



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2016 – 12:50 AM EDT

PDB ID : 5DFE
Title : 70S termination complex containing E. coli RF2
Authors : Hoffer, E.D.; Dunham, C.M.
Deposited on : 2015-08-26
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

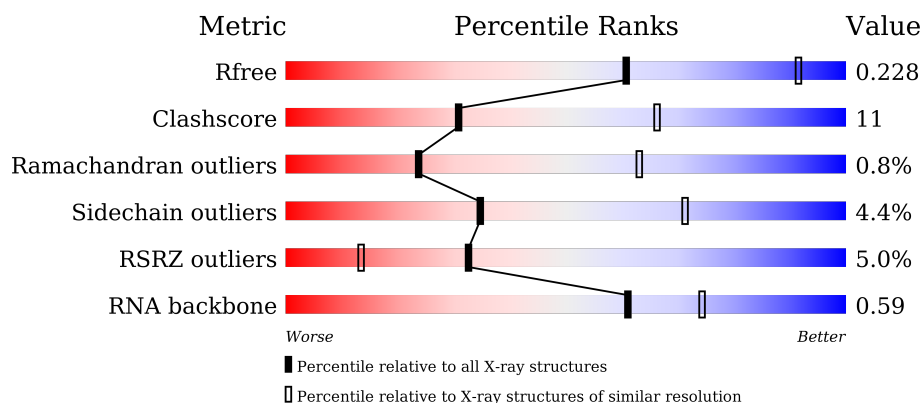
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)
RNA backbone	2183	1010 (3.52-2.68)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	QV	77	<div> <div>4%</div> <div>58%</div> <div>32%</div> <div>6%</div> <div>.</div> </div>
1	XV	77	<div> <div>3%</div> <div>64%</div> <div>27%</div> <div>8%</div> <div>.</div> </div>
2	QX	25	<div> <div>12%</div> <div>24%</div> <div>12%</div> <div>60%</div> </div>
2	XX	25	<div> <div>12%</div> <div>20%</div> <div>12%</div> <div>8%</div> <div>60%</div> </div>












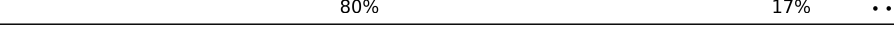








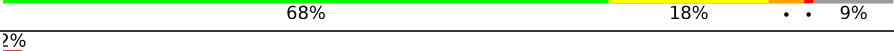
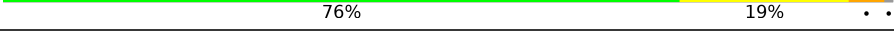

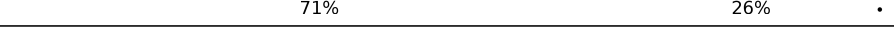

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Mol	Chain	Length	Quality of chain
3	QY	380	
3	XY	380	
4	RA	2915	
4	YA	2915	
5	RB	122	
5	YB	122	
6	RD	276	
6	YD	276	
7	RE	206	
7	YE	206	
8	RF	210	
8	YF	210	
9	RG	182	
9	YG	182	
10	RH	180	
10	YH	180	
11	RI	148	
11	YI	148	
12	RN	140	
12	YN	140	
13	RO	122	
13	YO	122	
14	RP	150	
14	YP	150	
15	RQ	141	

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Mol	Chain	Length	Quality of chain
15	YQ	141	
16	RR	118	
16	YR	118	
17	RS	112	
17	YS	112	
18	RT	146	
18	YT	146	
19	RU	118	
19	YU	118	
20	RV	101	
20	YV	101	
21	RW	113	
21	YW	113	
22	RX	96	
22	YX	96	
23	RY	110	
23	YY	110	
24	RZ	206	
24	YZ	206	
25	R0	85	
25	Y0	85	
26	R1	98	
26	Y1	98	
27	R2	72	
27	Y2	72	

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Mol	Chain	Length	Quality of chain
28	R3	60	<div> <div>5%</div> <div>78%</div> <div>20%</div> <div>.</div> </div>
28	Y3	60	<div> <div>2%</div> <div>82%</div> <div>15%</div> <div>..</div> </div>
29	R4	71	<div> <div>11%</div> <div>55%</div> <div>34%</div> <div>7%</div> <div>..</div> </div>
29	Y4	71	<div> <div>11%</div> <div>48%</div> <div>39%</div> <div>6%</div> <div>..</div> </div>
30	R5	60	<div> <div>2%</div> <div>75%</div> <div>22%</div> <div>..</div> </div>
30	Y5	60	<div> <div>78%</div> <div>15%</div> <div>5%</div> <div>.</div> </div>
31	R6	54	<div> <div>50%</div> <div>69%</div> <div>26%</div> <div>...</div> </div>
31	Y6	54	<div> <div>28%</div> <div>81%</div> <div>15%</div> <div>..</div> </div>
32	R7	49	<div> <div>2%</div> <div>61%</div> <div>33%</div> <div>..</div> </div>
32	Y7	49	<div> <div>73%</div> <div>18%</div> <div>..</div> <div>..</div> </div>
33	R8	65	<div> <div>66%</div> <div>29%</div> <div>...</div> </div>
33	Y8	65	<div> <div>60%</div> <div>37%</div> <div>..</div> </div>
34	R9	37	<div> <div>8%</div> <div>70%</div> <div>24%</div> <div>..</div> </div>
34	Y9	37	<div> <div>3%</div> <div>78%</div> <div>19%</div> <div>.</div> </div>
35	QA	1521	<div> <div>2%</div> <div>52%</div> <div>39%</div> <div>7%</div> <div>.</div> </div>
35	XA	1521	<div> <div>3%</div> <div>54%</div> <div>38%</div> <div>6%</div> <div>..</div> </div>
36	QB	256	<div> <div>5%</div> <div>51%</div> <div>33%</div> <div>.</div> <div>.</div> <div>10%</div> </div>
36	XB	256	<div> <div>4%</div> <div>48%</div> <div>34%</div> <div>5%</div> <div>.</div> <div>10%</div> </div>
37	QC	239	<div> <div>4%</div> <div>63%</div> <div>21%</div> <div>.</div> <div>14%</div> </div>
37	XC	239	<div> <div>3%</div> <div>60%</div> <div>23%</div> <div>.</div> <div>14%</div> </div>
38	QD	209	<div> <div>59%</div> <div>36%</div> <div>..</div> </div>
38	XD	209	<div> <div>65%</div> <div>31%</div> <div>..</div> </div>
39	QE	162	<div> <div>63%</div> <div>25%</div> <div>..</div> <div>9%</div> </div>
39	XE	162	<div> <div>%</div> <div>56%</div> <div>32%</div> <div>..</div> <div>9%</div> </div>
40	QF	101	<div> <div>%</div> <div>63%</div> <div>26%</div> <div>10%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
40	XF	101	
41	QG	156	
41	XG	156	
42	QH	138	
42	XH	138	
43	QI	128	
43	XI	128	
44	QJ	105	
44	XJ	105	
45	QK	129	
45	XK	129	
46	QL	132	
46	XL	132	
47	QM	126	
47	XM	126	
48	QN	61	
48	XN	61	
49	QO	89	
49	XO	89	
50	QP	88	
50	XP	88	
51	QQ	105	
51	XQ	105	
52	QR	88	
52	XR	88	

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Mol	Chain	Length	Quality of chain
53	QS	93	
53	XS	93	
54	QT	106	
54	XT	106	
55	QU	27	
55	XU	27	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	QA	1606	-	-	-	X
56	MG	QA	1610	-	-	-	X
56	MG	QA	1621	-	-	-	X
56	MG	QA	1622	-	-	-	X
56	MG	QA	1623	-	-	-	X
56	MG	QA	1625	-	-	-	X
56	MG	QA	1645	-	-	-	X
56	MG	QA	1647	-	-	-	X
56	MG	QA	1654	-	-	-	X
56	MG	QA	1655	-	-	-	X
56	MG	QA	1661	-	-	-	X
56	MG	QA	1665	-	-	-	X
56	MG	QA	1672	-	-	-	X
56	MG	QA	1680	-	-	-	X
56	MG	QA	1682	-	-	-	X
56	MG	QA	1703	-	-	-	X
56	MG	QA	1707	-	-	-	X
56	MG	QA	1710	-	-	-	X
56	MG	QA	1714	-	-	-	X
56	MG	QA	1719	-	-	-	X
56	MG	QA	1721	-	-	-	X
56	MG	QA	1722	-	-	-	X
56	MG	QA	1729	-	-	-	X
56	MG	QA	1734	-	-	-	X
56	MG	QA	1757	-	-	-	X
56	MG	QA	1768	-	-	-	X
56	MG	QA	1778	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	QA	1800	-	-	-	X
56	MG	QA	1812	-	-	-	X
56	MG	QA	1821	-	-	-	X
56	MG	QA	1830	-	-	-	X
56	MG	QA	1833	-	-	-	X
56	MG	QA	1841	-	-	-	X
56	MG	QA	1843	-	-	-	X
56	MG	QA	1847	-	-	-	X
56	MG	QA	1852	-	-	-	X
56	MG	QA	1855	-	-	-	X
56	MG	QA	1858	-	-	-	X
56	MG	QA	1870	-	-	-	X
56	MG	QA	1876	-	-	-	X
56	MG	QL	201	-	-	-	X
56	MG	QN	103	-	-	-	X
56	MG	QT	201	-	-	-	X
56	MG	QY	402	-	-	-	X
56	MG	R0	103	-	-	-	X
56	MG	R1	102	-	-	-	X
56	MG	R3	102	-	-	-	X
56	MG	R5	101	-	-	-	X
56	MG	R8	101	-	-	-	X
56	MG	RA	3001	-	-	-	X
56	MG	RA	3014	-	-	-	X
56	MG	RA	3021	-	-	-	X
56	MG	RA	3022	-	-	-	X
56	MG	RA	3023	-	-	-	X
56	MG	RA	3027	-	-	-	X
56	MG	RA	3029	-	-	-	X
56	MG	RA	3030	-	-	-	X
56	MG	RA	3040	-	-	-	X
56	MG	RA	3045	-	-	-	X
56	MG	RA	3050	-	-	-	X
56	MG	RA	3064	-	-	-	X
56	MG	RA	3070	-	-	-	X
56	MG	RA	3073	-	-	-	X
56	MG	RA	3075	-	-	-	X
56	MG	RA	3077	-	-	-	X
56	MG	RA	3082	-	-	-	X
56	MG	RA	3088	-	-	-	X
56	MG	RA	3092	-	-	-	X
56	MG	RA	3101	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3109	-	-	-	X
56	MG	RA	3116	-	-	-	X
56	MG	RA	3117	-	-	-	X
56	MG	RA	3118	-	-	-	X
56	MG	RA	3119	-	-	-	X
56	MG	RA	3122	-	-	-	X
56	MG	RA	3128	-	-	-	X
56	MG	RA	3132	-	-	-	X
56	MG	RA	3135	-	-	-	X
56	MG	RA	3141	-	-	-	X
56	MG	RA	3142	-	-	-	X
56	MG	RA	3146	-	-	-	X
56	MG	RA	3148	-	-	-	X
56	MG	RA	3163	-	-	-	X
56	MG	RA	3165	-	-	-	X
56	MG	RA	3168	-	-	-	X
56	MG	RA	3170	-	-	-	X
56	MG	RA	3177	-	-	-	X
56	MG	RA	3178	-	-	-	X
56	MG	RA	3184	-	-	-	X
56	MG	RA	3185	-	-	-	X
56	MG	RA	3196	-	-	-	X
56	MG	RA	3204	-	-	-	X
56	MG	RA	3207	-	-	-	X
56	MG	RA	3210	-	-	-	X
56	MG	RA	3216	-	-	-	X
56	MG	RA	3220	-	-	-	X
56	MG	RA	3225	-	-	-	X
56	MG	RA	3229	-	-	-	X
56	MG	RA	3230	-	-	-	X
56	MG	RA	3231	-	-	-	X
56	MG	RA	3233	-	-	-	X
56	MG	RA	3234	-	-	-	X
56	MG	RA	3240	-	-	-	X
56	MG	RA	3250	-	-	-	X
56	MG	RA	3264	-	-	-	X
56	MG	RA	3270	-	-	-	X
56	MG	RA	3274	-	-	-	X
56	MG	RA	3289	-	-	-	X
56	MG	RA	3298	-	-	-	X
56	MG	RA	3299	-	-	-	X
56	MG	RA	3301	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3306	-	-	-	X
56	MG	RA	3312	-	-	-	X
56	MG	RA	3315	-	-	-	X
56	MG	RA	3321	-	-	-	X
56	MG	RA	3323	-	-	-	X
56	MG	RA	3328	-	-	-	X
56	MG	RA	3330	-	-	-	X
56	MG	RA	3332	-	-	-	X
56	MG	RA	3333	-	-	-	X
56	MG	RA	3335	-	-	-	X
56	MG	RA	3342	-	-	-	X
56	MG	RA	3348	-	-	-	X
56	MG	RA	3349	-	-	-	X
56	MG	RA	3351	-	-	-	X
56	MG	RA	3353	-	-	-	X
56	MG	RA	3355	-	-	-	X
56	MG	RA	3358	-	-	-	X
56	MG	RA	3360	-	-	-	X
56	MG	RA	3363	-	-	-	X
56	MG	RA	3365	-	-	-	X
56	MG	RA	3374	-	-	-	X
56	MG	RA	3378	-	-	-	X
56	MG	RA	3380	-	-	-	X
56	MG	RA	3381	-	-	-	X
56	MG	RA	3383	-	-	-	X
56	MG	RA	3384	-	-	-	X
56	MG	RA	3385	-	-	-	X
56	MG	RA	3386	-	-	-	X
56	MG	RA	3389	-	-	-	X
56	MG	RA	3390	-	-	-	X
56	MG	RA	3391	-	-	-	X
56	MG	RA	3393	-	-	-	X
56	MG	RA	3398	-	-	-	X
56	MG	RA	3400	-	-	-	X
56	MG	RA	3407	-	-	-	X
56	MG	RA	3408	-	-	-	X
56	MG	RA	3411	-	-	-	X
56	MG	RA	3418	-	-	-	X
56	MG	RA	3419	-	-	-	X
56	MG	RA	3423	-	-	-	X
56	MG	RA	3430	-	-	-	X
56	MG	RA	3435	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3443	-	-	-	X
56	MG	RA	3451	-	-	-	X
56	MG	RA	3454	-	-	-	X
56	MG	RA	3457	-	-	-	X
56	MG	RA	3461	-	-	-	X
56	MG	RA	3464	-	-	-	X
56	MG	RA	3465	-	-	-	X
56	MG	RA	3467	-	-	-	X
56	MG	RA	3469	-	-	-	X
56	MG	RA	3470	-	-	-	X
56	MG	RA	3471	-	-	-	X
56	MG	RA	3472	-	-	-	X
56	MG	RA	3475	-	-	-	X
56	MG	RA	3476	-	-	-	X
56	MG	RA	3478	-	-	-	X
56	MG	RA	3482	-	-	-	X
56	MG	RA	3483	-	-	-	X
56	MG	RA	3485	-	-	-	X
56	MG	RA	3490	-	-	-	X
56	MG	RA	3495	-	-	-	X
56	MG	RA	3496	-	-	-	X
56	MG	RA	3500	-	-	-	X
56	MG	RA	3501	-	-	-	X
56	MG	RA	3504	-	-	-	X
56	MG	RA	3506	-	-	-	X
56	MG	RA	3511	-	-	-	X
56	MG	RA	3517	-	-	-	X
56	MG	RA	3520	-	-	-	X
56	MG	RA	3523	-	-	-	X
56	MG	RA	3525	-	-	-	X
56	MG	RA	3529	-	-	-	X
56	MG	RA	3531	-	-	-	X
56	MG	RA	3534	-	-	-	X
56	MG	RA	3535	-	-	-	X
56	MG	RA	3536	-	-	-	X
56	MG	RA	3538	-	-	-	X
56	MG	RA	3550	-	-	-	X
56	MG	RA	3553	-	-	-	X
56	MG	RA	3565	-	-	-	X
56	MG	RA	3567	-	-	-	X
56	MG	RA	3571	-	-	-	X
56	MG	RA	3573	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3587	-	-	-	X
56	MG	RA	3597	-	-	-	X
56	MG	RA	3600	-	-	-	X
56	MG	RA	3602	-	-	-	X
56	MG	RA	3606	-	-	-	X
56	MG	RA	3608	-	-	-	X
56	MG	RA	3610	-	-	-	X
56	MG	RA	3613	-	-	-	X
56	MG	RA	3615	-	-	-	X
56	MG	RA	3621	-	-	-	X
56	MG	RA	3622	-	-	-	X
56	MG	RA	3623	-	-	-	X
56	MG	RA	3629	-	-	-	X
56	MG	RA	3630	-	-	-	X
56	MG	RA	3633	-	-	-	X
56	MG	RA	3634	-	-	-	X
56	MG	RA	3637	-	-	-	X
56	MG	RA	3643	-	-	-	X
56	MG	RA	3649	-	-	-	X
56	MG	RA	3658	-	-	-	X
56	MG	RA	3676	-	-	-	X
56	MG	RA	3678	-	-	-	X
56	MG	RA	3683	-	-	-	X
56	MG	RA	3695	-	-	-	X
56	MG	RA	3696	-	-	-	X
56	MG	RA	3701	-	-	-	X
56	MG	RA	3706	-	-	-	X
56	MG	RA	3707	-	-	-	X
56	MG	RA	3708	-	-	-	X
56	MG	RA	3711	-	-	-	X
56	MG	RA	3712	-	-	-	X
56	MG	RA	3714	-	-	-	X
56	MG	RA	3721	-	-	-	X
56	MG	RA	3723	-	-	-	X
56	MG	RA	3737	-	-	-	X
56	MG	RA	3743	-	-	-	X
56	MG	RA	3745	-	-	-	X
56	MG	RA	3750	-	-	-	X
56	MG	RA	3753	-	-	-	X
56	MG	RA	3766	-	-	-	X
56	MG	RA	3769	-	-	-	X
56	MG	RA	3770	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3772	-	-	-	X
56	MG	RA	3773	-	-	-	X
56	MG	RA	3783	-	-	-	X
56	MG	RA	3785	-	-	-	X
56	MG	RA	3794	-	-	-	X
56	MG	RA	3802	-	-	-	X
56	MG	RA	3804	-	-	-	X
56	MG	RA	3806	-	-	-	X
56	MG	RA	3808	-	-	-	X
56	MG	RA	3809	-	-	-	X
56	MG	RA	3811	-	-	-	X
56	MG	RA	3813	-	-	-	X
56	MG	RA	3814	-	-	-	X
56	MG	RA	3820	-	-	-	X
56	MG	RA	3822	-	-	-	X
56	MG	RA	3828	-	-	-	X
56	MG	RA	3838	-	-	-	X
56	MG	RA	3849	-	-	-	X
56	MG	RA	3853	-	-	-	X
56	MG	RA	3855	-	-	-	X
56	MG	RA	3857	-	-	-	X
56	MG	RA	3861	-	-	-	X
56	MG	RA	3873	-	-	-	X
56	MG	RA	3874	-	-	-	X
56	MG	RA	3881	-	-	-	X
56	MG	RA	3888	-	-	-	X
56	MG	RA	3891	-	-	-	X
56	MG	RA	3892	-	-	-	X
56	MG	RA	3899	-	-	-	X
56	MG	RA	3900	-	-	-	X
56	MG	RA	3901	-	-	-	X
56	MG	RA	3902	-	-	-	X
56	MG	RA	3905	-	-	-	X
56	MG	RA	3910	-	-	-	X
56	MG	RA	3923	-	-	-	X
56	MG	RA	3927	-	-	-	X
56	MG	RA	3938	-	-	-	X
56	MG	RA	3940	-	-	-	X
56	MG	RA	3951	-	-	-	X
56	MG	RA	3952	-	-	-	X
56	MG	RA	3966	-	-	-	X
56	MG	RA	3968	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	3978	-	-	-	X
56	MG	RA	3988	-	-	-	X
56	MG	RA	3999	-	-	-	X
56	MG	RA	4000	-	-	-	X
56	MG	RA	4001	-	-	-	X
56	MG	RA	4003	-	-	-	X
56	MG	RA	4006	-	-	-	X
56	MG	RA	4009	-	-	-	X
56	MG	RA	4015	-	-	-	X
56	MG	RA	4016	-	-	-	X
56	MG	RA	4017	-	-	-	X
56	MG	RA	4018	-	-	-	X
56	MG	RA	4020	-	-	-	X
56	MG	RA	4022	-	-	-	X
56	MG	RA	4024	-	-	-	X
56	MG	RA	4028	-	-	-	X
56	MG	RA	4029	-	-	-	X
56	MG	RA	4030	-	-	-	X
56	MG	RA	4031	-	-	-	X
56	MG	RA	4032	-	-	-	X
56	MG	RA	4033	-	-	-	X
56	MG	RA	4034	-	-	-	X
56	MG	RA	4036	-	-	-	X
56	MG	RA	4037	-	-	-	X
56	MG	RA	4038	-	-	-	X
56	MG	RA	4039	-	-	-	X
56	MG	RA	4040	-	-	-	X
56	MG	RA	4041	-	-	-	X
56	MG	RA	4042	-	-	-	X
56	MG	RA	4043	-	-	-	X
56	MG	RA	4044	-	-	-	X
56	MG	RA	4045	-	-	-	X
56	MG	RA	4046	-	-	-	X
56	MG	RA	4047	-	-	-	X
56	MG	RA	4048	-	-	-	X
56	MG	RA	4049	-	-	-	X
56	MG	RA	4050	-	-	-	X
56	MG	RA	4052	-	-	-	X
56	MG	RA	4055	-	-	-	X
56	MG	RA	4057	-	-	-	X
56	MG	RA	4058	-	-	-	X
56	MG	RA	4059	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	RA	4060	-	-	-	X
56	MG	RA	4061	-	-	-	X
56	MG	RA	4062	-	-	-	X
56	MG	RA	4063	-	-	-	X
56	MG	RA	4064	-	-	-	X
56	MG	RA	4065	-	-	-	X
56	MG	RA	4066	-	-	-	X
56	MG	RB	209	-	-	-	X
56	MG	RB	215	-	-	-	X
56	MG	RB	225	-	-	-	X
56	MG	RD	301	-	-	-	X
56	MG	RD	302	-	-	-	X
56	MG	RD	304	-	-	-	X
56	MG	RD	305	-	-	-	X
56	MG	RD	307	-	-	-	X
56	MG	RD	308	-	-	-	X
56	MG	RD	311	-	-	-	X
56	MG	RD	312	-	-	-	X
56	MG	RE	301	-	-	-	X
56	MG	RE	302	-	-	-	X
56	MG	RE	305	-	-	-	X
56	MG	RE	306	-	-	-	X
56	MG	RF	301	-	-	-	X
56	MG	RF	303	-	-	-	X
56	MG	RF	305	-	-	-	X
56	MG	RF	306	-	-	-	X
56	MG	RF	308	-	-	-	X
56	MG	RF	310	-	-	-	X
56	MG	RG	201	-	-	-	X
56	MG	RN	201	-	-	-	X
56	MG	RO	201	-	-	-	X
56	MG	RP	201	-	-	-	X
56	MG	RQ	204	-	-	-	X
56	MG	RR	3201	-	-	-	X
56	MG	RR	3202	-	-	-	X
56	MG	RR	3203	-	-	-	X
56	MG	RU	203	-	-	-	X
56	MG	RV	202	-	-	-	X
56	MG	RV	203	-	-	-	X
56	MG	RX	101	-	-	-	X
56	MG	XA	1605	-	-	-	X
56	MG	XA	1608	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	XA	1611	-	-	-	X
56	MG	XA	1617	-	-	-	X
56	MG	XA	1620	-	-	-	X
56	MG	XA	1622	-	-	-	X
56	MG	XA	1626	-	-	-	X
56	MG	XA	1627	-	-	-	X
56	MG	XA	1628	-	-	-	X
56	MG	XA	1630	-	-	-	X
56	MG	XA	1631	-	-	-	X
56	MG	XA	1632	-	-	-	X
56	MG	XA	1658	-	-	-	X
56	MG	XA	1672	-	-	-	X
56	MG	XA	1682	-	-	-	X
56	MG	XA	1687	-	-	-	X
56	MG	XA	1695	-	-	-	X
56	MG	XA	1699	-	-	-	X
56	MG	XA	1706	-	-	-	X
56	MG	XA	1719	-	-	-	X
56	MG	XA	1726	-	-	-	X
56	MG	XA	1730	-	-	-	X
56	MG	XA	1736	-	-	-	X
56	MG	XA	1737	-	-	-	X
56	MG	XA	1740	-	-	-	X
56	MG	XA	1743	-	-	-	X
56	MG	XA	1746	-	-	-	X
56	MG	XA	1756	-	-	-	X
56	MG	XA	1757	-	-	-	X
56	MG	XA	1758	-	-	-	X
56	MG	XA	1761	-	-	-	X
56	MG	XA	1762	-	-	-	X
56	MG	XA	1767	-	-	-	X
56	MG	XA	1768	-	-	-	X
56	MG	XA	1770	-	-	-	X
56	MG	XA	1772	-	-	-	X
56	MG	XA	1774	-	-	-	X
56	MG	XA	1775	-	-	-	X
56	MG	XA	1778	-	-	-	X
56	MG	XA	1779	-	-	-	X
56	MG	XA	1784	-	-	-	X
56	MG	XA	1788	-	-	-	X
56	MG	XF	203	-	-	-	X
56	MG	XF	204	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	XR	101	-	-	-	X
56	MG	XX	101	-	-	-	X
56	MG	Y8	101	-	-	-	X
56	MG	YA	3010	-	-	-	X
56	MG	YA	3012	-	-	-	X
56	MG	YA	3014	-	-	-	X
56	MG	YA	3015	-	-	-	X
56	MG	YA	3021	-	-	-	X
56	MG	YA	3022	-	-	-	X
56	MG	YA	3029	-	-	-	X
56	MG	YA	3030	-	-	-	X
56	MG	YA	3032	-	-	-	X
56	MG	YA	3035	-	-	-	X
56	MG	YA	3038	-	-	-	X
56	MG	YA	3051	-	-	-	X
56	MG	YA	3055	-	-	-	X
56	MG	YA	3056	-	-	-	X
56	MG	YA	3060	-	-	-	X
56	MG	YA	3062	-	-	-	X
56	MG	YA	3073	-	-	-	X
56	MG	YA	3079	-	-	-	X
56	MG	YA	3087	-	-	-	X
56	MG	YA	3089	-	-	-	X
56	MG	YA	3090	-	-	-	X
56	MG	YA	3093	-	-	-	X
56	MG	YA	3094	-	-	-	X
56	MG	YA	3096	-	-	-	X
56	MG	YA	3097	-	-	-	X
56	MG	YA	3109	-	-	-	X
56	MG	YA	3112	-	-	-	X
56	MG	YA	3114	-	-	-	X
56	MG	YA	3116	-	-	-	X
56	MG	YA	3124	-	-	-	X
56	MG	YA	3131	-	-	-	X
56	MG	YA	3133	-	-	-	X
56	MG	YA	3135	-	-	-	X
56	MG	YA	3136	-	-	-	X
56	MG	YA	3141	-	-	-	X
56	MG	YA	3142	-	-	-	X
56	MG	YA	3149	-	-	-	X
56	MG	YA	3154	-	-	-	X
56	MG	YA	3155	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3156	-	-	-	X
56	MG	YA	3159	-	-	-	X
56	MG	YA	3169	-	-	-	X
56	MG	YA	3173	-	-	-	X
56	MG	YA	3179	-	-	-	X
56	MG	YA	3186	-	-	-	X
56	MG	YA	3195	-	-	-	X
56	MG	YA	3202	-	-	-	X
56	MG	YA	3212	-	-	-	X
56	MG	YA	3213	-	-	-	X
56	MG	YA	3219	-	-	-	X
56	MG	YA	3240	-	-	-	X
56	MG	YA	3243	-	-	-	X
56	MG	YA	3250	-	-	-	X
56	MG	YA	3252	-	-	-	X
56	MG	YA	3255	-	-	-	X
56	MG	YA	3256	-	-	-	X
56	MG	YA	3271	-	-	-	X
56	MG	YA	3272	-	-	-	X
56	MG	YA	3273	-	-	-	X
56	MG	YA	3275	-	-	-	X
56	MG	YA	3287	-	-	-	X
56	MG	YA	3288	-	-	-	X
56	MG	YA	3294	-	-	-	X
56	MG	YA	3295	-	-	-	X
56	MG	YA	3298	-	-	-	X
56	MG	YA	3300	-	-	-	X
56	MG	YA	3302	-	-	-	X
56	MG	YA	3303	-	-	-	X
56	MG	YA	3314	-	-	-	X
56	MG	YA	3319	-	-	-	X
56	MG	YA	3321	-	-	-	X
56	MG	YA	3323	-	-	-	X
56	MG	YA	3324	-	-	-	X
56	MG	YA	3326	-	-	-	X
56	MG	YA	3327	-	-	-	X
56	MG	YA	3328	-	-	-	X
56	MG	YA	3329	-	-	-	X
56	MG	YA	3331	-	-	-	X
56	MG	YA	3338	-	-	-	X
56	MG	YA	3339	-	-	-	X
56	MG	YA	3342	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3346	-	-	-	X
56	MG	YA	3348	-	-	-	X
56	MG	YA	3353	-	-	-	X
56	MG	YA	3354	-	-	-	X
56	MG	YA	3358	-	-	-	X
56	MG	YA	3363	-	-	-	X
56	MG	YA	3371	-	-	-	X
56	MG	YA	3377	-	-	-	X
56	MG	YA	3380	-	-	-	X
56	MG	YA	3381	-	-	-	X
56	MG	YA	3385	-	-	-	X
56	MG	YA	3387	-	-	-	X
56	MG	YA	3389	-	-	-	X
56	MG	YA	3390	-	-	-	X
56	MG	YA	3394	-	-	-	X
56	MG	YA	3400	-	-	-	X
56	MG	YA	3401	-	-	-	X
56	MG	YA	3404	-	-	-	X
56	MG	YA	3407	-	-	-	X
56	MG	YA	3410	-	-	-	X
56	MG	YA	3412	-	-	-	X
56	MG	YA	3416	-	-	-	X
56	MG	YA	3425	-	-	-	X
56	MG	YA	3433	-	-	-	X
56	MG	YA	3434	-	-	-	X
56	MG	YA	3443	-	-	-	X
56	MG	YA	3444	-	-	-	X
56	MG	YA	3452	-	-	-	X
56	MG	YA	3453	-	-	-	X
56	MG	YA	3460	-	-	-	X
56	MG	YA	3472	-	-	-	X
56	MG	YA	3478	-	-	-	X
56	MG	YA	3479	-	-	-	X
56	MG	YA	3480	-	-	-	X
56	MG	YA	3489	-	-	-	X
56	MG	YA	3491	-	-	-	X
56	MG	YA	3499	-	-	-	X
56	MG	YA	3503	-	-	-	X
56	MG	YA	3507	-	-	-	X
56	MG	YA	3515	-	-	-	X
56	MG	YA	3518	-	-	-	X
56	MG	YA	3520	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3521	-	-	-	X
56	MG	YA	3522	-	-	-	X
56	MG	YA	3536	-	-	-	X
56	MG	YA	3538	-	-	-	X
56	MG	YA	3542	-	-	-	X
56	MG	YA	3544	-	-	-	X
56	MG	YA	3548	-	-	-	X
56	MG	YA	3551	-	-	-	X
56	MG	YA	3554	-	-	-	X
56	MG	YA	3556	-	-	-	X
56	MG	YA	3569	-	-	-	X
56	MG	YA	3574	-	-	-	X
56	MG	YA	3575	-	-	-	X
56	MG	YA	3581	-	-	-	X
56	MG	YA	3582	-	-	-	X
56	MG	YA	3584	-	-	-	X
56	MG	YA	3586	-	-	-	X
56	MG	YA	3591	-	-	-	X
56	MG	YA	3592	-	-	-	X
56	MG	YA	3604	-	-	-	X
56	MG	YA	3605	-	-	-	X
56	MG	YA	3610	-	-	-	X
56	MG	YA	3611	-	-	-	X
56	MG	YA	3614	-	-	-	X
56	MG	YA	3615	-	-	-	X
56	MG	YA	3616	-	-	-	X
56	MG	YA	3618	-	-	-	X
56	MG	YA	3620	-	-	-	X
56	MG	YA	3625	-	-	-	X
56	MG	YA	3627	-	-	-	X
56	MG	YA	3634	-	-	-	X
56	MG	YA	3636	-	-	-	X
56	MG	YA	3646	-	-	-	X
56	MG	YA	3651	-	-	-	X
56	MG	YA	3652	-	-	-	X
56	MG	YA	3654	-	-	-	X
56	MG	YA	3660	-	-	-	X
56	MG	YA	3662	-	-	-	X
56	MG	YA	3664	-	-	-	X
56	MG	YA	3668	-	-	-	X
56	MG	YA	3669	-	-	-	X
56	MG	YA	3672	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YA	3678	-	-	-	X
56	MG	YA	3683	-	-	-	X
56	MG	YA	3685	-	-	-	X
56	MG	YA	3688	-	-	-	X
56	MG	YA	3692	-	-	-	X
56	MG	YA	3694	-	-	-	X
56	MG	YA	3704	-	-	-	X
56	MG	YA	3705	-	-	-	X
56	MG	YA	3707	-	-	-	X
56	MG	YA	3708	-	-	-	X
56	MG	YA	3712	-	-	-	X
56	MG	YA	3713	-	-	-	X
56	MG	YA	3718	-	-	-	X
56	MG	YA	3727	-	-	-	X
56	MG	YA	3728	-	-	-	X
56	MG	YA	3730	-	-	-	X
56	MG	YA	3734	-	-	-	X
56	MG	YA	3744	-	-	-	X
56	MG	YA	3747	-	-	-	X
56	MG	YA	3748	-	-	-	X
56	MG	YA	3749	-	-	-	X
56	MG	YA	3750	-	-	-	X
56	MG	YA	3751	-	-	-	X
56	MG	YA	3753	-	-	-	X
56	MG	YA	3754	-	-	-	X
56	MG	YA	3755	-	-	-	X
56	MG	YA	3756	-	-	-	X
56	MG	YA	3757	-	-	-	X
56	MG	YA	3758	-	-	-	X
56	MG	YA	3759	-	-	-	X
56	MG	YA	3760	-	-	-	X
56	MG	YB	217	-	-	-	X
56	MG	YD	303	-	-	-	X
56	MG	YD	304	-	-	-	X
56	MG	YD	305	-	-	-	X
56	MG	YD	306	-	-	-	X
56	MG	YD	308	-	-	-	X
56	MG	YD	309	-	-	-	X
56	MG	YE	302	-	-	-	X
56	MG	YE	303	-	-	-	X
56	MG	YE	304	-	-	-	X
56	MG	YE	305	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	YF	303	-	-	-	X
56	MG	YQ	201	-	-	-	X
56	MG	YR	201	-	-	-	X
56	MG	YT	202	-	-	-	X
56	MG	YW	201	-	-	-	X
56	MG	YX	101	-	-	-	X
57	ZN	R4	101	-	-	-	X
57	ZN	Y4	101	-	-	-	X

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 296662 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called Escherichia coli strain Ecol_745, complete genome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	QV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			
1	XV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			

- Molecule 2 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	QX	10	Total	C	N	O	P	0	0	0
			215	97	42	66	10			
2	XX	10	Total	C	N	O	P	0	0	0
			215	97	42	66	10			

- Molecule 3 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	QY	357	Total	C	N	O	S	0	0	0
			2833	1742	498	583	10			
3	XY	357	Total	C	N	O	S	0	0	0
			2833	1742	498	583	10			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
QY	-14	MET	-	initiating methionine	UNP P07012
QY	-13	GLY	-	expression tag	UNP P07012
QY	-12	SER	-	expression tag	UNP P07012
QY	-11	SER	-	expression tag	UNP P07012
QY	-10	HIS	-	expression tag	UNP P07012
QY	-9	HIS	-	expression tag	UNP P07012
QY	-8	HIS	-	expression tag	UNP P07012
QY	-7	HIS	-	expression tag	UNP P07012

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Chain	Residue	Modelled	Actual	Comment	Reference
QY	-6	HIS	-	expression tag	UNP P07012
QY	-5	HIS	-	expression tag	UNP P07012
QY	-4	SER	-	expression tag	UNP P07012
QY	-3	GLU	-	expression tag	UNP P07012
QY	-2	ASP	-	expression tag	UNP P07012
QY	-1	PRO	-	expression tag	UNP P07012
QY	0	ALA	-	expression tag	UNP P07012
XY	-14	MET	-	initiating methionine	UNP P07012
XY	-13	GLY	-	expression tag	UNP P07012
XY	-12	SER	-	expression tag	UNP P07012
XY	-11	SER	-	expression tag	UNP P07012
XY	-10	HIS	-	expression tag	UNP P07012
XY	-9	HIS	-	expression tag	UNP P07012
XY	-8	HIS	-	expression tag	UNP P07012
XY	-7	HIS	-	expression tag	UNP P07012
XY	-6	HIS	-	expression tag	UNP P07012
XY	-5	HIS	-	expression tag	UNP P07012
XY	-4	SER	-	expression tag	UNP P07012
XY	-3	GLU	-	expression tag	UNP P07012
XY	-2	ASP	-	expression tag	UNP P07012
XY	-1	PRO	-	expression tag	UNP P07012
XY	0	ALA	-	expression tag	UNP P07012

- Molecule 4 is a RNA chain called *Thermus thermophilus* HB8 genomic DNA, complete genome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	YA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			
4	RA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

- Molecule 5 is a RNA chain called *Thermus thermophilus* HB8 genomic DNA, complete genome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	YB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			
5	RB	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	YD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
6	RD	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	YE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
7	RE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	YF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			
8	RF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	YG	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			
9	RG	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	YH	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			
10	RH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	YI	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	RI	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	YN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
12	RN	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	YO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
13	RO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	YP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
14	RP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	YQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
15	RQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	YR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
16	RR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	YS	110	Total	C	N	O	0	0	0
			870	549	173	148			
17	RS	110	Total	C	N	O	0	0	0
			877	553	175	149			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	YT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			
18	RT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	YU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
19	RU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	YV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
20	RV	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	YW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
21	RW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	YX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
22	RX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	YY	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			
23	RY	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	YZ	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			
24	RZ	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Y0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
25	R0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Y1	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			
26	R1	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y2	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	R2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Y3	59	Total	C	N	O		0	0	0
			464	296	90	78				
28	R3	59	Total	C	N	O		0	0	0
			469	298	90	81				

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	Y4	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			
29	R4	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	Y5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
30	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	Y6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			
31	R6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	Y7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
32	R7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	Y8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
33	R8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	Y9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
34	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 35 is a RNA chain called Thermus thermophilus HB8 genomic DNA, complete genome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	XA	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			
35	QA	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	XB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			
36	QB	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	XC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			
37	QC	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	XD	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			
38	QD	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	XE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			
39	QE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	XF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			
40	QF	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	XG	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			
41	QG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	XH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
42	QH	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	XI	126	Total	C	N	O		0	0	0
			966	613	186	167				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
43	QI	127	Total	C	N	O	0	0	0
			986	625	193	168			

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
44	XJ	96	Total	C	N	O	0	0	0
			710	442	137	131			
44	QJ	97	Total	C	N	O	0	0	0
			719	446	142	131			

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	XK	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			
45	QK	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	XL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
46	QL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	XM	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			
47	QM	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			

- Molecule 48 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	XN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
48	QN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	XO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
49	QO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	XP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			
50	QP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	XQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
51	QQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	XR	68	Total	C	N	O	0	0	0
			555	355	108	92			
52	QR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	XS	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			
53	QS	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	XT	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			
54	QT	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			

- Molecule 55 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	XU	23	Total	C	N	O	0	0	0
			199	122	48	29			
55	QU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	QA	279	Total	Mg	0	0
			279	279		
56	YV	1	Total	Mg	0	0
			1	1		
56	RP	2	Total	Mg	0	0
			2	2		
56	R7	2	Total	Mg	0	0
			2	2		
56	YA	760	Total	Mg	0	0
			760	760		
56	Y5	1	Total	Mg	0	0
			1	1		
56	YR	1	Total	Mg	0	0
			1	1		
56	RT	3	Total	Mg	0	0
			3	3		
56	QD	3	Total	Mg	0	0
			3	3		
56	RN	3	Total	Mg	0	0
			3	3		
56	XE	2	Total	Mg	0	0
			2	2		
56	RG	4	Total	Mg	0	0
			4	4		
56	Y1	1	Total	Mg	0	0
			1	1		
56	YD	10	Total	Mg	0	0
			10	10		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	XX	1	Total Mg 1 1	0	0
56	QV	2	Total Mg 2 2	0	0
56	RX	1	Total Mg 1 1	0	0
56	Y8	2	Total Mg 2 2	0	0
56	YO	1	Total Mg 1 1	0	0
56	XA	190	Total Mg 190 190	0	0
56	QI	1	Total Mg 1 1	0	0
56	RQ	4	Total Mg 4 4	0	0
56	R0	4	Total Mg 4 4	0	0
56	XT	1	Total Mg 1 1	0	0
56	QR	1	Total Mg 1 1	0	0
56	QL	3	Total Mg 3 3	0	0
56	RU	3	Total Mg 3 3	0	0
56	QG	3	Total Mg 3 3	0	0
56	RO	1	Total Mg 1 1	0	0
56	XJ	1	Total Mg 1 1	0	0
56	QO	1	Total Mg 1 1	0	0
56	Y0	1	Total Mg 1 1	0	0
56	YG	3	Total Mg 3 3	0	0
56	YQ	2	Total Mg 2 2	0	0
56	YN	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	XF	4	Total Mg 4 4	0	0
56	YX	1	Total Mg 1 1	0	0
56	RR	5	Total Mg 5 5	0	0
56	RD	13	Total Mg 13 13	0	0
56	R1	3	Total Mg 3 3	0	0
56	QU	1	Total Mg 1 1	0	0
56	Y7	1	Total Mg 1 1	0	0
56	YT	3	Total Mg 3 3	0	0
56	RV	4	Total Mg 4 4	0	0
56	QF	1	Total Mg 1 1	0	0
56	RH	2	Total Mg 2 2	0	0
56	XK	1	Total Mg 1 1	0	0
56	QH	2	Total Mg 2 2	0	0
56	QQ	2	Total Mg 2 2	0	0
56	RA	1066	Total Mg 1066 1066	0	0
56	R4	1	Total Mg 1 1	0	0
56	YF	3	Total Mg 3 3	0	0
56	YP	1	Total Mg 1 1	0	0
56	RZ	1	Total Mg 1 1	0	0
56	QB	1	Total Mg 1 1	0	0
56	QM	1	Total Mg 1 1	0	0

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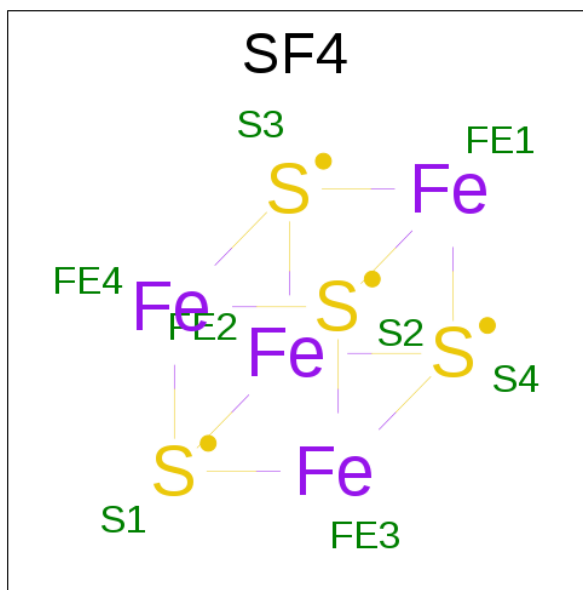
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	R9	2	Total 2	Mg 2	0	0
56	RE	6	Total 6	Mg 6	0	0
56	XL	1	Total 1	Mg 1	0	0
56	YB	19	Total 19	Mg 19	0	0
56	QT	1	Total 1	Mg 1	0	0
56	QN	2	Total 2	Mg 2	0	0
56	YW	2	Total 2	Mg 2	0	0
56	RW	2	Total 2	Mg 2	0	0
56	QY	3	Total 3	Mg 3	0	0
56	R8	1	Total 1	Mg 1	0	0
56	XH	1	Total 1	Mg 1	0	0
56	RB	29	Total 29	Mg 29	0	0
56	YI	1	Total 1	Mg 1	0	0
56	QE	2	Total 2	Mg 2	0	0
56	R5	3	Total 3	Mg 3	0	0
56	XR	1	Total 1	Mg 1	0	0
56	RF	12	Total 12	Mg 12	0	0
56	R3	2	Total 2	Mg 2	0	0
56	YE	7	Total 7	Mg 7	0	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	Y9	1	Total Zn 1 1	0	0
57	QN	1	Total Zn 1 1	0	0
57	Y6	1	Total Zn 1 1	0	0
57	XN	1	Total Zn 1 1	0	0
57	R9	1	Total Zn 1 1	0	0
57	Y4	1	Total Zn 1 1	0	0
57	R6	1	Total Zn 1 1	0	0
57	Y5	1	Total Zn 1 1	0	0
57	R5	1	Total Zn 1 1	0	0
57	YY	1	Total Zn 1 1	0	0
57	R4	1	Total Zn 1 1	0	0
57	RY	1	Total Zn 1 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).

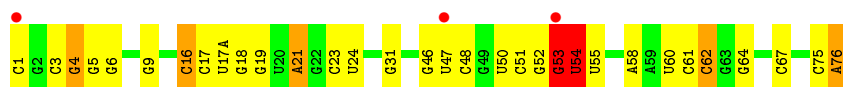


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	XD	1	Total 8	Fe 4	S 4	0	0
58	QD	1	Total 8	Fe 4	S 4	0	0

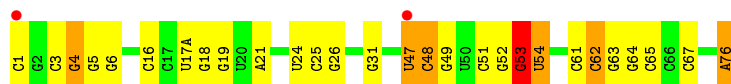
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Escherichia coli strain Ecol_745, complete genome



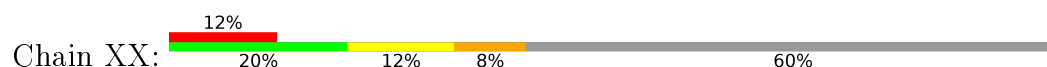
- Molecule 1: Escherichia coli strain Ecol_745, complete genome



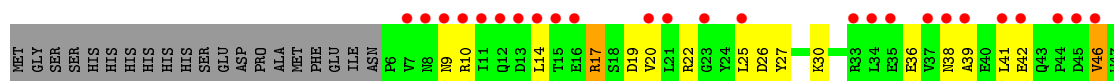
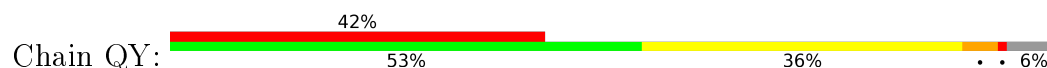
- Molecule 2: messenger RNA

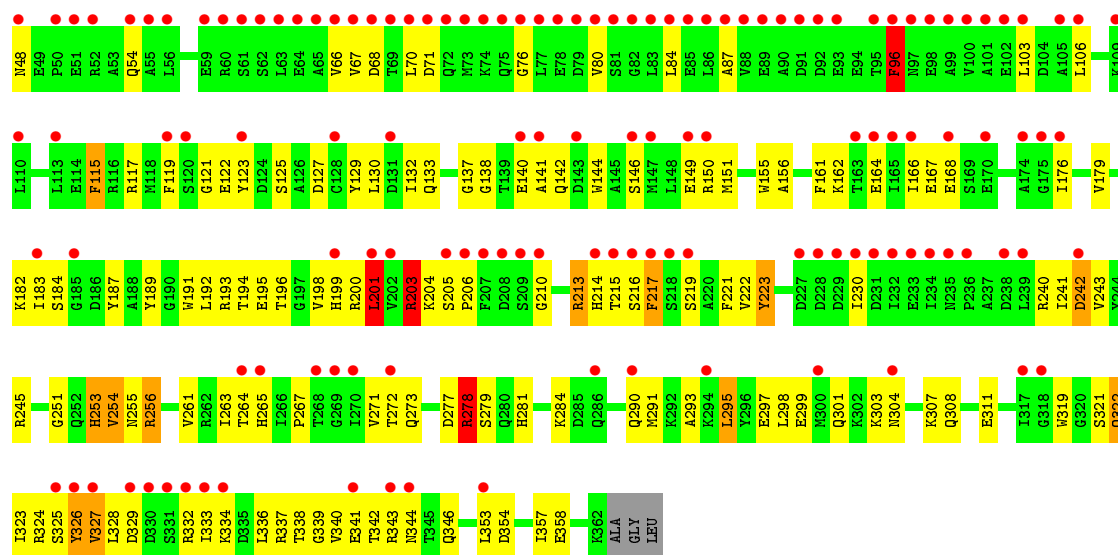


- Molecule 2: messenger RNA

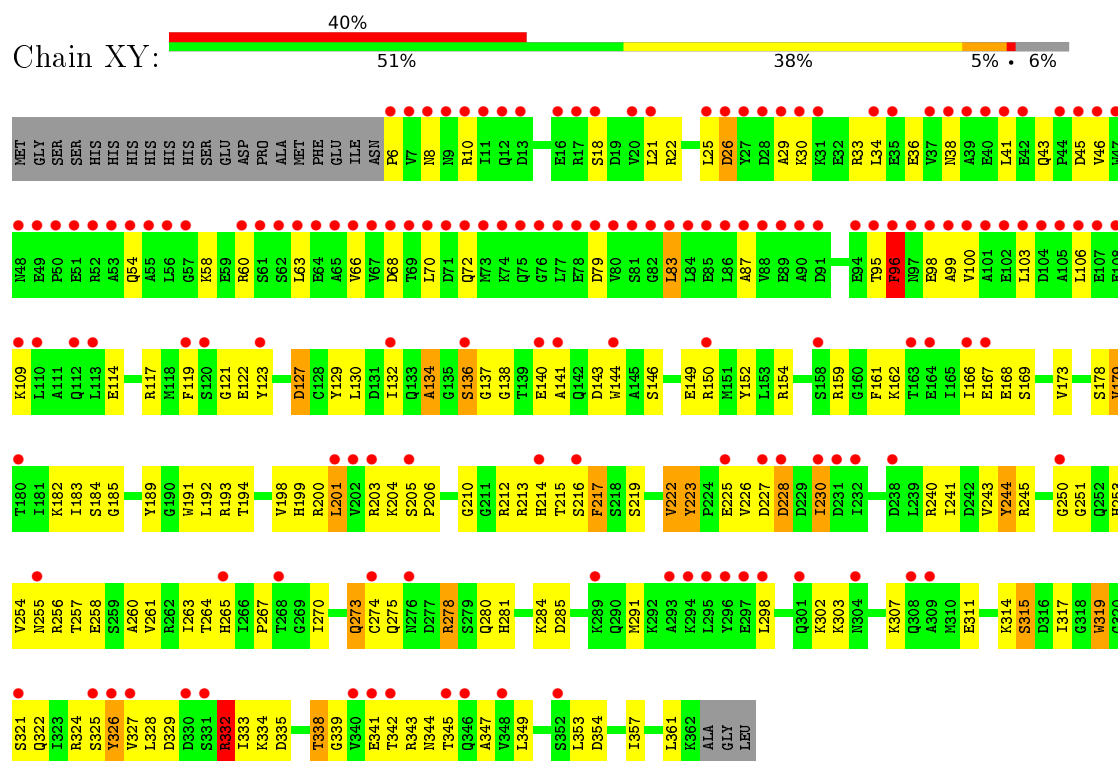


- Molecule 3: Peptide chain release factor 2

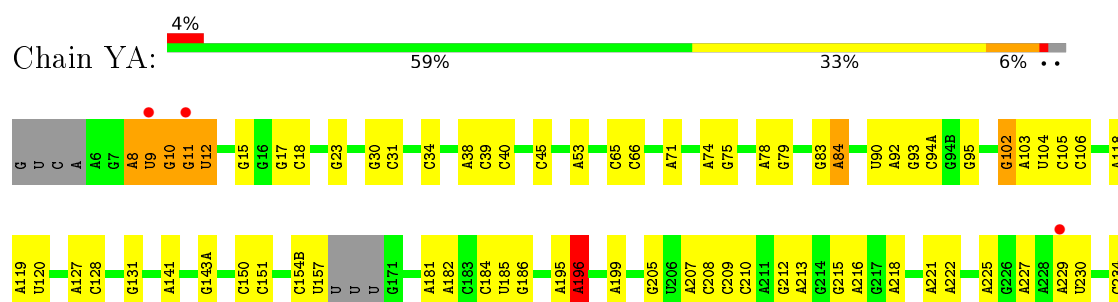




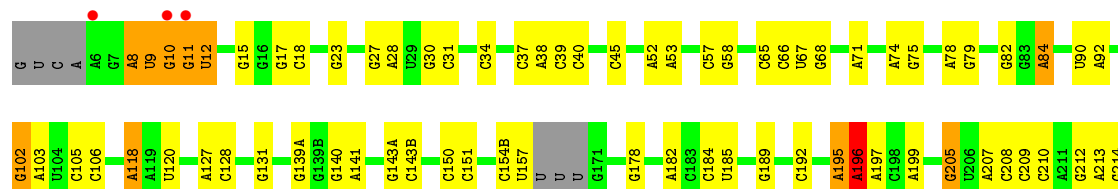
• Molecule 3: Peptide chain release factor 2



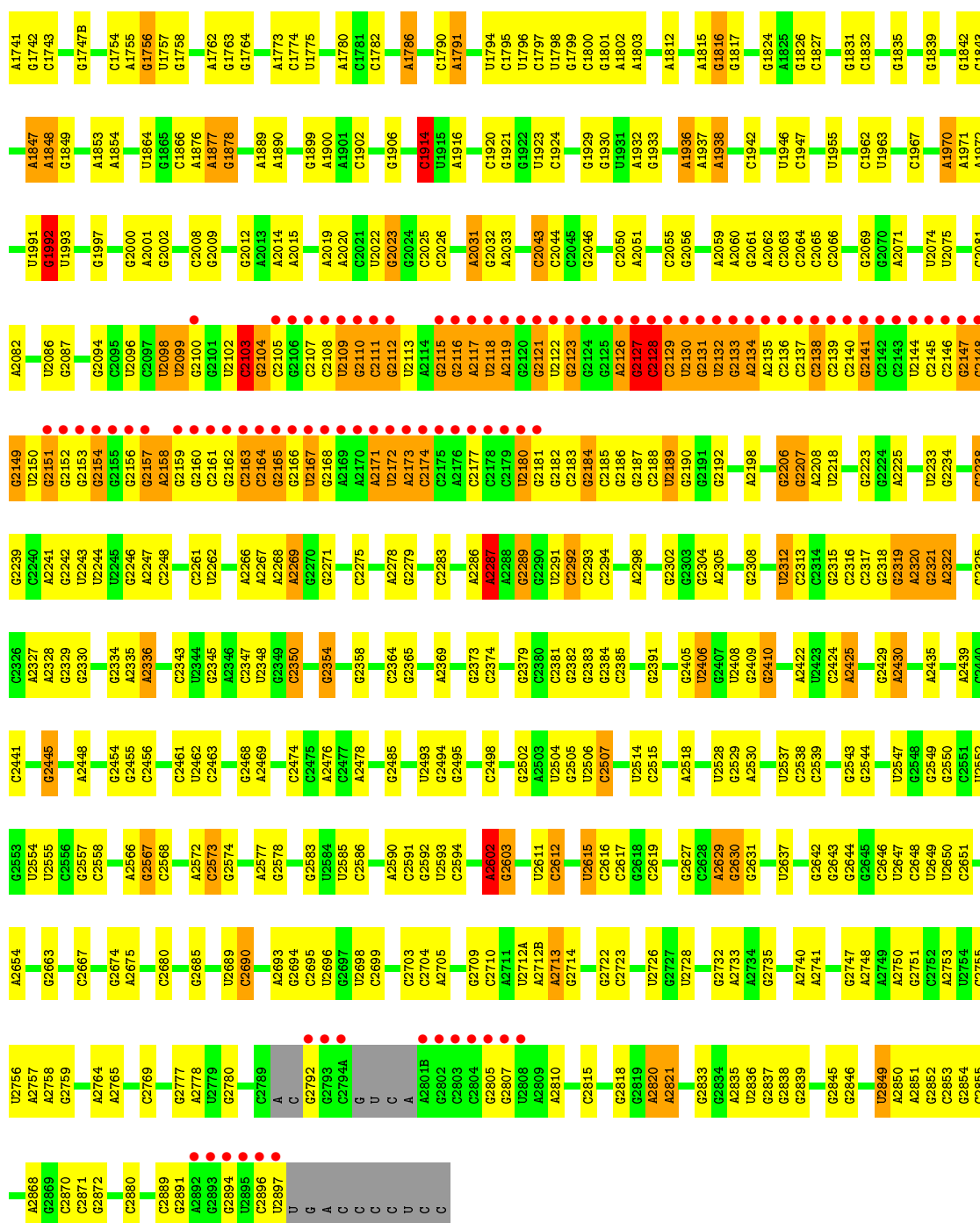
• Molecule 4: Thermus thermophilus HB8 genomic DNA, complete genome





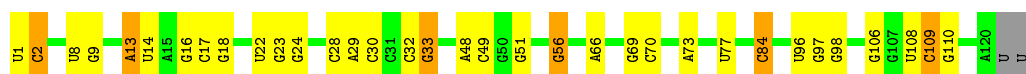






• Molecule 5: Thermus thermophilus HB8 genomic DNA, complete genome

Chain YB: 70% 23% 5%



• Molecule 5: Thermus thermophilus HB8 genomic DNA, complete genome

Chain RB: 75% 22%



• Molecule 6: 50S ribosomal protein L2

Chain YD: 76% 20%



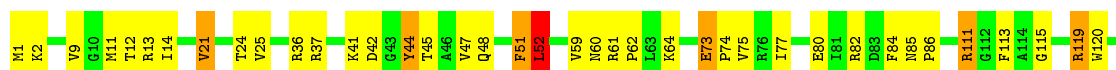
• Molecule 6: 50S ribosomal protein L2

Chain RD: 79% 18%



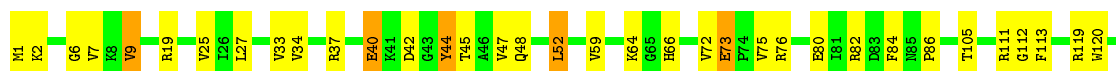
• Molecule 7: 50S ribosomal protein L3

Chain YE: 73% 23%



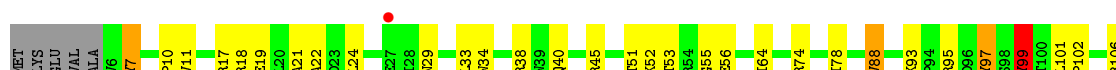
• Molecule 7: 50S ribosomal protein L3

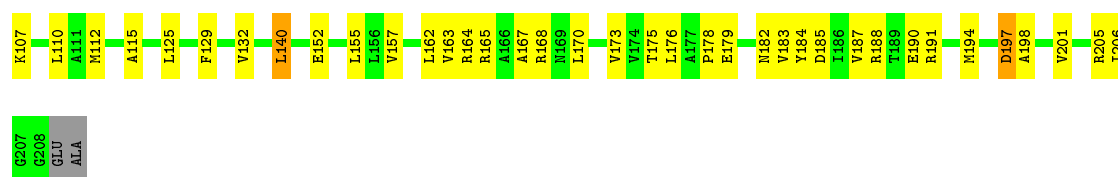
Chain RE: 75% 22%



• Molecule 8: 50S ribosomal protein L4

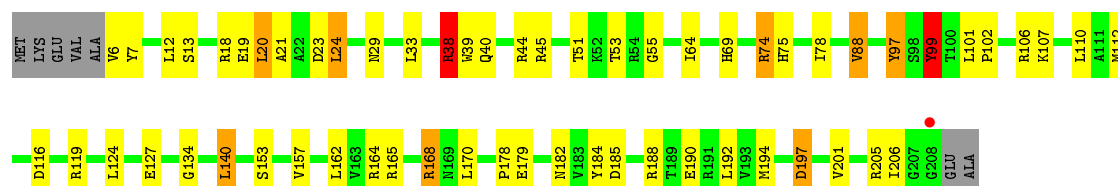
Chain YF: 64% 30%





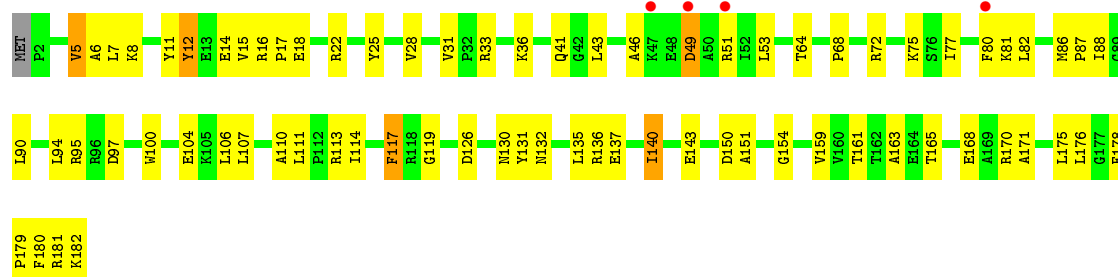
- Molecule 8: 50S ribosomal protein L4

Chain RF: 68% 24%



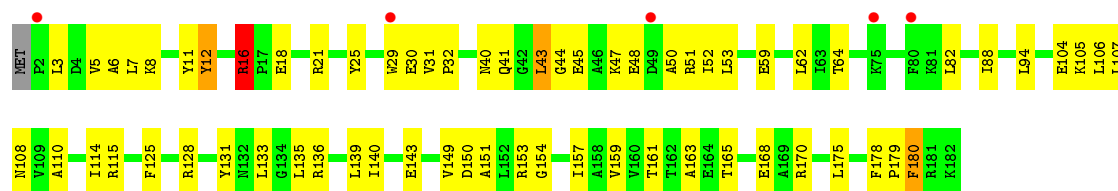
- Molecule 9: 50S ribosomal protein L5

Chain YG: 2% 59% 38%



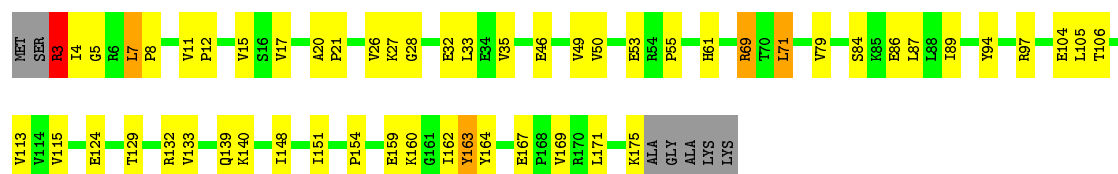
- Molecule 9: 50S ribosomal protein L5

Chain RG: 3% 64% 34%

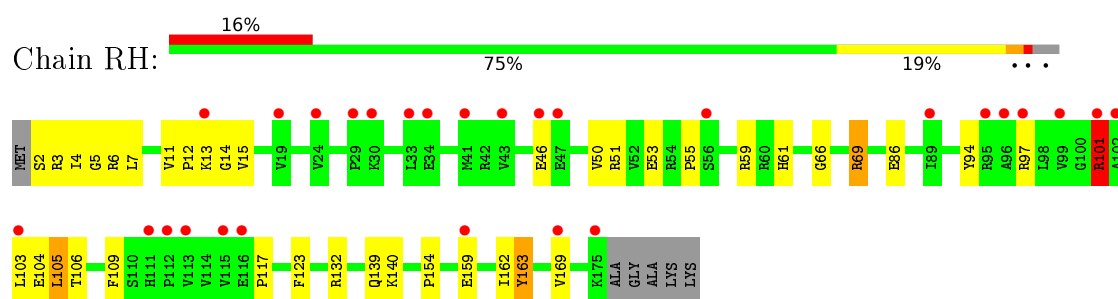


- Molecule 10: 50S ribosomal protein L6

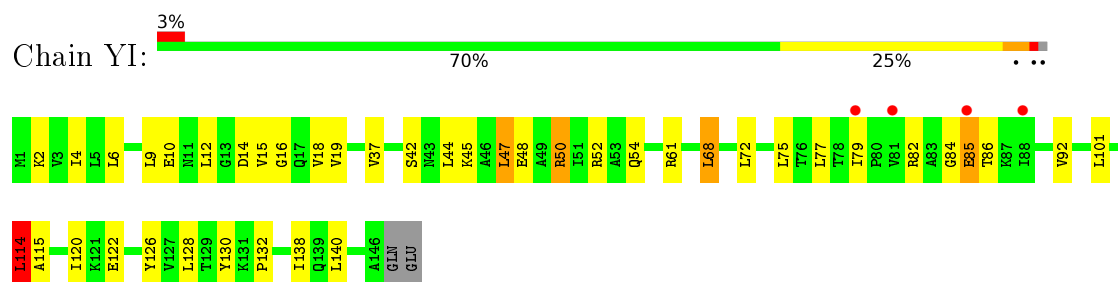
Chain YH: 66% 28%



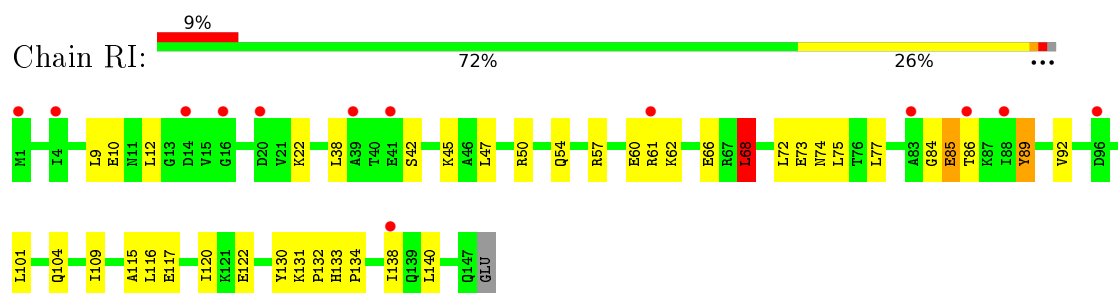
- Molecule 10: 50S ribosomal protein L6



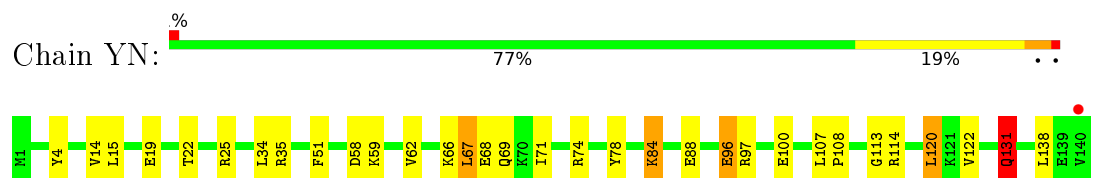
- Molecule 11: 50S ribosomal protein L9



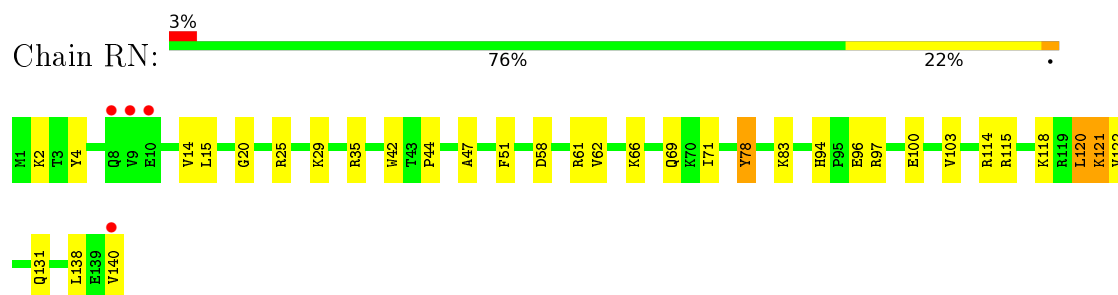
- Molecule 11: 50S ribosomal protein L9



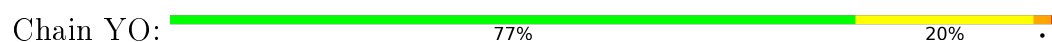
- Molecule 12: 50S ribosomal protein L13



- Molecule 12: 50S ribosomal protein L13



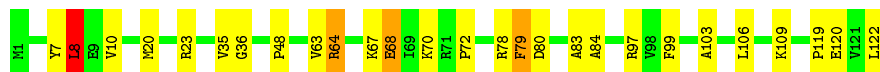
- Molecule 13: 50S ribosomal protein L14





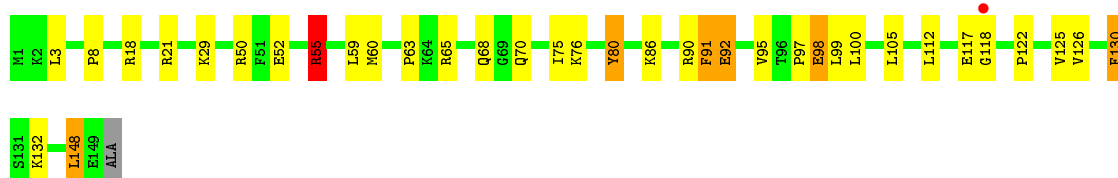
- Molecule 13: 50S ribosomal protein L14

Chain RO: 78% 19% ..



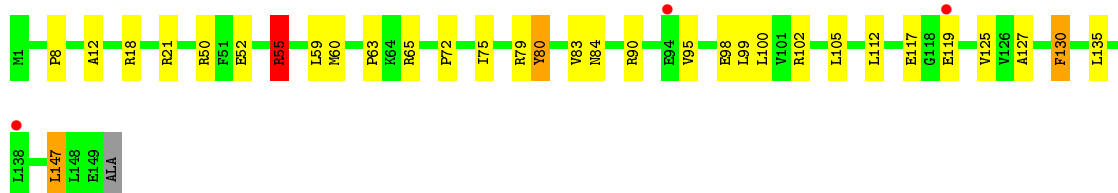
- Molecule 14: 50S ribosomal protein L15

Chain YP: 75% 19% ..



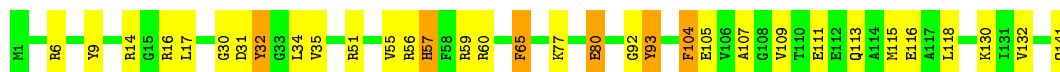
- Molecule 14: 50S ribosomal protein L15

Chain RP: 78% 19% ..



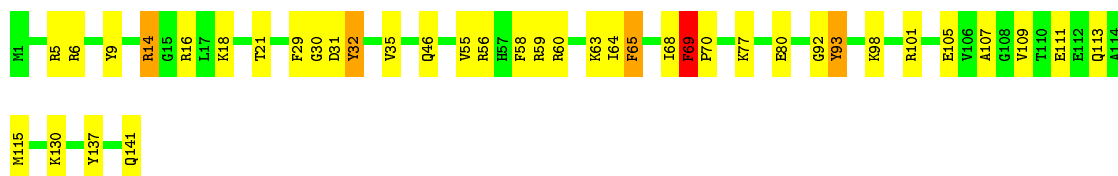
- Molecule 15: 50S ribosomal protein L16

Chain YQ: 77% 19% .



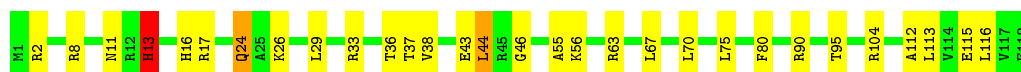
- Molecule 15: 50S ribosomal protein L16

Chain RQ: 72% 24% ..



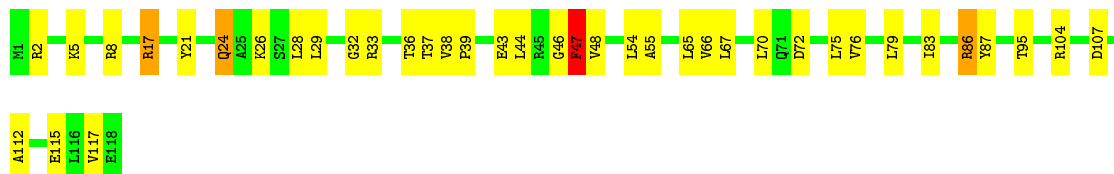
- Molecule 16: 50S ribosomal protein L17

Chain YR: 75% 23% ..



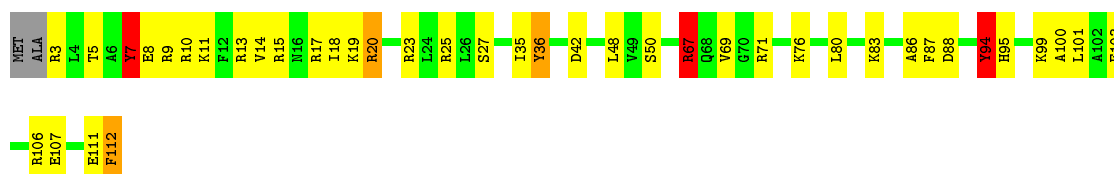
- Molecule 16: 50S ribosomal protein L17

Chain RR: 67% 30% . .



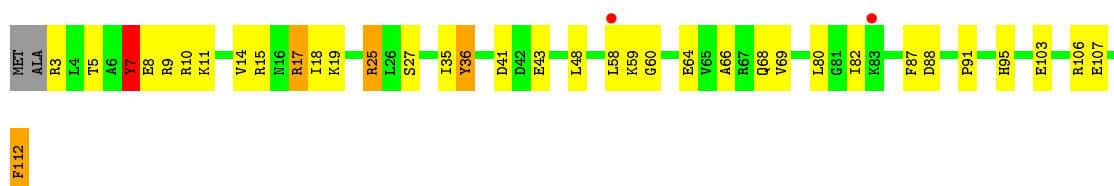
- Molecule 17: 50S ribosomal protein L18

Chain YS: 62% 31% . . .



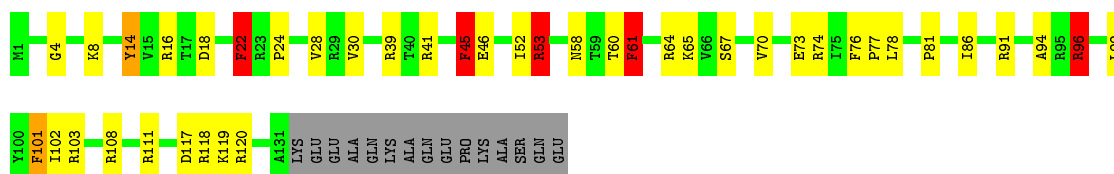
- Molecule 17: 50S ribosomal protein L18

Chain RS: 2% 66% 28% . . .



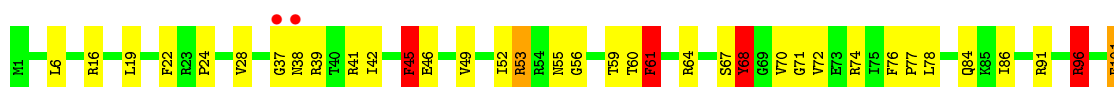
- Molecule 18: 50S ribosomal protein L19

Chain YT: 61% 24% 10% . .



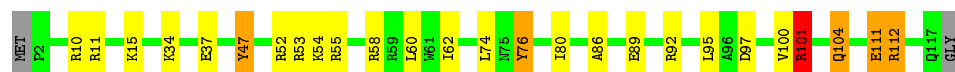
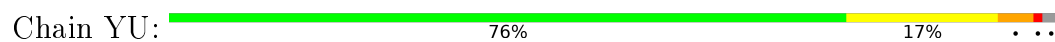
- Molecule 18: 50S ribosomal protein L19

Chain RT: 60% 25% 10% . .

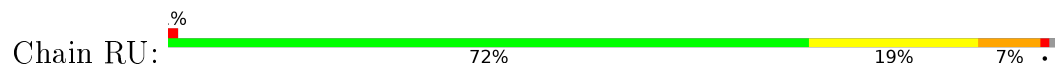




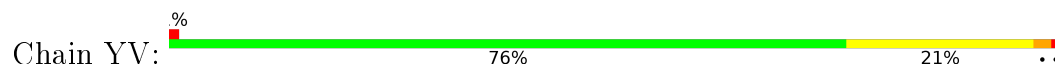
- Molecule 19: 50S ribosomal protein L20



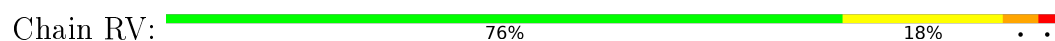
- Molecule 19: 50S ribosomal protein L20



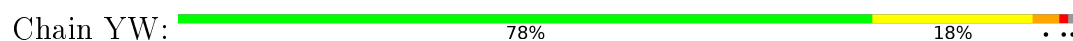
- Molecule 20: 50S ribosomal protein L21



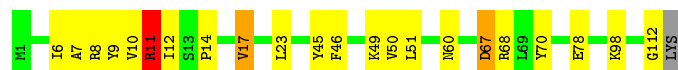
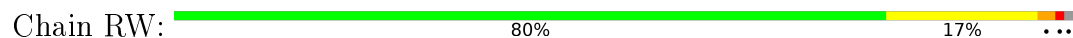
- Molecule 20: 50S ribosomal protein L21



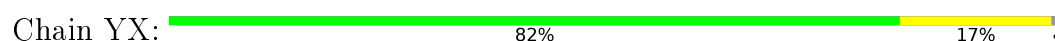
- Molecule 21: 50S ribosomal protein L22

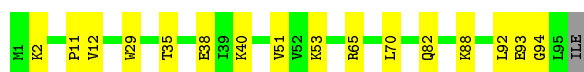


- Molecule 21: 50S ribosomal protein L22

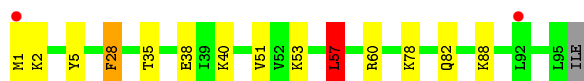
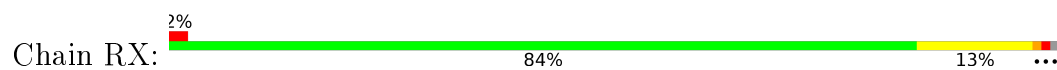


- Molecule 22: 50S ribosomal protein L23





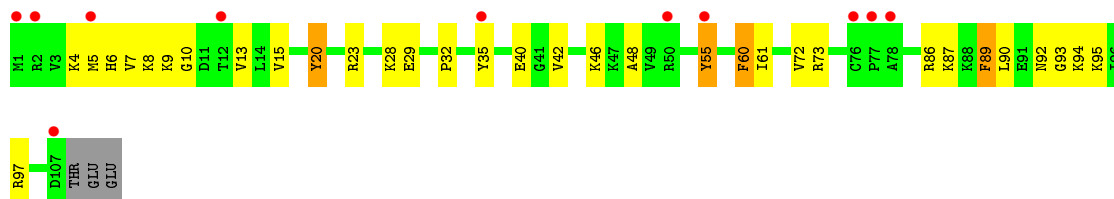
- Molecule 22: 50S ribosomal protein L23



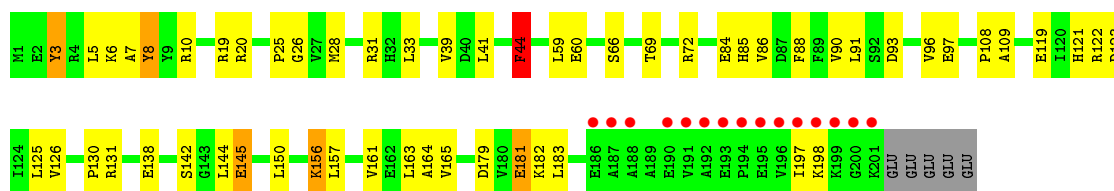
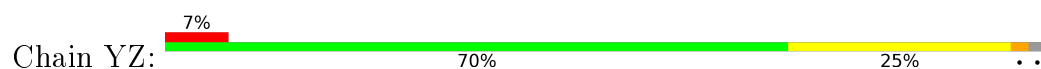
- Molecule 23: 50S ribosomal protein L24



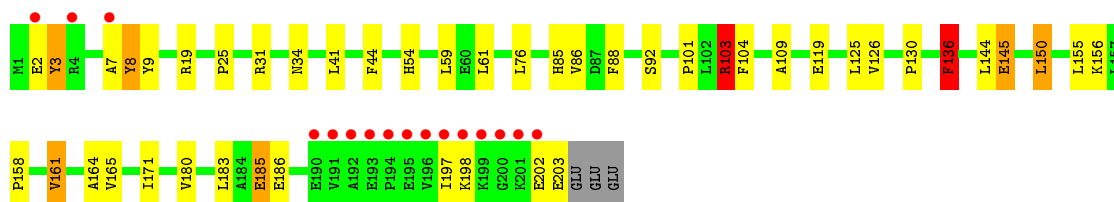
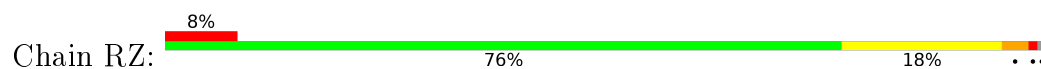
- Molecule 23: 50S ribosomal protein L24



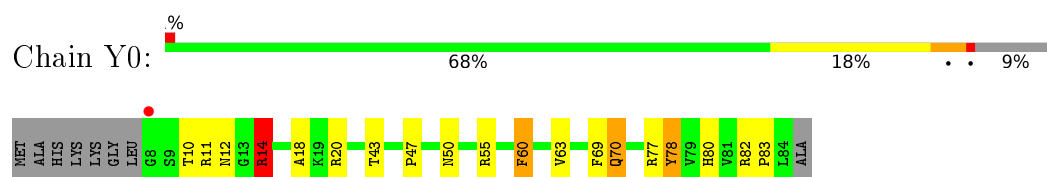
- Molecule 24: 50S ribosomal protein L25



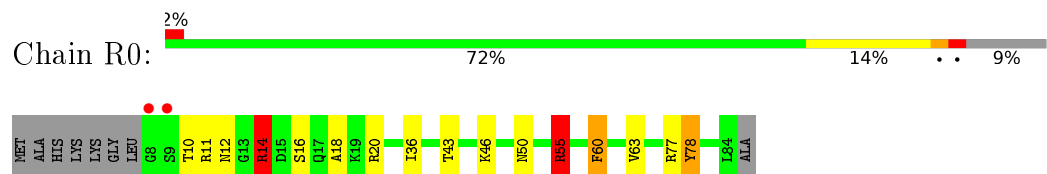
- Molecule 24: 50S ribosomal protein L25



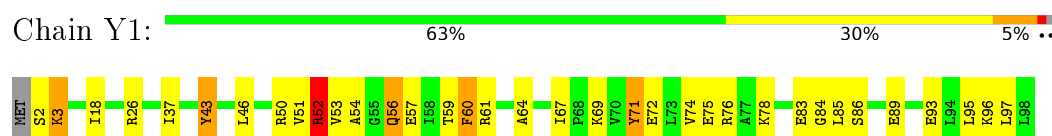
- Molecule 25: 50S ribosomal protein L27



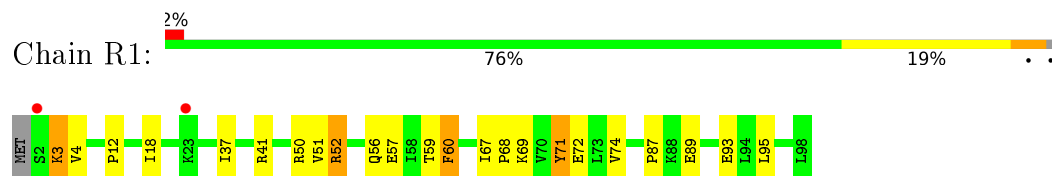
- Molecule 25: 50S ribosomal protein L27



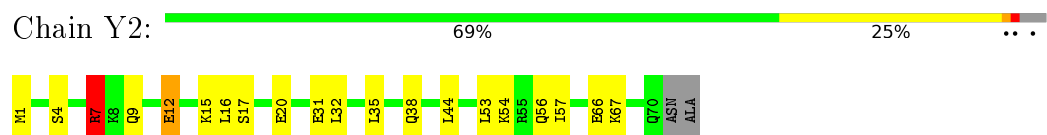
- Molecule 26: 50S ribosomal protein L28



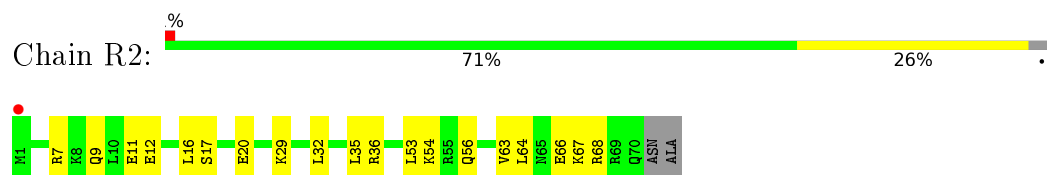
- Molecule 26: 50S ribosomal protein L28



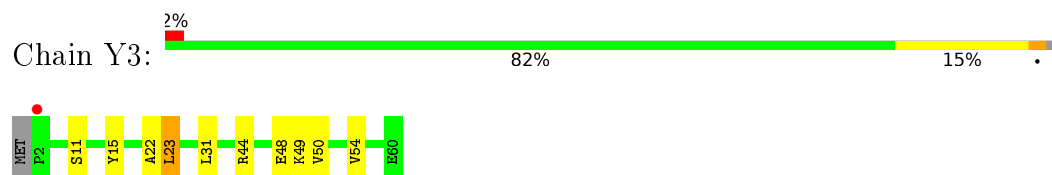
- Molecule 27: 50S ribosomal protein L29



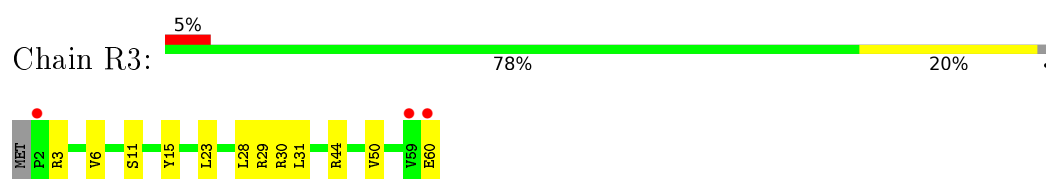
- Molecule 27: 50S ribosomal protein L29



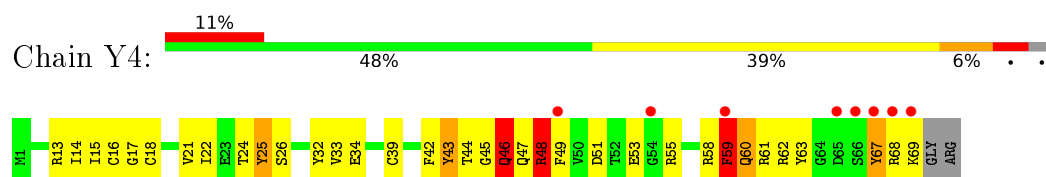
- Molecule 28: 50S ribosomal protein L30



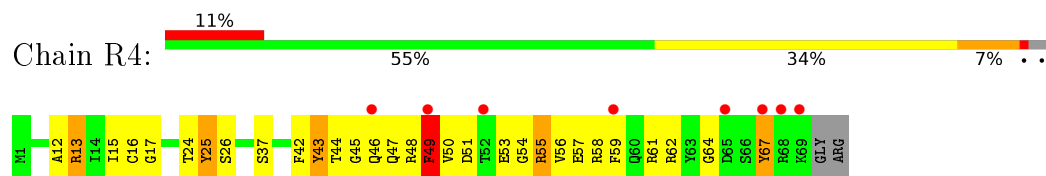
- Molecule 28: 50S ribosomal protein L30



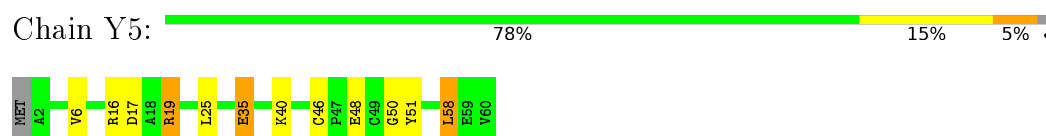
- Molecule 29: 50S ribosomal protein L31



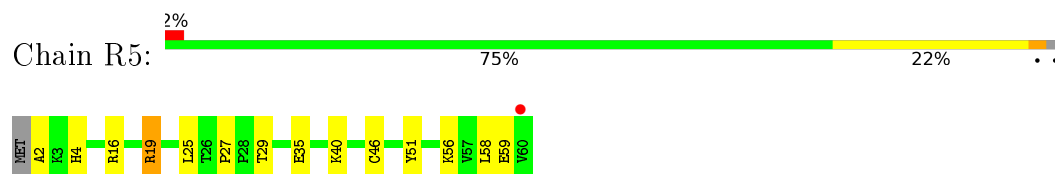
- Molecule 29: 50S ribosomal protein L31



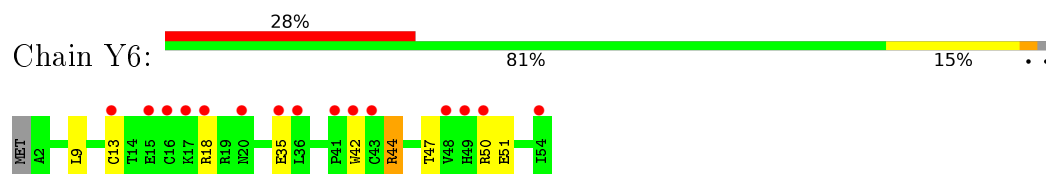
- Molecule 30: 50S ribosomal protein L32



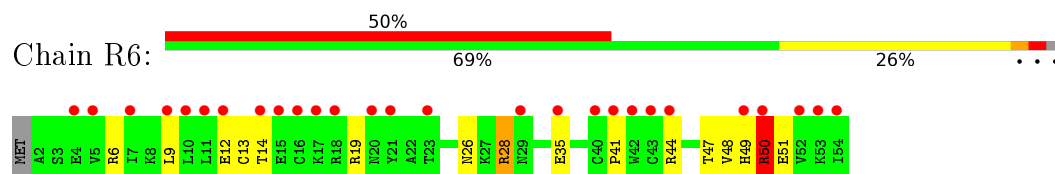
- Molecule 30: 50S ribosomal protein L32




- Molecule 31: 50S ribosomal protein L33



- Molecule 31: 50S ribosomal protein L33



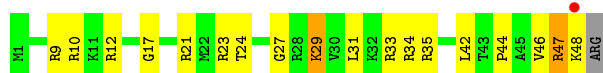
- Molecule 32: 50S ribosomal protein L34

Chain Y7:  73% 18% . . .



- Molecule 32: 50S ribosomal protein L34

Chain R7:  2% 61% 33% . . .



- Molecule 33: 50S ribosomal protein L35

Chain Y8:  60% 37% . . .




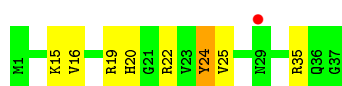
- Molecule 33: 50S ribosomal protein L35

Chain R8:  66% 29% . . .




- Molecule 34: 50S ribosomal protein L36

Chain Y9:  3% 78% 19% .



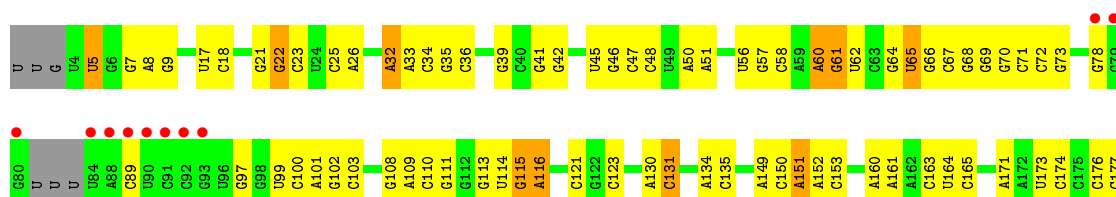
- Molecule 34: 50S ribosomal protein L36

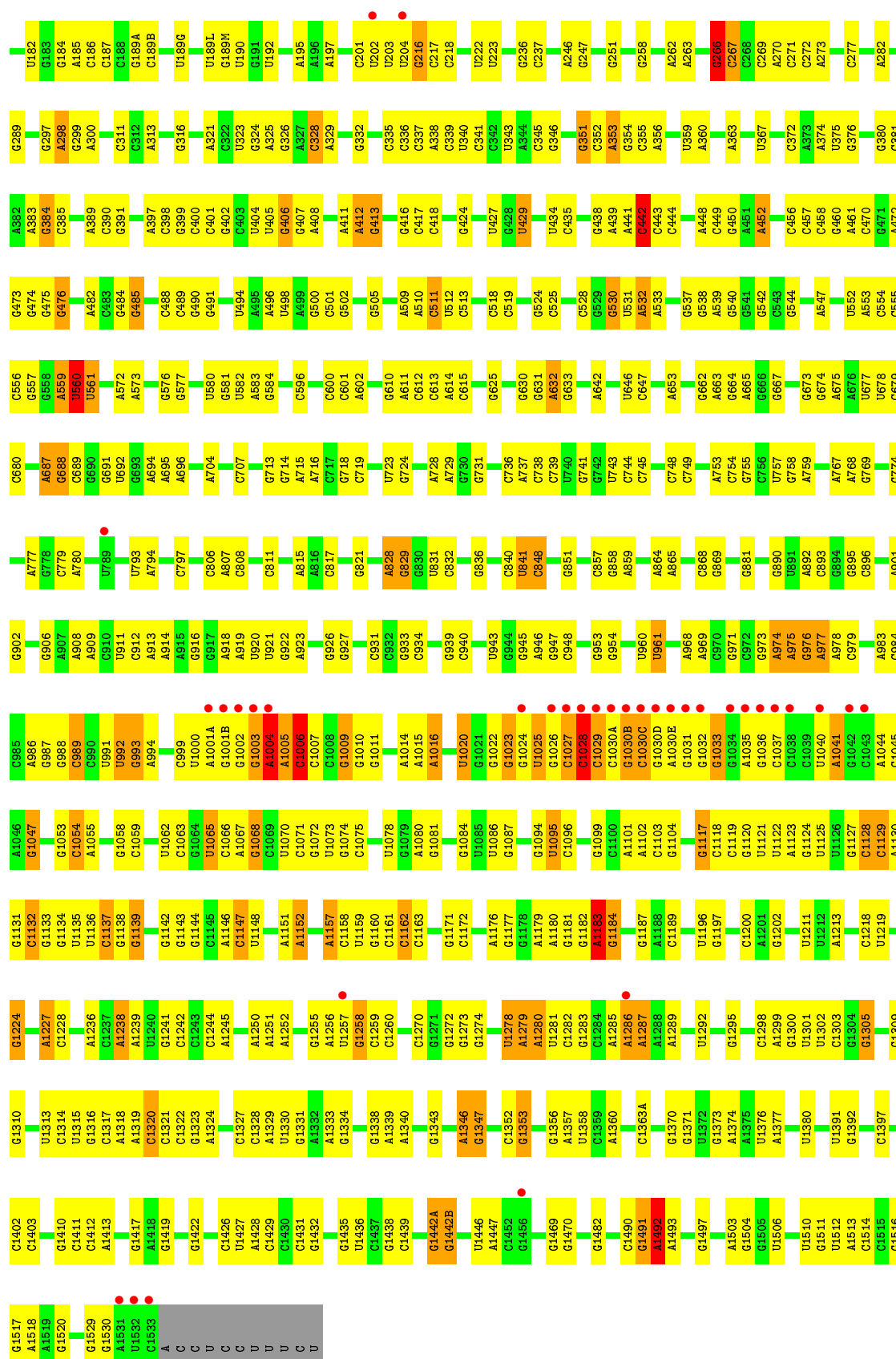
Chain R9:  8% 70% 24% . . .

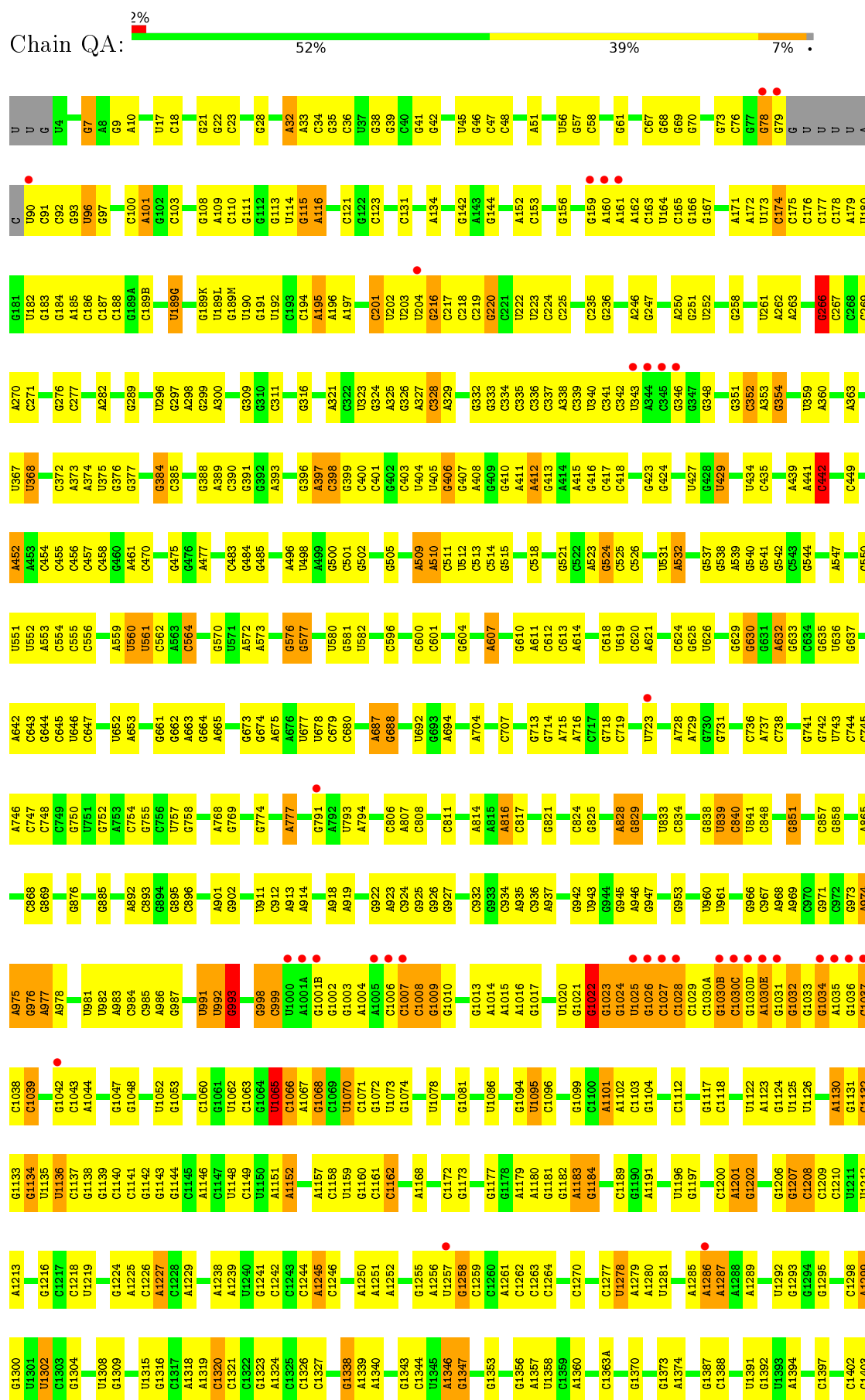


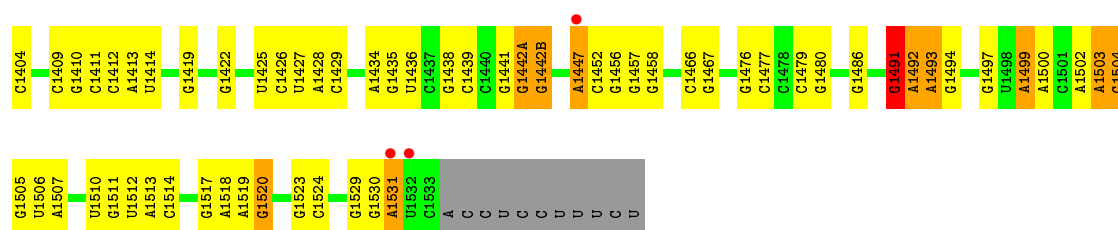
- Molecule 35: Thermus thermophilus HB8 genomic DNA, complete genome

Chain XA:  3% 54% 38% 6% . . .

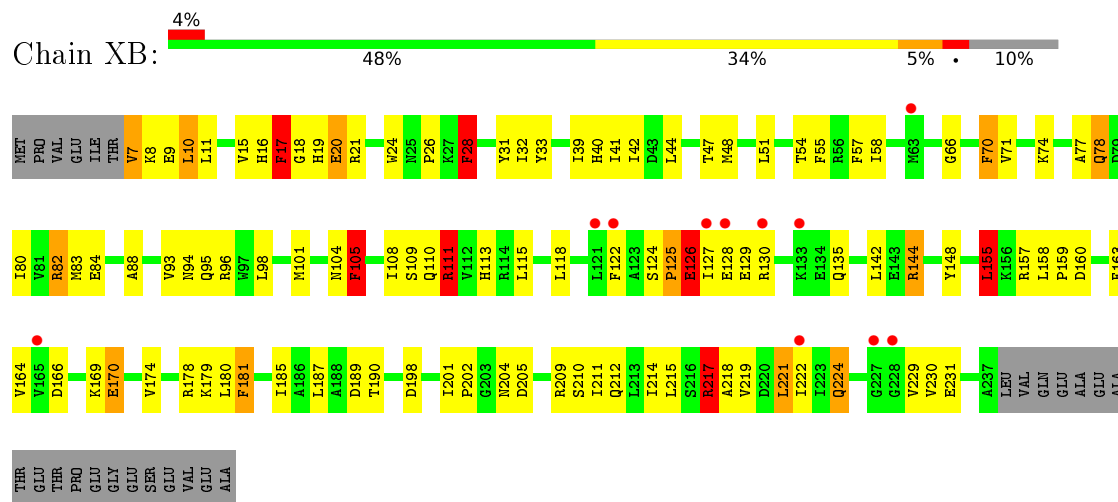




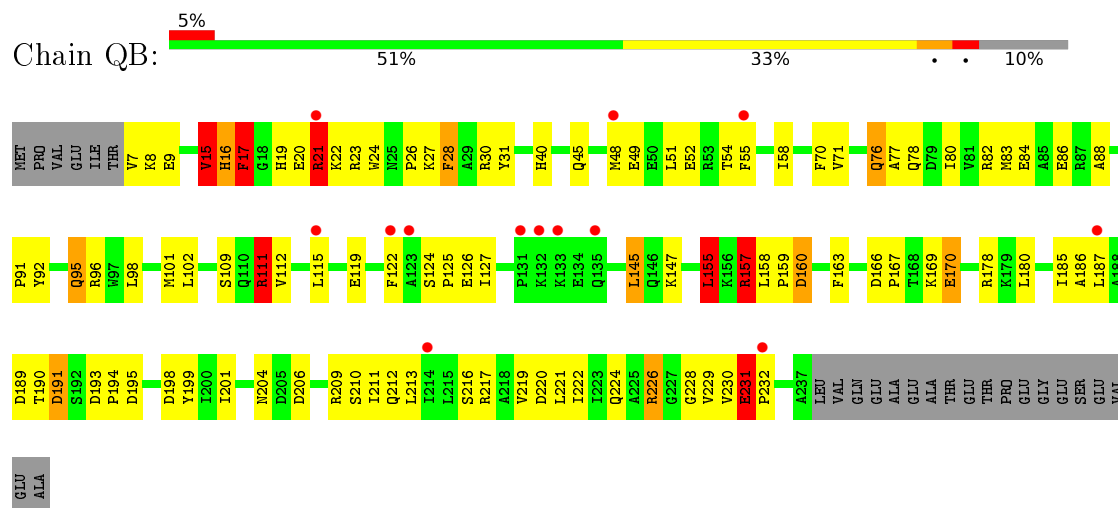




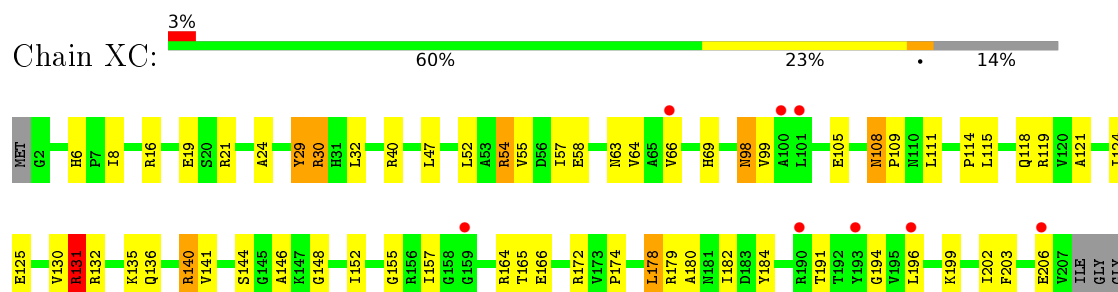
• Molecule 36: 30S ribosomal protein S2



• Molecule 36: 30S ribosomal protein S2



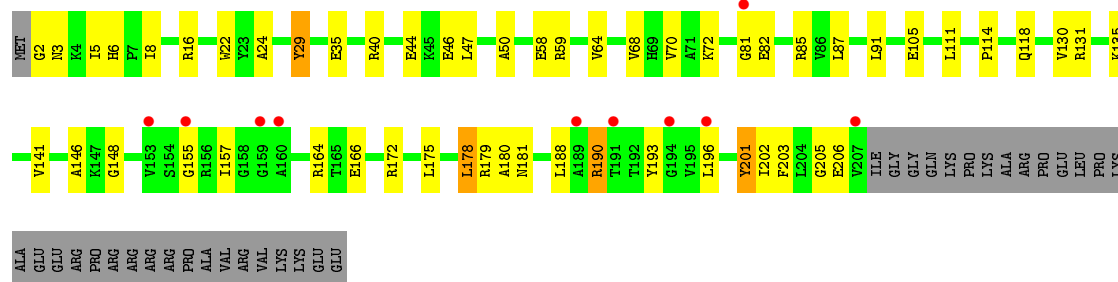
• Molecule 37: 30S ribosomal protein S3



GLN
LYS
PRO
LYS
LYS
ALA
ARG
PRO
GLU
LEU
PRO
LYS
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VAL
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GLU

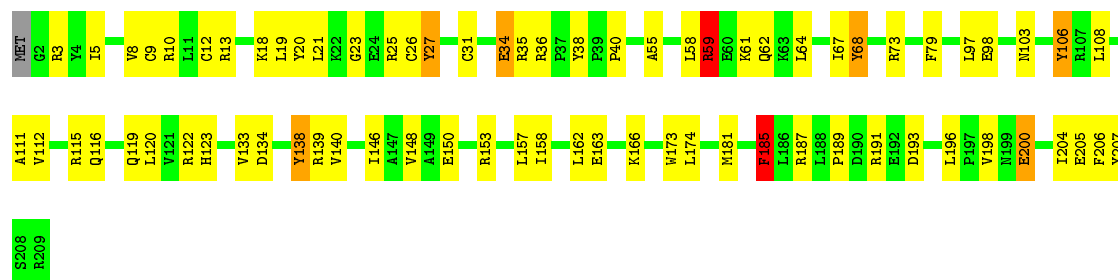
- Molecule 37: 30S ribosomal protein S3

Chain QC: 4% 63% 21% 14%



- Molecule 38: 30S ribosomal protein S4

Chain XD: 65% 31% 4%



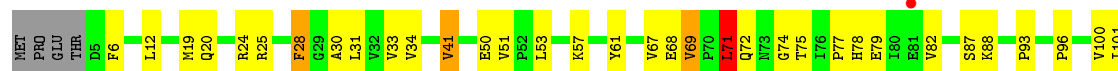
- Molecule 38: 30S ribosomal protein S4

Chain QD: 59% 36% 5%



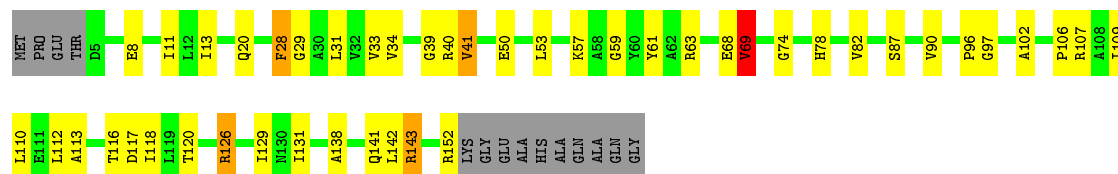
- Molecule 39: 30S ribosomal protein S5

Chain XE: 56% 32% 9% 3%





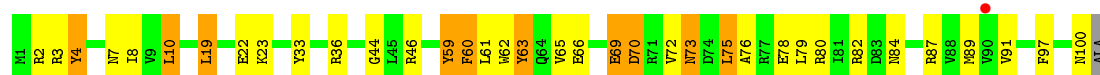
- Molecule 39: 30S ribosomal protein S5



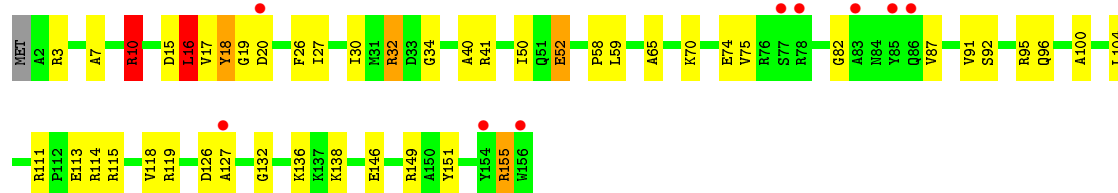
- Molecule 40: 30S ribosomal protein S6



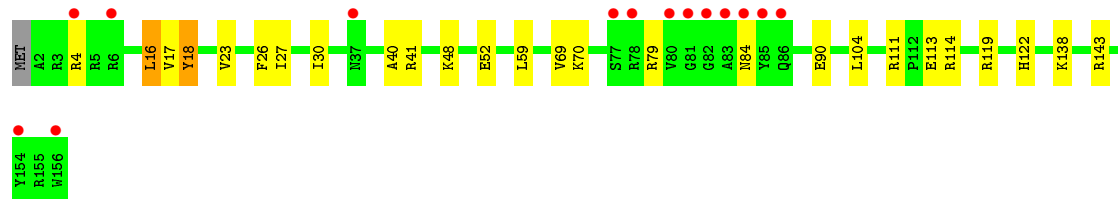
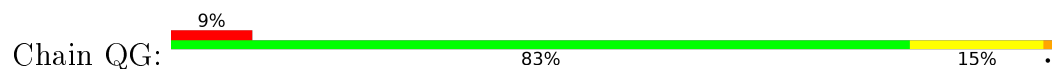
- Molecule 40: 30S ribosomal protein S6



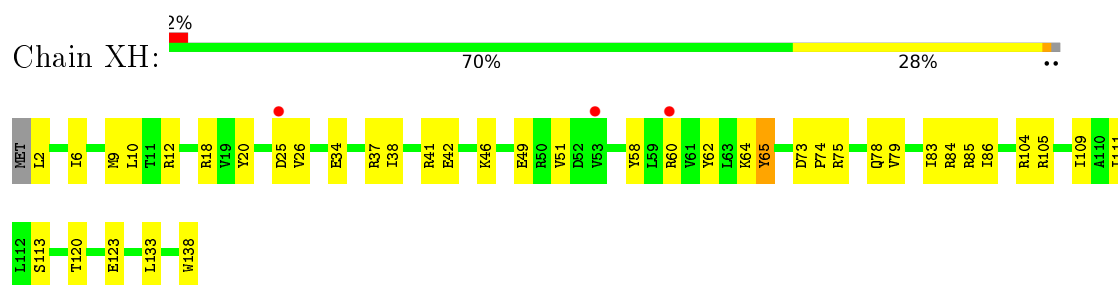
- Molecule 41: 30S ribosomal protein S7



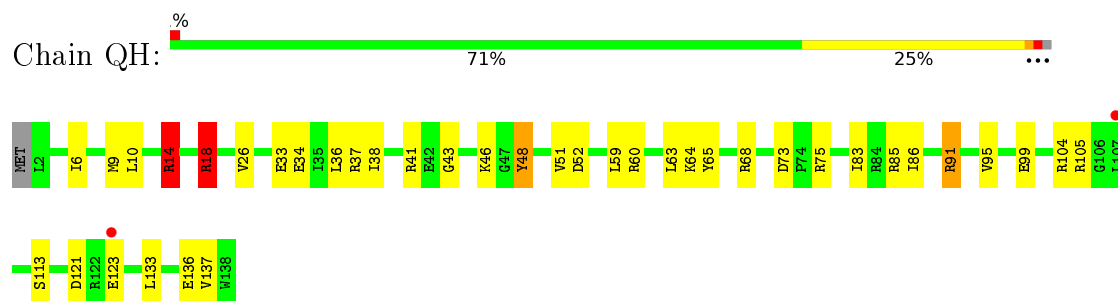
- Molecule 41: 30S ribosomal protein S7



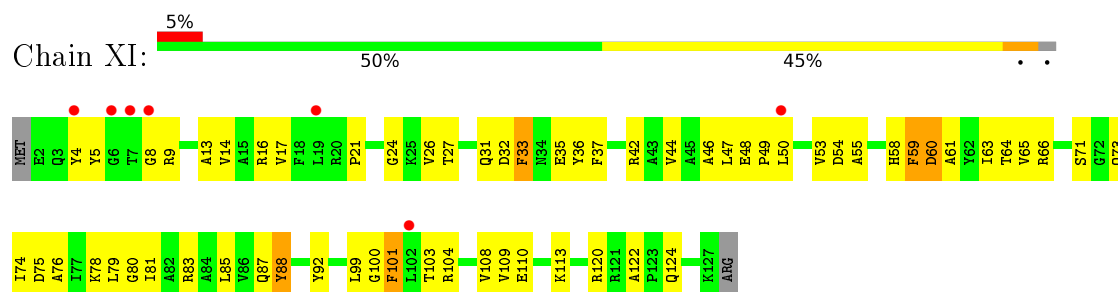
- Molecule 42: 30S ribosomal protein S8



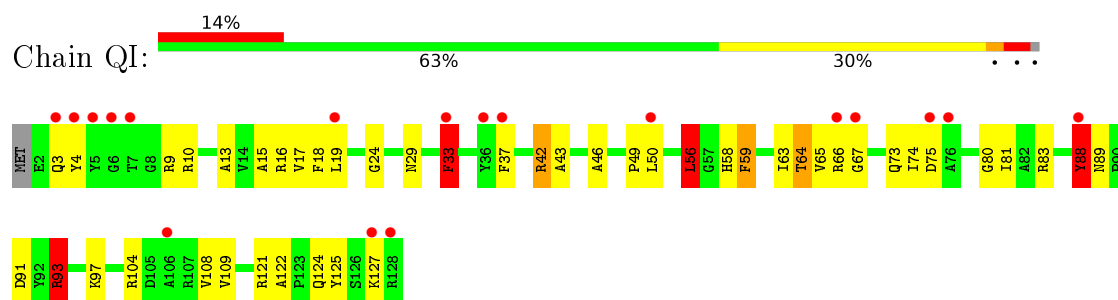
- Molecule 42: 30S ribosomal protein S8



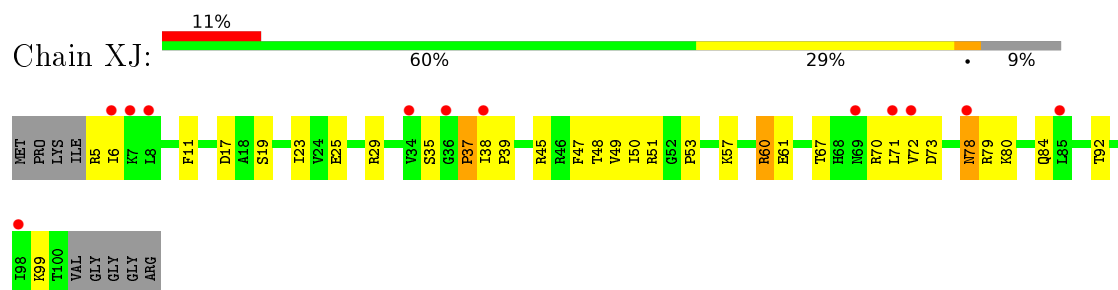
- Molecule 43: 30S ribosomal protein S9



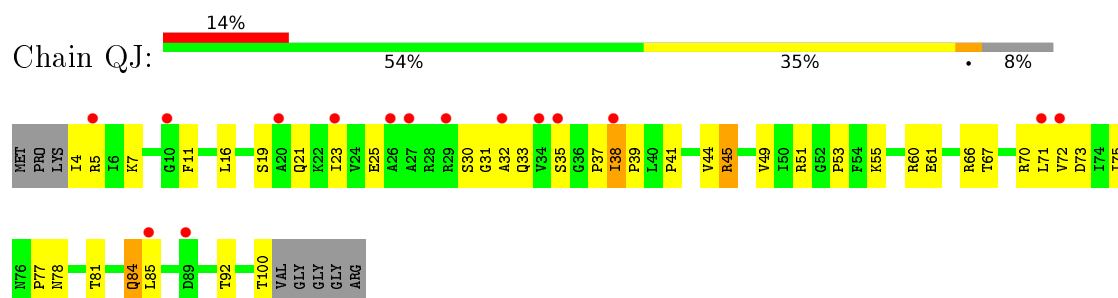
- Molecule 43: 30S ribosomal protein S9



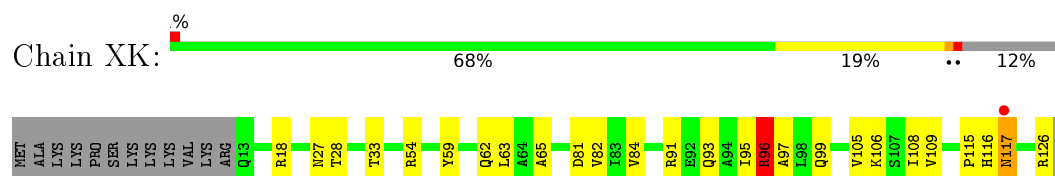
- Molecule 44: 30S ribosomal protein S10



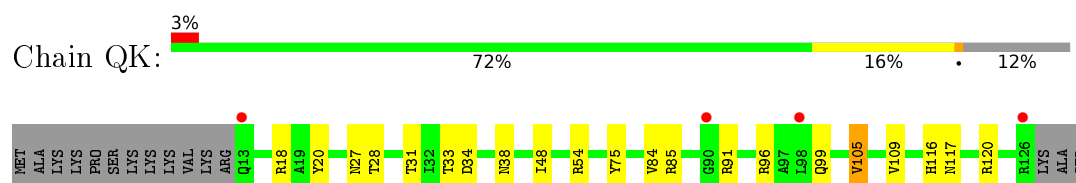
- Molecule 44: 30S ribosomal protein S10



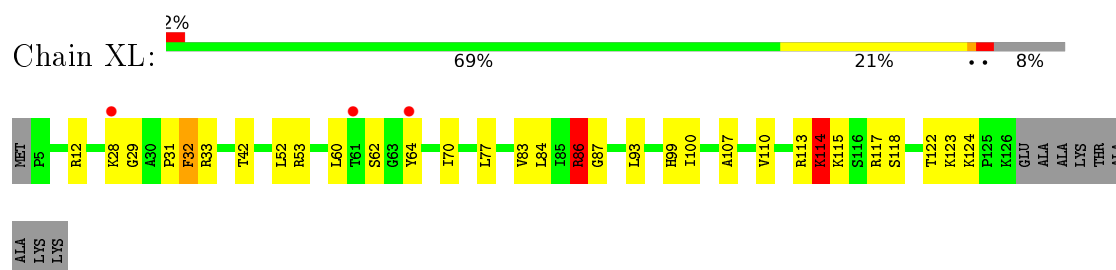
- Molecule 45: 30S ribosomal protein S11



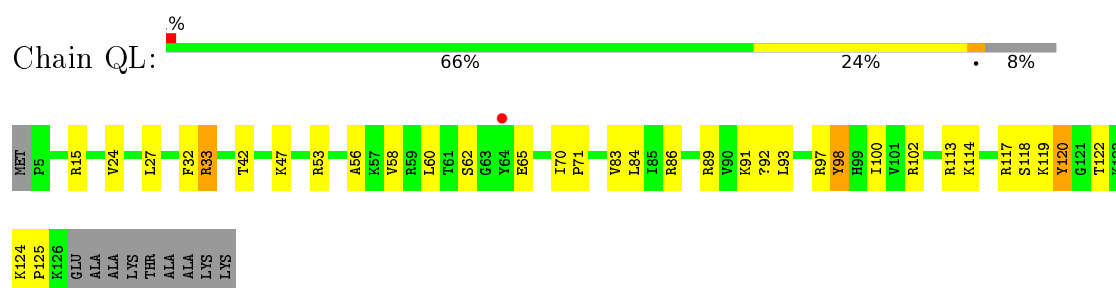
- Molecule 45: 30S ribosomal protein S11



- Molecule 46: 30S ribosomal protein S12

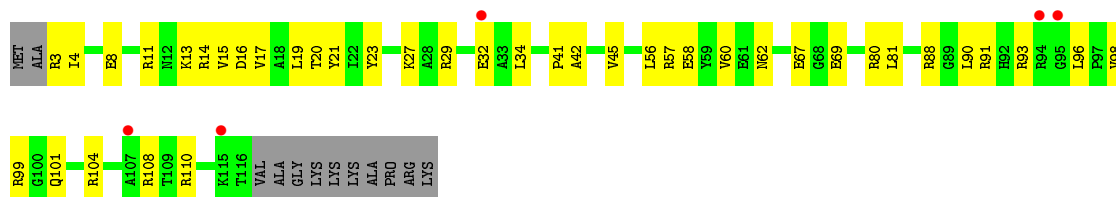


- Molecule 46: 30S ribosomal protein S12

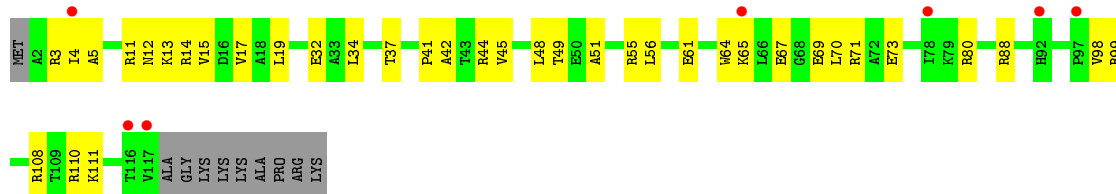


- Molecule 47: 30S ribosomal protein S13

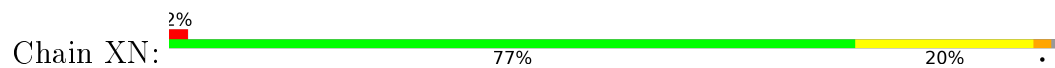




- Molecule 47: 30S ribosomal protein S13



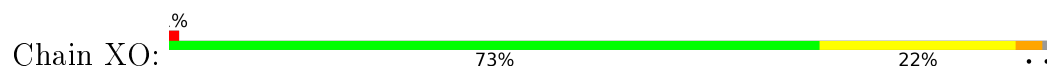
- Molecule 48: 30S ribosomal protein S14 type Z



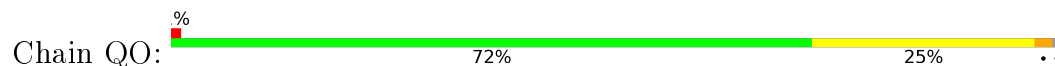
- Molecule 48: 30S ribosomal protein S14 type Z



- Molecule 49: 30S ribosomal protein S15



- Molecule 49: 30S ribosomal protein S15



- Molecule 50: 30S ribosomal protein S16

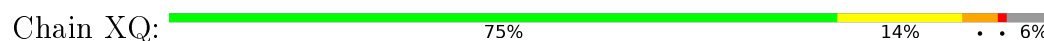




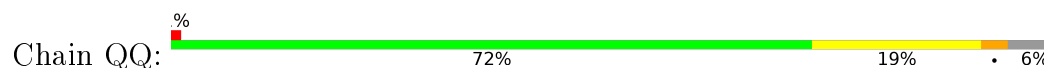
- Molecule 50: 30S ribosomal protein S16



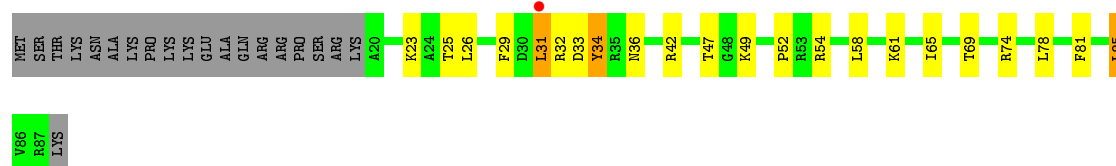
- Molecule 51: 30S ribosomal protein S17



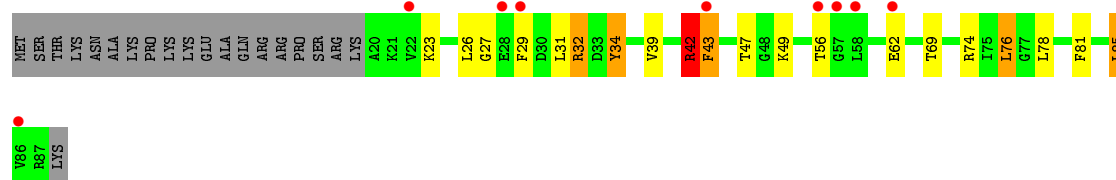
- Molecule 51: 30S ribosomal protein S17



- Molecule 52: 30S ribosomal protein S18




- Molecule 52: 30S ribosomal protein S18




- Molecule 53: 30S ribosomal protein S19



- Chain QS:
-
- | Category | Percentage |
|----------|------------|
| Red | 23% |
| Green | 66% |
| Yellow | 20% |
| Grey | 11% |

- Chain XT: 

- Chain QT: 
- | Chain | Percentage |
|--------|------------|
| Green | 74% |
| Yellow | 14% |
| Orange | 9% |
| Grey | 3% |
- NET
ALA
GLN
LYS
LYS
PRO
LYS
R8
R9
L10
S11
R15
L24
S31
K34
T35
L36
S37
K38
K39
A40
L43
O47
R57
E60
S61
L62
R79
R89
E93
A94
A95
L100
G103
LEU
SER
ALA

- Chain XU:
-
- | Amino Acid | Percentage |
|------------|------------|
| 19% | 19% |
| 59% | 59% |
| 22% | 22% |
| 1% | 1% |
| 15% | 15% |
- Legend:
- | Color | Amino Acid |
|--------------|------------|
| Red | MET |
| Yellow | G2 |
| Green | D6 |
| Orange | R6 |
| Light Green | R7 |
| Light Yellow | R10 |
| Light Green | G11 |
| Light Green | T17 |
| Light Green | Y18 |
| Light Yellow | R22 |
| Light Yellow | P23 |
| Light Yellow | R24 |
| Light Yellow | LYS |
| Light Yellow | LYS |
| Light Yellow | LYS |

- Chain QU:
-

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.48 Å 450.41 Å 622.55 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.88 – 3.10 49.88 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.88-3.10) 100.0 (49.88-3.10)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 3.12 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.10.1_2155)	Depositor
R, R_{free}	0.196 , 0.227 0.199 , 0.228	Depositor DCC
R_{free} test set	49511 reflections (4.91%)	DCC
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 74.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	296662	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ZN, OMG, MA6, SF4, 0TD, MG, 2MA, 2MU, 2MG, 5MC, UR3, 4OC, M2G, 7MG, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	QV	0.39	1/1836 (0.1%)	0.88	5/2859 (0.2%)
1	XV	0.35	1/1836 (0.1%)	0.81	2/2859 (0.1%)
2	QX	0.31	0/241	0.88	0/373
2	XX	0.29	0/241	0.85	0/373
3	QY	0.39	1/2873 (0.0%)	0.88	12/3870 (0.3%)
3	XY	0.38	1/2873 (0.0%)	0.77	9/3870 (0.2%)
4	RA	0.28	0/68901	0.90	93/107544 (0.1%)
4	YA	0.30	0/68901	0.88	81/107544 (0.1%)
5	RB	0.24	0/2876	0.85	0/4486
5	YB	0.27	0/2878	0.88	0/4490
6	RD	0.39	1/2181 (0.0%)	0.71	2/2940 (0.1%)
6	YD	0.47	2/2186 (0.1%)	0.88	9/2944 (0.3%)
7	RE	0.35	0/1592	0.68	0/2149
7	YE	0.48	3/1592 (0.2%)	0.74	4/2149 (0.2%)
8	RF	0.34	0/1619	0.75	4/2193 (0.2%)
8	YF	0.33	0/1615	0.71	2/2188 (0.1%)
9	RG	0.49	1/1451 (0.1%)	0.75	3/1961 (0.2%)
9	YG	0.36	0/1449	0.75	0/1957
10	RH	0.35	1/1356 (0.1%)	0.68	1/1834 (0.1%)
10	YH	0.40	1/1350 (0.1%)	0.79	5/1826 (0.3%)
11	RI	0.39	1/1109 (0.1%)	0.75	2/1512 (0.1%)
11	YI	0.41	1/1091 (0.1%)	0.82	6/1490 (0.4%)
12	RN	0.62	3/1148 (0.3%)	0.77	2/1547 (0.1%)
12	YN	0.44	1/1144 (0.1%)	0.71	3/1543 (0.2%)
13	RO	0.32	0/943	0.67	3/1269 (0.2%)
13	YO	0.38	1/943 (0.1%)	0.69	2/1269 (0.2%)
14	RP	0.35	0/1152	0.81	3/1533 (0.2%)
14	YP	0.36	0/1152	0.82	3/1533 (0.2%)
15	RQ	0.37	0/1143	0.78	5/1527 (0.3%)
15	YQ	0.39	0/1143	0.70	1/1527 (0.1%)
16	RR	0.42	1/982 (0.1%)	0.87	6/1312 (0.5%)
16	YR	0.41	1/982 (0.1%)	0.75	2/1312 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	RS	0.39	0/887	0.78	3/1180 (0.3%)
17	YS	0.40	0/880	0.96	4/1172 (0.3%)
18	RT	0.37	0/1105	0.87	6/1477 (0.4%)
18	YT	0.36	0/1097	0.90	7/1468 (0.5%)
19	RU	0.61	3/977 (0.3%)	1.20	9/1301 (0.7%)
19	YU	0.66	3/977 (0.3%)	1.09	8/1301 (0.6%)
20	RV	0.51	1/786 (0.1%)	1.31	5/1053 (0.5%)
20	YV	0.39	0/782	0.80	2/1049 (0.2%)
21	RW	0.31	0/897	0.71	3/1205 (0.2%)
21	YW	0.32	0/897	0.72	3/1205 (0.2%)
22	RX	0.31	0/764	0.66	1/1025 (0.1%)
22	YX	0.30	0/764	0.62	0/1025
23	RY	0.32	0/823	0.67	0/1099
23	YY	0.51	1/823 (0.1%)	0.92	4/1100 (0.4%)
24	RZ	0.36	0/1620	0.77	5/2200 (0.2%)
24	YZ	0.40	1/1590 (0.1%)	0.78	6/2162 (0.3%)
25	R0	0.46	0/616	1.07	5/821 (0.6%)
25	Y0	0.48	1/616 (0.2%)	0.87	2/821 (0.2%)
26	R1	0.33	0/761	0.75	2/1013 (0.2%)
26	Y1	0.73	5/766 (0.7%)	0.85	5/1018 (0.5%)
27	R2	0.35	0/590	0.70	0/781
27	Y2	0.56	2/594 (0.3%)	0.82	3/785 (0.4%)
28	R3	0.41	1/474 (0.2%)	0.63	0/635
28	Y3	0.28	0/469	0.61	0/630
29	R4	0.68	3/559 (0.5%)	1.06	4/754 (0.5%)
29	Y4	0.64	2/549 (0.4%)	1.05	6/741 (0.8%)
30	R5	0.54	1/473 (0.2%)	0.87	2/639 (0.3%)
30	Y5	0.52	0/469	0.73	0/635
31	R6	0.69	2/460 (0.4%)	1.23	5/613 (0.8%)
31	Y6	0.34	0/456	0.62	0/608
32	R7	0.59	2/426 (0.5%)	0.97	2/561 (0.4%)
32	Y7	0.37	0/426	0.92	4/561 (0.7%)
33	R8	0.33	0/525	0.87	2/691 (0.3%)
33	Y8	0.31	0/525	0.66	0/691
34	R9	0.48	1/310 (0.3%)	1.08	4/407 (1.0%)
34	Y9	0.29	0/310	0.69	0/407
35	QA	0.25	0/35795	0.86	32/55864 (0.1%)
35	XA	0.26	0/35890	0.88	34/56012 (0.1%)
36	QB	0.43	1/1876 (0.1%)	0.93	12/2533 (0.5%)
36	XB	0.47	1/1860 (0.1%)	1.14	14/2518 (0.6%)
37	QC	0.36	0/1582	0.69	1/2137 (0.0%)
37	XC	0.43	1/1566 (0.1%)	0.87	6/2119 (0.3%)
38	QD	0.36	0/1695	0.82	6/2274 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	XD	0.41	0/1698	0.79	2/2277 (0.1%)
39	QE	0.40	1/1149 (0.1%)	0.79	6/1548 (0.4%)
39	XE	0.41	1/1149 (0.1%)	0.65	1/1548 (0.1%)
40	QF	0.46	0/827	0.87	3/1120 (0.3%)
40	XF	0.39	0/829	0.83	1/1123 (0.1%)
41	QG	0.33	0/1254	0.66	1/1683 (0.1%)
41	XG	0.50	0/1248	0.84	7/1676 (0.4%)
42	QH	0.45	3/1118 (0.3%)	1.03	6/1506 (0.4%)
42	XH	0.41	0/1108	0.79	4/1494 (0.3%)
43	QI	0.71	1/1005 (0.1%)	0.92	5/1351 (0.4%)
43	XI	0.36	0/985	0.76	0/1329
44	QJ	0.36	0/732	0.80	3/993 (0.3%)
44	XJ	0.28	0/723	0.59	0/984
45	QK	0.34	0/849	0.71	2/1150 (0.2%)
45	XK	0.33	0/848	0.70	2/1149 (0.2%)
46	QL	0.34	0/937	0.71	1/1260 (0.1%)
46	XL	0.47	1/937 (0.1%)	0.74	2/1260 (0.2%)
47	QM	0.34	0/924	0.68	0/1242
47	XM	0.29	0/905	0.65	0/1217
48	QN	0.44	0/501	0.97	5/664 (0.8%)
48	XN	0.38	0/501	0.83	4/664 (0.6%)
49	QO	0.49	0/739	1.17	9/985 (0.9%)
49	XO	0.37	0/739	0.76	2/985 (0.2%)
50	QP	0.37	0/697	0.73	0/939
50	XP	0.60	1/693 (0.1%)	1.37	6/935 (0.6%)
51	QQ	0.34	0/836	0.69	0/1117
51	XQ	0.44	1/836 (0.1%)	0.68	1/1117 (0.1%)
52	QR	0.34	0/560	0.92	3/746 (0.4%)
52	XR	0.30	0/560	0.71	0/746
53	QS	0.61	2/663 (0.3%)	0.74	1/895 (0.1%)
53	XS	0.30	0/660	0.69	3/893 (0.3%)
54	QT	0.37	1/734 (0.1%)	0.65	1/969 (0.1%)
54	XT	0.41	1/736 (0.1%)	0.68	3/976 (0.3%)
55	QU	0.35	0/203	0.75	0/266
55	XU	0.32	0/203	0.68	0/266
All	All	0.33	67/318172 (0.0%)	0.86	571/475147 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	QY	0	3
8	RF	0	1
11	YI	0	1
17	RS	0	1
19	RU	0	1
25	R0	0	1
26	Y1	0	1
29	R4	0	1
29	Y4	0	1
31	R6	0	1
34	R9	0	1
36	QB	0	2
36	XB	0	2
37	QC	0	1
44	QJ	0	1
44	XJ	0	1
45	XK	0	1
46	XL	0	2
48	XN	0	1
51	XQ	0	1
All	All	0	25

All (67) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	QI	93	ARG	CB-CG	-17.94	1.04	1.52
53	QS	28	LYS	CD-CE	-11.05	1.23	1.51
26	Y1	52	ARG	CZ-NH2	10.67	1.47	1.33
1	QV	1	C	OP3-P	-10.63	1.48	1.61
1	XV	1	C	OP3-P	-10.63	1.48	1.61
12	RN	121	LYS	CD-CE	9.58	1.75	1.51
19	RU	112	ARG	CZ-NH1	8.99	1.44	1.33
36	XB	217	ARG	CG-CD	-8.88	1.29	1.51
31	R6	28	ARG	CG-CD	-8.79	1.29	1.51
46	XL	114	LYS	CB-CG	-8.75	1.28	1.52
12	YN	84	LYS	CD-CE	-8.63	1.29	1.51
6	RD	14	ARG	CZ-NH1	8.32	1.43	1.33
19	YU	101	ARG	CG-CD	8.20	1.72	1.51
29	R4	13	ARG	CG-CD	8.10	1.72	1.51
26	Y1	52	ARG	NE-CZ	7.89	1.43	1.33
39	XE	69	VAL	C-N	7.62	1.48	1.34
7	YE	73	GLU	CB-CG	-7.56	1.37	1.52
39	QE	69	VAL	C-N	7.40	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	YI	50	ARG	CB-CG	-7.28	1.32	1.52
7	YE	73	GLU	CD-OE1	-7.23	1.17	1.25
9	RG	16	ARG	CG-CD	7.06	1.69	1.51
6	YD	69	ARG	NE-CZ	-6.93	1.24	1.33
37	XC	131	ARG	CD-NE	-6.91	1.34	1.46
20	RV	21	ARG	CG-CD	-6.90	1.34	1.51
12	RN	83	LYS	CD-CE	-6.89	1.34	1.51
10	YH	53	GLU	C-N	6.88	1.49	1.34
7	YE	143	ASN	CA-C	-6.84	1.35	1.52
26	Y1	52	ARG	CD-NE	-6.67	1.35	1.46
19	YU	112	ARG	CZ-NH2	6.62	1.41	1.33
51	XQ	68	ARG	NE-CZ	-6.53	1.24	1.33
3	QY	278	ARG	NE-CZ	6.34	1.41	1.33
12	RN	121	LYS	CB-CG	-6.34	1.35	1.52
25	Y0	70	GLN	CB-CG	-6.24	1.35	1.52
42	QH	14	ARG	CG-CD	6.23	1.67	1.51
29	Y4	46	GLN	CD-NE2	6.21	1.48	1.32
42	QH	14	ARG	CB-CG	6.10	1.69	1.52
27	Y2	7	ARG	CZ-NH2	6.05	1.41	1.33
29	Y4	46	GLN	CD-OE1	-6.00	1.10	1.24
19	RU	92	ARG	NE-CZ	5.98	1.40	1.33
16	YR	24	GLN	CG-CD	5.88	1.64	1.51
53	QS	28	LYS	CE-NZ	-5.86	1.34	1.49
11	RI	104	GLN	CB-CG	-5.86	1.36	1.52
30	R5	27	PRO	CA-C	5.69	1.64	1.52
42	QH	14	ARG	NE-CZ	5.69	1.40	1.33
16	RR	24	GLN	CG-CD	5.62	1.64	1.51
27	Y2	7	ARG	CG-CD	5.62	1.66	1.51
23	YY	47	LYS	CE-NZ	5.60	1.63	1.49
32	R7	33	ARG	CG-CD	-5.59	1.38	1.51
29	R4	13	ARG	CZ-NH2	5.56	1.40	1.33
28	R3	44	ARG	CB-CG	-5.56	1.37	1.52
13	YO	3	GLN	CB-CG	-5.53	1.37	1.52
19	YU	101	ARG	CB-CG	5.51	1.67	1.52
50	XP	71	ARG	CZ-NH2	-5.40	1.26	1.33
34	R9	35	ARG	NE-CZ	5.39	1.40	1.33
10	RH	53	GLU	C-N	5.38	1.46	1.34
19	RU	112	ARG	CG-CD	-5.35	1.38	1.51
6	YD	103	ARG	NE-CZ	5.31	1.40	1.33
32	R7	29	LYS	CG-CD	-5.29	1.34	1.52
3	XY	278	ARG	NE-CZ	-5.26	1.26	1.33
29	R4	13	ARG	NE-CZ	5.25	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	R6	28	ARG	NE-CZ	5.21	1.39	1.33
36	QB	76	GLN	CB-CG	-5.21	1.38	1.52
26	Y1	56	GLN	CB-CG	5.19	1.66	1.52
54	QT	89	ARG	CB-CG	-5.18	1.38	1.52
24	YZ	20	ARG	CB-CG	-5.12	1.38	1.52
26	Y1	52	ARG	CZ-NH1	-5.12	1.26	1.33
54	XT	89	ARG	CD-NE	5.02	1.54	1.46

All (571) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	RA	2603	G	O5'-P-OP1	-35.76	67.78	110.70
36	XB	217	ARG	NE-CZ-NH2	-28.77	105.92	120.30
20	RV	21	ARG	NE-CZ-NH2	-27.66	106.47	120.30
50	XP	71	ARG	NE-CZ-NH2	-21.01	109.79	120.30
42	QH	14	ARG	NE-CZ-NH1	19.41	130.01	120.30
3	QY	278	ARG	NE-CZ-NH1	19.11	129.85	120.30
42	QH	14	ARG	NE-CZ-NH2	-18.98	110.81	120.30
31	R6	28	ARG	NE-CZ-NH1	18.96	129.78	120.30
19	YU	101	ARG	NE-CZ-NH1	18.03	129.31	120.30
49	QO	38	ARG	NE-CZ-NH2	-17.76	111.42	120.30
4	RA	2603	G	O5'-P-OP2	-17.75	89.41	110.70
19	RU	92	ARG	NE-CZ-NH1	16.46	128.53	120.30
50	XP	71	ARG	NE-CZ-NH1	16.35	128.48	120.30
37	XC	131	ARG	CG-CD-NE	-16.03	78.13	111.80
19	RU	112	ARG	NE-CZ-NH2	-15.82	112.39	120.30
36	XB	217	ARG	NE-CZ-NH1	15.80	128.20	120.30
4	RA	2602	A	OP1-P-O3'	-15.67	70.73	105.20
19	RU	92	ARG	NE-CZ-NH2	-15.45	112.58	120.30
20	RV	21	ARG	NE-CZ-NH1	15.26	127.93	120.30
6	YD	69	ARG	NE-CZ-NH2	15.08	127.84	120.30
23	YY	23	ARG	NE-CZ-NH1	14.20	127.40	120.30
50	XP	25	ARG	NE-CZ-NH1	13.99	127.30	120.30
3	QY	278	ARG	NE-CZ-NH2	-13.62	113.49	120.30
17	YS	67	ARG	CG-CD-NE	12.64	138.35	111.80
50	XP	25	ARG	NE-CZ-NH2	-12.53	114.04	120.30
43	QI	93	ARG	NE-CZ-NH2	12.48	126.54	120.30
49	QO	65	ARG	CG-CD-NE	12.02	137.04	111.80
39	QE	143	ARG	NE-CZ-NH1	11.77	126.19	120.30
25	R0	55	ARG	NE-CZ-NH2	-11.70	114.45	120.30
4	RA	1064	C	N1-C2-O2	11.52	125.81	118.90
19	YU	101	ARG	NE-CZ-NH2	-11.49	114.55	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	RV	21	ARG	CG-CD-NE	11.47	135.90	111.80
4	RA	2603	G	OP1-P-OP2	11.45	136.78	119.60
6	YD	69	ARG	NE-CZ-NH1	-11.36	114.62	120.30
35	QA	1409	C	N1-C2-O2	11.11	125.57	118.90
19	RU	112	ARG	NE-CZ-NH1	11.07	125.84	120.30
43	QI	93	ARG	CG-CD-NE	11.05	135.00	111.80
11	YI	50	ARG	CG-CD-NE	-11.04	88.61	111.80
10	YH	3	ARG	NE-CZ-NH1	-10.90	114.85	120.30
10	YH	3	ARG	CB-CG-CD	10.73	139.50	111.60
35	QA	576	G	OP2-P-O3'	-10.63	81.82	105.20
36	QB	226	ARG	NE-CZ-NH1	10.48	125.54	120.30
35	QA	576	G	OP1-P-O3'	-10.47	82.17	105.20
43	QI	93	ARG	NE-CZ-NH1	-10.29	115.15	120.30
49	QO	38	ARG	CA-CB-CG	10.12	135.66	113.40
27	Y2	7	ARG	NE-CZ-NH1	-10.12	115.24	120.30
33	R8	13	ARG	NE-CZ-NH1	10.11	125.35	120.30
41	XG	10	ARG	NE-CZ-NH2	-9.83	115.39	120.30
8	RF	38	ARG	NE-CZ-NH1	9.79	125.19	120.30
4	YA	1075	C	N1-C2-O2	9.75	124.75	118.90
49	QO	65	ARG	NE-CZ-NH1	-9.73	115.43	120.30
1	QV	54	U	O5'-P-OP1	-9.72	96.96	105.70
6	YD	103	ARG	NE-CZ-NH1	9.67	125.14	120.30
1	QV	53	G	O4'-C1'-N9	9.62	115.90	108.20
14	YP	55	ARG	NE-CZ-NH1	9.62	125.11	120.30
20	YV	21	ARG	CG-CD-NE	9.60	131.96	111.80
18	YT	53	ARG	NE-CZ-NH2	-9.52	115.54	120.30
33	R8	13	ARG	NE-CZ-NH2	-9.48	115.56	120.30
17	YS	67	ARG	CA-CB-CG	-9.43	92.67	113.40
24	RZ	103	ARG	CD-NE-CZ	9.38	136.74	123.60
4	RA	1075	C	N1-C2-O2	9.34	124.50	118.90
29	R4	13	ARG	CG-CD-NE	9.23	131.18	111.80
4	YA	1052	C	C2-N1-C1'	9.17	128.89	118.80
14	RP	55	ARG	NE-CZ-NH1	9.14	124.87	120.30
35	QA	1409	C	N3-C2-O2	-9.03	115.58	121.90
3	QY	278	ARG	CA-CB-CG	9.03	133.26	113.40
25	R0	55	ARG	CD-NE-CZ	8.98	136.17	123.60
34	R9	35	ARG	CB-CG-CD	8.98	134.95	111.60
49	QO	38	ARG	NE-CZ-NH1	8.95	124.78	120.30
4	YA	2128	C	C2-N1-C1'	8.77	128.45	118.80
36	QB	226	ARG	CG-CD-NE	8.73	130.13	111.80
37	XC	30	ARG	CG-CD-NE	8.72	130.11	111.80
31	R6	28	ARG	NE-CZ-NH2	-8.69	115.95	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	R9	35	ARG	NE-CZ-NH2	-8.69	115.96	120.30
4	RA	1052	C	C2-N1-C1'	8.67	128.34	118.80
50	XP	71	ARG	CA-CB-CG	8.65	132.43	113.40
3	QY	203	ARG	NE-CZ-NH1	8.62	124.61	120.30
36	QB	155	LEU	CB-CG-CD2	-8.59	96.40	111.00
7	YE	82	ARG	NE-CZ-NH1	8.57	124.58	120.30
4	RA	2128	C	C2-N1-C1'	8.51	128.16	118.80
42	XH	18	ARG	NE-CZ-NH2	8.44	124.52	120.30
8	RF	38	ARG	NE-CZ-NH2	-8.43	116.08	120.30
25	R0	55	ARG	NE-CZ-NH1	8.40	124.50	120.30
4	RA	1087	G	C8-N9-C1'	8.33	137.83	127.00
27	Y2	7	ARG	CG-CD-NE	8.32	129.28	111.80
38	QD	168	ARG	CG-CD-NE	-8.24	94.49	111.80
4	YA	1087	G	C8-N9-C1'	8.23	137.70	127.00
53	QS	28	LYS	CB-CG-CD	8.22	132.98	111.60
4	RA	1087	G	C4-N9-C1'	-8.22	115.81	126.50
4	YA	1087	G	C4-N9-C1'	-8.22	115.82	126.50
42	XH	84	ARG	NE-CZ-NH1	-8.18	116.21	120.30
44	QJ	45	ARG	NE-CZ-NH2	8.13	124.36	120.30
4	YA	1087	G	N3-C4-N9	-8.10	121.14	126.00
4	RA	1087	G	N3-C4-N9	-8.07	121.16	126.00
23	YY	23	ARG	NE-CZ-NH2	-8.05	116.28	120.30
36	QB	226	ARG	NE-CZ-NH2	-8.02	116.29	120.30
21	RW	11	ARG	NE-CZ-NH2	-8.02	116.29	120.30
21	YW	11	ARG	NE-CZ-NH2	-7.99	116.30	120.30
29	R4	13	ARG	CD-NE-CZ	7.99	134.78	123.60
26	Y1	52	ARG	NE-CZ-NH2	-7.99	116.31	120.30
36	XB	155	LEU	CA-CB-CG	7.99	133.66	115.30
44	QJ	45	ARG	CA-CB-CG	7.98	130.96	113.40
29	R4	13	ARG	CA-CB-CG	7.95	130.90	113.40
6	YD	211	ARG	CG-CD-NE	7.95	128.49	111.80
21	YW	11	ARG	NE-CZ-NH1	7.92	124.26	120.30
38	QD	168	ARG	CA-CB-CG	-7.90	96.03	113.40
21	RW	11	ARG	CG-CD-NE	7.89	128.36	111.80
36	QB	155	LEU	CA-CB-CG	7.86	133.38	115.30
24	RZ	103	ARG	NE-CZ-NH1	-7.84	116.38	120.30
19	YU	101	ARG	CD-NE-CZ	7.81	134.53	123.60
4	RA	2602	A	OP2-P-O3'	-7.80	88.04	105.20
3	QY	256	ARG	NE-CZ-NH1	-7.79	116.41	120.30
35	XA	442	C	C2-N1-C1'	7.77	127.35	118.80
14	YP	55	ARG	NE-CZ-NH2	-7.77	116.42	120.30
6	RD	14	ARG	NE-CZ-NH2	7.77	124.18	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	XY	332	ARG	CB-CG-CD	-7.76	91.43	111.60
35	QA	1022	G	C6-C5-N7	-7.72	125.77	130.40
4	YA	1531	C	C5-C6-N1	7.68	124.84	121.00
14	RP	55	ARG	NE-CZ-NH2	-7.64	116.48	120.30
35	XA	961	U	N1-C2-N3	7.63	119.48	114.90
20	RV	75	PHE	CB-CG-CD1	7.62	126.13	120.80
3	XY	278	ARG	NE-CZ-NH2	-7.62	116.49	120.30
42	XH	18	ARG	NE-CZ-NH1	-7.58	116.51	120.30
30	R5	19	ARG	CG-CD-NE	-7.58	95.89	111.80
11	YI	50	ARG	NE-CZ-NH1	-7.56	116.52	120.30
4	RA	1092	C	N1-C2-O2	7.55	123.43	118.90
12	RN	83	LYS	CD-CE-NZ	-7.54	94.35	111.70
4	RA	1075	C	N3-C2-O2	-7.54	116.62	121.90
44	QJ	45	ARG	NE-CZ-NH1	-7.53	116.53	120.30
4	YA	1092	C	N1-C2-O2	7.53	123.42	118.90
4	RA	1531	C	C5-C6-N1	7.52	124.76	121.00
4	YA	1092	C	C2-N1-C1'	7.51	127.06	118.80
24	YZ	20	ARG	NE-CZ-NH2	-7.50	116.55	120.30
4	RA	1530	C	C2-N1-C1'	7.50	127.05	118.80
4	YA	1075	C	N3-C2-O2	-7.50	116.65	121.90
35	XA	1003	G	N7-C8-N9	7.49	116.85	113.10
4	RA	1092	C	C2-N1-C1'	7.48	127.03	118.80
11	YI	68	LEU	CA-CB-CG	7.48	132.50	115.30
35	QA	78	G	N3-C4-N9	-7.46	121.52	126.00
42	QH	14	ARG	CD-NE-CZ	7.45	134.03	123.60
21	RW	11	ARG	NE-CZ-NH1	7.45	124.02	120.30
4	YA	1530	C	C2-N1-C1'	7.45	126.99	118.80
48	QN	31	ARG	NE-CZ-NH2	-7.41	116.59	120.30
4	YA	1097	U	C2-N1-C1'	7.39	126.57	117.70
35	QA	577	G	OP1-P-OP2	7.36	130.63	119.60
35	QA	1022	G	N9-C4-C5	-7.35	102.46	105.40
18	RT	53	ARG	CB-CG-CD	7.31	130.62	111.60
36	XB	217	ARG	CD-NE-CZ	7.31	133.84	123.60
24	YZ	44	PHE	CB-CG-CD1	7.27	125.89	120.80
4	YA	512	G	O4'-C1'-N9	7.27	114.02	108.20
34	R9	35	ARG	NE-CZ-NH1	7.26	123.93	120.30
35	XA	1158	C	C2-N1-C1'	7.26	126.78	118.80
24	RZ	103	ARG	CA-CB-CG	7.26	129.37	113.40
48	QN	31	ARG	NE-CZ-NH1	-7.24	116.68	120.30
7	YE	52	LEU	CA-CB-CG	7.24	131.94	115.30
36	XB	144	ARG	CA-CB-CG	7.22	129.28	113.40
16	RR	86	ARG	CG-CD-NE	7.21	126.95	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	RU	112	ARG	CB-CG-CD	-7.17	92.97	111.60
36	XB	28	PHE	CB-CG-CD2	-7.16	115.79	120.80
36	XB	155	LEU	CB-CG-CD2	-7.15	98.84	111.00
19	RU	112	ARG	CG-CD-NE	7.15	126.81	111.80
31	R6	28	ARG	CA-CB-CG	7.14	129.10	113.40
35	XA	1003	G	C8-N9-C4	-7.12	103.55	106.40
4	YA	1531	C	C2-N1-C1'	7.12	126.63	118.80
14	RP	147	LEU	CA-CB-CG	7.10	131.62	115.30
35	XA	1003	G	C4-N9-C1'	7.08	135.70	126.50
38	QD	168	ARG	CB-CG-CD	7.07	129.99	111.60
36	QB	111	ARG	CA-CB-CG	7.07	128.95	113.40
39	QE	143	ARG	NE-CZ-NH2	-7.07	116.77	120.30
26	Y1	26	ARG	NE-CZ-NH2	-7.06	116.77	120.30
49	QO	65	ARG	NE-CZ-NH2	7.05	123.83	120.30
29	R4	13	ARG	CB-CG-CD	7.04	129.89	111.60
11	RI	68	LEU	CA-CB-CG	7.03	131.47	115.30
4	RA	1097	U	C2-N1-C1'	7.03	126.13	117.70
31	R6	28	ARG	CG-CD-NE	-7.02	97.05	111.80
36	XB	144	ARG	CD-NE-CZ	7.01	133.41	123.60
41	XG	32	ARG	CG-CD-NE	-7.01	97.08	111.80
32	R7	33	ARG	NE-CZ-NH2	-7.01	116.80	120.30
25	Y0	14	ARG	CB-CG-CD	6.99	129.76	111.60
35	XA	1028	C	C2-N1-C1'	-6.98	111.12	118.80
3	QY	278	ARG	CB-CG-CD	-6.98	93.46	111.60
35	XA	1158	C	N1-C2-O2	6.97	123.08	118.90
4	YA	1052	C	C6-N1-C1'	-6.96	112.45	120.80
29	Y4	46	GLN	CG-CD-OE1	-6.96	107.69	121.60
41	XG	155	ARG	NE-CZ-NH2	6.93	123.76	120.30
35	XA	266	G	P-O3'-C3'	6.92	128.01	119.70
35	QA	78	G	C8-N9-C1'	6.92	136.00	127.00
25	R0	14	ARG	CB-CG-CD	6.91	129.57	111.60
35	XA	961	U	C2-N3-C4	-6.91	122.86	127.00
35	QA	78	G	C4-N9-C1'	-6.91	117.52	126.50
4	RA	1531	C	C2-N1-C1'	6.91	126.40	118.80
27	Y2	7	ARG	CB-CG-CD	6.90	129.54	111.60
19	YU	112	ARG	NE-CZ-NH2	6.89	123.75	120.30
53	XS	78	ARG	NE-CZ-NH2	-6.89	116.85	120.30
54	XT	89	ARG	NE-CZ-NH1	6.89	123.75	120.30
19	YU	101	ARG	CB-CG-CD	6.89	129.51	111.60
6	YD	176	ARG	CG-CD-NE	6.86	126.20	111.80
19	YU	101	ARG	CG-CD-NE	6.84	126.16	111.80
48	XN	31	ARG	CG-CD-NE	6.82	126.12	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	QC	190	ARG	NE-CZ-NH2	-6.78	116.91	120.30
4	RA	1313	U	C2-N1-C1'	6.77	125.83	117.70
9	RG	21	ARG	CB-CG-CD	-6.76	94.02	111.60
23	YY	23	ARG	CD-NE-CZ	6.76	133.06	123.60
4	RA	2160	G	N3-C4-N9	-6.75	121.95	126.00
36	QB	226	ARG	CD-NE-CZ	6.74	133.04	123.60
4	RA	1038	C	C2-N1-C1'	6.69	126.16	118.80
16	RR	17	ARG	CB-CG-CD	-6.68	94.23	111.60
35	QA	1022	G	C4-C5-N7	6.66	113.46	110.80
4	YA	1092	C	C5-C6-N1	6.65	124.32	121.00
35	XA	1028	C	C6-N1-C1'	6.65	128.78	120.80
4	YA	2160	G	N3-C4-N9	-6.65	122.01	126.00
7	YE	82	ARG	NE-CZ-NH2	-6.64	116.98	120.30
4	YA	847	U	C2-N1-C1'	6.64	125.67	117.70
4	YA	2128	C	C6-N1-C1'	-6.63	112.84	120.80
4	RA	1052	C	C6-N1-C1'	-6.61	112.86	120.80
15	RQ	5	ARG	NE-CZ-NH2	6.60	123.60	120.30
37	XC	131	ARG	NE-CZ-NH1	-6.60	117.00	120.30
3	QY	203	ARG	NE-CZ-NH2	-6.60	117.00	120.30
32	Y7	35	ARG	NE-CZ-NH1	6.59	123.59	120.30
12	RN	121	LYS	CG-CD-CE	6.58	131.62	111.90
1	QV	53	G	OP1-P-O3'	6.57	119.66	105.20
35	XA	1183	A	P-O3'-C3'	6.56	127.57	119.70
36	QB	28	PHE	CB-CG-CD2	-6.54	116.22	120.80
37	XC	30	ARG	NE-CZ-NH1	-6.54	117.03	120.30
24	YZ	44	PHE	CB-CG-CD2	-6.52	116.23	120.80
54	XT	89	ARG	NE-CZ-NH2	-6.52	117.04	120.30
45	XK	96	ARG	NE-CZ-NH2	-6.50	117.05	120.30
36	XB	144	ARG	NE-CZ-NH1	6.50	123.55	120.30
4	YA	1313	U	C2-N1-C1'	6.49	125.48	117.70
26	Y1	56	GLN	CA-CB-CG	6.45	127.58	113.40
52	QR	42	ARG	NE-CZ-NH1	-6.45	117.08	120.30
40	QF	46	ARG	NE-CZ-NH2	-6.44	117.08	120.30
41	XG	32	ARG	NE-CZ-NH1	-6.44	117.08	120.30
35	XA	1003	G	N3-C4-C5	-6.44	125.38	128.60
19	RU	117	GLN	CA-CB-CG	6.43	127.56	113.40
42	QH	14	ARG	CB-CG-CD	6.42	128.30	111.60
35	XA	754	C	C2-N1-C1'	6.42	125.86	118.80
10	YH	3	ARG	CA-CB-CG	6.41	127.51	113.40
35	QA	78	G	C6-C5-N7	6.38	134.23	130.40
35	QA	1022	G	N1-C6-O6	6.37	123.72	119.90
4	YA	1102	C	C2-N1-C1'	6.36	125.80	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	QA	1022	G	N3-C4-N9	6.36	129.82	126.00
4	RA	2128	C	C6-N1-C1'	-6.36	113.17	120.80
35	QA	1022	G	C8-N9-C1'	-6.35	118.74	127.00
30	R5	19	ARG	NE-CZ-NH2	-6.35	117.12	120.30
4	YA	1714	G	N3-C2-N2	-6.35	115.45	119.90
4	YA	1097	U	N1-C2-O2	6.34	127.24	122.80
16	RR	47	PHE	CB-CG-CD2	-6.34	116.36	120.80
1	XV	53	G	OP1-P-O3'	6.34	119.14	105.20
4	RA	1087	G	C6-C5-N7	6.33	134.20	130.40
32	Y7	35	ARG	NE-CZ-NH2	-6.31	117.15	120.30
35	QA	1030(C)	C	C2-N1-C1'	6.30	125.73	118.80
3	QY	96	PHE	CB-CG-CD2	-6.30	116.39	120.80
16	YR	13	HIS	CB-CA-C	6.29	122.99	110.40
26	Y1	52	ARG	NE-CZ-NH1	6.29	123.44	120.30
3	XY	96	PHE	CB-CG-CD2	-6.28	116.40	120.80
4	YA	277	C	N1-C2-O2	6.26	122.66	118.90
4	RA	1064	C	C2-N1-C1'	6.26	125.69	118.80
52	QR	32	ARG	NE-CZ-NH1	-6.26	117.17	120.30
24	YZ	20	ARG	NE-CZ-NH1	6.26	123.43	120.30
8	YF	191	ARG	NE-CZ-NH1	-6.25	117.17	120.30
36	XB	105	PHE	CB-CG-CD1	6.25	125.18	120.80
4	RA	1102	C	C2-N1-C1'	6.25	125.68	118.80
4	RA	847	U	C2-N1-C1'	6.24	125.19	117.70
4	RA	1073	A	C6-N1-C2	6.22	122.33	118.60
4	RA	1064	C	C5-C6-N1	6.22	124.11	121.00
35	XA	961	U	N3-C2-O2	-6.21	117.85	122.20
19	RU	92	ARG	CD-NE-CZ	6.21	132.29	123.60
4	RA	1073	A	N1-C2-N3	-6.20	126.20	129.30
24	YZ	156	LYS	C-N-CA	-6.20	106.21	121.70
45	XK	126	ARG	NE-CZ-NH1	6.19	123.39	120.30
4	YA	1087	G	C6-C5-N7	6.18	134.11	130.40
37	XC	140	ARG	CB-CG-CD	-6.17	95.56	111.60
35	QA	442	C	C2-N1-C1'	6.17	125.59	118.80
26	R1	52	ARG	NE-CZ-NH1	6.17	123.39	120.30
4	RA	1063	G	C8-N9-C1'	6.16	135.01	127.00
3	QY	295	LEU	CA-CB-CG	6.15	129.45	115.30
20	RV	75	PHE	CB-CG-CD2	-6.14	116.50	120.80
45	QK	96	ARG	CG-CD-NE	-6.13	98.92	111.80
15	RQ	69	PHE	CB-CG-CD2	-6.13	116.51	120.80
10	YH	3	ARG	NE-CZ-NH2	6.10	123.35	120.30
9	RG	16	ARG	NE-CZ-NH1	6.10	123.35	120.30
15	YQ	57	HIS	CB-CA-C	-6.10	98.20	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	YV	21	ARG	NE-CZ-NH1	-6.10	117.25	120.30
41	XG	16	LEU	CB-CG-CD2	6.09	121.36	111.00
4	RA	512	G	O4'-C1'-N9	6.09	113.07	108.20
4	YA	1097	U	N3-C2-O2	-6.09	117.94	122.20
16	YR	17	ARG	CB-CG-CD	-6.09	95.77	111.60
35	XA	1183	A	OP1-P-O3'	6.07	118.56	105.20
16	RR	47	PHE	CB-CG-CD1	6.07	125.05	120.80
4	RA	1064	C	C2-N3-C4	6.05	122.93	119.90
4	RA	1102	C	C6-N1-C2	-6.05	117.88	120.30
48	XN	31	ARG	CA-CB-CG	6.04	126.69	113.40
4	RA	1082	U	C2-N1-C1'	6.04	124.95	117.70
32	R7	29	LYS	CD-CE-NZ	-6.03	97.83	111.70
10	RH	101	ARG	NE-CZ-NH1	-6.03	117.29	120.30
36	QB	17	PHE	CB-CG-CD2	-6.02	116.59	120.80
4	YA	2792	G	N3-C4-N9	6.01	129.61	126.00
4	RA	1530	C	C6-N1-C1'	-6.01	113.59	120.80
4	YA	1058	G	N3-C4-N9	-5.99	122.41	126.00
35	XA	442	C	C6-N1-C1'	-5.98	113.62	120.80
41	QG	16	LEU	CB-CG-CD2	5.97	121.15	111.00
4	YA	1082	U	C2-N1-C1'	5.97	124.86	117.70
11	YI	61	ARG	CG-CD-NE	-5.97	99.27	111.80
21	YW	11	ARG	CG-CD-NE	5.97	124.33	111.80
4	RA	1712	C	N3-C2-O2	-5.95	117.73	121.90
4	YA	1063	G	C8-N9-C1'	5.95	134.73	127.00
11	YI	61	ARG	CA-CB-CG	-5.94	100.33	113.40
4	YA	1092	C	C6-N1-C2	-5.93	117.93	120.30
29	Y4	46	GLN	CA-CB-CG	-5.93	100.35	113.40
4	RA	2792	G	C6-C5-N7	-5.93	126.84	130.40
4	RA	1076	C	OP1-P-O3'	5.92	118.23	105.20
35	XA	530	G	C5-C6-O6	-5.92	125.05	128.60
18	YT	53	ARG	CB-CG-CD	5.92	126.98	111.60
46	QL	33	ARG	CG-CD-NE	5.91	124.22	111.80
4	RA	2792	G	N1-C6-O6	5.91	123.45	119.90
4	YA	1530	C	C6-N1-C1'	-5.89	113.73	120.80
35	XA	1045	C	C2-N1-C1'	5.89	125.28	118.80
35	QA	1022	G	C4-N9-C1'	5.88	134.14	126.50
15	RQ	69	PHE	CB-CG-CD1	5.87	124.91	120.80
4	RA	1314	C	C2-N1-C1'	5.87	125.26	118.80
4	YA	1038	C	C2-N1-C1'	5.86	125.24	118.80
4	YA	2103	C	N1-C2-O2	5.86	122.42	118.90
12	YN	67	LEU	CA-CB-CG	5.86	128.77	115.30
8	RF	24	LEU	CA-CB-CG	5.86	128.77	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	QB	17	PHE	CB-CG-CD1	5.85	124.89	120.80
48	QN	31	ARG	NH1-CZ-NH2	5.84	125.83	119.40
4	YA	1063	G	N3-C4-N9	-5.83	122.50	126.00
4	RA	1064	C	N3-C2-O2	-5.83	117.81	121.90
4	YA	1314	C	C2-N1-C1'	5.83	125.22	118.80
4	YA	1075	C	C6-N1-C2	-5.83	117.97	120.30
18	YT	45	PHE	CB-CG-CD2	-5.81	116.73	120.80
4	RA	1063	G	N3-C4-N9	-5.81	122.51	126.00
38	QD	185	PHE	CB-CG-CD2	-5.80	116.74	120.80
4	RA	2792	G	N3-C4-N9	5.79	129.48	126.00
4	YA	1076	C	OP1-P-O3'	5.79	117.93	105.20
46	XL	86	ARG	CG-CD-NE	5.78	123.94	111.80
16	RR	86	ARG	NE-CZ-NH2	-5.78	117.41	120.30
35	QA	993	G	N3-C4-N9	5.78	129.47	126.00
4	RA	1530	C	P-O3'-C3'	5.77	126.63	119.70
34	R9	35	ARG	CD-NE-CZ	5.76	131.67	123.60
51	XQ	26	GLN	CA-CB-CG	5.76	126.06	113.40
35	QA	1030(C)	C	N1-C2-O2	5.75	122.35	118.90
4	RA	1097	U	N1-C2-O2	5.75	126.83	122.80
13	RO	64	ARG	CB-CG-CD	-5.74	96.67	111.60
18	RT	45	PHE	CB-CG-CD2	-5.74	116.78	120.80
48	QN	36	PHE	CB-CG-CD2	-5.74	116.78	120.80
35	XA	1158	C	N3-C2-O2	-5.73	117.89	121.90
32	Y7	33	ARG	CB-CG-CD	-5.73	96.71	111.60
18	RT	53	ARG	NE-CZ-NH2	-5.73	117.44	120.30
10	YH	3	ARG	CB-CA-C	5.72	121.85	110.40
11	YI	114	LEU	CA-CB-CG	5.72	128.46	115.30
42	XH	84	ARG	NE-CZ-NH2	5.72	123.16	120.30
4	YA	2160	G	C8-N9-C1'	5.71	134.43	127.00
39	QE	143	ARG	CD-NE-CZ	5.69	131.56	123.60
24	RZ	103	ARG	CG-CD-NE	5.69	123.74	111.80
4	RA	2138	C	N1-C2-O2	5.68	122.31	118.90
36	XB	111	ARG	CA-CB-CG	5.68	125.90	113.40
4	RA	1092	C	N3-C2-O2	-5.68	117.93	121.90
36	XB	105	PHE	CB-CG-CD2	-5.67	116.83	120.80
4	YA	2138	C	N1-C2-O2	5.66	122.30	118.90
16	RR	86	ARG	NE-CZ-NH1	5.66	123.13	120.30
49	QO	7	GLU	CA-CB-CG	5.66	125.84	113.40
3	QY	213	ARG	NE-CZ-NH2	-5.65	117.48	120.30
37	XC	140	ARG	NE-CZ-NH1	5.65	123.12	120.30
4	RA	2128	C	N1-C2-O2	5.65	122.29	118.90
23	YY	23	ARG	CG-CD-NE	5.64	123.65	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	RA	1992	G	P-O3'-C3'	5.64	126.47	119.70
48	QN	36	PHE	CB-CG-CD1	5.63	124.74	120.80
7	YE	52	LEU	CB-CG-CD2	5.63	120.57	111.00
4	RA	2160	G	C8-N9-C1'	5.62	134.31	127.00
4	YA	196	A	O4'-C1'-N9	5.62	112.70	108.20
4	YA	2128	C	N1-C2-O2	5.62	122.27	118.90
49	QO	65	ARG	N-CA-CB	-5.62	100.49	110.60
49	XO	7	GLU	CA-CB-CG	5.62	125.75	113.40
4	YA	1052	C	N1-C2-O2	5.61	122.26	118.90
8	YF	99	TYR	CB-CG-CD2	-5.61	117.64	121.00
52	QR	42	ARG	CA-CB-CG	5.61	125.73	113.40
40	QF	19	LEU	CB-CG-CD1	-5.59	101.49	111.00
4	RA	1092	C	C5-C6-N1	5.59	123.80	121.00
4	YA	1530	C	P-O3'-C3'	5.59	126.41	119.70
4	RA	1073	A	N9-C4-C5	-5.59	103.56	105.80
26	R1	52	ARG	CA-CB-CG	5.59	125.69	113.40
4	RA	1714	G	N3-C2-N2	-5.58	115.99	119.90
4	RA	1087	G	N9-C4-C5	5.58	107.63	105.40
32	Y7	34	ARG	NE-CZ-NH1	-5.58	117.51	120.30
17	RS	17	ARG	NE-CZ-NH1	-5.57	117.52	120.30
25	Y0	14	ARG	NE-CZ-NH2	-5.56	117.52	120.30
4	YA	1992	G	P-O3'-C3'	5.56	126.37	119.70
40	XF	97	PHE	CB-CG-CD2	-5.56	116.91	120.80
4	YA	1102	C	C6-N1-C2	-5.56	118.08	120.30
4	YA	1075	C	C5-C6-N1	5.55	123.78	121.00
4	YA	277	C	C2-N1-C1'	5.55	124.91	118.80
11	RI	68	LEU	CB-CG-CD2	-5.55	101.57	111.00
36	XB	28	PHE	CB-CG-CD1	5.55	124.68	120.80
18	RT	96	ARG	NE-CZ-NH1	-5.55	117.53	120.30
4	RA	154(B)	C	C2-N1-C1'	5.54	124.89	118.80
4	YA	1087	G	N3-C4-C5	5.53	131.37	128.60
17	RS	7	TYR	CA-CB-CG	5.53	123.91	113.40
3	XY	96	PHE	CB-CG-CD1	5.53	124.67	120.80
4	RA	2735	G	N3-C2-N2	-5.53	116.03	119.90
1	QV	62	C	C6-N1-C2	-5.52	118.09	120.30
4	RA	1097	U	N3-C2-O2	-5.51	118.34	122.20
38	XD	185	PHE	CB-CG-CD2	-5.51	116.94	120.80
38	QD	135	LEU	CB-CG-CD2	-5.51	101.63	111.00
39	QE	143	ARG	CG-CD-NE	-5.51	100.23	111.80
4	RA	2602	A	O3'-P-O5'	5.50	114.45	104.00
25	R0	14	ARG	NE-CZ-NH2	-5.50	117.55	120.30
4	RA	1036	G	C8-N9-C1'	5.50	134.15	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	YA	873	G	N3-C4-N9	-5.49	122.71	126.00
4	YA	1530	C	N1-C2-O2	5.49	122.19	118.90
4	RA	1092	C	C6-N1-C2	-5.48	118.11	120.30
53	XS	10	PHE	CB-CG-CD2	-5.48	116.97	120.80
35	QA	754	C	C2-N1-C1'	5.48	124.82	118.80
15	RQ	14	ARG	NE-CZ-NH1	-5.47	117.56	120.30
4	RA	1058	G	N3-C4-N9	-5.46	122.72	126.00
4	YA	2896	C	C2-N1-C1'	5.46	124.81	118.80
6	YD	103	ARG	NE-CZ-NH2	-5.45	117.57	120.30
35	XA	1006	C	N1-C2-O2	-5.45	115.63	118.90
4	YA	2160	G	C4-N9-C1'	-5.45	119.42	126.50
35	XA	1158	C	C6-N1-C2	-5.45	118.12	120.30
40	QF	46	ARG	NE-CZ-NH1	5.43	123.02	120.30
18	YT	61	PHE	CB-CG-CD2	-5.43	117.00	120.80
18	RT	45	PHE	CB-CG-CD1	5.43	124.60	120.80
35	XA	1054	C	N1-C2-O2	5.42	122.16	118.90
4	RA	2127	G	C6-C5-N7	-5.42	127.15	130.40
29	Y4	60	GLN	N-CA-C	5.42	125.63	111.00
13	YO	3	GLN	CA-CB-CG	5.42	125.31	113.40
48	XN	31	ARG	CB-CA-C	5.42	121.23	110.40
4	RA	2128	C	C6-N1-C2	-5.41	118.14	120.30
17	YS	7	TYR	CA-CB-CG	5.41	123.68	113.40
42	QH	18	ARG	NE-CZ-NH2	-5.41	117.60	120.30
4	RA	1075	C	C6-N1-C2	-5.40	118.14	120.30
50	XP	16	HIS	N-CA-CB	5.40	120.32	110.60
49	QO	65	ARG	CA-CB-CG	5.40	125.28	113.40
17	YS	94	TYR	CB-CG-CD2	-5.40	117.76	121.00
3	XY	302	LYS	CD-CE-NZ	-5.39	99.29	111.70
18	RT	61	PHE	CB-CG-CD2	-5.39	117.03	120.80
18	YT	45	PHE	CB-CG-CD1	5.38	124.57	120.80
18	YT	22	PHE	CB-CG-CD2	-5.38	117.03	120.80
19	RU	101	ARG	CA-CB-CG	5.38	125.23	113.40
54	XT	56	MET	CG-SD-CE	-5.38	91.60	100.20
4	RA	2896	C	C2-N1-C1'	5.38	124.71	118.80
36	QB	157	ARG	CB-CG-CD	-5.37	97.64	111.60
35	QA	266	G	P-O3'-C3'	5.37	126.14	119.70
13	RO	8	LEU	CA-CB-CG	5.37	127.64	115.30
35	QA	191	G	N3-C4-N9	5.36	129.22	126.00
53	XS	10	PHE	CB-CG-CD1	5.36	124.55	120.80
15	RQ	5	ARG	NE-CZ-NH1	-5.36	117.62	120.30
36	QB	76	GLN	CA-CB-CG	5.36	125.18	113.40
4	YA	1092	C	N3-C2-O2	-5.35	118.15	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	XA	1004	A	O4'-C1'-N9	5.35	112.48	108.20
4	YA	1102	C	C5-C6-N1	5.35	123.67	121.00
35	XA	266	G	OP2-P-O3'	5.34	116.96	105.20
4	RA	2160	G	C4-N9-C1'	-5.34	119.55	126.50
4	YA	361	G	N3-C2-N2	-5.34	116.16	119.90
13	YO	8	LEU	CA-CB-CG	5.34	127.58	115.30
3	XY	222	VAL	C-N-CA	5.34	135.04	121.70
3	QY	278	ARG	N-CA-CB	-5.33	101.00	110.60
4	YA	2792	G	C8-N9-C1'	-5.33	120.06	127.00
38	QD	59	ARG	CA-CB-CG	5.33	125.14	113.40
35	QA	570	G	C4-N9-C1'	5.33	133.43	126.50
35	XA	442	C	N1-C2-O2	5.33	122.10	118.90
4	YA	1052	C	C5-C6-N1	5.33	123.67	121.00
1	XV	53	G	P-O3'-C3'	5.33	126.09	119.70
4	YA	1712	C	N3-C2-O2	-5.32	118.17	121.90
4	RA	1775	U	C5-C4-O4	-5.32	122.71	125.90
3	XY	278	ARG	NE-CZ-NH1	5.31	122.96	120.30
35	XA	999	C	C2-N1-C1'	5.31	124.64	118.80
1	QV	53	G	C4-N9-C1'	-5.30	119.60	126.50
4	YA	1063	G	N1-C6-O6	-5.30	116.72	119.90
4	RA	1914	C	N1-C2-O2	5.30	122.08	118.90
4	RA	1530	C	N1-C2-O2	5.30	122.08	118.90
4	RA	1774	C	N3-C2-O2	-5.29	118.19	121.90
54	QT	24	LEU	CA-CB-CG	5.29	127.47	115.30
4	YA	1747(B)	G	N3-C2-N2	-5.29	116.20	119.90
4	YA	2128	C	C6-N1-C2	-5.29	118.19	120.30
4	YA	2792	G	C4-N9-C1'	5.29	133.38	126.50
4	RA	887	A	O4'-C1'-N9	5.29	112.43	108.20
3	XY	98	GLU	CA-CB-CG	5.28	125.02	113.40
6	YD	176	ARG	CB-CG-CD	-5.28	97.88	111.60
39	QE	126	ARG	NE-CZ-NH2	-5.28	117.66	120.30
12	YN	84	LYS	CA-CB-CG	5.27	124.99	113.40
6	YD	242	ARG	CG-CD-NE	5.26	122.85	111.80
39	XE	71	LEU	CB-CG-CD2	-5.26	102.06	111.00
4	RA	196	A	O4'-C1'-N9	5.25	112.40	108.20
4	YA	2287	A	O4'-C1'-N9	5.25	112.40	108.20
6	RD	242	ARG	CG-CD-NE	5.25	122.83	111.80
17	RS	25	ARG	NE-CZ-NH1	-5.25	117.67	120.30
29	Y4	48	ARG	NE-CZ-NH2	-5.25	117.67	120.30
8	RF	99	TYR	CB-CG-CD2	-5.25	117.85	121.00
4	YA	549	G	C6-C5-N7	-5.25	127.25	130.40
24	RZ	136	PHE	CB-CG-CD2	-5.25	117.13	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	YD	84	TYR	CA-CB-CG	5.24	123.36	113.40
4	RA	873	G	N3-C4-N9	-5.24	122.85	126.00
4	YA	1058	G	C8-N9-C1'	5.24	133.81	127.00
43	QI	88	TYR	CA-CB-CG	5.24	123.36	113.40
4	RA	1063	G	C4-N9-C1'	-5.24	119.69	126.50
4	YA	2121	G	N3-C4-N9	5.24	129.14	126.00
26	Y1	52	ARG	CA-CB-CG	5.23	124.90	113.40
4	YA	2792	G	C6-C5-N7	-5.22	127.27	130.40
4	RA	752	A	P-O3'-C3'	5.22	125.97	119.70
43	QI	33	PHE	CB-CG-CD1	5.22	124.45	120.80
29	Y4	46	GLN	CB-CA-C	5.21	120.83	110.40
4	YA	1087	G	N9-C4-C5	5.21	107.48	105.40
19	YU	37	GLU	CA-CB-CG	5.21	124.87	113.40
4	RA	1087	G	N3-C4-C5	5.21	131.21	128.60
35	QA	991	U	P-O3'-C3'	5.21	125.95	119.70
39	QE	126	ARG	NE-CZ-NH1	5.21	122.90	120.30
38	XD	59	ARG	CA-CB-CG	5.20	124.85	113.40
4	RA	1058	G	N3-C2-N2	-5.20	116.26	119.90
4	RA	1076	C	P-O3'-C3'	5.20	125.94	119.70
4	RA	1052	C	N1-C2-O2	5.20	122.02	118.90
4	RA	1531	C	C6-N1-C2	-5.19	118.22	120.30
4	YA	887	A	O4'-C1'-N9	5.19	112.35	108.20
4	YA	1065	U	O4'-C1'-N1	5.19	112.35	108.20
4	YA	2127	G	C6-C5-N7	-5.18	127.29	130.40
35	XA	1045	C	N1-C2-O2	5.18	122.01	118.90
4	YA	1063	G	C4-N9-C1'	-5.18	119.77	126.50
35	XA	1492	A	O4'-C1'-N9	-5.17	104.06	108.20
29	Y4	59	PHE	CB-CG-CD2	-5.17	117.18	120.80
35	QA	368	U	C2-N3-C4	-5.17	123.90	127.00
4	YA	2103	C	N3-C2-O2	-5.17	118.28	121.90
19	YU	101	ARG	CA-CB-CG	5.16	124.76	113.40
35	QA	1491	G	O4'-C1'-N9	5.16	112.33	108.20
46	XL	114	LYS	CG-CD-CE	5.16	127.38	111.90
22	RX	57	LEU	CA-CB-CG	5.16	127.16	115.30
35	QA	1043	C	C2-N1-C1'	-5.15	113.13	118.80
4	YA	549	G	N3-C4-N9	5.14	129.09	126.00
4	RA	2121	G	N3-C4-N9	5.14	129.09	126.00
4	YA	893	C	N1-C2-O2	5.13	121.98	118.90
35	XA	1065	U	P-O3'-C3'	5.13	125.86	119.70
42	QH	18	ARG	NE-CZ-NH1	5.12	122.86	120.30
4	RA	1063	G	N1-C6-O6	-5.11	116.83	119.90
35	QA	78	G	N9-C4-C5	5.10	107.44	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	QA	1065	U	P-O3'-C3'	5.10	125.82	119.70
4	RA	2103	C	N1-C2-O2	5.10	121.96	118.90
9	RG	170	ARG	NE-CZ-NH1	-5.10	117.75	120.30
4	YA	1073	A	N9-C4-C5	-5.10	103.76	105.80
12	YN	84	LYS	CD-CE-NZ	-5.09	99.99	111.70
48	XN	31	ARG	CB-CG-CD	5.09	124.84	111.60
31	R6	50	ARG	NE-CZ-NH1	-5.09	117.76	120.30
4	YA	1531	C	C6-N1-C2	-5.08	118.27	120.30
3	QY	96	PHE	CB-CG-CD1	5.08	124.36	120.80
35	QA	570	G	C8-N9-C1'	-5.07	120.40	127.00
36	XB	82	ARG	NE-CZ-NH2	-5.07	117.77	120.30
24	YZ	31	ARG	NE-CZ-NH1	-5.06	117.77	120.30
4	RA	2287	A	O4'-C1'-N9	5.06	112.24	108.20
4	YA	1774	C	N3-C2-O2	-5.05	118.36	121.90
14	YP	55	ARG	CB-CG-CD	-5.05	98.46	111.60
18	YT	96	ARG	NE-CZ-NH1	-5.05	117.78	120.30
35	XA	1003	G	N3-C4-N9	5.05	129.03	126.00
35	XA	5	U	N1-C2-O2	5.05	126.33	122.80
41	XG	155	ARG	NE-CZ-NH1	-5.05	117.78	120.30
4	RA	2792	G	C5-C6-O6	-5.05	125.57	128.60
49	XO	65	ARG	NE-CZ-NH2	-5.04	117.78	120.30
13	RO	64	ARG	CA-CB-CG	5.04	124.50	113.40
4	RA	1063	G	N9-C4-C5	5.04	107.42	105.40
3	XY	278	ARG	CD-NE-CZ	5.04	130.65	123.60
45	QK	96	ARG	CA-CB-CG	-5.04	102.32	113.40
4	RA	1058	G	C8-N9-C1'	5.04	133.55	127.00
41	XG	16	LEU	CA-CB-CG	5.03	126.88	115.30
4	YA	847	U	N1-C2-O2	5.03	126.32	122.80
4	RA	1102	C	C5-C6-N1	5.03	123.52	121.00
35	XA	560	U	C2-N1-C1'	5.03	123.73	117.70
4	RA	1065	U	P-O3'-C3'	5.03	125.73	119.70
35	XA	1033	G	N3-C4-N9	-5.02	122.99	126.00
4	RA	997	G	O5'-P-OP1	-5.02	101.18	105.70
35	QA	570	G	N3-C4-N9	5.01	129.01	126.00
4	YA	154(B)	C	C2-N1-C1'	5.01	124.31	118.80
4	RA	1747(B)	G	N3-C2-N2	-5.01	116.39	119.90

There are no chirality outliers.

All (25) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	QB	15	VAL	Peptide

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Mol	Chain	Res	Type	Group
36	QB	231	GLU	Peptide
37	QC	105	GLU	Peptide
44	QJ	60	ARG	Peptide
3	QY	115	PHE	Peptide
3	QY	201	LEU	Peptide
3	QY	48	ASN	Sidechain
25	R0	55	ARG	Sidechain
29	R4	12	ALA	Peptide
31	R6	28	ARG	Sidechain
34	R9	35	ARG	Sidechain
8	RF	74	ARG	Peptide
17	RS	58	LEU	Peptide
19	RU	117	GLN	Sidechain
36	XB	217	ARG	Sidechain
36	XB	7	VAL	Peptide
44	XJ	60	ARG	Peptide
45	XK	117	ASN	Peptide
46	XL	114	LYS	Mainchain
46	XL	86	ARG	Peptide
48	XN	30	ALA	Peptide
51	XQ	26	GLN	Sidechain
26	Y1	52	ARG	Sidechain
29	Y4	46	GLN	Mainchain
11	YI	84	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	QV	1644	0	836	29	0
1	XV	1644	0	836	19	0
2	QX	215	0	109	3	0
2	XX	215	0	108	6	0
3	QY	2833	0	2729	139	0
3	XY	2833	0	2729	155	0
4	RA	61758	0	31149	799	0
4	YA	61758	0	31152	795	0
5	RB	2572	0	1305	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	YB	2573	0	1306	17	0
6	RD	2131	0	2207	63	0
6	YD	2136	0	2217	65	0
7	RE	1559	0	1618	41	0
7	YE	1559	0	1618	43	0
8	RF	1584	0	1625	58	0
8	YF	1580	0	1619	68	0
9	RG	1426	0	1445	51	0
9	YG	1424	0	1441	60	0
10	RH	1330	0	1407	30	0
10	YH	1324	0	1402	43	0
11	RI	1094	0	1127	34	0
11	YI	1076	0	1094	24	0
12	RN	1121	0	1195	27	0
12	YN	1117	0	1184	22	0
13	RO	933	0	996	28	0
13	YO	933	0	996	26	0
14	RP	1135	0	1212	33	0
14	YP	1135	0	1212	44	0
15	RQ	1122	0	1179	45	0
15	YQ	1122	0	1179	38	0
16	RR	968	0	1033	32	0
16	YR	968	0	1033	21	0
17	RS	877	0	938	38	0
17	YS	870	0	923	41	0
18	RT	1091	0	1151	44	0
18	YT	1083	0	1136	54	0
19	RU	959	0	1019	31	0
19	YU	959	0	1019	27	0
20	RV	775	0	841	23	0
20	YV	771	0	830	21	0
21	RW	886	0	940	18	0
21	YW	886	0	940	21	0
22	RX	750	0	814	13	0
22	YX	750	0	814	8	0
23	RY	810	0	892	35	0
23	YY	810	0	887	34	0
24	RZ	1587	0	1598	48	0
24	YZ	1557	0	1564	53	0
25	R0	608	0	622	19	0
25	Y0	608	0	622	21	0
26	R1	754	0	823	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	Y1	759	0	837	27	0
27	R2	588	0	643	13	0
27	Y2	592	0	654	17	0
28	R3	469	0	518	8	0
28	Y3	464	0	514	5	0
29	R4	546	0	522	37	0
29	Y4	536	0	514	45	0
30	R5	459	0	476	13	0
30	Y5	455	0	465	9	0
31	R6	453	0	473	9	0
31	Y6	449	0	469	6	0
32	R7	418	0	467	16	0
32	Y7	418	0	467	11	0
33	R8	517	0	582	21	0
33	Y8	517	0	582	26	0
34	R9	307	0	335	9	0
34	Y9	307	0	335	6	0
35	QA	32246	0	16294	525	0
35	XA	32331	0	16339	485	0
36	QB	1842	0	1862	88	0
36	XB	1825	0	1828	104	0
37	QC	1558	0	1557	50	0
37	XC	1542	0	1517	49	0
38	QD	1665	0	1688	86	0
38	XD	1668	0	1704	75	0
39	QE	1133	0	1191	33	0
39	XE	1133	0	1191	41	0
40	QF	814	0	808	44	0
40	XF	816	0	808	32	0
41	QG	1235	0	1249	23	0
41	XG	1229	0	1238	34	0
42	QH	1098	0	1143	33	0
42	XH	1088	0	1126	28	0
43	QI	986	0	990	50	0
43	XI	966	0	953	65	0
44	QJ	719	0	672	35	0
44	XJ	710	0	661	27	0
45	QK	834	0	838	13	0
45	XK	833	0	836	21	0
46	QL	932	0	981	36	0
46	XL	932	0	981	31	0
47	QM	914	0	954	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	XM	895	0	920	34	0
48	QN	492	0	529	29	0
48	XN	492	0	529	16	0
49	QO	728	0	760	16	0
49	XO	728	0	760	17	0
50	QP	681	0	697	30	0
50	XP	677	0	686	33	0
51	QQ	823	0	891	22	0
51	XQ	823	0	891	18	0
52	QR	555	0	618	22	0
52	XR	555	0	618	20	0
53	QS	648	0	658	22	0
53	XS	645	0	635	27	0
54	QT	732	0	809	13	0
54	XT	733	0	795	16	0
55	QU	199	0	208	10	0
55	XU	199	0	208	5	0
56	QA	279	0	0	0	0
56	QB	1	0	0	0	0
56	QD	3	0	0	0	0
56	QE	2	0	0	0	0
56	QF	1	0	0	0	0
56	QG	3	0	0	0	0
56	QH	2	0	0	0	0
56	QI	1	0	0	0	0
56	QL	3	0	0	0	0
56	QM	1	0	0	0	0
56	QN	2	0	0	0	0
56	QO	1	0	0	0	0
56	QQ	2	0	0	0	0
56	QR	1	0	0	0	0
56	QT	1	0	0	0	0
56	QU	1	0	0	0	0
56	QV	2	0	0	0	0
56	QY	3	0	0	0	0
56	R0	4	0	0	0	0
56	R1	3	0	0	0	0
56	R3	2	0	0	0	0
56	R4	1	0	0	0	0
56	R5	3	0	0	0	0
56	R7	2	0	0	0	0
56	R8	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	R9	2	0	0	0	0
56	RA	1066	0	0	0	0
56	RB	29	0	0	0	0
56	RD	13	0	0	0	0
56	RE	6	0	0	0	0
56	RF	12	0	0	0	0
56	RG	4	0	0	0	0
56	RH	2	0	0	0	0
56	RN	3	0	0	0	0
56	RO	1	0	0	0	0
56	RP	2	0	0	0	0
56	RQ	4	0	0	0	0
56	RR	5	0	0	0	0
56	RT	3	0	0	0	0
56	RU	3	0	0	0	0
56	RV	4	0	0	0	0
56	RW	2	0	0	0	0
56	RX	1	0	0	0	0
56	RZ	1	0	0	0	0
56	XA	190	0	0	0	0
56	XE	2	0	0	0	0
56	XF	4	0	0	0	0
56	XH	1	0	0	0	0
56	XJ	1	0	0	0	0
56	XK	1	0	0	0	0
56	XL	1	0	0	0	0
56	XR	1	0	0	0	0
56	XT	1	0	0	0	0
56	XX	1	0	0	0	0
56	Y0	1	0	0	0	0
56	Y1	1	0	0	0	0
56	Y5	1	0	0	0	0
56	Y7	1	0	0	0	0
56	Y8	2	0	0	0	0
56	YA	760	0	0	0	0
56	YB	19	0	0	0	0
56	YD	10	0	0	0	0
56	YE	7	0	0	0	0
56	YF	3	0	0	0	0
56	YG	3	0	0	0	0
56	YI	1	0	0	0	0
56	YN	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	YO	1	0	0	0	0
56	YP	1	0	0	0	0
56	YQ	2	0	0	0	0
56	YR	1	0	0	0	0
56	YT	3	0	0	0	0
56	YV	1	0	0	0	0
56	YW	2	0	0	0	0
56	YX	1	0	0	0	0
57	QN	1	0	0	0	0
57	R4	1	0	0	0	0
57	R5	1	0	0	0	0
57	R6	1	0	0	0	0
57	R9	1	0	0	0	0
57	RY	1	0	0	0	0
57	XN	1	0	0	0	0
57	Y4	1	0	0	0	0
57	Y5	1	0	0	0	0
57	Y6	1	0	0	0	0
57	Y9	1	0	0	0	0
57	YY	1	0	0	0	0
58	QD	8	0	0	0	0
58	XD	8	0	0	0	0
All	All	296662	0	200145	5370	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (5370) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:RN:121:LYS:CE	12:RN:121:LYS:CD	1.75	1.59
4:YA:2012:G:OP1	21:YW:11:ARG:NH2	1.88	1.07
36:QB:15:VAL:HG23	36:QB:209:ARG:HB3	1.36	1.06
35:XA:1003:G:H2'	35:XA:1004:A:H4'	1.33	1.05
3:XY:281:HIS:HE1	4:YA:2493:U:H1'	1.22	1.04
4:RA:2012:G:OP1	21:RW:11:ARG:NH2	1.92	1.02
29:R4:67:TYR:HD1	29:R4:67:TYR:H	1.02	0.98
27:Y2:12:GLU:OE1	27:Y2:15:LYS:NZ	1.97	0.97
36:XB:111:ARG:HA	36:XB:111:ARG:HE	1.27	0.96
46:QL:33:ARG:HH11	46:QL:62:SER:HB3	1.28	0.96
47:XM:3:ARG:HG3	47:XM:8:GLU:HG3	1.48	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:YP:52:GLU:HB3	14:YP:55:ARG:HH11	1.32	0.95
29:Y4:59:PHE:HA	29:Y4:61:ARG:N	1.83	0.94
22:RX:60:ARG:HH12	32:R7:47:ARG:HH22	1.06	0.94
35:XA:407:G:H5''	38:XD:115:ARG:HG2	1.49	0.94
4:YA:2131:G:H5''	4:YA:2132:U:H5'	1.46	0.94
4:YA:2304:G:H22	4:YA:2312:U:H3	1.13	0.93
4:RA:2131:G:H5''	4:RA:2132:U:H5'	1.48	0.93
36:QB:82:ARG:NH1	36:QB:92:TYR:OH	2.01	0.93
43:QI:17:VAL:HG21	43:QI:81:ILE:HG22	1.50	0.93
3:XY:83:LEU:HD22	3:XY:99:ALA:HB2	1.50	0.93
40:QF:97:PHE:HB2	52:QR:32:ARG:HD2	1.46	0.92
15:RQ:21:THR:HG21	15:RQ:101:ARG:HB2	1.49	0.92
4:YA:1041:C:H42	4:YA:1114:G:H1	1.16	0.92
9:RG:41:GLN:HB3	9:RG:43:LEU:HD13	1.52	0.92
3:XY:338:THR:HG23	3:XY:339:GLY:HA2	1.51	0.92
19:YU:97:ASP:O	19:YU:101:ARG:HB3	1.68	0.91
36:QB:155:LEU:HD21	36:QB:159:PRO:HG3	1.51	0.91
53:XS:50:ALA:HB1	53:XS:57:HIS:HB3	1.51	0.90
35:XA:427:U:OP1	38:XD:13:ARG:NH2	2.04	0.90
38:XD:18:LYS:NZ	38:XD:31:CYS:SG	2.44	0.90
18:RT:55:ASN:H	18:RT:59:THR:HG22	1.36	0.90
25:R0:10:THR:HG22	25:R0:12:ASN:H	1.33	0.90
6:RD:17:THR:O	6:RD:211:ARG:NH2	2.05	0.89
36:XB:17:PHE:HD1	36:XB:18:GLY:H	1.20	0.89
4:RA:1075:C:OP1	15:RQ:59:ARG:NH2	2.05	0.88
4:RA:1041:C:H42	4:RA:1114:G:H1	1.14	0.88
35:QA:1086:U:H3	35:QA:1099:G:H22	1.23	0.87
9:RG:161:THR:HG22	9:RG:163:ALA:H	1.40	0.86
35:XA:1292:U:OP2	41:XG:41:ARG:NH2	2.08	0.86
38:QD:18:LYS:NZ	38:QD:31:CYS:SG	2.49	0.86
4:RA:1798:U:OP2	6:RD:274:ARG:NH2	2.08	0.86
38:QD:59:ARG:HA	38:QD:59:ARG:HE	1.40	0.86
14:RP:52:GLU:HB3	14:RP:55:ARG:HH11	1.39	0.86
4:RA:2304:G:H22	4:RA:2312:U:H3	1.25	0.85
19:RU:49:HIS:HA	19:RU:52:ARG:HB3	1.58	0.85
37:QC:8:ILE:HG23	37:QC:16:ARG:HD3	1.58	0.85
36:XB:15:VAL:HB	36:XB:209:ARG:HB3	1.58	0.85
35:QA:981:U:H4'	48:QN:21:TYR:CE2	2.12	0.84
17:RS:59:LYS:HG3	17:RS:60:GLY:H	1.41	0.84
37:XC:119:ARG:HD3	37:XC:140:ARG:HH21	1.41	0.84
25:Y0:10:THR:HG22	25:Y0:12:ASN:H	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:QY:245:ARG:HE	4:RA:2573:C:H42	1.24	0.84
7:RE:47:VAL:HG21	7:RE:86:PRO:HD2	1.59	0.84
18:YT:22:PHE:H	18:YT:22:PHE:HD1	1.23	0.84
38:QD:3:ARG:HD3	38:QD:118:ARG:HE	1.43	0.84
35:QA:407:G:H5''	38:QD:115:ARG:HG2	1.59	0.84
35:QA:975:A:H4'	35:QA:976:G:H5''	1.59	0.84
4:RA:250:G:OP2	33:R8:13:ARG:NH2	2.10	0.83
35:XA:401:C:OP2	38:XD:73:ARG:NH2	2.10	0.83
54:XT:56:MET:HE1	54:XT:85:MET:HG2	1.61	0.83
52:QR:32:ARG:HA	52:QR:69:THR:HG21	1.60	0.83
40:XF:19:LEU:HD11	40:XF:59:TYR:CE2	2.14	0.83
35:QA:1422:G:H5''	13:RO:48:PRO:HB3	1.59	0.83
36:QB:195:ASP:O	42:QH:68:ARG:NH2	2.12	0.82
3:QY:168:GLU:HG2	3:QY:179:VAL:HG12	1.59	0.82
4:RA:956:G:OP2	15:RQ:14:ARG:NH2	2.12	0.82
35:XA:501:C:OP1	46:XL:117:ARG:NH2	2.11	0.82
35:QA:673:G:H2'	35:QA:674:G:C8	2.14	0.82
40:QF:19:LEU:HD11	40:QF:59:TYR:CE2	2.14	0.82
6:YD:13:ARG:NH1	6:YD:16:MET:SD	2.52	0.82
35:QA:1255:G:OP1	44:QJ:45:ARG:NH2	2.11	0.82
3:QY:245:ARG:NH1	4:RA:2555:U:O2	2.13	0.82
37:XC:8:ILE:HG23	37:XC:16:ARG:HD3	1.61	0.82
37:QC:40:ARG:O	37:QC:44:GLU:HB3	1.80	0.81
24:RZ:144:LEU:HD21	24:RZ:150:LEU:HD13	1.61	0.81
35:QA:677:U:H3	35:QA:713:G:H22	1.27	0.81
4:RA:1754:C:H5'	18:RT:101:PHE:CE1	2.15	0.81
3:XY:281:HIS:CE1	4:YA:2493:U:H1'	2.12	0.81
29:Y4:59:PHE:HA	29:Y4:61:ARG:H	1.43	0.81
36:QB:111:ARG:HE	36:QB:111:ARG:HA	1.45	0.81
23:RY:8:LYS:HG2	23:RY:97:ARG:HH12	1.44	0.81
35:XA:673:G:H2'	35:XA:674:G:C8	2.14	0.81
9:YG:41:GLN:HB3	9:YG:43:LEU:HD13	1.63	0.81
1:XV:53:G:O5'	24:YZ:198:LYS:NZ	2.13	0.81
36:QB:8:LYS:NZ	36:QB:52:GLU:HG2	1.94	0.81
3:QY:253:HIS:O	3:QY:255:ASN:N	2.12	0.81
27:Y2:1:MET:SD	27:Y2:56:GLN:NE2	2.54	0.81
11:YI:92:VAL:HG23	11:YI:120:ILE:HB	1.63	0.81
18:RT:61:PHE:CE1	18:RT:76:PHE:HB2	2.15	0.80
23:RY:92:ASN:HB2	23:RY:94:LYS:H	1.46	0.80
35:XA:559:A:OP1	39:XE:126:ARG:NH2	2.14	0.80
36:XB:110:GLN:O	36:XB:113:HIS:HB2	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XY:201:LEU:HD12	3:XY:326:TYR:HB2	1.63	0.80
4:YA:1754:C:H5'	18:YT:101:PHE:CE1	2.15	0.80
22:RX:60:ARG:HH12	32:R7:47:ARG:NH2	1.80	0.80
14:RP:100:LEU:HD12	14:RP:112:LEU:HD11	1.63	0.80
4:YA:2271:G:H5''	25:Y0:20:ARG:HE	1.46	0.80
4:YA:2572:A:C8	7:YE:144:ARG:HD2	2.16	0.80
6:RD:242:ARG:HB2	6:RD:242:ARG:HH11	1.46	0.80
8:YF:10:PRO:HB3	8:YF:17:ARG:HE	1.47	0.80
13:YO:35:VAL:HG11	13:YO:103:ALA:HB3	1.64	0.80
44:XJ:49:VAL:HG23	48:XN:41:ARG:HG3	1.63	0.80
9:YG:111:LEU:HB3	9:YG:117:PHE:CE2	2.16	0.80
10:YH:7:LEU:HB3	10:YH:69:ARG:NH1	1.95	0.80
4:RA:2365:G:H4'	25:R0:60:PHE:CE2	2.17	0.79
35:XA:582:U:OP1	49:XO:68:ARG:NH2	2.15	0.79
4:YA:1530:C:O2'	4:YA:1531:C:O5'	1.99	0.79
9:YG:111:LEU:HB3	9:YG:117:PHE:HE2	1.47	0.79
1:QV:53:G:O6	1:QV:62:C:N4	2.15	0.79
4:RA:1530:C:O2'	4:RA:1531:C:O5'	2.00	0.79
10:YH:46:GLU:HB2	10:YH:49:VAL:HG12	1.64	0.79
8:RF:157:VAL:HB	8:RF:194:MET:HG2	1.63	0.79
3:XY:203:ARG:HH12	3:XY:206:PRO:HD3	1.47	0.79
14:YP:100:LEU:HD12	14:YP:112:LEU:HD11	1.64	0.79
38:XD:122:ARG:NH1	38:XD:134:ASP:O	2.16	0.79
50:QP:38:TYR:H	50:QP:38:TYR:HD1	1.30	0.79
18:YT:39:ARG:NH2	35:XA:345:C:OP2	2.15	0.79
4:YA:1310:G:OP2	32:Y7:9:ARG:NH1	2.15	0.79
38:XD:59:ARG:HA	38:XD:59:ARG:HE	1.45	0.79
37:XC:54:ARG:HB3	37:XC:69:HIS:HB2	1.63	0.79
13:YO:48:PRO:HB3	35:XA:1422:G:H5''	1.65	0.78
35:QA:427:U:OP1	38:QD:13:ARG:NH2	2.16	0.78
9:YG:16:ARG:HE	9:YG:31:VAL:HG21	1.48	0.78
16:YR:33:ARG:HG3	16:YR:115:GLU:HG2	1.65	0.78
18:YT:61:PHE:CE1	18:YT:76:PHE:HB2	2.17	0.78
4:RA:587:C:OP2	14:RP:21:ARG:NH2	2.15	0.78
31:Y6:35:GLU:OE2	31:Y6:50:ARG:NH1	2.17	0.78
24:YZ:5:LEU:HD11	24:YZ:44:PHE:HB2	1.64	0.78
35:QA:946:A:H2'	35:QA:947:G:C8	2.19	0.78
13:RO:35:VAL:HG11	13:RO:103:ALA:HB3	1.66	0.78
21:RW:11:ARG:HD2	21:RW:11:ARG:C	2.03	0.78
7:YE:47:VAL:HG11	7:YE:86:PRO:HD2	1.66	0.78
15:YQ:57:HIS:HE1	15:YQ:116:GLU:HB3	1.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:QP:38:TYR:CE1	50:QP:50:LYS:HB3	2.19	0.78
40:QF:22:GLU:OE2	40:QF:82:ARG:NH1	2.17	0.77
35:XA:975:A:H4'	35:XA:976:G:H5''	1.65	0.77
14:YP:59:LEU:HD11	33:Y8:10:ALA:HB2	1.65	0.77
31:R6:35:GLU:HG2	31:R6:50:ARG:HD2	1.66	0.77
44:QJ:61:GLU:OE2	48:QN:49:HIS:NE2	2.17	0.77
43:XI:16:ARG:HB2	43:XI:64:THR:HG22	1.65	0.77
22:RX:60:ARG:NH1	32:R7:47:ARG:HH22	1.81	0.77
4:RA:2384:G:OP2	25:R0:55:ARG:NH1	2.16	0.77
35:XA:664:G:H22	35:XA:741:G:H1	1.29	0.77
36:XB:88:ALA:HB1	36:XB:222:ILE:HD11	1.67	0.77
36:QB:8:LYS:HZ1	36:QB:52:GLU:HG2	1.49	0.77
25:R0:11:ARG:O	25:R0:14:ARG:NH2	2.18	0.77
14:RP:59:LEU:HD11	33:R8:10:ALA:HB2	1.65	0.77
13:RO:64:ARG:NH1	18:RT:70:VAL:HG21	2.00	0.77
8:RF:12:LEU:HD13	8:RF:124:LEU:HD11	1.68	0.76
35:XA:1031:G:H2'	35:XA:1032:G:C8	2.20	0.76
3:XY:334:LYS:NZ	3:XY:341:GLU:OE2	2.18	0.76
4:YA:250:G:OP2	33:Y8:13:ARG:NH2	2.17	0.76
35:XA:677:U:H3	35:XA:713:G:H22	1.34	0.76
35:XA:390:C:O3'	50:XP:28:ARG:NH2	2.19	0.76
35:QA:17:U:H2'	35:QA:18:C:C6	2.21	0.76
40:QF:44:GLY:HA2	40:QF:59:TYR:CE1	2.21	0.76
35:XA:1189:C:OP1	44:XJ:51:ARG:NH2	2.19	0.76
36:XB:155:LEU:HD21	36:XB:159:PRO:HG3	1.68	0.76
43:QI:50:LEU:HD13	43:QI:56:LEU:HA	1.67	0.76
38:QD:53:ASP:HB3	38:QD:57:ARG:HH12	1.49	0.75
4:RA:1102:C:H2'	4:RA:1103:A:H8	1.51	0.75
37:QC:188:LEU:HD23	37:QC:190:ARG:HH11	1.50	0.75
11:YI:9:LEU:HD12	11:YI:12:LEU:HD12	1.68	0.75
35:XA:1075:C:OP1	36:XB:179:LYS:NZ	2.20	0.75
54:XT:42:GLN:NE2	54:XT:46:GLU:OE2	2.18	0.75
36:QB:185:ILE:HG22	36:QB:199:TYR:HB2	1.67	0.75
4:RA:848:G:H2'	4:RA:849:A:C8	2.21	0.75
6:YD:260:ARG:NH1	6:YD:264:LYS:HD3	2.01	0.75
35:QA:1189:C:OP1	44:QJ:51:ARG:NH2	2.20	0.75
36:QB:231:GLU:HB3	36:QB:232:PRO:HD3	1.68	0.75
3:QY:332:ARG:HH11	3:QY:334:LYS:HD2	1.52	0.75
3:XY:223:TYR:H	3:XY:223:TYR:HD1	1.33	0.75
7:YE:14:ILE:HB	18:YT:14:TYR:CE2	2.22	0.75
47:XM:81:LEU:HD13	47:XM:88:ARG:HD2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1318:A:H4'	53:QS:10:PHE:CE2	2.22	0.74
4:RA:2150:U:H2'	4:RA:2151:G:C8	2.21	0.74
8:RF:99:TYR:H	8:RF:99:TYR:HD1	1.32	0.74
17:RS:27:SER:HA	17:RS:88:ASP:HB3	1.69	0.74
37:QC:40:ARG:O	37:QC:44:GLU:CB	2.34	0.74
35:QA:943:U:H1'	43:QI:124:GLN:HE22	1.51	0.74
25:R0:60:PHE:HD1	25:R0:60:PHE:H	1.35	0.74
49:XO:26:GLU:OE2	49:XO:77:ARG:NE	2.21	0.74
23:YY:15:VAL:O	23:YY:22:GLY:N	2.15	0.74
3:QY:166:ILE:HG22	3:QY:167:GLU:HG3	1.68	0.74
1:QV:54:U:H5''	24:RZ:203:GLU:OE1	1.88	0.74
35:XA:581:G:OP1	49:XO:65:ARG:NH2	2.21	0.74
34:R9:22:ARG:HD3	34:R9:35:ARG:HD2	1.69	0.74
35:XA:17:U:H2'	35:XA:18:C:C6	2.21	0.74
37:XC:40:ARG:NH2	37:XC:55:VAL:O	2.20	0.74
43:XI:50:LEU:HD23	43:XI:85:LEU:HD11	1.70	0.74
6:YD:242:ARG:HB2	6:YD:242:ARG:HH11	1.53	0.74
35:QA:339:C:OP2	13:RO:97:ARG:NH1	2.20	0.74
35:QA:1435:G:H2'	35:QA:1436:U:C6	2.22	0.73
24:RZ:158:PRO:HG2	24:RZ:161:VAL:HG11	1.69	0.73
36:XB:163:PHE:CE2	36:XB:215:LEU:HD22	2.23	0.73
4:YA:1405:U:H2'	4:YA:1406:U:C6	2.23	0.73
4:YA:1816:G:O6	6:YD:35:LYS:NZ	2.20	0.73
4:YA:530:G:N1	4:YA:2023:G:OP1	2.18	0.73
18:YT:45:PHE:CE2	18:YT:74:ARG:HG3	2.22	0.73
51:QQ:66:SER:O	51:QQ:70:ARG:NH1	2.21	0.73
3:QY:279:SER:OG	15:RQ:80:GLU:OE2	2.06	0.73
37:XC:140:ARG:HB2	37:XC:140:ARG:HH11	1.51	0.73
51:XQ:66:SER:O	51:XQ:70:ARG:NH1	2.21	0.73
7:YE:11:MET:HG2	7:YE:24:THR:HG22	1.70	0.73
20:RV:72:VAL:HG13	20:RV:85:LYS:HB3	1.69	0.73
3:XY:241:ILE:HG12	3:XY:263:ILE:HG12	1.71	0.73
48:QN:41:ARG:HG2	48:QN:42:ILE:N	2.02	0.73
3:QY:130:LEU:HD22	3:QY:132:ILE:HG13	1.69	0.73
8:RF:53:THR:HG22	8:RF:55:GLY:H	1.53	0.73
44:XJ:17:ASP:OD1	44:XJ:70:ARG:NH1	2.22	0.73
4:YA:1064:C:H3'	4:YA:1065:U:C5'	2.19	0.73
4:YA:1798:U:OP2	6:YD:274:ARG:NH2	2.22	0.73
15:YQ:60:ARG:NH2	24:YZ:181:GLU:HG2	2.04	0.73
47:QM:19:LEU:HD21	47:QM:56:LEU:HD21	1.69	0.73
4:RA:1102:C:H2'	4:RA:1103:A:C8	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XE:69:VAL:HG11	39:XE:113:ALA:HB1	1.70	0.73
45:XK:84:VAL:HG11	45:XK:91:ARG:HD2	1.69	0.73
38:QD:162:LEU:HD13	38:QD:181:MET:HG2	1.70	0.73
4:RA:1802:A:H2'	4:RA:1803:A:C8	2.24	0.73
4:YA:2469:A:O2'	15:YQ:56:ARG:NH1	2.21	0.73
35:QA:1441:G:H5''	35:QA:1442(A):G:H5'	1.71	0.72
47:XM:58:GLU:O	47:XM:62:ASN:ND2	2.21	0.72
29:Y4:48:ARG:N	29:Y4:48:ARG:HD2	2.04	0.72
45:QK:84:VAL:HG11	45:QK:91:ARG:HD2	1.70	0.72
40:XF:44:GLY:HA2	40:XF:59:TYR:CE1	2.23	0.72
8:YF:18:ARG:HG2	8:YF:19:GLU:H	1.54	0.72
35:QA:1360:A:OP2	48:QN:35:ARG:NH2	2.21	0.72
4:RA:2292:C:OP1	17:RS:17:ARG:NH1	2.22	0.72
14:RP:99:LEU:HD23	14:RP:102:ARG:HH21	1.53	0.72
17:RS:3:ARG:HH21	17:RS:9:ARG:HH12	1.38	0.72
18:YT:61:PHE:HD1	18:YT:61:PHE:H	1.34	0.72
4:RA:1310:G:OP2	32:R7:9:ARG:NH1	2.22	0.72
4:RA:1064:C:H3'	4:RA:1065:U:C5'	2.20	0.72
4:RA:631:A:OP1	14:RP:65:ARG:NH1	2.22	0.72
43:XI:46:ALA:HB2	43:XI:74:ILE:HG23	1.72	0.72
49:XO:7:GLU:OE2	49:XO:38:ARG:NH2	2.23	0.72
49:XO:35:ARG:HH21	49:XO:59:MET:HE2	1.55	0.72
50:XP:13:HIS:O	50:XP:42:ARG:NH1	2.22	0.72
8:YF:179:GLU:OE1	8:YF:179:GLU:N	2.22	0.72
4:RA:1073:A:H2'	4:RA:1074:G:H8	1.54	0.72
4:RA:2680:C:OP2	7:RE:111:ARG:NH2	2.22	0.72
18:RT:68:TYR:H	18:RT:68:TYR:HD1	1.36	0.72
36:XB:47:THR:HA	36:XB:202:PRO:HG2	1.70	0.72
29:Y4:67:TYR:HB3	53:XS:16:LEU:HD11	1.71	0.72
4:RA:994:C:OP1	19:RU:53:ARG:NH2	2.23	0.72
4:YA:1801:G:OP2	6:YD:154:LYS:NZ	2.23	0.72
4:YA:2150:U:H2'	4:YA:2151:G:C8	2.25	0.72
8:YF:33:LEU:HD13	8:YF:112:MET:HE2	1.71	0.72
4:YA:631:A:OP1	14:YP:65:ARG:NH1	2.21	0.72
3:XY:251:GLY:O	3:XY:255:ASN:ND2	2.23	0.72
6:YD:242:ARG:HD3	6:YD:246:PRO:HG3	1.72	0.72
8:RF:179:GLU:N	8:RF:179:GLU:OE1	2.22	0.71
8:RF:74:ARG:O	8:RF:75:HIS:CD2	2.43	0.71
24:RZ:103:ARG:HG2	24:RZ:136:PHE:CD2	2.24	0.71
1:XV:76:A:H3'	3:XY:251:GLY:HA3	1.72	0.71
3:QY:54:GLN:OE1	4:RA:1095:A:N6	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:RE:40:GLU:OE1	7:RE:40:GLU:N	2.21	0.71
44:XJ:38:ILE:HG12	44:XJ:71:LEU:HB3	1.70	0.71
27:Y2:9:GLN:HE22	27:Y2:56:GLN:HB3	1.54	0.71
35:QA:532:A:N6	35:QA:1206:G:O2'	2.22	0.71
4:RA:143(A):G:H4'	22:RX:35:THR:HG21	1.71	0.71
10:RH:159:GLU:HG2	10:RH:169:VAL:HG11	1.73	0.71
46:QL:33:ARG:NH1	46:QL:62:SER:HB3	2.04	0.71
3:XY:245:ARG:HH22	4:YA:2508:G:H5'	1.56	0.71
28:R3:3:ARG:NH1	28:R3:60:GLU:OE2	2.24	0.71
9:RG:179:PRO:HB2	29:R4:42:PHE:HE2	1.55	0.71
24:YZ:10:ARG:NH2	24:YZ:26:GLY:O	2.24	0.71
49:QO:25:THR:HG21	49:QO:70:LEU:HB2	1.73	0.71
4:RA:1353:A:H2'	4:RA:1354:A:C8	2.25	0.71
40:XF:100:ASN:ND2	52:XR:26:LEU:O	2.23	0.71
29:Y4:59:PHE:H	29:Y4:59:PHE:HD1	1.39	0.71
4:RA:660:G:H5'	8:RF:99:TYR:CD2	2.25	0.71
6:RD:260:ARG:NH1	6:RD:264:LYS:HD3	2.05	0.71
35:XA:946:A:H2'	35:XA:947:G:C8	2.26	0.71
4:YA:587:C:OP2	14:YP:21:ARG:NH2	2.23	0.71
43:QI:19:LEU:HB3	43:QI:59:PHE:HD2	1.54	0.71
13:RO:68:GLU:HB3	13:RO:78:ARG:HB2	1.73	0.71
35:XA:1435:G:H2'	35:XA:1436:U:C6	2.25	0.71
13:YO:80:ASP:OD1	18:YT:64:ARG:NH2	2.24	0.70
48:QN:21:TYR:H	48:QN:21:TYR:HD1	1.36	0.70
4:RA:1165:U:H2'	4:RA:1166:C:C6	2.26	0.70
9:RG:59:GLU:OE2	9:RG:153:ARG:NH2	2.24	0.70
9:YG:12:TYR:HA	9:YG:16:ARG:HG2	1.71	0.70
53:QS:41:VAL:HG12	53:QS:44:MET:HG3	1.72	0.70
37:XC:131:ARG:HH11	37:XC:135:LYS:HE3	1.56	0.70
3:XY:130:LEU:HD11	3:XY:152:TYR:CD2	2.26	0.70
8:YF:178:PRO:HB2	8:YF:201:VAL:HG21	1.71	0.70
12:YN:96:GLU:N	12:YN:96:GLU:OE1	2.23	0.70
40:QF:72:VAL:HG13	40:QF:73:ASN:H	1.55	0.70
44:QJ:35:SER:HB3	44:QJ:73:ASP:HB2	1.72	0.70
35:XA:1047:G:H5''	48:XN:4:LYS:HD3	1.72	0.70
6:YD:176:ARG:HH11	6:YD:176:ARG:HG2	1.55	0.70
14:YP:91:PHE:CE2	14:YP:99:LEU:HD21	2.26	0.70
35:QA:1391:U:H2'	35:QA:1392:G:C8	2.27	0.70
36:XB:28:PHE:CE1	36:XB:31:TYR:HB2	2.26	0.70
14:YP:59:LEU:HD21	33:Y8:10:ALA:HA	1.73	0.70
35:QA:1356:G:H2'	35:QA:1357:A:C8	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:RX:53:LYS:HB3	22:RX:82:GLN:HB3	1.72	0.70
4:YA:2126:A:H4'	4:YA:2127:G:O5'	1.91	0.70
19:RU:104:GLN:OE1	19:RU:104:GLN:N	2.24	0.70
3:XY:213:ARG:HH22	35:XA:530:G:H2'	1.56	0.70
4:YA:1405:U:H2'	4:YA:1406:U:H6	1.56	0.70
40:QF:61:LEU:HB3	40:QF:63:TYR:HE1	1.57	0.70
4:RA:530:G:N1	4:RA:2023:G:OP1	2.22	0.70
24:RZ:103:ARG:HG2	24:RZ:136:PHE:HD2	1.56	0.70
8:RF:29:ASN:HB3	8:RF:112:MET:HE1	1.72	0.70
35:QA:664:G:H22	35:QA:741:G:H1	1.38	0.69
36:XB:128:GLU:OE1	36:XB:135:GLN:NE2	2.23	0.69
45:XK:99:GLN:HG2	45:XK:105:VAL:HG21	1.72	0.69
20:YV:72:VAL:HG13	20:YV:85:LYS:HB3	1.74	0.69
27:R2:9:GLN:HE22	27:R2:56:GLN:HB3	1.57	0.69
29:R4:67:TYR:CD1	29:R4:67:TYR:N	2.57	0.69
40:XF:61:LEU:HB3	40:XF:63:TYR:HE1	1.57	0.69
4:YA:660:G:H5'	8:YF:99:TYR:CD2	2.27	0.69
8:YF:21:ALA:HB3	8:YF:22:ALA:HA	1.73	0.69
30:R5:35:GLU:HG2	30:R5:51:TYR:CD2	2.28	0.69
4:RA:11:G:H2'	4:RA:12:U:H5'	1.73	0.69
35:XA:1513:A:H2'	35:XA:1514:C:C6	2.27	0.69
37:XC:6:HIS:CE1	37:XC:8:ILE:HB	2.27	0.69
3:XY:344:ASN:HB3	3:XY:347:ALA:HB3	1.74	0.69
3:XY:38:ASN:OD1	3:XY:60:ARG:NH1	2.23	0.69
50:QP:53:VAL:HG13	50:QP:79:VAL:HG12	1.75	0.69
6:RD:2:ALA:N	6:RD:200:ASP:OD2	2.25	0.69
1:QV:53:G:N2	24:RZ:202:GLU:OE2	2.26	0.69
35:XA:559:A:H4'	35:XA:560:U:H3'	1.74	0.69
11:RI:60:GLU:HG3	11:RI:61:ARG:NH1	2.07	0.69
35:XA:1005:A:H5''	35:XA:1006:C:C5	2.27	0.69
37:XC:152:ILE:HG12	37:XC:199:LYS:HB2	1.73	0.69
4:YA:1102:C:H2'	4:YA:1103:A:H8	1.57	0.69
19:YU:52:ARG:HG2	19:YU:52:ARG:HH11	1.57	0.69
35:QA:524:G:H2'	35:QA:525:C:C6	2.27	0.69
33:R8:31:HIS:ND1	33:R8:32:LEU:HD13	2.08	0.69
6:RD:242:ARG:HD3	6:RD:246:PRO:HG3	1.75	0.69
17:RS:106:ARG:HG3	17:RS:112:PHE:CE1	2.27	0.69
35:XA:1356:G:H2'	35:XA:1357:A:C8	2.27	0.69
4:YA:1073:A:H2'	4:YA:1074:G:C8	2.28	0.69
4:YA:2365:G:H4'	25:Y0:60:PHE:CE2	2.28	0.69
35:QA:164:U:H2'	35:QA:165:C:C6	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XY:136:SER:O	3:XY:138:GLY:N	2.24	0.69
43:QI:33:PHE:CE1	43:QI:37:PHE:HD2	2.11	0.69
4:RA:1073:A:H2'	4:RA:1074:G:C8	2.26	0.69
37:XC:21:ARG:NH2	37:XC:58:GLU:OE2	2.25	0.69
4:YA:1264:G:OP1	30:Y5:19:ARG:NH2	2.25	0.69
10:YH:97:ARG:NE	10:YH:104:GLU:OE1	2.22	0.69
21:YW:75:TYR:CE2	21:YW:104:THR:HB	2.28	0.69
3:QY:245:ARG:NH2	4:RA:2573:C:N3	2.36	0.69
6:RD:52:ARG:NH1	6:RD:249:PRO:HG2	2.08	0.69
11:RI:109:ILE:HG13	11:RI:130:TYR:CZ	2.27	0.69
35:XA:1218:C:H2'	35:XA:1219:U:C6	2.27	0.69
35:XA:262:A:H2'	35:XA:263:A:C8	2.27	0.69
53:XS:41:VAL:HG12	53:XS:44:MET:HG3	1.73	0.69
3:XY:245:ARG:NH2	4:YA:2508:G:H5'	2.07	0.69
40:XF:43:LEU:HD23	40:XF:46:ARG:HH22	1.57	0.69
3:QY:230:ILE:HG23	3:QY:299:GLU:HG3	1.75	0.68
38:XD:68:TYR:CE2	38:XD:97:LEU:HB3	2.28	0.68
43:XI:53:VAL:O	43:XI:55:ALA:N	2.26	0.68
21:YW:11:ARG:C	21:YW:11:ARG:HD2	2.13	0.68
38:QD:12:CYS:SG	38:QD:19:LEU:HB2	2.33	0.68
4:RA:2126:A:H4'	4:RA:2127:G:O5'	1.91	0.68
4:RA:2507:C:O3'	4:RA:2573:C:N4	2.26	0.68
43:XI:4:TYR:CD1	43:XI:88:TYR:HB2	2.28	0.68
9:YG:80:PHE:O	9:YG:82:LEU:N	2.26	0.68
35:QA:45:U:H2'	35:QA:46:G:C8	2.28	0.68
26:R1:50:ARG:HG2	26:R1:59:THR:HG22	1.74	0.68
36:XB:187:LEU:HA	36:XB:201:ILE:HB	1.73	0.68
4:YA:1076:C:H4'	4:YA:1077:A:OP1	1.92	0.68
4:YA:2292:C:OP1	17:YS:17:ARG:NH1	2.22	0.68
40:XF:22:GLU:OE2	40:XF:82:ARG:NH2	2.26	0.68
39:QE:69:VAL:HG11	39:QE:113:ALA:HB1	1.74	0.68
1:XV:63:G:H4'	25:Y0:11:ARG:HH22	1.58	0.68
4:YA:1073:A:H2'	4:YA:1074:G:H8	1.57	0.68
7:YE:51:PHE:CD2	7:YE:52:LEU:HD22	2.29	0.68
4:YA:272(P):C:O2'	11:YI:42:SER:OG	2.10	0.68
17:YS:50:SER:O	17:YS:76:LYS:NZ	2.22	0.68
1:QV:24:U:O2'	4:RA:1923:U:OP1	2.12	0.68
4:RA:922:U:H2'	4:RA:923:C:C6	2.27	0.68
10:RH:97:ARG:NE	10:RH:104:GLU:OE1	2.24	0.68
36:QB:16:HIS:HB3	36:QB:210:SER:HB2	1.75	0.68
43:QI:16:ARG:HB2	43:QI:64:THR:HG22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:RH:86:GLU:OE2	10:RH:132:ARG:NH2	2.26	0.68
18:RT:64:ARG:NH1	18:RT:103:ARG:HA	2.08	0.68
4:YA:1102:C:H2'	4:YA:1103:A:C8	2.29	0.68
8:YF:18:ARG:HG2	8:YF:19:GLU:N	2.09	0.68
38:XD:162:LEU:HD13	38:XD:181:MET:HG2	1.74	0.68
4:YA:2753:A:N3	34:Y9:15:LYS:NZ	2.42	0.68
7:RE:72:VAL:HG22	7:RE:73:GLU:OE1	1.94	0.68
13:RO:64:ARG:HG2	13:RO:79:PHE:CD2	2.29	0.68
23:YY:8:LYS:HG2	23:YY:97:ARG:HH12	1.59	0.68
3:QY:9:ASN:HB3	3:QY:10:ARG:NH1	2.09	0.67
4:RA:1076:C:H1'	4:RA:1077:A:H5'	1.75	0.67
35:XA:1086:U:H3	35:XA:1099:G:H22	1.41	0.67
35:XA:101:A:H5'	54:XT:10:LEU:HD21	1.75	0.67
9:YG:143:GLU:OE2	29:Y4:26:SER:OG	2.12	0.67
36:QB:88:ALA:O	36:QB:226:ARG:NH2	2.28	0.67
4:RA:1889:A:H2'	4:RA:1890:A:C8	2.28	0.67
4:RA:998:C:P	19:RU:92:ARG:HH22	2.16	0.67
32:Y7:35:ARG:HD3	32:Y7:42:LEU:HD11	1.77	0.67
4:YA:848:G:H2'	4:YA:849:A:C8	2.29	0.67
4:RA:2152:G:H2'	4:RA:2153:G:H8	1.59	0.67
18:RT:61:PHE:H	18:RT:61:PHE:HD1	1.43	0.67
4:YA:1657:C:H2'	4:YA:1658:C:H6	1.59	0.67
4:YA:2064:C:H2'	4:YA:2065:C:C6	2.29	0.67
8:YF:164:ARG:HD2	8:YF:175:THR:HG23	1.76	0.67
35:QA:1218:C:H2'	35:QA:1219:U:C6	2.30	0.67
10:RH:139:GLN:HG3	10:RH:140:LYS:N	2.09	0.67
40:QF:44:GLY:HA2	40:QF:59:TYR:CD1	2.30	0.67
35:XA:1310:G:OP2	47:XM:88:ARG:NH1	2.28	0.67
42:XH:41:ARG:NH2	42:XH:123:GLU:OE2	2.27	0.67
4:YA:11:G:H2'	4:YA:12:U:H5'	1.77	0.67
4:YA:1914:C:O2'	4:YA:1915:5MU:OP1	2.12	0.67
4:YA:2507:C:H5''	4:YA:2573:C:H41	1.60	0.67
4:YA:813:U:H2'	4:YA:814:C:C6	2.30	0.67
29:R4:67:TYR:HD1	29:R4:67:TYR:N	1.84	0.67
9:RG:16:ARG:NE	9:RG:31:VAL:HG21	2.09	0.67
18:YT:41:ARG:NH2	35:XA:346:G:OP1	2.24	0.67
47:XM:88:ARG:HG3	47:XM:98:VAL:HG11	1.76	0.67
4:YA:1802:A:H2'	4:YA:1803:A:C8	2.29	0.67
6:RD:71:ASP:HB3	6:RD:103:ARG:HH22	1.59	0.67
35:XA:539:A:H2'	35:XA:540:G:C8	2.29	0.67
48:XN:4:LYS:HA	48:XN:7:ILE:HG12	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:QB:16:HIS:C	36:QB:17:PHE:HD1	1.98	0.67
35:XA:537:G:H5''	46:XL:113:ARG:NH1	2.10	0.67
38:XD:153:ARG:HH12	38:XD:181:MET:HB2	1.60	0.67
42:XH:25:ASP:HB3	42:XH:58:TYR:HD2	1.59	0.67
4:YA:1071:G:N2	4:YA:1089:G:O6	2.20	0.67
4:YA:2152:G:H2'	4:YA:2153:G:H8	1.59	0.67
10:YH:139:GLN:HG3	10:YH:140:LYS:N	2.09	0.67
35:QA:159:G:N2	35:QA:162:A:OP2	2.21	0.67
35:QA:737:A:H2'	35:QA:738:C:C6	2.30	0.67
52:QR:42:ARG:HA	52:QR:42:ARG:NE	2.09	0.67
4:RA:1101:U:H2'	4:RA:1102:C:H6	1.60	0.67
7:RE:1:MET:O	7:RE:84:PHE:HB2	1.95	0.67
36:XB:98:LEU:O	36:XB:101:MET:HG3	1.95	0.67
22:YX:53:LYS:HB3	22:YX:82:GLN:HB3	1.77	0.67
35:QA:998:G:H2'	35:QA:999:C:C6	2.30	0.67
38:QD:116:GLN:NE2	38:QD:157:LEU:HD11	2.09	0.67
45:XK:116:HIS:N	45:XK:117:ASN:HA	2.09	0.67
35:QA:406:G:H5'	38:QD:5:ILE:HD11	1.77	0.66
41:XG:111:ARG:NH2	41:XG:126:ASP:OD2	2.28	0.66
6:YD:52:ARG:NH1	6:YD:249:PRO:HG2	2.10	0.66
19:YU:104:GLN:OE1	19:YU:104:GLN:N	2.28	0.66
38:QD:68:TYR:CE2	38:QD:97:LEU:HB3	2.30	0.66
42:QH:95:VAL:HB	42:QH:99:GLU:HG3	1.78	0.66
4:RA:1076:C:H4'	4:RA:1077:A:OP1	1.94	0.66
33:Y8:31:HIS:ND1	33:Y8:32:LEU:HD13	2.09	0.66
4:YA:286:C:H2'	4:YA:287:C:C6	2.30	0.66
8:YF:157:VAL:HB	8:YF:194:MET:HG2	1.77	0.66
24:YZ:144:LEU:HD21	24:YZ:150:LEU:HD13	1.76	0.66
37:QC:6:HIS:CE1	37:QC:8:ILE:HB	2.30	0.66
41:QG:27:ILE:HD12	41:QG:40:ALA:HA	1.77	0.66
48:QN:36:PHE:HD1	48:QN:36:PHE:O	1.78	0.66
4:YA:1165:U:H2'	4:YA:1166:C:C6	2.30	0.66
5:YB:66:A:H61	5:YB:109:C:H5'	1.58	0.66
35:XA:1005:A:OP2	35:XA:1024:G:N2	2.28	0.66
35:XA:625:G:H4'	50:XP:16:HIS:CD2	2.30	0.66
46:XL:33:ARG:HD3	46:XL:62:SER:HB3	1.78	0.66
35:QA:1030(A):C:N4	35:QA:1032:G:O6	2.28	0.66
35:QA:1103:C:OP1	36:QB:96:ARG:NH2	2.29	0.66
35:XA:1104:G:H4'	36:XB:111:ARG:NH1	2.10	0.66
4:YA:969:U:H2'	4:YA:970:C:C6	2.30	0.66
18:YT:64:ARG:NH1	18:YT:103:ARG:HA	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1513:A:H2'	35:QA:1514:C:C6	2.31	0.66
35:XA:1318:A:H5''	53:XS:3:ARG:HH22	1.60	0.66
3:XY:281:HIS:HB2	15:YQ:80:GLU:OE2	1.96	0.66
4:YA:1076:C:H1'	4:YA:1077:A:H5'	1.77	0.66
4:YA:2685:G:H5'	13:YO:68:GLU:OE2	1.96	0.66
35:QA:673:G:H5''	40:QF:87:ARG:NH1	2.11	0.66
4:RA:2271:G:H5''	25:R0:20:ARG:HE	1.59	0.66
13:RO:8:LEU:HD12	13:RO:84:ALA:HB2	1.78	0.66
13:RO:80:ASP:OD1	18:RT:64:ARG:NH2	2.29	0.66
20:RV:75:PHE:C	20:RV:75:PHE:HD1	1.98	0.66
43:XI:5:TYR:N	43:XI:87:GLN:OE1	2.24	0.66
4:RA:2753:A:N3	34:R9:15:LYS:NZ	2.44	0.66
35:XA:1510:U:H2'	35:XA:1511:G:C8	2.31	0.66
4:YA:83:G:H1	4:YA:102:G:HO2'	1.41	0.65
7:YE:1:MET:O	7:YE:84:PHE:HB2	1.95	0.65
24:RZ:136:PHE:N	24:RZ:136:PHE:HD1	1.94	0.65
35:XA:1073:U:O2'	36:XB:104:ASN:OD1	2.13	0.65
45:XK:27:ASN:OD1	45:XK:28:THR:N	2.30	0.65
3:XY:311:GLU:HA	3:XY:314:LYS:HD2	1.76	0.65
29:Y4:67:TYR:H	29:Y4:67:TYR:HD1	1.44	0.65
24:YZ:25:PRO:O	24:YZ:85:HIS:HA	1.97	0.65
4:RA:1405:U:H2'	4:RA:1406:U:C6	2.31	0.65
4:RA:2140:C:H2'	4:RA:2141:G:H8	1.62	0.65
4:RA:307:G:N1	4:RA:310:A:OP2	2.29	0.65
16:RR:29:LEU:HB3	16:RR:75:LEU:HD21	1.79	0.65
24:RZ:203:GLU:N	24:RZ:203:GLU:OE1	2.29	0.65
36:XB:101:MET:HA	36:XB:108:ILE:HG13	1.77	0.65
42:XH:10:LEU:HD22	42:XH:83:ILE:HD11	1.76	0.65
3:XY:33:ARG:NH1	3:XY:36:GLU:OE2	2.27	0.65
53:QS:50:ALA:HB1	53:QS:57:HIS:HB3	1.79	0.65
36:XB:78:GLN:NE2	36:XB:94:ASN:O	2.30	0.65
37:XC:131:ARG:NH1	37:XC:135:LYS:HE3	2.12	0.65
10:YH:3:ARG:HH12	10:YH:4:ILE:N	1.94	0.65
11:YI:50:ARG:O	11:YI:54:GLN:HG2	1.96	0.65
35:XA:1104:G:H4'	36:XB:111:ARG:HH11	1.61	0.65
37:XC:155:GLY:HA3	37:XC:196:LEU:HD22	1.78	0.65
39:XE:57:LYS:HG2	39:XE:61:TYR:HE2	1.62	0.65
4:YA:245:G:O6	33:Y8:8:LYS:NZ	2.27	0.65
4:YA:2785:C:OP1	7:YE:41:LYS:NZ	2.27	0.65
4:YA:643:A:H1'	31:Y6:44:ARG:HH21	1.60	0.65
24:YZ:91:LEU:HD11	24:YZ:96:VAL:HG11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:QY:241:ILE:HG12	3:QY:263:ILE:HG12	1.79	0.65
8:RF:165:ARG:HG2	8:RF:168:ARG:NH1	2.10	0.65
12:RN:96:GLU:N	12:RN:96:GLU:OE1	2.28	0.65
36:XB:9:GLU:O	36:XB:11:LEU:N	2.29	0.65
4:YA:2683:C:OP1	18:YT:53:ARG:NH2	2.29	0.65
35:QA:1414:U:H3	35:QA:1486:G:H1	1.44	0.65
50:XP:6:LEU:HB3	50:XP:17:TYR:HD2	1.61	0.65
6:YD:206:LEU:HD22	6:YD:211:ARG:HD2	1.77	0.65
35:QA:401:C:OP2	38:QD:73:ARG:NH2	2.30	0.65
4:RA:2137:C:H2'	4:RA:2138:C:C6	2.31	0.65
20:RV:75:PHE:CD1	20:RV:75:PHE:C	2.71	0.65
23:RY:55:TYR:HE2	23:RY:61:ILE:HG21	1.62	0.65
35:XA:524:G:H2'	35:XA:525:C:C6	2.31	0.65
4:YA:2836:U:H2'	4:YA:2837:G:C8	2.32	0.65
42:QH:51:VAL:HG11	42:QH:60:ARG:HH12	1.62	0.65
4:RA:1794:U:H2'	4:RA:1795:C:H6	1.62	0.65
35:XA:1402:4OC:HM22	35:XA:1403:C:H5'	1.78	0.65
18:YT:22:PHE:N	18:YT:22:PHE:CD1	2.64	0.65
1:XV:52:G:N3	24:YZ:198:LYS:HE3	2.12	0.65
37:XC:19:GLU:HG2	37:XC:54:ARG:HH12	1.60	0.64
3:XY:166:ILE:HG22	3:XY:167:GLU:HG3	1.79	0.64
35:QA:1323:G:H2'	35:QA:1324:A:C8	2.31	0.64
40:QF:19:LEU:HD11	40:QF:59:TYR:HE2	1.61	0.64
4:RA:856:C:H2'	4:RA:857:C:C6	2.32	0.64
37:XC:6:HIS:HE1	37:XC:8:ILE:HB	1.62	0.64
3:XY:144:TRP:CE3	3:XY:201:LEU:HD13	2.32	0.64
29:Y4:67:TYR:CD1	29:Y4:67:TYR:N	2.65	0.64
10:YH:35:VAL:HG13	10:YH:71:LEU:HD22	1.78	0.64
18:YT:22:PHE:N	18:YT:22:PHE:HD1	1.95	0.64
35:QA:1292:U:OP2	41:QG:41:ARG:NH2	2.28	0.64
20:RV:43:GLU:N	20:RV:43:GLU:OE1	2.30	0.64
37:XC:109:PRO:HB3	37:XC:115:LEU:HD23	1.78	0.64
4:YA:904:C:H2'	4:YA:905:U:C6	2.32	0.64
8:YF:185:ASP:HA	8:YF:188:ARG:HD3	1.78	0.64
35:QA:976:G:H5'	35:QA:1358:U:O2'	1.98	0.64
42:QH:86:ILE:HG13	42:QH:133:LEU:HD22	1.80	0.64
43:QI:121:ARG:NH1	43:QI:122:ALA:O	2.30	0.64
3:QY:273:GLN:NE2	4:RA:1942:5MC:OP1	2.30	0.64
13:RO:64:ARG:HH12	18:RT:70:VAL:HG21	1.62	0.64
4:YA:1064:C:H3'	4:YA:1065:U:H5'	1.79	0.64
18:YT:117:ASP:OD2	18:YT:120:ARG:NE	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:YW:8:ARG:HH21	21:YW:9:TYR:HE2	1.46	0.64
37:XC:47:LEU:HB2	37:XC:52:LEU:HD12	1.80	0.64
47:XM:20:THR:HG21	47:XM:27:LYS:HD2	1.78	0.64
12:YN:67:LEU:O	12:YN:88:GLU:HG3	1.97	0.64
24:YZ:126:VAL:HG11	24:YZ:161:VAL:HG13	1.78	0.64
35:QA:1492:A:H3'	35:QA:1493:A:H8	1.62	0.64
3:QY:213:ARG:NH1	3:QY:329:ASP:HB2	2.13	0.64
4:RA:1057:A:N6	4:RA:1087:G:OP1	2.31	0.64
4:RA:1141:U:OP1	12:RN:25:ARG:NH1	2.31	0.64
4:RA:2102:U:O2	4:RA:2187:G:O6	2.15	0.64
4:YA:1709:U:H2'	4:YA:1710:C:C6	2.33	0.64
8:YF:51:THR:HB	8:YF:88:VAL:HG11	1.80	0.64
11:RI:60:GLU:HG3	11:RI:61:ARG:HH12	1.62	0.64
37:XC:19:GLU:HB3	37:XC:40:ARG:HH22	1.61	0.64
4:YA:2137:C:H2'	4:YA:2138:C:C6	2.33	0.64
24:YZ:44:PHE:CE2	24:YZ:86:VAL:HG21	2.32	0.64
35:QA:544:G:OP1	38:QD:59:ARG:NH2	2.30	0.64
35:XA:976:G:H5'	35:XA:1358:U:O2'	1.97	0.64
3:XY:129:TYR:HE1	3:XY:182:LYS:HG3	1.63	0.64
4:YA:1057:A:N6	4:YA:1087:G:OP1	2.30	0.64
50:QP:13:HIS:O	50:QP:42:ARG:NH1	2.31	0.64
54:QT:89:ARG:O	54:QT:93:GLU:HG2	1.98	0.64
4:RA:1064:C:H3'	4:RA:1065:U:H5'	1.79	0.64
52:XR:32:ARG:HA	52:XR:69:THR:HG21	1.79	0.64
26:Y1:69:LYS:HE2	26:Y1:72:GLU:OE1	1.96	0.64
4:YA:1065:U:H4'	4:YA:1066:U:H5'	1.79	0.64
4:YA:1101:U:H2'	4:YA:1102:C:C6	2.33	0.64
4:YA:922:U:H2'	4:YA:923:C:C6	2.32	0.64
35:QA:269:C:H2'	35:QA:270:A:C8	2.33	0.64
4:RA:657:U:H2'	4:RA:658:C:C6	2.33	0.64
35:XA:954:G:H21	35:XA:1227:A:H62	1.45	0.64
35:XA:865:A:H5'	35:XA:1078:U:C5	2.33	0.64
35:QA:1117:G:O3'	43:QI:104:ARG:NH1	2.31	0.63
1:QV:61:C:H2'	1:QV:62:C:H6	1.63	0.63
47:XM:90:LEU:HD23	47:XM:93:ARG:HH21	1.61	0.63
3:XY:149:GLU:HG3	3:XY:150:ARG:N	2.13	0.63
27:Y2:17:SER:OG	27:Y2:20:GLU:HG3	1.98	0.63
6:YD:260:ARG:HH12	6:YD:264:LYS:HD3	1.63	0.63
18:RT:45:PHE:CE2	18:RT:74:ARG:HG3	2.33	0.63
20:RV:21:ARG:NH1	20:RV:93:GLU:OE1	2.31	0.63
43:XI:26:VAL:HA	43:XI:61:ALA:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1101:U:H2'	4:YA:1102:C:H6	1.62	0.63
14:RP:60:MET:HA	33:R8:13:ARG:NH1	2.13	0.63
3:XY:34:LEU:HD13	3:XY:63:LEU:HB2	1.80	0.63
29:Y4:18:CYS:SG	29:Y4:39:CYS:HB3	2.38	0.63
3:QY:144:TRP:CE3	3:QY:201:LEU:HD13	2.34	0.63
4:RA:813:U:H2'	4:RA:814:C:C6	2.33	0.63
16:RR:47:PHE:HD1	16:RR:47:PHE:O	1.81	0.63
4:YA:272(E):U:H2'	4:YA:272(F):C:C6	2.34	0.63
4:YA:483:A:O2'	23:YY:49:VAL:O	2.12	0.63
9:RG:11:TYR:HD2	9:RG:12:TYR:CD1	2.16	0.63
4:YA:1587:A:H2'	4:YA:1588:C:C6	2.33	0.63
10:YH:27:LYS:HD3	10:YH:32:GLU:HG3	1.79	0.63
12:YN:97:ARG:HA	12:YN:100:GLU:HG2	1.81	0.63
35:QA:222:U:H2'	35:QA:223:U:C6	2.34	0.63
37:XC:119:ARG:HD3	37:XC:140:ARG:NH2	2.11	0.63
35:XA:1318:A:H4'	53:XS:10:PHE:CE2	2.33	0.63
9:YG:150:ASP:OD1	9:YG:151:ALA:N	2.32	0.63
38:QD:79:PHE:HE1	38:QD:204:ILE:HD13	1.64	0.63
42:QH:37:ARG:HH21	42:QH:38:ILE:HD11	1.64	0.63
15:RQ:16:ARG:HG2	15:RQ:18:LYS:HG3	1.80	0.63
35:QA:90:U:H2'	35:QA:91:C:C6	2.34	0.63
4:RA:2138:C:H2'	4:RA:2139:C:C6	2.34	0.63
36:XB:127:ILE:HG12	36:XB:128:GLU:N	2.14	0.63
4:YA:38:A:H2'	4:YA:39:C:C6	2.32	0.63
4:YA:1695:G:N7	6:YD:14:ARG:NH2	2.46	0.63
4:YA:2319:G:H22	17:YS:3:ARG:NH1	1.97	0.63
36:QB:28:PHE:CE1	36:QB:31:TYR:HB2	2.34	0.63
55:QU:18:TYR:HB3	55:QU:22:ARG:O	1.98	0.63
28:R3:3:ARG:HD3	28:R3:60:GLU:OE2	1.99	0.63
33:R8:28:GLY:O	33:R8:36:LYS:NZ	2.30	0.63
4:RA:582:G:H2'	4:RA:583:G:C8	2.33	0.63
4:RA:923:C:H2'	4:RA:924:C:H6	1.63	0.63
18:RT:39:ARG:HH12	18:RT:41:ARG:HD3	1.63	0.63
36:XB:88:ALA:HB2	36:XB:219:VAL:HG13	1.80	0.63
4:YA:1292:U:H2'	4:YA:1293:C:C6	2.33	0.63
4:YA:2152:G:H2'	4:YA:2153:G:C8	2.33	0.63
8:YF:95:ARG:HG3	8:YF:97:TYR:CE1	2.34	0.63
18:YT:53:ARG:NH1	18:YT:53:ARG:O	2.32	0.63
35:QA:1143:G:H2'	35:QA:1144:G:H8	1.63	0.62
38:QD:108:LEU:HD21	38:QD:183:GLY:HA3	1.80	0.62
38:QD:116:GLN:HE21	38:QD:157:LEU:HD11	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:QT:10:LEU:HD23	54:QT:11:SER:H	1.63	0.62
27:R2:16:LEU:O	27:R2:67:LYS:NZ	2.31	0.62
35:XA:977:A:N6	35:XA:1224:G:OP1	2.28	0.62
35:XA:441:A:H3'	35:XA:442:C:H6	1.64	0.62
48:XN:9:LYS:O	48:XN:12:ARG:HG2	1.99	0.62
4:YA:1798:U:H5'	6:YD:259:THR:HG22	1.80	0.62
4:YA:2140:C:H2'	4:YA:2141:G:H8	1.64	0.62
10:YH:86:GLU:OE2	10:YH:132:ARG:NH2	2.32	0.62
46:QL:117:ARG:HG2	46:QL:122:THR:HB	1.81	0.62
4:RA:1936:A:OP2	4:RA:1962:5MC:N4	2.29	0.62
35:XA:1278:U:H5''	35:XA:1279:A:H5'	1.81	0.62
3:XY:273:GLN:HG2	3:XY:274:CYS:N	2.03	0.62
38:QD:53:ASP:HB3	38:QD:57:ARG:NH1	2.14	0.62
4:RA:1796:U:H2'	4:RA:1797:C:H6	1.64	0.62
4:RA:2836:U:H2'	4:RA:2837:G:C8	2.33	0.62
4:RA:286:C:H2'	4:RA:287:C:C6	2.34	0.62
8:RF:185:ASP:HA	8:RF:188:ARG:HD3	1.81	0.62
4:RA:272(K):U:H1'	11:RI:50:ARG:NH2	2.14	0.62
12:RN:120:LEU:HD22	12:RN:122:VAL:HG23	1.81	0.62
35:XA:1244:C:H2'	35:XA:1245:A:C8	2.34	0.62
35:XA:1391:U:H2'	35:XA:1392:G:C8	2.34	0.62
41:XG:18:TYR:CD2	41:XG:59:LEU:HB2	2.35	0.62
9:YG:113:ARG:HH21	29:Y4:33:VAL:HG12	1.63	0.62
23:YY:14:LEU:HD12	23:YY:22:GLY:O	1.99	0.62
40:QF:2:ARG:HB2	40:QF:4:TYR:HE1	1.63	0.62
4:RA:2271:G:C5'	25:R0:20:ARG:HE	2.12	0.62
4:RA:641:C:O2'	4:RA:2350:C:OP1	2.16	0.62
35:XA:1117:G:H4'	43:XI:104:ARG:HH12	1.63	0.62
35:XA:1244:C:H2'	35:XA:1245:A:H8	1.64	0.62
42:XH:42:GLU:HG3	42:XH:109:ILE:HD13	1.80	0.62
35:QA:316:G:OP2	35:QA:351:G:O2'	2.16	0.62
7:RE:48:GLN:NE2	7:RE:66:HIS:NE2	2.47	0.62
36:QB:76:GLN:NE2	36:QB:206:ASP:HA	2.14	0.62
4:RA:1639:U:H2'	4:RA:1640:C:H5''	1.81	0.62
13:YO:68:GLU:HB3	13:YO:78:ARG:HB2	1.82	0.62
35:QA:108:G:N1	54:QT:15:ARG:HG2	2.15	0.62
35:QA:1172:C:H2'	35:QA:1173:G:H8	1.65	0.62
36:QB:98:LEU:O	36:QB:101:MET:HG3	1.99	0.62
40:QF:2:ARG:HB2	40:QF:4:TYR:CE1	2.34	0.62
43:QI:4:TYR:CD1	43:QI:88:TYR:HB2	2.35	0.62
4:RA:1065:U:H4'	4:RA:1066:U:H5'	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:2206:G:H3'	4:RA:2207:G:C8	2.35	0.62
53:XS:10:PHE:HD1	53:XS:10:PHE:C	2.03	0.62
3:XY:21:LEU:HD11	3:XY:114:GLU:HG2	1.81	0.62
33:Y8:6:THR:HG22	33:Y8:63:PRO:HD2	1.82	0.62
4:YA:1249:U:H2'	14:YP:18:ARG:HH22	1.62	0.62
4:YA:1657:C:H2'	4:YA:1658:C:C6	2.34	0.62
14:RP:59:LEU:HD21	33:R8:10:ALA:HA	1.82	0.62
13:RO:68:GLU:N	13:RO:68:GLU:OE1	2.31	0.62
19:RU:76:TYR:CE1	19:RU:80:ILE:HG13	2.35	0.62
35:XA:1006:C:H2'	35:XA:1007:C:C6	2.35	0.62
35:XA:1309:G:OP1	47:XM:88:ARG:HD3	2.00	0.62
38:XD:12:CYS:SG	38:XD:19:LEU:HB2	2.39	0.62
43:XI:33:PHE:CE1	43:XI:37:PHE:HD2	2.17	0.62
4:YA:1429:G:H2'	4:YA:1430:C:C6	2.35	0.62
4:YA:2138:C:H2'	4:YA:2139:C:C6	2.35	0.62
6:YD:108:PRO:HG2	6:YD:111:LEU:HG	1.81	0.62
4:RA:607:U:OP1	8:RF:102:PRO:HA	1.99	0.62
1:XV:53:G:O4'	24:YZ:198:LYS:HD2	2.00	0.62
3:XY:161:PHE:HD1	3:XY:185:GLY:HA3	1.65	0.62
4:YA:1823:G:OP1	6:YD:54:ARG:NH1	2.32	0.62
4:YA:276:A:H5''	4:YA:277:C:H5'	1.82	0.62
4:YA:607:U:OP1	8:YF:102:PRO:HA	2.00	0.62
4:YA:657:U:H2'	4:YA:658:C:C6	2.35	0.62
23:YY:13:VAL:O	23:YY:24:VAL:HA	2.00	0.62
43:QI:108:VAL:HG12	43:QI:109:VAL:H	1.65	0.62
3:QY:38:ASN:O	3:QY:42:GLU:HB2	2.00	0.62
53:QS:67:VAL:HG21	29:R4:59:PHE:CE1	2.35	0.62
4:RA:1101:U:H2'	4:RA:1102:C:C6	2.34	0.62
4:RA:2839:G:H5'	16:RR:46:GLY:HA2	1.80	0.62
17:RS:106:ARG:HG3	17:RS:112:PHE:HE1	1.64	0.62
35:XA:1002:G:N3	35:XA:1003:G:H8	1.98	0.62
35:XA:501:C:H2'	35:XA:502:G:H8	1.64	0.62
36:XB:166:ASP:HB3	36:XB:169:LYS:HB3	1.80	0.62
50:XP:71:ARG:HH11	50:XP:71:ARG:HG3	1.64	0.62
35:QA:713:G:H2'	35:QA:714:G:C8	2.34	0.61
4:RA:1378:A:OP1	32:R7:10:ARG:NH2	2.33	0.61
4:RA:2243:U:H2'	4:RA:2244:U:C6	2.35	0.61
4:RA:2328:A:H2'	4:RA:2329:G:C8	2.35	0.61
8:RF:51:THR:HB	8:RF:88:VAL:HG11	1.81	0.61
9:RG:150:ASP:OD1	9:RG:151:ALA:N	2.33	0.61
21:RW:8:ARG:HH21	21:RW:9:TYR:HE2	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1796:U:H2'	4:YA:1797:C:C6	2.35	0.61
4:YA:1889:A:H2'	4:YA:1890:A:C8	2.35	0.61
4:YA:218:A:C2	4:YA:235:U:H4'	2.34	0.61
53:QS:3:ARG:NH1	53:QS:10:PHE:HB2	2.15	0.61
8:RF:40:GLN:NE2	8:RF:182:ASN:HB2	2.15	0.61
9:RG:139:LEU:HD21	9:RG:149:VAL:HG11	1.83	0.61
46:XL:70:ILE:HG12	46:XL:100:ILE:HD12	1.82	0.61
4:YA:2110:G:OP1	4:YA:2118:U:N3	2.30	0.61
15:YQ:60:ARG:HH21	24:YZ:181:GLU:HG2	1.64	0.61
35:QA:1003:G:H2'	35:QA:1004:A:H4'	1.82	0.61
4:RA:813:U:H2'	4:RA:814:C:H6	1.65	0.61
36:XB:16:HIS:HB2	36:XB:204:ASN:HB3	1.82	0.61
44:XJ:35:SER:HB3	44:XJ:73:ASP:H	1.65	0.61
3:XY:96:PHE:O	3:XY:96:PHE:HD1	1.84	0.61
4:YA:1028:A:N6	4:YA:1125:G:H2'	2.16	0.61
18:YT:101:PHE:HD2	18:YT:102:ILE:N	1.98	0.61
40:QF:70:ASP:OD1	40:QF:70:ASP:N	2.31	0.61
31:R6:9:LEU:HD22	31:R6:51:GLU:OE2	1.99	0.61
4:RA:2064:C:H2'	4:RA:2065:C:C6	2.35	0.61
3:XY:303:LYS:O	3:XY:307:LYS:HG2	2.00	0.61
24:YZ:44:PHE:C	24:YZ:44:PHE:HD1	2.04	0.61
4:RA:2152:G:H2'	4:RA:2153:G:C8	2.34	0.61
11:RI:84:GLY:N	11:RI:89:TYR:HE1	1.97	0.61
35:XA:189(L):U:H2'	35:XA:189(M):G:C8	2.36	0.61
47:XM:19:LEU:HD21	47:XM:56:LEU:HD21	1.81	0.61
4:YA:1067:A:H4'	4:YA:1068:G:OP2	2.00	0.61
35:QA:501:C:H2'	35:QA:502:G:H8	1.64	0.61
37:XC:58:GLU:HB3	44:XJ:92:THR:HG21	1.81	0.61
38:XD:27:TYR:N	38:XD:27:TYR:HD1	1.98	0.61
43:XI:49:PRO:HG3	43:XI:101:PHE:HD2	1.65	0.61
49:XO:6:GLU:N	49:XO:6:GLU:OE1	2.25	0.61
10:YH:28:GLY:HA3	10:YH:79:VAL:HB	1.81	0.61
15:YQ:34:LEU:HB2	15:YQ:118:LEU:HD22	1.81	0.61
35:QA:1207:2MG:H2'	35:QA:1208:C:H6	1.65	0.61
35:QA:270:A:H2'	35:QA:271:C:C6	2.36	0.61
35:QA:918:A:H2'	35:QA:919:A:C8	2.36	0.61
6:RD:69:ARG:NH2	6:RD:128:GLY:O	2.34	0.61
35:XA:449:C:O2	50:XP:42:ARG:HD2	2.00	0.61
27:Y2:16:LEU:O	27:Y2:67:LYS:NZ	2.33	0.61
8:YF:40:GLN:NE2	8:YF:182:ASN:HB2	2.16	0.61
17:YS:27:SER:HA	17:YS:88:ASP:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1402:4OC:HM22	35:QA:1403:C:H5'	1.82	0.61
35:QA:403:C:H4'	38:QD:122:ARG:NH1	2.15	0.61
3:QY:195:GLU:HG2	3:QY:357:ILE:HD11	1.81	0.61
4:RA:2074:U:H2'	4:RA:2075:U:C6	2.36	0.61
13:RO:119:PRO:HB2	18:RT:68:TYR:CE2	2.36	0.61
26:Y1:50:ARG:HG2	26:Y1:59:THR:HG22	1.82	0.61
9:YG:49:ASP:OD1	9:YG:49:ASP:N	2.32	0.61
22:YX:65:ARG:HB3	22:YX:70:LEU:HD23	1.83	0.61
35:QA:407:G:O2'	38:QD:116:GLN:HG3	2.01	0.61
38:QD:76:ARG:HD3	38:QD:207:TYR:CE1	2.35	0.61
35:QA:1289:A:OP1	55:QU:10:ARG:NH2	2.33	0.61
4:RA:1826:G:H4'	6:RD:242:ARG:NH2	2.16	0.61
7:RE:73:GLU:N	7:RE:73:GLU:OE1	2.32	0.61
38:XD:106:TYR:HD1	38:XD:106:TYR:C	2.03	0.61
39:XE:20:GLN:NE2	39:XE:25:ARG:HD2	2.16	0.61
43:XI:33:PHE:CD1	43:XI:37:PHE:HD2	2.18	0.61
51:XQ:4:LYS:H	51:XQ:61:GLU:HG2	1.66	0.61
3:XY:121:GLY:O	3:XY:123:TYR:N	2.33	0.61
37:QC:155:GLY:HA3	37:QC:196:LEU:HD22	1.83	0.61
38:QD:88:VAL:HG22	39:QE:96:PRO:HB2	1.83	0.61
39:QE:31:LEU:HD11	39:QE:129:ILE:HA	1.82	0.61
43:QI:33:PHE:HE1	43:QI:43:ALA:HB1	1.66	0.61
4:RA:2138:C:H2'	4:RA:2139:C:H6	1.65	0.61
4:RA:639:U:H2'	4:RA:640:C:C6	2.35	0.61
4:RA:923:C:H2'	4:RA:924:C:C6	2.36	0.61
16:RR:24:GLN:HB3	16:RR:44:LEU:HD11	1.83	0.61
36:XB:144:ARG:NH2	36:XB:148:TYR:OH	2.33	0.61
4:YA:813:U:H2'	4:YA:814:C:H6	1.65	0.61
7:YE:51:PHE:O	7:YE:77:ILE:HB	2.00	0.61
12:YN:131:GLN:N	12:YN:131:GLN:OE1	2.29	0.61
37:QC:47:LEU:HD13	37:QC:68:VAL:HG11	1.83	0.60
36:XB:8:LYS:HD2	36:XB:51:LEU:HD13	1.83	0.60
37:XC:119:ARG:NH1	37:XC:140:ARG:HE	1.98	0.60
27:Y2:35:LEU:HD12	27:Y2:53:LEU:HD12	1.83	0.60
4:YA:2134:A:N6	4:YA:2156:G:O2'	2.34	0.60
4:YA:534:U:H2'	4:YA:535:C:C6	2.36	0.60
35:QA:1286:A:H2'	35:QA:1287:A:H4'	1.83	0.60
37:QC:6:HIS:HE1	37:QC:8:ILE:HB	1.66	0.60
4:RA:1405:U:H2'	4:RA:1406:U:H6	1.65	0.60
37:XC:140:ARG:CB	37:XC:140:ARG:HH11	2.13	0.60
8:YF:99:TYR:HD1	8:YF:99:TYR:N	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:YN:120:LEU:HD22	12:YN:122:VAL:HG23	1.83	0.60
18:YT:53:ARG:HB3	18:YT:53:ARG:HH11	1.66	0.60
35:QA:341:C:H2'	35:QA:342:C:C6	2.37	0.60
35:QA:743:U:H2'	35:QA:744:C:C6	2.36	0.60
38:QD:191:ARG:HD3	38:QD:200:GLU:OE2	2.02	0.60
41:QG:48:LYS:O	41:QG:52:GLU:HG2	2.00	0.60
15:RQ:69:PHE:HD1	15:RQ:70:PRO:N	1.98	0.60
35:XA:1182:G:H4'	35:XA:1183:A:H3'	1.81	0.60
35:XA:316:G:OP2	35:XA:351:G:O2'	2.19	0.60
37:XC:114:PRO:O	37:XC:118:GLN:HG3	2.01	0.60
3:XY:130:LEU:HD22	3:XY:132:ILE:HG13	1.82	0.60
32:Y7:34:ARG:HG3	32:Y7:39:ARG:HG3	1.82	0.60
4:YA:1721:G:H8	4:YA:1741:A:H62	1.49	0.60
6:YD:71:ASP:HB3	6:YD:103:ARG:HH22	1.65	0.60
24:YZ:44:PHE:C	24:YZ:44:PHE:CD1	2.75	0.60
3:QY:162:LYS:HB3	3:QY:184:SER:HB3	1.84	0.60
4:RA:1587:A:H2'	4:RA:1588:C:C6	2.37	0.60
4:RA:2646:C:OP2	4:RA:2732:G:O2'	2.13	0.60
7:RE:34:VAL:CG2	7:RE:48:GLN:HE21	2.14	0.60
35:XA:184:G:H2'	35:XA:185:A:H8	1.66	0.60
36:XB:28:PHE:CD1	36:XB:31:TYR:HB2	2.36	0.60
35:XA:738:C:OP1	40:XF:2:ARG:NH1	2.34	0.60
40:XF:95:GLU:O	52:XR:32:ARG:NH2	2.29	0.60
3:XY:22:ARG:HG2	3:XY:70:LEU:HD13	1.84	0.60
4:YA:958:U:OP2	15:YQ:14:ARG:NH1	2.34	0.60
12:YN:62:VAL:HG13	12:YN:66:LYS:HD2	1.81	0.60
35:QA:1027:C:H2'	35:QA:1028:C:C5	2.37	0.60
35:QA:201:C:H42	35:QA:216:G:H1	1.50	0.60
35:QA:974:A:OP2	48:QN:29:ARG:NH2	2.32	0.60
36:QB:78:GLN:NE2	36:QB:95:GLN:OE1	2.35	0.60
4:RA:1709:U:H2'	4:RA:1710:C:C6	2.37	0.60
6:RD:10:THR:OG1	6:RD:13:ARG:HG2	2.01	0.60
35:XA:270:A:H2'	35:XA:271:C:C6	2.37	0.60
19:YU:58:ARG:NH2	19:YU:92:ARG:HH12	2.00	0.60
35:QA:277:C:P	51:QQ:68:ARG:HH12	2.24	0.60
4:RA:1920:4OC:HM22	4:RA:1921:G:H5'	1.83	0.60
35:XA:407:G:H2'	35:XA:408:A:C8	2.36	0.60
35:XA:715:A:H2'	35:XA:716:A:C8	2.37	0.60
4:YA:1371:G:HO2'	4:YA:1372:U:H5	1.50	0.60
4:YA:1379:A:H4'	4:YA:1380:G:OP2	2.01	0.60
4:YA:639:U:H2'	4:YA:640:C:C6	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:668:G:H5'	4:YA:669:G:OP2	2.02	0.60
38:QD:98:GLU:OE1	38:QD:103:ASN:ND2	2.29	0.60
4:RA:218:A:C2	4:RA:235:U:H4'	2.37	0.60
4:RA:969:U:H2'	4:RA:970:C:C6	2.37	0.60
6:RD:147:LEU:HD11	6:RD:183:ARG:HH21	1.65	0.60
7:RE:119:ARG:HD2	7:RE:120:TRP:CE2	2.37	0.60
9:RG:115:ARG:HB3	9:RG:136:ARG:HH22	1.66	0.60
11:RI:86:THR:O	11:RI:122:GLU:HB2	2.02	0.60
35:XA:1014:A:H2	35:XA:1219:U:H1'	1.66	0.60
35:XA:1329:A:OP2	55:XU:7:ARG:NH2	2.30	0.60
38:XD:79:PHE:HE1	38:XD:204:ILE:HD13	1.65	0.60
46:XL:86:ARG:HD2	46:XL:87:GLY:HA3	1.83	0.60
49:XO:25:THR:HG21	49:XO:70:LEU:HB2	1.83	0.60
53:XS:10:PHE:CD1	53:XS:10:PHE:C	2.75	0.60
4:YA:1530:C:O2'	4:YA:1531:C:H6	1.85	0.60
4:YA:2328:A:H2'	4:YA:2329:G:C8	2.36	0.60
22:RX:5:TYR:O	27:R2:36:ARG:NH2	2.33	0.60
4:RA:1292:U:H2'	4:RA:1293:C:C6	2.37	0.60
10:RH:163:TYR:HE2	10:RH:169:VAL:HG22	1.66	0.60
19:RU:111:GLU:OE1	19:RU:111:GLU:HA	2.02	0.60
19:RU:47:TYR:HE2	20:RV:74:LYS:HE2	1.66	0.60
39:XE:57:LYS:HG2	39:XE:61:TYR:CE2	2.37	0.60
40:XF:44:GLY:HA2	40:XF:59:TYR:CD1	2.37	0.60
4:YA:1353:A:H2'	4:YA:1354:A:C8	2.36	0.60
4:YA:641:C:O2'	4:YA:2350:C:OP1	2.18	0.60
4:YA:249:C:O2	33:Y8:12:LYS:NZ	2.30	0.60
42:QH:41:ARG:NH2	42:QH:123:GLU:OE2	2.33	0.60
49:QO:16:ALA:HB1	49:QO:21:ASP:HB3	1.82	0.60
4:RA:78:A:H2'	4:RA:79:G:H8	1.66	0.60
4:RA:1798:U:H5'	6:RD:259:THR:HG22	1.84	0.60
18:RT:55:ASN:N	18:RT:59:THR:HG22	2.12	0.60
35:XA:1014:A:C2	35:XA:1219:U:H1'	2.35	0.60
34:Y9:22:ARG:HB2	34:Y9:24:TYR:HE1	1.67	0.60
8:YF:197:ASP:OD1	8:YF:198:ALA:N	2.35	0.60
11:YI:14:ASP:OD1	11:YI:15:VAL:N	2.34	0.60
47:QM:3:ARG:HG3	47:QM:4:ILE:N	2.17	0.60
4:RA:1817:G:OP1	6:RD:88:ARG:NH2	2.34	0.60
35:XA:407:G:H2'	35:XA:408:A:H8	1.65	0.60
38:XD:116:GLN:NE2	38:XD:157:LEU:HD11	2.17	0.60
4:YA:2243:U:H2'	4:YA:2244:U:C6	2.36	0.60
40:QF:100:ASN:ND2	52:QR:26:LEU:O	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1794:U:H2'	4:RA:1795:C:C6	2.37	0.59
4:RA:38:A:H2'	4:RA:39:C:C6	2.37	0.59
15:RQ:31:ASP:C	15:RQ:32:TYR:HD1	2.05	0.59
19:RU:76:TYR:C	19:RU:76:TYR:HD1	2.06	0.59
23:RY:8:LYS:HG2	23:RY:97:ARG:NH1	2.14	0.59
35:XA:474:G:H2'	35:XA:475:G:H8	1.66	0.59
4:YA:2646:C:OP2	4:YA:2732:G:O2'	2.14	0.59
36:QB:80:ILE:HD11	36:QB:212:GLN:HB2	1.83	0.59
43:QI:10:ARG:HG2	43:QI:75:ASP:HB2	1.84	0.59
11:RI:115:ALA:HB2	11:RI:131:LYS:HE2	1.85	0.59
4:RA:272(K):U:H1'	11:RI:50:ARG:HH21	1.67	0.59
35:XA:67:C:H2'	35:XA:68:G:C8	2.37	0.59
4:YA:857:C:OP2	25:Y0:77:ARG:NH2	2.34	0.59
4:YA:1786:A:H1'	4:YA:1938:A:N6	2.17	0.59
4:YA:78:A:H2'	4:YA:79:G:H8	1.66	0.59
19:YU:76:TYR:HD1	19:YU:76:TYR:C	2.05	0.59
41:QG:111:ARG:NH1	41:QG:122:HIS:HB2	2.17	0.59
4:RA:1507:A:O2'	4:RA:1508:A:O5'	2.18	0.59
35:XA:406:G:H5'	38:XD:5:ILE:HD11	1.84	0.59
1:XV:53:G:H4'	1:XV:54:U:OP1	2.01	0.59
4:YA:30:G:H2'	4:YA:31:C:C6	2.37	0.59
10:YH:7:LEU:HB3	10:YH:69:ARG:HH11	1.68	0.59
21:YW:67:ASP:OD1	21:YW:67:ASP:N	2.35	0.59
35:QA:407:G:H2'	35:QA:408:A:C8	2.38	0.59
37:QC:131:ARG:NH1	37:QC:135:LYS:HE3	2.16	0.59
35:XA:737:A:H2'	35:XA:738:C:C6	2.37	0.59
38:XD:106:TYR:C	38:XD:106:TYR:CD1	2.76	0.59
13:YO:64:ARG:HG2	13:YO:79:PHE:CD2	2.36	0.59
18:YT:14:TYR:HD1	18:YT:14:TYR:N	2.00	0.59
4:RA:1721:G:H8	4:RA:1741:A:H62	1.47	0.59
4:RA:639:U:H2'	4:RA:640:C:H6	1.66	0.59
11:RI:101:LEU:HD11	11:RI:140:LEU:HD11	1.84	0.59
43:XI:60:ASP:OD1	43:XI:60:ASP:N	2.34	0.59
4:YA:1359:A:H61	4:YA:1372:U:H3	1.50	0.59
4:YA:336:C:O2'	23:YY:35:TYR:OH	2.21	0.59
7:YE:14:ILE:HG13	7:YE:21:VAL:HG13	1.84	0.59
9:YG:161:THR:HG22	9:YG:163:ALA:H	1.66	0.59
18:YT:65:LYS:HE2	18:YT:67:SER:HB2	1.85	0.59
35:QA:537:G:H5''	46:QL:113:ARG:NH1	2.17	0.59
3:QY:243:VAL:HG12	3:QY:261:VAL:HG12	1.85	0.59
3:QY:230:ILE:HG23	3:QY:299:GLU:CG	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:QM:65:LYS:HA	29:R4:50:VAL:HG11	1.83	0.59
35:XA:946:A:H2'	35:XA:947:G:H8	1.64	0.59
37:XC:141:VAL:HG11	37:XC:202:ILE:HG12	1.84	0.59
29:Y4:59:PHE:CD1	29:Y4:59:PHE:N	2.71	0.59
35:QA:642:A:N3	42:QH:113:SER:OG	2.32	0.59
4:RA:1796:U:H2'	4:RA:1797:C:C6	2.37	0.59
54:XT:50:GLU:HG3	54:XT:100:ILE:HD11	1.84	0.59
4:YA:660:G:H5'	8:YF:99:TYR:CE2	2.37	0.59
10:YH:159:GLU:HG2	10:YH:169:VAL:HG11	1.84	0.59
36:QB:17:PHE:HD1	36:QB:17:PHE:N	2.01	0.59
39:QE:33:VAL:HG13	39:QE:112:LEU:HD12	1.83	0.59
4:RA:2698:U:H2'	4:RA:2699:C:C6	2.37	0.59
7:RE:34:VAL:HG23	7:RE:48:GLN:HE21	1.67	0.59
38:XD:27:TYR:N	38:XD:27:TYR:CD1	2.71	0.59
40:XF:8:ILE:HG22	40:XF:10:LEU:HD13	1.84	0.59
3:XY:159:ARG:HH21	3:XY:354:ASP:CG	2.06	0.59
4:YA:2698:U:H2'	4:YA:2699:C:C6	2.37	0.59
14:YP:52:GLU:HB3	14:YP:55:ARG:NH1	2.12	0.59
16:YR:29:LEU:HB3	16:YR:75:LEU:HD21	1.85	0.59
22:YX:88:LYS:HG2	22:YX:93:GLU:HG3	1.84	0.59
37:QC:131:ARG:NE	37:QC:166:GLU:OE2	2.34	0.59
27:R2:63:VAL:O	27:R2:66:GLU:HB3	2.01	0.59
29:R4:57:GLU:HB2	29:R4:58:ARG:HA	1.85	0.59
4:RA:660:G:H5'	8:RF:99:TYR:CE2	2.38	0.59
5:RB:77:U:OP1	24:RZ:19:ARG:NH2	2.36	0.59
38:XD:138:TYR:HD1	38:XD:139:ARG:N	2.00	0.59
38:XD:173:TRP:CD1	38:XD:189:PRO:HG3	2.38	0.59
39:XE:31:LEU:HD11	39:XE:129:ILE:HA	1.84	0.59
44:XJ:11:PHE:HE1	44:XJ:67:THR:HG22	1.67	0.59
4:YA:1693:U:O2	6:YD:14:ARG:NH1	2.35	0.59
4:YA:2102:U:O2	4:YA:2187:G:O6	2.21	0.59
8:YF:178:PRO:HB2	8:YF:201:VAL:CG2	2.33	0.59
17:YS:67:ARG:HG2	17:YS:100:ALA:O	2.03	0.59
35:QA:737:A:H2'	35:QA:738:C:H6	1.66	0.59
38:QD:59:ARG:HH21	38:QD:62:GLN:HG3	1.68	0.59
40:QF:8:ILE:HG22	40:QF:10:LEU:HD13	1.84	0.59
53:QS:10:PHE:HD1	53:QS:11:VAL:N	2.01	0.59
4:RA:210:C:OP1	32:R7:29:LYS:HE2	2.02	0.59
14:RP:63:PRO:HG2	33:R8:25:MET:HB2	1.85	0.59
38:XD:191:ARG:NE	38:XD:200:GLU:OE2	2.34	0.59
47:XM:3:ARG:HH12	47:XM:11:ARG:HE	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:127:A:H5''	4:YA:128:C:C6	2.38	0.59
6:YD:52:ARG:HH12	6:YD:249:PRO:HG2	1.68	0.59
26:R1:3:LYS:HG3	26:R1:4:VAL:H	1.68	0.58
4:RA:2022:U:O2'	4:RA:2617:C:H5'	2.02	0.58
4:RA:2292:C:P	17:RS:17:ARG:HH12	2.25	0.58
35:XA:1103:C:OP1	36:XB:96:ARG:NH2	2.36	0.58
35:XA:266:G:O2'	35:XA:267:C:OP2	2.15	0.58
3:XY:33:ARG:HD2	3:XY:36:GLU:OE2	2.02	0.58
4:YA:2740:A:H2'	4:YA:2741:A:C8	2.38	0.58
7:YE:12:THR:HG22	7:YE:13:ARG:H	1.66	0.58
8:YF:53:THR:HG23	8:YF:55:GLY:H	1.68	0.58
16:YR:36:THR:HG22	16:YR:37:THR:H	1.68	0.58
36:QB:76:GLN:HE21	36:QB:206:ASP:CA	2.17	0.58
36:QB:229:VAL:HG12	36:QB:230:VAL:H	1.67	0.58
43:QI:65:VAL:HG21	43:QI:73:GLN:HB3	1.85	0.58
4:RA:486:C:H4'	21:RW:60:ASN:ND2	2.18	0.58
24:RZ:136:PHE:CD1	24:RZ:136:PHE:N	2.67	0.58
35:XA:1002:G:H2'	35:XA:1003:G:C8	2.37	0.58
39:XE:102:ALA:HB1	39:XE:106:PRO:HG2	1.85	0.58
35:XA:673:G:H5''	40:XF:87:ARG:NH1	2.17	0.58
42:XH:37:ARG:HH21	42:XH:38:ILE:HD11	1.67	0.58
46:XL:86:ARG:NH1	46:XL:99:HIS:HB2	2.18	0.58
29:Y4:16:CYS:SG	29:Y4:17:GLY:N	2.76	0.58
4:YA:2680:C:OP2	7:YE:111:ARG:NH2	2.36	0.58
35:QA:1510:U:H2'	35:QA:1511:G:C8	2.37	0.58
35:QA:184:G:H2'	35:QA:185:A:H8	1.68	0.58
40:QF:23:LYS:HG2	40:QF:61:LEU:HD21	1.84	0.58
37:XC:40:ARG:HH12	48:XN:52:GLN:HG2	1.69	0.58
25:Y0:60:PHE:HD1	25:Y0:60:PHE:H	1.49	0.58
27:Y2:38:GLN:HB3	27:Y2:44:LEU:HB2	1.85	0.58
4:YA:1385:G:O2'	4:YA:1396:U:O2	2.20	0.58
4:YA:2138:C:H2'	4:YA:2139:C:H6	1.66	0.58
4:YA:2206:G:H8	4:YA:2207:G:N7	2.01	0.58
4:YA:2648:C:H2'	4:YA:2649:U:C6	2.38	0.58
4:YA:1815:A:OP2	6:YD:54:ARG:NH2	2.36	0.58
3:QY:199:HIS:CD2	3:QY:324:ARG:HD2	2.38	0.58
4:RA:1068:G:H3'	4:RA:1096:A:OP2	2.04	0.58
4:RA:272(O):C:H2'	4:RA:272(P):C:C6	2.39	0.58
35:XA:1346:A:OP1	43:XI:120:ARG:NH1	2.34	0.58
43:XI:9:ARG:HG2	43:XI:14:VAL:HG12	1.85	0.58
4:YA:1507:A:O2'	4:YA:1508:A:O5'	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:639:U:H2'	4:YA:640:C:H6	1.69	0.58
35:QA:1062:U:H2'	35:QA:1063:C:C6	2.38	0.58
47:QM:80:ARG:HG2	47:QM:80:ARG:HH11	1.67	0.58
3:QY:129:TYR:HB2	3:QY:223:TYR:CE1	2.39	0.58
21:RW:23:LEU:HD11	30:R5:25:LEU:HB2	1.86	0.58
35:XA:1346:A:C5	41:XG:10:ARG:NH2	2.70	0.58
37:XC:140:ARG:HB2	37:XC:140:ARG:NH1	2.19	0.58
29:Y4:42:PHE:HD2	29:Y4:43:TYR:CE1	2.21	0.58
4:YA:581:C:H2'	4:YA:582:G:H8	1.67	0.58
6:YD:108:PRO:HB3	6:YD:143:HIS:CE1	2.37	0.58
35:QA:614:A:OP1	38:QD:85:LYS:NZ	2.36	0.58
35:XA:642:A:N3	42:XH:113:SER:OG	2.31	0.58
4:YA:2023:G:H5'	4:YA:2617:C:H4'	1.86	0.58
35:QA:1014:A:C2	35:QA:1219:U:H1'	2.38	0.58
35:QA:560:U:O2'	35:QA:561:U:OP2	2.18	0.58
35:QA:626:U:H4'	50:QP:38:TYR:CE2	2.37	0.58
4:RA:1062:G:N7	4:RA:1070:A:H1'	2.19	0.58
12:RN:62:VAL:HG13	12:RN:66:LYS:HD2	1.85	0.58
40:XF:75:LEU:HD22	40:XF:79:LEU:HG	1.85	0.58
43:XI:31:GLN:NE2	43:XI:36:TYR:HD1	2.02	0.58
8:YF:101:LEU:HD12	8:YF:102:PRO:HD2	1.84	0.58
4:YA:300:A:OP1	23:YY:86:ARG:NH2	2.36	0.58
35:QA:1309:G:OP1	47:QM:88:ARG:HD2	2.04	0.58
35:QA:343:U:O2'	35:QA:346:G:O6	2.13	0.58
35:QA:38:G:H22	35:QA:397:A:H5'	1.67	0.58
35:QA:714:G:H2'	35:QA:715:A:C8	2.38	0.58
36:QB:16:HIS:HB2	36:QB:204:ASN:HB3	1.85	0.58
36:QB:24:TRP:CZ3	36:QB:26:PRO:HA	2.38	0.58
4:RA:2740:A:H2'	4:RA:2741:A:C8	2.39	0.58
6:RD:8:PRO:HB3	6:RD:14:ARG:HG3	1.85	0.58
35:XA:1027:C:H3'	35:XA:1028:C:C6	2.38	0.58
50:XP:17:TYR:N	50:XP:17:TYR:HD1	2.01	0.58
54:XT:89:ARG:O	54:XT:93:GLU:HG2	2.03	0.58
5:YB:48:A:H2'	5:YB:49:C:C6	2.39	0.58
40:QF:36:ARG:NH2	40:QF:66:GLU:OE1	2.37	0.58
3:QY:132:ILE:HB	3:QY:179:VAL:HG23	1.86	0.58
3:QY:245:ARG:HE	4:RA:2573:C:N4	1.99	0.58
8:RF:164:ARG:O	8:RF:168:ARG:HB3	2.03	0.58
23:RY:55:TYR:CE2	23:RY:61:ILE:HG21	2.39	0.58
35:XA:1062:U:H2'	35:XA:1063:C:C6	2.39	0.58
35:XA:544:G:OP1	38:XD:59:ARG:NH2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:XB:7:VAL:O	36:XB:217:ARG:NE	2.37	0.58
29:Y4:61:ARG:HG2	53:XS:42:PRO:CG	2.34	0.58
4:YA:2591:C:H2'	4:YA:2592:G:C8	2.38	0.58
4:YA:994:C:OP1	19:YU:53:ARG:NH2	2.36	0.58
4:YA:2787:C:H1'	7:YE:62:PRO:HG3	1.86	0.58
8:YF:99:TYR:HD1	8:YF:99:TYR:H	1.51	0.58
11:YI:85:GLU:HG3	11:YI:86:THR:H	1.67	0.58
13:YO:115:VAL:HG13	13:YO:121:VAL:HG21	1.86	0.58
4:RA:1024:G:HO2'	4:RA:1144:G:HO2'	1.46	0.58
4:RA:2291:U:H2'	4:RA:2292:C:C6	2.38	0.58
19:RU:76:TYR:C	19:RU:76:TYR:CD1	2.77	0.58
35:XA:1001(A):A:H2'	35:XA:1001(B):G:C8	2.38	0.58
3:XY:332:ARG:NH1	35:XA:531:U:O4	2.28	0.58
35:XA:992:U:H4'	35:XA:993:G:O5'	2.04	0.58
3:XY:168:GLU:HG2	3:XY:179:VAL:HG12	1.85	0.58
3:XY:342:THR:HG22	3:XY:344:ASN:H	1.68	0.58
4:YA:1069:A:H5'	4:YA:1096:A:H5'	1.86	0.58
4:YA:2648:C:H2'	4:YA:2649:U:H6	1.69	0.58
19:YU:76:TYR:CE1	19:YU:80:ILE:HG13	2.38	0.58
37:QC:29:TYR:CD2	48:QN:36:PHE:HE1	2.22	0.57
3:QY:303:LYS:O	3:QY:307:LYS:HG2	2.03	0.57
27:R2:32:LEU:HD11	27:R2:54:LYS:HG2	1.84	0.57
16:RR:36:THR:HG22	16:RR:37:THR:H	1.69	0.57
40:XF:19:LEU:HD11	40:XF:59:TYR:HE2	1.69	0.57
3:XY:106:LEU:HD23	3:XY:109:LYS:HD3	1.85	0.57
3:XY:132:ILE:HB	3:XY:179:VAL:HG23	1.85	0.57
4:YA:2271:G:C5'	25:Y0:20:ARG:HE	2.16	0.57
4:YA:1639:U:H2'	4:YA:1640:C:H5''	1.85	0.57
4:YA:690:G:H2'	4:YA:691:C:C6	2.39	0.57
10:YH:89:ILE:O	10:YH:129:THR:HG23	2.04	0.57
35:QA:56:U:H2'	35:QA:57:G:C8	2.39	0.57
35:QA:992:U:H4'	35:QA:993:G:H5'	1.86	0.57
4:RA:2206:G:H3'	4:RA:2207:G:H8	1.68	0.57
6:RD:132:PRO:HG3	6:RD:190:TYR:CE1	2.39	0.57
4:RA:2751:G:C8	10:RH:2:SER:HA	2.39	0.57
35:XA:1030(B):G:H2'	35:XA:1030(C):C:H5''	1.87	0.57
53:XS:27:GLU:OE1	53:XS:47:HIS:NE2	2.33	0.57
4:YA:2074:U:H2'	4:YA:2075:U:C6	2.39	0.57
4:YA:923:C:H2'	4:YA:924:C:H6	1.69	0.57
6:YD:17:THR:O	6:YD:211:ARG:NH2	2.37	0.57
19:YU:47:TYR:HE2	20:YV:74:LYS:HE2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:QF:97:PHE:CD2	52:QR:31:LEU:HD23	2.40	0.57
42:QH:10:LEU:HD22	42:QH:83:ILE:HD11	1.86	0.57
48:QN:4:LYS:HA	48:QN:7:ILE:HG12	1.85	0.57
40:QF:97:PHE:HD2	52:QR:31:LEU:HD23	1.69	0.57
4:RA:2567:G:H2'	4:RA:2568:C:C6	2.39	0.57
35:XA:501:C:H2'	35:XA:502:G:C8	2.38	0.57
37:XC:108:ASN:HD21	37:XC:144:SER:HB3	1.69	0.57
44:XJ:49:VAL:HG23	48:YN:41:ARG:CG	2.33	0.57
29:Y4:67:TYR:HD1	29:Y4:67:TYR:N	2.00	0.57
4:YA:2206:G:H3'	4:YA:2207:G:C8	2.38	0.57
4:YA:2206:G:H3'	4:YA:2207:G:H8	1.69	0.57
4:YA:270:A:OP2	4:YA:272(X):G:N1	2.28	0.57
10:YH:11:VAL:HG21	10:YH:50:VAL:HG23	1.86	0.57
35:QA:34:C:H2'	35:QA:35:G:H8	1.67	0.57
35:QA:564:C:O2'	42:QH:91:ARG:NH2	2.34	0.57
29:R4:61:ARG:CG	29:R4:62:ARG:H	2.18	0.57
4:RA:1657:C:H2'	4:RA:1658:C:H6	1.69	0.57
4:RA:2572:A:N7	7:RE:144:ARG:HD2	2.20	0.57
10:RH:154:PRO:HG3	10:RH:163:TYR:CD1	2.39	0.57
35:XA:1302:U:OP2	47:XM:21:TYR:OH	2.17	0.57
35:XA:262:A:H2'	35:XA:263:A:H8	1.67	0.57
35:XA:407:G:O2'	38:XD:116:GLN:HG3	2.05	0.57
38:XD:116:GLN:HE21	38:XD:157:LEU:HD11	1.69	0.57
4:YA:1429:G:H2'	4:YA:1430:C:H6	1.69	0.57
9:YG:117:PHE:HD1	9:YG:119:GLY:H	1.53	0.57
35:QA:1071:C:H2'	35:QA:1072:G:H8	1.69	0.57
35:QA:1183:A:H3'	35:QA:1184:G:H5''	1.87	0.57
49:QO:6:GLU:N	49:QO:6:GLU:OE1	2.26	0.57
3:QY:41:LEU:HA	3:QY:46:VAL:HG21	1.86	0.57
4:RA:1067:A:H4'	4:RA:1068:G:OP2	2.03	0.57
4:RA:1467:C:C5	4:RA:1546:C:H2'	2.39	0.57
8:RF:178:PRO:HB2	8:RF:201:VAL:CG2	2.34	0.57
35:XA:164:U:H2'	35:XA:165:C:C6	2.40	0.57
47:XM:3:ARG:NH1	47:XM:11:ARG:HE	2.02	0.57
4:YA:658:C:H2'	4:YA:659:C:C6	2.40	0.57
10:YH:115:VAL:HG11	10:YH:148:ILE:HD11	1.87	0.57
35:QA:341:C:H2'	35:QA:342:C:H6	1.70	0.57
3:QY:230:ILE:HG22	3:QY:230:ILE:O	2.05	0.57
29:R4:16:CYS:SG	29:R4:17:GLY:N	2.77	0.57
4:RA:1530:C:O2'	4:RA:1531:C:H6	1.87	0.57
6:RD:52:ARG:HH12	6:RD:249:PRO:HG2	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:RE:37:ARG:HG3	7:RE:80:GLU:OE2	2.05	0.57
4:RA:1036:G:OP2	10:RH:59:ARG:NH1	2.37	0.57
19:RU:62:ILE:HG23	19:RU:76:TYR:CE2	2.40	0.57
35:XA:1029:C:N4	35:XA:1030(A):C:H41	2.02	0.57
3:XY:243:VAL:HG12	3:XY:261:VAL:HG12	1.87	0.57
11:YI:4:ILE:HD11	11:YI:44:LEU:HD12	1.85	0.57
35:QA:1020:U:H2'	35:QA:1021:G:C8	2.39	0.57
35:QA:390:C:H2'	35:QA:391:G:C8	2.40	0.57
37:QC:35:GLU:HG2	37:QC:59:ARG:HH22	1.70	0.57
43:QI:42:ARG:NH1	43:QI:75:ASP:OD1	2.35	0.57
2:QX:22:C:H41	3:QY:210:GLY:HA3	1.70	0.57
4:RA:184:C:H2'	4:RA:185:U:C6	2.40	0.57
4:RA:2156:G:N7	4:RA:2157:G:N2	2.52	0.57
4:RA:848:G:H2'	4:RA:849:A:H8	1.66	0.57
41:XG:18:TYR:HD2	41:XG:59:LEU:HB2	1.70	0.57
3:XY:191:TRP:O	3:XY:194:THR:HG22	2.05	0.57
29:Y4:59:PHE:CZ	53:XS:64:GLU:HB2	2.40	0.57
13:YO:8:LEU:HD12	13:YO:84:ALA:HB2	1.85	0.57
35:QA:269:C:H2'	35:QA:270:A:H8	1.70	0.57
36:QB:76:GLN:HE21	36:QB:206:ASP:C	2.08	0.57
54:QT:57:ARG:HH12	54:QT:100:ILE:HD12	1.69	0.57
8:RF:184:TYR:CE2	8:RF:188:ARG:HD2	2.39	0.57
35:XA:375:U:H4'	50:XP:17:TYR:HE2	1.69	0.57
4:YA:2156:G:N7	4:YA:2157:G:N2	2.53	0.57
4:YA:2279:G:N7	25:Y0:14:ARG:NH1	2.46	0.57
17:YS:35:ILE:C	17:YS:36:TYR:HD1	2.07	0.57
19:YU:76:TYR:C	19:YU:76:TYR:CD1	2.78	0.57
35:QA:100:C:H2'	35:QA:101:A:C8	2.40	0.57
35:QA:600:C:H2'	35:QA:601:C:H6	1.70	0.57
36:QB:17:PHE:CD1	36:QB:17:PHE:N	2.73	0.57
4:RA:876:C:H2'	4:RA:877:U:O4'	2.05	0.57
24:RZ:3:TYR:N	24:RZ:3:TYR:HD1	2.03	0.57
35:XA:222:U:H2'	35:XA:223:U:C6	2.40	0.57
41:XG:113:GLU:HG2	41:XG:119:ARG:HG2	1.86	0.57
4:YA:1292:U:H2'	4:YA:1293:C:H6	1.67	0.57
4:YA:881:G:H2'	4:YA:882:G:C8	2.39	0.57
14:YP:86:LYS:HB3	14:YP:118:GLY:HA3	1.87	0.57
21:YW:14:PRO:HG2	21:YW:78:GLU:HG3	1.85	0.57
35:QA:1412:C:H2'	35:QA:1413:A:C8	2.39	0.57
35:QA:1492:A:OP2	46:QL:47:LYS:NZ	2.38	0.57
14:RP:90:ARG:HH12	14:RP:105:LEU:HD21	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:RV:12:TYR:CD2	20:RV:20:LEU:HD11	2.40	0.57
24:RZ:126:VAL:HG11	24:RZ:161:VAL:HG23	1.87	0.57
36:XB:55:PHE:CD1	36:XB:221:LEU:HD12	2.39	0.57
36:XB:78:GLN:HA	36:XB:78:GLN:HE21	1.70	0.57
4:YA:2291:U:H2'	4:YA:2292:C:C6	2.40	0.57
4:YA:674:G:O2'	8:YF:74:ARG:HD3	2.04	0.57
4:YA:889:C:O2'	4:YA:890:A:O5'	2.23	0.57
12:YN:4:TYR:CD2	19:YU:100:VAL:HG11	2.40	0.57
19:YU:62:ILE:HG23	19:YU:76:TYR:CE2	2.40	0.57
24:YZ:3:TYR:HD1	24:YZ:3:TYR:N	2.02	0.57
35:QA:1072:G:H2'	35:QA:1073:U:C6	2.40	0.56
40:QF:33:TYR:HE2	40:QF:78:GLU:HG2	1.69	0.56
4:RA:1406:U:H2'	4:RA:1407:C:H6	1.70	0.56
4:RA:2110:G:OP1	4:RA:2118:U:N3	2.35	0.56
4:RA:2023:G:H5'	4:RA:2617:C:H4'	1.85	0.56
6:RD:148:GLU:HB2	6:RD:151:LYS:HD2	1.88	0.56
12:RN:4:TYR:CD2	19:RU:100:VAL:HG11	2.40	0.56
18:RT:60:THR:HG22	18:RT:77:PRO:HA	1.87	0.56
36:XB:18:GLY:HA2	36:XB:42:ILE:HD12	1.86	0.56
3:XY:244:TYR:CD1	3:XY:244:TYR:N	2.72	0.56
26:Y1:86:SER:OG	26:Y1:89:GLU:OE1	2.13	0.56
4:YA:2649:U:H2'	4:YA:2650:U:H6	1.70	0.56
19:YU:89:GLU:O	20:YV:11:GLN:NE2	2.32	0.56
3:QY:319:TRP:HE1	35:QA:1492:A:H2'	1.68	0.56
35:QA:501:C:H2'	35:QA:502:G:C8	2.40	0.56
37:QC:22:TRP:CZ2	48:QN:54:PRO:HG2	2.40	0.56
1:QV:76:A:H3'	3:QY:251:GLY:HA3	1.86	0.56
3:QY:324:ARG:HB3	3:QY:326:TYR:HE1	1.70	0.56
4:RA:2103:C:C4	4:RA:2104:G:N2	2.73	0.56
4:RA:608:A:H2'	4:RA:609:A:C8	2.40	0.56
8:RF:99:TYR:N	8:RF:99:TYR:HD1	2.01	0.56
4:RA:2405:G:H5'	14:RP:75:ILE:HD13	1.87	0.56
35:XA:692:U:O2'	35:XA:694:A:N7	2.36	0.56
38:XD:173:TRP:CD1	38:XD:174:LEU:HG	2.39	0.56
38:XD:59:ARG:HH21	38:XD:62:GLN:HG3	1.69	0.56
41:XG:146:GLU:OE2	41:XG:149:ARG:NE	2.38	0.56
43:XI:24:GLY:HA2	43:XI:59:PHE:O	2.05	0.56
3:XY:129:TYR:HB2	3:XY:223:TYR:CE1	2.39	0.56
3:XY:58:LYS:HD2	4:YA:1068:G:N2	2.21	0.56
4:YA:1062:G:H5'	4:YA:1070:A:H5''	1.87	0.56
17:YS:94:TYR:CE1	17:YS:99:LYS:HG3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1030(D):G:N7	35:QA:1031:G:N2	2.52	0.56
35:QA:449:C:O2	50:QP:42:ARG:HD2	2.06	0.56
51:QQ:62:SER:OG	51:QQ:72:ARG:HG3	2.03	0.56
8:RF:33:LEU:HD13	8:RF:112:MET:HE2	1.87	0.56
14:RP:52:GLU:HB3	14:RP:55:ARG:NH1	2.16	0.56
35:XA:266:G:H5''	35:XA:266:G:N3	2.19	0.56
35:XA:737:A:H2'	35:XA:738:C:H6	1.69	0.56
40:XF:70:ASP:OD1	40:XF:70:ASP:N	2.38	0.56
3:XY:68:ASP:O	3:XY:72:GLN:HG3	2.05	0.56
4:YA:2321:G:O2'	4:YA:2322:A:OP1	2.21	0.56
4:YA:30:G:H2'	4:YA:31:C:H6	1.70	0.56
4:YA:856:C:H2'	4:YA:857:C:C6	2.40	0.56
11:YI:101:LEU:HD11	11:YI:140:LEU:HD11	1.86	0.56
20:YV:76:LYS:HB2	20:YV:81:TYR:HB3	1.88	0.56
35:QA:1009:G:C2	35:QA:1010:G:C8	2.93	0.56
35:QA:1428:A:H2'	35:QA:1429:C:C6	2.40	0.56
35:QA:412:A:C6	38:QD:35:ARG:HD3	2.41	0.56
50:QP:38:TYR:N	50:QP:38:TYR:HD1	2.02	0.56
3:QY:203:ARG:HG3	3:QY:204:LYS:N	2.21	0.56
4:RA:589:C:H2'	4:RA:590:A:H8	1.69	0.56
4:RA:668:G:H5'	4:RA:669:G:OP2	2.05	0.56
35:XA:1129:C:H2'	35:XA:1139:G:N7	2.20	0.56
37:XC:124:ILE:HD12	37:XC:196:LEU:HD12	1.87	0.56
46:XL:28:LYS:N	46:XL:29:GLY:HA2	2.21	0.56
50:XP:17:TYR:N	50:XP:17:TYR:CD1	2.74	0.56
4:YA:1826:G:H4'	6:YD:242:ARG:NH2	2.21	0.56
35:QA:56:U:H2'	35:QA:57:G:H8	1.70	0.56
47:QM:15:VAL:HG11	47:QM:48:LEU:HD21	1.85	0.56
53:QS:3:ARG:HH21	53:QS:7:LYS:HE3	1.70	0.56
4:RA:1265:A:H3'	30:R5:19:ARG:NH1	2.20	0.56
4:RA:2849:U:H4'	4:RA:2868:A:C2	2.40	0.56
18:RT:28:VAL:O	18:RT:46:GLU:HA	2.05	0.56
36:XB:105:PHE:O	36:XB:105:PHE:HD1	1.89	0.56
36:XB:24:TRP:CZ3	36:XB:26:PRO:HA	2.40	0.56
4:YA:1406:U:H2'	4:YA:1407:C:H6	1.71	0.56
4:YA:994:C:H3'	19:YU:54:LYS:HE3	1.85	0.56
36:QB:55:PHE:HB3	36:QB:221:LEU:HD11	1.86	0.56
3:QY:138:GLY:O	3:QY:142:GLN:HG3	2.04	0.56
3:QY:217:PHE:N	3:QY:217:PHE:CD1	2.74	0.56
4:RA:1786:A:H1'	4:RA:1938:A:N6	2.20	0.56
4:RA:590:A:H2'	4:RA:591:C:C6	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:2748:A:H5'	10:RH:4:ILE:HD12	1.87	0.56
4:RA:1035:U:OP1	10:RH:59:ARG:NH2	2.38	0.56
24:RZ:198:LYS:HB2	24:RZ:203:GLU:C	2.25	0.56
35:XA:769:G:H4'	35:XA:1513:A:H4'	1.88	0.56
38:XD:8:VAL:HG22	38:XD:21:LEU:HD13	1.87	0.56
31:Y6:9:LEU:HD22	31:Y6:51:GLU:OE2	2.06	0.56
4:YA:2223:G:OP1	6:YD:172:TYR:OH	2.20	0.56
6:YD:142:VAL:HG23	6:YD:193:VAL:HA	1.87	0.56
8:YF:29:ASN:HB3	8:YF:112:MET:HE1	1.88	0.56
35:QA:600:C:H2'	35:QA:601:C:C6	2.40	0.56
50:QP:34:GLU:OE2	50:QP:55:ARG:NH2	2.38	0.56
3:QY:213:ARG:HH22	3:QY:327:VAL:HG23	1.70	0.56
4:RA:2180:U:H2'	4:RA:2181:G:C8	2.41	0.56
11:RI:92:VAL:HG13	11:RI:120:ILE:HB	1.88	0.56
16:RR:55:ALA:CB	16:RR:79:LEU:HD22	2.36	0.56
43:XI:21:PRO:HA	43:XI:59:PHE:HA	1.88	0.56
8:YF:99:TYR:CD1	8:YF:99:TYR:N	2.72	0.56
35:QA:1316:G:N1	35:QA:1319:A:OP2	2.38	0.56
3:QY:325:SER:O	3:QY:333:ILE:HA	2.05	0.56
4:RA:2336:A:H61	25:R0:43:THR:HG22	1.70	0.56
4:RA:2649:U:H2'	4:RA:2650:U:H6	1.70	0.56
4:RA:78:A:H2'	4:RA:79:G:C8	2.41	0.56
11:RI:54:GLN:HA	11:RI:57:ARG:HG2	1.87	0.56
35:XA:718:G:C4	45:XK:116:HIS:CD2	2.94	0.56
4:YA:414:C:H2'	4:YA:415:A:C8	2.40	0.56
4:YA:581:C:H2'	4:YA:582:G:C8	2.41	0.56
4:YA:1188:U:H4'	20:YV:79:VAL:HG22	1.87	0.56
35:QA:164:U:H2'	35:QA:165:C:H6	1.70	0.56
47:QM:32:GLU:HG2	47:QM:64:TRP:HZ2	1.71	0.56
44:QJ:45:ARG:NH1	48:QN:36:PHE:HD2	2.03	0.56
4:RA:1497:U:H5''	4:RA:1498:C:H5	1.71	0.56
4:RA:589:C:H2'	4:RA:590:A:C8	2.41	0.56
35:XA:390:C:H2'	35:XA:391:G:C8	2.41	0.56
3:XY:18:SER:O	3:XY:22:ARG:HG3	2.06	0.56
25:Y0:11:ARG:O	25:Y0:14:ARG:NH2	2.39	0.56
4:YA:1378:A:OP1	32:Y7:10:ARG:NH2	2.39	0.56
4:YA:590:A:H2'	4:YA:591:C:C6	2.41	0.56
35:QA:922:G:H2'	35:QA:923:A:C8	2.41	0.56
4:RA:1316:U:H2'	4:RA:1317:A:H8	1.71	0.56
4:RA:1379:A:H4'	4:RA:1380:G:OP2	2.05	0.56
15:RQ:92:GLY:C	15:RQ:93:TYR:HD1	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:RT:28:VAL:HG13	18:RT:86:ILE:HG23	1.88	0.56
24:RZ:25:PRO:O	24:RZ:85:HIS:HA	2.05	0.56
35:XA:1410:G:H2'	35:XA:1411:C:C6	2.40	0.56
35:XA:689:C:OP1	45:XK:27:ASN:ND2	2.35	0.56
36:XB:178:ARG:NH1	36:XB:198:ASP:OD1	2.39	0.56
37:XC:121:ALA:O	37:XC:125:GLU:HG3	2.06	0.56
39:XE:141:GLN:HA	39:XE:143:ARG:HH21	1.71	0.56
43:XI:58:HIS:C	43:XI:59:PHE:HD1	2.09	0.56
3:XY:244:TYR:HD1	3:XY:244:TYR:H	1.52	0.56
3:XY:34:LEU:HD11	3:XY:60:ARG:HG3	1.87	0.56
4:YA:2115:G:H21	4:YA:2171:A:H61	1.54	0.56
4:YA:305:U:H2'	4:YA:306:U:C6	2.40	0.56
6:YD:148:GLU:HB2	6:YD:151:LYS:HD2	1.87	0.56
18:YT:91:ARG:HD2	18:YT:120:ARG:NH1	2.21	0.56
23:YY:23:ARG:HH11	23:YY:23:ARG:HB2	1.71	0.56
35:QA:186:C:H2'	35:QA:187:C:H6	1.70	0.56
35:QA:945:G:C2	35:QA:946:A:C8	2.94	0.56
38:QD:81:GLU:OE2	38:QD:139:ARG:NH2	2.31	0.56
29:R4:53:GLU:HG3	29:R4:55:ARG:H	1.71	0.56
4:RA:1429:G:H2'	4:RA:1430:C:C6	2.41	0.56
4:RA:2128:C:H5'	4:RA:2129:C:OP2	2.06	0.56
4:RA:2206:G:H5''	4:RA:2207:G:C8	2.41	0.56
4:RA:674:G:H1'	8:RF:74:ARG:HD3	1.87	0.56
13:RO:36:GLY:HA3	13:RO:109:LYS:HD2	1.88	0.56
3:XY:136:SER:HA	35:XA:1493:A:H1'	1.88	0.56
35:XA:57:G:H2'	35:XA:58:C:C6	2.41	0.56
36:XB:16:HIS:O	36:XB:18:GLY:N	2.39	0.56
26:Y1:51:VAL:HG11	26:Y1:74:VAL:HG21	1.88	0.56
4:YA:2099:U:H3	4:YA:2190:G:H1	1.54	0.56
4:YA:2334:G:H5'	17:YS:9:ARG:HG2	1.88	0.56
8:YF:29:ASN:H	8:YF:112:MET:CE	2.18	0.56
35:QA:1104:G:H4'	36:QB:111:ARG:NH1	2.21	0.55
35:QA:1255:G:P	44:QJ:45:ARG:NH2	2.79	0.55
3:QY:115:PHE:HB3	3:QY:119:PHE:HD2	1.69	0.55
4:RA:285:C:H2'	4:RA:286:C:H6	1.71	0.55
4:RA:652(U):C:H2'	4:RA:652(V):G:C8	2.40	0.55
4:RA:904:C:H2'	4:RA:905:U:C6	2.42	0.55
8:RF:99:TYR:N	8:RF:99:TYR:CD1	2.72	0.55
14:RP:90:ARG:NH1	14:RP:105:LEU:HD11	2.22	0.55
4:YA:1165:U:H2'	4:YA:1166:C:H6	1.70	0.55
4:YA:2065:C:H2'	4:YA:2066:C:H6	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:YQ:31:ASP:C	15:YQ:32:TYR:HD1	2.08	0.55
35:QA:123:C:OP1	35:QA:311:C:O2'	2.23	0.55
40:QF:75:LEU:HD22	40:QF:79:LEU:HG	1.88	0.55
42:QH:33:GLU:HG2	42:QH:48:TYR:HE2	1.71	0.55
4:RA:1864:U:OP1	4:RA:2410:G:O2'	2.19	0.55
4:RA:582:G:H2'	4:RA:583:G:H8	1.70	0.55
18:RT:24:PRO:HD3	18:RT:52:ILE:HD12	1.87	0.55
39:XE:33:VAL:HG13	39:XE:112:LEU:HD12	1.87	0.55
4:YA:2180:U:H2'	4:YA:2181:G:C8	2.40	0.55
24:YZ:157:LEU:HD11	24:YZ:163:LEU:HB2	1.88	0.55
35:QA:1117:G:H5''	43:QI:104:ARG:HH12	1.70	0.55
35:QA:335:C:H2'	35:QA:336:C:C6	2.42	0.55
39:QE:33:VAL:HG21	39:QE:109:ILE:HA	1.89	0.55
39:QE:8:GLU:OE2	39:QE:63:ARG:NH2	2.39	0.55
50:QP:37:GLY:HA3	50:QP:50:LYS:O	2.07	0.55
27:R2:35:LEU:HD12	27:R2:53:LEU:HD12	1.88	0.55
6:RD:177:LEU:HD11	6:RD:183:ARG:HD3	1.88	0.55
4:YA:1593:G:H2'	4:YA:1594:G:C8	2.42	0.55
3:XY:315:SER:OG	4:YA:1914:C:N4	2.39	0.55
6:YD:177:LEU:HD11	6:YD:183:ARG:HD3	1.87	0.55
35:QA:1003:G:N2	35:QA:1004:A:N3	2.54	0.55
1:QV:51:C:H2'	1:QV:52:G:O4'	2.07	0.55
29:R4:54:GLY:O	29:R4:56:VAL:HA	2.06	0.55
4:RA:1688:U:O2	4:RA:1700:A:H5'	2.06	0.55
4:RA:1946:U:H2'	4:RA:1947:C:H6	1.72	0.55
4:RA:2130:U:H2'	4:RA:2158:A:H61	1.71	0.55
14:RP:98:GLU:OE1	14:RP:102:ARG:NH1	2.39	0.55
3:XY:280:GLN:HB2	4:YA:2493:U:H4'	1.88	0.55
26:Y1:2:SER:HB3	26:Y1:46:LEU:HD12	1.89	0.55
33:Y8:6:THR:HG23	33:Y8:64:TYR:HD2	1.71	0.55
4:YA:2206:G:H5''	4:YA:2207:G:C8	2.41	0.55
4:YA:234:C:H2'	4:YA:235:U:H6	1.71	0.55
8:YF:24:LEU:HD23	8:YF:115:ALA:HA	1.88	0.55
17:YS:36:TYR:N	17:YS:36:TYR:HD1	2.04	0.55
18:YT:14:TYR:CD1	18:YT:14:TYR:N	2.72	0.55
21:YW:12:ILE:HD13	21:YW:17:VAL:HG13	1.88	0.55
44:QJ:44:VAL:HG22	44:QJ:66:ARG:HE	1.70	0.55
3:QY:125:SER:HA	3:QY:187:TYR:HA	1.88	0.55
3:QY:141:ALA:HB2	3:QY:216:SER:HB2	1.88	0.55
4:RA:1406:U:H2'	4:RA:1407:C:C6	2.41	0.55
4:RA:2685:G:H5'	13:RO:68:GLU:OE2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:XB:77:ALA:HB2	36:XB:211:ILE:HD13	1.89	0.55
45:XK:18:ARG:HB2	45:XK:33:THR:OG1	2.07	0.55
35:XA:35:G:O2'	46:XL:118:SER:O	2.25	0.55
3:XY:241:ILE:HG21	3:XY:284:LYS:HE2	1.88	0.55
3:XY:244:TYR:HD1	3:XY:244:TYR:N	2.04	0.55
3:XY:326:TYR:HD1	3:XY:326:TYR:N	2.04	0.55
24:YZ:125:LEU:HB3	24:YZ:165:VAL:HG13	1.89	0.55
35:QA:1068:G:H8	35:QA:1068:G:OP2	1.90	0.55
36:QB:23:ARG:O	36:QB:23:ARG:HG2	2.07	0.55
3:QY:84:LEU:HD22	3:QY:96:PHE:CD1	2.42	0.55
4:RA:305:U:H2'	4:RA:306:U:C6	2.41	0.55
35:XA:1005:A:H5''	35:XA:1006:C:C6	2.41	0.55
35:XA:555:C:H2'	35:XA:556:C:C6	2.41	0.55
1:XV:53:G:O6	1:XV:62:C:N4	2.39	0.55
4:YA:1062:G:N7	4:YA:1070:A:H1'	2.22	0.55
15:YQ:59:ARG:NH1	15:YQ:60:ARG:HH11	2.04	0.55
35:QA:745:C:H2'	35:QA:746:A:C8	2.42	0.55
37:QC:3:ASN:N	37:QC:3:ASN:OD1	2.39	0.55
44:QJ:84:GLN:HG2	44:QJ:85:LEU:N	2.21	0.55
46:QL:120:TYR:N	46:QL:120:TYR:HD1	2.04	0.55
53:QS:74:PHE:CD1	53:QS:74:PHE:N	2.75	0.55
29:R4:13:ARG:HD3	29:R4:15:ILE:HD11	1.87	0.55
53:QS:45:VAL:HG21	29:R4:59:PHE:CZ	2.41	0.55
4:RA:127:A:H5''	4:RA:128:C:C6	2.42	0.55
4:RA:1842:G:H2'	4:RA:1843:C:C6	2.41	0.55
4:RA:2304:G:N2	4:RA:2312:U:H3	2.02	0.55
4:RA:272(E):U:H2'	4:RA:272(F):C:C6	2.41	0.55
7:RE:37:ARG:O	7:RE:45:THR:HA	2.07	0.55
17:RS:5:THR:OG1	17:RS:8:GLU:HG3	2.07	0.55
35:XA:500:G:H2'	35:XA:501:C:C6	2.42	0.55
35:XA:743:U:H2'	35:XA:744:C:C6	2.42	0.55
4:YA:2103:C:C4	4:YA:2104:G:N2	2.75	0.55
4:YA:247:G:H4'	4:YA:386:G:C5	2.42	0.55
35:QA:1024:G:H2'	35:QA:1025:U:H5''	1.88	0.55
35:QA:411:A:OP2	38:QD:25:ARG:NH2	2.40	0.55
36:QB:167:PRO:HG3	36:QB:186:ALA:HB1	1.87	0.55
3:QY:265:HIS:CD2	3:QY:267:PRO:HD2	2.42	0.55
8:RF:107:LYS:HG3	8:RF:206:ILE:HA	1.88	0.55
17:RS:59:LYS:HG3	17:RS:60:GLY:N	2.18	0.55
4:YA:1406:U:H2'	4:YA:1407:C:C6	2.42	0.55
4:YA:1588:C:H2'	4:YA:1589:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1709:U:H2'	4:YA:1710:C:H6	1.71	0.55
4:YA:1842:G:H2'	4:YA:1843:C:C6	2.42	0.55
35:QA:1143:G:H2'	35:QA:1144:G:C8	2.42	0.55
36:QB:109:SER:O	36:QB:112:VAL:HG22	2.07	0.55
40:QF:61:LEU:HD23	40:QF:63:TYR:OH	2.07	0.55
43:QI:16:ARG:HH11	43:QI:64:THR:HG21	1.71	0.55
37:QC:58:GLU:HB3	44:QJ:92:THR:HG21	1.89	0.55
46:QL:42:THR:HA	46:QL:53:ARG:O	2.07	0.55
3:QY:22:ARG:HG2	3:QY:70:LEU:HD13	1.89	0.55
8:RF:64:ILE:HG21	8:RF:78:ILE:HG23	1.89	0.55
4:RA:2319:G:H22	17:RS:3:ARG:HD2	1.71	0.55
35:XA:922:G:H4'	39:XE:20:GLN:HA	1.87	0.55
42:XH:65:TYR:CD1	42:XH:65:TYR:N	2.75	0.55
25:Y0:70:GLN:NE2	25:Y0:80:HIS:HE2	2.05	0.55
29:Y4:47:GLN:C	29:Y4:48:ARG:HD2	2.27	0.55
4:YA:1250:G:N7	14:YP:18:ARG:NH2	2.53	0.55
4:YA:2455:G:H2'	4:YA:2456:C:C6	2.42	0.55
8:YF:152:GLU:HG2	8:YF:190:GLU:OE1	2.06	0.55
4:YA:322:A:OP1	8:YF:168:ARG:HD2	2.07	0.55
22:YX:12:VAL:HG22	22:YX:29:TRP:CE2	2.41	0.55
35:QA:629:G:H2'	35:QA:630:G:O4'	2.08	0.55
35:QA:376:G:H5''	50:QP:5:ARG:HD2	1.89	0.55
4:RA:30:G:H2'	4:RA:31:C:C6	2.42	0.55
4:RA:414:C:H2'	4:RA:415:A:C8	2.42	0.55
35:XA:269:C:H2'	35:XA:270:A:C8	2.42	0.55
36:XB:77:ALA:HA	36:XB:80:ILE:HG22	1.89	0.55
35:XA:537:G:H5''	46:XL:113:ARG:HH12	1.71	0.55
4:YA:1796:U:H2'	4:YA:1797:C:H6	1.71	0.55
4:YA:2127:G:H2'	4:YA:2128:C:O4'	2.07	0.55
4:YA:2441:C:OP2	4:YA:2586:C:O2'	2.25	0.55
35:QA:176:C:H2'	35:QA:177:C:H6	1.72	0.54
38:QD:173:TRP:CD2	38:QD:189:PRO:HG3	2.43	0.54
3:QY:340:VAL:HG12	3:QY:341:GLU:H	1.72	0.54
11:RI:85:GLU:OE1	11:RI:85:GLU:HA	2.06	0.54
35:XA:1285:A:H4'	35:XA:1286:A:H5'	1.88	0.54
35:XA:411:A:OP2	38:XD:25:ARG:NH2	2.39	0.54
35:XA:678:U:H2'	35:XA:679:C:C6	2.42	0.54
38:XD:133:VAL:HG11	38:XD:138:TYR:CD2	2.42	0.54
35:XA:1117:G:H4'	43:XI:104:ARG:NH1	2.22	0.54
45:XK:81:ASP:OD1	45:XK:106:LYS:HB2	2.07	0.54
4:YA:2233:U:H2'	4:YA:2234:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:2304:G:N2	4:YA:2312:U:H3	1.95	0.54
4:YA:93:G:H2'	4:YA:94(A):C:C6	2.41	0.54
17:YS:67:ARG:HG3	17:YS:100:ALA:HB1	1.88	0.54
21:YW:86:LEU:HD22	21:YW:96:ILE:HD11	1.89	0.54
35:QA:17:U:H2'	35:QA:18:C:H6	1.71	0.54
37:QC:29:TYR:CD2	48:QN:36:PHE:CE1	2.95	0.54
41:QG:113:GLU:HG2	41:QG:119:ARG:HG2	1.88	0.54
1:QV:53:G:H4'	1:QV:54:U:OP1	2.07	0.54
3:QY:256:ARG:NH1	4:RA:2573:C:C2	2.68	0.54
4:RA:658:C:H2'	4:RA:659:C:C6	2.41	0.54
8:RF:18:ARG:HG2	8:RF:19:GLU:N	2.22	0.54
13:RO:79:PHE:N	13:RO:79:PHE:CD1	2.76	0.54
14:RP:83:VAL:HG12	14:RP:112:LEU:HD21	1.89	0.54
17:RS:36:TYR:HD1	17:RS:36:TYR:N	2.04	0.54
35:XA:1002:G:N3	35:XA:1003:G:C8	2.76	0.54
35:XA:1346:A:C4	41:XG:10:ARG:NH2	2.71	0.54
35:XA:714:G:H2'	35:XA:715:A:C8	2.43	0.54
36:XB:84:GLU:HB3	36:XB:219:VAL:HG21	1.89	0.54
38:XD:98:GLU:HA	38:XD:103:ASN:ND2	2.21	0.54
1:XV:51:C:H2'	1:XV:52:G:C8	2.42	0.54
13:YO:68:GLU:OE1	13:YO:68:GLU:N	2.34	0.54
18:YT:45:PHE:C	18:YT:45:PHE:CD1	2.81	0.54
24:YZ:3:TYR:N	24:YZ:3:TYR:CD1	2.75	0.54
35:QA:1148:U:H2'	35:QA:1149:C:O4'	2.07	0.54
35:QA:328:C:H4'	35:QA:329:A:H5'	1.89	0.54
26:R1:51:VAL:HG11	26:R1:74:VAL:HG21	1.88	0.54
9:RG:3:LEU:HD22	29:R4:25:TYR:CE2	2.43	0.54
34:R9:35:ARG:HG2	34:R9:36:GLN:N	2.21	0.54
4:RA:918:A:H5''	5:RB:98:G:O2'	2.07	0.54
17:RS:87:PHE:CD1	17:RS:112:PHE:HE2	2.25	0.54
18:RT:68:TYR:CD1	18:RT:68:TYR:N	2.74	0.54
24:RZ:185:GLU:HG3	24:RZ:186:GLU:N	2.23	0.54
36:XB:181:PHE:CD1	36:XB:181:PHE:N	2.76	0.54
3:XY:191:TRP:HE3	3:XY:357:ILE:HG21	1.72	0.54
3:XY:217:PHE:N	3:XY:217:PHE:CD1	2.74	0.54
3:XY:311:GLU:HA	3:XY:314:LYS:CD	2.38	0.54
29:Y4:46:GLN:N	29:Y4:46:GLN:OE1	2.40	0.54
4:YA:904:C:H2'	4:YA:905:U:H6	1.71	0.54
4:YA:923:C:H2'	4:YA:924:C:C6	2.43	0.54
9:YG:11:TYR:HD2	9:YG:12:TYR:CE1	2.25	0.54
10:YH:3:ARG:NH1	10:YH:3:ARG:C	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:YS:25:ARG:HD2	17:YS:42:ASP:OD2	2.07	0.54
4:YA:560:C:H5'	19:YU:52:ARG:HH21	1.73	0.54
24:YZ:156:LYS:HG3	24:YZ:156:LYS:O	2.07	0.54
35:QA:946:A:H2'	35:QA:947:G:H8	1.71	0.54
34:R9:22:ARG:HB2	34:R9:24:TYR:HE1	1.73	0.54
3:QY:256:ARG:NH1	4:RA:2573:C:N3	2.55	0.54
9:RG:114:ILE:HG12	9:RG:140:ILE:HG12	1.89	0.54
17:RS:87:PHE:HD1	17:RS:112:PHE:HE2	1.56	0.54
1:QV:54:U:OP2	24:RZ:203:GLU:HB2	2.07	0.54
24:RZ:3:TYR:N	24:RZ:3:TYR:CD1	2.76	0.54
35:XA:945:G:C2	35:XA:946:A:C8	2.95	0.54
43:XI:88:TYR:C	43:XI:88:TYR:HD1	2.10	0.54
4:YA:1588:C:H2'	4:YA:1589:C:H6	1.72	0.54
4:YA:484:C:H2'	4:YA:485:C:H6	1.73	0.54
8:YF:132:VAL:HG21	8:YF:163:VAL:HG22	1.89	0.54
15:YQ:57:HIS:CE1	15:YQ:116:GLU:HB3	2.35	0.54
18:YT:61:PHE:N	18:YT:61:PHE:CD1	2.74	0.54
41:QG:79:ARG:HA	41:QG:84:ASN:HA	1.88	0.54
46:QL:71:PRO:O	46:QL:102:ARG:NH1	2.41	0.54
47:QM:14:ARG:NE	47:QM:42:ALA:HA	2.23	0.54
53:QS:45:VAL:HG21	29:R4:59:PHE:HZ	1.73	0.54
34:R9:16:VAL:HG22	34:R9:25:VAL:HG22	1.88	0.54
4:RA:2321:G:O2'	4:RA:2322:A:OP1	2.21	0.54
4:RA:652(C):A:H61	4:RA:655:A:H1'	1.72	0.54
4:RA:657:U:H2'	4:RA:658:C:H6	1.72	0.54
6:RD:269:PHE:N	6:RD:269:PHE:CD1	2.75	0.54
11:RI:77:LEU:HD12	11:RI:101:LEU:HG	1.89	0.54
18:RT:45:PHE:CD1	18:RT:45:PHE:C	2.81	0.54
35:XA:1148:U:O2'	43:XI:66:ARG:NH1	2.35	0.54
35:XA:176:C:H2'	35:XA:177:C:H6	1.73	0.54
37:XC:54:ARG:HG3	37:XC:54:ARG:HH11	1.72	0.54
2:XX:22:C:H41	3:XY:210:GLY:HA3	1.72	0.54
27:Y2:4:SER:HA	27:Y2:7:ARG:NH1	2.23	0.54
4:YA:796:C:H2'	4:YA:797:C:C6	2.43	0.54
6:YD:84:TYR:HD1	6:YD:85:ASP:N	2.05	0.54
53:QS:10:PHE:HD1	53:QS:10:PHE:C	2.10	0.54
4:RA:2134:A:N6	4:RA:2156:G:O2'	2.41	0.54
4:RA:2469:A:O2'	15:RQ:56:ARG:NH1	2.40	0.54
4:RA:2649:U:H2'	4:RA:2650:U:C6	2.43	0.54
10:RH:3:ARG:HE	10:RH:5:GLY:H	1.56	0.54
23:RY:86:ARG:O	23:RY:97:ARG:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:116:A:H61	35:XA:313:A:H1'	1.72	0.54
36:XB:82:ARG:HB2	36:XB:94:ASN:ND2	2.22	0.54
8:YF:184:TYR:CE2	8:YF:188:ARG:HD2	2.43	0.54
4:YA:2727:G:O2'	13:YO:70:LYS:NZ	2.41	0.54
13:YO:79:PHE:N	13:YO:79:PHE:CD1	2.76	0.54
21:YW:11:ARG:HH21	21:YW:98:LYS:HA	1.72	0.54
35:QA:189(L):U:H2'	35:QA:189(M):G:H8	1.73	0.54
35:QA:736:C:H2'	35:QA:737:A:C8	2.42	0.54
35:QA:811:C:O2'	35:QA:901:A:N1	2.39	0.54
3:QY:223:TYR:CD1	3:QY:223:TYR:N	2.75	0.54
4:RA:1429:G:H2'	4:RA:1430:C:H6	1.70	0.54
4:RA:2115:G:H21	4:RA:2171:A:H61	1.56	0.54
4:RA:2291:U:H2'	4:RA:2292:C:H6	1.71	0.54
7:RE:134:ILE:HA	7:RE:137:HIS:CD2	2.42	0.54
11:RI:77:LEU:CD1	11:RI:101:LEU:HG	2.38	0.54
15:RQ:68:ILE:HG22	15:RQ:101:ARG:HE	1.72	0.54
53:XS:50:ALA:HA	53:XS:58:VAL:O	2.07	0.54
3:XY:255:ASN:O	4:YA:2507:C:H4'	2.06	0.54
3:XY:327:VAL:C	3:XY:329:ASP:H	2.10	0.54
27:Y2:4:SER:HA	27:Y2:7:ARG:HH11	1.72	0.54
4:YA:1467:C:C5	4:YA:1546:C:H2'	2.43	0.54
4:YA:1525:G:H2'	4:YA:1526:G:C8	2.42	0.54
14:YP:70:GLN:N	14:YP:70:GLN:OE1	2.41	0.54
35:QA:646:U:H2'	35:QA:647:C:C6	2.43	0.54
4:RA:8:A:H2'	4:RA:9:U:C6	2.42	0.54
11:RI:54:GLN:HG3	11:RI:57:ARG:HH11	1.72	0.54
35:XA:1118:C:H1'	35:XA:1179:A:C4	2.43	0.54
35:XA:189(A):G:H2'	35:XA:189(B):C:C6	2.43	0.54
35:XA:340:U:H2'	35:XA:341:C:H6	1.73	0.54
50:XP:71:ARG:CG	50:XP:71:ARG:NH1	2.70	0.54
52:XR:47:THR:HG23	52:XR:49:LYS:HG3	1.89	0.54
29:Y4:53:GLU:CD	29:Y4:53:GLU:H	2.10	0.54
6:YD:260:ARG:NH2	6:YD:270:ILE:HD12	2.22	0.54
35:QA:454:C:OP1	50:QP:75:ARG:NH2	2.41	0.54
36:QB:76:GLN:HE21	36:QB:206:ASP:HA	1.73	0.54
37:QC:148:GLY:HA3	37:QC:172:ARG:O	2.08	0.54
53:QS:64:GLU:HG3	29:R4:59:PHE:CE1	2.42	0.54
14:RP:63:PRO:HD3	33:R8:27:THR:HG22	1.89	0.54
4:RA:1816:G:O6	6:RD:35:LYS:NZ	2.31	0.54
4:RA:2223:G:OP1	6:RD:172:TYR:OH	2.23	0.54
24:RZ:126:VAL:CG1	24:RZ:161:VAL:HG23	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:41:G:H2'	35:XA:42:G:H8	1.73	0.54
29:Y4:42:PHE:HD2	29:Y4:43:TYR:CD1	2.26	0.54
4:YA:2591:C:H2'	4:YA:2592:G:H8	1.71	0.54
24:YZ:126:VAL:CG1	24:YZ:161:VAL:HG13	2.38	0.54
35:QA:1038:C:H2'	35:QA:1039:C:H6	1.73	0.54
35:QA:1124:G:N2	35:QA:1125:U:O4	2.40	0.54
35:QA:555:C:H2'	35:QA:556:C:C6	2.42	0.54
38:QD:138:TYR:HD1	38:QD:139:ARG:N	2.06	0.54
55:QU:18:TYR:CE2	55:QU:24:ARG:HB3	2.43	0.54
29:R4:64:GLY:O	29:R4:67:TYR:HE1	1.91	0.54
4:RA:1000:A:H2'	4:RA:1001:A:C8	2.43	0.54
9:RG:3:LEU:HD22	29:R4:25:TYR:HE2	1.72	0.54
4:RA:1188:U:H4'	20:RV:79:VAL:HG22	1.90	0.54
23:RY:92:ASN:N	23:RY:93:GLY:HA2	2.22	0.54
35:XA:1286:A:H2'	35:XA:1287:A:H4'	1.90	0.54
35:XA:189(A):G:H2'	35:XA:189(B):C:H6	1.72	0.54
35:XA:404:U:H2'	35:XA:405:U:H6	1.73	0.54
3:XY:322:GLN:NE2	35:XA:519:C:O5'	2.41	0.54
36:XB:105:PHE:CE1	36:XB:109:SER:HB3	2.43	0.54
36:XB:124:SER:HB2	36:XB:125:PRO:HD3	1.90	0.54
35:XA:429:U:H3'	38:XD:9:CYS:SG	2.48	0.54
54:XT:16:HIS:O	54:XT:19:SER:OG	2.22	0.54
3:XY:278:ARG:HG2	4:YA:2602:A:C5	2.43	0.54
26:Y1:76:ARG:HH22	26:Y1:97:LEU:HB3	1.73	0.54
4:YA:2291:U:H2'	4:YA:2292:C:H6	1.73	0.54
35:QA:769:G:H4'	35:QA:1513:A:H4'	1.90	0.53
38:QD:27:TYR:N	38:QD:27:TYR:HD1	2.06	0.53
39:QE:87:SER:HB3	39:QE:131:ILE:HD13	1.90	0.53
52:QR:47:THR:HG23	52:QR:49:LYS:HG3	1.90	0.53
53:QS:10:PHE:CD1	53:QS:10:PHE:C	2.79	0.53
35:QA:192:U:O2'	54:QT:60:GLU:OE2	2.18	0.53
4:RA:760:G:H2'	4:RA:761:A:O4'	2.08	0.53
12:RN:47:ALA:HB3	12:RN:115:ARG:HH21	1.73	0.53
19:RU:108:GLU:HG2	20:RV:45:THR:HG21	1.91	0.53
36:XB:8:LYS:HD2	36:XB:51:LEU:HB3	1.91	0.53
38:XD:18:LYS:HG2	38:XD:20:TYR:CE1	2.43	0.53
41:XG:114:ARG:HB2	41:XG:115:ARG:HH21	1.72	0.53
44:XJ:25:GLU:O	44:XJ:29:ARG:HG2	2.08	0.53
4:YA:184:C:H2'	4:YA:185:U:C6	2.43	0.53
4:YA:2119:A:H61	4:YA:2168:G:H21	1.55	0.53
8:YF:29:ASN:H	8:YF:112:MET:HE3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:YF:179:GLU:O	8:YF:205:ARG:NH2	2.40	0.53
11:YI:72:LEU:O	11:YI:75:LEU:HB3	2.08	0.53
35:QA:73:G:H1	35:QA:96:U:H3	1.56	0.53
45:QK:109:VAL:HG23	52:QR:85:LEU:O	2.08	0.53
3:QY:117:ARG:NH1	3:QY:358:GLU:O	2.39	0.53
4:RA:1503:U:H2'	4:RA:1504:C:C6	2.43	0.53
4:RA:1657:C:H2'	4:RA:1658:C:C6	2.44	0.53
4:RA:2119:A:H61	4:RA:2168:G:H21	1.56	0.53
9:RG:108:ASN:HA	29:R4:37:SER:HB3	1.89	0.53
38:XD:163:GLU:O	38:XD:166:LYS:HG2	2.08	0.53
35:XA:406:G:O2'	38:XD:3:ARG:NH2	2.41	0.53
41:XG:111:ARG:HD3	41:XG:113:GLU:OE2	2.08	0.53
3:XY:166:ILE:HD11	3:XY:182:LYS:HE3	1.90	0.53
31:Y6:13:CYS:SG	31:Y6:47:THR:HG21	2.47	0.53
4:YA:2650:U:H2'	4:YA:2651:C:H6	1.72	0.53
4:YA:2747:G:O6	4:YA:2755:C:H5''	2.09	0.53
4:YA:65:C:H2'	4:YA:66:C:H6	1.73	0.53
4:YA:856:C:H2'	4:YA:857:C:H6	1.73	0.53
4:YA:1652:A:N6	16:YR:11:ASN:OD1	2.39	0.53
35:QA:1304:G:OP1	55:QU:2:GLY:N	2.41	0.53
38:QD:60:GLU:HG3	38:QD:202:LEU:HD12	1.90	0.53
45:QK:27:ASN:OD1	45:QK:28:THR:N	2.40	0.53
48:QN:48:ALA:HB2	48:QN:53:LEU:HD12	1.91	0.53
3:QY:217:PHE:N	3:QY:217:PHE:HD1	2.05	0.53
4:RA:2127:G:H2'	4:RA:2128:C:O4'	2.08	0.53
4:RA:579:G:H2'	4:RA:580:C:C6	2.43	0.53
8:RF:101:LEU:O	8:RF:106:ARG:NH1	2.33	0.53
8:RF:197:ASP:N	8:RF:197:ASP:OD1	2.41	0.53
35:XA:1258:G:H2'	35:XA:1259:C:C6	2.44	0.53
35:XA:1314:C:OP2	53:XS:4:SER:OG	2.14	0.53
43:XI:8:GLY:HA3	43:XI:76:ALA:O	2.09	0.53
26:Y1:50:ARG:HD2	26:Y1:57:GLU:OE2	2.08	0.53
27:Y2:12:GLU:HA	27:Y2:15:LYS:NZ	2.24	0.53
4:YA:2315:G:H2'	4:YA:2316:C:C6	2.43	0.53
4:YA:657:U:H2'	4:YA:658:C:H6	1.73	0.53
8:YF:165:ARG:HG2	8:YF:168:ARG:HH21	1.72	0.53
35:QA:434:U:H2'	35:QA:435:C:C6	2.42	0.53
36:QB:76:GLN:NE2	36:QB:206:ASP:CA	2.71	0.53
43:QI:33:PHE:CD1	43:QI:37:PHE:HD2	2.26	0.53
35:QA:1124:G:H5'	44:QJ:38:ILE:HG22	1.89	0.53
47:QM:3:ARG:HG3	47:QM:4:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:QQ:86:GLU:O	51:QQ:90:ILE:HG12	2.07	0.53
1:QV:16:C:O2'	1:QV:61:C:OP1	2.27	0.53
18:RT:45:PHE:C	18:RT:45:PHE:HD1	2.11	0.53
35:XA:919:A:O2'	35:XA:1080:A:N1	2.33	0.53
43:XI:99:LEU:HB3	43:XI:101:PHE:HE1	1.72	0.53
35:XA:452:A:N3	50:XP:72:ARG:NH1	2.56	0.53
54:XT:57:ARG:HH12	54:XT:100:ILE:HB	1.72	0.53
4:YA:2364:C:OP1	25:Y0:55:ARG:NH1	2.40	0.53
4:YA:924:C:H2'	4:YA:925:C:C6	2.44	0.53
4:YA:997:G:OP1	19:YU:92:ARG:HG3	2.08	0.53
18:YT:53:ARG:CB	18:YT:53:ARG:HH11	2.21	0.53
35:QA:407:G:H2'	35:QA:408:A:H8	1.72	0.53
46:QL:120:TYR:N	46:QL:120:TYR:CD1	2.77	0.53
49:QO:54:ARG:HG2	49:QO:58:MET:HE2	1.91	0.53
4:RA:1064:C:N4	4:RA:1065:U:C2	2.76	0.53
15:RQ:65:PHE:N	15:RQ:65:PHE:CD1	2.77	0.53
18:RT:101:PHE:HD2	18:RT:102:ILE:N	2.05	0.53
35:XA:1025:U:H3	35:XA:1036:G:H1	1.55	0.53
53:XS:22:LEU:O	53:XS:26:GLY:N	2.41	0.53
4:YA:272(A):A:H8	4:YA:272(B):C:C6	2.27	0.53
4:YA:652(U):C:H2'	4:YA:652(V):G:C8	2.44	0.53
9:YG:97:ASP:HA	9:YG:100:TRP:HD1	1.74	0.53
38:QD:140:VAL:HG11	38:QD:146:ILE:HD11	1.89	0.53
35:QA:1326:C:OP1	55:QU:12:LYS:NZ	2.41	0.53
5:RB:91:C:OP1	15:RQ:16:ARG:HG3	2.08	0.53
23:RY:6:HIS:ND1	23:RY:7:VAL:HG23	2.24	0.53
35:XA:299:G:H2'	35:XA:300:A:C8	2.43	0.53
36:XB:105:PHE:C	36:XB:105:PHE:CD1	2.81	0.53
41:XG:15:ASP:OD1	41:XG:20:ASP:N	2.32	0.53
53:XS:30:LEU:HD11	53:XS:50:ALA:HB2	1.90	0.53
2:XX:14:A:H61	41:XG:82:GLY:HA3	1.74	0.53
28:Y3:23:LEU:HD13	28:Y3:50:VAL:HG11	1.91	0.53
4:YA:1265:A:H3'	30:Y5:19:ARG:NH1	2.23	0.53
18:YT:60:THR:HG22	18:YT:77:PRO:HA	1.89	0.53
35:QA:1030(D):G:H2'	35:QA:1030(E):A:C8	2.44	0.53
35:QA:1442(A):G:N3	35:QA:1442(A):G:H2'	2.24	0.53
35:QA:21:G:H2'	35:QA:22:G:C8	2.44	0.53
35:QA:339:C:H2'	35:QA:340:U:H6	1.74	0.53
38:QD:159:ARG:O	38:QD:163:GLU:HG3	2.09	0.53
39:QE:90:VAL:O	39:QE:120:THR:HA	2.09	0.53
43:QI:88:TYR:HD1	43:QI:88:TYR:C	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:QN:3:ARG:HH12	48:QN:28:GLY:HA3	1.74	0.53
4:RA:105:C:H2'	4:RA:106:C:H6	1.73	0.53
4:RA:2293:C:H2'	4:RA:2294:C:H6	1.74	0.53
18:RT:68:TYR:HD1	18:RT:68:TYR:N	2.02	0.53
35:XA:17:U:H2'	35:XA:18:C:H6	1.68	0.53
42:XH:86:ILE:HG13	42:XH:133:LEU:HD22	1.90	0.53
44:XJ:61:GLU:OE2	48:XN:49:HIS:NE2	2.31	0.53
45:XK:62:GLN:HB2	45:XK:93:GLN:HG3	1.91	0.53
3:XY:265:HIS:CD2	3:XY:267:PRO:HD2	2.44	0.53
4:YA:1587:A:H2'	4:YA:1588:C:H6	1.74	0.53
4:YA:1920:4OC:HM22	4:YA:1921:G:H5'	1.89	0.53
4:YA:2162:G:H2'	4:YA:2163:C:C6	2.44	0.53
4:YA:2327:A:H2'	4:YA:2328:A:C8	2.43	0.53
4:YA:2711:A:H5''	4:YA:2712(A):U:H5''	1.91	0.53
24:YZ:179:ASP:O	24:YZ:182:LYS:HG2	2.08	0.53
35:QA:911:U:H2'	35:QA:912:C:C6	2.44	0.53
41:QG:18:TYR:CD2	41:QG:59:LEU:HB2	2.44	0.53
43:QI:16:ARG:HD3	43:QI:64:THR:HG21	1.91	0.53
50:QP:38:TYR:CD1	50:QP:38:TYR:N	2.75	0.53
52:QR:43:PHE:N	52:QR:43:PHE:CD1	2.76	0.53
1:QV:58:A:O2'	1:QV:60:U:OP2	2.17	0.53
2:QX:19:U:O2	3:QY:137:GLY:O	2.27	0.53
3:QY:265:HIS:HB2	3:QY:291:MET:HE2	1.91	0.53
3:QY:293:ALA:O	3:QY:297:GLU:HG3	2.08	0.53
4:RA:1198:U:C2	4:RA:1199:U:C5	2.96	0.53
4:RA:2165:G:H2'	4:RA:2166:G:O4'	2.09	0.53
4:RA:2168:G:H22	4:RA:2171:A:H2'	1.74	0.53
4:RA:302:C:OP2	23:RY:73:ARG:NH2	2.38	0.53
4:RA:375:C:H2'	4:RA:376:C:C6	2.44	0.53
4:RA:690:G:H2'	4:RA:691:C:C6	2.43	0.53
4:RA:796:C:H2'	4:RA:797:C:C6	2.44	0.53
4:RA:911:A:H2'	15:RQ:9:TYR:OH	2.09	0.53
10:RH:7:LEU:HD23	10:RH:69:ARG:HH12	1.74	0.53
17:RS:36:TYR:CD1	17:RS:36:TYR:N	2.77	0.53
35:XA:41:G:H2'	35:XA:42:G:C8	2.44	0.53
39:XE:12:LEU:O	39:XE:30:ALA:HA	2.09	0.53
3:XY:217:PHE:CZ	3:XY:319:TRP:HA	2.44	0.53
25:Y0:70:GLN:NE2	25:Y0:80:HIS:NE2	2.55	0.53
29:Y4:13:ARG:NH2	29:Y4:21:VAL:HG11	2.24	0.53
4:YA:1430:C:H2'	4:YA:1431:U:C6	2.43	0.53
18:YT:45:PHE:C	18:YT:45:PHE:HD1	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1015:A:H2'	35:QA:1016:A:C8	2.44	0.53
35:QA:1070:U:P	39:QE:20:GLN:HE22	2.31	0.53
35:QA:1132:C:H2'	35:QA:1133:G:H8	1.73	0.53
35:QA:404:U:H2'	35:QA:405:U:H6	1.74	0.53
36:QB:88:ALA:HB2	36:QB:219:VAL:HG13	1.91	0.53
47:QM:34:LEU:HD13	47:QM:41:PRO:HA	1.90	0.53
44:QJ:53:PRO:HA	48:QN:41:ARG:HH21	1.74	0.53
35:XA:1128:C:H1'	35:XA:1147:C:H42	1.74	0.53
35:XA:679:C:H2'	35:XA:680:C:H6	1.74	0.53
4:YA:2001:A:H2'	4:YA:2002:G:C8	2.44	0.53
23:YY:23:ARG:HD3	23:YY:42:VAL:HG22	1.89	0.53
35:QA:1263:C:H2'	35:QA:1264:C:C6	2.43	0.53
35:QA:876:G:O5'	42:QH:14:ARG:NH1	2.42	0.53
29:R4:61:ARG:NH2	29:R4:67:TYR:OH	2.42	0.53
4:RA:2171:A:H4'	4:RA:2172:U:OP1	2.09	0.53
4:RA:919:G:N2	4:RA:2269:A:OP2	2.42	0.53
4:RA:2445:G:OP1	8:RF:74:ARG:NH2	2.42	0.53
37:XC:24:ALA:HB3	37:XC:29:TYR:HB2	1.91	0.53
39:XE:79:GLU:N	39:XE:79:GLU:OE1	2.31	0.53
35:XA:1298:C:C4	41:XG:114:ARG:HD3	2.43	0.53
3:XY:162:LYS:HB2	3:XY:184:SER:HB3	1.90	0.53
4:YA:1067:A:H5'	4:YA:1067:A:H8	1.74	0.53
4:YA:1068:G:H3'	4:YA:1096:A:OP2	2.09	0.53
4:YA:1688:U:O2	4:YA:1700:A:H5'	2.09	0.53
4:YA:1794:U:H2'	4:YA:1795:C:H6	1.74	0.53
4:YA:2128:C:H5'	4:YA:2129:C:OP2	2.09	0.53
4:YA:2649:U:H2'	4:YA:2650:U:C6	2.44	0.53
4:YA:375:C:H2'	4:YA:376:C:C6	2.44	0.53
4:YA:78:A:H2'	4:YA:79:G:C8	2.44	0.53
7:YE:37:ARG:HG3	7:YE:80:GLU:OE2	2.08	0.53
14:YP:97:PRO:HA	14:YP:112:LEU:HD12	1.91	0.53
35:QA:1425:U:H2'	35:QA:1426:C:C6	2.44	0.52
3:QY:326:TYR:O	3:QY:328:LEU:N	2.43	0.52
3:QY:332:ARG:HG3	3:QY:343:ARG:CD	2.40	0.52
3:QY:96:PHE:O	3:QY:96:PHE:HD1	1.93	0.52
4:RA:1264:G:OP1	30:R5:19:ARG:NH2	2.41	0.52
16:RR:8:ARG:HG3	16:RR:43:GLU:OE2	2.10	0.52
18:RT:39:ARG:NH1	18:RT:41:ARG:HD3	2.24	0.52
35:XA:45:U:H2'	35:XA:46:G:C8	2.45	0.52
4:YA:1063:G:N2	4:YA:1064:C:C5	2.77	0.52
4:YA:1316:U:H2'	4:YA:1317:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:589:C:H2'	4:YA:590:A:C8	2.44	0.52
24:YZ:93:ASP:HB2	24:YZ:131:ARG:HH22	1.74	0.52
35:QA:728:A:H2'	35:QA:729:A:C8	2.44	0.52
36:QB:91:PRO:HG2	36:QB:155:LEU:HB2	1.91	0.52
43:QI:33:PHE:O	43:QI:33:PHE:HD1	1.92	0.52
4:RA:184:C:H2'	4:RA:185:U:H6	1.74	0.52
4:RA:871:U:H2'	4:RA:872:A:C8	2.44	0.52
9:RG:179:PRO:HB2	29:R4:42:PHE:CE2	2.39	0.52
24:RZ:136:PHE:H	24:RZ:136:PHE:HD1	1.54	0.52
35:XA:1151:A:O2'	35:XA:1152:A:H8	1.91	0.52
41:XG:132:GLY:O	41:XG:136:LYS:HG2	2.08	0.52
43:XI:99:LEU:HB3	43:XI:101:PHE:CE1	2.44	0.52
4:YA:2390:U:P	33:Y8:35:GLN:HE22	2.32	0.52
4:YA:307:G:N1	4:YA:310:A:OP2	2.42	0.52
4:YA:272(P):C:H5''	11:YI:45:LYS:HD2	1.91	0.52
35:QA:539:A:H2'	35:QA:540:G:C8	2.44	0.52
35:QA:1216:G:OP1	48:QN:2:ALA:HA	2.08	0.52
3:QY:201:LEU:HD21	3:QY:203:ARG:HD3	1.92	0.52
47:QM:65:LYS:HD2	29:R4:51:ASP:CB	2.40	0.52
4:RA:150:C:H2'	4:RA:151:C:H6	1.74	0.52
4:RA:2122:U:H2'	4:RA:2123:G:C8	2.45	0.52
4:RA:2233:U:H2'	4:RA:2234:G:C8	2.45	0.52
35:XA:109:A:C6	35:XA:326:G:C6	2.97	0.52
40:XF:30:LEU:HD23	40:XF:75:LEU:HD11	1.90	0.52
4:YA:1843:C:H5'	6:YD:253:GLN:OE1	2.09	0.52
4:YA:2122:U:H2'	4:YA:2123:G:C8	2.45	0.52
4:YA:227:A:H5''	14:YP:76:LYS:HE2	1.91	0.52
6:YD:132:PRO:HG3	6:YD:190:TYR:CE1	2.45	0.52
4:YA:1791:A:H5'	6:YD:206:LEU:HD12	1.90	0.52
10:YH:163:TYR:CE2	10:YH:169:VAL:HG22	2.44	0.52
37:QC:87:LEU:O	37:QC:91:LEU:HB2	2.10	0.52
4:RA:2354:G:H21	25:R0:36:ILE:HD11	1.75	0.52
4:RA:284:U:H2'	4:RA:285:C:H6	1.75	0.52
4:RA:674:G:O2'	8:RF:74:ARG:HD3	2.09	0.52
10:RH:11:VAL:HG21	10:RH:50:VAL:HG23	1.91	0.52
23:RY:55:TYR:N	23:RY:55:TYR:CD1	2.78	0.52
42:XH:65:TYR:N	42:XH:65:TYR:HD1	2.07	0.52
3:XY:189:TYR:CE2	3:XY:193:ARG:HD3	2.44	0.52
17:YS:36:TYR:CD1	17:YS:36:TYR:N	2.78	0.52
24:YZ:6:LYS:HA	24:YZ:60:GLU:HB3	1.91	0.52
35:QA:1278:U:H5'	35:QA:1279:A:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:QF:22:GLU:OE1	40:QF:84:ASN:HB2	2.09	0.52
40:QF:4:TYR:HD1	40:QF:4:TYR:N	2.08	0.52
33:R8:62:LEU:HB3	33:R8:65:GLU:HG2	1.91	0.52
4:RA:1063:G:N2	4:RA:1064:C:C5	2.78	0.52
4:RA:1496:A:H2'	4:RA:1498:C:C5	2.45	0.52
15:RQ:69:PHE:CD1	15:RQ:69:PHE:C	2.83	0.52
35:XA:64:G:H4'	35:XA:65:U:H3'	1.90	0.52
35:XA:662:G:H2'	35:XA:663:A:C8	2.44	0.52
35:XA:890:G:O2'	35:XA:906:G:O6	2.22	0.52
36:XB:17:PHE:CD1	36:XB:18:GLY:N	2.72	0.52
39:XE:12:LEU:HD12	39:XE:128:PRO:HB2	1.91	0.52
46:XL:32:PHE:CD1	46:XL:32:PHE:N	2.77	0.52
35:XA:108:G:C6	54:XT:15:ARG:HG2	2.45	0.52
4:YA:1230:C:H2'	4:YA:1231:G:H8	1.75	0.52
4:YA:1497:U:H5''	4:YA:1498:C:H5	1.74	0.52
4:YA:2543:G:H2'	4:YA:2544:G:C8	2.44	0.52
4:YA:265:A:N1	4:YA:427:U:O2'	2.35	0.52
4:YA:823:G:H2'	4:YA:824:A:H8	1.75	0.52
10:YH:12:PRO:O	10:YH:15:VAL:HG22	2.08	0.52
52:QR:39:VAL:O	52:QR:42:ARG:HB2	2.09	0.52
4:RA:1164:G:H2'	4:RA:1165:U:C6	2.44	0.52
4:RA:2267:A:H5''	4:RA:2268:A:H5'	1.90	0.52
12:RN:96:GLU:HB2	12:RN:122:VAL:HG12	1.92	0.52
38:XD:112:VAL:HG22	38:XD:116:GLN:OE1	2.09	0.52
42:XH:46:LYS:HG3	42:XH:64:LYS:HB2	1.92	0.52
45:XK:117:ASN:N	45:XK:117:ASN:OD1	2.42	0.52
4:YA:2122:U:H2'	4:YA:2123:G:H8	1.75	0.52
4:YA:2635:C:H4'	7:YE:48:GLN:HE21	1.75	0.52
7:YE:134:ILE:HA	7:YE:137:HIS:CD2	2.44	0.52
9:YG:11:TYR:OH	9:YG:33:ARG:HG2	2.09	0.52
16:YR:8:ARG:HG3	16:YR:43:GLU:OE2	2.09	0.52
37:QC:40:ARG:O	37:QC:44:GLU:HB2	2.08	0.52
4:RA:686:G:N2	4:RA:788:A:H61	2.08	0.52
4:RA:886:C:O2'	4:RA:889:C:N4	2.38	0.52
4:RA:922:U:H2'	4:RA:923:C:H6	1.70	0.52
35:XA:1513:A:H2'	35:XA:1514:C:H6	1.75	0.52
36:XB:126:GLU:N	36:XB:126:GLU:OE1	2.43	0.52
37:XC:119:ARG:CD	37:XC:140:ARG:HH21	2.17	0.52
47:XM:88:ARG:HG3	47:XM:98:VAL:CG1	2.39	0.52
3:XY:326:TYR:N	3:XY:326:TYR:CD1	2.78	0.52
3:XY:325:SER:O	3:XY:333:ILE:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Y4:58:ARG:HG3	53:XS:64:GLU:O	2.10	0.52
4:YA:1936:A:OP2	4:YA:1962:5MC:N4	2.40	0.52
4:YA:881:G:H2'	4:YA:882:G:H8	1.74	0.52
24:YZ:44:PHE:HE2	24:YZ:86:VAL:HG11	1.74	0.52
35:QA:384:G:H2'	35:QA:385:C:C6	2.43	0.52
38:QD:20:TYR:HD1	38:QD:20:TYR:N	2.07	0.52
38:QD:68:TYR:N	38:QD:68:TYR:HD1	2.08	0.52
1:QV:62:C:O2	1:QV:62:C:H2'	2.10	0.52
3:QY:255:ASN:OD1	4:RA:2583:G:N2	2.38	0.52
25:R0:60:PHE:CD1	25:R0:60:PHE:N	2.75	0.52
33:R8:14:VAL:HG13	33:R8:22:VAL:HG13	1.92	0.52
4:RA:1946:U:H2'	4:RA:1947:C:C6	2.44	0.52
4:RA:2246:G:H2'	4:RA:2247:A:H8	1.75	0.52
7:RE:119:ARG:HG3	7:RE:160:TYR:HB2	1.91	0.52
11:RI:42:SER:O	11:RI:45:LYS:HB2	2.09	0.52
24:RZ:54:HIS:ND1	24:RZ:101:PRO:HG3	2.25	0.52
35:XA:1239:A:H62	35:XA:1299:A:H62	1.57	0.52
39:XE:28:PHE:N	39:XE:28:PHE:CD1	2.77	0.52
51:XQ:62:SER:OG	51:XQ:72:ARG:HG3	2.09	0.52
23:YY:19:LYS:HE3	23:YY:20:TYR:HE1	1.75	0.52
35:QA:1007:C:C2'	35:QA:1008:C:H5'	2.40	0.52
35:QA:456:C:H2'	35:QA:457:C:C6	2.44	0.52
35:QA:715:A:H2'	35:QA:716:A:C8	2.45	0.52
35:QA:838:G:H2'	35:QA:839:U:H2'	1.92	0.52
36:QB:178:ARG:NH2	36:QB:198:ASP:OD1	2.43	0.52
31:R6:12:GLU:O	31:R6:49:HIS:HA	2.10	0.52
33:R8:31:HIS:CE1	33:R8:32:LEU:HD13	2.44	0.52
4:RA:1525:G:H2'	4:RA:1526:G:H8	1.75	0.52
4:RA:336:C:O2'	23:RY:35:TYR:OH	2.28	0.52
14:RP:84:ASN:HB3	14:RP:117:GLU:O	2.09	0.52
24:RZ:8:TYR:HD1	24:RZ:8:TYR:N	2.08	0.52
35:XA:1003:G:H3'	35:XA:1003:G:N3	2.25	0.52
35:XA:323:U:H2'	35:XA:324:G:O4'	2.10	0.52
35:XA:632:A:H5'	35:XA:633:G:OP2	2.10	0.52
35:XA:911:U:H2'	35:XA:912:C:C6	2.45	0.52
36:XB:28:PHE:HE1	36:XB:31:TYR:HB2	1.72	0.52
4:YA:1057:A:N7	4:YA:1086:A:H2'	2.24	0.52
4:YA:1316:U:H2'	4:YA:1317:A:C8	2.44	0.52
4:YA:1525:G:H2'	4:YA:1526:G:H8	1.75	0.52
4:YA:2640:G:O3'	12:YN:74:ARG:NH2	2.25	0.52
4:YA:2693:A:H2'	4:YA:2694:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:823:G:H2'	4:YA:824:A:C8	2.44	0.52
17:YS:7:TYR:HE1	17:YS:11:LYS:CE	2.23	0.52
35:QA:679:C:H2'	35:QA:680:C:H6	1.74	0.52
43:QI:17:VAL:HG23	43:QI:63:ILE:HG12	1.90	0.52
53:QS:74:PHE:HD1	53:QS:74:PHE:N	2.08	0.52
1:QV:21:A:H61	1:QV:46:G:H2'	1.73	0.52
3:QY:265:HIS:HB2	3:QY:291:MET:CE	2.40	0.52
33:R8:24:ALA:HB3	33:R8:48:PHE:HE1	1.75	0.52
4:RA:1070:A:H2'	4:RA:1071:G:C8	2.45	0.52
4:RA:2206:G:H5''	4:RA:2207:G:N7	2.25	0.52
6:RD:70:TRP:HB3	6:RD:190:TYR:CE2	2.44	0.52
10:RH:103:LEU:HG	10:RH:105:LEU:HD13	1.92	0.52
11:RI:130:TYR:CE2	11:RI:132:PRO:HB3	2.45	0.52
15:RQ:55:VAL:HG12	15:RQ:64:ILE:HD12	1.92	0.52
23:RY:20:TYR:HD1	23:RY:20:TYR:N	2.08	0.52
35:XA:1004:A:N7	35:XA:1037:C:H2'	2.25	0.52
36:XB:16:HIS:CG	36:XB:210:SER:HB3	2.45	0.52
40:XF:61:LEU:HD23	40:XF:63:TYR:OH	2.10	0.52
53:XS:41:VAL:HG22	53:XS:42:PRO:HD2	1.92	0.52
3:XY:141:ALA:HB2	3:XY:216:SER:HB2	1.92	0.52
4:YA:1915:5MU:H2'	4:YA:1916:A:C8	2.44	0.52
4:YA:582:G:H2'	4:YA:583:G:C8	2.45	0.52
4:YA:848:G:H2'	4:YA:849:A:H8	1.75	0.52
4:YA:93:G:H2'	4:YA:94(A):C:H6	1.74	0.52
13:YO:64:ARG:NH1	18:YT:70:VAL:HG21	2.24	0.52
36:QB:166:ASP:HB3	36:QB:169:LYS:HB3	1.93	0.51
36:QB:28:PHE:CD1	36:QB:31:TYR:HB2	2.46	0.51
38:QD:61:LYS:HD2	38:QD:207:TYR:OH	2.09	0.51
54:QT:43:LEU:O	54:QT:47:GLY:N	2.43	0.51
4:RA:1431:U:H2'	4:RA:1432:C:C6	2.44	0.51
4:RA:2246:G:H2'	4:RA:2247:A:C8	2.44	0.51
4:RA:588:U:H2'	4:RA:589:C:C6	2.44	0.51
9:RG:44:GLY:N	9:RG:88:ILE:O	2.40	0.51
17:RS:11:LYS:HD3	17:RS:15:ARG:NH1	2.25	0.51
21:RW:14:PRO:HG2	21:RW:78:GLU:HG3	1.91	0.51
35:XA:1442(A):G:N3	35:XA:1442(A):G:H2'	2.25	0.51
3:XY:149:GLU:OE1	3:XY:179:VAL:HG11	2.10	0.51
4:YA:1069:A:H2'	4:YA:1073:A:N7	2.25	0.51
4:YA:2189:U:H2'	4:YA:2190:G:C8	2.44	0.51
4:YA:2206:G:H5''	4:YA:2207:G:N7	2.25	0.51
4:YA:309:G:N3	4:YA:329:G:O2'	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:YF:165:ARG:HG2	8:YF:168:ARG:NH2	2.25	0.51
7:YE:12:THR:HG23	18:YT:58:ASN:HD21	1.75	0.51
40:QF:69:GLU:O	40:QF:72:VAL:HG12	2.11	0.51
4:RA:1739:U:HO2'	4:RA:1740:G:H8	1.57	0.51
4:RA:2086:U:H2'	4:RA:2087:G:C8	2.46	0.51
24:RZ:125:LEU:HB3	24:RZ:165:VAL:HG13	1.91	0.51
35:XA:1431:C:H2'	35:XA:1432:G:O4'	2.10	0.51
35:XA:500:G:H2'	35:XA:501:C:H6	1.75	0.51
35:XA:678:U:H2'	35:XA:679:C:H6	1.75	0.51
37:XC:174:PRO:HD2	37:XC:182:ILE:HD11	1.92	0.51
38:XD:20:TYR:N	38:XD:20:TYR:HD1	2.08	0.51
47:XM:80:ARG:NH2	53:XS:65:ASN:O	2.42	0.51
2:XX:22:C:N4	3:XY:210:GLY:HA3	2.25	0.51
3:XY:217:PHE:HD1	3:XY:217:PHE:N	2.08	0.51
4:YA:2171:A:H4'	4:YA:2172:U:OP1	2.08	0.51
4:YA:2379:G:O2'	17:YS:17:ARG:NH2	2.30	0.51
4:YA:588:U:H2'	4:YA:589:C:C6	2.45	0.51
4:YA:876:C:H2'	4:YA:877:U:O4'	2.10	0.51
15:YQ:92:GLY:C	15:YQ:93:TYR:HD1	2.14	0.51
16:YR:33:ARG:HH11	16:YR:113:LEU:HD22	1.74	0.51
35:QA:1255:G:P	44:QJ:45:ARG:HH21	2.33	0.51
35:QA:339:C:H2'	35:QA:340:U:C6	2.46	0.51
35:QA:34:C:H2'	35:QA:35:G:C8	2.45	0.51
36:QB:55:PHE:HD1	36:QB:58:ILE:HD12	1.75	0.51
37:QC:175:LEU:HD21	37:QC:201:TYR:HD2	1.75	0.51
54:QT:34:LYS:O	54:QT:38:LYS:HG2	2.11	0.51
4:RA:1250:G:N7	14:RP:18:ARG:NH2	2.57	0.51
4:RA:1292:U:H2'	4:RA:1293:C:H6	1.74	0.51
4:RA:1798:U:H5''	6:RD:260:ARG:HB3	1.92	0.51
4:RA:286:C:H2'	4:RA:287:C:H6	1.75	0.51
10:RH:46:GLU:OE2	10:RH:51:ARG:NE	2.35	0.51
35:XA:135:C:O2	50:XP:1:MET:HB3	2.10	0.51
36:XB:127:ILE:HG12	36:XB:128:GLU:H	1.75	0.51
38:XD:23:GLY:N	38:XD:26:CYS:SG	2.76	0.51
38:XD:98:GLU:OE1	38:XD:103:ASN:ND2	2.35	0.51
53:XS:23:ASN:HA	53:XS:27:GLU:OE2	2.11	0.51
3:XY:281:HIS:O	3:XY:285:ASP:HB2	2.09	0.51
4:YA:1817:G:OP1	6:YD:88:ARG:NH2	2.42	0.51
4:YA:286:C:H2'	4:YA:287:C:H6	1.72	0.51
17:YS:23:ARG:HD2	17:YS:86:ALA:HB2	1.91	0.51
18:YT:28:VAL:O	18:YT:46:GLU:HA	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:YT:73:GLU:OE2	18:YT:103:ARG:NH2	2.35	0.51
18:YT:45:PHE:HE2	18:YT:74:ARG:HG3	1.74	0.51
24:YZ:145:GLU:HA	24:YZ:145:GLU:OE1	2.11	0.51
35:QA:1130:A:H2'	35:QA:1131:G:C8	2.45	0.51
35:QA:632:A:H5'	35:QA:633:G:OP2	2.11	0.51
36:QB:54:THR:HG21	36:QB:201:ILE:HD11	1.93	0.51
37:QC:81:GLY:O	37:QC:85:ARG:HG3	2.11	0.51
38:QD:27:TYR:CD1	38:QD:27:TYR:N	2.78	0.51
49:QO:15:PHE:CD1	49:QO:15:PHE:N	2.77	0.51
4:RA:102:G:OP1	27:R2:7:ARG:NH2	2.43	0.51
4:RA:1201:C:H2'	4:RA:1202:C:H6	1.75	0.51
4:RA:1311:G:C4	32:R7:47:ARG:NH2	2.78	0.51
4:RA:1628:G:H2'	4:RA:1629:U:C6	2.45	0.51
4:RA:2313:C:O4'	9:RG:40:ASN:ND2	2.43	0.51
4:RA:2591:C:H2'	4:RA:2592:G:C8	2.46	0.51
4:RA:2853:C:H2'	4:RA:2854:G:H8	1.76	0.51
9:RG:135:LEU:O	9:RG:154:GLY:HA3	2.11	0.51
24:RZ:145:GLU:OE1	24:RZ:145:GLU:HA	2.11	0.51
29:Y4:61:ARG:NH2	53:XS:9:VAL:HG11	2.25	0.51
33:Y8:24:ALA:HB3	33:Y8:48:PHE:HE1	1.76	0.51
4:YA:1682:G:H2'	4:YA:1683:C:C6	2.46	0.51
10:YH:3:ARG:NH1	10:YH:4:ILE:N	2.58	0.51
14:YP:91:PHE:HE2	14:YP:99:LEU:HD21	1.75	0.51
20:YV:35:LEU:HB2	20:YV:57:VAL:HG22	1.91	0.51
35:QA:1182:G:H4'	35:QA:1183:A:H5'	1.92	0.51
35:QA:337:C:H2'	35:QA:338:A:C8	2.46	0.51
35:QA:45:U:H2'	35:QA:46:G:H8	1.71	0.51
35:QA:865:A:H5'	35:QA:1078:U:C5	2.44	0.51
35:QA:1191:A:OP2	37:QC:3:ASN:ND2	2.44	0.51
40:QF:62:TRP:C	40:QF:63:TYR:HD1	2.14	0.51
4:RA:1518:U:H2'	4:RA:1519:G:O4'	2.09	0.51
9:RG:50:ALA:C	9:RG:52:ILE:H	2.14	0.51
23:RY:55:TYR:HD1	23:RY:55:TYR:N	2.08	0.51
35:XA:1289:A:N1	35:XA:1371:G:O2'	2.37	0.51
35:XA:70:G:H1	35:XA:99:U:H3	1.58	0.51
35:XA:943:U:H1'	43:XI:124:GLN:HE22	1.74	0.51
39:XE:78:HIS:ND1	42:XH:104:ARG:HD2	2.25	0.51
47:XM:4:ILE:HD11	47:XM:60:VAL:HG11	1.93	0.51
4:YA:1075:C:H2'	4:YA:1076:C:H5'	1.93	0.51
4:YA:8:A:H2'	4:YA:9:U:C6	2.46	0.51
9:YG:179:PRO:HB2	29:Y4:42:PHE:HE2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:YZ:138:GLU:O	24:YZ:156:LYS:HE3	2.10	0.51
35:QA:1013:G:N2	35:QA:1016:A:OP2	2.42	0.51
35:QA:134:A:H61	50:QP:25:ARG:NH1	2.08	0.51
36:QB:198:ASP:HA	42:QH:68:ARG:HH12	1.76	0.51
43:QI:46:ALA:HB2	43:QI:74:ILE:HG23	1.90	0.51
35:QA:750:G:O2'	49:QO:22:THR:O	2.23	0.51
31:R6:13:CYS:SG	31:R6:47:THR:HG21	2.50	0.51
4:RA:2153:G:H2'	4:RA:2154:G:C8	2.45	0.51
4:RA:861:A:N3	5:RB:79:C:O2'	2.38	0.51
17:RS:87:PHE:HB2	17:RS:112:PHE:CD2	2.46	0.51
24:RZ:92:SER:O	24:RZ:130:PRO:HG2	2.11	0.51
35:XA:1305:G:N2	35:XA:1331:G:H1'	2.25	0.51
35:XA:443:C:H2'	35:XA:444:C:C6	2.46	0.51
35:XA:580:U:H2'	35:XA:581:G:O4'	2.11	0.51
43:XI:9:ARG:H	43:XI:79:LEU:HD23	1.75	0.51
3:XY:215:THR:HG22	3:XY:217:PHE:CE1	2.45	0.51
29:Y4:25:TYR:HD1	29:Y4:25:TYR:N	2.09	0.51
33:Y8:28:GLY:O	33:Y8:36:LYS:NZ	2.42	0.51
4:YA:608:A:H2'	4:YA:609:A:C8	2.46	0.51
16:YR:26:LYS:HE2	16:YR:70:LEU:O	2.10	0.51
35:QA:266:G:O3'	51:QQ:67:LYS:HB2	2.11	0.51
35:QA:532:A:N6	37:QC:193:TYR:HA	2.25	0.51
49:QO:15:PHE:HD1	49:QO:15:PHE:N	2.08	0.51
3:QY:223:TYR:H	3:QY:223:TYR:HD1	1.56	0.51
3:QY:326:TYR:O	3:QY:328:LEU:HG	2.10	0.51
27:R2:64:LEU:HD21	27:R2:68:ARG:HE	1.74	0.51
4:RA:1166:C:H2'	4:RA:1167:U:C6	2.46	0.51
4:RA:1630:G:H2'	4:RA:1631(A):C:C6	2.46	0.51
13:RO:122:LEU:HD13	18:RT:72:VAL:HG11	1.91	0.51
4:RA:1287:A:H8	16:RR:104:ARG:HD3	1.74	0.51
17:RS:15:ARG:O	17:RS:19:LYS:HG2	2.10	0.51
42:XH:38:ILE:HG21	42:XH:111:ILE:HG12	1.91	0.51
43:XI:33:PHE:HE2	43:XI:47:LEU:HG	1.76	0.51
4:YA:248:G:H5'	4:YA:250:G:N7	2.25	0.51
4:YA:335:C:H4'	23:YY:73:ARG:NE	2.26	0.51
4:YA:956:G:H5''	15:YQ:77:LYS:HD2	1.92	0.51
9:YG:106:LEU:HA	9:YG:110:ALA:HB3	1.91	0.51
35:QA:1037:C:H2'	35:QA:1038:C:C6	2.46	0.51
35:QA:1241:G:H2'	35:QA:1242:C:C6	2.46	0.51
35:QA:179:A:H2'	35:QA:180:U:H6	1.75	0.51
35:QA:455:C:C2	35:QA:456:C:C5	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:646:U:H2'	35:QA:647:C:H6	1.75	0.51
35:QA:678:U:H2'	35:QA:679:C:H6	1.75	0.51
35:QA:7:G:H5'	35:QA:298:A:O4'	2.11	0.51
41:QG:111:ARG:NH1	41:QG:113:GLU:OE2	2.44	0.51
4:RA:1050:A:H2'	4:RA:1051:G:H8	1.75	0.51
4:RA:1053:C:H2'	4:RA:1054:A:C8	2.46	0.51
4:RA:1075:C:H2'	4:RA:1076:C:H5'	1.93	0.51
4:RA:1588:C:H2'	4:RA:1589:C:C6	2.46	0.51
4:RA:2293:C:H2'	4:RA:2294:C:C6	2.46	0.51
4:RA:463:G:N2	4:RA:466:A:OP2	2.33	0.51
4:RA:881:G:H2'	4:RA:882:G:C8	2.46	0.51
15:RQ:6:ARG:NH1	24:RZ:197:ILE:HG12	2.26	0.51
17:RS:103:GLU:O	17:RS:107:GLU:HG3	2.10	0.51
37:XC:179:ARG:NH1	37:XC:206:GLU:OE1	2.43	0.51
38:XD:13:ARG:HH12	38:XD:36:ARG:CZ	2.23	0.51
50:XP:6:LEU:HD23	50:XP:17:TYR:CD2	2.45	0.51
4:YA:184:C:H2'	4:YA:185:U:H6	1.75	0.51
4:YA:236:C:H2'	4:YA:237:C:H6	1.76	0.51
4:YA:414:C:H2'	4:YA:415:A:H8	1.76	0.51
7:YE:44:TYR:HD1	7:YE:44:TYR:H	1.59	0.51
10:YH:55:PRO:HG2	10:YH:61:HIS:CE1	2.45	0.51
24:YZ:119:GLU:OE1	24:YZ:122:ARG:NH1	2.43	0.51
35:QA:1003:G:C2'	35:QA:1004:A:H4'	2.41	0.51
35:QA:1007:C:H2'	35:QA:1008:C:H5'	1.92	0.51
36:QB:111:ARG:NE	36:QB:111:ARG:HA	2.21	0.51
35:QA:922:G:H4'	39:QE:20:GLN:HA	1.93	0.51
3:QY:223:TYR:HD1	3:QY:223:TYR:N	2.09	0.51
29:R4:25:TYR:HD1	29:R4:25:TYR:N	2.09	0.51
4:RA:1028:A:N6	4:RA:1125:G:H2'	2.26	0.51
4:RA:1525:G:H2'	4:RA:1526:G:C8	2.46	0.51
4:RA:263:C:H2'	4:RA:264:C:O4'	2.11	0.51
4:RA:2810:A:N6	4:RA:2891:G:O2'	2.35	0.51
4:RA:862:G:H2'	4:RA:863:A:O4'	2.11	0.51
7:RE:9:VAL:HG22	7:RE:25:VAL:HB	1.92	0.51
8:RF:178:PRO:HB2	8:RF:201:VAL:HG21	1.91	0.51
16:RR:54:LEU:HD21	16:RR:65:LEU:HB3	1.93	0.51
21:RW:45:TYR:OH	21:RW:49:LYS:NZ	2.44	0.51
36:XB:181:PHE:HD1	36:XB:181:PHE:N	2.09	0.51
52:XR:33:ASP:OD2	52:XR:36:ASN:HB2	2.10	0.51
1:XV:16:C:O2'	1:XV:61:C:OP1	2.27	0.51
4:YA:1721:G:N1	4:YA:1739:U:OP2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:579:G:H2'	4:YA:580:C:C6	2.46	0.51
21:YW:4:LYS:HE2	21:YW:6:ILE:HD11	1.92	0.51
35:QA:441:A:H3'	35:QA:442:C:H6	1.76	0.51
38:QD:13:ARG:HG2	38:QD:38:TYR:O	2.10	0.51
40:QF:4:TYR:CD1	40:QF:4:TYR:N	2.79	0.51
41:QG:111:ARG:HH12	41:QG:122:HIS:HB2	1.75	0.51
42:QH:83:ILE:HG13	42:QH:137:VAL:HG22	1.93	0.51
46:QL:98:TYR:N	46:QL:98:TYR:CD1	2.79	0.51
11:RI:38:LEU:HD12	11:RI:38:LEU:H	1.76	0.51
35:XA:920:U:H2'	35:XA:921:U:C6	2.46	0.51
35:XA:986:A:H2'	35:XA:987:G:C8	2.46	0.51
36:XB:155:LEU:CD2	36:XB:159:PRO:HG3	2.39	0.51
37:XC:111:LEU:HD22	37:XC:146:ALA:HB2	1.93	0.51
47:XM:99:ARG:HB2	47:XM:101:GLN:NE2	2.25	0.51
3:XY:152:TYR:HE1	3:XY:353:LEU:HD22	1.76	0.51
4:YA:2365:G:HO2'	25:Y0:60:PHE:HE2	1.57	0.51
26:Y1:75:GLU:HA	26:Y1:78:LYS:HE2	1.93	0.51
4:YA:53:A:C2	32:Y7:35:ARG:NH1	2.79	0.51
4:YA:301:G:OP2	23:YY:84:ARG:NH2	2.44	0.51
4:YA:839:U:H2'	4:YA:840:C:C6	2.46	0.51
5:YB:22:U:H2'	5:YB:23:G:C8	2.46	0.51
7:YE:37:ARG:O	7:YE:45:THR:HA	2.10	0.51
9:YG:117:PHE:C	9:YG:117:PHE:CD1	2.84	0.51
23:YY:37:VAL:HG21	23:YY:72:VAL:HG21	1.92	0.51
35:QA:1239:A:H62	35:QA:1299:A:N6	2.08	0.50
35:QA:22:G:H4'	35:QA:885:G:C8	2.46	0.50
35:QA:363:A:OP1	46:QL:33:ARG:HD3	2.11	0.50
36:QB:115:LEU:HD13	36:QB:145:LEU:HB3	1.93	0.50
38:QD:98:GLU:HA	38:QD:103:ASN:ND2	2.26	0.50
39:QE:57:LYS:HG2	39:QE:61:TYR:CE2	2.46	0.50
43:QI:42:ARG:O	43:QI:74:ILE:HG21	2.11	0.50
4:RA:1171:G:N2	4:RA:1178:C:O2	2.44	0.50
4:RA:2189:U:H2'	4:RA:2190:G:C8	2.46	0.50
4:RA:2590:A:H2'	4:RA:2591:C:H6	1.76	0.50
4:RA:658:C:H2'	4:RA:659:C:H6	1.74	0.50
4:RA:856:C:H2'	4:RA:857:C:H6	1.75	0.50
4:RA:909:A:H2'	4:RA:912:C:H5	1.74	0.50
4:RA:950:G:H2'	4:RA:951:C:H6	1.76	0.50
18:RT:91:ARG:HD2	18:RT:120:ARG:NH1	2.26	0.50
35:XA:8:A:N6	38:XD:205:GLU:O	2.45	0.50
39:XE:72:GLN:O	39:XE:75:THR:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:XG:16:LEU:HD11	43:XI:42:ARG:HA	1.93	0.50
43:XI:33:PHE:O	43:XI:33:PHE:HD1	1.93	0.50
43:XI:53:VAL:C	43:XI:55:ALA:H	2.12	0.50
43:XI:42:ARG:HH12	43:XI:75:ASP:CG	2.15	0.50
4:YA:1064:C:N4	4:YA:1065:U:C2	2.79	0.50
4:YA:1210:A:H5''	4:YA:1212:G:O4'	2.11	0.50
4:YA:2022:U:O2'	4:YA:2617:C:H5'	2.11	0.50
21:YW:11:ARG:HH21	21:YW:98:LYS:CA	2.24	0.50
45:QK:99:GLN:HG2	45:QK:105:VAL:HG21	1.93	0.50
46:QL:53:ARG:HG3	46:QL:93:LEU:HD21	1.93	0.50
52:QR:34:TYR:N	52:QR:34:TYR:CD1	2.79	0.50
4:RA:105:C:H2'	4:RA:106:C:C6	2.46	0.50
4:RA:285:C:H2'	4:RA:286:C:C6	2.46	0.50
24:RZ:7:ALA:C	24:RZ:8:TYR:HD1	2.15	0.50
24:RZ:8:TYR:N	24:RZ:8:TYR:CD1	2.80	0.50
35:XA:1412:C:H2'	35:XA:1413:A:C8	2.47	0.50
35:XA:25:C:H2'	35:XA:26:A:C8	2.47	0.50
35:XA:610:G:C4	35:XA:611:A:C8	2.99	0.50
37:XC:180:ALA:HB1	37:XC:203:PHE:HE1	1.77	0.50
51:XQ:27:PHE:CD1	51:XQ:27:PHE:N	2.79	0.50
1:XV:53:G:HO2'	1:XV:54:U:H5	1.60	0.50
29:Y4:24:THR:C	29:Y4:25:TYR:HD1	2.14	0.50
7:YE:119:ARG:HD2	7:YE:120:TRP:NE1	2.25	0.50
10:YH:164:TYR:HB2	10:YH:167:GLU:HB2	1.93	0.50
15:YQ:65:PHE:CD1	15:YQ:65:PHE:N	2.79	0.50
18:YT:30:VAL:HG22	18:YT:86:ILE:HG12	1.93	0.50
23:YY:60:PHE:CD1	23:YY:60:PHE:N	2.80	0.50
35:QA:189(B):C:H42	35:QA:189(K):G:H1	1.59	0.50
35:QA:824:C:H2'	35:QA:825:G:H8	1.76	0.50
36:QB:109:SER:C	36:QB:111:ARG:H	2.15	0.50
46:QL:83:VAL:HG13	46:QL:100:ILE:HG23	1.92	0.50
47:QM:3:ARG:HG3	47:QM:4:ILE:H	1.77	0.50
1:QV:54:U:C2	1:QV:58:A:N7	2.79	0.50
4:RA:11:G:C2'	4:RA:12:U:H5'	2.41	0.50
4:RA:2094:G:P	11:RI:22:LYS:HD2	2.51	0.50
4:RA:2182:G:H2'	4:RA:2183:C:C6	2.46	0.50
5:RB:2:C:H2'	5:RB:3:C:C6	2.46	0.50
10:RH:163:TYR:CE2	10:RH:169:VAL:HG22	2.46	0.50
15:RQ:21:THR:CG2	15:RQ:101:ARG:HB2	2.31	0.50
35:XA:1023:G:H3'	35:XA:1024:G:H8	1.76	0.50
35:XA:110:C:H2'	35:XA:111:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:384:G:H2'	35:XA:385:C:C6	2.46	0.50
36:XB:201:ILE:HG21	36:XB:214:ILE:HG21	1.93	0.50
43:XI:42:ARG:NH2	43:XI:71:SER:OG	2.44	0.50
35:XA:1360:A:OP2	48:XN:35:ARG:NH2	2.44	0.50
14:YP:63:PRO:HD3	33:Y8:27:THR:HG22	1.93	0.50
4:YA:2134:A:H8	4:YA:2156:G:H21	1.59	0.50
4:YA:784:A:C6	6:YD:229:VAL:HG11	2.46	0.50
7:YE:59:VAL:HG12	7:YE:64:LYS:HG3	1.93	0.50
10:YH:163:TYR:HE2	10:YH:169:VAL:HG22	1.77	0.50
14:YP:100:LEU:HD22	14:YP:105:LEU:HD12	1.92	0.50
19:YU:111:GLU:OE1	19:YU:111:GLU:HA	2.11	0.50
35:QA:246:A:C2	35:QA:282:A:C5	3.00	0.50
4:RA:1053:C:H2'	4:RA:1054:A:H8	1.76	0.50
4:RA:1889:A:N1	4:RA:2234:G:H1'	2.26	0.50
4:RA:2543:G:H2'	4:RA:2544:G:C8	2.46	0.50
4:RA:320:A:H4'	4:RA:322:A:N7	2.26	0.50
4:RA:321:G:O2'	4:RA:340:A:N3	2.41	0.50
6:RD:108:PRO:HD2	6:RD:111:LEU:CD1	2.41	0.50
8:RF:140:LEU:CD1	8:RF:170:LEU:HD21	2.41	0.50
9:RG:11:TYR:CD2	9:RG:12:TYR:CD1	2.99	0.50
11:RI:9:LEU:HD12	11:RI:12:LEU:HD12	1.93	0.50
4:RA:1141:U:P	12:RN:25:ARG:HH12	2.34	0.50
12:RN:97:ARG:HA	12:RN:100:GLU:HB2	1.92	0.50
18:RT:56:GLY:O	18:RT:59:THR:HG23	2.11	0.50
35:XA:632:A:H3'	35:XA:633:G:H8	1.75	0.50
3:XY:324:ARG:HA	3:XY:334:LYS:O	2.10	0.50
3:XY:58:LYS:HD2	4:YA:1068:G:H22	1.75	0.50
14:YP:91:PHE:N	14:YP:91:PHE:CD1	2.78	0.50
14:YP:92:GLU:HA	14:YP:92:GLU:OE1	2.12	0.50
17:YS:94:TYR:C	17:YS:94:TYR:HD1	2.15	0.50
23:YY:23:ARG:CD	23:YY:42:VAL:HG22	2.41	0.50
24:YZ:8:TYR:N	24:YZ:8:TYR:HD1	2.09	0.50
35:QA:1518:MA6:N6	35:QA:1519:MA6:H103	2.26	0.50
35:QA:679:C:H2'	35:QA:680:C:C6	2.47	0.50
35:QA:728:A:H2'	35:QA:729:A:H8	1.77	0.50
43:QI:88:TYR:C	43:QI:88:TYR:CD1	2.85	0.50
51:QQ:70:ARG:C	51:QQ:71:PHE:HD1	2.15	0.50
52:QR:43:PHE:N	52:QR:43:PHE:HD1	2.09	0.50
4:RA:2122:U:H2'	4:RA:2123:G:H8	1.76	0.50
4:RA:2164:C:H3'	4:RA:2165:G:H8	1.76	0.50
4:RA:2164:C:H5"	4:RA:2165:G:OP2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:RT:42:ILE:HD13	18:RT:84:GLN:OE1	2.11	0.50
35:XA:865:A:H5'	35:XA:1078:U:H5	1.74	0.50
35:XA:1491:G:H5''	35:XA:1492:A:OP2	2.11	0.50
35:XA:416:G:H2'	35:XA:417:C:C6	2.47	0.50
35:XA:612:C:H2'	35:XA:613:C:C6	2.46	0.50
3:XY:223:TYR:CD1	3:XY:223:TYR:N	2.78	0.50
4:YA:2086:U:H2'	4:YA:2087:G:C8	2.47	0.50
4:YA:218:A:H2	4:YA:235:U:H4'	1.76	0.50
4:YA:458:G:O2'	4:YA:469:G:O6	2.27	0.50
4:YA:2641:G:P	12:YN:74:ARG:HH12	2.35	0.50
35:QA:69:G:H2'	35:QA:70:G:H8	1.77	0.50
36:QB:163:PHE:CD1	36:QB:185:ILE:HG13	2.46	0.50
39:QE:96:PRO:HA	39:QE:117:ASP:OD2	2.11	0.50
39:QE:28:PHE:N	39:QE:28:PHE:CD1	2.78	0.50
4:RA:1991:U:H2'	4:RA:1992:G:H5''	1.94	0.50
4:RA:2266:A:H4'	4:RA:2267:A:N3	2.27	0.50
4:RA:863:A:H2'	4:RA:864:G:H8	1.76	0.50
9:RG:125:PHE:HE2	9:RG:180:PHE:HE2	1.57	0.50
22:RX:28:PHE:CD1	22:RX:28:PHE:N	2.80	0.50
3:XY:136:SER:CA	35:XA:1493:A:H1'	2.41	0.50
35:XA:184:G:H2'	35:XA:185:A:C8	2.46	0.50
35:XA:922:G:H2'	35:XA:923:A:C8	2.47	0.50
39:XE:28:PHE:N	39:XE:28:PHE:HD1	2.09	0.50
40:XF:15:ASP:HB3	38:QD:20:TYR:CE2	2.47	0.50
41:XG:113:GLU:HG3	41:XG:118:VAL:HG12	1.93	0.50
44:XJ:80:LYS:O	44:XJ:84:GLN:HB2	2.12	0.50
55:XU:17:THR:O	55:XU:22:ARG:NH1	2.41	0.50
29:Y4:14:ILE:HB	29:Y4:22:ILE:HB	1.93	0.50
4:YA:1171:G:N2	4:YA:1178:C:O2	2.43	0.50
4:YA:1991:U:H2'	4:YA:1992:G:H5''	1.92	0.50
4:YA:2162:G:O3'	4:YA:2172:U:O2'	2.25	0.50
35:QA:1020:U:H2'	35:QA:1021:G:H8	1.76	0.50
35:QA:678:U:H2'	35:QA:679:C:C6	2.47	0.50
1:QV:50:U:H3	1:QV:64:G:H1	1.59	0.50
4:RA:1022:G:N7	12:RN:66:LYS:HE2	2.26	0.50
4:RA:1084:A:H3'	4:RA:1085:A:C4'	2.42	0.50
4:RA:1316:U:H2'	4:RA:1317:A:C8	2.47	0.50
4:RA:143(A):G:H2'	4:RA:143(B):C:C6	2.47	0.50
4:RA:2690:C:N4	4:RA:2713:A:H1'	2.27	0.50
16:RR:33:ARG:NH1	16:RR:115:GLU:OE2	2.44	0.50
22:RX:57:LEU:CD1	22:RX:78:LYS:HG3	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:XI:59:PHE:HD1	43:XI:59:PHE:N	2.10	0.50
52:XR:23:LYS:HD2	52:XR:58:LEU:HD12	1.93	0.50
45:XK:109:VAL:HG23	52:XR:85:LEU:O	2.12	0.50
4:YA:1444:G:H2'	4:YA:1445(B):C:C5	2.47	0.50
4:YA:747:U:O2	4:YA:2014:A:H1'	2.12	0.50
4:YA:2752:C:OP2	10:YH:4:ILE:HD11	2.12	0.50
24:YZ:8:TYR:CD1	24:YZ:8:TYR:N	2.80	0.50
44:QJ:11:PHE:HE1	44:QJ:67:THR:HG22	1.77	0.50
54:QT:57:ARG:HH22	54:QT:100:ILE:HD12	1.76	0.50
3:QY:164:GLU:O	3:QY:182:LYS:N	2.41	0.50
3:QY:326:TYR:N	3:QY:326:TYR:HD1	2.10	0.50
8:RF:29:ASN:H	8:RF:112:MET:CE	2.25	0.50
15:RQ:32:TYR:N	15:RQ:32:TYR:HD1	2.09	0.50
1:QV:54:U:P	24:RZ:203:GLU:HB2	2.52	0.50
36:XB:155:LEU:HD13	36:XB:157:ARG:O	2.10	0.50
36:XB:32:ILE:HD13	36:XB:40:HIS:CD2	2.47	0.50
50:XP:68:ASP:O	50:XP:71:ARG:HB2	2.11	0.50
53:XS:10:PHE:HD1	53:XS:11:VAL:N	2.09	0.50
4:YA:1230:C:H2'	4:YA:1231:G:C8	2.46	0.50
15:YQ:57:HIS:CE1	15:YQ:116:GLU:CG	2.95	0.50
17:YS:87:PHE:HB2	17:YS:112:PHE:CD2	2.47	0.50
35:QA:1183:A:O2'	35:QA:1184:G:OP1	2.27	0.50
35:QA:807:A:H2'	35:QA:808:C:C6	2.46	0.50
35:QA:848:C:O5'	35:QA:848:C:H6	1.95	0.50
44:QJ:5:ARG:HD2	44:QJ:71:LEU:HD11	1.94	0.50
35:QA:452:A:H4'	50:QP:72:ARG:NH1	2.26	0.50
3:QY:183:ILE:HG13	3:QY:192:LEU:CD1	2.42	0.50
31:R6:41:PRO:O	31:R6:44:ARG:HG3	2.12	0.50
4:RA:2206:G:H8	4:RA:2207:G:N7	2.10	0.50
5:RB:2:C:H2'	5:RB:3:C:H6	1.77	0.50
12:RN:62:VAL:CG1	12:RN:66:LYS:HB2	2.42	0.50
15:RQ:69:PHE:C	15:RQ:69:PHE:HD1	2.15	0.50
35:XA:1376:U:H2'	35:XA:1377:A:H8	1.77	0.50
35:XA:719:C:O2'	52:XR:49:LYS:HB3	2.12	0.50
35:XA:757:U:H2'	35:XA:758:G:O4'	2.12	0.50
37:XC:63:ASN:HB2	37:XC:98:ASN:HB2	1.94	0.50
41:XG:65:ALA:HB1	41:XG:127:ALA:HB3	1.94	0.50
41:XG:15:ASP:OD1	41:XG:19:GLY:N	2.45	0.50
3:XY:198:VAL:HB	3:XY:321:SER:O	2.12	0.50
4:YA:1417:C:H2'	4:YA:1418:G:O4'	2.11	0.50
4:YA:2065:C:H2'	4:YA:2066:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YD:70:TRP:HB3	6:YD:190:TYR:CE2	2.47	0.50
15:YQ:51:ARG:O	15:YQ:55:VAL:HG12	2.11	0.50
35:QA:90:U:H2'	35:QA:91:C:H6	1.77	0.49
36:QB:187:LEU:HA	36:QB:201:ILE:HB	1.93	0.49
38:QD:200:GLU:N	38:QD:200:GLU:OE1	2.45	0.49
39:QE:8:GLU:HG2	39:QE:34:VAL:HG22	1.94	0.49
4:RA:1086:A:OP1	4:RA:1104:C:O2'	2.29	0.49
4:RA:2315:G:H2'	4:RA:2316:C:C6	2.47	0.49
4:RA:2648:C:H2'	4:RA:2649:U:H6	1.76	0.49
4:RA:272(O):C:H2'	4:RA:272(P):C:H6	1.77	0.49
4:RA:272(M):G:H21	11:RI:50:ARG:HD3	1.77	0.49
16:RR:33:ARG:HD2	16:RR:115:GLU:HG2	1.94	0.49
35:XA:1179:A:H2'	35:XA:1180:A:O4'	2.11	0.49
35:XA:1241:G:H2'	35:XA:1242:C:C6	2.47	0.49
43:XI:88:TYR:CD1	43:XI:88:TYR:C	2.83	0.49
52:XR:52:PRO:HB2	52:XR:54:ARG:HG2	1.92	0.49
3:XY:200:ARG:HB2	3:XY:322:GLN:HB3	1.92	0.49
3:XY:200:ARG:NH2	3:XY:325:SER:OG	2.38	0.49
4:YA:2218:U:C2	26:Y1:52:ARG:NH2	2.80	0.49
34:Y9:19:ARG:HG2	34:Y9:20:HIS:ND1	2.27	0.49
4:YA:1503:U:H2'	4:YA:1504:C:C6	2.47	0.49
4:YA:2849:U:H4'	4:YA:2868:A:C2	2.46	0.49
4:YA:284:U:H2'	4:YA:285:C:H6	1.77	0.49
13:YO:64:ARG:HB2	13:YO:83:ALA:HB3	1.94	0.49
4:YA:483:A:O4'	23:YY:48:ALA:HB1	2.12	0.49
38:QD:55:ALA:O	38:QD:59:ARG:HB2	2.12	0.49
38:QD:68:TYR:CD1	38:QD:68:TYR:N	2.80	0.49
39:QE:50:GLU:HB2	39:QE:53:LEU:HD13	1.94	0.49
4:RA:2064:C:H2'	4:RA:2065:C:H6	1.74	0.49
4:RA:774:A:H2'	4:RA:774:A:N3	2.27	0.49
35:XA:160:A:H2'	35:XA:161:A:O4'	2.11	0.49
33:Y8:31:HIS:CE1	33:Y8:32:LEU:HD13	2.47	0.49
4:YA:1799:G:H8	6:YD:181:GLU:OE1	1.94	0.49
35:QA:1308:U:H5'	47:QM:110:ARG:HH11	1.78	0.49
35:QA:512:U:H2'	35:QA:513:C:C6	2.47	0.49
36:QB:231:GLU:HB3	36:QB:232:PRO:CD	2.36	0.49
39:QE:74:GLY:HA3	39:QE:116:THR:HG22	1.95	0.49
43:QL:58:HIS:C	43:QL:59:PHE:HD1	2.15	0.49
46:QL:27:LEU:HD13	46:QL:98:TYR:CE2	2.46	0.49
4:RA:1386:C:H2'	4:RA:1387:C:C6	2.46	0.49
4:RA:607:U:C5	4:RA:620:G:C5	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:1490:C:H2'	35:XA:1491:G:O4'	2.12	0.49
42:XH:49:GLU:OE2	42:XH:62:TYR:OH	2.18	0.49
4:YA:2165:G:H2'	4:YA:2166:G:O4'	2.11	0.49
4:YA:2182:G:H2'	4:YA:2183:C:C6	2.47	0.49
4:YA:285:C:H2'	4:YA:286:C:H6	1.77	0.49
9:YG:36:LYS:HD3	9:YG:95:ARG:NH1	2.26	0.49
11:YI:114:LEU:HD11	11:YI:128:LEU:HB3	1.95	0.49
35:QA:134:A:H1'	35:QA:325:A:C5	2.47	0.49
38:QD:20:TYR:CD1	38:QD:20:TYR:N	2.78	0.49
3:QY:198:VAL:HB	3:QY:321:SER:O	2.12	0.49
4:RA:2408:U:H2'	4:RA:2409:G:C8	2.47	0.49
4:RA:276:A:H5''	4:RA:277:C:H5'	1.94	0.49
4:RA:484:C:H2'	4:RA:485:C:H6	1.77	0.49
9:RG:62:LEU:O	9:RG:143:GLU:HG2	2.12	0.49
18:RT:16:ARG:HD3	18:RT:19:LEU:HG	1.93	0.49
35:XA:186:C:H2'	35:XA:187:C:H6	1.76	0.49
36:XB:105:PHE:C	36:XB:105:PHE:HD1	2.16	0.49
36:XB:174:VAL:O	36:XB:178:ARG:HG2	2.12	0.49
38:XD:79:PHE:CE1	38:XD:204:ILE:HD13	2.47	0.49
43:XI:80:GLY:O	43:XI:83:ARG:HB2	2.12	0.49
47:XM:14:ARG:NE	47:XM:42:ALA:HA	2.28	0.49
4:YA:1946:U:H2'	4:YA:1947:C:H6	1.75	0.49
4:YA:2130:U:H2'	4:YA:2158:A:H61	1.77	0.49
4:YA:2246:G:H2'	4:YA:2247:A:C8	2.48	0.49
4:YA:1050:A:C2	4:YA:2751:G:C2	3.00	0.49
13:YO:87:ILE:HD12	13:YO:91:LEU:HA	1.94	0.49
24:YZ:72:ARG:NH2	24:YZ:97:GLU:O	2.40	0.49
35:QA:1158:C:C4	35:QA:1160:G:C8	3.00	0.49
37:QC:141:VAL:HG11	37:QC:202:ILE:HG12	1.95	0.49
38:QD:8:VAL:HG22	38:QD:21:LEU:HD13	1.93	0.49
39:QE:40:ARG:HG2	39:QE:68:GLU:OE1	2.12	0.49
47:QM:13:LYS:HA	47:QM:44:ARG:HH11	1.76	0.49
3:QY:342:THR:HG22	3:QY:344:ASN:H	1.77	0.49
4:RA:1084:A:H3'	4:RA:1085:A:H4'	1.93	0.49
4:RA:1289:C:H2'	4:RA:1290:C:H6	1.76	0.49
4:RA:2025:C:H2'	4:RA:2026:C:C6	2.47	0.49
4:RA:852:G:H2'	4:RA:853:G:C8	2.48	0.49
18:RT:101:PHE:CD2	18:RT:102:ILE:N	2.80	0.49
35:XA:473:G:H2'	35:XA:474:G:H8	1.77	0.49
52:XR:34:TYR:N	52:XR:34:TYR:CD1	2.80	0.49
4:YA:2461:C:H2'	4:YA:2462:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:2650:U:H2'	4:YA:2651:C:C6	2.48	0.49
4:YA:922:U:H2'	4:YA:923:C:H6	1.76	0.49
9:YG:18:GLU:O	9:YG:22:ARG:HG2	2.12	0.49
17:YS:69:VAL:HG13	17:YS:101:LEU:HD12	1.93	0.49
24:YZ:181:GLU:OE1	24:YZ:181:GLU:HA	2.12	0.49
35:QA:186:C:H2'	35:QA:187:C:C6	2.47	0.49
36:QB:27:LYS:HD2	36:QB:193:ASP:OD1	2.13	0.49
38:QD:107:ARG:HG3	38:QD:173:TRP:HH2	1.76	0.49
38:QD:107:ARG:HH21	38:QD:194:LEU:HD21	1.78	0.49
4:RA:2001:A:H2'	4:RA:2002:G:C8	2.48	0.49
4:RA:270:A:OP2	4:RA:272(X):G:N1	2.36	0.49
4:RA:272(A):A:H8	4:RA:272(B):C:C6	2.30	0.49
4:RA:863:A:H2'	4:RA:864:G:C8	2.48	0.49
6:RD:147:LEU:HD11	6:RD:183:ARG:NH2	2.28	0.49
12:RN:62:VAL:HG11	12:RN:66:LYS:HB2	1.94	0.49
13:RO:120:GLU:OE1	18:RT:67:SER:OG	2.24	0.49
19:RU:62:ILE:HG12	19:RU:76:TYR:CE2	2.47	0.49
24:RZ:198:LYS:HB3	24:RZ:202:GLU:HB3	1.93	0.49
15:RQ:141:GLN:NE2	24:RZ:76:LEU:HD13	2.27	0.49
35:XA:21:G:H2'	35:XA:22:G:C8	2.46	0.49
38:XD:55:ALA:O	38:XD:59:ARG:HB2	2.11	0.49
39:XE:6:PHE:HB2	39:XE:34:VAL:HG13	1.93	0.49
41:XG:27:ILE:HD12	41:XG:40:ALA:HA	1.93	0.49
43:XI:65:VAL:HG21	43:XI:73:GLN:HB3	1.94	0.49
3:XY:203:ARG:HG2	3:XY:204:LYS:O	2.13	0.49
3:XY:321:SER:H	3:XY:322:GLN:HG3	1.76	0.49
26:Y1:56:GLN:HE21	26:Y1:56:GLN:HA	1.77	0.49
4:YA:1179:C:H2'	4:YA:1180:C:C6	2.47	0.49
4:YA:2311:A:H3'	4:YA:2312:U:C6	2.47	0.49
4:YA:2698:U:H2'	4:YA:2699:C:H6	1.77	0.49
24:YZ:93:ASP:HB2	24:YZ:131:ARG:NH2	2.28	0.49
35:QA:1241:G:H2'	35:QA:1242:C:H6	1.78	0.49
35:QA:1504:G:OP1	35:QA:1507:A:H4'	2.13	0.49
35:QA:610:G:C4	35:QA:611:A:C8	3.00	0.49
35:QA:744:C:O2'	35:QA:851:G:N2	2.44	0.49
35:QA:92:C:H2'	35:QA:93:G:C8	2.48	0.49
1:QV:54:U:H2'	1:QV:55:U:O4'	2.12	0.49
31:R6:6:ARG:NH1	31:R6:26:ASN:HB2	2.27	0.49
4:RA:690:G:H2'	4:RA:691:C:H6	1.77	0.49
4:RA:740:U:H2'	4:RA:741:G:C8	2.48	0.49
6:RD:269:PHE:N	6:RD:269:PHE:HD1	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1815:A:OP2	6:RD:54:ARG:NH2	2.46	0.49
35:XA:713:G:H2'	35:XA:714:G:C8	2.48	0.49
35:XA:974:A:OP2	48:XN:29:ARG:NH2	2.42	0.49
38:XD:59:ARG:NE	38:XD:59:ARG:HA	2.22	0.49
3:XY:143:ASP:O	3:XY:146:SER:OG	2.26	0.49
4:YA:1431:U:H2'	4:YA:1432:C:C6	2.48	0.49
4:YA:2364:C:H2'	4:YA:2365:G:O4'	2.12	0.49
4:YA:658:C:H2'	4:YA:659:C:H6	1.78	0.49
35:QA:1014:A:H2	35:QA:1219:U:H1'	1.77	0.49
39:QE:28:PHE:N	39:QE:28:PHE:HD1	2.11	0.49
50:QP:38:TYR:CD1	50:QP:50:LYS:HB3	2.47	0.49
51:QQ:45:HIS:NE2	51:QQ:47:PRO:HG3	2.28	0.49
6:RD:260:ARG:HH12	6:RD:264:LYS:HD3	1.75	0.49
8:RF:184:TYR:O	8:RF:188:ARG:HG3	2.13	0.49
35:XA:601:C:H2'	35:XA:602:A:H8	1.78	0.49
36:XB:9:GLU:C	36:XB:11:LEU:H	2.14	0.49
50:XP:8:ARG:NH2	50:XP:15:PRO:HG3	2.28	0.49
33:Y8:23:VAL:HG11	33:Y8:47:LYS:HD3	1.95	0.49
8:YF:40:GLN:HE22	8:YF:182:ASN:HB2	1.78	0.49
8:YF:53:THR:HG22	8:YF:56:GLU:HG2	1.94	0.49
12:YN:69:GLN:O	12:YN:71:ILE:HD12	2.13	0.49
21:YW:78:GLU:OE2	21:YW:99:ARG:NH1	2.42	0.49
37:QC:24:ALA:HB3	37:QC:29:TYR:HB2	1.94	0.49
41:QG:26:PHE:CE2	41:QG:30:ILE:HD11	2.47	0.49
51:QQ:6:LEU:O	51:QQ:58:GLU:HA	2.12	0.49
3:QY:325:SER:C	3:QY:326:TYR:HD1	2.16	0.49
3:QY:87:ALA:CB	3:QY:96:PHE:HB2	2.42	0.49
4:RA:674:G:H1'	8:RF:74:ARG:CD	2.42	0.49
4:RA:855:G:H2'	4:RA:856:C:C6	2.48	0.49
4:RA:661:C:H5'	8:RF:38:ARG:HH12	1.78	0.49
9:RG:106:LEU:HA	9:RG:110:ALA:HB3	1.93	0.49
14:RP:84:ASN:OD1	14:RP:117:GLU:HB3	2.13	0.49
20:RV:12:TYR:CD1	20:RV:12:TYR:N	2.81	0.49
35:XA:696:A:N1	35:XA:797:C:O2'	2.38	0.49
43:XI:26:VAL:HG22	43:XI:61:ALA:HB3	1.94	0.49
33:Y8:65:GLU:OE1	33:Y8:65:GLU:HA	2.13	0.49
7:YE:174:ASP:OD1	7:YE:175:VAL:N	2.46	0.49
7:YE:51:PHE:CE2	7:YE:52:LEU:HD22	2.47	0.49
9:YG:114:ILE:HG23	9:YG:136:ARG:NH2	2.28	0.49
35:QA:1452:C:H4'	35:QA:1457:G:C8	2.48	0.49
35:QA:901:A:O2'	35:QA:1513:A:OP1	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:923:A:H2'	35:QA:924:C:C6	2.48	0.49
36:QB:84:GLU:HB3	36:QB:219:VAL:HG21	1.93	0.49
4:RA:2815:C:H5'	30:R5:29:THR:HG21	1.95	0.49
4:RA:1721:G:N1	4:RA:1739:U:OP2	2.46	0.49
4:RA:2647:U:H2'	4:RA:2648:C:C6	2.48	0.49
19:RU:108:GLU:OE2	19:RU:112:ARG:NH1	2.46	0.49
19:RU:86:ALA:HB2	19:RU:116:ALA:HB2	1.95	0.49
35:XA:1183:A:H1'	35:XA:1184:G:OP1	2.13	0.49
35:XA:1323:G:H2'	35:XA:1324:A:C8	2.48	0.49
35:XA:679:C:H2'	35:XA:680:C:C6	2.48	0.49
36:XB:55:PHE:CG	36:XB:221:LEU:HD12	2.47	0.49
42:XH:34:GLU:O	42:XH:37:ARG:HB3	2.13	0.49
47:XM:15:VAL:HG12	47:XM:45:VAL:HG22	1.94	0.49
4:YA:1050:A:H2'	4:YA:1051:G:H8	1.78	0.49
4:YA:2168:G:H22	4:YA:2171:A:H2'	1.78	0.49
4:YA:674:G:H1'	8:YF:74:ARG:CD	2.43	0.49
7:YE:170:LEU:HD23	7:YE:184:VAL:HG11	1.94	0.49
8:YF:107:LYS:HG3	8:YF:206:ILE:HA	1.94	0.49
4:YA:1665:A:H4'	13:YO:67:LYS:HB2	1.95	0.49
4:YA:911:A:H2'	15:YQ:9:TYR:OH	2.12	0.49
4:YA:143(A):G:H4'	22:YX:35:THR:HG21	1.95	0.49
35:QA:1492:A:O4'	46:QL:47:LYS:NZ	2.37	0.48
35:QA:407:G:OP1	38:QD:115:ARG:HD3	2.13	0.48
35:QA:692:U:O2'	35:QA:694:A:N7	2.40	0.48
35:QA:1151:A:H5''	44:QJ:41:PRO:HA	1.95	0.48
4:RA:1581:G:H2'	4:RA:1582:C:O4'	2.12	0.48
3:QY:256:ARG:NH1	4:RA:2573:C:C4	2.81	0.48
17:RS:35:ILE:C	17:RS:36:TYR:HD1	2.16	0.48
35:XA:1001(A):A:H2'	35:XA:1001(B):G:H8	1.78	0.48
35:XA:1135:U:H2'	35:XA:1137:C:N3	2.28	0.48
35:XA:806:C:H2'	35:XA:807:A:H8	1.77	0.48
35:XA:973:G:H3'	35:XA:974:A:H5''	1.94	0.48
36:XB:74:LYS:HE3	36:XB:166:ASP:HB2	1.95	0.48
38:XD:200:GLU:O	38:XD:204:ILE:HG12	2.13	0.48
47:XM:17:VAL:O	47:XM:20:THR:OG1	2.18	0.48
30:Y5:40:LYS:HD3	30:Y5:46:CYS:HA	1.95	0.48
3:XY:219:SER:CB	4:YA:1914:C:H42	2.26	0.48
4:YA:919:G:N2	4:YA:2269:A:OP2	2.46	0.48
4:YA:2286:A:H4'	4:YA:2287:A:O4'	2.13	0.48
4:YA:2748:A:H5'	10:YH:4:ILE:HD12	1.94	0.48
7:YE:9:VAL:HG22	7:YE:25:VAL:HB	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:YG:165:THR:OG1	9:YG:168:GLU:HG3	2.13	0.48
23:YY:20:TYR:N	23:YY:20:TYR:HD1	2.11	0.48
35:QA:1016:A:H2'	35:QA:1017:G:O4'	2.13	0.48
36:QB:28:PHE:HE1	36:QB:31:TYR:HB2	1.76	0.48
40:QF:3:ARG:HA	40:QF:65:VAL:O	2.14	0.48
48:QN:36:PHE:CD1	48:QN:36:PHE:C	2.86	0.48
27:R2:7:ARG:O	27:R2:11:GLU:HG3	2.12	0.48
4:RA:1588:C:H2'	4:RA:1589:C:H6	1.78	0.48
4:RA:247:G:H4'	4:RA:386:G:C5	2.48	0.48
7:RE:170:LEU:HB3	7:RE:184:VAL:CG2	2.43	0.48
35:XA:1238:A:N7	35:XA:1303:C:H1'	2.28	0.48
35:XA:1318:A:H5''	53:XS:3:ARG:NH2	2.28	0.48
35:XA:340:U:H2'	35:XA:341:C:C6	2.47	0.48
39:XE:74:GLY:HA3	39:XE:116:THR:HG22	1.94	0.48
43:XI:5:TYR:OH	43:XI:16:ARG:HG2	2.13	0.48
43:XI:8:GLY:HA2	43:XI:79:LEU:HD23	1.96	0.48
25:Y0:60:PHE:N	25:Y0:60:PHE:CD1	2.81	0.48
4:YA:1682:G:H2'	4:YA:1683:C:H6	1.77	0.48
4:YA:1946:U:H2'	4:YA:1947:C:C6	2.48	0.48
4:YA:2266:A:H4'	4:YA:2267:A:N3	2.28	0.48
4:YA:2455:G:H2'	4:YA:2456:C:H6	1.78	0.48
6:YD:176:ARG:HH11	6:YD:176:ARG:CG	2.21	0.48
9:YG:72:ARG:HG2	9:YG:87:PRO:HA	1.94	0.48
20:YV:12:TYR:HD1	20:YV:12:TYR:N	2.11	0.48
21:YW:75:TYR:CD2	21:YW:104:THR:HB	2.47	0.48
35:QA:18:C:H4'	35:QA:1078:U:O2	2.12	0.48
35:QA:1434:A:H2'	35:QA:1435:G:O4'	2.13	0.48
35:QA:340:U:H2'	35:QA:341:C:H6	1.77	0.48
55:QU:18:TYR:CE2	55:QU:24:ARG:HD3	2.47	0.48
14:RP:50:ARG:HD3	33:R8:7:HIS:CD2	2.48	0.48
4:RA:1530:C:HO2'	4:RA:1531:C:P	2.34	0.48
3:QY:221:PHE:HB2	4:RA:1914:C:H41	1.78	0.48
4:RA:2065:C:H2'	4:RA:2066:C:H6	1.79	0.48
4:RA:218:A:H2	4:RA:235:U:H4'	1.76	0.48
4:RA:2648:C:H2'	4:RA:2649:U:C6	2.49	0.48
4:RA:950:G:H2'	4:RA:951:C:C6	2.48	0.48
8:RF:74:ARG:O	8:RF:75:HIS:HD2	1.91	0.48
10:RH:3:ARG:HB3	10:RH:6:ARG:HG2	1.95	0.48
4:RA:2019:A:O4'	19:RU:34:LYS:HE3	2.13	0.48
21:RW:67:ASP:OD1	21:RW:67:ASP:N	2.45	0.48
23:RY:20:TYR:CD1	23:RY:20:TYR:N	2.80	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:RY:60:PHE:CD1	23:RY:60:PHE:N	2.81	0.48
35:XA:1053:G:N7	35:XA:1200:C:H5''	2.28	0.48
35:XA:1068:G:OP2	35:XA:1068:G:H8	1.96	0.48
35:XA:1171:G:H2'	35:XA:1172:C:C6	2.48	0.48
35:XA:8:A:H5'	39:XE:101:ILE:HG22	1.95	0.48
39:XE:87:SER:HB3	39:XE:131:ILE:HD13	1.95	0.48
45:XK:115:PRO:C	45:XK:117:ASN:HA	2.33	0.48
46:XL:86:ARG:NH1	46:XL:99:HIS:CB	2.76	0.48
46:XL:53:ARG:HG3	46:XL:93:LEU:HD21	1.94	0.48
35:XA:663:A:H5''	52:XR:61:LYS:NZ	2.28	0.48
3:XY:200:ARG:HG2	3:XY:201:LEU:N	2.27	0.48
3:XY:326:TYR:O	3:XY:328:LEU:HG	2.12	0.48
33:Y8:9:GLY:O	33:Y8:13:ARG:HG3	2.14	0.48
4:YA:1510:G:H2'	4:YA:1511:C:C6	2.48	0.48
9:YG:135:LEU:O	9:YG:154:GLY:HA3	2.14	0.48
21:YW:75:TYR:HD2	21:YW:75:TYR:O	1.95	0.48
35:QA:1512:U:H2'	35:QA:1513:A:C8	2.49	0.48
35:QA:580:U:H2'	35:QA:581:G:O4'	2.13	0.48
35:QA:983:A:H2	35:QA:984:C:C6	2.32	0.48
4:RA:615:G:OP1	8:RF:40:GLN:HG2	2.13	0.48
4:RA:623:G:H2'	4:RA:624:C:H6	1.78	0.48
6:RD:77:ALA:HB2	6:RD:97:TYR:CD1	2.48	0.48
37:XC:191:THR:OG1	37:XC:194:GLY:O	2.18	0.48
41:XG:70:LYS:O	41:XG:138:LYS:HE2	2.13	0.48
47:XM:3:ARG:HA	47:XM:57:ARG:HH21	1.79	0.48
4:YA:1514:U:H2'	4:YA:1515:G:C8	2.49	0.48
4:YA:1932:A:H2'	4:YA:1933:G:O4'	2.13	0.48
4:YA:576:U:H2'	4:YA:577:G:C8	2.49	0.48
8:YF:140:LEU:CD1	8:YF:170:LEU:HD21	2.44	0.48
8:YF:188:ARG:HA	14:YP:3:LEU:HD13	1.95	0.48
24:YZ:39:VAL:HG21	24:YZ:44:PHE:HD2	1.79	0.48
35:QA:1491:G:O2'	35:QA:1492:A:H5'	2.13	0.48
35:QA:399:G:H2'	35:QA:400:C:C6	2.49	0.48
41:QG:69:VAL:HG21	41:QG:104:LEU:HD13	1.95	0.48
44:QJ:49:VAL:HG23	48:QN:41:ARG:HB2	1.95	0.48
35:QA:523:A:N1	46:QL:92:0TD:H6	2.28	0.48
3:QY:195:GLU:CG	3:QY:357:ILE:HD11	2.43	0.48
25:R0:46:LYS:HD2	25:R0:78:TYR:CE1	2.48	0.48
29:R4:46:GLN:O	29:R4:48:ARG:N	2.46	0.48
4:RA:210:C:P	32:R7:29:LYS:HE2	2.52	0.48
4:RA:1057:A:N7	4:RA:1086:A:H2'	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1514:U:H2'	4:RA:1515:G:H8	1.79	0.48
4:RA:639:U:C2	4:RA:640:C:C5	3.01	0.48
11:RI:68:LEU:HD12	11:RI:68:LEU:O	2.14	0.48
35:XA:646:U:H2'	35:XA:647:C:C6	2.48	0.48
36:XB:109:SER:O	36:XB:113:HIS:CD2	2.66	0.48
38:XD:68:TYR:HD1	38:XD:68:TYR:N	2.11	0.48
49:XO:35:ARG:NH2	49:XO:59:MET:HE2	2.26	0.48
3:XY:240:ARG:NH2	3:XY:264:THR:HG21	2.29	0.48
4:YA:2336:A:H61	25:Y0:43:THR:HG22	1.78	0.48
29:Y4:25:TYR:CD1	29:Y4:25:TYR:N	2.82	0.48
4:YA:1518:U:H2'	4:YA:1519:G:O4'	2.14	0.48
4:YA:1794:U:H2'	4:YA:1795:C:C6	2.49	0.48
4:YA:2109:U:H2'	4:YA:2110:G:C8	2.48	0.48
4:YA:2126:A:N6	4:YA:2162:G:HO2'	2.11	0.48
4:YA:2741:A:H5''	34:Y9:22:ARG:HH12	1.77	0.48
6:YD:108:PRO:HD2	6:YD:111:LEU:HD12	1.94	0.48
7:YE:119:ARG:HH21	7:YE:158:GLY:HA3	1.78	0.48
4:YA:1287:A:H8	16:YR:104:ARG:HD3	1.79	0.48
17:YS:7:TYR:HD1	17:YS:7:TYR:O	1.96	0.48
4:YA:1187:G:H5'	20:YV:81:TYR:CE1	2.48	0.48
35:QA:1024:G:N2	35:QA:1025:U:O4'	2.42	0.48
35:QA:455:C:H2'	35:QA:456:C:H6	1.79	0.48
35:QA:501:C:OP1	46:QL:117:ARG:NH2	2.46	0.48
36:QB:212:GLN:O	36:QB:216:SER:OG	2.32	0.48
42:QH:37:ARG:HH21	42:QH:38:ILE:CD1	2.26	0.48
4:RA:1201:C:H2'	4:RA:1202:C:C6	2.48	0.48
4:RA:2854:G:H2'	4:RA:2855:C:H6	1.79	0.48
6:RD:85:ASP:OD2	6:RD:88:ARG:NH1	2.40	0.48
14:RP:130:PHE:HB2	14:RP:135:LEU:HG	1.95	0.48
16:RR:67:LEU:HD13	16:RR:76:VAL:HG21	1.94	0.48
18:RT:117:ASP:OD2	18:RT:120:ARG:NE	2.46	0.48
21:RW:6:ILE:HG22	21:RW:8:ARG:HG3	1.95	0.48
35:XA:416:G:H2'	35:XA:417:C:H6	1.79	0.48
38:XD:61:LYS:HD2	38:XD:207:TYR:OH	2.14	0.48
32:Y7:12:ARG:NH2	32:Y7:44:PRO:HB3	2.29	0.48
4:YA:1300:U:H4'	4:YA:1301:A:H5'	1.95	0.48
4:YA:774:A:N3	4:YA:774:A:H2'	2.29	0.48
11:YI:77:LEU:HD22	11:YI:79:ILE:HG13	1.94	0.48
15:YQ:6:ARG:NH2	24:YZ:197:ILE:HG12	2.29	0.48
17:YS:94:TYR:CD1	17:YS:94:TYR:C	2.87	0.48
18:YT:45:PHE:HD1	18:YT:46:GLU:N	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:1036:G:H5''	35:QA:1037:C:C5	2.49	0.48
35:QA:624:C:H2'	35:QA:625:G:H8	1.79	0.48
36:QB:160:ASP:OD1	36:QB:160:ASP:N	2.45	0.48
43:QL:59:PHE:N	43:QL:59:PHE:HD1	2.11	0.48
47:QM:11:ARG:C	47:QM:13:LYS:H	2.17	0.48
3:QY:36:GLU:HA	3:QY:39:ALA:HB3	1.95	0.48
4:RA:1069:A:C4	4:RA:1095:A:H4'	2.48	0.48
4:RA:1199:U:H2'	4:RA:1200:C:H6	1.79	0.48
4:RA:1351:C:H2'	4:RA:1352:U:C6	2.49	0.48
4:RA:1587:A:H2'	4:RA:1588:C:H6	1.77	0.48
4:RA:362:U:O2'	4:RA:363(A):G:H5'	2.14	0.48
4:RA:1568:G:H5''	6:RD:61:LEU:HD13	1.96	0.48
35:XA:176:C:H2'	35:XA:177:C:C6	2.48	0.48
35:XA:33:A:H2'	35:XA:34:C:C6	2.48	0.48
40:XF:43:LEU:CD2	40:XF:46:ARG:HH22	2.24	0.48
3:XY:26:ASP:HB3	3:XY:29:ALA:HB3	1.94	0.48
3:XY:319:TRP:O	3:XY:322:GLN:HG2	2.13	0.48
3:XY:96:PHE:O	3:XY:96:PHE:CD1	2.66	0.48
4:YA:1336:A:H2'	4:YA:1337:G:C8	2.49	0.48
4:YA:1514:U:H2'	4:YA:1515:G:H8	1.79	0.48
4:YA:2590:A:H2'	4:YA:2591:C:H6	1.77	0.48
4:YA:760:G:H2'	4:YA:761:A:O4'	2.14	0.48
5:YB:84:C:OP1	28:Y3:15:TYR:OH	2.21	0.48
8:YF:184:TYR:O	8:YF:188:ARG:HG3	2.13	0.48
19:YU:58:ARG:NH2	19:YU:92:ARG:NH1	2.60	0.48
35:QA:1151:A:O2'	35:QA:1152:A:H8	1.96	0.48
35:QA:1239:A:H62	35:QA:1299:A:H61	1.60	0.48
35:QA:1404:5MC:O2	35:QA:1519:MA6:O2'	2.24	0.48
35:QA:142:G:O2'	35:QA:196:A:N1	2.42	0.48
35:QA:335:C:H2'	35:QA:336:C:H6	1.79	0.48
36:QB:115:LEU:O	36:QB:119:GLU:HG2	2.13	0.48
38:QD:81:GLU:O	38:QD:85:LYS:HB2	2.14	0.48
44:QJ:45:ARG:HH11	48:QN:36:PHE:HD2	1.57	0.48
45:QK:84:VAL:CG1	45:QK:91:ARG:HD2	2.40	0.48
47:QM:67:GLU:O	47:QM:71:ARG:HG3	2.14	0.48
3:QY:149:GLU:HG3	3:QY:150:ARG:N	2.29	0.48
3:QY:261:VAL:HG21	3:QY:284:LYS:HA	1.95	0.48
3:QY:332:ARG:HD2	3:QY:334:LYS:HD2	1.96	0.48
29:R4:61:ARG:CG	29:R4:62:ARG:N	2.76	0.48
4:RA:1045:A:H5''	4:RA:1046:A:OP1	2.14	0.48
4:RA:1423:G:OP1	4:RA:1492:G:O2'	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:297:C:H2'	4:RA:298:G:O4'	2.14	0.48
35:XA:1015:A:H2'	35:XA:1016:A:C8	2.49	0.48
35:XA:1072:G:H2'	35:XA:1073:U:C6	2.49	0.48
35:XA:1162:C:H2'	35:XA:1163:C:C6	2.49	0.48
35:XA:189(L):U:H2'	35:XA:189(M):G:H8	1.77	0.48
36:XB:118:LEU:HB3	36:XB:142:LEU:HD12	1.95	0.48
37:XC:63:ASN:CB	37:XC:98:ASN:HB2	2.43	0.48
46:XL:117:ARG:NH2	46:XL:124:LYS:HB2	2.29	0.48
53:XS:66:MET:HB2	53:XS:74:PHE:CZ	2.48	0.48
4:YA:2567:G:H2'	4:YA:2568:C:C6	2.49	0.48
4:YA:2627:G:O2'	4:YA:2781:A:N1	2.36	0.48
4:YA:492:A:H2'	4:YA:493:G:O4'	2.14	0.48
9:YG:51:ARG:HD3	9:YG:87:PRO:HD2	1.94	0.48
17:YS:11:LYS:HD3	17:YS:15:ARG:CZ	2.44	0.48
24:YZ:7:ALA:C	24:YZ:8:TYR:CD1	2.87	0.48
35:QA:1036:G:H5'	35:QA:1037:C:OP2	2.13	0.48
35:QA:28:G:O2'	35:QA:296:U:OP1	2.26	0.48
35:QA:981:U:H4'	48:QN:21:TYR:HE2	1.71	0.48
40:QF:63:TYR:HD1	40:QF:63:TYR:N	2.11	0.48
48:QN:21:TYR:CD1	48:QN:21:TYR:N	2.75	0.48
30:R5:40:LYS:HD3	30:R5:46:CYS:HA	1.95	0.48
4:RA:904:C:H2'	4:RA:905:U:H6	1.79	0.48
6:RD:146:GLU:HB2	6:RD:189:CYS:HB3	1.96	0.48
4:RA:1843:C:H5'	6:RD:253:GLN:OE1	2.13	0.48
9:RG:143:GLU:OE2	29:R4:26:SER:OG	2.22	0.48
11:RI:84:GLY:N	11:RI:89:TYR:CE1	2.81	0.48
18:RT:45:PHE:HD1	18:RT:46:GLU:N	2.12	0.48
35:XA:1030(D):G:H2'	35:XA:1030(E):A:C8	2.49	0.48
35:XA:1132:C:C2	35:XA:1133:G:C8	3.02	0.48
35:XA:1352:C:H2'	35:XA:1353:G:C8	2.48	0.48
35:XA:246:A:C2	35:XA:282:A:C5	3.01	0.48
35:XA:674:G:H2'	35:XA:675:A:H8	1.78	0.48
36:XB:111:ARG:CA	36:XB:111:ARG:HE	2.06	0.48
38:XD:20:TYR:CD1	38:XD:20:TYR:N	2.79	0.48
42:XH:20:TYR:HA	42:XH:65:TYR:CE2	2.49	0.48
3:XY:33:ARG:O	3:XY:36:GLU:HG2	2.14	0.48
3:XY:334:LYS:HG3	3:XY:341:GLU:HG2	1.96	0.48
10:YH:20:ALA:HB1	10:YH:21:PRO:HD2	1.96	0.48
14:YP:126:VAL:HG12	14:YP:148:LEU:HD22	1.95	0.48
14:YP:50:ARG:HD3	33:Y8:7:HIS:CD2	2.49	0.48
1:XV:52:G:H2'	24:YZ:198:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:YZ:28:MET:HA	24:YZ:88:PHE:O	2.13	0.48
35:QA:1425:U:H2'	35:QA:1426:C:H6	1.79	0.48
36:QB:19:HIS:O	36:QB:20:GLU:HB3	2.14	0.48
46:QL:70:ILE:HG12	46:QL:100:ILE:HD12	1.95	0.48
3:QY:324:ARG:HA	3:QY:334:LYS:O	2.13	0.48
3:QY:151:MET:CE	3:QY:353:LEU:HD21	2.44	0.48
4:RA:1062:G:H5'	4:RA:1070:A:H5''	1.95	0.48
4:RA:2780:G:OP1	12:RN:118:LYS:HE2	2.14	0.48
4:RA:30:G:H2'	4:RA:31:C:H6	1.77	0.48
8:RF:101:LEU:HD12	8:RF:102:PRO:HD2	1.95	0.48
19:RU:32:PHE:CZ	19:RU:36:ARG:HD3	2.48	0.48
20:RV:12:TYR:HD1	20:RV:12:TYR:N	2.10	0.48
35:XA:1251:A:H2'	35:XA:1252:A:C8	2.49	0.48
35:XA:1315:U:H2'	35:XA:1316:G:O4'	2.13	0.48
35:XA:601:C:H2'	35:XA:602:A:C8	2.48	0.48
26:Y1:54:ALA:HB1	26:Y1:83:GLU:HG3	1.95	0.48
27:Y2:32:LEU:HD11	27:Y2:54:LYS:HG2	1.96	0.48
4:YA:1025:G:C4	4:YA:1135:C:H1'	2.49	0.48
4:YA:607:U:C5	4:YA:620:G:C5	3.02	0.48
8:YF:107:LYS:HE2	8:YF:205:ARG:O	2.14	0.48
35:QA:403:C:O2'	38:QD:122:ARG:NH1	2.47	0.47
35:QA:646:U:C2	35:QA:647:C:C5	3.01	0.47
38:QD:133:VAL:HG11	38:QD:138:TYR:CD2	2.49	0.47
47:QM:32:GLU:HG2	47:QM:64:TRP:CZ2	2.48	0.47
50:QP:9:PHE:N	50:QP:9:PHE:CD1	2.82	0.47
51:QQ:68:ARG:H	51:QQ:70:ARG:NH1	2.12	0.47
4:RA:143(A):G:H2'	4:RA:143(B):C:H6	1.78	0.47
4:RA:2298:A:H62	4:RA:2318:G:H8	1.62	0.47
4:RA:414:C:H2'	4:RA:415:A:H8	1.79	0.47
4:RA:793:A:OP2	4:RA:2071:A:O2'	2.32	0.47
8:RF:101:LEU:HB3	8:RF:106:ARG:HD3	1.95	0.47
41:XG:52:GLU:HA	41:XG:52:GLU:OE1	2.14	0.47
55:XU:5:ASP:O	55:XU:11:GLY:HA3	2.14	0.47
4:YA:1086:A:OP1	4:YA:1104:C:O2'	2.31	0.47
4:YA:1341:U:OP1	4:YA:1397:U:N3	2.40	0.47
4:YA:1386:C:H2'	4:YA:1387:C:C6	2.48	0.47
4:YA:2389:G:H5''	4:YA:2390:U:O4'	2.13	0.47
4:YA:574:C:N3	7:YE:145:LYS:NZ	2.49	0.47
4:YA:637:A:H8	14:YP:117:GLU:HG3	1.79	0.47
8:YF:101:LEU:O	8:YF:106:ARG:NH1	2.42	0.47
14:YP:90:ARG:HG2	14:YP:91:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:YU:86:ALA:O	20:YV:49:THR:HG23	2.14	0.47
35:QA:1112:C:O2	37:QC:179:ARG:HG2	2.13	0.47
35:QA:1245:A:H2'	35:QA:1246:C:C6	2.50	0.47
35:QA:1277:C:O2'	35:QA:1279:A:H1'	2.14	0.47
36:QB:102:LEU:HB3	36:QB:180:LEU:HD12	1.96	0.47
35:QA:1343:G:H4'	43:QI:122:ALA:HB3	1.96	0.47
3:QY:115:PHE:HB3	3:QY:119:PHE:CD2	2.48	0.47
3:QY:200:ARG:HB3	3:QY:324:ARG:O	2.14	0.47
3:QY:336:LEU:O	3:QY:336:LEU:HD12	2.14	0.47
4:RA:1084:A:C8	4:RA:1085:A:H4'	2.49	0.47
4:RA:2327:A:H2'	4:RA:2328:A:C8	2.49	0.47
4:RA:234:C:H2'	4:RA:235:U:H6	1.79	0.47
4:RA:2391:G:O6	4:RA:2425:A:H8	1.98	0.47
3:QY:245:ARG:NE	4:RA:2573:C:H42	2.01	0.47
17:RS:66:ALA:O	17:RS:69:VAL:HG22	2.13	0.47
35:XA:134:A:H1'	35:XA:325:A:C5	2.49	0.47
43:XI:9:ARG:HA	43:XI:13:ALA:O	2.14	0.47
44:XJ:78:ASN:O	44:XJ:80:LYS:N	2.47	0.47
3:XY:326:TYR:HD2	3:XY:349:LEU:HD21	1.79	0.47
4:YA:1063:G:O2'	4:YA:1063:G:N3	2.42	0.47
4:YA:1839:G:C2	4:YA:1840:G:C8	3.02	0.47
4:YA:2115:G:H3'	4:YA:2116:G:C5'	2.45	0.47
4:YA:2153:G:H2'	4:YA:2154:G:C8	2.48	0.47
4:YA:606:U:H4'	4:YA:658:C:H4'	1.96	0.47
6:YD:75:ILE:HD13	6:YD:99:ASP:OD2	2.15	0.47
8:YF:34:TRP:CH2	14:YP:8:PRO:HB3	2.49	0.47
4:YA:674:G:H1'	8:YF:74:ARG:HD2	1.96	0.47
9:YG:64:THR:HB	9:YG:94:LEU:HD21	1.96	0.47
4:YA:1143:A:OP1	12:YN:25:ARG:NH2	2.47	0.47
17:YS:112:PHE:CD1	17:YS:112:PHE:N	2.80	0.47
18:YT:101:PHE:CD2	18:YT:102:ILE:N	2.80	0.47
20:YV:12:TYR:CD1	20:YV:12:TYR:N	2.82	0.47
22:YX:2:LYS:NZ	22:YX:38:GLU:OE2	2.30	0.47
35:QA:1207:2MG:H2'	35:QA:1208:C:C6	2.48	0.47
35:QA:923:A:H2'	35:QA:924:C:H6	1.79	0.47
43:QI:125:TYR:CE1	43:QI:127:LYS:HB2	2.49	0.47
32:R7:24:THR:HG23	32:R7:27:GLY:H	1.78	0.47
4:RA:1593:G:H2'	4:RA:1594:G:C8	2.49	0.47
4:RA:587:C:P	14:RP:21:ARG:NH2	2.87	0.47
4:RA:854:G:H2'	4:RA:855:G:H8	1.79	0.47
15:RQ:65:PHE:N	15:RQ:65:PHE:HD1	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:RS:7:TYR:HE1	17:RS:11:LYS:CE	2.27	0.47
35:XA:1035:A:H2'	35:XA:1036:G:C8	2.49	0.47
35:XA:375:U:H4'	50:XP:17:TYR:CE2	2.47	0.47
35:XA:474:G:H2'	35:XA:475:G:C8	2.46	0.47
35:XA:539:A:H2'	35:XA:540:G:H8	1.74	0.47
39:XE:50:GLU:HB2	39:XE:53:LEU:HD13	1.97	0.47
40:XF:62:TRP:C	40:XF:63:TYR:HD1	2.16	0.47
35:XA:1295:G:O2'	47:XM:14:ARG:NH1	2.48	0.47
3:XY:150:ARG:O	3:XY:154:ARG:HG3	2.14	0.47
4:YA:1070:A:H2'	4:YA:1071:G:C8	2.49	0.47
4:YA:2329:G:H2'	4:YA:2330:G:C8	2.49	0.47
4:YA:2839:G:H5'	16:YR:46:GLY:HA2	1.96	0.47
4:YA:284:U:H2'	4:YA:285:C:C6	2.49	0.47
4:YA:2572:A:N7	7:YE:144:ARG:HD2	2.27	0.47
9:YG:113:ARG:NH2	29:Y4:33:VAL:HG12	2.27	0.47
35:QA:1003:G:N2	35:QA:1004:A:H1'	2.30	0.47
35:QA:513:C:H2'	35:QA:514:C:H6	1.78	0.47
35:QA:526:C:OP2	46:QL:91:LYS:HE3	2.15	0.47
3:QY:189:TYR:CE2	3:QY:193:ARG:HD3	2.49	0.47
3:QY:303:LYS:HE2	3:QY:307:LYS:NZ	2.29	0.47
4:RA:17:G:H2'	4:RA:18:C:C6	2.50	0.47
4:RA:2852:G:H2'	4:RA:2853:C:C6	2.49	0.47
14:RP:130:PHE:CD1	14:RP:130:PHE:N	2.83	0.47
24:RZ:156:LYS:O	24:RZ:156:LYS:HG3	2.14	0.47
4:YA:1084:A:H3'	4:YA:1085:A:H4'	1.96	0.47
4:YA:2788:C:OP1	7:YE:61:ARG:NH2	2.47	0.47
4:YA:998:C:P	19:YU:92:ARG:HH22	2.37	0.47
4:YA:2445:G:OP1	8:YF:74:ARG:NH2	2.47	0.47
17:YS:103:GLU:O	17:YS:107:GLU:HG3	2.14	0.47
24:YZ:144:LEU:HD21	24:YZ:150:LEU:CD1	2.44	0.47
35:QA:1158:C:C5	35:QA:1160:G:C8	3.02	0.47
35:QA:337:C:H2'	35:QA:338:A:H8	1.79	0.47
35:QA:645:C:H2'	35:QA:646:U:C6	2.49	0.47
47:QM:14:ARG:HE	47:QM:42:ALA:HA	1.78	0.47
47:QM:65:LYS:O	47:QM:70:LEU:HD12	2.15	0.47
48:QN:36:PHE:HD1	48:QN:36:PHE:C	2.18	0.47
51:QQ:4:LYS:H	51:QQ:61:GLU:HG2	1.79	0.47
35:QA:1318:A:H4'	53:QS:10:PHE:CD2	2.49	0.47
1:QV:54:U:OP1	24:RZ:203:GLU:N	2.39	0.47
29:R4:24:THR:C	29:R4:25:TYR:HD1	2.17	0.47
4:RA:1198:U:H2'	4:RA:1199:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1431:U:H2'	4:RA:1432:C:H6	1.78	0.47
4:RA:2134:A:C5	4:RA:2157:G:H5'	2.50	0.47
4:RA:2320:A:N3	4:RA:2320:A:H2'	2.29	0.47
4:RA:2650:U:H2'	4:RA:2651:C:H6	1.79	0.47
14:RP:130:PHE:N	14:RP:130:PHE:HD1	2.13	0.47
19:RU:50:ARG:O	19:RU:54:LYS:NZ	2.46	0.47
35:XA:34:C:H2'	35:XA:35:G:H8	1.80	0.47
36:XB:163:PHE:HA	36:XB:185:ILE:O	2.15	0.47
51:XQ:27:PHE:CE1	51:XQ:36:ILE:HG13	2.49	0.47
4:YA:105:C:H2'	4:YA:106:C:H6	1.79	0.47
4:YA:2313:C:H2'	4:YA:2314:C:C6	2.49	0.47
4:YA:2687:U:H2'	4:YA:2688:U:O4'	2.13	0.47
4:YA:272(O):C:H2'	4:YA:272(P):C:C6	2.50	0.47
4:YA:1500:G:O2'	6:YD:100:GLY:O	2.28	0.47
11:YI:130:TYR:CE2	11:YI:132:PRO:HB3	2.50	0.47
20:YV:35:LEU:HB2	20:YV:57:VAL:CG2	2.45	0.47
24:YZ:59:LEU:O	24:YZ:66:SER:HA	2.15	0.47
35:QA:1497:G:H1'	35:QA:1518:MA6:H2	1.97	0.47
35:QA:1302:U:H5	47:QM:17:VAL:HG21	1.79	0.47
1:QV:3:C:H2'	1:QV:4:G:H5'	1.97	0.47
3:QY:326:TYR:N	3:QY:326:TYR:CD1	2.83	0.47
29:R4:25:TYR:N	29:R4:25:TYR:CD1	2.82	0.47
4:RA:2615:U:H2'	4:RA:2616:C:H6	1.80	0.47
4:RA:284:U:H2'	4:RA:285:C:C6	2.49	0.47
4:RA:65:C:H2'	4:RA:66:C:H6	1.79	0.47
4:RA:852:G:H2'	4:RA:853:G:H8	1.80	0.47
9:RG:107:LEU:HD21	9:RG:178:PHE:CD1	2.50	0.47
16:RR:28:LEU:HD12	16:RR:48:VAL:HG21	1.95	0.47
17:RS:7:TYR:HB2	17:RS:10:ARG:NH2	2.29	0.47
18:RT:107:ASP:O	18:RT:111:ARG:HB2	2.14	0.47
35:XA:1086:U:C2	35:XA:1087:G:C8	3.02	0.47
35:XA:1161:C:C2	35:XA:1162:C:C5	3.02	0.47
36:XB:127:ILE:C	36:XB:129:GLU:H	2.18	0.47
36:XB:17:PHE:HD1	36:XB:18:GLY:N	2.01	0.47
42:XH:37:ARG:HH21	42:XH:38:ILE:CD1	2.28	0.47
47:XM:29:ARG:HA	47:XM:32:GLU:HB3	1.97	0.47
47:XM:81:LEU:CD1	47:XM:88:ARG:HD2	2.43	0.47
51:XQ:70:ARG:C	51:XQ:71:PHE:HD1	2.17	0.47
4:YA:2805:G:H2'	4:YA:2807:G:C8	2.50	0.47
4:YA:833:U:H2'	4:YA:834:C:C6	2.49	0.47
10:YH:46:GLU:HB2	10:YH:49:VAL:CG1	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:YT:22:PHE:CD2	18:YT:28:VAL:HG21	2.50	0.47
35:QA:1131:G:H2'	35:QA:1132:C:C6	2.49	0.47
38:QD:59:ARG:HA	38:QD:59:ARG:NE	2.20	0.47
43:QI:89:ASN:OD1	43:QI:91:ASP:N	2.47	0.47
46:QL:97:ARG:C	46:QL:98:TYR:CD1	2.88	0.47
46:QL:98:TYR:N	46:QL:98:TYR:HD1	2.13	0.47
3:QY:242:ASP:OD1	3:QY:242:ASP:N	2.48	0.47
26:R1:69:LYS:HE2	26:R1:72:GLU:OE1	2.15	0.47
4:RA:1045:A:H5'	4:RA:1047:G:O5'	2.14	0.47
4:RA:1198:U:H2'	4:RA:1199:U:H6	1.79	0.47
4:RA:1444:G:H2'	4:RA:1445(B):C:C5	2.50	0.47
4:RA:2365:G:H4'	25:R0:60:PHE:CZ	2.50	0.47
4:RA:2494:G:H2'	4:RA:2495:G:H8	1.79	0.47
4:RA:492:A:H2'	4:RA:493:G:O4'	2.15	0.47
4:RA:623:G:H2'	4:RA:624:C:C6	2.50	0.47
4:RA:900:A:C4	4:RA:901:A:C8	3.03	0.47
6:RD:72:LYS:HD3	6:RD:97:TYR:CE2	2.50	0.47
20:RV:11:GLN:C	20:RV:12:TYR:HD1	2.18	0.47
24:RZ:180:VAL:HG13	24:RZ:183:LEU:HD12	1.96	0.47
3:XY:322:GLN:NE2	35:XA:519:C:P	2.88	0.47
36:XB:111:ARG:NE	36:XB:111:ARG:HA	2.11	0.47
38:XD:61:LYS:HD3	38:XD:206:PHE:CD2	2.50	0.47
40:XF:60:PHE:CE2	52:XR:78:LEU:HD21	2.49	0.47
41:XG:32:ARG:O	41:XG:34:GLY:N	2.47	0.47
35:XA:1151:A:O4'	44:XJ:39:PRO:HB2	2.14	0.47
35:XA:363:A:OP1	46:XL:33:ARG:HG3	2.15	0.47
51:XQ:27:PHE:HD1	51:XQ:27:PHE:N	2.13	0.47
4:YA:11:G:C2'	4:YA:12:U:H5'	2.44	0.47
4:YA:534:U:H2'	4:YA:535:C:H6	1.79	0.47
5:YB:13:A:N1	5:YB:69:G:O2'	2.39	0.47
10:YH:3:ARG:HH12	10:YH:5:GLY:H	1.63	0.47
4:YA:2469:A:O3'	15:YQ:56:ARG:HD2	2.15	0.47
15:YQ:59:ARG:NH1	15:YQ:60:ARG:HG3	2.29	0.47
35:QA:953:G:C6	35:QA:1229:A:C6	3.03	0.47
35:QA:1251:A:H2'	35:QA:1252:A:C8	2.49	0.47
35:QA:35:G:H2'	35:QA:36:C:C6	2.49	0.47
35:QA:604:G:C6	35:QA:635:G:C6	3.03	0.47
38:QD:112:VAL:HG22	38:QD:116:GLN:OE1	2.14	0.47
4:RA:2629:A:H1'	4:RA:2630:G:H5''	1.97	0.47
5:RB:87:G:N2	5:RB:89:G:H3'	2.30	0.47
9:RG:25:TYR:HB3	9:RG:30:GLU:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:RP:127:ALA:O	14:RP:147:LEU:HA	2.14	0.47
20:RV:11:GLN:C	20:RV:12:TYR:CD1	2.88	0.47
35:XA:1435:G:H2'	35:XA:1436:U:H6	1.77	0.47
35:XA:32:A:H2'	35:XA:33:A:C8	2.50	0.47
36:XB:57:PHE:CE2	36:XB:185:ILE:HD11	2.49	0.47
36:XB:78:GLN:O	36:XB:94:ASN:ND2	2.48	0.47
38:XD:68:TYR:CD1	38:XD:68:TYR:N	2.83	0.47
3:XY:328:LEU:HD22	3:XY:345:THR:HB	1.96	0.47
3:XY:30:LYS:HD3	3:XY:66:VAL:HG11	1.97	0.47
4:YA:2028:U:H2'	4:YA:2029:G:O4'	2.14	0.47
4:YA:2119:A:H61	4:YA:2168:G:N2	2.13	0.47
4:YA:2267:A:H5''	4:YA:2268:A:H5'	1.96	0.47
4:YA:2317:C:H2'	4:YA:2318:G:H5'	1.96	0.47
4:YA:689:A:H2'	4:YA:690:G:C8	2.50	0.47
4:YA:2811:G:OP1	7:YE:60:ASN:HB2	2.15	0.47
14:YP:98:GLU:N	14:YP:98:GLU:OE1	2.35	0.47
17:YS:15:ARG:O	17:YS:19:LYS:HG2	2.15	0.47
24:YZ:7:ALA:C	24:YZ:8:TYR:HD1	2.17	0.47
35:QA:532:A:H61	37:QC:193:TYR:HA	1.80	0.47
35:QA:96:U:H2'	35:QA:97:G:C8	2.48	0.47
38:QD:170:VAL:HG12	38:QD:174:LEU:HB2	1.95	0.47
43:QI:59:PHE:CZ	43:QI:88:TYR:CE2	3.02	0.47
3:QY:200:ARG:HB2	3:QY:322:GLN:CB	2.45	0.47
32:R7:12:ARG:NH2	32:R7:44:PRO:HB3	2.30	0.47
4:RA:1057:A:O2'	4:RA:1058:G:OP1	2.29	0.47
4:RA:1711:C:H2'	4:RA:1712:C:C6	2.49	0.47
4:RA:1831:G:H2'	4:RA:1832:C:C6	2.49	0.47
4:RA:534:U:H2'	4:RA:535:C:C6	2.50	0.47
4:RA:538:G:H2'	4:RA:539:G:H8	1.79	0.47
17:RS:112:PHE:CD1	17:RS:112:PHE:N	2.82	0.47
4:RA:2319:G:H22	17:RS:3:ARG:NH1	2.12	0.47
17:RS:7:TYR:C	17:RS:7:TYR:HD1	2.18	0.47
24:RZ:7:ALA:C	24:RZ:8:TYR:CD1	2.88	0.47
35:XA:1273:G:H3'	35:XA:1274:G:H8	1.80	0.47
35:XA:1410:G:H2'	35:XA:1411:C:H6	1.77	0.47
35:XA:612:C:H2'	35:XA:613:C:H6	1.80	0.47
35:XA:614:A:H2'	35:XA:615:C:C6	2.50	0.47
38:XD:13:ARG:HG2	38:XD:38:TYR:O	2.15	0.47
4:YA:467:G:OP1	32:Y7:33:ARG:HD2	2.15	0.47
34:Y9:16:VAL:HG22	34:Y9:25:VAL:HG22	1.97	0.47
4:YA:1047:G:O2'	4:YA:1048:A:O5'	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1503:U:H2'	4:YA:1504:C:H6	1.79	0.47
4:YA:1571:A:H2'	4:YA:1572:A:C8	2.49	0.47
4:YA:1683:C:H2'	4:YA:1684:C:H6	1.79	0.47
4:YA:2016:U:H1'	30:Y5:6:VAL:HG13	1.96	0.47
4:YA:589:C:H2'	4:YA:590:A:H8	1.79	0.47
4:YA:84:A:C2	4:YA:103:A:C5	3.03	0.47
4:YA:994:C:O2'	4:YA:996:A:OP1	2.23	0.47
4:YA:615:G:OP1	8:YF:40:GLN:HG2	2.15	0.47
10:YH:94:TYR:HA	10:YH:106:THR:O	2.14	0.47
13:YO:63:VAL:HG12	13:YO:106:LEU:HD11	1.97	0.47
35:QA:1160:G:C5	35:QA:1161:C:C5	3.03	0.47
35:QA:824:C:H2'	35:QA:825:G:C8	2.49	0.47
35:QA:96:U:H2'	35:QA:97:G:H8	1.78	0.47
3:QY:41:LEU:HD23	3:QY:46:VAL:HG21	1.96	0.47
4:RA:1503:U:H2'	4:RA:1504:C:H6	1.77	0.47
4:RA:2099:U:H3	4:RA:2190:G:H1	1.62	0.47
4:RA:2647:U:H2'	4:RA:2648:C:H6	1.80	0.47
4:RA:479:A:N3	4:RA:481:G:H5''	2.30	0.47
35:XA:1030(B):G:H1'	35:XA:1030(D):G:N7	2.30	0.47
35:XA:1305:G:OP1	55:XU:2:GLY:N	2.48	0.47
35:XA:338:A:H2'	35:XA:339:C:H6	1.80	0.47
35:XA:728:A:H2'	35:XA:729:A:C8	2.50	0.47
35:XA:743:U:H2'	35:XA:744:C:H6	1.78	0.47
36:XB:28:PHE:CD2	36:XB:190:THR:HA	2.50	0.47
35:XA:538:G:H5''	46:XL:114:LYS:HB2	1.97	0.47
47:XM:91:ARG:HB2	47:XM:98:VAL:HG22	1.97	0.47
27:Y2:32:LEU:HD12	27:Y2:57:ILE:HD12	1.97	0.47
29:Y4:68:ARG:O	29:Y4:69:LYS:HB3	2.15	0.47
4:YA:1364:G:OP2	26:Y1:3:LYS:HG3	2.15	0.47
1:XV:24:U:O2'	4:YA:1923:U:OP1	2.30	0.47
4:YA:2298:A:H62	4:YA:2318:G:H8	1.59	0.47
6:YD:146:GLU:HG2	6:YD:152:GLY:C	2.36	0.47
9:YG:107:LEU:HD11	9:YG:178:PHE:CE1	2.48	0.47
12:YN:58:ASP:N	12:YN:58:ASP:OD1	2.48	0.47
35:QA:189(L):U:H2'	35:QA:189(M):G:C8	2.50	0.47
35:QA:235:C:H2'	35:QA:236:G:H8	1.79	0.47
35:QA:340:U:H2'	35:QA:341:C:C6	2.50	0.47
43:QI:42:ARG:O	43:QI:42:ARG:HD3	2.15	0.47
46:QL:27:LEU:HD13	46:QL:98:TYR:HE2	1.80	0.47
1:QV:3:C:C2'	1:QV:4:G:H5'	2.44	0.47
4:RA:1291:C:H2'	4:RA:1292:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1321:A:H2'	4:RA:1322:A:H8	1.80	0.47
4:RA:1629:U:H2'	4:RA:1630:G:C8	2.50	0.47
4:RA:594:U:H2'	4:RA:595:C:C6	2.50	0.47
7:RE:6:GLY:O	7:RE:195:LEU:HD12	2.15	0.47
11:RI:89:TYR:CD1	11:RI:89:TYR:N	2.83	0.47
4:RA:995:C:N4	12:RN:2:LYS:HG3	2.29	0.47
21:RW:12:ILE:HD13	21:RW:17:VAL:HG13	1.96	0.47
35:XA:222:U:H2'	35:XA:223:U:H6	1.79	0.47
35:XA:71:C:H2'	35:XA:72:C:C6	2.50	0.47
35:XA:542:G:OP1	38:XD:10:ARG:NH1	2.48	0.47
43:XI:31:GLN:HE21	43:XI:36:TYR:HD1	1.63	0.47
43:XI:59:PHE:CD1	43:XI:59:PHE:N	2.83	0.47
45:XK:65:ALA:HB3	45:XK:97:ALA:HB3	1.97	0.47
46:XL:110:VAL:HB	46:XL:113:ARG:HG2	1.97	0.47
26:Y1:43:TYR:HD1	26:Y1:43:TYR:N	2.12	0.47
28:Y3:44:ARG:O	28:Y3:48:GLU:HG3	2.14	0.47
30:Y5:16:ARG:NH1	30:Y5:17:ASP:OD1	2.48	0.47
4:YA:1182:A:H2'	4:YA:1183:G:C8	2.50	0.47
4:YA:1842:G:H2'	4:YA:1843:C:H6	1.79	0.47
4:YA:2118:U:O2'	4:YA:2119:A:H5''	2.14	0.47
4:YA:65:C:H2'	4:YA:66:C:C6	2.50	0.47
5:YB:96:U:H2'	5:YB:97:G:C8	2.50	0.47
9:YG:6:ALA:N	9:YG:104:GLU:OE2	2.48	0.47
9:YG:41:GLN:HG2	9:YG:154:GLY:O	2.15	0.47
37:QC:201:TYR:HD1	37:QC:201:TYR:N	2.13	0.46
38:QD:133:VAL:HG11	38:QD:138:TYR:HD2	1.79	0.46
38:QD:20:TYR:HD2	38:QD:27:TYR:CE1	2.32	0.46
39:QE:78:HIS:ND1	42:QH:104:ARG:HD2	2.30	0.46
40:QF:63:TYR:N	40:QF:63:TYR:CD1	2.82	0.46
49:QO:24:SER:O	49:QO:28:GLN:HG3	2.15	0.46
3:QY:196:THR:HG23	3:QY:222:VAL:HB	1.97	0.46
4:RA:140:G:N2	4:RA:1596:A:H4'	2.30	0.46
4:RA:1847:A:H3'	4:RA:1848:A:H5'	1.96	0.46
7:RE:34:VAL:HG22	7:RE:48:GLN:HG2	1.97	0.46
9:RG:131:TYR:HB3	9:RG:159:VAL:HG13	1.98	0.46
14:RP:95:VAL:HG22	14:RP:125:VAL:HA	1.97	0.46
14:RP:80:TYR:N	14:RP:80:TYR:HD1	2.13	0.46
35:XA:1119:C:H2'	35:XA:1120:G:H8	1.80	0.46
35:XA:1151:A:O2'	35:XA:1152:A:O5'	2.29	0.46
35:XA:1376:U:O4	41:XG:10:ARG:NH1	2.48	0.46
35:XA:1512:U:H2'	35:XA:1513:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:539:A:OP2	46:XL:115:LYS:NZ	2.47	0.46
35:XA:69:G:H2'	35:XA:70:G:H8	1.80	0.46
42:XH:65:TYR:HA	42:XH:79:VAL:HG23	1.98	0.46
50:XP:59:TRP:HA	50:XP:62:VAL:HG12	1.96	0.46
52:XR:61:LYS:O	52:XR:65:ILE:HG12	2.15	0.46
1:XV:52:G:C2	1:XV:63:G:C2	3.02	0.46
4:YA:1278:A:H2'	4:YA:1279:G:C8	2.51	0.46
4:YA:2064:C:H2'	4:YA:2065:C:H6	1.78	0.46
4:YA:2167:U:H2'	4:YA:2168:G:C4	2.50	0.46
12:YN:22:THR:HB	12:YN:25:ARG:HB2	1.96	0.46
17:YS:7:TYR:HE1	17:YS:11:LYS:HE3	1.80	0.46
35:QA:1037:C:H2'	35:QA:1038:C:H6	1.79	0.46
35:QA:973:G:H3'	35:QA:974:A:H5''	1.96	0.46
35:QA:1292:U:P	41:QG:41:ARG:NH2	2.88	0.46
47:QM:108:ARG:HD3	47:QM:108:ARG:HA	1.62	0.46
29:R4:61:ARG:HG2	29:R4:62:ARG:H	1.80	0.46
4:RA:1720:U:H2'	4:RA:1721:G:O4'	2.16	0.46
4:RA:2051:A:H5'	4:RA:2578:G:O4'	2.16	0.46
4:RA:2162:G:H2'	4:RA:2163:C:C6	2.50	0.46
4:RA:2591:C:H2'	4:RA:2592:G:H8	1.80	0.46
4:RA:580:C:H2'	4:RA:581:C:C6	2.50	0.46
4:RA:581:C:H2'	4:RA:582:G:H8	1.79	0.46
7:RE:175:VAL:HG12	7:RE:182:LEU:HD12	1.98	0.46
16:RR:21:TYR:HB3	16:RR:47:PHE:CD2	2.50	0.46
20:RV:40:LEU:HB2	20:RV:46:VAL:HG13	1.97	0.46
23:RY:20:TYR:HB3	23:RY:23:ARG:HG3	1.96	0.46
24:RZ:155:LEU:HD11	24:RZ:171:ILE:HD13	1.96	0.46
35:XA:1346:A:H61	35:XA:1374:A:H3'	1.80	0.46
35:XA:201:C:H42	35:XA:216:G:H1	1.63	0.46
35:XA:1202:G:O4'	48:XN:29:ARG:NH1	2.49	0.46
50:XP:75:ARG:HG3	50:XP:80:PHE:CD2	2.49	0.46
51:XQ:6:LEU:O	51:XQ:58:GLU:HA	2.14	0.46
4:YA:1201:C:H2'	4:YA:1202:C:H6	1.80	0.46
4:YA:1754:C:C5	18:YT:96:ARG:NH2	2.83	0.46
4:YA:1812:A:O2'	6:YD:45:ASN:N	2.48	0.46
4:YA:1915:5MU:H2'	4:YA:1916:A:H8	1.80	0.46
4:YA:2647:U:H2'	4:YA:2648:C:C6	2.51	0.46
4:YA:468:G:N7	32:Y7:39:ARG:NH2	2.54	0.46
6:YD:70:TRP:HB3	6:YD:190:TYR:CZ	2.50	0.46
15:YQ:57:HIS:HE1	15:YQ:116:GLU:CB	2.22	0.46
23:YY:20:TYR:N	23:YY:20:TYR:CD1	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:YZ:125:LEU:HG	24:YZ:164:ALA:HB3	1.98	0.46
35:QA:1343:G:H2'	35:QA:1344:C:C6	2.50	0.46
38:QD:57:ARG:NE	38:QD:205:GLU:HG2	2.30	0.46
43:QI:13:ALA:HA	43:QI:66:ARG:O	2.15	0.46
2:QX:22:C:N4	3:QY:210:GLY:HA3	2.30	0.46
3:QY:304:ASN:O	3:QY:308:GLN:HG2	2.15	0.46
3:QY:30:LYS:HD2	3:QY:66:VAL:HG11	1.97	0.46
4:RA:1199:U:H2'	4:RA:1200:C:C6	2.50	0.46
4:RA:1269:A:H2'	4:RA:1270:C:C6	2.50	0.46
4:RA:273(E):G:C2	4:RA:273(F):G:C8	3.03	0.46
6:RD:70:TRP:HB3	6:RD:190:TYR:CZ	2.51	0.46
6:RD:52:ARG:H	6:RD:52:ARG:HG2	1.43	0.46
15:RQ:32:TYR:N	15:RQ:32:TYR:CD1	2.83	0.46
16:RR:95:THR:HA	16:RR:115:GLU:O	2.16	0.46
35:XA:1002:G:C2	35:XA:1003:G:C8	3.03	0.46
35:XA:646:U:H2'	35:XA:647:C:H6	1.80	0.46
38:XD:196:LEU:O	38:XD:198:VAL:N	2.45	0.46
38:XD:64:LEU:HB2	38:XD:198:VAL:HG11	1.97	0.46
44:XJ:57:LYS:HE3	44:XJ:60:ARG:NH2	2.29	0.46
3:XY:335:ASP:O	3:XY:339:GLY:HA3	2.16	0.46
3:XY:159:ARG:NH2	3:XY:354:ASP:OD2	2.46	0.46
26:Y1:60:PHE:HD1	26:Y1:60:PHE:N	2.13	0.46
3:XY:255:ASN:ND2	4:YA:2584:U:O2'	2.42	0.46
4:YA:320:A:H4'	4:YA:322:A:N7	2.30	0.46
4:YA:950:G:H2'	4:YA:951:C:C6	2.51	0.46
9:YG:11:TYR:HD2	9:YG:12:TYR:CD1	2.33	0.46
4:YA:2864:G:OP1	18:YT:119:LYS:HE3	2.15	0.46
18:YT:28:VAL:HG13	18:YT:86:ILE:HG23	1.97	0.46
19:YU:34:LYS:HA	19:YU:34:LYS:HD3	1.64	0.46
20:YV:11:GLN:C	20:YV:12:TYR:HD1	2.19	0.46
36:QB:7:VAL:HG12	36:QB:217:ARG:HD2	1.97	0.46
46:QL:89:ARG:HA	46:QL:97:ARG:HA	1.96	0.46
3:QY:191:TRP:O	3:QY:194:THR:HG22	2.14	0.46
3:QY:254:VAL:H	4:RA:2602:A:N6	2.14	0.46
26:R1:3:LYS:HG3	26:R1:4:VAL:N	2.29	0.46
4:RA:1417:C:H2'	4:RA:1418:G:O4'	2.16	0.46
4:RA:1421:G:C2	4:RA:1422:G:C8	3.03	0.46
4:RA:197:A:N6	4:RA:2430:A:H2'	2.30	0.46
4:RA:38:A:H2'	4:RA:39:C:H6	1.80	0.46
12:RN:121:LYS:CE	12:RN:121:LYS:HD2	2.20	0.46
12:RN:94:HIS:HB3	12:RN:97:ARG:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:RX:28:PHE:HD1	22:RX:28:PHE:N	2.13	0.46
35:XA:115:G:H4'	35:XA:116:A:O5'	2.16	0.46
35:XA:1162:C:H2'	35:XA:1163:C:H6	1.80	0.46
35:XA:269:C:H2'	35:XA:270:A:H8	1.79	0.46
35:XA:270:A:H2'	35:XA:271:C:H6	1.77	0.46
35:XA:828:A:H2'	35:XA:829:G:O4'	2.15	0.46
36:XB:113:HIS:CD2	36:XB:113:HIS:H	2.33	0.46
43:XI:33:PHE:C	43:XI:33:PHE:CD1	2.89	0.46
43:XI:49:PRO:HG3	43:XI:101:PHE:CD2	2.48	0.46
2:XX:22:C:C6	3:XY:212:ARG:HD3	2.50	0.46
3:XY:265:HIS:HB2	3:XY:291:MET:HE1	1.96	0.46
4:YA:1278:A:H2'	4:YA:1279:G:H8	1.81	0.46
4:YA:1289:C:H2'	4:YA:1290:C:H6	1.81	0.46
4:YA:2693:A:H2'	4:YA:2694:G:C8	2.51	0.46
6:YD:69:ARG:C	6:YD:71:ASP:H	2.18	0.46
14:YP:90:ARG:NH1	14:YP:105:LEU:HD11	2.30	0.46
15:YQ:16:ARG:HG3	15:YQ:17:LEU:N	2.30	0.46
35:QA:1428:A:H2'	35:QA:1429:C:H6	1.80	0.46
38:QD:155:LEU:HB3	38:QD:158:ILE:HG12	1.97	0.46
38:QD:178:VAL:HG12	38:QD:179:GLU:H	1.80	0.46
39:QE:152:ARG:HB2	42:QH:43:GLY:O	2.15	0.46
47:QM:4:ILE:HA	47:QM:5:ALA:HA	1.61	0.46
47:QM:65:LYS:NZ	47:QM:73:GLU:OE1	2.41	0.46
3:QY:264:THR:HB	3:QY:271:VAL:HG12	1.98	0.46
31:R6:14:THR:HG21	31:R6:48:VAL:HG13	1.97	0.46
4:RA:1164:G:H2'	4:RA:1165:U:H6	1.80	0.46
4:RA:1628:G:H2'	4:RA:1629:U:H6	1.80	0.46
4:RA:1848:A:C4	4:RA:1849:G:C8	3.03	0.46
4:RA:719:C:H2'	4:RA:720:C:H6	1.81	0.46
4:RA:84:A:C2	4:RA:103:A:C5	3.04	0.46
11:RI:89:TYR:HD1	11:RI:89:TYR:N	2.13	0.46
4:RA:871:U:H4'	15:RQ:69:PHE:CE2	2.51	0.46
19:RU:34:LYS:HA	19:RU:34:LYS:HD3	1.67	0.46
35:XA:858:G:O6	35:XA:869:G:H3'	2.16	0.46
36:XB:122:PHE:CG	36:XB:127:ILE:HD12	2.51	0.46
35:XA:552:U:H4'	46:XL:87:GLY:HA2	1.96	0.46
26:Y1:43:TYR:CD1	26:Y1:43:TYR:N	2.84	0.46
4:YA:1639:U:C2'	4:YA:1640:C:H5''	2.45	0.46
4:YA:484:C:H2'	4:YA:485:C:C6	2.51	0.46
4:YA:566:U:H5''	14:YP:29:LYS:HE3	1.98	0.46
4:YA:639:U:C2	4:YA:640:C:C5	3.02	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:971:C:H2'	4:YA:972:G:O4'	2.16	0.46
6:YD:108:PRO:HD2	6:YD:111:LEU:CD1	2.45	0.46
4:YA:2506:U:OP1	7:YE:144:ARG:NH2	2.48	0.46
7:YE:24:THR:HG23	7:YE:186:GLY:O	2.16	0.46
8:YF:129:PHE:O	8:YF:132:VAL:HG22	2.16	0.46
8:YF:155:LEU:HD11	8:YF:176:LEU:HD12	1.97	0.46
4:YA:637:A:H5''	14:YP:117:GLU:HG2	1.97	0.46
16:YR:24:GLN:HE22	16:YR:36:THR:HG21	1.81	0.46
23:YY:60:PHE:HD1	23:YY:60:PHE:N	2.14	0.46
23:YY:89:PHE:CD1	23:YY:89:PHE:N	2.83	0.46
35:QA:1118:C:H1'	35:QA:1179:A:C4	2.50	0.46
35:QA:176:C:H2'	35:QA:177:C:C6	2.50	0.46
42:QH:63:LEU:HD23	42:QH:65:TYR:OH	2.16	0.46
42:QH:83:ILE:HA	42:QH:136:GLU:O	2.15	0.46
45:QK:18:ARG:HB2	45:QK:33:THR:OG1	2.16	0.46
49:QO:64:ARG:NH1	49:QO:68:ARG:HH21	2.13	0.46
26:R1:56:GLN:NE2	26:R1:87:PRO:HD3	2.31	0.46
26:R1:50:ARG:NH1	26:R1:57:GLU:OE2	2.49	0.46
4:RA:2103:C:N3	4:RA:2104:G:N2	2.63	0.46
4:RA:2109:U:H2'	4:RA:2110:G:C8	2.50	0.46
4:RA:2313:C:C4'	9:RG:40:ASN:HD22	2.29	0.46
4:RA:236:C:H2'	4:RA:237:C:H6	1.80	0.46
4:RA:614(A):U:H2'	4:RA:614(B):U:O4'	2.16	0.46
4:RA:747:U:O2	4:RA:2014:A:H1'	2.16	0.46
7:RE:170:LEU:HB3	7:RE:184:VAL:HG22	1.97	0.46
11:RI:130:TYR:HB3	11:RI:138:ILE:HB	1.96	0.46
18:RT:101:PHE:HD2	18:RT:101:PHE:C	2.18	0.46
20:RV:61:VAL:HA	20:RV:94:LEU:HD23	1.97	0.46
23:RY:9:LYS:HA	23:RY:10:GLY:HA2	1.62	0.46
35:XA:881:G:OP2	46:XL:12:ARG:NH2	2.49	0.46
36:XB:16:HIS:CB	36:XB:210:SER:HB3	2.46	0.46
46:XL:32:PHE:N	46:XL:32:PHE:HD1	2.14	0.46
50:XP:8:ARG:C	50:XP:9:PHE:HD1	2.19	0.46
28:Y3:11:SER:HA	28:Y3:31:LEU:HD21	1.97	0.46
4:YA:1420:U:O2'	4:YA:1421:G:OP1	2.31	0.46
4:YA:1629:U:H2'	4:YA:1630:G:C8	2.50	0.46
4:YA:2373:G:H2'	4:YA:2374:C:C6	2.51	0.46
4:YA:273(E):G:C2	4:YA:273(F):G:C8	3.03	0.46
4:YA:634:C:H2'	4:YA:635:C:C6	2.50	0.46
4:YA:706:A:H2'	4:YA:707:G:O4'	2.16	0.46
7:YE:44:TYR:CD1	7:YE:44:TYR:N	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:YG:117:PHE:C	9:YG:117:PHE:HD1	2.19	0.46
17:YS:87:PHE:HB2	17:YS:112:PHE:CE2	2.51	0.46
35:QA:1034:G:H3'	35:QA:1035:A:C8	2.51	0.46
35:QA:1038:C:H2'	35:QA:1039:C:C6	2.51	0.46
35:QA:171:A:H2'	35:QA:172:A:C8	2.51	0.46
35:QA:455:C:H2'	35:QA:456:C:C6	2.50	0.46
49:QO:29:VAL:HG11	49:QO:67:LEU:HD21	1.98	0.46
50:QP:1:MET:SD	50:QP:65:GLN:HG3	2.56	0.46
53:QS:22:LEU:HD12	53:QS:31:ILE:HD11	1.98	0.46
1:QV:54:U:N3	1:QV:58:A:C8	2.81	0.46
4:RA:1092:C:O2	4:RA:1092:C:H2'	2.15	0.46
4:RA:1514:U:H2'	4:RA:1515:G:C8	2.51	0.46
4:RA:338:G:OP1	23:RY:4:LYS:NZ	2.46	0.46
10:RH:3:ARG:CG	10:RH:6:ARG:HG2	2.46	0.46
13:RO:79:PHE:HD1	13:RO:79:PHE:N	2.14	0.46
14:RP:8:PRO:HB2	14:RP:12:ALA:HB3	1.98	0.46
20:RV:40:LEU:HB2	20:RV:46:VAL:CG1	2.46	0.46
23:RY:5:MET:HE3	23:RY:32:PRO:HA	1.97	0.46
35:XA:1346:A:N1	35:XA:1374:A:H5''	2.30	0.46
35:XA:272:C:C2	35:XA:273:A:C8	3.04	0.46
4:YA:1084:A:H3'	4:YA:1085:A:C4'	2.44	0.46
4:YA:836:G:H2'	4:YA:837:C:C6	2.50	0.46
9:YG:16:ARG:HB2	9:YG:17:PRO:HD3	1.96	0.46
9:YG:5:VAL:HG22	9:YG:8:LYS:HB3	1.97	0.46
12:YN:108:PRO:O	12:YN:113:GLY:HA3	2.16	0.46
12:YN:14:VAL:HG11	12:YN:138:LEU:HD12	1.98	0.46
15:YQ:65:PHE:HD1	15:YQ:65:PHE:N	2.12	0.46
22:YX:40:LYS:HG3	22:YX:51:VAL:HB	1.96	0.46
35:QA:1258:G:H2'	35:QA:1259:C:C6	2.51	0.46
35:QA:1410:G:H2'	35:QA:1411:C:C6	2.50	0.46
35:QA:410:G:OP1	38:QD:30:LYS:NZ	2.35	0.46
36:QB:82:ARG:NH1	36:QB:86:GLU:OE2	2.49	0.46
41:QG:70:LYS:O	41:QG:138:LYS:HE2	2.16	0.46
42:QH:6:ILE:HB	42:QH:85:ARG:NH1	2.31	0.46
43:QI:80:GLY:O	43:QI:83:ARG:HB2	2.16	0.46
35:QA:108:G:H1	54:QT:15:ARG:HG2	1.80	0.46
3:QY:295:LEU:HD12	3:QY:295:LEU:O	2.16	0.46
4:RA:1866:C:H2'	4:RA:1876:A:O4'	2.16	0.46
4:RA:2115:G:H3'	4:RA:2116:G:H5'	1.98	0.46
4:RA:2537:U:H2'	4:RA:2538:C:C6	2.51	0.46
11:RI:130:TYR:HE2	11:RI:132:PRO:HB3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:RO:64:ARG:HG2	13:RO:79:PHE:CG	2.50	0.46
15:RQ:109:VAL:HG13	15:RQ:113:GLN:HB2	1.97	0.46
23:RY:89:PHE:CD1	23:RY:89:PHE:N	2.84	0.46
35:XA:1171:G:H2'	35:XA:1172:C:H6	1.81	0.46
35:XA:35:G:H2'	35:XA:36:C:C6	2.51	0.46
35:XA:600:C:H2'	35:XA:601:C:C6	2.51	0.46
35:XA:831:U:H2'	35:XA:832:C:H6	1.80	0.46
38:XD:133:VAL:HG11	38:XD:138:TYR:HD2	1.81	0.46
39:XE:68:GLU:O	39:XE:68:GLU:HG3	2.15	0.46
50:XP:75:ARG:HG3	50:XP:80:PHE:HD2	1.81	0.46
26:Y1:71:TYR:N	26:Y1:71:TYR:HD1	2.14	0.46
4:YA:1496:A:H2'	4:YA:1498:C:C5	2.51	0.46
4:YA:1756:G:H4'	4:YA:1758:G:O4'	2.16	0.46
4:YA:2115:G:H22	4:YA:2119:A:H5'	1.80	0.46
4:YA:2164:C:H5''	4:YA:2165:G:OP2	2.16	0.46
4:YA:2793:G:H2'	4:YA:2794(A):C:O4'	2.15	0.46
4:YA:361:G:O2'	4:YA:362:U:H5'	2.16	0.46
4:YA:950:G:H2'	4:YA:951:C:H6	1.80	0.46
8:YF:187:VAL:HG12	14:YP:3:LEU:HD12	1.98	0.46
10:YH:87:LEU:HD23	10:YH:164:TYR:HA	1.98	0.46
11:YI:82:ARG:HD2	35:QA:368:U:O4	2.15	0.46
35:QA:1161:C:C2	35:QA:1162:C:C5	3.04	0.46
35:QA:333:G:H2'	35:QA:334:C:H6	1.81	0.46
35:QA:32:A:H2'	35:QA:33:A:C8	2.51	0.46
35:QA:417:C:H2'	35:QA:418:C:H6	1.80	0.46
36:QB:8:LYS:HZ3	36:QB:52:GLU:HG2	1.78	0.46
37:QC:180:ALA:HB1	37:QC:203:PHE:CE1	2.51	0.46
43:QI:88:TYR:HD1	43:QI:88:TYR:O	1.99	0.46
4:RA:2619:C:H4'	7:RE:151:TYR:O	2.15	0.46
4:RA:192:C:O2'	4:RA:802:A:N3	2.43	0.46
4:RA:1803:A:O2'	6:RD:259:THR:HG21	2.16	0.46
9:RG:16:ARG:NE	9:RG:31:VAL:CG2	2.78	0.46
23:RY:87:LYS:HB3	23:RY:95:LYS:HD2	1.97	0.46
35:XA:953:G:N7	47:XM:104:ARG:NH2	2.55	0.46
3:XY:152:TYR:OH	3:XY:199:HIS:NE2	2.39	0.46
27:Y2:31:GLU:OE1	27:Y2:53:LEU:HD11	2.15	0.46
4:YA:443:A:H1'	4:YA:1201:C:O4'	2.16	0.46
4:YA:1269:A:H2'	4:YA:1270:C:C6	2.50	0.46
4:YA:185:U:H4'	4:YA:218:A:H4'	1.98	0.46
15:YQ:35:VAL:HG12	15:YQ:130:LYS:O	2.15	0.46
35:QA:1410:G:C4	35:QA:1491:G:N2	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:22:G:H2'	35:QA:23:C:H6	1.80	0.46
35:QA:299:G:H2'	35:QA:300:A:C8	2.51	0.46
35:QA:359:U:H2'	35:QA:360:A:C8	2.51	0.46
35:QA:41:G:H2'	35:QA:42:G:H8	1.81	0.46
38:QD:185:PHE:HE1	38:QD:187:ARG:O	1.99	0.46
42:QH:121:ASP:N	42:QH:121:ASP:OD1	2.49	0.46
40:QF:60:PHE:CE2	52:QR:78:LEU:HD21	2.51	0.46
3:QY:14:LEU:HD23	3:QY:17:ARG:NH1	2.30	0.46
26:R1:18:ILE:HG12	26:R1:37:ILE:HG12	1.98	0.46
32:R7:46:VAL:HG13	32:R7:48:LYS:NZ	2.31	0.46
4:RA:1024:G:O2'	4:RA:1144:G:O2'	2.22	0.46
4:RA:1638:C:O3'	4:RA:2709:G:N2	2.49	0.46
4:RA:39:C:H2'	4:RA:40:C:C6	2.51	0.46
4:RA:458:G:O2'	4:RA:469:G:O6	2.26	0.46
4:RA:833:U:H2'	4:RA:834:C:C6	2.51	0.46
10:RH:162:ILE:C	10:RH:163:TYR:HD1	2.20	0.46
17:RS:64:GLU:O	17:RS:68:GLN:HG3	2.15	0.46
17:RS:7:TYR:O	17:RS:7:TYR:HD1	1.99	0.46
47:XM:99:ARG:HB2	47:XM:101:GLN:HE22	1.80	0.46
29:Y4:59:PHE:CA	29:Y4:61:ARG:H	2.23	0.46
4:YA:1084:A:C8	4:YA:1085:A:H4'	2.51	0.46
4:YA:1097:U:H2'	4:YA:1097:U:O2	2.15	0.46
4:YA:1239:G:H2'	4:YA:1240:U:O4'	2.16	0.46
4:YA:1431:U:H2'	4:YA:1432:C:H6	1.82	0.46
4:YA:2507:C:C5'	4:YA:2573:C:H41	2.29	0.46
4:YA:2637:U:H5'	7:YE:44:TYR:CE2	2.51	0.46
16:YR:95:THR:HG22	16:YR:116:LEU:HD23	1.98	0.46
35:QA:115:G:H4'	35:QA:116:A:O5'	2.16	0.45
35:QA:1245:A:H2'	35:QA:1246:C:H6	1.81	0.45
35:QA:736:C:H2'	35:QA:737:A:H8	1.82	0.45
35:QA:1239:A:O2'	41:QG:114:ARG:O	2.28	0.45
41:QG:18:TYR:CE2	41:QG:59:LEU:HB2	2.51	0.45
43:QI:24:GLY:HA2	43:QI:59:PHE:O	2.16	0.45
44:QJ:5:ARG:CD	44:QJ:71:LEU:HD11	2.46	0.45
53:QS:39:THR:HG22	53:QS:40:ILE:O	2.16	0.45
3:QY:133:GLN:HG2	4:RA:1914:C:O2	2.16	0.45
4:RA:1709:U:H2'	4:RA:1710:C:H6	1.77	0.45
3:QY:219:SER:HB2	4:RA:1914:C:H42	1.81	0.45
9:RG:131:TYR:HB3	9:RG:159:VAL:CG1	2.46	0.45
9:RG:5:VAL:HG22	9:RG:8:LYS:HB3	1.97	0.45
15:RQ:137:TYR:O	15:RQ:141:GLN:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:RR:17:ARG:HB2	16:RR:17:ARG:HE	1.56	0.45
18:RT:96:ARG:HH11	18:RT:96:ARG:HD2	1.48	0.45
42:XH:73:ASP:OD1	42:XH:75:ARG:HG3	2.16	0.45
47:XM:34:LEU:HD13	47:XM:41:PRO:HA	1.98	0.45
3:XY:201:LEU:HG	3:XY:203:ARG:HB2	1.96	0.45
3:XY:134:ALA:O	3:XY:317:ILE:HD13	2.16	0.45
3:XY:332:ARG:HG3	3:XY:343:ARG:HG2	1.99	0.45
4:YA:250:G:P	33:Y8:13:ARG:HH22	2.39	0.45
4:YA:2420:C:OP1	33:Y8:34:TRP:HB3	2.16	0.45
4:YA:1683:C:H2'	4:YA:1684:C:C6	2.51	0.45
4:YA:2109:U:N3	4:YA:2110:G:O6	2.50	0.45
4:YA:2838:G:C4	4:YA:2839:G:C8	3.05	0.45
7:YE:37:ARG:HA	7:YE:42:ASP:OD2	2.16	0.45
8:YF:167:ALA:HB1	8:YF:173:VAL:HG11	1.98	0.45
18:YT:4:GLY:O	18:YT:8:LYS:HG2	2.16	0.45
4:YA:2717:G:H1'	18:YT:96:ARG:NH2	2.31	0.45
35:QA:33:A:N3	46:QL:32:PHE:HE2	2.14	0.45
42:QH:46:LYS:HG3	42:QH:64:LYS:HB2	1.98	0.45
43:QI:59:PHE:CD1	43:QI:59:PHE:N	2.84	0.45
43:QI:49:PRO:HD2	43:QI:81:ILE:HD11	1.98	0.45
47:QM:37:THR:HB	47:QM:55:ARG:HD2	1.98	0.45
4:RA:1180:C:H2'	4:RA:1181:C:C6	2.52	0.45
4:RA:1636:C:H2'	4:RA:1637:A:C8	2.52	0.45
4:RA:1658:C:H2'	4:RA:1659:U:C6	2.51	0.45
4:RA:1790:C:H2'	4:RA:1791:A:C5	2.51	0.45
4:RA:2140:C:H2'	4:RA:2141:G:C8	2.47	0.45
4:RA:2286:A:H4'	4:RA:2287:A:O4'	2.16	0.45
4:RA:2698:U:H2'	4:RA:2699:C:H6	1.80	0.45
4:RA:610:G:H2'	4:RA:611:C:H6	1.81	0.45
4:RA:875:G:H2'	4:RA:876:C:O4'	2.16	0.45
6:RD:218:ARG:HB3	6:RD:219:PRO:HD2	1.98	0.45
9:RG:178:PHE:HB2	9:RG:180:PHE:HE1	1.81	0.45
15:RQ:59:ARG:HG2	15:RQ:59:ARG:HH11	1.81	0.45
16:RR:26:LYS:HE2	16:RR:70:LEU:O	2.16	0.45
17:RS:7:TYR:C	17:RS:7:TYR:CD1	2.90	0.45
19:RU:47:TYR:C	19:RU:47:TYR:CD1	2.90	0.45
35:XA:1006:C:H2'	35:XA:1007:C:H6	1.80	0.45
35:XA:102:G:O2'	35:XA:151:A:N3	2.36	0.45
35:XA:744:C:H2'	35:XA:745:C:C6	2.51	0.45
35:XA:744:C:H2'	35:XA:745:C:H6	1.81	0.45
37:XC:57:ILE:HG12	37:XC:66:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XE:28:PHE:CD2	39:XE:51:VAL:HG22	2.51	0.45
41:XG:17:VAL:HG12	41:XG:18:TYR:CD1	2.51	0.45
50:XP:19:ILE:HD11	50:XP:39:TYR:HB2	1.98	0.45
50:XP:23:ASP:OD1	50:XP:24:ALA:N	2.49	0.45
52:XR:74:ARG:HD3	52:XR:81:PHE:CD1	2.51	0.45
35:XA:108:G:N1	54:XT:15:ARG:HG2	2.31	0.45
54:XT:36:LEU:HD12	54:XT:62:LEU:HD12	1.98	0.45
4:YA:2246:G:H2'	4:YA:2247:A:H8	1.80	0.45
4:YA:493:G:H2'	4:YA:494:G:O4'	2.16	0.45
6:YD:77:ALA:HB2	6:YD:97:TYR:CD1	2.52	0.45
8:YF:110:LEU:HA	8:YF:183:VAL:HG12	1.98	0.45
9:YG:137:GLU:HG3	9:YG:140:ILE:HD12	1.97	0.45
10:YH:162:ILE:C	10:YH:163:TYR:HD1	2.20	0.45
4:YA:2839:G:H5'	16:YR:46:GLY:CA	2.47	0.45
17:YS:10:ARG:HA	17:YS:13:ARG:HH21	1.82	0.45
19:YU:92:ARG:HA	19:YU:95:LEU:HB2	1.98	0.45
35:QA:1002:G:C2	35:QA:1039:C:C2	3.05	0.45
35:QA:1073:U:C2	35:QA:1074:G:C8	3.04	0.45
35:QA:1132:C:C2	35:QA:1133:G:C8	3.04	0.45
35:QA:1263:C:H2'	35:QA:1264:C:H6	1.81	0.45
35:QA:250:A:O4'	35:QA:252:U:C6	2.69	0.45
35:QA:266:G:H2'	35:QA:266:G:N3	2.32	0.45
36:QB:40:HIS:HB3	36:QB:190:THR:HG21	1.97	0.45
48:QN:41:ARG:HE	48:QN:42:ILE:HG13	1.80	0.45
55:QU:17:THR:C	55:QU:18:TYR:HD1	2.19	0.45
3:QY:329:ASP:O	35:QA:1052:U:H4'	2.16	0.45
28:R3:11:SER:HA	28:R3:31:LEU:HD21	1.99	0.45
4:RA:1155:A:H5''	19:RU:55:ARG:HH11	1.82	0.45
4:RA:1430:C:H2'	4:RA:1431:U:C6	2.51	0.45
4:RA:207:A:H2'	4:RA:208:C:O4'	2.17	0.45
8:RF:192:LEU:HD22	8:RF:194:MET:HE2	1.97	0.45
15:RQ:93:TYR:N	15:RQ:93:TYR:HD1	2.13	0.45
16:RR:28:LEU:O	16:RR:32:GLY:N	2.47	0.45
16:RR:2:ARG:O	16:RR:2:ARG:HG2	2.16	0.45
21:RW:68:ARG:HH12	21:RW:112:GLY:H	1.63	0.45
35:XA:1512:U:H2'	35:XA:1513:A:H8	1.82	0.45
35:XA:266:G:H3'	51:XQ:67:LYS:HB2	1.98	0.45
35:XA:335:C:H2'	35:XA:336:C:C6	2.51	0.45
35:XA:512:U:H2'	35:XA:513:C:C6	2.51	0.45
35:XA:687:A:N3	35:XA:688:G:H1'	2.31	0.45
38:XD:122:ARG:HD2	38:XD:122:ARG:HA	1.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:XI:17:VAL:HG23	43:XI:63:ILE:HG12	1.99	0.45
44:XJ:37:PRO:HA	44:XJ:72:VAL:HG12	1.98	0.45
3:XY:21:LEU:O	3:XY:25:LEU:HB2	2.16	0.45
29:Y4:43:TYR:CD1	29:Y4:43:TYR:N	2.84	0.45
14:YP:60:MET:HA	33:Y8:13:ARG:NH1	2.30	0.45
4:YA:2115:G:H3'	4:YA:2116:G:H5'	1.97	0.45
4:YA:2164:C:H3'	4:YA:2165:G:H8	1.81	0.45
4:YA:2661:G:O6	10:YH:175:LYS:NZ	2.42	0.45
4:YA:285:C:H2'	4:YA:286:C:C6	2.51	0.45
4:YA:350:U:H2'	4:YA:351:G:O4'	2.16	0.45
4:YA:568:U:H5'	4:YA:945:A:N6	2.32	0.45
9:YG:11:TYR:CZ	9:YG:16:ARG:HD2	2.52	0.45
13:YO:79:PHE:N	13:YO:79:PHE:HD1	2.15	0.45
16:YR:55:ALA:HA	16:YR:80:PHE:CE1	2.51	0.45
35:QA:1158:C:H5	35:QA:1181:G:H1	1.60	0.45
35:QA:1295:G:O2'	47:QM:14:ARG:NH1	2.50	0.45
35:QA:159:G:N2	35:QA:161:A:H3'	2.31	0.45
35:QA:262:A:H2'	35:QA:263:A:C8	2.51	0.45
35:QA:514:C:C2	35:QA:515:G:C8	3.05	0.45
35:QA:936:C:C2	35:QA:937:A:C8	3.05	0.45
36:QB:224:GLN:HA	36:QB:228:GLY:O	2.16	0.45
36:QB:71:VAL:HG12	36:QB:170:GLU:HG3	1.98	0.45
37:QC:181:ASN:HB3	37:QC:205:GLY:O	2.16	0.45
38:QD:13:ARG:NH2	38:QD:40:PRO:HA	2.31	0.45
43:QI:33:PHE:CD1	43:QI:33:PHE:C	2.90	0.45
49:QO:18:PHE:HB2	49:QO:19:PRO:HD2	1.99	0.45
50:QP:74:LEU:O	50:QP:79:VAL:HG22	2.17	0.45
4:RA:1166:C:H2'	4:RA:1167:U:H6	1.82	0.45
4:RA:1500:G:H2'	4:RA:1501:C:C6	2.52	0.45
4:RA:1482:G:C6	4:RA:1507:A:C6	3.04	0.45
4:RA:1639:U:C2'	4:RA:1640:C:H5''	2.45	0.45
4:RA:2455:G:H2'	4:RA:2456:C:C6	2.52	0.45
4:RA:635:C:H2'	4:RA:636:G:O4'	2.17	0.45
4:RA:924:C:H2'	4:RA:925:C:C6	2.52	0.45
4:RA:934:G:H2'	4:RA:935:C:H6	1.82	0.45
35:XA:1127:G:H5'	35:XA:1280:A:O2'	2.16	0.45
35:XA:978:A:O2'	35:XA:1322:C:N3	2.43	0.45
35:XA:1376:U:H2'	35:XA:1377:A:C8	2.52	0.45
35:XA:36:C:H5''	46:XL:123:LYS:HD3	1.98	0.45
35:XA:438:G:O2'	35:XA:494:U:O4	2.27	0.45
42:XH:51:VAL:HG11	42:XH:60:ARG:HH11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:XO:16:ALA:HB1	49:XO:21:ASP:HB3	1.99	0.45
4:YA:1164:G:H2'	4:YA:1165:U:C6	2.51	0.45
4:YA:1188:U:C4'	20:YV:79:VAL:HG22	2.45	0.45
4:YA:212:G:H2'	4:YA:213:A:O4'	2.17	0.45
4:YA:2619:C:H4'	7:YE:151:TYR:O	2.17	0.45
4:YA:2522:U:O2'	4:YA:2647:U:OP1	2.24	0.45
4:YA:910:A:N1	4:YA:2277:G:H1'	2.31	0.45
4:YA:528:A:H2	12:YN:114:ARG:NH1	2.15	0.45
15:YQ:104:PHE:N	15:YQ:104:PHE:CD1	2.85	0.45
23:YY:19:LYS:HE3	23:YY:20:TYR:CE1	2.51	0.45
35:QA:110:C:H2'	35:QA:111:G:O4'	2.17	0.45
35:QA:636:U:H2'	35:QA:637:G:H8	1.81	0.45
35:QA:839:U:H1'	35:QA:840:C:OP1	2.16	0.45
37:QC:180:ALA:HB1	37:QC:203:PHE:HE1	1.81	0.45
37:QC:59:ARG:H	44:QJ:92:THR:CG2	2.30	0.45
37:QC:82:GLU:OE1	37:QC:85:ARG:NH2	2.48	0.45
39:QE:102:ALA:HB1	39:QE:106:PRO:HG2	1.98	0.45
44:QJ:45:ARG:HD3	44:QJ:45:ARG:HH11	1.53	0.45
46:QL:119:LYS:C	46:QL:120:TYR:HD1	2.20	0.45
47:QM:88:ARG:HG3	47:QM:98:VAL:CG1	2.47	0.45
3:QY:140:GLU:OE1	3:QY:206:PRO:HD2	2.17	0.45
3:QY:324:ARG:HB3	3:QY:326:TYR:CE1	2.51	0.45
4:RA:1055:G:H2'	4:RA:1056:G:O4'	2.17	0.45
4:RA:1165:U:H2'	4:RA:1166:C:H6	1.74	0.45
4:RA:2118:U:O2'	4:RA:2119:A:H5''	2.16	0.45
4:RA:250:G:H2'	4:RA:251:A:C8	2.52	0.45
4:RA:272(D):G:H2'	4:RA:272(E):U:C6	2.52	0.45
5:RB:48:A:H4'	17:RS:95:HIS:HD2	1.79	0.45
9:RG:32:PRO:HB3	9:RG:163:ALA:HB2	1.97	0.45
13:RO:64:ARG:HB2	13:RO:83:ALA:HB3	1.98	0.45
36:XB:170:GLU:HA	36:XB:170:GLU:OE1	2.17	0.45
38:XD:138:TYR:CD1	38:XD:138:TYR:C	2.90	0.45
35:XA:1187:G:H5'	43:XI:113:LYS:HE2	1.99	0.45
43:XI:53:VAL:HG11	43:XI:92:TYR:CE1	2.51	0.45
46:XL:83:VAL:HG13	46:XL:100:ILE:HG23	1.99	0.45
26:Y1:53:VAL:HG22	26:Y1:74:VAL:HG13	1.97	0.45
4:YA:2690:C:N4	4:YA:2713:A:H1'	2.31	0.45
4:YA:362:U:O2'	4:YA:363(A):G:H5'	2.17	0.45
6:YD:72:LYS:NZ	6:YD:99:ASP:OD2	2.36	0.45
15:YQ:59:ARG:HH12	15:YQ:60:ARG:HH11	1.63	0.45
20:YV:11:GLN:C	20:YV:12:TYR:CD1	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:652:U:O4	35:QA:752:G:O2'	2.26	0.45
35:QA:687:A:C2	35:QA:704:A:C5	3.05	0.45
3:QY:215:THR:HG22	3:QY:217:PHE:CE1	2.51	0.45
4:RA:1651:G:H5'	16:RR:39:PRO:HG2	1.98	0.45
4:RA:2462:U:H2'	4:RA:2463:C:C6	2.51	0.45
4:RA:581:C:H2'	4:RA:582:G:C8	2.51	0.45
4:RA:839:U:H2'	4:RA:840:C:C6	2.51	0.45
21:RW:11:ARG:HH21	21:RW:98:LYS:HA	1.81	0.45
23:RY:55:TYR:HE2	23:RY:61:ILE:HD13	1.82	0.45
35:XA:1143:G:H2'	35:XA:1144:G:C8	2.52	0.45
35:XA:475:G:C2'	35:XA:476:G:H5'	2.46	0.45
35:XA:531:U:O3'	35:XA:532:A:H4'	2.17	0.45
39:XE:72:GLN:OE1	39:XE:77:PRO:HB3	2.17	0.45
36:XB:178:ARG:NH2	42:XH:74:PRO:HB3	2.31	0.45
49:XO:24:SER:O	49:XO:28:GLN:HG3	2.16	0.45
1:XV:3:C:C2'	1:XV:4:G:H5'	2.46	0.45
26:Y1:3:LYS:HB2	26:Y1:61:ARG:NH1	2.32	0.45
30:Y5:35:GLU:HG3	30:Y5:51:TYR:CD2	2.52	0.45
4:YA:1092:C:O2	4:YA:1092:C:H2'	2.16	0.45
4:YA:2328:A:H2'	4:YA:2329:G:H8	1.81	0.45
4:YA:2359:C:H2'	4:YA:2360:A:O4'	2.16	0.45
4:YA:273(F):G:H2'	4:YA:273(G):C:H6	1.81	0.45
6:YD:9:TYR:CZ	6:YD:13:ARG:HG3	2.51	0.45
17:YS:71:ARG:NH1	17:YS:107:GLU:OE1	2.50	0.45
35:QA:828:A:H2'	35:QA:829:G:O4'	2.17	0.45
36:QB:16:HIS:CB	36:QB:210:SER:HB2	2.43	0.45
35:QA:1279:A:H5''	44:QJ:7:LYS:NZ	2.32	0.45
47:QM:11:ARG:O	47:QM:13:LYS:N	2.49	0.45
44:QJ:61:GLU:OE1	48:QN:58:LYS:NZ	2.49	0.45
50:QP:18:ARG:HD3	50:QP:35:LYS:HD2	1.98	0.45
4:RA:2630:G:H2'	4:RA:2631:G:C8	2.52	0.45
4:RA:273(A):G:N7	4:RA:421:U:H2'	2.31	0.45
9:RG:64:THR:HB	9:RG:94:LEU:HD21	1.99	0.45
15:RQ:111:GLU:O	15:RQ:115:MET:HG2	2.17	0.45
23:RY:15:VAL:HG21	23:RY:42:VAL:HG11	1.97	0.45
35:XA:1241:G:H2'	35:XA:1242:C:H6	1.80	0.45
35:XA:1338:G:H2'	35:XA:1339:A:C8	2.51	0.45
36:XB:160:ASP:N	36:XB:160:ASP:OD1	2.50	0.45
38:XD:148:VAL:HG11	38:XD:158:ILE:HG21	1.99	0.45
35:XA:667:G:H4'	49:XO:51:HIS:ND1	2.31	0.45
3:XY:87:ALA:HB2	3:XY:95:THR:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1057:A:HO2'	4:YA:1058:G:P	2.39	0.45
4:YA:1791:A:H3'	4:YA:1792:G:H8	1.82	0.45
4:YA:2113:U:H2'	4:YA:2114:A:O4'	2.17	0.45
4:YA:2722:G:H2'	4:YA:2723:C:C6	2.52	0.45
4:YA:740:U:H2'	4:YA:741:G:C8	2.52	0.45
8:YF:178:PRO:HG2	8:YF:179:GLU:OE1	2.16	0.45
15:YQ:16:ARG:HG3	15:YQ:17:LEU:H	1.82	0.45
35:QA:1298:C:C6	41:QG:114:ARG:NH1	2.85	0.45
35:QA:217:C:H2'	35:QA:218:C:C6	2.51	0.45
35:QA:376:G:H2'	35:QA:377:G:H8	1.82	0.45
35:QA:924:C:H2'	35:QA:925:G:C8	2.51	0.45
50:QP:79:VAL:HG23	50:QP:80:PHE:CD1	2.51	0.45
3:QY:96:PHE:O	3:QY:96:PHE:CD1	2.69	0.45
47:QM:65:LYS:N	29:R4:50:VAL:HG21	2.32	0.45
4:RA:1257:C:OP1	8:RF:75:HIS:HE1	1.99	0.45
4:RA:2115:G:H3'	4:RA:2116:G:C5'	2.46	0.45
4:RA:2238:G:H2'	4:RA:2238:G:N3	2.32	0.45
4:RA:881:G:H2'	4:RA:882:G:H8	1.80	0.45
8:RF:13:SER:OG	8:RF:127:GLU:OE2	2.27	0.45
13:RO:63:VAL:HG12	13:RO:106:LEU:HD11	1.97	0.45
13:RO:68:GLU:CB	13:RO:78:ARG:HB2	2.42	0.45
35:XA:1074:G:H2'	35:XA:1075:C:H6	1.81	0.45
38:XD:140:VAL:HG11	38:XD:146:ILE:HD11	1.98	0.45
38:XD:200:GLU:OE1	38:XD:200:GLU:N	2.50	0.45
43:XI:9:ARG:C	43:XI:104:ARG:HE	2.19	0.45
43:XI:17:VAL:HG11	43:XI:80:GLY:C	2.37	0.45
3:XY:6:PRO:O	3:XY:10:ARG:HG2	2.17	0.45
3:XY:321:SER:N	3:XY:322:GLN:HG3	2.32	0.45
4:YA:2183:C:H2'	4:YA:2184:G:C8	2.51	0.45
4:YA:616:G:H5'	8:YF:205:ARG:HD3	1.99	0.45
15:YQ:32:TYR:N	15:YQ:32:TYR:HD1	2.13	0.45
20:YV:5:VAL:HG11	20:YV:57:VAL:HG21	1.99	0.45
23:YY:19:LYS:CE	23:YY:20:TYR:HE1	2.29	0.45
35:QA:103:C:O2'	35:QA:172:A:N1	2.38	0.45
35:QA:611:A:C4	35:QA:612:C:C5	3.05	0.45
35:QA:611:A:H2'	35:QA:612:C:H6	1.82	0.45
38:QD:102:ASP:OD1	38:QD:103:ASN:N	2.50	0.45
42:QH:18:ARG:HA	42:QH:18:ARG:HD2	1.63	0.45
42:QH:33:GLU:HG2	42:QH:48:TYR:CE2	2.52	0.45
44:QJ:30:SER:OG	44:QJ:81:THR:HG22	2.17	0.45
50:QP:57:ARG:NH2	50:QP:78:GLY:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:2271:G:OP1	25:R0:18:ALA:HB1	2.17	0.45
26:R1:60:PHE:N	26:R1:60:PHE:HD1	2.15	0.45
33:R8:23:VAL:HG11	33:R8:47:LYS:HD3	1.97	0.45
4:RA:1179:C:H2'	4:RA:1180:C:C6	2.52	0.45
4:RA:1899:G:N3	4:RA:1899:G:H2'	2.32	0.45
4:RA:189:G:H2'	4:RA:205:G:N2	2.32	0.45
4:RA:208:C:H2'	4:RA:209:C:C6	2.52	0.45
4:RA:903:C:H2'	4:RA:904:C:H6	1.82	0.45
4:RA:921:G:H2'	4:RA:922:U:C6	2.51	0.45
4:RA:1798:U:H5	6:RD:274:ARG:NH1	2.14	0.45
14:RP:80:TYR:CD1	14:RP:80:TYR:N	2.85	0.45
16:RR:83:ILE:O	16:RR:86:ARG:HB2	2.17	0.45
18:RT:101:PHE:CD2	18:RT:101:PHE:C	2.90	0.45
35:XA:113:G:H2'	35:XA:114:U:C6	2.52	0.45
37:XC:148:GLY:HA3	37:XC:172:ARG:O	2.17	0.45
35:XA:407:G:HO2'	38:XD:116:GLN:HG3	1.82	0.45
35:XA:1148:U:C2'	43:XI:66:ARG:HH12	2.29	0.45
50:XP:66:PRO:HG2	50:XP:71:ARG:HG2	1.99	0.45
25:Y0:70:GLN:HE21	25:Y0:80:HIS:CD2	2.35	0.45
4:YA:1045:A:N3	4:YA:1045:A:H2'	2.31	0.45
4:YA:1321:A:C4	4:YA:1322:A:C8	3.05	0.45
4:YA:1581:G:H2'	4:YA:1582:C:O4'	2.16	0.45
4:YA:2774:C:H2'	4:YA:2775:A:O4'	2.17	0.45
4:YA:2820:A:O2'	4:YA:2821:A:OP1	2.32	0.45
4:YA:587:C:P	14:YP:21:ARG:NH2	2.90	0.45
4:YA:855:G:H2'	4:YA:856:C:C6	2.52	0.45
6:YD:70:TRP:NE1	6:YD:146:GLU:OE2	2.40	0.45
6:YD:84:TYR:C	6:YD:84:TYR:CD1	2.89	0.45
8:YF:11:VAL:HA	8:YF:125:LEU:O	2.17	0.45
10:YH:124:GLU:HB2	10:YH:132:ARG:HB3	1.98	0.45
15:YQ:93:TYR:N	15:YQ:93:TYR:HD1	2.15	0.45
4:YA:583:G:OP2	19:YU:10:ARG:HD2	2.17	0.45
23:YY:89:PHE:HD1	23:YY:89:PHE:N	2.15	0.45
35:QA:662:G:H2'	35:QA:663:A:C8	2.52	0.45
36:QB:167:PRO:HD3	36:QB:187:LEU:O	2.17	0.45
37:QC:201:TYR:N	37:QC:201:TYR:CD1	2.83	0.45
44:QJ:39:PRO:HA	44:QJ:70:ARG:HD3	1.99	0.45
52:QR:29:PHE:HE1	52:QR:31:LEU:HD13	1.81	0.45
3:QY:240:ARG:HB3	3:QY:264:THR:HG23	1.99	0.45
4:RA:2262:U:H4'	4:RA:2328:A:C2	2.53	0.45
4:RA:2693:A:H2'	4:RA:2694:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:630:G:N2	4:RA:633:A:OP2	2.45	0.45
9:RG:11:TYR:HD2	9:RG:12:TYR:CE1	2.34	0.45
23:RY:55:TYR:CE2	23:RY:61:ILE:HD13	2.52	0.45
24:RZ:44:PHE:CZ	24:RZ:86:VAL:HG11	2.52	0.45
35:XA:1030(B):G:HO2'	35:XA:1030(C):C:H6	1.64	0.45
35:XA:1146:A:H3'	35:XA:1147:C:H5''	1.98	0.45
35:XA:434:U:H2'	35:XA:435:C:C6	2.52	0.45
36:XB:218:ALA:O	36:XB:222:ILE:HG23	2.17	0.45
37:XC:178:LEU:HA	37:XC:178:LEU:HD12	1.77	0.45
39:XE:71:LEU:HD11	39:XE:115:VAL:HG22	1.98	0.45
40:XF:63:TYR:CD1	40:XF:63:TYR:N	2.85	0.45
41:XG:100:ALA:O	41:XG:104:LEU:HD13	2.17	0.45
43:XI:50:LEU:HD11	43:XI:81:ILE:HD11	1.97	0.45
46:XL:42:THR:HA	46:XL:53:ARG:O	2.17	0.45
51:XQ:83:ASP:OD1	51:XQ:83:ASP:N	2.50	0.45
1:XV:3:C:H2'	1:XV:4:G:H5'	1.99	0.45
3:XY:144:TRP:CD2	3:XY:201:LEU:HD13	2.52	0.45
4:YA:1180:C:H2'	4:YA:1181:C:C6	2.52	0.45
4:YA:643:A:H1'	31:Y6:44:ARG:NH2	2.31	0.45
9:YG:11:TYR:HA	9:YG:15:VAL:HB	1.99	0.45
14:YP:130:PHE:N	14:YP:130:PHE:CD1	2.85	0.45
17:YS:87:PHE:CD1	17:YS:112:PHE:HE2	2.35	0.45
21:YW:23:LEU:HD11	30:Y5:25:LEU:HB2	1.99	0.45
38:QD:61:LYS:HD3	38:QD:206:PHE:CD2	2.51	0.44
41:QG:23:VAL:O	41:QG:27:ILE:HG12	2.17	0.44
43:QI:108:VAL:HG12	43:QI:109:VAL:N	2.31	0.44
44:QJ:45:ARG:NH1	48:QN:36:PHE:CD2	2.82	0.44
49:QO:28:GLN:OE1	49:QO:66:LEU:HD21	2.16	0.44
51:QQ:42:TYR:N	51:QQ:42:TYR:HD1	2.14	0.44
4:RA:2328:A:H2'	4:RA:2329:G:H8	1.82	0.44
4:RA:889:C:O2'	4:RA:890:A:O5'	2.24	0.44
6:RD:106:ILE:O	6:RD:108:PRO:HD3	2.16	0.44
35:XA:1157:A:C2	35:XA:1181:G:C4	3.05	0.44
35:XA:1426:C:H2'	35:XA:1427:U:H6	1.82	0.44
35:XA:807:A:H2'	35:XA:808:C:C6	2.51	0.44
35:XA:1343:G:H4'	43:XI:122:ALA:HB3	1.99	0.44
51:XQ:42:TYR:HD1	51:XQ:42:TYR:N	2.14	0.44
26:Y1:60:PHE:CD1	26:Y1:60:PHE:N	2.84	0.44
26:Y1:83:GLU:HA	26:Y1:84:GLY:HA2	1.72	0.44
4:YA:1051:G:H2'	4:YA:1052:C:H6	1.81	0.44
4:YA:1057:A:O2'	4:YA:1058:G:OP1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1179:C:H2'	4:YA:1180:C:H6	1.82	0.44
4:YA:2845:G:H2'	4:YA:2846:G:H8	1.82	0.44
4:YA:306:U:H2'	4:YA:307:G:O4'	2.17	0.44
7:YE:2:LYS:HA	7:YE:84:PHE:CD1	2.52	0.44
9:YG:119:GLY:HA3	9:YG:181:ARG:HB2	1.98	0.44
12:YN:34:LEU:HD23	12:YN:107:LEU:HD11	1.98	0.44
35:QA:22:G:H2'	35:QA:23:C:C6	2.52	0.44
35:QA:384:G:H2'	35:QA:385:C:H6	1.82	0.44
35:QA:393:A:H5'	35:QA:483:C:O2'	2.18	0.44
35:QA:38:G:N2	35:QA:397:A:H5'	2.32	0.44
35:QA:645:C:H2'	35:QA:646:U:H6	1.83	0.44
35:QA:977:A:H1'	35:QA:982:U:O4	2.16	0.44
36:QB:95:GLN:HG3	36:QB:147:LYS:HG2	1.98	0.44
38:QD:185:PHE:C	38:QD:185:PHE:CD1	2.91	0.44
38:QD:205:GLU:OE2	39:QE:107:ARG:NE	2.50	0.44
35:QA:1047:G:H5''	48:QN:4:LYS:HD3	2.00	0.44
27:R2:17:SER:OG	27:R2:20:GLU:HG2	2.16	0.44
30:R5:58:LEU:HD23	30:R5:59:GLU:O	2.16	0.44
4:RA:1824:G:O3'	6:RD:249:PRO:HD3	2.17	0.44
4:RA:1923:U:H2'	4:RA:1924:C:C6	2.52	0.44
4:RA:52:A:H2'	4:RA:53:A:C8	2.52	0.44
4:RA:956:G:H5''	15:RQ:77:LYS:HD2	1.99	0.44
4:RA:971:C:H2'	4:RA:972:G:O4'	2.17	0.44
15:RQ:58:PHE:O	15:RQ:60:ARG:N	2.50	0.44
20:RV:14:VAL:HB	20:RV:96:ILE:HG13	1.98	0.44
35:XA:277:C:H5''	51:XQ:68:ARG:HH22	1.80	0.44
35:XA:411:A:O2'	35:XA:413:G:H5'	2.17	0.44
35:XA:979:C:H42	48:XN:18:VAL:HG12	1.82	0.44
36:XB:8:LYS:CD	36:XB:51:LEU:HB3	2.47	0.44
38:XD:59:ARG:NH2	38:XD:62:GLN:HG3	2.32	0.44
37:XC:131:ARG:CZ	39:XE:50:GLU:OE1	2.66	0.44
40:XF:60:PHE:N	40:XF:60:PHE:HD1	2.15	0.44
43:XI:108:VAL:HG12	43:XI:109:VAL:H	1.82	0.44
45:XK:84:VAL:HG21	45:XK:95:ILE:HD11	1.99	0.44
47:XM:16:ASP:N	47:XM:16:ASP:OD1	2.48	0.44
35:XA:1314:C:N4	53:XS:2:PRO:O	2.46	0.44
54:XT:18:GLN:O	54:XT:22:ARG:HG3	2.16	0.44
3:XY:161:PHE:CD1	3:XY:185:GLY:HA3	2.51	0.44
3:XY:144:TRP:CG	3:XY:201:LEU:HD22	2.52	0.44
4:YA:1051:G:C4	4:YA:1052:C:C5	3.05	0.44
4:YA:1357:U:H2'	4:YA:1358:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1957:C:H2'	4:YA:1958:C:C6	2.52	0.44
4:YA:2144:U:H1'	4:YA:2147:G:O6	2.17	0.44
4:YA:900:A:C4	4:YA:901:A:C8	3.05	0.44
5:YB:77:U:OP1	24:YZ:19:ARG:NH2	2.49	0.44
35:QA:1513:A:H2'	35:QA:1514:C:H6	1.78	0.44
35:QA:509:A:H2'	35:QA:510:A:C8	2.52	0.44
35:QA:553:A:H2'	35:QA:554:C:C6	2.52	0.44
38:QD:13:ARG:HH12	38:QD:36:ARG:CZ	2.30	0.44
38:QD:173:TRP:CG	38:QD:189:PRO:HG3	2.52	0.44
45:QK:20:TYR:HB2	45:QK:31:THR:HG23	2.00	0.44
32:R7:34:ARG:HB2	32:R7:42:LEU:HD22	1.99	0.44
4:RA:250:G:P	33:R8:13:ARG:HH22	2.39	0.44
4:RA:1115:G:H2'	4:RA:1116:C:C6	2.52	0.44
4:RA:2128:C:H3'	4:RA:2129:C:H5''	1.99	0.44
4:RA:2538:C:H2'	4:RA:2539:C:H6	1.82	0.44
4:RA:2820:A:O2'	4:RA:2821:A:OP1	2.35	0.44
4:RA:2854:G:H2'	4:RA:2855:C:C6	2.52	0.44
4:RA:858:U:O2	4:RA:2268:A:H2'	2.17	0.44
6:RD:142:VAL:HG23	6:RD:193:VAL:HA	1.99	0.44
4:RA:2406:U:C2	14:RP:72:PRO:HG2	2.52	0.44
4:RA:993:G:OP1	19:RU:50:ARG:HD2	2.16	0.44
4:RA:1188:U:C4'	20:RV:79:VAL:HG22	2.48	0.44
21:RW:11:ARG:HH21	21:RW:98:LYS:CA	2.30	0.44
35:XA:1176:A:H2'	35:XA:1177:G:C8	2.52	0.44
40:XF:63:TYR:HD1	40:XF:63:TYR:N	2.15	0.44
44:XJ:38:ILE:CG1	44:XJ:71:LEU:HB3	2.45	0.44
50:XP:9:PHE:N	50:XP:9:PHE:CD1	2.85	0.44
3:XY:146:SER:O	3:XY:149:GLU:HG2	2.16	0.44
4:YA:1359:A:N6	4:YA:1372:U:H3	2.15	0.44
4:YA:2023:G:H4'	4:YA:2617:C:O3'	2.17	0.44
4:YA:2119:A:N6	4:YA:2168:G:H21	2.15	0.44
4:YA:2391:G:O6	4:YA:2425:A:H8	2.01	0.44
4:YA:1818:U:O4	6:YD:154:LYS:HD2	2.17	0.44
6:YD:69:ARG:C	6:YD:71:ASP:N	2.70	0.44
10:YH:35:VAL:CG1	10:YH:71:LEU:HD22	2.46	0.44
12:YN:71:ILE:HG21	12:YN:84:LYS:HB3	1.99	0.44
14:YP:65:ARG:O	14:YP:68:GLN:NE2	2.50	0.44
15:YQ:109:VAL:HG13	15:YQ:113:GLN:HB2	1.99	0.44
15:YQ:30:GLY:HA2	15:YQ:107:ALA:HB2	1.97	0.44
22:YX:11:PRO:HB3	22:YX:92:LEU:HD11	1.99	0.44
35:QA:1227:A:OP2	47:QM:111:LYS:NZ	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QA:677:U:O2	35:QA:777:A:O2'	2.35	0.44
36:QB:155:LEU:HD12	36:QB:157:ARG:H	1.81	0.44
37:QC:164:ARG:HB3	37:QC:164:ARG:HE	1.65	0.44
37:QC:178:LEU:HA	37:QC:178:LEU:HD12	1.73	0.44
38:QD:59:ARG:HE	38:QD:59:ARG:CA	2.20	0.44
4:RA:610:G:H2'	4:RA:611:C:C6	2.53	0.44
7:RE:44:TYR:HD2	7:RE:82:ARG:HE	1.65	0.44
4:RA:2358:G:N2	14:RP:55:ARG:HH22	2.15	0.44
4:RA:2405:G:C5'	14:RP:75:ILE:HD13	2.47	0.44
22:RX:40:LYS:HG3	22:RX:51:VAL:HB	2.00	0.44
24:RZ:125:LEU:HG	24:RZ:164:ALA:HB3	2.00	0.44
35:XA:1030(A):C:N3	35:XA:1031:G:N2	2.65	0.44
35:XA:186:C:C2	35:XA:187:C:C5	3.06	0.44
35:XA:975:A:N1	44:XJ:48:THR:HB	2.32	0.44
40:XF:60:PHE:N	40:XF:60:PHE:CD1	2.85	0.44
42:XH:9:MET:HG3	42:XH:26:VAL:HG11	2.00	0.44
35:XA:1353:G:OP1	55:XU:10:ARG:NH1	2.50	0.44
2:XX:14:A:H61	41:XG:82:GLY:CA	2.30	0.44
4:YA:1155:A:H5''	19:YU:55:ARG:HD3	1.99	0.44
4:YA:2320:A:N3	4:YA:2320:A:H2'	2.31	0.44
4:YA:2507:C:H5''	4:YA:2573:C:N4	2.30	0.44
4:YA:573:G:O2'	4:YA:574:C:H3'	2.18	0.44
4:YA:690:G:H2'	4:YA:691:C:H6	1.79	0.44
4:YA:878:A:C6	4:YA:900:A:C8	3.06	0.44
5:YB:32:C:C4	5:YB:33:G:N7	2.86	0.44
15:YQ:32:TYR:N	15:YQ:32:TYR:CD1	2.85	0.44
35:QA:1095:U:H2'	35:QA:1096:C:C6	2.52	0.44
35:QA:1289:A:P	55:QU:10:ARG:HH22	2.41	0.44
35:QA:174:C:H2'	35:QA:175:C:C6	2.52	0.44
35:QA:309:G:O2'	35:QA:607:A:N1	2.49	0.44
35:QA:895:G:H2'	35:QA:896:C:C6	2.52	0.44
46:QL:117:ARG:CG	46:QL:122:THR:HB	2.46	0.44
46:QL:92:0TD:C	46:QL:92:0TD:OD2	2.65	0.44
52:QR:31:LEU:HD21	52:QR:62:GLU:HB3	1.99	0.44
26:R1:3:LYS:O	26:R1:12:PRO:HD3	2.17	0.44
29:R4:59:PHE:C	29:R4:61:ARG:H	2.20	0.44
4:RA:1065:U:H4'	4:RA:1066:U:C5'	2.46	0.44
4:RA:2063:C:C4	4:RA:2064:C:C5	3.06	0.44
4:RA:2287:A:C8	4:RA:2289:G:C8	3.06	0.44
4:RA:2590:A:H2'	4:RA:2591:C:C6	2.53	0.44
4:RA:2612:C:OP2	30:R5:2:ALA:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:2674:G:H2'	4:RA:2675:A:C8	2.53	0.44
4:RA:361:G:O2'	4:RA:362:U:H5'	2.17	0.44
4:RA:375:C:H2'	4:RA:376:C:H6	1.82	0.44
23:RY:89:PHE:HD1	23:RY:89:PHE:N	2.16	0.44
35:XA:152:A:C8	35:XA:153:C:C5	3.06	0.44
35:XA:663:A:H5''	52:XR:61:LYS:HZ2	1.82	0.44
35:XA:881:G:P	46:XL:12:ARG:HH22	2.41	0.44
39:XE:100:VAL:HA	39:XE:118:ILE:HG22	1.99	0.44
39:XE:19:MET:SD	39:XE:24:ARG:HB3	2.58	0.44
40:XF:69:GLU:O	40:XF:72:VAL:HG13	2.17	0.44
46:XL:31:PRO:HB2	46:XL:32:PHE:HD1	1.83	0.44
29:Y4:15:ILE:HD12	29:Y4:21:VAL:HG22	1.99	0.44
4:YA:1049:C:O2	4:YA:1113:U:H4'	2.17	0.44
4:YA:2241:A:H2'	4:YA:2242:G:C8	2.52	0.44
4:YA:754:C:H2'	4:YA:755:C:C6	2.53	0.44
4:YA:862:G:H2'	4:YA:863:A:O4'	2.18	0.44
5:YB:1:U:H2'	5:YB:2:C:H6	1.82	0.44
8:YF:7:TYR:O	8:YF:22:ALA:N	2.50	0.44
9:YG:77:ILE:HG21	9:YG:80:PHE:CD2	2.52	0.44
11:YI:130:TYR:HB3	11:YI:138:ILE:HB	2.00	0.44
16:YR:2:ARG:O	16:YR:2:ARG:HG2	2.17	0.44
18:YT:64:ARG:HH12	18:YT:103:ARG:HA	1.81	0.44
20:YV:52:VAL:CG2	20:YV:55:ALA:HB3	2.48	0.44
24:YZ:69:THR:HG22	24:YZ:90:VAL:HA	1.99	0.44
35:QA:10:A:OP2	39:QE:126:ARG:HD3	2.16	0.44
35:QA:297:G:N2	35:QA:300:A:OP2	2.47	0.44
35:QA:978:A:C4	35:QA:1319:A:C2	3.06	0.44
36:QB:19:HIS:NE2	36:QB:189:ASP:OD2	2.50	0.44
36:QB:55:PHE:CD1	36:QB:58:ILE:HD12	2.53	0.44
38:QD:121:VAL:O	38:QD:134:ASP:HA	2.18	0.44
4:RA:1069:A:H5'	4:RA:1096:A:H5'	2.00	0.44
4:RA:1196:C:C2	4:RA:1197:G:C8	3.05	0.44
4:RA:1668:A:H4'	4:RA:1669:A:O5'	2.18	0.44
4:RA:2557:G:H2'	4:RA:2558:C:C6	2.53	0.44
4:RA:574:C:N3	7:RE:145:LYS:NZ	2.65	0.44
9:RG:47:LYS:HG3	9:RG:48:GLU:N	2.33	0.44
24:RZ:104:PHE:CE2	24:RZ:119:GLU:HG2	2.53	0.44
35:XA:1005:A:H1'	35:XA:1025:U:C2	2.53	0.44
35:XA:1030(B):G:H21	35:XA:1030(D):G:H3'	1.80	0.44
36:XB:20:GLU:O	36:XB:39:ILE:HG12	2.17	0.44
37:XC:30:ARG:HH11	37:XC:30:ARG:HD3	1.62	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:XD:185:PHE:HE1	38:XD:187:ARG:O	2.01	0.44
43:XI:53:VAL:HG21	43:XI:92:TYR:CE1	2.52	0.44
47:XM:15:VAL:O	47:XM:19:LEU:HD13	2.17	0.44
54:XT:37:SER:O	54:XT:41:ILE:HG12	2.17	0.44
1:XV:49:G:H1	1:XV:65:C:H42	1.64	0.44
3:XY:203:ARG:CG	3:XY:204:LYS:N	2.80	0.44
26:Y1:85:LEU:HD23	26:Y1:89:GLU:HB3	1.99	0.44
29:Y4:15:ILE:HB	29:Y4:32:TYR:CD1	2.53	0.44
4:YA:1006:C:C2	4:YA:1138:G:N2	2.86	0.44
4:YA:250:G:H2'	4:YA:251:A:C8	2.51	0.44
4:YA:302:C:H2'	4:YA:303:U:C6	2.53	0.44
4:YA:518:G:H2'	4:YA:519:U:C6	2.53	0.44
5:YB:1:U:H2'	5:YB:2:C:C6	2.52	0.44
13:YO:111:PHE:N	13:YO:111:PHE:CD1	2.86	0.44
18:YT:24:PRO:HD3	18:YT:52:ILE:HD12	2.00	0.44
35:QA:1134:G:C2	35:QA:1141:C:C2	3.05	0.44
35:QA:1338:G:H2'	35:QA:1339:A:C8	2.53	0.44
35:QA:189(G):U:C4	51:QQ:72:ARG:NH1	2.85	0.44
35:QA:359:U:H2'	35:QA:360:A:H8	1.83	0.44
35:QA:500:G:H2'	35:QA:501:C:C6	2.53	0.44
35:QA:673:G:H2'	35:QA:674:G:H8	1.73	0.44
35:QA:707:C:OP1	45:QK:85:ARG:NH1	2.48	0.44
36:QB:9:GLU:OE1	36:QB:217:ARG:NH2	2.32	0.44
37:QC:111:LEU:HD22	37:QC:146:ALA:HB2	1.99	0.44
1:QV:58:A:H2	1:QV:60:U:HO2'	1.62	0.44
25:R0:10:THR:HG22	25:R0:12:ASN:N	2.16	0.44
26:R1:71:TYR:CD1	26:R1:71:TYR:N	2.86	0.44
27:R2:16:LEU:HB3	27:R2:20:GLU:HG3	2.00	0.44
4:RA:1278:A:H2'	4:RA:1279:G:C8	2.53	0.44
4:RA:1510:G:H2'	4:RA:1511:C:C6	2.53	0.44
4:RA:1692:U:O2'	4:RA:1693:U:H2'	2.18	0.44
4:RA:2321:G:N3	4:RA:2321:G:H2'	2.33	0.44
4:RA:900:A:H2'	4:RA:901:A:O4'	2.18	0.44
4:RA:998:C:P	19:RU:92:ARG:NH2	2.89	0.44
4:RA:2637:U:H5'	7:RE:44:TYR:CE2	2.52	0.44
10:RH:101:ARG:HH11	10:RH:101:ARG:HD2	1.55	0.44
11:RI:10:GLU:N	11:RI:10:GLU:OE1	2.50	0.44
4:RA:1754:C:C5	18:RT:96:ARG:NH2	2.86	0.44
24:RZ:103:ARG:NH2	24:RZ:136:PHE:CD2	2.80	0.44
35:XA:1426:C:H2'	35:XA:1427:U:C6	2.51	0.44
46:XL:117:ARG:HG2	46:XL:122:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XY:100:VAL:HA	3:XY:103:LEU:HB3	1.99	0.44
26:Y1:18:ILE:HG12	26:Y1:37:ILE:HG12	1.99	0.44
29:Y4:43:TYR:HD1	29:Y4:43:TYR:N	2.15	0.44
4:YA:1500:G:H2'	4:YA:1501:C:C6	2.53	0.44
4:YA:1754:C:H2'	4:YA:1755:A:O4'	2.18	0.44
4:YA:2070:G:H2'	4:YA:2071:A:C8	2.53	0.44
4:YA:2137:C:C2	4:YA:2154:G:N1	2.86	0.44
4:YA:2111:C:H42	4:YA:2147:G:H22	1.66	0.44
4:YA:1889:A:N1	4:YA:2234:G:H1'	2.33	0.44
4:YA:2630:G:H2'	4:YA:2631:G:C8	2.52	0.44
4:YA:484:C:C2	4:YA:485:C:C5	3.05	0.44
4:YA:522:G:H2'	4:YA:523:C:C6	2.53	0.44
4:YA:443:A:N7	8:YF:45:ARG:HG2	2.33	0.44
14:YP:90:ARG:HH12	14:YP:105:LEU:HD21	1.83	0.44
18:YT:101:PHE:HD2	18:YT:101:PHE:C	2.20	0.44
23:YY:86:ARG:O	23:YY:97:ARG:HA	2.17	0.44
35:QA:109:A:C6	35:QA:326:G:C6	3.06	0.44
35:QA:1394:A:N1	35:QA:1500:A:O2'	2.37	0.44
35:QA:1438:G:H2'	35:QA:1439:C:C6	2.53	0.44
35:QA:1503:A:OP1	35:QA:1531:A:O2'	2.28	0.44
35:QA:513:C:H2'	35:QA:514:C:C6	2.53	0.44
35:QA:924:C:H2'	35:QA:925:G:H8	1.83	0.44
36:QB:229:VAL:HG12	36:QB:230:VAL:N	2.30	0.44
43:QI:17:VAL:HG11	43:QI:80:GLY:C	2.38	0.44
1:QV:21:A:N6	1:QV:46:G:H2'	2.32	0.44
25:R0:50:ASN:HB3	25:R0:63:VAL:HG22	2.00	0.44
4:RA:1051:G:C4	4:RA:1052:C:C5	3.06	0.44
4:RA:150:C:H2'	4:RA:151:C:C6	2.51	0.44
4:RA:1598:C:H2'	4:RA:1599:C:H6	1.82	0.44
4:RA:1932:A:H2'	4:RA:1933:G:O4'	2.17	0.44
4:RA:2103:C:N3	4:RA:2104:G:C2	2.86	0.44
4:RA:2133:G:N2	4:RA:2157:G:H2'	2.33	0.44
4:RA:249:C:O2	33:R8:12:LYS:NZ	2.40	0.44
4:RA:675:A:C8	4:RA:804:A:C6	3.05	0.44
5:RB:48:A:H2'	5:RB:49:C:C6	2.53	0.44
10:RH:3:ARG:NH2	10:RH:66:GLY:HA3	2.33	0.44
12:RN:20:GLY:HA2	12:RN:61:ARG:HG2	1.99	0.44
12:RN:69:GLN:O	12:RN:71:ILE:HD12	2.17	0.44
35:XA:406:G:N2	38:XD:119:GLN:HE22	2.16	0.44
50:XP:9:PHE:N	50:XP:9:PHE:HD1	2.16	0.44
51:XQ:42:TYR:N	51:XQ:42:TYR:CD1	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XY:260:ALA:CB	3:XY:275:GLN:HG2	2.47	0.44
25:Y0:77:ARG:C	25:Y0:78:TYR:HD1	2.21	0.44
4:YA:1199:U:H2'	4:YA:1200:C:H6	1.83	0.44
4:YA:1899:G:N3	4:YA:1899:G:H2'	2.33	0.44
4:YA:39:C:H2'	4:YA:40:C:C6	2.53	0.44
11:YI:122:GLU:HB2	11:YI:126:TYR:OH	2.18	0.44
14:YP:130:PHE:N	14:YP:130:PHE:HD1	2.16	0.44
35:QA:1003:G:C2	35:QA:1004:A:H1'	2.53	0.44
35:QA:179:A:H2'	35:QA:180:U:C6	2.52	0.44
35:QA:417:C:C2	35:QA:418:C:C5	3.06	0.44
35:QA:553:A:H2'	35:QA:554:C:H6	1.82	0.44
35:QA:73:G:H2'	35:QA:76:C:C6	2.53	0.44
52:QR:34:TYR:N	52:QR:34:TYR:HD1	2.15	0.44
54:QT:36:LEU:HD12	54:QT:62:LEU:HD12	1.99	0.44
1:QV:52:G:C6	1:QV:53:G:N7	2.86	0.44
4:RA:1063:G:N3	4:RA:1063:G:O2'	2.42	0.44
4:RA:1289:C:H2'	4:RA:1290:C:C6	2.51	0.44
4:RA:1638:C:H2'	4:RA:1639:U:O4'	2.17	0.44
4:RA:2144:U:H1'	4:RA:2147:G:O6	2.18	0.44
4:RA:2134:A:H8	4:RA:2156:G:H21	1.65	0.44
4:RA:902:C:H2'	4:RA:903:C:C6	2.53	0.44
6:RD:72:LYS:HD2	6:RD:103:ARG:NH1	2.33	0.44
8:RF:97:TYR:N	8:RF:97:TYR:CD1	2.86	0.44
8:RF:97:TYR:N	8:RF:97:TYR:HD1	2.15	0.44
9:RG:180:PHE:CD1	9:RG:180:PHE:N	2.86	0.44
35:XA:1120:G:H2'	35:XA:1121:U:C6	2.53	0.44
35:XA:1124:G:H5'	44:XJ:38:ILE:HG22	1.98	0.44
35:XA:625:G:H4'	50:XP:16:HIS:CG	2.52	0.44
35:XA:939:G:H2'	35:XA:940:C:C6	2.52	0.44
36:XB:189:ASP:HB3	36:XB:205:ASP:H	1.82	0.44
36:XB:221:LEU:HD23	36:XB:224:GLN:OE1	2.18	0.44
36:XB:28:PHE:CE2	36:XB:190:THR:HA	2.53	0.44
41:XG:50:ILE:HD11	41:XG:58:PRO:HA	1.99	0.44
51:XQ:86:GLU:O	51:XQ:90:ILE:HG12	2.18	0.44
1:XV:47:U:H3'	1:XV:48:C:C5'	2.48	0.44
26:Y1:71:TYR:N	26:Y1:71:TYR:CD1	2.85	0.44
4:YA:1051:G:H2'	4:YA:1052:C:C6	2.53	0.44
4:YA:1067:A:O4'	4:YA:1068:G:N2	2.50	0.44
4:YA:1105:U:H2'	4:YA:1106:G:C8	2.53	0.44
4:YA:577:G:O2'	4:YA:1254:A:OP1	2.36	0.44
4:YA:1482:G:C6	4:YA:1507:A:C6	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:947:G:H2'	4:YA:948:G:C8	2.53	0.44
9:YG:170:ARG:NH2	9:YG:182:LYS:O	2.51	0.44
11:YI:2:LYS:HA	11:YI:19:VAL:O	2.18	0.44
16:YR:56:LYS:NZ	16:YR:90:ARG:O	2.51	0.44
18:YT:108:ARG:HG3	18:YT:111:ARG:NH2	2.33	0.44
35:QA:1183:A:H3'	35:QA:1184:G:C5'	2.48	0.43
35:QA:67:C:H2'	35:QA:68:G:C8	2.53	0.43
35:QA:966:M2G:HM13	35:QA:967:5MC:H1'	2.00	0.43
36:QB:8:LYS:O	36:QB:9:GLU:HB3	2.18	0.43
39:QE:141:GLN:HA	39:QE:143:ARG:HH21	1.83	0.43
41:QG:111:ARG:HH12	41:QG:122:HIS:CB	2.30	0.43
44:QJ:21:GLN:O	44:QJ:25:GLU:HG3	2.18	0.43
46:QL:32:PHE:HB3	46:QL:84:LEU:HD22	1.99	0.43
35:QA:1458:G:H5''	54:QT:31:SER:OG	2.18	0.43
3:QY:176:ILE:HD13	3:QY:179:VAL:CG1	2.48	0.43
3:QY:200:ARG:HB2	3:QY:322:GLN:HB3	2.00	0.43
26:R1:71:TYR:HD1	26:R1:71:TYR:N	2.16	0.43
4:RA:1045:A:N3	4:RA:1045:A:H2'	2.33	0.43
4:RA:1239:G:H2'	4:RA:1240:U:O4'	2.18	0.43
4:RA:1756:G:H4'	4:RA:1758:G:O4'	2.18	0.43
4:RA:2008:C:H2'	4:RA:2009:G:H8	1.83	0.43
4:RA:2111:C:H42	4:RA:2147:G:H22	1.66	0.43
4:RA:299:A:N1	4:RA:322:A:O2'	2.37	0.43
4:RA:706:A:H2'	4:RA:707:G:O4'	2.18	0.43
4:RA:952:G:C6	4:RA:966:G:C6	3.06	0.43
5:RB:84:C:OP1	28:R3:15:TYR:OH	2.23	0.43
5:RB:95:C:H2'	5:RB:96:U:C6	2.53	0.43
7:RE:37:ARG:HA	7:RE:42:ASP:OD2	2.18	0.43
7:RE:19:ARG:NH1	13:RO:72:PRO:HB3	2.33	0.43
40:XF:23:LYS:HG2	40:XF:61:LEU:HD21	1.99	0.43
41:XG:75:VAL:HA	41:XG:87:VAL:O	2.18	0.43
51:XQ:27:PHE:CD1	51:XQ:36:ILE:HG13	2.53	0.43
52:XR:26:LEU:HD11	52:XR:42:ARG:NE	2.33	0.43
3:XY:226:VAL:HG22	3:XY:227:ASP:H	1.83	0.43
17:YS:20:ARG:HH22	25:Y0:47:PRO:HB2	1.83	0.43
30:Y5:50:GLY:HA3	30:Y5:58:LEU:O	2.18	0.43
33:Y8:62:LEU:HB3	33:Y8:65:GLU:HG2	2.00	0.43
4:YA:721:C:H2'	4:YA:722:A:C8	2.52	0.43
4:YA:878:A:H3'	4:YA:879:G:H8	1.83	0.43
6:YD:147:LEU:HD11	6:YD:183:ARG:HE	1.83	0.43
7:YE:12:THR:HG22	7:YE:13:ARG:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:YG:15:VAL:HG21	9:YG:176:LEU:HD23	2.00	0.43
35:QA:610:G:C5	35:QA:611:A:N7	2.86	0.43
35:QA:857:C:H2'	35:QA:858:G:O4'	2.18	0.43
40:QF:60:PHE:N	40:QF:60:PHE:CD1	2.87	0.43
47:QM:88:ARG:HG3	47:QM:98:VAL:HG11	2.00	0.43
50:QP:40:ASP:HB3	50:QP:48:TRP:HB2	2.00	0.43
50:QP:9:PHE:HD1	50:QP:9:PHE:N	2.14	0.43
4:RA:1047:G:O2'	4:RA:1048:A:O5'	2.33	0.43
4:RA:1073:A:HO2'	4:RA:1074:G:C5'	2.30	0.43
4:RA:1097:U:H2'	4:RA:1097:U:O2	2.17	0.43
4:RA:2046:G:O5'	30:R5:19:ARG:HA	2.18	0.43
4:RA:2630:G:H2'	4:RA:2631:G:H8	1.83	0.43
5:RB:74:U:H1'	24:RZ:34:ASN:HD21	1.82	0.43
7:RE:52:LEU:O	7:RE:76:ARG:N	2.44	0.43
10:RH:3:ARG:HG2	10:RH:6:ARG:HG2	2.00	0.43
11:RI:133:HIS:ND1	11:RI:134:PRO:O	2.51	0.43
17:RS:14:VAL:O	17:RS:18:ILE:HG12	2.18	0.43
4:RA:1754:C:OP1	18:RT:96:ARG:HD3	2.17	0.43
35:XA:1030(B):G:H1'	35:XA:1030(D):G:C5	2.53	0.43
35:XA:1255:G:C2	35:XA:1283:G:C2	3.06	0.43
35:XA:892:A:H2'	35:XA:893:C:H6	1.82	0.43
37:XC:131:ARG:NH2	37:XC:166:GLU:OE2	2.42	0.43
39:XE:93:PRO:HG2	42:XH:105:ARG:HD2	2.00	0.43
42:XH:6:ILE:HB	42:XH:85:ARG:NH1	2.33	0.43
44:XJ:11:PHE:CE1	44:XJ:67:THR:HG22	2.50	0.43
44:XJ:50:ILE:HB	48:XN:41:ARG:HH21	1.83	0.43
4:YA:1198:U:C2	4:YA:1199:U:C5	3.05	0.43
4:YA:1614:A:C2	21:YW:93:ALA:HB2	2.53	0.43
4:YA:263:C:H2'	4:YA:264:C:O4'	2.17	0.43
4:YA:963:U:H2'	4:YA:964:C:C6	2.53	0.43
5:YB:14:U:OP2	5:YB:70:C:O2'	2.26	0.43
7:YE:42:ASP:HB3	7:YE:44:TYR:HE1	1.83	0.43
35:QA:1492:A:H3'	35:QA:1493:A:C8	2.49	0.43
35:QA:1512:U:H2'	35:QA:1513:A:H8	1.83	0.43
35:QA:742:G:H5'	49:QO:58:MET:HE3	2.01	0.43
35:QA:743:U:H2'	35:QA:744:C:H6	1.81	0.43
35:QA:757:U:H2'	35:QA:758:G:O4'	2.18	0.43
36:QB:16:HIS:C	36:QB:17:PHE:CD1	2.85	0.43
36:QB:189:ASP:O	36:QB:191:ASP:N	2.52	0.43
39:QE:39:GLY:HA2	39:QE:69:VAL:HG13	2.01	0.43
41:QG:18:TYR:N	41:QG:18:TYR:HD1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:QJ:16:LEU:HD21	44:QJ:70:ARG:HG2	2.00	0.43
3:QY:19:ASP:O	3:QY:22:ARG:HB2	2.19	0.43
26:R1:60:PHE:N	26:R1:60:PHE:CD1	2.86	0.43
33:R8:33:ASN:HA	33:R8:36:LYS:HD2	2.00	0.43
4:RA:1051:G:H2'	4:RA:1052:C:H6	1.83	0.43
4:RA:1803:A:H4'	6:RD:259:THR:HG23	2.00	0.43
4:RA:2115:G:H22	4:RA:2119:A:H5'	1.83	0.43
4:RA:212:G:H2'	4:RA:213:A:O4'	2.19	0.43
4:RA:2549:G:H2'	4:RA:2550:G:H8	1.84	0.43
4:RA:2845:G:H2'	4:RA:2846:G:C8	2.53	0.43
4:RA:67:U:C2	4:RA:68:G:C8	3.06	0.43
4:RA:814:C:H2'	4:RA:815:C:H6	1.82	0.43
7:RE:119:ARG:HG3	7:RE:160:TYR:CG	2.54	0.43
9:RG:105:LYS:HE3	9:RG:105:LYS:HB2	1.70	0.43
22:RX:2:LYS:NZ	22:RX:38:GLU:OE2	2.36	0.43
36:XB:9:GLU:HG3	36:XB:10:LEU:N	2.33	0.43
37:XC:8:ILE:HD12	37:XC:16:ARG:CD	2.48	0.43
39:XE:96:PRO:HA	39:XE:117:ASP:OD2	2.18	0.43
52:XR:25:THR:OG1	52:XR:26:LEU:HD13	2.17	0.43
4:YA:1166:C:H2'	4:YA:1167:U:C6	2.53	0.43
4:YA:1557:C:H5''	4:YA:1558:A:OP2	2.18	0.43
4:YA:1790:C:H5''	4:YA:1791:A:OP1	2.17	0.43
4:YA:1957:C:H2'	4:YA:1958:C:H6	1.82	0.43
4:YA:2025:C:H2'	4:YA:2026:C:C6	2.53	0.43
4:YA:2573:C:H3'	4:YA:2573:C:H6	1.83	0.43
4:YA:2695:C:H2'	4:YA:2696:U:C6	2.53	0.43
6:YD:84:TYR:C	6:YD:84:TYR:HD1	2.22	0.43
10:YH:105:LEU:HD21	10:YH:162:ILE:HD11	1.99	0.43
10:YH:8:PRO:HB2	10:YH:49:VAL:CG2	2.48	0.43
24:YZ:33:LEU:HD21	24:YZ:90:VAL:HG11	1.98	0.43
24:YZ:39:VAL:HG21	24:YZ:44:PHE:CD2	2.53	0.43
35:QA:1179:A:H2'	35:QA:1180:A:O4'	2.18	0.43
35:QA:1316:G:N2	35:QA:1318:A:H3'	2.34	0.43
35:QA:1410:G:H2'	35:QA:1411:C:H6	1.83	0.43
35:QA:687:A:N3	35:QA:688:G:H1'	2.33	0.43
43:QI:19:LEU:HB3	43:QI:59:PHE:CD2	2.43	0.43
51:QQ:42:TYR:N	51:QQ:42:TYR:CD1	2.86	0.43
3:QY:204:LYS:HB2	3:QY:329:ASP:OD2	2.18	0.43
4:RA:1491:G:O2'	6:RD:101:GLU:HB3	2.18	0.43
4:RA:1557:C:H5''	4:RA:1558:A:OP2	2.18	0.43
4:RA:1802:A:H2'	4:RA:1803:A:H8	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:1827:C:O2'	4:RA:1970:A:N3	2.45	0.43
4:RA:2115:G:N1	4:RA:2117:A:N7	2.67	0.43
4:RA:2577:A:H5''	4:RA:2578:G:H5'	2.01	0.43
4:RA:2850:A:H2'	4:RA:2851:A:C8	2.54	0.43
4:RA:764:A:H5'	6:RD:210:GLY:HA2	2.00	0.43
9:RG:180:PHE:HD1	9:RG:180:PHE:N	2.16	0.43
9:RG:6:ALA:N	9:RG:104:GLU:OE2	2.51	0.43
10:RH:12:PRO:O	10:RH:15:VAL:HG22	2.17	0.43
12:RN:58:ASP:N	12:RN:58:ASP:OD1	2.48	0.43
14:RP:79:ARG:C	14:RP:80:TYR:HD1	2.22	0.43
15:RQ:93:TYR:N	15:RQ:93:TYR:CD1	2.86	0.43
16:RR:38:VAL:HG22	16:RR:112:ALA:HB2	2.01	0.43
35:XA:130:A:O2'	35:XA:131:C:O5'	2.29	0.43
35:XA:554:C:C2	35:XA:555:C:C5	3.07	0.43
35:XA:767:A:H2'	35:XA:768:A:O4'	2.17	0.43
35:XA:857:C:H2'	35:XA:858:G:O4'	2.18	0.43
40:XF:59:TYR:CD1	40:XF:59:TYR:C	2.92	0.43
41:XG:92:SER:O	41:XG:96:GLN:HG3	2.18	0.43
44:XJ:19:SER:O	44:XJ:23:ILE:HG12	2.19	0.43
46:XL:53:ARG:CB	46:XL:93:LEU:HD11	2.48	0.43
3:XY:140:GLU:HG3	3:XY:216:SER:HB3	1.99	0.43
3:XY:250:GLY:HA3	3:XY:254:VAL:HB	2.00	0.43
3:XY:54:GLN:HA	4:YA:1068:G:O6	2.18	0.43
4:YA:1400:G:H2'	4:YA:1401:G:C8	2.54	0.43
4:YA:1866:C:H2'	4:YA:1876:A:O4'	2.18	0.43
4:YA:2846:G:H2'	4:YA:2847:U:C6	2.53	0.43
4:YA:2880:C:O3'	16:YR:90:ARG:NH1	2.52	0.43
4:YA:590:A:H2'	4:YA:591:C:H6	1.81	0.43
4:YA:732:C:H2'	4:YA:733:G:O4'	2.19	0.43
4:YA:923:C:C2	4:YA:924:C:C5	3.06	0.43
5:YB:16:G:N2	5:YB:69:G:H1'	2.33	0.43
7:YE:173:VAL:CG2	7:YE:185:LYS:HB2	2.49	0.43
9:YG:5:VAL:HG22	9:YG:8:LYS:CB	2.49	0.43
23:YY:86:ARG:NH1	23:YY:100:ALA:HA	2.34	0.43
35:QA:1499:A:H1'	35:QA:1520:G:H5'	2.00	0.43
35:QA:184:G:H2'	35:QA:185:A:C8	2.51	0.43
35:QA:224:C:H2'	35:QA:225:C:C6	2.54	0.43
35:QA:270:A:H2'	35:QA:271:C:H6	1.83	0.43
43:QI:93:ARG:HH11	43:QI:93:ARG:HD3	1.51	0.43
35:QA:718:G:H5'	45:QK:117:ASN:HB2	1.99	0.43
40:QF:100:ASN:ND2	52:QR:27:GLY:O	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:QS:66:MET:HB2	53:QS:74:PHE:CZ	2.54	0.43
1:QV:55:U:P	24:RZ:203:GLU:OE2	2.77	0.43
3:QY:195:GLU:OE2	3:QY:357:ILE:HD11	2.19	0.43
4:RA:1540:U:H2'	4:RA:1541:G:O4'	2.19	0.43
4:RA:1682:G:C4	4:RA:1757:U:C2	3.07	0.43
4:RA:1824:G:OP1	6:RD:52:ARG:HD3	2.18	0.43
10:RH:13:LYS:HA	10:RH:14:GLY:HA2	1.65	0.43
17:RS:7:TYR:HE1	17:RS:11:LYS:HE3	1.82	0.43
24:RZ:109:ALA:HB3	24:RZ:145:GLU:OE1	2.19	0.43
35:XA:1286:A:C8	35:XA:1287:A:H4'	2.54	0.43
35:XA:1301:U:O2'	35:XA:1302:U:H5'	2.19	0.43
35:XA:412:A:C5	38:XD:35:ARG:HG3	2.54	0.43
35:XA:449:C:H2'	35:XA:450:G:O4'	2.18	0.43
35:XA:864:A:H2'	35:XA:865:A:C8	2.54	0.43
36:XB:9:GLU:HG3	36:XB:10:LEU:H	1.82	0.43
3:XY:152:TYR:HE1	3:XY:353:LEU:CD2	2.31	0.43
4:YA:1050:A:H2'	4:YA:1051:G:C8	2.53	0.43
4:YA:1223:G:N2	4:YA:1226:A:OP2	2.44	0.43
4:YA:1721:G:H2'	4:YA:1740:G:O6	2.18	0.43
4:YA:1682:G:C4	4:YA:1757:U:C2	3.07	0.43
4:YA:1877:A:H5'	4:YA:1878:G:OP2	2.18	0.43
4:YA:1945:G:H2'	4:YA:1946:U:C6	2.53	0.43
4:YA:582:G:H2'	4:YA:583:G:H8	1.83	0.43
4:YA:671:C:H2'	4:YA:672:C:C6	2.54	0.43
4:YA:795:C:H2'	4:YA:796:C:C6	2.53	0.43
4:YA:569:U:O2'	4:YA:983:A:N1	2.44	0.43
8:YF:34:TRP:CZ3	14:YP:8:PRO:HB3	2.53	0.43
10:YH:55:PRO:HG2	10:YH:61:HIS:ND1	2.34	0.43
10:YH:7:LEU:HB3	10:YH:69:ARG:HH12	1.79	0.43
13:YO:64:ARG:HG2	13:YO:79:PHE:CE2	2.54	0.43
24:YZ:109:ALA:HB3	24:YZ:145:GLU:OE1	2.18	0.43
24:YZ:44:PHE:O	24:YZ:44:PHE:CD1	2.71	0.43
35:QA:1258:G:H2'	35:QA:1259:C:H6	1.83	0.43
35:QA:551:U:H2'	35:QA:552:U:C6	2.53	0.43
36:QB:27:LYS:O	36:QB:30:ARG:NH1	2.51	0.43
38:QD:163:GLU:O	38:QD:166:LYS:HG2	2.18	0.43
3:QY:193:ARG:O	3:QY:196:THR:OG1	2.31	0.43
4:RA:2153:G:H2'	4:RA:2154:G:H8	1.83	0.43
4:RA:225:A:O2'	4:RA:257:A:H4'	2.19	0.43
4:RA:2373:G:H2'	4:RA:2374:C:C6	2.54	0.43
4:RA:2461:C:H2'	4:RA:2462:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:RD:77:ALA:HA	6:RD:97:TYR:HA	2.01	0.43
15:RQ:29:PHE:HB3	15:RQ:65:PHE:CE2	2.53	0.43
20:RV:34:GLU:HA	20:RV:57:VAL:O	2.18	0.43
19:RU:40:PHE:CD2	20:RV:75:PHE:CE2	3.06	0.43
23:RY:13:VAL:HB	23:RY:72:VAL:HG13	1.99	0.43
35:XA:407:G:OP1	38:XD:115:ARG:NH2	2.44	0.43
35:XA:583:A:H2'	35:XA:584:G:O4'	2.18	0.43
35:XA:841:U:C5	35:XA:848:C:H1'	2.54	0.43
52:XR:34:TYR:N	52:XR:34:TYR:HD1	2.16	0.43
3:XY:117:ARG:HD2	3:XY:361:LEU:HB2	2.00	0.43
27:Y2:12:GLU:OE1	27:Y2:12:GLU:HA	2.18	0.43
4:YA:1092:C:C2	4:YA:1099:G:N1	2.87	0.43
4:YA:2096:U:H3	4:YA:2193:G:H1	1.66	0.43
4:YA:858:U:O2	4:YA:2268:A:H2'	2.19	0.43
4:YA:2376:A:C2	17:YS:94:TYR:CE2	3.06	0.43
8:YF:64:ILE:HG21	8:YF:78:ILE:HG23	2.00	0.43
8:YF:97:TYR:CD1	8:YF:97:TYR:N	2.87	0.43
11:YI:4:ILE:HG12	11:YI:18:VAL:HG22	2.01	0.43
21:YW:74:ALA:O	21:YW:75:TYR:HB3	2.18	0.43
35:QA:1225:A:H2'	35:QA:1226:C:C5	2.54	0.43
35:QA:1320:C:H2'	35:QA:1321:C:O4'	2.19	0.43
35:QA:636:U:H2'	35:QA:637:G:C8	2.53	0.43
35:QA:747:C:H3'	35:QA:748:C:C6	2.54	0.43
36:QB:219:VAL:HA	36:QB:222:ILE:HD12	2.01	0.43
40:QF:60:PHE:HD1	40:QF:60:PHE:N	2.17	0.43
45:QK:48:ILE:H	45:QK:48:ILE:HG13	1.67	0.43
50:QP:50:LYS:HD2	50:QP:50:LYS:HA	1.77	0.43
3:QY:319:TRP:HE1	35:QA:1492:A:C2'	2.32	0.43
4:RA:1094:U:H4'	4:RA:1096:A:N6	2.34	0.43
4:RA:1420:U:O2'	4:RA:1421:G:OP1	2.35	0.43
4:RA:1469:A:H2'	4:RA:1470:G:O4'	2.19	0.43
4:RA:1654:A:C2	7:RE:113:PHE:CD2	3.06	0.43
4:RA:321:G:H5'	8:RF:134:GLY:O	2.18	0.43
4:RA:539:G:H2'	4:RA:540:C:H6	1.82	0.43
7:RE:113:PHE:HB2	7:RE:159:HIS:CD2	2.54	0.43
20:RV:76:LYS:HB2	20:RV:81:TYR:HB3	2.01	0.43
24:RZ:2:GLU:C	24:RZ:3:TYR:HD1	2.21	0.43
24:RZ:9:TYR:OH	24:RZ:61:LEU:HD23	2.19	0.43
35:XA:1438:G:H2'	35:XA:1439:C:H6	1.84	0.43
35:XA:399:G:H2'	35:XA:400:C:C6	2.53	0.43
38:XD:111:ALA:HB2	38:XD:120:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XE:137:GLU:CG	39:XE:140:ARG:HH11	2.32	0.43
3:XY:192:LEU:HB3	3:XY:222:VAL:HG21	2.01	0.43
4:YA:150:C:H2'	4:YA:151:C:H6	1.83	0.43
4:YA:944:G:H5''	4:YA:945:A:O5'	2.18	0.43
7:YE:36:ARG:NH1	7:YE:85:ASN:OD1	2.50	0.43
8:YF:101:LEU:HB3	8:YF:106:ARG:HD3	2.00	0.43
8:YF:97:TYR:HD1	8:YF:97:TYR:N	2.17	0.43
14:YP:63:PRO:HB2	33:Y8:30:ARG:NH2	2.33	0.43
16:YR:24:GLN:HB3	16:YR:44:LEU:HD11	2.00	0.43
16:YR:24:GLN:NE2	16:YR:36:THR:HG21	2.33	0.43
23:YY:5:MET:CE	23:YY:32:PRO:HA	2.48	0.43
23:YY:5:MET:HE1	23:YY:35:TYR:HA	2.00	0.43
35:QA:1244:C:H2'	35:QA:1245:A:C8	2.54	0.43
35:QA:1244:C:H2'	35:QA:1245:A:H8	1.83	0.43
35:QA:1346:A:N1	35:QA:1374:A:H5''	2.34	0.43
35:QA:1427:U:H2'	35:QA:1428:A:C8	2.53	0.43
35:QA:160:A:H2'	35:QA:161:A:O4'	2.18	0.43
35:QA:41:G:H2'	35:QA:42:G:C8	2.53	0.43
35:QA:643:C:H2'	35:QA:644:G:H8	1.84	0.43
35:QA:553:A:H5''	46:QL:24:VAL:HG21	2.00	0.43
3:QY:176:ILE:HG21	3:QY:179:VAL:HG13	1.99	0.43
3:QY:338:THR:OG1	3:QY:339:GLY:HA2	2.19	0.43
21:RW:23:LEU:CD1	30:R5:25:LEU:HB2	2.49	0.43
4:RA:1385:G:C4	4:RA:1386:C:C5	3.07	0.43
4:RA:1799:G:H8	6:RD:181:GLU:OE1	2.02	0.43
4:RA:1946:U:C2	4:RA:1947:C:C5	3.07	0.43
4:RA:2173:A:H2'	4:RA:2174:C:H5'	2.00	0.43
4:RA:37:C:H2'	4:RA:38:A:C8	2.53	0.43
4:RA:671:C:H2'	4:RA:672:C:C6	2.54	0.43
11:RI:61:ARG:HD3	11:RI:61:ARG:HA	1.82	0.43
5:RB:8:U:H4'	17:RS:25:ARG:NH2	2.33	0.43
17:RS:48:LEU:HD23	17:RS:82:ILE:HD11	2.01	0.43
18:RT:37:GLY:HA2	18:RT:38:ASN:HA	1.65	0.43
35:XA:1009:G:H1	35:XA:1020:U:H3	1.67	0.43
35:XA:328:C:H4'	35:XA:329:A:H5'	2.00	0.43
35:XA:380:G:N2	35:XA:383:A:OP2	2.52	0.43
35:XA:73:G:C6	35:XA:97:G:C6	3.07	0.43
36:XB:113:HIS:CD2	36:XB:113:HIS:N	2.83	0.43
36:XB:163:PHE:CE1	36:XB:185:ILE:HG22	2.54	0.43
36:XB:66:GLY:HA3	36:XB:160:ASP:OD2	2.18	0.43
37:XC:64:VAL:O	37:XC:99:VAL:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XE:102:ALA:O	39:XE:107:ARG:NH1	2.51	0.43
48:YN:29:ARG:NH2	48:YN:41:ARG:HH11	2.16	0.43
3:XY:270:ILE:HD12	3:XY:298:LEU:HD11	2.00	0.43
4:YA:1125:G:C6	4:YA:1126:A:N6	2.87	0.43
4:YA:1637:A:H4'	4:YA:2711:A:O2'	2.18	0.43
4:YA:1720:U:H2'	4:YA:1721:G:O4'	2.18	0.43
4:YA:195:A:H5''	4:YA:196:A:O5'	2.19	0.43
4:YA:2059:A:C8	4:YA:2503:2MA:HM23	2.54	0.43
4:YA:721:C:H2'	4:YA:722:A:H8	1.83	0.43
9:YG:7:LEU:HD23	9:YG:100:TRP:HE3	1.84	0.43
9:YG:68:PRO:HB2	9:YG:90:LEU:HB3	2.00	0.43
13:YO:68:GLU:CB	13:YO:78:ARG:HB2	2.47	0.43
15:YQ:104:PHE:N	15:YQ:104:PHE:HD1	2.17	0.43
20:YV:14:VAL:HB	20:YV:96:ILE:HG13	2.01	0.43
35:QA:1160:G:C6	35:QA:1161:C:C5	3.06	0.43
35:QA:1157:A:C2	35:QA:1181:G:C4	3.07	0.43
35:QA:152:A:C8	35:QA:153:C:C5	3.07	0.43
35:QA:324:G:N1	35:QA:327:A:OP2	2.51	0.43
35:QA:892:A:H2'	35:QA:893:C:C6	2.54	0.43
35:QA:895:G:H2'	35:QA:896:C:H6	1.83	0.43
36:QB:15:VAL:O	36:QB:15:VAL:HG22	2.18	0.43
35:QA:1060:C:C4	37:QC:2:GLY:HA3	2.53	0.43
40:QF:59:TYR:C	40:QF:59:TYR:CD1	2.93	0.43
49:QO:82:ILE:O	49:QO:86:GLY:N	2.52	0.43
31:R6:12:GLU:HG2	31:R6:19:ARG:HG2	2.01	0.43
33:R8:65:GLU:OE1	33:R8:65:GLU:HA	2.18	0.43
4:RA:1033:U:O2'	4:RA:2750:A:N6	2.51	0.43
4:RA:2119:A:N6	4:RA:2168:G:H21	2.16	0.43
4:RA:2364:C:H2'	4:RA:2365:G:O4'	2.18	0.43
4:RA:1297:C:OP1	4:RA:2710:C:H4'	2.19	0.43
6:RD:145:VAL:HG12	6:RD:146:GLU:O	2.19	0.43
12:RN:42:TRP:CH2	12:RN:44:PRO:HB3	2.54	0.43
15:RQ:63:LYS:HG3	15:RQ:65:PHE:CE1	2.53	0.43
21:RW:10:VAL:HG12	21:RW:12:ILE:HG22	1.99	0.43
35:XA:1161:C:H2'	35:XA:1162:C:C6	2.54	0.43
35:XA:7:G:H5'	35:XA:298:A:O4'	2.19	0.43
36:XB:70:PHE:N	36:XB:70:PHE:CD1	2.87	0.43
43:XI:55:ALA:HA	43:XI:58:HIS:ND1	2.34	0.43
48:YN:23:ARG:NH1	48:YN:30:ALA:HB2	2.33	0.43
29:Y4:48:ARG:HB3	29:Y4:51:ASP:O	2.19	0.43
4:YA:1094:U:H4'	4:YA:1096:A:N6	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1358:G:O2'	4:YA:1359:A:H5'	2.18	0.43
4:YA:1754:C:OP1	18:YT:96:ARG:HD3	2.19	0.43
4:YA:234:C:H2'	4:YA:235:U:C6	2.52	0.43
4:YA:2557:G:H2'	4:YA:2558:C:C6	2.53	0.43
4:YA:2695:C:H2'	4:YA:2696:U:H6	1.84	0.43
4:YA:335:C:H4'	23:YY:73:ARG:HD2	2.00	0.43
4:YA:445:C:H2'	4:YA:446:G:O4'	2.18	0.43
4:YA:610:G:H2'	4:YA:611:C:H6	1.83	0.43
4:YA:871:U:H2'	4:YA:872:A:C8	2.54	0.43
4:YA:2303:G:O2'	9:YG:132:ASN:HB2	2.18	0.43
9:YG:170:ARG:HH21	9:YG:180:PHE:HB2	1.84	0.43
23:YY:21:LYS:HB2	23:YY:21:LYS:HE3	1.74	0.43
35:QA:1142:G:H2'	35:QA:1143:G:O4'	2.19	0.43
35:QA:554:C:C2	35:QA:555:C:C5	3.07	0.43
37:QC:157:ILE:HB	37:QC:164:ARG:HH21	1.83	0.43
37:QC:8:ILE:HD12	37:QC:16:ARG:CD	2.48	0.43
42:QH:36:LEU:HD12	42:QH:59:LEU:HD13	2.00	0.43
42:QH:51:VAL:HG11	42:QH:60:ARG:NH1	2.31	0.43
42:QH:73:ASP:OD1	42:QH:75:ARG:HG3	2.19	0.43
44:QJ:35:SER:N	44:QJ:73:ASP:O	2.37	0.43
4:RA:195:A:H5''	4:RA:196:A:O5'	2.18	0.43
4:RA:635:C:O2'	4:RA:639:U:OP1	2.35	0.43
4:RA:900:A:H2'	4:RA:901:A:H8	1.84	0.43
5:RB:66:A:H61	5:RB:109:C:H5'	1.84	0.43
4:RA:563:G:N2	19:RU:37:GLU:OE2	2.43	0.43
21:RW:7:ALA:HB2	21:RW:50:VAL:HG22	2.01	0.43
23:RY:6:HIS:HE1	23:RY:72:VAL:O	2.01	0.43
35:XA:1023:G:H3'	35:XA:1024:G:C8	2.54	0.43
35:XA:1131:G:H2'	35:XA:1132:C:C6	2.53	0.43
35:XA:1273:G:H3'	35:XA:1274:G:C8	2.54	0.43
35:XA:337:C:H2'	35:XA:338:A:C8	2.53	0.43
35:XA:911:U:H2'	35:XA:912:C:H6	1.84	0.43
36:XB:7:VAL:HG12	36:XB:8:LYS:H	1.84	0.43
38:XD:108:LEU:CD1	38:XD:174:LEU:HD13	2.49	0.43
44:XJ:6:ILE:HB	44:XJ:72:VAL:HG22	2.00	0.43
29:Y4:44:THR:O	29:Y4:46:GLN:N	2.52	0.43
30:Y5:35:GLU:HA	30:Y5:35:GLU:OE1	2.19	0.43
4:YA:105:C:H2'	4:YA:106:C:C6	2.54	0.43
4:YA:2365:G:O6	33:Y8:39:LYS:HE3	2.19	0.43
4:YA:2853:C:C2	4:YA:2854:G:C8	3.07	0.43
4:YA:302:C:H2'	4:YA:303:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:656:G:H2'	4:YA:657:U:O4'	2.19	0.43
4:YA:924:C:H2'	4:YA:925:C:H6	1.82	0.43
9:YG:171:ALA:O	9:YG:175:LEU:HD13	2.19	0.43
12:YN:19:GLU:HG3	12:YN:59:LYS:HB3	2.01	0.43
35:QA:1030(D):G:H2'	35:QA:1030(E):A:H8	1.82	0.42
35:QA:1030(A):C:N3	35:QA:1031:G:N2	2.66	0.42
35:QA:1261:A:H3'	35:QA:1262:C:H6	1.84	0.42
35:QA:396:G:O2'	35:QA:398:C:OP1	2.24	0.42
35:QA:868:C:H2'	35:QA:869:G:O4'	2.19	0.42
39:QE:41:VAL:HG13	39:QE:113:ALA:HA	2.01	0.42
41:QG:17:VAL:HG12	41:QG:18:TYR:CD1	2.54	0.42
35:QA:1149:C:P	43:QI:9:ARG:HH21	2.42	0.42
47:QM:14:ARG:HG2	47:QM:42:ALA:O	2.19	0.42
47:QM:49:THR:HG22	47:QM:51:ALA:H	1.84	0.42
49:QO:72:ARG:HB2	49:QO:72:ARG:HE	1.53	0.42
50:QP:60:LEU:HD21	50:QP:80:PHE:HE1	1.83	0.42
32:R7:17:GLY:O	32:R7:21:ARG:HG2	2.19	0.42
4:RA:1105:U:H2'	4:RA:1106:G:C8	2.54	0.42
4:RA:1321:A:H2'	4:RA:1322:A:C8	2.54	0.42
4:RA:2119:A:H61	4:RA:2168:G:N2	2.16	0.42
4:RA:2345:G:N3	4:RA:2381:C:H2'	2.34	0.42
4:RA:265:A:N1	4:RA:427:U:O2'	2.39	0.42
4:RA:272(A):A:C8	4:RA:272(B):C:C6	3.07	0.42
4:RA:2805:G:H2'	4:RA:2807:G:C8	2.54	0.42
4:RA:2845:G:H2'	4:RA:2846:G:H8	1.84	0.42
4:RA:302:C:H2'	4:RA:303:U:C6	2.54	0.42
4:RA:934:G:H2'	4:RA:935:C:C6	2.54	0.42
7:RE:7:VAL:CG1	7:RE:27:LEU:HB3	2.49	0.42
8:RF:110:LEU:HD11	8:RF:205:ARG:NH1	2.34	0.42
18:RT:45:PHE:CD2	18:RT:74:ARG:HG3	2.54	0.42
19:RU:47:TYR:C	19:RU:47:TYR:HD1	2.22	0.42
35:XA:1160:G:C5	35:XA:1161:C:C5	3.07	0.42
35:XA:56:U:H2'	35:XA:57:G:C8	2.54	0.42
35:XA:691:G:H2'	35:XA:692:U:C6	2.54	0.42
35:XA:933:G:O6	41:XG:3:ARG:NH2	2.51	0.42
39:XE:110:LEU:HD13	39:XE:118:ILE:HG21	2.01	0.42
44:XJ:6:ILE:HB	44:XJ:72:VAL:CG2	2.49	0.42
45:XK:96:ARG:HD2	45:XK:96:ARG:HA	1.50	0.42
29:Y4:58:ARG:HH11	47:XM:80:ARG:NH2	2.15	0.42
4:YA:242:G:H5''	33:Y8:64:TYR:CE2	2.53	0.42
4:YA:330:A:N7	4:YA:1210:A:O2'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1826:G:O2'	6:YD:242:ARG:NH2	2.52	0.42
9:YG:16:ARG:NH2	9:YG:28:VAL:O	2.52	0.42
4:YA:956:G:OP2	15:YQ:14:ARG:NH2	2.52	0.42
20:YV:29:PRO:HA	20:YV:61:VAL:CG2	2.49	0.42
35:QA:1002:G:H2'	35:QA:1003:G:C1'	2.49	0.42
35:QA:1072:G:H2'	35:QA:1073:U:H6	1.82	0.42
35:QA:323:U:H2'	35:QA:324:G:O4'	2.18	0.42
35:QA:375:U:OP1	50:QP:69:THR:HG21	2.18	0.42
35:QA:429:U:H3'	38:QD:9:CYS:SG	2.59	0.42
35:QA:624:C:H2'	35:QA:625:G:C8	2.54	0.42
35:QA:986:A:H2'	35:QA:987:G:C8	2.55	0.42
36:QB:15:VAL:HG11	36:QB:213:LEU:HD12	2.02	0.42
36:QB:163:PHE:HA	36:QB:185:ILE:O	2.19	0.42
37:QC:58:GLU:O	37:QC:64:VAL:HG23	2.19	0.42
35:QA:542:G:H5'	38:QD:41:GLY:HA3	2.00	0.42
35:QA:562:C:H1'	46:QL:15:ARG:HD2	2.01	0.42
48:QN:45:ARG:O	48:QN:49:HIS:HD2	2.02	0.42
35:QA:277:C:H5''	51:QQ:68:ARG:HH22	1.84	0.42
1:QV:16:C:H3'	1:QV:17:C:C6	2.54	0.42
4:RA:1322:A:C5	4:RA:1323:U:C5	3.07	0.42
4:RA:1400:G:H2'	4:RA:1401:G:C8	2.54	0.42
4:RA:2243:U:H2'	4:RA:2244:U:H6	1.81	0.42
4:RA:2321:G:HO2'	4:RA:2322:A:P	2.41	0.42
4:RA:2547:U:O2	13:RO:23:ARG:NH2	2.47	0.42
4:RA:2722:G:H2'	4:RA:2723:C:C6	2.54	0.42
4:RA:453:C:O2	4:RA:457:A:O2'	2.36	0.42
4:RA:493:G:H2'	4:RA:494:G:O4'	2.19	0.42
9:RG:125:PHE:CE2	9:RG:180:PHE:HE2	2.36	0.42
13:RO:64:ARG:NH2	13:RO:99:PHE:O	2.52	0.42
17:RS:41:ASP:OD1	17:RS:43:GLU:HB3	2.19	0.42
35:XA:1073:U:C2	35:XA:1074:G:C8	3.07	0.42
35:XA:384:G:H2'	35:XA:385:C:H6	1.83	0.42
36:XB:77:ALA:O	36:XB:78:GLN:C	2.57	0.42
35:XA:1070:U:OP1	39:XE:20:GLN:NE2	2.52	0.42
42:XH:120:THR:OG1	42:XH:123:GLU:HG3	2.19	0.42
43:XI:100:GLY:O	43:XI:103:THR:HG22	2.19	0.42
35:XA:375:U:OP1	50:XP:69:THR:HG21	2.19	0.42
4:YA:1045:A:H5''	4:YA:1046:A:OP1	2.18	0.42
4:YA:2358:G:N2	14:YP:55:ARG:HH22	2.17	0.42
4:YA:2845:G:H2'	4:YA:2846:G:C8	2.54	0.42
5:YB:24:G:N7	5:YB:56:G:H2'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YD:80:ALA:N	6:YD:94:LEU:O	2.51	0.42
7:YE:115:GLY:O	7:YE:119:ARG:HB2	2.19	0.42
11:YI:48:GLU:HG3	11:YI:52:ARG:NH1	2.33	0.42
17:YS:20:ARG:HA	17:YS:20:ARG:HD3	1.85	0.42
35:QA:1024:G:N3	35:QA:1024:G:H2'	2.34	0.42
35:QA:1412:C:H2'	35:QA:1413:A:H8	1.82	0.42
35:QA:194:C:H2'	35:QA:195:A:H5''	2.00	0.42
35:QA:32:A:H3'	35:QA:33:A:H8	1.83	0.42
35:QA:620:C:H2'	35:QA:621:A:O4'	2.20	0.42
36:QB:217:ARG:O	36:QB:220:ASP:HB2	2.19	0.42
39:QE:110:LEU:HD13	39:QE:118:ILE:HG21	2.01	0.42
44:QJ:81:THR:HA	44:QJ:84:GLN:OE1	2.19	0.42
35:QA:261:U:OP2	54:QT:79:ARG:NH2	2.52	0.42
1:QV:53:G:O6	1:QV:62:C:C4	2.72	0.42
30:R5:51:TYR:HE1	30:R5:56:LYS:HD3	1.83	0.42
31:R6:9:LEU:HD13	31:R6:51:GLU:HG3	2.01	0.42
4:RA:1357:U:H5'	32:R7:23:ARG:NH1	2.35	0.42
4:RA:579:G:O2'	4:RA:2019:A:OP1	2.30	0.42
4:RA:2188:C:H2'	4:RA:2189:U:O4'	2.20	0.42
4:RA:228:A:H8	4:RA:229:A:H5'	1.84	0.42
4:RA:721:C:H2'	4:RA:722:A:C8	2.55	0.42
6:RD:70:TRP:NE1	6:RD:146:GLU:OE2	2.48	0.42
6:RD:260:ARG:NH2	6:RD:270:ILE:HD12	2.35	0.42
8:RF:153:SER:OG	8:RF:190:GLU:HG3	2.19	0.42
15:RQ:30:GLY:HA2	15:RQ:107:ALA:HB2	2.01	0.42
16:RR:104:ARG:HD2	16:RR:107:ASP:OD1	2.19	0.42
22:RX:88:LYS:HB2	22:RX:88:LYS:HE3	1.75	0.42
35:XA:1000:U:N3	35:XA:1001(A):A:N7	2.68	0.42
35:XA:359:U:H2'	35:XA:360:A:C8	2.54	0.42
35:XA:806:C:H2'	35:XA:807:A:C8	2.55	0.42
35:XA:841:U:H6	35:XA:841:U:OP1	2.02	0.42
36:XB:70:PHE:N	36:XB:70:PHE:HD1	2.17	0.42
3:XY:261:VAL:HG21	3:XY:284:LYS:HA	1.99	0.42
3:XY:317:ILE:O	3:XY:317:ILE:HG22	2.19	0.42
4:YA:1499:C:C2	4:YA:1500:G:C8	3.07	0.42
4:YA:1567:A:OP2	6:YD:84:TYR:OH	2.24	0.42
4:YA:2298:A:N6	4:YA:2318:G:H8	2.17	0.42
4:YA:2345:G:N3	4:YA:2381:C:H2'	2.35	0.42
4:YA:623:G:H2'	4:YA:624:C:C6	2.54	0.42
4:YA:828:U:H4'	4:YA:831:G:N1	2.34	0.42
4:YA:90:U:H1'	4:YA:92:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:997:G:OP2	19:YU:58:ARG:NH1	2.53	0.42
9:YG:11:TYR:CD2	9:YG:12:TYR:CD1	3.07	0.42
4:YA:2306:C:N4	9:YG:43:LEU:O	2.51	0.42
4:YA:2657:A:O3'	10:YH:160:LYS:NZ	2.53	0.42
15:YQ:30:GLY:H	15:YQ:105:GLU:HG2	1.84	0.42
24:YZ:44:PHE:O	24:YZ:44:PHE:HD1	2.01	0.42
35:QA:582:U:OP1	49:QO:64:ARG:NH1	2.53	0.42
38:QD:18:LYS:HG2	38:QD:20:TYR:CE1	2.55	0.42
40:QF:7:ASN:OD1	40:QF:62:TRP:HD1	2.01	0.42
44:QJ:31:GLY:HA2	44:QJ:32:ALA:HA	1.66	0.42
32:R7:31:LEU:O	32:R7:35:ARG:HG3	2.20	0.42
4:RA:9:U:O2'	4:RA:10:G:OP1	2.34	0.42
4:RA:2514:U:H2'	4:RA:2515:C:C6	2.54	0.42
4:RA:2646:C:H2'	4:RA:2647:U:O4'	2.19	0.42
4:RA:2870:C:H2'	4:RA:2871:C:O4'	2.19	0.42
4:RA:840:C:H2'	4:RA:841:A:H8	1.85	0.42
5:RB:105:A:H2'	5:RB:106:G:O4'	2.19	0.42
8:RF:116:ASP:OD1	8:RF:119:ARG:NH2	2.47	0.42
4:RA:2667:C:H1'	10:RH:109:PHE:CD1	2.54	0.42
11:RI:109:ILE:HA	11:RI:109:ILE:HD12	1.88	0.42
4:RA:871:U:H4'	15:RQ:69:PHE:CD2	2.55	0.42
16:RR:47:PHE:C	16:RR:47:PHE:CD1	2.92	0.42
18:RT:61:PHE:CD1	18:RT:61:PHE:N	2.79	0.42
21:RW:46:PHE:O	21:RW:50:VAL:HG23	2.19	0.42
35:XA:189(M):G:H2'	35:XA:190:U:C6	2.54	0.42
35:XA:908:A:H2'	35:XA:909:A:C8	2.54	0.42
49:XO:4:THR:HG22	49:XO:7:GLU:HB2	2.01	0.42
50:XP:19:ILE:HG22	50:XP:36:ILE:HG13	2.01	0.42
3:XY:41:LEU:HD23	3:XY:46:VAL:HG21	2.01	0.42
4:YA:1065:U:H4'	4:YA:1066:U:C5'	2.46	0.42
4:YA:207:A:H2'	4:YA:208:C:O4'	2.20	0.42
4:YA:373:U:H2'	4:YA:374:A:H8	1.84	0.42
6:YD:242:ARG:CD	6:YD:246:PRO:HG3	2.47	0.42
10:YH:17:VAL:HG22	10:YH:26:VAL:HG22	2.02	0.42
16:YR:38:VAL:HG22	16:YR:112:ALA:HB2	2.01	0.42
20:YV:40:LEU:HB2	20:YV:46:VAL:HG12	2.01	0.42
23:YY:77:PRO:HD2	23:YY:106:LEU:HD23	2.00	0.42
35:QA:1048:G:C6	35:QA:1210:C:N4	2.87	0.42
35:QA:276:G:O3'	51:QQ:68:ARG:NH1	2.52	0.42
43:QI:42:ARG:HA	43:QI:42:ARG:HD3	1.95	0.42
3:QY:25:LEU:O	3:QY:30:LYS:HE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:RX:1:MET:O	27:R2:29:LYS:HE3	2.19	0.42
28:R3:23:LEU:HD13	28:R3:50:VAL:HG11	2.01	0.42
4:RA:2365:G:O6	33:R8:39:LYS:HE3	2.20	0.42
4:RA:1115:G:H2'	4:RA:1116:C:H6	1.85	0.42
4:RA:443:A:H1'	4:RA:1201:C:O4'	2.19	0.42
4:RA:1923:U:H2'	4:RA:1924:C:H6	1.84	0.42
4:RA:2695:C:H2'	4:RA:2696:U:C6	2.55	0.42
4:RA:638:G:H2'	4:RA:639:U:C6	2.54	0.42
7:RE:105:THR:OG1	7:RE:199:ARG:NH2	2.52	0.42
12:RN:29:LYS:HD3	12:RN:140:VAL:HB	2.01	0.42
17:RS:19:LYS:HE2	17:RS:25:ARG:HH11	1.83	0.42
35:XA:337:C:H2'	35:XA:338:A:H8	1.84	0.42
35:XA:947:G:H2'	35:XA:948:C:O4'	2.19	0.42
36:XB:48:MET:HA	36:XB:51:LEU:HB2	2.00	0.42
38:XD:119:GLN:HE21	38:XD:123:HIS:CE1	2.38	0.42
44:XJ:5:ARG:N	44:XJ:99:LYS:O	2.53	0.42
35:XA:718:G:C5	45:XK:116:HIS:HD2	2.38	0.42
48:XN:4:LYS:HG3	48:XN:7:ILE:HD11	2.00	0.42
52:XR:29:PHE:HE1	52:XR:31:LEU:CD1	2.33	0.42
35:XA:192:U:O2'	54:XT:60:GLU:OE2	2.19	0.42
3:XY:228:ASP:HB3	3:XY:230:ILE:HG13	2.01	0.42
26:Y1:93:GLU:O	26:Y1:96:LYS:HB2	2.20	0.42
4:YA:1430:C:H2'	4:YA:1431:U:H6	1.84	0.42
4:YA:2051:A:H5'	4:YA:2578:G:O4'	2.19	0.42
4:YA:2238:G:H2'	4:YA:2238:G:N3	2.35	0.42
4:YA:2462:U:H1'	4:YA:2491:U:O4	2.19	0.42
4:YA:277:C:H4'	4:YA:278:A:H8	1.84	0.42
4:YA:746:A:H2'	4:YA:2612:C:H5''	2.00	0.42
8:YF:18:ARG:CG	8:YF:19:GLU:H	2.29	0.42
4:YA:2312:U:H5'	9:YG:88:ILE:HD11	2.00	0.42
16:YR:13:HIS:HD2	16:YR:16:HIS:H	1.67	0.42
4:YA:481:G:OP2	23:YY:47:LYS:HD2	2.19	0.42
24:YZ:91:LEU:HG	24:YZ:130:PRO:HG3	2.01	0.42
35:QA:1030(B):G:H2'	35:QA:1030(D):G:OP2	2.19	0.42
35:QA:1131:G:H2'	35:QA:1132:C:H6	1.85	0.42
35:QA:512:U:H2'	35:QA:513:C:H6	1.84	0.42
35:QA:57:G:H2'	35:QA:58:C:C6	2.54	0.42
37:QC:130:VAL:HG21	37:QC:157:ILE:HG23	2.02	0.42
51:QQ:94:ASN:O	51:QQ:98:LEU:HD13	2.19	0.42
3:QY:80:VAL:HG11	3:QY:103:LEU:HD13	2.01	0.42
28:R3:29:ARG:HG3	28:R3:30:ARG:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:105:C:C2	4:RA:106:C:C5	3.08	0.42
4:RA:1667:G:O2'	4:RA:1991:U:O4	2.24	0.42
4:RA:2747:G:O6	4:RA:2755:C:H5''	2.19	0.42
4:RA:1815:A:P	6:RD:54:ARG:HH22	2.42	0.42
19:RU:104:GLN:CD	19:RU:104:GLN:H	2.16	0.42
23:RY:60:PHE:HD1	23:RY:60:PHE:N	2.16	0.42
24:RZ:144:LEU:HD21	24:RZ:150:LEU:CD1	2.42	0.42
35:XA:560:U:H4'	35:XA:561:U:O5'	2.20	0.42
38:XD:59:ARG:CA	38:XD:59:ARG:HE	2.22	0.42
40:XF:37:VAL:HA	40:XF:65:VAL:HG12	2.02	0.42
43:XI:59:PHE:CZ	43:XI:88:TYR:CE2	3.07	0.42
47:XM:108:ARG:HD3	47:XM:108:ARG:HA	1.63	0.42
49:XO:76:GLU:OE1	49:XO:76:GLU:HA	2.19	0.42
51:XQ:4:LYS:N	51:XQ:61:GLU:HG2	2.32	0.42
3:XY:200:ARG:CB	3:XY:322:GLN:HB3	2.50	0.42
27:Y2:7:ARG:HG2	27:Y2:7:ARG:H	1.20	0.42
4:YA:987:G:O2'	4:YA:1000:A:N3	2.47	0.42
3:XY:54:GLN:HG3	4:YA:1068:G:H1	1.85	0.42
4:YA:2128:C:H3'	4:YA:2129:C:H5''	2.02	0.42
4:YA:2395:C:H2'	4:YA:2396:G:O4'	2.19	0.42
4:YA:38:A:H2'	4:YA:39:C:H6	1.80	0.42
4:YA:875:G:H2'	4:YA:876:C:O4'	2.20	0.42
10:YH:154:PRO:HG3	10:YH:163:TYR:CD1	2.55	0.42
17:YS:83:LYS:HB3	17:YS:111:GLU:OE1	2.19	0.42
35:QA:1065:U:H1'	35:QA:1066:C:OP2	2.19	0.42
35:QA:1071:C:H2'	35:QA:1072:G:C8	2.52	0.42
35:QA:1326:C:H2'	35:QA:1327:C:C6	2.55	0.42
35:QA:932:C:H5''	41:QG:4:ARG:CZ	2.50	0.42
38:QD:173:TRP:CE3	38:QD:174:LEU:HG	2.55	0.42
42:QH:9:MET:HG3	42:QH:26:VAL:HG11	2.02	0.42
35:QA:1524:C:OP1	45:QK:120:ARG:NH1	2.52	0.42
35:QA:188:C:O4'	54:QT:89:ARG:NH2	2.52	0.42
3:QY:298:LEU:O	3:QY:301:GLN:N	2.52	0.42
3:QY:332:ARG:HG3	3:QY:343:ARG:HD2	2.01	0.42
34:R9:15:LYS:HE2	34:R9:17:ILE:HD11	2.01	0.42
34:R9:32:HIS:O	34:R9:34:GLN:HG3	2.19	0.42
4:RA:1475:G:H2'	4:RA:1476:C:H6	1.84	0.42
4:RA:1842:G:H2'	4:RA:1843:C:H6	1.84	0.42
4:RA:275:G:H2'	4:RA:276:A:O4'	2.20	0.42
4:RA:2852:G:H2'	4:RA:2853:C:H6	1.83	0.42
4:RA:568:U:H5'	4:RA:945:A:N6	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:743:G:OP1	7:RE:130:GLY:HA2	2.19	0.42
4:RA:1902:C:OP1	6:RD:242:ARG:HD2	2.19	0.42
7:RE:59:VAL:HG12	7:RE:64:LYS:HG3	2.01	0.42
9:RG:7:LEU:HA	9:RG:7:LEU:HD23	1.90	0.42
5:RB:91:C:OP2	15:RQ:16:ARG:NH1	2.53	0.42
16:RR:54:LEU:HD23	16:RR:66:VAL:HG23	2.01	0.42
35:XA:1095:U:H2'	35:XA:1096:C:C6	2.54	0.42
35:XA:1142:G:H2'	35:XA:1143:G:O4'	2.19	0.42
35:XA:1428:A:H2'	35:XA:1429:C:C6	2.55	0.42
35:XA:217:C:H2'	35:XA:218:C:C6	2.55	0.42
35:XA:376:G:H5''	50:XP:5:ARG:HB2	2.02	0.42
35:XA:389:A:H3'	35:XA:390:C:H6	1.84	0.42
35:XA:417:C:H2'	35:XA:418:C:C6	2.54	0.42
35:XA:456:C:H2'	35:XA:457:C:C6	2.55	0.42
35:XA:45:U:H2'	35:XA:46:G:H8	1.84	0.42
35:XA:56:U:H2'	35:XA:57:G:H8	1.85	0.42
35:XA:736:C:H2'	35:XA:737:A:C8	2.55	0.42
35:XA:811:C:O2'	35:XA:901:A:N1	2.50	0.42
37:XC:8:ILE:HG12	37:XC:184:TYR:HB3	2.01	0.42
44:XJ:50:ILE:HB	48:XN:41:ARG:NH2	2.34	0.42
47:XM:96:LEU:C	47:XM:110:ARG:HD3	2.40	0.42
35:XA:1330:U:H4'	47:XM:23:TYR:CE1	2.54	0.42
54:XT:67:ALA:HB2	54:XT:77:ALA:HB2	2.01	0.42
28:Y3:22:ALA:HB2	28:Y3:49:LYS:HD3	2.02	0.42
29:Y4:62:ARG:HH11	29:Y4:62:ARG:HA	1.85	0.42
4:YA:1092:C:OP2	4:YA:1092:C:H6	2.03	0.42
4:YA:1354:A:H4'	6:YD:38:LYS:NZ	2.34	0.42
4:YA:2115:G:N1	4:YA:2117:A:N7	2.67	0.42
5:YB:28:C:H2'	5:YB:29:A:O4'	2.20	0.42
5:YB:48:A:H4'	17:YS:95:HIS:HD2	1.85	0.42
8:YF:11:VAL:HG22	8:YF:125:LEU:HB2	2.02	0.42
15:YQ:93:TYR:N	15:YQ:93:TYR:CD1	2.87	0.42
35:QA:1026:G:H2'	35:QA:1026:G:N3	2.34	0.42
35:QA:1218:C:H2'	35:QA:1219:U:H6	1.81	0.42
35:QA:1438:G:H2'	35:QA:1439:C:H6	1.85	0.42
35:QA:58:C:O2'	35:QA:388:G:N7	2.50	0.42
35:QA:612:C:C2	35:QA:613:C:C5	3.08	0.42
38:QD:111:ALA:HB1	38:QD:116:GLN:HB3	2.01	0.42
35:QA:412:A:C5	38:QD:35:ARG:HD3	2.55	0.42
39:QE:13:ILE:HA	39:QE:29:GLY:O	2.20	0.42
38:QD:88:VAL:HG13	39:QE:97:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:QP:39:TYR:CE2	50:QP:41:PRO:HB3	2.55	0.42
51:QQ:45:HIS:CD2	51:QQ:47:PRO:HG3	2.55	0.42
4:RA:1021:A:H3'	4:RA:1021:A:N3	2.35	0.42
4:RA:2241:A:H2'	4:RA:2242:G:C8	2.55	0.42
4:RA:2247:A:H2'	4:RA:2248:C:H6	1.85	0.42
4:RA:2853:C:H2'	4:RA:2854:G:C8	2.55	0.42
4:RA:483:A:O4'	23:RY:48:ALA:HB1	2.19	0.42
7:RE:44:TYR:H	7:RE:44:TYR:HD1	1.67	0.42
8:RF:6:VAL:CB	8:RF:23:ASP:HA	2.50	0.42
9:RG:47:LYS:HG3	9:RG:48:GLU:H	1.85	0.42
23:RY:5:MET:CE	23:RY:32:PRO:HA	2.50	0.42
23:RY:92:ASN:CB	23:RY:94:LYS:H	2.24	0.42
35:XA:1438:G:H2'	35:XA:1439:C:C6	2.55	0.42
35:XA:34:C:H2'	35:XA:35:G:C8	2.55	0.42
35:XA:918:A:H2'	35:XA:919:A:C8	2.55	0.42
36:XB:80:ILE:HD11	36:XB:212:GLN:HB2	2.00	0.42
54:XT:56:MET:HE3	54:XT:85:MET:HA	2.02	0.42
1:XV:51:C:H2'	1:XV:52:G:O4'	2.19	0.42
3:XY:200:ARG:HH21	3:XY:325:SER:HG	1.60	0.42
3:XY:127:ASP:HB2	3:XY:225:GLU:OE1	2.20	0.42
4:YA:1053:C:H2'	4:YA:1054:A:H8	1.85	0.42
3:XY:58:LYS:HZ1	4:YA:1067:A:H5''	1.84	0.42
4:YA:17:G:H2'	4:YA:18:C:C6	2.54	0.42
4:YA:2115:G:N2	4:YA:2171:A:H61	2.16	0.42
4:YA:2031:A:C6	4:YA:2498:C:H1'	2.54	0.42
4:YA:273(F):G:C4	4:YA:273(G):C:C5	3.07	0.42
4:YA:18:C:O2'	4:YA:554:U:OP1	2.36	0.42
8:YF:56:GLU:OE2	8:YF:93:LYS:NZ	2.50	0.42
9:YG:46:ALA:HB2	9:YG:53:LEU:HD12	2.01	0.42
11:YI:48:GLU:HG3	11:YI:52:ARG:HH11	1.85	0.42
15:YQ:111:GLU:O	15:YQ:115:MET:HG2	2.20	0.42
16:YR:63:ARG:O	16:YR:67:LEU:HB2	2.19	0.42
18:YT:16:ARG:HG2	18:YT:18:ASP:OD1	2.19	0.42
19:YU:62:ILE:HG12	19:YU:76:TYR:CE2	2.55	0.42
23:YY:56:PRO:C	23:YY:58:GLY:H	2.23	0.42
35:QA:113:G:O4'	35:QA:354:G:H4'	2.20	0.42
35:QA:454:C:OP2	35:QA:455:C:N4	2.37	0.42
35:QA:814:A:H2'	35:QA:816:A:H5''	2.02	0.42
44:QJ:38:ILE:HG13	44:QJ:38:ILE:O	2.19	0.42
3:QY:151:MET:HE3	3:QY:353:LEU:HD21	2.02	0.42
3:QY:205:SER:HB2	3:QY:214:HIS:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:QY:272:THR:HG21	3:QY:290:GLN:HB2	2.00	0.42
4:RA:1510:G:H2'	4:RA:1511:C:H6	1.85	0.42
4:RA:2336:A:H61	25:R0:43:THR:CG2	2.32	0.42
4:RA:2023:G:H4'	4:RA:2617:C:O3'	2.19	0.42
4:RA:272(Z):C:H1'	4:RA:273(D):G:H1'	2.02	0.42
4:RA:27:G:O2'	4:RA:28:A:OP2	2.32	0.42
5:RB:31:C:H4'	9:RG:29:TRP:CH2	2.54	0.42
4:RA:1826:G:O2'	6:RD:242:ARG:NH2	2.52	0.42
10:RH:55:PRO:HG2	10:RH:61:HIS:CE1	2.55	0.42
11:RI:62:LYS:O	11:RI:66:GLU:HG2	2.20	0.42
15:RQ:35:VAL:HG12	15:RQ:130:LYS:O	2.19	0.42
35:XA:100:C:H2'	35:XA:101:A:O4'	2.19	0.42
35:XA:1084:G:H5'	35:XA:1102:A:OP2	2.20	0.42
35:XA:1417:G:N2	35:XA:1482:G:H2'	2.35	0.42
35:XA:779:C:H2'	35:XA:780:A:O4'	2.19	0.42
38:XD:108:LEU:HD13	38:XD:174:LEU:HD13	2.01	0.42
29:Y4:61:ARG:HH22	53:XS:9:VAL:HG21	1.85	0.42
3:XY:134:ALA:O	3:XY:317:ILE:HG21	2.19	0.42
29:Y4:47:GLN:C	29:Y4:49:PHE:H	2.22	0.42
4:YA:1453:U:O2'	4:YA:1455:G:N7	2.44	0.42
4:YA:1540:U:H2'	4:YA:1541:G:O4'	2.20	0.42
19:YU:47:TYR:C	19:YU:47:TYR:CD1	2.92	0.42
35:QA:1053:G:N7	35:QA:1200:C:H5''	2.34	0.42
35:QA:514:C:H2'	35:QA:515:G:H8	1.85	0.42
36:QB:157:ARG:HB3	36:QB:157:ARG:HE	1.23	0.42
37:QC:29:TYR:O	37:QC:29:TYR:HD1	2.03	0.42
1:QV:23:C:H2'	1:QV:24:U:C6	2.55	0.42
3:QY:27:TYR:CE1	3:QY:67:VAL:HG13	2.55	0.42
25:R0:77:ARG:C	25:R0:78:TYR:HD1	2.23	0.42
27:R2:12:GLU:HA	27:R2:12:GLU:OE1	2.19	0.42
9:RG:108:ASN:O	29:R4:37:SER:N	2.52	0.42
4:RA:1153:C:H2'	4:RA:1154:G:O4'	2.20	0.42
8:RF:178:PRO:HB2	8:RF:201:VAL:HG22	2.02	0.42
9:RG:165:THR:OG1	9:RG:168:GLU:HG3	2.18	0.42
12:RN:14:VAL:HG11	12:RN:138:LEU:HD12	2.02	0.42
4:RA:2642:G:H4'	12:RN:78:TYR:CE2	2.55	0.42
15:RQ:21:THR:HG21	15:RQ:101:ARG:CB	2.34	0.42
35:XA:1004:A:H5''	35:XA:1025:U:C5	2.55	0.42
35:XA:1132:C:H2'	35:XA:1133:G:H8	1.85	0.42
35:XA:1143:G:H2'	35:XA:1144:G:H8	1.85	0.42
35:XA:123:C:OP1	35:XA:311:C:O2'	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:1314:C:H2'	35:XA:1315:U:C6	2.55	0.42
35:XA:687:A:C2	35:XA:704:A:C5	3.07	0.42
35:XA:868:C:H2'	35:XA:869:G:O4'	2.19	0.42
36:XB:54:THR:HG21	36:XB:201:ILE:HD11	2.02	0.42
50:XP:60:LEU:HD21	50:XP:80:PHE:CZ	2.54	0.42
3:XY:324:ARG:HB3	3:XY:326:TYR:HE1	1.85	0.42
27:Y2:53:LEU:HD23	27:Y2:53:LEU:HA	1.89	0.42
31:Y6:18:ARG:HD2	31:Y6:42:TRP:CE2	2.55	0.42
4:YA:1021:A:N3	4:YA:1021:A:H3'	2.35	0.42
4:YA:1197:G:H2'	4:YA:1198:U:H6	1.84	0.42
4:YA:1199:U:H2'	4:YA:1200:C:C6	2.55	0.42
4:YA:225:A:O2'	4:YA:257:A:H4'	2.19	0.42
4:YA:236:C:H2'	4:YA:237:C:C6	2.54	0.42
4:YA:2564:A:OP1	4:YA:2648:C:H4'	2.20	0.42
4:YA:2674:G:H2'	4:YA:2675:A:C8	2.54	0.42
4:YA:476:G:H4'	4:YA:502:A:N1	2.35	0.42
4:YA:529:A:OP2	12:YN:114:ARG:NH2	2.52	0.42
4:YA:580:C:H2'	4:YA:581:C:C6	2.55	0.42
4:YA:668:G:H2'	4:YA:670:A:H62	1.85	0.42
4:YA:9:U:HO2'	4:YA:10:G:P	2.43	0.42
5:YB:17:C:H2'	5:YB:18:G:O4'	2.19	0.42
8:YF:52:LYS:HB3	8:YF:56:GLU:HG3	2.02	0.42
15:YQ:32:TYR:HB3	15:YQ:132:VAL:O	2.20	0.42
17:YS:13:ARG:HE	17:YS:13:ARG:HB3	1.64	0.42
17:YS:14:VAL:O	17:YS:18:ILE:HG12	2.20	0.42
35:QA:1387:G:H2'	35:QA:1388:C:H6	1.85	0.41
37:QC:114:PRO:O	37:QC:118:GLN:HG3	2.19	0.41
40:QF:8:ILE:CG2	40:QF:10:LEU:HD13	2.50	0.41
41:QG:18:TYR:CD1	41:QG:18:TYR:N	2.88	0.41
42:QH:34:GLU:O	42:QH:37:ARG:HB3	2.20	0.41
43:QI:4:TYR:O	43:QI:18:PHE:HA	2.19	0.41
53:QS:12:ASP:O	53:QS:14:HIS:N	2.43	0.41
3:QY:14:LEU:HD23	3:QY:17:ARG:HH11	1.84	0.41
3:QY:281:HIS:HB2	15:RQ:80:GLU:OE2	2.20	0.41
4:RA:1210:A:H5''	4:RA:1212:G:O4'	2.19	0.41
4:RA:1475:G:H2'	4:RA:1476:C:C6	2.55	0.41
4:RA:2137:C:C2	4:RA:2154:G:N1	2.87	0.41
4:RA:2149:G:H2'	4:RA:2150:U:O4'	2.20	0.41
4:RA:235:U:C2	4:RA:236:C:C5	3.08	0.41
4:RA:2031:A:C6	4:RA:2498:C:H1'	2.55	0.41
4:RA:643:A:N1	4:RA:2369:A:O2'	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:RD:108:PRO:HD2	6:RD:111:LEU:HG	2.02	0.41
6:RD:172:TYR:CE2	6:RD:269:PHE:CD2	3.07	0.41
8:RF:140:LEU:HD11	8:RF:170:LEU:HD21	2.01	0.41
35:XA:1333:A:H2'	35:XA:1334:G:O4'	2.19	0.41
35:XA:355:C:C4	35:XA:356:A:N7	2.87	0.41
35:XA:892:A:H2'	35:XA:893:C:C6	2.55	0.41
35:XA:412:A:C6	38:XD:35:ARG:HG3	2.55	0.41
43:XI:78:LYS:O	43:XI:81:ILE:HG22	2.20	0.41
43:XI:59:PHE:CE2	43:XI:88:TYR:CE2	3.08	0.41
45:XK:59:TYR:CE2	45:XK:63:LEU:HD11	2.55	0.41
51:XQ:94:ASN:O	51:XQ:98:LEU:HD13	2.19	0.41
35:XA:1313:U:P	53:XS:5:LEU:HG	2.60	0.41
3:XY:43:GLN:HG2	3:XY:45:ASP:H	1.85	0.41
4:YA:1570:A:H2'	4:YA:1571:A:C8	2.55	0.41
4:YA:1654:A:C2	7:YE:113:PHE:CD2	3.08	0.41
4:YA:1831:G:H2'	4:YA:1832:C:C6	2.55	0.41
4:YA:301:G:H1'	4:YA:302:C:C6	2.55	0.41
4:YA:738:G:H3'	4:YA:739:G:C8	2.54	0.41
4:YA:1491:G:O2'	6:YD:101:GLU:HB3	2.19	0.41
35:QA:222:U:H2'	35:QA:223:U:H6	1.84	0.41
35:QA:538:G:H5''	46:QL:114:LYS:HB2	2.02	0.41
35:QA:925:G:H1'	35:QA:1502:A:C4	2.55	0.41
36:QB:19:HIS:CE1	36:QB:20:GLU:OE1	2.73	0.41
36:QB:21:ARG:H	36:QB:21:ARG:HG3	1.32	0.41
36:QB:45:GLN:O	36:QB:48:MET:HB2	2.19	0.41
39:QE:142:LEU:C	39:QE:143:ARG:HG3	2.40	0.41
40:QF:3:ARG:C	40:QF:4:TYR:HD1	2.23	0.41
40:QF:72:VAL:O	40:QF:75:LEU:HB3	2.21	0.41
46:QL:86:ARG:O	46:QL:98:TYR:HB3	2.19	0.41
51:QQ:68:ARG:O	51:QQ:68:ARG:HG2	2.20	0.41
3:QY:340:VAL:HG12	3:QY:341:GLU:N	2.34	0.41
4:RA:1321:A:C4	4:RA:1322:A:C8	3.08	0.41
4:RA:2000:G:OP1	16:RR:5:LYS:NZ	2.50	0.41
4:RA:2109:U:N3	4:RA:2110:G:O6	2.54	0.41
4:RA:2704:C:H2'	4:RA:2705:A:O4'	2.20	0.41
4:RA:302:C:H2'	4:RA:303:U:H6	1.85	0.41
4:RA:391:G:C5	4:RA:392:C:C5	3.08	0.41
4:RA:539:G:H2'	4:RA:540:C:C6	2.54	0.41
4:RA:956:G:P	15:RQ:14:ARG:HH22	2.43	0.41
7:RE:178:GLU:CD	7:RE:178:GLU:H	2.23	0.41
7:RE:47:VAL:HG23	7:RE:84:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:RV:62:LEU:CD1	20:RV:95:LEU:HB2	2.50	0.41
23:RY:5:MET:HE1	23:RY:35:TYR:HA	2.02	0.41
35:XA:1347:G:N2	35:XA:1373:G:H2'	2.35	0.41
35:XA:554:C:H2'	35:XA:555:C:H6	1.84	0.41
35:XA:69:G:N3	35:XA:70:G:C8	2.88	0.41
38:XD:10:ARG:HB2	38:XD:40:PRO:HG3	2.02	0.41
41:XG:151:TYR:OH	45:XK:54:ARG:NH1	2.53	0.41
2:XX:21:A:N1	3:XY:213:ARG:NH2	2.67	0.41
25:Y0:50:ASN:HB3	25:Y0:63:VAL:HG22	2.03	0.41
4:YA:1289:C:H2'	4:YA:1290:C:C6	2.55	0.41
4:YA:2063:C:C4	4:YA:2064:C:C5	3.08	0.41
4:YA:285:C:C2	4:YA:286:C:C5	3.08	0.41
9:YG:131:TYR:HB3	9:YG:159:VAL:CG1	2.49	0.41
11:YI:16:GLY:O	11:YI:47:LEU:HD11	2.21	0.41
19:YU:11:ARG:O	19:YU:15:LYS:HG3	2.20	0.41
35:QA:1201:A:H1'	35:QA:1202:G:OP2	2.19	0.41
35:QA:1309:G:N7	47:QM:99:ARG:NH2	2.65	0.41
35:QA:1442(A):G:HO2'	35:QA:1442(B):G:P	2.43	0.41
35:QA:183:G:H2'	35:QA:184:G:C8	2.55	0.41
35:QA:768:A:H4'	35:QA:1523:G:N2	2.36	0.41
36:QB:55:PHE:HB3	36:QB:221:LEU:CD1	2.50	0.41
47:QM:64:TRP:C	29:R4:50:VAL:HG21	2.39	0.41
51:QQ:83:ASP:OD1	51:QQ:83:ASP:N	2.54	0.41
26:R1:52:ARG:HH21	26:R1:57:GLU:HB2	1.85	0.41
4:RA:1500:G:H2'	4:RA:1501:C:H6	1.86	0.41
4:RA:1790:C:H5''	4:RA:1791:A:OP1	2.20	0.41
4:RA:2081:C:H2'	4:RA:2082:A:H8	1.85	0.41
4:RA:2316:C:O2'	9:RG:128:ARG:NH2	2.53	0.41
4:RA:614(C):G:C1'	8:RF:44:ARG:HD2	2.50	0.41
4:RA:824:A:H1'	4:RA:2358:G:N7	2.35	0.41
4:RA:833:U:H2'	4:RA:834:C:H6	1.85	0.41
15:RQ:30:GLY:H	15:RQ:105:GLU:HG2	1.85	0.41
16:RR:36:THR:HG22	16:RR:37:THR:N	2.33	0.41
17:RS:11:LYS:HG3	17:RS:91:PRO:HD3	2.00	0.41
13:RO:80:ASP:OD2	18:RT:71:GLY:HA3	2.20	0.41
35:XA:1122:U:C4	35:XA:1123:A:N7	2.89	0.41
35:XA:1279:A:H2'	35:XA:1279:A:N3	2.35	0.41
35:XA:22:G:H2'	35:XA:23:C:C6	2.55	0.41
35:XA:511:C:C2	35:XA:512:U:C5	3.07	0.41
35:XA:691:G:H1'	35:XA:696:A:N6	2.36	0.41
35:XA:895:G:H2'	35:XA:896:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:XB:229:VAL:HG12	36:XB:230:VAL:H	1.85	0.41
38:XD:34:GLU:HA	38:XD:34:GLU:OE1	2.19	0.41
39:XE:82:VAL:HG21	39:XE:138:ALA:HA	2.03	0.41
40:XF:59:TYR:C	40:XF:59:TYR:HD1	2.23	0.41
42:XH:20:TYR:OH	42:XH:78:GLN:NE2	2.53	0.41
43:XI:32:ASP:HB3	43:XI:35:GLU:HG2	2.02	0.41
35:XA:718:G:C5	45:XK:116:HIS:CD2	3.09	0.41
46:XL:33:ARG:CD	46:XL:62:SER:HB3	2.48	0.41
27:Y2:12:GLU:HA	27:Y2:15:LYS:HZ3	1.83	0.41
4:YA:250:G:P	33:Y8:13:ARG:NH2	2.92	0.41
4:YA:1030:G:C6	4:YA:1125:G:N2	2.88	0.41
4:YA:1142(B):A:C4	4:YA:1144:G:N7	2.88	0.41
4:YA:1322:A:C5	4:YA:1323:U:C5	3.08	0.41
4:YA:1530:C:C2	4:YA:1531:C:C6	3.08	0.41
4:YA:2103:C:N3	4:YA:2104:G:C2	2.88	0.41
4:YA:2134:A:C5	4:YA:2157:G:H5'	2.55	0.41
4:YA:2293:C:H2'	4:YA:2294:C:H6	1.86	0.41
4:YA:2342:C:O2'	4:YA:2374:C:H5''	2.20	0.41
4:YA:557:U:H2'	4:YA:558:G:H8	1.85	0.41
4:YA:902:C:H2'	4:YA:903:C:C6	2.55	0.41
7:YE:170:LEU:HB3	7:YE:184:VAL:HG13	2.02	0.41
11:YI:77:LEU:CD1	11:YI:101:LEU:HG	2.50	0.41
13:YO:67:LYS:HD2	13:YO:68:GLU:OE1	2.21	0.41
35:QA:1101:A:H4'	35:QA:1102:A:O5'	2.21	0.41
35:QA:1172:C:H2'	35:QA:1173:G:C8	2.51	0.41
35:QA:1315:U:H2'	35:QA:1316:G:O4'	2.20	0.41
35:QA:389:A:H3'	35:QA:390:C:H6	1.85	0.41
35:QA:892:A:H2'	35:QA:893:C:H6	1.85	0.41
35:QA:93:G:H2'	35:QA:96:U:O4'	2.21	0.41
44:QJ:4:ILE:N	44:QJ:100:THR:HG22	2.34	0.41
4:RA:1656:C:H2'	4:RA:1657:C:H6	1.85	0.41
4:RA:2184:G:N1	4:RA:2185:C:O2	2.53	0.41
4:RA:840:C:H2'	4:RA:841:A:C8	2.56	0.41
4:RA:871:U:H5''	15:RQ:69:PHE:CE2	2.56	0.41
19:RU:97:ASP:O	19:RU:101:ARG:HB3	2.20	0.41
35:XA:687:A:C2	35:XA:704:A:C6	3.08	0.41
43:XI:101:PHE:CD1	43:XI:101:PHE:N	2.89	0.41
3:XY:205:SER:HB2	3:XY:214:HIS:HB2	2.02	0.41
4:YA:1055:G:H2'	4:YA:1056:G:O4'	2.20	0.41
4:YA:1500:G:H2'	4:YA:1501:C:H6	1.85	0.41
4:YA:1668:A:H4'	4:YA:1669:A:O5'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YA:1697:G:OP2	4:YA:1698:A:O2'	2.32	0.41
4:YA:2310:A:O2'	9:YG:75:LYS:NZ	2.44	0.41
4:YA:2321:G:N3	4:YA:2321:G:H2'	2.35	0.41
4:YA:918:A:H5''	5:YB:98:G:O2'	2.20	0.41
4:YA:2591:C:OP1	6:YD:239:ARG:HD2	2.20	0.41
10:YH:163:TYR:N	10:YH:163:TYR:CD1	2.89	0.41
15:YQ:55:VAL:HG11	24:YZ:183:LEU:HD21	2.02	0.41
17:YS:7:TYR:C	17:YS:7:TYR:HD1	2.24	0.41
18:YT:101:PHE:CD2	18:YT:101:PHE:C	2.93	0.41
37:QC:179:ARG:NH1	37:QC:206:GLU:OE1	2.53	0.41
40:QF:59:TYR:C	40:QF:59:TYR:HD1	2.23	0.41
43:QI:29:ASN:ND2	43:QI:65:VAL:HG12	2.35	0.41
46:QL:124:LYS:HA	46:QL:125:PRO:HD3	1.94	0.41
46:QL:58:VAL:O	46:QL:65:GLU:HA	2.20	0.41
35:QA:1216:G:H5''	48:QN:5:ALA:HB2	2.02	0.41
50:QP:8:ARG:C	50:QP:9:PHE:HD1	2.24	0.41
3:QY:155:TRP:HH2	3:QY:354:ASP:OD1	2.03	0.41
26:R1:67:ILE:N	26:R1:68:PRO:HD2	2.36	0.41
34:R9:17:ILE:HD13	34:R9:17:ILE:HA	1.89	0.41
4:RA:1069:A:H2'	4:RA:1073:A:N7	2.35	0.41
4:RA:1091:G:H2'	4:RA:1091:G:N3	2.35	0.41
4:RA:1877:A:H5'	4:RA:1878:G:OP2	2.21	0.41
4:RA:2261:C:C2	4:RA:2262:U:C5	3.08	0.41
4:RA:2354:G:H21	25:R0:36:ILE:CD1	2.32	0.41
4:RA:2643:G:H2'	4:RA:2644:G:O4'	2.20	0.41
4:RA:2627:G:N2	4:RA:2777:G:OP2	2.52	0.41
4:RA:376:C:H2'	4:RA:377:C:H6	1.86	0.41
4:RA:392:C:C2	4:RA:393:C:C5	3.08	0.41
4:RA:608:A:H2'	4:RA:609:A:H8	1.84	0.41
7:RE:7:VAL:HG13	7:RE:27:LEU:HB3	2.02	0.41
8:RF:45:ARG:CZ	8:RF:97:TYR:CE2	3.04	0.41
10:RH:94:TYR:HA	10:RH:106:THR:O	2.20	0.41
12:RN:103:VAL:HG11	12:RN:120:LEU:HD12	2.02	0.41
23:RY:28:LYS:HD2	23:RY:40:GLU:HG2	2.01	0.41
35:XA:1469:G:H2'	35:XA:1470:G:C8	2.56	0.41
35:XA:343:U:H2'	35:XA:345:C:C5	2.56	0.41
35:XA:674:G:H2'	35:XA:675:A:C8	2.55	0.41
37:XC:132:ARG:O	37:XC:136:GLN:HG3	2.21	0.41
37:XC:130:VAL:HG21	37:XC:157:ILE:HG23	2.02	0.41
37:XC:164:ARG:HG2	37:XC:165:THR:N	2.35	0.41
38:XD:67:ILE:HG22	38:XD:68:TYR:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:XH:104:ARG:NH2	42:XH:138:TRP:CZ2	2.88	0.41
3:XY:169:SER:OG	3:XY:178:SER:HB3	2.21	0.41
3:XY:79:ASP:O	3:XY:83:LEU:HB2	2.21	0.41
4:YA:628:G:H5''	33:Y8:18:ALA:HB2	2.02	0.41
4:YA:1073:A:H4'	4:YA:1074:G:OP1	2.20	0.41
4:YA:2159:G:N2	4:YA:2160:G:N3	2.69	0.41
4:YA:2756:U:H1'	4:YA:2757:A:H5''	2.02	0.41
4:YA:300:A:H2'	4:YA:334:C:H1'	2.02	0.41
4:YA:519:U:H2'	4:YA:520:G:C8	2.55	0.41
4:YA:657:U:C2	4:YA:658:C:C5	3.08	0.41
4:YA:754:C:H2'	4:YA:755:C:H6	1.86	0.41
4:YA:775:G:C4	4:YA:794:G:C8	3.08	0.41
4:YA:889:C:O2'	4:YA:890:A:H8	2.03	0.41
6:YD:165:ILE:HA	6:YD:175:LEU:HD23	2.02	0.41
11:YI:6:LEU:HD11	11:YI:37:VAL:HG23	2.02	0.41
13:YO:107:ARG:HG2	13:YO:115:VAL:HG11	2.03	0.41
35:QA:1037:C:C2	35:QA:1038:C:C5	3.08	0.41
35:QA:1130:A:H2'	35:QA:1131:G:H8	1.85	0.41
35:QA:833:U:H2'	35:QA:834:C:H6	1.84	0.41
37:QC:5:ILE:HD11	48:QN:49:HIS:HE1	1.85	0.41
38:QD:138:TYR:CD1	38:QD:138:TYR:C	2.94	0.41
39:QE:11:ILE:N	39:QE:31:LEU:O	2.49	0.41
39:QE:82:VAL:HG21	39:QE:138:ALA:HA	2.03	0.41
42:QH:86:ILE:CG1	42:QH:133:LEU:HD22	2.49	0.41
46:QL:56:ALA:HB2	46:QL:70:ILE:HD11	2.02	0.41
50:QP:71:ARG:HG3	50:QP:80:PHE:HE2	1.85	0.41
35:QA:719:C:O2'	52:QR:49:LYS:HB3	2.20	0.41
3:QY:194:THR:HG23	3:QY:357:ILE:HD12	2.03	0.41
3:QY:198:VAL:O	3:QY:323:ILE:HG12	2.20	0.41
3:QY:41:LEU:HD23	3:QY:46:VAL:CG2	2.51	0.41
4:RA:1798:U:H5'	6:RD:259:THR:CG2	2.49	0.41
4:RA:517:C:OP1	30:R5:16:ARG:NH2	2.54	0.41
4:RA:817:C:O2'	4:RA:839:U:H5''	2.20	0.41
5:RB:29:A:H2'	5:RB:30:C:C6	2.55	0.41
6:RD:260:ARG:NH2	6:RD:270:ILE:CD1	2.84	0.41
7:RE:112:GLY:O	7:RE:159:HIS:HA	2.21	0.41
23:RY:20:TYR:HB3	23:RY:23:ARG:CG	2.50	0.41
23:RY:46:LYS:HD3	23:RY:60:PHE:CD2	2.55	0.41
35:XA:189(A):G:C6	35:XA:189(M):G:C6	3.09	0.41
35:XA:417:C:H2'	35:XA:418:C:H6	1.84	0.41
35:XA:441:A:H3'	35:XA:442:C:C6	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:488:C:H2'	35:XA:489:C:H6	1.86	0.41
40:XF:36:ARG:NH2	40:XF:66:GLU:OE1	2.53	0.41
4:YA:1005:C:H2'	4:YA:1006:C:C6	2.55	0.41
4:YA:1091:G:N3	4:YA:1091:G:H2'	2.36	0.41
4:YA:1510:G:H2'	4:YA:1511:C:H6	1.85	0.41
4:YA:2010:G:H5''	21:YW:42:ARG:HB2	2.03	0.41
4:YA:2065:C:H4'	4:YA:2251:OMG:HM22	2.02	0.41
4:YA:2405:G:H5'	14:YP:75:ILE:HD13	2.01	0.41
4:YA:2742:C:OP1	34:Y9:35:ARG:HD3	2.20	0.41
4:YA:562:U:H6	4:YA:562:U:H2'	1.73	0.41
4:YA:863:A:H2'	4:YA:864:G:H8	1.85	0.41
9:YG:14:GLU:C	9:YG:17:PRO:HD2	2.41	0.41
13:YO:111:PHE:HD1	13:YO:111:PHE:N	2.19	0.41
17:YS:7:TYR:C	17:YS:7:TYR:CD1	2.94	0.41
4:YA:2682:U:O2'	18:YT:58:ASN:OD1	2.38	0.41
24:YZ:121:HIS:HB3	24:YZ:123:ASP:O	2.21	0.41
35:QA:1023:G:H2'	35:QA:1024:G:C8	2.55	0.41
35:QA:1004:A:C5	35:QA:1037:C:C2	3.08	0.41
35:QA:113:G:H2'	35:QA:114:U:C6	2.56	0.41
35:QA:1279:A:O2'	35:QA:1281:U:OP2	2.33	0.41
35:QA:1476:G:H2'	35:QA:1477:C:C6	2.55	0.41
36:QB:77:ALA:HB2	36:QB:211:ILE:HD13	2.03	0.41
38:QD:118:ARG:HH11	38:QD:118:ARG:HG3	1.85	0.41
55:QU:18:TYR:N	55:QU:18:TYR:HD1	2.19	0.41
29:R4:49:PHE:HB3	29:R4:50:VAL:H	1.64	0.41
4:RA:1530:C:C2	4:RA:1531:C:C6	3.09	0.41
4:RA:1721:G:H2'	4:RA:1740:G:O6	2.21	0.41
4:RA:2043:C:C2	4:RA:2044:C:C5	3.09	0.41
4:RA:2100:G:C6	4:RA:2190:G:C6	3.08	0.41
4:RA:2115:G:N2	4:RA:2171:A:H61	2.17	0.41
4:RA:2291:U:C2	4:RA:2292:C:C5	3.08	0.41
4:RA:2348:U:O4	4:RA:2382:G:N1	2.54	0.41
4:RA:2593:U:H2'	4:RA:2594:C:C6	2.56	0.41
4:RA:2712(A):U:O2'	4:RA:2713:A:H5'	2.20	0.41
4:RA:580:C:H2'	4:RA:581:C:H6	1.85	0.41
4:RA:784:A:C6	6:RD:229:VAL:HG11	2.56	0.41
7:RE:2:LYS:HA	7:RE:84:PHE:CD1	2.55	0.41
11:RI:72:LEU:HD12	11:RI:138:ILE:HG21	2.01	0.41
15:RQ:21:THR:HG23	15:RQ:98:LYS:O	2.21	0.41
19:RU:62:ILE:HG12	19:RU:76:TYR:HE2	1.84	0.41
35:XA:1516:G:H2'	35:XA:1518:MA6:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:986:A:H2'	35:XA:987:G:H8	1.86	0.41
36:XB:158:LEU:HD21	36:XB:180:LEU:HD13	2.03	0.41
36:XB:33:TYR:N	36:XB:41:ILE:O	2.47	0.41
38:XD:108:LEU:HD11	38:XD:174:LEU:HB3	2.03	0.41
39:XE:88:LYS:HB3	39:XE:123:LEU:HB2	2.03	0.41
3:XY:183:ILE:HG13	3:XY:192:LEU:CD1	2.51	0.41
3:XY:253:HIS:CD2	3:XY:257:THR:HG21	2.54	0.41
25:Y0:82:ARG:HA	25:Y0:83:PRO:HD3	1.87	0.41
4:YA:1590:U:H2'	4:YA:1591:G:H8	1.85	0.41
4:YA:2347:C:C2	4:YA:2348:U:C5	3.09	0.41
4:YA:2557:G:H2'	4:YA:2558:C:H6	1.85	0.41
4:YA:609:A:H2'	4:YA:610:G:O4'	2.21	0.41
6:YD:218:ARG:HB3	6:YD:219:PRO:HD2	2.02	0.41
11:YI:114:LEU:HD12	11:YI:115:ALA:N	2.36	0.41
14:YP:126:VAL:HG12	14:YP:148:LEU:CD2	2.50	0.41
17:YS:11:LYS:HD3	17:YS:15:ARG:NH1	2.36	0.41
20:YV:52:VAL:HG23	20:YV:55:ALA:HB3	2.03	0.41
20:YV:81:TYR:C	20:YV:82:ARG:HG3	2.41	0.41
21:YW:6:ILE:HG22	21:YW:8:ARG:HG3	2.02	0.41
23:YY:38:ILE:HD11	23:YY:66:PRO:HG3	2.02	0.41
35:QA:1208:C:H2'	35:QA:1209:C:H6	1.85	0.41
35:QA:219:C:H2'	35:QA:220:G:O4'	2.20	0.41
35:QA:540:G:H2'	35:QA:541:G:O4'	2.21	0.41
35:QA:791:G:N2	35:QA:1497:G:O3'	2.53	0.41
35:QA:806:C:H2'	35:QA:807:A:H8	1.86	0.41
37:QC:35:GLU:CG	37:QC:59:ARG:HH22	2.33	0.41
38:QD:164:ALA:O	38:QD:168:ARG:HD2	2.20	0.41
40:QF:73:ASN:HA	40:QF:73:ASN:HD22	1.55	0.41
42:QH:48:TYR:H	42:QH:48:TYR:HD1	1.67	0.41
42:QH:51:VAL:HG21	42:QH:60:ARG:HH11	1.86	0.41
43:QI:33:PHE:CE1	43:QI:43:ALA:HB1	2.50	0.41
40:QF:89:MET:SD	52:QR:76:LEU:HD13	2.60	0.41
53:QS:52:TYR:HB2	53:QS:57:HIS:CD2	2.56	0.41
26:R1:89:GLU:O	26:R1:93:GLU:HG2	2.21	0.41
4:RA:1117:G:H2'	4:RA:1118:C:C6	2.56	0.41
4:RA:1742:G:H2'	4:RA:1743:C:C6	2.56	0.41
4:RA:1754:C:H2'	4:RA:1755:A:O4'	2.20	0.41
4:RA:2059:A:O2'	8:RF:69:HIS:ND1	2.47	0.41
4:RA:23:G:OP1	4:RA:504:U:N3	2.46	0.41
4:RA:2839:G:H5'	16:RR:46:GLY:CA	2.48	0.41
4:RA:476:G:H4'	4:RA:502:A:N1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:510:C:C2	4:RA:511:U:C6	3.09	0.41
4:RA:57:C:H2'	4:RA:58:G:O4'	2.20	0.41
9:RG:133:LEU:HD11	9:RG:157:ILE:HD12	2.03	0.41
11:RI:72:LEU:C	11:RI:74:ASN:H	2.23	0.41
12:RN:114:ARG:O	12:RN:118:LYS:HG3	2.21	0.41
16:RR:24:GLN:HE22	16:RR:36:THR:HG21	1.85	0.41
20:RV:75:PHE:CD1	20:RV:76:LYS:N	2.88	0.41
35:XA:1070:U:H2'	35:XA:1071:C:H6	1.85	0.41
35:XA:1492:A:H3'	35:XA:1493:A:H8	1.85	0.41
35:XA:149:A:H2'	35:XA:150:C:C6	2.56	0.41
35:XA:67:C:O2	35:XA:171:A:H2	2.04	0.41
35:XA:297:G:H4'	35:XA:557:G:H4'	2.02	0.41
35:XA:581:G:N1	35:XA:759:A:OP2	2.37	0.41
35:XA:908:A:H2'	35:XA:909:A:H8	1.86	0.41
36:XB:19:HIS:O	36:XB:20:GLU:HB2	2.20	0.41
46:XL:53:ARG:HB3	46:XL:93:LEU:HD11	2.02	0.41
4:YA:1053:C:H2'	4:YA:1054:A:C8	2.56	0.41
4:YA:1946:U:C2	4:YA:1947:C:C5	3.09	0.41
4:YA:210:C:OP2	32:Y7:29:LYS:NZ	2.50	0.41
4:YA:2646:C:H2'	4:YA:2647:U:O4'	2.21	0.41
4:YA:2667:C:H2'	4:YA:2668:G:O4'	2.20	0.41
10:YH:84:SER:HA	10:YH:133:VAL:O	2.19	0.41
18:YT:16:ARG:HH21	18:YT:81:PRO:HA	1.85	0.41
35:QA:1323:G:H2'	35:QA:1324:A:H8	1.83	0.41
35:QA:985:C:H2'	35:QA:986:A:C8	2.55	0.41
37:QC:50:ALA:HB1	37:QC:70:VAL:HG21	2.01	0.41
40:QF:97:PHE:HB2	52:QR:32:ARG:CD	2.34	0.41
44:QJ:19:SER:O	44:QJ:23:ILE:HG12	2.20	0.41
44:QJ:37:PRO:HA	44:QJ:72:VAL:HG12	2.02	0.41
3:QY:357:ILE:HA	3:QY:357:ILE:HD13	1.83	0.41
4:RA:1053:C:O2'	4:RA:1054:A:O5'	2.36	0.41
4:RA:1179:C:H2'	4:RA:1180:C:H6	1.86	0.41
4:RA:1270:C:H5''	4:RA:1271:G:O5'	2.21	0.41
4:RA:1385:G:O2'	4:RA:1396:U:O2	2.37	0.41
4:RA:2015:A:N3	30:R5:4:HIS:NE2	2.65	0.41
4:RA:2050:C:H2'	4:RA:2051:A:O4'	2.20	0.41
4:RA:208:C:H2'	4:RA:209:C:H6	1.86	0.41
4:RA:2262:U:OP2	25:R0:16:SER:OG	2.34	0.41
4:RA:2302:G:C6	4:RA:2315:G:C6	3.09	0.41
4:RA:2462:U:H2'	4:RA:2463:C:H6	1.85	0.41
4:RA:2528:U:H2'	4:RA:2530:A:O5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RA:2838:G:C4	4:RA:2839:G:C8	3.08	0.41
4:RA:2889:C:H2'	4:RA:2891:G:O4'	2.21	0.41
4:RA:445:C:H2'	4:RA:446:G:O4'	2.20	0.41
9:RG:115:ARG:HB3	9:RG:136:ARG:NH2	2.32	0.41
10:RH:117:PRO:HG3	10:RH:123:PHE:CD2	2.55	0.41
16:RR:70:LEU:O	16:RR:72:ASP:N	2.54	0.41
18:RT:64:ARG:HH12	18:RT:103:ARG:HA	1.80	0.41
19:RU:47:TYR:HA	19:RU:50:ARG:HG2	2.03	0.41
35:XA:1058:G:H2'	35:XA:1059:C:C6	2.56	0.41
35:XA:236:G:H2'	35:XA:237:C:C6	2.56	0.41
35:XA:41:G:C6	35:XA:402:G:C6	3.09	0.41
35:XA:448:A:P	35:XA:485:G:H22	2.42	0.41
35:XA:553:A:H2'	35:XA:554:C:C6	2.56	0.41
35:XA:61:G:H2'	35:XA:62:U:O4'	2.21	0.41
36:XB:71:VAL:HG23	36:XB:164:VAL:HA	2.03	0.41
38:XD:173:TRP:CZ3	38:XD:193:ASP:HB3	2.56	0.41
39:XE:33:VAL:HG21	39:XE:109:ILE:HA	2.02	0.41
41:XG:74:GLU:HB2	41:XG:91:VAL:HG22	2.02	0.41
49:XO:26:GLU:HG3	49:XO:26:GLU:H	1.61	0.41
4:YA:1084:A:H8	4:YA:1085:A:H4'	1.86	0.41
4:YA:208:C:H2'	4:YA:209:C:C6	2.55	0.41
4:YA:2134:A:O2'	4:YA:2159:G:H1'	2.21	0.41
4:YA:2316:C:H2'	4:YA:2317:C:C6	2.55	0.41
4:YA:23:G:OP1	4:YA:504:U:N3	2.51	0.41
4:YA:2526:G:H5'	4:YA:2742:C:O2'	2.20	0.41
4:YA:2537:U:H2'	4:YA:2538:C:C6	2.55	0.41
4:YA:273(F):G:H2'	4:YA:273(G):C:C6	2.56	0.41
4:YA:556:G:H2'	4:YA:557:U:C6	2.55	0.41
4:YA:610:G:H2'	4:YA:611:C:C6	2.56	0.41
4:YA:644:A:H4'	4:YA:645:C:H5	1.86	0.41
9:YG:86:MET:HA	9:YG:87:PRO:HD3	1.95	0.41
13:YO:9:GLU:O	13:YO:83:ALA:HA	2.21	0.41
18:YT:94:ALA:HB1	18:YT:99:LEU:HD21	2.02	0.41
35:QA:1014:A:H2'	35:QA:1015:A:C8	2.56	0.41
35:QA:1158:C:H5	35:QA:1181:G:N1	2.18	0.41
35:QA:1387:G:H2'	35:QA:1388:C:C6	2.56	0.41
35:QA:224:C:H2'	35:QA:225:C:H6	1.86	0.41
36:QB:45:GLN:O	36:QB:49:GLU:HG2	2.20	0.41
38:QD:110:PHE:N	38:QD:110:PHE:CD1	2.89	0.41
35:QA:35:G:O2'	46:QL:118:SER:O	2.28	0.41
47:QM:5:ALA:HB1	47:QM:61:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:QQ:4:LYS:N	51:QQ:61:GLU:HG2	2.35	0.41
53:QS:41:VAL:CG2	29:R4:67:TYR:CE2	3.04	0.41
3:QY:277:ASP:HB3	3:QY:278:ARG:H	1.65	0.41
4:RA:1157:G:O2'	28:R3:31:LEU:HD12	2.21	0.41
32:R7:23:ARG:O	32:R7:23:ARG:HG2	2.20	0.41
4:RA:242:G:C8	33:R8:5:LYS:HG2	2.56	0.41
4:RA:82:G:N1	4:RA:103:A:OP2	2.41	0.41
4:RA:1394:U:H2'	4:RA:1395:A:O4'	2.21	0.41
4:RA:2059:A:O3'	8:RF:69:HIS:HA	2.20	0.41
4:RA:2098:U:H2'	4:RA:2099:U:O4'	2.21	0.41
4:RA:2112:G:H2'	4:RA:2113:U:C6	2.55	0.41
4:RA:903:C:H2'	4:RA:904:C:C6	2.55	0.41
4:RA:949:C:H2'	4:RA:950:G:H8	1.85	0.41
8:RF:40:GLN:HE22	8:RF:182:ASN:HB2	1.86	0.41
8:RF:29:ASN:H	8:RF:112:MET:HE3	1.85	0.41
4:RA:1665:A:H4'	13:RO:67:LYS:HB2	2.03	0.41
35:XA:1327:C:H2'	35:XA:1328:C:C6	2.56	0.41
35:XA:71:C:H2'	35:XA:72:C:H6	1.84	0.41
35:XA:988:G:H2'	35:XA:989:C:O4'	2.21	0.41
36:XB:20:GLU:HB3	36:XB:21:ARG:H	1.53	0.41
39:XE:144:THR:H	39:XE:147:ASP:HB2	1.86	0.41
43:XI:48:GLU:HB3	43:XI:101:PHE:HE2	1.85	0.41
49:XO:4:THR:HG22	49:XO:7:GLU:OE1	2.21	0.41
50:XP:8:ARG:HH21	50:XP:15:PRO:HG3	1.86	0.41
35:XA:375:U:C4'	50:XP:17:TYR:HE2	2.33	0.41
26:Y1:51:VAL:HG11	26:Y1:74:VAL:CG2	2.50	0.41
4:YA:103:A:C5	4:YA:104:U:C5	3.08	0.41
4:YA:1914:C:HO2'	4:YA:1915:5MU:P	2.41	0.41
4:YA:2103:C:N3	4:YA:2104:G:N2	2.69	0.41
3:XY:256:ARG:NH2	4:YA:2453:A:H5''	2.36	0.41
4:YA:684:G:OP1	32:Y7:16:HIS:ND1	2.54	0.41
4:YA:718:A:H3'	4:YA:719:C:H6	1.85	0.41
4:YA:861:A:H2'	4:YA:862:G:O4'	2.21	0.41
4:YA:1798:U:H5	6:YD:274:ARG:NH1	2.19	0.41
9:YG:110:ALA:O	9:YG:140:ILE:HG23	2.21	0.41
9:YG:25:TYR:CD2	9:YG:31:VAL:HG12	2.55	0.41
21:YW:10:VAL:HG12	21:YW:12:ILE:HG22	2.03	0.41
35:QA:1022:G:H5'	35:QA:1023:G:OP2	2.21	0.41
35:QA:1135:U:H4'	35:QA:1136:U:H5	1.85	0.41
35:QA:166:G:H2'	35:QA:167:G:H8	1.86	0.41
39:QE:59:GLY:O	39:QE:63:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:QP:59:TRP:HA	50:QP:62:VAL:HG12	2.03	0.41
51:QQ:10:VAL:HG13	51:QQ:19:VAL:HB	2.03	0.41
52:QR:23:LYS:HB2	52:QR:56:THR:O	2.21	0.41
1:QV:52:G:O2'	24:RZ:198:LYS:NZ	2.52	0.41
3:QY:68:ASP:HA	3:QY:71:ASP:HB2	2.03	0.41
3:QY:76:GLY:O	3:QY:80:VAL:HG23	2.21	0.41
29:R4:61:ARG:HG3	29:R4:62:ARG:N	2.36	0.41
34:R9:9:ARG:HH11	34:R9:16:VAL:HG23	1.85	0.41
4:RA:1007:C:OP1	12:RN:35:ARG:NH1	2.54	0.41
4:RA:1144:G:H2'	4:RA:1145:C:C6	2.56	0.41
4:RA:273(F):G:C4	4:RA:273(G):C:C5	3.09	0.41
4:RA:531:C:H4'	4:RA:532:A:H5''	2.03	0.41
4:RA:640:C:H2'	4:RA:641:C:C6	2.56	0.41
8:RF:20:LEU:CD2	8:RF:21:ALA:H	2.34	0.41
13:RO:7:TYR:CE1	13:RO:20:MET:HB2	2.56	0.41
21:RW:11:ARG:HD2	21:RW:12:ILE:N	2.35	0.41
24:RZ:31:ARG:H	24:RZ:31:ARG:HG2	1.65	0.41
35:XA:114:U:H1'	35:XA:353:A:H1'	2.03	0.41
35:XA:374:A:C6	35:XA:375:U:C4	3.08	0.41
35:XA:60:A:H4'	35:XA:61:G:O5'	2.21	0.41
50:XP:23:ASP:OD1	50:XP:25:ARG:HD2	2.19	0.41
4:YA:2162:G:H2'	4:YA:2163:C:C5	2.55	0.41
3:XY:258:GLU:OE1	4:YA:2492:U:H4'	2.21	0.41
4:YA:746:A:HO2'	4:YA:2611:U:HO2'	1.68	0.41
4:YA:2718:G:O2'	4:YA:2847:U:OP1	2.36	0.41
35:QA:93:G:C2'	35:QA:96:U:H5'	2.51	0.40
36:QB:51:LEU:HD23	36:QB:201:ILE:HD12	2.02	0.40
40:QF:4:TYR:HB3	40:QF:91:VAL:O	2.21	0.40
43:QI:15:ALA:HB2	43:QI:65:VAL:HG23	2.03	0.40
44:QJ:33:GLN:O	44:QJ:75:ILE:N	2.45	0.40
47:QM:11:ARG:HA	47:QM:45:VAL:HB	2.03	0.40
51:QQ:12:SER:HB3	51:QQ:20:THR:HB	2.03	0.40
3:QY:146:SER:O	3:QY:149:GLU:HG2	2.21	0.40
28:R3:6:VAL:HG12	28:R3:28:LEU:HD11	2.02	0.40
4:RA:1449:A:N3	4:RA:1529:G:H1'	2.36	0.40
4:RA:2118:U:H5	4:RA:2148:G:H1'	1.86	0.40
4:RA:301:G:C4	4:RA:302:C:C5	3.09	0.40
4:RA:375:C:C2	4:RA:376:C:C5	3.09	0.40
4:RA:485:C:C2	4:RA:486:C:C5	3.09	0.40
4:RA:719:C:H2'	4:RA:720:C:C6	2.56	0.40
4:RA:9:U:HO2'	4:RA:10:G:P	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:RT:22:PHE:CZ	18:RT:61:PHE:CD2	3.09	0.40
19:RU:17:ILE:HG23	19:RU:39:LEU:HD12	2.03	0.40
35:XA:1120:G:H2'	35:XA:1121:U:H6	1.86	0.40
35:XA:113:G:H2'	35:XA:114:U:H6	1.86	0.40
35:XA:983:A:H2	35:XA:984:C:C6	2.39	0.40
39:XE:41:VAL:O	39:XE:67:VAL:HG12	2.21	0.40
41:XG:26:PHE:CE2	41:XG:30:ILE:HD11	2.56	0.40
42:XH:12:ARG:HD2	42:XH:26:VAL:HG12	2.03	0.40
43:XI:16:ARG:HH11	43:XI:64:THR:HG21	1.86	0.40
46:XL:28:LYS:O	46:XL:28:LYS:HG2	2.21	0.40
3:XY:10:ARG:HA	3:XY:10:ARG:HD3	1.83	0.40
26:Y1:64:ALA:HA	26:Y1:67:ILE:HG13	2.03	0.40
4:YA:1007:C:OP1	12:YN:35:ARG:NH1	2.54	0.40
4:YA:1364:G:P	26:Y1:3:LYS:HG3	2.61	0.40
4:YA:1638:C:O3'	4:YA:2709:G:N2	2.54	0.40
4:YA:1798:U:H5'	6:YD:259:THR:CG2	2.49	0.40
4:YA:2271:G:OP1	25:Y0:18:ALA:HB1	2.21	0.40
4:YA:2647:U:H2'	4:YA:2648:C:H6	1.86	0.40
4:YA:2810:A:N6	4:YA:2891:G:O2'	2.38	0.40
9:YG:126:ASP:HB3	9:YG:130:ASN:H	1.85	0.40
9:YG:46:ALA:HB2	9:YG:53:LEU:CD1	2.50	0.40
18:YT:108:ARG:HA	18:YT:111:ARG:NH1	2.36	0.40
35:QA:1177:G:OP2	43:QI:97:LYS:NZ	2.29	0.40
35:QA:179:A:C4	35:QA:180:U:C5	3.09	0.40
35:QA:675:A:H1'	45:QK:116:HIS:CG	2.56	0.40
36:QB:27:LYS:HB2	36:QB:194:PRO:HD2	2.02	0.40
36:QB:71:VAL:CG1	36:QB:170:GLU:HG3	2.51	0.40
38:QD:188:LEU:HA	38:QD:189:PRO:HD3	1.87	0.40
41:QG:143:ARG:HE	41:QG:143:ARG:HB2	1.49	0.40
53:QS:11:VAL:HG11	53:QS:16:LEU:HB2	2.02	0.40
55:QU:18:TYR:N	55:QU:18:TYR:CD1	2.89	0.40
3:QY:281:HIS:HE1	4:RA:2493:U:H1'	1.86	0.40
29:R4:43:TYR:CD1	29:R4:43:TYR:N	2.90	0.40
4:RA:2065:C:C2	4:RA:2066:C:C5	3.10	0.40
4:RA:950:G:C5	4:RA:951:C:C5	3.10	0.40
6:RD:72:LYS:HD2	6:RD:101:GLU:OE2	2.21	0.40
8:RF:39:TRP:HA	8:RF:99:TYR:CE1	2.55	0.40
9:RG:18:GLU:HA	9:RG:18:GLU:OE1	2.21	0.40
4:RA:1035:U:P	10:RH:59:ARG:NH2	2.95	0.40
4:RA:2728:U:H5'	13:RO:70:LYS:HZ3	1.85	0.40
24:RZ:59:LEU:HD11	24:RZ:88:PHE:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:1036:G:H2'	35:XA:1037:C:O4'	2.22	0.40
35:XA:102:G:C5	35:XA:103:C:C5	3.09	0.40
35:XA:1040:U:H2'	35:XA:1041:A:O4'	2.21	0.40
35:XA:1320:C:H2'	35:XA:1321:C:O4'	2.21	0.40
35:XA:217:C:H2'	35:XA:218:C:H6	1.87	0.40
35:XA:553:A:H2'	35:XA:554:C:H6	1.87	0.40
39:XE:137:GLU:HG3	39:XE:140:ARG:HH11	1.85	0.40
42:XH:64:LYS:C	42:XH:65:TYR:CD1	2.94	0.40
29:Y4:67:TYR:CE2	53:XS:41:VAL:HG21	2.55	0.40
3:XY:260:ALA:HB2	3:XY:275:GLN:HG2	2.03	0.40
29:Y4:48:ARG:CD	29:Y4:48:ARG:N	2.80	0.40
32:Y7:31:LEU:O	32:Y7:35:ARG:HG2	2.21	0.40
4:YA:2660:A:N7	10:YH:175:LYS:HE3	2.36	0.40
8:YF:38:ARG:HG2	8:YF:99:TYR:OH	2.22	0.40
12:YN:62:VAL:HG11	12:YN:66:LYS:HB2	2.03	0.40
13:YO:120:GLU:OE2	13:YO:122:LEU:HD21	2.21	0.40
35:QA:1250:A:H4'	43:QI:67:GLY:HA2	2.03	0.40
35:QA:1261:A:H3'	35:QA:1262:C:C6	2.57	0.40
35:QA:1447:A:H5''	35:QA:1452:C:OP2	2.21	0.40
35:QA:177:C:H2'	35:QA:178:C:H6	1.85	0.40
35:QA:352:C:O2'	35:QA:354:G:OP1	2.27	0.40
35:QA:677:U:H2'	35:QA:678:U:H6	1.86	0.40
42:QH:105:ARG:HG3	42:QH:105:ARG:O	2.22	0.40
45:QK:34:ASP:OD2	45:QK:38:ASN:HB2	2.22	0.40
3:QY:156:ALA:HB1	3:QY:161:PHE:HB2	2.02	0.40
3:QY:176:ILE:HD13	3:QY:179:VAL:HG11	2.04	0.40
3:QY:307:LYS:O	3:QY:311:GLU:HG2	2.20	0.40
4:RA:1057:A:HO2'	4:RA:1058:G:P	2.44	0.40
4:RA:1300:U:H4'	4:RA:1301:A:H5'	2.03	0.40
4:RA:139(A):G:O6	4:RA:140:G:O2'	2.40	0.40
4:RA:1499:C:H2'	4:RA:1500:G:H8	1.86	0.40
4:RA:1853:A:H2'	4:RA:1854:A:C8	2.57	0.40
4:RA:2317:C:H2'	4:RA:2318:G:H5'	2.03	0.40
4:RA:2650:U:C2	4:RA:2651:C:C5	3.09	0.40
9:RG:7:LEU:HD12	9:RG:104:GLU:N	2.37	0.40
15:RQ:31:ASP:C	15:RQ:32:TYR:CD1	2.91	0.40
35:XA:978:A:C2	35:XA:1319:A:C4	3.09	0.40
36:XB:229:VAL:HG12	36:XB:230:VAL:N	2.37	0.40
36:XB:58:ILE:CG2	36:XB:222:ILE:HG22	2.52	0.40
41:XG:74:GLU:OE2	41:XG:95:ARG:NE	2.53	0.40
43:XI:27:THR:HG23	43:XI:31:GLN:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:XJ:45:ARG:HG2	44:XJ:47:PHE:CZ	2.56	0.40
45:XK:81:ASP:OD1	45:XK:106:LYS:HE3	2.22	0.40
45:XK:82:VAL:HB	45:XK:108:ILE:HG12	2.02	0.40
47:XM:13:LYS:HE3	47:XM:21:TYR:OH	2.21	0.40
49:XO:40:SER:O	49:XO:44:LYS:HG3	2.22	0.40
3:XY:58:LYS:NZ	4:YA:1067:A:H5''	2.36	0.40
4:YA:1153:C:H2'	4:YA:1154:G:O4'	2.20	0.40
4:YA:2311:A:H3'	4:YA:2312:U:C5	2.57	0.40
4:YA:1027:A:C2	4:YA:2488:A:H5'	2.56	0.40
4:YA:2712(A):U:O2'	4:YA:2713:A:H5'	2.22	0.40
4:YA:370:G:H4'	4:YA:371:A:OP2	2.21	0.40
4:YA:636:G:OP1	14:YP:132:LYS:HG3	2.20	0.40
4:YA:952:G:C6	4:YA:966:G:C6	3.10	0.40
13:YO:36:GLY:HA3	13:YO:109:LYS:HD2	2.04	0.40
14:YP:80:TYR:HD1	14:YP:80:TYR:N	2.19	0.40
18:YT:96:ARG:HH11	18:YT:96:ARG:HD2	1.49	0.40
23:YY:13:VAL:HB	23:YY:72:VAL:HG13	2.03	0.40
24:YZ:108:PRO:HA	24:YZ:142:SER:HA	2.03	0.40
35:QA:1466:C:H2'	35:QA:1467:G:O4'	2.21	0.40
35:QA:1479:C:H2'	35:QA:1480:G:C8	2.56	0.40
35:QA:374:A:C6	35:QA:375:U:C4	3.09	0.40
37:QC:70:VAL:HG22	37:QC:72:LYS:H	1.86	0.40
40:QF:76:ALA:HB1	40:QF:80:ARG:NH2	2.36	0.40
42:QH:51:VAL:HG12	42:QH:52:ASP:N	2.37	0.40
52:QR:74:ARG:HD3	52:QR:81:PHE:CD1	2.56	0.40
3:QY:76:GLY:HA3	3:QY:106:LEU:HD11	2.03	0.40
3:QY:256:ARG:NH2	4:RA:2573:C:O5'	2.54	0.40
26:R1:12:PRO:HB2	26:R1:41:ARG:NH2	2.36	0.40
4:RA:1358:G:O2'	4:RA:1359:A:H5'	2.21	0.40
4:RA:118:A:N3	4:RA:178:G:H1'	2.36	0.40
4:RA:2485:G:H5''	15:RQ:46:GLN:HE21	1.87	0.40
4:RA:2574:G:H8	4:RA:2574:G:O5'	2.04	0.40
4:RA:272(A):A:H8	4:RA:272(B):C:C5	2.39	0.40
4:RA:609:A:H2'	4:RA:610:G:O4'	2.22	0.40
4:RA:656:G:H2'	4:RA:657:U:C6	2.56	0.40
4:RA:878:A:C6	4:RA:900:A:C8	3.08	0.40
6:RD:53:PHE:CD2	6:RD:220:HIS:ND1	2.89	0.40
9:RG:18:GLU:HG3	9:RG:175:LEU:HD21	2.03	0.40
17:RS:87:PHE:HB2	17:RS:112:PHE:CE2	2.56	0.40
35:XA:1003:G:H1	35:XA:1035:A:N6	2.20	0.40
35:XA:1010:G:H2'	35:XA:1011:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XA:22:G:H2'	35:XA:23:C:H6	1.86	0.40
35:XA:490:G:H2'	35:XA:491:G:H8	1.86	0.40
36:XB:230:VAL:HG22	36:XB:231:GLU:H	1.87	0.40
40:XF:100:ASN:OD1	52:XR:23:LYS:HE2	2.21	0.40
43:XI:110:GLU:OE2	43:XI:113:LYS:NZ	2.49	0.40
46:XL:77:LEU:HD21	46:XL:107:ALA:HA	2.03	0.40
53:XS:43:GLU:N	53:XS:43:GLU:OE1	2.52	0.40
1:XV:25:C:H2'	1:XV:26:G:O4'	2.21	0.40
3:XY:203:ARG:NH1	3:XY:206:PRO:HD3	2.24	0.40
3:XY:217:PHE:CE2	3:XY:319:TRP:HA	2.56	0.40
29:Y4:13:ARG:HH21	29:Y4:21:VAL:HG11	1.87	0.40
29:Y4:62:ARG:HD3	29:Y4:62:ARG:HA	1.91	0.40
4:YA:1022:G:C5	4:YA:1140:C:C4	3.09	0.40
4:YA:1067:A:H5'	4:YA:1067:A:C8	2.55	0.40
4:YA:1268:A:H2'	4:YA:1269:A:O4'	2.21	0.40
4:YA:1790:C:H2'	4:YA:1791:A:C8	2.57	0.40
4:YA:185:U:C2	4:YA:186:G:C8	3.10	0.40
4:YA:687:C:H2'	4:YA:688:U:O4'	2.22	0.40
10:YH:113:VAL:HG11	10:YH:151:ILE:HD13	2.03	0.40
17:YS:106:ARG:HG2	17:YS:112:PHE:CE1	2.57	0.40
18:YT:22:PHE:CZ	18:YT:61:PHE:CE2	3.09	0.40
35:QA:1122:U:C4	35:QA:1123:A:N7	2.89	0.40
35:QA:1347:G:N2	35:QA:1373:G:H2'	2.35	0.40
35:QA:189(M):G:C2	35:QA:190:U:C4	3.09	0.40
35:QA:415:A:C4	35:QA:416:G:C8	3.10	0.40
35:QA:417:C:H2'	35:QA:418:C:C6	2.56	0.40
36:QB:124:SER:HA	36:QB:125:PRO:HA	1.71	0.40
37:QC:46:GLU:OE1	37:QC:46:GLU:HA	2.22	0.40
38:QD:148:VAL:HG11	38:QD:158:ILE:HD12	2.03	0.40
38:QD:59:ARG:NH2	38:QD:62:GLN:HG3	2.35	0.40
33:R8:23:VAL:HG13	33:R8:47:LYS:HB3	2.03	0.40
4:RA:1051:G:H2'	4:RA:1052:C:C6	2.57	0.40
4:RA:185:U:H4'	4:RA:218:A:H4'	2.04	0.40
4:RA:2167:U:H2'	4:RA:2168:G:C4	2.56	0.40
4:RA:2329:G:H2'	4:RA:2330:G:C8	2.56	0.40
4:RA:2454:G:C4	4:RA:2455:G:C8	3.10	0.40
4:RA:2552:2MU:O5'	4:RA:2552:2MU:H6	2.22	0.40
4:RA:39:C:H2'	4:RA:40:C:H6	1.85	0.40
4:RA:90:U:H1'	4:RA:92:A:C8	2.57	0.40
4:RA:923:C:C2	4:RA:924:C:C5	3.09	0.40
4:RA:946:G:H2'	4:RA:947:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:RB:8:U:O3'	17:RS:25:ARG:NH2	2.41	0.40
10:RH:163:TYR:N	10:RH:163:TYR:CD1	2.89	0.40
16:RR:87:TYR:OH	16:RR:117:VAL:O	2.28	0.40
16:RR:47:PHE:HD1	16:RR:47:PHE:C	2.25	0.40
35:XA:1129:C:N4	35:XA:1143:G:H1	2.19	0.40
35:XA:271:C:H2'	35:XA:272:C:H6	1.87	0.40
35:XA:277:C:H5''	51:XQ:68:ARG:NH2	2.37	0.40
35:XA:460:G:H1'	35:XA:472:A:H61	1.87	0.40
36:XB:111:ARG:NE	36:XB:111:ARG:CA	2.80	0.40
36:XB:71:VAL:HG12	36:XB:93:VAL:CG2	2.52	0.40
40:XF:97:PHE:HD1	40:XF:98:LEU:N	2.19	0.40
35:XA:1058:G:N2	44:XJ:53:PRO:HG3	2.36	0.40
35:XA:739:C:O2'	49:XO:42:HIS:ND1	2.45	0.40
54:XT:47:GLY:HA2	54:XT:48:LYS:C	2.42	0.40
4:YA:1073:A:HO2'	4:YA:1074:G:C5'	2.34	0.40
4:YA:1301:A:C8	4:YA:1303:G:C8	3.10	0.40
4:YA:1317:A:H2'	4:YA:1318:C:C6	2.57	0.40
4:YA:1321:A:H2'	4:YA:1322:A:H8	1.86	0.40
4:YA:1346:G:C6	4:YA:1601:G:C6	3.10	0.40
4:YA:1810:A:H2'	4:YA:1811:G:O4'	2.22	0.40
4:YA:2131:G:H5'	4:YA:2133:G:O5'	2.21	0.40
4:YA:594:U:H2'	4:YA:595:C:C6	2.57	0.40
4:YA:900:A:H2'	4:YA:901:A:H8	1.87	0.40
6:YD:80:ALA:HB3	6:YD:94:LEU:HB3	2.03	0.40
14:YP:95:VAL:HG22	14:YP:125:VAL:HG12	2.03	0.40
17:YS:5:THR:OG1	17:YS:8:GLU:HG3	2.22	0.40
18:YT:118:ARG:HG2	35:XA:1442(B):G:C8	2.57	0.40
21:YW:9:TYR:HA	21:YW:100:THR:CG2	2.52	0.40
24:YZ:19:ARG:NH1	24:YZ:84:GLU:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	QY	355/380 (93%)	304 (86%)	43 (12%)	8 (2%)	8	35
3	XY	355/380 (93%)	310 (87%)	33 (9%)	12 (3%)	5	25
6	RD	273/276 (99%)	258 (94%)	15 (6%)	0	100	100
6	YD	273/276 (99%)	257 (94%)	15 (6%)	1 (0%)	39	75
7	RE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	34	72
7	YE	202/206 (98%)	192 (95%)	8 (4%)	2 (1%)	19	58
8	RF	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
8	YF	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
9	RG	179/182 (98%)	166 (93%)	10 (6%)	3 (2%)	11	43
9	YG	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	30	68
10	RH	172/180 (96%)	163 (95%)	9 (5%)	0	100	100
10	YH	171/180 (95%)	159 (93%)	12 (7%)	0	100	100
11	RI	145/148 (98%)	130 (90%)	13 (9%)	2 (1%)	14	48
11	YI	144/148 (97%)	136 (94%)	6 (4%)	2 (1%)	14	48
12	RN	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
12	YN	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	26	65
13	RO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
13	YO	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
14	RP	147/150 (98%)	141 (96%)	6 (4%)	0	100	100
14	YP	147/150 (98%)	137 (93%)	8 (5%)	2 (1%)	14	48
15	RQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
15	YQ	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	26	65
16	RR	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
16	YR	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
17	RS	108/112 (96%)	103 (95%)	5 (5%)	0	100	100
17	YS	108/112 (96%)	104 (96%)	4 (4%)	0	100	100
18	RT	129/146 (88%)	120 (93%)	7 (5%)	2 (2%)	12	44
18	YT	129/146 (88%)	122 (95%)	7 (5%)	0	100	100
19	RU	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
19	YU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
20	RV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	19	58
20	YV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	19	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	RW	110/113 (97%)	110 (100%)	0	0	100	100
21	YW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
22	RX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
22	YX	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	17	55
23	RY	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
23	YY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
24	RZ	201/206 (98%)	192 (96%)	9 (4%)	0	100	100
24	YZ	199/206 (97%)	188 (94%)	11 (6%)	0	100	100
25	R0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
25	Y0	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
26	R1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	55
26	Y1	95/98 (97%)	91 (96%)	3 (3%)	1 (1%)	17	55
27	R2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
27	Y2	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
28	R3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	Y3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
29	R4	67/71 (94%)	52 (78%)	10 (15%)	5 (8%)	1	7
29	Y4	67/71 (94%)	57 (85%)	7 (10%)	3 (4%)	3	17
30	R5	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
30	Y5	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
31	R6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
31	Y6	51/54 (94%)	47 (92%)	4 (8%)	0	100	100
32	R7	46/49 (94%)	46 (100%)	0	0	100	100
32	Y7	46/49 (94%)	46 (100%)	0	0	100	100
33	R8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
33	Y8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
34	R9	35/37 (95%)	35 (100%)	0	0	100	100
34	Y9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
36	QB	229/256 (90%)	197 (86%)	20 (9%)	12 (5%)	2	15
36	XB	229/256 (90%)	198 (86%)	24 (10%)	7 (3%)	5	27
37	QC	204/239 (85%)	195 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	XC	204/239 (85%)	193 (95%)	9 (4%)	2 (1%)	19	58
38	QD	206/209 (99%)	190 (92%)	15 (7%)	1 (0%)	34	72
38	XD	206/209 (99%)	197 (96%)	8 (4%)	1 (0%)	34	72
39	QE	146/162 (90%)	143 (98%)	3 (2%)	0	100	100
39	XE	146/162 (90%)	141 (97%)	5 (3%)	0	100	100
40	QF	98/101 (97%)	90 (92%)	6 (6%)	2 (2%)	9	38
40	XF	98/101 (97%)	93 (95%)	3 (3%)	2 (2%)	9	38
41	QG	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
41	XG	153/156 (98%)	147 (96%)	4 (3%)	2 (1%)	15	50
42	QH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	26	65
42	XH	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
43	QI	125/128 (98%)	117 (94%)	7 (6%)	1 (1%)	24	63
43	XI	124/128 (97%)	113 (91%)	9 (7%)	2 (2%)	12	44
44	QJ	95/105 (90%)	84 (88%)	8 (8%)	3 (3%)	5	26
44	XJ	94/105 (90%)	82 (87%)	9 (10%)	3 (3%)	5	26
45	QK	112/129 (87%)	108 (96%)	3 (3%)	1 (1%)	21	61
45	XK	112/129 (87%)	110 (98%)	2 (2%)	0	100	100
46	QL	119/132 (90%)	117 (98%)	2 (2%)	0	100	100
46	XL	119/132 (90%)	113 (95%)	6 (5%)	0	100	100
47	QM	114/126 (90%)	106 (93%)	7 (6%)	1 (1%)	21	61
47	XM	112/126 (89%)	104 (93%)	7 (6%)	1 (1%)	21	61
48	QN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
48	XN	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
49	QO	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
49	XO	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
50	QP	80/88 (91%)	74 (92%)	6 (8%)	0	100	100
50	XP	80/88 (91%)	74 (92%)	6 (8%)	0	100	100
51	QQ	97/105 (92%)	91 (94%)	4 (4%)	2 (2%)	9	37
51	XQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
52	QR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
52	XR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	QS	81/93 (87%)	75 (93%)	6 (7%)	0	100	100
53	XS	81/93 (87%)	77 (95%)	4 (5%)	0	100	100
54	QT	94/106 (89%)	86 (92%)	5 (5%)	3 (3%)	5	26
54	XT	96/106 (91%)	91 (95%)	2 (2%)	3 (3%)	5	27
55	QU	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	3	17
55	XU	21/27 (78%)	19 (90%)	1 (5%)	1 (5%)	3	17
All	All	12150/12888 (94%)	11432 (94%)	615 (5%)	103 (1%)	24	63

All (103) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	QY	254	VAL
3	XY	122	GLU
3	XY	230	ILE
3	XY	315	SER
9	YG	81	LYS
11	YI	85	GLU
29	Y4	60	GLN
36	XB	10	LEU
36	XB	17	PHE
36	XB	20	GLU
38	XD	150	GLU
43	XI	54	ASP
36	QB	15	VAL
36	QB	17	PHE
36	QB	21	ARG
29	R4	47	GLN
29	R4	49	PHE
29	R4	55	ARG
3	QY	122	GLU
3	QY	327	VAL
3	QY	337	ARG
3	XY	137	GLY
3	XY	228	ASP
3	XY	319	TRP
20	YV	79	VAL
22	YX	94	GLY
26	Y1	3	LYS
40	XF	70	ASP
41	XG	155	ARG

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Mol	Chain	Res	Type
43	XI	44	VAL
54	XT	47	GLY
54	XT	95	ALA
36	QB	16	HIS
51	QQ	68	ARG
54	QT	47	GLY
54	QT	95	ALA
18	RT	68	TYR
18	RT	128	GLU
20	RV	79	VAL
29	R4	45	GLY
3	QY	127	ASP
3	XY	26	ASP
3	XY	127	ASP
3	XY	134	ALA
7	YE	51	PHE
15	YQ	80	GLU
36	XB	125	PRO
40	XF	69	GLU
44	XJ	78	ASN
44	XJ	79	ARG
36	QB	126	GLU
36	QB	157	ARG
36	QB	231	GLU
40	QF	70	ASP
42	QH	14	ARG
44	QJ	55	LYS
44	QJ	78	ASN
55	QU	3	LYS
9	RG	51	ARG
11	RI	73	GLU
26	R1	3	LYS
3	QY	46	VAL
3	QY	346	GLN
3	XY	136	SER
14	YP	98	GLU
36	QB	95	GLN
40	QF	69	GLU
44	QJ	77	PRO
7	RE	52	LEU
11	RI	117	GLU
3	XY	119	PHE

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Mol	Chain	Res	Type
7	YE	74	PRO
11	YI	10	GLU
29	Y4	55	ARG
36	XB	83	MET
36	XB	126	GLU
37	XC	98	ASN
41	XG	7	ALA
54	XT	100	ILE
55	XU	7	ARG
36	QB	83	MET
36	QB	127	ILE
38	QD	24	GLU
43	QI	56	LEU
47	QM	12	ASN
51	QQ	67	LYS
9	RG	43	LEU
29	R4	44	THR
12	YN	131	GLN
29	Y4	45	GLY
36	XB	95	GLN
47	XM	67	GLU
36	QB	22	LYS
54	QT	100	ILE
3	QY	121	GLY
36	QB	158	LEU
3	XY	173	VAL
14	YP	122	PRO
45	QK	105	VAL
9	RG	16	ARG
6	YD	241	PRO
37	XC	108	ASN
44	XJ	37	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	QY	304/324 (94%)	290 (95%)	14 (5%)	33	70
3	XY	304/324 (94%)	292 (96%)	12 (4%)	39	75
6	RD	214/218 (98%)	206 (96%)	8 (4%)	41	76
6	YD	215/218 (99%)	208 (97%)	7 (3%)	45	79
7	RE	164/166 (99%)	158 (96%)	6 (4%)	41	76
7	YE	164/166 (99%)	156 (95%)	8 (5%)	31	68
8	RF	160/166 (96%)	149 (93%)	11 (7%)	19	55
8	YF	159/166 (96%)	152 (96%)	7 (4%)	35	71
9	RG	144/156 (92%)	139 (96%)	5 (4%)	43	78
9	YG	142/156 (91%)	137 (96%)	5 (4%)	43	78
10	RH	144/148 (97%)	140 (97%)	4 (3%)	51	82
10	YH	143/148 (97%)	136 (95%)	7 (5%)	31	68
11	RI	111/124 (90%)	105 (95%)	6 (5%)	27	64
11	YI	108/124 (87%)	105 (97%)	3 (3%)	51	82
12	RN	119/119 (100%)	114 (96%)	5 (4%)	36	73
12	YN	118/119 (99%)	111 (94%)	7 (6%)	24	60
13	RO	100/100 (100%)	96 (96%)	4 (4%)	38	75
13	YO	100/100 (100%)	96 (96%)	4 (4%)	38	75
14	RP	115/116 (99%)	111 (96%)	4 (4%)	43	78
14	YP	115/116 (99%)	109 (95%)	6 (5%)	29	65
15	RQ	111/111 (100%)	107 (96%)	4 (4%)	42	77
15	YQ	111/111 (100%)	106 (96%)	5 (4%)	34	70
16	RR	101/101 (100%)	100 (99%)	1 (1%)	82	93
16	YR	101/101 (100%)	99 (98%)	2 (2%)	63	86
17	RS	87/88 (99%)	83 (95%)	4 (5%)	33	70
17	YS	85/88 (97%)	77 (91%)	8 (9%)	11	39
18	RT	115/127 (91%)	106 (92%)	9 (8%)	16	49
18	YT	113/127 (89%)	105 (93%)	8 (7%)	18	54
19	RU	93/94 (99%)	84 (90%)	9 (10%)	10	36
19	YU	93/94 (99%)	85 (91%)	8 (9%)	13	45
20	RV	81/82 (99%)	76 (94%)	5 (6%)	23	59
20	YV	80/82 (98%)	75 (94%)	5 (6%)	22	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	RW	90/92 (98%)	85 (94%)	5 (6%)	26	62
21	YW	90/92 (98%)	84 (93%)	6 (7%)	20	56
22	RX	77/78 (99%)	75 (97%)	2 (3%)	54	83
22	YX	77/78 (99%)	77 (100%)	0	100	100
23	RY	86/91 (94%)	80 (93%)	6 (7%)	19	54
23	YY	86/91 (94%)	82 (95%)	4 (5%)	32	70
24	RZ	169/179 (94%)	160 (95%)	9 (5%)	28	64
24	YZ	165/179 (92%)	159 (96%)	6 (4%)	42	77
25	R0	61/67 (91%)	57 (93%)	4 (7%)	21	56
25	Y0	61/67 (91%)	57 (93%)	4 (7%)	21	56
26	R1	79/83 (95%)	76 (96%)	3 (4%)	40	76
26	Y1	81/83 (98%)	77 (95%)	4 (5%)	31	68
27	R2	65/67 (97%)	65 (100%)	0	100	100
27	Y2	66/67 (98%)	63 (96%)	3 (4%)	34	70
28	R3	51/52 (98%)	51 (100%)	0	100	100
28	Y3	50/52 (96%)	48 (96%)	2 (4%)	38	75
29	R4	58/63 (92%)	54 (93%)	4 (7%)	19	55
29	Y4	54/63 (86%)	47 (87%)	7 (13%)	5	21
30	R5	51/52 (98%)	51 (100%)	0	100	100
30	Y5	50/52 (96%)	46 (92%)	4 (8%)	15	48
31	R6	51/52 (98%)	50 (98%)	1 (2%)	63	86
31	Y6	50/52 (96%)	49 (98%)	1 (2%)	63	86
32	R7	41/42 (98%)	40 (98%)	1 (2%)	57	84
32	Y7	41/42 (98%)	39 (95%)	2 (5%)	31	68
33	R8	54/55 (98%)	52 (96%)	2 (4%)	41	76
33	Y8	54/55 (98%)	53 (98%)	1 (2%)	65	87
34	R9	34/34 (100%)	32 (94%)	2 (6%)	24	60
34	Y9	34/34 (100%)	33 (97%)	1 (3%)	50	81
36	QB	191/220 (87%)	181 (95%)	10 (5%)	29	65
36	XB	187/220 (85%)	171 (91%)	16 (9%)	13	45
37	QC	144/188 (77%)	141 (98%)	3 (2%)	61	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	XC	140/188 (74%)	134 (96%)	6 (4%)	35	72
38	QD	171/181 (94%)	163 (95%)	8 (5%)	32	70
38	XD	172/181 (95%)	163 (95%)	9 (5%)	29	65
39	QE	114/123 (93%)	111 (97%)	3 (3%)	54	83
39	XE	114/123 (93%)	110 (96%)	4 (4%)	43	78
40	QF	85/90 (94%)	78 (92%)	7 (8%)	14	47
40	XF	85/90 (94%)	79 (93%)	6 (7%)	18	54
41	QG	120/127 (94%)	117 (98%)	3 (2%)	55	84
41	XG	119/127 (94%)	115 (97%)	4 (3%)	44	79
42	QH	116/119 (98%)	112 (97%)	4 (3%)	44	79
42	XH	114/119 (96%)	112 (98%)	2 (2%)	66	88
43	QI	91/99 (92%)	83 (91%)	8 (9%)	12	43
43	XI	88/99 (89%)	83 (94%)	5 (6%)	25	62
44	QJ	68/92 (74%)	66 (97%)	2 (3%)	50	81
44	XJ	68/92 (74%)	68 (100%)	0	100	100
45	QK	83/99 (84%)	81 (98%)	2 (2%)	57	84
45	XK	83/99 (84%)	82 (99%)	1 (1%)	78	92
46	QL	96/108 (89%)	93 (97%)	3 (3%)	47	80
46	XL	96/108 (89%)	89 (93%)	7 (7%)	17	52
47	QM	90/101 (89%)	89 (99%)	1 (1%)	80	93
47	XM	87/101 (86%)	86 (99%)	1 (1%)	80	93
48	QN	49/50 (98%)	43 (88%)	6 (12%)	6	24
48	XN	49/50 (98%)	49 (100%)	0	100	100
49	QO	78/80 (98%)	76 (97%)	2 (3%)	54	83
49	XO	78/80 (98%)	75 (96%)	3 (4%)	40	76
50	QP	69/74 (93%)	66 (96%)	3 (4%)	35	72
50	XP	68/74 (92%)	62 (91%)	6 (9%)	12	43
51	QQ	94/97 (97%)	93 (99%)	1 (1%)	80	93
51	XQ	94/97 (97%)	90 (96%)	4 (4%)	35	72
52	QR	59/77 (77%)	54 (92%)	5 (8%)	13	45
52	XR	59/77 (77%)	56 (95%)	3 (5%)	29	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	QS	68/80 (85%)	65 (96%)	3 (4%)	35	71
53	XS	67/80 (84%)	65 (97%)	2 (3%)	48	81
54	QT	71/82 (87%)	71 (100%)	0	100	100
54	XT	70/82 (85%)	70 (100%)	0	100	100
55	QU	18/22 (82%)	17 (94%)	1 (6%)	26	62
55	XU	18/22 (82%)	18 (100%)	0	100	100
All	All	9971/10712 (93%)	9532 (96%)	439 (4%)	35	71

All (439) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	QY	17	ARG
3	QY	20	VAL
3	QY	26	ASP
3	QY	96	PHE
3	QY	123	TYR
3	QY	201	LEU
3	QY	203	ARG
3	QY	217	PHE
3	QY	223	TYR
3	QY	242	ASP
3	QY	253	HIS
3	QY	278	ARG
3	QY	322	GLN
3	QY	326	TYR
3	XY	8	ASN
3	XY	83	LEU
3	XY	96	PHE
3	XY	179	VAL
3	XY	201	LEU
3	XY	217	PHE
3	XY	223	TYR
3	XY	244	TYR
3	XY	273	GLN
3	XY	326	TYR
3	XY	332	ARG
3	XY	338	THR
6	YD	61	LEU
6	YD	84	TYR
6	YD	97	TYR

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Mol	Chain	Res	Type
6	YD	172	TYR
6	YD	242	ARG
6	YD	260	ARG
6	YD	276	LYS
7	YE	21	VAL
7	YE	44	TYR
7	YE	52	LEU
7	YE	73	GLU
7	YE	75	VAL
7	YE	111	ARG
7	YE	119	ARG
7	YE	178	GLU
8	YF	7	TYR
8	YF	88	VAL
8	YF	97	TYR
8	YF	99	TYR
8	YF	140	LEU
8	YF	162	LEU
8	YF	197	ASP
9	YG	5	VAL
9	YG	12	TYR
9	YG	49	ASP
9	YG	117	PHE
9	YG	140	ILE
10	YH	3	ARG
10	YH	7	LEU
10	YH	33	LEU
10	YH	69	ARG
10	YH	71	LEU
10	YH	163	TYR
10	YH	171	LEU
11	YI	47	LEU
11	YI	68	LEU
11	YI	114	LEU
12	YN	15	LEU
12	YN	51	PHE
12	YN	68	GLU
12	YN	78	TYR
12	YN	96	GLU
12	YN	120	LEU
12	YN	131	GLN
13	YO	8	LEU

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Mol	Chain	Res	Type
13	YO	10	VAL
13	YO	79	PHE
13	YO	111	PHE
14	YP	55	ARG
14	YP	80	TYR
14	YP	91	PHE
14	YP	92	GLU
14	YP	130	PHE
14	YP	148	LEU
15	YQ	32	TYR
15	YQ	65	PHE
15	YQ	93	TYR
15	YQ	104	PHE
15	YQ	141	GLN
16	YR	13	HIS
16	YR	44	LEU
17	YS	7	TYR
17	YS	20	ARG
17	YS	36	TYR
17	YS	48	LEU
17	YS	67	ARG
17	YS	80	LEU
17	YS	94	TYR
17	YS	112	PHE
18	YT	14	TYR
18	YT	22	PHE
18	YT	45	PHE
18	YT	53	ARG
18	YT	61	PHE
18	YT	78	LEU
18	YT	96	ARG
18	YT	101	PHE
19	YU	47	TYR
19	YU	60	LEU
19	YU	74	LEU
19	YU	76	TYR
19	YU	101	ARG
19	YU	104	GLN
19	YU	111	GLU
19	YU	112	ARG
20	YV	12	TYR
20	YV	51	VAL

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Mol	Chain	Res	Type
20	YV	61	VAL
20	YV	79	VAL
20	YV	95	LEU
21	YW	11	ARG
21	YW	17	VAL
21	YW	51	LEU
21	YW	67	ASP
21	YW	70	TYR
21	YW	75	TYR
23	YY	20	TYR
23	YY	23	ARG
23	YY	60	PHE
23	YY	89	PHE
24	YZ	3	TYR
24	YZ	8	TYR
24	YZ	41	LEU
24	YZ	44	PHE
24	YZ	145	GLU
24	YZ	181	GLU
25	Y0	14	ARG
25	Y0	60	PHE
25	Y0	69	PHE
25	Y0	78	TYR
26	Y1	43	TYR
26	Y1	60	PHE
26	Y1	71	TYR
26	Y1	95	LEU
27	Y2	7	ARG
27	Y2	12	GLU
27	Y2	66	GLU
28	Y3	23	LEU
28	Y3	54	VAL
29	Y4	25	TYR
29	Y4	34	GLU
29	Y4	43	TYR
29	Y4	48	ARG
29	Y4	59	PHE
29	Y4	63	TYR
29	Y4	67	TYR
30	Y5	19	ARG
30	Y5	35	GLU
30	Y5	48	GLU

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Mol	Chain	Res	Type
30	Y5	58	LEU
31	Y6	44	ARG
32	Y7	34	ARG
32	Y7	35	ARG
33	Y8	48	PHE
34	Y9	24	TYR
36	XB	17	PHE
36	XB	28	PHE
36	XB	44	LEU
36	XB	70	PHE
36	XB	78	GLN
36	XB	105	PHE
36	XB	111	ARG
36	XB	115	LEU
36	XB	126	GLU
36	XB	130	ARG
36	XB	155	LEU
36	XB	170	GLU
36	XB	181	PHE
36	XB	217	ARG
36	XB	221	LEU
36	XB	224	GLN
37	XC	29	TYR
37	XC	32	LEU
37	XC	54	ARG
37	XC	105	GLU
37	XC	131	ARG
37	XC	178	LEU
38	XD	27	TYR
38	XD	34	GLU
38	XD	58	LEU
38	XD	59	ARG
38	XD	68	TYR
38	XD	106	TYR
38	XD	138	TYR
38	XD	185	PHE
38	XD	200	GLU
39	XE	28	PHE
39	XE	41	VAL
39	XE	71	LEU
39	XE	137	GLU
40	XF	10	LEU

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Mol	Chain	Res	Type
40	XF	59	TYR
40	XF	60	PHE
40	XF	63	TYR
40	XF	75	LEU
40	XF	97	PHE
41	XG	10	ARG
41	XG	16	LEU
41	XG	18	TYR
41	XG	52	GLU
42	XH	2	LEU
42	XH	65	TYR
43	XI	33	PHE
43	XI	59	PHE
43	XI	60	ASP
43	XI	88	TYR
43	XI	101	PHE
45	XK	96	ARG
46	XL	32	PHE
46	XL	52	LEU
46	XL	60	LEU
46	XL	64	TYR
46	XL	84	LEU
46	XL	86	ARG
46	XL	114	LYS
47	XM	69	GLU
49	XO	6	GLU
49	XO	54	ARG
49	XO	64	ARG
50	XP	9	PHE
50	XP	16	HIS
50	XP	17	TYR
50	XP	20	VAL
50	XP	25	ARG
50	XP	71	ARG
51	XQ	26	GLN
51	XQ	27	PHE
51	XQ	42	TYR
51	XQ	71	PHE
52	XR	31	LEU
52	XR	34	TYR
52	XR	85	LEU
53	XS	10	PHE

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Mol	Chain	Res	Type
53	XS	78	ARG
36	QB	17	PHE
36	QB	21	ARG
36	QB	70	PHE
36	QB	111	ARG
36	QB	122	PHE
36	QB	145	LEU
36	QB	155	LEU
36	QB	160	ASP
36	QB	170	GLU
36	QB	191	ASP
37	QC	29	TYR
37	QC	178	LEU
37	QC	201	TYR
38	QD	20	TYR
38	QD	27	TYR
38	QD	59	ARG
38	QD	68	TYR
38	QD	138	TYR
38	QD	185	PHE
38	QD	188	LEU
38	QD	200	GLU
39	QE	28	PHE
39	QE	41	VAL
39	QE	69	VAL
40	QF	4	TYR
40	QF	10	LEU
40	QF	59	TYR
40	QF	60	PHE
40	QF	63	TYR
40	QF	73	ASN
40	QF	75	LEU
41	QG	16	LEU
41	QG	18	TYR
41	QG	90	GLU
42	QH	14	ARG
42	QH	18	ARG
42	QH	48	TYR
42	QH	91	ARG
43	QI	3	GLN
43	QI	33	PHE
43	QI	42	ARG

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Mol	Chain	Res	Type
43	QI	56	LEU
43	QI	59	PHE
43	QI	64	THR
43	QI	88	TYR
43	QI	93	ARG
44	QJ	38	ILE
44	QJ	84	GLN
45	QK	54	ARG
45	QK	75	TYR
46	QL	60	LEU
46	QL	98	TYR
46	QL	120	TYR
47	QM	69	GLU
48	QN	3	ARG
48	QN	18	VAL
48	QN	21	TYR
48	QN	31	ARG
48	QN	36	PHE
48	QN	41	ARG
49	QO	6	GLU
49	QO	15	PHE
50	QP	9	PHE
50	QP	20	VAL
50	QP	38	TYR
51	QQ	42	TYR
52	QR	34	TYR
52	QR	42	ARG
52	QR	43	PHE
52	QR	76	LEU
52	QR	85	LEU
53	QS	10	PHE
53	QS	41	VAL
53	QS	74	PHE
55	QU	18	TYR
6	RD	97	TYR
6	RD	172	TYR
6	RD	176	ARG
6	RD	193	VAL
6	RD	221	VAL
6	RD	242	ARG
6	RD	260	ARG
6	RD	269	PHE

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Mol	Chain	Res	Type
7	RE	9	VAL
7	RE	33	VAL
7	RE	40	GLU
7	RE	44	TYR
7	RE	73	GLU
7	RE	75	VAL
8	RF	7	TYR
8	RF	20	LEU
8	RF	24	LEU
8	RF	38	ARG
8	RF	88	VAL
8	RF	97	TYR
8	RF	99	TYR
8	RF	140	LEU
8	RF	162	LEU
8	RF	168	ARG
8	RF	197	ASP
9	RG	12	TYR
9	RG	45	GLU
9	RG	53	LEU
9	RG	82	LEU
9	RG	180	PHE
10	RH	69	ARG
10	RH	101	ARG
10	RH	105	LEU
10	RH	163	TYR
11	RI	47	LEU
11	RI	68	LEU
11	RI	75	LEU
11	RI	85	GLU
11	RI	89	TYR
11	RI	116	LEU
12	RN	15	LEU
12	RN	51	PHE
12	RN	78	TYR
12	RN	120	LEU
12	RN	131	GLN
13	RO	8	LEU
13	RO	10	VAL
13	RO	68	GLU
13	RO	79	PHE
14	RP	55	ARG

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Mol	Chain	Res	Type
14	RP	80	TYR
14	RP	119	GLU
14	RP	130	PHE
15	RQ	32	TYR
15	RQ	65	PHE
15	RQ	69	PHE
15	RQ	93	TYR
16	RR	47	PHE
17	RS	7	TYR
17	RS	36	TYR
17	RS	80	LEU
17	RS	112	PHE
18	RT	6	LEU
18	RT	45	PHE
18	RT	49	VAL
18	RT	53	ARG
18	RT	61	PHE
18	RT	68	TYR
18	RT	78	LEU
18	RT	96	ARG
18	RT	101	PHE
19	RU	36	ARG
19	RU	47	TYR
19	RU	60	LEU
19	RU	74	LEU
19	RU	76	TYR
19	RU	92	ARG
19	RU	95	LEU
19	RU	104	GLN
19	RU	111	GLU
20	RV	12	TYR
20	RV	43	GLU
20	RV	72	VAL
20	RV	75	PHE
20	RV	79	VAL
21	RW	11	ARG
21	RW	17	VAL
21	RW	51	LEU
21	RW	67	ASP
21	RW	70	TYR
22	RX	28	PHE
22	RX	57	LEU

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Mol	Chain	Res	Type
23	RY	20	TYR
23	RY	29	GLU
23	RY	55	TYR
23	RY	60	PHE
23	RY	89	PHE
23	RY	90	LEU
24	RZ	3	TYR
24	RZ	8	TYR
24	RZ	41	LEU
24	RZ	103	ARG
24	RZ	136	PHE
24	RZ	145	GLU
24	RZ	150	LEU
24	RZ	161	VAL
24	RZ	185	GLU
25	R0	14	ARG
25	R0	55	ARG
25	R0	60	PHE
25	R0	78	TYR
26	R1	60	PHE
26	R1	71	TYR
26	R1	95	LEU
29	R4	25	TYR
29	R4	43	TYR
29	R4	49	PHE
29	R4	67	TYR
31	R6	50	ARG
32	R7	47	ARG
33	R8	13	ARG
33	R8	48	PHE
34	R9	24	TYR
34	R9	35	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
3	XY	214	HIS
3	XY	280	GLN
3	XY	281	HIS
11	YI	54	GLN
15	YQ	57	HIS
24	YZ	121	HIS

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Mol	Chain	Res	Type
26	Y1	56	GLN
27	Y2	9	GLN
36	XB	40	HIS
36	XB	78	GLN
36	XB	113	HIS
40	XF	73	ASN
42	XH	78	GLN
42	XH	82	HIS
43	XI	124	GLN
45	XK	116	HIS
36	QB	76	GLN
36	QB	78	GLN
36	QB	113	HIS
37	QC	69	HIS
40	QF	73	ASN
42	QH	82	HIS
43	QI	124	GLN
45	QK	116	HIS
6	RD	96	HIS
7	RE	48	GLN
8	RF	75	HIS
14	RP	27	HIS
21	RW	60	ASN
26	R1	56	GLN
27	R2	9	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	QV	76/77 (98%)	17 (22%)	1 (1%)
1	XV	76/77 (98%)	16 (21%)	1 (1%)
2	QX	9/25 (36%)	3 (33%)	0
2	XX	9/25 (36%)	4 (44%)	0
35	QA	1494/1521 (98%)	229 (15%)	14 (0%)
35	XA	1498/1521 (98%)	226 (15%)	18 (1%)
4	RA	2855/2915 (97%)	452 (15%)	28 (0%)
4	YA	2855/2915 (97%)	457 (16%)	26 (0%)
5	RB	119/122 (97%)	9 (7%)	0
5	YB	119/122 (97%)	14 (11%)	0
All	All	9110/9320 (97%)	1427 (15%)	88 (0%)

All (1427) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	QV	4	G
1	QV	5	G
1	QV	6	G
1	QV	9	G
1	QV	16	C
1	QV	17(A)	U
1	QV	18	G
1	QV	19	G
1	QV	21	A
1	QV	31	G
1	QV	47	U
1	QV	48	C
1	QV	53	G
1	QV	54	U
1	QV	67	C
1	QV	75	C
1	QV	76	A
2	QX	21	A
2	QX	22	C
2	QX	23	A
1	XV	4	G
1	XV	5	G
1	XV	6	G
1	XV	17(A)	U
1	XV	18	G
1	XV	19	G
1	XV	21	A
1	XV	31	G
1	XV	47	U
1	XV	48	C
1	XV	53	G
1	XV	54	U
1	XV	62	C
1	XV	64	G
1	XV	67	C
1	XV	76	A
2	XX	15	A
2	XX	21	A
2	XX	22	C
2	XX	23	A
4	YA	8	A
4	YA	10	G
4	YA	11	G

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Mol	Chain	Res	Type
4	YA	12	U
4	YA	15	G
4	YA	34	C
4	YA	45	C
4	YA	71	A
4	YA	74	A
4	YA	75	G
4	YA	84	A
4	YA	95	G
4	YA	102	G
4	YA	118	A
4	YA	119	A
4	YA	120	U
4	YA	131	G
4	YA	141	A
4	YA	157	U
4	YA	181	A
4	YA	182	A
4	YA	196	A
4	YA	199	A
4	YA	205	G
4	YA	215	G
4	YA	216	A
4	YA	221	A
4	YA	222	A
4	YA	229	A
4	YA	230	U
4	YA	248	G
4	YA	266	G
4	YA	272(K)	U
4	YA	272(L)	U
4	YA	272(M)	G
4	YA	272(N)	U
4	YA	272(O)	C
4	YA	272(P)	C
4	YA	273(B)	U
4	YA	273(C)	G
4	YA	277	C
4	YA	278	A
4	YA	311	A
4	YA	327	G
4	YA	329	G

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Mol	Chain	Res	Type
4	YA	330	A
4	YA	352	G
4	YA	362	U
4	YA	363(A)	G
4	YA	372	G
4	YA	386	G
4	YA	396	G
4	YA	405	U
4	YA	411	G
4	YA	412	A
4	YA	428	A
4	YA	444	C
4	YA	455	C
4	YA	456	C
4	YA	457	A
4	YA	470	A
4	YA	481	G
4	YA	505	A
4	YA	508	G
4	YA	509	C
4	YA	530	G
4	YA	531	C
4	YA	532	A
4	YA	533	G
4	YA	545	G
4	YA	563	G
4	YA	568	U
4	YA	573	G
4	YA	575	A
4	YA	603	A
4	YA	604	G
4	YA	607	U
4	YA	614(C)	G
4	YA	615	G
4	YA	627	A
4	YA	637	A
4	YA	645	C
4	YA	646	A
4	YA	652(C)	A
4	YA	652(D)	G
4	YA	652(V)	G
4	YA	653	A

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Mol	Chain	Res	Type
4	YA	668	G
4	YA	669	G
4	YA	686	G
4	YA	717	G
4	YA	730	C
4	YA	752	A
4	YA	753	C
4	YA	764	A
4	YA	775	G
4	YA	776	G
4	YA	782	A
4	YA	784	A
4	YA	785	G
4	YA	792	G
4	YA	805	G
4	YA	812	C
4	YA	827	U
4	YA	828	U
4	YA	857	C
4	YA	859	G
4	YA	877	U
4	YA	880	G
4	YA	886	C
4	YA	887	A
4	YA	888	C
4	YA	889	C
4	YA	890	A
4	YA	893	C
4	YA	895	U
4	YA	896	A
4	YA	897	C
4	YA	900	A
4	YA	901	A
4	YA	907	U
4	YA	910	A
4	YA	917	A
4	YA	932	G
4	YA	941	A
4	YA	945	A
4	YA	946	G
4	YA	953	A
4	YA	959	A

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Mol	Chain	Res	Type
4	YA	961	C
4	YA	974	G
4	YA	975(A)	C
4	YA	983	A
4	YA	996	A
4	YA	1012	U
4	YA	1013	C
4	YA	1017	G
4	YA	1026	U
4	YA	1033	U
4	YA	1041	C
4	YA	1045	A
4	YA	1046	A
4	YA	1047	G
4	YA	1048	A
4	YA	1052	C
4	YA	1053	C
4	YA	1054	A
4	YA	1058	G
4	YA	1060	U
4	YA	1063	G
4	YA	1064	C
4	YA	1065	U
4	YA	1066	U
4	YA	1067	A
4	YA	1068	G
4	YA	1069	A
4	YA	1070	A
4	YA	1071	G
4	YA	1072	C
4	YA	1073	A
4	YA	1074	G
4	YA	1076	C
4	YA	1077	A
4	YA	1078	U
4	YA	1079	C
4	YA	1082	U
4	YA	1083	U
4	YA	1084	A
4	YA	1085	A
4	YA	1086	A
4	YA	1088	A

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Mol	Chain	Res	Type
4	YA	1090	U
4	YA	1091	G
4	YA	1092	C
4	YA	1093	G
4	YA	1094	U
4	YA	1096	A
4	YA	1098	A
4	YA	1109	C
4	YA	1110	G
4	YA	1112	G
4	YA	1116	C
4	YA	1117	G
4	YA	1128	A
4	YA	1129	A
4	YA	1130	U
4	YA	1135	C
4	YA	1136	G
4	YA	1171	G
4	YA	1188	U
4	YA	1211	U
4	YA	1212	G
4	YA	1220	A
4	YA	1229	G
4	YA	1236	G
4	YA	1253	A
4	YA	1256	G
4	YA	1271	G
4	YA	1272	A
4	YA	1273	U
4	YA	1300	U
4	YA	1301	A
4	YA	1306	C
4	YA	1314	C
4	YA	1352	U
4	YA	1359	A
4	YA	1360	A
4	YA	1365	A
4	YA	1368	G
4	YA	1380	G
4	YA	1384	A
4	YA	1385	G
4	YA	1386	C

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Mol	Chain	Res	Type
4	YA	1416	G
4	YA	1417	C
4	YA	1421	G
4	YA	1428	C
4	YA	1445(A)	A
4	YA	1450(A)	G
4	YA	1451	C
4	YA	1455	G
4	YA	1459	G
4	YA	1467	C
4	YA	1471	A
4	YA	1482	G
4	YA	1493	C
4	YA	1494	A
4	YA	1497	U
4	YA	1508	A
4	YA	1509(A)	C
4	YA	1509(B)	A
4	YA	1531	C
4	YA	1542	A
4	YA	1543	C
4	YA	1547	C
4	YA	1558	A
4	YA	1566	A
4	YA	1569	A
4	YA	1578	U
4	YA	1580	A
4	YA	1584	C
4	YA	1586	A
4	YA	1608	A
4	YA	1609	A
4	YA	1610	A
4	YA	1640	C
4	YA	1647	G
4	YA	1648	C
4	YA	1674	G
4	YA	1696	G
4	YA	1700	A
4	YA	1701	A
4	YA	1721	G
4	YA	1722	A
4	YA	1750	G

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Mol	Chain	Res	Type
4	YA	1756	G
4	YA	1762	A
4	YA	1763	G
4	YA	1764	G
4	YA	1773	A
4	YA	1780	A
4	YA	1782	C
4	YA	1786	A
4	YA	1791	A
4	YA	1800	C
4	YA	1801	G
4	YA	1816	G
4	YA	1835	G
4	YA	1839	G
4	YA	1847	A
4	YA	1848	A
4	YA	1877	A
4	YA	1878	G
4	YA	1889	A
4	YA	1900	A
4	YA	1906	G
4	YA	1913	A
4	YA	1914	C
4	YA	1915	5MU
4	YA	1929	G
4	YA	1930	G
4	YA	1936	A
4	YA	1937	A
4	YA	1938	A
4	YA	1955	U
4	YA	1963	U
4	YA	1967	C
4	YA	1970	A
4	YA	1971	A
4	YA	1972	A
4	YA	1992	G
4	YA	1993	U
4	YA	1997	G
4	YA	2020	A
4	YA	2023	G
4	YA	2031	A
4	YA	2032	G

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Mol	Chain	Res	Type
4	YA	2033	A
4	YA	2043	C
4	YA	2055	C
4	YA	2056	G
4	YA	2060	A
4	YA	2061	G
4	YA	2062	A
4	YA	2069	G
4	YA	2096	U
4	YA	2098	U
4	YA	2099	U
4	YA	2103	C
4	YA	2104	G
4	YA	2105	C
4	YA	2107	C
4	YA	2108	C
4	YA	2109	U
4	YA	2110	G
4	YA	2111	C
4	YA	2112	G
4	YA	2115	G
4	YA	2116	G
4	YA	2117	A
4	YA	2118	U
4	YA	2119	A
4	YA	2121	G
4	YA	2123	G
4	YA	2126	A
4	YA	2127	G
4	YA	2128	C
4	YA	2129	C
4	YA	2130	U
4	YA	2131	G
4	YA	2132	U
4	YA	2133	G
4	YA	2134	A
4	YA	2135	A
4	YA	2136	C
4	YA	2141	G
4	YA	2145	C
4	YA	2146	C
4	YA	2147	G

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Mol	Chain	Res	Type
4	YA	2148	G
4	YA	2151	G
4	YA	2154	G
4	YA	2157	G
4	YA	2158	A
4	YA	2159	G
4	YA	2161	C
4	YA	2163	C
4	YA	2164	C
4	YA	2165	G
4	YA	2167	U
4	YA	2172	U
4	YA	2173	A
4	YA	2174	C
4	YA	2177	C
4	YA	2180	U
4	YA	2184	G
4	YA	2186	G
4	YA	2189	U
4	YA	2192	G
4	YA	2198	A
4	YA	2206	G
4	YA	2207	G
4	YA	2208	A
4	YA	2218	U
4	YA	2225	A
4	YA	2238	G
4	YA	2239	G
4	YA	2268	A
4	YA	2269	A
4	YA	2275	C
4	YA	2279	G
4	YA	2283	C
4	YA	2287	A
4	YA	2289	G
4	YA	2292	C
4	YA	2305	A
4	YA	2308	G
4	YA	2309	A
4	YA	2312	U
4	YA	2319	G
4	YA	2320	A

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Mol	Chain	Res	Type
4	YA	2321	G
4	YA	2322	A
4	YA	2325	G
4	YA	2334	G
4	YA	2335	A
4	YA	2336	A
4	YA	2343	C
4	YA	2347	C
4	YA	2350	C
4	YA	2354	G
4	YA	2383	G
4	YA	2385	C
4	YA	2406	U
4	YA	2410	G
4	YA	2422	A
4	YA	2424	C
4	YA	2425	A
4	YA	2429	G
4	YA	2430	A
4	YA	2435	A
4	YA	2439	A
4	YA	2441	C
4	YA	2448	A
4	YA	2468	G
4	YA	2474	C
4	YA	2476	A
4	YA	2478	A
4	YA	2498	C
4	YA	2502	G
4	YA	2504	U
4	YA	2505	G
4	YA	2506	U
4	YA	2518	A
4	YA	2529	G
4	YA	2554	U
4	YA	2566	A
4	YA	2567	G
4	YA	2573	C
4	YA	2582	G
4	YA	2585	U
4	YA	2586	C
4	YA	2602	A

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Mol	Chain	Res	Type
4	YA	2611	U
4	YA	2612	C
4	YA	2615	U
4	YA	2629	A
4	YA	2630	G
4	YA	2654	A
4	YA	2663	G
4	YA	2689	U
4	YA	2690	C
4	YA	2691	C
4	YA	2702	U
4	YA	2703	C
4	YA	2712(B)	A
4	YA	2713	A
4	YA	2714	G
4	YA	2726	U
4	YA	2733	A
4	YA	2744	G
4	YA	2757	A
4	YA	2758	A
4	YA	2764	A
4	YA	2765	A
4	YA	2766	G
4	YA	2769	C
4	YA	2778	A
4	YA	2818	G
4	YA	2820	A
4	YA	2821	A
4	YA	2833	G
4	YA	2835	A
4	YA	2872	G
4	YA	2880	C
4	YA	2894	G
4	YA	2897	U
5	YB	2	C
5	YB	8	U
5	YB	9	G
5	YB	13	A
5	YB	30	C
5	YB	33	G
5	YB	51	G
5	YB	56	G

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Mol	Chain	Res	Type
5	YB	73	A
5	YB	84	C
5	YB	106	G
5	YB	108	U
5	YB	109	C
5	YB	110	G
35	XA	5	U
35	XA	9	G
35	XA	22	G
35	XA	32	A
35	XA	39	G
35	XA	47	C
35	XA	48	C
35	XA	50	A
35	XA	51	A
35	XA	61	G
35	XA	66	G
35	XA	78	G
35	XA	89	C
35	XA	116	A
35	XA	121	C
35	XA	131	C
35	XA	151	A
35	XA	163	C
35	XA	173	U
35	XA	174	C
35	XA	182	U
35	XA	189(G)	U
35	XA	195	A
35	XA	197	A
35	XA	202	U
35	XA	203	U
35	XA	204	U
35	XA	216	G
35	XA	247	G
35	XA	251	G
35	XA	258	G
35	XA	266	G
35	XA	267	C
35	XA	289	G
35	XA	298	A
35	XA	321	A

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Mol	Chain	Res	Type
35	XA	328	C
35	XA	332	G
35	XA	351	G
35	XA	352	C
35	XA	353	A
35	XA	354	G
35	XA	367	U
35	XA	372	C
35	XA	381	C
35	XA	384	G
35	XA	397	A
35	XA	398	C
35	XA	406	G
35	XA	412	A
35	XA	413	G
35	XA	424	G
35	XA	429	U
35	XA	439	A
35	XA	442	C
35	XA	452	A
35	XA	458	C
35	XA	461	A
35	XA	470	C
35	XA	476	G
35	XA	482	A
35	XA	484	G
35	XA	485	G
35	XA	496	A
35	XA	498	U
35	XA	505	G
35	XA	509	A
35	XA	510	A
35	XA	511	C
35	XA	518	C
35	XA	528	C
35	XA	532	A
35	XA	533	A
35	XA	547	A
35	XA	559	A
35	XA	561	U
35	XA	572	A
35	XA	573	A

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Mol	Chain	Res	Type
35	XA	576	G
35	XA	577	G
35	XA	596	C
35	XA	630	G
35	XA	631	G
35	XA	632	A
35	XA	653	A
35	XA	665	A
35	XA	687	A
35	XA	688	G
35	XA	695	A
35	XA	707	C
35	XA	723	U
35	XA	724	G
35	XA	731	G
35	XA	749	C
35	XA	753	A
35	XA	755	G
35	XA	774	G
35	XA	777	A
35	XA	793	U
35	XA	794	A
35	XA	815	A
35	XA	817	C
35	XA	821	G
35	XA	828	A
35	XA	829	G
35	XA	836	G
35	XA	840	C
35	XA	841	U
35	XA	848	C
35	XA	851	G
35	XA	859	A
35	XA	902	G
35	XA	914	A
35	XA	916	G
35	XA	926	G
35	XA	927	G
35	XA	931	C
35	XA	934	C
35	XA	960	U
35	XA	961	U

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Mol	Chain	Res	Type
35	XA	968	A
35	XA	969	A
35	XA	971	G
35	XA	974	A
35	XA	975	A
35	XA	976	G
35	XA	977	A
35	XA	989	C
35	XA	992	U
35	XA	993	G
35	XA	994	A
35	XA	1004	A
35	XA	1005	A
35	XA	1006	C
35	XA	1009	G
35	XA	1016	A
35	XA	1020	U
35	XA	1022	G
35	XA	1023	G
35	XA	1025	U
35	XA	1026	G
35	XA	1027	C
35	XA	1028	C
35	XA	1029	C
35	XA	1030(B)	G
35	XA	1030(C)	C
35	XA	1033	G
35	XA	1041	A
35	XA	1044	A
35	XA	1047	G
35	XA	1054	C
35	XA	1055	A
35	XA	1065	U
35	XA	1066	C
35	XA	1068	G
35	XA	1081	G
35	XA	1094	G
35	XA	1095	U
35	XA	1101	A
35	XA	1117	G
35	XA	1125	U
35	XA	1129	C

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Mol	Chain	Res	Type
35	XA	1130	A
35	XA	1132	C
35	XA	1134	G
35	XA	1136	U
35	XA	1137	C
35	XA	1138	G
35	XA	1139	G
35	XA	1147	C
35	XA	1152	A
35	XA	1157	A
35	XA	1159	U
35	XA	1162	C
35	XA	1183	A
35	XA	1184	G
35	XA	1196	U
35	XA	1197	G
35	XA	1211	U
35	XA	1213	A
35	XA	1224	G
35	XA	1227	A
35	XA	1228	C
35	XA	1236	A
35	XA	1238	A
35	XA	1250	A
35	XA	1256	A
35	XA	1257	U
35	XA	1258	G
35	XA	1260	C
35	XA	1270	C
35	XA	1272	G
35	XA	1278	U
35	XA	1279	A
35	XA	1280	A
35	XA	1281	U
35	XA	1282	C
35	XA	1286	A
35	XA	1287	A
35	XA	1300	G
35	XA	1305	G
35	XA	1317	C
35	XA	1320	C
35	XA	1340	A

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Mol	Chain	Res	Type
35	XA	1346	A
35	XA	1347	G
35	XA	1353	G
35	XA	1363(A)	C
35	XA	1370	G
35	XA	1380	U
35	XA	1397	C
35	XA	1419	G
35	XA	1442(A)	G
35	XA	1442(B)	G
35	XA	1446	U
35	XA	1447	A
35	XA	1491	G
35	XA	1492	A
35	XA	1497	G
35	XA	1503	A
35	XA	1504	G
35	XA	1506	U
35	XA	1517	G
35	XA	1520	G
35	XA	1529	G
35	XA	1530	G
35	QA	7	G
35	QA	9	G
35	QA	32	A
35	QA	39	G
35	QA	47	C
35	QA	48	C
35	QA	51	A
35	QA	61	G
35	QA	78	G
35	QA	79	G
35	QA	96	U
35	QA	101	A
35	QA	116	A
35	QA	121	C
35	QA	131	C
35	QA	144	G
35	QA	156	G
35	QA	163	C
35	QA	173	U
35	QA	174	C

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Mol	Chain	Res	Type
35	QA	182	U
35	QA	189(G)	U
35	QA	195	A
35	QA	197	A
35	QA	201	C
35	QA	202	U
35	QA	203	U
35	QA	204	U
35	QA	216	G
35	QA	220	G
35	QA	247	G
35	QA	251	G
35	QA	258	G
35	QA	266	G
35	QA	267	C
35	QA	289	G
35	QA	321	A
35	QA	328	C
35	QA	332	G
35	QA	348	G
35	QA	352	C
35	QA	353	A
35	QA	354	G
35	QA	367	U
35	QA	372	C
35	QA	373	A
35	QA	384	G
35	QA	397	A
35	QA	398	C
35	QA	406	G
35	QA	412	A
35	QA	413	G
35	QA	423	G
35	QA	424	G
35	QA	429	U
35	QA	439	A
35	QA	442	C
35	QA	452	A
35	QA	458	C
35	QA	461	A
35	QA	470	C
35	QA	475	G

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Mol	Chain	Res	Type
35	QA	477	A
35	QA	484	G
35	QA	485	G
35	QA	496	A
35	QA	498	U
35	QA	505	G
35	QA	509	A
35	QA	510	A
35	QA	511	C
35	QA	518	C
35	QA	521	G
35	QA	524	G
35	QA	531	U
35	QA	532	A
35	QA	547	A
35	QA	550	G
35	QA	559	A
35	QA	561	U
35	QA	564	C
35	QA	572	A
35	QA	573	A
35	QA	576	G
35	QA	577	G
35	QA	596	C
35	QA	607	A
35	QA	618	C
35	QA	619	U
35	QA	630	G
35	QA	632	A
35	QA	653	A
35	QA	661	G
35	QA	665	A
35	QA	687	A
35	QA	688	G
35	QA	723	U
35	QA	731	G
35	QA	755	G
35	QA	774	G
35	QA	777	A
35	QA	793	U
35	QA	794	A
35	QA	816	A

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Mol	Chain	Res	Type
35	QA	817	C
35	QA	821	G
35	QA	828	A
35	QA	829	G
35	QA	839	U
35	QA	840	C
35	QA	841	U
35	QA	851	G
35	QA	902	G
35	QA	914	A
35	QA	926	G
35	QA	927	G
35	QA	934	C
35	QA	935	A
35	QA	942	G
35	QA	960	U
35	QA	961	U
35	QA	968	A
35	QA	969	A
35	QA	971	G
35	QA	974	A
35	QA	975	A
35	QA	976	G
35	QA	977	A
35	QA	992	U
35	QA	993	G
35	QA	998	G
35	QA	999	C
35	QA	1001(B)	G
35	QA	1006	C
35	QA	1007	C
35	QA	1008	C
35	QA	1009	G
35	QA	1022	G
35	QA	1023	G
35	QA	1024	G
35	QA	1025	U
35	QA	1026	G
35	QA	1027	C
35	QA	1028	C
35	QA	1029	C
35	QA	1030(B)	G

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Mol	Chain	Res	Type
35	QA	1030(C)	C
35	QA	1030(E)	A
35	QA	1032	G
35	QA	1033	G
35	QA	1034	G
35	QA	1037	C
35	QA	1039	C
35	QA	1042	G
35	QA	1044	A
35	QA	1065	U
35	QA	1066	C
35	QA	1068	G
35	QA	1070	U
35	QA	1081	G
35	QA	1094	G
35	QA	1095	U
35	QA	1101	A
35	QA	1126	U
35	QA	1130	A
35	QA	1132	C
35	QA	1134	G
35	QA	1136	U
35	QA	1137	C
35	QA	1138	G
35	QA	1139	G
35	QA	1140	C
35	QA	1146	A
35	QA	1152	A
35	QA	1159	U
35	QA	1162	C
35	QA	1168	A
35	QA	1183	A
35	QA	1184	G
35	QA	1196	U
35	QA	1197	G
35	QA	1202	G
35	QA	1208	C
35	QA	1212	U
35	QA	1213	A
35	QA	1224	G
35	QA	1227	A
35	QA	1238	A

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Mol	Chain	Res	Type
35	QA	1245	A
35	QA	1256	A
35	QA	1257	U
35	QA	1258	G
35	QA	1270	C
35	QA	1278	U
35	QA	1280	A
35	QA	1286	A
35	QA	1287	A
35	QA	1293	G
35	QA	1299	A
35	QA	1300	G
35	QA	1302	U
35	QA	1320	C
35	QA	1338	G
35	QA	1340	A
35	QA	1346	A
35	QA	1347	G
35	QA	1353	G
35	QA	1363(A)	C
35	QA	1370	G
35	QA	1397	C
35	QA	1419	G
35	QA	1442(A)	G
35	QA	1442(B)	G
35	QA	1447	A
35	QA	1456	G
35	QA	1491	G
35	QA	1492	A
35	QA	1493	A
35	QA	1494	G
35	QA	1499	A
35	QA	1503	A
35	QA	1504	G
35	QA	1505	G
35	QA	1506	U
35	QA	1517	G
35	QA	1520	G
35	QA	1529	G
35	QA	1530	G
35	QA	1531	A
4	RA	8	A

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Mol	Chain	Res	Type
4	RA	10	G
4	RA	11	G
4	RA	12	U
4	RA	15	G
4	RA	34	C
4	RA	45	C
4	RA	71	A
4	RA	74	A
4	RA	75	G
4	RA	84	A
4	RA	102	G
4	RA	118	A
4	RA	120	U
4	RA	131	G
4	RA	141	A
4	RA	157	U
4	RA	182	A
4	RA	196	A
4	RA	199	A
4	RA	205	G
4	RA	214	G
4	RA	215	G
4	RA	216	A
4	RA	221	A
4	RA	222	A
4	RA	229	A
4	RA	230	U
4	RA	248	G
4	RA	272(K)	U
4	RA	272(L)	U
4	RA	272(M)	G
4	RA	272(N)	U
4	RA	272(O)	C
4	RA	273(B)	U
4	RA	273(C)	G
4	RA	277	C
4	RA	278	A
4	RA	311	A
4	RA	317	G
4	RA	324	A
4	RA	329	G
4	RA	330	A

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Mol	Chain	Res	Type
4	RA	352	G
4	RA	362	U
4	RA	363(A)	G
4	RA	372	G
4	RA	386	G
4	RA	396	G
4	RA	405	U
4	RA	411	G
4	RA	412	A
4	RA	428	A
4	RA	444	C
4	RA	454	A
4	RA	455	C
4	RA	456	C
4	RA	457	A
4	RA	470	A
4	RA	481	G
4	RA	505	A
4	RA	508	G
4	RA	509	C
4	RA	530	G
4	RA	531	C
4	RA	532	A
4	RA	533	G
4	RA	545	G
4	RA	563	G
4	RA	568	U
4	RA	573	G
4	RA	575	A
4	RA	603	A
4	RA	604	G
4	RA	607	U
4	RA	614(C)	G
4	RA	615	G
4	RA	627	A
4	RA	637	A
4	RA	645	C
4	RA	646	A
4	RA	652(C)	A
4	RA	652(D)	G
4	RA	652(V)	G
4	RA	653	A

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Mol	Chain	Res	Type
4	RA	668	G
4	RA	669	G
4	RA	686	G
4	RA	730	C
4	RA	752	A
4	RA	753	C
4	RA	775	G
4	RA	776	G
4	RA	782	A
4	RA	784	A
4	RA	785	G
4	RA	792	G
4	RA	805	G
4	RA	812	C
4	RA	827	U
4	RA	857	C
4	RA	859	G
4	RA	877	U
4	RA	880	G
4	RA	886	C
4	RA	887	A
4	RA	888	C
4	RA	889	C
4	RA	890	A
4	RA	893	C
4	RA	895	U
4	RA	896	A
4	RA	897	C
4	RA	900	A
4	RA	901	A
4	RA	910	A
4	RA	915	C
4	RA	917	A
4	RA	931	G
4	RA	932	G
4	RA	936	C
4	RA	941	A
4	RA	945	A
4	RA	946	G
4	RA	953	A
4	RA	959	A
4	RA	961	C

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Mol	Chain	Res	Type
4	RA	974	G
4	RA	975(A)	C
4	RA	983	A
4	RA	996	A
4	RA	1012	U
4	RA	1013	C
4	RA	1015	G
4	RA	1017	G
4	RA	1026	U
4	RA	1033	U
4	RA	1045	A
4	RA	1046	A
4	RA	1047	G
4	RA	1048	A
4	RA	1052	C
4	RA	1053	C
4	RA	1054	A
4	RA	1058	G
4	RA	1060	U
4	RA	1063	G
4	RA	1064	C
4	RA	1065	U
4	RA	1066	U
4	RA	1067	A
4	RA	1068	G
4	RA	1069	A
4	RA	1070	A
4	RA	1071	G
4	RA	1072	C
4	RA	1073	A
4	RA	1074	G
4	RA	1076	C
4	RA	1077	A
4	RA	1078	U
4	RA	1079	C
4	RA	1080	C
4	RA	1082	U
4	RA	1083	U
4	RA	1084	A
4	RA	1085	A
4	RA	1086	A
4	RA	1088	A

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Mol	Chain	Res	Type
4	RA	1090	U
4	RA	1091	G
4	RA	1092	C
4	RA	1093	G
4	RA	1094	U
4	RA	1096	A
4	RA	1098	A
4	RA	1109	C
4	RA	1110	G
4	RA	1112	G
4	RA	1116	C
4	RA	1117	G
4	RA	1129	A
4	RA	1130	U
4	RA	1135	C
4	RA	1136	G
4	RA	1171	G
4	RA	1211	U
4	RA	1212	G
4	RA	1220	A
4	RA	1229	G
4	RA	1253	A
4	RA	1256	G
4	RA	1271	G
4	RA	1272	A
4	RA	1273	U
4	RA	1300	U
4	RA	1301	A
4	RA	1314	C
4	RA	1342	A
4	RA	1352	U
4	RA	1359	A
4	RA	1360	A
4	RA	1365	A
4	RA	1368	G
4	RA	1380	G
4	RA	1384	A
4	RA	1385	G
4	RA	1386	C
4	RA	1416	G
4	RA	1417	C
4	RA	1421	G

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Mol	Chain	Res	Type
4	RA	1428	C
4	RA	1445(A)	A
4	RA	1450(A)	G
4	RA	1451	C
4	RA	1455	G
4	RA	1459	G
4	RA	1467	C
4	RA	1471	A
4	RA	1482	G
4	RA	1493	C
4	RA	1494	A
4	RA	1497	U
4	RA	1508	A
4	RA	1509(A)	C
4	RA	1509(B)	A
4	RA	1531	C
4	RA	1542	A
4	RA	1543	C
4	RA	1545	A
4	RA	1547	C
4	RA	1558	A
4	RA	1566	A
4	RA	1569	A
4	RA	1578	U
4	RA	1580	A
4	RA	1583	A
4	RA	1584	C
4	RA	1586	A
4	RA	1608	A
4	RA	1609	A
4	RA	1610	A
4	RA	1640	C
4	RA	1647	G
4	RA	1648	C
4	RA	1674	G
4	RA	1696	G
4	RA	1700	A
4	RA	1701	A
4	RA	1721	G
4	RA	1722	A
4	RA	1740	G
4	RA	1756	G

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Mol	Chain	Res	Type
4	RA	1762	A
4	RA	1763	G
4	RA	1764	G
4	RA	1773	A
4	RA	1780	A
4	RA	1782	C
4	RA	1786	A
4	RA	1791	A
4	RA	1800	C
4	RA	1801	G
4	RA	1812	A
4	RA	1816	G
4	RA	1835	G
4	RA	1839	G
4	RA	1847	A
4	RA	1848	A
4	RA	1877	A
4	RA	1878	G
4	RA	1900	A
4	RA	1906	G
4	RA	1914	C
4	RA	1916	A
4	RA	1929	G
4	RA	1930	G
4	RA	1936	A
4	RA	1937	A
4	RA	1938	A
4	RA	1955	U
4	RA	1963	U
4	RA	1967	C
4	RA	1970	A
4	RA	1971	A
4	RA	1972	A
4	RA	1993	U
4	RA	1997	G
4	RA	2020	A
4	RA	2023	G
4	RA	2031	A
4	RA	2032	G
4	RA	2033	A
4	RA	2043	C
4	RA	2055	C

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Mol	Chain	Res	Type
4	RA	2056	G
4	RA	2060	A
4	RA	2061	G
4	RA	2062	A
4	RA	2069	G
4	RA	2096	U
4	RA	2098	U
4	RA	2099	U
4	RA	2103	C
4	RA	2104	G
4	RA	2105	C
4	RA	2107	C
4	RA	2108	C
4	RA	2109	U
4	RA	2110	G
4	RA	2111	C
4	RA	2112	G
4	RA	2115	G
4	RA	2116	G
4	RA	2117	A
4	RA	2118	U
4	RA	2119	A
4	RA	2121	G
4	RA	2123	G
4	RA	2126	A
4	RA	2127	G
4	RA	2128	C
4	RA	2129	C
4	RA	2130	U
4	RA	2131	G
4	RA	2132	U
4	RA	2133	G
4	RA	2134	A
4	RA	2135	A
4	RA	2136	C
4	RA	2141	G
4	RA	2145	C
4	RA	2146	C
4	RA	2147	G
4	RA	2148	G
4	RA	2149	G
4	RA	2151	G

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Mol	Chain	Res	Type
4	RA	2154	G
4	RA	2157	G
4	RA	2158	A
4	RA	2159	G
4	RA	2161	C
4	RA	2163	C
4	RA	2164	C
4	RA	2165	G
4	RA	2167	U
4	RA	2172	U
4	RA	2173	A
4	RA	2174	C
4	RA	2177	C
4	RA	2180	U
4	RA	2184	G
4	RA	2186	G
4	RA	2189	U
4	RA	2192	G
4	RA	2198	A
4	RA	2206	G
4	RA	2207	G
4	RA	2208	A
4	RA	2218	U
4	RA	2225	A
4	RA	2238	G
4	RA	2239	G
4	RA	2269	A
4	RA	2275	C
4	RA	2278	A
4	RA	2279	G
4	RA	2283	C
4	RA	2287	A
4	RA	2289	G
4	RA	2292	C
4	RA	2305	A
4	RA	2308	G
4	RA	2312	U
4	RA	2319	G
4	RA	2320	A
4	RA	2321	G
4	RA	2322	A
4	RA	2325	G

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Mol	Chain	Res	Type
4	RA	2334	G
4	RA	2335	A
4	RA	2336	A
4	RA	2343	C
4	RA	2347	C
4	RA	2350	C
4	RA	2354	G
4	RA	2379	G
4	RA	2383	G
4	RA	2385	C
4	RA	2406	U
4	RA	2410	G
4	RA	2422	A
4	RA	2424	C
4	RA	2425	A
4	RA	2429	G
4	RA	2430	A
4	RA	2435	A
4	RA	2439	A
4	RA	2441	C
4	RA	2445	G
4	RA	2448	A
4	RA	2468	G
4	RA	2474	C
4	RA	2476	A
4	RA	2478	A
4	RA	2502	G
4	RA	2504	U
4	RA	2505	G
4	RA	2506	U
4	RA	2507	C
4	RA	2518	A
4	RA	2529	G
4	RA	2554	U
4	RA	2566	A
4	RA	2567	G
4	RA	2573	C
4	RA	2585	U
4	RA	2586	C
4	RA	2602	A
4	RA	2603	G
4	RA	2611	U

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Mol	Chain	Res	Type
4	RA	2612	C
4	RA	2615	U
4	RA	2629	A
4	RA	2630	G
4	RA	2654	A
4	RA	2663	G
4	RA	2689	U
4	RA	2690	C
4	RA	2703	C
4	RA	2712(B)	A
4	RA	2713	A
4	RA	2714	G
4	RA	2726	U
4	RA	2733	A
4	RA	2757	A
4	RA	2758	A
4	RA	2759	G
4	RA	2764	A
4	RA	2765	A
4	RA	2769	C
4	RA	2778	A
4	RA	2818	G
4	RA	2820	A
4	RA	2821	A
4	RA	2833	G
4	RA	2835	A
4	RA	2849	U
4	RA	2872	G
4	RA	2880	C
4	RA	2894	G
4	RA	2897	U
5	RB	13	A
5	RB	24	G
5	RB	30	C
5	RB	45	A
5	RB	53	A
5	RB	56	G
5	RB	73	A
5	RB	84	C
5	RB	110	G

All (88) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	QV	53	G
1	XV	53	G
4	YA	9	U
4	YA	196	A
4	YA	272(M)	G
4	YA	277	C
4	YA	752	A
4	YA	827	U
4	YA	856	C
4	YA	900	A
4	YA	1047	G
4	YA	1053	C
4	YA	1057	A
4	YA	1065	U
4	YA	1067	A
4	YA	1073	A
4	YA	1076	C
4	YA	1210	A
4	YA	1379	A
4	YA	1420	U
4	YA	1530	C
4	YA	1992	G
4	YA	2126	A
4	YA	2171	A
4	YA	2172	U
4	YA	2321	G
4	YA	2689	U
4	YA	2756	U
35	XA	60	A
35	XA	65	U
35	XA	115	G
35	XA	266	G
35	XA	509	A
35	XA	560	U
35	XA	687	A
35	XA	748	C
35	XA	840	C
35	XA	913	A
35	XA	991	U
35	XA	992	U
35	XA	1065	U
35	XA	1067	A
35	XA	1128	C

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Mol	Chain	Res	Type
35	XA	1183	A
35	XA	1256	A
35	XA	1442(A)	G
35	QA	115	G
35	QA	266	G
35	QA	509	A
35	QA	560	U
35	QA	687	A
35	QA	839	U
35	QA	913	A
35	QA	991	U
35	QA	1065	U
35	QA	1067	A
35	QA	1201	A
35	QA	1207	2MG
35	QA	1285	A
35	QA	1442(A)	G
4	RA	9	U
4	RA	195	A
4	RA	272(M)	G
4	RA	277	C
4	RA	752	A
4	RA	827	U
4	RA	856	C
4	RA	900	A
4	RA	1047	G
4	RA	1053	C
4	RA	1057	A
4	RA	1065	U
4	RA	1067	A
4	RA	1073	A
4	RA	1076	C
4	RA	1210	A
4	RA	1379	A
4	RA	1420	U
4	RA	1530	C
4	RA	1992	G
4	RA	2126	A
4	RA	2171	A
4	RA	2172	U
4	RA	2321	G
4	RA	2406	U

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Mol	Chain	Res	Type
4	RA	2602	A
4	RA	2689	U
4	RA	2756	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

48 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
35	2MG	QA	1207	56,35	18,26,27	1.23	2 (11%)	21,38,41	2.36	7 (33%)
35	5MC	QA	1400	35	14,22,23	1.36	1 (7%)	17,32,35	0.84	1 (5%)
35	4OC	QA	1402	35	15,23,24	0.59	0	21,32,35	1.87	3 (14%)
35	5MC	QA	1404	35	14,22,23	1.32	1 (7%)	17,32,35	0.89	1 (5%)
35	5MC	QA	1407	35	14,22,23	1.31	1 (7%)	17,32,35	0.98	1 (5%)
35	UR3	QA	1498	35	13,22,23	0.71	0	18,32,35	0.75	0
35	MA6	QA	1518	35	18,26,27	0.97	1 (5%)	15,38,41	2.29	4 (26%)
35	MA6	QA	1519	35	18,26,27	0.98	1 (5%)	15,38,41	2.18	2 (13%)
35	PSU	QA	516	56,35	15,21,22	1.25	2 (13%)	16,30,33	2.20	3 (18%)
35	7MG	QA	527	56,35	20,26,27	1.45	2 (10%)	23,39,42	3.27	5 (21%)
35	M2G	QA	966	35	18,27,28	1.39	3 (16%)	22,40,43	1.84	4 (18%)
35	5MC	QA	967	35	14,22,23	1.31	1 (7%)	17,32,35	0.89	1 (5%)
46	0TD	QL	92	46	4,9,10	0.64	0	4,11,13	1.59	1 (25%)
4	PSU	RA	1911	4	15,21,22	1.38	1 (6%)	16,30,33	2.20	4 (25%)
4	5MU	RA	1915	56,4	13,22,23	0.55	0	16,32,35	2.83	2 (12%)
4	PSU	RA	1917	4	15,21,22	1.27	1 (6%)	16,30,33	2.25	4 (25%)
4	4OC	RA	1920	4	15,22,24	0.58	0	20,31,35	1.42	1 (5%)
4	5MU	RA	1939	4	13,22,23	0.59	0	16,32,35	2.55	2 (12%)
4	5MC	RA	1942	56,4	14,22,23	1.30	1 (7%)	17,32,35	0.93	1 (5%)
4	5MC	RA	1962	56,4	14,22,23	1.32	1 (7%)	17,32,35	0.88	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OMG	RA	2251	1,56,4	18,26,27	1.13	2 (11%)	21,38,41	1.83	4 (19%)
4	2MA	RA	2503	56,4	17,25,26	1.58	3 (17%)	18,37,40	2.95	1 (5%)
4	2MU	RA	2552	56,4	14,22,24	0.78	0	19,31,36	1.61	1 (5%)
4	PSU	RA	2605	4	15,21,22	1.30	1 (6%)	16,30,33	2.36	4 (25%)
35	2MG	XA	1207	35	18,26,27	1.20	2 (11%)	21,38,41	2.22	6 (28%)
35	5MC	XA	1400	35	14,22,23	1.30	1 (7%)	17,32,35	0.88	1 (5%)
35	4OC	XA	1402	35	15,23,24	0.60	0	21,32,35	1.90	3 (14%)
35	5MC	XA	1404	35	14,22,23	1.31	1 (7%)	17,32,35	0.93	1 (5%)
35	5MC	XA	1407	35	14,22,23	1.28	1 (7%)	17,32,35	1.01	1 (5%)
35	UR3	XA	1498	56,35	13,22,23	0.72	1 (7%)	18,32,35	0.73	0
35	MA6	XA	1518	35	18,26,27	0.96	1 (5%)	15,38,41	2.22	2 (13%)
35	MA6	XA	1519	35	18,26,27	0.96	1 (5%)	15,38,41	2.36	3 (20%)
35	PSU	XA	516	35	15,21,22	1.29	1 (6%)	16,30,33	2.14	3 (18%)
35	7MG	XA	527	35	20,26,27	1.46	2 (10%)	23,39,42	3.18	5 (21%)
35	M2G	XA	966	35	18,27,28	1.42	3 (16%)	22,40,43	1.91	5 (22%)
35	5MC	XA	967	35	14,22,23	1.31	1 (7%)	17,32,35	0.88	1 (5%)
46	0TD	XL	92	46	4,9,10	0.58	0	4,11,13	1.63	1 (25%)
4	PSU	YA	1911	4	15,21,22	1.36	1 (6%)	16,30,33	2.32	4 (25%)
4	5MU	YA	1915	4	13,22,23	0.57	0	16,32,35	2.70	2 (12%)
4	PSU	YA	1917	4	15,21,22	1.23	1 (6%)	16,30,33	2.22	4 (25%)
4	4OC	YA	1920	4	15,22,24	0.57	0	20,31,35	1.27	1 (5%)
4	5MU	YA	1939	56,4	13,22,23	0.64	0	16,32,35	2.43	2 (12%)
4	5MC	YA	1942	4	14,22,23	1.25	1 (7%)	17,32,35	0.96	1 (5%)
4	5MC	YA	1962	56,4	14,22,23	1.30	1 (7%)	17,32,35	0.95	1 (5%)
4	OMG	YA	2251	1,56,4	18,26,27	1.17	2 (11%)	21,38,41	1.82	4 (19%)
4	2MA	YA	2503	56,4	17,25,26	1.56	3 (17%)	18,37,40	2.90	1 (5%)
4	2MU	YA	2552	56,4	14,22,24	0.79	0	19,31,36	1.66	1 (5%)
4	PSU	YA	2605	4	15,21,22	1.43	1 (6%)	16,30,33	2.31	4 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	2MG	QA	1207	56,35	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	5MC	QA	1400	35	-	0/3/25/26	0/2/2/2
35	4OC	QA	1402	35	-	0/7/29/30	0/2/2/2
35	5MC	QA	1404	35	-	0/3/25/26	0/2/2/2
35	5MC	QA	1407	35	-	0/3/25/26	0/2/2/2
35	UR3	QA	1498	35	-	0/3/25/26	0/2/2/2
35	MA6	QA	1518	35	-	0/7/29/30	0/3/3/3
35	MA6	QA	1519	35	-	0/7/29/30	0/3/3/3
35	PSU	QA	516	56,35	-	0/7/25/26	0/2/2/2
35	7MG	QA	527	56,35	-	0/7/37/38	0/3/3/3
35	M2G	QA	966	35	-	0/7/29/30	0/3/3/3
35	5MC	QA	967	35	-	0/3/25/26	0/2/2/2
46	0TD	QL	92	46	-	0/2/12/14	0/0/0/0
4	PSU	RA	1911	4	-	0/7/25/26	0/2/2/2
4	5MU	RA	1915	56,4	-	0/3/25/26	0/2/2/2
4	PSU	RA	1917	4	-	0/7/25/26	0/2/2/2
4	4OC	RA	1920	4	-	0/5/27/30	0/2/2/2
4	5MU	RA	1939	4	-	0/3/25/26	0/2/2/2
4	5MC	RA	1942	56,4	-	0/3/25/26	0/2/2/2
4	5MC	RA	1962	56,4	-	0/3/25/26	0/2/2/2
4	OMG	RA	2251	1,56,4	-	0/5/27/28	0/3/3/3
4	2MA	RA	2503	56,4	-	0/3/25/26	0/3/3/3
4	2MU	RA	2552	56,4	-	0/5/27/28	0/2/2/2
4	PSU	RA	2605	4	-	0/7/25/26	0/2/2/2
35	2MG	XA	1207	35	-	0/5/27/28	0/3/3/3
35	5MC	XA	1400	35	-	0/3/25/26	0/2/2/2
35	4OC	XA	1402	35	-	2/7/29/30	0/2/2/2
35	5MC	XA	1404	35	-	0/3/25/26	0/2/2/2
35	5MC	XA	1407	35	-	0/3/25/26	0/2/2/2
35	UR3	XA	1498	56,35	-	0/3/25/26	0/2/2/2
35	MA6	XA	1518	35	-	0/7/29/30	0/3/3/3
35	MA6	XA	1519	35	-	0/7/29/30	0/3/3/3
35	PSU	XA	516	35	-	0/7/25/26	0/2/2/2
35	7MG	XA	527	35	-	0/7/37/38	0/3/3/3
35	M2G	XA	966	35	-	0/7/29/30	0/3/3/3
35	5MC	XA	967	35	-	0/3/25/26	0/2/2/2
46	0TD	XL	92	46	-	0/2/12/14	0/0/0/0
4	PSU	YA	1911	4	-	0/7/25/26	0/2/2/2
4	5MU	YA	1915	4	-	0/3/25/26	0/2/2/2
4	PSU	YA	1917	4	-	0/7/25/26	0/2/2/2
4	4OC	YA	1920	4	-	0/5/27/30	0/2/2/2
4	5MU	YA	1939	56,4	-	0/3/25/26	0/2/2/2
4	5MC	YA	1942	4	-	0/3/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	5MC	YA	1962	56,4	-	0/3/25/26	0/2/2/2
4	OMG	YA	2251	1,56,4	-	0/5/27/28	0/3/3/3
4	2MA	YA	2503	56,4	-	0/3/25/26	0/3/3/3
4	2MU	YA	2552	56,4	-	0/5/27/28	0/2/2/2
4	PSU	YA	2605	4	-	0/7/25/26	0/2/2/2

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	YA	2605	PSU	C5-C1'	-4.46	1.48	1.52
4	RA	1911	PSU	C5-C1'	-4.31	1.48	1.52
4	YA	1911	PSU	C5-C1'	-4.20	1.48	1.52
4	RA	2605	PSU	C5-C1'	-3.99	1.48	1.52
35	XA	516	PSU	C5-C1'	-3.84	1.48	1.52
4	RA	1917	PSU	C5-C1'	-3.70	1.49	1.52
4	YA	1917	PSU	C5-C1'	-3.54	1.49	1.52
35	QA	516	PSU	C5-C1'	-3.53	1.49	1.52
35	QA	516	PSU	O4'-C1'	-2.07	1.41	1.44
35	XA	1498	UR3	C4-N3	2.01	1.41	1.38
4	RA	2503	2MA	C5-C4	2.99	1.47	1.40
4	YA	2503	2MA	C5-C4	2.99	1.47	1.40
4	RA	2251	OMG	C5-C4	3.07	1.47	1.40
35	XA	966	M2G	C5-C4	3.09	1.47	1.40
35	XA	1207	2MG	C5-C4	3.09	1.47	1.40
35	QA	966	M2G	C5-C4	3.09	1.47	1.40
35	XA	1518	MA6	C5-C4	3.10	1.47	1.40
35	QA	1207	2MG	C5-C4	3.11	1.47	1.40
35	QA	1519	MA6	C5-C4	3.13	1.47	1.40
35	XA	1519	MA6	C5-C4	3.18	1.47	1.40
35	QA	1518	MA6	C5-C4	3.22	1.47	1.40
4	YA	2251	OMG	C5-C4	3.22	1.47	1.40
35	QA	527	7MG	C5-C4	3.24	1.47	1.39
35	XA	966	M2G	C2-N2	3.26	1.40	1.34
35	XA	527	7MG	C5-C4	3.29	1.47	1.39
35	QA	966	M2G	C2-N2	3.29	1.40	1.34
4	RA	2251	OMG	C6-C5	3.34	1.48	1.41
4	YA	2251	OMG	C6-C5	3.49	1.48	1.41
35	QA	966	M2G	C6-C5	3.54	1.48	1.41
4	YA	2503	2MA	C6-N6	3.65	1.35	1.29
35	QA	1207	2MG	C6-C5	3.68	1.48	1.41
4	RA	2503	2MA	C6-N6	3.68	1.35	1.29
35	XA	966	M2G	C6-C5	3.69	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	XA	1207	2MG	C6-C5	3.71	1.48	1.41
4	YA	2503	2MA	C6-C5	3.98	1.48	1.40
4	RA	2503	2MA	C6-C5	4.11	1.48	1.40
4	YA	1942	5MC	C5-C4	4.40	1.48	1.41
35	XA	1407	5MC	C5-C4	4.47	1.48	1.41
35	XA	1400	5MC	C5-C4	4.55	1.48	1.41
4	YA	1962	5MC	C5-C4	4.56	1.48	1.41
35	XA	527	7MG	C6-C5	4.58	1.47	1.41
35	QA	527	7MG	C6-C5	4.59	1.47	1.41
35	QA	1407	5MC	C5-C4	4.60	1.48	1.41
4	RA	1942	5MC	C5-C4	4.61	1.48	1.41
35	XA	1404	5MC	C5-C4	4.64	1.48	1.41
4	RA	1962	5MC	C5-C4	4.66	1.48	1.41
35	QA	967	5MC	C5-C4	4.67	1.48	1.41
35	XA	967	5MC	C5-C4	4.69	1.48	1.41
35	QA	1404	5MC	C5-C4	4.69	1.48	1.41
35	QA	1400	5MC	C5-C4	4.75	1.48	1.41

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	QA	527	7MG	C5-C4-N3	-8.85	117.73	126.74
35	XA	527	7MG	C5-C4-N3	-8.56	118.02	126.74
4	RA	1915	5MU	C5-C4-N3	-8.09	118.56	125.35
4	RA	1939	5MU	C5-C4-N3	-7.60	118.97	125.35
4	YA	1915	5MU	C5-C4-N3	-7.50	119.05	125.35
4	YA	1939	5MU	C5-C4-N3	-7.24	119.27	125.35
35	XA	1519	MA6	N3-C2-N1	-6.94	123.42	128.87
35	XA	1518	MA6	N3-C2-N1	-6.67	123.63	128.87
35	QA	1518	MA6	N3-C2-N1	-6.65	123.65	128.87
35	QA	1519	MA6	N3-C2-N1	-6.45	123.81	128.87
35	QA	527	7MG	C5-C6-N1	-5.10	115.80	123.39
35	XA	527	7MG	C5-C6-N1	-5.05	115.88	123.39
4	YA	2251	OMG	C5-C6-N1	-4.45	117.71	123.52
35	XA	966	M2G	C5-C6-N1	-4.32	117.88	123.52
35	QA	966	M2G	C5-C6-N1	-4.32	117.88	123.52
35	XA	1207	2MG	C5-C6-N1	-4.28	117.93	123.52
4	RA	2251	OMG	C5-C6-N1	-4.24	117.98	123.52
35	QA	1207	2MG	C5-C6-N1	-4.14	118.11	123.52
4	RA	2605	PSU	C5-C1'-C2'	-4.13	108.42	115.44
4	RA	2605	PSU	C5-C6-N1	-3.94	118.89	124.38
4	YA	1911	PSU	C5-C6-N1	-3.88	118.97	124.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	YA	2605	PSU	C5-C1'-C2'	-3.83	108.93	115.44
4	RA	1911	PSU	C5-C6-N1	-3.79	119.10	124.38
4	YA	1911	PSU	C5-C1'-C2'	-3.75	109.06	115.44
4	YA	2605	PSU	C5-C6-N1	-3.67	119.26	124.38
4	YA	1917	PSU	C5-C6-N1	-3.67	119.27	124.38
35	QA	1402	4OC	CM4-N4-C4	-3.61	119.82	122.87
35	XA	516	PSU	C5-C6-N1	-3.61	119.34	124.38
35	QA	516	PSU	C5-C6-N1	-3.48	119.52	124.38
4	RA	1917	PSU	C5-C6-N1	-3.42	119.62	124.38
35	XA	966	M2G	C6-C5-C4	-3.35	117.03	120.86
4	RA	2251	OMG	N3-C2-N1	-3.33	123.02	127.56
35	XA	1207	2MG	CM2-N2-C2	-3.27	119.35	123.03
35	QA	966	M2G	C6-C5-C4	-3.25	117.15	120.86
35	QA	527	7MG	C8-N9-C1'	-3.16	112.94	122.43
46	XL	92	0TD	O-C-CA	-3.12	117.18	125.69
35	QA	1207	2MG	C6-C5-C4	-3.11	117.30	120.86
46	QL	92	0TD	O-C-CA	-3.09	117.25	125.69
35	XA	1207	2MG	C6-C5-C4	-3.08	117.34	120.86
35	QA	1207	2MG	CM2-N2-C2	-3.05	119.61	123.03
35	XA	1402	4OC	CM4-N4-C4	-3.02	120.32	122.87
4	YA	2251	OMG	N3-C2-N1	-3.00	123.47	127.56
4	YA	1917	PSU	C5-C1'-C2'	-2.94	110.44	115.44
35	XA	527	7MG	C8-N9-C1'	-2.90	113.72	122.43
4	RA	1911	PSU	C5-C1'-C2'	-2.90	110.51	115.44
4	RA	2251	OMG	C6-C5-C4	-2.87	117.58	120.86
35	XA	1519	MA6	C10-N6-C9	-2.73	107.04	115.96
4	RA	1917	PSU	C5-C1'-C2'	-2.71	110.83	115.44
4	YA	2251	OMG	C6-C5-C4	-2.47	118.03	120.86
35	QA	1207	2MG	N3-C2-N1	-2.27	122.79	126.19
35	QA	1518	MA6	C1'-N9-C4	-2.25	124.30	126.81
35	QA	1518	MA6	C10-N6-C9	-2.15	108.95	115.96
35	XA	1207	2MG	N3-C2-N1	-2.08	123.07	126.19
35	XA	966	M2G	N3-C2-N1	-2.07	122.84	126.35
35	QA	966	M2G	N3-C2-N1	-2.07	122.84	126.35
35	QA	1207	2MG	O3'-C3'-C2'	2.05	118.48	111.86
35	QA	1400	5MC	N4-C4-N3	2.33	120.33	116.92
35	XA	967	5MC	N4-C4-N3	2.43	120.48	116.92
35	QA	1404	5MC	N4-C4-N3	2.44	120.50	116.92
4	RA	1942	5MC	N4-C4-N3	2.49	120.57	116.92
35	XA	966	M2G	N1-C2-N2	2.51	119.87	117.14
4	YA	2605	PSU	O4'-C1'-C2'	2.51	107.41	104.69
35	QA	967	5MC	N4-C4-N3	2.53	120.63	116.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	XA	1404	5MC	N4-C4-N3	2.57	120.68	116.92
4	YA	1917	PSU	O4'-C1'-C2'	2.60	107.50	104.69
4	RA	1962	5MC	N4-C4-N3	2.62	120.76	116.92
35	XA	1400	5MC	N4-C4-N3	2.63	120.77	116.92
4	RA	2605	PSU	O4'-C1'-C2'	2.63	107.54	104.69
35	QA	1407	5MC	N4-C4-N3	2.64	120.79	116.92
35	XA	1407	5MC	N4-C4-N3	2.65	120.80	116.92
4	RA	1917	PSU	O4'-C1'-C2'	2.65	107.56	104.69
4	YA	1962	5MC	N4-C4-N3	2.71	120.90	116.92
4	YA	1942	5MC	N4-C4-N3	2.72	120.90	116.92
4	YA	1911	PSU	O4'-C1'-C2'	2.82	107.74	104.69
4	RA	1911	PSU	O4'-C1'-C2'	2.90	107.82	104.69
35	XA	516	PSU	O4'-C1'-C2'	3.02	107.95	104.69
35	XA	1402	4OC	C2-N3-C4	3.34	119.67	115.43
35	QA	516	PSU	O4'-C1'-C2'	3.46	108.43	104.69
35	QA	1402	4OC	C2-N3-C4	3.72	120.16	115.43
35	QA	1519	MA6	C2-N1-C6	4.45	122.12	111.64
35	XA	1518	MA6	C2-N1-C6	4.47	122.19	111.64
4	YA	1920	4OC	C6-C5-C4	4.53	119.21	117.44
35	XA	1519	MA6	C2-N1-C6	4.61	122.52	111.64
35	QA	1518	MA6	C2-N1-C6	4.71	122.74	111.64
35	XA	1207	2MG	C6-N1-C2	4.82	122.14	115.24
35	QA	1207	2MG	C6-N1-C2	4.89	122.24	115.24
4	RA	1920	4OC	C6-C5-C4	5.15	119.45	117.44
4	YA	2251	OMG	C6-N1-C2	5.25	122.03	115.88
4	RA	2251	OMG	C6-N1-C2	5.32	122.11	115.88
35	QA	966	M2G	C2-N3-C4	5.34	120.84	114.99
35	XA	1207	2MG	C2-N3-C4	5.50	121.02	114.99
35	XA	966	M2G	C2-N3-C4	5.52	121.04	114.99
35	QA	1207	2MG	C2-N3-C4	5.66	121.20	114.99
35	QA	527	7MG	C6-N1-C2	5.86	122.75	115.88
35	XA	527	7MG	C6-N1-C2	5.91	122.81	115.88
4	YA	1939	5MU	C4-N3-C2	6.10	120.25	115.16
35	QA	1402	4OC	C6-C5-C4	6.14	119.83	117.42
4	RA	2552	2MU	C4-N3-C2	6.18	120.72	114.21
4	YA	2552	2MU	C4-N3-C2	6.20	120.74	114.21
4	RA	1939	5MU	C4-N3-C2	6.43	120.52	115.16
4	RA	1911	PSU	C4-N3-C2	6.51	120.59	115.16
4	RA	2605	PSU	C4-N3-C2	6.59	120.66	115.16
4	YA	1917	PSU	C4-N3-C2	6.67	120.72	115.16
35	XA	516	PSU	C4-N3-C2	6.68	120.73	115.16
4	YA	1911	PSU	C4-N3-C2	6.69	120.74	115.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	YA	2605	PSU	C4-N3-C2	6.73	120.78	115.16
35	XA	1402	4OC	C6-C5-C4	6.84	120.11	117.42
35	QA	516	PSU	C4-N3-C2	6.86	120.88	115.16
4	RA	1917	PSU	C4-N3-C2	7.05	121.04	115.16
4	YA	1915	5MU	C4-N3-C2	7.41	121.34	115.16
4	RA	1915	5MU	C4-N3-C2	7.54	121.45	115.16
35	XA	527	7MG	N3-C4-N9	8.93	138.53	126.98
35	QA	527	7MG	N3-C4-N9	9.21	138.90	126.98
4	YA	2503	2MA	C2-N3-C4	11.97	121.05	115.29
4	RA	2503	2MA	C2-N3-C4	12.19	121.16	115.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	XA	1402	4OC	N3-C4-N4-CM4
35	XA	1402	4OC	C5-C4-N4-CM4

There are no ring outliers.

19 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	QA	1207	2MG	2	0
35	QA	1402	4OC	1	0
35	QA	1404	5MC	1	0
35	QA	1518	MA6	2	0
35	QA	1519	MA6	2	0
35	QA	966	M2G	1	0
35	QA	967	5MC	1	0
46	QL	92	0TD	2	0
4	RA	1920	4OC	1	0
4	RA	1942	5MC	1	0
4	RA	1962	5MC	1	0
4	RA	2552	2MU	1	0
35	XA	1402	4OC	1	0
35	XA	1518	MA6	1	0
4	YA	1915	5MU	4	0
4	YA	1920	4OC	1	0
4	YA	1962	5MC	1	0
4	YA	2251	OMG	1	0
4	YA	2503	2MA	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2527 ligands modelled in this entry, 2525 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	SF4	QD	302	38	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	XD	301	38	0,12,12	0.00	-	0,24,24	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	QD	302	38	-	0/0/48/48	0/6/5/5
58	SF4	XD	301	38	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	QV	77/77 (100%)	0.23	3 (3%) 43 21	57, 94, 173, 210	0
1	XV	77/77 (100%)	0.30	2 (2%) 59 35	49, 84, 141, 212	0
2	QX	10/25 (40%)	1.09	3 (30%) 1 0	69, 105, 168, 212	0
2	XX	10/25 (40%)	1.03	3 (30%) 1 0	52, 112, 150, 183	0
3	QY	357/380 (93%)	2.04	158 (44%) 0 0	77, 135, 202, 220	0
3	XY	357/380 (93%)	2.11	151 (42%) 0 0	73, 132, 203, 228	0
4	RA	2856/2915 (97%)	0.01	131 (4%) 36 17	22, 55, 177, 347	0
4	YA	2856/2915 (97%)	-0.02	124 (4%) 39 18	14, 41, 183, 343	0
5	RB	120/122 (98%)	-0.21	0 100 100	56, 91, 116, 152	0
5	YB	120/122 (98%)	-0.32	0 100 100	39, 63, 85, 130	0
6	RD	275/276 (99%)	-0.31	1 (0%) 93 85	25, 47, 71, 109	0
6	YD	275/276 (99%)	-0.35	1 (0%) 93 85	16, 39, 69, 132	0
7	RE	204/206 (99%)	-0.19	0 100 100	26, 53, 85, 119	0
7	YE	204/206 (99%)	-0.19	0 100 100	19, 46, 86, 135	0
8	RF	203/210 (96%)	-0.16	1 (0%) 91 83	29, 67, 110, 133	0
8	YF	203/210 (96%)	-0.31	1 (0%) 91 83	15, 45, 89, 139	0
9	RG	181/182 (99%)	0.17	5 (2%) 56 32	76, 103, 134, 155	0
9	YG	181/182 (99%)	-0.11	4 (2%) 65 42	55, 78, 121, 184	0
10	RH	174/180 (96%)	0.79	28 (16%) 3 1	74, 111, 147, 158	0
10	YH	173/180 (96%)	-0.14	0 100 100	40, 64, 95, 139	0
11	RI	147/148 (99%)	0.59	13 (8%) 12 4	59, 103, 135, 164	0
11	YI	146/148 (98%)	0.32	4 (2%) 58 34	51, 92, 127, 150	0
12	RN	140/140 (100%)	0.03	4 (2%) 55 31	40, 62, 101, 140	0
12	YN	140/140 (100%)	-0.23	1 (0%) 89 78	27, 47, 87, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	RO	122/122 (100%)	-0.27	0 100 100	33, 52, 78, 113	0
13	YO	122/122 (100%)	-0.26	0 100 100	27, 45, 71, 83	0
14	RP	149/150 (99%)	0.10	3 (2%) 68 46	29, 72, 109, 138	0
14	YP	149/150 (99%)	-0.13	1 (0%) 89 78	18, 52, 84, 115	0
15	RQ	141/141 (100%)	-0.26	0 100 100	43, 67, 88, 112	0
15	YQ	141/141 (100%)	-0.30	0 100 100	30, 48, 74, 124	0
16	RR	118/118 (100%)	-0.25	0 100 100	31, 50, 77, 93	0
16	YR	118/118 (100%)	-0.31	0 100 100	28, 43, 67, 89	0
17	RS	110/112 (98%)	0.15	2 (1%) 71 50	66, 89, 113, 133	0
17	YS	110/112 (98%)	-0.08	0 100 100	47, 62, 89, 106	0
18	RT	131/146 (89%)	-0.23	2 (1%) 76 58	37, 59, 105, 155	0
18	YT	131/146 (89%)	-0.25	0 100 100	36, 53, 98, 122	0
19	RU	116/118 (98%)	-0.20	1 (0%) 85 72	33, 57, 91, 113	0
19	YU	116/118 (98%)	-0.41	0 100 100	23, 37, 67, 104	0
20	RV	101/101 (100%)	-0.21	0 100 100	37, 74, 100, 122	0
20	YV	101/101 (100%)	-0.13	1 (0%) 84 69	21, 50, 88, 109	0
21	RW	112/113 (99%)	-0.19	0 100 100	34, 48, 81, 122	0
21	YW	112/113 (99%)	-0.33	0 100 100	25, 37, 68, 143	0
22	RX	95/96 (98%)	0.02	2 (2%) 67 44	45, 60, 87, 120	0
22	YX	95/96 (98%)	-0.28	0 100 100	28, 42, 80, 115	0
23	RY	107/110 (97%)	0.85	11 (10%) 9 3	57, 83, 131, 176	0
23	YY	107/110 (97%)	0.14	2 (1%) 70 48	38, 64, 107, 150	0
24	RZ	203/206 (98%)	0.60	16 (7%) 15 5	71, 100, 156, 194	0
24	YZ	201/206 (97%)	0.17	15 (7%) 17 6	50, 77, 135, 178	0
25	R0	77/85 (90%)	0.22	2 (2%) 59 35	50, 62, 90, 109	0
25	Y0	77/85 (90%)	-0.06	1 (1%) 79 62	31, 45, 80, 110	0
26	R1	97/98 (98%)	0.01	2 (2%) 67 44	33, 58, 89, 111	0
26	Y1	97/98 (98%)	-0.06	0 100 100	27, 47, 95, 114	0
27	R2	70/72 (97%)	0.02	1 (1%) 78 60	53, 74, 106, 130	0
27	Y2	70/72 (97%)	-0.22	0 100 100	34, 55, 82, 142	0
28	R3	59/60 (98%)	0.46	3 (5%) 32 13	42, 63, 107, 148	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	Y3	59/60 (98%)	-0.06	1 (1%) 73 52	28, 43, 106, 122	0
29	R4	69/71 (97%)	0.79	8 (11%) 6 2	99, 136, 177, 184	0
29	Y4	69/71 (97%)	0.48	8 (11%) 6 2	75, 124, 168, 178	0
30	R5	59/60 (98%)	-0.16	1 (1%) 73 52	29, 51, 94, 160	0
30	Y5	59/60 (98%)	-0.32	0 100 100	18, 42, 91, 141	0
31	R6	53/54 (98%)	2.07	27 (50%) 0 0	82, 102, 143, 150	0
31	Y6	53/54 (98%)	1.49	15 (28%) 1 0	75, 88, 116, 130	0
32	R7	48/49 (97%)	-0.08	1 (2%) 67 44	28, 42, 83, 120	0
32	Y7	48/49 (97%)	-0.16	0 100 100	17, 31, 69, 115	0
33	R8	64/65 (98%)	-0.15	0 100 100	39, 54, 73, 107	0
33	Y8	64/65 (98%)	-0.26	0 100 100	24, 38, 58, 71	0
34	R9	37/37 (100%)	0.82	3 (8%) 15 5	58, 77, 101, 112	0
34	Y9	37/37 (100%)	0.60	1 (2%) 58 34	49, 61, 81, 93	0
35	QA	1488/1521 (97%)	0.01	38 (2%) 59 35	42, 86, 173, 260	0
35	XA	1492/1521 (98%)	0.02	44 (2%) 55 31	32, 84, 168, 253	0
36	QB	231/256 (90%)	0.39	13 (5%) 28 11	85, 122, 153, 178	0
36	XB	231/256 (90%)	0.27	11 (4%) 34 15	80, 110, 143, 161	0
37	QC	206/239 (86%)	0.35	10 (4%) 33 14	88, 115, 144, 168	0
37	XC	206/239 (86%)	0.24	8 (3%) 43 21	80, 104, 134, 167	0
38	QD	208/209 (99%)	-0.04	0 100 100	62, 91, 125, 150	0
38	XD	208/209 (99%)	0.09	0 100 100	68, 97, 133, 152	0
39	QE	148/162 (91%)	-0.03	0 100 100	64, 86, 114, 143	0
39	XE	148/162 (91%)	0.08	1 (0%) 89 78	62, 78, 114, 139	0
40	QF	100/101 (99%)	-0.04	1 (1%) 84 69	71, 95, 118, 132	0
40	XF	100/101 (99%)	-0.24	0 100 100	62, 81, 109, 124	0
41	QG	155/156 (99%)	0.52	14 (9%) 12 4	82, 109, 137, 157	0
41	XG	155/156 (99%)	0.44	9 (5%) 26 11	78, 100, 130, 155	0
42	QH	137/138 (99%)	0.19	2 (1%) 76 58	55, 86, 114, 123	0
42	XH	137/138 (99%)	0.09	3 (2%) 65 42	60, 86, 113, 120	0
43	QI	127/128 (99%)	0.93	18 (14%) 4 2	78, 123, 151, 175	0
43	XI	126/128 (98%)	0.43	7 (5%) 28 11	68, 111, 139, 165	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	QJ	97/105 (92%)	1.06	15 (15%) 3 1	90, 121, 149, 161	0
44	XJ	96/105 (91%)	0.82	12 (12%) 5 2	78, 116, 144, 146	0
45	QK	114/129 (88%)	0.35	4 (3%) 48 23	63, 86, 113, 138	0
45	XK	114/129 (88%)	0.13	1 (0%) 85 72	47, 75, 105, 132	0
46	QL	121/132 (91%)	-0.10	1 (0%) 87 75	47, 66, 90, 105	0
46	XL	121/132 (91%)	0.04	3 (2%) 61 37	48, 66, 94, 116	0
47	QM	116/126 (92%)	0.34	7 (6%) 25 10	85, 114, 138, 148	0
47	XM	114/126 (90%)	0.42	5 (4%) 38 17	84, 107, 128, 144	0
48	QN	60/61 (98%)	0.69	6 (10%) 9 3	88, 111, 129, 146	0
48	XN	60/61 (98%)	0.27	1 (1%) 73 52	73, 92, 115, 127	0
49	QO	88/89 (98%)	0.07	1 (1%) 82 66	60, 80, 109, 121	0
49	XO	88/89 (98%)	0.15	1 (1%) 82 66	48, 80, 112, 123	0
50	QP	82/88 (93%)	0.37	3 (3%) 45 22	58, 76, 104, 114	0
50	XP	82/88 (93%)	0.57	5 (6%) 25 10	71, 93, 118, 141	0
51	QQ	99/105 (94%)	0.27	1 (1%) 84 69	53, 78, 114, 138	0
51	XQ	99/105 (94%)	0.03	0 100 100	59, 78, 101, 126	0
52	QR	68/88 (77%)	0.76	9 (13%) 4 2	72, 90, 119, 139	0
52	XR	68/88 (77%)	0.32	1 (1%) 76 58	56, 83, 114, 124	0
53	QS	83/93 (89%)	1.21	21 (25%) 1 0	87, 120, 146, 161	0
53	XS	83/93 (89%)	1.01	12 (14%) 3 1	89, 118, 142, 183	0
54	QT	96/106 (90%)	0.15	1 (1%) 84 69	54, 80, 116, 120	0
54	XT	98/106 (92%)	0.46	5 (5%) 32 13	65, 88, 120, 128	0
55	QU	23/27 (85%)	2.09	14 (60%) 0 0	88, 103, 130, 145	0
55	XU	23/27 (85%)	1.31	5 (21%) 1 0	81, 102, 117, 119	0
All	All	21456/22208 (96%)	0.14	1081 (5%) 32 13	14, 73, 148, 347	0

All (1081) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
35	XA	88	A	13.9
4	YA	2141	G	11.3
3	XY	50	PRO	10.6
24	YZ	192	ALA	10.2
24	YZ	193	GLU	9.8

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Mol	Chain	Res	Type	RSRZ
24	RZ	192	ALA	9.2
4	YA	2116	G	9.1
4	YA	2140	C	9.1
4	YA	1076	C	8.9
3	QY	66	VAL	8.9
35	QA	1036	G	8.6
24	RZ	200	GLY	8.6
3	XY	84	LEU	8.4
4	RA	2110	G	8.2
4	YA	2139	C	8.1
24	RZ	202	GLU	8.0
4	RA	1067	A	7.9
28	R3	60	GLU	7.8
4	RA	2146	C	7.8
35	QA	1030(C)	C	7.6
3	QY	25	LEU	7.5
4	RA	1064	C	7.4
24	RZ	191	VAL	7.4
4	YA	2154	G	7.3
4	YA	2153	G	7.3
23	RY	1	MET	7.2
24	RZ	195	GLU	7.2
35	XA	90	U	7.1
4	YA	2793	G	7.1
4	RA	2138	C	7.1
4	RA	2125	G	7.1
41	QG	81	GLY	7.0
4	RA	2141	G	6.9
35	XA	1030(C)	C	6.9
4	RA	2169	A	6.9
35	XA	80	G	6.9
29	R4	68	ARG	6.9
4	YA	1083	U	6.8
3	QY	55	ALA	6.8
4	YA	2804	C	6.8
3	QY	102	GLU	6.8
3	QY	76	GLY	6.7
3	QY	74	LYS	6.7
4	RA	2147	G	6.7
3	QY	77	LEU	6.6
3	XY	46	VAL	6.5
4	RA	1062	G	6.5

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Mol	Chain	Res	Type	RSRZ
3	QY	330	ASP	6.5
4	RA	2162	G	6.4
23	YY	1	MET	6.4
3	XY	66	VAL	6.4
3	XY	88	VAL	6.3
3	QY	71	ASP	6.3
4	YA	2142	C	6.2
35	XA	89	C	6.2
4	YA	1091	G	6.2
3	QY	81	SER	6.2
4	RA	2154	G	6.2
3	QY	50	PRO	6.2
31	R6	42	TRP	6.2
3	XY	167	GLU	6.2
4	RA	2139	C	6.1
4	RA	2142	C	6.1
4	RA	2802	G	6.1
4	RA	2801(B)	A	6.1
3	QY	332	ARG	6.0
4	YA	1075	C	6.0
3	QY	230	ILE	6.0
24	YZ	200	GLY	6.0
4	RA	2137	C	6.0
4	RA	2172	U	6.0
3	XY	30	LYS	6.0
3	XY	45	ASP	6.0
3	XY	231	ASP	6.0
3	QY	72	GLN	6.0
3	XY	47	TRP	6.0
4	RA	2896	C	5.9
3	XY	53	ALA	5.9
4	RA	2161	C	5.9
4	RA	2124	G	5.9
3	XY	85	GLU	5.8
4	RA	229	A	5.8
4	RA	2793	G	5.8
4	YA	2805	G	5.8
3	XY	41	LEU	5.8
4	RA	2155	G	5.7
4	YA	2108	C	5.7
35	QA	344	A	5.7
4	YA	2173	A	5.6

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Mol	Chain	Res	Type	RSRZ
29	R4	69	LYS	5.6
3	XY	12	GLN	5.6
4	YA	2161	C	5.6
4	RA	2168	G	5.6
4	RA	2140	C	5.6
31	R6	4	GLU	5.6
4	YA	2160	G	5.6
4	YA	2138	C	5.6
3	QY	89	GLU	5.6
4	YA	2125	G	5.5
24	RZ	201	LYS	5.5
4	YA	2155	G	5.5
4	YA	2132	U	5.5
4	RA	1509(A)	C	5.4
4	RA	1076	C	5.4
24	RZ	199	LYS	5.4
4	RA	2805	G	5.4
29	Y4	68	ARG	5.4
31	R6	54	ILE	5.4
3	XY	69	THR	5.4
3	QY	231	ASP	5.4
3	QY	75	GLN	5.4
4	YA	1067	A	5.4
41	QG	82	GLY	5.3
4	RA	2804	C	5.3
24	YZ	187	ALA	5.3
41	QG	156	TRP	5.3
43	QI	128	ARG	5.3
45	QK	13	GLN	5.3
3	XY	163	THR	5.3
3	QY	68	ASP	5.3
3	XY	89	GLU	5.2
3	XY	73	MET	5.2
3	XY	101	ALA	5.2
35	QA	1030(B)	G	5.2
3	QY	73	MET	5.2
24	RZ	193	GLU	5.2
4	RA	2803	C	5.2
24	RZ	194	PRO	5.1
4	RA	2173	A	5.1
55	QU	18	TYR	5.1
3	QY	70	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
4	RA	2127	G	5.1
4	YA	2169	A	5.1
4	RA	2105	C	5.1
53	QS	12	ASP	5.1
4	RA	2176	A	5.1
35	QA	1531	A	5.1
3	QY	12	GLN	5.1
4	YA	2144	U	5.0
3	QY	88	VAL	5.0
4	YA	2801(B)	A	5.0
4	YA	1081	U	5.0
3	XY	38	ASN	5.0
44	QJ	89	ASP	5.0
4	RA	2120	G	5.0
35	XA	92	C	5.0
4	RA	2118	U	5.0
4	RA	2144	U	5.0
4	RA	2145	C	5.0
30	R5	60	VAL	5.0
4	RA	2159	G	5.0
4	YA	1077	A	5.0
3	XY	67	VAL	5.0
44	QJ	26	ALA	4.9
3	QY	235	ASN	4.9
4	YA	2152	G	4.9
3	QY	54	GLN	4.9
43	QI	127	LYS	4.9
4	RA	1079	C	4.9
25	Y0	8	GLY	4.9
3	XY	297	GLU	4.9
3	QY	175	GLY	4.9
4	YA	2162	G	4.9
3	XY	83	LEU	4.8
4	RA	2153	G	4.8
31	R6	50	ARG	4.8
4	YA	2143	C	4.8
3	XY	70	LEU	4.8
4	RA	1083	U	4.8
3	QY	174	ALA	4.8
24	RZ	198	LYS	4.8
24	YZ	191	VAL	4.8
3	XY	44	PRO	4.8

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Mol	Chain	Res	Type	RSRZ
3	QY	91	ASP	4.8
4	RA	2111	C	4.8
4	RA	1046	A	4.8
35	XA	1030(A)	C	4.7
3	XY	51	GLU	4.7
3	XY	42	GLU	4.7
4	YA	2130	U	4.7
3	QY	44	PRO	4.7
3	QY	8	ASN	4.7
3	XY	104	ASP	4.6
4	YA	280	C	4.6
4	RA	2131	G	4.6
4	YA	2145	C	4.6
4	YA	2803	C	4.6
4	RA	2170	A	4.6
4	RA	2128	C	4.5
4	RA	2174	C	4.5
3	QY	216	SER	4.5
55	QU	16	GLY	4.5
4	RA	2894	G	4.5
4	YA	1509(A)	C	4.5
24	YZ	196	VAL	4.5
35	QA	345	C	4.5
3	QY	229	ASP	4.5
35	XA	1001(B)	G	4.5
4	YA	1085	A	4.5
3	QY	38	ASN	4.5
4	RA	2112	G	4.5
3	QY	69	THR	4.5
3	QY	202	VAL	4.5
6	YD	276	LYS	4.5
3	XY	87	ALA	4.4
35	XA	84	U	4.4
3	QY	232	ILE	4.4
4	YA	2146	C	4.4
3	XY	80	VAL	4.4
35	XA	91	C	4.4
35	QA	1532	U	4.3
4	RA	2116	G	4.3
3	XY	8	ASN	4.3
41	QG	78	ARG	4.3
3	QY	14	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
3	XY	91	ASP	4.3
3	XY	62	SER	4.3
4	YA	1095	A	4.3
3	XY	95	THR	4.3
4	RA	2807	G	4.3
35	QA	1001(A)	A	4.3
4	YA	1064	C	4.3
4	YA	2167	U	4.2
35	XA	1257	U	4.2
3	QY	95	THR	4.2
3	QY	163	THR	4.2
4	RA	2143	C	4.2
3	XY	81	SER	4.2
3	QY	101	ALA	4.2
3	XY	110	LEU	4.2
24	YZ	197	ILE	4.2
3	XY	55	ALA	4.2
3	XY	75	GLN	4.2
25	R0	8	GLY	4.2
29	Y4	59	PHE	4.2
4	RA	1085	A	4.2
35	QA	1030(D)	G	4.2
4	RA	1095	A	4.2
4	RA	2121	G	4.2
3	XY	100	VAL	4.2
4	YA	2896	C	4.1
4	RA	2119	A	4.1
4	RA	2129	C	4.1
35	QA	1028	C	4.1
4	RA	2123	G	4.1
29	R4	49	PHE	4.1
53	XS	4	SER	4.1
41	QG	80	VAL	4.1
3	QY	16	GLU	4.1
29	Y4	66	SER	4.1
3	XY	71	ASP	4.1
3	XY	164	GLU	4.1
4	YA	2172	U	4.1
4	YA	1087	G	4.1
3	QY	60	ARG	4.1
4	YA	2174	C	4.1
3	XY	228	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
4	YA	1078	U	4.1
3	XY	7	VAL	4.1
4	RA	2106	G	4.1
44	QJ	32	ALA	4.1
3	XY	205	SER	4.1
4	YA	1080	C	4.1
9	YG	51	ARG	4.1
3	QY	93	GLU	4.1
44	QJ	10	GLY	4.0
4	RA	2126	A	4.0
44	QJ	27	ALA	4.0
4	RA	2794(A)	C	4.0
4	RA	2109	U	4.0
4	YA	2133	G	4.0
4	RA	2165	G	4.0
35	XA	1001(A)	A	4.0
4	YA	2151	G	4.0
22	RX	1	MET	4.0
4	RA	2897	U	4.0
4	YA	2129	C	4.0
31	R6	20	ASN	4.0
3	XY	94	GLU	4.0
10	RH	43	VAL	4.0
35	XA	1531	A	4.0
3	XY	11	ILE	4.0
4	RA	2179	C	4.0
4	YA	2165	G	3.9
3	QY	150	ARG	3.9
4	RA	2136	C	3.9
31	Y6	42	TRP	3.9
10	RH	159	GLU	3.9
4	YA	2147	G	3.9
4	RA	2148	G	3.9
35	XA	1036	G	3.9
3	QY	326	TYR	3.9
3	XY	352	SER	3.9
3	QY	290	GLN	3.9
4	YA	2107	C	3.8
41	XG	156	TRP	3.8
3	QY	201	LEU	3.8
4	YA	2117	A	3.8
4	RA	2180	U	3.8

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Mol	Chain	Res	Type	RSRZ
3	QY	234	ILE	3.8
3	XY	13	ASP	3.8
4	RA	652(D)	G	3.8
3	XY	97	ASN	3.8
3	XY	86	LEU	3.8
36	QB	131	PRO	3.8
3	QY	64	GLU	3.8
3	XY	72	GLN	3.8
3	XY	348	VAL	3.8
4	RA	1090	U	3.8
4	RA	2792	G	3.8
36	XB	130	ARG	3.8
4	YA	2137	C	3.8
35	QA	1037	C	3.8
24	YZ	199	LYS	3.8
44	XJ	38	ILE	3.8
3	QY	228	ASP	3.8
3	QY	90	ALA	3.8
4	YA	2894	G	3.8
41	QG	83	ALA	3.8
3	QY	84	LEU	3.8
4	YA	1082	U	3.7
3	QY	206	PRO	3.7
35	XA	202	U	3.7
3	QY	119	PHE	3.7
53	XS	69	HIS	3.7
55	QU	5	ASP	3.7
35	QA	1034	G	3.7
3	XY	74	LYS	3.7
35	XA	1533	C	3.7
4	RA	2152	G	3.7
4	RA	2156	G	3.7
3	XY	21	LEU	3.7
3	QY	327	VAL	3.7
3	XY	296	TYR	3.7
4	RA	2122	U	3.7
4	RA	1075	C	3.7
35	XA	1037	C	3.7
3	QY	56	LEU	3.7
23	RY	5	MET	3.7
1	QV	1	C	3.7
4	RA	2117	A	3.7

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Mol	Chain	Res	Type	RSRZ
3	XY	230	ILE	3.7
3	XY	60	ARG	3.7
3	QY	67	VAL	3.6
3	QY	80	VAL	3.6
53	QS	49	ILE	3.6
4	YA	1090	U	3.6
10	RH	97	ARG	3.6
55	QU	22	ARG	3.6
4	YA	1079	C	3.6
3	XY	40	GLU	3.6
4	YA	1093	G	3.6
3	XY	48	ASN	3.6
29	R4	65	ASP	3.6
4	RA	1078	U	3.6
35	QA	160	A	3.6
4	RA	2160	G	3.6
24	YZ	195	GLU	3.6
4	RA	2108	C	3.6
3	QY	9	ASN	3.6
3	XY	82	GLY	3.6
36	QB	115	LEU	3.6
10	RH	102	ALA	3.5
47	QM	4	ILE	3.5
4	YA	2794(A)	C	3.5
3	QY	92	ASP	3.5
4	RA	2132	U	3.5
11	RI	83	ALA	3.5
3	QY	268	THR	3.5
3	QY	46	VAL	3.5
3	QY	96	PHE	3.5
4	YA	1065	U	3.5
4	RA	1087	G	3.5
3	XY	298	LEU	3.5
3	QY	329	ASP	3.5
53	QS	66	MET	3.5
24	YZ	201	LYS	3.5
3	QY	83	LEU	3.5
35	XA	1532	U	3.5
3	QY	39	ALA	3.5
41	QG	85	TYR	3.5
3	XY	98	GLU	3.5
3	QY	106	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
3	XY	109	LYS	3.5
3	QY	233	GLU	3.4
3	QY	82	GLY	3.4
4	RA	888	C	3.4
31	R6	43	CYS	3.4
4	YA	2168	G	3.4
3	XY	96	PHE	3.4
4	RA	2167	U	3.4
24	RZ	197	ILE	3.4
3	QY	270	ILE	3.4
3	QY	65	ALA	3.4
35	XA	1286	A	3.4
4	YA	2118	U	3.4
31	Y6	20	ASN	3.4
3	XY	26	ASP	3.4
36	QB	187	LEU	3.4
3	XY	27	TYR	3.4
3	QY	205	SER	3.4
3	XY	28	ASP	3.4
3	XY	90	ALA	3.4
41	QG	84	ASN	3.4
4	YA	229	A	3.3
4	RA	2171	A	3.3
35	QA	1030(E)	A	3.3
10	RH	24	VAL	3.3
23	RY	77	PRO	3.3
2	XX	23	A	3.3
3	QY	140	GLU	3.3
4	RA	2107	C	3.3
4	RA	1082	U	3.3
4	RA	2115	G	3.3
35	XA	1026	G	3.3
3	QY	209	SER	3.3
3	QY	265	HIS	3.3
36	XB	227	GLY	3.3
27	R2	1	MET	3.3
2	QX	14	A	3.3
31	R6	49	HIS	3.3
46	QL	64	TYR	3.3
55	QU	17	THR	3.3
4	YA	2128	C	3.3
3	XY	64	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
24	RZ	190	GLU	3.3
3	QY	100	VAL	3.3
41	XG	78	ARG	3.3
3	XY	321	SER	3.3
3	QY	21	LEU	3.3
3	QY	103	LEU	3.3
3	XY	203	ARG	3.3
3	QY	210	GLY	3.3
31	Y6	49	HIS	3.3
10	RH	19	VAL	3.3
3	XY	68	ASP	3.3
48	QN	25	VAL	3.3
3	QY	164	GLU	3.3
31	Y6	43	CYS	3.3
41	XG	85	TYR	3.3
4	YA	2176	A	3.2
3	XY	120	SER	3.2
4	YA	2802	G	3.2
4	RA	1080	C	3.2
52	QR	58	LEU	3.2
1	XV	1	C	3.2
29	Y4	65	ASP	3.2
3	XY	65	ALA	3.2
4	RA	1065	U	3.2
35	XA	1029	C	3.2
35	QA	1006	C	3.2
1	QV	53	G	3.2
35	QA	79	G	3.2
3	XY	17	ARG	3.2
36	QB	135	GLN	3.2
41	QG	37	ASN	3.2
3	XY	140	GLU	3.2
3	QY	238	ASP	3.2
44	XJ	71	LEU	3.2
9	RG	2	PRO	3.2
3	QY	61	SER	3.2
47	QM	116	THR	3.2
4	RA	2133	G	3.2
3	QY	105	ALA	3.2
4	YA	2156	G	3.2
4	YA	2159	G	3.2
4	YA	277	C	3.2

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Mol	Chain	Res	Type	RSRZ
3	QY	11	ILE	3.2
54	XT	99	LEU	3.2
3	XY	216	SER	3.2
53	QS	35	SER	3.2
3	XY	308	GLN	3.2
35	QA	1257	U	3.2
3	XY	232	ILE	3.2
3	XY	119	PHE	3.2
3	QY	143	ASP	3.1
3	QY	97	ASN	3.1
9	YG	49	ASP	3.1
52	QR	57	GLY	3.1
3	XY	54	GLN	3.1
3	XY	345	THR	3.1
29	Y4	54	GLY	3.1
52	QR	62	GLU	3.1
4	RA	2164	C	3.1
31	Y6	36	LEU	3.1
3	QY	87	ALA	3.1
53	XS	49	ILE	3.1
3	QY	7	VAL	3.1
3	XY	342	THR	3.1
53	XS	40	ILE	3.1
3	QY	78	GLU	3.1
34	R9	12	ASP	3.1
41	XG	77	SER	3.1
4	YA	1088	A	3.1
3	QY	86	LEU	3.1
3	XY	103	LEU	3.1
4	RA	2175	C	3.1
3	XY	276	ASN	3.0
44	XJ	98	ILE	3.0
4	RA	1081	U	3.0
10	RH	101	ARG	3.0
35	XA	93	G	3.0
4	RA	2134	A	3.0
3	XY	108	GLU	3.0
29	R4	67	TYR	3.0
37	XC	193	TYR	3.0
4	YA	1058	G	3.0
4	YA	2131	G	3.0
4	RA	2157	G	3.0

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Mol	Chain	Res	Type	RSRZ
31	Y6	35	GLU	3.0
35	XA	79	G	3.0
4	YA	2164	C	3.0
41	QG	4	ARG	3.0
44	QJ	34	VAL	3.0
4	RA	2181	G	3.0
24	YZ	198	LYS	3.0
35	XA	1030(D)	G	3.0
4	YA	2163	C	3.0
35	XA	204	U	3.0
3	XY	9	ASN	3.0
29	Y4	67	TYR	3.0
31	R6	17	LYS	3.0
37	XC	206	GLU	3.0
50	QP	19	ILE	3.0
4	RA	2808	U	3.0
28	R3	59	VAL	3.0
48	QN	3	ARG	3.0
4	YA	276	A	3.0
3	XY	39	ALA	3.0
3	XY	57	GLY	3.0
3	XY	61	SER	3.0
24	YZ	194	PRO	3.0
43	QI	6	GLY	3.0
3	XY	79	ASP	3.0
52	QR	43	PHE	3.0
52	QR	56	THR	3.0
43	XI	8	GLY	3.0
4	YA	2122	U	3.0
37	QC	160	ALA	3.0
3	XY	106	LEU	3.0
4	YA	652(W)	C	3.0
35	XA	1028	C	3.0
43	QI	36	TYR	3.0
53	XS	71	LEU	3.0
26	R1	2	SER	3.0
3	XY	102	GLU	3.0
3	XY	107	GLU	2.9
10	RH	103	LEU	2.9
3	XY	238	ASP	2.9
31	R6	12	GLU	2.9
3	QY	331	SER	2.9

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Mol	Chain	Res	Type	RSRZ
31	Y6	54	ILE	2.9
35	QA	1026	G	2.9
37	QC	153	VAL	2.9
23	RY	2	ARG	2.9
3	XY	77	LEU	2.9
31	R6	41	PRO	2.9
4	RA	645	C	2.9
2	QX	23	A	2.9
4	YA	278	A	2.9
35	QA	1005	A	2.9
3	XY	56	LEU	2.9
4	RA	2895	U	2.9
22	RX	92	LEU	2.9
36	XB	121	LEU	2.9
3	XY	180	THR	2.9
48	QN	38	GLY	2.9
3	XY	166	ILE	2.9
10	RH	89	ILE	2.9
3	XY	325	SER	2.9
4	YA	1057	A	2.9
28	Y3	2	PRO	2.9
3	QY	85	GLU	2.9
3	XY	132	ILE	2.9
4	YA	2807	G	2.9
4	YA	1046	A	2.9
10	RH	116	GLU	2.9
3	XY	330	ASP	2.9
4	YA	2115	G	2.9
4	YA	2897	U	2.9
4	YA	2135	A	2.9
11	RI	86	THR	2.9
3	XY	105	ALA	2.9
43	QI	7	THR	2.9
35	XA	1003	G	2.9
53	QS	45	VAL	2.8
46	XL	61	THR	2.8
3	QY	149	GLU	2.8
4	YA	652(D)	G	2.8
4	YA	2792	G	2.8
3	QY	334	LYS	2.8
3	QY	13	ASP	2.8
3	XY	52	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
43	QI	33	PHE	2.8
35	XA	1456	G	2.8
41	QG	154	TYR	2.8
3	QY	269	GLY	2.8
18	RT	37	GLY	2.8
3	XY	10	ARG	2.8
35	QA	1007	C	2.8
4	RA	1057	A	2.8
3	XY	113	LEU	2.8
4	YA	2124	G	2.8
53	QS	15	LEU	2.8
3	XY	34	LEU	2.8
35	XA	1035	A	2.8
44	XJ	6	ILE	2.8
53	QS	41	VAL	2.8
53	QS	63	THR	2.8
35	QA	90	U	2.8
3	XY	31	LYS	2.8
35	QA	1000	U	2.8
55	QU	12	LYS	2.8
35	QA	1001(B)	G	2.8
4	RA	2130	U	2.8
31	R6	9	LEU	2.8
24	RZ	196	VAL	2.8
3	QY	120	SER	2.8
4	YA	275	G	2.8
4	RA	11	G	2.8
3	XY	227	ASP	2.8
10	RH	33	LEU	2.8
4	YA	272(K)	U	2.8
24	YZ	186	GLU	2.8
3	QY	63	LEU	2.8
3	XY	274	CYS	2.8
23	RY	55	TYR	2.8
31	R6	53	LYS	2.7
3	QY	20	VAL	2.7
3	XY	6	PRO	2.7
44	XJ	34	VAL	2.7
53	XS	27	GLU	2.7
2	QX	22	C	2.7
35	XA	1030(B)	G	2.7
3	QY	166	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
3	XY	304	ASN	2.7
10	RH	111	HIS	2.7
44	QJ	23	ILE	2.7
3	QY	79	ASP	2.7
31	R6	11	LEU	2.7
31	R6	5	VAL	2.7
10	RH	56	SER	2.7
53	XS	38	SER	2.7
3	XY	268	THR	2.7
35	XA	1034	G	2.7
4	RA	6	A	2.7
3	QY	217	PHE	2.7
31	Y6	48	VAL	2.7
10	RH	47	GLU	2.7
11	RI	138	ILE	2.7
11	RI	14	ASP	2.7
32	R7	48	LYS	2.7
4	YA	652(U)	C	2.7
53	QS	16	LEU	2.7
10	RH	99	VAL	2.7
11	RI	41	GLU	2.7
24	YZ	188	ALA	2.7
35	QA	1031	G	2.7
53	QS	20	LEU	2.7
3	QY	48	ASN	2.7
4	RA	2178	C	2.7
4	YA	1074	G	2.7
3	QY	99	ALA	2.7
4	YA	888	C	2.7
41	XG	154	TYR	2.7
43	XI	19	LEU	2.7
12	RN	8	GLN	2.7
4	RA	2892	A	2.7
11	RI	20	ASP	2.7
4	YA	2157	G	2.7
23	RY	12	THR	2.7
35	QA	1027	C	2.7
42	QH	107	LEU	2.7
44	QJ	5	ARG	2.7
10	RH	115	VAL	2.7
36	XB	165	VAL	2.7
3	QY	272	THR	2.7

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Mol	Chain	Res	Type	RSRZ
3	QY	147	MET	2.7
11	RI	16	GLY	2.7
41	QG	86	GLN	2.7
3	QY	165	ILE	2.7
41	QG	77	SER	2.6
9	YG	47	LYS	2.6
4	YA	1063	G	2.6
35	XA	1024	G	2.6
23	RY	107	ASP	2.6
3	QY	341	GLU	2.6
3	XY	78	GLU	2.6
52	QR	28	GLU	2.6
4	YA	2171	A	2.6
3	QY	146	SER	2.6
35	QA	346	G	2.6
31	Y6	16	CYS	2.6
4	YA	652(E)	C	2.6
4	RA	2163	C	2.6
25	R0	9	SER	2.6
47	XM	115	LYS	2.6
47	QM	65	LYS	2.6
28	R3	2	PRO	2.6
24	YZ	190	GLU	2.6
35	QA	1035	A	2.6
3	QY	214	HIS	2.6
4	YA	2109	U	2.6
4	YA	2150	U	2.6
4	YA	2121	G	2.6
31	R6	35	GLU	2.6
35	XA	1004	A	2.6
29	Y4	69	LYS	2.6
31	Y6	17	LYS	2.6
34	R9	13	LYS	2.6
11	RI	96	ASP	2.6
29	Y4	49	PHE	2.6
3	QY	37	VAL	2.6
52	QR	22	VAL	2.6
46	XL	64	TYR	2.6
34	R9	37	GLY	2.6
55	XU	2	GLY	2.6
10	RH	113	VAL	2.6
53	QS	65	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
4	RA	652(V)	G	2.5
3	XY	63	LEU	2.5
31	Y6	41	PRO	2.5
3	XY	225	GLU	2.5
23	RY	50	ARG	2.5
37	QC	159	GLY	2.5
3	QY	300	MET	2.5
31	R6	7	ILE	2.5
35	XA	1043	C	2.5
4	RA	10	G	2.5
36	QB	214	ILE	2.5
12	RN	9	VAL	2.5
11	RI	1	MET	2.5
3	XY	20	VAL	2.5
47	QM	117	VAL	2.5
3	XY	37	VAL	2.5
43	XI	102	LEU	2.5
3	QY	208	ASP	2.5
11	RI	61	ARG	2.5
37	XC	190	ARG	2.5
55	XU	22	ARG	2.5
11	RI	4	ILE	2.5
3	QY	325	SER	2.5
4	YA	2149	G	2.5
53	QS	47	HIS	2.5
29	R4	59	PHE	2.5
4	RA	1104	C	2.5
10	RH	112	PRO	2.5
31	R6	16	CYS	2.5
31	R6	40	CYS	2.5
31	Y6	50	ARG	2.5
43	QI	4	TYR	2.5
43	QI	5	TYR	2.5
3	QY	317	ILE	2.5
3	QY	333	ILE	2.5
36	XB	127	ILE	2.5
3	QY	98	GLU	2.5
47	XM	94	ARG	2.5
4	YA	2112	G	2.5
4	RA	2893	G	2.5
17	RS	58	LEU	2.5
40	QF	90	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
44	QJ	20	ALA	2.5
53	XS	47	HIS	2.5
3	XY	35	GLU	2.5
31	R6	18	ARG	2.5
3	XY	201	LEU	2.5
4	YA	2808	U	2.5
3	QY	45	ASP	2.5
55	QU	13	ILE	2.5
3	XY	25	LEU	2.4
9	RG	75	LYS	2.4
4	YA	1026	U	2.4
3	QY	286	GLN	2.4
4	YA	2166	G	2.4
4	RA	652(U)	C	2.4
4	RA	2100	G	2.4
3	XY	150	ARG	2.4
4	YA	2170	A	2.4
4	RA	1536	C	2.4
3	XY	202	VAL	2.4
37	XC	101	LEU	2.4
3	XY	144	TRP	2.4
55	QU	24	ARG	2.4
3	XY	29	ALA	2.4
3	QY	344	ASN	2.4
44	QJ	38	ILE	2.4
4	YA	279	C	2.4
3	QY	23	GLY	2.4
3	XY	326	TYR	2.4
44	QJ	35	SER	2.4
3	XY	295	LEU	2.4
43	QI	66	ARG	2.4
4	YA	1072	C	2.4
54	XT	7	LYS	2.4
35	QA	1286	A	2.4
48	XN	2	ALA	2.4
3	QY	218	SER	2.4
3	XY	49	GLU	2.4
4	YA	2127	G	2.4
3	XY	16	GLU	2.4
3	QY	10	ARG	2.4
3	QY	62	SER	2.4
55	XU	24	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
3	QY	239	LEU	2.4
4	RA	2135	A	2.4
35	XA	1030(E)	A	2.4
4	YA	652(V)	G	2.4
45	QK	90	GLY	2.4
47	XM	32	GLU	2.4
1	QV	47	U	2.4
4	YA	653	A	2.4
43	XI	7	THR	2.4
3	QY	199	HIS	2.4
3	XY	214	HIS	2.4
4	RA	1055	G	2.4
35	XA	1032	G	2.4
3	QY	294	LYS	2.4
41	XG	20	ASP	2.4
55	QU	14	TRP	2.4
42	XH	53	VAL	2.4
3	XY	141	ALA	2.4
3	XY	265	HIS	2.4
48	QN	7	ILE	2.4
4	RA	1089	G	2.4
2	XX	14	A	2.3
14	YP	118	GLY	2.3
41	QG	6	ARG	2.3
41	XG	86	GLN	2.3
43	QI	37	PHE	2.3
3	QY	59	GLU	2.3
37	QC	191	THR	2.3
36	QB	55	PHE	2.3
43	QI	19	LEU	2.3
48	QN	2	ALA	2.3
31	Y6	18	ARG	2.3
4	RA	2166	G	2.3
9	RG	29	TRP	2.3
10	RH	30	LYS	2.3
35	QA	791	G	2.3
4	YA	1536	C	2.3
4	RA	652(W)	C	2.3
4	RA	653	A	2.3
4	RA	1103	A	2.3
4	RA	1066	U	2.3
12	YN	140	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
9	RG	49	ASP	2.3
4	RA	2151	G	2.3
36	XB	133	LYS	2.3
37	XC	100	ALA	2.3
3	QY	353	LEU	2.3
31	Y6	13	CYS	2.3
31	R6	10	LEU	2.3
4	YA	2106	G	2.3
53	QS	4	SER	2.3
1	XV	47	U	2.3
24	RZ	2	GLU	2.3
36	XB	63	MET	2.3
53	XS	56	GLN	2.3
23	RY	35	TYR	2.3
50	XP	19	ILE	2.3
31	R6	44	ARG	2.3
11	RI	88	ILE	2.3
35	XA	1031	G	2.3
35	XA	1042	G	2.3
35	QA	1042	G	2.3
4	YA	2126	A	2.3
4	RA	1077	A	2.3
36	XB	228	GLY	2.3
47	XM	95	GLY	2.3
35	XA	789	U	2.3
4	RA	1070	A	2.3
36	XB	128	GLU	2.3
14	RP	138	LEU	2.3
3	XY	112	GLN	2.3
47	QM	78	ILE	2.3
36	QB	122	PHE	2.3
3	QY	41	LEU	2.3
3	QY	110	LEU	2.3
35	QA	159	G	2.3
23	RY	78	ALA	2.3
41	XG	127	ALA	2.3
52	QR	86	VAL	2.3
3	QY	215	THR	2.3
3	QY	227	ASP	2.3
37	XC	196	LEU	2.3
3	QY	318	GLY	2.2
3	XY	99	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
31	R6	52	VAL	2.3
54	XT	45	GLN	2.3
4	YA	11	G	2.2
4	RA	1044	G	2.2
43	XI	50	LEU	2.2
4	YA	1102	C	2.2
54	XT	6	PRO	2.2
36	XB	122	PHE	2.2
53	XS	60	VAL	2.2
3	XY	309	ALA	2.2
3	QY	52	ARG	2.2
4	YA	2123	G	2.2
44	XJ	69	ASN	2.2
53	QS	6	LYS	2.2
55	XU	23	PRO	2.2
24	RZ	7	ALA	2.2
35	XA	1027	C	2.2
37	XC	159	GLY	2.2
54	QT	40	ALA	2.2
55	QU	21	TYR	2.2
37	QC	196	LEU	2.2
31	R6	14	THR	2.2
43	QI	76	ALA	2.2
4	RA	2177	C	2.2
3	QY	176	ILE	2.2
3	XY	327	VAL	2.2
3	QY	168	GLU	2.2
3	XY	250	GLY	2.2
10	RH	175	LYS	2.2
43	QI	106	ALA	2.2
3	QY	34	LEU	2.2
3	QY	35	GLU	2.2
36	QB	133	LYS	2.2
43	QI	88	TYR	2.2
3	XY	158	SER	2.2
49	XO	88	ARG	2.2
55	QU	10	ARG	2.2
3	XY	341	GLU	2.2
50	XP	36	ILE	2.2
43	QI	67	GLY	2.2
50	QP	54	GLU	2.2
19	RU	116	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
53	QS	30	LEU	2.2
36	QB	48	MET	2.2
14	RP	94	GLU	2.2
31	Y6	15	GLU	2.2
3	QY	219	SER	2.2
4	YA	1070	A	2.2
3	QY	113	LEU	2.2
10	RH	13	LYS	2.2
36	QB	232	PRO	2.2
37	QC	155	GLY	2.2
42	XH	60	ARG	2.2
43	QI	50	LEU	2.2
48	QN	35	ARG	2.2
55	QU	6	ARG	2.2
3	XY	346	GLN	2.2
9	YG	80	PHE	2.2
3	QY	304	ASN	2.2
8	YF	27	GLU	2.2
11	YI	79	ILE	2.2
11	YI	81	VAL	2.2
29	R4	52	THR	2.2
42	QH	123	GLU	2.2
3	XY	289	LYS	2.2
11	RI	39	ALA	2.2
47	XM	107	ALA	2.2
3	QY	236	PRO	2.2
44	XJ	36	GLY	2.2
45	XK	117	ASN	2.2
55	QU	2	GLY	2.2
31	R6	21	TYR	2.1
43	XI	4	TYR	2.1
3	XY	136	SER	2.1
50	XP	1	MET	2.1
53	QS	64	GLU	2.1
4	YA	1103	A	2.1
53	XS	30	LEU	2.1
3	XY	301	GLN	2.1
2	XX	22	C	2.1
35	XA	1038	C	2.1
54	XT	55	ILE	2.1
53	QS	82	GLY	2.1
44	QJ	71	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
3	QY	128	CYS	2.1
3	QY	141	ALA	2.1
3	XY	255	ASN	2.1
4	RA	1058	G	2.1
9	RG	80	PHE	2.1
35	QA	78	G	2.1
10	RH	34	GLU	2.1
47	QM	97	PRO	2.1
4	YA	2136	C	2.1
34	Y9	29	ASN	2.1
44	XJ	7	LYS	2.1
53	QS	43	GLU	2.1
4	RA	1056	G	2.1
3	QY	131	ASP	2.1
4	YA	9	U	2.1
36	QB	123	ALA	2.1
36	QB	132	LYS	2.1
44	QJ	29	ARG	2.1
45	QK	126	ARG	2.1
50	QP	48	TRP	2.1
3	QY	51	GLU	2.1
3	QY	264	THR	2.1
11	YI	85	GLU	2.1
20	YV	1	MET	2.1
44	QJ	85	LEU	2.1
52	XR	31	LEU	2.1
17	RS	83	LYS	2.1
26	R1	23	LYS	2.1
3	XY	293	ALA	2.1
10	RH	96	ALA	2.1
42	XH	25	ASP	2.1
43	QI	75	ASP	2.1
35	XA	1040	U	2.1
3	XY	340	VAL	2.1
11	YI	88	ILE	2.1
12	RN	140	VAL	2.1
45	QK	98	LEU	2.1
3	QY	207	PHE	2.1
52	QR	29	PHE	2.1
53	QS	27	GLU	2.1
3	XY	76	GLY	2.1
8	RF	208	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
37	QC	81	GLY	2.1
49	QO	86	GLY	2.1
3	XY	123	TYR	2.1
39	XE	81	GLU	2.1
6	RD	276	LYS	2.1
24	RZ	4	ARG	2.1
31	R6	29	ASN	2.1
35	XA	78	G	2.1
3	QY	33	ARG	2.1
10	RH	169	VAL	2.1
44	QJ	72	VAL	2.1
51	QQ	11	VAL	2.1
53	QS	38	SER	2.1
29	R4	46	GLN	2.1
43	QI	3	GLN	2.1
3	QY	42	GLU	2.1
10	RH	46	GLU	2.1
44	XJ	72	VAL	2.1
4	YA	1089	G	2.1
23	RY	76	CYS	2.1
23	YY	60	PHE	2.1
18	RT	38	ASN	2.1
46	XL	28	LYS	2.1
3	QY	15	THR	2.1
55	XU	18	TYR	2.1
10	RH	41	MET	2.1
14	RP	119	GLU	2.0
36	QB	21	ARG	2.0
35	XA	1002	G	2.0
10	RH	29	PRO	2.0
31	R6	23	THR	2.0
35	QA	204	U	2.0
36	XB	222	ILE	2.0
3	QY	185	GLY	2.0
37	QC	194	GLY	2.0
3	XY	331	SER	2.0
10	RH	95	ARG	2.0
31	R6	15	GLU	2.0
37	QC	189	ALA	2.0
37	QC	207	VAL	2.0
50	XP	21	VAL	2.0
53	QS	80	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
35	QA	1025	U	2.0
3	QY	343	ARG	2.0
3	QY	170	GLU	2.0
35	QA	1447	A	2.0
43	XI	6	GLY	2.0
50	XP	55	ARG	2.0
35	QA	723	U	2.0
3	QY	242	ASP	2.0
3	XY	18	SER	2.0
47	QM	92	HIS	2.0
3	QY	109	LYS	2.0
3	QY	123	TYR	2.0
3	QY	183	ILE	2.0
3	XY	294	LYS	2.0
37	XC	66	VAL	2.0
41	XG	83	ALA	2.0
12	RN	10	GLU	2.0
53	XS	44	MET	2.0
35	QA	343	U	2.0
44	XJ	8	LEU	2.0
4	YA	2148	G	2.0
4	RA	352	G	2.0
35	QA	161	A	2.0
44	XJ	78	ASN	2.0
44	XJ	85	LEU	2.0
55	QU	9	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
35	5MC	XA	1404	21/22	0.97	0.18	-	34,45,58,63	0
4	4OC	YA	1920	21/23	0.97	0.16	-	40,47,55,60	0
35	4OC	XA	1402	22/23	0.94	0.23	-	45,57,67,81	0
4	PSU	YA	1917	20/21	0.93	0.17	-	51,62,88,91	0
35	MA6	XA	1519	24/25	0.98	0.18	-	28,45,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	MA6	XA	1518	24/25	0.98	0.20	-	31,41,46,52	0
4	2MU	YA	2552	21/23	0.98	0.18	-	19,28,42,46	0
35	5MC	XA	1407	21/22	0.97	0.20	-	46,49,58,59	0
4	2MA	YA	2503	23/24	0.98	0.18	-	8,22,36,38	0
35	2MG	QA	1207	24/25	0.94	0.13	-	101,124,131,134	0
4	5MC	YA	1942	21/22	0.98	0.16	-	25,38,47,50	0
35	UR3	QA	1498	21/22	0.97	0.18	-	44,57,69,72	0
35	UR3	XA	1498	21/22	0.98	0.15	-	34,43,57,66	0
4	OMG	RA	2251	24/25	0.98	0.18	-	31,38,50,55	0
4	PSU	RA	2605	20/21	0.97	0.17	-	19,36,47,48	0
35	5MC	QA	1400	21/22	0.96	0.21	-	66,75,85,88	0
4	5MC	YA	1962	21/22	0.98	0.15	-	25,33,47,55	0
4	PSU	RA	1917	20/21	0.93	0.17	-	53,73,89,103	0
4	5MC	RA	1962	21/22	0.98	0.15	-	39,46,52,62	0
35	5MC	QA	1407	21/22	0.98	0.15	-	44,51,62,68	0
4	OMG	YA	2251	24/25	0.98	0.19	-	13,25,35,41	0
4	PSU	YA	2605	20/21	0.97	0.21	-	10,25,42,59	0
35	7MG	QA	527	24/25	0.94	0.21	-	51,70,76,76	0
35	5MC	QA	967	21/22	0.94	0.22	-	71,84,95,99	0
4	5MU	YA	1915	21/22	0.91	0.18	-	52,76,85,87	0
4	5MU	RA	1915	21/22	0.91	0.13	-	92,100,114,117	0
35	M2G	XA	966	25/26	0.94	0.19	-	56,75,94,105	0
4	5MC	RA	1942	21/22	0.97	0.20	-	41,50,62,64	0
46	0TD	XL	92	10/11	0.92	0.20	-	58,67,84,87	0
35	5MC	QA	1404	21/22	0.96	0.20	-	55,62,67,73	0
35	MA6	QA	1518	24/25	0.96	0.19	-	48,58,67,72	0
35	PSU	QA	516	20/21	0.93	0.13	-	71,77,87,88	0
35	5MC	XA	1400	21/22	0.96	0.18	-	50,65,74,85	0
35	M2G	QA	966	25/26	0.93	0.21	-	71,80,92,93	0
4	2MU	RA	2552	21/23	0.98	0.17	-	19,33,40,48	0
35	MA6	QA	1519	24/25	0.96	0.25	-	41,56,68,79	0
4	4OC	RA	1920	21/23	0.95	0.20	-	55,62,85,94	0
4	5MU	RA	1939	21/22	0.97	0.19	-	23,37,44,52	0
35	7MG	XA	527	24/25	0.96	0.20	-	54,63,74,79	0
35	PSU	XA	516	20/21	0.93	0.18	-	75,86,95,95	0
46	0TD	QL	92	10/11	0.94	0.18	-	59,72,74,78	0
35	5MC	XA	967	21/22	0.95	0.20	-	62,75,84,92	0
4	PSU	YA	1911	20/21	0.97	0.17	-	45,57,62,63	0
4	PSU	RA	1911	20/21	0.96	0.15	-	55,66,73,74	0
35	4OC	QA	1402	22/23	0.92	0.23	-	55,67,72,74	0
4	5MU	YA	1939	21/22	0.98	0.17	-	15,27,36,48	0
4	2MA	RA	2503	23/24	0.98	0.16	-	16,24,31,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	2MG	XA	1207	24/25	0.94	0.17	-	85,98,106,107	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3264	1/1	0.75	1.24	138.91	63,63,63,63	0
56	MG	RA	4015	1/1	0.21	0.92	123.17	89,89,89,89	0
56	MG	RA	3696	1/1	0.86	1.18	109.91	74,74,74,74	0
56	MG	RA	3088	1/1	0.80	1.56	102.48	89,89,89,89	0
56	MG	RA	3457	1/1	0.50	1.10	100.26	81,81,81,81	0
56	MG	RA	3968	1/1	0.61	0.74	74.01	66,66,66,66	0
56	MG	RA	3511	1/1	0.38	1.14	72.77	62,62,62,62	0
56	MG	RA	3196	1/1	0.84	0.97	67.94	104,104,104,104	0
56	MG	RA	3360	1/1	0.70	0.93	67.86	66,66,66,66	0
56	MG	RA	3141	1/1	0.95	0.60	66.68	93,93,93,93	0
56	MG	YA	3491	1/1	0.73	0.66	66.06	53,53,53,53	0
56	MG	YA	3662	1/1	0.56	0.79	62.49	91,91,91,91	0
56	MG	YA	3654	1/1	0.92	0.78	61.24	54,54,54,54	0
56	MG	RA	3828	1/1	-0.18	1.87	61.21	94,94,94,94	0
56	MG	YA	3302	1/1	0.34	0.79	60.28	72,72,72,72	0
56	MG	YA	3273	1/1	0.53	0.90	59.55	72,72,72,72	0
56	MG	RA	3881	1/1	0.92	1.20	59.41	68,68,68,68	0
56	MG	YA	3056	1/1	0.17	1.07	59.27	81,81,81,81	0
56	MG	YA	3090	1/1	0.85	0.91	58.63	54,54,54,54	0
56	MG	YA	3377	1/1	0.89	0.81	56.63	52,52,52,52	0
56	MG	XA	1719	1/1	0.24	0.94	54.90	95,95,95,95	0
56	MG	RA	3177	1/1	0.68	0.70	54.29	72,72,72,72	0
56	MG	RA	3374	1/1	0.88	0.69	52.51	92,92,92,92	0
56	MG	RA	4039	1/1	0.92	1.34	50.16	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	R0	103	1/1	0.50	1.31	48.73	81,81,81,81	0
56	MG	RA	3630	1/1	0.64	0.64	48.42	90,90,90,90	0
56	MG	RA	3804	1/1	0.90	0.57	47.90	78,78,78,78	0
56	MG	QA	1812	1/1	0.53	0.97	47.81	68,68,68,68	0
56	MG	YA	3688	1/1	0.88	0.55	47.71	62,62,62,62	0
56	MG	RA	3637	1/1	0.63	0.66	46.70	66,66,66,66	0
56	MG	RA	3022	1/1	0.98	0.69	46.65	76,76,76,76	0
56	MG	YA	3574	1/1	0.92	0.45	46.10	30,30,30,30	0
56	MG	RA	3045	1/1	0.94	0.68	44.23	71,71,71,71	0
56	MG	RA	3855	1/1	0.91	0.82	44.22	62,62,62,62	0
56	MG	RA	3418	1/1	0.97	0.69	44.10	36,36,36,36	0
56	MG	YA	3712	1/1	0.97	0.54	43.82	51,51,51,51	0
56	MG	RA	3365	1/1	0.70	0.56	43.54	61,61,61,61	0
56	MG	RA	3750	1/1	0.93	0.93	43.15	66,66,66,66	0
56	MG	YA	3586	1/1	0.87	0.82	42.48	48,48,48,48	0
56	MG	RA	3853	1/1	0.86	1.12	41.47	64,64,64,64	0
56	MG	RA	3711	1/1	0.96	0.60	41.45	80,80,80,80	0
56	MG	YA	3155	1/1	0.73	0.81	40.95	65,65,65,65	0
56	MG	YA	3610	1/1	0.99	0.42	40.75	20,20,20,20	0
56	MG	QA	1870	1/1	0.87	0.62	40.10	47,47,47,47	0
56	MG	RA	3910	1/1	0.78	0.86	39.90	66,66,66,66	0
56	MG	RA	3363	1/1	0.87	0.50	39.78	50,50,50,50	0
56	MG	RA	3475	1/1	0.95	0.56	39.74	46,46,46,46	0
56	MG	RA	3386	1/1	0.95	0.40	38.90	26,26,26,26	0
56	MG	XA	1767	1/1	0.96	0.44	38.54	37,37,37,37	0
56	MG	RA	3978	1/1	0.95	0.52	38.54	55,55,55,55	0
56	MG	RA	3587	1/1	0.96	0.85	38.37	53,53,53,53	0
56	MG	RA	3523	1/1	0.56	0.93	38.29	64,64,64,64	0
56	MG	RA	3353	1/1	0.92	0.50	37.91	35,35,35,35	0
56	MG	RA	3118	1/1	0.93	0.48	37.52	76,76,76,76	0
56	MG	RA	3483	1/1	0.96	0.45	37.40	21,21,21,21	0
56	MG	RA	3301	1/1	0.88	0.83	37.28	66,66,66,66	0
56	MG	RA	3163	1/1	0.83	0.95	37.14	93,93,93,93	0
56	MG	RA	3204	1/1	0.93	0.68	37.07	59,59,59,59	0
56	MG	RA	3772	1/1	0.73	0.41	36.97	57,57,57,57	0
56	MG	YA	3404	1/1	0.97	0.53	36.80	13,13,13,13	0
56	MG	RA	3116	1/1	0.86	0.76	36.72	104,104,104,104	0
56	MG	RA	3029	1/1	0.86	0.73	36.72	66,66,66,66	0
56	MG	RA	3435	1/1	0.98	0.59	36.67	23,23,23,23	0
56	MG	RA	3383	1/1	0.89	0.54	36.39	40,40,40,40	0
56	MG	RA	4020	1/1	0.96	0.88	36.38	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	YA	3133	1/1	0.88	0.52	36.16	91,91,91,91	0
56	MG	RA	3207	1/1	0.74	0.82	36.00	69,69,69,69	0
56	MG	YA	3575	1/1	0.98	0.52	35.97	30,30,30,30	0
56	MG	RD	304	1/1	0.79	1.94	35.59	86,86,86,86	0
56	MG	YA	3416	1/1	0.84	0.84	35.40	39,39,39,39	0
56	MG	RU	203	1/1	0.94	0.79	35.34	64,64,64,64	0
56	MG	QA	1858	1/1	0.21	0.95	35.24	115,115,115,115	0
56	MG	RA	3082	1/1	0.90	0.96	34.44	62,62,62,62	0
56	MG	YE	305	1/1	0.82	0.42	34.01	57,57,57,57	0
56	MG	RA	3602	1/1	0.80	0.96	33.79	80,80,80,80	0
56	MG	QA	1623	1/1	0.84	0.48	33.52	74,74,74,74	0
56	MG	RA	3966	1/1	0.92	0.71	32.42	65,65,65,65	0
56	MG	XA	1784	1/1	0.79	0.78	32.41	72,72,72,72	0
56	MG	YA	3288	1/1	0.93	0.46	32.35	53,53,53,53	0
56	MG	YA	3327	1/1	0.98	0.48	32.35	7,7,7,7	0
56	MG	RA	3407	1/1	0.95	0.50	32.27	34,34,34,34	0
56	MG	RA	3888	1/1	0.97	0.47	32.05	24,24,24,24	0
56	MG	RA	3482	1/1	0.96	0.50	31.68	21,21,21,21	0
56	MG	YA	3298	1/1	0.94	0.56	31.41	19,19,19,19	0
56	MG	RA	3384	1/1	0.98	0.60	31.25	21,21,21,21	0
56	MG	QA	1778	1/1	0.79	0.83	31.25	61,61,61,61	0
56	MG	QA	1721	1/1	0.66	0.58	30.94	75,75,75,75	0
56	MG	RA	3814	1/1	0.87	0.79	30.72	63,63,63,63	0
56	MG	RA	3485	1/1	0.96	0.76	30.57	65,65,65,65	0
56	MG	YA	3634	1/1	0.93	0.77	30.43	48,48,48,48	0
56	MG	RA	3525	1/1	0.25	0.87	30.33	65,65,65,65	0
56	MG	RA	3469	1/1	0.97	0.66	30.33	40,40,40,40	0
56	MG	YA	3581	1/1	0.97	0.56	30.23	24,24,24,24	0
56	MG	RA	3391	1/1	0.98	0.48	30.20	17,17,17,17	0
56	MG	YA	3326	1/1	0.95	0.47	30.00	27,27,27,27	0
56	MG	RA	3613	1/1	0.98	0.41	29.83	35,35,35,35	0
56	MG	YA	3727	1/1	0.63	0.49	29.67	59,59,59,59	0
56	MG	RA	3467	1/1	0.98	0.39	29.61	21,21,21,21	0
56	MG	RA	3849	1/1	0.44	0.62	29.49	52,52,52,52	0
56	MG	YA	3708	1/1	0.89	0.64	29.29	37,37,37,37	0
56	MG	YA	3678	1/1	0.93	0.56	28.84	50,50,50,50	0
56	MG	XA	1626	1/1	0.64	0.82	28.77	77,77,77,77	0
56	MG	YA	3618	1/1	0.98	0.34	28.57	24,24,24,24	0
56	MG	YA	3759	1/1	0.89	0.59	28.11	64,64,64,64	0
56	MG	RA	3553	1/1	0.64	0.83	28.02	87,87,87,87	0
56	MG	YA	3713	1/1	0.87	0.70	27.83	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3342	1/1	0.93	0.45	27.68	60,60,60,60	0
56	MG	RA	3571	1/1	0.76	0.46	27.61	94,94,94,94	0
56	MG	RA	3822	1/1	0.71	0.41	27.56	37,37,37,37	0
56	MG	R3	102	1/1	0.78	1.19	27.43	80,80,80,80	0
56	MG	RA	3658	1/1	0.91	0.71	27.30	95,95,95,95	0
56	MG	QA	1847	1/1	0.59	1.06	27.11	64,64,64,64	0
56	MG	YA	3390	1/1	0.97	0.56	27.08	33,33,33,33	0
56	MG	RA	3988	1/1	0.80	0.65	26.85	75,75,75,75	0
56	MG	XA	1775	1/1	0.89	0.82	26.72	72,72,72,72	0
56	MG	YA	3518	1/1	0.98	0.35	26.68	16,16,16,16	0
56	MG	YA	3412	1/1	0.92	0.55	26.62	72,72,72,72	0
56	MG	YA	3760	1/1	0.95	0.49	26.43	85,85,85,85	0
56	MG	RA	3573	1/1	0.69	1.08	26.42	91,91,91,91	0
56	MG	RA	3633	1/1	0.91	0.40	26.40	74,74,74,74	0
56	MG	YA	3060	1/1	0.65	0.41	26.35	62,62,62,62	0
56	MG	RA	4063	1/1	0.84	1.41	26.33	68,68,68,68	0
56	MG	RF	306	1/1	0.90	0.66	26.28	79,79,79,79	0
56	MG	RA	3476	1/1	0.97	0.45	26.21	30,30,30,30	0
56	MG	RA	3606	1/1	0.93	0.80	26.19	53,53,53,53	0
56	MG	RA	3451	1/1	0.95	0.46	26.12	27,27,27,27	0
56	MG	XF	203	1/1	-0.28	1.43	25.95	109,109,109,109	0
56	MG	RA	3783	1/1	0.97	0.45	25.95	42,42,42,42	0
56	MG	QA	1661	1/1	0.62	0.61	25.86	81,81,81,81	0
56	MG	YA	3472	1/1	0.98	0.44	25.84	23,23,23,23	0
56	MG	RP	201	1/1	0.83	0.77	25.83	72,72,72,72	0
56	MG	YA	3363	1/1	0.99	0.58	25.74	11,11,11,11	0
56	MG	YA	3109	1/1	0.93	0.42	25.70	35,35,35,35	0
56	MG	RA	3109	1/1	0.86	0.54	25.66	66,66,66,66	0
56	MG	YA	3616	1/1	0.96	0.63	25.63	53,53,53,53	0
56	MG	XA	1682	1/1	0.37	0.73	25.56	86,86,86,86	0
56	MG	YA	3672	1/1	0.94	0.70	25.39	26,26,26,26	0
56	MG	RA	3122	1/1	0.73	0.67	25.36	92,92,92,92	0
56	MG	YA	3358	1/1	0.99	0.60	25.36	18,18,18,18	0
56	MG	YA	3756	1/1	0.95	0.61	25.31	80,80,80,80	0
56	MG	RA	3184	1/1	0.92	0.56	25.27	60,60,60,60	0
56	MG	RA	3389	1/1	0.97	0.39	25.22	23,23,23,23	0
56	MG	YA	3346	1/1	0.98	0.53	25.17	16,16,16,16	0
56	MG	RF	310	1/1	0.48	0.69	25.02	88,88,88,88	0
56	MG	YA	3615	1/1	0.99	0.52	24.87	11,11,11,11	0
56	MG	YA	3371	1/1	0.99	0.44	24.71	14,14,14,14	0
56	MG	RA	3892	1/1	0.77	0.52	24.57	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3548	1/1	0.91	0.56	24.34	32,32,32,32	0
56	MG	YA	3272	1/1	0.88	0.39	24.29	39,39,39,39	0
56	MG	YA	3683	1/1	0.91	0.56	24.19	39,39,39,39	0
56	MG	YA	3479	1/1	0.71	0.54	24.14	50,50,50,50	0
56	MG	YA	3627	1/1	0.87	0.45	24.11	38,38,38,38	0
56	MG	QA	1757	1/1	0.05	0.97	23.95	86,86,86,86	0
56	MG	RA	3378	1/1	0.98	0.41	23.84	25,25,25,25	0
56	MG	R5	101	1/1	0.81	1.13	23.83	105,105,105,105	0
56	MG	YA	3156	1/1	0.96	0.38	23.81	40,40,40,40	0
56	MG	YA	3694	1/1	0.75	0.47	23.73	80,80,80,80	0
56	MG	XA	1758	1/1	0.86	0.55	23.70	60,60,60,60	0
56	MG	YA	3089	1/1	0.81	0.37	23.69	80,80,80,80	0
56	MG	YA	3544	1/1	0.57	0.54	23.64	81,81,81,81	0
56	MG	YA	3271	1/1	0.94	0.36	23.54	70,70,70,70	0
56	MG	YA	3186	1/1	0.74	0.43	23.46	39,39,39,39	0
56	MG	YA	3124	1/1	0.94	0.56	23.00	54,54,54,54	0
56	MG	YA	3755	1/1	0.87	0.61	22.96	80,80,80,80	0
56	MG	RA	3940	1/1	0.47	0.65	22.80	83,83,83,83	0
56	MG	RA	3289	1/1	0.77	0.75	22.74	83,83,83,83	0
56	MG	YA	3240	1/1	0.90	0.71	22.65	70,70,70,70	0
56	MG	RN	201	1/1	0.65	0.82	22.51	85,85,85,85	0
56	MG	YA	3319	1/1	0.99	0.44	22.51	20,20,20,20	0
56	MG	YA	3029	1/1	0.82	0.55	22.40	57,57,57,57	0
56	MG	RA	3240	1/1	0.79	0.45	22.39	92,92,92,92	0
56	MG	YA	3169	1/1	0.80	0.59	22.24	91,91,91,91	0
56	MG	YA	3394	1/1	0.95	0.46	21.90	19,19,19,19	0
56	MG	YA	3718	1/1	0.62	0.35	21.87	60,60,60,60	0
56	MG	YA	3651	1/1	0.98	0.56	21.70	15,15,15,15	0
56	MG	RR	3201	1/1	0.89	0.59	21.59	62,62,62,62	0
56	MG	RA	3385	1/1	0.94	0.52	21.56	27,27,27,27	0
56	MG	RA	4045	1/1	0.94	0.73	21.48	71,71,71,71	0
56	MG	RA	3766	1/1	0.87	0.53	21.43	29,29,29,29	0
56	MG	RA	3951	1/1	0.50	0.51	21.43	87,87,87,87	0
56	MG	YA	3664	1/1	0.84	0.44	21.40	42,42,42,42	0
56	MG	R1	102	1/1	0.40	0.93	21.29	71,71,71,71	0
56	MG	RA	4041	1/1	0.80	1.06	21.25	77,77,77,77	0
56	MG	YA	3097	1/1	0.90	0.52	21.23	37,37,37,37	0
56	MG	RA	3838	1/1	0.97	0.53	21.11	17,17,17,17	0
56	MG	XA	1746	1/1	0.96	0.45	21.05	35,35,35,35	0
56	MG	XA	1774	1/1	0.96	0.38	21.03	59,59,59,59	0
56	MG	YA	3669	1/1	0.98	0.38	20.98	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3615	1/1	0.98	0.58	20.80	34,34,34,34	0
56	MG	YA	3478	1/1	0.41	0.46	20.76	67,67,67,67	0
56	MG	YA	3584	1/1	0.65	0.51	20.44	56,56,56,56	0
56	MG	RA	3443	1/1	0.97	0.55	20.38	20,20,20,20	0
56	MG	RA	3411	1/1	0.93	0.34	20.31	31,31,31,31	0
56	MG	YA	3400	1/1	0.69	0.57	20.27	74,74,74,74	0
56	MG	RA	3165	1/1	0.97	0.49	20.18	99,99,99,99	0
56	MG	YA	3401	1/1	0.97	0.52	20.14	19,19,19,19	0
56	MG	RA	3501	1/1	0.98	0.65	20.14	22,22,22,22	0
56	MG	RA	3891	1/1	0.66	0.55	19.95	59,59,59,59	0
56	MG	RA	3101	1/1	0.88	0.38	19.91	68,68,68,68	0
56	MG	RA	3496	1/1	0.98	0.43	19.80	16,16,16,16	0
56	MG	RA	3274	1/1	0.86	0.36	19.78	101,101,101,101	0
56	MG	RF	305	1/1	0.87	0.88	19.71	69,69,69,69	0
56	MG	RA	3623	1/1	0.98	0.53	19.70	34,34,34,34	0
56	MG	YA	3136	1/1	0.94	0.48	19.66	59,59,59,59	0
56	MG	XA	1632	1/1	0.76	0.83	19.62	59,59,59,59	0
56	MG	YA	3652	1/1	0.98	0.47	19.59	24,24,24,24	0
56	MG	RA	3753	1/1	0.95	0.51	19.59	48,48,48,48	0
56	MG	YA	3275	1/1	0.90	0.50	19.58	53,53,53,53	0
56	MG	RA	4061	1/1	0.89	0.48	19.55	96,96,96,96	0
56	MG	RA	3495	1/1	0.98	0.49	19.52	43,43,43,43	0
56	MG	YA	3252	1/1	0.88	0.50	19.48	70,70,70,70	0
56	MG	YA	3515	1/1	0.99	0.41	19.37	12,12,12,12	0
56	MG	RA	3027	1/1	0.89	0.48	19.30	103,103,103,103	0
56	MG	RA	3225	1/1	0.76	0.42	19.25	109,109,109,109	0
56	MG	YA	3380	1/1	0.98	0.37	19.00	7,7,7,7	0
56	MG	YA	3381	1/1	0.96	0.36	18.87	11,11,11,11	0
56	MG	RA	4030	1/1	0.96	0.85	18.87	71,71,71,71	0
56	MG	RA	3148	1/1	0.94	0.37	18.78	66,66,66,66	0
56	MG	RA	3536	1/1	0.89	0.37	18.65	64,64,64,64	0
56	MG	QN	103	1/1	0.45	0.95	18.53	80,80,80,80	0
56	MG	RA	3092	1/1	0.96	0.64	18.40	79,79,79,79	0
56	MG	RA	3465	1/1	0.98	0.37	18.35	27,27,27,27	0
56	MG	YA	3707	1/1	0.76	0.59	18.35	95,95,95,95	0
56	MG	YA	3321	1/1	0.96	0.43	18.31	29,29,29,29	0
56	MG	YA	3668	1/1	0.97	0.42	18.27	28,28,28,28	0
56	MG	YA	3250	1/1	0.84	0.30	18.26	45,45,45,45	0
56	MG	RD	308	1/1	0.78	0.57	18.23	80,80,80,80	0
56	MG	QA	1719	1/1	0.96	0.49	18.11	32,32,32,32	0
56	MG	RA	3419	1/1	0.96	0.45	18.09	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3714	1/1	0.96	0.39	18.02	36,36,36,36	0
56	MG	RA	3478	1/1	0.98	0.38	18.02	34,34,34,34	0
56	MG	XA	1779	1/1	0.85	0.82	18.00	60,60,60,60	0
56	MG	YA	3480	1/1	0.98	0.40	17.99	17,17,17,17	0
56	MG	RA	3629	1/1	0.86	0.43	17.84	60,60,60,60	0
56	MG	RA	3785	1/1	0.91	0.43	17.78	56,56,56,56	0
56	MG	RA	3220	1/1	0.92	0.39	17.71	75,75,75,75	0
56	MG	RA	3231	1/1	0.82	0.59	17.65	97,97,97,97	0
56	MG	XA	1788	1/1	0.72	0.68	17.63	62,62,62,62	0
56	MG	QA	1722	1/1	0.96	0.71	17.55	61,61,61,61	0
56	MG	RA	3332	1/1	0.83	0.33	17.51	53,53,53,53	0
56	MG	QA	1703	1/1	0.92	0.27	17.50	60,60,60,60	0
56	MG	YA	3685	1/1	0.97	0.46	17.49	19,19,19,19	0
56	MG	RA	3927	1/1	0.85	0.38	17.47	81,81,81,81	0
56	MG	QA	1734	1/1	0.64	0.63	17.46	85,85,85,85	0
56	MG	YA	3522	1/1	0.80	0.48	17.36	65,65,65,65	0
56	MG	RA	3901	1/1	0.98	0.38	17.36	16,16,16,16	0
56	MG	YA	3407	1/1	0.97	0.47	17.34	18,18,18,18	0
56	MG	XA	1672	1/1	0.49	0.64	17.21	91,91,91,91	0
56	MG	XA	1778	1/1	0.89	0.70	17.19	60,60,60,60	0
56	MG	YA	3434	1/1	0.90	0.36	17.02	55,55,55,55	0
56	MG	RA	3490	1/1	0.23	0.49	16.89	86,86,86,86	0
56	MG	XA	1737	1/1	0.97	0.45	16.84	47,47,47,47	0
56	MG	RA	3517	1/1	0.57	0.44	16.80	107,107,107,107	0
56	MG	YA	3173	1/1	0.72	0.42	16.80	85,85,85,85	0
56	MG	QA	1645	1/1	0.49	0.36	16.73	75,75,75,75	0
56	MG	YA	3331	1/1	0.95	0.41	16.72	9,9,9,9	0
56	MG	YA	3551	1/1	0.76	0.51	16.67	60,60,60,60	0
56	MG	YA	3605	1/1	0.99	0.31	16.61	19,19,19,19	0
56	MG	RA	3707	1/1	0.84	0.43	16.53	69,69,69,69	0
56	MG	YA	3354	1/1	0.94	0.47	16.52	47,47,47,47	0
56	MG	YA	3149	1/1	0.95	0.38	16.42	56,56,56,56	0
56	MG	RA	3408	1/1	0.95	0.33	16.41	24,24,24,24	0
56	MG	XA	1743	1/1	0.95	0.76	16.39	44,44,44,44	0
56	MG	RA	4064	1/1	0.88	1.01	16.19	64,64,64,64	0
56	MG	RD	312	1/1	0.67	0.47	16.16	76,76,76,76	0
56	MG	YA	3159	1/1	0.80	0.39	16.12	91,91,91,91	0
56	MG	RA	4059	1/1	0.67	0.61	16.05	101,101,101,101	0
56	MG	YA	3591	1/1	0.95	0.43	16.03	42,42,42,42	0
56	MG	YE	302	1/1	0.79	0.53	16.02	79,79,79,79	0
56	MG	YA	3489	1/1	0.98	0.37	15.94	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3461	1/1	0.64	0.78	15.88	76,76,76,76	0
56	MG	RA	3423	1/1	0.99	0.41	15.80	21,21,21,21	0
56	MG	XA	1627	1/1	0.87	0.48	15.75	62,62,62,62	0
56	MG	YA	3212	1/1	0.91	0.49	15.72	62,62,62,62	0
56	MG	YA	3303	1/1	0.85	0.39	15.71	85,85,85,85	0
56	MG	YA	3339	1/1	0.95	0.50	15.64	15,15,15,15	0
56	MG	RA	3538	1/1	0.45	0.36	15.56	80,80,80,80	0
56	MG	RA	3634	1/1	0.49	0.61	15.55	81,81,81,81	0
56	MG	RA	3794	1/1	0.90	0.71	15.51	86,86,86,86	0
56	MG	YW	201	1/1	0.87	0.66	15.44	75,75,75,75	0
56	MG	RA	3400	1/1	0.98	0.46	15.33	21,21,21,21	0
56	MG	YA	3324	1/1	0.82	0.51	15.12	39,39,39,39	0
56	MG	RA	3808	1/1	0.91	0.36	14.98	56,56,56,56	0
56	MG	RA	3809	1/1	0.31	0.65	14.98	76,76,76,76	0
56	MG	RA	4058	1/1	0.65	0.53	14.91	120,120,120,120	0
56	MG	RA	3621	1/1	0.91	0.35	14.87	61,61,61,61	0
56	MG	RA	3348	1/1	0.97	0.39	14.70	34,34,34,34	0
56	MG	YA	3705	1/1	0.91	0.41	14.61	32,32,32,32	0
56	MG	YA	3748	1/1	0.86	0.49	14.57	95,95,95,95	0
56	MG	RA	4040	1/1	0.85	0.54	14.54	69,69,69,69	0
56	MG	YA	3256	1/1	0.89	0.37	14.54	43,43,43,43	0
56	MG	RA	3393	1/1	0.98	0.47	14.53	14,14,14,14	0
56	MG	YA	3734	1/1	0.96	0.49	14.46	41,41,41,41	0
56	MG	YD	303	1/1	0.90	0.75	14.46	44,44,44,44	0
56	MG	RA	4017	1/1	0.83	0.59	14.46	90,90,90,90	0
56	MG	RA	4018	1/1	0.69	0.68	14.42	70,70,70,70	0
56	MG	YA	3294	1/1	0.91	0.36	14.37	52,52,52,52	0
56	MG	QA	1654	1/1	0.88	0.37	14.34	64,64,64,64	0
56	MG	RA	3706	1/1	0.77	0.43	14.28	58,58,58,58	0
56	MG	YX	101	1/1	0.97	0.31	14.26	31,31,31,31	0
56	MG	RA	4038	1/1	0.83	0.61	14.17	66,66,66,66	0
56	MG	YA	3338	1/1	0.99	0.43	14.17	16,16,16,16	0
56	MG	RA	3146	1/1	0.86	0.21	13.99	37,37,37,37	0
56	MG	XA	1772	1/1	0.84	0.41	13.99	51,51,51,51	0
56	MG	RA	3649	1/1	0.63	0.40	13.86	85,85,85,85	0
56	MG	YA	3757	1/1	0.90	0.51	13.84	70,70,70,70	0
56	MG	RD	302	1/1	0.94	0.67	13.71	53,53,53,53	0
56	MG	RA	3500	1/1	0.92	0.50	13.68	25,25,25,25	0
56	MG	RA	4048	1/1	0.85	0.55	13.59	81,81,81,81	0
56	MG	YA	3131	1/1	0.50	0.32	13.58	88,88,88,88	0
56	MG	RA	3695	1/1	0.61	0.34	13.51	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3660	1/1	0.96	0.25	13.45	34,34,34,34	0
56	MG	RA	4037	1/1	0.91	0.49	13.40	69,69,69,69	0
56	MG	YB	217	1/1	0.85	0.33	13.26	77,77,77,77	0
56	MG	RA	3178	1/1	0.82	0.57	13.24	79,79,79,79	0
56	MG	RA	3349	1/1	0.91	0.29	13.21	40,40,40,40	0
56	MG	RA	4036	1/1	0.97	0.75	13.20	85,85,85,85	0
56	MG	YA	3051	1/1	0.78	0.40	13.15	64,64,64,64	0
56	MG	RA	3873	1/1	0.98	0.45	13.11	31,31,31,31	0
56	MG	YA	3015	1/1	0.83	0.39	13.08	23,23,23,23	0
56	MG	YA	3444	1/1	0.97	0.43	13.04	27,27,27,27	0
56	MG	YA	3604	1/1	0.98	0.42	12.98	11,11,11,11	0
56	MG	YA	3614	1/1	0.99	0.44	12.94	26,26,26,26	0
56	MG	RA	3470	1/1	0.96	0.40	12.92	34,34,34,34	0
56	MG	RA	3229	1/1	0.75	0.46	12.89	82,82,82,82	0
56	MG	RA	4066	1/1	0.78	0.70	12.87	78,78,78,78	0
56	MG	RA	3355	1/1	0.99	0.57	12.86	24,24,24,24	0
56	MG	RA	3185	1/1	0.91	0.46	12.85	94,94,94,94	0
56	MG	YA	3443	1/1	0.58	0.79	12.82	81,81,81,81	0
56	MG	YA	3032	1/1	0.86	0.28	12.74	80,80,80,80	0
56	MG	RA	3643	1/1	0.83	0.75	12.71	71,71,71,71	0
56	MG	RA	3520	1/1	0.82	0.25	12.67	34,34,34,34	0
56	MG	YA	3329	1/1	0.97	0.34	12.63	19,19,19,19	0
56	MG	XA	1706	1/1	0.85	0.24	12.55	67,67,67,67	0
56	MG	RA	3900	1/1	0.91	0.26	12.54	30,30,30,30	0
56	MG	RA	3077	1/1	0.78	0.25	12.51	70,70,70,70	0
56	MG	RA	3380	1/1	0.95	0.46	12.48	43,43,43,43	0
56	MG	RA	3390	1/1	0.99	0.31	12.46	27,27,27,27	0
56	MG	RA	3075	1/1	0.78	0.32	12.36	56,56,56,56	0
56	MG	YA	3328	1/1	0.97	0.35	12.32	15,15,15,15	0
56	MG	RA	4006	1/1	0.85	0.80	12.31	81,81,81,81	0
56	MG	RA	3550	1/1	0.88	0.34	12.26	70,70,70,70	0
56	MG	YD	306	1/1	0.99	0.41	12.25	53,53,53,53	0
56	MG	QA	1621	1/1	0.86	0.41	12.19	71,71,71,71	0
56	MG	YA	3073	1/1	0.96	0.58	12.18	67,67,67,67	0
56	MG	RA	4032	1/1	0.98	0.46	12.09	76,76,76,76	0
56	MG	XA	1630	1/1	0.83	0.35	12.02	62,62,62,62	0
56	MG	RA	3021	1/1	0.89	0.71	11.90	101,101,101,101	0
56	MG	RA	4047	1/1	0.47	0.62	11.85	117,117,117,117	0
56	MG	YD	305	1/1	0.78	0.41	11.73	82,82,82,82	0
56	MG	QA	1833	1/1	0.91	0.55	11.71	51,51,51,51	0
56	MG	YA	3219	1/1	0.85	0.42	11.66	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3135	1/1	0.94	0.36	11.65	77,77,77,77	0
56	MG	YA	3750	1/1	0.99	0.43	11.60	22,22,22,22	0
56	MG	XA	1699	1/1	0.93	0.42	11.56	44,44,44,44	0
56	MG	YA	3094	1/1	0.41	0.40	11.53	68,68,68,68	0
56	MG	RA	3454	1/1	0.76	0.29	11.51	51,51,51,51	0
56	MG	XA	1740	1/1	0.75	0.30	11.47	65,65,65,65	0
56	MG	RA	4050	1/1	0.96	0.46	11.41	59,59,59,59	0
56	MG	RA	4060	1/1	0.87	0.58	11.39	82,82,82,82	0
56	MG	RA	3128	1/1	0.93	0.36	11.39	48,48,48,48	0
56	MG	RA	4043	1/1	0.93	0.60	11.14	86,86,86,86	0
56	MG	YA	3022	1/1	0.97	0.39	11.12	62,62,62,62	0
56	MG	RA	3472	1/1	0.72	0.27	11.11	51,51,51,51	0
56	MG	RA	3210	1/1	0.98	0.33	11.09	67,67,67,67	0
56	MG	YA	3348	1/1	0.94	0.33	11.07	17,17,17,17	0
56	MG	YA	3704	1/1	0.93	0.44	11.07	29,29,29,29	0
56	MG	RA	4057	1/1	0.91	0.67	11.06	77,77,77,77	0
56	MG	QA	1682	1/1	0.49	0.37	11.02	93,93,93,93	0
56	MG	RA	3770	1/1	0.97	0.35	11.02	22,22,22,22	0
56	MG	YA	3625	1/1	0.95	0.31	11.01	19,19,19,19	0
56	MG	RA	3142	1/1	0.47	0.41	10.99	76,76,76,76	0
56	MG	RF	303	1/1	0.95	0.46	10.97	80,80,80,80	0
56	MG	RD	301	1/1	0.81	0.57	10.93	76,76,76,76	0
56	MG	RA	3230	1/1	0.98	0.53	10.82	81,81,81,81	0
56	MG	RA	4031	1/1	0.71	0.40	10.78	102,102,102,102	0
56	MG	RR	3202	1/1	0.87	0.38	10.65	69,69,69,69	0
56	MG	RA	3806	1/1	0.82	0.30	10.63	78,78,78,78	0
56	MG	Y8	101	1/1	0.76	0.88	10.63	70,70,70,70	0
56	MG	RA	4029	1/1	0.88	0.72	10.59	91,91,91,91	0
56	MG	RA	4024	1/1	0.88	0.51	10.58	59,59,59,59	0
56	MG	XA	1695	1/1	0.81	0.64	10.56	52,52,52,52	0
56	MG	YA	3035	1/1	0.89	0.29	10.50	73,73,73,73	0
56	MG	RA	3802	1/1	0.86	1.16	10.46	89,89,89,89	0
56	MG	YA	3499	1/1	0.91	0.44	10.41	38,38,38,38	0
56	MG	RA	4065	1/1	0.71	0.61	10.38	86,86,86,86	0
56	MG	RA	3813	1/1	0.96	0.36	10.34	23,23,23,23	0
56	MG	YT	202	1/1	0.35	0.83	10.24	84,84,84,84	0
56	MG	RA	3857	1/1	0.97	0.34	10.22	35,35,35,35	0
56	MG	RA	3600	1/1	0.72	0.46	10.15	87,87,87,87	0
56	MG	YA	3179	1/1	0.79	0.43	10.09	69,69,69,69	0
56	MG	YA	3287	1/1	0.97	0.42	10.07	35,35,35,35	0
56	MG	RA	3471	1/1	0.96	0.42	10.01	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3170	1/1	0.90	0.24	9.96	66,66,66,66	0
56	MG	YA	3744	1/1	0.93	0.37	9.94	33,33,33,33	0
56	MG	RA	4003	1/1	0.70	0.34	9.94	51,51,51,51	0
56	MG	XA	1736	1/1	0.90	0.30	9.92	58,58,58,58	0
56	MG	YA	3195	1/1	0.96	0.26	9.82	33,33,33,33	0
56	MG	RA	3678	1/1	0.92	0.28	9.77	31,31,31,31	0
56	MG	YA	3342	1/1	0.96	0.29	9.75	20,20,20,20	0
56	MG	RB	225	1/1	0.60	0.45	9.75	76,76,76,76	0
56	MG	RA	3298	1/1	0.92	0.28	9.74	24,24,24,24	0
56	MG	RA	3683	1/1	0.60	0.50	9.73	96,96,96,96	0
56	MG	YA	3692	1/1	0.87	0.29	9.73	39,39,39,39	0
56	MG	RA	3040	1/1	0.73	0.48	9.72	76,76,76,76	0
56	MG	RA	3874	1/1	0.93	0.40	9.67	25,25,25,25	0
56	MG	RA	3070	1/1	0.97	0.59	9.67	78,78,78,78	0
56	MG	XA	1622	1/1	0.79	0.22	9.66	42,42,42,42	0
56	MG	YA	3135	1/1	0.91	1.19	9.61	89,89,89,89	0
56	MG	YA	3730	1/1	0.85	0.51	9.60	87,87,87,87	0
56	MG	YA	3758	1/1	0.90	0.55	9.58	76,76,76,76	0
56	MG	RA	4046	1/1	0.64	0.59	9.54	86,86,86,86	0
56	MG	YA	3569	1/1	0.96	0.41	9.50	32,32,32,32	0
56	MG	RA	4009	1/1	0.97	0.61	9.49	70,70,70,70	0
56	MG	XA	1611	1/1	0.97	0.42	9.42	73,73,73,73	0
56	MG	RA	3023	1/1	0.74	0.35	9.41	73,73,73,73	0
56	MG	RA	3721	1/1	0.82	0.58	9.36	73,73,73,73	0
56	MG	YA	3592	1/1	0.98	0.40	9.34	28,28,28,28	0
56	MG	YA	3520	1/1	0.89	0.65	9.32	68,68,68,68	0
56	MG	YA	3636	1/1	0.93	0.25	9.27	45,45,45,45	0
56	MG	YA	3433	1/1	0.90	0.29	9.23	19,19,19,19	0
56	MG	YA	3213	1/1	0.97	0.30	9.22	67,67,67,67	0
56	MG	QA	1647	1/1	-0.54	0.48	9.18	134,134,134,134	0
56	MG	RA	3335	1/1	0.96	0.29	9.17	46,46,46,46	0
56	MG	XA	1687	1/1	0.87	0.68	9.14	101,101,101,101	0
56	MG	RF	301	1/1	0.64	0.55	9.13	101,101,101,101	0
56	MG	RA	3358	1/1	0.70	0.50	9.07	99,99,99,99	0
56	MG	RA	3769	1/1	0.93	0.40	9.03	46,46,46,46	0
56	MG	RA	3743	1/1	0.86	0.29	9.03	35,35,35,35	0
56	MG	RA	3504	1/1	0.97	0.36	8.96	38,38,38,38	0
56	MG	YA	3425	1/1	0.90	0.27	8.93	49,49,49,49	0
56	MG	YA	3154	1/1	0.80	0.59	8.78	86,86,86,86	0
56	MG	RA	4034	1/1	0.86	0.71	8.76	73,73,73,73	0
56	MG	RA	4022	1/1	0.88	0.40	8.73	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3923	1/1	0.84	0.29	8.68	79,79,79,79	0
56	MG	RV	202	1/1	0.93	0.33	8.68	55,55,55,55	0
56	MG	QA	1622	1/1	0.91	0.31	8.51	62,62,62,62	0
56	MG	YA	3611	1/1	0.90	0.27	8.50	31,31,31,31	0
56	MG	RD	305	1/1	0.94	0.42	8.40	86,86,86,86	0
56	MG	RA	3321	1/1	0.98	0.28	8.32	19,19,19,19	0
56	MG	YA	3055	1/1	0.88	0.32	8.30	45,45,45,45	0
56	MG	RA	4062	1/1	0.90	0.38	8.22	78,78,78,78	0
56	MG	YA	3542	1/1	0.94	0.30	8.17	21,21,21,21	0
56	MG	QA	1729	1/1	0.93	0.38	8.16	50,50,50,50	0
56	MG	RF	308	1/1	0.86	0.51	8.14	74,74,74,74	0
56	MG	RB	209	1/1	0.73	0.42	8.14	92,92,92,92	0
56	MG	XF	204	1/1	0.77	0.67	8.02	101,101,101,101	0
56	MG	YD	304	1/1	0.92	0.34	8.00	49,49,49,49	0
56	MG	QA	1841	1/1	0.96	0.34	8.00	28,28,28,28	0
56	MG	RE	301	1/1	0.80	0.38	7.98	81,81,81,81	0
56	MG	RA	3737	1/1	0.83	0.28	7.98	77,77,77,77	0
56	MG	YA	3521	1/1	0.92	0.42	7.94	95,95,95,95	0
56	MG	RA	3398	1/1	0.98	0.44	7.90	20,20,20,20	0
56	MG	XA	1617	1/1	0.93	0.29	7.86	44,44,44,44	0
56	MG	YA	3353	1/1	0.96	0.29	7.81	14,14,14,14	0
56	MG	QA	1855	1/1	0.88	0.31	7.79	56,56,56,56	0
56	MG	XX	101	1/1	0.78	0.79	7.78	122,122,122,122	0
56	MG	YA	3620	1/1	0.93	0.27	7.77	34,34,34,34	0
56	MG	YA	3389	1/1	0.89	0.30	7.75	50,50,50,50	0
56	MG	RA	3312	1/1	0.46	1.07	7.71	124,124,124,124	0
56	MG	QA	1610	1/1	0.83	0.35	7.71	105,105,105,105	0
56	MG	YA	3749	1/1	0.90	0.32	7.71	54,54,54,54	0
56	MG	YA	3751	1/1	0.93	0.27	7.63	39,39,39,39	0
56	MG	RA	3565	1/1	0.91	0.30	7.63	44,44,44,44	0
56	MG	RA	3250	1/1	0.73	0.43	7.62	69,69,69,69	0
56	MG	XA	1628	1/1	0.89	0.25	7.58	56,56,56,56	0
56	MG	YA	3554	1/1	0.96	0.23	7.58	44,44,44,44	0
56	MG	RA	3745	1/1	0.96	0.30	7.46	21,21,21,21	0
56	MG	YA	3323	1/1	0.89	0.33	7.41	37,37,37,37	0
56	MG	RA	3712	1/1	0.94	0.66	7.40	53,53,53,53	0
56	MG	RA	3306	1/1	0.97	1.00	7.39	66,66,66,66	0
56	MG	YA	3753	1/1	0.94	0.50	7.37	54,54,54,54	0
56	MG	RA	3132	1/1	0.72	0.25	7.36	63,63,63,63	0
56	MG	RA	3535	1/1	0.74	0.26	7.33	57,57,57,57	0
56	MG	RA	4016	1/1	0.91	0.35	7.33	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1821	1/1	0.65	0.85	7.31	90,90,90,90	0
56	MG	RA	3333	1/1	0.98	0.37	7.25	24,24,24,24	0
56	MG	YA	3536	1/1	0.91	0.23	7.23	42,42,42,42	0
56	MG	YA	3021	1/1	0.92	0.38	7.16	69,69,69,69	0
56	MG	QA	1852	1/1	0.83	0.38	7.14	60,60,60,60	0
56	MG	QA	1768	1/1	0.34	0.29	7.09	91,91,91,91	0
56	MG	YA	3556	1/1	0.97	0.31	6.96	41,41,41,41	0
56	MG	RA	4028	1/1	0.97	0.30	6.91	78,78,78,78	0
56	MG	YA	3243	1/1	0.85	0.32	6.85	67,67,67,67	0
56	MG	RA	3315	1/1	0.98	0.30	6.85	29,29,29,29	0
56	MG	YA	3012	1/1	0.83	0.26	6.78	56,56,56,56	0
56	MG	XA	1608	1/1	0.41	0.47	6.75	76,76,76,76	0
56	MG	RO	201	1/1	0.71	0.56	6.71	93,93,93,93	0
56	MG	QA	1680	1/1	0.46	0.37	6.69	64,64,64,64	0
56	MG	YA	3014	1/1	0.98	0.28	6.64	39,39,39,39	0
56	MG	RA	3811	1/1	0.85	0.24	6.60	55,55,55,55	0
56	MG	RA	4044	1/1	0.97	0.50	6.52	95,95,95,95	0
56	MG	RA	3676	1/1	0.94	0.41	6.48	86,86,86,86	0
56	MG	RA	3030	1/1	0.87	0.72	6.48	113,113,113,113	0
56	MG	RA	3234	1/1	0.85	0.36	6.44	64,64,64,64	0
56	MG	R8	101	1/1	0.77	0.70	6.39	75,75,75,75	0
56	MG	RA	3861	1/1	0.79	0.25	6.34	43,43,43,43	0
56	MG	RA	3216	1/1	0.93	0.31	6.34	77,77,77,77	0
56	MG	YA	3646	1/1	0.77	0.40	6.33	69,69,69,69	0
56	MG	YA	3314	1/1	0.68	0.46	6.26	55,55,55,55	0
56	MG	XA	1757	1/1	0.94	0.27	6.24	30,30,30,30	0
56	MG	YD	309	1/1	0.94	0.32	6.21	14,14,14,14	0
56	MG	RA	4049	1/1	0.85	0.46	6.18	92,92,92,92	0
56	MG	RA	3820	1/1	0.98	0.26	6.16	28,28,28,28	0
56	MG	YA	3038	1/1	0.95	0.27	6.14	48,48,48,48	0
56	MG	QA	1672	1/1	0.78	0.50	6.13	45,45,45,45	0
56	MG	QA	1606	1/1	0.87	0.45	6.12	93,93,93,93	0
56	MG	YA	3385	1/1	0.99	0.34	6.12	23,23,23,23	0
56	MG	RA	3073	1/1	0.93	0.33	6.11	64,64,64,64	0
56	MG	YE	304	1/1	0.91	0.29	6.09	51,51,51,51	0
56	MG	QA	1843	1/1	0.67	0.31	6.02	89,89,89,89	0
56	MG	RA	3723	1/1	0.88	0.22	6.00	68,68,68,68	0
56	MG	RA	3701	1/1	0.77	0.50	5.99	64,64,64,64	0
56	MG	QA	1665	1/1	0.79	0.50	5.96	102,102,102,102	0
56	MG	QY	402	1/1	0.48	0.55	5.91	111,111,111,111	0
56	MG	YA	3754	1/1	0.97	0.31	5.89	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3773	1/1	0.96	0.24	5.89	25,25,25,25	0
56	MG	YA	3295	1/1	0.86	0.30	5.87	44,44,44,44	0
56	MG	YD	308	1/1	0.99	0.27	5.81	71,71,71,71	0
56	MG	RA	3529	1/1	0.90	0.27	5.78	77,77,77,77	0
56	MG	QA	1714	1/1	0.94	0.28	5.66	42,42,42,42	0
56	MG	RA	3464	1/1	0.92	0.27	5.60	71,71,71,71	0
56	MG	RA	3534	1/1	0.89	0.25	5.58	44,44,44,44	0
56	MG	YA	3387	1/1	0.93	0.39	5.57	37,37,37,37	0
56	MG	RA	4055	1/1	0.73	0.71	5.57	86,86,86,86	0
56	MG	YA	3114	1/1	0.89	0.29	5.54	90,90,90,90	0
56	MG	RA	3938	1/1	0.84	0.59	5.51	100,100,100,100	0
56	MG	YA	3538	1/1	0.92	0.39	5.49	44,44,44,44	0
56	MG	RA	3597	1/1	0.95	0.26	5.40	19,19,19,19	0
56	MG	QA	1710	1/1	0.98	0.29	5.35	28,28,28,28	0
56	MG	YA	3079	1/1	0.94	0.29	5.32	91,91,91,91	0
56	MG	QT	201	1/1	0.66	0.50	5.30	65,65,65,65	0
56	MG	QA	1707	1/1	0.95	0.30	5.29	28,28,28,28	0
56	MG	RE	305	1/1	0.73	0.30	5.27	33,33,33,33	0
56	MG	RA	3351	1/1	0.50	0.63	5.23	70,70,70,70	0
56	MG	RA	3531	1/1	0.81	0.24	5.21	34,34,34,34	0
56	MG	RA	3622	1/1	0.99	0.34	5.19	20,20,20,20	0
56	MG	RA	3119	1/1	0.95	0.45	5.16	74,74,74,74	0
56	MG	RA	3899	1/1	0.96	0.35	5.07	66,66,66,66	0
56	MG	RD	311	1/1	0.78	0.50	5.03	70,70,70,70	0
56	MG	YA	3030	1/1	0.92	0.25	4.96	39,39,39,39	0
56	MG	RV	203	1/1	0.82	0.35	4.94	55,55,55,55	0
56	MG	QA	1625	1/1	0.77	0.31	4.84	61,61,61,61	0
56	MG	RA	3381	1/1	0.93	0.27	4.82	39,39,39,39	0
56	MG	YA	3507	1/1	0.75	0.24	4.76	44,44,44,44	0
56	MG	RA	3905	1/1	0.95	0.42	4.74	41,41,41,41	0
56	MG	RA	3299	1/1	0.82	0.38	4.71	96,96,96,96	0
56	MG	RA	3608	1/1	0.80	0.74	4.67	104,104,104,104	0
56	MG	RA	3270	1/1	0.83	0.33	4.56	103,103,103,103	0
56	MG	YA	3202	1/1	0.93	0.28	4.53	38,38,38,38	0
56	MG	RX	101	1/1	0.91	0.35	4.51	51,51,51,51	0
56	MG	YF	303	1/1	0.95	0.26	4.49	85,85,85,85	0
56	MG	RD	307	1/1	0.73	0.37	4.49	83,83,83,83	0
56	MG	RA	3999	1/1	0.96	0.23	4.44	21,21,21,21	0
56	MG	XA	1770	1/1	0.75	0.35	4.39	104,104,104,104	0
56	MG	RB	215	1/1	0.54	0.32	4.37	91,91,91,91	0
56	MG	RA	3902	1/1	0.96	0.27	4.35	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1658	1/1	0.84	0.29	4.32	79,79,79,79	0
56	MG	RA	3323	1/1	0.93	0.25	4.31	38,38,38,38	0
56	MG	RA	3610	1/1	0.89	0.25	4.29	67,67,67,67	0
56	MG	RQ	204	1/1	0.88	0.36	4.28	72,72,72,72	0
56	MG	YE	303	1/1	0.59	0.43	4.27	103,103,103,103	0
56	MG	RA	3050	1/1	0.92	0.43	4.19	88,88,88,88	0
56	MG	RA	3506	1/1	0.97	0.22	4.16	26,26,26,26	0
56	MG	XA	1620	1/1	0.68	0.26	4.11	63,63,63,63	0
56	MG	YQ	201	1/1	0.92	0.26	4.07	33,33,33,33	0
56	MG	XA	1756	1/1	0.96	0.29	4.03	27,27,27,27	0
56	MG	YA	3062	1/1	0.89	0.22	4.02	57,57,57,57	0
56	MG	YA	3116	1/1	0.89	0.22	3.99	58,58,58,58	0
56	MG	XA	1762	1/1	0.86	0.26	3.98	48,48,48,48	0
56	MG	QA	1876	1/1	0.77	0.26	3.97	84,84,84,84	0
56	MG	YA	3453	1/1	0.88	0.24	3.96	35,35,35,35	0
56	MG	RA	4042	1/1	0.61	0.36	3.94	80,80,80,80	0
56	MG	YA	3096	1/1	0.92	0.20	3.94	26,26,26,26	0
56	MG	QA	1655	1/1	0.89	0.41	3.84	64,64,64,64	0
56	MG	YA	3093	1/1	0.88	0.23	3.83	18,18,18,18	0
56	MG	RA	3014	1/1	0.96	0.23	3.64	38,38,38,38	0
56	MG	RA	3567	1/1	0.76	0.27	3.59	81,81,81,81	0
56	MG	YR	201	1/1	0.82	0.34	3.59	66,66,66,66	0
56	MG	RA	3708	1/1	0.81	0.34	3.55	54,54,54,54	0
56	MG	YA	3410	1/1	0.97	0.31	3.54	31,31,31,31	0
56	MG	YA	3300	1/1	0.93	0.26	3.52	40,40,40,40	0
56	MG	RA	4001	1/1	0.89	0.33	3.48	58,58,58,58	0
56	MG	RA	3117	1/1	0.92	0.28	3.47	64,64,64,64	0
56	MG	YA	3503	1/1	0.93	0.19	3.46	18,18,18,18	0
56	MG	RA	3168	1/1	0.94	0.20	3.44	71,71,71,71	0
56	MG	QA	1830	1/1	0.24	0.24	3.34	85,85,85,85	0
56	MG	RA	4033	1/1	0.95	0.27	3.27	17,17,17,17	0
56	MG	RA	3430	1/1	0.97	0.26	3.26	9,9,9,9	0
56	MG	YA	3582	1/1	0.78	0.52	3.25	101,101,101,101	0
56	MG	RA	3952	1/1	0.93	0.24	3.21	49,49,49,49	0
56	MG	YA	3255	1/1	0.71	0.33	3.20	88,88,88,88	0
57	ZN	Y4	101	1/1	0.14	0.44	3.20	305,305,305,305	0
56	MG	XR	101	1/1	0.79	0.44	3.20	89,89,89,89	0
56	MG	RA	3233	1/1	0.87	0.30	3.16	72,72,72,72	0
56	MG	YA	3452	1/1	0.95	0.21	3.08	46,46,46,46	0
56	MG	QA	1800	1/1	0.97	0.21	3.08	41,41,41,41	0
56	MG	YA	3728	1/1	0.95	0.25	2.99	8,8,8,8	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3064	1/1	0.81	0.20	2.94	54,54,54,54	0
56	MG	RA	3001	1/1	0.88	0.32	2.87	68,68,68,68	0
56	MG	YA	3087	1/1	0.78	0.23	2.85	64,64,64,64	0
56	MG	RA	3328	1/1	0.88	0.21	2.83	34,34,34,34	0
56	MG	YA	3142	1/1	0.92	0.23	2.80	58,58,58,58	0
56	MG	XA	1726	1/1	0.91	0.21	2.73	74,74,74,74	0
56	MG	YA	3460	1/1	0.95	0.21	2.72	28,28,28,28	0
56	MG	RA	3330	1/1	0.80	0.20	2.61	41,41,41,41	0
56	MG	YA	3112	1/1	0.97	0.21	2.60	9,9,9,9	0
56	MG	QL	201	1/1	0.78	0.31	2.55	66,66,66,66	0
56	MG	XA	1761	1/1	0.90	0.21	2.47	38,38,38,38	0
56	MG	YA	3010	1/1	0.95	0.23	2.30	41,41,41,41	0
56	MG	RG	201	1/1	0.25	0.48	2.28	121,121,121,121	0
56	MG	RA	4000	1/1	0.93	0.26	2.24	30,30,30,30	0
56	MG	RE	306	1/1	0.83	0.30	2.23	59,59,59,59	0
56	MG	XA	1768	1/1	0.90	0.24	2.17	45,45,45,45	0
57	ZN	R4	101	1/1	0.73	0.34	2.15	269,269,269,269	0
56	MG	XA	1631	1/1	0.99	0.40	2.11	60,60,60,60	0
56	MG	XA	1730	1/1	0.81	0.18	2.10	47,47,47,47	0
56	MG	RR	3203	1/1	0.68	0.28	2.10	84,84,84,84	0
56	MG	RE	302	1/1	0.45	0.34	2.09	109,109,109,109	0
56	MG	XA	1605	1/1	0.74	0.50	2.07	72,72,72,72	0
56	MG	YA	3141	1/1	0.96	0.20	2.04	23,23,23,23	0
56	MG	RA	4052	1/1	0.66	0.70	2.00	90,90,90,90	0
56	MG	YA	3092	1/1	0.52	0.25	1.92	113,113,113,113	0
56	MG	XA	1689	1/1	0.80	0.26	1.91	64,64,64,64	0
56	MG	RA	3157	1/1	0.86	0.22	1.90	72,72,72,72	0
56	MG	QN	102	1/1	0.66	0.38	1.83	68,68,68,68	0
56	MG	YA	3013	1/1	0.91	0.19	1.74	23,23,23,23	0
56	MG	RA	4021	1/1	0.84	0.30	1.70	56,56,56,56	0
56	MG	RA	3716	1/1	0.87	0.21	1.68	52,52,52,52	0
56	MG	YV	201	1/1	0.87	0.27	1.67	44,44,44,44	0
56	MG	RA	3653	1/1	0.80	0.25	1.64	75,75,75,75	0
56	MG	RA	4025	1/1	0.83	0.26	1.64	32,32,32,32	0
56	MG	QA	1618	1/1	0.91	0.23	1.62	96,96,96,96	0
56	MG	YA	3317	1/1	0.95	0.19	1.61	24,24,24,24	0
56	MG	RA	3376	1/1	0.90	0.20	1.40	52,52,52,52	0
56	MG	QD	304	1/1	0.47	0.27	1.39	111,111,111,111	0
56	MG	QF	201	1/1	0.81	0.28	1.38	59,59,59,59	0
56	MG	XL	201	1/1	0.72	0.31	1.33	85,85,85,85	0
56	MG	YA	3747	1/1	0.75	0.43	1.32	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3673	1/1	0.99	0.22	1.32	13,13,13,13	0
56	MG	XA	1685	1/1	0.95	0.28	1.28	65,65,65,65	0
56	MG	RA	3507	1/1	0.95	0.19	1.26	109,109,109,109	0
56	MG	QA	1635	1/1	0.84	0.18	1.25	58,58,58,58	0
56	MG	RA	4051	1/1	0.92	0.27	1.23	63,63,63,63	0
56	MG	YB	214	1/1	0.90	0.16	1.20	45,45,45,45	0
56	MG	RB	205	1/1	0.97	0.22	1.15	47,47,47,47	0
56	MG	YA	3001	1/1	0.81	0.33	1.15	90,90,90,90	0
56	MG	RA	3125	1/1	0.98	0.20	1.06	36,36,36,36	0
56	MG	YA	3702	1/1	0.95	0.17	1.06	30,30,30,30	0
56	MG	RA	3670	1/1	0.81	0.23	0.99	80,80,80,80	0
56	MG	QA	1656	1/1	0.81	0.20	0.93	58,58,58,58	0
56	MG	YA	3177	1/1	0.42	0.20	0.83	71,71,71,71	0
56	MG	QA	1771	1/1	0.77	0.15	0.82	57,57,57,57	0
56	MG	RA	3401	1/1	0.85	0.19	0.80	44,44,44,44	0
56	MG	YF	301	1/1	0.85	0.19	0.79	54,54,54,54	0
56	MG	XA	1653	1/1	0.87	0.30	0.77	79,79,79,79	0
56	MG	QA	1678	1/1	0.84	0.22	0.75	80,80,80,80	0
56	MG	QA	1690	1/1	0.80	0.28	0.74	72,72,72,72	0
56	MG	QA	1619	1/1	0.88	0.23	0.72	75,75,75,75	0
56	MG	YA	3306	1/1	0.98	0.17	0.69	9,9,9,9	0
56	MG	RB	206	1/1	0.74	0.18	0.66	74,74,74,74	0
56	MG	RA	3937	1/1	0.83	0.19	0.66	38,38,38,38	0
56	MG	YA	3335	1/1	0.93	0.16	0.64	30,30,30,30	0
56	MG	XA	1635	1/1	0.91	0.20	0.57	29,29,29,29	0
56	MG	XT	201	1/1	0.66	0.29	0.52	65,65,65,65	0
56	MG	QA	1614	1/1	0.86	0.19	0.50	48,48,48,48	0
56	MG	RQ	201	1/1	0.90	0.20	0.44	47,47,47,47	0
56	MG	YA	3153	1/1	0.87	0.20	0.40	37,37,37,37	0
56	MG	QA	1872	1/1	0.87	0.22	0.26	85,85,85,85	0
56	MG	XA	1722	1/1	0.64	0.20	0.25	67,67,67,67	0
56	MG	XA	1790	1/1	0.78	0.25	0.24	98,98,98,98	0
56	MG	YA	3746	1/1	0.94	0.19	0.24	35,35,35,35	0
56	MG	RA	4023	1/1	0.95	0.19	0.20	49,49,49,49	0
56	MG	QA	1616	1/1	0.93	0.19	0.12	92,92,92,92	0
56	MG	RD	306	1/1	0.94	0.17	0.09	33,33,33,33	0
56	MG	YA	3117	1/1	0.71	0.16	0.09	42,42,42,42	0
56	MG	RA	3062	1/1	0.14	0.20	-0.03	82,82,82,82	0
56	MG	RA	3304	1/1	0.91	0.18	-0.04	39,39,39,39	0
56	MG	YG	202	1/1	0.89	0.18	-0.05	78,78,78,78	0
56	MG	YA	3187	1/1	0.85	0.23	-0.06	40,40,40,40	0
56	MG	QA	1779	1/1	0.86	0.22	-0.06	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1638	1/1	0.97	0.15	-0.15	41,41,41,41	0
56	MG	RA	3726	1/1	0.92	0.16	-0.21	53,53,53,53	0
56	MG	QA	1827	1/1	0.97	0.18	-0.21	52,52,52,52	0
56	MG	YA	3002	1/1	0.94	0.23	-0.25	64,64,64,64	0
56	MG	RA	3758	1/1	0.83	0.16	-0.30	49,49,49,49	0
56	MG	RA	3008	1/1	0.80	0.17	-0.37	46,46,46,46	0
56	MG	RA	3043	1/1	0.94	0.14	-0.39	38,38,38,38	0
56	MG	QA	1634	1/1	0.92	0.18	-0.39	44,44,44,44	0
56	MG	RA	3732	1/1	0.83	0.14	-0.45	54,54,54,54	0
56	MG	RA	3570	1/1	0.89	0.13	-0.51	35,35,35,35	0
56	MG	QA	1658	1/1	0.84	0.15	-0.52	94,94,94,94	0
56	MG	QQ	202	1/1	0.90	0.14	-0.54	68,68,68,68	0
56	MG	RB	219	1/1	0.98	0.14	-0.55	57,57,57,57	0
57	ZN	YY	201	1/1	0.72	0.18	-0.57	221,221,221,221	0
56	MG	QA	1869	1/1	0.68	0.18	-0.66	61,61,61,61	0
57	ZN	RY	201	1/1	0.55	0.21	-0.68	210,210,210,210	0
56	MG	RA	3867	1/1	0.61	0.14	-0.71	63,63,63,63	0
56	MG	XA	1615	1/1	0.84	0.21	-0.77	63,63,63,63	0
56	MG	QR	101	1/1	0.76	0.19	-0.85	71,71,71,71	0
56	MG	RG	204	1/1	0.76	0.19	-0.92	67,67,67,67	0
56	MG	XA	1752	1/1	0.98	0.18	-0.93	51,51,51,51	0
56	MG	RA	3584	1/1	0.91	0.13	-1.00	45,45,45,45	0
56	MG	YA	3736	1/1	0.92	0.15	-1.04	39,39,39,39	0
56	MG	RA	3420	1/1	0.95	0.15	-1.06	19,19,19,19	0
56	MG	QB	301	1/1	0.86	0.13	-1.06	91,91,91,91	0
56	MG	XA	1643	1/1	0.55	0.15	-1.08	80,80,80,80	0
56	MG	RA	3851	1/1	0.59	0.14	-1.08	91,91,91,91	0
56	MG	QA	1650	1/1	0.70	0.14	-1.11	72,72,72,72	0
56	MG	YA	3424	1/1	0.88	0.16	-1.16	27,27,27,27	0
56	MG	RF	309	1/1	0.93	0.14	-1.16	68,68,68,68	0
56	MG	RA	3866	1/1	0.92	0.11	-1.23	76,76,76,76	0
58	SF4	QD	302	8/8	0.99	0.15	-1.36	51,57,76,106	0
57	ZN	QN	101	1/1	0.96	0.13	-1.40	105,105,105,105	0
56	MG	YA	3457	1/1	0.95	0.12	-1.41	33,33,33,33	0
56	MG	RA	3532	1/1	0.74	0.12	-1.43	52,52,52,52	0
57	ZN	XN	101	1/1	0.98	0.10	-1.44	94,94,94,94	0
56	MG	YA	3279	1/1	0.93	0.15	-1.48	61,61,61,61	0
56	MG	YA	3190	1/1	0.82	0.12	-1.48	78,78,78,78	0
56	MG	XA	1696	1/1	0.85	0.14	-1.53	67,67,67,67	0
58	SF4	XD	301	8/8	0.99	0.14	-1.55	58,74,100,102	0
56	MG	YG	203	1/1	0.73	0.14	-1.65	54,54,54,54	0
56	MG	QA	1739	1/1	0.73	0.12	-1.66	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	ZN	Y9	101	1/1	0.97	0.10	-1.72	107,107,107,107	0
56	MG	YA	3023	1/1	0.95	0.13	-1.80	16,16,16,16	0
56	MG	YA	3204	1/1	0.89	0.14	-1.85	42,42,42,42	0
56	MG	RA	3025	1/1	0.97	0.14	-1.96	23,23,23,23	0
56	MG	RA	3032	1/1	0.88	0.14	-2.01	49,49,49,49	0
57	ZN	R9	102	1/1	0.99	0.05	-2.05	92,92,92,92	0
57	ZN	R6	101	1/1	0.92	0.16	-2.10	160,160,160,160	0
56	MG	RA	3131	1/1	0.71	0.09	-2.19	67,67,67,67	0
56	MG	QA	1626	1/1	0.87	0.09	-2.20	78,78,78,78	0
57	ZN	Y5	102	1/1	0.98	0.05	-2.40	119,119,119,119	0
56	MG	YA	3752	1/1	0.95	0.12	-2.50	52,52,52,52	0
56	MG	XK	201	1/1	0.93	0.07	-2.52	53,53,53,53	0
56	MG	RA	3006	1/1	0.79	0.12	-2.75	33,33,33,33	0
57	ZN	R5	102	1/1	0.99	0.03	-2.86	119,119,119,119	0
57	ZN	Y6	101	1/1	0.98	0.17	-3.05	169,169,169,169	0
56	MG	RA	3965	1/1	0.96	0.11	-3.05	45,45,45,45	0
56	MG	YA	3286	1/1	0.92	0.10	-3.05	35,35,35,35	0
56	MG	RA	3049	1/1	0.95	0.12	-3.20	48,48,48,48	0
56	MG	YA	3224	1/1	0.90	0.10	-3.28	66,66,66,66	0
56	MG	YA	3091	1/1	0.95	0.14	-3.38	36,36,36,36	0
56	MG	RA	3395	1/1	0.95	0.09	-3.60	22,22,22,22	0
56	MG	YA	3564	1/1	0.96	0.11	-3.80	42,42,42,42	0
56	MG	YA	3009	1/1	0.98	0.12	-3.87	37,37,37,37	0
56	MG	RA	3964	1/1	0.94	0.10	-4.22	44,44,44,44	0
56	MG	YA	3041	1/1	0.95	0.06	-4.70	35,35,35,35	0
56	MG	XA	1636	1/1	0.87	0.07	-4.84	60,60,60,60	0
56	MG	RA	3513	1/1	0.98	0.11	-4.90	14,14,14,14	0
56	MG	QA	1631	1/1	0.97	0.08	-5.18	34,34,34,34	0
56	MG	RA	3041	1/1	0.96	0.06	-5.71	44,44,44,44	0
56	MG	YA	3106	1/1	0.89	0.10	-7.45	30,30,30,30	0
56	MG	QA	1774	1/1	0.57	0.42	-	77,77,77,77	0
56	MG	YA	3559	1/1	0.96	0.40	-	54,54,54,54	0
56	MG	YA	3596	1/1	0.97	0.41	-	39,39,39,39	0
56	MG	RA	3607	1/1	0.75	0.35	-	98,98,98,98	0
56	MG	RA	3713	1/1	0.85	0.45	-	47,47,47,47	0
56	MG	XF	202	1/1	0.72	0.45	-	73,73,73,73	0
56	MG	YA	3530	1/1	0.82	0.69	-	59,59,59,59	0
56	MG	XA	1651	1/1	0.07	0.55	-	90,90,90,90	0
56	MG	RA	3803	1/1	0.88	0.14	-	64,64,64,64	0
56	MG	XE	201	1/1	0.55	0.48	-	79,79,79,79	0
56	MG	XA	1648	1/1	0.48	0.51	-	74,74,74,74	0
56	MG	QA	1673	1/1	0.83	0.41	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3897	1/1	0.95	0.37	-	61,61,61,61	0
56	MG	RB	226	1/1	0.15	0.66	-	99,99,99,99	0
56	MG	YA	3403	1/1	0.54	0.38	-	59,59,59,59	0
56	MG	YA	3606	1/1	0.98	0.62	-	25,25,25,25	0
56	MG	YA	3399	1/1	0.91	0.62	-	36,36,36,36	0
56	MG	QA	1801	1/1	0.66	0.30	-	78,78,78,78	0
56	MG	RA	3134	1/1	0.60	0.54	-	83,83,83,83	0
56	MG	QA	1846	1/1	0.91	0.57	-	47,47,47,47	0
56	MG	YA	3666	1/1	0.94	0.46	-	36,36,36,36	0
56	MG	QA	1867	1/1	0.16	1.16	-	99,99,99,99	0
56	MG	RA	3166	1/1	0.69	0.99	-	68,68,68,68	0
56	MG	RA	3934	1/1	0.81	0.17	-	62,62,62,62	0
56	MG	YA	3228	1/1	0.67	0.33	-	75,75,75,75	0
56	MG	RA	3484	1/1	0.98	0.46	-	30,30,30,30	0
56	MG	RA	3563	1/1	0.82	0.60	-	66,66,66,66	0
56	MG	YA	3158	1/1	0.85	0.68	-	49,49,49,49	0
56	MG	YA	3280	1/1	0.93	0.33	-	14,14,14,14	0
56	MG	RA	3143	1/1	0.90	0.15	-	72,72,72,72	0
56	MG	RB	210	1/1	0.62	1.00	-	109,109,109,109	0
56	MG	RA	3199	1/1	0.71	0.24	-	68,68,68,68	0
56	MG	RA	3886	1/1	0.92	0.60	-	52,52,52,52	0
56	MG	YA	3733	1/1	0.89	0.25	-	62,62,62,62	0
56	MG	QA	1765	1/1	0.90	0.20	-	83,83,83,83	0
56	MG	YA	3597	1/1	0.83	0.75	-	74,74,74,74	0
56	MG	YA	3576	1/1	0.93	0.35	-	37,37,37,37	0
56	MG	QA	1799	1/1	-0.38	0.83	-	83,83,83,83	0
56	MG	YA	3352	1/1	0.95	0.46	-	11,11,11,11	0
56	MG	QA	1603	1/1	0.77	0.40	-	105,105,105,105	0
56	MG	RA	3858	1/1	0.49	0.71	-	80,80,80,80	0
56	MG	RA	3247	1/1	0.85	0.60	-	88,88,88,88	0
56	MG	YA	3068	1/1	0.89	0.35	-	65,65,65,65	0
56	MG	RA	3396	1/1	0.89	0.47	-	58,58,58,58	0
56	MG	RA	3206	1/1	0.79	0.56	-	97,97,97,97	0
56	MG	YA	3227	1/1	0.81	0.46	-	64,64,64,64	0
56	MG	XA	1604	1/1	0.43	0.71	-	99,99,99,99	0
56	MG	YA	3052	1/1	0.74	0.31	-	45,45,45,45	0
56	MG	YA	3588	1/1	0.88	0.18	-	76,76,76,76	0
56	MG	YA	3549	1/1	0.94	0.31	-	34,34,34,34	0
56	MG	XA	1749	1/1	0.84	0.41	-	82,82,82,82	0
56	MG	RA	3918	1/1	0.95	0.52	-	71,71,71,71	0
56	MG	RB	229	1/1	0.44	0.52	-	108,108,108,108	0
56	MG	RA	3920	1/1	0.91	0.50	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3986	1/1	0.70	0.53	-	79,79,79,79	0
56	MG	YA	3332	1/1	0.96	0.33	-	28,28,28,28	0
56	MG	YA	3511	1/1	0.49	0.60	-	60,60,60,60	0
56	MG	RA	3499	1/1	0.77	0.50	-	77,77,77,77	0
56	MG	RA	3740	1/1	0.36	0.97	-	76,76,76,76	0
56	MG	RA	3558	1/1	0.71	0.56	-	82,82,82,82	0
56	MG	RA	3183	1/1	0.84	0.34	-	81,81,81,81	0
56	MG	YA	3567	1/1	0.86	0.23	-	42,42,42,42	0
56	MG	YA	3185	1/1	0.13	0.86	-	105,105,105,105	0
56	MG	RA	3236	1/1	0.79	0.69	-	69,69,69,69	0
56	MG	RA	3681	1/1	0.21	0.67	-	119,119,119,119	0
56	MG	XA	1711	1/1	0.12	0.61	-	92,92,92,92	0
56	MG	YA	3483	1/1	0.97	0.35	-	26,26,26,26	0
56	MG	RA	3211	1/1	0.79	0.55	-	88,88,88,88	0
56	MG	RA	3111	1/1	0.80	0.25	-	106,106,106,106	0
56	MG	RA	3059	1/1	0.90	0.13	-	76,76,76,76	0
56	MG	RA	3977	1/1	0.40	0.90	-	62,62,62,62	0
56	MG	RA	3276	1/1	0.50	0.64	-	91,91,91,91	0
56	MG	RA	3007	1/1	0.91	0.22	-	61,61,61,61	0
56	MG	RA	3152	1/1	0.74	0.45	-	106,106,106,106	0
56	MG	RA	3724	1/1	0.64	0.26	-	67,67,67,67	0
56	MG	QA	1667	1/1	0.94	0.21	-	67,67,67,67	0
56	MG	YA	3396	1/1	0.00	0.89	-	94,94,94,94	0
56	MG	YA	3085	1/1	0.60	0.28	-	86,86,86,86	0
56	MG	RA	3771	1/1	0.82	0.31	-	45,45,45,45	0
56	MG	RA	3542	1/1	0.60	0.55	-	76,76,76,76	0
56	MG	QA	1818	1/1	0.91	0.23	-	63,63,63,63	0
56	MG	RA	3123	1/1	0.93	0.23	-	30,30,30,30	0
56	MG	YA	3580	1/1	0.92	0.46	-	27,27,27,27	0
56	MG	RA	3172	1/1	0.96	0.51	-	80,80,80,80	0
56	MG	YA	3602	1/1	0.99	0.41	-	16,16,16,16	0
56	MG	YA	3535	1/1	0.31	0.98	-	75,75,75,75	0
56	MG	RA	3675	1/1	0.60	0.33	-	75,75,75,75	0
56	MG	QA	1848	1/1	0.47	0.57	-	68,68,68,68	0
56	MG	QA	1764	1/1	0.29	0.34	-	101,101,101,101	0
56	MG	YA	3706	1/1	0.95	0.28	-	79,79,79,79	0
56	MG	YA	3145	1/1	0.96	0.46	-	59,59,59,59	0
56	MG	YA	3162	1/1	0.91	0.15	-	27,27,27,27	0
56	MG	QA	1758	1/1	0.75	0.50	-	76,76,76,76	0
56	MG	XA	1656	1/1	0.81	0.37	-	80,80,80,80	0
56	MG	QY	401	1/1	-0.00	0.42	-	111,111,111,111	0
56	MG	YA	3632	1/1	0.85	0.34	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3875	1/1	0.48	0.59	-	90,90,90,90	0
56	MG	XA	1638	1/1	0.90	0.07	-	118,118,118,118	0
56	MG	RA	3674	1/1	0.87	0.59	-	77,77,77,77	0
56	MG	RA	3291	1/1	0.71	0.76	-	86,86,86,86	0
56	MG	RA	3601	1/1	0.93	0.79	-	87,87,87,87	0
56	MG	YA	3724	1/1	0.97	0.57	-	51,51,51,51	0
56	MG	YA	3711	1/1	0.92	0.67	-	47,47,47,47	0
56	MG	XA	1702	1/1	0.55	0.38	-	61,61,61,61	0
56	MG	YA	3254	1/1	0.88	0.32	-	67,67,67,67	0
56	MG	QA	1611	1/1	0.43	0.75	-	89,89,89,89	0
56	MG	RA	3819	1/1	0.81	0.23	-	33,33,33,33	0
56	MG	QA	1767	1/1	0.86	0.22	-	90,90,90,90	0
56	MG	RA	3552	1/1	0.85	0.17	-	97,97,97,97	0
56	MG	RA	3995	1/1	0.76	0.38	-	111,111,111,111	0
56	MG	YA	3656	1/1	0.99	0.29	-	34,34,34,34	0
56	MG	RA	3631	1/1	0.68	0.42	-	125,125,125,125	0
56	MG	YA	3519	1/1	0.78	0.44	-	79,79,79,79	0
56	MG	QA	1613	1/1	0.97	0.10	-	97,97,97,97	0
56	MG	QA	1747	1/1	0.65	0.46	-	72,72,72,72	0
56	MG	YA	3579	1/1	0.96	0.56	-	36,36,36,36	0
56	MG	RA	3257	1/1	0.94	0.55	-	100,100,100,100	0
56	MG	RA	3375	1/1	0.51	0.68	-	73,73,73,73	0
56	MG	RA	3827	1/1	0.81	0.34	-	57,57,57,57	0
56	MG	XA	1771	1/1	0.93	0.54	-	62,62,62,62	0
56	MG	YA	3017	1/1	0.82	0.57	-	60,60,60,60	0
56	MG	YA	3430	1/1	0.95	0.20	-	20,20,20,20	0
56	MG	XA	1721	1/1	0.68	0.60	-	86,86,86,86	0
56	MG	RA	3167	1/1	0.90	0.13	-	69,69,69,69	0
56	MG	QA	1750	1/1	0.88	0.35	-	67,67,67,67	0
56	MG	YA	3667	1/1	0.59	0.64	-	90,90,90,90	0
56	MG	YA	3192	1/1	0.88	0.21	-	71,71,71,71	0
56	MG	RA	3282	1/1	-0.37	2.52	-	109,109,109,109	0
56	MG	RA	3815	1/1	0.92	0.29	-	68,68,68,68	0
56	MG	YA	3084	1/1	0.87	0.37	-	66,66,66,66	0
56	MG	XA	1661	1/1	0.46	0.34	-	87,87,87,87	0
56	MG	XA	1610	1/1	0.70	0.36	-	79,79,79,79	0
56	MG	QA	1761	1/1	0.80	0.62	-	72,72,72,72	0
56	MG	YA	3448	1/1	0.62	0.32	-	81,81,81,81	0
56	MG	RA	3458	1/1	0.90	0.21	-	74,74,74,74	0
56	MG	RA	3840	1/1	0.46	0.55	-	83,83,83,83	0
56	MG	QA	1817	1/1	0.67	0.35	-	64,64,64,64	0
56	MG	QA	1842	1/1	0.36	0.37	-	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3467	1/1	0.52	0.93	-	82,82,82,82	0
56	MG	RA	3412	1/1	0.83	0.48	-	71,71,71,71	0
56	MG	YA	3677	1/1	0.96	0.74	-	42,42,42,42	0
56	MG	RA	3515	1/1	0.76	0.55	-	67,67,67,67	0
56	MG	XA	1780	1/1	0.94	0.62	-	40,40,40,40	0
56	MG	YA	3485	1/1	0.78	0.53	-	77,77,77,77	0
56	MG	RA	3832	1/1	0.84	0.36	-	74,74,74,74	0
56	MG	QA	1802	1/1	0.81	0.65	-	79,79,79,79	0
56	MG	RA	3660	1/1	0.92	0.23	-	46,46,46,46	0
56	MG	RA	3829	1/1	0.77	1.09	-	65,65,65,65	0
56	MG	RD	309	1/1	0.79	0.29	-	78,78,78,78	0
56	MG	RA	3679	1/1	0.89	0.84	-	54,54,54,54	0
56	MG	XA	1601	1/1	0.86	0.23	-	75,75,75,75	0
56	MG	RA	3038	1/1	0.87	0.20	-	63,63,63,63	0
56	MG	RA	3442	1/1	0.99	0.59	-	18,18,18,18	0
56	MG	YA	3261	1/1	0.88	0.24	-	55,55,55,55	0
56	MG	QA	1620	1/1	0.56	0.27	-	75,75,75,75	0
56	MG	RA	3944	1/1	0.96	0.18	-	22,22,22,22	0
56	MG	YA	3042	1/1	0.95	0.19	-	61,61,61,61	0
56	MG	XA	1684	1/1	0.90	0.48	-	40,40,40,40	0
56	MG	YA	3698	1/1	0.78	0.48	-	77,77,77,77	0
56	MG	RA	3477	1/1	0.87	0.39	-	46,46,46,46	0
56	MG	RA	3512	1/1	0.41	0.86	-	80,80,80,80	0
56	MG	RA	3147	1/1	0.98	0.20	-	39,39,39,39	0
56	MG	RA	3790	1/1	0.41	0.50	-	82,82,82,82	0
56	MG	YA	3700	1/1	0.81	0.36	-	71,71,71,71	0
56	MG	XA	1642	1/1	0.96	0.25	-	55,55,55,55	0
56	MG	RA	3314	1/1	0.66	0.65	-	58,58,58,58	0
56	MG	YA	3378	1/1	0.89	0.25	-	53,53,53,53	0
56	MG	QD	303	1/1	0.69	0.47	-	79,79,79,79	0
56	MG	YA	3203	1/1	0.61	0.54	-	84,84,84,84	0
56	MG	RA	3870	1/1	0.97	0.44	-	24,24,24,24	0
56	MG	YA	3577	1/1	0.71	0.67	-	53,53,53,53	0
56	MG	YA	3679	1/1	0.84	0.45	-	36,36,36,36	0
56	MG	QA	1875	1/1	0.83	0.42	-	75,75,75,75	0
56	MG	RA	3034	1/1	0.80	0.81	-	100,100,100,100	0
56	MG	XA	1718	1/1	0.15	1.23	-	73,73,73,73	0
56	MG	YA	3309	1/1	0.89	0.37	-	37,37,37,37	0
56	MG	RA	3936	1/1	0.83	1.03	-	74,74,74,74	0
56	MG	RA	3448	1/1	0.64	0.68	-	71,71,71,71	0
56	MG	YA	3137	1/1	0.94	0.34	-	40,40,40,40	0
56	MG	QA	1859	1/1	0.94	0.34	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3422	1/1	0.43	0.69	-	84,84,84,84	0
56	MG	YA	3274	1/1	0.95	0.39	-	48,48,48,48	0
56	MG	RA	3878	1/1	0.72	0.72	-	81,81,81,81	0
56	MG	RA	3042	1/1	0.77	0.31	-	80,80,80,80	0
56	MG	QA	1612	1/1	-0.13	0.93	-	97,97,97,97	0
56	MG	YA	3296	1/1	0.92	0.58	-	32,32,32,32	0
56	MG	RD	313	1/1	0.38	0.78	-	82,82,82,82	0
56	MG	YA	3613	1/1	0.91	0.65	-	53,53,53,53	0
56	MG	RA	4010	1/1	0.83	0.33	-	76,76,76,76	0
56	MG	RA	3514	1/1	0.77	0.25	-	87,87,87,87	0
56	MG	RA	3765	1/1	0.99	0.57	-	40,40,40,40	0
56	MG	YA	3076	1/1	0.95	0.29	-	4,4,4,4	0
56	MG	XA	1781	1/1	-0.11	0.82	-	110,110,110,110	0
56	MG	RA	3138	1/1	0.73	0.44	-	53,53,53,53	0
56	MG	QA	1605	1/1	0.81	0.29	-	67,67,67,67	0
56	MG	YA	3501	1/1	0.45	0.65	-	115,115,115,115	0
56	MG	RA	3406	1/1	0.81	0.27	-	60,60,60,60	0
56	MG	YA	3461	1/1	0.47	0.91	-	81,81,81,81	0
56	MG	YA	3626	1/1	0.98	0.30	-	25,25,25,25	0
56	MG	XA	1707	1/1	0.87	0.52	-	58,58,58,58	0
56	MG	XA	1782	1/1	0.92	0.20	-	46,46,46,46	0
56	MG	RA	3452	1/1	0.75	0.29	-	78,78,78,78	0
56	MG	XA	1709	1/1	0.51	0.17	-	72,72,72,72	0
56	MG	QA	1657	1/1	0.45	0.57	-	98,98,98,98	0
56	MG	RA	3576	1/1	0.93	0.39	-	43,43,43,43	0
56	MG	RA	3667	1/1	0.67	0.19	-	60,60,60,60	0
56	MG	RA	3181	1/1	0.79	0.29	-	90,90,90,90	0
56	MG	RA	3015	1/1	0.89	0.30	-	72,72,72,72	0
56	MG	QA	1742	1/1	0.90	0.72	-	58,58,58,58	0
56	MG	RA	3079	1/1	0.97	0.38	-	64,64,64,64	0
56	MG	RA	4014	1/1	0.81	0.57	-	83,83,83,83	0
56	MG	RB	218	1/1	0.84	0.28	-	79,79,79,79	0
56	MG	RA	3982	1/1	0.61	0.53	-	83,83,83,83	0
56	MG	QA	1809	1/1	0.83	0.26	-	67,67,67,67	0
56	MG	RA	3976	1/1	0.54	0.63	-	81,81,81,81	0
56	MG	RA	3583	1/1	0.62	0.61	-	72,72,72,72	0
56	MG	RA	3432	1/1	0.58	0.43	-	58,58,58,58	0
56	MG	RA	3604	1/1	0.80	0.28	-	91,91,91,91	0
56	MG	QA	1687	1/1	0.79	0.32	-	97,97,97,97	0
56	MG	XA	1694	1/1	0.98	0.34	-	30,30,30,30	0
56	MG	QA	1627	1/1	0.91	0.09	-	42,42,42,42	0
56	MG	YA	3594	1/1	0.90	0.33	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3662	1/1	0.35	0.96	-	89,89,89,89	0
56	MG	RA	3628	1/1	0.77	0.55	-	65,65,65,65	0
56	MG	RA	3797	1/1	0.74	0.49	-	84,84,84,84	0
56	MG	YA	3459	1/1	0.48	0.38	-	85,85,85,85	0
56	MG	XA	1785	1/1	0.52	0.42	-	81,81,81,81	0
56	MG	XA	1647	1/1	0.21	0.35	-	92,92,92,92	0
56	MG	YA	3100	1/1	0.64	0.28	-	87,87,87,87	0
56	MG	YA	3406	1/1	0.66	0.44	-	80,80,80,80	0
56	MG	YA	3033	1/1	0.95	0.12	-	13,13,13,13	0
56	MG	RA	3427	1/1	0.69	0.62	-	78,78,78,78	0
56	MG	XA	1621	1/1	0.56	0.59	-	68,68,68,68	0
56	MG	RH	202	1/1	0.40	0.50	-	96,96,96,96	0
56	MG	YA	3277	1/1	0.96	0.47	-	17,17,17,17	0
56	MG	YA	3193	1/1	0.18	0.70	-	101,101,101,101	0
56	MG	RA	3447	1/1	0.88	0.29	-	57,57,57,57	0
56	MG	RA	3505	1/1	0.80	0.26	-	64,64,64,64	0
56	MG	YA	3439	1/1	0.68	0.52	-	80,80,80,80	0
56	MG	RA	3636	1/1	0.34	1.23	-	91,91,91,91	0
56	MG	XA	1683	1/1	0.88	0.79	-	69,69,69,69	0
56	MG	RA	3672	1/1	0.40	0.69	-	75,75,75,75	0
56	MG	R7	102	1/1	0.63	0.52	-	72,72,72,72	0
56	MG	YA	3188	1/1	0.81	0.41	-	94,94,94,94	0
56	MG	QA	1844	1/1	0.89	0.17	-	80,80,80,80	0
56	MG	RA	3445	1/1	0.92	0.26	-	58,58,58,58	0
56	MG	QA	1624	1/1	0.72	0.54	-	73,73,73,73	0
56	MG	YA	3197	1/1	0.84	0.38	-	77,77,77,77	0
56	MG	RA	3956	1/1	0.66	0.33	-	77,77,77,77	0
56	MG	QA	1726	1/1	0.74	0.24	-	81,81,81,81	0
56	MG	RA	3324	1/1	0.97	0.37	-	14,14,14,14	0
56	MG	YA	3291	1/1	0.94	0.48	-	24,24,24,24	0
56	MG	RA	3776	1/1	0.69	0.36	-	73,73,73,73	0
56	MG	XA	1700	1/1	0.76	0.43	-	43,43,43,43	0
56	MG	RA	3377	1/1	0.86	0.47	-	42,42,42,42	0
56	MG	RA	3718	1/1	0.88	0.13	-	62,62,62,62	0
56	MG	YA	3171	1/1	0.67	0.38	-	104,104,104,104	0
56	MG	YA	3561	1/1	0.77	0.35	-	45,45,45,45	0
56	MG	RA	3437	1/1	0.20	0.64	-	77,77,77,77	0
56	MG	YA	3442	1/1	0.84	0.48	-	53,53,53,53	0
56	MG	YA	3526	1/1	0.88	0.43	-	43,43,43,43	0
56	MG	YA	3305	1/1	0.95	0.13	-	19,19,19,19	0
56	MG	YA	3239	1/1	0.83	0.38	-	94,94,94,94	0
56	MG	RA	3650	1/1	0.82	0.41	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3266	1/1	0.85	0.78	-	70,70,70,70	0
56	MG	YA	3061	1/1	0.60	0.58	-	57,57,57,57	0
56	MG	RA	3094	1/1	0.97	0.87	-	71,71,71,71	0
56	MG	QA	1715	1/1	0.33	0.44	-	77,77,77,77	0
56	MG	QA	1697	1/1	0.54	0.30	-	76,76,76,76	0
56	MG	RA	3612	1/1	0.89	0.76	-	64,64,64,64	0
56	MG	RA	3687	1/1	0.81	0.30	-	57,57,57,57	0
56	MG	YA	3264	1/1	0.86	0.56	-	88,88,88,88	0
56	MG	QA	1824	1/1	0.64	1.30	-	127,127,127,127	0
56	MG	RB	216	1/1	0.76	0.32	-	59,59,59,59	0
56	MG	QA	1743	1/1	0.62	0.33	-	71,71,71,71	0
56	MG	RA	3757	1/1	0.83	0.35	-	70,70,70,70	0
56	MG	QA	1692	1/1	0.90	0.37	-	52,52,52,52	0
56	MG	RA	3645	1/1	0.61	0.54	-	84,84,84,84	0
56	MG	RA	3198	1/1	0.25	1.31	-	84,84,84,84	0
56	MG	QA	1731	1/1	0.71	0.48	-	71,71,71,71	0
56	MG	RA	3722	1/1	0.64	0.36	-	82,82,82,82	0
56	MG	RA	3801	1/1	0.65	0.19	-	74,74,74,74	0
56	MG	YA	3587	1/1	0.97	0.27	-	31,31,31,31	0
56	MG	RA	3201	1/1	0.83	0.34	-	70,70,70,70	0
56	MG	YA	3607	1/1	0.93	0.58	-	53,53,53,53	0
56	MG	RA	3962	1/1	0.65	0.82	-	62,62,62,62	0
56	MG	YA	3020	1/1	0.86	0.26	-	80,80,80,80	0
56	MG	RA	3039	1/1	0.36	0.54	-	76,76,76,76	0
56	MG	RT	202	1/1	0.87	0.30	-	65,65,65,65	0
56	MG	YA	3655	1/1	0.66	0.81	-	86,86,86,86	0
56	MG	YE	307	1/1	0.84	0.24	-	64,64,64,64	0
56	MG	RA	3357	1/1	0.67	0.16	-	61,61,61,61	0
56	MG	RA	3126	1/1	0.50	1.12	-	79,79,79,79	0
56	MG	YA	3071	1/1	0.83	0.43	-	77,77,77,77	0
56	MG	QA	1756	1/1	0.45	0.55	-	114,114,114,114	0
56	MG	YA	3719	1/1	0.84	0.39	-	79,79,79,79	0
56	MG	QH	202	1/1	0.79	0.67	-	77,77,77,77	0
56	MG	XA	1787	1/1	0.81	1.38	-	84,84,84,84	0
56	MG	YA	3454	1/1	0.88	1.12	-	52,52,52,52	0
56	MG	RA	3481	1/1	0.21	0.21	-	81,81,81,81	0
56	MG	YN	201	1/1	0.09	0.83	-	87,87,87,87	0
56	MG	QI	201	1/1	0.68	0.55	-	106,106,106,106	0
56	MG	QA	1766	1/1	0.61	0.39	-	71,71,71,71	0
56	MG	R1	103	1/1	0.88	0.30	-	55,55,55,55	0
56	MG	RA	3154	1/1	0.87	0.11	-	88,88,88,88	0
56	MG	RA	3697	1/1	0.88	0.32	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3640	1/1	0.94	0.14	-	48,48,48,48	0
56	MG	YA	3659	1/1	0.88	0.43	-	29,29,29,29	0
56	MG	YA	3583	1/1	0.95	0.50	-	29,29,29,29	0
56	MG	QA	1860	1/1	0.14	0.63	-	100,100,100,100	0
56	MG	YA	3540	1/1	0.92	0.45	-	27,27,27,27	0
56	MG	RA	3239	1/1	0.37	0.81	-	112,112,112,112	0
56	MG	RA	3609	1/1	0.87	0.27	-	71,71,71,71	0
56	MG	RA	3136	1/1	0.66	0.41	-	84,84,84,84	0
56	MG	RA	3409	1/1	0.95	0.32	-	33,33,33,33	0
56	MG	QA	1789	1/1	-0.04	0.40	-	99,99,99,99	0
56	MG	RA	3862	1/1	0.74	0.41	-	79,79,79,79	0
56	MG	RA	3812	1/1	0.53	0.62	-	106,106,106,106	0
56	MG	YW	202	1/1	0.56	0.24	-	55,55,55,55	0
56	MG	YA	3139	1/1	0.78	0.47	-	66,66,66,66	0
56	MG	XA	1763	1/1	0.89	0.57	-	49,49,49,49	0
56	MG	QA	1834	1/1	0.91	0.35	-	43,43,43,43	0
56	MG	XA	1663	1/1	0.80	0.43	-	107,107,107,107	0
56	MG	YA	3695	1/1	0.61	0.94	-	76,76,76,76	0
56	MG	YA	3045	1/1	0.95	0.46	-	27,27,27,27	0
56	MG	RA	3915	1/1	0.97	0.31	-	41,41,41,41	0
56	MG	RA	3161	1/1	0.82	0.33	-	72,72,72,72	0
56	MG	RA	3746	1/1	-0.06	0.70	-	112,112,112,112	0
56	MG	RA	3044	1/1	0.94	0.32	-	29,29,29,29	0
56	MG	QA	1754	1/1	-0.02	0.82	-	108,108,108,108	0
56	MG	XA	1629	1/1	0.84	0.19	-	51,51,51,51	0
56	MG	YA	3449	1/1	0.19	0.78	-	81,81,81,81	0
56	MG	RA	3599	1/1	0.63	0.26	-	66,66,66,66	0
56	MG	RA	3212	1/1	0.71	0.61	-	95,95,95,95	0
56	MG	YA	3635	1/1	0.77	0.53	-	80,80,80,80	0
56	MG	RA	3150	1/1	0.74	0.16	-	74,74,74,74	0
56	MG	RA	3930	1/1	0.93	0.40	-	54,54,54,54	0
56	MG	YA	3176	1/1	0.57	0.45	-	102,102,102,102	0
56	MG	RA	3810	1/1	0.54	0.63	-	75,75,75,75	0
56	MG	RA	3689	1/1	0.88	0.89	-	70,70,70,70	0
56	MG	QA	1641	1/1	0.42	0.65	-	105,105,105,105	0
56	MG	RA	3762	1/1	0.81	0.26	-	76,76,76,76	0
56	MG	YA	3181	1/1	0.87	0.27	-	66,66,66,66	0
56	MG	RA	3085	1/1	0.78	0.45	-	76,76,76,76	0
56	MG	RA	3302	1/1	0.45	0.55	-	92,92,92,92	0
56	MG	XA	1649	1/1	0.30	0.36	-	92,92,92,92	0
56	MG	RA	3657	1/1	0.88	0.52	-	65,65,65,65	0
56	MG	QA	1688	1/1	0.84	0.71	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3265	1/1	0.75	0.42	-	64,64,64,64	0
56	MG	YA	3555	1/1	0.81	0.63	-	77,77,77,77	0
56	MG	YA	3236	1/1	0.54	0.36	-	106,106,106,106	0
56	MG	YA	3115	1/1	0.78	0.29	-	52,52,52,52	0
56	MG	XA	1654	1/1	0.09	0.90	-	89,89,89,89	0
56	MG	RA	3688	1/1	0.30	0.32	-	90,90,90,90	0
56	MG	RA	3761	1/1	0.99	0.44	-	22,22,22,22	0
56	MG	YA	3110	1/1	0.50	0.47	-	63,63,63,63	0
56	MG	YA	3102	1/1	0.88	0.52	-	60,60,60,60	0
56	MG	RA	4035	1/1	0.45	0.38	-	116,116,116,116	0
56	MG	RA	3856	1/1	0.94	0.30	-	33,33,33,33	0
56	MG	RA	3642	1/1	0.79	0.24	-	70,70,70,70	0
56	MG	RA	3752	1/1	0.14	0.61	-	102,102,102,102	0
56	MG	YA	3167	1/1	0.56	0.87	-	88,88,88,88	0
56	MG	XA	1742	1/1	0.91	0.39	-	52,52,52,52	0
56	MG	QA	1706	1/1	0.97	0.47	-	35,35,35,35	0
56	MG	RA	3789	1/1	0.81	0.33	-	95,95,95,95	0
56	MG	RA	3449	1/1	0.85	0.22	-	45,45,45,45	0
56	MG	XA	1644	1/1	0.87	0.34	-	61,61,61,61	0
56	MG	RA	3997	1/1	0.86	0.30	-	98,98,98,98	0
56	MG	YA	3246	1/1	0.11	0.52	-	118,118,118,118	0
56	MG	YA	3543	1/1	0.94	0.52	-	36,36,36,36	0
56	MG	RA	3341	1/1	0.95	0.52	-	30,30,30,30	0
56	MG	YA	3629	1/1	0.90	0.36	-	44,44,44,44	0
56	MG	YA	3058	1/1	0.85	0.20	-	75,75,75,75	0
56	MG	YA	3039	1/1	0.71	0.59	-	73,73,73,73	0
56	MG	RA	3058	1/1	0.20	1.00	-	88,88,88,88	0
56	MG	RA	3268	1/1	0.86	0.42	-	95,95,95,95	0
56	MG	R0	101	1/1	0.82	0.43	-	94,94,94,94	0
56	MG	YP	201	1/1	0.62	0.56	-	79,79,79,79	0
56	MG	YA	3693	1/1	0.83	0.29	-	60,60,60,60	0
56	MG	RA	3313	1/1	0.94	0.40	-	21,21,21,21	0
56	MG	YA	3648	1/1	0.93	0.28	-	40,40,40,40	0
56	MG	RA	3665	1/1	0.81	0.36	-	77,77,77,77	0
56	MG	RA	3246	1/1	0.81	0.77	-	69,69,69,69	0
56	MG	YA	3074	1/1	0.90	0.30	-	63,63,63,63	0
56	MG	RA	3618	1/1	0.85	0.33	-	48,48,48,48	0
56	MG	RA	3824	1/1	0.32	1.39	-	76,76,76,76	0
56	MG	YA	3691	1/1	0.95	0.29	-	38,38,38,38	0
56	MG	RA	3530	1/1	0.69	0.42	-	75,75,75,75	0
56	MG	YA	3031	1/1	0.88	0.38	-	46,46,46,46	0
56	MG	YA	3130	1/1	0.84	0.59	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3344	1/1	0.42	0.27	-	80,80,80,80	0
56	MG	XA	1678	1/1	0.94	0.61	-	81,81,81,81	0
56	MG	YA	3568	1/1	0.96	0.25	-	19,19,19,19	0
56	MG	RA	3704	1/1	0.62	0.60	-	91,91,91,91	0
56	MG	RA	3035	1/1	0.55	0.47	-	97,97,97,97	0
56	MG	YB	219	1/1	0.94	0.42	-	31,31,31,31	0
56	MG	YA	3653	1/1	0.88	0.54	-	55,55,55,55	0
56	MG	QA	1850	1/1	0.67	0.61	-	51,51,51,51	0
56	MG	RF	304	1/1	0.79	0.17	-	63,63,63,63	0
56	MG	RR	3205	1/1	0.76	0.41	-	60,60,60,60	0
56	MG	YA	3209	1/1	0.86	0.44	-	48,48,48,48	0
56	MG	RA	3825	1/1	-0.00	1.06	-	98,98,98,98	0
56	MG	QA	1785	1/1	0.59	0.51	-	84,84,84,84	0
56	MG	RA	3869	1/1	0.89	1.08	-	77,77,77,77	0
56	MG	RA	3344	1/1	0.97	0.38	-	51,51,51,51	0
56	MG	YA	3504	1/1	0.64	0.28	-	74,74,74,74	0
56	MG	YA	3067	1/1	0.93	1.04	-	53,53,53,53	0
56	MG	XA	1690	1/1	0.92	0.29	-	53,53,53,53	0
56	MG	RA	3763	1/1	0.83	0.47	-	61,61,61,61	0
56	MG	RA	3226	1/1	0.78	0.98	-	104,104,104,104	0
56	MG	RA	3494	1/1	0.94	0.89	-	55,55,55,55	0
56	MG	RA	3917	1/1	0.82	0.57	-	67,67,67,67	0
56	MG	RA	3115	1/1	-0.39	1.51	-	92,92,92,92	0
56	MG	RB	207	1/1	0.88	0.17	-	82,82,82,82	0
56	MG	RA	3093	1/1	0.93	0.12	-	72,72,72,72	0
56	MG	XA	1641	1/1	0.92	0.36	-	61,61,61,61	0
56	MG	YA	3637	1/1	0.13	1.13	-	101,101,101,101	0
56	MG	QA	1760	1/1	0.04	0.95	-	77,77,77,77	0
56	MG	RA	3877	1/1	0.98	0.37	-	23,23,23,23	0
56	MG	RA	3975	1/1	0.93	0.23	-	63,63,63,63	0
56	MG	YA	3680	1/1	0.98	0.73	-	50,50,50,50	0
56	MG	R9	101	1/1	0.57	0.42	-	92,92,92,92	0
56	MG	YA	3126	1/1	0.93	0.17	-	91,91,91,91	0
56	MG	QA	1724	1/1	0.79	0.23	-	76,76,76,76	0
56	MG	RA	3760	1/1	0.89	0.16	-	74,74,74,74	0
56	MG	YA	3351	1/1	0.87	0.51	-	51,51,51,51	0
56	MG	RA	3889	1/1	0.91	0.54	-	48,48,48,48	0
56	MG	RA	3848	1/1	0.97	0.68	-	50,50,50,50	0
56	MG	RA	3887	1/1	0.96	0.34	-	53,53,53,53	0
56	MG	YA	3716	1/1	0.85	0.38	-	65,65,65,65	0
56	MG	YE	306	1/1	0.96	0.41	-	13,13,13,13	0
56	MG	Y7	101	1/1	0.89	0.55	-	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3428	1/1	0.87	0.29	-	60,60,60,60	0
56	MG	RN	202	1/1	0.59	1.06	-	98,98,98,98	0
56	MG	QA	1644	1/1	0.68	0.53	-	108,108,108,108	0
56	MG	RA	3528	1/1	0.80	0.33	-	76,76,76,76	0
56	MG	YA	3119	1/1	0.61	0.55	-	78,78,78,78	0
56	MG	QA	1755	1/1	0.72	0.39	-	69,69,69,69	0
56	MG	YA	3349	1/1	0.94	0.36	-	49,49,49,49	0
56	MG	YA	3494	1/1	0.98	0.20	-	36,36,36,36	0
56	MG	YA	3040	1/1	0.86	0.19	-	66,66,66,66	0
56	MG	YA	3441	1/1	0.98	0.44	-	34,34,34,34	0
56	MG	RA	3002	1/1	0.93	0.28	-	70,70,70,70	0
56	MG	XA	1735	1/1	0.78	0.75	-	53,53,53,53	0
56	MG	RA	3402	1/1	0.68	0.80	-	71,71,71,71	0
56	MG	RA	3730	1/1	0.76	0.22	-	51,51,51,51	0
56	MG	YA	3595	1/1	0.98	0.51	-	12,12,12,12	0
56	MG	RA	3555	1/1	0.91	1.15	-	68,68,68,68	0
56	MG	YA	3225	1/1	0.85	0.30	-	74,74,74,74	0
56	MG	QA	1643	1/1	0.89	0.67	-	86,86,86,86	0
56	MG	QA	1845	1/1	0.73	0.77	-	77,77,77,77	0
56	MG	RA	3692	1/1	0.86	0.74	-	87,87,87,87	0
56	MG	RA	3382	1/1	0.98	0.31	-	20,20,20,20	0
56	MG	QA	1816	1/1	0.69	0.78	-	76,76,76,76	0
56	MG	QA	1879	1/1	0.75	0.44	-	78,78,78,78	0
56	MG	YA	3497	1/1	0.65	0.41	-	63,63,63,63	0
56	MG	RA	3387	1/1	0.95	0.64	-	50,50,50,50	0
56	MG	QA	1811	1/1	0.63	0.33	-	83,83,83,83	0
56	MG	RA	3686	1/1	0.69	0.37	-	62,62,62,62	0
56	MG	YA	3391	1/1	0.98	0.45	-	18,18,18,18	0
56	MG	YA	3253	1/1	0.21	0.63	-	98,98,98,98	0
56	MG	RA	3339	1/1	0.63	0.46	-	68,68,68,68	0
56	MG	YA	3322	1/1	0.97	0.29	-	9,9,9,9	0
56	MG	XA	1751	1/1	0.79	0.43	-	59,59,59,59	0
56	MG	RA	3921	1/1	0.62	2.25	-	88,88,88,88	0
56	MG	YA	3337	1/1	0.94	0.28	-	35,35,35,35	0
56	MG	YA	3725	1/1	0.86	0.40	-	68,68,68,68	0
56	MG	YA	3304	1/1	0.81	0.61	-	56,56,56,56	0
56	MG	YA	3550	1/1	0.74	0.82	-	76,76,76,76	0
56	MG	YA	3523	1/1	0.51	0.28	-	56,56,56,56	0
56	MG	YA	3375	1/1	0.80	0.42	-	55,55,55,55	0
56	MG	YA	3267	1/1	-0.10	1.03	-	100,100,100,100	0
56	MG	YA	3475	1/1	0.72	0.58	-	84,84,84,84	0
56	MG	RA	3076	1/1	0.73	0.68	-	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3659	1/1	0.78	0.58	-	62,62,62,62	0
56	MG	RA	3561	1/1	0.88	0.35	-	42,42,42,42	0
56	MG	RA	3816	1/1	0.84	0.55	-	102,102,102,102	0
56	MG	QA	1683	1/1	0.68	0.26	-	112,112,112,112	0
56	MG	YA	3214	1/1	0.46	0.74	-	111,111,111,111	0
56	MG	RA	3180	1/1	0.94	0.34	-	75,75,75,75	0
56	MG	QA	1711	1/1	0.84	0.27	-	63,63,63,63	0
56	MG	YA	3534	1/1	-0.20	0.53	-	124,124,124,124	0
56	MG	YA	3025	1/1	0.82	0.07	-	55,55,55,55	0
56	MG	XA	1625	1/1	0.85	0.70	-	74,74,74,74	0
56	MG	RA	3581	1/1	0.92	0.25	-	75,75,75,75	0
56	MG	RA	3258	1/1	0.66	0.62	-	96,96,96,96	0
56	MG	QA	1797	1/1	0.77	0.38	-	95,95,95,95	0
56	MG	QA	1795	1/1	0.80	0.34	-	61,61,61,61	0
56	MG	QA	1819	1/1	0.32	0.57	-	65,65,65,65	0
56	MG	QA	1636	1/1	0.56	0.30	-	66,66,66,66	0
56	MG	RA	3577	1/1	-0.29	1.14	-	94,94,94,94	0
56	MG	RA	3648	1/1	0.86	0.51	-	82,82,82,82	0
56	MG	RA	3228	1/1	0.75	0.55	-	101,101,101,101	0
56	MG	XA	1676	1/1	0.95	0.30	-	42,42,42,42	0
56	MG	YA	3043	1/1	0.85	0.77	-	62,62,62,62	0
56	MG	RA	3884	1/1	0.89	0.31	-	71,71,71,71	0
56	MG	RA	3744	1/1	0.92	0.43	-	41,41,41,41	0
56	MG	RA	3831	1/1	0.98	0.30	-	65,65,65,65	0
56	MG	RA	3095	1/1	0.87	0.58	-	88,88,88,88	0
56	MG	RA	3066	1/1	0.61	0.54	-	56,56,56,56	0
56	MG	RA	3083	1/1	0.91	0.37	-	80,80,80,80	0
56	MG	YA	3397	1/1	0.87	0.61	-	68,68,68,68	0
56	MG	YA	3663	1/1	0.98	0.71	-	38,38,38,38	0
56	MG	XA	1745	1/1	0.96	0.46	-	44,44,44,44	0
56	MG	RA	3598	1/1	0.83	0.37	-	94,94,94,94	0
56	MG	XA	1765	1/1	0.95	0.55	-	49,49,49,49	0
56	MG	RA	3241	1/1	0.92	0.32	-	108,108,108,108	0
56	MG	YA	3235	1/1	0.84	0.24	-	91,91,91,91	0
56	MG	YA	3445	1/1	0.72	0.66	-	72,72,72,72	0
56	MG	RA	3503	1/1	0.98	0.28	-	21,21,21,21	0
56	MG	QY	403	1/1	0.20	0.81	-	81,81,81,81	0
56	MG	YB	205	1/1	0.54	0.69	-	89,89,89,89	0
56	MG	QA	1684	1/1	0.86	0.50	-	97,97,97,97	0
56	MG	YA	3498	1/1	0.90	0.42	-	64,64,64,64	0
56	MG	RA	3218	1/1	0.89	0.55	-	65,65,65,65	0
56	MG	RA	3568	1/1	0.97	0.35	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3600	1/1	0.91	0.41	-	51,51,51,51	0
56	MG	RA	3144	1/1	0.76	0.76	-	84,84,84,84	0
56	MG	XA	1728	1/1	0.12	0.94	-	101,101,101,101	0
56	MG	QA	1782	1/1	0.71	0.26	-	69,69,69,69	0
56	MG	XA	1652	1/1	0.31	0.49	-	78,78,78,78	0
56	MG	RA	3160	1/1	0.88	0.94	-	83,83,83,83	0
56	MG	YA	3714	1/1	0.69	0.41	-	80,80,80,80	0
56	MG	XA	1614	1/1	0.96	0.24	-	60,60,60,60	0
56	MG	RA	3578	1/1	0.84	0.50	-	60,60,60,60	0
56	MG	QA	1738	1/1	0.44	0.60	-	98,98,98,98	0
56	MG	RA	3277	1/1	0.37	0.68	-	94,94,94,94	0
56	MG	YA	3281	1/1	0.87	0.93	-	60,60,60,60	0
56	MG	QO	101	1/1	0.46	0.66	-	79,79,79,79	0
56	MG	YA	3365	1/1	0.87	0.41	-	48,48,48,48	0
56	MG	YA	3455	1/1	0.76	0.54	-	79,79,79,79	0
56	MG	RA	3680	1/1	0.92	0.53	-	46,46,46,46	0
56	MG	RB	220	1/1	0.94	0.51	-	47,47,47,47	0
56	MG	YA	3622	1/1	0.91	0.51	-	49,49,49,49	0
56	MG	YA	3237	1/1	0.76	0.68	-	69,69,69,69	0
56	MG	RA	3909	1/1	0.76	0.73	-	73,73,73,73	0
56	MG	QA	1737	1/1	0.69	0.91	-	72,72,72,72	0
56	MG	RA	3575	1/1	0.89	0.38	-	62,62,62,62	0
56	MG	RQ	203	1/1	0.70	0.69	-	82,82,82,82	0
56	MG	RA	3673	1/1	0.97	0.41	-	45,45,45,45	0
56	MG	QA	1791	1/1	0.17	0.83	-	96,96,96,96	0
56	MG	QA	1700	1/1	0.77	0.44	-	66,66,66,66	0
56	MG	RA	4011	1/1	0.77	0.64	-	83,83,83,83	0
56	MG	YA	3258	1/1	0.89	0.36	-	68,68,68,68	0
56	MG	RA	3102	1/1	0.72	0.85	-	107,107,107,107	0
56	MG	YA	3557	1/1	0.72	0.73	-	67,67,67,67	0
56	MG	YA	3731	1/1	0.94	0.30	-	32,32,32,32	0
56	MG	QA	1649	1/1	0.93	0.18	-	50,50,50,50	0
56	MG	YA	3333	1/1	0.95	0.64	-	26,26,26,26	0
56	MG	YA	3393	1/1	0.88	0.20	-	66,66,66,66	0
56	MG	RA	3595	1/1	0.74	0.41	-	84,84,84,84	0
56	MG	YA	3318	1/1	0.98	0.41	-	26,26,26,26	0
56	MG	RA	3200	1/1	0.73	0.41	-	99,99,99,99	0
56	MG	QA	1823	1/1	0.49	0.60	-	70,70,70,70	0
56	MG	YA	3437	1/1	0.39	0.84	-	85,85,85,85	0
56	MG	RB	204	1/1	0.93	0.17	-	71,71,71,71	0
56	MG	YA	3386	1/1	0.96	0.55	-	23,23,23,23	0
56	MG	RA	3990	1/1	0.96	0.35	-	109,109,109,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3435	1/1	0.91	0.49	-	36,36,36,36	0
56	MG	QA	1825	1/1	0.86	0.39	-	74,74,74,74	0
56	MG	YA	3411	1/1	0.90	0.26	-	83,83,83,83	0
56	MG	XA	1675	1/1	0.32	0.73	-	82,82,82,82	0
56	MG	YA	3370	1/1	0.37	0.30	-	67,67,67,67	0
56	MG	YA	3107	1/1	0.33	0.65	-	80,80,80,80	0
56	MG	RA	3426	1/1	0.74	0.47	-	88,88,88,88	0
56	MG	RA	3139	1/1	0.87	0.28	-	72,72,72,72	0
56	MG	RA	3316	1/1	0.43	0.57	-	84,84,84,84	0
56	MG	YA	3105	1/1	0.86	0.39	-	37,37,37,37	0
56	MG	RA	3253	1/1	0.88	0.29	-	66,66,66,66	0
56	MG	RA	3715	1/1	0.87	0.41	-	76,76,76,76	0
56	MG	YB	215	1/1	0.85	0.22	-	92,92,92,92	0
56	MG	RD	303	1/1	0.89	0.28	-	41,41,41,41	0
56	MG	RA	3404	1/1	0.84	0.24	-	81,81,81,81	0
56	MG	XA	1692	1/1	0.09	0.77	-	75,75,75,75	0
56	MG	RA	3311	1/1	0.55	0.43	-	100,100,100,100	0
56	MG	XA	1723	1/1	0.49	0.28	-	75,75,75,75	0
56	MG	RA	3497	1/1	0.51	0.33	-	82,82,82,82	0
56	MG	RA	3800	1/1	-0.07	0.46	-	102,102,102,102	0
56	MG	XA	1708	1/1	0.73	0.38	-	78,78,78,78	0
56	MG	YB	213	1/1	0.85	0.40	-	57,57,57,57	0
56	MG	YA	3573	1/1	0.91	0.64	-	38,38,38,38	0
56	MG	RV	201	1/1	0.09	0.64	-	110,110,110,110	0
56	MG	XA	1624	1/1	0.52	0.61	-	76,76,76,76	0
56	MG	YB	218	1/1	0.29	0.40	-	80,80,80,80	0
56	MG	YA	3231	1/1	0.91	0.29	-	59,59,59,59	0
56	MG	RA	3545	1/1	0.75	0.51	-	70,70,70,70	0
56	MG	YA	3474	1/1	0.81	0.37	-	72,72,72,72	0
56	MG	YA	3420	1/1	0.92	0.46	-	39,39,39,39	0
56	MG	YA	3687	1/1	0.85	0.21	-	75,75,75,75	0
56	MG	QA	1752	1/1	0.83	0.24	-	77,77,77,77	0
56	MG	YA	3072	1/1	0.90	0.37	-	99,99,99,99	0
56	MG	RA	3182	1/1	0.83	0.50	-	85,85,85,85	0
56	MG	YA	3205	1/1	0.81	0.29	-	58,58,58,58	0
56	MG	YA	3471	1/1	0.92	0.61	-	58,58,58,58	0
56	MG	RA	3254	1/1	0.84	0.30	-	92,92,92,92	0
56	MG	RB	202	1/1	0.83	0.14	-	55,55,55,55	0
56	MG	YA	3689	1/1	0.92	0.44	-	67,67,67,67	0
56	MG	YA	3245	1/1	0.93	0.56	-	107,107,107,107	0
56	MG	RG	203	1/1	0.77	0.37	-	79,79,79,79	0
56	MG	YB	203	1/1	0.84	0.14	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3155	1/1	0.90	0.51	-	78,78,78,78	0
56	MG	RA	3047	1/1	0.96	0.10	-	12,12,12,12	0
56	MG	QA	1829	1/1	-0.01	0.94	-	94,94,94,94	0
56	MG	RA	3959	1/1	0.84	0.26	-	43,43,43,43	0
56	MG	YA	3463	1/1	0.85	0.23	-	47,47,47,47	0
56	MG	RA	3488	1/1	0.68	0.31	-	57,57,57,57	0
56	MG	QA	1862	1/1	0.64	0.50	-	101,101,101,101	0
56	MG	RA	3266	1/1	0.88	0.40	-	74,74,74,74	0
56	MG	RA	3847	1/1	0.61	0.45	-	102,102,102,102	0
56	MG	XA	1607	1/1	0.80	0.38	-	47,47,47,47	0
56	MG	RA	3219	1/1	0.89	0.20	-	66,66,66,66	0
56	MG	RA	3872	1/1	0.75	0.65	-	78,78,78,78	0
56	MG	RA	3439	1/1	0.41	0.71	-	89,89,89,89	0
56	MG	QA	1787	1/1	0.39	0.71	-	76,76,76,76	0
56	MG	YA	3578	1/1	0.40	0.88	-	95,95,95,95	0
56	MG	RA	3945	1/1	0.99	0.47	-	25,25,25,25	0
56	MG	YA	3598	1/1	0.91	0.47	-	49,49,49,49	0
56	MG	RA	3232	1/1	0.89	0.75	-	57,57,57,57	0
56	MG	YA	3601	1/1	0.97	0.60	-	29,29,29,29	0
56	MG	RA	3010	1/1	0.94	0.28	-	50,50,50,50	0
56	MG	RA	3787	1/1	0.14	1.12	-	105,105,105,105	0
56	MG	YA	3221	1/1	0.86	0.34	-	77,77,77,77	0
56	MG	RA	3137	1/1	0.96	0.80	-	97,97,97,97	0
56	MG	XA	1727	1/1	0.47	0.44	-	84,84,84,84	0
56	MG	RA	3777	1/1	0.87	0.45	-	93,93,93,93	0
56	MG	YA	3144	1/1	0.95	0.34	-	57,57,57,57	0
56	MG	RA	3953	1/1	0.58	0.30	-	86,86,86,86	0
56	MG	RA	3100	1/1	-0.13	1.07	-	93,93,93,93	0
56	MG	RA	3252	1/1	0.59	0.59	-	91,91,91,91	0
56	MG	YA	3183	1/1	0.81	0.36	-	47,47,47,47	0
56	MG	RA	3121	1/1	0.88	0.49	-	83,83,83,83	0
56	MG	YB	204	1/1	0.75	0.41	-	99,99,99,99	0
56	MG	RA	3998	1/1	0.15	0.88	-	87,87,87,87	0
56	MG	QA	1813	1/1	0.41	0.77	-	83,83,83,83	0
56	MG	RA	3895	1/1	0.95	0.67	-	54,54,54,54	0
56	MG	RA	3399	1/1	0.41	0.77	-	117,117,117,117	0
56	MG	YA	3657	1/1	0.90	0.60	-	34,34,34,34	0
56	MG	RA	3836	1/1	0.74	0.42	-	91,91,91,91	0
56	MG	QA	1630	1/1	0.49	0.64	-	81,81,81,81	0
56	MG	YA	3623	1/1	0.81	0.34	-	54,54,54,54	0
56	MG	RA	3237	1/1	0.48	0.52	-	100,100,100,100	0
56	MG	YA	3218	1/1	0.90	0.36	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QU	101	1/1	0.14	0.49	-	81,81,81,81	0
56	MG	RA	3764	1/1	0.82	0.48	-	60,60,60,60	0
56	MG	YA	3157	1/1	0.91	0.41	-	44,44,44,44	0
56	MG	RA	3989	1/1	0.95	0.30	-	39,39,39,39	0
56	MG	RA	3911	1/1	0.96	0.30	-	46,46,46,46	0
56	MG	YA	3312	1/1	0.73	0.41	-	73,73,73,73	0
56	MG	RA	3265	1/1	0.87	0.10	-	111,111,111,111	0
56	MG	YA	3108	1/1	0.48	0.48	-	98,98,98,98	0
56	MG	Y5	101	1/1	0.84	0.31	-	63,63,63,63	0
56	MG	QA	1705	1/1	0.85	0.27	-	37,37,37,37	0
56	MG	RA	4056	1/1	0.82	0.73	-	70,70,70,70	0
56	MG	XE	202	1/1	0.86	0.07	-	67,67,67,67	0
56	MG	YB	208	1/1	0.78	0.31	-	81,81,81,81	0
56	MG	RA	3782	1/1	0.03	0.60	-	94,94,94,94	0
56	MG	YA	3699	1/1	0.91	0.67	-	66,66,66,66	0
56	MG	RE	303	1/1	0.97	0.33	-	15,15,15,15	0
56	MG	RA	3641	1/1	0.77	0.57	-	65,65,65,65	0
56	MG	RA	3416	1/1	0.92	0.20	-	60,60,60,60	0
56	MG	YA	3477	1/1	0.78	0.52	-	70,70,70,70	0
56	MG	RA	3845	1/1	0.73	0.58	-	94,94,94,94	0
56	MG	YA	3599	1/1	0.76	0.41	-	70,70,70,70	0
56	MG	YA	3438	1/1	0.96	0.32	-	45,45,45,45	0
56	MG	RA	3972	1/1	0.89	0.43	-	81,81,81,81	0
56	MG	YA	3247	1/1	-0.23	0.92	-	106,106,106,106	0
56	MG	RA	3759	1/1	0.73	0.27	-	67,67,67,67	0
56	MG	QA	1632	1/1	0.77	0.76	-	70,70,70,70	0
56	MG	QA	1780	1/1	0.58	0.26	-	92,92,92,92	0
56	MG	YA	3118	1/1	0.90	0.38	-	91,91,91,91	0
56	MG	RA	3028	1/1	0.64	0.17	-	69,69,69,69	0
56	MG	RA	3319	1/1	0.83	0.71	-	54,54,54,54	0
56	MG	QA	1730	1/1	0.91	0.30	-	49,49,49,49	0
56	MG	YD	301	1/1	0.72	0.67	-	60,60,60,60	0
56	MG	RA	3779	1/1	0.90	0.23	-	86,86,86,86	0
56	MG	YA	3495	1/1	0.92	0.56	-	63,63,63,63	0
56	MG	RA	3624	1/1	0.98	0.23	-	38,38,38,38	0
56	MG	R1	101	1/1	0.69	0.65	-	82,82,82,82	0
56	MG	YA	3276	1/1	0.96	0.60	-	67,67,67,67	0
56	MG	XA	1753	1/1	0.53	0.69	-	99,99,99,99	0
56	MG	XA	1660	1/1	0.39	0.39	-	99,99,99,99	0
56	MG	RA	3120	1/1	0.88	0.24	-	63,63,63,63	0
56	MG	RA	3551	1/1	0.91	0.30	-	72,72,72,72	0
56	MG	RA	3842	1/1	0.76	0.40	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3196	1/1	0.88	0.35	-	109,109,109,109	0
56	MG	QA	1741	1/1	0.76	0.56	-	45,45,45,45	0
56	MG	YA	3722	1/1	0.27	0.49	-	89,89,89,89	0
56	MG	RA	4053	1/1	0.79	0.80	-	74,74,74,74	0
56	MG	RA	3805	1/1	0.79	0.31	-	98,98,98,98	0
56	MG	RA	3224	1/1	0.64	0.55	-	96,96,96,96	0
56	MG	RW	202	1/1	0.69	0.42	-	89,89,89,89	0
56	MG	YA	3036	1/1	0.89	0.31	-	55,55,55,55	0
56	MG	YA	3402	1/1	0.90	0.51	-	32,32,32,32	0
56	MG	YA	3619	1/1	0.96	0.20	-	38,38,38,38	0
56	MG	YA	3201	1/1	0.68	0.33	-	87,87,87,87	0
56	MG	QA	1836	1/1	0.60	0.44	-	89,89,89,89	0
56	MG	QA	1662	1/1	0.68	0.51	-	82,82,82,82	0
56	MG	RA	3943	1/1	0.82	0.33	-	86,86,86,86	0
56	MG	XA	1664	1/1	0.59	0.29	-	67,67,67,67	0
56	MG	RA	3592	1/1	0.83	0.57	-	56,56,56,56	0
56	MG	YA	3446	1/1	0.63	0.61	-	71,71,71,71	0
56	MG	RA	3175	1/1	0.84	0.51	-	70,70,70,70	0
56	MG	Y1	101	1/1	0.53	1.05	-	104,104,104,104	0
56	MG	RA	3361	1/1	0.67	0.34	-	76,76,76,76	0
56	MG	RA	3046	1/1	0.91	0.68	-	68,68,68,68	0
56	MG	YA	3743	1/1	0.97	0.40	-	43,43,43,43	0
56	MG	RA	3784	1/1	0.78	0.31	-	94,94,94,94	0
56	MG	RA	3837	1/1	0.91	0.22	-	59,59,59,59	0
56	MG	RA	3844	1/1	0.87	0.44	-	113,113,113,113	0
56	MG	YA	3565	1/1	0.30	0.78	-	85,85,85,85	0
56	MG	RA	3980	1/1	0.88	0.34	-	49,49,49,49	0
56	MG	YA	3168	1/1	0.86	0.39	-	88,88,88,88	0
56	MG	RA	3127	1/1	0.98	0.42	-	52,52,52,52	0
56	MG	RA	3557	1/1	0.81	0.42	-	63,63,63,63	0
56	MG	RA	3227	1/1	0.73	0.53	-	93,93,93,93	0
56	MG	RA	3368	1/1	0.78	1.34	-	76,76,76,76	0
56	MG	RA	3350	1/1	0.89	0.11	-	65,65,65,65	0
56	MG	RA	3646	1/1	0.66	0.69	-	92,92,92,92	0
56	MG	YA	3639	1/1	0.92	0.65	-	74,74,74,74	0
56	MG	XA	1786	1/1	0.77	0.24	-	72,72,72,72	0
56	MG	QA	1781	1/1	0.96	0.42	-	54,54,54,54	0
56	MG	YA	3208	1/1	0.63	1.12	-	60,60,60,60	0
56	MG	RA	3074	1/1	0.85	0.28	-	52,52,52,52	0
56	MG	RA	3961	1/1	0.22	1.07	-	114,114,114,114	0
56	MG	RA	3834	1/1	0.65	0.40	-	80,80,80,80	0
56	MG	YA	3690	1/1	0.95	0.30	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3446	1/1	0.66	1.11	-	63,63,63,63	0
56	MG	YA	3481	1/1	0.76	0.50	-	77,77,77,77	0
56	MG	XA	1662	1/1	0.57	0.22	-	80,80,80,80	0
56	MG	RA	3373	1/1	0.87	0.53	-	44,44,44,44	0
56	MG	RA	3065	1/1	0.51	0.59	-	89,89,89,89	0
56	MG	YA	3649	1/1	0.84	0.35	-	60,60,60,60	0
56	MG	YA	3674	1/1	0.86	0.59	-	74,74,74,74	0
56	MG	RA	3325	1/1	0.96	0.32	-	42,42,42,42	0
56	MG	YA	3199	1/1	0.93	0.64	-	102,102,102,102	0
56	MG	YA	3643	1/1	0.95	0.63	-	36,36,36,36	0
56	MG	RA	3906	1/1	0.97	0.30	-	20,20,20,20	0
56	MG	QG	201	1/1	0.80	0.88	-	91,91,91,91	0
56	MG	YA	3359	1/1	0.71	0.15	-	72,72,72,72	0
56	MG	YA	3257	1/1	0.87	0.21	-	84,84,84,84	0
56	MG	RA	3883	1/1	0.82	0.34	-	93,93,93,93	0
56	MG	YA	3080	1/1	0.76	0.38	-	80,80,80,80	0
56	MG	QA	1877	1/1	0.90	0.38	-	94,94,94,94	0
56	MG	YA	3373	1/1	0.89	0.38	-	41,41,41,41	0
56	MG	YA	3034	1/1	0.85	0.28	-	68,68,68,68	0
56	MG	YA	3658	1/1	0.45	0.27	-	77,77,77,77	0
56	MG	QA	1806	1/1	0.88	0.17	-	73,73,73,73	0
56	MG	RA	3459	1/1	0.65	0.52	-	78,78,78,78	0
56	MG	YB	201	1/1	0.53	0.52	-	89,89,89,89	0
56	MG	QA	1820	1/1	0.75	0.19	-	79,79,79,79	0
56	MG	RA	3821	1/1	0.97	0.48	-	29,29,29,29	0
56	MG	RA	3293	1/1	0.79	0.21	-	128,128,128,128	0
56	MG	RA	3436	1/1	0.75	0.93	-	56,56,56,56	0
56	MG	XA	1659	1/1	0.96	0.14	-	75,75,75,75	0
56	MG	RA	3099	1/1	0.71	0.31	-	102,102,102,102	0
56	MG	YA	3563	1/1	0.94	0.75	-	76,76,76,76	0
56	MG	XA	1704	1/1	0.36	0.32	-	83,83,83,83	0
56	MG	QA	1864	1/1	0.75	0.58	-	90,90,90,90	0
56	MG	YA	3531	1/1	0.29	0.32	-	66,66,66,66	0
56	MG	RA	3255	1/1	0.97	0.57	-	100,100,100,100	0
56	MG	YA	3278	1/1	0.91	0.24	-	38,38,38,38	0
56	MG	YA	3088	1/1	0.80	0.32	-	42,42,42,42	0
56	MG	RA	3950	1/1	0.32	0.80	-	87,87,87,87	0
56	MG	RA	3366	1/1	0.67	0.35	-	72,72,72,72	0
56	MG	YA	3121	1/1	0.92	0.70	-	47,47,47,47	0
56	MG	RA	3823	1/1	0.52	0.51	-	97,97,97,97	0
56	MG	YA	3077	1/1	0.91	0.28	-	35,35,35,35	0
56	MG	QA	1749	1/1	0.61	0.94	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3054	1/1	0.94	0.11	-	27,27,27,27	0
56	MG	XA	1669	1/1	-0.04	0.93	-	103,103,103,103	0
56	MG	YA	3251	1/1	0.76	0.38	-	100,100,100,100	0
56	MG	RA	3310	1/1	0.94	0.59	-	96,96,96,96	0
56	MG	YA	3075	1/1	0.78	0.40	-	43,43,43,43	0
56	MG	YA	3715	1/1	0.72	0.71	-	58,58,58,58	0
56	MG	RA	3186	1/1	0.83	0.33	-	77,77,77,77	0
56	MG	QA	1839	1/1	-0.16	0.48	-	93,93,93,93	0
56	MG	RA	3440	1/1	0.88	0.47	-	57,57,57,57	0
56	MG	YA	3293	1/1	0.84	1.21	-	70,70,70,70	0
56	MG	YA	3018	1/1	0.71	0.44	-	75,75,75,75	0
56	MG	YA	3682	1/1	0.91	0.33	-	37,37,37,37	0
56	MG	RA	3685	1/1	0.85	0.48	-	97,97,97,97	0
56	MG	XA	1729	1/1	0.88	0.24	-	58,58,58,58	0
56	MG	QA	1648	1/1	0.79	0.20	-	67,67,67,67	0
56	MG	RA	3486	1/1	0.88	0.40	-	78,78,78,78	0
56	MG	RA	3876	1/1	0.96	0.69	-	54,54,54,54	0
56	MG	RA	3524	1/1	0.49	0.63	-	71,71,71,71	0
56	MG	XA	1777	1/1	0.86	0.58	-	98,98,98,98	0
56	MG	RA	3924	1/1	0.63	0.48	-	65,65,65,65	0
56	MG	QA	1807	1/1	0.78	0.31	-	65,65,65,65	0
56	MG	YA	3469	1/1	0.85	0.35	-	88,88,88,88	0
56	MG	YA	3638	1/1	0.86	0.33	-	65,65,65,65	0
56	MG	RA	3498	1/1	0.86	0.46	-	58,58,58,58	0
56	MG	RA	3214	1/1	0.91	0.47	-	59,59,59,59	0
56	MG	YA	3066	1/1	0.95	0.28	-	50,50,50,50	0
56	MG	QA	1681	1/1	-0.01	1.05	-	85,85,85,85	0
56	MG	QA	1716	1/1	0.93	0.14	-	81,81,81,81	0
56	MG	QA	1674	1/1	0.35	0.39	-	85,85,85,85	0
56	MG	Y8	102	1/1	0.94	0.48	-	41,41,41,41	0
56	MG	RA	3868	1/1	0.70	0.44	-	48,48,48,48	0
56	MG	YA	3143	1/1	0.98	0.10	-	56,56,56,56	0
56	MG	RA	3799	1/1	0.87	0.42	-	54,54,54,54	0
56	MG	YA	3466	1/1	0.53	0.53	-	80,80,80,80	0
56	MG	QE	202	1/1	0.29	0.61	-	91,91,91,91	0
56	MG	QA	1776	1/1	0.71	0.37	-	80,80,80,80	0
56	MG	RB	217	1/1	0.62	0.81	-	94,94,94,94	0
56	MG	XA	1670	1/1	0.95	0.32	-	80,80,80,80	0
56	MG	YA	3409	1/1	0.52	0.28	-	120,120,120,120	0
56	MG	YA	3703	1/1	0.92	0.39	-	35,35,35,35	0
56	MG	XA	1679	1/1	0.95	0.41	-	52,52,52,52	0
56	MG	QA	1663	1/1	0.91	0.20	-	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3099	1/1	0.38	0.63	-	106,106,106,106	0
56	MG	RA	3590	1/1	0.17	0.89	-	104,104,104,104	0
56	MG	YA	3696	1/1	0.96	0.38	-	17,17,17,17	0
56	MG	RA	3818	1/1	0.61	0.65	-	67,67,67,67	0
56	MG	YA	3745	1/1	0.71	0.66	-	67,67,67,67	0
56	MG	RA	3060	1/1	0.96	0.14	-	21,21,21,21	0
56	MG	RA	3544	1/1	0.44	0.76	-	78,78,78,78	0
56	MG	RA	3493	1/1	0.93	0.43	-	60,60,60,60	0
56	MG	YA	3356	1/1	0.94	0.36	-	50,50,50,50	0
56	MG	YA	3426	1/1	0.79	0.52	-	50,50,50,50	0
56	MG	RA	3617	1/1	0.49	0.54	-	83,83,83,83	0
56	MG	XA	1776	1/1	0.94	0.56	-	61,61,61,61	0
56	MG	YA	3207	1/1	0.93	0.35	-	70,70,70,70	0
56	MG	RA	3626	1/1	0.81	0.43	-	68,68,68,68	0
56	MG	RA	3202	1/1	0.63	0.62	-	92,92,92,92	0
56	MG	YA	3011	1/1	0.96	0.21	-	40,40,40,40	0
56	MG	RA	3162	1/1	0.59	1.07	-	72,72,72,72	0
56	MG	RA	4012	1/1	0.81	0.79	-	89,89,89,89	0
56	MG	RA	3334	1/1	0.96	0.37	-	46,46,46,46	0
56	MG	RA	3055	1/1	0.83	0.53	-	85,85,85,85	0
56	MG	RA	3768	1/1	0.54	0.85	-	76,76,76,76	0
56	MG	QA	1835	1/1	0.31	0.75	-	89,89,89,89	0
56	MG	RA	3153	1/1	0.94	0.12	-	35,35,35,35	0
56	MG	RQ	202	1/1	0.88	0.34	-	51,51,51,51	0
56	MG	RA	3830	1/1	0.96	0.17	-	66,66,66,66	0
56	MG	RA	3272	1/1	0.59	0.34	-	83,83,83,83	0
56	MG	YA	3229	1/1	0.82	0.34	-	71,71,71,71	0
56	MG	RA	4027	1/1	0.97	0.36	-	39,39,39,39	0
56	MG	QA	1793	1/1	0.59	1.19	-	82,82,82,82	0
56	MG	XA	1741	1/1	0.80	0.23	-	67,67,67,67	0
56	MG	XA	1616	1/1	0.66	1.74	-	115,115,115,115	0
56	MG	YA	3083	1/1	0.64	0.44	-	99,99,99,99	0
56	MG	RA	3336	1/1	0.77	0.30	-	66,66,66,66	0
56	MG	RA	3292	1/1	0.97	0.10	-	83,83,83,83	0
56	MG	YA	3717	1/1	0.83	0.41	-	45,45,45,45	0
56	MG	XA	1703	1/1	0.40	0.67	-	60,60,60,60	0
56	MG	XA	1693	1/1	0.43	0.51	-	81,81,81,81	0
56	MG	RA	3369	1/1	0.96	0.58	-	47,47,47,47	0
56	MG	YA	3408	1/1	0.93	0.37	-	17,17,17,17	0
56	MG	YA	3473	1/1	0.64	0.53	-	77,77,77,77	0
56	MG	XA	1606	1/1	0.94	0.12	-	95,95,95,95	0
56	MG	XA	1738	1/1	0.90	0.62	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3963	1/1	0.55	2.00	-	110,110,110,110	0
56	MG	QV	101	1/1	0.60	0.64	-	118,118,118,118	0
56	MG	XA	1720	1/1	0.88	1.05	-	63,63,63,63	0
56	MG	RA	3521	1/1	0.69	0.40	-	81,81,81,81	0
56	MG	RA	3005	1/1	0.11	1.05	-	99,99,99,99	0
56	MG	QA	1828	1/1	0.97	0.24	-	41,41,41,41	0
56	MG	YA	3053	1/1	0.67	0.51	-	77,77,77,77	0
56	MG	YA	3419	1/1	0.61	0.47	-	66,66,66,66	0
56	MG	XA	1789	1/1	0.69	0.39	-	58,58,58,58	0
56	MG	RA	3081	1/1	0.72	0.54	-	91,91,91,91	0
56	MG	RA	3774	1/1	0.79	0.51	-	59,59,59,59	0
56	MG	YA	3369	1/1	0.48	0.17	-	63,63,63,63	0
56	MG	QA	1792	1/1	0.58	0.58	-	69,69,69,69	0
56	MG	QA	1718	1/1	0.64	0.75	-	82,82,82,82	0
56	MG	RA	3720	1/1	0.97	0.42	-	33,33,33,33	0
56	MG	YA	3738	1/1	0.58	0.54	-	68,68,68,68	0
56	MG	RA	3994	1/1	0.03	0.89	-	88,88,88,88	0
56	MG	QA	1728	1/1	0.49	0.31	-	64,64,64,64	0
56	MG	YA	3215	1/1	0.82	0.19	-	54,54,54,54	0
56	MG	RA	3655	1/1	0.97	0.30	-	25,25,25,25	0
56	MG	XA	1671	1/1	-0.47	1.25	-	108,108,108,108	0
56	MG	QA	1604	1/1	0.82	0.23	-	75,75,75,75	0
56	MG	RA	3654	1/1	0.58	0.47	-	87,87,87,87	0
56	MG	YA	3603	1/1	0.49	0.53	-	100,100,100,100	0
56	MG	RA	3487	1/1	0.96	0.18	-	17,17,17,17	0
56	MG	YA	3545	1/1	0.43	0.43	-	99,99,99,99	0
56	MG	YA	3347	1/1	-0.11	0.26	-	99,99,99,99	0
56	MG	QA	1633	1/1	0.86	0.20	-	95,95,95,95	0
56	MG	RA	3262	1/1	0.93	0.59	-	80,80,80,80	0
56	MG	YA	3630	1/1	0.96	0.50	-	32,32,32,32	0
56	MG	QA	1694	1/1	0.88	0.36	-	97,97,97,97	0
56	MG	YA	3189	1/1	0.94	0.28	-	96,96,96,96	0
56	MG	RA	3793	1/1	0.96	0.41	-	38,38,38,38	0
56	MG	YA	3364	1/1	0.79	0.43	-	67,67,67,67	0
56	MG	RA	3164	1/1	0.80	0.47	-	87,87,87,87	0
56	MG	RA	3052	1/1	0.90	0.23	-	85,85,85,85	0
56	MG	RA	3543	1/1	0.96	0.30	-	26,26,26,26	0
56	MG	RA	3403	1/1	0.95	0.35	-	25,25,25,25	0
56	MG	QA	1685	1/1	0.44	0.42	-	91,91,91,91	0
56	MG	YA	3552	1/1	0.82	0.70	-	52,52,52,52	0
56	MG	YA	3621	1/1	0.94	0.34	-	49,49,49,49	0
56	MG	QA	1615	1/1	0.79	0.25	-	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3509	1/1	0.95	1.03	-	69,69,69,69	0
56	MG	YA	3675	1/1	0.97	0.30	-	29,29,29,29	0
56	MG	RA	3518	1/1	0.63	0.60	-	82,82,82,82	0
56	MG	QA	1717	1/1	0.96	0.53	-	29,29,29,29	0
56	MG	YA	3737	1/1	0.23	1.27	-	107,107,107,107	0
56	MG	RA	3929	1/1	0.94	0.23	-	65,65,65,65	0
56	MG	RA	3327	1/1	0.69	0.61	-	62,62,62,62	0
56	MG	XA	1665	1/1	0.79	0.29	-	73,73,73,73	0
56	MG	YA	3418	1/1	0.67	0.77	-	56,56,56,56	0
56	MG	RA	3614	1/1	0.97	0.42	-	32,32,32,32	0
56	MG	YA	3633	1/1	0.81	0.69	-	47,47,47,47	0
56	MG	YA	3398	1/1	0.93	0.22	-	25,25,25,25	0
56	MG	QV	102	1/1	0.89	0.38	-	45,45,45,45	0
56	MG	RA	3729	1/1	0.73	0.39	-	59,59,59,59	0
56	MG	QA	1746	1/1	0.72	0.23	-	65,65,65,65	0
56	MG	RA	3067	1/1	0.73	0.39	-	83,83,83,83	0
56	MG	RA	3556	1/1	0.48	0.68	-	75,75,75,75	0
56	MG	QA	1798	1/1	-0.41	1.43	-	119,119,119,119	0
56	MG	QA	1770	1/1	0.75	0.25	-	73,73,73,73	0
56	MG	YA	3665	1/1	0.93	0.38	-	31,31,31,31	0
56	MG	YA	3537	1/1	0.92	0.37	-	57,57,57,57	0
56	MG	RA	3747	1/1	0.36	0.57	-	96,96,96,96	0
56	MG	RF	307	1/1	0.89	0.29	-	65,65,65,65	0
56	MG	YA	3496	1/1	0.97	0.42	-	18,18,18,18	0
56	MG	YA	3560	1/1	0.98	0.21	-	6,6,6,6	0
56	MG	RA	3434	1/1	0.83	0.33	-	61,61,61,61	0
56	MG	RA	3012	1/1	0.92	0.19	-	53,53,53,53	0
56	MG	YA	3325	1/1	0.97	0.33	-	20,20,20,20	0
56	MG	QA	1651	1/1	0.85	0.62	-	89,89,89,89	0
56	MG	YA	3612	1/1	0.99	0.23	-	23,23,23,23	0
56	MG	RA	3942	1/1	0.09	0.90	-	104,104,104,104	0
56	MG	YA	3464	1/1	0.56	0.67	-	73,73,73,73	0
56	MG	RA	3835	1/1	0.85	0.73	-	56,56,56,56	0
56	MG	RA	3223	1/1	0.92	0.64	-	63,63,63,63	0
56	MG	YA	3571	1/1	0.98	0.49	-	23,23,23,23	0
56	MG	YA	3104	1/1	0.87	0.55	-	85,85,85,85	0
56	MG	RA	3305	1/1	0.90	0.88	-	98,98,98,98	0
56	MG	YA	3670	1/1	0.97	0.35	-	12,12,12,12	0
56	MG	XA	1609	1/1	0.60	1.30	-	88,88,88,88	0
56	MG	YA	3230	1/1	0.86	0.58	-	57,57,57,57	0
56	MG	YA	3308	1/1	0.29	0.28	-	64,64,64,64	0
56	MG	RA	3133	1/1	0.87	0.29	-	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1674	1/1	0.51	0.31	-	73,73,73,73	0
56	MG	YA	3388	1/1	0.95	0.26	-	33,33,33,33	0
56	MG	R4	102	1/1	0.43	0.38	-	88,88,88,88	0
56	MG	YA	3210	1/1	0.87	0.30	-	65,65,65,65	0
56	MG	YA	3631	1/1	0.98	0.12	-	55,55,55,55	0
56	MG	RA	4007	1/1	0.91	0.63	-	49,49,49,49	0
56	MG	RA	3585	1/1	0.83	0.53	-	59,59,59,59	0
56	MG	XA	1691	1/1	0.91	0.43	-	60,60,60,60	0
56	MG	RA	3429	1/1	0.17	0.21	-	89,89,89,89	0
56	MG	QD	301	1/1	0.30	1.54	-	90,90,90,90	0
56	MG	YA	3383	1/1	0.80	0.45	-	70,70,70,70	0
56	MG	XJ	201	1/1	0.50	0.15	-	97,97,97,97	0
56	MG	RA	3916	1/1	0.62	0.70	-	72,72,72,72	0
56	MG	R5	103	1/1	0.93	0.77	-	59,59,59,59	0
56	MG	QA	1878	1/1	0.29	1.20	-	108,108,108,108	0
56	MG	RA	3149	1/1	0.87	0.27	-	39,39,39,39	0
56	MG	YA	3006	1/1	0.96	0.13	-	18,18,18,18	0
56	MG	YA	3558	1/1	0.94	0.27	-	25,25,25,25	0
56	MG	XA	1666	1/1	0.57	0.76	-	63,63,63,63	0
56	MG	RA	3388	1/1	0.92	0.52	-	49,49,49,49	0
56	MG	RA	3108	1/1	0.94	0.54	-	69,69,69,69	0
56	MG	YA	3140	1/1	0.85	0.56	-	65,65,65,65	0
56	MG	YA	3113	1/1	0.99	0.20	-	104,104,104,104	0
56	MG	YA	3701	1/1	0.95	0.56	-	60,60,60,60	0
56	MG	QA	1733	1/1	0.52	0.78	-	60,60,60,60	0
56	MG	XA	1764	1/1	0.83	0.54	-	52,52,52,52	0
56	MG	YA	3500	1/1	0.73	0.96	-	53,53,53,53	0
56	MG	YA	3493	1/1	0.74	0.34	-	74,74,74,74	0
56	MG	QA	1814	1/1	0.29	0.56	-	97,97,97,97	0
56	MG	YA	3200	1/1	0.87	0.33	-	70,70,70,70	0
56	MG	QA	1723	1/1	0.88	0.19	-	50,50,50,50	0
56	MG	YA	3506	1/1	0.84	0.35	-	53,53,53,53	0
56	MG	QA	1851	1/1	0.74	0.44	-	94,94,94,94	0
56	MG	RA	3480	1/1	0.95	0.47	-	42,42,42,42	0
56	MG	YA	3509	1/1	0.89	0.27	-	71,71,71,71	0
56	MG	RA	3221	1/1	0.83	0.57	-	63,63,63,63	0
56	MG	RA	3156	1/1	0.88	0.27	-	117,117,117,117	0
56	MG	RB	222	1/1	0.59	0.45	-	94,94,94,94	0
56	MG	YD	310	1/1	0.81	0.44	-	64,64,64,64	0
56	MG	RA	3931	1/1	0.89	0.27	-	73,73,73,73	0
56	MG	RA	3303	1/1	0.75	0.74	-	79,79,79,79	0
56	MG	RH	201	1/1	0.51	0.54	-	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1617	1/1	0.94	0.35	-	61,61,61,61	0
56	MG	RA	3009	1/1	0.80	0.30	-	53,53,53,53	0
56	MG	QA	1861	1/1	0.48	0.92	-	75,75,75,75	0
56	MG	RA	3939	1/1	0.91	0.26	-	58,58,58,58	0
56	MG	QA	1679	1/1	0.91	0.20	-	64,64,64,64	0
56	MG	RF	302	1/1	0.57	0.73	-	73,73,73,73	0
56	MG	RA	3560	1/1	0.96	0.61	-	23,23,23,23	0
56	MG	RA	3947	1/1	0.97	0.20	-	20,20,20,20	0
56	MG	RA	3992	1/1	0.79	0.16	-	74,74,74,74	0
56	MG	QA	1664	1/1	0.36	0.90	-	92,92,92,92	0
56	MG	YA	3362	1/1	0.99	0.50	-	18,18,18,18	0
56	MG	RA	3235	1/1	0.94	0.31	-	70,70,70,70	0
56	MG	QA	1784	1/1	0.70	0.47	-	64,64,64,64	0
56	MG	RA	3285	1/1	0.51	0.65	-	85,85,85,85	0
56	MG	RA	3572	1/1	0.91	0.38	-	83,83,83,83	0
56	MG	XA	1602	1/1	0.92	0.28	-	86,86,86,86	0
56	MG	YA	3589	1/1	0.98	0.43	-	31,31,31,31	0
56	MG	QA	1810	1/1	0.86	0.41	-	69,69,69,69	0
56	MG	RA	3069	1/1	0.90	0.29	-	55,55,55,55	0
56	MG	RA	3087	1/1	0.87	0.60	-	99,99,99,99	0
56	MG	RA	3705	1/1	0.89	0.56	-	50,50,50,50	0
56	MG	QA	1670	1/1	0.80	0.52	-	81,81,81,81	0
56	MG	QA	1786	1/1	0.90	0.30	-	54,54,54,54	0
56	MG	RA	3359	1/1	0.97	0.31	-	32,32,32,32	0
56	MG	RA	3176	1/1	0.84	0.69	-	96,96,96,96	0
56	MG	YA	3128	1/1	0.86	0.20	-	26,26,26,26	0
56	MG	YA	3151	1/1	0.97	0.13	-	8,8,8,8	0
56	MG	YA	3476	1/1	0.85	0.54	-	52,52,52,52	0
56	MG	YA	3340	1/1	0.68	0.24	-	59,59,59,59	0
56	MG	XA	1657	1/1	0.87	0.42	-	65,65,65,65	0
56	MG	YA	3249	1/1	0.83	0.54	-	72,72,72,72	0
56	MG	RA	3466	1/1	0.69	0.47	-	56,56,56,56	0
56	MG	QA	1607	1/1	0.75	0.23	-	71,71,71,71	0
56	MG	RA	3619	1/1	0.93	0.48	-	27,27,27,27	0
56	MG	YA	3585	1/1	0.92	0.42	-	75,75,75,75	0
56	MG	R3	101	1/1	0.52	1.02	-	95,95,95,95	0
56	MG	YA	3361	1/1	0.92	0.19	-	65,65,65,65	0
56	MG	RB	221	1/1	0.72	0.23	-	64,64,64,64	0
56	MG	XA	1623	1/1	0.67	0.78	-	73,73,73,73	0
56	MG	YA	3166	1/1	0.09	1.14	-	132,132,132,132	0
56	MG	YA	3617	1/1	0.95	0.29	-	17,17,17,17	0
56	MG	RA	3651	1/1	0.89	0.21	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3879	1/1	0.97	0.35	-	29,29,29,29	0
56	MG	YA	3468	1/1	0.70	0.94	-	58,58,58,58	0
56	MG	YA	3487	1/1	0.94	0.71	-	46,46,46,46	0
56	MG	YA	3132	1/1	0.96	0.58	-	86,86,86,86	0
56	MG	YA	3710	1/1	0.85	0.54	-	61,61,61,61	0
56	MG	RA	3193	1/1	0.37	0.60	-	94,94,94,94	0
56	MG	RA	3734	1/1	0.82	0.59	-	70,70,70,70	0
56	MG	YA	3514	1/1	0.91	0.38	-	62,62,62,62	0
56	MG	YB	207	1/1	0.65	0.47	-	110,110,110,110	0
56	MG	YA	3624	1/1	0.74	0.42	-	71,71,71,71	0
56	MG	YA	3374	1/1	0.97	0.55	-	34,34,34,34	0
56	MG	RA	3140	1/1	0.87	0.78	-	93,93,93,93	0
56	MG	RA	3337	1/1	0.85	0.46	-	81,81,81,81	0
56	MG	YA	3553	1/1	0.82	0.47	-	58,58,58,58	0
56	MG	YA	3367	1/1	0.89	0.15	-	56,56,56,56	0
56	MG	YA	3732	1/1	0.86	1.04	-	73,73,73,73	0
56	MG	RA	3912	1/1	0.71	0.65	-	76,76,76,76	0
56	MG	YG	201	1/1	0.62	1.62	-	116,116,116,116	0
56	MG	YA	3330	1/1	0.66	0.52	-	62,62,62,62	0
56	MG	YA	3297	1/1	0.97	0.49	-	19,19,19,19	0
56	MG	RA	3908	1/1	0.97	0.41	-	22,22,22,22	0
56	MG	QA	1837	1/1	0.48	0.42	-	69,69,69,69	0
56	MG	YA	3064	1/1	0.90	0.41	-	55,55,55,55	0
56	MG	RA	3421	1/1	0.90	0.31	-	42,42,42,42	0
56	MG	RA	3283	1/1	0.54	0.60	-	101,101,101,101	0
56	MG	QA	1838	1/1	0.92	0.28	-	85,85,85,85	0
56	MG	RA	3516	1/1	0.97	0.43	-	13,13,13,13	0
56	MG	YA	3423	1/1	0.89	0.65	-	59,59,59,59	0
56	MG	RZ	301	1/1	0.41	0.33	-	66,66,66,66	0
56	MG	RA	3890	1/1	0.68	0.82	-	57,57,57,57	0
56	MG	YA	3242	1/1	0.82	0.29	-	88,88,88,88	0
56	MG	R5	104	1/1	0.87	0.63	-	67,67,67,67	0
56	MG	YA	3152	1/1	0.96	0.25	-	50,50,50,50	0
56	MG	RA	3208	1/1	0.74	0.35	-	70,70,70,70	0
56	MG	RA	3871	1/1	0.54	0.49	-	77,77,77,77	0
56	MG	XA	1760	1/1	0.82	0.30	-	71,71,71,71	0
56	MG	RA	3833	1/1	0.98	0.40	-	29,29,29,29	0
56	MG	QA	1775	1/1	0.78	0.47	-	72,72,72,72	0
56	MG	RA	3071	1/1	0.93	0.62	-	63,63,63,63	0
56	MG	RA	4002	1/1	0.62	0.31	-	83,83,83,83	0
56	MG	RA	3194	1/1	0.96	0.28	-	67,67,67,67	0
56	MG	YA	3313	1/1	0.91	0.82	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3322	1/1	0.16	0.88	-	90,90,90,90	0
56	MG	RA	3297	1/1	0.85	0.15	-	39,39,39,39	0
56	MG	RA	3004	1/1	0.96	0.10	-	29,29,29,29	0
56	MG	RF	312	1/1	0.76	0.48	-	62,62,62,62	0
56	MG	RA	3748	1/1	0.84	0.22	-	61,61,61,61	0
56	MG	RA	3269	1/1	0.89	0.28	-	74,74,74,74	0
56	MG	RA	3993	1/1	0.75	0.45	-	86,86,86,86	0
56	MG	YA	3259	1/1	0.86	0.31	-	66,66,66,66	0
56	MG	YA	3709	1/1	0.92	0.86	-	58,58,58,58	0
56	MG	RA	3217	1/1	0.57	0.35	-	88,88,88,88	0
56	MG	RA	3540	1/1	0.74	0.26	-	73,73,73,73	0
56	MG	RA	3174	1/1	0.83	0.29	-	62,62,62,62	0
56	MG	RA	3826	1/1	0.81	0.28	-	62,62,62,62	0
56	MG	YA	3226	1/1	0.78	0.44	-	75,75,75,75	0
56	MG	RA	3970	1/1	0.93	0.37	-	31,31,31,31	0
56	MG	RA	3151	1/1	0.89	0.60	-	59,59,59,59	0
56	MG	RA	3158	1/1	0.85	0.35	-	67,67,67,67	0
56	MG	YA	3741	1/1	0.97	0.29	-	57,57,57,57	0
56	MG	RA	3260	1/1	0.88	0.99	-	71,71,71,71	0
56	MG	QA	1777	1/1	0.92	0.19	-	81,81,81,81	0
56	MG	RA	3791	1/1	0.69	0.31	-	64,64,64,64	0
56	MG	YB	211	1/1	0.59	0.34	-	70,70,70,70	0
56	MG	Y0	101	1/1	0.64	0.85	-	65,65,65,65	0
56	MG	RW	201	1/1	0.87	0.33	-	64,64,64,64	0
56	MG	RA	3173	1/1	0.77	0.35	-	50,50,50,50	0
56	MG	RA	3539	1/1	0.87	0.54	-	39,39,39,39	0
56	MG	YA	3739	1/1	0.98	0.47	-	79,79,79,79	0
56	MG	YA	3316	1/1	0.93	0.47	-	53,53,53,53	0
56	MG	RA	3669	1/1	0.25	0.61	-	81,81,81,81	0
56	MG	QA	1796	1/1	0.63	0.43	-	73,73,73,73	0
56	MG	RA	3788	1/1	0.67	0.10	-	75,75,75,75	0
56	MG	YA	3490	1/1	0.66	0.51	-	104,104,104,104	0
56	MG	RA	3456	1/1	0.72	0.21	-	58,58,58,58	0
56	MG	RA	3864	1/1	0.96	0.79	-	76,76,76,76	0
56	MG	QA	1804	1/1	0.69	0.39	-	71,71,71,71	0
56	MG	QA	1735	1/1	0.04	0.69	-	107,107,107,107	0
56	MG	RA	3564	1/1	0.61	0.59	-	101,101,101,101	0
56	MG	RA	3278	1/1	0.84	0.67	-	83,83,83,83	0
56	MG	QA	1769	1/1	0.10	0.54	-	95,95,95,95	0
56	MG	QA	1740	1/1	0.97	0.34	-	55,55,55,55	0
56	MG	YA	3456	1/1	0.61	0.66	-	68,68,68,68	0
56	MG	RA	3345	1/1	0.97	0.46	-	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3013	1/1	0.80	0.54	-	71,71,71,71	0
56	MG	RA	3739	1/1	0.90	0.31	-	78,78,78,78	0
56	MG	XA	1713	1/1	0.76	0.24	-	49,49,49,49	0
56	MG	RA	3903	1/1	0.74	0.28	-	57,57,57,57	0
56	MG	RA	3215	1/1	0.83	0.40	-	98,98,98,98	0
56	MG	RA	3635	1/1	0.68	0.30	-	112,112,112,112	0
56	MG	RA	3096	1/1	0.92	0.17	-	48,48,48,48	0
56	MG	YB	209	1/1	0.22	1.01	-	102,102,102,102	0
56	MG	QA	1866	1/1	0.40	1.84	-	89,89,89,89	0
56	MG	RA	3932	1/1	0.94	0.61	-	61,61,61,61	0
56	MG	QA	1608	1/1	0.71	0.68	-	110,110,110,110	0
56	MG	YA	3194	1/1	0.88	0.32	-	70,70,70,70	0
56	MG	YA	3376	1/1	0.90	0.16	-	58,58,58,58	0
56	MG	XA	1667	1/1	0.94	0.32	-	77,77,77,77	0
56	MG	YA	3484	1/1	0.96	0.34	-	21,21,21,21	0
56	MG	RA	3894	1/1	0.96	0.48	-	23,23,23,23	0
56	MG	YA	3431	1/1	0.61	0.59	-	57,57,57,57	0
56	MG	RA	3320	1/1	0.98	0.37	-	14,14,14,14	0
56	MG	YA	3049	1/1	0.93	0.31	-	78,78,78,78	0
56	MG	YA	3284	1/1	0.97	0.23	-	8,8,8,8	0
56	MG	RA	3985	1/1	0.41	0.68	-	81,81,81,81	0
56	MG	RA	3286	1/1	0.93	0.46	-	118,118,118,118	0
56	MG	YA	3647	1/1	0.96	0.49	-	27,27,27,27	0
56	MG	RA	3663	1/1	0.75	0.49	-	77,77,77,77	0
56	MG	YA	3004	1/1	0.96	0.14	-	43,43,43,43	0
56	MG	RA	3574	1/1	0.78	0.34	-	62,62,62,62	0
56	MG	RA	3979	1/1	0.96	0.20	-	37,37,37,37	0
56	MG	QA	1712	1/1	0.61	0.56	-	87,87,87,87	0
56	MG	QA	1659	1/1	0.90	1.38	-	84,84,84,84	0
56	MG	QQ	201	1/1	0.85	0.20	-	71,71,71,71	0
56	MG	RA	3048	1/1	0.67	0.32	-	78,78,78,78	0
56	MG	RA	3051	1/1	0.63	0.60	-	83,83,83,83	0
56	MG	RA	3275	1/1	0.71	0.46	-	72,72,72,72	0
56	MG	RA	3192	1/1	0.92	0.75	-	92,92,92,92	0
56	MG	YA	3095	1/1	0.76	0.17	-	68,68,68,68	0
56	MG	RA	3693	1/1	0.80	0.38	-	67,67,67,67	0
56	MG	RT	203	1/1	0.14	0.50	-	88,88,88,88	0
56	MG	YA	3008	1/1	0.91	0.20	-	47,47,47,47	0
56	MG	QA	1689	1/1	0.81	0.50	-	80,80,80,80	0
56	MG	YA	3262	1/1	0.38	0.68	-	88,88,88,88	0
56	MG	RA	3896	1/1	0.75	0.75	-	59,59,59,59	0
56	MG	YA	3211	1/1	0.58	0.53	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	QA	1822	1/1	0.71	0.56	-	65,65,65,65	0
56	MG	YA	3505	1/1	0.70	0.97	-	88,88,88,88	0
56	MG	YA	3263	1/1	0.83	0.58	-	81,81,81,81	0
56	MG	RA	3719	1/1	0.78	0.39	-	55,55,55,55	0
56	MG	RA	3925	1/1	0.88	0.28	-	83,83,83,83	0
56	MG	QA	1609	1/1	0.66	0.60	-	106,106,106,106	0
56	MG	YA	3232	1/1	0.48	0.37	-	104,104,104,104	0
56	MG	QA	1701	1/1	0.88	0.79	-	50,50,50,50	0
56	MG	YA	3292	1/1	0.85	0.75	-	81,81,81,81	0
56	MG	RA	3379	1/1	0.96	0.47	-	44,44,44,44	0
56	MG	YA	3645	1/1	0.89	0.62	-	67,67,67,67	0
56	MG	RA	3935	1/1	-0.02	0.51	-	91,91,91,91	0
56	MG	RA	3666	1/1	0.91	0.98	-	69,69,69,69	0
56	MG	RA	3450	1/1	0.86	1.24	-	53,53,53,53	0
56	MG	RA	3638	1/1	0.73	0.37	-	85,85,85,85	0
56	MG	RA	3949	1/1	0.39	0.67	-	80,80,80,80	0
56	MG	YA	3103	1/1	0.62	0.25	-	63,63,63,63	0
56	MG	QA	1652	1/1	0.32	0.62	-	83,83,83,83	0
56	MG	YI	201	1/1	0.81	0.34	-	110,110,110,110	0
56	MG	RA	3238	1/1	0.95	0.38	-	106,106,106,106	0
56	MG	RA	3694	1/1	0.43	0.53	-	107,107,107,107	0
56	MG	QA	1601	1/1	-0.53	0.53	-	129,129,129,129	0
56	MG	RA	3537	1/1	0.45	0.61	-	93,93,93,93	0
56	MG	RA	3019	1/1	0.83	0.27	-	113,113,113,113	0
56	MG	XA	1714	1/1	0.80	0.20	-	58,58,58,58	0
56	MG	RA	3741	1/1	0.72	0.21	-	61,61,61,61	0
56	MG	RA	3852	1/1	0.96	0.35	-	47,47,47,47	0
56	MG	YA	3357	1/1	0.90	0.30	-	39,39,39,39	0
56	MG	RA	3682	1/1	0.71	0.37	-	81,81,81,81	0
56	MG	QA	1783	1/1	0.54	0.21	-	77,77,77,77	0
56	MG	RA	3700	1/1	0.89	0.23	-	53,53,53,53	0
56	MG	RA	3502	1/1	0.98	0.31	-	20,20,20,20	0
56	MG	QA	1653	1/1	0.60	0.42	-	85,85,85,85	0
56	MG	RA	3189	1/1	0.96	0.24	-	39,39,39,39	0
56	MG	YA	3082	1/1	0.93	0.26	-	78,78,78,78	0
56	MG	RA	3171	1/1	0.65	0.51	-	89,89,89,89	0
56	MG	RA	3865	1/1	0.93	0.49	-	51,51,51,51	0
56	MG	RA	3699	1/1	0.41	1.14	-	98,98,98,98	0
56	MG	YQ	202	1/1	0.83	0.37	-	59,59,59,59	0
56	MG	YA	3046	1/1	0.87	0.38	-	75,75,75,75	0
56	MG	RA	3222	1/1	0.84	0.11	-	72,72,72,72	0
56	MG	YA	3355	1/1	0.76	0.11	-	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3632	1/1	0.86	0.49	-	55,55,55,55	0
56	MG	RA	3914	1/1	0.92	0.50	-	56,56,56,56	0
56	MG	YA	3451	1/1	0.60	0.37	-	64,64,64,64	0
56	MG	RA	4005	1/1	0.83	0.28	-	58,58,58,58	0
56	MG	YA	3697	1/1	0.92	0.64	-	38,38,38,38	0
56	MG	YA	3191	1/1	0.55	0.14	-	76,76,76,76	0
56	MG	QA	1863	1/1	0.80	0.28	-	80,80,80,80	0
56	MG	YA	3282	1/1	0.97	0.36	-	10,10,10,10	0
56	MG	RA	3627	1/1	0.87	0.62	-	76,76,76,76	0
56	MG	YA	3223	1/1	0.86	0.47	-	91,91,91,91	0
56	MG	XA	1734	1/1	0.89	0.17	-	78,78,78,78	0
56	MG	RA	3370	1/1	0.29	0.99	-	88,88,88,88	0
56	MG	RA	3933	1/1	0.73	0.85	-	76,76,76,76	0
56	MG	YA	3334	1/1	0.97	0.51	-	14,14,14,14	0
56	MG	YA	3640	1/1	0.96	0.56	-	40,40,40,40	0
56	MG	RA	3300	1/1	0.82	1.18	-	68,68,68,68	0
56	MG	YA	3063	1/1	0.92	0.23	-	35,35,35,35	0
56	MG	RA	3417	1/1	0.96	0.12	-	42,42,42,42	0
56	MG	RA	3987	1/1	0.72	0.65	-	80,80,80,80	0
56	MG	RA	3547	1/1	0.45	0.35	-	74,74,74,74	0
56	MG	RA	3742	1/1	0.59	0.60	-	81,81,81,81	0
56	MG	RA	3340	1/1	0.69	0.49	-	52,52,52,52	0
56	MG	YA	3086	1/1	0.02	0.93	-	95,95,95,95	0
56	MG	YA	3533	1/1	0.97	0.22	-	48,48,48,48	0
56	MG	XA	1673	1/1	-0.23	1.71	-	103,103,103,103	0
56	MG	RA	3097	1/1	0.95	0.49	-	93,93,93,93	0
56	MG	QA	1698	1/1	0.48	0.40	-	100,100,100,100	0
56	MG	RA	3579	1/1	0.98	0.30	-	24,24,24,24	0
56	MG	YA	3216	1/1	0.94	0.37	-	25,25,25,25	0
56	MG	RA	3080	1/1	0.82	0.60	-	81,81,81,81	0
56	MG	YA	3147	1/1	0.60	0.40	-	84,84,84,84	0
56	MG	XA	1680	1/1	0.66	0.18	-	77,77,77,77	0
56	MG	YA	3170	1/1	0.79	0.63	-	56,56,56,56	0
56	MG	RA	3086	1/1	0.40	0.77	-	124,124,124,124	0
56	MG	RA	3326	1/1	0.95	0.19	-	20,20,20,20	0
56	MG	R0	102	1/1	0.67	0.21	-	84,84,84,84	0
56	MG	QA	1629	1/1	0.88	0.31	-	51,51,51,51	0
56	MG	XA	1739	1/1	0.92	0.51	-	61,61,61,61	0
56	MG	RA	3755	1/1	0.74	0.56	-	71,71,71,71	0
56	MG	RA	3859	1/1	0.88	0.72	-	72,72,72,72	0
56	MG	RA	4054	1/1	0.39	0.99	-	97,97,97,97	0
56	MG	RA	3569	1/1	0.91	0.46	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3413	1/1	0.97	0.40	-	36,36,36,36	0
56	MG	QL	202	1/1	0.84	0.11	-	68,68,68,68	0
56	MG	RA	3671	1/1	0.84	0.29	-	71,71,71,71	0
56	MG	YA	3285	1/1	0.95	0.55	-	25,25,25,25	0
56	MG	RA	3893	1/1	0.98	0.62	-	34,34,34,34	0
56	MG	YA	3299	1/1	0.96	0.53	-	10,10,10,10	0
56	MG	YA	3527	1/1	0.91	0.38	-	50,50,50,50	0
56	MG	YA	3395	1/1	0.99	0.41	-	17,17,17,17	0
56	MG	XA	1650	1/1	0.79	0.64	-	84,84,84,84	0
56	MG	RA	3733	1/1	0.27	0.94	-	96,96,96,96	0
56	MG	XA	1783	1/1	0.17	1.23	-	99,99,99,99	0
56	MG	YA	3123	1/1	0.89	0.14	-	86,86,86,86	0
56	MG	RA	3197	1/1	0.31	1.25	-	85,85,85,85	0
56	MG	YA	3019	1/1	0.91	0.34	-	81,81,81,81	0
56	MG	RA	3455	1/1	0.82	0.41	-	48,48,48,48	0
56	MG	QA	1677	1/1	0.21	0.91	-	94,94,94,94	0
56	MG	RA	3661	1/1	0.80	0.32	-	89,89,89,89	0
56	MG	XA	1645	1/1	0.66	0.53	-	93,93,93,93	0
56	MG	QA	1693	1/1	0.09	0.39	-	88,88,88,88	0
56	MG	YA	3081	1/1	0.88	0.53	-	71,71,71,71	0
56	MG	RA	3508	1/1	0.98	0.46	-	42,42,42,42	0
56	MG	YA	3729	1/1	0.79	0.55	-	61,61,61,61	0
56	MG	RA	3103	1/1	0.38	0.50	-	104,104,104,104	0
56	MG	XA	1773	1/1	0.12	0.97	-	96,96,96,96	0
56	MG	RA	3188	1/1	0.91	0.75	-	115,115,115,115	0
56	MG	YA	3525	1/1	0.88	0.54	-	86,86,86,86	0
56	MG	RB	211	1/1	0.21	0.37	-	95,95,95,95	0
56	MG	RA	3969	1/1	0.65	0.45	-	98,98,98,98	0
56	MG	YA	3440	1/1	0.97	0.24	-	29,29,29,29	0
56	MG	YA	3161	1/1	0.78	0.52	-	76,76,76,76	0
56	MG	RB	228	1/1	0.61	0.56	-	93,93,93,93	0
56	MG	RA	3639	1/1	0.70	1.07	-	65,65,65,65	0
56	MG	YA	3125	1/1	0.96	0.37	-	58,58,58,58	0
56	MG	RA	3104	1/1	0.69	0.48	-	57,57,57,57	0
56	MG	QA	1808	1/1	0.80	0.48	-	54,54,54,54	0
56	MG	RA	3309	1/1	0.57	0.58	-	63,63,63,63	0
56	MG	RA	3329	1/1	0.84	0.28	-	86,86,86,86	0
56	MG	RA	3644	1/1	-0.05	1.01	-	84,84,84,84	0
56	MG	YA	3488	1/1	0.54	0.38	-	105,105,105,105	0
56	MG	YA	3735	1/1	0.89	0.56	-	71,71,71,71	0
56	MG	YA	3429	1/1	0.90	0.29	-	67,67,67,67	0
56	MG	QA	1639	1/1	0.85	0.20	-	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3138	1/1	0.95	0.23	-	61,61,61,61	0
56	MG	RA	3698	1/1	0.97	0.13	-	73,73,73,73	0
56	MG	YA	3541	1/1	0.89	0.41	-	20,20,20,20	0
56	MG	R9	103	1/1	0.91	0.23	-	67,67,67,67	0
56	MG	YA	3529	1/1	0.60	0.71	-	73,73,73,73	0
56	MG	RA	3473	1/1	0.99	0.37	-	26,26,26,26	0
56	MG	QA	1871	1/1	0.09	2.62	-	100,100,100,100	0
56	MG	RA	3756	1/1	0.82	0.48	-	83,83,83,83	0
56	MG	RA	3245	1/1	0.72	0.47	-	81,81,81,81	0
56	MG	RA	3290	1/1	0.80	0.35	-	74,74,74,74	0
56	MG	YA	3059	1/1	0.65	0.63	-	79,79,79,79	0
56	MG	YB	212	1/1	0.94	0.50	-	57,57,57,57	0
56	MG	QA	1702	1/1	0.86	0.35	-	64,64,64,64	0
56	MG	QG	202	1/1	0.79	0.31	-	92,92,92,92	0
56	MG	RA	3991	1/1	0.71	0.59	-	73,73,73,73	0
56	MG	RA	3397	1/1	0.82	0.44	-	65,65,65,65	0
56	MG	RF	311	1/1	0.74	0.62	-	74,74,74,74	0
56	MG	YA	3028	1/1	0.86	0.31	-	51,51,51,51	0
56	MG	YA	3590	1/1	0.98	0.68	-	41,41,41,41	0
56	MG	RA	3702	1/1	0.81	0.96	-	67,67,67,67	0
56	MG	XA	1677	1/1	0.87	0.26	-	71,71,71,71	0
56	MG	QA	1831	1/1	0.54	0.40	-	93,93,93,93	0
56	MG	QA	1853	1/1	0.65	0.63	-	107,107,107,107	0
56	MG	RA	3479	1/1	0.91	0.33	-	19,19,19,19	0
56	MG	YA	3220	1/1	0.79	0.30	-	87,87,87,87	0
56	MG	YA	3671	1/1	0.90	0.47	-	37,37,37,37	0
56	MG	XA	1637	1/1	0.36	0.69	-	89,89,89,89	0
56	MG	RA	3880	1/1	0.80	0.48	-	54,54,54,54	0
56	MG	YA	3307	1/1	0.77	0.34	-	73,73,73,73	0
56	MG	XA	1612	1/1	0.97	0.09	-	41,41,41,41	0
56	MG	XA	1747	1/1	0.88	0.51	-	59,59,59,59	0
56	MG	QM	201	1/1	0.31	0.63	-	85,85,85,85	0
56	MG	RA	3904	1/1	0.98	0.29	-	24,24,24,24	0
56	MG	RA	3588	1/1	0.84	0.48	-	63,63,63,63	0
56	MG	RA	3527	1/1	0.79	0.77	-	67,67,67,67	0
56	MG	YA	3486	1/1	0.96	0.55	-	30,30,30,30	0
56	MG	YA	3458	1/1	0.92	0.31	-	46,46,46,46	0
56	MG	YA	3642	1/1	0.97	0.69	-	58,58,58,58	0
56	MG	RA	3984	1/1	0.94	0.38	-	41,41,41,41	0
56	MG	RA	3090	1/1	0.31	0.43	-	93,93,93,93	0
56	MG	RA	3474	1/1	0.99	0.28	-	45,45,45,45	0
56	MG	XA	1748	1/1	0.76	0.46	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3033	1/1	0.87	0.26	-	91,91,91,91	0
56	MG	QA	1772	1/1	0.75	0.99	-	79,79,79,79	0
56	MG	RA	3967	1/1	0.59	0.57	-	61,61,61,61	0
56	MG	RA	3620	1/1	0.41	0.59	-	90,90,90,90	0
56	MG	YA	3650	1/1	0.92	0.61	-	48,48,48,48	0
56	MG	YA	3320	1/1	0.98	0.36	-	26,26,26,26	0
56	MG	YA	3234	1/1	0.72	0.53	-	76,76,76,76	0
56	MG	XA	1750	1/1	0.89	0.28	-	87,87,87,87	0
56	MG	RA	3352	1/1	0.92	0.57	-	65,65,65,65	0
56	MG	RA	3031	1/1	0.59	0.39	-	75,75,75,75	0
56	MG	RA	3983	1/1	0.56	0.70	-	84,84,84,84	0
56	MG	RB	212	1/1	0.85	0.17	-	74,74,74,74	0
56	MG	RA	3280	1/1	0.89	0.23	-	78,78,78,78	0
56	MG	YT	201	1/1	0.74	0.43	-	57,57,57,57	0
56	MG	RA	3113	1/1	0.93	0.58	-	65,65,65,65	0
56	MG	RA	3546	1/1	0.55	0.44	-	111,111,111,111	0
56	MG	YA	3384	1/1	0.93	0.55	-	38,38,38,38	0
56	MG	YA	3436	1/1	0.91	0.38	-	51,51,51,51	0
56	MG	RA	3405	1/1	0.88	0.56	-	32,32,32,32	0
56	MG	RA	3020	1/1	0.99	0.45	-	89,89,89,89	0
56	MG	QA	1640	1/1	0.77	0.73	-	75,75,75,75	0
56	MG	RA	3885	1/1	0.97	0.52	-	66,66,66,66	0
56	MG	RA	3603	1/1	0.28	0.50	-	101,101,101,101	0
56	MG	YA	3122	1/1	0.92	0.51	-	60,60,60,60	0
56	MG	QA	1873	1/1	0.46	0.60	-	70,70,70,70	0
56	MG	YA	3165	1/1	0.29	0.51	-	73,73,73,73	0
56	MG	QE	201	1/1	0.68	0.17	-	84,84,84,84	0
56	MG	RA	3971	1/1	0.97	0.38	-	19,19,19,19	0
56	MG	RA	3191	1/1	0.92	0.13	-	69,69,69,69	0
56	MG	RA	3296	1/1	0.62	0.43	-	102,102,102,102	0
56	MG	RA	3863	1/1	0.73	1.26	-	87,87,87,87	0
56	MG	RA	3738	1/1	0.95	0.40	-	53,53,53,53	0
56	MG	RA	3850	1/1	0.97	0.31	-	43,43,43,43	0
56	MG	YA	3516	1/1	0.84	0.60	-	78,78,78,78	0
56	MG	RB	224	1/1	0.60	0.65	-	78,78,78,78	0
56	MG	XA	1744	1/1	0.91	0.59	-	59,59,59,59	0
56	MG	RA	3841	1/1	0.81	0.44	-	64,64,64,64	0
56	MG	QA	1691	1/1	-0.06	0.46	-	104,104,104,104	0
56	MG	YA	3238	1/1	0.89	0.32	-	91,91,91,91	0
56	MG	RA	3413	1/1	0.97	0.39	-	34,34,34,34	0
56	MG	RA	3356	1/1	0.90	0.11	-	23,23,23,23	0
56	MG	XA	1731	1/1	0.85	0.26	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3269	1/1	0.75	0.54	-	78,78,78,78	0
56	MG	YA	3101	1/1	0.83	0.35	-	70,70,70,70	0
56	MG	YA	3005	1/1	0.95	0.29	-	63,63,63,63	0
56	MG	YA	3676	1/1	0.55	0.84	-	73,73,73,73	0
56	MG	RA	3106	1/1	0.96	0.26	-	102,102,102,102	0
56	MG	RA	3690	1/1	0.83	0.99	-	74,74,74,74	0
56	MG	RA	3371	1/1	0.88	0.54	-	75,75,75,75	0
56	MG	YA	3163	1/1	0.89	0.19	-	52,52,52,52	0
56	MG	QA	1762	1/1	-0.08	1.11	-	93,93,93,93	0
56	MG	XA	1639	1/1	0.52	0.52	-	98,98,98,98	0
56	MG	YA	3050	1/1	0.83	0.19	-	85,85,85,85	0
56	MG	YA	3343	1/1	0.96	0.40	-	21,21,21,21	0
56	MG	YA	3450	1/1	0.48	0.70	-	79,79,79,79	0
56	MG	YA	3470	1/1	0.83	0.31	-	59,59,59,59	0
56	MG	YA	3502	1/1	0.67	0.44	-	79,79,79,79	0
56	MG	RB	213	1/1	0.89	0.61	-	58,58,58,58	0
56	MG	QA	1695	1/1	0.82	0.47	-	48,48,48,48	0
56	MG	YA	3150	1/1	0.54	0.82	-	84,84,84,84	0
56	MG	YA	3289	1/1	0.96	0.24	-	38,38,38,38	0
56	MG	YE	301	1/1	0.34	0.49	-	95,95,95,95	0
56	MG	RA	3145	1/1	0.93	0.16	-	43,43,43,43	0
56	MG	QA	1699	1/1	0.76	0.57	-	65,65,65,65	0
56	MG	RA	3727	1/1	-0.47	0.55	-	108,108,108,108	0
56	MG	YA	3539	1/1	0.97	0.30	-	18,18,18,18	0
56	MG	RA	3954	1/1	0.36	0.63	-	77,77,77,77	0
56	MG	RA	3343	1/1	0.90	0.16	-	68,68,68,68	0
56	MG	RA	3263	1/1	0.69	0.23	-	67,67,67,67	0
56	MG	RA	3786	1/1	0.31	0.66	-	87,87,87,87	0
56	MG	YA	3428	1/1	0.82	0.32	-	44,44,44,44	0
56	MG	YA	3726	1/1	0.38	0.80	-	81,81,81,81	0
56	MG	XA	1634	1/1	0.18	0.46	-	75,75,75,75	0
56	MG	QA	1669	1/1	0.71	1.07	-	71,71,71,71	0
56	MG	YA	3070	1/1	0.70	0.42	-	62,62,62,62	0
56	MG	RB	201	1/1	0.94	0.19	-	72,72,72,72	0
56	MG	XA	1603	1/1	0.52	0.87	-	76,76,76,76	0
56	MG	YA	3174	1/1	0.21	0.99	-	95,95,95,95	0
56	MG	RA	3129	1/1	0.83	0.25	-	45,45,45,45	0
56	MG	QA	1720	1/1	-0.02	0.88	-	97,97,97,97	0
56	MG	QA	1794	1/1	0.60	0.46	-	79,79,79,79	0
56	MG	QA	1628	1/1	0.80	0.27	-	49,49,49,49	0
56	MG	RA	3652	1/1	0.69	0.62	-	88,88,88,88	0
56	MG	RA	3492	1/1	0.93	0.41	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3957	1/1	0.81	0.32	-	66,66,66,66	0
56	MG	RA	3057	1/1	0.63	0.52	-	93,93,93,93	0
56	MG	YO	201	1/1	0.76	0.35	-	78,78,78,78	0
56	MG	RA	3089	1/1	0.92	0.07	-	67,67,67,67	0
56	MG	YA	3609	1/1	0.92	0.26	-	51,51,51,51	0
56	MG	YA	3508	1/1	0.79	0.37	-	102,102,102,102	0
56	MG	YA	3007	1/1	0.93	0.25	-	63,63,63,63	0
56	MG	RA	3061	1/1	0.62	0.23	-	84,84,84,84	0
56	MG	YA	3414	1/1	0.66	0.68	-	83,83,83,83	0
56	MG	XA	1697	1/1	0.66	0.81	-	70,70,70,70	0
56	MG	YA	3405	1/1	0.84	0.42	-	86,86,86,86	0
56	MG	YA	3027	1/1	0.73	0.49	-	45,45,45,45	0
56	MG	RA	3018	1/1	0.85	0.32	-	89,89,89,89	0
56	MG	RA	3580	1/1	0.53	0.65	-	112,112,112,112	0
56	MG	RA	3063	1/1	0.95	0.30	-	41,41,41,41	0
56	MG	RA	3533	1/1	0.80	0.26	-	49,49,49,49	0
56	MG	XA	1733	1/1	0.90	0.25	-	72,72,72,72	0
56	MG	YA	3368	1/1	0.80	0.45	-	62,62,62,62	0
56	MG	RP	202	1/1	0.73	0.22	-	78,78,78,78	0
56	MG	YA	3447	1/1	0.84	0.59	-	68,68,68,68	0
56	MG	RA	3647	1/1	0.89	0.29	-	88,88,88,88	0
56	MG	RA	3946	1/1	0.96	0.15	-	18,18,18,18	0
56	MG	YA	3184	1/1	0.60	0.43	-	80,80,80,80	0
56	MG	YA	3686	1/1	0.99	0.35	-	15,15,15,15	0
56	MG	RA	3307	1/1	0.96	0.45	-	76,76,76,76	0
56	MG	XA	1766	1/1	0.97	0.72	-	52,52,52,52	0
56	MG	QA	1676	1/1	0.72	0.61	-	88,88,88,88	0
56	MG	XA	1710	1/1	0.85	0.35	-	66,66,66,66	0
56	MG	RA	4019	1/1	0.79	0.68	-	87,87,87,87	0
56	MG	RA	3860	1/1	0.94	0.48	-	25,25,25,25	0
56	MG	YA	3661	1/1	0.88	0.61	-	63,63,63,63	0
56	MG	RA	3541	1/1	0.68	0.87	-	74,74,74,74	0
56	MG	YA	3427	1/1	-0.06	1.07	-	75,75,75,75	0
56	MG	QA	1671	1/1	0.94	0.16	-	64,64,64,64	0
56	MG	RA	3519	1/1	0.58	0.44	-	82,82,82,82	0
56	MG	RA	3213	1/1	0.92	0.31	-	105,105,105,105	0
56	MG	RA	3179	1/1	0.44	0.84	-	77,77,77,77	0
56	MG	RA	3796	1/1	0.47	0.94	-	67,67,67,67	0
56	MG	RA	3244	1/1	0.90	0.08	-	71,71,71,71	0
56	MG	RA	3960	1/1	0.75	0.69	-	89,89,89,89	0
56	MG	RA	3261	1/1	0.16	0.49	-	82,82,82,82	0
56	MG	YA	3723	1/1	0.77	0.37	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3172	1/1	0.83	0.28	-	69,69,69,69	0
56	MG	RA	3898	1/1	0.86	0.32	-	48,48,48,48	0
56	MG	YB	202	1/1	0.89	0.17	-	56,56,56,56	0
56	MG	RA	3107	1/1	0.80	0.53	-	109,109,109,109	0
56	MG	RA	3091	1/1	0.86	1.44	-	104,104,104,104	0
56	MG	YA	3517	1/1	0.78	0.41	-	92,92,92,92	0
56	MG	YA	3134	1/1	0.76	0.45	-	89,89,89,89	0
56	MG	RA	3596	1/1	0.71	0.42	-	83,83,83,83	0
56	MG	RD	310	1/1	0.53	0.41	-	94,94,94,94	0
56	MG	XA	1705	1/1	0.74	0.26	-	67,67,67,67	0
56	MG	YA	3198	1/1	0.72	0.60	-	80,80,80,80	0
56	MG	YF	302	1/1	0.39	0.53	-	85,85,85,85	0
56	MG	YA	3417	1/1	0.14	0.70	-	106,106,106,106	0
56	MG	RA	3728	1/1	0.90	0.32	-	74,74,74,74	0
56	MG	YA	3421	1/1	0.30	1.11	-	75,75,75,75	0
56	MG	YA	3270	1/1	0.57	0.45	-	83,83,83,83	0
56	MG	RA	3248	1/1	0.86	0.34	-	56,56,56,56	0
56	MG	RA	3003	1/1	0.73	0.40	-	73,73,73,73	0
56	MG	QA	1642	1/1	0.43	0.66	-	83,83,83,83	0
56	MG	RA	3554	1/1	0.87	0.51	-	55,55,55,55	0
56	MG	QH	201	1/1	0.54	0.49	-	76,76,76,76	0
56	MG	RA	3817	1/1	0.50	0.81	-	76,76,76,76	0
56	MG	RA	3036	1/1	0.59	0.41	-	69,69,69,69	0
56	MG	RA	3562	1/1	0.92	0.16	-	59,59,59,59	0
56	MG	RA	3124	1/1	0.78	0.19	-	46,46,46,46	0
56	MG	RA	3522	1/1	0.85	0.29	-	55,55,55,55	0
56	MG	RA	3593	1/1	0.90	0.56	-	66,66,66,66	0
56	MG	RA	3347	1/1	0.95	0.47	-	23,23,23,23	0
56	MG	YA	3160	1/1	0.87	0.47	-	67,67,67,67	0
56	MG	RA	3926	1/1	0.69	0.50	-	83,83,83,83	0
56	MG	RA	3279	1/1	0.28	0.57	-	103,103,103,103	0
56	MG	RA	3958	1/1	0.60	0.54	-	104,104,104,104	0
56	MG	RA	3996	1/1	0.87	0.86	-	73,73,73,73	0
56	MG	YD	302	1/1	0.81	0.38	-	71,71,71,71	0
56	MG	YA	3180	1/1	0.85	0.41	-	43,43,43,43	0
56	MG	RA	3308	1/1	0.91	0.50	-	64,64,64,64	0
56	MG	RB	227	1/1	0.67	0.53	-	74,74,74,74	0
56	MG	QA	1826	1/1	-0.17	0.47	-	74,74,74,74	0
56	MG	YA	3233	1/1	0.41	0.47	-	95,95,95,95	0
56	MG	RA	4013	1/1	0.83	0.42	-	76,76,76,76	0
56	MG	RA	3392	1/1	0.86	0.27	-	28,28,28,28	0
56	MG	RA	3749	1/1	0.87	0.31	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3625	1/1	0.47	0.67	-	91,91,91,91	0
56	MG	YB	210	1/1	0.94	0.40	-	57,57,57,57	0
56	MG	QA	1660	1/1	0.66	0.19	-	77,77,77,77	0
56	MG	YA	3510	1/1	0.64	0.61	-	80,80,80,80	0
56	MG	RA	3068	1/1	0.61	0.49	-	79,79,79,79	0
56	MG	QA	1666	1/1	0.69	0.22	-	74,74,74,74	0
56	MG	YA	3311	1/1	0.20	1.31	-	94,94,94,94	0
56	MG	QA	1849	1/1	0.85	0.69	-	81,81,81,81	0
56	MG	YA	3512	1/1	0.80	0.48	-	62,62,62,62	0
56	MG	YA	3547	1/1	0.67	0.41	-	80,80,80,80	0
56	MG	YA	3175	1/1	0.90	0.48	-	123,123,123,123	0
56	MG	QA	1686	1/1	-0.13	1.02	-	103,103,103,103	0
56	MG	RA	3287	1/1	0.94	0.16	-	83,83,83,83	0
56	MG	XA	1754	1/1	0.83	0.57	-	86,86,86,86	0
56	MG	YA	3608	1/1	0.95	0.64	-	44,44,44,44	0
56	MG	QA	1736	1/1	0.29	0.81	-	86,86,86,86	0
56	MG	RA	3941	1/1	0.93	0.14	-	69,69,69,69	0
56	MG	RR	3204	1/1	0.63	0.50	-	83,83,83,83	0
56	MG	XA	1717	1/1	0.93	0.49	-	59,59,59,59	0
56	MG	RA	3424	1/1	0.91	0.35	-	80,80,80,80	0
56	MG	RA	3913	1/1	0.87	0.43	-	43,43,43,43	0
56	MG	YA	3528	1/1	0.37	0.63	-	104,104,104,104	0
56	MG	RA	3736	1/1	0.78	0.37	-	74,74,74,74	0
56	MG	RA	3394	1/1	0.99	0.45	-	31,31,31,31	0
56	MG	RA	3110	1/1	0.96	0.21	-	70,70,70,70	0
56	MG	YA	3524	1/1	0.45	0.38	-	96,96,96,96	0
56	MG	RA	3948	1/1	0.49	0.57	-	89,89,89,89	0
56	MG	QA	1675	1/1	0.56	1.02	-	94,94,94,94	0
56	MG	YA	3465	1/1	0.17	0.79	-	82,82,82,82	0
56	MG	YA	3111	1/1	0.68	0.57	-	58,58,58,58	0
56	MG	YA	3432	1/1	0.67	0.47	-	84,84,84,84	0
56	MG	RA	3843	1/1	0.79	0.29	-	72,72,72,72	0
56	MG	QA	1708	1/1	0.70	0.17	-	77,77,77,77	0
56	MG	YA	3016	1/1	0.99	0.16	-	29,29,29,29	0
56	MG	RA	3605	1/1	0.88	0.33	-	70,70,70,70	0
56	MG	YA	3078	1/1	0.83	0.34	-	60,60,60,60	0
56	MG	YA	3248	1/1	0.69	0.42	-	105,105,105,105	0
56	MG	RA	3431	1/1	0.67	0.39	-	88,88,88,88	0
56	MG	QA	1815	1/1	0.86	0.33	-	65,65,65,65	0
56	MG	QA	1865	1/1	0.59	0.77	-	75,75,75,75	0
56	MG	RA	4026	1/1	0.85	0.48	-	71,71,71,71	0
56	MG	QA	1854	1/1	0.62	0.34	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YB	216	1/1	0.97	0.40	-	45,45,45,45	0
56	MG	RA	3331	1/1	0.74	0.76	-	73,73,73,73	0
56	MG	RA	3011	1/1	0.33	0.58	-	84,84,84,84	0
56	MG	XF	201	1/1	0.89	0.21	-	39,39,39,39	0
56	MG	QA	1874	1/1	0.84	0.37	-	74,74,74,74	0
56	MG	RA	3854	1/1	0.95	0.28	-	47,47,47,47	0
56	MG	RA	3754	1/1	0.36	0.83	-	92,92,92,92	0
56	MG	RA	3078	1/1	0.60	0.89	-	70,70,70,70	0
56	MG	RA	3795	1/1	0.84	0.55	-	75,75,75,75	0
56	MG	XA	1681	1/1	0.87	0.29	-	106,106,106,106	0
56	MG	QA	1646	1/1	0.78	0.59	-	46,46,46,46	0
56	MG	YA	3044	1/1	0.93	0.19	-	35,35,35,35	0
56	MG	RA	3338	1/1	0.96	0.67	-	38,38,38,38	0
56	MG	QA	1759	1/1	0.69	0.15	-	78,78,78,78	0
56	MG	RA	3362	1/1	0.74	0.33	-	93,93,93,93	0
56	MG	RA	3105	1/1	0.46	0.58	-	71,71,71,71	0
56	MG	RT	201	1/1	0.64	0.98	-	77,77,77,77	0
56	MG	XA	1716	1/1	0.65	0.29	-	57,57,57,57	0
56	MG	YA	3628	1/1	0.50	0.46	-	105,105,105,105	0
56	MG	QL	203	1/1	0.59	0.22	-	60,60,60,60	0
56	MG	YA	3379	1/1	0.62	0.34	-	70,70,70,70	0
56	MG	YA	3720	1/1	0.92	0.50	-	83,83,83,83	0
56	MG	RA	3024	1/1	0.84	0.44	-	74,74,74,74	0
56	MG	YA	3178	1/1	0.78	0.89	-	62,62,62,62	0
56	MG	RA	3710	1/1	0.70	0.84	-	70,70,70,70	0
56	MG	RA	3919	1/1	0.85	0.55	-	47,47,47,47	0
56	MG	YA	3492	1/1	0.83	0.57	-	63,63,63,63	0
56	MG	RA	3195	1/1	0.56	0.56	-	115,115,115,115	0
56	MG	RA	4008	1/1	0.61	0.36	-	86,86,86,86	0
56	MG	RA	3668	1/1	0.92	0.33	-	49,49,49,49	0
56	MG	YA	3127	1/1	0.88	0.29	-	50,50,50,50	0
56	MG	XA	1732	1/1	0.88	0.67	-	44,44,44,44	0
56	MG	RA	3410	1/1	0.81	0.12	-	76,76,76,76	0
56	MG	RA	3781	1/1	0.66	0.39	-	60,60,60,60	0
56	MG	QA	1704	1/1	0.72	0.81	-	74,74,74,74	0
56	MG	RB	208	1/1	0.31	0.31	-	90,90,90,90	0
56	MG	YA	3222	1/1	0.64	0.54	-	71,71,71,71	0
56	MG	RA	3526	1/1	0.92	0.59	-	51,51,51,51	0
56	MG	XA	1640	1/1	0.98	0.15	-	66,66,66,66	0
56	MG	QA	1745	1/1	0.23	0.80	-	98,98,98,98	0
56	MG	YT	203	1/1	0.54	0.35	-	78,78,78,78	0
56	MG	QA	1805	1/1	0.48	0.22	-	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3907	1/1	0.88	0.61	-	78,78,78,78	0
56	MG	RA	3444	1/1	0.90	0.96	-	83,83,83,83	0
56	MG	RA	3037	1/1	0.90	0.37	-	88,88,88,88	0
56	MG	YA	3681	1/1	0.96	0.76	-	38,38,38,38	0
56	MG	XA	1701	1/1	0.94	0.43	-	51,51,51,51	0
56	MG	XA	1686	1/1	0.78	0.26	-	68,68,68,68	0
56	MG	RA	3973	1/1	0.72	0.57	-	84,84,84,84	0
56	MG	YA	3513	1/1	0.91	0.28	-	80,80,80,80	0
56	MG	YA	3372	1/1	0.89	0.29	-	49,49,49,49	0
56	MG	RA	3611	1/1	0.76	0.29	-	80,80,80,80	0
56	MG	XA	1688	1/1	0.81	0.28	-	56,56,56,56	0
56	MG	RA	3780	1/1	0.83	0.94	-	74,74,74,74	0
56	MG	YA	3037	1/1	-0.20	0.92	-	88,88,88,88	0
56	MG	RN	203	1/1	0.77	0.33	-	86,86,86,86	0
56	MG	XA	1633	1/1	0.98	0.34	-	51,51,51,51	0
56	MG	RA	3242	1/1	0.93	0.31	-	54,54,54,54	0
56	MG	RA	4004	1/1	0.55	0.42	-	93,93,93,93	0
56	MG	YD	307	1/1	0.78	0.68	-	64,64,64,64	0
56	MG	YA	3336	1/1	0.65	0.41	-	71,71,71,71	0
56	MG	RA	3294	1/1	0.93	0.28	-	61,61,61,61	0
56	MG	YA	3146	1/1	0.85	0.13	-	60,60,60,60	0
56	MG	RA	3433	1/1	0.81	0.38	-	66,66,66,66	0
56	MG	RA	3839	1/1	0.58	0.66	-	72,72,72,72	0
56	MG	QA	1602	1/1	0.48	0.15	-	95,95,95,95	0
56	MG	RA	3731	1/1	0.81	0.40	-	83,83,83,83	0
56	MG	RA	3725	1/1	0.63	0.47	-	80,80,80,80	0
56	MG	XA	1646	1/1	0.89	0.56	-	63,63,63,63	0
56	MG	YA	3024	1/1	0.83	0.88	-	59,59,59,59	0
56	MG	YA	3057	1/1	-0.03	0.73	-	99,99,99,99	0
56	MG	QA	1790	1/1	0.93	0.84	-	56,56,56,56	0
56	MG	R7	101	1/1	0.82	0.44	-	66,66,66,66	0
56	MG	QA	1763	1/1	0.17	1.00	-	100,100,100,100	0
56	MG	YA	3026	1/1	0.68	0.24	-	93,93,93,93	0
56	MG	RA	3243	1/1	0.83	0.30	-	73,73,73,73	0
56	MG	RA	3460	1/1	0.95	0.86	-	51,51,51,51	0
56	MG	YA	3350	1/1	0.90	0.25	-	23,23,23,23	0
56	MG	RA	3510	1/1	0.76	0.21	-	38,38,38,38	0
56	MG	XA	1618	1/1	0.43	0.74	-	72,72,72,72	0
56	MG	YA	3566	1/1	0.76	0.20	-	60,60,60,60	0
56	MG	XA	1613	1/1	0.91	0.12	-	51,51,51,51	0
56	MG	RA	3591	1/1	0.69	0.56	-	77,77,77,77	0
56	MG	RA	3594	1/1	0.95	0.21	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3148	1/1	0.25	0.77	-	92,92,92,92	0
56	MG	RA	3026	1/1	0.93	0.72	-	72,72,72,72	0
56	MG	RU	202	1/1	0.82	0.30	-	78,78,78,78	0
56	MG	QA	1856	1/1	-0.05	1.28	-	89,89,89,89	0
56	MG	RA	3098	1/1	0.95	0.19	-	12,12,12,12	0
56	MG	RA	3974	1/1	0.62	1.33	-	70,70,70,70	0
56	MG	YA	3422	1/1	0.70	0.80	-	122,122,122,122	0
56	MG	YA	3260	1/1	0.72	0.45	-	71,71,71,71	0
56	MG	XA	1724	1/1	0.85	0.37	-	65,65,65,65	0
56	MG	RA	3453	1/1	0.90	0.25	-	64,64,64,64	0
56	MG	YA	3366	1/1	0.93	0.67	-	59,59,59,59	0
56	MG	RA	3955	1/1	0.80	0.27	-	74,74,74,74	0
56	MG	YA	3532	1/1	0.81	0.92	-	60,60,60,60	0
56	MG	YA	3206	1/1	0.66	0.45	-	100,100,100,100	0
56	MG	RA	3414	1/1	0.94	0.35	-	34,34,34,34	0
56	MG	RA	3130	1/1	0.87	0.06	-	69,69,69,69	0
56	MG	RA	3441	1/1	0.69	0.69	-	61,61,61,61	0
56	MG	RA	3928	1/1	0.93	0.36	-	59,59,59,59	0
56	MG	YA	3003	1/1	0.38	0.93	-	106,106,106,106	0
56	MG	RA	3205	1/1	0.62	0.45	-	76,76,76,76	0
56	MG	RA	3438	1/1	0.83	0.17	-	71,71,71,71	0
56	MG	QA	1773	1/1	0.91	0.31	-	71,71,71,71	0
56	MG	XA	1755	1/1	0.97	0.58	-	43,43,43,43	0
56	MG	YA	3069	1/1	0.32	0.79	-	78,78,78,78	0
56	MG	RA	3751	1/1	0.48	0.31	-	51,51,51,51	0
56	MG	RA	3548	1/1	0.92	0.43	-	38,38,38,38	0
56	MG	YB	206	1/1	0.42	0.63	-	99,99,99,99	0
56	MG	RE	304	1/1	0.29	0.73	-	75,75,75,75	0
56	MG	QA	1788	1/1	0.32	0.66	-	81,81,81,81	0
56	MG	YA	3241	1/1	0.47	0.49	-	85,85,85,85	0
56	MG	RB	223	1/1	0.63	0.94	-	102,102,102,102	0
56	MG	YA	3593	1/1	0.93	0.50	-	28,28,28,28	0
56	MG	RA	3259	1/1	0.76	0.30	-	87,87,87,87	0
56	MG	RA	3846	1/1	0.71	0.72	-	80,80,80,80	0
56	MG	XA	1769	1/1	0.73	0.73	-	64,64,64,64	0
56	MG	QA	1732	1/1	0.67	0.42	-	96,96,96,96	0
56	MG	RA	3203	1/1	0.41	0.71	-	97,97,97,97	0
56	MG	RA	3159	1/1	0.87	0.41	-	107,107,107,107	0
56	MG	RA	3468	1/1	0.92	0.19	-	40,40,40,40	0
56	MG	RA	3586	1/1	0.77	0.50	-	73,73,73,73	0
56	MG	YA	3283	1/1	0.95	0.26	-	36,36,36,36	0
56	MG	RA	3053	1/1	0.84	0.43	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	YA	3217	1/1	0.89	0.21	-	75,75,75,75	0
56	MG	RA	3778	1/1	0.95	0.68	-	41,41,41,41	0
56	MG	RA	3251	1/1	0.71	0.49	-	69,69,69,69	0
56	MG	RA	3072	1/1	0.94	0.94	-	93,93,93,93	0
56	MG	XA	1655	1/1	0.69	0.55	-	84,84,84,84	0
56	MG	RA	3284	1/1	0.90	0.35	-	97,97,97,97	0
56	MG	XA	1759	1/1	0.90	0.31	-	56,56,56,56	0
56	MG	RA	3709	1/1	0.90	0.20	-	75,75,75,75	0
56	MG	RA	3491	1/1	0.54	0.82	-	81,81,81,81	0
56	MG	RB	203	1/1	0.56	0.48	-	106,106,106,106	0
56	MG	RA	3209	1/1	0.91	1.06	-	100,100,100,100	0
56	MG	YA	3268	1/1	0.93	0.40	-	73,73,73,73	0
56	MG	RA	3616	1/1	0.96	0.36	-	33,33,33,33	0
56	MG	RA	3367	1/1	0.30	0.63	-	74,74,74,74	0
56	MG	RU	201	1/1	0.89	0.38	-	70,70,70,70	0
56	MG	RA	3288	1/1	0.73	0.33	-	95,95,95,95	0
56	MG	QA	1725	1/1	0.23	0.63	-	90,90,90,90	0
56	MG	RA	3267	1/1	0.94	0.26	-	47,47,47,47	0
56	MG	RV	204	1/1	0.33	0.51	-	70,70,70,70	0
56	MG	YA	3684	1/1	0.94	0.57	-	39,39,39,39	0
56	MG	YA	3462	1/1	0.34	0.74	-	75,75,75,75	0
56	MG	YA	3310	1/1	0.97	0.48	-	38,38,38,38	0
56	MG	RA	3489	1/1	0.77	0.85	-	50,50,50,50	0
56	MG	RA	3112	1/1	0.51	0.52	-	117,117,117,117	0
56	MG	RA	3656	1/1	0.85	0.56	-	44,44,44,44	0
56	MG	QA	1840	1/1	0.67	0.57	-	89,89,89,89	0
56	MG	YA	3382	1/1	0.97	0.26	-	29,29,29,29	0
56	MG	QA	1668	1/1	0.20	0.69	-	102,102,102,102	0
56	MG	XA	1712	1/1	0.83	0.31	-	61,61,61,61	0
56	MG	XA	1668	1/1	0.27	0.69	-	87,87,87,87	0
56	MG	RA	3190	1/1	0.81	0.31	-	62,62,62,62	0
56	MG	QA	1751	1/1	0.75	0.31	-	83,83,83,83	0
56	MG	YA	3301	1/1	0.87	0.22	-	42,42,42,42	0
56	MG	RA	3691	1/1	0.62	0.47	-	64,64,64,64	0
56	MG	RA	3273	1/1	0.90	0.57	-	76,76,76,76	0
56	MG	RA	3281	1/1	0.86	1.19	-	85,85,85,85	0
56	MG	RA	3703	1/1	0.69	0.72	-	71,71,71,71	0
56	MG	RA	3295	1/1	0.91	0.15	-	73,73,73,73	0
56	MG	RA	3717	1/1	0.93	0.46	-	38,38,38,38	0
56	MG	QA	1709	1/1	0.84	0.46	-	53,53,53,53	0
56	MG	RA	3169	1/1	0.88	0.17	-	82,82,82,82	0
56	MG	RA	3792	1/1	0.98	0.41	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	XA	1715	1/1	0.68	0.62	-	55,55,55,55	0
56	MG	RA	3084	1/1	0.88	0.48	-	79,79,79,79	0
56	MG	QA	1637	1/1	0.62	0.72	-	93,93,93,93	0
56	MG	RA	3775	1/1	0.84	0.41	-	56,56,56,56	0
56	MG	RA	3589	1/1	0.49	0.62	-	100,100,100,100	0
56	MG	R0	104	1/1	0.48	0.46	-	90,90,90,90	0
56	MG	YA	3415	1/1	0.13	0.98	-	84,84,84,84	0
56	MG	YA	3742	1/1	0.89	0.39	-	36,36,36,36	0
56	MG	YA	3290	1/1	0.94	0.43	-	47,47,47,47	0
56	MG	RA	3582	1/1	0.87	0.76	-	72,72,72,72	0
56	MG	QA	1868	1/1	0.95	0.68	-	58,58,58,58	0
56	MG	XA	1725	1/1	0.48	0.69	-	87,87,87,87	0
56	MG	YA	3182	1/1	0.89	0.24	-	68,68,68,68	0
56	MG	YA	3098	1/1	0.88	0.13	-	49,49,49,49	0
56	MG	XA	1698	1/1	0.73	0.41	-	66,66,66,66	0
56	MG	RA	3372	1/1	0.76	0.58	-	61,61,61,61	0
56	MG	YA	3641	1/1	0.61	0.83	-	86,86,86,86	0
56	MG	RA	3016	1/1	0.78	0.83	-	77,77,77,77	0
56	MG	YA	3644	1/1	0.93	0.66	-	57,57,57,57	0
56	MG	RA	3882	1/1	0.43	0.70	-	77,77,77,77	0
56	MG	RA	3981	1/1	0.92	0.09	-	69,69,69,69	0
56	MG	QA	1727	1/1	-0.11	0.78	-	100,100,100,100	0
56	MG	QA	1803	1/1	0.88	0.51	-	49,49,49,49	0
56	MG	QA	1744	1/1	0.85	0.67	-	65,65,65,65	0
56	MG	YA	3482	1/1	0.91	0.39	-	65,65,65,65	0
56	MG	QG	203	1/1	0.33	1.46	-	100,100,100,100	0
56	MG	RA	3566	1/1	0.92	0.24	-	57,57,57,57	0
56	MG	RA	3054	1/1	0.86	0.34	-	78,78,78,78	0
56	MG	XH	201	1/1	0.47	0.61	-	78,78,78,78	0
56	MG	RA	3684	1/1	0.67	0.50	-	71,71,71,71	0
56	MG	RA	3767	1/1	0.86	0.37	-	37,37,37,37	0
56	MG	RA	3317	1/1	0.76	0.33	-	73,73,73,73	0
56	MG	YA	3740	1/1	0.83	0.38	-	52,52,52,52	0
56	MG	YA	3345	1/1	0.95	0.43	-	39,39,39,39	0
56	MG	RA	3249	1/1	0.53	0.73	-	94,94,94,94	0
56	MG	YA	3129	1/1	0.78	0.33	-	31,31,31,31	0
56	MG	QA	1753	1/1	0.35	0.47	-	71,71,71,71	0
56	MG	RA	3462	1/1	0.89	0.44	-	52,52,52,52	0
56	MG	RA	3922	1/1	0.81	0.44	-	70,70,70,70	0
56	MG	RA	3271	1/1	0.35	0.48	-	93,93,93,93	0
56	MG	YA	3047	1/1	0.96	0.11	-	44,44,44,44	0
56	MG	RA	3664	1/1	0.96	0.24	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	RA	3346	1/1	0.85	0.82	-	72,72,72,72	0
56	MG	YA	3546	1/1	0.87	0.53	-	47,47,47,47	0
56	MG	RA	3318	1/1	0.99	0.32	-	19,19,19,19	0
56	MG	YA	3120	1/1	0.83	0.52	-	72,72,72,72	0
56	MG	RA	3807	1/1	0.51	0.62	-	70,70,70,70	0
56	MG	YA	3721	1/1	0.83	0.55	-	65,65,65,65	0
56	MG	YA	3562	1/1	0.93	0.32	-	70,70,70,70	0
56	MG	YA	3065	1/1	0.74	0.70	-	88,88,88,88	0
56	MG	RA	3735	1/1	0.78	0.62	-	66,66,66,66	0
56	MG	YA	3570	1/1	0.84	0.52	-	59,59,59,59	0
56	MG	QA	1748	1/1	0.29	0.54	-	92,92,92,92	0
56	MG	RA	3677	1/1	0.92	1.04	-	61,61,61,61	0
56	MG	YA	3244	1/1	0.91	0.66	-	39,39,39,39	0
56	MG	RA	3559	1/1	0.62	0.37	-	97,97,97,97	0
56	MG	YA	3360	1/1	0.92	0.73	-	53,53,53,53	0
56	MG	QA	1857	1/1	0.71	0.71	-	71,71,71,71	0
56	MG	YA	3341	1/1	0.94	0.50	-	42,42,42,42	0
56	MG	RA	3017	1/1	0.91	0.59	-	68,68,68,68	0
56	MG	RA	3549	1/1	-0.17	1.05	-	78,78,78,78	0
56	MG	YA	3164	1/1	0.24	0.87	-	87,87,87,87	0
56	MG	XA	1619	1/1	0.70	0.12	-	74,74,74,74	0
56	MG	RA	3114	1/1	0.85	0.32	-	91,91,91,91	0
56	MG	YA	3048	1/1	0.97	0.26	-	57,57,57,57	0
56	MG	RA	3056	1/1	0.95	0.57	-	70,70,70,70	0
56	MG	QA	1713	1/1	0.77	0.43	-	79,79,79,79	0
56	MG	RB	214	1/1	0.91	0.49	-	44,44,44,44	0
56	MG	QA	1696	1/1	0.65	0.35	-	73,73,73,73	0
56	MG	YA	3392	1/1	0.91	0.56	-	54,54,54,54	0
56	MG	RA	3364	1/1	0.59	0.39	-	96,96,96,96	0
56	MG	RG	202	1/1	0.86	0.09	-	85,85,85,85	0
56	MG	RA	3463	1/1	0.60	0.50	-	78,78,78,78	0
56	MG	YA	3315	1/1	0.81	0.79	-	62,62,62,62	0
56	MG	YA	3572	1/1	0.97	0.25	-	28,28,28,28	0
56	MG	RA	3256	1/1	0.67	0.40	-	103,103,103,103	0
56	MG	RA	3187	1/1	0.73	0.53	-	106,106,106,106	0
56	MG	RA	3798	1/1	0.44	1.16	-	99,99,99,99	0
56	MG	RA	3425	1/1	0.46	0.49	-	94,94,94,94	0
56	MG	RA	3415	1/1	0.95	0.54	-	42,42,42,42	0
56	MG	QA	1832	1/1	0.53	0.63	-	92,92,92,92	0
56	MG	RA	3354	1/1	0.89	0.18	-	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.