



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:40 PM GMT

PDB ID : 1VY5
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in the post-catalysis state of peptide bond formation containing dipeptidyl-tRNA in the A site and deacylated tRNA in the P site.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.55 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

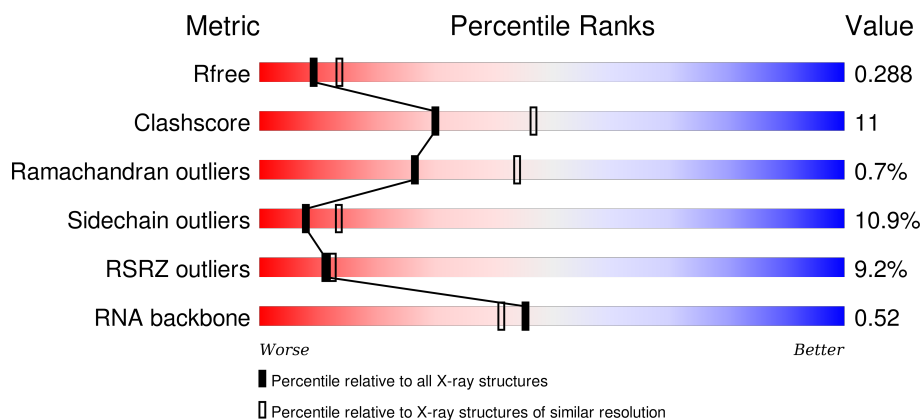
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)
RNA backbone	2183	1093 (3.00-2.08)

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	AA	1521	<div> <div>2%</div> <div>52%</div> <div>37%</div> <div>9%</div> <div>..</div> </div>
1	CA	1521	<div> <div>5%</div> <div>45%</div> <div>42%</div> <div>10%</div> <div>..</div> </div>
2	AB	256	<div> <div>13%</div> <div>42%</div> <div>41%</div> <div>6%</div> <div>10%</div> </div>
2	CB	256	<div> <div>23%</div> <div>36%</div> <div>43%</div> <div>11%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	

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Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	76	
23	CW	76	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
27	DB	121	

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Mol	Chain	Length	Quality of chain
28	BD	276	
28	DD	276	
29	BE	206	
29	DE	206	
30	BF	210	
30	DF	210	
31	BG	182	
31	DG	182	
32	BH	180	
32	DH	180	
33	BI	148	
33	DI	148	
34	BN	140	
34	DN	140	
35	BO	122	
35	DO	122	
36	BP	150	
36	DP	150	
37	BQ	141	
37	DQ	141	
38	BR	118	
38	DR	118	
39	BS	112	
39	DS	112	
40	BT	146	

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Mol	Chain	Length	Quality of chain
40	DT	146	
41	BU	118	
41	DU	118	
42	BV	101	
42	DV	101	
43	BW	113	
43	DW	113	
44	BX	96	
44	DX	96	
45	BY	110	
45	DY	110	
46	BZ	206	
46	DZ	206	
47	B0	85	
47	D0	85	
48	B1	98	
48	D1	98	
49	B2	72	
49	D2	72	
50	B3	60	
50	D3	60	
51	B4	71	
51	D4	71	
52	B5	60	
52	D5	60	

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Mol	Chain	Length	Quality of chain
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

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
57	MG	AA	3018	-	-	-	X
57	MG	AA	3080	-	-	-	X
57	MG	AA	3084	-	-	-	X
57	MG	AA	3095	-	-	-	X
57	MG	AA	3138	-	-	-	X
57	MG	AA	3156	-	-	-	X
57	MG	AA	3205	-	-	-	X
57	MG	AF	3001	-	-	-	X
57	MG	AY	3003	-	-	-	X
57	MG	B1	101	-	-	-	X
57	MG	BA	3029	-	-	-	X
57	MG	BA	3040	-	-	-	X
57	MG	BA	3046	-	-	-	X
57	MG	BA	3054	-	-	-	X
57	MG	BA	3069	-	-	-	X
57	MG	BA	3082	-	-	-	X
57	MG	BA	3085	-	-	-	X
57	MG	BA	3115	-	-	-	X
57	MG	BA	3139	-	-	-	X
57	MG	BA	3141	-	-	-	X
57	MG	BA	3143	-	-	-	X
57	MG	BA	3151	-	-	-	X
57	MG	BA	3153	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BA	3156	-	-	-	X
57	MG	BA	3196	-	-	-	X
57	MG	BA	3203	-	-	-	X
57	MG	BA	3213	-	-	-	X
57	MG	BA	3215	-	-	-	X
57	MG	BA	3232	-	-	-	X
57	MG	BA	3239	-	-	-	X
57	MG	BA	3240	-	-	-	X
57	MG	BA	3246	-	-	-	X
57	MG	BA	3248	-	-	-	X
57	MG	BA	3250	-	-	-	X
57	MG	BA	3284	-	-	-	X
57	MG	BA	3289	-	-	-	X
57	MG	BA	3290	-	-	-	X
57	MG	BA	3328	-	-	-	X
57	MG	BA	3330	-	-	-	X
57	MG	BA	3335	-	-	-	X
57	MG	BA	3367	-	-	-	X
57	MG	BA	3549	-	-	-	X
57	MG	BA	3613	-	-	-	X
57	MG	BA	3626	-	-	-	X
57	MG	BA	3639	-	-	-	X
57	MG	BA	3670	-	-	-	X
57	MG	BA	3698	-	-	-	X
57	MG	BA	3699	-	-	-	X
57	MG	BA	3728	-	-	-	X
57	MG	BA	3732	-	-	-	X
57	MG	BA	3771	-	-	-	X
57	MG	BA	3801	-	-	-	X
57	MG	BA	3802	-	-	-	X
57	MG	BA	3804	-	-	-	X
57	MG	BA	3812	-	-	-	X
57	MG	BB	202	-	-	-	X
57	MG	BB	218	-	-	-	X
57	MG	BD	302	-	-	-	X
57	MG	BD	306	-	-	-	X
57	MG	BF	303	-	-	-	X
57	MG	BF	306	-	-	-	X
57	MG	BN	3001	-	-	-	X
57	MG	BP	201	-	-	-	X
57	MG	BU	206	-	-	-	X
57	MG	BV	201	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BX	3001	-	-	-	X
57	MG	CA	3045	-	-	-	X
57	MG	CA	3057	-	-	-	X
57	MG	CA	3061	-	-	-	X
57	MG	CA	3079	-	-	-	X
57	MG	CA	3087	-	-	-	X
57	MG	CA	3133	-	-	-	X
57	MG	CA	3152	-	-	-	X
57	MG	CA	3169	-	-	-	X
57	MG	DA	3016	-	-	-	X
57	MG	DA	3019	-	-	-	X
57	MG	DA	3027	-	-	-	X
57	MG	DA	3028	-	-	-	X
57	MG	DA	3029	-	-	-	X
57	MG	DA	3031	-	-	-	X
57	MG	DA	3045	-	-	-	X
57	MG	DA	3059	-	-	-	X
57	MG	DA	3067	-	-	-	X
57	MG	DA	3081	-	-	-	X
57	MG	DA	3096	-	-	-	X
57	MG	DA	3115	-	-	-	X
57	MG	DA	3116	-	-	-	X
57	MG	DA	3119	-	-	-	X
57	MG	DA	3132	-	-	-	X
57	MG	DA	3168	-	-	-	X
57	MG	DA	3182	-	-	-	X
57	MG	DA	3208	-	-	-	X
57	MG	DA	3213	-	-	-	X
57	MG	DA	3226	-	-	-	X
57	MG	DA	3236	-	-	-	X
57	MG	DA	3426	-	-	-	X
57	MG	DA	3439	-	-	-	X
57	MG	DA	3471	-	-	-	X
57	MG	DA	3481	-	-	-	X
57	MG	DA	3510	-	-	-	X
57	MG	DA	3518	-	-	-	X
57	MG	DA	3588	-	-	-	X
57	MG	DA	3594	-	-	-	X
57	MG	DA	3610	-	-	-	X
57	MG	DA	3629	-	-	-	X
57	MG	DA	3637	-	-	-	X
57	MG	DA	3642	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	DA	3668	-	-	-	X
57	MG	DA	3669	-	-	-	X
57	MG	DA	3676	-	-	-	X
57	MG	DB	3008	-	-	-	X
57	MG	DB	3009	-	-	-	X
57	MG	DD	304	-	-	-	X
57	MG	DD	307	-	-	-	X
57	MG	DD	308	-	-	-	X
57	MG	DE	301	-	-	-	X
57	MG	DF	3003	-	-	-	X
57	MG	DU	3002	-	-	-	X
59	ZN	B5	102	-	-	-	X
59	ZN	B6	103	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297141 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1498	Total	C	N	O	P	0	0	0
			32205	14333	5970	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			983	623	193	167			
9	CI	127	Total	C	N	O	0	0	0
			978	619	190	169			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O	0	0	0
			709	440	138	131			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O			
			714	445	138	131	0	0	0

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	AK	114	Total	C	N	O	S		
			829	516	155	155	3	0	0
11	CK	114	Total	C	N	O	S		
			833	519	156	155	3	0	0

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0
12	CL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	AM	123	Total	C	N	O	S		
			958	592	198	166	2	0	0
13	CM	122	Total	C	N	O	S		
			950	586	197	165	2	0	0

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0
14	CN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0
15	CO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	12	Total	C	N	O	P	0	0	0
			252	115	46	80	11			

- Molecule 23 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1607	727	288	516	73	3			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1560	702	281	503	72	2			

- Molecule 24 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	AX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
24	CX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 25 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
25	AY	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
25	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

- Molecule 26 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BA	2819	Total	C	N	O	P	0	0	0
			60729	27026	11370	19515	2818			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

- Molecule 27 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			
27	DB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
28	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
29	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
31	DG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
32	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
33	DI	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 34 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
34	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
35	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
36	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
37	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
38	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 39 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BS	110	Total	C	N	O		0	0	0
			877	553	175	149				
39	DS	110	Total	C	N	O		0	0	0
			870	549	173	148				

- Molecule 40 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
40	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 41 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
41	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 42 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 43 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
43	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
44	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
45	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 46 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BZ	171	Total	C	N	O	S	0	0	0
			1349	862	243	242	2			
46	DZ	174	Total	C	N	O	S	0	0	0
			1360	870	243	245	2			

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
47	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 48 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
48	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
49	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
50	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
50	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 51 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B4	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			
51	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 52 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
52	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 53 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
53	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
54	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B8	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
55	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
56	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B4	1	Total	Mg	0	0
			1	1		
57	BA	812	Total	Mg	0	0
			812	812		
57	AK	1	Total	Mg	0	0
			1	1		
57	DQ	4	Total	Mg	0	0
			4	4		
57	D3	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	DF	4	Total 4	Mg 4	0	0
57	CV	1	Total 1	Mg 1	0	0
57	B8	1	Total 1	Mg 1	0	0
57	BE	8	Total 8	Mg 8	0	0
57	AW	4	Total 4	Mg 4	0	0
57	DU	2	Total 2	Mg 2	0	0
57	B1	1	Total 1	Mg 1	0	0
57	AN	2	Total 2	Mg 2	0	0
57	BP	5	Total 5	Mg 5	0	0
57	AX	15	Total 15	Mg 15	0	0
57	DN	1	Total 1	Mg 1	0	0
57	CA	170	Total 170	Mg 170	0	0
57	B5	1	Total 1	Mg 1	0	0
57	BB	20	Total 20	Mg 20	0	0
57	D8	1	Total 1	Mg 1	0	0
57	AE	3	Total 3	Mg 3	0	0
57	DG	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	BF	9	Total 9	Mg 9	0	0
57	BX	3	Total 3	Mg 3	0	0
57	B2	1	Total 1	Mg 1	0	0

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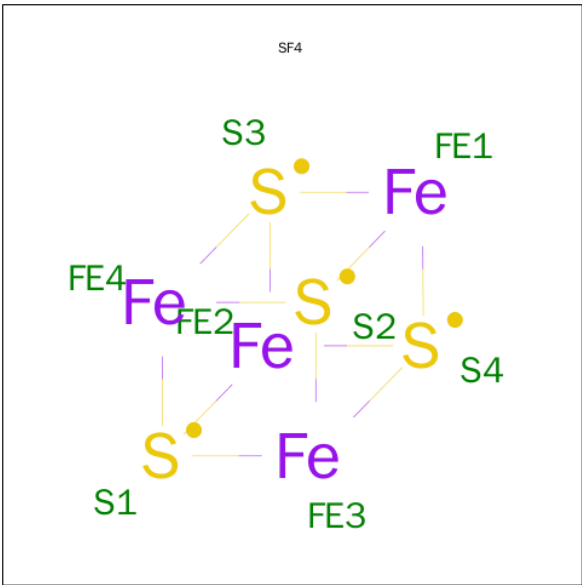
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	214	Total 214	Mg 214	0	0
57	BQ	5	Total 5	Mg 5	0	0
57	CX	3	Total 3	Mg 3	0	0
57	DV	3	Total 3	Mg 3	0	0
57	B6	2	Total 2	Mg 2	0	0
57	AM	1	Total 1	Mg 1	0	0
57	BU	8	Total 8	Mg 8	0	0
57	DR	1	Total 1	Mg 1	0	0
57	BN	6	Total 6	Mg 6	0	0
57	CT	1	Total 1	Mg 1	0	0
57	D0	1	Total 1	Mg 1	0	0
57	BG	3	Total 3	Mg 3	0	0
57	BY	1	Total 1	Mg 1	0	0
57	DE	4	Total 4	Mg 4	0	0
57	B3	2	Total 2	Mg 2	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	BR	2	Total 2	Mg 2	0	0
57	DA	677	Total 677	Mg 677	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DW	4	Total 4	Mg 4	0	0
57	B7	5	Total 5	Mg 5	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	CF	1	Total 1	Mg 1	0	0
57	BV	5	Total 5	Mg 5	0	0
57	DO	1	Total 1	Mg 1	0	0
57	BO	2	Total 2	Mg 2	0	0
57	DX	1	Total 1	Mg 1	0	0
57	BZ	1	Total 1	Mg 1	0	0
57	DY	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	CD	1	Total 1	Mg 1	0	0
57	BD	9	Total 9	Mg 9	0	0
57	B0	3	Total 3	Mg 3	0	0
57	CE	1	Total 1	Mg 1	0	0
57	BW	4	Total 4	Mg 4	0	0
57	AY	3	Total 3	Mg 3	0	0
57	DD	9	Total 9	Mg 9	0	0
57	CK	1	Total 1	Mg 1	0	0
57	AF	1	Total 1	Mg 1	0	0
57	DB	13	Total 13	Mg 13	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	AD	1	Total	Fe	S	0	0
			8	4	4		
58	CD	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	B5	1	Total	Zn	0	0
			1	1		
59	B4	1	Total	Zn	0	0
			1	1		
59	CN	1	Total	Zn	0	0
			1	1		
59	BY	1	Total	Zn	0	0
			1	1		
59	B9	1	Total	Zn	0	0
			1	1		
59	DY	1	Total	Zn	0	0
			1	1		
59	D5	1	Total	Zn	0	0
			1	1		
59	D4	1	Total	Zn	0	0
			1	1		
59	AN	1	Total	Zn	0	0
			1	1		
59	D6	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	D9	1	Total 1	Zn 1	0	0
59	B6	1	Total 1	Zn 1	0	0

- Molecule 60 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	AX	1	Total 1	K 1	0	0
60	CX	1	Total 1	K 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	227	Total 227	O 227	0	0
61	AE	2	Total 2	O 2	0	0
61	AJ	1	Total 1	O 1	0	0
61	AL	1	Total 1	O 1	0	0
61	AM	1	Total 1	O 1	0	0
61	AU	1	Total 1	O 1	0	0
61	AV	3	Total 3	O 3	0	0
61	AW	3	Total 3	O 3	0	0
61	AX	6	Total 6	O 6	0	0
61	AY	1	Total 1	O 1	0	0
61	BA	1383	Total 1383	O 1383	0	0
61	BB	36	Total 36	O 36	0	0
61	BD	12	Total 12	O 12	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BE	14	Total 14	O 14	0	0
61	BF	8	Total 8	O 8	0	0
61	BG	3	Total 3	O 3	0	0
61	BI	1	Total 1	O 1	0	0
61	BO	4	Total 4	O 4	0	0
61	BP	16	Total 16	O 16	0	0
61	BQ	4	Total 4	O 4	0	0
61	BR	2	Total 2	O 2	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	3	Total 3	O 3	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	1	Total 1	O 1	0	0
61	BX	4	Total 4	O 4	0	0
61	BZ	1	Total 1	O 1	0	0
61	B0	3	Total 3	O 3	0	0
61	B1	1	Total 1	O 1	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	2	Total 2	O 2	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	2	Total 2	O 2	0	0
61	B8	8	Total 8	O 8	0	0

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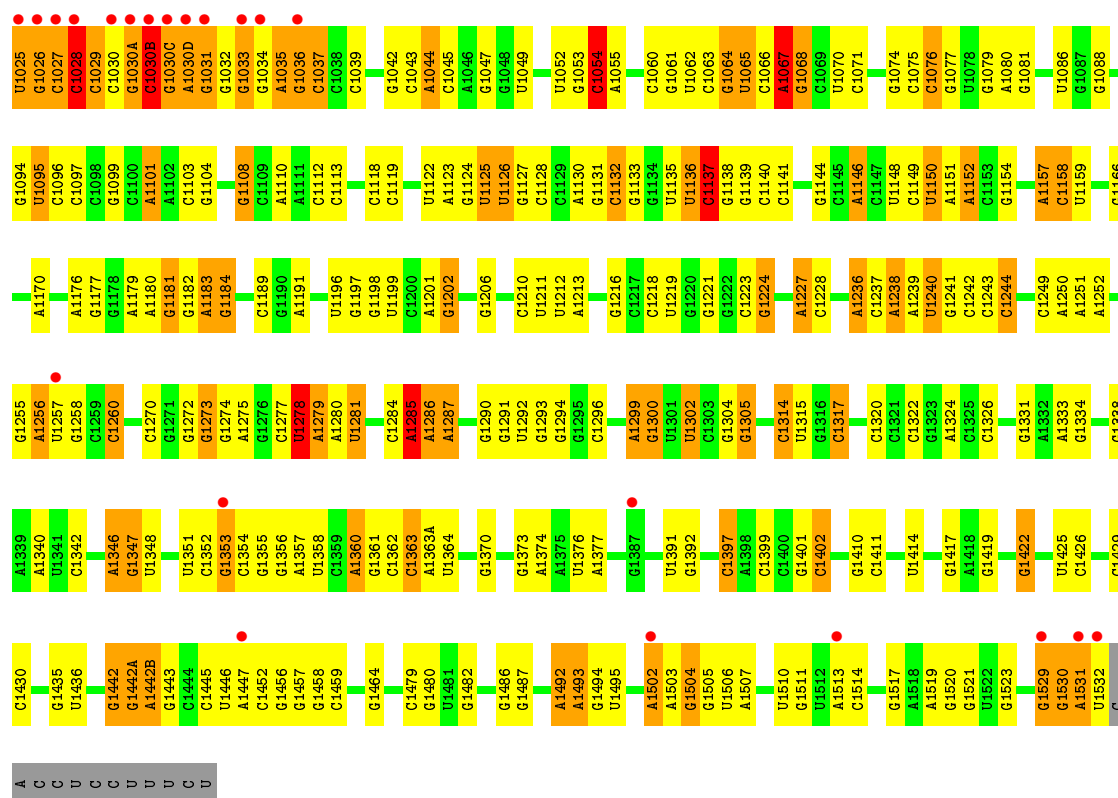
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CA	185	Total 185	O 185	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CV	1	Total 1	O 1	0	0
61	CW	2	Total 2	O 2	0	0
61	DA	1025	Total 1025	O 1025	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	19	Total 19	O 19	0	0
61	DE	11	Total 11	O 11	0	0
61	DF	3	Total 3	O 3	0	0
61	DN	2	Total 2	O 2	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	16	Total 16	O 16	0	0
61	DR	1	Total 1	O 1	0	0
61	DT	3	Total 3	O 3	0	0
61	DU	2	Total 2	O 2	0	0
61	DX	3	Total 3	O 3	0	0
61	DY	2	Total 2	O 2	0	0
61	D0	3	Total 3	O 3	0	0
61	D1	1	Total 1	O 1	0	0

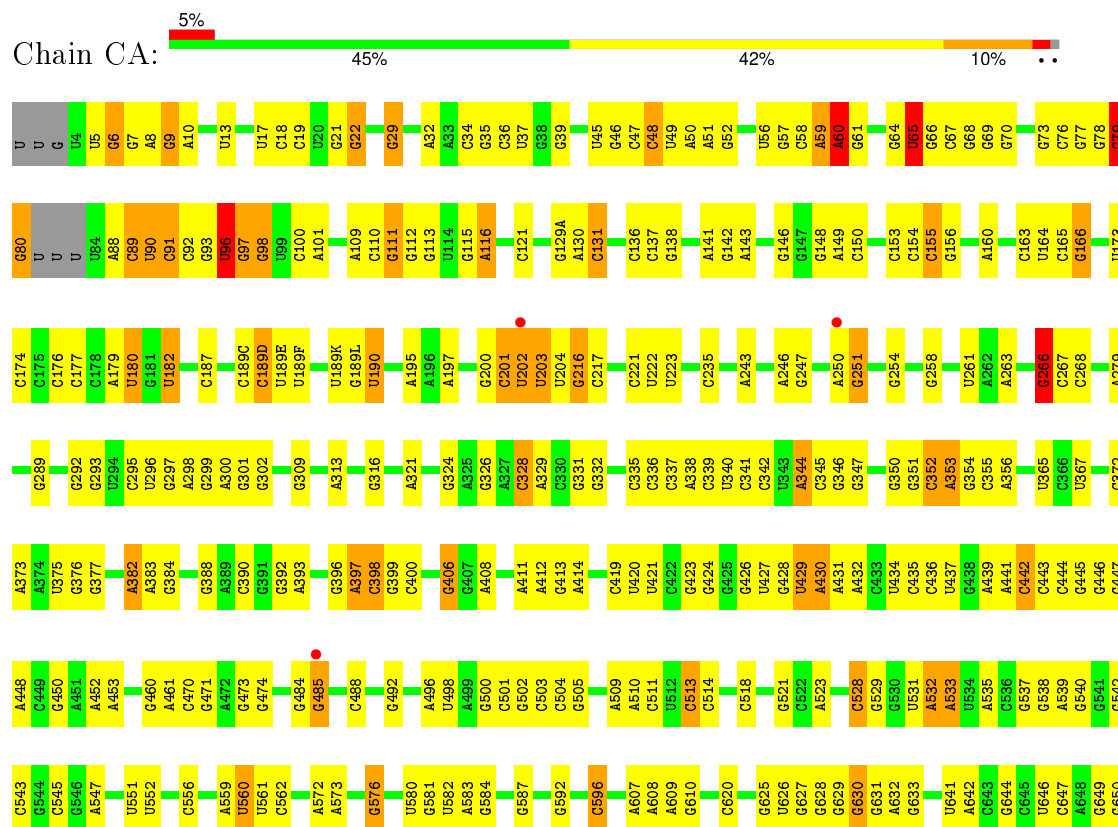
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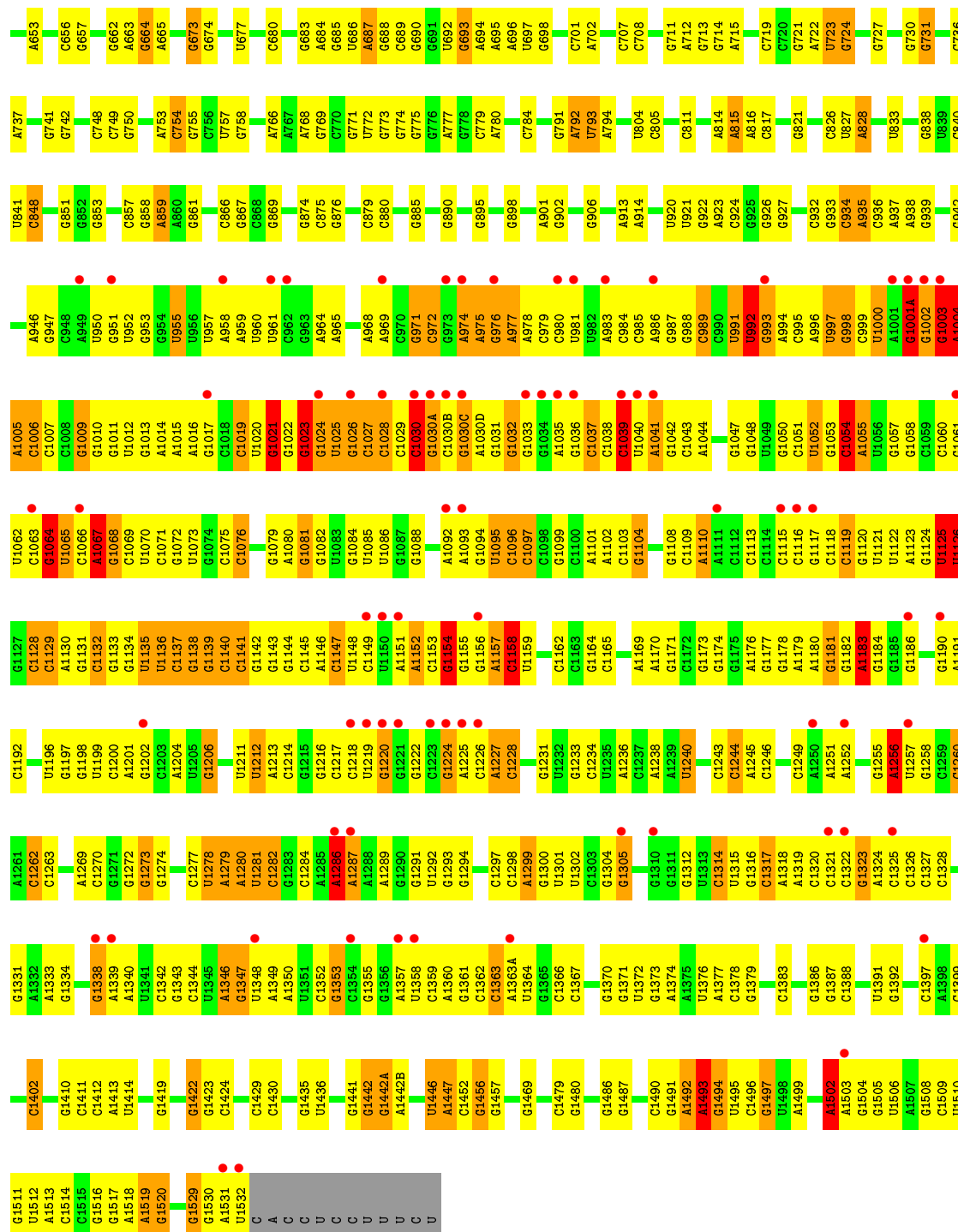
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	D3	1	Total	O	0	0
			1	1		
61	D7	3	Total	O	0	0
			3	3		
61	D8	4	Total	O	0	0
			4	4		

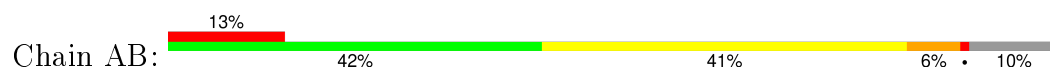


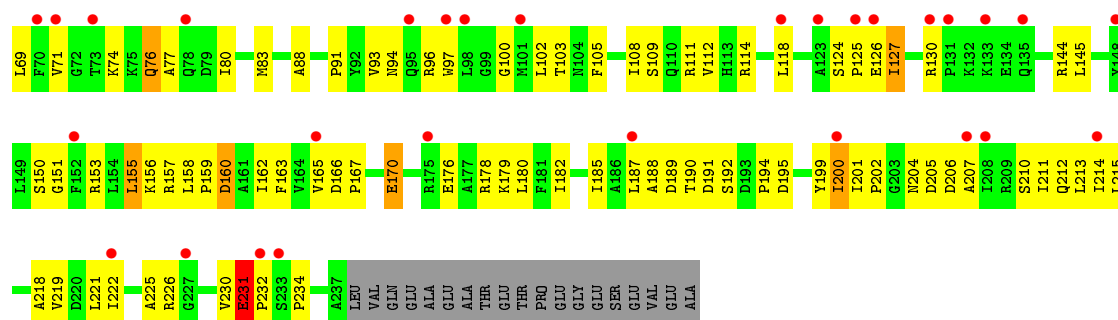
• Molecule 1: 16S Ribosomal RNA



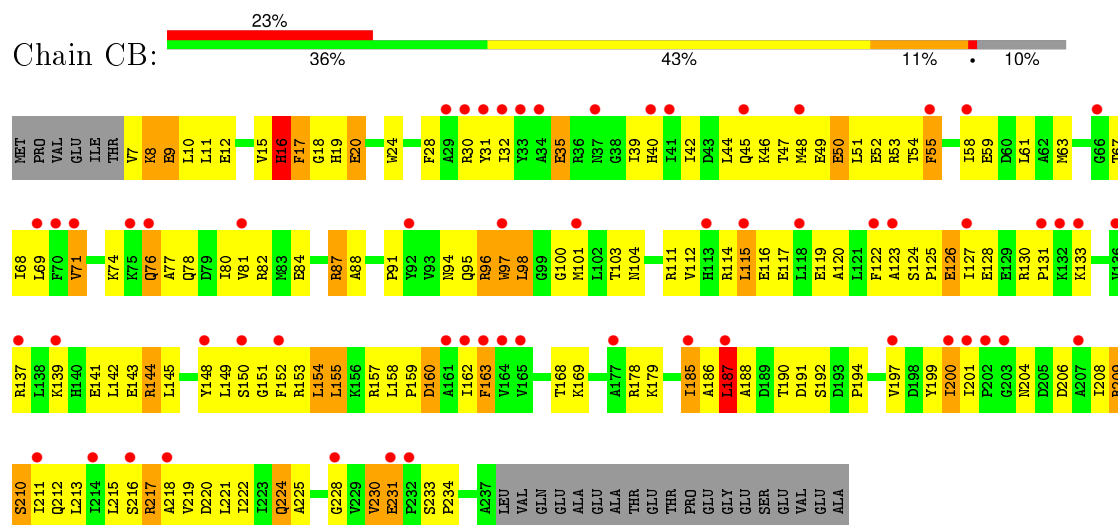


• Molecule 2: 30S ribosomal protein S2

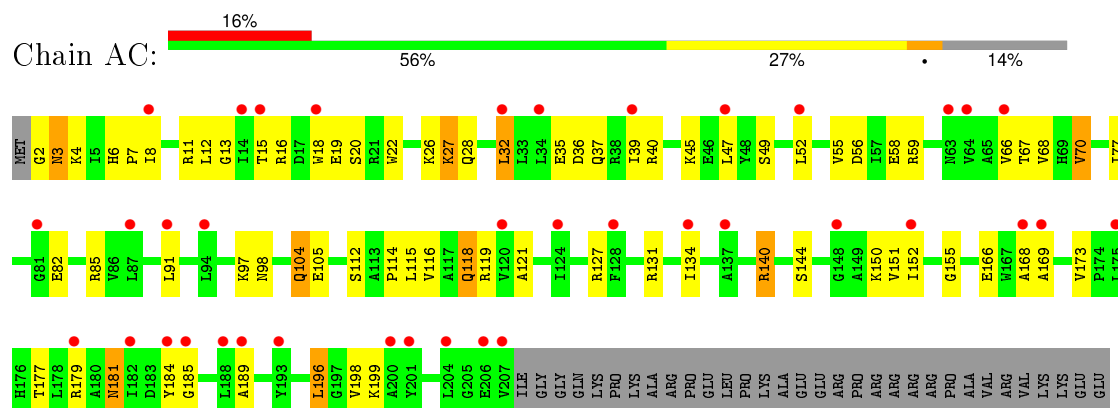




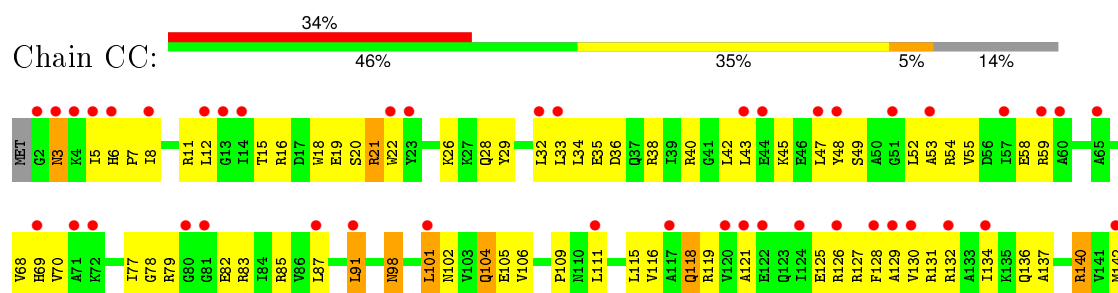
• Molecule 2: 30S ribosomal protein S2

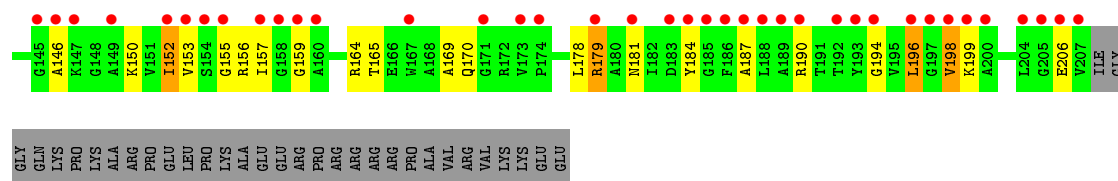


• Molecule 3: 30S ribosomal protein S3

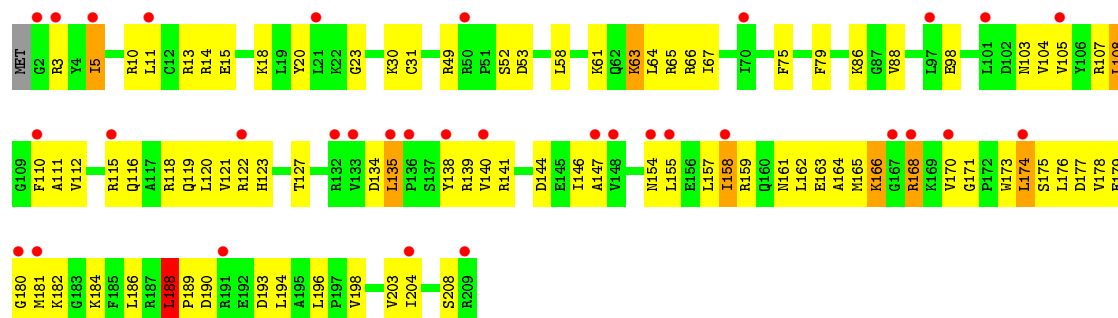


• Molecule 3: 30S ribosomal protein S3

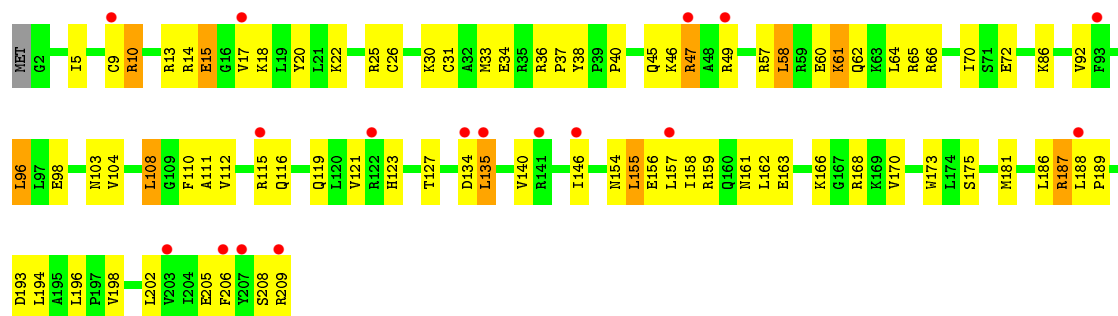




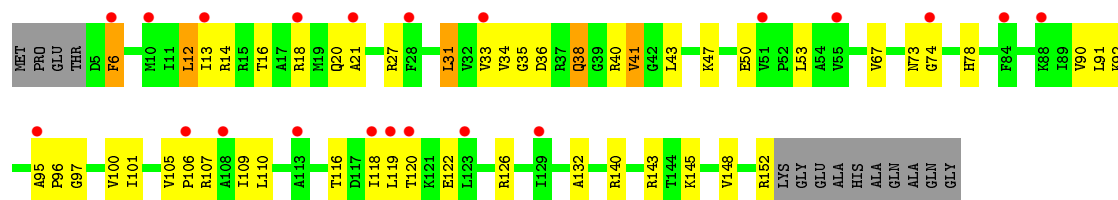
• Molecule 4: 30S ribosomal protein S4



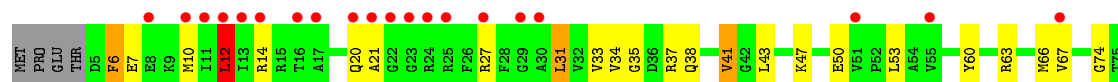
• Molecule 4: 30S ribosomal protein S4

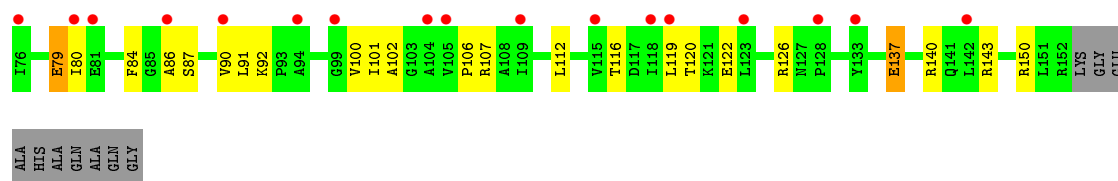


• Molecule 5: 30S ribosomal protein S5

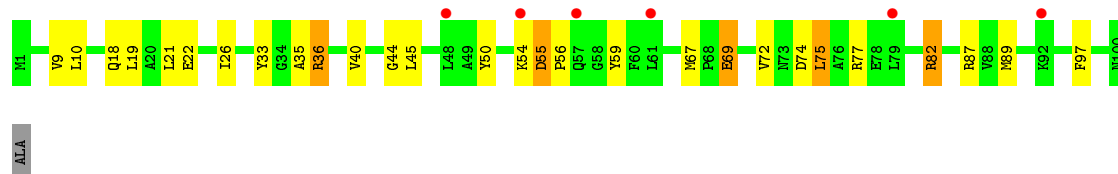
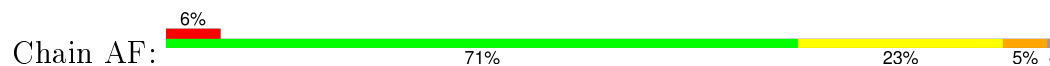


• Molecule 5: 30S ribosomal protein S5

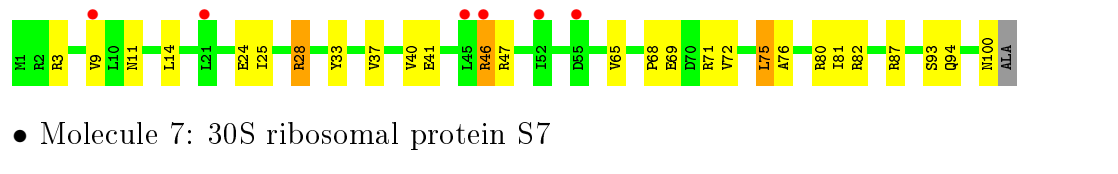
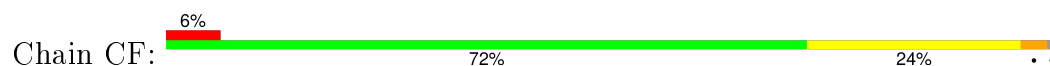




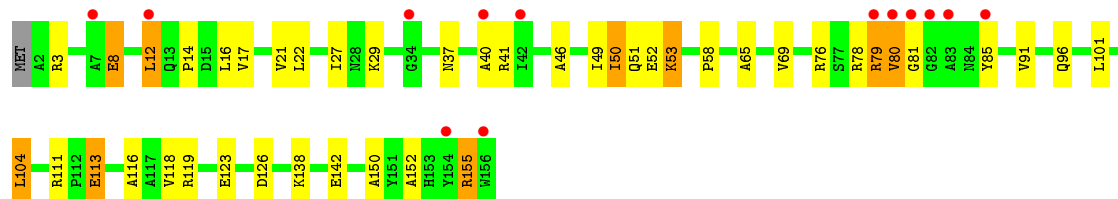
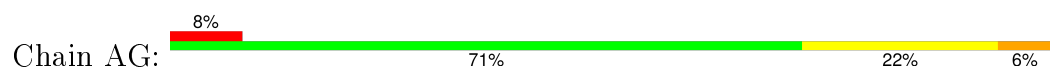
- Molecule 6: 30S ribosomal protein S6



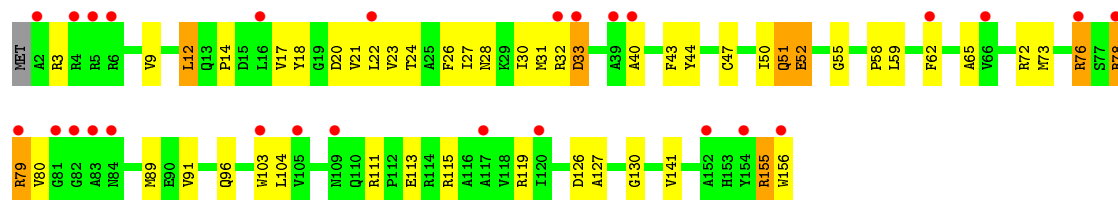
- Molecule 6: 30S ribosomal protein S6



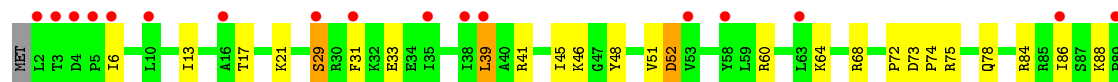
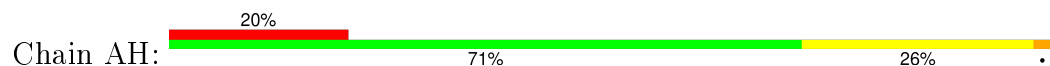
- Molecule 7: 30S ribosomal protein S7

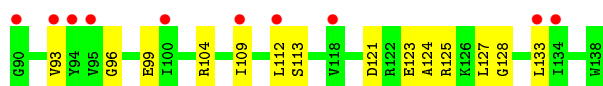


- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8

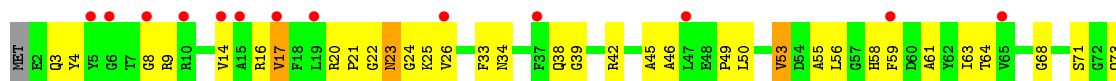




- Molecule 8: 30S ribosomal protein S8



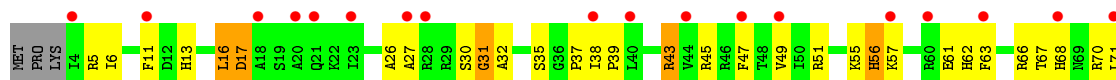
- Molecule 9: 30S ribosomal protein S9



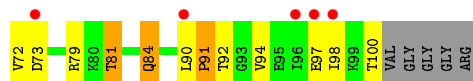
- Molecule 9: 30S ribosomal protein S9

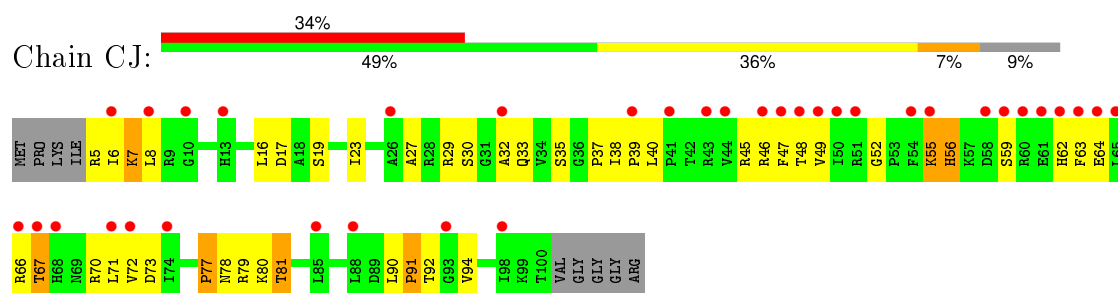


- Molecule 10: 30S ribosomal protein S10

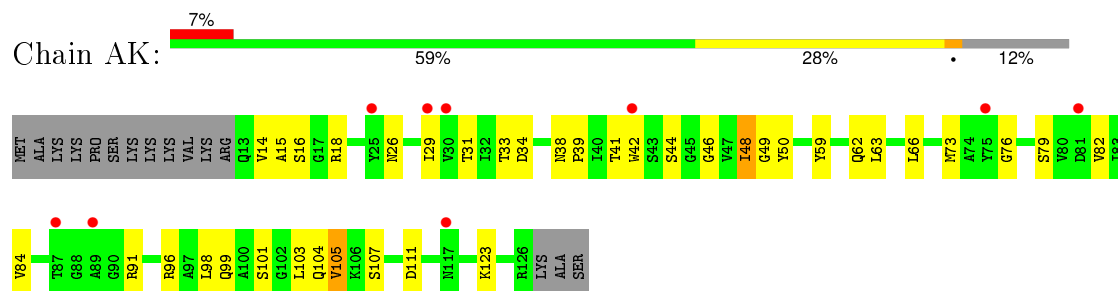


- Molecule 10: 30S ribosomal protein S10

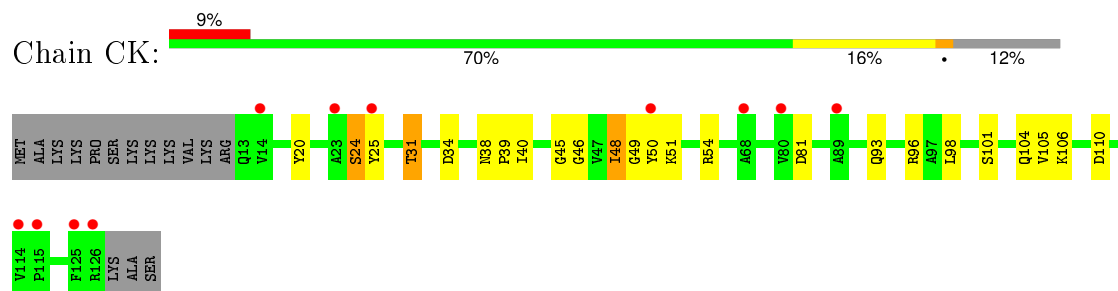




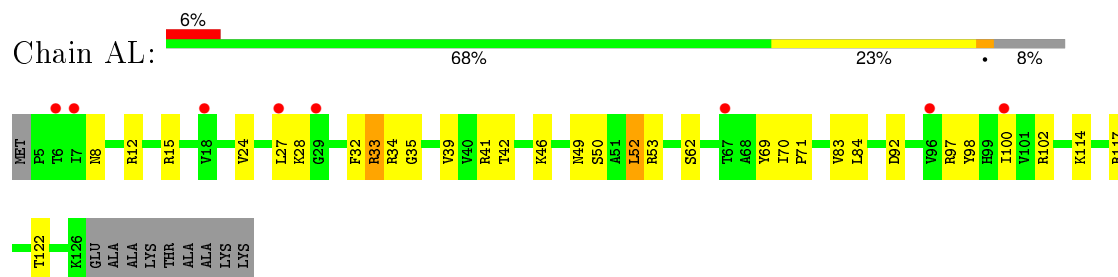
- Molecule 11: 30S ribosomal protein S11



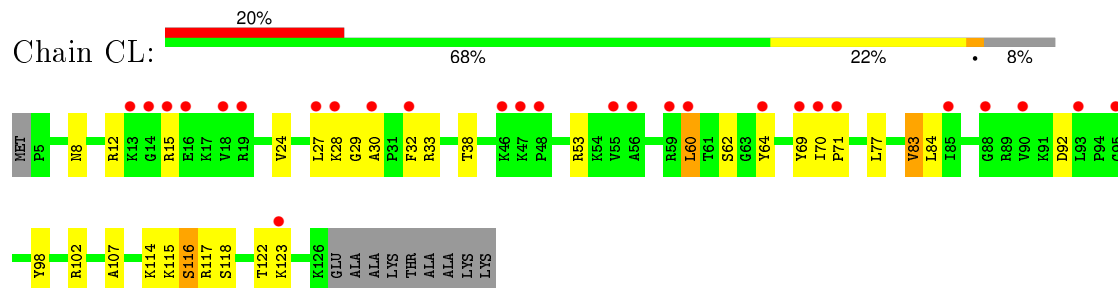
- Molecule 11: 30S ribosomal protein S11



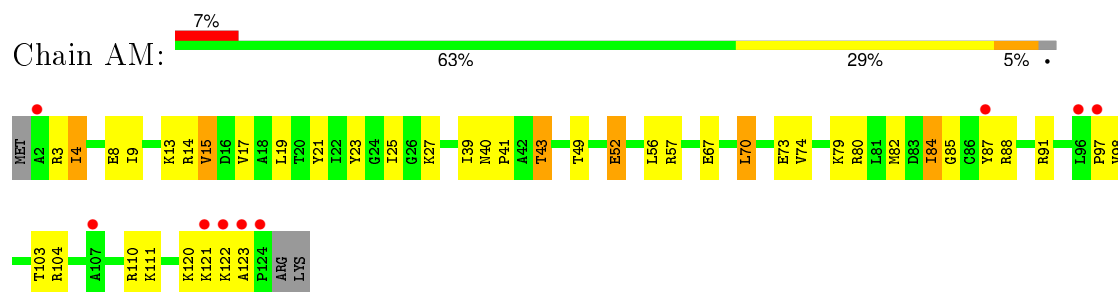
- Molecule 12: 30S ribosomal protein S12



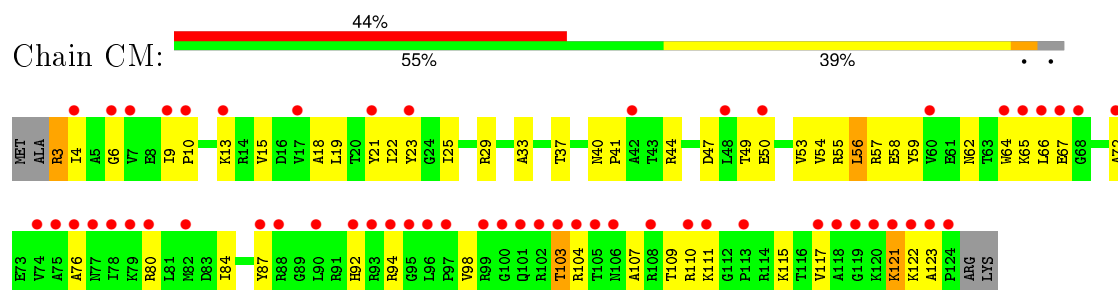
- Molecule 12: 30S ribosomal protein S12



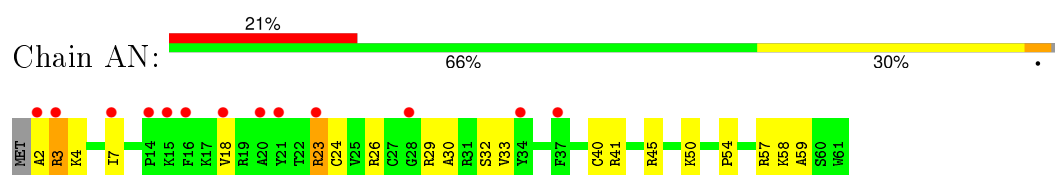
- Molecule 13: 30S ribosomal protein S13



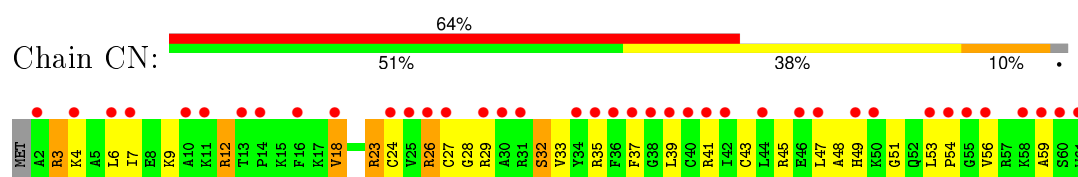
- Molecule 13: 30S ribosomal protein S13



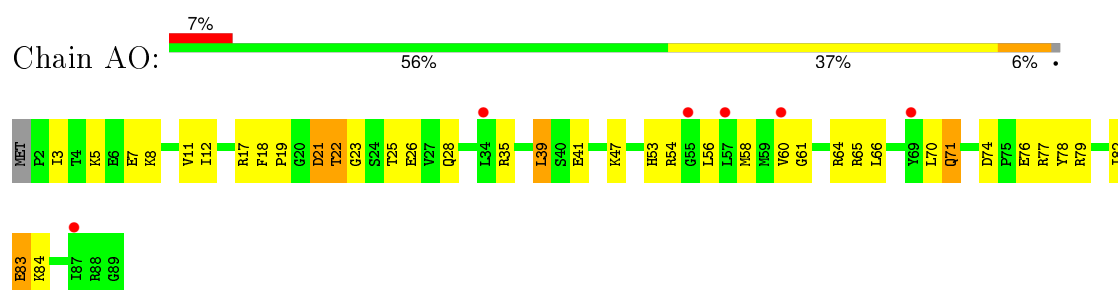
- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S14 type Z

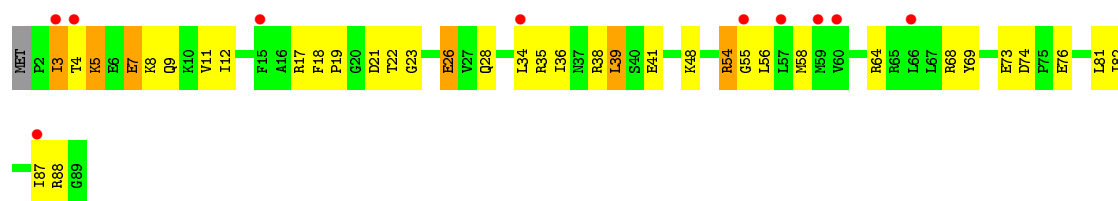


- Molecule 15: 30S ribosomal protein S15

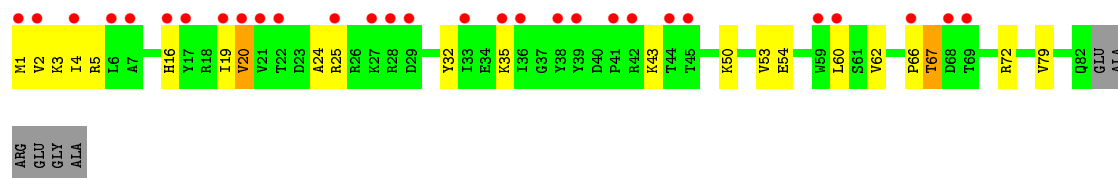


- Molecule 15: 30S ribosomal protein S15





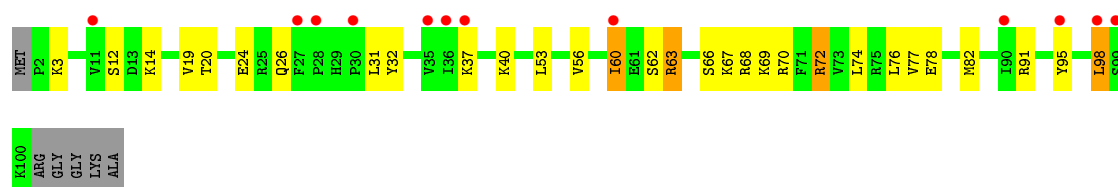
- Molecule 16: 30S ribosomal protein S16



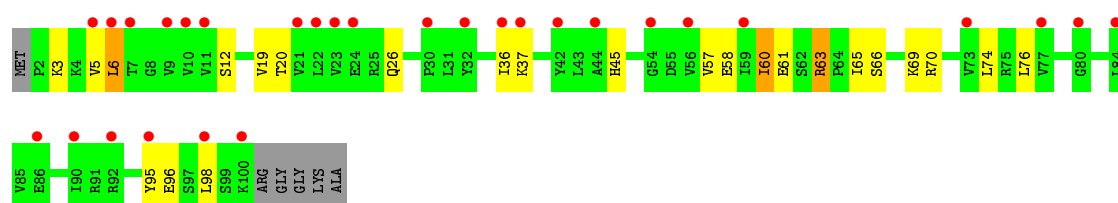
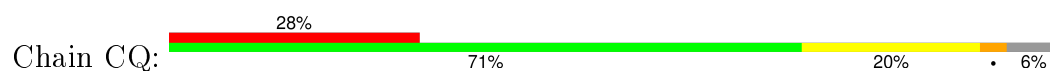
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

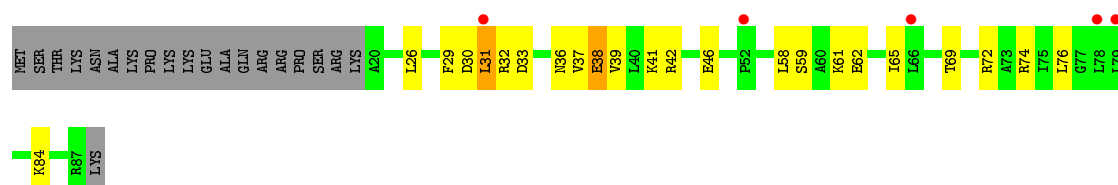


- Molecule 17: 30S ribosomal protein S17

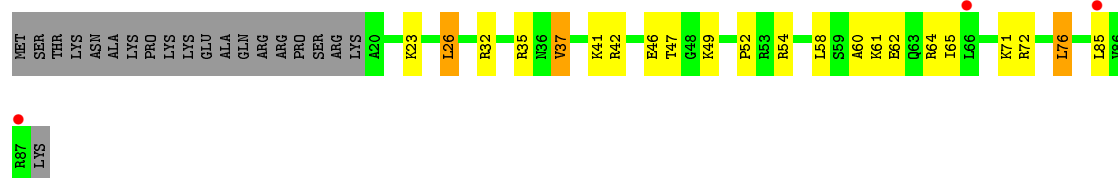


- Molecule 18: 30S ribosomal protein S18

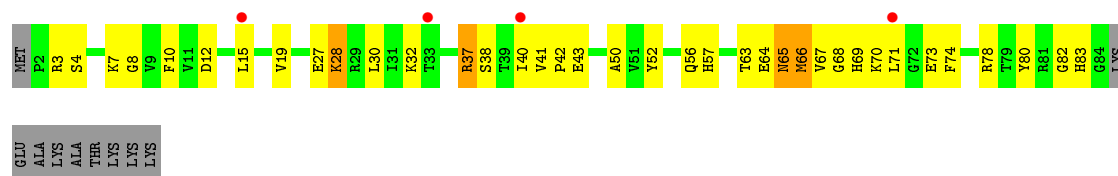




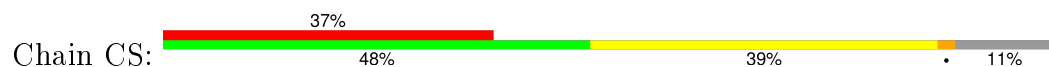
- Molecule 18: 30S ribosomal protein S18



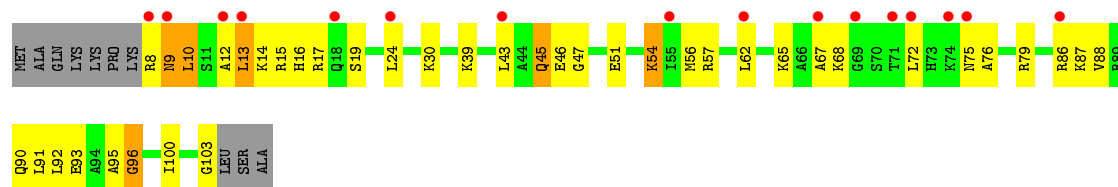
- Molecule 19: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S19

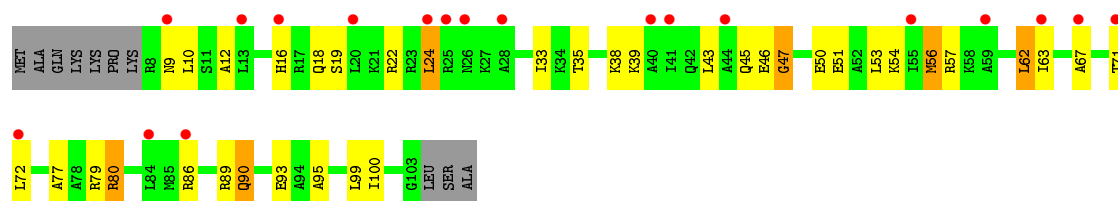


- Molecule 20: 30S ribosomal protein S20

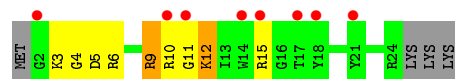


- Molecule 20: 30S ribosomal protein S20





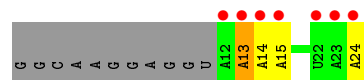
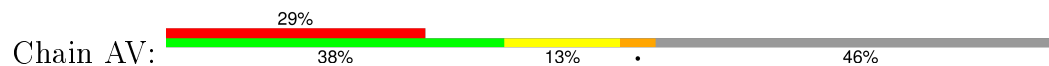
- Molecule 21: 30S ribosomal protein Thx



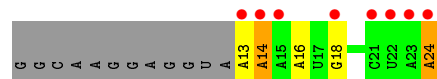
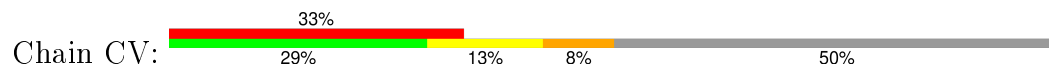
- Molecule 21: 30S ribosomal protein Thx



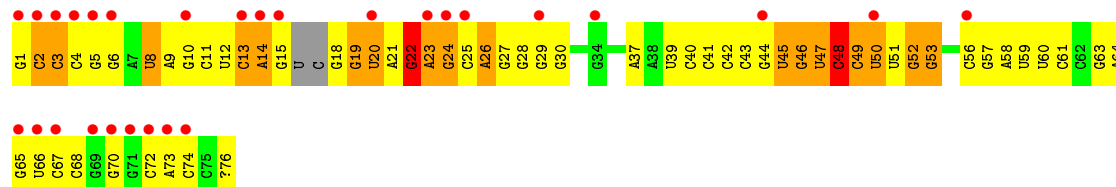
- Molecule 22: mRNA



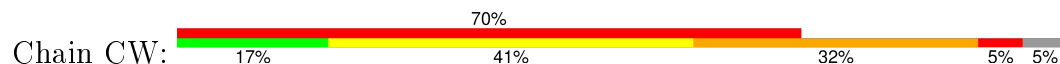
- Molecule 22: mRNA

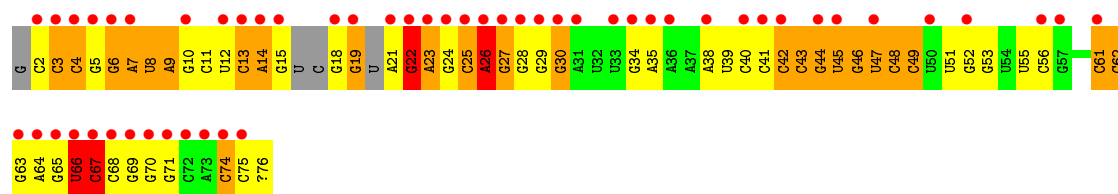


- Molecule 23: A-site tRNA



- Molecule 23: A-site tRNA

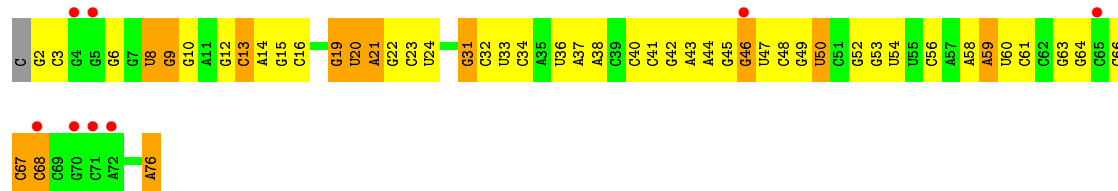




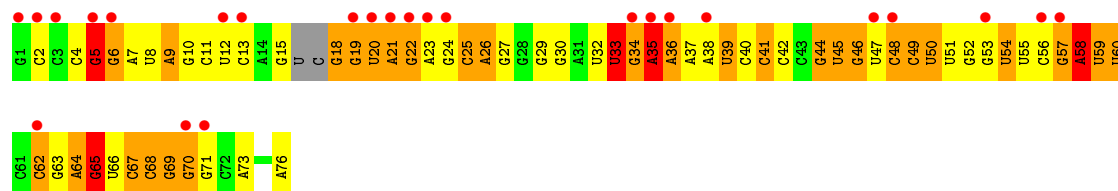
• Molecule 24: P-site tRNA



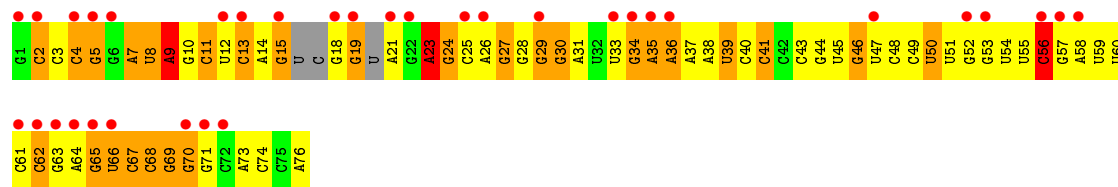
• Molecule 24: P-site tRNA



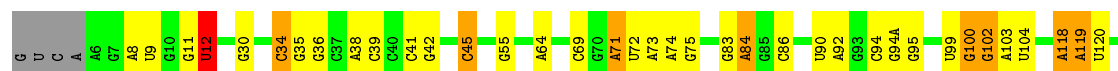
• Molecule 25: E-site tRNA



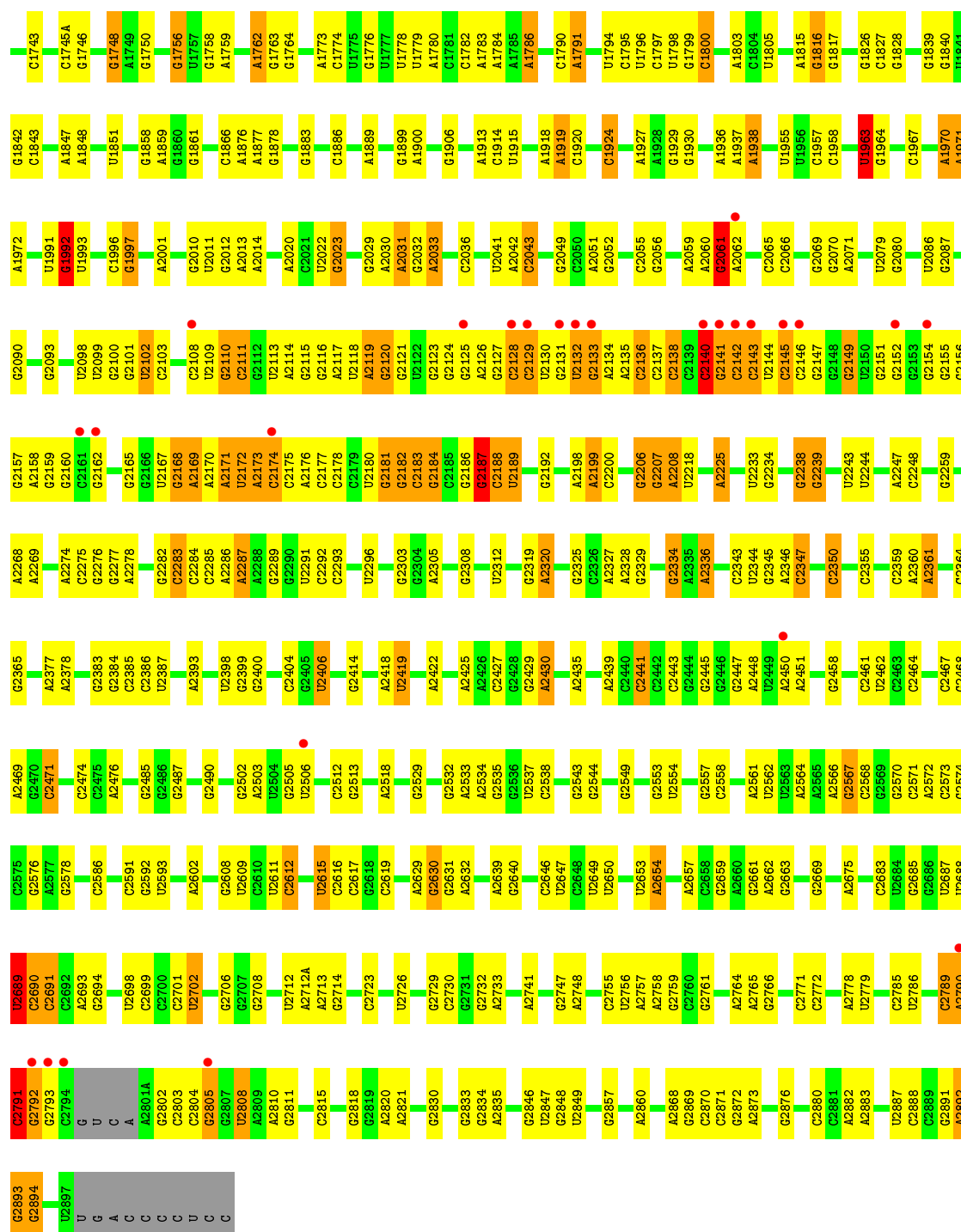
• Molecule 25: E-site tRNA



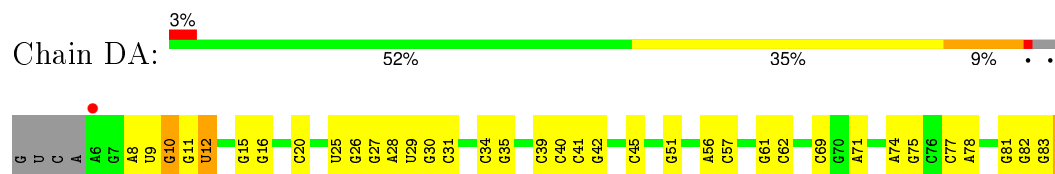
• Molecule 26: 23S Ribosomal RNA





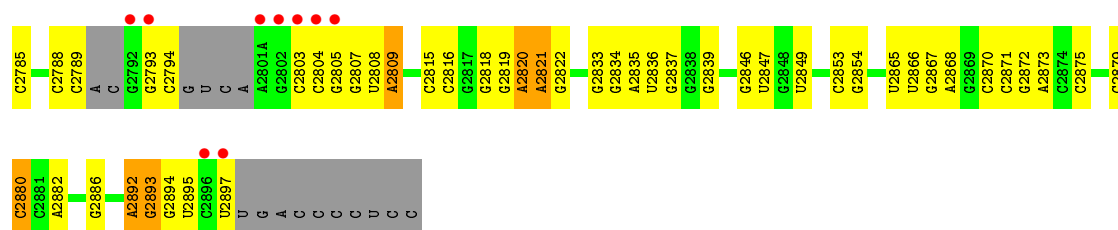


- Molecule 26: 23S Ribosomal RNA



U1263	G1179	C	4887	G966	G809	C721	A637	A	C456	C364	G272B	A204	A82
G1264	C1180	A	C888	C967	G810	C721	G638	G549	A457	C365	G272E	G205	G93
A1265	G1266	U	C889	C971	U811	U724	U639	G556	G465	C366	C272J	C208	C94
G1266	G1184	G	A890	C971	U812	G725	G641	U557	G468	G370	G275	C209	G94A
A1267	G1185	G	C892	G974	U813	G726	G642	G563	G469	A371	G275	G212	G95
G1268	G1186	U	C894	C975	C816	G729	A643	G564	A470	G372	A276	G213	G100
A1269	G1187	C	U895	A983	C817	C730	A644	C565	A478	G373	C277	G214	A103
C1270	U1188	G	A896	C987	G818	C731	G645	U566	A479	A374	A278	G215	G102
G1271	A1189	A	C898	C987	A819	C731	A646	U567	A478	G375	C277	G216	G109
U1272	U1273	C	A899	C987	A820	A734	G648	A567	A479	C376	C285	A216	G117
A1278	G1196	C	A900	A988	A821	U740	G649	U568	G480	U380	C286	A221	G118
G1283	G1197	A	A901	A990	A821	U741	G650	U569	G481	G381	C287	A222	A118
A1284	U1199	G	A902	A991	U827	G741	A652B	G570	A482	G382	C288	A223	A119
G1285	G1200	A	C903	C992	U828	G744	G652C	A571	A483	U383	A289	G224	U120
C1286	C1201	G	C904	C993	A829	G744	G652D	G572	C484	G384	C292	A225	G121
G1287	G1202	G	G930	C994	G830	G745	G652E	G573	C485	U385	C293	G226	G125
A1287	A1203	U	U910	C995	A831	A746	G	A575	A492	G386	A294	A227	G131
U1288	U1204	U	A911	A996	G832	U747	G	G582	G493	G389	A299	A228	G140
C1293	U1205	G	C912	A997	U833	U748	C	G583	G494	A390	A300	A229	A141
G1299	G1209	G	U913	C998	U839	A752	G	G586	G498	G391	G301	A233	G143
A1210	U1211	C	C914	A1000	C940	C753	C	A587	U499	G396	U305	C234	C143A
U1211	A1201	U	A917	A1001	G848	C754	A	U588	G500	G397	U306	U235	C144
G1219	G1219	A	A918	G1002	G848	C755	C	C589	A503	G399	G307	A241	G145
A1220	A1220	G	G921	C1005	U851	G760	G	G592	A505	U405	G309	G245	A149
C1221	C1221	A	U922	C1006	G852	A761	G	G600	G509	G406	A310	C246	C154A
C1221A	C1221A	G	C923	C1007	G853	U762	G	G601	G510	G407	A311	G247	U
G1222	C1222	C	G927	C1008	G854	G763	C	G602	G511	G410	G315	G248	U
G1223	G1223	A	G928	G1011	G855	A764	C	G603	G512	G411	C316	G249	G171
C1225	C1225	G	U932	U1012	U856	G765	C	G604	G513	A412	A320	G250	G173
A1226	A1226	C	G934	U1013	U857	G770	G	G605	G516	C413	G321	G251	G178
G1229	G1231	U	G937	U1014	U858	A774	G	U606	C517	C414	A322	G252	A181
C1230	G1231	C	U937	U1015	U859	G775	G	U607	G528	A421	G326	G253	A182
G1231	G1231	U	G938	U1016	A861	G776	G	A608	A529	A422	G327	A270	C183
C1232	G1232	C	U938	G1017	G862	A782	G	A609	G531	A428	U328	G271	U185
G1235	G1235	U	A941	U1018	G864	A783	G662	U614	A526	A429	G329	G271J	A188
A1236	A1236	A	G942	U1019	C865	A784	G663	G614A	A527	A428	A330	U271K	A189
G1237	A1237	A	U943	A1020	A866	G785	G668	A614C	A528	A429	A331	G271L	A191
A1238	G1238	A	G944	U1021	C867	G785	G669	G614B	A529	A429	A332	G271M	U193
G1239	G1239	A	A945	U1022	U868	G785	G674	A614C	A530	A429	A333	G271N	C192
U1240	U1240	G	G946	G1023	G869	A788	G674	G615	G531	A429	A334	G271R	G194
A1241	A1241	U	G946	G1024	A870	G788	G674	G616	A532	A429	A335	G271S	A195
G1242	G1242	C	G950	G1025	A871	C790	G674	G617	A533	A429	A336	G271T	A196
A1242	A1242	U	U951	U1026	G874	C791	G674	G618	A534	A429	A337	G271U	A197
G1246	A1246	C	G952	A1027	G875	G792	G674	G619	U534	A429	A338	G271V	C198
A1247	A1247	G	A953	A1028	A878	A793	G674	G620	C535	A442	G339	G271W	A199
G1248	G1248	U	G954	U1032	G879	C795	G674	G621	A536	A443	G340	G271X	C203
A1253	A1253	A	G955	G1033	G880	C796	G674	G622	C537	A444	G341	G271Y	
G1256	G1256	U	A957	U1035	G881	C797	G674	G623	A538	A445	G342	G271Z	
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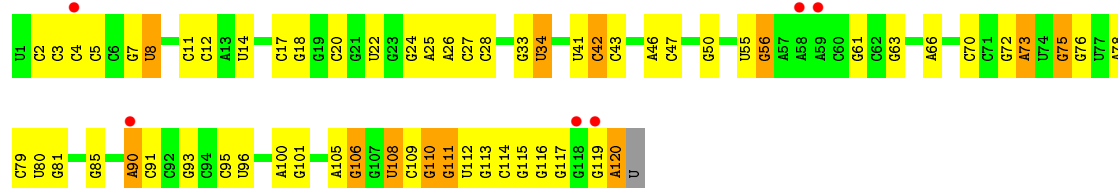
• Molecule 27: 5S Ribosomal RNA

Chain BB: 75% 18% 6% .



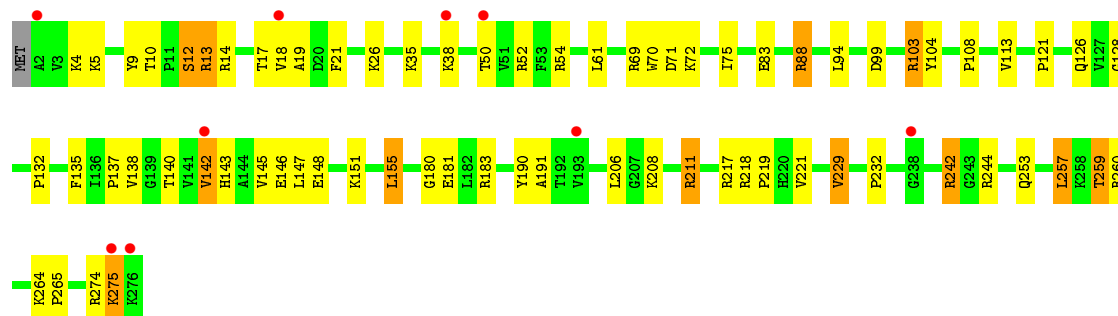
• Molecule 27: 5S Ribosomal RNA

Chain DB: 5% 48% 41% 10% .



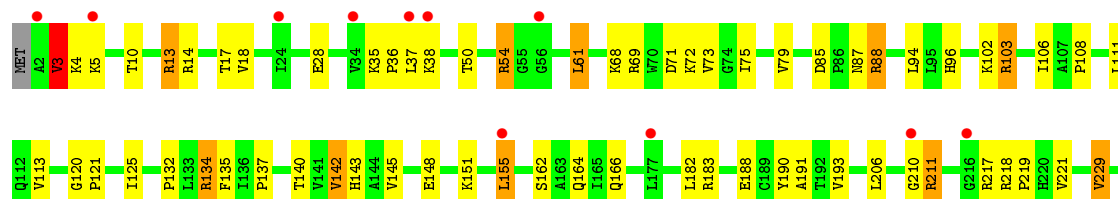
• Molecule 28: 50S ribosomal protein L2

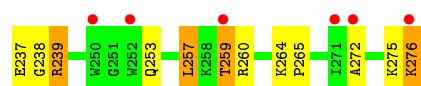
Chain BD: 3% 74% 21% .



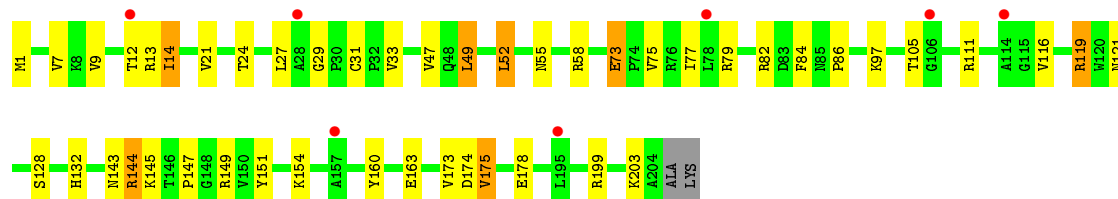
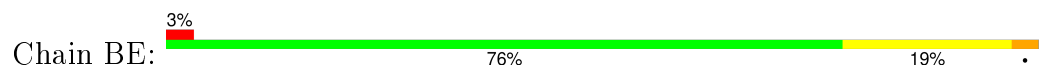
• Molecule 28: 50S ribosomal protein L2

Chain DD: 6% 72% 22% 5% .

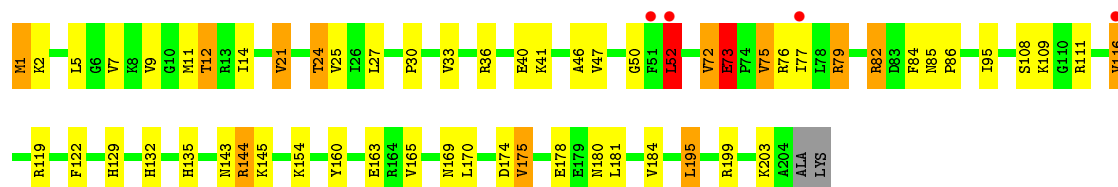




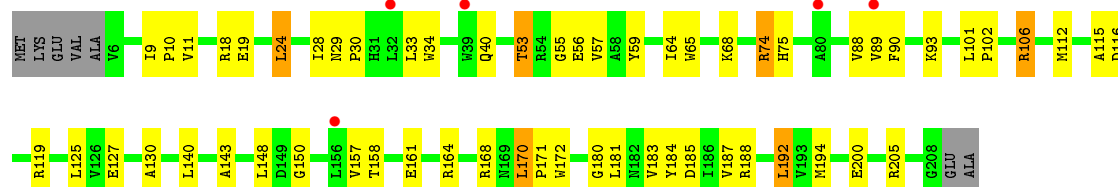
- Molecule 29: 50S ribosomal protein L3



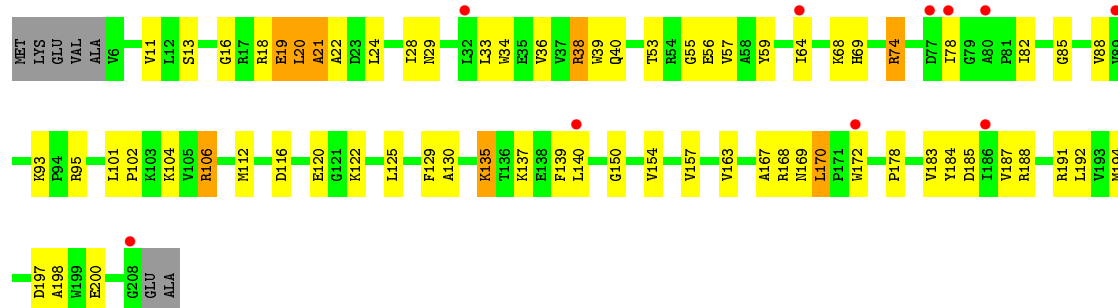
- Molecule 29: 50S ribosomal protein L3



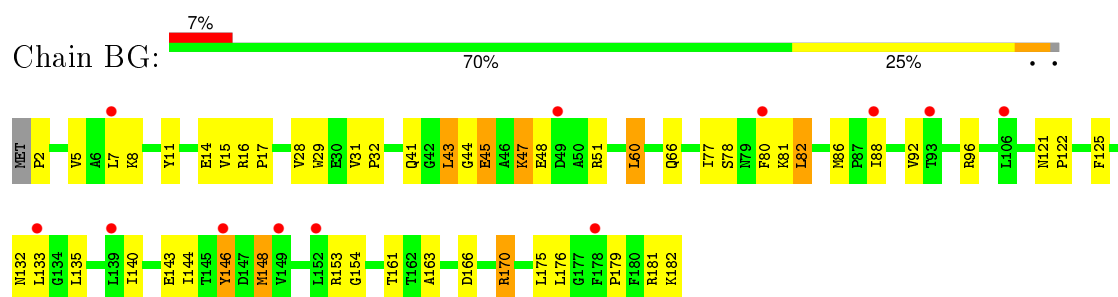
- Molecule 30: 50S ribosomal protein L4



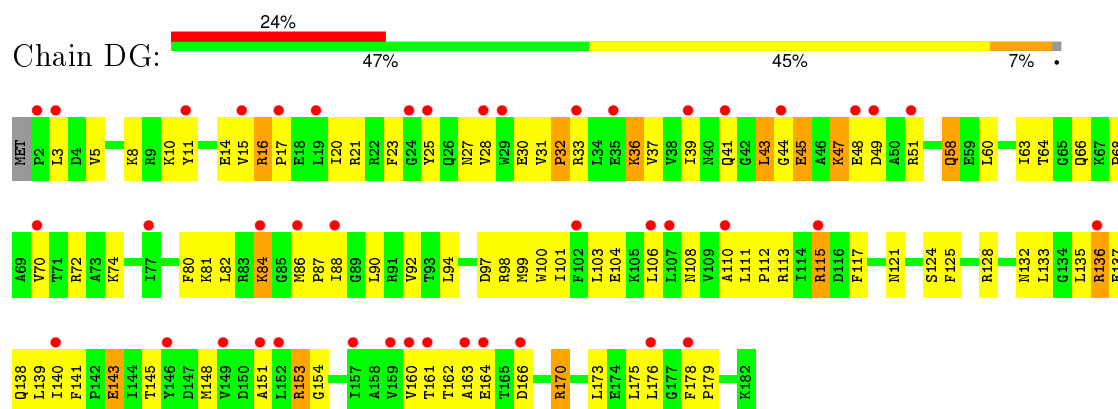
- Molecule 30: 50S ribosomal protein L4



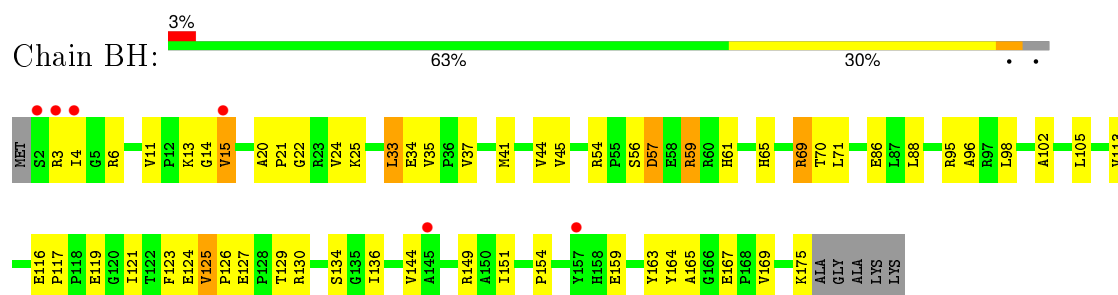
- Molecule 31: 50S ribosomal protein L5



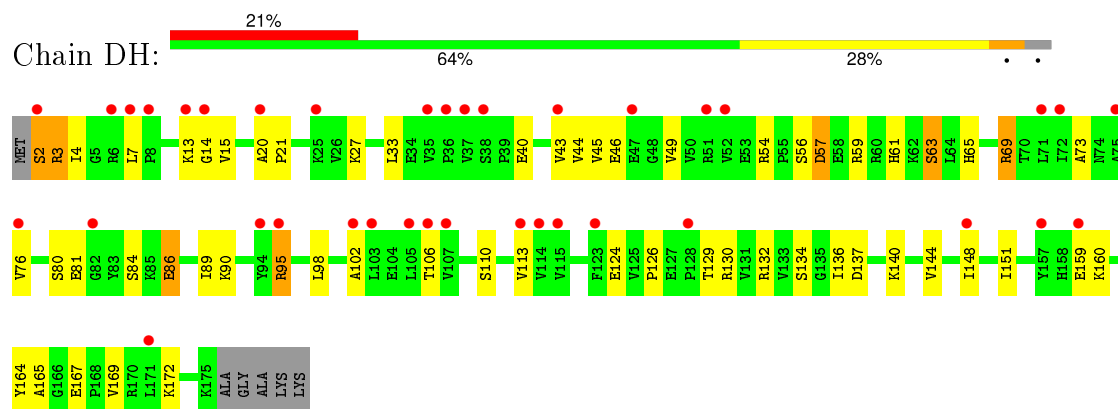
• Molecule 31: 50S ribosomal protein L5



• Molecule 32: 50S ribosomal protein L6

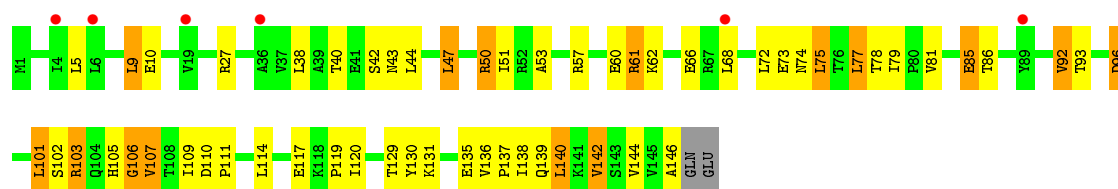


• Molecule 32: 50S ribosomal protein L6

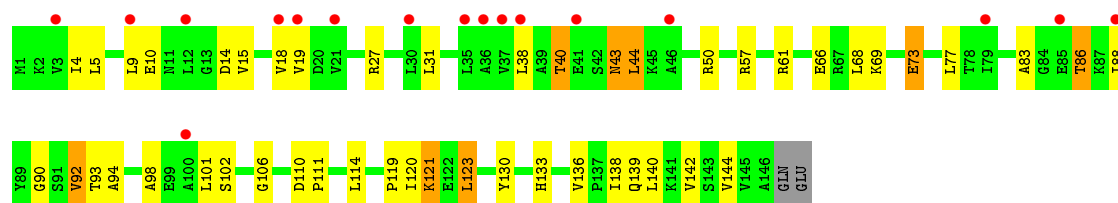


• Molecule 33: 50S ribosomal protein L9

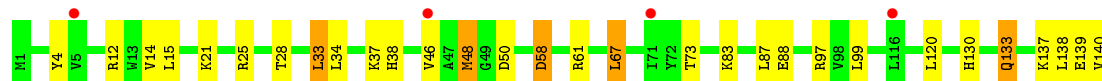
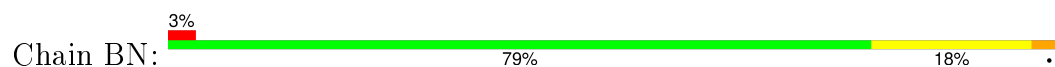




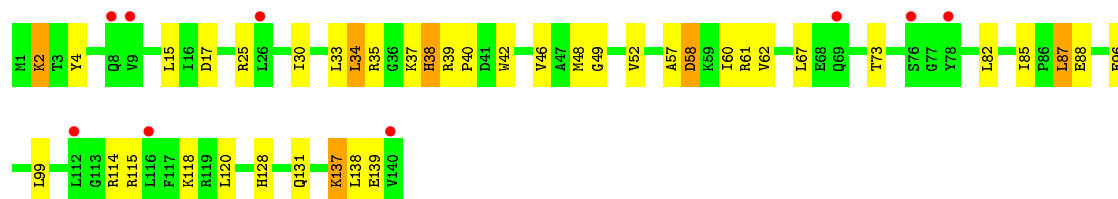
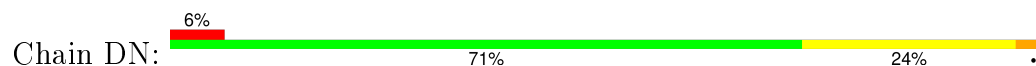
• Molecule 33: 50S ribosomal protein L9



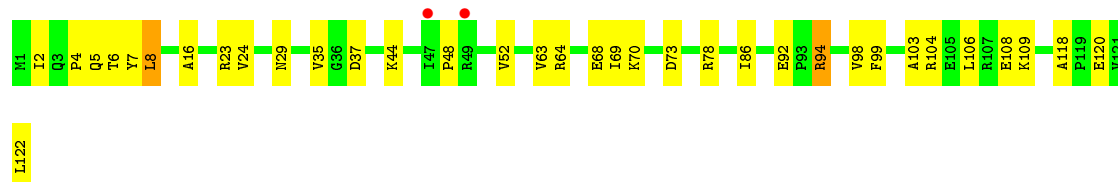
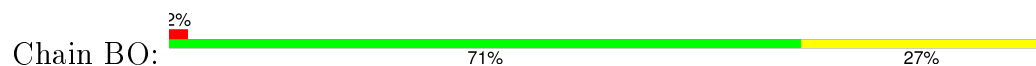
• Molecule 34: 50S ribosomal protein L13



• Molecule 34: 50S ribosomal protein L13

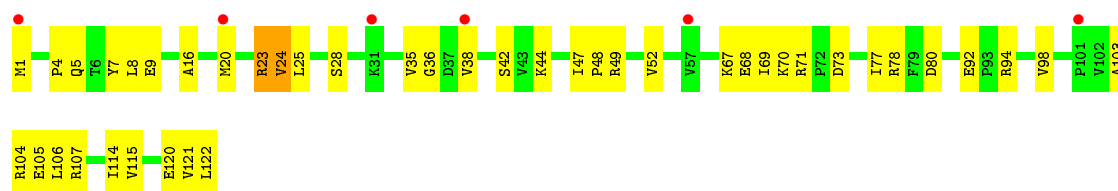


• Molecule 35: 50S ribosomal protein L14

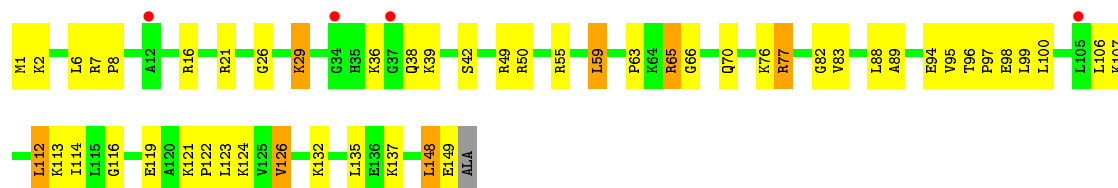


• Molecule 35: 50S ribosomal protein L14

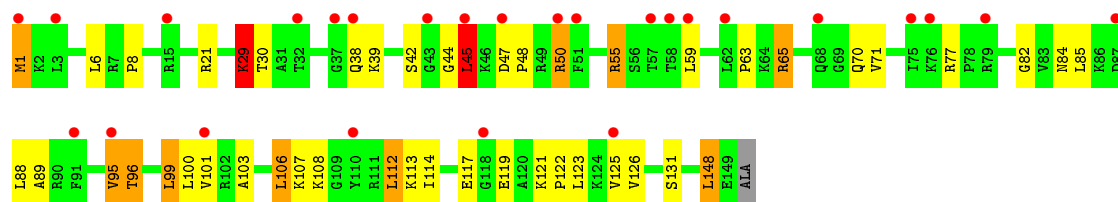




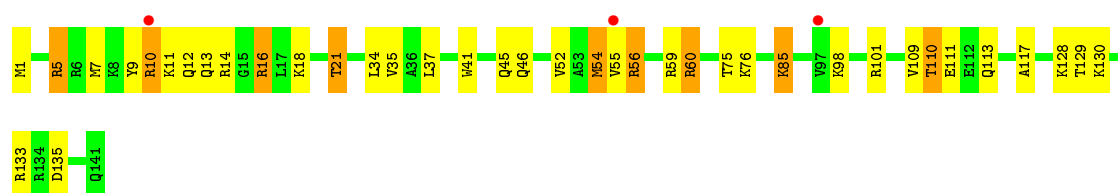
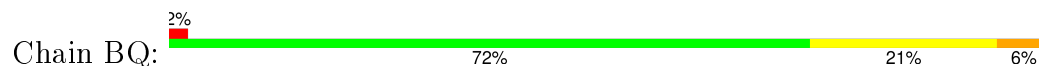
- Molecule 36: 50S ribosomal protein L15



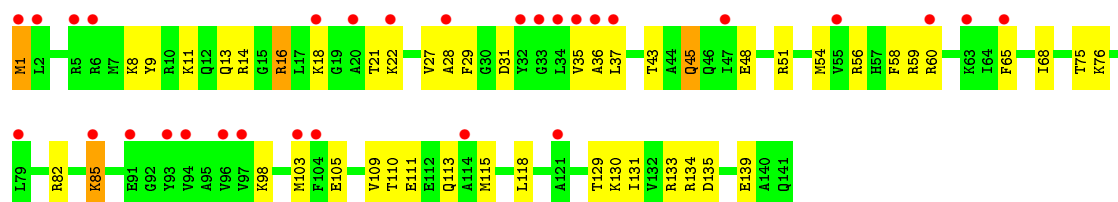
- Molecule 36: 50S ribosomal protein L15



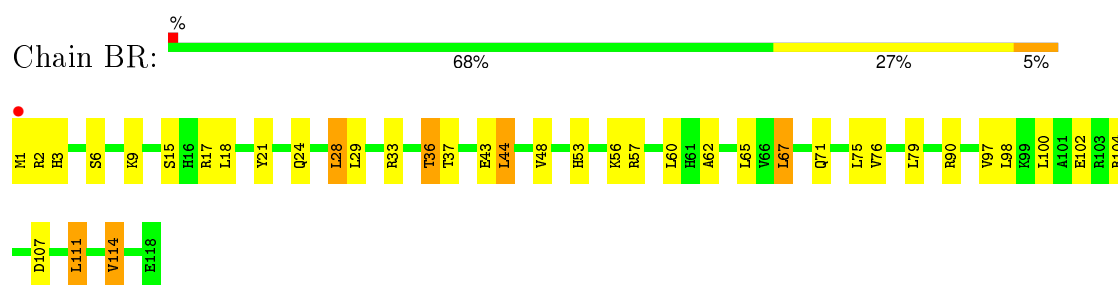
- Molecule 37: 50S ribosomal protein L16



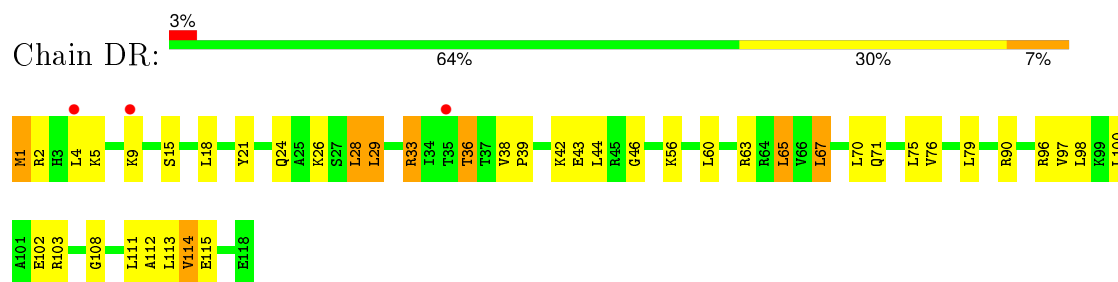
- Molecule 37: 50S ribosomal protein L16



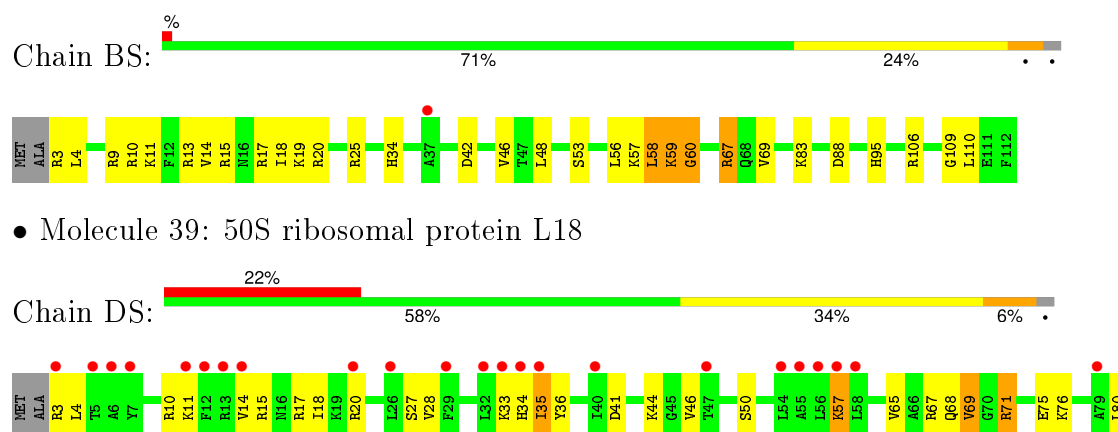
- Molecule 38: 50S ribosomal protein L17



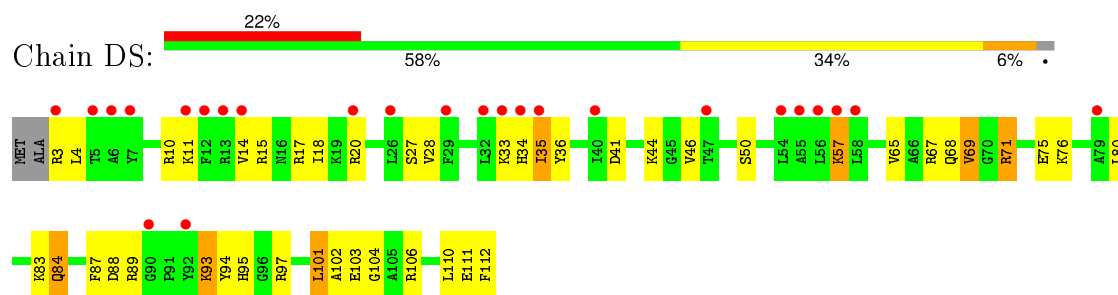
- Molecule 38: 50S ribosomal protein L17



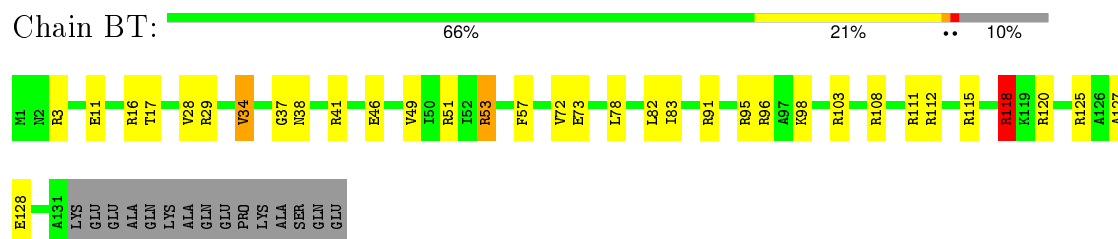
- Molecule 39: 50S ribosomal protein L18



- Molecule 39: 50S ribosomal protein L18

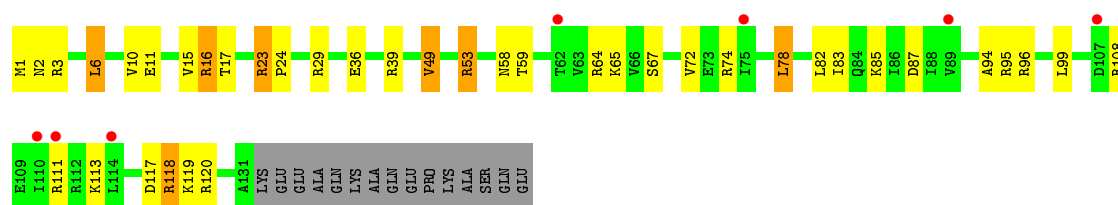


- Molecule 40: 50S ribosomal protein L19

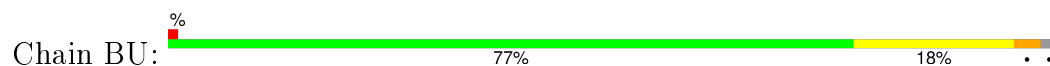


- Molecule 40: 50S ribosomal protein L19

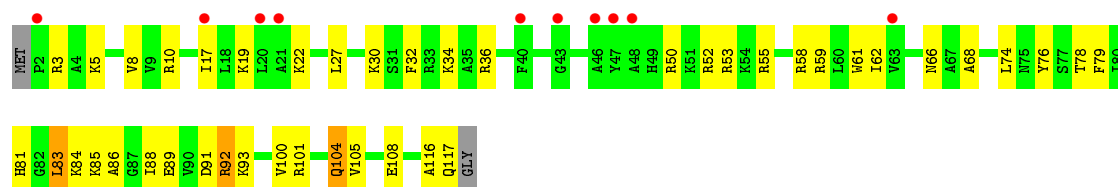




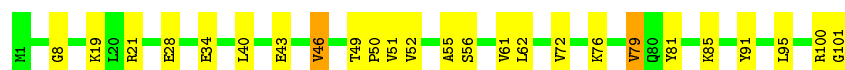
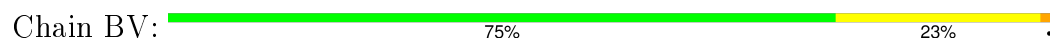
- Molecule 41: 50S ribosomal protein L20



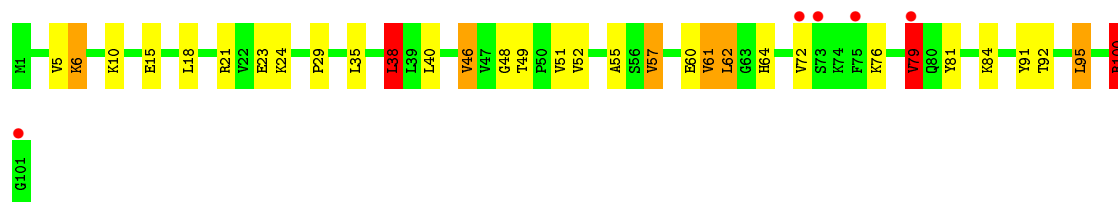
- Molecule 41: 50S ribosomal protein L20



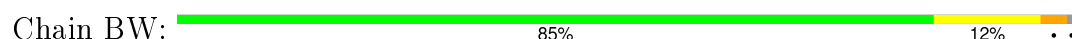
- Molecule 42: 50S ribosomal protein L21



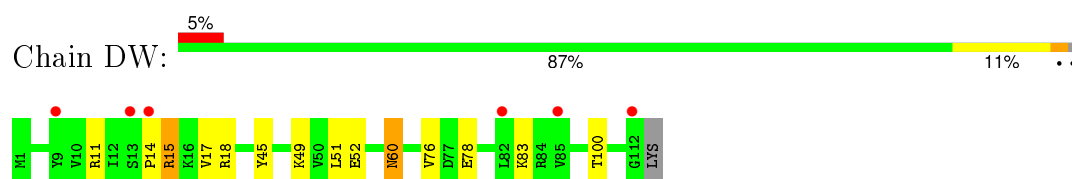
- Molecule 42: 50S ribosomal protein L21



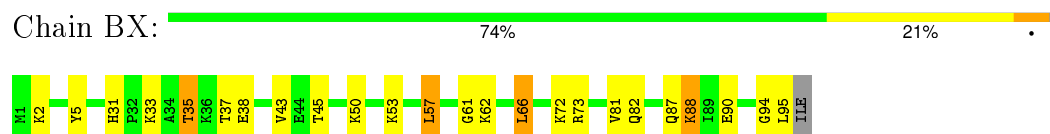
- Molecule 43: 50S ribosomal protein L22



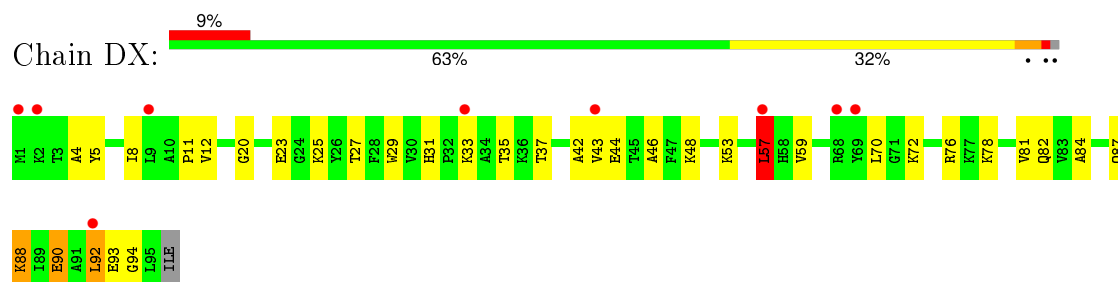
- Molecule 43: 50S ribosomal protein L22



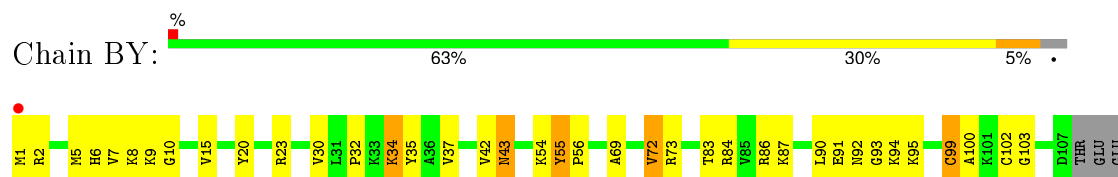
- Molecule 44: 50S ribosomal protein L23



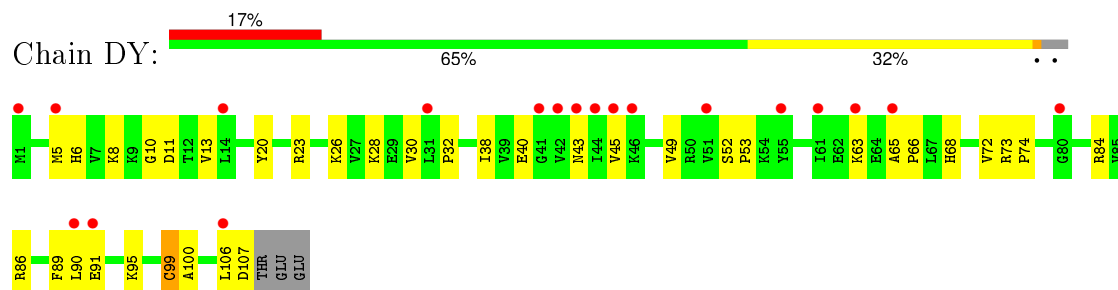
- Molecule 44: 50S ribosomal protein L23



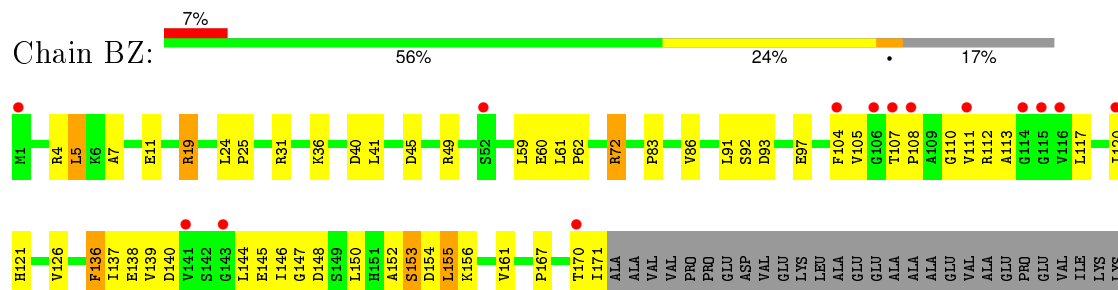
- Molecule 45: 50S ribosomal protein L24



- Molecule 45: 50S ribosomal protein L24

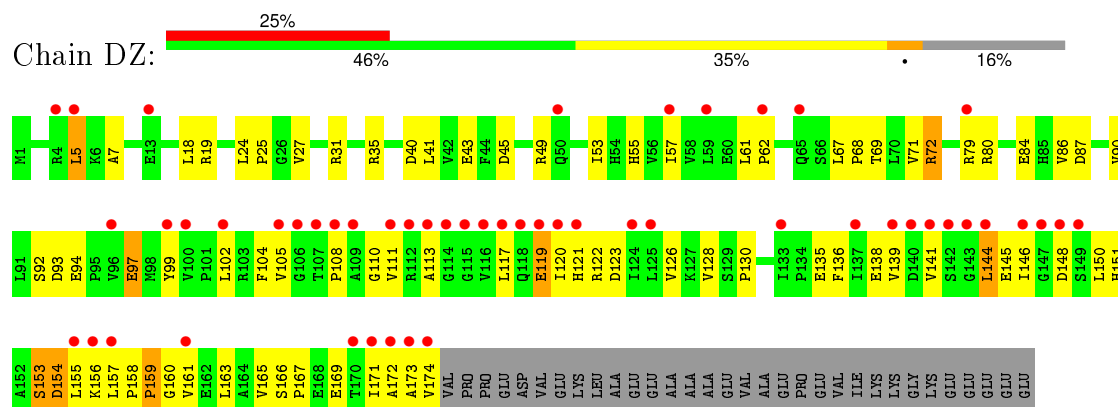


- Molecule 46: 50S ribosomal protein L25

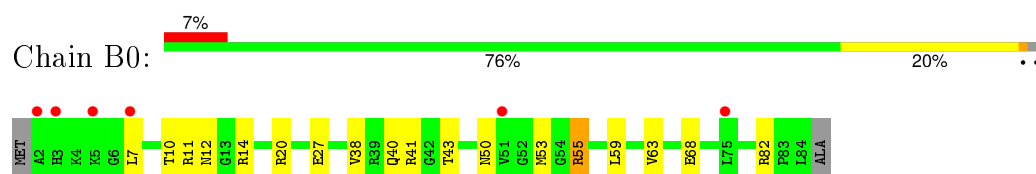


GLY
LYS
GLU
GLU
GLU
GLU

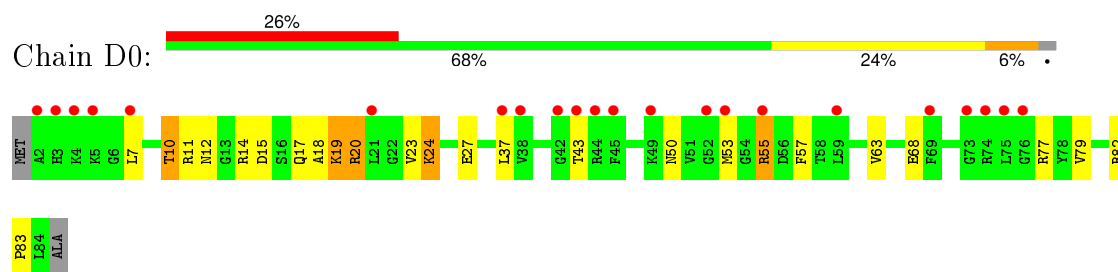
- Molecule 46: 50S ribosomal protein L25



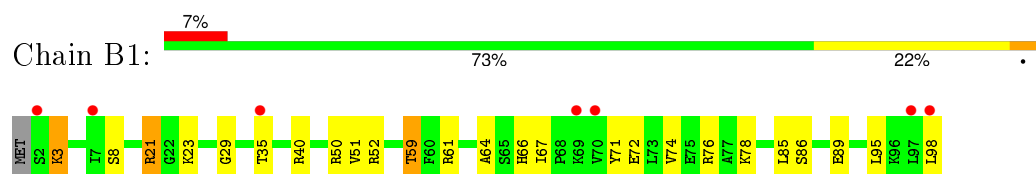
- Molecule 47: 50S ribosomal protein L27



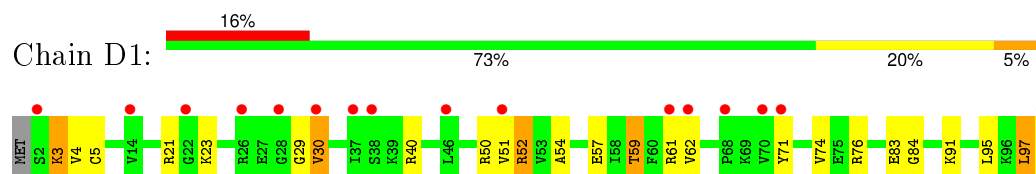
- Molecule 47: 50S ribosomal protein L27



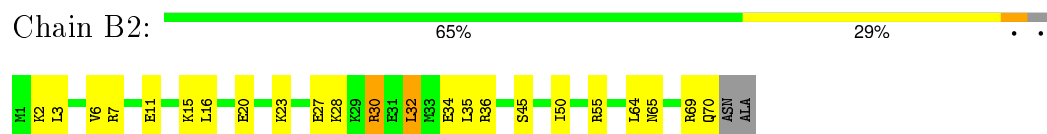
- Molecule 48: 50S ribosomal protein L28



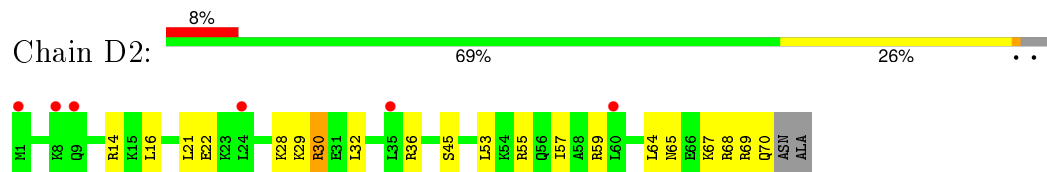
- Molecule 48: 50S ribosomal protein L28



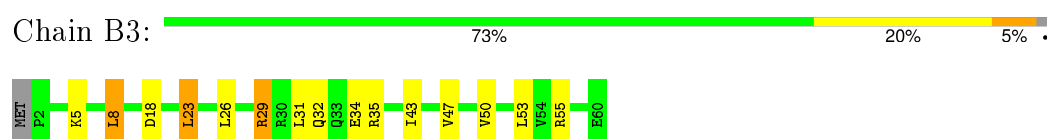
- Molecule 49: 50S ribosomal protein L29



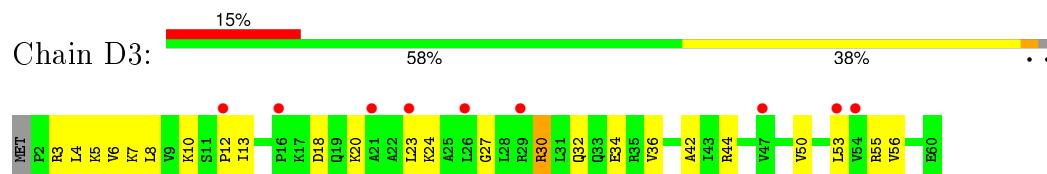
- Molecule 49: 50S ribosomal protein L29



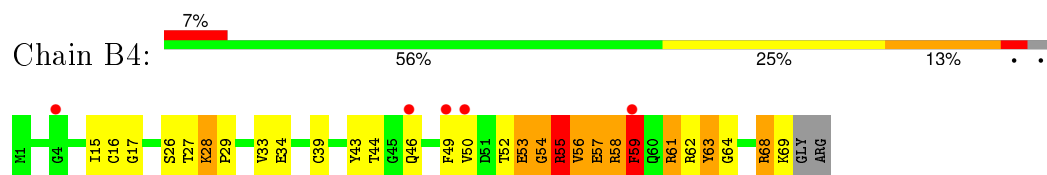
- Molecule 50: 50S ribosomal protein L30



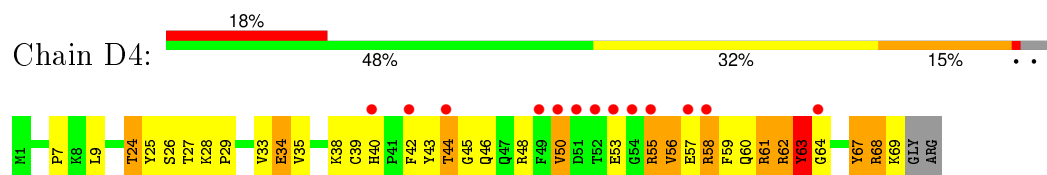
- Molecule 50: 50S ribosomal protein L30



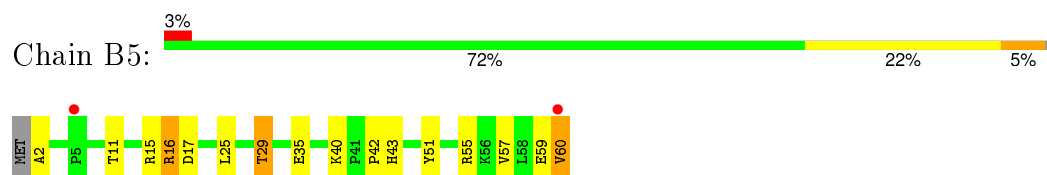
- Molecule 51: 50S ribosomal protein L31



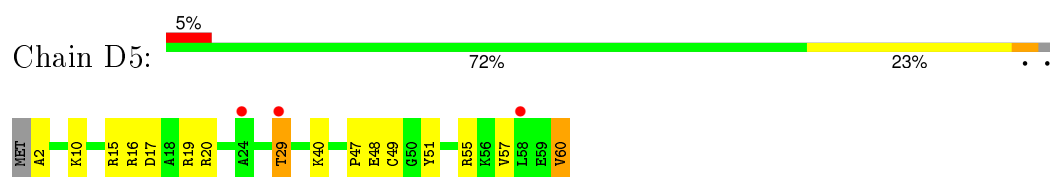
- Molecule 51: 50S ribosomal protein L31



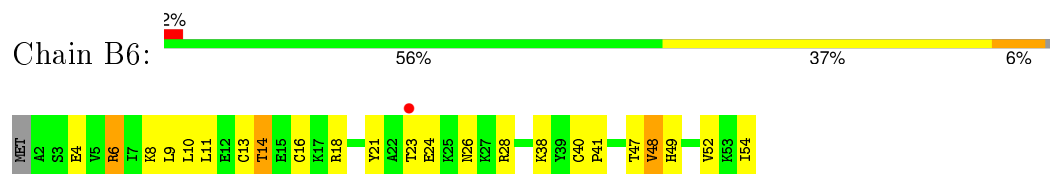
- Molecule 52: 50S ribosomal protein L32



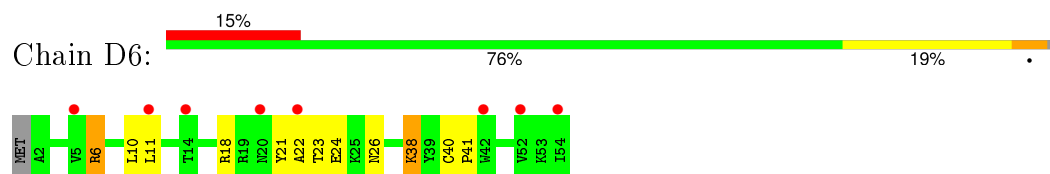
- Molecule 52: 50S ribosomal protein L32



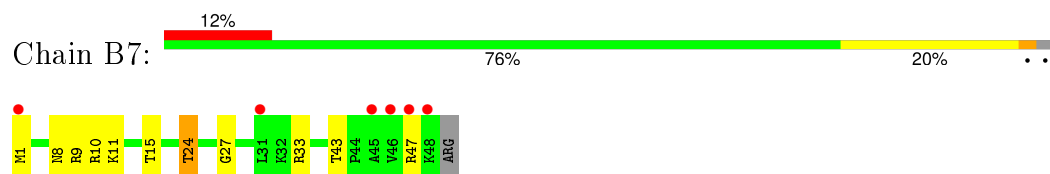
- Molecule 53: 50S ribosomal protein L33



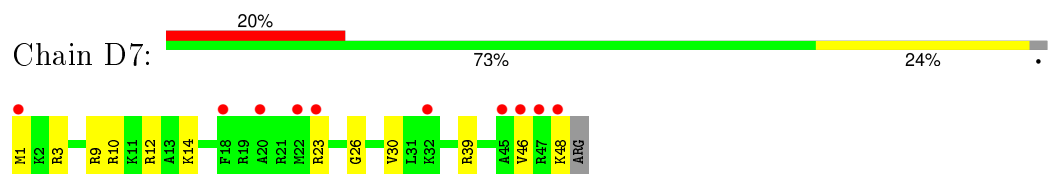
- Molecule 53: 50S ribosomal protein L33



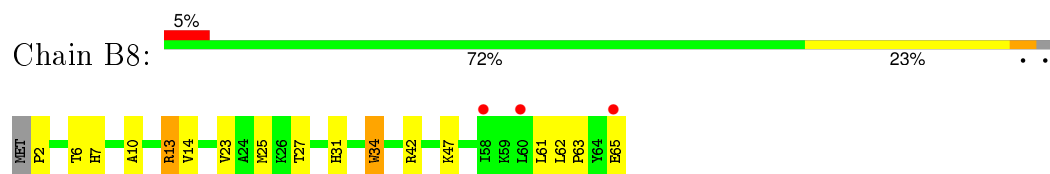
- Molecule 54: 50S ribosomal protein L34



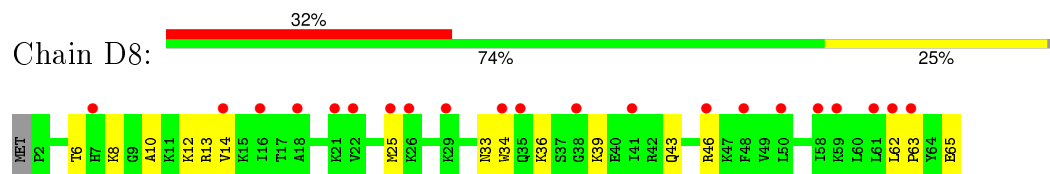
- Molecule 54: 50S ribosomal protein L34



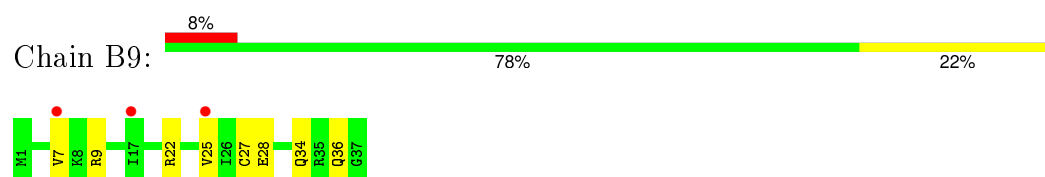
- Molecule 55: 50S ribosomal protein L35



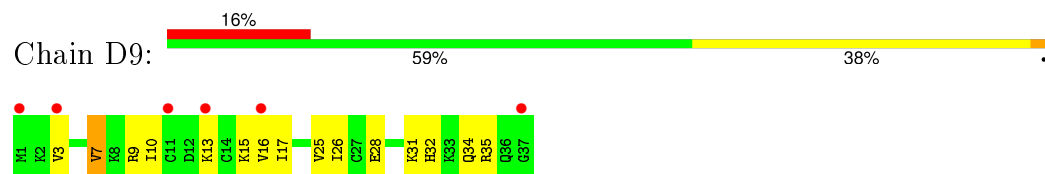
- Molecule 55: 50S ribosomal protein L35



- Molecule 56: 50S ribosomal protein L36



- Molecule 56: 50S ribosomal protein L36



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.32Å 450.06Å 622.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	152.51 – 2.55 255.92 – 2.55	Depositor EDS
% Data completeness (in resolution range)	95.8 (152.51-2.55) 95.8 (255.92-2.55)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.233 , 0.280 0.244 , 0.288	Depositor DCC
R_{free} test set	90444 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 58.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 1802139 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	297141	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.64% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, 31M, MIA, SF4, MG, 5MC, 4SU, 7MG, K, 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	AA	0.37	0/36049	0.91	42/56261 (0.1%)
1	CA	0.40	6/36170 (0.0%)	1.00	88/56452 (0.2%)
2	AB	0.31	0/1881	0.60	0/2542
2	CB	0.33	0/1860	0.65	1/2518 (0.0%)
3	AC	0.28	0/1576	0.52	0/2130
3	CC	0.32	0/1566	0.61	0/2119
4	AD	0.29	0/1689	0.58	2/2267 (0.1%)
4	CD	0.30	0/1704	0.54	0/2284
5	AE	0.30	0/1145	0.55	0/1543
5	CE	0.31	0/1149	0.62	1/1548 (0.1%)
6	AF	0.28	0/819	0.49	0/1111
6	CF	0.31	0/829	0.52	0/1123
7	AG	0.27	0/1250	0.51	0/1679
7	CG	0.28	0/1254	0.53	0/1683
8	AH	0.27	0/1108	0.50	0/1494
8	CH	0.27	0/1108	0.52	0/1494
9	AI	0.30	0/1002	0.59	0/1346
9	CI	0.30	0/997	0.57	0/1343
10	AJ	0.28	0/722	0.59	0/982
10	CJ	0.31	0/727	0.59	0/988
11	AK	0.28	0/844	0.60	1/1145 (0.1%)
11	CK	0.28	0/848	0.53	0/1149
12	AL	0.30	0/946	0.52	0/1274
12	CL	0.30	0/946	0.55	0/1274
13	AM	0.28	0/969	0.61	0/1302
13	CM	0.29	0/961	0.57	0/1291
14	AN	0.30	0/501	0.50	0/664
14	CN	0.33	0/501	0.57	0/664
15	AO	0.28	0/739	0.55	0/985
15	CO	0.30	0/739	0.54	0/985
16	AP	0.28	0/697	0.52	0/939
16	CP	0.31	0/693	0.51	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.28	0/836	0.53	0/1117
17	CQ	0.29	0/836	0.50	0/1117
18	AR	0.27	0/560	0.56	0/746
18	CR	0.28	0/560	0.56	0/746
19	AS	0.29	0/667	0.58	0/900
19	CS	0.32	0/661	0.67	0/893
20	AT	0.28	0/730	0.58	0/965
20	CT	0.28	0/729	0.52	0/965
21	AU	0.26	0/203	0.52	0/266
21	CU	0.35	0/203	0.52	0/266
22	AV	0.41	0/310	0.94	0/480
22	CV	0.45	0/282	1.06	1/437 (0.2%)
23	AW	0.47	0/1577	1.18	6/2454 (0.2%)
23	CW	0.59	0/1531	1.46	25/2379 (1.1%)
24	AX	0.51	0/1725	1.17	14/2689 (0.5%)
24	CX	0.44	0/1725	1.12	10/2689 (0.4%)
25	AY	0.62	0/1602	1.43	22/2493 (0.9%)
25	CY	0.64	0/1579	1.46	32/2455 (1.3%)
26	BA	0.48	2/68013 (0.0%)	0.95	84/106165 (0.1%)
26	DA	0.42	1/67542 (0.0%)	0.94	72/105428 (0.1%)
27	BB	0.41	0/2878	0.88	0/4490
27	DB	0.44	0/2878	0.94	0/4490
28	BD	0.37	0/2186	0.59	0/2944
28	DD	0.33	0/2186	0.55	0/2944
29	BE	0.36	0/1592	0.57	0/2149
29	DE	0.34	0/1592	0.60	1/2149 (0.0%)
30	BF	0.35	0/1619	0.55	0/2193
30	DF	0.32	0/1615	0.58	0/2188
31	BG	0.31	0/1450	0.54	0/1959
31	DG	0.33	0/1449	0.57	0/1958
32	BH	0.33	0/1356	0.54	0/1834
32	DH	0.30	0/1356	0.52	0/1834
33	BI	0.29	0/1100	0.60	0/1501
33	DI	0.28	0/1076	0.57	0/1471
34	BN	0.32	0/1144	0.53	0/1543
34	DN	0.31	0/1144	0.54	0/1543
35	BO	0.34	0/943	0.58	1/1269 (0.1%)
35	DO	0.31	0/943	0.51	0/1269
36	BP	0.34	0/1152	0.58	0/1533
36	DP	0.31	0/1152	0.59	0/1533
37	BQ	0.34	0/1143	0.53	0/1527
37	DQ	0.31	0/1143	0.52	0/1527
38	BR	0.35	0/982	0.58	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.29	0/982	0.52	0/1312
39	BS	0.31	0/887	0.63	2/1180 (0.2%)
39	DS	0.29	0/880	0.61	0/1172
40	BT	0.33	0/1105	0.59	1/1477 (0.1%)
40	DT	0.29	0/1097	0.56	0/1468
41	BU	0.37	0/977	0.56	0/1301
41	DU	0.31	0/977	0.50	0/1301
42	BV	0.39	0/782	0.58	0/1049
42	DV	0.32	0/782	0.64	2/1049 (0.2%)
43	BW	0.38	0/897	0.57	0/1205
43	DW	0.31	0/897	0.52	0/1205
44	BX	0.39	0/764	0.59	1/1025 (0.1%)
44	DX	0.32	0/764	0.56	1/1025 (0.1%)
45	BY	0.34	0/819	0.57	0/1095
45	DY	0.31	0/819	0.55	0/1095
46	BZ	0.31	0/1379	0.61	0/1873
46	DZ	0.29	0/1390	0.57	0/1890
47	B0	0.35	0/662	0.57	0/881
47	D0	0.29	0/662	0.49	0/881
48	B1	0.34	0/762	0.56	0/1014
48	D1	0.32	0/762	0.54	0/1014
49	B2	0.32	0/590	0.56	0/781
49	D2	0.27	0/590	0.46	0/781
50	B3	0.36	0/474	0.58	0/635
50	D3	0.27	0/469	0.50	0/630
51	B4	0.35	0/571	0.71	0/768
51	D4	0.34	0/545	0.70	0/737
52	B5	0.38	0/469	0.60	0/635
52	D5	0.33	0/469	0.52	0/635
53	B6	0.36	0/460	0.51	0/613
53	D6	0.30	0/456	0.48	0/608
54	B7	0.39	0/426	0.55	0/561
54	D7	0.33	0/426	0.59	0/561
55	B8	0.36	0/519	0.58	0/684
55	D8	0.32	0/525	0.52	0/691
56	B9	0.35	0/310	0.51	0/407
56	D9	0.31	0/310	0.56	0/407
All	All	0.40	9/316594 (0.0%)	0.88	410/473970 (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
2	AB	0	4
7	AG	0	2
7	CG	0	1
20	CT	0	1
28	BD	0	1
39	BS	0	1
51	B4	0	2
51	D4	0	1
All	All	0	13

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	N1-C2	-11.01	1.28	1.37
1	CA	1154	G	C6-N1	-10.68	1.32	1.39
1	CA	1119	C	N3-C4	-9.86	1.27	1.33
1	CA	1154	G	N7-C5	-7.17	1.34	1.39
26	BA	330	A	N9-C4	-6.79	1.33	1.37
26	BA	1021	A	N9-C4	-5.85	1.34	1.37
26	DA	2287	A	N9-C4	-5.40	1.34	1.37
1	CA	1154	G	C5-C4	5.28	1.42	1.38
1	CA	1119	C	C2-N3	-5.06	1.31	1.35

All (410) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	32.18	138.21	118.90
1	CA	1154	G	N3-C2-N2	24.48	137.03	119.90
1	CA	1154	G	C5-C6-O6	24.01	143.00	128.60
1	CA	1154	G	N1-C2-N2	-21.95	96.45	116.20
1	CA	1119	C	N3-C2-O2	-20.26	107.72	121.90
1	CA	1119	C	C2-N3-C4	18.04	128.92	119.90
1	CA	1119	C	C2-N1-C1'	16.83	137.32	118.80
1	CA	1154	G	C5-C6-N1	-16.70	103.15	111.50
1	CA	1154	G	C6-N1-C2	15.37	134.32	125.10
1	CA	1119	C	C5-C4-N4	13.49	129.64	120.20
1	CA	1119	C	C6-N1-C1'	-13.30	104.84	120.80
26	DA	2139	C	N1-C2-O2	11.63	125.88	118.90
1	CA	1119	C	N3-C4-N4	-11.16	110.19	118.00
1	CA	1001(A)	G	N3-C4-N9	10.62	132.37	126.00
23	CW	67	C	C5-C6-N1	10.56	126.28	121.00
1	CA	1154	G	C4-N9-C1'	10.47	140.11	126.50
25	AY	64	A	N1-C6-N6	-10.40	112.36	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	CY	23	A	N1-C6-N6	10.31	124.79	118.60
1	CA	1154	G	N1-C6-O6	-10.16	113.81	119.90
25	CY	66	U	C5-C4-O4	-10.02	119.89	125.90
25	AY	64	A	C5-C6-N6	9.87	131.59	123.70
26	BA	330	A	C2-N3-C4	-9.84	105.68	110.60
1	CA	1154	G	C2-N3-C4	-9.82	106.99	111.90
26	DA	2585	U	C5-C4-O4	-9.67	120.10	125.90
26	BA	2140	C	N1-C2-O2	9.55	124.63	118.90
1	CA	1119	C	C6-N1-C2	-9.51	116.49	120.30
26	DA	2174	C	C2-N1-C1'	9.37	129.11	118.80
1	CA	1119	C	C5-C6-N1	9.24	125.62	121.00
26	DA	2139	C	C2-N1-C1'	9.23	128.95	118.80
26	BA	1639	U	O5'-P-OP2	-9.22	97.40	105.70
1	CA	1054	C	P-O3'-C3'	9.21	130.75	119.70
26	DA	2152	G	C5-C6-O6	-9.21	123.08	128.60
1	CA	79	G	C5-C6-O6	9.02	134.01	128.60
24	AX	14	A	C4-C5-C6	8.97	121.48	117.00
1	CA	1154	G	C8-N9-C1'	-8.97	115.34	127.00
25	CY	4	C	N1-C2-O2	8.94	124.27	118.90
24	AX	46	G	C6-N1-C2	-8.94	119.74	125.10
24	CX	46	G	C6-N1-C2	-8.92	119.75	125.10
26	DA	2152	G	N1-C6-O6	8.87	125.22	119.90
26	BA	2140	C	N3-C2-O2	-8.83	115.72	121.90
1	CA	1004	A	O4'-C1'-N9	8.50	115.00	108.20
1	CA	1119	C	N1-C2-N3	-8.44	113.29	119.20
23	CW	7	A	N1-C6-N6	8.42	123.65	118.60
24	AX	14	A	C5-N7-C8	8.39	108.10	103.90
26	BA	1021	A	C2-N3-C4	-8.31	106.45	110.60
1	AA	1030(B)	C	C2-N1-C1'	8.24	127.86	118.80
26	DA	2136	C	N1-C2-O2	8.23	123.84	118.90
1	CA	1001(A)	G	N3-C4-C5	-8.21	124.49	128.60
23	CW	67	C	C2-N3-C4	8.09	123.95	119.90
1	AA	1137	C	C6-N1-C2	-8.06	117.07	120.30
26	BA	2140	C	C2-N1-C1'	8.06	127.67	118.80
25	CY	68	C	C2-N1-C1'	7.99	127.59	118.80
26	DA	2152	G	N9-C4-C5	-7.99	102.20	105.40
26	DA	2152	G	N3-C4-N9	7.99	130.79	126.00
24	CX	14	A	C4-C5-C6	7.97	120.98	117.00
39	BS	67	ARG	NE-CZ-NH1	-7.95	116.32	120.30
1	AA	1036	G	C4-N9-C1'	7.92	136.79	126.50
11	AK	18	ARG	NE-CZ-NH1	-7.89	116.36	120.30
1	CA	1001(A)	G	C4-N9-C1'	7.85	136.70	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C4-C5-C6	7.84	123.51	118.80
26	BA	2140	C	C6-N1-C2	-7.82	117.17	120.30
23	CW	22	G	N3-C2-N2	-7.75	114.47	119.90
1	AA	1030(B)	C	N1-C2-O2	7.75	123.55	118.90
26	DA	2139	C	N3-C2-O2	-7.71	116.50	121.90
26	DA	2152	G	C6-C5-N7	-7.69	125.79	130.40
1	CA	1126	U	C2-N1-C1'	7.68	126.92	117.70
26	BA	226	G	O4'-C1'-N9	7.68	114.34	108.20
26	DA	2167	U	N1-C2-O2	7.67	128.17	122.80
25	CY	66	U	N3-C4-O4	7.66	124.76	119.40
1	AA	1054	C	P-O3'-C3'	7.60	128.81	119.70
1	AA	346	G	C4-N9-C1'	7.56	136.32	126.50
25	CY	68	C	N3-C2-O2	-7.46	116.67	121.90
25	CY	56	C	C2-N1-C1'	7.45	126.99	118.80
1	CA	1001(A)	G	C8-N9-C1'	-7.43	117.34	127.00
25	CY	7	A	C6-N1-C2	-7.43	114.14	118.60
25	CY	68	C	N1-C2-O2	7.39	123.34	118.90
1	CA	1054	C	O4'-C1'-N1	7.39	114.11	108.20
26	BA	887	A	O4'-C1'-N9	7.35	114.08	108.20
26	BA	12	U	C2-N1-C1'	7.29	126.45	117.70
26	BA	1022	G	N3-C2-N2	-7.29	114.80	119.90
26	BA	1963	U	C2-N1-C1'	7.25	126.40	117.70
26	DA	2167	U	C2-N1-C1'	7.25	126.40	117.70
26	DA	2139	C	C6-N1-C1'	-7.22	112.13	120.80
26	DA	2152	G	C4-C5-N7	7.19	113.68	110.80
35	BO	8	LEU	CA-CB-CG	7.19	131.83	115.30
23	CW	45	U	C2-N1-C1'	7.17	126.31	117.70
26	DA	2174	C	C6-N1-C1'	-7.16	112.20	120.80
26	DA	2206	G	C4-N9-C1'	-7.14	117.22	126.50
24	AX	14	A	C5-C6-N1	-7.14	114.13	117.70
23	CW	44	G	C5-C6-O6	-7.13	124.32	128.60
1	AA	254	G	O5'-P-OP1	-7.09	99.32	105.70
1	AA	1036	G	C8-N9-C1'	-7.08	117.79	127.00
26	DA	2155	G	N3-C2-N2	7.07	124.85	119.90
26	BA	512	G	O4'-C1'-N9	7.04	113.83	108.20
26	DA	2167	U	N3-C2-O2	-7.03	117.28	122.20
24	AX	22	G	C5-N7-C8	-7.00	100.80	104.30
26	DA	2152	G	C8-N9-C1'	-6.95	117.96	127.00
26	DA	1372	U	C5-C4-O4	-6.92	121.75	125.90
26	DA	2137	C	C6-N1-C2	-6.90	117.54	120.30
1	AA	1137	C	C5-C6-N1	6.88	124.44	121.00
25	CY	23	A	C6-C5-N7	-6.85	127.51	132.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	67	C	C2-N1-C1'	6.84	126.32	118.80
26	DA	2155	G	C6-N1-C2	6.83	129.20	125.10
23	CW	22	G	N3-C4-N9	-6.82	121.91	126.00
26	DA	893	C	C2-N1-C1'	6.82	126.30	118.80
26	DA	2585	U	C6-N1-C1'	-6.80	111.67	121.20
25	AY	5	G	N3-C4-N9	6.80	130.08	126.00
44	DX	57	LEU	CA-CB-CG	6.80	130.94	115.30
26	DA	2585	U	C2-N1-C1'	6.79	125.85	117.70
1	AA	346	G	O4'-C1'-N9	6.76	113.61	108.20
26	BA	271(M)	G	OP1-P-O3'	6.75	120.05	105.20
44	BX	57	LEU	CA-CB-CG	6.75	130.82	115.30
26	BA	624	C	O5'-P-OP1	-6.73	99.64	105.70
1	CA	1003	G	C4-N9-C1'	6.73	135.25	126.50
24	AX	22	G	C4-C5-C6	-6.69	114.79	118.80
23	CW	45	U	N1-C2-O2	6.69	127.48	122.80
1	CA	1154	G	N3-C4-N9	6.66	130.00	126.00
25	AY	4	C	N3-C2-O2	-6.61	117.27	121.90
26	BA	748	G	O4'-C1'-N9	6.61	113.49	108.20
1	CA	754	C	C2-N1-C1'	6.59	126.05	118.80
23	CW	7	A	C5-C6-N6	-6.57	118.45	123.70
26	DA	2152	G	C4-N9-C1'	6.55	135.02	126.50
25	CY	7	A	C5-C6-N1	6.53	120.96	117.70
1	CA	1001(A)	G	C6-C5-N7	-6.51	126.49	130.40
26	BA	2061	G	O5'-P-OP2	-6.50	99.84	105.70
23	CW	67	C	N1-C2-O2	6.49	122.79	118.90
25	AY	4	C	N1-C2-O2	6.48	122.79	118.90
26	BA	1142(A)	A	C2-N3-C4	-6.48	107.36	110.60
25	CY	56	C	C6-N1-C1'	-6.48	113.03	120.80
24	CX	22	G	N1-C6-O6	-6.45	116.03	119.90
25	CY	7	A	N3-C4-N9	6.45	132.56	127.40
23	CW	67	C	C6-N1-C2	-6.44	117.72	120.30
25	AY	33	U	N3-C2-O2	-6.42	117.71	122.20
26	DA	1372	U	N3-C4-O4	6.41	123.89	119.40
26	BA	330	A	N1-C2-N3	6.39	132.50	129.30
1	CA	998	G	N3-C4-N9	-6.39	122.17	126.00
26	BA	141	A	N7-C8-N9	6.38	116.99	113.80
25	AY	58	A	C4-N9-C1'	6.37	137.76	126.30
23	CW	66	U	C2-N1-C1'	6.36	125.33	117.70
26	BA	1992	G	P-O3'-C3'	6.36	127.33	119.70
24	AX	22	G	N3-C4-N9	-6.32	122.21	126.00
26	DA	2206	G	C8-N9-C1'	6.31	135.21	127.00
1	AA	1054	C	N3-C2-O2	-6.31	117.48	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	372	G	O4'-C1'-N9	6.30	113.24	108.20
23	CW	3	C	N1-C2-O2	6.29	122.67	118.90
26	BA	1256	G	N9-C4-C5	-6.28	102.89	105.40
1	AA	1397	C	C2-N1-C1'	6.28	125.70	118.80
1	AA	346	G	C8-N9-C4	-6.27	103.89	106.40
26	BA	330	A	N3-C4-C5	6.27	131.19	126.80
26	DA	1531	C	C2-N1-C1'	6.25	125.68	118.80
26	BA	1300	U	P-O3'-C3'	6.25	127.19	119.70
24	CX	46	G	C5-C6-N1	6.24	114.62	111.50
23	AW	15	G	N3-C2-N2	6.24	124.27	119.90
25	AY	69	G	N3-C4-N9	6.24	129.74	126.00
1	CA	1003	G	N7-C8-N9	6.20	116.20	113.10
23	AW	48	C	N1-C2-O2	-6.20	115.18	118.90
1	CA	1154	G	N3-C4-C5	-6.19	125.50	128.60
1	CA	96	U	O4'-C1'-N1	6.19	113.15	108.20
25	CY	23	A	C4-C5-C6	6.18	120.09	117.00
25	CY	23	A	C5-C6-N6	-6.17	118.77	123.70
25	AY	33	U	C2-N1-C1'	6.16	125.09	117.70
1	CA	1030(B)	C	C5-C6-N1	6.15	124.08	121.00
25	AY	68	C	N1-C2-O2	6.13	122.58	118.90
24	AX	14	A	C8-N9-C1'	-6.13	116.67	127.70
26	BA	1176	G	OP1-P-O3'	6.13	118.69	105.20
25	CY	4	C	N3-C2-O2	-6.13	117.61	121.90
1	AA	1054	C	C6-N1-C2	-6.12	117.85	120.30
1	CA	1052	U	N1-C2-O2	6.11	127.08	122.80
1	AA	1030(B)	C	N3-C2-O2	-6.11	117.62	121.90
1	CA	1256	A	O4'-C1'-N9	-6.11	103.31	108.20
1	CA	1119	C	C4-C5-C6	-6.11	114.35	117.40
26	BA	528	A	C2-N3-C4	-6.10	107.55	110.60
24	CX	46	G	N3-C2-N2	-6.07	115.65	119.90
1	CA	1064	G	P-O3'-C3'	6.07	126.98	119.70
25	AY	50	U	C2-N3-C4	6.05	130.63	127.00
26	BA	2036	C	O5'-P-OP1	-6.04	100.26	105.70
26	BA	330	A	N3-C4-N9	-6.04	122.57	127.40
1	CA	754	C	N1-C2-O2	6.00	122.50	118.90
26	BA	141	A	C5-N7-C8	-6.00	100.90	103.90
26	BA	787	U	O5'-P-OP1	-5.99	100.31	105.70
26	BA	271(M)	G	P-O3'-C3'	5.99	126.89	119.70
26	DA	1531	C	N1-C2-O2	5.98	122.49	118.90
26	DA	2140	C	C2-N1-C1'	5.98	125.38	118.80
25	AY	33	U	N1-C2-O2	5.97	126.98	122.80
1	CA	1030	C	C2-N1-C1'	5.96	125.36	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	2248	C	O5'-P-OP2	-5.95	100.34	105.70
1	CA	65	U	P-O3'-C3'	5.95	126.84	119.70
1	AA	1030(B)	C	C6-N1-C1'	-5.94	113.67	120.80
26	BA	1992	G	C8-N9-C4	-5.94	104.02	106.40
26	BA	1776	G	O5'-P-OP2	-5.94	100.35	105.70
23	CW	22	G	N9-C4-C5	5.94	107.78	105.40
26	BA	2615	U	O5'-P-OP1	-5.92	100.37	105.70
39	BS	67	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	CA	1030(B)	C	C6-N1-C2	-5.92	117.93	120.30
26	BA	933	A	O4'-C1'-N9	5.92	112.93	108.20
25	AY	69	G	N3-C4-C5	-5.91	125.64	128.60
1	AA	347	G	P-O3'-C3'	5.91	126.79	119.70
23	AW	3	C	C2-N1-C1'	5.91	125.30	118.80
26	BA	1021	A	N1-C2-N3	5.91	132.25	129.30
25	CY	56	C	N1-C2-O2	5.89	122.43	118.90
24	AX	46	G	C5-C6-N1	5.88	114.44	111.50
26	DA	614	U	N3-C2-O2	-5.88	118.08	122.20
24	AX	22	G	C8-N9-C1'	5.86	134.62	127.00
24	AX	14	A	C4-N9-C1'	5.86	136.84	126.30
1	CA	687	A	P-O3'-C3'	5.85	126.72	119.70
23	CW	3	C	C2-N3-C4	5.84	122.82	119.90
1	CA	1023	G	N3-C4-N9	5.83	129.50	126.00
24	CX	14	A	C5-N7-C8	5.82	106.81	103.90
1	CA	1067	A	P-O3'-C3'	5.81	126.67	119.70
26	DA	2139	C	C5-C6-N1	5.81	123.91	121.00
1	CA	997	U	C5-C4-O4	5.79	129.38	125.90
26	BA	1022	G	N3-C4-N9	-5.76	122.54	126.00
1	AA	839	U	P-O3'-C3'	5.75	126.60	119.70
23	CW	66	U	P-O3'-C3'	5.74	126.59	119.70
26	BA	1828	G	C5-C6-O6	-5.73	125.16	128.60
26	BA	528	A	C5-N7-C8	-5.73	101.04	103.90
25	AY	35	A	O5'-P-OP2	-5.72	100.55	105.70
26	BA	845	G	O4'-C1'-N9	5.71	112.77	108.20
26	DA	1204	A	O4'-C1'-N9	5.70	112.76	108.20
1	CA	1039	C	N1-C2-O2	5.69	122.32	118.90
26	BA	1493	C	N1-C2-O2	5.69	122.31	118.90
1	CA	1125	U	O3'-P-O5'	5.69	114.81	104.00
26	BA	1963	U	N1-C2-O2	5.68	126.78	122.80
23	CW	45	U	C6-N1-C1'	-5.68	113.25	121.20
1	AA	1067	A	P-O3'-C3'	5.68	126.51	119.70
1	CA	1039	C	C5-C4-N4	-5.68	116.23	120.20
1	CA	1001(A)	G	N9-C4-C5	-5.67	103.13	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	DE	72	VAL	C-N-CA	5.66	135.86	121.70
1	CA	79	G	N1-C6-O6	-5.66	116.50	119.90
1	AA	1054	C	C2-N1-C1'	5.66	125.02	118.80
25	CY	5	G	N3-C4-C5	-5.64	125.78	128.60
1	AA	1125	U	P-O3'-C3'	5.64	126.47	119.70
25	CY	50	U	C5-C4-O4	5.64	129.28	125.90
1	AA	346	G	N3-C4-C5	-5.63	125.79	128.60
42	DV	100	ARG	NE-CZ-NH1	5.63	123.11	120.30
26	DA	214	G	O4'-C1'-N9	5.62	112.70	108.20
26	DA	2137	C	O4'-C1'-N1	5.61	112.69	108.20
26	DA	893	C	N1-C2-O2	5.60	122.26	118.90
23	AW	22	G	N1-C6-O6	5.60	123.26	119.90
26	BA	1372	U	N3-C4-O4	5.59	123.32	119.40
1	CA	1154	G	C5-N7-C8	5.59	107.09	104.30
26	DA	748	G	C4-N9-C1'	-5.59	119.24	126.50
1	CA	1021	G	O4'-C1'-N9	5.58	112.66	108.20
1	AA	346	G	C8-N9-C1'	-5.57	119.76	127.00
26	BA	1176	G	P-O3'-C3'	5.57	126.38	119.70
26	DA	1937	A	O4'-C1'-N9	5.56	112.65	108.20
42	DV	38	LEU	CA-CB-CG	5.56	128.09	115.30
25	AY	58	A	C8-N9-C1'	-5.56	117.69	127.70
1	AA	1022	G	N3-C2-N2	5.55	123.78	119.90
1	CA	1126	U	N1-C2-O2	5.55	126.68	122.80
1	CA	1493	A	P-O3'-C3'	5.55	126.36	119.70
26	DA	2174	C	C5-C6-N1	5.54	123.77	121.00
1	CA	1225	A	C5-C6-N6	5.53	128.13	123.70
23	CW	6	G	C4-C5-N7	5.53	113.01	110.80
23	CW	6	G	N9-C4-C5	-5.53	103.19	105.40
24	AX	22	G	N3-C4-C5	5.53	131.36	128.60
1	AA	991	U	P-O3'-C3'	5.52	126.33	119.70
25	AY	58	A	P-O3'-C3'	5.52	126.33	119.70
25	CY	69	G	N3-C4-N9	5.52	129.31	126.00
26	DA	2140	C	N1-C2-O2	5.52	122.21	118.90
26	BA	570	G	C5-C6-O6	-5.52	125.29	128.60
26	BA	1256	G	C4-C5-N7	5.52	113.01	110.80
24	CX	34	C	C2-N1-C1'	5.52	124.87	118.80
25	CY	68	C	C6-N1-C1'	-5.51	114.19	120.80
24	AX	67	C	N1-C2-O2	5.50	122.20	118.90
26	DA	2139	C	N3-C4-C5	5.49	124.10	121.90
1	AA	1028	C	O4'-C1'-N1	5.48	112.59	108.20
1	CA	1154	G	C6-C5-N7	-5.48	127.11	130.40
26	DA	383	U	O4'-C1'-N1	5.48	112.58	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	1936	A	O4'-C1'-N9	5.46	112.57	108.20
1	CA	90	U	N1-C2-N3	5.46	118.18	114.90
26	BA	1187	G	N1-C6-O6	-5.46	116.62	119.90
26	BA	383	U	C2-N1-C1'	-5.46	111.15	117.70
26	BA	2789	C	N1-C2-O2	-5.46	115.62	118.90
1	AA	1054	C	N1-C2-O2	5.46	122.17	118.90
1	CA	1286	A	C8-N9-C4	-5.45	103.62	105.80
26	BA	2689	U	N3-C2-O2	-5.45	118.39	122.20
1	AA	1285	A	P-O3'-C3'	5.44	126.23	119.70
26	BA	847	U	C2-N1-C1'	-5.44	111.17	117.70
26	BA	12	U	N1-C2-O2	5.43	126.60	122.80
26	DA	1300	U	P-O3'-C3'	5.43	126.22	119.70
24	CX	22	G	C5-N7-C8	-5.43	101.59	104.30
26	DA	2685	G	N1-C6-O6	-5.42	116.65	119.90
1	AA	347	G	OP1-P-O3'	5.41	117.09	105.20
26	DA	2585	U	O4'-C1'-N1	-5.40	103.88	108.20
26	DA	2321	G	C4-N9-C1'	5.40	133.52	126.50
1	AA	1502	A	N1-C2-N3	5.39	132.00	129.30
1	AA	97	G	N3-C4-N9	5.39	129.24	126.00
26	BA	1530	C	P-O3'-C3'	5.38	126.16	119.70
23	CW	26	A	C5-C6-N6	-5.38	119.39	123.70
26	DA	1313	U	C2-N1-C1'	5.38	124.16	117.70
23	AW	50	U	C5-C4-O4	-5.38	122.67	125.90
26	BA	1204	A	O4'-C1'-N9	5.38	112.50	108.20
25	CY	7	A	C6-C5-N7	-5.38	128.54	132.30
26	BA	945	A	C2-N3-C4	-5.38	107.91	110.60
26	BA	576	U	O5'-P-OP1	-5.37	100.86	105.70
26	BA	1698	A	O4'-C1'-N9	5.37	112.50	108.20
1	CA	1286	A	N7-C8-N9	5.37	116.48	113.80
26	BA	944	G	C4-N9-C1'	5.36	133.47	126.50
25	CY	5	G	O4'-C1'-N9	5.36	112.49	108.20
1	CA	1529	G	C4-N9-C1'	5.36	133.47	126.50
1	AA	1278	U	C5-C6-N1	5.36	125.38	122.70
26	DA	1530	C	P-O3'-C3'	5.36	126.13	119.70
25	CY	68	C	C6-N1-C2	-5.35	118.16	120.30
25	CY	5	G	C2-N3-C4	5.35	114.58	111.90
24	CX	46	G	C5-C6-O6	-5.35	125.39	128.60
26	DA	1698	A	O4'-C1'-N9	5.35	112.48	108.20
23	CW	67	C	C4-C5-C6	-5.34	114.73	117.40
1	AA	1042	G	O4'-C1'-N9	5.34	112.47	108.20
2	CB	187	LEU	CA-CB-CG	5.34	127.58	115.30
26	BA	12	U	N3-C2-O2	-5.33	118.47	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	2593	U	N3-C4-O4	-5.33	115.67	119.40
1	AA	1030(B)	C	C6-N1-C2	-5.32	118.17	120.30
25	CY	5	G	N3-C4-N9	5.32	129.19	126.00
1	CA	1126	U	C6-N1-C1'	-5.31	113.76	121.20
25	CY	24	G	N3-C4-N9	5.31	129.19	126.00
25	AY	50	U	N3-C4-C5	-5.31	111.42	114.60
1	CA	992	U	P-O3'-C3'	5.30	126.06	119.70
1	CA	1206	G	C5-C6-O6	-5.30	125.42	128.60
26	BA	1614	A	O5'-P-OP1	-5.30	100.93	105.70
26	BA	1045	A	O5'-P-OP1	5.29	117.04	110.70
1	CA	1502	A	N1-C2-N3	5.29	131.94	129.30
26	BA	1175	U	P-O3'-C3'	5.28	126.04	119.70
23	CW	66	U	C5-C6-N1	5.28	125.34	122.70
4	AD	174	LEU	CA-CB-CG	5.26	127.41	115.30
23	AW	3	C	N1-C2-O2	5.26	122.06	118.90
1	CA	79	G	C6-N1-C2	5.26	128.25	125.10
26	DA	2629	A	O4'-C1'-N9	5.25	112.40	108.20
4	AD	188	LEU	CA-CB-CG	5.24	127.36	115.30
1	CA	1323	G	N3-C4-N9	5.24	129.15	126.00
5	CE	12	LEU	CA-CB-CG	5.24	127.35	115.30
25	CY	60	U	N3-C2-O2	-5.24	118.53	122.20
24	AX	22	G	C4-N9-C1'	-5.24	119.69	126.50
26	BA	1315	C	O5'-P-OP2	-5.24	100.99	105.70
1	CA	1126	U	P-O5'-C5'	5.23	129.27	120.90
1	CA	1126	U	C5-C6-N1	5.22	125.31	122.70
1	CA	1158	C	C2-N1-C1'	5.22	124.55	118.80
25	CY	7	A	N9-C4-C5	-5.22	103.71	105.80
26	BA	2789	C	C2-N1-C1'	-5.21	113.07	118.80
26	BA	1963	U	C6-N1-C1'	-5.21	113.91	121.20
1	CA	1003	G	C8-N9-C4	-5.21	104.32	106.40
1	CA	1183	A	P-O3'-C3'	5.21	125.95	119.70
1	CA	1158	C	N1-C2-O2	5.20	122.02	118.90
26	DA	2554	U	O5'-P-OP2	-5.20	101.02	105.70
26	DA	2154	G	N9-C1'-C2'	-5.20	106.28	112.00
1	CA	1220	G	N3-C4-N9	-5.20	122.88	126.00
1	CA	998	G	N9-C4-C5	5.19	107.48	105.40
26	BA	481	G	O4'-C1'-N9	5.19	112.35	108.20
26	BA	195	A	P-O3'-C3'	5.19	125.92	119.70
26	BA	141	A	O4'-C1'-N9	5.18	112.35	108.20
26	BA	527	C	N3-C2-O2	-5.18	118.27	121.90
26	DA	945	A	O4'-C1'-N9	5.18	112.35	108.20
25	CY	7	A	C5-C6-N6	-5.18	119.56	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1150	U	C2-N3-C4	5.17	130.10	127.00
1	AA	1502	A	N7-C8-N9	5.17	116.39	113.80
1	CA	1030	C	C6-N1-C1'	-5.17	114.59	120.80
1	AA	754	C	C2-N1-C1'	5.17	124.49	118.80
26	BA	2791	C	C6-N1-C2	-5.17	118.23	120.30
25	AY	5	G	N3-C4-C5	-5.17	126.02	128.60
1	AA	97	G	N3-C4-C5	-5.16	126.02	128.60
1	CA	848	C	C5-C6-N1	5.16	123.58	121.00
26	DA	2137	C	C6-N1-C1'	5.16	126.99	120.80
26	DA	914	C	N1-C2-O2	5.15	121.99	118.90
26	DA	748	G	C8-N9-C1'	5.15	133.69	127.00
1	CA	266	G	C4-N9-C1'	5.14	133.19	126.50
26	BA	265	A	O4'-C1'-N9	5.14	112.31	108.20
26	BA	1021	A	C5-N7-C8	-5.13	101.33	103.90
26	BA	2471	C	N1-C2-O2	5.13	121.98	118.90
25	AY	6	G	N9-C4-C5	-5.12	103.35	105.40
25	AY	18	G	C4-N9-C1'	-5.12	119.84	126.50
25	AY	45	U	C5-C6-N1	5.12	125.26	122.70
1	CA	60	A	P-O3'-C3'	5.12	125.84	119.70
1	CA	1158	C	C6-N1-C2	-5.11	118.26	120.30
25	CY	69	G	N3-C4-C5	-5.11	126.05	128.60
24	CX	22	G	C4-C5-C6	-5.10	115.74	118.80
26	BA	517	C	C6-N1-C2	-5.10	118.26	120.30
26	BA	2187	G	C5-C6-O6	5.10	131.66	128.60
23	CW	66	U	C5-C4-O4	-5.10	122.84	125.90
22	CV	24	A	O4'-C1'-N9	5.09	112.28	108.20
25	CY	9	A	C4-C5-C6	-5.09	114.45	117.00
1	AA	1397	C	O4'-C1'-N1	5.09	112.27	108.20
26	DA	893	C	C6-N1-C2	-5.08	118.27	120.30
26	DA	2430	A	O4'-C1'-N9	5.08	112.26	108.20
26	DA	893	C	C5-C6-N1	5.08	123.54	121.00
26	DA	2621	A	C8-N9-C4	5.07	107.83	105.80
26	DA	214	G	C4-N9-C1'	-5.07	119.91	126.50
26	DA	1992	G	P-O3'-C3'	5.06	125.78	119.70
1	CA	1003	G	C8-N9-C1'	-5.06	120.42	127.00
1	CA	955	U	C2-N3-C4	5.06	130.04	127.00
1	AA	346	G	N7-C8-N9	5.06	115.63	113.10
1	CA	79	G	N3-C4-N9	-5.06	122.97	126.00
1	CA	90	U	O4'-C1'-N1	5.06	112.25	108.20
26	BA	2848	G	O4'-C1'-N9	5.05	112.24	108.20
26	DA	1558	A	P-O3'-C3'	5.05	125.77	119.70
23	CW	22	G	N1-C2-N2	5.05	120.75	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	1791	A	O5'-P-OP1	-5.05	101.16	105.70
26	DA	2136	C	N3-C2-O2	-5.04	118.37	121.90
26	BA	2553	G	N3-C4-C5	-5.04	126.08	128.60
25	AY	65	G	N9-C4-C5	5.04	107.42	105.40
1	AA	98	G	N3-C4-N9	5.04	129.02	126.00
26	BA	383	U	O4'-C1'-N1	5.04	112.23	108.20
1	AA	1035	A	N1-C2-N3	5.03	131.82	129.30
40	BT	118	ARG	NE-CZ-NH1	5.02	122.81	120.30
26	DA	512	G	O4'-C1'-N9	5.02	112.22	108.20
26	DA	1131	G	O4'-C1'-N9	5.01	112.21	108.20
26	DA	1899	G	N3-C4-N9	5.01	129.01	126.00
26	BA	774	A	C8-N9-C4	-5.01	103.80	105.80
26	BA	933	A	N7-C8-N9	5.01	116.30	113.80
26	DA	90	U	C2-N1-C1'	5.00	123.70	117.70
26	DA	2140	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	18	GLY	Peptide
2	AB	231	GLU	Peptide
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	78	ARG	Peptide
7	AG	79	ARG	Peptide
51	B4	52	THR	Peptide
51	B4	59	PHE	Peptide
28	BD	274	ARG	Peptide
39	BS	58	LEU	Peptide
7	CG	78	ARG	Peptide
20	CT	9	ASN	Peptide
51	D4	67	TYR	Peptide

5.2 Too-close contacts ⓘ

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	AA	32205	0	16254	495	0
1	CA	32312	0	16307	663	0
2	AB	1846	0	1867	92	0
2	CB	1825	0	1828	102	0
3	AC	1552	0	1546	53	0
3	CC	1542	0	1517	81	0
4	AD	1659	0	1676	73	0
4	CD	1674	0	1714	61	0
5	AE	1129	0	1185	34	0
5	CE	1133	0	1191	33	0
6	AF	806	0	793	24	0
6	CF	816	0	808	18	0
7	AG	1231	0	1238	28	0
7	CG	1235	0	1249	37	0
8	AH	1088	0	1126	26	0
8	CH	1088	0	1126	42	0
9	AI	983	0	986	47	0
9	CI	978	0	966	47	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	36	0
11	AK	829	0	825	20	0
11	CK	833	0	836	14	0
12	AL	930	0	980	24	0
12	CL	930	0	980	27	0
13	AM	958	0	1002	31	0
13	CM	950	0	988	39	0
14	AN	492	0	529	16	0
14	CN	492	0	529	33	0
15	AO	728	0	760	20	0
15	CO	728	0	760	31	0
16	AP	681	0	697	12	0
16	CP	677	0	686	23	0
17	AQ	823	0	891	22	0
17	CQ	823	0	891	15	0
18	AR	555	0	618	17	0
18	CR	555	0	618	16	0
19	AS	652	0	662	31	0
19	CS	646	0	644	42	0
20	AT	728	0	798	32	0
20	CT	727	0	796	25	0
21	AU	199	0	208	8	0
21	CU	199	0	208	10	0
22	AV	277	0	140	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	CV	252	0	130	7	0
23	AW	1607	0	839	55	0
23	CW	1560	0	803	55	0
24	AX	1625	0	828	34	0
24	CX	1625	0	828	33	0
25	AY	1581	0	805	96	0
25	CY	1561	0	796	79	0
26	BA	60729	0	30621	669	0
26	DA	60311	0	30409	876	0
27	BB	2573	0	1306	19	0
27	DB	2573	0	1306	50	0
28	BD	2136	0	2218	51	0
28	DD	2136	0	2218	61	0
29	BE	1559	0	1618	30	0
29	DE	1559	0	1618	45	0
30	BF	1584	0	1625	47	0
30	DF	1580	0	1619	50	0
31	BG	1425	0	1443	38	0
31	DG	1424	0	1434	66	0
32	BH	1330	0	1407	28	0
32	DH	1330	0	1407	30	0
33	BI	1085	0	1114	41	0
33	DI	1061	0	1080	25	0
34	BN	1117	0	1183	17	0
34	DN	1117	0	1184	27	0
35	BO	933	0	996	20	0
35	DO	933	0	996	29	0
36	BP	1135	0	1212	38	0
36	DP	1135	0	1212	43	0
37	BQ	1122	0	1179	31	0
37	DQ	1122	0	1179	35	0
38	BR	968	0	1033	18	0
38	DR	968	0	1033	28	0
39	BS	877	0	938	23	0
39	DS	870	0	923	34	0
40	BT	1091	0	1151	27	0
40	DT	1083	0	1136	31	0
41	BU	959	0	1019	17	0
41	DU	959	0	1019	38	0
42	BV	771	0	830	13	0
42	DV	771	0	830	25	0
43	BW	886	0	939	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	DW	886	0	940	9	0
44	BX	750	0	814	16	0
44	DX	750	0	814	23	0
45	BY	806	0	881	23	0
45	DY	806	0	881	26	0
46	BZ	1349	0	1355	44	0
46	DZ	1360	0	1363	61	0
47	B0	653	0	674	14	0
47	D0	653	0	674	20	0
48	B1	755	0	826	18	0
48	D1	755	0	826	18	0
49	B2	588	0	643	11	0
49	D2	588	0	643	12	0
50	B3	469	0	518	9	0
50	D3	464	0	514	12	0
51	B4	558	0	544	22	0
51	D4	532	0	503	31	0
52	B5	455	0	465	11	0
52	D5	455	0	465	12	0
53	B6	453	0	473	13	0
53	D6	449	0	469	9	0
54	B7	418	0	467	9	0
54	D7	418	0	467	10	0
55	B8	511	0	571	21	0
55	D8	517	0	582	10	0
56	B9	307	0	335	7	0
56	D9	307	0	335	13	0
57	AA	214	0	0	0	0
57	AE	3	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AM	1	0	0	0	0
57	AN	2	0	0	0	0
57	AW	4	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	3	0	0	0	0
57	B1	1	0	0	0	0
57	B2	1	0	0	0	0
57	B3	2	0	0	0	0
57	B4	1	0	0	0	0
57	B5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	1	0	0	0	0
57	B9	1	0	0	0	0
57	BA	812	0	0	0	0
57	BB	20	0	0	0	0
57	BD	9	0	0	0	0
57	BE	8	0	0	0	0
57	BF	9	0	0	0	0
57	BG	3	0	0	0	0
57	BN	6	0	0	0	0
57	BO	2	0	0	0	0
57	BP	5	0	0	0	0
57	BQ	5	0	0	0	0
57	BR	2	0	0	0	0
57	BU	8	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	3	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	1	0	0	0	0
57	CA	170	0	0	0	0
57	CD	1	0	0	0	0
57	CE	1	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CV	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	3	0	0	1	0
57	D0	1	0	0	0	0
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0
57	DA	677	0	0	0	0
57	DB	13	0	0	0	0
57	DD	9	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	DP	2	0	0	0	0
57	DQ	4	0	0	0	0
57	DR	1	0	0	0	0
57	DU	2	0	0	0	0
57	DV	3	0	0	0	0
57	DW	4	0	0	0	0
57	DX	1	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	0	0
58	CD	8	0	0	0	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	227	0	0	17	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	1	0	0	1	0
61	AM	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	3	0	0	0	0
61	AW	3	0	0	0	0
61	AX	6	0	0	2	0
61	AY	1	0	0	0	0
61	B0	3	0	0	0	0
61	B1	1	0	0	0	0
61	B3	2	0	0	0	0
61	B5	2	0	0	0	0
61	B6	1	0	0	0	0
61	B7	2	0	0	0	0
61	B8	8	0	0	1	0
61	BA	1383	0	0	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BB	36	0	0	1	0
61	BD	12	0	0	1	0
61	BE	14	0	0	4	0
61	BF	8	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BO	4	0	0	0	0
61	BP	16	0	0	3	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	3	0	0	0	0
61	BV	2	0	0	0	0
61	BW	1	0	0	0	0
61	BX	4	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	185	0	0	17	0
61	CJ	2	0	0	1	0
61	CL	1	0	0	0	0
61	CT	1	0	0	0	0
61	CV	1	0	0	0	0
61	CW	2	0	0	0	0
61	D0	3	0	0	0	0
61	D1	1	0	0	0	0
61	D3	1	0	0	1	0
61	D7	3	0	0	0	0
61	D8	4	0	0	0	0
61	DA	1025	0	0	79	0
61	DB	9	0	0	0	0
61	DD	19	0	0	4	0
61	DE	11	0	0	0	0
61	DF	3	0	0	0	0
61	DN	2	0	0	1	0
61	DO	1	0	0	0	0
61	DP	16	0	0	2	0
61	DR	1	0	0	0	0
61	DT	3	0	0	0	0
61	DU	2	0	0	0	0
61	DX	3	0	0	0	0
61	DY	2	0	0	0	0
All	All	297141	0	196251	5228	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 (5228) 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)
25:CY:7:A:N6	25:CY:66:U:H3	1.37	1.21
25:AY:49:C:N4	25:AY:65:G:H1	1.44	1.16
26:DA:2139:C:N4	26:DA:2152:G:H1	1.42	1.16
1:CA:1000:U:H3	1:CA:1041:A:N6	1.44	1.15
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.12
26:BA:2136:C:N4	26:BA:2155:G:H1	1.51	1.08
26:DA:2138:C:N4	26:DA:2153:G:H1	1.54	1.03
26:DA:2121:G:H1	26:DA:2177:C:N4	1.54	1.02
23:AW:26:A:H61	23:AW:44:G:H1	1.04	1.02
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.36	1.01
25:CY:19:G:N2	25:CY:56:C:N3	2.08	1.01
25:CY:19:G:H1	25:CY:56:C:N4	1.58	1.01
1:CA:999:C:H42	1:CA:1042:G:H1	1.07	1.01
25:CY:50:U:H3	25:CY:64:A:N6	1.58	1.00
26:BA:1019:U:HO2'	26:BA:1021:A:H2	1.07	1.00
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.44	1.00
1:CA:1162:C:H42	1:CA:1174:G:H1	1.01	0.99
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.41	0.98
25:CY:8:4SU:HN3	25:CY:14:A:H62	1.10	0.98
26:DA:2124:G:H1	26:DA:2174:C:N4	1.62	0.97
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.47	0.97
26:BA:993:G:OP1	41:BU:50:ARG:NH2	1.98	0.97
25:AY:7:A:H61	25:AY:66:U:H3	1.11	0.97
1:CA:1162:C:N4	1:CA:1174:G:H1	1.63	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.10	0.96
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.48	0.95
23:CW:66:U:H3'	23:CW:67:C:H5''	1.49	0.95
26:BA:2123:G:H1	26:BA:2175:C:H42	1.12	0.95
25:CY:51:U:H3	25:CY:63:G:H1	1.13	0.95
27:DB:22:U:H3	27:DB:61:G:H1	1.11	0.94
25:AY:49:C:N3	25:AY:65:G:N2	2.14	0.94
24:AX:5:G:H1	24:AX:68:C:N4	1.65	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.66	0.93
42:DV:100:ARG:HH11	42:DV:100:ARG:HG3	1.33	0.93
23:AW:29:G:H1	23:AW:41:C:H42	1.16	0.93
25:CY:50:U:H3	25:CY:64:A:H61	0.96	0.92
1:CA:76:C:H42	1:CA:93:G:H1	0.97	0.92
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2136:C:H42	26:BA:2155:G:H1	0.96	0.92
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.02	0.92
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.51	0.91
23:AW:50:U:H3	23:AW:64:A:H61	1.02	0.91
26:DA:2124:G:H1	26:DA:2174:C:H42	1.17	0.91
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.04	0.91
26:DA:1204:A:H2	26:DA:1241:A:H62	1.19	0.90
24:AX:5:G:H1	24:AX:68:C:H42	0.92	0.90
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.07	0.89
25:CY:15:G:N1	25:CY:48:C:N3	2.19	0.89
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
25:AY:26:A:H61	25:AY:44:G:H1	1.14	0.88
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.56	0.88
1:CA:1000:U:H3	1:CA:1041:A:H61	0.88	0.88
1:CA:1502:A:H2	1:CA:1505:G:H1	1.22	0.87
1:CA:1002:G:N2	1:CA:1038:C:N3	2.23	0.87
1:AA:664:G:H22	1:AA:741:G:H1	1.19	0.87
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.07	0.87
23:AW:50:U:H3	23:AW:64:A:N6	1.71	0.87
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.08	0.87
23:AW:76:31M:H5'	23:AW:76:31M:H8	1.56	0.87
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.86
26:DA:1689:A:H62	26:DA:1698:A:H2	1.20	0.86
29:BE:47:VAL:HG21	29:BE:86:PRO:HD2	1.57	0.86
1:AA:1025:U:O2	1:AA:1036:G:O6	1.93	0.86
26:DA:397:G:N7	61:DA:4625:HOH:O	2.08	0.86
1:CA:664:G:H22	1:CA:741:G:H1	1.24	0.86
26:DA:827:U:OP1	61:DA:4303:HOH:O	1.91	0.85
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.10	0.85
26:DA:1169:G:H1	26:DA:1180:C:H42	1.23	0.85
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.58	0.85
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.59	0.85
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.58	0.84
26:DA:2430:A:OP2	61:DA:4303:HOH:O	1.94	0.84
26:BA:1689:A:H62	26:BA:1698:A:H2	1.25	0.84
26:DA:2138:C:N3	26:DA:2153:G:N2	2.24	0.84
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
7:CG:79:ARG:HE	7:CG:80:VAL:HG23	1.42	0.84
26:BA:100:G:O2'	49:B2:7:ARG:NH2	2.10	0.84
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.60	0.84
26:BA:2287:A:H62	26:BA:2344:U:H3	1.23	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.11	0.84
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.60	0.83
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.11	0.83
23:AW:26:A:N6	23:AW:44:G:H1	1.75	0.83
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.44	0.83
29:DE:11:MET:HG2	29:DE:24:THR:HB	1.61	0.82
10:CJ:7:LYS:HG3	10:CJ:71:LEU:HD12	1.60	0.82
23:AW:6:G:H1	23:AW:67:C:N4	1.77	0.82
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.59	0.82
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.62	0.82
25:AY:50:U:O4	25:AY:64:A:N1	2.13	0.82
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.12	0.82
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.59	0.82
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.60	0.82
26:BA:885:C:H3'	26:BA:886:C:H5''	1.61	0.82
25:CY:31:A:N1	25:CY:39:PSU:O2	2.13	0.82
25:CY:19:G:H1	25:CY:56:C:H42	0.85	0.82
23:CW:4:C:N4	23:CW:69:G:H1	1.77	0.82
26:BA:2100:G:H1	26:BA:2189:U:H3	1.27	0.82
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
4:AD:158:ILE:H	4:AD:158:ILE:HD13	1.45	0.81
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.29	0.81
26:DA:2139:C:H42	26:DA:2152:G:H1	0.83	0.81
1:CA:1029:C:N4	1:CA:1032:G:N1	2.29	0.81
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.62	0.81
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.61	0.81
1:CA:1153:C:H42	1:CA:1154:G:H21	1.28	0.81
26:DA:2124:G:N2	26:DA:2174:C:N3	2.28	0.81
26:BA:279:C:H42	26:BA:361:G:H1	1.26	0.81
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.61	0.81
26:BA:1530:C:O2'	26:BA:1531:C:O5'	1.99	0.81
26:DA:2114:A:N6	26:DA:2119:A:N7	2.28	0.81
1:CA:999:C:N4	1:CA:1042:G:H1	1.77	0.81
26:DA:2121:G:N2	26:DA:2177:C:N3	2.27	0.81
26:BA:2723:C:OP1	38:BR:3:HIS:ND1	2.12	0.81
1:CA:201:C:H42	1:CA:216:G:H1	1.28	0.80
26:DA:2114:A:N1	26:DA:2171:A:N6	2.29	0.80
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.62	0.80
32:BH:59:ARG:HB2	32:BH:59:ARG:HH11	1.43	0.80
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.14	0.80
1:AA:407:G:H5''	4:AD:115:ARG:HG2	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1315:C:OP2	61:DA:4172:HOH:O	1.99	0.80
26:DA:529:A:N6	26:DA:2041:U:O2	2.14	0.80
1:CA:985:C:H42	1:CA:1220:G:H1	1.24	0.80
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.12	0.80
26:DA:2819:G:N7	61:DA:4078:HOH:O	2.15	0.80
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.30	0.80
26:BA:1466:G:HO2'	26:BA:1546:C:HO2'	1.22	0.79
25:CY:53:G:O6	25:CY:61:C:N4	2.16	0.79
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.79
25:AY:19:G:N2	25:AY:56:C:N3	2.30	0.79
25:CY:19:G:N1	25:CY:56:C:N4	2.23	0.79
25:CY:8:4SU:S4	25:CY:14:A:N7	2.56	0.79
26:DA:2682:U:OP2	61:DA:3832:HOH:O	2.00	0.79
1:CA:1133:G:H1	1:CA:1141:C:H42	1.26	0.79
1:CA:1000:U:O2	1:CA:1041:A:N1	2.15	0.79
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.01	0.79
26:DA:2138:C:H42	26:DA:2153:G:H1	0.80	0.79
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.62	0.79
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.15	0.79
26:BA:1506:C:H2'	26:BA:1507:A:H8	1.47	0.79
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.64	0.79
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.65	0.78
23:CW:29:G:H1	23:CW:41:C:H42	1.29	0.78
26:DA:1324:G:N7	61:DA:3887:HOH:O	2.15	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.15	0.78
26:BA:2808:U:O2	26:BA:2892:A:N6	2.15	0.78
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.16	0.78
1:CA:975:A:H4'	1:CA:976:G:H5''	1.64	0.78
26:BA:2141:G:H1	26:BA:2149:G:H22	1.31	0.78
1:AA:1158:C:H5	1:AA:1181:G:H1	1.32	0.78
1:AA:156:G:N2	1:AA:165:C:O2	2.17	0.78
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.16	0.78
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.17	0.78
26:BA:2123:G:H1	26:BA:2175:C:N4	1.81	0.78
25:CY:15:G:N2	25:CY:48:C:H42	1.82	0.78
26:DA:2608:G:N7	61:DA:4023:HOH:O	2.17	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
26:DA:1648:C:OP1	61:DA:4215:HOH:O	2.01	0.78
25:CY:62:C:H2'	25:CY:63:G:H8	1.49	0.77
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.67	0.77
26:DA:2287:A:H62	26:DA:2344:U:H3	1.30	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.18	0.77
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.32	0.77
1:CA:985:C:N4	1:CA:1220:G:H1	1.81	0.77
26:BA:2136:C:N3	26:BA:2155:G:N2	2.27	0.77
1:CA:1255:G:OP1	10:CJ:45:ARG:NH2	2.17	0.77
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.65	0.77
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.67	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.18	0.77
25:CY:25:C:H2'	25:CY:26:A:H8	1.47	0.77
26:BA:998:C:OP1	61:BA:4663:HOH:O	2.02	0.77
1:AA:1260:C:O2	1:AA:1275:A:N6	2.17	0.77
33:BI:129:THR:HG22	33:BI:139:GLN:HE22	1.48	0.77
23:CW:19:G:H1	23:CW:56:C:H42	1.33	0.77
25:AY:7:A:N6	25:AY:66:U:H3	1.82	0.77
23:AW:53:G:OP1	37:BQ:60:ARG:NH2	2.17	0.77
1:CA:1025:U:H3	1:CA:1036:G:H1	1.32	0.76
26:BA:927:G:N7	61:BA:4413:HOH:O	2.17	0.76
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.18	0.76
1:AA:1422:G:H5''	35:BO:48:PRO:HB3	1.67	0.76
1:CA:838:G:H1	1:CA:848:C:N4	1.84	0.76
26:BA:400:G:N7	61:BA:5004:HOH:O	2.17	0.76
26:BA:1452:A:OP2	61:BA:4011:HOH:O	2.02	0.76
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.67	0.76
23:CW:4:C:N3	23:CW:69:G:N2	2.34	0.76
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.68	0.76
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.66	0.76
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.18	0.76
1:CA:1422:G:H5''	35:DO:48:PRO:HB3	1.67	0.76
28:DD:238:GLY:O	61:DD:408:HOH:O	2.03	0.76
26:BA:2103:C:H42	26:BA:2186:G:H1	1.30	0.76
1:AA:975:A:H4'	1:AA:976:G:H5''	1.67	0.76
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.66	0.76
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.18	0.76
1:CA:1054:C:O2'	1:CA:1055:A:O5'	2.02	0.76
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.19	0.76
26:DA:880:G:N1	26:DA:898:C:O2	2.18	0.76
26:BA:11:G:H2'	26:BA:12:U:H5''	1.68	0.76
51:D4:38:LYS:O	51:D4:40:HIS:N	2.17	0.76
13:CM:25:ILE:HD11	13:CM:66:LEU:HD13	1.68	0.75
2:CB:17:PHE:HB2	2:CB:44:LEU:HD11	1.66	0.75
26:DA:792:G:O6	61:DA:4162:HOH:O	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.01	0.75
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.66	0.75
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.68	0.75
1:AA:532:A:H2	1:AA:1206:G:H21	1.35	0.75
26:BA:1332:G:OP1	61:BA:4653:HOH:O	2.03	0.75
24:AX:6:G:H1	24:AX:67:C:H42	1.34	0.75
23:CW:4:C:H42	23:CW:69:G:H1	1.33	0.75
23:CW:49:C:N4	23:CW:65:G:O6	2.20	0.75
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.68	0.75
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.68	0.75
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.20	0.75
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.19	0.75
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.20	0.75
26:DA:2638:G:OP2	29:DE:82:ARG:NH2	2.19	0.75
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.16	0.75
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.69	0.75
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.18	0.75
26:BA:271(R):G:OP1	48:B1:76:ARG:NH1	2.19	0.75
26:BA:307:G:H21	26:BA:330:A:H62	1.35	0.75
23:AW:29:G:H1	23:AW:41:C:N4	1.84	0.75
23:AW:6:G:N2	23:AW:67:C:N3	2.34	0.75
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.59	0.75
1:AA:574:A:OP2	61:AA:4005:HOH:O	2.05	0.75
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.20	0.75
1:AA:78:G:N2	1:AA:91:C:N3	2.35	0.75
3:CC:179:ARG:HD2	3:CC:206:GLU:HB2	1.68	0.75
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.19	0.74
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.05	0.74
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.51	0.74
19:CS:42:PRO:HG3	51:D4:61:ARG:HG2	1.69	0.74
26:DA:1189:A:OP2	61:DA:4184:HOH:O	2.04	0.74
26:BA:2741:A:OP1	56:B9:22:ARG:NH2	2.17	0.74
27:DB:76:G:N2	27:DB:101:G:O6	2.19	0.74
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.68	0.74
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.68	0.74
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.21	0.74
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.52	0.74
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.53	0.74
26:DA:449:A:OP2	61:DA:4657:HOH:O	2.05	0.74
1:CA:958:A:N6	19:CS:77:THR:O	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2467:C:OP2	61:BA:5096:HOH:O	2.05	0.74
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.19	0.74
1:CA:811:C:N4	61:CA:4023:HOH:O	2.20	0.74
26:DA:2169:A:O2'	26:DA:2170:A:O5'	2.06	0.74
23:CW:7:A:N1	23:CW:66:U:O4	2.19	0.74
25:AY:50:U:H3	25:AY:64:A:H2	1.35	0.74
23:CW:2:C:N3	23:CW:71:G:O6	2.21	0.74
27:DB:75:G:N2	46:DZ:87:ASP:OD1	2.21	0.74
26:DA:2049:G:N7	61:DA:3798:HOH:O	2.19	0.74
26:DA:884:C:N4	26:DA:892:G:O6	2.20	0.74
26:BA:1840:G:N7	61:BA:4332:HOH:O	2.20	0.74
26:DA:1314:C:OP1	61:DA:4172:HOH:O	2.04	0.74
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.21	0.74
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.20	0.74
3:CC:150:LYS:HG3	3:CC:169:ALA:HB2	1.70	0.74
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.21	0.74
26:BA:568:U:O4	61:BA:4141:HOH:O	2.05	0.74
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.53	0.74
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.69	0.74
25:CY:62:C:H2'	25:CY:63:G:C8	2.23	0.73
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.21	0.73
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.69	0.73
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.21	0.73
26:DA:2121:G:H1	26:DA:2177:C:H42	0.80	0.73
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.05	0.73
25:CY:31:A:C6	25:CY:39:PSU:O2	2.41	0.73
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.07	0.73
29:DE:77:ILE:HD13	29:DE:195:LEU:HD13	1.70	0.73
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.68	0.73
26:BA:1602:U:O4	61:BA:4228:HOH:O	2.06	0.73
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.71	0.73
51:D4:40:HIS:O	51:D4:44:THR:N	2.17	0.73
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.71	0.73
27:DB:20:C:N4	27:DB:63:G:O6	2.19	0.73
51:B4:53:GLU:C	51:B4:55:ARG:H	1.92	0.73
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.71	0.73
26:DA:1959:G:N7	61:DA:4503:HOH:O	2.21	0.73
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.21	0.73
26:DA:1352:U:OP2	61:DA:3767:HOH:O	2.06	0.73
25:CY:18:G:N2	25:CY:55:PSU:N3	2.37	0.73
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.71	0.73
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.05	0.73
26:DA:11:G:N7	61:DA:4280:HOH:O	2.20	0.73
11:CK:20:TYR:HB2	11:CK:31:THR:HG22	1.69	0.73
27:DB:24:G:N2	27:DB:27:C:N3	2.32	0.73
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.69	0.73
51:B4:59:PHE:HD1	51:B4:59:PHE:H	1.35	0.73
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.71	0.73
25:AY:26:A:N6	25:AY:44:G:H1	1.85	0.72
23:AW:52:G:H4'	37:BQ:56:ARG:HH22	1.54	0.72
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.53	0.72
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	1.70	0.72
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.22	0.72
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.53	0.72
25:CY:36:A:H2'	25:CY:37:MIA:O4'	1.89	0.72
36:BP:94:GLU:OE2	36:BP:124:LYS:NZ	2.22	0.72
26:DA:741:G:OP2	61:DA:4224:HOH:O	2.05	0.72
25:CY:31:A:N1	25:CY:39:PSU:C2	2.57	0.72
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.72	0.72
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.52	0.72
26:BA:1507:A:O2'	26:BA:1508:A:O4'	2.06	0.72
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.89	0.72
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.22	0.72
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.71	0.72
42:DV:6:LYS:HB2	42:DV:38:LEU:HD21	1.69	0.72
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.35	0.72
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
25:CY:26:A:N1	25:CY:44:G:O6	2.23	0.72
1:CA:1055:A:N7	1:CA:1200:C:N4	2.37	0.72
25:AY:76:A:N6	26:BA:2422:A:O4'	2.22	0.72
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.21	0.72
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.23	0.72
1:AA:266:G:H5''	1:AA:268:C:H41	1.53	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.06	0.72
25:CY:5:G:H1	25:CY:68:C:H42	1.36	0.72
26:BA:739:G:OP1	61:BA:5196:HOH:O	2.06	0.72
1:AA:347:G:O2'	1:AA:348:G:OP1	2.08	0.72
1:CA:324:G:N7	61:CA:4089:HOH:O	2.23	0.72
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.70	0.72
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.22	0.72
25:AY:62:C:H2'	25:AY:63:G:H8	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.54	0.72
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.04	0.72
1:CA:977:A:N6	1:CA:1224:G:OP1	2.21	0.72
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.07	0.72
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.23	0.72
28:DD:28:GLU:OE1	61:DD:416:HOH:O	2.06	0.72
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.71	0.72
9:CI:53:VAL:O	9:CI:55:ALA:N	2.22	0.72
26:DA:1670:C:OP1	61:DA:3752:HOH:O	2.06	0.72
26:BA:1714:G:H1	26:BA:1745(A):C:H42	1.38	0.72
26:DA:1604:C:OP2	61:DA:4546:HOH:O	2.08	0.72
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.14	0.72
1:AA:1445:C:O2	1:AA:1457:G:N2	2.20	0.72
1:CA:1162:C:N3	1:CA:1174:G:N2	2.34	0.71
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.07	0.71
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.70	0.71
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.21	0.71
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.07	0.71
26:DA:1890:A:OP2	61:DA:4472:HOH:O	2.08	0.71
26:BA:957:A:H5'	37:BQ:76:LYS:HG3	1.72	0.71
1:AA:1086:U:H3	1:AA:1099:G:H22	1.37	0.71
25:CY:15:G:N2	25:CY:48:C:N4	2.38	0.71
25:AY:25:C:O2'	25:AY:26:A:O5'	2.09	0.71
1:CA:1054:C:C4	23:CW:34:G:H1'	2.25	0.71
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.37	0.71
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	1.71	0.71
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.73	0.71
23:CW:29:G:H1	23:CW:41:C:N4	1.87	0.71
10:CJ:5:ARG:N	61:CJ:5101:HOH:O	2.22	0.71
26:DA:370:G:N7	61:DA:3786:HOH:O	2.23	0.71
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.72	0.71
36:BP:116:GLY:O	36:BP:137:LYS:NZ	2.22	0.71
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.73	0.71
26:BA:528:A:H2'	26:BA:529:A:H5''	1.72	0.71
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.72	0.71
26:BA:2124:G:H1	26:BA:2174:C:H42	1.37	0.71
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.73	0.71
26:BA:2130:U:H4'	26:BA:2133:G:H4'	1.72	0.71
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.24	0.71
23:CW:27:G:H1	23:CW:43:C:H42	1.37	0.71
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.72	0.71
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.71	0.71
61:DA:4209:HOH:O	29:DE:135:HIS:NE2	2.24	0.71
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	1.91	0.71
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.73	0.71
26:BA:1022:G:H22	26:BA:1142(A):A:H2	1.39	0.70
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.72	0.70
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.22	0.70
26:DA:643:A:N1	26:DA:2369:A:O2'	2.22	0.70
26:DA:731:C:OP1	61:DA:4348:HOH:O	2.08	0.70
31:DG:63:ILE:HA	31:DG:143:GLU:HG3	1.72	0.70
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.54	0.70
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.57	0.70
1:AA:972:C:OP1	61:AA:4173:HOH:O	2.09	0.70
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.24	0.70
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.70	0.70
26:BA:2239:G:OP2	61:BA:4335:HOH:O	2.08	0.70
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.70
26:DA:1637:A:OP2	61:DA:4569:HOH:O	2.09	0.70
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.72	0.70
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.73	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.08	0.70
1:CA:771:G:N7	61:CA:4042:HOH:O	2.24	0.70
26:BA:1310:G:OP2	54:B7:9:ARG:NH1	2.25	0.70
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.24	0.70
23:AW:6:G:H1	23:AW:67:C:H42	1.32	0.70
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.56	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.74	0.70
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.21	0.70
25:CY:51:U:O2	25:CY:63:G:N2	2.23	0.70
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.70
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.24	0.70
26:BA:2102:U:O2	26:BA:2187:G:N2	2.25	0.70
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.57	0.70
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.24	0.70
26:BA:2102:U:H3	26:BA:2187:G:H1	1.40	0.70
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.39	0.70
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.24	0.70
26:DA:2138:C:N4	26:DA:2153:G:N1	2.27	0.70
1:AA:1027:C:O2	1:AA:1034:G:C2	2.45	0.70
26:BA:729:G:OP2	28:BD:13:ARG:NH1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.73	0.70
23:AW:47:U:H5'	23:AW:47:U:H6	1.57	0.70
1:AA:1076:C:H5'	1:AA:1076:C:H6	1.57	0.70
26:DA:987:G:O2'	26:DA:1000:A:N3	2.23	0.69
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.74	0.69
1:AA:96:U:HO2'	1:AA:97:G:H8	1.40	0.69
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.24	0.69
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.73	0.69
26:BA:1250:G:OP2	36:BP:21:ARG:NH1	2.26	0.69
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.25	0.69
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.74	0.69
26:DA:2504:U:OP2	61:DA:4169:HOH:O	2.11	0.69
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.25	0.69
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.25	0.69
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.75	0.69
1:CA:76:C:N3	1:CA:93:G:N2	2.34	0.69
28:BD:147:LEU:HD13	28:BD:155:LEU:HD21	1.73	0.69
1:AA:1414:U:H3	1:AA:1486:G:H1	1.40	0.69
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.24	0.69
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.26	0.69
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.25	0.69
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.25	0.69
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.57	0.69
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.75	0.69
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.28	0.69
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.23	0.69
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.74	0.69
1:CA:200:G:H1	1:CA:217:C:H42	1.40	0.69
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.69
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.73	0.69
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.57	0.69
1:AA:78:G:N1	1:AA:91:C:N4	2.40	0.69
10:CJ:49:VAL:HG23	14:CN:41:ARG:HD2	1.75	0.69
39:DS:93:LYS:HD2	39:DS:95:HIS:HB2	1.74	0.69
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.75	0.69
26:DA:2060:A:N3	61:DA:4112:HOH:O	2.25	0.69
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.69
26:BA:527:C:OP1	61:BA:4682:HOH:O	2.11	0.69
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.26	0.69
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.75	0.69
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:882:G:N2	26:DA:894:C:O2	2.18	0.68
1:CA:560:U:OP2	61:CA:4161:HOH:O	2.11	0.68
2:AB:20:GLU:HG2	2:AB:191:ASP:HB3	1.74	0.68
26:BA:1352:U:OP1	61:BA:4087:HOH:O	2.11	0.68
26:BA:1140:C:O3'	34:BN:25:ARG:NH1	2.27	0.68
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.08	0.68
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.59	0.68
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.26	0.68
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.76	0.68
29:DE:72:VAL:HG13	29:DE:73:GLU:O	1.93	0.68
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.26	0.68
26:DA:1223:G:N2	26:DA:1226:A:OP2	2.23	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.58	0.68
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.74	0.68
26:DA:880:G:H22	26:DA:898:C:H1'	1.59	0.68
26:DA:89:G:H3'	26:DA:90:U:H5''	1.76	0.68
26:BA:2612:C:OP2	52:B5:2:ALA:N	2.27	0.68
5:CE:7:GLU:OE1	5:CE:37:ARG:NH2	2.26	0.68
26:DA:2139:C:N4	26:DA:2152:G:N1	2.16	0.68
26:DA:2127:G:O6	26:DA:2161:C:N3	2.26	0.68
26:BA:1843:C:H5'	28:BD:253:GLN:NE2	2.09	0.68
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.73	0.68
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.26	0.68
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.76	0.68
26:DA:194:G:N7	61:DA:4296:HOH:O	2.26	0.68
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.27	0.68
26:BA:1045:A:OP1	26:BA:1045:A:H4'	1.92	0.68
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.76	0.68
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	1.93	0.68
26:DA:2165:G:H22	26:DA:2172:U:H5	1.40	0.68
26:BA:2110:G:O2'	26:BA:2120:G:OP2	2.12	0.68
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.26	0.68
26:DA:1647:G:OP1	61:DA:4215:HOH:O	2.12	0.68
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.10	0.68
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.76	0.68
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.76	0.68
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.68
1:CA:952:U:O2'	1:CA:965:A:N6	2.27	0.68
1:AA:1027:C:N3	1:AA:1034:G:C6	2.63	0.67
23:AW:66:U:H2'	23:AW:67:C:C6	2.29	0.67
26:BA:271(L):U:OP1	33:BI:50:ARG:NH1	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:446:G:H1	1:CA:488:C:H42	1.39	0.67
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.26	0.67
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.24	0.67
25:CY:25:C:H2'	25:CY:26:A:C8	2.30	0.67
51:B4:55:ARG:HB2	51:B4:56:VAL:O	1.94	0.67
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.42	0.67
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.75	0.67
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.94	0.67
1:CA:1133:G:H1	1:CA:1141:C:N4	1.92	0.67
26:DA:1449:A:HO2'	26:DA:1529:G:N2	1.92	0.67
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.75	0.67
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.76	0.67
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.74	0.67
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.58	0.67
25:AY:66:U:H2'	25:AY:67:C:C6	2.29	0.67
26:BA:692:C:O2'	28:BD:38:LYS:NZ	2.26	0.67
1:AA:324:G:N7	61:AA:4166:HOH:O	2.27	0.67
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.77	0.67
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.24	0.67
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.67
46:BZ:11:GLU:O	46:BZ:36:LYS:NZ	2.23	0.67
26:BA:1783:A:N7	61:BA:5061:HOH:O	2.26	0.67
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.24	0.67
26:BA:662:G:H5''	36:BP:16:ARG:HG2	1.75	0.67
1:CA:999:C:N3	1:CA:1042:G:N2	2.38	0.67
24:AX:5:G:N2	24:AX:68:C:N3	2.40	0.67
25:AY:22:G:H2'	25:AY:23:A:C8	2.29	0.67
28:DD:28:GLU:OE2	61:DD:417:HOH:O	2.13	0.67
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.77	0.67
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.27	0.67
26:DA:307:G:N1	26:DA:310:A:OP2	2.26	0.67
26:DA:2886:G:N7	61:DA:4141:HOH:O	2.26	0.67
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.28	0.67
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.28	0.67
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.13	0.67
13:CM:80:ARG:HH22	19:CS:69:HIS:CE1	2.12	0.67
26:BA:2759:G:N7	61:BA:4124:HOH:O	2.28	0.67
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.77	0.67
26:DA:600:G:O6	61:DA:4398:HOH:O	2.11	0.67
29:BE:149:ARG:O	61:BE:406:HOH:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2639:A:OP2	61:DA:3839:HOH:O	2.12	0.67
1:CA:316:G:OP2	1:CA:351:G:O2'	2.12	0.67
1:CA:664:G:P	18:CR:64:ARG:HH22	2.18	0.66
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.66
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.77	0.66
26:DA:1993:U:OP2	61:DA:4714:HOH:O	2.13	0.66
3:CC:34:LEU:HG	3:CC:38:ARG:HH12	1.59	0.66
1:AA:1238:A:OP2	61:AA:4160:HOH:O	2.12	0.66
23:CW:51:U:H3	23:CW:63:G:H1	1.41	0.66
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.28	0.66
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.75	0.66
26:BA:568:U:O2'	61:BA:5168:HOH:O	2.13	0.66
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.30	0.66
26:DA:2499:C:OP2	61:DA:4653:HOH:O	2.12	0.66
26:BA:1238:G:OP2	61:BA:5012:HOH:O	2.14	0.66
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.41	0.66
13:CM:3:ARG:NH2	13:CM:9:ILE:O	2.28	0.66
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.60	0.66
25:AY:9:A:H5''	25:AY:46:7MG:HN22	1.60	0.66
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.26	0.66
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.23	0.66
26:DA:20:C:OP1	41:DU:22:LYS:NZ	2.25	0.66
26:BA:84:A:H5'	45:BY:8:LYS:HG2	1.76	0.66
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.42	0.66
26:BA:278:A:H2'	26:BA:279:C:C6	2.30	0.66
26:DA:307:G:H21	26:DA:330:A:H62	1.44	0.66
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.77	0.66
25:CY:2:C:H2'	25:CY:3:C:H6	1.61	0.66
26:DA:2552:U:H2'	26:DA:2554:U:OP2	1.95	0.66
24:AX:8:4SU:O2	24:AX:21:A:H2	1.79	0.66
25:AY:35:A:H2'	25:AY:36:A:C8	2.30	0.66
26:DA:770:G:OP2	61:DA:4267:HOH:O	2.12	0.66
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.78	0.66
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.78	0.66
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.76	0.66
13:CM:6:GLY:H	13:CM:67:GLU:HG3	1.61	0.66
1:CA:972:C:OP1	61:CA:4167:HOH:O	2.13	0.66
26:BA:250:G:OP2	55:B8:13:ARG:NH2	2.28	0.66
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.78	0.66
1:AA:1278:U:H5'	1:AA:1279:A:O4'	1.96	0.66
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.66
2:CB:125:PRO:O	2:CB:127:ILE:N	2.27	0.66
25:AY:9:A:O2'	25:AY:10:G:N7	2.28	0.66
1:AA:165:C:H2'	1:AA:166:G:C8	2.31	0.66
1:AA:567:G:N3	61:AA:4131:HOH:O	2.28	0.66
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.19	0.66
26:BA:624:C:O2'	26:BA:657:U:OP1	2.12	0.66
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.43	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.29	0.66
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.78	0.66
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.77	0.66
40:DT:108:ARG:HG2	40:DT:111:ARG:HH12	1.60	0.66
26:DA:2171:A:N3	26:DA:2172:U:N3	2.44	0.66
27:DB:4:C:H42	27:DB:117:G:H1	1.45	0.66
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.29	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.64	0.65
26:DA:740:U:OP2	61:DA:4223:HOH:O	2.13	0.65
25:CY:28:G:N2	25:CY:43:C:H1'	2.10	0.65
3:CC:137:ALA:HA	3:CC:140:ARG:HH12	1.61	0.65
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.28	0.65
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.27	0.65
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.29	0.65
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.78	0.65
26:BA:84:A:H5''	45:BY:8:LYS:HE3	1.77	0.65
51:D4:62:ARG:O	51:D4:64:GLY:N	2.29	0.65
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.78	0.65
1:CA:673:G:H2'	1:CA:674:G:C8	2.31	0.65
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.60	0.65
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.78	0.65
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.79	0.65
20:AT:9:ASN:O	20:AT:10:LEU:HB2	1.95	0.65
9:AI:53:VAL:HG11	9:AI:92:TYR:CZ	2.31	0.65
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.29	0.65
2:CB:178:ARG:HH22	8:CH:68:ARG:HH22	1.43	0.65
1:CA:460:G:O6	1:CA:470:C:H5''	1.96	0.65
26:DA:2492:U:OP1	61:DA:4150:HOH:O	2.15	0.65
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.24	0.65
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.29	0.65
26:DA:2260:C:OP1	61:DA:4688:HOH:O	2.14	0.65
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.15	0.65
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.78	0.65
26:BA:744:G:OP1	61:BA:4704:HOH:O	2.14	0.65
29:DE:72:VAL:HG22	29:DE:73:GLU:HG3	1.78	0.65
26:BA:1267:U:OP1	61:BA:5106:HOH:O	2.14	0.65
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.60	0.65
1:CA:396:G:O2'	1:CA:398:C:OP1	2.05	0.65
10:AJ:5:ARG:NE	10:AJ:73:ASP:OD1	2.30	0.65
27:BB:66:A:H61	27:BB:108:U:H2'	1.62	0.65
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.26	0.65
31:DG:36:LYS:HG2	31:DG:160:VAL:HB	1.78	0.65
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.12	0.65
1:CA:1402:C:N4	22:CV:18:G:OP2	2.28	0.65
27:DB:5:C:H42	27:DB:116:G:H1	1.43	0.65
1:AA:1028:C:H42	1:AA:1033:G:H1	1.45	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.77	0.65
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.29	0.65
30:DF:140:LEU:HD21	30:DF:170:LEU:HD11	1.79	0.65
8:CH:29:SER:HB2	8:CH:32:LYS:HG3	1.78	0.65
36:DP:42:SER:O	61:DP:304:HOH:O	2.14	0.65
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.61	0.65
26:BA:1314:C:OP1	61:BA:4653:HOH:O	2.14	0.65
1:CA:1011:G:N2	1:CA:1019:C:H1'	2.12	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.29	0.65
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.79	0.65
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.79	0.65
26:DA:1642:G:N7	61:DA:4099:HOH:O	2.28	0.65
26:BA:2079:U:OP1	48:B1:21:ARG:NH2	2.29	0.65
1:AA:1502:A:H2	1:AA:1505:G:N1	1.91	0.64
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.77	0.64
26:BA:2287:A:N6	26:BA:2344:U:H3	1.93	0.64
1:AA:166:G:H2'	1:AA:167:G:C8	2.32	0.64
26:BA:568:U:H5'	26:BA:945:A:N1	2.12	0.64
2:AB:16:HIS:HE1	2:AB:214:ILE:HD11	1.63	0.64
1:CA:35:G:O2'	12:CL:118:SER:O	2.15	0.64
26:BA:2608:G:N7	61:BA:4411:HOH:O	2.29	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.29	0.64
26:BA:1113:U:H2'	26:BA:1114:G:H8	1.62	0.64
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.27	0.64
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.78	0.64
31:DG:80:PHE:O	31:DG:82:LEU:N	2.30	0.64
26:DA:299:A:N1	26:DA:322:A:O2'	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.27	0.64
26:BA:2131:G:H5''	26:BA:2132:U:H3'	1.80	0.64
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.79	0.64
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.27	0.64
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.80	0.64
26:BA:1434:A:H61	26:BA:1558:A:H62	1.44	0.64
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.25	0.64
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.28	0.64
1:CA:96:U:O2'	1:CA:97:G:H5'	1.97	0.64
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.30	0.64
25:AY:19:G:N1	25:AY:56:C:N4	2.45	0.64
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.10	0.64
26:DA:2624:G:N7	61:DA:4478:HOH:O	2.29	0.64
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.64
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.98	0.64
20:CT:16:HIS:O	20:CT:19:SER:OG	2.13	0.64
26:BA:607:U:OP1	30:BF:102:PRO:HA	1.98	0.64
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.80	0.64
25:CY:12:U:O4	25:CY:23:A:N1	2.31	0.64
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.79	0.64
26:BA:887:A:O2'	26:BA:888:C:OP2	2.13	0.64
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.63	0.64
1:CA:1118:C:C2	1:CA:1119:C:H5	2.16	0.64
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.64
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.26	0.64
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.62	0.64
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.33	0.64
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.62	0.64
22:CV:16:A:H61	24:CX:36:U:H3	1.46	0.64
26:DA:2161:C:H2'	26:DA:2162:G:C8	2.33	0.64
26:BA:1047:G:H2'	26:BA:1110:G:H1	1.62	0.64
26:BA:187:G:OP2	61:BA:4468:HOH:O	2.14	0.64
2:AB:83:MET:HB3	2:AB:234:PRO:HG2	1.80	0.64
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.80	0.64
35:BO:37:ASP:OD1	35:BO:109:LYS:NZ	2.30	0.64
40:DT:95:ARG:HG2	40:DT:95:ARG:HH11	1.62	0.64
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.30	0.64
26:DA:568:U:H5'	26:DA:945:A:N1	2.13	0.64
25:AY:26:A:N6	25:AY:44:G:N1	2.43	0.63
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.63
26:DA:918:A:N3	27:DB:80:U:O2'	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.32	0.63
1:AA:11:G:O2'	1:AA:506:G:N2	2.31	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH2	2.31	0.63
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.13	0.63
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.79	0.63
1:CA:1157:A:H4'	1:CA:1158:C:O5'	1.98	0.63
26:BA:526:A:OP1	61:BA:4682:HOH:O	2.15	0.63
26:DA:2893:G:H5'	26:DA:2893:G:H8	1.63	0.63
26:BA:700:G:O2'	26:BA:1632:A:N3	2.29	0.63
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.33	0.63
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.80	0.63
1:CA:148:G:H2'	1:CA:149:A:H8	1.63	0.63
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.63
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.30	0.63
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.78	0.63
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.62	0.63
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.42	0.63
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.80	0.63
26:DA:248:G:OP1	61:DA:4415:HOH:O	2.16	0.63
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.80	0.63
1:CA:683:G:O6	61:CA:4143:HOH:O	2.14	0.63
26:BA:2632:A:HO2'	26:BA:2811:G:HO2'	1.43	0.63
26:DA:2143:C:H2'	26:DA:2144:U:O4'	1.98	0.63
1:AA:1157:A:H4'	1:AA:1158:C:O5'	1.98	0.63
1:CA:991:U:O2'	1:CA:992:U:O5'	2.14	0.63
55:B8:23:VAL:HG11	55:B8:47:LYS:HD3	1.80	0.63
26:BA:2022:U:OP1	61:BA:4666:HOH:O	2.15	0.63
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.25	0.63
25:AY:55:PSU:C2	25:AY:57:G:H5'	2.34	0.63
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.46	0.63
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.80	0.63
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.33	0.63
21:CU:5:ASP:O	21:CU:11:GLY:HA3	1.98	0.63
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	1.99	0.63
26:BA:625:G:O6	36:BP:107:LYS:NZ	2.31	0.63
1:CA:266:G:H5''	1:CA:268:C:H41	1.64	0.63
26:DA:662:G:OP1	61:DA:4188:HOH:O	2.15	0.63
31:DG:113:ARG:NH1	31:DG:141:PHE:O	2.32	0.63
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.81	0.63
1:AA:557:G:OP1	61:AA:4076:HOH:O	2.16	0.63
55:B8:62:LEU:HB3	55:B8:65:GLU:HG3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:125:GLU:HG3	3:CC:190:ARG:O	1.99	0.63
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.34	0.63
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.33	0.63
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.81	0.63
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.79	0.63
26:DA:852:G:H2'	26:DA:853:G:H8	1.63	0.63
1:AA:1003:G:C2	1:AA:1004:A:H1'	2.34	0.63
26:BA:1371:G:O6	61:BA:4345:HOH:O	2.12	0.63
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.13	0.63
25:CY:27:G:O6	25:CY:43:C:N3	2.32	0.63
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.80	0.63
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.80	0.63
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.80	0.63
1:AA:352:C:OP2	61:AA:4116:HOH:O	2.15	0.63
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.79	0.63
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.81	0.63
25:CY:50:U:O2	25:CY:64:A:N1	2.32	0.62
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.98	0.62
26:BA:1174:A:H4'	26:BA:1175:U:OP1	1.98	0.62
1:AA:346:G:C4	1:AA:347:G:H1'	2.33	0.62
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.80	0.62
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.32	0.62
49:D2:65:ASN:OD1	49:D2:69:ARG:NH1	2.32	0.62
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.63	0.62
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.81	0.62
1:AA:1047:G:H5''	14:AN:4:LYS:HD2	1.81	0.62
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	1.99	0.62
3:CC:22:TRP:CG	3:CC:59:ARG:HD2	2.34	0.62
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.22	0.62
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	1.82	0.62
1:CA:1029:C:N4	1:CA:1032:G:H1	1.96	0.62
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.80	0.62
1:AA:157:G:H1	1:AA:164:U:H3	1.47	0.62
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.13	0.62
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.27	0.62
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.64	0.62
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.33	0.62
1:CA:1076:C:H6	1:CA:1076:C:H5'	1.62	0.62
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.80	0.62
26:BA:2689:U:H4'	26:BA:2690:C:H5'	1.82	0.62
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:473:G:H2'	1:CA:474:G:H8	1.62	0.62
23:CW:47:U:O2'	23:CW:48:C:OP1	2.16	0.62
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.81	0.62
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.81	0.62
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.32	0.62
1:AA:56:U:H2'	1:AA:57:G:C8	2.34	0.62
15:AO:22:THR:OG1	15:AO:23:GLY:N	2.31	0.62
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.32	0.62
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.32	0.62
38:DR:97:VAL:HG22	38:DR:114:VAL:HG13	1.80	0.62
26:BA:2830:G:O6	61:BA:5189:HOH:O	2.13	0.62
1:CA:1054:C:N4	23:CW:34:G:H1'	2.14	0.62
26:DA:880:G:N2	26:DA:898:C:H1'	2.14	0.62
1:CA:983:A:N1	1:CA:1222:G:N2	2.47	0.62
1:CA:1244:C:H42	1:CA:1293:G:H1	1.47	0.62
25:AY:22:G:N7	25:AY:46:7MG:O6	2.32	0.62
23:CW:19:G:N2	23:CW:56:C:N3	2.45	0.62
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.65	0.62
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.15	0.62
1:AA:202:U:O2'	1:AA:203:U:O5'	2.16	0.62
12:CL:60:LEU:N	12:CL:64:TYR:O	2.25	0.62
25:CY:9:A:O2'	25:CY:10:G:N7	2.32	0.62
26:BA:2893:G:O2'	26:BA:2894:G:OP2	2.14	0.62
1:AA:406:G:OP2	61:AA:4123:HOH:O	2.15	0.62
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.64	0.62
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.82	0.62
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.81	0.62
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.81	0.62
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.82	0.62
26:BA:2572:A:N7	29:BE:144:ARG:HD2	2.15	0.62
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.82	0.62
8:AH:121:ASP:OD1	8:AH:125:ARG:NH2	2.32	0.62
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.15	0.62
1:CA:959:A:O2'	1:CA:984:C:O2'	2.17	0.62
2:CB:50:GLU:HG3	2:CB:200:ILE:O	1.98	0.62
23:AW:56:C:H5	26:BA:897:C:O4'	1.83	0.62
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.82	0.62
1:AA:92:C:H2'	1:AA:93:G:C8	2.35	0.62
13:CM:121:LYS:H	13:CM:121:LYS:NZ	1.97	0.62
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.65	0.62
26:DA:882:G:N1	26:DA:894:C:N3	2.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:179:PRO:HB2	51:D4:42:PHE:HE1	1.64	0.62
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.81	0.62
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.30	0.62
26:DA:900:A:H2'	26:DA:901:A:H8	1.65	0.62
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.62
18:AR:38:GLU:HA	18:AR:41:LYS:HD3	1.82	0.62
1:CA:977:A:O2'	1:CA:981:U:N3	2.33	0.61
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.35	0.61
26:DA:509:C:OP1	61:DA:4324:HOH:O	2.16	0.61
26:BA:732:C:OP2	61:BA:4004:HOH:O	2.16	0.61
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.35	0.61
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.65	0.61
25:CY:8:4SU:HN3	25:CY:14:A:N6	1.91	0.61
1:AA:1027:C:C2	1:AA:1034:G:N1	2.67	0.61
24:AX:6:G:H1	24:AX:67:C:N4	1.97	0.61
27:DB:24:G:N3	27:DB:26:A:N6	2.48	0.61
27:DB:24:G:N7	27:DB:56:G:H2'	2.15	0.61
26:BA:2168:G:C6	26:BA:2171:A:H8	2.18	0.61
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.30	0.61
27:BB:45:A:OP2	31:BG:96:ARG:NH2	2.28	0.61
1:AA:953:G:H5'	1:AA:965:A:H61	1.65	0.61
26:DA:373:U:H2'	26:DA:374:A:H8	1.65	0.61
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.81	0.61
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.99	0.61
29:DE:52:LEU:O	29:DE:76:ARG:N	2.25	0.61
26:DA:1261:C:OP2	43:DW:83:LYS:NZ	2.33	0.61
26:BA:2049:G:N7	61:BA:5165:HOH:O	2.31	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.00	0.61
1:CA:757:U:H2'	1:CA:758:G:O4'	1.99	0.61
25:CY:26:A:N1	25:CY:44:G:C6	2.69	0.61
36:DP:99:LEU:O	36:DP:103:ALA:N	2.32	0.61
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.32	0.61
2:AB:74:LYS:NZ	2:AB:205:ASP:OD2	2.33	0.61
1:AA:677:U:H3	1:AA:713:G:H22	1.47	0.61
15:AO:79:ARG:O	15:AO:83:GLU:HB2	1.99	0.61
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.65	0.61
1:CA:1120:G:O6	1:CA:1154:G:N2	2.33	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
26:BA:1816:G:O6	28:BD:35:LYS:NZ	2.28	0.61
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.14	0.61
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.34	0.61
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.83	0.61
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.61
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.82	0.61
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.36	0.61
50:D3:12:PRO:HB2	50:D3:20:LYS:HG2	1.81	0.61
26:DA:2431:U:OP1	61:DA:3906:HOH:O	2.16	0.61
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.66	0.61
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.36	0.61
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.35	0.61
1:CA:985:C:N3	1:CA:1220:G:N2	2.46	0.61
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.33	0.61
46:DZ:117:LEU:HD12	46:DZ:174:VAL:HG22	1.80	0.61
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.47	0.61
1:CA:1148:U:H1'	9:CI:66:ARG:HH12	1.66	0.61
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	1.81	0.61
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.14	0.61
44:DX:46:ALA:O	49:D2:30:ARG:NH2	2.33	0.61
1:AA:189:G:H1	1:AA:189(K):U:H3	1.48	0.61
26:BA:2350:C:OP2	61:BA:4049:HOH:O	2.16	0.61
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.18	0.61
41:BU:76:TYR:OH	41:BU:92:ARG:NH1	2.33	0.61
25:CY:5:G:H1	25:CY:68:C:N4	1.99	0.61
1:CA:952:U:H2'	1:CA:953:G:C8	2.36	0.61
26:DA:301:G:OP2	45:DY:84:ARG:NH2	2.33	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.29	0.61
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.83	0.61
26:BA:2714:G:OP1	61:BA:4546:HOH:O	2.16	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.35	0.61
10:CJ:27:ALA:HA	10:CJ:81:THR:HG22	1.83	0.61
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.33	0.61
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.29	0.61
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.33	0.61
1:AA:166:G:H2'	1:AA:167:G:H8	1.65	0.61
27:DB:110:G:H2'	27:DB:111:G:C8	2.36	0.61
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.82	0.61
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.64	0.61
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.19	0.61
26:DA:526:A:OP1	61:DA:4194:HOH:O	2.16	0.61
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:920:U:H2'	1:CA:921:U:C6	2.35	0.61
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.83	0.61
1:CA:692:U:O2'	1:CA:694:A:N7	2.31	0.61
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.16	0.61
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.19	0.61
26:BA:528:A:C2'	26:BA:529:A:H5''	2.31	0.61
1:CA:1067:A:O2'	1:CA:1068:G:OP2	2.17	0.61
1:CA:957:U:H2'	1:CA:959:A:OP2	2.01	0.61
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.82	0.61
40:DT:85:LYS:NZ	40:DT:87:ASP:OD2	2.28	0.61
26:BA:2791:C:H2'	26:BA:2792:G:C8	2.36	0.60
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.60
2:AB:55:PHE:HA	2:AB:58:ILE:HB	1.83	0.60
1:CA:646:U:H2'	1:CA:647:C:C6	2.36	0.60
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.83	0.60
2:CB:47:THR:O	2:CB:51:LEU:N	2.32	0.60
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.36	0.60
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.65	0.60
13:AM:80:ARG:HH22	19:AS:69:HIS:HE1	1.48	0.60
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.82	0.60
39:BS:56:LEU:HD12	39:BS:69:VAL:HG12	1.82	0.60
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.36	0.60
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.25	0.60
26:BA:1204:A:H2	26:BA:1241:A:H62	1.49	0.60
29:BE:9:VAL:HB	40:BT:3:ARG:HG2	1.82	0.60
1:CA:148:G:H2'	1:CA:149:A:C8	2.37	0.60
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.35	0.60
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.84	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.81	0.60
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.82	0.60
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.36	0.60
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.33	0.60
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.83	0.60
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.83	0.60
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.16	0.60
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.45	0.60
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.66	0.60
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.33	0.60
26:DA:954:G:H5''	37:DQ:13:GLN:HB3	1.83	0.60
51:B4:57:GLU:HB3	51:B4:58:ARG:HA	1.83	0.60
26:DA:1739:U:HO2'	26:DA:1740:G:H8	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:29:GLY:HA3	61:BE:408:HOH:O	2.01	0.60
31:BG:47:LYS:HG3	31:BG:48:GLU:H	1.66	0.60
1:AA:413:G:N2	1:AA:428:G:H1'	2.16	0.60
1:CA:1120:G:C6	1:CA:1154:G:N2	2.69	0.60
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.02	0.60
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	1.84	0.60
25:AY:59:U:H3'	25:AY:60:U:C6	2.35	0.60
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.35	0.60
1:AA:865:A:H2	1:AA:918:A:H4'	1.67	0.60
36:BP:26:GLY:O	61:BP:311:HOH:O	2.16	0.60
11:CK:98:LEU:O	11:CK:101:SER:OG	2.19	0.60
28:BD:71:ASP:HB3	28:BD:103:ARG:NH2	2.16	0.60
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.84	0.60
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.82	0.60
1:CA:9:G:H2'	1:CA:10:A:H8	1.66	0.60
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.84	0.60
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.02	0.60
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.34	0.60
1:AA:1026:G:O6	1:AA:1034:G:N2	2.32	0.60
25:AY:19:G:H1	25:AY:56:C:N4	2.00	0.60
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.67	0.60
51:B4:53:GLU:O	51:B4:55:ARG:N	2.34	0.60
26:DA:1226:A:OP1	42:DV:84:LYS:HE2	2.01	0.60
1:CA:1075:C:H2'	1:CA:1076:C:H5''	1.84	0.60
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.83	0.60
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.02	0.60
26:DA:1007:C:OP1	34:DN:35:ARG:NH1	2.34	0.60
1:AA:662:G:H2'	1:AA:663:A:C8	2.37	0.60
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.37	0.60
26:BA:2033:A:OP1	61:BA:4308:HOH:O	2.17	0.60
26:DA:2747:G:H1	26:DA:2754:U:H2'	1.66	0.60
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.60
26:BA:2447:G:OP2	61:BA:4563:HOH:O	2.16	0.60
26:DA:774:A:N6	61:DA:3733:HOH:O	2.35	0.60
19:AS:28:LYS:HZ2	19:AS:28:LYS:HB3	1.66	0.60
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.35	0.60
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.60
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.34	0.60
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.02	0.60
23:AW:56:C:P	26:BA:897:C:H5'	2.42	0.60
26:BA:880:G:N2	26:BA:898:C:O2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2808:U:C2'	26:DA:2809:A:H5'	2.32	0.60
32:DH:20:ALA:HB1	32:DH:21:PRO:HD2	1.84	0.60
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.84	0.60
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.85	0.60
1:CA:1505:G:HO2'	22:CV:13:A:H2	1.49	0.60
26:BA:1048:A:OP2	26:BA:1109:C:N4	2.30	0.60
26:DA:2499:C:N3	61:DA:3930:HOH:O	2.31	0.60
26:DA:1247:A:OP1	30:DF:95:ARG:NH2	2.32	0.60
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	1.82	0.60
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.27	0.60
26:BA:2155:G:H2'	26:BA:2156:G:O4'	2.01	0.59
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.84	0.59
26:DA:2638:G:P	29:DE:82:ARG:HH22	2.25	0.59
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.35	0.59
40:BT:118:ARG:HH22	40:BT:125:ARG:HH12	1.50	0.59
26:BA:2206:G:H3'	26:BA:2207:G:C8	2.37	0.59
26:BA:2871:C:N3	61:BA:4781:HOH:O	2.31	0.59
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.24	0.59
46:BZ:139:VAL:HG22	46:BZ:155:LEU:HD11	1.84	0.59
26:BA:1418:G:OP2	61:BA:4580:HOH:O	2.16	0.59
26:DA:247:G:H4'	26:DA:386:G:C5	2.36	0.59
14:CN:6:LEU:HB3	14:CN:23:ARG:HH21	1.67	0.59
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.37	0.59
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.20	0.59
22:CV:14:A:C4	25:CY:34:G:C6	2.90	0.59
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.66	0.59
26:BA:898:C:H2'	26:BA:899:A:C8	2.37	0.59
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.67	0.59
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.17	0.59
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.83	0.59
26:DA:2846:G:N7	61:DA:4073:HOH:O	2.32	0.59
26:DA:1434:A:H61	26:DA:1558:A:H62	1.49	0.59
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.84	0.59
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.67	0.59
14:CN:32:SER:OG	14:CN:32:SER:O	2.19	0.59
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.17	0.59
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.83	0.59
23:CW:14:A:H61	23:CW:21:A:H2	1.49	0.59
23:CW:61:C:O2'	23:CW:62:C:O5'	2.14	0.59
1:CA:539:A:H2'	1:CA:540:G:C8	2.37	0.59
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	1.82	0.59
1:AA:200:G:H1	1:AA:217:C:H42	1.51	0.59
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.35	0.59
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.31	0.59
36:DP:85:LEU:HA	36:DP:88:LEU:HD12	1.85	0.59
1:CA:113:G:OP1	61:CA:4148:HOH:O	2.17	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
1:CA:596:C:O2	1:CA:644:G:N2	2.17	0.59
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.35	0.59
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.03	0.59
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.18	0.59
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.67	0.59
25:AY:59:U:H3'	25:AY:60:U:H6	1.68	0.59
26:BA:2103:C:N4	26:BA:2186:G:H1	1.98	0.59
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.84	0.59
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.17	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
51:D4:33:VAL:HG12	51:D4:35:VAL:H	1.66	0.59
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.35	0.59
1:CA:538:G:H5''	12:CL:114:LYS:HB2	1.82	0.59
26:DA:1446:C:H42	26:DA:1465:G:H1	1.50	0.59
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.34	0.59
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.85	0.59
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.20	0.59
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.84	0.59
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.83	0.59
1:AA:736:C:H2'	1:AA:737:A:C8	2.37	0.59
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.01	0.59
3:AC:82:GLU:HG2	3:AC:85:ARG:NH2	2.17	0.59
1:AA:189(A):C:H42	1:AA:189(J):G:H1	1.51	0.59
26:DA:2140:C:H1'	26:DA:2152:G:N2	2.18	0.59
26:BA:1040:C:H2'	26:BA:1041:C:O4'	2.01	0.59
26:BA:1649:G:O2'	38:BR:107:ASP:OD2	2.17	0.59
23:AW:22:G:O2'	23:AW:23:A:OP1	2.18	0.59
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.85	0.59
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.37	0.59
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.85	0.59
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.35	0.59
26:DA:2002:G:OP2	38:DR:9:LYS:NZ	2.35	0.59
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.85	0.59
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.38	0.59
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.84	0.59
25:CY:18:G:N2	25:CY:55:PSU:C4	2.71	0.59
26:BA:652(E):G:O6	26:BA:652(T):C:N4	2.30	0.59
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.32	0.59
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.59
23:CW:11:C:H42	23:CW:24:G:H1	1.50	0.59
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.03	0.59
25:AY:58:A:H3'	25:AY:58:A:P	2.43	0.59
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.84	0.59
26:DA:271(R):G:H5''	48:D1:97:LEU:HD21	1.84	0.59
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.36	0.59
26:DA:2062:A:OP1	61:DA:3829:HOH:O	2.17	0.59
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.38	0.59
26:DA:2173:A:H2'	26:DA:2174:C:O4'	2.03	0.59
23:AW:5:G:H2'	23:AW:6:G:H8	1.67	0.59
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.02	0.59
1:CA:1010:G:C2	1:CA:1011:G:C8	2.91	0.59
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.84	0.59
1:AA:1239:A:H62	1:AA:1299:A:N6	2.01	0.59
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.37	0.59
19:AS:30:LEU:HD11	19:AS:50:ALA:HB2	1.85	0.59
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.49	0.59
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.85	0.59
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.85	0.59
26:DA:249:C:O2	55:D8:12:LYS:NZ	2.29	0.59
26:BA:1913:A:H4'	26:BA:1914:C:H5''	1.83	0.59
26:BA:322:A:OP1	30:BF:168:ARG:HD2	2.03	0.59
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.68	0.59
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.67	0.58
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.03	0.58
26:BA:2789:C:O2	26:BA:2894:G:N2	2.35	0.58
26:DA:848:G:N3	26:DA:933:A:H1'	2.18	0.58
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.17	0.58
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.23	0.58
45:DY:5:MET:HE1	45:DY:32:PRO:HA	1.84	0.58
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.36	0.58
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.37	0.58
2:AB:162:ILE:O	2:AB:185:ILE:HG12	2.03	0.58
26:BA:526:A:O2'	26:BA:2043:C:O2	2.20	0.58
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.02	0.58
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.58
4:CD:64:LEU:HB2	4:CD:198:VAL:HG11	1.84	0.58
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.02	0.58
1:AA:17:U:H2'	1:AA:18:C:C6	2.38	0.58
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.85	0.58
1:CA:1338:G:H21	24:CX:41:C:H1'	1.68	0.58
25:AY:53:G:C5	25:AY:54:5MU:H72	2.38	0.58
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.22	0.58
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.03	0.58
37:DQ:48:GLU:OE1	37:DQ:51:ARG:NH2	2.33	0.58
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.84	0.58
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.36	0.58
26:BA:1021:A:H62	26:BA:1141:U:H3	1.51	0.58
23:AW:66:U:H2'	23:AW:67:C:H6	1.66	0.58
1:AA:46:G:O6	61:AA:4200:HOH:O	2.15	0.58
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.86	0.58
1:CA:504:C:OP1	61:CA:4008:HOH:O	2.17	0.58
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.85	0.58
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.38	0.58
23:AW:47:U:O2'	23:AW:48:C:OP1	2.20	0.58
26:BA:2485:G:OP1	37:BQ:46:GLN:NE2	2.35	0.58
26:DA:2365:G:O6	55:D8:43:GLN:NE2	2.36	0.58
24:CX:50:U:H3	24:CX:64:G:H1	1.51	0.58
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.16	0.58
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.85	0.58
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.84	0.58
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.84	0.58
26:DA:900:A:H2'	26:DA:901:A:C8	2.39	0.58
26:BA:184:C:H2'	26:BA:185:U:C6	2.38	0.58
1:AA:1302:U:C5	13:AM:17:VAL:HG21	2.38	0.58
1:CA:48:C:OP2	61:CA:4100:HOH:O	2.16	0.58
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.03	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
1:CA:420:U:O2'	1:CA:423:G:O6	2.18	0.58
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.38	0.58
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.68	0.58
1:AA:473:G:H2'	1:AA:474:G:C8	2.39	0.58
1:AA:1125:U:H1'	1:AA:1126:U:H2'	1.86	0.58
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.85	0.58
6:CF:24:GLU:HG3	6:CF:28:ARG:NH1	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.21	0.58
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.19	0.58
46:DZ:117:LEU:HA	46:DZ:174:VAL:HA	1.86	0.58
26:BA:2144:U:O2'	26:BA:2145:C:H2'	2.04	0.58
1:CA:473:G:H2'	1:CA:474:G:C8	2.39	0.58
26:DA:2438:U:O2'	26:DA:2440:C:OP1	2.20	0.58
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.14	0.58
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.04	0.58
26:DA:1300:U:H4'	26:DA:1301:A:H5''	1.86	0.58
15:CO:3:ILE:H	15:CO:3:ILE:HD13	1.67	0.58
26:BA:871:U:OP1	37:BQ:5:ARG:HD3	2.04	0.58
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.69	0.58
26:BA:2659:G:O2'	32:BH:175:LYS:NZ	2.37	0.58
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.33	0.58
23:AW:28:G:H2'	23:AW:29:G:H8	1.67	0.58
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.04	0.58
26:BA:801:G:O6	30:BF:53:THR:OG1	2.20	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.69	0.58
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.15	0.58
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.36	0.58
26:DA:1253:A:N6	61:DA:3721:HOH:O	2.33	0.58
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.86	0.58
25:CY:40:C:C2'	25:CY:41:C:H5'	2.34	0.58
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.33	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
1:AA:347:G:H2'	1:AA:348:G:O4'	2.03	0.58
1:CA:1277:C:O2'	1:CA:1279:A:H8	1.86	0.58
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.67	0.58
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.03	0.58
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.21	0.58
26:BA:303:U:O4	61:BA:4677:HOH:O	2.13	0.58
1:CA:971:G:OP2	1:CA:1231:G:N2	2.26	0.58
1:AA:727:G:N2	1:AA:730:G:OP2	2.36	0.58
9:CI:5:TYR:O	9:CI:87:GLN:NE2	2.37	0.58
1:CA:1153:C:H42	1:CA:1154:G:N2	2.01	0.57
33:BI:129:THR:HG22	33:BI:139:GLN:NE2	2.17	0.57
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.37	0.57
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.69	0.57
26:BA:566:U:H5''	36:BP:29:LYS:HE3	1.86	0.57
50:B3:18:ASP:N	50:B3:18:ASP:OD1	2.37	0.57
1:CA:995:C:O2	14:CN:4:LYS:NZ	2.28	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:34:C:H2'	1:CA:35:G:H8	1.69	0.57
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.86	0.57
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.86	0.57
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.57
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.85	0.57
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.04	0.57
26:BA:2430:A:N3	26:BA:2430:A:H2'	2.18	0.57
27:BB:75:G:H8	27:BB:75:G:H5'	1.69	0.57
25:AY:38:A:H2'	25:AY:39:PSU:O4'	2.04	0.57
26:BA:1166:C:H2'	26:BA:1167:U:C6	2.39	0.57
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.33	0.57
23:AW:5:G:H2'	23:AW:6:G:C8	2.39	0.57
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.04	0.57
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.29	0.57
33:BI:140:LEU:HD22	33:BI:142:VAL:HG13	1.86	0.57
26:DA:399:G:OP2	61:DA:4406:HOH:O	2.17	0.57
1:CA:1026:G:O6	1:CA:1036:G:N2	2.37	0.57
2:AB:16:HIS:HD2	2:AB:17:PHE:N	2.00	0.57
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.05	0.57
25:AY:63:G:H2'	25:AY:64:A:O4'	2.04	0.57
1:CA:975:A:N1	10:CJ:48:THR:HB	2.19	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.38	0.57
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.39	0.57
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.40	0.57
26:BA:893:C:H2'	26:BA:894:C:C6	2.39	0.57
1:AA:757:U:H2'	1:AA:758:G:O4'	2.04	0.57
15:CO:82:ILE:HB	15:CO:87:ILE:HB	1.87	0.57
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.68	0.57
26:DA:1448:G:H4'	26:DA:1542:A:OP1	2.05	0.57
26:DA:1359:A:H61	26:DA:1372:U:H3	1.52	0.57
41:BU:89:GLU:HG3	42:BV:50:PRO:HB3	1.86	0.57
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.68	0.57
1:AA:1392:G:N2	1:AA:1502:A:H8	2.01	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.40	0.57
26:DA:1264:G:OP1	52:D5:19:ARG:NH2	2.35	0.57
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.69	0.57
26:DA:531:C:H4'	26:DA:532:A:H5'	1.86	0.57
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.70	0.57
26:DA:903:C:H2'	26:DA:904:C:C6	2.40	0.57
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.01	0.57
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.37	0.57
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.40	0.57
26:BA:2334:G:H5'	39:BS:9:ARG:HG2	1.85	0.57
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.69	0.57
27:BB:14:U:OP2	27:BB:70:C:O2'	2.20	0.57
26:DA:1209:G:O2'	26:DA:1237:A:N1	2.32	0.57
2:CB:63:MET:HG3	2:CB:225:ALA:HB1	1.86	0.57
1:CA:1099:G:OP2	2:CB:144:ARG:NH2	2.34	0.57
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.37	0.57
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.35	0.57
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.70	0.57
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.86	0.57
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.70	0.57
25:CY:2:C:H2'	25:CY:3:C:C6	2.39	0.57
26:BA:878:A:H61	26:BA:899:A:H1'	1.70	0.57
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.05	0.57
26:BA:30:G:OP2	41:BU:5:LYS:NZ	2.29	0.57
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.86	0.57
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.87	0.57
27:DB:41:U:H5	31:DG:70:VAL:H	1.51	0.57
26:BA:2001:A:OP1	38:BR:9:LYS:NZ	2.36	0.57
1:CA:992:U:H3	1:CA:1044:A:H62	1.53	0.57
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.21	0.57
26:DA:1013:C:H2'	26:DA:1014:U:H6	1.69	0.57
26:BA:579:G:H2'	26:BA:580:C:C6	2.40	0.57
26:DA:658:C:H2'	26:DA:659:C:C6	2.40	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.35	0.57
1:CA:1000:U:N3	1:CA:1041:A:N6	2.22	0.57
1:AA:993:G:H2'	1:AA:995:C:H41	1.69	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.33	0.57
25:CY:27:G:N1	25:CY:43:C:O2	2.38	0.57
14:CN:24:CYS:O	14:CN:28:GLY:N	2.30	0.57
24:CX:67:C:H2'	24:CX:68:C:H5'	1.86	0.57
1:AA:69:G:H2'	1:AA:70:G:C8	2.39	0.57
26:BA:576:U:H2'	26:BA:577:G:C8	2.39	0.57
11:CK:48:ILE:O	11:CK:50:TYR:N	2.37	0.57
26:DA:197:A:O2'	61:DA:3732:HOH:O	2.16	0.57
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	1.87	0.57
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.70	0.57
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.86	0.57
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.40	0.57
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.70	0.57
25:AY:59:U:H5'	25:AY:60:U:H5	1.70	0.57
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.31	0.57
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.20	0.57
1:CA:1086:U:H3	1:CA:1099:G:H22	1.53	0.57
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.38	0.57
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.57
32:DH:80:SER:OG	32:DH:81:GLU:OE1	2.17	0.57
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.70	0.57
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.37	0.57
26:BA:880:G:H2'	26:BA:881:G:H8	1.69	0.56
26:DA:2808:U:H2'	26:DA:2809:A:H5'	1.87	0.56
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.22	0.56
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.40	0.56
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.87	0.56
26:BA:1799:G:O2'	28:BD:181:GLU:OE2	2.22	0.56
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.70	0.56
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.38	0.56
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.86	0.56
25:CY:9:A:OP2	25:CY:13:C:N4	2.38	0.56
40:DT:53:ARG:HB3	40:DT:53:ARG:HH11	1.70	0.56
1:CA:953:G:H5'	1:CA:965:A:N6	2.20	0.56
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.87	0.56
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.38	0.56
1:AA:977:A:N6	1:AA:1224:G:OP1	2.29	0.56
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.88	0.56
26:DA:1864:U:OP1	26:DA:2410:G:O2'	2.17	0.56
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.85	0.56
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.68	0.56
1:CA:1502:A:H2	1:CA:1505:G:N1	1.99	0.56
1:CA:1154:G:N7	1:CA:1155:G:C8	2.73	0.56
46:BZ:137:ILE:HA	46:BZ:156:LYS:NZ	2.20	0.56
3:CC:126:ARG:HB3	3:CC:128:PHE:CE1	2.40	0.56
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.87	0.56
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.87	0.56
23:CW:30:G:H1	23:CW:40:C:H42	1.51	0.56
33:DI:110:ASP:N	33:DI:130:TYR:OH	2.34	0.56
26:DA:866:A:H2	26:DA:867:C:C4	2.23	0.56
1:AA:333:G:H4'	20:AT:16:HIS:CE1	2.41	0.56
1:CA:426:G:OP1	4:CD:36:ARG:HD2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.88	0.56
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.70	0.56
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	1.87	0.56
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.05	0.56
27:DB:110:G:H2'	27:DB:111:G:H8	1.70	0.56
1:AA:952:U:H2'	1:AA:953:G:C8	2.41	0.56
26:BA:453:C:O2	26:BA:457:A:O2'	2.22	0.56
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.88	0.56
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.39	0.56
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.40	0.56
1:CA:222:U:H2'	1:CA:223:U:C6	2.39	0.56
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.40	0.56
46:BZ:111:VAL:HG21	46:BZ:117:LEU:HB2	1.88	0.56
1:AA:96:U:O2'	1:AA:97:G:H8	1.88	0.56
26:DA:1805:U:O2	28:DD:50:THR:HB	2.05	0.56
26:DA:534:U:H2'	26:DA:535:C:C6	2.41	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
13:AM:84:ILE:HD12	19:AS:74:PHE:HE2	1.70	0.56
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.87	0.56
1:CA:1392:G:N2	1:CA:1502:A:H8	2.03	0.56
1:CA:9:G:H2'	1:CA:10:A:C8	2.41	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.88	0.56
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.88	0.56
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.20	0.56
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.56
1:AA:58:C:O2'	1:AA:388:G:N7	2.33	0.56
26:DA:1639:U:H2'	26:DA:1640:C:H5'	1.88	0.56
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.88	0.56
26:BA:2708:G:H1'	38:BR:71:GLN:HE22	1.70	0.56
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	1.88	0.56
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	1.88	0.56
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.05	0.56
26:DA:2167:U:O2'	26:DA:2168:G:O4'	2.23	0.56
1:AA:976:G:N2	1:AA:1363:C:OP2	2.38	0.56
31:BG:41:GLN:HG3	31:BG:60:LEU:HD21	1.88	0.56
26:BA:171:G:O2'	26:BA:172:C:H5'	2.06	0.56
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.06	0.56
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.04	0.56
30:BF:161:GLU:HG2	30:BF:164:ARG:NH2	2.20	0.56
26:DA:245:G:O6	55:D8:8:LYS:NZ	2.31	0.56
1:AA:671:G:H5'	6:AF:77:ARG:HH22	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DY:99:CYS:HB2	45:DY:106:LEU:HD21	1.88	0.56
26:BA:668:G:H5'	26:BA:669:G:OP2	2.06	0.56
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.25	0.56
26:BA:588:U:H2'	26:BA:589:C:C6	2.41	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
26:DA:125:G:O2'	54:D7:48:LYS:NZ	2.36	0.56
26:DA:1787:A:N3	61:DA:3727:HOH:O	2.33	0.56
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.53	0.56
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.88	0.56
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.06	0.56
1:AA:103:C:O2'	1:AA:172:A:N1	2.34	0.56
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.41	0.56
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	1.87	0.56
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.41	0.56
21:CU:7:ARG:HD2	21:CU:21:TYR:HE2	1.69	0.56
28:DD:4:LYS:HB3	28:DD:18:VAL:HG23	1.88	0.56
37:DQ:1:MET:SD	37:DQ:1:MET:N	2.66	0.56
26:BA:71:A:OP2	26:BA:71:A:H3'	2.06	0.56
26:DA:2138:C:H2'	26:DA:2139:C:H5''	1.87	0.56
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.41	0.56
26:BA:2124:G:H1	26:BA:2174:C:N4	2.04	0.56
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.88	0.56
1:CA:1047:G:H5''	14:CN:4:LYS:HD2	1.87	0.56
8:CH:39:LEU:HD12	8:CH:44:PHE:HB2	1.88	0.56
31:BG:77:ILE:HG22	31:BG:80:PHE:H	1.69	0.56
36:BP:89:ALA:O	36:BP:121:LYS:NZ	2.27	0.56
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.24	0.56
10:CJ:47:PHE:N	10:CJ:63:PHE:O	2.33	0.56
1:AA:139:G:N2	1:AA:224:C:O2	2.35	0.56
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.41	0.56
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.19	0.56
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.21	0.56
26:DA:1265:A:OP2	61:DA:4004:HOH:O	2.18	0.56
32:DH:113:VAL:HG11	32:DH:151:ILE:HD13	1.87	0.56
26:BA:784:A:H5'	26:BA:785:G:OP1	2.06	0.56
1:CA:1120:G:C6	1:CA:1121:U:C4	2.94	0.55
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.27	0.55
1:AA:736:C:H2'	1:AA:737:A:H8	1.71	0.55
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.37	0.55
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.71	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1392:G:H21	1:AA:1502:A:H8	1.54	0.55
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.53	0.55
24:CX:40:C:H2'	24:CX:41:C:H6	1.71	0.55
1:CA:450:G:OP1	16:CP:43:LYS:NZ	2.38	0.55
1:CA:442:C:H42	1:CA:492:G:H1	1.53	0.55
4:AD:175:SER:HB3	4:AD:186:LEU:HD11	1.88	0.55
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.41	0.55
26:DA:1527:G:HO2'	26:DA:1544:A:H62	1.53	0.55
26:BA:1309:G:O6	61:BA:4912:HOH:O	2.17	0.55
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.55
26:BA:592:G:O6	61:BA:4937:HOH:O	2.16	0.55
2:CB:8:LYS:HG3	2:CB:9:GLU:HG3	1.87	0.55
26:DA:1039:G:O6	26:DA:1116:C:N4	2.37	0.55
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.55
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.41	0.55
25:AY:19:G:H3'	25:AY:20:U:C6	2.41	0.55
12:AL:24:VAL:HG13	12:AL:98:TYR:CE1	2.41	0.55
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.88	0.55
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.36	0.55
5:CE:50:GLU:HB2	5:CE:53:LEU:HD12	1.88	0.55
26:DA:140:G:N2	26:DA:1596:A:H4'	2.21	0.55
26:BA:2662:A:H2'	26:BA:2663:G:O4'	2.07	0.55
34:DN:17:ASP:HB2	34:DN:137:LYS:HZ1	1.71	0.55
26:BA:2238:G:H2'	26:BA:2238:G:N3	2.20	0.55
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.88	0.55
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.87	0.55
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.41	0.55
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.05	0.55
26:BA:2791:C:H2'	26:BA:2792:G:H8	1.71	0.55
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.39	0.55
3:CC:6:HIS:CD2	3:CC:8:ILE:H	2.23	0.55
13:CM:65:LYS:HA	51:D4:50:VAL:HG11	1.87	0.55
30:BF:158:THR:O	30:BF:164:ARG:NH1	2.38	0.55
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.41	0.55
11:AK:34:ASP:OD1	11:AK:38:ASN:N	2.40	0.55
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.39	0.55
33:DI:38:LEU:HB2	33:DI:40:THR:HG22	1.89	0.55
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.03	0.55
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.40	0.55
1:AA:442:C:H42	1:AA:492:G:H1	1.53	0.55
1:CA:1154:G:N7	1:CA:1155:G:N9	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.88	0.55
1:AA:1445:C:N3	1:AA:1457:G:N1	2.37	0.55
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.88	0.55
3:CC:33:LEU:HD21	14:CN:53:LEU:HD23	1.88	0.55
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.70	0.55
26:DA:320:A:OP2	30:DF:137:LYS:NZ	2.33	0.55
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.06	0.55
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.18	0.55
26:BA:222:A:H5''	26:BA:421:U:OP1	2.07	0.55
26:DA:2882:A:H5'	38:DR:96:ARG:HG3	1.87	0.55
26:DA:859:G:N2	26:DA:917:A:OP2	2.39	0.55
26:BA:2171:A:H1'	26:BA:2172:U:O4'	2.07	0.55
26:BA:2110:G:C2	26:BA:2120:G:H1'	2.42	0.55
26:DA:848:G:C2	26:DA:933:A:H1'	2.42	0.55
55:B8:62:LEU:HB3	55:B8:65:GLU:CG	2.36	0.55
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.41	0.55
2:CB:48:MET:HA	2:CB:51:LEU:HB2	1.89	0.55
44:BX:2:LYS:NZ	44:BX:38:GLU:OE2	2.30	0.55
11:CK:24:SER:OG	11:CK:25:TYR:N	2.38	0.55
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.37	0.55
26:DA:84:A:H5''	45:DY:8:LYS:HE3	1.88	0.55
1:AA:123:C:OP1	1:AA:311:C:O2'	2.20	0.55
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.41	0.55
27:BB:91:C:H5'	37:BQ:18:LYS:HA	1.87	0.55
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.89	0.55
1:CA:1002:G:H1	1:CA:1038:C:H42	0.70	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
26:DA:1530:C:HO2'	26:DA:1531:C:P	2.29	0.55
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.54	0.55
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.40	0.55
27:DB:24:G:H4'	27:DB:25:A:C8	2.41	0.55
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.88	0.55
26:DA:330:A:H2	26:DA:1210:A:HO2'	1.54	0.55
51:D4:46:GLN:C	51:D4:48:ARG:H	2.10	0.55
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.72	0.55
33:BI:106:GLY:HA2	33:BI:107:VAL:O	2.06	0.55
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.07	0.55
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.21	0.55
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.88	0.55
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.55
10:CJ:55:LYS:HG3	10:CJ:56:HIS:CD2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:353:A:H5'	1:AA:353:A:H8	1.72	0.55
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.72	0.55
26:BA:898:C:H2'	26:BA:899:A:H8	1.70	0.55
31:DG:179:PRO:HB2	51:D4:42:PHE:CE1	2.41	0.55
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.20	0.55
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.70	0.55
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.55
2:CB:45:GLN:O	2:CB:49:GLU:HB2	2.06	0.55
24:AX:64:G:H4'	37:BQ:10:ARG:HH21	1.71	0.55
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.25	0.55
1:CA:328:C:H4'	1:CA:329:A:H5'	1.89	0.55
1:CA:1023:G:C4	1:CA:1024:G:C8	2.94	0.55
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.71	0.55
2:AB:16:HIS:O	2:AB:17:PHE:HD1	1.89	0.55
25:AY:50:U:N3	25:AY:64:A:C2	2.69	0.55
26:BA:2141:G:H1	26:BA:2149:G:N2	2.02	0.55
26:DA:900:A:O2'	26:DA:901:A:OP1	2.24	0.55
4:CD:196:LEU:O	4:CD:198:VAL:N	2.36	0.55
26:BA:2336:A:H61	47:B0:43:THR:HG22	1.71	0.55
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.71	0.55
34:DN:128:HIS:O	34:DN:131:GLN:NE2	2.40	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.22	0.55
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.55	0.55
36:BP:36:LYS:O	61:BP:306:HOH:O	2.18	0.55
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.41	0.55
7:CG:78:ARG:HB2	7:CG:156:TRP:HZ3	1.72	0.55
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.88	0.55
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.89	0.55
36:DP:84:ASN:CG	36:DP:117:GLU:HB2	2.27	0.55
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	1.88	0.55
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.06	0.55
26:DA:2349:G:OP1	61:DA:3781:HOH:O	2.18	0.55
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.88	0.55
25:CY:29:G:H1	25:CY:41:C:N4	2.05	0.54
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.89	0.54
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.70	0.54
25:AY:33:U:H2'	25:AY:35:A:OP2	2.07	0.54
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.54
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.42	0.54
46:DZ:163:LEU:HG	46:DZ:165:VAL:HG22	1.88	0.54
26:DA:223:A:O2'	26:DA:420:C:O2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:109:A:OP1	61:AA:4215:HOH:O	2.18	0.54
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	1.89	0.54
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.41	0.54
26:DA:2155:G:H2'	26:DA:2156:G:H5'	1.89	0.54
25:CY:39:PSU:C2	25:CY:40:C:C2	2.95	0.54
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.89	0.54
39:DS:93:LYS:HD3	39:DS:94:TYR:N	2.22	0.54
15:CO:5:LYS:N	15:CO:5:LYS:HD3	2.23	0.54
26:DA:191:A:N1	61:DA:4228:HOH:O	2.34	0.54
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.37	0.54
16:CP:8:ARG:HG3	16:CP:17:TYR:CE1	2.42	0.54
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.72	0.54
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.42	0.54
26:DA:637:A:H2'	36:DP:117:GLU:OE2	2.08	0.54
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.06	0.54
48:D1:54:ALA:HB1	48:D1:83:GLU:HG3	1.88	0.54
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.39	0.54
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.87	0.54
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.90	0.54
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.40	0.54
1:CA:419:C:OP1	1:CA:513:C:O2'	2.23	0.54
26:BA:1253:A:OP1	61:BA:4931:HOH:O	2.18	0.54
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.25	0.54
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.22	0.54
26:BA:1047:G:HO2'	26:BA:1048:A:H8	1.55	0.54
1:AA:1007:C:N3	1:AA:1022:G:O6	2.41	0.54
26:BA:404:C:H4'	26:BA:405:U:H5'	1.89	0.54
31:DG:23:PHE:HB2	31:DG:25:TYR:CZ	2.42	0.54
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.31	0.54
46:BZ:4:ARG:NE	46:BZ:60:GLU:OE1	2.28	0.54
26:BA:226:G:H21	26:BA:228:A:H62	1.54	0.54
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.36	0.54
7:AG:152:ALA:HB1	7:AG:155:ARG:HH21	1.72	0.54
26:BA:69:C:O2	26:BA:73:A:O2'	2.23	0.54
26:DA:276:A:H5''	26:DA:277:C:H5'	1.88	0.54
1:AA:501:C:H2'	1:AA:502:G:C8	2.43	0.54
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.42	0.54
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.89	0.54
26:BA:2180:U:H2'	26:BA:2181:G:O4'	2.08	0.54
26:DA:2612:C:OP2	52:D5:2:ALA:N	2.41	0.54
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:51:U:H3	25:AY:63:G:H1	1.55	0.54
26:BA:2129:C:H2'	26:BA:2130:U:C6	2.42	0.54
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.41	0.54
26:DA:300:A:P	45:DY:86:ARG:HH22	2.30	0.54
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.40	0.54
26:DA:2733:A:N1	29:DE:203:LYS:HA	2.23	0.54
26:DA:796:C:H2'	26:DA:797:C:C6	2.42	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.38	0.54
1:CA:1378:C:H5	1:CA:1379:G:C4	2.25	0.54
1:CA:859:A:OP2	1:CA:869:G:N1	2.34	0.54
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.88	0.54
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.90	0.54
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.72	0.54
5:AE:91:LEU:HB3	5:AE:118:ILE:HD11	1.89	0.54
26:BA:2116:G:N1	26:BA:2162:G:OP1	2.41	0.54
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.43	0.54
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.06	0.54
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.41	0.54
26:BA:1721:G:H3'	26:BA:1722:A:H5''	1.88	0.54
1:AA:848:C:H2'	1:AA:849:C:C6	2.43	0.54
3:AC:104:GLN:HE21	3:AC:105:GLU:N	2.05	0.54
32:DH:56:SER:OG	32:DH:57:ASP:N	2.41	0.54
26:DA:641:C:H42	26:DA:647:G:H1	1.56	0.54
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.24	0.54
25:AY:67:C:H2'	25:AY:68:C:O4'	2.08	0.54
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.23	0.54
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.72	0.54
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.22	0.54
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.88	0.54
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	1.88	0.54
1:AA:1292:U:H5'	9:AI:38:GLN:NE2	2.22	0.54
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.54
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.90	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.90	0.54
1:CA:701:C:OP1	1:CA:702:A:O2'	2.14	0.54
33:DI:14:ASP:OD1	33:DI:15:VAL:N	2.38	0.54
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	1.89	0.54
26:DA:1183:G:H5''	50:D3:30:ARG:HH12	1.73	0.54
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.40	0.54
18:CR:61:LYS:O	18:CR:65:ILE:HG12	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1971:A:N1	61:BA:4352:HOH:O	2.33	0.54
6:CF:46:ARG:HG3	6:CF:47:ARG:N	2.21	0.54
1:CA:1003:G:N2	1:CA:1025:U:O4	2.40	0.54
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.23	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:HB3	1.88	0.54
26:DA:855:G:H2'	26:DA:856:C:C6	2.43	0.54
3:CC:6:HIS:CG	14:CN:49:HIS:HB3	2.43	0.54
26:BA:2327:A:H2'	26:BA:2328:A:C8	2.42	0.54
1:AA:45:U:H2'	1:AA:46:G:C8	2.42	0.54
1:AA:171:A:H2'	1:AA:172:A:C8	2.42	0.54
24:CX:58:A:H4'	24:CX:59:A:OP1	2.08	0.54
26:DA:252:G:P	36:DP:50:ARG:HH12	2.31	0.54
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.07	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.06	0.54
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.88	0.54
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.07	0.54
26:DA:879:G:H3'	26:DA:880:G:H8	1.72	0.54
51:B4:54:GLY:C	51:B4:56:VAL:HA	2.28	0.54
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.23	0.54
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.89	0.54
1:CA:723:U:HO2'	1:CA:724:G:C5'	2.21	0.54
1:AA:159:G:O2'	1:AA:161:A:N7	2.30	0.54
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.43	0.54
1:CA:441:A:H3'	1:CA:442:C:C6	2.43	0.54
26:DA:971:C:OP2	61:DA:4647:HOH:O	2.18	0.54
26:BA:271(E):U:H2'	26:BA:271(F):C:C6	2.43	0.54
1:AA:934:C:OP1	61:AA:4110:HOH:O	2.18	0.54
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.07	0.54
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.73	0.54
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.08	0.54
26:BA:2243:U:OP1	61:BA:4017:HOH:O	2.17	0.54
1:AA:524:G:H2'	1:AA:525:C:C6	2.43	0.54
1:CA:399:G:H2'	1:CA:400:C:C6	2.43	0.54
1:AA:539:A:H2'	1:AA:540:G:C8	2.43	0.54
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.40	0.54
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.20	0.54
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.90	0.54
26:BA:1174:A:H1'	26:BA:1175:U:H5''	1.89	0.54
26:BA:887:A:H4'	26:BA:888:C:C5	2.43	0.54
3:CC:55:VAL:HG22	3:CC:68:VAL:HG22	1.88	0.54
1:CA:428:G:OP2	4:CD:10:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.08	0.54
26:DA:1013:C:H2'	26:DA:1014:U:C6	2.43	0.54
26:BA:272:G:O2'	26:BA:421:U:OP2	2.22	0.54
26:DA:391:G:O2'	26:DA:410:G:OP1	2.19	0.54
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.41	0.54
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.90	0.54
1:AA:316:G:OP2	1:AA:351:G:O2'	2.25	0.54
1:AA:222:U:H2'	1:AA:223:U:C6	2.43	0.54
23:AW:9:A:O2'	23:AW:10:G:N7	2.40	0.54
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.89	0.54
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.43	0.54
1:CA:1490:C:H2'	1:CA:1491:G:H8	1.72	0.54
25:AY:6:G:O6	25:AY:7:A:N6	2.40	0.54
2:CB:16:HIS:CB	2:CB:210:SER:HB2	2.28	0.54
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.41	0.54
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.89	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.42	0.54
1:AA:26:A:N6	1:AA:558:G:O2'	2.39	0.54
26:BA:271(H):G:O2'	26:BA:271(I):G:H8	1.90	0.54
26:DA:2102:U:H3	26:DA:2187:G:H1	1.56	0.54
1:CA:59:A:H5''	1:CA:60:A:H5''	1.89	0.54
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.40	0.54
1:AA:880:C:OP1	12:AL:8:ASN:ND2	2.39	0.54
26:BA:2630:G:H2'	26:BA:2631:G:C8	2.43	0.54
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.41	0.54
26:BA:1470:G:N2	26:BA:1520:G:OP2	2.34	0.54
2:CB:15:VAL:HG12	2:CB:16:HIS:H	1.73	0.53
23:CW:66:U:C3'	23:CW:67:C:H5''	2.32	0.53
1:CA:93:G:O2'	1:CA:96:U:H5'	2.08	0.53
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.23	0.53
25:AY:9:A:H5''	25:AY:46:7MG:N2	2.23	0.53
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.90	0.53
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.43	0.53
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.31	0.53
54:B7:24:THR:CG2	54:B7:27:GLY:H	2.20	0.53
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.89	0.53
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.89	0.53
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.41	0.53
26:DA:625:G:O6	36:DP:107:LYS:NZ	2.36	0.53
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:49:ILE:HD13	19:CS:62:ILE:HD13	1.90	0.53
1:CA:299:G:H2'	1:CA:300:A:C8	2.43	0.53
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.89	0.53
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.08	0.53
26:DA:203:C:OP2	61:DA:4309:HOH:O	2.19	0.53
26:BA:2142:C:H2'	26:BA:2143:C:C6	2.43	0.53
1:CA:1011:G:C6	1:CA:1012:U:C2	2.97	0.53
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.90	0.53
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.91	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.53
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.44	0.53
1:AA:159:G:N2	1:AA:162:A:OP2	2.37	0.53
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.43	0.53
33:DI:27:ARG:HD2	48:D1:71:TYR:CE1	2.43	0.53
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.72	0.53
26:DA:500:G:N1	26:DA:503:A:OP2	2.40	0.53
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.40	0.53
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.29	0.53
10:AJ:13:HIS:O	10:AJ:17:ASP:HB2	2.09	0.53
27:DB:90:A:C5	27:DB:91:C:H1'	2.44	0.53
36:DP:121:LYS:O	36:DP:123:LEU:N	2.40	0.53
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.89	0.53
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.90	0.53
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.74	0.53
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.90	0.53
1:CA:890:G:O2'	1:CA:906:G:O6	2.20	0.53
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.23	0.53
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.23	0.53
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.90	0.53
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.72	0.53
4:CD:61:LYS:HD2	4:CD:206:PHE:CE2	2.43	0.53
2:CB:95:GLN:HG3	2:CB:148:TYR:HA	1.90	0.53
26:DA:1203:G:O2'	26:DA:1242:A:N6	2.39	0.53
1:CA:1272:G:C2	1:CA:1273:G:H1'	2.43	0.53
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.53
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.73	0.53
23:CW:27:G:H1	23:CW:43:C:N4	2.03	0.53
26:BA:2115:G:H21	26:BA:2171:A:H61	1.57	0.53
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.36	0.53
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.89	0.53
13:AM:80:ARG:HH22	19:AS:69:HIS:CE1	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1007:C:P	34:DN:37:LYS:HZ1	2.31	0.53
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.44	0.53
29:DE:36:ARG:HD3	29:DE:85:ASN:HD21	1.73	0.53
1:CA:382:A:H2'	1:CA:383:A:C8	2.43	0.53
51:B4:15:ILE:O	51:B4:33:VAL:N	2.39	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.91	0.53
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.44	0.53
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.24	0.53
17:AQ:95:TYR:HA	17:AQ:98:LEU:HD22	1.89	0.53
1:AA:346:G:OP1	40:BT:41:ARG:NH2	2.41	0.53
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.91	0.53
13:CM:22:ILE:HG23	13:CM:67:GLU:HG2	1.91	0.53
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.90	0.53
27:DB:95:C:H2'	27:DB:96:U:C6	2.44	0.53
1:CA:543:C:OP1	4:CD:14:ARG:NE	2.36	0.53
39:DS:67:ARG:HG3	39:DS:104:GLY:HA3	1.90	0.53
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.41	0.53
26:BA:2537:U:H2'	26:BA:2538:C:C6	2.44	0.53
1:AA:198:G:O6	1:AA:219:C:N4	2.42	0.53
33:BI:61:ARG:HA	33:BI:61:ARG:HH11	1.73	0.53
1:AA:715:A:H2'	1:AA:716:A:C8	2.44	0.53
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.44	0.53
36:BP:42:SER:O	61:BP:305:HOH:O	2.18	0.53
26:DA:2070:G:OP2	61:DA:4495:HOH:O	2.18	0.53
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.74	0.53
25:AY:49:C:H42	25:AY:65:G:H1	0.68	0.53
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.09	0.53
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.23	0.53
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.53
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.53
1:AA:848:C:H2'	1:AA:849:C:H6	1.74	0.53
26:BA:2693:A:H2'	26:BA:2694:G:C8	2.44	0.53
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.90	0.53
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.09	0.53
26:BA:548:A:H61	42:BV:19:LYS:H	1.56	0.53
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.53
23:AW:18:G:H4'	23:AW:60:U:C5	2.43	0.53
26:DA:922:U:H2'	26:DA:923:C:C6	2.43	0.53
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.91	0.53
26:DA:2177:C:H2'	26:DA:2178:C:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1120:G:C6	1:CA:1154:G:C2	2.96	0.53
26:DA:1658:C:OP1	61:DA:4209:HOH:O	2.18	0.53
26:BA:2116:G:H2'	26:BA:2117:A:C6	2.44	0.53
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.74	0.53
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.33	0.53
2:CB:46:LYS:O	2:CB:50:GLU:N	2.42	0.53
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.08	0.53
42:DV:24:LYS:HG3	42:DV:64:HIS:HD2	1.73	0.53
26:DA:1423:G:OP1	26:DA:1492:G:O2'	2.26	0.53
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.09	0.53
26:DA:644:A:H4'	26:DA:645:C:C5	2.43	0.53
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.43	0.53
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.23	0.53
1:CA:895:G:N7	61:CA:4069:HOH:O	2.34	0.53
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.53
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.39	0.53
26:BA:2115:G:N2	26:BA:2171:A:H61	2.06	0.53
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.90	0.53
23:AW:9:A:H1'	23:AW:45:U:O2'	2.09	0.53
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.44	0.53
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.08	0.53
12:AL:39:VAL:HG11	12:AL:41:ARG:NH1	2.24	0.53
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.08	0.53
1:AA:946:A:H2'	1:AA:947:G:C8	2.43	0.53
46:BZ:126:VAL:HG11	46:BZ:161:VAL:HG23	1.89	0.53
23:AW:1:G:H2'	23:AW:2:C:C6	2.44	0.53
23:CW:75:C:H2'	23:CW:76:31M:C4	2.39	0.53
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	1.92	0.53
24:AX:7:G:H1	24:AX:66:C:H42	1.56	0.53
26:DA:144:C:H2'	26:DA:145:G:H8	1.73	0.53
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.25	0.53
6:AF:9:VAL:HB	6:AF:87:ARG:HB2	1.90	0.53
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.73	0.53
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.07	0.53
1:AA:520:A:N1	1:AA:536:C:H1'	2.23	0.53
1:AA:270:A:H2'	1:AA:271:C:C6	2.44	0.53
39:DS:87:PHE:CZ	39:DS:102:ALA:HB2	2.44	0.53
26:DA:2112:G:N7	26:DA:2169:A:N6	2.57	0.53
1:CA:1125:U:C3'	1:CA:1126:U:H5''	2.38	0.53
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.73	0.53
1:CA:1122:U:C4	1:CA:1123:A:N7	2.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:97:G:O2'	1:AA:98:G:H5''	2.09	0.53
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.91	0.53
1:AA:262:A:H2'	1:AA:263:A:C8	2.44	0.53
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.09	0.53
26:BA:639:U:H2'	26:BA:640:C:C6	2.44	0.53
26:DA:1532:C:N4	26:DA:1537:G:O6	2.20	0.53
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.89	0.53
1:CA:1125:U:O2	10:CJ:38:ILE:HG21	2.09	0.52
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.45	0.52
28:BD:10:THR:OG1	28:BD:13:ARG:HB2	2.08	0.52
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.91	0.52
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.09	0.52
26:DA:1415:U:O2'	26:DA:1417:C:OP1	2.25	0.52
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.91	0.52
2:CB:91:PRO:HD3	2:CB:154:LEU:HD12	1.91	0.52
1:CA:620:C:C2	4:CD:135:LEU:HG	2.43	0.52
16:CP:52:ASP:O	16:CP:54:GLU:N	2.33	0.52
49:B2:11:GLU:O	49:B2:15:LYS:HG3	2.09	0.52
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.08	0.52
26:DA:2684:U:O2'	35:DO:68:GLU:OE1	2.28	0.52
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.40	0.52
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.74	0.52
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	1.90	0.52
26:DA:878:A:N6	26:DA:899:A:O2'	2.43	0.52
26:BA:252:G:OP1	36:BP:50:ARG:NH1	2.42	0.52
25:AY:67:C:H2'	25:AY:68:C:C6	2.44	0.52
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.44	0.52
1:CA:1119:C:N3	1:CA:1154:G:O6	2.42	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.75	0.52
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.09	0.52
26:BA:330:A:H2	26:BA:1210:A:O2'	1.92	0.52
26:BA:1359:A:H2'	26:BA:1360:A:H5'	1.91	0.52
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.09	0.52
1:CA:164:U:H2'	1:CA:165:C:C6	2.44	0.52
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.09	0.52
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.91	0.52
24:AX:56:C:O5'	24:AX:56:C:H6	1.92	0.52
1:AA:1027:C:N3	1:AA:1028:C:N4	2.57	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:CD1	2.39	0.52
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.08	0.52
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:B3:50:VAL:HB	50:B3:53:LEU:HD12	1.90	0.52
1:AA:67:C:H2'	1:AA:68:G:C8	2.44	0.52
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.52
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.52
1:CA:625:G:H2'	1:CA:626:U:H6	1.74	0.52
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.91	0.52
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.10	0.52
34:DN:67:LEU:O	34:DN:88:GLU:HG3	2.10	0.52
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.90	0.52
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.09	0.52
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.52
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.44	0.52
26:BA:1482:G:O6	26:BA:1507:A:N6	2.42	0.52
12:AL:24:VAL:HG13	12:AL:98:TYR:HE1	1.73	0.52
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.43	0.52
26:BA:1843:C:H5'	28:BD:253:GLN:HE22	1.74	0.52
32:BH:56:SER:OG	32:BH:57:ASP:N	2.42	0.52
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.42	0.52
33:DI:40:THR:O	33:DI:44:LEU:HB2	2.09	0.52
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.45	0.52
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.45	0.52
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.92	0.52
3:CC:111:LEU:HD22	3:CC:146:ALA:HB2	1.92	0.52
44:DX:44:GLU:O	44:DX:48:LYS:N	2.42	0.52
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.92	0.52
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.44	0.52
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.92	0.52
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.92	0.52
27:BB:7:G:H5''	27:BB:7:G:H8	1.75	0.52
1:AA:1053:G:C3'	1:AA:1054:C:H5'	2.39	0.52
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.90	0.52
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.10	0.52
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.74	0.52
26:BA:1429:G:H2'	26:BA:1430:C:C6	2.44	0.52
26:DA:2803:C:H2'	26:DA:2804:C:H6	1.74	0.52
26:BA:2136:C:N4	26:BA:2155:G:N1	2.32	0.52
26:BA:1187:G:H5''	42:BV:81:TYR:CE1	2.43	0.52
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.52
1:CA:1243:C:H42	1:CA:1294:G:H1	1.58	0.52
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.44	0.52
23:AW:1:G:O6	23:AW:72:C:N3	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:49:ARG:NH1	55:B8:61:LEU:HD23	2.24	0.52
50:D3:13:ILE:O	61:D3:3101:HOH:O	2.19	0.52
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.91	0.52
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.45	0.52
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.42	0.52
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.52
25:CY:61:C:H2'	25:CY:62:C:C6	2.45	0.52
7:AG:49:ILE:O	7:AG:53:LYS:HG3	2.10	0.52
24:AX:4:G:H2'	24:AX:5:G:C8	2.44	0.52
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.09	0.52
26:BA:957:A:N1	26:BA:2458:G:H4'	2.25	0.52
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.43	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.43	0.52
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.91	0.52
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.74	0.52
1:CA:1469:G:N7	61:CA:4124:HOH:O	2.34	0.52
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.24	0.52
1:AA:685:G:N2	1:AA:704:A:OP2	2.33	0.52
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.74	0.52
26:DA:821:A:N1	61:DA:4093:HOH:O	2.34	0.52
1:AA:1320:C:OP1	19:AS:70:LYS:HE3	2.09	0.52
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.75	0.52
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.54	0.52
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.09	0.52
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.43	0.52
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.10	0.52
26:DA:2171:A:C4	26:DA:2172:U:C4	2.98	0.52
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.09	0.52
1:CA:1154:G:N7	1:CA:1155:G:C4	2.78	0.52
20:CT:43:LEU:O	20:CT:47:GLY:N	2.42	0.52
1:CA:1075:C:C2'	1:CA:1076:C:H5''	2.40	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.92	0.52
1:AA:838:G:H2'	1:AA:839:U:H2'	1.92	0.52
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.45	0.52
8:CH:49:GLU:HG2	8:CH:62:TYR:HE1	1.75	0.52
1:CA:296:U:O2'	1:CA:556:C:O2	2.27	0.52
17:CQ:5:VAL:HG22	17:CQ:60:ILE:HG12	1.91	0.52
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.38	0.52
1:CA:189(L):G:H2'	1:CA:190:U:H6	1.74	0.52
39:BS:106:ARG:O	39:BS:109:GLY:N	2.40	0.52
4:AD:107:ARG:HH22	4:AD:194:LEU:HD21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:53:ARG:NH1	2:CB:53:ARG:HB3	2.25	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.10	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.92	0.52
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.45	0.52
1:AA:346:G:H3'	1:AA:347:G:H4'	1.92	0.52
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	1.92	0.52
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.43	0.52
26:DA:657:U:H2'	26:DA:658:C:C6	2.44	0.52
3:CC:126:ARG:HB3	3:CC:128:PHE:HE1	1.75	0.52
1:AA:649:G:H2'	1:AA:650:G:H8	1.74	0.52
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.75	0.52
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.34	0.52
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.91	0.52
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	1.92	0.52
26:BA:2051:A:H5'	26:BA:2578:G:O4'	2.10	0.52
11:AK:15:ALA:HA	11:AK:76:GLY:O	2.09	0.52
26:BA:2747:G:O6	26:BA:2755:C:H5''	2.10	0.52
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	1.91	0.52
25:AY:5:G:H1'	25:AY:69:G:N2	2.25	0.52
26:BA:1177:A:H3'	26:BA:1178:C:C6	2.44	0.52
23:CW:19:G:H1	23:CW:56:C:N4	2.04	0.52
26:DA:942:G:OP2	36:DP:39:LYS:NZ	2.42	0.52
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.22	0.52
1:AA:428:G:H4'	1:AA:429:U:O5'	2.10	0.52
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.25	0.52
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.92	0.52
26:BA:2404:C:O3'	36:BP:77:ARG:NH2	2.43	0.52
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.74	0.52
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.42	0.52
1:CA:768:A:OP2	61:CA:4019:HOH:O	2.19	0.52
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.43	0.52
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.38	0.52
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.27	0.52
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.10	0.52
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.75	0.52
26:DA:171:G:H2'	26:DA:172:C:H6	1.75	0.52
26:DA:373:U:H2'	26:DA:374:A:C8	2.44	0.52
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.09	0.52
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.45	0.52
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.52
1:CA:551:U:H2'	1:CA:552:U:C6	2.44	0.52
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.92	0.52
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.91	0.52
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.92	0.52
7:AG:12:LEU:H	7:AG:12:LEU:HD12	1.74	0.52
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.43	0.52
26:DA:81:G:N7	61:DA:4166:HOH:O	2.33	0.52
1:AA:664:G:N2	1:AA:741:G:H1	2.00	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.45	0.51
1:CA:1304:G:C6	1:CA:1305:G:N1	2.78	0.51
19:AS:65:ASN:HD22	19:AS:66:MET:N	2.09	0.51
8:AH:73:ASP:OD1	8:AH:75:ARG:HD3	2.10	0.51
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.45	0.51
26:DA:2299:G:H2'	26:DA:2300:G:H8	1.75	0.51
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.76	0.51
26:BA:1858:G:N2	26:BA:1883:G:H2'	2.24	0.51
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.91	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.56	0.51
29:DE:12:THR:HG22	40:DT:58:ASN:OD1	2.10	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.10	0.51
25:AY:7:A:N1	25:AY:66:U:O2	2.42	0.51
8:CH:67:PRO:O	8:CH:69:ARG:HG3	2.10	0.51
26:DA:1803:A:HO2'	28:DD:259:THR:HG21	1.76	0.51
29:BE:47:VAL:HG23	29:BE:84:PHE:O	2.10	0.51
1:AA:1036:G:H5'	1:AA:1037:C:OP2	2.09	0.51
1:CA:1118:C:C2	1:CA:1119:C:C5	2.96	0.51
1:AA:78:G:C2	1:AA:91:C:N3	2.78	0.51
29:DE:50:GLY:HA3	29:DE:75:VAL:HG11	1.91	0.51
9:CI:53:VAL:C	9:CI:55:ALA:H	2.10	0.51
1:CA:1129:C:P	9:CI:16:ARG:HH12	2.33	0.51
26:DA:1006:C:OP2	61:DA:4190:HOH:O	2.19	0.51
32:DH:81:GLU:OE1	32:DH:81:GLU:N	2.44	0.51
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.92	0.51
26:BA:2361:A:OP1	55:B8:27:THR:OG1	2.13	0.51
1:CA:17:U:H2'	1:CA:18:C:C6	2.44	0.51
1:CA:1327:C:H5''	21:CU:20:LYS:HB3	1.93	0.51
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.74	0.51
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:793:A:OP2	26:BA:2071:A:O2'	2.27	0.51
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.09	0.51
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.92	0.51
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.44	0.51
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.93	0.51
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.93	0.51
26:BA:2277:G:OP2	47:B0:10:THR:HG21	2.10	0.51
26:DA:867:C:H2'	26:DA:868:U:H5'	1.92	0.51
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.92	0.51
26:BA:8:A:H2'	26:BA:9:U:H6	1.74	0.51
1:CA:955:U:O2'	19:CS:83:HIS:HD2	1.93	0.51
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.24	0.51
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.09	0.51
44:DX:88:LYS:HG2	44:DX:93:GLU:HG3	1.92	0.51
4:CD:38:TYR:CE1	4:CD:45:GLN:HG2	2.45	0.51
26:DA:62:C:H42	26:DA:93:G:H1	1.57	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.75	0.51
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.30	0.51
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.76	0.51
1:AA:1035:A:H2	1:AA:1036:G:N7	2.09	0.51
1:CA:34:C:H2'	1:CA:35:G:C8	2.45	0.51
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.92	0.51
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.92	0.51
26:DA:832:G:OP1	61:DA:4285:HOH:O	2.19	0.51
29:DE:52:LEU:HB2	29:DE:76:ARG:HB2	1.92	0.51
26:BA:1164:G:H2'	26:BA:1165:U:C6	2.46	0.51
23:CW:74:C:N4	26:DA:2507:C:O2'	2.44	0.51
26:BA:637:A:H4'	26:BA:638:G:O5'	2.11	0.51
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.10	0.51
1:CA:352:C:N3	1:CA:356:A:N6	2.58	0.51
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.10	0.51
1:CA:179:A:H2'	1:CA:180:U:C6	2.46	0.51
26:DA:710:G:H1	26:DA:721:C:H42	1.56	0.51
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	1.92	0.51
9:CI:96:LEU:O	9:CI:100:GLY:N	2.43	0.51
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.90	0.51
3:CC:118:GLN:HA	3:CC:121:ALA:HB3	1.92	0.51
3:CC:187:ALA:O	3:CC:198:VAL:HG23	2.11	0.51
42:DV:10:LYS:HZ1	42:DV:23:GLU:HG3	1.74	0.51
26:BA:602:G:O2'	26:BA:655:A:N6	2.43	0.51
26:BA:1420:U:O2'	26:BA:1421:G:OP1	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.10	0.51
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD13	1.91	0.51
26:DA:1155:A:H5''	41:DU:55:ARG:HD3	1.93	0.51
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.10	0.51
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.11	0.51
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.24	0.51
23:CW:47:U:H3'	23:CW:48:C:H5'	1.92	0.51
1:CA:1050:G:H1'	1:CA:1214:C:O2	2.10	0.51
26:DA:652(T):C:H2'	26:DA:652(U):G:C8	2.46	0.51
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.76	0.51
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.92	0.51
19:CS:11:VAL:HB	19:CS:16:LEU:HD12	1.93	0.51
26:BA:34:C:H5''	26:BA:35:G:OP2	2.09	0.51
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.51
51:D4:7:PRO:HB2	51:D4:27:THR:HG21	1.93	0.51
26:DA:621:A:OP2	36:DP:108:LYS:NZ	2.43	0.51
1:AA:997:U:H3	1:AA:1044:A:H61	1.59	0.51
26:BA:45:C:OP2	26:BA:215:G:H2'	2.10	0.51
45:DY:6:HIS:CD2	45:DY:6:HIS:H	2.28	0.51
26:BA:2123:G:N2	26:BA:2175:C:N3	2.48	0.51
1:CA:1392:G:H21	1:CA:1502:A:H8	1.57	0.51
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.26	0.51
1:AA:1025:U:C2	1:AA:1036:G:O6	2.63	0.51
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.10	0.51
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.09	0.51
31:DG:37:VAL:HG23	31:DG:99:MET:HG3	1.92	0.51
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.11	0.51
33:BI:72:LEU:O	33:BI:74:ASN:N	2.44	0.51
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.43	0.51
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	1.91	0.51
26:BA:859:G:O2'	26:BA:916:G:O6	2.21	0.51
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.44	0.51
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.10	0.51
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.92	0.51
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.11	0.51
4:CD:65:ARG:HD3	4:CD:70:ILE:O	2.11	0.51
23:AW:28:G:H2'	23:AW:29:G:C8	2.46	0.51
26:BA:1506:C:H2'	26:BA:1507:A:C8	2.36	0.51
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.25	0.51
1:AA:164:U:H2'	1:AA:165:C:C6	2.46	0.51
26:DA:10:G:H2'	26:DA:11:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.42	0.51
1:CA:662:G:H2'	1:CA:663:A:C8	2.46	0.51
26:DA:1639:U:H4'	26:DA:2699:C:H4'	1.92	0.51
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.25	0.51
26:BA:848:G:C4	26:BA:933:A:H8	2.29	0.51
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.91	0.51
26:DA:2218:U:O4'	48:D1:52:ARG:NH2	2.44	0.51
26:BA:1790:C:H5''	26:BA:1791:A:OP1	2.11	0.51
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.43	0.51
26:DA:1023:U:OP2	61:DA:4648:HOH:O	2.20	0.51
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.40	0.51
1:CA:1004:A:C6	1:CA:1037:C:C2	2.98	0.51
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.93	0.51
26:BA:529:A:H62	26:BA:2041:U:H3	1.59	0.51
26:BA:271(K):U:C2	33:BI:50:ARG:HD3	2.46	0.51
1:CA:950:U:H2'	1:CA:951:G:H8	1.76	0.51
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.92	0.51
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.45	0.51
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.10	0.51
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.51
26:DA:82:G:N1	26:DA:103:A:OP2	2.37	0.51
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.93	0.51
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.93	0.51
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.44	0.51
1:CA:375:U:O4	61:CA:4093:HOH:O	2.17	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51
1:AA:954:G:H21	1:AA:1227:A:H62	1.59	0.51
24:AX:61:C:H2'	24:AX:62:C:H6	1.75	0.51
1:AA:145:G:H1	1:AA:177:C:H42	1.59	0.51
24:AX:76:A:O3'	61:AX:3101:HOH:O	2.19	0.51
26:DA:2121:G:O6	26:DA:2176:A:N6	2.44	0.51
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.45	0.51
1:AA:1004:A:N7	1:AA:1036:G:C2	2.79	0.51
1:CA:1120:G:N1	1:CA:1154:G:N3	2.59	0.51
25:AY:19:G:H1	25:AY:56:C:H42	1.48	0.51
44:DX:5:TYR:CE1	49:D2:30:ARG:HB2	2.46	0.51
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.51	0.51
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.44	0.51
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.35	0.51
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.46	0.51
26:BA:467:G:OP1	54:B7:33:ARG:NH1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:53:ALA:HB3	3:CC:106:VAL:HG21	1.93	0.51
1:CA:587:G:N1	1:CA:754:C:OP2	2.41	0.51
9:CI:8:GLY:HA3	9:CI:76:ALA:O	2.10	0.51
1:AA:600:C:H2'	1:AA:601:C:C6	2.45	0.51
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.11	0.51
1:CA:69:G:H2'	1:CA:70:G:H8	1.76	0.51
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.46	0.51
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.11	0.51
9:AI:128:ARG:NH1	24:AX:35:A:OP2	2.44	0.51
26:BA:2168:G:C6	26:BA:2171:A:C8	2.99	0.51
26:BA:1365:A:OP2	48:B1:3:LYS:HG2	2.10	0.51
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.11	0.51
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.46	0.51
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.74	0.51
41:DU:52:ARG:HA	41:DU:55:ARG:HE	1.74	0.51
1:CA:533:A:O2'	1:CA:535:A:OP2	2.25	0.51
8:AH:124:ALA:O	8:AH:128:GLY:N	2.43	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
1:AA:460:G:O5'	1:AA:460:G:H8	1.93	0.51
26:DA:309:G:N3	26:DA:329:G:O2'	2.43	0.51
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.26	0.51
41:DU:104:GLN:OE1	41:DU:105:VAL:N	2.34	0.51
25:CY:7:A:H61	25:CY:66:U:H3	0.60	0.50
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.46	0.50
19:AS:3:ARG:HH21	19:AS:7:LYS:HE2	1.76	0.50
4:AD:108:LEU:HD12	4:AD:176:LEU:HB2	1.93	0.50
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.11	0.50
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.40	0.50
1:AA:749:C:H2'	1:AA:750:G:H8	1.76	0.50
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.75	0.50
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.12	0.50
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.93	0.50
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.26	0.50
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.27	0.50
25:AY:40:C:H2'	25:AY:41:C:H6	1.76	0.50
26:DA:1671:U:HO2'	26:DA:1673:U:H5	1.57	0.50
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.93	0.50
17:AQ:12:SER:HB3	17:AQ:20:THR:HB	1.92	0.50
25:CY:11:C:N3	25:CY:24:G:O6	2.44	0.50
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.44	0.50
51:D4:62:ARG:HD3	51:D4:62:ARG:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.26	0.50
24:AX:61:C:H2'	24:AX:62:C:C6	2.46	0.50
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.11	0.50
1:CA:431:A:H2'	1:CA:432:A:C8	2.46	0.50
7:CG:28:ASN:HA	7:CG:31:MET:HE2	1.93	0.50
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.50
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.93	0.50
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.92	0.50
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.43	0.50
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.92	0.50
36:BP:88:LEU:HD11	36:BP:114:ILE:HD12	1.93	0.50
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	1.93	0.50
26:DA:479:A:N3	26:DA:481:G:H5''	2.26	0.50
26:DA:376:C:OP1	61:DA:4418:HOH:O	2.19	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.10	0.50
25:AY:62:C:H2'	25:AY:63:G:C8	2.40	0.50
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.46	0.50
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.10	0.50
27:DB:17:C:H2'	27:DB:18:G:O4'	2.11	0.50
31:DG:70:VAL:HA	31:DG:90:LEU:HD23	1.92	0.50
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	1.92	0.50
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.25	0.50
7:CG:26:PHE:HE2	7:CG:104:LEU:HD23	1.76	0.50
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.46	0.50
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	1.92	0.50
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.93	0.50
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.43	0.50
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.47	0.50
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.26	0.50
26:BA:1423:G:OP1	26:BA:1492:G:O2'	2.23	0.50
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.12	0.50
26:BA:1030:G:OP2	37:BQ:128:LYS:NZ	2.44	0.50
26:DA:2153:G:C2	26:DA:2154:G:C4	2.99	0.50
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.21	0.50
1:CA:1119:C:H2'	1:CA:1120:G:H8	1.75	0.50
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.44	0.50
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.94	0.50
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.26	0.50
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.11	0.50
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.54	0.50
27:BB:2:C:H2'	27:BB:3:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.46	0.50
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.31	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.45	0.50
26:BA:796:C:H2'	26:BA:797:C:C6	2.46	0.50
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.46	0.50
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.11	0.50
1:CA:1030:C:N4	1:CA:1032:G:O6	2.44	0.50
1:AA:78:G:H1	1:AA:91:C:N4	2.07	0.50
2:CB:233:SER:HB2	2:CB:234:PRO:HD2	1.93	0.50
26:DA:2318:G:N2	39:DS:3:ARG:HH11	2.09	0.50
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.76	0.50
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
9:AI:4:TYR:CD2	9:AI:88:TYR:HA	2.47	0.50
1:AA:1067:A:O2'	1:AA:1068:G:OP2	2.21	0.50
8:CH:43:GLY:O	8:CH:64:LYS:NZ	2.42	0.50
26:DA:483:A:O2'	45:DY:49:VAL:O	2.25	0.50
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.10	0.50
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.12	0.50
27:DB:11:C:OP2	27:DB:12:C:N4	2.32	0.50
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.26	0.50
26:BA:2512:C:H2'	26:BA:2513:G:O4'	2.12	0.50
26:DA:286:C:H2'	26:DA:287:C:H6	1.77	0.50
1:CA:67:C:H2'	1:CA:68:G:C8	2.47	0.50
1:AA:1521:G:N3	61:AA:4065:HOH:O	2.35	0.50
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.93	0.50
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	1.94	0.50
25:CY:23:A:H8	25:CY:23:A:O5'	1.94	0.50
4:AD:15:GLU:HG2	4:AD:63:LYS:CB	2.41	0.50
17:CQ:45:HIS:HA	17:CQ:69:LYS:HE3	1.94	0.50
26:BA:1045:A:H1'	26:BA:1047:G:N3	2.26	0.50
23:CW:14:A:H2'	23:CW:15:G:O4'	2.11	0.50
26:BA:456:C:H4'	61:BA:3946:HOH:O	2.11	0.50
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.14	0.50
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.50
26:DA:1266:G:O4'	43:DW:15:ARG:NH2	2.45	0.50
23:AW:58:A:O2'	23:AW:60:U:OP2	2.24	0.50
26:BA:1448:G:H4'	26:BA:1542:A:OP1	2.11	0.50
26:DA:885:C:H2'	26:DA:886:C:H4'	1.94	0.50
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.94	0.50
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.93	0.50
55:B8:6:THR:HG22	55:B8:63:PRO:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AL:28:LYS:HG3	12:AL:62:SER:HB2	1.94	0.50
18:AR:42:ARG:HH21	18:AR:42:ARG:HA	1.75	0.50
26:BA:1449:A:H5'	26:BA:1450:G:OP2	2.12	0.50
25:AY:69:G:C2	25:AY:70:G:H1'	2.47	0.50
26:DA:2139:C:N4	26:DA:2153:G:C2	2.79	0.50
27:DB:75:G:H1'	46:DZ:27:VAL:HG11	1.94	0.50
26:DA:854:G:H2'	26:DA:855:G:H8	1.76	0.50
23:AW:37:MIA:O2'	26:BA:1913:A:N1	2.44	0.50
5:AE:78:HIS:HD1	8:AH:104:ARG:CD	2.24	0.50
24:CX:6:G:H1	24:CX:67:C:H42	1.58	0.50
36:DP:89:ALA:O	36:DP:121:LYS:NZ	2.39	0.50
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.92	0.50
1:CA:677:U:H3	1:CA:713:G:H22	1.58	0.50
26:BA:1379:A:H4'	26:BA:1380:G:OP2	2.10	0.50
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.94	0.50
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.11	0.50
23:CW:9:A:O2'	23:CW:10:G:N7	2.43	0.50
21:CU:6:ARG:O	21:CU:12:LYS:NZ	2.37	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
1:AA:376:G:P	16:AP:67:THR:HG21	2.51	0.50
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.11	0.50
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.12	0.50
31:DG:11:TYR:HB2	31:DG:176:LEU:HD21	1.93	0.50
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.45	0.50
26:DA:11:G:H2'	26:DA:12:U:H5''	1.93	0.50
39:DS:93:LYS:CD	39:DS:95:HIS:HB2	2.40	0.50
1:CA:952:U:H2'	1:CA:953:G:H8	1.77	0.50
3:CC:136:GLN:O	3:CC:140:ARG:NH1	2.45	0.50
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.76	0.50
19:AS:68:GLY:H	51:B4:58:ARG:HH11	1.59	0.50
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.47	0.50
26:DA:1021:A:H62	26:DA:1141:U:H3	1.59	0.50
1:AA:714:G:H2'	1:AA:715:A:C8	2.47	0.50
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.76	0.50
26:BA:272(H):C:H42	26:BA:363(B):G:H1	1.58	0.50
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.77	0.50
26:BA:2319:G:H22	39:BS:3:ARG:NE	2.09	0.50
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.46	0.50
23:AW:49:C:H42	23:AW:65:G:H1	1.60	0.50
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.93	0.50
45:BY:6:HIS:CD2	45:BY:6:HIS:H	2.30	0.50
6:AF:36:ARG:HH11	6:AF:36:ARG:HB3	1.77	0.50
26:BA:1866:C:H2'	26:BA:1876:A:O4'	2.11	0.50
26:DA:586:A:N1	26:DA:809:G:O2'	2.35	0.50
46:DZ:93:ASP:OD1	46:DZ:94:GLU:HG3	2.12	0.50
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	1.93	0.50
7:CG:76:ARG:HB3	7:CG:156:TRP:CH2	2.47	0.50
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.09	0.50
1:CA:950:U:H2'	1:CA:951:G:C8	2.47	0.50
25:AY:33:U:C3'	25:AY:34:G:H5''	2.41	0.50
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.41	0.50
1:CA:1244:C:N4	1:CA:1293:G:H1	2.10	0.50
26:BA:2712:U:H2'	26:BA:2714:G:H5''	1.93	0.50
26:DA:1300:U:O2'	26:DA:1635:G:OP1	2.27	0.50
1:CA:936:C:H2'	1:CA:937:A:O4'	2.10	0.50
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.42	0.50
2:CB:186:ALA:HB3	2:CB:197:VAL:HG11	1.93	0.50
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.47	0.50
26:BA:548:A:N6	42:BV:19:LYS:H	2.09	0.50
1:AA:673:G:H2'	1:AA:674:G:C8	2.47	0.50
1:AA:1131:G:O2'	1:AA:1132:C:H5'	2.12	0.50
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.50
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.46	0.50
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.11	0.50
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.12	0.50
1:CA:933:G:N2	1:CA:935:A:O4'	2.45	0.50
26:BA:2441:C:OP2	26:BA:2586:C:O2'	2.26	0.50
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.45	0.50
23:AW:11:C:H42	23:AW:24:G:H1	1.58	0.50
26:DA:1996:C:H4'	26:DA:1997:G:OP1	2.11	0.50
40:BT:29:ARG:HG3	40:BT:46:GLU:HB2	1.93	0.50
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.11	0.50
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.41	0.50
16:AP:4:ILE:HB	16:AP:66:PRO:HA	1.94	0.50
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.50
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.45	0.50
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.11	0.49
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.47	0.49
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.47	0.49
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.77	0.49
51:B4:61:ARG:HG3	51:B4:62:ARG:N	2.26	0.49
4:AD:196:LEU:O	4:AD:198:VAL:N	2.41	0.49
26:BA:2278:A:OP2	47:B0:12:ASN:ND2	2.45	0.49
48:B1:85:LEU:HB3	48:B1:89:GLU:HG2	1.94	0.49
46:DZ:117:LEU:HD11	46:DZ:144:LEU:HD13	1.93	0.49
26:BA:2128:C:O2'	26:BA:2129:C:H5'	2.12	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.47	0.49
26:BA:1779:U:H2'	61:BA:5061:HOH:O	2.11	0.49
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.41	0.49
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.47	0.49
26:DA:1359:A:N6	26:DA:1372:U:H3	2.08	0.49
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.77	0.49
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.12	0.49
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.94	0.49
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.92	0.49
26:BA:747:U:O2	26:BA:2014:A:H1'	2.12	0.49
26:BA:646:A:H2'	26:BA:647:G:O4'	2.12	0.49
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.93	0.49
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.12	0.49
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.94	0.49
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.47	0.49
47:D0:37:LEU:HD13	47:D0:79:VAL:HG11	1.94	0.49
26:BA:1009:A:P	34:BN:37:LYS:HZ1	2.32	0.49
41:BU:74:LEU:H	41:BU:74:LEU:HD12	1.77	0.49
26:BA:282:A:H2'	26:BA:282:A:N3	2.27	0.49
10:CJ:67:THR:O	10:CJ:67:THR:OG1	2.30	0.49
1:AA:991:U:O2'	1:AA:992:U:OP2	2.23	0.49
1:AA:1399:C:C2	1:AA:1502:A:N6	2.80	0.49
26:DA:996:A:C2	26:DA:997:G:C8	3.00	0.49
45:BY:92:ASN:HB3	45:BY:94:LYS:N	2.25	0.49
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.35	0.49
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.94	0.49
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.95	0.49
26:DA:1721:G:H8	26:DA:1741:A:H62	1.60	0.49
1:AA:1125:U:O2'	1:AA:1127:G:N7	2.24	0.49
26:DA:1359:A:H2'	26:DA:1360:A:H5'	1.94	0.49
1:AA:1053:G:O2'	61:AA:4100:HOH:O	2.19	0.49
2:AB:103:THR:HA	2:AB:180:LEU:HD11	1.93	0.49
1:AA:1095:U:P	1:AA:1108:G:H1	2.35	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2294:C:H5''	39:DS:10:ARG:HD2	1.94	0.49
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.11	0.49
26:BA:2259:G:C8	26:BA:2427:C:C4	3.00	0.49
26:BA:1774:C:H6	26:BA:1774:C:O5'	1.95	0.49
1:CA:137:C:H2'	1:CA:138:G:H8	1.76	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.11	0.49
1:CA:155:C:H2'	1:CA:156:G:O4'	2.11	0.49
4:CD:57:ARG:NE	4:CD:205:GLU:OE2	2.44	0.49
46:BZ:117:LEU:CD1	46:BZ:144:LEU:HD22	2.39	0.49
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.78	0.49
26:BA:271(K):U:H1'	33:BI:50:ARG:CZ	2.43	0.49
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.75	0.49
1:CA:984:C:O5'	1:CA:984:C:H6	1.94	0.49
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.12	0.49
28:BD:70:TRP:HB3	28:BD:190:TYR:CE1	2.46	0.49
46:DZ:104:PHE:HA	46:DZ:139:VAL:HB	1.95	0.49
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.13	0.49
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.47	0.49
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.13	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
42:DV:62:LEU:HD11	42:DV:95:LEU:HB2	1.93	0.49
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.49
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.48	0.49
26:DA:335:C:H4'	45:DY:73:ARG:CZ	2.42	0.49
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.13	0.49
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	2.12	0.49
1:CA:110:C:H2'	1:CA:111:G:O4'	2.12	0.49
26:BA:2345:G:H4'	26:BA:2346:A:H5''	1.94	0.49
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.12	0.49
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.46	0.49
26:BA:196:A:O2'	26:BA:805:G:O6	2.26	0.49
23:AW:63:G:H2'	23:AW:64:A:O4'	2.13	0.49
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.92	0.49
26:DA:10:G:H2'	26:DA:11:G:C8	2.47	0.49
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.45	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.27	0.49
37:BQ:16:ARG:HG2	37:BQ:18:LYS:HE2	1.94	0.49
34:DN:67:LEU:HD13	34:DN:87:LEU:HD13	1.94	0.49
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.94	0.49
26:DA:528:A:C2	26:DA:2042:A:H2'	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:920:U:H2'	1:AA:921:U:C6	2.48	0.49
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.44	0.49
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.93	0.49
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.94	0.49
1:AA:110:C:H2'	1:AA:111:G:O4'	2.12	0.49
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.93	0.49
26:BA:83:G:N2	26:BA:103:A:OP2	2.44	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.26	0.49
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.77	0.49
1:CA:91:C:H2'	1:CA:92:C:C6	2.48	0.49
42:DV:100:ARG:NH1	42:DV:100:ARG:HG3	2.10	0.49
1:CA:923:A:OP1	5:CE:21:ALA:HB2	2.11	0.49
25:AY:50:U:N3	25:AY:64:A:H2	2.05	0.49
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.47	0.49
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	1.93	0.49
26:BA:956:G:P	37:BQ:14:ARG:HH22	2.36	0.49
27:DB:41:U:H5	31:DG:70:VAL:N	2.09	0.49
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.95	0.49
26:BA:8:A:H2'	26:BA:9:U:C6	2.47	0.49
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.94	0.49
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.77	0.49
1:CA:528:C:H5'	1:CA:529:G:OP2	2.13	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.26	0.49
1:CA:444:C:H2'	1:CA:445:G:H8	1.78	0.49
26:DA:2558:C:H2'	26:DA:2559:C:O4'	2.13	0.49
26:BA:2029:G:H2'	26:BA:2031:A:OP1	2.12	0.49
26:DA:2471:C:N4	26:DA:2476:A:O2'	2.43	0.49
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.94	0.49
1:AA:1523:G:OP1	11:AK:123:LYS:NZ	2.30	0.49
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.46	0.49
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.28	0.49
26:DA:2123:G:H2'	26:DA:2124:G:C8	2.47	0.49
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.42	0.49
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.93	0.49
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.48	0.49
26:DA:300:A:H3'	45:DY:84:ARG:HH22	1.77	0.49
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	1.94	0.49
2:CB:77:ALA:HB2	2:CB:211:ILE:HD13	1.94	0.49
1:CA:45:U:H2'	1:CA:46:G:C8	2.47	0.49
31:DG:16:ARG:HB2	31:DG:17:PRO:HD3	1.94	0.49
1:CA:1287:A:N3	1:CA:1353:G:O2'	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:76:31M:O	24:CX:76:A:O2'	2.19	0.49
1:AA:674:G:OP1	6:AF:87:ARG:NH2	2.43	0.49
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.94	0.49
26:BA:2319:G:N1	39:BS:3:ARG:HA	2.28	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:CZ	2.42	0.49
26:BA:1356:G:OP1	61:BA:5239:HOH:O	2.20	0.49
31:DG:103:LEU:HD22	31:DG:178:PHE:HZ	1.77	0.49
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.47	0.49
26:DA:639:U:H2'	26:DA:640:C:C6	2.48	0.49
26:BA:55:G:O2'	26:BA:127:A:N1	2.39	0.49
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.78	0.49
26:DA:2058:A:N7	61:DA:3876:HOH:O	2.34	0.49
1:AA:630:G:O2'	1:AA:631:G:H5'	2.13	0.49
1:AA:1244:C:OP1	21:AU:9:ARG:HB2	2.13	0.49
1:CA:1002:G:N3	1:CA:1003:G:H8	2.10	0.49
25:AY:51:U:H2'	25:AY:52:G:C8	2.48	0.49
1:CA:838:G:N2	1:CA:848:C:N3	2.58	0.49
24:AX:66:C:H2'	24:AX:67:C:O4'	2.13	0.49
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.45	0.49
26:BA:548:A:O2'	26:BA:549:G:OP1	2.27	0.49
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.78	0.49
26:BA:1278:A:OP1	38:BR:36:THR:HG23	2.12	0.49
26:DA:989:G:H4'	26:DA:990:A:OP1	2.12	0.49
26:DA:764:A:H5'	28:DD:210:GLY:HA2	1.94	0.49
1:CA:8:A:H5'	5:CE:101:ILE:HG22	1.95	0.49
49:D2:32:LEU:HD23	49:D2:53:LEU:HB3	1.94	0.49
26:DA:588:U:H2'	26:DA:589:C:C6	2.46	0.49
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.95	0.49
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.47	0.49
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.48	0.49
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD22	1.94	0.49
25:AY:22:G:H2'	25:AY:23:A:H8	1.75	0.49
24:AX:21:A:N6	24:AX:46:G:H2'	2.27	0.49
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.10	0.49
1:AA:865:A:C2	1:AA:918:A:H4'	2.45	0.49
1:CA:539:A:H2'	1:CA:540:G:H8	1.76	0.49
3:AC:114:PRO:HA	3:AC:185:GLY:HA3	1.94	0.49
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.13	0.49
23:AW:58:A:H2	23:AW:60:U:HO2'	1.59	0.49
26:DA:25:U:C4	26:DA:26:G:C6	3.00	0.49
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:B4:26:SER:OG	51:B4:27:THR:N	2.45	0.49
61:BA:4985:HOH:O	36:BP:39:LYS:HE3	2.12	0.49
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.48	0.49
1:CA:815:A:N7	1:CA:1509:C:O2'	2.41	0.49
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.13	0.49
26:DA:2154:G:C2	26:DA:2155:G:C8	3.01	0.49
26:BA:885:C:H3'	26:BA:886:C:C5'	2.40	0.49
1:CA:1029:C:N4	1:CA:1033:G:O6	2.46	0.49
26:BA:2140:C:H1'	26:BA:2152:G:H22	1.77	0.49
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.13	0.49
1:CA:1494:G:H4'	26:DA:1913:A:N7	2.28	0.49
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.27	0.49
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.59	0.49
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.13	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.46	0.49
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.59	0.49
5:CE:34:VAL:HG11	5:CE:63:ARG:HG3	1.94	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HG3	1.78	0.49
19:AS:41:VAL:O	19:AS:43:GLU:N	2.45	0.49
46:DZ:5:LEU:HD21	46:DZ:43:GLU:HB3	1.94	0.49
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.94	0.49
7:CG:126:ASP:O	7:CG:130:GLY:N	2.46	0.49
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.28	0.49
26:DA:812:C:H2'	26:DA:813:U:H6	1.77	0.49
25:CY:18:G:C2	25:CY:55:PSU:C4	3.00	0.49
26:BA:2042:A:OP1	61:BA:5120:HOH:O	2.20	0.49
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.47	0.49
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.78	0.49
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.47	0.49
46:BZ:41:LEU:HD21	46:BZ:83:PRO:HG2	1.94	0.49
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.48	0.49
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.48	0.49
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.46	0.49
1:CA:78:G:H2'	1:CA:79:G:H5''	1.95	0.49
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.48	0.49
24:AX:57:A:O4'	31:BG:78:SER:OG	2.31	0.49
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.12	0.49
1:AA:72:C:H2'	1:AA:73:G:O4'	2.13	0.49
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.94	0.49
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.13	0.49
35:DO:122:LEU:HD13	40:DT:72:VAL:HG11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:183:C:N4	26:BA:213:A:H61	2.10	0.49
8:CH:83:ILE:HB	8:CH:137:VAL:HG13	1.94	0.49
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.95	0.49
24:CX:9:G:N2	24:CX:46:G:OP2	2.46	0.49
26:BA:2347:C:O2'	53:B6:21:TYR:OH	2.30	0.49
23:AW:25:C:C2'	23:AW:26:A:H5'	2.43	0.48
25:CY:29:G:N2	25:CY:41:C:N3	2.61	0.48
1:CA:1118:C:H1'	1:CA:1179:A:C4	2.48	0.48
26:DA:2037:G:H2'	26:DA:2038:G:C8	2.48	0.48
26:DA:2278:A:OP1	37:DQ:11:LYS:HD2	2.12	0.48
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.52	0.48
24:AX:47:U:H5''	24:AX:48:C:OP1	2.13	0.48
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.95	0.48
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.94	0.48
27:BB:102:A:N7	61:BB:318:HOH:O	2.35	0.48
1:AA:236:G:OP1	17:AQ:40:LYS:NZ	2.45	0.48
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.19	0.48
26:DA:2137:C:H42	26:DA:2154:G:H1	1.59	0.48
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.28	0.48
1:CA:976:G:OP1	14:CN:32:SER:N	2.34	0.48
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.48	0.48
26:BA:1364:G:P	48:B1:3:LYS:HG3	2.53	0.48
23:CW:21:A:O2'	23:CW:22:G:OP1	2.28	0.48
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.12	0.48
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.14	0.48
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.77	0.48
1:CA:189(L):G:H2'	1:CA:190:U:C6	2.48	0.48
2:CB:119:GLU:OE2	2:CB:153:ARG:NH2	2.41	0.48
53:B6:8:LYS:HG2	55:B8:34:TRP:CG	2.49	0.48
56:D9:10:ILE:HD12	56:D9:32:HIS:HA	1.94	0.48
1:CA:50:A:H1'	1:CA:52:G:C8	2.48	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.77	0.48
39:DS:41:ASP:OD2	39:DS:44:LYS:HE2	2.13	0.48
26:DA:652(B):A:N1	26:DA:655:A:H1'	2.29	0.48
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.11	0.48
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.76	0.48
26:DA:222:A:H5''	26:DA:421:U:OP1	2.13	0.48
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.13	0.48
25:CY:7:A:N6	25:CY:66:U:N3	2.17	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48
51:B4:53:GLU:C	51:B4:55:ARG:N	2.65	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:163:PHE:CD2	2:AB:185:ILE:HG13	2.48	0.48
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.48	0.48
25:AY:32:PSU:C2	25:AY:33:U:H5	2.32	0.48
26:DA:1478:G:HO2'	26:DA:1558:A:H2	1.62	0.48
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.13	0.48
26:BA:2138:C:C2	26:BA:2154:G:C2	3.02	0.48
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.48
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.94	0.48
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	1.95	0.48
1:AA:1284:C:OP2	1:AA:1285:A:O2'	2.29	0.48
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.77	0.48
37:BQ:52:VAL:HA	37:BQ:55:VAL:HG12	1.94	0.48
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.13	0.48
26:DA:1922:G:H2'	26:DA:1923:U:O4'	2.13	0.48
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.40	0.48
2:AB:76:GLN:H	2:AB:76:GLN:CD	2.16	0.48
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.48	0.48
1:AA:621:A:H2'	1:AA:622:A:C8	2.48	0.48
26:BA:247:G:H4'	26:BA:386:G:C5	2.48	0.48
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.78	0.48
7:CG:20:ASP:HB3	7:CG:23:VAL:HB	1.95	0.48
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.48	0.48
23:AW:26:A:N1	23:AW:44:G:N2	2.61	0.48
26:DA:2126:A:H4'	26:DA:2127:G:OP1	2.13	0.48
25:CY:35:A:H2'	25:CY:36:A:O4'	2.13	0.48
26:BA:2119:A:C2	26:BA:2170:A:H2'	2.48	0.48
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.20	0.48
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.43	0.48
26:BA:630:G:OP1	55:B8:47:LYS:NZ	2.41	0.48
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.42	0.48
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.94	0.48
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.94	0.48
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.11	0.48
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.96	0.48
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.13	0.48
26:BA:2771:C:H2'	26:BA:2772:C:C6	2.48	0.48
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.28	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:H8	2.11	0.48
28:DD:137:PRO:O	28:DD:140:THR:HG23	2.14	0.48
26:DA:2853:C:H2'	26:DA:2854:G:H8	1.77	0.48
26:BA:800:A:H8	26:BA:800:A:OP1	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.96	0.48
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.48	0.48
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.14	0.48
1:AA:627:G:H2'	1:AA:628:G:H8	1.78	0.48
26:BA:2640:G:OP1	34:BN:97:ARG:NH2	2.46	0.48
1:CA:339:C:H2'	1:CA:340:U:C6	2.49	0.48
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.78	0.48
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.49	0.48
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.17	0.48
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.95	0.48
25:CY:69:G:C2	25:CY:70:G:H1'	2.48	0.48
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.96	0.48
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.96	0.48
2:CB:71:VAL:HG23	2:CB:163:PHE:O	2.14	0.48
26:BA:1405:U:H2'	26:BA:1406:U:H6	1.78	0.48
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.95	0.48
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.27	0.48
41:DU:78:THR:O	41:DU:117:GLN:NE2	2.46	0.48
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.28	0.48
7:AG:150:ALA:HB2	11:AK:50:TYR:OH	2.13	0.48
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.52	0.48
26:BA:323:G:C8	30:BF:171:PRO:HG3	2.48	0.48
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.42	0.48
19:CS:17:GLU:O	19:CS:17:GLU:HG2	2.14	0.48
1:CA:141:A:H1'	1:CA:182:U:O2	2.13	0.48
1:CA:1029:C:N4	1:CA:1032:G:C6	2.77	0.48
26:BA:2141:G:N3	26:BA:2142:C:H1'	2.29	0.48
48:B1:72:GLU:O	48:B1:76:ARG:HG3	2.13	0.48
9:CI:16:ARG:HH11	9:CI:66:ARG:HH11	1.62	0.48
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.10	0.48
1:CA:428:G:H4'	1:CA:429:U:O5'	2.12	0.48
26:BA:184:C:H2'	26:BA:185:U:H6	1.78	0.48
26:BA:893:C:H2'	26:BA:894:C:H6	1.79	0.48
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.94	0.48
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.38	0.48
33:BI:61:ARG:HD2	33:BI:61:ARG:N	2.28	0.48
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.53	0.48
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.14	0.48
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.13	0.48
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.13	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H6	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1668:A:H4'	26:BA:1669:A:O5'	2.14	0.48
26:DA:184:C:H2'	26:DA:185:U:C6	2.48	0.48
29:BE:178:GLU:OE2	29:BE:178:GLU:N	2.46	0.48
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.96	0.48
26:DA:861:A:N3	27:DB:79:C:O2'	2.41	0.48
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.48
1:CA:742:G:P	15:CO:35:ARG:HH22	2.36	0.48
25:AY:63:G:C2	25:AY:64:A:H1'	2.48	0.48
1:CA:1119:C:C4	1:CA:1154:G:O6	2.66	0.48
1:CA:1135:U:H2'	1:CA:1137:C:O2	2.14	0.48
26:BA:2140:C:C2	26:BA:2151:G:N2	2.82	0.48
26:BA:2129:C:H2'	26:BA:2130:U:H6	1.77	0.48
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.28	0.48
26:DA:952:G:H5''	26:DA:953:A:OP2	2.14	0.48
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.28	0.48
31:DG:125:PHE:HB3	31:DG:166:ASP:OD1	2.14	0.48
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.14	0.48
26:BA:288:C:H2'	26:BA:289:A:H8	1.79	0.48
1:AA:62:U:OP1	1:AA:385:C:O2'	2.26	0.48
26:BA:1231:G:H2'	26:BA:1232:G:C8	2.48	0.48
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.48	0.48
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.12	0.48
44:DX:20:GLY:HA2	44:DX:23:GLU:OE2	2.14	0.48
1:CA:408:A:H4'	4:CD:112:VAL:HG21	1.96	0.48
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.77	0.48
26:BA:2386:C:H2'	26:BA:2387:U:C6	2.49	0.48
26:DA:2162:G:H4'	26:DA:2172:U:O2'	2.13	0.48
1:CA:1125:U:H3'	1:CA:1126:U:H5''	1.96	0.48
1:AA:1158:C:H5	1:AA:1181:G:N1	2.06	0.48
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.14	0.48
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.96	0.48
7:AG:111:ARG:HD2	7:AG:123:GLU:HB2	1.95	0.48
26:DA:171:G:H2'	26:DA:172:C:C6	2.49	0.48
26:BA:2328:A:H2'	26:BA:2329:G:H8	1.75	0.48
28:BD:70:TRP:HB3	28:BD:190:TYR:CZ	2.49	0.48
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.48	0.48
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.49	0.48
6:AF:69:GLU:CD	6:AF:69:GLU:H	2.16	0.48
30:DF:120:GLU:CB	30:DF:122:LYS:HG2	2.44	0.48
26:BA:196:A:H2'	26:BA:196:A:N3	2.27	0.48
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:DE:108:SER:HB3	29:DE:165:VAL:HG21	1.96	0.48
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.49	0.48
31:BG:66:GLN:HB3	31:BG:92:VAL:HG21	1.94	0.48
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.14	0.48
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.79	0.48
26:DA:1472:A:H2'	26:DA:1473:G:O4'	2.13	0.48
7:CG:12:LEU:HD12	7:CG:12:LEU:H	1.78	0.48
26:DA:851:U:O2'	50:D3:42:ALA:O	2.30	0.48
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.23	0.48
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.53	0.48
2:CB:81:VAL:HB	2:CB:94:ASN:HD21	1.78	0.48
53:D6:11:LEU:HB2	53:D6:21:TYR:HB2	1.95	0.48
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.48	0.48
26:DA:828:U:H2'	26:DA:829:A:C8	2.49	0.48
1:CA:1133:G:N2	1:CA:1141:C:N3	2.58	0.48
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.14	0.48
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.78	0.48
26:BA:2791:C:OP2	26:BA:2791:C:H6	1.96	0.48
4:AD:3:ARG:HD3	4:AD:118:ARG:CD	2.44	0.48
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.46	0.48
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.96	0.48
3:CC:32:LEU:HD12	3:CC:59:ARG:HH22	1.79	0.48
2:CB:46:LYS:O	2:CB:50:GLU:HB2	2.14	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.12	0.48
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.45	0.48
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.77	0.48
26:DA:390:A:H4'	26:DA:391:G:H5'	1.94	0.48
26:DA:77:C:H42	26:DA:109:G:H1	1.61	0.48
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.95	0.48
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.54	0.48
26:BA:848:G:H2'	26:BA:849:A:C8	2.48	0.48
5:AE:36:ASP:OD1	5:AE:38:GLN:N	2.38	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.49	0.48
1:CA:707:C:H2'	1:CA:708:C:C6	2.49	0.48
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.96	0.48
26:DA:2540:C:H2'	26:DA:2541:A:O4'	2.14	0.48
5:CE:84:PHE:N	5:CE:87:SER:O	2.45	0.48
26:DA:1363:C:O2'	26:DA:1809:A:N3	2.37	0.48
26:DA:2293:C:H42	26:DA:2339:G:H1	1.61	0.48
47:B0:53:MET:HG3	47:B0:59:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:582:G:H2'	26:BA:583:G:C8	2.49	0.48
1:AA:328:C:H4'	1:AA:329:A:H5'	1.96	0.48
26:BA:2183:C:H2'	26:BA:2184:G:H8	1.78	0.48
1:CA:93:G:C2'	1:CA:96:U:H5'	2.44	0.48
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.14	0.48
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.49	0.48
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.48
46:DZ:138:GLU:H	46:DZ:156:LYS:HZ1	1.62	0.48
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.42	0.48
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.49	0.48
3:CC:87:LEU:O	3:CC:91:LEU:N	2.36	0.48
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.49	0.48
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.13	0.48
26:DA:2820:A:OP1	38:DR:4:LEU:HD23	2.14	0.48
23:AW:47:U:H5'	23:AW:47:U:C6	2.45	0.48
26:BA:2572:A:C8	29:BE:144:ARG:HD2	2.49	0.48
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.96	0.48
1:CA:1058:G:H1	1:CA:1199:U:H3	1.62	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.49	0.48
1:AA:501:C:H2'	1:AA:502:G:H8	1.78	0.48
12:CL:53:ARG:HH12	12:CL:92:ASP:HB2	1.79	0.48
10:AJ:49:VAL:HG23	14:AN:41:ARG:HD2	1.96	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.81	0.48
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.28	0.48
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.95	0.48
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.25	0.48
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.49	0.48
26:DA:272(E):G:C2	26:DA:364:C:C2	3.02	0.48
26:BA:493:G:O6	61:BA:4550:HOH:O	2.19	0.48
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.96	0.48
6:CF:33:TYR:CD2	6:CF:75:LEU:HD23	2.49	0.48
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.14	0.48
25:AY:5:G:C2	25:AY:6:G:C4	3.02	0.47
1:CA:89:C:H2'	1:CA:90:U:O4'	2.14	0.47
1:CA:1121:U:C4	1:CA:1122:U:C4	3.01	0.47
25:AY:58:A:H4'	25:AY:59:U:OP1	2.14	0.47
26:BA:527:C:C5	26:BA:2779:U:H2'	2.49	0.47
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.46	0.47
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.47
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.79	0.47
26:DA:1365:A:OP2	48:D1:3:LYS:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.49	0.47
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.34	0.47
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.47	0.47
2:CB:139:LYS:O	2:CB:143:GLU:HG3	2.14	0.47
1:CA:1371:G:O3'	9:CI:69:GLY:HA3	2.14	0.47
27:DB:14:U:H5'	27:DB:70:C:O2	2.13	0.47
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.49	0.47
1:AA:1137:C:H6	1:AA:1137:C:H3'	1.77	0.47
3:CC:101:LEU:HD12	3:CC:102:ASN:N	2.29	0.47
1:CA:130:A:O2'	1:CA:131:C:O5'	2.28	0.47
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.14	0.47
1:CA:1125:U:C2'	1:CA:1126:U:H5''	2.44	0.47
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.96	0.47
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.14	0.47
33:BI:130:TYR:N	33:BI:138:ILE:O	2.42	0.47
23:CW:8:4SU:S4	23:CW:14:A:N7	2.88	0.47
1:CA:646:U:H2'	1:CA:647:C:H6	1.75	0.47
24:CX:67:C:C2'	24:CX:68:C:H5'	2.43	0.47
19:AS:40:ILE:HD11	19:AS:74:PHE:HE1	1.78	0.47
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.95	0.47
26:DA:93:G:H2'	26:DA:94:C:C6	2.49	0.47
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.47
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.13	0.47
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.49	0.47
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.96	0.47
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.14	0.47
1:AA:950:U:H2'	1:AA:951:G:H8	1.80	0.47
26:DA:817:C:H2'	26:DA:818:G:O4'	2.14	0.47
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.96	0.47
26:DA:2304:G:H22	26:DA:2312:U:H3	1.61	0.47
26:DA:2776:A:H4'	26:DA:2777:G:H5''	1.96	0.47
20:CT:24:LEU:HD13	20:CT:24:LEU:HA	1.69	0.47
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.14	0.47
5:AE:90:VAL:O	5:AE:120:THR:HA	2.14	0.47
1:AA:165:C:H2'	1:AA:166:G:H8	1.79	0.47
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.25	0.47
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.13	0.47
33:BI:114:LEU:HD13	33:BI:130:TYR:HD1	1.78	0.47
26:DA:322:A:OP1	30:DF:168:ARG:HD2	2.14	0.47
26:BA:900:A:H2'	26:BA:901:A:O4'	2.14	0.47
3:AC:118:GLN:HG2	3:AC:118:GLN:H	1.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.96	0.47
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.96	0.47
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.48	0.47
21:CU:12:LYS:HD3	21:CU:22:ARG:HB3	1.96	0.47
1:AA:950:U:H2'	1:AA:951:G:C8	2.49	0.47
26:BA:446:G:OP1	41:BU:3:ARG:NH1	2.42	0.47
1:AA:371:G:O2'	1:AA:373:A:N7	2.47	0.47
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.95	0.47
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.95	0.47
28:DD:71:ASP:HB3	28:DD:103:ARG:NH2	2.28	0.47
55:B8:42:ARG:HD2	61:B8:205:HOH:O	2.15	0.47
26:DA:615:G:OP1	30:DF:40:GLN:HG2	2.14	0.47
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	1.95	0.47
1:AA:596:C:OP2	61:AA:4083:HOH:O	2.20	0.47
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.40	0.47
1:CA:934:C:OP1	61:CA:4164:HOH:O	2.20	0.47
26:DA:39:C:H2'	26:DA:40:C:C6	2.49	0.47
29:DE:178:GLU:N	29:DE:178:GLU:OE2	2.42	0.47
37:DQ:37:LEU:HD21	37:DQ:130:LYS:HE2	1.96	0.47
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.48	0.47
19:CS:32:LYS:HE3	19:CS:57:HIS:CD2	2.49	0.47
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.47	0.47
26:DA:816:C:OP1	26:DA:1185:C:O2'	2.22	0.47
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
27:BB:66:A:N6	27:BB:108:U:H2'	2.28	0.47
26:BA:899:A:HO2'	26:BA:900:A:H8	1.60	0.47
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.14	0.47
1:CA:1057:G:H5'	3:CC:155:GLY:HA2	1.95	0.47
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.30	0.47
35:DO:7:TYR:CZ	35:DO:44:LYS:HG3	2.50	0.47
1:AA:461:A:O2'	1:AA:470:C:H5'	2.13	0.47
1:AA:1495:U:O2'	26:BA:1919:A:N1	2.40	0.47
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.96	0.47
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.96	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.49	0.47
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.49	0.47
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.14	0.47
26:BA:1701:A:OP2	61:BA:5017:HOH:O	2.20	0.47
26:BA:616:G:H5'	30:BF:205:ARG:HD2	1.96	0.47
23:AW:76:31M:HNM1	26:BA:2061:G:H22	1.62	0.47
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:727:G:P	1:CA:742:G:H21	2.38	0.47
25:AY:50:U:H2'	25:AY:51:U:C6	2.48	0.47
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.49	0.47
4:CD:173:TRP:NE1	4:CD:189:PRO:HG3	2.29	0.47
25:AY:32:PSU:C2	25:AY:33:U:C5	3.02	0.47
2:CB:120:ALA:O	2:CB:122:PHE:N	2.43	0.47
28:DD:4:LYS:HB3	28:DD:18:VAL:CG2	2.44	0.47
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.96	0.47
26:DA:709:U:H2'	26:DA:710:G:C8	2.50	0.47
8:CH:33:GLU:HG2	8:CH:48:TYR:CE1	2.49	0.47
35:BO:120:GLU:HG2	35:BO:122:LEU:HG	1.97	0.47
26:BA:1031:G:H21	56:B9:36:GLN:HE22	1.62	0.47
29:DE:1:MET:HE1	29:DE:199:ARG:HD2	1.95	0.47
26:BA:302:C:OP2	45:BY:73:ARG:NH2	2.46	0.47
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.45	0.47
21:CU:15:ARG:HB2	21:CU:15:ARG:HH11	1.79	0.47
3:CC:69:HIS:CD2	3:CC:104:GLN:HB3	2.49	0.47
32:BH:20:ALA:HB1	32:BH:21:PRO:HD2	1.97	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.28	0.47
26:BA:1178:C:O5'	26:BA:1178:C:H6	1.96	0.47
25:AY:18:G:H1	25:AY:55:PSU:H1'	1.80	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
1:CA:952:U:H4'	1:CA:964:A:N1	2.30	0.47
26:DA:310:A:H1'	26:DA:311:A:H2'	1.95	0.47
25:AY:36:A:N6	25:AY:37:MIA:C6	2.78	0.47
61:DA:3829:HOH:O	30:DF:68:LYS:HE2	2.14	0.47
4:AD:175:SER:OG	4:AD:184:LYS:HB2	2.14	0.47
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.97	0.47
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.79	0.47
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.49	0.47
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.47	0.47
1:AA:1210:C:N4	1:AA:1211:U:O4	2.47	0.47
7:CG:89:MET:SD	7:CG:155:ARG:HB2	2.55	0.47
3:CC:42:LEU:HA	3:CC:45:LYS:HZ2	1.80	0.47
26:BA:143:G:H1'	44:BX:37:THR:HG21	1.97	0.47
24:CX:23:C:H2'	24:CX:24:U:C6	2.49	0.47
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.54	0.47
2:AB:166:ASP:O	2:AB:170:GLU:N	2.39	0.47
26:DA:2528:U:H5''	56:D9:31:LYS:HE2	1.97	0.47
25:AY:27:G:N2	25:AY:44:G:N3	2.63	0.47
26:BA:1173:G:N2	26:BA:1177:A:OP2	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.49	0.47
26:DA:897:C:H3'	26:DA:898:C:C6	2.50	0.47
1:CA:988:G:C4'	1:CA:1014:A:H61	2.28	0.47
22:CV:14:A:H8	22:CV:14:A:OP1	1.97	0.47
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.30	0.47
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.96	0.47
26:BA:2117:A:O2'	26:BA:2118:U:H5''	2.15	0.47
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.15	0.47
26:BA:2110:G:H4'	26:BA:2111:C:OP2	2.15	0.47
26:DA:855:G:O2'	47:D0:27:GLU:OE2	2.31	0.47
26:DA:2788:C:H2'	26:DA:2789:C:C6	2.50	0.47
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.96	0.47
1:AA:46:G:O2'	1:AA:365:U:O2	2.31	0.47
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.47
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.14	0.47
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.49	0.47
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.97	0.47
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.50	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.30	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.80	0.47
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.24	0.47
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.96	0.47
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	1.97	0.47
9:CI:88:TYR:CD1	9:CI:89:ASN:HB2	2.49	0.47
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.44	0.47
2:AB:188:ALA:HB1	2:AB:192:SER:OG	2.15	0.47
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.80	0.47
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.30	0.47
1:CA:1186:G:O3'	9:CI:113:LYS:NZ	2.46	0.47
29:DE:5:LEU:HD11	29:DE:79:ARG:HB2	1.96	0.47
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.97	0.47
26:DA:2751:G:C8	32:DH:2:SER:HA	2.49	0.47
53:B6:16:CYS:SG	53:B6:18:ARG:HD3	2.54	0.47
31:DG:121:ASN:HB3	31:DG:124:SER:HB2	1.97	0.47
26:BA:2701:C:H2'	26:BA:2702:U:H2'	1.96	0.47
28:DD:5:LYS:HE3	28:DD:5:LYS:HB3	1.52	0.47
45:BY:30:VAL:HG13	45:BY:37:VAL:HG12	1.97	0.47
41:BU:85:LYS:HE2	41:BU:117:GLN:HA	1.97	0.47
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.15	0.47
1:CA:627:G:H2'	1:CA:628:G:H8	1.78	0.47
13:CM:92:HIS:CE1	13:CM:98:VAL:HG11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:118:A:N3	26:DA:178:G:H1'	2.30	0.47
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.97	0.47
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	1.95	0.47
26:DA:1196:C:H2'	26:DA:1197:G:H8	1.79	0.47
40:BT:53:ARG:NH1	40:BT:53:ARG:HB3	2.30	0.47
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.15	0.47
1:CA:109:A:C6	1:CA:326:G:C6	3.03	0.47
1:AA:1360:A:H2'	1:AA:1361:G:O4'	2.15	0.47
1:CA:1027:C:OP1	1:CA:1027:C:H4'	2.14	0.47
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.15	0.47
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.77	0.47
1:CA:1179:A:C6	1:CA:1180:A:C4	3.03	0.47
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.48	0.47
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.50	0.47
3:CC:6:HIS:HB3	14:CN:49:HIS:ND1	2.30	0.47
26:DA:797:C:H2'	26:DA:798:G:O4'	2.14	0.47
26:DA:2506:U:OP1	29:DE:144:ARG:NH2	2.48	0.47
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.97	0.47
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.50	0.47
26:BA:1311:G:O2'	54:B7:47:ARG:NH2	2.47	0.47
1:AA:1293:G:H2'	1:AA:1294:G:C8	2.49	0.47
51:D4:53:GLU:HG2	51:D4:55:ARG:N	2.29	0.47
26:BA:41:C:H2'	26:BA:42:G:O4'	2.15	0.47
26:DA:1270:C:H5''	26:DA:1271:G:O5'	2.15	0.47
26:DA:2306:C:H3'	26:DA:2307:G:H2'	1.97	0.47
26:DA:121:G:H4'	26:DA:149:A:H5'	1.97	0.47
24:CX:44:A:C6	24:CX:45:G:C6	3.02	0.47
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.49	0.47
1:CA:337:C:H2'	1:CA:338:A:H8	1.79	0.47
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.48	0.47
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.40	0.47
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.96	0.47
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.50	0.47
19:CS:32:LYS:HA	19:CS:50:ALA:HB3	1.96	0.47
1:CA:1139:G:H4'	1:CA:1140:C:OP1	2.14	0.47
9:CI:16:ARG:HH11	9:CI:64:THR:HG21	1.80	0.47
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.97	0.47
1:CA:1305:G:H5'	21:CU:4:GLY:C	2.36	0.47
26:DA:77:C:OP1	49:D2:59:ARG:HD3	2.14	0.47
1:AA:1132:C:H2'	1:AA:1133:G:C8	2.50	0.47
1:AA:1227:A:P	13:AM:111:LYS:HZ2	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2563:U:H4'	35:DO:28:SER:HA	1.97	0.47
1:AA:299:G:O6	61:AA:4081:HOH:O	2.14	0.47
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.47
28:BD:72:LYS:HB3	28:BD:75:ILE:HD12	1.97	0.47
1:AA:1443:G:N2	1:AA:1459:C:O2	2.37	0.47
26:DA:315:G:H2'	26:DA:316:C:C6	2.50	0.47
26:BA:1243:G:O2'	36:BP:7:ARG:NH2	2.47	0.47
23:CW:29:G:N2	23:CW:41:C:N3	2.56	0.47
1:AA:156:G:N1	1:AA:165:C:N3	2.55	0.47
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.95	0.47
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.41	0.47
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.97	0.47
2:AB:19:HIS:O	2:AB:39:ILE:HG23	2.15	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.47	0.47
27:DB:115:G:H2'	27:DB:116:G:O4'	2.15	0.47
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	1.97	0.47
2:CB:185:ILE:HG22	2:CB:199:TYR:HD2	1.79	0.47
46:DZ:57:ILE:HD12	46:DZ:71:VAL:HG23	1.97	0.47
26:DA:2319:G:N2	39:DS:3:ARG:HA	2.30	0.47
26:DA:2298:A:C8	26:DA:2299:G:C8	3.03	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.50	0.47
7:CG:44:TYR:O	7:CG:47:CYS:HB2	2.15	0.47
26:DA:511:U:H4'	26:DA:1235:G:H4'	1.96	0.47
1:CA:136:C:O2'	16:CP:63:GLY:O	2.24	0.47
8:CH:124:ALA:O	8:CH:128:GLY:N	2.48	0.47
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.15	0.47
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.35	0.47
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.96	0.46
1:AA:1028:C:N4	1:AA:1033:G:H1	2.10	0.46
26:DA:1169:G:O5'	26:DA:1169:G:H8	1.98	0.46
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.35	0.46
1:AA:163:C:H2'	1:AA:164:U:C6	2.49	0.46
1:CA:1456:G:N1	20:CT:51:GLU:OE1	2.45	0.46
23:AW:52:G:H4'	37:BQ:56:ARG:HH12	1.80	0.46
1:AA:346:G:C3'	1:AA:347:G:H4'	2.45	0.46
26:DA:854:G:H2'	26:DA:855:G:C8	2.50	0.46
1:AA:953:G:N7	13:AM:104:ARG:NH2	2.63	0.46
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.14	0.46
26:BA:303:U:H2'	26:BA:304:G:H8	1.80	0.46
1:AA:161:A:H2'	1:AA:162:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1116:C:H2'	26:DA:1117:G:H8	1.79	0.46
26:DA:1797:C:H4'	28:DD:257:LEU:O	2.15	0.46
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.48	0.46
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.14	0.46
1:AA:625:G:H2'	1:AA:626:U:H6	1.79	0.46
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.50	0.46
26:BA:1641:A:H2'	26:BA:1642:G:O4'	2.14	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.49	0.46
38:BR:104:ARG:HG3	38:BR:111:LEU:HD21	1.97	0.46
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.50	0.46
26:BA:620:G:N3	26:BA:620:G:H5'	2.30	0.46
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.46
26:DA:2516:G:O6	26:DA:2517:C:N4	2.48	0.46
1:CA:309:G:O2'	1:CA:607:A:N1	2.48	0.46
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.46
26:DA:2141:G:C8	26:DA:2151:G:N2	2.83	0.46
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.96	0.46
1:AA:1002:G:H3'	1:AA:1003:G:H8	1.81	0.46
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.80	0.46
23:AW:6:G:N1	23:AW:67:C:N4	2.39	0.46
26:BA:1179:C:H2'	26:BA:1180:C:H6	1.80	0.46
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.44	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.43	0.46
25:CY:74:C:H4'	48:D1:23:LYS:HE3	1.97	0.46
37:DQ:133:ARG:HG2	37:DQ:134:ARG:N	2.30	0.46
26:DA:2318:G:H4'	26:DA:2319:G:OP1	2.14	0.46
26:DA:2647:U:H2'	26:DA:2648:C:C6	2.51	0.46
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.16	0.46
23:CW:76:31M:N	24:CX:76:A:O3'	2.49	0.46
40:DT:16:ARG:HH11	40:DT:16:ARG:HB3	1.80	0.46
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.15	0.46
2:AB:102:LEU:HD23	2:AB:182:ILE:HD12	1.98	0.46
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.97	0.46
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.48	0.46
26:DA:2516:G:C6	26:DA:2517:C:C4	3.03	0.46
26:DA:229:A:H5''	26:DA:230:U:H5'	1.96	0.46
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.15	0.46
1:AA:382:A:H2'	1:AA:383:A:C8	2.49	0.46
26:BA:2010:G:H5''	43:BW:42:ARG:HB2	1.98	0.46
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.50	0.46
26:DA:1630:G:H2'	26:DA:1631:C:C6	2.51	0.46
26:BA:2887:U:H2'	26:BA:2888:C:C6	2.49	0.46
5:AE:43:LEU:HD21	5:AE:132:ALA:HB1	1.97	0.46
1:CA:772:U:H2'	1:CA:773:G:O4'	2.15	0.46
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.30	0.46
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.30	0.46
10:CJ:23:ILE:HA	10:CJ:23:ILE:HD13	1.77	0.46
30:BF:93:LYS:HD3	30:BF:93:LYS:HA	1.68	0.46
31:BG:146:TYR:O	31:BG:146:TYR:HD1	1.98	0.46
25:AY:69:G:C5	25:AY:70:G:C8	3.03	0.46
26:BA:278:A:O2'	26:BA:279:C:OP1	2.23	0.46
29:DE:50:GLY:HA2	29:DE:77:ILE:O	2.14	0.46
25:CY:69:G:C6	25:CY:70:G:C8	3.04	0.46
26:BA:527:C:C4	26:BA:2779:U:H2'	2.50	0.46
1:AA:406:G:H4'	4:AD:3:ARG:HH22	1.80	0.46
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.51	0.46
22:CV:16:A:N6	24:CX:36:U:H3	2.12	0.46
46:BZ:137:ILE:HA	46:BZ:156:LYS:HZ1	1.80	0.46
15:AO:18:PHE:CZ	15:AO:21:ASP:HB3	2.50	0.46
45:BY:55:TYR:CD2	45:BY:55:TYR:N	2.84	0.46
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.51	0.46
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.98	0.46
2:AB:59:GLU:HG3	2:AB:225:ALA:HB2	1.96	0.46
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.47	0.46
4:AD:163:GLU:O	4:AD:165:MET:N	2.48	0.46
1:AA:743:U:H2'	1:AA:744:C:C6	2.51	0.46
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.15	0.46
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.96	0.46
56:D9:13:LYS:HD3	56:D9:28:GLU:OE2	2.15	0.46
26:DA:724:U:H2'	26:DA:725:G:O4'	2.15	0.46
25:AY:12:U:C2	25:AY:24:G:C2	3.03	0.46
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.15	0.46
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.29	0.46
26:BA:615:G:OP1	30:BF:40:GLN:HG2	2.15	0.46
26:DA:8:A:H2'	26:DA:9:U:H6	1.81	0.46
26:DA:2510:C:C4	26:DA:2511:U:C4	3.03	0.46
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.16	0.46
25:CY:15:G:C2	25:CY:48:C:N3	2.82	0.46
26:BA:2792:G:N2	26:BA:2805:G:H1'	2.31	0.46
29:BE:149:ARG:N	61:BE:406:HOH:O	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.96	0.46
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.80	0.46
26:DA:1359:A:N1	26:DA:1372:U:O4	2.47	0.46
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.15	0.46
26:DA:647:G:O5'	26:DA:647:G:H8	1.98	0.46
24:AX:17:C:H5'	24:AX:61:C:OP1	2.16	0.46
43:BW:9:TYR:HA	43:BW:100:THR:HG23	1.98	0.46
26:DA:28:A:C2	26:DA:513:A:C8	3.03	0.46
26:DA:2870:C:H5''	38:DR:65:LEU:HD21	1.97	0.46
1:CA:1499:A:H1'	1:CA:1520:G:H5'	1.96	0.46
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.49	0.46
26:DA:995:C:N3	34:DN:2:LYS:HA	2.31	0.46
26:DA:2745:C:C4	26:DA:2746:U:C4	3.03	0.46
23:AW:19:G:H4'	23:AW:20:U:OP1	2.16	0.46
23:AW:8:4SU:O2'	23:AW:46:7MG:N2	2.49	0.46
24:CX:37:A:H2'	24:CX:38:A:O4'	2.16	0.46
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HB2	1.98	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
1:AA:1003:G:C2	1:AA:1004:A:N3	2.84	0.46
10:AJ:70:ARG:HA	10:AJ:70:ARG:HD3	1.83	0.46
2:CB:149:LEU:HD22	2:CB:152:PHE:HD2	1.80	0.46
26:BA:2130:U:H2'	26:BA:2131:G:N2	2.31	0.46
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.15	0.46
1:AA:224:C:H2'	1:AA:225:C:H6	1.81	0.46
1:CA:992:U:H6	1:CA:992:U:H5''	1.80	0.46
19:CS:27:GLU:HB2	19:CS:28:LYS:NZ	2.31	0.46
19:CS:27:GLU:HG2	19:CS:47:HIS:HE2	1.80	0.46
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.46
1:CA:69:G:H2'	1:CA:70:G:C8	2.51	0.46
29:DE:1:MET:O	29:DE:84:PHE:HB2	2.15	0.46
32:DH:86:GLU:HB3	32:DH:165:ALA:HB2	1.97	0.46
26:DA:811:U:H2'	36:DP:21:ARG:HA	1.96	0.46
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.97	0.46
30:BF:28:ILE:O	30:BF:30:PRO:HD3	2.15	0.46
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.15	0.46
11:AK:82:VAL:N	11:AK:107:SER:O	2.45	0.46
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.30	0.46
26:DA:195:A:H2'	26:DA:198:C:N4	2.31	0.46
26:DA:383:U:H2'	26:DA:385:C:H5	1.81	0.46
26:BA:236:C:H2'	26:BA:237:C:C6	2.50	0.46
26:DA:2502:G:H5''	26:DA:2503:A:H5''	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:55:U:O3'	31:DG:27:ASN:ND2	2.49	0.46
26:DA:783:A:O2'	26:DA:785:G:OP1	2.24	0.46
1:CA:1002:G:N3	1:CA:1003:G:C8	2.84	0.46
26:BA:1021:A:H3'	26:BA:1021:A:C8	2.50	0.46
1:AA:1025:U:O2	1:AA:1036:G:C6	2.66	0.46
26:BA:1697:G:OP2	26:BA:1698:A:O2'	2.14	0.46
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.38	0.46
1:CA:1134:G:H2'	1:CA:1135:U:H5'	1.98	0.46
1:CA:1291:G:C6	1:CA:1292:U:C4	3.04	0.46
25:CY:35:A:N6	25:CY:36:A:N1	2.63	0.46
26:DA:740:U:H2'	26:DA:741:G:C8	2.51	0.46
26:BA:2128:C:H2'	26:BA:2129:C:C6	2.50	0.46
52:D5:16:ARG:HD2	52:D5:20:ARG:NH1	2.31	0.46
26:DA:191:A:H2'	26:DA:192:C:C6	2.50	0.46
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.46
4:AD:110:PHE:HE1	4:AD:176:LEU:HD13	1.80	0.46
14:CN:6:LEU:HB3	14:CN:23:ARG:NH2	2.30	0.46
26:BA:191:A:H2'	26:BA:192:C:C6	2.51	0.46
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.48	0.46
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.49	0.46
1:AA:1136:U:H5''	1:AA:1137:C:N3	2.30	0.46
18:CR:26:LEU:CD2	18:CR:42:ARG:HD2	2.46	0.46
18:AR:65:ILE:O	18:AR:69:THR:HG23	2.16	0.46
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.49	0.46
26:DA:1611:C:H2'	26:DA:1612:C:H5'	1.98	0.46
1:CA:630:G:H2'	1:CA:631:G:H8	1.81	0.46
1:CA:1095:U:C4	1:CA:1096:C:C4	3.03	0.46
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.96	0.46
26:BA:484:C:H2'	26:BA:485:C:C6	2.51	0.46
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.96	0.46
26:BA:1495:A:H2'	26:BA:1496:A:C8	2.51	0.46
25:CY:50:U:C2	25:CY:64:A:N1	2.84	0.46
26:BA:2141:G:N7	26:BA:2151:G:C2	2.84	0.46
4:AD:3:ARG:HD3	4:AD:118:ARG:HD2	1.97	0.46
26:DA:999:U:O2'	26:DA:1000:A:H5'	2.16	0.46
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.15	0.46
26:BA:1300:U:H4'	26:BA:1301:A:H5'	1.97	0.46
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.79	0.46
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.16	0.46
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.30	0.46
31:BG:47:LYS:O	31:BG:51:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2291:U:O2'	26:DA:2374:C:H1'	2.16	0.46
1:CA:937:A:H1'	1:CA:1379:G:N2	2.30	0.46
26:BA:2630:G:H2'	26:BA:2631:G:H8	1.80	0.46
26:DA:2347:C:O2'	53:D6:21:TYR:OH	2.34	0.46
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.98	0.46
26:DA:195:A:H2'	26:DA:198:C:H41	1.80	0.46
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.51	0.46
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.96	0.46
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.39	0.46
33:DI:77:LEU:HD11	33:DI:101:LEU:HB2	1.98	0.46
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.51	0.46
26:BA:882:G:H2'	26:BA:883:G:O4'	2.15	0.46
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.16	0.46
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.99	0.46
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.16	0.46
7:CG:79:ARG:HB3	7:CG:80:VAL:H	1.37	0.46
3:AC:20:SER:OG	3:AC:40:ARG:NH1	2.48	0.46
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.15	0.46
1:AA:93:G:O2'	1:AA:96:U:H5'	2.16	0.46
26:DA:774:A:N3	26:DA:774:A:H2'	2.30	0.46
1:CA:450:G:H4'	16:CP:41:PRO:HB2	1.98	0.46
31:DG:25:TYR:HB3	31:DG:30:GLU:HB3	1.98	0.46
2:CB:28:PHE:HD1	2:CB:194:PRO:HG3	1.81	0.46
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.37	0.46
33:BI:85:GLU:OE1	33:BI:85:GLU:HA	2.16	0.46
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.80	0.46
26:BA:271(V):G:O6	61:BA:4948:HOH:O	2.20	0.46
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	1.98	0.46
61:BA:5273:HOH:O	47:B0:41:ARG:HA	2.15	0.46
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.16	0.46
2:CB:30:ARG:HG3	2:CB:31:TYR:CD1	2.50	0.46
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.49	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.81	0.46
26:BA:536:A:H2'	26:BA:537:C:C6	2.50	0.46
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.31	0.46
1:CA:1006:C:H2'	1:CA:1007:C:O4'	2.16	0.46
1:CA:1317:C:H5	14:CN:18:VAL:HG21	1.80	0.46
26:BA:2141:G:C4	26:BA:2142:C:H1'	2.51	0.46
2:CB:218:ALA:O	2:CB:222:ILE:HG23	2.15	0.46
26:DA:307:G:H22	26:DA:310:A:P	2.38	0.46
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.24	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.03	0.46
44:DX:92:LEU:HA	44:DX:92:LEU:HD12	1.83	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
30:BF:29:ASN:H	30:BF:112:MET:CE	2.28	0.46
2:CB:150:SER:OG	2:CB:151:GLY:N	2.48	0.46
1:AA:6:G:O2'	1:AA:7:G:H5'	2.16	0.46
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.16	0.46
26:DA:1484:G:C6	26:DA:1485:G:N7	2.84	0.46
25:CY:76:A:O2'	26:DA:2394:C:N3	2.44	0.46
26:BA:857:C:N4	26:BA:858:U:O4	2.49	0.46
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.43	0.46
26:DA:2687:U:H2'	26:DA:2688:U:O4'	2.16	0.46
31:DG:44:GLY:O	31:DG:47:LYS:HB2	2.15	0.46
1:CA:202:U:O2'	1:CA:203:U:O5'	2.31	0.46
2:CB:100:GLY:HA2	2:CB:103:THR:OG1	2.15	0.46
46:DZ:150:LEU:HD12	46:DZ:150:LEU:HA	1.78	0.46
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.49	0.46
26:DA:1032:A:H2	26:DA:1122:G:H22	1.61	0.46
52:B5:42:PRO:HB2	52:B5:43:HIS:ND1	2.31	0.46
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.49	0.46
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.81	0.46
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.31	0.46
13:AM:4:ILE:HD12	13:AM:57:ARG:HA	1.97	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
26:BA:2803:C:H2'	26:BA:2804:C:C6	2.51	0.46
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.51	0.46
1:AA:93:G:C2'	1:AA:96:U:H5'	2.46	0.46
26:DA:517:C:O2'	43:DW:18:ARG:NH2	2.49	0.46
26:DA:330:A:HO2'	26:DA:331:A:H8	1.61	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.51	0.46
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.16	0.46
26:DA:1477:A:H2'	26:DA:1478:G:O4'	2.14	0.46
2:CB:96:ARG:HD2	2:CB:98:LEU:HD22	1.97	0.46
26:DA:1857:G:C6	26:DA:1858:G:N1	2.84	0.46
3:CC:121:ALA:HB2	3:CC:198:VAL:HG21	1.98	0.46
26:BA:2011:U:OP1	43:BW:42:ARG:HD3	2.16	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.78	0.46
38:DR:98:LEU:HB2	38:DR:113:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.98	0.46
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.16	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.51	0.46
26:BA:2675:A:H5'	35:BO:29:ASN:O	2.15	0.46
33:DI:90:GLY:O	33:DI:121:LYS:HE3	2.16	0.46
26:BA:2359:C:H2'	26:BA:2360:A:O4'	2.16	0.46
26:BA:1178:C:H2'	26:BA:1179:C:C6	2.51	0.45
1:CA:976:G:C8	1:CA:1362:C:N4	2.84	0.45
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.16	0.45
1:AA:1075:C:H2'	1:AA:1076:C:H5''	1.98	0.45
1:CA:920:U:H2'	1:CA:921:U:H6	1.77	0.45
26:DA:1300:U:H4'	26:DA:1301:A:O5'	2.16	0.45
33:BI:77:LEU:HB2	33:BI:142:VAL:HG12	1.97	0.45
1:CA:1084:G:C5	1:CA:1085:U:C4	3.04	0.45
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.96	0.45
1:CA:59:A:H3'	1:CA:331:G:H22	1.81	0.45
28:DD:72:LYS:HB3	28:DD:75:ILE:HD12	1.98	0.45
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.16	0.45
26:BA:271(O):C:H2'	26:BA:271(P):C:C6	2.51	0.45
26:DA:601:C:O2'	30:DF:104:LYS:NZ	2.44	0.45
2:AB:45:GLN:O	2:AB:49:GLU:HB2	2.16	0.45
15:CO:74:ASP:OD1	15:CO:76:GLU:HB2	2.16	0.45
26:DA:754:C:H2'	26:DA:755:C:C6	2.50	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.51	0.45
1:AA:691:G:OP2	11:AK:26:ASN:ND2	2.38	0.45
1:CA:689:C:P	11:CK:46:GLY:HA3	2.56	0.45
33:DI:102:SER:O	33:DI:106:GLY:N	2.37	0.45
50:B3:43:ILE:O	50:B3:47:VAL:HG23	2.16	0.45
1:CA:1423:G:H2'	1:CA:1424:C:H6	1.80	0.45
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.31	0.45
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.98	0.45
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.51	0.45
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.51	0.45
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.16	0.45
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.49	0.45
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	2.12	0.45
13:CM:37:THR:HG21	13:CM:56:LEU:HA	1.97	0.45
31:BG:16:ARG:NE	31:BG:31:VAL:HG11	2.30	0.45
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.81	0.45
4:AD:162:LEU:CD1	4:AD:181:MET:HG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2846:G:H2'	26:BA:2847:U:O4'	2.16	0.45
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.16	0.45
33:DI:93:THR:HG22	33:DI:119:PRO:HB3	1.97	0.45
1:CA:775:G:N2	1:CA:804:U:O4	2.48	0.45
1:AA:59:A:H3'	1:AA:331:G:H22	1.81	0.45
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.36	0.45
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.97	0.45
3:AC:155:GLY:HA3	3:AC:196:LEU:HD22	1.97	0.45
5:AE:27:ARG:HB2	5:AE:27:ARG:HE	1.48	0.45
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.52	0.45
9:CI:99:LEU:HB3	9:CI:101:PHE:CE2	2.51	0.45
26:DA:698:C:O2'	26:DA:734:A:N6	2.49	0.45
26:DA:752:A:P	54:D7:3:ARG:HH22	2.39	0.45
38:DR:29:LEU:HA	38:DR:29:LEU:HD12	1.78	0.45
47:D0:53:MET:HG2	47:D0:57:PHE:HA	1.98	0.45
26:DA:1027:A:C6	26:DA:1126:A:C4	3.04	0.45
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.16	0.45
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.51	0.45
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.98	0.45
2:AB:16:HIS:CE1	2:AB:214:ILE:HD11	2.46	0.45
26:DA:2127:G:N1	26:DA:2161:C:O2	2.34	0.45
26:BA:2141:G:C6	26:BA:2142:C:C2	3.04	0.45
1:CA:1053:G:C3'	1:CA:1054:C:H5'	2.45	0.45
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.45
26:BA:1301:A:C8	26:BA:1303:G:C8	3.04	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.51	0.45
39:DS:3:ARG:HE	39:DS:4:LEU:N	2.15	0.45
34:BN:38:HIS:NE2	34:BN:50:ASP:OD2	2.50	0.45
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.50	0.45
26:DA:2468:G:C2	26:DA:2481:G:N3	2.85	0.45
26:BA:90:U:H4'	26:BA:92:A:H5'	1.99	0.45
26:DA:2653:U:O2'	32:DH:110:SER:HB3	2.15	0.45
19:CS:41:VAL:HG12	19:CS:43:GLU:H	1.80	0.45
11:CK:81:ASP:OD1	11:CK:106:LYS:HB2	2.17	0.45
31:BG:45:GLU:HG2	31:BG:45:GLU:H	1.36	0.45
28:BD:52:ARG:NH2	61:BD:411:HOH:O	2.22	0.45
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.44	0.45
16:CP:19:ILE:N	16:CP:37:GLY:O	2.49	0.45
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.52	0.45
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.81	0.45
4:AD:138:TYR:HE1	4:AD:140:VAL:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DY:86:ARG:HD2	45:DY:100:ALA:HA	1.98	0.45
1:CA:991:U:H3'	1:CA:1212:U:N3	2.32	0.45
6:CF:28:ARG:HB2	6:CF:28:ARG:HH11	1.82	0.45
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.17	0.45
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.17	0.45
31:BG:31:VAL:HA	31:BG:32:PRO:HD2	1.79	0.45
36:BP:121:LYS:O	36:BP:123:LEU:N	2.45	0.45
26:DA:2019:A:C4'	41:DU:34:LYS:HD2	2.47	0.45
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.64	0.45
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.16	0.45
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.16	0.45
7:AG:91:VAL:HB	7:AG:96:GLN:HG2	1.99	0.45
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.45
1:CA:56:U:H2'	1:CA:57:G:C8	2.52	0.45
26:DA:241:A:H8	26:DA:241:A:OP1	2.00	0.45
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.52	0.45
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.49	0.45
1:AA:356:A:N7	61:AA:4035:HOH:O	2.36	0.45
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.17	0.45
3:CC:79:ARG:H	3:CC:82:GLU:HB3	1.82	0.45
26:DA:2287:A:N1	26:DA:2346:A:N7	2.65	0.45
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.49	0.45
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.98	0.45
1:CA:22:G:H4'	1:CA:885:G:C8	2.52	0.45
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.32	0.45
46:BZ:105:VAL:N	46:BZ:139:VAL:O	2.41	0.45
18:AR:31:LEU:HD11	18:AR:62:GLU:HB2	1.98	0.45
1:AA:1305:G:H5"	21:AU:4:GLY:HA3	1.98	0.45
6:CF:46:ARG:HH21	18:CR:37:VAL:HG11	1.81	0.45
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.47	0.45
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.52	0.45
1:CA:1097:C:O2'	1:CA:1169:A:N3	2.41	0.45
20:CT:53:LEU:O	20:CT:57:ARG:HG3	2.16	0.45
26:DA:25:U:H5'	43:DW:78:GLU:O	2.16	0.45
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.32	0.45
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.46	0.45
1:CA:189(F):U:O2	17:CQ:63:ARG:NH2	2.50	0.45
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.99	0.45
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	1.98	0.45
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.63	0.45
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:150:SER:OG	2:AB:151:GLY:N	2.49	0.45
35:BO:7:TYR:CZ	35:BO:44:LYS:HG3	2.52	0.45
12:CL:69:TYR:CE2	12:CL:71:PRO:HA	2.52	0.45
2:AB:22:LYS:H	2:AB:40:HIS:CE1	2.35	0.45
1:CA:93:G:C6	1:CA:96:U:C4	3.05	0.45
1:CA:97:G:O2'	1:CA:98:G:H5''	2.17	0.45
42:DV:100:ARG:HH11	42:DV:100:ARG:CG	2.17	0.45
25:CY:21:A:N6	25:CY:46:7MG:H81	2.32	0.45
1:CA:1054:C:O2'	1:CA:1055:A:C5'	2.64	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.20	0.45
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.50	0.45
26:BA:528:A:N1	26:BA:2042:A:H2'	2.31	0.45
26:BA:1300:U:H4'	26:BA:1301:A:H5''	1.99	0.45
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.81	0.45
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.45	0.45
1:AA:836:G:OP1	18:AR:61:LYS:NZ	2.49	0.45
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.30	0.45
26:BA:2544:G:H1'	26:BA:2646:C:H4'	1.99	0.45
26:DA:251:A:H5''	36:DP:50:ARG:HH11	1.81	0.45
26:DA:93:G:H2'	26:DA:94:C:H6	1.82	0.45
1:AA:300:A:O2'	1:AA:564:C:N3	2.39	0.45
26:DA:2450:A:OP1	26:DA:2497:A:O2'	2.35	0.45
1:AA:8:A:N7	4:AD:208:SER:OG	2.48	0.45
46:DZ:113:ALA:HB3	46:DZ:146:ILE:HD11	1.97	0.45
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.50	0.45
33:BI:102:SER:OG	33:BI:103:ARG:N	2.50	0.45
29:BE:7:VAL:HG12	29:BE:27:LEU:HB3	1.98	0.45
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.81	0.45
41:DU:27:LEU:HD23	41:DU:30:LYS:HB2	1.98	0.45
55:D8:62:LEU:HB3	55:D8:65:GLU:HG3	1.97	0.45
26:DA:1782:C:H1'	26:DA:2609:U:H5''	1.98	0.45
26:DA:686:G:H21	26:DA:788:A:H61	1.65	0.45
45:DY:13:VAL:HG12	45:DY:74:PRO:HA	1.99	0.45
1:CA:1000:U:C2	1:CA:1041:A:N1	2.83	0.45
25:AY:50:U:C4	25:AY:64:A:N1	2.84	0.45
15:CO:54:ARG:HD3	15:CO:58:MET:CE	2.47	0.45
1:AA:78:G:C6	1:AA:91:C:N4	2.83	0.45
25:CY:70:G:H2'	25:CY:71:G:H5'	1.99	0.45
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.83	0.45
23:CW:47:U:H3'	23:CW:48:C:C5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:55:PHE:O	2:CB:59:GLU:N	2.33	0.45
37:BQ:18:LYS:HB2	37:BQ:18:LYS:HE3	1.72	0.45
1:CA:297:G:N2	1:CA:300:A:OP2	2.49	0.45
44:DX:92:LEU:C	44:DX:94:GLY:H	2.18	0.45
26:BA:141:A:H8	26:BA:1408:C:O2'	2.00	0.45
33:BI:136:VAL:N	33:BI:137:PRO:HD3	2.32	0.45
16:AP:5:ARG:NH1	16:AP:24:ALA:HA	2.31	0.45
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.50	0.45
26:DA:2348:U:O4	26:DA:2382:G:N1	2.50	0.45
1:CA:335:C:H2'	1:CA:336:C:C6	2.51	0.45
3:CC:156:ARG:NH2	3:CC:159:GLY:O	2.27	0.45
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.56	0.45
26:DA:30:G:H2'	26:DA:31:C:C6	2.52	0.45
26:DA:864:G:C6	26:DA:865:C:N4	2.85	0.45
1:AA:692:U:O2'	1:AA:694:A:N7	2.42	0.45
35:DO:107:ARG:CZ	40:DT:36:GLU:HG2	2.46	0.45
31:DG:74:LYS:O	31:DG:84:LYS:HD2	2.16	0.45
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.98	0.45
28:BD:5:LYS:HE3	28:BD:5:LYS:HB3	1.56	0.45
36:BP:135:LEU:HD23	36:BP:135:LEU:HA	1.77	0.45
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.47	0.45
26:DA:848:G:C4	26:DA:933:A:H8	2.35	0.45
26:BA:1783:A:H5'	26:BA:2608:G:H4'	1.98	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
26:DA:1740:G:H2'	26:DA:1741:A:C8	2.51	0.45
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.17	0.45
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.51	0.45
26:DA:443:A:OP2	26:DA:614(B):G:N2	2.38	0.45
24:CX:9:G:O2'	24:CX:10:G:N7	2.37	0.45
1:AA:300:A:H2'	1:AA:301:G:O4'	2.17	0.45
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.52	0.45
26:DA:94(A):G:C6	26:DA:95:G:C5	3.05	0.45
1:CA:58:C:O2'	1:CA:388:G:N7	2.40	0.45
26:DA:2637:U:H1'	26:DA:2782:G:N2	2.32	0.45
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.99	0.45
26:DA:270:A:N1	26:DA:366:C:H4'	2.32	0.45
37:DQ:118:LEU:HB3	37:DQ:131:ILE:HD12	1.97	0.45
4:AD:121:VAL:O	4:AD:134:ASP:HA	2.15	0.45
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.98	0.45
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.33	0.45
25:AY:7:A:O2'	25:AY:49:C:OP2	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.34	0.45
2:CB:15:VAL:HG21	2:CB:213:LEU:HD12	1.98	0.45
42:DV:40:LEU:HB2	42:DV:46:VAL:HG22	1.99	0.45
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.82	0.45
26:DA:1395:A:OP1	61:DA:4546:HOH:O	2.21	0.45
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.52	0.45
27:DB:66:A:N6	27:DB:108:U:H3'	2.32	0.45
26:BA:897:C:C4	26:BA:898:C:N4	2.85	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
1:AA:662:G:H2'	1:AA:663:A:H8	1.79	0.45
1:AA:189(A):C:N4	1:AA:189(J):G:H1	2.15	0.45
31:BG:11:TYR:O	31:BG:16:ARG:HG2	2.17	0.45
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.52	0.45
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.86	0.45
23:AW:18:G:O2'	23:AW:57:G:N2	2.39	0.45
23:CW:76:31M:HD1	23:CW:76:31M:HA	1.41	0.45
1:CA:1374:A:O2'	7:CG:28:ASN:HB3	2.16	0.45
27:DB:11:C:H3'	27:DB:12:C:C6	2.52	0.45
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.99	0.45
26:DA:2305:A:H2'	26:DA:2306:C:O4'	2.17	0.45
28:DD:96:HIS:HD2	28:DD:102:LYS:HG2	1.81	0.45
26:DA:263:C:H2'	26:DA:264:C:O4'	2.17	0.45
34:BN:14:VAL:HG11	34:BN:138:LEU:HD12	1.99	0.45
26:BA:1957:C:H2'	26:BA:1958:C:C6	2.52	0.45
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.17	0.45
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.17	0.45
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.16	0.45
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.51	0.45
45:BY:34:LYS:O	45:BY:34:LYS:HG3	2.15	0.45
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.16	0.45
40:DT:117:ASP:OD2	40:DT:120:ARG:NE	2.41	0.45
1:CA:1028:C:N3	1:CA:1033:G:C6	2.84	0.45
25:AY:54:5MU:H73	25:AY:55:PSU:O2	2.17	0.45
1:CA:1133:G:C4	1:CA:1134:G:C8	3.04	0.45
1:CA:582:U:OP2	1:CA:758:G:N1	2.45	0.45
26:BA:973:A:OP2	61:BA:4141:HOH:O	2.20	0.45
26:BA:2893:G:HO2'	26:BA:2894:G:P	2.38	0.45
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.17	0.45
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.45
1:CA:200:G:H1	1:CA:217:C:N4	2.09	0.45
26:BA:2168:G:O6	26:BA:2171:A:H8	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:250:G:P	55:B8:13:ARG:HH22	2.39	0.45
1:AA:1442(B):A:N3	40:BT:118:ARG:NH2	2.65	0.45
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.49	0.45
26:BA:899:A:O2'	26:BA:900:A:H8	2.00	0.45
34:DN:37:LYS:NZ	61:DN:5101:HOH:O	2.49	0.45
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	1.99	0.45
1:CA:1338:G:C6	1:CA:1339:A:C6	3.05	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.15	0.45
26:DA:2303:G:O2'	31:DG:132:ASN:ND2	2.44	0.45
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.51	0.45
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.99	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.99	0.45
26:BA:2576:G:H1'	61:BA:4454:HOH:O	2.17	0.45
5:CE:79:GLU:OE1	8:CH:104:ARG:HA	2.17	0.45
32:BH:98:LEU:HD12	32:BH:102:ALA:O	2.16	0.45
26:DA:492:A:H2'	26:DA:493:G:O4'	2.17	0.45
26:DA:2607:G:O6	61:DA:4661:HOH:O	2.20	0.45
61:BA:4103:HOH:O	30:BF:68:LYS:HE2	2.17	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.78	0.45
25:CY:66:U:H2'	25:CY:67:C:O4'	2.17	0.44
46:DZ:157:LEU:C	46:DZ:161:VAL:HG11	2.37	0.44
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.81	0.44
26:BA:1371:G:H2'	26:BA:1372:U:C5	2.50	0.44
26:DA:307:G:H21	26:DA:330:A:N6	2.10	0.44
27:DB:66:A:H61	27:DB:109:C:H5'	1.82	0.44
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.98	0.44
36:BP:50:ARG:NH2	55:B8:7:HIS:HD2	2.15	0.44
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.44
26:DA:2298:A:H2'	26:DA:2299:G:O4'	2.16	0.44
1:CA:1386:G:C2	1:CA:1387:G:C8	3.04	0.44
1:AA:6:G:H4'	1:AA:298:A:H4'	1.99	0.44
26:BA:271(P):C:O3'	33:BI:42:SER:OG	2.27	0.44
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.53	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.16	0.44
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.99	0.44
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.17	0.44
37:DQ:58:PHE:CE2	37:DQ:109:VAL:HG21	2.52	0.44
1:CA:866:C:C4	1:CA:867:G:H1'	2.52	0.44
26:BA:2615:U:H2'	26:BA:2616:C:H6	1.82	0.44
1:CA:353:A:H8	1:CA:353:A:H5'	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:46:GLU:O	20:CT:46:GLU:HG2	2.16	0.44
1:CA:501:C:H2'	1:CA:502:G:C8	2.52	0.44
1:AA:636:U:H2'	1:AA:637:G:C8	2.52	0.44
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.17	0.44
2:CB:213:LEU:O	2:CB:217:ARG:HB2	2.17	0.44
26:BA:1019:U:H3	26:BA:1142(A):A:N6	2.10	0.44
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.17	0.44
15:CO:54:ARG:HD3	15:CO:58:MET:HE2	1.99	0.44
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.82	0.44
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.40	0.44
25:AY:41:C:H2'	25:AY:42:C:C6	2.53	0.44
9:CI:99:LEU:HB3	9:CI:101:PHE:CD2	2.52	0.44
26:DA:686:G:N2	26:DA:788:A:H61	2.14	0.44
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.50	0.44
26:BA:1630:G:H2'	26:BA:1631:C:C6	2.53	0.44
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.18	0.44
1:AA:767:A:N7	61:AA:4048:HOH:O	2.36	0.44
45:DY:52:SER:HB2	45:DY:53:PRO:HD2	1.99	0.44
26:BA:305:U:H2'	26:BA:306:U:C6	2.52	0.44
31:DG:138:GLN:OE1	31:DG:138:GLN:N	2.43	0.44
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.52	0.44
33:DI:133:HIS:HD2	33:DI:136:VAL:HG23	1.82	0.44
26:BA:470:A:OP1	30:BF:59:TYR:HE1	1.99	0.44
27:DB:72:G:H1'	27:DB:105:A:H61	1.82	0.44
26:BA:2649:U:H2'	26:BA:2650:U:C6	2.51	0.44
1:CA:153:C:H2'	1:CA:154:C:C6	2.52	0.44
26:DA:2153:G:N2	26:DA:2154:G:N3	2.65	0.44
3:AC:52:LEU:HA	3:AC:70:VAL:HG23	1.99	0.44
46:BZ:108:PRO:CG	46:BZ:117:LEU:HD22	2.47	0.44
19:CS:30:LEU:CD1	19:CS:50:ALA:HB2	2.48	0.44
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.80	0.44
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.51	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.52	0.44
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.32	0.44
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.99	0.44
36:DP:88:LEU:HD11	36:DP:114:ILE:HD12	1.99	0.44
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.32	0.44
26:BA:2661:G:H2'	26:BA:2662:A:C8	2.51	0.44
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.53	0.44
1:AA:620:C:H2'	1:AA:621:A:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:128:VAL:HG23	46:DZ:160:GLY:O	2.17	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
31:DG:28:VAL:O	31:DG:31:VAL:HG12	2.18	0.44
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.71	0.44
26:BA:1378:A:OP1	54:B7:10:ARG:NH2	2.51	0.44
26:BA:675:A:C8	26:BA:804:A:C6	3.05	0.44
4:CD:47:ARG:HH11	4:CD:49:ARG:HH21	1.65	0.44
29:BE:79:ARG:HA	29:BE:79:ARG:HD3	1.82	0.44
25:CY:7:A:N1	25:CY:66:U:O2	2.50	0.44
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.40	0.44
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.17	0.44
1:CA:1054:C:HO2'	1:CA:1055:A:P	2.36	0.44
23:AW:51:U:H2'	23:AW:52:G:H8	1.83	0.44
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.32	0.44
10:CJ:5:ARG:HA	10:CJ:73:ASP:HA	2.00	0.44
17:CQ:66:SER:H	17:CQ:69:LYS:HB3	1.82	0.44
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.99	0.44
2:CB:80:ILE:HD11	2:CB:212:GLN:CA	2.48	0.44
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.70	0.44
33:BI:101:LEU:HD13	33:BI:107:VAL:O	2.16	0.44
26:BA:141:A:C8	26:BA:1408:C:O2'	2.69	0.44
1:CA:551:U:H2'	1:CA:552:U:H6	1.81	0.44
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.98	0.44
25:AY:40:C:H2'	25:AY:41:C:C6	2.52	0.44
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.52	0.44
26:DA:1219:G:H1	26:DA:1230:C:H42	1.64	0.44
26:BA:1268:A:C2	26:BA:2013:A:C4	3.05	0.44
26:DA:2370:G:C6	26:DA:2371:G:C6	3.06	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
44:DX:59:VAL:HB	44:DX:76:ARG:HB2	1.99	0.44
26:BA:2384:G:OP2	47:B0:55:ARG:NH1	2.51	0.44
4:CD:163:GLU:O	4:CD:166:LYS:N	2.44	0.44
27:BB:4:C:H2'	27:BB:5:C:C6	2.52	0.44
26:BA:1184:G:H5'	50:B3:29:ARG:NH1	2.32	0.44
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.44
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.47	0.44
29:DE:181:LEU:HD12	29:DE:181:LEU:HA	1.84	0.44
3:AC:27:LYS:NZ	3:AC:27:LYS:HA	2.32	0.44
26:BA:311:A:C6	26:BA:328:U:C4	3.06	0.44
1:CA:142:G:H2'	1:CA:143:A:O4'	2.16	0.44
26:DA:2156:G:O5'	26:DA:2156:G:H8	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
26:DA:1153:C:H5''	41:DU:62:ILE:HD13	2.00	0.44
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.47	0.44
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.44
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.17	0.44
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.50	0.44
2:AB:21:ARG:CD	2:AB:21:ARG:H	2.30	0.44
26:DA:2892:A:N6	26:DA:2893:G:O6	2.51	0.44
3:CC:33:LEU:HD12	3:CC:36:ASP:HB3	1.99	0.44
3:AC:12:LEU:O	14:AN:57:ARG:NH2	2.50	0.44
26:DA:900:A:HO2'	26:DA:901:A:P	2.40	0.44
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	1.99	0.44
1:CA:537:G:H2'	1:CA:538:G:C8	2.53	0.44
2:CB:74:LYS:HB3	2:CB:169:LYS:HE2	1.98	0.44
1:AA:162:A:O5'	1:AA:162:A:H8	2.01	0.44
33:BI:27:ARG:HD2	48:B1:71:TYR:CZ	2.51	0.44
26:DA:250:G:C6	26:DA:251:A:C6	3.05	0.44
26:BA:2052:G:H4'	29:BE:143:ASN:O	2.17	0.44
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.69	0.44
26:BA:848:G:O6	26:BA:928:G:H2'	2.17	0.44
4:AD:177:ASP:HB3	4:AD:182:LYS:HG2	2.00	0.44
26:DA:1894:C:H2'	26:DA:1895:C:C6	2.53	0.44
26:DA:1472:A:N6	26:DA:1519:G:H1'	2.32	0.44
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.99	0.44
37:DQ:35:VAL:HG12	37:DQ:130:LYS:O	2.18	0.44
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.53	0.44
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.48	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.16	0.44
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	2.00	0.44
26:BA:1001:A:H2'	26:BA:1002:G:O4'	2.18	0.44
1:CA:938:A:C6	1:CA:939:G:C5	3.06	0.44
1:CA:1441:G:O5'	1:CA:1441:G:H8	2.00	0.44
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.53	0.44
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.82	0.44
26:BA:1178:C:H2'	26:BA:1179:C:H6	1.82	0.44
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.46	0.44
12:CL:24:VAL:HG12	12:CL:24:VAL:O	2.17	0.44
26:BA:910:A:N1	26:BA:2277:G:H1'	2.32	0.44
1:AA:92:C:H2'	1:AA:93:G:H8	1.80	0.44
26:BA:2115:G:C2	26:BA:2117:A:N7	2.86	0.44
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:3:C:H2'	27:DB:4:C:H6	1.83	0.44
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.29	0.44
23:AW:56:C:OP1	26:BA:897:C:H5'	2.18	0.44
26:BA:1153:C:OP1	41:BU:92:ARG:NH1	2.50	0.44
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.51	0.44
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.33	0.44
23:CW:39:PSU:H2'	23:CW:40:C:H6	1.83	0.44
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.36	0.44
1:CA:1508:G:H2'	1:CA:1509:C:C6	2.52	0.44
4:CD:161:ASN:HD22	4:CD:161:ASN:N	2.16	0.44
1:CA:826:C:H2'	1:CA:827:U:C6	2.53	0.44
1:AA:636:U:H2'	1:AA:637:G:H8	1.83	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.91	0.44
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.52	0.44
26:BA:2303:G:O2'	31:BG:132:ASN:ND2	2.44	0.44
26:DA:556:G:H2'	26:DA:557:U:C6	2.52	0.44
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.53	0.44
31:DG:128:ARG:HE	31:DG:128:ARG:HB2	1.67	0.44
26:BA:2093:G:C6	26:BA:2225:A:C8	3.06	0.44
1:CA:37:U:O2'	1:CA:500:G:H4'	2.17	0.44
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	2.00	0.44
27:DB:46:A:H2'	27:DB:47:C:C6	2.52	0.44
26:DA:2144:U:O3'	26:DA:2145:C:H2'	2.17	0.44
7:AG:46:ALA:O	7:AG:50:ILE:HG23	2.18	0.44
26:DA:828:U:H4'	26:DA:831:G:N1	2.32	0.44
33:BI:79:ILE:HB	33:BI:144:VAL:HG12	2.00	0.44
1:CA:1134:G:C2'	1:CA:1135:U:H5'	2.48	0.44
1:AA:346:G:N3	1:AA:347:G:H1'	2.33	0.44
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.32	0.44
30:DF:39:TRP:HB3	30:DF:101:LEU:HD22	2.00	0.44
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	1.99	0.44
23:CW:14:A:N6	23:CW:21:A:H2	2.15	0.44
1:AA:952:U:H2'	1:AA:953:G:H8	1.80	0.44
1:CA:684:A:O2'	11:CK:39:PRO:O	2.34	0.44
46:BZ:155:LEU:HD12	46:BZ:156:LYS:H	1.81	0.44
23:AW:22:G:H2'	23:AW:23:A:C8	2.53	0.44
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.99	0.44
26:DA:1016:G:H2'	26:DA:1017:G:O4'	2.18	0.44
26:DA:656:G:H2'	26:DA:657:U:O4'	2.18	0.44
23:CW:38:A:H2'	23:CW:39:PSU:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B2:30:ARG:O	49:B2:34:GLU:HG3	2.17	0.44
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.18	0.44
23:CW:76:31M:H4'	26:DA:2506:U:O2'	2.17	0.44
1:AA:674:G:H2'	1:AA:675:A:H8	1.83	0.44
26:BA:251:A:C5	26:BA:252:G:H1'	2.52	0.44
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.99	0.44
1:CA:1170:A:H2'	1:CA:1171:G:O4'	2.17	0.44
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.33	0.44
6:CF:69:GLU:H	6:CF:69:GLU:CD	2.17	0.44
1:AA:630:G:H2'	1:AA:631:G:H8	1.83	0.44
1:CA:79:G:N2	1:CA:80:G:C4	2.86	0.44
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.99	0.44
26:DA:582:G:H2'	26:DA:583:G:C8	2.53	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
1:AA:1326:C:OP1	21:AU:12:LYS:NZ	2.50	0.44
1:CA:576:G:O6	1:CA:880:C:O2'	2.30	0.44
13:CM:40:ASN:ND2	13:CM:41:PRO:HD2	2.33	0.44
28:DD:164:GLN:NE2	28:DD:166:GLN:OE1	2.46	0.44
50:D3:18:ASP:OD1	50:D3:18:ASP:N	2.44	0.44
3:AC:140:ARG:HB2	3:AC:140:ARG:HE	1.51	0.44
1:CA:696:A:H8	1:CA:696:A:O5'	2.01	0.44
26:BA:530:G:N3	26:BA:530:G:O4'	2.50	0.44
39:BS:58:LEU:HD23	39:BS:58:LEU:HA	1.70	0.44
1:AA:434:U:H2'	1:AA:435:C:C6	2.52	0.44
54:B7:11:LYS:HE3	54:B7:15:THR:OG1	2.18	0.44
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.99	0.44
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.18	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
25:CY:65:G:H2'	25:CY:66:U:C6	2.53	0.44
1:CA:1040:U:C4	1:CA:1041:A:C8	3.05	0.44
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.15	0.44
23:AW:51:U:H2'	23:AW:52:G:C8	2.53	0.44
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.60	0.44
26:DA:330:A:H2	26:DA:1210:A:H2'	1.83	0.44
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.50	0.44
1:AA:68:G:C2	1:AA:69:G:H1'	2.53	0.44
34:DN:15:LEU:HD12	34:DN:137:LYS:HG2	1.99	0.44
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.83	0.44
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.53	0.44
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.99	0.44
26:BA:2030:A:H4'	26:BA:2031:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:4:TYR:CZ	9:CI:88:TYR:HD2	2.36	0.44
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.00	0.44
1:AA:299:G:H2'	1:AA:300:A:C8	2.53	0.44
28:DD:13:ARG:HD2	28:DD:13:ARG:HA	1.71	0.44
4:CD:47:ARG:NH1	4:CD:49:ARG:HH21	2.16	0.44
26:DA:1288:U:C2	26:DA:1327:C:O2	2.71	0.44
26:DA:888:C:H5''	26:DA:889:C:OP2	2.18	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.50	0.44
1:AA:731:G:H5'	1:AA:766:A:H4'	2.00	0.44
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.21	0.44
26:BA:2059:A:OP2	61:BA:4337:HOH:O	2.21	0.44
20:AT:72:LEU:HD23	20:AT:72:LEU:HA	1.84	0.44
15:AO:54:ARG:O	15:AO:58:MET:HG3	2.18	0.44
29:BE:73:GLU:H	29:BE:73:GLU:HG3	1.63	0.44
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.82	0.44
50:D3:23:LEU:O	50:D3:27:GLY:N	2.50	0.44
26:BA:875:G:H2'	26:BA:876:C:O4'	2.17	0.44
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.99	0.44
1:AA:184:G:H2'	1:AA:185:A:H8	1.81	0.44
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.17	0.44
1:CA:35:G:H2'	1:CA:36:C:C6	2.53	0.44
25:CY:30:G:C2	25:CY:31:A:C8	3.06	0.44
26:DA:1301:A:H2	26:DA:1626:G:N3	2.14	0.44
8:CH:39:LEU:HA	8:CH:39:LEU:HD13	1.74	0.44
26:DA:2615:U:OP1	61:DA:4004:HOH:O	2.21	0.44
11:AK:33:THR:HA	11:AK:39:PRO:HA	2.00	0.44
26:DA:2070:G:H2'	26:DA:2071:A:H8	1.83	0.44
29:BE:143:ASN:HD22	29:BE:147:PRO:CD	2.31	0.44
2:CB:192:SER:O	2:CB:194:PRO:HD3	2.17	0.44
26:DA:26:G:C6	26:DA:27:G:N1	2.86	0.44
28:BD:83:GLU:OE1	28:BD:104:TYR:OH	2.28	0.44
26:DA:1032:A:H4'	56:D9:16:VAL:HG11	2.00	0.44
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.83	0.44
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	2.00	0.44
32:BH:3:ARG:HH12	32:BH:65:HIS:HB3	1.83	0.44
26:BA:876:C:H2'	26:BA:877:U:O4'	2.18	0.44
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	2.00	0.44
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.53	0.44
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.33	0.44
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:265:A:C8	26:DA:266:G:H1'	2.53	0.44
39:DS:35:ILE:HD11	39:DS:101:LEU:HD12	1.99	0.44
26:BA:574:C:N3	29:BE:145:LYS:NZ	2.63	0.44
1:AA:958:A:C6	1:AA:959:A:N1	2.86	0.44
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.52	0.44
31:DG:111:LEU:HB3	31:DG:117:PHE:CE2	2.53	0.44
1:CA:292:G:N7	1:CA:293:G:H1'	2.33	0.44
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.18	0.44
26:DA:927:G:H2'	26:DA:928:G:O4'	2.17	0.44
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.18	0.44
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.17	0.44
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.99	0.44
2:AB:16:HIS:HD2	2:AB:17:PHE:H	1.56	0.43
26:DA:2164:C:H5	26:DA:2165:G:N3	2.16	0.43
41:DU:76:TYR:HH	41:DU:92:ARG:HH11	1.63	0.43
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.06	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
1:CA:1118:C:N1	1:CA:1119:C:H5	2.16	0.43
1:CA:1136:U:H5''	1:CA:1137:C:C5	2.53	0.43
25:CY:37:MIA:H3'	25:CY:38:A:H8	1.82	0.43
37:DQ:139:GLU:HG2	46:DZ:122:ARG:HG3	2.00	0.43
37:DQ:27:VAL:O	37:DQ:29:PHE:N	2.51	0.43
37:DQ:29:PHE:O	46:DZ:122:ARG:NH2	2.51	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.71	0.43
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.51	0.43
26:DA:2732:G:OP1	29:DE:203:LYS:NZ	2.43	0.43
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.52	0.43
2:CB:7:VAL:HG12	2:CB:8:LYS:HG2	2.00	0.43
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.53	0.43
39:BS:3:ARG:HE	39:BS:4:LEU:H	1.66	0.43
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.18	0.43
26:DA:2347:C:H2'	26:DA:2348:U:C6	2.53	0.43
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.18	0.43
1:CA:1423:G:H2'	1:CA:1424:C:C6	2.53	0.43
26:DA:2742:C:OP1	56:D9:35:ARG:HD3	2.18	0.43
13:CM:72:ALA:O	13:CM:76:ALA:N	2.42	0.43
9:AI:22:GLY:N	9:AI:58:HIS:O	2.39	0.43
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.99	0.43
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	2.00	0.43
26:BA:1826:G:H2'	26:BA:1827:C:O4'	2.17	0.43
26:DA:668:G:H5'	26:DA:669:G:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2685:G:H5'	35:BO:68:GLU:OE1	2.18	0.43
1:AA:858:G:O6	1:AA:869:G:H3'	2.18	0.43
1:AA:401:C:H2'	1:AA:402:G:C8	2.53	0.43
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.18	0.43
30:BF:140:LEU:HD21	30:BF:170:LEU:HD11	2.00	0.43
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.99	0.43
26:BA:970:C:H2'	26:BA:971:C:C6	2.53	0.43
45:DY:10:GLY:O	45:DY:26:LYS:HD3	2.18	0.43
33:DI:88:ILE:HD11	33:DI:144:VAL:HG11	2.00	0.43
26:BA:1440:G:H2'	26:BA:1441:G:O4'	2.18	0.43
2:CB:20:GLU:HG3	2:CB:191:ASP:HB3	1.99	0.43
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.43
1:CA:1152:A:C6	1:CA:1153:C:C4	3.06	0.43
25:AY:57:G:C2	25:AY:58:A:H5'	2.53	0.43
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.43
26:BA:1358:G:N2	26:BA:1372:U:C5	2.86	0.43
3:CC:18:TRP:CE3	3:CC:18:TRP:N	2.85	0.43
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.18	0.43
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.18	0.43
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	2.00	0.43
26:DA:288:C:H2'	26:DA:289:A:H8	1.82	0.43
26:DA:910:A:N1	26:DA:2277:G:H1'	2.32	0.43
26:BA:2447:G:N2	26:BA:2450:A:OP2	2.51	0.43
46:BZ:150:LEU:HA	46:BZ:150:LEU:HD12	1.78	0.43
26:DA:903:C:H2'	26:DA:904:C:H6	1.81	0.43
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.82	0.43
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.80	0.43
7:CG:26:PHE:CD2	7:CG:62:PHE:HE1	2.36	0.43
51:D4:26:SER:OG	51:D4:27:THR:N	2.51	0.43
37:DQ:68:ILE:HD13	37:DQ:103:MET:HG2	2.00	0.43
26:BA:363(A):A:H2'	26:BA:363(B):G:C8	2.53	0.43
26:BA:127:A:H5''	26:BA:128:C:C6	2.53	0.43
26:DA:817:C:OP2	61:DA:4676:HOH:O	2.21	0.43
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.99	0.43
41:BU:117:GLN:H	41:BU:117:GLN:HG2	1.42	0.43
26:DA:601:C:O2	26:DA:605:C:H4'	2.18	0.43
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.18	0.43
1:AA:646:U:H2'	1:AA:647:C:C6	2.53	0.43
38:DR:21:TYR:CZ	38:DR:43:GLU:HG2	2.52	0.43
26:BA:94:C:H2'	26:BA:94(A):G:O4'	2.19	0.43
9:CI:108:VAL:HG12	9:CI:109:VAL:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BO:78:ARG:NH2	40:BT:73:GLU:OE2	2.49	0.43
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.53	0.43
1:CA:1115:C:H2'	1:CA:1116:C:C6	2.53	0.43
1:CA:766:A:OP2	61:CA:4021:HOH:O	2.21	0.43
46:DZ:154:ASP:OD1	46:DZ:154:ASP:N	2.39	0.43
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.00	0.43
26:BA:2320:A:H2'	26:BA:2320:A:N3	2.34	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.33	0.43
1:CA:1002:G:N2	1:CA:1039:C:C4	2.86	0.43
3:AC:52:LEU:HD11	3:AC:55:VAL:CG2	2.48	0.43
1:CA:757:U:O2'	1:CA:879:C:O2	2.31	0.43
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.18	0.43
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.18	0.43
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.45	0.43
26:BA:1970:A:H4'	26:BA:1971:A:OP1	2.18	0.43
26:BA:1594:G:H2'	26:BA:1595:G:O4'	2.18	0.43
14:AN:24:CYS:HB2	14:AN:33:VAL:HG12	2.01	0.43
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.43
30:BF:33:LEU:HD13	30:BF:112:MET:HE2	2.00	0.43
51:D4:56:VAL:HG13	51:D4:57:GLU:H	1.83	0.43
26:DA:324:A:H2'	26:DA:325:G:O4'	2.19	0.43
9:AI:61:ALA:HB1	9:AI:63:ILE:HD11	2.01	0.43
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.19	0.43
26:DA:623:G:H2'	26:DA:624:C:C6	2.54	0.43
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	2.00	0.43
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.53	0.43
6:CF:94:GLN:NE2	18:CR:72:ARG:HH12	2.16	0.43
16:CP:60:LEU:HA	16:CP:60:LEU:HD13	1.84	0.43
26:BA:2406:U:H2'	26:BA:2406:U:OP2	2.19	0.43
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.44	0.43
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	2.00	0.43
35:DO:25:LEU:HD12	35:DO:38:VAL:HG12	1.99	0.43
1:AA:335:C:H2'	1:AA:336:C:C6	2.54	0.43
20:CT:90:GLN:O	20:CT:93:GLU:HB3	2.18	0.43
20:AT:92:LEU:HA	20:AT:92:LEU:HD23	1.84	0.43
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	2.00	0.43
1:CA:1399:C:C2	1:CA:1502:A:N6	2.87	0.43
23:AW:76:31M:HE1	26:BA:2451:A:C6	2.53	0.43
26:BA:886:C:OP1	26:BA:886:C:H4'	2.17	0.43
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DF:33:LEU:HB3	36:DP:6:LEU:HD21	2.01	0.43
26:DA:2820:A:C5	38:DR:4:LEU:HD11	2.53	0.43
26:BA:2168:G:H5'	26:BA:2169:A:H5''	2.00	0.43
3:CC:34:LEU:HG	3:CC:38:ARG:NH1	2.31	0.43
14:CN:37:PHE:HZ	14:CN:56:VAL:HG21	1.83	0.43
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.18	0.43
1:AA:1302:U:H5	13:AM:17:VAL:HG21	1.83	0.43
26:DA:2410:G:H2'	26:DA:2411:A:O4'	2.19	0.43
26:BA:590:A:H2'	26:BA:591:C:O4'	2.18	0.43
26:BA:2543:G:H2'	26:BA:2544:G:C8	2.53	0.43
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.54	0.43
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.53	0.43
26:DA:813:U:HO2'	26:DA:1225:G:HO2'	1.67	0.43
1:AA:374:A:C6	1:AA:375:U:C4	3.05	0.43
26:DA:1881:C:H2'	26:DA:1882:C:O4'	2.19	0.43
34:DN:57:ALA:HB1	34:DN:96:GLU:HA	2.01	0.43
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.48	0.43
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.19	0.43
51:D4:68:ARG:O	51:D4:69:LYS:HB3	2.18	0.43
26:DA:627:A:H4'	26:DA:628:G:H5'	2.00	0.43
26:DA:540:C:H2'	26:DA:541:C:C6	2.53	0.43
45:DY:89:PHE:CE2	45:DY:95:LYS:HB2	2.53	0.43
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.53	0.43
1:AA:814:A:H2'	1:AA:816:A:H5''	1.99	0.43
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.17	0.43
26:DA:2134:A:C2	26:DA:2159:G:H4'	2.53	0.43
26:DA:2134:A:H3'	26:DA:2135:A:C8	2.53	0.43
26:BA:1171:G:H3'	26:BA:1173:G:H5'	2.01	0.43
26:BA:1177:A:H2'	26:BA:1177:A:N3	2.33	0.43
27:DB:28:C:OP2	39:DS:33:LYS:NZ	2.32	0.43
25:CY:4:C:H2'	25:CY:5:G:H5'	2.00	0.43
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.52	0.43
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.51	0.43
31:DG:45:GLU:H	31:DG:45:GLU:HG2	1.43	0.43
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.54	0.43
23:AW:56:C:H5'	26:BA:896:A:H1'	2.00	0.43
1:CA:722:A:N6	1:CA:724:G:C2	2.87	0.43
45:DY:43:ASN:OD1	45:DY:65:ALA:HB3	2.19	0.43
5:AE:105:VAL:O	5:AE:109:ILE:HD12	2.19	0.43
1:AA:262:A:H4'	20:AT:75:ASN:HB2	2.00	0.43
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	2.01	0.43
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.53	0.43
26:DA:2516:G:C6	26:DA:2517:C:N4	2.86	0.43
33:BI:81:VAL:O	33:BI:146:ALA:HA	2.19	0.43
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.00	0.43
26:BA:1918:A:O2'	26:BA:1920:C:N4	2.51	0.43
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.82	0.43
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.00	0.43
32:DH:98:LEU:HD12	32:DH:102:ALA:O	2.18	0.43
16:CP:55:ARG:HD2	16:CP:55:ARG:HA	1.88	0.43
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	2.01	0.43
26:BA:1431:U:H2'	26:BA:1432:C:C6	2.54	0.43
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	2.01	0.43
25:AY:71:G:H4'	26:BA:1851:U:H4'	2.00	0.43
9:CI:43:ALA:HB2	9:CI:74:ILE:CD1	2.49	0.43
1:CA:750:G:N2	15:CO:23:GLY:O	2.48	0.43
1:CA:1009:G:N2	1:CA:1010:G:H1'	2.33	0.43
26:BA:2791:C:H5'	26:BA:2893:G:N2	2.34	0.43
51:B4:59:PHE:C	51:B4:61:ARG:H	2.21	0.43
25:AY:33:U:H2'	25:AY:34:G:H5''	2.00	0.43
40:BT:118:ARG:HD2	40:BT:118:ARG:HA	1.61	0.43
1:CA:693:G:H2'	1:CA:694:A:C8	2.53	0.43
26:BA:1720:U:H2'	26:BA:1721:G:O4'	2.18	0.43
24:CX:15:G:H2'	24:CX:59:A:N1	2.34	0.43
23:CW:76:31M:HAM	24:CX:76:A:O3'	2.19	0.43
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.55	0.43
1:CA:1030(A):G:C2	1:CA:1030(C):G:H8	2.36	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.84	0.43
26:BA:2183:C:O2'	26:BA:2184:G:OP1	2.35	0.43
26:DA:782:A:H5'	26:DA:783:A:N7	2.34	0.43
34:BN:67:LEU:HA	34:BN:67:LEU:HD12	1.80	0.43
19:AS:52:TYR:HA	19:AS:56:GLN:O	2.18	0.43
26:BA:2591:C:H2'	26:BA:2592:G:C8	2.54	0.43
28:DD:142:VAL:HG13	28:DD:191:ALA:HB1	2.00	0.43
13:AM:120:LYS:HE3	23:AW:40:C:O2'	2.19	0.43
26:DA:69:C:N4	61:DA:4335:HOH:O	2.52	0.43
14:CN:47:LEU:O	14:CN:51:GLY:N	2.51	0.43
26:BA:1258:C:H2'	26:BA:1259:G:O4'	2.19	0.43
46:DZ:153:SER:HB3	46:DZ:167:PRO:HA	2.00	0.43
28:BD:137:PRO:O	28:BD:140:THR:HG23	2.18	0.43
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:8:4SU:C2	25:CY:14:A:H62	2.30	0.43
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	2.01	0.43
1:CA:1011:G:C2	1:CA:1012:U:H1'	2.54	0.43
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.54	0.43
1:AA:90:U:O2'	1:AA:91:C:H5'	2.19	0.43
26:BA:1045:A:H1'	26:BA:1047:G:C2	2.53	0.43
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.18	0.43
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	2.01	0.43
26:DA:2805:G:C6	26:DA:2807:G:C6	3.07	0.43
13:CM:50:GLU:HA	13:CM:53:VAL:HB	2.01	0.43
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	2.01	0.43
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.48	0.43
30:DF:18:ARG:HG2	30:DF:19:GLU:H	1.84	0.43
26:BA:2292:C:H2'	26:BA:2293:C:H6	1.83	0.43
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.19	0.43
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.54	0.43
1:AA:1198:G:H2'	1:AA:1199:U:C6	2.54	0.43
2:AB:36:ARG:C	2:AB:38:GLY:H	2.21	0.43
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.00	0.43
43:BW:19:LEU:HB3	52:B5:25:LEU:HD11	2.01	0.43
26:DA:991:C:OP2	26:DA:1186:G:H5'	2.18	0.43
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	2.00	0.43
32:DH:59:ARG:O	32:DH:63:SER:OG	2.36	0.43
48:B1:50:ARG:HG2	48:B1:59:THR:HB	2.00	0.43
26:BA:2706:G:N7	61:BA:4733:HOH:O	2.37	0.43
1:CA:1110:A:OP2	61:CA:4091:HOH:O	2.21	0.43
2:AB:200:ILE:HD13	2:AB:200:ILE:H	1.84	0.43
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.51	0.43
33:DI:73:GLU:HG3	33:DI:139:GLN:O	2.18	0.43
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.19	0.43
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.99	0.43
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.43
7:CG:78:ARG:CZ	7:CG:79:ARG:HH12	2.32	0.43
26:BA:11:G:C2'	26:BA:12:U:H5''	2.45	0.43
12:AL:24:VAL:O	12:AL:24:VAL:HG12	2.18	0.43
4:AD:64:LEU:HB2	4:AD:198:VAL:HG21	2.00	0.43
1:CA:1320:C:C1'	19:CS:73:GLU:HG3	2.49	0.43
23:CW:61:C:O2'	23:CW:62:C:H6	2.02	0.43
31:DG:37:VAL:O	31:DG:94:LEU:N	2.50	0.43
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.43
26:BA:197:A:N6	26:BA:2430:A:O2'	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.54	0.43
1:AA:452:A:HO2'	1:AA:453:A:H8	1.65	0.43
26:DA:644:A:H5''	26:DA:645:C:OP1	2.19	0.43
1:CA:165:C:H2'	1:CA:166:G:C8	2.54	0.43
1:CA:302:G:N3	1:CA:556:C:H4'	2.33	0.43
4:CD:38:TYR:CZ	4:CD:45:GLN:HG2	2.54	0.43
26:BA:848:G:N9	26:BA:933:A:H8	2.17	0.43
26:DA:974:G:C4	26:DA:989:G:C2	3.07	0.43
49:D2:53:LEU:HA	49:D2:53:LEU:HD23	1.89	0.43
26:DA:1487:G:H2'	26:DA:1488:G:O4'	2.18	0.43
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.48	0.43
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	2.00	0.43
26:DA:265:A:H1'	26:DA:266:G:O4'	2.19	0.43
20:CT:86:ARG:O	20:CT:90:GLN:HB2	2.19	0.43
5:AE:148:VAL:O	5:AE:152:ARG:HG3	2.18	0.43
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	2.01	0.43
49:B2:16:LEU:HB3	49:B2:20:GLU:HB2	1.99	0.43
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.83	0.43
36:DP:101:VAL:HA	36:DP:106:LEU:O	2.18	0.43
26:BA:2233:U:H2'	26:BA:2234:G:C8	2.54	0.43
26:DA:2494:G:C4	26:DA:2495:G:C8	3.07	0.43
26:DA:1656:C:H2'	26:DA:1657:C:H6	1.84	0.43
31:DG:164:GLU:OE2	31:DG:164:GLU:N	2.51	0.43
26:BA:2790:A:N3	26:BA:2790:A:H2'	2.34	0.43
2:CB:84:GLU:OE1	2:CB:216:SER:HA	2.18	0.43
1:AA:1151:A:O4'	10:AJ:39:PRO:HB2	2.19	0.43
25:AY:49:C:N4	25:AY:65:G:N1	2.28	0.43
26:BA:1175:U:O3'	26:BA:1176:G:H4'	2.17	0.43
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.19	0.43
46:DZ:156:LYS:HE3	46:DZ:158:PRO:HD3	2.01	0.43
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.84	0.43
26:BA:1372:U:H2'	26:BA:1373:A:O4'	2.18	0.43
3:AC:6:HIS:HD2	3:AC:8:ILE:N	2.11	0.43
31:DG:43:LEU:C	31:DG:45:GLU:H	2.22	0.43
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.47	0.43
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.83	0.43
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.50	0.43
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.33	0.43
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.52	0.43
26:DA:224:G:N7	26:DA:420:C:H4'	2.33	0.43
26:BA:2181:G:O2'	26:BA:2182:G:OP1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DI:14:ASP:OD1	33:DI:15:VAL:HG12	2.19	0.43
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.19	0.43
2:AB:88:ALA:O	2:AB:226:ARG:NH1	2.51	0.43
26:BA:288:C:H2'	26:BA:289:A:C8	2.53	0.43
1:CA:607:A:C2	16:CP:31:LYS:HG3	2.54	0.43
1:AA:402:G:C6	1:AA:403:C:C4	3.07	0.43
26:DA:2228:G:C5	26:DA:2229:C:C4	3.07	0.43
24:CX:54:5MU:O5'	24:CX:54:5MU:H6	2.02	0.43
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.19	0.43
52:D5:48:GLU:O	52:D5:60:VAL:HG11	2.18	0.43
35:BO:104:ARG:NH1	40:BT:34:VAL:HG21	2.34	0.43
32:BH:121:ILE:HG13	32:BH:144:VAL:HG21	2.01	0.43
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.83	0.43
1:CA:1289:A:H2	1:CA:1372:U:O4'	2.01	0.43
26:DA:380:U:H2'	26:DA:381:G:H8	1.83	0.43
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.54	0.43
1:CA:397:A:N3	1:CA:397:A:H3'	2.34	0.43
26:DA:208:C:H2'	26:DA:209:C:C6	2.54	0.43
26:BA:2653:U:H2'	26:BA:2654:A:C8	2.53	0.43
25:AY:6:G:H2'	25:AY:7:A:H5'	2.01	0.43
1:CA:92:C:H2'	1:CA:93:G:O4'	2.19	0.43
42:DV:55:ALA:HA	42:DV:100:ARG:O	2.19	0.43
28:BD:206:LEU:HD22	28:BD:211:ARG:HG2	2.00	0.43
4:AD:63:LYS:HG3	4:AD:64:LEU:N	2.33	0.43
25:CY:34:G:C6	25:CY:35:A:C6	3.07	0.43
26:DA:816:C:O2'	26:DA:932:G:O6	2.37	0.43
26:DA:855:G:C6	26:DA:856:C:N4	2.86	0.43
26:BA:657:U:H2'	26:BA:658:C:C6	2.53	0.43
26:BA:881:G:N3	26:BA:881:G:H2'	2.34	0.43
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.52	0.43
26:BA:892:G:C5	26:BA:893:C:C4	3.07	0.43
31:BG:77:ILE:HD12	31:BG:82:LEU:HD12	2.00	0.43
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.18	0.43
26:DA:140:G:H22	26:DA:1596:A:H4'	1.83	0.43
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.19	0.43
1:AA:584:G:H2'	1:AA:585:G:C8	2.54	0.43
1:AA:130:A:N3	1:AA:263:A:O2'	2.38	0.43
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.54	0.43
26:BA:1380:G:OP2	61:BA:5152:HOH:O	2.22	0.43
26:BA:2292:C:P	39:BS:17:ARG:HH12	2.41	0.43
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:337:C:H2'	1:CA:338:A:C8	2.53	0.43
26:BA:882:G:N2	26:BA:895:U:O2	2.52	0.43
31:DG:44:GLY:N	31:DG:88:ILE:O	2.52	0.43
26:BA:1826:G:H4'	28:BD:242:ARG:CZ	2.49	0.43
26:BA:1664:A:H1'	26:BA:2685:G:O2'	2.19	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
26:BA:224:G:H2'	26:BA:225:A:O4'	2.18	0.43
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.54	0.43
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.19	0.43
1:AA:943:U:H2'	1:AA:944:G:H5'	2.00	0.43
36:BP:96:THR:OG1	36:BP:99:LEU:HG	2.18	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	2.01	0.43
26:DA:2028:U:H2'	26:DA:2029:G:O4'	2.19	0.43
27:BB:110:G:H2'	27:BB:111:G:H8	1.84	0.43
27:DB:114:C:H4'	39:DS:46:VAL:HG22	2.01	0.43
7:CG:33:ASP:OD1	7:CG:33:ASP:N	2.51	0.43
44:BX:66:LEU:HD23	44:BX:66:LEU:HA	1.73	0.43
1:AA:1342:C:H4'	9:AI:125:TYR:HB3	2.01	0.43
26:DA:1668:A:O2'	26:DA:1674:G:N7	2.43	0.43
48:D1:50:ARG:HD2	48:D1:57:GLU:OE1	2.19	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.19	0.43
10:CJ:90:LEU:HA	10:CJ:91:PRO:HD3	1.83	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.87	0.43
26:BA:340:A:H2'	26:BA:341:G:O4'	2.19	0.43
26:DA:2137:C:O2'	26:DA:2138:C:H5'	2.19	0.42
26:DA:827:U:H4'	26:DA:828:U:C6	2.53	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.22	0.42
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.00	0.42
26:BA:2173:A:H2'	26:BA:2174:C:O4'	2.18	0.42
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.26	0.42
1:AA:96:U:OP2	1:AA:96:U:H6	2.02	0.42
2:AB:21:ARG:HB3	2:AB:39:ILE:HA	2.00	0.42
24:CX:8:4SU:H5''	24:CX:49:G:H5'	2.01	0.42
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.53	0.42
37:DQ:31:ASP:HA	37:DQ:134:ARG:HH11	1.83	0.42
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.51	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.33	0.42
1:CA:1286:A:H3'	1:CA:1286:A:C8	2.54	0.42
26:DA:140:G:H1'	26:DA:141:A:H2	1.84	0.42
1:AA:839:U:H3'	1:AA:840:C:C5	2.53	0.42
3:AC:104:GLN:HE21	3:AC:105:GLU:H	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:19:G:H3'	24:AX:20:U:H6	1.84	0.42
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.84	0.42
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.84	0.42
24:CX:21:A:N6	24:CX:46:G:H2'	2.34	0.42
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.54	0.42
1:CA:130:A:N3	1:CA:263:A:O2'	2.49	0.42
1:CA:532:A:N6	3:CC:156:ARG:HH22	2.16	0.42
26:DA:325:G:H2'	26:DA:326:G:O4'	2.20	0.42
26:DA:414:C:O2'	26:DA:415:A:H5'	2.19	0.42
26:BA:614(C):A:C4	30:BF:180:GLY:HA2	2.54	0.42
28:BD:145:VAL:HG12	28:BD:146:GLU:O	2.18	0.42
13:AM:19:LEU:HB3	13:AM:25:ILE:HG21	2.01	0.42
17:AQ:62:SER:OG	17:AQ:72:ARG:HD2	2.19	0.42
2:AB:28:PHE:CD1	2:AB:190:THR:HG22	2.54	0.42
26:DA:1161:C:H2'	26:DA:1162:G:C8	2.53	0.42
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.19	0.42
26:DA:2865:U:C4	26:DA:2866:U:C4	3.07	0.42
28:DD:36:PRO:HA	28:DD:61:LEU:HD13	2.01	0.42
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.84	0.42
33:DI:94:ALA:O	33:DI:98:ALA:N	2.44	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.18	0.42
26:BA:2561:A:H2'	26:BA:2562:U:O4'	2.18	0.42
24:AX:7:G:O2'	24:AX:49:G:H5'	2.19	0.42
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.33	0.42
1:AA:346:G:H2'	1:AA:347:G:H4'	2.01	0.42
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.84	0.42
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.41	0.42
26:BA:528:A:C2	26:BA:2043:C:H4'	2.53	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.19	0.42
3:CC:6:HIS:HD2	3:CC:8:ILE:N	2.14	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
40:BT:118:ARG:HH11	40:BT:118:ARG:CG	2.30	0.42
1:CA:684:A:H1'	11:CK:39:PRO:HD2	2.01	0.42
26:DA:746:A:H2'	26:DA:2612:C:H5''	2.00	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:N	2.33	0.42
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.84	0.42
26:DA:1471:A:OP2	26:DA:1519:G:N1	2.42	0.42
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	2.01	0.42
26:DA:1235:G:C6	26:DA:1236:G:N1	2.87	0.42
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.53	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.83	0.42
53:D6:40:CYS:HA	53:D6:41:PRO:HD3	1.90	0.42
1:CA:49:U:O4	1:CA:365:U:H5	2.01	0.42
48:B1:8:SER:HB3	48:B1:66:HIS:CD2	2.55	0.42
7:CG:103:TRP:CH2	7:CG:141:VAL:HG21	2.54	0.42
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.54	0.42
51:B4:39:CYS:HA	51:B4:44:THR:HG21	2.01	0.42
26:DA:760:G:H2'	26:DA:761:A:O4'	2.18	0.42
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.54	0.42
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.35	0.42
26:DA:212:G:H2'	26:DA:213:A:O4'	2.18	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.49	0.42
1:CA:1051:C:N4	61:CA:4001:HOH:O	2.51	0.42
26:BA:1991:U:H2'	26:BA:1992:G:H5''	2.00	0.42
1:AA:126:G:H4'	1:AA:634:C:O2	2.19	0.42
26:DA:2345:G:OP2	53:D6:38:LYS:NZ	2.42	0.42
26:DA:2168:G:O3'	26:DA:2169:A:H8	2.02	0.42
25:CY:9:A:C8	25:CY:11:C:N4	2.87	0.42
1:CA:922:G:C6	1:CA:923:A:C6	3.07	0.42
4:CD:13:ARG:HB2	4:CD:40:PRO:HD3	2.01	0.42
46:DZ:138:GLU:H	46:DZ:156:LYS:NZ	2.16	0.42
25:AY:55:PSU:N3	25:AY:57:G:H5'	2.33	0.42
51:B4:59:PHE:N	51:B4:59:PHE:CD1	2.77	0.42
30:DF:33:LEU:HA	30:DF:33:LEU:HD12	1.75	0.42
26:DA:2272:U:H5''	26:DA:2273:A:OP1	2.18	0.42
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	2.00	0.42
46:BZ:136:PHE:O	46:BZ:137:ILE:HG13	2.20	0.42
1:AA:1299:A:H5''	1:AA:1299:A:N3	2.35	0.42
30:BF:24:LEU:HB3	30:BF:115:ALA:HB2	2.02	0.42
20:AT:16:HIS:O	20:AT:19:SER:OG	2.25	0.42
26:DA:1545:A:H2'	26:DA:1546:C:O4'	2.20	0.42
26:BA:226:G:N2	26:BA:228:A:H62	2.15	0.42
26:BA:192:C:OP1	61:BA:4017:HOH:O	2.21	0.42
1:AA:540:G:H2'	1:AA:541:G:O4'	2.19	0.42
26:BA:1797:C:H4'	28:BD:257:LEU:O	2.18	0.42
39:DS:67:ARG:HG3	39:DS:104:GLY:CA	2.49	0.42
23:CW:74:C:C4	23:CW:75:C:C2	3.07	0.42
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	2.01	0.42
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.79	0.42
1:CA:935:A:O2'	1:CA:1383:C:N3	2.44	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.81	0.42
26:DA:2745:C:H2'	26:DA:2746:U:O4'	2.19	0.42
26:DA:699:A:H2'	26:DA:700:G:O4'	2.19	0.42
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.42
1:AA:8:A:H5'	5:AE:101:ILE:HG22	2.00	0.42
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	2.01	0.42
26:DA:1656:C:H2'	26:DA:1657:C:C6	2.54	0.42
24:CX:53:G:H3'	24:CX:54:5MU:H71	2.01	0.42
26:DA:1970:A:H4'	26:DA:1971:A:OP1	2.19	0.42
53:D6:10:LEU:HD23	53:D6:22:ALA:HB2	2.01	0.42
30:BF:89:VAL:HG12	30:BF:90:PHE:CD2	2.55	0.42
19:CS:51:VAL:HB	19:CS:75:ALA:HB2	2.00	0.42
26:BA:644:A:H4'	26:BA:645:C:H5	1.83	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.19	0.42
24:AX:13:C:O2'	26:BA:1924:C:H4'	2.20	0.42
13:AM:39:ILE:HD12	13:AM:52:GLU:HG2	2.00	0.42
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.19	0.42
37:DQ:43:THR:OG1	37:DQ:45:GLN:HG2	2.19	0.42
1:AA:1236:A:O2'	1:AA:1304:G:H4'	2.19	0.42
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.63	0.42
30:BF:9:ILE:HA	30:BF:10:PRO:HD2	1.82	0.42
41:DU:17:ILE:HG13	41:DU:32:PHE:HE1	1.83	0.42
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.53	0.42
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.99	0.42
26:BA:1188:U:H4'	42:BV:79:VAL:HG22	2.01	0.42
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	2.00	0.42
25:CY:50:U:H2'	25:CY:51:U:C6	2.53	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.55	0.42
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.06	0.42
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.19	0.42
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.34	0.42
42:DV:48:GLY:HA2	42:DV:52:VAL:HG12	2.01	0.42
1:CA:924:C:O2'	1:CA:1502:A:N6	2.49	0.42
1:AA:741:G:H2'	1:AA:742:G:O4'	2.19	0.42
26:DA:996:A:C6	26:DA:1160:G:N1	2.87	0.42
25:AY:50:U:H2'	25:AY:51:U:O4'	2.20	0.42
1:CA:1122:U:N3	1:CA:1123:A:N7	2.67	0.42
26:BA:1530:C:H1'	26:BA:1531:C:OP1	2.19	0.42
1:CA:583:A:N6	1:CA:758:G:O2'	2.52	0.42
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.78	0.42
26:BA:2116:G:H2'	26:BA:2117:A:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:D4:33:VAL:HG12	51:D4:34:GLU:N	2.34	0.42
1:CA:1410:G:H2'	1:CA:1411:C:H6	1.84	0.42
26:DA:910:A:C5	37:DQ:13:GLN:HG3	2.55	0.42
23:CW:11:C:N4	23:CW:24:G:H1	2.14	0.42
33:BI:93:THR:H	33:BI:96:ASP:HB2	1.84	0.42
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.85	0.42
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.20	0.42
20:AT:67:ALA:HA	20:AT:72:LEU:O	2.18	0.42
34:BN:130:HIS:O	34:BN:133:GLN:HG2	2.19	0.42
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.84	0.42
4:CD:121:VAL:O	4:CD:134:ASP:HA	2.20	0.42
26:BA:466:A:N3	26:BA:683:C:H1'	2.34	0.42
26:DA:1847:A:H3'	26:DA:1848:A:H5'	2.00	0.42
1:CA:898:G:N2	1:CA:901:A:OP2	2.50	0.42
24:AX:9:G:O2'	24:AX:10:G:N7	2.47	0.42
26:DA:729:G:O2'	26:DA:763:G:H4'	2.19	0.42
27:DB:33:G:N3	27:DB:50:G:N2	2.67	0.42
38:BR:98:LEU:HD12	52:B5:57:VAL:HG11	2.01	0.42
22:AV:15:A:O5'	22:AV:15:A:H8	2.02	0.42
2:CB:160:ASP:N	2:CB:160:ASP:OD1	2.52	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.49	0.42
26:DA:2251:G:OP1	37:DQ:82:ARG:NH1	2.52	0.42
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.84	0.42
26:DA:2171:A:OP1	26:DA:2171:A:H3'	2.19	0.42
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.52	0.42
46:DZ:144:LEU:CD1	46:DZ:172:ALA:HB1	2.47	0.42
30:DF:184:TYR:CZ	30:DF:188:ARG:HD2	2.54	0.42
1:AA:1125:U:H4'	1:AA:1126:U:OP1	2.19	0.42
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.55	0.42
1:AA:109:A:C6	1:AA:326:G:C6	3.07	0.42
1:CA:1297:C:P	13:CM:44:ARG:HH22	2.42	0.42
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.34	0.42
53:B6:11:LEU:HA	53:B6:11:LEU:HD23	1.82	0.42
26:DA:864:G:N2	26:DA:913:U:C2	2.87	0.42
31:BG:121:ASN:HA	31:BG:122:PRO:HD3	1.87	0.42
8:AH:46:LYS:HG3	8:AH:64:LYS:HB2	2.02	0.42
6:CF:68:PRO:HB2	6:CF:71:ARG:HG3	2.01	0.42
26:BA:375:C:H2'	26:BA:376:C:C6	2.54	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.00	0.42
26:DA:352:G:N2	61:DA:3734:HOH:O	2.32	0.42
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.55	0.42
30:DF:139:PHE:CD2	30:DF:167:ALA:HB2	2.55	0.42
26:DA:744:G:OP1	29:DE:132:HIS:ND1	2.47	0.42
39:DS:57:LYS:HE3	39:DS:57:LYS:HB2	1.80	0.42
24:AX:2:G:H2'	24:AX:2:G:N3	2.34	0.42
1:AA:1079:G:O3'	5:AE:14:ARG:NH2	2.52	0.42
28:BD:218:ARG:HB3	28:BD:219:PRO:HD2	2.01	0.42
32:BH:22:GLY:HA2	32:BH:37:VAL:O	2.20	0.42
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.18	0.42
25:AY:52:G:H1	25:AY:62:C:H42	1.67	0.42
25:CY:18:G:C2	25:CY:55:PSU:O4	2.72	0.42
27:DB:28:C:P	39:DS:36:TYR:HH	2.43	0.42
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	2.01	0.42
31:DG:136:ARG:H	31:DG:136:ARG:HH11	1.68	0.42
2:CB:133:LYS:O	2:CB:137:ARG:HG3	2.20	0.42
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.55	0.42
29:DE:72:VAL:HA	29:DE:73:GLU:CB	2.50	0.42
26:DA:1354:A:H5''	28:DD:38:LYS:HD3	2.01	0.42
26:BA:606:U:H4'	26:BA:658:C:H4'	2.00	0.42
13:CM:65:LYS:CA	51:D4:50:VAL:HG11	2.49	0.42
1:CA:1057:G:C5	1:CA:1204:A:C2	3.07	0.42
26:DA:2365:G:O6	55:D8:39:LYS:HE3	2.19	0.42
1:CA:971:G:OP1	1:CA:971:G:H3'	2.19	0.42
31:BG:77:ILE:N	31:BG:82:LEU:O	2.48	0.42
26:BA:2181:G:HO2'	26:BA:2182:G:P	2.42	0.42
26:DA:251:A:C5	26:DA:252:G:H1'	2.55	0.42
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.53	0.42
1:AA:60:A:OP1	1:AA:111:G:N2	2.51	0.42
4:AD:166:LYS:HD3	4:AD:166:LYS:HA	1.79	0.42
1:CA:444:C:H2'	1:CA:445:G:C8	2.55	0.42
26:DA:1488:G:H5'	26:DA:1489:U:OP2	2.20	0.42
1:AA:299:G:H8	1:AA:299:G:O5'	2.02	0.42
26:DA:896:A:N6	46:DZ:146:ILE:HD13	2.34	0.42
27:DB:73:A:C4	27:DB:105:A:C2	3.07	0.42
28:BD:242:ARG:HD3	28:BD:242:ARG:N	2.33	0.42
27:BB:110:G:H2'	27:BB:111:G:C8	2.54	0.42
27:DB:33:G:C6	27:DB:34:U:C4	3.07	0.42
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.18	0.42
28:DD:264:LYS:HA	28:DD:265:PRO:HD3	1.88	0.42
26:DA:608:A:C6	26:DA:609:A:C6	3.08	0.42
26:DA:1151:G:C2	26:DA:1152:C:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:715:A:H5''	1:CA:805:C:H1'	2.02	0.42
30:BF:34:TRP:CH2	36:BP:8:PRO:HB3	2.54	0.42
35:DO:36:GLY:HA2	35:DO:106:LEU:HD23	2.01	0.42
1:CA:1092:A:C6	1:CA:1093:A:C6	3.07	0.42
26:DA:2271:G:OP1	47:D0:18:ALA:HB1	2.19	0.42
33:DI:66:GLU:OE2	33:DI:69:LYS:HD3	2.18	0.42
2:AB:24:TRP:HD1	2:AB:24:TRP:H	1.68	0.42
26:DA:29:U:OP1	41:DU:5:LYS:NZ	2.52	0.42
1:CA:979:C:H2'	1:CA:980:C:H5'	2.01	0.42
1:CA:792:A:H4'	1:CA:793:U:H5''	2.01	0.42
23:CW:25:C:C2'	23:CW:26:A:H5'	2.49	0.42
26:BA:1675:C:O2	29:BE:128:SER:OG	2.37	0.42
46:BZ:110:GLY:CA	46:BZ:145:GLU:HA	2.50	0.42
46:BZ:145:GLU:H	46:BZ:148:ASP:HB2	1.84	0.42
1:CA:1053:G:C4'	1:CA:1054:C:H5'	2.50	0.42
19:CS:27:GLU:HB2	19:CS:28:LYS:HZ3	1.83	0.42
26:DA:868:U:C4	26:DA:869:G:N7	2.88	0.42
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	2.02	0.42
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.52	0.42
26:BA:493:G:H2'	26:BA:494:G:O4'	2.19	0.42
26:DA:698:C:H5''	26:DA:699:A:OP1	2.20	0.42
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.18	0.42
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.18	0.42
40:BT:91:ARG:HD2	40:BT:120:ARG:NH1	2.35	0.42
1:CA:1446:U:H4'	1:CA:1447:A:C5	2.54	0.42
26:DA:937:U:H2'	26:DA:938:G:O4'	2.20	0.42
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	2.01	0.42
26:DA:1167:U:C2	26:DA:1168:G:C8	3.07	0.42
47:B0:38:VAL:HG12	47:B0:40:GLN:HG2	2.01	0.42
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.55	0.42
11:AK:111:ASP:HB2	18:AR:84:LYS:HD3	2.01	0.42
26:BA:118:A:H3'	26:BA:119:A:H5''	2.02	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
1:AA:877:C:OP1	8:AH:88:LYS:NZ	2.33	0.42
1:CA:116:A:H61	1:CA:313:A:H1'	1.84	0.42
1:CA:779:C:H2'	1:CA:780:A:O4'	2.19	0.42
26:BA:1748:G:H5''	26:BA:1748:G:H8	1.85	0.42
28:DD:37:LEU:HD13	28:DD:87:ASN:ND2	2.34	0.42
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.54	0.42
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.45	0.42
25:AY:52:G:H1	25:AY:62:C:N4	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:583:A:H2'	1:CA:584:G:O4'	2.20	0.42
56:D9:7:VAL:HG12	56:D9:34:GLN:HB3	2.01	0.42
2:CB:137:ARG:O	2:CB:141:GLU:N	2.36	0.42
24:AX:32:5MC:HM53	24:AX:33:U:O4	2.20	0.42
26:BA:1714:G:H1	26:BA:1745(A):C:N4	2.13	0.42
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.19	0.42
1:CA:1067:A:H1'	1:CA:1068:G:O4'	2.20	0.42
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.51	0.42
31:BG:77:ILE:HG21	31:BG:80:PHE:CD2	2.55	0.42
15:CO:36:ILE:HG23	15:CO:56:LEU:HD11	2.01	0.42
4:AD:107:ARG:HH22	4:AD:194:LEU:CD2	2.33	0.42
34:DN:40:PRO:HB3	41:DU:68:ALA:HB2	2.01	0.42
26:BA:570:G:H2'	26:BA:2030:A:C5	2.55	0.42
49:B2:32:LEU:HD13	49:B2:36:ARG:HH11	1.85	0.42
29:DE:9:VAL:HB	40:DT:3:ARG:HG2	2.02	0.42
1:AA:1287:A:H2	1:AA:1353:G:N3	2.18	0.42
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	2.00	0.42
1:CA:1072:G:C6	1:CA:1073:U:C4	3.08	0.42
56:B9:27:CYS:SG	56:B9:28:GLU:N	2.93	0.42
46:DZ:24:LEU:HA	46:DZ:25:PRO:HD3	1.90	0.42
1:AA:938:A:C6	1:AA:939:G:C5	3.07	0.42
26:DA:536:A:H2'	26:DA:537:C:C6	2.55	0.42
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.55	0.42
26:DA:2107:C:H2'	26:DA:2108:C:O4'	2.20	0.42
45:DY:45:VAL:N	45:DY:63:LYS:O	2.45	0.42
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.84	0.42
28:DD:145:VAL:HB	28:DD:155:LEU:HB2	2.02	0.42
6:AF:35:ALA:HA	6:AF:67:MET:HB3	2.02	0.42
26:DA:1198:U:H2'	26:DA:1199:U:C6	2.55	0.42
1:CA:685:G:C2	1:CA:686:U:C4	3.08	0.42
51:D4:9:LEU:HA	51:D4:9:LEU:HD23	1.90	0.42
26:BA:1512:U:O2'	26:BA:1513:C:H5'	2.20	0.42
1:CA:1233:G:H2'	1:CA:1234:C:C6	2.55	0.42
26:BA:717:G:H2'	26:BA:718:A:O4'	2.20	0.42
1:AA:1029:C:N3	1:AA:1032:G:O6	2.53	0.42
25:AY:56:C:C2	25:AY:57:G:C8	3.08	0.42
23:CW:29:G:N2	23:CW:42:C:C2	2.88	0.42
1:AA:1182:G:C3'	1:AA:1183:A:H5'	2.50	0.42
26:BA:2111:C:OP2	26:BA:2145:C:N4	2.51	0.42
17:AQ:66:SER:H	17:AQ:69:LYS:HB3	1.85	0.42
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:344:A:H5''	1:CA:345:C:H5	1.84	0.42
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.20	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.80	0.42
1:CA:1357:A:N6	1:CA:1363(A):A:N1	2.67	0.42
1:AA:583:A:N6	1:AA:758:G:O2'	2.53	0.42
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.85	0.42
26:BA:222:A:H3'	26:BA:421:U:H5'	2.00	0.42
1:AA:130:A:O2'	1:AA:131:C:O5'	2.32	0.42
26:BA:1858:G:H21	26:BA:1883:G:H2'	1.84	0.42
33:BI:131:LYS:HA	33:BI:137:PRO:HA	2.02	0.42
3:CC:77:ILE:HG13	3:CC:78:GLY:N	2.35	0.42
26:DA:1470:G:HO2'	26:DA:1471:A:H8	1.63	0.42
28:DD:73:VAL:O	28:DD:75:ILE:HG13	2.19	0.42
40:BT:53:ARG:CZ	40:BT:53:ARG:HB3	2.50	0.42
46:DZ:146:ILE:H	46:DZ:146:ILE:HG13	1.62	0.42
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.85	0.42
29:BE:14:ILE:HG12	29:BE:21:VAL:HG13	2.00	0.42
1:AA:152:A:N6	1:AA:170:U:C2	2.88	0.42
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.55	0.42
26:DA:234:C:H2'	26:DA:235:U:C6	2.54	0.42
26:DA:839:U:H2'	26:DA:840:C:C6	2.55	0.42
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.60	0.42
1:CA:6:G:H4'	1:CA:298:A:H4'	2.00	0.42
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.35	0.42
31:DG:72:ARG:NH1	31:DG:87:PRO:HG3	2.35	0.42
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.84	0.42
34:DN:138:LEU:HA	34:DN:138:LEU:HD23	1.73	0.42
1:CA:1269:A:H2	1:CA:1312:G:N3	2.17	0.42
26:BA:2090:G:O6	61:BA:4756:HOH:O	2.19	0.42
26:BA:2461:C:H2'	26:BA:2462:U:C6	2.55	0.42
1:AA:108:G:O6	20:AT:15:ARG:HD2	2.19	0.42
24:CX:3:C:H5'	26:DA:2255:G:O2'	2.20	0.42
15:AO:78:TYR:CZ	15:AO:82:ILE:HD13	2.55	0.42
25:AY:68:C:N3	25:AY:69:G:C8	2.88	0.42
1:AA:922:G:C6	1:AA:923:A:C6	3.08	0.42
4:CD:57:ARG:HD3	4:CD:205:GLU:HB2	2.00	0.42
25:CY:15:G:H22	25:CY:48:C:N4	2.15	0.42
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
1:CA:989:C:HO2'	1:CA:1016:A:H2	1.67	0.42
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.54	0.42
13:CM:94:ARG:CZ	19:CS:80:TYR:HD2	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2101:G:H2'	26:BA:2102:U:C6	2.55	0.42
51:B4:62:ARG:HB2	51:B4:63:TYR:CD1	2.54	0.42
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.55	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.13	0.42
26:DA:300:A:H3'	45:DY:84:ARG:NH2	2.35	0.42
26:DA:526:A:N3	26:DA:2044:C:H1'	2.35	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HB2	2.02	0.42
25:AY:38:A:C5	25:AY:39:PSU:C6	3.08	0.42
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.20	0.42
26:DA:2262:U:H4'	26:DA:2328:A:H2	1.84	0.42
10:CJ:56:HIS:CD2	10:CJ:56:HIS:H	2.38	0.42
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.20	0.42
46:DZ:5:LEU:HA	46:DZ:5:LEU:HD22	1.82	0.42
26:DA:2853:C:H2'	26:DA:2854:G:C8	2.54	0.42
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.42
26:BA:1762:A:H2'	61:BA:5184:HOH:O	2.19	0.42
2:AB:62:ALA:HB3	2:AB:225:ALA:HB3	2.02	0.42
26:DA:2307:G:H8	26:DA:2307:G:OP1	2.03	0.42
26:BA:2443:C:OP1	30:BF:68:LYS:HD3	2.20	0.42
9:AI:16:ARG:HB2	9:AI:64:THR:HB	2.01	0.42
26:BA:2619:C:H4'	29:BE:151:TYR:O	2.20	0.42
3:AC:131:ARG:NE	3:AC:166:GLU:OE2	2.53	0.42
1:CA:641:U:O3'	1:CA:642:A:H8	2.03	0.42
13:AM:14:ARG:NH2	13:AM:41:PRO:O	2.53	0.42
20:CT:33:ILE:HG13	20:CT:62:LEU:HD22	2.02	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
3:AC:56:ASP:HB2	3:AC:67:THR:HB	2.02	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.42
50:B3:5:LYS:NZ	50:B3:34:GLU:OE2	2.40	0.42
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.71	0.42
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	2.02	0.42
39:DS:80:LEU:HA	39:DS:80:LEU:HD12	1.84	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.80	0.42
26:DA:2252:G:H2'	26:DA:2253:G:O4'	2.19	0.42
1:AA:881:G:P	12:AL:12:ARG:HH22	2.42	0.42
1:CA:1039:C:C4	1:CA:1040:U:C4	3.07	0.41
1:CA:998:G:C6	1:CA:999:C:C4	3.08	0.41
26:DA:994:C:O2'	26:DA:996:A:OP1	2.16	0.41
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.34	0.41
1:AA:1035:A:H8	1:AA:1035:A:O5'	2.02	0.41
1:AA:78:G:N2	1:AA:91:C:C2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2815:C:H2'	26:DA:2816:C:H6	1.85	0.41
51:B4:63:TYR:CD1	51:B4:63:TYR:N	2.86	0.41
26:DA:2788:C:C4	26:DA:2789:C:N4	2.88	0.41
26:DA:1843:C:H5'	28:DD:253:GLN:NE2	2.34	0.41
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.20	0.41
26:DA:867:C:C2'	26:DA:868:U:H5'	2.50	0.41
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	2.02	0.41
23:CW:76:31M:N3'	26:DA:2585:U:O4	2.53	0.41
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	2.02	0.41
44:DX:88:LYS:NZ	44:DX:90:GLU:HG2	2.34	0.41
2:AB:71:VAL:HG13	2:AB:93:VAL:CG2	2.50	0.41
40:BT:73:GLU:OE1	40:BT:103:ARG:NE	2.41	0.41
45:BY:7:VAL:HG21	45:BY:72:VAL:HG12	2.02	0.41
1:AA:555:C:H2'	1:AA:556:C:C6	2.55	0.41
46:DZ:166:SER:O	46:DZ:169:GLU:HB2	2.20	0.41
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.19	0.41
33:BI:110:ASP:HA	33:BI:111:PRO:HD2	1.78	0.41
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.85	0.41
1:AA:591:U:H2'	1:AA:592:G:C8	2.54	0.41
1:AA:688:G:H5'	11:AK:46:GLY:C	2.40	0.41
26:DA:2505:G:O6	26:DA:2576:G:H2'	2.20	0.41
3:AC:47:LEU:CD1	3:AC:68:VAL:HG11	2.50	0.41
4:CD:17:VAL:HG12	4:CD:18:LYS:N	2.35	0.41
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.93	0.41
26:DA:569:U:H5''	61:DA:4096:HOH:O	2.20	0.41
9:AI:93:ARG:HB2	9:AI:93:ARG:NH1	2.35	0.41
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.20	0.41
26:DA:776:G:C8	26:DA:793:A:C2	3.08	0.41
23:AW:25:C:H2'	23:AW:26:A:H5'	2.02	0.41
26:DA:2124:G:N1	26:DA:2174:C:N4	2.34	0.41
8:CH:72:PRO:O	8:CH:73:ASP:HB3	2.20	0.41
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.69	0.41
26:BA:1530:C:HO2'	26:BA:1531:C:P	2.37	0.41
25:AY:22:G:C2	25:AY:23:A:C5	3.08	0.41
1:CA:1135:U:HO2'	1:CA:1136:U:H5	1.66	0.41
1:CA:657:G:H1'	1:CA:750:G:N2	2.35	0.41
25:CY:5:G:N2	25:CY:68:C:N3	2.63	0.41
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.49	0.41
17:CQ:65:ILE:HB	17:CQ:69:LYS:HB3	2.03	0.41
1:CA:986:A:N3	19:CS:52:TYR:OH	2.42	0.41
1:AA:1417:G:H22	1:AA:1482:G:H2'	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:56:LEU:HD23	13:CM:57:ARG:N	2.35	0.41
27:DB:108:U:H2'	27:DB:109:C:H5''	2.03	0.41
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.35	0.41
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	2.01	0.41
46:BZ:104:PHE:CD2	46:BZ:139:VAL:HB	2.55	0.41
1:AA:1296:C:H4'	1:AA:1302:U:C4	2.55	0.41
1:CA:971:G:H22	1:CA:1363(A):A:P	2.42	0.41
25:AY:39:PSU:H5'	25:AY:39:PSU:H6	1.86	0.41
26:DA:1885:A:H2'	26:DA:1886:C:O4'	2.20	0.41
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.41
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.52	0.41
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.34	0.41
26:DA:27:G:O2'	26:DA:28:A:OP2	2.36	0.41
11:AK:59:TYR:CZ	11:AK:63:LEU:HD11	2.55	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.20	0.41
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.55	0.41
3:CC:82:GLU:O	3:CC:85:ARG:HB2	2.20	0.41
26:BA:2012:G:OP1	43:BW:11:ARG:NH2	2.45	0.41
31:DG:86:MET:HA	31:DG:87:PRO:HD3	1.97	0.41
26:BA:355:G:H2'	26:BA:356:G:O4'	2.20	0.41
1:CA:434:U:H2'	1:CA:435:C:C6	2.55	0.41
41:BU:17:ILE:HG13	41:BU:32:PHE:HE1	1.84	0.41
4:AD:178:VAL:C	4:AD:180:GLY:H	2.23	0.41
1:CA:814:A:N7	1:CA:816:A:C4	2.88	0.41
26:BA:479:A:N3	26:BA:481:G:H5''	2.35	0.41
1:AA:309:G:H1'	1:AA:608:A:C2	2.55	0.41
12:AL:42:THR:OG1	12:AL:52:LEU:HD13	2.20	0.41
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.19	0.41
26:DA:1905:C:H1'	26:DA:1928:A:H2	1.85	0.41
32:BH:96:ALA:HB2	32:BH:105:LEU:HD13	2.02	0.41
26:BA:954:G:H5''	37:BQ:13:GLN:HB3	2.01	0.41
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.21	0.41
38:DR:26:LYS:HE2	38:DR:70:LEU:O	2.20	0.41
34:BN:33:LEU:HD12	34:BN:33:LEU:HA	1.84	0.41
1:CA:791:G:N2	1:CA:1497:G:O3'	2.50	0.41
26:DA:2519:U:C4	26:DA:2542:A:C5	3.08	0.41
3:CC:116:VAL:HG13	3:CC:119:ARG:HD3	2.02	0.41
1:AA:890:G:O2'	1:AA:906:G:O6	2.24	0.41
1:AA:765:G:N1	1:AA:812:C:O2'	2.43	0.41
39:BS:10:ARG:HG3	39:BS:13:ARG:NH2	2.35	0.41
19:AS:38:SER:HB2	19:AS:71:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:27:LYS:HB2	2:AB:194:PRO:HD2	2.01	0.41
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.41
26:DA:2172:U:O2'	26:DA:2173:A:P	2.78	0.41
42:DV:46:VAL:HG23	42:DV:52:VAL:HG11	2.01	0.41
23:AW:76:31M:HD2	26:BA:2506:U:O4'	2.20	0.41
1:AA:1027:C:C2	1:AA:1034:G:C6	3.07	0.41
1:CA:741:G:H2'	1:CA:742:G:O4'	2.20	0.41
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.56	0.41
46:DZ:126:VAL:HG11	46:DZ:161:VAL:CG2	2.41	0.41
25:AY:19:G:C4'	25:AY:57:G:H22	2.33	0.41
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.20	0.41
26:BA:528:A:C8	26:BA:528:A:H3'	2.54	0.41
24:AX:15:G:H21	24:AX:21:A:H1'	1.84	0.41
1:AA:663:A:H5'	1:AA:836:G:OP1	2.19	0.41
46:BZ:105:VAL:O	46:BZ:140:ASP:HA	2.20	0.41
26:BA:303:U:H2'	26:BA:304:G:C8	2.55	0.41
26:DA:1372:U:O5'	26:DA:1372:U:H6	2.03	0.41
1:AA:977:A:H1'	1:AA:982:U:O4	2.20	0.41
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.21	0.41
26:DA:275:G:H2'	26:DA:276:A:O4'	2.20	0.41
32:BH:88:LEU:HD23	32:BH:165:ALA:HA	2.01	0.41
26:DA:2541:A:N7	61:DA:3999:HOH:O	2.37	0.41
10:AJ:47:PHE:N	10:AJ:63:PHE:O	2.47	0.41
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.40	0.41
26:BA:615:G:OP1	30:BF:40:GLN:NE2	2.53	0.41
27:BB:110:G:O2'	27:BB:111:G:H5'	2.20	0.41
37:DQ:45:GLN:CD	37:DQ:45:GLN:H	2.23	0.41
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.41
5:CE:41:VAL:O	5:CE:66:MET:HA	2.20	0.41
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.67	0.41
1:CA:250:A:H4'	1:CA:251:G:O5'	2.18	0.41
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.41
38:BR:57:ARG:HH21	38:BR:62:ALA:HB2	1.85	0.41
1:AA:589:C:H5''	8:AH:29:SER:OG	2.20	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
17:CQ:3:LYS:HD3	17:CQ:61:GLU:O	2.20	0.41
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.55	0.41
4:AD:190:ASP:H	4:AD:193:ASP:HB2	1.86	0.41
39:DS:83:LYS:HE2	39:DS:83:LYS:HB3	1.90	0.41
17:AQ:31:LEU:HD23	17:AQ:32:TYR:CZ	2.56	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1008:C:H4'	41:DU:59:ARG:NH2	2.35	0.41
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.20	0.41
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.35	0.41
1:CA:1240:U:OP2	7:CG:115:ARG:HA	2.19	0.41
1:CA:1041:A:H2'	1:CA:1042:G:O4'	2.20	0.41
2:CB:12:GLU:O	2:CB:15:VAL:N	2.50	0.41
25:AY:19:G:H4'	25:AY:20:U:OP2	2.19	0.41
25:AY:57:G:N3	25:AY:58:A:H5'	2.35	0.41
4:AD:64:LEU:HB2	4:AD:198:VAL:HG11	2.03	0.41
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.76	0.41
26:BA:2119:A:C5	26:BA:2171:A:C6	3.08	0.41
14:CN:45:ARG:O	14:CN:49:HIS:HD2	2.04	0.41
29:BE:119:ARG:HG2	29:BE:160:TYR:CG	2.56	0.41
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.54	0.41
8:CH:51:VAL:HG12	8:CH:52:ASP:N	2.35	0.41
33:DI:110:ASP:OD1	33:DI:111:PRO:HD2	2.21	0.41
1:AA:103:C:OP2	20:AT:14:LYS:NZ	2.44	0.41
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.55	0.41
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	2.03	0.41
26:BA:443:A:H5''	26:BA:444:C:OP1	2.21	0.41
41:DU:81:HIS:O	41:DU:84:LYS:HB3	2.20	0.41
33:BI:93:THR:H	33:BI:96:ASP:CG	2.23	0.41
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.80	0.41
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	2.02	0.41
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.55	0.41
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.34	0.41
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.41
1:AA:382:A:H2'	1:AA:383:A:H8	1.85	0.41
26:DA:8:A:H2'	26:DA:9:U:C6	2.55	0.41
26:DA:752:A:OP1	54:D7:3:ARG:NH2	2.50	0.41
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.47	0.41
1:CA:501:C:H2'	1:CA:502:G:H8	1.84	0.41
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.21	0.41
1:AA:826:C:H2'	1:AA:827:U:C6	2.56	0.41
26:BA:1266:G:O4'	43:BW:15:ARG:NH2	2.50	0.41
26:BA:816:C:H2'	26:BA:817:C:C6	2.55	0.41
26:BA:1750:G:O2'	26:BA:2860:A:N1	2.38	0.41
26:BA:1403:C:H5''	26:BA:1471:A:H1'	2.01	0.41
26:BA:2785:C:H2'	26:BA:2786:U:O4'	2.20	0.41
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.21	0.41
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:562:C:H1'	12:CL:15:ARG:HB3	2.02	0.41
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.56	0.41
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	2.01	0.41
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	2.02	0.41
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.50	0.41
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.20	0.41
32:DH:27:LYS:HB3	32:DH:27:LYS:HE3	1.82	0.41
3:CC:28:GLN:HE21	3:CC:28:GLN:HB2	1.59	0.41
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	2.03	0.41
26:BA:601:C:O2'	26:BA:605:C:H5''	2.20	0.41
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.02	0.41
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	2.02	0.41
1:CA:1173:G:H2'	1:CA:1174:G:C8	2.55	0.41
26:DA:2169:A:C2	26:DA:2170:A:C2	3.08	0.41
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.19	0.41
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.49	0.41
26:DA:932:G:H4'	26:DA:933:A:O5'	2.19	0.41
1:CA:723:U:HO2'	1:CA:724:G:H5'	1.85	0.41
29:DE:169:ASN:HB2	29:DE:203:LYS:HG3	2.03	0.41
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.51	0.41
26:DA:1580:A:OP2	26:DA:1580:A:H8	2.03	0.41
1:AA:103:C:OP2	20:AT:17:ARG:NH2	2.53	0.41
26:DA:1024:G:C6	26:DA:1025:G:C6	3.08	0.41
26:DA:1127:A:C2'	26:DA:1128:A:H5''	2.50	0.41
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	2.02	0.41
26:DA:324:A:N6	26:DA:338:G:O2'	2.49	0.41
6:CF:94:GLN:HE22	18:CR:72:ARG:HH12	1.69	0.41
26:DA:1882:C:H3'	26:DA:1883:G:H8	1.85	0.41
26:BA:465:G:H2'	26:BA:466:A:C8	2.55	0.41
33:BI:109:ILE:HG23	33:BI:110:ASP:N	2.35	0.41
26:BA:634:C:H2'	26:BA:635:C:C6	2.56	0.41
26:BA:1456:G:OP2	61:BA:4012:HOH:O	2.21	0.41
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.85	0.41
26:DA:2550:G:C6	26:DA:2551:C:C4	3.08	0.41
1:CA:730:G:C5	1:CA:731:G:H1'	2.55	0.41
40:DT:6:LEU:O	40:DT:10:VAL:HG23	2.20	0.41
1:CA:29:G:O2'	1:CA:295:C:H4'	2.20	0.41
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.41
20:CT:72:LEU:HA	20:CT:72:LEU:HD23	1.84	0.41
30:DF:135:LYS:HE2	30:DF:135:LYS:HA	2.02	0.41
1:CA:978:A:C6	1:CA:1319:A:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2283:C:H2'	26:BA:2284:C:O4'	2.20	0.41
26:DA:2154:G:N1	26:DA:2155:G:N7	2.69	0.41
1:CA:998:G:H2'	1:CA:999:C:O4'	2.20	0.41
26:DA:2114:A:N1	26:DA:2117:A:N6	2.69	0.41
4:AD:138:TYR:CE1	4:AD:140:VAL:HA	2.56	0.41
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.51	0.41
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.21	0.41
14:CN:37:PHE:HB3	14:CN:39:LEU:HG	2.03	0.41
1:CA:983:A:O2'	1:CA:1050:G:OP2	2.33	0.41
1:CA:722:A:C8	1:CA:724:G:H1'	2.55	0.41
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.41
1:CA:942:G:C2	1:CA:1342:C:C2	3.09	0.41
26:DA:869:G:C6	26:DA:870:A:C5	3.08	0.41
33:DI:43:ASN:C	33:DI:43:ASN:HD22	2.24	0.41
1:CA:513:C:H2'	1:CA:514:C:O4'	2.19	0.41
26:DA:1021:A:C3'	26:DA:1021:A:C8	3.02	0.41
27:BB:6:C:H2'	27:BB:7:G:H5''	2.02	0.41
1:AA:600:C:H2'	1:AA:601:C:H6	1.85	0.41
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.20	0.41
35:DO:20:MET:HE3	35:DO:44:LYS:HE3	2.02	0.41
26:BA:719:C:H2'	26:BA:720:C:H6	1.85	0.41
33:BI:103:ARG:HE	33:BI:103:ARG:HB3	1.53	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.21	0.41
3:AC:27:LYS:HA	3:AC:27:LYS:HD2	1.76	0.41
21:AU:6:ARG:O	21:AU:12:LYS:HD2	2.21	0.41
20:CT:86:ARG:CZ	20:CT:86:ARG:HB3	2.49	0.41
27:DB:8:U:H3	27:DB:113:G:H1	1.69	0.41
10:AJ:27:ALA:HA	10:AJ:81:THR:HG21	2.03	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.01	0.41
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	2.02	0.41
53:B6:9:LEU:HD11	53:B6:23:THR:HG23	2.03	0.41
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.41
20:AT:57:ARG:HH22	20:AT:100:ILE:HD12	1.86	0.41
26:BA:1756:G:H4'	26:BA:1758:G:O4'	2.21	0.41
32:DH:54:ARG:HD3	32:DH:65:HIS:ND1	2.34	0.41
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.68	0.41
1:CA:857:C:H2'	1:CA:858:G:O4'	2.21	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.78	0.41
8:AH:33:GLU:HG2	8:AH:48:TYR:CZ	2.56	0.41
39:DS:65:VAL:O	39:DS:69:VAL:HG12	2.20	0.41
26:DA:1766:U:H2'	26:DA:1767:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2639:A:OP2	61:BA:4129:HOH:O	2.22	0.41
26:DA:775:G:O3'	61:DA:4253:HOH:O	2.21	0.41
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.88	0.41
26:DA:2152:G:C2	26:DA:2153:G:H1'	2.54	0.41
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.50	0.41
23:CW:34:G:H2'	23:CW:35:A:C8	2.56	0.41
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.44	0.41
24:AX:31:G:C8	24:AX:32:5MC:HM52	2.56	0.41
26:DA:2025:C:H2'	26:DA:2026:C:C6	2.56	0.41
26:DA:2026:C:H2'	26:DA:2027:G:O4'	2.21	0.41
1:AA:993:G:N3	1:AA:993:G:H2'	2.36	0.41
30:BF:157:VAL:HG21	30:BF:181:LEU:HD13	2.02	0.41
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	2.02	0.41
30:BF:101:LEU:HA	30:BF:101:LEU:HD12	1.84	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.56	0.41
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.86	0.41
25:AY:38:A:H3'	25:AY:39:PSU:H5'	2.02	0.41
1:AA:161:A:O5'	1:AA:161:A:H8	2.02	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.92	0.41
36:DP:55:ARG:HA	61:DP:309:HOH:O	2.21	0.41
39:DS:67:ARG:HG2	39:DS:71:ARG:HH11	1.85	0.41
26:DA:62:C:N4	26:DA:93:G:H1	2.19	0.41
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	2.03	0.41
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.02	0.41
26:DA:2228:G:C6	26:DA:2229:C:C4	3.09	0.41
1:AA:1286:A:H2'	1:AA:1287:A:H4'	2.01	0.41
27:DB:33:G:C2	27:DB:50:G:C2	3.08	0.41
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.41
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.45	0.41
26:BA:271(A):A:N1	26:BA:272(D):G:O2'	2.47	0.41
1:CA:176:C:H2'	1:CA:177:C:C6	2.55	0.41
23:AW:13:C:O2'	23:AW:14:A:O5'	2.37	0.41
26:DA:340:A:H2'	26:DA:341:G:O4'	2.20	0.41
26:DA:1498:C:O4'	26:DA:1577:C:H4'	2.21	0.41
1:AA:37:U:O2'	1:AA:500:G:H4'	2.20	0.41
36:BP:6:LEU:HA	36:BP:6:LEU:HD23	1.80	0.41
20:AT:46:GLU:HG2	20:AT:46:GLU:O	2.20	0.41
33:BI:9:LEU:HD22	33:BI:9:LEU:HA	1.79	0.41
3:CC:26:LYS:HE3	3:CC:26:LYS:HB3	1.88	0.41
45:BY:5:MET:HE1	45:BY:32:PRO:HA	2.03	0.41
26:BA:1338:G:N7	44:BX:62:LYS:NZ	2.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:42:C:C4	27:DB:43:C:C4	3.09	0.41
27:DB:119:G:C6	27:DB:120:A:C6	3.09	0.41
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.56	0.41
26:DA:2432:A:C6	26:DA:2433:A:C6	3.09	0.41
34:DN:42:TRP:HD1	34:DN:48:MET:HE2	1.86	0.41
25:CY:64:A:H2'	25:CY:65:G:C8	2.56	0.41
25:AY:70:G:C6	25:AY:71:G:C5	3.09	0.41
26:BA:2061:G:H5''	26:BA:2503:A:C2	2.56	0.41
36:BP:65:ARG:HD3	36:BP:66:GLY:N	2.36	0.41
25:AY:20:U:H4'	25:AY:21:A:OP1	2.20	0.41
25:AY:59:U:H3'	25:AY:60:U:C5	2.56	0.41
26:DA:1449:A:C2	26:DA:1529:G:H1'	2.55	0.41
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.21	0.41
54:B7:24:THR:HG22	54:B7:27:GLY:N	2.30	0.41
1:AA:1256:A:N6	1:AA:1278:U:O4'	2.52	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.01	0.41
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.55	0.41
23:CW:21:A:N6	23:CW:46:7MG:C4	2.89	0.41
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.39	0.41
26:BA:1203:G:OP2	26:BA:1204:A:O2'	2.28	0.41
1:CA:1102:A:O3'	2:CB:96:ARG:NH1	2.47	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
41:DU:85:LYS:HE2	41:DU:85:LYS:HB3	1.77	0.41
1:AA:109:A:H2'	1:AA:326:G:N2	2.35	0.41
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.54	0.41
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.56	0.41
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.41
2:AB:103:THR:HG23	2:AB:176:GLU:OE1	2.21	0.41
1:CA:8:A:C6	4:CD:209:ARG:HG3	2.56	0.41
37:DQ:58:PHE:CZ	37:DQ:109:VAL:HG21	2.55	0.41
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.85	0.41
52:D5:47:PRO:HG2	52:D5:48:GLU:OE1	2.21	0.41
20:AT:54:LYS:HB2	20:AT:100:ILE:HD11	2.03	0.41
26:DA:674:G:H1'	30:DF:74:ARG:HD3	2.03	0.41
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.20	0.41
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	2.02	0.41
26:BA:2418:A:H2'	26:BA:2419:U:C6	2.55	0.41
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	2.02	0.41
15:AO:71:GLN:HA	15:AO:71:GLN:HE21	1.85	0.41
15:AO:7:GLU:H	15:AO:7:GLU:HG3	1.65	0.41
31:DG:58:GLN:OE1	31:DG:58:GLN:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.81	0.41
26:DA:117:G:C6	26:DA:119:A:C6	3.09	0.41
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.21	0.41
1:AA:358:U:H2'	1:AA:359:U:C6	2.56	0.41
1:AA:519:C:OP2	12:AL:50:SER:OG	2.26	0.41
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.21	0.41
25:AY:69:G:H2'	25:AY:70:G:O4'	2.21	0.41
26:DA:2133:G:O2'	26:DA:2134:A:P	2.79	0.41
1:CA:1002:G:C2	1:CA:1003:G:C8	3.09	0.41
1:CA:1003:G:C6	1:CA:1004:A:C2	3.09	0.41
25:CY:8:4SU:S4	25:CY:14:A:C8	3.13	0.41
26:DA:2113:U:N3	26:DA:2114:A:N7	2.69	0.41
26:BA:100:G:H3'	26:BA:102:G:C5'	2.50	0.41
9:CI:56:LEU:HD23	9:CI:56:LEU:HA	1.86	0.41
26:BA:1170:G:C2	26:BA:1171:G:H1'	2.55	0.41
4:AD:157:LEU:HD23	4:AD:161:ASN:HD21	1.85	0.41
1:CA:1029:C:N3	1:CA:1032:G:C2	2.89	0.41
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.85	0.41
25:AY:21:A:H4'	25:AY:22:G:OP1	2.21	0.41
25:AY:58:A:H8	25:AY:58:A:H2'	1.72	0.41
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.20	0.41
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.86	0.41
1:AA:1422:G:C5'	35:BO:48:PRO:HB3	2.44	0.41
30:BF:11:VAL:HB	30:BF:18:ARG:HB3	2.03	0.41
1:CA:1015:A:H2'	1:CA:1016:A:C8	2.56	0.41
29:DE:46:ALA:HB2	29:DE:82:ARG:HA	2.02	0.41
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	2.01	0.41
27:DB:24:G:H4'	27:DB:25:A:N7	2.36	0.41
26:BA:528:A:C3'	26:BA:529:A:H5''	2.51	0.41
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.21	0.41
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.20	0.41
26:BA:1047:G:O2'	26:BA:1048:A:H8	2.03	0.41
31:DG:101:ILE:O	31:DG:104:GLU:HB3	2.20	0.41
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.55	0.41
26:DA:571:A:H5'	26:DA:2030:A:N7	2.36	0.41
1:AA:1278:U:H6	1:AA:1278:U:H3'	1.85	0.41
6:AF:97:PHE:CB	18:AR:32:ARG:HD3	2.51	0.41
1:CA:1243:C:H2'	1:CA:1244:C:H6	1.85	0.41
1:AA:277:C:H5''	17:AQ:68:ARG:HH22	1.86	0.41
26:DA:516:C:H1'	26:DA:1261:C:O2'	2.21	0.41
2:CB:48:MET:O	2:CB:52:GLU:N	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:429:U:H1'	1:CA:430:A:H5''	2.03	0.41
28:BD:121:PRO:HB3	28:BD:135:PHE:CE2	2.56	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.21	0.41
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.56	0.41
39:DS:4:LEU:HD23	39:DS:4:LEU:HA	1.76	0.41
24:CX:31:G:C8	24:CX:32:5MC:HM52	2.56	0.41
26:DA:921:G:C6	26:DA:922:U:C4	3.09	0.41
26:DA:2803:C:H2'	26:DA:2804:C:C6	2.53	0.41
26:DA:821:A:H2'	26:DA:946:G:H5''	2.02	0.41
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.56	0.41
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.21	0.41
1:CA:447:G:O6	1:CA:485:G:O2'	2.19	0.41
24:AX:76:A:OP2	61:AX:3106:HOH:O	2.20	0.41
6:AF:36:ARG:NH1	6:AF:36:ARG:HB3	2.36	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
26:DA:1268:A:C2	26:DA:2013:A:C4	3.09	0.41
2:CB:100:GLY:O	2:CB:104:ASN:N	2.49	0.41
26:DA:446:G:OP1	41:DU:3:ARG:NH1	2.52	0.41
26:BA:2857:G:N2	26:BA:2860:A:OP2	2.43	0.41
1:AA:192:U:O3'	20:AT:57:ARG:HD2	2.20	0.41
1:AA:551:U:H2'	1:AA:552:U:C6	2.55	0.41
26:BA:2570:G:H2'	26:BA:2571:C:O4'	2.21	0.41
44:DX:57:LEU:HD22	44:DX:78:LYS:HG2	2.03	0.41
26:BA:1550:C:H4'	26:BA:1743:C:O2	2.21	0.41
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.92	0.41
26:BA:947:G:H2'	26:BA:948:G:C8	2.56	0.41
26:DA:1283:G:O2'	26:DA:1285:G:N7	2.44	0.41
26:BA:2065:C:H2'	26:BA:2066:C:C6	2.56	0.41
26:BA:86:C:H4'	26:BA:104:U:H1'	2.03	0.41
32:DH:95:ARG:HB3	32:DH:95:ARG:HE	1.77	0.41
26:DA:2275:C:H5'	26:DA:2275:C:H6	1.86	0.41
2:CB:112:VAL:O	2:CB:116:GLU:HB2	2.21	0.41
38:DR:28:LEU:HD23	38:DR:28:LEU:HA	1.93	0.41
26:BA:687:C:H42	26:BA:787:U:H4'	1.86	0.41
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.01	0.41
35:BO:86:ILE:HG22	35:BO:94:ARG:HG3	2.03	0.41
31:DG:108:ASN:O	31:DG:112:PRO:HG2	2.21	0.41
26:DA:1910:G:H2'	26:DA:1911:U:H6	1.85	0.41
26:BA:1033:U:OP1	56:B9:9:ARG:NH2	2.54	0.41
1:AA:1324:A:O4'	1:AA:1362:C:H4'	2.21	0.41
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:104:LEU:HD13	7:AG:104:LEU:HA	1.96	0.41
26:DA:2761:G:N3	26:DA:2761:G:H2'	2.35	0.41
26:BA:2729:G:H2'	26:BA:2730:C:O4'	2.21	0.41
1:AA:1003:G:N2	1:AA:1004:A:N3	2.69	0.41
25:AY:21:A:H8	25:AY:21:A:OP2	2.04	0.41
44:DX:35:THR:HG22	44:DX:37:THR:N	2.36	0.41
1:CA:1053:G:H4'	1:CA:1054:C:H5'	2.03	0.41
26:BA:2893:G:H4'	26:BA:2894:G:O5'	2.21	0.41
26:BA:1359:A:C2	26:BA:1372:U:O4	2.74	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5''	2.51	0.41
26:BA:887:A:H4'	26:BA:888:C:H5	1.82	0.41
14:CN:37:PHE:CE2	14:CN:53:LEU:HD22	2.56	0.41
1:CA:344:A:H4'	1:CA:345:C:OP2	2.21	0.41
1:CA:946:A:H2'	1:CA:947:G:C8	2.56	0.41
1:CA:436:C:H2'	1:CA:437:U:H6	1.86	0.41
6:AF:19:LEU:HD11	6:AF:59:TYR:CZ	2.56	0.41
26:DA:753:C:H6	26:DA:753:C:OP2	2.03	0.41
1:CA:1030(A):G:N2	1:CA:1030(C):G:H8	2.19	0.41
1:CA:1030(A):G:H2'	1:CA:1030(C):G:OP2	2.20	0.41
10:CJ:6:ILE:N	10:CJ:72:VAL:O	2.36	0.41
26:BA:719:C:H2'	26:BA:720:C:C6	2.56	0.41
34:BN:138:LEU:HD23	34:BN:138:LEU:HA	1.81	0.41
44:BX:88:LYS:HE3	44:BX:88:LYS:HB3	1.87	0.41
7:CG:24:THR:O	7:CG:27:ILE:HB	2.21	0.41
26:DA:1161:C:H2'	26:DA:1162:G:H8	1.86	0.41
1:CA:609:A:C5	1:CA:610:G:C8	3.09	0.41
4:CD:18:LYS:HE3	4:CD:20:TYR:CE1	2.55	0.41
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.36	0.41
31:BG:125:PHE:HB3	31:BG:166:ASP:OD1	2.20	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.85	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
35:DO:98:VAL:HG11	35:DO:114:ILE:HG23	2.02	0.41
38:DR:38:VAL:HG12	38:DR:42:LYS:HE3	2.03	0.41
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.03	0.41
26:DA:41:C:H2'	26:DA:42:G:C8	2.56	0.41
26:DA:649:G:H4'	55:D8:46:ARG:HH22	1.86	0.41
4:CD:33:MET:O	4:CD:37:PRO:HB3	2.20	0.41
56:D9:17:ILE:HD12	56:D9:17:ILE:HA	1.92	0.41
33:DI:83:ALA:CB	33:DI:123:LEU:HD21	2.50	0.41
33:DI:86:THR:O	33:DI:123:LEU:HD23	2.21	0.41
26:DA:2706:G:H2'	26:DA:2707:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:966:G:H2'	26:DA:967:C:C6	2.55	0.41
46:DZ:120:ILE:HD11	46:DZ:173:ALA:CB	2.51	0.41
25:AY:6:G:C6	25:AY:7:A:C5	3.08	0.40
42:DV:52:VAL:CG2	42:DV:55:ALA:HB3	2.51	0.40
1:CA:861:G:OP1	8:CH:75:ARG:NH2	2.54	0.40
3:AC:52:LEU:HD11	3:AC:55:VAL:HG23	2.02	0.40
46:DZ:161:VAL:O	46:DZ:161:VAL:HG13	2.20	0.40
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.35	0.40
26:BA:2804:C:H2'	26:BA:2805:G:O4'	2.21	0.40
23:CW:27:G:H2'	23:CW:28:G:C8	2.56	0.40
26:BA:2113:U:C4	26:BA:2114:A:N7	2.89	0.40
2:AB:21:ARG:NH2	2:AB:23:ARG:HE	2.19	0.40
40:DT:108:ARG:HG2	40:DT:111:ARG:NH1	2.32	0.40
26:DA:299:A:H5''	45:DY:86:ARG:NH2	2.36	0.40
26:DA:2849:U:O4	40:DT:23:ARG:NH2	2.43	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.55	0.40
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.56	0.40
5:CE:31:LEU:HA	5:CE:31:LEU:HD23	1.86	0.40
4:AD:120:LEU:HA	4:AD:120:LEU:HD23	1.82	0.40
26:DA:1853:A:N1	26:DA:2087:G:H1'	2.37	0.40
31:BG:14:GLU:C	31:BG:17:PRO:HD2	2.42	0.40
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.57	0.40
26:DA:478:A:N1	26:DA:500:G:H4'	2.35	0.40
26:DA:1309:G:H3'	54:D7:9:ARG:NH1	2.36	0.40
1:AA:1152:A:OP1	10:AJ:68:HIS:ND1	2.52	0.40
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.35	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.86	0.40
1:CA:1497:G:HO2'	1:CA:1518:A:H2	1.62	0.40
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.54	0.40
26:BA:2282:G:OP1	26:BA:2283:C:H1'	2.21	0.40
26:BA:1185:C:H5''	26:BA:1186:G:OP1	2.20	0.40
26:DA:1336:A:H2'	26:DA:1337:G:C8	2.56	0.40
1:CA:19:C:H5''	5:CE:86:ALA:HB3	2.03	0.40
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.56	0.40
46:BZ:92:SER:OG	46:BZ:93:ASP:N	2.55	0.40
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.77	0.40
1:CA:64:G:H4'	1:CA:65:U:H3'	2.02	0.40
1:CA:690:G:H8	1:CA:690:G:O5'	2.04	0.40
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.86	0.40
27:DB:78:A:C2	27:DB:100:A:C4	3.09	0.40
7:CG:14:PRO:HG3	7:CG:21:VAL:HG13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:319:G:H1	1:AA:334:C:H42	1.69	0.40
26:DA:225:A:N6	26:DA:226:G:C2	2.89	0.40
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.53	0.40
9:AI:50:LEU:HB2	9:AI:55:ALA:HB3	2.04	0.40
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.04	0.40
22:CV:14:A:C2	25:CY:34:G:C2	3.10	0.40
26:BA:2278:A:OP1	37:BQ:11:LYS:HD2	2.22	0.40
26:DA:1394:U:C4	26:DA:1395:A:C5	3.10	0.40
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.66	0.40
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.21	0.40
19:CS:69:HIS:HD2	19:CS:73:GLU:OE1	2.05	0.40
25:AY:36:A:C6	25:AY:37:MIA:C5	3.03	0.40
27:DB:110:G:O2'	27:DB:111:G:H5'	2.21	0.40
1:CA:149:A:H2'	1:CA:150:C:C6	2.56	0.40
14:CN:23:ARG:HG3	14:CN:28:GLY:O	2.21	0.40
38:DR:63:ARG:O	38:DR:67:LEU:HB2	2.22	0.40
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.22	0.40
8:AH:39:LEU:HD12	8:AH:39:LEU:HA	1.86	0.40
23:CW:9:A:OP2	23:CW:13:C:N4	2.47	0.40
31:DG:125:PHE:HB3	31:DG:166:ASP:CG	2.42	0.40
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.56	0.40
24:CX:43:A:H2'	24:CX:44:A:C8	2.56	0.40
1:CA:993:G:O2'	1:CA:994:A:N7	2.51	0.40
54:B7:8:ASN:HB3	54:B7:11:LYS:HB3	2.02	0.40
20:AT:92:LEU:O	20:AT:96:GLY:HA2	2.22	0.40
27:DB:33:G:C6	27:DB:34:U:N3	2.89	0.40
26:BA:817:C:H4'	26:BA:932:G:C5	2.56	0.40
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.21	0.40
15:AO:7:GLU:O	15:AO:11:VAL:HG23	2.21	0.40
38:DR:38:VAL:HG22	38:DR:112:ALA:HB2	2.03	0.40
26:BA:1161:C:O2'	42:BV:8:GLY:HA2	2.21	0.40
30:DF:59:TYR:HE2	30:DF:85:GLY:O	2.04	0.40
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.02	0.40
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.21	0.40
24:CX:2:G:H5'	57:CX:3002:MG:MG	1.46	0.40
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	2.03	0.40
1:AA:955:U:O2'	19:AS:83:HIS:HD2	2.03	0.40
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.44	0.40
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.94	0.40
26:BA:828:U:C5	26:BA:2247:A:H4'	2.56	0.40
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1414:U:H3	1:CA:1486:G:H1	1.68	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.40
2:AB:118:LEU:HA	2:AB:118:LEU:HD23	1.84	0.40
30:DF:93:LYS:HD3	30:DF:93:LYS:HA	1.86	0.40
1:AA:613:C:H2'	1:AA:614:A:C8	2.55	0.40
26:DA:820:A:N3	26:DA:943:U:H4'	2.36	0.40
26:BA:1805:U:O2	28:BD:50:THR:HB	2.21	0.40
29:DE:30:PRO:HD3	29:DE:180:ASN:ND2	2.35	0.40
26:BA:1223:G:N2	26:BA:1226:A:OP2	2.47	0.40
53:B6:14:THR:HB	53:B6:48:VAL:O	2.22	0.40
26:DA:2155:G:C2'	26:DA:2156:G:H5'	2.52	0.40
26:BA:1174:A:H1'	26:BA:1175:U:C5'	2.50	0.40
25:AY:58:A:O2'	25:AY:60:U:OP2	2.29	0.40
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.22	0.40
12:CL:27:LEU:HD23	12:CL:30:ALA:O	2.22	0.40
31:DG:115:ARG:HG2	31:DG:136:ARG:HH21	1.85	0.40
1:AA:936:C:H2'	1:AA:937:A:O4'	2.20	0.40
26:DA:856:C:H2'	26:DA:857:C:C6	2.56	0.40
51:D4:62:ARG:N	51:D4:62:ARG:HD3	2.35	0.40
26:DA:2022:U:OP2	52:D5:15:ARG:NH2	2.54	0.40
1:CA:1084:G:H1'	1:CA:1102:A:N7	2.36	0.40
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.55	0.40
26:DA:866:A:C6	26:DA:914:C:C5	3.10	0.40
1:CA:1286:A:H3'	1:CA:1286:A:H8	1.85	0.40
3:CC:29:TYR:CZ	14:CN:54:PRO:HG2	2.57	0.40
29:DE:85:ASN:HA	29:DE:86:PRO:HD2	1.84	0.40
7:CG:26:PHE:HE1	7:CG:30:ILE:HD11	1.87	0.40
42:DV:24:LYS:HA	42:DV:92:THR:OG1	2.21	0.40
1:AA:271:C:H2'	1:AA:272:C:H6	1.87	0.40
2:CB:28:PHE:O	2:CB:32:ILE:HG13	2.21	0.40
26:BA:570:G:H2'	26:BA:2030:A:N7	2.37	0.40
26:DA:1611:C:C2'	26:DA:1612:C:H5'	2.50	0.40
1:CA:630:G:O2'	1:CA:631:G:H5'	2.21	0.40
26:BA:2615:U:H2'	26:BA:2616:C:C6	2.56	0.40
4:AD:11:LEU:HG	4:AD:66:ARG:HD3	2.03	0.40
1:AA:189(F):U:C2	17:AQ:72:ARG:NH2	2.90	0.40
26:DA:234:C:H2'	26:DA:235:U:H6	1.87	0.40
26:DA:1669:A:H5''	26:DA:2550:G:OP1	2.21	0.40
46:DZ:79:ARG:HB2	46:DZ:80:ARG:NH1	2.36	0.40
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	2.04	0.40
34:DN:60:ILE:HG13	34:DN:61:ARG:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:923:C:H2'	26:BA:924:C:C6	2.56	0.40
1:CA:453:A:H4'	16:CP:72:ARG:HG3	2.02	0.40
28:BD:4:LYS:HB3	28:BD:18:VAL:HG23	2.04	0.40
20:AT:56:MET:HE3	20:AT:88:VAL:HG21	2.03	0.40
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.61	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.02	0.40
10:AJ:90:LEU:HA	10:AJ:91:PRO:HD3	1.92	0.40
1:CA:828:A:H4'	1:CA:828:A:OP1	2.21	0.40
33:DI:92:VAL:HG22	33:DI:120:ILE:HB	2.03	0.40
26:BA:2274:A:C5	26:BA:2276:G:C8	3.10	0.40
1:CA:697:U:H2'	1:CA:698:G:H5'	2.04	0.40
9:AI:33:PHE:HD1	9:AI:34:ASN:ND2	2.20	0.40
1:AA:542:G:O3'	4:AD:14:ARG:NH2	2.53	0.40
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.56	0.40
2:CB:16:HIS:ND1	2:CB:17:PHE:N	2.68	0.40
26:DA:2174:C:H2'	26:DA:2174:C:O2	2.21	0.40
26:DA:996:A:O3'	41:DU:91:ASP:HB2	2.22	0.40
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.04	0.40
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.21	0.40
26:DA:892:G:H2'	26:DA:893:C:C4'	2.52	0.40
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.57	0.40
49:D2:64:LEU:O	49:D2:68:ARG:HG3	2.22	0.40
2:AB:19:HIS:CG	2:AB:20:GLU:H	2.39	0.40
26:DA:570:G:H2'	26:DA:2030:A:C5	2.56	0.40
1:CA:1075:C:H42	1:CA:1082:G:H1	1.68	0.40
1:AA:148:G:H2'	1:AA:149:A:C8	2.50	0.40
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.05	0.40
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.20	0.40
26:BA:1406:U:H2'	26:BA:1407:C:H6	1.86	0.40
26:BA:589:C:H2'	26:BA:590:A:C8	2.56	0.40
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.52	0.40
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.20	0.40
24:AX:19:G:H5''	24:AX:60:U:O4	2.21	0.40
1:AA:390:C:H2'	1:AA:391:G:C8	2.56	0.40
2:CB:53:ARG:CZ	2:CB:53:ARG:HB3	2.50	0.40
26:BA:2070:G:H2'	26:BA:2071:A:C8	2.57	0.40
26:DA:443:A:H5''	26:DA:444:C:OP1	2.21	0.40
30:BF:64:ILE:HG13	30:BF:65:TRP:N	2.37	0.40
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.37	0.40
1:CA:1479:C:H2'	1:CA:1480:G:C8	2.56	0.40
26:DA:1486:A:O2'	26:DA:1487:G:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BV:49:THR:HG22	42:BV:49:THR:O	2.21	0.40
1:CA:57:G:H2'	1:CA:58:C:C6	2.57	0.40
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.21	0.40
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.72	0.40
50:D3:23:LEU:HD13	50:D3:50:VAL:HG11	2.02	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.57	0.40
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.22	0.40
26:BA:2398:U:H2'	26:BA:2399:G:C8	2.57	0.40
26:DA:428:A:H3'	26:DA:429:A:H8	1.87	0.40
40:DT:94:ALA:HB1	40:DT:99:LEU:HD21	2.02	0.40
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.52	0.40
26:DA:2462:U:H2'	26:DA:2463:C:C6	2.56	0.40
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.36	0.40
28:BD:19:ALA:HB3	28:BD:21:PHE:CE1	2.56	0.40
45:BY:83:THR:HG21	45:BY:99:CYS:HB2	2.02	0.40
24:CX:12:G:H4'	26:DA:1908:C:O2	2.21	0.40
26:DA:2756:U:H1'	26:DA:2757:A:H5''	2.02	0.40
8:CH:119:LEU:HB3	8:CH:123:GLU:CB	2.51	0.40
7:AG:14:PRO:HG3	7:AG:21:VAL:HG13	2.03	0.40
26:BA:2355:C:H5'	61:BA:3944:HOH:O	2.22	0.40
13:AM:97:PRO:HG2	13:AM:103:THR:HG22	2.04	0.40
8:CH:25:ASP:N	8:CH:25:ASP:OD1	2.55	0.40
2:AB:8:LYS:HG2	2:AB:8:LYS:H	1.51	0.40
3:CC:178:LEU:HA	3:CC:178:LEU:HD13	1.93	0.40
19:AS:15:LEU:O	19:AS:19:VAL:HG23	2.21	0.40
10:AJ:26:ALA:O	10:AJ:30:SER:OG	2.39	0.40
48:D1:5:CYS:SG	48:D1:62:VAL:HG23	2.62	0.40
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.57	0.40
26:DA:1241:A:O2'	26:DA:1242:A:H5'	2.21	0.40
25:AY:26:A:N1	25:AY:44:G:N2	2.54	0.40
1:AA:1002:G:C6	1:AA:1003:G:C2	3.10	0.40
25:CY:29:G:N1	25:CY:41:C:N4	2.69	0.40
1:CA:1154:G:O6	1:CA:1155:G:C6	2.75	0.40
14:CN:9:LYS:HG3	14:CN:12:ARG:HH11	1.86	0.40
26:DA:933:A:H2'	26:DA:934:G:O4'	2.22	0.40
26:DA:832:G:H5'	36:DP:45:LEU:HD21	2.04	0.40
30:BF:106:ARG:HG2	30:BF:106:ARG:H	1.70	0.40
3:AC:82:GLU:HA	3:AC:85:ARG:CZ	2.51	0.40
24:CX:66:C:H2'	24:CX:67:C:O4'	2.22	0.40
26:BA:674:G:O2'	30:BF:74:ARG:HD3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.22	0.40
6:AF:22:GLU:O	6:AF:26:ILE:HG13	2.22	0.40
2:CB:28:PHE:CD2	2:CB:190:THR:HA	2.56	0.40
26:DA:2294:C:P	39:DS:89:ARG:HH22	2.44	0.40
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	2.04	0.40
1:AA:1151:A:O2'	1:AA:1152:A:H8	2.05	0.40
13:AM:39:ILE:HG13	13:AM:56:LEU:HD12	2.03	0.40
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.20	0.40
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.02	0.40
26:BA:370:G:H4'	26:BA:371:A:OP2	2.21	0.40
4:AD:18:LYS:HE3	4:AD:20:TYR:CZ	2.56	0.40
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	2.02	0.40
6:AF:55:ASP:HA	6:AF:56:PRO:HD2	1.98	0.40
26:DA:1001:A:H2'	26:DA:1002:G:O4'	2.21	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.21	0.40
46:DZ:171:ILE:HG13	46:DZ:171:ILE:H	1.65	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.62	0.40
2:AB:215:LEU:HD23	2:AB:215:LEU:HA	1.79	0.40
1:AA:512:U:H2'	1:AA:513:C:C6	2.56	0.40
26:DA:56:A:H2'	26:DA:57:C:O4'	2.22	0.40
26:DA:305:U:H2'	26:DA:306:U:C6	2.56	0.40
51:D4:28:LYS:HA	51:D4:29:PRO:HD3	1.84	0.40
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.09	0.40
1:CA:243:A:C2	1:CA:246:A:C8	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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
2	AB	229/256 (90%)	208 (91%)	14 (6%)	7 (3%)	5 6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CB	229/256 (90%)	206 (90%)	16 (7%)	7 (3%)	5	6
3	AC	204/239 (85%)	195 (96%)	8 (4%)	1 (0%)	34	54
3	CC	204/239 (85%)	189 (93%)	15 (7%)	0	100	100
4	AD	206/209 (99%)	197 (96%)	7 (3%)	2 (1%)	19	33
4	CD	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	34	54
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
5	CE	146/162 (90%)	140 (96%)	6 (4%)	0	100	100
6	AF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
7	AG	153/156 (98%)	144 (94%)	5 (3%)	4 (3%)	7	9
7	CG	153/156 (98%)	144 (94%)	8 (5%)	1 (1%)	26	44
8	AH	135/138 (98%)	134 (99%)	1 (1%)	0	100	100
8	CH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
9	AI	125/128 (98%)	117 (94%)	8 (6%)	0	100	100
9	CI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	24	40
10	AJ	95/105 (90%)	85 (90%)	6 (6%)	4 (4%)	3	3
10	CJ	94/105 (90%)	85 (90%)	4 (4%)	5 (5%)	2	2
11	AK	112/129 (87%)	104 (93%)	6 (5%)	2 (2%)	11	17
11	CK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	11	17
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
12	CL	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
13	AM	121/126 (96%)	116 (96%)	5 (4%)	0	100	100
13	CM	120/126 (95%)	113 (94%)	7 (6%)	0	100	100
14	AN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	AP	80/88 (91%)	79 (99%)	1 (1%)	0	100	100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	15	25
17	AQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
19	AS	81/93 (87%)	73 (90%)	7 (9%)	1 (1%)	16	27
19	CS	81/93 (87%)	72 (89%)	9 (11%)	0	100	100
20	AT	94/106 (89%)	87 (93%)	3 (3%)	4 (4%)	3	3
20	CT	94/106 (89%)	88 (94%)	3 (3%)	3 (3%)	5	6
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
21	CU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
28	BD	273/276 (99%)	264 (97%)	8 (3%)	1 (0%)	39	60
28	DD	273/276 (99%)	263 (96%)	8 (3%)	2 (1%)	26	44
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	34	54
29	DE	202/206 (98%)	196 (97%)	4 (2%)	2 (1%)	19	33
30	BF	201/210 (96%)	200 (100%)	0	1 (0%)	34	54
30	DF	201/210 (96%)	199 (99%)	0	2 (1%)	19	33
31	BG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	30	48
31	DG	179/182 (98%)	171 (96%)	5 (3%)	3 (2%)	11	18
32	BH	172/180 (96%)	168 (98%)	3 (2%)	1 (1%)	30	48
32	DH	172/180 (96%)	166 (96%)	5 (3%)	1 (1%)	30	48
33	BI	144/148 (97%)	130 (90%)	11 (8%)	3 (2%)	9	13
33	DI	144/148 (97%)	133 (92%)	10 (7%)	1 (1%)	26	44
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
34	DN	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	26	44
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	DO	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
36	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	26	44
36	DP	147/150 (98%)	138 (94%)	7 (5%)	2 (1%)	14	23
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	26	44
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
39	BS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	21	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	DS	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	21	36
40	BT	129/146 (88%)	122 (95%)	7 (5%)	0	100	100
40	DT	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	114 (100%)	0	0	100	100
42	BV	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	19	33
43	BW	110/113 (97%)	110 (100%)	0	0	100	100
43	DW	110/113 (97%)	110 (100%)	0	0	100	100
44	BX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
44	DX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
45	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
45	DY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
46	BZ	169/206 (82%)	153 (90%)	15 (9%)	1 (1%)	30	48
46	DZ	172/206 (84%)	161 (94%)	11 (6%)	0	100	100
47	B0	81/85 (95%)	81 (100%)	0	0	100	100
47	D0	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	17	30
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	30
49	B2	68/72 (94%)	68 (100%)	0	0	100	100
49	D2	68/72 (94%)	68 (100%)	0	0	100	100
50	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	3	3
51	D4	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	1	1
52	B5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
52	D5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
53	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
53	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
54	B7	46/49 (94%)	46 (100%)	0	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	8	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	B8	62/65 (95%)	62 (100%)	0	0	100	100
55	D8	62/65 (95%)	62 (100%)	0	0	100	100
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10908 (96%)	416 (4%)	85 (1%)	26	44

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	126	GLU
7	AG	80	VAL
20	AT	10	LEU
20	AT	96	GLY
28	BD	275	LYS
29	BE	52	LEU
30	BF	130	ALA
33	BI	107	VAL
51	B4	55	ARG
2	CB	16	HIS
2	CB	20	GLU
2	CB	126	GLU
4	CD	46	LYS
9	CI	54	ASP
10	CJ	79	ARG
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
33	DI	10	GLU
36	DP	29	LYS
51	D4	39	CYS
51	D4	63	TYR
54	D7	46	VAL
2	AB	10	LEU
2	AB	19	HIS
4	AD	166	LYS
7	AG	8	GLU
7	AG	81	GLY
10	AJ	31	GLY
10	AJ	56	HIS
11	AK	49	GLY
20	AT	47	GLY

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Mol	Chain	Res	Type
33	BI	106	GLY
48	B1	3	LYS
51	B4	54	GLY
51	B4	57	GLU
2	CB	8	LYS
2	CB	9	GLU
10	CJ	56	HIS
10	CJ	77	PRO
11	CK	49	GLY
20	CT	47	GLY
20	CT	95	ALA
29	DE	52	LEU
31	DG	81	LYS
32	DH	126	PRO
37	DQ	28	ALA
51	D4	45	GLY
2	AB	20	GLU
4	AD	164	ALA
10	AJ	79	ARG
19	AS	42	PRO
20	AT	95	ALA
31	BG	47	LYS
32	BH	126	PRO
39	BS	60	GLY
46	BZ	152	ALA
11	CK	105	VAL
28	DD	239	ARG
34	DN	2	LYS
39	DS	84	GLN
33	BI	73	GLU
36	BP	29	LYS
2	CB	10	LEU
10	CJ	55	LYS
28	DD	3	VAL
31	DG	32	PRO
31	DG	47	LYS
36	DP	45	LEU
48	D1	3	LYS
51	D4	55	ARG
10	AJ	91	PRO
29	DE	73	GLU
51	D4	62	ARG

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Mol	Chain	Res	Type
2	AB	231	GLU
3	AC	66	VAL
2	CB	231	GLU
7	CG	17	VAL
16	CP	53	VAL
11	AK	105	VAL
2	AB	124	SER
10	CJ	91	PRO
42	DV	79	VAL
7	AG	17	VAL
2	AB	125	PRO

5.3.2 Protein sidechains ⓘ

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	
2	AB	192/220 (87%)	163 (85%)	29 (15%)	3	6
2	CB	187/220 (85%)	149 (80%)	38 (20%)	1	2
3	AC	143/188 (76%)	121 (85%)	22 (15%)	3	5
3	CC	140/188 (74%)	124 (89%)	16 (11%)	7	12
4	AD	170/181 (94%)	152 (89%)	18 (11%)	8	15
4	CD	173/181 (96%)	152 (88%)	21 (12%)	6	10
5	AE	113/123 (92%)	105 (93%)	8 (7%)	18	32
5	CE	114/123 (93%)	101 (89%)	13 (11%)	7	12
6	AF	83/90 (92%)	76 (92%)	7 (8%)	14	24
6	CF	85/90 (94%)	80 (94%)	5 (6%)	24	42
7	AG	119/127 (94%)	108 (91%)	11 (9%)	11	20
7	CG	120/127 (94%)	109 (91%)	11 (9%)	11	20
8	AH	114/119 (96%)	105 (92%)	9 (8%)	15	27
8	CH	114/119 (96%)	107 (94%)	7 (6%)	23	40
9	AI	90/99 (91%)	76 (84%)	14 (16%)	3	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	CI	89/99 (90%)	76 (85%)	13 (15%)	4	6
10	AJ	66/92 (72%)	58 (88%)	8 (12%)	6	10
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	13	22
11	AK	82/99 (83%)	77 (94%)	5 (6%)	23	40
11	CK	83/99 (84%)	76 (92%)	7 (8%)	14	24
12	AL	97/109 (89%)	93 (96%)	4 (4%)	37	61
12	CL	97/109 (89%)	93 (96%)	4 (4%)	37	61
13	AM	93/101 (92%)	82 (88%)	11 (12%)	6	11
13	CM	92/101 (91%)	80 (87%)	12 (13%)	5	9
14	AN	49/50 (98%)	42 (86%)	7 (14%)	4	7
14	CN	49/50 (98%)	41 (84%)	8 (16%)	3	4
15	AO	78/80 (98%)	64 (82%)	14 (18%)	2	3
15	CO	78/80 (98%)	69 (88%)	9 (12%)	7	12
16	AP	69/74 (93%)	60 (87%)	9 (13%)	5	9
16	CP	68/74 (92%)	61 (90%)	7 (10%)	9	15
17	AQ	94/97 (97%)	85 (90%)	9 (10%)	10	18
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	17	30
18	AR	59/77 (77%)	54 (92%)	5 (8%)	13	23
18	CR	59/77 (77%)	52 (88%)	7 (12%)	6	11
19	AS	69/80 (86%)	64 (93%)	5 (7%)	18	31
19	CS	67/80 (84%)	63 (94%)	4 (6%)	24	41
20	AT	70/82 (85%)	62 (89%)	8 (11%)	7	12
20	CT	70/82 (85%)	62 (89%)	8 (11%)	7	12
21	AU	18/22 (82%)	15 (83%)	3 (17%)	3	4
21	CU	18/22 (82%)	17 (94%)	1 (6%)	26	45
28	BD	215/218 (99%)	195 (91%)	20 (9%)	11	19
28	DD	215/218 (99%)	193 (90%)	22 (10%)	9	16
29	BE	164/166 (99%)	146 (89%)	18 (11%)	8	13
29	DE	164/166 (99%)	145 (88%)	19 (12%)	7	12
30	BF	160/166 (96%)	149 (93%)	11 (7%)	19	34
30	DF	159/166 (96%)	144 (91%)	15 (9%)	11	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	BG	143/156 (92%)	128 (90%)	15 (10%)	8	15
31	DG	142/156 (91%)	122 (86%)	20 (14%)	4	7
32	BH	144/148 (97%)	126 (88%)	18 (12%)	6	10
32	DH	144/148 (97%)	126 (88%)	18 (12%)	6	10
33	BI	110/124 (89%)	86 (78%)	24 (22%)	1	2
33	DI	104/124 (84%)	88 (85%)	16 (15%)	3	5
34	BN	118/119 (99%)	103 (87%)	15 (13%)	5	9
34	DN	118/119 (99%)	106 (90%)	12 (10%)	9	16
35	BO	100/100 (100%)	93 (93%)	7 (7%)	19	33
35	DO	100/100 (100%)	93 (93%)	7 (7%)	19	33
36	BP	115/116 (99%)	98 (85%)	17 (15%)	4	6
36	DP	115/116 (99%)	100 (87%)	15 (13%)	5	9
37	BQ	111/111 (100%)	95 (86%)	16 (14%)	4	6
37	DQ	111/111 (100%)	99 (89%)	12 (11%)	8	14
38	BR	101/101 (100%)	82 (81%)	19 (19%)	2	3
38	DR	101/101 (100%)	83 (82%)	18 (18%)	2	3
39	BS	87/88 (99%)	81 (93%)	6 (7%)	19	34
39	DS	85/88 (97%)	75 (88%)	10 (12%)	6	11
40	BT	115/127 (91%)	106 (92%)	9 (8%)	16	28
40	DT	113/127 (89%)	103 (91%)	10 (9%)	12	22
41	BU	93/94 (99%)	84 (90%)	9 (10%)	10	18
41	DU	93/94 (99%)	85 (91%)	8 (9%)	13	23
42	BV	80/82 (98%)	68 (85%)	12 (15%)	3	6
42	DV	80/82 (98%)	67 (84%)	13 (16%)	3	4
43	BW	90/92 (98%)	83 (92%)	7 (8%)	16	28
43	DW	90/92 (98%)	83 (92%)	7 (8%)	16	28
44	BX	77/78 (99%)	71 (92%)	6 (8%)	16	28
44	DX	77/78 (99%)	71 (92%)	6 (8%)	16	28
45	BY	85/91 (93%)	75 (88%)	10 (12%)	6	11
45	DY	85/91 (93%)	79 (93%)	6 (7%)	18	32
46	BZ	145/179 (81%)	133 (92%)	12 (8%)	14	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	DZ	145/179 (81%)	129 (89%)	16 (11%)	8	13
47	B0	65/67 (97%)	62 (95%)	3 (5%)	33	55
47	D0	65/67 (97%)	60 (92%)	5 (8%)	16	28
48	B1	80/83 (96%)	73 (91%)	7 (9%)	12	22
48	D1	80/83 (96%)	71 (89%)	9 (11%)	7	12
49	B2	65/67 (97%)	57 (88%)	8 (12%)	6	10
49	D2	65/67 (97%)	59 (91%)	6 (9%)	11	20
50	B3	51/52 (98%)	46 (90%)	5 (10%)	10	17
50	D3	50/52 (96%)	44 (88%)	6 (12%)	6	11
51	B4	60/63 (95%)	47 (78%)	13 (22%)	1	2
51	D4	53/63 (84%)	43 (81%)	10 (19%)	2	3
52	B5	50/52 (96%)	45 (90%)	5 (10%)	9	17
52	D5	50/52 (96%)	46 (92%)	4 (8%)	15	26
53	B6	51/52 (98%)	44 (86%)	7 (14%)	4	7
53	D6	50/52 (96%)	48 (96%)	2 (4%)	38	62
54	B7	41/42 (98%)	38 (93%)	3 (7%)	17	31
54	D7	41/42 (98%)	38 (93%)	3 (7%)	17	31
55	B8	53/55 (96%)	49 (92%)	4 (8%)	17	30
55	D8	54/55 (98%)	51 (94%)	3 (6%)	26	45
56	B9	34/34 (100%)	34 (100%)	0	100	100
56	D9	34/34 (100%)	32 (94%)	2 (6%)	24	42
All	All	9320/10066 (93%)	8304 (89%)	1016 (11%)	8	13

All (1016) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	10	LEU
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	21	ARG
2	AB	23	ARG
2	AB	24	TRP
2	AB	49	GLU

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Mol	Chain	Res	Type
2	AB	64	ARG
2	AB	67	THR
2	AB	76	GLN
2	AB	94	ASN
2	AB	108	ILE
2	AB	111	ARG
2	AB	114	ARG
2	AB	127	ILE
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	160	ASP
2	AB	170	GLU
2	AB	187	LEU
2	AB	200	ILE
2	AB	221	LEU
2	AB	230	VAL
3	AC	3	ASN
3	AC	26	LYS
3	AC	27	LYS
3	AC	28	GLN
3	AC	32	LEU
3	AC	37	GLN
3	AC	45	LYS
3	AC	49	SER
3	AC	70	VAL
3	AC	77	ILE
3	AC	97	LYS
3	AC	98	ASN
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	119	ARG
3	AC	127	ARG
3	AC	140	ARG
3	AC	144	SER
3	AC	181	ASN
3	AC	196	LEU
3	AC	198	VAL

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Mol	Chain	Res	Type
4	AD	5	ILE
4	AD	31	CYS
4	AD	49	ARG
4	AD	52	SER
4	AD	53	ASP
4	AD	58	LEU
4	AD	63	LYS
4	AD	86	LYS
4	AD	108	LEU
4	AD	122	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	139	ARG
4	AD	141	ARG
4	AD	144	ASP
4	AD	158	ILE
4	AD	168	ARG
4	AD	188	LEU
5	AE	6	PHE
5	AE	12	LEU
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	73	ASN
5	AE	145	LYS
6	AF	36	ARG
6	AF	40	VAL
6	AF	55	ASP
6	AF	69	GLU
6	AF	74	ASP
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	50	ILE
7	AG	51	GLN
7	AG	52	GLU
7	AG	53	LYS
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU

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Mol	Chain	Res	Type
7	AG	113	GLU
7	AG	155	ARG
8	AH	21	LYS
8	AH	29	SER
8	AH	39	LEU
8	AH	52	ASP
8	AH	78	GLN
8	AH	84	ARG
8	AH	109	ILE
8	AH	112	LEU
8	AH	127	LEU
9	AI	14	VAL
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	53	VAL
9	AI	56	LEU
9	AI	81	ILE
9	AI	86	VAL
9	AI	89	ASN
9	AI	103	THR
9	AI	108	VAL
9	AI	121	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	16	LEU
10	AJ	17	ASP
10	AJ	43	ARG
10	AJ	66	ARG
10	AJ	81	THR
10	AJ	84	GLN
10	AJ	94	VAL
10	AJ	100	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
12	AL	33	ARG
12	AL	46	LYS
12	AL	52	LEU
12	AL	83	VAL

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Mol	Chain	Res	Type
13	AM	4	ILE
13	AM	15	VAL
13	AM	27	LYS
13	AM	43	THR
13	AM	49	THR
13	AM	52	GLU
13	AM	70	LEU
13	AM	73	GLU
13	AM	84	ILE
13	AM	110	ARG
13	AM	121	LYS
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	23	ARG
14	AN	26	ARG
14	AN	32	SER
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	21	ASP
15	AO	22	THR
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN
15	AO	76	GLU
15	AO	83	GLU
15	AO	84	LYS
16	AP	1	MET
16	AP	2	VAL
16	AP	19	ILE
16	AP	20	VAL
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
17	AQ	14	LYS

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Mol	Chain	Res	Type
17	AQ	19	VAL
17	AQ	24	GLU
17	AQ	60	ILE
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	98	LEU
18	AR	31	LEU
18	AR	37	VAL
18	AR	38	GLU
18	AR	46	GLU
18	AR	76	LEU
19	AS	12	ASP
19	AS	28	LYS
19	AS	37	ARG
19	AS	65	ASN
19	AS	66	MET
20	AT	8	ARG
20	AT	9	ASN
20	AT	13	LEU
20	AT	24	LEU
20	AT	30	LYS
20	AT	45	GLN
20	AT	54	LYS
20	AT	62	LEU
21	AU	9	ARG
21	AU	10	ARG
21	AU	12	LYS
28	BD	12	SER
28	BD	13	ARG
28	BD	61	LEU
28	BD	88	ARG
28	BD	94	LEU
28	BD	99	ASP
28	BD	103	ARG
28	BD	113	VAL
28	BD	126	GLN
28	BD	138	VAL
28	BD	142	VAL
28	BD	155	LEU
28	BD	211	ARG

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Mol	Chain	Res	Type
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	242	ARG
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG
29	BE	1	MET
29	BE	14	ILE
29	BE	24	THR
29	BE	33	VAL
29	BE	49	LEU
29	BE	52	LEU
29	BE	73	GLU
29	BE	75	VAL
29	BE	77	ILE
29	BE	82	ARG
29	BE	97	LYS
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	203	LYS
30	BF	19	GLU
30	BF	24	LEU
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	125	LEU
30	BF	170	LEU
30	BF	192	LEU
30	BF	200	GLU
31	BG	7	LEU
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	81	LYS
31	BG	82	LEU

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Mol	Chain	Res	Type
31	BG	86	MET
31	BG	133	LEU
31	BG	135	LEU
31	BG	140	ILE
31	BG	143	GLU
31	BG	146	TYR
31	BG	148	MET
31	BG	170	ARG
31	BG	175	LEU
32	BH	6	ARG
32	BH	15	VAL
32	BH	33	LEU
32	BH	41	MET
32	BH	44	VAL
32	BH	45	VAL
32	BH	57	ASP
32	BH	59	ARG
32	BH	69	ARG
32	BH	71	LEU
32	BH	86	GLU
32	BH	95	ARG
32	BH	116	GLU
32	BH	119	GLU
32	BH	124	GLU
32	BH	125	VAL
32	BH	129	THR
32	BH	134	SER
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	38	LEU
33	BI	43	ASN
33	BI	47	LEU
33	BI	50	ARG
33	BI	57	ARG
33	BI	60	GLU
33	BI	61	ARG
33	BI	62	LYS
33	BI	66	GLU
33	BI	68	LEU
33	BI	75	LEU
33	BI	77	LEU

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Mol	Chain	Res	Type
33	BI	78	THR
33	BI	85	GLU
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	103	ARG
33	BI	117	GLU
33	BI	140	LEU
33	BI	142	VAL
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	46	VAL
34	BN	48	MET
34	BN	58	ASP
34	BN	61	ARG
34	BN	67	LEU
34	BN	73	THR
34	BN	83	LYS
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	133	GLN
34	BN	139	GLU
35	BO	8	LEU
35	BO	23	ARG
35	BO	24	VAL
35	BO	69	ILE
35	BO	92	GLU
35	BO	94	ARG
35	BO	108	GLU
36	BP	1	MET
36	BP	2	LYS
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	70	GLN
36	BP	76	LYS
36	BP	77	ARG
36	BP	83	VAL
36	BP	95	VAL
36	BP	98	GLU

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Mol	Chain	Res	Type
36	BP	106	LEU
36	BP	112	LEU
36	BP	119	GLU
36	BP	126	VAL
36	BP	148	LEU
36	BP	149	GLU
37	BQ	1	MET
37	BQ	5	ARG
37	BQ	7	MET
37	BQ	10	ARG
37	BQ	16	ARG
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	54	MET
37	BQ	56	ARG
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR
37	BQ	85	LYS
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	6	SER
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	60	LEU
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	20	ARG

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Mol	Chain	Res	Type
39	BS	57	LYS
39	BS	59	LYS
39	BS	67	ARG
39	BS	83	LYS
39	BS	110	LEU
40	BT	17	THR
40	BT	28	VAL
40	BT	34	VAL
40	BT	49	VAL
40	BT	53	ARG
40	BT	78	LEU
40	BT	96	ARG
40	BT	108	ARG
40	BT	118	ARG
41	BU	8	VAL
41	BU	31	SER
41	BU	36	ARG
41	BU	74	LEU
41	BU	83	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
41	BU	117	GLN
42	BV	28	GLU
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
42	BV	85	LYS
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	15	ARG
43	BW	17	VAL
43	BW	51	LEU
43	BW	67	ASP
43	BW	100	THR

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Mol	Chain	Res	Type
44	BX	35	THR
44	BX	45	THR
44	BX	57	LEU
44	BX	66	LEU
44	BX	72	LYS
44	BX	88	LYS
45	BY	1	MET
45	BY	2	ARG
45	BY	23	ARG
45	BY	34	LYS
45	BY	43	ASN
45	BY	55	TYR
45	BY	72	VAL
45	BY	90	LEU
45	BY	91	GLU
45	BY	99	CYS
46	BZ	5	LEU
46	BZ	19	ARG
46	BZ	40	ASP
46	BZ	72	ARG
46	BZ	86	VAL
46	BZ	91	LEU
46	BZ	120	ILE
46	BZ	136	PHE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	170	THR
47	B0	20	ARG
47	B0	55	ARG
47	B0	82	ARG
48	B1	21	ARG
48	B1	40	ARG
48	B1	52	ARG
48	B1	59	THR
48	B1	78	LYS
48	B1	95	LEU
48	B1	98	LEU
49	B2	3	LEU
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU

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Mol	Chain	Res	Type
49	B2	45	SER
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	8	LEU
50	B3	23	LEU
50	B3	29	ARG
50	B3	32	GLN
50	B3	55	ARG
51	B4	28	LYS
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	50	VAL
51	B4	53	GLU
51	B4	55	ARG
51	B4	56	VAL
51	B4	58	ARG
51	B4	59	PHE
51	B4	61	ARG
51	B4	63	TYR
51	B4	68	ARG
52	B5	16	ARG
52	B5	29	THR
52	B5	40	LYS
52	B5	55	ARG
52	B5	60	VAL
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
53	B6	52	VAL
54	B7	1	MET
54	B7	24	THR
54	B7	43	THR
55	B8	13	ARG
55	B8	14	VAL
55	B8	31	HIS
55	B8	34	TRP
2	CB	11	LEU

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Mol	Chain	Res	Type
2	CB	16	HIS
2	CB	17	PHE
2	CB	24	TRP
2	CB	35	GLU
2	CB	39	ILE
2	CB	50	GLU
2	CB	55	PHE
2	CB	67	THR
2	CB	71	VAL
2	CB	76	GLN
2	CB	82	ARG
2	CB	87	ARG
2	CB	96	ARG
2	CB	97	TRP
2	CB	98	LEU
2	CB	114	ARG
2	CB	115	LEU
2	CB	117	GLU
2	CB	124	SER
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	144	ARG
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	160	ASP
2	CB	163	PHE
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	209	ARG
2	CB	210	SER
2	CB	217	ARG
2	CB	221	LEU
2	CB	224	GLN
2	CB	230	VAL
3	CC	3	ASN
3	CC	21	ARG
3	CC	35	GLU
3	CC	49	SER
3	CC	70	VAL

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Mol	Chain	Res	Type
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	118	GLN
3	CC	140	ARG
3	CC	152	ILE
3	CC	179	ARG
3	CC	196	LEU
3	CC	198	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	86	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	115	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	155	LEU
4	CD	157	LEU
4	CD	168	ARG
4	CD	170	VAL
4	CD	181	MET
4	CD	187	ARG
4	CD	188	LEU
4	CD	194	LEU
5	CE	6	PHE
5	CE	10	MET
5	CE	12	LEU
5	CE	27	ARG
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	60	TYR
5	CE	67	VAL

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Mol	Chain	Res	Type
5	CE	79	GLU
5	CE	137	GLU
5	CE	150	ARG
6	CF	28	ARG
6	CF	40	VAL
6	CF	41	GLU
6	CF	46	ARG
6	CF	75	LEU
7	CG	9	VAL
7	CG	12	LEU
7	CG	32	ARG
7	CG	33	ASP
7	CG	51	GLN
7	CG	52	GLU
7	CG	72	ARG
7	CG	73	MET
7	CG	76	ARG
7	CG	79	ARG
7	CG	155	ARG
8	CH	21	LYS
8	CH	29	SER
8	CH	39	LEU
8	CH	84	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	112	LEU
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN
9	CI	50	LEU
9	CI	56	LEU
9	CI	81	ILE
9	CI	89	ASN
9	CI	102	LEU
9	CI	108	VAL
9	CI	112	LYS
9	CI	121	ARG
9	CI	125	TYR
9	CI	128	ARG
10	CJ	7	LYS
10	CJ	19	SER
10	CJ	29	ARG

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Mol	Chain	Res	Type
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
11	CK	24	SER
11	CK	31	THR
11	CK	48	ILE
11	CK	51	LYS
11	CK	54	ARG
11	CK	96	ARG
11	CK	104	GLN
12	CL	38	THR
12	CL	60	LEU
12	CL	83	VAL
12	CL	116	SER
13	CM	3	ARG
13	CM	15	VAL
13	CM	19	LEU
13	CM	47	ASP
13	CM	49	THR
13	CM	56	LEU
13	CM	84	ILE
13	CM	103	THR
13	CM	104	ARG
13	CM	110	ARG
13	CM	117	VAL
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	12	ARG
14	CN	18	VAL
14	CN	23	ARG
14	CN	26	ARG
14	CN	32	SER
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	7	GLU
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	48	LYS

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Mol	Chain	Res	Type
15	CO	54	ARG
16	CP	2	VAL
16	CP	5	ARG
16	CP	27	LYS
16	CP	60	LEU
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	19	VAL
17	CQ	36	ILE
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	74	LEU
17	CQ	96	GLU
18	CR	26	LEU
18	CR	32	ARG
18	CR	35	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	46	GLU
18	CR	76	LEU
19	CS	28	LYS
19	CS	37	ARG
19	CS	56	GLN
19	CS	78	ARG
20	CT	24	LEU
20	CT	38	LYS
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	10	ARG
28	DD	3	VAL
28	DD	13	ARG
28	DD	54	ARG
28	DD	61	LEU
28	DD	88	ARG
28	DD	94	LEU
28	DD	103	ARG

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Mol	Chain	Res	Type
28	DD	106	ILE
28	DD	113	VAL
28	DD	134	ARG
28	DD	142	VAL
28	DD	155	LEU
28	DD	162	SER
28	DD	193	VAL
28	DD	211	ARG
28	DD	217	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG
28	DD	276	LYS
29	DE	1	MET
29	DE	12	THR
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	40	GLU
29	DE	47	VAL
29	DE	52	LEU
29	DE	73	GLU
29	DE	75	VAL
29	DE	79	ARG
29	DE	82	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	195	LEU
30	DF	19	GLU
30	DF	20	LEU
30	DF	24	LEU
30	DF	28	ILE
30	DF	38	ARG
30	DF	57	VAL
30	DF	74	ARG
30	DF	82	ILE

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Mol	Chain	Res	Type
30	DF	88	VAL
30	DF	106	ARG
30	DF	135	LYS
30	DF	170	LEU
30	DF	192	LEU
30	DF	197	ASP
30	DF	200	GLU
31	DG	16	ARG
31	DG	21	ARG
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	49	ASP
31	DG	58	GLN
31	DG	60	LEU
31	DG	84	LYS
31	DG	98	ARG
31	DG	115	ARG
31	DG	133	LEU
31	DG	135	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	145	THR
31	DG	148	MET
31	DG	153	ARG
31	DG	170	ARG
32	DH	2	SER
32	DH	3	ARG
32	DH	15	VAL
32	DH	33	LEU
32	DH	43	VAL
32	DH	44	VAL
32	DH	45	VAL
32	DH	57	ASP
32	DH	63	SER
32	DH	69	ARG
32	DH	84	SER
32	DH	86	GLU
32	DH	95	ARG
32	DH	106	THR
32	DH	124	GLU

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Mol	Chain	Res	Type
32	DH	134	SER
32	DH	136	ILE
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	19	VAL
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	50	ARG
33	DI	68	LEU
33	DI	73	GLU
33	DI	86	THR
33	DI	92	VAL
33	DI	114	LEU
33	DI	121	LYS
33	DI	123	LEU
33	DI	140	LEU
33	DI	142	VAL
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	58	ASP
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	99	LEU
34	DN	120	LEU
34	DN	137	LYS
34	DN	139	GLU
35	DO	8	LEU
35	DO	9	GLU
35	DO	23	ARG
35	DO	24	VAL
35	DO	69	ILE
35	DO	92	GLU
35	DO	94	ARG
36	DP	1	MET
36	DP	29	LYS
36	DP	45	LEU
36	DP	50	ARG

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Mol	Chain	Res	Type
36	DP	55	ARG
36	DP	65	ARG
36	DP	70	GLN
36	DP	95	VAL
36	DP	96	THR
36	DP	99	LEU
36	DP	106	LEU
36	DP	112	LEU
36	DP	119	GLU
36	DP	131	SER
36	DP	148	LEU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET
37	DQ	56	ARG
37	DQ	59	ARG
37	DQ	60	ARG
37	DQ	65	PHE
37	DQ	75	THR
37	DQ	85	LYS
37	DQ	110	THR
38	DR	1	MET
38	DR	15	SER
38	DR	18	LEU
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU
38	DR	60	LEU
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU
38	DR	102	GLU
38	DR	111	LEU
38	DR	114	VAL
39	DS	20	ARG

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Mol	Chain	Res	Type
39	DS	35	ILE
39	DS	57	LYS
39	DS	69	VAL
39	DS	71	ARG
39	DS	75	GLU
39	DS	93	LYS
39	DS	101	LEU
39	DS	103	GLU
39	DS	110	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	23	ARG
40	DT	49	VAL
40	DT	53	ARG
40	DT	78	LEU
40	DT	96	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	8	VAL
41	DU	36	ARG
41	DU	74	LEU
41	DU	83	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	104	GLN
41	DU	108	GLU
42	DV	6	LYS
42	DV	15	GLU
42	DV	18	LEU
42	DV	38	LEU
42	DV	46	VAL
42	DV	51	VAL
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	95	LEU
42	DV	100	ARG
43	DW	11	ARG
43	DW	15	ARG

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Mol	Chain	Res	Type
43	DW	17	VAL
43	DW	51	LEU
43	DW	52	GLU
43	DW	60	ASN
43	DW	100	THR
44	DX	57	LEU
44	DX	70	LEU
44	DX	72	LYS
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	11	ASP
45	DY	23	ARG
45	DY	90	LEU
45	DY	91	GLU
45	DY	99	CYS
45	DY	107	ASP
46	DZ	5	LEU
46	DZ	18	LEU
46	DZ	35	ARG
46	DZ	40	ASP
46	DZ	41	LEU
46	DZ	72	ARG
46	DZ	86	VAL
46	DZ	97	GLU
46	DZ	102	LEU
46	DZ	119	GLU
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	153	SER
46	DZ	154	ASP
46	DZ	155	LEU
46	DZ	159	PRO
47	D0	10	THR
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
47	D0	55	ARG
48	D1	4	VAL
48	D1	21	ARG
48	D1	30	VAL
48	D1	40	ARG

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Mol	Chain	Res	Type
48	D1	52	ARG
48	D1	59	THR
48	D1	95	LEU
48	D1	97	LEU
48	D1	98	LEU
49	D2	21	LEU
49	D2	28	LYS
49	D2	30	ARG
49	D2	45	SER
49	D2	55	ARG
49	D2	70	GLN
50	D3	3	ARG
50	D3	8	LEU
50	D3	24	LYS
50	D3	30	ARG
50	D3	44	ARG
50	D3	55	ARG
51	D4	24	THR
51	D4	34	GLU
51	D4	44	THR
51	D4	50	VAL
51	D4	56	VAL
51	D4	58	ARG
51	D4	61	ARG
51	D4	63	TYR
51	D4	67	TYR
51	D4	68	ARG
52	D5	29	THR
52	D5	40	LYS
52	D5	55	ARG
52	D5	60	VAL
53	D6	6	ARG
53	D6	38	LYS
54	D7	1	MET
54	D7	14	LYS
54	D7	23	ARG
55	D8	13	ARG
55	D8	14	VAL
55	D8	34	TRP
56	D9	7	VAL
56	D9	26	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (130) such

sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
4	AD	161	ASN
5	AE	20	GLN
5	AE	38	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	34	ASN
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
13	AM	92	HIS
15	AO	9	GLN
15	AO	28	GLN
15	AO	46	HIS
15	AO	71	GLN
16	AP	76	GLN
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS
20	AT	9	ASN
20	AT	90	GLN

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Mol	Chain	Res	Type
28	BD	87	ASN
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
31	BG	26	GLN
31	BG	40	ASN
33	BI	43	ASN
33	BI	54	GLN
35	BO	5	GLN
36	BP	38	GLN
38	BR	71	GLN
40	BT	43	GLN
40	BT	58	ASN
40	BT	123	GLN
41	BU	94	ASN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	43	ASN
49	B2	9	GLN
49	B2	70	GLN
51	B4	46	GLN
56	B9	36	GLN
2	CB	40	HIS
2	CB	94	ASN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	69	HIS
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	77	ASN
4	CD	119	GLN
4	CD	123	HIS
4	CD	125	HIS
4	CD	161	ASN
5	CE	20	GLN

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Mol	Chain	Res	Type
5	CE	141	GLN
6	CF	94	GLN
7	CG	28	ASN
7	CG	51	GLN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	89	ASN
9	CI	124	GLN
10	CJ	62	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
13	CM	92	HIS
15	CO	28	GLN
15	CO	62	GLN
19	CS	56	GLN
19	CS	57	HIS
19	CS	65	ASN
19	CS	69	HIS
19	CS	83	HIS
28	DD	96	HIS
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	85	ASN
30	DF	69	HIS
30	DF	169	ASN
30	DF	203	GLN
31	DG	26	GLN
31	DG	40	ASN
33	DI	43	ASN
38	DR	71	GLN
39	DS	68	GLN
40	DT	58	ASN
40	DT	123	GLN
41	DU	117	GLN
42	DV	64	HIS
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN

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Mol	Chain	Res	Type
46	DZ	55	HIS
46	DZ	151	HIS
56	D9	20	HIS
56	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	304 (20%)	25 (1%)
1	CA	1501/1521 (98%)	316 (21%)	28 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	2 (18%)	0
23	AW	70/76 (92%)	30 (42%)	2 (2%)
23	CW	67/76 (88%)	32 (47%)	2 (2%)
24	AX	75/77 (97%)	16 (21%)	0
24	CX	75/77 (97%)	21 (28%)	0
25	AY	71/76 (93%)	35 (49%)	4 (5%)
25	CY	69/76 (90%)	32 (46%)	1 (1%)
26	BA	2811/2915 (96%)	450 (16%)	34 (1%)
26	DA	2791/2915 (95%)	552 (19%)	30 (1%)
27	BB	119/121 (98%)	14 (11%)	0
27	DB	119/121 (98%)	17 (14%)	0
All	All	9286/9620 (96%)	1824 (19%)	126 (1%)

All (1824) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	73	G

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Mol	Chain	Res	Type
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	101	A
1	AA	111	G
1	AA	112	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	146	G
1	AA	155	C
1	AA	163	C
1	AA	166	G
1	AA	173	U
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	279	A
1	AA	289	G

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Mol	Chain	Res	Type
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	412	A
1	AA	414	A
1	AA	421	U
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	484	G
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C

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Mol	Chain	Res	Type
1	AA	518	C
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	592	G
1	AA	596	C
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	649	G
1	AA	653	A
1	AA	665	A
1	AA	673	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	695	A
1	AA	711	G
1	AA	712	A
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	753	A
1	AA	755	G
1	AA	774	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	815	A

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Mol	Chain	Res	Type
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	833	U
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	874	G
1	AA	902	G
1	AA	914	A
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1019	C

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Mol	Chain	Res	Type
1	AA	1021	G
1	AA	1022	G
1	AA	1023	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(B)	C
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1037	C
1	AA	1039	C
1	AA	1043	C
1	AA	1044	A
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1097	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1110	A
1	AA	1113	C
1	AA	1124	G
1	AA	1126	U
1	AA	1130	A
1	AA	1132	C

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Mol	Chain	Res	Type
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1224	G
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1286	A
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U

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Mol	Chain	Res	Type
1	AA	1305	G
1	AA	1314	C
1	AA	1317	C
1	AA	1322	C
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1355	G
1	AA	1360	A
1	AA	1363	C
1	AA	1364	U
1	AA	1370	G
1	AA	1397	C
1	AA	1402	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1519	A
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	14	A
22	AV	24	A
23	AW	2	C

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Mol	Chain	Res	Type
23	AW	3	C
23	AW	4	C
23	AW	8	4SU
23	AW	12	U
23	AW	14	A
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G
23	AW	23	A
23	AW	24	G
23	AW	26	A
23	AW	27	G
23	AW	30	G
23	AW	42	C
23	AW	43	C
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	52	G
23	AW	53	G
23	AW	59	U
23	AW	61	C
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	3	C
24	AX	9	G
24	AX	13	C
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	42	G
24	AX	48	C
24	AX	56	C
24	AX	59	A
24	AX	63	G
24	AX	67	C

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Mol	Chain	Res	Type
24	AX	68	C
24	AX	70	G
24	AX	76	A
25	AY	2	C
25	AY	5	G
25	AY	9	A
25	AY	11	C
25	AY	13	C
25	AY	15	G
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	22	G
25	AY	26	A
25	AY	29	G
25	AY	30	G
25	AY	33	U
25	AY	34	G
25	AY	35	A
25	AY	36	A
25	AY	39	PSU
25	AY	41	C
25	AY	44	G
25	AY	45	U
25	AY	46	7MG
25	AY	47	U
25	AY	48	C
25	AY	49	C
25	AY	54	5MU
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	62	C
25	AY	65	G
25	AY	67	C
25	AY	70	G
25	AY	73	A
26	BA	12	U
26	BA	34	C
26	BA	36	G
26	BA	45	C

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Mol	Chain	Res	Type
26	BA	64	A
26	BA	71	A
26	BA	72	U
26	BA	74	A
26	BA	75	G
26	BA	84	A
26	BA	95	G
26	BA	99	U
26	BA	100	G
26	BA	102	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	151	C
26	BA	154(A)	C
26	BA	172	C
26	BA	181	A
26	BA	182	A
26	BA	188	G
26	BA	196	A
26	BA	197	A
26	BA	199	A
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	223	A
26	BA	229	A
26	BA	233	A
26	BA	248	G
26	BA	271(E)	U
26	BA	271(I)	G
26	BA	271(K)	U
26	BA	271(L)	U
26	BA	271(M)	G
26	BA	271(N)	U
26	BA	271(S)	G
26	BA	272(A)	U
26	BA	272(B)	G
26	BA	272(G)	C
26	BA	272(I)	U

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Mol	Chain	Res	Type
26	BA	279	C
26	BA	282	A
26	BA	283	A
26	BA	311	A
26	BA	329	G
26	BA	330	A
26	BA	352	G
26	BA	363	G
26	BA	363(B)	G
26	BA	372	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	405	U
26	BA	411	G
26	BA	428	A
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	454	A
26	BA	456	C
26	BA	470	A
26	BA	479	A
26	BA	481	G
26	BA	504	U
26	BA	505	A
26	BA	509	C
26	BA	528	A
26	BA	529	A
26	BA	530	G
26	BA	531	C
26	BA	532	A
26	BA	533	G
26	BA	545	G
26	BA	549	G
26	BA	563	G
26	BA	573	G
26	BA	575	A
26	BA	592	G
26	BA	603	A
26	BA	604	G
26	BA	607	U

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Mol	Chain	Res	Type
26	BA	614(A)	U
26	BA	614(B)	G
26	BA	615	G
26	BA	616	G
26	BA	627	A
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	652(F)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	669	G
26	BA	677	A
26	BA	686	G
26	BA	730	C
26	BA	732	C
26	BA	764	A
26	BA	765	G
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	784	A
26	BA	785	G
26	BA	792	G
26	BA	805	G
26	BA	812	C
26	BA	819	A
26	BA	824	A
26	BA	827	U
26	BA	828	U
26	BA	830	G
26	BA	855	G
26	BA	859	G
26	BA	862	G
26	BA	866	A
26	BA	877	U
26	BA	879	G
26	BA	880	G
26	BA	882	G
26	BA	884	C
26	BA	885	C
26	BA	886	C

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Mol	Chain	Res	Type
26	BA	887	A
26	BA	888	C
26	BA	889	C
26	BA	890	A
26	BA	892	G
26	BA	893	C
26	BA	894	C
26	BA	895	U
26	BA	896	A
26	BA	897	C
26	BA	898	C
26	BA	899	A
26	BA	900	A
26	BA	901	A
26	BA	907	U
26	BA	910	A
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	958	U
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	983	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C
26	BA	1022	G
26	BA	1033	U
26	BA	1038	C
26	BA	1041	C
26	BA	1045	A
26	BA	1046	A
26	BA	1047	G
26	BA	1048	A
26	BA	1051	G
26	BA	1107	G
26	BA	1108	U
26	BA	1110	G
26	BA	1112	G

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Mol	Chain	Res	Type
26	BA	1128	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1170	G
26	BA	1171	G
26	BA	1173	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1177	A
26	BA	1178	C
26	BA	1210	A
26	BA	1211	U
26	BA	1220	A
26	BA	1244	G
26	BA	1248	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A
26	BA	1273	U
26	BA	1289	C
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1314	C
26	BA	1319	G
26	BA	1352	U
26	BA	1359	A
26	BA	1360	A
26	BA	1365	A
26	BA	1370	C
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1416	G
26	BA	1417	C
26	BA	1420	U
26	BA	1421	G
26	BA	1428	C
26	BA	1445	A

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Mol	Chain	Res	Type
26	BA	1449	A
26	BA	1450	G
26	BA	1459	G
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1484	G
26	BA	1493	C
26	BA	1507	A
26	BA	1508	A
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1531	C
26	BA	1538	G
26	BA	1543	C
26	BA	1558	A
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U
26	BA	1580	A
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1648	C
26	BA	1654	A
26	BA	1664	A
26	BA	1674	G
26	BA	1694	C
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1722	A
26	BA	1739	U
26	BA	1746	G
26	BA	1748	G
26	BA	1756	G
26	BA	1759	A
26	BA	1762	A
26	BA	1763	G

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Mol	Chain	Res	Type
26	BA	1764	G
26	BA	1773	A
26	BA	1780	A
26	BA	1782	C
26	BA	1786	A
26	BA	1791	A
26	BA	1800	C
26	BA	1816	G
26	BA	1839	G
26	BA	1847	A
26	BA	1848	A
26	BA	1861	G
26	BA	1877	A
26	BA	1878	G
26	BA	1886	C
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1915	U
26	BA	1919	A
26	BA	1924	C
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1937	A
26	BA	1938	A
26	BA	1955	U
26	BA	1963	U
26	BA	1967	C
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1992	G
26	BA	1993	U
26	BA	1997	G
26	BA	2020	A
26	BA	2023	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2043	C
26	BA	2055	C

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Mol	Chain	Res	Type
26	BA	2056	G
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2069	G
26	BA	2098	U
26	BA	2102	U
26	BA	2110	G
26	BA	2111	C
26	BA	2119	A
26	BA	2120	G
26	BA	2121	G
26	BA	2125	G
26	BA	2126	A
26	BA	2127	G
26	BA	2128	C
26	BA	2129	C
26	BA	2132	U
26	BA	2133	G
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2138	C
26	BA	2140	C
26	BA	2141	G
26	BA	2142	C
26	BA	2143	C
26	BA	2145	C
26	BA	2146	C
26	BA	2147	G
26	BA	2149	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2165	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A
26	BA	2171	A
26	BA	2172	U
26	BA	2173	A

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Mol	Chain	Res	Type
26	BA	2174	C
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2192	G
26	BA	2198	A
26	BA	2199	A
26	BA	2206	G
26	BA	2207	G
26	BA	2208	A
26	BA	2218	U
26	BA	2225	A
26	BA	2238	G
26	BA	2239	G
26	BA	2268	A
26	BA	2269	A
26	BA	2275	C
26	BA	2283	C
26	BA	2287	A
26	BA	2289	G
26	BA	2305	A
26	BA	2308	G
26	BA	2320	A
26	BA	2325	G
26	BA	2334	G
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A
26	BA	2383	G
26	BA	2385	C
26	BA	2393	A
26	BA	2400	G
26	BA	2406	U
26	BA	2414	G
26	BA	2419	U
26	BA	2425	A
26	BA	2429	G

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Mol	Chain	Res	Type
26	BA	2430	A
26	BA	2435	A
26	BA	2439	A
26	BA	2441	C
26	BA	2448	A
26	BA	2464	C
26	BA	2468	G
26	BA	2469	A
26	BA	2471	C
26	BA	2474	C
26	BA	2476	A
26	BA	2487	G
26	BA	2490	G
26	BA	2502	G
26	BA	2505	G
26	BA	2518	A
26	BA	2529	G
26	BA	2535	G
26	BA	2549	G
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2574	G
26	BA	2602	A
26	BA	2609	U
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2654	A
26	BA	2669	G
26	BA	2689	U
26	BA	2690	C
26	BA	2691	C
26	BA	2702	U
26	BA	2712(A)	A
26	BA	2713	A
26	BA	2726	U
26	BA	2733	A
26	BA	2757	A
26	BA	2758	A

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Mol	Chain	Res	Type
26	BA	2761	G
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A
26	BA	2790	A
26	BA	2791	C
26	BA	2792	G
26	BA	2793	G
26	BA	2802	G
26	BA	2805	G
26	BA	2808	U
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A
26	BA	2833	G
26	BA	2834	G
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2876	G
26	BA	2880	C
26	BA	2882	A
26	BA	2883	A
26	BA	2892	A
26	BA	2894	G
27	BB	2	C
27	BB	7	G
27	BB	34	U
27	BB	42	C
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	93	G
27	BB	106	G
27	BB	110	G
27	BB	111	G
27	BB	112	U
27	BB	120	A
1	CA	5	U
1	CA	6	G

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Mol	Chain	Res	Type
1	CA	7	G
1	CA	9	G
1	CA	13	U
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	77	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	100	C
1	CA	101	A
1	CA	111	G
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	146	G
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(K)	U
1	CA	190	U
1	CA	195	A

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Mol	Chain	Res	Type
1	CA	197	A
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	279	A
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	346	G
1	CA	350	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	382	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A

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Mol	Chain	Res	Type
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	461	A
1	CA	471	G
1	CA	484	G
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	545	C
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	592	G
1	CA	596	C
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	649	G
1	CA	650	G
1	CA	653	A
1	CA	664	G
1	CA	665	A
1	CA	673	G
1	CA	680	C
1	CA	687	A
1	CA	688	G

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Mol	Chain	Res	Type
1	CA	693	G
1	CA	695	A
1	CA	711	G
1	CA	712	A
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	753	A
1	CA	755	G
1	CA	774	G
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	815	A
1	CA	817	C
1	CA	821	G
1	CA	828	A
1	CA	833	U
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	935	A
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	974	A
1	CA	975	A

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Mol	Chain	Res	Type
1	CA	976	G
1	CA	977	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	997	U
1	CA	1000	U
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1009	G
1	CA	1019	C
1	CA	1021	G
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1031	G
1	CA	1032	G
1	CA	1037	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G

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Mol	Chain	Res	Type
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1097	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1109	C
1	CA	1110	A
1	CA	1113	C
1	CA	1117	G
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
1	CA	1131	G
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1183	A
1	CA	1184	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1224	G

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Mol	Chain	Res	Type
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1286	A
1	CA	1287	A
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1314	C
1	CA	1317	C
1	CA	1322	C
1	CA	1338	G
1	CA	1340	A
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1355	G
1	CA	1363	C
1	CA	1364	U
1	CA	1370	G
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A

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Mol	Chain	Res	Type
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1456	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1519	A
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	24	A
23	CW	3	C
23	CW	4	C
23	CW	5	G
23	CW	6	G
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	14	A
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	25	C
23	CW	26	A
23	CW	27	G
23	CW	30	G
23	CW	42	C
23	CW	43	C
23	CW	45	U
23	CW	46	7MG
23	CW	47	U

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Mol	Chain	Res	Type
23	CW	48	C
23	CW	49	C
23	CW	52	G
23	CW	53	G
23	CW	61	C
23	CW	62	C
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	70	G
23	CW	74	C
24	CX	8	4SU
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	31	G
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	50	U
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	63	G
24	CX	67	C
24	CX	68	C
24	CX	76	A
25	CY	2	C
25	CY	8	4SU
25	CY	9	A
25	CY	11	C
25	CY	13	C
25	CY	15	G
25	CY	19	G
25	CY	23	A
25	CY	27	G

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Mol	Chain	Res	Type
25	CY	29	G
25	CY	30	G
25	CY	33	U
25	CY	34	G
25	CY	35	A
25	CY	36	A
25	CY	39	PSU
25	CY	41	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G
25	CY	54	5MU
25	CY	56	C
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	70	G
25	CY	73	A
26	DA	10	G
26	DA	12	U
26	DA	15	G
26	DA	16	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	51	G
26	DA	61	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	95	G
26	DA	100	G
26	DA	102	G

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Mol	Chain	Res	Type
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	173	G
26	DA	181	A
26	DA	182	A
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	214	G
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	225	A
26	DA	228	A
26	DA	229	A
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(V)	G
26	DA	271(W)	G
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	272(C)	G
26	DA	272(J)	C
26	DA	274	G
26	DA	277	C
26	DA	278	A
26	DA	285	C
26	DA	288	C
26	DA	292	C
26	DA	294	A
26	DA	311	A

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Mol	Chain	Res	Type
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	333	G
26	DA	352	G
26	DA	363	G
26	DA	372	G
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	399	G
26	DA	405	U
26	DA	407	G
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	421	U
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	447	A
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	481	G
26	DA	485	C
26	DA	494	G
26	DA	498	G
26	DA	504	U
26	DA	505	A
26	DA	509	C
26	DA	521	G
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	545	G
26	DA	563	G
26	DA	568	U

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Mol	Chain	Res	Type
26	DA	573	G
26	DA	574	C
26	DA	575	A
26	DA	586	A
26	DA	587	C
26	DA	588	U
26	DA	592	G
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	614(C)	A
26	DA	615	G
26	DA	616	G
26	DA	620	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(D)	C
26	DA	652(U)	G
26	DA	656	G
26	DA	668	G
26	DA	669	G
26	DA	686	G
26	DA	698	C
26	DA	699	A
26	DA	715	G
26	DA	726	G
26	DA	730	C
26	DA	752	A
26	DA	753	C
26	DA	765	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C

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Mol	Chain	Res	Type
26	DA	792	G
26	DA	794	G
26	DA	803	U
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	851	U
26	DA	852	G
26	DA	854	G
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	868	U
26	DA	874	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	893	C
26	DA	896	A
26	DA	897	C
26	DA	898	C
26	DA	900	A
26	DA	901	A
26	DA	903	C
26	DA	910	A
26	DA	917	A
26	DA	932	G
26	DA	938	G
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	950	G
26	DA	952	G
26	DA	953	A
26	DA	958	U

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Mol	Chain	Res	Type
26	DA	959	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	983	A
26	DA	996	A
26	DA	1005	C
26	DA	1006	C
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1033	U
26	DA	1034	G
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1118	C
26	DA	1126	A
26	DA	1128	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1144	G
26	DA	1171	G
26	DA	1180	C
26	DA	1196	C
26	DA	1205	U
26	DA	1210	A
26	DA	1211	U
26	DA	1220	A
26	DA	1221	C
26	DA	1229	G
26	DA	1242	A
26	DA	1247	A
26	DA	1253	A

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Mol	Chain	Res	Type
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1287	A
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1305	C
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U
26	DA	1359	A
26	DA	1360	A
26	DA	1365	A
26	DA	1368	G
26	DA	1370	C
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A
26	DA	1445(A)	C
26	DA	1449	A
26	DA	1450	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1490	A
26	DA	1493	C
26	DA	1494	A
26	DA	1495	A
26	DA	1496	A
26	DA	1497	U

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Mol	Chain	Res	Type
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1523	U
26	DA	1525	G
26	DA	1531	C
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1547	C
26	DA	1554	A
26	DA	1558	A
26	DA	1559	G
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1580	A
26	DA	1583	A
26	DA	1584	C
26	DA	1586	A
26	DA	1595	G
26	DA	1598	C
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1612	C
26	DA	1639	U
26	DA	1640	C
26	DA	1647	G
26	DA	1648	C
26	DA	1654	A
26	DA	1674	G
26	DA	1696	G
26	DA	1700	A
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1756	G
26	DA	1758	G
26	DA	1763	G
26	DA	1764	G

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Mol	Chain	Res	Type
26	DA	1773	A
26	DA	1780	A
26	DA	1782	C
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1835	G
26	DA	1836	C
26	DA	1847	A
26	DA	1848	A
26	DA	1866	C
26	DA	1877	A
26	DA	1887	C
26	DA	1889	A
26	DA	1895	C
26	DA	1900	A
26	DA	1906	G
26	DA	1914	C
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
26	DA	1963	U
26	DA	1964	G
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2031	A
26	DA	2032	G
26	DA	2033	A
26	DA	2043	C
26	DA	2046	G

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Mol	Chain	Res	Type
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2082	A
26	DA	2093	G
26	DA	2095	C
26	DA	2096	U
26	DA	2099	U
26	DA	2101	G
26	DA	2102	U
26	DA	2103	C
26	DA	2104	G
26	DA	2105	C
26	DA	2108	C
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G
26	DA	2117	A
26	DA	2119	A
26	DA	2122	U
26	DA	2124	G
26	DA	2125	G
26	DA	2126	A
26	DA	2127	G
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2143	C
26	DA	2145	C

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Mol	Chain	Res	Type
26	DA	2146	C
26	DA	2148	G
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2155	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2163	C
26	DA	2164	C
26	DA	2165	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2186	G
26	DA	2189	U
26	DA	2192	G
26	DA	2193	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2235	G
26	DA	2238	G
26	DA	2239	G
26	DA	2259	G
26	DA	2273	A

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Mol	Chain	Res	Type
26	DA	2275	C
26	DA	2278	A
26	DA	2280	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2294	C
26	DA	2299	G
26	DA	2302	G
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2312	U
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2325	G
26	DA	2327	A
26	DA	2328	A
26	DA	2334	G
26	DA	2336	A
26	DA	2339	G
26	DA	2343	C
26	DA	2347	C
26	DA	2350	C
26	DA	2354	G
26	DA	2366	A
26	DA	2376	A
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2400	G
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2441	C

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Mol	Chain	Res	Type
26	DA	2445	G
26	DA	2448	A
26	DA	2465	C
26	DA	2468	G
26	DA	2469	A
26	DA	2474	C
26	DA	2476	A
26	DA	2478	A
26	DA	2490	G
26	DA	2494	G
26	DA	2497	A
26	DA	2502	G
26	DA	2505	G
26	DA	2506	U
26	DA	2518	A
26	DA	2529	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2573	C
26	DA	2586	C
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2629	A
26	DA	2630	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2691	C
26	DA	2703	C
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G

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Mol	Chain	Res	Type
26	DA	2726	U
26	DA	2733	A
26	DA	2734	A
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2760	C
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2784	C
26	DA	2793	G
26	DA	2794	C
26	DA	2809	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2833	G
26	DA	2834	G
26	DA	2835	A
26	DA	2872	G
26	DA	2873	A
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	34	U
27	DB	42	C
27	DB	56	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	90	A
27	DB	93	G
27	DB	106	G
27	DB	108	U

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Mol	Chain	Res	Type
27	DB	110	G
27	DB	111	G
27	DB	112	U
27	DB	120	A

All (126) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	96	U
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1181	G
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
1	AA	1492	A
23	AW	13	C
23	AW	22	G
25	AY	19	G
25	AY	21	A
25	AY	25	C
25	AY	58	A
26	BA	71	A
26	BA	196	A
26	BA	271(J)	C

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Mol	Chain	Res	Type
26	BA	271(K)	U
26	BA	271(M)	G
26	BA	278	A
26	BA	746	A
26	BA	764	A
26	BA	774	A
26	BA	899	A
26	BA	974	G
26	BA	1047	G
26	BA	1142(A)	A
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1210	A
26	BA	1300	U
26	BA	1301	A
26	BA	1379	A
26	BA	1420	U
26	BA	1530	C
26	BA	1653	G
26	BA	1992	G
26	BA	2110	G
26	BA	2126	A
26	BA	2181	G
26	BA	2183	C
26	BA	2187	G
26	BA	2406	U
26	BA	2430	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	840	C

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Mol	Chain	Res	Type
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1027	C
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1181	G
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1299	A
1	CA	1442	G
1	CA	1492	A
23	CW	4	C
23	CW	13	C
25	CY	46	7MG
26	DA	271(K)	U
26	DA	271(M)	G
26	DA	277	C
26	DA	587	C
26	DA	752	A
26	DA	764	A
26	DA	774	A
26	DA	827	U
26	DA	856	C
26	DA	900	A
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2110	G

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Mol	Chain	Res	Type
26	DA	2126	A
26	DA	2136	C
26	DA	2169	A
26	DA	2177	C
26	DA	2318	G
26	DA	2689	U
26	DA	2756	U
26	DA	2893	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

38 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$
23	PSU	AW	32	23	13,21,22	1.17	1 (7%)	18,30,33	3.46	6 (33%)
23	MIA	AW	37	23	21,31,32	1.70	2 (9%)	26,44,47	1.54	6 (23%)
23	PSU	AW	39	23	13,21,22	1.43	1 (7%)	18,30,33	3.54	6 (33%)
23	7MG	AW	46	23	19,26,27	1.11	1 (5%)	24,39,42	3.10	7 (29%)
23	5MU	AW	54	23	12,22,23	0.32	0	14,32,35	2.50	2 (14%)
23	PSU	AW	55	23	13,21,22	1.28	1 (7%)	18,30,33	3.56	6 (33%)
23	31M	AW	76	23	35,44,45	1.39	4 (11%)	40,61,64	2.17	6 (15%)
23	4SU	AW	8	23	11,21,22	1.20	1 (9%)	13,30,33	1.13	1 (7%)
24	5MC	AX	32	24	13,22,23	1.42	1 (7%)	15,32,35	1.02	1 (6%)
24	5MU	AX	54	24,57	12,22,23	0.31	0	14,32,35	2.40	2 (14%)
24	PSU	AX	55	24,57	13,21,22	1.49	1 (7%)	18,30,33	3.39	6 (33%)
24	4SU	AX	8	24	11,21,22	1.17	1 (9%)	13,30,33	1.64	1 (7%)
25	PSU	AY	32	25	13,21,22	1.02	1 (7%)	18,30,33	3.34	6 (33%)
25	MIA	AY	37	25	15,24,32	1.21	2 (13%)	16,35,47	2.01	2 (12%)
25	PSU	AY	39	25	13,21,22	1.30	2 (15%)	18,30,33	3.68	4 (22%)
25	7MG	AY	46	25	19,26,27	1.11	1 (5%)	24,39,42	3.34	8 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	5MU	AY	54	25	12,22,23	0.43	0	14,32,35	2.26	2 (14%)
25	PSU	AY	55	25	13,21,22	1.74	2 (15%)	18,30,33	3.07	6 (33%)
25	4SU	AY	8	25	11,21,22	1.22	1 (9%)	13,30,33	1.22	1 (7%)
23	PSU	CW	32	23	13,21,22	1.33	1 (7%)	18,30,33	3.29	5 (27%)
23	MIA	CW	37	23	15,24,32	1.21	2 (13%)	16,35,47	1.95	2 (12%)
23	PSU	CW	39	23	13,21,22	1.48	1 (7%)	18,30,33	3.63	6 (33%)
23	7MG	CW	46	23	19,26,27	1.06	1 (5%)	24,39,42	2.89	6 (25%)
23	5MU	CW	54	23	12,22,23	0.42	0	14,32,35	2.46	2 (14%)
23	PSU	CW	55	23	13,21,22	1.09	1 (7%)	18,30,33	3.37	6 (33%)
23	31M	CW	76	23	35,44,45	1.40	4 (11%)	40,61,64	1.97	3 (7%)
23	4SU	CW	8	23	11,21,22	1.25	1 (9%)	13,30,33	1.21	1 (7%)
24	5MC	CX	32	24	13,22,23	1.34	1 (7%)	15,32,35	0.95	1 (6%)
24	5MU	CX	54	24	12,22,23	0.36	0	14,32,35	2.17	2 (14%)
24	PSU	CX	55	24	13,21,22	1.21	1 (7%)	18,30,33	3.31	6 (33%)
24	4SU	CX	8	24	11,21,22	1.15	1 (9%)	13,30,33	1.67	1 (7%)
25	PSU	CY	32	25	13,21,22	1.13	1 (7%)	18,30,33	3.38	5 (27%)
25	MIA	CY	37	25	15,24,32	1.26	2 (13%)	16,35,47	1.96	2 (12%)
25	PSU	CY	39	25	13,21,22	1.32	1 (7%)	18,30,33	2.98	6 (33%)
25	7MG	CY	46	25	19,26,27	1.02	1 (5%)	24,39,42	2.92	7 (29%)
25	5MU	CY	54	25	12,22,23	0.37	0	14,32,35	2.16	2 (14%)
25	PSU	CY	55	25	13,21,22	0.82	1 (7%)	18,30,33	3.36	6 (33%)
25	4SU	CY	8	25	11,21,22	1.32	1 (9%)	13,30,33	1.02	1 (7%)

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
23	PSU	AW	32	23	-	0/7/25/26	0/2/2/2
23	MIA	AW	37	23	-	0/11/33/34	0/3/3/3
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
23	7MG	AW	46	23	-	0/7/37/38	0/3/3/3
23	5MU	AW	54	23	-	0/3/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
23	31M	AW	76	23	-	0/27/49/50	0/4/4/4
23	4SU	AW	8	23	-	0/3/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	5MC	AX	32	24	-	0/3/25/26	0/2/2/2
24	5MU	AX	54	24,57	-	0/3/25/26	0/2/2/2
24	PSU	AX	55	24,57	-	0/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/3/25/26	0/2/2/2
25	PSU	AY	32	25	-	0/7/25/26	0/2/2/2
25	MIA	AY	37	25	-	0/3/25/34	0/3/3/3
25	PSU	AY	39	25	-	0/7/25/26	0/2/2/2
25	7MG	AY	46	25	-	0/7/37/38	0/3/3/3
25	5MU	AY	54	25	-	0/3/25/26	0/2/2/2
25	PSU	AY	55	25	-	0/7/25/26	0/2/2/2
25	4SU	AY	8	25	-	0/3/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/3/25/34	0/3/3/3
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	0/7/37/38	0/3/3/3
23	5MU	CW	54	23	-	0/3/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
23	31M	CW	76	23	-	0/27/49/50	0/4/4/4
23	4SU	CW	8	23	-	0/3/25/26	0/2/2/2
24	5MC	CX	32	24	-	0/3/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/3/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	0/3/25/26	0/2/2/2
25	PSU	CY	32	25	-	0/7/25/26	0/2/2/2
25	MIA	CY	37	25	-	0/3/25/34	0/3/3/3
25	PSU	CY	39	25	-	0/7/25/26	0/2/2/2
25	7MG	CY	46	25	-	0/7/37/38	0/3/3/3
25	5MU	CY	54	25	-	0/3/25/26	0/2/2/2
25	PSU	CY	55	25	-	0/7/25/26	0/2/2/2
25	4SU	CY	8	25	-	0/3/25/26	0/2/2/2

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-6.35	1.70	1.75
25	AY	55	PSU	C5-C1'	-5.72	1.47	1.52
23	AW	76	31M	CB-CG	-4.92	1.39	1.51
23	CW	39	PSU	C5-C1'	-4.87	1.48	1.52
24	AX	55	PSU	C5-C1'	-4.77	1.48	1.52
23	CW	76	31M	CB-CG	-4.74	1.39	1.51
23	AW	39	PSU	C5-C1'	-4.71	1.48	1.52
23	CW	32	PSU	C5-C1'	-4.27	1.48	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	55	PSU	C5-C1'	-4.16	1.48	1.52
25	CY	8	4SU	C4-S4	-4.06	1.59	1.67
25	CY	39	PSU	C5-C1'	-3.89	1.48	1.52
25	AY	8	4SU	C4-S4	-3.81	1.60	1.67
24	CX	55	PSU	C5-C1'	-3.79	1.48	1.52
23	AW	32	PSU	C5-C1'	-3.79	1.48	1.52
23	AW	8	4SU	C4-S4	-3.77	1.60	1.67
24	AX	8	4SU	C4-S4	-3.74	1.60	1.67
23	CW	8	4SU	C4-S4	-3.67	1.60	1.67
24	CX	8	4SU	C4-S4	-3.66	1.60	1.67
25	AY	39	PSU	C5-C1'	-3.65	1.49	1.52
23	AW	76	31M	C5-C4	-3.41	1.32	1.40
23	CW	76	31M	C5-C4	-3.37	1.32	1.40
25	CY	32	PSU	C5-C1'	-3.32	1.49	1.52
23	CW	55	PSU	C5-C1'	-3.31	1.49	1.52
25	AY	32	PSU	C5-C1'	-3.12	1.49	1.52
25	AY	55	PSU	O4'-C1'	-2.45	1.40	1.44
25	AY	39	PSU	O4'-C1'	-2.38	1.40	1.44
25	CY	55	PSU	C5-C1'	-2.21	1.50	1.52
23	CW	76	31M	C5-N7	-2.20	1.32	1.39
23	AW	76	31M	C2-N1	2.31	1.38	1.33
25	CY	37	MIA	C2-N3	2.34	1.36	1.32
25	AY	37	MIA	C2-N3	2.37	1.36	1.32
23	CW	37	MIA	C2-N3	2.44	1.36	1.32
25	CY	46	7MG	C5-C4	3.04	1.47	1.39
25	AY	46	7MG	C5-C4	3.09	1.47	1.39
23	CW	46	7MG	C5-C4	3.11	1.48	1.39
23	AW	37	MIA	C5-C4	3.13	1.47	1.40
23	AW	46	7MG	C5-C4	3.15	1.48	1.39
23	CW	37	MIA	C5-C4	3.35	1.48	1.40
25	AY	37	MIA	C5-C4	3.40	1.48	1.40
23	AW	76	31M	O4'-C1'	3.52	1.45	1.41
25	CY	37	MIA	C5-C4	3.58	1.48	1.40
23	CW	76	31M	O4'-C1'	3.65	1.45	1.41
24	CX	32	5MC	C5-C4	4.70	1.48	1.41
24	AX	32	5MC	C5-C4	4.81	1.48	1.41

All (149) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	76	31M	N3-C2-N1	-11.49	120.09	128.89
25	AY	39	PSU	N1-C2-N3	-11.29	121.13	128.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	39	PSU	N1-C2-N3	-11.15	121.22	128.33
23	CW	76	31M	N3-C2-N1	-11.12	120.38	128.89
23	AW	39	PSU	N1-C2-N3	-10.87	121.40	128.33
25	AY	46	7MG	C5-C4-N3	-10.69	116.40	126.82
25	CY	32	PSU	N1-C2-N3	-10.67	121.53	128.33
23	AW	55	PSU	N1-C2-N3	-10.64	121.55	128.33
25	AY	32	PSU	N1-C2-N3	-10.55	121.60	128.33
23	AW	32	PSU	N1-C2-N3	-10.49	121.64	128.33
24	AX	55	PSU	N1-C2-N3	-10.47	121.65	128.33
23	CW	32	PSU	N1-C2-N3	-10.41	121.69	128.33
24	CX	55	PSU	N1-C2-N3	-10.26	121.79	128.33
23	CW	55	PSU	N1-C2-N3	-10.18	121.84	128.33
25	CY	55	PSU	N1-C2-N3	-9.42	122.33	128.33
25	AY	55	PSU	N1-C2-N3	-9.00	122.59	128.33
23	CW	46	7MG	C5-C4-N3	-8.76	118.28	126.82
25	CY	39	PSU	N1-C2-N3	-8.71	122.77	128.33
23	AW	46	7MG	C5-C4-N3	-8.35	118.68	126.82
25	CY	46	7MG	C5-C4-N3	-8.06	118.96	126.82
25	AY	37	MIA	N3-C2-N1	-6.86	123.64	128.89
23	CW	37	MIA	N3-C2-N1	-6.72	123.75	128.89
25	CY	37	MIA	N3-C2-N1	-6.65	123.80	128.89
25	CY	55	PSU	C5-C1'-C2'	-6.52	103.95	115.52
23	CW	54	5MU	C5-C4-N3	-5.64	118.86	125.14
23	AW	54	5MU	C5-C4-N3	-5.62	118.88	125.14
24	CX	54	5MU	C5-C4-N3	-5.55	118.96	125.14
24	CX	8	4SU	C5-C4-N3	-5.52	118.22	123.63
24	AX	8	4SU	C5-C4-N3	-5.50	118.24	123.63
24	AX	54	5MU	C5-C4-N3	-5.39	119.14	125.14
23	AW	46	7MG	C5-C6-N1	-5.30	115.31	123.46
23	AW	55	PSU	C5-C1'-C2'	-5.17	106.33	115.52
25	AY	54	5MU	C5-C4-N3	-5.14	119.41	125.14
23	CW	46	7MG	C5-C6-N1	-5.08	115.65	123.46
25	CY	46	7MG	C5-C6-N1	-5.02	115.75	123.46
25	CY	54	5MU	C5-C4-N3	-4.73	119.87	125.14
23	CW	39	PSU	C5-C1'-C2'	-4.49	107.55	115.52
23	AW	32	PSU	C5-C1'-C2'	-4.41	107.69	115.52
25	AY	46	7MG	C5-C6-N1	-4.41	116.69	123.46
23	CW	55	PSU	C5-C1'-C2'	-4.31	107.87	115.52
23	AW	76	31M	C4'-C3'-N3'	-3.99	105.29	113.61
24	AX	55	PSU	C5-C6-N1	-3.91	118.87	124.39
25	AY	55	PSU	C5-C6-N1	-3.90	118.88	124.39
25	CY	39	PSU	C5-C1'-C2'	-3.90	108.59	115.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	8	4SU	C5-C4-N3	-3.86	119.85	123.63
25	AY	32	PSU	C5-C6-N1	-3.85	118.95	124.39
24	CX	55	PSU	C5-C6-N1	-3.82	119.00	124.39
25	CY	55	PSU	C5-C6-N1	-3.80	119.03	124.39
23	CW	8	4SU	C5-C4-N3	-3.76	119.95	123.63
23	AW	32	PSU	C5-C6-N1	-3.64	119.25	124.39
23	CW	39	PSU	C5-C6-N1	-3.62	119.29	124.39
23	AW	39	PSU	C5-C6-N1	-3.62	119.29	124.39
23	AW	37	MIA	C12-N6-C6	-3.58	118.97	123.42
23	AW	8	4SU	C5-C4-N3	-3.57	120.13	123.63
23	CW	55	PSU	C5-C6-N1	-3.50	119.45	124.39
23	CW	32	PSU	C5-C6-N1	-3.49	119.47	124.39
25	CY	39	PSU	C5-C6-N1	-3.43	119.55	124.39
23	AW	39	PSU	C5-C1'-C2'	-3.37	109.53	115.52
23	AW	55	PSU	C5-C6-N1	-3.26	119.80	124.39
24	AX	55	PSU	C5-C1'-C2'	-3.24	109.77	115.52
23	AW	37	MIA	C4-C5-N7	-3.17	106.56	109.48
25	AY	37	MIA	C4-C5-N7	-3.17	106.56	109.48
23	CW	37	MIA	C4-C5-N7	-3.12	106.61	109.48
25	AY	55	PSU	C5-C1'-C2'	-2.96	110.26	115.52
25	CY	32	PSU	C5-C6-N1	-2.94	120.25	124.39
25	CY	46	7MG	CM7-N7-C8	-2.79	112.61	120.52
23	AW	37	MIA	C11-S10-C2	-2.76	100.49	102.26
23	AW	46	7MG	CM7-N7-C8	-2.69	112.89	120.52
24	CX	55	PSU	C5-C1'-C2'	-2.60	110.90	115.52
23	AW	37	MIA	C5-C6-N1	-2.60	117.80	120.48
25	AY	46	7MG	CM7-N7-C8	-2.59	113.18	120.52
23	CW	76	31M	C2'-C1'-N9	-2.56	110.39	114.29
23	CW	46	7MG	CM7-N7-C8	-2.52	113.39	120.52
23	AW	76	31M	OTM-CTM-CAM	-2.49	113.55	119.80
23	AW	46	7MG	C5-C4-N9	-2.49	102.51	106.18
25	CY	8	4SU	C5-C4-N3	-2.44	121.24	123.63
25	AY	32	PSU	C5-C1'-C2'	-2.43	111.21	115.52
23	CW	76	31M	OTM-CTM-CAM	-2.40	113.79	119.80
25	CY	37	MIA	C4-C5-N7	-2.37	107.30	109.48
23	AW	37	MIA	N3-C2-N1	-2.37	122.26	126.79
23	AW	76	31M	C4-C5-N7	-2.18	107.47	109.48
25	AY	46	7MG	C5-C4-N9	-2.13	103.05	106.18
23	CW	46	7MG	CM7-N7-C5	2.02	130.86	124.09
25	CY	46	7MG	CM7-N7-C5	2.05	130.96	124.09
23	AW	76	31M	C2'-C3'-C4'	2.07	104.83	102.27
25	CY	46	7MG	N2-C2-N1	2.10	120.67	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	46	7MG	CM7-N7-C5	2.14	131.26	124.09
25	AY	46	7MG	C2-N3-C4	2.18	120.88	114.53
23	AW	46	7MG	CM7-N7-C5	2.18	131.40	124.09
25	CY	39	PSU	O4'-C1'-C2'	2.22	106.99	104.73
23	CW	55	PSU	O4'-C1'-C2'	2.34	107.12	104.73
23	AW	55	PSU	O4'-C1'-C2'	2.49	107.27	104.73
24	CX	32	5MC	N4-C4-N3	2.57	120.67	116.95
24	AX	32	5MC	N4-C4-N3	2.69	120.84	116.95
25	CY	55	PSU	O4'-C1'-C2'	2.75	107.53	104.73
23	AW	76	31M	O4'-C4'-C3'	2.78	107.90	103.93
23	CW	39	PSU	O4'-C1'-C2'	2.81	107.60	104.73
25	AY	32	PSU	O4'-C1'-C2'	2.83	107.61	104.73
25	AY	39	PSU	O4'-C1'-C2'	2.85	107.64	104.73
25	AY	39	PSU	C6-N1-C2	2.87	120.08	115.47
23	AW	32	PSU	O4'-C1'-C2'	2.95	107.74	104.73
23	AW	39	PSU	O4'-C1'-C2'	3.03	107.81	104.73
24	CX	55	PSU	O4'-C1'-C2'	3.07	107.86	104.73
23	CW	32	PSU	O4'-C1'-C2'	3.07	107.86	104.73
23	AW	37	MIA	C2-N1-C6	3.08	122.38	113.35
24	AX	55	PSU	O4'-C1'-C2'	3.12	107.91	104.73
25	CY	32	PSU	O4'-C1'-C2'	3.30	108.09	104.73
25	AY	55	PSU	C6-N1-C2	3.71	121.44	115.47
25	AY	55	PSU	O4'-C1'-C2'	3.74	108.55	104.73
25	CY	32	PSU	C6-N1-C2	3.94	121.80	115.47
23	AW	55	PSU	C6-N1-C2	3.95	121.82	115.47
23	AW	39	PSU	C6-N1-C2	4.00	121.90	115.47
25	CY	39	PSU	C6-N1-C2	4.06	121.99	115.47
23	CW	32	PSU	C6-N1-C2	4.10	122.06	115.47
23	CW	55	PSU	C6-N1-C2	4.11	122.08	115.47
23	CW	39	PSU	C6-N1-C2	4.15	122.15	115.47
24	AX	55	PSU	C6-N1-C2	4.28	122.36	115.47
24	CX	55	PSU	C6-N1-C2	4.30	122.38	115.47
23	AW	32	PSU	C6-N1-C2	4.34	122.44	115.47
25	AY	46	7MG	C6-N1-C2	4.37	122.00	115.94
25	CY	55	PSU	C4-N3-C2	4.50	119.14	115.25
25	AY	32	PSU	C6-N1-C2	4.50	122.71	115.47
25	CY	55	PSU	C6-N1-C2	4.76	123.13	115.47
23	CW	46	7MG	C6-N1-C2	4.92	122.77	115.94
25	CY	39	PSU	C4-N3-C2	5.37	119.89	115.25
25	CY	46	7MG	C6-N1-C2	5.39	123.42	115.94
24	CX	54	5MU	C4-N3-C2	5.50	120.00	115.25
25	AY	55	PSU	C4-N3-C2	5.56	120.05	115.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	32	PSU	C4-N3-C2	5.97	120.41	115.25
23	AW	46	7MG	C6-N1-C2	6.13	124.44	115.94
24	AX	55	PSU	C4-N3-C2	6.14	120.55	115.25
25	CY	54	5MU	C4-N3-C2	6.17	120.58	115.25
23	CW	55	PSU	C4-N3-C2	6.20	120.61	115.25
25	AY	54	5MU	C4-N3-C2	6.21	120.61	115.25
24	CX	55	PSU	C4-N3-C2	6.22	120.62	115.25
23	AW	32	PSU	C4-N3-C2	6.32	120.71	115.25
23	CW	32	PSU	C4-N3-C2	6.44	120.81	115.25
25	CY	32	PSU	C4-N3-C2	6.93	121.23	115.25
24	AX	54	5MU	C4-N3-C2	6.93	121.23	115.25
23	CW	39	PSU	C4-N3-C2	6.94	121.24	115.25
23	AW	55	PSU	C4-N3-C2	6.95	121.25	115.25
23	CW	54	5MU	C4-N3-C2	6.97	121.27	115.25
25	CY	46	7MG	N3-C4-N9	7.04	137.32	126.75
23	AW	54	5MU	C4-N3-C2	7.16	121.44	115.25
23	CW	46	7MG	N3-C4-N9	7.21	137.58	126.75
23	AW	39	PSU	C4-N3-C2	7.32	121.58	115.25
23	AW	46	7MG	N3-C4-N9	8.03	138.81	126.75
25	AY	46	7MG	N3-C4-N9	9.19	140.54	126.75
25	AY	39	PSU	C4-N3-C2	9.31	123.29	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

28 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AW	37	MIA	1	0
23	AW	39	PSU	1	0
23	AW	46	7MG	1	0
23	AW	76	31M	4	0
23	AW	8	4SU	1	0
24	AX	32	5MC	3	0
24	AX	55	PSU	1	0
24	AX	8	4SU	2	0
25	AY	32	PSU	2	0
25	AY	37	MIA	3	0
25	AY	39	PSU	4	0
25	AY	46	7MG	3	0
25	AY	54	5MU	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	AY	55	PSU	4	0
25	AY	8	4SU	1	0
23	CW	39	PSU	3	0
23	CW	46	7MG	1	0
23	CW	55	PSU	1	0
23	CW	76	31M	7	0
23	CW	8	4SU	2	0
24	CX	32	5MC	2	0
24	CX	54	5MU	2	0
24	CX	8	4SU	2	0
25	CY	37	MIA	2	0
25	CY	39	PSU	4	0
25	CY	46	7MG	1	0
25	CY	55	PSU	4	0
25	CY	8	4SU	5	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 2093 ligands modelled in this entry, 2091 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	AD	501	4	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	CD	302	4	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	AD	501	4	-	0/0/48/48	0/6/5/5
58	SF4	CD	302	4	-	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 [i](#)

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	AA	1498/1521 (98%)	0.52	34 (2%) 64 69	42, 72, 93, 108	0
1	CA	1503/1521 (98%)	0.55	81 (5%) 29 34	44, 74, 94, 109	0
2	AB	231/256 (90%)	0.85	33 (14%) 4 4	72, 82, 90, 94	0
2	CB	231/256 (90%)	1.53	59 (25%) 1 1	73, 84, 90, 95	0
3	AC	206/239 (86%)	1.04	38 (18%) 2 2	68, 79, 87, 94	0
3	CC	206/239 (86%)	1.95	82 (39%) 0 0	71, 81, 89, 94	0
4	AD	208/209 (99%)	1.05	33 (15%) 3 3	57, 72, 81, 90	0
4	CD	208/209 (99%)	0.88	17 (8%) 14 16	58, 71, 80, 91	0
5	AE	148/162 (91%)	1.09	21 (14%) 4 4	58, 71, 80, 85	0
5	CE	148/162 (91%)	1.30	37 (25%) 1 1	60, 73, 81, 86	0
6	AF	100/101 (99%)	0.62	6 (6%) 25 29	56, 69, 78, 82	0
6	CF	100/101 (99%)	0.50	6 (6%) 25 29	57, 70, 78, 82	0
7	AG	155/156 (99%)	0.92	13 (8%) 14 15	65, 75, 83, 91	0
7	CG	155/156 (99%)	1.22	27 (17%) 2 2	66, 76, 84, 92	0
8	AH	137/138 (99%)	1.05	27 (19%) 1 1	62, 72, 79, 87	0
8	CH	137/138 (99%)	1.17	30 (21%) 1 1	64, 74, 80, 87	0
9	AI	127/128 (99%)	1.20	28 (22%) 1 1	65, 80, 86, 89	0
9	CI	127/128 (99%)	2.63	76 (59%) 0 0	68, 82, 88, 91	0
10	AJ	97/105 (92%)	1.27	23 (23%) 1 1	64, 82, 90, 93	0
10	CJ	96/105 (91%)	1.83	36 (37%) 0 0	67, 84, 91, 93	0
11	AK	114/129 (88%)	0.90	9 (7%) 15 17	48, 70, 79, 84	0
11	CK	114/129 (88%)	0.83	11 (9%) 10 11	51, 71, 79, 84	0
12	AL	122/132 (92%)	0.84	8 (6%) 22 25	50, 65, 73, 78	0
12	CL	122/132 (92%)	1.26	27 (22%) 1 1	53, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.78	9 (7%) 18 20	55, 70, 81, 89	0
13	CM	122/126 (96%)	2.18	56 (45%) 0 0	70, 84, 91, 99	0
14	AN	60/61 (98%)	1.29	13 (21%) 1 1	67, 74, 83, 84	0
14	CN	60/61 (98%)	3.14	39 (65%) 0 0	69, 77, 84, 88	0
15	AO	88/89 (98%)	0.74	6 (6%) 20 23	56, 67, 80, 81	0
15	CO	88/89 (98%)	1.01	10 (11%) 7 7	59, 69, 80, 83	0
16	AP	82/88 (93%)	1.68	29 (35%) 0 0	57, 71, 80, 84	0
16	CP	82/88 (93%)	1.05	8 (9%) 10 11	58, 70, 80, 84	0
17	AQ	99/105 (94%)	0.89	12 (12%) 6 6	59, 71, 80, 84	0
17	CQ	99/105 (94%)	1.39	29 (29%) 1 0	61, 71, 81, 85	0
18	AR	68/88 (77%)	0.82	5 (7%) 17 20	59, 68, 81, 83	0
18	CR	68/88 (77%)	0.67	3 (4%) 38 44	61, 70, 80, 84	0
19	AS	83/93 (89%)	0.68	4 (4%) 34 40	71, 80, 86, 95	0
19	CS	83/93 (89%)	2.05	34 (40%) 0 0	74, 82, 89, 96	0
20	AT	96/106 (90%)	1.03	16 (16%) 2 2	57, 71, 81, 85	0
20	CT	96/106 (90%)	1.24	19 (19%) 1 1	58, 70, 82, 85	0
21	AU	23/27 (85%)	1.76	8 (34%) 0 0	67, 74, 77, 81	0
21	CU	23/27 (85%)	2.92	15 (65%) 0 0	71, 75, 80, 84	0
22	AV	13/24 (54%)	3.01	7 (53%) 0 0	58, 81, 96, 99	0
22	CV	12/24 (50%)	3.80	8 (66%) 0 0	63, 84, 93, 94	0
23	AW	66/76 (86%)	2.11	28 (42%) 0 0	68, 96, 103, 105	0
23	CW	64/76 (84%)	3.73	53 (82%) 0 0	73, 97, 103, 106	0
24	AX	72/77 (93%)	0.61	1 (1%) 78 81	39, 68, 87, 91	0
24	CX	72/77 (93%)	0.89	8 (11%) 7 8	53, 82, 93, 97	0
25	AY	67/76 (88%)	1.57	25 (37%) 0 0	44, 97, 102, 105	0
25	CY	66/76 (86%)	2.48	34 (51%) 0 0	47, 97, 102, 105	0
26	BA	2819/2915 (96%)	0.84	37 (1%) 79 83	26, 45, 89, 104	0
26	DA	2800/2915 (96%)	0.35	73 (2%) 59 64	30, 49, 90, 108	0
27	BB	120/121 (99%)	0.72	0 100 100	40, 64, 73, 86	0
27	DB	120/121 (99%)	0.38	6 (5%) 32 38	46, 69, 76, 90	0
28	BD	275/276 (99%)	0.89	9 (3%) 50 56	27, 43, 58, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	0.77	17 (6%) 24 27	29, 45, 61, 81	0
29	BE	204/206 (99%)	0.87	7 (3%) 49 55	25, 48, 66, 80	0
29	DE	204/206 (99%)	0.64	4 (1%) 68 73	29, 52, 67, 81	0
30	BF	203/210 (96%)	0.82	5 (2%) 61 66	26, 53, 76, 87	0
30	DF	203/210 (96%)	0.64	10 (4%) 33 39	30, 58, 77, 87	0
31	BG	181/182 (99%)	0.89	12 (6%) 22 25	51, 69, 81, 88	0
31	DG	181/182 (99%)	1.36	43 (23%) 1 1	56, 73, 82, 90	0
32	BH	174/180 (96%)	0.82	6 (3%) 49 55	51, 65, 75, 88	0
32	DH	174/180 (96%)	1.17	37 (21%) 1 1	55, 70, 78, 88	0
33	BI	146/148 (98%)	0.63	6 (4%) 41 47	50, 74, 82, 87	0
33	DI	146/148 (98%)	0.67	17 (11%) 6 7	52, 75, 82, 86	0
34	BN	140/140 (100%)	0.98	4 (2%) 55 61	32, 50, 67, 76	0
34	DN	140/140 (100%)	0.75	9 (6%) 23 26	36, 55, 70, 77	0
35	BO	122/122 (100%)	0.65	2 (1%) 74 79	30, 43, 59, 70	0
35	DO	122/122 (100%)	0.83	6 (4%) 33 39	45, 59, 73, 78	0
36	BP	149/150 (99%)	0.90	4 (2%) 58 63	26, 55, 75, 83	0
36	DP	149/150 (99%)	1.03	26 (17%) 2 2	30, 59, 77, 85	0
37	BQ	141/141 (100%)	0.91	3 (2%) 67 72	36, 52, 67, 80	0
37	DQ	141/141 (100%)	1.34	30 (21%) 1 1	41, 57, 70, 82	0
38	BR	118/118 (100%)	0.76	1 (0%) 87 89	25, 36, 54, 59	0
38	DR	118/118 (100%)	0.72	3 (2%) 61 66	41, 54, 65, 72	0
39	BS	110/112 (98%)	0.57	1 (0%) 85 88	38, 51, 65, 72	0
39	DS	110/112 (98%)	1.31	25 (22%) 1 1	63, 77, 84, 92	0
40	BT	131/146 (89%)	0.58	0 100 100	32, 47, 69, 82	0
40	DT	131/146 (89%)	0.74	7 (5%) 30 35	48, 63, 79, 85	0
41	BU	116/118 (98%)	0.88	1 (0%) 85 88	18, 33, 49, 59	0
41	DU	116/118 (98%)	0.90	10 (8%) 13 14	42, 61, 78, 84	0
42	BV	101/101 (100%)	0.62	0 100 100	21, 41, 58, 67	0
42	DV	101/101 (100%)	0.70	5 (4%) 32 38	41, 71, 83, 91	0
43	BW	112/113 (99%)	0.81	0 100 100	23, 34, 54, 79	0
43	DW	112/113 (99%)	0.77	6 (5%) 29 34	39, 50, 67, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.63	0	100 100	23, 38, 61, 84	0
44	DX	95/96 (98%)	1.06	9 (9%)	10 11	43, 60, 76, 79	0
45	BY	107/110 (97%)	0.58	1 (0%)	85 88	32, 50, 69, 83	0
45	DY	107/110 (97%)	1.29	19 (17%)	2 2	57, 71, 81, 88	0
46	BZ	171/206 (83%)	0.77	14 (8%)	14 16	39, 64, 91, 95	0
46	DZ	174/206 (84%)	1.64	52 (29%)	1 0	66, 84, 94, 101	0
47	B0	83/85 (97%)	0.96	6 (7%)	18 21	27, 39, 61, 73	0
47	D0	83/85 (97%)	1.60	22 (26%)	1 1	47, 66, 75, 82	0
48	B1	97/98 (98%)	0.88	7 (7%)	18 21	30, 48, 70, 76	0
48	D1	97/98 (98%)	1.04	16 (16%)	2 2	38, 58, 74, 83	0
49	B2	70/72 (97%)	0.64	0	100 100	34, 50, 64, 79	0
49	D2	70/72 (97%)	0.73	6 (8%)	13 14	56, 70, 80, 86	0
50	B3	59/60 (98%)	0.70	0	100 100	24, 37, 63, 71	0
50	D3	59/60 (98%)	1.05	9 (15%)	3 3	49, 64, 79, 85	0
51	B4	69/71 (97%)	0.55	5 (7%)	18 21	54, 73, 87, 92	0
51	D4	69/71 (97%)	1.21	13 (18%)	2 2	74, 88, 94, 99	0
52	B5	59/60 (98%)	0.71	2 (3%)	49 55	20, 33, 54, 67	0
52	D5	59/60 (98%)	0.63	3 (5%)	32 37	36, 51, 67, 73	0
53	B6	53/54 (98%)	0.67	1 (1%)	70 74	31, 44, 61, 68	0
53	D6	53/54 (98%)	1.20	8 (15%)	3 3	52, 63, 76, 79	0
54	B7	48/49 (97%)	1.12	6 (12%)	5 6	21, 30, 62, 76	0
54	D7	48/49 (97%)	1.41	10 (20%)	1 1	33, 42, 61, 70	0
55	B8	64/65 (98%)	0.82	3 (4%)	35 41	25, 36, 45, 60	0
55	D8	64/65 (98%)	1.61	21 (32%)	0 0	46, 58, 66, 72	0
56	B9	37/37 (100%)	1.16	3 (8%)	15 16	31, 49, 73, 74	0
56	D9	37/37 (100%)	1.37	6 (16%)	3 2	46, 57, 73, 76	0
All	All	20897/21748 (96%)	0.86	1915 (9%)	11 12	18, 64, 89, 109	0

All (1915) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	13.3
2	CB	165	VAL	13.0

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Mol	Chain	Res	Type	RSRZ
13	AM	124	PRO	11.8
7	CG	83	ALA	11.1
23	CW	71	G	10.9
13	CM	123	ALA	10.2
3	CC	155	GLY	9.5
7	CG	82	GLY	9.4
23	CW	70	G	9.0
14	CN	25	VAL	8.7
23	CW	73	A	8.5
3	CC	198	VAL	8.4
9	CI	7	THR	8.4
13	AM	123	ALA	8.4
23	AW	71	G	8.3
46	DZ	114	GLY	8.3
51	D4	49	PHE	8.2
23	CW	72	C	8.2
7	AG	82	GLY	8.2
13	CM	90	LEU	8.2
13	CM	78	ILE	8.1
9	CI	109	VAL	8.1
23	AW	70	G	8.1
9	CI	76	ALA	8.1
23	CW	2	C	8.0
3	CC	8	ILE	7.9
23	CW	4	C	7.8
10	CJ	47	PHE	7.7
22	CV	23	A	7.7
13	CM	4	ILE	7.6
14	CN	34	TYR	7.6
14	CN	39	LEU	7.5
3	CC	189	ALA	7.4
21	CU	14	TRP	7.4
5	CE	12	LEU	7.3
19	CS	80	TYR	7.3
46	DZ	155	LEU	7.3
31	DG	28	VAL	7.2
22	CV	13	A	7.2
9	CI	36	TYR	7.2
13	CM	122	LYS	7.2
10	CJ	85	LEU	7.2
23	CW	3	C	7.1
46	DZ	120	ILE	7.1

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Mol	Chain	Res	Type	RSRZ
45	DY	1	MET	7.1
13	CM	94	ARG	7.0
25	CY	1	G	7.0
19	CS	82	GLY	7.0
14	CN	61	TRP	6.9
19	CS	79	THR	6.9
9	CI	61	ALA	6.7
26	DA	2155	G	6.7
2	CB	187	LEU	6.7
9	CI	115	GLY	6.7
23	CW	31	A	6.7
13	CM	120	LYS	6.7
25	CY	18	G	6.7
3	CC	124	ILE	6.6
13	CM	121	LYS	6.6
25	CY	34	G	6.6
25	CY	36	A	6.6
1	CA	1030(B)	C	6.6
22	AV	13	A	6.6
3	CC	157	ILE	6.6
7	AG	83	ALA	6.6
39	DS	32	LEU	6.5
9	CI	66	ARG	6.5
54	B7	46	VAL	6.5
10	CJ	55	LYS	6.5
13	CM	102	ARG	6.5
26	DA	229	A	6.4
31	DG	29	TRP	6.4
14	CN	29	ARG	6.3
13	CM	119	GLY	6.3
46	DZ	113	ALA	6.2
14	CN	37	PHE	6.2
9	CI	14	VAL	6.2
44	DX	92	LEU	6.2
46	DZ	107	THR	6.2
3	CC	71	ALA	6.2
51	D4	57	GLU	6.2
14	AN	2	ALA	6.2
5	CE	22	GLY	6.2
2	CB	122	PHE	6.1
9	CI	9	ARG	6.1
26	DA	2132	U	6.1

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Mol	Chain	Res	Type	RSRZ
51	D4	52	THR	6.0
3	CC	153	VAL	6.0
21	CU	6	ARG	5.9
14	CN	44	LEU	5.9
26	DA	2112	G	5.9
26	DA	2125	G	5.9
2	CB	123	ALA	5.9
3	CC	190	ARG	5.9
54	D7	46	VAL	5.9
2	CB	164	VAL	5.8
23	CW	69	G	5.8
14	CN	53	LEU	5.8
3	CC	53	ALA	5.8
13	CM	6	GLY	5.8
26	DA	2154	G	5.7
47	D0	45	PHE	5.7
25	CY	35	A	5.7
42	DV	72	VAL	5.7
22	AV	24	A	5.6
22	CV	24	A	5.6
45	DY	106	LEU	5.6
8	AH	3	THR	5.6
9	CI	123	PRO	5.6
2	CB	92	TYR	5.6
48	B1	98	LEU	5.6
48	D1	2	SER	5.6
21	CU	16	GLY	5.6
7	CG	81	GLY	5.5
1	CA	1030(A)	G	5.5
25	CY	53	G	5.5
46	BZ	114	GLY	5.5
25	CY	56	C	5.5
19	CS	41	VAL	5.4
46	DZ	116	VAL	5.4
46	DZ	96	VAL	5.4
28	BD	276	LYS	5.4
5	CE	90	VAL	5.3
17	AQ	27	PHE	5.3
3	CC	167	TRP	5.3
45	DY	5	MET	5.3
5	CE	94	ALA	5.2
25	AY	36	A	5.2

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Mol	Chain	Res	Type	RSRZ
13	CM	87	TYR	5.2
23	CW	38	A	5.2
12	CL	64	TYR	5.2
9	CI	15	ALA	5.2
23	CW	13	C	5.2
25	CY	64	A	5.2
46	DZ	108	PRO	5.1
7	AG	79	ARG	5.1
10	CJ	63	PHE	5.1
9	CI	67	GLY	5.1
22	CV	22	U	5.1
14	CN	2	ALA	5.0
2	CB	32	ILE	5.0
2	CB	132	LYS	5.0
13	AM	122	LYS	5.0
1	CA	1532	U	5.0
2	AB	101	MET	5.0
3	CC	197	GLY	5.0
47	D0	3	HIS	5.0
17	CQ	54	GLY	5.0
23	CW	75	C	5.0
22	CV	21	C	5.0
46	DZ	111	VAL	4.9
2	CB	97	TRP	4.9
13	CM	60	VAL	4.9
32	DH	105	LEU	4.9
56	D9	37	GLY	4.9
23	AW	4	C	4.9
37	DQ	33	GLY	4.9
1	CA	1035	A	4.9
26	DA	2173	A	4.9
16	AP	2	VAL	4.9
2	CB	207	ALA	4.9
31	DG	48	GLU	4.9
1	AA	1532	U	4.8
23	CW	5	G	4.8
46	DZ	156	LYS	4.8
26	DA	2133	G	4.8
47	B0	7	LEU	4.8
1	AA	1036	G	4.8
56	D9	16	VAL	4.8
22	AV	14	A	4.8

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Mol	Chain	Res	Type	RSRZ
46	DZ	171	ILE	4.8
7	CG	156	TRP	4.8
2	CB	201	ILE	4.8
19	CS	52	TYR	4.8
9	CI	110	GLU	4.8
19	CS	75	ALA	4.7
19	CS	84	GLY	4.7
46	DZ	143	GLY	4.7
23	CW	56	C	4.7
1	AA	1031	G	4.7
23	CW	24	G	4.7
19	CS	71	LEU	4.7
45	DY	45	VAL	4.7
5	CE	13	ILE	4.7
9	AI	15	ALA	4.7
9	CI	122	ALA	4.7
21	AU	17	THR	4.7
51	D4	54	GLY	4.7
26	DA	2145	C	4.7
1	CA	1036	G	4.7
25	AY	34	G	4.7
31	DG	140	ILE	4.7
9	CI	49	PRO	4.6
9	AI	113	LYS	4.6
3	CC	194	GLY	4.6
9	AI	106	ALA	4.6
9	CI	106	ALA	4.6
10	CJ	46	ARG	4.6
9	CI	125	TYR	4.6
31	DG	19	LEU	4.6
9	CI	18	PHE	4.6
23	AW	3	C	4.6
10	CJ	71	LEU	4.6
1	AA	1028	C	4.6
54	D7	48	LYS	4.6
1	AA	1257	U	4.6
22	AV	12	A	4.6
46	DZ	147	GLY	4.6
3	AC	204	LEU	4.6
10	CJ	74	ILE	4.6
17	CQ	36	ILE	4.6
14	CN	36	PHE	4.6

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Mol	Chain	Res	Type	RSRZ
3	CC	120	VAL	4.5
26	BA	2140	C	4.5
4	AD	2	GLY	4.5
10	CJ	44	VAL	4.5
12	CL	18	VAL	4.5
26	DA	896	A	4.5
14	CN	10	ALA	4.5
23	CW	40	C	4.5
3	CC	101	LEU	4.5
26	DA	2802	G	4.5
20	CT	9	ASN	4.5
8	CH	130	GLY	4.5
9	CI	124	GLN	4.5
5	CE	109	ILE	4.5
9	AI	81	ILE	4.5
9	CI	79	LEU	4.5
1	CA	1030	C	4.5
23	CW	28	G	4.4
9	AI	19	LEU	4.4
3	AC	39	ILE	4.4
23	CW	14	A	4.4
14	CN	4	LYS	4.4
19	CS	30	LEU	4.4
25	CY	5	G	4.4
3	CC	129	ALA	4.4
19	CS	49	ILE	4.4
10	CJ	62	HIS	4.4
12	CL	32	PHE	4.4
8	CH	93	VAL	4.4
14	CN	42	ILE	4.4
5	CE	133	TYR	4.4
44	DX	69	TYR	4.4
21	CU	13	ILE	4.4
25	CY	2	C	4.3
14	CN	38	GLY	4.3
23	CW	15	G	4.3
9	CI	10	ARG	4.3
9	CI	85	LEU	4.3
54	B7	47	ARG	4.3
9	CI	112	LYS	4.3
9	CI	75	ASP	4.3
22	AV	23	A	4.3

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Mol	Chain	Res	Type	RSRZ
15	CO	57	LEU	4.3
7	CG	154	TYR	4.3
9	CI	116	LYS	4.3
3	CC	126	ARG	4.3
9	CI	114	TYR	4.3
23	AW	20	U	4.3
10	AJ	98	ILE	4.3
23	CW	10	G	4.3
26	DA	888	C	4.3
32	DH	107	VAL	4.3
37	DQ	5	ARG	4.3
16	AP	19	ILE	4.2
3	CC	4	LYS	4.2
23	CW	6	G	4.2
10	CJ	49	VAL	4.2
13	CM	101	GLN	4.2
53	D6	54	ILE	4.2
10	CJ	54	PHE	4.2
32	DH	6	ARG	4.2
1	CA	1220	G	4.2
10	CJ	72	VAL	4.2
16	CP	51	VAL	4.2
14	CN	50	LYS	4.2
12	CL	90	VAL	4.2
25	CY	57	G	4.2
53	D6	52	VAL	4.2
3	CC	185	GLY	4.2
13	CM	88	ARG	4.2
46	DZ	172	ALA	4.2
2	CB	71	VAL	4.2
25	CY	6	G	4.2
2	CB	70	PHE	4.2
16	AP	38	TYR	4.2
2	CB	101	MET	4.2
21	CU	2	GLY	4.2
26	DA	2156	G	4.1
7	CG	4	ARG	4.1
54	D7	47	ARG	4.1
20	CT	72	LEU	4.1
23	AW	73	A	4.1
46	DZ	149	SER	4.1
26	BA	2132	U	4.1

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Mol	Chain	Res	Type	RSRZ
46	DZ	139	VAL	4.1
9	CI	4	TYR	4.1
26	BA	2145	C	4.1
9	CI	69	GLY	4.1
53	D6	11	LEU	4.1
23	CW	30	G	4.1
28	BD	2	ALA	4.1
1	CA	1531	A	4.1
3	CC	60	ALA	4.1
32	DH	113	VAL	4.1
46	BZ	106	GLY	4.1
7	CG	22	LEU	4.1
9	CI	127	LYS	4.1
25	CY	61	C	4.1
23	AW	5	G	4.1
13	CM	97	PRO	4.1
32	DH	72	ILE	4.1
46	DZ	125	LEU	4.1
1	CA	1001	A	4.1
45	DY	55	TYR	4.1
9	AI	109	VAL	4.0
41	DU	2	PRO	4.0
1	AA	1027	C	4.0
14	CN	59	ALA	4.0
25	AY	24	G	4.0
39	DS	56	LEU	4.0
25	CY	62	C	4.0
51	D4	50	VAL	4.0
45	DY	44	ILE	4.0
3	CC	145	GLY	4.0
14	CN	58	LYS	4.0
2	CB	131	PRO	4.0
21	CU	11	GLY	4.0
3	CC	184	TYR	4.0
23	AW	69	G	4.0
48	B1	2	SER	4.0
4	CD	134	ASP	4.0
46	BZ	108	PRO	4.0
21	AU	2	GLY	4.0
3	CC	160	ALA	4.0
7	CG	79	ARG	4.0
26	DA	2153	G	4.0

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Mol	Chain	Res	Type	RSRZ
37	DQ	22	LYS	4.0
14	CN	49	HIS	4.0
19	CS	66	MET	4.0
47	D0	44	ARG	4.0
54	B7	48	LYS	3.9
25	CY	19	G	3.9
46	BZ	141	VAL	3.9
9	CI	19	LEU	3.9
2	AB	126	GLU	3.9
32	DH	106	THR	3.9
23	CW	41	C	3.9
31	DG	159	VAL	3.9
33	DI	38	LEU	3.9
37	DQ	104	PHE	3.9
46	DZ	115	GLY	3.9
1	CA	1034	G	3.9
3	CC	134	ILE	3.9
3	CC	57	ILE	3.9
9	AI	47	LEU	3.9
23	CW	36	A	3.9
21	CU	8	THR	3.9
21	CU	17	THR	3.9
11	AK	25	TYR	3.9
16	AP	39	TYR	3.9
46	DZ	141	VAL	3.9
3	AC	87	LEU	3.9
37	DQ	65	PHE	3.9
10	CJ	48	THR	3.9
2	CB	228	GLY	3.9
3	AC	81	GLY	3.9
4	CD	47	ARG	3.9
23	CW	74	C	3.9
13	CM	82	MET	3.9
14	CN	55	GLY	3.9
19	CS	53	ASN	3.9
8	CH	2	LEU	3.9
10	CJ	50	ILE	3.9
10	AJ	18	ALA	3.8
2	CB	152	PHE	3.8
9	CI	17	VAL	3.8
39	DS	11	LYS	3.8
26	DA	2170	A	3.8

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Mol	Chain	Res	Type	RSRZ
3	CC	206	GLU	3.8
28	DD	37	LEU	3.8
8	CH	95	VAL	3.8
55	D8	26	LYS	3.8
26	DA	1509	C	3.8
39	DS	3	ARG	3.8
2	CB	163	PHE	3.8
1	CA	1202	G	3.8
54	D7	1	MET	3.8
26	BA	2794	C	3.8
17	CQ	84	LEU	3.8
46	DZ	170	THR	3.8
26	BA	2793	G	3.8
23	CW	25	C	3.8
14	CN	41	ARG	3.8
9	CI	80	GLY	3.8
47	D0	21	LEU	3.8
47	D0	69	PHE	3.8
2	CB	29	ALA	3.8
20	CT	28	ALA	3.8
26	BA	1509	C	3.8
26	DA	2793	G	3.8
51	D4	51	ASP	3.8
2	AB	133	LYS	3.8
39	DS	54	LEU	3.8
46	BZ	120	ILE	3.7
48	B1	97	LEU	3.7
3	CC	187	ALA	3.7
4	CD	146	ILE	3.7
20	AT	67	ALA	3.7
51	D4	40	HIS	3.7
16	AP	68	ASP	3.7
9	CI	81	ILE	3.7
31	DG	41	GLN	3.7
31	DG	25	TYR	3.7
21	AU	15	ARG	3.7
26	BA	885	C	3.7
2	CB	33	TYR	3.7
3	CC	6	HIS	3.7
12	CL	28	LYS	3.7
5	CE	81	GLU	3.7
9	CI	108	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
21	CU	10	ARG	3.7
44	DX	68	ARG	3.7
1	AA	1034	G	3.7
1	CA	1002	G	3.7
1	CA	1224	G	3.7
22	CV	14	A	3.7
22	AV	22	U	3.7
39	DS	12	PHE	3.7
46	DZ	137	ILE	3.7
26	DA	2119	A	3.7
30	DF	208	GLY	3.6
17	AQ	35	VAL	3.6
39	DS	40	ILE	3.6
1	AA	1030(A)	G	3.6
25	AY	47	U	3.6
26	DA	2160	G	3.6
9	CI	30	GLY	3.6
23	CW	65	G	3.6
7	CG	78	ARG	3.6
13	CM	7	VAL	3.6
9	CI	27	THR	3.6
37	DQ	28	ALA	3.6
17	CQ	23	VAL	3.6
7	AG	156	TRP	3.6
26	DA	2113	U	3.6
16	AP	60	LEU	3.6
36	DP	59	LEU	3.6
13	CM	105	THR	3.6
46	DZ	173	ALA	3.6
23	AW	72	C	3.6
26	BA	2146	C	3.6
21	CU	15	ARG	3.6
39	DS	5	THR	3.6
13	CM	118	ALA	3.6
41	DU	21	ALA	3.6
31	DG	39	ILE	3.6
1	CA	1001(A)	G	3.6
25	CY	63	G	3.6
26	DA	2116	G	3.6
26	DA	2149	G	3.6
19	CS	14	HIS	3.6
3	AC	206	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
20	AT	74	LYS	3.6
3	AC	184	TYR	3.6
8	CH	94	TYR	3.6
3	CC	128	PHE	3.5
9	CI	28	VAL	3.5
23	AW	14	A	3.5
40	DT	75	ILE	3.5
3	CC	154	SER	3.5
39	DS	7	TYR	3.5
44	DX	2	LYS	3.5
3	AC	8	ILE	3.5
26	DA	2146	C	3.5
4	AD	155	LEU	3.5
19	CS	35	SER	3.5
13	CM	104	ARG	3.5
25	AY	1	G	3.5
31	DG	11	TYR	3.5
2	CB	177	ALA	3.5
10	AJ	73	ASP	3.5
32	DH	102	ALA	3.5
32	DH	123	PHE	3.5
10	CJ	93	GLY	3.5
25	AY	35	A	3.5
2	CB	31	TYR	3.5
9	CI	105	ASP	3.5
2	CB	37	ASN	3.5
31	DG	136	ARG	3.5
31	DG	149	VAL	3.5
39	DS	35	ILE	3.5
19	CS	81	ARG	3.5
8	CH	124	ALA	3.5
9	CI	62	TYR	3.5
4	AD	5	ILE	3.5
17	AQ	36	ILE	3.5
21	CU	5	ASP	3.5
47	D0	37	LEU	3.5
20	AT	55	ILE	3.5
18	AR	78	LEU	3.5
28	DD	38	LYS	3.5
49	D2	60	LEU	3.5
25	CY	13	C	3.4
51	B4	59	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
3	CC	204	LEU	3.4
9	CI	102	LEU	3.4
1	AA	1030(B)	C	3.4
6	CF	55	ASP	3.4
17	AQ	28	PRO	3.4
31	DG	35	GLU	3.4
5	CE	105	VAL	3.4
3	CC	171	GLY	3.4
9	AI	117	HIS	3.4
26	DA	2123	G	3.4
44	DX	33	LYS	3.4
25	AY	56	C	3.4
26	DA	2144	U	3.4
2	AB	232	PRO	3.4
9	AI	126	SER	3.4
12	AL	29	GLY	3.4
4	CD	188	LEU	3.4
12	CL	13	LYS	3.4
1	AA	1030(C)	G	3.4
23	AW	6	G	3.4
25	AY	5	G	3.4
25	CY	47	U	3.4
26	BA	2131	G	3.4
5	AE	28	PHE	3.4
9	AI	98	PRO	3.4
26	DA	886	C	3.4
36	DP	118	GLY	3.4
47	D0	59	LEU	3.4
11	CK	126	ARG	3.4
51	D4	55	ARG	3.4
1	CA	1150	U	3.4
55	D8	35	GLN	3.4
32	DH	36	PRO	3.4
2	CB	214	ILE	3.4
20	CT	41	ILE	3.4
12	CL	55	VAL	3.4
16	AP	59	TRP	3.4
28	DD	2	ALA	3.4
31	DG	2	PRO	3.4
2	CB	48	MET	3.4
23	AW	13	C	3.4
14	CN	31	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
46	DZ	146	ILE	3.4
9	CI	126	SER	3.3
31	DG	49	ASP	3.3
46	DZ	118	GLN	3.3
47	D0	4	LYS	3.3
2	CB	200	ILE	3.3
12	CL	27	LEU	3.3
23	CW	23	A	3.3
26	DA	2131	G	3.3
42	DV	73	SER	3.3
19	CS	40	ILE	3.3
24	AX	67	C	3.3
3	CC	12	LEU	3.3
1	AA	1531	A	3.3
1	AA	1002	G	3.3
21	CU	24	ARG	3.3
26	DA	2319	G	3.3
5	CE	11	ILE	3.3
7	CG	84	ASN	3.3
16	AP	17	TYR	3.3
52	D5	58	LEU	3.3
26	BA	2062	A	3.3
23	AW	65	G	3.3
13	CM	64	TRP	3.3
8	CH	112	LEU	3.3
31	DG	152	LEU	3.3
36	DP	45	LEU	3.3
3	CC	23	TYR	3.3
23	AW	25	C	3.3
23	CW	47	U	3.3
25	AY	13	C	3.3
26	BA	2161	C	3.3
26	DA	2138	C	3.3
10	CJ	26	ALA	3.3
25	AY	38	A	3.3
31	DG	163	ALA	3.3
23	CW	27	G	3.3
10	AJ	63	PHE	3.3
3	AC	14	ILE	3.3
5	AE	118	ILE	3.3
14	CN	7	ILE	3.3
16	CP	48	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
36	DP	32	THR	3.3
5	CE	30	ALA	3.3
13	CM	99	ARG	3.3
25	CY	21	A	3.3
26	DA	2115	G	3.3
2	CB	115	LEU	3.2
10	CJ	65	LEU	3.2
14	CN	24	CYS	3.2
7	AG	154	TYR	3.2
10	CJ	13	HIS	3.2
15	CO	60	VAL	3.2
9	CI	128	ARG	3.2
2	CB	34	ALA	3.2
3	CC	121	ALA	3.2
22	CV	15	A	3.2
2	CB	203	GLY	3.2
23	CW	34	G	3.2
25	CY	65	G	3.2
26	DA	883	G	3.2
2	AB	165	VAL	3.2
17	CQ	73	VAL	3.2
36	DP	57	THR	3.2
26	DA	2128	C	3.2
46	DZ	99	TYR	3.2
13	AM	2	ALA	3.2
1	AA	1030(D)	A	3.2
3	CC	47	LEU	3.2
13	CM	74	VAL	3.2
3	CC	65	ALA	3.2
13	CM	75	ALA	3.2
8	CH	9	MET	3.2
17	CQ	92	ARG	3.2
44	DX	1	MET	3.2
4	AD	135	LEU	3.2
19	CS	32	LYS	3.2
20	CT	26	ASN	3.2
27	DB	119	G	3.2
26	DA	2140	C	3.2
3	CC	147	LYS	3.2
3	CC	199	LYS	3.2
1	CA	1363(A)	A	3.2
3	CC	87	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
7	CG	16	LEU	3.2
23	CW	64	A	3.2
25	CY	26	A	3.2
10	CJ	6	ILE	3.2
36	DP	75	ILE	3.2
5	CE	16	THR	3.2
32	DH	52	VAL	3.2
9	CI	12	GLU	3.2
1	AA	1447	A	3.2
3	AC	168	ALA	3.2
21	AU	18	TYR	3.2
1	AA	163	C	3.2
26	DA	2164	C	3.2
47	D0	74	ARG	3.1
14	CN	27	CYS	3.1
17	CQ	90	ILE	3.1
26	DA	652(B)	A	3.1
47	D0	42	GLY	3.1
32	DH	25	LYS	3.1
14	CN	47	LEU	3.1
19	CS	20	LEU	3.1
1	AA	1026	G	3.1
9	CI	103	THR	3.1
11	AK	29	ILE	3.1
51	D4	44	THR	3.1
3	CC	146	ALA	3.1
23	CW	26	A	3.1
27	DB	59	A	3.1
2	CB	197	VAL	3.1
46	BZ	111	VAL	3.1
13	AM	97	PRO	3.1
29	BE	195	LEU	3.1
46	DZ	5	LEU	3.1
13	CM	95	GLY	3.1
23	CW	19	G	3.1
4	CD	141	ARG	3.1
7	AG	40	ALA	3.1
32	BH	145	ALA	3.1
47	B0	3	HIS	3.1
1	CA	1219	U	3.1
12	CL	69	TYR	3.1
5	AE	6	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
10	AJ	40	LEU	3.1
32	DH	128	PRO	3.1
40	DT	111	ARG	3.1
20	AT	12	ALA	3.1
25	AY	19	G	3.1
31	BG	146	TYR	3.1
2	CB	118	LEU	3.1
37	DQ	6	ARG	3.1
39	DS	58	LEU	3.1
2	CB	211	ILE	3.1
31	DG	157	ILE	3.1
32	DH	2	SER	3.1
32	DH	115	VAL	3.1
27	DB	118	G	3.1
7	CG	32	ARG	3.1
8	CH	131	GLY	3.1
14	CN	35	ARG	3.1
5	CE	123	LEU	3.1
17	CQ	98	LEU	3.1
46	DZ	117	LEU	3.1
26	BA	2143	C	3.1
26	DA	2803	C	3.1
9	CI	63	ILE	3.1
39	BS	37	ALA	3.1
9	CI	65	VAL	3.1
17	CQ	56	VAL	3.1
25	CY	22	G	3.0
25	CY	25	C	3.0
9	AI	120	ARG	3.0
14	CN	60	SER	3.0
31	DG	51	ARG	3.0
9	AI	65	VAL	3.0
17	CQ	9	VAL	3.0
44	DX	43	VAL	3.0
14	CN	16	PHE	3.0
32	DH	103	LEU	3.0
36	DP	51	PHE	3.0
13	CM	72	ALA	3.0
23	AW	2	C	3.0
31	DG	88	ILE	3.0
39	DS	33	LYS	3.0
17	AQ	30	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
14	CN	6	LEU	3.0
33	DI	35	LEU	3.0
2	AB	200	ILE	3.0
3	CC	5	ILE	3.0
5	CE	21	ALA	3.0
13	CM	76	ALA	3.0
26	BA	271(K)	U	3.0
26	DA	1026	U	3.0
41	DU	17	ILE	3.0
56	D9	3	VAL	3.0
55	D8	61	LEU	3.0
9	CI	5	TYR	3.0
11	CK	25	TYR	3.0
45	DY	63	LYS	3.0
8	CH	134	ILE	3.0
14	CN	30	ALA	3.0
1	AA	1001(A)	G	3.0
25	AY	57	G	3.0
4	AD	3	ARG	3.0
8	CH	92	ARG	3.0
9	CI	42	ARG	3.0
19	CS	36	ARG	3.0
36	DP	50	ARG	3.0
8	AH	5	PRO	3.0
51	B4	50	VAL	3.0
13	CM	77	ASN	3.0
47	D0	5	LYS	3.0
4	AD	11	LEU	3.0
45	DY	90	LEU	3.0
25	CY	12	U	3.0
25	CY	33	U	3.0
31	DG	146	TYR	3.0
32	DH	157	TYR	3.0
1	AA	161	A	3.0
1	AA	162	A	3.0
2	AB	130	ARG	3.0
26	DA	885	C	3.0
26	DA	2174	C	3.0
5	AE	55	VAL	3.0
17	CQ	10	VAL	3.0
49	D2	1	MET	3.0
9	CI	33	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
2	AB	227	GLY	3.0
25	AY	23	A	3.0
1	CA	1116	C	3.0
13	CM	117	VAL	2.9
26	DA	2139	C	3.0
45	DY	42	VAL	2.9
1	AA	1023	G	2.9
19	AS	71	LEU	2.9
37	DQ	2	LEU	2.9
4	AD	180	GLY	2.9
9	CI	107	ARG	2.9
10	AJ	21	GLN	2.9
18	CR	87	ARG	2.9
32	BH	2	SER	2.9
5	AE	108	ALA	2.9
11	AK	75	TYR	2.9
11	CK	114	VAL	2.9
26	DA	645	C	2.9
39	DS	14	VAL	2.9
2	AB	175	ARG	2.9
2	CB	133	LYS	2.9
37	DQ	18	LYS	2.9
43	DW	82	LEU	2.9
47	D0	7	LEU	2.9
55	D8	25	MET	2.9
45	DY	61	ILE	2.9
46	DZ	121	HIS	2.9
14	CN	40	CYS	2.9
1	CA	983	A	2.9
9	CI	83	ARG	2.9
39	DS	20	ARG	2.9
16	AP	21	VAL	2.9
3	CC	159	GLY	2.9
8	CH	133	LEU	2.9
26	DA	2142	C	2.9
1	CA	1030(C)	G	2.9
9	CI	52	ALA	2.9
23	CW	29	G	2.9
48	D1	37	ILE	2.9
4	CD	9	CYS	2.9
46	BZ	115	GLY	2.9
24	CX	65	C	2.9

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Mol	Chain	Res	Type	RSRZ
34	DN	116	LEU	2.9
45	DY	31	LEU	2.9
7	CG	152	ALA	2.9
3	CC	152	ILE	2.9
20	CT	63	ILE	2.9
32	BH	4	ILE	2.9
4	AD	138	TYR	2.9
13	CM	21	TYR	2.9
19	CS	12	ASP	2.9
46	BZ	143	GLY	2.9
3	AC	94	LEU	2.9
16	AP	1	MET	2.9
23	CW	21	A	2.9
23	CW	67	C	2.9
31	BG	93	THR	2.9
7	CG	39	ALA	2.9
2	CB	162	ILE	2.9
8	CH	111	ILE	2.9
7	AG	81	GLY	2.9
17	AQ	99	SER	2.9
8	CH	119	LEU	2.9
54	D7	23	ARG	2.9
1	CA	1149	C	2.9
8	CH	135	CYS	2.9
15	CO	4	THR	2.9
13	AM	107	ALA	2.9
47	D0	2	ALA	2.9
10	CJ	58	ASP	2.9
28	BD	38	LYS	2.9
39	DS	57	LYS	2.9
28	DD	216	GLY	2.9
2	CB	137	ARG	2.8
37	DQ	32	TYR	2.8
2	CB	136	VAL	2.8
12	CL	60	LEU	2.8
20	AT	43	LEU	2.8
26	DA	2124	G	2.8
50	D3	53	LEU	2.8
26	DA	2801(A)	A	2.8
19	CS	68	GLY	2.8
2	AB	214	ILE	2.8
37	DQ	47	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
46	DZ	50	GLN	2.8
8	CH	65	TYR	2.8
6	AF	79	LEU	2.8
32	DH	7	LEU	2.8
37	DQ	1	MET	2.8
46	DZ	144	LEU	2.8
1	CA	1033	G	2.8
23	AW	44	G	2.8
1	CA	1115	C	2.8
1	CA	1286	A	2.8
23	CW	35	A	2.8
46	DZ	57	ILE	2.8
9	CI	88	TYR	2.8
26	DA	2897	U	2.8
32	DH	94	TYR	2.8
4	AD	174	LEU	2.8
10	AJ	90	LEU	2.8
32	DH	71	LEU	2.8
33	DI	30	LEU	2.8
30	BF	89	VAL	2.8
46	DZ	119	GLU	2.8
48	D1	62	VAL	2.8
4	AD	110	PHE	2.8
14	CN	26	ARG	2.8
46	BZ	107	THR	2.8
16	AP	7	ALA	2.8
23	AW	15	G	2.8
23	CW	57	G	2.8
26	DA	2147	G	2.8
2	CB	139	LYS	2.8
26	DA	2161	C	2.8
26	DA	2896	C	2.8
10	CJ	59	SER	2.8
34	BN	71	ILE	2.8
3	AC	193	TYR	2.8
3	CC	91	LEU	2.8
19	CS	16	LEU	2.8
30	DF	32	LEU	2.8
34	DN	26	LEU	2.8
3	CC	173	VAL	2.8
53	D6	5	VAL	2.8
56	B9	25	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
10	CJ	67	THR	2.8
9	CI	72	GLY	2.8
46	BZ	104	PHE	2.8
10	CJ	41	PRO	2.8
1	CA	973	G	2.8
1	CA	1322	C	2.8
14	CN	46	GLU	2.8
23	CW	52	G	2.8
19	CS	69	HIS	2.8
16	AP	28	ARG	2.8
5	AE	123	LEU	2.8
55	D8	29	LYS	2.8
3	CC	158	GLY	2.8
5	CE	99	GLY	2.8
33	BI	19	VAL	2.8
55	D8	38	GLY	2.8
56	B9	7	VAL	2.8
12	CL	30	ALA	2.8
37	DQ	114	ALA	2.8
1	CA	1066	C	2.8
1	CA	1354	C	2.8
2	CB	40	HIS	2.8
8	AH	4	ASP	2.8
1	CA	1357	A	2.8
12	CL	70	ILE	2.8
31	BG	88	ILE	2.8
25	AY	12	U	2.8
18	AR	31	LEU	2.8
45	DY	14	LEU	2.8
5	CE	55	VAL	2.8
7	AG	85	TYR	2.8
46	DZ	106	GLY	2.8
8	CH	11	THR	2.8
14	CN	13	THR	2.8
19	CS	77	THR	2.8
4	CD	206	PHE	2.8
9	AI	37	PHE	2.8
50	D3	21	ALA	2.8
13	CM	65	LYS	2.8
22	AV	15	A	2.7
33	DI	12	LEU	2.7
3	CC	186	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
4	CD	49	ARG	2.7
5	CE	14	ARG	2.7
17	CQ	5	VAL	2.7
32	DH	37	VAL	2.7
48	B1	35	THR	2.7
17	CQ	100	LYS	2.7
16	AP	29	ASP	2.7
48	D1	38	SER	2.7
5	CE	8	GLU	2.7
32	DH	47	GLU	2.7
5	CE	80	ILE	2.7
48	B1	7	ILE	2.7
3	CC	81	GLY	2.7
9	CI	8	GLY	2.7
47	D0	52	GLY	2.7
18	AR	79	LEU	2.7
9	CI	93	ARG	2.7
28	BD	275	LYS	2.7
36	DP	79	ARG	2.7
8	CH	58	TYR	2.7
13	CM	10	PRO	2.7
41	DU	63	VAL	2.7
10	AJ	68	HIS	2.7
20	CT	59	ALA	2.7
33	DI	36	ALA	2.7
39	DS	34	HIS	2.7
4	CD	122	ARG	2.7
5	AE	129	ILE	2.7
9	AI	10	ARG	2.7
2	AB	97	TRP	2.7
16	AP	6	LEU	2.7
1	CA	1250	A	2.7
5	AE	120	THR	2.7
53	D6	14	THR	2.7
3	AC	120	VAL	2.7
8	AH	93	VAL	2.7
31	DG	102	PHE	2.7
46	DZ	174	VAL	2.7
48	B1	70	VAL	2.7
41	DU	47	TYR	2.7
1	CA	1190	G	2.7
3	AC	200	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
2	CB	66	GLY	2.7
31	DG	115	ARG	2.7
12	CL	85	ILE	2.7
46	DZ	59	LEU	2.7
26	BA	2128	C	2.7
1	CA	1092	A	2.7
2	AB	70	PHE	2.7
9	CI	26	VAL	2.7
31	DG	70	VAL	2.7
32	DH	38	SER	2.7
3	CC	200	ALA	2.7
5	CE	17	ALA	2.7
4	AD	50	ARG	2.7
12	CL	88	GLY	2.7
25	CY	15	G	2.7
55	D8	41	ILE	2.7
5	CE	142	LEU	2.7
10	CJ	68	HIS	2.7
31	DG	86	MET	2.7
2	AB	123	ALA	2.7
3	CC	122	GLU	2.7
26	DA	2062	A	2.7
31	DG	160	VAL	2.7
34	DN	9	VAL	2.7
55	B8	65	GLU	2.7
9	CI	57	GLY	2.7
23	CW	66	U	2.7
32	DH	82	GLY	2.7
2	AB	135	GLN	2.7
2	CB	76	GLN	2.7
8	AH	35	ILE	2.7
9	AI	77	ILE	2.7
12	AL	7	ILE	2.7
20	CT	55	ILE	2.7
28	DD	271	ILE	2.7
28	DD	177	LEU	2.7
8	CH	122	ARG	2.7
14	AN	14	PRO	2.7
1	CA	1039	C	2.7
26	BA	2108	C	2.7
9	CI	46	ALA	2.7
11	CK	68	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
36	DP	125	VAL	2.7
46	DZ	105	VAL	2.7
55	D8	34	TRP	2.7
1	CA	1041	A	2.7
27	DB	58	A	2.7
4	AD	158	ILE	2.6
5	AE	18	ARG	2.6
37	DQ	91	GLU	2.6
3	AC	32	LEU	2.6
10	AJ	71	LEU	2.6
20	AT	72	LEU	2.6
23	CW	18	G	2.6
23	CW	22	G	2.6
25	AY	71	G	2.6
14	AN	15	LYS	2.6
25	AY	48	C	2.6
36	DP	76	LYS	2.6
2	CB	81	VAL	2.6
3	AC	207	VAL	2.6
11	CK	125	PHE	2.6
12	CL	56	ALA	2.6
32	DH	76	VAL	2.6
1	AA	204	U	2.6
23	AW	50	U	2.6
26	DA	2114	A	2.6
9	CI	20	ARG	2.6
19	CS	83	HIS	2.6
5	AE	119	LEU	2.6
18	CR	85	LEU	2.6
31	DG	17	PRO	2.6
49	D2	8	LYS	2.6
1	AA	1024	G	2.6
1	CA	1061	G	2.6
1	CA	1338	G	2.6
36	BP	37	GLY	2.6
11	CK	89	ALA	2.6
23	AW	56	C	2.6
37	DQ	96	VAL	2.6
45	DY	91	GLU	2.6
9	CI	121	ARG	2.6
47	D0	55	ARG	2.6
11	AK	42	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
39	DS	92	TYR	2.6
1	CA	949	A	2.6
1	CA	969	A	2.6
13	CM	92	HIS	2.6
3	CC	188	LEU	2.6
8	AH	2	LEU	2.6
10	AJ	4	ILE	2.6
13	CM	66	LEU	2.6
2	CB	45	GLN	2.6
16	AP	41	PRO	2.6
3	AC	15	THR	2.6
3	CC	2	GLY	2.6
3	CC	205	GLY	2.6
10	CJ	51	ARG	2.6
32	DH	95	ARG	2.6
1	CA	976	G	2.6
1	CA	1040	U	2.6
23	CW	12	U	2.6
36	DP	101	VAL	2.6
48	D1	70	VAL	2.6
14	CN	11	LYS	2.6
4	AD	204	ILE	2.6
17	CQ	22	LEU	2.6
20	CT	20	LEU	2.6
33	DI	41	GLU	2.6
50	D3	16	PRO	2.6
3	CC	181	ASN	2.6
3	CC	117	ALA	2.6
5	AE	95	ALA	2.6
3	CC	207	VAL	2.6
16	AP	20	VAL	2.6
37	DQ	97	VAL	2.6
23	AW	34	G	2.6
26	BA	888	C	2.6
20	AT	18	GLN	2.6
9	AI	114	TYR	2.6
3	AC	175	LEU	2.6
8	CH	104	ARG	2.6
8	CH	83	ILE	2.6
12	CL	48	PRO	2.6
21	AU	14	TRP	2.6
37	DQ	60	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
29	DE	77	ILE	2.6
20	AT	75	ASN	2.6
23	CW	45	U	2.6
9	CI	43	ALA	2.6
14	AN	20	ALA	2.6
33	DI	46	ALA	2.6
54	D7	20	ALA	2.6
3	AC	66	VAL	2.6
10	AJ	49	VAL	2.6
1	CA	962	C	2.6
10	CJ	60	ARG	2.6
33	DI	9	LEU	2.6
3	AC	18	TRP	2.6
9	CI	77	ILE	2.6
53	D6	42	TRP	2.6
1	CA	1225	A	2.6
15	CO	59	MET	2.6
7	CG	117	ALA	2.6
9	CI	117	HIS	2.6
10	AJ	47	PHE	2.6
3	CC	130	VAL	2.5
31	BG	149	VAL	2.5
25	AY	3	C	2.5
14	CN	14	PRO	2.5
15	AO	34	LEU	2.5
25	AY	53	G	2.5
36	DP	58	THR	2.5
26	BA	1026	U	2.5
35	DO	20	MET	2.5
11	AK	89	ALA	2.5
55	D8	7	HIS	2.5
3	AC	128	PHE	2.5
4	AD	148	VAL	2.5
15	AO	60	VAL	2.5
32	DH	35	VAL	2.5
16	CP	30	GLY	2.5
28	DD	56	GLY	2.5
31	DG	164	GLU	2.5
39	DS	90	GLY	2.5
53	D6	20	ASN	2.5
23	CW	42	C	2.5
33	BI	6	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
50	D3	26	LEU	2.5
16	AP	44	THR	2.5
32	DH	148	ILE	2.5
5	AE	10	MET	2.5
26	DA	614(B)	G	2.5
3	CC	22	TRP	2.5
5	CE	104	ALA	2.5
27	DB	90	A	2.5
47	B0	2	ALA	2.5
54	D7	18	PHE	2.5
4	AD	170	VAL	2.5
17	AQ	11	VAL	2.5
34	BN	5	VAL	2.5
45	DY	51	VAL	2.5
9	AI	127	LYS	2.5
13	CM	79	LYS	2.5
6	CF	21	LEU	2.5
16	AP	25	ARG	2.5
2	AB	148	TYR	2.5
3	AC	201	TYR	2.5
16	AP	36	ILE	2.5
25	CY	66	U	2.5
3	CC	69	HIS	2.5
37	DQ	20	ALA	2.5
39	DS	6	ALA	2.5
36	DP	91	PHE	2.5
39	DS	29	PHE	2.5
41	DU	40	PHE	2.5
7	CG	105	VAL	2.5
8	AH	118	VAL	2.5
8	CH	61	VAL	2.5
9	AI	108	VAL	2.5
6	CF	46	ARG	2.5
10	CJ	66	ARG	2.5
21	AU	10	ARG	2.5
55	D8	63	PRO	2.5
10	CJ	88	LEU	2.5
26	BA	2129	C	2.5
1	CA	961	U	2.5
15	AO	69	TYR	2.5
47	D0	43	THR	2.5
37	DQ	63	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
20	CT	44	ALA	2.5
37	DQ	121	ALA	2.5
41	DU	43	GLY	2.5
41	DU	48	ALA	2.5
1	AA	1529	G	2.5
4	AD	209	ARG	2.5
5	CE	20	GLN	2.5
10	AJ	11	PHE	2.5
20	AT	8	ARG	2.5
36	DP	15	ARG	2.5
33	DI	21	VAL	2.5
48	D1	30	VAL	2.5
6	AF	48	LEU	2.5
20	AT	24	LEU	2.5
29	DE	52	LEU	2.5
36	BP	105	LEU	2.5
2	CB	41	ILE	2.5
8	AH	6	ILE	2.5
17	AQ	90	ILE	2.5
28	DD	259	THR	2.5
31	DG	161	THR	2.5
8	CH	128	GLY	2.5
17	CQ	44	ALA	2.5
9	CI	71	SER	2.5
34	BN	46	VAL	2.5
6	AF	92	LYS	2.5
17	CQ	37	LYS	2.5
23	AW	10	G	2.5
26	BA	2805	G	2.5
31	DG	84	LYS	2.5
46	DZ	148	ASP	2.5
3	AC	188	LEU	2.5
8	AH	112	LEU	2.5
20	CT	24	LEU	2.5
37	DQ	37	LEU	2.5
13	CM	103	THR	2.5
2	AB	208	ILE	2.5
5	AE	13	ILE	2.5
14	AN	7	ILE	2.5
15	AO	87	ILE	2.5
21	CU	22	ARG	2.5
40	DT	110	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
8	AH	94	TYR	2.5
17	CQ	86	GLU	2.5
23	AW	67	C	2.5
48	D1	71	TYR	2.5
54	D7	22	MET	2.5
13	CM	13	LYS	2.4
28	DD	276	LYS	2.4
2	CB	232	PRO	2.4
28	BD	142	VAL	2.4
28	DD	34	VAL	2.4
26	DA	887	A	2.4
20	AT	13	LEU	2.4
1	CA	1305	G	2.4
2	AB	95	GLN	2.4
9	CI	111	ARG	2.4
32	DH	159	GLU	2.4
50	D3	29	ARG	2.4
4	AD	167	GLY	2.4
12	AL	67	THR	2.4
10	AJ	23	ILE	2.4
1	CA	1397	C	2.4
3	CC	142	MET	2.4
4	AD	147	ALA	2.4
13	CM	42	ALA	2.4
21	AU	21	TYR	2.4
36	DP	110	TYR	2.4
37	DQ	93	TYR	2.4
9	AI	59	PHE	2.4
3	CC	174	PRO	2.4
36	DP	47	ASP	2.4
46	DZ	62	PRO	2.4
2	AB	71	VAL	2.4
7	CG	5	ARG	2.4
10	CJ	64	GLU	2.4
16	AP	16	HIS	2.4
37	BQ	97	VAL	2.4
6	AF	61	LEU	2.4
28	DD	252	TRP	2.4
31	DG	106	LEU	2.4
3	CC	80	GLY	2.4
1	CA	1156	G	2.4
1	CA	1221	G	2.4

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Mol	Chain	Res	Type	RSRZ
3	CC	14	ILE	2.4
5	CE	118	ILE	2.4
19	AS	40	ILE	2.4
2	AB	48	MET	2.4
24	CX	46	G	2.4
25	AY	22	G	2.4
26	DA	2127	G	2.4
26	DA	2318	G	2.4
9	CI	119	ALA	2.4
33	DI	100	ALA	2.4
2	CB	55	PHE	2.4
8	AH	31	PHE	2.4
13	CM	67	GLU	2.4
46	DZ	140	ASP	2.4
7	CG	6	ARG	2.4
3	AC	148	GLY	2.4
8	AH	133	LEU	2.4
10	CJ	8	LEU	2.4
17	CQ	80	GLY	2.4
23	CW	50	U	2.4
47	D0	73	GLY	2.4
23	AW	23	A	2.4
45	BY	1	MET	2.4
1	AA	927	G	2.4
13	CM	23	TYR	2.4
16	AP	42	ARG	2.4
37	DQ	36	ALA	2.4
1	CA	1321	C	2.4
23	CW	68	C	2.4
25	CY	70	G	2.4
26	BA	2792	G	2.4
26	DA	2110	G	2.4
26	DA	2804	C	2.4
34	DN	69	GLN	2.4
3	AC	64	VAL	2.4
4	AD	140	VAL	2.4
15	CO	55	GLY	2.4
36	DP	95	VAL	2.4
55	D8	14	VAL	2.4
2	AB	187	LEU	2.4
3	CC	111	LEU	2.4
39	DS	47	THR	2.4

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Mol	Chain	Res	Type	RSRZ
55	D8	58	ILE	2.4
35	DO	31	LYS	2.4
41	DU	46	ALA	2.4
1	AA	1030	C	2.4
1	CA	980	C	2.4
1	CA	1117	G	2.4
9	CI	37	PHE	2.4
48	D1	68	PRO	2.4
1	CA	1257	U	2.4
2	AB	61	LEU	2.4
3	AC	91	LEU	2.4
14	CN	18	VAL	2.4
33	BI	68	LEU	2.4
33	DI	37	VAL	2.4
47	D0	38	VAL	2.4
55	D8	50	LEU	2.4
10	AJ	28	ARG	2.4
36	DP	87	ASP	2.4
39	DS	13	ARG	2.4
2	CB	127	ILE	2.4
55	D8	16	ILE	2.4
1	CA	1151	A	2.4
7	AG	7	ALA	2.4
4	AD	154	ASN	2.4
17	CQ	32	TYR	2.4
20	AT	69	GLY	2.4
43	DW	9	TYR	2.4
23	AW	66	U	2.4
9	CI	11	LYS	2.4
4	CD	135	LEU	2.4
8	AH	10	LEU	2.4
12	AL	18	VAL	2.4
17	CQ	11	VAL	2.4
25	CY	29	G	2.4
26	DA	2168	G	2.4
46	BZ	116	VAL	2.4
46	DZ	161	VAL	2.4
48	D1	61	ARG	2.4
19	CS	13	ASP	2.4
50	D3	23	LEU	2.4
2	AB	78	GLN	2.4
2	CB	231	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
8	AH	134	ILE	2.4
10	CJ	98	ILE	2.4
3	AC	169	ALA	2.4
19	CS	44	MET	2.4
1	CA	1287	A	2.3
46	DZ	4	ARG	2.3
4	CD	157	LEU	2.3
8	AH	95	VAL	2.3
13	CM	17	VAL	2.3
15	CO	34	LEU	2.3
31	BG	152	LEU	2.3
48	D1	98	LEU	2.3
1	AA	1353	G	2.3
26	DA	2159	G	2.3
26	DA	2792	G	2.3
20	CT	16	HIS	2.3
8	CH	15	ASN	2.3
39	DS	55	ALA	2.3
3	AC	185	GLY	2.3
4	AD	122	ARG	2.3
13	CM	100	GLY	2.3
13	CM	113	PRO	2.3
48	D1	28	GLY	2.3
3	CC	183	ASP	2.3
30	DF	77	ASP	2.3
33	BI	89	TYR	2.3
1	CA	1325	C	2.3
3	CC	196	LEU	2.3
26	BA	2142	C	2.3
31	BG	7	LEU	2.3
2	AB	233	SER	2.3
35	DO	57	VAL	2.3
43	DW	85	VAL	2.3
55	D8	21	LYS	2.3
10	CJ	43	ARG	2.3
20	CT	86	ARG	2.3
23	CW	44	G	2.3
2	AB	207	ALA	2.3
3	CC	13	GLY	2.3
5	CE	10	MET	2.3
8	AH	38	ILE	2.3
32	DH	8	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
52	D5	24	ALA	2.3
4	AD	133	VAL	2.3
5	CE	51	VAL	2.3
23	CW	61	C	2.3
25	AY	62	C	2.3
25	CY	4	C	2.3
4	AD	132	ARG	2.3
14	AN	23	ARG	2.3
16	AP	69	THR	2.3
28	DD	210	GLY	2.3
32	DH	14	GLY	2.3
9	AI	110	GLU	2.3
33	DI	88	ILE	2.3
36	DP	68	GLN	2.3
29	BE	28	ALA	2.3
45	DY	65	ALA	2.3
47	D0	53	MET	2.3
23	AW	1	G	2.3
23	CW	63	G	2.3
19	CS	10	PHE	2.3
31	DG	178	PHE	2.3
2	AB	98	LEU	2.3
4	CD	207	TYR	2.3
12	AL	27	LEU	2.3
32	DH	171	LEU	2.3
39	DS	26	LEU	2.3
44	DX	57	LEU	2.3
3	AC	63	ASN	2.3
4	CD	203	VAL	2.3
13	CM	106	ASN	2.3
45	DY	43	ASN	2.3
7	AG	34	GLY	2.3
31	DG	44	GLY	2.3
48	D1	22	GLY	2.3
51	B4	4	GLY	2.3
31	BG	49	ASP	2.3
56	D9	11	CYS	2.3
2	AB	222	ILE	2.3
3	AC	134	ILE	2.3
10	CJ	39	PRO	2.3
30	DF	186	ILE	2.3
46	DZ	109	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
50	D3	12	PRO	2.3
3	CC	179	ARG	2.3
26	BA	2141	G	2.3
26	DA	2157	G	2.3
55	D8	46	ARG	2.3
4	AD	97	LEU	2.3
13	CM	50	GLU	2.3
7	CG	109	ASN	2.3
28	DD	155	LEU	2.3
46	DZ	157	LEU	2.3
49	D2	24	LEU	2.3
49	D2	35	LEU	2.3
26	BA	529	A	2.3
26	BA	2790	A	2.3
14	AN	18	VAL	2.3
14	CN	56	VAL	2.3
15	AO	55	GLY	2.3
43	DW	14	PRO	2.3
3	AC	182	ILE	2.3
5	AE	21	ALA	2.3
8	AH	16	ALA	2.3
39	DS	79	ALA	2.3
14	AN	3	ARG	2.3
12	CL	16	GLU	2.3
17	CQ	24	GLU	2.3
51	B4	49	PHE	2.3
1	AA	1033	G	2.3
2	CB	75	LYS	2.3
15	CO	66	LEU	2.3
18	AR	66	LEU	2.3
19	AS	15	LEU	2.3
24	CX	4	G	2.3
29	BE	78	LEU	2.3
31	DG	107	LEU	2.3
47	B0	75	LEU	2.3
47	D0	75	LEU	2.3
5	AE	33	VAL	2.3
24	CX	72	A	2.3
37	DQ	35	VAL	2.3
48	D1	51	VAL	2.3
1	CA	1028	C	2.3
2	CB	30	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
11	CK	115	PRO	2.3
33	DI	79	ILE	2.2
46	DZ	124	ILE	2.2
1	CA	1348	U	2.2
26	DA	614(A)	U	2.2
7	CG	62	PHE	2.2
31	BG	80	PHE	2.2
8	AH	39	LEU	2.2
9	CI	54	ASP	2.2
10	CJ	10	GLY	2.2
31	DG	176	LEU	2.2
55	B8	60	LEU	2.2
1	CA	951	G	2.2
1	CA	1186	G	2.2
3	CC	48	TYR	2.2
8	AH	58	TYR	2.2
11	AK	87	THR	2.2
4	AD	115	ARG	2.2
4	CD	115	ARG	2.2
9	AI	14	VAL	2.2
10	AJ	44	VAL	2.2
13	AM	87	TYR	2.2
17	CQ	42	TYR	2.2
19	CS	51	VAL	2.2
26	BA	2154	G	2.2
30	DF	89	VAL	2.2
34	DN	140	VAL	2.2
51	D4	53	GLU	2.2
55	D8	22	VAL	2.2
26	DA	6	A	2.2
25	CY	72	C	2.2
5	AE	113	ALA	2.2
6	AF	54	LYS	2.2
7	CG	2	ALA	2.2
12	CL	47	LYS	2.2
29	BE	157	ALA	2.2
53	D6	22	ALA	2.2
1	CA	981	U	2.2
13	CM	9	ILE	2.2
25	AY	20	U	2.2
16	CP	9	PHE	2.2
2	CB	69	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
3	CC	43	LEU	2.2
6	CF	45	LEU	2.2
8	AH	63	LEU	2.2
9	AI	79	LEU	2.2
17	AQ	98	LEU	2.2
17	CQ	6	LEU	2.2
18	CR	66	LEU	2.2
34	DN	112	LEU	2.2
44	DX	9	LEU	2.2
14	AN	21	TYR	2.2
17	AQ	37	LYS	2.2
17	CQ	95	TYR	2.2
18	AR	52	PRO	2.2
28	BD	193	VAL	2.2
32	DH	13	LYS	2.2
41	BU	8	VAL	2.2
47	B0	5	LYS	2.2
8	AH	89	PRO	2.2
47	B0	51	VAL	2.2
1	CA	485	G	2.2
1	CA	1003	G	2.2
26	DA	652(U)	G	2.2
26	DA	2148	G	2.2
10	AJ	20	ALA	2.2
20	CT	67	ALA	2.2
36	BP	12	ALA	2.2
34	DN	76	SER	2.2
43	DW	13	SER	2.2
46	BZ	52	SER	2.2
13	CM	80	ARG	2.2
20	CT	25	ARG	2.2
45	DY	41	GLY	2.2
3	CC	72	LYS	2.2
15	AO	57	LEU	2.2
16	AP	27	LYS	2.2
19	CS	6	LYS	2.2
41	DU	20	LEU	2.2
53	B6	23	THR	2.2
2	AB	125	PRO	2.2
36	DP	38	GLN	2.2
8	AH	53	VAL	2.2
17	CQ	21	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
21	CU	18	TYR	2.2
29	DE	116	VAL	2.2
9	CI	82	ALA	2.2
29	BE	114	ALA	2.2
31	DG	110	ALA	2.2
1	CA	1024	G	2.2
3	CC	3	ASN	2.2
7	CG	33	ASP	2.2
11	AK	117	ASN	2.2
7	CG	76	ARG	2.2
8	AH	100	ILE	2.2
26	BA	229	A	2.2
13	CM	110	ARG	2.2
26	BA	2133	G	2.2
26	BA	2162	G	2.2
26	DA	2805	G	2.2
30	DF	78	ILE	2.2
32	DH	51	ARG	2.2
51	D4	58	ARG	2.2
5	CE	29	GLY	2.2
38	DR	9	LYS	2.2
51	D4	42	PHE	2.2
3	CC	33	LEU	2.2
37	DQ	34	LEU	2.2
20	AT	71	THR	2.2
2	AB	15	VAL	2.2
52	B5	60	VAL	2.2
11	AK	81	ASP	2.2
28	DD	272	ALA	2.2
33	BI	36	ALA	2.2
37	DQ	103	MET	2.2
46	BZ	1	MET	2.2
5	CE	76	ILE	2.2
8	AH	86	ILE	2.2
8	CH	45	ILE	2.2
1	CA	1218	C	2.2
12	CL	95	GLY	2.2
31	DG	77	ILE	2.2
7	CG	103	TRP	2.2
22	CV	18	G	2.2
25	CY	52	G	2.2
26	BA	2125	G	2.2

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Mol	Chain	Res	Type	RSRZ
29	DE	51	PHE	2.2
3	AC	34	LEU	2.2
3	AC	52	LEU	2.2
4	AD	101	LEU	2.2
5	CE	119	LEU	2.2
13	AM	96	LEU	2.2
29	BE	12	THR	2.2
12	CL	123	LYS	2.2
13	AM	121	LYS	2.2
13	CM	93	ARG	2.2
16	CP	41	PRO	2.2
46	DZ	79	ARG	2.2
9	AI	17	VAL	2.2
9	AI	26	VAL	2.2
16	CP	20	VAL	2.2
42	DV	79	VAL	2.2
3	CC	193	TYR	2.2
8	CH	28	ALA	2.2
11	CK	50	TYR	2.2
32	DH	75	ALA	2.2
3	CC	51	GLY	2.2
31	DG	24	GLY	2.2
42	DV	101	GLY	2.2
56	D9	1	MET	2.2
7	CG	120	ILE	2.2
15	CO	87	ILE	2.2
10	CJ	61	GLU	2.2
3	AC	179	ARG	2.2
4	CD	209	ARG	2.2
5	AE	88	LYS	2.2
12	CL	15	ARG	2.2
13	CM	111	LYS	2.2
19	CS	15	LEU	2.2
40	DT	114	LEU	2.2
16	CP	18	ARG	2.2
45	DY	46	LYS	2.2
46	DZ	112	ARG	2.2
47	D0	49	LYS	2.2
28	BD	50	THR	2.2
38	DR	35	THR	2.2
2	AB	131	PRO	2.2
31	DG	166	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	AA	841	U	2.2
36	DP	43	GLY	2.1
2	CB	58	ILE	2.1
8	AH	109	ILE	2.1
10	AJ	96	ILE	2.1
10	AJ	57	LYS	2.1
4	AD	191	ARG	2.1
10	AJ	60	ARG	2.1
27	DB	4	C	2.1
31	DG	33	ARG	2.1
1	CA	958	A	2.1
1	CA	1503	A	2.1
20	AT	62	LEU	2.1
26	DA	2126	A	2.1
31	BG	106	LEU	2.1
31	BG	178	PHE	2.1
36	DP	3	LEU	2.1
1	CA	1017	G	2.1
2	CB	202	PRO	2.1
8	CH	138	TRP	2.1
9	AI	8	GLY	2.1
11	CK	80	VAL	2.1
12	CL	14	GLY	2.1
29	BE	106	GLY	2.1
33	DI	18	VAL	2.1
16	AP	35	LYS	2.1
17	AQ	95	TYR	2.1
6	CF	52	ILE	2.1
12	CL	19	ARG	2.1
48	D1	26	ARG	2.1
1	CA	1223	C	2.1
4	AD	21	LEU	2.1
26	BA	2174	C	2.1
26	DA	912	C	2.1
30	DF	140	LEU	2.1
31	BG	133	LEU	2.1
55	D8	48	PHE	2.1
1	CA	974	A	2.1
1	CA	986	A	2.1
19	CS	43	GLU	2.1
25	CY	58	A	2.1
52	B5	5	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
26	BA	2506	U	2.1
34	DN	8	GLN	2.1
5	CE	23	GLY	2.1
56	D9	13	LYS	2.1
1	CA	993	G	2.1
1	CA	1310	G	2.1
26	BA	1176	G	2.1
3	CC	149	ALA	2.1
7	CG	40	ALA	2.1
32	BH	3	ARG	2.1
4	AD	181	MET	2.1
35	DO	1	MET	2.1
16	AP	4	ILE	2.1
28	DD	24	ILE	2.1
2	AB	118	LEU	2.1
9	AI	112	LYS	2.1
9	CI	40	LEU	2.1
12	CL	93	LEU	2.1
19	CS	5	LEU	2.1
30	BF	32	LEU	2.1
30	BF	156	LEU	2.1
31	BG	139	LEU	2.1
31	DG	3	LEU	2.1
37	DQ	79	LEU	2.1
48	B1	69	LYS	2.1
2	CB	113	HIS	2.1
3	CC	192	THR	2.1
5	AE	106	PRO	2.1
46	BZ	170	THR	2.1
21	AU	11	GLY	2.1
8	AH	29	SER	2.1
21	CU	9	ARG	2.1
3	AC	137	ALA	2.1
4	AD	105	VAL	2.1
5	CE	86	ALA	2.1
20	CT	40	ALA	2.1
32	DH	20	ALA	2.1
33	DI	3	VAL	2.1
40	DT	89	VAL	2.1
50	D3	47	VAL	2.1
54	D7	45	ALA	2.1
3	CC	44	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
25	CY	71	G	2.1
26	BA	2152	G	2.1
38	BR	1	MET	2.1
46	DZ	13	GLU	2.1
2	AB	33	TYR	2.1
17	AQ	60	ILE	2.1
28	DD	5	LYS	2.1
51	B4	46	GLN	2.1
13	CM	48	LEU	2.1
20	CT	13	LEU	2.1
38	DR	4	LEU	2.1
54	B7	31	LEU	2.1
2	AB	73	THR	2.1
5	CE	25	ARG	2.1
9	AI	6	GLY	2.1
14	AN	28	GLY	2.1
16	AP	22	THR	2.1
24	CX	71	C	2.1
43	DW	112	GLY	2.1
45	DY	80	GLY	2.1
47	D0	76	GLY	2.1
51	D4	64	GLY	2.1
26	DA	2585	U	2.1
2	CB	150	SER	2.1
2	CB	216	SER	2.1
46	DZ	142	SER	2.1
1	CA	1093	A	2.1
26	DA	899	A	2.1
2	CB	218	ALA	2.1
3	AC	189	ALA	2.1
5	CE	115	VAL	2.1
7	CG	66	VAL	2.1
10	AJ	27	ALA	2.1
12	AL	96	VAL	2.1
30	BF	39	TRP	2.1
30	BF	80	ALA	2.1
30	DF	172	TRP	2.1
33	DI	19	VAL	2.1
37	DQ	55	VAL	2.1
37	DQ	94	VAL	2.1
36	DP	1	MET	2.1
20	AT	9	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
2	CB	148	TYR	2.1
7	AG	42	ILE	2.1
8	CH	86	ILE	2.1
9	CI	74	ILE	2.1
17	CQ	59	ILE	2.1
23	AW	24	G	2.1
24	CX	5	G	2.1
25	AY	70	G	2.1
30	DF	64	ILE	2.1
33	BI	4	ILE	2.1
12	CL	59	ARG	2.1
37	BQ	10	ARG	2.1
2	AB	152	PHE	2.1
3	AC	47	LEU	2.1
9	CI	90	PRO	2.1
16	CP	60	LEU	2.1
36	DP	37	GLY	2.1
36	DP	62	LEU	2.1
48	D1	46	LEU	2.1
10	AJ	97	GLU	2.1
20	CT	71	THR	2.1
23	CW	33	U	2.1
1	CA	1063	C	2.1
1	CA	1226	C	2.1
25	AY	2	C	2.1
40	DT	107	ASP	2.1
8	CH	16	ALA	2.1
23	CW	7	A	2.1
31	DG	151	ALA	2.1
54	B7	45	ALA	2.1
5	AE	51	VAL	2.1
7	AG	80	VAL	2.1
31	DG	15	VAL	2.1
3	CC	132	ARG	2.1
5	CE	24	ARG	2.1
35	BO	49	ARG	2.1
3	AC	152	ILE	2.1
16	AP	33	ILE	2.1
13	CM	68	GLY	2.1
1	AA	306	G	2.1
1	AA	821	G	2.1
4	CD	93	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
13	CM	96	LEU	2.1
14	AN	16	PHE	2.1
14	CN	54	PRO	2.1
17	CQ	30	PRO	2.1
24	CX	70	G	2.1
25	AY	6	G	2.1
26	BA	948	G	2.1
1	CA	1358	U	2.1
12	AL	6	THR	2.1
16	AP	45	THR	2.1
24	CX	68	C	2.0
46	DZ	65	GLN	2.0
49	D2	9	GLN	2.0
1	AA	1502	A	2.0
1	CA	250	A	2.0
3	CC	59	ARG	2.0
13	CM	108	ARG	2.0
30	DF	80	ALA	2.0
6	CF	9	VAL	2.0
11	CK	14	VAL	2.0
25	AY	21	A	2.0
26	BA	1664	A	2.0
26	BA	2450	A	2.0
26	DA	2134	A	2.0
28	BD	18	VAL	2.0
2	CB	185	ILE	2.0
3	AC	124	ILE	2.0
4	AD	70	ILE	2.0
8	AH	90	GLY	2.0
10	AJ	38	ILE	2.0
12	CL	46	LYS	2.0
28	BD	238	GLY	2.0
36	BP	34	GLY	2.0
37	DQ	85	LYS	2.0
5	CE	128	PRO	2.0
9	AI	5	TYR	2.0
9	CI	21	PRO	2.0
32	BH	157	TYR	2.0
34	DN	78	TYR	2.0
1	AA	1025	U	2.0
5	AE	84	PHE	2.0
46	DZ	102	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
52	D5	29	THR	2.0
1	CA	1026	G	2.0
26	BA	975(A)	G	2.0
4	AD	168	ARG	2.0
20	AT	86	ARG	2.0
2	CB	161	ALA	2.0
11	CK	23	ALA	2.0
55	D8	18	ALA	2.0
8	CH	116	LYS	2.0
4	CD	17	VAL	2.0
11	AK	30	VAL	2.0
17	CQ	77	VAL	2.0
32	BH	15	VAL	2.0
32	DH	43	VAL	2.0
32	DH	114	VAL	2.0
37	BQ	55	VAL	2.0
48	D1	14	VAL	2.0
50	D3	54	VAL	2.0
1	AA	1513	A	2.0
35	BO	47	ILE	2.0
46	DZ	133	ILE	2.0
55	B8	58	ILE	2.0
3	CC	32	LEU	2.0
4	AD	136	PRO	2.0
6	AF	57	GLN	2.0
7	AG	12	LEU	2.0
12	CL	71	PRO	2.0
16	AP	66	PRO	2.0
9	CI	92	TYR	2.0
14	AN	34	TYR	2.0
20	CT	84	LEU	2.0
34	BN	116	LEU	2.0
14	AN	37	PHE	2.0
17	CQ	7	THR	2.0
42	DV	75	PHE	2.0
5	CE	27	ARG	2.0
1	AA	1387	G	2.0
10	CJ	32	ALA	2.0
19	CS	50	ALA	2.0
23	AW	29	G	2.0
23	AW	74	C	2.0
26	DA	2137	C	2.0

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Mol	Chain	Res	Type	RSRZ
26	DA	2143	C	2.0
5	AE	74	GLY	2.0
5	CE	67	VAL	2.0
35	DO	38	VAL	2.0
46	DZ	100	VAL	2.0
54	B7	1	MET	2.0
1	CA	1111	A	2.0
1	CA	1252	A	2.0
1	CA	1339	A	2.0
12	AL	100	ILE	2.0
15	CO	3	ILE	2.0
33	DI	85	GLU	2.0
35	DO	101	PRO	2.0
56	B9	17	ILE	2.0
1	CA	202	U	2.0
26	DA	2118	U	2.0
55	D8	62	LEU	2.0
15	CO	15	PHE	2.0
19	AS	33	THR	2.0
28	DD	250	TRP	2.0
40	DT	62	THR	2.0
54	D7	32	LYS	2.0
55	D8	59	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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
23	5MU	CW	54	21/22	0.84	0.23	-	74,88,99,101	0
24	5MC	AX	32	21/22	0.95	0.21	-	43,53,62,78	0
23	MIA	AW	37	29/30	0.94	0.26	-	59,71,81,86	0
25	PSU	CY	55	20/21	0.67	0.49	-	94,102,110,124	0
23	4SU	AW	8	20/21	0.81	0.19	-	86,95,112,128	0
23	PSU	CW	39	20/21	0.87	0.42	-	78,84,97,98	0
25	MIA	CY	37	22/30	0.61	0.38	-	72,95,113,138	0
24	5MC	CX	32	21/22	0.96	0.21	-	63,76,86,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	PSU	AW	32	20/21	0.88	0.25	-	77,83,92,98	0
23	PSU	CW	32	20/21	0.88	0.45	-	81,87,94,103	0
25	7MG	CY	46	24/25	0.48	0.37	-	86,105,111,137	0
23	31M	CW	76	41/42	0.89	0.41	-	50,63,73,88	20
25	4SU	AY	8	20/21	0.78	0.16	-	82,96,103,118	0
23	PSU	AW	55	20/21	0.84	0.26	-	77,90,98,104	0
24	PSU	AX	55	20/21	0.95	0.21	-	50,63,73,83	0
25	PSU	AY	55	20/21	0.70	0.29	-	93,101,108,122	0
25	PSU	CY	32	20/21	0.79	0.21	-	80,92,101,107	0
23	PSU	CW	55	20/21	0.79	0.30	-	79,89,99,104	0
24	5MU	CX	54	21/22	0.92	0.22	-	70,81,89,99	0
24	4SU	CX	8	20/21	0.91	0.17	-	77,87,95,97	0
25	PSU	AY	32	20/21	0.83	0.24	-	78,93,100,106	0
24	4SU	AX	8	20/21	0.94	0.18	-	54,66,82,89	0
23	MIA	CW	37	22/30	0.84	0.32	-	75,85,92,100	0
23	5MU	AW	54	21/22	0.91	0.20	-	65,82,91,93	0
23	7MG	AW	46	24/25	0.72	0.23	-	84,99,117,133	0
24	PSU	CX	55	20/21	0.89	0.15	-	70,80,91,96	0
23	7MG	CW	46	24/25	0.67	0.27	-	79,96,109,133	0
25	PSU	CY	39	20/21	0.77	0.30	-	79,90,116,130	0
23	PSU	AW	39	20/21	0.93	0.23	-	73,82,95,97	0
25	MIA	AY	37	22/30	0.80	0.22	-	77,90,111,119	0
23	31M	AW	76	41/42	0.94	0.33	-	37,54,66,83	9
25	5MU	AY	54	21/22	0.73	0.26	-	80,96,105,131	0
25	4SU	CY	8	20/21	0.68	0.22	-	93,103,113,128	0
25	5MU	CY	54	21/22	0.63	0.53	-	78,94,109,140	0
25	PSU	AY	39	20/21	0.76	0.30	-	78,90,117,123	0
25	7MG	AY	46	24/25	0.76	0.28	-	75,101,111,123	0
24	5MU	AX	54	21/22	0.95	0.20	-	49,68,79,84	0
23	4SU	CW	8	20/21	0.69	0.30	-	81,98,120,127	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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
57	MG	BA	3639	1/1	0.93	0.46	38.70	48,48,48,48	0
57	MG	BF	303	1/1	0.96	0.54	32.51	49,49,49,49	0
57	MG	BX	3001	1/1	0.92	0.83	32.24	48,48,48,48	0
57	MG	DA	3116	1/1	0.91	0.48	27.40	52,52,52,52	0
57	MG	DA	3226	1/1	0.95	0.38	22.29	45,45,45,45	0
57	MG	BA	3250	1/1	0.93	0.67	21.11	42,42,42,42	0
57	MG	BA	3367	1/1	0.98	0.25	16.63	29,29,29,29	0
57	MG	DA	3031	1/1	0.99	0.43	16.26	43,43,43,43	0
57	MG	BA	3054	1/1	0.94	0.28	15.40	36,36,36,36	0
57	MG	DA	3213	1/1	0.64	0.32	12.85	63,63,63,63	0
57	MG	DA	3208	1/1	0.89	0.37	12.01	58,58,58,58	0
57	MG	B1	101	1/1	0.91	0.50	11.81	51,51,51,51	0
57	MG	DA	3168	1/1	0.97	0.29	11.65	45,45,45,45	0
57	MG	BA	3239	1/1	0.92	0.34	11.60	48,48,48,48	0
57	MG	BA	3029	1/1	0.97	0.49	11.56	37,37,37,37	0
57	MG	DA	3016	1/1	0.97	0.34	10.49	50,50,50,50	0
57	MG	BA	3804	1/1	0.96	0.42	10.05	53,53,53,53	0
57	MG	BA	3248	1/1	0.96	0.30	9.77	42,42,42,42	0
57	MG	BA	3802	1/1	0.83	0.47	9.63	54,54,54,54	0
57	MG	BA	3246	1/1	0.95	0.35	9.56	39,39,39,39	0
57	MG	BA	3240	1/1	0.91	0.40	9.54	47,47,47,47	0
57	MG	AA	3156	1/1	0.95	0.25	9.33	63,63,63,63	0
57	MG	BA	3115	1/1	0.97	0.23	9.29	59,59,59,59	0
57	MG	DA	3588	1/1	0.91	0.30	9.19	65,65,65,65	0
57	MG	BA	3328	1/1	0.93	0.27	9.14	40,40,40,40	0
57	MG	DA	3019	1/1	0.97	0.29	9.06	37,37,37,37	0
57	MG	DA	3067	1/1	0.94	0.26	8.76	57,57,57,57	0
57	MG	DA	3045	1/1	0.93	0.29	8.34	51,51,51,51	0
57	MG	DU	3002	1/1	0.85	0.40	8.22	55,55,55,55	0
57	MG	DA	3594	1/1	0.94	0.31	8.03	54,54,54,54	0
57	MG	DA	3081	1/1	0.96	0.28	7.99	55,55,55,55	0
57	MG	BA	3670	1/1	0.43	0.25	7.81	61,61,61,61	0
57	MG	DA	3028	1/1	0.97	0.36	7.66	52,52,52,52	0
57	MG	BA	3728	1/1	0.80	0.33	7.42	48,48,48,48	0
57	MG	DA	3481	1/1	0.89	0.41	7.36	55,55,55,55	0
57	MG	BA	3613	1/1	0.96	0.42	7.18	42,42,42,42	0
57	MG	DA	3027	1/1	0.99	0.57	7.18	51,51,51,51	0
57	MG	BA	3771	1/1	0.78	0.29	7.12	50,50,50,50	0
57	MG	DD	308	1/1	0.98	0.29	7.00	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3132	1/1	0.90	0.23	6.91	52,52,52,52	0
57	MG	DA	3236	1/1	0.91	0.26	6.82	47,47,47,47	0
57	MG	DA	3642	1/1	0.76	0.28	6.77	54,54,54,54	0
57	MG	BA	3069	1/1	0.99	0.27	6.68	22,22,22,22	0
57	MG	CA	3152	1/1	0.80	0.20	6.41	76,76,76,76	0
57	MG	BA	3732	1/1	0.87	0.26	6.38	51,51,51,51	0
57	MG	BU	206	1/1	0.99	0.40	6.17	35,35,35,35	0
57	MG	BA	3156	1/1	0.95	0.29	6.05	41,41,41,41	0
57	MG	DA	3676	1/1	0.87	0.33	5.70	67,67,67,67	0
57	MG	DA	3637	1/1	0.92	0.59	5.65	58,58,58,58	0
57	MG	DA	3029	1/1	0.93	0.35	5.65	49,49,49,49	0
57	MG	BA	3139	1/1	0.97	0.33	5.63	40,40,40,40	0
57	MG	BA	3040	1/1	0.98	0.36	5.54	35,35,35,35	0
57	MG	AY	3003	1/1	0.92	0.30	5.53	53,53,53,53	0
57	MG	BA	3046	1/1	0.97	0.28	5.28	41,41,41,41	0
57	MG	DE	301	1/1	0.98	0.40	5.26	46,46,46,46	0
57	MG	BA	3232	1/1	0.97	0.21	5.08	52,52,52,52	0
57	MG	BA	3812	1/1	0.92	0.28	5.08	47,47,47,47	0
57	MG	BB	202	1/1	0.86	0.28	5.05	59,59,59,59	0
57	MG	AA	3095	1/1	0.93	0.29	5.02	60,60,60,60	0
57	MG	BA	3549	1/1	0.97	0.29	4.92	39,39,39,39	0
57	MG	BA	3085	1/1	0.98	0.27	4.87	35,35,35,35	0
57	MG	DD	307	1/1	0.97	0.32	4.81	43,43,43,43	0
57	MG	BA	3213	1/1	0.86	0.26	4.80	40,40,40,40	0
57	MG	BA	3153	1/1	0.96	0.31	4.76	47,47,47,47	0
57	MG	BP	201	1/1	0.95	0.28	4.46	41,41,41,41	0
57	MG	BA	3335	1/1	0.82	0.23	4.46	52,52,52,52	0
57	MG	BA	3801	1/1	0.94	0.31	4.32	50,50,50,50	0
57	MG	BA	3143	1/1	0.91	0.26	4.26	45,45,45,45	0
57	MG	DB	3008	1/1	0.76	0.20	4.14	67,67,67,67	0
57	MG	DA	3059	1/1	0.96	0.26	4.12	43,43,43,43	0
57	MG	CA	3169	1/1	0.95	0.24	4.04	51,51,51,51	0
57	MG	DA	3182	1/1	0.97	0.24	3.94	51,51,51,51	0
57	MG	DA	3668	1/1	0.92	0.39	3.81	60,60,60,60	0
57	MG	DA	3629	1/1	0.95	0.27	3.69	62,62,62,62	0
57	MG	DF	3003	1/1	0.97	0.40	3.67	43,43,43,43	0
57	MG	AA	3084	1/1	0.78	0.24	3.62	51,51,51,51	0
57	MG	DA	3426	1/1	0.93	0.22	3.60	49,49,49,49	0
57	MG	BA	3082	1/1	0.97	0.22	3.54	39,39,39,39	0
57	MG	BA	3196	1/1	0.94	0.25	3.53	38,38,38,38	0
57	MG	DA	3669	1/1	0.81	0.25	3.52	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3439	1/1	0.95	0.23	3.51	42,42,42,42	0
57	MG	BA	3290	1/1	0.92	0.28	3.47	40,40,40,40	0
57	MG	BA	3141	1/1	0.98	0.28	3.42	42,42,42,42	0
57	MG	CA	3057	1/1	0.90	0.18	3.42	76,76,76,76	0
57	MG	BA	3284	1/1	0.86	0.26	3.35	43,43,43,43	0
57	MG	BA	3626	1/1	0.95	0.25	3.32	44,44,44,44	0
57	MG	DD	304	1/1	0.92	0.38	3.28	52,52,52,52	0
57	MG	BA	3699	1/1	0.96	0.23	3.17	35,35,35,35	0
57	MG	CA	3061	1/1	0.89	0.28	3.13	66,66,66,66	0
57	MG	BV	201	1/1	0.98	0.31	3.13	33,33,33,33	0
57	MG	BF	306	1/1	0.97	0.28	3.10	31,31,31,31	0
57	MG	AA	3018	1/1	0.97	0.24	2.91	56,56,56,56	0
57	MG	AA	3138	1/1	0.81	0.18	2.83	71,71,71,71	0
57	MG	DA	3115	1/1	0.98	0.24	2.79	40,40,40,40	0
57	MG	BA	3151	1/1	0.92	0.26	2.76	52,52,52,52	0
57	MG	DA	3119	1/1	0.90	0.21	2.69	39,39,39,39	0
57	MG	DA	3471	1/1	0.98	0.22	2.54	50,50,50,50	0
57	MG	CA	3133	1/1	0.98	0.21	2.53	59,59,59,59	0
59	ZN	B6	103	1/1	0.98	0.24	2.50	49,49,49,49	0
57	MG	BA	3203	1/1	0.92	0.25	2.49	40,40,40,40	0
57	MG	BD	306	1/1	0.97	0.25	2.48	38,38,38,38	0
57	MG	BA	3289	1/1	0.94	0.21	2.47	56,56,56,56	0
57	MG	BA	3215	1/1	0.95	0.27	2.46	36,36,36,36	0
57	MG	DB	3009	1/1	0.94	0.18	2.46	59,59,59,59	0
57	MG	BA	3330	1/1	0.97	0.23	2.44	37,37,37,37	0
57	MG	BN	3001	1/1	0.96	0.31	2.43	53,53,53,53	0
57	MG	DA	3610	1/1	0.78	0.22	2.41	64,64,64,64	0
57	MG	CA	3087	1/1	0.83	0.19	2.38	67,67,67,67	0
57	MG	BD	302	1/1	0.91	0.28	2.37	50,50,50,50	0
57	MG	CA	3045	1/1	0.96	0.24	2.36	54,54,54,54	0
57	MG	AA	3205	1/1	0.95	0.22	2.24	51,51,51,51	0
57	MG	AF	3001	1/1	0.95	0.26	2.20	44,44,44,44	0
57	MG	CA	3079	1/1	0.94	0.21	2.19	66,66,66,66	0
57	MG	DA	3096	1/1	0.97	0.23	2.17	42,42,42,42	0
57	MG	AA	3080	1/1	0.92	0.21	2.16	58,58,58,58	0
57	MG	BA	3698	1/1	0.97	0.22	2.14	31,31,31,31	0
59	ZN	B5	102	1/1	0.99	0.22	2.10	48,48,48,48	0
57	MG	DA	3510	1/1	0.95	0.25	2.10	49,49,49,49	0
57	MG	DA	3518	1/1	0.66	0.24	2.04	54,54,54,54	0
57	MG	BB	218	1/1	0.82	0.22	2.00	77,77,77,77	0
57	MG	B7	104	1/1	0.91	0.27	1.99	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3014	1/1	0.93	0.29	1.96	42,42,42,42	0
57	MG	BU	205	1/1	0.94	0.24	1.95	47,47,47,47	0
57	MG	DA	3113	1/1	0.95	0.19	1.89	60,60,60,60	0
57	MG	BA	3228	1/1	0.93	0.25	1.85	59,59,59,59	0
57	MG	BA	3742	1/1	0.87	0.24	1.81	65,65,65,65	0
57	MG	BA	3279	1/1	0.94	0.24	1.78	43,43,43,43	0
57	MG	DA	3014	1/1	0.96	0.21	1.73	46,46,46,46	0
57	MG	DD	306	1/1	0.94	0.28	1.73	39,39,39,39	0
57	MG	CA	3067	1/1	0.96	0.31	1.71	61,61,61,61	0
57	MG	BA	3796	1/1	0.95	0.25	1.69	45,45,45,45	0
57	MG	DV	3002	1/1	0.97	0.31	1.67	49,49,49,49	0
57	MG	BA	3212	1/1	0.88	0.24	1.65	54,54,54,54	0
57	MG	BA	3159	1/1	0.97	0.25	1.65	50,50,50,50	0
57	MG	DA	3117	1/1	0.95	0.20	1.64	52,52,52,52	0
57	MG	AA	3025	1/1	0.84	0.25	1.62	62,62,62,62	0
57	MG	BA	3087	1/1	0.95	0.24	1.56	42,42,42,42	0
57	MG	DA	3347	1/1	0.99	0.20	1.56	27,27,27,27	0
59	ZN	D5	501	1/1	0.99	0.20	1.45	58,58,58,58	0
57	MG	BA	3321	1/1	0.91	0.24	1.39	55,55,55,55	0
57	MG	BA	3628	1/1	0.92	0.25	1.38	49,49,49,49	0
57	MG	BA	3078	1/1	0.93	0.24	1.36	51,51,51,51	0
57	MG	DV	3001	1/1	0.93	0.23	1.24	70,70,70,70	0
57	MG	BA	3607	1/1	0.98	0.24	1.24	38,38,38,38	0
57	MG	BA	3787	1/1	0.97	0.23	1.23	45,45,45,45	0
57	MG	DW	3004	1/1	0.97	0.22	1.22	52,52,52,52	0
57	MG	DA	3462	1/1	0.86	0.20	1.21	42,42,42,42	0
57	MG	BA	3096	1/1	0.94	0.23	1.14	54,54,54,54	0
57	MG	BA	3443	1/1	0.85	0.23	1.14	37,37,37,37	0
57	MG	BA	3794	1/1	0.84	0.26	1.09	51,51,51,51	0
57	MG	DA	3104	1/1	0.94	0.29	1.08	53,53,53,53	0
57	MG	DA	3431	1/1	0.84	0.23	1.04	50,50,50,50	0
57	MG	BA	3543	1/1	0.94	0.23	1.03	37,37,37,37	0
57	MG	BA	3206	1/1	0.87	0.23	1.03	49,49,49,49	0
57	MG	DA	3169	1/1	0.96	0.24	1.03	47,47,47,47	0
57	MG	CA	3138	1/1	0.87	0.19	0.97	80,80,80,80	0
57	MG	CA	3150	1/1	0.91	0.21	0.92	56,56,56,56	0
57	MG	BE	302	1/1	0.97	0.23	0.89	39,39,39,39	0
57	MG	BA	3264	1/1	0.96	0.21	0.89	58,58,58,58	0
57	MG	DA	3413	1/1	0.66	0.23	0.88	48,48,48,48	0
57	MG	AA	3155	1/1	0.93	0.24	0.87	48,48,48,48	0
57	MG	AA	3125	1/1	0.97	0.24	0.85	37,37,37,37	0
57	MG	DA	3470	1/1	0.89	0.19	0.79	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	BA	3254	1/1	0.97	0.22	0.78	25,25,25,25	0
57	MG	BA	3216	1/1	0.99	0.23	0.74	37,37,37,37	0
57	MG	BA	3098	1/1	0.92	0.22	0.73	40,40,40,40	0
57	MG	AA	3071	1/1	0.93	0.22	0.72	53,53,53,53	0
57	MG	BF	307	1/1	0.97	0.24	0.71	37,37,37,37	0
57	MG	BA	3273	1/1	0.82	0.22	0.67	54,54,54,54	0
57	MG	DQ	3004	1/1	0.87	0.28	0.65	54,54,54,54	0
57	MG	BA	3041	1/1	0.96	0.23	0.63	40,40,40,40	0
57	MG	CA	3116	1/1	0.84	0.22	0.62	68,68,68,68	0
57	MG	BA	3044	1/1	0.98	0.22	0.61	20,20,20,20	0
57	MG	BA	3412	1/1	0.92	0.23	0.49	40,40,40,40	0
57	MG	BQ	3002	1/1	0.96	0.23	0.49	43,43,43,43	0
57	MG	DA	3180	1/1	0.85	0.20	0.46	42,42,42,42	0
57	MG	DA	3336	1/1	0.94	0.19	0.45	40,40,40,40	0
57	MG	BD	301	1/1	0.95	0.23	0.44	40,40,40,40	0
57	MG	BA	3209	1/1	0.95	0.24	0.44	54,54,54,54	0
57	MG	BG	202	1/1	0.92	0.21	0.43	41,41,41,41	0
57	MG	DA	3459	1/1	0.98	0.19	0.43	47,47,47,47	0
57	MG	DA	3256	1/1	0.67	0.19	0.41	62,62,62,62	0
57	MG	BA	3747	1/1	0.94	0.20	0.40	52,52,52,52	0
57	MG	BA	3259	1/1	0.98	0.21	0.39	25,25,25,25	0
57	MG	DA	3558	1/1	0.87	0.17	0.38	61,61,61,61	0
57	MG	BA	3079	1/1	0.93	0.19	0.36	39,39,39,39	0
57	MG	DA	3210	1/1	0.94	0.17	0.32	53,53,53,53	0
57	MG	DU	3001	1/1	0.98	0.32	0.29	55,55,55,55	0
57	MG	BA	3268	1/1	0.94	0.22	0.26	55,55,55,55	0
57	MG	BA	3518	1/1	0.97	0.20	0.25	44,44,44,44	0
57	MG	DA	3268	1/1	0.83	0.17	0.18	51,51,51,51	0
57	MG	CA	3167	1/1	0.97	0.17	0.13	60,60,60,60	0
57	MG	BA	3399	1/1	0.89	0.20	0.10	45,45,45,45	0
57	MG	BA	3056	1/1	0.95	0.21	0.09	40,40,40,40	0
57	MG	CA	3051	1/1	0.66	0.19	0.03	81,81,81,81	0
59	ZN	B4	501	1/1	0.95	0.15	0.03	89,89,89,89	0
57	MG	AA	3120	1/1	0.97	0.19	-0.00	45,45,45,45	0
57	MG	DA	3630	1/1	0.82	0.19	0.00	61,61,61,61	0
57	MG	DA	3578	1/1	0.93	0.18	-0.02	59,59,59,59	0
57	MG	CA	3134	1/1	0.97	0.16	-0.04	69,69,69,69	0
57	MG	DA	3641	1/1	0.86	0.20	-0.06	69,69,69,69	0
57	MG	AX	3002	1/1	0.88	0.17	-0.08	58,58,58,58	0
57	MG	AA	3148	1/1	0.97	0.22	-0.08	57,57,57,57	0
57	MG	DA	3015	1/1	0.95	0.20	-0.08	52,52,52,52	0
57	MG	BA	3583	1/1	0.87	0.21	-0.11	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3416	1/1	0.98	0.21	-0.14	21,21,21,21	0
59	ZN	AN	501	1/1	0.98	0.19	-0.15	69,69,69,69	0
57	MG	AA	3213	1/1	0.95	0.23	-0.19	54,54,54,54	0
57	MG	BD	304	1/1	0.95	0.22	-0.25	32,32,32,32	0
57	MG	BX	3002	1/1	0.87	0.19	-0.27	46,46,46,46	0
57	MG	BA	3357	1/1	0.92	0.23	-0.28	25,25,25,25	0
57	MG	DA	3020	1/1	0.97	0.16	-0.29	55,55,55,55	0
57	MG	DA	3640	1/1	0.95	0.19	-0.33	43,43,43,43	0
57	MG	BA	3588	1/1	0.98	0.23	-0.34	31,31,31,31	0
57	MG	DA	3295	1/1	0.95	0.21	-0.34	44,44,44,44	0
57	MG	BA	3245	1/1	0.97	0.23	-0.34	34,34,34,34	0
57	MG	BW	203	1/1	0.96	0.20	-0.34	44,44,44,44	0
57	MG	BA	3283	1/1	0.95	0.20	-0.35	35,35,35,35	0
57	MG	BA	3094	1/1	0.96	0.21	-0.36	36,36,36,36	0
57	MG	D3	3001	1/1	0.92	0.20	-0.38	57,57,57,57	0
57	MG	BA	3028	1/1	0.97	0.22	-0.39	51,51,51,51	0
57	MG	AA	3099	1/1	0.97	0.20	-0.39	51,51,51,51	0
57	MG	DA	3267	1/1	0.92	0.16	-0.40	49,49,49,49	0
57	MG	BA	3530	1/1	0.86	0.22	-0.40	49,49,49,49	0
57	MG	DF	3002	1/1	0.98	0.17	-0.43	48,48,48,48	0
57	MG	BA	3045	1/1	0.99	0.21	-0.45	36,36,36,36	0
59	ZN	D6	501	1/1	0.99	0.17	-0.45	71,71,71,71	0
57	MG	D8	5001	1/1	0.65	0.23	-0.45	66,66,66,66	0
57	MG	DA	3322	1/1	0.97	0.19	-0.47	51,51,51,51	0
57	MG	AK	3001	1/1	0.97	0.18	-0.48	44,44,44,44	0
57	MG	BA	3135	1/1	0.98	0.20	-0.57	43,43,43,43	0
57	MG	BA	3050	1/1	0.98	0.20	-0.58	38,38,38,38	0
57	MG	BA	3124	1/1	0.98	0.21	-0.58	19,19,19,19	0
57	MG	CK	3001	1/1	0.95	0.17	-0.61	45,45,45,45	0
57	MG	DA	3143	1/1	0.97	0.18	-0.61	38,38,38,38	0
57	MG	BA	3042	1/1	0.97	0.20	-0.63	43,43,43,43	0
57	MG	AA	3214	1/1	0.86	0.17	-0.68	73,73,73,73	0
57	MG	BA	3641	1/1	0.75	0.21	-0.68	68,68,68,68	0
57	MG	DE	302	1/1	0.96	0.17	-0.69	33,33,33,33	0
57	MG	BD	307	1/1	0.99	0.21	-0.72	40,40,40,40	0
57	MG	BA	3449	1/1	0.98	0.21	-0.72	35,35,35,35	0
57	MG	AA	3085	1/1	0.93	0.18	-0.75	48,48,48,48	0
57	MG	BA	3529	1/1	0.96	0.20	-0.76	56,56,56,56	0
59	ZN	BY	501	1/1	0.98	0.15	-0.77	58,58,58,58	0
57	MG	BA	3286	1/1	0.98	0.21	-0.79	34,34,34,34	0
57	MG	AA	3065	1/1	0.86	0.20	-0.80	63,63,63,63	0
57	MG	BA	3388	1/1	0.92	0.19	-0.81	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3070	1/1	0.61	0.15	-0.81	63,63,63,63	0
57	MG	DA	3308	1/1	0.82	0.15	-0.82	61,61,61,61	0
59	ZN	DY	501	1/1	0.90	0.15	-0.82	96,96,96,96	0
57	MG	DA	3118	1/1	0.81	0.15	-0.82	77,77,77,77	0
57	MG	BA	3011	1/1	0.97	0.19	-0.86	35,35,35,35	0
57	MG	CA	3065	1/1	0.98	0.17	-0.87	49,49,49,49	0
57	MG	BA	3023	1/1	0.89	0.22	-0.90	36,36,36,36	0
57	MG	BA	3426	1/1	0.87	0.20	-0.91	37,37,37,37	0
57	MG	AA	3014	1/1	0.94	0.21	-0.91	32,32,32,32	0
57	MG	DA	3540	1/1	0.93	0.17	-0.92	42,42,42,42	0
57	MG	DA	3191	1/1	0.97	0.17	-0.93	37,37,37,37	0
57	MG	BB	215	1/1	0.59	0.18	-0.95	73,73,73,73	0
57	MG	BA	3144	1/1	0.97	0.19	-0.95	41,41,41,41	0
57	MG	BP	202	1/1	0.93	0.21	-0.97	36,36,36,36	0
57	MG	DA	3675	1/1	0.94	0.13	-0.99	52,52,52,52	0
57	MG	DA	3586	1/1	0.92	0.16	-0.99	60,60,60,60	0
57	MG	CA	3048	1/1	0.96	0.12	-1.00	67,67,67,67	0
57	MG	DX	101	1/1	0.89	0.12	-1.04	51,51,51,51	0
57	MG	BU	203	1/1	0.98	0.21	-1.04	47,47,47,47	0
57	MG	DA	3145	1/1	0.96	0.17	-1.05	43,43,43,43	0
57	MG	BA	3158	1/1	0.97	0.20	-1.05	41,41,41,41	0
57	MG	AA	3004	1/1	0.63	0.15	-1.07	67,67,67,67	0
57	MG	DA	3367	1/1	0.88	0.14	-1.07	61,61,61,61	0
57	MG	DA	3206	1/1	0.89	0.13	-1.09	50,50,50,50	0
57	MG	AX	3005	1/1	0.97	0.14	-1.09	47,47,47,47	0
57	MG	BU	208	1/1	0.94	0.21	-1.09	40,40,40,40	0
57	MG	AX	3015	1/1	0.95	0.21	-1.09	42,42,42,42	0
58	SF4	AD	501	8/8	0.98	0.16	-1.11	62,68,73,86	0
57	MG	BA	3427	1/1	0.41	0.20	-1.12	61,61,61,61	0
57	MG	CE	3001	1/1	0.86	0.10	-1.13	79,79,79,79	0
57	MG	BA	3202	1/1	0.97	0.19	-1.13	60,60,60,60	0
57	MG	AE	203	1/1	0.93	0.18	-1.15	63,63,63,63	0
57	MG	DA	3673	1/1	0.60	0.14	-1.15	69,69,69,69	0
57	MG	BA	3190	1/1	0.93	0.20	-1.18	52,52,52,52	0
57	MG	BA	3798	1/1	0.95	0.20	-1.19	28,28,28,28	0
57	MG	BA	3060	1/1	0.98	0.20	-1.20	30,30,30,30	0
57	MG	DA	3607	1/1	0.79	0.14	-1.21	65,65,65,65	0
57	MG	CA	3164	1/1	0.93	0.16	-1.25	60,60,60,60	0
57	MG	CV	101	1/1	0.84	0.13	-1.25	72,72,72,72	0
57	MG	DA	3099	1/1	0.97	0.17	-1.26	32,32,32,32	0
57	MG	DA	3375	1/1	0.95	0.16	-1.26	39,39,39,39	0
57	MG	DA	3435	1/1	0.97	0.15	-1.28	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3030	1/1	0.88	0.18	-1.29	46,46,46,46	0
57	MG	BA	3333	1/1	0.88	0.20	-1.30	38,38,38,38	0
57	MG	BN	3003	1/1	0.97	0.19	-1.30	48,48,48,48	0
57	MG	BA	3531	1/1	0.93	0.21	-1.32	26,26,26,26	0
57	MG	BA	3405	1/1	0.91	0.19	-1.34	63,63,63,63	0
57	MG	BA	3781	1/1	0.80	0.20	-1.35	41,41,41,41	0
57	MG	DA	3433	1/1	0.95	0.18	-1.36	46,46,46,46	0
57	MG	BA	3810	1/1	0.89	0.19	-1.36	41,41,41,41	0
57	MG	CX	3004	1/1	0.95	0.18	-1.38	63,63,63,63	0
57	MG	CA	3034	1/1	0.97	0.13	-1.42	59,59,59,59	0
57	MG	CA	3147	1/1	0.98	0.12	-1.42	64,64,64,64	0
57	MG	CA	3166	1/1	0.80	0.14	-1.42	66,66,66,66	0
59	ZN	B9	501	1/1	0.99	0.18	-1.42	38,38,38,38	0
57	MG	AM	201	1/1	0.89	0.16	-1.43	51,51,51,51	0
57	MG	CA	3037	1/1	0.95	0.14	-1.44	73,73,73,73	0
57	MG	AA	3015	1/1	0.95	0.15	-1.44	65,65,65,65	0
58	SF4	CD	302	8/8	0.98	0.16	-1.44	60,68,83,86	0
57	MG	BV	203	1/1	0.89	0.19	-1.46	38,38,38,38	0
57	MG	DA	3004	1/1	0.91	0.17	-1.46	40,40,40,40	0
57	MG	BA	3677	1/1	0.97	0.17	-1.48	60,60,60,60	0
57	MG	AA	3032	1/1	0.94	0.19	-1.50	67,67,67,67	0
57	MG	CA	3071	1/1	0.97	0.15	-1.52	68,68,68,68	0
57	MG	BQ	3001	1/1	0.95	0.22	-1.52	45,45,45,45	0
57	MG	BA	3806	1/1	0.96	0.16	-1.53	30,30,30,30	0
57	MG	DA	3037	1/1	0.94	0.16	-1.54	43,43,43,43	0
57	MG	DA	3514	1/1	0.93	0.13	-1.54	42,42,42,42	0
57	MG	DA	3672	1/1	0.93	0.16	-1.55	71,71,71,71	0
57	MG	B6	101	1/1	0.98	0.17	-1.57	48,48,48,48	0
57	MG	DA	3042	1/1	0.97	0.17	-1.57	38,38,38,38	0
57	MG	BA	3295	1/1	0.93	0.19	-1.58	38,38,38,38	0
57	MG	AN	503	1/1	0.93	0.15	-1.58	54,54,54,54	0
57	MG	CA	3033	1/1	0.86	0.19	-1.59	71,71,71,71	0
57	MG	DA	3613	1/1	0.97	0.15	-1.59	54,54,54,54	0
57	MG	BA	3049	1/1	0.98	0.21	-1.62	36,36,36,36	0
57	MG	DA	3173	1/1	0.92	0.12	-1.62	53,53,53,53	0
57	MG	DA	3575	1/1	0.87	0.14	-1.62	64,64,64,64	0
57	MG	BA	3465	1/1	0.90	0.18	-1.62	43,43,43,43	0
57	MG	AA	3133	1/1	0.92	0.16	-1.63	56,56,56,56	0
57	MG	BA	3320	1/1	0.93	0.22	-1.63	48,48,48,48	0
57	MG	DA	3281	1/1	0.98	0.16	-1.63	53,53,53,53	0
57	MG	BA	3713	1/1	0.93	0.18	-1.64	33,33,33,33	0
57	MG	AA	3001	1/1	0.85	0.14	-1.64	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	ZN	D4	501	1/1	0.79	0.07	-1.65	144,144,144,144	0
57	MG	BA	3807	1/1	0.93	0.17	-1.68	47,47,47,47	0
57	MG	B0	101	1/1	0.98	0.17	-1.69	36,36,36,36	0
57	MG	BN	3006	1/1	0.93	0.20	-1.69	49,49,49,49	0
57	MG	BA	3509	1/1	0.94	0.21	-1.69	31,31,31,31	0
57	MG	DA	3271	1/1	0.90	0.15	-1.70	48,48,48,48	0
57	MG	DA	3313	1/1	0.89	0.16	-1.70	47,47,47,47	0
57	MG	BA	3057	1/1	0.88	0.19	-1.70	34,34,34,34	0
57	MG	DA	3205	1/1	0.77	0.10	-1.72	56,56,56,56	0
57	MG	DA	3183	1/1	0.95	0.15	-1.73	38,38,38,38	0
57	MG	DA	3663	1/1	0.96	0.13	-1.73	60,60,60,60	0
59	ZN	D9	501	1/1	0.97	0.12	-1.74	68,68,68,68	0
59	ZN	CN	501	1/1	0.98	0.08	-1.76	93,93,93,93	0
57	MG	DW	3002	1/1	0.96	0.15	-1.78	45,45,45,45	0
57	MG	BA	3722	1/1	0.92	0.19	-1.78	47,47,47,47	0
57	MG	BA	3740	1/1	0.88	0.16	-1.78	28,28,28,28	0
57	MG	CA	3099	1/1	0.98	0.15	-1.79	44,44,44,44	0
57	MG	AA	3137	1/1	0.97	0.15	-1.81	51,51,51,51	0
57	MG	DA	3174	1/1	0.95	0.13	-1.85	44,44,44,44	0
57	MG	DA	3388	1/1	0.88	0.15	-1.85	53,53,53,53	0
57	MG	BA	3433	1/1	0.91	0.20	-1.88	32,32,32,32	0
57	MG	DB	3004	1/1	0.90	0.15	-1.88	55,55,55,55	0
57	MG	BA	3456	1/1	0.85	0.18	-1.89	49,49,49,49	0
57	MG	DA	3237	1/1	0.93	0.14	-1.90	56,56,56,56	0
57	MG	CA	3040	1/1	0.93	0.11	-1.90	51,51,51,51	0
57	MG	BA	3587	1/1	0.83	0.17	-1.95	36,36,36,36	0
57	MG	DA	3366	1/1	0.96	0.14	-1.96	42,42,42,42	0
57	MG	BN	3002	1/1	0.91	0.16	-1.97	39,39,39,39	0
57	MG	BA	3763	1/1	0.96	0.19	-2.00	24,24,24,24	0
57	MG	CA	3053	1/1	0.94	0.15	-2.05	41,41,41,41	0
57	MG	BA	3539	1/1	0.95	0.20	-2.06	52,52,52,52	0
57	MG	DA	3127	1/1	0.93	0.15	-2.06	35,35,35,35	0
57	MG	DA	3492	1/1	0.89	0.12	-2.07	55,55,55,55	0
57	MG	BA	3009	1/1	0.94	0.17	-2.07	28,28,28,28	0
57	MG	AA	3002	1/1	0.83	0.15	-2.08	71,71,71,71	0
57	MG	BA	3510	1/1	0.95	0.16	-2.10	46,46,46,46	0
57	MG	DA	3344	1/1	0.99	0.16	-2.11	31,31,31,31	0
57	MG	CA	3009	1/1	0.83	0.11	-2.12	64,64,64,64	0
57	MG	BA	3463	1/1	0.81	0.20	-2.12	48,48,48,48	0
57	MG	AA	3030	1/1	0.91	0.18	-2.14	60,60,60,60	0
57	MG	CA	3109	1/1	0.82	0.13	-2.16	67,67,67,67	0
57	MG	BA	3541	1/1	0.90	0.16	-2.16	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3212	1/1	0.96	0.13	-2.16	42,42,42,42	0
57	MG	BV	202	1/1	0.96	0.17	-2.17	50,50,50,50	0
57	MG	BA	3133	1/1	0.95	0.19	-2.17	45,45,45,45	0
57	MG	BE	304	1/1	0.96	0.19	-2.17	42,42,42,42	0
57	MG	CT	3001	1/1	0.58	0.12	-2.18	56,56,56,56	0
57	MG	DA	3101	1/1	0.96	0.16	-2.20	49,49,49,49	0
57	MG	DA	3261	1/1	0.97	0.12	-2.21	49,49,49,49	0
57	MG	DA	3285	1/1	0.99	0.13	-2.22	32,32,32,32	0
57	MG	DE	303	1/1	0.85	0.12	-2.24	54,54,54,54	0
57	MG	DA	3177	1/1	0.98	0.15	-2.24	42,42,42,42	0
57	MG	DA	3545	1/1	0.93	0.13	-2.24	35,35,35,35	0
57	MG	DB	3003	1/1	0.88	0.12	-2.26	57,57,57,57	0
57	MG	DA	3592	1/1	0.86	0.08	-2.26	51,51,51,51	0
57	MG	DA	3424	1/1	0.90	0.09	-2.27	61,61,61,61	0
57	MG	DA	3061	1/1	0.87	0.13	-2.28	48,48,48,48	0
57	MG	CA	3083	1/1	0.94	0.10	-2.33	79,79,79,79	0
57	MG	BA	3565	1/1	0.97	0.17	-2.33	40,40,40,40	0
57	MG	BA	3219	1/1	0.94	0.17	-2.35	36,36,36,36	0
57	MG	BA	3646	1/1	0.93	0.17	-2.37	42,42,42,42	0
57	MG	DA	3353	1/1	0.96	0.16	-2.38	42,42,42,42	0
57	MG	CA	3028	1/1	0.91	0.13	-2.40	41,41,41,41	0
57	MG	BF	302	1/1	0.92	0.18	-2.42	46,46,46,46	0
57	MG	AA	3094	1/1	0.88	0.16	-2.44	59,59,59,59	0
57	MG	BA	3797	1/1	0.92	0.17	-2.44	53,53,53,53	0
57	MG	BE	308	1/1	0.93	0.17	-2.45	40,40,40,40	0
57	MG	CA	3038	1/1	0.90	0.14	-2.45	58,58,58,58	0
57	MG	BA	3458	1/1	0.99	0.18	-2.46	18,18,18,18	0
57	MG	DQ	3001	1/1	0.98	0.13	-2.49	47,47,47,47	0
57	MG	DA	3201	1/1	0.93	0.14	-2.49	61,61,61,61	0
57	MG	AA	3009	1/1	0.94	0.18	-2.52	57,57,57,57	0
57	MG	DA	3043	1/1	0.94	0.15	-2.53	38,38,38,38	0
57	MG	CA	3124	1/1	0.87	0.12	-2.53	59,59,59,59	0
57	MG	AA	3117	1/1	0.90	0.12	-2.58	79,79,79,79	0
57	MG	DA	3171	1/1	0.97	0.12	-2.58	31,31,31,31	0
57	MG	BA	3430	1/1	0.88	0.16	-2.60	37,37,37,37	0
57	MG	AA	3211	1/1	0.90	0.12	-2.61	47,47,47,47	0
57	MG	BA	3730	1/1	0.31	0.19	-2.61	71,71,71,71	0
57	MG	AA	3139	1/1	0.83	0.14	-2.63	59,59,59,59	0
57	MG	DA	3030	1/1	0.95	0.14	-2.63	39,39,39,39	0
57	MG	CA	3046	1/1	0.91	0.09	-2.64	69,69,69,69	0
57	MG	AA	3091	1/1	0.81	0.14	-2.65	60,60,60,60	0
57	MG	CA	3112	1/1	0.93	0.15	-2.65	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3366	1/1	0.91	0.12	-2.67	57,57,57,57	0
57	MG	DA	3310	1/1	0.97	0.13	-2.68	38,38,38,38	0
57	MG	DA	3537	1/1	0.96	0.08	-2.69	44,44,44,44	0
57	MG	DA	3270	1/1	0.90	0.10	-2.69	46,46,46,46	0
57	MG	BA	3332	1/1	0.98	0.18	-2.69	38,38,38,38	0
57	MG	BA	3563	1/1	0.98	0.17	-2.71	36,36,36,36	0
57	MG	DA	3135	1/1	0.92	0.12	-2.71	38,38,38,38	0
57	MG	AA	3023	1/1	0.83	0.13	-2.74	74,74,74,74	0
57	MG	BA	3236	1/1	0.94	0.20	-2.75	49,49,49,49	0
57	MG	BB	204	1/1	0.97	0.18	-2.76	41,41,41,41	0
57	MG	DA	3501	1/1	0.95	0.15	-2.77	37,37,37,37	0
57	MG	BA	3211	1/1	0.96	0.16	-2.78	55,55,55,55	0
57	MG	BA	3319	1/1	0.93	0.19	-2.82	46,46,46,46	0
57	MG	BA	3214	1/1	0.97	0.17	-2.82	41,41,41,41	0
57	MG	DA	3425	1/1	0.85	0.12	-2.82	61,61,61,61	0
57	MG	BD	303	1/1	0.97	0.14	-2.84	39,39,39,39	0
57	MG	BA	3351	1/1	0.90	0.17	-2.85	30,30,30,30	0
57	MG	DA	3671	1/1	0.99	0.13	-2.86	74,74,74,74	0
57	MG	B7	102	1/1	0.93	0.16	-2.87	47,47,47,47	0
57	MG	BA	3423	1/1	0.91	0.18	-2.90	44,44,44,44	0
57	MG	CA	3123	1/1	0.97	0.14	-2.91	58,58,58,58	0
57	MG	B7	103	1/1	0.97	0.16	-2.92	42,42,42,42	0
57	MG	BA	3480	1/1	0.84	0.20	-2.93	35,35,35,35	0
57	MG	BA	3526	1/1	0.88	0.17	-2.95	44,44,44,44	0
57	MG	CA	3043	1/1	0.98	0.11	-2.97	47,47,47,47	0
57	MG	BA	3459	1/1	0.92	0.19	-2.98	48,48,48,48	0
57	MG	AA	3182	1/1	0.97	0.14	-2.98	49,49,49,49	0
57	MG	DA	3472	1/1	0.94	0.16	-3.04	44,44,44,44	0
57	MG	BA	3788	1/1	0.83	0.15	-3.06	51,51,51,51	0
57	MG	DA	3363	1/1	0.98	0.15	-3.06	29,29,29,29	0
57	MG	DA	3122	1/1	0.84	0.11	-3.06	49,49,49,49	0
57	MG	BA	3792	1/1	0.98	0.14	-3.07	54,54,54,54	0
57	MG	BA	3415	1/1	0.94	0.16	-3.10	28,28,28,28	0
57	MG	DA	3326	1/1	0.97	0.16	-3.12	43,43,43,43	0
57	MG	DA	3667	1/1	0.86	0.12	-3.12	50,50,50,50	0
57	MG	BA	3334	1/1	0.97	0.14	-3.13	37,37,37,37	0
57	MG	DA	3464	1/1	0.96	0.10	-3.13	46,46,46,46	0
57	MG	BA	3790	1/1	0.89	0.18	-3.17	34,34,34,34	0
57	MG	DD	305	1/1	0.98	0.12	-3.17	36,36,36,36	0
57	MG	DA	3003	1/1	0.98	0.15	-3.18	27,27,27,27	0
57	MG	BA	3550	1/1	0.90	0.19	-3.20	36,36,36,36	0
57	MG	BA	3381	1/1	0.95	0.15	-3.21	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3419	1/1	0.94	0.11	-3.21	32,32,32,32	0
57	MG	BA	3102	1/1	0.97	0.18	-3.22	44,44,44,44	0
57	MG	BA	3350	1/1	0.94	0.20	-3.25	28,28,28,28	0
57	MG	BA	3581	1/1	0.90	0.19	-3.31	30,30,30,30	0
57	MG	AA	3045	1/1	0.87	0.12	-3.33	58,58,58,58	0
57	MG	BD	305	1/1	0.97	0.15	-3.33	35,35,35,35	0
57	MG	DA	3319	1/1	0.96	0.12	-3.33	41,41,41,41	0
57	MG	DA	3539	1/1	0.95	0.12	-3.34	53,53,53,53	0
57	MG	CA	3089	1/1	0.98	0.12	-3.35	47,47,47,47	0
57	MG	DA	3666	1/1	0.89	0.14	-3.36	35,35,35,35	0
57	MG	DA	3337	1/1	0.90	0.13	-3.37	41,41,41,41	0
57	MG	CA	3132	1/1	0.95	0.13	-3.38	66,66,66,66	0
57	MG	BA	3477	1/1	0.92	0.18	-3.38	61,61,61,61	0
57	MG	BA	3411	1/1	0.90	0.19	-3.39	33,33,33,33	0
57	MG	BF	301	1/1	0.97	0.16	-3.41	35,35,35,35	0
57	MG	DA	3198	1/1	0.98	0.13	-3.45	40,40,40,40	0
57	MG	DA	3324	1/1	0.94	0.11	-3.45	33,33,33,33	0
57	MG	DG	3001	1/1	0.81	0.09	-3.46	55,55,55,55	0
57	MG	BA	3398	1/1	0.95	0.21	-3.47	32,32,32,32	0
57	MG	DA	3422	1/1	0.83	0.08	-3.48	46,46,46,46	0
57	MG	BA	3425	1/1	0.97	0.15	-3.48	40,40,40,40	0
57	MG	BA	3379	1/1	0.97	0.18	-3.51	31,31,31,31	0
57	MG	DA	3284	1/1	0.93	0.12	-3.53	47,47,47,47	0
57	MG	BA	3789	1/1	0.97	0.18	-3.58	12,12,12,12	0
57	MG	DA	3306	1/1	0.96	0.13	-3.59	55,55,55,55	0
57	MG	DA	3486	1/1	0.95	0.09	-3.61	47,47,47,47	0
57	MG	BA	3067	1/1	0.97	0.15	-3.65	41,41,41,41	0
57	MG	BA	3407	1/1	0.92	0.15	-3.66	47,47,47,47	0
57	MG	BA	3752	1/1	0.97	0.19	-3.66	32,32,32,32	0
57	MG	D0	101	1/1	0.85	0.08	-3.68	71,71,71,71	0
57	MG	AA	3033	1/1	0.85	0.14	-3.68	59,59,59,59	0
57	MG	BA	3630	1/1	0.97	0.14	-3.68	58,58,58,58	0
57	MG	BA	3791	1/1	0.98	0.18	-3.69	28,28,28,28	0
57	MG	DA	3465	1/1	0.90	0.12	-3.70	46,46,46,46	0
57	MG	BA	3570	1/1	0.95	0.16	-3.72	42,42,42,42	0
57	MG	DA	3074	1/1	0.93	0.12	-3.72	37,37,37,37	0
57	MG	AW	3004	1/1	0.57	0.14	-3.73	49,49,49,49	0
57	MG	BA	3755	1/1	0.85	0.15	-3.74	55,55,55,55	0
57	MG	DA	3192	1/1	0.97	0.10	-3.74	60,60,60,60	0
57	MG	CA	3003	1/1	0.88	0.12	-3.74	57,57,57,57	0
57	MG	DA	3632	1/1	0.87	0.15	-3.78	36,36,36,36	0
57	MG	BA	3274	1/1	0.86	0.14	-3.78	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3636	1/1	0.57	0.14	-3.85	64,64,64,64	0
57	MG	DA	3434	1/1	0.94	0.10	-3.85	39,39,39,39	0
57	MG	AA	3146	1/1	0.90	0.13	-3.94	66,66,66,66	0
57	MG	AA	3121	1/1	0.87	0.12	-3.95	70,70,70,70	0
57	MG	DA	3530	1/1	0.51	0.13	-3.95	74,74,74,74	0
57	MG	BA	3629	1/1	0.96	0.16	-3.97	43,43,43,43	0
57	MG	BU	207	1/1	0.95	0.17	-3.98	38,38,38,38	0
57	MG	BA	3365	1/1	0.94	0.13	-4.00	62,62,62,62	0
57	MG	BA	3420	1/1	0.97	0.16	-4.01	40,40,40,40	0
57	MG	CF	3001	1/1	0.94	0.11	-4.02	46,46,46,46	0
57	MG	DA	3246	1/1	0.93	0.14	-4.02	43,43,43,43	0
57	MG	BU	201	1/1	0.89	0.15	-4.03	43,43,43,43	0
57	MG	BA	3249	1/1	0.95	0.13	-4.07	49,49,49,49	0
57	MG	DA	3286	1/1	0.95	0.14	-4.08	42,42,42,42	0
57	MG	BA	3013	1/1	0.99	0.14	-4.10	32,32,32,32	0
57	MG	DA	3053	1/1	0.94	0.10	-4.10	47,47,47,47	0
57	MG	BA	3538	1/1	0.75	0.15	-4.14	40,40,40,40	0
57	MG	BA	3605	1/1	0.98	0.17	-4.16	43,43,43,43	0
57	MG	DA	3609	1/1	0.88	0.10	-4.18	46,46,46,46	0
57	MG	DA	3455	1/1	0.97	0.10	-4.19	47,47,47,47	0
57	MG	AA	3145	1/1	0.88	0.12	-4.19	66,66,66,66	0
57	MG	BA	3542	1/1	0.92	0.18	-4.19	45,45,45,45	0
57	MG	CA	3157	1/1	0.88	0.11	-4.24	58,58,58,58	0
57	MG	BB	208	1/1	0.97	0.14	-4.28	45,45,45,45	0
57	MG	BA	3369	1/1	0.92	0.15	-4.29	44,44,44,44	0
57	MG	DA	3325	1/1	0.92	0.12	-4.31	35,35,35,35	0
57	MG	BA	3701	1/1	0.96	0.15	-4.31	43,43,43,43	0
57	MG	DA	3103	1/1	0.91	0.10	-4.33	58,58,58,58	0
57	MG	DA	3373	1/1	0.97	0.15	-4.34	44,44,44,44	0
57	MG	AA	3020	1/1	0.83	0.13	-4.36	76,76,76,76	0
57	MG	CA	3020	1/1	0.89	0.11	-4.36	56,56,56,56	0
57	MG	BA	3436	1/1	0.94	0.14	-4.36	40,40,40,40	0
57	MG	AA	3152	1/1	0.93	0.10	-4.37	62,62,62,62	0
57	MG	BA	3736	1/1	0.98	0.16	-4.37	42,42,42,42	0
57	MG	DA	3509	1/1	0.96	0.12	-4.37	59,59,59,59	0
57	MG	DA	3342	1/1	0.82	0.11	-4.42	42,42,42,42	0
57	MG	BA	3793	1/1	0.89	0.13	-4.42	40,40,40,40	0
57	MG	BR	202	1/1	0.98	0.14	-4.43	31,31,31,31	0
57	MG	DA	3157	1/1	0.98	0.11	-4.46	47,47,47,47	0
57	MG	DA	3365	1/1	0.96	0.08	-4.46	36,36,36,36	0
57	MG	BA	3562	1/1	0.91	0.14	-4.52	37,37,37,37	0
57	MG	DA	3498	1/1	0.85	0.08	-4.52	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	BX	3003	1/1	0.92	0.17	-4.55	35,35,35,35	0
57	MG	BA	3247	1/1	0.98	0.16	-4.58	25,25,25,25	0
57	MG	BA	3183	1/1	0.94	0.18	-4.60	42,42,42,42	0
57	MG	AA	3054	1/1	0.86	0.13	-4.60	53,53,53,53	0
57	MG	DA	3430	1/1	0.84	0.11	-4.61	37,37,37,37	0
57	MG	DA	3596	1/1	0.96	0.10	-4.64	56,56,56,56	0
57	MG	BA	3175	1/1	0.95	0.20	-4.65	20,20,20,20	0
57	MG	DA	3648	1/1	0.96	0.14	-4.65	57,57,57,57	0
57	MG	DA	3006	1/1	0.93	0.10	-4.66	38,38,38,38	0
57	MG	DA	3580	1/1	0.96	0.16	-4.66	36,36,36,36	0
57	MG	BU	204	1/1	0.95	0.16	-4.73	35,35,35,35	0
57	MG	AA	3115	1/1	0.92	0.08	-4.75	79,79,79,79	0
57	MG	DA	3635	1/1	0.76	0.11	-4.76	38,38,38,38	0
57	MG	BB	217	1/1	0.98	0.18	-4.76	29,29,29,29	0
57	MG	DA	3447	1/1	0.93	0.15	-4.77	58,58,58,58	0
57	MG	BA	3222	1/1	0.97	0.18	-4.80	37,37,37,37	0
57	MG	CA	3023	1/1	0.96	0.14	-4.81	44,44,44,44	0
57	MG	BA	3387	1/1	0.92	0.15	-4.84	54,54,54,54	0
57	MG	DA	3334	1/1	0.88	0.15	-4.86	52,52,52,52	0
57	MG	DA	3039	1/1	0.94	0.10	-4.86	43,43,43,43	0
57	MG	BA	3051	1/1	0.92	0.19	-4.87	43,43,43,43	0
57	MG	DA	3515	1/1	0.96	0.15	-4.96	45,45,45,45	0
57	MG	AA	3158	1/1	0.97	0.13	-4.98	45,45,45,45	0
57	MG	AA	3042	1/1	0.89	0.09	-4.98	57,57,57,57	0
57	MG	BA	3418	1/1	0.82	0.17	-5.00	30,30,30,30	0
57	MG	BE	301	1/1	0.89	0.14	-5.04	35,35,35,35	0
57	MG	BA	3772	1/1	0.98	0.19	-5.05	33,33,33,33	0
57	MG	CA	3096	1/1	0.94	0.10	-5.07	44,44,44,44	0
57	MG	BA	3299	1/1	0.97	0.16	-5.08	25,25,25,25	0
57	MG	DA	3417	1/1	0.79	0.11	-5.10	52,52,52,52	0
57	MG	AA	3019	1/1	0.88	0.11	-5.11	66,66,66,66	0
57	MG	BA	3354	1/1	0.95	0.10	-5.11	48,48,48,48	0
57	MG	BA	3025	1/1	0.98	0.16	-5.12	27,27,27,27	0
57	MG	DA	3529	1/1	0.97	0.08	-5.14	38,38,38,38	0
57	MG	BA	3326	1/1	0.97	0.19	-5.16	20,20,20,20	0
57	MG	BA	3472	1/1	0.98	0.16	-5.17	20,20,20,20	0
57	MG	DA	3562	1/1	0.95	0.12	-5.18	64,64,64,64	0
57	MG	BA	3409	1/1	0.88	0.16	-5.20	30,30,30,30	0
57	MG	DA	3345	1/1	0.97	0.09	-5.22	44,44,44,44	0
57	MG	BA	3402	1/1	0.89	0.14	-5.23	40,40,40,40	0
57	MG	DA	3011	1/1	0.91	0.08	-5.25	48,48,48,48	0
57	MG	DA	3500	1/1	0.98	0.10	-5.27	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3318	1/1	0.95	0.14	-5.27	40,40,40,40	0
57	MG	DA	3440	1/1	0.87	0.09	-5.30	61,61,61,61	0
57	MG	DA	3330	1/1	0.98	0.11	-5.32	45,45,45,45	0
57	MG	DA	3148	1/1	0.88	0.12	-5.36	54,54,54,54	0
57	MG	DA	3296	1/1	0.96	0.12	-5.36	28,28,28,28	0
57	MG	CA	3077	1/1	0.94	0.08	-5.41	66,66,66,66	0
57	MG	DA	3369	1/1	0.97	0.15	-5.41	28,28,28,28	0
57	MG	AA	3178	1/1	0.93	0.15	-5.42	59,59,59,59	0
57	MG	DA	3358	1/1	0.93	0.14	-5.42	45,45,45,45	0
57	MG	BQ	3005	1/1	0.89	0.13	-5.43	49,49,49,49	0
57	MG	BA	3532	1/1	0.89	0.15	-5.46	52,52,52,52	0
57	MG	BA	3441	1/1	0.96	0.13	-5.49	35,35,35,35	0
57	MG	BA	3048	1/1	0.97	0.13	-5.50	47,47,47,47	0
57	MG	BA	3486	1/1	0.85	0.13	-5.51	57,57,57,57	0
57	MG	BA	3353	1/1	0.76	0.12	-5.56	50,50,50,50	0
57	MG	BV	205	1/1	0.96	0.09	-5.57	38,38,38,38	0
57	MG	B3	3001	1/1	0.95	0.12	-5.59	34,34,34,34	0
57	MG	DA	3008	1/1	0.98	0.09	-5.63	36,36,36,36	0
57	MG	BA	3269	1/1	0.91	0.16	-5.69	53,53,53,53	0
57	MG	CA	3068	1/1	0.94	0.15	-5.69	48,48,48,48	0
57	MG	BA	3234	1/1	0.98	0.15	-5.73	38,38,38,38	0
57	MG	BA	3715	1/1	0.81	0.14	-5.74	63,63,63,63	0
57	MG	BA	3750	1/1	0.91	0.17	-5.74	27,27,27,27	0
57	MG	DA	3287	1/1	0.95	0.10	-5.74	41,41,41,41	0
57	MG	BA	3343	1/1	0.97	0.15	-5.76	53,53,53,53	0
57	MG	BA	3517	1/1	0.96	0.14	-5.77	45,45,45,45	0
57	MG	CA	3041	1/1	0.89	0.13	-5.79	59,59,59,59	0
57	MG	BA	3555	1/1	0.93	0.14	-5.81	29,29,29,29	0
57	MG	AA	3074	1/1	0.96	0.09	-5.89	50,50,50,50	0
57	MG	DA	3618	1/1	0.88	0.12	-5.89	53,53,53,53	0
57	MG	BA	3483	1/1	0.97	0.15	-5.92	28,28,28,28	0
57	MG	BA	3132	1/1	0.96	0.14	-5.93	40,40,40,40	0
57	MG	BA	3558	1/1	0.98	0.14	-5.93	32,32,32,32	0
57	MG	DA	3341	1/1	0.96	0.13	-5.93	51,51,51,51	0
57	MG	BA	3692	1/1	0.96	0.15	-5.95	40,40,40,40	0
57	MG	BA	3167	1/1	0.98	0.12	-5.98	41,41,41,41	0
57	MG	BA	3119	1/1	0.93	0.13	-6.01	45,45,45,45	0
57	MG	BA	3598	1/1	0.86	0.14	-6.03	63,63,63,63	0
57	MG	BA	3217	1/1	0.94	0.16	-6.06	37,37,37,37	0
57	MG	DA	3351	1/1	0.93	0.12	-6.06	48,48,48,48	0
57	MG	BA	3027	1/1	0.95	0.11	-6.09	26,26,26,26	0
57	MG	BA	3309	1/1	0.97	0.18	-6.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BN	3004	1/1	0.90	0.12	-6.10	60,60,60,60	0
57	MG	AA	3164	1/1	0.97	0.10	-6.13	61,61,61,61	0
57	MG	DA	3414	1/1	0.84	0.13	-6.14	43,43,43,43	0
57	MG	BA	3487	1/1	0.98	0.14	-6.32	50,50,50,50	0
57	MG	DA	3040	1/1	0.96	0.12	-6.33	31,31,31,31	0
57	MG	AA	3093	1/1	0.89	0.12	-6.47	66,66,66,66	0
57	MG	BA	3410	1/1	0.97	0.16	-6.48	27,27,27,27	0
57	MG	DA	3272	1/1	0.95	0.10	-6.49	41,41,41,41	0
57	MG	BA	3764	1/1	0.84	0.17	-6.50	51,51,51,51	0
57	MG	BA	3620	1/1	0.95	0.15	-6.55	40,40,40,40	0
57	MG	DA	3612	1/1	0.94	0.09	-6.62	62,62,62,62	0
57	MG	BA	3768	1/1	0.93	0.12	-6.63	47,47,47,47	0
57	MG	DA	3579	1/1	0.97	0.10	-6.65	48,48,48,48	0
57	MG	DA	3502	1/1	0.90	0.10	-6.73	55,55,55,55	0
57	MG	DA	3401	1/1	0.90	0.10	-6.74	38,38,38,38	0
57	MG	DA	3356	1/1	0.87	0.10	-6.77	36,36,36,36	0
57	MG	BA	3511	1/1	0.94	0.14	-6.95	30,30,30,30	0
57	MG	AA	3100	1/1	0.90	0.12	-7.08	65,65,65,65	0
57	MG	DA	3021	1/1	0.98	0.09	-7.08	31,31,31,31	0
57	MG	DA	3446	1/1	0.83	0.11	-7.10	45,45,45,45	0
57	MG	BA	3043	1/1	0.92	0.15	-7.24	48,48,48,48	0
57	MG	DA	3387	1/1	0.96	0.10	-7.31	42,42,42,42	0
57	MG	CA	3117	1/1	0.93	0.10	-7.31	71,71,71,71	0
57	MG	BA	3008	1/1	0.89	0.17	-7.35	47,47,47,47	0
57	MG	BA	3318	1/1	0.87	0.12	-7.36	41,41,41,41	0
57	MG	AA	3063	1/1	0.91	0.10	-7.38	35,35,35,35	0
57	MG	DA	3265	1/1	0.97	0.12	-7.40	30,30,30,30	0
57	MG	DA	3549	1/1	0.93	0.10	-7.43	57,57,57,57	0
57	MG	DA	3377	1/1	0.95	0.09	-7.48	38,38,38,38	0
57	MG	BA	3395	1/1	0.95	0.17	-7.49	38,38,38,38	0
57	MG	AA	3200	1/1	0.88	0.08	-7.51	73,73,73,73	0
57	MG	CA	3110	1/1	0.94	0.09	-7.53	65,65,65,65	0
57	MG	DA	3321	1/1	0.81	0.08	-7.54	48,48,48,48	0
57	MG	BA	3010	1/1	0.98	0.16	-7.54	39,39,39,39	0
57	MG	BA	3649	1/1	0.94	0.11	-7.56	40,40,40,40	0
57	MG	DA	3460	1/1	0.97	0.13	-7.57	41,41,41,41	0
57	MG	DA	3570	1/1	0.95	0.13	-7.70	31,31,31,31	0
57	MG	BA	3548	1/1	0.87	0.17	-7.71	40,40,40,40	0
57	MG	CA	3081	1/1	0.89	0.09	-7.74	46,46,46,46	0
57	MG	BA	3661	1/1	0.96	0.09	-7.80	44,44,44,44	0
57	MG	CA	3086	1/1	0.93	0.13	-7.83	64,64,64,64	0
57	MG	BA	3609	1/1	0.98	0.11	-7.87	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3535	1/1	0.92	0.19	-7.94	31,31,31,31	0
57	MG	AA	3081	1/1	0.95	0.11	-7.95	48,48,48,48	0
57	MG	AA	3130	1/1	0.93	0.08	-8.00	56,56,56,56	0
57	MG	DA	3328	1/1	0.90	0.08	-8.09	47,47,47,47	0
57	MG	BA	3650	1/1	0.91	0.12	-8.20	52,52,52,52	0
57	MG	BA	3371	1/1	0.97	0.14	-8.21	35,35,35,35	0
57	MG	BA	3406	1/1	0.93	0.09	-8.41	50,50,50,50	0
57	MG	BA	3585	1/1	0.93	0.09	-8.65	46,46,46,46	0
57	MG	BA	3497	1/1	0.98	0.14	-8.81	28,28,28,28	0
57	MG	BA	3744	1/1	0.98	0.14	-8.82	39,39,39,39	0
57	MG	BA	3716	1/1	0.78	0.12	-8.84	65,65,65,65	0
57	MG	BA	3363	1/1	0.97	0.15	-8.86	22,22,22,22	0
57	MG	DA	3477	1/1	0.95	0.09	-9.22	43,43,43,43	0
57	MG	BF	305	1/1	0.98	0.09	-9.40	49,49,49,49	0
57	MG	CA	3016	1/1	0.85	0.11	-9.40	57,57,57,57	0
57	MG	BA	3258	1/1	0.87	0.13	-9.41	44,44,44,44	0
57	MG	CA	3069	1/1	0.96	0.12	-9.42	60,60,60,60	0
57	MG	DA	3289	1/1	0.98	0.10	-9.53	53,53,53,53	0
57	MG	BA	3256	1/1	0.96	0.15	-9.63	40,40,40,40	0
57	MG	AA	3022	1/1	0.92	0.10	-9.64	71,71,71,71	0
57	MG	DA	3149	1/1	0.93	0.06	-9.67	56,56,56,56	0
57	MG	BA	3643	1/1	0.97	0.13	-9.84	46,46,46,46	0
57	MG	BA	3648	1/1	0.90	0.11	-9.84	65,65,65,65	0
57	MG	BA	3604	1/1	0.93	0.15	-9.86	36,36,36,36	0
57	MG	DA	3303	1/1	0.95	0.09	-9.87	48,48,48,48	0
57	MG	BA	3316	1/1	0.81	0.12	-10.12	66,66,66,66	0
57	MG	BA	3644	1/1	0.96	0.14	-10.25	35,35,35,35	0
57	MG	DA	3279	1/1	0.91	0.12	-10.44	56,56,56,56	0
57	MG	DA	3619	1/1	0.96	0.11	-10.61	69,69,69,69	0
57	MG	BA	3378	1/1	0.99	0.12	-10.77	28,28,28,28	0
57	MG	BA	3647	1/1	0.95	0.09	-11.48	56,56,56,56	0
57	MG	BA	3026	1/1	0.95	0.15	-11.57	41,41,41,41	0
57	MG	AA	3016	1/1	0.94	0.09	-11.70	63,63,63,63	0
57	MG	AA	3086	1/1	0.98	0.07	-11.88	57,57,57,57	0
57	MG	DA	3538	1/1	0.91	0.11	-12.06	58,58,58,58	0
57	MG	BA	3162	1/1	0.88	0.15	-12.29	38,38,38,38	0
57	MG	BA	3594	1/1	0.83	0.12	-12.41	40,40,40,40	0
57	MG	BA	3092	1/1	0.89	0.16	-12.53	37,37,37,37	0
57	MG	DA	3315	1/1	0.99	0.08	-12.65	42,42,42,42	0
57	MG	BA	3580	1/1	0.93	0.13	-13.63	55,55,55,55	0
57	MG	DA	3278	1/1	0.97	0.06	-14.02	43,43,43,43	0
57	MG	BA	3786	1/1	0.97	0.13	-14.14	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3002	1/1	0.89	0.10	-16.88	50,50,50,50	0
57	MG	BA	3146	1/1	0.95	0.17	-17.32	40,40,40,40	0
57	MG	DA	3254	1/1	0.94	0.07	-19.23	52,52,52,52	0
57	MG	DA	3445	1/1	0.96	0.10	-21.95	32,32,32,32	0
57	MG	BA	3522	1/1	0.94	0.09	-25.68	52,52,52,52	0
57	MG	DA	3069	1/1	0.85	0.23	-	57,57,57,57	0
57	MG	BA	3462	1/1	0.96	0.19	-	36,36,36,36	0
57	MG	BA	3038	1/1	0.98	0.25	-	35,35,35,35	0
57	MG	BA	3568	1/1	0.63	0.10	-	59,59,59,59	0
57	MG	BA	3770	1/1	0.94	0.16	-	45,45,45,45	0
57	MG	BA	3021	1/1	0.93	0.18	-	49,49,49,49	0
57	MG	BA	3384	1/1	0.99	0.19	-	41,41,41,41	0
57	MG	BA	3091	1/1	0.96	0.39	-	56,56,56,56	0
57	MG	CA	3144	1/1	0.91	0.19	-	71,71,71,71	0
57	MG	AA	3124	1/1	0.87	0.09	-	47,47,47,47	0
57	MG	BA	3062	1/1	0.95	0.27	-	42,42,42,42	0
57	MG	BA	3385	1/1	0.92	0.16	-	59,59,59,59	0
57	MG	CA	3142	1/1	0.93	0.13	-	69,69,69,69	0
57	MG	DA	3408	1/1	0.81	0.08	-	58,58,58,58	0
57	MG	DA	3012	1/1	0.96	0.12	-	33,33,33,33	0
57	MG	B3	3002	1/1	0.96	0.12	-	66,66,66,66	0
57	MG	DR	5001	1/1	0.58	0.24	-	70,70,70,70	0
57	MG	DA	3398	1/1	0.92	0.14	-	45,45,45,45	0
57	MG	AA	3039	1/1	0.95	0.15	-	56,56,56,56	0
57	MG	BA	3536	1/1	0.94	0.27	-	49,49,49,49	0
57	MG	DA	3215	1/1	0.90	0.13	-	59,59,59,59	0
57	MG	BA	3454	1/1	0.98	0.23	-	27,27,27,27	0
57	MG	DA	3535	1/1	0.99	0.18	-	56,56,56,56	0
57	MG	CA	3090	1/1	0.87	0.10	-	67,67,67,67	0
57	MG	BA	3712	1/1	0.95	0.18	-	53,53,53,53	0
57	MG	CA	3159	1/1	0.89	0.18	-	70,70,70,70	0
57	MG	BA	3488	1/1	0.96	0.19	-	60,60,60,60	0
57	MG	DA	3599	1/1	0.97	0.20	-	36,36,36,36	0
57	MG	DA	3163	1/1	0.93	0.15	-	49,49,49,49	0
57	MG	AA	3169	1/1	0.74	0.13	-	62,62,62,62	0
57	MG	BA	3205	1/1	0.95	0.27	-	50,50,50,50	0
57	MG	BD	309	1/1	0.90	0.32	-	57,57,57,57	0
57	MG	BA	3705	1/1	0.98	0.11	-	62,62,62,62	0
57	MG	DA	3442	1/1	0.98	0.12	-	39,39,39,39	0
57	MG	DA	3476	1/1	0.84	0.14	-	62,62,62,62	0
57	MG	DA	3346	1/1	0.96	0.12	-	48,48,48,48	0
57	MG	AA	3059	1/1	0.90	0.12	-	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3653	1/1	0.91	0.14	-	52,52,52,52	0
57	MG	BA	3377	1/1	0.94	0.14	-	44,44,44,44	0
57	MG	AA	3058	1/1	0.90	0.28	-	59,59,59,59	0
57	MG	BA	3337	1/1	0.88	0.17	-	58,58,58,58	0
57	MG	AA	3072	1/1	0.88	0.12	-	66,66,66,66	0
57	MG	DA	3178	1/1	0.85	0.22	-	50,50,50,50	0
57	MG	CA	3151	1/1	0.95	0.27	-	59,59,59,59	0
57	MG	DA	3129	1/1	0.90	0.12	-	46,46,46,46	0
57	MG	BA	3651	1/1	0.92	0.19	-	45,45,45,45	0
57	MG	BA	3514	1/1	0.88	0.23	-	48,48,48,48	0
57	MG	BA	3164	1/1	0.91	0.21	-	48,48,48,48	0
57	MG	BA	3556	1/1	0.98	0.21	-	36,36,36,36	0
57	MG	DA	3202	1/1	0.94	0.11	-	57,57,57,57	0
57	MG	CA	3140	1/1	0.84	0.15	-	67,67,67,67	0
57	MG	DA	3311	1/1	0.89	0.17	-	54,54,54,54	0
57	MG	DA	3602	1/1	0.95	0.10	-	65,65,65,65	0
57	MG	DA	3134	1/1	0.91	0.21	-	41,41,41,41	0
57	MG	BA	3554	1/1	0.92	0.13	-	51,51,51,51	0
57	MG	DA	3397	1/1	0.93	0.09	-	57,57,57,57	0
57	MG	BA	3136	1/1	0.92	0.14	-	30,30,30,30	0
57	MG	BA	3761	1/1	0.82	0.16	-	59,59,59,59	0
57	MG	BA	3323	1/1	0.94	0.20	-	30,30,30,30	0
57	MG	BA	3601	1/1	0.86	0.12	-	55,55,55,55	0
57	MG	BA	3312	1/1	0.90	0.18	-	32,32,32,32	0
57	MG	BA	3180	1/1	0.86	0.17	-	47,47,47,47	0
57	MG	BA	3681	1/1	0.85	0.08	-	66,66,66,66	0
57	MG	BY	502	1/1	0.92	0.25	-	40,40,40,40	0
57	MG	BA	3645	1/1	0.96	0.20	-	33,33,33,33	0
57	MG	DA	3123	1/1	0.96	0.20	-	56,56,56,56	0
57	MG	DA	3418	1/1	0.95	0.11	-	52,52,52,52	0
57	MG	DA	3249	1/1	0.94	0.14	-	45,45,45,45	0
57	MG	DA	3393	1/1	0.98	0.10	-	50,50,50,50	0
57	MG	BP	203	1/1	0.98	0.15	-	33,33,33,33	0
57	MG	AA	3029	1/1	0.93	0.23	-	53,53,53,53	0
57	MG	BA	3767	1/1	0.92	0.12	-	73,73,73,73	0
57	MG	BA	3084	1/1	0.94	0.22	-	38,38,38,38	0
57	MG	DA	3617	1/1	0.93	0.07	-	56,56,56,56	0
57	MG	BA	3622	1/1	0.89	0.19	-	48,48,48,48	0
57	MG	BA	3233	1/1	0.99	0.31	-	56,56,56,56	0
57	MG	DA	3421	1/1	0.84	0.13	-	50,50,50,50	0
57	MG	DA	3065	1/1	0.93	0.18	-	43,43,43,43	0
57	MG	DA	3572	1/1	0.88	0.06	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3799	1/1	0.92	0.06	-	49,49,49,49	0
57	MG	BA	3593	1/1	0.95	0.22	-	38,38,38,38	0
57	MG	DA	3300	1/1	0.94	0.20	-	45,45,45,45	0
57	MG	DA	3108	1/1	0.93	0.07	-	52,52,52,52	0
57	MG	DA	3647	1/1	0.97	0.11	-	54,54,54,54	0
57	MG	BA	3221	1/1	0.97	0.17	-	37,37,37,37	0
57	MG	BA	3616	1/1	0.62	0.20	-	65,65,65,65	0
57	MG	DA	3058	1/1	0.97	0.14	-	29,29,29,29	0
57	MG	CA	3100	1/1	0.91	0.09	-	52,52,52,52	0
57	MG	BA	3200	1/1	0.93	0.15	-	67,67,67,67	0
57	MG	DA	3590	1/1	0.88	0.10	-	51,51,51,51	0
57	MG	BA	3422	1/1	0.99	0.24	-	33,33,33,33	0
57	MG	BA	3355	1/1	0.93	0.17	-	61,61,61,61	0
57	MG	BA	3432	1/1	0.85	0.14	-	58,58,58,58	0
57	MG	DA	3244	1/1	0.69	0.11	-	71,71,71,71	0
57	MG	BA	3359	1/1	0.95	0.30	-	62,62,62,62	0
57	MG	BA	3424	1/1	0.92	0.25	-	39,39,39,39	0
57	MG	DA	3438	1/1	0.93	0.20	-	47,47,47,47	0
57	MG	DA	3166	1/1	0.97	0.11	-	55,55,55,55	0
57	MG	BA	3637	1/1	0.87	0.11	-	39,39,39,39	0
57	MG	BA	3360	1/1	0.96	0.16	-	41,41,41,41	0
57	MG	DB	3002	1/1	0.88	0.17	-	65,65,65,65	0
57	MG	AA	3174	1/1	0.94	0.10	-	50,50,50,50	0
57	MG	DA	3224	1/1	0.95	0.17	-	49,49,49,49	0
57	MG	DA	3250	1/1	0.92	0.18	-	69,69,69,69	0
57	MG	DA	3625	1/1	0.93	0.07	-	69,69,69,69	0
57	MG	AA	3087	1/1	0.96	0.11	-	41,41,41,41	0
57	MG	DA	3626	1/1	0.89	0.07	-	67,67,67,67	0
57	MG	BA	3719	1/1	0.98	0.18	-	53,53,53,53	0
57	MG	AA	3062	1/1	0.98	0.28	-	51,51,51,51	0
57	MG	BA	3125	1/1	0.89	0.17	-	47,47,47,47	0
57	MG	DA	3644	1/1	0.97	0.08	-	55,55,55,55	0
57	MG	DA	3047	1/1	0.92	0.15	-	49,49,49,49	0
57	MG	BO	201	1/1	0.91	0.19	-	50,50,50,50	0
57	MG	CA	3063	1/1	0.95	0.23	-	58,58,58,58	0
57	MG	DA	3187	1/1	0.97	0.11	-	42,42,42,42	0
57	MG	BA	3017	1/1	0.92	0.25	-	48,48,48,48	0
57	MG	DA	3488	1/1	0.95	0.07	-	41,41,41,41	0
57	MG	DA	3079	1/1	0.92	0.17	-	55,55,55,55	0
57	MG	DA	3454	1/1	0.96	0.16	-	56,56,56,56	0
57	MG	DA	3144	1/1	0.98	0.11	-	38,38,38,38	0
57	MG	BA	3191	1/1	0.96	0.18	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	DA	3164	1/1	0.92	0.12	-	51,51,51,51	0
57	MG	BA	3690	1/1	0.93	0.18	-	58,58,58,58	0
57	MG	BA	3186	1/1	0.93	0.45	-	45,45,45,45	0
57	MG	BA	3066	1/1	0.81	0.19	-	49,49,49,49	0
57	MG	DA	3392	1/1	0.92	0.19	-	70,70,70,70	0
57	MG	DA	3269	1/1	0.96	0.06	-	49,49,49,49	0
57	MG	DA	3297	1/1	0.99	0.11	-	39,39,39,39	0
57	MG	DA	3654	1/1	0.86	0.12	-	56,56,56,56	0
57	MG	DA	3107	1/1	0.93	0.14	-	51,51,51,51	0
57	MG	BG	203	1/1	0.96	0.16	-	42,42,42,42	0
57	MG	BA	3780	1/1	0.87	0.11	-	62,62,62,62	0
57	MG	DA	3126	1/1	0.90	0.08	-	55,55,55,55	0
57	MG	DA	3552	1/1	0.97	0.11	-	54,54,54,54	0
57	MG	BA	3403	1/1	0.93	0.08	-	54,54,54,54	0
57	MG	DA	3564	1/1	0.89	0.16	-	61,61,61,61	0
57	MG	DA	3527	1/1	0.88	0.12	-	60,60,60,60	0
57	MG	DA	3070	1/1	0.90	0.13	-	58,58,58,58	0
57	MG	DA	3262	1/1	0.77	0.10	-	65,65,65,65	0
57	MG	AW	3001	1/1	0.81	0.11	-	60,60,60,60	0
57	MG	DA	3593	1/1	0.89	0.11	-	40,40,40,40	0
57	MG	DA	3162	1/1	0.92	0.35	-	50,50,50,50	0
57	MG	DA	3360	1/1	0.86	0.16	-	46,46,46,46	0
57	MG	BA	3154	1/1	0.83	0.23	-	47,47,47,47	0
57	MG	BA	3103	1/1	0.97	0.17	-	38,38,38,38	0
57	MG	BA	3735	1/1	0.98	0.43	-	57,57,57,57	0
57	MG	BA	3229	1/1	0.91	0.22	-	54,54,54,54	0
57	MG	BA	3696	1/1	0.96	0.14	-	33,33,33,33	0
57	MG	CA	3025	1/1	0.94	0.14	-	51,51,51,51	0
57	MG	DA	3228	1/1	0.97	0.30	-	38,38,38,38	0
57	MG	DA	3546	1/1	0.73	0.11	-	71,71,71,71	0
57	MG	BZ	3001	1/1	0.89	0.29	-	55,55,55,55	0
57	MG	BA	3557	1/1	0.95	0.16	-	33,33,33,33	0
57	MG	BA	3658	1/1	0.87	0.26	-	61,61,61,61	0
57	MG	AA	3083	1/1	0.94	0.31	-	57,57,57,57	0
57	MG	DA	3536	1/1	0.93	0.10	-	48,48,48,48	0
57	MG	AX	3014	1/1	0.67	0.19	-	72,72,72,72	0
57	MG	DA	3646	1/1	0.85	0.14	-	59,59,59,59	0
57	MG	BA	3537	1/1	0.93	0.16	-	45,45,45,45	0
57	MG	BA	3627	1/1	0.96	0.17	-	56,56,56,56	0
57	MG	BA	3122	1/1	0.88	0.15	-	41,41,41,41	0
57	MG	DA	3407	1/1	0.91	0.04	-	66,66,66,66	0
57	MG	DA	3573	1/1	0.94	0.11	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3624	1/1	0.88	0.10	-	68,68,68,68	0
57	MG	AA	3181	1/1	0.93	0.16	-	51,51,51,51	0
57	MG	BA	3024	1/1	0.91	0.19	-	49,49,49,49	0
57	MG	CA	3129	1/1	0.91	0.09	-	43,43,43,43	0
57	MG	BA	3039	1/1	0.98	0.20	-	32,32,32,32	0
57	MG	BA	3123	1/1	0.95	0.22	-	32,32,32,32	0
57	MG	BA	3720	1/1	0.96	0.14	-	65,65,65,65	0
57	MG	BA	3729	1/1	0.96	0.19	-	47,47,47,47	0
57	MG	BA	3090	1/1	0.95	0.31	-	53,53,53,53	0
57	MG	DA	3571	1/1	0.85	0.12	-	56,56,56,56	0
57	MG	DA	3483	1/1	0.95	0.32	-	55,55,55,55	0
57	MG	BA	3114	1/1	0.79	0.18	-	53,53,53,53	0
57	MG	AA	3082	1/1	0.98	0.13	-	46,46,46,46	0
57	MG	DA	3551	1/1	0.93	0.08	-	55,55,55,55	0
57	MG	DA	3277	1/1	0.95	0.12	-	55,55,55,55	0
57	MG	BA	3474	1/1	0.97	0.18	-	55,55,55,55	0
57	MG	CA	3019	1/1	0.95	0.10	-	65,65,65,65	0
57	MG	BA	3578	1/1	0.88	0.10	-	46,46,46,46	0
57	MG	DA	3323	1/1	0.88	0.11	-	50,50,50,50	0
57	MG	DA	3410	1/1	0.85	0.13	-	53,53,53,53	0
57	MG	DA	3252	1/1	0.76	0.08	-	37,37,37,37	0
57	MG	AA	3196	1/1	0.85	0.21	-	74,74,74,74	0
57	MG	BA	3120	1/1	0.91	0.21	-	55,55,55,55	0
57	MG	DA	3233	1/1	0.96	0.19	-	53,53,53,53	0
57	MG	CA	3108	1/1	0.94	0.31	-	68,68,68,68	0
57	MG	AA	3092	1/1	0.97	0.14	-	63,63,63,63	0
57	MG	BA	3108	1/1	0.96	0.32	-	44,44,44,44	0
57	MG	BA	3683	1/1	0.91	0.15	-	73,73,73,73	0
57	MG	BA	3018	1/1	0.84	0.20	-	56,56,56,56	0
57	MG	CA	3111	1/1	0.91	0.16	-	64,64,64,64	0
57	MG	BW	204	1/1	0.96	0.22	-	42,42,42,42	0
57	MG	BA	3088	1/1	0.96	0.35	-	48,48,48,48	0
57	MG	DA	3128	1/1	0.92	0.15	-	58,58,58,58	0
57	MG	DA	3372	1/1	0.95	0.08	-	56,56,56,56	0
57	MG	DA	3485	1/1	0.95	0.12	-	52,52,52,52	0
57	MG	DA	3222	1/1	0.80	0.15	-	57,57,57,57	0
57	MG	BA	3288	1/1	0.95	0.20	-	56,56,56,56	0
57	MG	BA	3774	1/1	0.97	0.07	-	46,46,46,46	0
57	MG	BA	3297	1/1	0.88	0.14	-	43,43,43,43	0
57	MG	BA	3447	1/1	0.86	0.10	-	72,72,72,72	0
57	MG	AA	3051	1/1	0.87	0.23	-	73,73,73,73	0
57	MG	DA	3185	1/1	0.86	0.11	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3304	1/1	0.91	0.15	-	67,67,67,67	0
57	MG	DA	3674	1/1	0.95	0.16	-	37,37,37,37	0
57	MG	CD	301	1/1	0.95	0.19	-	56,56,56,56	0
57	MG	BA	3300	1/1	0.74	0.25	-	57,57,57,57	0
57	MG	DA	3151	1/1	0.89	0.09	-	55,55,55,55	0
57	MG	CA	3084	1/1	0.97	0.13	-	60,60,60,60	0
57	MG	CA	3156	1/1	0.89	0.10	-	73,73,73,73	0
57	MG	DA	3197	1/1	0.98	0.14	-	55,55,55,55	0
57	MG	BA	3672	1/1	0.94	0.20	-	43,43,43,43	0
57	MG	DA	3041	1/1	0.93	0.09	-	38,38,38,38	0
57	MG	BB	213	1/1	0.96	0.19	-	60,60,60,60	0
57	MG	BA	3746	1/1	0.91	0.11	-	51,51,51,51	0
57	MG	DA	3060	1/1	0.74	0.15	-	64,64,64,64	0
57	MG	BA	3686	1/1	0.90	0.25	-	60,60,60,60	0
57	MG	DA	3432	1/1	0.93	0.12	-	37,37,37,37	0
57	MG	DA	3452	1/1	0.90	0.16	-	51,51,51,51	0
57	MG	BA	3470	1/1	0.65	0.13	-	62,62,62,62	0
57	MG	DA	3035	1/1	0.86	0.20	-	52,52,52,52	0
57	MG	AA	3194	1/1	0.90	0.11	-	56,56,56,56	0
57	MG	DA	3082	1/1	0.81	0.14	-	47,47,47,47	0
57	MG	BA	3500	1/1	0.95	0.15	-	56,56,56,56	0
57	MG	BA	3569	1/1	0.99	0.19	-	49,49,49,49	0
57	MG	DA	3348	1/1	0.95	0.10	-	34,34,34,34	0
57	MG	AA	3118	1/1	0.95	0.17	-	47,47,47,47	0
57	MG	AX	3008	1/1	0.92	0.19	-	70,70,70,70	0
57	MG	BA	3691	1/1	0.96	0.16	-	55,55,55,55	0
57	MG	CA	3024	1/1	0.79	0.10	-	74,74,74,74	0
57	MG	DA	3466	1/1	0.97	0.11	-	41,41,41,41	0
57	MG	BA	3527	1/1	0.95	0.16	-	54,54,54,54	0
57	MG	BA	3074	1/1	0.87	0.21	-	46,46,46,46	0
57	MG	BA	3336	1/1	0.95	0.15	-	64,64,64,64	0
57	MG	DB	3007	1/1	0.96	0.20	-	58,58,58,58	0
57	MG	BA	3490	1/1	0.97	0.10	-	54,54,54,54	0
57	MG	DA	3450	1/1	0.84	0.10	-	40,40,40,40	0
57	MG	DA	3001	1/1	0.92	0.17	-	60,60,60,60	0
57	MG	CA	3008	1/1	0.92	0.27	-	51,51,51,51	0
57	MG	DA	3212	1/1	0.80	0.15	-	45,45,45,45	0
57	MG	DA	3034	1/1	0.98	0.17	-	38,38,38,38	0
57	MG	BA	3003	1/1	0.72	0.19	-	60,60,60,60	0
57	MG	BA	3282	1/1	0.93	0.16	-	39,39,39,39	0
57	MG	DA	3584	1/1	0.94	0.18	-	53,53,53,53	0
57	MG	BA	3784	1/1	0.97	0.21	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3179	1/1	0.84	0.18	-	50,50,50,50	0
57	MG	DA	3526	1/1	0.88	0.11	-	48,48,48,48	0
57	MG	AA	3031	1/1	0.87	0.23	-	70,70,70,70	0
57	MG	BA	3340	1/1	0.94	0.14	-	39,39,39,39	0
57	MG	BA	3745	1/1	0.89	0.08	-	75,75,75,75	0
57	MG	DA	3655	1/1	0.94	0.11	-	64,64,64,64	0
57	MG	BA	3287	1/1	0.98	0.14	-	42,42,42,42	0
57	MG	DA	3036	1/1	0.93	0.14	-	48,48,48,48	0
57	MG	BA	3731	1/1	0.97	0.30	-	37,37,37,37	0
57	MG	AA	3157	1/1	0.95	0.17	-	45,45,45,45	0
57	MG	B4	502	1/1	0.75	0.14	-	71,71,71,71	0
57	MG	BA	3394	1/1	0.90	0.18	-	40,40,40,40	0
57	MG	DA	3146	1/1	0.90	0.10	-	55,55,55,55	0
57	MG	AA	3163	1/1	0.92	0.18	-	56,56,56,56	0
57	MG	BA	3101	1/1	0.92	0.19	-	53,53,53,53	0
57	MG	BA	3140	1/1	0.96	0.14	-	47,47,47,47	0
57	MG	CA	3148	1/1	0.98	0.11	-	70,70,70,70	0
57	MG	BA	3036	1/1	0.97	0.17	-	40,40,40,40	0
57	MG	BA	3189	1/1	0.94	0.19	-	39,39,39,39	0
57	MG	AA	3147	1/1	0.97	0.10	-	70,70,70,70	0
57	MG	BA	3749	1/1	0.89	0.12	-	56,56,56,56	0
57	MG	BA	3275	1/1	0.88	0.18	-	58,58,58,58	0
57	MG	BA	3501	1/1	0.90	0.22	-	71,71,71,71	0
57	MG	AX	3011	1/1	0.80	0.20	-	78,78,78,78	0
57	MG	BA	3016	1/1	0.92	0.13	-	38,38,38,38	0
57	MG	DA	3114	1/1	0.94	0.15	-	55,55,55,55	0
57	MG	BA	3528	1/1	0.96	0.18	-	56,56,56,56	0
57	MG	BA	3007	1/1	0.91	0.19	-	55,55,55,55	0
57	MG	AA	3180	1/1	0.96	0.10	-	73,73,73,73	0
57	MG	BA	3064	1/1	0.94	0.13	-	43,43,43,43	0
57	MG	DA	3007	1/1	0.87	0.14	-	50,50,50,50	0
57	MG	BA	3172	1/1	0.81	0.19	-	46,46,46,46	0
57	MG	DA	3087	1/1	0.95	0.18	-	58,58,58,58	0
57	MG	BA	3223	1/1	0.93	0.13	-	41,41,41,41	0
57	MG	AA	3161	1/1	0.92	0.23	-	65,65,65,65	0
57	MG	BA	3015	1/1	0.95	0.16	-	32,32,32,32	0
57	MG	BA	3225	1/1	0.76	0.16	-	61,61,61,61	0
57	MG	BA	3466	1/1	0.91	0.17	-	49,49,49,49	0
57	MG	CA	3036	1/1	0.89	0.14	-	66,66,66,66	0
57	MG	AX	3016	1/1	0.90	0.10	-	56,56,56,56	0
57	MG	B2	3001	1/1	0.85	0.21	-	56,56,56,56	0
57	MG	CA	3127	1/1	0.95	0.18	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3161	1/1	0.94	0.09	-	56,56,56,56	0
57	MG	BA	3265	1/1	0.93	0.21	-	54,54,54,54	0
57	MG	BB	211	1/1	0.87	0.10	-	51,51,51,51	0
57	MG	DA	3152	1/1	0.93	0.20	-	51,51,51,51	0
57	MG	BA	3611	1/1	0.97	0.17	-	46,46,46,46	0
57	MG	BA	3618	1/1	0.89	0.14	-	65,65,65,65	0
57	MG	BA	3612	1/1	0.90	0.14	-	21,21,21,21	0
57	MG	CA	3137	1/1	0.97	0.16	-	56,56,56,56	0
57	MG	BA	3695	1/1	0.82	0.18	-	67,67,67,67	0
57	MG	DA	3327	1/1	0.92	0.12	-	57,57,57,57	0
57	MG	AA	3175	1/1	0.94	0.18	-	63,63,63,63	0
57	MG	DA	3511	1/1	0.94	0.16	-	49,49,49,49	0
57	MG	BA	3523	1/1	0.94	0.11	-	48,48,48,48	0
57	MG	DB	3012	1/1	0.86	0.33	-	61,61,61,61	0
57	MG	DA	3338	1/1	0.97	0.15	-	61,61,61,61	0
57	MG	AA	3027	1/1	0.93	0.15	-	50,50,50,50	0
57	MG	BA	3176	1/1	0.94	0.17	-	45,45,45,45	0
57	MG	BA	3476	1/1	0.97	0.15	-	55,55,55,55	0
57	MG	BB	216	1/1	0.96	0.23	-	51,51,51,51	0
57	MG	DP	202	1/1	0.89	0.11	-	53,53,53,53	0
57	MG	DA	3639	1/1	0.96	0.48	-	59,59,59,59	0
57	MG	DA	3332	1/1	0.89	0.11	-	53,53,53,53	0
57	MG	BA	3118	1/1	0.93	0.17	-	48,48,48,48	0
57	MG	BA	3503	1/1	0.75	0.12	-	49,49,49,49	0
57	MG	CA	3130	1/1	0.90	0.09	-	57,57,57,57	0
57	MG	CA	3155	1/1	0.97	0.12	-	53,53,53,53	0
57	MG	AA	3040	1/1	0.98	0.11	-	60,60,60,60	0
57	MG	AA	3150	1/1	0.95	0.19	-	57,57,57,57	0
57	MG	DA	3582	1/1	0.82	0.07	-	56,56,56,56	0
57	MG	CA	3093	1/1	0.96	0.10	-	55,55,55,55	0
57	MG	DA	3555	1/1	0.98	0.29	-	53,53,53,53	0
57	MG	CA	3107	1/1	0.82	0.20	-	80,80,80,80	0
57	MG	BA	3734	1/1	0.92	0.16	-	52,52,52,52	0
57	MG	BA	3754	1/1	0.85	0.18	-	48,48,48,48	0
57	MG	DA	3207	1/1	0.95	0.30	-	63,63,63,63	0
57	MG	BA	3400	1/1	0.91	0.21	-	33,33,33,33	0
57	MG	DA	3531	1/1	0.76	0.18	-	61,61,61,61	0
57	MG	DA	3282	1/1	0.96	0.06	-	52,52,52,52	0
57	MG	BB	214	1/1	0.77	0.17	-	49,49,49,49	0
57	MG	BA	3302	1/1	0.93	0.12	-	69,69,69,69	0
60	K	AX	3001	1/1	0.94	0.12	-	65,65,65,65	0
57	MG	DA	3097	1/1	0.91	0.21	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3083	1/1	0.92	0.19	-	40,40,40,40	0
57	MG	CW	3001	1/1	0.91	0.22	-	67,67,67,67	0
57	MG	AA	3068	1/1	0.94	0.14	-	69,69,69,69	0
57	MG	AA	3176	1/1	0.89	0.10	-	67,67,67,67	0
57	MG	CA	3158	1/1	0.85	0.13	-	67,67,67,67	0
57	MG	BA	3808	1/1	0.95	0.17	-	42,42,42,42	0
57	MG	BA	3769	1/1	0.83	0.18	-	52,52,52,52	0
57	MG	BA	3113	1/1	0.97	0.25	-	53,53,53,53	0
57	MG	DA	3581	1/1	0.95	0.23	-	57,57,57,57	0
57	MG	AA	3159	1/1	0.94	0.12	-	66,66,66,66	0
57	MG	CA	3031	1/1	0.95	0.10	-	68,68,68,68	0
57	MG	BA	3668	1/1	0.91	0.17	-	53,53,53,53	0
57	MG	BA	3231	1/1	0.85	0.32	-	63,63,63,63	0
57	MG	CA	3026	1/1	0.90	0.20	-	63,63,63,63	0
57	MG	DA	3018	1/1	0.90	0.20	-	62,62,62,62	0
57	MG	DA	3448	1/1	0.43	0.21	-	70,70,70,70	0
57	MG	BA	3452	1/1	0.94	0.16	-	55,55,55,55	0
57	MG	AE	202	1/1	0.79	0.12	-	80,80,80,80	0
57	MG	BA	3777	1/1	0.94	0.17	-	40,40,40,40	0
57	MG	BU	202	1/1	0.93	0.28	-	40,40,40,40	0
57	MG	BA	3147	1/1	0.88	0.16	-	45,45,45,45	0
57	MG	BA	3551	1/1	0.95	0.19	-	36,36,36,36	0
57	MG	BA	3505	1/1	0.93	0.12	-	55,55,55,55	0
57	MG	DA	3238	1/1	0.94	0.26	-	44,44,44,44	0
57	MG	AA	3149	1/1	0.93	0.10	-	46,46,46,46	0
57	MG	DA	3444	1/1	0.89	0.06	-	44,44,44,44	0
57	MG	AA	3034	1/1	0.85	0.11	-	47,47,47,47	0
57	MG	DA	3051	1/1	0.90	0.11	-	48,48,48,48	0
57	MG	AA	3166	1/1	0.85	0.14	-	69,69,69,69	0
57	MG	BA	3080	1/1	0.98	0.17	-	60,60,60,60	0
57	MG	BB	207	1/1	0.96	0.22	-	54,54,54,54	0
57	MG	BA	3266	1/1	0.88	0.19	-	39,39,39,39	0
57	MG	DA	3650	1/1	0.93	0.12	-	67,67,67,67	0
57	MG	CA	3092	1/1	0.95	0.10	-	50,50,50,50	0
57	MG	DA	3595	1/1	0.92	0.17	-	59,59,59,59	0
57	MG	DA	3080	1/1	0.95	0.10	-	55,55,55,55	0
57	MG	DA	3404	1/1	0.98	0.12	-	48,48,48,48	0
57	MG	CA	3017	1/1	0.78	0.19	-	53,53,53,53	0
57	MG	BA	3625	1/1	0.98	0.18	-	39,39,39,39	0
57	MG	BA	3401	1/1	0.75	0.16	-	35,35,35,35	0
57	MG	BA	3061	1/1	0.91	0.23	-	29,29,29,29	0
57	MG	BA	3226	1/1	0.91	0.27	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3054	1/1	0.90	0.30	-	69,69,69,69	0
57	MG	BA	3376	1/1	0.94	0.16	-	48,48,48,48	0
57	MG	BA	3055	1/1	0.93	0.21	-	45,45,45,45	0
57	MG	BQ	3003	1/1	0.94	0.27	-	49,49,49,49	0
57	MG	BA	3375	1/1	0.96	0.13	-	68,68,68,68	0
57	MG	DA	3458	1/1	0.94	0.05	-	52,52,52,52	0
57	MG	CA	3056	1/1	0.96	0.10	-	64,64,64,64	0
57	MG	DA	3110	1/1	0.87	0.32	-	58,58,58,58	0
57	MG	DB	3013	1/1	0.94	0.17	-	64,64,64,64	0
57	MG	AX	3012	1/1	0.96	0.17	-	59,59,59,59	0
57	MG	DA	3258	1/1	0.98	0.14	-	48,48,48,48	0
57	MG	BA	3442	1/1	0.88	0.17	-	44,44,44,44	0
57	MG	DA	3620	1/1	0.76	0.11	-	68,68,68,68	0
57	MG	DA	3553	1/1	0.82	0.10	-	49,49,49,49	0
57	MG	BA	3177	1/1	0.90	0.19	-	46,46,46,46	0
57	MG	AA	3116	1/1	0.95	0.11	-	55,55,55,55	0
57	MG	BA	3765	1/1	0.93	0.22	-	48,48,48,48	0
57	MG	BA	3434	1/1	0.83	0.13	-	55,55,55,55	0
57	MG	BA	3134	1/1	0.92	0.17	-	48,48,48,48	0
57	MG	AA	3151	1/1	0.96	0.14	-	45,45,45,45	0
57	MG	BA	3131	1/1	0.89	0.11	-	58,58,58,58	0
57	MG	BA	3688	1/1	0.93	0.16	-	46,46,46,46	0
57	MG	CA	3030	1/1	0.94	0.22	-	57,57,57,57	0
57	MG	AX	3009	1/1	0.92	0.18	-	64,64,64,64	0
57	MG	DA	3357	1/1	0.98	0.07	-	50,50,50,50	0
57	MG	BA	3519	1/1	0.93	0.08	-	55,55,55,55	0
57	MG	DA	3469	1/1	0.88	0.28	-	44,44,44,44	0
57	MG	DA	3349	1/1	0.97	0.07	-	52,52,52,52	0
57	MG	BA	3489	1/1	0.97	0.07	-	59,59,59,59	0
57	MG	DA	3247	1/1	0.84	0.09	-	45,45,45,45	0
57	MG	DA	3199	1/1	0.96	0.10	-	47,47,47,47	0
57	MG	BA	3679	1/1	0.88	0.12	-	62,62,62,62	0
57	MG	DA	3090	1/1	0.89	0.10	-	52,52,52,52	0
57	MG	BA	3621	1/1	0.91	0.17	-	53,53,53,53	0
57	MG	DA	3453	1/1	0.98	0.22	-	60,60,60,60	0
57	MG	DA	3175	1/1	0.97	0.12	-	41,41,41,41	0
57	MG	BA	3220	1/1	0.94	0.22	-	29,29,29,29	0
57	MG	BA	3811	1/1	0.90	0.14	-	65,65,65,65	0
57	MG	BA	3461	1/1	0.90	0.10	-	62,62,62,62	0
57	MG	BA	3329	1/1	0.94	0.19	-	60,60,60,60	0
57	MG	CA	3165	1/1	0.93	0.11	-	45,45,45,45	0
57	MG	BA	3065	1/1	0.94	0.19	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3053	1/1	0.72	0.21	-	54,54,54,54	0
57	MG	BA	3507	1/1	0.91	0.20	-	49,49,49,49	0
57	MG	CA	3080	1/1	0.95	0.09	-	49,49,49,49	0
57	MG	BA	3553	1/1	0.97	0.10	-	59,59,59,59	0
57	MG	BA	3704	1/1	0.76	0.13	-	77,77,77,77	0
57	MG	BA	3479	1/1	0.97	0.07	-	50,50,50,50	0
57	MG	CA	3153	1/1	0.91	0.16	-	70,70,70,70	0
57	MG	BA	3152	1/1	0.97	0.30	-	43,43,43,43	0
57	MG	DA	3550	1/1	0.91	0.13	-	57,57,57,57	0
57	MG	BA	3235	1/1	0.98	0.16	-	42,42,42,42	0
57	MG	BA	3703	1/1	0.89	0.10	-	64,64,64,64	0
57	MG	AA	3135	1/1	0.90	0.24	-	65,65,65,65	0
57	MG	DA	3026	1/1	0.99	0.55	-	59,59,59,59	0
57	MG	DA	3614	1/1	0.88	0.07	-	65,65,65,65	0
57	MG	DA	3317	1/1	0.91	0.12	-	44,44,44,44	0
57	MG	BA	3591	1/1	0.96	0.17	-	35,35,35,35	0
57	MG	DA	3402	1/1	0.81	0.10	-	66,66,66,66	0
57	MG	BB	205	1/1	0.96	0.20	-	60,60,60,60	0
57	MG	DA	3063	1/1	0.92	0.23	-	54,54,54,54	0
57	MG	DA	3320	1/1	0.61	0.15	-	55,55,55,55	0
57	MG	DA	3264	1/1	0.94	0.13	-	40,40,40,40	0
57	MG	DA	3160	1/1	0.96	0.10	-	56,56,56,56	0
57	MG	DA	3467	1/1	0.95	0.25	-	40,40,40,40	0
57	MG	DA	3292	1/1	0.98	0.17	-	30,30,30,30	0
57	MG	BA	3759	1/1	0.83	0.18	-	33,33,33,33	0
57	MG	CA	3018	1/1	0.72	0.16	-	69,69,69,69	0
57	MG	DA	3463	1/1	0.90	0.14	-	55,55,55,55	0
57	MG	BA	3589	1/1	0.96	0.21	-	27,27,27,27	0
57	MG	AN	502	1/1	0.91	0.29	-	63,63,63,63	0
57	MG	CA	3094	1/1	0.94	0.11	-	70,70,70,70	0
57	MG	BA	3097	1/1	0.97	0.14	-	44,44,44,44	0
57	MG	BA	3678	1/1	0.70	0.08	-	65,65,65,65	0
57	MG	DA	3054	1/1	0.94	0.23	-	48,48,48,48	0
57	MG	BA	3809	1/1	0.94	0.14	-	63,63,63,63	0
57	MG	BA	3383	1/1	0.95	0.12	-	53,53,53,53	0
57	MG	BA	3035	1/1	0.93	0.25	-	39,39,39,39	0
57	MG	DA	3094	1/1	0.98	0.22	-	50,50,50,50	0
57	MG	DA	3156	1/1	0.96	0.09	-	51,51,51,51	0
57	MG	DA	3033	1/1	0.90	0.10	-	42,42,42,42	0
57	MG	DA	3608	1/1	0.75	0.13	-	68,68,68,68	0
57	MG	DA	3395	1/1	0.96	0.12	-	47,47,47,47	0
57	MG	BA	3595	1/1	0.93	0.09	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3168	1/1	0.97	0.17	-	47,47,47,47	0
57	MG	AA	3044	1/1	0.96	0.25	-	60,60,60,60	0
57	MG	BA	3244	1/1	0.96	0.22	-	53,53,53,53	0
57	MG	BA	3339	1/1	0.98	0.21	-	23,23,23,23	0
57	MG	DA	3657	1/1	0.85	0.10	-	63,63,63,63	0
57	MG	BA	3281	1/1	0.98	0.28	-	60,60,60,60	0
57	MG	DA	3263	1/1	0.92	0.13	-	41,41,41,41	0
57	MG	BA	3148	1/1	0.98	0.33	-	44,44,44,44	0
57	MG	DA	3243	1/1	0.91	0.12	-	55,55,55,55	0
57	MG	DA	3304	1/1	0.95	0.06	-	48,48,48,48	0
57	MG	CA	3044	1/1	0.89	0.23	-	62,62,62,62	0
57	MG	AA	3013	1/1	0.76	0.18	-	69,69,69,69	0
57	MG	BA	3706	1/1	0.93	0.12	-	53,53,53,53	0
57	MG	BA	3077	1/1	0.93	0.17	-	49,49,49,49	0
57	MG	BA	3165	1/1	0.86	0.17	-	45,45,45,45	0
57	MG	DA	3489	1/1	0.96	0.13	-	51,51,51,51	0
57	MG	AA	3043	1/1	0.96	0.23	-	51,51,51,51	0
57	MG	AA	3191	1/1	0.92	0.21	-	47,47,47,47	0
57	MG	BA	3610	1/1	0.94	0.09	-	61,61,61,61	0
57	MG	DA	3391	1/1	0.92	0.09	-	45,45,45,45	0
57	MG	BQ	3004	1/1	0.95	0.27	-	42,42,42,42	0
57	MG	DA	3643	1/1	0.91	0.13	-	61,61,61,61	0
57	MG	DA	3503	1/1	0.92	0.14	-	52,52,52,52	0
57	MG	AA	3024	1/1	0.97	0.11	-	54,54,54,54	0
57	MG	AA	3056	1/1	0.93	0.13	-	61,61,61,61	0
57	MG	BA	3414	1/1	0.96	0.19	-	41,41,41,41	0
57	MG	DA	3560	1/1	0.99	0.07	-	40,40,40,40	0
57	MG	BB	219	1/1	0.92	0.11	-	67,67,67,67	0
57	MG	DA	3181	1/1	0.95	0.13	-	50,50,50,50	0
57	MG	BA	3659	1/1	0.90	0.19	-	61,61,61,61	0
57	MG	AA	3202	1/1	0.92	0.14	-	57,57,57,57	0
57	MG	BA	3582	1/1	0.96	0.17	-	74,74,74,74	0
57	MG	DA	3532	1/1	0.66	0.24	-	69,69,69,69	0
57	MG	CA	3114	1/1	0.93	0.04	-	57,57,57,57	0
57	MG	DA	3556	1/1	0.90	0.11	-	67,67,67,67	0
57	MG	DA	3147	1/1	0.84	0.15	-	56,56,56,56	0
57	MG	BA	3089	1/1	0.97	0.17	-	19,19,19,19	0
57	MG	BA	3617	1/1	0.95	0.16	-	51,51,51,51	0
57	MG	BA	3469	1/1	0.96	0.14	-	49,49,49,49	0
57	MG	DA	3621	1/1	0.89	0.08	-	44,44,44,44	0
57	MG	DA	3494	1/1	0.91	0.12	-	47,47,47,47	0
57	MG	BA	3495	1/1	0.91	0.13	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3110	1/1	0.95	0.17	-	41,41,41,41	0
57	MG	AA	3112	1/1	0.97	0.16	-	63,63,63,63	0
57	MG	DA	3066	1/1	0.89	0.10	-	42,42,42,42	0
57	MG	DA	3232	1/1	0.94	0.13	-	62,62,62,62	0
57	MG	DA	3194	1/1	0.92	0.10	-	56,56,56,56	0
57	MG	BA	3694	1/1	0.96	0.10	-	51,51,51,51	0
57	MG	BA	3702	1/1	0.90	0.27	-	51,51,51,51	0
57	MG	BA	3107	1/1	0.96	0.16	-	53,53,53,53	0
57	MG	DA	3102	1/1	0.94	0.19	-	40,40,40,40	0
57	MG	BA	3019	1/1	0.91	0.15	-	42,42,42,42	0
57	MG	AX	3006	1/1	0.97	0.10	-	65,65,65,65	0
57	MG	B0	102	1/1	0.92	0.22	-	48,48,48,48	0
57	MG	DA	3105	1/1	0.97	0.19	-	48,48,48,48	0
57	MG	DA	3022	1/1	0.96	0.27	-	51,51,51,51	0
57	MG	DA	3525	1/1	0.98	0.13	-	59,59,59,59	0
57	MG	CA	3095	1/1	0.92	0.14	-	64,64,64,64	0
57	MG	BA	3184	1/1	0.96	0.32	-	43,43,43,43	0
57	MG	AA	3010	1/1	0.95	0.17	-	52,52,52,52	0
57	MG	DA	3451	1/1	0.81	0.16	-	55,55,55,55	0
57	MG	DA	3049	1/1	0.91	0.27	-	52,52,52,52	0
57	MG	DA	3493	1/1	0.96	0.30	-	66,66,66,66	0
57	MG	BA	3348	1/1	0.95	0.18	-	36,36,36,36	0
57	MG	DA	3223	1/1	0.89	0.14	-	50,50,50,50	0
57	MG	DA	3333	1/1	0.82	0.13	-	41,41,41,41	0
57	MG	DA	3371	1/1	0.89	0.13	-	58,58,58,58	0
57	MG	CA	3160	1/1	0.91	0.17	-	62,62,62,62	0
57	MG	BA	3349	1/1	0.96	0.09	-	56,56,56,56	0
57	MG	AA	3195	1/1	0.95	0.12	-	57,57,57,57	0
57	MG	DA	3335	1/1	0.79	0.16	-	47,47,47,47	0
57	MG	CA	3170	1/1	0.93	0.18	-	58,58,58,58	0
57	MG	DB	3006	1/1	0.95	0.14	-	57,57,57,57	0
57	MG	BA	3682	1/1	0.94	0.19	-	53,53,53,53	0
57	MG	AA	3104	1/1	0.94	0.28	-	59,59,59,59	0
57	MG	AA	3167	1/1	0.95	0.09	-	57,57,57,57	0
57	MG	BA	3795	1/1	0.95	0.15	-	35,35,35,35	0
57	MG	CA	3014	1/1	0.92	0.21	-	58,58,58,58	0
57	MG	BA	3571	1/1	0.95	0.18	-	58,58,58,58	0
57	MG	B6	102	1/1	0.92	0.12	-	68,68,68,68	0
57	MG	DA	3543	1/1	0.91	0.08	-	53,53,53,53	0
57	MG	CA	3154	1/1	0.95	0.17	-	56,56,56,56	0
57	MG	BA	3631	1/1	0.91	0.18	-	42,42,42,42	0
57	MG	AA	3126	1/1	0.98	0.09	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3437	1/1	0.87	0.16	-	52,52,52,52	0
57	MG	DA	3050	1/1	0.92	0.17	-	59,59,59,59	0
57	MG	BD	308	1/1	0.96	0.23	-	46,46,46,46	0
57	MG	DA	3229	1/1	0.94	0.22	-	50,50,50,50	0
57	MG	BA	3419	1/1	0.87	0.23	-	37,37,37,37	0
57	MG	CA	3139	1/1	0.94	0.14	-	62,62,62,62	0
57	MG	DA	3314	1/1	0.90	0.12	-	43,43,43,43	0
57	MG	DA	3380	1/1	0.88	0.07	-	55,55,55,55	0
57	MG	AA	3060	1/1	0.93	0.27	-	46,46,46,46	0
57	MG	DA	3275	1/1	0.89	0.17	-	42,42,42,42	0
57	MG	DA	3259	1/1	0.58	0.21	-	43,43,43,43	0
57	MG	DA	3487	1/1	0.82	0.21	-	62,62,62,62	0
57	MG	BA	3111	1/1	0.97	0.13	-	54,54,54,54	0
57	MG	DA	3423	1/1	0.92	0.12	-	49,49,49,49	0
57	MG	BA	3739	1/1	0.94	0.23	-	40,40,40,40	0
57	MG	CA	3027	1/1	0.87	0.20	-	64,64,64,64	0
57	MG	DA	3563	1/1	0.57	0.15	-	74,74,74,74	0
57	MG	DA	3211	1/1	0.93	0.14	-	48,48,48,48	0
57	MG	CA	3035	1/1	0.94	0.09	-	59,59,59,59	0
57	MG	DA	3364	1/1	0.95	0.07	-	40,40,40,40	0
57	MG	DA	3379	1/1	0.94	0.14	-	63,63,63,63	0
57	MG	BA	3756	1/1	0.97	0.20	-	48,48,48,48	0
57	MG	BA	3327	1/1	0.98	0.18	-	38,38,38,38	0
57	MG	BA	3506	1/1	0.85	0.10	-	58,58,58,58	0
57	MG	BA	3352	1/1	0.94	0.22	-	53,53,53,53	0
57	MG	BA	3068	1/1	0.95	0.18	-	43,43,43,43	0
57	MG	DA	3288	1/1	0.88	0.14	-	52,52,52,52	0
57	MG	DA	3052	1/1	0.96	0.13	-	61,61,61,61	0
57	MG	BA	3075	1/1	0.93	0.24	-	45,45,45,45	0
57	MG	DA	3591	1/1	0.88	0.16	-	55,55,55,55	0
57	MG	AA	3198	1/1	0.91	0.12	-	61,61,61,61	0
57	MG	AA	3193	1/1	0.93	0.08	-	72,72,72,72	0
57	MG	DA	3179	1/1	0.94	0.12	-	52,52,52,52	0
57	MG	AA	3050	1/1	0.95	0.15	-	33,33,33,33	0
57	MG	BA	3596	1/1	0.89	0.10	-	64,64,64,64	0
57	MG	BA	3513	1/1	0.87	0.15	-	59,59,59,59	0
57	MG	DA	3658	1/1	0.86	0.12	-	62,62,62,62	0
57	MG	BA	3293	1/1	0.85	0.26	-	50,50,50,50	0
57	MG	AX	3003	1/1	0.92	0.13	-	71,71,71,71	0
57	MG	DA	3399	1/1	0.98	0.13	-	59,59,59,59	0
57	MG	AA	3089	1/1	0.87	0.15	-	60,60,60,60	0
57	MG	AW	3002	1/1	0.95	0.22	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3642	1/1	0.93	0.12	-	48,48,48,48	0
57	MG	BA	3285	1/1	0.91	0.27	-	50,50,50,50	0
57	MG	BA	3440	1/1	0.95	0.12	-	42,42,42,42	0
57	MG	BA	3545	1/1	0.87	0.15	-	65,65,65,65	0
57	MG	AA	3037	1/1	0.92	0.22	-	55,55,55,55	0
57	MG	DA	3161	1/1	0.98	0.19	-	38,38,38,38	0
57	MG	DA	3428	1/1	0.94	0.18	-	37,37,37,37	0
57	MG	BP	204	1/1	0.96	0.06	-	46,46,46,46	0
57	MG	CA	3074	1/1	0.92	0.23	-	64,64,64,64	0
57	MG	DA	3368	1/1	0.94	0.24	-	50,50,50,50	0
57	MG	BA	3317	1/1	0.82	0.18	-	53,53,53,53	0
57	MG	DA	3420	1/1	0.89	0.24	-	60,60,60,60	0
57	MG	AE	201	1/1	0.93	0.15	-	59,59,59,59	0
57	MG	BA	3723	1/1	0.95	0.07	-	47,47,47,47	0
57	MG	BA	3310	1/1	0.92	0.24	-	58,58,58,58	0
57	MG	BA	3757	1/1	0.80	0.20	-	76,76,76,76	0
57	MG	CA	3088	1/1	0.62	0.14	-	74,74,74,74	0
57	MG	DA	3219	1/1	0.92	0.17	-	53,53,53,53	0
57	MG	BA	3253	1/1	0.84	0.23	-	55,55,55,55	0
57	MG	DA	3670	1/1	0.93	0.42	-	60,60,60,60	0
57	MG	DA	3495	1/1	0.86	0.11	-	47,47,47,47	0
57	MG	BA	3708	1/1	0.92	0.21	-	50,50,50,50	0
57	MG	DA	3189	1/1	0.97	0.20	-	41,41,41,41	0
57	MG	CA	3050	1/1	0.97	0.20	-	61,61,61,61	0
57	MG	BA	3572	1/1	0.96	0.16	-	61,61,61,61	0
57	MG	BA	3012	1/1	0.96	0.20	-	39,39,39,39	0
57	MG	BA	3194	1/1	0.95	0.18	-	47,47,47,47	0
57	MG	BA	3278	1/1	0.98	0.18	-	34,34,34,34	0
57	MG	BA	3776	1/1	0.97	0.20	-	43,43,43,43	0
57	MG	BA	3560	1/1	0.77	0.14	-	56,56,56,56	0
57	MG	BA	3301	1/1	0.85	0.13	-	60,60,60,60	0
57	MG	DA	3057	1/1	0.96	0.20	-	42,42,42,42	0
57	MG	CA	3085	1/1	0.98	0.12	-	54,54,54,54	0
57	MG	CJ	5001	1/1	0.76	0.08	-	73,73,73,73	0
57	MG	BA	3052	1/1	0.80	0.16	-	56,56,56,56	0
57	MG	BA	3037	1/1	1.00	0.24	-	34,34,34,34	0
57	MG	AA	3170	1/1	0.81	0.13	-	75,75,75,75	0
57	MG	AA	3005	1/1	0.84	0.14	-	62,62,62,62	0
57	MG	BA	3573	1/1	0.89	0.16	-	51,51,51,51	0
57	MG	BA	3492	1/1	0.96	0.14	-	46,46,46,46	0
57	MG	CA	3002	1/1	0.90	0.12	-	63,63,63,63	0
57	MG	AA	3007	1/1	0.93	0.13	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3113	1/1	0.95	0.11	-	67,67,67,67	0
57	MG	BA	3308	1/1	0.86	0.19	-	43,43,43,43	0
57	MG	DA	3381	1/1	0.93	0.16	-	56,56,56,56	0
57	MG	BA	3437	1/1	0.96	0.14	-	36,36,36,36	0
57	MG	CA	3032	1/1	0.95	0.24	-	62,62,62,62	0
57	MG	DA	3095	1/1	0.89	0.15	-	58,58,58,58	0
57	MG	DA	3312	1/1	0.86	0.10	-	54,54,54,54	0
57	MG	DA	3078	1/1	0.80	0.18	-	57,57,57,57	0
57	MG	BA	3464	1/1	0.93	0.14	-	45,45,45,45	0
57	MG	BA	3272	1/1	0.96	0.61	-	48,48,48,48	0
57	MG	BA	3473	1/1	0.82	0.19	-	56,56,56,56	0
57	MG	DA	3583	1/1	0.95	0.15	-	51,51,51,51	0
57	MG	BA	3737	1/1	0.98	0.29	-	43,43,43,43	0
60	K	CX	3001	1/1	0.97	0.19	-	82,82,82,82	0
57	MG	BA	3714	1/1	0.92	0.11	-	57,57,57,57	0
57	MG	BA	3584	1/1	0.87	0.20	-	63,63,63,63	0
57	MG	BA	3448	1/1	0.95	0.24	-	32,32,32,32	0
57	MG	DA	3044	1/1	0.85	0.10	-	62,62,62,62	0
57	MG	DA	3218	1/1	0.78	0.13	-	59,59,59,59	0
57	MG	DA	3636	1/1	0.88	0.32	-	63,63,63,63	0
57	MG	DA	3217	1/1	0.87	0.14	-	38,38,38,38	0
57	MG	DA	3378	1/1	0.90	0.13	-	57,57,57,57	0
57	MG	DA	3098	1/1	0.89	0.17	-	53,53,53,53	0
57	MG	BA	3652	1/1	0.92	0.14	-	67,67,67,67	0
57	MG	AA	3038	1/1	0.87	0.33	-	68,68,68,68	0
57	MG	BA	3374	1/1	0.99	0.17	-	40,40,40,40	0
57	MG	DA	3220	1/1	0.96	0.15	-	46,46,46,46	0
57	MG	BA	3298	1/1	0.89	0.17	-	51,51,51,51	0
57	MG	BA	3491	1/1	0.96	0.15	-	45,45,45,45	0
57	MG	DA	3354	1/1	0.92	0.19	-	44,44,44,44	0
57	MG	DA	3517	1/1	0.93	0.05	-	51,51,51,51	0
57	MG	DA	3412	1/1	0.98	0.20	-	50,50,50,50	0
57	MG	BA	3031	1/1	0.95	0.19	-	52,52,52,52	0
57	MG	CA	3073	1/1	0.86	0.15	-	57,57,57,57	0
57	MG	BB	209	1/1	0.75	0.32	-	65,65,65,65	0
57	MG	AA	3197	1/1	0.87	0.27	-	70,70,70,70	0
57	MG	BA	3370	1/1	0.96	0.20	-	39,39,39,39	0
57	MG	BA	3579	1/1	0.95	0.17	-	49,49,49,49	0
57	MG	BA	3606	1/1	0.91	0.14	-	61,61,61,61	0
57	MG	BA	3243	1/1	0.94	0.17	-	53,53,53,53	0
57	MG	DA	3597	1/1	0.96	0.06	-	51,51,51,51	0
57	MG	BA	3356	1/1	0.96	0.16	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3053	1/1	0.98	0.20	-	61,61,61,61	0
57	MG	DA	3406	1/1	0.82	0.11	-	51,51,51,51	0
57	MG	BA	3561	1/1	0.91	0.11	-	45,45,45,45	0
57	MG	DA	3519	1/1	0.95	0.18	-	63,63,63,63	0
57	MG	AA	3067	1/1	0.93	0.26	-	57,57,57,57	0
57	MG	CA	3163	1/1	0.88	0.09	-	63,63,63,63	0
57	MG	DA	3257	1/1	0.97	0.18	-	50,50,50,50	0
57	MG	DA	3370	1/1	0.97	0.14	-	51,51,51,51	0
57	MG	CA	3146	1/1	0.81	0.19	-	66,66,66,66	0
57	MG	CA	3006	1/1	0.90	0.14	-	64,64,64,64	0
57	MG	DA	3165	1/1	0.91	0.23	-	57,57,57,57	0
57	MG	DA	3521	1/1	0.87	0.13	-	58,58,58,58	0
57	MG	B0	103	1/1	0.96	0.08	-	53,53,53,53	0
57	MG	AA	3106	1/1	0.95	0.10	-	57,57,57,57	0
57	MG	DA	3628	1/1	0.82	0.24	-	76,76,76,76	0
57	MG	AA	3008	1/1	0.83	0.27	-	73,73,73,73	0
57	MG	DA	3092	1/1	0.88	0.17	-	45,45,45,45	0
57	MG	DA	3273	1/1	0.92	0.11	-	47,47,47,47	0
57	MG	CA	3097	1/1	0.86	0.15	-	69,69,69,69	0
57	MG	BA	3664	1/1	0.90	0.16	-	55,55,55,55	0
57	MG	BA	3195	1/1	0.90	0.11	-	46,46,46,46	0
57	MG	BA	3104	1/1	0.90	0.13	-	42,42,42,42	0
57	MG	BA	3689	1/1	0.96	0.17	-	42,42,42,42	0
57	MG	DA	3283	1/1	0.87	0.11	-	51,51,51,51	0
57	MG	BA	3112	1/1	0.96	0.23	-	30,30,30,30	0
57	MG	BA	3261	1/1	0.93	0.11	-	61,61,61,61	0
57	MG	BA	3185	1/1	0.88	0.19	-	57,57,57,57	0
57	MG	BA	3666	1/1	0.91	0.19	-	50,50,50,50	0
57	MG	BB	201	1/1	0.93	0.17	-	55,55,55,55	0
57	MG	DA	3235	1/1	0.94	0.20	-	45,45,45,45	0
57	MG	BA	3603	1/1	0.96	0.13	-	53,53,53,53	0
57	MG	BA	3633	1/1	0.94	0.12	-	49,49,49,49	0
57	MG	AA	3143	1/1	0.90	0.08	-	60,60,60,60	0
57	MG	DA	3190	1/1	0.98	0.20	-	54,54,54,54	0
57	MG	DW	3003	1/1	0.93	0.09	-	72,72,72,72	0
57	MG	BA	3482	1/1	0.95	0.15	-	51,51,51,51	0
57	MG	BA	3178	1/1	0.95	0.13	-	46,46,46,46	0
57	MG	DA	3024	1/1	0.94	0.21	-	59,59,59,59	0
57	MG	DA	3574	1/1	0.96	0.11	-	53,53,53,53	0
57	MG	DA	3384	1/1	0.97	0.10	-	49,49,49,49	0
57	MG	BA	3450	1/1	0.98	0.13	-	48,48,48,48	0
57	MG	CA	3168	1/1	0.87	0.11	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3490	1/1	0.94	0.13	-	47,47,47,47	0
57	MG	AA	3035	1/1	0.95	0.21	-	56,56,56,56	0
57	MG	DA	3139	1/1	0.85	0.17	-	53,53,53,53	0
57	MG	DA	3524	1/1	0.90	0.17	-	61,61,61,61	0
57	MG	BA	3743	1/1	0.94	0.17	-	44,44,44,44	0
57	MG	DA	3071	1/1	0.84	0.13	-	59,59,59,59	0
57	MG	CA	3004	1/1	0.89	0.25	-	66,66,66,66	0
57	MG	DA	3604	1/1	0.91	0.17	-	59,59,59,59	0
57	MG	BA	3614	1/1	0.96	0.10	-	63,63,63,63	0
57	MG	CA	3015	1/1	0.95	0.22	-	56,56,56,56	0
57	MG	DA	3002	1/1	0.87	0.10	-	48,48,48,48	0
57	MG	DA	3606	1/1	0.88	0.10	-	71,71,71,71	0
57	MG	DA	3298	1/1	0.96	0.15	-	59,59,59,59	0
57	MG	DA	3130	1/1	0.91	0.18	-	52,52,52,52	0
57	MG	DA	3561	1/1	0.97	0.04	-	57,57,57,57	0
57	MG	BA	3174	1/1	0.98	0.18	-	37,37,37,37	0
57	MG	BA	3033	1/1	0.88	0.30	-	53,53,53,53	0
57	MG	DA	3557	1/1	0.93	0.15	-	51,51,51,51	0
57	MG	DA	3009	1/1	0.93	0.15	-	48,48,48,48	0
57	MG	DQ	3003	1/1	0.94	0.15	-	51,51,51,51	0
57	MG	AA	3192	1/1	0.86	0.14	-	71,71,71,71	0
57	MG	DA	3032	1/1	0.93	0.14	-	48,48,48,48	0
57	MG	BA	3421	1/1	0.78	0.17	-	32,32,32,32	0
57	MG	DA	3396	1/1	0.93	0.10	-	40,40,40,40	0
57	MG	DA	3251	1/1	0.92	0.17	-	62,62,62,62	0
57	MG	BA	3408	1/1	0.96	0.20	-	36,36,36,36	0
57	MG	DA	3227	1/1	0.93	0.28	-	41,41,41,41	0
57	MG	DA	3605	1/1	0.89	0.12	-	58,58,58,58	0
57	MG	BA	3267	1/1	0.88	0.19	-	65,65,65,65	0
57	MG	DA	3528	1/1	0.86	0.15	-	62,62,62,62	0
57	MG	DA	3038	1/1	0.91	0.16	-	47,47,47,47	0
57	MG	DE	304	1/1	0.95	0.15	-	43,43,43,43	0
57	MG	DA	3508	1/1	0.98	0.10	-	44,44,44,44	0
57	MG	BA	3599	1/1	0.90	0.21	-	43,43,43,43	0
57	MG	CA	3102	1/1	0.93	0.08	-	68,68,68,68	0
57	MG	BA	3322	1/1	0.92	0.17	-	52,52,52,52	0
57	MG	B7	105	1/1	0.88	0.16	-	56,56,56,56	0
57	MG	CA	3062	1/1	0.89	0.17	-	64,64,64,64	0
57	MG	BA	3161	1/1	0.93	0.17	-	52,52,52,52	0
57	MG	BA	3224	1/1	0.96	0.21	-	65,65,65,65	0
57	MG	BA	3238	1/1	0.96	0.24	-	62,62,62,62	0
57	MG	DA	3245	1/1	0.91	0.12	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3134	1/1	0.95	0.14	-	66,66,66,66	0
57	MG	BA	3760	1/1	0.82	0.19	-	44,44,44,44	0
57	MG	CA	3128	1/1	0.89	0.15	-	65,65,65,65	0
57	MG	DA	3076	1/1	0.69	0.14	-	58,58,58,58	0
57	MG	DA	3137	1/1	0.92	0.22	-	54,54,54,54	0
57	MG	BA	3392	1/1	0.99	0.16	-	53,53,53,53	0
57	MG	AA	3188	1/1	0.91	0.08	-	69,69,69,69	0
57	MG	BA	3654	1/1	0.91	0.20	-	57,57,57,57	0
57	MG	DA	3479	1/1	0.94	0.17	-	43,43,43,43	0
57	MG	BA	3305	1/1	0.85	0.09	-	62,62,62,62	0
57	MG	BA	3564	1/1	0.94	0.16	-	44,44,44,44	0
57	MG	DA	3159	1/1	0.96	0.15	-	58,58,58,58	0
57	MG	AA	3021	1/1	0.91	0.13	-	63,63,63,63	0
57	MG	BA	3515	1/1	0.92	0.12	-	53,53,53,53	0
57	MG	DA	3665	1/1	0.98	0.14	-	42,42,42,42	0
57	MG	CA	3029	1/1	0.94	0.17	-	63,63,63,63	0
57	MG	BA	3291	1/1	0.93	0.21	-	33,33,33,33	0
57	MG	DA	3048	1/1	0.92	0.06	-	53,53,53,53	0
57	MG	BA	3109	1/1	0.89	0.18	-	51,51,51,51	0
57	MG	CA	3001	1/1	0.95	0.10	-	75,75,75,75	0
57	MG	DA	3652	1/1	0.93	0.39	-	67,67,67,67	0
57	MG	BA	3169	1/1	0.96	0.17	-	45,45,45,45	0
57	MG	BA	3373	1/1	0.95	0.17	-	48,48,48,48	0
57	MG	CA	3091	1/1	0.91	0.12	-	55,55,55,55	0
57	MG	BA	3451	1/1	0.95	0.16	-	31,31,31,31	0
57	MG	BA	3192	1/1	0.90	0.28	-	46,46,46,46	0
57	MG	BA	3460	1/1	0.96	0.10	-	62,62,62,62	0
57	MG	AA	3105	1/1	0.97	0.32	-	69,69,69,69	0
57	MG	DA	3506	1/1	0.97	0.09	-	42,42,42,42	0
57	MG	DA	3359	1/1	0.95	0.14	-	47,47,47,47	0
57	MG	DA	3507	1/1	0.95	0.14	-	43,43,43,43	0
57	MG	AA	3061	1/1	0.92	0.34	-	55,55,55,55	0
57	MG	DA	3616	1/1	0.74	0.11	-	71,71,71,71	0
57	MG	DA	3196	1/1	0.95	0.22	-	49,49,49,49	0
57	MG	DA	3299	1/1	0.96	0.20	-	55,55,55,55	0
57	MG	DA	3214	1/1	0.90	0.24	-	59,59,59,59	0
57	MG	AA	3047	1/1	0.85	0.16	-	63,63,63,63	0
57	MG	AA	3012	1/1	0.93	0.16	-	46,46,46,46	0
57	MG	BA	3546	1/1	0.85	0.19	-	40,40,40,40	0
57	MG	AY	3001	1/1	0.95	0.39	-	65,65,65,65	0
57	MG	CA	3141	1/1	0.85	0.04	-	92,92,92,92	0
57	MG	CA	3115	1/1	0.86	0.08	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3779	1/1	0.92	0.29	-	66,66,66,66	0
57	MG	AX	3007	1/1	0.91	0.10	-	67,67,67,67	0
57	MG	DA	3482	1/1	0.93	0.10	-	50,50,50,50	0
57	MG	BA	3149	1/1	0.93	0.18	-	40,40,40,40	0
57	MG	AA	3077	1/1	0.98	0.25	-	56,56,56,56	0
57	MG	BA	3073	1/1	0.91	0.22	-	61,61,61,61	0
57	MG	AA	3136	1/1	0.93	0.10	-	70,70,70,70	0
57	MG	DA	3073	1/1	0.95	0.09	-	42,42,42,42	0
57	MG	BA	3669	1/1	0.83	0.09	-	62,62,62,62	0
57	MG	AA	3079	1/1	0.85	0.13	-	68,68,68,68	0
57	MG	DA	3248	1/1	0.89	0.12	-	56,56,56,56	0
57	MG	BA	3208	1/1	0.96	0.16	-	44,44,44,44	0
57	MG	DA	3339	1/1	0.87	0.15	-	61,61,61,61	0
57	MG	BA	3342	1/1	0.82	0.10	-	46,46,46,46	0
57	MG	CA	3022	1/1	0.89	0.19	-	78,78,78,78	0
57	MG	DA	3559	1/1	0.96	0.12	-	43,43,43,43	0
57	MG	DA	3461	1/1	0.96	0.11	-	62,62,62,62	0
57	MG	DA	3443	1/1	0.96	0.10	-	54,54,54,54	0
57	MG	CA	3105	1/1	0.98	0.18	-	52,52,52,52	0
57	MG	DA	3172	1/1	0.94	0.09	-	62,62,62,62	0
57	MG	DA	3361	1/1	0.87	0.12	-	44,44,44,44	0
57	MG	AA	3108	1/1	0.89	0.28	-	67,67,67,67	0
57	MG	BA	3313	1/1	0.98	0.07	-	53,53,53,53	0
57	MG	DA	3125	1/1	0.71	0.26	-	70,70,70,70	0
57	MG	AA	3052	1/1	0.94	0.29	-	65,65,65,65	0
57	MG	BA	3193	1/1	0.97	0.20	-	48,48,48,48	0
57	MG	DA	3389	1/1	0.95	0.14	-	46,46,46,46	0
57	MG	BA	3623	1/1	0.90	0.26	-	55,55,55,55	0
57	MG	BA	3187	1/1	0.98	0.25	-	29,29,29,29	0
57	MG	DA	3100	1/1	0.92	0.16	-	43,43,43,43	0
57	MG	DA	3513	1/1	0.83	0.16	-	52,52,52,52	0
57	MG	DA	3124	1/1	0.89	0.15	-	57,57,57,57	0
57	MG	BA	3207	1/1	0.92	0.24	-	54,54,54,54	0
57	MG	DA	3624	1/1	0.94	0.19	-	56,56,56,56	0
57	MG	BA	3201	1/1	0.93	0.20	-	62,62,62,62	0
57	MG	BA	3020	1/1	0.80	0.22	-	53,53,53,53	0
57	MG	BA	3093	1/1	0.97	0.26	-	56,56,56,56	0
57	MG	CA	3060	1/1	0.93	0.09	-	65,65,65,65	0
57	MG	DA	3405	1/1	0.91	0.16	-	46,46,46,46	0
57	MG	BA	3081	1/1	0.95	0.21	-	46,46,46,46	0
57	MG	BA	3296	1/1	0.85	0.18	-	53,53,53,53	0
57	MG	BA	3364	1/1	0.98	0.27	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3055	1/1	0.96	0.17	-	49,49,49,49	0
57	MG	BA	3324	1/1	0.89	0.17	-	45,45,45,45	0
57	MG	DA	3520	1/1	0.96	0.11	-	57,57,57,57	0
57	MG	AA	3131	1/1	0.91	0.15	-	71,71,71,71	0
57	MG	DA	3603	1/1	0.88	0.06	-	41,41,41,41	0
57	MG	DA	3475	1/1	0.96	0.17	-	51,51,51,51	0
57	MG	BA	3372	1/1	0.83	0.16	-	28,28,28,28	0
57	MG	CA	3136	1/1	0.95	0.14	-	72,72,72,72	0
57	MG	AA	3111	1/1	0.94	0.09	-	79,79,79,79	0
57	MG	CA	3106	1/1	0.95	0.07	-	56,56,56,56	0
57	MG	DA	3468	1/1	0.84	0.27	-	66,66,66,66	0
57	MG	BA	3721	1/1	0.46	0.32	-	82,82,82,82	0
57	MG	BA	3634	1/1	0.90	0.14	-	62,62,62,62	0
57	MG	DA	3456	1/1	0.92	0.07	-	50,50,50,50	0
57	MG	DB	3001	1/1	0.91	0.17	-	64,64,64,64	0
57	MG	DA	3131	1/1	0.93	0.21	-	46,46,46,46	0
57	MG	BA	3277	1/1	0.93	0.64	-	47,47,47,47	0
57	MG	CA	3010	1/1	0.94	0.17	-	56,56,56,56	0
57	MG	DA	3253	1/1	0.96	0.13	-	45,45,45,45	0
57	MG	DA	3089	1/1	0.97	0.38	-	52,52,52,52	0
57	MG	DA	3240	1/1	0.87	0.09	-	48,48,48,48	0
57	MG	BA	3121	1/1	0.91	0.21	-	64,64,64,64	0
57	MG	AA	3073	1/1	0.85	0.10	-	56,56,56,56	0
57	MG	DA	3329	1/1	0.54	0.13	-	54,54,54,54	0
57	MG	DA	3005	1/1	0.99	0.22	-	57,57,57,57	0
57	MG	DA	3291	1/1	0.93	0.20	-	44,44,44,44	0
57	MG	DA	3231	1/1	0.97	0.10	-	62,62,62,62	0
57	MG	BR	201	1/1	0.94	0.26	-	57,57,57,57	0
57	MG	DA	3662	1/1	0.94	0.13	-	62,62,62,62	0
57	MG	BA	3389	1/1	0.94	0.13	-	55,55,55,55	0
57	MG	CA	3122	1/1	0.94	0.22	-	64,64,64,64	0
57	MG	BA	3575	1/1	0.91	0.12	-	48,48,48,48	0
57	MG	AA	3173	1/1	0.96	0.15	-	54,54,54,54	0
57	MG	DD	303	1/1	0.74	0.62	-	87,87,87,87	0
57	MG	DA	3623	1/1	0.94	0.09	-	66,66,66,66	0
57	MG	DA	3394	1/1	0.83	0.18	-	65,65,65,65	0
57	MG	DA	3234	1/1	0.77	0.21	-	63,63,63,63	0
57	MG	AA	3055	1/1	0.93	0.21	-	57,57,57,57	0
57	MG	BA	3478	1/1	0.91	0.19	-	58,58,58,58	0
57	MG	BA	3667	1/1	0.95	0.15	-	61,61,61,61	0
57	MG	AA	3162	1/1	0.91	0.07	-	66,66,66,66	0
57	MG	DA	3309	1/1	0.86	0.09	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3660	1/1	0.94	0.09	-	61,61,61,61	0
57	MG	BA	3413	1/1	0.91	0.13	-	47,47,47,47	0
57	MG	DA	3473	1/1	0.92	0.11	-	50,50,50,50	0
57	MG	AA	3046	1/1	0.88	0.22	-	55,55,55,55	0
57	MG	DA	3611	1/1	0.95	0.14	-	48,48,48,48	0
57	MG	DA	3484	1/1	0.86	0.12	-	62,62,62,62	0
57	MG	DA	3109	1/1	0.96	0.15	-	40,40,40,40	0
57	MG	BA	3783	1/1	0.95	0.12	-	56,56,56,56	0
57	MG	BA	3368	1/1	0.97	0.19	-	40,40,40,40	0
57	MG	DP	201	1/1	0.79	0.30	-	70,70,70,70	0
57	MG	DA	3142	1/1	0.97	0.13	-	47,47,47,47	0
57	MG	CA	3064	1/1	0.80	0.17	-	60,60,60,60	0
57	MG	DA	3383	1/1	0.77	0.20	-	54,54,54,54	0
57	MG	CA	3101	1/1	0.95	0.11	-	49,49,49,49	0
57	MG	DA	3239	1/1	0.91	0.24	-	56,56,56,56	0
57	MG	BA	3331	1/1	0.97	0.17	-	49,49,49,49	0
57	MG	AA	3185	1/1	0.89	0.12	-	82,82,82,82	0
57	MG	DA	3436	1/1	0.97	0.12	-	54,54,54,54	0
57	MG	DA	3343	1/1	0.95	0.16	-	50,50,50,50	0
57	MG	BA	3512	1/1	0.84	0.18	-	52,52,52,52	0
57	MG	DA	3280	1/1	0.90	0.16	-	33,33,33,33	0
57	MG	BA	3502	1/1	0.88	0.12	-	56,56,56,56	0
57	MG	BA	3130	1/1	0.95	0.08	-	44,44,44,44	0
57	MG	DA	3362	1/1	0.85	0.21	-	44,44,44,44	0
57	MG	BA	3341	1/1	0.93	0.12	-	51,51,51,51	0
57	MG	BB	220	1/1	0.85	0.13	-	57,57,57,57	0
57	MG	DW	3001	1/1	0.97	0.40	-	54,54,54,54	0
57	MG	BA	3230	1/1	0.98	0.20	-	53,53,53,53	0
57	MG	BA	3687	1/1	0.95	0.21	-	22,22,22,22	0
57	MG	BA	3001	1/1	0.87	0.14	-	53,53,53,53	0
57	MG	AX	3013	1/1	0.96	0.13	-	58,58,58,58	0
57	MG	DQ	3002	1/1	0.95	0.10	-	51,51,51,51	0
57	MG	BA	3386	1/1	0.87	0.16	-	53,53,53,53	0
57	MG	AA	3103	1/1	0.73	0.23	-	73,73,73,73	0
57	MG	AA	3006	1/1	0.96	0.12	-	52,52,52,52	0
57	MG	AA	3110	1/1	0.96	0.13	-	48,48,48,48	0
57	MG	BA	3632	1/1	0.95	0.07	-	50,50,50,50	0
57	MG	BA	3534	1/1	0.97	0.21	-	44,44,44,44	0
57	MG	BA	3307	1/1	0.92	0.17	-	29,29,29,29	0
57	MG	BA	3635	1/1	0.95	0.13	-	58,58,58,58	0
57	MG	BA	3198	1/1	0.99	0.24	-	37,37,37,37	0
57	MG	BA	3382	1/1	0.96	0.08	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3493	1/1	0.92	0.16	-	58,58,58,58	0
57	MG	BA	3071	1/1	0.87	0.35	-	59,59,59,59	0
57	MG	DA	3522	1/1	0.95	0.12	-	71,71,71,71	0
57	MG	BE	307	1/1	0.92	0.16	-	62,62,62,62	0
57	MG	AA	3128	1/1	0.88	0.08	-	57,57,57,57	0
57	MG	BA	3199	1/1	0.90	0.15	-	46,46,46,46	0
57	MG	DA	3255	1/1	0.93	0.09	-	51,51,51,51	0
57	MG	CA	3039	1/1	0.88	0.11	-	68,68,68,68	0
57	MG	BA	3435	1/1	0.97	0.27	-	45,45,45,45	0
57	MG	BA	3170	1/1	0.94	0.16	-	38,38,38,38	0
57	MG	CA	3098	1/1	0.84	0.09	-	65,65,65,65	0
57	MG	DB	3010	1/1	0.97	0.17	-	57,57,57,57	0
57	MG	BA	3773	1/1	0.93	0.25	-	52,52,52,52	0
57	MG	BA	3257	1/1	0.73	0.23	-	53,53,53,53	0
57	MG	BA	3171	1/1	0.95	0.25	-	31,31,31,31	0
57	MG	BA	3741	1/1	0.89	0.74	-	64,64,64,64	0
57	MG	DA	3403	1/1	0.45	0.14	-	57,57,57,57	0
57	MG	CX	3003	1/1	0.81	0.22	-	54,54,54,54	0
57	MG	BA	3738	1/1	0.94	0.15	-	43,43,43,43	0
57	MG	BA	3775	1/1	0.95	0.16	-	33,33,33,33	0
57	MG	AA	3209	1/1	0.89	0.08	-	59,59,59,59	0
57	MG	BA	3753	1/1	0.96	0.15	-	33,33,33,33	0
57	MG	BB	206	1/1	0.91	0.30	-	47,47,47,47	0
57	MG	DA	3209	1/1	0.90	0.24	-	53,53,53,53	0
57	MG	DA	3548	1/1	0.95	0.06	-	60,60,60,60	0
57	MG	DA	3386	1/1	0.95	0.11	-	35,35,35,35	0
57	MG	BA	3390	1/1	0.97	0.26	-	38,38,38,38	0
57	MG	DA	3091	1/1	0.92	0.10	-	48,48,48,48	0
57	MG	BA	3126	1/1	0.91	0.16	-	54,54,54,54	0
57	MG	BA	3099	1/1	0.92	0.22	-	41,41,41,41	0
57	MG	DA	3631	1/1	0.93	0.12	-	57,57,57,57	0
57	MG	BF	308	1/1	0.76	0.20	-	46,46,46,46	0
57	MG	DA	3677	1/1	0.90	0.47	-	52,52,52,52	0
57	MG	BA	3428	1/1	0.97	0.19	-	46,46,46,46	0
57	MG	AA	3129	1/1	0.95	0.11	-	47,47,47,47	0
57	MG	BA	3524	1/1	0.93	0.13	-	42,42,42,42	0
57	MG	AA	3165	1/1	0.95	0.19	-	54,54,54,54	0
57	MG	DA	3225	1/1	0.95	0.07	-	49,49,49,49	0
57	MG	BA	3592	1/1	0.95	0.20	-	28,28,28,28	0
57	MG	DA	3062	1/1	0.86	0.20	-	63,63,63,63	0
57	MG	BA	3567	1/1	0.95	0.15	-	34,34,34,34	0
57	MG	DA	3075	1/1	0.84	0.29	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3121	1/1	0.93	0.07	-	44,44,44,44	0
57	MG	BA	3762	1/1	0.98	0.20	-	46,46,46,46	0
57	MG	BA	3227	1/1	0.91	0.24	-	57,57,57,57	0
57	MG	CA	3058	1/1	0.83	0.13	-	68,68,68,68	0
57	MG	DA	3138	1/1	0.86	0.13	-	55,55,55,55	0
57	MG	DA	3565	1/1	0.95	0.08	-	59,59,59,59	0
57	MG	AA	3127	1/1	0.83	0.16	-	65,65,65,65	0
57	MG	BA	3697	1/1	0.89	0.16	-	61,61,61,61	0
57	MG	BA	3615	1/1	0.77	0.21	-	68,68,68,68	0
57	MG	BA	3494	1/1	0.96	0.09	-	49,49,49,49	0
57	MG	BA	3032	1/1	0.89	0.20	-	47,47,47,47	0
57	MG	AA	3078	1/1	0.93	0.27	-	66,66,66,66	0
57	MG	BA	3294	1/1	0.94	0.24	-	61,61,61,61	0
57	MG	AA	3140	1/1	0.93	0.15	-	53,53,53,53	0
57	MG	B5	101	1/1	0.83	0.25	-	51,51,51,51	0
57	MG	DA	3316	1/1	0.72	0.11	-	45,45,45,45	0
57	MG	BA	3034	1/1	0.96	0.25	-	56,56,56,56	0
57	MG	BA	3252	1/1	0.90	0.41	-	60,60,60,60	0
57	MG	DA	3627	1/1	0.93	0.17	-	63,63,63,63	0
57	MG	BA	3145	1/1	0.92	0.10	-	44,44,44,44	0
57	MG	CA	3135	1/1	0.92	0.15	-	63,63,63,63	0
57	MG	AA	3190	1/1	0.87	0.10	-	58,58,58,58	0
57	MG	AA	3160	1/1	0.80	0.21	-	59,59,59,59	0
57	MG	BA	3674	1/1	0.97	0.15	-	63,63,63,63	0
57	MG	BA	3748	1/1	0.94	0.14	-	29,29,29,29	0
57	MG	AA	3090	1/1	0.98	0.22	-	66,66,66,66	0
57	MG	BA	3204	1/1	0.94	0.23	-	36,36,36,36	0
57	MG	BA	3263	1/1	0.97	0.35	-	49,49,49,49	0
57	MG	BA	3676	1/1	0.96	0.21	-	33,33,33,33	0
57	MG	BA	3467	1/1	0.98	0.23	-	50,50,50,50	0
57	MG	DA	3415	1/1	0.85	0.11	-	68,68,68,68	0
57	MG	DA	3155	1/1	0.97	0.24	-	48,48,48,48	0
57	MG	BA	3718	1/1	0.85	0.11	-	71,71,71,71	0
57	MG	AA	3199	1/1	0.94	0.15	-	73,73,73,73	0
57	MG	BA	3496	1/1	0.95	0.17	-	41,41,41,41	0
57	MG	BA	3544	1/1	0.98	0.22	-	44,44,44,44	0
57	MG	AA	3098	1/1	0.94	0.18	-	55,55,55,55	0
57	MG	CA	3121	1/1	0.95	0.14	-	63,63,63,63	0
57	MG	BA	3397	1/1	0.89	0.15	-	30,30,30,30	0
57	MG	BA	3693	1/1	0.81	0.19	-	56,56,56,56	0
57	MG	BA	3344	1/1	0.94	0.12	-	66,66,66,66	0
57	MG	BP	205	1/1	0.95	0.18	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3782	1/1	0.95	0.16	-	65,65,65,65	0
57	MG	BA	3439	1/1	0.93	0.13	-	33,33,33,33	0
57	MG	BA	3128	1/1	0.87	0.14	-	69,69,69,69	0
57	MG	DA	3512	1/1	0.98	0.09	-	47,47,47,47	0
57	MG	AA	3003	1/1	0.91	0.30	-	72,72,72,72	0
57	MG	DA	3416	1/1	0.96	0.12	-	50,50,50,50	0
57	MG	BB	210	1/1	0.90	0.07	-	61,61,61,61	0
57	MG	DA	3568	1/1	0.95	0.08	-	52,52,52,52	0
57	MG	DA	3150	1/1	0.96	0.08	-	56,56,56,56	0
57	MG	BA	3525	1/1	0.96	0.17	-	34,34,34,34	0
57	MG	BA	3116	1/1	0.97	0.28	-	50,50,50,50	0
57	MG	DA	3010	1/1	0.98	0.17	-	47,47,47,47	0
57	MG	DA	3355	1/1	0.89	0.12	-	58,58,58,58	0
57	MG	CA	3076	1/1	0.89	0.14	-	57,57,57,57	0
57	MG	DA	3638	1/1	0.89	0.10	-	51,51,51,51	0
57	MG	DA	3301	1/1	0.90	0.19	-	52,52,52,52	0
57	MG	BA	3218	1/1	0.95	0.20	-	47,47,47,47	0
57	MG	BA	3766	1/1	0.97	0.15	-	28,28,28,28	0
57	MG	BA	3671	1/1	0.92	0.16	-	63,63,63,63	0
57	MG	AA	3201	1/1	0.93	0.13	-	52,52,52,52	0
57	MG	DA	3307	1/1	0.97	0.09	-	42,42,42,42	0
57	MG	BA	3137	1/1	0.97	0.24	-	39,39,39,39	0
57	MG	DA	3158	1/1	0.94	0.16	-	60,60,60,60	0
57	MG	DD	309	1/1	0.91	0.21	-	59,59,59,59	0
57	MG	AA	3070	1/1	0.92	0.18	-	52,52,52,52	0
57	MG	BA	3095	1/1	0.76	0.24	-	51,51,51,51	0
57	MG	CA	3119	1/1	0.94	0.16	-	64,64,64,64	0
57	MG	DA	3204	1/1	0.96	0.31	-	46,46,46,46	0
57	MG	DA	3390	1/1	0.97	0.12	-	43,43,43,43	0
57	MG	BA	3255	1/1	0.91	0.15	-	47,47,47,47	0
57	MG	AA	3107	1/1	0.88	0.18	-	64,64,64,64	0
57	MG	BA	3362	1/1	0.76	0.20	-	41,41,41,41	0
57	MG	BA	3404	1/1	0.84	0.13	-	59,59,59,59	0
57	MG	DA	3385	1/1	0.83	0.11	-	52,52,52,52	0
57	MG	AA	3183	1/1	0.81	0.15	-	65,65,65,65	0
57	MG	DA	3120	1/1	0.90	0.13	-	49,49,49,49	0
57	MG	BA	3047	1/1	0.90	0.21	-	60,60,60,60	0
57	MG	BB	212	1/1	0.97	0.13	-	55,55,55,55	0
57	MG	CA	3052	1/1	0.86	0.21	-	72,72,72,72	0
57	MG	DA	3651	1/1	0.48	0.54	-	75,75,75,75	0
57	MG	BA	3396	1/1	0.91	0.15	-	50,50,50,50	0
57	MG	BB	203	1/1	0.97	0.24	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3086	1/1	0.97	0.09	-	43,43,43,43	0
57	MG	BA	3711	1/1	0.96	0.19	-	54,54,54,54	0
57	MG	CA	3103	1/1	0.98	0.13	-	46,46,46,46	0
57	MG	BE	306	1/1	0.95	0.20	-	26,26,26,26	0
57	MG	DA	3084	1/1	0.96	0.08	-	39,39,39,39	0
57	MG	BA	3619	1/1	0.88	0.20	-	58,58,58,58	0
57	MG	AA	3097	1/1	0.92	0.34	-	56,56,56,56	0
57	MG	BA	3680	1/1	0.86	0.11	-	68,68,68,68	0
57	MG	AA	3049	1/1	0.87	0.21	-	64,64,64,64	0
57	MG	DA	3195	1/1	0.94	0.09	-	43,43,43,43	0
57	MG	BA	3574	1/1	0.96	0.19	-	66,66,66,66	0
57	MG	AA	3206	1/1	0.75	0.19	-	64,64,64,64	0
57	MG	BA	3657	1/1	0.96	0.26	-	47,47,47,47	0
57	MG	AA	3123	1/1	0.94	0.26	-	51,51,51,51	0
57	MG	BA	3276	1/1	0.90	0.31	-	54,54,54,54	0
57	MG	BA	3241	1/1	0.98	0.19	-	36,36,36,36	0
57	MG	BA	3303	1/1	0.91	0.17	-	36,36,36,36	0
57	MG	CA	3145	1/1	0.94	0.14	-	66,66,66,66	0
57	MG	CA	3125	1/1	0.94	0.08	-	63,63,63,63	0
57	MG	BA	3188	1/1	0.97	0.30	-	49,49,49,49	0
57	MG	BA	3520	1/1	0.94	0.16	-	61,61,61,61	0
57	MG	AA	3101	1/1	0.93	0.16	-	43,43,43,43	0
57	MG	BA	3345	1/1	0.97	0.14	-	38,38,38,38	0
57	MG	DA	3544	1/1	0.83	0.12	-	65,65,65,65	0
57	MG	BA	3475	1/1	0.97	0.13	-	42,42,42,42	0
57	MG	BA	3727	1/1	0.96	0.13	-	51,51,51,51	0
57	MG	BA	3504	1/1	0.94	0.13	-	56,56,56,56	0
57	MG	DA	3064	1/1	0.92	0.20	-	49,49,49,49	0
57	MG	DA	3013	1/1	0.93	0.09	-	40,40,40,40	0
57	MG	CA	3075	1/1	0.91	0.18	-	59,59,59,59	0
57	MG	AA	3177	1/1	0.86	0.08	-	66,66,66,66	0
57	MG	DA	3221	1/1	0.90	0.28	-	52,52,52,52	0
57	MG	DF	3004	1/1	0.99	0.38	-	44,44,44,44	0
57	MG	DA	3622	1/1	0.91	0.21	-	61,61,61,61	0
57	MG	DD	301	1/1	0.96	0.15	-	47,47,47,47	0
57	MG	BA	3499	1/1	0.89	0.10	-	58,58,58,58	0
57	MG	BA	3655	1/1	0.94	0.14	-	50,50,50,50	0
57	MG	BA	3707	1/1	0.82	0.24	-	44,44,44,44	0
57	MG	AA	3096	1/1	0.93	0.22	-	63,63,63,63	0
57	MG	DA	3533	1/1	0.94	0.11	-	43,43,43,43	0
57	MG	AA	3011	1/1	0.96	0.34	-	57,57,57,57	0
57	MG	DA	3184	1/1	0.97	0.16	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3576	1/1	0.92	0.09	-	53,53,53,53	0
57	MG	CA	3049	1/1	0.96	0.20	-	63,63,63,63	0
57	MG	DA	3266	1/1	0.97	0.09	-	57,57,57,57	0
57	MG	CA	3012	1/1	0.91	0.20	-	60,60,60,60	0
57	MG	DA	3167	1/1	0.95	0.13	-	41,41,41,41	0
57	MG	BA	3805	1/1	0.94	0.12	-	44,44,44,44	0
57	MG	BA	3181	1/1	0.98	0.25	-	43,43,43,43	0
57	MG	DA	3290	1/1	0.95	0.15	-	59,59,59,59	0
57	MG	AY	3002	1/1	0.94	0.24	-	56,56,56,56	0
57	MG	AA	3141	1/1	0.93	0.23	-	61,61,61,61	0
57	MG	BA	3576	1/1	0.93	0.07	-	57,57,57,57	0
57	MG	BA	3155	1/1	0.94	0.27	-	44,44,44,44	0
57	MG	DA	3046	1/1	0.97	0.16	-	47,47,47,47	0
57	MG	BA	3251	1/1	0.96	0.19	-	44,44,44,44	0
57	MG	BA	3292	1/1	0.92	0.15	-	48,48,48,48	0
57	MG	AA	3203	1/1	0.96	0.13	-	59,59,59,59	0
57	MG	BA	3086	1/1	0.97	0.21	-	22,22,22,22	0
57	MG	BA	3638	1/1	0.79	0.14	-	63,63,63,63	0
57	MG	CA	3059	1/1	0.92	0.25	-	72,72,72,72	0
57	MG	BA	3004	1/1	0.97	0.19	-	33,33,33,33	0
57	MG	DA	3331	1/1	0.94	0.17	-	37,37,37,37	0
57	MG	BA	3516	1/1	0.94	0.19	-	52,52,52,52	0
57	MG	BA	3438	1/1	0.84	0.14	-	60,60,60,60	0
57	MG	AA	3113	1/1	0.96	0.12	-	58,58,58,58	0
57	MG	AA	3026	1/1	0.88	0.13	-	70,70,70,70	0
57	MG	DA	3242	1/1	0.87	0.11	-	52,52,52,52	0
57	MG	DA	3085	1/1	0.91	0.08	-	53,53,53,53	0
57	MG	DO	5001	1/1	0.95	0.13	-	59,59,59,59	0
57	MG	BA	3315	1/1	0.89	0.19	-	31,31,31,31	0
57	MG	AA	3057	1/1	0.90	0.22	-	64,64,64,64	0
57	MG	DA	3023	1/1	0.95	0.29	-	40,40,40,40	0
57	MG	DA	3659	1/1	0.87	0.13	-	48,48,48,48	0
57	MG	DV	3003	1/1	0.92	0.10	-	65,65,65,65	0
57	MG	BA	3100	1/1	0.92	0.17	-	39,39,39,39	0
57	MG	BA	3586	1/1	0.96	0.09	-	53,53,53,53	0
57	MG	BA	3800	1/1	0.93	0.22	-	38,38,38,38	0
57	MG	DA	3457	1/1	0.96	0.07	-	54,54,54,54	0
57	MG	CA	3013	1/1	0.80	0.13	-	69,69,69,69	0
57	MG	DA	3600	1/1	0.95	0.35	-	70,70,70,70	0
57	MG	DA	3400	1/1	0.87	0.12	-	54,54,54,54	0
57	MG	AW	3003	1/1	0.94	0.13	-	72,72,72,72	0
57	MG	BA	3358	1/1	0.97	0.21	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3516	1/1	0.94	0.07	-	67,67,67,67	0
57	MG	BA	3105	1/1	0.97	0.18	-	37,37,37,37	0
57	MG	BE	303	1/1	0.94	0.20	-	51,51,51,51	0
57	MG	DA	3154	1/1	0.94	0.17	-	48,48,48,48	0
57	MG	AA	3036	1/1	0.90	0.17	-	61,61,61,61	0
57	MG	CA	3066	1/1	0.84	0.14	-	66,66,66,66	0
57	MG	CA	3126	1/1	0.94	0.11	-	67,67,67,67	0
57	MG	DA	3429	1/1	0.91	0.14	-	41,41,41,41	0
57	MG	AA	3207	1/1	0.97	0.09	-	65,65,65,65	0
57	MG	BA	3468	1/1	0.96	0.17	-	62,62,62,62	0
57	MG	AA	3171	1/1	0.92	0.10	-	51,51,51,51	0
57	MG	BA	3306	1/1	0.94	0.17	-	37,37,37,37	0
57	MG	BA	3552	1/1	0.95	0.25	-	29,29,29,29	0
57	MG	BA	3271	1/1	0.92	0.17	-	58,58,58,58	0
57	MG	AA	3208	1/1	0.97	0.17	-	60,60,60,60	0
57	MG	DA	3106	1/1	0.89	0.13	-	52,52,52,52	0
57	MG	BA	3325	1/1	0.95	0.15	-	48,48,48,48	0
57	MG	BA	3785	1/1	0.94	0.23	-	59,59,59,59	0
57	MG	DA	3504	1/1	0.97	0.07	-	47,47,47,47	0
57	MG	BA	3700	1/1	0.90	0.16	-	61,61,61,61	0
57	MG	DA	3274	1/1	0.88	0.15	-	58,58,58,58	0
57	MG	AA	3069	1/1	0.80	0.19	-	68,68,68,68	0
57	MG	BA	3142	1/1	0.98	0.18	-	49,49,49,49	0
57	MG	DA	3141	1/1	0.90	0.27	-	61,61,61,61	0
57	MG	BA	3380	1/1	0.97	0.10	-	48,48,48,48	0
57	MG	DA	3230	1/1	0.94	0.22	-	73,73,73,73	0
57	MG	DA	3656	1/1	0.94	0.13	-	58,58,58,58	0
57	MG	BA	3709	1/1	0.82	0.20	-	62,62,62,62	0
57	MG	AA	3109	1/1	0.92	0.14	-	62,62,62,62	0
57	MG	BA	3717	1/1	0.92	0.16	-	50,50,50,50	0
57	MG	BA	3446	1/1	0.83	0.17	-	40,40,40,40	0
57	MG	BA	3005	1/1	0.91	0.16	-	30,30,30,30	0
57	MG	AA	3142	1/1	0.90	0.11	-	41,41,41,41	0
57	MG	BA	3311	1/1	0.97	0.27	-	48,48,48,48	0
57	MG	BG	201	1/1	0.97	0.20	-	58,58,58,58	0
57	MG	DA	3411	1/1	0.94	0.22	-	53,53,53,53	0
57	MG	DA	3645	1/1	0.95	0.07	-	45,45,45,45	0
57	MG	BA	3566	1/1	0.88	0.21	-	67,67,67,67	0
57	MG	DA	3056	1/1	0.88	0.09	-	51,51,51,51	0
57	MG	DA	3093	1/1	0.88	0.09	-	62,62,62,62	0
57	MG	CA	3120	1/1	0.92	0.18	-	64,64,64,64	0
57	MG	BA	3653	1/1	0.97	0.21	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3170	1/1	0.91	0.12	-	53,53,53,53	0
57	MG	BA	3533	1/1	0.93	0.10	-	59,59,59,59	0
57	MG	AA	3076	1/1	0.93	0.26	-	77,77,77,77	0
57	MG	DA	3186	1/1	0.95	0.16	-	54,54,54,54	0
57	MG	DA	3072	1/1	0.97	0.14	-	47,47,47,47	0
57	MG	BA	3006	1/1	0.88	0.19	-	48,48,48,48	0
57	MG	DA	3661	1/1	0.85	0.16	-	62,62,62,62	0
57	MG	BA	3481	1/1	0.97	0.18	-	41,41,41,41	0
57	MG	BA	3444	1/1	0.89	0.21	-	29,29,29,29	0
57	MG	DA	3112	1/1	0.92	0.16	-	59,59,59,59	0
57	MG	BA	3346	1/1	0.93	0.10	-	27,27,27,27	0
57	MG	BA	3663	1/1	0.94	0.19	-	41,41,41,41	0
57	MG	CA	3011	1/1	0.91	0.23	-	61,61,61,61	0
57	MG	BA	3726	1/1	0.99	0.19	-	63,63,63,63	0
57	MG	BA	3429	1/1	0.90	0.10	-	65,65,65,65	0
57	MG	BV	204	1/1	0.93	0.21	-	49,49,49,49	0
57	MG	BA	3724	1/1	0.79	0.18	-	62,62,62,62	0
57	MG	DA	3577	1/1	0.86	0.14	-	58,58,58,58	0
57	MG	DA	3542	1/1	0.97	0.17	-	24,24,24,24	0
57	MG	DA	3499	1/1	0.90	0.10	-	53,53,53,53	0
57	MG	DA	3136	1/1	0.95	0.14	-	52,52,52,52	0
57	MG	BA	3347	1/1	0.92	0.15	-	44,44,44,44	0
57	MG	BA	3314	1/1	0.89	0.13	-	58,58,58,58	0
57	MG	DA	3615	1/1	0.90	0.09	-	65,65,65,65	0
57	MG	DA	3077	1/1	0.89	0.23	-	61,61,61,61	0
57	MG	CA	3118	1/1	0.91	0.19	-	68,68,68,68	0
57	MG	DA	3350	1/1	0.96	0.12	-	51,51,51,51	0
57	MG	BA	3540	1/1	0.73	0.23	-	37,37,37,37	0
57	MG	DA	3241	1/1	0.96	0.13	-	45,45,45,45	0
57	MG	AA	3122	1/1	0.92	0.11	-	56,56,56,56	0
57	MG	BA	3498	1/1	0.98	0.18	-	36,36,36,36	0
57	MG	DA	3541	1/1	0.95	0.14	-	44,44,44,44	0
57	MG	BA	3508	1/1	0.91	0.20	-	51,51,51,51	0
57	MG	AA	3132	1/1	0.94	0.19	-	55,55,55,55	0
57	MG	DA	3587	1/1	0.94	0.12	-	56,56,56,56	0
57	MG	DA	3153	1/1	0.92	0.19	-	47,47,47,47	0
57	MG	DA	3176	1/1	0.96	0.19	-	41,41,41,41	0
57	MG	BA	3022	1/1	0.92	0.20	-	60,60,60,60	0
57	MG	DD	302	1/1	0.94	0.15	-	42,42,42,42	0
57	MG	BA	3577	1/1	0.95	0.19	-	51,51,51,51	0
57	MG	BA	3656	1/1	0.93	0.27	-	53,53,53,53	0
57	MG	DA	3601	1/1	0.97	0.09	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3075	1/1	0.94	0.11	-	49,49,49,49	0
57	MG	DA	3474	1/1	0.95	0.14	-	51,51,51,51	0
57	MG	DA	3305	1/1	0.97	0.19	-	50,50,50,50	0
57	MG	AA	3210	1/1	0.89	0.27	-	59,59,59,59	0
57	MG	BA	3197	1/1	0.96	0.29	-	41,41,41,41	0
57	MG	CX	3002	1/1	0.67	0.14	-	70,70,70,70	0
57	MG	BA	3260	1/1	0.97	0.30	-	39,39,39,39	0
57	MG	AA	3041	1/1	0.85	0.21	-	46,46,46,46	0
57	MG	BA	3072	1/1	0.88	0.14	-	47,47,47,47	0
57	MG	DA	3496	1/1	0.95	0.07	-	53,53,53,53	0
57	MG	BA	3117	1/1	0.88	0.20	-	59,59,59,59	0
57	MG	DA	3649	1/1	0.95	0.05	-	58,58,58,58	0
57	MG	AA	3168	1/1	0.98	0.11	-	59,59,59,59	0
57	MG	BA	3361	1/1	0.89	0.13	-	49,49,49,49	0
57	MG	AA	3102	1/1	0.89	0.24	-	59,59,59,59	0
57	MG	BA	3484	1/1	0.94	0.13	-	54,54,54,54	0
57	MG	DA	3478	1/1	0.92	0.12	-	59,59,59,59	0
57	MG	AA	3184	1/1	0.85	0.12	-	60,60,60,60	0
57	MG	DA	3523	1/1	0.86	0.10	-	59,59,59,59	0
57	MG	BW	201	1/1	0.95	0.31	-	44,44,44,44	0
57	MG	DA	3449	1/1	0.97	0.10	-	54,54,54,54	0
57	MG	DA	3203	1/1	0.94	0.57	-	50,50,50,50	0
57	MG	DA	3374	1/1	0.96	0.16	-	56,56,56,56	0
57	MG	BA	3166	1/1	0.94	0.14	-	38,38,38,38	0
57	MG	CA	3104	1/1	0.95	0.12	-	68,68,68,68	0
57	MG	DB	3005	1/1	0.93	0.08	-	59,59,59,59	0
57	MG	BA	3471	1/1	0.88	0.27	-	53,53,53,53	0
57	MG	AA	3088	1/1	0.93	0.27	-	65,65,65,65	0
57	MG	BA	3242	1/1	0.82	0.21	-	55,55,55,55	0
57	MG	AA	3064	1/1	0.89	0.24	-	60,60,60,60	0
57	MG	BA	3083	1/1	0.96	0.14	-	56,56,56,56	0
57	MG	BA	3685	1/1	0.94	0.19	-	53,53,53,53	0
57	MG	DA	3017	1/1	0.93	0.06	-	55,55,55,55	0
57	MG	DA	3340	1/1	0.80	0.18	-	58,58,58,58	0
57	MG	DA	3547	1/1	0.90	0.14	-	54,54,54,54	0
57	MG	BA	3778	1/1	0.96	0.16	-	48,48,48,48	0
57	MG	BA	3665	1/1	0.96	0.16	-	49,49,49,49	0
57	MG	DA	3585	1/1	0.78	0.12	-	43,43,43,43	0
57	MG	BA	3393	1/1	0.97	0.18	-	51,51,51,51	0
57	MG	BA	3280	1/1	0.97	0.14	-	37,37,37,37	0
57	MG	BA	3106	1/1	0.89	0.22	-	42,42,42,42	0
57	MG	AA	3066	1/1	0.91	0.31	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3270	1/1	0.97	0.17	-	48,48,48,48	0
57	MG	DA	3534	1/1	0.98	0.15	-	55,55,55,55	0
57	MG	BA	3391	1/1	0.84	0.24	-	63,63,63,63	0
57	MG	DA	3068	1/1	0.96	0.10	-	58,58,58,58	0
57	MG	BA	3521	1/1	0.98	0.20	-	39,39,39,39	0
57	MG	BA	3431	1/1	0.89	0.17	-	59,59,59,59	0
57	MG	DA	3302	1/1	0.94	0.28	-	70,70,70,70	0
57	MG	BA	3063	1/1	0.93	0.15	-	59,59,59,59	0
57	MG	DA	3409	1/1	0.92	0.15	-	57,57,57,57	0
57	MG	DA	3664	1/1	0.97	0.39	-	48,48,48,48	0
57	MG	BA	3675	1/1	0.92	0.19	-	67,67,67,67	0
57	MG	BA	3157	1/1	0.94	0.24	-	45,45,45,45	0
57	MG	DA	3111	1/1	0.96	0.19	-	61,61,61,61	0
57	MG	DA	3491	1/1	0.98	0.16	-	51,51,51,51	0
57	MG	DA	3382	1/1	0.92	0.07	-	48,48,48,48	0
57	MG	BA	3547	1/1	0.96	0.23	-	39,39,39,39	0
57	MG	DA	3505	1/1	0.92	0.08	-	56,56,56,56	0
57	MG	BA	3338	1/1	0.97	0.13	-	40,40,40,40	0
57	MG	CA	3078	1/1	0.93	0.14	-	44,44,44,44	0
57	MG	CA	3042	1/1	0.95	0.12	-	59,59,59,59	0
57	MG	AA	3114	1/1	0.96	0.17	-	59,59,59,59	0
57	MG	CA	3072	1/1	0.97	0.17	-	54,54,54,54	0
57	MG	BA	3210	1/1	0.91	0.33	-	49,49,49,49	0
57	MG	DA	3480	1/1	0.99	0.10	-	40,40,40,40	0
57	MG	DA	3260	1/1	0.94	0.09	-	55,55,55,55	0
57	MG	AA	3179	1/1	0.95	0.13	-	69,69,69,69	0
57	MG	BA	3150	1/1	0.91	0.17	-	55,55,55,55	0
57	MG	BF	304	1/1	0.76	0.18	-	45,45,45,45	0
57	MG	DA	3293	1/1	0.96	0.14	-	54,54,54,54	0
57	MG	BA	3182	1/1	0.92	0.14	-	55,55,55,55	0
57	MG	AA	3154	1/1	0.97	0.11	-	69,69,69,69	0
57	MG	BE	305	1/1	0.86	0.17	-	43,43,43,43	0
57	MG	CA	3149	1/1	0.82	0.14	-	52,52,52,52	0
57	MG	BA	3127	1/1	0.92	0.29	-	57,57,57,57	0
57	MG	DN	5001	1/1	0.98	0.11	-	66,66,66,66	0
57	MG	DA	3276	1/1	0.82	0.12	-	49,49,49,49	0
57	MG	CA	3055	1/1	0.91	0.09	-	69,69,69,69	0
57	MG	BA	3608	1/1	0.95	0.31	-	62,62,62,62	0
57	MG	BA	3058	1/1	0.89	0.15	-	49,49,49,49	0
57	MG	DA	3140	1/1	0.87	0.15	-	58,58,58,58	0
57	MG	AA	3187	1/1	0.90	0.13	-	62,62,62,62	0
57	MG	CA	3143	1/1	0.96	0.10	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3186	1/1	0.97	0.12	-	42,42,42,42	0
57	MG	AA	3028	1/1	0.91	0.23	-	76,76,76,76	0
57	MG	BA	3590	1/1	0.89	0.16	-	50,50,50,50	0
57	MG	BA	3725	1/1	0.97	0.14	-	44,44,44,44	0
57	MG	BA	3163	1/1	0.95	0.13	-	55,55,55,55	0
57	MG	AX	3010	1/1	0.88	0.21	-	59,59,59,59	0
57	MG	BA	3453	1/1	0.85	0.32	-	45,45,45,45	0
57	MG	DA	3088	1/1	0.84	0.18	-	47,47,47,47	0
57	MG	DA	3376	1/1	0.95	0.16	-	61,61,61,61	0
57	MG	BA	3237	1/1	0.94	0.15	-	45,45,45,45	0
57	MG	DA	3566	1/1	0.64	0.13	-	69,69,69,69	0
57	MG	BA	3070	1/1	0.72	0.37	-	59,59,59,59	0
57	MG	BA	3138	1/1	0.92	0.33	-	42,42,42,42	0
57	MG	BA	3684	1/1	0.87	0.12	-	68,68,68,68	0
57	MG	B9	502	1/1	0.93	0.19	-	48,48,48,48	0
57	MG	CA	3131	1/1	0.97	0.07	-	55,55,55,55	0
57	MG	BA	3710	1/1	0.88	0.17	-	57,57,57,57	0
57	MG	BW	202	1/1	0.95	0.22	-	54,54,54,54	0
57	MG	BN	3005	1/1	0.97	0.17	-	36,36,36,36	0
57	MG	DA	3188	1/1	0.94	0.19	-	48,48,48,48	0
57	MG	DA	3216	1/1	0.88	0.22	-	56,56,56,56	0
57	MG	DA	3441	1/1	0.95	0.11	-	45,45,45,45	0
57	MG	BA	3733	1/1	0.77	0.11	-	58,58,58,58	0
57	MG	BA	3059	1/1	0.96	0.21	-	26,26,26,26	0
57	MG	DA	3567	1/1	0.88	0.27	-	62,62,62,62	0
57	MG	BA	3417	1/1	0.94	0.23	-	38,38,38,38	0
57	MG	DA	3352	1/1	0.97	0.19	-	63,63,63,63	0
57	MG	BA	3662	1/1	0.92	0.10	-	61,61,61,61	0
57	MG	AA	3048	1/1	0.96	0.22	-	57,57,57,57	0
57	MG	BA	3076	1/1	0.96	0.17	-	43,43,43,43	0
57	MG	AA	3204	1/1	0.90	0.13	-	53,53,53,53	0
57	MG	DA	3598	1/1	0.95	0.08	-	61,61,61,61	0
57	MG	DA	3633	1/1	0.71	0.12	-	58,58,58,58	0
57	MG	CA	3021	1/1	0.84	0.14	-	61,61,61,61	0
57	MG	DB	3011	1/1	0.69	0.14	-	72,72,72,72	0
57	MG	BA	3445	1/1	0.89	0.30	-	63,63,63,63	0
57	MG	BA	3602	1/1	0.76	0.16	-	53,53,53,53	0
57	MG	BA	3457	1/1	0.93	0.19	-	32,32,32,32	0
57	MG	DA	3025	1/1	0.80	0.16	-	54,54,54,54	0
57	MG	DA	3193	1/1	0.96	0.13	-	57,57,57,57	0
57	MG	DA	3427	1/1	0.94	0.14	-	45,45,45,45	0
57	MG	AA	3017	1/1	0.83	0.18	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BF	309	1/1	0.97	0.15	-	53,53,53,53	0
57	MG	BA	3660	1/1	0.96	0.11	-	61,61,61,61	0
57	MG	DA	3294	1/1	0.98	0.16	-	43,43,43,43	0
57	MG	CA	3162	1/1	0.96	0.10	-	66,66,66,66	0
57	MG	DA	3634	1/1	0.94	0.14	-	60,60,60,60	0
57	MG	AA	3189	1/1	0.83	0.12	-	65,65,65,65	0
57	MG	CA	3082	1/1	0.93	0.15	-	79,79,79,79	0
57	MG	DA	3200	1/1	0.94	0.09	-	66,66,66,66	0
57	MG	BA	3600	1/1	0.95	0.30	-	44,44,44,44	0
57	MG	BA	3758	1/1	0.93	0.11	-	45,45,45,45	0
57	MG	BA	3262	1/1	0.95	0.14	-	41,41,41,41	0
57	MG	BA	3751	1/1	0.95	0.17	-	26,26,26,26	0
57	MG	BA	3485	1/1	0.90	0.09	-	42,42,42,42	0
57	MG	AA	3119	1/1	0.92	0.12	-	51,51,51,51	0
57	MG	BA	3673	1/1	0.88	0.17	-	55,55,55,55	0
57	MG	BA	3559	1/1	0.94	0.08	-	47,47,47,47	0
57	MG	DA	3554	1/1	0.79	0.10	-	62,62,62,62	0
57	MG	DA	3497	1/1	0.84	0.11	-	55,55,55,55	0
57	MG	BA	3160	1/1	0.96	0.32	-	55,55,55,55	0
57	MG	AA	3144	1/1	0.95	0.14	-	46,46,46,46	0
57	MG	DY	502	1/1	0.95	0.13	-	50,50,50,50	0
57	MG	DA	3133	1/1	0.90	0.22	-	50,50,50,50	0
57	MG	BA	3129	1/1	0.84	0.28	-	58,58,58,58	0
57	MG	CA	3007	1/1	0.91	0.13	-	57,57,57,57	0
57	MG	CA	3047	1/1	0.98	0.14	-	53,53,53,53	0
57	MG	AA	3172	1/1	0.94	0.10	-	72,72,72,72	0
57	MG	AA	3153	1/1	0.66	0.18	-	74,74,74,74	0
57	MG	BO	202	1/1	0.91	0.09	-	65,65,65,65	0
57	MG	B8	101	1/1	0.97	0.21	-	44,44,44,44	0
57	MG	BA	3597	1/1	0.99	0.21	-	25,25,25,25	0
57	MG	BA	3173	1/1	0.93	0.15	-	48,48,48,48	0
57	MG	DA	3589	1/1	0.81	0.07	-	68,68,68,68	0
57	MG	CA	3005	1/1	0.96	0.15	-	62,62,62,62	0
57	MG	BA	3803	1/1	0.94	0.23	-	44,44,44,44	0
57	MG	DF	3001	1/1	0.87	0.20	-	44,44,44,44	0
57	MG	AX	3004	1/1	0.94	0.15	-	64,64,64,64	0
57	MG	BA	3455	1/1	0.91	0.16	-	64,64,64,64	0
57	MG	B7	101	1/1	0.97	0.24	-	39,39,39,39	0
57	MG	BA	3640	1/1	0.89	0.17	-	53,53,53,53	0
57	MG	DA	3569	1/1	0.96	0.23	-	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.