



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jan 11, 2017 – 05:56 AM EST

PDB ID : 5MC6  
EMDB ID: : EMD-3461  
Title : Cryo-EM structure of a native ribosome-Ski2-Ski3-Ski8 complex from *S. cerevisiae*  
Authors : Schmidt, C.; Kowalinski, E.; Shanmuganathan, V.; Defenouillere, Q.; Braunger, K.; Heuer, A.; Pech, M.; Namane, A.; Berninghausen, O.; Fromont-Racine, M.; Jacquier, A.; Conti, E.; Becker, T.; Beckmann, R.  
Deposited on : 2016-11-09  
Resolution : 3.80 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

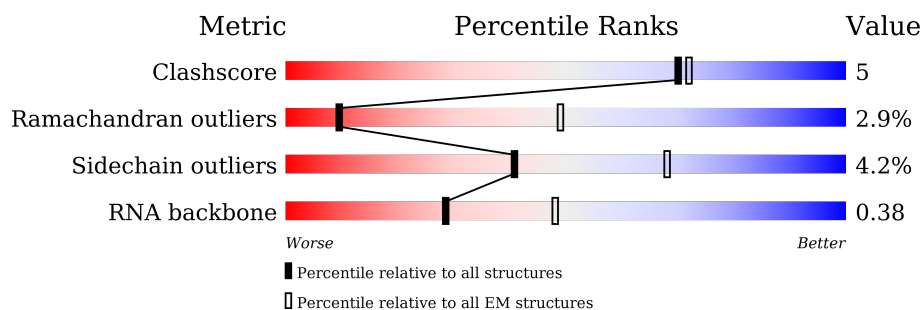
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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.






















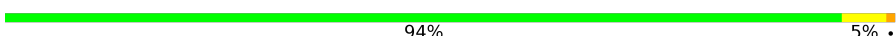
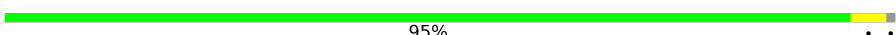
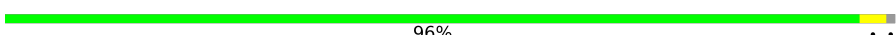



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	2	1800	
2	A	240	
3	B	225	
4	C	105	
5	D	143	
6	E	142	
7	F	143	
8	G	136	






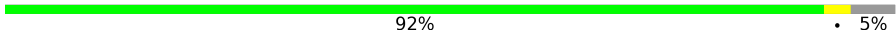
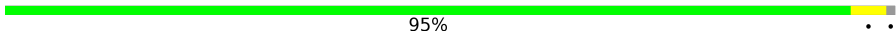
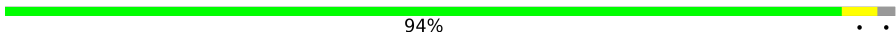








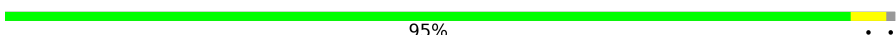








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Mol	Chain	Length	Quality of chain
9	H	146	
10	I	144	
11	J	121	
12	K	108	
13	L	67	
14	M	56	
15	N	152	
16	O	319	
17	P	252	
18	Q	255	
19	R	254	
20	S	261	
21	T	236	
22	U	190	
23	V	200	
24	W	197	
25	X	156	
26	Y	151	
27	Z	137	
28	a	87	
29	b	130	
30	c	145	
31	d	135	
32	e	119	
33	f	82	

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Mol	Chain	Length	Quality of chain
34	g	63	 92% • 5%
35	l	34	 38% 62%
36	m	76	 55% 43% •
37	n	77	 60% 40%
38	h	1287	 83% • 13%
39	i	1432	 92% • 5%
40	j	397	 95% • •
40	k	397	 94% • •
41	AA	256	 79% 11% 9%
42	AB	137	 86% 13% •
43	AC	100	 82% 17% •
44	AD	191	 86% 12% •
45	AE	155	 56% 6% • 37%
46	AF	88	 80% 16% • •
47	AG	174	 83% 13% • •
48	AH	142	 75% 11% 15%
49	AI	78	 95% • •
50	AJ	199	 86% 10% • •
51	AK	127	 90% 9% •
52	AL	51	 86% 12% •
53	AM	138	 87% 12% •
54	AN	136	 82% 17% •
55	AO	128	 36% • • 59%
56	AP	106	 89% 9% • •
57	AQ	204	 85% 13% •

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Mol	Chain	Length	Quality of chain
58	AR	149	81% 13% . ..
59	AS	25	44% 52% .
60	AT	92	84% 14% ..
61	AU	199	92% 7% .
62	AV	59	93% . . .
63	AW	254	80% 19% .
64	AX	184	85% 13% ..
65	AY	105	82% 10% . 8%
66	AZ	210	99% .
67	BA	387	84% 15% .
68	BB	186	84% 16% .
69	BC	113	76% 19% . .
70	BD	221	85% 13% .
71	BE	362	84% 15% .
72	BF	189	86% 13% ..
73	BG	130	87% 11% .
74	BH	172	91% 9% .
75	BI	297	87% 11% .
76	BJ	160	87% 13% .
77	BK	107	83% 15% ..
78	BL	121	78% 5% 17%
79	BM	176	75% 12% . 11%
80	BN	121	83% 9% . 7%
81	BO	244	80% 10% . 9%
82	BP	120	89% 9% ..

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Mol	Chain	Length	Quality of chain
83	BQ	3396	<div><div></div><div>51%36%6%7%</div></div>
84	BR	121	<div><div></div><div>54%40%6%</div></div>
85	BS	158	<div><div></div><div>53%41%7%</div></div>
86	BT	157	<div><div></div><div>50%41%5%..</div></div>

## 2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 229285 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1767	Total	C	N	O	P	0	0
			37645	16830	6656	12392	1767		

- Molecule 2 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	96	Total	C	N	O	S	0	0
			813	527	133	151	2		

- Molecule 5 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	121	Total	C	N	O	S	0	0
			877	552	153	170	2		

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	91	Total	C	N	O	S	0	0
			746	467	144	133	2		

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 11 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	K	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 13 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 14 is a protein called 40S ribosomal protein S29-A.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 19 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	178	Total	C	N	O	S	0	0
			1434	905	276	252	1		

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 26 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 27 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	132	Total	C	N	O	S	0	0
			1060	669	206	185			

- Molecule 32 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	34	Total	C	N	O	P	0	0
			692	311	84	263	34		

- Molecule 36 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 37 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 38 is a protein called Antiviral helicase SKI2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	1121	Total	C	N	O	S	0	0
			8814	5643	1504	1625	42		

- Molecule 39 is a protein called Superciller protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	1365	Total	C	N	O	S	0	0
			9827	6302	1663	1825	37		

- Molecule 40 is a protein called Antiviral protein SKI8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	392	Total	C	N	O	S	0	0
			2933	1861	500	558	14		
40	k	388	Total	C	N	O	S	0	0
			2919	1851	502	552	14		

- Molecule 41 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 42 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AB	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AC	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AD	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AE	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AF	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 47 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 48 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AH	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 49 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	AI	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	AJ	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 51 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	AK	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 52 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AL	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	AN	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 55 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AO	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 56 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 57 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 58 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 59 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 60 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 61 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	AV	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 63 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 64 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AX	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AY	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 66 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 67 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BA	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 68 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BC	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 70 is a protein called 60S ribosomal protein L10.



Mol	Chain	Residues	Atoms					AltConf	Trace
70	BD	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 71 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BE	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 72 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BF	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 73 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 74 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 75 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BI	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 76 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 77 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 78 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BL	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 79 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BM	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 80 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 81 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BO	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 82 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BP	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 83 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BQ	3165	Total	C	N	O	P	0	0
			67695	30238	12201	22091	3165		

- Molecule 84 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BR	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BS	158	Total	C	N	O	P	0	0
			3352	1500	586	1108	158		

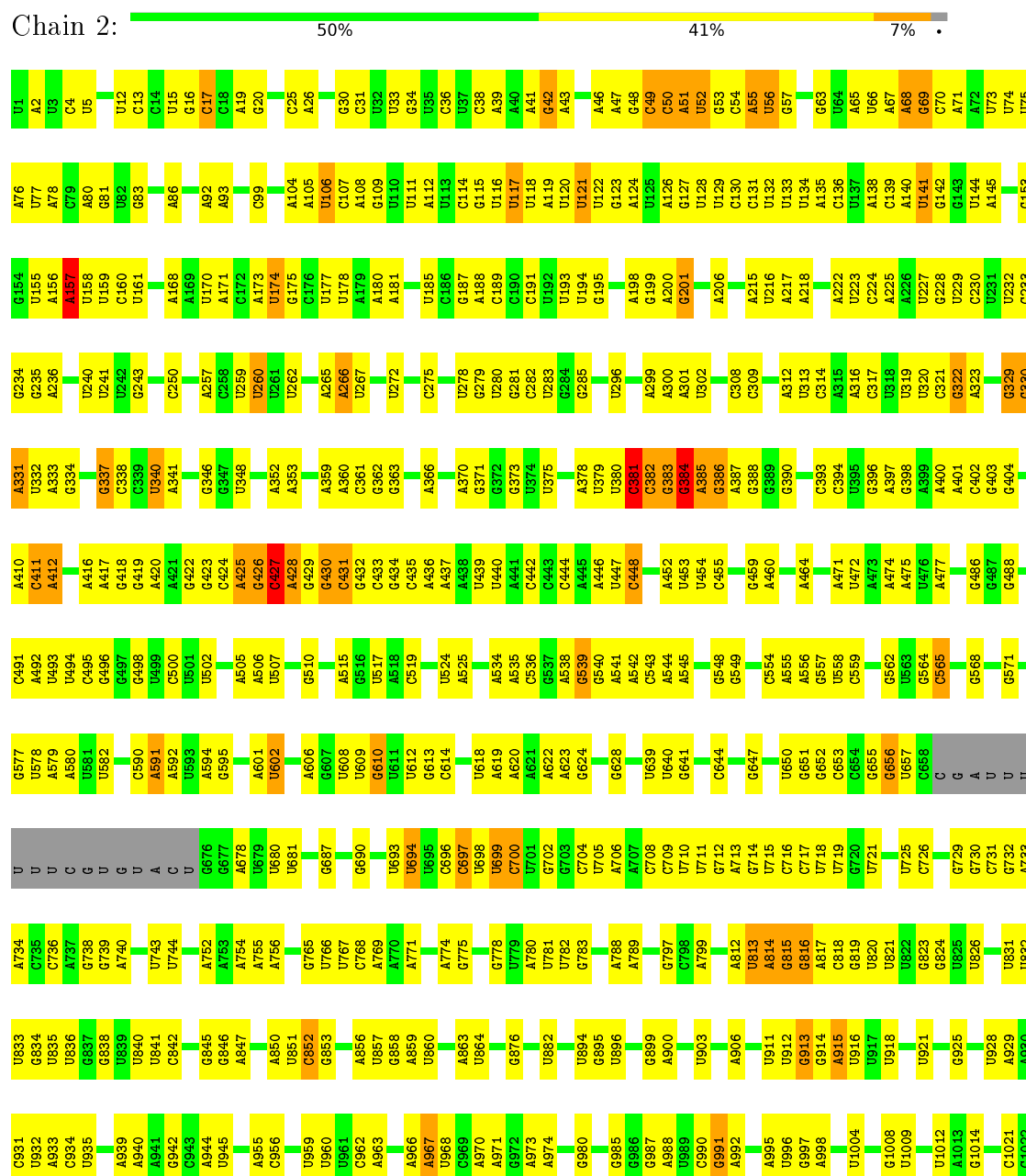
- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

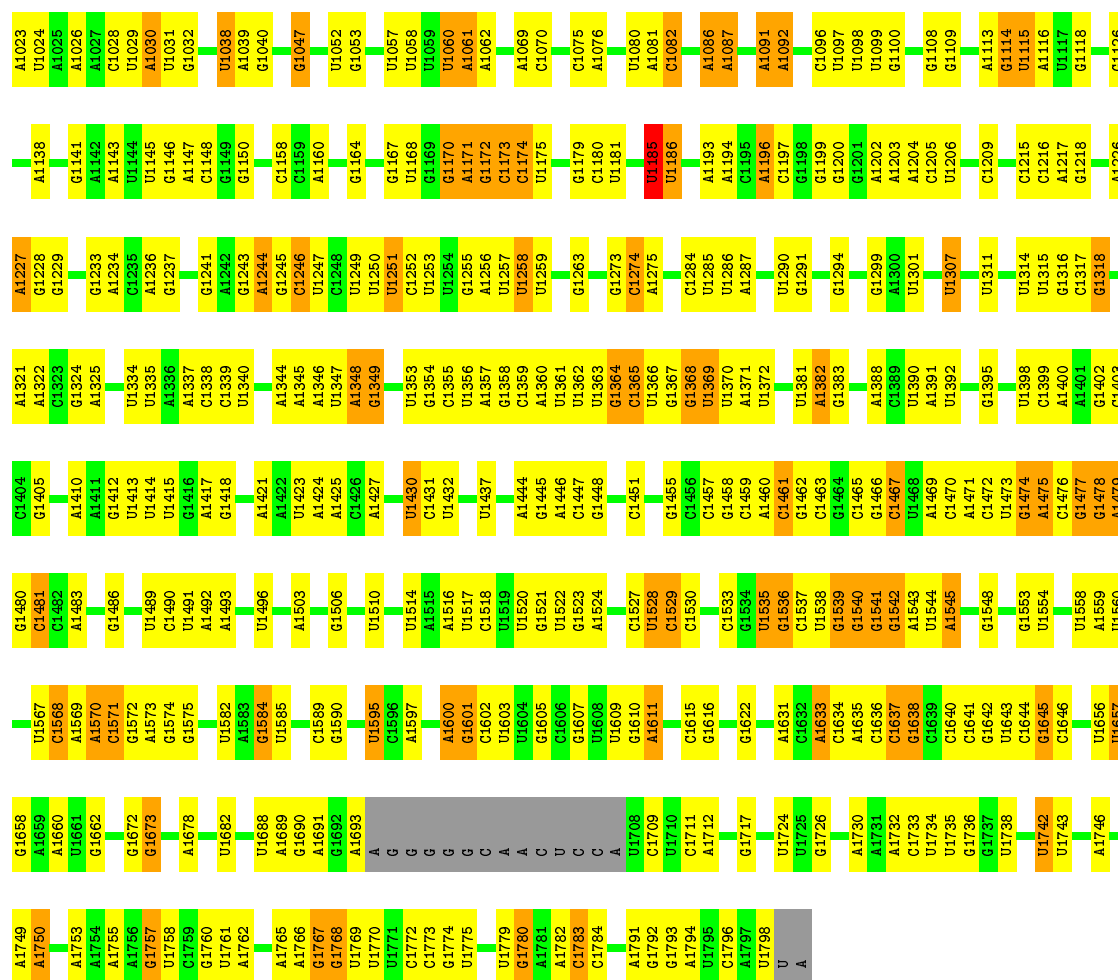
Mol	Chain	Residues	Atoms					AltConf	Trace
86	BT	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

### 3 Residue-property plots

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

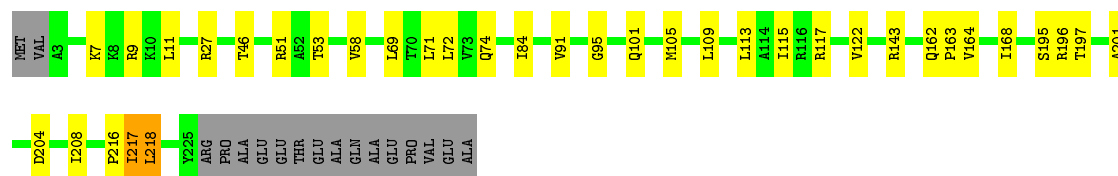
- Molecule 1: 18S ribosomal RNA





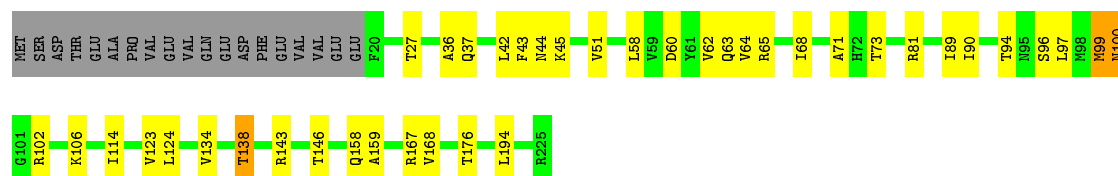
### • Molecule 2: 40S ribosomal protein S3

Chain A: 78% 14% 7%

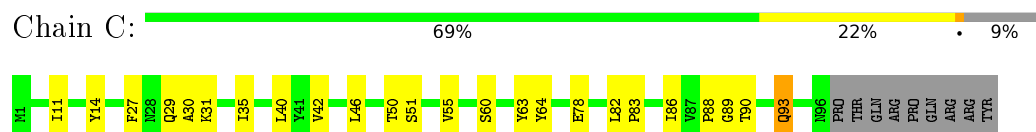


### • Molecule 3: 40S ribosomal protein S5

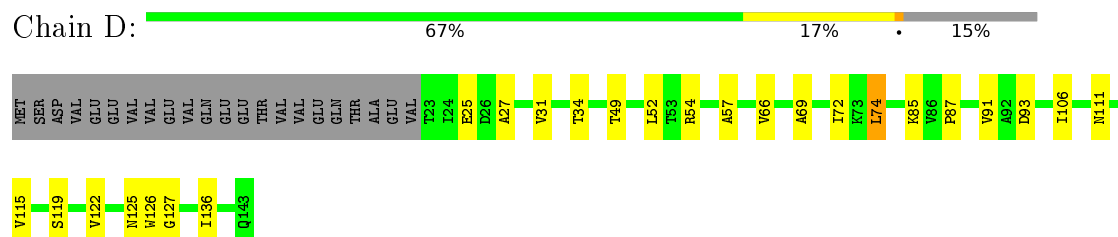
Chain B: 74% 16% 8%



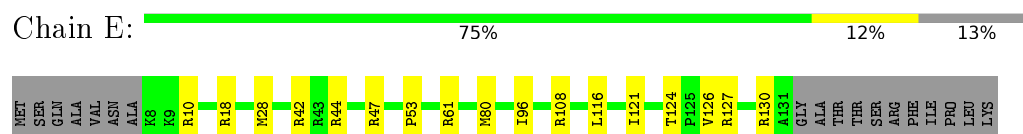
### • Molecule 4: 40S ribosomal protein S10-A



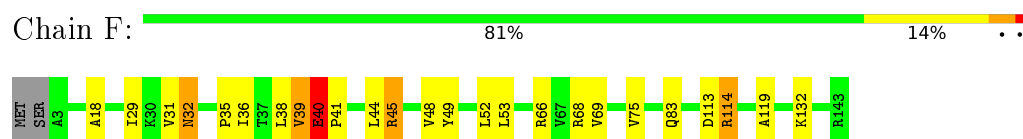
- Molecule 5: 40S ribosomal protein S12



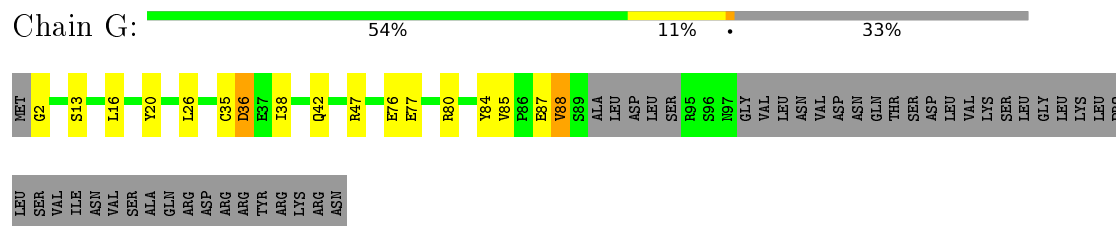
- Molecule 6: 40S ribosomal protein S15



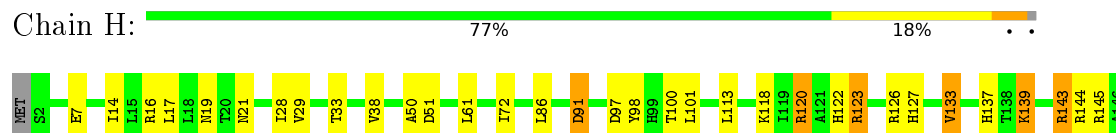
- Molecule 7: 40S ribosomal protein S16-A



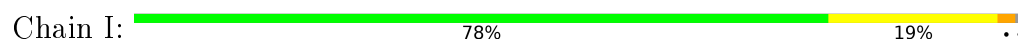
- Molecule 8: 40S ribosomal protein S17-B

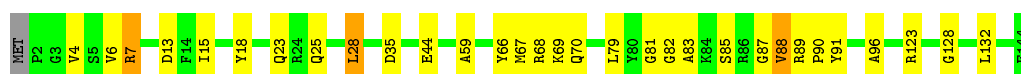


- Molecule 9: 40S ribosomal protein S18-A



- Molecule 10: 40S ribosomal protein S19-A





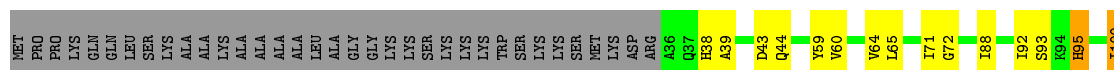
- Molecule 11: 40S ribosomal protein S20

Chain J: 74% 13% 12%



- Molecule 12: 40S ribosomal protein S25-A

Chain K: 50% 13% 35%



- Molecule 13: 40S ribosomal protein S28-B

Chain L: 85% 9% 6%



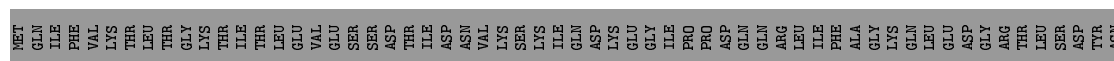
- Molecule 14: 40S ribosomal protein S29-A

Chain M: 86% 7% 5%



- Molecule 15: Ubiquitin-40S ribosomal protein S31

Chain N: 29% 5% 66%



- Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein

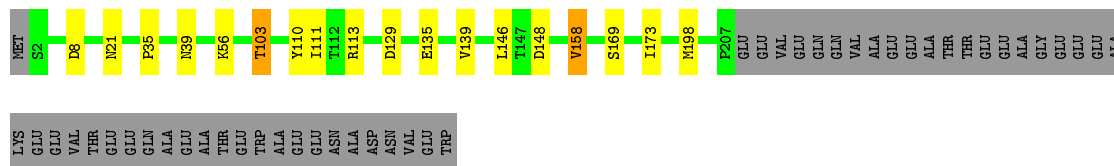
Chain O: 89% 10%





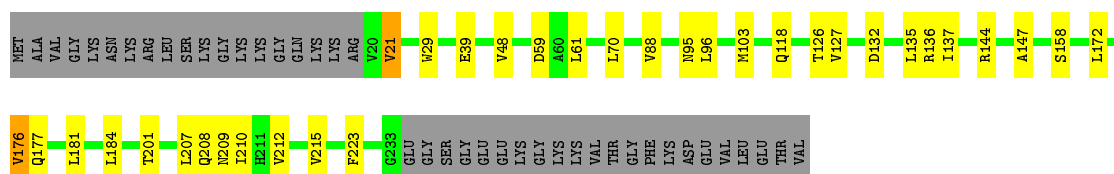
• Molecule 17: 40S ribosomal protein S0-A

Chain P: 75% 6% 18%



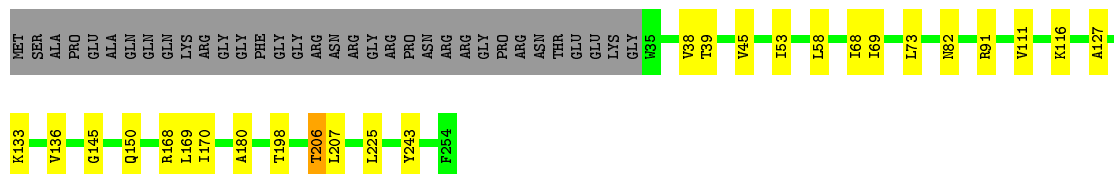
• Molecule 18: 40S ribosomal protein S1-A

Chain Q: 71% 13% 16%



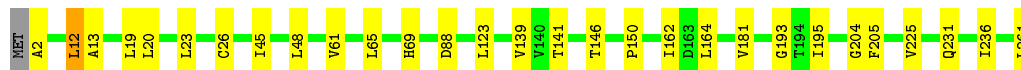
• Molecule 19: 40S ribosomal protein S2

Chain R: 76% 10% 13%



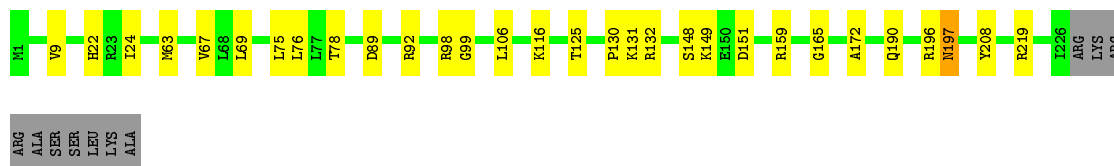
• Molecule 20: 40S ribosomal protein S4-A

Chain S: 89% 11%



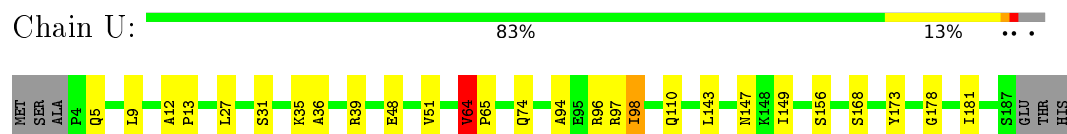
• Molecule 21: 40S ribosomal protein S6-A

Chain T: 83% 12%

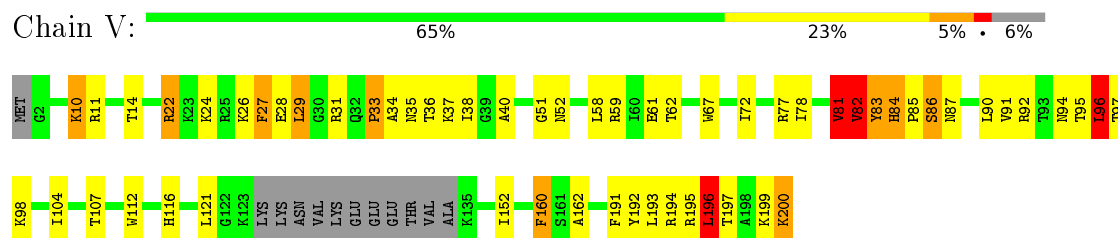


• Molecule 22: 40S ribosomal protein S7-A

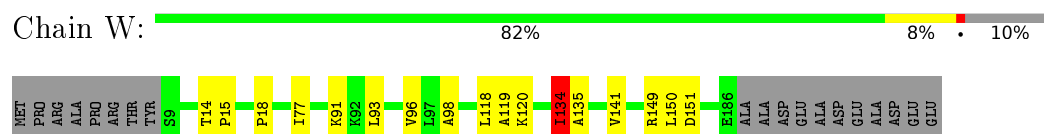




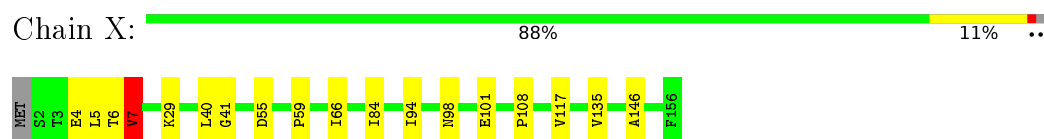
- Molecule 23: 40S ribosomal protein S8-A



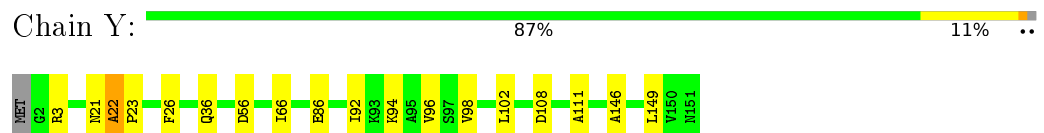
- Molecule 24: 40S ribosomal protein S9-A



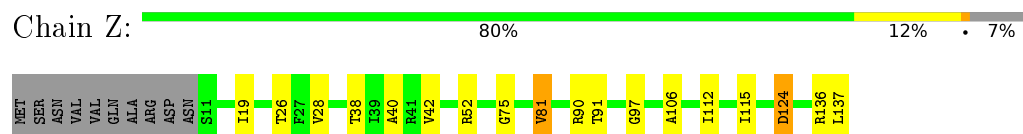
- Molecule 25: 40S ribosomal protein S11-A



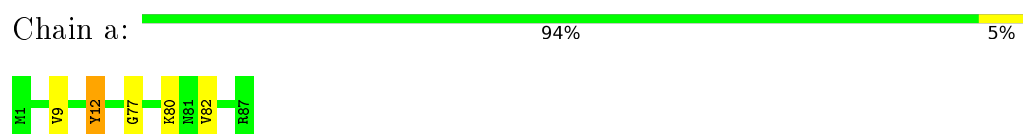
- Molecule 26: 40S ribosomal protein S13



- Molecule 27: 40S ribosomal protein S14-A



- Molecule 28: 40S ribosomal protein S21-A



- Molecule 29: 40S ribosomal protein S22-A

Chain b:  95% ..



- Molecule 30: 40S ribosomal protein S23-A

Chain c:  96% ..



- Molecule 31: 40S ribosomal protein S24-A

Chain d:  87% 9% ..



- Molecule 32: 40S ribosomal protein S26-A

Chain e:  68% 13% 18%




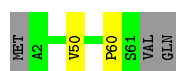
- Molecule 33: 40S ribosomal protein S27-A

Chain f:  93% 6% .




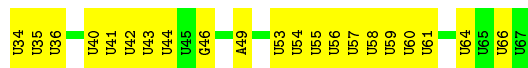
- Molecule 34: 40S ribosomal protein S30-A

Chain g:  92% . 5%



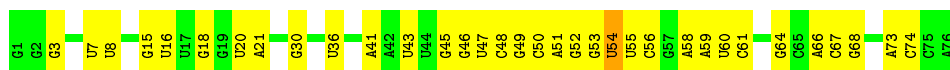
- Molecule 35: mRNA

Chain l:  38% 62%



- Molecule 36: A-site tRNA

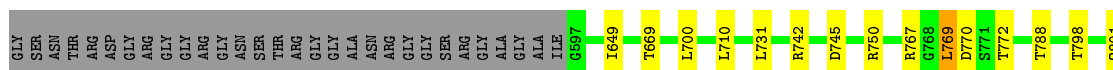
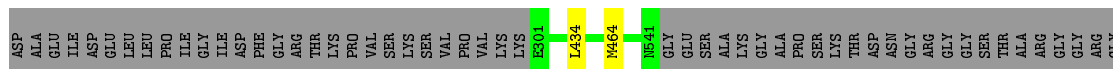
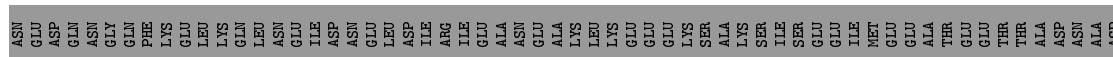
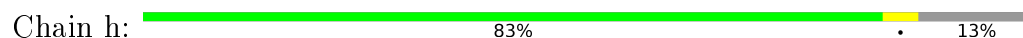
Chain m:  55% 43% .



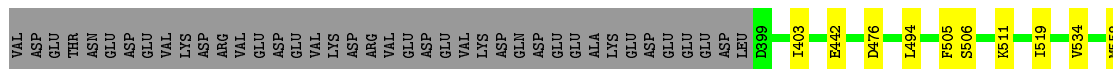
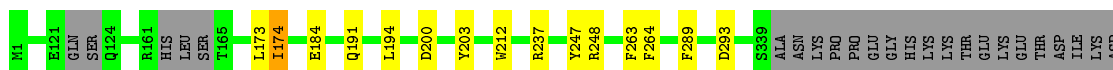
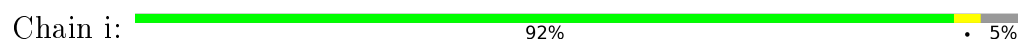
- Molecule 37: P-site tRNA



- Molecule 38: Antiviral helicase SKI2




- Molecule 39: Superkiller protein 3



- Molecule 40: Antiviral protein SKI8




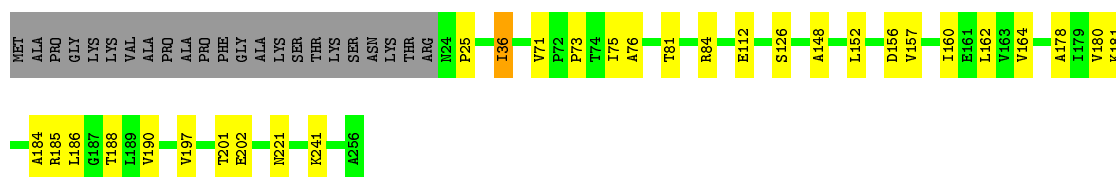
- Molecule 40: Antiviral protein SKI8

Chain k:  94%




- Molecule 41: 60S ribosomal protein L8-A

Chain AA:  79% 11% 9%




- Molecule 42: 60S ribosomal protein L23-A

Chain AB:  86% 13%




- Molecule 43: 60S ribosomal protein L36-A

Chain AC:  82% 17%



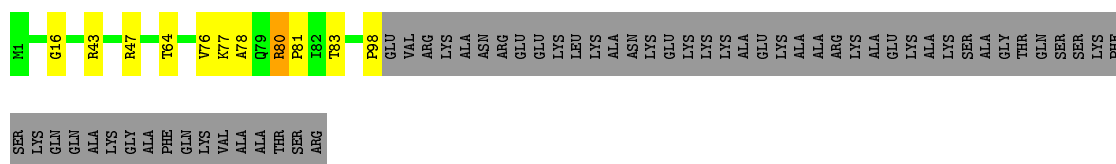
- Molecule 44: 60S ribosomal protein L9-A

Chain AD:  86% 12%




- Molecule 45: 60S ribosomal protein L24-A

Chain AE:  56% 6% 37%



- Molecule 46: 60S ribosomal protein L37-A

Chain AF:  80% 16%



- Molecule 47: 60S ribosomal protein L11-A

Chain AG: 83% 13% ..



- Molecule 48: 60S ribosomal protein L25

Chain AH: 75% 11% 15%



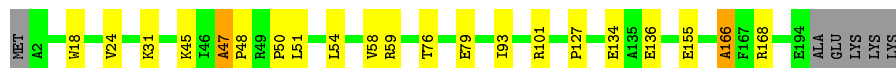
- Molecule 49: 60S ribosomal protein L38

Chain AI: 95% ..



- Molecule 50: 60S ribosomal protein L13-A

Chain AJ: 86% 10% ..



- Molecule 51: 60S ribosomal protein L26-A

Chain AK: 90% 9% .



- Molecule 52: 60S ribosomal protein L39

Chain AL: 86% 12% .

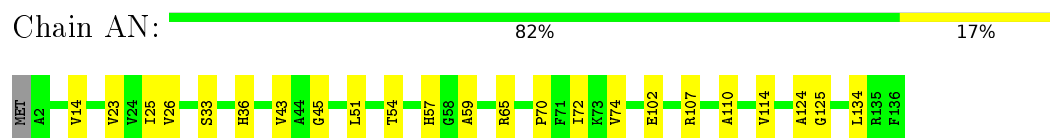


- Molecule 53: 60S ribosomal protein L14-A

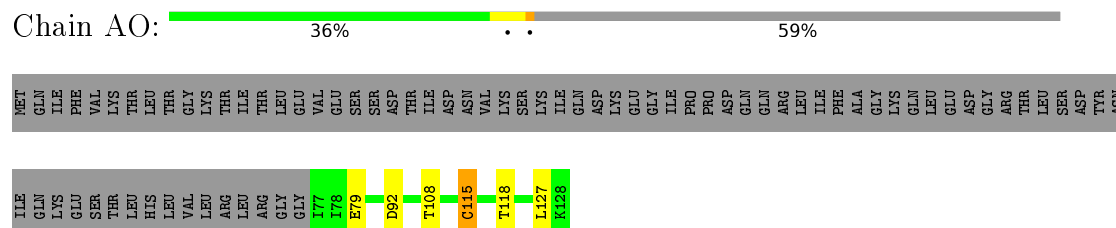
Chain AM: 87% 12% .



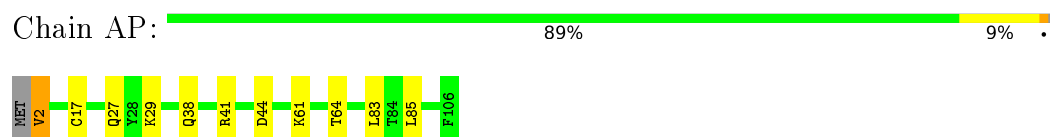
- Molecule 54: 60S ribosomal protein L27-A



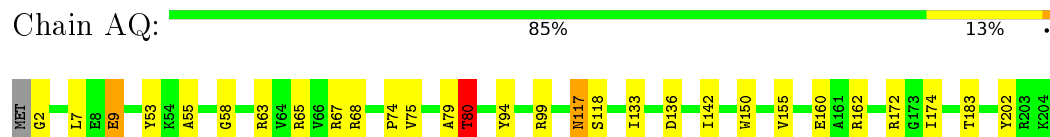
- Molecule 55: Ubiquitin-60S ribosomal protein L40



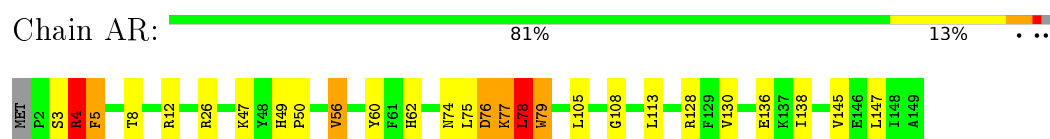
- Molecule 56: 60S ribosomal protein L42-A



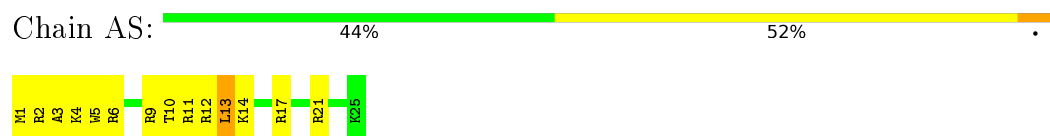
- Molecule 57: 60S ribosomal protein L15-A



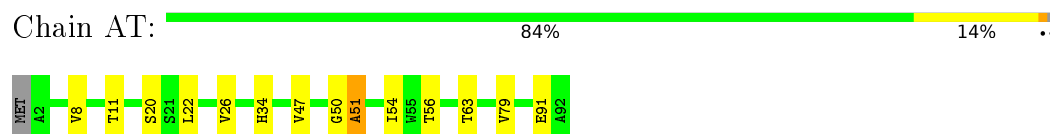
- Molecule 58: 60S ribosomal protein L28



- Molecule 59: 60S ribosomal protein L41-A

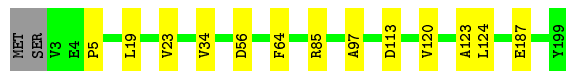


- Molecule 60: 60S ribosomal protein L43-A



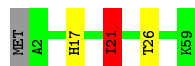
- Molecule 61: 60S ribosomal protein L16-A

Chain AU:  92% 7%




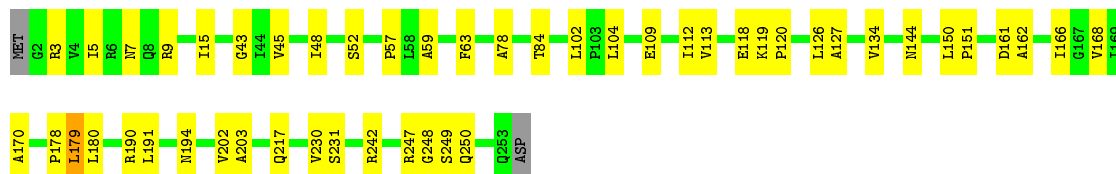
- Molecule 62: 60S ribosomal protein L29

Chain AV:  93%




- Molecule 63: 60S ribosomal protein L2-A

Chain AW:  80% 19%




- Molecule 64: 60S ribosomal protein L17-A

Chain AX:  85% 13%



- Molecule 65: 60S ribosomal protein L30

Chain AY:  82% 10% 8%




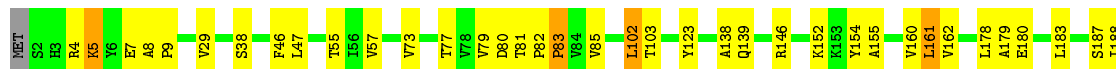
- Molecule 66: uL1

Chain AZ:  99%



- Molecule 67: 60S ribosomal protein L3

Chain BA:  84% 15%





- Molecule 68: 60S ribosomal protein L18-A

Chain BB: 84% 16%



- Molecule 69: 60S ribosomal protein L31-A

Chain BC: 76% 19%



- Molecule 70: 60S ribosomal protein L10

Chain BD: 85% 13%



- Molecule 71: 60S ribosomal protein L4-A

Chain BE: 84% 15%



- Molecule 72: 60S ribosomal protein L19-A

Chain BF: 86% 13%



- Molecule 73: 60S ribosomal protein L32

Chain BG: 87% 11%





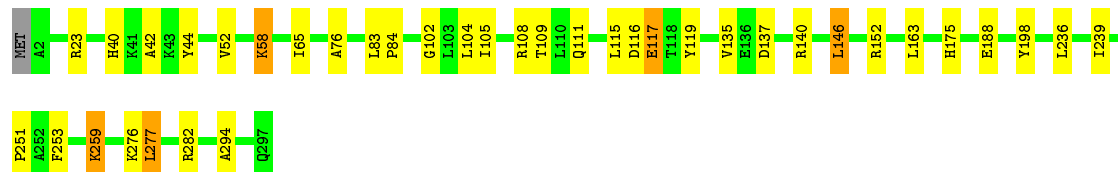
- Molecule 74: 60S ribosomal protein L20-A

Chain BH:  91% 9%



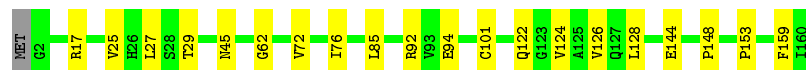
- Molecule 75: 60S ribosomal protein L5

Chain BI:  87% 11% 2%



- Molecule 76: 60S ribosomal protein L21-A

Chain BJ:  87% 13%



- Molecule 77: 60S ribosomal protein L33-A

Chain BK:  83% 15% ..

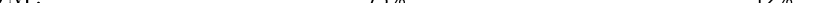


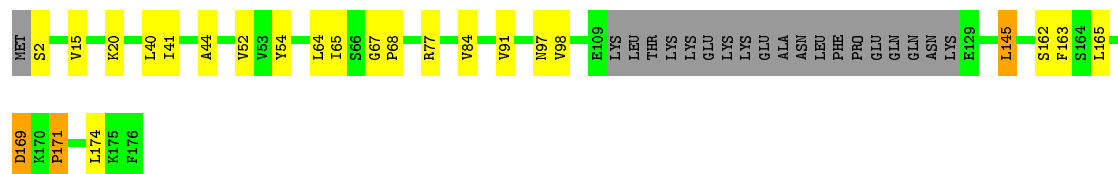
- Molecule 78: 60S ribosomal protein L22-A

Chain BL:  78% 5% 17%




- Molecule 79: 60S ribosomal protein L6-A

Chain BM:  75% 12% • 11%



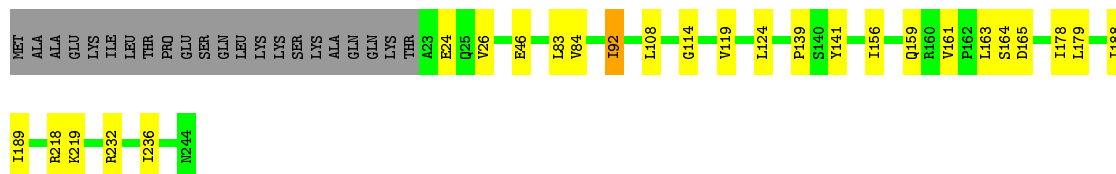
- Molecule 80: 60S ribosomal protein L34-A

Chain BN:  83% 9% 7%



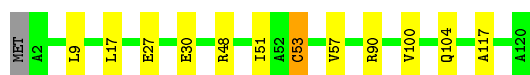
- Molecule 81: 60S ribosomal protein L7-A

Chain BO: 80% 10% 9%



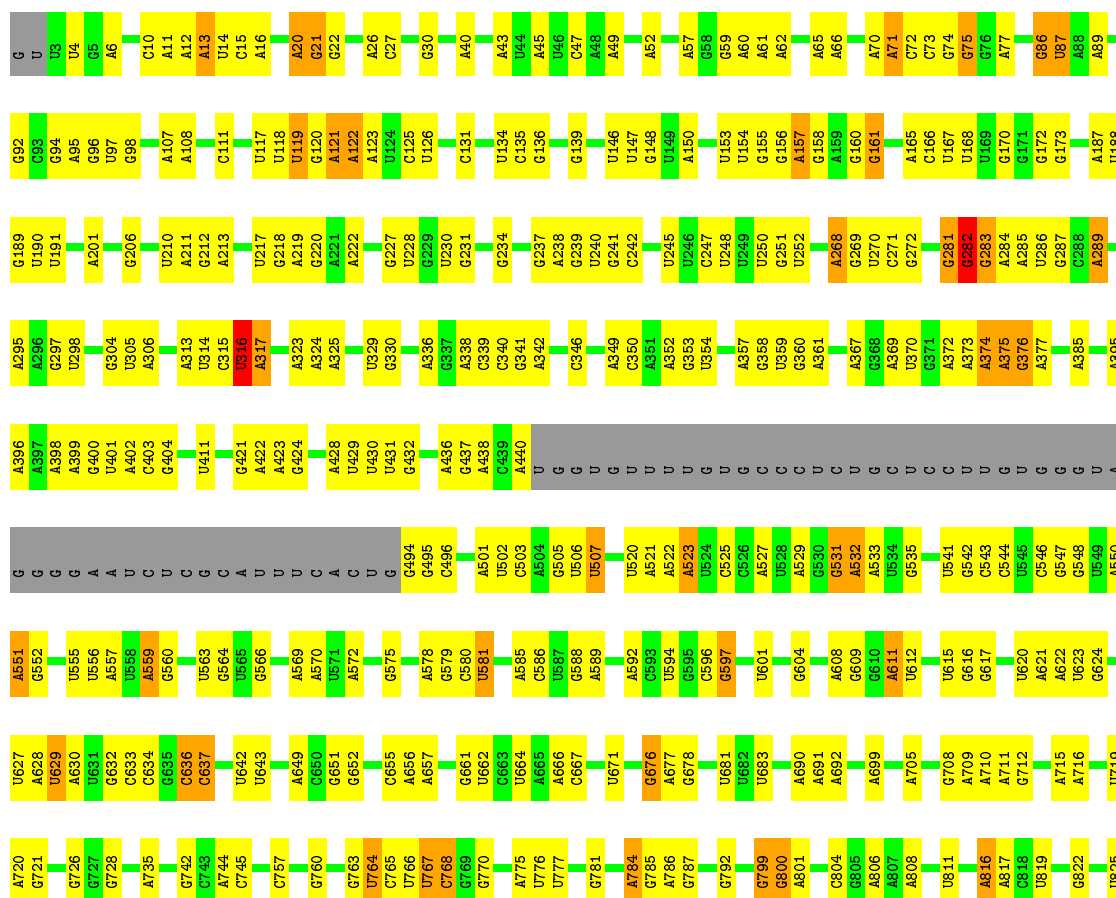
- Molecule 82: 60S ribosomal protein L35-A

Chain BP: 89% 9% ..



- Molecule 83: 25S ribosomal RNA

Chain BQ: 51% 36% 6% 7%



U2162	C1854	A1760	A1656	C1556	A1449	C1333	G1261	G1194	A1102	G1019	G934	G826
C2163	U1855	C1761	C1657	A1557	G1450	U1334	G1262	A1195	A1103	G1020		
A2167	C1856	C1762	G1658	A1558	C1451		A1263	C1196	G1104	C1023	6937	U829
A2168	C1857	U1763	U1659	A1559	A1452	A1337	G1264	A1197	A1105		6938	A830
G2169	A1858	U1764	C1660	G1561	A1456	C1338	U1265	C1198	G1106	G1024	U939	G831
U2170	G	U1765	G1661	C1562			G1266	C1199		A1025		G832
G	A	G1766	G1662	C1563	A1462	G1345	U1267	A1200	U1110	U1028	U942	G833
C	A				U1463			C1201	U1111		6943	U834
U2175	A1865	G1769	G1668	U1567	U1463	U1348	A1270	A1202		G1029	6944	
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G2177	A1867			U1569		A1350	C1272	A1204	G1117	G1031	U946	A846
A2178	G1868	G1775	A1676	U1570	A1467	U1351	A1273	C1205		C1032		A847
C2179	U1871		G1677	A1571	A1468	A1352	C1274	G1206		U1033	6949	A848
G2180	U	G1780		U1572		U1353	C1275		U1125		6950	C849
	C	U1781	U1684	U1577	U1479			U1240	A1126	A1036		
U2184	U1877	U1782	U1683	G1576	G1480	G1354	U1276		U1127		6953	G857
G2185	G1878	U1783	U1684	U1577	A1481	A1355	C1277	G1213	C1037	C1038	U954	A858
U2186	A1879	G1784	U1692	G1577	A1482	U1356	A1278	G1222	A1129			G859
G2187	U1880	U1785	C1693	C1578	G1483	G1357	C1280	A1217	A1130	U1042	6959	G860
A2188	A1881	G1786	U1694	C1579	U1484	C1358	C1281		G1134	C1043	U960	G861
	A	U1787	U1695	A1580	U1485	C1359	G1282	U1220		C1045	6961	
U2191	U1885	C1788	A1696	C1581	G1486	C1364	C1283	G1221	G1140	A1046	A962	
G2192	A1886		A1697	C1582	G1487		C1284	G1222				
G2193	G1887	C1792	U1702	A1583		G1380	G1285	A1223	C1141	A1047	6964	U874
G2194	U1888	G1794	U1703	A1587	U1494	A1381	A1286	C1224	G1142	A1048		G875
	C	U1797	A1704	A1588	U1495	G1382	A1287	A1225	A1143	C1049	6974	A876
C2197	A1893	A1798		A1589	A1504	C1385	A1290	G1227	U1144	U1051	C977	C877
A2198	U1894	A1798	C1708	C1596	C1505	A1386	A1291	C1228	G1145	U1052	6978	G878
G2199	G1895	A1798	G1713	C1597	U1506	C1391	A1294	G1229	G1149	A1055	U979	G880
	C	G1897	U1714	C1596	G1507	G1392		A1231			A980	G881
U2202	G1898	G1809		C1597	C1508	A1393	A1301	G1232		G1063	U981	A882
C2203	A1900	A1813	U1717	U1511	U1511	A1399	A1302	G1233	A1151	A1064	6984	U885
U2204	U1901	A1814	G1718	A1602	U1512	G1400	A1303	G1234	A1153	A1065		
C2205	G1905	U1815	U1719	A1603	G1513		U1304	U1235	U1071		U988	A895
A2206	U1906	A1816	U1720	G1604	G1514	G1408	U1305	G1236	G1072		A989	A896
U2209	G1906	G1817	U1721	A1605			G1306	G1237	U1073	U1074	U990	U897
G2210	U1912	U1818	U1722	U1606	G1520	G1417	U1307	C1238	U1073		6991	U898
U2211	G	U1819	U1723	U1607	U1522	A1418	A1308	C1239	A1075	G993	A992	U899
C2212	C	U1820	U1724	U1607	U1523	A1419	U1309	A1240	G1076	U1077	U995	G907
	A	C1822	C1725	A1613	A1524		G1313	G1242	G1171		A996	G908
U2225	C			G1617	G1525	C1424	C1314	G1243	G1172			
	U	U1834	G1728	G1618	U1526		U1315	A1244		U1081		C911
A2228	G	A1835	A1729	G1619	C1527	A1429	C1316	A1245	G1177	U1082	G1001	G912
U2229	C	U1731	G1730	U1620		U1430	A1317	G1246	G1178	G1083		A913
A2243	A1930	A1839	G1735	A1621	C1532	G1431	A1318	U1247	A1179	A1084	G1005	A914
A2244	U1931	U1840		U1533	U1533	C1432	G1319	C1248	A1180	A1085	A1006	A915
C2245	A1932	A1841		G1624		A1433	C1320	G1249	U1181	C1086	U1007	G916
G2246	C	A1842		A1625	G1536	G1434	G1321	G1250	A1182	G1087	U1008	A917
	U	U1740	U1741	U1630		A1435		A1251			A1009	
G2249	U1942	G1747	G1747	U1631	A1539	U1436	U1325	A1252	C1185	C1092	G1010	A921
A2255	G	A1846	G1748	C1632	G1542	C1437	A1326	U1253	G1186	A1093	G1013	U922
A2256	U	G1848	A1749	C1633			C1327	C1254	G1187	U1094	U1014	C923
C2257	C	C1849	A1750	A1645	U1549	G1444	G1328	C1255	U1188	U1095	G1013	G924
U2258	U	U1851	G1751	U1645		U1445	U1329	G1256	U1191	U1096	U1015	A925
G2160	U	G1851	A1752	G1646	U1554	A1446	A1330	C1257	C1192	G1097	C1016	A926
U2260	G				U1555	U1448	A1332		C1192	A1098	C1017	A933

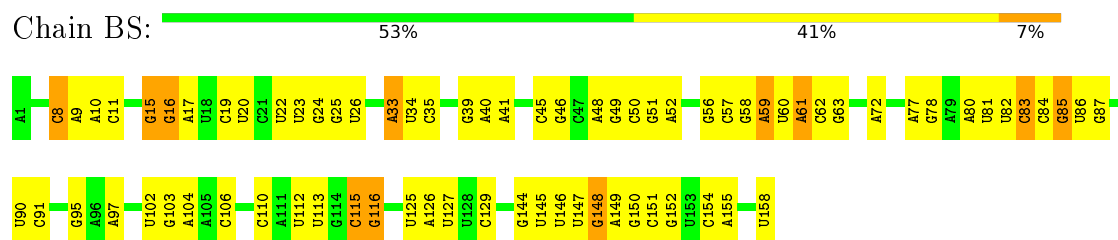
G3364	A3279	U3196	G3112	A2911	U2716	G2614	G2530	C2374	G2261
U3366	U3280	G3197	A3113	G2912	G2817	U2617	C2531	G2375	A2262
G3369	U3287	U3198	A3114	U2923	C2821	G2618	U2532	C2378	C2263
A3370	G3289	G3202	G3116	C2925	G2824	G2619	G2533	C2383	A2270
A3375	U3293	U3203	G3118	C2928	U2829	G2624	A2535	C2386	A2271
A3376	A3294	C3206	U3119	C2929	U2834	C2625	A2536	A2387	G2272
C3378	A3295	U3207	C3120	C2930	U2835	C2626	U2537	U2388	U2274
U3382	U3304	G3208	A3121	U2932	G2836	A2628	U2538	C2392	A2279
G3383	A3305	A3209	A3122	A2933	U2837	U2629	C2539	G2393	A2280
U3384	U3306	A3210	A3123	A2934	G2838	U2630	U2540	U2394	A2281
U3385	U3307	U3214	G3124	U2935	A2839	U2633	U2541	G2399	U2282
G3386	C3308	A3215	U3126	A2936	G2840	U2634	U2542	C2399	G2283
G3390	U3313	C3217	A3130	U2938	U2842	U2641	U2544	A2397	C2284
U3396	U3316	G3219	U3131	C2942	A2845	A2642	A2547	A2398	G2288
	U3317	G3220	U3138	C2944	U2846	U2643	C2549	A2402	A2291
	G3318	G3224	A3142	G2945	A2746	U2652	U2550	G2403	U2292
	U3319	A3227	A3143	U2946	A2747	C2653	U2551	C2406	U2298
	A3320	C3228	G3144	G2947	U2750	A2655	C2552	C2407	
	A3321	G3229	U3152	G2950	G2751	A2656	U2553	U2411	G2302
	A3322	C3230	C3154	G2951	U2752	A2657	A2554	G2412	A2303
	A3323	U3231	U3155	G2952	G2753	U2658	U2555	U2416	C2304
	C3324	U3237	C3156	U2953	G2754	C2666	C2560	U2417	C2306
	U3329	G3238	U3157	U2954	A2758	G2672	C2567	G2418	G2307
	A3330	U3241	G3158	U2955	U2761	A2673	C2568	A2419	C2308
	U3331	G3242	C3159	C2960	A2762	A2674	A2569	C2420	
	A3332	A3243	U3160	G2961	U2767	G2677	U2570	A2424	G2311
	A3334	A3244	A3168	G2966	C2772	A2678	U2571	A2433	A2312
	A3335	A3245	U3171	C2970	C2776	A2679	C2572	U2434	U2314
	A3339	G3246	A3172	A2971	G2777	U2680	C2577	G2435	G2315
	A3342	G3247	A3173	C2972	G2778	C2682	U2578	U2436	G2316
	G3343	G3256	G3174	G2977	A2779	C2683	A2585	G2437	A2317
	A3344	U3258	A3175	U2978	G2784	U2684	U2586	U2318	U2319
	G3345	U3259	G3176	U2979	U2785	A2688	U2587	A2438	U2328
	U3346	G3260	U3177	U2983	U2883	C2689	U2588	A2441	C2329
	A3347	C3261	A3178	C2983	U2884	A2691	A2590	G2442	A2332
	G3348	U3262	U3179	C2988	U2885	A2694	A2593	U2443	C2333
	C3349	G3263	A3180	U2990	U2886	A2695	C2594	C2444	U2334
	U3351	A3268	G3182	U2996	U2888	A2696	A2595	U2445	G2335
	U3352	U3269	A3183	G2997	C2889	A2697	U2600	U2446	U2336
	G3353	C3270	U3184	U2998	G2890	U2703	C2606	G2451	U2340
	U3354	G3271	A3185	U2999	A2802	A2704	G2607	U2452	G2345
	G3355	C3272	U3186	A3000	A2804	U2705	U2610	U	U2346
	U3357	A3273	A3187	C3001	U2806	C2709	U2611	G	A2357
	U3358	C3274	G3188	A3004	A2903	U2713	U2612	U	A2364
	U3361	U2775	C3193	C3007	C2906	G2714	U2613	A	G2373
	A3362	G3276	C3194	U3007	G2907	U2715			
	U3363	C3278	U3195	A3008	G2815				

• Molecule 84: 5S ribosomal RNA

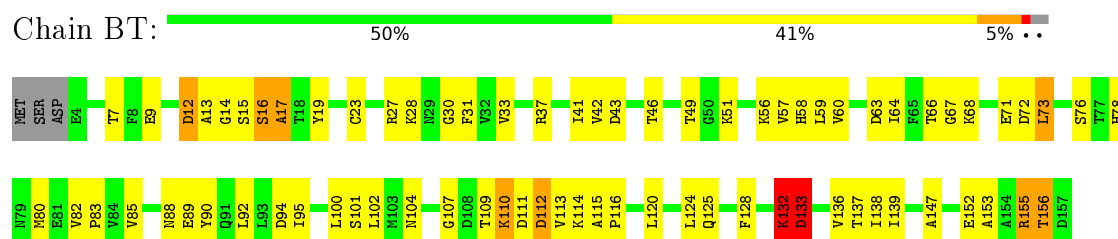
Chain BR:  54% 40% 6%

G91	G8	G109	G71	G61	G48	U53	U62	G71	G61
G99	C100	G110	A72	A63	G49	A330	A66	A72	A63
G101	C101	U111	C73	A64	U33	U331	A65	C73	A64
A102	A103	G112	C74	A65	U32	U332	A66	C74	A65
A103		C113	C75	A66	A42	G332	A67	C75	A66
		U114	A76	A67	U48	A333	A68	A76	A67
		U121	G77	A68	G49	A334	A69	G77	A68
			U78	A69	U53	A335	A70	U78	A69
			A79	A70	U33	A336	A71	A79	A70
			G80	A71	U32	A337	A72	G80	A71
			U81	A72	U48	A338	A73	U81	A72
			A84	A73	G49	A339	A74	A84	A73
			G85	A74	U53	A340	A75	G85	A74
			U86	A75	U33	A341	A76	U86	A75
			G87	A76	U32	A342	A77	G87	A76

- Molecule 85: 5.8S ribosomal RNA



- Molecule 86: Eukaryotic translation initiation factor 5A-1



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	31503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	2	0.33	2/42103 (0.0%)	0.73	20/65603 (0.0%)
10	I	0.42	0/1130	0.68	0/1517
11	J	0.36	0/865	0.62	0/1169
12	K	0.40	0/571	0.65	0/768
13	L	0.37	0/499	0.69	0/670
14	M	0.38	0/452	0.63	0/600
15	N	0.39	0/404	0.61	0/542
16	O	0.35	0/2489	0.52	0/3389
17	P	0.39	0/1617	0.62	0/2215
18	Q	0.40	0/1735	0.62	0/2335
19	R	0.35	0/1702	0.57	0/2310
2	A	0.37	0/1759	0.62	0/2368
20	S	0.39	0/2109	0.61	0/2839
21	T	0.38	0/1823	0.62	0/2439
22	U	0.40	0/1506	0.57	0/2028
23	V	0.46	0/1514	0.78	1/2021 (0.0%)
24	W	0.40	0/1456	0.65	0/1949
25	X	0.42	2/1239 (0.2%)	0.56	0/1673
26	Y	0.39	0/1215	0.66	0/1638
27	Z	0.41	0/901	0.71	0/1217
28	a	0.38	0/693	0.64	0/935
29	b	0.35	0/1038	0.65	1/1395 (0.1%)
3	B	0.39	0/1629	0.67	0/2202
30	c	0.36	0/1139	0.61	0/1518
31	d	0.41	0/1074	0.70	2/1431 (0.1%)
32	e	0.61	0/782	0.80	0/1047
33	f	0.37	0/620	0.57	0/838
34	g	0.39	0/481	0.60	0/640
35	l	0.47	1/764 (0.1%)	0.79	0/1179
36	m	0.26	0/1799	0.72	1/2801 (0.0%)
37	n	0.36	1/1835 (0.1%)	0.71	0/2858
38	h	0.40	2/8985 (0.0%)	0.56	1/12155 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	i	0.38	0/10027	0.54	0/13707
4	C	0.39	0/833	0.59	0/1126
40	j	0.37	0/3001	0.52	0/4083
40	k	0.37	0/2988	0.54	0/4060
41	AA	0.42	0/1836	0.63	0/2481
42	AB	0.39	0/1018	0.66	0/1369
43	AC	0.43	0/778	0.73	0/1034
44	AD	0.41	0/1539	0.66	0/2073
45	AE	0.42	0/712	0.66	1/958 (0.1%)
46	AF	0.45	0/696	0.74	0/923
47	AG	0.43	0/1374	0.71	0/1842
48	AH	0.38	0/979	0.64	0/1321
49	AI	0.40	0/618	0.61	0/826
5	D	0.40	0/885	0.61	0/1202
50	AJ	0.45	0/1568	0.74	0/2106
51	AK	0.39	0/1004	0.67	0/1341
52	AL	0.44	0/443	0.74	0/588
53	AM	0.40	0/1068	0.70	0/1438
54	AN	0.41	0/1118	0.65	0/1497
55	AO	0.42	0/423	0.69	0/562
56	AP	0.41	0/860	0.66	0/1136
57	AQ	0.44	0/1757	0.77	1/2354 (0.0%)
58	AR	0.42	0/1204	0.73	1/1612 (0.1%)
59	AS	0.50	0/234	0.86	0/300
6	E	0.40	0/998	0.64	0/1341
60	AT	0.39	0/701	0.72	0/934
61	AU	0.41	0/1585	0.66	0/2128
62	AV	0.39	0/473	0.66	0/629
63	AW	0.39	0/1948	0.75	0/2617
64	AX	0.42	0/1443	0.73	0/1944
65	AY	0.41	0/750	0.63	0/1008
67	BA	0.41	0/3146	0.69	0/4228
68	BB	0.40	0/1465	0.73	0/1965
69	BC	0.39	0/890	0.67	0/1196
7	F	0.40	0/1125	0.69	1/1510 (0.1%)
70	BD	0.43	0/1807	0.71	0/2425
71	BE	0.41	0/2800	0.68	0/3790
72	BF	0.43	0/1538	0.71	0/2050
73	BG	0.39	0/1041	0.64	0/1394
74	BH	0.41	0/1481	0.67	0/1990
75	BI	0.42	0/2425	0.66	0/3271
76	BJ	0.40	0/1300	0.68	0/1743
77	BK	0.41	0/868	0.69	0/1168



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	BL	0.44	0/812	0.60	0/1099
79	BM	0.40	0/1260	0.65	0/1694
8	G	0.49	2/754 (0.3%)	0.74	1/1005 (0.1%)
80	BN	0.41	0/890	0.71	0/1189
81	BO	0.42	0/1821	0.67	0/2451
82	BP	0.39	0/978	0.69	0/1301
83	BQ	0.34	4/75774 (0.0%)	0.75	37/118137 (0.0%)
84	BR	0.31	0/2883	0.73	1/4491 (0.0%)
85	BS	0.32	0/3745	0.73	1/5829 (0.0%)
86	BT	0.32	0/1142	0.61	0/1537
9	H	0.41	0/1211	0.75	0/1628
All	All	0.37	14/243945 (0.0%)	0.70	70/355920 (0.0%)

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
10	I	0	2
21	T	0	2
22	U	0	1
23	V	0	3
32	e	0	2
57	AQ	0	1
58	AR	0	2
63	AW	0	1
69	BC	0	1
70	BD	0	1
86	BT	0	1
9	H	0	1
All	All	0	18

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	52	U	O3'-P	23.25	1.89	1.61
83	BQ	683	U	N1-C2	10.32	1.47	1.38
37	n	1	G	OP3-P	-10.19	1.49	1.61
35	l	34	U	OP3-P	-10.13	1.49	1.61
83	BQ	683	U	C4-C5	8.78	1.51	1.43
38	h	832	GLU	CD-OE2	7.78	1.34	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	BQ	683	U	N1-C6	7.31	1.44	1.38
1	2	1589	C	N1-C6	7.31	1.41	1.37
83	BQ	683	U	N3-C4	7.13	1.44	1.38
38	h	832	GLU	CD-OE1	6.90	1.33	1.25
8	G	36	ASP	CG-OD1	6.01	1.39	1.25
25	X	101	GLU	CD-OE2	5.35	1.31	1.25
25	X	101	GLU	CD-OE1	5.06	1.31	1.25
8	G	36	ASP	CG-OD2	5.01	1.36	1.25

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	52	U	P-O3'-C3'	-14.01	102.89	119.70
1	2	52	U	C5'-C4'-O4'	-13.02	93.47	109.10
83	BQ	2972	G	N9-C1'-C2'	-11.36	99.23	114.00
1	2	428	A	N9-C1'-C2'	-10.27	100.66	114.00
83	BQ	933	A	C2'-C3'-O3'	9.73	130.90	109.50
83	BQ	1808	G	C2'-C3'-O3'	9.26	129.86	109.50
83	BQ	282	G	C2'-C3'-O3'	8.92	129.12	109.50
1	2	157	A	N9-C1'-C2'	-8.65	102.48	112.00
83	BQ	2970	C	N1-C1'-C2'	-8.24	102.93	112.00
7	F	40	GLU	C-N-CD	-8.22	102.51	120.60
83	BQ	1429	G	C2'-C3'-O3'	8.03	127.17	109.50
83	BQ	1511	U	C2'-C3'-O3'	8.01	127.11	109.50
83	BQ	2116	G	C2'-C3'-O3'	7.71	126.45	109.50
83	BQ	316	U	C2'-C3'-O3'	7.15	125.23	109.50
83	BQ	2972	G	C4'-C3'-O3'	7.03	127.05	113.00
1	2	428	A	C4'-C3'-O3'	6.91	126.83	113.00
83	BQ	1913	A	C2'-C3'-O3'	6.88	124.71	113.70
83	BQ	1241	U	C4'-C3'-O3'	6.64	126.29	113.00
1	2	1185	U	C2'-C3'-O3'	6.45	124.02	113.70
83	BQ	2177	G	C2'-C3'-O3'	6.44	124.00	113.70
1	2	384	G	C4'-C3'-O3'	6.42	125.84	113.00
1	2	427	C	N1-C1'-C2'	-6.39	104.97	112.00
83	BQ	3047	U	O4'-C1'-N1	6.21	113.17	108.20
83	BQ	1467	A	C2'-C3'-O3'	6.06	123.39	113.70
1	2	1274	C	C2'-C3'-O3'	6.04	123.36	113.70
1	2	1430	U	C2'-C3'-O3'	6.00	123.30	113.70
83	BQ	1483	G	C2'-C3'-O3'	5.97	123.26	113.70
83	BQ	1840	U	N1-C1'-C2'	5.96	121.75	114.00
58	AR	4	ARG	N-CA-C	5.94	127.03	111.00
1	2	412	A	N9-C1'-C2'	-5.90	105.51	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	d	132	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	2	1742	U	C2'-C3'-O3'	5.84	123.05	113.70
29	b	28	ARG	C-N-CD	-5.83	107.77	120.60
83	BQ	611	A	C2'-C3'-O3'	5.74	122.89	113.70
1	2	49	C	C1'-C2'-O2'	-5.70	93.49	110.60
83	BQ	2593	A	C2'-C3'-O3'	5.68	122.80	113.70
23	V	200	LYS	N-CA-C	5.67	126.30	111.00
1	2	1251	U	C2'-C3'-O3'	5.63	122.71	113.70
83	BQ	2495	C	C2'-C3'-O3'	5.63	122.71	113.70
83	BQ	1839	A	C2'-C3'-O3'	5.62	122.69	113.70
83	BQ	683	U	N3-C4-C5	5.58	117.95	114.60
83	BQ	1751	G	C2'-C3'-O3'	5.57	122.61	113.70
83	BQ	916	G	C4'-C3'-O3'	5.53	124.06	113.00
83	BQ	2273	G	C2'-C3'-O3'	5.51	122.52	113.70
83	BQ	2954	U	C4'-C3'-O3'	-5.42	98.01	109.40
83	BQ	2727	A	C2'-C3'-O3'	5.41	122.36	113.70
83	BQ	3156	U	C2'-C3'-O3'	5.39	122.33	113.70
1	2	381	C	N1-C1'-C2'	5.37	120.99	114.00
83	BQ	1392	G	C2'-C3'-O3'	5.37	122.29	113.70
83	BQ	3078	U	C2'-C3'-O3'	5.35	122.26	113.70
83	BQ	3219	G	C2'-C3'-O3'	5.33	122.22	113.70
83	BQ	1724	U	C4'-C3'-O3'	5.30	123.60	113.00
45	AE	80	ARG	C-N-CA	5.27	144.12	122.00
83	BQ	2500	A	C2'-C3'-O3'	5.22	122.05	113.70
83	BQ	1900	A	C2'-C3'-O3'	5.21	122.04	113.70
83	BQ	3152	U	N1-C1'-C2'	5.21	120.77	114.00
1	2	1382	A	C2'-C3'-O3'	5.21	122.03	113.70
85	BS	33	A	C4'-C3'-O3'	5.20	123.40	113.00
1	2	322	G	C2'-C3'-O3'	5.20	122.02	113.70
8	G	36	ASP	CB-CG-OD2	-5.19	113.63	118.30
1	2	141	U	C4'-C3'-O3'	5.16	123.32	113.00
38	h	899	LEU	CA-CB-CG	5.16	127.16	115.30
1	2	1244	A	C2'-C3'-O3'	5.14	121.93	113.70
83	BQ	2972	G	C1'-C2'-O2'	-5.13	95.22	110.60
1	2	539	G	C2'-C3'-O3'	5.09	121.85	113.70
83	BQ	2665	U	C4'-C3'-O3'	5.09	123.17	113.00
84	BR	77	G	C2'-C3'-O3'	5.07	121.81	113.70
36	m	54	U	C4'-C3'-O3'	5.05	123.11	113.00
31	d	132	ARG	NE-CZ-NH1	5.02	122.81	120.30
57	AQ	63	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
57	AQ	202	TYR	Peptide
58	AR	3	SER	Peptide
58	AR	5	PHE	Peptide
63	AW	250	GLN	Peptide
69	BC	12	TYR	Peptide
70	BD	171	GLY	Peptide
86	BT	76	SER	Peptide
9	H	143	ARG	Peptide
10	I	88	VAL	Peptide
10	I	89	ARG	Peptide
21	T	196	ARG	Peptide
21	T	197	ASN	Peptide
22	U	64	VAL	Peptide
23	V	33	PRO	Peptide
23	V	82	VAL	Peptide
23	V	84	HIS	Peptide
32	e	5	ARG	Peptide
32	e	6	ALA	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	2	37645	0	18938	393	0
2	A	1734	0	1817	17	0
3	B	1609	0	1675	18	0
4	C	813	0	800	9	0
5	D	877	0	883	8	0
6	E	977	0	1002	8	0
7	F	1105	0	1166	14	0
8	G	746	0	781	9	0
9	H	1192	0	1220	49	0
10	I	1112	0	1124	9	0
11	J	855	0	917	8	0
12	K	563	0	603	11	0
13	L	497	0	535	2	0
14	M	442	0	428	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	N	397	0	399	2	0
16	O	2436	0	2386	12	0
17	P	1577	0	1567	3	0
18	Q	1709	0	1784	10	0
19	R	1671	0	1768	12	0
20	S	2068	0	2154	12	0
21	T	1799	0	1879	41	0
22	U	1481	0	1572	16	0
23	V	1489	0	1525	33	0
24	W	1434	0	1511	7	0
25	X	1213	0	1257	5	0
26	Y	1192	0	1255	8	0
27	Z	891	0	883	4	0
28	a	684	0	672	0	0
29	b	1021	0	1060	0	0
30	c	1121	0	1196	0	0
31	d	1060	0	1123	0	0
32	e	769	0	818	0	0
33	f	610	0	633	0	0
34	g	473	0	518	0	0
35	l	692	0	347	0	0
36	m	1611	0	817	0	0
37	n	1644	0	831	0	0
38	h	8814	0	8710	0	0
39	i	9827	0	8617	0	0
40	j	2933	0	2695	0	0
40	k	2919	0	2682	0	0
41	AA	1804	0	1877	14	0
42	AB	1003	0	1048	10	0
43	AC	771	0	849	5	0
44	AD	1518	0	1587	13	0
45	AE	699	0	638	37	0
46	AF	681	0	684	8	0
47	AG	1353	0	1381	30	0
48	AH	964	0	1025	4	0
49	AI	612	0	682	1	0
50	AJ	1543	0	1608	9	0
51	AK	993	0	1081	5	0
52	AL	436	0	475	1	0
53	AM	1053	0	1149	4	0
54	AN	1092	0	1155	9	0
55	AO	417	0	459	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AP	847	0	918	24	0
57	AQ	1720	0	1779	14	0
58	AR	1173	0	1215	13	0
59	AS	233	0	282	57	0
60	AT	694	0	738	11	0
61	AU	1555	0	1659	3	0
62	AV	462	0	491	2	0
63	AW	1914	0	1980	53	0
64	AX	1420	0	1437	14	0
65	AY	742	0	797	4	0
66	AZ	1050	0	245	1	0
67	BA	3075	0	3142	33	0
68	BB	1441	0	1543	18	0
69	BC	876	0	912	8	0
70	BD	1770	0	1808	6	0
71	BE	2748	0	2859	19	0
72	BF	1521	0	1611	72	0
73	BG	1020	0	1090	5	0
74	BH	1445	0	1487	7	0
75	BI	2375	0	2325	15	0
76	BJ	1276	0	1323	5	0
77	BK	850	0	880	8	0
78	BL	796	0	812	2	0
79	BM	1239	0	1326	12	0
80	BN	880	0	945	5	0
81	BO	1784	0	1862	12	0
82	BP	969	0	1078	5	0
83	BQ	67695	0	34019	435	0
84	BR	2579	0	1304	16	0
85	BS	3352	0	1695	19	0
86	BT	1143	0	1102	96	0
All	All	229285	0	172910	1453	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 5.

All (1453) 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)
83:BQ:2418:G:C2	86:BT:73:LEU:HD11	1.29	1.63
1:2:1645:G:C5'	83:BQ:2255:A:N6	1.76	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:815:G:N3	72:BF:162:ARG:CZ	1.82	1.42
56:AP:27:GLN:HE22	86:BT:14:GLY:N	1.03	1.40
1:2:987:G:C6	63:AW:249:SER:HA	1.58	1.38
1:2:55:A:C2	1:2:403:G:N3	1.91	1.37
1:2:55:A:H2	1:2:403:G:C2	1.43	1.36
1:2:813:U:C1'	72:BF:163:ARG:NH1	1.71	1.36
1:2:1645:G:H5''	83:BQ:2255:A:N6	1.03	1.34
1:2:815:G:N3	72:BF:162:ARG:NH2	1.74	1.33
1:2:1724:U:H4'	45:AE:47:ARG:NH2	1.43	1.33
1:2:815:G:C2	72:BF:162:ARG:NH2	1.97	1.31
9:H:16:ARG:NH1	47:AG:110:ILE:C	1.84	1.31
9:H:16:ARG:HH12	47:AG:111:ASP:N	1.29	1.30
1:2:987:G:N1	63:AW:249:SER:HA	1.42	1.30
1:2:987:G:C2	63:AW:249:SER:CA	2.15	1.29
1:2:55:A:C2	1:2:403:G:C2	2.19	1.28
1:2:850:A:OP1	72:BF:165:LYS:NZ	1.65	1.28
21:T:151:ASP:OD2	45:AE:98:PRO:HG3	1.17	1.27
56:AP:27:GLN:NE2	86:BT:14:GLY:N	1.80	1.27
1:2:1779:U:O4	59:AS:12:ARG:NH1	1.66	1.26
83:BQ:2418:G:C2	86:BT:73:LEU:CD1	2.18	1.25
1:2:1735:U:P	42:AB:32:ARG:HH12	1.58	1.25
1:2:987:G:C2	63:AW:249:SER:N	2.05	1.23
86:BT:132:LYS:HB3	86:BT:152:GLU:OE2	1.14	1.23
1:2:1595:U:O4	1:2:1600:A:N1	1.71	1.23
21:T:9:VAL:CG1	45:AE:78:ALA:HB3	1.70	1.22
1:2:55:A:H2	1:2:403:G:N3	1.26	1.21
1:2:1080:U:O4	1:2:1091:A:N1	1.71	1.21
1:2:813:U:C2'	72:BF:163:ARG:NH1	2.03	1.20
21:T:22:HIS:NE2	67:BA:298:PHE:CD1	2.10	1.20
1:2:1784:C:C5	59:AS:5:TRP:CZ2	2.10	1.19
1:2:1118:G:P	59:AS:21:ARG:HH12	1.67	1.17
1:2:1724:U:C4'	45:AE:47:ARG:HH22	1.58	1.16
83:BQ:2433:U:O4	83:BQ:2595:A:N1	1.79	1.16
1:2:42:G:C2'	1:2:430:G:O6	1.93	1.16
1:2:1642:G:H4'	59:AS:1:MET:SD	1.85	1.15
1:2:815:G:C1'	72:BF:162:ARG:NH1	2.07	1.14
83:BQ:1554:U:O4	83:BQ:1559:A:N1	1.79	1.14
1:2:1735:U:OP1	42:AB:32:ARG:NH1	1.80	1.13
1:2:42:G:H2'	1:2:430:G:O6	0.97	1.13
1:2:816:G:N7	72:BF:170:ARG:NH2	1.96	1.12
21:T:130:PRO:HA	45:AE:83:THR:CB	1.80	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:120:ARG:HE	83:BQ:1025:A:H1'	1.16	1.09
86:BT:132:LYS:CB	86:BT:152:GLU:OE2	1.91	1.09
22:U:39:ARG:CZ	72:BF:181:ARG:O	1.99	1.09
21:T:131:LYS:O	45:AE:83:THR:O	1.70	1.08
21:T:9:VAL:HG11	45:AE:78:ALA:CB	1.84	1.07
1:2:971:A:H61	83:BQ:846:A:N6	1.51	1.07
83:BQ:2418:G:N2	86:BT:73:LEU:HD11	1.67	1.07
1:2:1057:U:O4	1:2:1062:A:N1	1.88	1.07
21:T:22:HIS:NE2	67:BA:298:PHE:HD1	1.49	1.06
83:BQ:829:U:N3	83:BQ:895:A:N6	2.03	1.06
1:2:1757:G:O2'	83:BQ:2255:A:O2'	1.73	1.06
1:2:815:G:H1'	72:BF:162:ARG:NH1	1.69	1.05
1:2:1585:U:C4	1:2:1611:A:N1	2.24	1.05
21:T:130:PRO:CA	45:AE:83:THR:CB	2.34	1.04
1:2:1784:C:H5	59:AS:5:TRP:CZ2	1.42	1.04
56:AP:64:THR:O	86:BT:17:ALA:CB	2.06	1.04
83:BQ:1554:U:C4	83:BQ:1559:A:N1	2.26	1.04
1:2:814:A:C2	72:BF:170:ARG:NH1	2.26	1.04
1:2:42:G:H2'	1:2:430:G:C6	1.93	1.03
1:2:850:A:H5''	72:BF:165:LYS:HZ1	1.20	1.03
1:2:1735:U:P	42:AB:32:ARG:NH1	2.31	1.03
1:2:987:G:C2	63:AW:249:SER:HA	1.83	1.03
1:2:850:A:H5''	72:BF:165:LYS:NZ	1.72	1.03
1:2:813:U:H1'	72:BF:163:ARG:NH1	1.68	1.03
1:2:971:A:N6	83:BQ:846:A:N6	2.04	1.03
83:BQ:3047:U:C4	83:BQ:3094:A:N1	2.28	1.00
83:BQ:2418:G:N1	86:BT:73:LEU:CD1	2.24	1.00
1:2:1645:G:C5'	83:BQ:2255:A:C6	2.44	0.99
21:T:151:ASP:OD2	45:AE:98:PRO:CG	2.09	0.99
1:2:913:G:C6	83:BQ:2207:A:O2'	2.13	0.99
9:H:16:ARG:NH1	47:AG:111:ASP:N	2.06	0.99
1:2:1080:U:C4	1:2:1091:A:N1	2.30	0.98
83:BQ:1188:U:N3	83:BQ:1317:A:N6	2.10	0.98
1:2:816:G:O6	72:BF:170:ARG:NH2	1.95	0.98
83:BQ:2612:U:N3	83:BQ:2804:A:N6	2.10	0.98
1:2:1724:U:H4'	45:AE:47:ARG:HH22	0.91	0.98
83:BQ:2966:G:O6	86:BT:56:LYS:NZ	1.97	0.98
1:2:1038:U:O4	1:2:1092:A:N1	1.96	0.97
1:2:816:G:C6	72:BF:170:ARG:NH2	2.32	0.97
1:2:987:G:N2	63:AW:248:GLY:C	2.18	0.97
1:2:55:A:N3	1:2:403:G:N2	2.13	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:814:A:N3	72:BF:170:ARG:NH1	2.12	0.96
1:2:815:G:C4	72:BF:162:ARG:CZ	2.48	0.95
21:T:22:HIS:NE2	67:BA:298:PHE:CE1	2.33	0.95
1:2:913:G:C5	83:BQ:2207:A:O2'	2.17	0.95
1:2:1585:U:O4	1:2:1611:A:N1	1.99	0.95
21:T:131:LYS:HE2	45:AE:81:PRO:HA	1.47	0.95
56:AP:27:GLN:HE22	86:BT:13:ALA:C	1.69	0.95
56:AP:64:THR:O	86:BT:17:ALA:HB3	1.64	0.94
1:2:987:G:N2	63:AW:249:SER:N	2.16	0.94
1:2:1012:U:H4'	63:AW:247:ARG:HB3	1.48	0.94
83:BQ:2612:U:N3	83:BQ:2804:A:C6	2.36	0.94
1:2:987:G:H2'	63:AW:249:SER:CB	1.98	0.94
1:2:816:G:C5	72:BF:170:ARG:NH2	2.30	0.93
9:H:16:ARG:HH11	47:AG:110:ILE:C	1.69	0.93
1:2:815:G:C1'	72:BF:162:ARG:HH11	1.80	0.93
1:2:1645:G:H5''	83:BQ:2255:A:H62	1.12	0.92
1:2:1080:U:O4	1:2:1091:A:C2	2.23	0.92
1:2:1783:C:C5	59:AS:5:TRP:CD2	2.58	0.92
1:2:1645:G:H5''	83:BQ:2255:A:H61	1.10	0.92
56:AP:27:GLN:HE22	86:BT:14:GLY:H	1.11	0.92
83:BQ:1188:U:O4	83:BQ:1317:A:N1	2.02	0.92
1:2:1118:G:OP1	59:AS:21:ARG:NH1	2.03	0.91
1:2:850:A:C5'	72:BF:165:LYS:HZ1	1.84	0.91
83:BQ:2418:G:N1	86:BT:73:LEU:HD11	1.83	0.91
1:2:1311:U:HO2'	8:G:2:GLY:N	1.69	0.91
83:BQ:3047:U:C5	83:BQ:3094:A:C2	2.58	0.91
9:H:16:ARG:NH1	47:AG:110:ILE:HG13	1.86	0.91
1:2:813:U:H2'	72:BF:163:ARG:NH1	1.82	0.90
1:2:55:A:O2'	1:2:56:U:OP1	1.90	0.90
21:T:131:LYS:N	45:AE:83:THR:CB	2.36	0.89
21:T:9:VAL:HG11	45:AE:78:ALA:HB3	0.92	0.89
9:H:120:ARG:NE	83:BQ:1025:A:H1'	1.88	0.88
21:T:131:LYS:CE	45:AE:81:PRO:HA	2.03	0.88
56:AP:27:GLN:NE2	86:BT:14:GLY:CA	2.36	0.88
9:H:16:ARG:HH12	47:AG:110:ILE:C	1.57	0.88
1:2:1772:C:H3'	59:AS:2:ARG:HH21	1.39	0.88
1:2:1185:U:O2'	1:2:1186:U:OP2	1.92	0.88
1:2:987:G:N1	63:AW:249:SER:CA	2.23	0.88
1:2:815:G:C4	72:BF:162:ARG:NH2	2.42	0.87
1:2:1038:U:C4	1:2:1092:A:N1	2.42	0.87
1:2:1126:G:C5'	59:AS:11:ARG:NH1	2.37	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1783:C:H5	59:AS:5:TRP:CG	1.92	0.87
1:2:851:U:P	72:BF:165:LYS:HE3	2.15	0.87
1:2:1757:G:HO2'	83:BQ:2255:A:HO2'	1.09	0.86
3:B:123:VAL:HG21	12:K:100:ILE:HD11	1.54	0.86
1:2:813:U:C2'	72:BF:163:ARG:HH11	1.83	0.86
1:2:1783:C:C5	59:AS:5:TRP:CG	2.63	0.86
1:2:987:G:C6	63:AW:249:SER:CA	2.53	0.86
1:2:1126:G:H5'	59:AS:11:ARG:NH1	1.91	0.86
1:2:1660:A:H5'	42:AB:67:PRO:HG2	1.58	0.85
83:BQ:2418:G:N2	86:BT:73:LEU:HD21	1.91	0.85
1:2:1113:A:H5''	59:AS:6:ARG:HH22	1.40	0.85
1:2:971:A:C6	83:BQ:846:A:N6	2.44	0.85
83:BQ:816:A:O2'	83:BQ:819:U:O4	1.94	0.85
56:AP:64:THR:O	86:BT:17:ALA:HB2	1.75	0.84
1:2:1126:G:H4'	59:AS:11:ARG:HH12	1.40	0.84
1:2:1118:G:P	59:AS:21:ARG:NH1	2.51	0.84
83:BQ:2612:U:O2	83:BQ:2804:A:N7	2.11	0.83
1:2:1595:U:C4	1:2:1600:A:N1	2.46	0.83
1:2:1642:G:C4'	59:AS:1:MET:SD	2.65	0.83
1:2:987:G:H2'	63:AW:249:SER:HB3	1.59	0.83
1:2:1780:G:H1'	83:BQ:2262:A:O3'	1.79	0.83
21:T:22:HIS:CD2	67:BA:298:PHE:CD1	2.66	0.83
21:T:22:HIS:CD2	67:BA:298:PHE:CE1	2.67	0.83
67:BA:305:ILE:HD11	67:BA:317:ILE:HG21	1.60	0.82
1:2:1645:G:H5'	83:BQ:2255:A:N6	1.94	0.82
83:BQ:2612:U:C4	83:BQ:2804:A:N6	2.47	0.82
1:2:815:G:H1'	72:BF:162:ARG:HH11	1.37	0.82
22:U:39:ARG:NH2	72:BF:181:ARG:O	2.10	0.82
23:V:162:ALA:HA	83:BQ:3353:G:OP2	1.80	0.82
1:2:55:A:H2	1:2:403:G:C4	1.98	0.82
9:H:16:ARG:HH11	47:AG:110:ILE:CB	1.94	0.81
21:T:130:PRO:C	45:AE:83:THR:CB	2.48	0.81
26:Y:22:ALA:HB1	26:Y:23:PRO:HA	1.62	0.81
3:B:94:THR:HG22	3:B:114:ILE:HG13	1.63	0.81
56:AP:27:GLN:OE1	86:BT:12:ASP:O	1.99	0.80
83:BQ:1554:U:O4	83:BQ:1559:A:C2	2.35	0.80
4:C:11:ILE:HD11	4:C:42:VAL:HG22	1.63	0.80
9:H:120:ARG:HE	83:BQ:1025:A:C1'	1.95	0.80
83:BQ:2418:G:N1	86:BT:73:LEU:HD12	1.95	0.79
1:2:1724:U:H4'	45:AE:47:ARG:CZ	2.11	0.79
1:2:853:G:N7	72:BF:173:ARG:NH2	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1645:G:C4'	83:BQ:2255:A:C6	2.66	0.79
21:T:131:LYS:CD	45:AE:81:PRO:HA	2.12	0.79
1:2:1113:A:H5''	59:AS:6:ARG:NH2	1.96	0.78
1:2:1783:C:N4	59:AS:5:TRP:CE3	2.52	0.78
1:2:55:A:C2	1:2:403:G:C4	2.72	0.78
9:H:16:ARG:HH11	47:AG:110:ILE:HB	1.49	0.78
1:2:815:G:N9	72:BF:162:ARG:NH1	2.32	0.78
1:2:1660:A:H5'	42:AB:67:PRO:CG	2.13	0.78
21:T:151:ASP:CG	45:AE:98:PRO:HG3	2.04	0.77
10:I:15:ILE:HG23	10:I:59:ALA:HB3	1.65	0.77
83:BQ:1447:G:HO2'	83:BQ:2355:G:H1	1.31	0.77
1:2:813:U:H2'	72:BF:163:ARG:HH11	1.42	0.77
1:2:987:G:C2	63:AW:248:GLY:C	2.55	0.77
83:BQ:1524:A:O2'	83:BQ:1526:U:OP2	2.02	0.77
1:2:1642:G:C5'	59:AS:1:MET:SD	2.73	0.77
9:H:16:ARG:NH1	47:AG:110:ILE:CG1	2.48	0.76
1:2:1779:U:O4	59:AS:12:ARG:CZ	2.33	0.76
83:BQ:1084:A:H2'	83:BQ:1085:A:C8	2.21	0.76
83:BQ:2273:G:O2'	83:BQ:2274:U:OP2	2.04	0.76
58:AR:138:ILE:HD13	58:AR:145:VAL:HG22	1.66	0.75
1:2:815:G:C4	72:BF:162:ARG:NH1	2.55	0.75
1:2:1641:C:H4'	59:AS:1:MET:H2	1.52	0.75
86:BT:90:TYR:CE1	86:BT:104:ASN:OD1	2.39	0.75
1:2:815:G:N2	72:BF:162:ARG:HH21	1.85	0.75
1:2:1114:G:OP1	59:AS:6:ARG:NH1	2.19	0.74
83:BQ:2806:U:OP1	86:BT:49:THR:OG1	2.03	0.74
6:E:108:ARG:NH2	83:BQ:1025:A:C2	2.55	0.74
56:AP:64:THR:HG21	86:BT:19:TYR:HB3	1.69	0.74
1:2:1656:U:HO2'	83:BQ:2292:U:HO2'	1.23	0.74
1:2:1038:U:H3	1:2:1092:A:N6	1.85	0.74
83:BQ:12:A:H2'	83:BQ:13:A:C8	2.22	0.74
1:2:300:A:H2'	1:2:301:A:C8	2.23	0.73
9:H:16:ARG:HH12	47:AG:111:ASP:CA	2.01	0.73
9:H:16:ARG:NH1	47:AG:110:ILE:CB	2.50	0.73
1:2:55:A:C2	1:2:403:G:N2	2.53	0.73
1:2:853:G:C8	72:BF:173:ARG:NH2	2.57	0.73
86:BT:133:ASP:O	86:BT:152:GLU:HG3	1.88	0.73
23:V:81:VAL:O	23:V:94:ASN:HA	1.89	0.73
1:2:850:A:C5'	72:BF:165:LYS:NZ	2.47	0.73
1:2:1750:A:P	59:AS:13:LEU:HD11	2.29	0.73
1:2:1645:G:C4'	83:BQ:2255:A:N6	2.50	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1641:C:H4'	59:AS:1:MET:N	2.04	0.73
63:AW:113:VAL:HG12	63:AW:166:ILE:HD13	1.71	0.72
1:2:1775:U:O4	59:AS:4:LYS:HE2	1.88	0.72
1:2:1118:G:OP2	59:AS:21:ARG:NH2	2.22	0.72
21:T:131:LYS:HE2	45:AE:81:PRO:CA	2.19	0.72
9:H:19:ASN:HA	47:AG:111:ASP:OD2	1.89	0.72
1:2:1080:U:O4	1:2:1091:A:C6	2.42	0.72
56:AP:41:ARG:NH1	83:BQ:284:A:OP2	2.23	0.72
1:2:813:U:C5	72:BF:163:ARG:CD	2.72	0.72
1:2:851:U:C5'	72:BF:172:ARG:HH22	2.03	0.72
86:BT:43:ASP:HB2	86:BT:60:VAL:HB	1.72	0.72
1:2:987:G:C5	63:AW:249:SER:HA	1.94	0.72
1:2:815:G:N3	72:BF:162:ARG:NE	2.37	0.71
1:2:1481:C:OP2	10:I:4:VAL:HA	1.91	0.71
9:H:16:ARG:NH1	47:AG:110:ILE:O	2.23	0.71
1:2:1734:U:OP1	42:AB:32:ARG:NH2	2.24	0.71
9:H:118:LYS:O	83:BQ:1025:A:C2	2.43	0.71
7:F:44:LEU:HD11	7:F:75:VAL:HG22	1.73	0.71
1:2:1773:C:OP2	59:AS:4:LYS:HB2	1.91	0.71
1:2:1012:U:H4'	63:AW:247:ARG:CB	2.21	0.71
1:2:913:G:N1	83:BQ:2207:A:H1'	2.06	0.71
41:AA:160:ILE:HG22	41:AA:164:VAL:HG13	1.73	0.71
83:BQ:3152:U:O2	83:BQ:3152:U:H2'	1.89	0.71
23:V:91:VAL:CG2	23:V:95:THR:HG21	2.20	0.71
1:2:1038:U:N3	1:2:1092:A:N6	2.38	0.70
1:2:815:G:H1'	72:BF:162:ARG:CZ	2.21	0.70
1:2:851:U:OP1	72:BF:165:LYS:HE3	1.89	0.70
1:2:851:U:OP2	72:BF:165:LYS:HE3	1.90	0.70
8:G:20:TYR:CG	8:G:38:ILE:HD11	2.25	0.70
1:2:1774:G:N7	59:AS:4:LYS:NZ	2.39	0.70
21:T:131:LYS:HD3	45:AE:81:PRO:N	2.07	0.70
86:BT:111:ASP:O	86:BT:112:ASP:O	2.09	0.70
41:AA:152:LEU:HD23	41:AA:178:ALA:HB3	1.73	0.70
1:2:853:G:P	72:BF:176:ARG:HE	2.14	0.70
1:2:1116:A:OP2	59:AS:14:LYS:NZ	2.25	0.69
1:2:987:G:C2'	63:AW:249:SER:CB	2.71	0.69
74:BH:77:VAL:HG13	74:BH:126:VAL:HG22	1.73	0.69
1:2:1645:G:H5'	83:BQ:2255:A:C6	2.26	0.69
19:R:53:ILE:HD11	19:R:73:LEU:HB2	1.74	0.69
67:BA:215:ILE:HG21	67:BA:282:ILE:HD11	1.74	0.69
21:T:151:ASP:OD1	45:AE:98:PRO:HB3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1724:U:C4'	45:AE:47:ARG:NH2	2.31	0.69
67:BA:46:PHE:CE2	67:BA:81:THR:HG23	2.28	0.68
1:2:1643:U:H5'	59:AS:9:ARG:HH12	1.58	0.68
86:BT:101:SER:HA	86:BT:111:ASP:HA	1.75	0.68
56:AP:27:GLN:NE2	86:BT:14:GLY:HA3	2.07	0.68
2:A:208:ILE:HD12	8:G:16:LEU:HD21	1.76	0.68
1:2:330:G:H2'	1:2:331:A:C8	2.29	0.68
71:BE:313:LEU:HD21	83:BQ:505:G:H4'	1.75	0.68
1:2:55:A:N3	1:2:403:G:C2	2.54	0.68
86:BT:33:VAL:HG23	86:BT:83:PRO:HD3	1.75	0.68
1:2:815:G:O4'	72:BF:162:ARG:NH1	2.27	0.68
1:2:697:C:O2	1:2:697:C:H2'	1.94	0.68
1:2:850:A:P	72:BF:165:LYS:NZ	2.67	0.68
83:BQ:2418:G:N2	86:BT:73:LEU:CG	2.57	0.67
83:BQ:800:G:N3	83:BQ:800:G:H2'	2.09	0.67
83:BQ:1188:U:C4	83:BQ:1317:A:N1	2.61	0.67
83:BQ:3047:U:O4	83:BQ:3094:A:N1	2.27	0.67
83:BQ:1898:G:O6	83:BQ:1899:G:N2	2.27	0.67
83:BQ:2418:G:N2	86:BT:73:LEU:CD1	2.41	0.67
10:I:18:TYR:CD2	10:I:59:ALA:HB2	2.30	0.67
1:2:1642:G:H5'	59:AS:1:MET:SD	2.33	0.67
1:2:1080:U:N3	1:2:1091:A:N6	2.43	0.67
1:2:55:A:O2'	1:2:56:U:P	2.51	0.67
1:2:851:U:H5'	72:BF:172:ARG:HH22	1.60	0.67
83:BQ:1188:U:C2	83:BQ:1317:A:N6	2.62	0.67
56:AP:27:GLN:NE2	86:BT:14:GLY:H	1.77	0.67
85:BS:145:U:H2'	85:BS:146:U:C6	2.30	0.67
1:2:1595:U:N3	1:2:1600:A:N6	2.42	0.66
18:Q:201:THR:HG21	18:Q:207:LEU:HD22	1.77	0.66
1:2:55:A:N3	1:2:55:A:H2'	2.09	0.66
1:2:987:G:H22	63:AW:248:GLY:C	1.97	0.66
83:BQ:3294:A:H2'	83:BQ:3295:A:O4'	1.96	0.66
16:O:180:ALA:HB3	16:O:190:ALA:HB3	1.78	0.66
1:2:383:G:O2'	1:2:384:G:O5'	2.12	0.66
83:BQ:2418:G:N2	86:BT:73:LEU:CD2	2.59	0.66
83:BQ:430:U:H2'	83:BQ:431:U:O4'	1.95	0.65
1:2:1749:A:O3'	59:AS:13:LEU:HD11	1.96	0.65
1:2:1082:C:N4	1:2:1091:A:N7	2.44	0.65
1:2:1116:A:C5'	59:AS:17:ARG:NH1	2.60	0.65
56:AP:27:GLN:HE21	86:BT:14:GLY:HA3	1.59	0.65
86:BT:155:ARG:C	86:BT:156:THR:HG23	2.16	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:559:A:H2'	83:BQ:560:G:O4'	1.97	0.65
1:2:1783:C:OP2	59:AS:1:MET:HB2	1.97	0.65
1:2:987:G:C5	63:AW:249:SER:CA	2.59	0.65
1:2:1584:G:N2	1:2:1611:A:OP2	2.30	0.64
60:AT:79:VAL:HG22	63:AW:112:ILE:HD13	1.79	0.64
1:2:1540:G:H2'	1:2:1541:G:C4	2.32	0.64
48:AH:103:TYR:HB3	48:AH:135:ILE:HD11	1.78	0.64
19:R:180:ALA:HB2	19:R:198:THR:HG21	1.79	0.64
21:T:131:LYS:HD3	45:AE:81:PRO:HA	1.78	0.64
1:2:1080:U:H3	1:2:1091:A:N6	1.95	0.64
83:BQ:3047:U:C4	83:BQ:3094:A:C2	2.82	0.64
83:BQ:3152:U:O2'	83:BQ:3294:A:C8	2.47	0.64
1:2:340:U:C2	23:V:86:SER:HB3	2.33	0.64
83:BQ:829:U:C2	83:BQ:895:A:N6	2.65	0.64
1:2:331:A:H2'	1:2:332:U:O4'	1.98	0.64
67:BA:8:ALA:HB1	67:BA:9:PRO:HD2	1.78	0.64
83:BQ:708:G:O2'	83:BQ:710:A:N7	2.24	0.64
1:2:1645:G:O4'	83:BQ:2255:A:C5	2.51	0.64
1:2:1645:G:O4'	83:BQ:2255:A:C6	2.51	0.63
86:BT:46:THR:HG22	86:BT:57:VAL:HG22	1.80	0.63
26:Y:22:ALA:HB1	26:Y:23:PRO:CA	2.28	0.63
21:T:131:LYS:HD3	45:AE:81:PRO:CA	2.28	0.63
54:AN:51:LEU:HD12	54:AN:65:ARG:HD2	1.79	0.63
1:2:1126:G:C4'	59:AS:11:ARG:HH12	2.11	0.63
83:BQ:2960:C:H2'	83:BQ:2961:G:C8	2.33	0.63
2:A:105:MET:HG2	2:A:122:VAL:HG21	1.80	0.63
83:BQ:1554:U:N3	83:BQ:1559:A:N6	2.46	0.63
86:BT:100:LEU:O	86:BT:111:ASP:O	2.16	0.63
86:BT:64:ILE:HG21	86:BT:139:ILE:HD11	1.78	0.63
21:T:9:VAL:HG13	45:AE:78:ALA:O	1.98	0.63
48:AH:105:VAL:HG11	48:AH:126:LEU:HD22	1.80	0.63
81:BO:156:ILE:HD12	81:BO:161:VAL:HG21	1.79	0.63
83:BQ:1188:U:H3	83:BQ:1317:A:N6	1.92	0.63
21:T:131:LYS:CE	45:AE:81:PRO:CA	2.75	0.63
54:AN:25:ILE:HA	54:AN:43:VAL:HG12	1.80	0.62
1:2:1116:A:H5''	59:AS:17:ARG:NH1	2.14	0.62
83:BQ:829:U:H3	83:BQ:895:A:N6	1.81	0.62
83:BQ:1786:G:H2'	83:BQ:1787:A:C8	2.34	0.62
83:BQ:1808:G:O2'	83:BQ:1809:A:OP2	2.11	0.62
86:BT:138:ILE:HG22	86:BT:147:ALA:HA	1.80	0.62
1:2:851:U:C5'	72:BF:172:ARG:NH2	2.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:2333:C:H2'	83:BQ:2334:U:O2	2.00	0.62
86:BT:113:VAL:O	86:BT:115:ALA:N	2.33	0.62
1:2:1645:G:C5'	83:BQ:2255:A:H61	1.76	0.62
1:2:55:A:H2'	1:2:403:G:H21	1.65	0.62
86:BT:109:THR:HG22	86:BT:110:LYS:N	2.13	0.62
83:BQ:3047:U:C5	83:BQ:3048:A:C5	2.88	0.62
83:BQ:1188:U:N3	83:BQ:1317:A:C6	2.68	0.61
16:O:243:LEU:HD23	16:O:254:ALA:HB2	1.80	0.61
1:2:1642:G:O3'	59:AS:9:ARG:NH2	2.33	0.61
1:2:987:G:N2	63:AW:248:GLY:CA	2.63	0.61
22:U:12:ALA:HB3	22:U:13:PRO:HD3	1.82	0.61
64:AX:36:ILE:CD1	64:AX:95:LEU:HD11	2.31	0.61
9:H:16:ARG:NH1	47:AG:110:ILE:CA	2.63	0.61
57:AQ:58:GLY:HA3	57:AQ:142:ILE:HD11	1.81	0.61
3:B:96:SER:HB3	3:B:176:THR:HG21	1.83	0.61
22:U:39:ARG:NH2	72:BF:181:ARG:C	2.54	0.61
83:BQ:2315:G:C2	83:BQ:2316:G:N7	2.69	0.61
12:K:60:VAL:HG11	12:K:65:LEU:HD11	4.18	0.61
83:BQ:11:A:O4'	83:BQ:1558:A:N6	2.34	0.61
83:BQ:2433:U:C4	83:BQ:2595:A:N1	2.68	0.61
1:2:1080:U:C4	1:2:1091:A:C6	2.89	0.60
83:BQ:1317:A:O2'	83:BQ:1318:A:H2'	2.01	0.60
1:2:1595:U:O4	1:2:1600:A:C2	2.53	0.60
1:2:1642:G:H5'	59:AS:1:MET:HG2	1.82	0.60
83:BQ:1073:U:H2'	83:BQ:1074:U:C6	2.36	0.60
9:H:16:ARG:HH11	47:AG:110:ILE:CA	2.13	0.60
44:AD:43:VAL:HG12	44:AD:57:VAL:HG23	1.82	0.60
53:AM:17:VAL:HG21	53:AM:74:ARG:HB3	1.83	0.60
83:BQ:2273:G:HO2'	83:BQ:2311:G:H1	1.40	0.60
86:BT:88:ASN:HD22	86:BT:138:ILE:HD11	1.66	0.60
1:2:1541:G:C4	1:2:1570:A:N6	2.70	0.60
1:2:432:G:C6	1:2:433:C:C4	2.89	0.60
83:BQ:2683:U:H2'	83:BQ:2684:C:C6	2.36	0.60
23:V:78:ILE:HD12	23:V:96:LEU:HD13	1.84	0.60
77:BK:15:SER:HA	77:BK:94:PHE:CE1	2.37	0.59
86:BT:94:ASP:O	86:BT:101:SER:OG	2.14	0.59
1:2:55:A:N7	1:2:426:G:N1	2.50	0.59
3:B:58:LEU:HD12	3:B:138:THR:HG22	1.84	0.59
68:BB:92:ARG:NH1	83:BQ:784:A:O2'	2.35	0.59
83:BQ:829:U:N3	83:BQ:895:A:C6	2.60	0.59
5:D:57:ALA:HB2	5:D:122:VAL:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:81:GLY:N	10:I:96:ALA:HB2	2.17	0.59
1:2:1642:G:H5'	59:AS:1:MET:CG	2.32	0.59
1:2:42:G:HO2'	1:2:430:G:H1	1.49	0.59
79:BM:169:ASP:HB3	79:BM:174:LEU:HD11	1.85	0.59
83:BQ:2333:C:C2	83:BQ:2334:U:O2	2.56	0.59
72:BF:99:LEU:HD21	72:BF:103:ARG:CZ	2.33	0.59
86:BT:155:ARG:O	86:BT:156:THR:HG23	2.02	0.59
1:2:431:C:C4	1:2:432:G:C6	2.91	0.58
63:AW:15:ILE:HD12	63:AW:194:ASN:HD22	1.68	0.58
83:BQ:2416:U:H3	83:BQ:2804:A:H2	1.50	0.58
1:2:1057:U:C4	1:2:1062:A:N1	2.68	0.58
1:2:384:G:H2'	1:2:385:A:H4'	1.84	0.58
1:2:987:G:H2'	63:AW:249:SER:HB2	1.83	0.58
67:BA:256:HIS:HA	67:BA:257:PRO:C	2.24	0.58
83:BQ:1696:A:H2'	83:BQ:1697:A:C8	2.38	0.58
83:BQ:2199:G:O2'	86:BT:71:GLU:OE2	2.18	0.58
11:J:34:LEU:HD21	11:J:89:ARG:HG3	1.84	0.58
86:BT:23:CYS:SG	86:BT:80:MET:N	2.76	0.58
19:R:82:ASN:HB2	19:R:207:LEU:HD12	1.85	0.58
86:BT:63:ASP:HB2	86:BT:67:GLY:H	1.68	0.58
1:2:813:U:C5	72:BF:163:ARG:HD2	2.37	0.58
65:AY:22:LYS:HB3	65:AY:93:LEU:HD11	1.84	0.58
75:BI:236:LEU:HA	75:BI:239:ILE:HD12	1.85	0.58
83:BQ:632:G:H2'	83:BQ:633:C:O4'	2.03	0.58
1:2:425:A:P	1:2:425:A:H3'	2.44	0.58
57:AQ:2:GLY:N	83:BQ:117:U:OP2	2.37	0.57
1:2:851:U:OP1	72:BF:165:LYS:CD	2.52	0.57
83:BQ:550:A:H2'	83:BQ:551:A:C8	2.39	0.57
23:V:81:VAL:HG13	23:V:82:VAL:N	2.19	0.57
1:2:967:A:H2'	1:2:968:U:O4'	2.04	0.57
46:AF:19:CYS:SG	46:AF:22:CYS:N	2.75	0.57
50:AJ:166:ALA:HB1	58:AR:147:LEU:HD11	1.86	0.57
75:BI:104:LEU:HD11	75:BI:108:ARG:NH2	2.18	0.57
75:BI:277:LEU:HD23	75:BI:282:ARG:HG3	1.86	0.57
86:BT:89:GLU:HA	86:BT:137:THR:HG22	1.85	0.57
19:R:45:VAL:HG21	19:R:68:ILE:HG23	1.87	0.57
26:Y:108:ASP:OD2	26:Y:111:ALA:HB3	2.04	0.57
1:2:1585:U:O4	1:2:1611:A:C6	2.57	0.57
1:2:987:G:N2	63:AW:248:GLY:HA2	2.20	0.57
67:BA:266:ARG:NH2	83:BQ:2392:C:O2'	2.37	0.57
83:BQ:628:A:H2'	83:BQ:629:U:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:3047:U:C4	83:BQ:3048:A:C6	2.92	0.57
1:2:697:C:C2'	1:2:697:C:O2	2.53	0.57
69:BC:36:ILE:CD1	69:BC:59:ILE:HD11	2.35	0.57
83:BQ:107:A:O2'	83:BQ:324:A:N3	2.32	0.57
9:H:120:ARG:NE	83:BQ:1025:A:N3	2.53	0.57
1:2:1474:G:H2'	1:2:1475:A:C8	2.40	0.57
85:BS:145:U:H2'	85:BS:146:U:O4'	2.04	0.57
56:AP:64:THR:CG2	86:BT:19:TYR:HB3	2.33	0.57
47:AG:59:ILE:HG21	47:AG:65:ILE:HD12	1.86	0.56
83:BQ:2186:U:H2'	83:BQ:2187:G:O4'	2.05	0.56
83:BQ:316:U:HO2'	83:BQ:317:A:P	2.27	0.56
9:H:50:ALA:HB2	9:H:72:ILE:HD12	1.87	0.56
77:BK:49:ILE:HD11	77:BK:71:VAL:HG23	1.86	0.56
43:AC:26:ILE:HD13	83:BQ:157:A:C8	2.40	0.56
1:2:815:G:H1'	72:BF:162:ARG:HD2	1.85	0.56
9:H:14:ILE:CD1	47:AG:118:PRO:HB3	2.35	0.56
21:T:131:LYS:H	45:AE:83:THR:CB	2.14	0.56
21:T:9:VAL:CG1	45:AE:78:ALA:CB	2.62	0.56
1:2:1542:G:N2	1:2:1568:C:O2'	2.39	0.56
83:BQ:1554:U:O4	83:BQ:1559:A:C6	2.57	0.56
56:AP:64:THR:HG22	86:BT:19:TYR:HA	1.86	0.56
19:R:38:VAL:HG13	19:R:39:THR:HG23	1.87	0.56
1:2:15:U:H2'	1:2:16:G:O4'	2.04	0.56
1:2:1773:C:OP1	59:AS:3:ALA:HB3	2.05	0.56
3:B:90:ILE:O	3:B:94:THR:HG23	2.05	0.56
9:H:143:ARG:HB3	9:H:144:ARG:HB2	1.88	0.56
26:Y:22:ALA:CB	26:Y:23:PRO:HA	2.35	0.56
68:BB:4:ASP:HB2	81:BO:92:ILE:HD13	1.86	0.56
83:BQ:2612:U:O4	83:BQ:2805:G:O6	2.23	0.56
44:AD:4:ILE:HD12	74:BH:143:PHE:CE1	2.40	0.56
77:BK:102:LEU:HD11	79:BM:165:LEU:HD11	1.88	0.56
1:2:1779:U:O4	59:AS:12:ARG:NH2	2.39	0.56
54:AN:54:THR:HG22	54:AN:57:HIS:CD2	2.41	0.56
84:BR:67:G:H2'	84:BR:68:C:O4'	2.05	0.56
4:C:90:THR:HG22	4:C:93:GLN:HE22	1.70	0.56
1:2:1038:U:O4	1:2:1092:A:C2	2.58	0.55
51:AK:59:VAL:HG12	51:AK:103:LYS:O	2.06	0.55
83:BQ:2328:U:H2'	83:BQ:2329:C:C6	2.42	0.55
83:BQ:2612:U:C2	83:BQ:2804:A:N6	2.74	0.55
5:D:74:LEU:HD11	15:N:106:TYR:HB3	1.88	0.55
16:O:89:LEU:HD21	16:O:110:VAL:HG11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:BD:189:VAL:HG13	70:BD:196:VAL:HG13	1.88	0.55
83:BQ:1241:U:H4'	83:BQ:1242:G:OP1	2.06	0.55
16:O:83:ALA:HA	16:O:89:LEU:HD22	1.88	0.55
21:T:130:PRO:CB	45:AE:83:THR:CB	2.84	0.55
83:BQ:3256:G:H2'	83:BQ:3257:C:O4'	2.06	0.55
1:2:852:C:H5'	72:BF:176:ARG:CD	2.37	0.55
54:AN:23:VAL:HG12	54:AN:45:GLY:HA3	1.89	0.55
86:BT:16:SER:O	86:BT:17:ALA:HB2	2.06	0.55
83:BQ:656:A:H2'	83:BQ:657:A:C8	2.42	0.55
1:2:913:G:N2	83:BQ:2206:G:O2'	2.40	0.55
64:AX:36:ILE:HD12	64:AX:95:LEU:HD11	1.89	0.55
83:BQ:829:U:C4	83:BQ:895:A:N6	2.70	0.55
1:2:174:U:C4	1:2:266:A:N6	2.75	0.55
56:AP:64:THR:HG21	86:BT:19:TYR:CB	2.36	0.55
79:BM:54:TYR:HA	79:BM:65:ILE:HG22	1.89	0.55
83:BQ:1482:A:H2'	83:BQ:1482:A:N3	2.22	0.55
83:BQ:3047:U:O4	83:BQ:3094:A:C6	2.60	0.55
83:BQ:358:G:N2	83:BQ:361:A:OP2	2.39	0.55
2:A:201:ALA:HB3	8:G:42:GLN:NE2	2.22	0.55
83:BQ:1554:U:C4	83:BQ:1559:A:C6	2.94	0.55
83:BQ:2452:G:N3	83:BQ:2452:G:H2'	2.22	0.55
81:BO:163:LEU:O	81:BO:165:ASP:N	2.40	0.54
83:BQ:1724:U:H4'	83:BQ:1725:C:OP1	2.07	0.54
83:BQ:3121:U:C4	83:BQ:3124:G:O6	2.60	0.54
1:2:1672:G:H2'	1:2:1673:G:C8	2.42	0.54
1:2:107:C:OP1	1:2:382:C:O2'	2.24	0.54
1:2:851:U:OP1	72:BF:165:LYS:CE	2.56	0.54
67:BA:57:VAL:HG22	67:BA:73:VAL:HG12	1.89	0.54
1:2:851:U:H5"	72:BF:172:ARG:CZ	2.28	0.54
14:M:21:CYS:SG	14:M:39:CYS:N	2.77	0.54
1:2:1601:G:C4	10:I:88:VAL:HG11	2.43	0.54
41:AA:148:ALA:HA	41:AA:201:THR:HG22	1.90	0.54
42:AB:6:ALA:HB2	42:AB:126:TRP:CZ3	2.42	0.54
67:BA:8:ALA:HB1	67:BA:9:PRO:CD	2.37	0.54
75:BI:52:VAL:HG21	75:BI:65:ILE:HD12	1.90	0.54
1:2:973:A:H5'	83:BQ:848:A:C2	2.43	0.54
6:E:121:ILE:HD12	9:H:122:HIS:CD2	2.43	0.54
77:BK:90:PRO:O	77:BK:92:LYS:N	2.40	0.54
6:E:108:ARG:NH2	83:BQ:1025:A:N1	2.54	0.54
86:BT:109:THR:O	86:BT:110:LYS:HB2	2.07	0.54
1:2:1012:U:C4'	63:AW:247:ARG:HB3	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:2433:U:O4	83:BQ:2595:A:C2	2.58	0.54
83:BQ:2858:U:C4	83:BQ:2859:U:O4	2.61	0.54
77:BK:16:TYR:CD1	77:BK:25:PRO:HA	2.43	0.54
86:BT:94:ASP:HA	86:BT:128:PHE:CZ	2.43	0.54
4:C:11:ILE:HD13	4:C:35:ILE:HD13	1.90	0.54
83:BQ:3202:G:H2'	83:BQ:3203:U:O4'	2.08	0.54
83:BQ:3375:A:O2'	83:BQ:3376:A:O4'	2.21	0.54
1:2:1645:G:C4'	83:BQ:2255:A:C5	2.91	0.54
41:AA:162:LEU:HD23	57:AQ:7:LEU:HD21	1.90	0.54
78:BL:43:VAL:HG11	78:BL:69:ALA:HB1	1.90	0.54
83:BQ:1194:G:H2'	83:BQ:1195:A:C8	2.43	0.54
20:S:181:VAL:HG13	20:S:225:VAL:HG13	1.88	0.54
74:BH:77:VAL:HG11	74:BH:106:LEU:HD13	1.90	0.53
77:BK:13:HIS:ND1	77:BK:93:THR:O	2.42	0.53
86:BT:59:LEU:HB2	86:BT:72:ASP:OD1	2.08	0.53
83:BQ:3152:U:H1'	83:BQ:3294:A:C4	2.43	0.53
83:BQ:2418:G:N3	86:BT:73:LEU:HD11	2.05	0.53
26:Y:26:PHE:CE2	26:Y:66:ILE:HD11	2.42	0.53
83:BQ:3237:U:H2'	83:BQ:3238:G:O4'	2.08	0.53
83:BQ:877:C:H2'	83:BQ:878:G:O4'	2.08	0.53
3:B:123:VAL:HG13	12:K:102:THR:HG22	1.89	0.53
1:2:1535:U:O2'	1:2:1536:G:O5'	2.26	0.53
9:H:16:ARG:NH1	47:AG:111:ASP:CA	2.66	0.53
1:2:1783:C:C4	59:AS:5:TRP:CE3	2.97	0.53
1:2:1544:U:C5	1:2:1545:A:N7	2.77	0.53
55:AO:115:CYS:SG	55:AO:118:THR:HG22	2.49	0.53
83:BQ:3055:U:O2'	83:BQ:3057:U:OP2	2.23	0.53
60:AT:26:VAL:HG22	63:AW:178:PRO:HD2	1.91	0.53
63:AW:5:ILE:HD11	63:AW:7:ASN:OD1	2.09	0.53
83:BQ:2418:G:H22	86:BT:73:LEU:CG	2.22	0.53
1:2:1637:C:H3'	1:2:1638:G:H5'	1.91	0.53
1:2:411:C:H2'	1:2:412:A:H8	1.74	0.53
44:AD:128:VAL:HA	44:AD:157:ASN:HD21	1.73	0.53
58:AR:105:LEU:HD21	58:AR:128:ARG:NH1	2.24	0.53
58:AR:77:LYS:O	58:AR:79:TRP:N	2.42	0.53
83:BQ:1046:A:H2'	83:BQ:1049:C:C5	2.44	0.53
83:BQ:1580:A:O2'	83:BQ:1581:C:O5'	2.26	0.53
1:2:591:A:H2'	1:2:592:A:C8	2.44	0.53
44:AD:23:ARG:NE	83:BQ:3187:A:OP1	2.40	0.53
21:T:131:LYS:HB2	45:AE:81:PRO:HA	1.89	0.53
61:AU:97:ALA:HB1	83:BQ:3172:A:O2'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:52:LEU:HD22	5:D:85:LYS:HE3	1.89	0.53
19:R:180:ALA:HB2	19:R:198:THR:CG2	2.39	0.53
21:T:159:ARG:NE	21:T:172:ALA:HB2	2.24	0.53
1:2:1038:U:H3	1:2:1092:A:H61	1.43	0.52
86:BT:28:LYS:HE3	86:BT:42:VAL:HA	1.91	0.52
63:AW:52:SER:HB3	63:AW:191:LEU:HD23	1.91	0.52
73:BG:82:LEU:HD21	73:BG:117:ILE:HD12	1.92	0.52
79:BM:2:SER:N	83:BQ:1385:C:HO2'	2.07	0.52
83:BQ:531:G:H2'	83:BQ:532:A:C8	2.43	0.52
7:F:31:VAL:HG12	7:F:32:ASN:HD22	1.73	0.52
12:K:59:TYR:CE1	12:K:100:ILE:HD13	2.44	0.52
1:2:1571:C:O2	1:2:1571:C:O4'	2.25	0.52
82:BP:53:CYS:O	82:BP:57:VAL:HG23	2.08	0.52
85:BS:41:A:N6	85:BS:103:G:O2'	2.38	0.52
7:F:32:ASN:HD21	7:F:69:VAL:HG13	1.74	0.52
76:BJ:62:GLY:HA3	76:BJ:76:ILE:HD13	1.90	0.52
9:H:120:ARG:HG3	83:BQ:1025:A:C2	2.44	0.52
1:2:329:G:O2'	23:V:84:HIS:CB	2.58	0.52
76:BJ:92:ARG:NH1	83:BQ:2736:A:OP1	2.42	0.52
21:T:116:LYS:HD2	21:T:125:THR:HG21	1.90	0.52
1:2:1477:G:H2'	1:2:1478:G:O4'	2.09	0.52
1:2:411:C:H2'	1:2:412:A:C8	2.45	0.52
75:BI:146:LEU:HD12	75:BI:163:LEU:HD12	1.91	0.52
63:AW:127:ALA:HB2	63:AW:134:VAL:HG13	1.91	0.52
69:BC:14:ILE:HD12	69:BC:39:PHE:CG	2.44	0.52
1:2:850:A:P	72:BF:165:LYS:HZ1	2.33	0.52
83:BQ:1784:G:H2'	83:BQ:1785:U:O4'	2.09	0.52
9:H:16:ARG:NH1	47:AG:110:ILE:HB	2.20	0.52
68:BB:80:THR:HG22	68:BB:100:THR:HB	1.92	0.52
82:BP:48:ARG:HA	82:BP:51:ILE:HD12	1.89	0.52
83:BQ:2794:G:N7	83:BQ:2795:U:C4	2.78	0.52
83:BQ:2804:A:C2	83:BQ:2805:G:C8	2.97	0.52
83:BQ:2804:A:OP2	86:BT:78:HIS:CD2	2.63	0.52
23:V:91:VAL:HG23	23:V:95:THR:HG21	1.90	0.52
1:2:565:C:H2'	1:2:577:G:N3	2.25	0.52
67:BA:160:VAL:HG12	67:BA:162:VAL:CG1	2.40	0.52
83:BQ:3187:A:H2'	83:BQ:3188:G:O4'	2.09	0.52
86:BT:116:PRO:HB3	86:BT:147:ALA:HB3	1.91	0.52
21:T:22:HIS:NE2	67:BA:298:PHE:HE1	1.99	0.52
1:2:55:A:N7	1:2:426:G:C6	2.78	0.52
74:BH:12:ARG:HD3	74:BH:59:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AN:14:VAL:HG21	80:BN:90:ILE:HD11	1.92	0.52
83:BQ:70:A:H2'	83:BQ:71:A:C8	2.45	0.52
85:BS:59:A:N3	85:BS:61:A:N6	2.58	0.52
1:2:1258:U:O2	1:2:1258:U:O4'	2.28	0.51
2:A:71:LEU:HD23	2:A:74:GLN:HE21	1.75	0.51
64:AX:6:ALA:HB2	85:BS:11:C:H1'	1.91	0.51
3:B:43:PHE:O	3:B:45:LYS:N	2.43	0.51
83:BQ:1696:A:H2'	83:BQ:1697:A:H8	1.74	0.51
56:AP:64:THR:CG2	86:BT:19:TYR:CB	2.87	0.51
9:H:126:ARG:HB2	9:H:133:VAL:HG23	1.91	0.51
9:H:86:LEU:HD22	9:H:97:ASP:HB3	1.92	0.51
24:W:134:ILE:HD12	24:W:135:ALA:N	2.26	0.51
1:2:1347:U:H2'	1:2:1347:U:O2	2.09	0.51
1:2:1780:G:N3	83:BQ:2262:A:O2'	2.35	0.51
83:BQ:708:G:N2	83:BQ:711:A:OP2	2.42	0.51
12:K:60:VAL:CG1	12:K:65:LEU:HD11	4.48	0.51
1:2:913:G:C6	83:BQ:2207:A:H1'	2.45	0.51
58:AR:4:ARG:NE	58:AR:4:ARG:O	2.43	0.51
72:BF:99:LEU:HD22	83:BQ:1722:U:H5''	1.92	0.51
83:BQ:1556:C:O2	83:BQ:1556:C:O4'	2.24	0.51
83:BQ:1661:G:H2'	83:BQ:1662:G:C8	2.45	0.51
23:V:34:ALA:HB1	23:V:91:VAL:HG23	1.92	0.51
1:2:1172:G:N2	1:2:1467:C:O2	2.43	0.51
51:AK:3:LYS:HG3	51:AK:8:VAL:HG13	1.92	0.51
53:AM:60:LEU:HA	53:AM:63:VAL:HG12	1.93	0.51
83:BQ:1897:G:H2'	83:BQ:1898:G:O4'	2.11	0.51
83:BQ:3214:U:O4'	83:BQ:3214:U:O2	2.27	0.51
83:BQ:3346:U:O2'	83:BQ:3347:A:H5'	2.10	0.51
83:BQ:2418:G:H21	86:BT:73:LEU:HD21	1.74	0.51
13:L:44:VAL:HG21	13:L:48:VAL:HG21	1.91	0.51
67:BA:29:VAL:CG2	67:BA:337:THR:HG21	2.40	0.51
67:BA:47:LEU:HD21	67:BA:179:ALA:HB3	1.91	0.51
83:BQ:1160:C:H2'	83:BQ:1160:C:O2	2.11	0.51
83:BQ:1177:G:O2'	83:BQ:1178:G:O5'	2.27	0.51
83:BQ:431:U:C2	83:BQ:432:G:C8	2.98	0.51
1:2:1477:G:H2'	1:2:1478:G:C1'	2.41	0.51
1:2:1585:U:H2'	1:2:1585:U:O2	2.09	0.51
47:AG:59:ILE:HG21	47:AG:65:ILE:CD1	2.41	0.51
83:BQ:1817:G:H2'	83:BQ:1818:U:O4'	2.10	0.51
23:V:34:ALA:CB	23:V:91:VAL:HG23	2.40	0.51
1:2:694:U:C5	22:U:98:ILE:HD12	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:55:A:HO2'	1:2:56:U:P	2.31	0.51
22:U:173:TYR:CE2	22:U:181:ILE:HD11	2.46	0.51
1:2:1246:C:O2	1:2:1246:C:O4'	2.26	0.51
50:AJ:76:THR:HG22	50:AJ:101:ARG:HG3	1.93	0.51
53:AM:40:ASP:OD1	53:AM:43:LYS:N	2.44	0.51
72:BF:96:ILE:HG12	83:BQ:1722:U:O4'	2.11	0.51
63:AW:230:VAL:HG21	83:BQ:2424:A:N1	2.26	0.51
83:BQ:859:G:C5	83:BQ:861:C:C5	2.99	0.51
84:BR:75:G:C8	84:BR:76:A:H2'	2.46	0.51
86:BT:109:THR:CG2	86:BT:110:LYS:N	2.74	0.51
83:BQ:2508:U:H2'	83:BQ:2509:U:O4'	2.11	0.50
68:BB:57:ILE:HD12	83:BQ:671:U:OP2	2.11	0.50
72:BF:106:LEU:HD11	72:BF:138:LEU:HD21	1.94	0.50
22:U:39:ARG:HD2	72:BF:181:ARG:HB2	1.94	0.50
70:BD:169:LYS:HB3	70:BD:176:ASP:HA	1.93	0.50
76:BJ:94:GLU:N	76:BJ:94:GLU:OE1	2.44	0.50
83:BQ:1554:U:H3	83:BQ:1559:A:N6	2.10	0.50
83:BQ:2419:A:H1'	83:BQ:2804:A:C8	2.46	0.50
84:BR:11:A:O2'	84:BR:13:A:OP2	2.29	0.50
1:2:610:G:N3	1:2:610:G:H2'	2.26	0.50
1:2:1174:C:O2'	1:2:1196:A:N6	2.44	0.50
1:2:427:C:H2'	1:2:428:A:H8	1.76	0.50
43:AC:77:LEU:HD11	43:AC:86:LYS:HG2	1.93	0.50
51:AK:59:VAL:HG13	51:AK:60:ARG:HG2	1.93	0.50
5:D:27:ALA:HB3	5:D:136:ILE:HG23	1.94	0.50
83:BQ:1632:A:H2'	83:BQ:1633:C:C6	2.47	0.50
1:2:1290:U:H2'	1:2:1291:G:C8	2.47	0.50
1:2:1362:U:O2	1:2:1362:U:O4'	2.30	0.50
1:2:1479:A:C2	1:2:1529:C:C2	3.00	0.50
68:BB:131:ALA:HB1	68:BB:135:GLN:H	1.76	0.50
73:BG:78:ASN:HA	73:BG:108:ILE:HD11	1.93	0.50
83:BQ:1134:G:O2'	83:BQ:2642:A:N3	2.37	0.50
83:BQ:268:A:H2'	83:BQ:268:A:N3	2.27	0.50
86:BT:111:ASP:O	86:BT:112:ASP:C	2.50	0.50
86:BT:156:THR:OG1	86:BT:156:THR:O	2.30	0.50
71:BE:71:VAL:HG22	71:BE:76:ARG:NH2	2.26	0.50
83:BQ:1326:A:H2'	83:BQ:1327:C:O4'	2.11	0.50
83:BQ:2836:C:O2	83:BQ:2836:C:O4'	2.30	0.50
23:V:162:ALA:HA	83:BQ:3353:G:P	2.52	0.50
83:BQ:373:A:C6	83:BQ:375:A:C6	3.00	0.50
4:C:83:PRO:HB2	4:C:86:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:103:MET:HB3	18:Q:215:VAL:HG12	1.93	0.50
21:T:131:LYS:CB	45:AE:81:PRO:HA	2.42	0.50
1:2:1145:U:C5	1:2:1633:A:C2	2.97	0.49
58:AR:26:ARG:NH1	83:BQ:938:C:OP2	2.43	0.49
1:2:337:G:O2'	23:V:10:LYS:NZ	2.44	0.49
3:B:146:THR:HG22	3:B:159:ALA:HA	1.94	0.49
9:H:118:LYS:O	83:BQ:1025:A:H2	1.89	0.49
86:BT:31:PHE:O	86:BT:82:VAL:HG13	2.12	0.49
5:D:69:ALA:HA	5:D:72:ILE:HD12	1.93	0.49
50:AJ:47:ALA:HB1	50:AJ:48:PRO:HD3	1.94	0.49
83:BQ:423:A:N6	83:BQ:637:C:OP1	2.45	0.49
86:BT:132:LYS:HB3	86:BT:152:GLU:CD	2.17	0.49
24:W:134:ILE:HD11	24:W:141:VAL:HB	1.94	0.49
1:2:1600:A:H2'	1:2:1600:A:N3	2.28	0.49
1:2:1784:C:C5	59:AS:5:TRP:HZ2	2.09	0.49
50:AJ:76:THR:HG1	50:AJ:79:GLU:H	1.59	0.49
60:AT:79:VAL:HG21	63:AW:168:VAL:HG13	1.93	0.49
83:BQ:1188:U:OP1	83:BQ:1210:U:O2'	2.28	0.49
83:BQ:313:A:H2'	83:BQ:314:U:O4'	2.12	0.49
23:V:81:VAL:HG12	23:V:95:THR:C	2.32	0.49
23:V:78:ILE:HD12	23:V:96:LEU:CD1	2.42	0.49
1:2:1461:C:C2	9:H:139:LYS:HD3	2.48	0.49
47:AG:163:PHE:CE2	47:AG:169:ALA:HB1	2.47	0.49
1:2:1750:A:OP1	59:AS:13:LEU:CD1	2.61	0.49
83:BQ:2577:C:C4	83:BQ:2578:U:C4	3.01	0.49
23:V:81:VAL:HG22	23:V:83:TYR:CD1	2.48	0.49
57:AQ:117:ASN:O	57:AQ:133:ILE:HG22	2.13	0.49
71:BE:286:VAL:HG12	71:BE:290:ILE:HD11	1.95	0.49
83:BQ:1188:U:C4	83:BQ:1317:A:N6	2.79	0.49
85:BS:83:C:O2'	85:BS:85:G:N2	2.46	0.49
86:BT:90:TYR:CD1	86:BT:104:ASN:OD1	2.65	0.49
20:S:61:VAL:HG12	20:S:65:LEU:HD12	1.94	0.49
1:2:1086:A:H2'	1:2:1087:A:C8	2.47	0.49
1:2:1560:U:O4'	1:2:1560:U:O2	2.29	0.49
83:BQ:2886:U:C4	83:BQ:2911:A:C6	3.01	0.49
64:AX:30:ARG:HA	64:AX:119:VAL:HG21	1.94	0.49
83:BQ:1625:A:N6	83:BQ:1818:U:O4	2.45	0.49
83:BQ:2328:U:H2'	83:BQ:2329:C:H6	1.77	0.49
1:2:1479:A:H2'	10:I:6:VAL:HG21	1.94	0.49
22:U:64:VAL:CG2	22:U:94:ALA:HB1	2.43	0.49
67:BA:339:ARG:NE	67:BA:342:LEU:HD21	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:831:G:O2'	83:BQ:1864:A:N3	2.40	0.49
83:BQ:2418:G:H2'	83:BQ:2418:G:N3	2.26	0.49
85:BS:25:G:H2'	85:BS:26:U:C6	2.47	0.49
18:Q:137:ILE:HD12	18:Q:172:LEU:HD22	1.94	0.49
1:2:903:U:O2	1:2:906:A:N7	2.46	0.49
41:AA:81:THR:HG21	41:AA:181:LYS:HD2	1.94	0.49
46:AF:31:LYS:HB2	46:AF:33:THR:HG22	1.94	0.49
83:BQ:2162:U:H2'	83:BQ:2163:C:O4'	2.12	0.49
83:BQ:359:U:H2'	83:BQ:360:G:O4'	2.13	0.49
83:BQ:86:G:H1'	83:BQ:87:U:OP2	2.13	0.49
1:2:1116:A:H5'	59:AS:17:ARG:NH1	2.27	0.48
1:2:472:U:O2'	1:2:769:A:N3	2.42	0.48
3:B:123:VAL:CG2	12:K:92:ILE:HD11	2.43	0.48
75:BI:76:ALA:HB3	75:BI:109:THR:HG22	1.94	0.48
9:H:14:ILE:HG23	9:H:14:ILE:O	2.13	0.48
20:S:141:THR:HG21	20:S:162:ILE:HD11	1.95	0.48
41:AA:184:ALA:O	41:AA:188:THR:HG23	2.13	0.48
83:BQ:10:C:O2'	83:BQ:1558:A:N6	2.47	0.48
16:O:222:LEU:CD2	16:O:265:LEU:HD21	2.44	0.48
2:A:162:GLN:N	2:A:163:PRO:CD	2.77	0.48
54:AN:110:ALA:O	54:AN:114:VAL:HG23	2.13	0.48
68:BB:86:THR:HG22	68:BB:105:ARG:HB2	1.94	0.48
83:BQ:431:U:N3	83:BQ:628:A:C2	2.82	0.48
83:BQ:2418:G:C6	86:BT:73:LEU:HD12	2.48	0.48
20:S:48:LEU:HD22	20:S:61:VAL:HG13	1.95	0.48
23:V:61:GLU:HG2	23:V:62:THR:HG23	1.95	0.48
1:2:1057:U:N3	1:2:1062:A:N6	2.60	0.48
1:2:1585:U:O4	1:2:1611:A:C2	2.63	0.48
51:AK:58:VAL:HG22	51:AK:104:LEU:HD22	1.96	0.48
57:AQ:53:TYR:CB	57:AQ:133:ILE:HD11	2.43	0.48
1:2:1126:G:C4'	59:AS:11:ARG:NH1	2.74	0.48
77:BK:49:ILE:HD11	77:BK:71:VAL:CG2	2.43	0.48
9:H:120:ARG:CD	83:BQ:1025:A:N3	2.77	0.48
83:BQ:1110:U:H2'	83:BQ:1111:U:C6	2.49	0.48
83:BQ:3079:U:O4'	83:BQ:3079:U:O2	2.32	0.48
16:O:144:LEU:HD23	16:O:181:TRP:CD2	2.48	0.48
25:X:5:LEU:O	25:X:7:VAL:N	2.47	0.48
1:2:381:C:O2	1:2:381:C:C2'	2.61	0.48
1:2:788:A:C2	20:S:19:LEU:HD13	2.48	0.48
2:A:216:PRO:HB2	2:A:217:ILE:HD12	1.95	0.48
83:BQ:2191:U:H2'	83:BQ:2192:C:O4'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:34:LEU:HD21	11:J:89:ARG:CG	2.43	0.48
13:L:12:VAL:HG13	13:L:28:VAL:HG13	1.94	0.48
1:2:260:U:O2	1:2:260:U:O4'	2.29	0.48
1:2:656:G:H2'	1:2:656:G:N3	2.27	0.48
46:AF:5:THR:HG22	46:AF:6:PRO:HD3	1.95	0.48
3:B:62:VAL:HG13	3:B:89:ILE:HD13	1.95	0.48
83:BQ:3182:G:C6	83:BQ:3183:A:N1	2.81	0.48
84:BR:113:C:H2'	84:BR:114:U:O4'	2.14	0.48
86:BT:132:LYS:HA	86:BT:132:LYS:HD2	1.58	0.48
4:C:11:ILE:HD13	4:C:35:ILE:HG21	1.95	0.48
19:R:69:ILE:HD11	19:R:133:LYS:HD3	1.94	0.48
1:2:1249:U:O4	1:2:1250:U:O4	2.32	0.48
9:H:16:ARG:HH12	47:AG:110:ILE:HG13	1.73	0.48
9:H:21:ASN:OD1	47:AG:116:TYR:CG	2.66	0.48
72:BF:23:TRP:CZ3	72:BF:25:ASP:HB3	2.49	0.48
81:BO:84:VAL:HG13	81:BO:119:VAL:CG2	2.44	0.48
24:W:14:THR:HB	24:W:15:PRO:CD	2.43	0.48
1:2:1116:A:H5'	59:AS:17:ARG:HH12	1.79	0.48
1:2:381:C:O2	1:2:381:C:H2'	2.14	0.48
1:2:850:A:H5''	72:BF:165:LYS:HZ2	1.68	0.48
2:A:69:LEU:HA	2:A:72:LEU:HD12	1.96	0.48
83:BQ:501:A:H2'	83:BQ:502:U:C6	2.49	0.48
86:BT:104:ASN:HB2	86:BT:107:GLY:O	2.13	0.48
86:BT:112:ASP:OD1	86:BT:113:VAL:HG13	2.13	0.48
71:BE:4:PRO:HD2	71:BE:22:LEU:HD12	1.96	0.48
81:BO:218:ARG:HA	83:BQ:1170:A:OP1	2.14	0.48
83:BQ:1203:A:H2'	83:BQ:1204:A:C8	2.49	0.48
83:BQ:1188:U:C4	83:BQ:1317:A:C6	3.02	0.48
83:BQ:1302:A:N7	83:BQ:2857:C:O2'	2.45	0.48
83:BQ:3019:U:C4	83:BQ:3020:U:C4	3.01	0.48
1:2:1145:U:C4	1:2:1146:G:C5	3.02	0.47
1:2:329:G:O2'	23:V:84:HIS:HB2	2.13	0.47
68:BB:86:THR:HG21	83:BQ:676:G:O6	2.14	0.47
71:BE:210:ALA:HB2	71:BE:254:ALA:N	2.29	0.47
83:BQ:3329:U:H2'	83:BQ:3330:A:O4'	2.14	0.47
63:AW:9:ARG:NH1	83:BQ:912:G:OP2	2.40	0.47
11:J:106:ILE:HG23	11:J:107:THR:HG23	1.96	0.47
1:2:300:A:H5''	20:S:2:ALA:HB2	1.96	0.47
1:2:1170:G:N3	1:2:1170:G:H2'	2.30	0.47
1:2:1772:C:O5'	59:AS:2:ARG:NE	2.47	0.47
1:2:55:A:N3	1:2:55:A:C2'	2.75	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AD:112:ILE:HG21	44:AD:161:LEU:HD11	1.96	0.47
63:AW:104:LEU:HD13	63:AW:162:ALA:O	2.14	0.47
69:BC:14:ILE:HG23	69:BC:16:LEU:CD1	2.44	0.47
69:BC:72:ARG:HB3	69:BC:96:VAL:CG2	2.44	0.47
83:BQ:2302:G:H2'	83:BQ:2303:A:O4'	2.14	0.47
83:BQ:2744:U:H2'	83:BQ:2745:G:O4'	2.13	0.47
1:2:995:A:H2'	1:2:996:U:O4'	2.14	0.47
50:AJ:47:ALA:CB	50:AJ:48:PRO:CD	2.93	0.47
69:BC:36:ILE:HD12	69:BC:59:ILE:HD11	1.95	0.47
79:BM:162:SER:N	83:BQ:3216:G:OP1	2.48	0.47
79:BM:68:PRO:HG3	79:BM:145:LEU:HD13	1.96	0.47
83:BQ:1063:G:N7	83:BQ:1097:G:H2'	2.29	0.47
83:BQ:1719:G:H2'	83:BQ:1720:U:O4'	2.14	0.47
83:BQ:2656:A:C4	83:BQ:2658:G:N7	2.83	0.47
83:BQ:629:U:C2	83:BQ:630:A:C8	3.02	0.47
9:H:123:ARG:HG3	9:H:133:VAL:HG22	1.97	0.47
16:O:22:SER:HB3	16:O:36:ALA:HB3	1.95	0.47
1:2:382:C:C2'	1:2:382:C:O2	2.63	0.47
1:2:50:C:O2	1:2:50:C:H2'	2.15	0.47
41:AA:36:ILE:O	83:BQ:2550:U:N3	2.47	0.47
7:F:39:VAL:O	7:F:40:GLU:HB2	2.14	0.47
2:A:95:GLY:HA2	2:A:101:GLN:HE21	1.79	0.47
60:AT:63:THR:HG22	63:AW:48:ILE:HD11	1.95	0.47
72:BF:45:VAL:HG22	72:BF:50:ILE:HB	1.95	0.47
83:BQ:580:C:H2'	83:BQ:581:U:O4'	2.14	0.47
83:BQ:897:U:C2	83:BQ:898:U:C5	3.03	0.47
1:2:1533:C:H4'	1:2:1539:G:N1	2.29	0.47
2:A:46:THR:HB	2:A:84:ILE:HD12	1.96	0.47
64:AX:129:THR:HG22	83:BQ:1507:G:C8	2.49	0.47
69:BC:29:ALA:HB3	69:BC:30:PRO:HD3	1.97	0.47
83:BQ:1127:G:N2	83:BQ:1130:A:OP2	2.43	0.47
83:BQ:436:A:H2'	83:BQ:437:G:O4'	2.14	0.47
18:Q:176:VAL:HG22	18:Q:184:LEU:HD21	1.96	0.47
1:2:987:G:N1	63:AW:248:GLY:O	2.48	0.47
1:2:851:U:H4'	72:BF:172:ARG:NH2	2.27	0.47
83:BQ:1046:A:H2'	83:BQ:1049:C:H5	1.79	0.47
83:BQ:1282:G:H2'	83:BQ:1283:C:O4'	2.15	0.47
83:BQ:1494:U:O4'	83:BQ:1495:U:C5	2.68	0.47
49:AI:53:THR:HG21	83:BQ:1747:G:O3'	2.14	0.47
83:BQ:1657:C:N4	83:BQ:1798:A:OP2	2.47	0.47
83:BQ:3078:U:C2'	83:BQ:3078:U:O2	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:3083:G:H2'	83:BQ:3084:C:O4'	2.15	0.47
16:O:225:LEU:HD12	16:O:228:LYS:HG3	1.97	0.47
83:BQ:1834:U:H3'	83:BQ:1835:A:H5'	1.95	0.47
58:AR:8:THR:HG21	83:BQ:662:U:OP1	2.14	0.47
9:H:113:LEU:HD21	9:H:127:HIS:HB3	1.97	0.47
17:P:139:VAL:O	17:P:139:VAL:HG22	2.15	0.47
26:Y:94:LYS:O	26:Y:98:VAL:HG23	2.14	0.47
2:A:113:LEU:HD22	2:A:117:ARG:HD2	1.97	0.47
73:BG:63:THR:HA	73:BG:66:LEU:HD12	1.97	0.47
83:BQ:1224:C:H2'	83:BQ:1225:A:O4'	2.15	0.47
1:2:1644:C:O2'	83:BQ:2255:A:N1	2.38	0.47
86:BT:42:VAL:HG13	86:BT:43:ASP:H	1.79	0.47
8:G:20:TYR:CD1	8:G:38:ILE:HD11	2.50	0.47
47:AG:18:VAL:HG22	47:AG:70:THR:HG22	1.97	0.47
83:BQ:1462:A:H2'	83:BQ:1463:U:O4'	2.14	0.47
63:AW:202:VAL:HG23	83:BQ:2185:G:OP1	2.15	0.47
1:2:1597:A:C8	14:M:14:TYR:CD1	3.02	0.47
24:W:14:THR:HB	24:W:15:PRO:HD2	1.95	0.47
27:Z:26:THR:HG21	27:Z:97:GLY:HA3	1.96	0.47
1:2:1358:G:N3	1:2:1358:G:H2'	2.30	0.47
1:2:1595:U:C4	1:2:1600:A:N6	2.82	0.47
1:2:628:G:O2'	83:BQ:846:A:C4	2.68	0.47
50:AJ:93:ILE:O	50:AJ:93:ILE:HG22	2.15	0.47
22:U:39:ARG:HH21	72:BF:181:ARG:HA	1.80	0.47
75:BI:146:LEU:HD12	75:BI:163:LEU:CD1	2.45	0.47
83:BQ:2696:A:H2'	83:BQ:2697:A:C8	2.50	0.47
83:BQ:374:A:HO2'	83:BQ:376:G:H8	1.59	0.47
83:BQ:829:U:O4	83:BQ:895:A:N1	2.48	0.47
42:AB:46:LEU:HD22	67:BA:8:ALA:HB2	1.97	0.46
57:AQ:94:TYR:O	83:BQ:289:A:O2'	2.33	0.46
58:AR:4:ARG:NH2	58:AR:5:PHE:HA	2.31	0.46
60:AT:54:ILE:HG23	63:AW:48:ILE:HD11	1.97	0.46
75:BI:83:LEU:N	75:BI:84:PRO:HD2	2.30	0.46
83:BQ:1748:G:C6	83:BQ:1749:A:C6	3.04	0.46
1:2:1757:G:H4'	83:BQ:2256:A:H2'	1.97	0.46
22:U:143:LEU:HD11	22:U:149:ILE:CD1	2.45	0.46
1:2:1236:A:H2'	1:2:1237:G:H8	1.79	0.46
1:2:1585:U:C4	1:2:1611:A:C2	3.00	0.46
46:AF:34:CYS:SG	46:AF:35:SER:N	2.88	0.46
79:BM:40:LEU:HD11	79:BM:54:TYR:HB2	1.97	0.46
83:BQ:506:U:C4	83:BQ:507:U:C5	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1060:U:H3'	1:2:1061:A:H5''	1.97	0.46
1:2:1172:G:O2'	1:2:1173:C:O4'	2.33	0.46
1:2:1775:U:O4	59:AS:4:LYS:CE	2.59	0.46
44:AD:20:ILE:HG12	44:AD:25:VAL:HG22	1.96	0.46
63:AW:118:GLU:CG	63:AW:126:LEU:HD21	2.46	0.46
79:BM:40:LEU:HB3	79:BM:84:VAL:CG1	2.45	0.46
84:BR:80:G:H2'	84:BR:81:U:O4'	2.14	0.46
10:I:18:TYR:CE2	10:I:59:ALA:HB2	2.49	0.46
11:J:63:LEU:HD11	11:J:86:ILE:HD11	1.98	0.46
18:Q:126:THR:HG22	18:Q:136:ARG:CG	2.45	0.46
44:AD:85:GLY:HA3	44:AD:187:ILE:HD12	1.98	0.46
64:AX:67:ILE:HD12	64:AX:82:ARG:NE	2.31	0.46
3:B:73:THR:HG23	7:F:114:ARG:HD2	1.97	0.46
68:BB:81:VAL:HG21	68:BB:140:LEU:HD12	1.96	0.46
83:BQ:523:A:N6	83:BQ:570:A:C2	2.83	0.46
84:BR:62:U:O4	84:BR:63:A:N6	2.49	0.46
1:2:1236:A:H2'	1:2:1237:G:C8	2.50	0.46
67:BA:161:LEU:N	67:BA:161:LEU:HD23	2.30	0.46
80:BN:38:LEU:N	80:BN:38:LEU:HD12	2.30	0.46
83:BQ:2612:U:O2	83:BQ:2804:A:C5	2.69	0.46
83:BQ:542:G:N3	83:BQ:542:G:H2'	2.31	0.46
71:BE:98:ARG:NH2	83:BQ:804:C:OP1	2.49	0.46
21:T:9:VAL:CG1	45:AE:78:ALA:O	2.63	0.46
9:H:14:ILE:HG21	47:AG:118:PRO:HD3	1.97	0.46
81:BO:232:ARG:HD2	81:BO:236:ILE:HD12	1.96	0.46
1:2:1570:A:C5	1:2:1570:A:OP2	2.68	0.46
1:2:42:G:C2'	1:2:430:G:C6	2.74	0.46
44:AD:161:LEU:CD2	44:AD:179:ILE:HG21	2.45	0.46
69:BC:63:GLY:O	69:BC:65:LYS:N	2.49	0.46
70:BD:21:TYR:CZ	83:BQ:1048:A:H2'	2.51	0.46
83:BQ:2117:A:H2'	83:BQ:2118:C:O4'	2.16	0.46
83:BQ:563:U:H2'	83:BQ:564:G:O4'	2.15	0.46
83:BQ:898:U:H2'	83:BQ:899:U:O4'	2.15	0.46
10:I:4:VAL:HG12	10:I:79:LEU:HD21	1.97	0.46
1:2:1641:C:O2'	59:AS:1:MET:HB3	2.15	0.46
1:2:1657:U:O2	83:BQ:2125:A:O4'	2.34	0.46
1:2:393:C:H2'	1:2:394:C:C6	2.51	0.46
68:BB:131:ALA:HB1	68:BB:135:GLN:N	2.30	0.46
83:BQ:20:A:C6	83:BQ:21:G:C6	3.04	0.46
83:BQ:2862:U:C2	83:BQ:2863:G:C8	3.04	0.46
83:BQ:2906:C:H2'	83:BQ:2907:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:BT:7:THR:O	86:BT:9:GLU:N	2.46	0.46
9:H:29:VAL:O	9:H:33:THR:HG23	2.15	0.46
75:BI:119:TYR:CE1	75:BI:135:VAL:HG23	2.51	0.46
70:BD:216:PHE:CD1	75:BI:294:ALA:HB1	2.50	0.46
83:BQ:1448:U:O2	83:BQ:1448:U:H2'	2.15	0.46
83:BQ:2418:G:H22	86:BT:73:LEU:HG	1.80	0.46
1:2:1553:G:N7	6:E:47:ARG:NH2	2.63	0.46
7:F:83:GLN:HE22	7:F:119:ALA:HB2	1.81	0.46
1:2:1038:U:O4	1:2:1092:A:C6	2.67	0.46
1:2:1724:U:C4'	45:AE:47:ARG:NH1	2.79	0.46
68:BB:64:VAL:HA	68:BB:67:ILE:HD12	1.98	0.46
71:BE:354:VAL:O	71:BE:358:THR:HG23	2.16	0.46
79:BM:41:ILE:HG21	79:BM:163:PHE:CD2	2.50	0.46
83:BQ:357:A:H2'	83:BQ:358:G:O4'	2.16	0.46
83:BQ:877:C:O2'	83:BQ:880:G:H1'	2.16	0.46
83:BQ:942:U:OP1	83:BQ:1434:G:N7	2.49	0.46
4:C:27:PHE:CD1	4:C:40:LEU:HD13	2.51	0.46
1:2:1185:U:O2'	1:2:1455:G:O2'	2.29	0.45
1:2:1368:G:N2	1:2:1369:U:O4'	2.49	0.45
1:2:348:U:H4'	23:V:14:THR:HG22	1.96	0.45
2:A:201:ALA:HB3	8:G:42:GLN:HE22	1.81	0.45
23:V:36:THR:O	23:V:36:THR:HG23	2.16	0.45
57:AQ:79:ALA:O	57:AQ:80:THR:HG23	2.16	0.45
81:BO:83:LEU:CD2	81:BO:139:PRO:HG3	2.46	0.45
83:BQ:1337:A:H2'	83:BQ:1338:C:O4'	2.16	0.45
83:BQ:2998:U:H2'	83:BQ:2999:U:O4'	2.16	0.45
16:O:103:PHE:HB3	16:O:134:TRP:CZ3	2.51	0.45
61:AU:120:VAL:O	61:AU:124:LEU:HD13	2.16	0.45
41:AA:241:LYS:HB3	83:BQ:2586:G:N7	2.31	0.45
83:BQ:3306:U:O4'	83:BQ:3306:U:O2	2.33	0.45
8:G:84:TYR:CD2	8:G:85:VAL:HG23	2.51	0.45
1:2:987:G:N1	63:AW:248:GLY:C	2.70	0.45
60:AT:8:VAL:O	60:AT:11:THR:HG22	2.17	0.45
63:AW:59:ALA:HB2	63:AW:78:ALA:HB2	1.98	0.45
83:BQ:1520:G:H2'	83:BQ:1521:G:O4'	2.16	0.45
83:BQ:2228:A:H2'	83:BQ:2229:A:C8	2.51	0.45
83:BQ:623:U:H2'	83:BQ:624:G:O4'	2.16	0.45
19:R:168:ARG:HD3	19:R:170:ILE:HD11	1.99	0.45
23:V:121:LEU:HD23	23:V:160:PHE:CG	2.51	0.45
23:V:26:LYS:O	23:V:28:GLU:N	2.49	0.45
71:BE:261:VAL:O	71:BE:270:SER:OG	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:BH:77:VAL:HG13	74:BH:126:VAL:CG2	2.43	0.45
86:BT:90:TYR:CE1	86:BT:104:ASN:CG	2.89	0.45
1:2:987:G:H22	63:AW:248:GLY:CA	2.28	0.45
64:AX:60:PHE:CE2	64:AX:82:ARG:HB3	2.51	0.45
68:BB:103:ALA:HB3	68:BB:106:PHE:CE2	2.51	0.45
68:BB:16:ARG:HD2	68:BB:53:PHE:O	2.17	0.45
71:BE:210:ALA:HB2	71:BE:254:ALA:CA	2.46	0.45
75:BI:115:LEU:O	75:BI:117:GLU:N	2.50	0.45
79:BM:52:VAL:HG23	79:BM:67:GLY:HA2	1.98	0.45
83:BQ:1077:U:O2	83:BQ:1083:G:C2	2.70	0.45
83:BQ:1192:C:N4	83:BQ:1302:A:OP1	2.50	0.45
83:BQ:3077:A:N6	83:BQ:3080:G:C5	2.84	0.45
7:F:18:ALA:HA	7:F:69:VAL:HG12	1.99	0.45
9:H:143:ARG:HB3	9:H:144:ARG:CB	2.46	0.45
20:S:139:VAL:HG13	20:S:150:PRO:HG3	1.97	0.45
1:2:1118:G:OP2	59:AS:21:ARG:NH1	2.48	0.45
71:BE:181:VAL:O	71:BE:182:LEU:HB2	2.16	0.45
62:AV:26:THR:HG23	83:BQ:1065:A:N1	2.31	0.45
83:BQ:1696:A:C2	83:BQ:1697:A:C5	3.05	0.45
83:BQ:3007:U:C2	83:BQ:3008:A:C8	3.05	0.45
1:2:699:U:H2'	1:2:700:C:C5	2.51	0.45
41:AA:81:THR:HG21	41:AA:181:LYS:CD	2.47	0.45
64:AX:67:ILE:HG23	64:AX:82:ARG:HE	1.82	0.45
83:BQ:118:U:C5	83:BQ:119:U:C5	3.04	0.45
83:BQ:2610:G:H2'	83:BQ:2611:U:O4'	2.17	0.45
85:BS:8:C:H2'	85:BS:9:A:C8	2.52	0.45
11:J:19:ILE:HA	11:J:96:PRO:HA	1.99	0.45
23:V:72:ILE:HG21	23:V:112:TRP:CE2	2.52	0.45
24:W:93:LEU:O	24:W:96:VAL:HG22	2.17	0.45
64:AX:41:LEU:HD13	64:AX:112:LEU:HD23	1.99	0.45
75:BI:102:GLY:O	75:BI:105:ILE:HG22	2.17	0.45
9:H:120:ARG:NH1	83:BQ:1025:A:O2'	2.50	0.45
83:BQ:1105:A:H2'	83:BQ:1106:G:O4'	2.17	0.45
83:BQ:2612:U:C2	83:BQ:2804:A:C6	3.04	0.45
83:BQ:908:G:N3	83:BQ:925:A:N7	2.64	0.45
83:BQ:989:A:H2'	83:BQ:990:U:O4'	2.17	0.45
86:BT:58:HIS:ND1	86:BT:72:ASP:O	2.50	0.45
1:2:1116:A:OP1	59:AS:14:LYS:HG2	2.17	0.45
1:2:1126:G:O5'	59:AS:11:ARG:NH1	2.48	0.45
1:2:1732:A:H2'	1:2:1733:C:C6	2.52	0.45
64:AX:139:TYR:CE1	83:BQ:2355:G:H4'	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:BB:150:VAL:HG23	68:BB:153:PHE:CD2	2.52	0.45
73:BG:23:ASP:OD1	73:BG:23:ASP:N	2.50	0.45
83:BQ:125:C:H2'	83:BQ:126:U:C6	2.52	0.45
83:BQ:1782:U:H2'	83:BQ:1783:U:O4'	2.17	0.45
83:BQ:1914:G:C8	83:BQ:2115:G:C2	3.05	0.45
83:BQ:2886:U:C4	83:BQ:2911:A:C5	3.05	0.45
86:BT:51:5CT:H10	86:BT:51:5CT:H3	1.58	0.45
7:F:18:ALA:CB	7:F:69:VAL:HG12	2.47	0.45
1:2:385:A:H2'	1:2:386:G:C8	2.53	0.44
1:2:55:A:H2'	1:2:403:G:N2	2.32	0.44
21:T:131:LYS:NZ	45:AE:81:PRO:CB	2.80	0.44
46:AF:22:CYS:HB3	46:AF:37:CYS:HB3	1.85	0.44
56:AP:85:LEU:HD12	56:AP:85:LEU:N	2.31	0.44
57:AQ:99:ARG:NH2	57:AQ:118:SER:O	2.50	0.44
83:BQ:1185:C:C4	83:BQ:1186:G:N7	2.85	0.44
72:BF:100:ARG:NH1	83:BQ:1722:U:OP1	2.51	0.44
52:AL:2:ALA:O	52:AL:4:GLN:N	2.51	0.44
50:AJ:58:VAL:HG13	83:BQ:75:G:H5'	1.98	0.44
83:BQ:907:G:N2	83:BQ:925:A:O2'	2.50	0.44
56:AP:27:GLN:NE2	86:BT:13:ALA:C	2.46	0.44
67:BA:161:LEU:HD22	67:BA:180:GLU:HG2	1.98	0.44
2:A:164:VAL:HG13	2:A:168:ILE:HD11	1.98	0.44
71:BE:20:LEU:HD11	71:BE:252:GLU:HG3	1.99	0.44
71:BE:74:ILE:HB	71:BE:75:PRO:HD2	2.00	0.44
83:BQ:2373:A:N3	83:BQ:2824:G:O2'	2.42	0.44
83:BQ:3343:G:C2	83:BQ:3361:G:C2	3.05	0.44
9:H:143:ARG:HG2	9:H:144:ARG:HD2	1.99	0.44
12:K:93:SER:HA	12:K:100:ILE:HG23	1.99	0.44
19:R:169:LEU:HD23	19:R:198:THR:HG22	1.99	0.44
26:Y:96:VAL:HG22	26:Y:146:ALA:HB1	1.99	0.44
1:2:360:A:O2'	1:2:362:G:OP1	2.29	0.44
1:2:851:U:H5''	72:BF:172:ARG:NH2	2.30	0.44
1:2:851:U:OP1	72:BF:165:LYS:HD2	2.16	0.44
66:AZ:56:UNK:O	66:AZ:57:UNK:CB	2.65	0.44
83:BQ:1317:A:O2'	83:BQ:1318:A:C2'	2.66	0.44
83:BQ:1481:A:N3	83:BQ:1481:A:H2'	2.32	0.44
83:BQ:1930:A:C8	83:BQ:1932:A:O4'	2.70	0.44
83:BQ:2612:U:C2	83:BQ:2804:A:C5	3.05	0.44
86:BT:152:GLU:HG2	86:BT:153:ALA:O	2.17	0.44
56:AP:64:THR:C	86:BT:17:ALA:HB3	2.36	0.44
4:C:46:LEU:O	4:C:50:THR:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:19:A:H2'	1:2:20:G:O4'	2.17	0.44
63:AW:230:VAL:HG22	63:AW:231:SER:H	1.83	0.44
20:S:123:LEU:HD13	20:S:236:ILE:HD11	1.99	0.44
24:W:77:ILE:HG21	24:W:91:LYS:HG3	1.99	0.44
9:H:16:ARG:HD2	47:AG:110:ILE:HB	2.00	0.44
56:AP:64:THR:O	86:BT:16:SER:O	2.34	0.44
83:BQ:2243:A:H1'	83:BQ:2313:A:H2'	1.99	0.44
83:BQ:2535:A:H2'	83:BQ:2536:A:O4'	2.18	0.44
83:BQ:2902:A:H2'	83:BQ:2903:A:O4'	2.18	0.44
6:E:96:ILE:HD13	6:E:116:LEU:O	2.17	0.44
8:G:35:CYS:HA	8:G:38:ILE:HG22	2.00	0.44
26:Y:26:PHE:CD2	26:Y:66:ILE:HD11	2.52	0.44
41:AA:75:ILE:O	41:AA:76:ALA:HB3	2.18	0.44
64:AX:29:THR:HA	64:AX:32:THR:HG22	2.00	0.44
83:BQ:160:G:H2'	83:BQ:161:G:O4'	2.18	0.44
83:BQ:2193:U:O4'	83:BQ:2193:U:O2	2.35	0.44
83:BQ:3078:U:O2	83:BQ:3078:U:H2'	2.17	0.44
25:X:59:PRO:HG3	25:X:66:ILE:HD11	1.99	0.44
1:2:330:G:H1'	23:V:200:LYS:O	2.18	0.44
1:2:973:A:H5'	83:BQ:848:A:H2	1.82	0.44
60:AT:54:ILE:HG23	63:AW:48:ILE:CD1	2.48	0.44
83:BQ:283:G:OP2	83:BQ:285:A:H4'	2.18	0.44
83:BQ:3084:C:O2'	83:BQ:3332:U:H5''	2.18	0.44
86:BT:66:THR:HG22	86:BT:68:LYS:HG2	1.99	0.44
1:2:1114:G:HO2'	1:2:1115:U:P	2.41	0.43
43:AC:6:GLY:O	43:AC:7:ILE:HG23	2.18	0.43
1:2:813:U:H5	72:BF:163:ARG:HD2	1.79	0.43
83:BQ:2208:A:O2'	83:BQ:2209:U:OP1	2.26	0.43
56:AP:2:VAL:HG11	83:BQ:2654:C:C5	2.52	0.43
1:2:1545:A:H5'	9:H:133:VAL:HG12	1.99	0.43
1:2:1147:A:H2'	1:2:1148:C:O4'	2.17	0.43
1:2:1595:U:C4	1:2:1600:A:C6	3.04	0.43
54:AN:54:THR:HG22	54:AN:57:HIS:CG	2.53	0.43
58:AR:49:HIS:N	58:AR:50:PRO:CD	2.80	0.43
83:BQ:2433:U:H3	83:BQ:2595:A:N6	2.16	0.43
83:BQ:2503:G:H2'	83:BQ:2504:U:O4'	2.18	0.43
83:BQ:2733:A:H2'	83:BQ:2734:A:O4'	2.18	0.43
83:BQ:2873:U:O2	83:BQ:2873:U:O4'	2.33	0.43
83:BQ:632:G:H2'	83:BQ:633:C:C6	2.53	0.43
1:2:1475:A:O2'	1:2:1540:G:O3'	2.37	0.43
1:2:173:A:H2'	1:2:174:U:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:432:G:C6	1:2:433:C:N3	2.86	0.43
41:AA:180:VAL:HG11	41:AA:186:LEU:HD21	2.01	0.43
64:AX:165:VAL:HG13	64:AX:165:VAL:O	2.18	0.43
86:BT:95:ILE:O	86:BT:95:ILE:HG13	2.18	0.43
22:U:143:LEU:HD12	22:U:147:ASN:HB2	1.99	0.43
1:2:1171:A:O2'	1:2:1172:G:P	2.77	0.43
1:2:16:G:H2'	1:2:17:C:C6	2.54	0.43
83:BQ:3375:A:H2'	83:BQ:3375:A:N3	2.33	0.43
84:BR:13:A:OP1	84:BR:111:U:H1'	2.18	0.43
9:H:21:ASN:OD1	47:AG:116:TYR:CB	2.67	0.43
17:P:146:LEU:HD22	17:P:173:ILE:HG21	2.00	0.43
21:T:131:LYS:O	45:AE:83:THR:C	2.49	0.43
25:X:108:PRO:HB2	25:X:135:VAL:HG22	1.99	0.43
27:Z:106:ALA:HA	27:Z:112:ILE:HD11	1.99	0.43
1:2:1038:U:C4	1:2:1092:A:C6	3.06	0.43
1:2:1145:U:C4	1:2:1146:G:C4	3.06	0.43
1:2:990:C:H2'	1:2:991:G:O4'	2.18	0.43
43:AC:44:VAL:HG21	57:AQ:9:GLU:HB3	2.00	0.43
3:B:97:LEU:HD21	3:B:194:LEU:HD22	2.01	0.43
3:B:36:ALA:HB1	3:B:42:LEU:HD11	1.99	0.43
81:BO:84:VAL:HG13	81:BO:119:VAL:HG21	2.00	0.43
83:BQ:1319:G:C6	83:BQ:1320:C:C4	3.07	0.43
83:BQ:2696:A:N7	83:BQ:2758:A:N6	2.66	0.43
5:D:125:ASN:O	5:D:127:GLY:N	2.49	0.43
18:Q:88:VAL:HG13	18:Q:96:LEU:HD13	2.00	0.43
23:V:72:ILE:HG21	23:V:112:TRP:CZ2	2.53	0.43
1:2:1227:A:C8	1:2:1229:G:N2	2.86	0.43
1:2:601:A:H2'	1:2:602:U:O4'	2.18	0.43
1:2:814:A:C2	72:BF:170:ARG:CZ	2.99	0.43
65:AY:10:ILE:HD11	65:AY:104:LEU:HD23	2.01	0.43
83:BQ:2855:U:H2'	83:BQ:2856:G:O4'	2.18	0.43
85:BS:15:G:C2	85:BS:16:G:N2	2.87	0.43
19:R:116:LYS:HG2	19:R:127:ALA:HB3	2.00	0.43
20:S:181:VAL:CG1	20:S:225:VAL:HG13	2.48	0.43
23:V:195:ARG:HB2	23:V:196:LEU:HD13	2.01	0.43
47:AG:17:LEU:HD13	47:AG:129:VAL:HG22	2.00	0.43
80:BN:41:ARG:HG2	80:BN:56:THR:HG21	2.00	0.43
83:BQ:1481:A:O2'	83:BQ:1482:A:OP2	2.37	0.43
60:AT:34:HIS:NE2	83:BQ:1792:C:OP2	2.50	0.43
10:I:82:GLY:O	10:I:83:ALA:HB3	2.18	0.43
12:K:39:ALA:O	12:K:72:GLY:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1746:A:N1	83:BQ:2302:G:O2'	2.47	0.43
1:2:30:G:H2'	1:2:31:C:C6	2.54	0.43
2:A:109:LEU:HD21	2:A:115:ILE:CD1	2.49	0.43
83:BQ:2433:U:N3	83:BQ:2595:A:N6	2.67	0.43
83:BQ:316:U:O2'	83:BQ:317:A:OP2	2.29	0.43
83:BQ:431:U:N3	83:BQ:432:G:N7	2.66	0.43
84:BR:8:G:H2'	84:BR:9:C:O4'	2.19	0.43
7:F:35:PRO:CG	7:F:38:LEU:HD12	2.48	0.43
1:2:329:G:O2'	23:V:84:HIS:HB3	2.19	0.43
1:2:1646:C:OP1	83:BQ:2259:A:C2	2.72	0.43
44:AD:112:ILE:HG21	44:AD:161:LEU:CD1	2.49	0.43
57:AQ:133:ILE:HG23	57:AQ:133:ILE:O	2.18	0.43
63:AW:179:LEU:HD13	83:BQ:1793:C:C5	2.53	0.43
81:BO:141:TYR:HA	81:BO:189:ILE:HD12	2.00	0.43
68:BB:4:ASP:CB	81:BO:92:ILE:HD13	2.49	0.43
83:BQ:3000:A:H2'	83:BQ:3001:C:C6	2.53	0.43
83:BQ:324:A:H2'	83:BQ:325:A:C8	2.53	0.43
83:BQ:859:G:C6	83:BQ:861:C:C4	3.07	0.43
85:BS:45:C:H2'	85:BS:46:G:O4'	2.19	0.43
11:J:48:HIS:NE2	11:J:99:ILE:HD13	2.34	0.43
16:O:67:ILE:HD12	16:O:85:TRP:CE3	2.54	0.43
1:2:121:U:C4	1:2:122:U:C4	3.07	0.43
1:2:1317:C:H2'	1:2:1318:G:O4'	2.19	0.43
46:AF:12:HIS:ND1	46:AF:12:HIS:O	2.52	0.43
57:AQ:160:GLU:OE1	57:AQ:160:GLU:N	2.52	0.43
72:BF:99:LEU:HD21	72:BF:103:ARG:NE	2.34	0.43
83:BQ:1047:A:N3	83:BQ:2633:U:O2'	2.51	0.43
83:BQ:1286:A:O2'	83:BQ:1287:A:H4'	2.19	0.43
1:2:123:G:O2'	20:S:146:THR:N	2.52	0.43
1:2:106:U:H2'	1:2:107:C:O4'	2.18	0.42
67:BA:247:ARG:HD2	83:BQ:1888:U:OP1	2.19	0.42
67:BA:29:VAL:HG22	67:BA:337:THR:HG21	1.99	0.42
83:BQ:2612:U:C2	83:BQ:2804:A:N7	2.85	0.42
86:BT:30:GLY:O	86:BT:41:ILE:HD12	2.19	0.42
1:2:50:C:C2'	1:2:50:C:O2	2.67	0.42
1:2:955:A:H2'	1:2:956:C:O4'	2.19	0.42
1:2:956:C:O3'	1:2:1047:G:N2	2.52	0.42
50:AJ:18:TRP:HE1	83:BQ:799:G:HO2'	1.67	0.42
57:AQ:172:ARG:NE	57:AQ:174:ILE:HD11	2.34	0.42
63:AW:203:ALA:HA	63:AW:217:GLN:HE21	1.84	0.42
63:AW:57:PRO:HD2	63:AW:170:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:123:VAL:HG22	12:K:92:ILE:HD11	2.01	0.42
3:B:68:ILE:HD12	3:B:71:ALA:HA	2.01	0.42
67:BA:82:PRO:O	67:BA:83:PRO:C	2.57	0.42
82:BP:9:LEU:HB3	82:BP:17:LEU:HD21	2.01	0.42
83:BQ:2167:A:N6	83:BQ:2168:A:N1	2.67	0.42
83:BQ:2794:G:C8	83:BQ:2795:U:C4	3.07	0.42
83:BQ:281:G:C6	83:BQ:282:G:C6	3.07	0.42
85:BS:77:A:H2'	85:BS:78:G:O4'	2.18	0.42
22:U:143:LEU:HD11	22:U:149:ILE:HD12	2.01	0.42
27:Z:81:VAL:HB	27:Z:115:ILE:HG22	2.01	0.42
1:2:12:U:H2'	1:2:13:C:C6	2.54	0.42
56:AP:38:GLN:OE1	56:AP:41:ARG:NH1	2.52	0.42
57:AQ:155:VAL:O	57:AQ:162:ARG:NH2	2.52	0.42
63:AW:150:LEU:HB3	63:AW:151:PRO:HD2	2.01	0.42
83:BQ:1064:A:H4'	83:BQ:1065:A:O5'	2.19	0.42
83:BQ:2273:G:O2'	83:BQ:2274:U:P	2.77	0.42
83:BQ:2886:U:C5	83:BQ:2911:A:C5	3.07	0.42
11:J:53:LYS:HB2	11:J:92:ASP:HB2	2.02	0.42
23:V:29:LEU:HD21	23:V:31:ARG:CZ	2.49	0.42
1:2:68:A:H4'	1:2:69:G:OP2	2.19	0.42
75:BI:40:HIS:CD2	75:BI:42:ALA:HB3	2.55	0.42
81:BO:219:LYS:HD3	83:BQ:1169:A:H4'	2.02	0.42
83:BQ:3159:C:H2'	83:BQ:3160:U:O4'	2.19	0.42
83:BQ:767:U:C2	83:BQ:768:C:C6	3.08	0.42
83:BQ:45:A:O2'	83:BQ:95:A:N1	2.46	0.42
84:BR:84:A:H2'	84:BR:85:G:C8	2.54	0.42
1:2:1030:A:C8	6:E:10:ARG:O	119.67	0.42
9:H:120:ARG:HG3	83:BQ:1025:A:H2	1.84	0.42
1:2:1233:G:H2'	1:2:1234:A:O4'	2.19	0.42
1:2:371:G:N2	1:2:612:U:O2	2.53	0.42
60:AT:47:VAL:HA	60:AT:56:THR:O	2.19	0.42
64:AX:31:GLU:N	64:AX:31:GLU:OE1	2.53	0.42
69:BC:20:LEU:HD11	69:BC:32:ALA:HB2	2.01	0.42
83:BQ:1203:A:N3	83:BQ:2855:U:O2'	2.41	0.42
83:BQ:1721:U:O2'	83:BQ:1723:A:N7	2.38	0.42
83:BQ:94:G:H2'	83:BQ:95:A:C8	2.54	0.42
85:BS:19:C:C4	85:BS:20:U:C4	3.07	0.42
86:BT:42:VAL:HG13	86:BT:43:ASP:N	2.35	0.42
1:2:1069:A:H2'	1:2:1070:C:O4'	2.19	0.42
1:2:1767:G:H4'	1:2:1768:G:O5'	2.20	0.42
1:2:1783:C:C5	59:AS:5:TRP:CE2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AH:79:GLY:HA3	48:AH:81:ILE:HD12	2.02	0.42
58:AR:74:ASN:HA	58:AR:113:LEU:O	2.20	0.42
83:BQ:1856:C:H2'	83:BQ:1857:C:C6	2.55	0.42
83:BQ:1481:A:O2'	83:BQ:1858:A:C2	2.71	0.42
83:BQ:1912:U:N3	83:BQ:2122:G:OP2	2.47	0.42
83:BQ:2193:U:C5	83:BQ:2313:A:N7	2.87	0.42
83:BQ:2406:C:H2'	83:BQ:2407:C:C6	2.54	0.42
83:BQ:2516:U:O2	83:BQ:2594:C:N4	2.53	0.42
83:BQ:3357:U:H2'	83:BQ:3358:U:C6	2.54	0.42
83:BQ:833:G:H2'	83:BQ:834:U:O4'	2.19	0.42
23:V:77:ARG:O	23:V:104:ILE:HG22	2.19	0.42
1:2:1784:C:H5	59:AS:5:TRP:CE2	2.17	0.42
1:2:431:C:H2'	1:2:432:G:C8	2.54	0.42
1:2:962:C:C4	1:2:963:A:C2	3.08	0.42
44:AD:41:ILE:O	44:AD:42:ASP:HB2	2.20	0.42
46:AF:21:ARG:NH2	46:AF:41:ALA:O	2.53	0.42
63:AW:3:ARG:HD3	83:BQ:911:C:N4	2.34	0.42
67:BA:77:THR:HG23	67:BA:326:GLY:O	2.20	0.42
22:U:39:ARG:NH1	72:BF:181:ARG:O	2.49	0.42
74:BH:124:LEU:HD23	76:BJ:153:PRO:HB2	2.01	0.42
80:BN:56:THR:O	80:BN:57:LEU:HD23	2.19	0.42
83:BQ:1504:A:C5	83:BQ:1505:C:C5	3.08	0.42
83:BQ:1532:C:H2'	83:BQ:1533:U:O4'	2.20	0.42
83:BQ:636:C:C3'	83:BQ:637:C:H5'	2.50	0.42
41:AA:185:ARG:CZ	85:BS:155:A:H4'	2.49	0.42
51:AK:52:ARG:NH2	85:BS:72:A:N7	2.68	0.42
5:D:31:VAL:HG21	5:D:136:ILE:HD11	2.02	0.42
20:S:12:LEU:HD23	20:S:13:ALA:N	2.35	0.42
63:AW:43:GLY:HA3	63:AW:63:PHE:CD1	2.55	0.42
23:V:162:ALA:CA	83:BQ:3353:G:OP2	2.60	0.42
85:BS:115:C:H2'	85:BS:116:G:O4'	2.20	0.42
85:BS:149:A:H2'	85:BS:150:G:C8	2.54	0.42
86:BT:124:LEU:HD11	86:BT:136:VAL:HG21	2.00	0.42
1:2:1147:A:H2'	1:2:1148:C:C6	2.55	0.42
1:2:200:A:H2'	1:2:201:G:O4'	2.20	0.42
42:AB:17:LEU:HD21	42:AB:98:ASN:CG	2.40	0.42
45:AE:16:GLY:N	67:BA:73:VAL:HG11	2.35	0.42
58:AR:75:LEU:HD23	58:AR:78:LEU:HD13	2.00	0.42
81:BO:108:LEU:HD22	81:BO:114:GLY:HA2	2.02	0.42
83:BQ:1624:G:H2'	83:BQ:1625:A:C8	2.55	0.42
83:BQ:271:C:H2'	83:BQ:272:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:3385:U:H2'	83:BQ:3386:G:O4'	2.20	0.42
83:BQ:340:C:N4	83:BQ:341:G:O6	2.53	0.42
1:2:628:G:O2'	83:BQ:846:A:C5	2.73	0.42
86:BT:155:ARG:C	86:BT:156:THR:CG2	2.86	0.42
7:F:45:ARG:O	7:F:48:VAL:HG12	2.19	0.42
8:G:87:GLU:O	8:G:88:VAL:HG12	2.18	0.42
1:2:1530:C:OP2	12:K:95:HIS:HB2	2.20	0.42
1:2:156:A:C2'	1:2:157:A:H5'	2.49	0.42
54:AN:36:HIS:NE2	54:AN:74:VAL:HG11	2.35	0.42
57:AQ:136:ASP:O	57:AQ:142:ILE:HD13	2.19	0.42
58:AR:62:HIS:CG	58:AR:62:HIS:O	2.72	0.42
62:AV:17:HIS:CD2	62:AV:21:ILE:HD11	2.55	0.42
3:B:99:MET:O	3:B:100:ASN:HB2	2.19	0.42
71:BE:129:THR:HG21	71:BE:248:VAL:HG21	2.02	0.42
80:BN:107:GLU:O	80:BN:111:ALA:HB3	2.20	0.42
83:BQ:339:C:OP1	83:BQ:1380:G:O2'	2.36	0.42
83:BQ:423:A:H2'	83:BQ:424:G:O4'	2.20	0.42
83:BQ:61:A:H2'	83:BQ:62:A:O4'	2.19	0.42
83:BQ:988:U:H2'	83:BQ:989:A:O4'	2.20	0.42
22:U:51:VAL:HG11	22:U:168:SER:HA	2.02	0.42
50:AJ:48:PRO:HB2	82:BP:117:ALA:HB2	2.02	0.41
65:AY:43:ILE:CD1	65:AY:92:ILE:HD11	2.50	0.41
78:BL:43:VAL:HG11	78:BL:69:ALA:CB	2.49	0.41
83:BQ:2332:A:C6	83:BQ:2333:C:C2	3.08	0.41
83:BQ:3346:U:H1'	83:BQ:3347:A:H5''	2.02	0.41
83:BQ:3355:U:H3'	83:BQ:3356:G:C5'	2.50	0.41
83:BQ:651:G:H2'	83:BQ:652:G:O4'	2.19	0.41
84:BR:86:U:O2'	84:BR:87:G:P	2.77	0.41
86:BT:102:LEU:HD23	86:BT:113:VAL:HG21	2.02	0.41
16:O:222:LEU:HD21	16:O:265:LEU:HD21	2.02	0.41
23:V:95:THR:O	23:V:97:THR:HG23	2.20	0.41
1:2:1609:U:H2'	1:2:1610:G:O4'	2.19	0.41
1:2:1746:A:H2	83:BQ:2302:G:N3	2.17	0.41
1:2:915:A:H2'	1:2:915:A:N3	2.35	0.41
1:2:1783:C:C4	59:AS:5:TRP:CD2	3.07	0.41
64:AX:32:THR:HG21	64:AX:87:SER:HB3	2.02	0.41
68:BB:103:ALA:HB3	68:BB:106:PHE:CZ	2.55	0.41
70:BD:95:VAL:HG22	70:BD:124:LEU:HD21	2.01	0.41
53:AM:55:ARG:HD3	74:BH:70:THR:HB	2.00	0.41
83:BQ:1260:A:C2	83:BQ:1261:G:N7	2.89	0.41
83:BQ:2577:C:N4	83:BQ:2578:U:C4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BQ:655:C:H2'	83:BQ:656:A:H8	1.85	0.41
83:BQ:763:G:C2	83:BQ:764:U:H1'	2.55	0.41
83:BQ:835:G:H2'	83:BQ:857:G:N2	2.35	0.41
84:BR:113:C:C4	84:BR:114:U:C4	3.08	0.41
4:C:29:GLN:O	4:C:30:ALA:HB3	2.21	0.41
1:2:42:G:O2'	1:2:430:G:N1	2.51	0.41
68:BB:18:ALA:HA	68:BB:53:PHE:CE1	2.55	0.41
71:BE:234:ASN:HD21	71:BE:236:LEU:HD12	1.85	0.41
71:BE:300:ARG:HB2	71:BE:301:PRO:CD	2.51	0.41
76:BJ:17:ARG:NH1	76:BJ:45:ASN:OD1	2.52	0.41
83:BQ:1238:C:H2'	83:BQ:1239:C:C6	2.55	0.41
83:BQ:1447:G:O2'	83:BQ:1448:U:P	2.78	0.41
83:BQ:1668:G:H2'	83:BQ:1669:C:O4'	2.20	0.41
83:BQ:3103:A:H2'	83:BQ:3104:U:O4'	2.20	0.41
83:BQ:3279:A:H2'	83:BQ:3280:U:O4'	2.19	0.41
83:BQ:825:U:C2	83:BQ:826:G:C8	3.09	0.41
84:BR:24:A:H2'	84:BR:25:G:O4'	2.21	0.41
86:BT:92:LEU:HD12	86:BT:101:SER:O	2.20	0.41
6:E:108:ARG:NH2	83:BQ:1025:A:H2	2.15	0.41
7:F:29:ILE:HG22	7:F:36:ILE:HD12	2.02	0.41
15:N:132:LEU:HD13	15:N:139:LEU:HD23	2.00	0.41
18:Q:126:THR:HG22	18:Q:136:ARG:HG3	2.02	0.41
18:Q:144:ARG:HB3	18:Q:208:GLN:HB3	2.02	0.41
22:U:35:LYS:O	22:U:36:ALA:HB3	2.20	0.41
1:2:1180:C:H2'	1:2:1181:U:O4'	2.20	0.41
1:2:1533:C:H4'	1:2:1539:G:C6	2.55	0.41
1:2:425:A:H3'	1:2:425:A:OP1	2.21	0.41
43:AC:33:ALA:O	43:AC:37:THR:OG1	2.31	0.41
65:AY:25:LEU:HD23	65:AY:90:VAL:HG13	2.01	0.41
67:BA:152:LYS:O	67:BA:188:ILE:HD11	2.20	0.41
67:BA:221:THR:OG1	67:BA:273:HIS:O	2.34	0.41
77:BK:32:ILE:HD12	77:BK:81:VAL:HG21	2.02	0.41
1:2:1780:G:C1'	83:BQ:2262:A:O3'	2.60	0.41
83:BQ:2719:U:C2	83:BQ:2720:G:C8	3.08	0.41
83:BQ:3293:U:H4'	83:BQ:3294:A:OP1	2.20	0.41
75:BI:58:LYS:HD2	84:BR:49:G:C8	2.55	0.41
86:BT:95:ILE:HD11	86:BT:125:GLN:HE22	1.85	0.41
17:P:56:LYS:HZ2	17:P:158:VAL:HA	1.85	0.41
19:R:53:ILE:HD11	19:R:73:LEU:HD22	2.02	0.41
20:S:45:ILE:HA	20:S:61:VAL:HG11	2.02	0.41
23:V:95:THR:HG22	23:V:95:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:117:U:H2'	1:2:118:U:O4'	2.21	0.41
1:2:1724:U:H4'	45:AE:47:ARG:NH1	2.35	0.41
1:2:447:U:H2'	1:2:448:C:O4'	2.21	0.41
1:2:51:A:P	1:2:51:A:O4'	2.79	0.41
42:AB:58:VAL:HG23	42:AB:76:ALA:HB3	2.01	0.41
63:AW:102:LEU:N	63:AW:102:LEU:HD12	2.35	0.41
1:2:987:G:C2'	63:AW:249:SER:HB2	2.45	0.41
83:BQ:13:A:C6	83:BQ:15:C:C5	3.08	0.41
12:K:59:TYR:HE1	12:K:100:ILE:HD13	1.84	0.41
1:2:1334:U:H2'	1:2:1335:U:O4'	2.20	0.41
1:2:1364:G:N7	1:2:1365:C:C2	2.89	0.41
54:AN:72:ILE:HD11	54:AN:107:ARG:HD3	2.02	0.41
61:AU:19:LEU:O	61:AU:23:VAL:HG23	2.21	0.41
63:AW:45:VAL:HG13	63:AW:84:THR:HA	2.02	0.41
83:BQ:227:G:C2	83:BQ:228:U:C2	3.09	0.41
83:BQ:238:A:H2'	83:BQ:239:G:O4'	2.20	0.41
79:BM:44:ALA:HB1	83:BQ:3273:A:H4'	2.01	0.41
22:U:64:VAL:O	22:U:64:VAL:HG12	2.20	0.41
25:X:84:ILE:HD13	25:X:117:VAL:HG11	2.01	0.41
1:2:106:U:HO2'	1:2:383:G:N2	2.18	0.41
1:2:108:A:H2'	1:2:109:G:C8	2.56	0.41
1:2:1348:A:H2'	1:2:1349:G:O4'	2.21	0.41
1:2:1585:U:C2'	1:2:1585:U:O2	2.68	0.41
46:AF:64:MET:O	46:AF:68:LYS:HB2	2.21	0.41
63:AW:119:LYS:HB2	63:AW:120:PRO:CD	2.51	0.41
70:BD:48:CYS:SG	70:BD:49:VAL:N	2.93	0.41
71:BE:286:VAL:HG12	71:BE:290:ILE:CD1	2.51	0.41
79:BM:52:VAL:HG21	79:BM:65:ILE:HD13	2.02	0.41
83:BQ:1227:C:N4	83:BQ:1281:G:O6	2.54	0.41
83:BQ:1562:C:C4	83:BQ:1563:C:N4	2.89	0.41
83:BQ:2416:U:O4	83:BQ:2804:A:N1	2.53	0.41
83:BQ:3047:U:C5	83:BQ:3094:A:H2	2.29	0.41
83:BQ:374:A:H4'	83:BQ:375:A:OP1	2.21	0.41
83:BQ:945:C:H2'	83:BQ:946:U:C6	2.55	0.41
85:BS:147:U:N3	85:BS:148:G:C8	2.88	0.41
85:BS:56:G:H2'	85:BS:57:C:O4'	2.20	0.41
86:BT:31:PHE:CE2	86:BT:85:VAL:HG21	2.56	0.41
86:BT:7:THR:C	86:BT:9:GLU:H	2.24	0.41
4:C:14:TYR:CD2	4:C:35:ILE:HD11	2.55	0.41
9:H:28:ILE:HD12	9:H:61:LEU:CD1	2.51	0.41
27:Z:19:ILE:HG23	27:Z:28:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:853:G:P	72:BF:176:ARG:NE	2.79	0.41
44:AD:120:ASP:OD2	44:AD:124:ARG:NH2	2.51	0.41
44:AD:57:VAL:HB	44:AD:68:LEU:HD13	2.03	0.41
67:BA:102:LEU:O	67:BA:103:THR:HG23	2.20	0.41
83:BQ:1160:C:C2'	83:BQ:1160:C:O2	2.69	0.41
86:BT:33:VAL:HA	86:BT:37:ARG:O	2.21	0.41
7:F:49:TYR:HA	7:F:52:LEU:HD12	2.03	0.41
19:R:133:LYS:O	19:R:136:VAL:HG23	2.19	0.41
25:X:94:ILE:N	25:X:94:ILE:HD12	2.36	0.41
47:AG:54:VAL:HG11	47:AG:57:PHE:CD2	2.55	0.41
60:AT:22:LEU:O	60:AT:26:VAL:HG23	2.20	0.41
73:BG:32:TRP:O	73:BG:33:ARG:HG2	2.21	0.41
83:BQ:585:A:H2'	83:BQ:586:C:C6	2.56	0.41
84:BR:109:G:C6	84:BR:110:G:N7	2.89	0.41
18:Q:61:LEU:HD11	18:Q:96:LEU:HD21	2.01	0.41
1:2:1365:C:C2'	1:2:1366:U:O5'	2.69	0.41
1:2:51:A:C4'	1:2:51:A:OP2	2.69	0.41
48:AH:82:LEU:HD21	48:AH:135:ILE:HG23	2.03	0.41
3:B:58:LEU:HD12	3:B:138:THR:CG2	2.49	0.41
68:BB:150:VAL:HG23	68:BB:153:PHE:CE2	2.56	0.41
68:BB:81:VAL:CG2	68:BB:140:LEU:HD12	2.51	0.41
83:BQ:121:A:H3'	83:BQ:122:A:C5'	2.51	0.41
83:BQ:1617:G:H2'	83:BQ:1618:G:O4'	2.21	0.41
83:BQ:2513:U:H4'	83:BQ:2514:U:OP1	2.21	0.41
83:BQ:2522:G:C2'	83:BQ:2522:G:N3	2.84	0.41
41:AA:241:LYS:CB	83:BQ:2586:G:N7	2.83	0.41
83:BQ:3183:A:C6	83:BQ:3184:A:N1	2.89	0.41
21:T:76:LEU:HD22	21:T:92:ARG:HB3	2.01	0.41
1:2:1307:U:O2	1:2:1307:U:O4'	2.39	0.41
2:A:53:THR:HA	2:A:91:VAL:HG12	2.02	0.41
71:BE:148:ILE:HA	71:BE:149:PRO:C	2.41	0.41
71:BE:32:PRO:HA	71:BE:244:LEU:HD11	2.03	0.41
75:BI:163:LEU:HD21	75:BI:175:HIS:CE1	2.56	0.41
83:BQ:1332:A:H2'	83:BQ:1333:C:C6	2.55	0.41
1:2:1746:A:H1'	83:BQ:2291:A:H1'	2.01	0.41
83:BQ:2419:A:C2	83:BQ:2420:C:C4	3.09	0.41
83:BQ:423:A:H2'	83:BQ:424:G:C8	2.56	0.41
2:A:11:LEU:HD13	11:J:29:THR:HG23	2.02	0.41
1:2:1423:U:H2'	1:2:1424:A:O4'	2.21	0.40
2:A:217:ILE:HG22	2:A:218:LEU:N	2.36	0.40
44:AD:103:ILE:HD11	44:AD:134:ILE:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AR:76:ASP:OD1	58:AR:76:ASP:N	2.53	0.40
67:BA:154:TYR:CE1	83:BQ:3242:G:H5''	2.56	0.40
83:BQ:1444:G:C6	83:BQ:1445:U:O2	2.74	0.40
83:BQ:3331:U:H2'	83:BQ:3332:U:O4'	2.21	0.40
21:T:63:MET:SD	21:T:106:LEU:HD21	2.61	0.40
21:T:67:VAL:HG23	21:T:99:GLY:HA2	2.02	0.40
1:2:1145:U:O2	1:2:1145:U:O4'	2.39	0.40
2:A:195:SER:O	2:A:197:THR:N	2.54	0.40
67:BA:4:ARG:O	67:BA:5:LYS:CB	2.69	0.40
83:BQ:1049:C:H2'	83:BQ:1050:U:C6	2.56	0.40
83:BQ:1051:U:C5	83:BQ:1052:U:C6	3.10	0.40
83:BQ:1479:U:O4	83:BQ:1480:G:C2	2.74	0.40
83:BQ:1676:A:C6	83:BQ:1677:G:N7	2.89	0.40
83:BQ:1840:U:O2	83:BQ:1840:U:C2'	2.69	0.40
83:BQ:2202:C:H2'	83:BQ:2203:U:O4'	2.21	0.40
83:BQ:744:A:H2'	83:BQ:745:C:O4'	2.20	0.40
86:BT:92:LEU:HA	86:BT:102:LEU:HD13	2.03	0.40
5:D:52:LEU:HD21	5:D:57:ALA:HB3	2.02	0.40
23:V:83:TYR:CB	23:V:84:HIS:HA	2.51	0.40
1:2:144:U:H2'	1:2:145:A:O4'	2.21	0.40
1:2:1479:A:N6	1:2:1528:U:O4	2.51	0.40
1:2:119:A:H1'	1:2:397:A:C8	2.57	0.40
1:2:816:G:N7	72:BF:170:ARG:CZ	2.76	0.40
1:2:93:A:O2'	1:2:398:G:N2	2.54	0.40
60:AT:50:GLY:O	60:AT:51:ALA:HB3	2.22	0.40
83:BQ:1047:A:H2'	83:BQ:1048:A:C8	2.57	0.40
83:BQ:1765:U:H2'	83:BQ:1766:G:O4'	2.22	0.40
67:BA:278:ILE:HD11	83:BQ:3098:G:H4'	2.02	0.40
16:O:38:ARG:HA	16:O:67:ILE:HG23	2.04	0.40
1:2:107:C:H2'	1:2:108:A:C8	2.57	0.40
83:BQ:2553:U:H3'	83:BQ:2554:A:H5''	2.02	0.40
83:BQ:306:A:N6	83:BQ:2784:G:C2	2.89	0.40
83:BQ:3345:G:H2'	83:BQ:3346:U:C6	2.56	0.40
83:BQ:52:A:N3	83:BQ:811:U:O2'	2.52	0.40
84:BR:48:U:N3	84:BR:49:G:N7	2.69	0.40
85:BS:9:A:H2'	85:BS:10:A:C8	2.56	0.40
7:F:41:PRO:HD2	7:F:44:LEU:HB2	2.04	0.40
9:H:21:ASN:OD1	47:AG:116:TYR:CD2	2.74	0.40
6:E:18:ARG:NH1	9:H:91:ASP:O	2.54	0.40
21:T:159:ARG:HE	21:T:172:ALA:HB2	1.86	0.40
23:V:91:VAL:HG13	23:V:200:LYS:HA	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:149:ARG:O	24:W:151:ASP:N	2.53	0.40
1:2:1126:G:O3'	59:AS:11:ARG:NH2	2.54	0.40
41:AA:160:ILE:HG22	41:AA:164:VAL:CG1	2.46	0.40
67:BA:81:THR:HG21	67:BA:205:VAL:CG1	2.52	0.40
71:BE:275:THR:HG22	71:BE:276:LEU:O	2.21	0.40
82:BP:100:VAL:HG22	82:BP:104:GLN:HB3	2.03	0.40
83:BQ:1055:A:N3	84:BR:81:U:O2'	2.46	0.40
83:BQ:1230:G:C6	83:BQ:1231:A:C6	3.09	0.40
83:BQ:1290:A:H2'	83:BQ:1291:A:C8	2.57	0.40
83:BQ:2876:C:H2'	83:BQ:2877:G:O4'	2.21	0.40
83:BQ:596:C:H2'	83:BQ:597:G:O4'	2.21	0.40
83:BQ:949:C:H2'	83:BQ:950:G:O4'	2.21	0.40
86:BT:16:SER:O	86:BT:17:ALA:CB	2.69	0.40
86:BT:27:ARG:HD3	86:BT:27:ARG:HA	1.93	0.40
3:B:37:GLN:HB3	7:F:53:LEU:HD22	2.03	0.40
18:Q:127:VAL:HG11	18:Q:176:VAL:HG21	2.03	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 PDB entries followed by that with respect to all EM entries.

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	A	221/240 (92%)	194 (88%)	24 (11%)	3 (1%)	14	59
3	B	204/225 (91%)	172 (84%)	24 (12%)	8 (4%)	4	38
4	C	94/105 (90%)	72 (77%)	16 (17%)	6 (6%)	2	26
5	D	119/143 (83%)	92 (77%)	17 (14%)	10 (8%)	1	17
6	E	122/142 (86%)	101 (83%)	18 (15%)	3 (2%)	7	49
7	F	139/143 (97%)	119 (86%)	15 (11%)	5 (4%)	4	41
8	G	87/136 (64%)	73 (84%)	11 (13%)	3 (3%)	5	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	H	143/146 (98%)	123 (86%)	17 (12%)	3 (2%)	9	53
10	I	141/144 (98%)	112 (79%)	21 (15%)	8 (6%)	2	28
11	J	105/121 (87%)	94 (90%)	10 (10%)	1 (1%)	19	66
12	K	68/108 (63%)	54 (79%)	9 (13%)	5 (7%)	1	21
13	L	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
14	M	51/56 (91%)	41 (80%)	10 (20%)	0	100	100
15	N	49/152 (32%)	40 (82%)	6 (12%)	3 (6%)	2	27
16	O	316/319 (99%)	274 (87%)	37 (12%)	5 (2%)	12	58
17	P	204/252 (81%)	176 (86%)	20 (10%)	8 (4%)	4	38
18	Q	212/255 (83%)	170 (80%)	31 (15%)	11 (5%)	2	30
19	R	218/254 (86%)	184 (84%)	30 (14%)	4 (2%)	11	55
20	S	258/261 (99%)	213 (83%)	36 (14%)	9 (4%)	4	42
21	T	224/236 (95%)	188 (84%)	29 (13%)	7 (3%)	5	45
22	U	182/190 (96%)	142 (78%)	31 (17%)	9 (5%)	3	32
23	V	184/200 (92%)	128 (70%)	30 (16%)	26 (14%)	0	6
24	W	176/197 (89%)	149 (85%)	21 (12%)	6 (3%)	5	43
25	X	153/156 (98%)	129 (84%)	17 (11%)	7 (5%)	3	34
26	Y	148/151 (98%)	134 (90%)	11 (7%)	3 (2%)	9	54
27	Z	125/137 (91%)	103 (82%)	17 (14%)	5 (4%)	4	38
28	a	85/87 (98%)	67 (79%)	14 (16%)	4 (5%)	3	33
29	b	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	7	50
30	c	142/145 (98%)	120 (84%)	21 (15%)	1 (1%)	26	72
31	d	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	2	30
32	e	95/119 (80%)	70 (74%)	17 (18%)	8 (8%)	1	17
33	f	79/82 (96%)	61 (77%)	14 (18%)	4 (5%)	2	31
34	g	58/63 (92%)	48 (83%)	8 (14%)	2 (3%)	5	43
38	h	1107/1287 (86%)	965 (87%)	124 (11%)	18 (2%)	12	58
39	i	1355/1432 (95%)	1158 (86%)	172 (13%)	25 (2%)	11	55
40	j	388/397 (98%)	335 (86%)	46 (12%)	7 (2%)	11	55
40	k	382/397 (96%)	333 (87%)	40 (10%)	9 (2%)	7	50
41	AA	231/256 (90%)	194 (84%)	32 (14%)	5 (2%)	8	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	AB	134/137 (98%)	117 (87%)	14 (10%)	3 (2%)	8	52
43	AC	97/100 (97%)	80 (82%)	13 (13%)	4 (4%)	3	37
44	AD	189/191 (99%)	166 (88%)	19 (10%)	4 (2%)	9	53
45	AE	96/155 (62%)	73 (76%)	18 (19%)	5 (5%)	2	30
46	AF	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	16	63
47	AG	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	4	41
48	AH	119/142 (84%)	103 (87%)	14 (12%)	2 (2%)	11	56
49	AI	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	15	61
50	AJ	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	5	45
51	AK	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
52	AL	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	9	53
53	AM	134/138 (97%)	119 (89%)	12 (9%)	3 (2%)	8	52
54	AN	133/136 (98%)	118 (89%)	10 (8%)	5 (4%)	4	39
55	AO	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	4	38
56	AP	103/106 (97%)	86 (84%)	16 (16%)	1 (1%)	19	66
57	AQ	201/204 (98%)	175 (87%)	21 (10%)	5 (2%)	7	49
58	AR	146/149 (98%)	118 (81%)	21 (14%)	7 (5%)	3	32
59	AS	23/25 (92%)	23 (100%)	0	0	100	100
60	AT	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	17	65
61	AU	195/199 (98%)	177 (91%)	15 (8%)	3 (2%)	13	59
62	AV	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	11	55
63	AW	250/254 (98%)	218 (87%)	31 (12%)	1 (0%)	39	80
64	AX	181/184 (98%)	158 (87%)	19 (10%)	4 (2%)	8	52
65	AY	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	17	65
67	BA	384/387 (99%)	332 (86%)	41 (11%)	11 (3%)	6	46
68	BB	183/186 (98%)	163 (89%)	17 (9%)	3 (2%)	12	58
69	BC	107/113 (95%)	94 (88%)	11 (10%)	2 (2%)	10	54
70	BD	218/221 (99%)	185 (85%)	24 (11%)	9 (4%)	3	37
71	BE	359/362 (99%)	306 (85%)	38 (11%)	15 (4%)	3	36
72	BF	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	12	58
73	BG	125/130 (96%)	110 (88%)	13 (10%)	2 (2%)	12	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	BH	170/172 (99%)	151 (89%)	16 (9%)	3 (2%)	11	55
75	BI	294/297 (99%)	263 (90%)	22 (8%)	9 (3%)	5	45
76	BJ	157/160 (98%)	133 (85%)	18 (12%)	6 (4%)	4	39
77	BK	104/107 (97%)	93 (89%)	9 (9%)	2 (2%)	10	54
78	BL	98/121 (81%)	79 (81%)	16 (16%)	3 (3%)	5	45
79	BM	152/176 (86%)	137 (90%)	11 (7%)	4 (3%)	7	48
80	BN	110/121 (91%)	104 (94%)	3 (3%)	3 (3%)	6	48
81	BO	220/244 (90%)	199 (90%)	16 (7%)	5 (2%)	8	51
82	BP	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	21	68
86	BT	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	25
All	All	14299/15550 (92%)	12246 (86%)	1644 (12%)	409 (3%)	9	46

All (409) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	196	ARG
3	B	100	ASN
5	D	115	VAL
5	D	126	TRP
7	F	32	ASN
7	F	40	GLU
7	F	45	ARG
7	F	113	ASP
10	I	69	LYS
17	P	110	TYR
18	Q	132	ASP
18	Q	176	VAL
20	S	12	LEU
20	S	69	HIS
20	S	231	GLN
23	V	11	ARG
23	V	27	PHE
23	V	33	PRO
23	V	35	ASN
23	V	83	TYR
23	V	85	PRO
23	V	192	TYR
23	V	193	LEU

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Mol	Chain	Res	Type
23	V	194	ARG
24	W	98	ALA
24	W	134	ILE
25	X	7	VAL
26	Y	22	ALA
27	Z	91	THR
27	Z	124	ASP
30	c	12	ALA
38	h	126	VAL
38	h	900	LYS
38	h	1203	PHE
39	i	203	TYR
39	i	1032	LYS
40	k	278	THR
40	k	365	LYS
42	AB	29	SER
44	AD	42	ASP
44	AD	50	ASN
45	AE	64	THR
47	AG	8	PRO
50	AJ	47	ALA
50	AJ	166	ALA
53	AM	136	ALA
57	AQ	75	VAL
58	AR	12	ARG
58	AR	78	LEU
62	AV	21	ILE
63	AW	144	ASN
67	BA	5	LYS
67	BA	138	ALA
69	BC	64	VAL
70	BD	135	PHE
70	BD	138	ARG
71	BE	292	SER
75	BI	116	ASP
76	BJ	25	VAL
76	BJ	124	VAL
76	BJ	144	GLU
76	BJ	159	PHE
77	BK	92	LYS
79	BM	171	PRO
81	BO	164	SER

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Mol	Chain	Res	Type
86	BT	110	LYS
86	BT	112	ASP
86	BT	133	ASP
2	A	217	ILE
2	A	218	LEU
3	B	44	ASN
3	B	60	ASP
4	C	60	SER
4	C	64	TYR
5	D	25	GLU
5	D	91	VAL
5	D	106	ILE
7	F	39	VAL
8	G	76	GLU
8	G	77	GLU
8	G	88	VAL
9	H	7	GLU
9	H	51	ASP
10	I	7	ARG
11	J	55	PRO
12	K	71	ILE
15	N	107	LYS
15	N	146	SER
17	P	21	ASN
17	P	39	ASN
17	P	169	SER
18	Q	158	SER
19	R	91	ARG
19	R	145	GLY
19	R	206	THR
20	S	23	LEU
21	T	148	SER
21	T	219	ARG
22	U	74	GLN
22	U	110	GLN
23	V	10	LYS
23	V	24	LYS
23	V	52	ASN
23	V	86	SER
23	V	152	ILE
23	V	191	PHE
24	W	119	ALA

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Mol	Chain	Res	Type
25	X	6	THR
27	Z	42	VAL
29	b	78	ARG
31	d	35	VAL
31	d	51	GLU
31	d	52	LYS
31	d	60	PHE
31	d	127	LYS
32	e	36	ILE
32	e	63	ALA
38	h	649	ILE
38	h	986	ARG
38	h	1052	ILE
39	i	200	ASP
39	i	264	PHE
39	i	624	ASP
40	j	255	ASN
40	j	323	LYS
40	k	266	GLU
41	AA	156	ASP
42	AB	45	ARG
43	AC	99	ARG
45	AE	77	LYS
48	AH	109	LYS
50	AJ	51	LEU
52	AL	3	ALA
57	AQ	55	ALA
58	AR	47	LYS
61	AU	123	ALA
61	AU	187	GLU
64	AX	68	GLY
64	AX	166	VAL
67	BA	38	SER
67	BA	332	ARG
67	BA	348	ARG
67	BA	352	GLU
70	BD	113	GLY
70	BD	194	ALA
71	BE	131	VAL
71	BE	140	HIS
71	BE	293	SER
72	BF	130	ASN

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Mol	Chain	Res	Type
73	BG	50	ILE
74	BH	24	LEU
74	BH	97	VAL
75	BI	276	LYS
82	BP	90	ARG
86	BT	15	SER
86	BT	132	LYS
86	BT	156	THR
3	B	81	ARG
4	C	93	GLN
5	D	87	PRO
9	H	139	LYS
10	I	28	LEU
10	I	67	MET
10	I	128	GLY
17	P	35	PRO
18	Q	177	GLN
18	Q	209	ASN
18	Q	223	PHE
20	S	20	LEU
20	S	205	PHE
22	U	97	ARG
22	U	156	SER
23	V	96	LEU
23	V	98	LYS
23	V	116	HIS
23	V	196	LEU
24	W	120	LYS
24	W	150	LEU
25	X	55	ASP
29	b	30	SER
31	d	4	ALA
32	e	83	ILE
33	f	3	LEU
33	f	10	PRO
38	h	28	LEU
38	h	53	ASP
38	h	769	LEU
39	i	442	GLU
39	i	494	LEU
39	i	506	SER
39	i	621	LYS

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Mol	Chain	Res	Type
39	i	658	ASP
39	i	1254	SER
40	j	365	LYS
40	k	77	ASP
42	AB	112	SER
43	AC	27	SER
47	AG	112	LEU
49	AI	33	LYS
54	AN	59	ALA
54	AN	102	GLU
54	AN	125	GLY
57	AQ	80	THR
58	AR	77	LYS
58	AR	108	GLY
61	AU	5	PRO
64	AX	155	GLU
67	BA	7	GLU
68	BB	23	ASN
70	BD	2	ARG
71	BE	232	SER
71	BE	338	LYS
72	BF	53	LYS
76	BJ	29	THR
77	BK	91	ALA
78	BL	91	ASP
79	BM	20	LYS
79	BM	97	ASN
81	BO	159	GLN
86	BT	16	SER
86	BT	17	ALA
86	BT	114	LYS
3	B	63	GLN
3	B	64	VAL
5	D	93	ASP
10	I	132	LEU
12	K	44	GLN
15	N	118	ARG
17	P	103	THR
18	Q	39	GLU
18	Q	147	ALA
21	T	132	ARG
21	T	197	ASN

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Mol	Chain	Res	Type
23	V	22	ARG
23	V	37	LYS
23	V	81	VAL
23	V	87	ASN
25	X	29	LYS
26	Y	3	ARG
27	Z	75	GLY
28	a	9	VAL
32	e	59	TYR
32	e	62	TYR
33	f	15	GLU
34	g	60	PRO
38	h	125	GLU
38	h	133	ASN
39	i	174	ILE
39	i	212	TRP
39	i	939	ILE
39	i	1175	ASP
40	j	282	GLN
40	k	47	ASP
40	k	284	SER
44	AD	2	LYS
44	AD	41	ILE
46	AF	11	ARG
48	AH	62	VAL
53	AM	29	ALA
55	AO	79	GLU
55	AO	92	ASP
56	AP	17	CYS
57	AQ	150	TRP
67	BA	187	SER
68	BB	162	ALA
70	BD	100	LYS
70	BD	107	ALA
71	BE	14	GLU
71	BE	266	THR
71	BE	270	SER
71	BE	320	ASN
72	BF	81	ARG
75	BI	188	GLU
75	BI	259	LYS
79	BM	98	VAL

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Mol	Chain	Res	Type
3	B	65	ARG
5	D	111	ASN
5	D	119	SER
6	E	28	MET
6	E	53	PRO
6	E	127	ARG
10	I	90	PRO
12	K	38	HIS
12	K	43	ASP
12	K	88	ILE
16	O	120	SER
16	O	162	ALA
16	O	283	LYS
17	P	111	ILE
18	Q	210	ILE
19	R	150	GLN
20	S	195	ILE
21	T	69	LEU
23	V	40	ALA
23	V	51	GLY
25	X	146	ALA
26	Y	21	ASN
27	Z	40	ALA
29	b	120	HIS
31	d	5	VAL
32	e	97	PRO
38	h	767	ARG
39	i	263	PHE
39	i	1177	ARG
40	j	256	SER
40	k	22	VAL
45	AE	43	ARG
47	AG	94	ARG
47	AG	108	GLU
50	AJ	155	GLU
54	AN	70	PRO
54	AN	124	ALA
58	AR	56	VAL
58	AR	79	TRP
64	AX	3	ARG
67	BA	155	ALA
69	BC	83	GLU

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Mol	Chain	Res	Type
70	BD	112	GLN
70	BD	175	LEU
71	BE	5	GLN
71	BE	155	ASP
71	BE	175	HIS
71	BE	317	PRO
73	BG	12	LYS
75	BI	44	TYR
75	BI	137	ASP
75	BI	253	PHE
75	BI	277	LEU
78	BL	11	ILE
80	BN	59	PRO
86	BT	12	ASP
4	C	51	SER
10	I	87	GLY
21	T	149	LYS
22	U	64	VAL
22	U	96	ARG
22	U	98	ILE
23	V	82	VAL
25	X	4	GLU
28	a	12	TYR
28	a	82	VAL
33	f	75	GLU
38	h	114	ILE
38	h	150	GLY
39	i	403	ILE
39	i	570	LYS
39	i	876	LEU
39	i	1067	GLY
39	i	1213	ILE
40	j	52	LYS
40	k	394	ALA
41	AA	25	PRO
41	AA	36	ILE
41	AA	157	VAL
43	AC	3	VAL
45	AE	80	ARG
47	AG	120	ILE
50	AJ	50	PRO
60	AT	51	ALA

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Mol	Chain	Res	Type
76	BJ	148	PRO
80	BN	77	GLY
81	BO	178	ILE
5	D	66	VAL
18	Q	21	VAL
22	U	178	GLY
32	e	16	GLY
34	g	50	VAL
38	h	1029	GLY
39	i	1197	GLY
39	i	1203	ILE
43	AC	9	ILE
47	AG	117	ASP
53	AM	6	ILE
67	BA	245	GLY
78	BL	27	VAL
81	BO	188	ILE
16	O	63	GLY
21	T	165	GLY
32	e	84	VAL
57	AQ	74	PRO
71	BE	78	GLY
75	BI	251	PRO
4	C	88	PRO
4	C	89	GLY
16	O	105	GLY
28	a	77	GLY
38	h	206	PRO
38	h	1232	PRO
40	k	349	GLY
65	AY	87	VAL
74	BH	167	ARG
81	BO	26	VAL
17	P	158	VAL
20	S	204	GLY
22	U	65	PRO
38	h	1221	GLY
41	AA	73	PRO
50	AJ	127	PRO
68	BB	59	ARG
80	BN	12	PRO
3	B	51	VAL

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Mol	Chain	Res	Type
18	Q	48	VAL
20	S	193	GLY
24	W	18	PRO
25	X	41	GLY
39	i	1192	ILE
40	j	277	PRO
45	AE	76	VAL
67	BA	83	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 PDB entries followed by that with respect to all EM entries.

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	A	182/195 (93%)	175 (96%)	7 (4%)	40	76
3	B	173/191 (91%)	162 (94%)	11 (6%)	22	63
4	C	88/98 (90%)	83 (94%)	5 (6%)	25	67
5	D	89/119 (75%)	85 (96%)	4 (4%)	34	73
6	E	101/118 (86%)	94 (93%)	7 (7%)	19	60
7	F	117/119 (98%)	113 (97%)	4 (3%)	44	79
8	G	80/124 (64%)	75 (94%)	5 (6%)	22	63
9	H	128/129 (99%)	117 (91%)	11 (9%)	13	51
10	I	115/116 (99%)	102 (89%)	13 (11%)	7	38
11	J	100/114 (88%)	94 (94%)	6 (6%)	24	65
12	K	61/89 (68%)	58 (95%)	3 (5%)	31	70
13	L	56/60 (93%)	54 (96%)	2 (4%)	42	77
14	M	47/49 (96%)	44 (94%)	3 (6%)	22	63
15	N	43/135 (32%)	42 (98%)	1 (2%)	58	84
16	O	259/262 (99%)	250 (96%)	9 (4%)	43	78
17	P	164/210 (78%)	157 (96%)	7 (4%)	35	74
18	Q	191/224 (85%)	182 (95%)	9 (5%)	32	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	R	180/205 (88%)	175 (97%)	5 (3%)	51	81
20	S	221/222 (100%)	217 (98%)	4 (2%)	66	88
21	T	188/201 (94%)	181 (96%)	7 (4%)	41	76
22	U	165/170 (97%)	160 (97%)	5 (3%)	48	80
23	V	150/161 (93%)	133 (89%)	17 (11%)	7	38
24	W	152/166 (92%)	150 (99%)	2 (1%)	76	91
25	X	129/137 (94%)	126 (98%)	3 (2%)	58	84
26	Y	127/128 (99%)	121 (95%)	6 (5%)	32	72
27	Z	81/105 (77%)	74 (91%)	7 (9%)	13	51
28	a	74/74 (100%)	72 (97%)	2 (3%)	52	82
29	b	110/111 (99%)	109 (99%)	1 (1%)	84	93
30	c	119/120 (99%)	115 (97%)	4 (3%)	44	79
31	d	111/113 (98%)	103 (93%)	8 (7%)	18	58
32	e	83/101 (82%)	77 (93%)	6 (7%)	18	58
33	f	70/71 (99%)	69 (99%)	1 (1%)	74	90
34	g	50/54 (93%)	50 (100%)	0	100	100
38	h	936/1139 (82%)	901 (96%)	35 (4%)	41	76
39	i	849/1279 (66%)	823 (97%)	26 (3%)	47	80
40	j	296/347 (85%)	288 (97%)	8 (3%)	52	82
40	k	295/347 (85%)	290 (98%)	5 (2%)	68	89
41	AA	187/208 (90%)	179 (96%)	8 (4%)	35	74
42	AB	104/105 (99%)	98 (94%)	6 (6%)	25	66
43	AC	81/82 (99%)	76 (94%)	5 (6%)	23	64
44	AD	171/171 (100%)	165 (96%)	6 (4%)	43	78
45	AE	57/129 (44%)	57 (100%)	0	100	100
46	AF	70/71 (99%)	65 (93%)	5 (7%)	18	59
47	AG	147/150 (98%)	140 (95%)	7 (5%)	31	71
48	AH	104/118 (88%)	98 (94%)	6 (6%)	25	66
49	AI	68/69 (99%)	67 (98%)	1 (2%)	72	90
50	AJ	154/159 (97%)	146 (95%)	8 (5%)	29	69
51	AK	109/110 (99%)	105 (96%)	4 (4%)	41	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AL	45/46 (98%)	42 (93%)	3 (7%)	20	62
53	AM	107/109 (98%)	101 (94%)	6 (6%)	26	67
54	AN	115/116 (99%)	112 (97%)	3 (3%)	54	82
55	AO	47/116 (40%)	44 (94%)	3 (6%)	22	63
56	AP	90/91 (99%)	85 (94%)	5 (6%)	26	67
57	AQ	175/176 (99%)	168 (96%)	7 (4%)	38	75
58	AR	118/119 (99%)	111 (94%)	7 (6%)	24	66
59	AS	23/23 (100%)	21 (91%)	2 (9%)	13	50
60	AT	71/72 (99%)	69 (97%)	2 (3%)	51	81
61	AU	160/162 (99%)	155 (97%)	5 (3%)	47	80
62	AV	46/47 (98%)	45 (98%)	1 (2%)	60	85
63	AW	193/196 (98%)	187 (97%)	6 (3%)	47	80
64	AX	140/146 (96%)	133 (95%)	7 (5%)	30	70
65	AY	81/88 (92%)	78 (96%)	3 (4%)	41	76
67	BA	320/323 (99%)	304 (95%)	16 (5%)	30	70
68	BB	150/151 (99%)	144 (96%)	6 (4%)	38	75
69	BC	92/97 (95%)	84 (91%)	8 (9%)	13	50
70	BD	184/187 (98%)	169 (92%)	15 (8%)	14	53
71	BE	288/289 (100%)	277 (96%)	11 (4%)	40	76
72	BF	153/154 (99%)	148 (97%)	5 (3%)	45	79
73	BG	109/111 (98%)	106 (97%)	3 (3%)	51	81
74	BH	156/156 (100%)	150 (96%)	6 (4%)	40	76
75	BI	244/245 (100%)	235 (96%)	9 (4%)	41	76
76	BJ	136/137 (99%)	129 (95%)	7 (5%)	29	69
77	BK	90/91 (99%)	87 (97%)	3 (3%)	45	79
78	BL	87/107 (81%)	86 (99%)	1 (1%)	80	92
79	BM	134/153 (88%)	127 (95%)	7 (5%)	29	69
80	BN	95/103 (92%)	94 (99%)	1 (1%)	80	92
81	BO	186/205 (91%)	181 (97%)	5 (3%)	52	82
82	BP	104/105 (99%)	101 (97%)	3 (3%)	50	81
86	BT	118/132 (89%)	113 (96%)	5 (4%)	36	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	11689/13228 (88%)	11203 (96%)	486 (4%)	41 74

All (486) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	7	LYS
2	A	9	ARG
2	A	27	ARG
2	A	51	ARG
2	A	58	VAL
2	A	143	ARG
2	A	204	ASP
3	B	27	THR
3	B	99	MET
3	B	102	ARG
3	B	106	LYS
3	B	124	LEU
3	B	134	VAL
3	B	138	THR
3	B	143	ARG
3	B	158	GLN
3	B	167	ARG
3	B	168	VAL
4	C	31	LYS
4	C	55	VAL
4	C	63	TYR
4	C	78	GLU
4	C	82	LEU
5	D	34	THR
5	D	49	THR
5	D	54	ARG
5	D	74	LEU
6	E	42	ARG
6	E	44	ARG
6	E	61	ARG
6	E	80	MET
6	E	124	THR
6	E	126	VAL
6	E	130	ARG
7	F	66	ARG
7	F	68	ARG
7	F	114	ARG

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Mol	Chain	Res	Type
7	F	132	LYS
8	G	13	SER
8	G	26	LEU
8	G	36	ASP
8	G	47	ARG
8	G	80	ARG
9	H	17	LEU
9	H	38	VAL
9	H	91	ASP
9	H	98	TYR
9	H	100	THR
9	H	101	LEU
9	H	120	ARG
9	H	123	ARG
9	H	133	VAL
9	H	137	HIS
9	H	145	ARG
10	I	7	ARG
10	I	13	ASP
10	I	23	GLN
10	I	25	GLN
10	I	28	LEU
10	I	35	ASP
10	I	44	GLU
10	I	66	TYR
10	I	68	ARG
10	I	70	GLN
10	I	85	SER
10	I	91	TYR
10	I	123	ARG
11	J	20	ILE
11	J	47	GLN
11	J	52	LYS
11	J	92	ASP
11	J	99	ILE
11	J	118	VAL
12	K	64	VAL
12	K	95	HIS
12	K	100	ILE
13	L	32	PHE
13	L	50	GLU
14	M	19	ARG

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Mol	Chain	Res	Type
14	M	28	THR
14	M	39	CYS
15	N	103	LEU
16	O	58	VAL
16	O	59	ARG
16	O	114	ASP
16	O	185	GLN
16	O	202	LEU
16	O	228	LYS
16	O	250	TYR
16	O	274	LEU
16	O	308	ASN
17	P	8	ASP
17	P	103	THR
17	P	113	ARG
17	P	129	ASP
17	P	135	GLU
17	P	148	ASP
17	P	198	MET
18	Q	21	VAL
18	Q	29	TRP
18	Q	59	ASP
18	Q	70	LEU
18	Q	95	ASN
18	Q	118	GLN
18	Q	135	LEU
18	Q	181	LEU
18	Q	212	VAL
19	R	58	LEU
19	R	111	VAL
19	R	206	THR
19	R	225	LEU
19	R	243	TYR
20	S	26	CYS
20	S	88	ASP
20	S	164	LEU
20	S	261	LEU
21	T	24	ILE
21	T	75	LEU
21	T	78	THR
21	T	89	ASP
21	T	98	ARG

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Mol	Chain	Res	Type
21	T	190	GLN
21	T	208	TYR
22	U	5	GLN
22	U	9	LEU
22	U	27	LEU
22	U	31	SER
22	U	48	GLU
23	V	22	ARG
23	V	27	PHE
23	V	29	LEU
23	V	38	ILE
23	V	58	LEU
23	V	59	ARG
23	V	67	TRP
23	V	81	VAL
23	V	82	VAL
23	V	90	LEU
23	V	92	ARG
23	V	96	LEU
23	V	107	THR
23	V	160	PHE
23	V	196	LEU
23	V	197	THR
23	V	199	LYS
24	W	118	LEU
24	W	134	ILE
25	X	7	VAL
25	X	40	LEU
25	X	98	ASN
26	Y	36	GLN
26	Y	56	ASP
26	Y	86	GLU
26	Y	92	ILE
26	Y	102	LEU
26	Y	149	LEU
27	Z	38	THR
27	Z	52	ARG
27	Z	81	VAL
27	Z	90	ARG
27	Z	124	ASP
27	Z	136	ARG
27	Z	137	LEU

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Mol	Chain	Res	Type
28	a	12	TYR
28	a	80	LYS
29	b	37	PHE
30	c	17	VAL
30	c	18	HIS
30	c	107	PHE
30	c	121	ARG
31	d	17	LEU
31	d	63	GLN
31	d	125	LEU
31	d	127	LYS
31	d	129	VAL
31	d	131	ARG
31	d	132	ARG
31	d	133	ASN
32	e	3	LYS
32	e	10	ARG
32	e	11	ASN
32	e	12	LYS
32	e	21	VAL
32	e	92	ARG
33	f	9	HIS
38	h	54	ARG
38	h	69	MET
38	h	186	LEU
38	h	434	LEU
38	h	464	MET
38	h	669	THR
38	h	700	LEU
38	h	710	LEU
38	h	731	LEU
38	h	742	ARG
38	h	745	ASP
38	h	750	ARG
38	h	769	LEU
38	h	770	ASP
38	h	772	THR
38	h	788	THR
38	h	798	THR
38	h	801	GLN
38	h	824	GLU
38	h	847	LYS

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Mol	Chain	Res	Type
38	h	856	ILE
38	h	865	ASP
38	h	892	SER
38	h	899	LEU
38	h	900	LYS
38	h	908	ARG
38	h	1000	VAL
38	h	1036	LEU
38	h	1089	LEU
38	h	1106	ASP
38	h	1112	LEU
38	h	1126	GLU
38	h	1186	LEU
38	h	1229	GLU
38	h	1244	TRP
39	i	173	LEU
39	i	174	ILE
39	i	184	GLU
39	i	191	GLN
39	i	194	LEU
39	i	237	ARG
39	i	247	TYR
39	i	248	ARG
39	i	289	PHE
39	i	293	ASP
39	i	476	ASP
39	i	505	PHE
39	i	511	LYS
39	i	519	ILE
39	i	534	VAL
39	i	558	MET
39	i	637	TYR
39	i	644	HIS
39	i	646	ARG
39	i	687	ARG
39	i	718	GLU
39	i	907	LEU
39	i	1189	PHE
39	i	1272	ASP
39	i	1323	LEU
39	i	1341	TYR
40	j	18	ASP

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Mol	Chain	Res	Type
40	j	61	HIS
40	j	99	THR
40	j	173	LEU
40	j	226	GLN
40	j	347	GLU
40	j	350	ASP
40	j	383	CYS
40	k	83	LEU
40	k	127	LEU
40	k	176	GLN
40	k	259	CYS
40	k	358	PHE
41	AA	71	VAL
41	AA	84	ARG
41	AA	112	GLU
41	AA	126	SER
41	AA	190	VAL
41	AA	197	VAL
41	AA	202	GLU
41	AA	221	ASN
42	AB	56	ASP
42	AB	57	MET
42	AB	61	THR
42	AB	68	GLU
42	AB	91	VAL
42	AB	104	ASN
43	AC	16	LYS
43	AC	20	MET
43	AC	46	GLU
43	AC	71	LYS
43	AC	88	GLU
44	AD	43	VAL
44	AD	68	LEU
44	AD	71	VAL
44	AD	72	LYS
44	AD	92	TYR
44	AD	177	ASP
46	AF	5	THR
46	AF	13	ASN
46	AF	17	THR
46	AF	19	CYS
46	AF	37	CYS

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Mol	Chain	Res	Type
47	AG	28	ASP
47	AG	59	ILE
47	AG	107	ASP
47	AG	112	LEU
47	AG	132	ASN
47	AG	165	GLN
47	AG	170	ASP
48	AH	31	THR
48	AH	39	LYS
48	AH	58	ASP
48	AH	61	LYS
48	AH	78	ASP
48	AH	108	LEU
49	AI	31	LEU
50	AJ	24	VAL
50	AJ	31	LYS
50	AJ	45	LYS
50	AJ	54	LEU
50	AJ	59	ARG
50	AJ	134	GLU
50	AJ	136	GLU
50	AJ	168	ARG
51	AK	28	ARG
51	AK	74	TYR
51	AK	108	LYS
51	AK	111	LEU
52	AL	6	SER
52	AL	28	ARG
52	AL	37	TYR
53	AM	4	ASP
53	AM	28	SER
53	AM	38	ILE
53	AM	44	VAL
53	AM	50	LYS
53	AM	128	ARG
54	AN	26	VAL
54	AN	33	SER
54	AN	134	LEU
55	AO	108	THR
55	AO	115	CYS
55	AO	127	LEU
56	AP	2	VAL

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Mol	Chain	Res	Type
56	AP	29	LYS
56	AP	44	ASP
56	AP	61	LYS
56	AP	83	LEU
57	AQ	9	GLU
57	AQ	65	ARG
57	AQ	67	ARG
57	AQ	68	ARG
57	AQ	80	THR
57	AQ	117	ASN
57	AQ	183	THR
58	AR	4	ARG
58	AR	56	VAL
58	AR	60	TYR
58	AR	76	ASP
58	AR	78	LEU
58	AR	130	VAL
58	AR	136	GLU
59	AS	10	THR
59	AS	13	LEU
60	AT	20	SER
60	AT	91	GLU
61	AU	34	VAL
61	AU	56	ASP
61	AU	64	PHE
61	AU	85	ARG
61	AU	113	ASP
62	AV	21	ILE
63	AW	109	GLU
63	AW	161	ASP
63	AW	179	LEU
63	AW	180	LEU
63	AW	190	ARG
63	AW	242	ARG
64	AX	31	GLU
64	AX	82	ARG
64	AX	94	LEU
64	AX	113	TYR
64	AX	118	GLN
64	AX	128	ARG
64	AX	168	LEU
65	AY	24	THR

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Mol	Chain	Res	Type
65	AY	48	THR
65	AY	104	LEU
67	BA	55	THR
67	BA	79	VAL
67	BA	80	ASP
67	BA	85	VAL
67	BA	102	LEU
67	BA	123	TYR
67	BA	139	GLN
67	BA	146	ARG
67	BA	161	LEU
67	BA	178	LEU
67	BA	183	LEU
67	BA	211	GLN
67	BA	221	THR
67	BA	238	LEU
67	BA	296	THR
67	BA	320	ASP
68	BB	49	LEU
68	BB	69	ARG
68	BB	113	LYS
68	BB	138	LEU
68	BB	168	THR
68	BB	174	ARG
69	BC	31	ARG
69	BC	64	VAL
69	BC	68	GLU
69	BC	79	ARG
69	BC	82	GLU
69	BC	106	THR
69	BC	107	VAL
69	BC	110	GLU
70	BD	34	ASP
70	BD	43	ASP
70	BD	51	LEU
70	BD	70	CYS
70	BD	90	VAL
70	BD	101	MET
70	BD	137	VAL
70	BD	138	ARG
70	BD	143	ASN
70	BD	155	ARG

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Mol	Chain	Res	Type
70	BD	161	GLN
70	BD	162	GLN
70	BD	175	LEU
70	BD	199	LEU
70	BD	216	PHE
71	BE	98	ARG
71	BE	108	LYS
71	BE	150	LEU
71	BE	156	LEU
71	BE	194	TYR
71	BE	203	ARG
71	BE	206	LEU
71	BE	247	PHE
71	BE	326	ARG
71	BE	349	THR
71	BE	362	ASP
72	BF	10	LEU
72	BF	22	VAL
72	BF	160	GLU
72	BF	167	ARG
72	BF	181	ARG
73	BG	8	LYS
73	BG	19	ARG
73	BG	106	VAL
74	BH	61	ILE
74	BH	71	LYS
74	BH	106	LEU
74	BH	109	ASP
74	BH	119	ARG
74	BH	172	TYR
75	BI	23	ARG
75	BI	58	LYS
75	BI	111	GLN
75	BI	117	GLU
75	BI	140	ARG
75	BI	146	LEU
75	BI	152	ARG
75	BI	198	TYR
75	BI	259	LYS
76	BJ	27	LEU
76	BJ	72	VAL
76	BJ	85	LEU

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Mol	Chain	Res	Type
76	BJ	101	CYS
76	BJ	122	GLN
76	BJ	126	VAL
76	BJ	128	LEU
77	BK	5	HIS
77	BK	31	LYS
77	BK	87	ASN
78	BL	75	TYR
79	BM	15	VAL
79	BM	64	LEU
79	BM	77	ARG
79	BM	91	VAL
79	BM	145	LEU
79	BM	169	ASP
79	BM	171	PRO
80	BN	98	GLN
81	BO	24	GLU
81	BO	46	GLU
81	BO	92	ILE
81	BO	124	LEU
81	BO	179	LEU
82	BP	27	GLU
82	BP	30	GLU
82	BP	53	CYS
86	BT	73	LEU
86	BT	120	LEU
86	BT	132	LYS
86	BT	133	ASP
86	BT	155	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (92) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	74	GLN
2	A	101	GLN
3	B	104	ASN
3	B	139	ASN
7	F	83	GLN
8	G	42	GLN
9	H	44	ASN
9	H	90	ASN
9	H	122	HIS

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Mol	Chain	Res	Type
10	I	25	GLN
11	J	17	GLN
14	M	53	ASN
15	N	123	ASN
16	O	185	GLN
16	O	198	ASN
18	Q	49	ASN
18	Q	74	GLN
18	Q	99	ASN
18	Q	146	GLN
18	Q	183	GLN
18	Q	211	HIS
19	R	89	GLN
20	S	96	ASN
20	S	98	ASN
21	T	176	GLN
22	U	29	ASN
23	V	88	ASN
23	V	119	GLN
26	Y	36	GLN
29	b	15	ASN
31	d	63	GLN
34	g	51	ASN
38	h	680	GLN
38	h	1261	ASN
39	i	69	HIS
39	i	172	ASN
39	i	191	GLN
39	i	507	ASN
39	i	701	ASN
39	i	773	GLN
39	i	853	GLN
39	i	982	GLN
39	i	1066	GLN
39	i	1228	ASN
39	i	1250	GLN
40	j	187	GLN
40	k	176	GLN
41	AA	240	ASN
44	AD	37	ASN
44	AD	157	ASN
47	AG	132	ASN

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Mol	Chain	Res	Type
50	AJ	37	ASN
52	AL	32	ASN
52	AL	33	ASN
52	AL	50	ASN
53	AM	56	GLN
53	AM	62	GLN
56	AP	27	GLN
58	AR	44	ASN
58	AR	65	GLN
61	AU	14	HIS
61	AU	26	GLN
63	AW	19	HIS
63	AW	47	GLN
63	AW	194	ASN
63	AW	209	HIS
63	AW	211	HIS
63	AW	217	GLN
64	AX	97	ASN
65	AY	11	ASN
65	AY	47	ASN
65	AY	71	GLN
70	BD	161	GLN
70	BD	207	ASN
71	BE	48	GLN
71	BE	59	GLN
71	BE	114	ASN
71	BE	116	ASN
71	BE	260	GLN
72	BF	144	GLN
72	BF	166	ASN
75	BI	63	GLN
76	BJ	98	HIS
76	BJ	122	GLN
77	BK	87	ASN
79	BM	167	ASN
81	BO	157	ASN
82	BP	16	GLN
82	BP	20	GLN
82	BP	99	GLN
86	BT	88	ASN
86	BT	125	GLN

## 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1800 (98%)	729 (41%)	100 (5%)
35	l	33/34 (97%)	20 (60%)	0
36	m	75/76 (98%)	34 (45%)	0
37	n	76/77 (98%)	30 (39%)	0
83	BQ	3162/3396 (93%)	1066 (33%)	177 (5%)
84	BR	120/121 (99%)	35 (29%)	7 (5%)
85	BS	157/158 (99%)	50 (31%)	10 (6%)
All	All	5387/5662 (95%)	1964 (36%)	294 (5%)

All (1964) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	17	C
1	2	25	C
1	2	26	A
1	2	33	U
1	2	34	G
1	2	36	C
1	2	38	C
1	2	39	A
1	2	41	A
1	2	42	G
1	2	43	A
1	2	46	A
1	2	47	A
1	2	48	G
1	2	49	C
1	2	50	C
1	2	51	A
1	2	52	U
1	2	53	G
1	2	54	C
1	2	55	A
1	2	56	U
1	2	57	G
1	2	63	G
1	2	65	A
1	2	66	U

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Mol	Chain	Res	Type
1	2	67	A
1	2	68	A
1	2	69	G
1	2	70	C
1	2	71	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	76	A
1	2	78	A
1	2	80	A
1	2	81	G
1	2	83	G
1	2	86	A
1	2	92	A
1	2	99	C
1	2	104	A
1	2	105	A
1	2	106	U
1	2	111	U
1	2	112	A
1	2	114	C
1	2	115	G
1	2	116	U
1	2	117	U
1	2	120	U
1	2	121	U
1	2	124	A
1	2	127	G
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	138	A
1	2	139	C
1	2	140	A
1	2	141	U
1	2	142	G

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Mol	Chain	Res	Type
1	2	153	G
1	2	155	U
1	2	157	A
1	2	158	U
1	2	159	U
1	2	160	C
1	2	161	U
1	2	168	A
1	2	170	U
1	2	171	A
1	2	174	U
1	2	175	G
1	2	177	U
1	2	178	U
1	2	180	A
1	2	181	A
1	2	185	U
1	2	187	G
1	2	188	A
1	2	189	C
1	2	191	C
1	2	193	U
1	2	194	U
1	2	195	G
1	2	198	A
1	2	199	G
1	2	201	G
1	2	206	A
1	2	215	A
1	2	216	U
1	2	217	A
1	2	218	A
1	2	222	A
1	2	223	U
1	2	224	C
1	2	225	A
1	2	227	U
1	2	228	G
1	2	229	U
1	2	230	C
1	2	232	U
1	2	233	C

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Mol	Chain	Res	Type
1	2	234	G
1	2	235	G
1	2	236	A
1	2	240	U
1	2	241	U
1	2	243	G
1	2	250	C
1	2	257	A
1	2	259	U
1	2	260	U
1	2	262	U
1	2	265	A
1	2	266	A
1	2	267	U
1	2	272	U
1	2	275	C
1	2	278	U
1	2	279	G
1	2	280	U
1	2	281	G
1	2	282	C
1	2	283	U
1	2	285	G
1	2	296	U
1	2	299	A
1	2	302	U
1	2	308	C
1	2	309	C
1	2	312	A
1	2	313	U
1	2	314	C
1	2	316	A
1	2	317	C
1	2	319	U
1	2	320	U
1	2	321	C
1	2	322	G
1	2	323	A
1	2	329	G
1	2	330	G
1	2	331	A
1	2	333	A

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Mol	Chain	Res	Type
1	2	334	G
1	2	337	G
1	2	338	C
1	2	340	U
1	2	341	A
1	2	346	G
1	2	352	A
1	2	353	A
1	2	359	A
1	2	361	C
1	2	363	G
1	2	366	A
1	2	370	A
1	2	373	G
1	2	375	U
1	2	378	A
1	2	380	U
1	2	381	C
1	2	382	C
1	2	383	G
1	2	384	G
1	2	385	A
1	2	386	G
1	2	387	A
1	2	388	G
1	2	390	G
1	2	396	G
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	411	C
1	2	416	A
1	2	417	A
1	2	418	G
1	2	419	G
1	2	420	A
1	2	422	G
1	2	423	G
1	2	424	C
1	2	425	A
1	2	426	G

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Mol	Chain	Res	Type
1	2	427	C
1	2	429	G
1	2	430	G
1	2	431	C
1	2	434	G
1	2	435	C
1	2	436	A
1	2	437	A
1	2	439	U
1	2	440	U
1	2	442	C
1	2	444	C
1	2	446	A
1	2	448	C
1	2	452	A
1	2	453	U
1	2	454	U
1	2	455	C
1	2	459	G
1	2	460	A
1	2	464	A
1	2	471	A
1	2	474	A
1	2	475	A
1	2	477	A
1	2	486	G
1	2	488	G
1	2	491	C
1	2	492	A
1	2	493	U
1	2	494	U
1	2	495	C
1	2	496	G
1	2	498	G
1	2	500	C
1	2	502	U
1	2	505	A
1	2	506	A
1	2	507	U
1	2	510	G
1	2	515	A
1	2	517	U

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Mol	Chain	Res	Type
1	2	519	C
1	2	524	U
1	2	525	A
1	2	534	A
1	2	535	A
1	2	536	C
1	2	538	A
1	2	540	G
1	2	541	A
1	2	542	A
1	2	543	C
1	2	544	A
1	2	545	A
1	2	548	G
1	2	549	G
1	2	554	C
1	2	555	A
1	2	556	A
1	2	557	G
1	2	558	U
1	2	559	C
1	2	562	G
1	2	564	G
1	2	565	C
1	2	568	G
1	2	571	G
1	2	578	U
1	2	579	A
1	2	580	A
1	2	582	U
1	2	590	C
1	2	591	A
1	2	594	A
1	2	595	G
1	2	602	U
1	2	606	A
1	2	608	U
1	2	610	G
1	2	614	C
1	2	618	U
1	2	619	A
1	2	620	A

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Mol	Chain	Res	Type
1	2	622	A
1	2	623	A
1	2	624	G
1	2	639	U
1	2	640	U
1	2	641	G
1	2	644	C
1	2	647	G
1	2	650	U
1	2	651	G
1	2	652	G
1	2	653	C
1	2	655	G
1	2	656	G
1	2	657	U
1	2	678	A
1	2	680	U
1	2	681	U
1	2	687	G
1	2	690	G
1	2	693	U
1	2	694	U
1	2	696	C
1	2	697	C
1	2	698	U
1	2	699	U
1	2	700	C
1	2	702	G
1	2	704	C
1	2	705	U
1	2	706	A
1	2	708	C
1	2	709	C
1	2	710	U
1	2	711	U
1	2	712	G
1	2	713	A
1	2	714	G
1	2	715	U
1	2	716	C
1	2	717	C
1	2	718	U

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Mol	Chain	Res	Type
1	2	719	U
1	2	721	U
1	2	725	U
1	2	726	C
1	2	729	G
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	738	G
1	2	739	G
1	2	740	A
1	2	743	U
1	2	744	U
1	2	752	A
1	2	754	A
1	2	755	A
1	2	756	A
1	2	765	G
1	2	766	U
1	2	767	U
1	2	768	C
1	2	771	A
1	2	774	A
1	2	775	G
1	2	778	G
1	2	780	A
1	2	781	U
1	2	782	U
1	2	783	G
1	2	789	A
1	2	797	G
1	2	799	A
1	2	812	A
1	2	813	U
1	2	814	A
1	2	815	G
1	2	816	G
1	2	817	A
1	2	818	C

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Mol	Chain	Res	Type
1	2	819	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	824	G
1	2	826	U
1	2	831	U
1	2	832	U
1	2	833	U
1	2	834	G
1	2	835	U
1	2	836	U
1	2	838	G
1	2	840	U
1	2	841	U
1	2	842	C
1	2	845	G
1	2	846	G
1	2	847	A
1	2	852	C
1	2	856	A
1	2	857	U
1	2	858	G
1	2	859	A
1	2	860	U
1	2	863	A
1	2	864	U
1	2	876	G
1	2	882	U
1	2	894	U
1	2	895	G
1	2	896	U
1	2	899	G
1	2	900	A
1	2	911	U
1	2	912	U
1	2	913	G
1	2	914	G
1	2	915	A
1	2	916	U
1	2	918	U
1	2	921	U

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Mol	Chain	Res	Type
1	2	925	G
1	2	929	A
1	2	931	C
1	2	932	U
1	2	933	A
1	2	934	C
1	2	935	U
1	2	939	A
1	2	940	A
1	2	942	G
1	2	944	A
1	2	945	U
1	2	959	U
1	2	960	U
1	2	966	A
1	2	967	A
1	2	970	A
1	2	974	A
1	2	980	G
1	2	985	G
1	2	988	A
1	2	991	G
1	2	992	A
1	2	997	G
1	2	998	A
1	2	1004	U
1	2	1008	G
1	2	1009	U
1	2	1014	G
1	2	1021	C
1	2	1023	A
1	2	1024	U
1	2	1026	A
1	2	1028	C
1	2	1029	U
1	2	1030	A
1	2	1031	U
1	2	1032	G
1	2	1038	U
1	2	1039	A
1	2	1040	G
1	2	1047	G

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Mol	Chain	Res	Type
1	2	1052	U
1	2	1053	G
1	2	1058	U
1	2	1060	U
1	2	1061	A
1	2	1075	C
1	2	1076	A
1	2	1081	A
1	2	1082	C
1	2	1086	A
1	2	1087	A
1	2	1091	A
1	2	1092	A
1	2	1096	C
1	2	1097	U
1	2	1098	U
1	2	1099	U
1	2	1100	G
1	2	1108	G
1	2	1109	G
1	2	1114	G
1	2	1115	U
1	2	1138	A
1	2	1141	G
1	2	1143	A
1	2	1150	G
1	2	1158	C
1	2	1160	A
1	2	1164	G
1	2	1167	G
1	2	1168	U
1	2	1170	G
1	2	1171	A
1	2	1172	G
1	2	1173	C
1	2	1174	C
1	2	1175	U
1	2	1179	G
1	2	1185	U
1	2	1186	U
1	2	1193	A
1	2	1194	A

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Mol	Chain	Res	Type
1	2	1196	A
1	2	1197	C
1	2	1199	G
1	2	1200	G
1	2	1202	A
1	2	1203	A
1	2	1204	A
1	2	1205	C
1	2	1206	U
1	2	1209	C
1	2	1215	C
1	2	1216	C
1	2	1217	A
1	2	1218	G
1	2	1227	A
1	2	1228	G
1	2	1241	G
1	2	1243	G
1	2	1244	A
1	2	1245	G
1	2	1246	C
1	2	1247	U
1	2	1251	U
1	2	1252	C
1	2	1253	U
1	2	1255	G
1	2	1256	A
1	2	1257	U
1	2	1258	U
1	2	1259	U
1	2	1263	G
1	2	1273	G
1	2	1274	C
1	2	1275	A
1	2	1284	C
1	2	1285	U
1	2	1286	U
1	2	1287	A
1	2	1294	G
1	2	1299	G
1	2	1301	U
1	2	1307	U

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Mol	Chain	Res	Type
1	2	1314	U
1	2	1315	U
1	2	1316	G
1	2	1318	G
1	2	1321	A
1	2	1322	A
1	2	1324	G
1	2	1325	A
1	2	1337	A
1	2	1338	C
1	2	1339	C
1	2	1340	U
1	2	1344	A
1	2	1345	A
1	2	1346	A
1	2	1348	A
1	2	1349	G
1	2	1353	U
1	2	1354	G
1	2	1355	C
1	2	1356	U
1	2	1359	C
1	2	1360	A
1	2	1361	U
1	2	1363	U
1	2	1364	G
1	2	1365	C
1	2	1367	G
1	2	1368	G
1	2	1369	U
1	2	1370	U
1	2	1371	A
1	2	1372	U
1	2	1381	U
1	2	1382	A
1	2	1383	G
1	2	1388	A
1	2	1390	U
1	2	1391	A
1	2	1392	U
1	2	1395	G
1	2	1398	U

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Mol	Chain	Res	Type
1	2	1399	C
1	2	1400	A
1	2	1402	G
1	2	1403	C
1	2	1405	G
1	2	1410	A
1	2	1413	U
1	2	1414	U
1	2	1415	U
1	2	1417	A
1	2	1418	G
1	2	1421	A
1	2	1425	A
1	2	1427	A
1	2	1431	C
1	2	1432	U
1	2	1437	U
1	2	1444	A
1	2	1445	G
1	2	1446	A
1	2	1447	C
1	2	1448	G
1	2	1451	C
1	2	1458	G
1	2	1459	C
1	2	1460	A
1	2	1461	C
1	2	1462	G
1	2	1463	C
1	2	1465	C
1	2	1466	G
1	2	1467	C
1	2	1469	A
1	2	1470	C
1	2	1471	A
1	2	1472	C
1	2	1473	U
1	2	1474	G
1	2	1475	A
1	2	1476	C
1	2	1477	G
1	2	1478	G

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Mol	Chain	Res	Type
1	2	1479	A
1	2	1480	G
1	2	1481	C
1	2	1483	A
1	2	1486	G
1	2	1489	U
1	2	1490	C
1	2	1491	U
1	2	1492	A
1	2	1493	A
1	2	1496	U
1	2	1503	A
1	2	1506	G
1	2	1510	U
1	2	1514	U
1	2	1516	A
1	2	1517	U
1	2	1518	C
1	2	1520	U
1	2	1521	G
1	2	1522	U
1	2	1523	G
1	2	1524	A
1	2	1527	C
1	2	1528	U
1	2	1529	C
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1538	U
1	2	1540	G
1	2	1541	G
1	2	1542	G
1	2	1543	A
1	2	1545	A
1	2	1548	G
1	2	1554	U
1	2	1558	U
1	2	1559	A
1	2	1567	U
1	2	1568	C
1	2	1569	A

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Mol	Chain	Res	Type
1	2	1570	A
1	2	1571	C
1	2	1572	G
1	2	1573	A
1	2	1574	G
1	2	1575	G
1	2	1582	U
1	2	1584	G
1	2	1590	G
1	2	1595	U
1	2	1600	A
1	2	1601	G
1	2	1602	C
1	2	1603	U
1	2	1605	G
1	2	1607	G
1	2	1611	A
1	2	1616	G
1	2	1622	G
1	2	1631	A
1	2	1633	A
1	2	1634	C
1	2	1635	A
1	2	1636	C
1	2	1637	C
1	2	1638	G
1	2	1640	C
1	2	1645	G
1	2	1657	U
1	2	1658	G
1	2	1662	G
1	2	1673	G
1	2	1678	A
1	2	1682	U
1	2	1688	U
1	2	1689	A
1	2	1690	G
1	2	1691	A
1	2	1693	A
1	2	1709	C
1	2	1711	C
1	2	1712	A

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Mol	Chain	Res	Type
1	2	1717	G
1	2	1726	G
1	2	1730	A
1	2	1736	G
1	2	1738	U
1	2	1742	U
1	2	1743	U
1	2	1750	A
1	2	1753	A
1	2	1755	A
1	2	1757	G
1	2	1758	U
1	2	1760	G
1	2	1762	A
1	2	1765	A
1	2	1766	A
1	2	1767	G
1	2	1768	G
1	2	1769	U
1	2	1770	U
1	2	1780	G
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1793	G
1	2	1794	A
1	2	1796	C
1	2	1798	U
35	1	35	U
35	1	36	U
35	1	40	U
35	1	41	U
35	1	42	U
35	1	43	U
35	1	44	U
35	1	46	G
35	1	49	A
35	1	53	U
35	1	54	U
35	1	55	U
35	1	56	U
35	1	57	U

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Mol	Chain	Res	Type
35	l	58	U
35	l	59	U
35	l	60	U
35	l	61	U
35	l	64	U
35	l	66	U
36	m	3	G
36	m	7	U
36	m	8	U
36	m	15	G
36	m	16	U
36	m	18	G
36	m	20	U
36	m	21	A
36	m	30	G
36	m	36	U
36	m	41	A
36	m	43	U
36	m	45	G
36	m	46	G
36	m	47	U
36	m	48	C
36	m	49	G
36	m	50	C
36	m	51	A
36	m	52	G
36	m	53	G
36	m	54	U
36	m	55	U
36	m	56	C
36	m	58	A
36	m	59	A
36	m	60	U
36	m	61	C
36	m	64	G
36	m	66	A
36	m	67	C
36	m	68	G
36	m	73	A
36	m	74	C
37	n	2	G
37	n	3	A

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Mol	Chain	Res	Type
37	n	8	U
37	n	9	A
37	n	11	U
37	n	13	C
37	n	14	A
37	n	15	G
37	n	16	U
37	n	17	C
37	n	17(A)	G
37	n	18	G
37	n	19	U
37	n	20	U
37	n	21	A
37	n	44	G
37	n	47	U
37	n	48	C
37	n	49	G
37	n	52	G
37	n	53	G
37	n	57	G
37	n	59	G
37	n	60	U
37	n	61	C
37	n	62	C
37	n	68	G
37	n	69	U
37	n	74	C
37	n	76	A
83	BQ	4	U
83	BQ	6	A
83	BQ	13	A
83	BQ	14	U
83	BQ	16	A
83	BQ	20	A
83	BQ	21	G
83	BQ	22	G
83	BQ	26	A
83	BQ	27	C
83	BQ	30	G
83	BQ	40	A
83	BQ	43	A
83	BQ	47	C

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Mol	Chain	Res	Type
83	BQ	49	A
83	BQ	57	A
83	BQ	59	G
83	BQ	60	A
83	BQ	65	A
83	BQ	66	A
83	BQ	71	A
83	BQ	72	C
83	BQ	73	C
83	BQ	74	G
83	BQ	75	G
83	BQ	77	A
83	BQ	86	G
83	BQ	87	U
83	BQ	89	A
83	BQ	92	G
83	BQ	96	G
83	BQ	97	U
83	BQ	98	G
83	BQ	108	A
83	BQ	111	C
83	BQ	119	U
83	BQ	120	G
83	BQ	121	A
83	BQ	122	A
83	BQ	123	A
83	BQ	131	C
83	BQ	134	U
83	BQ	135	C
83	BQ	136	G
83	BQ	139	G
83	BQ	146	U
83	BQ	147	U
83	BQ	148	G
83	BQ	150	A
83	BQ	153	U
83	BQ	154	U
83	BQ	155	G
83	BQ	156	G
83	BQ	157	A
83	BQ	158	G
83	BQ	161	G

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Mol	Chain	Res	Type
83	BQ	165	A
83	BQ	166	C
83	BQ	167	U
83	BQ	168	U
83	BQ	170	G
83	BQ	172	G
83	BQ	173	G
83	BQ	187	A
83	BQ	188	U
83	BQ	189	G
83	BQ	190	U
83	BQ	191	U
83	BQ	201	A
83	BQ	206	G
83	BQ	210	U
83	BQ	211	A
83	BQ	212	G
83	BQ	213	A
83	BQ	217	U
83	BQ	218	G
83	BQ	219	A
83	BQ	220	G
83	BQ	222	A
83	BQ	230	U
83	BQ	231	G
83	BQ	234	G
83	BQ	237	G
83	BQ	240	U
83	BQ	241	G
83	BQ	242	C
83	BQ	245	U
83	BQ	247	C
83	BQ	248	U
83	BQ	250	U
83	BQ	251	G
83	BQ	252	U
83	BQ	268	A
83	BQ	269	G
83	BQ	270	U
83	BQ	281	G
83	BQ	282	G
83	BQ	283	G

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Mol	Chain	Res	Type
83	BQ	286	U
83	BQ	287	G
83	BQ	289	A
83	BQ	295	A
83	BQ	297	G
83	BQ	298	U
83	BQ	304	G
83	BQ	305	U
83	BQ	315	C
83	BQ	317	A
83	BQ	323	A
83	BQ	329	U
83	BQ	330	G
83	BQ	336	A
83	BQ	338	A
83	BQ	342	A
83	BQ	346	C
83	BQ	349	A
83	BQ	350	C
83	BQ	353	G
83	BQ	354	U
83	BQ	367	A
83	BQ	370	U
83	BQ	372	A
83	BQ	375	A
83	BQ	376	G
83	BQ	377	A
83	BQ	385	A
83	BQ	395	A
83	BQ	396	A
83	BQ	398	A
83	BQ	399	A
83	BQ	400	G
83	BQ	401	U
83	BQ	402	A
83	BQ	403	C
83	BQ	404	G
83	BQ	421	G
83	BQ	422	A
83	BQ	428	A
83	BQ	429	U
83	BQ	438	A

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Mol	Chain	Res	Type
83	BQ	440	A
83	BQ	495	G
83	BQ	496	C
83	BQ	503	C
83	BQ	507	U
83	BQ	520	U
83	BQ	521	A
83	BQ	522	A
83	BQ	523	A
83	BQ	525	C
83	BQ	527	A
83	BQ	529	A
83	BQ	531	G
83	BQ	532	A
83	BQ	533	A
83	BQ	535	G
83	BQ	541	U
83	BQ	543	C
83	BQ	544	C
83	BQ	546	C
83	BQ	547	G
83	BQ	548	G
83	BQ	551	A
83	BQ	552	G
83	BQ	555	U
83	BQ	557	A
83	BQ	559	A
83	BQ	566	G
83	BQ	569	A
83	BQ	572	A
83	BQ	575	G
83	BQ	578	A
83	BQ	579	G
83	BQ	581	U
83	BQ	588	G
83	BQ	589	A
83	BQ	592	A
83	BQ	594	U
83	BQ	597	G
83	BQ	601	U
83	BQ	604	G
83	BQ	608	A

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Mol	Chain	Res	Type
83	BQ	609	G
83	BQ	611	A
83	BQ	612	U
83	BQ	615	U
83	BQ	616	G
83	BQ	617	G
83	BQ	620	U
83	BQ	621	A
83	BQ	622	A
83	BQ	627	U
83	BQ	629	U
83	BQ	634	C
83	BQ	636	C
83	BQ	637	C
83	BQ	642	U
83	BQ	643	U
83	BQ	649	A
83	BQ	661	G
83	BQ	664	U
83	BQ	666	A
83	BQ	667	C
83	BQ	676	G
83	BQ	677	A
83	BQ	678	G
83	BQ	681	U
83	BQ	690	A
83	BQ	691	A
83	BQ	692	A
83	BQ	699	A
83	BQ	705	A
83	BQ	709	A
83	BQ	712	G
83	BQ	715	A
83	BQ	716	A
83	BQ	719	U
83	BQ	720	A
83	BQ	721	G
83	BQ	726	G
83	BQ	728	G
83	BQ	735	A
83	BQ	742	G
83	BQ	757	C

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Mol	Chain	Res	Type
83	BQ	760	G
83	BQ	764	U
83	BQ	765	C
83	BQ	766	U
83	BQ	767	U
83	BQ	768	C
83	BQ	770	G
83	BQ	776	U
83	BQ	777	U
83	BQ	781	G
83	BQ	784	A
83	BQ	785	G
83	BQ	787	G
83	BQ	792	G
83	BQ	799	G
83	BQ	800	G
83	BQ	801	A
83	BQ	806	A
83	BQ	808	A
83	BQ	816	A
83	BQ	817	A
83	BQ	826	G
83	BQ	830	A
83	BQ	835	G
83	BQ	847	A
83	BQ	849	C
83	BQ	861	C
83	BQ	871	U
83	BQ	874	U
83	BQ	875	G
83	BQ	879	U
83	BQ	880	G
83	BQ	882	A
83	BQ	885	U
83	BQ	895	A
83	BQ	896	A
83	BQ	897	U
83	BQ	907	G
83	BQ	913	A
83	BQ	914	A
83	BQ	915	A
83	BQ	916	G

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Mol	Chain	Res	Type
83	BQ	917	A
83	BQ	921	A
83	BQ	922	U
83	BQ	923	C
83	BQ	924	G
83	BQ	925	A
83	BQ	926	A
83	BQ	933	A
83	BQ	934	G
83	BQ	937	G
83	BQ	938	C
83	BQ	939	U
83	BQ	944	C
83	BQ	953	G
83	BQ	954	U
83	BQ	959	C
83	BQ	960	U
83	BQ	961	C
83	BQ	962	A
83	BQ	964	G
83	BQ	974	G
83	BQ	977	C
83	BQ	979	U
83	BQ	980	A
83	BQ	981	U
83	BQ	984	G
83	BQ	991	G
83	BQ	993	G
83	BQ	994	G
83	BQ	995	U
83	BQ	996	A
83	BQ	1001	G
83	BQ	1005	G
83	BQ	1007	U
83	BQ	1008	U
83	BQ	1010	G
83	BQ	1013	G
83	BQ	1015	U
83	BQ	1016	C
83	BQ	1017	C
83	BQ	1018	G
83	BQ	1019	G

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Mol	Chain	Res	Type
83	BQ	1020	G
83	BQ	1023	C
83	BQ	1025	A
83	BQ	1028	U
83	BQ	1029	G
83	BQ	1030	A
83	BQ	1032	C
83	BQ	1033	U
83	BQ	1036	A
83	BQ	1038	C
83	BQ	1042	U
83	BQ	1043	C
83	BQ	1045	C
83	BQ	1047	A
83	BQ	1049	C
83	BQ	1050	U
83	BQ	1063	G
83	BQ	1065	A
83	BQ	1071	U
83	BQ	1076	C
83	BQ	1077	U
83	BQ	1081	U
83	BQ	1083	G
83	BQ	1087	G
83	BQ	1092	C
83	BQ	1093	A
83	BQ	1094	U
83	BQ	1095	U
83	BQ	1096	U
83	BQ	1097	G
83	BQ	1098	A
83	BQ	1102	A
83	BQ	1103	A
83	BQ	1104	G
83	BQ	1117	G
83	BQ	1125	U
83	BQ	1128	U
83	BQ	1131	G
83	BQ	1140	G
83	BQ	1142	G
83	BQ	1143	A
83	BQ	1144	U

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Mol	Chain	Res	Type
83	BQ	1145	G
83	BQ	1149	G
83	BQ	1150	A
83	BQ	1151	U
83	BQ	1153	A
83	BQ	1154	A
83	BQ	1155	C
83	BQ	1159	A
83	BQ	1171	G
83	BQ	1172	G
83	BQ	1177	G
83	BQ	1178	G
83	BQ	1180	A
83	BQ	1181	U
83	BQ	1182	A
83	BQ	1186	G
83	BQ	1191	U
83	BQ	1192	C
83	BQ	1193	A
83	BQ	1197	A
83	BQ	1199	C
83	BQ	1200	A
83	BQ	1201	C
83	BQ	1202	A
83	BQ	1206	G
83	BQ	1213	G
83	BQ	1217	A
83	BQ	1220	U
83	BQ	1222	G
83	BQ	1223	A
83	BQ	1225	A
83	BQ	1228	C
83	BQ	1230	G
83	BQ	1233	G
83	BQ	1234	G
83	BQ	1235	U
83	BQ	1236	G
83	BQ	1237	G
83	BQ	1238	C
83	BQ	1239	C
83	BQ	1240	A
83	BQ	1241	U

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Mol	Chain	Res	Type
83	BQ	1242	G
83	BQ	1243	G
83	BQ	1245	A
83	BQ	1246	G
83	BQ	1247	U
83	BQ	1248	C
83	BQ	1249	G
83	BQ	1251	A
83	BQ	1252	A
83	BQ	1253	U
83	BQ	1254	C
83	BQ	1256	G
83	BQ	1257	C
83	BQ	1260	A
83	BQ	1262	G
83	BQ	1263	A
83	BQ	1264	G
83	BQ	1265	U
83	BQ	1266	G
83	BQ	1267	U
83	BQ	1270	A
83	BQ	1271	A
83	BQ	1272	C
83	BQ	1273	A
83	BQ	1274	A
83	BQ	1275	C
83	BQ	1276	U
83	BQ	1277	C
83	BQ	1278	A
83	BQ	1279	C
83	BQ	1280	C
83	BQ	1281	G
83	BQ	1282	G
83	BQ	1285	G
83	BQ	1286	A
83	BQ	1287	A
83	BQ	1294	A
83	BQ	1301	A
83	BQ	1303	A
83	BQ	1305	U
83	BQ	1308	A
83	BQ	1309	U

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Mol	Chain	Res	Type
83	BQ	1313	G
83	BQ	1315	U
83	BQ	1316	C
83	BQ	1317	A
83	BQ	1318	A
83	BQ	1321	G
83	BQ	1325	U
83	BQ	1329	U
83	BQ	1330	A
83	BQ	1332	A
83	BQ	1334	U
83	BQ	1345	G
83	BQ	1348	U
83	BQ	1349	G
83	BQ	1351	U
83	BQ	1353	U
83	BQ	1354	G
83	BQ	1355	A
83	BQ	1356	U
83	BQ	1357	G
83	BQ	1359	C
83	BQ	1364	C
83	BQ	1382	G
83	BQ	1386	A
83	BQ	1391	C
83	BQ	1392	G
83	BQ	1393	A
83	BQ	1399	A
83	BQ	1400	G
83	BQ	1408	G
83	BQ	1418	A
83	BQ	1419	A
83	BQ	1424	C
83	BQ	1429	G
83	BQ	1430	U
83	BQ	1432	C
83	BQ	1434	G
83	BQ	1435	A
83	BQ	1437	C
83	BQ	1446	A
83	BQ	1447	G
83	BQ	1448	U

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Mol	Chain	Res	Type
83	BQ	1450	G
83	BQ	1452	A
83	BQ	1456	A
83	BQ	1464	G
83	BQ	1468	A
83	BQ	1480	G
83	BQ	1481	A
83	BQ	1482	A
83	BQ	1483	G
83	BQ	1484	U
83	BQ	1485	G
83	BQ	1487	G
83	BQ	1508	C
83	BQ	1512	U
83	BQ	1514	G
83	BQ	1523	U
83	BQ	1527	C
83	BQ	1533	U
83	BQ	1536	G
83	BQ	1539	A
83	BQ	1542	G
83	BQ	1549	U
83	BQ	1554	U
83	BQ	1555	U
83	BQ	1556	C
83	BQ	1557	A
83	BQ	1558	A
83	BQ	1559	A
83	BQ	1560	G
83	BQ	1561	G
83	BQ	1563	C
83	BQ	1567	U
83	BQ	1568	U
83	BQ	1569	U
83	BQ	1570	U
83	BQ	1571	A
83	BQ	1572	U
83	BQ	1576	G
83	BQ	1577	G
83	BQ	1578	C
83	BQ	1579	C
83	BQ	1580	A

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Mol	Chain	Res	Type
83	BQ	1581	C
83	BQ	1582	C
83	BQ	1583	A
83	BQ	1587	A
83	BQ	1588	A
83	BQ	1589	A
83	BQ	1593	A
83	BQ	1596	C
83	BQ	1597	C
83	BQ	1602	A
83	BQ	1603	A
83	BQ	1605	A
83	BQ	1613	A
83	BQ	1619	A
83	BQ	1620	U
83	BQ	1621	A
83	BQ	1630	U
83	BQ	1631	C
83	BQ	1632	A
83	BQ	1645	U
83	BQ	1646	G
83	BQ	1656	A
83	BQ	1657	C
83	BQ	1658	G
83	BQ	1659	U
83	BQ	1662	G
83	BQ	1683	A
83	BQ	1684	U
83	BQ	1692	U
83	BQ	1694	U
83	BQ	1696	A
83	BQ	1697	A
83	BQ	1702	U
83	BQ	1704	A
83	BQ	1708	C
83	BQ	1713	G
83	BQ	1714	A
83	BQ	1717	U
83	BQ	1718	G
83	BQ	1724	U
83	BQ	1725	C
83	BQ	1728	G

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Mol	Chain	Res	Type
83	BQ	1729	A
83	BQ	1730	G
83	BQ	1731	A
83	BQ	1735	G
83	BQ	1740	U
83	BQ	1741	A
83	BQ	1750	A
83	BQ	1751	G
83	BQ	1752	A
83	BQ	1760	A
83	BQ	1761	C
83	BQ	1762	C
83	BQ	1763	U
83	BQ	1765	U
83	BQ	1769	G
83	BQ	1770	G
83	BQ	1775	G
83	BQ	1780	G
83	BQ	1785	U
83	BQ	1788	C
83	BQ	1794	G
83	BQ	1797	A
83	BQ	1809	A
83	BQ	1813	A
83	BQ	1814	A
83	BQ	1815	U
83	BQ	1816	A
83	BQ	1817	G
83	BQ	1819	U
83	BQ	1820	U
83	BQ	1821	U
83	BQ	1822	C
83	BQ	1834	U
83	BQ	1835	A
83	BQ	1839	A
83	BQ	1840	U
83	BQ	1841	A
83	BQ	1842	A
83	BQ	1845	G
83	BQ	1846	C
83	BQ	1847	A
83	BQ	1848	G

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Mol	Chain	Res	Type
83	BQ	1849	C
83	BQ	1851	G
83	BQ	1854	C
83	BQ	1855	U
83	BQ	1856	C
83	BQ	1866	C
83	BQ	1868	G
83	BQ	1871	U
83	BQ	1877	U
83	BQ	1879	A
83	BQ	1880	U
83	BQ	1881	A
83	BQ	1884	A
83	BQ	1885	U
83	BQ	1886	A
83	BQ	1893	A
83	BQ	1894	U
83	BQ	1895	A
83	BQ	1899	G
83	BQ	1900	A
83	BQ	1901	A
83	BQ	1905	G
83	BQ	1906	G
83	BQ	1914	G
83	BQ	1918	C
83	BQ	1927	G
83	BQ	1930	A
83	BQ	1931	U
83	BQ	1932	A
83	BQ	1936	A
83	BQ	1942	U
83	BQ	1947	G
83	BQ	1948	G
83	BQ	1949	G
83	BQ	1952	G
83	BQ	1953	G
83	BQ	1954	G
83	BQ	2095	G
83	BQ	2099	A
83	BQ	2100	A
83	BQ	2101	C
83	BQ	2102	U

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Mol	Chain	Res	Type
83	BQ	2106	A
83	BQ	2107	A
83	BQ	2108	C
83	BQ	2111	G
83	BQ	2112	U
83	BQ	2113	A
83	BQ	2116	G
83	BQ	2117	A
83	BQ	2121	G
83	BQ	2122	G
83	BQ	2126	A
83	BQ	2131	A
83	BQ	2138	A
83	BQ	2139	A
83	BQ	2140	U
83	BQ	2158	A
83	BQ	2159	U
83	BQ	2160	G
83	BQ	2163	C
83	BQ	2169	G
83	BQ	2170	U
83	BQ	2175	U
83	BQ	2178	A
83	BQ	2179	C
83	BQ	2180	G
83	BQ	2184	U
83	BQ	2186	U
83	BQ	2188	A
83	BQ	2192	C
83	BQ	2193	U
83	BQ	2194	G
83	BQ	2197	C
83	BQ	2198	A
83	BQ	2205	U
83	BQ	2206	G
83	BQ	2207	A
83	BQ	2208	A
83	BQ	2209	U
83	BQ	2210	G
83	BQ	2212	C
83	BQ	2225	U
83	BQ	2243	A

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Mol	Chain	Res	Type
83	BQ	2244	A
83	BQ	2246	G
83	BQ	2249	G
83	BQ	2255	A
83	BQ	2256	A
83	BQ	2257	C
83	BQ	2261	G
83	BQ	2263	C
83	BQ	2270	A
83	BQ	2272	G
83	BQ	2274	U
83	BQ	2279	A
83	BQ	2280	A
83	BQ	2281	A
83	BQ	2282	U
83	BQ	2283	G
83	BQ	2284	C
83	BQ	2288	G
83	BQ	2298	U
83	BQ	2303	A
83	BQ	2306	C
83	BQ	2307	G
83	BQ	2308	C
83	BQ	2313	A
83	BQ	2314	U
83	BQ	2315	G
83	BQ	2318	U
83	BQ	2319	U
83	BQ	2336	U
83	BQ	2340	U
83	BQ	2357	A
83	BQ	2364	G
83	BQ	2373	A
83	BQ	2374	C
83	BQ	2375	G
83	BQ	2378	C
83	BQ	2383	C
83	BQ	2386	A
83	BQ	2388	U
83	BQ	2393	G
83	BQ	2394	G
83	BQ	2397	A

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Mol	Chain	Res	Type
83	BQ	2398	A
83	BQ	2402	A
83	BQ	2403	G
83	BQ	2411	U
83	BQ	2412	G
83	BQ	2418	G
83	BQ	2419	A
83	BQ	2433	U
83	BQ	2435	G
83	BQ	2436	U
83	BQ	2437	G
83	BQ	2439	A
83	BQ	2441	A
83	BQ	2442	G
83	BQ	2444	C
83	BQ	2445	A
83	BQ	2446	U
83	BQ	2447	A
83	BQ	2451	G
83	BQ	2452	G
83	BQ	2493	U
83	BQ	2494	A
83	BQ	2496	C
83	BQ	2497	U
83	BQ	2498	U
83	BQ	2501	U
83	BQ	2502	A
83	BQ	2508	U
83	BQ	2509	U
83	BQ	2514	U
83	BQ	2515	A
83	BQ	2522	G
83	BQ	2523	A
83	BQ	2524	A
83	BQ	2526	C
83	BQ	2530	G
83	BQ	2531	C
83	BQ	2533	G
83	BQ	2534	G
83	BQ	2537	U
83	BQ	2538	U
83	BQ	2539	C

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Mol	Chain	Res	Type
83	BQ	2540	A
83	BQ	2541	U
83	BQ	2542	U
83	BQ	2544	U
83	BQ	2546	C
83	BQ	2547	A
83	BQ	2550	U
83	BQ	2552	C
83	BQ	2554	A
83	BQ	2555	G
83	BQ	2559	U
83	BQ	2560	C
83	BQ	2567	C
83	BQ	2568	C
83	BQ	2570	U
83	BQ	2571	U
83	BQ	2572	C
83	BQ	2578	U
83	BQ	2585	G
83	BQ	2587	U
83	BQ	2589	G
83	BQ	2590	A
83	BQ	2593	A
83	BQ	2594	C
83	BQ	2600	C
83	BQ	2606	G
83	BQ	2607	G
83	BQ	2614	G
83	BQ	2618	G
83	BQ	2619	G
83	BQ	2624	G
83	BQ	2626	A
83	BQ	2627	C
83	BQ	2629	U
83	BQ	2641	U
83	BQ	2642	A
83	BQ	2652	U
83	BQ	2655	U
83	BQ	2656	A
83	BQ	2657	A
83	BQ	2666	C
83	BQ	2672	G

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Mol	Chain	Res	Type
83	BQ	2674	A
83	BQ	2678	A
83	BQ	2679	A
83	BQ	2681	U
83	BQ	2688	U
83	BQ	2689	A
83	BQ	2690	G
83	BQ	2691	A
83	BQ	2694	A
83	BQ	2695	A
83	BQ	2703	A
83	BQ	2704	A
83	BQ	2709	C
83	BQ	2713	U
83	BQ	2714	G
83	BQ	2716	U
83	BQ	2726	C
83	BQ	2727	A
83	BQ	2728	G
83	BQ	2737	C
83	BQ	2740	A
83	BQ	2747	A
83	BQ	2749	G
83	BQ	2751	G
83	BQ	2752	U
83	BQ	2753	G
83	BQ	2754	G
83	BQ	2755	C
83	BQ	2761	G
83	BQ	2762	A
83	BQ	2772	C
83	BQ	2776	C
83	BQ	2777	G
83	BQ	2778	G
83	BQ	2779	A
83	BQ	2795	U
83	BQ	2796	G
83	BQ	2800	G
83	BQ	2801	A
83	BQ	2802	A
83	BQ	2803	A
83	BQ	2804	A

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Mol	Chain	Res	Type
83	BQ	2810	C
83	BQ	2814	G
83	BQ	2816	G
83	BQ	2817	A
83	BQ	2821	C
83	BQ	2829	U
83	BQ	2834	G
83	BQ	2837	A
83	BQ	2839	G
83	BQ	2842	U
83	BQ	2845	A
83	BQ	2849	C
83	BQ	2855	U
83	BQ	2859	U
83	BQ	2860	U
83	BQ	2862	U
83	BQ	2863	G
83	BQ	2864	A
83	BQ	2867	C
83	BQ	2870	C
83	BQ	2871	G
83	BQ	2872	A
83	BQ	2875	U
83	BQ	2877	G
83	BQ	2883	U
83	BQ	2888	U
83	BQ	2889	C
83	BQ	2898	G
83	BQ	2901	G
83	BQ	2911	A
83	BQ	2912	G
83	BQ	2923	U
83	BQ	2925	C
83	BQ	2928	C
83	BQ	2930	A
83	BQ	2933	A
83	BQ	2935	U
83	BQ	2936	A
83	BQ	2938	G
83	BQ	2941	A
83	BQ	2942	C
83	BQ	2945	G

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Mol	Chain	Res	Type
83	BQ	2947	G
83	BQ	2950	G
83	BQ	2951	G
83	BQ	2953	U
83	BQ	2954	U
83	BQ	2955	U
83	BQ	2971	A
83	BQ	2972	G
83	BQ	2977	G
83	BQ	2978	U
83	BQ	2979	U
83	BQ	2983	C
83	BQ	2990	G
83	BQ	2996	U
83	BQ	2997	G
83	BQ	3004	C
83	BQ	3012	A
83	BQ	3013	U
83	BQ	3022	G
83	BQ	3023	U
83	BQ	3026	G
83	BQ	3030	G
83	BQ	3034	C
83	BQ	3039	C
83	BQ	3040	A
83	BQ	3047	U
83	BQ	3048	A
83	BQ	3049	A
83	BQ	3056	U
83	BQ	3057	U
83	BQ	3058	U
83	BQ	3059	G
83	BQ	3061	G
83	BQ	3074	G
83	BQ	3077	A
83	BQ	3078	U
83	BQ	3079	U
83	BQ	3080	G
83	BQ	3086	A
83	BQ	3090	U
83	BQ	3092	C
83	BQ	3094	A

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Mol	Chain	Res	Type
83	BQ	3099	C
83	BQ	3100	U
83	BQ	3104	U
83	BQ	3109	G
83	BQ	3111	U
83	BQ	3112	G
83	BQ	3113	A
83	BQ	3115	C
83	BQ	3116	G
83	BQ	3117	C
83	BQ	3119	U
83	BQ	3120	C
83	BQ	3122	A
83	BQ	3123	A
83	BQ	3126	C
83	BQ	3129	A
83	BQ	3130	A
83	BQ	3131	U
83	BQ	3138	U
83	BQ	3142	A
83	BQ	3143	C
83	BQ	3144	G
83	BQ	3152	U
83	BQ	3153	U
83	BQ	3154	C
83	BQ	3155	U
83	BQ	3156	U
83	BQ	3157	U
83	BQ	3158	G
83	BQ	3168	A
83	BQ	3171	U
83	BQ	3172	A
83	BQ	3173	G
83	BQ	3174	A
83	BQ	3175	U
83	BQ	3176	G
83	BQ	3178	A
83	BQ	3179	U
83	BQ	3180	A
83	BQ	3181	C
83	BQ	3183	A
83	BQ	3185	U

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Mol	Chain	Res	Type
83	BQ	3187	A
83	BQ	3193	C
83	BQ	3194	C
83	BQ	3195	U
83	BQ	3197	G
83	BQ	3198	U
83	BQ	3206	C
83	BQ	3207	U
83	BQ	3208	G
83	BQ	3209	A
83	BQ	3210	A
83	BQ	3216	G
83	BQ	3217	C
83	BQ	3218	A
83	BQ	3220	G
83	BQ	3224	G
83	BQ	3227	A
83	BQ	3228	C
83	BQ	3229	G
83	BQ	3231	U
83	BQ	3237	U
83	BQ	3238	G
83	BQ	3241	G
83	BQ	3242	G
83	BQ	3244	A
83	BQ	3245	A
83	BQ	3246	G
83	BQ	3247	G
83	BQ	3259	U
83	BQ	3261	C
83	BQ	3262	U
83	BQ	3263	G
83	BQ	3268	A
83	BQ	3269	U
83	BQ	3270	U
83	BQ	3271	G
83	BQ	3272	C
83	BQ	3273	A
83	BQ	3274	A
83	BQ	3275	U
83	BQ	3276	G
83	BQ	3277	U

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Mol	Chain	Res	Type
83	BQ	3278	C
83	BQ	3279	A
83	BQ	3287	U
83	BQ	3288	G
83	BQ	3289	G
83	BQ	3294	A
83	BQ	3295	A
83	BQ	3304	U
83	BQ	3305	A
83	BQ	3308	C
83	BQ	3313	U
83	BQ	3316	A
83	BQ	3317	U
83	BQ	3318	G
83	BQ	3319	U
83	BQ	3320	A
83	BQ	3322	A
83	BQ	3324	C
83	BQ	3330	A
83	BQ	3334	U
83	BQ	3335	A
83	BQ	3339	A
83	BQ	3342	A
83	BQ	3345	G
83	BQ	3346	U
83	BQ	3347	A
83	BQ	3348	G
83	BQ	3351	U
83	BQ	3352	U
83	BQ	3353	G
83	BQ	3354	U
83	BQ	3355	U
83	BQ	3356	G
83	BQ	3357	U
83	BQ	3362	A
83	BQ	3364	C
83	BQ	3368	U
83	BQ	3369	G
83	BQ	3370	A
83	BQ	3375	A
83	BQ	3378	C
83	BQ	3382	U

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Mol	Chain	Res	Type
83	BQ	3383	G
83	BQ	3390	G
84	BR	10	C
84	BR	11	A
84	BR	13	A
84	BR	14	U
84	BR	19	C
84	BR	20	A
84	BR	22	A
84	BR	23	A
84	BR	26	C
84	BR	29	C
84	BR	32	U
84	BR	33	U
84	BR	41	G
84	BR	42	A
84	BR	49	G
84	BR	53	U
84	BR	54	U
84	BR	55	A
84	BR	56	A
84	BR	65	G
84	BR	71	G
84	BR	73	C
84	BR	74	C
84	BR	77	G
84	BR	78	U
84	BR	79	A
84	BR	87	G
84	BR	91	G
84	BR	99	G
84	BR	101	G
84	BR	102	A
84	BR	103	A
84	BR	111	U
84	BR	112	G
84	BR	121	U
85	BS	8	C
85	BS	15	G
85	BS	16	G
85	BS	17	A
85	BS	22	U

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Mol	Chain	Res	Type
85	BS	23	U
85	BS	24	G
85	BS	34	U
85	BS	35	C
85	BS	39	G
85	BS	40	A
85	BS	49	G
85	BS	50	C
85	BS	51	G
85	BS	52	A
85	BS	59	A
85	BS	60	U
85	BS	61	A
85	BS	62	C
85	BS	63	G
85	BS	80	A
85	BS	81	U
85	BS	82	U
85	BS	83	C
85	BS	84	C
85	BS	85	G
85	BS	86	U
85	BS	87	G
85	BS	90	U
85	BS	91	C
85	BS	95	G
85	BS	97	A
85	BS	102	U
85	BS	104	A
85	BS	106	C
85	BS	110	C
85	BS	112	U
85	BS	113	U
85	BS	115	C
85	BS	116	G
85	BS	125	U
85	BS	126	A
85	BS	127	U
85	BS	129	C
85	BS	144	G
85	BS	148	G
85	BS	151	C

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Mol	Chain	Res	Type
85	BS	152	G
85	BS	154	C
85	BS	158	U

All (294) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	42	G
1	2	51	A
1	2	52	U
1	2	53	G
1	2	54	C
1	2	55	A
1	2	66	U
1	2	68	A
1	2	77	U
1	2	104	A
1	2	114	C
1	2	115	G
1	2	126	A
1	2	128	U
1	2	132	U
1	2	139	C
1	2	141	U
1	2	158	U
1	2	159	U
1	2	174	U
1	2	224	C
1	2	266	A
1	2	278	U
1	2	280	U
1	2	312	A
1	2	313	U
1	2	322	G
1	2	352	A
1	2	379	U
1	2	380	U
1	2	381	C
1	2	385	A
1	2	387	A
1	2	400	A
1	2	410	A

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Mol	Chain	Res	Type
1	2	411	C
1	2	425	A
1	2	429	G
1	2	430	G
1	2	439	U
1	2	454	U
1	2	539	G
1	2	541	A
1	2	555	A
1	2	578	U
1	2	609	U
1	2	613	G
1	2	619	A
1	2	639	U
1	2	696	C
1	2	699	U
1	2	705	U
1	2	711	U
1	2	754	A
1	2	765	G
1	2	766	U
1	2	782	U
1	2	819	G
1	2	913	G
1	2	928	U
1	2	944	A
1	2	1023	A
1	2	1081	A
1	2	1092	A
1	2	1108	G
1	2	1114	G
1	2	1173	C
1	2	1185	U
1	2	1193	A
1	2	1226	A
1	2	1244	A
1	2	1245	G
1	2	1251	U
1	2	1256	A
1	2	1273	G
1	2	1274	C
1	2	1314	U

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Mol	Chain	Res	Type
1	2	1344	A
1	2	1357	A
1	2	1369	U
1	2	1370	U
1	2	1382	A
1	2	1399	C
1	2	1412	G
1	2	1430	U
1	2	1457	C
1	2	1472	C
1	2	1481	C
1	2	1520	U
1	2	1539	G
1	2	1570	A
1	2	1573	A
1	2	1601	G
1	2	1615	C
1	2	1633	A
1	2	1636	C
1	2	1742	U
1	2	1761	U
1	2	1767	G
1	2	1791	A
83	BQ	13	A
83	BQ	21	G
83	BQ	40	A
83	BQ	43	A
83	BQ	66	A
83	BQ	71	A
83	BQ	86	G
83	BQ	97	U
83	BQ	154	U
83	BQ	155	G
83	BQ	189	G
83	BQ	211	A
83	BQ	269	G
83	BQ	282	G
83	BQ	316	U
83	BQ	349	A
83	BQ	352	A
83	BQ	353	G
83	BQ	369	A

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Mol	Chain	Res	Type
83	BQ	374	A
83	BQ	376	G
83	BQ	400	G
83	BQ	411	U
83	BQ	494	G
83	BQ	547	G
83	BQ	556	U
83	BQ	588	G
83	BQ	611	A
83	BQ	621	A
83	BQ	677	A
83	BQ	715	A
83	BQ	764	U
83	BQ	767	U
83	BQ	775	A
83	BQ	786	A
83	BQ	806	A
83	BQ	816	A
83	BQ	822	G
83	BQ	895	A
83	BQ	896	A
83	BQ	916	G
83	BQ	921	A
83	BQ	923	C
83	BQ	924	G
83	BQ	933	A
83	BQ	961	C
83	BQ	978	G
83	BQ	979	U
83	BQ	980	A
83	BQ	993	G
83	BQ	1064	A
83	BQ	1095	U
83	BQ	1096	U
83	BQ	1103	A
83	BQ	1116	G
83	BQ	1144	U
83	BQ	1152	G
83	BQ	1154	A
83	BQ	1177	G
83	BQ	1222	G
83	BQ	1241	U

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Mol	Chain	Res	Type
83	BQ	1253	U
83	BQ	1307	G
83	BQ	1352	A
83	BQ	1355	A
83	BQ	1392	G
83	BQ	1417	G
83	BQ	1418	A
83	BQ	1429	G
83	BQ	1467	A
83	BQ	1481	A
83	BQ	1482	A
83	BQ	1483	G
83	BQ	1511	U
83	BQ	1554	U
83	BQ	1568	U
83	BQ	1580	A
83	BQ	1607	U
83	BQ	1695	U
83	BQ	1724	U
83	BQ	1729	A
83	BQ	1730	G
83	BQ	1751	G
83	BQ	1808	G
83	BQ	1815	U
83	BQ	1816	A
83	BQ	1820	U
83	BQ	1839	A
83	BQ	1840	U
83	BQ	1846	C
83	BQ	1847	A
83	BQ	1849	C
83	BQ	1850	A
83	BQ	1885	U
83	BQ	1900	A
83	BQ	1913	A
83	BQ	2101	C
83	BQ	2112	U
83	BQ	2116	G
83	BQ	2138	A
83	BQ	2144	A
83	BQ	2159	U
83	BQ	2177	G

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Mol	Chain	Res	Type
83	BQ	2178	A
83	BQ	2198	A
83	BQ	2208	A
83	BQ	2256	A
83	BQ	2273	G
83	BQ	2279	A
83	BQ	2281	A
83	BQ	2282	U
83	BQ	2283	G
83	BQ	2305	G
83	BQ	2313	A
83	BQ	2433	U
83	BQ	2434	U
83	BQ	2445	A
83	BQ	2493	U
83	BQ	2495	C
83	BQ	2500	A
83	BQ	2501	U
83	BQ	2513	U
83	BQ	2514	U
83	BQ	2525	G
83	BQ	2539	C
83	BQ	2541	U
83	BQ	2549	G
83	BQ	2554	A
83	BQ	2586	G
83	BQ	2593	A
83	BQ	2617	U
83	BQ	2625	C
83	BQ	2665	U
83	BQ	2677	G
83	BQ	2680	A
83	BQ	2689	A
83	BQ	2703	A
83	BQ	2727	A
83	BQ	2754	G
83	BQ	2794	G
83	BQ	2801	A
83	BQ	2803	A
83	BQ	2816	G
83	BQ	2898	G
83	BQ	2911	A

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Mol	Chain	Res	Type
83	BQ	2941	A
83	BQ	2950	G
83	BQ	2953	U
83	BQ	2954	U
83	BQ	2971	A
83	BQ	3011	A
83	BQ	3021	A
83	BQ	3022	G
83	BQ	3047	U
83	BQ	3048	A
83	BQ	3057	U
83	BQ	3078	U
83	BQ	3093	C
83	BQ	3143	C
83	BQ	3156	U
83	BQ	3172	A
83	BQ	3175	U
83	BQ	3179	U
83	BQ	3196	U
83	BQ	3216	G
83	BQ	3219	G
83	BQ	3241	G
83	BQ	3269	U
83	BQ	3272	C
83	BQ	3274	A
83	BQ	3293	U
83	BQ	3317	U
83	BQ	3344	A
83	BQ	3345	G
83	BQ	3350	C
83	BQ	3353	G
83	BQ	3382	U
84	BR	12	U
84	BR	32	U
84	BR	41	G
84	BR	54	U
84	BR	77	G
84	BR	86	U
84	BR	111	U
85	BS	22	U
85	BS	23	U
85	BS	33	A

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Mol	Chain	Res	Type
85	BS	34	U
85	BS	39	G
85	BS	48	A
85	BS	58	G
85	BS	85	G
85	BS	112	U
85	BS	125	U

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z  > 2$
86	5CT	BT	51	86	12,14,15	0.36	0	12,15,17	1.37	3 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	5CT	BT	51	86	-	0/12/14/16	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	BT	51	5CT	C4-C3-C2	-2.58	109.19	113.70
86	BT	51	5CT	C1-NZ-CE	-2.36	108.27	113.83
86	BT	51	5CT	O-C-CA	-2.01	120.34	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	BT	51	5CT	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	52:U	O3'	53:G	P	1.89