



## Full wwPDB EM Validation Report ⓘ

Dec 22, 2022 – 04:31 pm GMT

PDB ID : 7QJH  
EMDB ID : EMD-14020  
Title : Spraguea lophii ribosome dimer  
Authors : Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Connors, R.; Williams, B.  
Deposited on : 2021-12-16  
Resolution : 10.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

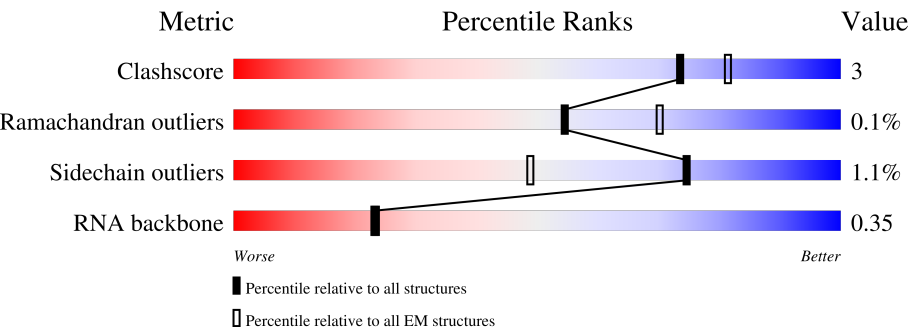
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 10.00 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	K50	2618	<div><div></div><div>62%29%5%</div></div>
1	L50	2618	<div><div></div><div>62%29%5%</div></div>
2	K70	119	<div><div></div><div>59%36%5%</div></div>
2	L70	119	<div><div></div><div>60%35%5%</div></div>
3	KA0	246	<div><div></div><div>96%</div></div>
3	LA0	246	<div><div></div><div>96%</div></div>
4	KAA	147	<div><div>10%</div><div>93%7%</div></div>

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Mol	Chain	Length	Quality of chain
4	LAA	147	
5	KB0	392	
5	LB0	392	
6	KC0	328	
6	LC0	328	
7	KCC	110	
7	LCC	110	
8	KD0	291	
8	LD0	291	
9	KDD	110	
9	LDD	110	
10	KE0	171	
10	LE0	171	
11	KEE	139	
11	LEE	139	
12	KF0	235	
12	LF0	235	
13	KFF	111	
13	LFF	111	
14	KG0	206	
14	LG0	206	
15	KGG	106	
15	LGG	106	
16	KH0	187	
16	LH0	187	


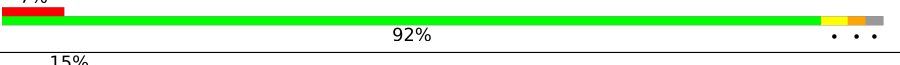
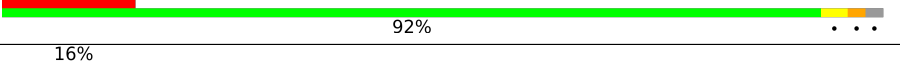
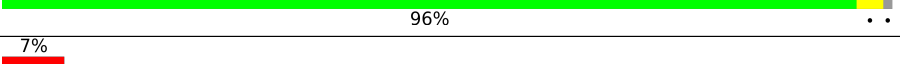
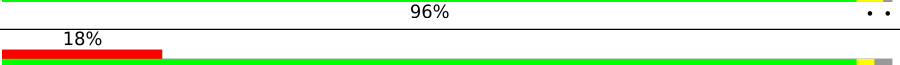
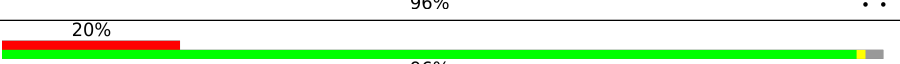
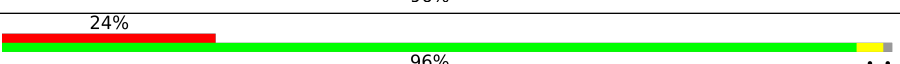
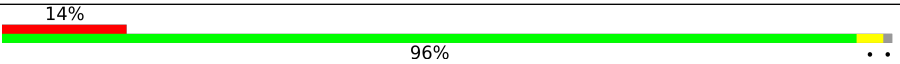
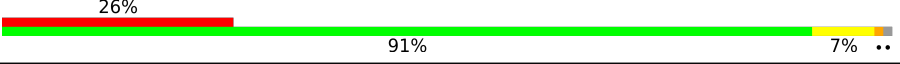
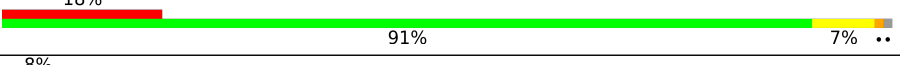
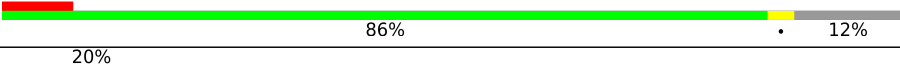
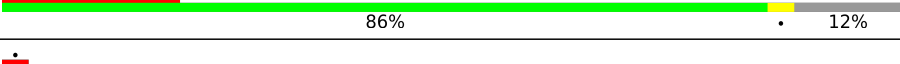
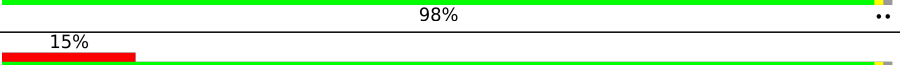
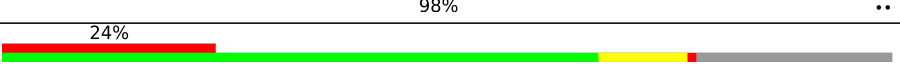
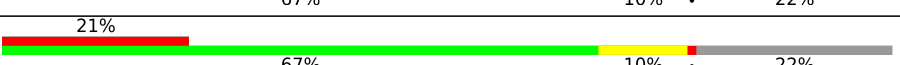
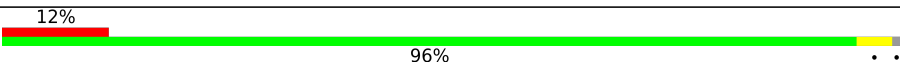
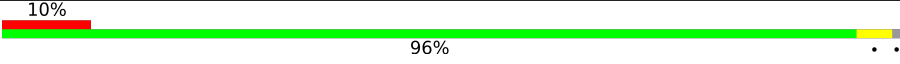
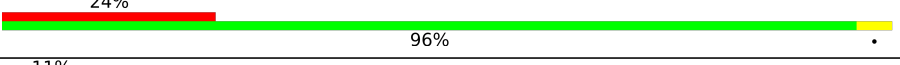
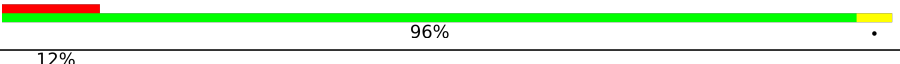


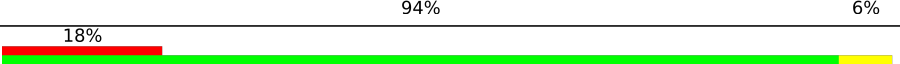
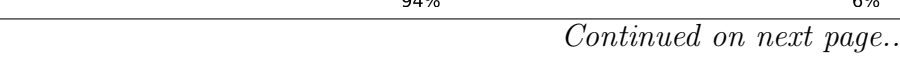

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Mol	Chain	Length	Quality of chain
17	KHH	119	
17	LHH	119	
18	KI0	218	
18	LI0	218	
19	KII	98	
19	LII	98	
20	KJ0	171	
20	LJ0	171	
21	KJJ	92	
21	LJJ	92	
22	KL0	165	
22	LL0	165	
23	KLL	52	
23	LLL	52	
24	KM0	115	
24	LM0	115	
25	KMM	127	
25	LMM	127	
26	KN0	204	
26	LN0	204	
27	KO0	198	
27	LO0	198	
28	KOO	104	
28	LOO	104	
29	KP0	167	



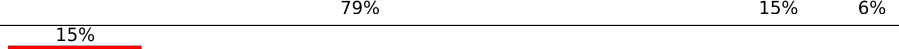
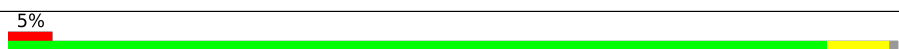



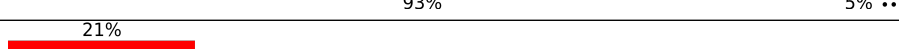



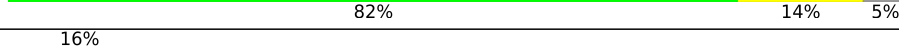

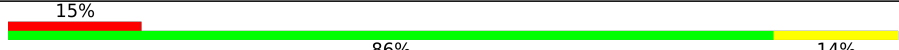


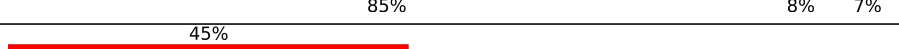







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Mol	Chain	Length	Quality of chain
29	LP0	167	
30	KPP	89	
30	LPP	89	
31	KQ0	183	
31	LQ0	183	
32	KR0	168	
32	LR0	168	
33	KS0	171	
33	LS0	171	
34	KT0	158	
35	KU0	113	
35	LU0	113	
36	KV0	142	
36	LV0	142	
37	KW0	131	
37	LW0	131	
38	KX0	113	
38	LX0	113	
39	KY0	131	
39	LY0	131	
40	KZ0	153	
40	LZ0	153	
41	MD1	151	
41	MD2	151	

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Mol	Chain	Length	Quality of chain
42	R60	1368	
42	S60	1368	
43	RA0	233	
43	SA0	233	
44	RAA	102	
44	SAA	102	
45	RB0	230	
45	SB0	230	
46	RBB	82	
46	SBB	82	
47	RC0	248	
47	SC0	248	
48	RCC	65	
48	SCC	65	
49	RD0	242	
49	SD0	242	
50	RDD	65	
50	SDD	65	
51	RE0	280	
51	SE0	280	
52	REE	60	
52	SEE	60	
53	RF0	195	
53	SF0	195	
54	RFF	150	

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Mol	Chain	Length	Quality of chain
54	SFF	150	
55	RG0	230	
55	SG0	230	
56	RGG	326	
56	SGG	326	
57	RH0	164	
57	SH0	164	
58	RI0	173	
58	SI0	173	
59	RJ0	184	
59	SJ0	184	
60	RK0	107	
60	SK0	107	
61	RL0	155	
61	SL0	155	
62	RM0	130	
62	SM0	130	
63	RN0	143	
63	SN0	143	
64	RO0	135	
64	SO0	135	
65	RQ0	143	
65	SQ0	143	
66	RR0	120	
66	SR0	120	

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Mol	Chain	Length	Quality of chain
67	RS0	160	
67	SS0	160	
68	RT0	143	
68	ST0	143	
69	RU0	119	
69	SU0	119	
70	RV0	67	
70	SV0	67	
71	RW0	128	
71	SW0	128	
72	RX0	141	
72	SX0	141	
73	RY0	146	
73	SY0	146	
74	RZ0	128	
74	SZ0	128	
75	RP0	163	
75	SP0	163	

## 2 Entry composition [i](#)

There are 76 unique types of molecules in this entry. The entry contains 343629 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 RNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		
1	K50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		

- Molecule 2 is a RNA chain called RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		
2	K70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		
3	KA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		

- Molecule 4 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		
4	KAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
5	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
6	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
7	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
8	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
9	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	KE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		
11	KEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		
12	KF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		
13	KFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		
14	KG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		
15	KGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		
16	KH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		
17	KHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		
18	KI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		
19	KII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
20	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
21	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
22	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
23	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
24	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
25	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
27	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
28	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
29	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
30	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
31	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
32	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
33	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		
34	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		
35	KU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		
36	KV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		
37	KW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		
38	KX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		
39	KY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		
40	KZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a protein called DNL-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		
41	MD2	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 42 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	R60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

- Molecule 43 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		
43	RA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		
44	RAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 45 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		
45	RB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 46 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		
46	RBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		
47	RC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		

- Molecule 48 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
48	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		
49	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 50 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
50	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
51	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 52 is a protein called eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SEE	56	Total	C	N	O	0	0
			447	284	89	74		
52	REE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
53	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 54 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SFF	58	Total	C	N	O	S	0	0
			422	261	77	79	5		
54	RFF	58	Total	C	N	O	S	0	0
			417	259	74	79	5		

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		
55	RG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		

- Molecule 56 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		
56	RGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
57	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	RI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		
59	RJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		
60	RK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		
61	RL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		
62	RM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		
63	RN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
64	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
65	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 66 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
66	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
67	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 68 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
68	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
69	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 70 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
70	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 71 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
71	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 72 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
72	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 73 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
73	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 75 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
75	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	LGG	1	Total	Zn	0
			1	1	
76	LJJ	1	Total	Zn	0
			1	1	
76	LMM	1	Total	Zn	0
			1	1	
76	LOO	1	Total	Zn	0
			1	1	
76	LPP	1	Total	Zn	0
			1	1	
76	SAA	1	Total	Zn	0
			1	1	
76	SBB	1	Total	Zn	0
			1	1	
76	SDD	1	Total	Zn	0
			1	1	
76	SFF	1	Total	Zn	0
			1	1	
76	KGG	1	Total	Zn	0
			1	1	
76	KJJ	1	Total	Zn	0
			1	1	
76	KMM	1	Total	Zn	0
			1	1	
76	KOO	1	Total	Zn	0
			1	1	
76	KPP	1	Total	Zn	0
			1	1	

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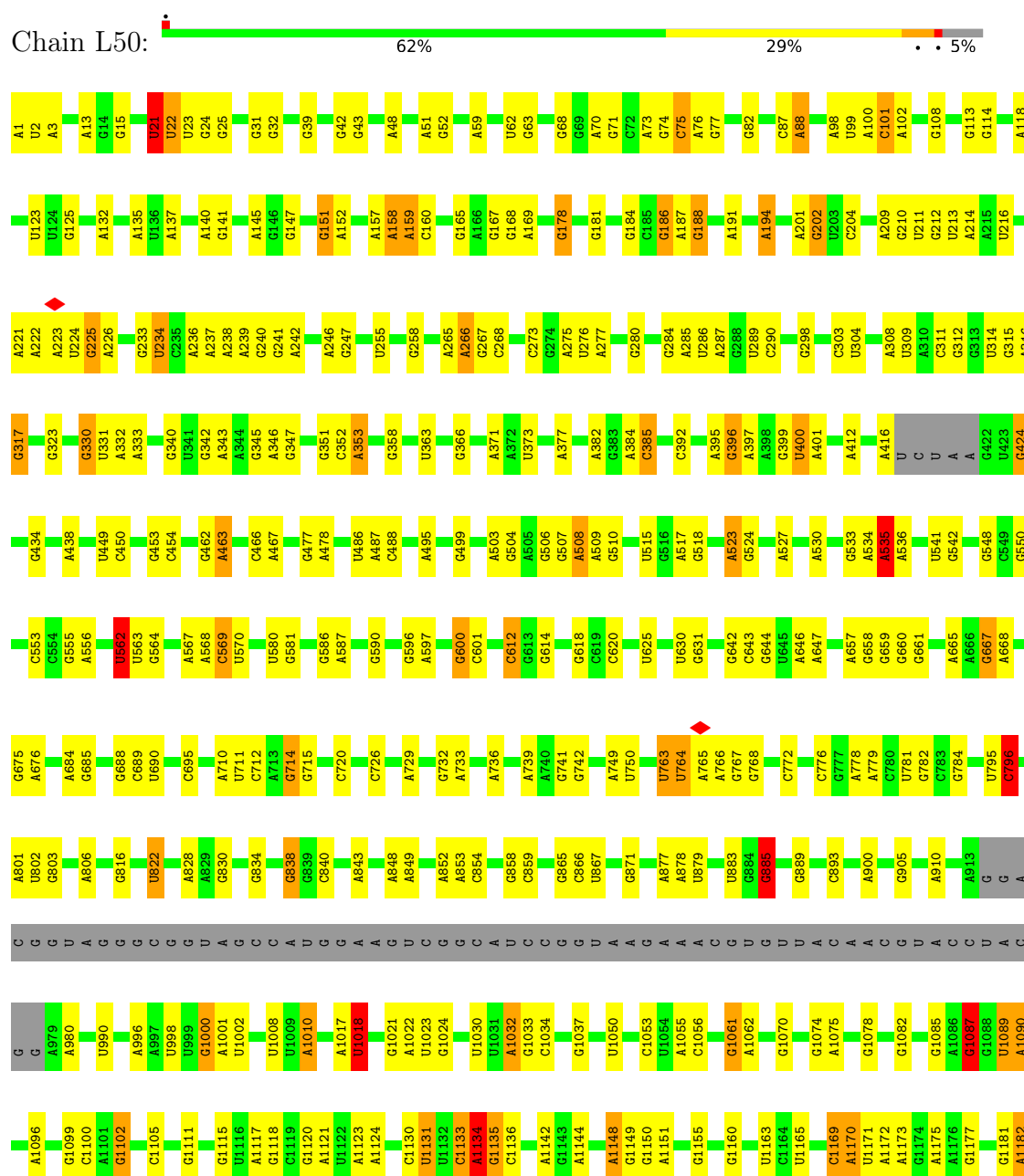
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Mol	Chain	Residues	Atoms		AltConf
76	RAA	1	Total 1	Zn 1	0
76	RBB	1	Total 1	Zn 1	0
76	RDD	1	Total 1	Zn 1	0
76	RFF	1	Total 1	Zn 1	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

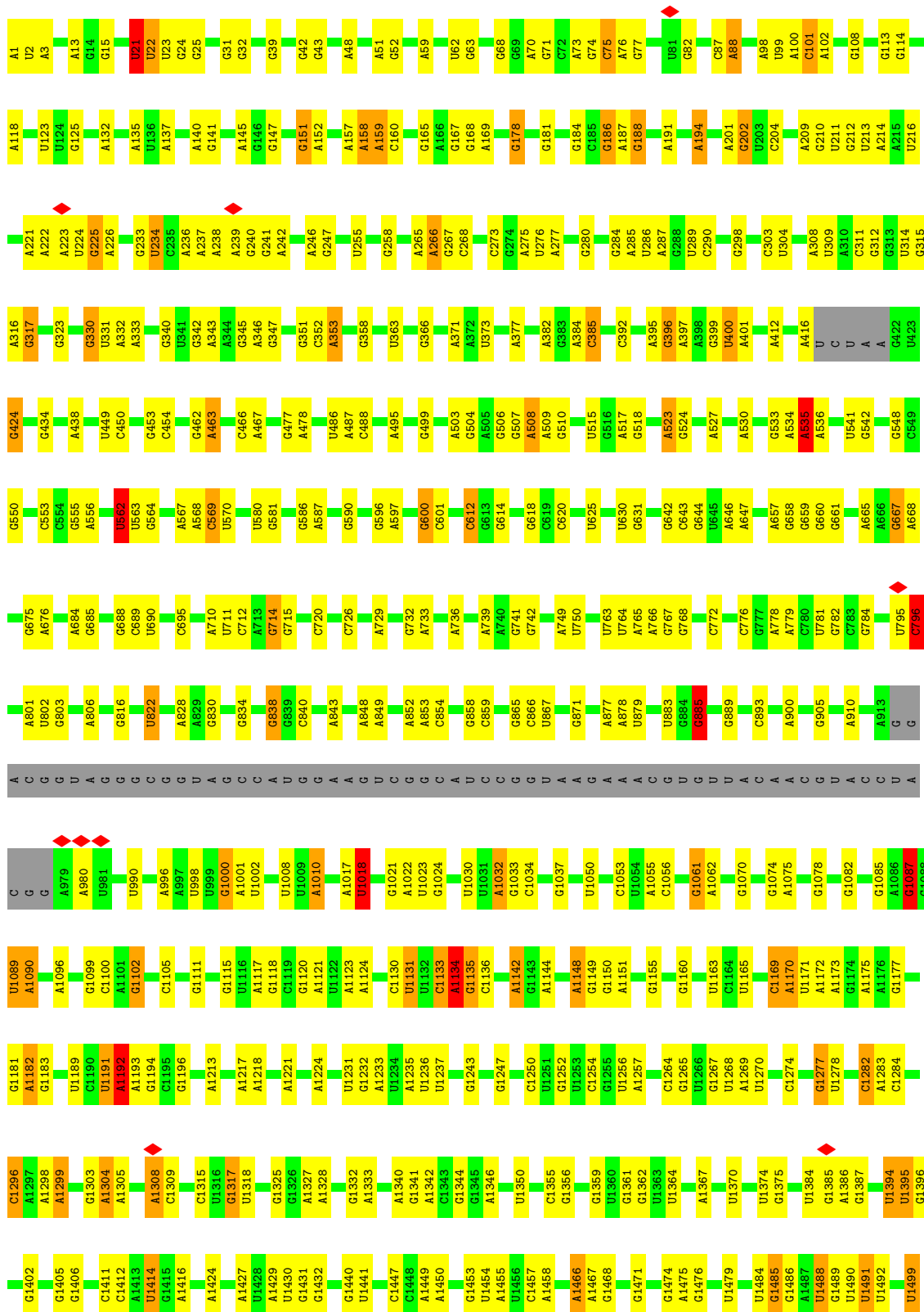
#### • Molecule 1: RNA 28S



U2544	A2434	A2314	A2211	C2096	A2014	A1859	G1724	U1623	G1524	G1406	A1298	G1183
G2548	A2435	G2315	G2212	U2097	C2015	G1860	G1733	G1624	G1527	C1411	A1299	U1189
G2551	G2436	G2319	A2213	A2098	G2019	A1868	A1733	G1625	U1527	C1412	G1303	C1190
G2552	U2437	G2322	G2217	C2099	G2020	A1969	A1735	G1626	C1533	U1413	A1305	U1191
A2555	A2441	U2322	G2221	G2108	C2021	U1871	G1738	C1634	G1534	U1414	A1308	A1192
U2556	A2447	U2323	G2224	G2109	G2022	U1872	A1739	G1638	G1535	G1415	G1309	A1193
G2557	G2451	G2325	G2225	A2110	A2026	U1873	C1742	G1642	G1536	A1416	A1306	G1194
A2558	A2452	G2332	U2226	G2114	A2027	U1874	G1743	G1643	G1537	A1424	G1317	G1196
G2559	C2453	U2227	U2228	A2115	G2030	A1877	U1746	U1644	G1538	U1427	U1318	A1213
U2562	C2459	A2337	U2229	A2117	U2031	G1878	U1749	G1645	G1547	U1428	A1322	A1217
U2563	A2460	C2336	G2234	G2122	A2032	A1879	A1749	U1554	G1549	U1429	A1325	A1218
G2564	C2461	G2340	U2234	G2123	A2036	U1880	U1750	G1555	U1554	U1430	G1326	A1221
U2565	A2462	G2341	G2235	G2124	C2037	U1881	G1751	U1556	G1557	G1431	A1327	A1224
A2566	A2463	G2345	G2239	G2130	A2038	G1882	U1755	A1651	A1563	G1432	A1328	U1231
U2567	G2473	U2346	U2240	A2131	G2039	A1883	U1760	G1652	U1564	C1436	U1232	G1232
U2568	A2474	U2347	G2241	A2136	A2042	G1884	A1783	G1653	U1565	G1440	A1333	A1233
G	A2475	U2351	G2242	A2140	G2043	G1885	U1783	A1665	G1566	U1441	A1340	U1234
U	G2476	A2355	U2243	G2141	A2044	G1886	A1783	A1668	U1567	C1447	G1341	A1235
G	C2477	A2355	G2253	G2142	G2045	G1887	A1783	G1673	U1568	U1448	A1342	U1237
G2572	U2481	G2358	U2254	U2141	G2046	A1888	A1783	G1675	U1569	A1450	A1346	G1243
U2573	A2482	G2368	G2255	A2142	A2047	U	A1797	G1677	U1570	G1453	U1380	G1247
A2574	A2487	A2368	G2257	A2146	G2048	U	U1798	G1679	C1571	U1454	C1355	C1250
G2575	A2490	A2363	G2260	G2146	A2049	U	U1799	A1681	U1572	A1455	G1356	U1251
G2578	A2491	G2373	G2261	A2149	C2051	U	U1800	G1682	U1573	U1456	U1363	U1252
U2587	A2492	G2376	G2262	C2150	A2052	G	G1801	G1685	U1574	C1457	U1364	U1253
G2588	G2493	G2377	G2266	U2151	G2053	U	A1808	G1686	U1583	A1458	U1365	C1254
C2593	C2497	U2378	C2267	U2152	U2054	U	A1809	C1686	U1585	A1466	U1366	U1254
C2594	A2501	G2379	G2272	G2150	G2057	U	A1810	U1689	G1586	A1467	G1361	G1255
U2595	C2502	A2394	G2275	G2162	U2059	U	G1811	U1690	U1591	A1475	U1362	U1256
G2597	U2503	G2399	G2275	U2163	A2060	G	A1820	A1691	U1592	G1471	U1363	U1257
U2598	A2508	C2400	A2279	G2164	A2061	U	G1820	A1692	A1596	G1474	A1367	C1264
G2600	A2509	C2401	G2286	A2167	C2063	U	G1821	U1693	A1601	A1475	U1370	G1265
C2605	G2518	A2410	U2291	C2168	C2064	U	G1822	U1694	G1602	G1476	U1374	U1266
A2606	G2519	C2411	U2292	A2169	U2065	U	G1828	A1695	U1605	U1479	U1375	G1267
G2610	A2520	U2412	C2293	A2170	A2067	U	A1832	G1697	U1609	U1484	U1384	C1274
U2612	G2525	U2413	G2296	A2171	A2067	U	A1833	A1698	G1485	U1485	G1385	G1277
U	C2416	G2416	C2296	C2177	U2073	U	A1834	C1699	A1610	G1486	A1386	U1278
U	G2419	C2420	C2303	C2178	A2075	U	G1835	U1705	A1611	A1487	A1387	C1282
A	C2421	A2532	A2304	A2181	A2076	U	A1836	G1708	G1612	U1488	U1394	U1395
U	C2423	G2305	G2305	G2184	G2077	U	A1837	U1709	A1613	G1489	A1283	C1284
U	C2424	G2306	G2306	A2185	A2078	U	A1839	U1710	G1614	U1490	G1396	C1296
C2538	G2431	A2309	G2310	C2189	G2085	U	U1846	A1711	A1617	U1491	G1402	A1297
A2539	G2432	G2310	G2313	G2198	G2087	U	A1854	A1717	U1618	U1492	G1513	
	G2433	G2313			G2093	U	U1858	G1719	G1619	U1499		
						U		C1720	G1622			

● Molecule 1: RNA 28S

Chain K50:  62% 29% 5%







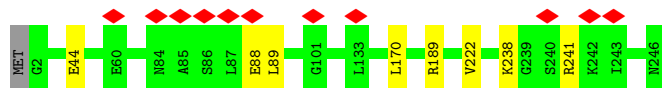
- Molecule 2: RNA 5S

Chain K70: 59% 36% 5%



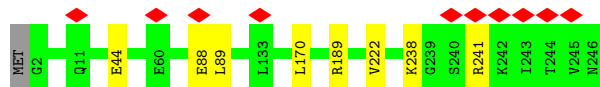
- Molecule 3: 60S ribosomal protein L8

Chain LA0: 96%



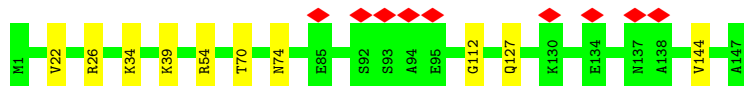
- Molecule 3: 60S ribosomal protein L8

Chain KA0: 96%



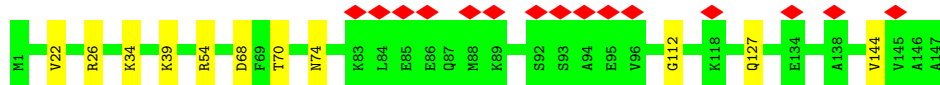
- Molecule 4: uL15

Chain LAA: 6% 93% 7%



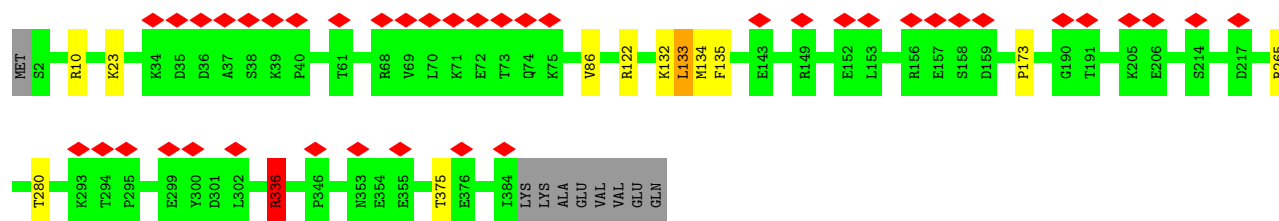
- Molecule 4: uL15

Chain KAA: 10% 93% 7%

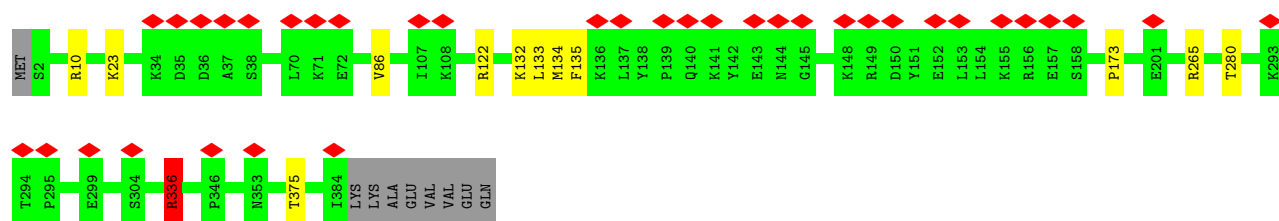


- Molecule 5: 60S ribosomal protein L3

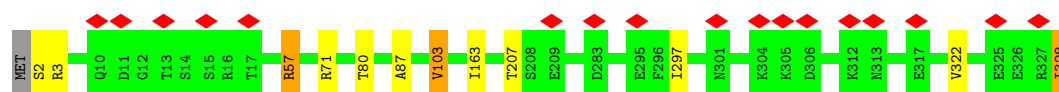
Chain LB0: 10% 94%



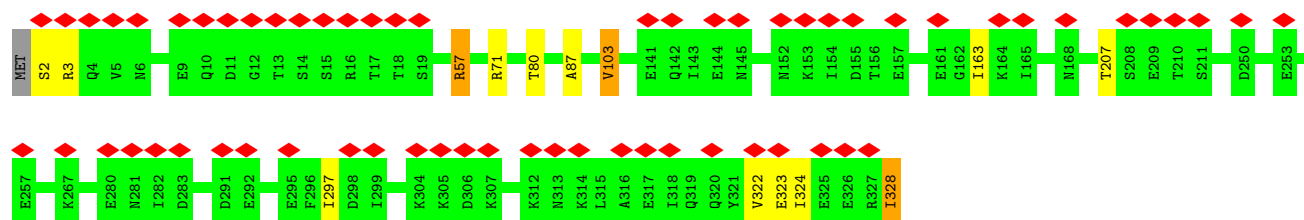
• Molecule 5: 60S ribosomal protein L3



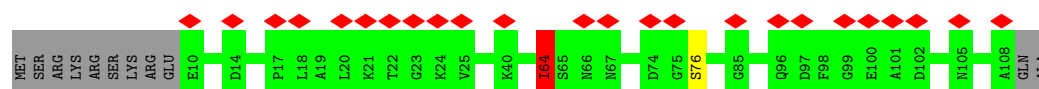
• Molecule 6: 60S ribosomal protein L4



• Molecule 6: 60S ribosomal protein L4

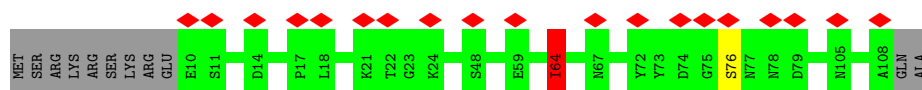


• Molecule 7: 60S ribosomal protein L3

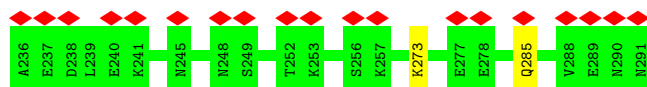
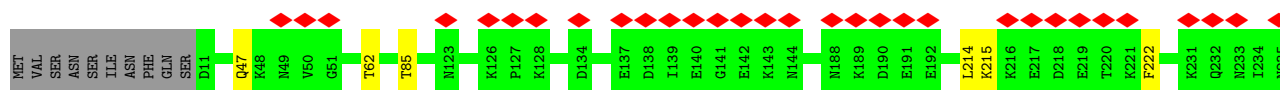


• Molecule 7: 60S ribosomal protein L3

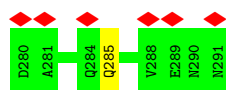
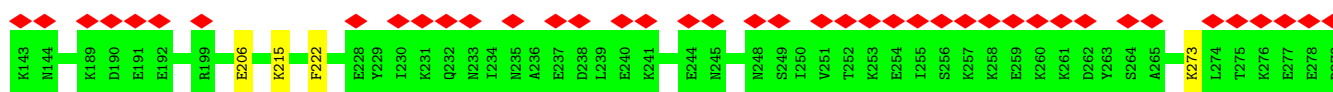
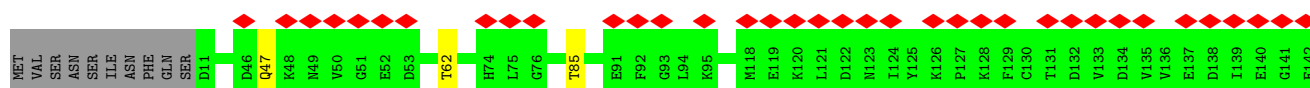




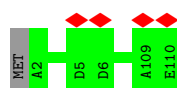
- Molecule 8: 60S ribosomal protein L5



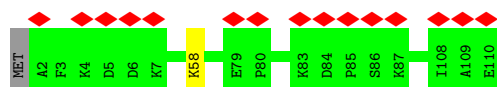
- Molecule 8: 60S ribosomal protein L5



- Molecule 9: 60S ribosomal protein L31

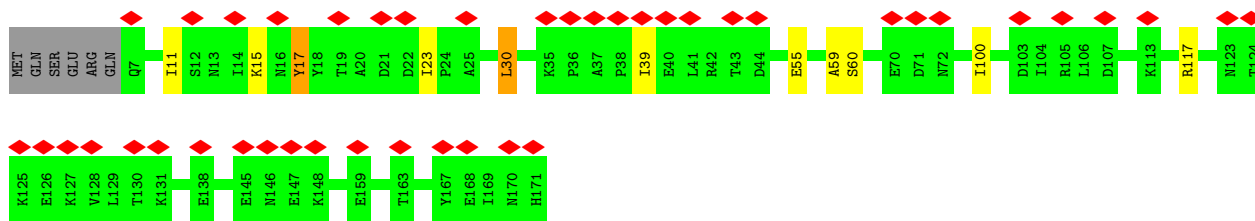


- Molecule 9: 60S ribosomal protein L31

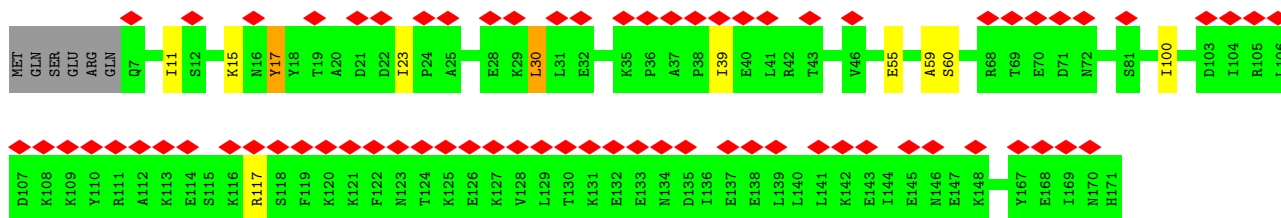
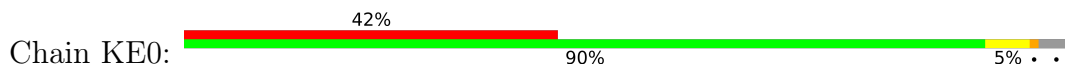


- Molecule 10: 60S ribosomal protein L6

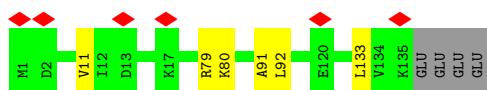




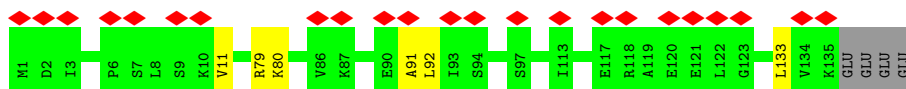
- Molecule 10: 60S ribosomal protein L6



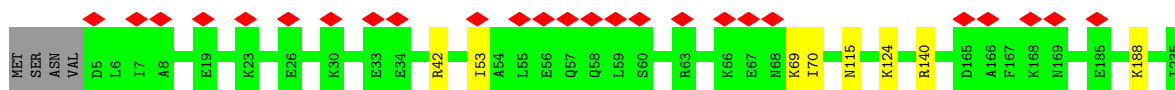
- Molecule 11: 60S ribosomal protein L32



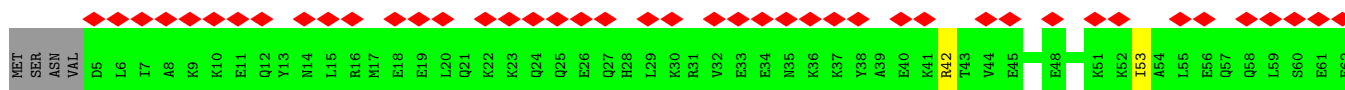
- Molecule 11: 60S ribosomal protein L32

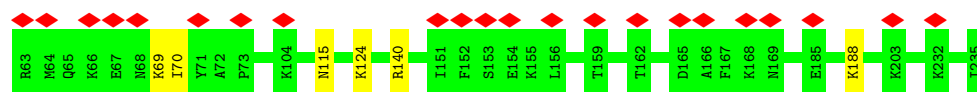


- Molecule 12: 60S ribosomal protein L7



- Molecule 12: 60S ribosomal protein L7

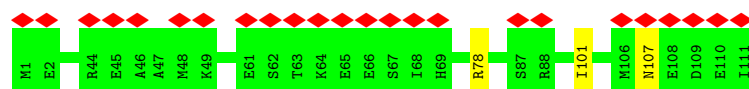




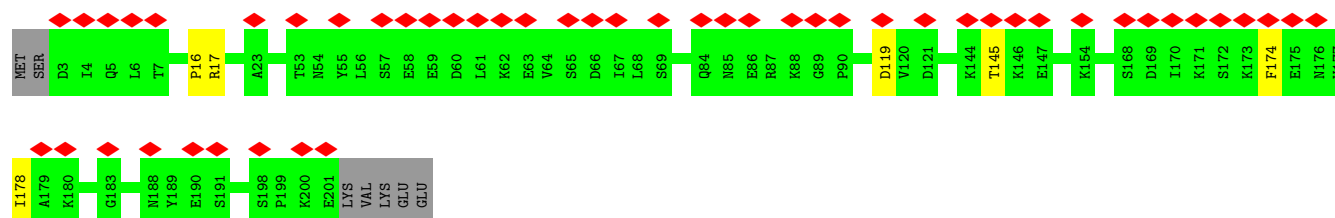
- Molecule 13: 60S ribosomal protein L35a



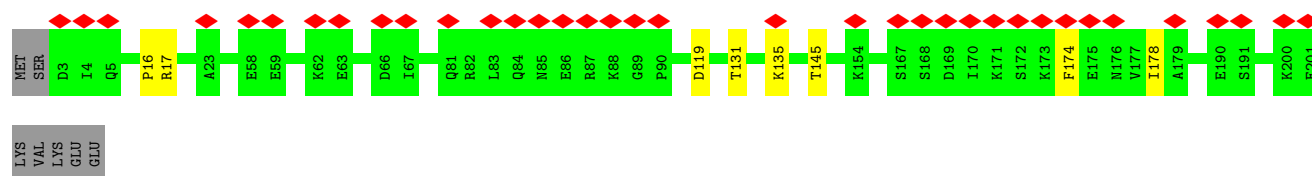
- Molecule 13: 60S ribosomal protein L35a



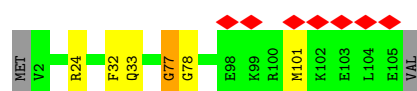
- Molecule 14: 60S ribosomal protein L8



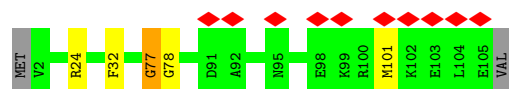
- Molecule 14: 60S ribosomal protein L8



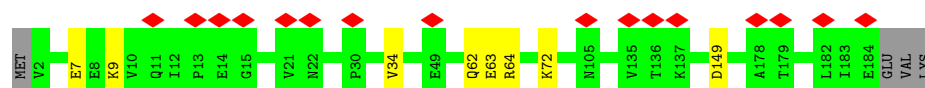
- Molecule 15: Ribosomal protein L34



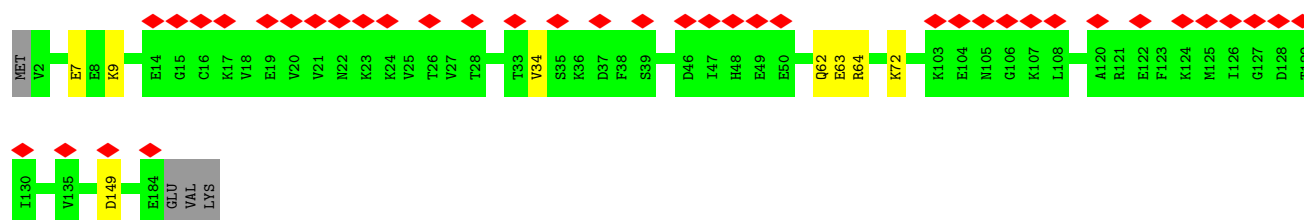
- Molecule 15: Ribosomal protein L34



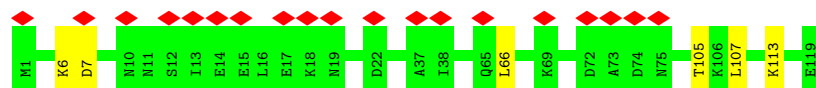
- Molecule 16: 60S ribosomal protein L9



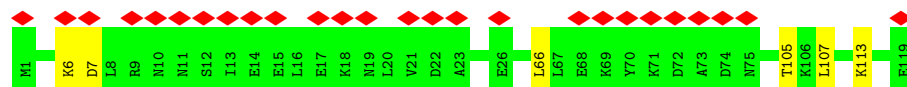
- Molecule 16: 60S ribosomal protein L9



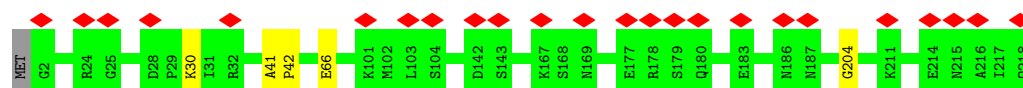
- Molecule 17: Ribosomal L29 protein



- Molecule 17: Ribosomal L29 protein

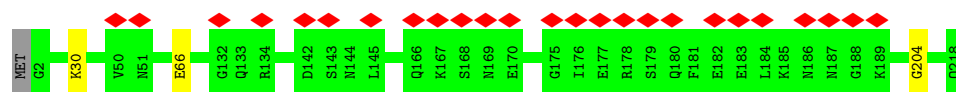


- Molecule 18: S60 ribosomal protein L10



- Molecule 18: S60 ribosomal protein L10

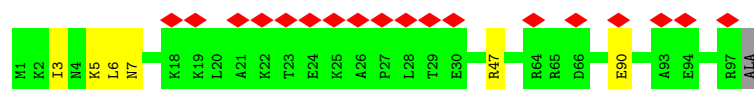




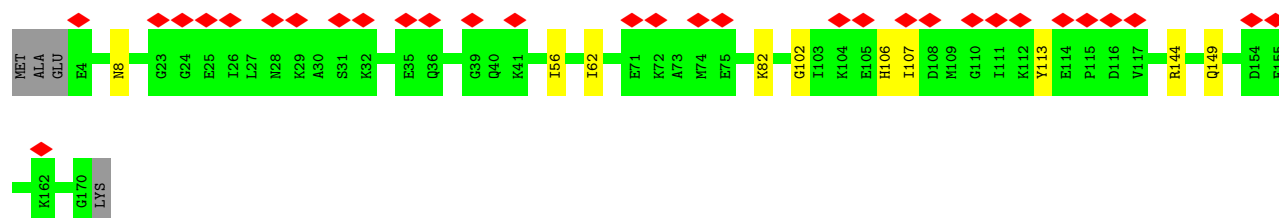
- Molecule 19: 60S ribosomal protein L36



- Molecule 19: 60S ribosomal protein L36



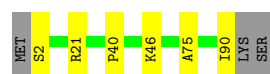
- Molecule 20: 60S ribosomal protein L11



- Molecule 20: 60S ribosomal protein L11

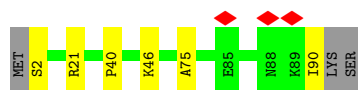


- Molecule 21: eL37

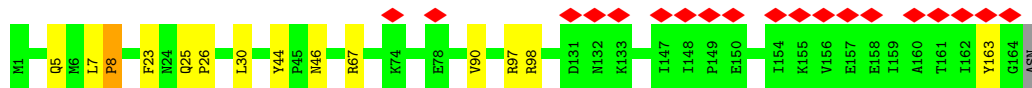


- Molecule 21: eL37

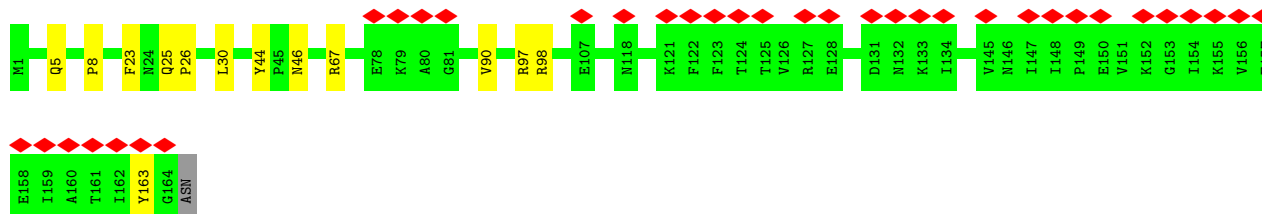




- Molecule 22: 60S ribosomal protein L13



- Molecule 22: 60S ribosomal protein L13



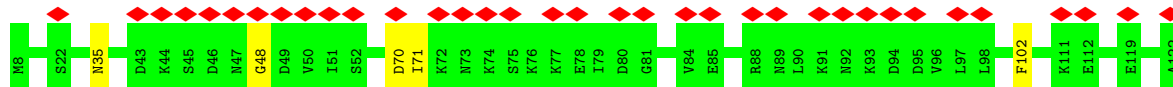
- Molecule 23: 60S ribosomal protein L39



- Molecule 23: 60S ribosomal protein L39

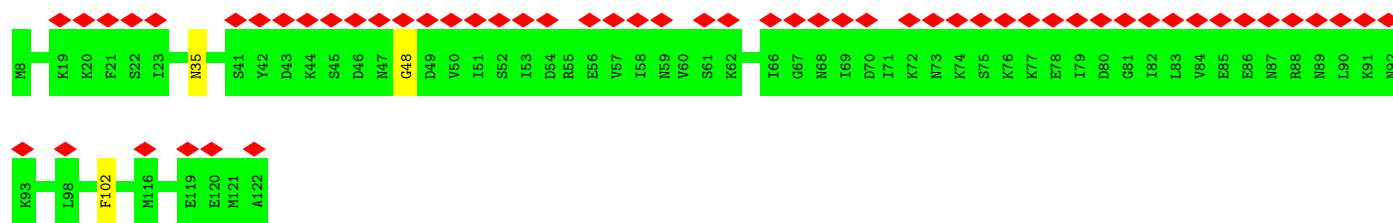


- Molecule 24: Transposase

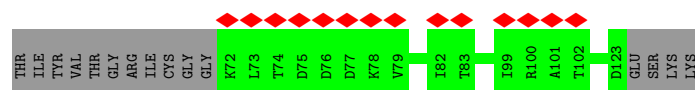
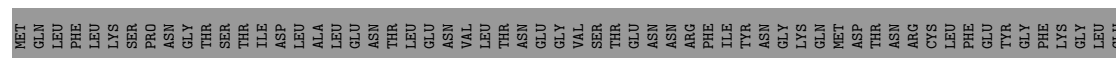
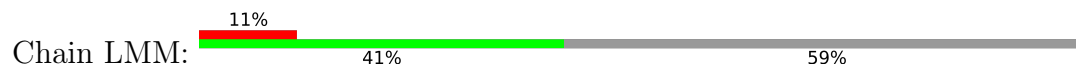


- Molecule 24: Transposase

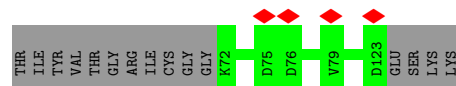
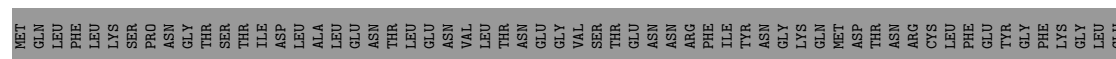




• Molecule 25: Ubiquitin



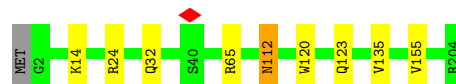
• Molecule 25: Ubiquitin



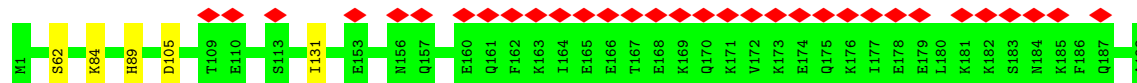
• Molecule 26: Ribosomal protein L15



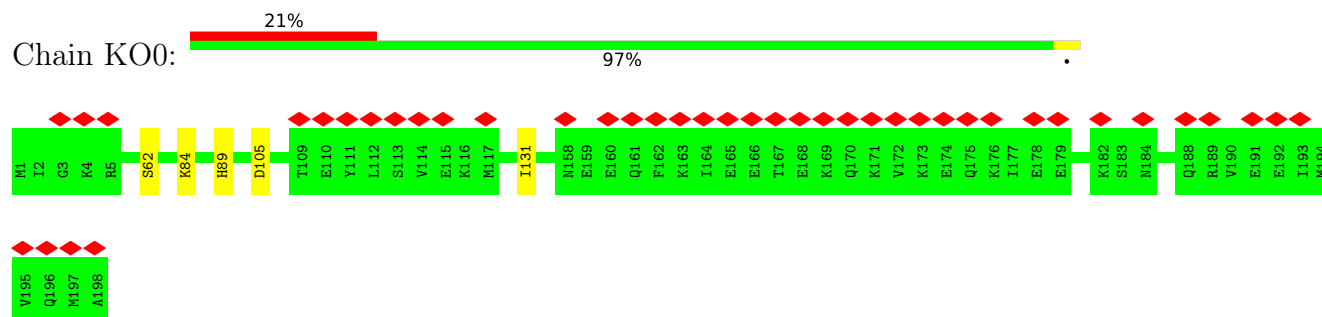
• Molecule 26: Ribosomal protein L15



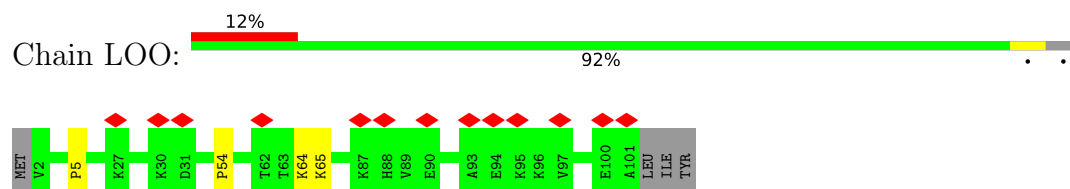
• Molecule 27: Ribosomal protein L13A



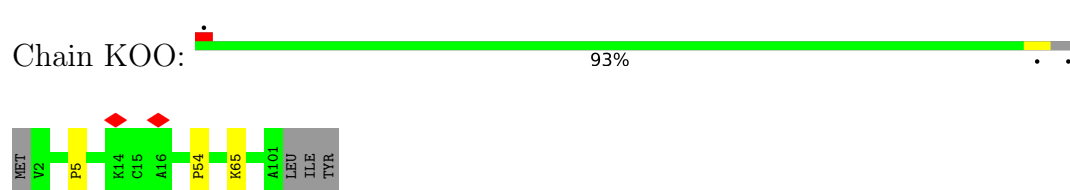
- Molecule 27: Ribosomal protein L13A



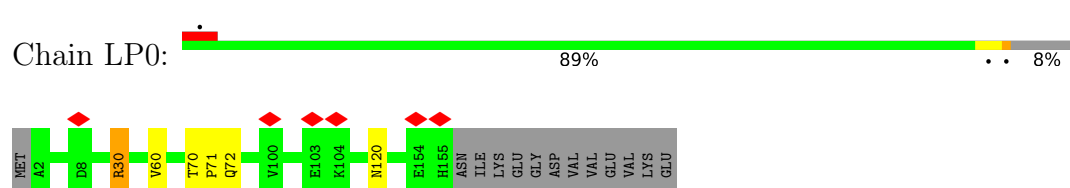
- Molecule 28: 60S ribosomal protein L44



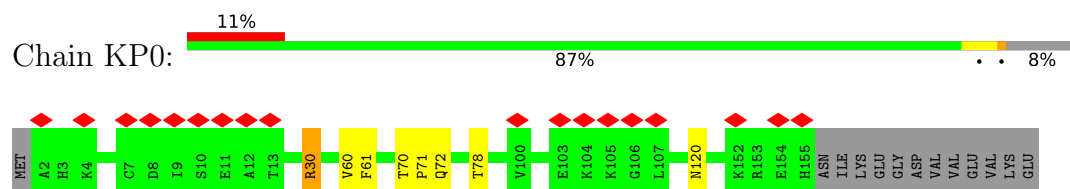
- Molecule 28: 60S ribosomal protein L44



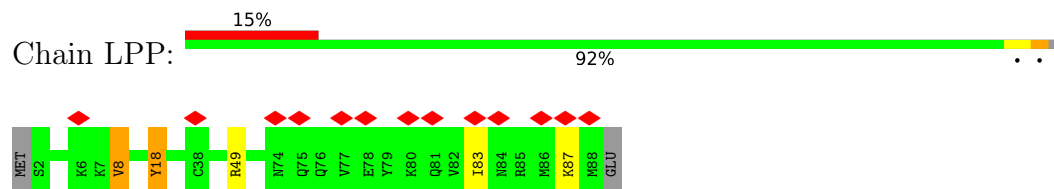
- Molecule 29: 60S ribosomal protein L17



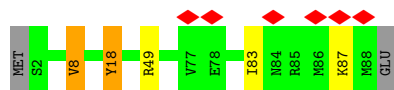
- Molecule 29: 60S ribosomal protein L17



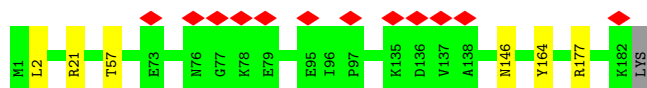
- Molecule 30: 60S ribosomal protein L37a



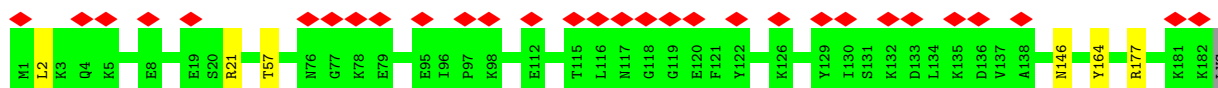
- Molecule 30: 60S ribosomal protein L37a



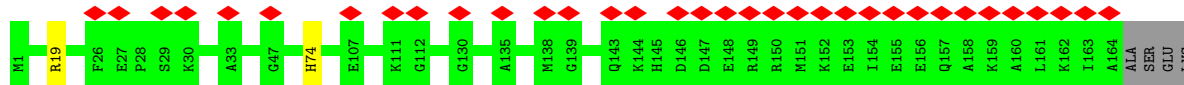
- Molecule 31: 60S ribosomal protein L18



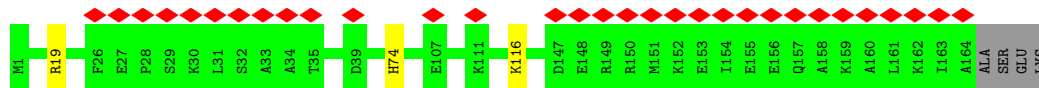
- Molecule 31: 60S ribosomal protein L18



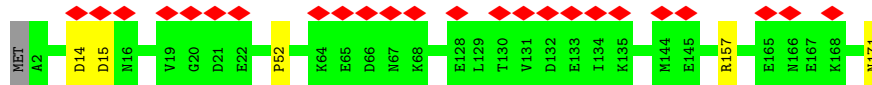
- Molecule 32: 60S ribosomal protein L19



- Molecule 32: 60S ribosomal protein L19

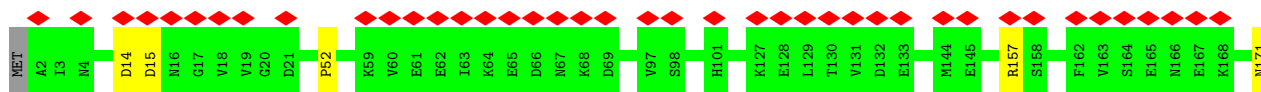


- Molecule 33: 60S ribosomal protein L20

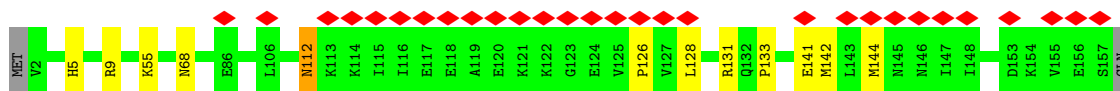


- Molecule 33: 60S ribosomal protein L20

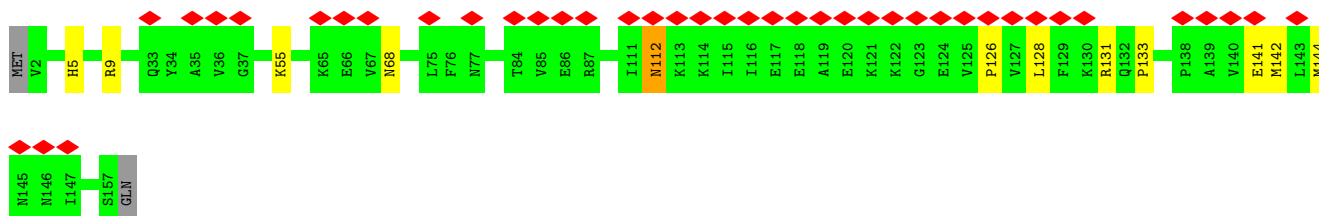




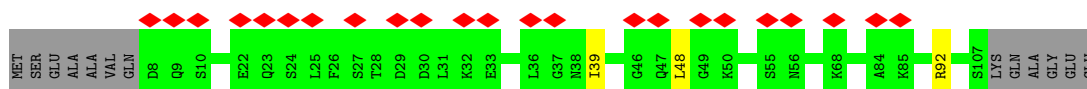
- Molecule 34: 60s ribosomal protein L21



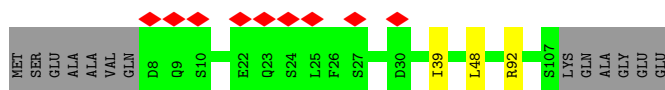
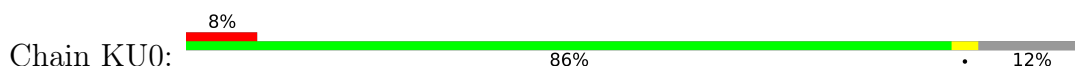
- Molecule 34: 60s ribosomal protein L21



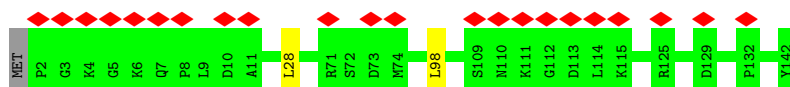
- Molecule 35: 60S ribosomal protein L22



- Molecule 35: 60S ribosomal protein L22

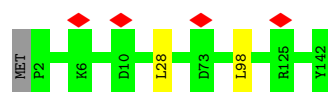


- Molecule 36: Ribosomal protein L23

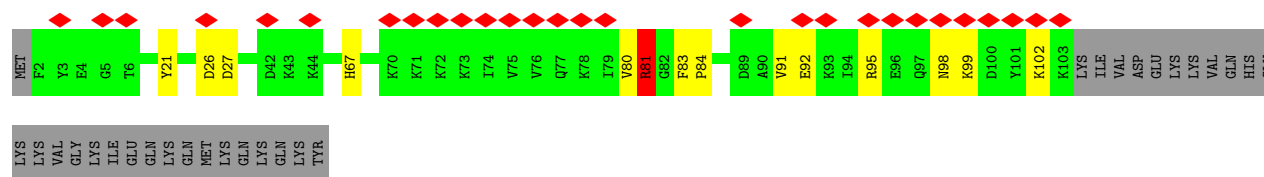
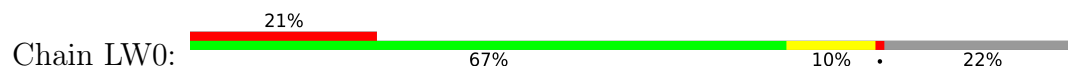


- Molecule 36: Ribosomal protein L23

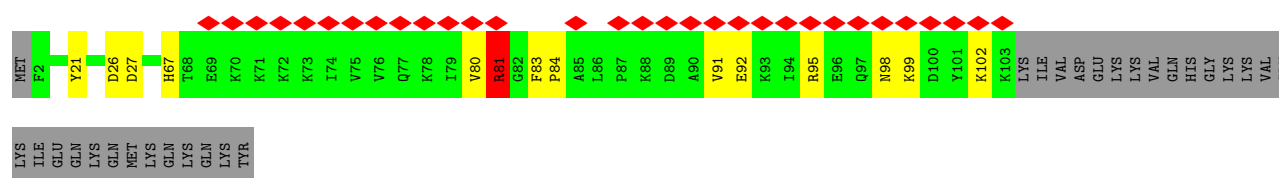
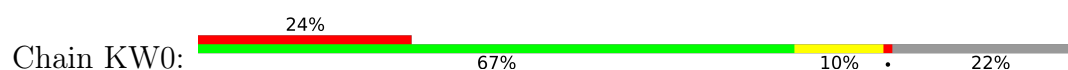




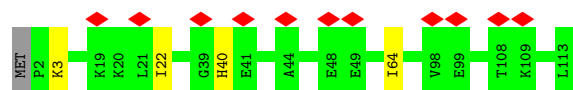
- Molecule 37: Ribosomal protein L24E



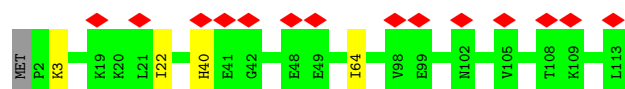
- Molecule 37: Ribosomal protein L24E



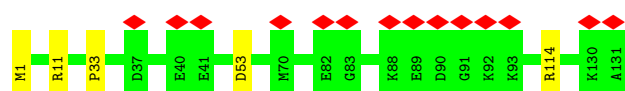
- Molecule 38: 60S ribosomal protein L23a



- Molecule 38: 60S ribosomal protein L23a

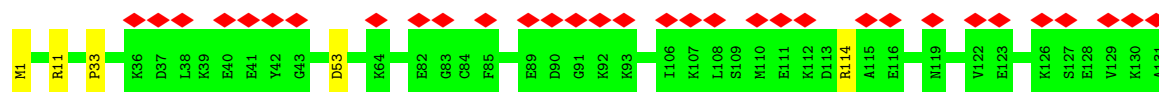


- Molecule 39: 60S ribosomal protein L26

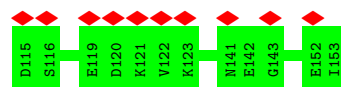
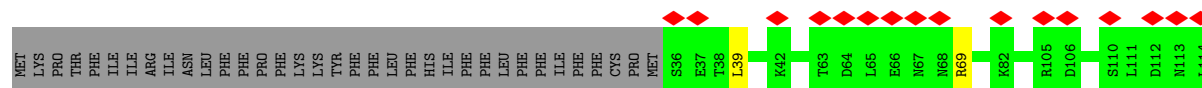
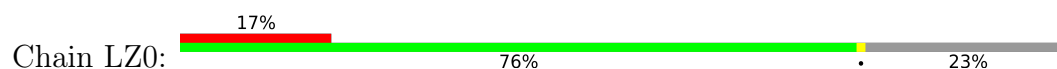


- Molecule 39: 60S ribosomal protein L26

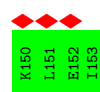
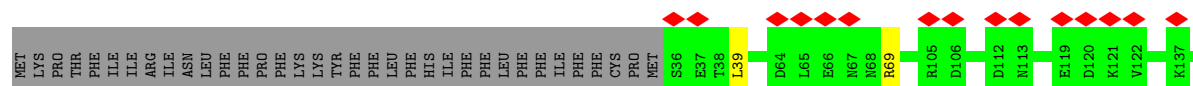
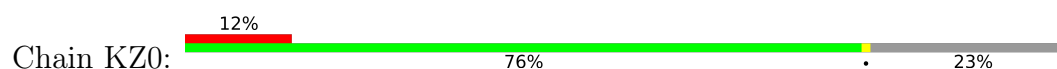




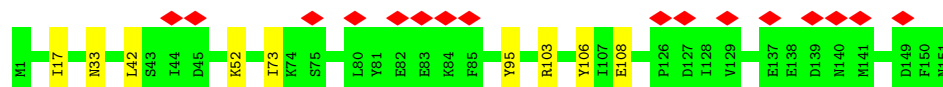
- Molecule 40: 60S ribosomal protein L27



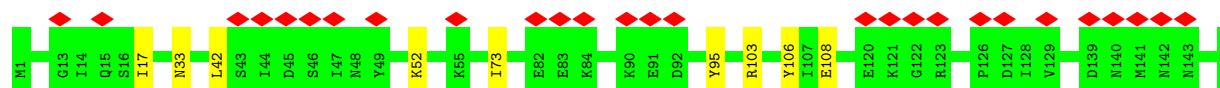
- Molecule 40: 60S ribosomal protein L27



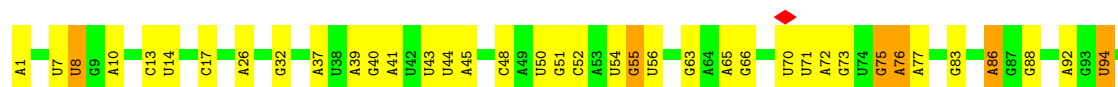
- Molecule 41: DNL-type domain-containing protein

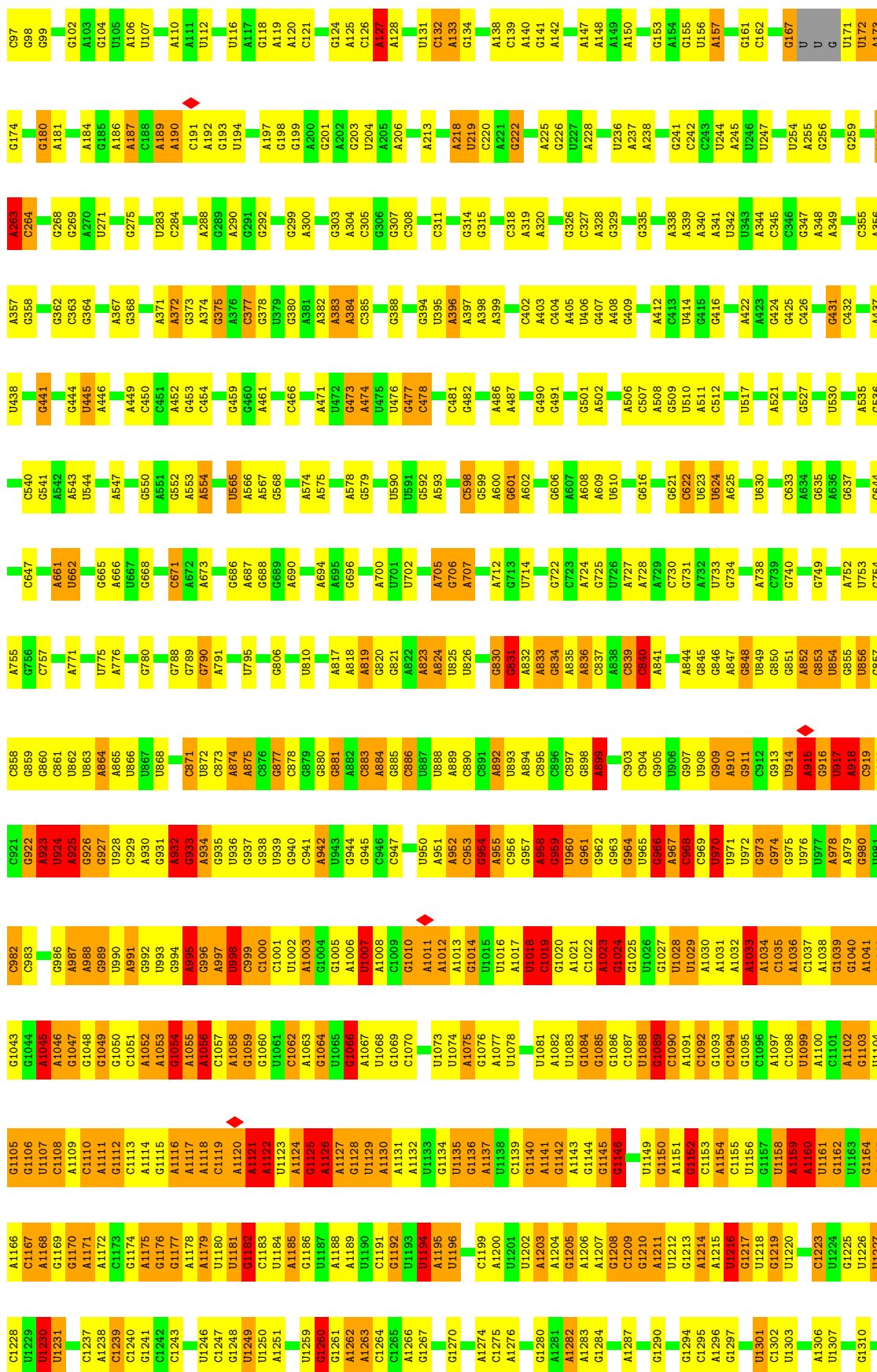


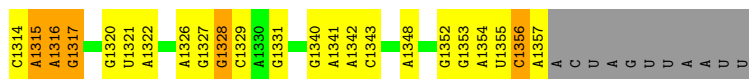
- Molecule 41: DNL-type domain-containing protein



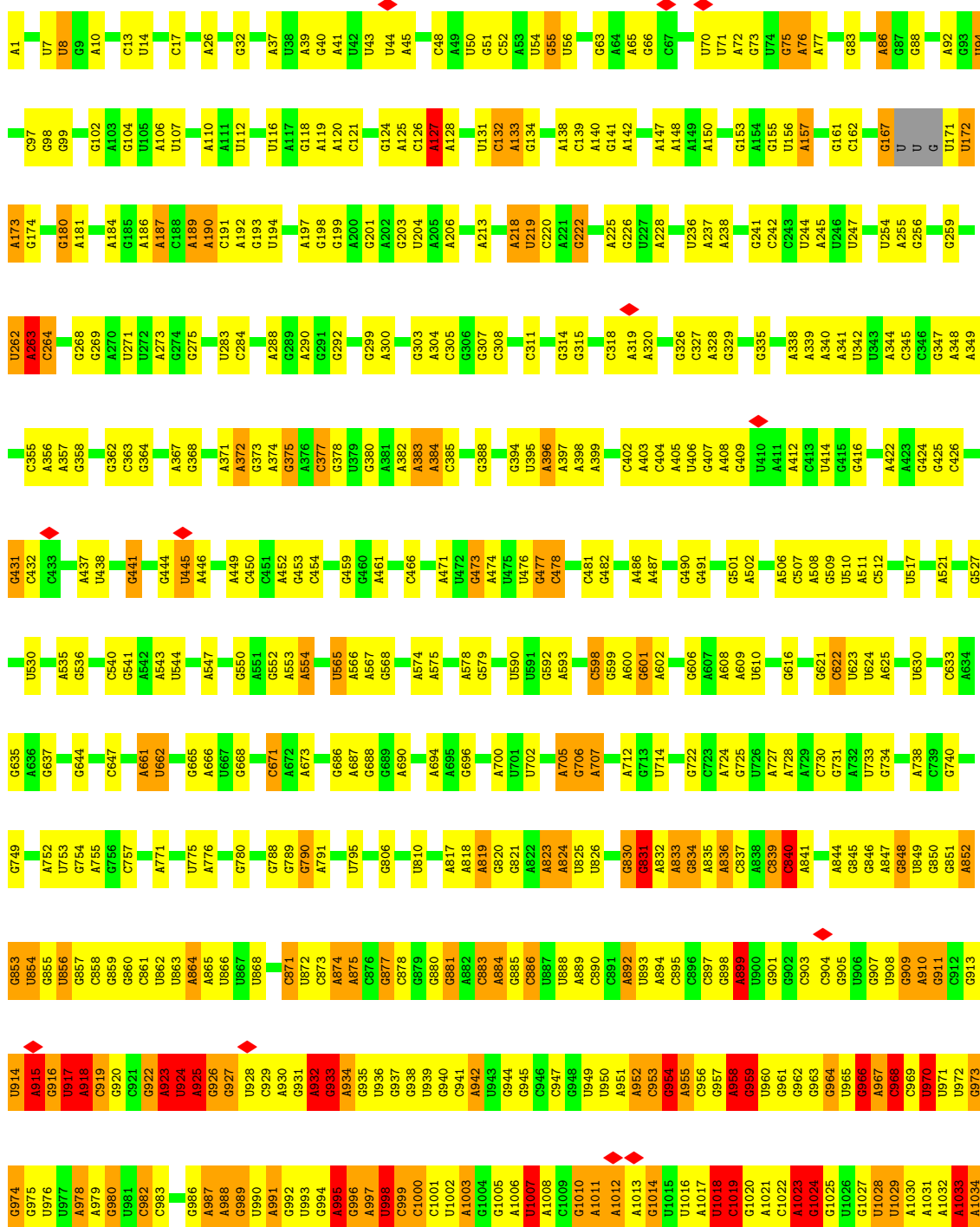
- Molecule 42: RNA 16S

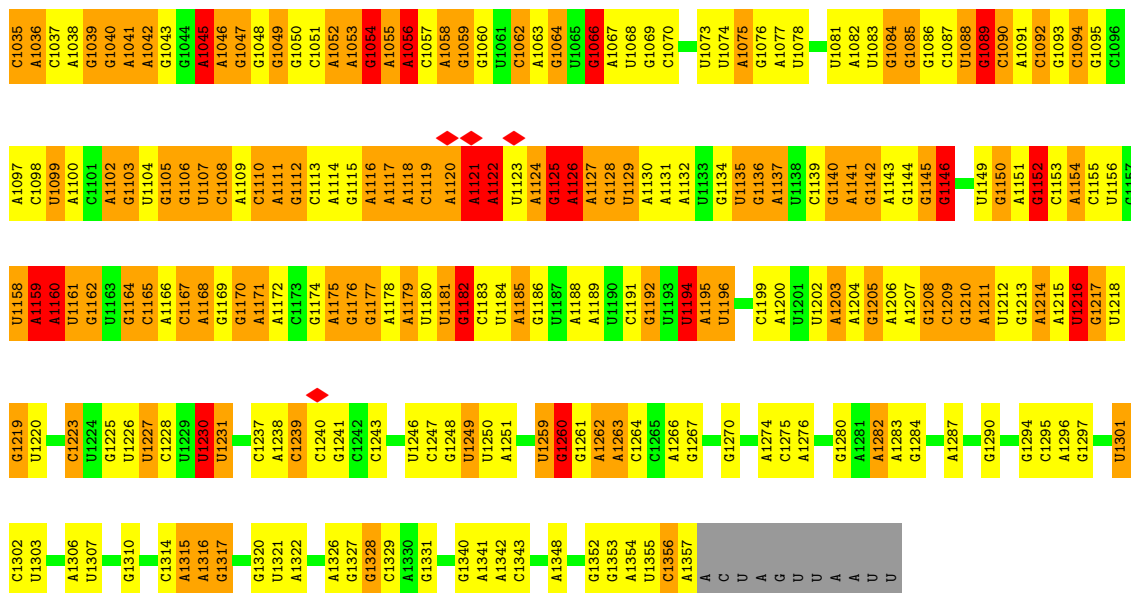




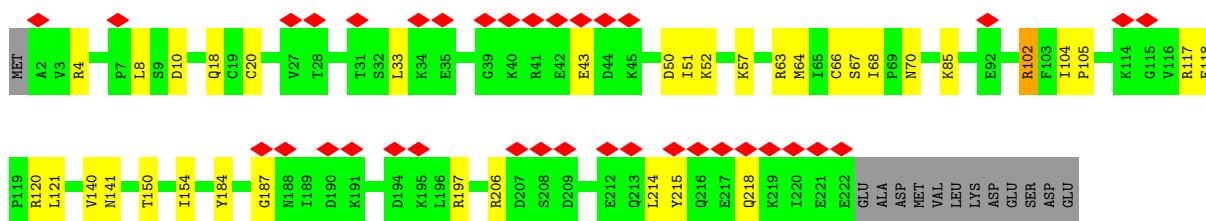
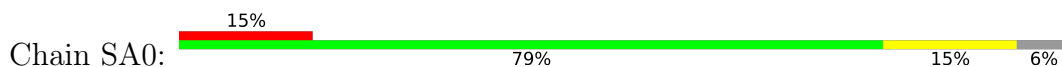


● Molecule 42: RNA 16S

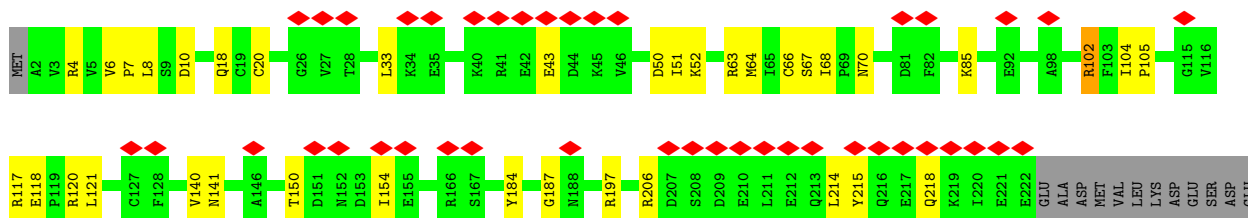
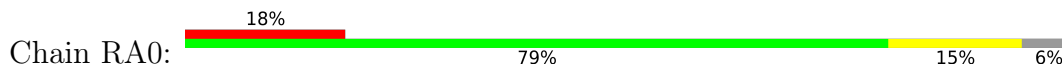




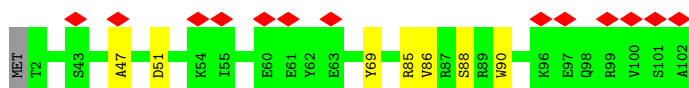
• Molecule 43: 40S ribosomal protein S0



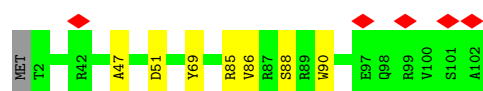
• Molecule 43: 40S ribosomal protein S0



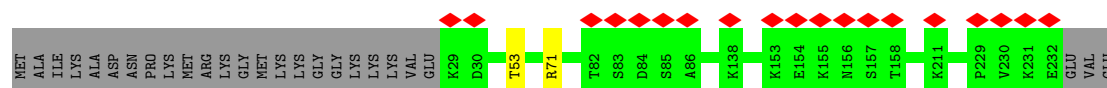
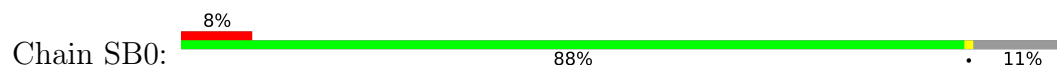
• Molecule 44: 40S ribosomal protein S26



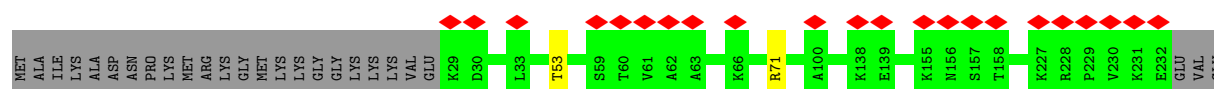
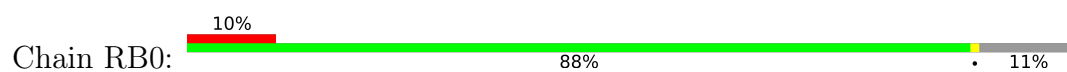
• Molecule 44: 40S ribosomal protein S26



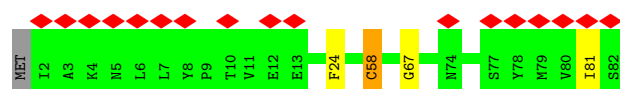
- Molecule 45: eS1



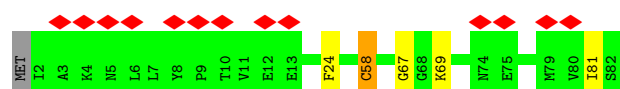
- Molecule 45: eS1



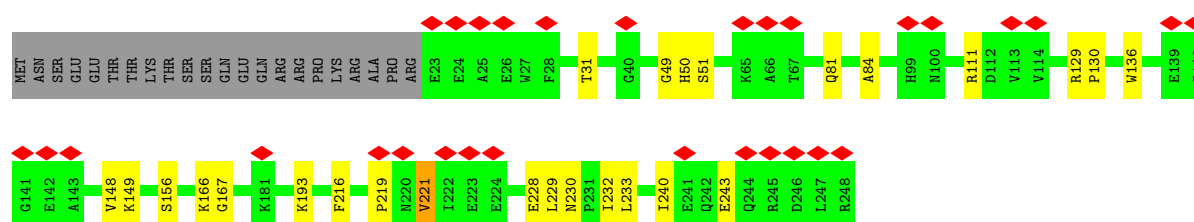
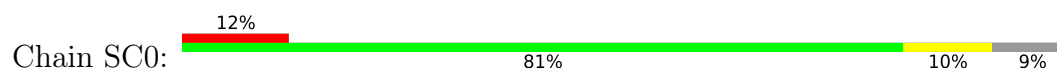
- Molecule 46: eS27



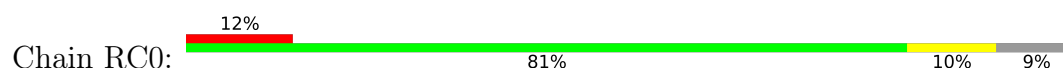
- Molecule 46: eS27

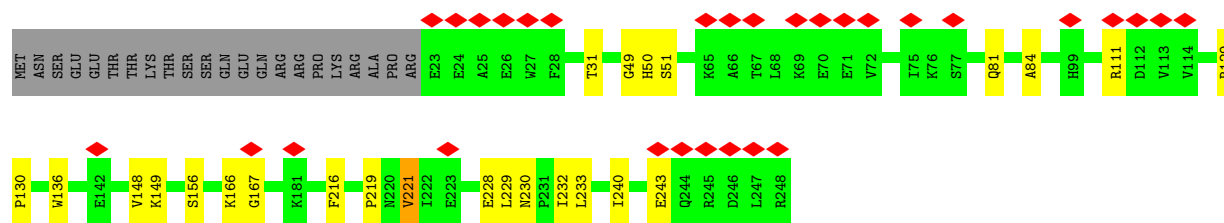


- Molecule 47: 40S ribosomal protein S2

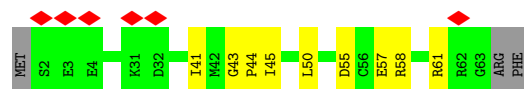
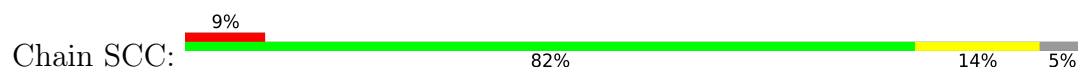


- Molecule 47: 40S ribosomal protein S2

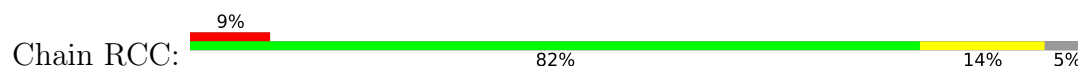




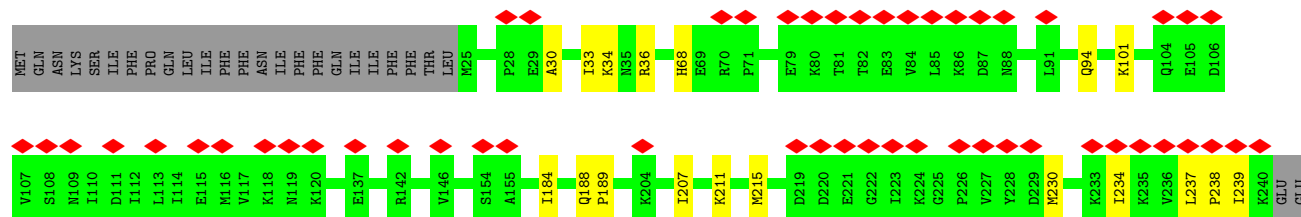
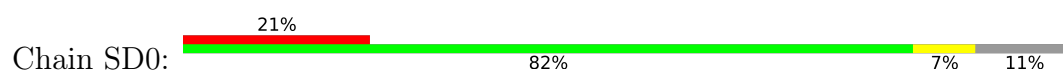
• Molecule 48: eS28



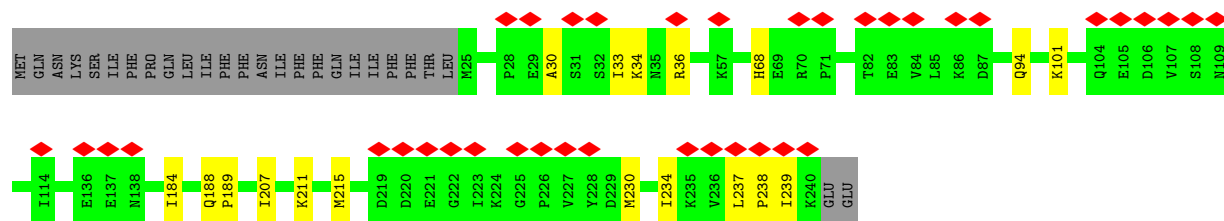
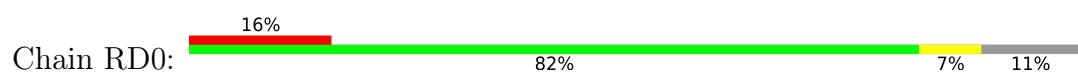
• Molecule 48: eS28



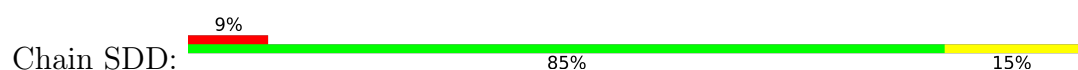
• Molecule 49: 40S ribosomal protein S3



• Molecule 49: 40S ribosomal protein S3

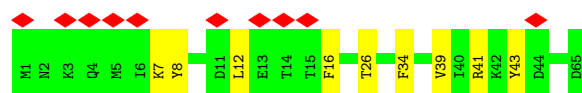
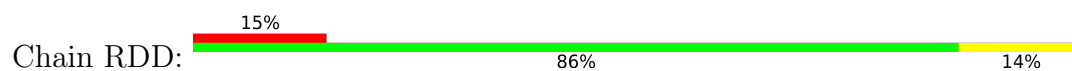


• Molecule 50: 40S ribosomal protein S29

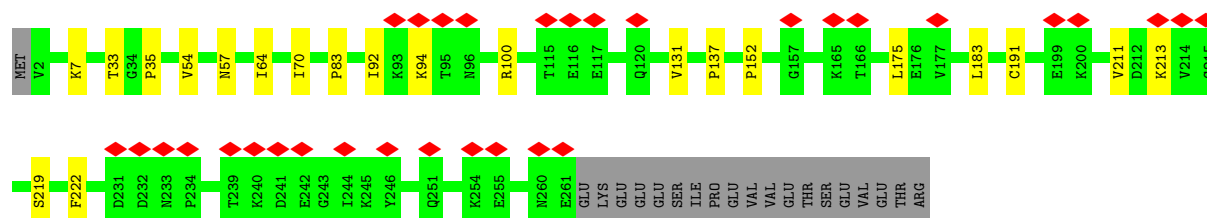
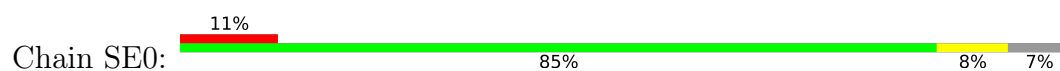




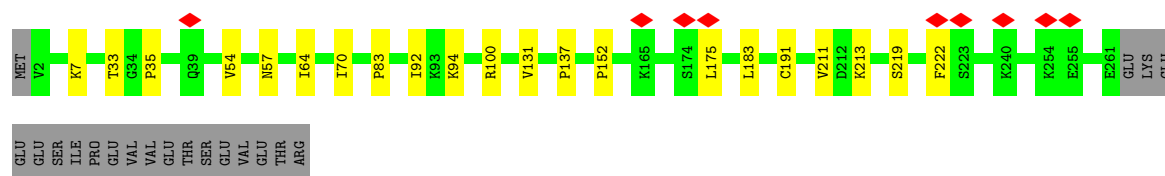
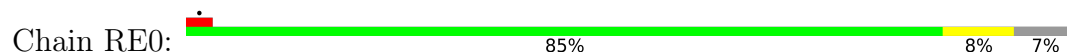
- Molecule 50: 40S ribosomal protein S29



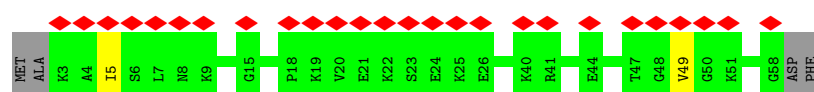
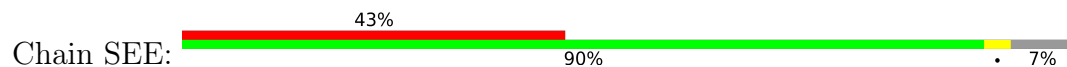
- Molecule 51: 40S ribosomal protein S4



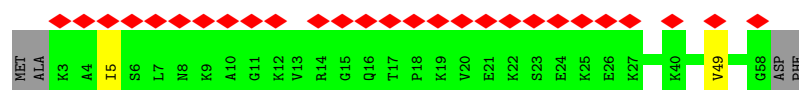
- Molecule 51: 40S ribosomal protein S4



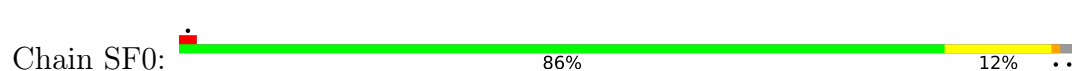
- Molecule 52: eS30



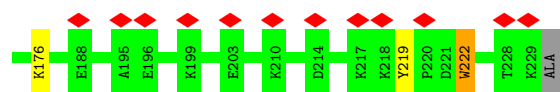
- Molecule 52: eS30



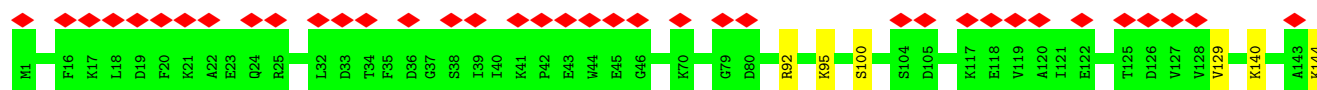
- Molecule 53: 40S ribosomal protein S5



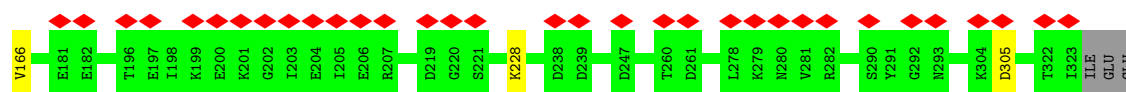
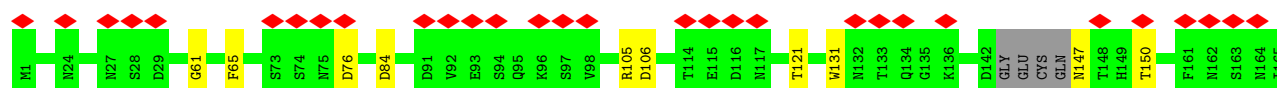




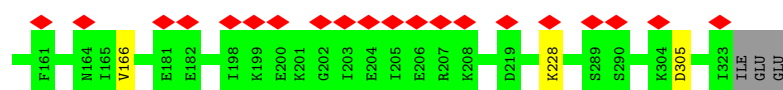
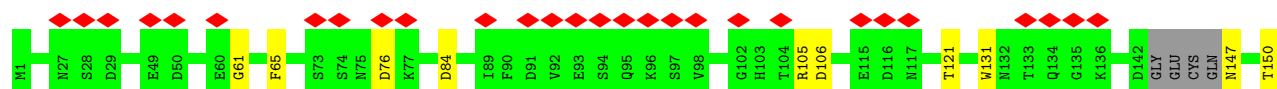
- Molecule 55: 40S ribosomal protein S6



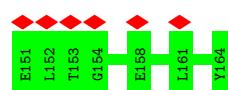
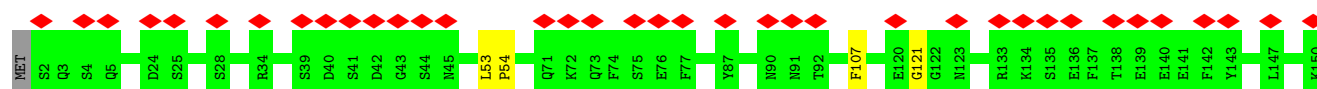
- Molecule 56: Guanine nucleotide binding protein beta subunit



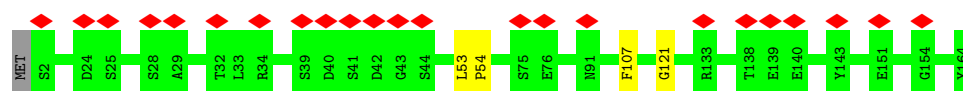
- Molecule 56: Guanine nucleotide binding protein beta subunit



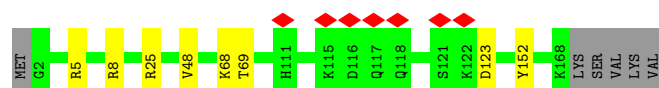
- Molecule 57: 40S ribosomal protein S7



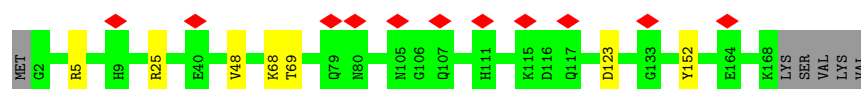
- Molecule 57: 40S ribosomal protein S7



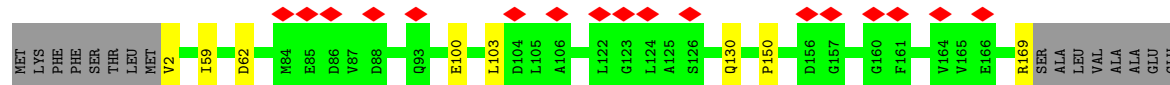
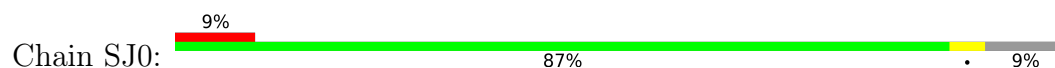
- Molecule 58: 40S ribosomal protein S8



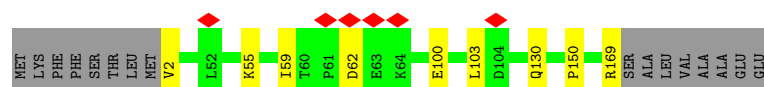
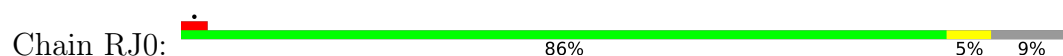
- Molecule 58: 40S ribosomal protein S8



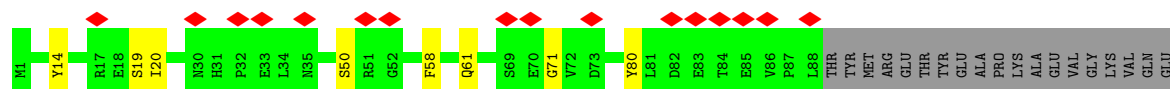
- Molecule 59: 40S ribosomal protein S9



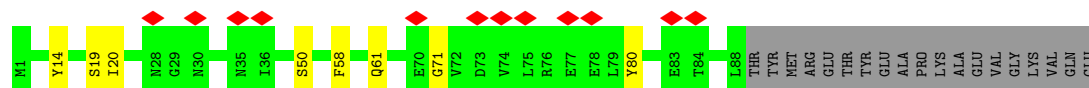
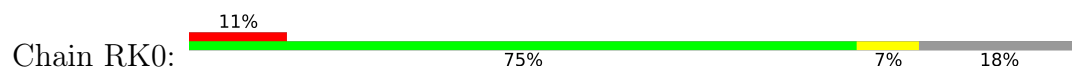
- Molecule 59: 40S ribosomal protein S9



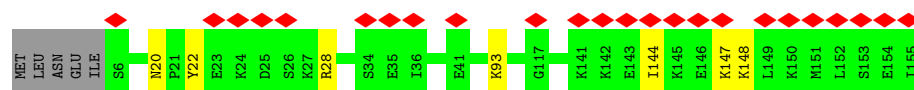
- Molecule 60: 40S ribosomal protein S10



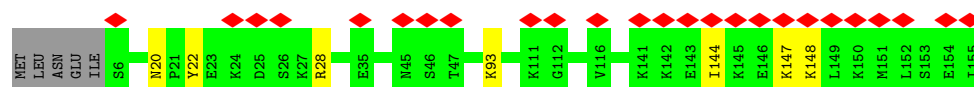
- Molecule 60: 40S ribosomal protein S10



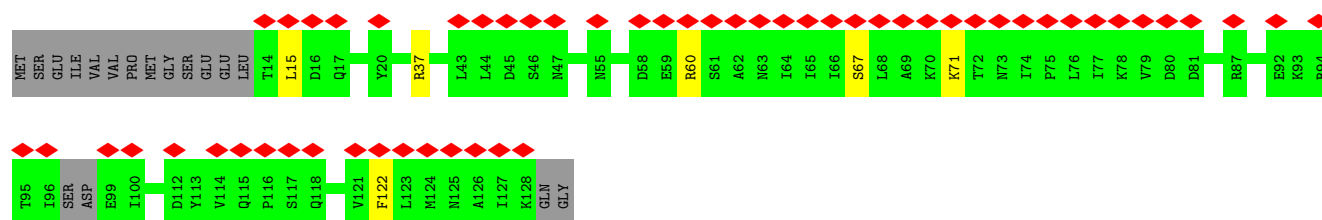
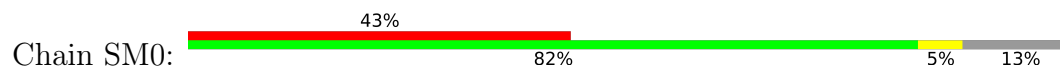
- Molecule 61: 40S ribosomal protein S11



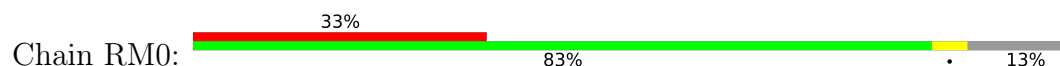
- Molecule 61: 40S ribosomal protein S11



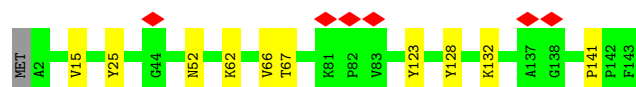
- Molecule 62: 40S ribosomal protein S12



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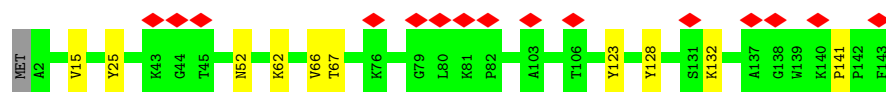


- Molecule 63: 40S ribosomal protein S13



- Molecule 63: 40S ribosomal protein S13





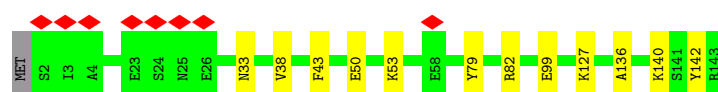
- Molecule 64: 40S ribosomal protein S14



- Molecule 64: 40S ribosomal protein S14



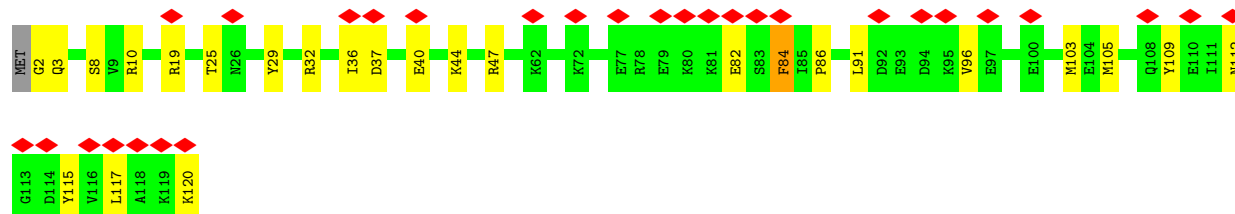
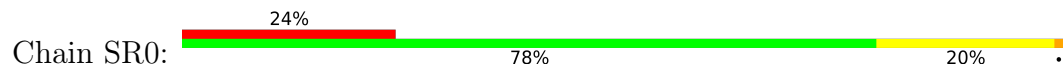
- Molecule 65: 40S ribosomal protein S16



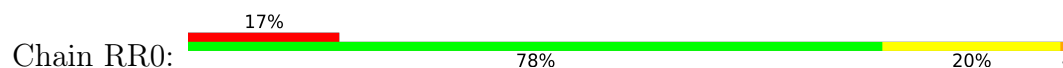
- Molecule 65: 40S ribosomal protein S16



- Molecule 66: eS17

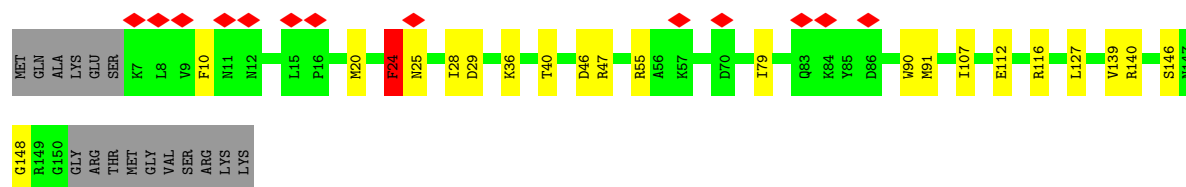
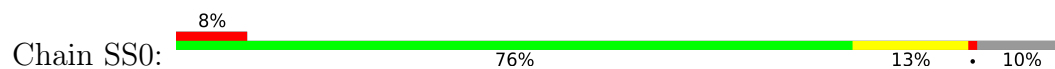


- Molecule 66: eS17

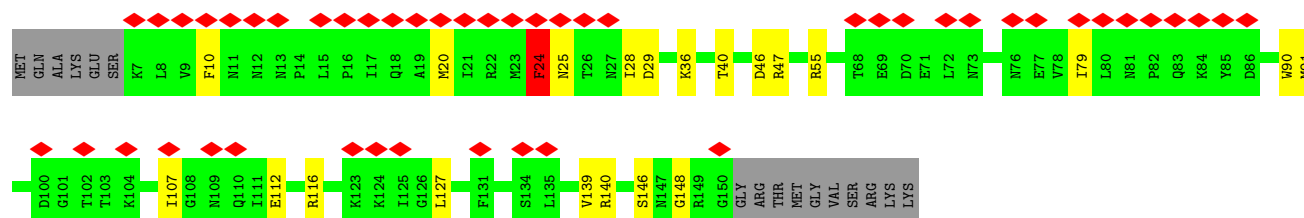
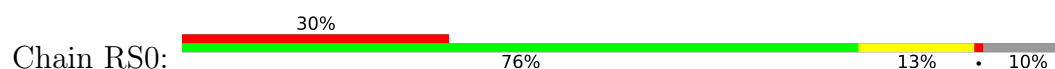




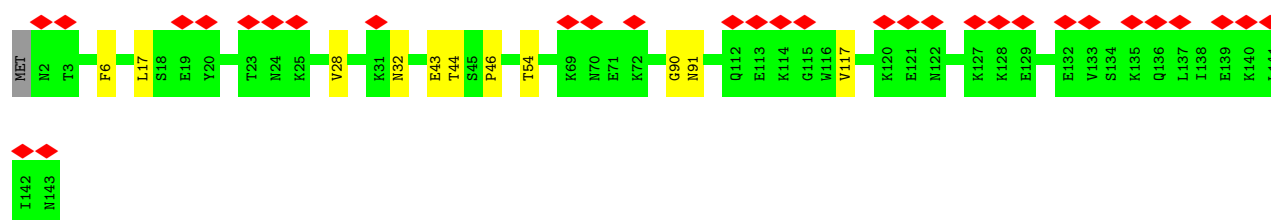
- Molecule 67: 40S ribosomal protein S18



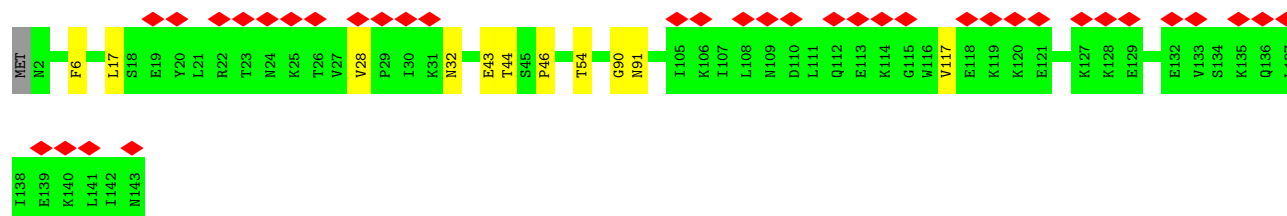
- Molecule 67: 40S ribosomal protein S18



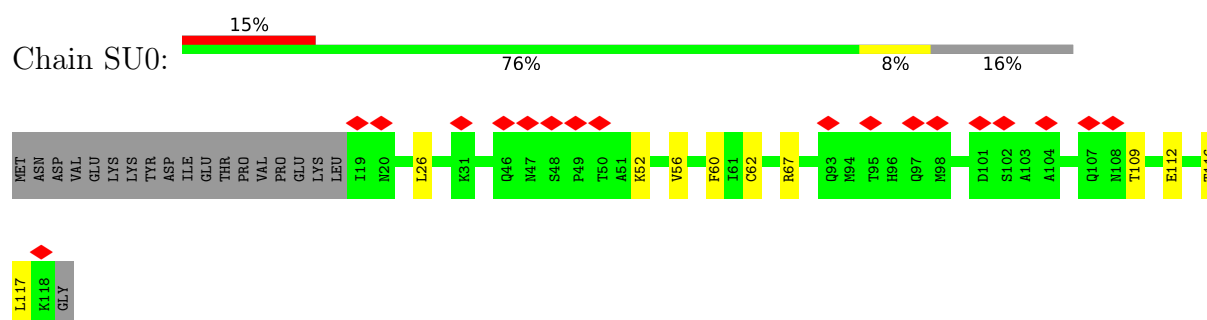
- Molecule 68: 40S Ribosomal protein S19



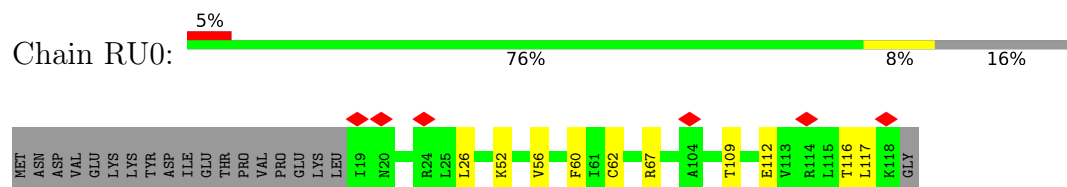
- Molecule 68: 40S Ribosomal protein S19



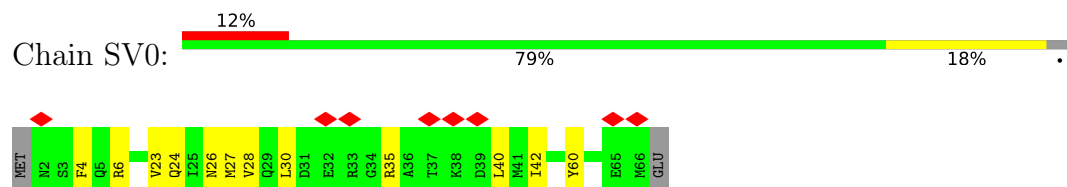
- Molecule 69: 40S ribosomal protein S20



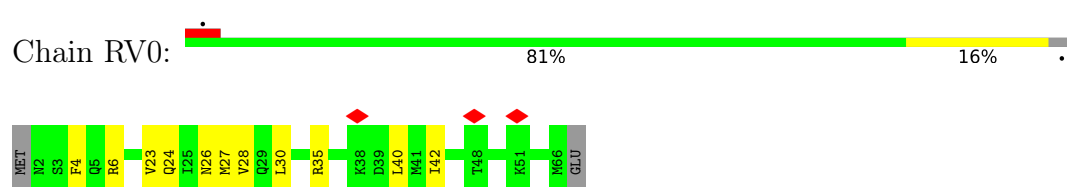
- Molecule 69: 40S ribosomal protein S20



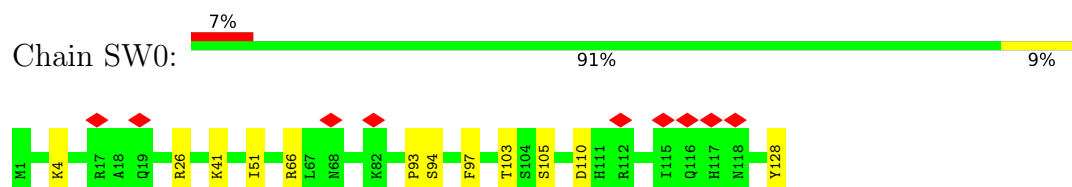
- Molecule 70: Ribosomal protein S21E



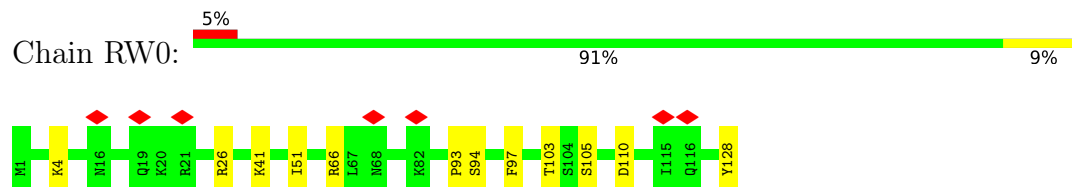
- Molecule 70: Ribosomal protein S21E



- Molecule 71: 40S ribosomal protein S15A

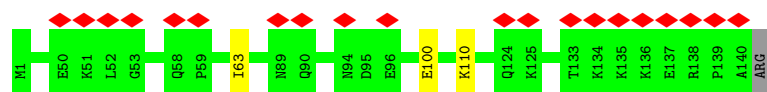


- Molecule 71: 40S ribosomal protein S15A

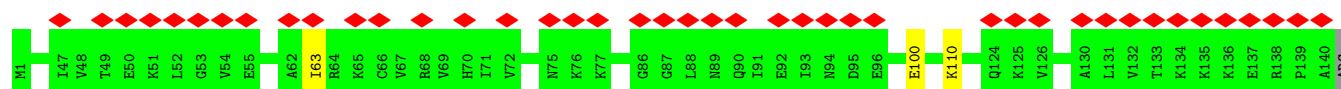


- Molecule 72: uS12

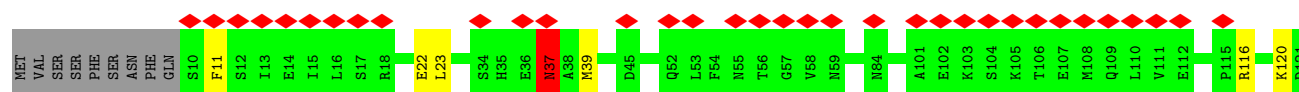




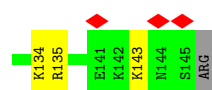
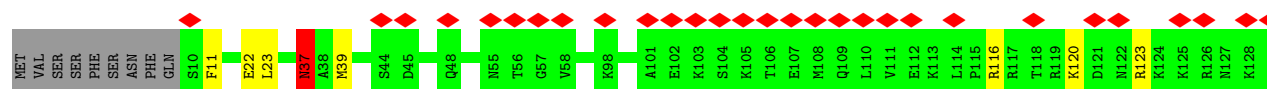
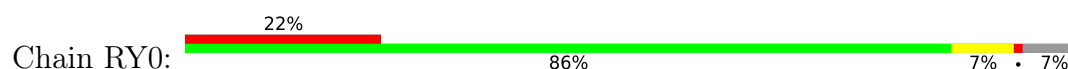
- Molecule 72: uS12



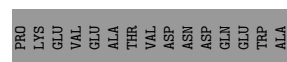
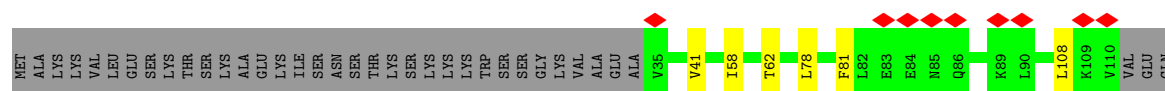
- Molecule 73: 40s ribosomal protein s24



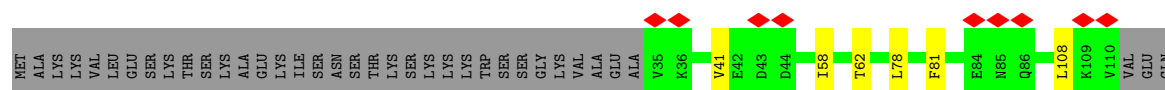
- Molecule 73: 40s ribosomal protein s24



- Molecule 74: 40S ribosomal protein S25



- Molecule 74: 40S ribosomal protein S25





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	1344	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	120, 120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.055	Depositor
Minimum map value	-1.175	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.156	Depositor
Recommended contour level	0.26	Depositor
Map size ( $\text{\AA}$ )	772.8, 772.8, 772.8	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	4.6, 4.6, 4.6	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	K50	0.75	1/60107 (0.0%)	1.19	160/93753 (0.2%)
1	L50	0.75	1/60107 (0.0%)	1.19	160/93753 (0.2%)
2	K70	0.75	1/2844 (0.0%)	1.11	6/4429 (0.1%)
2	L70	0.75	1/2844 (0.0%)	1.11	6/4429 (0.1%)
3	KA0	0.32	0/1926	0.74	0/2590
3	LA0	0.32	0/1926	0.74	0/2590
4	KAA	0.34	0/1191	0.66	0/1586
4	LAA	0.34	0/1191	0.66	0/1586
5	KB0	0.32	0/3092	0.70	1/4144 (0.0%)
5	LB0	0.32	0/3092	0.70	1/4144 (0.0%)
6	KC0	0.33	0/2646	0.75	1/3555 (0.0%)
6	LC0	0.33	0/2646	0.75	1/3555 (0.0%)
7	KCC	0.32	0/794	0.62	0/1067
7	LCC	0.32	0/794	0.62	0/1067
8	KD0	0.28	0/2328	0.67	0/3098
8	LD0	0.28	0/2328	0.67	0/3098
9	KDD	0.30	0/913	0.66	0/1223
9	LDD	0.30	0/913	0.66	0/1223
10	KE0	0.28	0/1394	0.65	0/1875
10	LE0	0.28	0/1394	0.65	0/1875
11	KEE	0.32	0/1108	0.69	0/1477
11	LEE	0.32	0/1108	0.69	0/1477
12	KF0	0.30	0/1963	0.68	0/2618
12	LF0	0.30	0/1963	0.68	0/2618
13	KFF	0.33	0/906	0.70	0/1207
13	LFF	0.33	0/906	0.70	0/1207
14	KG0	0.28	0/1612	0.63	0/2163
14	LG0	0.28	0/1612	0.63	0/2163
15	KGG	0.34	0/825	0.78	1/1090 (0.1%)
15	LGG	0.34	0/825	0.78	1/1090 (0.1%)
16	KH0	0.30	0/1503	0.65	0/2018
16	LH0	0.30	0/1503	0.65	0/2018

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	KHH	0.28	0/999	0.65	0/1324
17	LHH	0.28	0/999	0.65	0/1324
18	KI0	0.32	0/1781	0.69	0/2382
18	LI0	0.32	0/1781	0.69	0/2382
19	KII	0.29	0/790	0.59	0/1041
19	LII	0.29	0/790	0.59	0/1041
20	KJ0	0.30	0/1350	0.66	0/1797
20	LJ0	0.30	0/1350	0.66	0/1797
21	KJJ	0.40	0/710	0.82	2/932 (0.2%)
21	LJJ	0.40	0/710	0.83	2/932 (0.2%)
22	KL0	0.30	0/1374	0.76	1/1827 (0.1%)
22	LL0	0.30	0/1374	0.77	1/1827 (0.1%)
23	KLL	0.34	0/435	0.72	0/576
23	LLL	0.34	0/435	0.72	0/576
24	KM0	0.32	0/935	0.66	0/1251
24	LM0	0.32	0/935	0.65	0/1251
25	KMM	0.41	0/431	0.68	0/568
25	LMM	0.41	0/431	0.68	0/568
26	KN0	0.35	0/1722	0.74	1/2297 (0.0%)
26	LN0	0.35	0/1722	0.74	1/2297 (0.0%)
27	KO0	0.30	0/1626	0.65	0/2168
27	LO0	0.30	0/1626	0.65	0/2168
28	KOO	0.34	0/811	0.69	0/1071
28	LOO	0.34	0/811	0.70	0/1071
29	KP0	0.31	0/1262	0.77	0/1689
29	LP0	0.31	0/1262	0.77	0/1689
30	KPP	0.40	0/693	0.78	2/918 (0.2%)
30	LPP	0.40	0/693	0.78	2/918 (0.2%)
31	KQ0	0.30	0/1512	0.64	0/2014
31	LQ0	0.30	0/1512	0.64	0/2014
32	KR0	0.31	0/1352	0.65	1/1790 (0.1%)
32	LR0	0.31	0/1352	0.65	1/1790 (0.1%)
33	KS0	0.30	0/1422	0.67	0/1898
33	LS0	0.30	0/1422	0.66	0/1898
34	KT0	0.31	0/1294	0.68	0/1736
34	LT0	0.31	0/1294	0.68	0/1736
35	KU0	0.31	0/826	0.67	0/1104
35	LU0	0.30	0/826	0.67	0/1104
36	KV0	0.31	0/1068	0.70	0/1429
36	LV0	0.31	0/1068	0.70	0/1429
37	KW0	0.43	0/849	0.72	0/1129
37	LW0	0.43	0/849	0.72	0/1129
38	KX0	0.28	0/883	0.67	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
38	LX0	0.28	0/883	0.67	0/1175
39	KY0	0.29	0/1058	0.69	1/1399 (0.1%)
39	LY0	0.29	0/1058	0.69	1/1399 (0.1%)
40	KZ0	0.29	0/976	0.73	1/1302 (0.1%)
40	LZ0	0.29	0/976	0.73	1/1302 (0.1%)
41	MD1	0.66	0/1249	0.87	1/1677 (0.1%)
41	MD2	0.66	0/1249	0.87	1/1677 (0.1%)
42	R60	1.40	347/32725 (1.1%)	1.41	369/51066 (0.7%)
42	S60	1.40	351/32725 (1.1%)	1.41	376/51066 (0.7%)
43	RA0	0.36	1/1751 (0.1%)	0.64	0/2358
43	SA0	0.35	1/1751 (0.1%)	0.64	0/2358
44	RAA	0.38	0/839	0.73	0/1120
44	SAA	0.38	0/839	0.72	0/1120
45	RB0	0.29	0/1623	0.67	0/2169
45	SB0	0.29	0/1623	0.67	0/2169
46	RBB	0.47	1/634 (0.2%)	0.65	0/844
46	SBB	0.47	1/634 (0.2%)	0.65	0/844
47	RC0	0.31	0/1751	0.69	2/2359 (0.1%)
47	SC0	0.31	0/1751	0.69	2/2359 (0.1%)
48	RCC	0.33	0/480	0.73	0/644
48	SCC	0.32	0/480	0.73	0/644
49	RD0	0.30	0/1721	0.66	0/2304
49	SD0	0.30	0/1721	0.66	0/2304
50	RDD	0.40	0/559	0.75	1/742 (0.1%)
50	SDD	0.40	0/559	0.75	1/742 (0.1%)
51	RE0	0.32	0/2080	0.72	2/2804 (0.1%)
51	SE0	0.32	0/2080	0.72	2/2804 (0.1%)
52	REE	0.35	0/453	0.74	1/596 (0.2%)
52	SEE	0.36	0/453	0.74	1/596 (0.2%)
53	RF0	0.31	0/1527	0.69	0/2045
53	SF0	0.31	0/1527	0.68	0/2045
54	RFF	0.43	0/422	0.66	0/568
54	SFF	0.43	0/427	0.68	0/573
55	RG0	0.29	0/1864	0.68	0/2485
55	SG0	0.29	0/1864	0.68	0/2485
56	RGG	0.34	0/2517	0.71	1/3397 (0.0%)
56	SGG	0.34	0/2517	0.71	1/3397 (0.0%)
57	RH0	0.31	0/1356	0.66	0/1820
57	SH0	0.31	0/1356	0.66	0/1820
58	RI0	0.33	0/1369	0.67	0/1825
58	SI0	0.33	0/1369	0.67	0/1825
59	RJ0	0.33	0/1403	0.68	0/1880
59	SJ0	0.33	0/1403	0.68	0/1880

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
60	RK0	0.29	0/750	0.71	0/1009
60	SK0	0.29	0/750	0.71	0/1009
61	RL0	0.32	0/1252	0.72	2/1672 (0.1%)
61	SL0	0.32	0/1252	0.72	2/1672 (0.1%)
62	RM0	0.32	0/881	0.71	0/1182
62	SM0	0.32	0/881	0.71	0/1182
63	RN0	0.38	0/1154	0.78	0/1557
63	SN0	0.38	0/1154	0.78	0/1557
64	RO0	0.33	0/993	0.72	0/1326
64	SO0	0.32	0/993	0.72	0/1326
65	RQ0	0.33	0/1163	0.74	3/1556 (0.2%)
65	SQ0	0.32	0/1163	0.74	3/1556 (0.2%)
66	RR0	0.64	0/985	0.97	2/1315 (0.2%)
66	SR0	0.64	0/985	0.97	2/1315 (0.2%)
67	RS0	0.34	0/1165	0.74	0/1566
67	SS0	0.34	0/1165	0.74	0/1566
68	RT0	0.34	0/1181	0.75	1/1585 (0.1%)
68	ST0	0.34	0/1181	0.75	1/1585 (0.1%)
69	RU0	0.33	0/824	0.74	2/1110 (0.2%)
69	SU0	0.33	0/824	0.74	2/1110 (0.2%)
70	RV0	0.33	0/525	0.66	0/700
70	SV0	0.33	0/525	0.66	0/700
71	RW0	0.32	0/1037	0.71	0/1389
71	SW0	0.32	0/1037	0.71	0/1389
72	RX0	0.31	0/1113	0.70	0/1486
72	SX0	0.31	0/1113	0.70	0/1486
73	RY0	0.30	0/1131	0.72	1/1503 (0.1%)
73	SY0	0.30	0/1131	0.72	1/1503 (0.1%)
74	RZ0	0.33	0/640	0.75	0/855
74	SZ0	0.33	0/640	0.75	0/855
75	RP0	0.33	0/964	0.71	0/1289
75	SP0	0.33	0/964	0.71	0/1289
All	All	0.77	706/366789 (0.2%)	1.06	1139/533031 (0.2%)

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
6	KC0	0	1
6	LC0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	KFF	0	1
13	LFF	0	1
15	KGG	0	1
15	LGG	0	1
All	All	0	6

All (706) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	934	A	P-O5'	10.41	1.70	1.59
42	R60	934	A	P-O5'	10.38	1.70	1.59
42	R60	988	A	N9-C4	-8.53	1.32	1.37
42	S60	988	A	N9-C4	-8.53	1.32	1.37
43	RA0	20	CYS	C-N	8.45	1.53	1.34
43	SA0	20	CYS	C-N	8.41	1.53	1.34
1	L50	1	A	OP3-P	-8.40	1.51	1.61
42	S60	1052	A	N9-C4	-8.37	1.32	1.37
42	S60	1049	G	N7-C5	-8.33	1.34	1.39
1	K50	1	A	OP3-P	-8.32	1.51	1.61
42	R60	1052	A	N9-C4	-8.31	1.32	1.37
42	S60	968	C	N1-C6	-8.28	1.32	1.37
42	R60	968	C	N1-C6	-8.28	1.32	1.37
42	R60	1049	G	N7-C5	-8.24	1.34	1.39
42	R60	835	A	N7-C5	-7.85	1.34	1.39
42	S60	835	A	N7-C5	-7.81	1.34	1.39
42	R60	989	G	N7-C5	-7.76	1.34	1.39
42	S60	989	G	N7-C5	-7.74	1.34	1.39
42	R60	978	A	N9-C4	-7.69	1.33	1.37
42	S60	979	A	N7-C5	-7.69	1.34	1.39
42	R60	1	A	OP3-P	-7.59	1.52	1.61
42	S60	1011	A	N7-C5	-7.59	1.34	1.39
42	R60	1011	A	N7-C5	-7.59	1.34	1.39
42	S60	1	A	OP3-P	-7.54	1.52	1.61
42	S60	1045	A	N3-C4	-7.54	1.30	1.34
42	R60	979	A	N7-C5	-7.48	1.34	1.39
42	S60	978	A	N9-C4	-7.46	1.33	1.37
42	S60	1178	A	N9-C4	-7.44	1.33	1.37
42	R60	1089	G	C8-N7	7.43	1.35	1.30
2	L70	1	A	OP3-P	-7.39	1.52	1.61
2	K70	1	A	OP3-P	-7.37	1.52	1.61
42	R60	1178	A	N9-C4	-7.36	1.33	1.37
42	R60	849	U	C2-N3	-7.35	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1045	A	N3-C4	-7.32	1.30	1.34
42	S60	1058	A	N9-C4	-7.30	1.33	1.37
42	S60	1089	G	C8-N7	7.30	1.35	1.30
42	S60	835	A	N3-C4	-7.28	1.30	1.34
42	R60	1058	A	N9-C4	-7.28	1.33	1.37
42	S60	849	U	C2-N3	-7.27	1.32	1.37
42	S60	952	A	N9-C4	-7.27	1.33	1.37
42	R60	847	A	N3-C4	-7.27	1.30	1.34
42	S60	847	A	N3-C4	-7.27	1.30	1.34
42	R60	1045	A	N7-C5	-7.25	1.34	1.39
42	S60	1045	A	N7-C5	-7.25	1.34	1.39
42	R60	1164	G	N7-C5	7.24	1.43	1.39
42	R60	835	A	N3-C4	-7.22	1.30	1.34
42	R60	952	A	N9-C4	-7.21	1.33	1.37
42	S60	951	A	N9-C4	-7.17	1.33	1.37
42	R60	989	G	C6-N1	-7.15	1.34	1.39
42	S60	885	G	N9-C8	-7.14	1.32	1.37
42	S60	1084	G	C8-N7	7.12	1.35	1.30
42	R60	1036	A	C5-C4	-7.12	1.33	1.38
42	R60	987	A	N9-C4	-7.12	1.33	1.37
42	R60	1084	G	C8-N7	7.11	1.35	1.30
42	S60	1164	G	N7-C5	7.10	1.43	1.39
42	S60	989	G	C6-N1	-7.07	1.34	1.39
42	R60	1181	U	C2-N3	-7.06	1.32	1.37
42	S60	987	A	N9-C4	-7.06	1.33	1.37
42	S60	1036	A	C5-C4	-7.06	1.33	1.38
42	R60	885	G	N9-C8	-7.05	1.32	1.37
42	S60	963	G	C5-C4	-7.04	1.33	1.38
42	R60	963	G	C5-C4	-7.00	1.33	1.38
42	S60	1228	C	C4-C5	-6.95	1.37	1.43
42	R60	979	A	N3-C4	-6.95	1.30	1.34
42	R60	951	A	N9-C4	-6.94	1.33	1.37
42	R60	848	G	N9-C8	-6.93	1.32	1.37
42	S60	836	A	N3-C4	-6.92	1.30	1.34
42	S60	1182	G	C8-N7	-6.92	1.26	1.30
42	R60	1014	G	N7-C5	-6.91	1.35	1.39
42	S60	848	G	N9-C8	-6.91	1.33	1.37
42	S60	1181	U	C2-N3	-6.90	1.32	1.37
42	R60	1182	G	C8-N7	-6.88	1.26	1.30
42	S60	1176	G	N7-C5	6.87	1.43	1.39
42	S60	1014	G	N7-C5	-6.86	1.35	1.39
42	R60	1121	A	N9-C4	6.84	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	979	A	N3-C4	-6.84	1.30	1.34
42	S60	1121	A	N9-C4	6.83	1.42	1.37
42	S60	851	G	N7-C5	6.82	1.43	1.39
42	S60	1027	G	C5-C4	-6.82	1.33	1.38
42	S60	1053	A	N3-C4	6.81	1.39	1.34
42	S60	994	G	N7-C5	-6.81	1.35	1.39
42	R60	877	G	N9-C8	-6.79	1.33	1.37
42	R60	1027	G	C5-C4	-6.79	1.33	1.38
42	S60	877	G	N9-C8	-6.78	1.33	1.37
42	R60	1095	G	C8-N7	6.78	1.35	1.30
42	S60	1154	A	N9-C4	6.77	1.42	1.37
42	S60	1028	U	C2-N3	-6.75	1.33	1.37
42	S60	884	A	N9-C4	6.74	1.41	1.37
42	R60	1028	U	C2-N3	-6.74	1.33	1.37
42	R60	1228	C	C4-C5	-6.73	1.37	1.43
42	R60	1053	A	N3-C4	6.72	1.38	1.34
42	R60	1154	A	N9-C4	6.72	1.41	1.37
42	S60	1095	G	C8-N7	6.72	1.34	1.30
42	R60	836	A	N3-C4	-6.71	1.30	1.34
42	R60	1066	G	N9-C8	-6.70	1.33	1.37
42	R60	994	G	N7-C5	-6.70	1.35	1.39
42	S60	1086	G	P-O5'	6.69	1.66	1.59
42	R60	1176	G	N7-C5	6.68	1.43	1.39
42	R60	884	A	N9-C4	6.66	1.41	1.37
42	R60	1120	A	N3-C4	6.66	1.38	1.34
42	S60	1066	G	N9-C8	-6.65	1.33	1.37
42	S60	1038	A	N9-C4	-6.64	1.33	1.37
42	S60	1022	C	P-O5'	6.63	1.66	1.59
42	R60	1022	C	P-O5'	6.63	1.66	1.59
42	R60	1086	G	P-O5'	6.63	1.66	1.59
42	S60	1120	A	N3-C4	6.63	1.38	1.34
42	S60	877	G	P-O5'	6.62	1.66	1.59
42	R60	851	G	N7-C5	6.61	1.43	1.39
42	R60	1038	A	N9-C4	-6.61	1.33	1.37
42	R60	1036	A	C6-N6	-6.61	1.28	1.33
42	S60	1102	A	N9-C4	6.60	1.41	1.37
42	R60	859	G	C8-N7	6.60	1.34	1.30
42	R60	1114	A	P-O5'	6.60	1.66	1.59
42	S60	1036	A	C6-N6	-6.58	1.28	1.33
42	R60	1102	A	N9-C4	6.57	1.41	1.37
42	S60	1114	A	P-O5'	6.56	1.66	1.59
42	R60	877	G	P-O5'	6.55	1.66	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	871	C	N1-C6	-6.54	1.33	1.37
42	R60	871	C	N1-C6	-6.54	1.33	1.37
42	R60	856	U	P-O5'	6.53	1.66	1.59
42	R60	1174	G	C2-N3	6.53	1.38	1.32
42	S60	1162	G	C8-N7	6.53	1.34	1.30
42	R60	1053	A	N7-C5	6.52	1.43	1.39
42	R60	1162	G	C8-N7	6.52	1.34	1.30
42	S60	1053	A	N7-C5	6.52	1.43	1.39
42	R60	1050	G	N9-C8	-6.52	1.33	1.37
42	S60	856	U	P-O5'	6.50	1.66	1.59
42	S60	970	U	C2-N3	-6.50	1.33	1.37
42	R60	989	G	N3-C4	-6.49	1.30	1.35
42	S60	1110	C	C4-C5	6.48	1.48	1.43
42	S60	1032	A	C8-N7	-6.47	1.27	1.31
42	R60	885	G	C6-N1	-6.47	1.35	1.39
42	R60	1116	A	N3-C4	6.46	1.38	1.34
42	S60	1179	A	N3-C4	-6.46	1.30	1.34
42	S60	839	C	C4-C5	-6.45	1.37	1.43
42	S60	1116	A	N3-C4	6.45	1.38	1.34
42	R60	1003	A	C5-C4	-6.45	1.34	1.38
42	R60	1110	C	C4-C5	6.44	1.48	1.43
42	S60	1140	G	N7-C5	6.44	1.43	1.39
42	S60	1050	G	N9-C8	-6.42	1.33	1.37
42	S60	1174	G	C2-N3	6.42	1.37	1.32
42	R60	978	A	N7-C5	-6.42	1.35	1.39
42	S60	859	G	C8-N7	6.41	1.34	1.30
42	S60	1003	A	C5-C4	-6.41	1.34	1.38
42	S60	1183	C	C4-C5	-6.41	1.37	1.43
42	R60	1053	A	C6-N1	6.40	1.40	1.35
42	R60	1179	A	N3-C4	-6.39	1.31	1.34
42	R60	1140	G	N7-C5	6.38	1.43	1.39
42	S60	978	A	N7-C5	-6.38	1.35	1.39
42	R60	1183	C	C4-C5	-6.38	1.37	1.43
42	R60	1111	A	P-O5'	6.37	1.66	1.59
42	S60	1159	A	N9-C4	6.36	1.41	1.37
42	R60	839	C	C4-C5	-6.36	1.37	1.43
42	S60	885	G	C6-N1	-6.35	1.35	1.39
42	R60	970	U	C2-N3	-6.35	1.33	1.37
42	S60	989	G	N3-C4	-6.34	1.31	1.35
42	S60	1067	A	N7-C5	6.33	1.43	1.39
42	S60	1171	A	N3-C4	6.33	1.38	1.34
42	R60	1032	A	C8-N7	-6.32	1.27	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1067	A	N7-C5	6.32	1.43	1.39
42	S60	1062	C	N1-C6	-6.32	1.33	1.37
42	S60	1111	A	P-O5'	6.32	1.66	1.59
42	R60	1062	C	N1-C6	-6.31	1.33	1.37
42	R60	983	C	N1-C6	-6.28	1.33	1.37
42	R60	1159	A	N9-C4	6.28	1.41	1.37
42	S60	850	G	N9-C4	-6.27	1.32	1.38
42	R60	850	G	N9-C4	-6.27	1.32	1.38
42	S60	1106	G	N7-C5	6.26	1.43	1.39
42	S60	954	G	N7-C5	-6.26	1.35	1.39
42	S60	1058	A	N7-C5	-6.26	1.35	1.39
42	S60	983	C	N1-C6	-6.26	1.33	1.37
42	R60	1219	G	C5-C4	-6.25	1.33	1.38
42	R60	1112	G	P-O5'	6.25	1.66	1.59
42	R60	1155	C	P-O5'	6.24	1.66	1.59
42	R60	892	A	P-O5'	6.23	1.66	1.59
42	R60	1106	G	N7-C5	6.23	1.43	1.39
42	S60	835	A	C6-N1	-6.22	1.31	1.35
42	R60	847	A	N7-C5	-6.22	1.35	1.39
42	S60	892	A	P-O5'	6.22	1.66	1.59
42	R60	1046	A	C5-C4	-6.21	1.34	1.38
42	S60	1112	G	P-O5'	6.21	1.66	1.59
42	S60	847	A	N7-C5	-6.21	1.35	1.39
42	S60	1219	G	C5-C4	-6.21	1.34	1.38
42	R60	1171	A	N3-C4	6.21	1.38	1.34
42	R60	892	A	N3-C4	6.21	1.38	1.34
42	S60	1053	A	C6-N1	6.20	1.39	1.35
42	R60	915	A	N9-C4	6.20	1.41	1.37
42	R60	877	G	N3-C4	-6.20	1.31	1.35
42	S60	875	A	C5-C4	-6.20	1.34	1.38
42	S60	892	A	N3-C4	6.19	1.38	1.34
42	S60	877	G	N3-C4	-6.19	1.31	1.35
42	S60	1155	C	P-O5'	6.19	1.66	1.59
42	R60	1003	A	N9-C4	6.18	1.41	1.37
42	R60	1018	U	C2-N3	-6.18	1.33	1.37
42	S60	1136	G	P-O5'	6.17	1.66	1.59
42	S60	1046	A	C5-C4	-6.17	1.34	1.38
42	R60	1058	A	N7-C5	-6.16	1.35	1.39
42	R60	1111	A	N9-C4	6.16	1.41	1.37
42	S60	885	G	N3-C4	-6.15	1.31	1.35
42	S60	1046	A	C6-N6	-6.15	1.29	1.33
42	R60	1046	A	C6-N6	-6.15	1.29	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	847	A	C6-N1	-6.14	1.31	1.35
42	S60	1177	G	C8-N7	-6.14	1.27	1.30
42	S60	1111	A	N9-C4	6.14	1.41	1.37
42	S60	877	G	C6-N1	-6.14	1.35	1.39
42	S60	1064	G	C8-N7	6.14	1.34	1.30
42	S60	1018	U	C2-N3	-6.13	1.33	1.37
42	R60	1113	C	P-O5'	6.13	1.65	1.59
42	R60	861	C	P-O5'	6.13	1.65	1.59
42	R60	875	A	C5-C4	-6.12	1.34	1.38
42	R60	1064	G	C8-N7	6.12	1.34	1.30
42	S60	1113	C	P-O5'	6.11	1.65	1.59
42	S60	1030	A	N7-C5	-6.11	1.35	1.39
42	R60	1067	A	N3-C4	6.11	1.38	1.34
42	R60	954	G	N7-C5	-6.10	1.35	1.39
42	R60	1136	G	P-O5'	6.09	1.65	1.59
42	R60	865	A	N9-C4	6.08	1.41	1.37
42	S60	915	A	N9-C4	6.08	1.41	1.37
42	S60	1067	A	N3-C4	6.08	1.38	1.34
42	R60	877	G	C8-N7	6.08	1.34	1.30
42	S60	1046	A	N7-C5	6.07	1.42	1.39
42	R60	1046	A	N7-C5	6.07	1.42	1.39
42	R60	877	G	C6-N1	-6.06	1.35	1.39
42	R60	847	A	C6-N1	-6.06	1.31	1.35
42	S60	857	G	P-O5'	6.06	1.65	1.59
42	S60	1003	A	N9-C4	6.05	1.41	1.37
42	R60	1116	A	C6-N1	6.05	1.39	1.35
42	S60	886	C	C4-N4	-6.04	1.28	1.33
42	R60	1086	G	N7-C5	6.04	1.42	1.39
42	S60	939	U	P-O5'	6.04	1.65	1.59
42	R60	1177	G	C8-N7	-6.03	1.27	1.30
42	S60	1045	A	C6-N1	-6.02	1.31	1.35
42	R60	935	G	C8-N7	6.02	1.34	1.30
42	S60	1129	U	C2-N3	-6.01	1.33	1.37
42	R60	835	A	C6-N1	-6.01	1.31	1.35
42	S60	877	G	C8-N7	6.01	1.34	1.30
42	R60	857	G	P-O5'	6.01	1.65	1.59
42	R60	1086	G	C6-N1	6.01	1.43	1.39
42	S60	913	G	C6-N1	6.00	1.43	1.39
42	R60	913	G	C6-N1	6.00	1.43	1.39
42	S60	938	G	P-O5'	6.00	1.65	1.59
42	S60	1120	A	C6-N1	6.00	1.39	1.35
42	R60	1092	C	P-O5'	6.00	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1120	A	C6-N1	5.99	1.39	1.35
42	S60	1086	G	N3-C4	5.99	1.39	1.35
42	S60	1116	A	C6-N1	5.99	1.39	1.35
42	S60	861	C	P-O5'	5.99	1.65	1.59
42	R60	1049	G	C6-N1	-5.99	1.35	1.39
42	S60	1086	G	C6-N1	5.98	1.43	1.39
42	S60	1174	G	C8-N7	5.98	1.34	1.30
42	S60	865	A	N9-C4	5.98	1.41	1.37
42	R60	1165	C	N3-C4	5.97	1.38	1.33
42	S60	1161	U	C2-N3	-5.96	1.33	1.37
42	R60	1045	A	C6-N1	-5.96	1.31	1.35
42	R60	1161	U	C2-N3	-5.95	1.33	1.37
42	R60	1152	G	C8-N7	5.94	1.34	1.30
42	R60	1174	G	C8-N7	5.94	1.34	1.30
42	S60	1152	G	C8-N7	5.94	1.34	1.30
42	S60	1156	U	P-O5'	5.94	1.65	1.59
42	S60	1092	C	P-O5'	5.93	1.65	1.59
42	S60	1049	G	C6-N1	-5.93	1.35	1.39
42	R60	885	G	N3-C4	-5.93	1.31	1.35
42	R60	939	U	P-O5'	5.93	1.65	1.59
42	R60	1086	G	N3-C4	5.93	1.39	1.35
42	R60	1129	U	C2-N3	-5.92	1.33	1.37
42	S60	1103	G	N3-C4	5.92	1.39	1.35
42	S60	1092	C	N3-C4	5.92	1.38	1.33
42	S60	1086	G	N7-C5	5.91	1.42	1.39
42	S60	1154	A	P-O5'	5.91	1.65	1.59
42	R60	988	A	N7-C5	-5.91	1.35	1.39
42	R60	848	G	C6-N1	-5.91	1.35	1.39
42	S60	935	G	C8-N7	5.90	1.34	1.30
42	R60	863	U	C2-N3	5.90	1.41	1.37
42	S60	995	A	C5-C4	-5.89	1.34	1.38
42	R60	1092	C	N3-C4	5.89	1.38	1.33
42	S60	1048	G	N9-C4	-5.89	1.33	1.38
42	R60	886	C	C4-N4	-5.89	1.28	1.33
42	S60	863	U	C2-N3	5.88	1.41	1.37
42	S60	932	A	N7-C5	5.88	1.42	1.39
42	R60	1154	A	P-O5'	5.88	1.65	1.59
42	R60	938	G	P-O5'	5.88	1.65	1.59
42	S60	1117	A	N7-C5	5.88	1.42	1.39
42	R60	1103	G	N3-C4	5.88	1.39	1.35
42	R60	1051	C	C4-N4	-5.87	1.28	1.33
42	S60	899	A	N9-C4	5.87	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	1165	C	N3-C4	5.87	1.38	1.33
42	R60	1030	A	N7-C5	-5.87	1.35	1.39
42	S60	1117	A	N3-C4	5.86	1.38	1.34
42	S60	1066	G	C5-C4	-5.86	1.34	1.38
42	S60	1171	A	C6-N1	5.86	1.39	1.35
42	S60	836	A	N7-C5	-5.85	1.35	1.39
42	R60	938	G	N7-C5	5.85	1.42	1.39
42	S60	1084	G	C2-N3	5.84	1.37	1.32
42	R60	860	G	C2-N3	5.84	1.37	1.32
42	S60	1051	C	C4-N4	-5.84	1.28	1.33
42	S60	848	G	C6-N1	-5.83	1.35	1.39
42	R60	1117	A	N7-C5	5.83	1.42	1.39
42	R60	1156	U	P-O5'	5.83	1.65	1.59
42	R60	1066	G	C5-C4	-5.83	1.34	1.38
42	R60	1171	A	C6-N1	5.83	1.39	1.35
42	R60	889	A	P-O5'	5.83	1.65	1.59
42	S60	1050	G	C5-C4	-5.82	1.34	1.38
42	S60	885	G	N7-C5	-5.82	1.35	1.39
42	S60	988	A	N7-C5	-5.81	1.35	1.39
42	R60	899	A	N9-C4	5.81	1.41	1.37
42	R60	1084	G	C2-N3	5.81	1.37	1.32
42	S60	1180	U	C2-N3	-5.81	1.33	1.37
42	R60	913	G	N3-C4	5.80	1.39	1.35
42	R60	1048	G	N9-C4	-5.80	1.33	1.38
42	S60	1067	A	C6-N1	5.80	1.39	1.35
42	R60	1122	A	N9-C4	5.80	1.41	1.37
42	S60	938	G	N7-C5	5.80	1.42	1.39
42	S60	1030	A	N3-C4	-5.80	1.31	1.34
42	R60	973	G	P-O5'	5.80	1.65	1.59
42	R60	1088	U	P-O5'	5.80	1.65	1.59
42	S60	892	A	C6-N1	5.79	1.39	1.35
42	S60	920	G	C8-N7	5.79	1.34	1.30
42	S60	1088	U	P-O5'	5.79	1.65	1.59
42	R60	932	A	N7-C5	5.79	1.42	1.39
42	R60	920	G	C8-N7	5.79	1.34	1.30
42	R60	1050	G	C5-C4	-5.78	1.34	1.38
42	R60	952	A	C5-C6	-5.78	1.35	1.41
42	R60	995	A	C5-C4	-5.77	1.34	1.38
42	S60	913	G	N3-C4	5.76	1.39	1.35
42	R60	836	A	N7-C5	-5.76	1.35	1.39
42	R60	1073	U	P-O5'	5.76	1.65	1.59
42	S60	1134	G	N7-C5	5.76	1.42	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	932	A	N9-C4	5.76	1.41	1.37
42	S60	889	A	P-O5'	5.76	1.65	1.59
42	R60	892	A	C6-N1	5.76	1.39	1.35
42	S60	969	C	C4-N4	-5.76	1.28	1.33
42	S60	973	G	P-O5'	5.75	1.65	1.59
42	S60	1122	A	N9-C4	5.75	1.41	1.37
42	S60	989	G	N9-C8	-5.75	1.33	1.37
42	S60	860	G	C2-N3	5.74	1.37	1.32
42	R60	1117	A	N3-C4	5.74	1.38	1.34
42	R60	885	G	N7-C5	-5.74	1.35	1.39
42	S60	1207	A	N9-C4	5.74	1.41	1.37
42	R60	989	G	N9-C8	-5.74	1.33	1.37
42	R60	1059	G	N7-C5	5.73	1.42	1.39
42	S60	991	A	C5-C4	-5.73	1.34	1.38
42	R60	991	A	C5-C4	-5.72	1.34	1.38
42	S60	1203	A	P-O5'	5.72	1.65	1.59
42	R60	1087	C	N3-C4	5.72	1.38	1.33
42	S60	1087	C	N3-C4	5.72	1.38	1.33
42	R60	864	A	N3-C4	-5.72	1.31	1.34
42	R60	1129	U	P-O5'	5.72	1.65	1.59
42	S60	1040	G	C5-C4	-5.71	1.34	1.38
42	R60	1030	A	N3-C4	-5.71	1.31	1.34
42	S60	1052	A	N7-C5	-5.70	1.35	1.39
42	R60	852	A	N3-C4	5.70	1.38	1.34
42	R60	1067	A	C6-N1	5.69	1.39	1.35
42	R60	1134	G	N7-C5	5.68	1.42	1.39
42	R60	1180	U	C2-N3	-5.68	1.33	1.37
42	S60	932	A	N9-C4	5.68	1.41	1.37
42	S60	1031	A	C5-C4	-5.68	1.34	1.38
42	S60	1165	C	N1-C6	5.68	1.40	1.37
42	S60	1206	A	N3-C4	-5.68	1.31	1.34
42	S60	1117	A	N9-C4	5.68	1.41	1.37
42	R60	1092	C	N1-C6	5.67	1.40	1.37
42	R60	875	A	C6-N6	-5.67	1.29	1.33
42	S60	875	A	C6-N6	-5.67	1.29	1.33
42	R60	1203	A	P-O5'	5.67	1.65	1.59
42	S60	1027	G	N1-C2	-5.66	1.33	1.37
42	S60	852	A	N3-C4	5.66	1.38	1.34
42	S60	1073	U	P-O5'	5.66	1.65	1.59
42	S60	1129	U	P-O5'	5.66	1.65	1.59
42	S60	952	A	C5-C6	-5.66	1.35	1.41
42	S60	844	A	N9-C4	-5.66	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	1141	A	N3-C4	5.66	1.38	1.34
42	S60	1200	A	P-O5'	5.66	1.65	1.59
42	R60	1031	A	C5-C4	-5.65	1.34	1.38
42	R60	1040	G	C5-C4	-5.65	1.34	1.38
42	S60	1051	C	C2-N3	-5.65	1.31	1.35
42	R60	1051	C	C5-C6	-5.64	1.29	1.34
42	R60	1117	A	N9-C4	5.64	1.41	1.37
42	R60	1209	C	N1-C6	5.63	1.40	1.37
42	R60	969	C	C4-N4	-5.62	1.28	1.33
42	R60	1176	G	C2-N3	5.62	1.37	1.32
42	R60	1207	A	N9-C4	5.62	1.41	1.37
42	R60	1200	A	P-O5'	5.62	1.65	1.59
42	S60	1141	A	N7-C5	5.61	1.42	1.39
42	R60	1051	C	C2-N3	-5.61	1.31	1.35
42	R60	1016	U	C2-N3	-5.60	1.33	1.37
42	R60	1160	A	N9-C4	5.60	1.41	1.37
42	S60	1092	C	N1-C6	5.60	1.40	1.37
42	S60	1002	U	N1-C6	-5.60	1.32	1.38
42	S60	1195	A	C8-N7	5.59	1.35	1.31
42	S60	1047	G	P-O5'	5.59	1.65	1.59
42	S60	1209	C	N1-C6	5.59	1.40	1.37
42	R60	1047	G	P-O5'	5.59	1.65	1.59
42	R60	1141	A	N7-C5	5.58	1.42	1.39
42	S60	1059	G	N7-C5	5.58	1.42	1.39
42	R60	844	A	N9-C4	-5.58	1.34	1.37
42	S60	864	A	N3-C4	-5.57	1.31	1.34
42	R60	857	G	N3-C4	5.57	1.39	1.35
42	S60	1174	G	N9-C4	5.57	1.42	1.38
42	S60	1186	G	C2'-C1'	-5.57	1.47	1.53
42	R60	907	G	N7-C5	5.57	1.42	1.39
42	R60	1141	A	N3-C4	5.57	1.38	1.34
42	R60	1052	A	N7-C5	-5.57	1.35	1.39
42	R60	852	A	P-O5'	5.57	1.65	1.59
42	S60	1051	C	C5-C6	-5.56	1.29	1.34
42	R60	1164	G	C6-N1	5.56	1.43	1.39
42	R60	1121	A	N7-C5	5.56	1.42	1.39
42	S60	1037	C	C4-N4	-5.55	1.28	1.33
42	R60	1002	U	N1-C6	-5.55	1.32	1.38
42	R60	1165	C	N1-C6	5.55	1.40	1.37
42	R60	954	G	P-O5'	5.55	1.65	1.59
42	S60	954	G	P-O5'	5.54	1.65	1.59
42	R60	1027	G	N1-C2	-5.54	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	852	A	P-O5'	5.54	1.65	1.59
42	S60	1055	A	N7-C5	-5.54	1.35	1.39
42	R60	1037	C	C4-N4	-5.54	1.28	1.33
42	S60	1230	U	N1-C6	-5.53	1.32	1.38
42	S60	990	U	N1-C6	-5.53	1.32	1.38
42	R60	1230	U	N1-C6	-5.53	1.32	1.38
42	R60	877	G	C2-N3	5.52	1.37	1.32
42	S60	833	A	N9-C4	-5.52	1.34	1.37
42	S60	907	G	N7-C5	5.52	1.42	1.39
42	S60	995	A	N3-C4	-5.52	1.31	1.34
42	R60	990	U	N1-C6	-5.52	1.32	1.38
42	R60	1206	A	N3-C4	-5.52	1.31	1.34
42	R60	1186	G	C2'-C1'	-5.51	1.47	1.53
42	S60	1164	G	C6-N1	5.51	1.43	1.39
42	S60	1016	U	C2-N3	-5.50	1.33	1.37
42	S60	991	A	N9-C8	-5.50	1.33	1.37
42	S60	1075	A	P-O5'	5.50	1.65	1.59
42	S60	1106	G	P-O5'	5.49	1.65	1.59
42	R60	1174	G	N9-C4	5.49	1.42	1.38
42	S60	1029	U	C2-N3	-5.49	1.33	1.37
42	S60	1160	A	N9-C4	5.49	1.41	1.37
42	S60	1176	G	C2-N3	5.49	1.37	1.32
42	S60	1220	U	C2-N3	-5.49	1.33	1.37
42	S60	877	G	C2-N3	5.49	1.37	1.32
42	S60	1039	G	N7-C5	-5.49	1.35	1.39
42	R60	953	C	P-O5'	5.48	1.65	1.59
42	S60	1049	G	N3-C4	-5.48	1.31	1.35
42	S60	1185	A	C8-N7	-5.48	1.27	1.31
42	S60	953	C	P-O5'	5.48	1.65	1.59
42	S60	944	G	C2-N3	5.47	1.37	1.32
42	R60	1113	C	N3-C4	5.47	1.37	1.33
42	R60	1145	G	C2'-C1'	-5.47	1.47	1.53
42	S60	1087	C	N1-C6	5.47	1.40	1.37
42	R60	944	G	C2-N3	5.47	1.37	1.32
42	R60	1115	G	C8-N7	5.47	1.34	1.30
42	R60	995	A	N3-C4	-5.46	1.31	1.34
42	S60	992	G	C5-C4	-5.46	1.34	1.38
42	R60	991	A	N9-C8	-5.46	1.33	1.37
42	R60	987	A	C5-C6	-5.46	1.36	1.41
42	R60	1074	U	C2-N3	5.46	1.41	1.37
42	R60	1220	U	C2-N3	-5.46	1.33	1.37
42	S60	857	G	N3-C4	5.45	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	975	G	C8-N7	-5.45	1.27	1.30
42	R60	1195	A	C8-N7	5.45	1.35	1.31
42	S60	1098	C	P-O5'	5.45	1.65	1.59
42	R60	857	G	C6-N1	5.45	1.43	1.39
42	R60	1098	C	P-O5'	5.44	1.65	1.59
42	R60	992	G	C5-C4	-5.44	1.34	1.38
42	R60	1049	G	N3-C4	-5.44	1.31	1.35
42	R60	1131	A	N3-C4	5.44	1.38	1.34
42	S60	886	C	C5-C6	-5.44	1.30	1.34
42	S60	1192	G	C8-N7	5.43	1.34	1.30
42	S60	1121	A	N7-C5	5.43	1.42	1.39
42	S60	968	C	N3-C4	-5.43	1.30	1.33
42	S60	1047	G	C8-N7	-5.42	1.27	1.30
42	S60	1047	G	N3-C4	5.42	1.39	1.35
42	S60	969	C	C5-C6	-5.42	1.30	1.34
42	R60	1075	A	P-O5'	5.42	1.65	1.59
42	R60	969	C	C2-N3	-5.41	1.31	1.35
42	R60	1047	G	C8-N7	-5.41	1.27	1.30
42	S60	1145	G	C2'-C1'	-5.41	1.47	1.53
42	S60	1115	G	C8-N7	5.41	1.34	1.30
42	R60	969	C	C5-C6	-5.41	1.30	1.34
42	R60	1039	G	N7-C5	-5.41	1.36	1.39
42	R60	1185	A	C8-N7	-5.41	1.27	1.31
42	R60	1055	A	N7-C5	-5.40	1.36	1.39
42	R60	886	C	C5-C6	-5.40	1.30	1.34
42	R60	1047	G	N3-C4	5.40	1.39	1.35
42	R60	833	A	N9-C4	-5.39	1.34	1.37
42	S60	975	G	C8-N7	-5.39	1.27	1.30
42	R60	1000	C	C4-C5	-5.39	1.38	1.43
42	S60	987	A	C5-C6	-5.39	1.36	1.41
42	R60	1120	A	N7-C5	5.39	1.42	1.39
42	R60	968	C	N3-C4	-5.39	1.30	1.33
42	S60	864	A	N7-C5	-5.38	1.36	1.39
42	R60	1209	C	N3-C4	5.38	1.37	1.33
42	R60	950	U	P-O5'	5.38	1.65	1.59
42	S60	1113	C	N3-C4	5.38	1.37	1.33
42	R60	1194	U	N1-C2	5.38	1.43	1.38
42	S60	1093	G	P-O5'	5.37	1.65	1.59
42	R60	1176	G	N9-C4	5.37	1.42	1.38
42	R60	1165	C	P-O5'	5.37	1.65	1.59
42	S60	1117	A	C6-N1	5.37	1.39	1.35
42	R60	1117	A	C6-N1	5.37	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	840	C	N1-C6	5.36	1.40	1.37
42	S60	969	C	C2-N3	-5.36	1.31	1.35
42	R60	1192	G	C8-N7	5.36	1.34	1.30
42	S60	974	G	C5-C4	-5.36	1.34	1.38
42	R60	1066	G	C2-N3	5.36	1.37	1.32
42	R60	1106	G	P-O5'	5.36	1.65	1.59
42	S60	1000	C	C4-C5	-5.35	1.38	1.43
42	S60	1194	U	N1-C2	5.35	1.43	1.38
42	R60	1010	G	N9-C4	-5.35	1.33	1.38
42	R60	1036	A	N1-C2	-5.35	1.29	1.34
42	S60	995	A	N9-C8	-5.35	1.33	1.37
42	S60	913	G	P-O5'	5.35	1.65	1.59
42	S60	979	A	C6-N1	-5.34	1.31	1.35
42	S60	1165	C	P-O5'	5.34	1.65	1.59
42	S60	1209	C	N3-C4	5.34	1.37	1.33
42	R60	855	G	C2-N3	5.34	1.37	1.32
42	S60	1118	A	C5-C4	5.34	1.42	1.38
42	S60	1010	G	N9-C4	-5.33	1.33	1.38
42	S60	1164	G	P-O5'	5.33	1.65	1.59
42	R60	1209	C	P-O5'	5.33	1.65	1.59
42	S60	1161	U	C4-O4	-5.33	1.19	1.23
42	R60	1093	G	P-O5'	5.33	1.65	1.59
42	S60	1097	A	N7-C5	5.33	1.42	1.39
42	R60	1054	G	N9-C8	5.33	1.41	1.37
42	R60	1182	G	C5-C4	-5.33	1.34	1.38
42	S60	1137	A	C5-C4	5.32	1.42	1.38
42	S60	857	G	C6-N1	5.32	1.43	1.39
42	S60	1132	A	C6-N1	5.32	1.39	1.35
42	R60	979	A	C6-N1	-5.32	1.31	1.35
42	S60	1054	G	N9-C8	5.32	1.41	1.37
42	S60	950	U	P-O5'	5.31	1.65	1.59
42	R60	1029	U	C2-N3	-5.31	1.34	1.37
42	S60	836	A	N9-C8	-5.31	1.33	1.37
42	S60	1036	A	N1-C2	-5.31	1.29	1.34
42	R60	1179	A	N7-C5	-5.31	1.36	1.39
42	S60	1018	U	C4-O4	-5.30	1.19	1.23
42	R60	913	G	P-O5'	5.30	1.65	1.59
42	R60	836	A	N9-C8	-5.30	1.33	1.37
42	R60	955	A	N9-C4	-5.30	1.34	1.37
42	R60	1118	A	C5-C4	5.30	1.42	1.38
42	S60	1074	U	C2-N3	5.30	1.41	1.37
42	R60	864	A	N7-C5	-5.30	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1172	A	P-O5'	5.29	1.65	1.59
42	S60	1066	G	C2-N3	5.29	1.36	1.32
42	S60	1176	G	N9-C4	5.29	1.42	1.38
42	S60	1209	C	P-O5'	5.29	1.65	1.59
42	R60	1018	U	C4-O4	-5.29	1.19	1.23
42	R60	963	G	N1-C2	-5.29	1.33	1.37
42	R60	1227	U	C2-N3	-5.28	1.34	1.37
42	S60	855	G	C2-N3	5.28	1.36	1.32
42	S60	1028	U	C4-O4	-5.28	1.19	1.23
42	S60	1172	A	P-O5'	5.28	1.65	1.59
42	R60	963	G	N9-C8	-5.27	1.34	1.37
42	S60	1120	A	N7-C5	5.27	1.42	1.39
42	R60	974	G	C5-C4	-5.27	1.34	1.38
42	R60	1162	G	C2-N3	5.26	1.36	1.32
42	S60	1182	G	C5-C4	-5.26	1.34	1.38
42	R60	952	A	C2-N3	-5.26	1.28	1.33
42	S60	1127	A	C5-C4	-5.26	1.35	1.38
42	S60	1179	A	N7-C5	-5.26	1.36	1.39
42	R60	1081	U	P-O5'	5.26	1.65	1.59
42	R60	840	C	N1-C6	5.26	1.40	1.37
42	R60	1132	A	C6-N1	5.26	1.39	1.35
42	R60	1164	G	P-O5'	5.25	1.65	1.59
42	R60	1175	A	C5-C4	5.25	1.42	1.38
42	S60	963	G	N1-C2	-5.25	1.33	1.37
42	S60	1131	A	N3-C4	5.25	1.38	1.34
42	S60	931	G	N7-C5	5.24	1.42	1.39
42	R60	1127	A	C5-C4	-5.24	1.35	1.38
42	S60	955	A	N7-C5	-5.24	1.36	1.39
42	R60	1226	U	C2-N3	-5.24	1.34	1.37
42	R60	1059	G	N3-C4	5.24	1.39	1.35
42	R60	884	A	N7-C5	5.23	1.42	1.39
42	R60	995	A	N9-C8	-5.23	1.33	1.37
42	R60	1116	A	N7-C5	5.22	1.42	1.39
42	S60	1206	A	N7-C5	-5.22	1.36	1.39
42	R60	886	C	C2-N3	-5.22	1.31	1.35
42	S60	935	G	C2-N3	5.22	1.36	1.32
42	S60	952	A	C2-N3	-5.22	1.28	1.33
42	R60	1185	A	C5-C4	-5.22	1.35	1.38
46	SBB	58	CYS	CB-SG	-5.22	1.73	1.81
42	R60	931	G	N7-C5	5.22	1.42	1.39
42	R60	1018	U	P-O5'	5.21	1.65	1.59
42	R60	1161	U	C4-O4	-5.21	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1087	C	N1-C6	5.21	1.40	1.37
42	S60	963	G	N9-C8	-5.21	1.34	1.37
42	R60	1206	A	N7-C5	-5.21	1.36	1.39
42	S60	886	C	C2-N3	-5.21	1.31	1.35
42	R60	970	U	C4-O4	-5.21	1.19	1.23
42	S60	840	C	N3-C4	5.20	1.37	1.33
42	S60	955	A	N9-C4	-5.20	1.34	1.37
42	S60	1207	A	C5-C4	-5.20	1.35	1.38
42	S60	1226	U	C2-N3	-5.20	1.34	1.37
42	R60	847	A	N9-C8	-5.20	1.33	1.37
42	R60	1103	G	N9-C8	5.19	1.41	1.37
42	R60	953	C	C4-N4	-5.19	1.29	1.33
42	S60	847	A	N9-C8	-5.19	1.33	1.37
42	R60	853	G	C8-N7	5.19	1.34	1.30
42	R60	1176	G	N3-C4	5.19	1.39	1.35
42	S60	1018	U	P-O5'	5.18	1.65	1.59
42	S60	1140	G	C6-N1	5.18	1.43	1.39
42	R60	1097	A	N7-C5	5.18	1.42	1.39
42	S60	1081	U	P-O5'	5.18	1.65	1.59
42	R60	935	G	C2-N3	5.18	1.36	1.32
42	S60	1059	G	N3-C4	5.18	1.39	1.35
42	R60	1129	U	O3'-P	-5.18	1.54	1.61
42	R60	1186	G	N7-C5	-5.18	1.36	1.39
42	S60	892	A	N7-C5	5.18	1.42	1.39
42	S60	1175	A	C5-C4	5.17	1.42	1.38
42	R60	1137	A	C5-C4	5.17	1.42	1.38
42	S60	853	G	C8-N7	5.17	1.34	1.30
42	S60	1227	U	C2-N3	-5.17	1.34	1.37
46	RBB	58	CYS	CB-SG	-5.16	1.73	1.81
42	S60	836	A	C6-N1	-5.16	1.31	1.35
42	S60	1185	A	C5-C4	-5.16	1.35	1.38
42	S60	953	C	C4-N4	-5.16	1.29	1.33
42	S60	979	A	N9-C8	-5.16	1.33	1.37
42	R60	892	A	N7-C5	5.16	1.42	1.39
42	S60	884	A	N7-C5	5.15	1.42	1.39
42	S60	1085	G	C2-N3	5.15	1.36	1.32
42	R60	1055	A	N3-C4	-5.15	1.31	1.34
42	S60	1116	A	N7-C5	5.15	1.42	1.39
42	S60	839	C	P-O5'	5.15	1.64	1.59
42	S60	1186	G	N7-C5	-5.15	1.36	1.39
42	S60	970	U	C4-O4	-5.14	1.19	1.23
42	R60	955	A	N7-C5	-5.14	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	1176	G	N3-C4	5.14	1.39	1.35
42	R60	990	U	N3-C4	-5.14	1.33	1.38
42	R60	837	C	N1-C6	-5.14	1.34	1.37
42	R60	1223	C	P-O5'	5.14	1.64	1.59
42	S60	1164	G	N3-C4	5.14	1.39	1.35
42	R60	1028	U	C4-O4	-5.14	1.19	1.23
42	R60	1047	G	C6-N1	5.14	1.43	1.39
42	R60	1126	A	N9-C4	5.14	1.41	1.37
42	R60	1132	A	N3-C4	5.13	1.38	1.34
42	R60	1140	G	C6-N1	5.13	1.43	1.39
42	S60	837	C	N1-C6	-5.13	1.34	1.37
42	S60	1142	G	C2-N3	5.13	1.36	1.32
42	S60	1085	G	N7-C5	5.13	1.42	1.39
42	S60	938	G	N3-C4	5.13	1.39	1.35
42	S60	1126	A	N9-C4	5.13	1.41	1.37
42	R60	1186	G	P-O5'	5.12	1.64	1.59
42	S60	1011	A	N3-C4	-5.12	1.31	1.34
42	S60	1137	A	P-O5'	5.12	1.64	1.59
42	R60	938	G	N3-C4	5.12	1.39	1.35
42	R60	979	A	N9-C8	-5.12	1.33	1.37
42	R60	1142	G	C2-N3	5.12	1.36	1.32
42	S60	1129	U	O3'-P	-5.11	1.55	1.61
42	R60	1002	U	N3-C4	-5.11	1.33	1.38
42	R60	1207	A	C5-C4	-5.11	1.35	1.38
42	R60	1122	A	C8-N7	5.10	1.35	1.31
42	R60	1137	A	P-O5'	5.10	1.64	1.59
42	S60	1160	A	N7-C5	5.10	1.42	1.39
42	S60	1055	A	N3-C4	-5.10	1.31	1.34
42	R60	1085	G	C2-N3	5.10	1.36	1.32
42	S60	990	U	N3-C4	-5.10	1.33	1.38
42	S60	1141	A	C6-N1	5.10	1.39	1.35
42	S60	862	U	P-O5'	5.09	1.64	1.59
42	S60	1132	A	N3-C4	5.09	1.38	1.34
42	S60	844	A	C8-N7	-5.09	1.27	1.31
42	S60	1002	U	N3-C4	-5.09	1.33	1.38
42	R60	1164	G	N3-C4	5.08	1.39	1.35
42	S60	931	G	C2-N3	5.08	1.36	1.32
42	S60	1095	G	N7-C5	-5.08	1.36	1.39
42	S60	1103	G	N9-C8	5.08	1.41	1.37
42	R60	836	A	C6-N1	-5.08	1.31	1.35
42	R60	1085	G	N7-C5	5.08	1.42	1.39
42	S60	1047	G	C6-N1	5.07	1.43	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	1098	C	N1-C6	5.07	1.40	1.37
42	S60	1162	G	C2-N3	5.07	1.36	1.32
42	S60	1178	A	N7-C5	-5.07	1.36	1.39
42	S60	1059	G	C6-N1	5.07	1.43	1.39
42	R60	1049	G	C8-N7	5.07	1.33	1.30
42	R60	1178	A	N7-C5	-5.07	1.36	1.39
42	S60	1152	G	C5-C4	5.07	1.41	1.38
42	S60	1186	G	P-O5'	5.07	1.64	1.59
42	R60	855	G	N9-C4	5.06	1.42	1.38
42	R60	862	U	P-O5'	5.06	1.64	1.59
42	R60	951	A	P-O5'	5.06	1.64	1.59
42	S60	1130	A	N9-C4	5.06	1.40	1.37
42	S60	849	U	C4-O4	-5.06	1.19	1.23
42	S60	1120	A	N9-C8	5.06	1.41	1.37
42	R60	1052	A	C5-C6	-5.06	1.36	1.41
42	R60	1059	G	C6-N1	5.05	1.43	1.39
42	R60	839	C	P-O5'	5.05	1.64	1.59
42	R60	849	U	C4-O4	-5.05	1.19	1.23
42	S60	1106	G	N3-C4	5.04	1.39	1.35
42	R60	1098	C	N1-C6	5.04	1.40	1.37
42	S60	932	A	N3-C4	5.04	1.37	1.34
42	S60	1223	C	P-O5'	5.04	1.64	1.59
42	R60	1011	A	N3-C4	-5.04	1.31	1.34
42	R60	901	G	C6-N1	5.03	1.43	1.39
42	R60	1095	G	N7-C5	-5.03	1.36	1.39
42	S60	1206	A	C6-N1	-5.03	1.32	1.35
42	R60	853	G	C5-C4	5.03	1.41	1.38
42	R60	1055	A	C8-N7	5.03	1.35	1.31
42	S60	937	G	P-O5'	5.03	1.64	1.59
42	S60	951	A	P-O5'	5.03	1.64	1.59
42	S60	1127	A	C6-N6	-5.02	1.29	1.33
42	S60	982	C	C4-C5	-5.02	1.39	1.43
42	R60	1213	G	C5-C4	-5.02	1.34	1.38
42	S60	937	G	N9-C4	5.01	1.42	1.38
42	R60	840	C	N3-C4	5.01	1.37	1.33
42	R60	982	C	C4-C5	-5.01	1.39	1.43
42	S60	1122	A	C8-N7	5.01	1.35	1.31
42	S60	853	G	C5-C4	5.01	1.41	1.38
42	R60	1206	A	C6-N1	-5.01	1.32	1.35
42	R60	949	U	P-O5'	5.01	1.64	1.59
42	S60	1045	A	N9-C8	-5.00	1.33	1.37
42	R60	937	G	N9-C4	5.00	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	R60	1127	A	C6-N6	-5.00	1.29	1.33

All (1139) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	1356	C	O5'-P-OP1	-18.09	89.00	110.70
42	S60	1356	C	O5'-P-OP1	-18.08	89.00	110.70
42	S60	910	A	P-O3'-C3'	-11.69	105.67	119.70
42	R60	910	A	P-O3'-C3'	-11.66	105.71	119.70
42	S60	850	G	C5-N7-C8	-11.29	98.66	104.30
42	S60	1034	A	P-O3'-C3'	-11.28	106.16	119.70
42	R60	850	G	C5-N7-C8	-11.26	98.67	104.30
42	R60	1034	A	P-O3'-C3'	-11.25	106.20	119.70
42	R60	904	C	P-O3'-C3'	-10.88	106.64	119.70
42	S60	904	C	P-O3'-C3'	-10.88	106.65	119.70
1	K50	330	G	C2'-C3'-O3'	10.41	132.40	109.50
1	L50	330	G	C2'-C3'-O3'	10.39	132.36	109.50
42	R60	917	U	P-O3'-C3'	-10.36	107.26	119.70
42	S60	917	U	P-O3'-C3'	-10.31	107.33	119.70
42	S60	1108	C	P-O3'-C3'	-10.23	107.42	119.70
42	R60	996	G	P-O3'-C3'	-10.18	107.49	119.70
42	R60	1108	C	P-O3'-C3'	-10.17	107.49	119.70
42	S60	996	G	P-O3'-C3'	-10.17	107.50	119.70
42	R60	1033	A	P-O3'-C3'	-9.99	107.71	119.70
42	S60	1033	A	P-O3'-C3'	-9.98	107.72	119.70
42	S60	1261	G	P-O3'-C3'	-9.95	107.76	119.70
42	R60	1261	G	P-O3'-C3'	-9.91	107.81	119.70
1	K50	1265	G	OP1-P-OP2	-9.87	104.79	119.60
1	L50	1265	G	OP1-P-OP2	-9.84	104.85	119.60
42	S60	958	A	P-O3'-C3'	-9.83	107.91	119.70
42	S60	965	U	P-O3'-C3'	-9.81	107.92	119.70
42	R60	958	A	P-O3'-C3'	-9.80	107.93	119.70
42	R60	965	U	P-O3'-C3'	-9.79	107.95	119.70
42	R60	964	G	P-O3'-C3'	-9.52	108.27	119.70
42	S60	964	G	P-O3'-C3'	-9.50	108.30	119.70
1	L50	535	A	P-O3'-C3'	9.45	131.04	119.70
1	K50	535	A	P-O3'-C3'	9.43	131.01	119.70
42	R60	956	C	P-O3'-C3'	-9.39	108.43	119.70
42	S60	956	C	P-O3'-C3'	-9.35	108.47	119.70
42	S60	845	G	P-O3'-C3'	-9.30	108.54	119.70
42	R60	845	G	P-O3'-C3'	-9.30	108.55	119.70
42	S60	877	G	N9-C4-C5	9.29	109.12	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	877	G	N9-C4-C5	9.22	109.09	105.40
1	L50	1395	U	C2'-C3'-O3'	9.05	129.42	109.50
42	S60	995	A	P-O3'-C3'	-9.05	108.84	119.70
42	R60	995	A	P-O3'-C3'	-9.05	108.84	119.70
1	K50	1395	U	C2'-C3'-O3'	9.02	129.34	109.50
42	S60	1170	G	C1'-O4'-C4'	-9.02	102.69	109.90
42	R60	1260	G	P-O3'-C3'	-9.02	108.88	119.70
42	S60	1260	G	P-O3'-C3'	-9.01	108.89	119.70
1	K50	1282	C	N1-C2-O2	9.01	124.31	118.90
42	R60	1170	G	C1'-O4'-C4'	-9.00	102.70	109.90
42	S60	998	U	P-O3'-C3'	-8.98	108.92	119.70
42	R60	923	A	P-O3'-C3'	-8.97	108.94	119.70
42	S60	923	A	P-O3'-C3'	-8.95	108.97	119.70
42	R60	998	U	P-O3'-C3'	-8.94	108.97	119.70
1	L50	1282	C	N1-C2-O2	8.92	124.25	118.90
42	R60	850	G	C4-C5-N7	8.86	114.34	110.80
42	S60	850	G	C4-C5-N7	8.85	114.34	110.80
1	L50	1959	A	C2'-C3'-O3'	8.83	128.93	109.50
42	S60	877	G	C4-C5-N7	-8.82	107.27	110.80
1	K50	1959	A	C2'-C3'-O3'	8.81	128.89	109.50
42	R60	824	A	P-O3'-C3'	-8.81	109.12	119.70
42	S60	824	A	P-O3'-C3'	-8.80	109.14	119.70
1	L50	1148	A	C4'-C3'-O3'	8.78	130.55	113.00
1	L50	1585	U	P-O3'-C3'	-8.77	109.18	119.70
1	K50	1148	A	C4'-C3'-O3'	8.76	130.52	113.00
1	K50	1585	U	P-O3'-C3'	-8.72	109.24	119.70
42	R60	961	G	P-O3'-C3'	-8.71	109.25	119.70
42	R60	877	G	C4-C5-N7	-8.70	107.32	110.80
42	S60	961	G	P-O3'-C3'	-8.70	109.27	119.70
42	R60	1135	U	C3'-C2'-C1'	-8.69	94.55	101.50
42	S60	1135	U	C3'-C2'-C1'	-8.67	94.57	101.50
42	R60	394	G	O5'-P-OP1	-8.55	98.00	105.70
42	S60	1125	G	C3'-C2'-C1'	-8.51	94.69	101.50
42	R60	1125	G	C3'-C2'-C1'	-8.50	94.70	101.50
42	S60	394	G	O5'-P-OP1	-8.50	98.05	105.70
68	RT0	117	VAL	CA-CB-CG1	8.39	123.49	110.90
68	ST0	117	VAL	CA-CB-CG1	8.37	123.45	110.90
42	S60	997	A	P-O3'-C3'	-8.27	109.77	119.70
1	K50	424	G	O4'-C1'-N9	8.27	114.81	108.20
42	S60	831	G	P-O3'-C3'	-8.26	109.79	119.70
1	K50	1709	G	C1'-O4'-C4'	-8.25	103.30	109.90
42	R60	831	G	P-O3'-C3'	-8.25	109.80	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	997	A	P-O3'-C3'	-8.24	109.81	119.70
42	S60	919	C	N3-C4-C5	-8.21	118.61	121.90
42	R60	1046	A	C8-N9-C4	8.21	109.08	105.80
1	L50	424	G	O4'-C1'-N9	8.19	114.75	108.20
1	L50	1709	G	C1'-O4'-C4'	-8.18	103.36	109.90
42	S60	1107	U	P-O3'-C3'	-8.18	109.89	119.70
1	L50	141	G	O4'-C1'-N9	8.17	114.74	108.20
42	S60	850	G	N7-C8-N9	8.16	117.18	113.10
1	K50	141	G	O4'-C1'-N9	8.15	114.72	108.20
42	R60	1107	U	P-O3'-C3'	-8.15	109.92	119.70
42	R60	919	C	N3-C4-C5	-8.14	118.64	121.90
42	R60	1150	G	P-O3'-C3'	-8.09	109.99	119.70
42	S60	1150	G	P-O3'-C3'	-8.09	109.99	119.70
42	R60	850	G	N7-C8-N9	8.09	117.14	113.10
42	R60	1174	G	C3'-C2'-C1'	8.09	107.97	101.50
1	K50	1000	G	C1'-O4'-C4'	-8.08	103.43	109.90
42	S60	1046	A	C8-N9-C4	8.07	109.03	105.80
1	L50	1000	G	C1'-O4'-C4'	-8.06	103.45	109.90
42	S60	848	G	OP2-P-O3'	8.06	122.93	105.20
1	L50	2431	C	O5'-P-OP1	-8.05	98.45	105.70
42	S60	1174	G	C3'-C2'-C1'	8.04	107.93	101.50
42	R60	848	G	OP2-P-O3'	8.04	122.88	105.20
42	S60	1167	C	P-O3'-C3'	-8.03	110.06	119.70
1	K50	2431	C	O5'-P-OP1	-8.03	98.47	105.70
1	K50	2597	G	C2'-C3'-O3'	8.01	127.12	109.50
42	S60	1168	A	P-O3'-C3'	-8.01	110.09	119.70
1	L50	2597	G	C2'-C3'-O3'	8.00	127.11	109.50
42	R60	1167	C	P-O3'-C3'	-8.00	110.10	119.70
1	K50	600	G	O4'-C1'-N9	7.99	114.59	108.20
42	R60	1168	A	P-O3'-C3'	-7.99	110.11	119.70
21	KJJ	21	ARG	NE-CZ-NH2	7.97	124.28	120.30
42	R60	1231	U	P-O3'-C3'	-7.92	110.20	119.70
1	L50	600	G	O4'-C1'-N9	7.92	114.54	108.20
42	S60	933	G	O3'-P-O5'	7.92	119.04	104.00
42	R60	262	U	C2'-C3'-O3'	7.91	126.91	109.50
1	K50	1277	G	C2'-C3'-O3'	7.91	126.91	109.50
42	S60	989	G	N9-C4-C5	7.91	108.56	105.40
42	R60	933	G	O3'-P-O5'	7.91	119.03	104.00
42	R60	1066	G	N3-C4-C5	-7.91	124.65	128.60
42	S60	1231	U	P-O3'-C3'	-7.90	110.22	119.70
1	L50	1277	G	C2'-C3'-O3'	7.90	126.88	109.50
42	S60	262	U	C2'-C3'-O3'	7.88	126.84	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	LJJ	21	ARG	NE-CZ-NH2	7.87	124.24	120.30
42	S60	1066	G	N3-C4-C5	-7.86	124.67	128.60
42	R60	989	G	N9-C4-C5	7.83	108.53	105.40
42	S60	473	G	C2'-C3'-O3'	7.80	126.67	109.50
42	R60	473	G	C2'-C3'-O3'	7.80	126.66	109.50
42	R60	1023	A	P-O3'-C3'	-7.75	110.41	119.70
1	K50	1192	A	C2'-C3'-O3'	7.73	126.50	109.50
1	L50	1192	A	C2'-C3'-O3'	7.72	126.49	109.50
42	S60	1023	A	P-O3'-C3'	-7.72	110.43	119.70
42	R60	1111	A	N7-C8-N9	-7.72	109.94	113.80
42	R60	127	A	C2'-C3'-O3'	7.71	126.46	109.50
42	S60	127	A	C2'-C3'-O3'	7.71	126.45	109.50
42	S60	1111	A	N7-C8-N9	-7.69	109.95	113.80
42	S60	383	A	C2'-C3'-O3'	7.66	126.36	109.50
42	R60	264	C	O5'-P-OP1	7.64	119.87	110.70
42	R60	383	A	C2'-C3'-O3'	7.64	126.31	109.50
42	R60	1095	G	N9-C4-C5	7.63	108.45	105.40
42	S60	264	C	O5'-P-OP1	7.61	119.83	110.70
42	S60	180	G	C4'-C3'-O3'	7.59	128.18	113.00
42	S60	1001	C	N3-C4-C5	-7.58	118.87	121.90
42	S60	1049	G	C8-N9-C4	-7.58	103.37	106.40
42	S60	1095	G	N9-C4-C5	7.58	108.43	105.40
42	R60	819	A	P-O3'-C3'	7.58	128.79	119.70
42	R60	1043	G	P-O3'-C3'	-7.58	110.61	119.70
42	R60	180	G	C4'-C3'-O3'	7.57	128.14	113.00
1	L50	796	C	O4'-C1'-N1	7.56	114.25	108.20
42	S60	1043	G	P-O3'-C3'	-7.55	110.64	119.70
1	K50	1838	G	O4'-C1'-C2'	-7.55	98.25	105.80
1	L50	385	C	O5'-P-OP1	-7.55	98.90	105.70
42	S60	819	A	P-O3'-C3'	7.55	128.76	119.70
42	R60	1041	A	P-O3'-C3'	-7.55	110.64	119.70
42	S60	1041	A	P-O3'-C3'	-7.54	110.65	119.70
42	R60	1192	G	C8-N9-C4	-7.54	103.39	106.40
56	SGG	166	VAL	CA-CB-CG1	7.53	122.19	110.90
42	R60	1049	G	C8-N9-C4	-7.52	103.39	106.40
1	L50	1838	G	O4'-C1'-C2'	-7.52	98.28	105.80
42	R60	1066	G	C4-C5-N7	-7.52	107.79	110.80
56	RGG	166	VAL	CA-CB-CG1	7.51	122.17	110.90
42	R60	1089	G	N9-C4-C5	7.50	108.40	105.40
42	S60	1216	U	P-O3'-C3'	-7.49	110.71	119.70
42	R60	1216	U	P-O3'-C3'	-7.49	110.72	119.70
1	L50	1966	A	C2'-C3'-O3'	7.48	125.96	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	463	A	OP1-P-OP2	-7.47	108.39	119.60
1	K50	796	C	O4'-C1'-N1	7.47	114.18	108.20
1	K50	385	C	O5'-P-OP1	-7.47	98.98	105.70
73	SY0	37	ASN	CB-CA-C	7.46	125.33	110.40
1	K50	1966	A	C2'-C3'-O3'	7.46	125.92	109.50
1	L50	463	A	OP1-P-OP2	-7.46	108.41	119.60
42	R60	1046	A	C2-N3-C4	7.45	114.33	110.60
73	RY0	37	ASN	CB-CA-C	7.43	125.27	110.40
1	K50	159	A	OP1-P-OP2	-7.42	108.46	119.60
42	S60	1192	G	C8-N9-C4	-7.42	103.43	106.40
42	S60	1186	G	C3'-C2'-C1'	-7.42	95.56	101.50
42	R60	1003	A	C5-N7-C8	7.41	107.60	103.90
42	R60	1186	G	C3'-C2'-C1'	-7.41	95.57	101.50
42	S60	1003	A	C5-N7-C8	7.39	107.60	103.90
1	L50	159	A	OP1-P-OP2	-7.39	108.51	119.60
42	S60	994	G	C4'-C3'-C2'	-7.39	95.21	102.60
42	R60	1001	C	N3-C4-C5	-7.39	118.94	121.90
50	RDD	39	VAL	CA-CB-CG1	7.38	121.97	110.90
42	R60	994	G	C4'-C3'-C2'	-7.38	95.22	102.60
42	S60	1046	A	C2-N3-C4	7.36	114.28	110.60
50	SDD	39	VAL	CA-CB-CG1	7.36	121.94	110.90
42	S60	598	C	C2'-C3'-O3'	7.35	125.68	109.50
42	S60	944	G	P-O3'-C3'	-7.34	110.89	119.70
42	R60	944	G	P-O3'-C3'	-7.34	110.89	119.70
1	K50	1967	A	C2'-C3'-O3'	7.34	125.64	109.50
42	S60	1066	G	C4-C5-N7	-7.33	107.87	110.80
42	R60	598	C	C2'-C3'-O3'	7.33	125.63	109.50
42	S60	847	A	N9-C4-C5	7.32	108.73	105.80
1	L50	1967	A	C2'-C3'-O3'	7.31	125.58	109.50
42	S60	960	U	P-O3'-C3'	-7.31	110.93	119.70
42	R60	960	U	P-O3'-C3'	-7.27	110.97	119.70
1	K50	644	G	O5'-P-OP1	7.27	119.43	110.70
1	L50	644	G	O5'-P-OP1	7.27	119.42	110.70
42	S60	1089	G	N9-C4-C5	7.27	108.31	105.40
42	S60	848	G	C4-C5-N7	-7.26	107.89	110.80
42	R60	847	A	N9-C4-C5	7.26	108.70	105.80
42	S60	966	G	P-O3'-C3'	-7.25	111.00	119.70
42	R60	966	G	P-O3'-C3'	-7.25	111.00	119.70
42	R60	848	G	C4-C5-N7	-7.22	107.91	110.80
42	R60	1055	A	N9-C4-C5	7.21	108.69	105.80
42	S60	1055	A	N9-C4-C5	7.17	108.67	105.80
1	L50	1394	U	C2'-C3'-O3'	7.17	125.28	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L50	586	G	O4'-C1'-N9	7.16	113.93	108.20
42	S60	1095	G	C8-N9-C4	-7.16	103.54	106.40
42	R60	1230	U	P-O3'-C3'	-7.16	111.11	119.70
1	K50	1394	U	C2'-C3'-O3'	7.15	125.24	109.50
42	S60	1230	U	P-O3'-C3'	-7.15	111.12	119.70
42	R60	859	G	C8-N9-C4	-7.15	103.54	106.40
42	R60	1095	G	C8-N9-C4	-7.14	103.54	106.40
42	S60	1195	A	N9-C4-C5	7.14	108.66	105.80
1	K50	586	G	O4'-C1'-N9	7.12	113.90	108.20
42	S60	933	G	C4'-C3'-O3'	7.11	127.23	113.00
1	L50	353	A	O5'-P-OP1	-7.11	99.30	105.70
42	R60	933	G	C4'-C3'-O3'	7.11	127.22	113.00
1	K50	353	A	O5'-P-OP1	-7.09	99.32	105.70
52	REE	49	VAL	CA-CB-CG1	7.07	121.51	110.90
42	R60	830	G	P-O3'-C3'	-7.04	111.25	119.70
52	SEE	49	VAL	CA-CB-CG1	7.04	121.45	110.90
1	K50	21	U	C2'-C3'-O3'	7.03	124.97	109.50
42	S60	830	G	P-O3'-C3'	-7.03	111.27	119.70
1	L50	21	U	C2'-C3'-O3'	7.03	124.95	109.50
42	S60	859	G	C8-N9-C4	-7.01	103.60	106.40
42	R60	1195	A	N9-C4-C5	7.00	108.60	105.80
42	R60	1094	C	N3-C4-C5	-7.00	119.10	121.90
1	L50	1182	A	P-O3'-C3'	6.98	128.07	119.70
42	S60	1094	C	N3-C4-C5	-6.96	119.11	121.90
42	R60	1206	A	N9-C4-C5	6.95	108.58	105.80
42	R60	1062	C	N3-C4-C5	-6.92	119.13	121.90
1	K50	1182	A	P-O3'-C3'	6.92	128.00	119.70
42	S60	1206	A	N9-C4-C5	6.91	108.57	105.80
42	R60	1048	G	C4'-C3'-C2'	-6.91	95.69	102.60
42	S60	1048	G	C4'-C3'-C2'	-6.91	95.69	102.60
42	R60	1111	A	C5-N7-C8	6.91	107.35	103.90
42	S60	894	A	P-O3'-C3'	-6.90	111.42	119.70
42	R60	894	A	P-O3'-C3'	-6.89	111.43	119.70
42	S60	864	A	N9-C4-C5	6.89	108.56	105.80
42	S60	1003	A	C2-N3-C4	6.88	114.04	110.60
42	R60	1014	G	C8-N9-C4	-6.87	103.65	106.40
42	S60	1111	A	C5-N7-C8	6.86	107.33	103.90
42	R60	1046	A	N7-C8-N9	-6.85	110.37	113.80
42	S60	1051	C	C6-N1-C2	6.85	123.04	120.30
42	R60	1003	A	C2-N3-C4	6.85	114.02	110.60
42	S60	1134	G	P-O3'-C3'	-6.85	111.48	119.70
42	R60	1192	G	N9-C4-C5	6.84	108.14	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	1134	G	P-O3'-C3'	-6.84	111.49	119.70
66	RR0	47	ARG	NE-CZ-NH2	6.84	123.72	120.30
42	R60	1014	G	N9-C4-C5	6.83	108.13	105.40
42	S60	1049	G	N9-C4-C5	6.83	108.13	105.40
42	S60	883	C	C6-N1-C2	6.82	123.03	120.30
42	R60	1207	A	C5-N7-C8	6.82	107.31	103.90
42	R60	1049	G	N9-C4-C5	6.82	108.13	105.40
42	S60	1192	G	N9-C4-C5	6.81	108.12	105.40
42	R60	864	A	N9-C4-C5	6.80	108.52	105.80
42	S60	1062	C	N3-C4-C5	-6.80	119.18	121.90
1	K50	562	U	P-O5'-C5'	-6.80	110.03	120.90
42	S60	1046	A	N7-C8-N9	-6.79	110.41	113.80
42	R60	918	A	P-O3'-C3'	-6.79	111.56	119.70
42	S60	1207	A	C5-N7-C8	6.78	107.29	103.90
1	L50	562	U	P-O5'-C5'	-6.78	110.05	120.90
66	SR0	47	ARG	NE-CZ-NH2	6.78	123.69	120.30
42	R60	883	C	C6-N1-C2	6.77	123.01	120.30
42	R60	1051	C	C6-N1-C2	6.76	123.00	120.30
42	S60	918	A	P-O3'-C3'	-6.76	111.59	119.70
42	R60	565	U	C2'-C3'-O3'	6.75	124.50	113.70
42	S60	565	U	C2'-C3'-O3'	6.75	124.49	113.70
42	R60	1207	A	N7-C8-N9	-6.75	110.43	113.80
1	L50	147	G	P-O3'-C3'	-6.74	111.61	119.70
42	S60	1207	A	N7-C8-N9	-6.74	110.43	113.80
42	S60	963	G	P-O3'-C3'	-6.74	111.61	119.70
42	R60	13	C	OP1-P-OP2	-6.73	109.50	119.60
42	R60	1011	A	C8-N9-C4	-6.73	103.11	105.80
1	K50	1808	A	C4'-C3'-O3'	6.73	126.45	113.00
42	R60	963	G	P-O3'-C3'	-6.72	111.63	119.70
42	S60	13	C	OP1-P-OP2	-6.72	109.52	119.60
42	S60	1182	G	N9-C4-C5	-6.72	102.71	105.40
1	L50	1808	A	C4'-C3'-O3'	6.72	126.44	113.00
42	S60	1014	G	C8-N9-C4	-6.71	103.72	106.40
1	K50	1488	U	O4'-C1'-N1	6.71	113.57	108.20
42	S60	1185	A	C8-N9-C4	6.71	108.48	105.80
42	R60	1001	C	C6-N1-C2	-6.71	117.62	120.30
42	R60	1182	G	N9-C4-C5	-6.70	102.72	105.40
42	S60	1014	G	N9-C4-C5	6.70	108.08	105.40
42	R60	1053	A	C8-N9-C4	6.69	108.48	105.80
1	L50	600	G	O4'-C1'-C2'	-6.69	99.11	105.80
42	S60	954	G	C8-N9-C4	-6.69	103.72	106.40
1	K50	600	G	O4'-C1'-C2'	-6.69	99.11	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	147	G	P-O3'-C3'	-6.69	111.68	119.70
1	K50	1134	A	C2'-C3'-O3'	6.68	124.39	113.70
42	S60	1011	A	C8-N9-C4	-6.67	103.13	105.80
42	S60	848	G	N3-C4-C5	-6.67	125.27	128.60
1	L50	1488	U	O4'-C1'-N1	6.66	113.53	108.20
1	K50	1317	G	P-O3'-C3'	-6.66	111.71	119.70
1	L50	1317	G	P-O3'-C3'	-6.66	111.71	119.70
1	K50	667	G	P-O3'-C3'	6.65	127.68	119.70
42	R60	1070	C	N3-C4-C5	-6.65	119.24	121.90
42	R60	919	C	C6-N1-C2	-6.65	117.64	120.30
42	S60	1070	C	N3-C4-C5	-6.64	119.24	121.90
1	L50	1134	A	C2'-C3'-O3'	6.63	124.31	113.70
42	S60	1053	A	C8-N9-C4	6.62	108.45	105.80
42	R60	848	G	N3-C4-C5	-6.62	125.29	128.60
42	S60	919	C	C6-N1-C2	-6.62	117.65	120.30
42	S60	1001	C	C6-N1-C2	-6.62	117.65	120.30
1	L50	667	G	P-O3'-C3'	6.61	127.63	119.70
42	R60	1185	A	C8-N9-C4	6.61	108.44	105.80
1	L50	1771	G	P-O3'-C3'	6.60	127.62	119.70
41	MD2	103	ARG	NE-CZ-NH2	6.60	123.60	120.30
42	R60	1205	G	C8-N9-C4	-6.60	103.76	106.40
1	K50	1771	G	P-O3'-C3'	6.59	127.61	119.70
41	MD1	103	ARG	NE-CZ-NH2	6.58	123.59	120.30
42	S60	877	G	N3-C4-C5	-6.58	125.31	128.60
42	R60	1212	U	O4'-C1'-N1	6.58	113.46	108.20
42	S60	1205	G	C8-N9-C4	-6.57	103.77	106.40
42	R60	954	G	C8-N9-C4	-6.56	103.78	106.40
42	S60	854	U	P-O3'-C3'	-6.55	111.83	119.70
42	S60	857	G	C4-C5-N7	6.55	113.42	110.80
42	R60	213	A	P-O3'-C3'	-6.55	111.84	119.70
42	R60	1356	C	OP1-P-OP2	6.55	129.43	119.60
42	R60	1153	C	P-O3'-C3'	-6.55	111.84	119.70
42	R60	671	C	O5'-P-OP1	6.54	118.55	110.70
42	S60	1356	C	OP1-P-OP2	6.54	129.41	119.60
42	S60	671	C	O5'-P-OP1	6.54	118.55	110.70
42	R60	875	A	C2-N3-C4	6.54	113.87	110.60
42	S60	1003	A	N7-C8-N9	-6.53	110.53	113.80
42	R60	1038	A	C4'-C3'-C2'	-6.53	96.07	102.60
42	S60	213	A	P-O3'-C3'	-6.53	111.86	119.70
42	S60	1038	A	C4'-C3'-C2'	-6.53	96.07	102.60
42	S60	1212	U	O4'-C1'-N1	6.53	113.42	108.20
42	S60	1179	A	N9-C4-C5	6.52	108.41	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	1153	C	P-O3'-C3'	-6.52	111.88	119.70
1	K50	1783	A	P-O3'-C3'	-6.51	111.89	119.70
42	R60	854	U	P-O3'-C3'	-6.51	111.89	119.70
1	L50	1783	A	P-O3'-C3'	-6.51	111.89	119.70
42	S60	875	A	C2-N3-C4	6.50	113.85	110.60
42	S60	874	A	N9-C4-C5	6.49	108.40	105.80
1	K50	2355	A	OP1-P-OP2	-6.49	109.87	119.60
1	L50	2355	A	OP1-P-OP2	-6.48	109.88	119.60
42	R60	982	C	N3-C4-C5	-6.48	119.31	121.90
47	SC0	221	VAL	CA-CB-CG1	6.46	120.59	110.90
42	R60	1003	A	N7-C8-N9	-6.46	110.57	113.80
47	RC0	221	VAL	CA-CB-CG1	6.46	120.60	110.90
42	S60	982	C	N3-C4-C5	-6.46	119.32	121.90
42	R60	877	G	N3-C4-C5	-6.45	125.37	128.60
2	L70	46	C	P-O3'-C3'	-6.44	111.97	119.70
42	R60	874	A	N9-C4-C5	6.43	108.37	105.80
42	R60	1179	A	N9-C4-C5	6.41	108.36	105.80
42	R60	903	C	P-O3'-C3'	-6.41	112.01	119.70
42	R60	857	G	C4-C5-N7	6.40	113.36	110.80
42	S60	903	C	P-O3'-C3'	-6.40	112.02	119.70
42	R60	1177	G	C4-C5-N7	6.39	113.36	110.80
1	K50	371	A	N7-C8-N9	-6.38	110.61	113.80
2	K70	46	C	P-O3'-C3'	-6.38	112.05	119.70
22	KL0	67	ARG	CG-CD-NE	6.37	125.18	111.80
22	LL0	67	ARG	CG-CD-NE	6.36	125.16	111.80
42	S60	1066	G	C5-N7-C8	6.36	107.48	104.30
42	R60	1066	G	C5-N7-C8	6.36	107.48	104.30
1	L50	2114	G	C4'-C3'-C2'	-6.35	96.25	102.60
1	K50	2114	G	C4'-C3'-C2'	-6.35	96.25	102.60
1	L50	400	U	O5'-P-OP2	-6.34	99.99	105.70
1	K50	548	G	OP1-P-OP2	-6.34	110.09	119.60
42	R60	920	G	N9-C4-C5	6.33	107.93	105.40
1	L50	548	G	OP1-P-OP2	-6.33	110.11	119.60
1	L50	371	A	N7-C8-N9	-6.31	110.64	113.80
42	R60	1047	G	C4-C5-N7	6.30	113.32	110.80
1	K50	400	U	O5'-P-OP2	-6.29	100.03	105.70
6	LC0	57	ARG	CG-CD-NE	-6.28	98.61	111.80
6	KC0	57	ARG	CG-CD-NE	-6.28	98.61	111.80
1	L50	1102	G	O4'-C1'-C2'	-6.28	99.52	105.80
42	R60	1047	G	N9-C4-C5	-6.28	102.89	105.40
42	R60	885	G	N9-C4-C5	6.28	107.91	105.40
1	K50	342	G	P-O3'-C3'	-6.28	112.17	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	1047	G	C4-C5-N7	6.27	113.31	110.80
1	L50	342	G	P-O3'-C3'	-6.27	112.18	119.70
1	K50	1102	G	O4'-C1'-C2'	-6.27	99.53	105.80
42	R60	1053	A	N9-C4-C5	-6.26	103.30	105.80
5	KB0	336	ARG	CG-CD-NE	6.26	124.95	111.80
5	LB0	336	ARG	CG-CD-NE	6.25	124.92	111.80
1	K50	1277	G	C4'-C3'-O3'	6.25	125.50	113.00
26	LN0	123	GLN	CB-CA-C	-6.25	97.91	110.40
42	S60	1053	A	N9-C4-C5	-6.24	103.30	105.80
1	L50	1277	G	C4'-C3'-O3'	6.24	125.48	113.00
42	R60	1127	A	C8-N9-C4	6.24	108.30	105.80
42	S60	1052	A	C5-N7-C8	-6.23	100.79	103.90
26	KN0	123	GLN	CB-CA-C	-6.23	97.95	110.40
42	S60	1177	G	C4-C5-N7	6.22	113.29	110.80
1	K50	2481	U	P-O3'-C3'	6.21	127.15	119.70
42	R60	954	G	N7-C8-N9	6.21	116.20	113.10
1	L50	2481	U	P-O3'-C3'	6.21	127.15	119.70
42	S60	1047	G	N9-C4-C5	-6.20	102.92	105.40
42	S60	1127	A	C8-N9-C4	6.20	108.28	105.80
1	L50	412	A	OP1-P-OP2	-6.19	110.31	119.60
1	K50	412	A	OP1-P-OP2	-6.19	110.31	119.60
42	S60	989	G	C8-N9-C4	-6.19	103.92	106.40
42	S60	201	G	P-O3'-C3'	-6.19	112.27	119.70
42	R60	1048	G	C5-N7-C8	-6.19	101.21	104.30
42	S60	954	G	N7-C8-N9	6.18	116.19	113.10
42	R60	1052	A	C5-N7-C8	-6.18	100.81	103.90
42	S60	1093	G	C4-C5-N7	6.18	113.27	110.80
42	R60	1055	A	C8-N9-C4	-6.17	103.33	105.80
42	R60	858	C	C2-N3-C4	6.17	122.98	119.90
42	S60	1048	G	C5-N7-C8	-6.16	101.22	104.30
42	R60	1093	G	C4-C5-N7	6.16	113.27	110.80
42	S60	1195	A	C8-N9-C4	-6.16	103.34	105.80
42	R60	989	G	C8-N9-C4	-6.16	103.94	106.40
42	R60	1056	A	N9-C4-C5	6.16	108.26	105.80
1	L50	462	G	OP1-P-OP2	-6.16	110.36	119.60
42	S60	1089	G	C8-N9-C4	-6.15	103.94	106.40
1	K50	462	G	OP1-P-OP2	-6.15	110.38	119.60
42	R60	1089	G	C8-N9-C4	-6.14	103.94	106.40
42	R60	1195	A	C8-N9-C4	-6.14	103.34	105.80
42	R60	973	G	N9-C4-C5	6.13	107.85	105.40
42	S60	1182	G	C8-N9-C4	6.13	108.85	106.40
42	R60	1103	G	O4'-C1'-C2'	-6.13	99.67	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	920	G	N9-C4-C5	6.12	107.85	105.40
42	R60	201	G	P-O3'-C3'	-6.12	112.36	119.70
42	S60	885	G	N9-C4-C5	6.12	107.85	105.40
42	S60	1103	G	O4'-C1'-C2'	-6.12	99.68	105.80
42	S60	877	G	C8-N9-C4	-6.12	103.95	106.40
69	SU0	67	ARG	CG-CD-NE	6.12	124.64	111.80
42	R60	877	G	C8-N9-C4	-6.12	103.95	106.40
1	L50	125	G	OP1-P-OP2	-6.11	110.43	119.60
42	R60	885	G	C4-C5-N7	-6.11	108.35	110.80
69	RU0	67	ARG	CG-CD-NE	6.11	124.62	111.80
42	S60	1055	A	C8-N9-C4	-6.10	103.36	105.80
47	SC0	129	ARG	CB-CA-C	-6.10	98.21	110.40
42	S60	973	G	N9-C4-C5	6.09	107.84	105.40
1	K50	125	G	OP1-P-OP2	-6.09	110.47	119.60
47	RC0	129	ARG	CB-CA-C	-6.09	98.22	110.40
42	S60	1067	A	C8-N9-C4	6.09	108.23	105.80
1	L50	562	U	C5'-C4'-C3'	-6.08	106.28	116.00
42	S60	835	A	C8-N9-C4	-6.07	103.37	105.80
42	R60	1182	G	C8-N9-C4	6.06	108.83	106.40
1	K50	1835	G	C3'-C2'-C1'	6.06	106.34	101.50
42	R60	835	A	C8-N9-C4	-6.05	103.38	105.80
42	S60	858	C	C2-N3-C4	6.05	122.93	119.90
42	S60	987	A	C5-N7-C8	-6.05	100.88	103.90
42	S60	1066	G	C2-N3-C4	6.05	114.92	111.90
1	K50	562	U	C5'-C4'-C3'	-6.05	106.33	116.00
42	S60	895	C	P-O3'-C3'	-6.04	112.45	119.70
1	L50	1835	G	C3'-C2'-C1'	6.04	106.33	101.50
1	L50	140	A	P-O3'-C3'	6.04	126.94	119.70
1	K50	477	G	P-O3'-C3'	6.03	126.93	119.70
42	S60	952	A	C4-C5-N7	6.02	113.71	110.70
42	R60	1119	C	C2-N3-C4	6.02	122.91	119.90
42	R60	1067	A	C8-N9-C4	6.02	108.21	105.80
42	S60	1056	A	N9-C4-C5	6.02	108.21	105.80
42	R60	895	C	P-O3'-C3'	-6.02	112.48	119.70
42	S60	262	U	C4'-C3'-O3'	6.01	125.03	113.00
42	R60	262	U	C4'-C3'-O3'	6.01	125.03	113.00
42	S60	1050	G	C4-C5-N7	-6.01	108.40	110.80
1	L50	477	G	P-O3'-C3'	6.01	126.91	119.70
42	S60	1208	G	C2-N3-C4	6.00	114.90	111.90
1	K50	140	A	P-O3'-C3'	6.00	126.90	119.70
42	R60	987	A	C5-N7-C8	-5.99	100.90	103.90
42	S60	933	G	C3'-C2'-C1'	-5.99	96.71	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	952	A	C4-C5-N7	5.99	113.70	110.70
42	S60	1046	A	C5-C6-N1	5.98	120.69	117.70
42	R60	933	G	C3'-C2'-C1'	-5.98	96.71	101.50
42	S60	1119	C	C2-N3-C4	5.98	122.89	119.90
42	R60	884	A	C3'-C2'-C1'	5.97	106.28	101.50
42	S60	853	G	C8-N9-C4	-5.97	104.01	106.40
42	R60	1050	G	C4-C5-N7	-5.97	108.41	110.80
42	R60	180	G	P-O3'-C3'	5.96	126.85	119.70
42	R60	1019	C	C3'-C2'-C1'	5.96	106.27	101.50
42	R60	859	G	N9-C4-C5	5.96	107.78	105.40
42	S60	1019	C	C3'-C2'-C1'	5.96	106.26	101.50
1	L50	1061	G	O4'-C1'-N9	5.95	112.96	108.20
42	S60	847	A	C4-C5-C6	5.95	119.97	117.00
42	R60	1066	G	C2-N3-C4	5.94	114.87	111.90
42	S60	884	A	C3'-C2'-C1'	5.94	106.25	101.50
42	S60	859	G	N9-C4-C5	5.94	107.77	105.40
1	K50	1061	G	O4'-C1'-N9	5.94	112.95	108.20
42	S60	885	G	C4-C5-N7	-5.93	108.43	110.80
21	LJJ	21	ARG	NE-CZ-NH1	-5.93	117.33	120.30
42	S60	1054	G	C4-C5-N7	5.93	113.17	110.80
42	S60	953	C	C6-N1-C2	5.93	122.67	120.30
42	S60	180	G	P-O3'-C3'	5.93	126.81	119.70
42	R60	853	G	C8-N9-C4	-5.92	104.03	106.40
42	R60	1215	A	C8-N9-C4	5.92	108.17	105.80
42	S60	954	G	C2-N3-C4	-5.92	108.94	111.90
42	R60	1053	A	N1-C2-N3	-5.92	126.34	129.30
61	RL0	28	ARG	NE-CZ-NH2	-5.92	117.34	120.30
42	R60	1046	A	C5-C6-N1	5.91	120.66	117.70
42	R60	1177	G	N9-C4-C5	-5.91	103.04	105.40
21	KJJ	21	ARG	NE-CZ-NH1	-5.91	117.35	120.30
15	LGG	24	ARG	CG-CD-NE	-5.91	99.40	111.80
42	S60	1053	A	N1-C2-N3	-5.91	126.35	129.30
15	KGG	24	ARG	CG-CD-NE	-5.90	99.41	111.80
42	S60	924	U	P-O3'-C3'	-5.90	112.62	119.70
42	S60	848	G	N9-C4-C5	5.90	107.76	105.40
42	R60	924	U	P-O3'-C3'	-5.90	112.62	119.70
42	R60	1208	G	C2-N3-C4	5.90	114.85	111.90
61	RL0	28	ARG	NE-CZ-NH1	5.90	123.25	120.30
42	R60	969	C	C6-N1-C2	5.90	122.66	120.30
42	R60	1054	G	C4-C5-N7	5.89	113.16	110.80
2	K70	31	G	P-O3'-C3'	-5.89	112.63	119.70
42	R60	865	A	C5-N7-C8	5.89	106.84	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	848	G	N9-C4-C5	5.88	107.75	105.40
2	L70	31	G	P-O3'-C3'	-5.88	112.64	119.70
42	R60	1011	A	C5-C6-N1	-5.88	114.76	117.70
1	K50	317	G	C3'-C2'-C1'	-5.86	96.81	101.50
42	R60	1064	G	N9-C4-C5	5.86	107.74	105.40
42	S60	1182	G	C5-C6-O6	-5.86	125.09	128.60
42	R60	1128	G	C4-C5-N7	5.85	113.14	110.80
51	RE0	100	ARG	NE-CZ-NH1	-5.85	117.37	120.30
42	S60	1182	G	C2-N3-C4	5.85	114.83	111.90
42	R60	1182	G	C2-N3-C4	5.85	114.83	111.90
42	S60	875	A	N7-C8-N9	-5.85	110.88	113.80
1	L50	317	G	C3'-C2'-C1'	-5.84	96.83	101.50
42	S60	952	A	N9-C4-C5	-5.84	103.46	105.80
42	R60	847	A	C4-C5-C6	5.84	119.92	117.00
42	R60	954	G	C2-N3-C4	-5.84	108.98	111.90
42	R60	1024	G	P-O3'-C3'	-5.84	112.70	119.70
42	R60	959	G	P-O3'-C3'	-5.83	112.70	119.70
42	S60	1011	A	C5-C6-N1	-5.83	114.78	117.70
1	L50	1277	G	C3'-C2'-C1'	-5.83	96.84	101.50
42	R60	1010	G	C1'-O4'-C4'	-5.83	105.24	109.90
42	R60	1058	A	C1'-O4'-C4'	-5.83	105.24	109.90
42	S60	969	C	C6-N1-C2	5.83	122.63	120.30
61	SL0	28	ARG	NE-CZ-NH2	-5.83	117.39	120.30
1	L50	523	A	C1'-C2'-O2'	-5.82	93.13	110.60
1	L50	2235	C	O5'-P-OP2	-5.82	100.46	105.70
1	K50	1491	U	P-O3'-C3'	5.82	126.69	119.70
42	R60	953	C	C6-N1-C2	5.82	122.63	120.30
1	K50	2235	C	O5'-P-OP2	-5.82	100.46	105.70
42	S60	1010	G	C1'-O4'-C4'	-5.82	105.25	109.90
61	SL0	28	ARG	NE-CZ-NH1	5.82	123.21	120.30
42	S60	865	A	C5-N7-C8	5.81	106.81	103.90
42	S60	959	G	P-O3'-C3'	-5.81	112.72	119.70
42	S60	952	A	N1-C6-N6	5.81	122.09	118.60
42	R60	955	A	C4'-C3'-C2'	-5.81	96.79	102.60
42	S60	947	C	P-O3'-C3'	-5.81	112.73	119.70
69	RU0	56	VAL	CA-CB-CG1	5.81	119.61	110.90
51	SE0	100	ARG	NE-CZ-NH1	-5.80	117.40	120.30
1	K50	1277	G	C3'-C2'-C1'	-5.80	96.86	101.50
42	S60	1064	G	N9-C4-C5	5.80	107.72	105.40
1	K50	280	G	C4'-C3'-C2'	-5.80	96.80	102.60
1	L50	225	G	C2'-C3'-O3'	5.80	122.98	113.70
30	LPP	8	VAL	CA-CB-CG1	5.80	119.60	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	523	A	C1'-C2'-O2'	-5.80	93.20	110.60
42	S60	897	C	P-O3'-C3'	-5.80	112.74	119.70
42	S60	1176	G	C2-N3-C4	5.80	114.80	111.90
1	L50	1491	U	P-O3'-C3'	5.80	126.66	119.70
42	S60	942	A	C8-N9-C4	-5.80	103.48	105.80
65	RQ0	38	VAL	CA-CB-CG1	5.80	119.59	110.90
42	S60	1186	G	O4'-C1'-N9	5.79	112.84	108.20
42	S60	888	U	C3'-C2'-C1'	-5.79	96.87	101.50
42	S60	1024	G	P-O3'-C3'	-5.79	112.75	119.70
42	S60	1058	A	C1'-O4'-C4'	-5.79	105.26	109.90
42	R60	897	C	P-O3'-C3'	-5.79	112.75	119.70
42	R60	875	A	N7-C8-N9	-5.79	110.90	113.80
42	R60	947	C	P-O3'-C3'	-5.79	112.75	119.70
42	R60	1203	A	C5-N7-C8	5.79	106.79	103.90
42	R60	920	G	C4-C5-N7	-5.79	108.49	110.80
1	L50	1838	G	O5'-P-OP2	-5.78	100.50	105.70
30	KPP	8	VAL	CA-CB-CG1	5.78	119.58	110.90
42	R60	952	A	N1-C6-N6	5.78	122.07	118.60
42	S60	874	A	C4-C5-N7	-5.78	107.81	110.70
1	L50	395	A	C4'-C3'-O3'	-5.78	97.27	109.40
42	S60	1128	G	C4-C5-N7	5.78	113.11	110.80
42	R60	1186	G	O4'-C1'-N9	5.78	112.82	108.20
1	K50	395	A	C4'-C3'-O3'	-5.78	97.27	109.40
42	R60	942	A	C8-N9-C4	-5.77	103.49	105.80
65	SQ0	38	VAL	CA-CB-CG1	5.77	119.56	110.90
42	R60	1062	C	C4-C5-C6	5.77	120.28	117.40
1	L50	280	G	C4'-C3'-C2'	-5.76	96.84	102.60
69	SU0	56	VAL	CA-CB-CG1	5.76	119.54	110.90
1	K50	225	G	C2'-C3'-O3'	5.76	122.92	113.70
42	S60	1215	A	C8-N9-C4	5.76	108.10	105.80
1	K50	1838	G	O5'-P-OP2	-5.76	100.52	105.70
42	R60	952	A	N9-C4-C5	-5.76	103.50	105.80
1	K50	1835	G	P-O5'-C5'	-5.75	111.69	120.90
42	R60	874	A	C4-C5-N7	-5.75	107.82	110.70
42	R60	1182	G	C5-C6-O6	-5.75	125.15	128.60
42	R60	915	A	P-O3'-C3'	-5.75	112.80	119.70
42	R60	1185	A	N9-C4-C5	-5.75	103.50	105.80
1	L50	234	U	O5'-P-OP2	-5.74	100.53	105.70
1	L50	1835	G	P-O5'-C5'	-5.74	111.71	120.90
42	R60	944	G	C4-C5-N7	-5.74	108.50	110.80
1	L50	1102	G	O5'-P-OP1	5.74	117.58	110.70
42	S60	222	G	C4'-C3'-C2'	-5.73	96.87	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	919	C	C2-N3-C4	5.73	122.77	119.90
42	S60	1106	G	P-O3'-C3'	-5.73	112.82	119.70
42	R60	1106	G	P-O3'-C3'	-5.73	112.83	119.70
1	K50	1303	G	C4'-C3'-C2'	-5.72	96.88	102.60
30	LPP	49	ARG	CG-CD-NE	5.72	123.81	111.80
42	R60	888	U	C3'-C2'-C1'	-5.72	96.93	101.50
42	S60	955	A	C4'-C3'-C2'	-5.72	96.88	102.60
42	S60	1203	A	C5-N7-C8	5.71	106.76	103.90
42	S60	262	U	O4'-C4'-C3'	-5.71	98.29	104.00
42	S60	915	A	P-O3'-C3'	-5.71	112.85	119.70
1	L50	2452	A	C4'-C3'-O3'	5.70	124.40	113.00
42	S60	1185	A	N9-C4-C5	-5.70	103.52	105.80
1	K50	1102	G	O5'-P-OP1	5.70	117.54	110.70
30	KPP	49	ARG	CG-CD-NE	5.70	123.77	111.80
1	L50	1303	G	C4'-C3'-C2'	-5.70	96.90	102.60
1	L50	2373	G	C4'-C3'-C2'	-5.70	96.90	102.60
1	K50	234	U	O5'-P-OP2	-5.70	100.57	105.70
42	R60	875	A	C8-N9-C4	5.70	108.08	105.80
42	S60	1062	C	C4-C5-C6	5.70	120.25	117.40
42	S60	840	C	P-O3'-C3'	-5.69	112.87	119.70
32	KR0	74	HIS	CB-CA-C	5.69	121.78	110.40
42	R60	222	G	C4'-C3'-C2'	-5.69	96.91	102.60
42	R60	1045	A	N9-C4-C5	5.69	108.08	105.80
42	S60	960	U	C4'-C3'-C2'	-5.69	96.91	102.60
42	R60	840	C	P-O3'-C3'	-5.69	112.88	119.70
42	R60	1048	G	C6-C5-N7	-5.69	126.99	130.40
42	R60	1094	C	C2-N3-C4	5.68	122.74	119.90
1	K50	2452	A	C4'-C3'-O3'	5.68	124.36	113.00
1	L50	1733	A	C4'-C3'-O3'	-5.68	97.47	109.40
42	S60	864	A	C8-N9-C4	-5.68	103.53	105.80
42	R60	262	U	O4'-C4'-C3'	-5.68	98.32	104.00
42	R60	839	C	C2-N3-C4	5.68	122.74	119.90
32	LR0	74	HIS	CB-CA-C	5.68	121.76	110.40
1	K50	2373	G	C4'-C3'-C2'	-5.68	96.92	102.60
42	S60	1177	G	N9-C4-C5	-5.67	103.13	105.40
42	R60	960	U	C4'-C3'-C2'	-5.67	96.93	102.60
1	L50	1277	G	C4'-C3'-C2'	-5.67	96.93	102.60
42	S60	1146	G	C3'-C2'-C1'	-5.67	96.97	101.50
1	L50	822	U	P-O3'-C3'	-5.66	112.90	119.70
42	S60	1184	U	C3'-C2'-C1'	-5.66	96.97	101.50
42	S60	922	G	P-O3'-C3'	-5.66	112.91	119.70
1	K50	1733	A	C4'-C3'-O3'	-5.66	97.51	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	886	C	C6-N1-C2	5.66	122.56	120.30
42	R60	835	A	N9-C4-C5	5.66	108.06	105.80
1	L50	1304	A	P-O3'-C3'	-5.66	112.91	119.70
1	K50	1277	G	C4'-C3'-C2'	-5.66	96.94	102.60
42	R60	1146	G	C3'-C2'-C1'	-5.65	96.98	101.50
42	R60	1176	G	C2-N3-C4	5.65	114.73	111.90
42	S60	1176	G	O4'-C4'-C3'	5.65	110.62	106.10
1	K50	822	U	P-O3'-C3'	-5.65	112.92	119.70
42	R60	963	G	C2-N3-C4	5.65	114.72	111.90
42	S60	835	A	N9-C4-C5	5.65	108.06	105.80
42	R60	864	A	C8-N9-C4	-5.64	103.54	105.80
42	S60	839	C	C2-N3-C4	5.64	122.72	119.90
1	K50	600	G	N9-C1'-C2'	-5.64	105.80	112.00
1	K50	1304	A	P-O3'-C3'	-5.64	112.93	119.70
42	S60	1093	G	C5-N7-C8	-5.64	101.48	104.30
42	S60	944	G	C4-C5-N7	-5.63	108.55	110.80
42	R60	1125	G	C2'-C3'-O3'	5.63	122.71	113.70
42	S60	1207	A	C2-N3-C4	5.63	113.42	110.60
42	S60	1125	G	C2'-C3'-O3'	5.63	122.70	113.70
42	S60	1127	A	C2-N3-C4	5.63	113.41	110.60
42	R60	922	G	P-O3'-C3'	-5.63	112.95	119.70
42	R60	1259	U	P-O3'-C3'	-5.63	112.95	119.70
42	R60	919	C	C2-N3-C4	5.62	122.71	119.90
42	S60	1067	A	N9-C4-C5	-5.62	103.55	105.80
42	S60	1094	C	C2-N3-C4	5.62	122.71	119.90
42	S60	871	C	N3-C4-C5	-5.62	119.65	121.90
42	S60	1048	G	C6-C5-N7	-5.62	127.03	130.40
42	R60	1067	A	N9-C4-C5	-5.62	103.55	105.80
42	S60	951	A	C5-N7-C8	-5.61	101.09	103.90
1	K50	1485	G	O4'-C1'-N9	5.61	112.69	108.20
1	K50	1832	A	O5'-P-OP2	-5.61	100.65	105.70
42	S60	1259	U	P-O3'-C3'	-5.61	112.97	119.70
42	S60	875	A	C8-N9-C4	5.61	108.04	105.80
42	R60	836	A	N9-C4-C5	5.61	108.04	105.80
1	L50	2587	U	C3'-C2'-C1'	-5.61	97.02	101.50
42	R60	1184	U	C3'-C2'-C1'	-5.60	97.02	101.50
42	R60	1007	U	O4'-C1'-N1	5.60	112.68	108.20
42	S60	1045	A	N9-C4-C5	5.60	108.04	105.80
42	S60	963	G	C2-N3-C4	5.59	114.70	111.90
51	SE0	100	ARG	NE-CZ-NH2	5.59	123.10	120.30
1	L50	1832	A	O5'-P-OP2	-5.59	100.67	105.70
42	R60	1089	G	C4-C5-N7	-5.59	108.57	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L50	600	G	N9-C1'-C2'	-5.58	105.86	112.00
1	K50	2587	U	C3'-C2'-C1'	-5.58	97.03	101.50
42	R60	1035	C	P-O3'-C3'	-5.58	113.00	119.70
42	R60	1056	A	C4-C5-N7	-5.58	107.91	110.70
2	L70	64	G	OP1-P-OP2	-5.58	111.23	119.60
42	S60	1005	G	C4'-C3'-C2'	-5.58	97.02	102.60
42	S60	1106	G	C8-N9-C4	5.58	108.63	106.40
42	R60	1055	A	C4-C5-C6	5.58	119.79	117.00
42	R60	1093	G	C5-N7-C8	-5.57	101.51	104.30
42	S60	1089	G	C4-C5-N7	-5.57	108.57	110.80
42	R60	1207	A	C2-N3-C4	5.57	113.38	110.60
42	S60	848	G	C5-N7-C8	5.57	107.08	104.30
42	R60	1176	G	O4'-C4'-C3'	5.57	110.55	106.10
2	K70	64	G	OP1-P-OP2	-5.56	111.25	119.60
42	S60	1035	C	P-O3'-C3'	-5.56	113.03	119.70
42	R60	1182	G	N1-C2-N3	-5.56	120.56	123.90
1	K50	178	G	C5-C6-O6	5.56	131.94	128.60
42	S60	920	G	C4-C5-N7	-5.55	108.58	110.80
42	R60	856	U	C3'-C2'-C1'	-5.55	97.06	101.50
1	L50	1485	G	O4'-C1'-N9	5.55	112.64	108.20
1	L50	1471	G	OP1-P-OP2	-5.55	111.27	119.60
42	S60	856	U	C3'-C2'-C1'	-5.55	97.06	101.50
42	S60	1127	A	N7-C8-N9	-5.55	111.03	113.80
42	R60	865	A	C4-C5-N7	-5.55	107.93	110.70
1	K50	1711	A	O5'-P-OP2	-5.54	100.71	105.70
42	R60	951	A	C5-N7-C8	-5.54	101.13	103.90
42	S60	871	C	C4-C5-C6	5.54	120.17	117.40
40	LZ0	69	ARG	CB-CG-CD	5.54	126.01	111.60
42	S60	1007	U	O4'-C1'-N1	5.54	112.63	108.20
1	K50	1471	G	OP1-P-OP2	-5.54	111.29	119.60
42	R60	622	C	P-O3'-C3'	-5.54	113.06	119.70
51	RE0	100	ARG	NE-CZ-NH2	5.54	123.07	120.30
42	R60	1005	G	C4'-C3'-C2'	-5.53	97.07	102.60
42	S60	865	A	C4-C5-N7	-5.53	107.93	110.70
1	L50	667	G	OP1-P-OP2	-5.53	111.31	119.60
42	R60	1183	C	C2-N3-C4	5.53	122.66	119.90
42	S60	1055	A	C4-C5-C6	5.53	119.76	117.00
42	S60	877	G	C4-C5-C6	5.52	122.11	118.80
1	L50	1282	C	C2-N3-C4	5.52	122.66	119.90
40	KZ0	69	ARG	CB-CG-CD	5.52	125.95	111.60
42	R60	1127	A	C2-N3-C4	5.52	113.36	110.60
42	S60	968	C	O5'-P-OP2	-5.51	100.74	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	RR0	32	ARG	NE-CZ-NH2	5.51	123.05	120.30
42	S60	839	C	C5-C6-N1	5.50	123.75	121.00
1	K50	667	G	OP1-P-OP2	-5.50	111.34	119.60
1	K50	714	G	O5'-P-OP1	5.50	117.31	110.70
42	S60	886	C	C6-N1-C2	5.50	122.50	120.30
42	S60	1206	A	C8-N9-C4	-5.50	103.60	105.80
42	R60	1003	A	C4-C5-N7	-5.50	107.95	110.70
42	R60	968	C	O5'-P-OP2	-5.49	100.76	105.70
42	R60	1127	A	N7-C8-N9	-5.49	111.05	113.80
42	S60	982	C	C6-N1-C2	-5.49	118.11	120.30
1	L50	1711	A	O5'-P-OP2	-5.49	100.76	105.70
42	S60	944	G	C5-N7-C8	5.49	107.04	104.30
42	S60	1195	A	C4-C5-C6	5.49	119.74	117.00
42	S60	1239	C	O5'-P-OP2	-5.49	100.76	105.70
1	K50	1282	C	C2-N3-C4	5.49	122.64	119.90
42	R60	1106	G	C8-N9-C4	5.49	108.59	106.40
1	L50	714	G	O5'-P-OP1	5.48	117.28	110.70
42	S60	1003	A	C4-C5-N7	-5.48	107.96	110.70
42	R60	944	G	C5-N7-C8	5.48	107.04	104.30
42	R60	1228	C	C2-N3-C4	5.48	122.64	119.90
42	R60	877	G	C4-C5-C6	5.48	122.09	118.80
42	S60	1049	G	C4-C5-C6	5.47	122.08	118.80
2	K70	86	G	C4'-C3'-C2'	-5.47	97.12	102.60
42	R60	986	G	C3'-C2'-C1'	5.47	105.88	101.50
2	L70	75	G	C3'-C2'-C1'	-5.47	97.12	101.50
42	S60	622	C	P-O3'-C3'	-5.47	113.13	119.70
42	S60	986	G	C3'-C2'-C1'	5.47	105.88	101.50
42	R60	848	G	C5-N7-C8	5.47	107.03	104.30
42	R60	1239	C	O5'-P-OP2	-5.47	100.78	105.70
42	S60	1228	C	C2-N3-C4	5.46	122.63	119.90
42	R60	1049	G	C4-C5-C6	5.46	122.08	118.80
2	L70	86	G	C4'-C3'-C2'	-5.46	97.14	102.60
1	K50	1614	G	O4'-C1'-N9	5.46	112.57	108.20
1	L50	1614	G	O4'-C1'-N9	5.46	112.56	108.20
1	L50	2441	A	P-O3'-C3'	-5.46	113.15	119.70
42	R60	269	G	OP1-P-OP2	-5.46	111.42	119.60
42	S60	1052	A	N7-C8-N9	5.45	116.53	113.80
42	R60	954	G	C5-C6-N1	-5.45	108.78	111.50
42	S60	973	G	C4-C5-N7	-5.45	108.62	110.80
42	S60	1056	A	C4-C5-N7	-5.45	107.98	110.70
42	R60	1052	A	N7-C8-N9	5.45	116.52	113.80
1	L50	178	G	C5-C6-O6	5.44	131.87	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	1183	C	C2-N3-C4	5.44	122.62	119.90
42	S60	836	A	N9-C4-C5	5.44	107.97	105.80
42	R60	954	G	C5-N7-C8	-5.44	101.58	104.30
1	K50	1074	G	C2'-C3'-O3'	5.43	122.39	113.70
1	K50	2441	A	P-O3'-C3'	-5.43	113.18	119.70
42	S60	1328	G	C3'-C2'-C1'	5.43	105.85	101.50
42	S60	269	G	OP1-P-OP2	-5.43	111.45	119.60
42	R60	10	A	P-O3'-C3'	-5.43	113.19	119.70
1	L50	838	G	OP1-P-OP2	-5.42	111.46	119.60
1	K50	1634	C	C1'-O4'-C4'	-5.42	105.56	109.90
1	K50	2473	G	OP1-P-OP2	-5.42	111.47	119.60
42	R60	861	C	C6-N1-C2	5.42	122.47	120.30
42	R60	973	G	C4-C5-N7	-5.42	108.63	110.80
42	R60	1195	A	C4-C5-C6	5.42	119.71	117.00
1	L50	1074	G	C2'-C3'-O3'	5.42	122.37	113.70
42	R60	982	C	C6-N1-C2	-5.42	118.13	120.30
2	K70	75	G	C3'-C2'-C1'	-5.42	97.17	101.50
1	K50	141	G	O4'-C1'-C2'	-5.41	100.39	105.80
42	R60	839	C	C5-C6-N1	5.41	123.71	121.00
42	S60	1182	G	N1-C2-N3	-5.41	120.65	123.90
42	R60	952	A	C5-N7-C8	-5.41	101.19	103.90
42	R60	979	A	N9-C4-C5	5.41	107.96	105.80
42	R60	1206	A	C4-C5-C6	5.40	119.70	117.00
42	R60	1206	A	C8-N9-C4	-5.40	103.64	105.80
1	L50	2473	G	OP1-P-OP2	-5.40	111.50	119.60
1	L50	141	G	O4'-C1'-C2'	-5.40	100.40	105.80
42	S60	1205	G	N7-C8-N9	5.40	115.80	113.10
1	K50	838	G	OP1-P-OP2	-5.40	111.50	119.60
1	K50	518	G	OP1-P-OP2	-5.40	111.50	119.60
42	S60	1084	G	N9-C4-C5	5.40	107.56	105.40
42	R60	477	G	C3'-C2'-C1'	5.40	105.82	101.50
1	L50	330	G	C8-N9-C4	-5.39	104.24	106.40
42	R60	1205	G	N7-C8-N9	5.39	115.80	113.10
42	S60	10	A	P-O3'-C3'	-5.39	113.23	119.70
1	K50	1282	C	N3-C2-O2	-5.39	118.13	121.90
42	S60	1094	C	C6-N1-C2	-5.39	118.14	120.30
42	R60	1328	G	C3'-C2'-C1'	5.39	105.81	101.50
42	S60	979	A	N9-C4-C5	5.38	107.95	105.80
1	K50	1808	A	P-O3'-C3'	5.38	126.16	119.70
42	S60	873	C	C5-C6-N1	-5.38	118.31	121.00
42	S60	1206	A	C4-C5-C6	5.38	119.69	117.00
1	L50	42	G	C4'-C3'-C2'	-5.38	97.22	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	995	A	C5-N7-C8	5.38	106.59	103.90
66	SR0	32	ARG	NE-CZ-NH2	5.38	122.99	120.30
1	L50	1634	C	C1'-O4'-C4'	-5.37	105.60	109.90
42	S60	477	G	C3'-C2'-C1'	5.37	105.80	101.50
1	K50	330	G	C8-N9-C4	-5.37	104.25	106.40
1	L50	518	G	OP1-P-OP2	-5.37	111.55	119.60
1	L50	1808	A	P-O3'-C3'	5.36	126.14	119.70
42	S60	954	G	C5-C6-N1	-5.36	108.82	111.50
42	S60	1054	G	C1'-O4'-C4'	-5.36	105.61	109.90
1	L50	1282	C	N3-C2-O2	-5.36	118.15	121.90
1	K50	42	G	C4'-C3'-C2'	-5.36	97.25	102.60
1	K50	1466	A	C3'-C2'-C1'	5.35	105.78	101.50
42	R60	954	G	C6-C5-N7	-5.35	127.19	130.40
42	R60	871	C	N3-C4-C5	-5.34	119.76	121.90
42	R60	873	C	C5-C6-N1	-5.34	118.33	121.00
42	R60	1054	G	C1'-O4'-C4'	-5.34	105.62	109.90
1	L50	141	G	C1'-O4'-C4'	-5.34	105.63	109.90
42	S60	10	A	O5'-P-OP2	5.34	117.10	110.70
42	R60	860	G	C4-C5-N7	-5.33	108.67	110.80
1	L50	1466	A	C3'-C2'-C1'	5.33	105.76	101.50
42	S60	1089	G	C3'-C2'-C1'	5.33	105.76	101.50
42	R60	1154	A	P-O3'-C3'	-5.33	113.31	119.70
42	R60	1208	G	C5-N7-C8	5.33	106.96	104.30
42	S60	952	A	C5-N7-C8	-5.33	101.24	103.90
1	K50	141	G	C1'-O4'-C4'	-5.32	105.64	109.90
1	K50	2184	G	P-O3'-C3'	5.32	126.09	119.70
42	R60	888	U	OP1-P-OP2	-5.32	111.62	119.60
42	S60	888	U	OP1-P-OP2	-5.32	111.62	119.60
42	S60	925	A	P-O3'-C3'	-5.32	113.32	119.70
42	S60	851	G	C5-C6-O6	-5.31	125.41	128.60
42	S60	860	G	C4-C5-N7	-5.31	108.67	110.80
42	R60	1084	G	N9-C4-C5	5.31	107.53	105.40
42	R60	1089	G	C3'-C2'-C1'	5.31	105.75	101.50
42	R60	963	G	C4-C5-N7	-5.31	108.68	110.80
42	R60	10	A	O5'-P-OP2	5.30	117.06	110.70
42	R60	851	G	C5-C6-O6	-5.30	125.42	128.60
1	L50	2184	G	P-O3'-C3'	5.30	126.06	119.70
42	S60	1154	A	P-O3'-C3'	-5.30	113.34	119.70
42	S60	893	U	P-O3'-C3'	-5.30	113.34	119.70
42	R60	834	G	P-O3'-C3'	-5.30	113.34	119.70
42	R60	849	U	O5'-P-OP2	-5.30	100.93	105.70
42	S60	1213	G	C8-N9-C4	5.30	108.52	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	1176	G	C5-C6-N1	5.30	114.15	111.50
42	S60	849	U	O5'-P-OP2	-5.29	100.94	105.70
42	R60	925	A	P-O3'-C3'	-5.29	113.35	119.70
42	R60	1018	U	N3-C4-C5	5.29	117.78	114.60
42	S60	847	A	C4-C5-N7	-5.29	108.06	110.70
42	S60	1032	A	N9-C4-C5	-5.29	103.68	105.80
1	K50	515	U	P-O3'-C3'	-5.29	113.35	119.70
42	R60	847	A	C4-C5-N7	-5.29	108.06	110.70
42	S60	954	G	C5-N7-C8	-5.29	101.66	104.30
42	R60	1003	A	C6-N1-C2	-5.29	115.43	118.60
42	R60	601	G	C4'-C3'-C2'	-5.28	97.32	102.60
1	K50	371	A	C5-N7-C8	5.28	106.54	103.90
42	R60	1032	A	N9-C4-C5	-5.28	103.69	105.80
1	K50	614	G	N3-C4-C5	-5.28	125.96	128.60
42	R60	893	U	P-O3'-C3'	-5.28	113.36	119.70
42	S60	601	G	C4'-C3'-C2'	-5.28	97.32	102.60
42	R60	871	C	C4-C5-C6	5.28	120.04	117.40
42	S60	1208	G	C5-C6-N1	5.28	114.14	111.50
42	S60	861	C	C6-N1-C2	5.27	122.41	120.30
42	S60	954	G	C6-C5-N7	-5.27	127.24	130.40
42	R60	1118	A	C5-C6-N1	-5.27	115.06	117.70
1	L50	2332	G	C4'-C3'-C2'	-5.27	97.33	102.60
42	S60	864	A	C4-C5-C6	5.27	119.63	117.00
42	S60	1003	A	C6-N1-C2	-5.27	115.44	118.60
42	R60	1010	G	C4-C5-N7	5.27	112.91	110.80
42	R60	1213	G	C8-N9-C4	5.27	108.51	106.40
42	S60	947	C	N3-C4-C5	-5.27	119.79	121.90
42	S60	1010	G	C5-N7-C8	-5.26	101.67	104.30
42	R60	850	G	C4'-C3'-C2'	-5.26	97.34	102.60
1	K50	1605	U	P-O3'-C3'	-5.26	113.38	119.70
42	R60	864	A	C4-C5-C6	5.26	119.63	117.00
42	S60	834	G	P-O3'-C3'	-5.26	113.39	119.70
42	S60	860	G	N3-C4-C5	-5.26	125.97	128.60
42	R60	947	C	N3-C4-C5	-5.26	119.80	121.90
1	K50	323	G	C4'-C3'-C2'	-5.26	97.34	102.60
1	K50	2332	G	C4'-C3'-C2'	-5.26	97.34	102.60
65	SQ0	82	ARG	NE-CZ-NH1	-5.26	117.67	120.30
42	S60	1118	A	C5-C6-N1	-5.26	115.07	117.70
42	R60	275	G	C4'-C3'-C2'	-5.25	97.35	102.60
42	R60	1118	A	C8-N9-C4	-5.25	103.70	105.80
42	S60	1010	G	C4-C5-N7	5.25	112.90	110.80
1	L50	515	U	P-O3'-C3'	-5.25	113.40	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	275	G	C4'-C3'-C2'	-5.25	97.35	102.60
1	K50	141	G	C3'-C2'-C1'	-5.25	97.30	101.50
1	L50	323	G	C4'-C3'-C2'	-5.25	97.36	102.60
42	S60	1018	U	N3-C4-C5	5.25	117.75	114.60
42	R60	993	U	P-O3'-C3'	-5.25	113.41	119.70
42	S60	1194	U	C5-C6-N1	-5.24	120.08	122.70
42	R60	1012	A	C4'-C3'-C2'	-5.24	97.36	102.60
1	K50	885	G	P-O3'-C3'	-5.24	113.41	119.70
42	R60	1203	A	C2-N3-C4	5.24	113.22	110.60
1	L50	1605	U	P-O3'-C3'	-5.24	113.41	119.70
1	L50	1839	A	P-O3'-C3'	-5.24	113.41	119.70
42	S60	963	G	C4-C5-N7	-5.24	108.71	110.80
42	S60	993	U	P-O3'-C3'	-5.24	113.42	119.70
42	R60	858	C	C5-C6-N1	5.24	123.62	121.00
42	R60	1218	U	C3'-C2'-C1'	5.23	105.69	101.50
42	S60	850	G	C4'-C3'-C2'	-5.23	97.37	102.60
42	S60	1012	A	C4'-C3'-C2'	-5.23	97.37	102.60
1	L50	885	G	P-O3'-C3'	-5.23	113.42	119.70
42	S60	1218	U	C3'-C2'-C1'	5.23	105.68	101.50
1	K50	1499	U	C2'-C3'-O3'	5.23	122.07	113.70
1	K50	1839	A	P-O3'-C3'	-5.23	113.43	119.70
1	L50	1499	U	C2'-C3'-O3'	5.22	122.06	113.70
42	R60	860	G	N3-C4-C5	-5.22	125.99	128.60
42	R60	1010	G	C5-N7-C8	-5.22	101.69	104.30
1	K50	1160	G	O4'-C1'-N9	5.22	112.38	108.20
1	K50	2447	A	P-O5'-C5'	-5.22	112.54	120.90
42	S60	1039	G	C8-N9-C4	-5.22	104.31	106.40
42	S60	1052	A	C5-C6-N1	-5.22	115.09	117.70
1	L50	2447	A	P-O5'-C5'	-5.21	112.56	120.90
42	R60	918	A	C3'-C2'-C1'	-5.21	97.33	101.50
42	S60	918	A	C3'-C2'-C1'	-5.21	97.33	101.50
42	S60	1176	G	C5-C6-N1	5.21	114.11	111.50
1	L50	1602	G	C4'-C3'-C2'	-5.21	97.39	102.60
42	S60	1054	G	C5-N7-C8	-5.20	101.70	104.30
1	K50	596	G	C4'-C3'-C2'	-5.20	97.40	102.60
42	R60	934	A	P-O3'-C3'	-5.20	113.46	119.70
42	R60	1011	A	N9-C4-C5	5.20	107.88	105.80
42	S60	1059	G	N9-C4-C5	-5.20	103.32	105.40
1	L50	141	G	C3'-C2'-C1'	-5.20	97.34	101.50
42	S60	1018	U	C6-N1-C2	5.20	124.12	121.00
42	R60	1194	U	C5-C6-N1	-5.20	120.10	122.70
1	L50	371	A	C5-N7-C8	5.20	106.50	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	1000	G	C1'-C2'-O2'	-5.20	95.01	110.60
1	L50	1010	A	O5'-P-OP2	-5.20	101.02	105.70
42	S60	441	G	C4'-C3'-C2'	-5.20	97.40	102.60
42	S60	1053	A	C3'-C2'-C1'	-5.19	97.34	101.50
42	R60	1054	G	C5-N7-C8	-5.19	101.70	104.30
1	L50	1513	G	P-O3'-C3'	5.19	125.93	119.70
42	S60	1051	C	N3-C4-C5	5.19	123.98	121.90
42	R60	1097	A	C8-N9-C4	5.19	107.88	105.80
1	L50	1000	G	C1'-C2'-O2'	-5.19	95.04	110.60
42	S60	1128	G	N9-C4-C5	-5.19	103.33	105.40
42	R60	1059	G	N9-C4-C5	-5.19	103.33	105.40
65	RQ0	82	ARG	NE-CZ-NH1	-5.19	117.71	120.30
1	K50	1010	A	O5'-P-OP2	-5.19	101.03	105.70
42	R60	1208	G	C5-C6-N1	5.19	114.09	111.50
1	L50	1575	G	C4'-C3'-C2'	-5.18	97.42	102.60
42	S60	934	A	P-O3'-C3'	-5.18	113.48	119.70
42	S60	1048	G	N7-C8-N9	5.18	115.69	113.10
42	S60	1097	A	C8-N9-C4	5.18	107.87	105.80
42	S60	989	G	C4-C5-N7	-5.18	108.73	110.80
42	S60	995	A	C5-N7-C8	5.18	106.49	103.90
42	S60	1208	G	C5-N7-C8	5.18	106.89	104.30
42	R60	1003	A	N1-C6-N6	-5.18	115.49	118.60
42	R60	1053	A	C3'-C2'-C1'	-5.18	97.36	101.50
42	S60	1003	A	C5-C6-N1	5.18	120.29	117.70
42	S60	1203	A	C2-N3-C4	5.18	113.19	110.60
1	L50	1586	G	OP1-P-OP2	-5.18	111.83	119.60
1	L50	2009	U	O5'-P-OP2	-5.18	101.04	105.70
1	L50	2181	A	O5'-P-OP1	-5.18	101.04	105.70
42	S60	994	G	C8-N9-C4	-5.17	104.33	106.40
1	K50	462	G	OP1-P-O3'	5.17	116.58	105.20
1	K50	1513	G	P-O3'-C3'	5.17	125.91	119.70
1	K50	1575	G	C4'-C3'-C2'	-5.17	97.42	102.60
42	R60	1048	G	N7-C8-N9	5.17	115.69	113.10
42	R60	1003	A	C5-C6-N1	5.17	120.29	117.70
42	S60	1161	U	C6-N1-C2	5.17	124.10	121.00
1	K50	2452	A	P-O3'-C3'	5.17	125.91	119.70
1	K50	2315	G	C4'-C3'-C2'	-5.17	97.43	102.60
1	L50	1364	U	P-O3'-C3'	-5.17	113.50	119.70
1	K50	1602	G	C4'-C3'-C2'	-5.17	97.43	102.60
1	K50	541	U	P-O3'-C3'	-5.17	113.50	119.70
42	R60	441	G	C4'-C3'-C2'	-5.17	97.44	102.60
1	K50	690	U	C4'-C3'-C2'	-5.16	97.44	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L50	1160	G	O4'-C1'-N9	5.16	112.33	108.20
42	R60	951	A	C4-C5-N7	5.16	113.28	110.70
42	R60	994	G	C8-N9-C4	-5.16	104.34	106.40
42	R60	1128	G	N9-C4-C5	-5.16	103.34	105.40
1	L50	462	G	OP1-P-O3'	5.16	116.55	105.20
1	L50	2315	G	C4'-C3'-C2'	-5.16	97.44	102.60
1	K50	2009	U	O5'-P-OP2	-5.16	101.06	105.70
42	R60	1189	A	N7-C8-N9	-5.16	111.22	113.80
1	L50	596	G	C4'-C3'-C2'	-5.15	97.45	102.60
42	R60	989	G	C4-C5-N7	-5.15	108.74	110.80
1	L50	690	U	C4'-C3'-C2'	-5.15	97.45	102.60
42	R60	1018	U	C6-N1-C2	5.15	124.09	121.00
42	R60	1094	C	C6-N1-C2	-5.15	118.24	120.30
42	S60	1069	G	C5-N7-C8	-5.15	101.73	104.30
1	K50	1364	U	P-O3'-C3'	-5.15	113.52	119.70
42	R60	1097	A	C2-N3-C4	5.15	113.17	110.60
42	R60	1179	A	C4-C5-N7	-5.15	108.13	110.70
1	L50	1165	U	P-O3'-C3'	-5.15	113.52	119.70
39	LY0	53	ASP	CB-CA-C	5.15	120.69	110.40
42	S60	858	C	C5-C6-N1	5.15	123.57	121.00
42	S60	1118	A	C8-N9-C4	-5.14	103.74	105.80
1	L50	541	U	P-O3'-C3'	-5.14	113.53	119.70
42	R60	1039	G	C8-N9-C4	-5.14	104.34	106.40
42	R60	1011	A	C4-C5-C6	5.14	119.57	117.00
1	L50	2447	A	O4'-C1'-N9	5.14	112.31	108.20
1	K50	2447	A	O4'-C1'-N9	5.13	112.31	108.20
39	KY0	53	ASP	CB-CA-C	5.13	120.67	110.40
1	L50	1192	A	OP1-P-OP2	-5.13	111.90	119.60
1	K50	1165	U	P-O3'-C3'	-5.13	113.54	119.70
1	K50	1586	G	OP1-P-OP2	-5.13	111.90	119.60
1	L50	614	G	N3-C4-C5	-5.13	126.04	128.60
42	R60	459	G	C4'-C3'-C2'	-5.13	97.47	102.60
42	R60	1208	G	N7-C8-N9	-5.13	110.54	113.10
1	L50	2452	A	P-O3'-C3'	5.12	125.85	119.70
1	K50	1192	A	OP1-P-OP2	-5.12	111.91	119.60
42	S60	1189	A	N7-C8-N9	-5.12	111.24	113.80
1	K50	194	A	OP1-P-OP2	-5.12	111.92	119.60
42	R60	1069	G	C5-N7-C8	-5.12	101.74	104.30
42	S60	459	G	C4'-C3'-C2'	-5.12	97.48	102.60
42	S60	1208	G	N7-C8-N9	-5.12	110.54	113.10
2	K70	93	A	P-O3'-C3'	-5.12	113.56	119.70
42	R60	1161	U	N3-C4-C5	5.12	117.67	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	1001	C	C2-N3-C4	5.12	122.46	119.90
2	L70	93	A	P-O3'-C3'	-5.12	113.56	119.70
42	S60	1088	U	C5-C6-N1	-5.12	120.14	122.70
42	R60	162	C	P-O3'-C3'	-5.12	113.56	119.70
42	R60	1052	A	C5-C6-N1	-5.12	115.14	117.70
42	R60	1095	G	C4-C5-C6	5.12	121.87	118.80
1	L50	194	A	OP1-P-OP2	-5.11	111.93	119.60
42	S60	835	A	C4-C5-C6	5.11	119.56	117.00
42	S60	1097	A	C2-N3-C4	5.11	113.15	110.60
42	S60	1179	A	C4-C5-N7	-5.11	108.15	110.70
42	S60	857	G	N9-C4-C5	-5.11	103.36	105.40
42	R60	881	G	OP1-P-OP2	-5.11	111.94	119.60
1	L50	2011	A	P-O3'-C3'	-5.11	113.57	119.70
42	R60	1048	G	C5-C6-N1	-5.11	108.95	111.50
42	S60	1011	A	N9-C4-C5	5.10	107.84	105.80
1	K50	1476	G	N3-C4-C5	-5.10	126.05	128.60
1	L50	690	U	OP1-P-O3'	5.10	116.42	105.20
42	S60	987	A	C4-C5-N7	5.10	113.25	110.70
1	L50	1476	G	N3-C4-C5	-5.10	126.05	128.60
42	R60	1161	U	C6-N1-C2	5.10	124.06	121.00
42	R60	1211	A	N9-C4-C5	5.10	107.84	105.80
1	K50	2181	A	O5'-P-OP1	-5.09	101.12	105.70
42	R60	844	A	P-O3'-C3'	-5.09	113.59	119.70
42	S60	881	G	OP1-P-OP2	-5.09	111.96	119.60
42	S60	951	A	C4-C5-N7	5.09	113.25	110.70
42	S60	1052	A	C2-N3-C4	-5.09	108.05	110.60
1	K50	2341	G	C4'-C3'-C2'	-5.09	97.51	102.60
42	S60	263	A	C5'-C4'-C3'	-5.09	107.86	116.00
42	S60	989	G	C4-C5-C6	5.09	121.85	118.80
1	K50	690	U	OP1-P-O3'	5.09	116.39	105.20
1	L50	1622	G	C4'-C3'-C2'	-5.09	97.51	102.60
42	S60	1048	G	C5-C6-N1	-5.09	108.96	111.50
1	L50	330	G	P-O3'-C3'	5.08	125.80	119.70
1	K50	2011	A	P-O3'-C3'	-5.08	113.60	119.70
42	R60	1051	C	N3-C4-C5	5.08	123.93	121.90
1	L50	266	A	O5'-P-OP1	-5.08	101.13	105.70
42	S60	1011	A	C4-C5-C6	5.08	119.54	117.00
42	S60	1064	G	OP1-P-OP2	-5.08	111.98	119.60
42	R60	1052	A	C2-N3-C4	-5.08	108.06	110.60
42	S60	162	C	P-O3'-C3'	-5.08	113.60	119.70
42	R60	1064	G	C8-N9-C4	-5.08	104.37	106.40
1	L50	1018	U	C1'-C2'-O2'	-5.08	95.37	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	1053	A	C2-N3-C4	5.08	113.14	110.60
42	R60	263	A	C5'-C4'-C3'	-5.08	107.88	116.00
1	K50	569	C	O5'-P-OP2	-5.07	101.13	105.70
1	K50	2313	G	O5'-P-OP1	-5.07	101.14	105.70
1	L50	612	C	OP1-P-OP2	-5.07	111.99	119.60
1	L50	2341	G	C4'-C3'-C2'	-5.07	97.53	102.60
42	S60	1111	A	C8-N9-C4	5.07	107.83	105.80
42	R60	885	G	C4'-C3'-C2'	-5.07	97.53	102.60
42	R60	1064	G	OP1-P-OP2	-5.07	112.00	119.60
42	S60	844	A	P-O3'-C3'	-5.07	113.62	119.70
42	S60	1094	C	C5-C6-N1	5.07	123.53	121.00
42	R60	1111	A	C8-N9-C4	5.07	107.83	105.80
42	S60	1095	G	C4-C5-C6	5.07	121.84	118.80
42	S60	1062	C	C6-N1-C2	-5.06	118.28	120.30
42	S60	1214	A	P-O3'-C3'	-5.06	113.63	119.70
1	K50	330	G	P-O3'-C3'	5.06	125.78	119.70
42	R60	8	U	O5'-P-OP2	-5.06	101.15	105.70
1	L50	1087	G	C4'-C3'-C2'	-5.06	97.54	102.60
42	S60	1050	G	N3-C4-C5	-5.06	126.07	128.60
1	K50	1087	G	C4'-C3'-C2'	-5.06	97.54	102.60
1	K50	1622	G	C4'-C3'-C2'	-5.06	97.54	102.60
42	R60	835	A	C4-C5-C6	5.06	119.53	117.00
65	RQ0	82	ARG	NE-CZ-NH2	5.06	122.83	120.30
42	R60	833	A	P-O3'-C3'	-5.06	113.63	119.70
1	L50	569	C	O5'-P-OP2	-5.06	101.15	105.70
1	L50	1182	A	O5'-P-OP2	5.06	116.77	110.70
42	R60	989	G	C4-C5-C6	5.05	121.83	118.80
1	L50	2313	G	O5'-P-OP1	-5.05	101.15	105.70
1	L50	2145	A	O5'-P-OP1	-5.05	101.16	105.70
42	S60	885	G	C4'-C3'-C2'	-5.05	97.55	102.60
1	K50	1018	U	C1'-C2'-O2'	-5.05	95.45	110.60
1	L50	1614	G	C1'-O4'-C4'	-5.05	105.86	109.90
42	S60	8	U	O5'-P-OP2	-5.05	101.16	105.70
1	K50	612	C	OP1-P-OP2	-5.05	112.03	119.60
1	L50	1018	U	C1'-O4'-C4'	-5.04	105.87	109.90
42	S60	308	C	P-O3'-C3'	-5.04	113.65	119.70
42	R60	1209	C	C6-N1-C2	5.04	122.32	120.30
42	S60	875	A	C5-N7-C8	5.04	106.42	103.90
1	K50	266	A	O5'-P-OP1	-5.04	101.16	105.70
42	R60	1214	A	P-O3'-C3'	-5.04	113.65	119.70
1	K50	1018	U	C1'-O4'-C4'	-5.04	105.87	109.90
42	R60	975	G	C4-C5-N7	5.04	112.81	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	833	A	P-O3'-C3'	-5.04	113.66	119.70
1	L50	590	G	N3-C4-C5	-5.04	126.08	128.60
1	L50	1484	U	O5'-P-OP2	5.04	116.74	110.70
1	K50	590	G	N3-C4-C5	-5.04	126.08	128.60
1	K50	2019	G	C4'-C3'-C2'	-5.04	97.56	102.60
1	K50	2145	A	O5'-P-OP1	-5.04	101.17	105.70
1	L50	2019	G	C4'-C3'-C2'	-5.03	97.57	102.60
42	S60	1053	A	C2-N3-C4	5.03	113.12	110.60
1	K50	1115	G	C3'-C2'-C1'	-5.03	97.47	101.50
42	R60	308	C	P-O3'-C3'	-5.03	113.66	119.70
42	S60	1161	U	N3-C4-C5	5.03	117.62	114.60
1	K50	1414	U	P-O5'-C5'	-5.03	112.85	120.90
42	S60	883	C	N3-C4-C5	5.03	123.91	121.90
1	K50	1971	C	P-O3'-C3'	-5.03	113.66	119.70
1	L50	2167	A	C3'-C2'-C1'	5.03	105.52	101.50
1	K50	1614	G	C1'-O4'-C4'	-5.03	105.88	109.90
42	R60	987	A	C4-C5-N7	5.03	113.21	110.70
42	S60	952	A	C6-N1-C2	5.03	121.62	118.60
42	R60	1086	G	C3'-C2'-C1'	-5.03	97.48	101.50
42	S60	624	U	P-O3'-C3'	-5.03	113.67	119.70
42	S60	1064	G	C8-N9-C4	-5.03	104.39	106.40
1	K50	75	C	C2'-C3'-O3'	5.03	121.74	113.70
42	S60	987	A	N1-C6-N6	5.02	121.61	118.60
1	L50	1625	A	O5'-P-OP2	-5.02	101.18	105.70
42	S60	1003	A	N1-C6-N6	-5.02	115.59	118.60
42	S60	1048	G	N1-C6-O6	5.02	122.91	119.90
65	SQ0	82	ARG	NE-CZ-NH2	5.02	122.81	120.30
1	L50	75	C	C2'-C3'-O3'	5.02	121.73	113.70
42	S60	1000	C	C2-N3-C4	5.02	122.41	119.90
42	R60	1048	G	N1-C6-O6	5.02	122.91	119.90
1	L50	1115	G	C3'-C2'-C1'	-5.02	97.49	101.50
1	L50	1414	U	P-O5'-C5'	-5.02	112.87	120.90
1	L50	2556	U	P-O3'-C3'	-5.02	113.68	119.70
1	L50	151	G	P-O3'-C3'	5.01	125.72	119.70
42	S60	859	G	C4-C5-C6	5.01	121.81	118.80
42	S60	1070	C	C6-N1-C2	-5.01	118.29	120.30
1	L50	1182	A	OP1-P-OP2	-5.01	112.08	119.60
42	S60	1086	G	C3'-C2'-C1'	-5.01	97.49	101.50
1	K50	1484	U	O5'-P-OP2	5.01	116.72	110.70
1	K50	1838	G	C8-N9-C4	-5.01	104.39	106.40
1	K50	1315	C	O5'-P-OP2	-5.01	101.19	105.70
1	K50	1182	A	O5'-P-OP2	5.01	116.71	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	1182	A	OP1-P-OP2	-5.01	112.09	119.60
42	R60	1070	C	C6-N1-C2	-5.01	118.30	120.30
1	L50	1386	A	C3'-C2'-C1'	-5.01	97.49	101.50
1	K50	2154	U	P-O3'-C3'	-5.01	113.69	119.70
42	R60	1001	C	C2-N3-C4	5.00	122.40	119.90
42	R60	1062	C	C6-N1-C2	-5.00	118.30	120.30
1	K50	151	G	P-O3'-C3'	5.00	125.70	119.70
42	R60	1178	A	C5-C6-N1	-5.00	115.20	117.70
42	R60	1228	C	C5-C6-N1	5.00	123.50	121.00
42	S60	1211	A	P-O3'-C3'	-5.00	113.70	119.70

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	KC0	87	ALA	Peptide
13	KFF	101	ILE	Peptide
15	KGG	77	GLY	Peptide
6	LC0	87	ALA	Peptide
13	LFF	101	ILE	Peptide
15	LGG	77	GLY	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	K50	53655	0	26955	121	0
1	L50	53655	0	26955	121	0
2	K70	2542	0	1282	9	0
2	L70	2542	0	1282	8	0
3	KA0	1889	0	1985	12	0
3	LA0	1889	0	1985	12	0
4	KAA	1167	0	1214	7	0
4	LAA	1167	0	1214	6	0
5	KB0	3039	0	3183	5	0
5	LB0	3039	0	3183	6	0
6	KC0	2604	0	2638	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	LC0	2604	0	2638	10	0
7	KCC	781	0	803	2	0
7	LCC	781	0	803	2	0
8	KD0	2298	0	2384	7	0
8	LD0	2298	0	2384	7	0
9	KDD	895	0	948	1	0
9	LDD	895	0	948	0	0
10	KE0	1371	0	1389	15	0
10	LE0	1371	0	1389	14	0
11	KEE	1090	0	1173	11	0
11	LEE	1090	0	1173	11	0
12	KF0	1933	0	2011	10	0
12	LF0	1933	0	2011	10	0
13	KFF	893	0	945	2	0
13	LFF	893	0	945	2	0
14	KG0	1590	0	1709	5	0
14	LG0	1590	0	1709	4	0
15	KGG	819	0	882	2	0
15	LGG	819	0	882	3	0
16	KH0	1477	0	1528	3	0
16	LH0	1477	0	1528	3	0
17	KHH	992	0	1097	5	0
17	LHH	992	0	1097	5	0
18	KI0	1750	0	1797	2	0
18	LI0	1750	0	1797	3	0
19	KII	784	0	874	4	0
19	LII	784	0	874	3	0
20	KJ0	1332	0	1411	12	0
20	LJ0	1332	0	1411	12	0
21	KJJ	701	0	753	4	0
21	LJJ	701	0	753	4	0
22	KL0	1353	0	1433	4	0
22	LL0	1353	0	1433	5	0
23	KLL	427	0	468	0	0
23	LLL	427	0	468	0	0
24	KM0	927	0	961	4	0
24	LM0	927	0	961	5	0
25	KMM	427	0	461	0	0
25	LMM	427	0	461	0	0
26	KN0	1688	0	1752	5	0
26	LN0	1688	0	1752	5	0
27	KO0	1598	0	1681	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	LO0	1598	0	1681	3	0
28	KOO	801	0	886	3	0
28	LOO	801	0	886	4	0
29	KP0	1238	0	1304	4	0
29	LP0	1238	0	1304	3	0
30	KPP	684	0	720	2	0
30	LPP	684	0	720	2	0
31	KQ0	1491	0	1587	6	0
31	LQ0	1491	0	1587	7	0
32	KR0	1336	0	1430	1	0
32	LR0	1336	0	1430	0	0
33	KS0	1400	0	1450	1	0
33	LS0	1400	0	1450	1	0
34	KT0	1270	0	1321	16	0
34	LT0	1270	0	1321	16	0
35	KU0	810	0	834	1	0
35	LU0	810	0	834	1	0
36	KV0	1057	0	1139	1	0
36	LV0	1057	0	1139	1	0
37	KW0	832	0	873	45	0
37	LW0	832	0	873	45	0
38	KX0	874	0	956	5	0
38	LX0	874	0	956	5	0
39	KY0	1048	0	1135	2	0
39	LY0	1048	0	1135	2	0
40	KZ0	963	0	1022	2	0
40	LZ0	963	0	1022	2	0
41	MD1	1229	0	1216	10	0
41	MD2	1229	0	1216	9	0
42	R60	29181	0	14605	318	0
42	S60	29181	0	14604	321	0
43	RA0	1725	0	1750	140	0
43	SA0	1725	0	1750	138	0
44	RAA	827	0	859	17	0
44	SAA	827	0	859	17	0
45	RB0	1609	0	1728	6	0
45	SB0	1609	0	1728	6	0
46	RBB	627	0	651	4	0
46	SBB	627	0	651	3	0
47	RC0	1727	0	1802	95	0
47	SC0	1727	0	1802	94	0
48	RCC	476	0	488	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	SCC	476	0	488	17	0
49	RD0	1700	0	1815	32	0
49	SD0	1700	0	1815	32	0
50	RDD	550	0	542	28	0
50	SDD	550	0	542	30	0
51	RE0	2044	0	2116	26	0
51	SE0	2044	0	2116	26	0
52	REE	447	0	483	1	0
52	SEE	447	0	483	1	0
53	RF0	1509	0	1604	39	0
53	SF0	1509	0	1604	41	0
54	RFF	417	0	402	42	0
54	SFF	422	0	412	44	0
55	RG0	1836	0	1972	40	0
55	SG0	1836	0	1972	39	0
56	RGG	2478	0	2458	24	0
56	SGG	2478	0	2458	24	0
57	RH0	1335	0	1356	2	0
57	SH0	1335	0	1356	2	0
58	RI0	1347	0	1379	9	0
58	SI0	1347	0	1379	10	0
59	RJ0	1379	0	1436	16	0
59	SJ0	1379	0	1436	15	0
60	RK0	737	0	746	16	0
60	SK0	737	0	746	16	0
61	RL0	1229	0	1302	5	0
61	SL0	1229	0	1302	5	0
62	RM0	876	0	937	6	0
62	SM0	876	0	937	5	0
63	RN0	1130	0	1189	10	0
63	SN0	1130	0	1189	10	0
64	RO0	983	0	1028	14	0
64	SO0	983	0	1028	14	0
65	RQ0	1143	0	1171	20	0
65	SQ0	1143	0	1171	21	0
66	RR0	974	0	1003	99	0
66	SR0	974	0	1003	98	0
67	RS0	1150	0	1207	32	0
67	SS0	1150	0	1207	33	0
68	RT0	1161	0	1219	10	0
68	ST0	1161	0	1219	10	0
69	RU0	809	0	838	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	SU0	809	0	838	14	0
70	RV0	521	0	525	74	0
70	SV0	521	0	525	74	0
71	RW0	1022	0	1052	20	0
71	SW0	1022	0	1052	19	0
72	RX0	1098	0	1183	3	0
72	SX0	1098	0	1183	3	0
73	RY0	1118	0	1166	13	0
73	SY0	1118	0	1166	13	0
74	RZ0	633	0	678	14	0
74	SZ0	633	0	678	14	0
75	RP0	950	0	984	56	0
75	SP0	950	0	984	59	0
76	KGG	1	0	0	0	0
76	KJJ	1	0	0	0	0
76	KMM	1	0	0	0	0
76	KOO	1	0	0	0	0
76	KPP	1	0	0	0	0
76	LGG	1	0	0	0	0
76	LJJ	1	0	0	0	0
76	LMM	1	0	0	0	0
76	LOO	1	0	0	0	0
76	LPP	1	0	0	0	0
76	RAA	1	0	0	0	0
76	RBB	1	0	0	0	0
76	RDD	1	0	0	0	0
76	RFF	1	0	0	0	0
76	SAA	1	0	0	0	0
76	SBB	1	0	0	0	0
76	SDD	1	0	0	0	0
76	SFF	1	0	0	0	0
All	All	343629	0	266537	1984	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 3.

All (1984) 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)
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CD1	1.35	1.54
43:RA0:70:ASN:HB2	47:RC0:240:ILE:CD1	1.35	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SC0:51:SER:HB2	70:SV0:6:ARG:NH2	1.30	1.45
47:RC0:51:SER:HB2	70:RV0:6:ARG:NH2	1.30	1.42
49:SD0:238:PRO:C	66:SR0:19:ARG:HH12	1.27	1.38
20:KJ0:82:LYS:HB3	75:RP0:30:PHE:CE2	1.62	1.35
49:RD0:238:PRO:C	66:RR0:19:ARG:HH12	1.27	1.34
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CG1	1.56	1.34
43:RA0:70:ASN:HB2	47:RC0:240:ILE:CG1	1.56	1.34
43:RA0:70:ASN:CB	47:RC0:240:ILE:HD11	1.59	1.33
20:LJ0:82:LYS:HB3	75:SP0:30:PHE:CE2	1.62	1.32
43:SA0:141:ASN:O	70:SV0:23:VAL:HG23	1.21	1.31
43:SA0:70:ASN:CB	47:SC0:240:ILE:HD11	1.59	1.30
43:RA0:141:ASN:O	70:RV0:23:VAL:HG23	1.21	1.29
3:LA0:241:ARG:NH1	42:S60:592:G:H4'	1.51	1.25
49:SD0:239:ILE:N	66:SR0:19:ARG:HH12	1.35	1.25
3:KA0:241:ARG:NH1	42:R60:592:G:H4'	1.51	1.24
49:RD0:239:ILE:N	66:RR0:19:ARG:HH12	1.35	1.23
50:RDD:8:TYR:CE2	75:RP0:72:ARG:HD2	1.75	1.22
50:SDD:8:TYR:CE2	75:SP0:72:ARG:HD2	1.75	1.20
43:SA0:63:ARG:CZ	70:SV0:30:LEU:HG	1.75	1.17
49:RD0:238:PRO:C	66:RR0:19:ARG:NH1	1.98	1.17
43:RA0:63:ARG:CZ	70:RV0:30:LEU:HG	1.75	1.16
49:SD0:238:PRO:C	66:SR0:19:ARG:NH1	1.98	1.16
47:RC0:51:SER:CB	70:RV0:6:ARG:HH21	1.60	1.15
47:SC0:51:SER:CB	70:SV0:6:ARG:HH21	1.60	1.15
37:KW0:99:LYS:HA	37:KW0:102:LYS:HE2	1.30	1.13
47:SC0:51:SER:CB	70:SV0:6:ARG:NH2	2.11	1.13
37:LW0:99:LYS:HA	37:LW0:102:LYS:HE2	1.30	1.13
47:RC0:51:SER:CB	70:RV0:6:ARG:NH2	2.11	1.12
43:SA0:63:ARG:HG2	70:SV0:30:LEU:HD21	1.31	1.11
54:SFF:104:THR:HG22	54:RFF:98:ILE:O	1.50	1.11
20:LJ0:82:LYS:CB	75:SP0:30:PHE:HE2	1.65	1.09
20:KJ0:82:LYS:CB	75:RP0:30:PHE:HE2	1.65	1.09
54:SFF:104:THR:HG21	54:RFF:99:LYS:HA	1.35	1.09
43:RA0:70:ASN:CB	47:RC0:240:ILE:CD1	2.22	1.08
47:RC0:219:PRO:HB3	71:RW0:66:ARG:NH2	1.68	1.08
47:SC0:219:PRO:HB3	71:SW0:66:ARG:NH2	1.68	1.08
1:L50:1691:A:N6	42:S60:1248:G:H4'	1.68	1.08
73:SY0:22:GLU:O	73:SY0:23:LEU:HG	1.53	1.07
34:LT0:126:PRO:HB2	34:LT0:128:LEU:HG	1.34	1.07
43:SA0:70:ASN:CG	47:SC0:240:ILE:HG12	1.74	1.07
1:K50:1691:A:N6	42:R60:1248:G:H4'	1.68	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:70:ASN:CB	47:SC0:240:ILE:CD1	2.22	1.07
43:RA0:70:ASN:CG	47:RC0:240:ILE:HG12	1.73	1.06
43:SA0:141:ASN:C	70:SV0:23:VAL:HG23	1.76	1.06
43:RA0:187:GLY:HA2	70:RV0:35:ARG:NH2	1.71	1.05
1:L50:535:A:O2'	31:LQ0:146:ASN:HB3	1.55	1.05
37:LW0:83:PHE:CD1	55:SG0:144:LYS:HG2	1.92	1.05
43:SA0:63:ARG:O	70:SV0:28:VAL:HG22	1.55	1.05
43:RA0:63:ARG:HG2	70:RV0:30:LEU:HD21	1.31	1.05
43:RA0:70:ASN:CB	47:RC0:240:ILE:CG1	2.35	1.05
49:RD0:239:ILE:N	66:RR0:19:ARG:NH1	2.05	1.05
1:K50:535:A:O2'	31:KQ0:146:ASN:HB3	1.55	1.05
43:RA0:141:ASN:C	70:RV0:23:VAL:HG23	1.76	1.05
73:RY0:22:GLU:O	73:RY0:23:LEU:HG	1.54	1.05
3:LA0:241:ARG:HH12	42:S60:592:G:C4'	1.69	1.05
43:RA0:63:ARG:O	70:RV0:28:VAL:HG22	1.55	1.05
50:RDD:12:LEU:HD21	75:RP0:67:PHE:CD2	1.92	1.05
43:SA0:70:ASN:CB	47:SC0:240:ILE:CG1	2.35	1.04
1:K50:1695:A:N1	42:R60:1249:U:C5'	2.20	1.04
34:KT0:126:PRO:HB2	34:KT0:128:LEU:HG	1.34	1.04
50:SDD:12:LEU:HD21	75:SP0:67:PHE:CD2	1.92	1.04
3:KA0:241:ARG:HH12	42:R60:592:G:C4'	1.69	1.04
43:SA0:141:ASN:O	70:SV0:23:VAL:CG2	2.05	1.04
47:SC0:136:TRP:HH2	59:SJ0:59:ILE:CG2	1.71	1.04
43:RA0:64:MET:HB3	70:RV0:27:MET:HG2	1.38	1.03
1:L50:1695:A:N1	42:S60:1249:U:C5'	2.20	1.03
37:LW0:83:PHE:CD1	37:LW0:84:PRO:HD2	1.93	1.03
37:KW0:83:PHE:CD1	55:RG0:144:LYS:CG	2.41	1.03
37:KW0:83:PHE:CD1	55:RG0:144:LYS:HG2	1.92	1.03
47:RC0:136:TRP:HH2	59:RJ0:59:ILE:CG2	1.71	1.03
43:RA0:141:ASN:O	70:RV0:23:VAL:CG2	2.05	1.03
43:RA0:215:TYR:CD1	66:RR0:84:PHE:CE2	2.46	1.03
55:RG0:140:LYS:O	55:RG0:144:LYS:HD3	1.58	1.03
37:LW0:83:PHE:CD1	55:SG0:144:LYS:CG	2.41	1.03
43:SA0:215:TYR:CD1	66:SR0:84:PHE:CE2	2.46	1.03
55:SG0:140:LYS:O	55:SG0:144:LYS:HD3	1.58	1.03
43:SA0:64:MET:HB3	70:SV0:27:MET:HG2	1.38	1.02
43:SA0:187:GLY:HA2	70:SV0:35:ARG:NH2	1.71	1.02
10:KE0:55:GLU:OE2	10:KE0:117:ARG:HG3	1.59	1.02
43:SA0:63:ARG:CG	70:SV0:30:LEU:HD21	1.90	1.02
50:SDD:12:LEU:CD1	75:SP0:75:ILE:HG21	1.90	1.02
37:KW0:83:PHE:CD1	37:KW0:84:PRO:HD2	1.93	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RDD:12:LEU:CD1	75:RP0:75:ILE:HG21	1.90	1.02
10:LE0:55:GLU:OE2	10:LE0:117:ARG:HG3	1.59	1.01
43:SA0:117:ARG:HH12	47:SC0:243:GLU:CD	1.64	1.01
1:L50:1695:A:N1	42:S60:1249:U:H5'	1.76	1.00
1:K50:1695:A:N1	42:R60:1249:U:H5'	1.76	1.00
55:SG0:147:PHE:HZ	55:SG0:160:LYS:HE2	1.22	1.00
55:RG0:147:PHE:HZ	55:RG0:160:LYS:HE2	1.23	1.00
43:RA0:63:ARG:CG	70:RV0:30:LEU:HD21	1.89	0.99
1:K50:1695:A:C2	42:R60:1249:U:H5''	1.97	0.99
1:L50:1695:A:C2	42:S60:1249:U:H5''	1.97	0.99
54:SFF:145:VAL:HG11	54:RFF:136:LYS:CB	1.93	0.99
49:SD0:239:ILE:N	66:SR0:19:ARG:NH1	2.05	0.98
43:RA0:117:ARG:HH12	47:RC0:243:GLU:CD	1.64	0.98
42:S60:973:G:H1	44:SAA:90:TRP:HZ2	1.09	0.98
3:LA0:241:ARG:HH12	42:S60:592:G:H4'	1.13	0.97
42:R60:973:G:H1	44:RAA:90:TRP:HZ2	1.09	0.97
47:RC0:230:ASN:N	70:RV0:24:GLN:HE22	1.61	0.97
47:SC0:230:ASN:N	70:SV0:24:GLN:HE22	1.61	0.96
37:LW0:98:ASN:ND2	55:SG0:147:PHE:HA	1.81	0.96
43:RA0:215:TYR:HA	66:RR0:84:PHE:CD2	2.01	0.96
37:KW0:98:ASN:ND2	55:RG0:147:PHE:HA	1.81	0.96
44:SAA:47:ALA:CB	48:SCC:61:ARG:HE	1.78	0.96
43:RA0:63:ARG:NE	70:RV0:30:LEU:HG	1.81	0.96
43:SA0:215:TYR:HA	66:SR0:84:PHE:CD2	2.01	0.95
44:RAA:47:ALA:CB	48:RCC:61:ARG:HE	1.78	0.95
43:SA0:63:ARG:NE	70:SV0:30:LEU:HG	1.81	0.95
56:SGG:65:PHE:CE2	66:SR0:29:TYR:CE2	2.55	0.95
56:RGG:65:PHE:CE2	66:RR0:29:TYR:CE2	2.55	0.95
42:S60:554:A:N3	71:SW0:103:THR:HG22	1.83	0.94
20:KJ0:82:LYS:CB	75:RP0:30:PHE:CE2	2.44	0.93
43:RA0:70:ASN:HB2	47:RC0:240:ILE:HD11	0.95	0.93
43:RA0:184:TYR:CD1	70:RV0:35:ARG:NH1	2.36	0.93
50:SDD:8:TYR:O	75:SP0:67:PHE:N	2.01	0.93
20:KJ0:82:LYS:HB3	75:RP0:30:PHE:CD2	2.03	0.93
1:L50:1691:A:N6	42:S60:1248:G:C4'	2.32	0.93
43:SA0:51:ILE:HG13	66:SR0:105:MET:SD	2.09	0.93
47:SC0:51:SER:HB2	70:SV0:6:ARG:HH22	1.15	0.93
43:RA0:70:ASN:CA	47:RC0:240:ILE:HD11	1.98	0.93
50:RDD:8:TYR:O	75:RP0:67:PHE:N	2.01	0.93
43:SA0:70:ASN:CA	47:SC0:240:ILE:HD11	1.98	0.93
43:RA0:51:ILE:HG13	66:RR0:105:MET:SD	2.09	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LJ0:82:LYS:HB3	75:SP0:30:PHE:CD2	2.03	0.92
43:SA0:70:ASN:HB2	47:SC0:240:ILE:HD11	0.95	0.92
1:K50:1691:A:N6	42:R60:1248:G:C4'	2.32	0.92
42:R60:554:A:N3	71:RW0:103:THR:HG22	1.83	0.92
43:SA0:184:TYR:CD1	70:SV0:35:ARG:NH1	2.36	0.92
1:K50:1695:A:N1	42:R60:1249:U:H5''	1.85	0.92
43:SA0:63:ARG:HD3	70:SV0:30:LEU:HD23	1.52	0.91
10:LE0:100:ILE:HD11	24:LM0:102:PHE:HB2	1.49	0.91
43:RA0:120:ARG:HE	47:RC0:232:ILE:HG21	1.35	0.91
43:SA0:4:ARG:O	70:SV0:30:LEU:HD12	1.69	0.91
10:KE0:100:ILE:HD11	24:KM0:102:PHE:HB2	1.49	0.91
43:RA0:63:ARG:HD3	70:RV0:30:LEU:HD23	1.52	0.91
37:KW0:99:LYS:CA	37:KW0:102:LYS:HE2	2.00	0.91
42:R60:973:G:N1	44:RAA:90:TRP:CZ2	2.39	0.91
43:SA0:51:ILE:HD12	66:SR0:105:MET:HG2	1.53	0.90
43:RA0:51:ILE:HD12	66:RR0:105:MET:HG2	1.53	0.90
50:RDD:8:TYR:CE2	75:RP0:72:ARG:CD	2.54	0.90
42:S60:958:A:H3'	42:S60:959:G:H21	1.37	0.90
42:R60:958:A:H3'	42:R60:959:G:H21	1.37	0.90
43:SA0:120:ARG:HE	47:SC0:232:ILE:HG21	1.35	0.90
1:L50:1695:A:N1	42:S60:1249:U:H5''	1.85	0.90
43:RA0:4:ARG:O	70:RV0:30:LEU:HD12	1.69	0.90
43:RA0:184:TYR:O	70:RV0:35:ARG:HD2	1.72	0.90
3:KA0:241:ARG:HH12	42:R60:592:G:H4'	1.13	0.90
47:RC0:136:TRP:CH2	59:RJ0:59:ILE:CG2	2.54	0.90
42:S60:973:G:N1	44:SAA:90:TRP:CZ2	2.39	0.89
47:SC0:136:TRP:CH2	59:SJ0:59:ILE:CG2	2.54	0.89
37:LW0:99:LYS:CA	37:LW0:102:LYS:HE2	2.00	0.89
50:SDD:8:TYR:CE2	75:SP0:72:ARG:CD	2.54	0.89
42:S60:203:G:N3	51:SE0:33:THR:HG21	1.88	0.89
47:RC0:130:PRO:HB2	70:RV0:4:PHE:CZ	2.07	0.89
42:R60:203:G:N3	51:RE0:33:THR:HG21	1.88	0.89
43:RA0:70:ASN:ND2	47:RC0:240:ILE:HG12	1.88	0.89
50:RDD:8:TYR:CD2	75:RP0:72:ARG:HD2	2.08	0.89
43:SA0:184:TYR:O	70:SV0:35:ARG:HD2	1.72	0.89
47:SC0:130:PRO:HB2	70:SV0:4:PHE:CZ	2.07	0.89
47:RC0:230:ASN:H	70:RV0:24:GLN:HE22	0.91	0.89
43:RA0:67:SER:OG	70:RV0:40:LEU:CD2	2.21	0.89
43:RA0:117:ARG:NH1	47:RC0:243:GLU:OE2	2.06	0.88
47:RC0:51:SER:HB2	70:RV0:6:ARG:HH22	1.15	0.88
37:LW0:99:LYS:HA	37:LW0:102:LYS:CE	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LA0:241:ARG:NH1	42:S60:592:G:C4'	2.33	0.88
43:SA0:67:SER:OG	70:SV0:40:LEU:CD2	2.21	0.88
43:SA0:117:ARG:NH1	47:SC0:243:GLU:OE2	2.06	0.88
43:SA0:70:ASN:ND2	47:SC0:240:ILE:HG12	1.88	0.88
43:RA0:63:ARG:HD3	70:RV0:30:LEU:CD2	2.03	0.88
43:SA0:63:ARG:HD3	70:SV0:30:LEU:CD2	2.03	0.88
37:KW0:99:LYS:HA	37:KW0:102:LYS:CE	2.03	0.88
20:LJ0:82:LYS:CB	75:SP0:30:PHE:CE2	2.44	0.87
48:SCC:58:ARG:HH12	64:SO0:101:ARG:HH22	1.19	0.87
50:RDD:12:LEU:CD2	75:RP0:67:PHE:CD2	2.57	0.87
50:RDD:8:TYR:CZ	75:RP0:72:ARG:HD2	2.09	0.87
42:S60:973:G:N1	44:SAA:90:TRP:HZ2	1.72	0.87
47:SC0:230:ASN:H	70:SV0:24:GLN:HE22	0.91	0.87
47:RC0:230:ASN:H	70:RV0:24:GLN:NE2	1.73	0.87
43:SA0:67:SER:OG	70:SV0:40:LEU:HD22	1.75	0.87
50:SDD:8:TYR:CZ	75:SP0:72:ARG:HD2	2.09	0.87
47:SC0:230:ASN:H	70:SV0:24:GLN:NE2	1.73	0.86
50:SDD:12:LEU:CD2	75:SP0:67:PHE:CD2	2.57	0.86
50:SDD:8:TYR:CD2	75:SP0:72:ARG:HD2	2.08	0.86
43:SA0:70:ASN:CB	47:SC0:240:ILE:HG12	1.99	0.86
42:R60:973:G:N1	44:RAA:90:TRP:HZ2	1.72	0.86
47:SC0:230:ASN:HB2	70:SV0:24:GLN:CD	1.96	0.86
37:LW0:26:ASP:O	37:LW0:27:ASP:OD1	1.94	0.86
48:RCC:58:ARG:HH12	64:RO0:101:ARG:HH22	1.19	0.85
43:RA0:70:ASN:CB	47:RC0:240:ILE:HG12	1.99	0.85
42:R60:1084:G:N2	75:RP0:117:GLY:O	2.09	0.85
47:RC0:230:ASN:HB2	70:RV0:24:GLN:CD	1.96	0.85
42:R60:914:U:H3	42:R60:918:A:H61	1.23	0.85
42:S60:706:G:H2'	42:S60:706:G:N3	1.92	0.85
43:SA0:120:ARG:HE	47:SC0:232:ILE:CG2	1.88	0.85
43:RA0:67:SER:OG	70:RV0:40:LEU:HD22	1.75	0.85
43:RA0:120:ARG:HE	47:RC0:232:ILE:CG2	1.89	0.85
42:S60:1084:G:N2	75:SP0:117:GLY:O	2.09	0.84
20:KJ0:82:LYS:HB3	75:RP0:30:PHE:HE2	1.06	0.84
37:KW0:26:ASP:O	37:KW0:27:ASP:OD1	1.94	0.84
42:S60:1149:U:OP1	67:SS0:139:VAL:N	2.10	0.84
42:R60:826:U:O2'	47:RC0:81:GLN:O	1.94	0.84
50:SDD:12:LEU:HD11	75:SP0:75:ILE:HG21	1.59	0.84
47:RC0:219:PRO:HB3	71:RW0:66:ARG:HH22	1.39	0.84
42:S60:995:A:H3'	42:S60:996:G:H8	1.42	0.84
42:R60:1149:U:OP1	67:RS0:139:VAL:N	2.10	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S60:826:U:O2'	47:SC0:81:GLN:O	1.94	0.84
42:S60:914:U:H3	42:S60:918:A:H61	1.24	0.84
1:K50:1728:U:HO2'	42:R60:1259:U:HO2'	0.93	0.84
42:R60:706:G:N3	42:R60:706:G:H2'	1.92	0.83
42:S60:705:A:N3	42:S60:706:G:C6	2.46	0.83
55:SG0:147:PHE:CZ	55:SG0:160:LYS:HE2	2.13	0.83
42:R60:995:A:H3'	42:R60:996:G:H8	1.42	0.83
47:SC0:219:PRO:HB3	71:SW0:66:ARG:HH22	1.39	0.83
53:SF0:118:ARG:HD2	53:SF0:125:MET:HB3	1.59	0.83
42:R60:705:A:N3	42:R60:706:G:C6	2.46	0.83
43:SA0:215:TYR:O	66:SR0:84:PHE:HE2	1.62	0.83
43:RA0:63:ARG:CD	70:RV0:30:LEU:CD2	2.57	0.83
42:S60:923:A:H4'	42:S60:924:U:H2'	1.61	0.83
41:MD2:52:LYS:HG3	42:R60:606:G:N2	1.93	0.83
43:SA0:63:ARG:CD	70:SV0:30:LEU:CD2	2.57	0.83
41:MD1:52:LYS:HG3	42:S60:606:G:N2	1.93	0.83
54:SFF:147:ILE:HD11	54:RFF:147:ILE:HD11	1.59	0.83
42:S60:973:G:H22	44:SAA:90:TRP:HH2	1.27	0.82
42:S60:1159:A:O2'	75:SP0:100:ASN:ND2	2.11	0.82
54:SFF:150:LYS:HD2	42:R60:915:A:O2'	1.77	0.82
42:R60:1159:A:O2'	75:RP0:100:ASN:ND2	2.12	0.82
42:R60:923:A:H4'	42:R60:924:U:H2'	1.61	0.82
50:RDD:12:LEU:HD11	75:RP0:75:ILE:HG21	1.59	0.82
53:RF0:118:ARG:HD2	53:RF0:125:MET:HB3	1.59	0.82
55:RG0:147:PHE:CZ	55:RG0:160:LYS:HE2	2.13	0.82
49:SD0:101:LYS:NZ	60:SK0:14:TYR:OH	2.13	0.82
49:SD0:234:ILE:HD12	66:SR0:8:SER:HB2	1.62	0.81
50:RDD:8:TYR:N	75:RP0:67:PHE:O	2.13	0.81
56:RGG:65:PHE:HE2	66:RR0:29:TYR:CE2	1.96	0.81
50:SDD:8:TYR:N	75:SP0:67:PHE:O	2.14	0.81
42:R60:173:A:C8	51:RE0:131:VAL:CG1	2.64	0.81
43:RA0:215:TYR:O	66:RR0:84:PHE:HE2	1.62	0.81
47:RC0:230:ASN:HB2	70:RV0:24:GLN:OE1	1.80	0.81
53:RF0:39:ILE:HG21	65:RQ0:50:GLU:HB2	1.62	0.81
42:S60:173:A:C8	51:SE0:131:VAL:CG1	2.64	0.81
20:LJ0:82:LYS:HB3	75:SP0:30:PHE:HE2	1.06	0.81
54:SFF:93:LYS:HB3	54:SFF:94:PRO:HD2	1.63	0.81
42:R60:1055:A:O3'	47:RC0:84:ALA:HB2	1.81	0.81
1:L50:1691:A:C6	42:S60:1248:G:O4'	2.34	0.81
53:SF0:39:ILE:HG21	65:SQ0:50:GLU:HB2	1.62	0.81
47:SC0:230:ASN:HB2	70:SV0:24:GLN:OE1	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SF0:39:ILE:CG2	65:SQ0:50:GLU:HB2	2.11	0.81
53:RF0:39:ILE:CG2	65:RQ0:50:GLU:HB2	2.11	0.81
56:RGG:65:PHE:CZ	66:RR0:29:TYR:CE2	2.69	0.81
43:RA0:215:TYR:HA	66:RR0:84:PHE:CE2	2.16	0.81
56:SGG:65:PHE:CZ	66:SR0:29:TYR:CE2	2.69	0.80
43:RA0:63:ARG:HG2	70:RV0:30:LEU:CD2	2.11	0.80
42:S60:1055:A:O3'	47:SC0:84:ALA:HB2	1.81	0.80
10:KE0:23:ILE:HD11	11:KEE:79:ARG:HH12	1.45	0.80
43:SA0:215:TYR:HA	66:SR0:84:PHE:CE2	2.16	0.80
47:RC0:136:TRP:HH2	59:RJ0:59:ILE:HG21	1.46	0.80
49:RD0:234:ILE:HD12	66:RR0:8:SER:HB2	1.62	0.80
65:SQ0:33:ASN:ND2	68:ST0:6:PHE:CD2	2.50	0.80
56:SGG:65:PHE:HE2	66:SR0:29:TYR:CE2	1.96	0.80
1:K50:1691:A:C6	42:R60:1248:G:O4'	2.34	0.80
34:KT0:126:PRO:HB2	34:KT0:128:LEU:CG	2.13	0.79
42:R60:988:A:O2'	43:RA0:105:PRO:O	2.00	0.79
10:LE0:23:ILE:HD11	11:LEE:79:ARG:HH12	1.45	0.79
43:SA0:67:SER:CA	70:SV0:28:VAL:HG13	2.13	0.79
47:SC0:136:TRP:HH2	59:SJ0:59:ILE:HG21	1.46	0.79
47:SC0:166:LYS:HD2	59:SJ0:100:GLU:OE2	1.83	0.79
53:RF0:96:GLY:O	74:RZ0:108:LEU:CD2	2.31	0.79
54:RFF:93:LYS:HB3	54:RFF:94:PRO:HD2	1.63	0.79
65:RQ0:33:ASN:ND2	68:RT0:6:PHE:CD2	2.50	0.79
1:L50:796:C:H5''	34:LT0:131:ARG:H	1.48	0.79
53:SF0:96:GLY:O	74:SZ0:108:LEU:CD2	2.31	0.79
37:LW0:83:PHE:CG	37:LW0:84:PRO:HD2	2.18	0.79
37:LW0:83:PHE:CE1	55:SG0:144:LYS:HG2	2.17	0.79
1:L50:1695:A:C2	42:S60:1249:U:C5'	2.66	0.79
37:KW0:83:PHE:CD1	55:RG0:144:LYS:HG3	2.17	0.79
42:S60:988:A:O2'	43:SA0:105:PRO:O	2.00	0.79
37:KW0:83:PHE:CG	37:KW0:84:PRO:HD2	2.18	0.79
37:LW0:83:PHE:CD1	55:SG0:144:LYS:HG3	2.17	0.78
3:KA0:241:ARG:NH1	42:R60:592:G:C4'	2.33	0.78
43:RA0:67:SER:CA	70:RV0:28:VAL:HG13	2.12	0.78
47:RC0:166:LYS:HD2	59:RJ0:100:GLU:OE2	1.83	0.78
54:SFF:99:LYS:HE2	54:SFF:102:ILE:HG12	1.63	0.78
43:RA0:215:TYR:HA	66:RR0:84:PHE:HD2	1.48	0.78
43:SA0:52:LYS:HB2	66:SR0:109:TYR:CZ	2.19	0.78
50:SDD:12:LEU:CD1	75:SP0:75:ILE:CG2	2.62	0.78
42:R60:973:G:H22	44:RAA:90:TRP:HH2	1.27	0.78
43:RA0:63:ARG:O	70:RV0:28:VAL:CG2	2.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SFF:132:ARG:O	42:R60:918:A:H4'	1.84	0.78
1:K50:796:C:H5''	34:KT0:131:ARG:H	1.48	0.78
48:RCC:58:ARG:HH12	64:RO0:101:ARG:NH2	1.82	0.78
43:SA0:215:TYR:HA	66:SR0:84:PHE:HD2	1.48	0.78
55:SG0:169:VAL:CG1	55:SG0:176:LYS:HE2	2.14	0.78
42:R60:1045:A:OP2	66:RR0:2:GLY:N	2.17	0.78
37:KW0:83:PHE:CE1	55:RG0:144:LYS:HG2	2.17	0.78
43:RA0:187:GLY:HA2	70:RV0:35:ARG:CZ	2.14	0.78
43:SA0:63:ARG:O	70:SV0:28:VAL:CG2	2.32	0.77
43:SA0:118:GLU:OE2	47:SC0:31:THR:HA	1.83	0.77
43:SA0:206:ARG:NE	66:SR0:86:PRO:HG2	1.99	0.77
3:KA0:241:ARG:CZ	42:R60:592:G:H4'	2.15	0.77
42:R60:1055:A:O3'	47:RC0:84:ALA:CB	2.33	0.77
53:SF0:6:THR:HG23	65:SQ0:53:LYS:NZ	2.00	0.77
54:SFF:104:THR:CG2	54:RFF:98:ILE:O	2.31	0.77
34:LT0:126:PRO:HB2	34:LT0:128:LEU:CG	2.13	0.77
54:SFF:104:THR:CG2	54:RFF:99:LYS:HA	2.11	0.77
43:RA0:52:LYS:HB2	66:RR0:109:TYR:CZ	2.19	0.77
42:S60:1045:A:OP2	66:SR0:2:GLY:N	2.17	0.77
42:S60:1055:A:O3'	47:SC0:84:ALA:CB	2.33	0.77
55:RG0:169:VAL:CG1	55:RG0:176:LYS:HE2	2.14	0.77
43:SA0:63:ARG:HG2	70:SV0:30:LEU:CD2	2.10	0.77
49:RD0:238:PRO:CA	66:RR0:19:ARG:HH12	1.98	0.77
42:R60:1188:A:H5''	65:RQ0:136:ALA:HB2	1.65	0.77
43:RA0:70:ASN:N	47:RC0:240:ILE:HD11	2.00	0.77
43:RA0:118:GLU:OE2	47:RC0:31:THR:HA	1.84	0.77
43:SA0:215:TYR:HD1	66:SR0:84:PHE:CD2	2.03	0.77
49:SD0:238:PRO:CA	66:SR0:19:ARG:HH12	1.98	0.77
54:SFF:97:ASP:CB	54:RFF:104:THR:O	2.32	0.76
43:RA0:67:SER:HA	70:RV0:28:VAL:HG13	1.66	0.76
44:RAA:47:ALA:HB1	48:RCC:61:ARG:HE	1.49	0.76
50:RDD:12:LEU:CD1	75:RP0:75:ILE:CG2	2.62	0.76
43:SA0:70:ASN:N	47:SC0:240:ILE:HD11	2.00	0.76
37:KW0:98:ASN:ND2	55:RG0:147:PHE:CA	2.48	0.76
42:R60:840:C:H4'	42:R60:1182:G:H5''	1.68	0.76
43:SA0:102:ARG:H	43:SA0:102:ARG:HD2	1.49	0.76
43:SA0:187:GLY:HA2	70:SV0:35:ARG:CZ	2.14	0.76
48:SCC:58:ARG:HH12	64:SO0:101:ARG:NH2	1.82	0.76
42:S60:915:A:C2	54:RFF:150:LYS:HG3	2.19	0.76
42:S60:1188:A:H5''	65:SQ0:136:ALA:HB2	1.65	0.76
53:SF0:40:LEU:HD23	65:SQ0:43:PHE:CE1	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA0:206:ARG:NE	66:RR0:86:PRO:HG2	1.99	0.76
53:RF0:6:THR:HG23	65:RQ0:53:LYS:NZ	2.00	0.76
53:RF0:40:LEU:HD23	65:RQ0:43:PHE:CE1	2.20	0.76
42:R60:173:A:H8	51:RE0:131:VAL:HG12	1.50	0.76
43:RA0:52:LYS:HB2	66:RR0:109:TYR:CE1	2.21	0.76
1:L50:883:U:H5''	24:LM0:35:ASN:HD21	1.51	0.76
3:LA0:241:ARG:CZ	42:S60:592:G:H4'	2.15	0.76
44:SAA:47:ALA:HB1	48:SCC:61:ARG:HE	1.49	0.76
42:R60:982:C:H4'	66:RR0:10:ARG:NH1	2.01	0.76
50:RDD:12:LEU:CD2	75:RP0:67:PHE:HD2	1.98	0.76
55:RG0:170:ASN:HD21	55:RG0:176:LYS:HD3	1.50	0.76
1:L50:883:U:H5''	24:LM0:35:ASN:ND2	2.01	0.76
43:SA0:52:LYS:HB2	66:SR0:109:TYR:CE1	2.21	0.76
43:SA0:67:SER:HA	70:SV0:28:VAL:HG13	1.66	0.76
43:RA0:102:ARG:HD2	43:RA0:102:ARG:H	1.49	0.76
1:K50:883:U:H5''	24:KM0:35:ASN:HD21	1.51	0.75
1:L50:2497:C:H5''	5:LB0:280:THR:HG21	1.68	0.75
42:S60:840:C:H4'	42:S60:1182:G:H5''	1.68	0.75
37:LW0:98:ASN:HD22	55:SG0:147:PHE:HA	1.52	0.75
37:LW0:98:ASN:ND2	55:SG0:147:PHE:CA	2.48	0.75
54:SFF:104:THR:HG21	54:RFF:99:LYS:HD3	1.67	0.75
49:RD0:101:LYS:NZ	60:RK0:14:TYR:OH	2.13	0.75
42:S60:982:C:H4'	66:SR0:10:ARG:NH1	2.01	0.75
55:SG0:170:ASN:HD21	55:SG0:176:LYS:HD3	1.50	0.75
42:S60:173:A:H8	51:SE0:131:VAL:HG12	1.50	0.75
43:RA0:215:TYR:HD1	66:RR0:84:PHE:CD2	2.03	0.75
56:RGG:228:LYS:NZ	66:RR0:25:THR:HG22	2.02	0.75
43:SA0:120:ARG:NE	47:SC0:232:ILE:HG21	2.02	0.75
50:SDD:12:LEU:CD2	75:SP0:67:PHE:HD2	1.98	0.75
1:K50:883:U:H5''	24:KM0:35:ASN:ND2	2.01	0.75
41:MD2:106:TYR:CE1	64:RO0:47:LYS:NZ	2.53	0.75
1:K50:2052:A:H5'	20:KJ0:62:ILE:HD11	1.69	0.74
41:MD1:106:TYR:CE1	64:SO0:47:LYS:NZ	2.54	0.74
1:K50:1695:A:C2	42:R60:1249:U:C5'	2.66	0.74
5:KB0:336:ARG:HH11	5:KB0:336:ARG:HG3	1.51	0.74
43:RA0:52:LYS:CB	66:RR0:109:TYR:CZ	2.70	0.74
43:SA0:52:LYS:CB	66:SR0:109:TYR:CZ	2.70	0.74
42:R60:173:A:C8	51:RE0:131:VAL:HG12	2.23	0.74
54:SFF:145:VAL:HG21	54:RFF:136:LYS:N	2.03	0.74
42:S60:173:A:C8	51:SE0:131:VAL:HG12	2.23	0.74
43:SA0:215:TYR:CD1	66:SR0:84:PHE:CD2	2.76	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB0:336:ARG:HH11	5:LB0:336:ARG:HG3	1.51	0.74
42:S60:982:C:O3'	66:SR0:10:ARG:NH1	2.21	0.74
43:RA0:120:ARG:NE	47:RC0:232:ILE:HG21	2.02	0.74
44:SAA:51:ASP:OD2	48:SCC:57:GLU:O	2.06	0.74
2:L70:27:A:OP2	8:LD0:62:THR:HG23	1.88	0.73
1:K50:2497:C:H5''	5:KB0:280:THR:HG21	1.68	0.73
42:R60:203:G:N3	51:RE0:33:THR:CG2	2.51	0.73
37:KW0:99:LYS:CB	37:KW0:102:LYS:HE2	2.18	0.73
42:S60:203:G:N3	51:SE0:33:THR:CG2	2.51	0.73
43:SA0:184:TYR:CE2	70:SV0:35:ARG:HD3	2.23	0.73
37:LW0:99:LYS:CB	37:LW0:102:LYS:HE2	2.18	0.73
67:SS0:20:MET:HG2	67:SS0:29:ASP:HA	1.71	0.73
43:RA0:64:MET:CB	70:RV0:27:MET:HG2	2.17	0.73
56:SGG:228:LYS:NZ	66:SR0:25:THR:HG22	2.02	0.73
2:K70:27:A:OP2	8:KD0:62:THR:HG23	1.88	0.73
42:R60:982:C:O3'	66:RR0:10:ARG:NH1	2.21	0.73
42:R60:1315:A:H2'	42:R60:1316:A:H8	1.54	0.73
49:RD0:36:ARG:NH1	69:RU0:112:GLU:OE2	2.21	0.73
53:RF0:96:GLY:O	74:RZ0:108:LEU:HD21	1.88	0.73
43:SA0:184:TYR:O	70:SV0:35:ARG:CD	2.36	0.73
45:SB0:53:THR:HG22	64:SO0:30:ASP:OD2	1.88	0.73
44:RAA:51:ASP:OD2	48:RCC:57:GLU:O	2.06	0.73
1:L50:2052:A:H5'	20:LJ0:62:ILE:HD11	1.69	0.73
49:SD0:36:ARG:NH1	69:SU0:112:GLU:OE2	2.21	0.73
45:RB0:53:THR:HG22	64:RO0:30:ASP:OD2	1.88	0.73
53:SF0:96:GLY:O	74:SZ0:108:LEU:HD21	1.88	0.73
54:SFF:143:TYR:O	54:RFF:134:GLY:HA3	1.89	0.73
42:S60:982:C:O2'	66:SR0:10:ARG:NH1	2.22	0.72
43:RA0:184:TYR:CE2	70:RV0:35:ARG:HD3	2.24	0.72
42:R60:438:U:H4'	72:RX0:110:LYS:HD2	1.72	0.72
43:RA0:184:TYR:O	70:RV0:35:ARG:CD	2.36	0.72
67:RS0:20:MET:HG2	67:RS0:29:ASP:HA	1.71	0.72
42:S60:438:U:H4'	72:SX0:110:LYS:HD2	1.72	0.72
42:S60:995:A:H3'	42:S60:996:G:C8	2.24	0.72
1:K50:1691:A:N1	42:R60:1248:G:O4'	2.23	0.72
48:RCC:41:ILE:HG23	53:RF0:131:ASP:O	1.90	0.72
7:LCC:64:ILE:HG22	40:LZ0:39:LEU:HD11	1.72	0.71
53:SF0:95:THR:HG21	53:SF0:102:ILE:HG12	1.72	0.71
43:RA0:52:LYS:HD2	66:RR0:109:TYR:CE1	2.25	0.71
42:S60:1034:A:H2'	42:S60:1035:C:C6	2.26	0.71
43:SA0:64:MET:CB	70:SV0:27:MET:HG2	2.17	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:705:A:C2	42:R60:706:G:O6	2.43	0.71
42:R60:995:A:H3'	42:R60:996:G:C8	2.24	0.71
43:RA0:215:TYR:CD1	66:RR0:84:PHE:CD2	2.76	0.71
42:S60:854:U:OP2	67:SS0:148:GLY:N	2.24	0.71
43:SA0:118:GLU:CD	47:SC0:31:THR:HG1	1.93	0.71
2:L70:3:U:H3	2:L70:116:G:H1	1.37	0.71
42:S60:705:A:C2	42:S60:706:G:O6	2.43	0.71
42:R60:854:U:OP2	67:RS0:148:GLY:N	2.24	0.71
2:K70:63:A:H2'	18:KI0:204:GLY:O	1.91	0.71
1:L50:1691:A:N1	42:S60:1248:G:O4'	2.23	0.71
47:SC0:219:PRO:CB	71:SW0:66:ARG:NH2	2.51	0.71
53:RF0:95:THR:HG21	53:RF0:102:ILE:HG12	1.72	0.71
7:KCC:64:ILE:HG22	40:KZ0:39:LEU:HD11	1.72	0.71
37:KW0:98:ASN:HD22	55:RG0:147:PHE:HA	1.52	0.71
2:L70:63:A:H2'	18:LI0:204:GLY:O	1.91	0.71
42:S60:237:A:H5'	58:SI0:48:VAL:CG1	2.21	0.71
42:S60:1315:A:H2'	42:S60:1316:A:H8	1.54	0.71
43:RA0:63:ARG:CG	70:RV0:30:LEU:CD2	2.67	0.70
53:RF0:40:LEU:CD2	65:RQ0:43:PHE:CD1	2.74	0.70
48:SCC:41:ILE:HG23	53:SF0:131:ASP:O	1.90	0.70
2:K70:3:U:H3	2:K70:116:G:H1	1.37	0.70
42:R60:1034:A:H2'	42:R60:1035:C:C6	2.26	0.70
43:SA0:52:LYS:HD2	66:SR0:109:TYR:CE1	2.25	0.70
47:RC0:136:TRP:CH2	59:RJ0:59:ILE:HG21	2.23	0.70
42:S60:1040:G:N2	42:S60:1042:A:H3'	2.06	0.70
53:SF0:40:LEU:CD2	65:SQ0:43:PHE:CD1	2.73	0.70
55:SG0:147:PHE:HZ	55:SG0:160:LYS:CE	2.03	0.70
42:R60:982:C:O2'	66:RR0:10:ARG:NH1	2.22	0.70
47:SC0:136:TRP:CH2	59:SJ0:59:ILE:HG21	2.23	0.70
54:SFF:138:TYR:CB	54:RFF:133:SER:CB	2.69	0.70
26:KN0:112:ASN:H	26:KN0:112:ASN:HD22	1.40	0.70
43:RA0:120:ARG:HH11	47:RC0:232:ILE:HG21	1.57	0.70
67:RS0:24:PHE:CZ	67:RS0:107:ILE:HG21	2.27	0.70
42:S60:666:A:OP1	63:SN0:132:LYS:NZ	2.25	0.70
43:SA0:120:ARG:HH11	47:SC0:232:ILE:HG21	1.57	0.70
52:SEE:5:ILE:HD12	72:SX0:63:ILE:HD12	1.74	0.70
1:L50:796:C:H5''	34:LT0:131:ARG:N	2.06	0.69
47:SC0:49:GLY:O	70:SV0:6:ARG:HB2	1.92	0.69
42:R60:237:A:H5'	58:RI0:48:VAL:CG1	2.21	0.69
47:RC0:49:GLY:O	70:RV0:6:ARG:HB2	1.92	0.69
52:REE:5:ILE:HD12	72:RX0:63:ILE:HD12	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:237:A:H5'	58:RI0:48:VAL:HG13	1.74	0.69
42:R60:1040:G:N2	42:R60:1042:A:H3'	2.06	0.69
42:S60:237:A:H5'	58:SI0:48:VAL:HG13	1.74	0.69
67:SS0:24:PHE:CZ	67:SS0:107:ILE:HG21	2.27	0.69
1:K50:796:C:H5''	34:KT0:131:ARG:N	2.06	0.69
45:SB0:53:THR:HG21	64:SO0:32:THR:OG1	1.92	0.69
51:RE0:64:ILE:HD12	73:RY0:23:LEU:HD13	1.75	0.69
14:LG0:119:ASP:OD1	14:LG0:145:THR:HA	1.92	0.69
42:S60:1315:A:H2'	42:S60:1316:A:C8	2.28	0.69
53:SF0:92:GLU:HG3	74:SZ0:108:LEU:HD12	1.73	0.69
1:K50:535:A:O2'	31:KQ0:146:ASN:CB	2.39	0.69
47:RC0:219:PRO:CB	71:RW0:66:ARG:NH2	2.51	0.69
42:S60:915:A:H1'	54:RFF:150:LYS:HD2	1.73	0.69
14:KG0:119:ASP:OD1	14:KG0:145:THR:HA	1.92	0.69
42:R60:1315:A:H2'	42:R60:1316:A:C8	2.28	0.69
43:RA0:67:SER:HA	70:RV0:28:VAL:CG1	2.22	0.69
53:RF0:92:GLU:HG3	74:RZ0:108:LEU:HD12	1.73	0.69
51:SE0:64:ILE:HD12	73:SY0:23:LEU:HD13	1.75	0.69
42:R60:666:A:OP1	63:RN0:132:LYS:NZ	2.25	0.69
10:LE0:55:GLU:CD	10:LE0:117:ARG:HG3	2.13	0.69
10:KE0:55:GLU:CD	10:KE0:117:ARG:HG3	2.13	0.69
42:R60:173:A:H8	51:RE0:131:VAL:CG1	2.04	0.68
45:RB0:53:THR:HG21	64:RO0:32:THR:OG1	1.92	0.68
26:LN0:112:ASN:HD22	26:LN0:112:ASN:H	1.40	0.68
43:SA0:67:SER:HA	70:SV0:28:VAL:CG1	2.22	0.68
53:SF0:6:THR:HG23	65:SQ0:53:LYS:HZ3	1.58	0.68
42:R60:1035:C:H2'	42:R60:1036:A:C8	2.29	0.68
42:S60:705:A:C2	42:S60:706:G:C6	2.82	0.68
42:S60:1035:C:H2'	42:S60:1036:A:C8	2.29	0.68
42:S60:1056:A:OP1	47:SC0:84:ALA:HB1	1.93	0.68
43:RA0:67:SER:CB	70:RV0:28:VAL:HG13	2.24	0.68
36:LV0:98:LEU:HD23	37:LW0:21:TYR:HB2	1.75	0.68
42:S60:915:A:N3	54:RFF:150:LYS:HG3	2.08	0.68
56:SGG:65:PHE:HZ	66:SR0:29:TYR:OH	1.77	0.68
56:RGG:65:PHE:HZ	66:RR0:29:TYR:OH	1.77	0.68
1:L50:535:A:HO2'	31:LQ0:146:ASN:HB3	1.59	0.68
42:R60:1056:A:OP1	47:RC0:84:ALA:HB1	1.93	0.68
43:RA0:141:ASN:C	70:RV0:23:VAL:CG2	2.55	0.67
42:S60:173:A:H8	51:SE0:131:VAL:CG1	2.04	0.67
43:SA0:141:ASN:C	70:SV0:23:VAL:CG2	2.55	0.67
49:SD0:94:GLN:HE21	60:SK0:19:SER:HB3	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:2109:G:H8	1:L50:2109:G:H5''	1.59	0.67
42:R60:705:A:C2	42:R60:706:G:C6	2.82	0.67
42:R60:1066:G:C5	60:RK0:58:PHE:CD1	2.83	0.67
55:RG0:147:PHE:HZ	55:RG0:160:LYS:CE	2.03	0.67
47:RC0:130:PRO:HB2	70:RV0:4:PHE:CE1	2.29	0.67
36:KV0:98:LEU:HD23	37:KW0:21:TYR:HB2	1.75	0.67
1:L50:535:A:O2'	31:LQ0:146:ASN:CB	2.38	0.67
47:SC0:130:PRO:HB2	70:SV0:4:PHE:CE1	2.29	0.67
50:SDD:12:LEU:HD23	75:SP0:67:PHE:HD2	1.59	0.67
66:RR0:103:MET:CE	66:RR0:117:LEU:HG	2.25	0.67
43:SA0:67:SER:CB	70:SV0:28:VAL:HG13	2.24	0.67
47:SC0:166:LYS:CD	59:SJ0:100:GLU:OE2	2.43	0.67
37:KW0:98:ASN:ND2	55:RG0:147:PHE:N	2.43	0.67
47:RC0:166:LYS:CD	59:RJ0:100:GLU:OE2	2.43	0.67
43:SA0:51:ILE:CG1	66:SR0:105:MET:SD	2.82	0.66
1:K50:2045:C:H5'	20:KJ0:102:GLY:HA3	1.77	0.66
42:R60:823:A:H2'	42:R60:824:A:C8	2.31	0.66
1:K50:2109:G:H5''	1:K50:2109:G:H8	1.59	0.66
43:RA0:51:ILE:CG1	66:RR0:105:MET:SD	2.82	0.66
56:RGG:65:PHE:CZ	66:RR0:29:TYR:CZ	2.83	0.66
20:LJ0:107:ILE:HD11	20:LJ0:113:TYR:HD1	1.60	0.66
37:LW0:98:ASN:ND2	55:SG0:147:PHE:N	2.43	0.66
42:S60:1066:G:C5	60:SK0:58:PHE:CD1	2.83	0.66
43:RA0:70:ASN:CA	47:RC0:240:ILE:CD1	2.68	0.66
49:RD0:94:GLN:HE21	60:RK0:19:SER:HB3	1.59	0.66
50:RDD:12:LEU:HD23	75:RP0:67:PHE:HD2	1.59	0.66
42:S60:823:A:H2'	42:S60:824:A:C8	2.31	0.66
43:SA0:63:ARG:CD	70:SV0:30:LEU:HD21	2.24	0.66
54:SFF:145:VAL:HG21	54:RFF:136:LYS:CB	2.25	0.66
42:R60:958:A:OP1	47:RC0:111:ARG:NH2	2.28	0.66
10:LE0:30:LEU:HD22	11:LEE:11:VAL:CG1	2.26	0.66
42:S60:914:U:H3	42:S60:918:A:N6	1.94	0.66
10:KE0:30:LEU:HD22	11:KEE:11:VAL:CG1	2.26	0.66
42:R60:661:A:H4'	63:RN0:62:LYS:HE2	1.78	0.66
56:SGG:65:PHE:CZ	66:SR0:29:TYR:CZ	2.83	0.66
42:R60:1230:U:O2'	44:RAA:88:SER:HB3	1.96	0.66
42:S60:958:A:OP1	47:SC0:111:ARG:NH2	2.28	0.66
42:S60:1230:U:O2'	44:SAA:88:SER:HB3	1.96	0.66
54:SFF:104:THR:CB	54:RFF:99:LYS:HD3	2.26	0.66
66:SR0:103:MET:CE	66:SR0:117:LEU:HG	2.25	0.66
67:RS0:139:VAL:O	67:RS0:139:VAL:HG12	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K50:1191:U:H2'	1:K50:1192:A:H5''	1.77	0.65
43:SA0:70:ASN:CA	47:SC0:240:ILE:CD1	2.68	0.65
56:SGG:228:LYS:HZ2	66:SR0:25:THR:HG22	1.58	0.65
45:RB0:71:ARG:HD3	64:RO0:32:THR:HG21	1.78	0.65
56:RGG:65:PHE:HZ	66:RR0:29:TYR:HH	1.40	0.65
48:SCC:55:ASP:OD2	53:SF0:195:ARG:HD3	1.96	0.65
48:RCC:55:ASP:OD2	53:RF0:195:ARG:HD3	1.96	0.65
1:L50:1018:U:O2'	13:LFF:78:ARG:HD2	1.97	0.65
1:L50:1191:U:H2'	1:L50:1192:A:H5''	1.77	0.65
45:SB0:71:ARG:HD3	64:SO0:32:THR:HG21	1.78	0.65
67:SS0:139:VAL:O	67:SS0:139:VAL:HG12	1.96	0.65
20:KJ0:107:ILE:HD11	20:KJ0:113:TYR:HD1	1.60	0.65
42:R60:1066:G:C6	60:RK0:58:PHE:CZ	2.84	0.65
42:S60:661:A:H4'	63:SN0:62:LYS:HE2	1.78	0.65
42:S60:826:U:O2	47:SC0:81:GLN:HB3	1.96	0.65
1:K50:1018:U:O2'	13:KFF:78:ARG:HD2	1.97	0.65
42:R60:910:A:H62	42:R60:922:G:H21	1.44	0.65
42:R60:982:C:H4'	66:RR0:10:ARG:HH11	1.62	0.65
42:S60:1066:G:C6	60:SK0:58:PHE:CZ	2.84	0.65
42:S60:840:C:O2'	42:S60:1182:G:OP1	2.14	0.65
42:S60:892:A:N3	75:SP0:115:TYR:OH	2.29	0.65
42:R60:840:C:O2'	42:R60:1182:G:OP1	2.14	0.65
51:SE0:137:PRO:HG3	55:SG0:222:TRP:HE1	1.63	0.64
55:SG0:169:VAL:HG11	55:SG0:176:LYS:HE2	1.79	0.64
67:SS0:24:PHE:O	67:SS0:25:ASN:OD1	2.15	0.64
47:RC0:136:TRP:HH2	59:RJ0:59:ILE:HG23	1.60	0.64
53:RF0:6:THR:HG23	65:RQ0:53:LYS:HZ3	1.60	0.64
1:K50:1691:A:C6	42:R60:1248:G:C4'	2.80	0.64
1:L50:1691:A:C6	42:S60:1248:G:C4'	2.80	0.64
56:SGG:65:PHE:HZ	66:SR0:29:TYR:HH	1.41	0.64
42:R60:826:U:O2	47:RC0:81:GLN:HB3	1.96	0.64
42:R60:1160:A:H2'	75:RP0:58:LYS:HD3	1.80	0.64
67:RS0:24:PHE:O	67:RS0:25:ASN:OD1	2.15	0.64
1:L50:2045:C:H5'	20:LJ0:102:GLY:HA3	1.77	0.64
37:LW0:99:LYS:HA	37:LW0:102:LYS:CD	2.27	0.64
42:S60:1144:G:C2'	42:S60:1145:G:H5'	2.27	0.64
49:SD0:33:ILE:HG21	69:SU0:26:LEU:HD21	1.79	0.64
54:SFF:145:VAL:HG22	54:RFF:133:SER:O	1.98	0.64
37:LW0:99:LYS:O	37:LW0:102:LYS:HG2	1.97	0.64
42:S60:982:C:H4'	66:SR0:10:ARG:HH11	1.62	0.64
1:K50:1694:U:O4	42:R60:1249:U:H4'	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:KT0:5:HIS:HA	34:KT0:9:ARG:HD2	1.80	0.64
37:KW0:99:LYS:HG2	37:KW0:102:LYS:HE2	1.80	0.64
56:RGG:105:ARG:HH22	66:RR0:37:ASP:CA	2.11	0.64
1:K50:535:A:HO2'	31:KQ0:146:ASN:HB3	1.61	0.64
37:KW0:99:LYS:O	37:KW0:102:LYS:HG2	1.98	0.64
42:R60:1144:G:C2'	42:R60:1145:G:H5'	2.27	0.64
20:LJ0:107:ILE:HD11	20:LJ0:113:TYR:CD1	2.33	0.64
37:LW0:99:LYS:HG2	37:LW0:102:LYS:NZ	2.13	0.64
54:SFF:150:LYS:HB2	42:R60:915:A:H1'	1.80	0.64
48:RCC:50:LEU:CD1	53:RF0:26:ILE:HD12	2.28	0.64
49:RD0:33:ILE:HG21	69:RU0:26:LEU:HD21	1.79	0.64
53:RF0:96:GLY:O	74:RZ0:108:LEU:HD23	1.97	0.64
42:S60:1160:A:H2'	75:SP0:58:LYS:HD3	1.80	0.63
53:SF0:42:HIS:HD1	65:SQ0:79:TYR:HH	1.45	0.63
49:RD0:94:GLN:HE21	60:RK0:19:SER:CB	2.11	0.63
48:SCC:50:LEU:HD13	53:SF0:26:ILE:HD12	1.80	0.63
20:KJ0:107:ILE:HD11	20:KJ0:113:TYR:CD1	2.33	0.63
43:RA0:70:ASN:ND2	47:RC0:240:ILE:CG1	2.61	0.63
41:MD1:52:LYS:HG3	42:S60:606:G:C2	2.32	0.63
54:SFF:104:THR:CG2	54:RFF:99:LYS:HD3	2.29	0.63
56:SGG:105:ARG:HH22	66:SR0:37:ASP:CA	2.11	0.63
41:MD2:52:LYS:HG3	42:R60:606:G:C2	2.32	0.63
43:RA0:118:GLU:CD	47:RC0:31:THR:HG1	2.02	0.63
49:SD0:94:GLN:HE21	60:SK0:19:SER:CB	2.11	0.63
42:R60:1091:A:O4'	75:RP0:146:HIS:HD2	1.81	0.63
51:RE0:137:PRO:HG3	55:RG0:222:TRP:HE1	1.63	0.63
34:LT0:5:HIS:HA	34:LT0:9:ARG:HD2	1.80	0.63
42:S60:1158:U:H4'	50:SDD:7:LYS:HE3	1.81	0.63
54:SFF:145:VAL:CG2	54:RFF:133:SER:O	2.47	0.63
66:SR0:3:GLN:HG3	66:SR0:3:GLN:O	1.99	0.63
37:KW0:99:LYS:HA	37:KW0:102:LYS:CD	2.27	0.63
43:RA0:206:ARG:NE	66:RR0:86:PRO:CG	2.62	0.63
47:SC0:49:GLY:O	70:SV0:6:ARG:HD2	1.99	0.63
42:S60:1085:G:H5''	75:SP0:140:THR:HG21	1.81	0.63
53:SF0:96:GLY:O	74:SZ0:108:LEU:HD23	1.97	0.63
37:LW0:99:LYS:HG2	37:LW0:102:LYS:HE2	1.80	0.63
67:SS0:24:PHE:CE1	67:SS0:107:ILE:HG21	2.34	0.63
1:L50:1694:U:O4	42:S60:1249:U:H4'	1.98	0.63
42:S60:910:A:H62	42:S60:922:G:H21	1.44	0.63
42:R60:892:A:N3	75:RP0:115:TYR:OH	2.29	0.63
47:RC0:49:GLY:O	70:RV0:6:ARG:HD2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S60:1034:A:H2'	42:S60:1035:C:H6	1.63	0.62
49:RD0:184:ILE:HD11	49:RD0:230:MET:SD	2.39	0.62
42:S60:1091:A:O4'	75:SP0:146:HIS:HD2	1.81	0.62
48:SCC:50:LEU:CD1	53:SF0:26:ILE:HD12	2.28	0.62
42:S60:1105:G:C8	42:S60:1105:G:H5''	2.34	0.62
43:SA0:206:ARG:NE	66:SR0:86:PRO:CG	2.62	0.62
42:R60:914:U:H3	42:R60:918:A:N6	1.94	0.62
56:RGG:65:PHE:HZ	66:RR0:29:TYR:CZ	2.17	0.62
49:SD0:184:ILE:HD11	49:SD0:230:MET:SD	2.39	0.62
54:SFF:135:ASN:HB2	54:RFF:145:VAL:HG23	1.80	0.62
42:R60:1181:U:OP1	65:RQ0:142:TYR:HE2	1.82	0.62
56:SGG:65:PHE:HZ	66:SR0:29:TYR:CZ	2.17	0.62
37:KW0:99:LYS:HG2	37:KW0:102:LYS:NZ	2.13	0.62
55:RG0:169:VAL:HG11	55:RG0:176:LYS:HE2	1.79	0.62
43:RA0:52:LYS:HB3	66:RR0:109:TYR:CZ	2.35	0.62
43:RA0:140:VAL:O	43:RA0:141:ASN:OD1	2.17	0.62
48:RCC:50:LEU:HD13	53:RF0:26:ILE:HD12	1.79	0.62
67:RS0:24:PHE:CE1	67:RS0:107:ILE:HG21	2.34	0.62
42:S60:1181:U:OP1	65:SQ0:142:TYR:HE2	1.82	0.62
53:SF0:40:LEU:CD2	65:SQ0:43:PHE:HD1	2.12	0.62
66:RR0:3:GLN:HG3	66:RR0:3:GLN:O	1.99	0.62
47:SC0:136:TRP:HH2	59:SJ0:59:ILE:HG23	1.60	0.62
42:R60:1085:G:H5''	75:RP0:140:THR:HG21	1.81	0.62
43:SA0:140:VAL:O	43:SA0:141:ASN:OD1	2.17	0.62
42:R60:1158:U:O2'	50:RDD:7:LYS:NZ	2.19	0.62
53:RF0:40:LEU:CD2	65:RQ0:43:PHE:HD1	2.12	0.61
53:RF0:40:LEU:O	53:RF0:42:HIS:N	2.33	0.61
43:SA0:51:ILE:HG13	66:SR0:105:MET:CE	2.30	0.61
2:K70:26:C:OP1	8:KD0:62:THR:HG21	2.01	0.61
43:SA0:215:TYR:O	66:SR0:84:PHE:CE2	2.51	0.61
42:S60:982:C:C3'	66:SR0:10:ARG:NH1	2.63	0.61
37:KW0:83:PHE:CE1	37:KW0:84:PRO:HD2	2.34	0.61
42:R60:982:C:C3'	66:RR0:10:ARG:NH1	2.63	0.61
43:SA0:102:ARG:HD2	43:SA0:102:ARG:N	2.16	0.61
48:SCC:58:ARG:NH1	64:SO0:101:ARG:NH2	2.49	0.61
42:R60:1158:U:H4'	50:RDD:7:LYS:HE3	1.81	0.61
55:RG0:169:VAL:HG12	55:RG0:176:LYS:HE2	1.82	0.61
42:S60:924:U:H1'	42:S60:925:A:N7	2.16	0.61
42:S60:1099:U:H1'	68:ST0:91:ASN:OD1	2.01	0.61
62:SM0:67:SER:O	62:SM0:71:LYS:HG2	2.01	0.61
42:R60:1034:A:H2'	42:R60:1035:C:H6	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA0:102:ARG:HD2	43:RA0:102:ARG:N	2.16	0.61
43:RA0:118:GLU:OE2	47:RC0:31:THR:OG1	2.18	0.61
43:RA0:4:ARG:O	70:RV0:30:LEU:CD1	2.47	0.61
42:S60:924:U:H1'	42:S60:925:A:C5	2.36	0.61
42:R60:1105:G:C8	42:R60:1105:G:H5''	2.34	0.61
43:RA0:63:ARG:CD	70:RV0:30:LEU:HD21	2.24	0.61
42:S60:554:A:N3	71:SW0:103:THR:CG2	2.62	0.61
12:LF0:115:ASN:HD21	34:LT0:133:PRO:HB2	1.66	0.60
42:S60:988:A:H4'	43:SA0:105:PRO:HG2	1.83	0.60
43:RA0:51:ILE:HG13	66:RR0:105:MET:CE	2.30	0.60
43:RA0:67:SER:OG	70:RV0:40:LEU:HD21	2.01	0.60
43:RA0:120:ARG:NH1	47:RC0:232:ILE:HG21	2.15	0.60
56:RGG:228:LYS:HZ3	66:RR0:25:THR:HG22	1.66	0.60
2:L70:26:C:OP1	8:LD0:62:THR:HG21	2.01	0.60
1:K50:2042:A:H61	1:K50:2054:U:H3	1.48	0.60
42:R60:1099:U:H1'	68:RT0:91:ASN:OD1	2.01	0.60
21:LJJ:90:ILE:O	21:LJJ:90:ILE:HG22	2.02	0.60
43:SA0:120:ARG:NH1	47:SC0:232:ILE:HG21	2.15	0.60
21:KJJ:90:ILE:O	21:KJJ:90:ILE:HG22	2.02	0.60
42:R60:1166:A:O2'	67:RS0:90:TRP:O	2.19	0.60
42:R60:924:U:H1'	42:R60:925:A:N7	2.16	0.60
43:RA0:52:LYS:CB	66:RR0:109:TYR:CE1	2.84	0.60
43:RA0:184:TYR:CE1	70:RV0:35:ARG:NH1	2.69	0.60
62:RM0:67:SER:O	62:RM0:71:LYS:HG2	2.01	0.60
37:LW0:83:PHE:CE1	37:LW0:84:PRO:HD2	2.34	0.60
43:SA0:52:LYS:CB	66:SR0:109:TYR:CE1	2.84	0.60
42:R60:924:U:H1'	42:R60:925:A:C5	2.36	0.60
43:SA0:70:ASN:ND2	47:SC0:240:ILE:CG1	2.61	0.60
43:SA0:184:TYR:CE1	70:SV0:35:ARG:NH1	2.69	0.60
42:R60:705:A:N3	42:R60:706:G:O6	2.35	0.60
43:RA0:63:ARG:NH1	70:RV0:30:LEU:HG	2.17	0.60
1:K50:733:A:O3'	12:KF0:124:LYS:NZ	2.35	0.60
62:RM0:15:LEU:HB3	62:RM0:122:PHE:HE2	1.67	0.60
42:S60:1166:A:O2'	67:SS0:90:TRP:O	2.19	0.60
42:S60:1143:A:H5'	67:SS0:36:LYS:HE3	1.84	0.60
1:L50:2042:A:H61	1:L50:2054:U:H3	1.48	0.60
42:S60:856:U:O4	67:SS0:146:SER:HB3	2.02	0.60
42:S60:999:C:H2'	42:S60:1000:C:C6	2.37	0.60
43:SA0:52:LYS:HB3	66:SR0:109:TYR:CZ	2.35	0.60
55:SG0:169:VAL:HG12	55:SG0:176:LYS:HE2	1.82	0.60
55:SG0:170:ASN:HD21	55:SG0:176:LYS:CD	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:554:A:N3	71:RW0:103:THR:CG2	2.62	0.60
42:R60:856:U:O4	67:RS0:146:SER:HB3	2.02	0.60
43:SA0:4:ARG:O	70:SV0:30:LEU:CD1	2.47	0.59
12:KF0:115:ASN:HD21	34:KT0:133:PRO:HB2	1.66	0.59
37:KW0:99:LYS:HG2	37:KW0:102:LYS:CE	2.33	0.59
42:R60:988:A:H4'	43:RA0:105:PRO:HG2	1.83	0.59
50:RDD:34:PHE:CE1	60:RK0:61:GLN:NE2	2.70	0.59
53:SF0:90:ILE:HG23	74:SZ0:58:ILE:CD1	2.32	0.59
49:RD0:94:GLN:HG2	60:RK0:20:ILE:HG23	1.84	0.59
44:SAA:69:TYR:HE2	64:SO0:90:LYS:O	1.86	0.59
42:R60:1143:A:H5'	67:RS0:36:LYS:HE3	1.84	0.59
55:RG0:170:ASN:HD21	55:RG0:176:LYS:CD	2.15	0.59
67:RS0:24:PHE:O	67:RS0:25:ASN:CG	2.41	0.59
42:R60:403:A:H2'	42:R60:404:C:C6	2.37	0.59
1:L50:733:A:O3'	12:LF0:124:LYS:NZ	2.35	0.59
42:S60:403:A:H2'	42:S60:404:C:C6	2.37	0.59
42:S60:1007:U:C4	56:SGG:84:ASP:OD2	2.56	0.59
43:SA0:18:GLN:HE22	66:SR0:96:VAL:HB	1.67	0.59
42:R60:945:G:OP1	49:RD0:211:LYS:HE3	2.03	0.59
42:R60:1007:U:C4	56:RGG:84:ASP:OD2	2.56	0.59
50:RDD:12:LEU:HD11	75:RP0:75:ILE:HD13	1.84	0.59
53:RF0:90:ILE:HG23	74:RZ0:58:ILE:CD1	2.32	0.59
37:LW0:99:LYS:HG2	37:LW0:102:LYS:CE	2.33	0.59
42:S60:405:A:H2'	42:S60:406:U:C6	2.38	0.59
42:S60:918:A:C8	42:S60:919:C:C5	2.90	0.59
50:SDD:12:LEU:HD11	75:SP0:75:ILE:HD13	1.84	0.59
54:SFF:143:TYR:HB3	54:RFF:134:GLY:HA2	1.85	0.59
42:R60:999:C:H2'	42:R60:1000:C:C6	2.37	0.59
54:RFF:96:GLN:O	54:RFF:96:GLN:HG2	2.02	0.59
42:R60:918:A:C8	42:R60:919:C:C5	2.90	0.59
42:R60:1125:G:H2'	42:R60:1126:A:O4'	2.03	0.59
47:RC0:148:VAL:CG2	71:RW0:97:PHE:HE1	2.15	0.59
42:S60:203:G:C2	51:SE0:33:THR:HG21	2.38	0.59
42:S60:705:A:N3	42:S60:706:G:O6	2.35	0.59
53:SF0:40:LEU:O	53:SF0:42:HIS:N	2.33	0.59
54:SFF:96:GLN:HG2	54:SFF:96:GLN:O	2.02	0.59
54:SFF:132:ARG:CA	42:R60:918:A:O5'	2.51	0.59
7:KCC:64:ILE:CG2	40:KZ0:39:LEU:HD11	2.33	0.59
47:RC0:148:VAL:CG2	71:RW0:97:PHE:CE1	2.86	0.59
10:LE0:30:LEU:CD2	11:LEE:11:VAL:HG13	2.33	0.59
67:SS0:24:PHE:O	67:SS0:25:ASN:CG	2.41	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:KE0:30:LEU:CD2	11:KEE:11:VAL:HG13	2.33	0.59
43:RA0:63:ARG:NH1	70:RV0:30:LEU:H	2.01	0.59
47:SC0:148:VAL:CG2	71:SW0:97:PHE:CE1	2.86	0.59
54:SFF:118:ARG:NH1	54:RFF:97:ASP:CB	2.66	0.59
37:KW0:95:ARG:HG2	37:KW0:99:LYS:HE3	1.85	0.59
51:RE0:64:ILE:CD1	73:RY0:23:LEU:HD13	2.33	0.59
49:SD0:94:GLN:HG2	60:SK0:20:ILE:HG23	1.84	0.58
10:KE0:23:ILE:CD1	11:KEE:79:ARG:HH12	2.16	0.58
12:LF0:188:LYS:HE3	31:LQ0:2:LEU:HD23	1.85	0.58
42:S60:945:G:OP1	49:SD0:211:LYS:HE3	2.03	0.58
43:SA0:102:ARG:H	43:SA0:102:ARG:CD	2.15	0.58
12:KF0:188:LYS:HE3	31:KQ0:2:LEU:HD23	1.85	0.58
42:R60:203:G:C2	51:RE0:33:THR:HG21	2.38	0.58
50:SDD:34:PHE:CE1	60:SK0:61:GLN:NE2	2.70	0.58
43:RA0:18:GLN:HE22	66:RR0:96:VAL:HB	1.67	0.58
42:S60:1125:G:H2'	42:S60:1126:A:O4'	2.03	0.58
44:RAA:69:TYR:HE2	64:RO0:90:LYS:O	1.86	0.58
53:RF0:40:LEU:HD23	65:RQ0:43:PHE:CD1	2.38	0.58
42:S60:999:C:H42	42:S60:1049:G:H1	1.52	0.58
43:SA0:63:ARG:NH1	70:SV0:30:LEU:H	2.01	0.58
43:SA0:67:SER:OG	70:SV0:40:LEU:HD21	2.01	0.58
51:SE0:64:ILE:CD1	73:SY0:23:LEU:HD13	2.33	0.58
67:SS0:55:ARG:HH22	68:ST0:32:ASN:HD22	1.51	0.58
48:RCC:58:ARG:NH1	64:RO0:101:ARG:NH2	2.49	0.58
43:SA0:206:ARG:CZ	66:SR0:86:PRO:HG2	2.34	0.58
42:R60:187:A:H62	42:R60:194:U:H3	1.51	0.58
10:LE0:23:ILE:CD1	11:LEE:79:ARG:HH12	2.16	0.58
37:LW0:95:ARG:HG2	37:LW0:99:LYS:HE3	1.85	0.58
42:S60:1144:G:H2'	42:S60:1145:G:H5'	1.84	0.58
42:R60:1144:G:H2'	42:R60:1145:G:H5'	1.84	0.58
43:RA0:102:ARG:H	43:RA0:102:ARG:CD	2.15	0.58
1:L50:2596:G:O2'	5:LB0:173:PRO:HG2	2.04	0.58
43:SA0:51:ILE:HD12	66:SR0:105:MET:CG	2.32	0.58
42:R60:405:A:H2'	42:R60:406:U:C6	2.38	0.58
49:RD0:238:PRO:CA	66:RR0:19:ARG:NH1	2.63	0.58
56:RGG:228:LYS:HZ2	66:RR0:25:THR:HG22	1.68	0.58
43:SA0:118:GLU:OE2	47:SC0:31:THR:OG1	2.18	0.58
50:RDD:8:TYR:CZ	75:RP0:72:ARG:CD	2.84	0.58
54:SFF:147:ILE:CD1	54:RFF:147:ILE:HD11	2.31	0.58
37:KW0:99:LYS:CG	37:KW0:102:LYS:HE2	2.34	0.58
42:R60:1107:U:H5''	68:RT0:43:GLU:HG2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:197:ARG:HB3	66:SR0:91:LEU:CB	2.34	0.57
54:SFF:145:VAL:HG21	54:RFF:136:LYS:H	1.69	0.57
37:LW0:83:PHE:CD1	37:LW0:84:PRO:CD	2.81	0.57
42:S60:1107:U:H5''	68:ST0:43:GLU:HG2	1.86	0.57
43:SA0:51:ILE:N	66:SR0:105:MET:SD	2.77	0.57
53:SF0:40:LEU:HD23	65:SQ0:43:PHE:CD1	2.38	0.57
37:KW0:99:LYS:HA	37:KW0:102:LYS:HG2	1.85	0.57
43:RA0:206:ARG:CZ	66:RR0:86:PRO:HG2	2.34	0.57
37:LW0:99:LYS:HA	37:LW0:102:LYS:HG2	1.85	0.57
47:SC0:148:VAL:CG2	71:SW0:97:PHE:HE1	2.15	0.57
43:RA0:52:LYS:CD	66:RR0:109:TYR:CE1	2.87	0.57
7:LCC:64:ILE:CG2	40:LZ0:39:LEU:HD11	2.33	0.57
43:RA0:51:ILE:N	66:RR0:105:MET:SD	2.77	0.57
43:SA0:52:LYS:CD	66:SR0:109:TYR:CE1	2.87	0.57
43:SA0:120:ARG:NH1	47:SC0:232:ILE:HD13	2.19	0.57
62:SM0:15:LEU:HB3	62:SM0:122:PHE:HE2	1.67	0.57
37:KW0:98:ASN:HD22	55:RG0:147:PHE:CA	2.15	0.57
42:R60:999:C:H42	42:R60:1049:G:H1	1.52	0.57
42:R60:1091:A:O4'	75:RP0:146:HIS:CD2	2.57	0.57
43:SA0:215:TYR:CA	66:SR0:84:PHE:CE2	2.87	0.57
1:K50:1691:A:C6	42:R60:1248:G:C1'	2.87	0.57
43:RA0:66:CYS:HB2	70:RV0:28:VAL:HG21	1.85	0.57
43:RA0:197:ARG:HB3	66:RR0:91:LEU:CB	2.34	0.57
43:RA0:206:ARG:CD	66:RR0:86:PRO:HG2	2.35	0.57
53:RF0:90:ILE:HG23	74:RZ0:58:ILE:HD13	1.86	0.57
43:SA0:206:ARG:CD	66:SR0:86:PRO:HG2	2.35	0.57
37:LW0:99:LYS:CG	37:LW0:102:LYS:HE2	2.34	0.57
43:SA0:63:ARG:CG	70:SV0:30:LEU:CD2	2.67	0.57
51:SE0:152:PRO:HD2	55:SG0:219:TYR:CE1	2.40	0.57
1:K50:2596:G:O2'	5:KB0:173:PRO:HG2	2.04	0.57
42:R60:1160:A:H5'	75:RP0:133:ARG:NH2	2.20	0.57
42:R60:1290:G:H5''	42:R60:1290:G:H8	1.70	0.57
43:RA0:120:ARG:NH1	47:RC0:232:ILE:HD13	2.19	0.57
43:RA0:215:TYR:CA	66:RR0:84:PHE:CE2	2.87	0.57
43:SA0:63:ARG:NH1	70:SV0:30:LEU:HG	2.17	0.57
49:SD0:237:LEU:O	66:SR0:19:ARG:CZ	2.53	0.57
42:R60:923:A:H5'	42:R60:924:U:C4	2.40	0.56
67:RS0:55:ARG:HH22	68:RT0:32:ASN:HD22	1.51	0.56
1:L50:796:C:H5'	34:LT0:131:ARG:HE	1.70	0.56
42:S60:187:A:H62	42:S60:194:U:H3	1.51	0.56
42:S60:1007:U:O4	56:SGG:84:ASP:OD2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:70:ASN:HB2	47:SC0:240:ILE:HG13	1.75	0.56
47:SC0:230:ASN:HB2	70:SV0:24:GLN:NE2	2.20	0.56
42:R60:864:A:N7	75:RP0:118:ARG:NH2	2.53	0.56
1:L50:1405:G:H2'	1:L50:1406:G:C8	2.40	0.56
1:L50:1691:A:C6	42:S60:1248:G:C1'	2.87	0.56
37:LW0:98:ASN:HD22	55:SG0:146:GLY:C	2.08	0.56
37:LW0:98:ASN:HD22	55:SG0:147:PHE:CA	2.15	0.56
42:S60:864:A:N7	75:SP0:118:ARG:NH2	2.53	0.56
42:S60:1230:U:H4'	44:SAA:88:SER:HB3	1.88	0.56
42:S60:1290:G:H5''	42:S60:1290:G:H8	1.70	0.56
43:SA0:66:CYS:HB2	70:SV0:28:VAL:HG21	1.86	0.56
20:LJ0:82:LYS:HB2	75:SP0:30:PHE:HE2	1.65	0.56
42:S60:1066:G:C6	60:SK0:58:PHE:CE1	2.93	0.56
4:KAA:70:THR:HG21	19:KII:6:LEU:HG	1.88	0.56
42:R60:1230:U:H4'	44:RAA:88:SER:HB3	1.88	0.56
42:S60:1089:G:O4'	75:SP0:141:ARG:HD3	2.06	0.56
42:S60:1091:A:O4'	75:SP0:146:HIS:CD2	2.57	0.56
53:SF0:90:ILE:HG23	74:SZ0:58:ILE:HD13	1.86	0.56
2:K70:60:A:H5'	8:KD0:273:LYS:HG2	1.88	0.56
42:R60:1066:G:C6	60:RK0:58:PHE:CE1	2.93	0.56
42:S60:1160:A:H5'	75:SP0:133:ARG:NH2	2.20	0.56
53:SF0:118:ARG:HD2	53:SF0:125:MET:CB	2.34	0.56
37:KW0:98:ASN:HD22	55:RG0:146:GLY:C	2.08	0.56
42:S60:1108:C:H5''	68:ST0:44:THR:O	2.05	0.56
42:R60:856:U:O4	67:RS0:146:SER:CB	2.54	0.56
42:R60:1089:G:O4'	75:RP0:141:ARG:HD3	2.06	0.56
1:K50:1405:G:H2'	1:K50:1406:G:C8	2.40	0.56
47:RC0:230:ASN:HB2	70:RV0:24:GLN:NE2	2.20	0.56
51:RE0:152:PRO:HD2	55:RG0:219:TYR:CE1	2.40	0.56
42:S60:923:A:H5'	42:S60:924:U:C4	2.40	0.56
1:K50:2198:G:H1	1:K50:2226:U:H3	1.54	0.56
42:R60:852:A:H2'	42:R60:853:G:C8	2.41	0.56
43:RA0:51:ILE:HD12	66:RR0:105:MET:CG	2.32	0.56
42:R60:982:C:C4'	66:RR0:10:ARG:NH1	2.68	0.56
42:S60:852:A:H2'	42:S60:853:G:C8	2.41	0.55
42:S60:932:A:H2'	42:S60:933:G:C8	2.42	0.55
42:R60:171:U:H5'	42:R60:172:U:H2'	1.88	0.55
4:LAA:70:THR:HG21	19:LII:6:LEU:HG	1.88	0.55
51:SE0:54:VAL:HG22	73:SY0:23:LEU:HD11	1.88	0.55
42:R60:203:G:H21	51:RE0:33:THR:HG21	1.70	0.55
42:R60:1108:C:H5''	68:RT0:44:THR:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:1152:G:OP1	75:RP0:36:LYS:NZ	2.37	0.55
43:RA0:63:ARG:NE	70:RV0:30:LEU:CG	2.64	0.55
42:S60:203:G:H21	51:SE0:33:THR:HG21	1.70	0.55
42:S60:915:A:N3	54:RFF:150:LYS:CG	2.69	0.55
55:SG0:170:ASN:HD21	55:SG0:176:LYS:CE	2.19	0.55
41:MD2:106:TYR:CE2	41:MD2:108:GLU:HA	2.41	0.55
42:R60:1007:U:O4	56:RGG:84:ASP:OD2	2.23	0.55
42:R60:1066:G:C5	60:RK0:58:PHE:CE1	2.95	0.55
43:RA0:67:SER:HB2	70:RV0:28:VAL:HG13	1.88	0.55
49:RD0:237:LEU:O	66:RR0:19:ARG:CZ	2.53	0.55
55:RG0:170:ASN:HD21	55:RG0:176:LYS:CE	2.19	0.55
42:S60:1066:G:C5	60:SK0:58:PHE:CE1	2.95	0.55
37:KW0:83:PHE:CG	55:RG0:144:LYS:HG3	2.42	0.55
42:S60:982:C:C4'	66:SR0:10:ARG:NH1	2.68	0.55
42:S60:1152:G:OP1	75:SP0:36:LYS:NZ	2.37	0.55
42:R60:1084:G:O3'	75:RP0:99:ARG:HD3	2.06	0.55
53:RF0:153:THR:HG21	53:RF0:160:LEU:HD13	1.88	0.55
43:SA0:117:ARG:NH1	47:SC0:243:GLU:CD	2.48	0.55
37:KW0:83:PHE:CG	55:RG0:144:LYS:CG	2.90	0.55
42:R60:932:A:H2'	42:R60:933:G:C8	2.42	0.55
42:R60:958:A:H3'	42:R60:959:G:N2	2.16	0.55
37:LW0:83:PHE:CG	55:SG0:144:LYS:HG3	2.42	0.55
42:S60:1084:G:O3'	75:SP0:99:ARG:HD3	2.06	0.55
50:SDD:7:LYS:HA	75:SP0:67:PHE:O	2.07	0.55
53:SF0:153:THR:HG21	53:SF0:160:LEU:HD13	1.88	0.55
1:K50:796:C:H5'	34:KT0:131:ARG:HE	1.70	0.55
47:RC0:229:LEU:HD12	70:RV0:42:ILE:HG12	1.89	0.55
50:RDD:7:LYS:HA	75:RP0:67:PHE:O	2.07	0.55
2:L70:60:A:H5'	8:LD0:273:LYS:HG2	1.88	0.55
42:R60:1010:G:OP1	69:RU0:52:LYS:NZ	2.39	0.55
43:RA0:68:ILE:HD12	43:RA0:121:LEU:HD22	1.89	0.55
1:L50:1940:C:H2'	1:L50:1941:A:C8	2.42	0.55
41:MD1:106:TYR:CE2	41:MD1:108:GLU:HA	2.41	0.55
42:S60:856:U:O4	67:SS0:146:SER:CB	2.54	0.55
43:SA0:10:ASP:CG	66:SR0:112:ASN:HD21	2.10	0.55
43:RA0:10:ASP:CG	66:RR0:112:ASN:HD21	2.10	0.55
43:RA0:215:TYR:O	66:RR0:84:PHE:CE2	2.51	0.55
47:SC0:130:PRO:HG2	70:SV0:4:PHE:CE1	2.42	0.55
42:R60:1150:G:H2'	42:R60:1151:A:C8	2.42	0.55
1:L50:275:A:N6	6:LC0:163:ILE:CD1	2.71	0.54
42:S60:958:A:H3'	42:S60:959:G:N2	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:68:ILE:HD12	43:SA0:121:LEU:HD22	1.89	0.54
42:R60:132:C:H3'	42:R60:133:A:H8	1.72	0.54
42:R60:932:A:H3'	42:R60:933:G:H8	1.72	0.54
42:R60:1160:A:OP1	75:RP0:133:ARG:NH1	2.39	0.54
49:RD0:188:GLN:N	49:RD0:189:PRO:HD2	2.22	0.54
53:RF0:42:HIS:ND1	65:RQ0:79:TYR:OH	2.36	0.54
42:S60:1160:A:OP1	75:SP0:133:ARG:NH1	2.39	0.54
42:S60:1181:U:OP1	65:SQ0:142:TYR:CE2	2.61	0.54
51:RE0:54:VAL:HG22	73:RY0:23:LEU:HD11	1.88	0.54
42:S60:932:A:H3'	42:S60:933:G:H8	1.72	0.54
42:S60:171:U:H5'	42:S60:172:U:H2'	1.88	0.54
42:S60:823:A:H2'	42:S60:824:A:H8	1.73	0.54
42:S60:1158:U:O2'	50:SDD:7:LYS:NZ	2.19	0.54
54:SFF:98:ILE:O	54:RFF:104:THR:HG22	2.08	0.54
10:KE0:30:LEU:HD22	11:KEE:11:VAL:HG13	1.89	0.54
63:RN0:123:TYR:OH	63:RN0:141:PRO:HG2	2.07	0.54
47:SC0:229:LEU:HD12	70:SV0:42:ILE:HG12	1.89	0.54
48:SCC:44:PRO:O	53:SF0:133:SER:CB	2.55	0.54
1:K50:275:A:N6	6:KC0:163:ILE:CD1	2.71	0.54
37:KW0:83:PHE:CG	55:RG0:144:LYS:HB3	2.43	0.54
42:R60:167:G:H21	42:R60:173:A:H2	1.55	0.54
42:S60:1150:G:H2'	42:S60:1151:A:C8	2.42	0.54
43:SA0:63:ARG:NE	70:SV0:30:LEU:CG	2.64	0.54
67:SS0:24:PHE:CZ	67:SS0:107:ILE:HG12	2.42	0.54
42:S60:288:A:H5''	58:SI0:25:ARG:NH2	2.23	0.54
56:SGG:105:ARG:HH21	66:SR0:36:ILE:HG22	1.73	0.54
42:S60:982:C:C4'	66:SR0:10:ARG:HH11	2.21	0.54
49:SD0:188:GLN:N	49:SD0:189:PRO:HD2	2.22	0.54
49:SD0:237:LEU:HD21	66:SR0:40:GLU:OE2	2.08	0.54
37:KW0:83:PHE:CD1	37:KW0:84:PRO:CD	2.81	0.54
42:S60:1023:A:H5''	66:SR0:3:GLN:HG2	1.90	0.54
42:S60:1208:G:OP2	65:SQ0:127:LYS:HE3	2.07	0.54
50:RDD:34:PHE:CZ	60:RK0:61:GLN:HG2	2.43	0.54
42:S60:1056:A:H5'	47:SC0:84:ALA:HA	1.89	0.54
42:S60:1167:C:H2'	42:S60:1168:A:O4'	2.08	0.54
43:SA0:67:SER:HB2	70:SV0:28:VAL:HG13	1.88	0.54
43:SA0:197:ARG:CB	66:SR0:91:LEU:CB	2.86	0.54
50:SDD:34:PHE:CZ	60:SK0:61:GLN:HG2	2.43	0.54
42:R60:1056:A:H5'	47:RC0:84:ALA:HA	1.89	0.54
42:R60:1108:C:H4'	68:RT0:46:PRO:HA	1.90	0.54
54:SFF:150:LYS:NZ	42:R60:917:U:OP1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:823:A:H2'	42:R60:824:A:H8	1.73	0.53
67:RS0:24:PHE:CZ	67:RS0:107:ILE:HG12	2.42	0.53
1:L50:2198:G:H1	1:L50:2226:U:H3	1.54	0.53
37:LW0:83:PHE:CG	55:SG0:144:LYS:CG	2.90	0.53
42:S60:1108:C:H4'	68:ST0:46:PRO:HA	1.90	0.53
42:R60:288:A:H5''	58:RI0:25:ARG:NH2	2.23	0.53
42:R60:886:C:O2'	50:RDD:26:THR:HB	2.08	0.53
42:R60:1208:G:OP2	65:RQ0:127:LYS:HE3	2.07	0.53
50:RDD:12:LEU:HD21	75:RP0:67:PHE:CE2	2.41	0.53
42:S60:915:A:H2	54:RFF:150:LYS:HG3	1.73	0.53
42:S60:982:C:C3'	66:SR0:10:ARG:HH11	2.22	0.53
1:K50:1169:C:H1'	1:K50:1170:A:H8	1.73	0.53
43:RA0:197:ARG:CB	66:RR0:91:LEU:CB	2.86	0.53
48:RCC:44:PRO:O	53:RF0:133:SER:CB	2.55	0.53
37:LW0:83:PHE:CG	55:SG0:144:LYS:HB3	2.43	0.53
42:S60:1090:C:O2	75:SP0:146:HIS:CE1	2.62	0.53
48:SCC:43:GLY:HA3	53:SF0:133:SER:OG	2.09	0.53
12:KF0:115:ASN:ND2	34:KT0:133:PRO:HB2	2.24	0.53
42:R60:982:C:C3'	66:RR0:10:ARG:HH11	2.22	0.53
42:R60:982:C:C4'	66:RR0:10:ARG:HH11	2.21	0.53
47:RC0:130:PRO:HG2	70:RV0:4:PHE:CE1	2.42	0.53
49:RD0:237:LEU:HD21	66:RR0:40:GLU:OE2	2.08	0.53
3:LA0:89:LEU:HD13	30:LPP:83:ILE:CD1	2.39	0.53
24:LM0:70:ASP:O	24:LM0:71:ILE:HG12	2.09	0.53
42:S60:167:G:H21	42:S60:173:A:H2	1.55	0.53
1:K50:1738:G:N3	42:R60:1306:A:H2	2.06	0.53
1:K50:1940:C:H2'	1:K50:1941:A:C8	2.42	0.53
42:R60:1023:A:P	66:RR0:3:GLN:CD	2.87	0.53
42:R60:1066:G:N7	60:RK0:58:PHE:CG	2.76	0.53
49:RD0:36:ARG:NH1	69:RU0:112:GLU:CD	2.62	0.53
49:RD0:94:GLN:NE2	60:RK0:19:SER:OG	2.42	0.53
51:RE0:137:PRO:HG3	55:RG0:222:TRP:NE1	2.23	0.53
42:S60:132:C:H3'	42:S60:133:A:H8	1.72	0.53
42:S60:932:A:H3'	42:S60:933:G:C8	2.44	0.53
1:K50:1880:U:H3	1:K50:1938:A:H61	1.56	0.53
42:R60:918:A:N7	42:R60:919:C:C4	2.77	0.53
43:RA0:184:TYR:CZ	70:RV0:35:ARG:HD3	2.44	0.53
67:RS0:28:ILE:CD1	67:RS0:40:THR:HB	2.39	0.53
1:L50:401:A:N1	6:LC0:80:THR:HG22	2.24	0.53
42:S60:864:A:C8	75:SP0:118:ARG:NH2	2.77	0.53
42:R60:1055:A:O3'	47:RC0:84:ALA:HB1	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:1738:G:N3	42:S60:1306:A:H2	2.06	0.53
41:MD1:42:LEU:HG	41:MD1:73:ILE:HD11	1.91	0.53
42:S60:1066:G:N7	60:SK0:58:PHE:CG	2.76	0.53
49:SD0:36:ARG:NH1	69:SU0:112:GLU:CD	2.62	0.53
34:KT0:112:ASN:C	34:KT0:112:ASN:HD22	2.11	0.53
42:R60:1056:A:P	47:RC0:84:ALA:HB1	2.49	0.53
67:RS0:139:VAL:O	67:RS0:139:VAL:CG1	2.57	0.53
54:SFF:147:ILE:HD11	54:RFF:147:ILE:CD1	2.35	0.53
1:K50:22:U:OP2	39:KY0:11:ARG:NH1	2.39	0.53
42:R60:1181:U:OP1	65:RQ0:142:TYR:CE2	2.61	0.53
2:L70:27:A:OP2	8:LD0:62:THR:CG2	2.57	0.53
12:LF0:115:ASN:ND2	34:LT0:133:PRO:HB2	2.24	0.53
42:S60:1023:A:P	66:SR0:3:GLN:CD	2.87	0.53
67:SS0:28:ILE:CD1	67:SS0:40:THR:HB	2.39	0.53
42:R60:1035:C:H2'	42:R60:1036:A:H8	1.74	0.53
42:R60:1167:C:H2'	42:R60:1168:A:O4'	2.08	0.53
43:RA0:63:ARG:CD	70:RV0:30:LEU:HG	2.39	0.53
48:SCC:44:PRO:O	53:SF0:133:SER:HB2	2.09	0.52
10:KE0:11:ILE:HD11	11:KEE:92:LEU:HD23	1.90	0.52
37:KW0:83:PHE:CD2	55:RG0:144:LYS:HB3	2.44	0.52
42:R60:1090:C:O2	75:RP0:146:HIS:CE1	2.62	0.52
42:R60:1181:U:H4'	65:RQ0:140:LYS:O	2.08	0.52
50:SDD:8:TYR:CZ	75:SP0:72:ARG:CD	2.84	0.52
51:SE0:137:PRO:HG3	55:SG0:222:TRP:NE1	2.23	0.52
10:LE0:11:ILE:HD11	11:LEE:92:LEU:HD23	1.90	0.52
37:LW0:81:ARG:HH12	55:SG0:148:SER:HB2	1.74	0.52
37:LW0:98:ASN:ND2	55:SG0:146:GLY:C	2.63	0.52
42:S60:1056:A:P	47:SC0:84:ALA:HB1	2.49	0.52
42:S60:1181:U:H4'	65:SQ0:140:LYS:O	2.08	0.52
54:SFF:135:ASN:HB2	54:RFF:145:VAL:CG2	2.39	0.52
63:SN0:123:TYR:OH	63:SN0:141:PRO:HG2	2.07	0.52
42:R60:203:G:N2	51:RE0:33:THR:HG21	2.25	0.52
1:L50:796:C:H4'	34:LT0:131:ARG:O	2.10	0.52
37:LW0:83:PHE:CD2	55:SG0:144:LYS:HB3	2.44	0.52
42:S60:244:U:H2'	42:S60:245:A:C8	2.44	0.52
43:SA0:63:ARG:CD	70:SV0:30:LEU:HG	2.39	0.52
49:SD0:94:GLN:NE2	60:SK0:19:SER:OG	2.42	0.52
42:R60:244:U:H2'	42:R60:245:A:C8	2.44	0.52
42:R60:932:A:H3'	42:R60:933:G:C8	2.44	0.52
42:R60:1007:U:C5	56:RGG:84:ASP:OD2	2.62	0.52
43:RA0:120:ARG:CZ	47:RC0:232:ILE:HG21	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:RAA:47:ALA:CB	48:RCC:61:ARG:NE	2.61	0.52
1:L50:1169:C:H1'	1:L50:1170:A:H8	1.73	0.52
47:SC0:130:PRO:HG2	70:SV0:4:PHE:HE1	1.74	0.52
49:SD0:238:PRO:CA	66:SR0:19:ARG:NH1	2.63	0.52
1:K50:796:C:H4'	34:KT0:131:ARG:O	2.10	0.52
3:KA0:89:LEU:HD13	30:KPP:83:ILE:CD1	2.39	0.52
37:KW0:98:ASN:ND2	55:RG0:146:GLY:C	2.63	0.52
48:RCC:43:GLY:HA3	53:RF0:133:SER:OG	2.09	0.52
56:RGG:105:ARG:HH21	66:RR0:36:ILE:HG22	1.73	0.52
34:LT0:112:ASN:HD22	34:LT0:112:ASN:C	2.11	0.52
42:S60:372:A:C4	59:SJ0:2:VAL:HG21	2.45	0.52
42:S60:886:C:O2'	50:SDD:26:THR:HB	2.08	0.52
43:SA0:184:TYR:CZ	70:SV0:35:ARG:HD3	2.44	0.52
1:K50:401:A:N1	6:KC0:80:THR:HG22	2.24	0.52
1:K50:2596:G:H5'	1:K50:2597:G:H5''	1.92	0.52
51:RE0:70:ILE:HD13	51:RE0:92:ILE:HG12	1.92	0.52
53:RF0:92:GLU:HG3	74:RZ0:108:LEU:CD1	2.40	0.52
55:RG0:170:ASN:ND2	55:RG0:176:LYS:HD3	2.22	0.52
1:L50:22:U:OP2	39:LY0:11:ARG:NH1	2.39	0.52
37:LW0:99:LYS:C	37:LW0:102:LYS:HG2	2.30	0.52
67:SS0:139:VAL:O	67:SS0:139:VAL:CG1	2.57	0.52
12:KF0:69:LYS:HD3	34:KT0:141:GLU:HG2	1.91	0.52
42:R60:1023:A:H5''	66:RR0:3:GLN:HG2	1.90	0.52
67:RS0:24:PHE:CE1	67:RS0:107:ILE:CG2	2.92	0.52
42:S60:1007:U:C5	56:SGG:84:ASP:OD2	2.62	0.52
67:SS0:46:ASP:OD1	67:SS0:47:ARG:N	2.43	0.52
41:MD2:42:LEU:HG	41:MD2:73:ILE:HD11	1.91	0.52
42:S60:995:A:H2'	42:S60:996:G:O4'	2.10	0.52
43:SA0:18:GLN:HE22	66:SR0:96:VAL:CB	2.23	0.52
1:K50:290:C:O3'	39:KY0:33:PRO:HG3	2.09	0.52
42:R60:372:A:C4	59:RJ0:2:VAL:HG21	2.45	0.52
1:L50:1131:U:H3	1:L50:1135:G:H1	1.57	0.52
37:LW0:99:LYS:HA	37:LW0:102:LYS:CG	2.40	0.52
42:S60:203:G:N2	51:SE0:33:THR:HG21	2.25	0.52
1:K50:1131:U:H3	1:K50:1135:G:H1	1.57	0.52
37:KW0:99:LYS:C	37:KW0:102:LYS:HG2	2.30	0.52
43:RA0:18:GLN:HE22	66:RR0:96:VAL:CB	2.23	0.52
55:RG0:176:LYS:N	55:RG0:176:LYS:HD2	2.25	0.52
42:S60:918:A:N7	42:S60:919:C:C4	2.77	0.51
43:SA0:120:ARG:CZ	47:SC0:232:ILE:HG21	2.39	0.51
50:SDD:12:LEU:HD21	75:SP0:67:PHE:CE2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SDD:12:LEU:HD12	75:SP0:75:ILE:HG21	1.86	0.51
43:RA0:70:ASN:HB2	47:RC0:240:ILE:HG13	1.75	0.51
42:S60:1010:G:OP1	69:SU0:52:LYS:NZ	2.39	0.51
37:KW0:99:LYS:HA	37:KW0:102:LYS:CG	2.40	0.51
43:RA0:117:ARG:NH1	47:RC0:243:GLU:CD	2.48	0.51
64:RO0:27:HIS:CE1	64:RO0:36:THR:HG23	2.45	0.51
42:S60:1055:A:O3'	47:SC0:84:ALA:HB1	2.07	0.51
55:SG0:176:LYS:N	55:SG0:176:LYS:HD2	2.25	0.51
1:K50:555:G:H1'	6:KC0:71:ARG:HH11	1.75	0.51
42:R60:999:C:H2'	42:R60:1000:C:H6	1.76	0.51
50:RDD:12:LEU:HD13	75:RP0:75:ILE:CG2	2.41	0.51
1:L50:2544:U:OP1	5:LB0:375:THR:HG22	2.11	0.51
56:SGG:105:ARG:HH22	66:SR0:37:ASP:CB	2.24	0.51
1:K50:2544:U:OP1	5:KB0:375:THR:HG22	2.11	0.51
2:K70:27:A:OP2	8:KD0:62:THR:CG2	2.57	0.51
48:RCC:44:PRO:O	53:RF0:133:SER:HB2	2.09	0.51
59:RJ0:100:GLU:OE1	59:RJ0:103:LEU:HD12	2.11	0.51
73:RY0:116:ARG:NH2	73:RY0:120:LYS:HZ1	2.08	0.51
42:S60:1066:G:N7	60:SK0:58:PHE:CD1	2.79	0.51
67:SS0:24:PHE:CE1	67:SS0:107:ILE:CG2	2.92	0.51
42:R60:1066:G:N7	60:RK0:58:PHE:CD1	2.79	0.51
12:LF0:69:LYS:HD3	34:LT0:141:GLU:HG2	1.91	0.51
12:KF0:70:ILE:HG12	34:KT0:144:MET:HG3	1.92	0.51
42:R60:864:A:C8	75:RP0:118:ARG:NH2	2.77	0.51
42:S60:1315:A:C2	42:S60:1316:A:N6	2.79	0.51
53:SF0:92:GLU:HG3	74:SZ0:108:LEU:CD1	2.40	0.51
1:K50:1328:A:H62	1:K50:1367:A:H61	1.59	0.51
4:KAA:74:ASN:HD22	4:KAA:112:GLY:H	1.59	0.51
47:RC0:130:PRO:HG2	70:RV0:4:PHE:HE1	1.74	0.51
1:L50:1880:U:H3	1:L50:1938:A:H61	1.56	0.51
56:SGG:65:PHE:HZ	66:SR0:29:TYR:CE2	2.27	0.51
64:SO0:27:HIS:CE1	64:SO0:36:THR:HG23	2.45	0.51
3:KAA:88:GLU:HG2	30:KPP:87:LYS:HE2	1.93	0.51
10:KE0:23:ILE:HD11	11:KEE:79:ARG:NH1	2.21	0.51
42:R60:995:A:H2'	42:R60:996:G:O4'	2.10	0.51
49:RD0:34:LYS:HE3	69:RU0:60:PHE:HB3	1.93	0.51
1:L50:396:G:N3	1:L50:396:G:H5''	2.26	0.51
37:KW0:81:ARG:HH12	55:RG0:148:SER:HB2	1.73	0.51
43:RA0:51:ILE:HG13	66:RR0:105:MET:HE3	1.91	0.51
1:L50:290:C:O3'	39:LY0:33:PRO:HG3	2.09	0.51
1:L50:1328:A:H62	1:L50:1367:A:H61	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S60:1124:A:H2'	42:S60:1125:G:C8	2.46	0.51
43:SA0:51:ILE:CD1	66:SR0:105:MET:CE	2.89	0.51
42:R60:1149:U:C5	67:RS0:140:ARG:NH2	2.79	0.51
56:RGG:105:ARG:HH22	66:RR0:37:ASP:CB	2.24	0.51
1:L50:1601:A:H4'	3:LA0:170:LEU:O	2.11	0.50
4:LAA:74:ASN:HD22	4:LAA:112:GLY:H	1.59	0.50
41:MD1:33:ASN:ND2	64:SO0:56:TYR:CE2	2.80	0.50
51:SE0:70:ILE:HD13	51:SE0:92:ILE:HG12	1.92	0.50
1:K50:1942:U:H2'	1:K50:1943:C:C5	2.46	0.50
1:L50:555:G:H1'	6:LC0:71:ARG:HH11	1.75	0.50
42:S60:1160:A:C2'	75:SP0:58:LYS:HD3	2.41	0.50
56:SGG:65:PHE:CE2	66:SR0:29:TYR:CZ	3.00	0.50
56:SGG:65:PHE:HE2	66:SR0:29:TYR:CD2	2.29	0.50
67:SS0:10:PHE:HD1	74:SZ0:81:PHE:CD2	2.29	0.50
69:SU0:116:THR:C	69:SU0:117:LEU:HG	2.32	0.50
1:K50:396:G:N3	1:K50:396:G:H5''	2.26	0.50
42:R60:1143:A:C4	67:RS0:36:LYS:HB2	2.46	0.50
53:RF0:40:LEU:HD21	65:RQ0:43:PHE:HD1	1.76	0.50
67:RS0:46:ASP:OD1	67:RS0:47:ARG:N	2.43	0.50
42:S60:1149:U:C5	67:SS0:140:ARG:NH2	2.79	0.50
43:SA0:51:ILE:HG13	66:SR0:105:MET:HE1	1.93	0.50
42:R60:926:G:H2'	42:R60:927:G:N7	2.26	0.50
67:RS0:10:PHE:HD1	74:RZ0:81:PHE:CD2	2.29	0.50
1:L50:1942:U:H2'	1:L50:1943:C:C5	2.46	0.50
49:SD0:237:LEU:O	66:SR0:19:ARG:NH1	2.45	0.50
56:SGG:228:LYS:HZ3	66:SR0:25:THR:HG22	1.76	0.50
42:R60:1167:C:H4'	67:RS0:91:MET:O	2.12	0.50
74:RZ0:41:VAL:HG21	74:RZ0:78:LEU:HD22	1.93	0.50
1:L50:562:U:H6	1:L50:562:U:H5''	1.76	0.50
1:L50:2596:G:H5'	1:L50:2597:G:H5''	1.92	0.50
42:S60:917:U:H5'	42:S60:918:A:N3	2.27	0.50
42:S60:1143:A:C4	67:SS0:36:LYS:HB2	2.46	0.50
54:SFF:145:VAL:CG1	54:RFF:136:LYS:CB	2.80	0.50
41:MD2:33:ASN:ND2	64:RO0:56:TYR:CE2	2.80	0.50
43:RA0:51:ILE:CD1	66:RR0:105:MET:CE	2.89	0.50
53:RF0:6:THR:CG2	65:RQ0:53:LYS:NZ	2.74	0.50
53:RF0:90:ILE:O	53:RF0:94:VAL:HG23	2.12	0.50
69:RU0:116:THR:C	69:RU0:117:LEU:HG	2.32	0.50
1:L50:2473:G:OP1	16:LH0:72:LYS:HG3	2.12	0.50
12:LF0:70:ILE:HG12	34:LT0:144:MET:HG3	1.92	0.50
42:S60:966:G:H2'	42:S60:967:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K50:562:U:H6	1:K50:562:U:H5''	1.76	0.50
20:KJ0:82:LYS:HB2	75:RP0:30:PHE:HE2	1.65	0.50
42:R60:966:G:H2'	42:R60:967:A:C8	2.46	0.50
42:R60:1216:U:H2'	42:R60:1217:G:C8	2.47	0.50
42:S60:926:G:H2'	42:S60:927:G:N7	2.26	0.50
42:S60:1216:U:H2'	42:S60:1217:G:C8	2.47	0.50
45:SB0:71:ARG:HB3	64:SO0:32:THR:HG21	1.93	0.50
42:R60:1124:A:H2'	42:R60:1125:G:C8	2.46	0.50
42:R60:1315:A:C2	42:R60:1316:A:N6	2.79	0.50
42:S60:139:C:O3'	55:SG0:95:LYS:NZ	2.45	0.50
1:K50:1424:A:H5'	15:KGG:77:GLY:HA3	1.94	0.50
42:R60:834:G:H5'	44:RAA:85:ARG:HD2	1.93	0.50
42:R60:917:U:H5'	42:R60:918:A:N3	2.27	0.50
42:R60:923:A:H5'	42:R60:924:U:N3	2.27	0.50
42:R60:1160:A:C2'	75:RP0:58:LYS:HD3	2.41	0.50
53:RF0:118:ARG:HD2	53:RF0:125:MET:CB	2.34	0.50
42:S60:999:C:H2'	42:S60:1000:C:H6	1.76	0.50
42:S60:1167:C:H4'	67:SS0:91:MET:O	2.12	0.50
54:SFF:118:ARG:HH12	54:RFF:97:ASP:CB	2.24	0.50
56:SGG:121:THR:HG21	56:SGG:131:TRP:CH2	2.47	0.50
59:SJ0:100:GLU:OE1	59:SJ0:103:LEU:HD12	2.11	0.50
43:RA0:215:TYR:C	66:RR0:84:PHE:HE2	2.14	0.50
45:RB0:71:ARG:HB3	64:RO0:32:THR:HG21	1.93	0.50
42:S60:55:G:H5'	73:SY0:123:ARG:HH11	1.77	0.49
42:S60:923:A:H5'	42:S60:924:U:N3	2.27	0.49
55:SG0:170:ASN:ND2	55:SG0:176:LYS:HD3	2.22	0.49
1:K50:1601:A:H4'	3:KA0:170:LEU:O	2.11	0.49
33:KS0:14:ASP:CG	33:KS0:15:ASP:H	2.15	0.49
53:RF0:92:GLU:CG	74:RZ0:108:LEU:HD12	2.41	0.49
66:SR0:36:ILE:HD11	66:SR0:44:LYS:NZ	2.27	0.49
1:K50:2051:C:C6	20:KJ0:56:ILE:HD11	2.48	0.49
42:R60:55:G:H5'	73:RY0:123:ARG:HH11	1.77	0.49
56:RGG:65:PHE:HE2	66:RR0:29:TYR:CD2	2.29	0.49
56:RGG:121:THR:HG21	56:RGG:131:TRP:CH2	2.47	0.49
3:LA0:88:GLU:HG2	30:LPP:87:LYS:HE2	1.93	0.49
53:SF0:90:ILE:O	53:SF0:94:VAL:HG23	2.12	0.49
56:SGG:105:ARG:HH22	66:SR0:37:ASP:HB2	1.77	0.49
1:K50:1089:U:H2'	1:K50:1090:A:C8	2.47	0.49
37:LW0:99:LYS:CA	37:LW0:102:LYS:HG2	2.42	0.49
42:S60:1019:C:H2'	42:S60:1020:G:C8	2.47	0.49
43:SA0:52:LYS:HD2	66:SR0:109:TYR:CD1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SD0:34:LYS:HE3	69:SU0:60:PHE:HB3	1.93	0.49
53:SF0:92:GLU:CG	74:SZ0:108:LEU:HD12	2.41	0.49
73:SY0:116:ARG:NH2	73:SY0:120:LYS:HZ1	2.10	0.49
42:R60:236:U:O2	58:RI0:5:ARG:NH1	2.46	0.49
42:R60:832:A:H2'	42:R60:833:A:C8	2.47	0.49
42:R60:1019:C:H2'	42:R60:1020:G:C8	2.47	0.49
56:RGG:65:PHE:CE2	66:RR0:29:TYR:CZ	2.99	0.49
1:L50:1089:U:H2'	1:L50:1090:A:C8	2.47	0.49
53:SF0:6:THR:CG2	65:SQ0:53:LYS:HZ3	2.26	0.49
42:R60:1066:G:O6	60:RK0:58:PHE:CE2	2.66	0.49
49:RD0:237:LEU:O	66:RR0:19:ARG:NH1	2.45	0.49
10:LE0:23:ILE:HD11	11:LEE:79:ARG:NH1	2.21	0.49
33:LS0:14:ASP:CG	33:LS0:15:ASP:H	2.15	0.49
42:S60:834:G:H5'	44:SAA:85:ARG:HD2	1.93	0.49
53:SF0:40:LEU:HD21	65:SQ0:43:PHE:HD1	1.76	0.49
74:SZ0:41:VAL:HG21	74:SZ0:78:LEU:HD22	1.93	0.49
66:RR0:36:ILE:HD11	66:RR0:44:LYS:NZ	2.27	0.49
16:LH0:7:GLU:OE2	16:LH0:9:LYS:HE3	2.13	0.49
42:S60:918:A:OP1	54:RFF:132:ARG:CB	2.60	0.49
42:S60:1260:G:H1	42:S60:1303:U:H3	1.61	0.49
51:SE0:92:ILE:HG22	51:SE0:94:LYS:O	2.13	0.49
42:R60:139:C:O3'	55:RG0:95:LYS:NZ	2.45	0.49
42:R60:1165:C:H2'	42:R60:1166:A:C8	2.48	0.49
43:RA0:120:ARG:HE	47:RC0:232:ILE:HG22	1.76	0.49
56:RGG:105:ARG:HH22	66:RR0:37:ASP:HB2	1.77	0.49
1:L50:1424:A:H5'	15:LGG:77:GLY:HA3	1.94	0.49
45:SB0:53:THR:CG2	64:SO0:32:THR:OG1	2.58	0.49
47:SC0:230:ASN:N	70:SV0:24:GLN:NE2	2.45	0.49
42:R60:65:A:H62	42:R60:75:G:H21	1.60	0.49
45:RB0:53:THR:CG2	64:RO0:32:THR:OG1	2.58	0.49
1:L50:2051:C:C6	20:LJ0:56:ILE:HD11	2.48	0.49
42:S60:126:C:H2'	42:S60:127:A:C8	2.48	0.49
42:S60:832:A:H2'	42:S60:833:A:C8	2.47	0.49
42:S60:1083:U:O2'	75:SP0:97:ASN:ND2	2.46	0.49
47:SC0:216:PHE:HZ	71:SW0:128:TYR:HD1	1.59	0.49
53:SF0:6:THR:HG23	65:SQ0:53:LYS:HZ1	1.77	0.49
54:SFF:150:LYS:HD2	42:R60:915:A:HO2'	1.76	0.49
1:K50:1441:U:H4'	38:KX0:64:ILE:HD11	1.95	0.49
37:KW0:99:LYS:CA	37:KW0:102:LYS:HG2	2.42	0.49
1:L50:486:U:H2'	1:L50:487:A:C8	2.48	0.49
42:S60:404:C:H4'	73:SY0:37:ASN:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:215:TYR:CD1	66:SR0:84:PHE:CZ	3.01	0.49
14:LG0:17:ARG:NH1	26:LN0:32:GLN:HE22	2.10	0.48
42:S60:995:A:C2'	42:S60:996:G:H5'	2.43	0.48
45:RB0:71:ARG:HB3	64:RO0:32:THR:CG2	2.43	0.48
47:RC0:166:LYS:CE	59:RJ0:100:GLU:OE2	2.61	0.48
51:RE0:92:ILE:HG22	51:RE0:94:LYS:O	2.13	0.48
1:L50:1441:U:H4'	38:LX0:64:ILE:HD11	1.94	0.48
50:SDD:12:LEU:HD13	75:SP0:75:ILE:CG2	2.41	0.48
53:SF0:158:LYS:HA	74:SZ0:62:THR:HG21	1.95	0.48
47:RC0:229:LEU:HB2	70:RV0:42:ILE:HD11	1.94	0.48
56:RGG:105:ARG:NH2	66:RR0:36:ILE:HG22	2.28	0.48
1:L50:1643:G:H1	1:L50:1672:A:H61	1.61	0.48
42:S60:1066:G:O6	60:SK0:58:PHE:CE2	2.66	0.48
42:S60:1262:A:H3'	42:S60:1263:A:H8	1.78	0.48
44:SAA:47:ALA:CB	48:SCC:61:ARG:NE	2.61	0.48
45:SB0:71:ARG:HB3	64:SO0:32:THR:CG2	2.43	0.48
47:SC0:229:LEU:HB2	70:SV0:42:ILE:HD11	1.94	0.48
56:SGG:105:ARG:NH2	66:SR0:36:ILE:HG22	2.28	0.48
1:K50:1691:A:C2	42:R60:1317:G:N2	2.81	0.48
1:K50:2447:A:H5''	1:K50:2447:A:H8	1.78	0.48
42:R60:404:C:H4'	73:RY0:37:ASN:HA	1.95	0.48
42:R60:1091:A:C8	75:RP0:146:HIS:CD2	3.01	0.48
43:RA0:118:GLU:CD	47:RC0:31:THR:OG1	2.51	0.48
42:S60:1091:A:C8	75:SP0:146:HIS:CD2	3.01	0.48
42:S60:1209:C:H2'	42:S60:1210:G:C8	2.49	0.48
1:K50:1643:G:H1	1:K50:1672:A:H61	1.61	0.48
37:LW0:83:PHE:CG	37:LW0:84:PRO:CD	2.92	0.48
42:S60:65:A:H62	42:S60:75:G:H21	1.60	0.48
42:S60:1165:C:H2'	42:S60:1166:A:C8	2.48	0.48
1:K50:486:U:H2'	1:K50:487:A:C8	2.48	0.48
37:KW0:83:PHE:CG	37:KW0:84:PRO:CD	2.92	0.48
50:RDD:8:TYR:CE2	75:RP0:72:ARG:NE	2.82	0.48
42:S60:236:U:O2	58:SI0:5:ARG:NH1	2.46	0.48
43:SA0:215:TYR:C	66:SR0:84:PHE:HE2	2.14	0.48
14:KG0:17:ARG:NH1	26:KN0:32:GLN:HE22	2.11	0.48
42:R60:126:C:H2'	42:R60:127:A:C8	2.48	0.48
42:R60:1083:U:O2'	75:RP0:97:ASN:ND2	2.46	0.48
42:R60:1209:C:H2'	42:R60:1210:G:C8	2.49	0.48
1:L50:1691:A:C2	42:S60:1317:G:N2	2.81	0.48
41:MD1:52:LYS:HG3	42:S60:606:G:H22	1.78	0.48
43:SA0:215:TYR:CA	66:SR0:84:PHE:HE2	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SF0:6:THR:CG2	65:SQ0:53:LYS:NZ	2.74	0.48
54:SFF:132:ARG:CA	42:R60:918:A:P	3.02	0.48
1:K50:399:G:O6	6:KC0:57:ARG:NH1	2.46	0.48
16:KH0:7:GLU:OE2	16:KH0:9:LYS:HE3	2.13	0.48
42:R60:1262:A:H3'	42:R60:1263:A:H8	1.78	0.48
47:RC0:216:PHE:HZ	71:RW0:128:TYR:HD1	1.59	0.48
50:RDD:43:TYR:CE2	69:RU0:62:CYS:HB2	2.49	0.48
1:L50:399:G:O6	6:LC0:57:ARG:NH1	2.46	0.48
42:S60:237:A:C5'	58:SI0:48:VAL:HG13	2.43	0.48
42:R60:377:C:OP1	59:RJ0:150:PRO:HD2	2.13	0.48
43:RA0:52:LYS:HD2	66:RR0:109:TYR:CD1	2.47	0.48
53:RF0:158:LYS:HA	74:RZ0:62:THR:HG21	1.95	0.48
1:L50:1325:G:H22	1:L50:1370:U:H3	1.62	0.48
49:SD0:239:ILE:CA	66:SR0:19:ARG:NH1	2.77	0.48
42:S60:1035:C:H2'	42:S60:1036:A:H8	1.74	0.48
49:SD0:68:HIS:NE2	69:SU0:109:THR:O	2.47	0.48
1:K50:2109:G:H5''	1:K50:2109:G:C8	2.45	0.48
1:K50:2473:G:OP1	16:KH0:72:LYS:HG3	2.12	0.48
37:KW0:95:ARG:O	37:KW0:99:LYS:HG3	2.14	0.48
42:R60:999:C:H2'	42:R60:1000:C:O4'	2.14	0.48
1:L50:1609:G:N2	1:L50:1614:G:O2'	2.47	0.47
1:L50:2116:A:H2'	1:L50:2117:A:C8	2.49	0.47
37:LW0:95:ARG:O	37:LW0:99:LYS:HG3	2.14	0.47
42:S60:125:A:H2'	42:S60:126:C:C6	2.49	0.47
1:K50:2116:A:H2'	1:K50:2117:A:C8	2.49	0.47
42:R60:995:A:C2'	42:R60:996:G:H5'	2.43	0.47
57:RH0:121:GLY:HA3	71:RW0:41:LYS:HG3	1.96	0.47
1:L50:2108:U:H6	1:L50:2108:U:H5''	1.78	0.47
8:LD0:215:LYS:HE2	8:LD0:222:PHE:CE2	2.49	0.47
1:K50:1325:G:H22	1:K50:1370:U:H3	1.62	0.47
42:R60:1260:G:H1	42:R60:1303:U:H3	1.61	0.47
10:LE0:30:LEU:HD22	11:LEE:11:VAL:HG13	1.89	0.47
20:LJ0:8:ASN:HD22	20:LJ0:149:GLN:HE22	1.61	0.47
42:S60:916:G:H5'	42:S60:916:G:H8	1.80	0.47
42:S60:932:A:C6	42:S60:933:G:C6	3.03	0.47
43:SA0:67:SER:HG	70:SV0:40:LEU:HD22	1.77	0.47
47:SC0:166:LYS:CE	59:SJ0:100:GLU:OE2	2.61	0.47
50:SDD:43:TYR:CE2	69:SU0:62:CYS:HB2	2.49	0.47
53:SF0:96:GLY:C	74:SZ0:108:LEU:HD21	2.34	0.47
1:K50:2108:U:H6	1:K50:2108:U:H5''	1.78	0.47
3:KA0:238:LYS:HD3	42:R60:714:U:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:KH0:63:GLU:OE2	27:KO0:131:ILE:HG21	2.13	0.47
37:KW0:83:PHE:HB2	55:RG0:144:LYS:HG3	1.97	0.47
42:R60:1160:A:P	75:RP0:62:SER:HG	2.36	0.47
42:R60:1168:A:H3'	42:R60:1169:G:H8	1.80	0.47
1:L50:2060:A:H2'	1:L50:2060:A:N3	2.29	0.47
42:S60:349:A:OP1	51:SE0:57:ASN:ND2	2.48	0.47
42:S60:910:A:H62	42:S60:922:G:N2	2.11	0.47
42:S60:967:A:H8	42:S60:967:A:O5'	1.97	0.47
42:S60:1140:G:H5'	42:S60:1143:A:N7	2.29	0.47
43:SA0:50:ASP:OD1	66:SR0:109:TYR:OH	2.33	0.47
67:SS0:112:GLU:O	67:SS0:116:ARG:HG2	2.15	0.47
1:K50:1609:G:N2	1:K50:1614:G:O2'	2.47	0.47
1:K50:1869:A:H5'	26:KN0:24:ARG:HD2	1.97	0.47
42:R60:466:C:H4'	72:RX0:100:GLU:HG2	1.97	0.47
42:R60:911:G:OP2	42:R60:911:G:H8	1.97	0.47
42:R60:970:U:H6	42:R60:970:U:H5''	1.80	0.47
42:R60:1140:G:H5'	42:R60:1143:A:N7	2.29	0.47
43:RA0:215:TYR:CD1	66:RR0:84:PHE:CZ	3.01	0.47
43:RA0:215:TYR:CA	66:RR0:84:PHE:HE2	2.26	0.47
44:RAA:47:ALA:HB2	48:RCC:61:ARG:HE	1.71	0.47
53:RF0:40:LEU:HD23	65:RQ0:43:PHE:HE1	1.73	0.47
3:LA0:238:LYS:HD3	42:S60:714:U:H5'	1.96	0.47
16:LH0:63:GLU:OE2	27:LO0:131:ILE:HG21	2.13	0.47
42:S60:1151:A:C2	42:S60:1152:G:H1'	2.49	0.47
54:SFF:135:ASN:OD1	54:RFF:143:TYR:O	2.32	0.47
3:KA0:238:LYS:HZ2	42:R60:714:U:H5''	1.80	0.47
8:KD0:215:LYS:HE2	8:KD0:222:PHE:CE2	2.49	0.47
37:KW0:98:ASN:CG	55:RG0:147:PHE:HA	2.35	0.47
42:R60:125:A:H2'	42:R60:126:C:C6	2.49	0.47
42:R60:997:A:H3'	42:R60:998:U:C5	2.50	0.47
47:RC0:216:PHE:HZ	71:RW0:128:TYR:CD1	2.33	0.47
53:RF0:6:THR:CG2	65:RQ0:53:LYS:HZ3	2.27	0.47
1:L50:1869:A:H5'	26:LN0:24:ARG:HD2	1.96	0.47
1:L50:2447:A:H8	1:L50:2447:A:H5''	1.79	0.47
42:S60:958:A:OP1	47:SC0:111:ARG:CZ	2.63	0.47
42:S60:1126:A:H8	42:S60:1164:G:H21	1.61	0.47
73:SY0:116:ARG:CZ	73:SY0:120:LYS:HZ2	2.27	0.47
1:K50:1878:G:H2'	1:K50:1879:A:C8	2.50	0.47
42:R60:507:C:H2'	42:R60:508:A:C8	2.50	0.47
42:R60:1208:G:C2'	42:R60:1209:C:H5'	2.44	0.47
47:RC0:233:LEU:HD13	70:RV0:26:ASN:ND2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RF0:96:GLY:C	74:RZ0:108:LEU:HD21	2.34	0.47
63:RN0:128:TYR:HE1	63:RN0:132:LYS:HZ2	1.62	0.47
67:RS0:55:ARG:HH22	68:RT0:32:ASN:ND2	2.12	0.47
1:L50:2109:G:H5'	1:L50:2109:G:C8	2.45	0.47
42:S60:507:C:H2'	42:S60:508:A:C8	2.50	0.47
42:S60:911:G:H8	42:S60:911:G:OP2	1.97	0.47
42:S60:995:A:C8	42:S60:996:G:C8	3.03	0.47
42:S60:1085:G:C5'	75:SP0:140:THR:HG21	2.44	0.47
47:SC0:233:LEU:HD13	70:SV0:26:ASN:ND2	2.30	0.47
57:SH0:121:GLY:HA3	71:SW0:41:LYS:HG3	1.96	0.47
20:KJ0:8:ASN:HD22	20:KJ0:149:GLN:HE22	1.61	0.47
37:KW0:98:ASN:HD22	55:RG0:147:PHE:N	2.10	0.47
42:R60:1085:G:C5'	75:RP0:140:THR:HG21	2.44	0.47
42:R60:1151:A:C2	42:R60:1152:G:H1'	2.49	0.47
49:RD0:68:HIS:NE2	69:RU0:109:THR:O	2.47	0.47
50:RDD:12:LEU:HD12	75:RP0:75:ILE:HG21	1.86	0.47
67:RS0:10:PHE:CD1	74:RZ0:81:PHE:CD2	3.03	0.47
67:RS0:112:GLU:O	67:RS0:116:ARG:HG2	2.15	0.47
37:LW0:83:PHE:HB2	55:SG0:144:LYS:HG3	1.97	0.47
42:S60:705:A:C2	42:S60:706:G:N1	2.83	0.47
42:S60:997:A:H3'	42:S60:998:U:C5	2.50	0.47
42:S60:999:C:H2'	42:S60:1000:C:O4'	2.14	0.47
42:S60:1208:G:C2'	42:S60:1209:C:H5'	2.44	0.47
42:R60:237:A:C5'	58:RI0:48:VAL:HG13	2.43	0.47
42:R60:967:A:H8	42:R60:967:A:O5'	1.97	0.47
42:R60:1068:U:H5'	49:RD0:207:ILE:HD11	1.96	0.47
47:RC0:50:HIS:O	70:RV0:6:ARG:NH2	2.48	0.47
53:RF0:6:THR:HG23	65:RQ0:53:LYS:HZ1	1.75	0.47
67:RS0:20:MET:CE	67:RS0:29:ASP:OD1	2.63	0.47
42:S60:377:C:OP1	59:SJ0:150:PRO:HD2	2.13	0.47
42:S60:1168:A:H3'	42:S60:1169:G:H8	1.80	0.47
47:SC0:50:HIS:O	70:SV0:6:ARG:NH2	2.48	0.47
42:R60:63:G:H2'	42:R60:76:A:C2	2.50	0.47
42:R60:916:G:H5'	42:R60:916:G:H8	1.80	0.47
55:RG0:144:LYS:HD2	55:RG0:144:LYS:N	2.30	0.47
42:S60:1110:C:H5'	68:ST0:54:THR:HG22	1.97	0.47
50:SDD:8:TYR:CE2	75:SP0:72:ARG:NE	2.82	0.47
63:SN0:128:TYR:HE1	63:SN0:132:LYS:HZ2	1.61	0.47
42:R60:995:A:C8	42:R60:996:G:C8	3.03	0.47
43:RA0:10:ASP:CB	66:RR0:112:ASN:HD21	2.28	0.47
43:RA0:52:LYS:HB2	66:RR0:109:TYR:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:RBB:24:PHE:CZ	71:RW0:51:ILE:HG23	2.49	0.47
4:LAA:127:GLN:HE22	19:LII:7:ASN:H	1.63	0.46
42:S60:384:A:C2	59:SJ0:169:ARG:HB2	2.50	0.46
42:S60:1068:U:H5'	49:SD0:207:ILE:HD11	1.96	0.46
43:SA0:197:ARG:HD3	66:SR0:91:LEU:CB	2.46	0.46
63:SN0:66:VAL:HG23	63:SN0:67:THR:HG23	1.97	0.46
73:SY0:116:ARG:NH1	73:SY0:120:LYS:HZ2	2.13	0.46
42:R60:517:U:H5'	51:RE0:219:SER:O	2.15	0.46
42:R60:932:A:C6	42:R60:933:G:C6	3.03	0.46
42:R60:958:A:OP1	47:RC0:111:ARG:CZ	2.63	0.46
42:R60:1018:U:H4'	42:R60:1019:C:OP2	2.15	0.46
46:SBB:24:PHE:CZ	71:SW0:51:ILE:HG23	2.49	0.46
49:SD0:36:ARG:NH1	69:SU0:112:GLU:OE1	2.48	0.46
55:SG0:144:LYS:N	55:SG0:144:LYS:HD2	2.30	0.46
67:SS0:20:MET:CE	67:SS0:29:ASP:OD1	2.63	0.46
42:R60:909:G:O6	62:RM0:37:ARG:HB3	2.15	0.46
42:R60:997:A:C2	42:R60:998:U:H1'	2.50	0.46
49:RD0:36:ARG:NH1	69:RU0:112:GLU:OE1	2.48	0.46
54:RFF:128:VAL:HG21	54:RFF:141:ARG:HE	1.80	0.46
1:L50:1878:G:H2'	1:L50:1879:A:C8	2.50	0.46
3:LA0:238:LYS:HZ3	42:S60:714:U:P	2.38	0.46
10:LE0:39:ILE:HG22	13:LFF:107:ASN:ND2	2.30	0.46
43:SA0:118:GLU:CD	47:SC0:31:THR:OG1	2.51	0.46
47:SC0:216:PHE:HZ	71:SW0:128:TYR:CD1	2.33	0.46
47:SC0:233:LEU:HD13	70:SV0:26:ASN:CG	2.35	0.46
1:K50:2060:A:H2'	1:K50:2060:A:N3	2.29	0.46
42:R60:1126:A:H8	42:R60:1164:G:H21	1.61	0.46
1:L50:2140:A:O2'	1:L50:2141:U:H2'	2.15	0.46
42:S60:63:G:H2'	42:S60:76:A:C2	2.50	0.46
42:S60:86:A:H1'	51:SE0:7:LYS:HD2	1.97	0.46
42:S60:517:U:H5'	51:SE0:219:SER:O	2.15	0.46
67:SS0:55:ARG:HH22	68:ST0:32:ASN:ND2	2.13	0.46
1:K50:2140:A:O2'	1:K50:2141:U:H2'	2.15	0.46
42:R60:705:A:C2	42:R60:706:G:N1	2.83	0.46
2:L70:1:A:H61	2:L70:118:U:H3	1.63	0.46
42:S60:662:U:H1'	63:SN0:52:ASN:ND2	2.29	0.46
42:R60:396:A:H2'	42:R60:397:A:C8	2.51	0.46
42:S60:396:A:H2'	42:S60:397:A:C8	2.51	0.46
42:S60:1018:U:H4'	42:S60:1019:C:OP2	2.15	0.46
43:SA0:52:LYS:HB2	66:SR0:109:TYR:CE2	2.50	0.46
42:R60:964:G:N2	42:R60:966:G:H3'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S60:997:A:C2	42:S60:998:U:H1'	2.50	0.46
54:SFF:99:LYS:HB3	54:RFF:104:THR:HG21	1.98	0.46
67:SS0:10:PHE:CD1	74:SZ0:81:PHE:CD2	3.03	0.46
1:K50:1308:A:H61	1:K50:2434:A:H2	1.63	0.46
42:R60:86:A:H1'	51:RE0:7:LYS:HD2	1.97	0.46
42:R60:864:A:N1	75:RP0:118:ARG:HB2	2.31	0.46
47:RC0:233:LEU:HD13	70:RV0:26:ASN:CG	2.35	0.46
63:RN0:66:VAL:HG23	63:RN0:67:THR:HG23	1.97	0.46
1:L50:303:C:H2'	1:L50:304:U:C6	2.51	0.46
43:SA0:10:ASP:CB	66:SR0:112:ASN:HD21	2.28	0.46
47:SC0:50:HIS:HA	70:SV0:6:ARG:HD2	1.98	0.46
53:SF0:40:LEU:HD23	65:SQ0:43:PHE:HE1	1.73	0.46
1:K50:202:G:O2'	17:KHH:105:THR:HG22	2.16	0.46
2:K70:1:A:H61	2:K70:118:U:H3	1.63	0.46
42:R60:349:A:OP1	51:RE0:57:ASN:ND2	2.48	0.46
47:RC0:148:VAL:HG21	71:RW0:97:PHE:CE1	2.51	0.46
1:L50:202:G:O2'	17:LHH:105:THR:HG22	2.16	0.46
42:S60:970:U:H6	42:S60:970:U:H5''	1.80	0.46
1:K50:303:C:H2'	1:K50:304:U:C6	2.51	0.46
10:KE0:39:ILE:HG22	13:KFF:107:ASN:ND2	2.30	0.46
42:R60:910:A:H62	42:R60:922:G:N2	2.11	0.46
42:R60:1110:C:H5'	68:RT0:54:THR:HG22	1.97	0.46
29:LP0:30:ARG:C	29:LP0:30:ARG:HD3	2.36	0.46
37:LW0:98:ASN:CG	55:SG0:147:PHE:HA	2.35	0.46
42:S60:989:G:H5'	43:SA0:104:ILE:HG23	1.98	0.46
47:SC0:130:PRO:CB	70:SV0:4:PHE:CE1	2.98	0.46
49:SD0:34:LYS:HD3	69:SU0:62:CYS:HB3	1.98	0.46
49:SD0:184:ILE:HD12	49:SD0:215:MET:HE3	1.98	0.46
22:KL0:25:GLN:HB3	22:KL0:26:PRO:HD3	1.97	0.46
29:KP0:30:ARG:C	29:KP0:30:ARG:HD3	2.36	0.46
29:KP0:70:THR:HG22	29:KP0:72:GLN:H	1.81	0.46
42:R60:131:U:H2'	42:R60:132:C:C6	2.51	0.46
42:R60:384:A:C2	59:RJ0:169:ARG:HB2	2.51	0.46
42:S60:466:C:H4'	72:SX0:100:GLU:HG2	1.97	0.45
42:R60:864:A:C2	75:RP0:118:ARG:HB2	2.51	0.45
43:RA0:197:ARG:HD3	66:RR0:91:LEU:CB	2.45	0.45
22:LL0:25:GLN:HB3	22:LL0:26:PRO:HD3	1.97	0.45
42:S60:244:U:H2'	42:S60:245:A:H8	1.81	0.45
42:S60:1085:G:H4'	75:SP0:140:THR:CG2	2.47	0.45
42:S60:1109:A:H2'	42:S60:1110:C:C6	2.52	0.45
47:SC0:148:VAL:HG21	71:SW0:97:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:662:U:H1'	63:RN0:52:ASN:ND2	2.29	0.45
42:S60:131:U:H2'	42:S60:132:C:C6	2.51	0.45
42:S60:864:A:N1	75:SP0:118:ARG:HB2	2.31	0.45
54:SFF:128:VAL:HG21	54:SFF:141:ARG:HE	1.80	0.45
4:KAA:127:GLN:HE22	19:KII:7:ASN:H	1.63	0.45
49:RD0:239:ILE:CA	66:RR0:19:ARG:NH1	2.77	0.45
73:RY0:116:ARG:NH1	73:RY0:120:LYS:HZ2	2.15	0.45
3:LA0:238:LYS:HZ2	42:S60:714:U:H5''	1.81	0.45
37:LW0:98:ASN:HD22	55:SG0:147:PHE:N	2.10	0.45
42:S60:864:A:C4	75:SP0:118:ARG:HD3	2.51	0.45
42:S60:909:G:O6	62:SM0:37:ARG:HB3	2.15	0.45
42:R60:1085:G:OP1	75:RP0:99:ARG:NE	2.46	0.45
49:RD0:34:LYS:HD3	69:RU0:62:CYS:HB3	1.98	0.45
54:RFF:96:GLN:OE1	54:RFF:96:GLN:N	2.50	0.45
1:L50:1308:A:H61	1:L50:2434:A:H2	1.63	0.45
1:L50:2416:G:H5''	1:L50:2416:G:H8	1.82	0.45
6:LC0:322:VAL:O	12:LF0:140:ARG:NH2	2.49	0.45
29:LP0:70:THR:HG22	29:LP0:72:GLN:H	1.81	0.45
31:LQ0:21:ARG:HB3	31:LQ0:57:THR:HG21	1.98	0.45
1:K50:158:A:N6	1:K50:168:G:H1'	2.32	0.45
1:K50:2267:C:O2	1:K50:2267:C:O4'	2.33	0.45
3:KA0:238:LYS:HZ3	42:R60:714:U:P	2.39	0.45
42:R60:1194:U:H2'	42:R60:1196:U:C5	2.51	0.45
43:RA0:10:ASP:HB3	66:RR0:112:ASN:OD1	2.16	0.45
47:RC0:50:HIS:HA	70:RV0:6:ARG:HD2	1.98	0.45
47:RC0:130:PRO:CB	70:RV0:4:PHE:CE1	2.98	0.45
54:RFF:93:LYS:HB3	54:RFF:94:PRO:CD	2.42	0.45
1:L50:1032:A:H8	1:L50:1032:A:H5''	1.82	0.45
1:L50:1691:A:H62	42:S60:1248:G:H4'	1.71	0.45
42:S60:661:A:H5'	63:SN0:15:VAL:O	2.17	0.45
42:S60:864:A:C2	75:SP0:118:ARG:HB2	2.52	0.45
12:KF0:69:LYS:HG3	34:KT0:142:MET:O	2.17	0.45
42:R60:1085:G:H4'	75:RP0:140:THR:CG2	2.47	0.45
43:RA0:218:GLN:HB3	66:RR0:84:PHE:CE2	2.51	0.45
67:RS0:24:PHE:CE2	67:RS0:107:ILE:HG12	2.52	0.45
1:L50:158:A:N6	1:L50:168:G:H1'	2.32	0.45
42:S60:55:G:H5'	73:SY0:123:ARG:NH1	2.32	0.45
42:S60:1194:U:H2'	42:S60:1196:U:C5	2.51	0.45
67:SS0:24:PHE:CE2	67:SS0:107:ILE:HG12	2.52	0.45
6:KC0:322:VAL:O	12:KF0:140:ARG:NH2	2.49	0.45
51:RE0:183:LEU:HD22	51:RE0:191:CYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:RY0:116:ARG:CZ	73:RY0:120:LYS:HZ2	2.30	0.45
42:S60:478:C:O2	61:SL0:93:LYS:HE2	2.17	0.45
42:S60:964:G:N2	42:S60:966:G:H3'	2.31	0.45
1:K50:1032:A:H5''	1:K50:1032:A:H8	1.82	0.45
42:S60:899:A:O2'	60:SK0:50:SER:OG	2.18	0.45
42:S60:1082:A:H2'	42:S60:1083:U:C6	2.52	0.45
67:SS0:127:LEU:HD22	75:SP0:132:ARG:NH2	2.32	0.45
6:KC0:103:VAL:HG13	22:KL0:23:PHE:CZ	2.52	0.45
37:KW0:99:LYS:O	37:KW0:102:LYS:CG	2.64	0.45
43:RA0:50:ASP:OD1	66:RR0:109:TYR:OH	2.33	0.45
47:RC0:167:GLY:HA3	59:RJ0:103:LEU:O	2.17	0.45
67:RS0:127:LEU:HD22	75:RP0:132:ARG:NH2	2.32	0.45
6:LC0:103:VAL:HG13	22:LL0:23:PHE:CZ	2.52	0.45
43:SA0:85:LYS:NZ	66:SR0:82:GLU:OE2	2.48	0.45
48:SCC:45:ILE:HG12	53:SF0:133:SER:HB3	1.99	0.45
51:SE0:183:LEU:HD22	51:SE0:191:CYS:HB2	1.98	0.45
54:SFF:93:LYS:HB3	54:SFF:94:PRO:CD	2.42	0.45
1:K50:2416:G:H8	1:K50:2416:G:H5''	1.82	0.45
42:R60:864:A:C4	75:RP0:118:ARG:HD3	2.52	0.45
42:R60:989:G:H5'	43:RA0:104:ILE:HG23	1.98	0.45
1:L50:1885:G:H1	1:L50:1933:C:H42	1.66	0.44
6:LC0:328:ILE:HG13	12:LF0:53:ILE:HG22	1.99	0.44
42:S60:94:U:H3'	42:S60:263:A:H61	1.83	0.44
58:SI0:69:THR:HG21	61:SL0:22:TYR:CE2	2.52	0.44
71:RW0:26:ARG:O	71:RW0:26:ARG:HG2	2.18	0.44
1:L50:2267:C:O2	1:L50:2267:C:O4'	2.33	0.44
42:S60:431:G:H2'	42:S60:445:U:N3	2.32	0.44
43:SA0:10:ASP:HB3	66:SR0:112:ASN:OD1	2.16	0.44
47:SC0:148:VAL:HG21	71:SW0:97:PHE:CZ	2.53	0.44
51:SE0:175:LEU:HD22	51:SE0:222:PHE:CD1	2.52	0.44
35:KU0:39:ILE:HG23	35:KU0:48:LEU:HD21	2.00	0.44
42:R60:1109:A:H2'	42:R60:1110:C:C6	2.51	0.44
43:RA0:52:LYS:HB2	66:RR0:109:TYR:CD1	2.51	0.44
49:RD0:184:ILE:HD12	49:RD0:215:MET:HE3	2.00	0.44
64:RO0:27:HIS:HE1	64:RO0:36:THR:HG23	1.82	0.44
42:S60:1107:U:H2'	42:S60:1108:C:C6	2.53	0.44
43:SA0:218:GLN:HB3	66:SR0:84:PHE:CE2	2.51	0.44
73:SY0:116:ARG:CZ	73:SY0:120:LYS:NZ	2.80	0.44
2:K70:70:U:H3	2:K70:105:G:H1	1.65	0.44
31:KQ0:21:ARG:HB3	31:KQ0:57:THR:HG21	1.98	0.44
42:R60:478:C:O2	61:RL0:93:LYS:HE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R60:661:A:H5'	63:RN0:15:VAL:O	2.17	0.44
42:R60:1144:G:O2'	42:R60:1145:G:H5'	2.17	0.44
51:RE0:175:LEU:HD22	51:RE0:222:PHE:CD1	2.52	0.44
42:S60:662:U:H1'	63:SN0:52:ASN:HD21	1.83	0.44
42:S60:995:A:C3'	42:S60:996:G:H8	2.23	0.44
42:S60:1010:G:OP1	69:SU0:52:LYS:CE	2.65	0.44
3:KA0:238:LYS:NZ	42:R60:714:U:H5''	2.32	0.44
42:R60:171:U:H5'	42:R60:172:U:H6	1.82	0.44
42:R60:1010:G:OP1	69:RU0:52:LYS:CE	2.65	0.44
58:RI0:69:THR:HG21	61:RL0:22:TYR:CE2	2.52	0.44
1:L50:188:G:OP2	4:LAA:34:LYS:HG2	2.17	0.44
12:LF0:69:LYS:HG3	34:LT0:142:MET:O	2.17	0.44
42:S60:997:A:H3'	42:S60:998:U:C6	2.53	0.44
67:SS0:24:PHE:CE2	67:SS0:79:ILE:HG21	2.53	0.44
42:R60:55:G:H5'	73:RY0:123:ARG:NH1	2.32	0.44
42:R60:244:U:H2'	42:R60:245:A:H8	1.81	0.44
47:RC0:148:VAL:HG21	71:RW0:97:PHE:CZ	2.53	0.44
35:LU0:39:ILE:HG23	35:LU0:48:LEU:HD21	1.99	0.44
43:SA0:63:ARG:CD	70:SV0:30:LEU:CG	2.95	0.44
42:R60:1082:A:H2'	42:R60:1083:U:C6	2.52	0.44
42:R60:1121:A:H3'	42:R60:1122:A:H8	1.82	0.44
10:LE0:11:ILE:HD12	11:LEE:91:ALA:HB1	1.98	0.44
44:SAA:47:ALA:HB2	48:SCC:61:ARG:HE	1.71	0.44
34:KT0:126:PRO:HB2	34:KT0:128:LEU:CD2	2.47	0.44
73:RY0:116:ARG:CZ	73:RY0:120:LYS:NZ	2.80	0.44
1:L50:2551:C:H2'	1:L50:2552:G:O4'	2.18	0.44
2:L70:70:U:H3	2:L70:105:G:H1	1.65	0.44
42:S60:171:U:H5'	42:S60:172:U:H6	1.82	0.44
42:S60:1149:U:C5	67:SS0:140:ARG:CZ	3.00	0.44
51:SE0:54:VAL:CG2	73:SY0:23:LEU:HD11	2.47	0.44
10:KE0:11:ILE:HD12	11:KEE:91:ALA:HB1	1.99	0.44
42:R60:914:U:C5	42:R60:916:G:C5	3.06	0.44
43:RA0:33:LEU:HD13	43:RA0:150:THR:HA	2.00	0.44
43:RA0:117:ARG:CZ	47:RC0:243:GLU:OE2	2.65	0.44
47:RC0:166:LYS:O	59:RJ0:103:LEU:HB3	2.18	0.44
56:RGG:228:LYS:HZ3	66:RR0:25:THR:CG2	2.29	0.44
41:MD1:106:TYR:HE2	41:MD1:108:GLU:HA	1.83	0.44
42:S60:517:U:C5'	51:SE0:219:SER:O	2.66	0.44
64:SO0:27:HIS:HE1	64:SO0:36:THR:HG23	1.82	0.44
1:K50:188:G:OP2	4:KAA:34:LYS:HG2	2.17	0.44
1:K50:2551:C:H2'	1:K50:2552:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:MD2:106:TYR:HE2	41:MD2:108:GLU:HA	1.83	0.44
42:S60:1160:A:P	75:SP0:62:SER:HG	2.40	0.43
42:S60:1167:C:H4'	67:SS0:91:MET:C	2.38	0.43
47:SC0:148:VAL:HG22	71:SW0:94:SER:HB2	2.00	0.43
17:KHH:113:LYS:HE2	22:KL0:46:ASN:HD22	1.83	0.43
41:MD2:17:ILE:HD12	41:MD2:95:TYR:CD2	2.53	0.43
3:LA0:238:LYS:NZ	42:S60:714:U:H5''	2.32	0.43
42:S60:218:A:H4'	42:S60:219:U:H5''	2.00	0.43
42:S60:1144:G:O2'	42:S60:1145:G:H5'	2.17	0.43
69:SU0:116:THR:O	69:SU0:117:LEU:HG	2.18	0.43
42:R60:94:U:H3'	42:R60:263:A:H61	1.83	0.43
42:R60:1149:U:C5	67:RS0:140:ARG:CZ	3.00	0.43
43:RA0:63:ARG:CD	70:RV0:30:LEU:CG	2.95	0.43
49:RD0:30:ALA:HB2	69:RU0:60:PHE:CE2	2.53	0.43
42:S60:132:C:H3'	42:S60:133:A:C8	2.53	0.43
42:S60:1121:A:H3'	42:S60:1122:A:H8	1.82	0.43
42:S60:1160:A:OP1	75:SP0:62:SER:OG	2.22	0.43
43:SA0:33:LEU:HD13	43:SA0:150:THR:HA	2.00	0.43
47:SC0:167:GLY:HA3	59:SJ0:103:LEU:O	2.17	0.43
54:SFF:96:GLN:OE1	54:SFF:96:GLN:N	2.50	0.43
71:SW0:26:ARG:HG2	71:SW0:26:ARG:O	2.18	0.43
1:K50:1875:G:H2'	1:K50:1876:A:C8	2.53	0.43
42:R60:995:A:C3'	42:R60:996:G:H8	2.23	0.43
42:R60:1167:C:H4'	67:RS0:91:MET:C	2.38	0.43
51:RE0:54:VAL:CG2	73:RY0:23:LEU:HD11	2.47	0.43
69:RU0:116:THR:O	69:RU0:117:LEU:HG	2.18	0.43
41:MD1:52:LYS:CG	42:S60:606:G:N2	2.74	0.43
43:SA0:214:LEU:HD13	66:SR0:86:PRO:HG3	2.00	0.43
58:SI0:123:ASP:HB2	61:SL0:22:TYR:HE1	1.84	0.43
1:K50:32:G:H21	1:K50:377:A:H62	1.66	0.43
1:K50:1089:U:H2'	1:K50:1090:A:H8	1.84	0.43
27:K00:84:LYS:HE2	27:K00:89:HIS:CD2	2.54	0.43
42:R60:1107:U:H2'	42:R60:1108:C:C6	2.53	0.43
1:L50:32:G:H21	1:L50:377:A:H62	1.66	0.43
1:L50:2525:G:H5'	29:LP0:71:PRO:HD3	2.00	0.43
5:LB0:133:LEU:H	5:LB0:133:LEU:HG	1.69	0.43
11:LEE:133:LEU:O	11:LEE:133:LEU:HG	2.19	0.43
42:S60:50:U:H2'	42:S60:51:G:C8	2.54	0.43
42:S60:705:A:H2'	42:S60:707:A:N7	2.34	0.43
42:S60:1230:U:O3'	44:SAA:88:SER:HA	2.18	0.43
43:SA0:52:LYS:HB2	66:SR0:109:TYR:CD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KAA:144:VAL:HG21	22:KL0:163:TYR:O	2.19	0.43
41:MD2:52:LYS:CG	42:R60:606:G:N2	2.74	0.43
42:R60:218:A:H4'	42:R60:219:U:H5''	2.00	0.43
42:R60:517:U:C5'	51:RE0:219:SER:O	2.66	0.43
42:R60:1230:U:O3'	44:RAA:88:SER:HA	2.18	0.43
1:L50:597:A:H4'	63:SN0:123:TYR:CD1	2.53	0.43
14:LG0:174:PHE:CE2	14:LG0:178:ILE:HD11	2.53	0.43
34:LT0:126:PRO:HB2	34:LT0:128:LEU:CD2	2.47	0.43
42:S60:189:A:H2'	42:S60:190:A:H4'	2.01	0.43
1:K50:1885:G:H1	1:K50:1933:C:H42	1.66	0.43
42:R60:916:G:O3'	42:R60:917:U:O2	2.37	0.43
43:RA0:50:ASP:OD1	66:RR0:109:TYR:CE2	2.72	0.43
48:RCC:45:ILE:HG12	53:RF0:133:SER:HB3	1.99	0.43
62:RM0:15:LEU:HB3	62:RM0:122:PHE:CE2	2.52	0.43
12:LF0:69:LYS:HD3	34:LT0:141:GLU:CG	2.49	0.43
42:S60:914:U:C5	42:S60:916:G:C5	3.06	0.43
10:KE0:100:ILE:CD1	24:KM0:102:PHE:HB2	2.36	0.43
14:KG0:174:PHE:CE2	14:KG0:178:ILE:HD11	2.53	0.43
42:R60:431:G:H2'	42:R60:445:U:N3	2.32	0.43
42:R60:997:A:H3'	42:R60:998:U:C6	2.53	0.43
43:RA0:85:LYS:NZ	66:RR0:82:GLU:OE2	2.48	0.43
44:RAA:51:ASP:OD2	48:RCC:57:GLU:C	2.57	0.43
1:L50:21:U:H5'	1:L50:1087:G:OP1	2.19	0.43
26:LN0:14:LYS:HE2	26:LN0:120:TRP:CZ3	2.53	0.43
42:S60:502:A:O3'	71:SW0:4:LYS:NZ	2.52	0.43
42:S60:933:G:H8	42:S60:933:G:O5'	2.02	0.43
50:SDD:16:PHE:HE1	75:SP0:66:GLY:HA3	1.82	0.43
58:SI0:69:THR:HG22	61:SL0:20:ASN:OD1	2.18	0.43
1:K50:2462:A:H2'	1:K50:2463:A:C8	2.54	0.43
12:KF0:69:LYS:HD3	34:KT0:141:GLU:CG	2.49	0.43
42:R60:790:G:H5''	42:R60:790:G:H8	1.84	0.43
42:R60:1107:U:H2'	42:R60:1108:C:H6	1.84	0.43
1:L50:1698:A:H1'	42:S60:1247:C:H1'	2.01	0.43
43:SA0:43:GLU:HG2	66:SR0:120:LYS:HE2	2.01	0.43
47:SC0:149:LYS:HB3	71:SW0:93:PRO:HA	2.01	0.43
49:SD0:30:ALA:HB2	69:SU0:60:PHE:CE2	2.53	0.43
6:KC0:2:SER:O	6:KC0:3:ARG:HG2	2.19	0.43
42:R60:830:G:O3'	42:R60:831:G:H8	2.02	0.43
50:RDD:16:PHE:HE1	75:RP0:66:GLY:HA3	1.82	0.43
1:L50:88:A:H5'	21:LJJ:75:ALA:HB2	2.01	0.43
1:L50:1441:U:H4'	38:LX0:64:ILE:CD1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:1875:G:H2'	1:L50:1876:A:C8	2.53	0.43
17:LHH:113:LYS:HE2	22:LL0:46:ASN:HD22	1.83	0.43
42:S60:790:G:H5''	42:S60:790:G:H8	1.84	0.43
42:S60:1262:A:C8	42:S60:1262:A:H5''	2.54	0.43
53:SF0:42:HIS:ND1	65:SQ0:79:TYR:OH	2.36	0.43
1:K50:597:A:H4'	63:RN0:123:TYR:CD1	2.53	0.43
1:K50:1936:U:HO2'	1:K50:1937:G:H8	1.67	0.43
42:R60:1208:G:H2'	42:R60:1209:C:H5'	2.01	0.43
58:RI0:123:ASP:HB2	61:RL0:22:TYR:HE1	1.84	0.43
1:L50:1691:A:C2	42:S60:1248:G:H1'	2.55	0.42
1:L50:1936:U:HO2'	1:L50:1937:G:H8	1.66	0.42
24:LM0:71:ILE:O	24:LM0:71:ILE:HG13	2.18	0.42
27:LO0:84:LYS:HE2	27:LO0:89:HIS:CD2	2.54	0.42
37:LW0:67:HIS:HB2	42:S60:1282:A:N3	2.34	0.42
41:MD1:17:ILE:HD12	41:MD1:95:TYR:CD2	2.53	0.42
58:SI0:8:ARG:HH11	58:SI0:8:ARG:HD3	1.72	0.42
1:K50:21:U:H5'	1:K50:1087:G:OP1	2.19	0.42
1:K50:1441:U:H4'	38:KX0:64:ILE:CD1	2.49	0.42
43:RA0:10:ASP:CB	66:RR0:112:ASN:OD1	2.67	0.42
47:RC0:148:VAL:HG22	71:RW0:94:SER:HB2	2.00	0.42
42:S60:999:C:O2'	42:S60:1000:C:H5'	2.20	0.42
43:SA0:10:ASP:CB	66:SR0:112:ASN:OD1	2.67	0.42
49:SD0:34:LYS:CE	69:SU0:60:PHE:HB3	2.49	0.42
1:K50:145:A:H5''	21:KJJ:46:LYS:HD2	2.01	0.42
6:KC0:328:ILE:HG13	12:KF0:53:ILE:HG22	1.99	0.42
37:KW0:67:HIS:HB2	42:R60:1282:A:N3	2.34	0.42
42:R60:502:A:O3'	71:RW0:4:LYS:NZ	2.52	0.42
43:RA0:118:GLU:OE2	47:RC0:31:THR:CA	2.61	0.42
58:RI0:68:LYS:HE2	58:RI0:152:TYR:CD2	2.54	0.42
67:RS0:24:PHE:CE2	67:RS0:79:ILE:HG21	2.53	0.42
1:L50:145:A:H5''	21:LJJ:46:LYS:HD2	2.01	0.42
1:L50:1933:C:H2'	1:L50:1934:C:C6	2.55	0.42
1:L50:2170:A:C8	28:LOO:54:PRO:HB3	2.55	0.42
4:LAA:144:VAL:HG21	22:LL0:163:TYR:O	2.19	0.42
37:LW0:99:LYS:O	37:LW0:102:LYS:CG	2.64	0.42
54:SFF:93:LYS:CB	54:SFF:94:PRO:HD2	2.43	0.42
42:R60:50:U:H2'	42:R60:51:G:C8	2.54	0.42
42:R60:662:U:H1'	63:RN0:52:ASN:HD21	1.83	0.42
42:R60:1230:U:O3'	44:RAA:88:SER:CB	2.67	0.42
42:R60:1231:U:H4'	44:RAA:86:VAL:CG1	2.50	0.42
49:RD0:34:LYS:CE	69:RU0:60:PHE:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RI0:69:THR:HG22	61:RL0:20:ASN:OD1	2.18	0.42
1:L50:555:G:H1'	6:LC0:71:ARG:NH1	2.34	0.42
1:L50:2160:G:H5''	28:LOO:65:LYS:HD2	2.02	0.42
43:SA0:50:ASP:OD1	66:SR0:109:TYR:CE2	2.72	0.42
47:SC0:166:LYS:O	59:SJ0:103:LEU:HB3	2.18	0.42
1:K50:2525:G:H5'	29:KP0:71:PRO:HD3	2.00	0.42
26:KN0:14:LYS:HE2	26:KN0:120:TRP:CZ3	2.53	0.42
42:R60:996:G:H2'	42:R60:997:A:O4'	2.20	0.42
42:R60:1023:A:P	66:RR0:3:GLN:OE1	2.78	0.42
42:R60:1262:A:C8	42:R60:1262:A:H5''	2.54	0.42
43:RA0:70:ASN:N	47:RC0:240:ILE:CD1	2.78	0.42
43:RA0:184:TYR:CD2	70:RV0:35:ARG:HD3	2.54	0.42
43:RA0:214:LEU:HD13	66:RR0:86:PRO:HG3	2.00	0.42
56:RGG:147:ASN:HD22	56:RGG:147:ASN:N	2.17	0.42
1:L50:2462:A:H2'	1:L50:2463:A:C8	2.54	0.42
17:LHH:6:LYS:HG3	17:LHH:7:ASP:OD1	2.19	0.42
42:S60:916:G:O3'	42:S60:917:U:O2	2.37	0.42
42:S60:1033:A:H2'	42:S60:1034:A:H5'	2.00	0.42
42:S60:1208:G:H2'	42:S60:1209:C:H5'	2.01	0.42
42:S60:1231:U:H4'	44:SAA:86:VAL:CG1	2.50	0.42
43:SA0:70:ASN:N	47:SC0:240:ILE:CD1	2.78	0.42
43:SA0:184:TYR:CD2	70:SV0:35:ARG:HD3	2.54	0.42
54:SFF:98:ILE:C	54:RFF:104:THR:HG22	2.40	0.42
66:SR0:103:MET:SD	66:SR0:117:LEU:HG	2.60	0.42
5:KB0:265:ARG:NH1	27:KOO:62:SER:OG	2.53	0.42
11:KEE:133:LEU:HG	11:KEE:133:LEU:O	2.19	0.42
17:KHH:66:LEU:HD12	38:KX0:22:ILE:HD11	2.01	0.42
42:R60:189:A:H2'	42:R60:190:A:H4'	2.01	0.42
42:R60:705:A:H2'	42:R60:707:A:N7	2.34	0.42
43:RA0:215:TYR:CE1	66:RR0:84:PHE:CZ	3.08	0.42
66:RR0:103:MET:SD	66:RR0:117:LEU:HG	2.60	0.42
42:S60:926:G:H2'	42:S60:927:G:C8	2.54	0.42
43:SA0:118:GLU:OE2	47:SC0:31:THR:CA	2.61	0.42
43:SA0:120:ARG:HE	47:SC0:232:ILE:HG22	1.75	0.42
49:SD0:184:ILE:HD12	49:SD0:215:MET:CE	2.50	0.42
1:K50:1933:C:H2'	1:K50:1934:C:C6	2.55	0.42
1:K50:2160:G:H5''	28:KOO:65:LYS:HD2	2.02	0.42
31:KQ0:164:TYR:CE2	31:KQ0:177:ARG:HD2	2.55	0.42
42:R60:696:G:H1	42:R60:712:A:H2	1.68	0.42
42:R60:1199:C:OP2	50:RDD:41:ARG:NH2	2.47	0.42
46:RBB:69:LYS:HB2	46:RBB:69:LYS:HE3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC0:2:SER:O	6:LC0:3:ARG:HG2	2.19	0.42
42:S60:830:G:O3'	42:S60:831:G:H8	2.02	0.42
42:S60:967:A:H5''	42:S60:968:C:C6	2.55	0.42
43:SA0:215:TYR:CG	66:SR0:84:PHE:CE2	3.05	0.42
56:SGG:147:ASN:HD22	56:SGG:147:ASN:N	2.17	0.42
42:S60:552:G:O2'	71:SW0:105:SER:HB3	2.20	0.42
42:S60:1023:A:P	66:SR0:3:GLN:OE1	2.78	0.42
42:S60:1230:U:O3'	44:SAA:88:SER:CB	2.68	0.42
43:SA0:64:MET:HB3	70:SV0:27:MET:CG	2.28	0.42
43:SA0:215:TYR:CE1	66:SR0:84:PHE:CZ	3.08	0.42
67:SS0:127:LEU:HD22	75:SP0:132:ARG:CZ	2.50	0.42
1:K50:88:A:H5'	21:KJJ:75:ALA:HB2	2.01	0.42
1:K50:2211:A:H5''	1:K50:2212:G:N2	2.35	0.42
42:R60:1024:G:C2	42:R60:1025:G:C8	3.08	0.42
47:RC0:149:LYS:HB3	71:RW0:93:PRO:HA	2.01	0.42
1:L50:222:A:H2'	1:L50:223:A:C8	2.55	0.42
1:L50:2026:G:C2	28:LOO:5:PRO:HG2	2.55	0.42
42:S60:173:A:N7	51:SE0:131:VAL:CG1	2.82	0.42
42:S60:915:A:N3	54:RFF:150:LYS:CD	2.83	0.42
42:S60:1168:A:H3'	42:S60:1169:G:C8	2.55	0.42
1:K50:2026:G:C2	28:KOO:5:PRO:HG2	2.55	0.42
42:R60:1033:A:H2'	42:R60:1034:A:H5'	2.00	0.42
42:R60:1108:C:H5'	68:RT0:44:THR:OG1	2.20	0.42
47:RC0:230:ASN:N	70:RV0:24:GLN:NE2	2.45	0.42
31:LQ0:164:TYR:CE2	31:LQ0:177:ARG:HD2	2.55	0.42
42:S60:1024:G:C2	42:S60:1025:G:C8	3.08	0.42
43:SA0:57:LYS:NZ	70:SV0:60:TYR:CD1	2.84	0.42
44:SAA:51:ASP:OD2	48:SCC:57:GLU:C	2.57	0.42
47:SC0:228:GLU:O	70:SV0:42:ILE:HG21	2.20	0.42
49:SD0:94:GLN:NE2	60:SK0:19:SER:CB	2.81	0.42
54:SFF:99:LYS:HE2	54:SFF:102:ILE:CG1	2.40	0.42
1:K50:1325:G:H1	1:K50:1370:U:H3	1.67	0.42
1:K50:1691:A:C2	42:R60:1248:G:H1'	2.55	0.42
1:K50:1698:A:H1'	42:R60:1247:C:H1'	2.01	0.42
1:K50:2170:A:C8	28:KOO:54:PRO:HB3	2.55	0.42
1:K50:2573:U:H2'	1:K50:2574:A:C8	2.55	0.42
42:R60:156:U:H2'	42:R60:157:A:C8	2.55	0.42
42:R60:933:G:H8	42:R60:933:G:O5'	2.02	0.42
42:R60:954:G:H5'	42:R60:980:G:OP1	2.20	0.42
42:S60:924:U:H1'	42:S60:925:A:C8	2.55	0.41
1:K50:1298:A:H5'	1:K50:1299:A:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K50:2610:U:H2'	1:K50:2611:C:C6	2.55	0.41
42:R60:375:G:H5''	42:R60:375:G:H8	1.85	0.41
42:R60:899:A:O2'	60:RK0:50:SER:OG	2.18	0.41
42:R60:967:A:H5''	42:R60:968:C:C6	2.55	0.41
43:RA0:141:ASN:CA	70:RV0:23:VAL:HG23	2.48	0.41
57:RH0:53:LEU:HB3	57:RH0:54:PRO:HD3	2.02	0.41
1:L50:1325:G:H1	1:L50:1370:U:H3	1.67	0.41
1:L50:2211:A:H5''	1:L50:2212:G:N2	2.35	0.41
5:LB0:265:ARG:NH1	27:LO0:62:SER:OG	2.53	0.41
8:LD0:214:LEU:HD23	8:LD0:214:LEU:HA	1.94	0.41
42:S60:954:G:H5'	42:S60:980:G:OP1	2.20	0.41
42:S60:1107:U:H2'	42:S60:1108:C:H6	1.84	0.41
1:K50:506:G:H2'	1:K50:508:A:N7	2.36	0.41
17:KHH:6:LYS:HG3	17:KHH:7:ASP:OD1	2.19	0.41
42:R60:924:U:H1'	42:R60:925:A:C8	2.55	0.41
42:R60:926:G:H2'	42:R60:927:G:C8	2.54	0.41
42:R60:995:A:H2'	42:R60:996:G:H5'	2.02	0.41
42:R60:999:C:O2'	42:R60:1000:C:H5'	2.20	0.41
55:RG0:156:GLU:O	55:RG0:160:LYS:HG3	2.20	0.41
1:L50:1298:A:H5'	1:L50:1299:A:OP2	2.20	0.41
42:S60:864:A:C6	75:SP0:118:ARG:HB2	2.55	0.41
42:S60:996:G:H2'	42:S60:997:A:O4'	2.20	0.41
47:SC0:229:LEU:CD1	70:SV0:42:ILE:HG12	2.50	0.41
58:SI0:68:LYS:HE2	58:SI0:152:TYR:CD2	2.54	0.41
62:SM0:15:LEU:C	62:SM0:15:LEU:HD12	2.41	0.41
43:RA0:43:GLU:HG2	66:RR0:120:LYS:HE2	2.01	0.41
47:RC0:228:GLU:O	70:RV0:42:ILE:HG21	2.20	0.41
51:RE0:35:PRO:HD2	51:RE0:83:PRO:HG2	2.03	0.41
62:RM0:15:LEU:CB	62:RM0:122:PHE:HE2	2.31	0.41
1:L50:885:G:C8	1:L50:885:G:H5''	2.56	0.41
1:L50:1089:U:H2'	1:L50:1090:A:H8	1.84	0.41
37:LW0:102:LYS:HB3	55:SG0:150:ASP:HB3	2.03	0.41
42:S60:1090:C:O2	75:SP0:146:HIS:HE1	2.02	0.41
42:S60:1262:A:H61	42:S60:1301:U:H3	1.68	0.41
61:SL0:144:ILE:HD13	61:SL0:147:LYS:HE2	2.03	0.41
1:K50:1424:A:H4'	15:KGG:77:GLY:H	1.85	0.41
1:K50:2492:U:H2'	1:K50:2493:G:C8	2.55	0.41
42:R60:552:G:O2'	71:RW0:105:SER:HB3	2.20	0.41
47:RC0:130:PRO:CG	70:RV0:4:PHE:CE1	3.03	0.41
62:RM0:15:LEU:HD12	62:RM0:15:LEU:C	2.41	0.41
1:L50:1488:U:H6	1:L50:1488:U:H2'	1.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:1940:C:H2'	1:L50:1941:A:H8	1.86	0.41
42:S60:1085:G:OP1	75:SP0:99:ARG:NE	2.46	0.41
8:KD0:47:GLN:HB2	34:KT0:68:ASN:O	2.21	0.41
14:KG0:16:PRO:HG2	26:KN0:32:GLN:HE21	1.86	0.41
47:RC0:149:LYS:HB2	71:RW0:93:PRO:O	2.21	0.41
47:RC0:229:LEU:CD1	70:RV0:42:ILE:HG12	2.50	0.41
28:LOO:64:LYS:HE2	28:LOO:64:LYS:HB3	1.92	0.41
42:S60:474:A:O2'	47:SC0:193:LYS:NZ	2.48	0.41
42:S60:696:G:H1	42:S60:712:A:H2	1.68	0.41
42:S60:1054:G:H2'	42:S60:1055:A:O4'	2.21	0.41
42:S60:1199:C:OP2	50:SDD:41:ARG:NH2	2.47	0.41
50:SDD:13:GLU:OE2	75:SP0:76:LYS:NZ	2.37	0.41
1:K50:1642:G:H2'	1:K50:1643:G:C8	2.56	0.41
43:RA0:64:MET:HB3	70:RV0:27:MET:CG	2.29	0.41
1:L50:2610:U:H2'	1:L50:2611:C:C6	2.55	0.41
14:LG0:16:PRO:HG2	26:LN0:32:GLN:HE21	1.86	0.41
50:SDD:7:LYS:CA	75:SP0:67:PHE:O	2.68	0.41
53:SF0:49:THR:O	53:SF0:49:THR:HG22	2.20	0.41
73:SY0:116:ARG:NH2	73:SY0:120:LYS:NZ	2.69	0.41
1:K50:222:A:H2'	1:K50:223:A:C8	2.55	0.41
1:K50:1078:G:O2'	11:KEE:80:LYS:NZ	2.54	0.41
4:KAA:70:THR:OG1	19:KII:5:LYS:HB2	2.21	0.41
18:KI0:30:LYS:HE2	18:KI0:66:GLU:HG2	2.02	0.41
42:R60:918:A:C5	42:R60:919:C:C4	3.09	0.41
42:R60:1090:C:O2	75:RP0:146:HIS:HE1	2.02	0.41
67:RS0:127:LEU:HD22	75:RP0:132:ARG:CZ	2.50	0.41
1:L50:506:G:H2'	1:L50:508:A:N7	2.36	0.41
1:L50:1296:C:H6	1:L50:1296:C:H5''	1.85	0.41
10:LE0:59:ALA:O	10:LE0:60:SER:HB2	2.21	0.41
42:S60:999:C:C4	42:S60:1000:C:C4	3.09	0.41
42:S60:1108:C:H5'	68:ST0:44:THR:OG1	2.20	0.41
47:SC0:230:ASN:CB	70:SV0:24:GLN:NE2	2.84	0.41
57:SH0:53:LEU:HB3	57:SH0:54:PRO:HD3	2.02	0.41
1:K50:186:G:H2'	1:K50:187:A:C8	2.56	0.41
1:K50:555:G:H1'	6:KC0:71:ARG:NH1	2.34	0.41
2:K70:34:C:O2'	8:KD0:206:GLU:OE1	2.27	0.41
17:KHH:66:LEU:CD1	38:KX0:22:ILE:HD11	2.51	0.41
42:R60:173:A:N7	51:RE0:131:VAL:CG1	2.82	0.41
42:R60:864:A:C6	75:RP0:118:ARG:HB2	2.55	0.41
42:R60:1054:G:H2'	42:R60:1055:A:O4'	2.21	0.41
47:RC0:219:PRO:CB	71:RW0:66:ARG:HH21	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:885:G:H5''	1:L50:885:G:H8	1.86	0.41
1:L50:1642:G:H2'	1:L50:1643:G:C8	2.56	0.41
1:L50:2492:U:H2'	1:L50:2493:G:C8	2.55	0.41
1:L50:2573:U:H2'	1:L50:2574:A:C8	2.55	0.41
42:S60:375:G:H8	42:S60:375:G:H5''	1.85	0.41
47:SC0:149:LYS:HB2	71:SW0:93:PRO:O	2.21	0.41
51:SE0:35:PRO:HD2	51:SE0:83:PRO:HG2	2.03	0.41
1:K50:885:G:H8	1:K50:885:G:H5''	1.85	0.41
1:K50:1133:C:H4'	1:K50:1134:A:H5'	2.02	0.41
10:KE0:59:ALA:O	10:KE0:60:SER:HB2	2.21	0.41
42:R60:132:C:H3'	42:R60:133:A:C8	2.53	0.41
42:R60:999:C:C4	42:R60:1000:C:C4	3.09	0.41
42:R60:1024:G:O2'	42:R60:1025:G:H5'	2.21	0.41
43:RA0:120:ARG:HH11	47:RC0:232:ILE:HD13	1.84	0.41
49:RD0:184:ILE:HD12	49:RD0:215:MET:CE	2.50	0.41
53:RF0:49:THR:O	53:RF0:49:THR:HG22	2.20	0.41
61:RL0:144:ILE:HD13	61:RL0:147:LYS:HE2	2.03	0.41
66:RR0:103:MET:HE2	66:RR0:115:TYR:CD1	2.56	0.41
74:RZ0:58:ILE:O	74:RZ0:58:ILE:HG13	2.21	0.41
1:L50:1078:G:O2'	11:LEE:80:LYS:NZ	2.54	0.41
42:S60:156:U:H2'	42:S60:157:A:C8	2.55	0.41
42:S60:574:A:H1'	46:SBB:67:GLY:CA	2.51	0.41
42:S60:910:A:N6	42:S60:922:G:H21	2.15	0.41
42:S60:1143:A:C5	67:SS0:36:LYS:HB2	2.56	0.41
46:SBB:81:ILE:CD1	63:SN0:25:TYR:HB2	2.51	0.41
74:SZ0:58:ILE:HG13	74:SZ0:58:ILE:O	2.21	0.41
42:R60:1262:A:H61	42:R60:1301:U:H3	1.69	0.41
46:RBB:81:ILE:CD1	63:RN0:25:TYR:HB2	2.51	0.41
1:L50:186:G:H2'	1:L50:187:A:C8	2.56	0.40
1:L50:401:A:N1	6:LC0:80:THR:CG2	2.84	0.40
1:L50:763:U:H2'	1:L50:764:U:O4'	2.22	0.40
18:LI0:30:LYS:HE2	18:LI0:66:GLU:HG2	2.02	0.40
42:S60:405:A:H2'	42:S60:406:U:H6	1.84	0.40
42:S60:995:A:H2'	42:S60:996:G:H5'	2.02	0.40
43:SA0:117:ARG:CZ	47:SC0:243:GLU:OE2	2.65	0.40
47:SC0:130:PRO:CG	70:SV0:4:PHE:CE1	3.03	0.40
1:K50:1296:C:H5''	1:K50:1296:C:H6	1.85	0.40
1:K50:1738:G:N3	42:R60:1306:A:C2	2.89	0.40
6:KC0:323:GLU:HG2	6:KC0:324:ILE:N	2.36	0.40
21:KJJ:40:PRO:O	38:KX0:3:LYS:HE3	2.21	0.40
42:R60:910:A:N6	42:R60:922:G:H21	2.15	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA0:51:ILE:CG1	66:RR0:105:MET:CE	2.99	0.40
55:RG0:176:LYS:CD	55:RG0:176:LYS:N	2.84	0.40
73:RY0:116:ARG:NH2	73:RY0:120:LYS:NZ	2.69	0.40
1:L50:1133:C:H4'	1:L50:1134:A:H5'	2.02	0.40
1:L50:1424:A:H4'	15:LGG:77:GLY:H	1.85	0.40
10:LE0:17:TYR:CE1	11:LEE:79:ARG:HD3	2.56	0.40
17:LHH:66:LEU:HD12	38:LX0:22:ILE:HD11	2.01	0.40
21:LJJ:40:PRO:O	38:LX0:3:LYS:HE3	2.21	0.40
42:S60:918:A:C5	42:S60:919:C:C4	3.09	0.40
55:SG0:156:GLU:O	55:SG0:160:LYS:HG3	2.20	0.40
56:SGG:65:PHE:CZ	66:SR0:29:TYR:OH	2.62	0.40
62:SM0:60:ARG:NH1	54:RFF:100:GLN:HE22	2.19	0.40
66:SR0:103:MET:HE2	66:SR0:115:TYR:CD1	2.56	0.40
1:K50:1142:A:H4'	9:KDD:58:LYS:HE3	2.03	0.40
1:K50:1344:G:H4'	32:KR0:116:LYS:HD2	2.04	0.40
10:KE0:17:TYR:CE1	11:KEE:79:ARG:HD3	2.56	0.40
37:KW0:102:LYS:HB3	55:RG0:150:ASP:HB3	2.03	0.40
43:RA0:6:VAL:HA	43:RA0:7:PRO:HD3	1.97	0.40
49:RD0:94:GLN:NE2	60:RK0:19:SER:CB	2.81	0.40
17:LHH:66:LEU:CD1	38:LX0:22:ILE:HD11	2.51	0.40
18:LI0:41:ALA:HA	18:LI0:42:PRO:HD3	2.00	0.40
42:S60:899:A:C6	42:S60:932:A:H1'	2.57	0.40
47:SC0:166:LYS:CB	59:SJ0:100:GLU:OE2	2.69	0.40
1:K50:101:C:H2'	1:K50:102:A:C8	2.56	0.40
1:K50:885:G:H5''	1:K50:885:G:C8	2.56	0.40
1:K50:1874:U:H3	1:K50:1944:A:H61	1.69	0.40
14:KG0:131:THR:O	14:KG0:135:LYS:HG2	2.21	0.40
42:R60:1146:G:H5'	68:RT0:90:GLY:HA3	2.03	0.40
47:RC0:166:LYS:CB	59:RJ0:100:GLU:OE2	2.69	0.40
55:RG0:169:VAL:HG11	55:RG0:176:LYS:HG2	2.04	0.40
59:RJ0:55:LYS:O	59:RJ0:59:ILE:HG12	2.21	0.40
1:L50:158:A:H61	1:L50:168:G:H1'	1.86	0.40
1:L50:2473:G:H2'	1:L50:2474:A:O4'	2.21	0.40
8:LD0:47:GLN:HB2	34:LT0:68:ASN:O	2.21	0.40
22:LL0:7:LEU:HA	22:LL0:8:PRO:HD3	1.90	0.40
31:LQ0:57:THR:O	31:LQ0:57:THR:HG22	2.22	0.40
53:SF0:95:THR:CG2	53:SF0:169:ILE:HG12	2.52	0.40
1:K50:158:A:H61	1:K50:168:G:H1'	1.87	0.40
4:KAA:68:ASP:OD2	19:KII:3:ILE:HG23	2.22	0.40
29:KP0:61:PHE:CE1	29:KP0:78:THR:HG21	2.57	0.40
47:RC0:230:ASN:CB	70:RV0:24:GLN:NE2	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L50:101:C:H2'	1:L50:102:A:C8	2.56	0.40
1:L50:1322:A:H5'	15:LGG:33:GLN:NE2	2.37	0.40
4:LAA:70:THR:OG1	19:LII:5:LYS:HB2	2.21	0.40
42:S60:960:U:C4	42:S60:961:G:N7	2.89	0.40
42:S60:1146:G:H5'	68:ST0:90:GLY:HA3	2.03	0.40
55:SG0:176:LYS:CD	55:SG0:176:LYS:N	2.84	0.40
1:K50:401:A:N1	6:KC0:80:THR:CG2	2.84	0.40
1:K50:2492:U:H2'	1:K50:2493:G:H8	1.87	0.40
42:R60:132:C:O2	42:R60:132:C:H2'	2.21	0.40
42:R60:574:A:H1'	46:RBB:67:GLY:CA	2.51	0.40
42:R60:933:G:C8	42:R60:933:G:O5'	2.74	0.40
42:R60:1023:A:H5''	66:RR0:3:GLN:CG	2.52	0.40
43:RA0:184:TYR:O	70:RV0:35:ARG:CZ	2.69	0.40
56:RGG:105:ARG:HH22	66:RR0:37:ASP:N	2.20	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	
3	KA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
3	LA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
4	KAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
4	LAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
5	KB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
5	LB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
6	KC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	41	77
6	LC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	41	77
7	KCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	15	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	LCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	15	55
8	KD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
8	LD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
9	KDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
9	LDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
10	KE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
10	LE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
11	KEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
11	LEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
12	KF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
12	LF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
13	KFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
13	LFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
14	KG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
14	LG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
15	KGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	15	55
15	LGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	15	55
16	KH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
16	LH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
17	KHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
17	LHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	KI0	215/218 (99%)	213 (99%)	2 (1%)	0	100	100
18	LI0	215/218 (99%)	214 (100%)	1 (0%)	0	100	100
19	KII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
19	LII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
20	KJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
20	LJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
21	KJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
21	LJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
22	KL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	25	66
22	LL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	25	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	KLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
23	LLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
24	KM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	17	57
24	LM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	17	57
25	KMM	50/127 (39%)	50 (100%)	0	0	100	100
25	LMM	50/127 (39%)	50 (100%)	0	0	100	100
26	KN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
26	LN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
27	KO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
27	LO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
28	KOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
28	LOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
29	KP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
29	LP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
30	KPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	13	50
30	LPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	13	50
31	KQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
31	LQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
32	KR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
32	LR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
33	KS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
33	LS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
34	KT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
34	LT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
35	KU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
35	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
36	KV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
36	LV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
37	KW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	15	55
37	LW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	15	55
38	KX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
39	KY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
39	LY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
40	KZ0	116/153 (76%)	116 (100%)	0	0	100	100
40	LZ0	116/153 (76%)	116 (100%)	0	0	100	100
41	MD1	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
41	MD2	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
43	RA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
43	SA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
44	RAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
44	SAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
45	RB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
45	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
46	RBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
46	SBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
47	RC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
47	SC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
48	RCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
48	SCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
49	RD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
49	SD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
50	RDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	SDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
51	RE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
51	SE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
52	REE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
52	SEE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
53	RF0	190/195 (97%)	181 (95%)	9 (5%)	0	100	100
53	SF0	190/195 (97%)	180 (95%)	10 (5%)	0	100	100
54	RFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
54	SFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	RG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
55	SG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
56	RGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	41	77
56	SGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	41	77
57	RH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	25	66
57	SH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	25	66
58	RI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
58	SI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
59	RJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
59	SJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
60	RK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	13	50
60	SK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	13	50
61	RL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
61	SL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
62	RM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
62	SM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
63	RN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
63	SN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
64	RO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
64	SO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
65	RQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
65	SQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
66	RR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
66	SR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
67	RS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	22	63
67	SS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	22	63
68	RT0	140/143 (98%)	140 (100%)	0	0	100	100
68	ST0	140/143 (98%)	140 (100%)	0	0	100	100
69	RU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
69	SU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
70	RV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	SV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
71	RW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
71	SW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
72	RX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
72	SX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
73	RY0	134/146 (92%)	121 (90%)	11 (8%)	2 (2%)	10	46
73	SY0	134/146 (92%)	122 (91%)	10 (8%)	2 (2%)	10	46
74	RZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
74	SZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
75	RP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
75	SP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
All	All	21258/22938 (93%)	20523 (96%)	709 (3%)	26 (0%)	54	86

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LGG	78	GLY
73	SY0	134	LYS
15	KGG	78	GLY
73	RY0	134	LYS
30	LPP	18	TYR
37	LW0	81	ARG
67	SS0	24	PHE
73	SY0	37	ASN
30	KPP	18	TYR
37	KW0	81	ARG
67	RS0	24	PHE
73	RY0	37	ASN
56	SGG	61	GLY
56	RGG	61	GLY
24	LM0	48	GLY
57	SH0	107	PHE
24	KM0	48	GLY
57	RH0	107	PHE
60	SK0	71	GLY
60	RK0	71	GLY
7	LCC	64	ILE
22	LL0	8	PRO

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Mol	Chain	Res	Type
7	KCC	64	ILE
22	KL0	8	PRO
6	LC0	297	ILE
6	KC0	297	ILE

### 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	
3	KA0	202/203 (100%)	199 (98%)	3 (2%)	65	80
3	LA0	202/203 (100%)	199 (98%)	3 (2%)	65	80
4	KAA	123/123 (100%)	119 (97%)	4 (3%)	38	61
4	LAA	123/123 (100%)	119 (97%)	4 (3%)	38	61
5	KB0	328/336 (98%)	319 (97%)	9 (3%)	44	65
5	LB0	328/336 (98%)	319 (97%)	9 (3%)	44	65
6	KC0	277/278 (100%)	274 (99%)	3 (1%)	73	84
6	LC0	277/278 (100%)	274 (99%)	3 (1%)	73	84
7	KCC	87/97 (90%)	85 (98%)	2 (2%)	50	70
7	LCC	87/97 (90%)	85 (98%)	2 (2%)	50	70
8	KD0	251/261 (96%)	249 (99%)	2 (1%)	81	89
8	LD0	251/261 (96%)	249 (99%)	2 (1%)	81	89
9	KDD	99/100 (99%)	99 (100%)	0	100	100
9	LDD	99/100 (99%)	99 (100%)	0	100	100
10	KE0	153/159 (96%)	150 (98%)	3 (2%)	55	74
10	LE0	153/159 (96%)	150 (98%)	3 (2%)	55	74
11	KEE	118/122 (97%)	118 (100%)	0	100	100
11	LEE	118/122 (97%)	118 (100%)	0	100	100
12	KF0	212/216 (98%)	211 (100%)	1 (0%)	88	93
12	LF0	212/216 (98%)	211 (100%)	1 (0%)	88	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	KFF	98/98 (100%)	98 (100%)	0	100	100
13	LFF	98/98 (100%)	98 (100%)	0	100	100
14	KG0	183/190 (96%)	183 (100%)	0	100	100
14	LG0	183/190 (96%)	183 (100%)	0	100	100
15	KGG	88/90 (98%)	86 (98%)	2 (2%)	50	70
15	LGG	88/90 (98%)	86 (98%)	2 (2%)	50	70
16	KH0	165/169 (98%)	161 (98%)	4 (2%)	49	69
16	LH0	165/169 (98%)	161 (98%)	4 (2%)	49	69
17	KHH	110/110 (100%)	109 (99%)	1 (1%)	78	87
17	LHH	110/110 (100%)	109 (99%)	1 (1%)	78	87
18	KI0	188/189 (100%)	188 (100%)	0	100	100
18	LI0	188/189 (100%)	188 (100%)	0	100	100
19	KII	84/84 (100%)	82 (98%)	2 (2%)	49	69
19	LII	84/84 (100%)	82 (98%)	2 (2%)	49	69
20	KJ0	146/149 (98%)	144 (99%)	2 (1%)	67	80
20	LJ0	146/149 (98%)	144 (99%)	2 (1%)	67	80
21	KJJ	78/81 (96%)	77 (99%)	1 (1%)	69	81
21	LJJ	78/81 (96%)	77 (99%)	1 (1%)	69	81
22	KL0	148/149 (99%)	142 (96%)	6 (4%)	30	55
22	LL0	148/149 (99%)	142 (96%)	6 (4%)	30	55
23	KLL	46/47 (98%)	46 (100%)	0	100	100
23	LLL	46/47 (98%)	46 (100%)	0	100	100
24	KM0	110/110 (100%)	110 (100%)	0	100	100
24	LM0	110/110 (100%)	110 (100%)	0	100	100
25	KMM	46/112 (41%)	46 (100%)	0	100	100
25	LMM	46/112 (41%)	46 (100%)	0	100	100
26	KN0	175/176 (99%)	171 (98%)	4 (2%)	50	70
26	LN0	175/176 (99%)	171 (98%)	4 (2%)	50	70
27	KO0	178/178 (100%)	177 (99%)	1 (1%)	86	92
27	LO0	178/178 (100%)	177 (99%)	1 (1%)	86	92
28	KOO	85/89 (96%)	85 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	LOO	85/89 (96%)	85 (100%)	0	100	100
29	KP0	135/147 (92%)	132 (98%)	3 (2%)	52	71
29	LP0	135/147 (92%)	132 (98%)	3 (2%)	52	71
30	KPP	75/77 (97%)	73 (97%)	2 (3%)	44	65
30	LPP	75/77 (97%)	73 (97%)	2 (3%)	44	65
31	KQ0	165/166 (99%)	165 (100%)	0	100	100
31	LQ0	165/166 (99%)	165 (100%)	0	100	100
32	KR0	142/145 (98%)	141 (99%)	1 (1%)	84	90
32	LR0	142/145 (98%)	141 (99%)	1 (1%)	84	90
33	KS0	155/156 (99%)	152 (98%)	3 (2%)	57	75
33	LS0	155/156 (99%)	152 (98%)	3 (2%)	57	75
34	KT0	140/142 (99%)	138 (99%)	2 (1%)	67	80
34	LT0	140/142 (99%)	138 (99%)	2 (1%)	67	80
35	KU0	89/98 (91%)	88 (99%)	1 (1%)	73	84
35	LU0	89/98 (91%)	88 (99%)	1 (1%)	73	84
36	KV0	113/114 (99%)	112 (99%)	1 (1%)	78	87
36	LV0	113/114 (99%)	112 (99%)	1 (1%)	78	87
37	KW0	93/120 (78%)	89 (96%)	4 (4%)	29	53
37	LW0	93/120 (78%)	89 (96%)	4 (4%)	29	53
38	KX0	92/93 (99%)	91 (99%)	1 (1%)	73	84
38	LX0	92/93 (99%)	91 (99%)	1 (1%)	73	84
39	KY0	116/116 (100%)	114 (98%)	2 (2%)	60	78
39	LY0	116/116 (100%)	114 (98%)	2 (2%)	60	78
40	KZ0	106/141 (75%)	106 (100%)	0	100	100
40	LZ0	106/141 (75%)	106 (100%)	0	100	100
41	MD1	139/139 (100%)	139 (100%)	0	100	100
41	MD2	139/139 (100%)	139 (100%)	0	100	100
43	RA0	194/206 (94%)	191 (98%)	3 (2%)	65	80
43	SA0	194/206 (94%)	191 (98%)	3 (2%)	65	80
44	RAA	92/93 (99%)	92 (100%)	0	100	100
44	SAA	92/93 (99%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	RB0	182/203 (90%)	182 (100%)	0	100	100
45	SB0	182/203 (90%)	182 (100%)	0	100	100
46	RBB	72/73 (99%)	71 (99%)	1 (1%)	67	80
46	SBB	72/73 (99%)	71 (99%)	1 (1%)	67	80
47	RC0	187/209 (90%)	185 (99%)	2 (1%)	73	84
47	SC0	187/209 (90%)	185 (99%)	2 (1%)	73	84
48	RCC	51/54 (94%)	51 (100%)	0	100	100
48	SCC	51/54 (94%)	51 (100%)	0	100	100
49	RD0	189/215 (88%)	189 (100%)	0	100	100
49	SD0	189/215 (88%)	189 (100%)	0	100	100
50	RDD	57/57 (100%)	57 (100%)	0	100	100
50	SDD	57/57 (100%)	57 (100%)	0	100	100
51	RE0	231/251 (92%)	229 (99%)	2 (1%)	78	87
51	SE0	231/251 (92%)	229 (99%)	2 (1%)	78	87
52	REE	44/47 (94%)	44 (100%)	0	100	100
52	SEE	44/47 (94%)	44 (100%)	0	100	100
53	RF0	167/170 (98%)	163 (98%)	4 (2%)	49	69
53	SF0	167/170 (98%)	163 (98%)	4 (2%)	49	69
54	RFF	45/136 (33%)	44 (98%)	1 (2%)	52	71
54	SFF	46/136 (34%)	45 (98%)	1 (2%)	52	71
55	RG0	199/199 (100%)	195 (98%)	4 (2%)	55	74
55	SG0	199/199 (100%)	195 (98%)	4 (2%)	55	74
56	RGG	282/288 (98%)	278 (99%)	4 (1%)	67	80
56	SGG	282/288 (98%)	278 (99%)	4 (1%)	67	80
57	RH0	153/154 (99%)	153 (100%)	0	100	100
57	SH0	153/154 (99%)	153 (100%)	0	100	100
58	RI0	147/153 (96%)	147 (100%)	0	100	100
58	SI0	147/153 (96%)	147 (100%)	0	100	100
59	RJ0	152/165 (92%)	150 (99%)	2 (1%)	69	81
59	SJ0	152/165 (92%)	150 (99%)	2 (1%)	69	81
60	RK0	83/99 (84%)	82 (99%)	1 (1%)	71	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	SK0	83/99 (84%)	82 (99%)	1 (1%)	71	83
61	RL0	140/145 (97%)	139 (99%)	1 (1%)	84	90
61	SL0	140/145 (97%)	139 (99%)	1 (1%)	84	90
62	RM0	99/114 (87%)	99 (100%)	0	100	100
62	SM0	99/114 (87%)	99 (100%)	0	100	100
63	RN0	126/127 (99%)	126 (100%)	0	100	100
63	SN0	126/127 (99%)	126 (100%)	0	100	100
64	RO0	102/108 (94%)	101 (99%)	1 (1%)	76	86
64	SO0	102/108 (94%)	101 (99%)	1 (1%)	76	86
65	RQ0	120/121 (99%)	119 (99%)	1 (1%)	81	89
65	SQ0	120/121 (99%)	119 (99%)	1 (1%)	81	89
66	RR0	109/111 (98%)	108 (99%)	1 (1%)	78	87
66	SR0	109/111 (98%)	108 (99%)	1 (1%)	78	87
67	RS0	125/138 (91%)	124 (99%)	1 (1%)	81	89
67	SS0	125/138 (91%)	124 (99%)	1 (1%)	81	89
68	RT0	129/130 (99%)	127 (98%)	2 (2%)	62	79
68	ST0	129/130 (99%)	127 (98%)	2 (2%)	62	79
69	RU0	92/110 (84%)	92 (100%)	0	100	100
69	SU0	92/110 (84%)	92 (100%)	0	100	100
70	RV0	61/63 (97%)	61 (100%)	0	100	100
70	SV0	61/63 (97%)	61 (100%)	0	100	100
71	RW0	111/111 (100%)	110 (99%)	1 (1%)	78	87
71	SW0	111/111 (100%)	110 (99%)	1 (1%)	78	87
72	RX0	115/116 (99%)	115 (100%)	0	100	100
72	SX0	115/116 (99%)	115 (100%)	0	100	100
73	RY0	126/136 (93%)	121 (96%)	5 (4%)	31	55
73	SY0	126/136 (93%)	121 (96%)	5 (4%)	31	55
74	RZ0	73/118 (62%)	73 (100%)	0	100	100
74	SZ0	73/118 (62%)	73 (100%)	0	100	100
75	RP0	107/144 (74%)	106 (99%)	1 (1%)	78	87
75	SP0	107/144 (74%)	106 (99%)	1 (1%)	78	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	19001/20268 (94%)	18785 (99%)	216 (1%)	74	84

All (216) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	LA0	44	GLU
3	LA0	189	ARG
3	LA0	222	VAL
4	LAA	22	VAL
4	LAA	26	ARG
4	LAA	39	LYS
4	LAA	54	ARG
5	LB0	10	ARG
5	LB0	23	LYS
5	LB0	86	VAL
5	LB0	122	ARG
5	LB0	132	LYS
5	LB0	133	LEU
5	LB0	134	MET
5	LB0	135	PHE
5	LB0	336	ARG
6	LC0	103	VAL
6	LC0	207	THR
6	LC0	328	ILE
7	LCC	64	ILE
7	LCC	76	SER
8	LD0	85	THR
8	LD0	285	GLN
10	LE0	15	LYS
10	LE0	17	TYR
10	LE0	30	LEU
12	LF0	42	ARG
15	LGG	32	PHE
15	LGG	101	MET
16	LH0	34	VAL
16	LH0	62	GLN
16	LH0	64	ARG
16	LH0	149	ASP
17	LHH	107	LEU
19	LII	47	ARG
19	LII	90	GLU
20	LJ0	106	HIS

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Mol	Chain	Res	Type
20	LJ0	144	ARG
21	LJJ	2	SER
22	LL0	5	GLN
22	LL0	30	LEU
22	LL0	44	TYR
22	LL0	90	VAL
22	LL0	97	ARG
22	LL0	98	ARG
26	LN0	65	ARG
26	LN0	112	ASN
26	LN0	135	VAL
26	LN0	155	VAL
27	LO0	105	ASP
29	LP0	30	ARG
29	LP0	60	VAL
29	LP0	120	ASN
30	LPP	8	VAL
30	LPP	18	TYR
32	LR0	19	ARG
33	LS0	52	PRO
33	LS0	157	ARG
33	LS0	171	ASN
34	LT0	55	LYS
34	LT0	112	ASN
35	LU0	92	ARG
36	LV0	28	LEU
37	LW0	80	VAL
37	LW0	81	ARG
37	LW0	91	VAL
37	LW0	92	GLU
38	LX0	40	HIS
39	LY0	1	MET
39	LY0	114	ARG
43	SA0	8	LEU
43	SA0	102	ARG
43	SA0	154	ILE
46	SBB	58	CYS
47	SC0	156	SER
47	SC0	221	VAL
51	SE0	211	VAL
51	SE0	213	LYS
53	SF0	18	TYR

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Mol	Chain	Res	Type
53	SF0	61	GLU
53	SF0	92	GLU
53	SF0	97	GLN
54	SFF	93	LYS
55	SG0	92	ARG
55	SG0	100	SER
55	SG0	129	VAL
55	SG0	222	TRP
56	SGG	76	ASP
56	SGG	106	ASP
56	SGG	150	THR
56	SGG	305	ASP
59	SJ0	62	ASP
59	SJ0	130	GLN
60	SK0	80	TYR
61	SL0	148	LYS
64	SO0	122	ASP
65	SQ0	99	GLU
66	SR0	84	PHE
67	SS0	24	PHE
68	ST0	17	LEU
68	ST0	28	VAL
71	SW0	110	ASP
73	SY0	11	PHE
73	SY0	37	ASN
73	SY0	39	MET
73	SY0	135	ARG
73	SY0	143	LYS
3	KA0	44	GLU
3	KA0	189	ARG
3	KA0	222	VAL
4	KAA	22	VAL
4	KAA	26	ARG
4	KAA	39	LYS
4	KAA	54	ARG
5	KB0	10	ARG
5	KB0	23	LYS
5	KB0	86	VAL
5	KB0	122	ARG
5	KB0	132	LYS
5	KB0	133	LEU
5	KB0	134	MET

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Mol	Chain	Res	Type
5	KB0	135	PHE
5	KB0	336	ARG
6	KC0	103	VAL
6	KC0	207	THR
6	KC0	328	ILE
7	KCC	64	ILE
7	KCC	76	SER
8	KD0	85	THR
8	KD0	285	GLN
10	KE0	15	LYS
10	KE0	17	TYR
10	KE0	30	LEU
12	KF0	42	ARG
15	KGG	32	PHE
15	KGG	101	MET
16	KH0	34	VAL
16	KH0	62	GLN
16	KH0	64	ARG
16	KH0	149	ASP
17	KHH	107	LEU
19	KII	47	ARG
19	KII	90	GLU
20	KJ0	106	HIS
20	KJ0	144	ARG
21	KJJ	2	SER
22	KL0	5	GLN
22	KL0	30	LEU
22	KL0	44	TYR
22	KL0	90	VAL
22	KL0	97	ARG
22	KL0	98	ARG
26	KN0	65	ARG
26	KN0	112	ASN
26	KN0	135	VAL
26	KN0	155	VAL
27	KO0	105	ASP
29	KP0	30	ARG
29	KP0	60	VAL
29	KP0	120	ASN
30	KPP	8	VAL
30	KPP	18	TYR
32	KR0	19	ARG

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Mol	Chain	Res	Type
33	KS0	52	PRO
33	KS0	157	ARG
33	KS0	171	ASN
34	KT0	55	LYS
34	KT0	112	ASN
35	KU0	92	ARG
36	KV0	28	LEU
37	KW0	80	VAL
37	KW0	81	ARG
37	KW0	91	VAL
37	KW0	92	GLU
38	KX0	40	HIS
39	KY0	1	MET
39	KY0	114	ARG
43	RA0	8	LEU
43	RA0	102	ARG
43	RA0	154	ILE
46	RBB	58	CYS
47	RC0	156	SER
47	RC0	221	VAL
51	RE0	211	VAL
51	RE0	213	LYS
53	RF0	18	TYR
53	RF0	61	GLU
53	RF0	92	GLU
53	RF0	97	GLN
54	RFF	93	LYS
55	RG0	92	ARG
55	RG0	100	SER
55	RG0	129	VAL
55	RG0	222	TRP
56	RGG	76	ASP
56	RGG	106	ASP
56	RGG	150	THR
56	RGG	305	ASP
59	RJ0	62	ASP
59	RJ0	130	GLN
60	RK0	80	TYR
61	RL0	148	LYS
64	RO0	122	ASP
65	RQ0	99	GLU
66	RR0	84	PHE

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Mol	Chain	Res	Type
67	RS0	24	PHE
68	RT0	17	LEU
68	RT0	28	VAL
71	RW0	110	ASP
73	RY0	11	PHE
73	RY0	37	ASN
73	RY0	39	MET
73	RY0	135	ARG
73	RY0	143	LYS
75	SP0	135	ARG
75	RP0	135	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	K50	2494/2618 (95%)	738 (29%)	103 (4%)
1	L50	2494/2618 (95%)	738 (29%)	102 (4%)
2	K70	118/119 (99%)	36 (30%)	4 (3%)
2	L70	118/119 (99%)	36 (30%)	4 (3%)
42	R60	1352/1368 (98%)	518 (38%)	70 (5%)
42	S60	1352/1368 (98%)	517 (38%)	70 (5%)
All	All	7928/8210 (96%)	2583 (32%)	353 (4%)

All (2583) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	13	A
1	L50	15	G
1	L50	21	U
1	L50	22	U
1	L50	23	U
1	L50	24	G
1	L50	25	G
1	L50	31	G
1	L50	39	G
1	L50	43	G

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Mol	Chain	Res	Type
1	L50	48	A
1	L50	51	A
1	L50	52	G
1	L50	59	A
1	L50	62	U
1	L50	63	G
1	L50	68	G
1	L50	70	A
1	L50	71	G
1	L50	73	A
1	L50	74	G
1	L50	75	C
1	L50	76	A
1	L50	77	G
1	L50	82	G
1	L50	87	C
1	L50	88	A
1	L50	98	A
1	L50	99	U
1	L50	100	A
1	L50	101	C
1	L50	108	G
1	L50	113	G
1	L50	114	G
1	L50	118	A
1	L50	123	U
1	L50	132	A
1	L50	135	A
1	L50	137	A
1	L50	151	G
1	L50	152	A
1	L50	157	A
1	L50	158	A
1	L50	159	A
1	L50	160	C
1	L50	165	G
1	L50	167	G
1	L50	169	A
1	L50	178	G
1	L50	181	G
1	L50	184	G
1	L50	186	G

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Mol	Chain	Res	Type
1	L50	188	G
1	L50	191	A
1	L50	194	A
1	L50	201	A
1	L50	202	G
1	L50	204	C
1	L50	209	A
1	L50	210	G
1	L50	211	U
1	L50	212	G
1	L50	213	U
1	L50	214	A
1	L50	216	U
1	L50	221	A
1	L50	224	U
1	L50	225	G
1	L50	226	A
1	L50	233	G
1	L50	234	U
1	L50	237	A
1	L50	238	A
1	L50	239	A
1	L50	240	G
1	L50	241	G
1	L50	242	A
1	L50	246	A
1	L50	247	G
1	L50	255	U
1	L50	258	G
1	L50	266	A
1	L50	267	G
1	L50	268	C
1	L50	273	C
1	L50	276	U
1	L50	277	A
1	L50	284	G
1	L50	285	A
1	L50	286	U
1	L50	287	A
1	L50	289	U
1	L50	298	G
1	L50	309	U

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Mol	Chain	Res	Type
1	L50	311	C
1	L50	312	G
1	L50	314	U
1	L50	315	G
1	L50	316	A
1	L50	317	G
1	L50	330	G
1	L50	331	U
1	L50	332	A
1	L50	333	A
1	L50	340	G
1	L50	343	A
1	L50	345	G
1	L50	346	A
1	L50	347	G
1	L50	352	C
1	L50	353	A
1	L50	358	G
1	L50	366	G
1	L50	373	U
1	L50	382	A
1	L50	384	A
1	L50	385	C
1	L50	392	C
1	L50	396	G
1	L50	397	A
1	L50	400	U
1	L50	416	A
1	L50	434	G
1	L50	438	A
1	L50	449	U
1	L50	450	C
1	L50	453	G
1	L50	454	C
1	L50	467	A
1	L50	478	A
1	L50	488	C
1	L50	495	A
1	L50	499	G
1	L50	503	A
1	L50	504	G
1	L50	507	G

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Mol	Chain	Res	Type
1	L50	508	A
1	L50	509	A
1	L50	510	G
1	L50	517	A
1	L50	523	A
1	L50	524	G
1	L50	527	A
1	L50	530	A
1	L50	533	G
1	L50	534	A
1	L50	535	A
1	L50	536	A
1	L50	542	G
1	L50	553	C
1	L50	556	A
1	L50	562	U
1	L50	563	U
1	L50	564	G
1	L50	567	A
1	L50	568	A
1	L50	569	C
1	L50	570	U
1	L50	580	U
1	L50	581	G
1	L50	587	A
1	L50	601	C
1	L50	612	C
1	L50	618	G
1	L50	620	C
1	L50	625	U
1	L50	630	U
1	L50	631	G
1	L50	642	G
1	L50	643	C
1	L50	646	A
1	L50	647	A
1	L50	658	G
1	L50	659	G
1	L50	660	G
1	L50	661	G
1	L50	665	A
1	L50	667	G

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Mol	Chain	Res	Type
1	L50	668	A
1	L50	675	G
1	L50	676	A
1	L50	684	A
1	L50	685	G
1	L50	688	G
1	L50	689	C
1	L50	695	C
1	L50	710	A
1	L50	711	U
1	L50	714	G
1	L50	715	G
1	L50	720	C
1	L50	726	C
1	L50	729	A
1	L50	732	G
1	L50	736	A
1	L50	739	A
1	L50	742	G
1	L50	749	A
1	L50	750	U
1	L50	763	U
1	L50	764	U
1	L50	765	A
1	L50	766	A
1	L50	767	G
1	L50	768	G
1	L50	772	C
1	L50	776	C
1	L50	778	A
1	L50	779	A
1	L50	781	U
1	L50	782	G
1	L50	784	G
1	L50	795	U
1	L50	796	C
1	L50	801	A
1	L50	802	U
1	L50	803	G
1	L50	806	A
1	L50	816	G
1	L50	822	U

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Mol	Chain	Res	Type
1	L50	828	A
1	L50	830	G
1	L50	834	G
1	L50	838	G
1	L50	840	C
1	L50	843	A
1	L50	848	A
1	L50	849	A
1	L50	852	A
1	L50	854	C
1	L50	858	G
1	L50	859	C
1	L50	865	G
1	L50	866	C
1	L50	867	U
1	L50	871	G
1	L50	877	A
1	L50	878	A
1	L50	879	U
1	L50	885	G
1	L50	889	G
1	L50	893	C
1	L50	900	A
1	L50	905	G
1	L50	910	A
1	L50	980	A
1	L50	990	U
1	L50	998	U
1	L50	1001	A
1	L50	1002	U
1	L50	1010	A
1	L50	1017	A
1	L50	1018	U
1	L50	1021	G
1	L50	1022	A
1	L50	1023	U
1	L50	1024	G
1	L50	1030	U
1	L50	1032	A
1	L50	1033	G
1	L50	1034	C
1	L50	1037	G

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Mol	Chain	Res	Type
1	L50	1050	U
1	L50	1053	C
1	L50	1055	A
1	L50	1056	C
1	L50	1061	G
1	L50	1062	A
1	L50	1070	G
1	L50	1075	A
1	L50	1082	G
1	L50	1085	G
1	L50	1087	G
1	L50	1089	U
1	L50	1090	A
1	L50	1096	A
1	L50	1099	G
1	L50	1100	C
1	L50	1102	G
1	L50	1105	C
1	L50	1111	G
1	L50	1117	A
1	L50	1118	G
1	L50	1120	G
1	L50	1121	A
1	L50	1123	A
1	L50	1124	A
1	L50	1130	C
1	L50	1131	U
1	L50	1133	C
1	L50	1134	A
1	L50	1135	G
1	L50	1136	C
1	L50	1142	A
1	L50	1144	A
1	L50	1148	A
1	L50	1149	G
1	L50	1150	G
1	L50	1151	A
1	L50	1155	G
1	L50	1163	U
1	L50	1169	C
1	L50	1170	A
1	L50	1171	U

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Mol	Chain	Res	Type
1	L50	1172	A
1	L50	1173	A
1	L50	1175	A
1	L50	1177	G
1	L50	1181	G
1	L50	1182	A
1	L50	1183	G
1	L50	1189	U
1	L50	1191	U
1	L50	1192	A
1	L50	1193	A
1	L50	1194	G
1	L50	1196	G
1	L50	1213	A
1	L50	1217	A
1	L50	1218	A
1	L50	1221	A
1	L50	1224	A
1	L50	1231	U
1	L50	1232	G
1	L50	1233	A
1	L50	1235	A
1	L50	1236	U
1	L50	1237	U
1	L50	1243	G
1	L50	1247	G
1	L50	1250	C
1	L50	1252	G
1	L50	1254	C
1	L50	1256	U
1	L50	1257	A
1	L50	1264	C
1	L50	1267	G
1	L50	1268	U
1	L50	1269	A
1	L50	1270	U
1	L50	1274	C
1	L50	1277	G
1	L50	1278	U
1	L50	1282	C
1	L50	1283	A
1	L50	1284	C

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Mol	Chain	Res	Type
1	L50	1296	C
1	L50	1299	A
1	L50	1304	A
1	L50	1305	A
1	L50	1308	A
1	L50	1309	C
1	L50	1317	G
1	L50	1318	U
1	L50	1327	A
1	L50	1332	G
1	L50	1333	A
1	L50	1340	A
1	L50	1341	G
1	L50	1342	A
1	L50	1346	A
1	L50	1350	U
1	L50	1355	C
1	L50	1356	G
1	L50	1359	G
1	L50	1361	G
1	L50	1362	G
1	L50	1374	U
1	L50	1375	G
1	L50	1384	U
1	L50	1385	G
1	L50	1386	A
1	L50	1387	G
1	L50	1395	U
1	L50	1396	G
1	L50	1402	G
1	L50	1411	C
1	L50	1412	C
1	L50	1414	U
1	L50	1416	A
1	L50	1427	A
1	L50	1429	A
1	L50	1430	U
1	L50	1431	G
1	L50	1432	G
1	L50	1440	G
1	L50	1447	C
1	L50	1449	A

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Mol	Chain	Res	Type
1	L50	1450	A
1	L50	1453	G
1	L50	1455	A
1	L50	1457	C
1	L50	1458	A
1	L50	1466	A
1	L50	1467	A
1	L50	1468	G
1	L50	1474	G
1	L50	1475	A
1	L50	1479	U
1	L50	1485	G
1	L50	1486	G
1	L50	1488	U
1	L50	1489	G
1	L50	1490	U
1	L50	1491	U
1	L50	1492	U
1	L50	1499	U
1	L50	1513	G
1	L50	1524	G
1	L50	1527	U
1	L50	1533	C
1	L50	1534	G
1	L50	1535	G
1	L50	1536	G
1	L50	1538	G
1	L50	1547	G
1	L50	1554	U
1	L50	1555	G
1	L50	1556	U
1	L50	1557	G
1	L50	1563	A
1	L50	1564	U
1	L50	1565	U
1	L50	1566	G
1	L50	1568	G
1	L50	1569	A
1	L50	1571	A
1	L50	1573	G
1	L50	1574	G
1	L50	1575	G

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Mol	Chain	Res	Type
1	L50	1583	A
1	L50	1591	G
1	L50	1592	U
1	L50	1602	G
1	L50	1610	A
1	L50	1611	A
1	L50	1612	G
1	L50	1613	A
1	L50	1614	G
1	L50	1617	A
1	L50	1619	G
1	L50	1624	G
1	L50	1626	G
1	L50	1638	G
1	L50	1643	G
1	L50	1644	U
1	L50	1645	C
1	L50	1646	G
1	L50	1649	A
1	L50	1651	A
1	L50	1653	G
1	L50	1665	A
1	L50	1668	A
1	L50	1674	G
1	L50	1675	G
1	L50	1680	A
1	L50	1682	G
1	L50	1685	G
1	L50	1686	G
1	L50	1689	G
1	L50	1692	A
1	L50	1693	C
1	L50	1697	G
1	L50	1698	A
1	L50	1699	C
1	L50	1705	U
1	L50	1708	G
1	L50	1709	G
1	L50	1710	U
1	L50	1711	A
1	L50	1717	A
1	L50	1718	C

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Mol	Chain	Res	Type
1	L50	1720	C
1	L50	1724	G
1	L50	1733	A
1	L50	1735	G
1	L50	1739	A
1	L50	1742	C
1	L50	1743	G
1	L50	1746	U
1	L50	1749	A
1	L50	1751	G
1	L50	1755	U
1	L50	1760	A
1	L50	1770	U
1	L50	1772	U
1	L50	1797	A
1	L50	1799	U
1	L50	1800	U
1	L50	1801	C
1	L50	1808	A
1	L50	1809	A
1	L50	1810	C
1	L50	1811	G
1	L50	1820	C
1	L50	1821	G
1	L50	1822	G
1	L50	1828	G
1	L50	1832	A
1	L50	1833	A
1	L50	1835	G
1	L50	1836	A
1	L50	1837	A
1	L50	1838	G
1	L50	1839	A
1	L50	1846	U
1	L50	1854	A
1	L50	1858	U
1	L50	1860	G
1	L50	1868	A
1	L50	1869	A
1	L50	1870	G
1	L50	1872	U
1	L50	1873	G

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Mol	Chain	Res	Type
1	L50	1874	U
1	L50	1881	U
1	L50	1883	A
1	L50	1885	G
1	L50	1887	G
1	L50	1888	A
1	L50	1931	C
1	L50	1934	C
1	L50	1935	A
1	L50	1937	G
1	L50	1938	A
1	L50	1939	U
1	L50	1940	C
1	L50	1941	A
1	L50	1942	U
1	L50	1943	C
1	L50	1946	G
1	L50	1949	A
1	L50	1950	C
1	L50	1955	G
1	L50	1956	U
1	L50	1957	U
1	L50	1958	U
1	L50	1959	A
1	L50	1960	A
1	L50	1961	G
1	L50	1963	A
1	L50	1966	A
1	L50	1967	A
1	L50	1968	G
1	L50	1973	G
1	L50	1977	G
1	L50	1978	G
1	L50	1985	G
1	L50	1991	G
1	L50	1995	G
1	L50	1997	A
1	L50	2007	A
1	L50	2008	A
1	L50	2011	A
1	L50	2013	A
1	L50	2019	G

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Mol	Chain	Res	Type
1	L50	2020	U
1	L50	2022	G
1	L50	2023	A
1	L50	2027	A
1	L50	2030	G
1	L50	2031	U
1	L50	2032	A
1	L50	2036	A
1	L50	2037	C
1	L50	2039	G
1	L50	2042	A
1	L50	2043	G
1	L50	2045	C
1	L50	2046	G
1	L50	2047	A
1	L50	2048	G
1	L50	2049	A
1	L50	2052	A
1	L50	2057	U
1	L50	2059	U
1	L50	2060	A
1	L50	2061	G
1	L50	2062	A
1	L50	2063	G
1	L50	2065	A
1	L50	2067	A
1	L50	2073	U
1	L50	2075	A
1	L50	2076	A
1	L50	2077	G
1	L50	2078	A
1	L50	2085	G
1	L50	2087	G
1	L50	2093	G
1	L50	2096	C
1	L50	2097	U
1	L50	2098	A
1	L50	2099	C
1	L50	2108	U
1	L50	2109	G
1	L50	2110	A
1	L50	2111	G

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Mol	Chain	Res	Type
1	L50	2114	G
1	L50	2122	G
1	L50	2124	C
1	L50	2130	G
1	L50	2131	A
1	L50	2136	A
1	L50	2140	A
1	L50	2141	U
1	L50	2142	A
1	L50	2145	A
1	L50	2146	G
1	L50	2149	A
1	L50	2150	C
1	L50	2152	U
1	L50	2160	G
1	L50	2162	G
1	L50	2164	G
1	L50	2167	A
1	L50	2168	G
1	L50	2169	A
1	L50	2170	A
1	L50	2171	A
1	L50	2177	C
1	L50	2178	C
1	L50	2185	A
1	L50	2189	C
1	L50	2211	A
1	L50	2212	G
1	L50	2213	A
1	L50	2217	C
1	L50	2221	G
1	L50	2224	G
1	L50	2228	U
1	L50	2229	U
1	L50	2234	U
1	L50	2235	C
1	L50	2239	G
1	L50	2241	U
1	L50	2243	U
1	L50	2253	C
1	L50	2254	U
1	L50	2255	A

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Mol	Chain	Res	Type
1	L50	2257	C
1	L50	2260	G
1	L50	2262	C
1	L50	2266	G
1	L50	2272	G
1	L50	2275	G
1	L50	2279	A
1	L50	2286	G
1	L50	2291	U
1	L50	2293	C
1	L50	2296	C
1	L50	2303	C
1	L50	2304	A
1	L50	2306	G
1	L50	2309	A
1	L50	2310	C
1	L50	2313	G
1	L50	2319	G
1	L50	2322	U
1	L50	2323	U
1	L50	2325	G
1	L50	2337	A
1	L50	2339	A
1	L50	2340	G
1	L50	2345	G
1	L50	2347	U
1	L50	2351	U
1	L50	2355	A
1	L50	2358	G
1	L50	2364	A
1	L50	2376	A
1	L50	2377	G
1	L50	2379	G
1	L50	2394	A
1	L50	2399	A
1	L50	2401	C
1	L50	2410	A
1	L50	2412	C
1	L50	2413	U
1	L50	2416	G
1	L50	2419	G
1	L50	2420	C

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Mol	Chain	Res	Type
1	L50	2423	C
1	L50	2424	G
1	L50	2432	G
1	L50	2434	A
1	L50	2436	G
1	L50	2437	U
1	L50	2441	A
1	L50	2447	A
1	L50	2451	U
1	L50	2452	A
1	L50	2453	C
1	L50	2459	C
1	L50	2460	U
1	L50	2473	G
1	L50	2475	A
1	L50	2476	G
1	L50	2477	C
1	L50	2482	A
1	L50	2487	A
1	L50	2490	A
1	L50	2491	A
1	L50	2501	A
1	L50	2503	U
1	L50	2508	A
1	L50	2509	A
1	L50	2518	G
1	L50	2519	G
1	L50	2520	A
1	L50	2529	C
1	L50	2532	A
1	L50	2533	G
1	L50	2534	U
1	L50	2535	U
1	L50	2538	C
1	L50	2539	A
1	L50	2548	G
1	L50	2555	A
1	L50	2558	A
1	L50	2559	G
1	L50	2562	U
1	L50	2563	U
1	L50	2565	U

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Mol	Chain	Res	Type
1	L50	2568	U
1	L50	2578	G
1	L50	2588	G
1	L50	2593	A
1	L50	2595	U
1	L50	2596	G
1	L50	2597	G
1	L50	2598	U
1	L50	2600	G
1	L50	2605	C
1	L50	2606	A
1	L50	2612	G
2	L70	2	G
2	L70	10	C
2	L70	14	U
2	L70	15	C
2	L70	18	C
2	L70	22	A
2	L70	25	A
2	L70	27	A
2	L70	32	A
2	L70	33	U
2	L70	35	C
2	L70	41	G
2	L70	42	A
2	L70	49	A
2	L70	50	A
2	L70	51	G
2	L70	53	U
2	L70	63	A
2	L70	64	G
2	L70	65	A
2	L70	67	C
2	L70	69	A
2	L70	88	C
2	L70	89	G
2	L70	91	C
2	L70	93	A
2	L70	100	A
2	L70	101	A
2	L70	104	C
2	L70	105	G

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Mol	Chain	Res	Type
2	L70	107	G
2	L70	108	G
2	L70	109	U
2	L70	110	G
2	L70	115	A
2	L70	119	U
42	S60	7	U
42	S60	8	U
42	S60	14	U
42	S60	17	C
42	S60	26	A
42	S60	32	G
42	S60	37	A
42	S60	39	A
42	S60	40	G
42	S60	41	A
42	S60	43	U
42	S60	44	U
42	S60	45	A
42	S60	48	C
42	S60	52	C
42	S60	54	U
42	S60	55	G
42	S60	56	U
42	S60	66	G
42	S60	70	U
42	S60	71	U
42	S60	72	A
42	S60	73	G
42	S60	75	G
42	S60	76	A
42	S60	77	A
42	S60	83	G
42	S60	86	A
42	S60	88	G
42	S60	92	A
42	S60	94	U
42	S60	97	C
42	S60	98	G
42	S60	99	G
42	S60	102	G
42	S60	104	G

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Mol	Chain	Res	Type
42	S60	106	A
42	S60	107	U
42	S60	110	A
42	S60	112	U
42	S60	116	U
42	S60	118	G
42	S60	119	A
42	S60	120	A
42	S60	121	C
42	S60	124	G
42	S60	127	A
42	S60	128	A
42	S60	132	C
42	S60	133	A
42	S60	134	G
42	S60	138	A
42	S60	140	A
42	S60	141	G
42	S60	142	A
42	S60	147	A
42	S60	148	A
42	S60	150	A
42	S60	153	G
42	S60	155	G
42	S60	157	A
42	S60	161	G
42	S60	167	G
42	S60	172	U
42	S60	173	A
42	S60	174	G
42	S60	180	G
42	S60	181	A
42	S60	184	A
42	S60	186	A
42	S60	187	A
42	S60	189	A
42	S60	190	A
42	S60	191	C
42	S60	192	A
42	S60	193	G
42	S60	197	A
42	S60	198	G

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Mol	Chain	Res	Type
42	S60	199	G
42	S60	204	U
42	S60	206	A
42	S60	219	U
42	S60	220	C
42	S60	222	G
42	S60	226	G
42	S60	228	A
42	S60	238	A
42	S60	241	G
42	S60	242	C
42	S60	247	U
42	S60	254	U
42	S60	255	A
42	S60	256	G
42	S60	259	G
42	S60	262	U
42	S60	263	A
42	S60	264	C
42	S60	268	G
42	S60	271	U
42	S60	283	U
42	S60	284	C
42	S60	290	A
42	S60	292	G
42	S60	299	G
42	S60	300	A
42	S60	303	G
42	S60	304	A
42	S60	305	C
42	S60	307	G
42	S60	311	C
42	S60	314	G
42	S60	315	G
42	S60	318	C
42	S60	319	A
42	S60	320	A
42	S60	326	G
42	S60	327	C
42	S60	328	A
42	S60	329	G
42	S60	335	G

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Mol	Chain	Res	Type
42	S60	338	A
42	S60	340	A
42	S60	341	A
42	S60	342	U
42	S60	344	A
42	S60	345	C
42	S60	347	G
42	S60	348	A
42	S60	355	C
42	S60	356	A
42	S60	357	A
42	S60	358	G
42	S60	362	G
42	S60	363	C
42	S60	364	G
42	S60	367	A
42	S60	368	G
42	S60	371	A
42	S60	372	A
42	S60	373	G
42	S60	374	A
42	S60	375	G
42	S60	377	C
42	S60	378	G
42	S60	380	G
42	S60	382	A
42	S60	383	A
42	S60	384	A
42	S60	385	C
42	S60	388	G
42	S60	395	U
42	S60	396	A
42	S60	398	A
42	S60	399	A
42	S60	402	C
42	S60	407	G
42	S60	408	A
42	S60	409	G
42	S60	412	A
42	S60	414	U
42	S60	416	G
42	S60	422	A

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Mol	Chain	Res	Type
42	S60	424	G
42	S60	425	G
42	S60	426	C
42	S60	431	G
42	S60	432	C
42	S60	437	A
42	S60	441	G
42	S60	444	G
42	S60	445	U
42	S60	446	A
42	S60	449	A
42	S60	450	C
42	S60	452	A
42	S60	453	G
42	S60	454	C
42	S60	461	A
42	S60	471	A
42	S60	473	G
42	S60	474	A
42	S60	476	U
42	S60	477	G
42	S60	478	C
42	S60	481	C
42	S60	482	G
42	S60	486	A
42	S60	487	A
42	S60	490	G
42	S60	491	G
42	S60	501	G
42	S60	506	A
42	S60	509	G
42	S60	510	U
42	S60	511	A
42	S60	512	C
42	S60	521	A
42	S60	527	G
42	S60	530	U
42	S60	535	A
42	S60	536	G
42	S60	540	C
42	S60	541	G
42	S60	543	A

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Mol	Chain	Res	Type
42	S60	544	U
42	S60	547	A
42	S60	550	G
42	S60	553	A
42	S60	554	A
42	S60	565	U
42	S60	566	A
42	S60	567	A
42	S60	568	G
42	S60	575	A
42	S60	578	A
42	S60	579	G
42	S60	590	U
42	S60	593	A
42	S60	598	C
42	S60	599	G
42	S60	600	A
42	S60	601	G
42	S60	602	A
42	S60	608	A
42	S60	609	A
42	S60	610	U
42	S60	616	G
42	S60	621	G
42	S60	622	C
42	S60	623	U
42	S60	624	U
42	S60	625	A
42	S60	630	U
42	S60	633	C
42	S60	635	G
42	S60	637	G
42	S60	644	G
42	S60	647	C
42	S60	661	A
42	S60	662	U
42	S60	665	G
42	S60	668	G
42	S60	671	C
42	S60	673	A
42	S60	686	G
42	S60	687	A

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Mol	Chain	Res	Type
42	S60	688	G
42	S60	690	A
42	S60	694	A
42	S60	700	A
42	S60	702	U
42	S60	705	A
42	S60	706	G
42	S60	707	A
42	S60	722	G
42	S60	724	A
42	S60	725	G
42	S60	727	A
42	S60	728	A
42	S60	730	C
42	S60	731	G
42	S60	733	U
42	S60	734	G
42	S60	738	A
42	S60	740	G
42	S60	749	G
42	S60	752	A
42	S60	753	U
42	S60	754	G
42	S60	755	A
42	S60	757	C
42	S60	771	A
42	S60	775	U
42	S60	776	A
42	S60	780	G
42	S60	789	G
42	S60	790	G
42	S60	791	A
42	S60	795	U
42	S60	806	G
42	S60	810	U
42	S60	817	A
42	S60	818	A
42	S60	820	G
42	S60	821	G
42	S60	823	A
42	S60	825	U
42	S60	831	G

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Mol	Chain	Res	Type
42	S60	836	A
42	S60	839	C
42	S60	840	C
42	S60	841	A
42	S60	846	G
42	S60	848	G
42	S60	866	U
42	S60	868	U
42	S60	871	C
42	S60	872	U
42	S60	874	A
42	S60	875	A
42	S60	877	G
42	S60	878	C
42	S60	880	G
42	S60	881	G
42	S60	883	C
42	S60	884	A
42	S60	890	C
42	S60	898	G
42	S60	899	A
42	S60	905	G
42	S60	908	U
42	S60	909	G
42	S60	911	G
42	S60	915	A
42	S60	916	G
42	S60	917	U
42	S60	918	A
42	S60	924	U
42	S60	925	A
42	S60	926	G
42	S60	927	G
42	S60	928	U
42	S60	929	C
42	S60	930	A
42	S60	932	A
42	S60	933	G
42	S60	934	A
42	S60	936	U
42	S60	940	G
42	S60	941	C

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Mol	Chain	Res	Type
42	S60	942	A
42	S60	952	A
42	S60	953	C
42	S60	955	A
42	S60	957	G
42	S60	958	A
42	S60	959	G
42	S60	962	G
42	S60	966	G
42	S60	967	A
42	S60	968	C
42	S60	970	U
42	S60	971	U
42	S60	972	U
42	S60	974	G
42	S60	976	U
42	S60	978	A
42	S60	980	G
42	S60	987	A
42	S60	991	A
42	S60	995	A
42	S60	998	U
42	S60	999	C
42	S60	1003	A
42	S60	1006	A
42	S60	1007	U
42	S60	1008	A
42	S60	1011	A
42	S60	1012	A
42	S60	1013	A
42	S60	1014	G
42	S60	1017	A
42	S60	1018	U
42	S60	1019	C
42	S60	1021	A
42	S60	1023	A
42	S60	1024	G
42	S60	1028	U
42	S60	1029	U
42	S60	1033	A
42	S60	1039	G
42	S60	1041	A

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Mol	Chain	Res	Type
42	S60	1042	A
42	S60	1045	A
42	S60	1046	A
42	S60	1047	G
42	S60	1052	A
42	S60	1053	A
42	S60	1054	G
42	S60	1056	A
42	S60	1057	C
42	S60	1058	A
42	S60	1059	G
42	S60	1060	G
42	S60	1062	C
42	S60	1063	A
42	S60	1064	G
42	S60	1066	G
42	S60	1075	A
42	S60	1076	G
42	S60	1077	A
42	S60	1078	U
42	S60	1088	U
42	S60	1089	G
42	S60	1090	C
42	S60	1092	C
42	S60	1094	C
42	S60	1099	U
42	S60	1100	A
42	S60	1102	A
42	S60	1103	G
42	S60	1104	U
42	S60	1105	G
42	S60	1106	G
42	S60	1111	A
42	S60	1112	G
42	S60	1116	A
42	S60	1117	A
42	S60	1118	A
42	S60	1119	C
42	S60	1120	A
42	S60	1121	A
42	S60	1122	A
42	S60	1123	U

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Mol	Chain	Res	Type
42	S60	1124	A
42	S60	1125	G
42	S60	1126	A
42	S60	1127	A
42	S60	1128	G
42	S60	1129	U
42	S60	1130	A
42	S60	1135	U
42	S60	1136	G
42	S60	1137	A
42	S60	1139	C
42	S60	1141	A
42	S60	1142	G
42	S60	1146	G
42	S60	1152	G
42	S60	1154	A
42	S60	1158	U
42	S60	1159	A
42	S60	1160	A
42	S60	1161	U
42	S60	1162	G
42	S60	1170	G
42	S60	1171	A
42	S60	1175	A
42	S60	1176	G
42	S60	1177	G
42	S60	1179	A
42	S60	1182	G
42	S60	1185	A
42	S60	1191	C
42	S60	1192	G
42	S60	1194	U
42	S60	1195	A
42	S60	1196	U
42	S60	1202	U
42	S60	1203	A
42	S60	1204	A
42	S60	1205	G
42	S60	1210	G
42	S60	1211	A
42	S60	1214	A
42	S60	1216	U

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Mol	Chain	Res	Type
42	S60	1217	G
42	S60	1219	G
42	S60	1223	C
42	S60	1225	G
42	S60	1227	U
42	S60	1230	U
42	S60	1237	C
42	S60	1238	A
42	S60	1239	C
42	S60	1240	C
42	S60	1241	G
42	S60	1243	C
42	S60	1246	U
42	S60	1249	U
42	S60	1250	U
42	S60	1251	A
42	S60	1260	G
42	S60	1262	A
42	S60	1263	A
42	S60	1264	C
42	S60	1266	A
42	S60	1267	G
42	S60	1270	G
42	S60	1274	A
42	S60	1275	C
42	S60	1276	A
42	S60	1280	G
42	S60	1282	A
42	S60	1283	A
42	S60	1284	G
42	S60	1287	A
42	S60	1294	G
42	S60	1295	C
42	S60	1296	A
42	S60	1297	G
42	S60	1301	U
42	S60	1302	C
42	S60	1307	U
42	S60	1310	G
42	S60	1314	C
42	S60	1315	A
42	S60	1316	A

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Mol	Chain	Res	Type
42	S60	1317	G
42	S60	1320	G
42	S60	1322	A
42	S60	1326	A
42	S60	1327	G
42	S60	1328	G
42	S60	1329	C
42	S60	1331	G
42	S60	1340	G
42	S60	1341	A
42	S60	1342	A
42	S60	1343	C
42	S60	1348	A
42	S60	1352	G
42	S60	1353	G
42	S60	1354	A
42	S60	1355	U
42	S60	1356	C
42	S60	1357	A
1	K50	2	U
1	K50	3	A
1	K50	13	A
1	K50	15	G
1	K50	21	U
1	K50	22	U
1	K50	23	U
1	K50	24	G
1	K50	25	G
1	K50	31	G
1	K50	39	G
1	K50	43	G
1	K50	48	A
1	K50	51	A
1	K50	52	G
1	K50	59	A
1	K50	62	U
1	K50	63	G
1	K50	68	G
1	K50	70	A
1	K50	71	G
1	K50	73	A
1	K50	74	G

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Mol	Chain	Res	Type
1	K50	75	C
1	K50	76	A
1	K50	77	G
1	K50	82	G
1	K50	87	C
1	K50	88	A
1	K50	98	A
1	K50	99	U
1	K50	100	A
1	K50	101	C
1	K50	108	G
1	K50	113	G
1	K50	114	G
1	K50	118	A
1	K50	123	U
1	K50	132	A
1	K50	135	A
1	K50	137	A
1	K50	151	G
1	K50	152	A
1	K50	157	A
1	K50	158	A
1	K50	159	A
1	K50	160	C
1	K50	165	G
1	K50	167	G
1	K50	169	A
1	K50	178	G
1	K50	181	G
1	K50	184	G
1	K50	186	G
1	K50	188	G
1	K50	191	A
1	K50	194	A
1	K50	201	A
1	K50	202	G
1	K50	204	C
1	K50	209	A
1	K50	210	G
1	K50	211	U
1	K50	212	G
1	K50	213	U

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Mol	Chain	Res	Type
1	K50	214	A
1	K50	216	U
1	K50	221	A
1	K50	224	U
1	K50	225	G
1	K50	226	A
1	K50	233	G
1	K50	234	U
1	K50	237	A
1	K50	238	A
1	K50	239	A
1	K50	240	G
1	K50	241	G
1	K50	242	A
1	K50	246	A
1	K50	247	G
1	K50	255	U
1	K50	258	G
1	K50	266	A
1	K50	267	G
1	K50	268	C
1	K50	273	C
1	K50	276	U
1	K50	277	A
1	K50	284	G
1	K50	285	A
1	K50	286	U
1	K50	287	A
1	K50	289	U
1	K50	298	G
1	K50	309	U
1	K50	311	C
1	K50	312	G
1	K50	314	U
1	K50	315	G
1	K50	316	A
1	K50	317	G
1	K50	330	G
1	K50	331	U
1	K50	332	A
1	K50	333	A
1	K50	340	G

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Mol	Chain	Res	Type
1	K50	343	A
1	K50	345	G
1	K50	346	A
1	K50	347	G
1	K50	352	C
1	K50	353	A
1	K50	358	G
1	K50	366	G
1	K50	373	U
1	K50	382	A
1	K50	384	A
1	K50	385	C
1	K50	392	C
1	K50	396	G
1	K50	397	A
1	K50	400	U
1	K50	416	A
1	K50	434	G
1	K50	438	A
1	K50	449	U
1	K50	450	C
1	K50	453	G
1	K50	454	C
1	K50	467	A
1	K50	478	A
1	K50	488	C
1	K50	495	A
1	K50	499	G
1	K50	503	A
1	K50	504	G
1	K50	507	G
1	K50	508	A
1	K50	509	A
1	K50	510	G
1	K50	517	A
1	K50	523	A
1	K50	524	G
1	K50	527	A
1	K50	530	A
1	K50	533	G
1	K50	534	A
1	K50	535	A

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Mol	Chain	Res	Type
1	K50	536	A
1	K50	542	G
1	K50	553	C
1	K50	556	A
1	K50	562	U
1	K50	563	U
1	K50	564	G
1	K50	567	A
1	K50	568	A
1	K50	569	C
1	K50	570	U
1	K50	580	U
1	K50	581	G
1	K50	587	A
1	K50	601	C
1	K50	612	C
1	K50	618	G
1	K50	620	C
1	K50	625	U
1	K50	630	U
1	K50	631	G
1	K50	642	G
1	K50	643	C
1	K50	646	A
1	K50	647	A
1	K50	658	G
1	K50	659	G
1	K50	660	G
1	K50	661	G
1	K50	665	A
1	K50	667	G
1	K50	668	A
1	K50	675	G
1	K50	676	A
1	K50	684	A
1	K50	685	G
1	K50	688	G
1	K50	689	C
1	K50	695	C
1	K50	710	A
1	K50	711	U
1	K50	714	G

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Mol	Chain	Res	Type
1	K50	715	G
1	K50	720	C
1	K50	726	C
1	K50	729	A
1	K50	732	G
1	K50	736	A
1	K50	739	A
1	K50	742	G
1	K50	749	A
1	K50	750	U
1	K50	763	U
1	K50	764	U
1	K50	765	A
1	K50	766	A
1	K50	767	G
1	K50	768	G
1	K50	772	C
1	K50	776	C
1	K50	778	A
1	K50	779	A
1	K50	781	U
1	K50	782	G
1	K50	784	G
1	K50	795	U
1	K50	796	C
1	K50	801	A
1	K50	802	U
1	K50	803	G
1	K50	806	A
1	K50	816	G
1	K50	822	U
1	K50	828	A
1	K50	830	G
1	K50	834	G
1	K50	838	G
1	K50	840	C
1	K50	843	A
1	K50	848	A
1	K50	849	A
1	K50	852	A
1	K50	854	C
1	K50	858	G

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Mol	Chain	Res	Type
1	K50	859	C
1	K50	865	G
1	K50	866	C
1	K50	867	U
1	K50	871	G
1	K50	877	A
1	K50	878	A
1	K50	879	U
1	K50	885	G
1	K50	889	G
1	K50	893	C
1	K50	900	A
1	K50	905	G
1	K50	910	A
1	K50	980	A
1	K50	990	U
1	K50	998	U
1	K50	1001	A
1	K50	1002	U
1	K50	1010	A
1	K50	1017	A
1	K50	1018	U
1	K50	1021	G
1	K50	1022	A
1	K50	1023	U
1	K50	1024	G
1	K50	1030	U
1	K50	1032	A
1	K50	1033	G
1	K50	1034	C
1	K50	1037	G
1	K50	1050	U
1	K50	1053	C
1	K50	1055	A
1	K50	1056	C
1	K50	1061	G
1	K50	1062	A
1	K50	1070	G
1	K50	1075	A
1	K50	1082	G
1	K50	1085	G
1	K50	1087	G

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Mol	Chain	Res	Type
1	K50	1089	U
1	K50	1090	A
1	K50	1096	A
1	K50	1099	G
1	K50	1100	C
1	K50	1102	G
1	K50	1105	C
1	K50	1111	G
1	K50	1117	A
1	K50	1118	G
1	K50	1120	G
1	K50	1121	A
1	K50	1123	A
1	K50	1124	A
1	K50	1130	C
1	K50	1131	U
1	K50	1133	C
1	K50	1134	A
1	K50	1135	G
1	K50	1136	C
1	K50	1142	A
1	K50	1144	A
1	K50	1148	A
1	K50	1149	G
1	K50	1150	G
1	K50	1151	A
1	K50	1155	G
1	K50	1163	U
1	K50	1169	C
1	K50	1170	A
1	K50	1171	U
1	K50	1172	A
1	K50	1173	A
1	K50	1175	A
1	K50	1177	G
1	K50	1181	G
1	K50	1182	A
1	K50	1183	G
1	K50	1189	U
1	K50	1191	U
1	K50	1192	A
1	K50	1193	A

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Mol	Chain	Res	Type
1	K50	1194	G
1	K50	1196	G
1	K50	1213	A
1	K50	1217	A
1	K50	1218	A
1	K50	1221	A
1	K50	1224	A
1	K50	1231	U
1	K50	1232	G
1	K50	1233	A
1	K50	1235	A
1	K50	1236	U
1	K50	1237	U
1	K50	1243	G
1	K50	1247	G
1	K50	1250	C
1	K50	1252	G
1	K50	1254	C
1	K50	1256	U
1	K50	1257	A
1	K50	1264	C
1	K50	1267	G
1	K50	1268	U
1	K50	1269	A
1	K50	1270	U
1	K50	1274	C
1	K50	1277	G
1	K50	1278	U
1	K50	1282	C
1	K50	1283	A
1	K50	1284	C
1	K50	1296	C
1	K50	1299	A
1	K50	1304	A
1	K50	1305	A
1	K50	1308	A
1	K50	1309	C
1	K50	1317	G
1	K50	1318	U
1	K50	1327	A
1	K50	1332	G
1	K50	1333	A

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Mol	Chain	Res	Type
1	K50	1340	A
1	K50	1341	G
1	K50	1342	A
1	K50	1346	A
1	K50	1350	U
1	K50	1355	C
1	K50	1356	G
1	K50	1359	G
1	K50	1361	G
1	K50	1362	G
1	K50	1374	U
1	K50	1375	G
1	K50	1384	U
1	K50	1385	G
1	K50	1386	A
1	K50	1387	G
1	K50	1395	U
1	K50	1396	G
1	K50	1402	G
1	K50	1411	C
1	K50	1412	C
1	K50	1414	U
1	K50	1416	A
1	K50	1427	A
1	K50	1429	A
1	K50	1430	U
1	K50	1431	G
1	K50	1432	G
1	K50	1440	G
1	K50	1447	C
1	K50	1449	A
1	K50	1450	A
1	K50	1453	G
1	K50	1455	A
1	K50	1457	C
1	K50	1458	A
1	K50	1466	A
1	K50	1467	A
1	K50	1468	G
1	K50	1474	G
1	K50	1475	A
1	K50	1479	U

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Mol	Chain	Res	Type
1	K50	1485	G
1	K50	1486	G
1	K50	1488	U
1	K50	1489	G
1	K50	1490	U
1	K50	1491	U
1	K50	1492	U
1	K50	1499	U
1	K50	1513	G
1	K50	1524	G
1	K50	1527	U
1	K50	1533	C
1	K50	1534	G
1	K50	1535	G
1	K50	1536	G
1	K50	1538	G
1	K50	1547	G
1	K50	1554	U
1	K50	1555	G
1	K50	1556	U
1	K50	1557	G
1	K50	1563	A
1	K50	1564	U
1	K50	1565	U
1	K50	1566	G
1	K50	1568	G
1	K50	1569	A
1	K50	1571	A
1	K50	1573	G
1	K50	1574	G
1	K50	1575	G
1	K50	1583	A
1	K50	1591	G
1	K50	1592	U
1	K50	1602	G
1	K50	1610	A
1	K50	1611	A
1	K50	1612	G
1	K50	1613	A
1	K50	1614	G
1	K50	1617	A
1	K50	1619	G

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Mol	Chain	Res	Type
1	K50	1624	G
1	K50	1626	G
1	K50	1638	G
1	K50	1643	G
1	K50	1644	U
1	K50	1645	C
1	K50	1646	G
1	K50	1649	A
1	K50	1651	A
1	K50	1653	G
1	K50	1665	A
1	K50	1668	A
1	K50	1674	G
1	K50	1675	G
1	K50	1680	A
1	K50	1682	G
1	K50	1685	G
1	K50	1686	G
1	K50	1689	G
1	K50	1692	A
1	K50	1693	C
1	K50	1697	G
1	K50	1698	A
1	K50	1699	C
1	K50	1705	U
1	K50	1708	G
1	K50	1709	G
1	K50	1710	U
1	K50	1711	A
1	K50	1717	A
1	K50	1718	C
1	K50	1720	C
1	K50	1724	G
1	K50	1733	A
1	K50	1735	G
1	K50	1739	A
1	K50	1742	C
1	K50	1743	G
1	K50	1746	U
1	K50	1749	A
1	K50	1751	G
1	K50	1755	U

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Mol	Chain	Res	Type
1	K50	1760	A
1	K50	1770	U
1	K50	1772	U
1	K50	1797	A
1	K50	1799	U
1	K50	1800	U
1	K50	1801	C
1	K50	1808	A
1	K50	1809	A
1	K50	1810	C
1	K50	1811	G
1	K50	1820	C
1	K50	1821	G
1	K50	1822	G
1	K50	1828	G
1	K50	1832	A
1	K50	1833	A
1	K50	1835	G
1	K50	1836	A
1	K50	1837	A
1	K50	1838	G
1	K50	1839	A
1	K50	1846	U
1	K50	1854	A
1	K50	1858	U
1	K50	1860	G
1	K50	1868	A
1	K50	1869	A
1	K50	1870	G
1	K50	1872	U
1	K50	1873	G
1	K50	1874	U
1	K50	1881	U
1	K50	1883	A
1	K50	1885	G
1	K50	1887	G
1	K50	1888	A
1	K50	1931	C
1	K50	1934	C
1	K50	1935	A
1	K50	1937	G
1	K50	1938	A

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Mol	Chain	Res	Type
1	K50	1939	U
1	K50	1940	C
1	K50	1941	A
1	K50	1942	U
1	K50	1943	C
1	K50	1946	G
1	K50	1949	A
1	K50	1950	C
1	K50	1955	G
1	K50	1956	U
1	K50	1957	U
1	K50	1958	U
1	K50	1959	A
1	K50	1960	A
1	K50	1961	G
1	K50	1963	A
1	K50	1966	A
1	K50	1967	A
1	K50	1968	G
1	K50	1973	G
1	K50	1977	G
1	K50	1978	G
1	K50	1985	G
1	K50	1991	G
1	K50	1995	G
1	K50	1997	A
1	K50	2007	A
1	K50	2008	A
1	K50	2011	A
1	K50	2013	A
1	K50	2019	G
1	K50	2020	U
1	K50	2022	G
1	K50	2023	A
1	K50	2027	A
1	K50	2030	G
1	K50	2031	U
1	K50	2032	A
1	K50	2036	A
1	K50	2037	C
1	K50	2039	G
1	K50	2042	A

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Mol	Chain	Res	Type
1	K50	2043	G
1	K50	2045	C
1	K50	2046	G
1	K50	2047	A
1	K50	2048	G
1	K50	2049	A
1	K50	2052	A
1	K50	2057	U
1	K50	2059	U
1	K50	2060	A
1	K50	2061	G
1	K50	2062	A
1	K50	2063	G
1	K50	2065	A
1	K50	2067	A
1	K50	2073	U
1	K50	2075	A
1	K50	2076	A
1	K50	2077	G
1	K50	2078	A
1	K50	2085	G
1	K50	2087	G
1	K50	2093	G
1	K50	2096	C
1	K50	2097	U
1	K50	2098	A
1	K50	2099	C
1	K50	2108	U
1	K50	2109	G
1	K50	2110	A
1	K50	2111	G
1	K50	2114	G
1	K50	2122	G
1	K50	2124	C
1	K50	2130	G
1	K50	2131	A
1	K50	2136	A
1	K50	2140	A
1	K50	2141	U
1	K50	2142	A
1	K50	2145	A
1	K50	2146	G

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Mol	Chain	Res	Type
1	K50	2149	A
1	K50	2150	C
1	K50	2152	U
1	K50	2160	G
1	K50	2162	G
1	K50	2164	G
1	K50	2167	A
1	K50	2168	G
1	K50	2169	A
1	K50	2170	A
1	K50	2171	A
1	K50	2177	C
1	K50	2178	C
1	K50	2185	A
1	K50	2189	C
1	K50	2211	A
1	K50	2212	G
1	K50	2213	A
1	K50	2217	C
1	K50	2221	G
1	K50	2224	G
1	K50	2228	U
1	K50	2229	U
1	K50	2234	U
1	K50	2235	C
1	K50	2239	G
1	K50	2241	U
1	K50	2243	U
1	K50	2253	C
1	K50	2254	U
1	K50	2255	A
1	K50	2257	C
1	K50	2260	G
1	K50	2262	C
1	K50	2266	G
1	K50	2272	G
1	K50	2275	G
1	K50	2279	A
1	K50	2286	G
1	K50	2291	U
1	K50	2293	C
1	K50	2296	C

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Mol	Chain	Res	Type
1	K50	2303	C
1	K50	2304	A
1	K50	2306	G
1	K50	2309	A
1	K50	2310	C
1	K50	2313	G
1	K50	2319	G
1	K50	2322	U
1	K50	2323	U
1	K50	2325	G
1	K50	2337	A
1	K50	2339	A
1	K50	2340	G
1	K50	2345	G
1	K50	2347	U
1	K50	2351	U
1	K50	2355	A
1	K50	2358	G
1	K50	2364	A
1	K50	2376	A
1	K50	2377	G
1	K50	2379	G
1	K50	2394	A
1	K50	2399	A
1	K50	2401	C
1	K50	2410	A
1	K50	2412	C
1	K50	2413	U
1	K50	2416	G
1	K50	2419	G
1	K50	2420	C
1	K50	2423	C
1	K50	2424	G
1	K50	2432	G
1	K50	2434	A
1	K50	2436	G
1	K50	2437	U
1	K50	2441	A
1	K50	2447	A
1	K50	2451	U
1	K50	2452	A
1	K50	2453	C

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Mol	Chain	Res	Type
1	K50	2459	C
1	K50	2460	U
1	K50	2473	G
1	K50	2475	A
1	K50	2476	G
1	K50	2477	C
1	K50	2482	A
1	K50	2487	A
1	K50	2490	A
1	K50	2491	A
1	K50	2501	A
1	K50	2503	U
1	K50	2508	A
1	K50	2509	A
1	K50	2518	G
1	K50	2519	G
1	K50	2520	A
1	K50	2529	C
1	K50	2532	A
1	K50	2533	G
1	K50	2534	U
1	K50	2535	U
1	K50	2538	C
1	K50	2539	A
1	K50	2548	G
1	K50	2555	A
1	K50	2558	A
1	K50	2559	G
1	K50	2562	U
1	K50	2563	U
1	K50	2565	U
1	K50	2568	U
1	K50	2578	G
1	K50	2588	G
1	K50	2593	A
1	K50	2595	U
1	K50	2596	G
1	K50	2597	G
1	K50	2598	U
1	K50	2600	G
1	K50	2605	C
1	K50	2606	A

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Mol	Chain	Res	Type
1	K50	2612	G
2	K70	2	G
2	K70	10	C
2	K70	14	U
2	K70	15	C
2	K70	18	C
2	K70	22	A
2	K70	25	A
2	K70	27	A
2	K70	32	A
2	K70	33	U
2	K70	35	C
2	K70	41	G
2	K70	42	A
2	K70	49	A
2	K70	50	A
2	K70	51	G
2	K70	53	U
2	K70	63	A
2	K70	64	G
2	K70	65	A
2	K70	67	C
2	K70	69	A
2	K70	88	C
2	K70	89	G
2	K70	91	C
2	K70	93	A
2	K70	100	A
2	K70	101	A
2	K70	104	C
2	K70	105	G
2	K70	107	G
2	K70	108	G
2	K70	109	U
2	K70	110	G
2	K70	115	A
2	K70	119	U
42	R60	7	U
42	R60	8	U
42	R60	14	U
42	R60	17	C
42	R60	26	A

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Mol	Chain	Res	Type
42	R60	32	G
42	R60	37	A
42	R60	39	A
42	R60	40	G
42	R60	41	A
42	R60	43	U
42	R60	44	U
42	R60	45	A
42	R60	48	C
42	R60	52	C
42	R60	54	U
42	R60	55	G
42	R60	56	U
42	R60	66	G
42	R60	70	U
42	R60	71	U
42	R60	72	A
42	R60	73	G
42	R60	75	G
42	R60	76	A
42	R60	77	A
42	R60	83	G
42	R60	86	A
42	R60	88	G
42	R60	92	A
42	R60	94	U
42	R60	97	C
42	R60	98	G
42	R60	99	G
42	R60	102	G
42	R60	104	G
42	R60	106	A
42	R60	107	U
42	R60	110	A
42	R60	112	U
42	R60	116	U
42	R60	118	G
42	R60	119	A
42	R60	120	A
42	R60	121	C
42	R60	124	G
42	R60	127	A

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Mol	Chain	Res	Type
42	R60	128	A
42	R60	132	C
42	R60	133	A
42	R60	134	G
42	R60	138	A
42	R60	140	A
42	R60	141	G
42	R60	142	A
42	R60	147	A
42	R60	148	A
42	R60	150	A
42	R60	153	G
42	R60	155	G
42	R60	157	A
42	R60	161	G
42	R60	167	G
42	R60	172	U
42	R60	173	A
42	R60	174	G
42	R60	180	G
42	R60	181	A
42	R60	184	A
42	R60	186	A
42	R60	187	A
42	R60	189	A
42	R60	190	A
42	R60	191	C
42	R60	192	A
42	R60	193	G
42	R60	197	A
42	R60	198	G
42	R60	199	G
42	R60	204	U
42	R60	206	A
42	R60	219	U
42	R60	220	C
42	R60	222	G
42	R60	226	G
42	R60	228	A
42	R60	238	A
42	R60	241	G
42	R60	242	C

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Mol	Chain	Res	Type
42	R60	247	U
42	R60	254	U
42	R60	255	A
42	R60	256	G
42	R60	259	G
42	R60	262	U
42	R60	263	A
42	R60	264	C
42	R60	268	G
42	R60	271	U
42	R60	273	A
42	R60	283	U
42	R60	284	C
42	R60	290	A
42	R60	292	G
42	R60	299	G
42	R60	300	A
42	R60	303	G
42	R60	304	A
42	R60	305	C
42	R60	307	G
42	R60	311	C
42	R60	314	G
42	R60	315	G
42	R60	318	C
42	R60	319	A
42	R60	320	A
42	R60	326	G
42	R60	327	C
42	R60	328	A
42	R60	329	G
42	R60	335	G
42	R60	338	A
42	R60	340	A
42	R60	341	A
42	R60	342	U
42	R60	344	A
42	R60	345	C
42	R60	347	G
42	R60	348	A
42	R60	355	C
42	R60	356	A

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Mol	Chain	Res	Type
42	R60	357	A
42	R60	358	G
42	R60	362	G
42	R60	363	C
42	R60	364	G
42	R60	367	A
42	R60	368	G
42	R60	371	A
42	R60	372	A
42	R60	373	G
42	R60	374	A
42	R60	375	G
42	R60	377	C
42	R60	378	G
42	R60	380	G
42	R60	382	A
42	R60	383	A
42	R60	384	A
42	R60	385	C
42	R60	388	G
42	R60	395	U
42	R60	396	A
42	R60	398	A
42	R60	399	A
42	R60	402	C
42	R60	407	G
42	R60	408	A
42	R60	409	G
42	R60	412	A
42	R60	414	U
42	R60	416	G
42	R60	422	A
42	R60	424	G
42	R60	425	G
42	R60	426	C
42	R60	431	G
42	R60	432	C
42	R60	437	A
42	R60	441	G
42	R60	444	G
42	R60	445	U
42	R60	446	A

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Mol	Chain	Res	Type
42	R60	449	A
42	R60	450	C
42	R60	452	A
42	R60	453	G
42	R60	454	C
42	R60	461	A
42	R60	471	A
42	R60	473	G
42	R60	474	A
42	R60	476	U
42	R60	477	G
42	R60	478	C
42	R60	481	C
42	R60	482	G
42	R60	486	A
42	R60	487	A
42	R60	490	G
42	R60	491	G
42	R60	501	G
42	R60	506	A
42	R60	509	G
42	R60	510	U
42	R60	511	A
42	R60	512	C
42	R60	521	A
42	R60	527	G
42	R60	530	U
42	R60	535	A
42	R60	536	G
42	R60	540	C
42	R60	541	G
42	R60	543	A
42	R60	544	U
42	R60	547	A
42	R60	550	G
42	R60	553	A
42	R60	554	A
42	R60	565	U
42	R60	566	A
42	R60	567	A
42	R60	568	G
42	R60	575	A

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Mol	Chain	Res	Type
42	R60	578	A
42	R60	579	G
42	R60	590	U
42	R60	593	A
42	R60	598	C
42	R60	599	G
42	R60	600	A
42	R60	601	G
42	R60	602	A
42	R60	608	A
42	R60	609	A
42	R60	610	U
42	R60	616	G
42	R60	621	G
42	R60	622	C
42	R60	623	U
42	R60	624	U
42	R60	625	A
42	R60	630	U
42	R60	633	C
42	R60	635	G
42	R60	637	G
42	R60	644	G
42	R60	647	C
42	R60	661	A
42	R60	662	U
42	R60	665	G
42	R60	668	G
42	R60	671	C
42	R60	673	A
42	R60	686	G
42	R60	687	A
42	R60	688	G
42	R60	690	A
42	R60	694	A
42	R60	700	A
42	R60	702	U
42	R60	705	A
42	R60	706	G
42	R60	707	A
42	R60	722	G
42	R60	724	A

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Mol	Chain	Res	Type
42	R60	725	G
42	R60	727	A
42	R60	728	A
42	R60	730	C
42	R60	731	G
42	R60	733	U
42	R60	734	G
42	R60	738	A
42	R60	740	G
42	R60	749	G
42	R60	752	A
42	R60	753	U
42	R60	754	G
42	R60	755	A
42	R60	757	C
42	R60	771	A
42	R60	775	U
42	R60	776	A
42	R60	780	G
42	R60	789	G
42	R60	790	G
42	R60	791	A
42	R60	795	U
42	R60	806	G
42	R60	810	U
42	R60	817	A
42	R60	818	A
42	R60	820	G
42	R60	821	G
42	R60	823	A
42	R60	825	U
42	R60	831	G
42	R60	836	A
42	R60	839	C
42	R60	840	C
42	R60	841	A
42	R60	846	G
42	R60	848	G
42	R60	866	U
42	R60	868	U
42	R60	871	C
42	R60	872	U

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Mol	Chain	Res	Type
42	R60	874	A
42	R60	875	A
42	R60	877	G
42	R60	878	C
42	R60	880	G
42	R60	881	G
42	R60	883	C
42	R60	884	A
42	R60	890	C
42	R60	898	G
42	R60	899	A
42	R60	905	G
42	R60	908	U
42	R60	909	G
42	R60	911	G
42	R60	915	A
42	R60	916	G
42	R60	917	U
42	R60	918	A
42	R60	924	U
42	R60	925	A
42	R60	926	G
42	R60	927	G
42	R60	928	U
42	R60	929	C
42	R60	930	A
42	R60	932	A
42	R60	933	G
42	R60	934	A
42	R60	936	U
42	R60	940	G
42	R60	941	C
42	R60	942	A
42	R60	952	A
42	R60	953	C
42	R60	955	A
42	R60	957	G
42	R60	958	A
42	R60	959	G
42	R60	962	G
42	R60	966	G
42	R60	967	A

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Mol	Chain	Res	Type
42	R60	968	C
42	R60	970	U
42	R60	971	U
42	R60	972	U
42	R60	974	G
42	R60	976	U
42	R60	978	A
42	R60	980	G
42	R60	987	A
42	R60	991	A
42	R60	995	A
42	R60	998	U
42	R60	999	C
42	R60	1003	A
42	R60	1006	A
42	R60	1007	U
42	R60	1008	A
42	R60	1011	A
42	R60	1012	A
42	R60	1013	A
42	R60	1014	G
42	R60	1017	A
42	R60	1018	U
42	R60	1019	C
42	R60	1021	A
42	R60	1023	A
42	R60	1024	G
42	R60	1028	U
42	R60	1029	U
42	R60	1033	A
42	R60	1039	G
42	R60	1041	A
42	R60	1042	A
42	R60	1045	A
42	R60	1046	A
42	R60	1047	G
42	R60	1052	A
42	R60	1053	A
42	R60	1054	G
42	R60	1056	A
42	R60	1057	C
42	R60	1058	A

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Mol	Chain	Res	Type
42	R60	1059	G
42	R60	1060	G
42	R60	1062	C
42	R60	1063	A
42	R60	1064	G
42	R60	1066	G
42	R60	1075	A
42	R60	1076	G
42	R60	1077	A
42	R60	1078	U
42	R60	1088	U
42	R60	1089	G
42	R60	1090	C
42	R60	1092	C
42	R60	1094	C
42	R60	1099	U
42	R60	1100	A
42	R60	1102	A
42	R60	1103	G
42	R60	1104	U
42	R60	1105	G
42	R60	1106	G
42	R60	1111	A
42	R60	1112	G
42	R60	1116	A
42	R60	1117	A
42	R60	1118	A
42	R60	1119	C
42	R60	1120	A
42	R60	1121	A
42	R60	1122	A
42	R60	1123	U
42	R60	1124	A
42	R60	1125	G
42	R60	1126	A
42	R60	1127	A
42	R60	1128	G
42	R60	1129	U
42	R60	1130	A
42	R60	1135	U
42	R60	1136	G
42	R60	1137	A

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Mol	Chain	Res	Type
42	R60	1139	C
42	R60	1141	A
42	R60	1142	G
42	R60	1146	G
42	R60	1152	G
42	R60	1154	A
42	R60	1158	U
42	R60	1159	A
42	R60	1160	A
42	R60	1161	U
42	R60	1162	G
42	R60	1170	G
42	R60	1171	A
42	R60	1175	A
42	R60	1176	G
42	R60	1177	G
42	R60	1179	A
42	R60	1182	G
42	R60	1185	A
42	R60	1191	C
42	R60	1192	G
42	R60	1194	U
42	R60	1195	A
42	R60	1196	U
42	R60	1202	U
42	R60	1203	A
42	R60	1204	A
42	R60	1205	G
42	R60	1210	G
42	R60	1211	A
42	R60	1214	A
42	R60	1216	U
42	R60	1217	G
42	R60	1219	G
42	R60	1223	C
42	R60	1225	G
42	R60	1227	U
42	R60	1230	U
42	R60	1237	C
42	R60	1238	A
42	R60	1239	C
42	R60	1240	C

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Mol	Chain	Res	Type
42	R60	1241	G
42	R60	1243	C
42	R60	1246	U
42	R60	1249	U
42	R60	1250	U
42	R60	1251	A
42	R60	1260	G
42	R60	1262	A
42	R60	1263	A
42	R60	1264	C
42	R60	1266	A
42	R60	1267	G
42	R60	1270	G
42	R60	1274	A
42	R60	1275	C
42	R60	1276	A
42	R60	1280	G
42	R60	1282	A
42	R60	1283	A
42	R60	1284	G
42	R60	1287	A
42	R60	1294	G
42	R60	1295	C
42	R60	1296	A
42	R60	1297	G
42	R60	1301	U
42	R60	1302	C
42	R60	1307	U
42	R60	1310	G
42	R60	1314	C
42	R60	1315	A
42	R60	1316	A
42	R60	1317	G
42	R60	1320	G
42	R60	1322	A
42	R60	1326	A
42	R60	1327	G
42	R60	1328	G
42	R60	1329	C
42	R60	1331	G
42	R60	1340	G
42	R60	1341	A

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Mol	Chain	Res	Type
42	R60	1342	A
42	R60	1343	C
42	R60	1348	A
42	R60	1352	G
42	R60	1353	G
42	R60	1354	A
42	R60	1355	U
42	R60	1356	C
42	R60	1357	A

All (353) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	21	U
1	L50	22	U
1	L50	73	A
1	L50	75	C
1	L50	135	A
1	L50	211	U
1	L50	214	A
1	L50	225	G
1	L50	236	A
1	L50	265	A
1	L50	276	U
1	L50	308	A
1	L50	330	G
1	L50	351	G
1	L50	363	U
1	L50	396	G
1	L50	424	G
1	L50	463	A
1	L50	466	C
1	L50	523	A
1	L50	535	A
1	L50	550	G
1	L50	563	U
1	L50	567	A
1	L50	600	G
1	L50	657	A
1	L50	659	G

*Continued on next page...*

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Mol	Chain	Res	Type
1	L50	667	G
1	L50	710	A
1	L50	712	C
1	L50	732	G
1	L50	741	G
1	L50	778	A
1	L50	782	G
1	L50	853	A
1	L50	996	A
1	L50	1000	G
1	L50	1008	U
1	L50	1017	A
1	L50	1018	U
1	L50	1032	A
1	L50	1061	G
1	L50	1089	U
1	L50	1134	A
1	L50	1148	A
1	L50	1172	A
1	L50	1182	A
1	L50	1256	U
1	L50	1277	G
1	L50	1384	U
1	L50	1394	U
1	L50	1395	U
1	L50	1449	A
1	L50	1454	U
1	L50	1474	G
1	L50	1485	G
1	L50	1491	U
1	L50	1564	U
1	L50	1596	A
1	L50	1611	A
1	L50	1644	U
1	L50	1697	G
1	L50	1709	G
1	L50	1717	A
1	L50	1743	G
1	L50	1749	A
1	L50	1798	U
1	L50	1800	U
1	L50	1808	A

*Continued on next page...*

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Mol	Chain	Res	Type
1	L50	1809	A
1	L50	1835	G
1	L50	1838	G
1	L50	1931	C
1	L50	1942	U
1	L50	1945	C
1	L50	1959	A
1	L50	1966	A
1	L50	1967	A
1	L50	2015	C
1	L50	2036	A
1	L50	2051	C
1	L50	2060	A
1	L50	2075	A
1	L50	2212	G
1	L50	2240	A
1	L50	2254	U
1	L50	2255	A
1	L50	2347	U
1	L50	2351	U
1	L50	2363	A
1	L50	2419	G
1	L50	2420	C
1	L50	2447	A
1	L50	2452	A
1	L50	2476	G
1	L50	2481	U
1	L50	2519	G
1	L50	2532	A
1	L50	2596	G
1	L50	2597	G
2	L70	32	A
2	L70	41	G
2	L70	62	A
2	L70	109	U
42	S60	71	U
42	S60	76	A
42	S60	118	G
42	S60	127	A
42	S60	180	G
42	S60	186	A
42	S60	190	A

*Continued on next page...*

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Mol	Chain	Res	Type
42	S60	191	C
42	S60	218	A
42	S60	225	A
42	S60	226	G
42	S60	256	G
42	S60	262	U
42	S60	283	U
42	S60	303	G
42	S60	328	A
42	S60	339	A
42	S60	355	C
42	S60	372	A
42	S60	383	A
42	S60	407	G
42	S60	408	A
42	S60	424	G
42	S60	425	G
42	S60	445	U
42	S60	473	G
42	S60	509	G
42	S60	511	A
42	S60	553	A
42	S60	565	U
42	S60	598	C
42	S60	661	A
42	S60	724	A
42	S60	753	U
42	S60	776	A
42	S60	788	G
42	S60	819	A
42	S60	877	G
42	S60	914	U
42	S60	916	G
42	S60	917	U
42	S60	918	A
42	S60	923	A
42	S60	925	A
42	S60	927	G
42	S60	934	A
42	S60	954	G
42	S60	970	U
42	S60	980	G

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Mol	Chain	Res	Type
42	S60	1007	U
42	S60	1018	U
42	S60	1021	A
42	S60	1023	A
42	S60	1045	A
42	S60	1057	C
42	S60	1077	A
42	S60	1088	U
42	S60	1089	G
42	S60	1103	G
42	S60	1105	G
42	S60	1125	G
42	S60	1135	U
42	S60	1141	A
42	S60	1175	A
42	S60	1176	G
42	S60	1262	A
42	S60	1314	C
42	S60	1321	U
42	S60	1328	G
42	S60	1356	C
1	K50	2	U
1	K50	3	A
1	K50	21	U
1	K50	22	U
1	K50	73	A
1	K50	75	C
1	K50	135	A
1	K50	211	U
1	K50	214	A
1	K50	225	G
1	K50	236	A
1	K50	265	A
1	K50	276	U
1	K50	308	A
1	K50	330	G
1	K50	351	G
1	K50	363	U
1	K50	396	G
1	K50	424	G
1	K50	463	A
1	K50	466	C

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Mol	Chain	Res	Type
1	K50	523	A
1	K50	535	A
1	K50	550	G
1	K50	563	U
1	K50	567	A
1	K50	600	G
1	K50	657	A
1	K50	659	G
1	K50	667	G
1	K50	710	A
1	K50	712	C
1	K50	732	G
1	K50	741	G
1	K50	778	A
1	K50	782	G
1	K50	853	A
1	K50	996	A
1	K50	1000	G
1	K50	1008	U
1	K50	1017	A
1	K50	1018	U
1	K50	1032	A
1	K50	1061	G
1	K50	1089	U
1	K50	1134	A
1	K50	1148	A
1	K50	1172	A
1	K50	1182	A
1	K50	1256	U
1	K50	1277	G
1	K50	1384	U
1	K50	1394	U
1	K50	1395	U
1	K50	1449	A
1	K50	1454	U
1	K50	1474	G
1	K50	1485	G
1	K50	1491	U
1	K50	1564	U
1	K50	1596	A
1	K50	1611	A
1	K50	1614	G

*Continued on next page...*

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Mol	Chain	Res	Type
1	K50	1644	U
1	K50	1697	G
1	K50	1709	G
1	K50	1717	A
1	K50	1743	G
1	K50	1749	A
1	K50	1798	U
1	K50	1800	U
1	K50	1808	A
1	K50	1809	A
1	K50	1835	G
1	K50	1838	G
1	K50	1931	C
1	K50	1942	U
1	K50	1945	C
1	K50	1959	A
1	K50	1966	A
1	K50	1967	A
1	K50	2015	C
1	K50	2036	A
1	K50	2051	C
1	K50	2060	A
1	K50	2075	A
1	K50	2212	G
1	K50	2240	A
1	K50	2254	U
1	K50	2255	A
1	K50	2347	U
1	K50	2351	U
1	K50	2363	A
1	K50	2419	G
1	K50	2420	C
1	K50	2447	A
1	K50	2452	A
1	K50	2476	G
1	K50	2481	U
1	K50	2519	G
1	K50	2532	A
1	K50	2596	G
1	K50	2597	G
2	K70	32	A
2	K70	41	G

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Mol	Chain	Res	Type
2	K70	62	A
2	K70	109	U
42	R60	71	U
42	R60	76	A
42	R60	118	G
42	R60	127	A
42	R60	180	G
42	R60	186	A
42	R60	190	A
42	R60	191	C
42	R60	218	A
42	R60	225	A
42	R60	226	G
42	R60	256	G
42	R60	262	U
42	R60	283	U
42	R60	303	G
42	R60	328	A
42	R60	339	A
42	R60	355	C
42	R60	372	A
42	R60	383	A
42	R60	407	G
42	R60	408	A
42	R60	424	G
42	R60	425	G
42	R60	445	U
42	R60	473	G
42	R60	509	G
42	R60	511	A
42	R60	553	A
42	R60	565	U
42	R60	598	C
42	R60	661	A
42	R60	724	A
42	R60	753	U
42	R60	776	A
42	R60	788	G
42	R60	819	A
42	R60	877	G
42	R60	914	U
42	R60	916	G

*Continued on next page...*

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Mol	Chain	Res	Type
42	R60	917	U
42	R60	918	A
42	R60	923	A
42	R60	925	A
42	R60	927	G
42	R60	934	A
42	R60	954	G
42	R60	970	U
42	R60	980	G
42	R60	1007	U
42	R60	1018	U
42	R60	1021	A
42	R60	1023	A
42	R60	1045	A
42	R60	1057	C
42	R60	1077	A
42	R60	1088	U
42	R60	1089	G
42	R60	1103	G
42	R60	1105	G
42	R60	1125	G
42	R60	1135	U
42	R60	1141	A
42	R60	1175	A
42	R60	1176	G
42	R60	1262	A
42	R60	1314	C
42	R60	1321	U
42	R60	1328	G
42	R60	1356	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

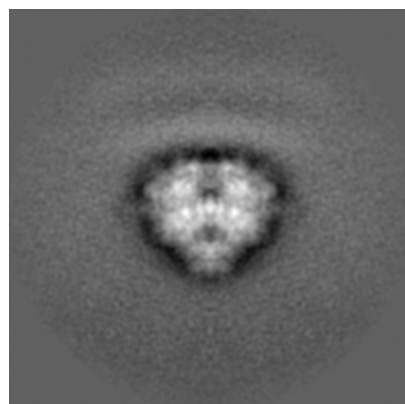
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14020. These allow visual inspection of the internal detail of the map and identification of artifacts.

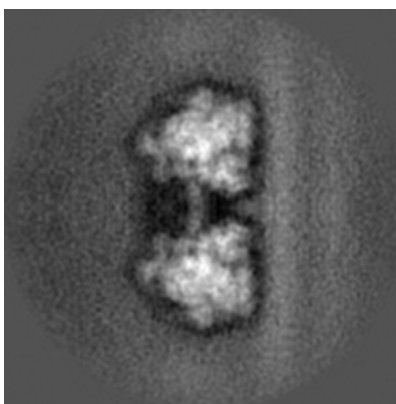
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

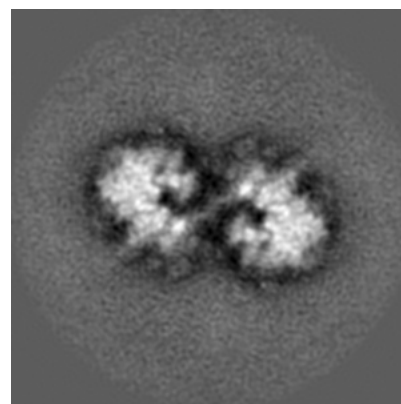
#### 6.1.1 Primary map



X

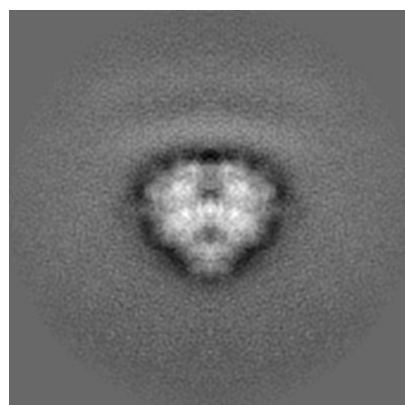


Y

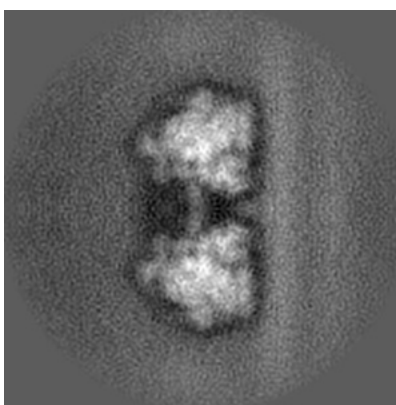


Z

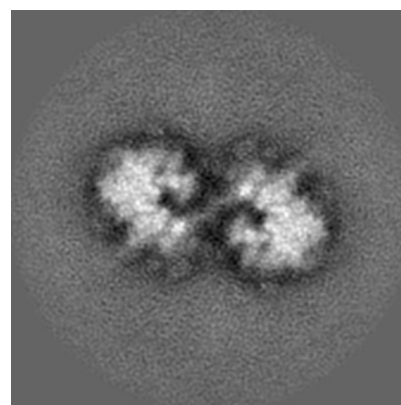
#### 6.1.2 Raw map



X



Y

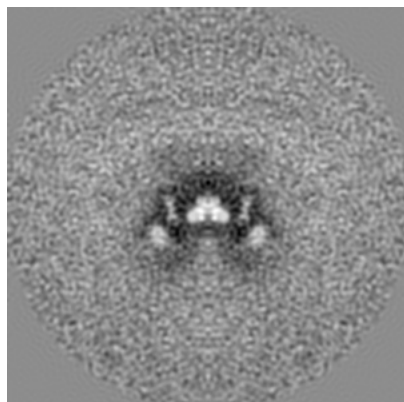


Z

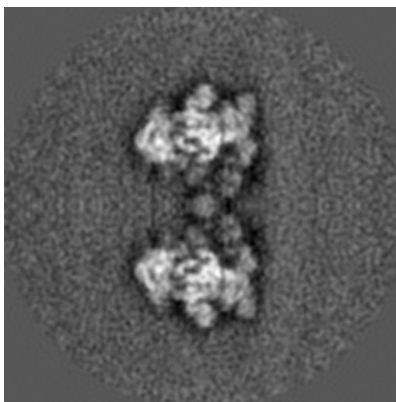
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

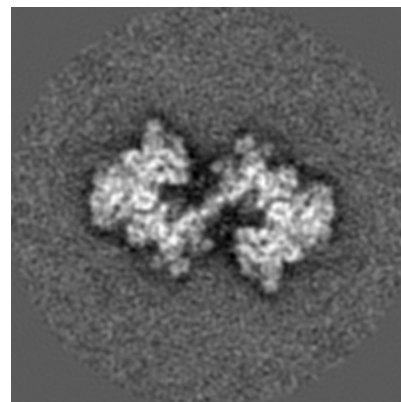
### 6.2.1 Primary map



X Index: 84

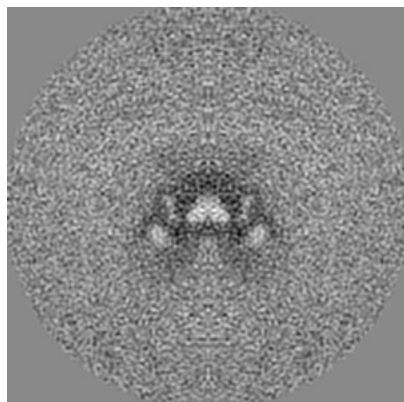


Y Index: 84

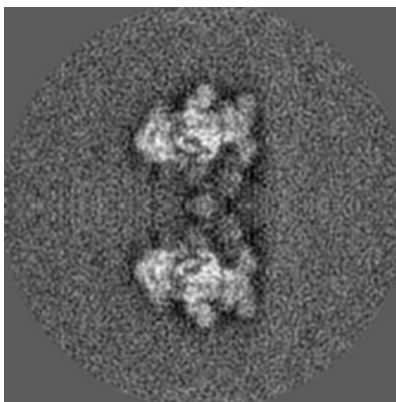


Z Index: 84

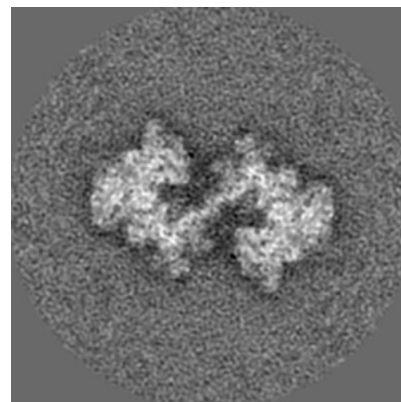
### 6.2.2 Raw map



X Index: 84



Y Index: 84

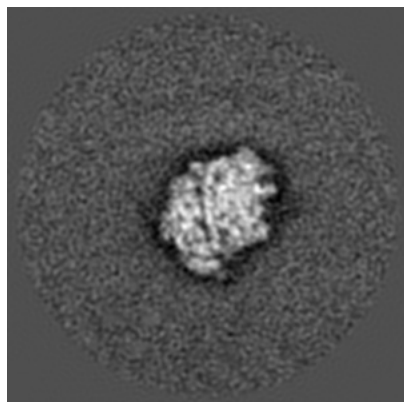


Z Index: 84

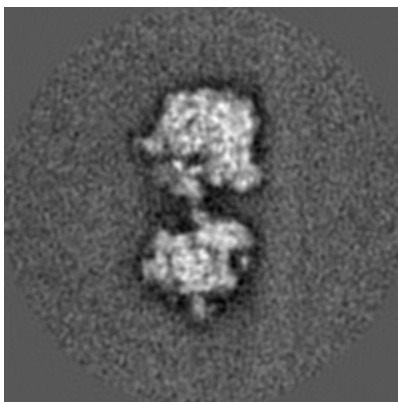
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

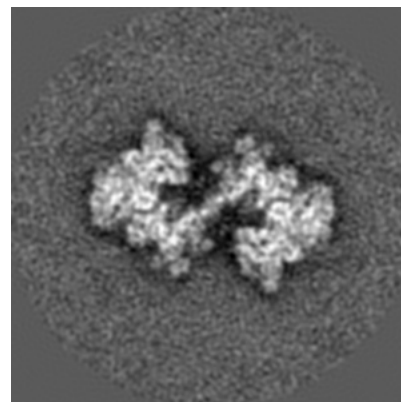
### 6.3.1 Primary map



X Index: 54

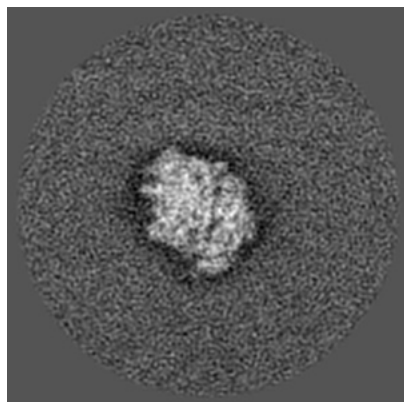


Y Index: 75

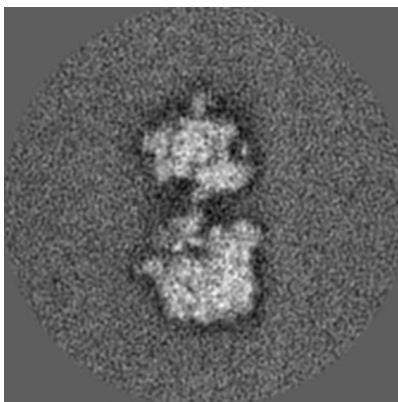


Z Index: 84

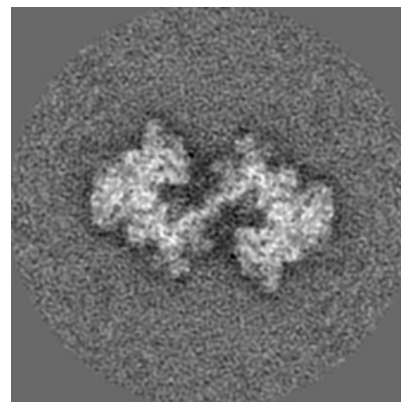
### 6.3.2 Raw map



X Index: 114



Y Index: 93

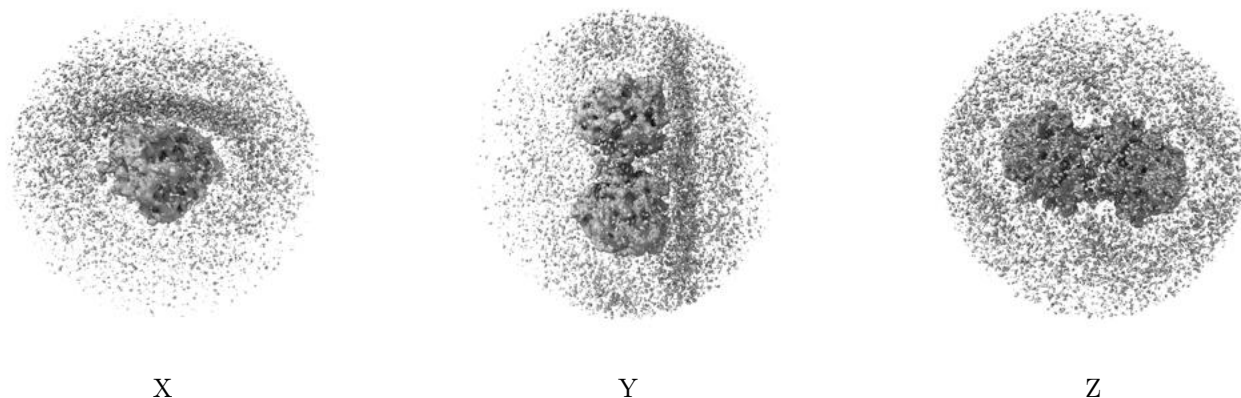


Z Index: 84

The images above show the largest variance slices of the map in three orthogonal directions.

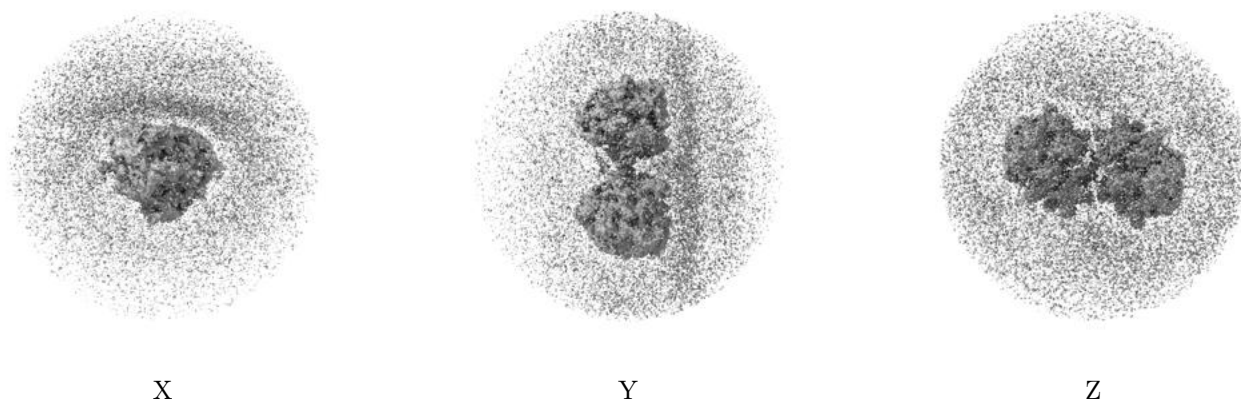
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

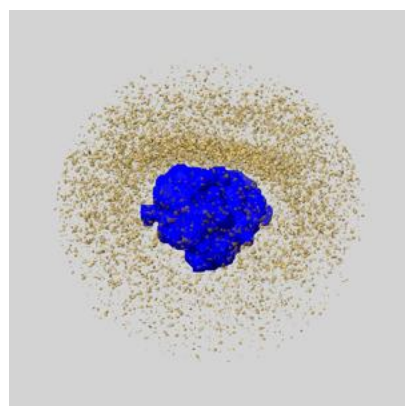
## 6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

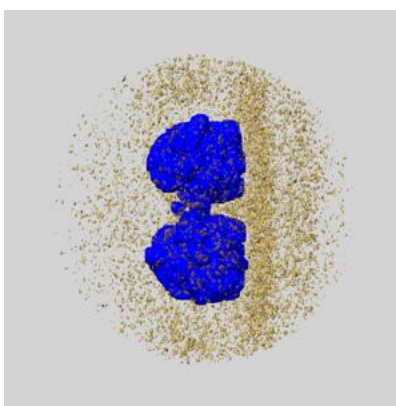
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

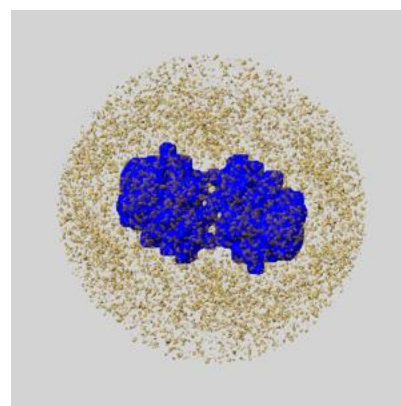
### 6.5.1 emd\_14020\_msk\_1.map [i](#)



X



Y

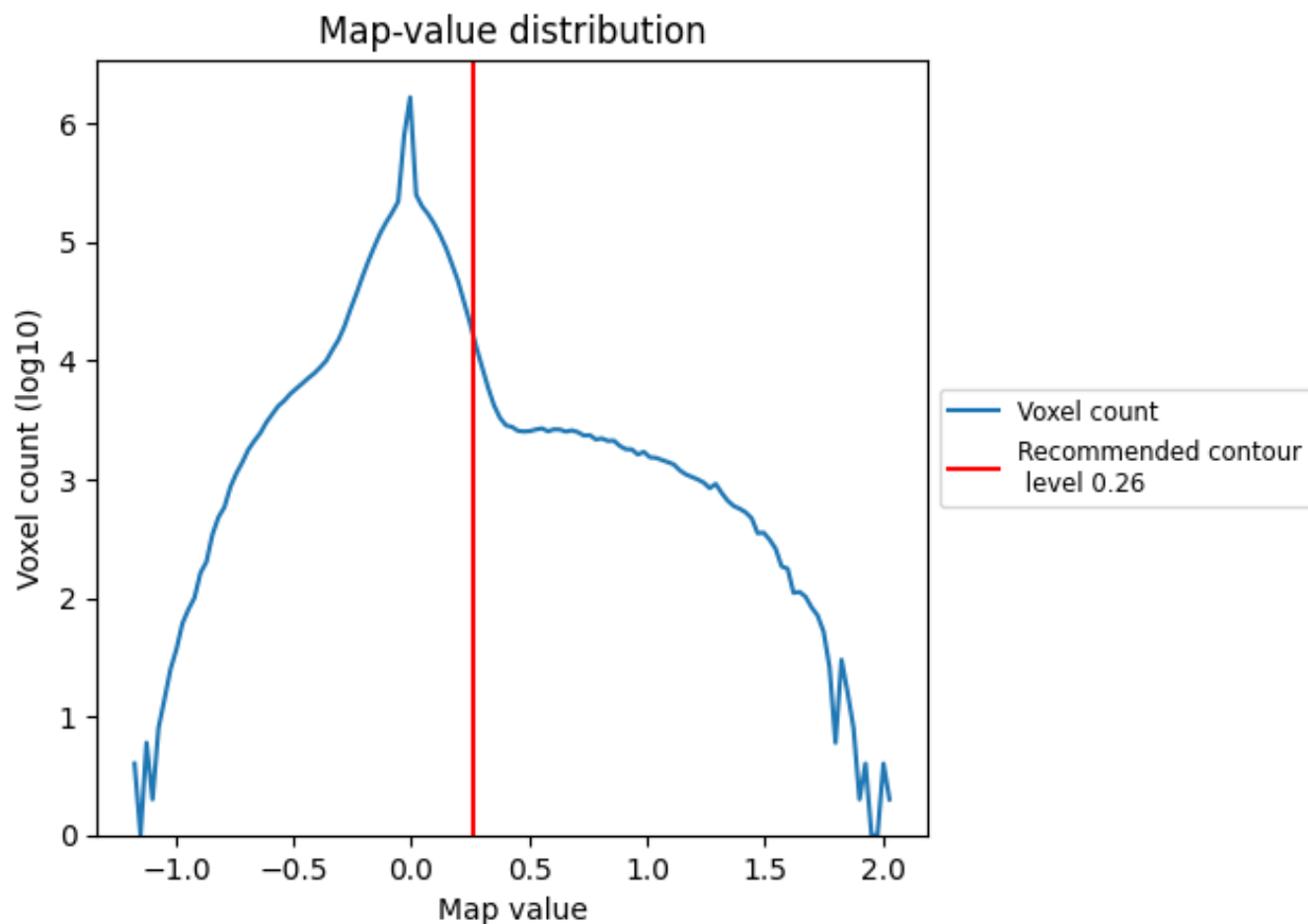


Z

## 7 Map analysis [i](#)

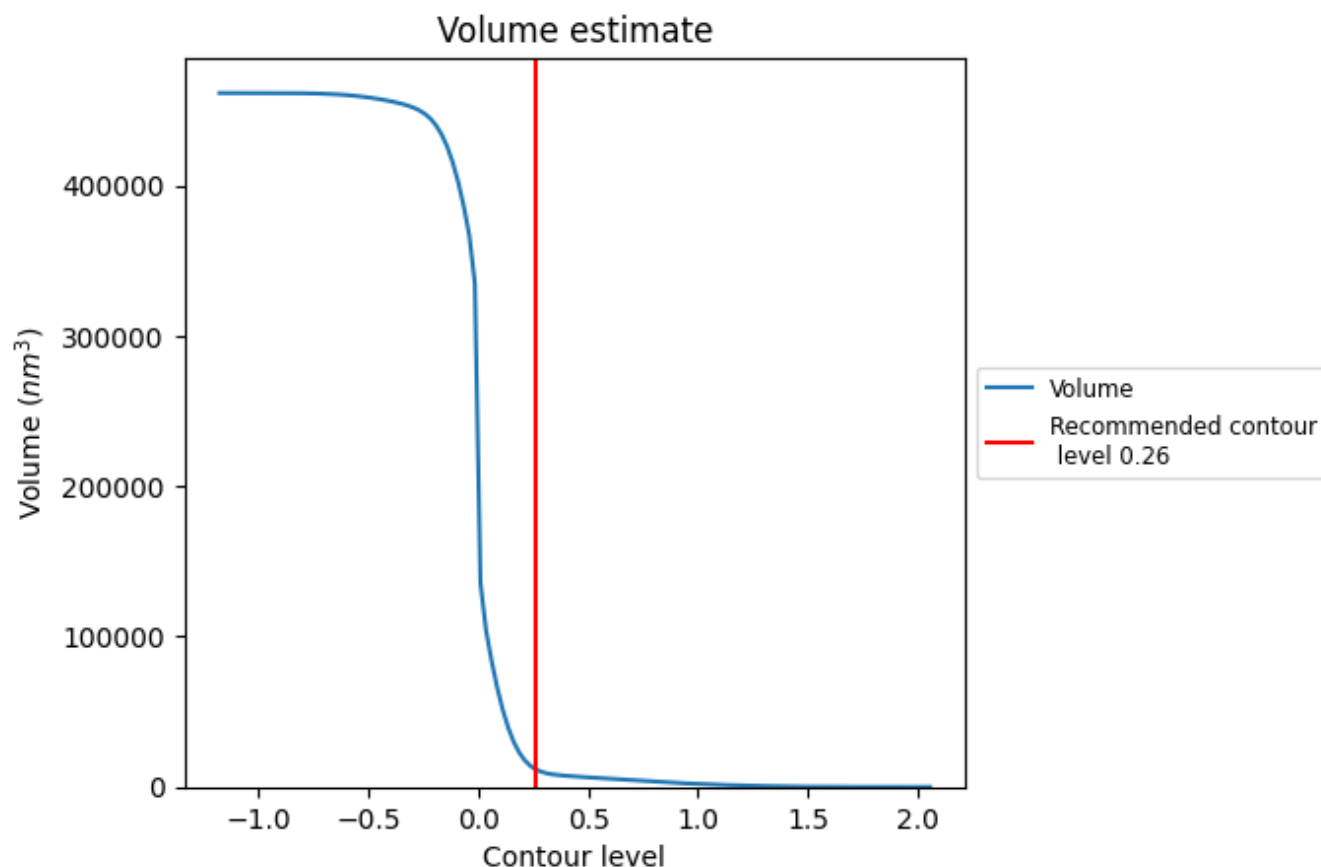
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

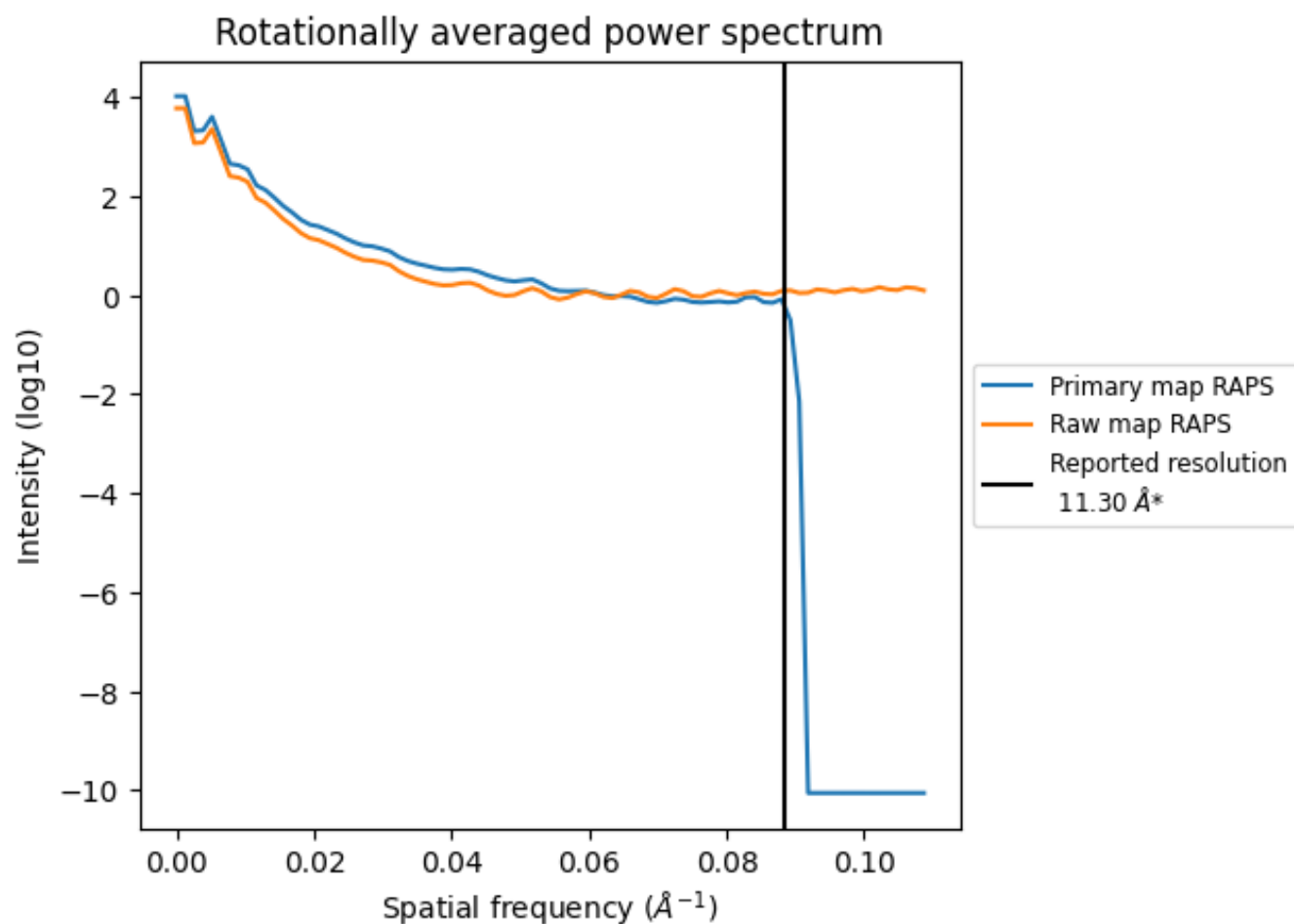
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11920 nm<sup>3</sup>; this corresponds to an approximate mass of 10768 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

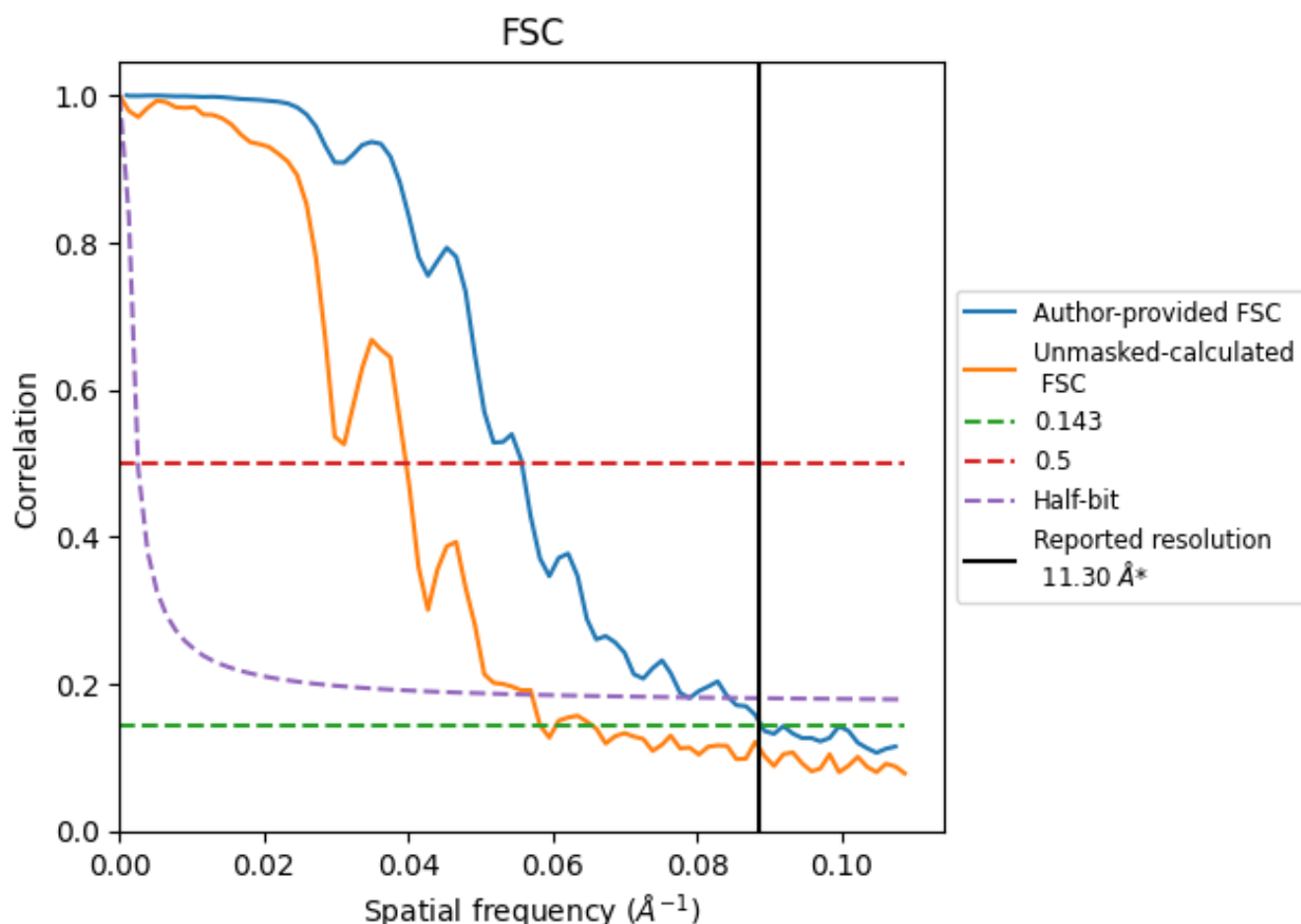


\*Reported resolution corresponds to spatial frequency of 0.088 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.088  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

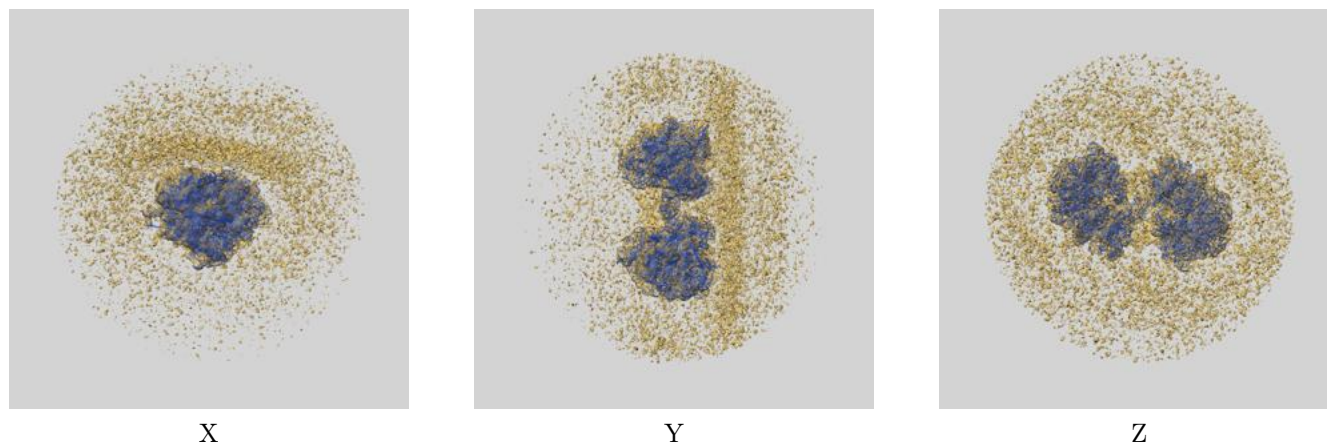
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	11.30	-	-
Author-provided FSC curve	11.26	17.95	12.69
Unmasked-calculated*	17.15	25.19	17.51

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 17.15 differs from the reported value 11.3 by more than 10 %

## 9 Map-model fit [i](#)

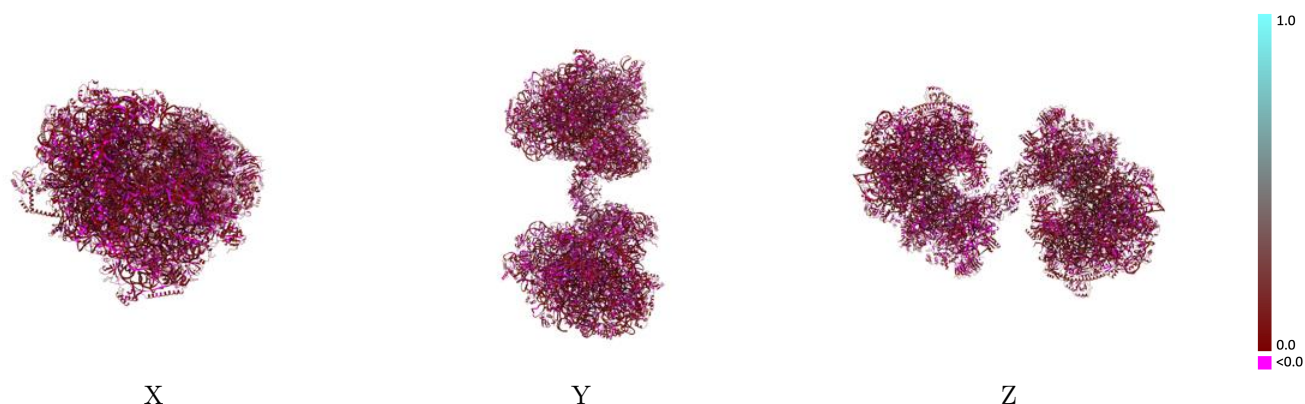
This section contains information regarding the fit between EMDB map EMD-14020 and PDB model 7QJH. Per-residue inclusion information can be found in section 3 on page 25.

### 9.1 Map-model overlay [i](#)



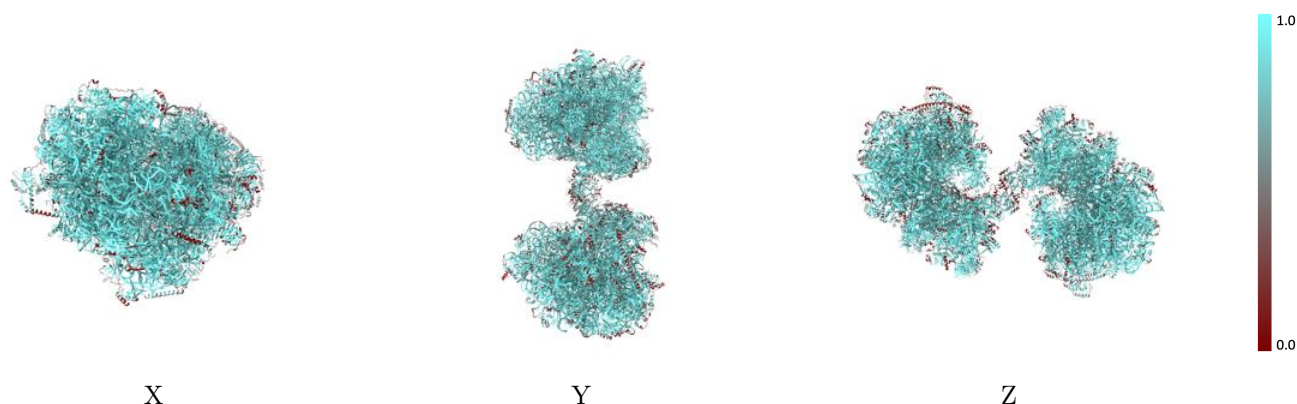
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



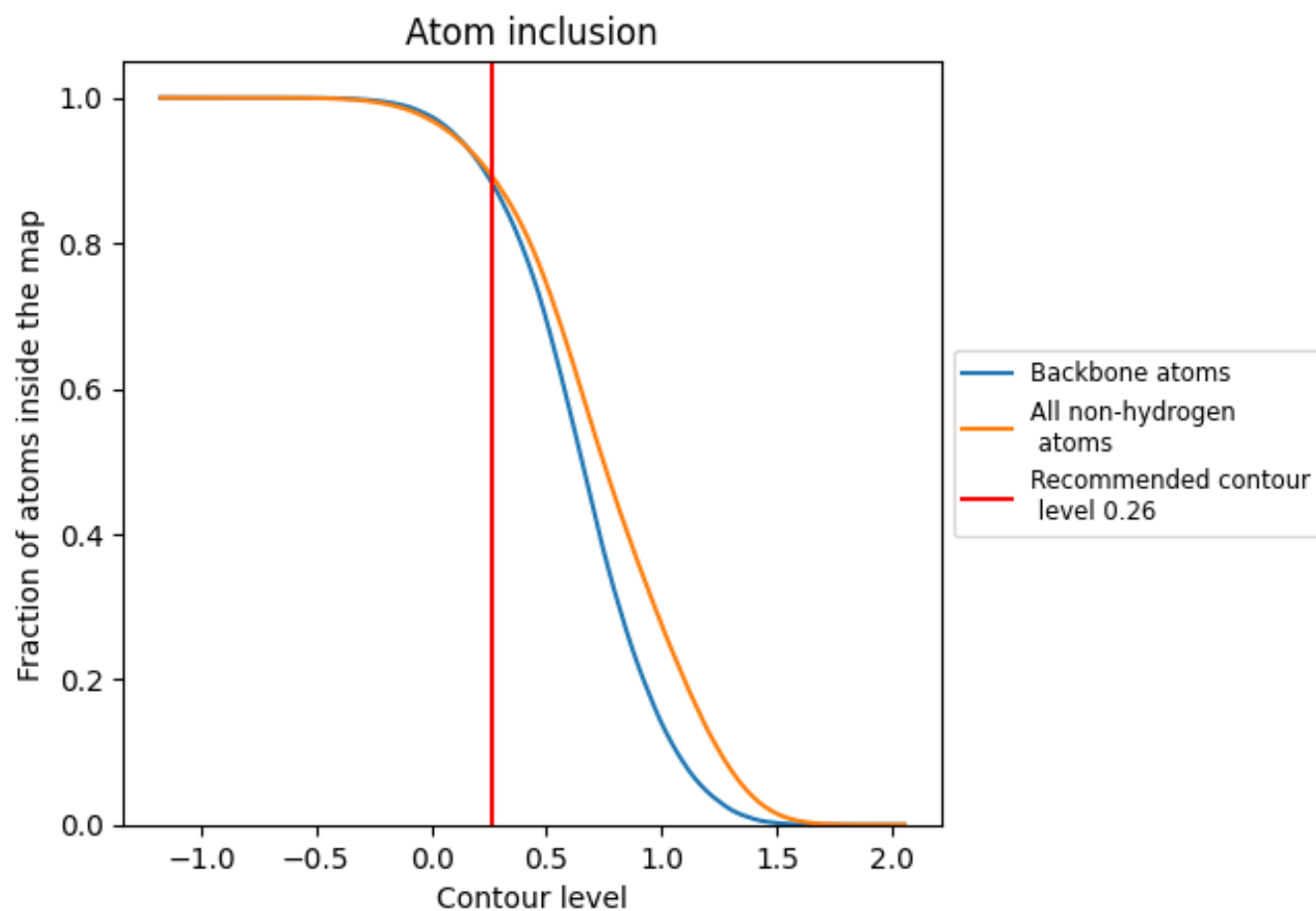
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.26).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ




















































































The table lists the average atom inclusion at the recommended contour level (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8938	 0.0580
K50	 0.9740	 0.0750
K70	 0.9237	 0.0640
KA0	 0.9243	 0.0230
KAA	 0.8761	 0.0130
KB0	 0.8760	 0.0170
KC0	 0.7802	 0.0190
KCC	 0.7938	 0.0520
KD0	 0.6530	 0.0380
KDD	 0.8465	 0.0400
KE0	 0.5112	 0.0470
KEE	 0.8083	 0.0300
KF0	 0.6800	 0.0500
KFF	 0.7652	 0.0450
KG0	 0.7572	 0.0620
KGG	 0.8904	 0.0100
KH0	 0.7608	 0.0350
KHH	 0.7603	 0.0580
KI0	 0.8608	 0.0020
KII	 0.7650	 0.0560
KJ0	 0.8337	 0.0430
KJJ	 0.9591	 0.0130
KL0	 0.7519	 0.0470
KLL	 0.9830	 -0.0090
KM0	 0.4891	 0.0600
KMM	 0.8927	 0.0300
KN0	 0.9950	 0.0020
KO0	 0.7545	 0.0450
KOO	 0.9602	 0.0280
KP0	 0.8594	 0.0400
KPP	 0.9065	 0.0450
KQ0	 0.8011	 0.0280
KR0	 0.7904	 0.0270
KS0	 0.7413	 0.0420
KT0	 0.6992	 0.0280























































































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Chain	Atom inclusion	Q-score
KU0	 0.8494	 0.0750
KV0	 0.9448	 0.0080
KW0	 0.6699	 0.0200
KX0	 0.8413	 0.0300
KY0	 0.7211	 0.0360
KZ0	 0.7992	 0.0570
L50	 0.9829	 0.0820
L70	 0.9843	 0.1000
LA0	 0.9200	 0.0270
LAA	 0.9244	 0.0190
LB0	 0.8679	 0.0190
LC0	 0.9073	 0.0320
LCC	 0.7393	 0.0720
LD0	 0.7678	 0.0410
LDD	 0.9347	 0.0280
LE0	 0.6741	 0.0590
LEE	 0.9226	 0.0270
LF0	 0.8345	 0.0690
LFF	 0.8923	 0.0400
LG0	 0.7170	 0.0500
LGG	 0.9030	 0.0020
LH0	 0.8502	 0.0500
LHH	 0.8099	 0.0360
LI0	 0.8696	 0.0390
LII	 0.8316	 0.0480
LJ0	 0.7747	 0.0430
LJJ	 0.9971	 0.0300
LL0	 0.8589	 0.0250
LLL	 1.0000	 -0.0100
LM0	 0.6416	 0.0950
LMM	 0.7195	 0.0340
LN0	 0.9907	 0.0030
LO0	 0.8060	 0.0600
LOO	 0.8331	 0.0230
LP0	 0.9309	 0.0320
LPP	 0.8084	 0.0220
LQ0	 0.9108	 0.0530
LR0	 0.7766	 0.0080
LS0	 0.8132	 0.0760
LT0	 0.8024	 0.0410
LU0	 0.7691	 0.0490
LV0	 0.8372	 0.0300

































































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Chain	Atom inclusion	Q-score
LW0	 0.6663	 0.0280
LX0	 0.8586	 0.0120
LY0	 0.8445	 0.0400
LZ0	 0.7463	 0.0490
MD1	 0.8376	 0.0700
MD2	 0.7763	 0.0590
R60	 0.9608	 0.0630
RA0	 0.7619	 0.0400
RAA	 0.9311	 0.0230
RB0	 0.8703	 0.0560
RBB	 0.7887	 0.0390
RC0	 0.8247	 0.0240
RCC	 0.8966	 0.0420
RD0	 0.7777	 0.0370
RDD	 0.8277	 0.0060
RE0	 0.9233	 0.0270
REE	 0.5229	 0.0270
RF0	 0.8957	 0.0480
RFF	 0.3952	 0.0250
RG0	 0.7427	 0.0520
RGG	 0.8174	 0.0370
RH0	 0.8176	 0.0640
RI0	 0.8972	 0.0420
RJ0	 0.9449	 0.0350
RK0	 0.8014	 0.0380
RL0	 0.8163	 0.0290
RM0	 0.5575	 0.0460
RN0	 0.8873	 0.0280
RO0	 0.9101	 0.0310
RP0	 0.6002	 0.0280
RQ0	 0.9166	 0.0240
RR0	 0.7983	 0.0430
RS0	 0.6307	 0.0480
RT0	 0.7069	 0.0310
RU0	 0.8851	 0.0430
RV0	 0.9055	 0.0490
RW0	 0.9343	 0.0030
RX0	 0.6791	 0.0060
RY0	 0.7507	 0.0470
RZ0	 0.8182	 0.0760
S60	 0.9833	 0.0840
SA0	 0.7761	 0.0570

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Chain	Atom inclusion	Q-score
SAA	 0.8584	 0.0090
SB0	 0.8627	 0.0690
SBB	 0.7194	 0.0440
SC0	 0.8159	 0.0580
SCC	 0.8513	 0.0480
SD0	 0.7268	 0.0530
SDD	 0.8428	 0.0230
SE0	 0.8456	 0.0460
SEE	 0.5482	 0.0330
SF0	 0.9356	 0.0520
SFF	 0.3086	 0.0270
SG0	 0.7692	 0.0460
SGG	 0.7596	 0.0610
SH0	 0.6953	 0.0780
SI0	 0.9360	 0.0220
SJ0	 0.8481	 0.0460
SK0	 0.7875	 0.0610
SL0	 0.8063	 0.0330
SM0	 0.4657	 0.0470
SN0	 0.9324	 0.0200
SO0	 0.9592	 0.0180
SP0	 0.7844	 0.0680
SQ0	 0.9112	 0.0350
SR0	 0.6838	 0.0370
SS0	 0.8653	 0.0650
ST0	 0.7377	 0.0590
SU0	 0.7942	 0.0370
SV0	 0.8425	 0.0640
SW0	 0.8970	 0.0390
SX0	 0.8279	 0.0160
SY0	 0.6618	 0.0680
SZ0	 0.8312	 0.0760