



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:56 PM UTC

PDB ID : 6T4Q / pdb_00006t4q
EMDB ID : EMD-10377
Title : Structure of yeast 80S ribosome stalled on the CGA-CCG inhibitory codon combination.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-14
Resolution : 2.60 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

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>.

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

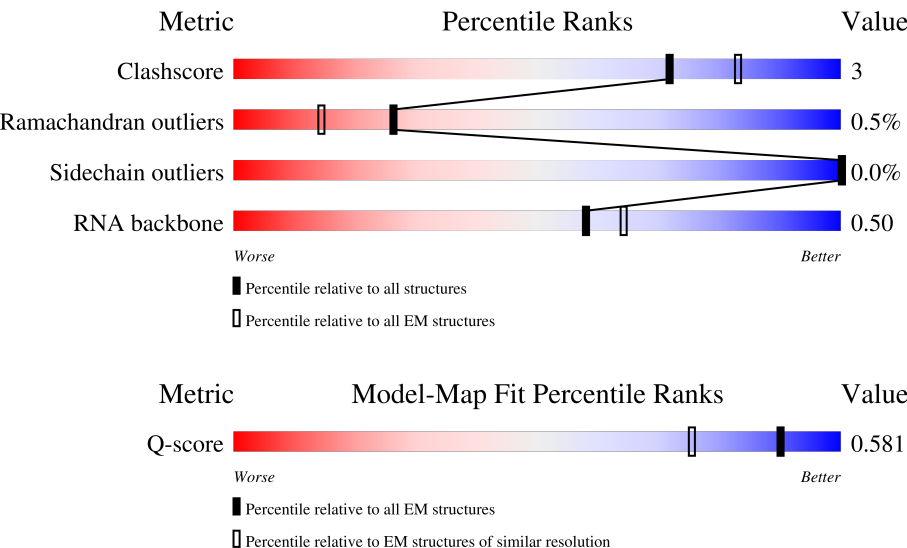
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.60 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.



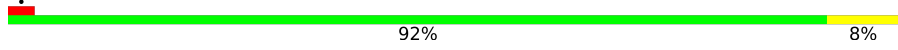
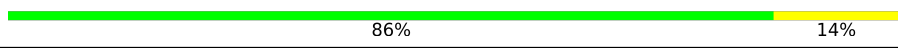
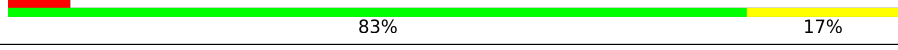
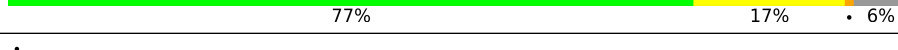
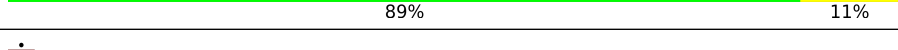
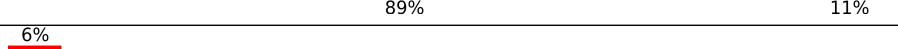
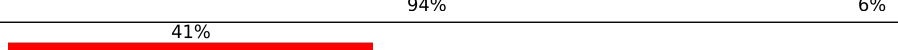
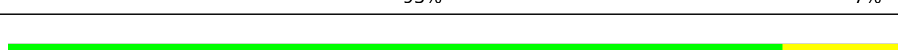
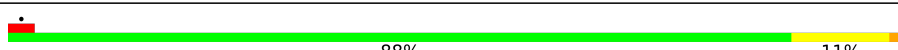
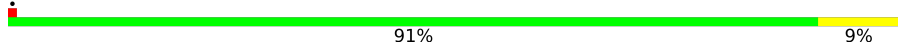
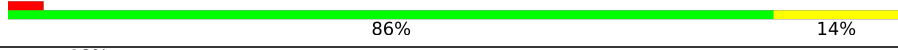
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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 ≥ 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	C2	1798	6% 65% 27% 7% .
2	SB	232	. 84% 12% . .
3	SP	117	9% 86% 14%

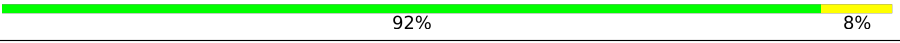
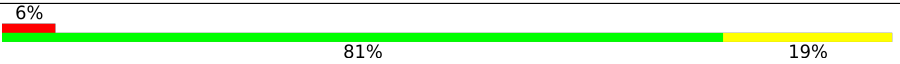
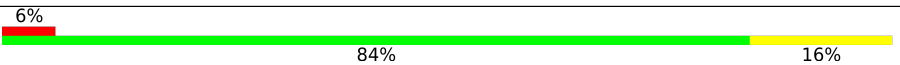
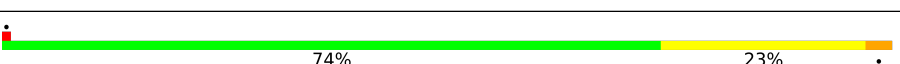
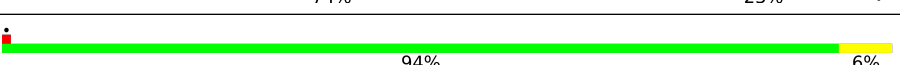
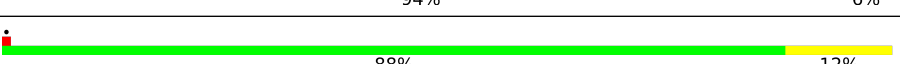
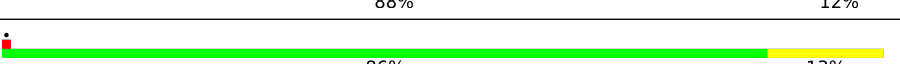
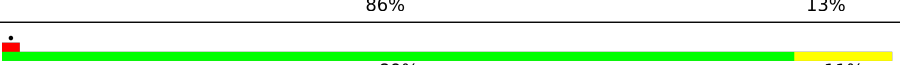
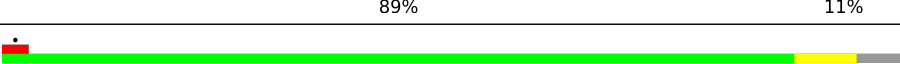
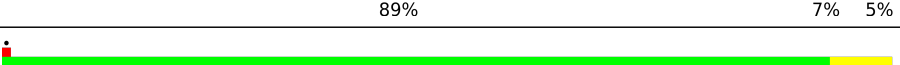
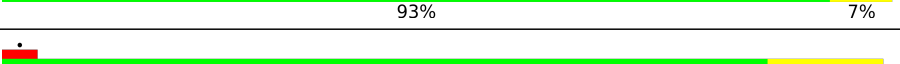
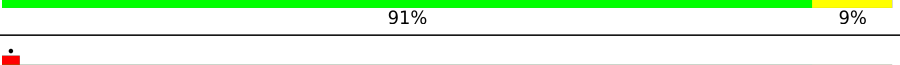
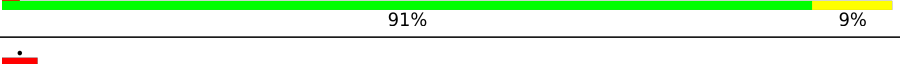
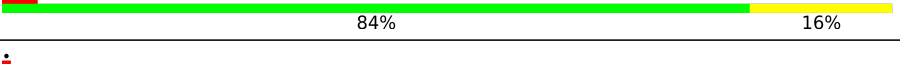
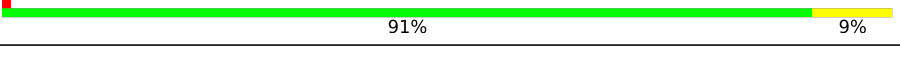
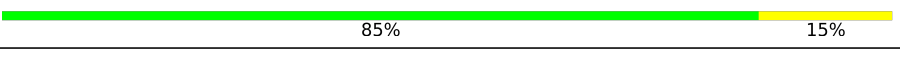
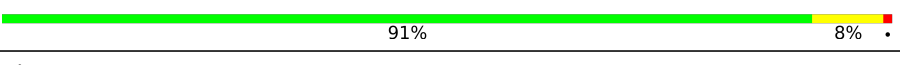
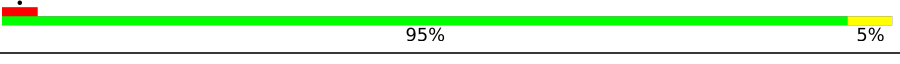
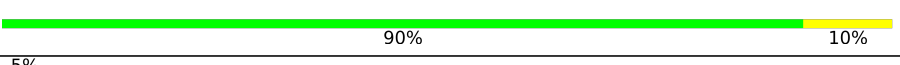
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Mol	Chain	Length	Quality of chain
4	SC	216	
5	SD	222	
6	SE	258	
7	SF	206	
8	SG	228	
9	SH	184	
10	SI	198	
11	SJ	184	
12	SK	92	
13	SL	144	
14	SM	121	
15	SN	150	
16	SO	127	
17	SQ	141	
18	SR	125	
19	SS	145	
20	ST	143	
21	SU	100	
22	SV	87	
23	SW	129	
24	SX	144	
25	SY	134	
26	SZ	82	
27	Sa	97	
28	Sb	81	

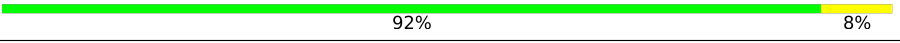
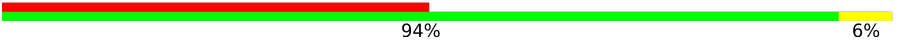
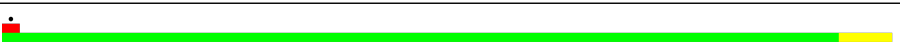
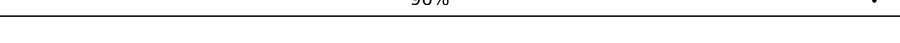
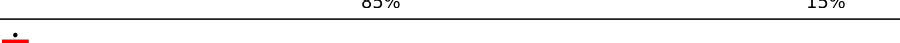
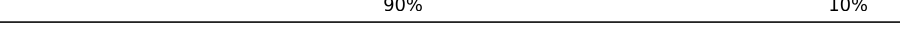
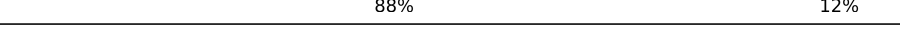
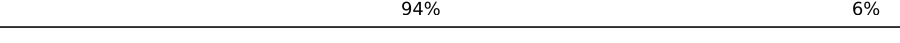
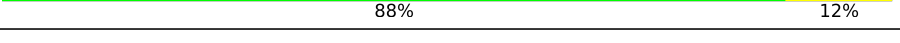
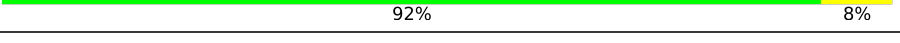
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Mol	Chain	Length	Quality of chain
29	Sd	53	
30	Se	60	
31	Sf	73	
32	Sg	312	
33	Sc	63	
34	C4	121	
35	C3	158	
36	LA	251	
37	LB	386	
38	LC	361	
39	LD	294	
40	LE	175	
41	LF	222	
42	LG	233	
43	LH	191	
44	LI	218	
45	LJ	169	
46	LL	193	
47	LM	136	
48	LN	203	
49	LO	197	
50	LP	183	
51	LQ	185	
52	LR	188	
53	LS	171	

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Mol	Chain	Length	Quality of chain
54	LT	159	
55	LU	100	
56	LV	136	
57	LW	126	
58	LX	121	
59	LY	125	
60	LZ	135	
61	La	148	
62	Lb	58	
63	Lc	96	
64	Ld	109	
65	Le	127	
66	Lf	106	
67	Lg	112	
68	Lh	119	
69	Li	99	
70	Lj	85	
71	Lk	77	
72	Ll	50	
73	Lm	52	
74	Ln	25	
75	Lo	103	
76	Lp	91	
77	C1	3184	
78	5	30	

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Mol	Chain	Length	Quality of chain
79	6	76	5% 78% 21%
80	7	75	65% 31%
81	8	6	17% 67% 33%
82	SA	206	89% 11%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 203581 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 3 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 7 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SH	184	Total	C	N	O	S	0	0
			1473	946	263	264			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 19 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	SY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	SZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 31 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Sf	97	ALA	LYS	conflict	UNP P05759

- Molecule 32 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sg	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 33 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 34 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 35 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 36 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 37 is a protein called 60S ribosomal protein L3.

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

- Molecule 38 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 40 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	132	ALA	THR	conflict	UNP P05739
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 41 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 44 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 45 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 46 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LP	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 51 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LR	188	Total	C	N	O	S	0	0
			1515	932	323	260			

- Molecule 53 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 54 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LW	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 58 is a protein called 60S ribosomal protein L25.

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

- Molecule 59 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LY	125	Total	C	N	O	S	0	0
			984	620	191	173			

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

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

- Molecule 61 is a protein called 60S ribosomal protein L28.

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

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

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

- Molecule 63 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 64 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 65 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 66 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 70 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 71 is a protein called 60S ribosomal protein L38.

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

- Molecule 72 is a protein called 60S ribosomal protein L39.

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

- Molecule 73 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 74 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 75 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 76 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 77 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	C1	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	5	30	Total	C	N	O	P	1	0
			666	298	127	210	31		

- Molecule 79 is a RNA chain called ICG tRNA Arg (P/P).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	6	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 80 is a RNA chain called tRNA (E/E).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	7	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	11	C	U	conflict	GB 176418

- Molecule 81 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	8	6	Total	C	N	O	S	0	0
			53	33	10	9	1		

- Molecule 82 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	C2	84	Total	Mg	0
			84	84	
83	SF	1	Total	Mg	0
			1	1	
83	C4	1	Total	Mg	0
			1	1	
83	C3	1	Total	Mg	0
			1	1	
83	LA	2	Total	Mg	0
			2	2	
83	LB	2	Total	Mg	0
			2	2	
83	LF	1	Total	Mg	0
			1	1	
83	LN	2	Total	Mg	0
			2	2	
83	LP	1	Total	Mg	0
			1	1	
83	LR	2	Total	Mg	0
			2	2	
83	LV	1	Total	Mg	0
			1	1	
83	La	1	Total	Mg	0
			1	1	
83	Le	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
83	Lg	1	Total 1	Mg 1	0
83	Lj	1	Total 1	Mg 1	0
83	C1	187	Total 187	Mg 187	0
83	6	1	Total 1	Mg 1	0

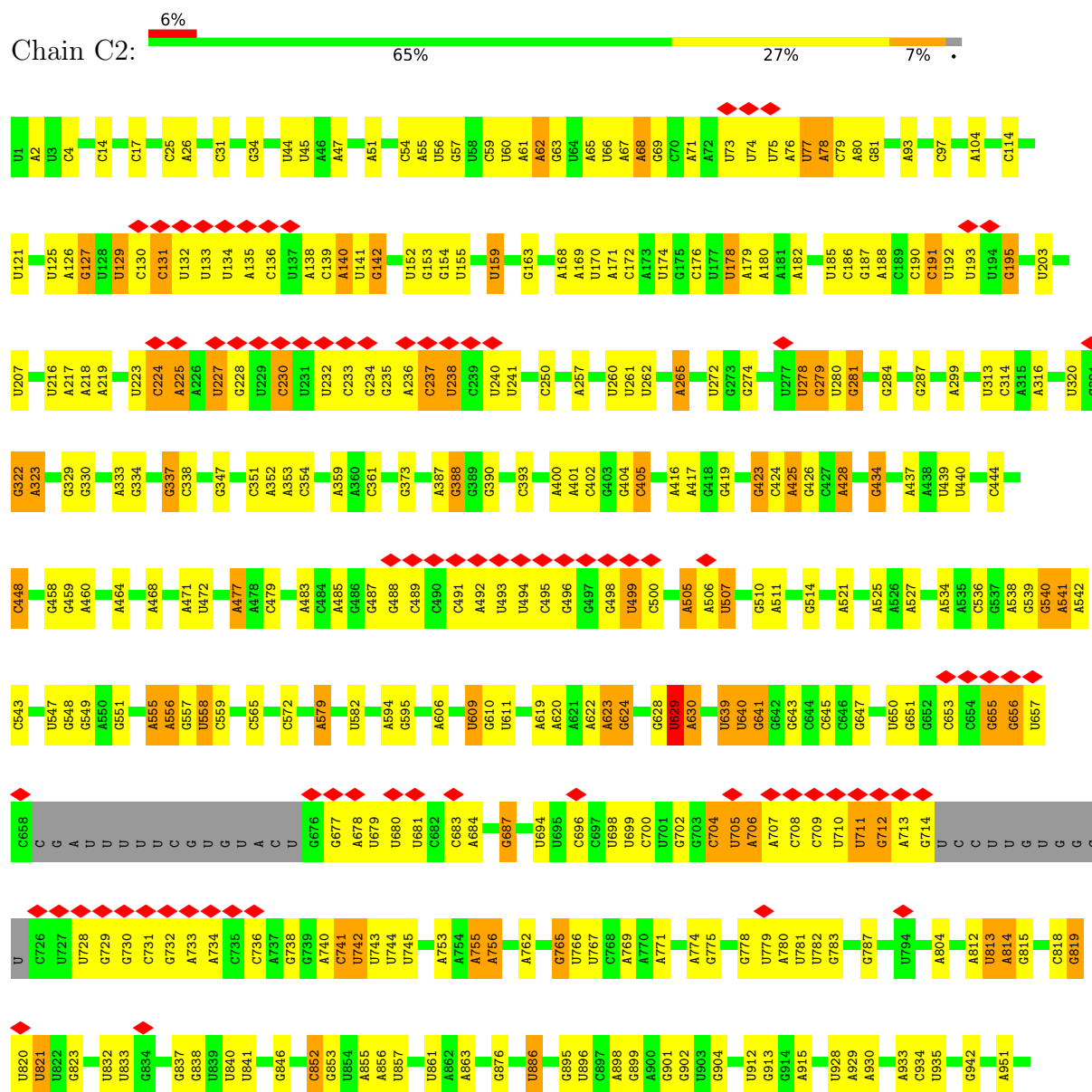
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Sd	1	Total 1	Zn 1	0
84	Sf	1	Total 1	Zn 1	0
84	Lg	1	Total 1	Zn 1	0
84	Lj	1	Total 1	Zn 1	0
84	Lm	1	Total 1	Zn 1	0
84	Lo	1	Total 1	Zn 1	0
84	Lp	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: 18S rRNA

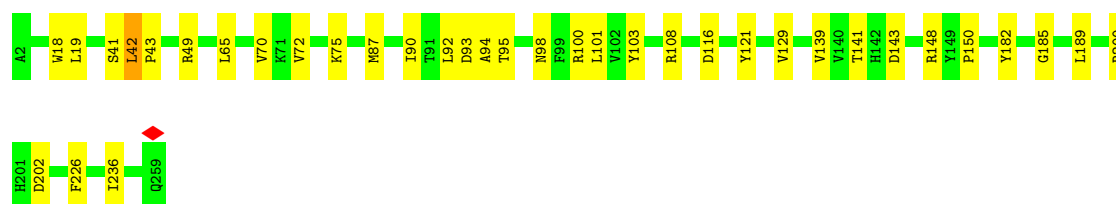
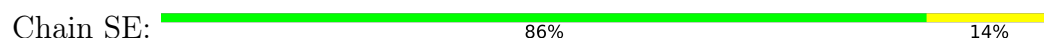




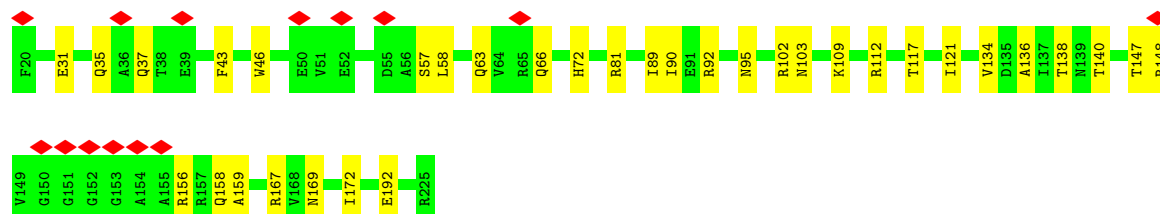
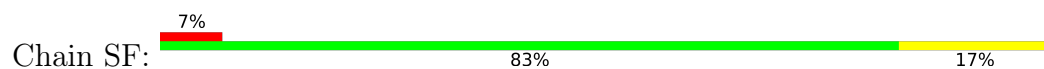
- Molecule 5: 40S ribosomal protein S3



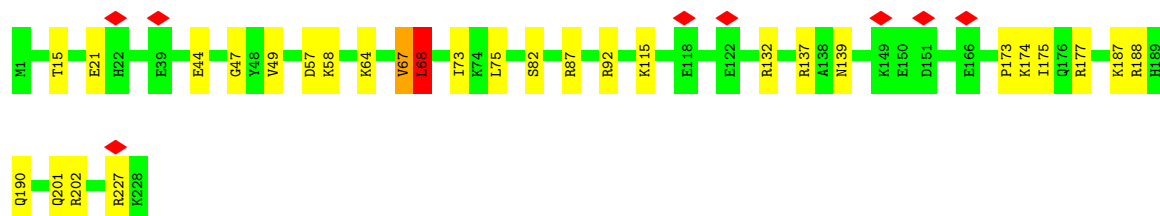
- Molecule 6: 40S ribosomal protein S4-A



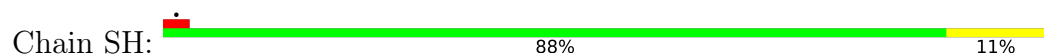
- Molecule 7: Rps5p



- Molecule 8: 40S ribosomal protein S6-A



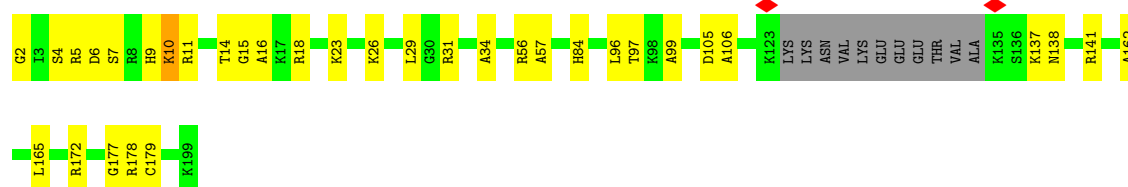
- Molecule 9: 40S ribosomal protein S7-A





- Molecule 10: 40S ribosomal protein S8-A

Chain SI: 77% 17% 6%



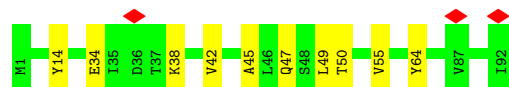
- Molecule 11: 40S ribosomal protein S9-A

Chain SJ: 89% 11%



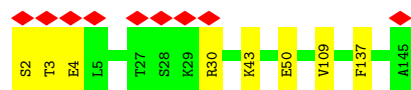
- Molecule 12: 40S ribosomal protein S10-A

Chain SK: 89% 11%



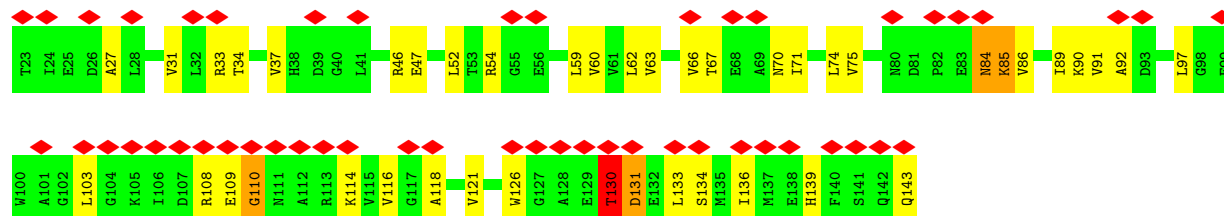
- Molecule 13: 40S ribosomal protein S11-A

Chain SL: 6% 94% 6%

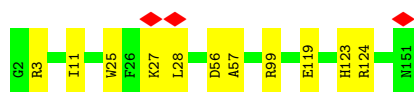


- Molecule 14: 40S ribosomal protein S12

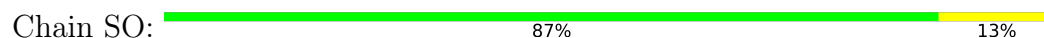
Chain SM: 41% 64% 31%



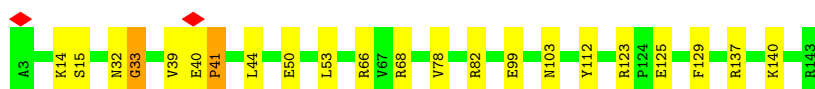
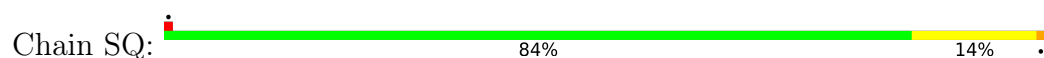
- Molecule 15: 40S ribosomal protein S13



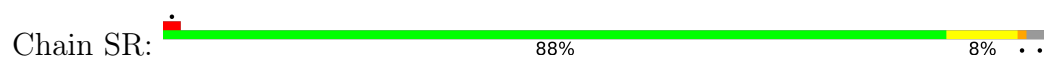
- Molecule 16: 40S ribosomal protein S14-B



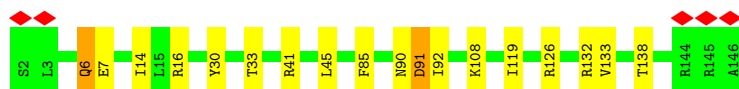
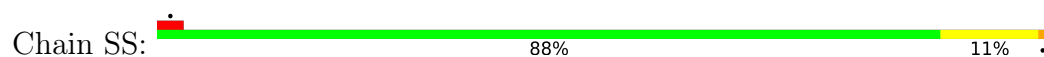
- Molecule 17: 40S ribosomal protein S16-A



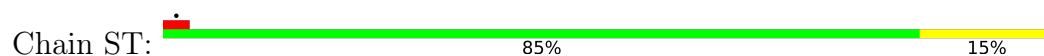
- Molecule 18: 40S ribosomal protein S17-A



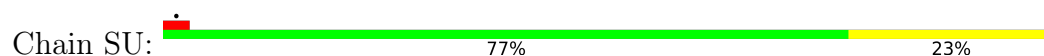
- Molecule 19: 40S ribosomal protein S18-A



- Molecule 20: 40S ribosomal protein S19-A



- Molecule 21: 40S ribosomal protein S20

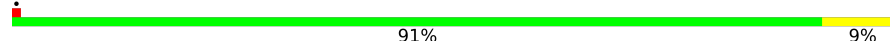


- Molecule 22: 40S ribosomal protein S21-A

Chain SV:  79% 21%



- Molecule 23: 40S ribosomal protein S22-A

Chain SW:  91% 9%



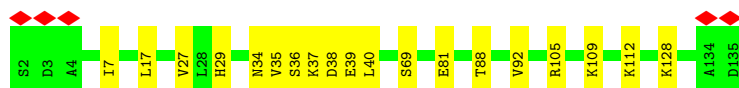
- Molecule 24: 40S ribosomal protein S23-A

Chain SX:  90% 10%



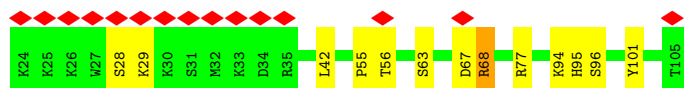
- Molecule 25: 40S ribosomal protein S24-A

Chain SY:  86% 14%



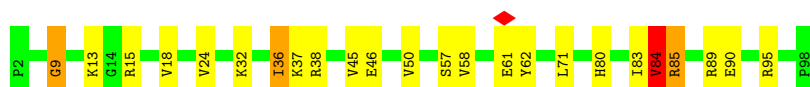
- Molecule 26: 40S ribosomal protein S25-A

Chain SZ:  18% 84% 15%



- Molecule 27: 40S ribosomal protein S26-B

Chain Sa:  75% 21%



- Molecule 28: 40S ribosomal protein S27-A

Chain Sb:  78% 20%



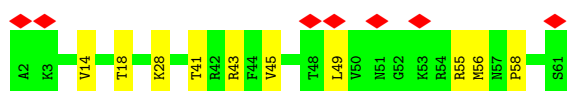
- Molecule 29: 40S ribosomal protein S29-A

Chain Sd: 92% 8%



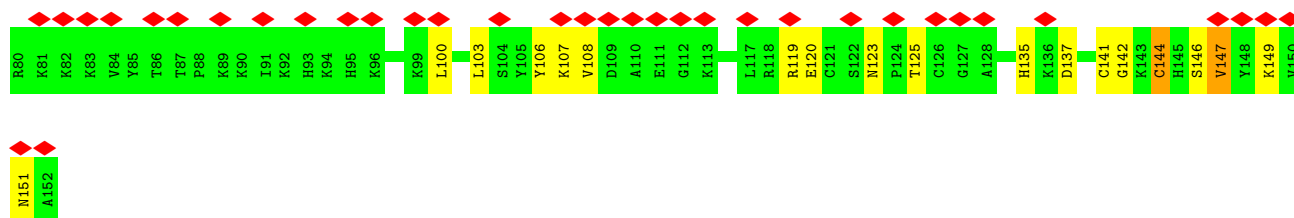
- Molecule 30: 40S ribosomal protein S30-A

Chain Se: 12% 83% 17%



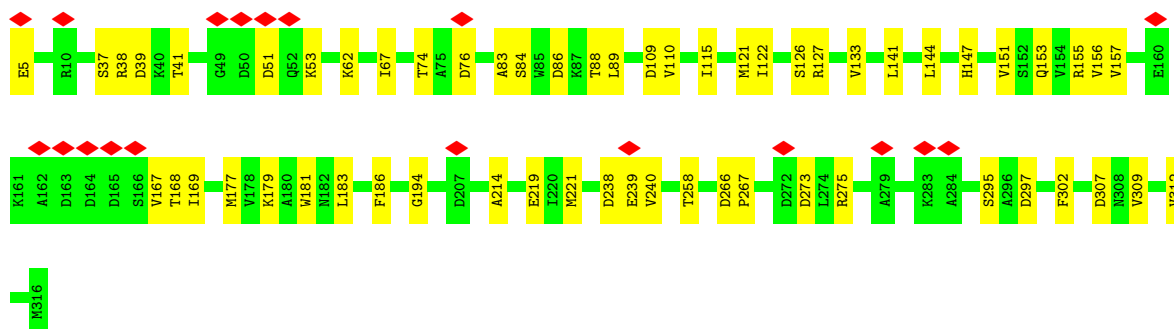
- Molecule 31: Ubiquitin-40S ribosomal protein S31

Chain Sf: 48% 75% 22%



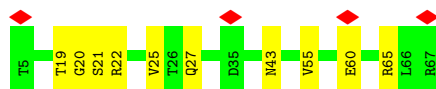
- Molecule 32: Guanine nucleotide-binding protein subunit beta-like protein

Chain Sg: 6% 81% 19%



- Molecule 33: 40S ribosomal protein S28-A

Chain Sc: 6% 84% 16%



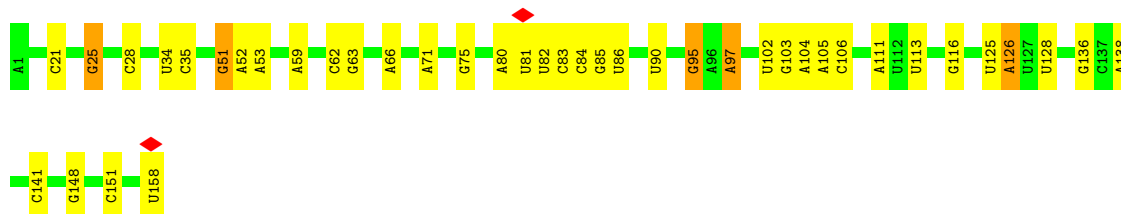
- Molecule 34: 5S rRNA

Chain C4:  85% 13%

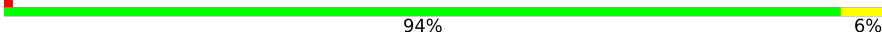


- Molecule 35: 5.8S rRNA

Chain C3:  74% 23%



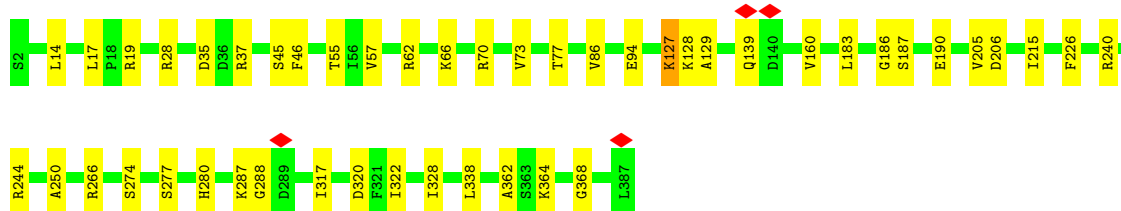
- Molecule 36: 60S ribosomal protein L2-A

Chain LA:  94% 6%



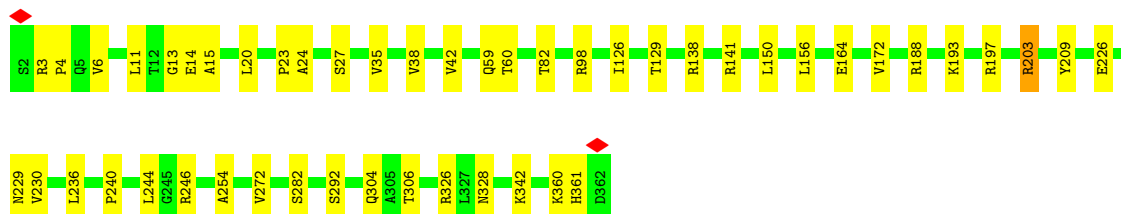
- Molecule 37: 60S ribosomal protein L3

Chain LB:  88% 12%



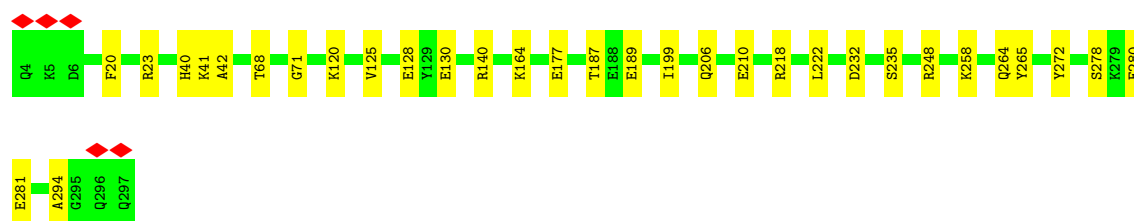
- Molecule 38: 60S ribosomal protein L4-A

Chain LC:  86% 13%



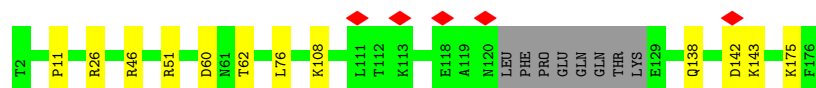
- Molecule 39: 60S ribosomal protein L5

Chain LD:  89% 11%

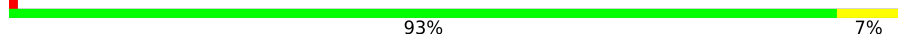


- Molecule 40: 60S ribosomal protein L6-B

Chain LE:  89% 7% 5%



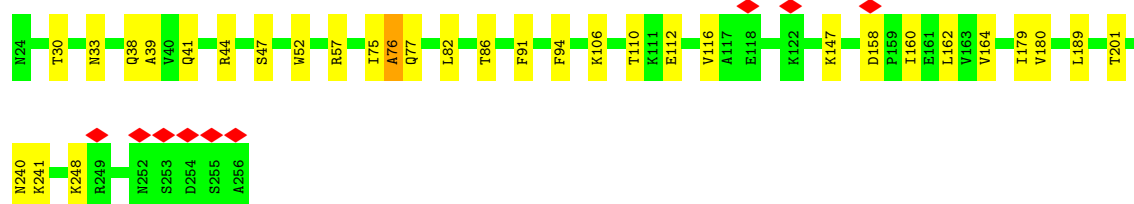
- Molecule 41: 60S ribosomal protein L7-A

Chain LF:  93% 7%

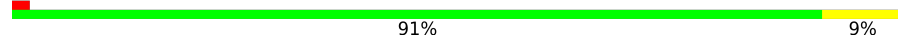


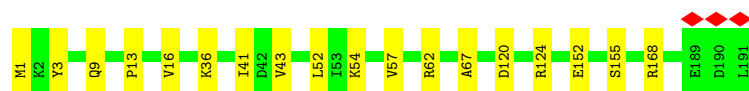
- Molecule 42: 60S ribosomal protein L8-A

Chain LG:  86% 13%



- Molecule 43: 60S ribosomal protein L9-A

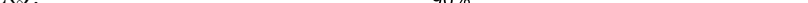
Chain LH:  91% 9%



- Molecule 44: 60S ribosomal protein L10

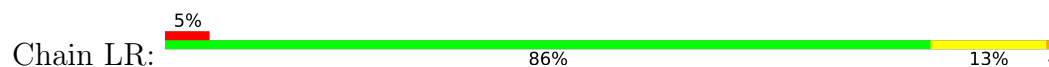
Chain LI:  91% 9%



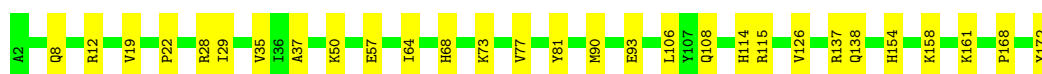
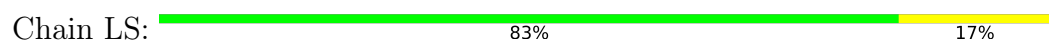
- Chain LQ: 



- Molecule 52: 60S ribosomal protein L19-A



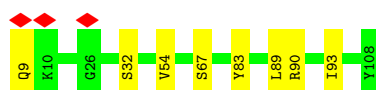
- Molecule 53: 60S ribosomal protein L20-A



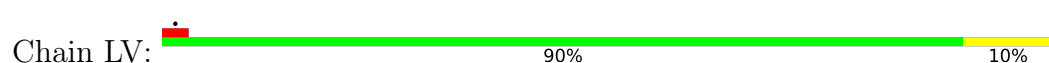
- Molecule 54: 60S ribosomal protein L21-A



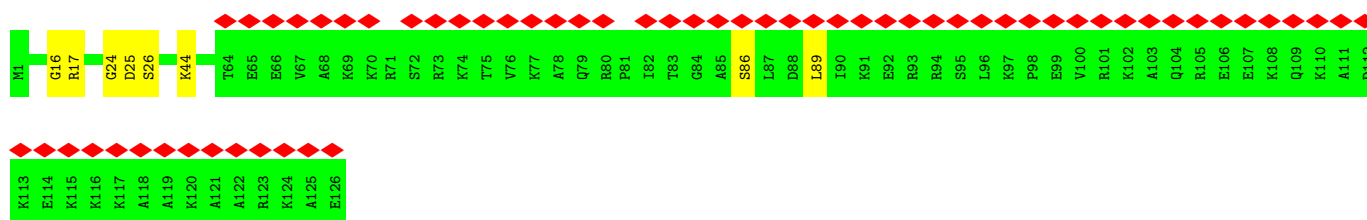
- Molecule 55: 60S ribosomal protein L22-A



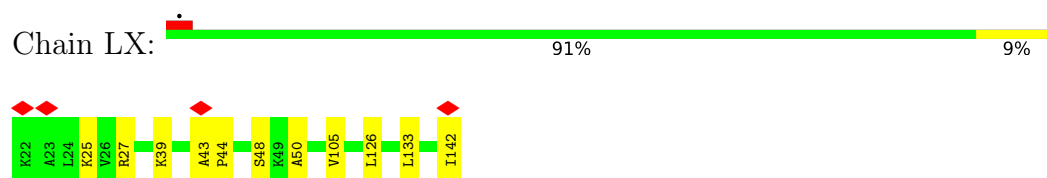
- Molecule 56: 60S ribosomal protein L23-A



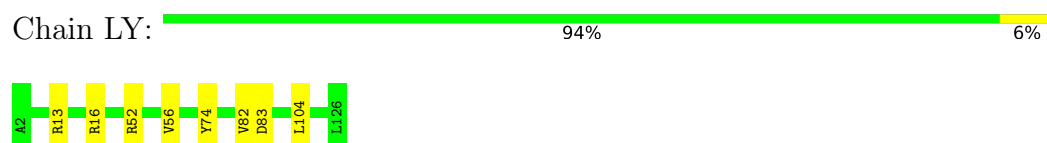
- Molecule 57: 60S ribosomal protein L24-A



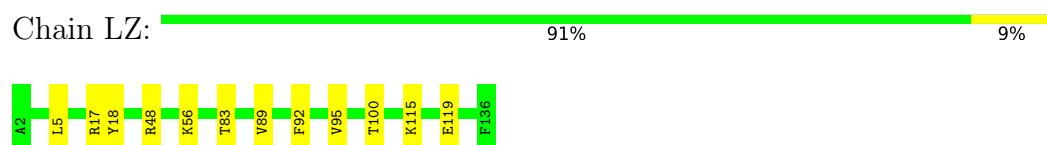
• Molecule 58: 60S ribosomal protein L25



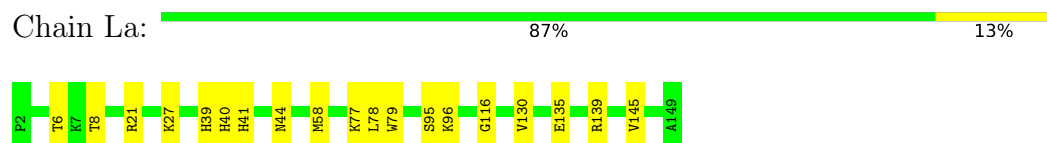
• Molecule 59: 60S ribosomal protein L26-A



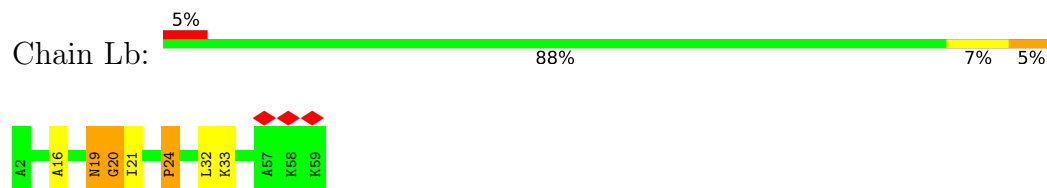
• Molecule 60: 60S ribosomal protein L27-A



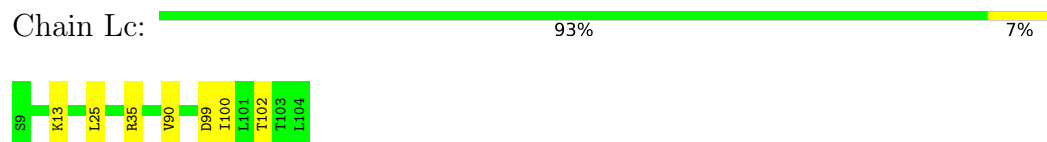
• Molecule 61: 60S ribosomal protein L28



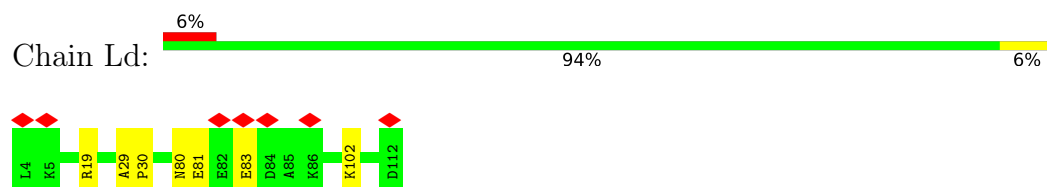
• Molecule 62: 60S ribosomal protein L29



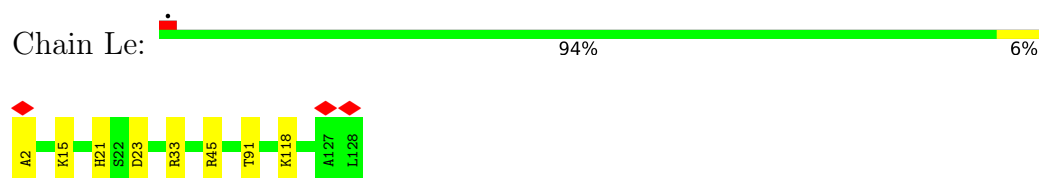
• Molecule 63: 60S ribosomal protein L30



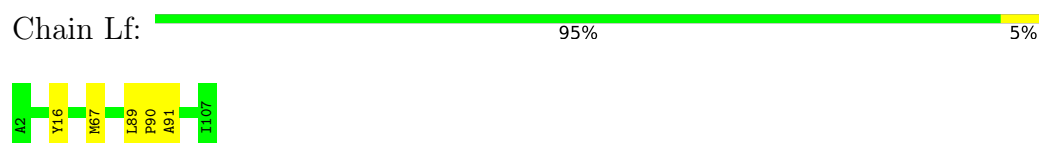
• Molecule 64: 60S ribosomal protein L31-A



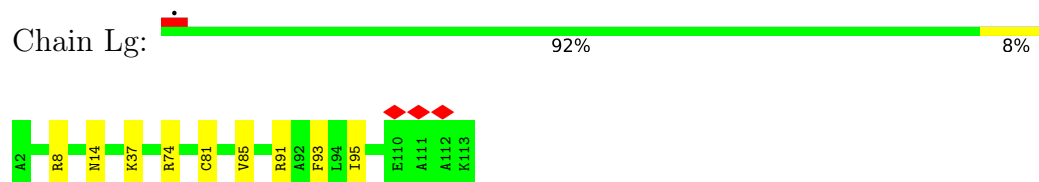
- Molecule 65: 60S ribosomal protein L32



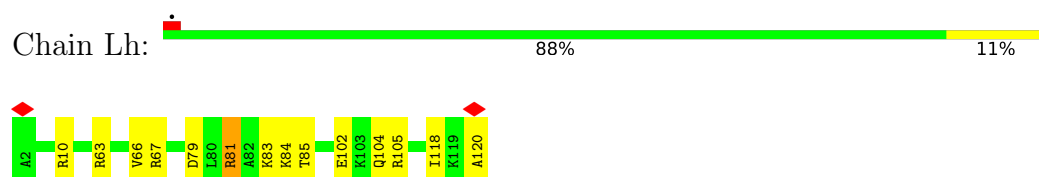
- Molecule 66: 60S ribosomal protein L33-A



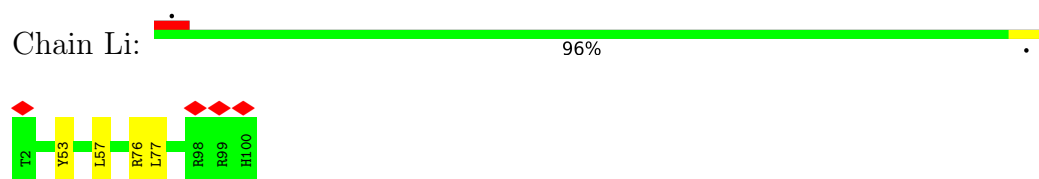
- Molecule 67: 60S ribosomal protein L34-A



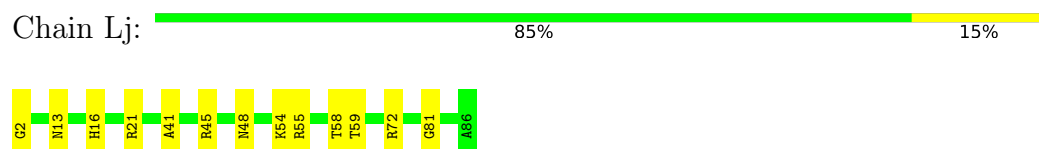
- Molecule 68: 60S ribosomal protein L35-A



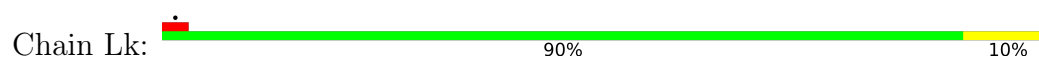
- Molecule 69: 60S ribosomal protein L36-A

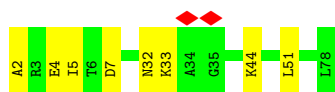


- Molecule 70: 60S ribosomal protein L37-A



- Molecule 71: 60S ribosomal protein L38





- Molecule 72: 60S ribosomal protein L39

Chain Ll: 88% 12%



- Molecule 73: Ubiquitin-60S ribosomal protein L40

Chain Lm: 94% 6%



- Molecule 74: 60S ribosomal protein L41-A

Chain Ln: 88% 12%



- Molecule 75: 60S ribosomal protein L42-A

Chain Lo: 92% 8%



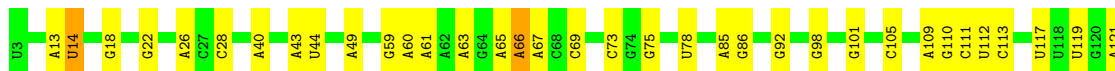
- Molecule 76: 60S ribosomal protein L43-A

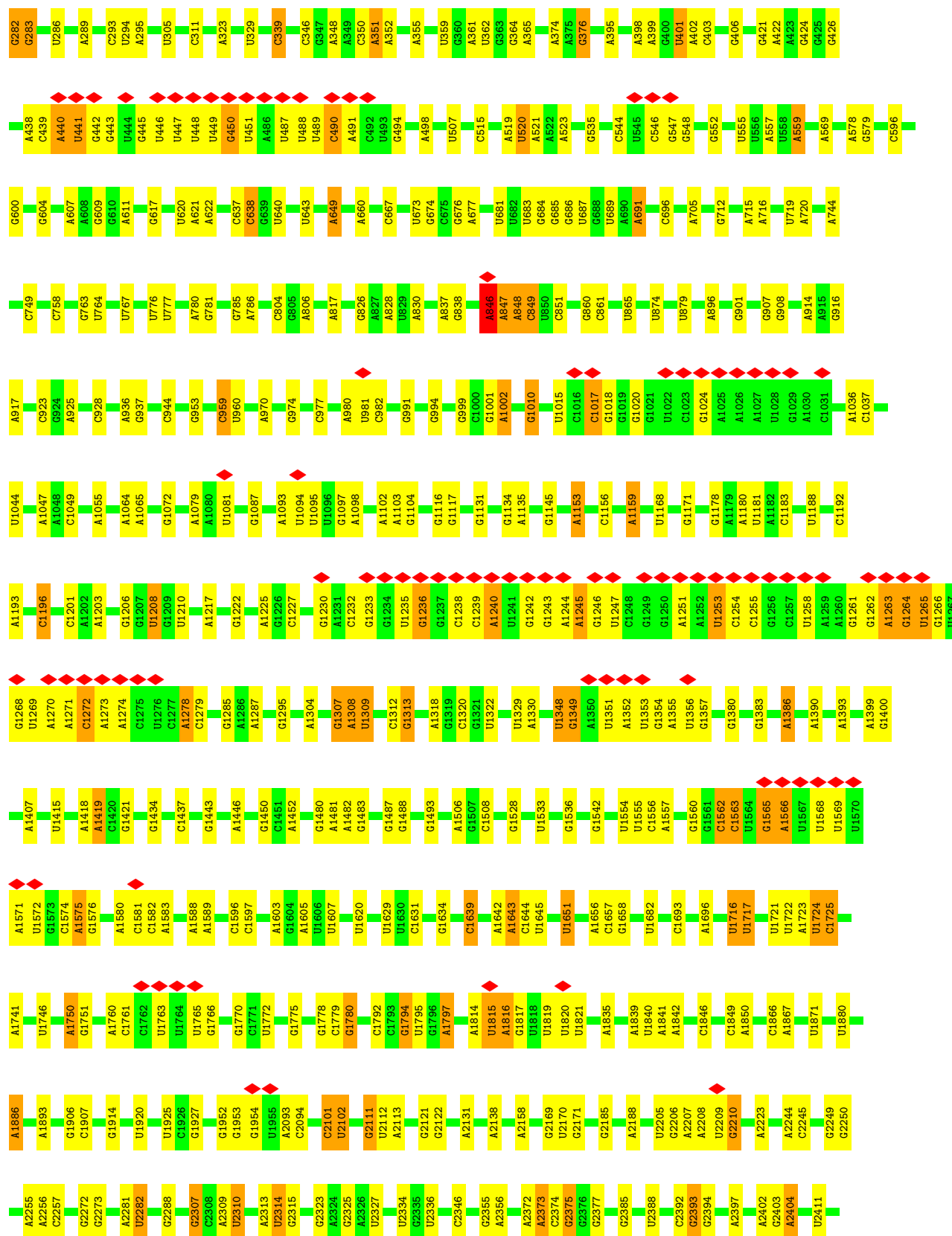
Chain Lp: 86% 14%

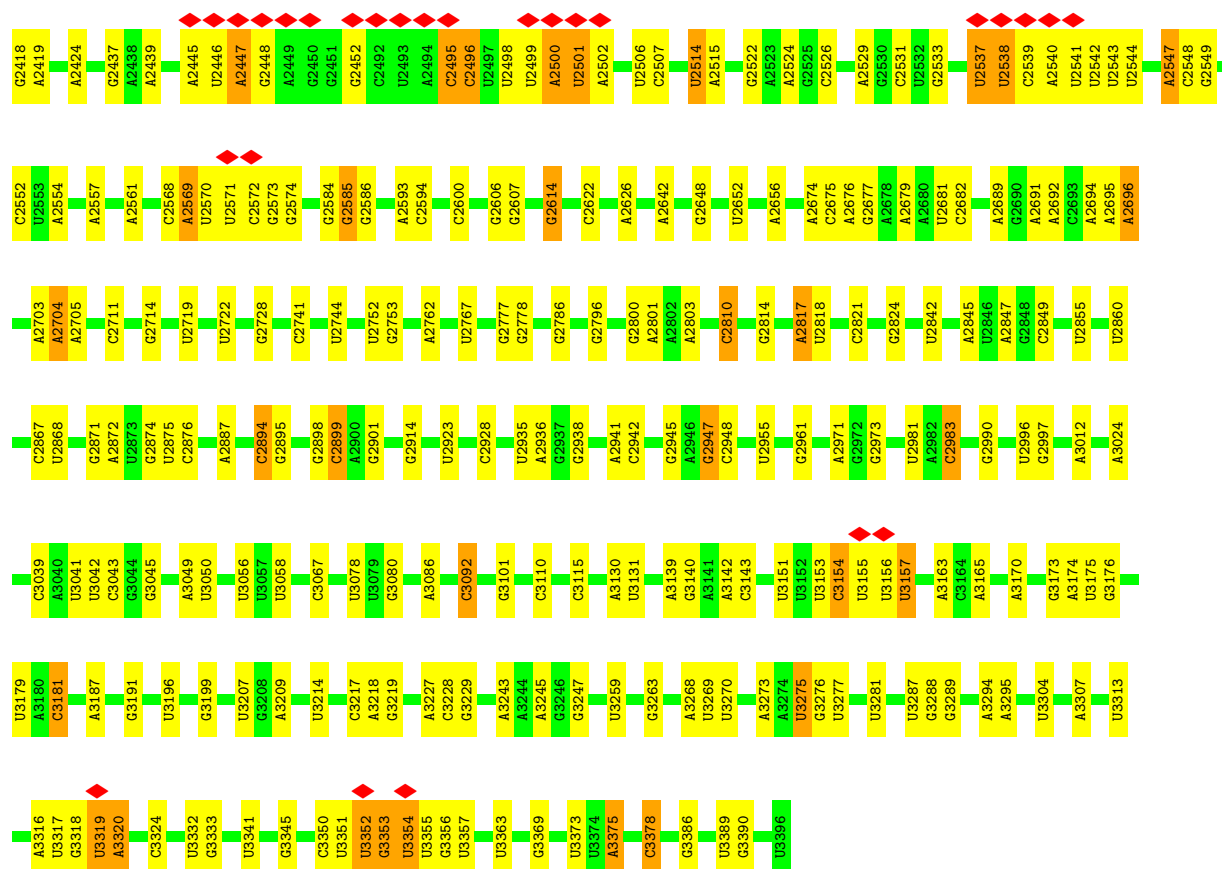


- Molecule 77: 25S rRNA

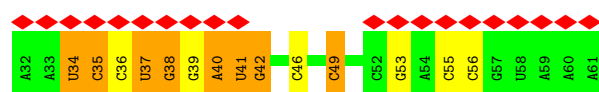
Chain C1: 75% 21%



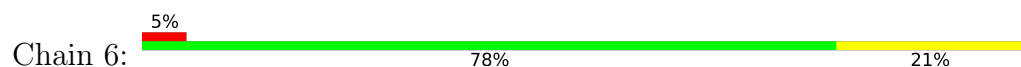




- Molecule 78: mRNA



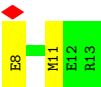
- Molecule 79: ICG tRNA Arg (P/P)



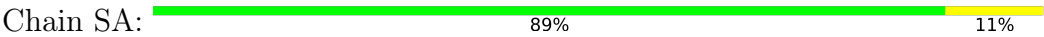
- Molecule 80: tRNA (E/E)



- Molecule 81: nascent chain



• Molecule 82: 40S ribosomal protein S0-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	550205	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.531	Depositor
Minimum map value	-0.739	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.0612	Depositor
Map size ($\text{\AA}$)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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, MG

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	C2	0.45	6/42053 (0.0%)	0.39	5/65522 (0.0%)
2	SB	0.30	0/1823	0.55	0/2447
3	SP	0.21	0/936	0.49	0/1259
4	SC	0.34	0/1656	0.48	0/2251
5	SD	0.24	0/1754	0.46	0/2361
6	SE	0.30	0/2097	0.51	0/2823
7	SF	0.24	0/1625	0.47	0/2197
8	SG	0.26	0/1839	0.52	0/2460
9	SH	0.26	0/1498	0.53	0/2019
10	SI	0.34	0/1501	0.58	0/2006
11	SJ	0.30	0/1504	0.54	0/2016
12	SK	0.21	0/769	0.48	0/1039
13	SL	0.38	0/1185	0.52	0/1598
14	SM	0.31	0/883	0.80	0/1199
15	SN	0.34	0/1215	0.60	0/1638
16	SO	0.33	0/937	0.55	0/1261
17	SQ	0.27	0/1125	0.51	0/1510
18	SR	0.24	0/957	0.50	0/1283
19	SS	0.23	0/1211	0.53	0/1628
20	ST	0.24	0/1130	0.46	0/1517
21	SU	0.25	0/807	0.51	0/1091
22	SV	0.30	0/682	0.58	1/921 (0.1%)
23	SW	0.38	0/1038	0.52	1/1395 (0.1%)
24	SX	0.34	0/1139	0.54	0/1518
25	SY	0.26	0/1087	0.49	0/1449
26	SZ	0.22	0/661	0.54	0/888
27	Sa	0.37	0/782	0.77	0/1047
28	Sb	0.30	0/620	0.59	0/838
29	Sd	0.26	0/452	0.45	0/600
30	Se	0.25	0/480	0.47	0/639
31	Sf	0.23	0/567	0.68	1/764 (0.1%)
32	Sg	0.21	0/2436	0.48	0/3318

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sc	0.25	0/493	0.49	0/663
34	C4	0.25	0/2883	0.31	0/4491
35	C3	0.35	0/3746	0.36	0/5832
36	LA	0.44	0/1933	0.59	0/2598
37	LB	0.39	0/3146	0.50	0/4228
38	LC	0.39	0/2800	0.51	0/3790
39	LD	0.28	0/2400	0.45	0/3239
40	LE	0.30	0/1327	0.45	0/1790
41	LF	0.38	0/1821	0.46	0/2451
42	LG	0.35	0/1836	0.49	0/2481
43	LH	0.30	0/1529	0.44	0/2060
44	LI	0.32	0/1801	0.45	0/2416
45	LJ	0.26	0/1371	0.48	0/1838
46	LL	0.38	0/1568	0.58	0/2106
47	LM	0.31	0/1068	0.48	0/1438
48	LN	0.44	0/1757	0.53	0/2354
49	LO	0.38	0/1585	0.49	0/2128
50	LP	0.39	0/1439	0.55	0/1938
51	LQ	0.38	0/1465	0.51	0/1965
52	LR	0.36	0/1532	0.56	0/2043
53	LS	0.35	0/1473	0.48	0/1980
54	LT	0.34	0/1300	0.43	0/1743
55	LU	0.27	0/812	0.43	0/1099
56	LV	0.37	0/1018	0.45	0/1369
57	LW	0.31	0/850	0.43	0/1152
58	LX	0.35	0/979	0.50	0/1321
59	LY	0.36	0/995	0.48	0/1329
60	LZ	0.34	0/1118	0.47	0/1497
61	La	0.42	0/1204	0.57	0/1612
62	Lb	0.31	0/473	0.53	0/629
63	Lc	0.33	0/745	0.47	0/1001
64	Ld	0.37	0/890	0.54	0/1196
65	Le	0.37	0/1038	0.44	0/1390
66	Lf	0.41	0/868	0.48	0/1168
67	Lg	0.39	0/890	0.51	0/1189
68	Lh	0.32	0/978	0.48	0/1301
69	Li	0.31	0/772	0.50	0/1026
70	Lj	0.46	0/685	0.57	0/908
71	Lk	0.31	0/618	0.46	0/826
72	Ll	0.42	0/443	0.46	0/588
73	Lm	0.34	0/423	0.43	0/562
74	Ln	0.41	0/230	0.63	0/296
75	Lo	0.35	0/836	0.48	0/1104

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lp	0.36	0/701	0.52	0/934
77	C1	0.46	6/76214 (0.0%)	0.38	3/118821 (0.0%)
78	5	0.16	0/746	0.35	0/1161
79	6	0.24	0/1810	0.38	0/2817
80	7	0.15	0/1773	0.29	0/2759
81	8	0.27	0/54	0.78	0/71
82	SA	0.28	0/1644	0.47	0/2249
All	All	0.40	12/218529 (0.0%)	0.43	11/321449 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	SB	0	1
6	SE	0	1
8	SG	0	1
9	SH	0	1
13	SL	0	1
14	SM	0	3
15	SN	0	1
17	SQ	0	2
19	SS	0	2
27	Sa	0	4
28	Sb	0	1
31	Sf	0	2
37	LB	0	2
38	LC	0	1
42	LG	0	2
45	LJ	0	1
49	LO	0	1
58	LX	0	1
61	La	0	1
62	Lb	0	3
64	Ld	0	1
68	Lh	0	1
All	All	0	34

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C2	629	U	C5-C6	68.63	2.71	1.34
77	C1	846	A	C5-C6	60.98	2.63	1.41
77	C1	846	A	C6-N1	29.36	1.94	1.35
77	C1	846	A	C5-C4	28.83	1.96	1.38
77	C1	846	A	N1-C2	27.85	1.90	1.34
77	C1	846	A	C2-N3	26.84	1.87	1.33
77	C1	846	A	N3-C4	26.68	1.88	1.34
1	C2	629	U	N3-C4	16.32	1.71	1.38
1	C2	629	U	C2-N3	14.72	1.67	1.37
1	C2	629	U	C4-C5	7.87	1.59	1.43
1	C2	629	U	N1-C6	7.35	1.52	1.38
1	C2	629	U	N1-C2	5.38	1.49	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	629	U	C4'-C3'-O3'	10.18	128.26	113.00
1	C2	629	U	C2-N3-C4	8.80	153.40	127.00
77	C1	846	A	C6-C5-N7	7.42	154.55	132.30
1	C2	629	U	C4-C5-C6	-7.28	97.87	119.70
77	C1	846	A	C2-N3-C4	6.82	131.06	110.60
22	SV	41	GLU	N-CA-CB	-6.61	106.64	114.17
23	SW	28	ARG	C-N-CD	-6.56	106.17	120.60
1	C2	629	U	C5'-C4'-C3'	6.53	125.79	116.00
77	C1	846	A	C4-C5-N7	-6.46	91.32	110.70
31	Sf	147	VAL	N-CA-C	5.54	112.14	106.21
1	C2	629	U	O5'-C5'-C4'	5.45	119.67	111.50

There are no chirality outliers.

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	LB	127	LYS	Peptide
37	LB	139	GLN	Peptide
38	LC	13	GLY	Peptide
42	LG	30	THR	Peptide
42	LG	76	ALA	Peptide
45	LJ	172	LEU	Peptide
49	LO	110[A]	PRO	Peptide
58	LX	43	ALA	Peptide
61	La	116	GLY	Peptide
62	Lb	19	ASN	Peptide

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Mol	Chain	Res	Type	Group
62	Lb	20	GLY	Peptide
62	Lb	24	PRO	Peptide
64	Ld	83	GLU	Peptide
68	Lh	83	LYS	Peptide
2	SB	81	PHE	Peptide
6	SE	42	LEU	Peptide
8	SG	68	LEU	Peptide
9	SH	64	VAL	Peptide
13	SL	4	GLU	Peptide
14	SM	110	GLY	Peptide
14	SM	130	THR	Peptide
14	SM	84	ASN	Peptide
15	SN	25	TRP	Peptide
17	SQ	33	GLY	Peptide
17	SQ	40	GLU	Peptide
19	SS	6	GLN	Peptide
19	SS	90	ASN	Peptide
27	Sa	36	ILE	Peptide
27	Sa	61	GLU	Peptide
27	Sa	84	VAL	Peptide
27	Sa	9	GLY	Peptide
28	Sb	61	THR	Peptide
31	Sf	106	TYR	Peptide
31	Sf	144	CYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C2	37604	0	18919	230	0
2	SB	1798	0	1890	20	0
3	SP	916	0	941	11	0
4	SC	1626	0	1715	21	0
5	SD	1729	0	1812	12	0
6	SE	2056	0	2140	24	0
7	SF	1605	0	1669	27	0
8	SG	1815	0	1894	23	0
9	SH	1473	0	1555	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	SI	1476	0	1501	26	0
11	SJ	1479	0	1556	12	0
12	SK	752	0	719	6	0
13	SL	1159	0	1225	4	0
14	SM	875	0	878	27	0
15	SN	1192	0	1255	6	0
16	SO	926	0	950	14	0
17	SQ	1105	0	1166	15	0
18	SR	948	0	990	8	0
19	SS	1192	0	1222	18	0
20	ST	1112	0	1124	19	0
21	SU	797	0	863	16	0
22	SV	673	0	662	10	0
23	SW	1021	0	1060	7	0
24	SX	1121	0	1196	11	0
25	SY	1073	0	1132	15	0
26	SZ	651	0	682	9	0
27	Sa	769	0	818	17	0
28	Sb	610	0	633	12	0
29	Sd	442	0	428	4	0
30	Se	472	0	521	7	0
31	Sf	556	0	551	11	0
32	Sg	2383	0	2332	37	0
33	Sc	491	0	524	8	0
34	C4	2579	0	1304	9	0
35	C3	3353	0	1695	15	0
36	LA	1899	0	1957	12	0
37	LB	3075	0	3142	35	0
38	LC	2748	0	2859	37	0
39	LD	2351	0	2294	22	0
40	LE	1305	0	1373	10	0
41	LF	1784	0	1862	13	0
42	LG	1804	0	1877	18	0
43	LH	1508	0	1572	15	0
44	LI	1764	0	1804	13	0
45	LJ	1350	0	1381	22	0
46	LL	1543	0	1608	17	0
47	LM	1053	0	1149	11	0
48	LN	1720	0	1779	21	0
49	LO	1555	0	1659	11	0
50	LP	1416	0	1433	6	0
51	LQ	1441	0	1543	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	LR	1515	0	1606	20	0
53	LS	1437	0	1475	26	0
54	LT	1276	0	1323	9	0
55	LU	796	0	812	5	0
56	LV	1003	0	1048	9	0
57	LW	836	0	709	6	0
58	LX	964	0	1025	7	0
59	LY	984	0	1075	6	0
60	LZ	1092	0	1155	10	0
61	La	1173	0	1215	11	0
62	Lb	462	0	491	8	0
63	Lc	737	0	792	4	0
64	Ld	876	0	912	4	0
65	Le	1017	0	1081	11	0
66	Lf	850	0	880	3	0
67	Lg	880	0	943	7	0
68	Lh	969	0	1078	10	0
69	Li	766	0	844	3	0
70	Lj	670	0	673	12	0
71	Lk	612	0	682	5	0
72	Ll	436	0	475	6	0
73	Lm	417	0	456	2	0
74	Ln	229	0	273	2	0
75	Lo	824	0	890	6	0
76	Lp	694	0	736	9	0
77	C1	68091	0	34216	302	0
78	5	666	0	338	7	0
79	6	1621	0	820	3	0
80	7	1589	0	810	10	0
81	8	53	0	44	2	0
82	SA	1603	0	1610	14	0
83	6	1	0	0	0	0
83	C1	187	0	0	0	0
83	C2	84	0	0	0	0
83	C3	1	0	0	0	0
83	C4	1	0	0	0	0
83	LA	2	0	0	0	0
83	LB	2	0	0	0	0
83	LF	1	0	0	0	0
83	LN	2	0	0	0	0
83	LP	1	0	0	0	0
83	LR	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	LV	1	0	0	0	0
83	La	1	0	0	0	0
83	Le	2	0	0	0	0
83	Lg	1	0	0	0	0
83	Lj	1	0	0	0	0
83	SF	1	0	0	0	0
84	Lg	1	0	0	0	0
84	Lj	1	0	0	0	0
84	Lm	1	0	0	0	0
84	Lo	1	0	0	0	0
84	Lp	1	0	0	0	0
84	Sd	1	0	0	0	0
84	Sf	1	0	0	0	0
All	All	203581	0	149301	1167	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 (1167) 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)
1:C2:629:U:C4	1:C2:629:U:N3	1.71	1.58
1:C2:629:U:C4	77:C1:846:A:C5	1.94	1.52
77:C1:846:A:C5	77:C1:846:A:C4	1.96	1.43
1:C2:629:U:C4	77:C1:846:A:C6	2.06	1.41
77:C1:846:A:C4	77:C1:846:A:N3	1.88	1.41
77:C1:846:A:C2	77:C1:846:A:N3	1.87	1.41
77:C1:846:A:C2	77:C1:846:A:N1	1.90	1.38
77:C1:846:A:C6	77:C1:846:A:N1	1.94	1.35
1:C2:629:U:N3	77:C1:846:A:C6	1.95	1.32
1:C2:629:U:C5	77:C1:846:A:C6	2.32	1.16
1:C2:629:U:C5	77:C1:846:A:C5	2.36	1.12
1:C2:629:U:C6	77:C1:846:A:C5	2.41	1.07
1:C2:629:U:C6	77:C1:846:A:C6	2.44	1.06
1:C2:629:U:C6	77:C1:846:A:C4	2.50	0.99
1:C2:629:U:C5	77:C1:846:A:C2	2.51	0.99
1:C2:629:U:C5	77:C1:846:A:C4	2.55	0.94
1:C2:629:U:C6	77:C1:846:A:C2	2.56	0.94
1:C2:629:U:C5	77:C1:846:A:N1	2.36	0.93
1:C2:992:A:O2'	1:C2:1785:U:O2	1.91	0.89
1:C2:1459:C:OP2	19:SS:138:THR:OG1	1.90	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:LO:176[A]:LYS:NZ	77:C1:3191:G:OP1	2.08	0.87
1:C2:227:U:O4	1:C2:230:C:N4	2.08	0.86
77:C1:846:A:C5	77:C1:846:A:C6	2.63	0.86
56:LV:81:GLN:O	56:LV:98:ASN:ND2	2.10	0.85
1:C2:1534:G:O2'	1:C2:1535:U:O2	1.93	0.85
1:C2:1339:C:O2'	1:C2:1341:A:N7	2.10	0.84
43:LH:41:ILE:HD11	43:LH:67:ALA:HB1	1.59	0.84
63:Lc:99:ASP:OD1	63:Lc:102:THR:OG1	1.96	0.83
19:SS:16:ARG:NH1	45:LJ:111:ASP:OD1	2.11	0.83
1:C2:629:U:C6	77:C1:846:A:N3	2.46	0.83
1:C2:629:U:C6	77:C1:846:A:N1	2.46	0.83
80:7:9:A:O2'	80:7:10:G:N7	2.13	0.82
1:C2:629:U:C2	77:C1:846:A:C6	2.67	0.82
77:C1:1716:U:O2'	77:C1:1717:U:O5'	1.97	0.82
33:Sc:27:GLN:OE1	33:Sc:43:ASN:ND2	2.13	0.81
1:C2:629:U:C5	77:C1:846:A:N3	2.48	0.81
37:LB:266:ARG:NH2	77:C1:2392:C:O2'	2.12	0.81
56:LV:10:LYS:NZ	56:LV:56:ASP:OD1	2.13	0.81
1:C2:521:A:N3	25:SY:34:ASN:ND2	2.28	0.81
1:C2:819:G:C6	1:C2:853:G:C2	2.69	0.81
15:SN:99:ARG:NH2	15:SN:119:GLU:OE2	2.14	0.81
50:LP:141:SER:OG	77:C1:2355:G:OP1	1.99	0.81
75:Lo:56:PRO:O	80:7:74:C:O2'	1.98	0.81
36:LA:70:ARG:NH1	77:C1:1651:U:OP1	2.14	0.80
36:LA:69:TYR:OH	77:C1:2557:A:OP1	1.97	0.80
67:Lg:74:ARG:NH2	77:C1:1639:C:OP2	2.14	0.80
77:C1:2307:G:O2'	77:C1:2310:U:OP2	1.99	0.80
32:Sg:156:VAL:HG12	32:Sg:169:ILE:HG22	1.64	0.80
77:C1:2495:C:O2'	77:C1:2496:C:OP1	2.00	0.80
1:C2:886:U:OP1	2:SB:214:LYS:NZ	2.13	0.80
52:LR:128:LYS:NZ	77:C1:1724:U:OP2	2.14	0.80
61:La:58:MET:SD	77:C1:2786:G:N2	2.53	0.80
27:Sa:83:ILE:O	27:Sa:85:ARG:N	2.15	0.79
35:C3:95:G:OP2	70:Lj:72:ARG:NH1	2.15	0.79
1:C2:322:G:O2'	1:C2:323:A:OP2	2.01	0.79
76:Lp:46:THR:OG1	76:Lp:57:CYS:SG	2.39	0.79
36:LA:220:GLY:O	77:C1:2245:C:O2'	2.01	0.79
79:6:58:A:O2'	79:6:60:U:OP2	1.98	0.79
1:C2:142:G:N7	8:SG:177:ARG:NH2	2.30	0.79
77:C1:2568:C:O2'	77:C1:2569:A:O4'	2.00	0.78
1:C2:337:G:O2'	10:SI:10:LYS:NZ	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:629:U:C5	1:C2:629:U:C6	2.71	0.78
1:C2:1594:G:OP2	1:C2:1596:C:N4	2.17	0.78
48:LN:93:LYS:NZ	77:C1:2600:C:OP1	2.16	0.78
76:Lp:4:ARG:NH2	77:C1:838:G:O6	2.17	0.78
77:C1:1778:G:O2'	77:C1:1780:G:OP2	2.02	0.78
77:C1:2899:C:O2'	77:C1:2901:G:OP2	2.01	0.78
1:C2:1135:U:OP2	24:SX:121:ARG:NH2	2.17	0.78
10:SI:162:ALA:O	77:C1:3352:U:O2'	2.01	0.77
62:Lb:16:ALA:O	62:Lb:20:GLY:HA3	1.84	0.77
1:C2:1227:A:OP1	1:C2:1229:G:O2'	2.01	0.77
27:Sa:32:LYS:O	27:Sa:37:LYS:NZ	2.17	0.77
51:LQ:21:SER:OG	77:C1:673:U:OP1	2.03	0.77
55:LU:90:ARG:NH1	77:C1:1682:U:O4	2.18	0.77
60:LZ:95:VAL:O	60:LZ:100:THR:OG1	2.02	0.77
61:La:21:ARG:NH2	77:C1:640:U:OP1	2.18	0.77
1:C2:705:U:O2'	1:C2:706:A:O5'	2.03	0.77
31:Sf:119:ARG:NH2	31:Sf:120:GLU:O	2.18	0.77
37:LB:215:ILE:HD12	37:LB:338:LEU:HD12	1.67	0.77
1:C2:1069:A:OP1	82:SA:28:ASN:ND2	2.18	0.76
6:SE:100:ARG:NH2	6:SE:121:TYR:O	2.18	0.76
35:C3:21:C:OP1	38:LC:193:LYS:NZ	2.18	0.76
37:LB:244:ARG:NH2	77:C1:2948:C:OP1	2.18	0.76
56:LV:12:ARG:NH1	77:C1:3041:U:OP1	2.18	0.76
77:C1:1693:C:HO2'	77:C1:1772:U:HO2'	1.28	0.76
70:Lj:2:GLY:N	77:C1:2138:A:HO2'	1.83	0.76
26:SZ:94:LYS:NZ	26:SZ:101:TYR:OH	2.19	0.76
1:C2:1296:A:OP1	82:SA:138:TYR:OH	2.04	0.76
65:Le:23:ASP:OD2	77:C1:424:G:O2'	2.02	0.76
77:C1:282:G:O2'	77:C1:283:G:OP2	2.02	0.75
34:C4:44:C:OP2	45:LJ:137:ARG:NH2	2.19	0.75
1:C2:623:A:N6	1:C2:970:A:OP1	2.19	0.75
57:LW:16:GLY:O	77:C1:3050:U:O2'	2.04	0.75
1:C2:1791:A:O2'	1:C2:1792:G:OP2	2.05	0.75
60:LZ:17:ARG:NH1	77:C1:1634:G:N7	2.35	0.75
42:LG:33:ASN:ND2	42:LG:38:GLN:OE1	2.19	0.74
1:C2:61:A:O2'	1:C2:62:A:O4'	2.05	0.74
31:Sf:123:ASN:ND2	31:Sf:144:CYS:SG	2.60	0.74
46:LL:36:ARG:NH2	77:C1:687:U:OP2	2.18	0.74
77:C1:2373:A:N3	77:C1:2824:G:O2'	2.20	0.74
42:LG:240:ASN:OD1	77:C1:2584:G:O2'	2.04	0.74
1:C2:1430:U:O2'	1:C2:1431:C:OP1	2.04	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Sg:295:SER:OG	32:Sg:297:ASP:OD1	2.04	0.73
77:C1:86:G:O2'	77:C1:98:G:O6	2.06	0.73
1:C2:742:U:O2	9:SH:107:ARG:NH2	2.21	0.73
1:C2:896:U:O2	16:SO:41:ARG:NH1	2.21	0.73
1:C2:1081:A:O2'	1:C2:1083:G:N7	2.19	0.73
31:Sf:123:ASN:ND2	31:Sf:125:THR:OG1	2.21	0.73
10:SI:4:SER:OG	10:SI:6:ASP:OD1	2.04	0.73
11:SJ:41:GLU:OE1	11:SJ:44:ARG:NH2	2.21	0.73
48:LN:5:LYS:NZ	77:C1:265:A:O2'	2.21	0.73
77:C1:221:A:O2'	77:C1:223:U:OP2	2.05	0.73
7:SF:63:GLN:NE2	7:SF:66:GLN:OE1	2.21	0.73
8:SG:64:LYS:NZ	8:SG:82:SER:O	2.21	0.73
9:SH:14:THR:OG1	9:SH:15:GLU:OE1	2.07	0.73
38:LC:126:ILE:O	38:LC:129:THR:OG1	2.07	0.73
2:SB:33:LYS:NZ	2:SB:42:ASN:OD1	2.21	0.72
39:LD:68:THR:OG1	39:LD:71:GLY:O	2.07	0.72
17:SQ:50:GLU:OE2	17:SQ:112:TYR:OH	2.07	0.72
53:LS:12:ARG:NH1	53:LS:57:GLU:OE2	2.22	0.72
68:Lh:81:ARG:O	68:Lh:81:ARG:NH1	2.21	0.72
42:LG:147:LYS:O	42:LG:201:THR:OG1	2.06	0.72
73:Lm:100:TYR:O	77:C1:2895:G:O2'	2.07	0.72
3:SP:123:TYR:OH	19:SS:126:ARG:NH1	2.23	0.72
40:LE:175:LYS:O	47:LM:117:ARG:NH2	2.22	0.72
1:C2:1584:G:N2	1:C2:1611:A:OP2	2.23	0.72
53:LS:161:LYS:NZ	77:C1:3209:A:OP2	2.21	0.71
77:C1:449:U:O2'	77:C1:450:G:N2	2.23	0.71
1:C2:159:U:O2'	8:SG:87:ARG:NH1	2.23	0.71
6:SE:19:LEU:HD11	6:SE:108:ARG:HD2	1.72	0.71
28:Sb:34:ASP:OD2	28:Sb:82:LYS:NZ	2.22	0.71
38:LC:361:HIS:O	53:LS:28:ARG:NH2	2.23	0.71
1:C2:1562:G:OP1	20:ST:89:ARG:NH2	2.23	0.71
2:SB:194:ASN:ND2	2:SB:210:ILE:O	2.23	0.71
14:SM:84:ASN:O	14:SM:86:VAL:HG22	1.91	0.71
61:La:135:GLU:OE2	61:La:139:ARG:NH2	2.24	0.71
27:Sa:13:LYS:O	27:Sa:15:ARG:NH1	2.23	0.71
80:7:57:A:O2'	80:7:59:U:OP2	2.07	0.71
77:C1:1244:A:O2'	77:C1:1247:U:OP1	2.07	0.71
1:C2:765:G:O6	11:SJ:149:ARG:NH2	2.24	0.71
1:C2:1502:G:N7	20:ST:102:ARG:NH2	2.39	0.71
31:Sf:100:LEU:HD11	31:Sf:103:LEU:HD11	1.72	0.71
35:C3:95:G:O2'	70:Lj:81:GLY:O	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:LG:248:LYS:NZ	77:C1:2529:A:OP1	2.17	0.71
40:LE:46:ARG:NH1	77:C1:3268:A:OP1	2.24	0.70
1:C2:1459:C:OP1	19:SS:126:ARG:NH2	2.24	0.70
76:Lp:5:THR:OG1	77:C1:837:A:OP1	2.07	0.70
77:C1:2537:U:O2'	77:C1:2538:U:O5'	2.10	0.70
34:C4:76:A:O2'	53:LS:50:LYS:NZ	2.24	0.70
1:C2:687:G:OP1	23:SW:118:ARG:NH1	2.25	0.70
1:C2:821:U:O4	1:C2:852:C:N3	2.25	0.70
10:SI:5:ARG:NH1	10:SI:29:LEU:O	2.24	0.70
1:C2:623:A:O2'	1:C2:624:G:OP1	2.09	0.70
77:C1:1724:U:O2'	77:C1:1725:C:OP2	2.10	0.70
1:C2:1435:G:O6	12:SK:64:TYR:OH	2.05	0.70
10:SI:162:ALA:HA	77:C1:3352:U:H2'	1.74	0.69
1:C2:235:G:O2'	1:C2:236:A:O5'	2.11	0.69
35:C3:136:G:OP1	58:LX:48:SER:OG	2.07	0.69
52:LR:100:ARG:NH1	77:C1:1722:U:OP1	2.25	0.69
1:C2:1615:C:O2'	1:C2:1616:G:OP2	2.07	0.69
57:LW:86:SER:O	57:LW:89:LEU:N	2.24	0.69
77:C1:3375:A:O2'	77:C1:3378:C:OP2	2.11	0.69
47:LM:84:LYS:NZ	77:C1:559:A:O2'	2.25	0.69
75:Lo:2:VAL:N	75:Lo:90:HIS:O	2.26	0.69
75:Lo:30:ALA:O	77:C1:2767:U:O2'	2.10	0.69
10:SI:138:ASN:OD1	10:SI:141:ARG:NH2	2.26	0.69
40:LE:11:PRO:HG2	65:Le:91:THR:HG21	1.74	0.69
51:LQ:86:THR:HG21	77:C1:676:G:O6	1.93	0.69
1:C2:1797:A:N6	27:Sa:84:VAL:O	2.26	0.69
43:LH:168:ARG:NH2	77:C1:2894:C:OP2	2.25	0.69
1:C2:129:U:O2'	1:C2:131:C:N4	2.26	0.69
60:LZ:56:LYS:NZ	77:C1:2574:G:OP2	2.26	0.69
80:7:15:A:N6	80:7:47:C:O2	2.22	0.68
1:C2:351:C:OP1	1:C2:630:A:O2'	2.05	0.68
18:SR:82:ASP:OD2	82:SA:88:LYS:NZ	2.25	0.68
77:C1:1716:U:HO2'	77:C1:1717:U:P	2.17	0.68
77:C1:1348:U:O2	77:C1:1349:G:N2	2.27	0.68
1:C2:405:C:O2'	8:SG:92:ARG:O	2.12	0.68
1:C2:1799:U:O2'	2:SB:152:ARG:NH1	2.27	0.68
77:C1:239:G:O2'	77:C1:240:U:OP1	2.05	0.68
16:SO:47:LYS:NZ	16:SO:66:ASP:OD2	2.19	0.68
70:Lj:48:ASN:OD1	70:Lj:54:LYS:NZ	2.27	0.68
23:SW:15:ASN:ND2	23:SW:72:CYS:O	2.26	0.68
22:SV:15:ARG:NH1	22:SV:33:GLN:OE1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:LH:120:ASP:OD1	43:LH:124:ARG:NH2	2.27	0.68
68:Lh:63:ARG:NH2	68:Lh:79:ASP:O	2.27	0.68
1:C2:819:G:C5	1:C2:853:G:C2	2.83	0.67
46:LL:4:SER:O	61:La:44:ASN:ND2	2.27	0.67
48:LN:4:TYR:OH	77:C1:148:G:OP2	2.08	0.67
3:SP:86:VAL:HG22	3:SP:87:PRO:HD2	1.76	0.67
6:SE:129:VAL:HG12	6:SE:139:VAL:HG12	1.75	0.67
37:LB:55:THR:OG1	77:C1:3049:A:O2'	2.11	0.67
43:LH:36:LYS:NZ	43:LH:152:GLU:OE2	2.27	0.67
5:SD:178:ARG:NH1	5:SD:179:GLN:OE1	2.28	0.67
61:La:27:LYS:NZ	77:C1:936:A:OP2	2.23	0.67
3:SP:64:LYS:NZ	3:SP:90:ILE:O	2.28	0.67
35:C3:75:G:OP2	59:LY:74:TYR:OH	2.13	0.67
77:C1:117:U:O2'	77:C1:119:U:OP2	2.11	0.67
1:C2:330:G:OP2	10:SI:172:ARG:NH1	2.28	0.67
53:LS:90:MET:HE1	53:LS:114:HIS:NE2	2.09	0.67
10:SI:34:ALA:HB2	10:SI:56:ARG:HD2	1.77	0.67
34:C4:121:U:OP2	39:LD:265:TYR:OH	2.09	0.66
1:C2:459:G:OP2	25:SY:105:ARG:NH2	2.28	0.66
33:Sc:21:SER:OG	33:Sc:22:ARG:NH1	2.27	0.66
77:C1:2874:G:N2	81:8:11:MET:SD	2.69	0.66
1:C2:1362:U:O2'	1:C2:1363:U:O2	2.08	0.66
10:SI:7:SER:O	10:SI:18:ARG:NH2	2.28	0.66
39:LD:130:GLU:OE1	39:LD:130:GLU:N	2.28	0.66
42:LG:52:TRP:O	42:LG:57:ARG:NH1	2.28	0.66
39:LD:128:GLU:O	39:LD:164:LYS:NZ	2.28	0.66
77:C1:3042:U:OP2	77:C1:3092:C:N4	2.26	0.66
1:C2:142:G:OP2	8:SG:139:ASN:ND2	2.28	0.66
59:LY:56:VAL:HG21	59:LY:104:LEU:HD13	1.78	0.66
1:C2:219:A:OP1	8:SG:227:ARG:NH2	2.29	0.66
31:Sf:137:ASP:O	31:Sf:151:ASN:ND2	2.28	0.66
10:SI:34:ALA:HB2	10:SI:56:ARG:CD	2.26	0.65
17:SQ:32:ASN:O	17:SQ:68:ARG:NH1	2.29	0.65
7:SF:136:ALA:O	7:SF:140:THR:HG22	1.96	0.65
54:LT:88:ARG:O	77:C1:2722:U:O2'	2.13	0.65
55:LU:32:SER:HG	55:LU:83:TYR:HH	1.42	0.65
1:C2:1089:U:OP1	27:Sa:89:ARG:NH1	2.29	0.65
35:C3:103:G:OP2	35:C3:105:A:O2'	2.15	0.65
1:C2:821:U:N3	1:C2:852:C:O2	2.29	0.65
80:7:10:G:O6	80:7:45:G:N2	2.26	0.65
28:Sb:59:CYS:SG	28:Sb:61:THR:OG1	2.55	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:5:34:U:O2'	78:5:35:C:OP1	2.09	0.65
36:LA:33:ASP:O	36:LA:37:ARG:NH1	2.30	0.65
64:Ld:102:LYS:NZ	77:C1:3373:U:OP2	2.20	0.65
4:SC:222:TYR:OH	22:SV:11:LEU:O	2.11	0.65
31:Sf:141:CYS:SG	31:Sf:142:GLY:N	2.70	0.65
7:SF:37:GLN:CB	17:SQ:53:LEU:HD22	2.28	0.64
25:SY:27:VAL:HG11	25:SY:35:VAL:HG21	1.79	0.64
77:C1:1565:G:C2	77:C1:1575:A:C6	2.84	0.64
12:SK:14:TYR:OH	12:SK:34:GLU:OE1	2.15	0.64
14:SM:133:LEU:HA	14:SM:136:ILE:HG22	1.79	0.64
47:LM:124:ARG:NH1	77:C1:3214:U:O4	2.30	0.64
48:LN:96:ARG:NH2	48:LN:104:GLU:OE2	2.31	0.64
70:Lj:13:ASN:ND2	77:C1:901:G:OP1	2.30	0.64
77:C1:1761:C:O2'	77:C1:1763:U:OP2	2.15	0.64
1:C2:140:A:OP1	8:SG:187:LYS:NZ	2.25	0.64
34:C4:21:G:O2'	39:LD:272:TYR:OH	2.02	0.64
37:LB:206:ASP:OD1	37:LB:287:LYS:NZ	2.29	0.64
16:SO:107:ARG:NH1	33:Sc:60:GLU:OE1	2.31	0.64
42:LG:160:ILE:O	42:LG:164:VAL:HG13	1.98	0.64
1:C2:861:U:O2'	23:SW:56:HIS:O	2.16	0.64
1:C2:1563:C:OP1	20:ST:84:LYS:NZ	2.19	0.64
32:Sg:302:PHE:HD1	32:Sg:312:VAL:HG12	1.62	0.64
40:LE:76:LEU:N	40:LE:138:GLN:OE1	2.29	0.64
68:Lh:102:GLU:OE1	68:Lh:105:ARG:NH2	2.31	0.64
82:SA:188:LEU:HD21	82:SA:195:TRP:CD1	2.33	0.64
49:LO:83[A]:ALA:O	77:C1:1312:C:O2'	2.16	0.64
1:C2:1365:C:OP1	17:SQ:66:ARG:NH1	2.30	0.64
4:SC:90:THR:OG1	4:SC:93:GLY:O	2.12	0.64
1:C2:1387:G:N7	18:SR:44:LYS:NZ	2.44	0.64
2:SB:212:VAL:HG13	2:SB:213:ARG:H	1.63	0.64
5:SD:105:MET:HG2	5:SD:122:VAL:HG21	1.80	0.64
6:SE:94:ALA:O	6:SE:95:THR:OG1	2.16	0.64
10:SI:84:HIS:NE2	10:SI:97:THR:OG1	2.30	0.64
21:SU:95:ALA:HB1	21:SU:99:ILE:CG2	2.27	0.64
65:Le:2:ALA:HB2	77:C1:440:A:N6	2.13	0.64
4:SC:38:VAL:O	4:SC:39:THR:HG23	1.98	0.63
35:C3:126:A:O2'	35:C3:128:U:OP2	2.12	0.63
1:C2:1382:A:O2'	1:C2:1383:G:OP1	2.11	0.63
1:C2:334:G:O6	10:SI:5:ARG:NH2	2.31	0.63
16:SO:102:LEU:HD23	27:Sa:45:VAL:HG12	1.79	0.63
39:LD:41:LYS:NZ	54:LT:30:TYR:O	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:LE:51:ARG:NH1	47:LM:114:ASP:OD2	2.31	0.63
62:Lb:33:LYS:HZ1	77:C1:2722:U:P	2.21	0.63
22:SV:64:GLU:OE2	28:Sb:2:VAL:N	2.32	0.63
46:LL:100:ARG:NH2	77:C1:66:A:OP2	2.32	0.63
24:SX:41:SER:O	24:SX:43:PHE:N	2.31	0.63
4:SC:81:MET:HE1	4:SC:186:LYS:HB3	1.79	0.63
37:LB:35:ASP:OD2	37:LB:37:ARG:NH1	2.32	0.63
61:La:6:THR:HG22	61:La:8:THR:H	1.63	0.63
77:C1:1253:U:N3	77:C1:1264:G:OP1	2.31	0.63
77:C1:1480:G:O2'	77:C1:1871:U:O4	2.15	0.63
53:LS:22:PRO:O	54:LT:146:ASN:ND2	2.32	0.63
54:LT:86:GLU:OE1	54:LT:88:ARG:NH2	2.32	0.63
56:LV:104:ASN:OD1	56:LV:108:GLU:N	2.32	0.63
60:LZ:17:ARG:NH2	60:LZ:18:TYR:OH	2.32	0.63
77:C1:2514:U:OP2	77:C1:2586:G:N2	2.30	0.63
1:C2:224:C:O2'	1:C2:225:A:OP1	2.12	0.63
21:SU:80:GLU:OE1	29:Sd:44:ARG:NH1	2.31	0.63
24:SX:42:PRO:O	24:SX:79:ASN:ND2	2.32	0.63
35:C3:52:A:OP1	72:Ll:21:ARG:NH1	2.30	0.63
65:Le:118:LYS:NZ	77:C1:438:A:OP1	2.25	0.63
1:C2:195:G:N7	10:SI:137:LYS:NZ	2.42	0.62
7:SF:92:ARG:NH2	7:SF:169:ASN:OD1	2.32	0.62
37:LB:368:GLY:O	57:LW:17:ARG:NH1	2.32	0.62
51:LQ:38:ARG:NH2	77:C1:1348:U:OP2	2.32	0.62
19:SS:30:TYR:O	19:SS:33:THR:OG1	2.17	0.62
41:LF:48:ASN:ND2	41:LF:182:ASP:OD2	2.32	0.62
58:LX:105:VAL:HG11	58:LX:126:LEU:HD22	1.81	0.62
77:C1:1255:C:N4	77:C1:1263:A:OP2	2.32	0.62
77:C1:1393:A:N3	77:C1:1419:A:O2'	2.32	0.62
77:C1:3319:U:O2'	77:C1:3320:A:OP1	2.15	0.62
45:LJ:112:LEU:O	45:LJ:114:ILE:HD12	1.99	0.62
65:Le:21:HIS:NE2	77:C1:638:C:OP1	2.29	0.62
47:LM:128:ARG:NH1	77:C1:3214:U:OP2	2.33	0.62
77:C1:1657:C:O2'	77:C1:1797:A:OP2	2.15	0.62
1:C2:819:G:C5	1:C2:853:G:N2	2.67	0.62
3:SP:103:ASN:OD1	3:SP:120:SER:OG	2.15	0.62
47:LM:62:GLN:N	47:LM:62:GLN:OE1	2.33	0.62
77:C1:2282:U:OP1	77:C1:2973:G:O2'	2.17	0.62
38:LC:82:THR:HG21	77:C1:364:G:O2'	2.00	0.62
6:SE:103:TYR:O	6:SE:182:TYR:OH	2.17	0.62
37:LB:55:THR:HG1	77:C1:3049:A:HO2'	1.42	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Lf:16:TYR:OH	66:Lf:89:LEU:O	2.16	0.62
77:C1:2568:C:O2'	77:C1:2569:A:O5'	2.18	0.62
71:Lk:44:LYS:NZ	77:C1:1750:A:OP1	2.28	0.62
3:SP:28:MET:HE1	3:SP:36:LEU:HD21	1.82	0.61
41:LF:233:GLU:OE2	53:LS:35:VAL:HG22	2.01	0.61
77:C1:339:C:OP1	77:C1:1380:G:O2'	2.17	0.61
32:Sg:39:ASP:OD1	32:Sg:41:THR:OG1	2.16	0.61
37:LB:240:ARG:NH2	77:C1:1907:C:O2	2.33	0.61
20:ST:38:LYS:O	20:ST:39:THR:OG1	2.16	0.61
52:LR:98:ARG:NH2	52:LR:130:ASN:OD1	2.33	0.61
1:C2:477:A:OP2	30:Se:28:LYS:NZ	2.28	0.61
1:C2:629:U:H5''	77:C1:846:A:H3'	1.82	0.61
45:LJ:99:THR:O	45:LJ:154:THR:OG1	2.15	0.61
48:LN:93:LYS:O	77:C1:289:A:O2'	2.19	0.61
1:C2:895:G:H21	16:SO:38:THR:HG21	1.66	0.61
17:SQ:50:GLU:OE1	17:SQ:82:ARG:NH2	2.33	0.61
1:C2:967:A:OP2	15:SN:124:ARG:NH2	2.33	0.61
35:C3:97:A:OP1	68:Lh:67:ARG:NH2	2.22	0.61
43:LH:1:MET:HE1	53:LS:138:GLN:HB3	1.83	0.61
37:LB:62:ARG:NH1	77:C1:3039:C:OP2	2.34	0.61
61:La:130:VAL:HG11	61:La:145:VAL:HG11	1.82	0.61
34:C4:81:U:O2'	77:C1:1055:A:N3	2.33	0.61
39:LD:281:GLU:OE1	39:LD:281:GLU:N	2.33	0.61
1:C2:59:C:O2'	1:C2:60:U:O4'	2.18	0.60
1:C2:1550:A:OP2	3:SP:42:ARG:NH2	2.34	0.60
1:C2:1066:C:O2'	2:SB:148:ASN:OD1	2.16	0.60
7:SF:158:GLN:NE2	7:SF:159:ALA:O	2.35	0.60
37:LB:187:SER:O	37:LB:190:GLU:N	2.34	0.60
28:Sb:67:THR:HG22	28:Sb:68:GLY:H	1.67	0.60
77:C1:1565:G:N2	77:C1:1575:A:C6	2.69	0.60
1:C2:804:A:N3	23:SW:105:THR:HG22	2.17	0.60
53:LS:158:LYS:NZ	77:C1:1183:C:OP1	2.32	0.60
53:LS:77:VAL:HG11	53:LS:106:LEU:HD13	1.83	0.60
1:C2:1565:C:OP1	19:SS:41:ARG:NH1	2.34	0.60
14:SM:91:VAL:HG22	14:SM:92:ALA:H	1.67	0.60
1:C2:479:C:O3'	11:SJ:120:LYS:NZ	2.34	0.59
32:Sg:153:GLN:OE1	32:Sg:155:ARG:NH1	2.35	0.59
51:LQ:123:THR:OG1	51:LQ:125:ASP:OD1	2.20	0.59
45:LJ:22:SER:O	77:C1:2676:A:N6	2.35	0.59
42:LG:47:SER:OG	77:C1:2585:G:O6	2.21	0.59
49:LO:110[A]:PRO:O	49:LO:112[A]:TYR:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:SA:180:GLU:OE2	82:SA:191:ARG:NH2	2.36	0.59
14:SM:71:ILE:O	14:SM:75:VAL:HG23	2.02	0.59
43:LH:155:SER:OG	77:C1:3110:C:O3'	2.18	0.59
62:Lb:16:ALA:O	62:Lb:20:GLY:CA	2.49	0.59
5:SD:23:GLU:OE2	5:SD:27:ARG:NE	2.34	0.59
66:Lf:67:MET:SD	66:Lf:89:LEU:HD23	2.43	0.59
17:SQ:129:PHE:O	17:SQ:137:ARG:NH1	2.35	0.59
1:C2:488:G:N2	1:C2:499:U:O4	2.35	0.59
2:SB:32:ILE:HD11	2:SB:46:THR:OG1	2.03	0.58
21:SU:33:GLN:N	21:SU:33:GLN:OE1	2.36	0.58
21:SU:95:ALA:HB1	21:SU:99:ILE:HG23	1.84	0.58
35:C3:141:C:O3'	48:LN:62:TYR:OH	2.21	0.58
48:LN:18:VAL:HG13	48:LN:19:LEU:HD12	1.85	0.58
30:Se:49:LEU:HD13	30:Se:58:PRO:HG3	1.85	0.58
54:LT:99:SER:OG	54:LT:101:CYS:SG	2.47	0.58
1:C2:1584:G:O2'	1:C2:1585:U:OP2	2.15	0.58
32:Sg:67:ILE:O	32:Sg:84:SER:OG	2.09	0.58
22:SV:28:ASP:OD2	22:SV:31:SER:OG	2.20	0.58
37:LB:94:GLU:OE1	37:LB:94:GLU:N	2.36	0.58
1:C2:1159:C:O2'	17:SQ:140:LYS:NZ	2.37	0.58
44:LI:90:ARG:NH1	77:C1:1044:U:OP1	2.37	0.58
1:C2:458:G:OP1	25:SY:109:LYS:NZ	2.25	0.58
57:LW:44:LYS:NZ	77:C1:2111:G:O2'	2.34	0.58
1:C2:853:G:OP2	52:LR:173:ARG:NH1	2.37	0.58
19:SS:91:ASP:OD2	19:SS:108:LYS:NZ	2.37	0.58
36:LA:93:LYS:NZ	77:C1:2547:A:O3'	2.37	0.58
48:LN:192:LYS:O	48:LN:196:THR:OG1	2.16	0.58
6:SE:148:ARG:NH1	8:SG:201:GLN:OE1	2.37	0.58
38:LC:226:GLU:OE1	38:LC:246:ARG:NH1	2.37	0.58
44:LI:54:SER:OG	44:LI:130:ASP:O	2.22	0.58
26:SZ:55:PRO:O	26:SZ:56:THR:OG1	2.18	0.58
30:Se:49:LEU:HD13	30:Se:58:PRO:CG	2.33	0.58
52:LR:105:LEU:HD23	52:LR:138:LEU:HD22	1.86	0.58
51:LQ:36:LEU:O	51:LQ:40:THR:OG1	2.22	0.57
82:SA:27:ARG:NH2	82:SA:43:ASP:O	2.37	0.57
1:C2:976:G:H1	1:C2:1023:A:HO2'	1.50	0.57
37:LB:19:ARG:NH2	77:C1:3045:G:OP1	2.36	0.57
6:SE:87:MET:HE1	6:SE:236:ILE:HD13	1.86	0.57
39:LD:278:SER:OG	39:LD:280:GLU:OE1	2.21	0.57
45:LJ:40:LEU:HD22	45:LJ:125:MET:HE1	1.86	0.57
1:C2:1796:C:O2'	27:Sa:95:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:41:LEU:HD22	4:SC:68:ILE:HD13	1.86	0.57
37:LB:77:THR:HG21	37:LB:328:ILE:HG12	1.87	0.57
51:LQ:66:ARG:NH2	77:C1:744:A:OP1	2.37	0.57
77:C1:1015:U:O2'	77:C1:1017:C:OP2	2.12	0.57
14:SM:59:LEU:HD23	14:SM:60:VAL:N	2.20	0.57
14:SM:70:ASN:OD1	14:SM:71:ILE:N	2.37	0.57
38:LC:98:ARG:NH2	77:C1:804:C:OP1	2.38	0.57
76:Lp:75:ALA:O	76:Lp:79:VAL:HG23	2.03	0.57
1:C2:127:G:N2	1:C2:178:U:O2'	2.38	0.57
1:C2:1529:C:OP1	26:SZ:95:HIS:NE2	2.37	0.57
1:C2:1022:C:O2'	1:C2:1125:A:N1	2.36	0.57
38:LC:328:ASN:OD1	41:LF:48:ASN:ND2	2.38	0.57
72:Ll:13:MET:SD	77:C1:1493:G:O2'	2.60	0.57
77:C1:2393:G:O2'	77:C1:2394:G:OP2	2.19	0.57
80:7:15:A:N1	80:7:47:C:N3	2.53	0.57
7:SF:58:LEU:HD12	7:SF:138:THR:HG22	1.87	0.56
49:LO:171[A]:LYS:NZ	77:C1:3181:C:OP2	2.29	0.56
82:SA:92:HIS:ND1	82:SA:202:TYR:OH	2.33	0.56
8:SG:174:LYS:O	8:SG:175:ILE:HD13	2.06	0.56
12:SK:47:GLN:O	12:SK:50:THR:OG1	2.18	0.56
44:LI:66:GLU:OE1	44:LI:69:ARG:NH2	2.38	0.56
77:C1:2495:C:HO2'	77:C1:2496:C:P	2.26	0.56
82:SA:156:VAL:HG12	82:SA:157:ASP:O	2.05	0.56
21:SU:71:PRO:O	29:Sd:40:ARG:NH2	2.38	0.56
60:LZ:48:ARG:NH2	77:C1:1631:C:OP2	2.35	0.56
1:C2:55:A:OP1	25:SY:112:LYS:NZ	2.35	0.56
9:SH:39:ARG:NH2	52:LR:188:ASP:OD2	2.38	0.56
1:C2:388:G:OP1	1:C2:423:G:O2'	2.23	0.56
45:LJ:65:ILE:HD11	77:C1:2681:U:H5'	1.88	0.56
65:Le:15:LYS:NZ	77:C1:426:G:OP1	2.38	0.56
77:C1:1196:C:OP1	77:C1:1309:U:O2'	2.19	0.56
31:Sf:146:SER:O	31:Sf:149:LYS:NZ	2.37	0.56
48:LN:186:GLY:O	48:LN:190:THR:HG23	2.05	0.56
6:SE:18:TRP:NE1	6:SE:41:SER:O	2.38	0.56
1:C2:1063:U:OP1	28:Sb:72:LYS:NZ	2.39	0.56
1:C2:1597:A:OP2	29:Sd:32:ARG:NH1	2.38	0.56
21:SU:106:ILE:HG13	21:SU:107:THR:HG23	1.88	0.56
71:Lk:4:GLU:OE2	77:C1:1746:U:O2'	2.22	0.55
14:SM:97:LEU:HD23	14:SM:118:ALA:O	2.06	0.55
77:C1:63:A:N3	77:C1:78:U:O2'	2.34	0.55
1:C2:125:U:OP1	8:SG:201:GLN:NE2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:108:ASP:OD1	2:SB:109:LYS:N	2.39	0.55
5:SD:59:LEU:HD23	5:SD:66:ILE:HG13	1.88	0.55
67:Lg:8:ARG:NH2	77:C1:1597:C:OP2	2.39	0.55
68:Lh:84:LYS:O	68:Lh:85:THR:HG23	2.07	0.55
70:Lj:21:ARG:NH2	70:Lj:41:ALA:O	2.33	0.55
1:C2:771:A:O2'	11:SJ:6:ARG:NH2	2.39	0.55
26:SZ:95:HIS:ND1	26:SZ:96:SER:O	2.39	0.55
32:Sg:238:ASP:OD2	32:Sg:258:THR:N	2.37	0.55
1:C2:237:C:O2'	1:C2:238:U:O5'	2.25	0.55
77:C1:2101:C:O2'	77:C1:2102:U:O5'	2.21	0.55
1:C2:169:A:OP2	8:SG:137:ARG:NH1	2.38	0.55
39:LD:294:ALA:HB1	44:LI:217:PHE:HB3	1.89	0.55
77:C1:3154:C:N3	77:C1:3157:U:O4	2.40	0.55
1:C2:1706:C:O2'	1:C2:1707:A:O4'	2.23	0.55
14:SM:74:LEU:HA	31:Sf:108:VAL:HG21	1.89	0.55
43:LH:62:ARG:NH1	77:C1:1210:U:OP1	2.39	0.55
56:LV:108:GLU:N	56:LV:108:GLU:OE2	2.40	0.55
1:C2:448:C:OP2	6:SE:49:ARG:NH2	2.40	0.55
1:C2:1515:A:O2'	1:C2:1517:U:OP2	2.15	0.55
2:SB:180:THR:OG1	2:SB:181:LEU:N	2.38	0.55
19:SS:14:ILE:HD12	45:LJ:116:TYR:CZ	2.42	0.55
1:C2:1226:A:H61	14:SM:114:LYS:CB	2.20	0.54
54:LT:80:VAL:O	54:LT:83:ARG:NH1	2.40	0.54
71:Lk:2:ALA:N	71:Lk:51:LEU:O	2.41	0.54
77:C1:1307:G:O2'	77:C1:1308:A:OP2	2.13	0.54
51:LQ:74:GLU:N	51:LQ:74:GLU:OE1	2.41	0.54
52:LR:88:ARG:O	77:C1:1779:C:N4	2.35	0.54
26:SZ:67:ASP:OD1	26:SZ:68:ARG:N	2.39	0.54
32:Sg:238:ASP:OD1	32:Sg:239:GLU:N	2.40	0.54
38:LC:193:LYS:HZ2	77:C1:1419:A:H5''	1.73	0.54
35:C3:51:G:OP2	72:LI:21:ARG:NH1	2.39	0.54
60:LZ:115:LYS:NZ	60:LZ:119:GLU:OE1	2.41	0.54
1:C2:393:C:OP2	10:SI:2:GLY:N	2.40	0.54
6:SE:141:THR:OG1	6:SE:143:ASP:OD1	2.13	0.54
7:SF:148:ARG:NH2	80:7:32:C:O2'	2.41	0.54
25:SY:38:ASP:OD1	25:SY:39:GLU:N	2.41	0.54
27:Sa:18:VAL:HG12	27:Sa:18:VAL:O	2.07	0.54
75:Lo:77:CYS:SG	75:Lo:79:THR:OG1	2.52	0.54
1:C2:1245:G:O2'	1:C2:1247:U:OP2	2.22	0.54
1:C2:1251:U:O2	31:Sf:135:HIS:NE2	2.41	0.54
53:LS:81:TYR:CE1	53:LS:90:MET:HE3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:C1:239:G:HO2'	77:C1:240:U:P	2.26	0.54
1:C2:68:A:N6	8:SG:132:ARG:O	2.40	0.54
1:C2:640:U:O2'	1:C2:641:G:OP1	2.26	0.54
6:SE:98:ASN:ND2	6:SE:116:ASP:OD1	2.40	0.54
9:SH:114:ARG:O	9:SH:117:THR:HG22	2.06	0.54
9:SH:181:ILE:HD12	9:SH:183:PHE:CE2	2.43	0.54
48:LN:90:ASN:ND2	77:C1:2424:A:OP1	2.41	0.54
77:C1:1015:U:O2	77:C1:1017:C:O2'	2.26	0.54
11:SJ:59:LEU:HD22	11:SJ:69:ARG:HA	1.89	0.54
77:C1:1562:C:HO2'	77:C1:1563:C:C5'	2.18	0.54
1:C2:1585:U:OP1	17:SQ:125:GLU:N	2.38	0.54
2:SB:72:ASP:OD1	16:SO:114:ARG:NH1	2.41	0.54
37:LB:266:ARG:HH22	77:C1:2392:C:HO2'	1.49	0.54
69:Li:76:ARG:O	77:C1:293:C:O2'	2.19	0.54
1:C2:1637:C:O2	78:5:49:C:N4	2.41	0.54
18:SR:82:ASP:O	82:SA:84:ARG:NH2	2.41	0.54
27:Sa:57:SER:OG	27:Sa:58:VAL:O	2.26	0.54
47:LM:59:ASN:OD1	47:LM:60:LEU:N	2.41	0.54
77:C1:2447:A:N6	77:C1:2448:G:O6	2.40	0.54
38:LC:360:LYS:NZ	77:C1:519:A:N7	2.55	0.53
52:LR:124:TYR:OH	77:C1:1721:U:OP2	2.25	0.53
3:SP:110:GLU:CG	19:SS:119:ILE:HD11	2.39	0.53
22:SV:58:TYR:OH	22:SV:62:ARG:NH1	2.41	0.53
1:C2:1436:A:OP2	5:SD:27:ARG:NH2	2.41	0.53
11:SJ:133:HIS:O	11:SJ:134:ILE:HG23	2.09	0.53
41:LF:70:LYS:NZ	77:C1:520:U:OP2	2.40	0.53
70:Lj:16:HIS:HD1	77:C1:359:U:HO2'	1.56	0.53
14:SM:66:VAL:HG23	14:SM:67:THR:H	1.74	0.53
1:C2:1611:A:O2'	7:SF:95:ASN:O	2.25	0.53
27:Sa:45:VAL:HG23	27:Sa:46:GLU:H	1.73	0.53
20:ST:23:GLN:NE2	20:ST:51:GLU:O	2.42	0.53
1:C2:1698:G:O2'	1:C2:1699:G:O5'	2.25	0.53
2:SB:210:ILE:O	2:SB:210:ILE:HG22	2.09	0.53
14:SM:33:ARG:O	14:SM:37:VAL:HG23	2.08	0.53
21:SU:22:ILE:HG22	21:SU:118:VAL:HG22	1.90	0.53
54:LT:124:VAL:HG12	54:LT:124:VAL:O	2.09	0.53
77:C1:2945:G:O2'	77:C1:2948:C:OP2	2.19	0.53
1:C2:629:U:H5'	77:C1:847:A:C8	2.44	0.53
47:LM:65:LEU:HD13	53:LS:172:TYR:OH	2.09	0.53
52:LR:115:ILE:HG13	52:LR:119:LEU:HD23	1.90	0.53
48:LN:204:LYS:NZ	77:C1:683:U:OP1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:C1:2185:G:O2'	77:C1:2314:U:OP2	2.24	0.53
4:SC:139:ILE:HD12	4:SC:218:ILE:HB	1.90	0.53
24:SX:102:VAL:HG12	24:SX:127:VAL:HG12	1.91	0.53
32:Sg:74:THR:OG1	32:Sg:76:ASP:OD1	2.20	0.53
36:LA:37:ARG:NH2	77:C1:2526:C:OP1	2.37	0.53
58:LX:50:ALA:O	68:Lh:66:VAL:HG21	2.08	0.53
77:C1:1596:C:O2'	77:C1:1696:A:N3	2.39	0.53
77:C1:1721:U:O2'	77:C1:1723:A:N7	2.40	0.53
16:SO:80:HIS:ND1	16:SO:113:GLY:O	2.30	0.52
32:Sg:194:GLY:O	32:Sg:221:MET:HE1	2.09	0.52
77:C1:848:A:O2'	77:C1:849:C:OP1	2.25	0.52
1:C2:278:U:OP1	1:C2:279:G:N2	2.42	0.52
1:C2:472:U:O2'	1:C2:769:A:N3	2.42	0.52
1:C2:629:U:C5'	77:C1:846:A:H3'	2.38	0.52
1:C2:1558:U:O2'	1:C2:1559:A:OP2	2.26	0.52
32:Sg:307:ASP:OD2	32:Sg:309:VAL:HG12	2.09	0.52
39:LD:206:GLN:NE2	39:LD:210:GLU:OE1	2.42	0.52
46:LL:76:THR:O	46:LL:79:GLU:N	2.39	0.52
1:C2:1504:G:OP1	20:ST:97:SER:OG	2.24	0.52
4:SC:206:THR:O	4:SC:210:THR:HG23	2.09	0.52
37:LB:215:ILE:CD1	37:LB:338:LEU:HD12	2.39	0.52
38:LC:59:GLN:OE1	70:Lj:55:ARG:NH2	2.40	0.52
61:La:95:SER:OG	61:La:96:LYS:O	2.23	0.52
1:C2:31:C:O2'	1:C2:547:U:OP1	2.28	0.52
1:C2:428:A:N3	1:C2:440:U:O2'	2.26	0.52
17:SQ:44:LEU:HB3	17:SQ:78:VAL:HG11	1.91	0.52
44:LI:54:SER:HB3	44:LI:135:ILE:HD11	1.92	0.52
56:LV:38:ALA:HB3	56:LV:59:MET:HB2	1.91	0.52
77:C1:1643:A:O2'	77:C1:1644:C:O4'	2.25	0.52
1:C2:629:U:N3	1:C2:630:A:N7	2.39	0.52
82:SA:188:LEU:HD21	82:SA:195:TRP:CG	2.44	0.52
37:LB:274:SER:OG	77:C1:3139:A:OP1	2.21	0.52
77:C1:1268:G:O2'	77:C1:1269:U:O2	2.28	0.52
1:C2:14:C:OP2	4:SC:206:THR:HG21	2.09	0.52
1:C2:742:U:O2'	9:SH:107:ARG:NE	2.41	0.52
34:C4:121:U:N3	39:LD:264:GLN:O	2.42	0.52
7:SF:192:GLU:OE2	26:SZ:63:SER:OG	2.15	0.52
37:LB:160:VAL:HG23	37:LB:183:LEU:HD11	1.92	0.52
77:C1:1261:G:HO2'	77:C1:1278:A:H61	1.56	0.52
82:SA:146:LEU:HD22	82:SA:173:ILE:HG21	1.91	0.52
43:LH:1:MET:HE1	53:LS:138:GLN:CG	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:LI:140:THR:HG21	44:LI:148:VAL:HG11	1.91	0.52
51:LQ:56:LYS:NZ	77:C1:674:G:O6	2.43	0.52
77:C1:2500:A:O2'	77:C1:2501:U:OP1	2.26	0.52
1:C2:555:A:O2'	1:C2:556:A:OP1	2.25	0.51
1:C2:647:G:N2	1:C2:687:G:H22	2.08	0.51
1:C2:1383:G:O5'	21:SU:89:ARG:NH1	2.43	0.51
1:C2:1601:G:OP1	20:ST:86:ARG:NH1	2.37	0.51
2:SB:77:GLU:OE2	16:SO:114:ARG:NH2	2.43	0.51
10:SI:96:LEU:HD13	10:SI:179:CYS:SG	2.51	0.51
37:LB:14:LEU:HA	37:LB:17:LEU:HD13	1.92	0.51
65:Le:2:ALA:HB2	77:C1:440:A:H61	1.75	0.51
1:C2:224:C:HO2'	1:C2:225:A:P	2.31	0.51
1:C2:1473:U:O2'	7:SF:103:ASN:ND2	2.42	0.51
3:SP:110:GLU:HG2	19:SS:119:ILE:HD11	1.92	0.51
30:Se:14:VAL:O	30:Se:18:THR:HG23	2.10	0.51
1:C2:629:U:N3	77:C1:846:A:N6	2.52	0.51
4:SC:116:LYS:HG2	4:SC:127:ALA:HB3	1.92	0.51
9:SH:150:GLN:HB2	9:SH:181:ILE:HG22	1.91	0.51
50:LP:56:ARG:NH1	50:LP:75:GLU:OE2	2.40	0.51
54:LT:84:TYR:HE2	62:Lb:21:ILE:HG22	1.76	0.51
7:SF:57:SER:OG	7:SF:167:ARG:NH2	2.43	0.51
14:SM:130:THR:OG1	14:SM:131:ASP:N	2.42	0.51
32:Sg:214:ALA:HB1	32:Sg:240:VAL:HG11	1.92	0.51
33:Sc:55:VAL:HG23	33:Sc:55:VAL:O	2.11	0.51
37:LB:317:ILE:HG22	37:LB:317:ILE:O	2.10	0.51
1:C2:762:A:OP1	11:SJ:79:ARG:NH1	2.42	0.51
1:C2:819:G:O6	1:C2:853:G:C6	2.64	0.51
1:C2:819:G:C4	1:C2:853:G:N2	2.79	0.51
16:SO:88:GLY:O	16:SO:92:LYS:NZ	2.43	0.51
20:ST:144:GLU:N	20:ST:144:GLU:OE1	2.44	0.51
24:SX:69:ARG:NH2	24:SX:116:ASP:OD2	2.43	0.51
10:SI:57:ALA:HB2	10:SI:177:GLY:HA2	1.93	0.51
38:LC:203:ARG:HB2	38:LC:203:ARG:CZ	2.41	0.51
46:LL:39:ARG:NH2	77:C1:686:G:OP2	2.44	0.51
77:C1:376:G:O2'	77:C1:401:U:O4	2.23	0.51
1:C2:755:A:O2'	1:C2:756:A:OP1	2.27	0.51
14:SM:103:LEU:HD11	14:SM:116:VAL:HG12	1.92	0.51
38:LC:164:GLU:OE1	38:LC:164:GLU:N	2.43	0.51
38:LC:342:LYS:O	77:C1:515:C:O2'	2.29	0.51
1:C2:540:G:O2'	1:C2:541:A:O5'	2.24	0.50
1:C2:1172:G:H21	20:ST:88:VAL:CG2	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SH:64:VAL:O	9:SH:64:VAL:HG22	2.11	0.50
47:LM:65:LEU:HD22	53:LS:172:TYR:OH	2.11	0.50
77:C1:2309:A:N3	77:C1:2961:G:O2'	2.42	0.50
1:C2:44:U:OP2	1:C2:437:A:N6	2.43	0.50
9:SH:34:LEU:HB2	9:SH:38:LEU:HD23	1.93	0.50
10:SI:106:ALA:HB2	10:SI:165:LEU:HG	1.92	0.50
20:ST:28:LEU:HD23	20:ST:29:GLU:N	2.26	0.50
20:ST:100:ILE:O	20:ST:104:VAL:HG23	2.12	0.50
32:Sg:115:ILE:HD13	32:Sg:122:ILE:HG12	1.93	0.50
49:LO:43[A]:ILE:HD11	49:LO:138[A]:LEU:CD1	2.41	0.50
51:LQ:141:ARG:NH2	77:C1:977:C:OP1	2.38	0.50
8:SG:49:VAL:HG12	8:SG:115:LYS:HB3	1.93	0.50
1:C2:579:A:N6	1:C2:1438:G:O2'	2.43	0.50
21:SU:44:ASN:OD1	21:SU:103:ILE:HD11	2.12	0.50
9:SH:138:LYS:NZ	9:SH:150:GLN:OE1	2.45	0.50
77:C1:3353:G:H3'	77:C1:3354:U:O4'	2.12	0.50
27:Sa:90:GLU:N	27:Sa:90:GLU:OE1	2.45	0.50
37:LB:277:SER:OG	37:LB:280:HIS:NE2	2.42	0.50
75:Lo:20:HIS:ND1	77:C1:2741:C:O2'	2.32	0.50
1:C2:1558:U:OP2	1:C2:1559:A:O2'	2.21	0.50
6:SE:19:LEU:HD11	6:SE:108:ARG:CD	2.40	0.50
58:LX:105:VAL:CG1	58:LX:126:LEU:HD22	2.41	0.50
32:Sg:5:GLU:OE1	32:Sg:5:GLU:N	2.45	0.50
32:Sg:144:LEU:HD12	32:Sg:181:TRP:CZ3	2.47	0.50
38:LC:60:THR:OG1	77:C1:364:G:OP1	2.19	0.50
41:LF:34:LYS:NZ	77:C1:596:C:OP2	2.21	0.50
45:LJ:133:ARG:NH1	45:LJ:153:LYS:O	2.45	0.50
76:Lp:49:ARG:NE	76:Lp:68:ALA:O	2.44	0.50
1:C2:1245:G:O2'	1:C2:1246:C:O5'	2.30	0.50
16:SO:61:MET:HE3	16:SO:65:GLN:NE2	2.27	0.50
27:Sa:45:VAL:HG23	27:Sa:46:GLU:N	2.27	0.50
38:LC:82:THR:HG23	77:C1:355:A:N1	2.26	0.50
76:Lp:50:GLY:O	77:C1:1795:U:N3	2.45	0.50
77:C1:69:C:O2'	77:C1:101:G:O2'	2.19	0.50
1:C2:655:G:N3	1:C2:678:A:N6	2.60	0.49
1:C2:1553:G:O2'	29:Sd:14:TYR:OH	2.12	0.49
6:SE:90:ILE:HD12	6:SE:101:LEU:HD13	1.94	0.49
24:SX:130:VAL:HG12	24:SX:130:VAL:O	2.12	0.49
25:SY:81:GLU:OE1	25:SY:81:GLU:N	2.45	0.49
33:Sc:65:ARG:NH2	78:5:38:G:O6	2.45	0.49
77:C1:362:U:HO2'	77:C1:928:C:HO2'	1.58	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:168:ILE:HG12	2:SB:197:ILE:HD12	1.94	0.49
7:SF:134:VAL:O	7:SF:138:THR:HG23	2.12	0.49
27:Sa:36:ILE:O	27:Sa:38:ARG:NH1	2.45	0.49
32:Sg:115:ILE:HD12	32:Sg:121:MET:O	2.11	0.49
18:SR:24:LEU:O	18:SR:58:MET:HE2	2.12	0.49
48:LN:98:LEU:HA	48:LN:101:THR:HG22	1.95	0.49
4:SC:183:ALA:CB	4:SC:207:LEU:HD11	2.42	0.49
6:SE:93:ASP:OD2	6:SE:94:ALA:N	2.43	0.49
52:LR:38:ARG:NH1	77:C1:1603:A:OP1	2.46	0.49
69:Li:53:TYR:O	69:Li:57:LEU:HD23	2.13	0.49
7:SF:43:PHE:CZ	7:SF:90:ILE:HG21	2.48	0.49
48:LN:8:GLU:OE2	48:LN:50:ARG:NH2	2.46	0.49
77:C1:1245:A:N6	77:C1:1272:C:O2'	2.46	0.49
1:C2:505:A:O2'	1:C2:507:U:OP1	2.23	0.49
49:LO:121[A]:PRO:HA	49:LO:124[A]:LEU:HD12	1.95	0.49
22:SV:80:LYS:O	22:SV:82:VAL:N	2.46	0.49
51:LQ:125:ASP:OD1	51:LQ:126:GLN:N	2.46	0.49
1:C2:1483:A:N3	1:C2:1607:G:O2'	2.40	0.49
4:SC:140:ARG:NH2	4:SC:228:ASN:OD1	2.46	0.49
36:LA:101:VAL:HG12	36:LA:101:VAL:O	2.13	0.49
38:LC:272:VAL:HG22	77:C1:696:C:OP1	2.12	0.49
77:C1:1261:G:O2'	77:C1:1278:A:N6	2.42	0.49
1:C2:1610:G:N7	17:SQ:14:LYS:NZ	2.60	0.48
19:SS:41:ARG:NH2	20:ST:36:ILE:O	2.45	0.48
32:Sg:177:MET:SD	32:Sg:179:LYS:NZ	2.73	0.48
38:LC:188:ARG:NE	38:LC:197:ARG:O	2.42	0.48
71:Lk:5:ILE:HG22	71:Lk:7:ASP:H	1.78	0.48
1:C2:813:U:O2'	1:C2:814:A:OP2	2.29	0.48
46:LL:76:THR:OG1	46:LL:101:ARG:NH1	2.46	0.48
1:C2:129:U:HO2'	1:C2:131:C:N4	2.08	0.48
1:C2:1615:C:OP1	7:SF:81:ARG:NH2	2.45	0.48
3:SP:75:PRO:HA	3:SP:93:VAL:HG23	1.95	0.48
14:SM:62:LEU:HD23	14:SM:63:VAL:O	2.14	0.48
32:Sg:273:ASP:OD1	32:Sg:275:ARG:NH1	2.46	0.48
38:LC:3:ARG:NH1	38:LC:27:SER:OG	2.44	0.48
77:C1:649:A:OP2	77:C1:2868:U:O2'	2.31	0.48
77:C1:1188:U:OP1	77:C1:1210:U:O2'	2.18	0.48
35:C3:28:C:O2'	77:C1:691:A:N1	2.45	0.48
77:C1:1390:A:N6	77:C1:1418:A:O2'	2.46	0.48
1:C2:163:G:OP2	1:C2:163:G:N2	2.38	0.48
1:C2:1344:A:O2'	1:C2:1345:A:OP1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SD:31:GLU:N	5:SD:31:GLU:OE1	2.46	0.48
6:SE:65:LEU:HD23	6:SE:70:VAL:CG1	2.43	0.48
11:SJ:129:ILE:HG12	11:SJ:134:ILE:HD11	1.95	0.48
36:LA:108:PRO:HG2	76:Lp:86:LEU:HD13	1.96	0.48
1:C2:354:C:H5''	10:SI:16:ALA:HB2	1.95	0.48
1:C2:558:U:OP2	30:Se:55:ARG:NH1	2.47	0.48
1:C2:639:U:OP1	9:SH:112:ARG:NH2	2.46	0.48
9:SH:133:THR:OG1	9:SH:134:GLU:N	2.35	0.48
37:LB:28:ARG:NH2	77:C1:3140:G:N7	2.55	0.48
77:C1:999:G:N3	77:C1:1002:A:N6	2.62	0.48
1:C2:1390:U:OP1	18:SR:5:ARG:NH1	2.46	0.48
55:LU:89:LEU:HB3	55:LU:93:ILE:HD12	1.94	0.48
65:Le:33:ARG:HH21	77:C1:1407:A:H4'	1.78	0.48
72:Ll:2:ALA:N	77:C1:1493:G:O6	2.46	0.48
77:C1:441:U:OP2	77:C1:490:C:N4	2.43	0.48
77:C1:1236:G:N1	77:C1:1244:A:OP1	2.46	0.48
28:Sb:76:GLY:O	28:Sb:77:THR:HG23	2.14	0.48
31:Sf:147:VAL:HG13	31:Sf:147:VAL:O	2.13	0.48
43:LH:9:GLN:OE1	43:LH:54:LYS:NZ	2.46	0.48
45:LJ:48:SER:OG	45:LJ:66:ALA:HB3	2.13	0.48
52:LR:62:ARG:HH12	77:C1:3067:C:H3'	1.77	0.48
80:7:17:G:N2	80:7:57:A:O4'	2.46	0.48
1:C2:1173:C:OP1	19:SS:132:ARG:NH2	2.47	0.48
2:SB:199:ASN:OD1	2:SB:202:LYS:NZ	2.47	0.48
4:SC:229:LEU:HD21	22:SV:10:GLU:OE2	2.13	0.48
53:LS:108:GLN:NE2	77:C1:1322:U:O2	2.40	0.48
70:Lj:45:ARG:NH2	77:C1:361:A:O3'	2.46	0.48
77:C1:643:U:O2'	77:C1:1153:A:N1	2.35	0.48
1:C2:63:G:O2'	1:C2:170:U:OP1	2.30	0.48
1:C2:1458:G:OP1	19:SS:138:THR:N	2.45	0.48
2:SB:61:LEU:HD21	2:SB:96:LEU:HD13	1.95	0.48
52:LR:114:LYS:NZ	77:C1:2093:A:N1	2.54	0.48
53:LS:90:MET:HE1	53:LS:114:HIS:CE1	2.48	0.48
1:C2:333:A:OP2	10:SI:31:ARG:NH2	2.47	0.47
1:C2:609:U:N3	24:SX:22:ASN:O	2.45	0.47
46:LL:166:ALA:HB3	61:La:135:GLU:OE2	2.13	0.47
52:LR:105:LEU:HD22	52:LR:135:LYS:HG3	1.95	0.47
8:SG:73:ILE:HD12	8:SG:75:LEU:HD21	1.96	0.47
15:SN:119:GLU:O	15:SN:123:HIS:ND1	2.46	0.47
50:LP:126:ARG:NH2	50:LP:140:GLU:OE2	2.46	0.47
1:C2:152:U:O2'	8:SG:15:THR:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:190:C:N4	1:C2:191:C:O2	2.47	0.47
30:Se:41:THR:HA	30:Se:45:VAL:HG22	1.96	0.47
77:C1:1268:G:N2	77:C1:1269:U:O4	2.47	0.47
23:SW:53:ILE:HD11	28:Sb:8:LEU:HD23	1.97	0.47
24:SX:41:SER:O	24:SX:41:SER:OG	2.31	0.47
45:LJ:18:VAL:HG11	77:C1:2682:C:O2'	2.15	0.47
53:LS:19:VAL:O	53:LS:19:VAL:HG13	2.14	0.47
1:C2:1474:G:OP2	7:SF:109:LYS:NZ	2.38	0.47
42:LG:112:GLU:O	42:LG:116:VAL:HG23	2.14	0.47
48:LN:136:ASP:OD1	48:LN:138:GLN:NE2	2.48	0.47
60:LZ:89:VAL:HG23	60:LZ:89:VAL:O	2.15	0.47
77:C1:2404:A:H61	81:8:8:GLU:HA	1.80	0.47
4:SC:102:VAL:HG11	4:SC:129:ILE:HG13	1.96	0.47
7:SF:43:PHE:HZ	7:SF:90:ILE:HG21	1.79	0.47
24:SX:36:THR:O	24:SX:40:SER:OG	2.21	0.47
24:SX:40:SER:O	24:SX:41:SER:OG	2.29	0.47
44:LI:205:SER:OG	44:LI:208:ASN:OD1	2.33	0.47
67:Lg:37:LYS:NZ	77:C1:1656:A:OP2	2.48	0.47
75:Lo:46:LYS:NZ	77:C1:44:U:O2	2.45	0.47
1:C2:1610:G:OP1	7:SF:72:HIS:NE2	2.42	0.47
4:SC:135:SER:O	4:SC:135:SER:OG	2.22	0.47
4:SC:146:THR:O	4:SC:148:LEU:N	2.48	0.47
5:SD:198:GLY:O	5:SD:200:LYS:NZ	2.43	0.47
6:SE:65:LEU:HD23	6:SE:70:VAL:HG11	1.97	0.47
7:SF:43:PHE:N	7:SF:46:TRP:O	2.36	0.47
11:SJ:18:PRO:O	11:SJ:23:ARG:NH2	2.48	0.47
30:Se:43:ARG:NH1	30:Se:56:MET:SD	2.87	0.47
32:Sg:126:SER:OG	32:Sg:127:ARG:N	2.47	0.47
39:LD:232:ASP:N	39:LD:235:SER:OG	2.47	0.47
62:Lb:32:LEU:HD12	77:C1:749:C:H5''	1.97	0.47
1:C2:1529:C:OP1	7:SF:112:ARG:NH2	2.46	0.47
4:SC:38:VAL:O	4:SC:38:VAL:HG13	2.15	0.47
25:SY:36:SER:O	25:SY:36:SER:OG	2.30	0.47
32:Sg:266:ASP:OD1	32:Sg:266:ASP:N	2.43	0.47
39:LD:40:HIS:CE1	39:LD:42:ALA:HB3	2.50	0.47
80:7:22:U:OP2	80:7:46:A:N6	2.48	0.47
1:C2:755:A:HO2'	1:C2:756:A:P	2.38	0.47
1:C2:819:G:C6	1:C2:853:G:N1	2.83	0.47
18:SR:109:LEU:O	18:SR:112:SER:OG	2.25	0.47
26:SZ:28:SER:OG	26:SZ:29:LYS:N	2.48	0.47
43:LH:62:ARG:NH2	77:C1:3115:C:OP1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LL:62:THR:O	46:LL:64:LYS:N	2.48	0.47
77:C1:2901:G:O2'	77:C1:3024:A:N1	2.46	0.47
1:C2:97:C:O2	1:C2:425:A:O2'	2.32	0.46
5:SD:9:ARG:HA	5:SD:12:VAL:HG22	1.97	0.46
38:LC:229:ASN:OD1	38:LC:230:VAL:N	2.47	0.46
57:LW:25:ASP:O	57:LW:26:SER:OG	2.23	0.46
62:Lb:19:ASN:ND2	77:C1:970:A:OP2	2.43	0.46
72:Ll:25:GLN:OE1	72:Ll:28:ARG:NE	2.49	0.46
77:C1:406:G:OP1	77:C1:1415:U:O2'	2.28	0.46
1:C2:629:U:N1	77:C1:846:A:C6	2.84	0.46
32:Sg:115:ILE:HD13	32:Sg:122:ILE:CG1	2.45	0.46
4:SC:53:ILE:HD13	4:SC:73:LEU:HD11	1.97	0.46
22:SV:32:VAL:HG11	22:SV:60:ARG:NH2	2.30	0.46
42:LG:241:LYS:NZ	77:C1:2586:G:O2'	2.45	0.46
49:LO:127[A]:LEU:HD11	53:LS:168:PRO:HG3	1.97	0.46
59:LY:16:ARG:NH1	77:C1:216:G:OP1	2.44	0.46
77:C1:2675:C:OP2	77:C1:2676:A:O2'	2.26	0.46
1:C2:235:G:N2	1:C2:236:A:N7	2.56	0.46
1:C2:741:C:OP2	13:SL:43:LYS:NZ	2.32	0.46
14:SM:66:VAL:HG23	14:SM:67:THR:N	2.30	0.46
18:SR:25:THR:O	18:SR:31:ASN:ND2	2.44	0.46
41:LF:94:LYS:NZ	77:C1:1156:C:OP2	2.45	0.46
56:LV:45:ARG:NE	77:C1:3043:C:OP1	2.48	0.46
1:C2:959:U:O2	28:Sb:30:SER:OG	2.33	0.46
5:SD:217:ILE:HG21	32:Sg:194:GLY:HA2	1.98	0.46
13:SL:109:VAL:HG12	13:SL:137:PHE:HB2	1.97	0.46
14:SM:131:ASP:HA	14:SM:134:SER:OG	2.15	0.46
21:SU:26:LEU:CD2	21:SU:114:VAL:HG22	2.46	0.46
61:La:77:LYS:O	61:La:79:TRP:N	2.45	0.46
1:C2:1127:G:OP1	74:Ln:11:ARG:NH1	2.49	0.46
35:C3:71:A:O2'	59:LY:52:ARG:NH2	2.49	0.46
38:LC:209:TYR:OH	77:C1:689:U:O4	2.23	0.46
42:LG:75:ILE:O	42:LG:76:ALA:HB3	2.16	0.46
46:LL:43:ALA:O	46:LL:47:ALA:HA	2.15	0.46
58:LX:25:LYS:HE2	58:LX:27:ARG:HH11	1.81	0.46
65:Le:45:ARG:O	77:C1:1145:G:O2'	2.28	0.46
19:SS:126:ARG:HB3	19:SS:133:VAL:HG12	1.97	0.46
60:LZ:5:LEU:HD11	63:Lc:35:ARG:HD2	1.98	0.46
77:C1:2208:A:O2'	77:C1:2210:G:OP2	2.30	0.46
77:C1:2500:A:HO2'	77:C1:2501:U:P	2.39	0.46
79:6:22:C:OP2	79:6:46:A:N6	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:164:ILE:HD13	2:SB:207:LEU:HD11	1.97	0.46
6:SE:87:MET:HE3	6:SE:226:PHE:HE2	1.80	0.46
36:LA:126:LEU:HD13	36:LA:150:LEU:HD22	1.98	0.46
38:LC:304:GLN:NE2	38:LC:306:THR:O	2.44	0.46
8:SG:44:GLU:OE2	8:SG:44:GLU:N	2.45	0.46
14:SM:97:LEU:HD11	14:SM:121:VAL:HG21	1.98	0.46
36:LA:36:GLU:OE1	36:LA:163:ARG:NH1	2.46	0.46
41:LF:29:GLU:OE1	41:LF:29:GLU:N	2.49	0.46
47:LM:133:LYS:NZ	77:C1:3227:A:O3'	2.47	0.46
77:C1:1240:A:H61	77:C1:1244:A:C5'	2.29	0.46
1:C2:628:G:H2'	77:C1:846:A:C2	2.51	0.45
1:C2:704:C:H42	1:C2:734:A:N6	2.14	0.45
1:C2:1216:C:HO2'	1:C2:1217:A:P	2.39	0.45
21:SU:96:PRO:O	21:SU:100:VAL:HG23	2.16	0.45
52:LR:70:LYS:NZ	52:LR:75:HIS:O	2.46	0.45
20:ST:125:SER:OG	20:ST:126:GLU:N	2.50	0.45
64:Ld:80:ASN:OD1	64:Ld:81:GLU:N	2.47	0.45
77:C1:1566:A:N1	77:C1:1571:A:N6	2.65	0.45
77:C1:3153:U:HO2'	77:C1:3154:C:C1'	2.24	0.45
1:C2:930:A:N3	2:SB:111:ARG:NH2	2.65	0.45
7:SF:31:GLU:O	7:SF:35:GLN:NE2	2.49	0.45
39:LD:218:ARG:O	39:LD:222:LEU:HD23	2.17	0.45
43:LH:1:MET:HE1	53:LS:138:GLN:CB	2.45	0.45
45:LJ:20:ASN:ND2	77:C1:2681:U:O2	2.49	0.45
8:SG:47:GLY:O	8:SG:115:LYS:NZ	2.28	0.45
9:SH:165:LYS:O	9:SH:168:SER:OG	2.29	0.45
17:SQ:39:VAL:HG23	17:SQ:41:PRO:HD2	1.98	0.45
32:Sg:89:LEU:HD21	32:Sg:110:VAL:HG11	1.98	0.45
32:Sg:133:VAL:O	32:Sg:141:LEU:N	2.50	0.45
53:LS:115:ARG:NH2	77:C1:1320:C:O2	2.50	0.45
77:C1:1562:C:O2'	77:C1:1563:C:O5'	2.14	0.45
1:C2:207:U:O2	10:SI:178:ARG:NH1	2.43	0.45
1:C2:976:G:N1	1:C2:1023:A:O2'	2.44	0.45
8:SG:21:GLU:OE1	8:SG:21:GLU:N	2.47	0.45
37:LB:57:VAL:HG22	37:LB:73:VAL:HG22	1.98	0.45
40:LE:11:PRO:CG	65:Le:91:THR:HG21	2.44	0.45
53:LS:77:VAL:HG13	53:LS:126:VAL:HG22	1.99	0.45
6:SE:87:MET:HE3	6:SE:226:PHE:CE2	2.51	0.45
11:SJ:109:LEU:O	11:SJ:113:VAL:HG23	2.17	0.45
33:Sc:19:THR:HG22	33:Sc:20:GLY:H	1.82	0.45
37:LB:66:LYS:O	37:LB:70:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LC:35:VAL:HG21	38:LC:244:LEU:HD21	1.98	0.45
1:C2:1229:G:H21	1:C2:1256:A:H62	1.65	0.45
9:SH:63:PRO:O	9:SH:64:VAL:HG12	2.17	0.45
25:SY:29:HIS:NE2	25:SY:69:SER:OG	2.46	0.45
32:Sg:302:PHE:CD1	32:Sg:312:VAL:HG12	2.47	0.45
38:LC:42:VAL:HG13	38:LC:236:LEU:HD21	1.98	0.45
44:LI:110:ARG:NH1	79:6:75:C:OP2	2.49	0.45
1:C2:1488:G:O2'	1:C2:1494:C:O2	2.26	0.45
39:LD:120:LYS:O	39:LD:248:ARG:NH2	2.47	0.45
42:LG:91:PHE:HE1	42:LG:180:VAL:HG21	1.81	0.45
77:C1:348:A:N3	77:C1:352:A:O2'	2.49	0.45
77:C1:440:A:N7	77:C1:441:U:O2'	2.43	0.45
39:LD:23:ARG:NE	77:C1:2703:A:OP2	2.46	0.45
42:LG:33:ASN:O	42:LG:39:ALA:HB3	2.16	0.45
45:LJ:40:LEU:CD2	45:LJ:125:MET:HE1	2.47	0.45
55:LU:9:GLN:N	55:LU:9:GLN:OE1	2.49	0.45
1:C2:629:U:H3'	77:C1:846:A:C4	2.52	0.45
1:C2:1303:U:O2'	1:C2:1322:A:OP2	2.34	0.45
1:C2:1371:A:O2'	1:C2:1373:C:OP1	2.34	0.45
12:SK:45:ALA:O	12:SK:49:LEU:HD23	2.17	0.45
14:SM:108:ARG:O	14:SM:110:GLY:N	2.50	0.45
22:SV:73:ALA:HB3	22:SV:79:LEU:HD12	1.99	0.45
28:Sb:61:THR:O	28:Sb:62:ILE:HG12	2.17	0.45
38:LC:82:THR:HG22	77:C1:365:A:H1'	1.99	0.45
43:LH:9:GLN:HB3	43:LH:52:LEU:HD11	1.98	0.45
48:LN:15:GLN:NE2	77:C1:294:U:OP2	2.46	0.45
70:Lj:2:GLY:N	77:C1:2138:A:O2'	2.46	0.45
73:Lm:79:GLU:O	73:Lm:81:SER:N	2.50	0.45
77:C1:1792:C:HO2'	77:C1:1794:G:H8	1.64	0.45
77:C1:2356:A:H61	77:C1:2983:C:H5	1.64	0.45
20:ST:22:LEU:HD23	20:ST:28:LEU:HD13	1.98	0.44
21:SU:70:THR:HG23	21:SU:72:ASN:O	2.16	0.44
22:SV:73:ALA:HB1	22:SV:78:LEU:CD1	2.47	0.44
41:LF:197:GLN:OE1	41:LF:197:GLN:N	2.47	0.44
46:LL:122:LYS:O	68:Lh:120:ALA:N	2.49	0.44
51:LQ:30:VAL:O	51:LQ:34:THR:HG22	2.16	0.44
77:C1:1313:G:O2'	77:C1:1318:A:N1	2.39	0.44
3:SP:21:ASP:O	3:SP:25:LEU:HD23	2.17	0.44
37:LB:205:VAL:CG2	37:LB:322:ILE:HD11	2.48	0.44
37:LB:362:ALA:O	37:LB:364:LYS:NZ	2.44	0.44
48:LN:153:ASP:OD2	48:LN:155:VAL:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:656:G:O6	1:C2:679:U:C2	2.71	0.44
2:SB:212:VAL:HG13	2:SB:213:ARG:N	2.28	0.44
21:SU:99:ILE:HD12	21:SU:102:ARG:HD3	1.99	0.44
51:LQ:40:THR:OG1	51:LQ:45:ASN:OD1	2.19	0.44
28:Sb:40:CYS:HG	28:Sb:58:SER:HG	1.58	0.44
34:C4:86:U:O2'	77:C1:1171:G:OP1	2.33	0.44
46:LL:57:VAL:HG23	46:LL:147:ILE:HG23	2.00	0.44
46:LL:164:GLU:OE1	46:LL:164:GLU:N	2.50	0.44
7:SF:89:ILE:HD11	7:SF:172:ILE:HD11	1.99	0.44
37:LB:244:ARG:NH1	77:C1:2981:U:OP2	2.50	0.44
37:LB:288:GLY:N	37:LB:320:ASP:OD1	2.45	0.44
53:LS:29:ILE:HG21	53:LS:37:ALA:HA	1.99	0.44
64:Ld:19:ARG:NH1	77:C1:3324:C:OP1	2.44	0.44
77:C1:2704:A:O2'	77:C1:2705:A:O5'	2.34	0.44
9:SH:150:GLN:CB	9:SH:181:ILE:HG22	2.48	0.44
17:SQ:14:LYS:O	17:SQ:123:ARG:NH2	2.51	0.44
27:Sa:50:VAL:HG21	78:5:37:U:O4	2.18	0.44
34:C4:85:G:O3'	41:LF:218:ARG:NH2	2.50	0.44
51:LQ:95:GLU:N	51:LQ:95:GLU:OE1	2.51	0.44
53:LS:8:GLN:HB2	53:LS:64:ILE:HD11	2.00	0.44
77:C1:3332:U:H2'	77:C1:3333:G:O4'	2.18	0.44
1:C2:1471:A:HO2'	7:SF:102:ARG:HH12	1.65	0.44
1:C2:1533:C:OP2	26:SZ:77:ARG:NH1	2.49	0.44
9:SH:133:THR:HG21	9:SH:162:ILE:HD11	1.99	0.44
25:SY:27:VAL:HG21	25:SY:40:LEU:HD21	2.00	0.44
44:LI:189:GLU:OE1	44:LI:189:GLU:N	2.45	0.44
1:C2:265:A:N7	8:SG:190:GLN:NE2	2.65	0.44
14:SM:139:HIS:O	14:SM:143:GLN:NE2	2.51	0.44
21:SU:40:ASN:OD1	21:SU:41:ILE:N	2.50	0.44
34:C4:119:U:OP2	39:LD:258:LYS:NZ	2.37	0.44
41:LF:119:VAL:HG13	41:LF:124:LEU:HD21	2.00	0.44
51:LQ:44:PHE:CD1	51:LQ:139:ILE:HD11	2.52	0.44
65:Le:33:ARG:NH2	77:C1:1407:A:O3'	2.50	0.44
77:C1:1565:G:C2	77:C1:1575:A:N1	2.85	0.44
1:C2:1273:G:H4'	1:C2:1274:C:H3'	2.00	0.44
6:SE:72:VAL:N	6:SE:75:LYS:O	2.48	0.44
14:SM:103:LEU:CD1	14:SM:116:VAL:HG12	2.47	0.44
37:LB:127:LYS:O	37:LB:129:ALA:N	2.51	0.44
38:LC:38:VAL:O	38:LC:42:VAL:HG12	2.18	0.44
38:LC:230:VAL:CG2	38:LC:254:ALA:HB1	2.48	0.44
52:LR:82:LYS:O	77:C1:1914:G:O2'	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:C1:3163:A:N6	77:C1:3288:G:O6	2.51	0.44
77:C1:3275:U:N3	77:C1:3277:U:O4'	2.49	0.44
1:C2:235:G:N2	1:C2:236:A:H62	2.15	0.43
1:C2:895:G:N2	16:SO:38:THR:HG21	2.31	0.43
37:LB:250:ALA:HB1	77:C1:2947:G:N3	2.33	0.43
38:LC:203:ARG:HH21	38:LC:240:PRO:HG2	1.83	0.43
38:LC:282:SER:N	51:LQ:125:ASP:OD2	2.49	0.43
48:LN:62:TYR:HD2	48:LN:134:LEU:HD13	1.82	0.43
54:LT:71:SER:OG	54:LT:72:VAL:N	2.51	0.43
9:SH:64:VAL:HB	9:SH:94:ALA:HB1	1.99	0.43
37:LB:226:PHE:O	77:C1:1886:A:O2'	2.35	0.43
39:LD:187:THR:O	39:LD:189:GLU:N	2.49	0.43
45:LJ:114:ILE:HG22	45:LJ:114:ILE:O	2.18	0.43
77:C1:1562:C:HO2'	77:C1:1563:C:P	2.35	0.43
77:C1:2323:G:O2'	77:C1:2325:G:OP2	2.28	0.43
80:7:10:G:C6	80:7:45:G:N2	2.84	0.43
1:C2:182:A:H61	1:C2:203:U:H3	1.66	0.43
1:C2:623:A:H3'	1:C2:624:G:H5''	2.00	0.43
7:SF:147:THR:HG21	33:Sc:25:VAL:HG21	2.00	0.43
24:SX:131:SER:O	24:SX:134:ALA:N	2.52	0.43
26:SZ:42:LEU:H	26:SZ:42:LEU:HD23	1.84	0.43
32:Sg:41:THR:HG22	32:Sg:62:LYS:HG2	2.00	0.43
38:LC:150:LEU:HD21	38:LC:172:VAL:HG12	2.00	0.43
44:LI:116:ARG:HH22	77:C1:2622:C:H42	1.66	0.43
55:LU:54:VAL:HG12	55:LU:67:SER:HB2	2.00	0.43
77:C1:2711:C:O2'	77:C1:2744:U:OP1	2.34	0.43
82:SA:177:LEU:O	82:SA:181:VAL:HG23	2.19	0.43
10:SI:10:LYS:O	10:SI:18:ARG:NH2	2.49	0.43
37:LB:205:VAL:HG21	37:LB:322:ILE:HD11	2.00	0.43
46:LL:35:ARG:NE	77:C1:685:G:OP1	2.50	0.43
61:La:39:HIS:O	61:La:41:HIS:N	2.51	0.43
1:C2:127:G:O6	8:SG:202:ARG:NH2	2.52	0.43
1:C2:821:U:C4	1:C2:852:C:N3	2.85	0.43
43:LH:13:PRO:HD2	43:LH:16:VAL:HG21	2.01	0.43
45:LJ:38:GLU:OE1	45:LJ:39:GLN:NE2	2.51	0.43
47:LM:19:ARG:HB3	47:LM:35:ILE:HD12	2.00	0.43
1:C2:1229:G:N1	14:SM:47:GLU:OE1	2.52	0.43
1:C2:1472:C:OP1	7:SF:102:ARG:NH1	2.45	0.43
6:SE:185:GLY:H	6:SE:189:LEU:HD13	1.83	0.43
23:SW:41:MET:SD	23:SW:129:VAL:HG21	2.58	0.43
32:Sg:167:VAL:HG22	32:Sg:183:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LB:86:VAL:HG13	37:LB:160:VAL:CG1	2.48	0.43
44:LI:211:ARG:NH1	44:LI:212:GLU:OE1	2.52	0.43
45:LJ:82:ARG:HB3	45:LJ:112:LEU:HD13	2.00	0.43
50:LP:127:ARG:NH1	77:C1:1506:A:OP2	2.49	0.43
66:Lf:90:PRO:O	66:Lf:91:ALA:HB3	2.18	0.43
77:C1:1815:U:O2'	77:C1:1816:A:OP2	2.29	0.43
1:C2:284:G:O6	8:SG:188:ARG:NH1	2.50	0.43
6:SE:139:VAL:HG13	6:SE:150:PRO:HG3	2.01	0.43
27:Sa:24:VAL:HG11	27:Sa:71:LEU:HD12	2.00	0.43
32:Sg:219:GLU:OE2	32:Sg:219:GLU:N	2.51	0.43
69:Li:77:LEU:HD23	77:C1:294:U:H4'	2.01	0.43
16:SO:102:LEU:CD2	27:Sa:45:VAL:HG12	2.46	0.43
42:LG:77:GLN:OE1	42:LG:179:ILE:HD11	2.19	0.43
43:LH:43:VAL:HG12	43:LH:57:VAL:CG2	2.49	0.43
46:LL:76:THR:O	46:LL:78:ALA:N	2.52	0.43
46:LL:145:PHE:CE2	68:Lh:118:ILE:HD11	2.54	0.43
53:LS:68:HIS:O	53:LS:73:LYS:NZ	2.52	0.43
9:SH:133:THR:O	9:SH:134:GLU:HG2	2.19	0.43
10:SI:105:ASP:O	10:SI:106:ALA:HB3	2.19	0.43
12:SK:38:LYS:O	12:SK:42:VAL:HG23	2.19	0.43
17:SQ:39:VAL:HG23	17:SQ:41:PRO:CD	2.49	0.43
39:LD:177:GLU:OE1	39:LD:177:GLU:N	2.49	0.43
64:Ld:29:ALA:HB3	64:Ld:30:PRO:HD3	2.01	0.43
67:Lg:91:ARG:HG2	67:Lg:95:ILE:HD12	2.00	0.43
77:C1:1116:G:N2	77:C1:2817:A:O4'	2.52	0.43
77:C1:1134:G:O2'	77:C1:2642:A:N3	2.36	0.43
1:C2:630:A:OP2	77:C1:846:A:H5'	2.19	0.43
1:C2:656:G:O6	1:C2:679:U:O2	2.37	0.43
1:C2:1786:G:OP2	16:SO:133:ARG:NH2	2.40	0.43
8:SG:57:ASP:OD2	8:SG:58:LYS:N	2.51	0.43
19:SS:14:ILE:HD12	45:LJ:116:TYR:CE2	2.54	0.43
25:SY:88:THR:O	25:SY:92:VAL:HG23	2.19	0.43
38:LC:11:LEU:HD21	38:LC:156:LEU:HB2	2.01	0.43
42:LG:82:LEU:HG	42:LG:86:THR:HG23	2.01	0.43
1:C2:77:U:O2'	1:C2:78:A:OP2	2.30	0.42
68:Lh:104:GLN:NE2	77:C1:112:U:OP1	2.48	0.42
82:SA:139:VAL:CG1	82:SA:141:ILE:HD12	2.49	0.42
1:C2:1681:A:H2	1:C2:1720:G:H21	1.67	0.42
9:SH:14:THR:HG22	9:SH:17:GLU:CD	2.45	0.42
52:LR:130:ASN:O	52:LR:131:ALA:HB3	2.19	0.42
1:C2:629:U:H6	77:C1:846:A:C2	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SM:31:VAL:HA	14:SM:34:THR:HG22	2.01	0.42
41:LF:144:ILE:HD12	41:LF:189:ILE:HD12	2.01	0.42
50:LP:33:ALA:HB1	50:LP:117:ILE:HG12	2.00	0.42
32:Sg:83:ALA:HA	32:Sg:89:LEU:HD23	2.00	0.42
37:LB:186:GLY:C	37:LB:187:SER:HG	2.26	0.42
39:LD:140:ARG:O	77:C1:1079:A:H4'	2.18	0.42
40:LE:108:LYS:NZ	77:C1:617:G:OP1	2.52	0.42
41:LF:107:ARG:NH2	41:LF:199:ASN:O	2.45	0.42
59:LY:82:VAL:HG12	59:LY:83:ASP:O	2.19	0.42
6:SE:200:ARG:NE	6:SE:202:ASP:OD1	2.51	0.42
19:SS:85:PHE:HE2	20:ST:36:ILE:HG23	1.85	0.42
40:LE:142:ASP:OD1	40:LE:143:LYS:N	2.53	0.42
42:LG:94:PHE:HB3	42:LG:189:LEU:HD11	2.01	0.42
77:C1:209:A:O2'	77:C1:211:A:OP2	2.34	0.42
1:C2:1274:C:O2'	1:C2:1275:A:OP2	2.27	0.42
23:SW:6:VAL:HG23	23:SW:29:PRO:HD2	2.02	0.42
25:SY:35:VAL:O	25:SY:35:VAL:HG12	2.20	0.42
32:Sg:147:HIS:CD2	32:Sg:151:VAL:HG22	2.55	0.42
52:LR:6:THR:O	52:LR:10:LEU:HD13	2.20	0.42
25:SY:7:ILE:CD1	25:SY:40:LEU:HD23	2.49	0.42
49:LO:126[A]:VAL:O	53:LS:154:HIS:NE2	2.45	0.42
63:Lc:13:LYS:HB3	63:Lc:100:ILE:HG23	2.01	0.42
71:Lk:32:ASN:OD1	71:Lk:33:LYS:N	2.52	0.42
1:C2:852:C:OP1	52:LR:176:ARG:NH2	2.52	0.42
4:SC:178:ILE:HD11	4:SC:193:VAL:O	2.20	0.42
40:LE:26:ARG:NH1	77:C1:607:A:OP1	2.51	0.42
48:LN:147:ARG:NE	77:C1:113:C:OP1	2.53	0.42
48:LN:44:ARG:NH2	77:C1:269:G:OP2	2.53	0.42
70:Lj:45:ARG:NH2	77:C1:362:U:OP1	2.53	0.42
77:C1:28:C:O2'	77:C1:61:A:N3	2.49	0.42
4:SC:165:VAL:HG11	4:SC:210:THR:HA	2.02	0.42
15:SN:56:ASP:OD1	15:SN:57:ALA:N	2.53	0.42
16:SO:126:THR:OG1	16:SO:127:ARG:N	2.52	0.42
19:SS:85:PHE:CE2	20:ST:36:ILE:HG23	2.55	0.42
36:LA:243:THR:HG21	77:C1:2244:A:O4'	2.20	0.42
39:LD:232:ASP:O	39:LD:235:SER:OG	2.35	0.42
77:C1:1925:U:O2'	77:C1:1927:G:N7	2.47	0.42
8:SG:67:VAL:O	8:SG:68:LEU:HG	2.20	0.41
10:SI:11:ARG:NH1	10:SI:15:GLY:O	2.52	0.41
38:LC:14:GLU:HG2	38:LC:15:ALA:H	1.84	0.41
44:LI:39:LYS:NZ	77:C1:1010:G:OP1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:LJ:53:THR:HG22	45:LJ:60:ARG:HA	2.01	0.41
46:LL:165:SER:O	46:LL:167:PHE:N	2.51	0.41
58:LX:39:LYS:NZ	77:C1:14:U:OP1	2.48	0.41
67:Lg:14:ASN:ND2	77:C1:828:A:OP1	2.46	0.41
70:Lj:58:THR:OG1	70:Lj:59:THR:N	2.50	0.41
72:Ll:37:TYR:O	77:C1:351:A:N6	2.53	0.41
1:C2:1254:U:OP2	14:SM:46:ARG:NH1	2.48	0.41
1:C2:1478:G:OP1	20:ST:39:THR:OG1	2.38	0.41
5:SD:32:GLU:OE1	5:SD:32:GLU:N	2.53	0.41
38:LC:14:GLU:HG2	38:LC:15:ALA:N	2.35	0.41
45:LJ:52:TYR:OH	77:C1:2679:A:O2'	2.36	0.41
77:C1:2810:C:OP2	77:C1:2955:U:O2'	2.37	0.41
78:5:40:A:O2'	78:5:41:U:O5'	2.36	0.41
1:C2:140:A:H61	1:C2:281:G:C5'	2.33	0.41
1:C2:1060:U:H3'	1:C2:1061:A:H5''	2.01	0.41
1:C2:1241:G:OP1	3:SP:77:ARG:NH2	2.53	0.41
4:SC:148:LEU:HD21	11:SJ:95:TYR:CZ	2.55	0.41
14:SM:84:ASN:OD1	14:SM:85:LYS:N	2.53	0.41
45:LJ:155:THR:OG1	45:LJ:158:ASP:OD1	2.38	0.41
76:Lp:17:ARG:NH1	77:C1:860:G:OP1	2.47	0.41
77:C1:187:A:N3	77:C1:208:C:O2'	2.49	0.41
1:C2:1615:C:P	7:SF:81:ARG:HE	2.44	0.41
2:SB:88:VAL:CG2	2:SB:96:LEU:HD12	2.50	0.41
4:SC:102:VAL:HG11	4:SC:129:ILE:CG1	2.49	0.41
13:SL:30:ARG:NH1	13:SL:50:GLU:OE1	2.53	0.41
38:LC:141:ARG:NH1	77:C1:1386:A:O4'	2.52	0.41
45:LJ:51:ARG:NH2	77:C1:2681:U:OP2	2.49	0.41
51:LQ:2:GLY:N	77:C1:1159:A:OP1	2.52	0.41
76:Lp:8:VAL:O	76:Lp:11:THR:OG1	2.32	0.41
1:C2:647:G:H22	1:C2:687:G:H1	1.68	0.41
1:C2:962:C:H2'	1:C2:963:A:O4'	2.20	0.41
32:Sg:51:ASP:O	32:Sg:53:LYS:N	2.54	0.41
35:C3:25:G:N7	59:LY:13:ARG:NH1	2.61	0.41
63:Lc:25:LEU:HD23	63:Lc:90:VAL:HG23	2.02	0.41
77:C1:1264:G:N2	77:C1:1265:U:O4	2.53	0.41
77:C1:2375:G:O2'	77:C1:2377:G:OP2	2.34	0.41
7:SF:121:ILE:O	7:SF:121:ILE:HG22	2.21	0.41
21:SU:27:THR:O	21:SU:27:THR:HG23	2.20	0.41
40:LE:60:ASP:OD1	40:LE:62:THR:OG1	2.36	0.41
1:C2:154:G:O6	25:SY:128:LYS:NZ	2.51	0.41
1:C2:904:G:O4'	78:5:42:G:O2'	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SI:26:LYS:O	10:SI:29:LEU:HD22	2.21	0.41
14:SM:52:LEU:O	14:SM:54:ARG:N	2.50	0.41
42:LG:41:GLN:OE1	42:LG:44:ARG:NH1	2.50	0.41
53:LS:93:GLU:OE2	53:LS:137:ARG:N	2.54	0.41
56:LV:96:GLU:OE2	57:LW:24:GLY:N	2.54	0.41
62:Lb:21:ILE:HG22	62:Lb:21:ILE:O	2.20	0.41
1:C2:1608:U:OP1	17:SQ:15:SER:OG	2.28	0.41
36:LA:96:LEU:HD12	36:LA:166:ILE:HD13	2.03	0.41
37:LB:45:SER:OG	37:LB:46:PHE:N	2.53	0.41
38:LC:138:ARG:NH2	77:C1:1383:G:O2'	2.53	0.41
49:LO:15[A]:LEU:HD11	49:LO:129[A]:LEU:CD1	2.51	0.41
50:LP:108:ASP:OD2	50:LP:110:THR:HG22	2.21	0.41
74:Ln:17:ARG:HA	74:Ln:20:VAL:HG12	2.01	0.41
77:C1:498:A:O2'	77:C1:3273:A:N1	2.50	0.41
77:C1:1724:U:H1'	77:C1:1725:C:C6	2.56	0.41
1:C2:434:G:N1	1:C2:437:A:OP2	2.48	0.41
1:C2:711:U:O2'	1:C2:712:G:OP2	2.35	0.41
1:C2:955:A:OP1	15:SN:3:ARG:NE	2.51	0.41
1:C2:1206:U:OP2	1:C2:1207:C:O2'	2.29	0.41
11:SJ:63:ASP:OD1	11:SJ:64:GLU:N	2.53	0.41
27:Sa:80:HIS:NE2	78:5:42:G:OP1	2.54	0.41
31:Sf:100:LEU:CD1	31:Sf:103:LEU:HD11	2.44	0.41
32:Sg:37:SER:OG	32:Sg:38:ARG:N	2.53	0.41
32:Sg:86:ASP:OD2	32:Sg:88:THR:OG1	2.39	0.41
32:Sg:109:ASP:OD2	32:Sg:127:ARG:NH1	2.54	0.41
32:Sg:144:LEU:HD11	32:Sg:186:PHE:HB3	2.02	0.41
38:LC:23:PRO:O	38:LC:24:ALA:HB3	2.21	0.41
44:LI:103:LEU:O	44:LI:112:GLN:NE2	2.53	0.41
48:LN:148:TYR:O	48:LN:151:ILE:HG22	2.21	0.41
49:LO:67[A]:THR:O	49:LO:67[A]:THR:HG22	2.21	0.41
60:LZ:83:THR:HG22	67:Lg:93:PHE:CZ	2.56	0.41
77:C1:2695:A:O2'	77:C1:2696:A:O5'	2.31	0.41
15:SN:11:ILE:HG13	15:SN:11:ILE:O	2.21	0.41
19:SS:45:LEU:HD22	19:SS:85:PHE:CE2	2.55	0.41
28:Sb:56:CYS:SG	28:Sb:58:SER:OG	2.57	0.41
42:LG:106:LYS:O	42:LG:110:THR:HG23	2.20	0.41
43:LH:1:MET:HE2	43:LH:3:TYR:CE1	2.55	0.41
1:C2:347:G:N2	10:SI:14:THR:O	2.48	0.40
2:SB:154:SER:O	2:SB:154:SER:OG	2.38	0.40
20:ST:49:ASP:OD1	20:ST:51:GLU:N	2.54	0.40
45:LJ:112:LEU:O	45:LJ:114:ILE:N	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:LR:44:LEU:HB2	52:LR:50:ILE:HD12	2.03	0.40
56:LV:29:SER:O	56:LV:66:LYS:NZ	2.54	0.40
77:C1:959:C:O2	77:C1:2614:G:O2'	2.38	0.40
77:C1:1452:A:N3	77:C1:2346:C:O2'	2.52	0.40
7:SF:117:THR:HG22	7:SF:121:ILE:HD12	2.03	0.40
13:SL:2:SER:O	13:SL:3:THR:OG1	2.23	0.40
14:SM:27:ALA:O	14:SM:31:VAL:HG13	2.22	0.40
14:SM:62:LEU:HD12	14:SM:75:VAL:HG11	2.03	0.40
28:Sb:36:LYS:HG3	28:Sb:43:ILE:HG22	2.03	0.40
33:Sc:19:THR:HG22	33:Sc:20:GLY:N	2.36	0.40
60:LZ:89:VAL:HG12	60:LZ:92:PHE:CZ	2.55	0.40
62:Lb:33:LYS:NZ	77:C1:2722:U:OP1	2.53	0.40
67:Lg:81:CYS:O	67:Lg:85:VAL:HG23	2.21	0.40
5:SD:32:GLU:OE2	5:SD:65:ARG:NH2	2.48	0.40
12:SK:50:THR:CG2	12:SK:55:VAL:HG13	2.51	0.40
32:Sg:157:VAL:HG22	32:Sg:168:THR:O	2.21	0.40
38:LC:6:VAL:N	38:LC:20:LEU:O	2.54	0.40
41:LF:168:ILE:HD12	41:LF:168:ILE:H	1.85	0.40
42:LG:162:LEU:HA	48:LN:7:LEU:HD11	2.04	0.40
77:C1:1203:A:N3	77:C1:2855:U:O2'	2.39	0.40
1:C2:329:G:H5'	10:SI:99:ALA:HB3	2.04	0.40
1:C2:1615:C:HO2'	1:C2:1616:G:P	2.38	0.40
5:SD:209:ILE:O	18:SR:20:TYR:OH	2.23	0.40
6:SE:42:LEU:HD23	6:SE:101:LEU:HD21	2.02	0.40
17:SQ:99:GLU:OE2	17:SQ:103:ASN:ND2	2.52	0.40
21:SU:60:THR:HG23	21:SU:60:THR:O	2.22	0.40
32:Sg:266:ASP:CG	32:Sg:267:PRO:HD3	2.47	0.40
35:C3:66:A:OP1	68:Lh:10:ARG:NH2	2.55	0.40
38:LC:326:ARG:NE	77:C1:596:C:O2	2.54	0.40
46:LL:90:ALA:HB1	46:LL:95:ILE:HB	2.04	0.40
49:LO:8[A]:VAL:HG22	49:LO:34[A]:VAL:CG1	2.51	0.40
77:C1:1168:U:O4	77:C1:1329:U:O2'	2.36	0.40
77:C1:1208:U:O2'	77:C1:3115:C:N4	2.54	0.40
6:SE:92:LEU:HD23	25:SY:17:LEU:HD11	2.04	0.40
20:ST:29:GLU:O	20:ST:30:VAL:HG13	2.21	0.40
39:LD:125:VAL:HG11	39:LD:199:ILE:HD13	2.02	0.40
52:LR:52:LYS:O	52:LR:53:LYS:HB2	2.22	0.40
58:LX:133:LEU:HD12	58:LX:142:ILE:HD11	2.04	0.40
77:C1:1565:G:N3	77:C1:1575:A:N1	2.69	0.40
82:SA:121:VAL:CG1	82:SA:143:VAL:HG22	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SB	222/232 (96%)	192 (86%)	27 (12%)	3 (1%)	9	19
3	SP	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
4	SC	214/216 (99%)	197 (92%)	16 (8%)	1 (0%)	24	46
5	SD	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
6	SE	256/258 (99%)	235 (92%)	20 (8%)	1 (0%)	30	51
7	SF	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
8	SG	226/228 (99%)	209 (92%)	14 (6%)	3 (1%)	9	21
9	SH	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	24	46
10	SI	183/198 (92%)	166 (91%)	14 (8%)	3 (2%)	7	16
11	SJ	182/184 (99%)	162 (89%)	18 (10%)	2 (1%)	11	25
12	SK	90/92 (98%)	75 (83%)	15 (17%)	0	100	100
13	SL	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
14	SM	119/121 (98%)	80 (67%)	32 (27%)	7 (6%)	1	1
15	SN	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	9	19
16	SO	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
17	SQ	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	19
18	SR	117/125 (94%)	109 (93%)	6 (5%)	2 (2%)	7	15
19	SS	143/145 (99%)	126 (88%)	13 (9%)	4 (3%)	4	6
20	ST	141/143 (99%)	127 (90%)	14 (10%)	0	100	100
21	SU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
22	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	10	23
23	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
24	SX	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	18	38
25	SY	132/134 (98%)	123 (93%)	8 (6%)	1 (1%)	16	34
26	SZ	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	9	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Sa	95/97 (98%)	77 (81%)	14 (15%)	4 (4%)	2	3
28	Sb	79/81 (98%)	70 (89%)	8 (10%)	1 (1%)	9	21
29	Sd	51/53 (96%)	51 (100%)	0	0	100	100
30	Se	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
31	Sf	71/73 (97%)	45 (63%)	25 (35%)	1 (1%)	9	19
32	Sg	310/312 (99%)	279 (90%)	31 (10%)	0	100	100
33	Sc	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
36	LA	249/251 (99%)	234 (94%)	14 (6%)	1 (0%)	30	51
37	LB	384/386 (100%)	357 (93%)	26 (7%)	1 (0%)	36	58
38	LC	359/361 (99%)	326 (91%)	31 (9%)	2 (1%)	21	42
39	LD	292/294 (99%)	273 (94%)	18 (6%)	1 (0%)	36	58
40	LE	163/175 (93%)	156 (96%)	7 (4%)	0	100	100
41	LF	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
42	LG	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
43	LH	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
44	LI	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
45	LJ	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
46	LL	191/193 (99%)	171 (90%)	18 (9%)	2 (1%)	12	28
47	LM	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
48	LN	201/203 (99%)	188 (94%)	12 (6%)	1 (0%)	24	46
49	LO	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	12	28
50	LP	181/183 (99%)	168 (93%)	13 (7%)	0	100	100
51	LQ	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
52	LR	186/188 (99%)	180 (97%)	4 (2%)	2 (1%)	11	25
53	LS	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
54	LT	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
55	LU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
56	LV	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
57	LW	124/126 (98%)	113 (91%)	11 (9%)	0	100	100
58	LX	119/121 (98%)	114 (96%)	4 (3%)	1 (1%)	16	34
59	LY	123/125 (98%)	119 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
61	La	146/148 (99%)	127 (87%)	17 (12%)	2 (1%)	9	19
62	Lb	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	14
63	Lc	94/96 (98%)	94 (100%)	0	0	100	100
64	Ld	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
65	Le	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
66	Lf	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
67	Lg	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
68	Lh	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
69	Li	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
70	Lj	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
71	Lk	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
72	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
73	Lm	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
74	Ln	23/25 (92%)	23 (100%)	0	0	100	100
75	Lo	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
76	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
81	8	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
82	SA	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	12	28
All	All	10988/11175 (98%)	10103 (92%)	826 (8%)	59 (0%)	26	46

All (59) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	SE	43	PRO
8	SG	68	LEU
10	SI	10	LYS
27	Sa	84	VAL
49	LO	111[A]	PRO
61	La	78	LEU
11	SJ	99	LEU
11	SJ	100	LYS
14	SM	90	LYS
14	SM	130	THR
14	SM	131	ASP

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Mol	Chain	Res	Type
15	SN	28	LEU
18	SR	24	LEU
19	SS	91	ASP
27	Sa	62	TYR
36	LA	126	LEU
37	LB	128	LYS
46	LL	63	VAL
58	LX	44	PRO
2	SB	213	ARG
8	SG	173	PRO
14	SM	109	GLU
19	SS	6	GLN
22	SV	81	ASN
25	SY	37	LYS
31	Sf	107	LYS
38	LC	292	SER
39	LD	20	PHE
46	LL	77	LEU
48	LN	95	GLN
49	LO	110[A]	PRO
61	La	40	HIS
2	SB	82	ARG
2	SB	212	VAL
4	SC	147	ASN
9	SH	134	GLU
10	SI	9	HIS
10	SI	23	LYS
14	SM	126	TRP
27	Sa	9	GLY
38	LC	4	PRO
52	LR	53	LYS
62	Lb	24	PRO
82	SA	196	SER
14	SM	85	LYS
18	SR	23	LYS
19	SS	7	GLU
24	SX	42	PRO
27	Sa	85	ARG
52	LR	52	LYS
82	SA	157	ASP
15	SN	27	LYS
26	SZ	68	ARG

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Mol	Chain	Res	Type
8	SG	67	VAL
17	SQ	33	GLY
17	SQ	41	PRO
19	SS	92	ILE
28	Sb	62	ILE
14	SM	89	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	
2	SB	200/205 (98%)	200 (100%)	0	100	100
3	SP	95/98 (97%)	95 (100%)	0	100	100
4	SC	175/175 (100%)	175 (100%)	0	100	100
5	SD	182/182 (100%)	182 (100%)	0	100	100
6	SE	220/220 (100%)	220 (100%)	0	100	100
7	SF	172/173 (99%)	171 (99%)	1 (1%)	78	91
8	SG	189/195 (97%)	189 (100%)	0	100	100
9	SH	163/165 (99%)	163 (100%)	0	100	100
10	SI	148/159 (93%)	148 (100%)	0	100	100
11	SJ	156/157 (99%)	156 (100%)	0	100	100
12	SK	77/85 (91%)	77 (100%)	0	100	100
13	SL	129/129 (100%)	129 (100%)	0	100	100
14	SM	88/98 (90%)	88 (100%)	0	100	100
15	SN	127/127 (100%)	127 (100%)	0	100	100
16	SO	91/96 (95%)	91 (100%)	0	100	100
17	SQ	117/117 (100%)	117 (100%)	0	100	100
18	SR	101/113 (89%)	101 (100%)	0	100	100
19	SS	128/128 (100%)	128 (100%)	0	100	100
20	ST	115/115 (100%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	SU	93/93 (100%)	93 (100%)	0	100	100
22	SV	71/74 (96%)	71 (100%)	0	100	100
23	SW	110/110 (100%)	110 (100%)	0	100	100
24	SX	119/119 (100%)	119 (100%)	0	100	100
25	SY	112/112 (100%)	112 (100%)	0	100	100
26	SZ	67/73 (92%)	67 (100%)	0	100	100
27	Sa	83/83 (100%)	83 (100%)	0	100	100
28	Sb	70/70 (100%)	70 (100%)	0	100	100
29	Sd	47/47 (100%)	47 (100%)	0	100	100
30	Se	50/51 (98%)	50 (100%)	0	100	100
31	Sf	56/63 (89%)	56 (100%)	0	100	100
32	Sg	250/257 (97%)	250 (100%)	0	100	100
33	Sc	55/56 (98%)	55 (100%)	0	100	100
36	LA	190/193 (98%)	190 (100%)	0	100	100
37	LB	319/322 (99%)	319 (100%)	0	100	100
38	LC	288/288 (100%)	287 (100%)	1 (0%)	86	94
39	LD	241/243 (99%)	241 (100%)	0	100	100
40	LE	138/153 (90%)	138 (100%)	0	100	100
41	LF	186/186 (100%)	186 (100%)	0	100	100
42	LG	187/191 (98%)	186 (100%)	1 (0%)	81	92
43	LH	168/171 (98%)	168 (100%)	0	100	100
44	LI	185/185 (100%)	185 (100%)	0	100	100
45	LJ	146/147 (99%)	146 (100%)	0	100	100
46	LL	154/154 (100%)	154 (100%)	0	100	100
47	LM	107/107 (100%)	107 (100%)	0	100	100
48	LN	175/175 (100%)	175 (100%)	0	100	100
49	LO	160/160 (100%)	160 (100%)	0	100	100
50	LP	138/145 (95%)	138 (100%)	0	100	100
51	LQ	150/150 (100%)	150 (100%)	0	100	100
52	LR	152/153 (99%)	152 (100%)	0	100	100
53	LS	155/155 (100%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	LT	136/136 (100%)	136 (100%)	0	100	100
55	LU	87/87 (100%)	87 (100%)	0	100	100
56	LV	104/104 (100%)	104 (100%)	0	100	100
57	LW	56/107 (52%)	56 (100%)	0	100	100
58	LX	104/105 (99%)	104 (100%)	0	100	100
59	LY	108/108 (100%)	108 (100%)	0	100	100
60	LZ	115/115 (100%)	115 (100%)	0	100	100
61	La	118/118 (100%)	118 (100%)	0	100	100
62	Lb	46/46 (100%)	46 (100%)	0	100	100
63	Lc	81/81 (100%)	81 (100%)	0	100	100
64	Ld	92/96 (96%)	92 (100%)	0	100	100
65	Le	108/109 (99%)	108 (100%)	0	100	100
66	Lf	90/90 (100%)	90 (100%)	0	100	100
67	Lg	95/95 (100%)	95 (100%)	0	100	100
68	Lh	104/104 (100%)	103 (99%)	1 (1%)	68	86
69	Li	80/81 (99%)	80 (100%)	0	100	100
70	Lj	69/69 (100%)	69 (100%)	0	100	100
71	Lk	68/68 (100%)	68 (100%)	0	100	100
72	Ll	45/45 (100%)	45 (100%)	0	100	100
73	Lm	47/47 (100%)	47 (100%)	0	100	100
74	Ln	22/23 (96%)	22 (100%)	0	100	100
75	Lo	87/88 (99%)	87 (100%)	0	100	100
76	Lp	71/71 (100%)	71 (100%)	0	100	100
81	8	5/6 (83%)	5 (100%)	0	100	100
82	SA	170/173 (98%)	170 (100%)	0	100	100
All	All	9203/9395 (98%)	9199 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	SF	156	ARG
38	LC	203	ARG
42	LG	158	ASP

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Mol	Chain	Res	Type
68	Lh	81	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (76) such sidechains are listed below:

Mol	Chain	Res	Type
3	SP	70	ASN
4	SC	59	HIS
7	SF	35	GLN
7	SF	44	ASN
7	SF	63	GLN
7	SF	103	ASN
8	SG	197	ASN
12	SK	12	HIS
12	SK	58	GLN
15	SN	5	HIS
16	SO	65	GLN
19	SS	127	HIS
20	ST	127	ASN
22	SV	81	ASN
23	SW	12	ASN
23	SW	56	HIS
24	SX	18	HIS
24	SX	27	ASN
24	SX	89	ASN
24	SX	99	ASN
25	SY	107	GLN
26	SZ	38	HIS
29	Sd	48	ASN
30	Se	17	GLN
31	Sf	123	ASN
32	Sg	16	HIS
32	Sg	148	ASN
32	Sg	182	ASN
33	Sc	27	GLN
33	Sc	43	ASN
36	LA	205	ASN
36	LA	211	HIS
37	LB	224	HIS
37	LB	231	HIS
38	LC	5	GLN
38	LC	18	ASN
39	LD	264	GLN

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Mol	Chain	Res	Type
39	LD	274	GLN
41	LF	172	ASN
41	LF	194	HIS
42	LG	192	GLN
42	LG	252	ASN
43	LH	125	ASN
44	LI	73	ASN
46	LL	102	GLN
46	LL	120	GLN
50	LP	54	HIS
50	LP	55	GLN
50	LP	116	HIS
51	LQ	9	GLN
51	LQ	126	GLN
52	LR	7	GLN
52	LR	92	GLN
52	LR	150	GLN
52	LR	166	ASN
53	LS	49	HIS
53	LS	65	ASN
53	LS	68	HIS
54	LT	5	HIS
54	LT	127	GLN
54	LT	134	GLN
55	LU	9	GLN
55	LU	101	ASN
56	LV	98	ASN
57	LW	42	GLN
60	LZ	122	HIS
61	La	39	HIS
64	Ld	21	HIS
66	Lf	75	HIS
66	Lf	106	ASN
67	Lg	108	GLN
70	Lj	12	HIS
71	Lk	10	GLN
72	Ll	32	ASN
75	Lo	82	GLN
82	SA	69	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1768/1798 (98%)	463 (26%)	50 (2%)
34	C4	120/121 (99%)	11 (9%)	1 (0%)
35	C3	157/158 (99%)	30 (19%)	1 (0%)
77	C1	3180/3184 (99%)	564 (17%)	38 (1%)
78	5	28/30 (93%)	12 (42%)	2 (7%)
79	6	73/76 (96%)	13 (17%)	0
80	7	74/75 (98%)	17 (22%)	0
All	All	5400/5442 (99%)	1110 (20%)	92 (1%)

All (1110) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	17	C
1	C2	25	C
1	C2	26	A
1	C2	34	G
1	C2	45	U
1	C2	47	A
1	C2	51	A
1	C2	54	C
1	C2	56	U
1	C2	57	G
1	C2	62	A
1	C2	65	A
1	C2	66	U
1	C2	67	A
1	C2	68	A
1	C2	69	G
1	C2	71	A
1	C2	73	U
1	C2	74	U
1	C2	75	U
1	C2	76	A
1	C2	78	A
1	C2	79	C
1	C2	81	G
1	C2	93	A
1	C2	104	A
1	C2	114	C
1	C2	121	U
1	C2	126	A

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Mol	Chain	Res	Type
1	C2	127	G
1	C2	129	U
1	C2	130	C
1	C2	131	C
1	C2	132	U
1	C2	133	U
1	C2	134	U
1	C2	135	A
1	C2	136	C
1	C2	138	A
1	C2	140	A
1	C2	141	U
1	C2	142	G
1	C2	153	G
1	C2	155	U
1	C2	159	U
1	C2	168	A
1	C2	171	A
1	C2	172	C
1	C2	174	U
1	C2	176	C
1	C2	178	U
1	C2	179	A
1	C2	180	A
1	C2	185	U
1	C2	186	C
1	C2	187	G
1	C2	188	A
1	C2	191	C
1	C2	192	U
1	C2	193	U
1	C2	195	G
1	C2	216	U
1	C2	217	A
1	C2	218	A
1	C2	223	U
1	C2	224	C
1	C2	225	A
1	C2	227	U
1	C2	228	G
1	C2	230	C
1	C2	232	U

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Mol	Chain	Res	Type
1	C2	233	C
1	C2	234	G
1	C2	237	C
1	C2	238	U
1	C2	240	U
1	C2	241	U
1	C2	250	C
1	C2	257	A
1	C2	260	U
1	C2	262	U
1	C2	265	A
1	C2	272	U
1	C2	274	G
1	C2	278	U
1	C2	279	G
1	C2	280	U
1	C2	281	G
1	C2	287	G
1	C2	299	A
1	C2	314	C
1	C2	316	A
1	C2	320	U
1	C2	322	G
1	C2	323	A
1	C2	337	G
1	C2	338	C
1	C2	352	A
1	C2	353	A
1	C2	359	A
1	C2	361	C
1	C2	373	G
1	C2	388	G
1	C2	390	G
1	C2	400	A
1	C2	401	A
1	C2	402	C
1	C2	404	G
1	C2	405	C
1	C2	416	A
1	C2	417	A
1	C2	419	G
1	C2	423	G

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Mol	Chain	Res	Type
1	C2	424	C
1	C2	425	A
1	C2	426	G
1	C2	428	A
1	C2	434	G
1	C2	439	U
1	C2	444	C
1	C2	448	C
1	C2	460	A
1	C2	464	A
1	C2	468	A
1	C2	471	A
1	C2	477	A
1	C2	483	A
1	C2	485	A
1	C2	487	G
1	C2	489	C
1	C2	491	C
1	C2	492	A
1	C2	493	U
1	C2	494	U
1	C2	495	C
1	C2	496	G
1	C2	498	G
1	C2	499	U
1	C2	500	C
1	C2	505	A
1	C2	506	A
1	C2	507	U
1	C2	510	G
1	C2	511	A
1	C2	514	G
1	C2	525	A
1	C2	527	A
1	C2	534	A
1	C2	536	C
1	C2	538	A
1	C2	539	G
1	C2	540	G
1	C2	541	A
1	C2	542	A
1	C2	543	C

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Mol	Chain	Res	Type
1	C2	548	G
1	C2	549	G
1	C2	551	G
1	C2	556	A
1	C2	557	G
1	C2	558	U
1	C2	559	C
1	C2	565	C
1	C2	572	C
1	C2	579	A
1	C2	582	U
1	C2	594	A
1	C2	595	G
1	C2	606	A
1	C2	610	G
1	C2	611	U
1	C2	619	A
1	C2	620	A
1	C2	622	A
1	C2	623	A
1	C2	624	G
1	C2	630	A
1	C2	639	U
1	C2	640	U
1	C2	641	G
1	C2	643	G
1	C2	645	C
1	C2	650	U
1	C2	651	G
1	C2	653	C
1	C2	655	G
1	C2	656	G
1	C2	657	U
1	C2	677	G
1	C2	680	U
1	C2	681	U
1	C2	683	C
1	C2	684	A
1	C2	687	G
1	C2	694	U
1	C2	696	C
1	C2	698	U

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Mol	Chain	Res	Type
1	C2	699	U
1	C2	700	C
1	C2	702	G
1	C2	704	C
1	C2	705	U
1	C2	706	A
1	C2	707	A
1	C2	708	C
1	C2	709	C
1	C2	710	U
1	C2	711	U
1	C2	712	G
1	C2	713	A
1	C2	714	G
1	C2	728	U
1	C2	729	G
1	C2	730	G
1	C2	731	C
1	C2	732	G
1	C2	733	A
1	C2	736	C
1	C2	738	G
1	C2	740	A
1	C2	741	C
1	C2	742	U
1	C2	743	U
1	C2	744	U
1	C2	745	U
1	C2	753	A
1	C2	756	A
1	C2	765	G
1	C2	766	U
1	C2	767	U
1	C2	774	A
1	C2	775	G
1	C2	778	G
1	C2	779	U
1	C2	780	A
1	C2	781	U
1	C2	782	U
1	C2	783	G
1	C2	787	G

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Mol	Chain	Res	Type
1	C2	812	A
1	C2	813	U
1	C2	814	A
1	C2	815	G
1	C2	818	C
1	C2	819	G
1	C2	820	U
1	C2	821	U
1	C2	823	G
1	C2	832	U
1	C2	833	U
1	C2	837	G
1	C2	838	G
1	C2	840	U
1	C2	841	U
1	C2	846	G
1	C2	852	C
1	C2	855	A
1	C2	856	A
1	C2	857	U
1	C2	863	A
1	C2	876	G
1	C2	886	U
1	C2	898	A
1	C2	899	G
1	C2	901	G
1	C2	902	G
1	C2	913	G
1	C2	915	A
1	C2	928	U
1	C2	929	A
1	C2	933	A
1	C2	934	C
1	C2	935	U
1	C2	942	G
1	C2	951	A
1	C2	960	U
1	C2	966	A
1	C2	970	A
1	C2	984	G
1	C2	988	A
1	C2	992	A

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Mol	Chain	Res	Type
1	C2	993	A
1	C2	1004	U
1	C2	1005	A
1	C2	1012	U
1	C2	1024	U
1	C2	1026	A
1	C2	1028	C
1	C2	1031	U
1	C2	1032	G
1	C2	1039	A
1	C2	1053	G
1	C2	1058	U
1	C2	1059	U
1	C2	1060	U
1	C2	1061	A
1	C2	1063	U
1	C2	1074	G
1	C2	1076	A
1	C2	1082	C
1	C2	1092	A
1	C2	1096	C
1	C2	1100	G
1	C2	1113	A
1	C2	1138	A
1	C2	1150	G
1	C2	1158	C
1	C2	1160	A
1	C2	1164	G
1	C2	1167	G
1	C2	1170	G
1	C2	1185	U
1	C2	1191	U
1	C2	1194	A
1	C2	1196	A
1	C2	1199	G
1	C2	1200	G
1	C2	1208	A
1	C2	1212	G
1	C2	1217	A
1	C2	1218	G
1	C2	1227	A
1	C2	1229	G

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Mol	Chain	Res	Type
1	C2	1241	G
1	C2	1242	A
1	C2	1243	G
1	C2	1244	A
1	C2	1245	G
1	C2	1246	C
1	C2	1251	U
1	C2	1252	C
1	C2	1256	A
1	C2	1257	U
1	C2	1258	U
1	C2	1274	C
1	C2	1275	A
1	C2	1285	U
1	C2	1286	U
1	C2	1291	G
1	C2	1301	U
1	C2	1308	G
1	C2	1314	U
1	C2	1315	U
1	C2	1316	G
1	C2	1318	G
1	C2	1321	A
1	C2	1322	A
1	C2	1325	A
1	C2	1337	A
1	C2	1344	A
1	C2	1345	A
1	C2	1346	A
1	C2	1348	A
1	C2	1349	G
1	C2	1360	A
1	C2	1361	U
1	C2	1363	U
1	C2	1364	G
1	C2	1367	G
1	C2	1370	U
1	C2	1371	A
1	C2	1373	C
1	C2	1381	U
1	C2	1382	A
1	C2	1383	G

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Mol	Chain	Res	Type
1	C2	1390	U
1	C2	1398	U
1	C2	1399	C
1	C2	1400	A
1	C2	1402	G
1	C2	1410	A
1	C2	1414	U
1	C2	1425	A
1	C2	1427	A
1	C2	1431	C
1	C2	1432	U
1	C2	1433	G
1	C2	1444	A
1	C2	1446	A
1	C2	1459	C
1	C2	1469	A
1	C2	1471	A
1	C2	1472	C
1	C2	1479	A
1	C2	1490	C
1	C2	1491	U
1	C2	1492	A
1	C2	1493	A
1	C2	1496	U
1	C2	1506	G
1	C2	1514	U
1	C2	1516	A
1	C2	1517	U
1	C2	1518	C
1	C2	1520	U
1	C2	1521	G
1	C2	1522	U
1	C2	1523	G
1	C2	1524	A
1	C2	1528	U
1	C2	1530	C
1	C2	1531	G
1	C2	1535	U
1	C2	1537	C
1	C2	1540	G
1	C2	1543	A
1	C2	1554	U

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Mol	Chain	Res	Type
1	C2	1557	U
1	C2	1558	U
1	C2	1559	A
1	C2	1570	A
1	C2	1573	A
1	C2	1574	G
1	C2	1575	G
1	C2	1576	A
1	C2	1583	A
1	C2	1584	G
1	C2	1590	G
1	C2	1601	G
1	C2	1602	C
1	C2	1607	G
1	C2	1611	A
1	C2	1616	G
1	C2	1622	G
1	C2	1631	A
1	C2	1634	C
1	C2	1635	A
1	C2	1636	C
1	C2	1637	C
1	C2	1657	U
1	C2	1658	G
1	C2	1682	U
1	C2	1688	U
1	C2	1689	A
1	C2	1696	G
1	C2	1697	G
1	C2	1698	G
1	C2	1699	G
1	C2	1700	C
1	C2	1701	A
1	C2	1702	A
1	C2	1707	A
1	C2	1708	U
1	C2	1715	G
1	C2	1716	C
1	C2	1717	G
1	C2	1757	G
1	C2	1760	G
1	C2	1766	A

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Mol	Chain	Res	Type
1	C2	1767	G
1	C2	1769	U
1	C2	1770	U
1	C2	1780	G
1	C2	1782	A
1	C2	1783	C
1	C2	1791	A
1	C2	1792	G
1	C2	1793	G
1	C2	1794	A
1	C2	1796	C
1	C2	1799	U
34	C4	7	G
34	C4	11	A
34	C4	53	U
34	C4	54	U
34	C4	65	G
34	C4	73	C
34	C4	76	A
34	C4	91	G
34	C4	102	A
34	C4	112	G
34	C4	121	U
35	C3	25	G
35	C3	34	U
35	C3	35	C
35	C3	51	G
35	C3	53	A
35	C3	59	A
35	C3	62	C
35	C3	63	G
35	C3	80	A
35	C3	81	U
35	C3	82	U
35	C3	83	C
35	C3	84	C
35	C3	85	G
35	C3	86	U
35	C3	90	U
35	C3	95	G
35	C3	97	A
35	C3	102	U

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Mol	Chain	Res	Type
35	C3	104	A
35	C3	106	C
35	C3	111	A
35	C3	113	U
35	C3	116	G
35	C3	125	U
35	C3	126	A
35	C3	138	A
35	C3	148	G
35	C3	151	C
35	C3	158	U
77	C1	13	A
77	C1	14	U
77	C1	18	G
77	C1	22	G
77	C1	26	A
77	C1	40	A
77	C1	43	A
77	C1	49	A
77	C1	59	G
77	C1	60	A
77	C1	65	A
77	C1	66	A
77	C1	67	A
77	C1	73	C
77	C1	75	G
77	C1	85	A
77	C1	92	G
77	C1	105	C
77	C1	109	A
77	C1	110	G
77	C1	111	C
77	C1	121	A
77	C1	122	A
77	C1	133	U
77	C1	135	C
77	C1	136	G
77	C1	148	G
77	C1	156	G
77	C1	157	A
77	C1	165	A
77	C1	166	C

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Mol	Chain	Res	Type
77	C1	172	G
77	C1	173	G
77	C1	187	A
77	C1	190	U
77	C1	191	U
77	C1	200	C
77	C1	210	U
77	C1	218	G
77	C1	219	A
77	C1	234	G
77	C1	237	G
77	C1	240	U
77	C1	241	G
77	C1	243	G
77	C1	245	U
77	C1	249	U
77	C1	251	G
77	C1	252	U
77	C1	269	G
77	C1	283	G
77	C1	286	U
77	C1	295	A
77	C1	305	U
77	C1	311	C
77	C1	323	A
77	C1	329	U
77	C1	339	C
77	C1	346	C
77	C1	350	C
77	C1	351	A
77	C1	374	A
77	C1	376	G
77	C1	395	A
77	C1	398	A
77	C1	399	A
77	C1	401	U
77	C1	402	A
77	C1	403	C
77	C1	421	G
77	C1	422	A
77	C1	439	C
77	C1	440	A

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Mol	Chain	Res	Type
77	C1	441	U
77	C1	442	G
77	C1	443	G
77	C1	445	G
77	C1	446	U
77	C1	447	U
77	C1	448	U
77	C1	450	G
77	C1	451	U
77	C1	487	U
77	C1	488	U
77	C1	489	U
77	C1	490	C
77	C1	491	A
77	C1	494	G
77	C1	507	U
77	C1	520	U
77	C1	521	A
77	C1	523	A
77	C1	535	G
77	C1	544	C
77	C1	546	C
77	C1	547	G
77	C1	548	G
77	C1	552	G
77	C1	555	U
77	C1	557	A
77	C1	559	A
77	C1	569	A
77	C1	578	A
77	C1	579	G
77	C1	600	G
77	C1	604	G
77	C1	609	G
77	C1	611	A
77	C1	620	U
77	C1	621	A
77	C1	622	A
77	C1	637	C
77	C1	638	C
77	C1	649	A
77	C1	660	A

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Mol	Chain	Res	Type
77	C1	667	C
77	C1	677	A
77	C1	681	U
77	C1	684	G
77	C1	691	A
77	C1	705	A
77	C1	712	G
77	C1	715	A
77	C1	716	A
77	C1	719	U
77	C1	720	A
77	C1	758	C
77	C1	763	G
77	C1	764	U
77	C1	767	U
77	C1	776	U
77	C1	777	U
77	C1	780	A
77	C1	781	G
77	C1	785	G
77	C1	786	A
77	C1	806	A
77	C1	817	A
77	C1	826	G
77	C1	830	A
77	C1	846	A
77	C1	847	A
77	C1	848	A
77	C1	849	C
77	C1	851	C
77	C1	861	C
77	C1	865	U
77	C1	874	U
77	C1	879	U
77	C1	896	A
77	C1	907	G
77	C1	908	G
77	C1	914	A
77	C1	916	G
77	C1	917	A
77	C1	923	C
77	C1	925	A

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Mol	Chain	Res	Type
77	C1	937	G
77	C1	944	C
77	C1	953	G
77	C1	959	C
77	C1	960	U
77	C1	974	G
77	C1	980	A
77	C1	981	U
77	C1	982	C
77	C1	991	G
77	C1	994	G
77	C1	1001	G
77	C1	1002	A
77	C1	1010	G
77	C1	1017	C
77	C1	1018	G
77	C1	1020	G
77	C1	1024	G
77	C1	1036	A
77	C1	1037	C
77	C1	1047	A
77	C1	1049	C
77	C1	1064	A
77	C1	1065	A
77	C1	1072	G
77	C1	1081	U
77	C1	1087	G
77	C1	1093	A
77	C1	1094	U
77	C1	1095	U
77	C1	1097	G
77	C1	1098	A
77	C1	1102	A
77	C1	1103	A
77	C1	1104	G
77	C1	1117	G
77	C1	1131	G
77	C1	1135	A
77	C1	1153	A
77	C1	1159	A
77	C1	1178	G
77	C1	1180	A

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Mol	Chain	Res	Type
77	C1	1181	U
77	C1	1192	C
77	C1	1193	A
77	C1	1196	C
77	C1	1201	C
77	C1	1206	G
77	C1	1208	U
77	C1	1217	A
77	C1	1222	G
77	C1	1225	A
77	C1	1227	C
77	C1	1230	G
77	C1	1232	C
77	C1	1233	G
77	C1	1235	U
77	C1	1236	G
77	C1	1238	C
77	C1	1239	C
77	C1	1240	A
77	C1	1242	G
77	C1	1243	G
77	C1	1245	A
77	C1	1246	G
77	C1	1251	A
77	C1	1253	U
77	C1	1254	C
77	C1	1258	U
77	C1	1262	G
77	C1	1263	A
77	C1	1264	G
77	C1	1265	U
77	C1	1266	G
77	C1	1270	A
77	C1	1271	A
77	C1	1272	C
77	C1	1274	A
77	C1	1278	A
77	C1	1279	C
77	C1	1285	G
77	C1	1287	A
77	C1	1295	G
77	C1	1304	A

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Mol	Chain	Res	Type
77	C1	1307	G
77	C1	1308	A
77	C1	1309	U
77	C1	1313	G
77	C1	1330	A
77	C1	1348	U
77	C1	1349	G
77	C1	1351	U
77	C1	1352	A
77	C1	1353	U
77	C1	1354	G
77	C1	1356	U
77	C1	1357	G
77	C1	1386	A
77	C1	1399	A
77	C1	1400	G
77	C1	1419	A
77	C1	1421	G
77	C1	1434	G
77	C1	1437	C
77	C1	1443	G
77	C1	1446	A
77	C1	1450	G
77	C1	1481	A
77	C1	1482	A
77	C1	1483	G
77	C1	1487	G
77	C1	1488	G
77	C1	1508	C
77	C1	1528	G
77	C1	1533	U
77	C1	1536	G
77	C1	1542	G
77	C1	1555	U
77	C1	1556	C
77	C1	1557	A
77	C1	1560	G
77	C1	1562	C
77	C1	1563	C
77	C1	1565	G
77	C1	1566	A
77	C1	1568	U

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Mol	Chain	Res	Type
77	C1	1569	U
77	C1	1572	U
77	C1	1574	C
77	C1	1575	A
77	C1	1576	G
77	C1	1580	A
77	C1	1581	C
77	C1	1582	C
77	C1	1583	A
77	C1	1588	A
77	C1	1589	A
77	C1	1605	A
77	C1	1607	U
77	C1	1620	U
77	C1	1629	U
77	C1	1639	C
77	C1	1642	A
77	C1	1643	A
77	C1	1645	U
77	C1	1651	U
77	C1	1658	G
77	C1	1717	U
77	C1	1724	U
77	C1	1725	C
77	C1	1741	A
77	C1	1750	A
77	C1	1751	G
77	C1	1760	A
77	C1	1765	U
77	C1	1766	G
77	C1	1770	G
77	C1	1775	G
77	C1	1780	G
77	C1	1794	G
77	C1	1797	A
77	C1	1814	A
77	C1	1816	A
77	C1	1817	G
77	C1	1819	U
77	C1	1820	U
77	C1	1821	U
77	C1	1835	A

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Mol	Chain	Res	Type
77	C1	1839	A
77	C1	1840	U
77	C1	1841	A
77	C1	1842	A
77	C1	1846	C
77	C1	1849	C
77	C1	1850	A
77	C1	1866	C
77	C1	1867	A
77	C1	1880	U
77	C1	1886	A
77	C1	1893	A
77	C1	1906	G
77	C1	1920	U
77	C1	1952	G
77	C1	1953	G
77	C1	1954	G
77	C1	2094	C
77	C1	2101	C
77	C1	2102	U
77	C1	2111	G
77	C1	2112	U
77	C1	2113	A
77	C1	2121	G
77	C1	2122	G
77	C1	2131	A
77	C1	2158	A
77	C1	2169	G
77	C1	2170	U
77	C1	2171	G
77	C1	2188	A
77	C1	2205	U
77	C1	2206	G
77	C1	2207	A
77	C1	2209	U
77	C1	2210	G
77	C1	2223	A
77	C1	2249	G
77	C1	2250	G
77	C1	2255	A
77	C1	2256	A
77	C1	2257	C

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Mol	Chain	Res	Type
77	C1	2272	G
77	C1	2273	G
77	C1	2281	A
77	C1	2282	U
77	C1	2288	G
77	C1	2307	G
77	C1	2310	U
77	C1	2313	A
77	C1	2314	U
77	C1	2315	G
77	C1	2327	U
77	C1	2334	U
77	C1	2336	U
77	C1	2372	A
77	C1	2373	A
77	C1	2374	C
77	C1	2375	G
77	C1	2385	G
77	C1	2388	U
77	C1	2393	G
77	C1	2397	A
77	C1	2402	A
77	C1	2403	G
77	C1	2404	A
77	C1	2411	U
77	C1	2418	G
77	C1	2419	A
77	C1	2437	G
77	C1	2439	A
77	C1	2445	A
77	C1	2446	U
77	C1	2447	A
77	C1	2452	G
77	C1	2496	C
77	C1	2498	U
77	C1	2499	U
77	C1	2501	U
77	C1	2502	A
77	C1	2506	U
77	C1	2507	C
77	C1	2514	U
77	C1	2515	A

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Mol	Chain	Res	Type
77	C1	2522	G
77	C1	2524	A
77	C1	2531	C
77	C1	2533	G
77	C1	2537	U
77	C1	2538	U
77	C1	2539	C
77	C1	2540	A
77	C1	2541	U
77	C1	2542	U
77	C1	2543	U
77	C1	2544	U
77	C1	2547	A
77	C1	2548	C
77	C1	2549	G
77	C1	2552	C
77	C1	2554	A
77	C1	2561	A
77	C1	2569	A
77	C1	2570	U
77	C1	2571	U
77	C1	2572	C
77	C1	2573	G
77	C1	2585	G
77	C1	2593	A
77	C1	2594	C
77	C1	2606	G
77	C1	2607	G
77	C1	2614	G
77	C1	2626	A
77	C1	2648	G
77	C1	2652	U
77	C1	2656	A
77	C1	2674	A
77	C1	2677	G
77	C1	2689	A
77	C1	2691	A
77	C1	2692	A
77	C1	2694	A
77	C1	2696	A
77	C1	2704	A
77	C1	2714	G

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Mol	Chain	Res	Type
77	C1	2719	U
77	C1	2728	G
77	C1	2752	U
77	C1	2753	G
77	C1	2762	A
77	C1	2777	G
77	C1	2778	G
77	C1	2796	G
77	C1	2800	G
77	C1	2801	A
77	C1	2803	A
77	C1	2810	C
77	C1	2814	G
77	C1	2817	A
77	C1	2818	U
77	C1	2821	C
77	C1	2842	U
77	C1	2845	A
77	C1	2847	A
77	C1	2849	C
77	C1	2860	U
77	C1	2867	C
77	C1	2871	G
77	C1	2872	A
77	C1	2875	U
77	C1	2876	C
77	C1	2887	A
77	C1	2894	C
77	C1	2898	G
77	C1	2899	C
77	C1	2914	G
77	C1	2923	U
77	C1	2928	C
77	C1	2935	U
77	C1	2936	A
77	C1	2938	G
77	C1	2941	A
77	C1	2942	C
77	C1	2947	G
77	C1	2971	A
77	C1	2983	C
77	C1	2990	G

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Mol	Chain	Res	Type
77	C1	2996	U
77	C1	2997	G
77	C1	3012	A
77	C1	3056	U
77	C1	3058	U
77	C1	3078	U
77	C1	3080	G
77	C1	3086	A
77	C1	3092	C
77	C1	3101	G
77	C1	3130	A
77	C1	3131	U
77	C1	3142	A
77	C1	3143	C
77	C1	3151	U
77	C1	3154	C
77	C1	3155	U
77	C1	3156	U
77	C1	3157	U
77	C1	3165	A
77	C1	3170	A
77	C1	3173	G
77	C1	3174	A
77	C1	3175	U
77	C1	3176	G
77	C1	3179	U
77	C1	3181	C
77	C1	3187	A
77	C1	3196	U
77	C1	3199	G
77	C1	3207	U
77	C1	3217	C
77	C1	3218	A
77	C1	3219	G
77	C1	3229	G
77	C1	3243	A
77	C1	3245	A
77	C1	3247	G
77	C1	3259	U
77	C1	3263	G
77	C1	3270	U
77	C1	3276	G

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Mol	Chain	Res	Type
77	C1	3281	U
77	C1	3287	U
77	C1	3289	G
77	C1	3294	A
77	C1	3295	A
77	C1	3304	U
77	C1	3307	A
77	C1	3313	U
77	C1	3316	A
77	C1	3317	U
77	C1	3318	G
77	C1	3319	U
77	C1	3320	A
77	C1	3341	U
77	C1	3345	G
77	C1	3351	U
77	C1	3352	U
77	C1	3353	G
77	C1	3354	U
77	C1	3355	U
77	C1	3356	G
77	C1	3357	U
77	C1	3363	U
77	C1	3369	G
77	C1	3375	A
77	C1	3378	C
77	C1	3386	G
77	C1	3389	U
77	C1	3390	G
78	5	35	C
78	5	36	C
78	5	37	U
78	5	38	G
78	5	39	G
78	5	40	A
78	5	42	G
78	5	46	C
78	5	49	C
78	5	53	G
78	5	55	C
78	5	56	C
79	6	16	U

Continued on next page...

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Mol	Chain	Res	Type
79	6	17	G
79	6	19	U
79	6	21	A
79	6	23	G
79	6	41	A
79	6	42	G
79	6	47	U
79	6	48	U
79	6	58	A
79	6	59	G
79	6	73	G
79	6	76	A
80	7	16	C
80	7	17	G
80	7	18	G
80	7	19	C
80	7	20	U
80	7	28	C
80	7	29	A
80	7	31	G
80	7	32	C
80	7	33	U
80	7	37	A
80	7	43	G
80	7	44	A
80	7	55	C
80	7	59	U
80	7	72	G
80	7	75	A

All (92) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C2	68	A
1	C2	77	U
1	C2	80	A
1	C2	139	C
1	C2	141	U
1	C2	224	C
1	C2	237	C
1	C2	261	U
1	C2	278	U

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Mol	Chain	Res	Type
1	C2	280	U
1	C2	313	U
1	C2	322	G
1	C2	352	A
1	C2	387	A
1	C2	400	A
1	C2	424	C
1	C2	539	G
1	C2	541	A
1	C2	555	A
1	C2	609	U
1	C2	629	U
1	C2	639	U
1	C2	640	U
1	C2	705	U
1	C2	711	U
1	C2	755	A
1	C2	765	G
1	C2	813	U
1	C2	819	G
1	C2	912	U
1	C2	928	U
1	C2	1226	A
1	C2	1245	G
1	C2	1251	U
1	C2	1256	A
1	C2	1273	G
1	C2	1274	C
1	C2	1344	A
1	C2	1382	A
1	C2	1399	C
1	C2	1430	U
1	C2	1471	A
1	C2	1556	A
1	C2	1558	U
1	C2	1573	A
1	C2	1601	G
1	C2	1615	C
1	C2	1633	A
1	C2	1636	C
1	C2	1791	A
34	C4	52	G

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Mol	Chain	Res	Type
35	C3	85	G
77	C1	13	A
77	C1	65	A
77	C1	239	G
77	C1	282	G
77	C1	439	C
77	C1	637	C
77	C1	715	A
77	C1	763	G
77	C1	848	A
77	C1	916	G
77	C1	1064	A
77	C1	1097	G
77	C1	1273	A
77	C1	1307	G
77	C1	1352	A
77	C1	1355	A
77	C1	1554	U
77	C1	1562	C
77	C1	1582	C
77	C1	1716	U
77	C1	1815	U
77	C1	1820	U
77	C1	2101	C
77	C1	2112	U
77	C1	2249	G
77	C1	2495	C
77	C1	2500	A
77	C1	2501	U
77	C1	2537	U
77	C1	2541	U
77	C1	2547	A
77	C1	3218	A
77	C1	3228	C
77	C1	3269	U
77	C1	3275	U
77	C1	3319	U
77	C1	3350	C
77	C1	3351	U
78	5	34	U
78	5	41	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 298 ligands modelled in this entry, 298 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	C1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C1	1955:U	O3'	2093:A	P	25.82
1	C1	2452:G	O3'	2492:C	P	17.25
1	C1	451:U	O3'	486:A	P	9.70

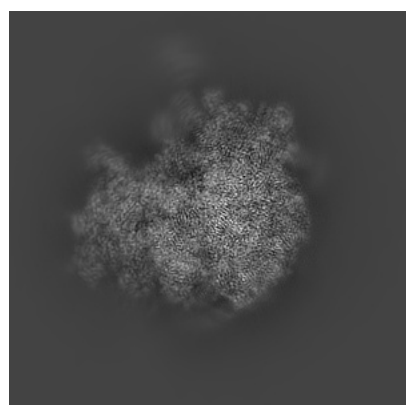
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10377. These allow visual inspection of the internal detail of the map and identification of artifacts.

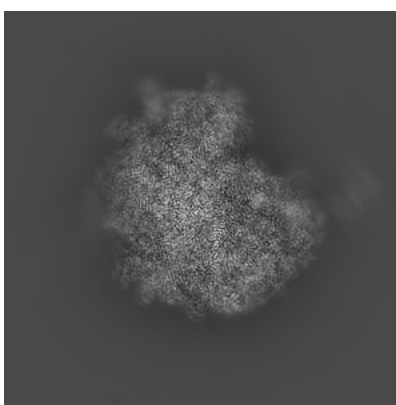
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

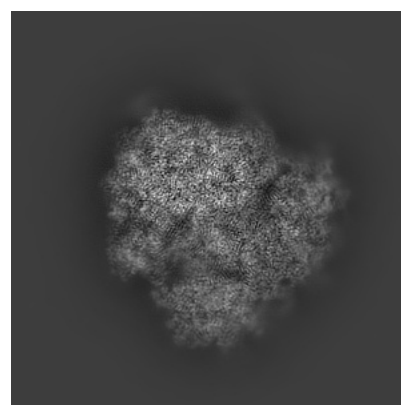
6.1.1 Primary map



X



Y

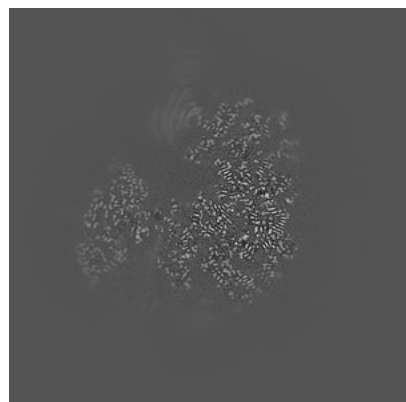


Z

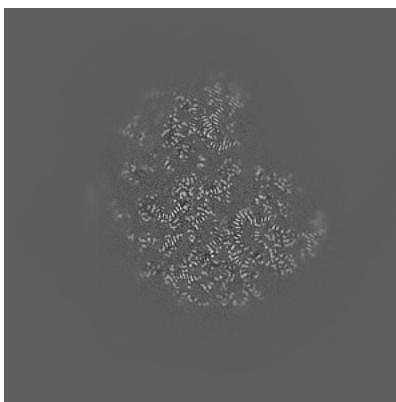
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

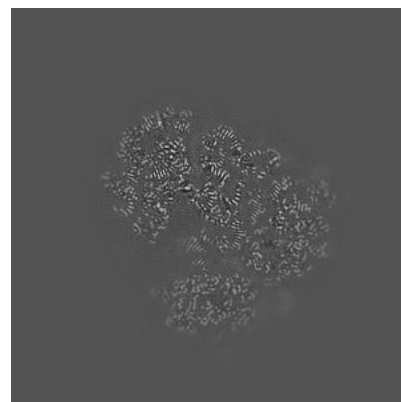
6.2.1 Primary map



X Index: 200



Y Index: 200

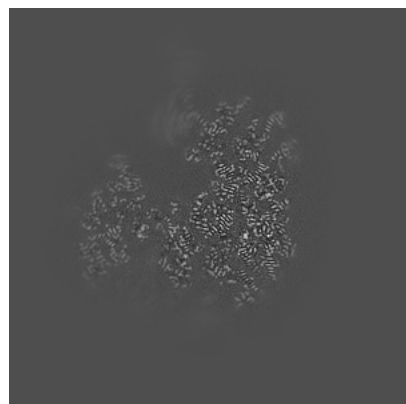


Z Index: 200

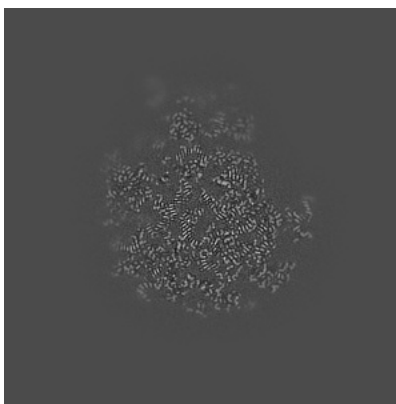
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

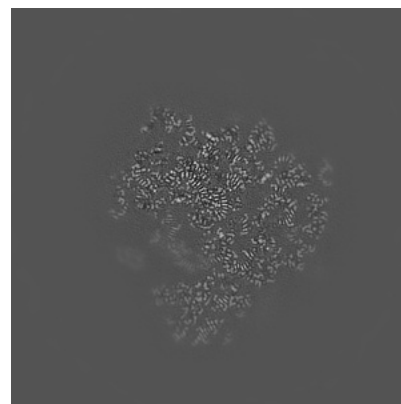
6.3.1 Primary map



X Index: 203



Y Index: 232

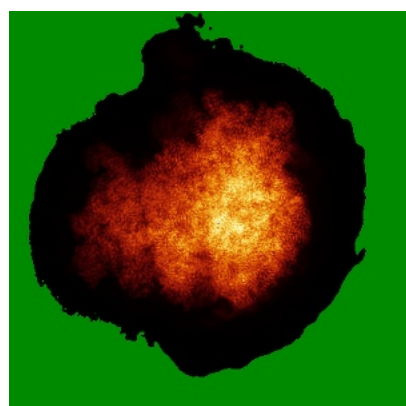


Z Index: 181

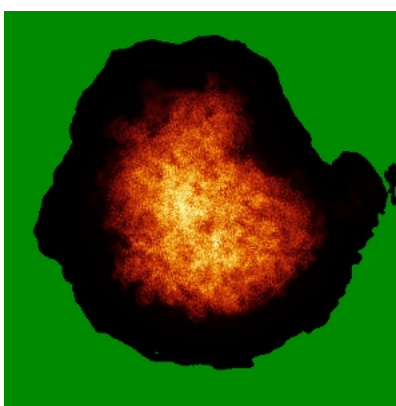
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

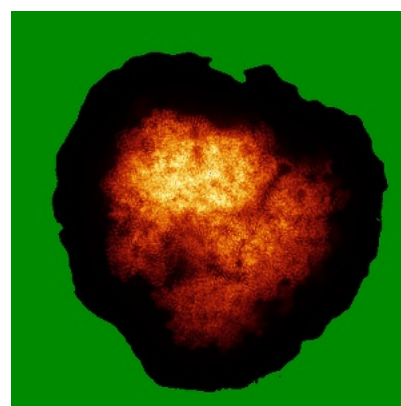
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

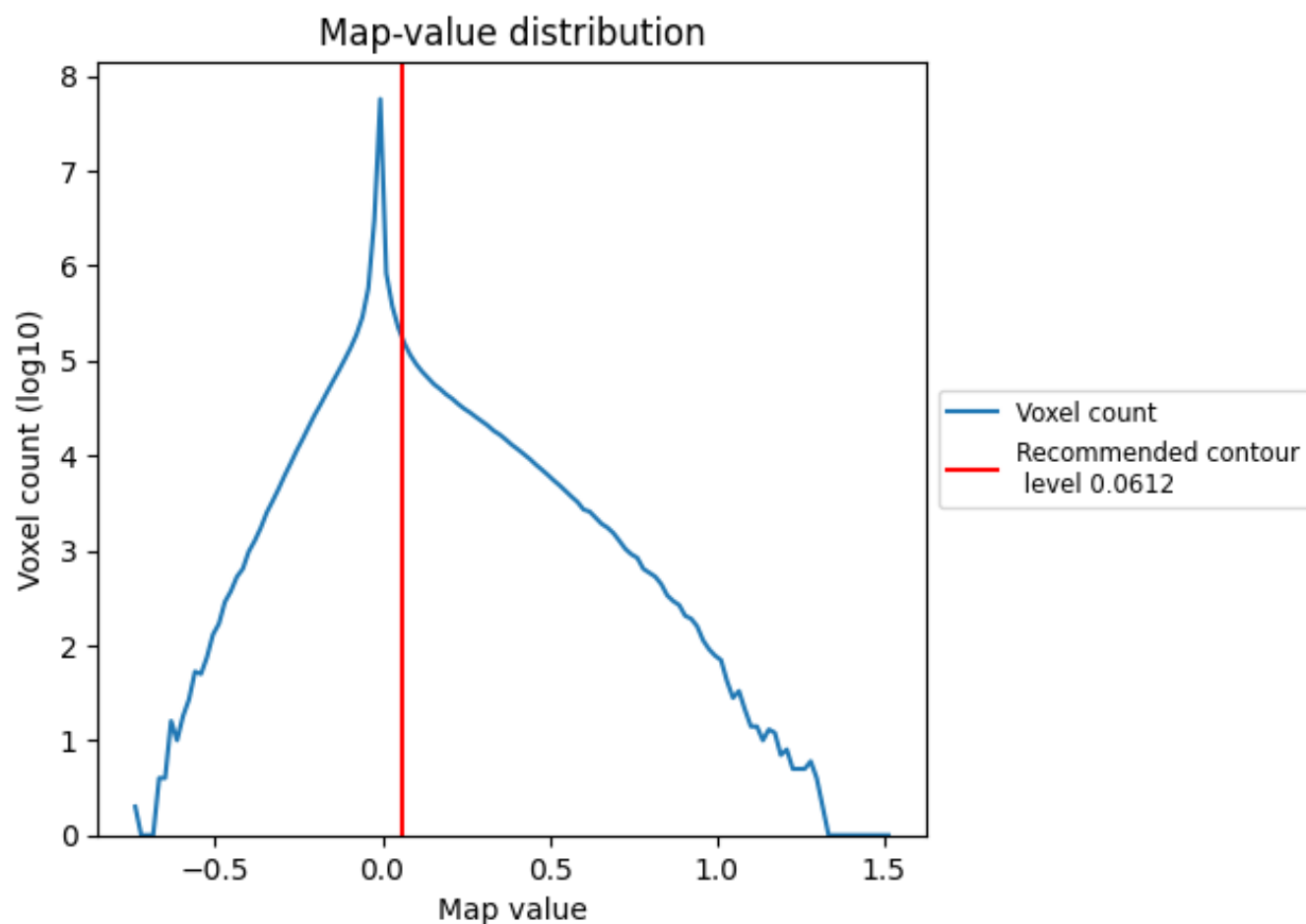
6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

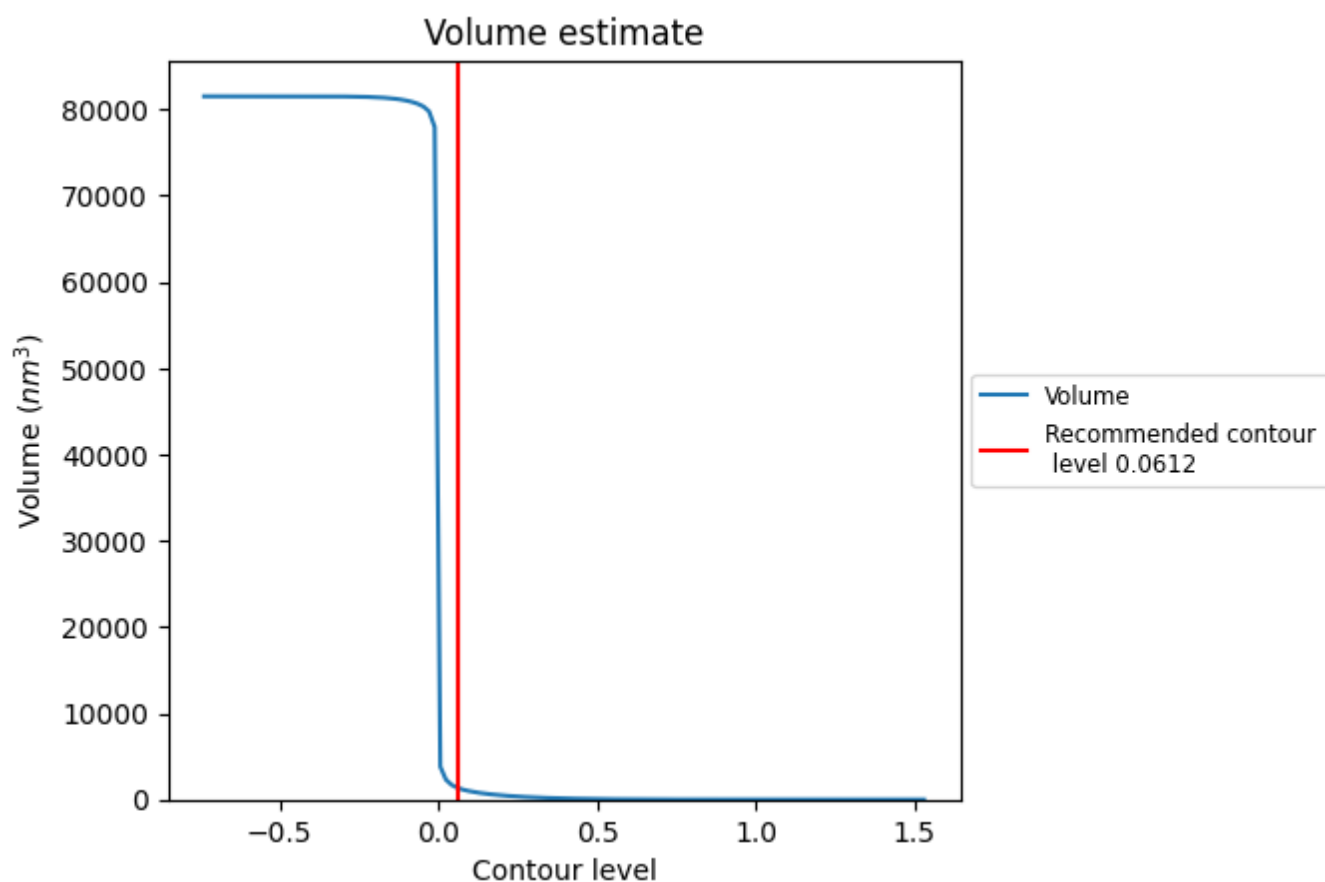
This section contains the results of statistical analysis of the map.

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.

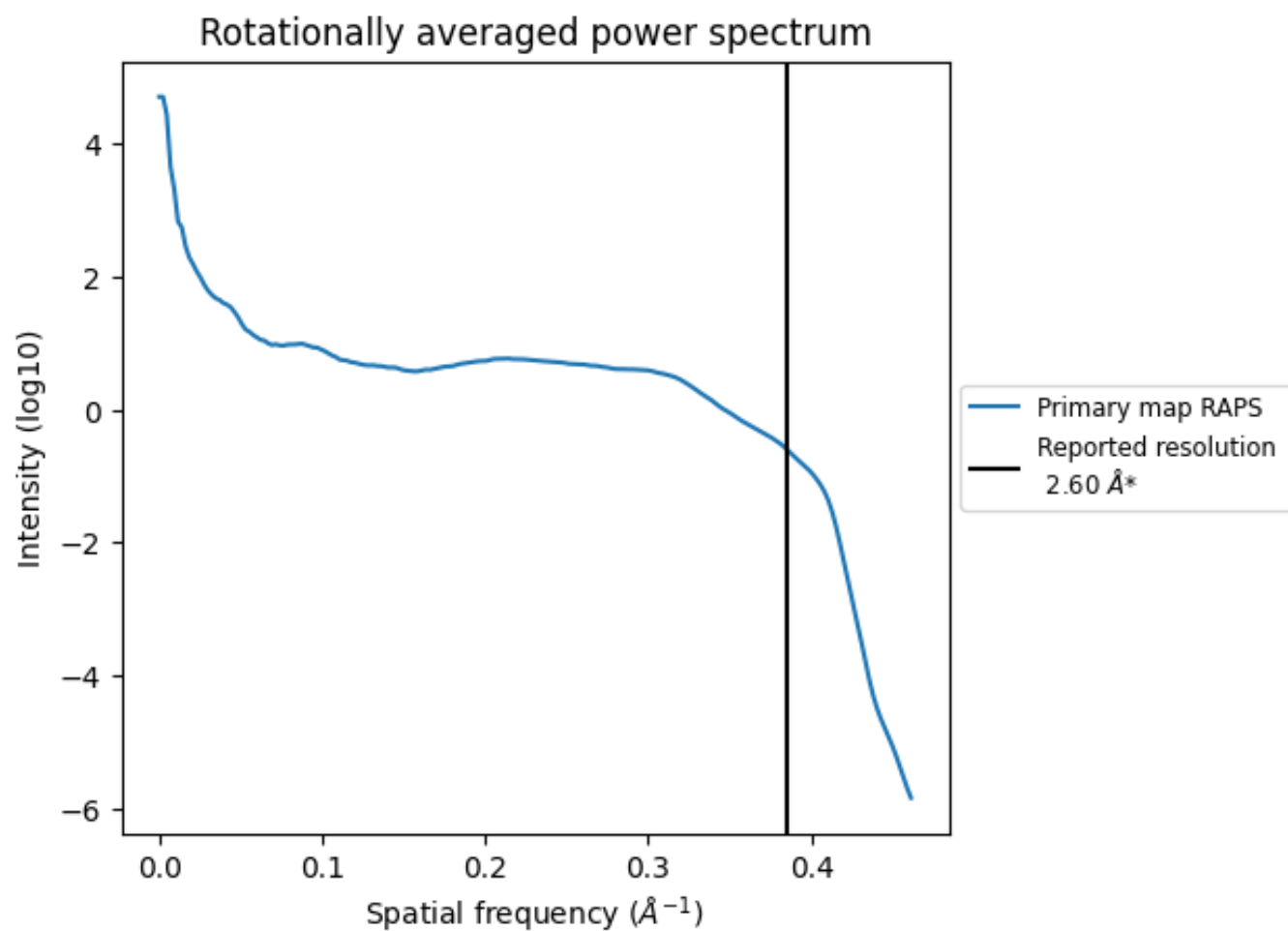
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1353 nm³; this corresponds to an approximate mass of 1222 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 ⓘ

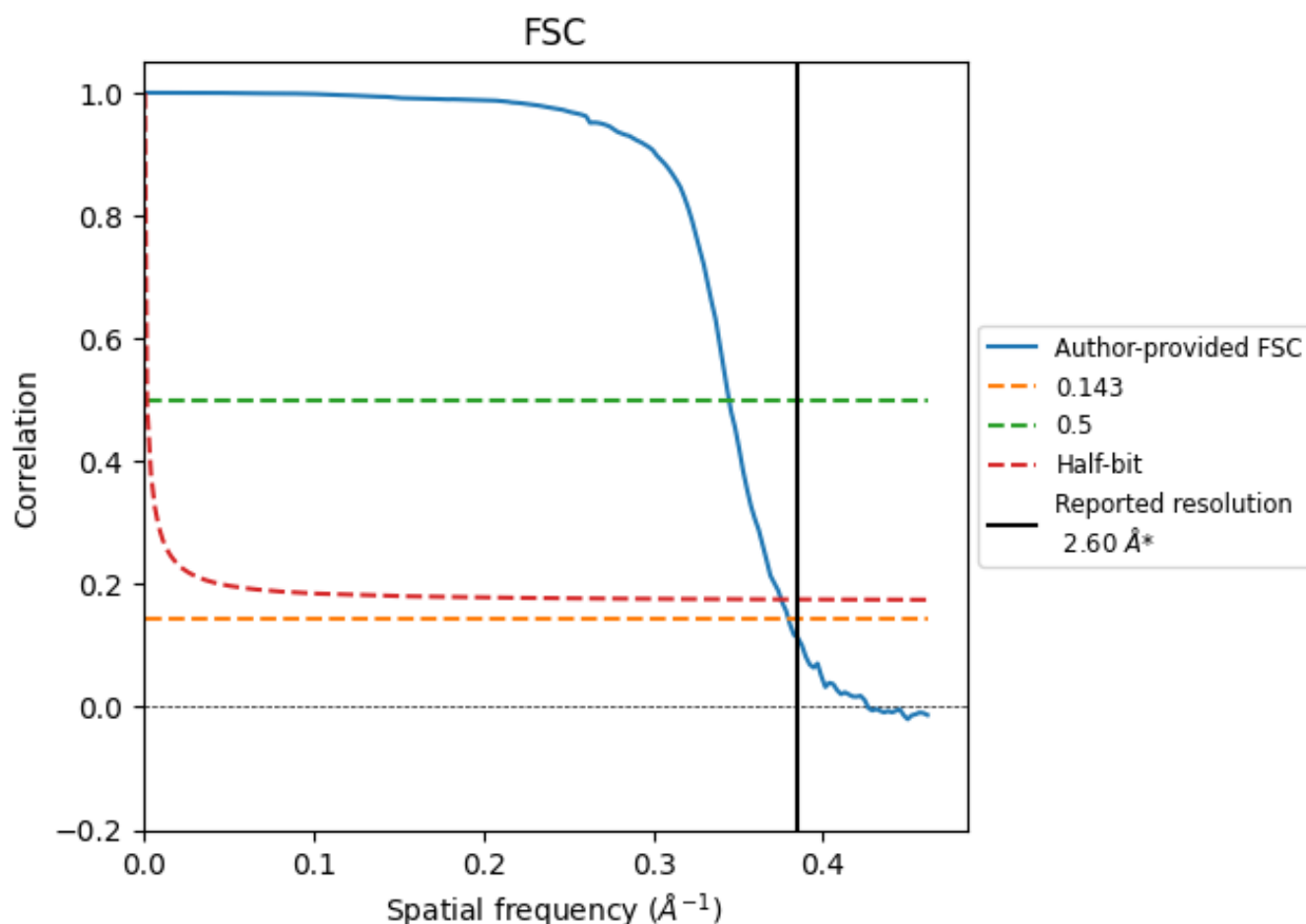


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

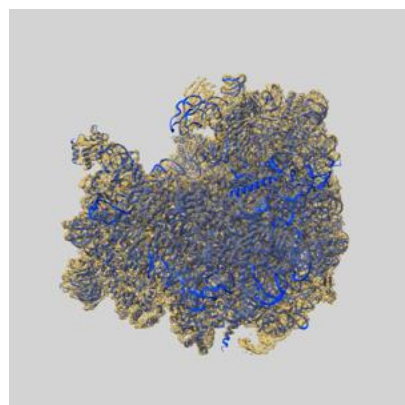
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.63	2.90	2.66
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

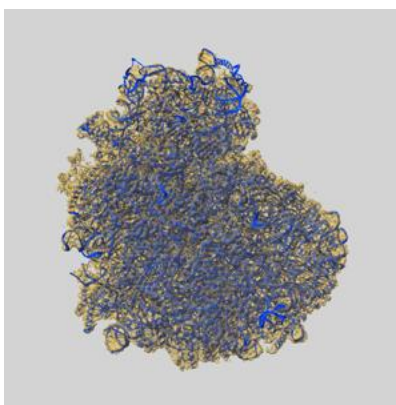
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10377 and PDB model 6T4Q. Per-residue inclusion information can be found in section 3 on page 21.

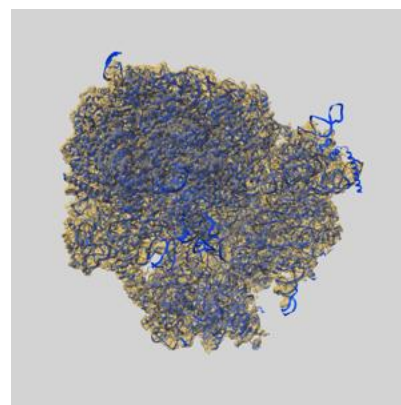
9.1 Map-model overlay [i](#)



X



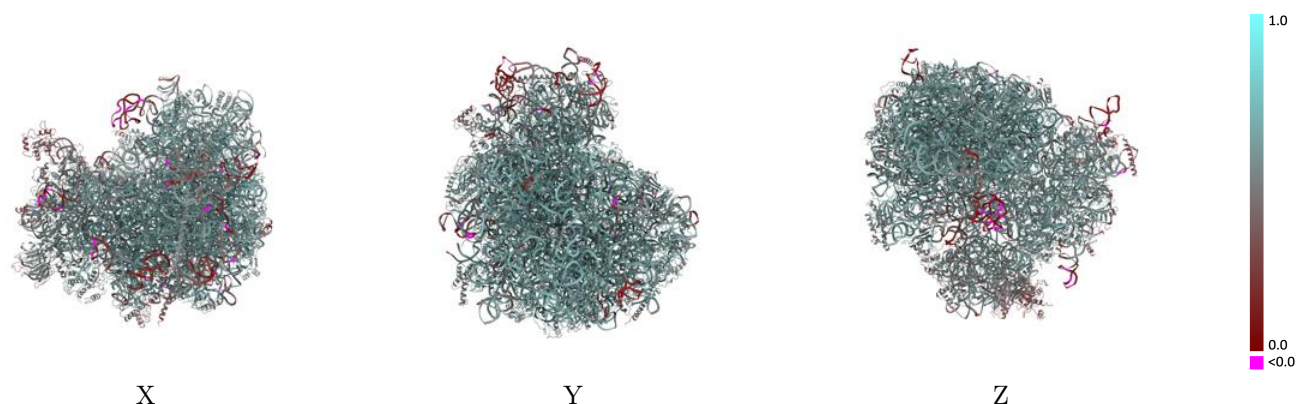
Y



Z

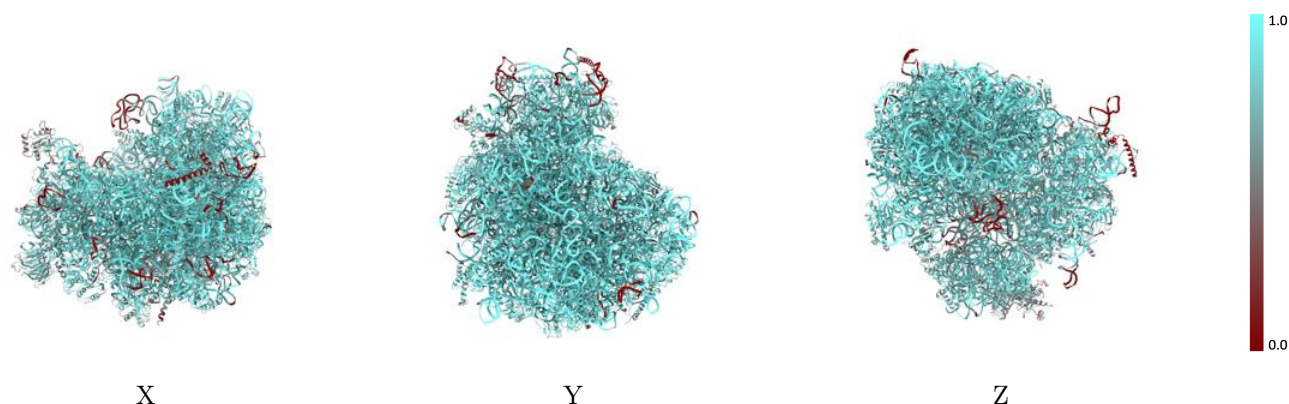
The images above show the 3D surface view of the map at the recommended contour level 0.0612 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



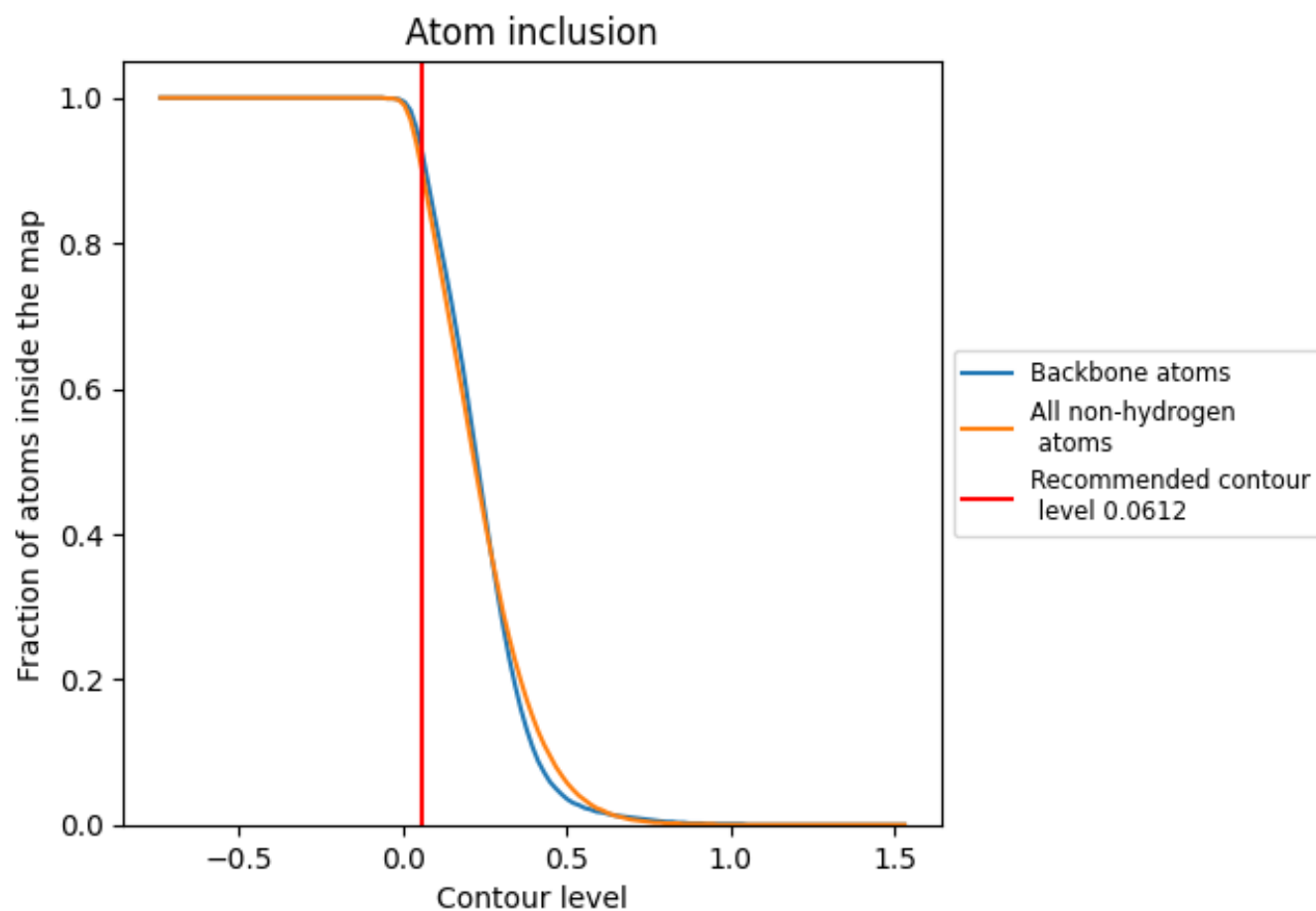
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0612).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.0612) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.5810
5	 0.3570	 0.3060
6	 0.8510	 0.5020
7	 0.7840	 0.4560
8	 0.6800	 0.4490
C1	 0.9450	 0.6100
C2	 0.9050	 0.5580
C3	 0.9720	 0.6360
C4	 0.9860	 0.6100
LA	 0.9500	 0.6530
LB	 0.9310	 0.6220
LC	 0.9150	 0.6150
LD	 0.8400	 0.5450
LE	 0.8640	 0.5640
LF	 0.9030	 0.6030
LG	 0.8590	 0.5660
LH	 0.8820	 0.5850
LI	 0.8610	 0.5850
LJ	 0.8060	 0.5300
LL	 0.8890	 0.5950
LM	 0.8810	 0.5820
LN	 0.9680	 0.6520
LO	 0.9230	 0.6160
LP	 0.9020	 0.6240
LQ	 0.9200	 0.6200
LR	 0.8500	 0.5850
LS	 0.9100	 0.6110
LT	 0.9060	 0.6070
LU	 0.8350	 0.5370
LV	 0.9080	 0.6270
LW	 0.5920	 0.5090
LX	 0.9040	 0.6010
LY	 0.9040	 0.6050
LZ	 0.8740	 0.5870
La	 0.9270	 0.6320



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Chain	Atom inclusion	Q-score
Lb	 0.8300	 0.5600
Lc	 0.8980	 0.6050
Ld	 0.8850	 0.6020
Le	 0.9260	 0.6370
Lf	 0.9460	 0.6440
Lg	 0.9030	 0.6240
Lh	 0.8840	 0.5950
Li	 0.8540	 0.5680
Lj	 0.9710	 0.6660
Lk	 0.8200	 0.5570
Ll	 0.9470	 0.6550
Lm	 0.8840	 0.5910
Ln	 0.9380	 0.6330
Lo	 0.8930	 0.6130
Lp	 0.9060	 0.6310
SA	 0.8720	 0.5610
SB	 0.8190	 0.5610
SC	 0.8890	 0.5940
SD	 0.7670	 0.5140
SE	 0.8770	 0.5820
SF	 0.7460	 0.5070
SG	 0.7870	 0.5170
SH	 0.7810	 0.5070
SI	 0.8890	 0.5910
SJ	 0.8290	 0.5460
SK	 0.7570	 0.4790
SL	 0.8790	 0.6100
SM	 0.4430	 0.3060
SN	 0.8710	 0.5750
SO	 0.8760	 0.5760
SP	 0.7060	 0.4700
SQ	 0.8200	 0.5410
SR	 0.7800	 0.5120
SS	 0.7500	 0.4880
ST	 0.7820	 0.5060
SU	 0.7560	 0.5060
SV	 0.8710	 0.5710
SW	 0.9110	 0.6200
SX	 0.8870	 0.5910
SY	 0.8100	 0.5200
SZ	 0.6490	 0.4540
Sa	 0.8750	 0.5780

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Chain	Atom inclusion	Q-score
Sb	 0.8550	 0.5700
Sc	 0.7590	 0.5310
Sd	 0.9010	 0.5780
Se	 0.7390	 0.5250
Sf	 0.4490	 0.2770
Sg	 0.7160	 0.4840