



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:14 PM UTC

PDB ID : 9QLP / pdb_00009qlp
EMDB ID : EMD-53231
Title : NMT1-NAC bound human RNC with full length ARF1 - State 2
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-03-21
Resolution : 2.75 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:

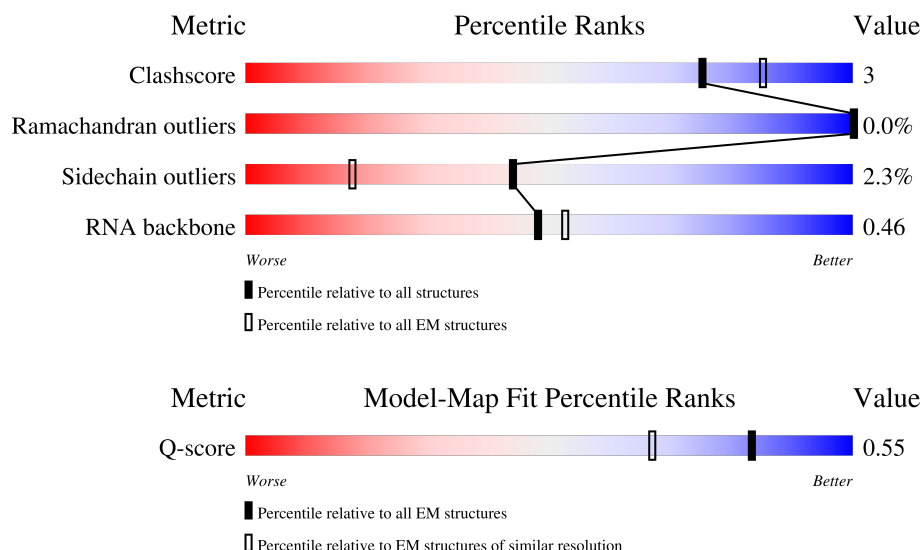
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.75 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	10570 (2.25 - 3.25)

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	CM	952	
2	CP	75	
3	CR	437	







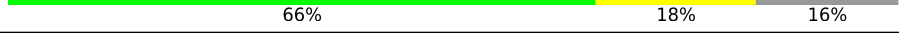
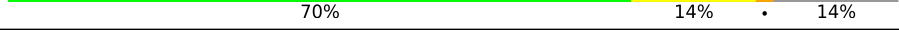
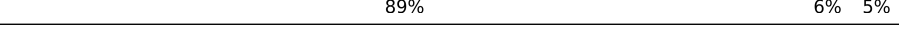
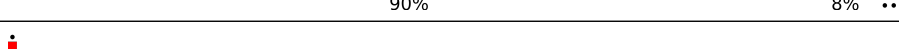
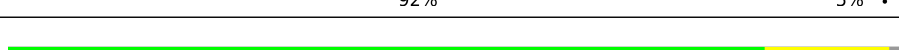

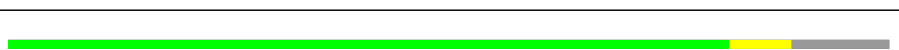







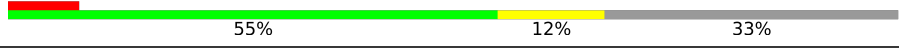
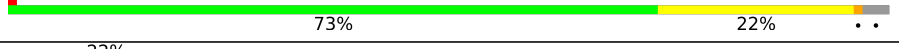



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Mol	Chain	Length	Quality of chain
4	CZ	217	
5	L5	5070	
6	L7	121	
7	L8	157	
8	LA	257	
9	LB	403	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	









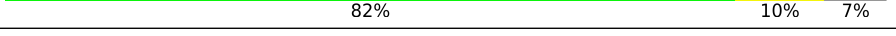



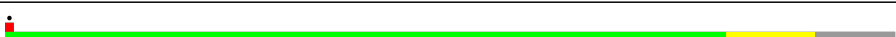

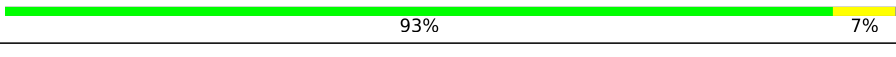

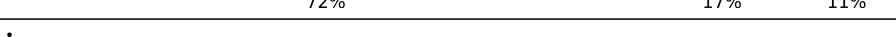

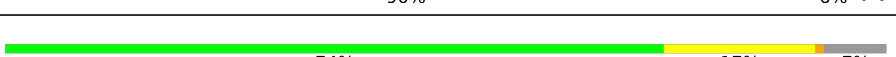


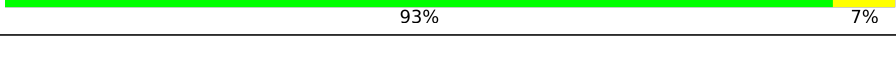
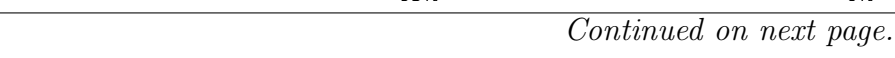


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Mol	Chain	Length	Quality of chain
29	LW	157	
30	LX	156	
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Ln	25	
47	Lo	106	
48	Lp	91	
49	Lr	137	
50	Ls	317	
51	Lt	165	
52	NA	215	
53	NB	162	




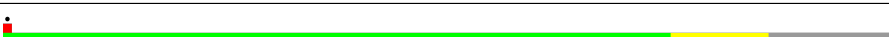
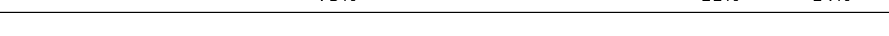
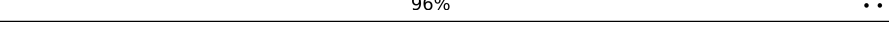




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Mol	Chain	Length	Quality of chain
54	NM	496	
55	S2	1869	
56	SA	295	
57	SB	264	
58	SC	293	
59	SD	243	
60	SE	263	
61	SF	204	
62	SG	249	
63	SH	194	
64	SI	208	
65	SJ	194	
66	SK	165	
67	SL	158	
68	SM	132	
69	SN	151	
70	SO	151	
71	SP	145	
72	SQ	146	
73	SR	135	
74	SS	152	
75	ST	145	
76	SU	119	
77	SV	83	
78	SW	130	

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Mol	Chain	Length	Quality of chain
79	SX	143	 87% 10% ..
80	SY	133	 80% 11% • 8%
81	SZ	125	 53% 7% 40%
82	Sa	115	 75% 11% 14%
83	Sb	84	 96% ..
84	Sc	69	 78% 12% • 9%
85	Sd	56	 88% 7% 5%
86	Se	133	 36% 5% 59%
87	Sf	156	 35% • • 60%
88	Sg	317	 83% 13% • •

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 223418 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 Full length ARF1-V5-hCMV staller mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CM	12	Total	C	N	O	P	0	0
			247	111	37	87	12		

- Molecule 2 is a RNA chain called prolyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CP	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 3 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CR	414	Total	C	N	O	S	0	0
			3269	2080	557	621	11		

- Molecule 4 is a protein called ADP-ribosylation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CZ	206	Total	C	N	O	S	0	0
			1491	947	250	286	8		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CZ	1	GLN	-	expression tag	UNP P84077
CZ	4	SER	ILE	conflict	UNP P84077
CZ	6	SER	ALA	conflict	UNP P84077
CZ	7	LYS	ASN	conflict	UNP P84077
CZ	8	PRO	LEU	conflict	UNP P84077
CZ	9	ARG	PHE	conflict	UNP P84077
CZ	182	GLY	-	expression tag	UNP P84077
CZ	183	LYS	-	expression tag	UNP P84077
CZ	184	PRO	-	expression tag	UNP P84077

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Chain	Residue	Modelled	Actual	Comment	Reference
CZ	185	ILE	-	expression tag	UNP P84077
CZ	186	PRO	-	expression tag	UNP P84077
CZ	187	ASN	-	expression tag	UNP P84077
CZ	188	PRO	-	expression tag	UNP P84077
CZ	189	LEU	-	expression tag	UNP P84077
CZ	190	LEU	-	expression tag	UNP P84077
CZ	191	GLY	-	expression tag	UNP P84077
CZ	192	LEU	-	expression tag	UNP P84077
CZ	193	ASP	-	expression tag	UNP P84077
CZ	194	SER	-	expression tag	UNP P84077
CZ	195	THR	-	expression tag	UNP P84077
CZ	196	MET	-	expression tag	UNP P84077
CZ	197	GLU	-	expression tag	UNP P84077
CZ	198	PRO	-	expression tag	UNP P84077
CZ	199	LEU	-	expression tag	UNP P84077
CZ	200	VAL	-	expression tag	UNP P84077
CZ	201	LEU	-	expression tag	UNP P84077
CZ	202	SER	-	expression tag	UNP P84077
CZ	203	ALA	-	expression tag	UNP P84077
CZ	204	LYS	-	expression tag	UNP P84077
CZ	205	LYS	-	expression tag	UNP P84077
CZ	206	LEU	-	expression tag	UNP P84077
CZ	207	SER	-	expression tag	UNP P84077
CZ	208	SER	-	expression tag	UNP P84077
CZ	209	LEU	-	expression tag	UNP P84077
CZ	210	LEU	-	expression tag	UNP P84077
CZ	211	THR	-	expression tag	UNP P84077
CZ	212	CYS	-	expression tag	UNP P84077
CZ	213	LYS	-	expression tag	UNP P84077
CZ	214	TYR	-	expression tag	UNP P84077
CZ	215	ILE	-	expression tag	UNP P84077
CZ	216	PRO	-	expression tag	UNP P84077
CZ	217	PRO	-	expression tag	UNP P84077

- Molecule 5 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L5	3648	Total	C	N	O	P	0	0
			78199	34823	14307	25422	3647		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 7 is a RNA chain called RNA (156-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 12 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 15 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 16 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	207	Total	C	N	O	S	0	0
			1666	1059	323	270	14		

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 20 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 21 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 22 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 23 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 25 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 26 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 27 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LU	101	Total	C	N	O	S	0	0
			806	520	141	143	2		

- Molecule 28 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

- Molecule 29 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 30 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 31 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 32 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 33 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 34 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 36 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 37 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 38 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 39 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 40 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 42 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 46 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 48 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ls	212	Total	C	N	O	S	0	0
			1640	1042	284	305	9		

- Molecule 51 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lt	160	Total	C	N	O	S	0	0
			1208	749	226	229	4		

- Molecule 52 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	NA	73	Total	C	N	O	S	0	0
			573	361	105	106	1		

- Molecule 53 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	NB	127	Total	C	N	O	S	0	0
			980	606	178	193	3		

- Molecule 54 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	NM	380	Total	C	N	O	S	3	0
			3122	2024	527	555	16		

- Molecule 55 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S2	1713	Total	C	N	O	P	0	0
			36562	16320	6564	11966	1712		

- Molecule 56 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 57 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 58 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 59 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SD	223	Total	C	N	O	S	0	0
			1594	1023	291	273	7		

- Molecule 60 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 61 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SF	181	Total	C	N	O	S	0	0
			1403	879	269	248	7		

- Molecule 62 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 63 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- Molecule 64 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 65 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 66 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 67 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 68 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SM	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 69 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 70 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 71 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SP	129	Total	C	N	O	S	0	0
			990	626	190	168	6		

- Molecule 72 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SQ	142	Total	C	N	O	S	0	0
			1075	689	204	179	3		

- Molecule 73 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 74 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SS	141	Total	C	N	O	S	0	0
			1130	712	232	185	1		

- Molecule 75 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 77 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 78 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 79 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 80 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 81 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 82 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 83 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 84 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 85 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 86 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Se	55	Total	C	N	O	S	0	0
			416	254	93	68	1		

- Molecule 87 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sf	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

- Molecule 88 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	Sg	308	Total	C	N	O	S	0	0
			2180	1393	381	395	11		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

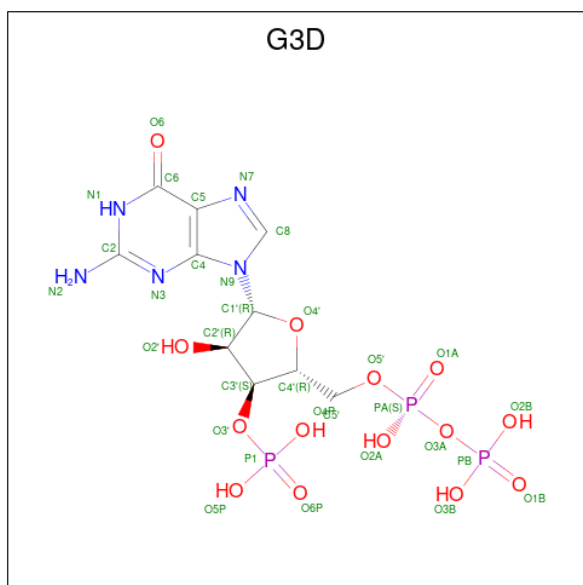
Mol	Chain	Residues	Atoms		AltConf
89	CM	1	Total	Mg	0
			1	1	
89	L5	126	Total	Mg	0
			126	126	
89	L7	3	Total	Mg	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
89	L8	3	Total	Mg	0
			3	3	
89	LA	1	Total	Mg	0
			1	1	
89	LC	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	
89	LN	1	Total	Mg	0
			1	1	
89	LP	1	Total	Mg	0
			1	1	
89	LV	1	Total	Mg	0
			1	1	
89	S2	51	Total	Mg	0
			51	51	
89	ST	1	Total	Mg	0
			1	1	

- Molecule 90 is GUANOSINE-3'-MONOPHOSPHATE-5'-DIPHOSPHATE (CCD ID: G3D) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				AltConf	
90	CZ	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 91 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
91	Lg	1	Total 1	Zn 1	0
91	Lj	1	Total 1	Zn 1	0
91	Lm	1	Total 1	Zn 1	0
91	Lo	1	Total 1	Zn 1	0
91	Lp	1	Total 1	Zn 1	0
91	Sa	1	Total 1	Zn 1	0
91	Sd	1	Total 1	Zn 1	0
91	Sf	1	Total 1	Zn 1	0

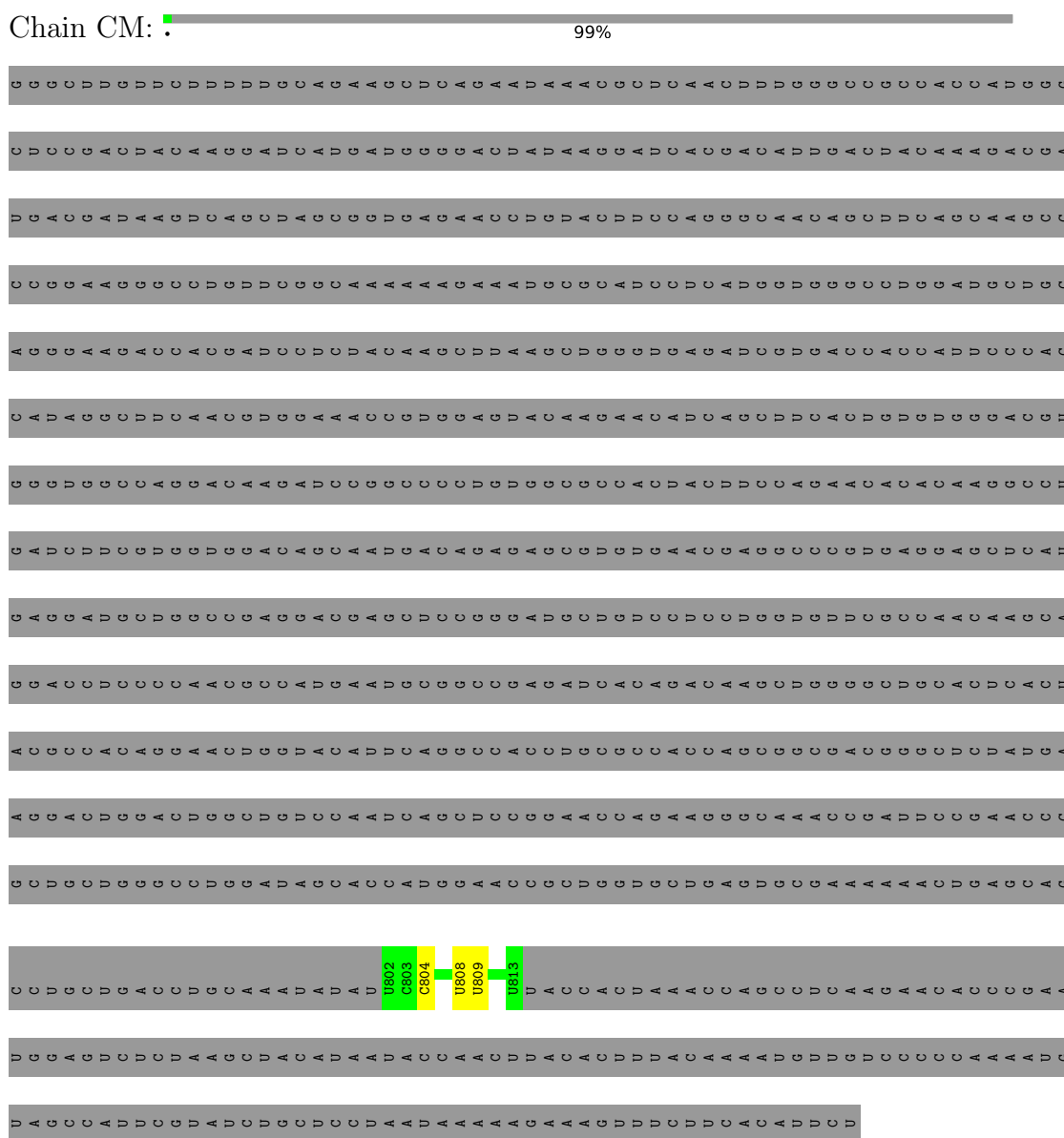
- Molecule 92 is water.

Mol	Chain	Residues	Atoms		AltConf
92	L5	3	Total 3	O 3	0
92	L7	1	Total 1	O 1	0
92	LI	1	Total 1	O 1	0
92	LN	1	Total 1	O 1	0
92	La	1	Total 1	O 1	0
92	Lp	1	Total 1	O 1	0
92	S2	3	Total 3	O 3	0

3 Residue-property plots

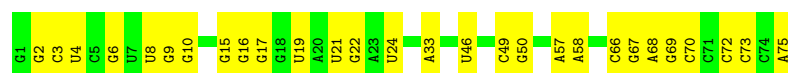
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Full length ARF1-V5-hCMV staller mRNA



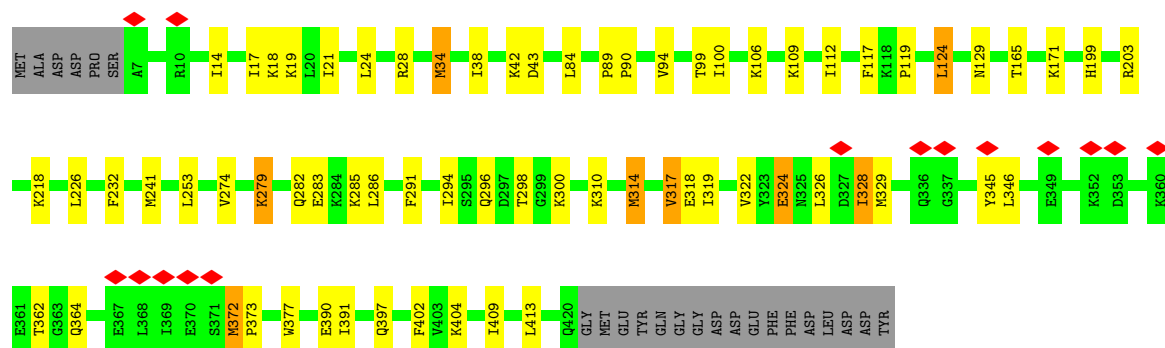
- Molecule 2: prolyl-tRNA

Chain CP:  63% 37%




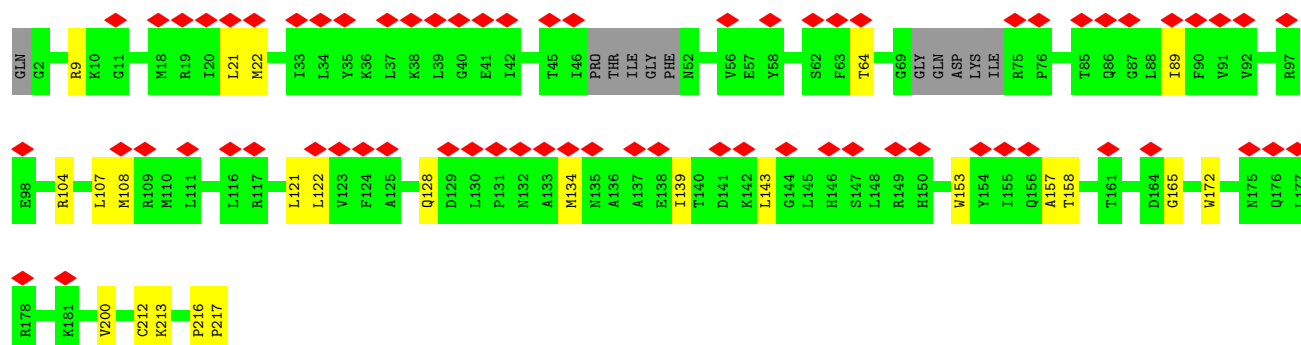
- Molecule 3: Eukaryotic peptide chain release factor subunit 1

Chain CR:  79% 14% 5%



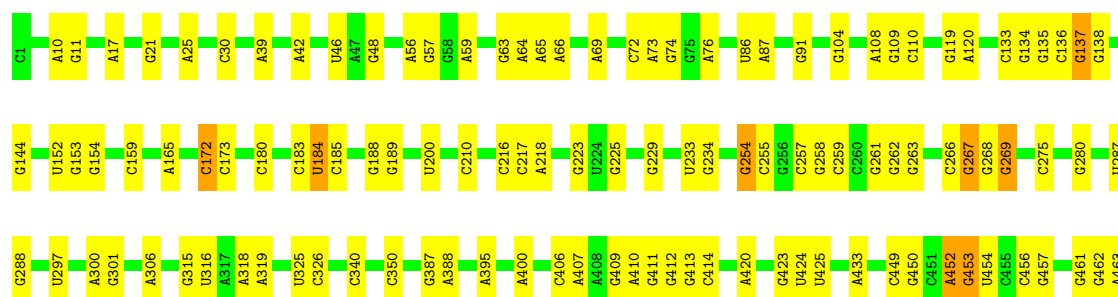
- Molecule 4: ADP-ribosylation factor 1

Chain CZ:  31% 84% 11% 5%



- Molecule 5: 28S rRNA

Chain L5:  51% 20% 28%







C4990	U4882	G4735	U4574	U4438	U4296	G4175	G4089	G	U3848	A3711	C3585
U4991	C4863	C4736	G4575	C4444	U4301	G4178	G4093	G	A3849	A3712	C3586
G4993	U4888	G4737	A4584	G4448	U4302	C4179	G4094	G	U3713	U3713	C3587
U5006	G4889	G4740	A4590	G4449	U4303	G4183	G4097	U	A3861	A3717	C3588
A5007	A4894	C4741	U4591	U4452	G4302	G4184	A4988	C	A3862	A3718	C3591
A5011	C4896	G4743	C4592	U4453	U4306	U4188	G4099	C	A3867	A3719	C3592
A5014	C4900	G4745	G4600	C4453	U4309	U4189	C4102	C	A3868	U3721	C3593
G5015	G4901	G4754	U4601	U4457	G4314	U4190	G4103	C	C3869	U3722	C3594
A5016	C4906	C4757	G4608	C4458	U4319	G4191	G4104	C	A3877	A3723	U3595
G5017	G4907	U4758	G4617	U4459	G4320	A4203	A4105	C	C3878	A3726	C3596
C5018	C4908	U4759	G4618	U4460	G4321	C4206	G4106	C	C3879	A3727	C3597
A5019	G4909	G4760	G4619	U4461	U4322	U4207	G4107	C	G3885	A3728	C3598
U5022	G4910	G4761	C4621	U4465	G4329	U4208	U4113	C	U3892	U3729	A3604
C5023	A4911	G4765	A4622	U4466	G4330	G4209	C4114	C	A3733	A3733	C3605
C5024	G4912	C4771	U4626	U4467	U4331	U4219	C4115	C	U3734	U3734	U3606
U5025	G4913	C4772	U4627	U4468	G4332	C4221	G4116	C	G3735	A3736	U3607
U5026	C4914	C4773	U4632	U4469	G4338	G4222	C4119	C	A3746	A3746	A3610
C5027	U4925	G4774	U4636	U4470	U4344	G4225	G4122	C	A3747	A3747	C3612
G5028	G4926	C4775	U4637	U4471	U4345	U4228	C4125	C	A3748	A3748	U3613
C5029	A4927	G4776	G4638	U4472	U4346	U4229	A4128	C	C3749	C3749	C3614
U5030	C4928	C4777	G4639	U4473	G4347	U4233	C4130	C	A3905	A3905	C3615
C5031	G4931	C4778	G4640	U4474	U4348	U4234	G4131	C	A3906	A3906	U3616
A5034	U4934	C4779	U4641	U4475	U4349	U4235	G4132	C	G3907	A3907	C3617
U5037	C4935	C4780	U4642	U4476	U4350	U4236	C4133	C	A3908	A3908	C3618
G5041	G4936	C4781	U4643	U4477	U4351	U4237	C4134	C	C3909	C3909	C3619
C5050	C4937	C4782	U4644	U4478	U4352	U4238	G4135	C	C3910	C3910	A3624
C5054	U4940	C4783	U4645	U4479	U4353	U4239	G4136	C	U3911	U3911	C3625
C5057	C4941	C4784	U4646	U4480	U4354	U4240	C4137	C	A3760	A3760	C3626
A5058	A4942	C4785	U4647	U4481	U4355	U4241	C4138	C	C3771	C3771	A3630
C5062	G4943	C4786	U4648	U4482	U4356	U4242	C4139	C	A3775	A3775	A3635
U5069	C4944	C4787	U4649	U4483	U4357	U4243	C4140	C	G3776	G3776	U3641
C	U4949	C4788	U4650	U4484	U4358	U4244	C4141	C	G3777	G3777	C3644
	G4954	C4789	U4651	U4485	U4359	U4245	C4142	C	A3784	A3784	U3644
	A4955	C4790	U4652	U4486	U4360	U4246	C4143	C	A3785	A3785	U3645
	U4959	C4791	U4653	U4487	U4361	U4247	C4144	C	U3786	U3786	A3646
	G4960	C4792	U4654	U4488	U4362	U4248	C4145	C	C3810	C3810	A3648
	C4963	C4793	U4655	U4489	U4363	U4249	G4150	C	U3814	U3814	A3662
	A4966	C4794	U4656	U4490	U4364	U4250	G4151	C	A3817	A3817	A3663
	A4967	C4795	U4657	U4491	U4365	U4251	G4152	C	U3818	U3818	C3664
	A4968	C4796	U4658	U4492	U4366	U4252	G4153	C	G3819	G3819	C3665
	U4976	C4797	U4659	U4493	U4367	U4253	C4164	C	G3673	G3673	C3674
	A4979	C4798	U4660	U4494	U4368	U4254	G4165	C	U3827	U3827	A3697
	U4988	C4799	U4661	U4495	U4369	U4255	G4166	C	A3838	A3838	C3698
	U4989	C4800	U4662	U4496	U4370	U4256	G4167	C	G3839	G3839	U3707
		C4801	U4663	U4497	U4371	U4257	G4168	C	U3840	U3840	C3708
		C4802	U4664	U4498	U4372	U4258	G4169	C			
		C4803	U4665	U4499	U4373	U4259	A4170	C			
		C4804	U4666	U4500	U4374	U4260	C4171	C			
		C4805	U4667	U4501	U4375	U4261	G4172	C			
		C4806	U4668	U4502	U4376	U4262	G4173	C			
		C4807	U4669	U4503	U4377	U4263	G4174	C			
		C4808	U4670	U4504	U4378	U4264	G4175	C			
		C4809	U4671	U4505	U4379	U4265	G4176	C			
		C4810	U4672	U4506	U4380	U4266	G4177	C			
		C4811	U4673	U4507	U4381	U4267	G4178	C			
		C4812	U4674	U4508	U4382	U4268	G4179	C			
		C4813	U4675	U4509	U4383	U4269	G4180	C			
		C4814	U4676	U4510	U4384	U4270	G4181	C			
		C4815	U4677	U4511	U4385	U4271	G4182	C			
		C4816	U4678	U4512	U4386	U4272	G4183	C			
		C4817	U4679	U4513	U4387	U4273	G4184	C			
		C4818	U4680	U4514	U4388	U4274	G4185	C			
		C4819	U4681	U4515	U4389	U4275	G4186	C			
		C4820	U4682	U4516	U4390	U4276	G4187	C			
		C4821	U4683	U4517	U4391	U4277	G4188	C			
		C4822	U4684	U4518	U4392	U4278	G4189	C			
		C4823	U4685	U4519	U4393	U4279	G4190	C			
		C4824	U4686	U4520	U4394	U4280	G4191	C			
		C4825	U4687	U4521	U4395	U4281	G4192	C			
		C4826	U4688	U4522	U4396	U4282	G4193	C			
		C4827	U4689	U4523	U4397	U4283	G4194	C			
		C4828	U4690	U4524	U4398	U4284	G4195	C			
		C4829	U4691	U4525	U4399	U4285	G4196	C			
		C4830	U4692	U4526	U4400	U4286	G4197	C			
		C4831	U4693	U4527	U4401	U4287	G4198	C			
		C4832	U4694	U4528	U4402	U4288	G4199	C			
		C4833	U4695	U4529	U4403	U4289	G4200	C			
		C4834	U4696	U4530	U4404	U4290	G4201	C			
		C4835	U4697	U4531	U4405	U4291	G4202	C			
		C4836	U4698	U4532	U4406	U4292	G4203	C			
		C4837	U4699	U4533	U4407	U4293	G4204	C			
		C4838	U4700	U4534	U4408	U4294	G4205	C			
		C4839	U4701	U4535	U4409	U4295	G4206	C			
		C4840	U4702	U4536	U4410	U4296	G4207	C			
		C4841	U4703	U4537	U4411	U4297	G4208	C			
		C4842	U4704	U4538	U4412	U4298	G4209	C			
		C4843	U4705	U4539	U4413	U4299	G4210	C			
		C4844	U4706	U4540	U4414	U4300	G4211	C			
		C4845	U4707	U4541	U4415	U4301	G4212	C			
		C4846	U4708	U4542	U4416	U4302	G4213	C			
		C4847	U4709	U4543	U4417	U4303	G4214	C			
		C4848	U4710	U4544	U4418	U4304	G4215	C			
		C4849	U4711	U4545	U4419	U4305	G4216	C			
		C4850	U4712	U4546	U4420	U4306	G4217	C			
		C4851	U4713	U4547	U4421	U4307	G4218	C			
		C4852	U4714	U4548	U4422	U4308	G4219	C			
		C4853	U4715	U4549	U4423	U4309	G4220	C			
		C4854	U4716	U4550	U4424	U4310	G4221	C			
		C4855	U4717	U4551	U4425	U4311	G4222	C			
		C4856	U4718	U4552	U4426	U4312	G4223	C			
		C4857	U4719	U4553	U4427	U4313	G4224	C			
		C4858	U4720	U4554	U4428	U4314	G4225	C			
		C4859	U4721	U4555	U4429	U4315	G4226	C			
		C4860	U4722	U4556	U4430	U4316	G4227	C			
		C4861	U4723	U4557	U4431	U4317	G4228	C			
		C4862	U4724	U4558	U4432	U4318	G4229	C			
		C4863	U4725	U4559	U4433	U4319	G4230	C			
		C4864	U4726	U4560	U4434	U4320	G4231	C			
		C4865	U4727	U4561	U4435	U4321	G4232	C			
		C4866	U4728	U4562	U4436	U4322	G4233	C			
		C4867	U4729	U4563	U4437	U4323	G4234	C			
		C4868	U4730	U4564	U4438	U4324	G4235	C			
		C4869	U4731	U4565	U4439	U4325	G4236	C			
		C4870	U4732	U4566	U4440	U4326	G4237	C			
		C4871	U4733	U4567	U4441	U4327	G4238	C			
		C4872	U4734	U4568	U4442	U4328	G4239	C			
		C4873	U4735	U4569	U4443	U4329	G4240	C			
		C4874	U4736	U4570	U4444	U4330	G4241	C			
		C4875	U4737	U4571	U4445	U4331	G4242	C			
		C4876	U4738	U4572	U4446	U4332	G4243	C			
		C4877	U4739	U4573	U4447	U4333	G4244	C			
		C4878	U4740	U4574	U4448	U4334	G4245	C			
		C4879	U4741	U4575	U4449	U4335	G4246	C			
		C4880	U4742	U4576	U4450	U4336	G4247	C			
		C4881	U4743	U4577	U4451	U4337	G4248	C			
		C4882	U4744	U4578	U4452	U43					

K294	ALA	GLU	SER	ME1	G2	K41	K48	I60	I61	C62	A80	H81	E82	L83	P84	K89	T93	Y99	L105	I118	V125	T126	Y145	L146	L163	K164	L211	Y219	F223	Y226	M236	M239	I247	K256	V261	M271	D278	Q282
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|------|------|-----|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|-----|------|-----|-----|------|-----|-----|------|------|-----|------|------|-----|------|-----|-----|------|------|-----|------|------|-----|
| L271 | K100 | ALA | GLY | L276 | K108 | GLY | L281 | K111 | VAL | L282 | K114 | GLY | L283 | E119 | ASP | L288 | R123 | LYS | L294 | K124 | GLY | L295 | L125 | LYS | L296 | H128 | PRO | L297 | T145 | ALA | L298 | F146 | LYS | L299 | G147 | LYS | L300 | T148 | VAL | L301 | T149 | ASP | L302 | ALA | L303 | F164 | ALA | L304 | L165 | GLY | L305 | V175 | LYS | L306 | T176 | VAL | L307 | R183 | ASN | L308 | V184 | LEU | L309 | H190 | LYS | L310 | F193 | ALA | L311 | I203 | LYS | L312 | K221 | LEU | L313 | ARG | GLY | L314 | LYS | ARG | L315 | HIS | LYS | L316 | GLN | SER | L317 | GLY | GLY | L318 | GLU | VAL | L319 | ILE | GLY | L320 | PHE | LYS | L321 | THR | ASP | LYS | L322 | THR | LYS | L323 | GLU | LYS | L324 | K237 | GLY | L325 | D254 | VAL | L326 | LEU | LYS | L327 | I257 | ALA | L328 | T261 | THR |
|------|------|-----|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|------|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|-----|------|-----|-----|------|-----|-----|------|------|-----|------|------|-----|------|-----|-----|------|------|-----|------|------|-----|

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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|
| Met | GLU | GLY | VAL | GLU | GLY | LYS | LYS | GLU | VAL | PRO | ALA | VAL | PRO | GLU | THR | LEU | LYS | LYS | ARG | ARG | P24 | | | | | | | | | | | |
| K222 | H226 | G231 | D332 | A233 | R236 | E237 | D238 | Q239 | I240 | M241 | R245 | R246 | M247 | R248 | L28 | K31 | M41 | K59 | Q63 | V83 | F91 | V92 | V105 | G120 | K127 | V136 | P145 | M151 | M157 | K199 | L208 | P216 |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|
| V194 | H195 | T198 | G213 | K217 | T222 | R223 | N227 | Y230 | V241 | P244 | V247 | L261 | A262 | T263 | K264 | LEU | GLY | MET | PRO | GLY | LYS | ALA | GLY | LYS | VAL | ALA | PRO | ALA | PRO | ALA | VAL | VAL | LYS | GLN | GLU | ALA | LYS | V27 | R35 | I45 | V55 | I80 | T106 | K121 | ALA | ALA | GLY | LYS | ASP | VAL | PRO | THR | K131 | A138 | I164 | R175 | K187 | L190 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|

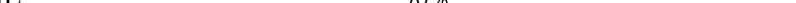
- [illegible]

- 

Amino Acid	Percentage (%)
MET	~1
C2	~1
I31	~1
R38	~1
A41	~1
L48	~1
S61	~1
S62	~1
R69	~1
M76	~1
L91	~1
I99	~1
L103	~1
SER	~1
CYS	~1
ALA	~1
GLY	~1
ALA	~1
ASP	~1
M10	~1
Q123	~1
V126	~1
I136	~1
M136	~1
S137	~1
I138	~1
R139	~1
K208	~1
V211	~1
S214	~1

- Chain LJ: 85% 10% 5%

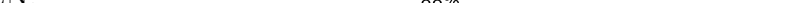
[illegible]

- Chain LL:  87% 9% .

MET	A2	R5	L10	K16	D17	W18	Q19	V22	I33	R36	I46	A47	A51	I58	V59	V70	S106	S109	S122	L124	K145	L146	V157	E164	D206	VAL	GUJ	LVS	LVS	LVS
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- Chain LM:  61% . 35%

[illegible]

- Chain LN:  88% 10%

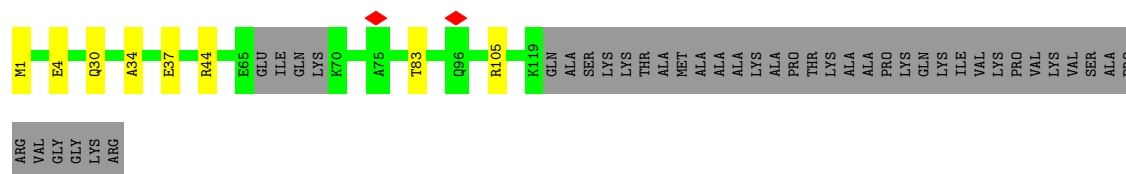
Met	G2	Q15	V18	Y53	V60	P84	H87	G88	Y89	E103	V115	W120	E123 D124	Y127	I133	F138 H139	K140	R143	P154	H178	H181	H182	T183 I184	R194	R204
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- Chain LO:  88% 10%

ME1	ALA	GLU	V4	L9	L16	V34	F47	R61	P70	F80	P89	K103	G107	M118	V126	V127	K130	R133	E144	K161	E186	D190	E194	T198	V203
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- Chain LP:  71% 11% 17%

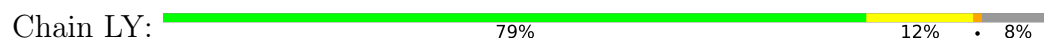
Met	V2	P8	K16	S20	N21	K27	N28	T32	Q64	C57	V58	Y63	T79	W83	N94	L95	K96	Q118	P123	H133	M140	M146	I149	E154	GLN	ILE	VAL	PRO	LYS	PRO	GLU	GLU	VAL	ALA	GLN	LYS	LYS	LVS	ILE	SER
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- Molecule 30: 60S ribosomal protein L23a



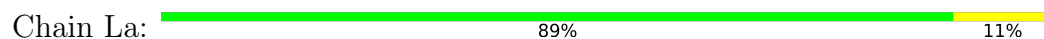
- Molecule 31: 60S ribosomal protein L26



- Molecule 32: 60S ribosomal protein L27



- Molecule 33: 60S ribosomal protein L27a

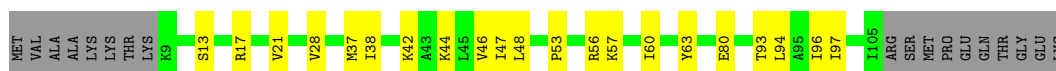


- Molecule 34: 60S ribosomal protein L29

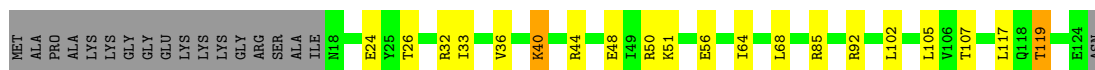


- Molecule 35: 60S ribosomal protein L30

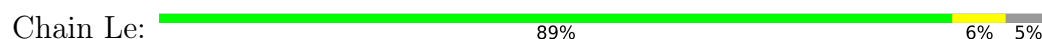




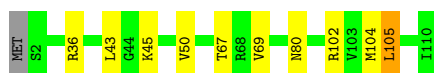
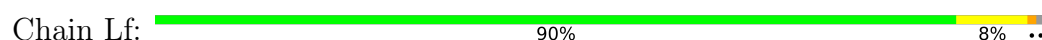
- Molecule 36: 60S ribosomal protein L31



- Molecule 37: 60S ribosomal protein L32



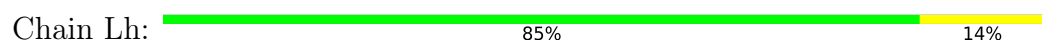
- Molecule 38: 60S ribosomal protein L35a



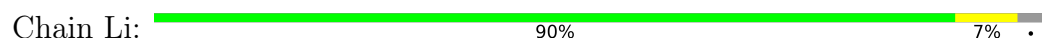
- Molecule 39: 60S ribosomal protein L34



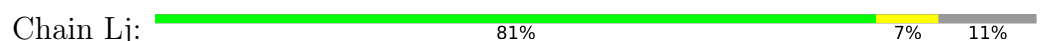
- Molecule 40: 60S ribosomal protein L35



- Molecule 41: 60S ribosomal protein L36



- Molecule 42: Large ribosomal subunit protein eL37





- Molecule 43: 60S ribosomal protein L38

Chain Lk: 83% 16%



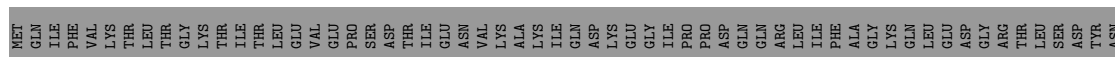
- Molecule 44: 60S ribosomal protein L39

Chain Ll: 90% 6%



- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain Lm: 38% 59%



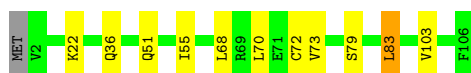
- Molecule 46: 60S ribosomal protein L41

Chain Ln: 92%



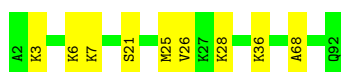
- Molecule 47: 60S ribosomal protein L36a

Chain Lo: 89% 9%



- Molecule 48: 60S ribosomal protein L37a

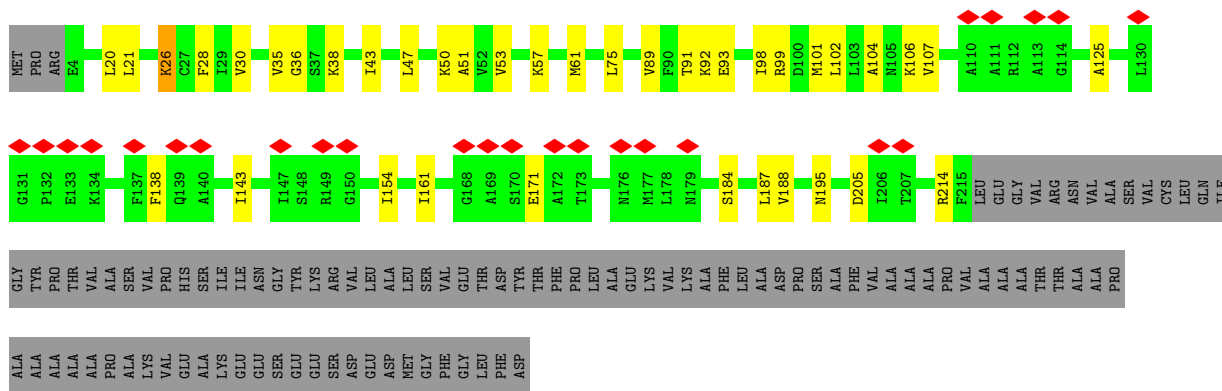
Chain Lp: 90% 10%



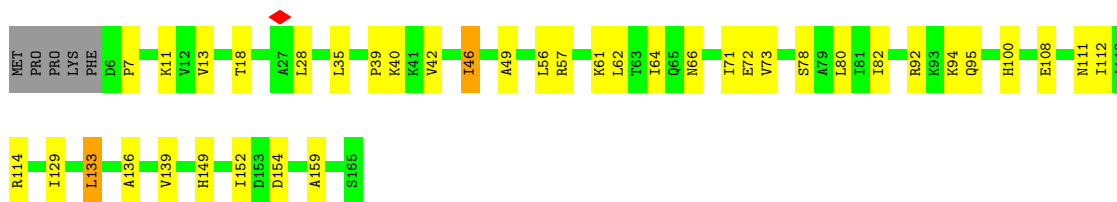
- Molecule 49: 60S ribosomal protein L28

MET
S2
F16
K19
T27
I44
V63 I64
R67
P73
S76
R79
R87
M96
S115
V126
LYS
ARG
LYS
ARG
THR
ARG
PRO
THR
LYS
SER
SER

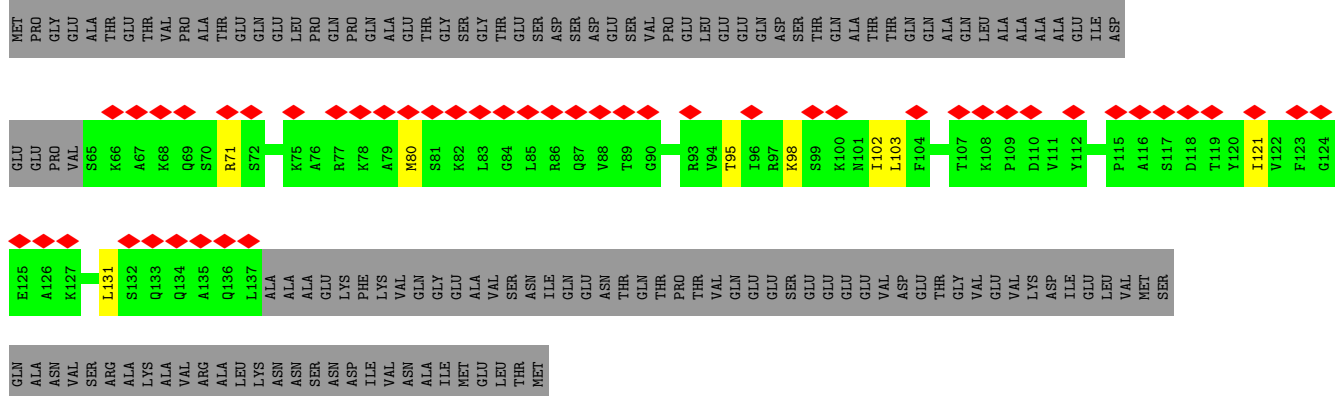
- Chain Ls: 



- Chain Lt:  73% 22% ..

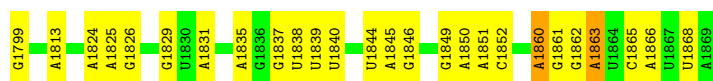


- Chain NA: 

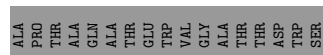
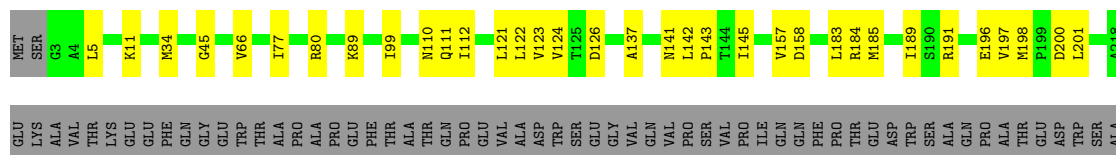


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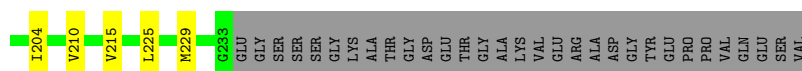
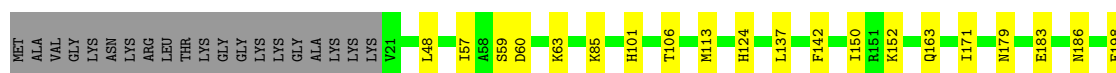




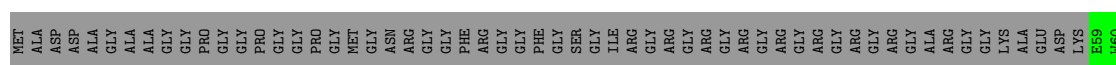
- Molecule 56: 40S ribosomal protein SA



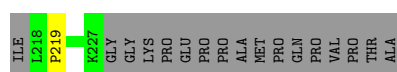
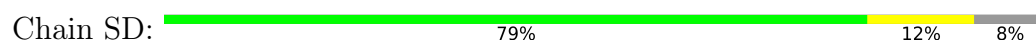
- Molecule 57: 40S ribosomal protein S3a




- Molecule 58: 40S ribosomal protein S2

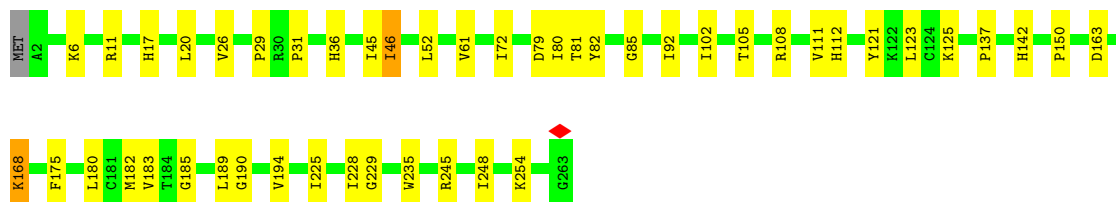


- Molecule 59: 40S ribosomal protein S3




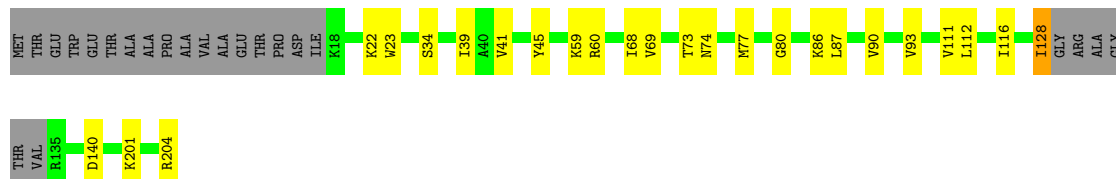
- Molecule 60: Small ribosomal subunit protein eS4, X isoform

Chain SE:  82% 17% .




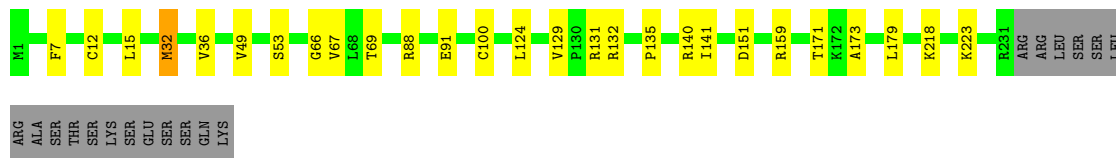
- Molecule 61: 40S ribosomal protein S5

Chain SF:  76% 12% 11%




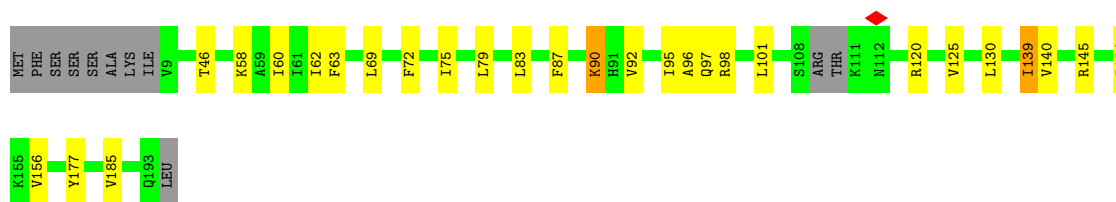
- Molecule 62: 40S ribosomal protein S6

Chain SG:  82% 10% 7%




- Molecule 63: 40S ribosomal protein S7

Chain SH:  80% 13% 6%




- Molecule 64: 40S ribosomal protein S8

Chain SI:  91% 8% .



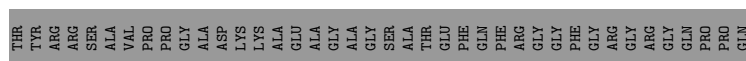
- Molecule 65: 40S ribosomal protein S9

Chain SJ:  85% 8% 8%



- Molecule 66: 40S ribosomal protein S10

Chain SK: 48% 10% 42%



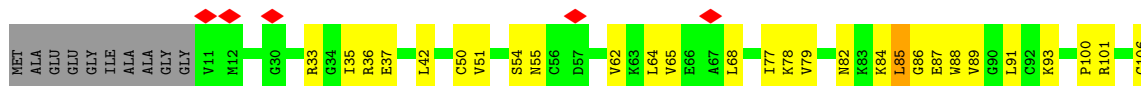
- Molecule 67: 40S ribosomal protein S11

Chain SL: 81% 10% 9%



- Molecule 68: 40S ribosomal protein S12

Chain SM: 6% 67% 24% 8%



- Molecule 69: 40S ribosomal protein S13

Chain SN: 93% 7%



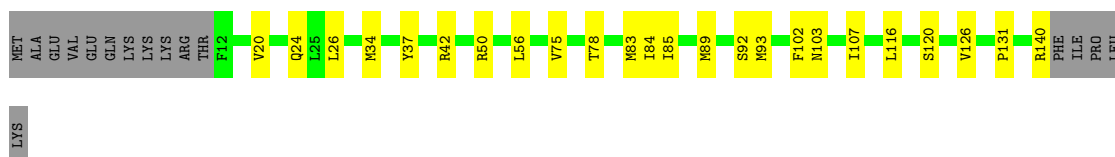
- Molecule 70: 40S ribosomal protein S14

Chain SO: 79% 9% 11%

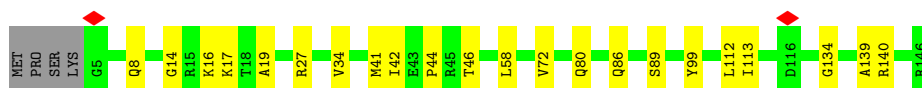
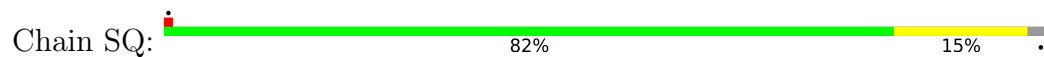


- Molecule 71: 40S ribosomal protein S15

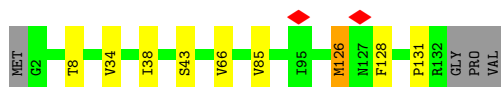
Chain SP: 72% 17% 11%



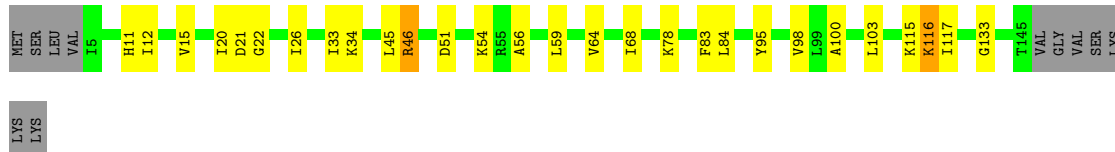
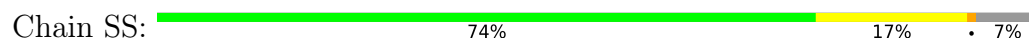
- Molecule 72: 40S ribosomal protein S16



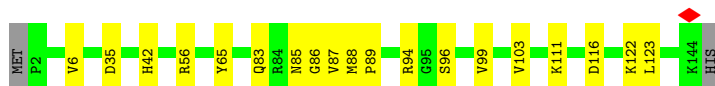
- Molecule 73: 40S ribosomal protein S17



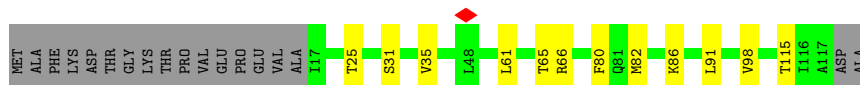
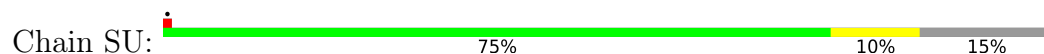
- Molecule 74: 40S ribosomal protein S18



- Molecule 75: 40S ribosomal protein S19




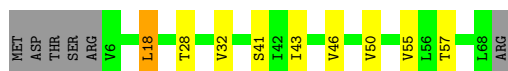
- Molecule 76: 40S ribosomal protein S20



- Molecule 77: 40S ribosomal protein S21



Chain Sc:  78% 12% 9%




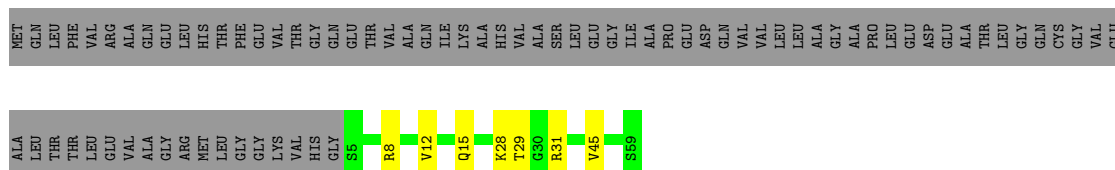
- Molecule 85: 40S ribosomal protein S29

Chain Sd:  88% 7% 5%



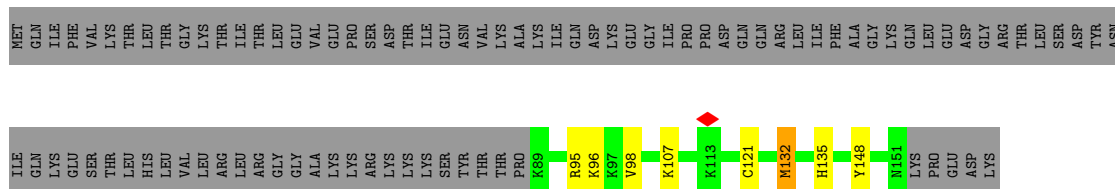
- Molecule 86: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se:  36% 5% 59%




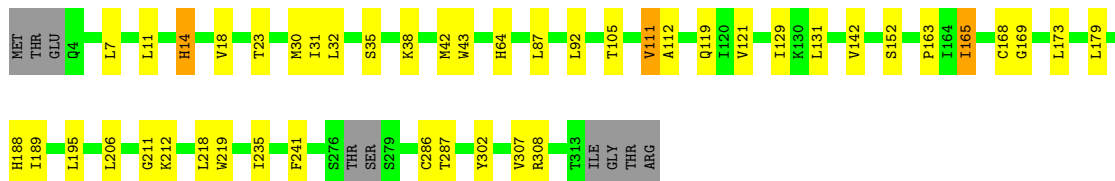
- Molecule 87: Ubiquitin

Chain Sf:  35% 60%



- Molecule 88: Receptor of activated protein C kinase 1

Chain Sg:  83% 13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21642	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.803	Depositor
Minimum map value	-2.734	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.119	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G3D, LYO, 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	CM	0.20	0/273	0.42	0/421
2	CP	0.19	0/1789	0.44	0/2788
3	CR	0.25	0/3311	0.60	5/4452 (0.1%)
4	CZ	0.22	0/1515	0.60	0/2063
5	L5	0.20	0/87471	0.35	1/136443 (0.0%)
6	L7	0.19	0/2858	0.32	0/4455
7	L8	0.19	0/3701	0.33	0/5766
8	LA	0.23	0/1936	0.56	0/2596
9	LB	0.22	0/3251	0.51	0/4352
10	LC	0.20	0/2938	0.47	0/3947
11	LD	0.22	0/2407	0.54	0/3227
12	LE	0.24	0/1788	0.57	1/2399 (0.0%)
13	LF	0.21	0/1905	0.48	0/2539
14	LG	0.21	0/1849	0.52	2/2496 (0.1%)
15	LH	0.23	0/1529	0.54	0/2058
16	LI	0.21	0/1705	0.51	0/2277
17	LJ	0.19	0/1352	0.48	0/1813
18	LL	0.20	0/1661	0.51	0/2229
19	LM	0.20	0/1145	0.46	0/1536
20	LN	0.20	0/1746	0.42	0/2338
21	LO	0.21	0/1665	0.49	0/2229
22	LP	0.21	0/1260	0.49	0/1692
23	LQ	0.20	0/1526	0.46	0/2038
24	LR	0.20	0/1468	0.47	0/1945
25	LS	0.19	0/1492	0.45	0/2003
26	LT	0.21	0/1310	0.54	0/1752
27	LU	0.19	0/820	0.54	0/1102
28	LV	0.21	0/985	0.53	0/1323
29	LW	0.20	0/820	0.47	0/1104
30	LX	0.22	0/998	0.49	0/1341
31	LY	0.21	0/1128	0.47	0/1500
32	LZ	0.20	0/1130	0.44	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.18	0/1183	0.40	0/1582
34	Lb	0.20	0/600	0.47	0/796
35	Lc	0.20	0/752	0.49	0/1011
36	Ld	0.21	0/889	0.49	0/1198
37	Le	0.21	0/1067	0.48	0/1425
38	Lf	0.23	0/891	0.53	0/1194
39	Lg	0.20	0/899	0.48	0/1200
40	Lh	0.17	0/1014	0.41	0/1340
41	Li	0.22	0/824	0.54	0/1093
42	Lj	0.21	0/720	0.50	0/952
43	Lk	0.25	0/548	0.61	0/730
44	Ll	0.22	0/454	0.49	0/599
45	Lm	0.18	0/431	0.46	0/570
46	Ln	0.20	0/231	0.37	0/294
47	Lo	0.18	0/876	0.44	0/1156
48	Lp	0.19	0/706	0.51	0/939
49	Lr	0.23	0/1012	0.50	0/1358
50	Ls	0.24	0/1666	0.62	2/2250 (0.1%)
51	Lt	0.29	0/1224	0.80	4/1651 (0.2%)
52	NA	0.13	0/578	0.38	0/771
53	NB	0.15	0/989	0.40	0/1327
54	NM	0.28	0/3211	0.71	1/4365 (0.0%)
55	S2	0.20	0/40882	0.39	2/63715 (0.0%)
56	SA	0.23	0/1708	0.55	0/2324
57	SB	0.19	0/1745	0.49	0/2337
58	SC	0.21	0/1697	0.48	1/2301 (0.0%)
59	SD	0.21	0/1620	0.52	0/2198
60	SE	0.19	0/2014	0.51	2/2726 (0.1%)
61	SF	0.20	0/1423	0.53	0/1913
62	SG	0.27	0/1657	0.55	0/2247
63	SH	0.21	0/1295	0.47	0/1763
64	SI	0.20	0/1603	0.49	0/2161
65	SJ	0.18	0/1456	0.48	0/1957
66	SK	0.20	0/750	0.49	0/1026
67	SL	0.19	0/1163	0.43	0/1562
68	SM	0.21	0/960	0.59	1/1286 (0.1%)
69	SN	0.21	0/1206	0.49	1/1626 (0.1%)
70	SO	0.22	0/982	0.58	0/1320
71	SP	0.18	0/1010	0.48	0/1362
72	SQ	0.21	0/1093	0.61	0/1470
73	SR	0.21	0/955	0.56	0/1294
74	SS	0.24	0/1148	0.62	0/1542
75	ST	0.19	0/1100	0.44	0/1479

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SU	0.17	0/722	0.45	0/983
77	SV	0.18	0/625	0.42	0/837
78	SW	0.20	0/1043	0.43	0/1396
79	SX	0.22	0/1096	0.56	0/1467
80	SY	0.18	0/944	0.50	0/1271
81	SZ	0.21	0/565	0.54	0/764
82	Sa	0.20	0/794	0.47	0/1065
83	Sb	0.22	0/632	0.51	0/851
84	Sc	0.21	0/474	0.61	0/638
85	Sd	0.17	0/443	0.44	0/589
86	Se	0.18	0/420	0.56	0/554
87	Sf	0.18	0/525	0.52	0/695
88	Sg	0.23	0/2235	0.65	0/3068
All	All	0.20	0/239482	0.43	23/351319 (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
4	CZ	0	1
18	LL	0	1
62	SG	0	2
74	SS	0	1
77	SV	0	1
All	All	0	6

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	S2	1145	A	O4'-C1'-N9	9.02	122.04	108.50
50	Ls	26	LYS	CB-CG-CD	5.92	124.91	111.30
54	NM	169	LEU	CA-CB-CG	5.88	136.90	116.30
14	LG	164	ILE	CA-C-N	5.82	130.84	122.23
14	LG	164	ILE	C-N-CA	5.82	130.84	122.23
12	LE	100	LYS	CB-CG-CD	5.72	124.45	111.30
51	Lt	40	LYS	CA-CB-CG	5.67	125.44	114.10
3	CR	314	MET	CB-CG-SD	5.52	129.27	112.70
68	SM	91	LEU	CA-CB-CG	5.52	135.61	116.30
58	SC	61	MET	CB-CG-SD	5.44	129.02	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CR	397	GLN	CA-CB-CG	5.42	124.94	114.10
69	SN	27	LYS	CB-CG-CD	5.26	123.41	111.30
3	CR	372	MET	CA-CB-CG	5.25	124.59	114.10
5	L5	2117	G	P-O3'-C3'	5.24	128.06	120.20
50	Ls	38	LYS	CA-CB-CG	5.23	124.56	114.10
51	Lt	73	VAL	CA-C-N	-5.21	118.84	122.59
51	Lt	73	VAL	C-N-CA	-5.21	118.84	122.59
60	SE	92	ILE	CA-C-N	5.14	131.36	121.54
60	SE	92	ILE	C-N-CA	5.14	131.36	121.54
3	CR	372	MET	CB-CG-SD	5.12	128.06	112.70
51	Lt	46	ILE	CA-CB-CG1	5.08	119.04	110.40
3	CR	279	LYS	CA-CB-CG	5.07	124.24	114.10
55	S2	688	U	P-O3'-C3'	5.03	127.74	120.20

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CZ	9	ARG	Peptide
18	LL	47	ALA	Peptide
62	SG	140	ARG	Sidechain
62	SG	32	MET	Peptide
74	SS	11	HIS	Peptide
77	SV	71	ARG	Sidechain

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	CM	247	0	128	1	0
2	CP	1602	0	809	3	0
3	CR	3269	0	3312	39	0
4	CZ	1491	0	1365	14	0
5	L5	78199	0	39524	259	0
6	L7	2558	0	1296	9	0
7	L8	3314	0	1683	13	0
8	LA	1898	0	1993	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LB	3183	0	3316	30	0
10	LC	2884	0	3050	19	0
11	LD	2361	0	2378	19	0
12	LE	1754	0	1899	14	0
13	LF	1870	0	1996	15	0
14	LG	1818	0	1911	11	0
15	LH	1510	0	1579	14	0
16	LI	1666	0	1711	9	0
17	LJ	1329	0	1348	10	0
18	LL	1630	0	1715	15	0
19	LM	1122	0	1174	4	0
20	LN	1701	0	1749	13	0
21	LO	1633	0	1771	12	0
22	LP	1234	0	1254	15	0
23	LQ	1502	0	1616	14	0
24	LR	1452	0	1580	8	0
25	LS	1452	0	1490	10	0
26	LT	1282	0	1336	16	0
27	LU	806	0	826	3	0
28	LV	971	0	1024	7	0
29	LW	808	0	726	6	0
30	LX	981	0	1055	8	0
31	LY	1111	0	1194	11	0
32	LZ	1107	0	1182	9	0
33	La	1154	0	1198	10	0
34	Lb	590	0	613	9	0
35	Lc	742	0	774	9	0
36	Ld	874	0	918	12	0
37	Le	1049	0	1136	6	0
38	Lf	872	0	901	5	0
39	Lg	889	0	968	3	0
40	Lh	1006	0	1132	11	0
41	Li	813	0	887	4	0
42	Lj	705	0	737	3	0
43	Lk	542	0	590	7	0
44	Ll	444	0	483	2	0
45	Lm	425	0	462	0	0
46	Ln	230	0	276	0	0
47	Lo	862	0	929	4	0
48	Lp	696	0	744	6	0
49	Lr	997	0	1054	6	0
50	Ls	1640	0	1687	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	Lt	1208	0	1257	21	0
52	NA	573	0	620	6	0
53	NB	980	0	994	5	0
54	NM	3122	0	3103	48	0
55	S2	36562	0	18472	161	0
56	SA	1671	0	1672	16	0
57	SB	1718	0	1786	16	0
58	SC	1661	0	1710	12	0
59	SD	1594	0	1568	17	0
60	SE	1972	0	2012	24	0
61	SF	1403	0	1421	17	0
62	SG	1634	0	1568	14	0
63	SH	1274	0	1196	16	0
64	SI	1574	0	1540	11	0
65	SJ	1431	0	1497	11	0
66	SK	726	0	674	12	0
67	SL	1143	0	1177	8	0
68	SM	950	0	987	17	0
69	SN	1182	0	1249	6	0
70	SO	969	0	982	9	0
71	SP	990	0	974	15	0
72	SQ	1075	0	1110	13	0
73	SR	942	0	913	4	0
74	SS	1130	0	1167	15	0
75	ST	1081	0	1093	11	0
76	SU	713	0	692	6	0
77	SV	618	0	617	2	0
78	SW	1026	0	1072	6	0
79	SX	1078	0	1130	8	0
80	SY	927	0	914	10	0
81	SZ	559	0	594	6	0
82	Sa	781	0	831	9	0
83	Sb	618	0	604	1	0
84	Sc	472	0	484	4	0
85	Sd	433	0	415	3	0
86	Se	416	0	439	4	0
87	Sf	515	0	521	5	0
88	Sg	2180	0	1968	23	0
89	CM	1	0	0	0	0
89	L5	126	0	0	0	0
89	L7	3	0	0	0	0
89	L8	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	LA	1	0	0	0	0
89	LC	1	0	0	0	0
89	LI	1	0	0	0	0
89	LN	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	S2	51	0	0	0	0
89	ST	1	0	0	0	0
90	CZ	32	0	10	0	0
91	Lg	1	0	0	0	0
91	Lj	1	0	0	0	0
91	Lm	1	0	0	0	0
91	Lo	1	0	0	0	0
91	Lp	1	0	0	0	0
91	Sa	1	0	0	0	0
91	Sd	1	0	0	0	0
91	Sf	1	0	0	0	0
92	L5	3	0	0	0	0
92	L7	1	0	0	0	0
92	LI	1	0	0	0	0
92	LN	1	0	0	0	0
92	La	1	0	0	0	0
92	Lp	1	0	0	0	0
92	S2	3	0	0	0	0
All	All	223418	0	165512	1205	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 (1205) 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)
55:S2:1748:G:H1	55:S2:1786:U:H3	1.21	0.85
55:S2:529:A:H61	55:S2:556:U:H3	1.29	0.79
54:NМ:182:GLU:HB3	54:NМ:189:ARG:HH21	1.48	0.79
5:L5:1443:A:N6	5:L5:2103:G:C6	2.51	0.77
54:NМ:278:GLN:HG3	54:NМ:480:ASN:HB3	1.68	0.76
3:CR:328:ILE:HD11	3:CR:345:TYR:HB2	1.67	0.75
5:L5:1465:G:H5'	34:Lb:44:ARG:HH21	1.53	0.73
16:LI:48:LEU:O	16:LI:139:ARG:HA	1.88	0.73
5:L5:1732:C:H5''	26:LT:43:LYS:HD3	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SH:63:PHE:HA	63:SH:95:ILE:O	1.89	0.72
17:LJ:141:ILE:HA	17:LJ:144:LYS:HD3	1.72	0.71
5:L5:4745:G:H1	5:L5:4955:A:H61	1.38	0.70
5:L5:3751:G:H21	5:L5:3775:A:H8	1.38	0.70
54:NM:302:ASN:HA	54:NM:304:ARG:HH11	1.57	0.69
60:SE:185:GLY:H	60:SE:189:LEU:HD13	1.57	0.69
5:L5:2611:A:H5'	5:L5:2688:G:H4'	1.74	0.69
57:SB:152:LYS:HB2	73:SR:131:PRO:HB3	1.74	0.69
55:S2:1098:C:H5	55:S2:1134:G:H1	1.41	0.69
67:SL:80:MET:HE1	67:SL:120:VAL:HG13	1.74	0.69
5:L5:1443:A:H62	5:L5:2104:G:N2	1.91	0.68
5:L5:4618:G:H5''	28:LV:15:ARG:HB2	1.76	0.68
8:LA:117:GLU:HB2	8:LA:162:ASN:HB2	1.76	0.68
5:L5:1443:A:N6	5:L5:2103:G:N1	2.41	0.67
12:LE:278:THR:HG23	12:LE:281:ILE:HD13	1.76	0.67
68:SM:33:ARG:H	68:SM:37:GLU:HB2	1.60	0.67
5:L5:4691:A:H4'	15:LH:71:ARG:HG2	1.77	0.67
7:L8:55:U:H3	7:L8:62:A:H2	1.43	0.67
31:LY:30:MET:HB3	31:LY:101:PRO:HG2	1.76	0.67
48:Lp:6:LYS:HE3	48:Lp:7:LYS:HE2	1.77	0.66
55:S2:433:A:H5''	64:SI:22:HIS:HB3	1.78	0.66
3:CR:286:LEU:HD11	3:CR:390:GLU:HG3	1.77	0.66
5:L5:468:U:H3	5:L5:688:U:H3	1.41	0.66
5:L5:1443:A:N6	5:L5:2104:G:C2	2.63	0.66
59:SD:48:ILE:O	59:SD:86:LEU:HA	1.96	0.65
3:CR:317:VAL:HA	3:CR:413:LEU:HA	1.77	0.65
50:Ls:47:LEU:HD12	50:Ls:51:ALA:HB3	1.79	0.65
71:SP:20:VAL:HG13	71:SP:24:GLN:HG2	1.78	0.65
55:S2:1348:G:H1	55:S2:1381:G:H22	1.44	0.65
17:LJ:95:ARG:O	17:LJ:98:ASN:HB2	1.97	0.64
5:L5:1940:G:H22	5:L5:4434:C:H5''	1.62	0.64
55:S2:1107:G:H1	55:S2:1125:C:H5	1.44	0.64
56:SA:137:ALA:HB1	56:SA:142:LEU:HB3	1.80	0.63
55:S2:165:G:H4'	62:SG:53:SER:HB3	1.80	0.63
51:Lt:11:LYS:HG3	51:Lt:35:LEU:HD11	1.80	0.63
8:LA:120:PRO:HA	8:LA:162:ASN:HB3	1.80	0.63
55:S2:1649:U:H3	55:S2:1675:A:H2	1.46	0.63
57:SB:48:LEU:HB3	70:SO:51:GLU:HG2	1.80	0.63
57:SB:183:GLU:HA	57:SB:186:ASN:HB2	1.80	0.63
55:S2:1308:U:H1'	87:Sf:135:HIS:HE1	1.64	0.62
41:Li:16:LYS:HE2	41:Li:16:LYS:H	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:928:G:H1	55:S2:1013:U:H3	1.47	0.62
3:CR:279:LYS:O	3:CR:283:GLU:HB2	1.99	0.62
8:LA:247:ARG:HD3	55:S2:1069:U:H4'	1.81	0.62
56:SA:66:VAL:HG21	56:SA:185:MET:HB3	1.80	0.62
55:S2:563:G:H1	55:S2:592:C:H5	1.46	0.62
4:CZ:22:MET:HB2	4:CZ:89:ILE:HB	1.81	0.62
5:L5:958:G:H21	12:LE:125:LEU:H	1.48	0.62
36:Ld:36:VAL:HG21	36:Ld:44:ARG:HG2	1.82	0.62
57:SB:179:ASN:HB3	57:SB:183:GLU:HG3	1.82	0.62
26:LT:84:ILE:HD13	34:Lb:23:LYS:HZ3	1.63	0.62
3:CR:318:GLU:HG3	3:CR:319:ILE:HG13	1.81	0.61
35:Lc:37:MET:HG3	35:Lc:97:ILE:HD11	1.80	0.61
55:S2:803:C:H5	55:S2:860:G:H22	1.48	0.61
74:SS:51:ASP:HB3	74:SS:54:LYS:HG3	1.82	0.61
26:LT:48:VAL:HG21	26:LT:94:GLU:HG2	1.82	0.61
31:LY:10:ASP:HB3	31:LY:13:LYS:HB2	1.82	0.61
5:L5:3615:G:H21	29:LW:44:ARG:HD3	1.65	0.61
5:L5:966:A:H5''	5:L5:2092:G:H22	1.66	0.61
22:LP:94:MET:HG2	22:LP:148:MET:HE3	1.82	0.61
51:Lt:61:LYS:HB3	51:Lt:72:GLU:HB2	1.83	0.61
63:SH:79:LEU:O	63:SH:83:LEU:HB2	1.99	0.61
13:LF:28:LEU:HA	13:LF:31:LYS:HG2	1.82	0.61
47:Lo:70:LEU:HD11	47:Lo:83:LEU:HD12	1.83	0.61
70:SO:41:PHE:HA	70:SO:57:THR:HG22	1.83	0.61
51:Lt:11:LYS:HB2	51:Lt:64:ILE:HB	1.82	0.60
70:SO:91:THR:HG22	70:SO:92:ALA:H	1.64	0.60
54:Nm:119:PHE:HB2	54:Nm:258:ARG:HH22	1.66	0.60
1:CM:808:U:H3	2:CP:33:A:H61	1.49	0.60
55:S2:617:G:H4'	79:SX:88:ASP:HB3	1.82	0.60
5:L5:3868:G:H22	5:L5:3900:G:H1'	1.66	0.60
55:S2:1679:A:H2'	61:SF:60:ARG:HD3	1.83	0.60
16:LI:31:ILE:HG22	16:LI:62:SER:HB2	1.84	0.60
74:SS:15:VAL:HB	74:SS:68:ILE:HD11	1.84	0.60
17:LJ:146:ARG:HG2	17:LJ:147:ARG:HG2	1.84	0.60
55:S2:560:A:H5'	65:SJ:174:LYS:HG2	1.84	0.60
11:LD:236:MET:HB3	11:LD:239:MET:HE2	1.84	0.60
24:LR:105:LEU:HD22	24:LR:135:LYS:HG2	1.84	0.60
5:L5:2469:C:H5	5:L5:2471:G:H1	1.50	0.60
13:LF:236:ARG:HB2	13:LF:239:GLN:HB2	1.84	0.60
5:L5:4139:G:H4'	5:L5:4146:G:H22	1.67	0.59
5:L5:1332:C:H2'	5:L5:1333:A:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:1228:A:H2'	55:S2:1229:G:C8	2.37	0.59
88:Sg:30:MET:HE1	88:Sg:92:LEU:HD13	1.83	0.59
55:S2:925:G:H1	55:S2:1017:U:H3	1.50	0.59
60:SE:17:HIS:HB2	60:SE:108:ARG:HA	1.84	0.59
5:L5:5011:A:H62	5:L5:5037:U:H3	1.51	0.59
65:SJ:127:ARG:HD3	86:Se:31:ARG:HD3	1.85	0.59
59:SD:163:PRO:O	59:SD:167:TYR:HB2	2.03	0.59
25:LS:15:ARG:HB3	25:LS:27:LEU:HD23	1.85	0.59
55:S2:1536:G:H2'	55:S2:1537:A:C8	2.38	0.59
56:SA:184:ARG:HD3	56:SA:191:ARG:HD3	1.84	0.59
59:SD:16:ILE:HD11	85:Sd:36:LEU:HD23	1.84	0.59
5:L5:1994:C:H2'	5:L5:1995:G:H8	1.67	0.59
55:S2:851:C:H5''	55:S2:852:G:H5'	1.83	0.59
5:L5:3946:G:H22	5:L5:4067:U:H3	1.51	0.58
76:SU:80:PHE:HB3	85:Sd:52:PHE:HB3	1.84	0.58
5:L5:703:G:H2'	5:L5:704:C:H4'	1.85	0.58
28:LV:43:LYS:HE2	28:LV:62:MET:HE3	1.85	0.58
50:Ls:138:PHE:HB2	50:Ls:143:ILE:HB	1.84	0.58
54:Nm:441:LEU:HA	54:Nm:444:MET:HE1	1.86	0.58
70:SO:101:GLY:HA3	70:SO:134:PRO:HG2	1.86	0.58
68:SM:55:ASN:HB2	68:SM:82:ASN:HB2	1.86	0.58
60:SE:45:ILE:HA	60:SE:61:VAL:HG11	1.85	0.57
8:LA:101:VAL:HG22	8:LA:165:VAL:HG22	1.85	0.57
36:Ld:26:THR:HG23	36:Ld:85:ARG:HH11	1.68	0.57
5:L5:4626:A:H62	5:L5:4669:A:H2	1.51	0.57
63:SH:87:PHE:HB3	63:SH:90:LYS:HZ3	1.70	0.57
5:L5:423:G:H21	22:LP:118:GLN:HE22	1.50	0.57
54:Nm:404:PRO:HA	54:Nm:417:LYS:HA	1.86	0.57
50:Ls:21:LEU:HD11	50:Ls:75:LEU:HD11	1.86	0.57
55:S2:1276:A:H62	55:S2:1321:G:H8	1.53	0.57
5:L5:74:G:H5''	18:LL:59:VAL:HB	1.84	0.57
5:L5:4302:U:H4'	26:LT:5:LYS:HD3	1.85	0.57
5:L5:2411:C:H2'	5:L5:2412:A:H8	1.69	0.56
55:S2:1265:A:H2	55:S2:1517:G:H22	1.52	0.56
70:SO:34:PHE:HB3	70:SO:41:PHE:HB2	1.87	0.56
55:S2:192:C:H41	55:S2:207:G:H21	1.51	0.56
60:SE:80:ILE:HG23	60:SE:81:THR:HG23	1.87	0.56
29:LW:4:GLU:HG3	29:LW:30:GLN:HG3	1.87	0.56
30:LX:82:THR:HG21	40:Lh:37:THR:HG22	1.87	0.56
58:SC:78:LEU:HD12	58:SC:81:ILE:HD11	1.87	0.56
68:SM:54:SER:HB3	68:SM:78:LYS:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:4699:U:H1'	5:L5:4700:A:H5''	1.87	0.56
28:LV:48:ARG:HG3	28:LV:49:LEU:H	1.71	0.56
36:Ld:33:ILE:HG22	36:Ld:44:ARG:HG3	1.88	0.56
8:LA:130:SER:HB2	8:LA:171:GLY:HA3	1.87	0.56
10:LC:159:GLU:HA	10:LC:217:ILE:HB	1.88	0.56
11:LD:62:CYS:HB3	11:LD:105:LEU:HD22	1.88	0.56
4:CZ:21:LEU:HA	4:CZ:64:THR:O	2.05	0.55
56:SA:77:ILE:HB	56:SA:124:VAL:HG12	1.87	0.55
88:Sg:119:GLN:HB3	88:Sg:131:LEU:HD11	1.88	0.55
30:LX:87:MET:HE1	30:LX:156:ILE:HD11	1.88	0.55
87:Sf:121:CYS:HB3	87:Sf:132:MET:HE1	1.86	0.55
5:L5:1942:A:H2'	5:L5:1943:A:C8	2.40	0.55
48:Lp:25:MET:HA	48:Lp:28:LYS:HE3	1.89	0.55
61:SF:140:ASP:HB2	84:Sc:46:VAL:HG22	1.87	0.55
10:LC:221:PHE:HB3	10:LC:227:ILE:HG21	1.88	0.55
17:LJ:90:ARG:HH22	17:LJ:110:GLN:HE22	1.55	0.55
32:LZ:50:PRO:HD3	32:LZ:68:ILE:HG12	1.89	0.55
51:Lt:18:THR:HA	51:Lt:57:ARG:HA	1.88	0.55
55:S2:5:U:H2'	55:S2:6:G:H8	1.72	0.55
57:SB:163:GLN:HB3	57:SB:204:ILE:HD13	1.88	0.55
63:SH:87:PHE:HB3	63:SH:90:LYS:NZ	2.22	0.55
3:CR:38:ILE:HG12	3:CR:94:VAL:HG13	1.89	0.55
5:L5:4258:C:H5'	17:LJ:68:ILE:HD11	1.87	0.55
50:Ls:101:MET:HE3	50:Ls:101:MET:H	1.72	0.55
59:SD:105:LEU:HB2	59:SD:122:VAL:HG21	1.88	0.55
20:LN:15:GLN:HG2	41:Li:52:PRO:HD2	1.89	0.55
17:LJ:35:ARG:HB3	17:LJ:123:ILE:HG23	1.89	0.55
51:Lt:111:ASN:HA	51:Lt:114:ARG:HD2	1.89	0.55
54:Nm:203:PRO:HD2	54:Nm:206:TRP:HB3	1.89	0.55
55:S2:28:U:H2'	55:S2:29:G:H8	1.71	0.55
63:SH:72:PHE:O	63:SH:75:ILE:O	2.24	0.55
55:S2:508:A:H3'	55:S2:509:G:H8	1.71	0.55
88:Sg:30:MET:HE2	88:Sg:42:MET:HE3	1.88	0.55
2:CP:66:C:H2'	2:CP:67:G:H8	1.72	0.54
5:L5:229:G:H5''	31:LY:11:ARG:HG3	1.89	0.54
9:LB:168:MET:HA	9:LB:171:LEU:HD12	1.89	0.54
56:SA:198:MET:HG2	56:SA:200:ASP:H	1.72	0.54
62:SG:88:ARG:HB2	62:SG:91:GLU:HB2	1.88	0.54
26:LT:82:GLY:HA3	34:Lb:16:TRP:HB2	1.88	0.54
28:LV:45:ILE:HG21	28:LV:53:PRO:HB3	1.88	0.54
55:S2:943:U:H2'	55:S2:944:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:NM:228:ALA:HA	54:NM:244:GLU:O	2.07	0.54
80:SY:91:LEU:HB3	80:SY:96:LEU:HD22	1.89	0.54
6:L7:30:C:H5	6:L7:47:G:H1	1.54	0.54
72:SQ:16:LYS:H	72:SQ:19:ALA:HB3	1.72	0.54
5:L5:2411:C:H2'	5:L5:2412:A:C8	2.43	0.54
5:L5:4992:G:H2'	5:L5:4993:G:C8	2.42	0.54
40:Lh:12:LYS:HD2	40:Lh:16:GLU:HG3	1.89	0.54
50:Ls:101:MET:HA	50:Ls:104:ALA:HB3	1.88	0.54
55:S2:803:C:H41	55:S2:860:G:H1	1.56	0.54
55:S2:895:G:H8	55:S2:896:U:H4'	1.72	0.54
55:S2:1204:A:H62	55:S2:1694:U:H3	1.56	0.54
13:LF:105:VAL:HG13	13:LF:136:VAL:HG12	1.89	0.54
54:NM:264:ILE:HA	54:NM:267:ILE:HG22	1.88	0.54
54:NM:319:THR:H	54:NM:322:ARG:HB2	1.73	0.54
35:Lc:48:LEU:HD21	35:Lc:60:ILE:HG21	1.89	0.54
67:SL:58:LYS:HE2	67:SL:59:LYS:HE3	1.89	0.54
75:ST:96:SER:HB3	75:ST:99:VAL:HB	1.89	0.54
25:LS:127:MET:HB3	26:LT:153:PRO:HG2	1.89	0.54
55:S2:1512:C:H5''	85:Sd:8:TRP:HZ3	1.73	0.54
55:S2:176:U:H2'	55:S2:177:G:C8	2.42	0.54
67:SL:93:LEU:HB3	67:SL:102:PHE:HB3	1.90	0.54
5:L5:1176:C:H42	5:L5:1184:A:H61	1.55	0.54
5:L5:3946:G:H21	5:L5:3947:A:H62	1.56	0.54
5:L5:4537:C:H2'	5:L5:4538:G:C8	2.43	0.54
10:LC:152:LEU:HD23	10:LC:251:ILE:HG12	1.89	0.54
20:LN:184:ILE:HG23	20:LN:194:ARG:HH22	1.72	0.54
5:L5:420:A:H61	7:L8:15:G:H1'	1.73	0.53
5:L5:4927:G:H5'	5:L5:4928:C:H5	1.73	0.53
14:LG:223:ARG:HG2	14:LG:227:ASN:HB2	1.90	0.53
55:S2:587:A:H5'	55:S2:592:C:H42	1.72	0.53
63:SH:140:VAL:HG12	69:SN:19:ARG:HD3	1.90	0.53
74:SS:34:LYS:HB3	74:SS:100:ALA:HA	1.89	0.53
88:Sg:14:HIS:CE1	88:Sg:35:SER:HB2	2.43	0.53
5:L5:2337:C:H4'	49:Lr:19:LYS:HB2	1.90	0.53
24:LR:105:LEU:HD23	24:LR:138:LEU:HD23	1.90	0.53
61:SF:73:THR:HG22	61:SF:93:VAL:HG21	1.91	0.53
10:LC:163:LYS:HB2	10:LC:166:GLU:HG2	1.90	0.53
48:Lp:6:LYS:HG2	48:Lp:7:LYS:HG2	1.91	0.53
76:SU:25:THR:HG22	76:SU:86:LYS:HG3	1.90	0.53
9:LB:107:ALA:HB2	9:LB:201:LEU:HG	1.91	0.53
56:SA:45:GLY:HA3	73:SR:126:MET:HE3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SB:150:ILE:HG21	73:SR:128:PHE:HD2	1.74	0.53
60:SE:11:ARG:HE	60:SE:20:LEU:HB3	1.74	0.53
67:SL:75:GLY:HA3	67:SL:88:ILE:HD12	1.91	0.53
50:Ls:26:LYS:HZ1	50:Ls:195:ASN:H	1.57	0.53
57:SB:137:LEU:HG	57:SB:215:VAL:HG22	1.91	0.53
60:SE:180:LEU:HA	60:SE:194:VAL:HA	1.89	0.53
3:CR:362:THR:HG23	3:CR:364:GLN:H	1.74	0.53
5:L5:2745:A:H2'	5:L5:2746:A:C8	2.44	0.53
5:L5:4363:A:H5''	47:Lo:36:GLN:HG2	1.91	0.53
55:S2:1616:U:H3	55:S2:1620:A:H2	1.55	0.53
5:L5:518:G:H1	5:L5:643:C:H2'	1.73	0.52
5:L5:1994:C:H2'	5:L5:1995:G:C8	2.44	0.52
25:LS:80:ILE:HG12	25:LS:129:VAL:HG13	1.90	0.52
52:NA:98:LYS:O	52:NA:102:ILE:HB	2.09	0.52
74:SS:26:ILE:HG13	74:SS:45:LEU:HD21	1.90	0.52
5:L5:46:U:H5''	18:LL:16:LYS:HG3	1.92	0.52
5:L5:1538:U:H2'	5:L5:1539:G:H8	1.74	0.52
56:SA:123:VAL:HG12	56:SA:145:ILE:HB	1.91	0.52
60:SE:105:THR:HG23	60:SE:245:ARG:HA	1.90	0.52
64:SI:174:CYS:HB2	64:SI:190:LEU:HD21	1.92	0.52
75:ST:65:TYR:HB2	75:ST:123:LEU:HD22	1.90	0.52
33:La:72:THR:HG22	33:La:110:LYS:HB3	1.92	0.52
20:LN:103:GLU:HG2	20:LN:115:VAL:HG11	1.91	0.52
55:S2:1521:C:H5'	71:SP:126:VAL:HB	1.92	0.52
66:SK:23:ALA:HB3	66:SK:69:TRP:HZ3	1.73	0.52
5:L5:137:G:H2'	5:L5:138:G:H8	1.73	0.52
11:LD:146:LEU:HD22	11:LD:163:LEU:HD22	1.92	0.52
51:Lt:56:LEU:HD21	51:Lt:82:ILE:HG23	1.92	0.52
8:LA:181:LYS:HB2	8:LA:184:ARG:HG3	1.90	0.52
20:LN:124:ASP:HB3	20:LN:127:TYR:H	1.74	0.52
36:Ld:32:ARG:HB3	36:Ld:48:GLU:HG3	1.92	0.52
80:SY:62:THR:HG23	80:SY:69:THR:HG22	1.92	0.52
88:Sg:195:LEU:HA	88:Sg:211:GLY:HA3	1.90	0.52
9:LB:220:ILE:HG12	9:LB:278:THR:HG23	1.92	0.52
21:LO:61:ARG:HA	21:LO:70:PRO:HD2	1.92	0.52
26:LT:14:MET:HE2	26:LT:58:HIS:HB3	1.92	0.52
70:SO:92:ALA:HB2	70:SO:125:LYS:HB2	1.91	0.52
5:L5:4274:A:H2'	5:L5:4275:G:C8	2.45	0.52
50:Ls:30:VAL:HG11	50:Ls:187:LEU:HD23	1.92	0.52
56:SA:80:ARG:HH21	56:SA:126:ASP:HB2	1.75	0.52
62:SG:7:PHE:HB3	62:SG:12:CYS:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:303:C:H5''	64:SI:75:LYS:HE2	1.91	0.52
55:S2:1531:A:H4'	55:S2:1605:G:H4'	1.91	0.52
5:L5:3717:A:H2'	5:L5:3718:A:C8	2.45	0.51
60:SE:123:LEU:HD11	60:SE:228:ILE:HG22	1.92	0.51
55:S2:940:U:H3	55:S2:1002:U:H3	1.59	0.51
56:SA:89:LYS:HD2	56:SA:201:LEU:HG	1.92	0.51
74:SS:64:VAL:O	74:SS:68:ILE:HD12	2.11	0.51
5:L5:1755:C:H1'	11:LD:2:GLY:HA3	1.91	0.51
55:S2:562:U:H2'	55:S2:563:G:C8	2.44	0.51
55:S2:1550:G:H3'	55:S2:1579:A:H61	1.74	0.51
5:L5:679:C:H2'	5:L5:680:G:H8	1.76	0.51
88:Sg:11:LEU:HB2	88:Sg:307:VAL:HB	1.91	0.51
5:L5:3697:U:H5''	5:L5:3698:G:H5'	1.93	0.51
68:SM:87:GLU:HG3	68:SM:100:PRO:HG3	1.92	0.51
5:L5:2894:A:H62	5:L5:3607:U:H3	1.58	0.51
55:S2:874:G:H2'	55:S2:875:A:H8	1.76	0.51
55:S2:1513:C:H2'	55:S2:1514:G:H8	1.75	0.51
5:L5:1332:C:H2'	5:L5:1333:A:C8	2.46	0.51
5:L5:4627:U:H4'	9:LB:373:LYS:HE2	1.92	0.51
5:L5:4537:C:H2'	5:L5:4538:G:H8	1.75	0.51
50:Ls:28:PHE:HB3	50:Ls:89:VAL:HG12	1.92	0.51
55:S2:1217:A:H2'	55:S2:1218:C:H6	1.76	0.51
71:SP:103:ASN:HB2	71:SP:120:SER:HB2	1.92	0.51
72:SQ:42:ILE:HG22	72:SQ:44:PRO:HD2	1.92	0.51
5:L5:679:C:H2'	5:L5:680:G:C8	2.46	0.51
5:L5:4499:G:C2	5:L5:4529:G:H1'	2.46	0.51
7:L8:141:C:H5''	20:LN:60:VAL:HG11	1.93	0.51
54:NM:152:LEU:HD13	54:NM:157:THR:HA	1.93	0.51
55:S2:639:C:H2'	55:S2:640:A:H8	1.75	0.51
60:SE:31:PRO:HA	60:SE:81:THR:HB	1.93	0.51
5:L5:4910:G:H22	21:LO:107:GLY:HA3	1.76	0.51
26:LT:72:VAL:HG11	26:LT:96:ILE:HD13	1.92	0.51
56:SA:77:ILE:HD13	56:SA:99:ILE:HB	1.93	0.51
61:SF:41:VAL:HG11	61:SF:68:ILE:HG22	1.92	0.51
64:SI:76:THR:HG22	64:SI:108:PRO:HG2	1.92	0.51
68:SM:116:LYS:HG3	68:SM:119:GLN:HE22	1.75	0.51
62:SG:67:VAL:HG12	62:SG:69:THR:HG22	1.93	0.50
72:SQ:134:GLY:HA3	72:SQ:140:ARG:HA	1.92	0.50
79:SX:100:VAL:HG12	79:SX:125:VAL:HA	1.93	0.50
3:CR:218:LYS:HE2	3:CR:218:LYS:H	1.76	0.50
5:L5:4163:U:H5'	5:L5:4164:C:H5''	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lc:47:ILE:HB	35:Lc:94:LEU:HG	1.93	0.50
39:Lg:42:PRO:HB2	39:Lg:53:LEU:HD12	1.93	0.50
55:S2:1692:U:H2'	55:S2:1693:G:C8	2.47	0.50
59:SD:132:LYS:HD3	59:SD:189:MET:HE3	1.93	0.50
28:LV:13:LYS:HB2	28:LV:128:LEU:HD11	1.92	0.50
3:CR:326:LEU:HG	3:CR:328:ILE:HG23	1.93	0.50
5:L5:4745:G:H1	5:L5:4955:A:N6	2.07	0.50
12:LE:190:HIS:HB3	12:LE:193:PHE:HD2	1.76	0.50
55:S2:848:U:H2'	55:S2:849:A:H8	1.77	0.50
55:S2:1536:G:H2'	55:S2:1537:A:H8	1.75	0.50
57:SB:57:ILE:HG22	57:SB:59:SER:H	1.75	0.50
60:SE:72:ILE:HD12	60:SE:82:TYR:HD1	1.76	0.50
5:L5:4128:A:H8	14:LG:35:ARG:H	1.59	0.50
57:SB:198:GLU:HG2	57:SB:210:VAL:HB	1.94	0.50
61:SF:201:LYS:HA	61:SF:204:ARG:HG3	1.94	0.50
4:CZ:121:LEU:O	4:CZ:153:TRP:HA	2.10	0.50
5:L5:2777:G:H5''	5:L5:2778:G:H5'	1.92	0.50
59:SD:109:LEU:HD12	59:SD:184:ILE:HD11	1.92	0.50
20:LN:138:PHE:HA	20:LN:143:ARG:HD2	1.94	0.50
23:LQ:36:ALA:HB1	23:LQ:45:GLN:HG3	1.93	0.50
27:LU:28:PRO:HB2	27:LU:34:MET:HB3	1.93	0.50
54:NM:233:ILE:HG21	54:NM:280:VAL:HG11	1.92	0.50
55:S2:639:C:H2'	55:S2:640:A:C8	2.46	0.50
55:S2:1752:C:H42	55:S2:1781:A:H2	1.60	0.50
59:SD:7:LYS:HD2	76:SU:25:THR:HG21	1.94	0.50
88:Sg:121:VAL:HG21	88:Sg:165:ILE:HG21	1.93	0.50
3:CR:279:LYS:HA	3:CR:282:GLN:HG2	1.94	0.50
5:L5:153:G:H2'	5:L5:154:G:H8	1.76	0.50
5:L5:2745:A:H2'	5:L5:2746:A:H8	1.76	0.50
5:L5:3917:A:H2'	5:L5:3918:G:H8	1.77	0.50
5:L5:5027:C:H42	64:SI:170:LYS:HE2	1.76	0.50
9:LB:283:LYS:HZ1	9:LB:361:GLU:H	1.60	0.50
15:LH:8:GLN:HG2	15:LH:74:CYS:SG	2.52	0.50
54:NM:245:ILE:HB	54:NM:281:TYR:HB3	1.94	0.50
54:NM:301:LEU:HD12	54:NM:443:LYS:HD3	1.93	0.50
55:S2:377:G:H5'	64:SI:98:LYS:HB3	1.94	0.50
63:SH:69:LEU:HD22	63:SH:96:ALA:HB2	1.93	0.50
66:SK:3:MET:HE1	66:SK:48:ALA:HB2	1.93	0.50
4:CZ:89:ILE:HG12	4:CZ:122:LEU:HB3	1.94	0.49
5:L5:4130:C:H41	5:L5:4154:G:H1	1.60	0.49
5:L5:4125:C:H5'	14:LG:45:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:4740:G:O6	5:L5:4959:U:O2	2.30	0.49
9:LB:29:VAL:HA	9:LB:220:ILE:HD13	1.94	0.49
9:LB:367:PHE:HB2	29:LW:1:MET:HE1	1.94	0.49
55:S2:150:A:H2'	55:S2:151:C:C6	2.46	0.49
55:S2:837:A:H61	80:SY:9:THR:H	1.60	0.49
3:CR:18:LYS:HG3	3:CR:19:LYS:HD3	1.94	0.49
5:L5:2487:G:H22	5:L5:2492:C:HI'	1.77	0.49
9:LB:153:MET:HE2	9:LB:194:LEU:HD21	1.92	0.49
54:NM:328:ARG:HH12	54:NM:330:PRO:HD3	1.77	0.49
78:SW:86:LEU:O	78:SW:90:GLN:HG3	2.12	0.49
5:L5:268:G:H2'	5:L5:269:G:H8	1.77	0.49
13:LF:92:VAL:O	13:LF:120:GLY:HA2	2.12	0.49
52:NA:121:ILE:HD11	53:NB:44:LEU:HD11	1.94	0.49
54:NM:403:LEU:HB3	54:NM:420:TYR:CE1	2.47	0.49
3:CR:24:LEU:HD21	3:CR:112:ILE:HD13	1.94	0.49
3:CR:119:PRO:HB2	3:CR:165:THR:HG21	1.94	0.49
16:LI:61:SER:HA	16:LI:126:VAL:HG12	1.93	0.49
36:Ld:40:LYS:O	36:Ld:44:ARG:HB3	2.12	0.49
64:SI:130:THR:HG23	64:SI:132:GLU:H	1.78	0.49
71:SP:92:SER:H	71:SP:107:ILE:HB	1.76	0.49
88:Sg:163:PRO:HG2	88:Sg:179:LEU:HD22	1.95	0.49
5:L5:515:C:H41	5:L5:647:G:H21	1.60	0.49
66:SK:63:ALA:HB2	66:SK:68:TYR:HE1	1.78	0.49
74:SS:78:LYS:HE2	74:SS:78:LYS:HA	1.94	0.49
5:L5:496:G:H2'	5:L5:498:C:H5''	1.93	0.49
5:L5:3720:G:H22	5:L5:3733:A:H2	1.60	0.49
13:LF:59:LYS:O	13:LF:63:GLN:HG2	2.13	0.49
51:Lt:39:PRO:HA	51:Lt:42:VAL:HG22	1.95	0.49
55:S2:1347:U:H2'	55:S2:1348:G:C8	2.48	0.49
63:SH:46:THR:HG21	63:SH:97:GLN:HG3	1.95	0.49
13:LF:91:PHE:HB2	13:LF:145:PRO:HG3	1.95	0.49
30:LX:122:ALA:HB3	30:LX:139:ARG:HG2	1.95	0.49
68:SM:79:VAL:HG11	68:SM:85:LEU:HB2	1.94	0.49
5:L5:300:A:H2'	5:L5:301:G:H8	1.77	0.49
5:L5:943:A:H62	13:LF:151:ASN:HD21	1.59	0.49
12:LE:254:ASP:HA	12:LE:257:ILE:HB	1.95	0.49
5:L5:1501:C:H2'	23:LQ:68:ARG:HH12	1.78	0.49
5:L5:4238:G:H2'	5:L5:4239:A:C8	2.48	0.49
32:LZ:57:MET:HE1	32:LZ:65:ARG:HD3	1.94	0.49
54:NM:388:GLU:HB2	54:NM:394:VAL:HG22	1.95	0.49
54:NM:421:SER:HB3	54:NM:450:PHE:HE1	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:928:G:H2'	55:S2:929:G:C8	2.48	0.49
55:S2:1845:A:H2'	55:S2:1846:G:C8	2.48	0.49
58:SC:104:ASP:HB3	58:SC:130:ILE:HG13	1.95	0.49
81:SZ:68:ILE:HB	81:SZ:109:TYR:HB2	1.94	0.49
5:L5:2520:C:H2'	5:L5:2521:G:H8	1.78	0.48
8:LA:172:GLY:HA3	48:Lp:68:ALA:H	1.78	0.48
55:S2:804:U:H5	55:S2:859:G:H1	1.60	0.48
79:SX:49:GLY:O	79:SX:99:GLU:HA	2.13	0.48
88:Sg:188:HIS:HB3	88:Sg:219:TRP:CH2	2.48	0.48
9:LB:56:ILE:HD13	9:LB:365:LEU:HD22	1.95	0.48
43:Lk:8:ILE:O	43:Lk:12:LEU:HD22	2.13	0.48
54:Nm:287:LEU:HD12	54:Nm:288:PRO:HD2	1.94	0.48
54:Nm:288:PRO:HA	54:Nm:289:LYS:HA	1.63	0.48
55:S2:323:C:H2'	55:S2:327:G:H22	1.78	0.48
88:Sg:31:ILE:HG13	88:Sg:43:TRP:HB2	1.95	0.48
30:LX:156:ILE:HG21	54:Nm:318:MET:HE2	1.95	0.48
35:Lc:38:ILE:HG21	35:Lc:63:TYR:HB3	1.95	0.48
55:S2:981:A:H2'	55:S2:982:G:C8	2.49	0.48
59:SD:150:MET:HE3	59:SD:152:PHE:HZ	1.79	0.48
18:LL:47:ALA:HB1	40:Lh:118:LYS:HE3	1.95	0.48
24:LR:23:TRP:HB3	24:LR:51:ILE:HG13	1.95	0.48
60:SE:229:GLY:HA2	60:SE:235:TRP:CD1	2.48	0.48
68:SM:50:CYS:HB2	68:SM:110:VAL:HG22	1.95	0.48
80:SY:35:VAL:HG23	80:SY:40:ILE:HD11	1.95	0.48
13:LF:216:PRO:HD3	13:LF:247:MET:HE2	1.95	0.48
27:LU:117:ILE:HG23	53:NB:31:LYS:HB3	1.95	0.48
54:Nm:453:LEU:HD12	54:Nm:455:LEU:HD22	1.94	0.48
55:S2:1665:G:H5''	75:ST:89:PRO:HD2	1.94	0.48
29:LW:83:THR:HA	62:SG:131:ARG:HB3	1.95	0.48
55:S2:1017:U:H5'	69:SN:55:ARG:HD3	1.95	0.48
55:S2:1240:A:H5''	71:SP:140:ARG:HH12	1.79	0.48
68:SM:51:VAL:HG22	68:SM:77:ILE:HB	1.95	0.48
5:L5:257:C:H2'	5:L5:258:G:C8	2.48	0.48
31:LY:2:LYS:HB3	31:LY:2:LYS:HE3	1.66	0.48
38:Lf:45:LYS:HD2	38:Lf:105:LEU:HA	1.96	0.48
48:Lp:21:SER:O	48:Lp:25:MET:HG2	2.14	0.48
55:S2:528:A:H2'	55:S2:529:A:C8	2.48	0.48
55:S2:616:A:H5'	86:Se:8:ARG:HG3	1.95	0.48
74:SS:22:GLY:HA2	74:SS:56:ALA:HB3	1.95	0.48
79:SX:57:VAL:HG22	79:SX:67:ARG:HB2	1.95	0.48
88:Sg:112:ALA:HB3	88:Sg:121:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:222:LYS:HB3	13:LF:231:GLY:HA2	1.96	0.48
15:LH:93:ARG:HD2	15:LH:143:GLU:HB2	1.95	0.48
55:S2:28:U:H2'	55:S2:29:G:C8	2.48	0.48
55:S2:640:A:H2'	55:S2:641:A:C8	2.49	0.48
5:L5:1500:A:H5''	5:L5:1501:C:H5'	1.96	0.48
5:L5:2082:G:H5''	23:LQ:12:LYS:HE3	1.96	0.48
22:LP:28:ASN:O	22:LP:32:THR:HG23	2.14	0.48
49:Lr:73:PRO:HA	49:Lr:76:SER:HB2	1.96	0.48
50:Ls:26:LYS:HZ1	50:Ls:195:ASN:N	2.12	0.48
74:SS:116:LYS:HB2	74:SS:116:LYS:HE3	1.62	0.48
5:L5:4093:G:H2'	5:L5:4094:G:C8	2.49	0.48
11:LD:236:MET:HA	11:LD:239:MET:HB3	1.95	0.48
55:S2:5:U:H2'	55:S2:6:G:C8	2.49	0.48
61:SF:74:ASN:HA	61:SF:77:MET:HE3	1.96	0.48
3:CR:199:HIS:CE1	3:CR:241:MET:HE1	2.48	0.47
8:LA:173:GLY:O	8:LA:176:ASP:HB2	2.14	0.47
3:CR:84:LEU:HD13	71:SP:131:PRO:HA	1.95	0.47
5:L5:1463:C:H5''	34:Lb:31:SER:HB2	1.95	0.47
5:L5:1969:G:H4'	50:Ls:36:GLY:HA2	1.95	0.47
5:L5:2493:G:H21	7:L8:126:C:H5''	1.79	0.47
9:LB:220:ILE:HB	9:LB:346:THR:HB	1.96	0.47
25:LS:70:LYS:HA	25:LS:70:LYS:HD3	1.65	0.47
25:LS:147:ASP:HB3	25:LS:150:ILE:HB	1.96	0.47
55:S2:150:A:N6	55:S2:168:C:O2	2.47	0.47
88:Sg:152:SER:H	88:Sg:169:GLY:HA2	1.79	0.47
3:CR:372:MET:HE1	3:CR:377:TRP:HB2	1.96	0.47
5:L5:678:C:H4'	49:Lr:96:MET:HE2	1.95	0.47
5:L5:2335:C:H2'	5:L5:2336:G:H8	1.79	0.47
11:LD:211:LEU:HB3	11:LD:219:TYR:HB2	1.95	0.47
23:LQ:50:ARG:HA	23:LQ:53:MET:HE3	1.96	0.47
55:S2:1304:U:H5''	87:Sf:95:ARG:HG2	1.96	0.47
84:Sc:32:VAL:O	84:Sc:41:SER:HA	2.14	0.47
8:LA:158:ILE:HB	8:LA:162:ASN:HD21	1.78	0.47
12:LE:108:LYS:HE3	12:LE:111:LYS:HA	1.97	0.47
13:LF:127:LYS:HB2	26:LT:133:ALA:HB3	1.97	0.47
60:SE:102:ILE:HG23	60:SE:182:MET:HE1	1.97	0.47
68:SM:86:GLY:HA2	68:SM:106:CYS:HB3	1.97	0.47
88:Sg:7:LEU:HD11	88:Sg:308:ARG:HB3	1.96	0.47
5:L5:3932:U:H2'	5:L5:3933:G:H8	1.79	0.47
22:LP:32:THR:HG22	22:LP:58:VAL:HG21	1.96	0.47
31:LY:47:MET:HE3	31:LY:48:PRO:HD2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Ld:64:ILE:HG23	36:Ld:68:LEU:HD23	1.95	0.47
61:SF:59:LYS:HZ3	61:SF:60:ARG:H	1.62	0.47
63:SH:98:ARG:HB3	63:SH:125:VAL:HG22	1.95	0.47
70:SO:32:HIS:CE1	70:SO:96:LYS:HD3	2.50	0.47
87:Sf:96:LYS:H	87:Sf:96:LYS:HD2	1.80	0.47
5:L5:1503:A:H4'	5:L5:1504:G:H5'	1.97	0.47
5:L5:4239:A:H2'	5:L5:4240:G:C8	2.50	0.47
9:LB:92:TYR:HB2	9:LB:159:VAL:HG13	1.96	0.47
10:LC:218:ILE:O	10:LC:222:ARG:HG3	2.15	0.47
54:Nm:406:THR:HG22	54:Nm:415[B]:SER:HB2	1.96	0.47
69:SN:19:ARG:HH21	83:Sb:84:HIS:HD2	1.62	0.47
5:L5:262:G:H2'	5:L5:263:G:H8	1.78	0.47
5:L5:2520:C:H2'	5:L5:2521:G:C8	2.50	0.47
7:L8:19:C:H2'	7:L8:20:A:C8	2.49	0.47
36:Ld:51:LYS:HB2	36:Ld:51:LYS:HE3	1.73	0.47
58:SC:259:THR:HG21	77:SV:16:LYS:H	1.80	0.47
68:SM:62:VAL:HA	68:SM:65:VAL:HG12	1.97	0.47
69:SN:93:LYS:HA	69:SN:150:VAL:HG21	1.97	0.47
71:SP:56:LEU:HD23	71:SP:83:MET:HG2	1.97	0.47
75:ST:116:ASP:HB3	75:ST:122:LYS:HE3	1.96	0.47
5:L5:512:U:H2'	5:L5:513:U:H4'	1.97	0.47
5:L5:1558:A:H2'	5:L5:1559:G:C8	2.50	0.47
5:L5:1308:C:H2'	5:L5:1309:C:C6	2.50	0.47
5:L5:3932:U:H2'	5:L5:3933:G:C8	2.50	0.47
11:LD:278:ASP:O	11:LD:282:GLN:HG3	2.15	0.47
44:Ll:34:LYS:HB2	44:Ll:34:LYS:HE3	1.65	0.47
56:SA:158:ASP:HB3	77:SV:69:ILE:HD12	1.96	0.47
15:LH:10:VAL:HG22	15:LH:55:LEU:HB3	1.97	0.47
55:S2:150:A:N6	55:S2:168:C:C2	2.83	0.47
64:SI:87:ASN:HB3	64:SI:90:LEU:HG	1.96	0.47
4:CZ:128:GLN:HG3	4:CZ:157:ALA:HB1	1.95	0.46
25:LS:15:ARG:HD2	25:LS:25:PRO:HG2	1.96	0.46
55:S2:1281:G:H3'	55:S2:1282:A:H8	1.79	0.46
22:LP:96:LYS:HB3	22:LP:96:LYS:HE2	1.74	0.46
40:Lh:6:ALA:O	40:Lh:10:ARG:HG2	2.15	0.46
41:Li:76:ARG:HA	41:Li:76:ARG:HD2	1.81	0.46
55:S2:4:C:H4'	58:SC:207:ALA:HB2	1.95	0.46
55:S2:491:C:H5''	80:SY:104:ARG:HG3	1.97	0.46
55:S2:1010:G:H2'	55:S2:1011:A:C8	2.50	0.46
55:S2:1748:G:O6	55:S2:1786:U:O4	2.33	0.46
75:ST:42:HIS:HB2	75:ST:83:GLN:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:ST:111:LYS:HB2	75:ST:111:LYS:HE2	1.65	0.46
80:SY:83:LYS:HE3	80:SY:96:LEU:HD11	1.97	0.46
82:Sa:53:ILE:HD11	82:Sa:64:LEU:HD11	1.97	0.46
5:L5:86:U:H2'	5:L5:87:A:H8	1.81	0.46
26:LT:78:LYS:HB3	26:LT:87:LYS:HG3	1.97	0.46
32:LZ:115:LYS:O	32:LZ:119:GLU:HG3	2.15	0.46
55:S2:150:A:H2'	55:S2:151:C:H6	1.81	0.46
3:CR:34:MET:HG3	3:CR:129:ASN:HA	1.96	0.46
3:CR:291:PHE:HZ	3:CR:402:PHE:HB2	1.81	0.46
5:L5:86:U:H2'	5:L5:87:A:C8	2.50	0.46
5:L5:2764:A:H2'	5:L5:2765:A:H8	1.81	0.46
5:L5:2838:G:H5'	9:LB:247:GLY:HA2	1.97	0.46
10:LC:301:ALA:HB1	23:LQ:132:LYS:HD3	1.98	0.46
40:Lh:26:VAL:O	40:Lh:30:GLN:HG3	2.15	0.46
55:S2:1189:A:H4'	79:SX:34:THR:HG21	1.97	0.46
5:L5:2708:U:H4'	5:L5:2709:C:H5''	1.97	0.46
8:LA:5:ILE:HG12	8:LA:8:GLN:HB2	1.97	0.46
11:LD:60:ILE:HD11	11:LD:93:THR:HA	1.98	0.46
50:Ls:43:ILE:O	50:Ls:47:LEU:HB2	2.16	0.46
51:Lt:129:ILE:O	51:Lt:133:LEU:HD12	2.15	0.46
51:Lt:136:ALA:HA	51:Lt:139:VAL:HG22	1.98	0.46
55:S2:1396:A:H4'	55:S2:1396:A:OP1	2.14	0.46
72:SQ:89:SER:HB3	72:SQ:112:LEU:HD13	1.98	0.46
82:Sa:24:THR:HG21	82:Sa:71:LEU:HA	1.97	0.46
84:Sc:18:LEU:HD11	84:Sc:43:ILE:HD12	1.96	0.46
3:CR:28:ARG:HE	3:CR:28:ARG:HB2	1.58	0.46
14:LG:138:ALA:HB2	14:LG:194:VAL:HG11	1.98	0.46
23:LQ:81:VAL:HG22	23:LQ:101:CYS:HB3	1.96	0.46
33:La:43:ILE:O	33:La:47:LYS:HB2	2.15	0.46
54:NM:406:THR:HG22	54:NM:415[A]:SER:HB3	1.97	0.46
55:S2:996:A:H2'	55:S2:997:A:C8	2.51	0.46
14:LG:187:LYS:HG3	14:LG:198:THR:HA	1.98	0.46
15:LH:53:LYS:HA	15:LH:53:LYS:HD3	1.72	0.46
21:LO:47:PHE:HZ	21:LO:144:GLU:HG3	1.81	0.46
36:Ld:105:LEU:HG	36:Ld:107:THR:HG23	1.97	0.46
63:SH:139:ILE:HG23	63:SH:156:VAL:HG13	1.96	0.46
81:SZ:65:TYR:HB2	81:SZ:68:ILE:HG12	1.98	0.46
88:Sg:168:CYS:HB2	88:Sg:195:LEU:HG	1.98	0.46
5:L5:318:A:H2'	5:L5:319:A:C8	2.51	0.46
5:L5:3610:A:H2'	5:L5:3611:A:C8	2.51	0.46
9:LB:149:ASP:O	9:LB:153:MET:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LC:71:ARG:HB2	10:LC:73:VAL:HG22	1.96	0.46
14:LG:213:GLY:O	14:LG:217:LYS:HG3	2.15	0.46
30:LX:82:THR:HB	54:NM:317:ASN:HD21	1.80	0.46
43:Lk:24:LYS:HD2	43:Lk:69:LEU:HD21	1.96	0.46
51:Lt:13:VAL:HB	51:Lt:62:LEU:HB2	1.98	0.46
55:S2:145:G:H2'	55:S2:146:G:C8	2.51	0.46
55:S2:1499:U:H4'	59:SD:176:LEU:HD13	1.98	0.46
61:SF:34:SER:HA	84:Sc:55:VAL:HB	1.97	0.46
5:L5:267:G:H4'	40:Lh:113:LEU:HD11	1.97	0.46
5:L5:662:C:H2'	5:L5:663:G:C8	2.51	0.46
6:L7:117:G:H5'	11:LD:256:LYS:HE3	1.97	0.46
20:LN:178:HIS:HA	20:LN:181:HIS:CE1	2.50	0.46
21:LO:126:VAL:HG13	21:LO:127:VAL:HG13	1.98	0.46
55:S2:1395:C:H1'	55:S2:1474:A:C4	2.51	0.46
74:SS:20:ILE:HD11	74:SS:33:ILE:HD11	1.98	0.46
5:L5:2765:A:H2'	5:L5:2766:A:C8	2.51	0.46
11:LD:89:LYS:HE3	11:LD:89:LYS:HB3	1.76	0.46
20:LN:53:TYR:HB2	20:LN:133:ILE:HG21	1.98	0.46
33:La:79:TRP:CE3	33:La:87:ARG:HG3	2.51	0.46
48:Lp:3:LYS:HB2	48:Lp:3:LYS:HE3	1.77	0.46
54:NM:163:LEU:HD11	54:NM:202:ARG:HG3	1.98	0.46
64:SI:119:LEU:HD23	64:SI:119:LEU:HA	1.86	0.46
5:L5:1553:A:N6	5:L5:1574:G:H1'	2.31	0.45
5:L5:1558:A:H2'	5:L5:1559:G:H8	1.80	0.45
9:LB:14:LEU:HD22	9:LB:17:LEU:HD11	1.98	0.45
12:LE:164:PHE:HA	12:LE:175:VAL:HG23	1.97	0.45
24:LR:135:LYS:O	24:LR:139:MET:HG3	2.15	0.45
63:SH:145:ARG:HA	63:SH:145:ARG:HD3	1.78	0.45
70:SO:28:PHE:HA	70:SO:92:ALA:O	2.16	0.45
76:SU:61:LEU:HD22	76:SU:82:MET:HG2	1.98	0.45
5:L5:4935:C:H2'	5:L5:4936:G:C8	2.51	0.45
15:LH:140:GLN:HB3	15:LH:143:GLU:HB3	1.98	0.45
66:SK:49:MET:HG2	66:SK:69:TRP:CG	2.51	0.45
71:SP:34:MET:HB3	71:SP:42:ARG:HG3	1.99	0.45
5:L5:4457:U:H1'	9:LB:252:ALA:HB3	1.99	0.45
5:L5:4621:C:OP1	28:LV:48:ARG:HD2	2.15	0.45
6:L7:119:U:H2'	11:LD:261:VAL:HG11	1.98	0.45
11:LD:41:LYS:HA	11:LD:41:LYS:HD3	1.77	0.45
17:LJ:56:THR:HG23	17:LJ:63:ARG:HA	1.98	0.45
51:Lt:94:LYS:NZ	51:Lt:95:GLN:HE21	2.14	0.45
55:S2:527:C:H2'	55:S2:528:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:1743:G:H21	55:S2:1791:A:H62	1.65	0.45
65:SJ:3:VAL:HG11	65:SJ:5:ARG:HH21	1.81	0.45
3:CR:203:ARG:HB2	3:CR:241:MET:HE2	1.99	0.45
4:CZ:107:LEU:HB3	4:CZ:108:MET:HE2	1.98	0.45
4:CZ:212:CYS:HB2	4:CZ:213:LYS:HD2	1.99	0.45
5:L5:1333:A:H2'	5:L5:1334:A:C8	2.51	0.45
14:LG:106:THR:HG22	14:LG:195:HIS:CD2	2.51	0.45
16:LI:76:MET:HE2	16:LI:138:ILE:HG21	1.97	0.45
29:LW:34:ALA:HA	29:LW:37:GLU:HB3	1.98	0.45
35:Lc:21:VAL:HG11	35:Lc:96:ILE:HD12	1.98	0.45
55:S2:1745:A:H1'	62:SG:66:GLY:HA2	1.98	0.45
55:S2:1860:A:H3'	82:Sa:8:ASN:HB3	1.98	0.45
62:SG:132:ARG:HD2	62:SG:132:ARG:HA	1.70	0.45
62:SG:159:ARG:HH11	62:SG:173:ALA:HB2	1.80	0.45
66:SK:20:VAL:HA	66:SK:69:TRP:O	2.16	0.45
3:CR:298:THR:HG23	3:CR:300:LYS:HE2	1.97	0.45
5:L5:184:U:H1'	5:L5:254:G:H22	1.81	0.45
21:LO:130:LYS:HB2	21:LO:133:ARG:HG2	1.97	0.45
22:LP:27:LYS:HG2	22:LP:63:TYR:CG	2.52	0.45
25:LS:30:MET:HE2	25:LS:30:MET:HB3	1.80	0.45
51:Lt:92:ARG:HD2	51:Lt:92:ARG:HA	1.79	0.45
55:S2:948:C:H2'	55:S2:949:G:H8	1.82	0.45
55:S2:1562:C:H2'	55:S2:1563:G:H8	1.81	0.45
71:SP:83:MET:HE3	71:SP:84:ILE:H	1.82	0.45
5:L5:1852:U:H5''	33:La:22:ILE:HD12	1.98	0.45
5:L5:3664:G:H2'	5:L5:3665:G:H8	1.81	0.45
10:LC:40:VAL:HG22	10:LC:115:VAL:HG11	1.99	0.45
18:LL:18:TRP:CD1	18:LL:18:TRP:H	2.35	0.45
18:LL:106:SER:HB3	18:LL:109:SER:HG	1.81	0.45
32:LZ:41:ALA:HB2	32:LZ:77:TYR:HE1	1.82	0.45
51:Lt:78:SER:O	51:Lt:82:ILE:HG22	2.16	0.45
54:Nm:357:LEU:HB3	54:Nm:363:THR:HB	1.99	0.45
55:S2:527:C:H4'	65:SJ:121:LYS:HD2	1.98	0.45
57:SB:85:LYS:HD3	57:SB:85:LYS:HA	1.86	0.45
63:SH:154:ILE:O	63:SH:185:VAL:HA	2.16	0.45
71:SP:85:ILE:HA	71:SP:89:MET:HE2	1.99	0.45
5:L5:1933:G:H2'	5:L5:1934:A:C8	2.52	0.45
5:L5:4260:U:H2'	5:L5:4261:C:C6	2.52	0.45
5:L5:4347:G:H2'	5:L5:4348:A:C8	2.52	0.45
22:LP:8:PRO:HD3	22:LP:149:ILE:HD13	1.99	0.45
22:LP:21:ASN:HD22	22:LP:123:PRO:HD2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LY:85:VAL:HG12	31:LY:97:VAL:HB	1.99	0.45
55:S2:107:A:H2'	55:S2:108:G:C8	2.52	0.45
55:S2:1285:G:H5'	68:SM:35:ILE:HG23	1.97	0.45
65:SJ:131:ARG:HD2	65:SJ:131:ARG:HA	1.82	0.45
80:SY:104:ARG:O	80:SY:108:LYS:HG3	2.17	0.45
5:L5:1382:G:H2'	5:L5:1383:G:H8	1.82	0.45
50:Ls:125:ALA:HA	50:Ls:154:ILE:HG23	1.99	0.45
54:NM:461:PHE:HB2	54:NM:465:LEU:HD23	1.99	0.45
55:S2:1705:C:H2'	55:S2:1706:G:C8	2.52	0.45
56:SA:123:VAL:HA	56:SA:145:ILE:O	2.17	0.45
5:L5:513:U:H3'	5:L5:514:U:H4'	1.99	0.45
5:L5:4174:U:H2'	5:L5:4175:G:H8	1.82	0.45
10:LC:328:LEU:HD13	13:LF:187:MET:HE2	1.99	0.45
12:LE:165:LEU:HD11	12:LE:176:THR:HG22	1.99	0.45
20:LN:120:TRP:HZ2	20:LN:123:GLU:HB2	1.82	0.45
20:LN:140:LYS:HD3	20:LN:140:LYS:HA	1.76	0.45
23:LQ:22:ASP:O	23:LQ:26:ARG:HG2	2.17	0.45
32:LZ:60:LYS:HE2	32:LZ:60:LYS:HB2	1.77	0.45
55:S2:455:A:H2'	55:S2:456:C:H6	1.82	0.45
58:SC:187:ARG:HE	58:SC:187:ARG:HB3	1.61	0.45
4:CZ:158:THR:HG22	4:CZ:165:GLY:HA3	1.98	0.45
5:L5:10:A:H2'	5:L5:11:G:C8	2.52	0.45
5:L5:325:U:H2'	5:L5:326:C:C6	2.52	0.45
5:L5:462:G:H2'	5:L5:463:A:C8	2.52	0.45
5:L5:4274:A:H2'	5:L5:4275:G:H8	1.82	0.45
11:LD:80:ALA:HA	11:LD:83:LEU:HG	1.99	0.45
14:LG:175:ARG:HG3	14:LG:230:TYR:CG	2.52	0.45
15:LH:12:ILE:HB	15:LH:53:LYS:O	2.17	0.45
26:LT:11:THR:HA	26:LT:14:MET:HB3	1.99	0.45
37:Le:64:LYS:HB2	37:Le:64:LYS:HE2	1.78	0.45
50:Ls:20:LEU:HD12	50:Ls:20:LEU:HA	1.88	0.45
51:Lt:49:ALA:HB1	51:Lt:71:ILE:HD13	1.98	0.45
56:SA:34:MET:HE3	56:SA:34:MET:HB3	1.80	0.45
56:SA:183:LEU:HB3	56:SA:189:ILE:HG12	1.99	0.45
64:SI:117:TYR:HD1	64:SI:152:ARG:HB3	1.81	0.45
80:SY:27:VAL:HG21	80:SY:35:VAL:HG21	1.98	0.45
3:CR:42:LYS:HB2	3:CR:42:LYS:HE2	1.78	0.44
5:L5:452:A:H4'	5:L5:453:G:H5'	1.98	0.44
5:L5:717:U:H2'	5:L5:718:C:C6	2.52	0.44
5:L5:1344:C:H1'	18:LL:10:LEU:HD11	1.99	0.44
5:L5:4238:G:H2'	5:L5:4239:A:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LD:223:PHE:HB3	11:LD:226:TYR:HB2	1.99	0.44
19:LM:86:TRP:CE2	19:LM:92:ALA:HB2	2.52	0.44
21:LO:194:GLU:O	21:LO:198:THR:HG23	2.17	0.44
59:SD:8:LYS:H	59:SD:8:LYS:HG3	1.58	0.44
64:SI:106:SER:O	64:SI:110:ARG:HB2	2.17	0.44
67:SL:111:VAL:HG12	67:SL:140:PHE:HB2	1.99	0.44
75:ST:56:ARG:HG3	75:ST:103:VAL:HG21	1.97	0.44
88:Sg:38:LYS:HG2	88:Sg:64:HIS:N	2.32	0.44
5:L5:57:G:H5''	20:LN:154:PRO:HB2	2.00	0.44
5:L5:1971:C:H5	5:L5:2000:G:H2'	1.83	0.44
5:L5:4188:U:H2'	5:L5:4189:U:C6	2.52	0.44
9:LB:29:VAL:HG12	9:LB:31:SER:H	1.82	0.44
22:LP:21:ASN:ND2	22:LP:123:PRO:HD2	2.32	0.44
31:LY:30:MET:HE2	31:LY:49:ILE:HD11	1.99	0.44
55:S2:1217:A:H2'	55:S2:1218:C:C6	2.52	0.44
67:SL:79:LYS:HE3	67:SL:79:LYS:HB2	1.75	0.44
3:CR:285:LYS:HA	3:CR:285:LYS:HD3	1.79	0.44
5:L5:1307:A:H2'	5:L5:1308:C:C6	2.53	0.44
12:LE:114:ARG:HH21	49:Lr:87:ARG:HH22	1.65	0.44
37:Le:89:LEU:HD23	37:Le:90:MET:HG2	1.99	0.44
44:Ll:23:ILE:HD12	44:Ll:27:ILE:HD11	2.00	0.44
50:Ls:50:LYS:HB2	50:Ls:93:GLU:HG3	1.99	0.44
54:Nm:426:HIS:CD2	54:Nm:434:LEU:HD21	2.52	0.44
55:S2:530:U:H2'	55:S2:531:A:H8	1.83	0.44
3:CR:17:ILE:O	3:CR:21:ILE:HG12	2.17	0.44
5:L5:959:G:C5	12:LE:123:ARG:HG3	2.53	0.44
5:L5:1508:A:H5''	10:LC:113:ARG:HD2	2.00	0.44
5:L5:1604:G:H2'	5:L5:1605:G:C8	2.53	0.44
5:L5:1662:C:H2'	5:L5:1663:C:C6	2.53	0.44
5:L5:4128:A:H2	5:L5:4156:G:H21	1.66	0.44
5:L5:4967:A:H2'	5:L5:4968:A:C8	2.53	0.44
34:Lb:56:LYS:H	34:Lb:56:LYS:HG2	1.59	0.44
47:Lo:22:LYS:HE3	47:Lo:73:VAL:HG12	1.98	0.44
55:S2:943:U:H2'	55:S2:944:A:C8	2.52	0.44
58:SC:191:VAL:HG11	58:SC:236:PHE:HA	1.98	0.44
59:SD:123:LEU:HD22	59:SD:134:CYS:SG	2.57	0.44
4:CZ:104:ARG:HG3	4:CZ:143:LEU:HA	1.99	0.44
5:L5:1298:C:H2'	5:L5:1299:G:H8	1.81	0.44
7:L8:47:C:H1'	7:L8:61:A:H2'	2.00	0.44
8:LA:54:ARG:HG2	8:LA:56:ALA:H	1.82	0.44
8:LA:119:LYS:HD3	8:LA:120:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LG:80:ILE:HD11	20:LN:18:VAL:HG23	1.99	0.44
25:LS:136:LYS:HE3	25:LS:136:LYS:HB2	1.91	0.44
54:NM:329:LEU:HD13	54:NM:330:PRO:HD2	1.99	0.44
58:SC:61:MET:HE3	58:SC:61:MET:HA	1.99	0.44
60:SE:137:PRO:HB2	60:SE:150:PRO:HD2	2.00	0.44
63:SH:58:LYS:HZ3	63:SH:90:LYS:HD3	1.83	0.44
65:SJ:47:LYS:HG2	65:SJ:102:ILE:HD12	2.00	0.44
68:SM:121:LYS:HE2	68:SM:121:LYS:HB2	1.79	0.44
5:L5:1849:U:H3'	18:LL:5:ARG:HH21	1.83	0.44
5:L5:4685:U:H2'	5:L5:4686:G:C8	2.53	0.44
6:L7:27:G:H2'	6:L7:28:C:H6	1.83	0.44
9:LB:52:GLY:HA2	9:LB:341:LYS:HE3	1.99	0.44
11:LD:48:LYS:HD2	11:LD:145:TYR:HE2	1.83	0.44
16:LI:38:ARG:HG2	16:LI:41:ALA:HB2	2.00	0.44
31:LY:111:LEU:HD12	31:LY:116:LYS:HG3	1.99	0.44
52:NA:95:THR:HB	52:NA:103:LEU:HD11	1.98	0.44
55:S2:16:G:H2'	55:S2:17:C:C6	2.52	0.44
60:SE:182:MET:HE2	60:SE:190:GLY:HA2	1.98	0.44
80:SY:37:LYS:HD2	80:SY:57:VAL:HG23	1.98	0.44
5:L5:258:G:H2'	5:L5:259:C:C6	2.53	0.44
5:L5:2568:C:H2'	5:L5:2569:G:H8	1.81	0.44
5:L5:4309:G:H5'	5:L5:4338:G:H5''	2.00	0.44
22:LP:54:GLN:HA	22:LP:83:TRP:CD1	2.53	0.44
30:LX:39:LYS:HB2	30:LX:39:LYS:HE2	1.73	0.44
55:S2:1597:C:H4'	55:S2:1603:G:C6	2.53	0.44
60:SE:79:ASP:HB3	60:SE:82:TYR:HB2	2.00	0.44
71:SP:75:VAL:HG23	71:SP:93:MET:HB3	1.99	0.44
82:Sa:12:LYS:HG3	82:Sa:15:ARG:HB2	2.00	0.44
3:CR:99:THR:HG22	3:CR:109:LYS:HD2	2.00	0.44
5:L5:4760:G:H4'	21:LO:161:LYS:HG2	2.00	0.44
13:LF:241:ASN:O	13:LF:245:ARG:HG2	2.18	0.44
39:Lg:9:ARG:HD2	39:Lg:34:TYR:CZ	2.53	0.44
53:NB:106:ILE:HD12	53:NB:106:ILE:HA	1.90	0.44
54:NM:386:VAL:HG12	54:NM:397:PHE:HB3	1.99	0.44
55:S2:1183:A:H2'	55:S2:1184:G:H8	1.82	0.44
57:SB:225:LEU:O	57:SB:229:MET:HG2	2.18	0.44
60:SE:52:LEU:HD21	60:SE:111:VAL:HG21	1.98	0.44
60:SE:125:LYS:HG2	60:SE:142:HIS:HB3	2.00	0.44
5:L5:1298:C:H2'	5:L5:1299:G:C8	2.53	0.44
5:L5:4954:G:H2'	5:L5:4955:A:C8	2.53	0.44
9:LB:63:PRO:HD2	9:LB:357:ARG:HH12	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LZ:89:ILE:HG22	32:LZ:91:LEU:HG	2.00	0.44
37:Le:106:LYS:HB3	37:Le:106:LYS:HE2	1.81	0.44
38:Lf:50:VAL:HG22	38:Lf:69:VAL:HG22	2.00	0.44
55:S2:186:C:H2'	55:S2:187:G:H8	1.83	0.44
58:SC:66:LEU:HD11	58:SC:81:ILE:HG21	1.99	0.44
62:SG:218:LYS:HB3	62:SG:218:LYS:HZ2	1.83	0.44
5:L5:4736:C:H2'	5:L5:4737:G:H8	1.83	0.43
10:LC:60:HIS:HA	10:LC:92:PHE:HE1	1.83	0.43
17:LJ:74:VAL:HG23	17:LJ:79:ALA:HB2	2.00	0.43
23:LQ:63:LEU:HD12	23:LQ:66:MET:HE2	2.00	0.43
33:La:100:ILE:HG13	33:La:123:ILE:HB	2.00	0.43
55:S2:12:U:H2'	55:S2:13:C:C6	2.52	0.43
55:S2:609:U:H2'	55:S2:610:G:H8	1.83	0.43
66:SK:27:VAL:HG13	66:SK:43:LEU:HD13	2.00	0.43
81:SZ:78:LYS:HD3	81:SZ:78:LYS:HA	1.81	0.43
3:CR:14:ILE:HG12	3:CR:117:PHE:CG	2.53	0.43
5:L5:1392:A:H2'	5:L5:1393:G:C8	2.53	0.43
5:L5:4694:G:H4'	15:LH:71:ARG:HH12	1.83	0.43
35:Lc:38:ILE:HD11	35:Lc:46:VAL:HG21	2.00	0.43
42:Lj:48:ASN:HA	42:Lj:54:LYS:HE2	2.00	0.43
51:Lt:7:PRO:HB2	51:Lt:66:ASN:HA	1.99	0.43
51:Lt:149:HIS:HA	51:Lt:152:ILE:HG13	2.00	0.43
54:NM:339:ARG:HH22	54:NM:388:GLU:HB3	1.83	0.43
60:SE:175:PHE:HE1	60:SE:225:ILE:HG21	1.84	0.43
61:SF:69:VAL:O	61:SF:73:THR:HG23	2.17	0.43
5:L5:1590:C:H4'	5:L5:2857:A:H5'	1.99	0.43
5:L5:2362:U:H2'	5:L5:2363:A:H8	1.82	0.43
5:L5:4389:C:H2'	5:L5:4390:A:C8	2.53	0.43
6:L7:4:U:H2'	6:L7:5:A:C8	2.53	0.43
36:Ld:50:ARG:HG2	36:Ld:64:ILE:HD11	2.00	0.43
38:Lf:102:ARG:HB2	38:Lf:104:MET:HE2	1.99	0.43
55:S2:1736:G:H2'	55:S2:1737:G:H8	1.83	0.43
66:SK:3:MET:HG2	66:SK:8:ARG:HH21	1.83	0.43
72:SQ:14:GLY:HA2	72:SQ:86:GLN:HE21	1.84	0.43
3:CR:106:LYS:HA	3:CR:106:LYS:HD3	1.74	0.43
5:L5:1824:G:H5''	26:LT:35:LYS:HD3	1.99	0.43
5:L5:2554:U:O2	5:L5:2764:A:N7	2.51	0.43
5:L5:3612:C:H1'	5:L5:5016:A:C8	2.54	0.43
5:L5:3717:A:H2'	5:L5:3718:A:H8	1.83	0.43
20:LN:84:PRO:HA	20:LN:87:HIS:CG	2.53	0.43
30:LX:76:ILE:HG22	30:LX:77:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LY:50:ARG:HB2	31:LY:115:ARG:HH12	1.84	0.43
51:Lt:42:VAL:O	51:Lt:46:ILE:HG13	2.18	0.43
55:S2:106:C:H2'	55:S2:107:A:H8	1.83	0.43
55:S2:1839:U:H2'	55:S2:1840:U:C6	2.54	0.43
60:SE:36:HIS:CG	60:SE:85:GLY:HA3	2.53	0.43
79:SX:54:LYS:HE3	79:SX:91:LEU:HG	1.98	0.43
5:L5:1199:G:H2'	5:L5:1200:G:C8	2.54	0.43
8:LA:118:GLU:HB2	8:LA:126:LEU:HD21	2.00	0.43
9:LB:286:LYS:HE3	9:LB:286:LYS:HB2	1.81	0.43
12:LE:149:ILE:HD12	12:LE:271:LEU:HD21	2.01	0.43
12:LE:183:ARG:HA	12:LE:183:ARG:HD2	1.83	0.43
21:LO:34:VAL:HG22	21:LO:103:LYS:HB2	2.00	0.43
52:NA:80:MET:HE3	53:NB:51:LEU:HD11	2.01	0.43
53:NB:64:MET:HB2	53:NB:72:ILE:HB	2.01	0.43
54:NM:240:LYS:HG3	54:NM:242:MET:SD	2.58	0.43
61:SF:41:VAL:HA	61:SF:45:TYR:HB2	2.01	0.43
61:SF:86:LYS:O	61:SF:90:VAL:HG13	2.18	0.43
66:SK:1:MET:HG2	66:SK:3:MET:HB3	2.00	0.43
75:ST:85:ASN:HB2	75:ST:88:MET:HB2	2.00	0.43
5:L5:1397:A:C8	33:La:114:LYS:HD2	2.54	0.43
5:L5:1857:C:H2'	5:L5:1858:A:H8	1.82	0.43
5:L5:1914:C:H4'	21:LO:89:PRO:HD3	2.00	0.43
5:L5:2539:C:H2'	5:L5:2540:C:C6	2.52	0.43
9:LB:57:VAL:HG22	9:LB:73:VAL:HG22	2.00	0.43
17:LJ:160:GLU:CD	17:LJ:160:GLU:H	2.27	0.43
32:LZ:57:MET:HE2	32:LZ:57:MET:HB3	1.70	0.43
50:Ls:26:LYS:HB2	50:Ls:91:THR:O	2.19	0.43
50:Ls:92:LYS:HA	50:Ls:92:LYS:HE3	2.01	0.43
55:S2:118:C:H1'	55:S2:445:A:C5	2.53	0.43
55:S2:1650:A:H5''	72:SQ:139:ALA:HB2	2.01	0.43
59:SD:66:ILE:O	59:SD:70:THR:HG23	2.18	0.43
81:SZ:58:LEU:HA	81:SZ:62:VAL:HG23	2.00	0.43
88:Sg:23:THR:HG22	88:Sg:31:ILE:HG22	2.00	0.43
3:CR:171:LYS:HE3	3:CR:171:LYS:HB2	1.81	0.43
5:L5:4622:A:H4'	9:LB:13:SER:HB2	1.99	0.43
15:LH:76:HIS:O	15:LH:80:MET:HG3	2.18	0.43
23:LQ:159:PRO:HA	23:LQ:160:HIS:HA	1.61	0.43
28:LV:84:GLN:HE21	28:LV:86:LYS:HB3	1.84	0.43
50:Ls:106:LYS:HE3	50:Ls:184:SER:HB2	2.01	0.43
54:NM:195:GLU:HB3	54:NM:381:ILE:HD11	2.00	0.43
55:S2:64:A:H2	55:S2:83:A:H62	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:455:A:H2'	55:S2:456:C:C6	2.54	0.43
55:S2:1004:U:H2'	55:S2:1005:G:C8	2.53	0.43
57:SB:113:MET:HE3	57:SB:142:PHE:HE2	1.83	0.43
59:SD:219:PRO:HB2	88:Sg:189:ILE:HD13	2.01	0.43
3:CR:226:LEU:O	3:CR:253:LEU:HA	2.18	0.43
3:CR:329:MET:O	3:CR:346:LEU:HB2	2.18	0.43
7:L8:141:C:H2'	7:L8:142:U:C6	2.53	0.43
10:LC:210:ILE:HA	10:LC:230:LEU:O	2.18	0.43
22:LP:95:LEU:HG	22:LP:148:MET:HE1	2.00	0.43
25:LS:84:TYR:CE1	25:LS:93:MET:HE3	2.53	0.43
55:S2:319:C:H2'	55:S2:320:G:H8	1.83	0.43
55:S2:352:U:H2'	55:S2:353:C:C6	2.54	0.43
55:S2:1679:A:C8	61:SF:60:ARG:HB2	2.54	0.43
69:SN:64:ARG:HD3	69:SN:70:LYS:HD3	2.01	0.43
88:Sg:206:LEU:HD12	88:Sg:218:LEU:HD22	2.01	0.43
3:CR:38:ILE:HB	3:CR:124:LEU:HB3	2.01	0.43
5:L5:153:G:H2'	5:L5:154:G:C8	2.54	0.43
5:L5:3746:A:H5''	8:LA:244:GLY:HA3	2.00	0.43
5:L5:4088:C:H2'	5:L5:4089:G:C8	2.54	0.43
5:L5:4704:C:H2'	5:L5:4705:A:C8	2.54	0.43
21:LO:16:LEU:HD12	21:LO:80:PHE:HD1	1.84	0.43
22:LP:140:MET:HE3	22:LP:140:MET:HB3	1.82	0.43
30:LX:82:THR:HG22	30:LX:155:ILE:HG23	2.00	0.43
33:La:7:LYS:HB3	33:La:7:LYS:HE2	1.86	0.43
35:Lc:48:LEU:HD13	35:Lc:57:LYS:HG3	2.01	0.43
40:Lh:4:ILE:HD12	40:Lh:53:SER:HB3	2.01	0.43
50:Ls:57:LYS:O	50:Ls:61:MET:HG2	2.18	0.43
74:SS:12:ILE:HG22	74:SS:21:ASP:HA	1.99	0.43
5:L5:223:G:H4'	5:L5:225:G:N7	2.34	0.43
5:L5:1077:C:H4'	5:L5:1215:C:C4	2.54	0.43
6:L7:22:A:H3'	6:L7:23:A:H8	1.83	0.43
10:LC:73:VAL:HB	10:LC:78:ARG:NH2	2.34	0.43
55:S2:1405:A:H2'	55:S2:1406:G:O4'	2.19	0.43
55:S2:1413:G:H2'	55:S2:1414:A:H8	1.84	0.43
55:S2:1866:A:H4'	82:Sa:95:ARG:HD3	2.01	0.43
65:SJ:66:LYS:HA	65:SJ:71:LEU:HD11	2.01	0.43
66:SK:80:ARG:HG3	66:SK:85:LEU:HD12	2.01	0.43
74:SS:115:LYS:C	74:SS:117:ILE:H	2.27	0.43
5:L5:424:U:H2'	5:L5:425:U:C6	2.54	0.42
5:L5:3707:U:H2'	5:L5:3708:C:C6	2.53	0.42
5:L5:4174:U:H2'	5:L5:4175:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LG:244:PRO:HA	14:LG:247:VAL:HG22	2.01	0.42
19:LM:113:MET:HE3	19:LM:113:MET:HB3	1.79	0.42
50:Ls:99:ARG:HH22	50:Ls:205:ASP:HA	1.84	0.42
55:S2:1004:U:H2'	55:S2:1005:G:H8	1.84	0.42
55:S2:1351:G:H4'	56:SA:110:ASN:HA	2.00	0.42
5:L5:662:C:H2'	5:L5:663:G:H8	1.83	0.42
5:L5:1464:C:H5''	34:Lb:32:LEU:HD12	2.01	0.42
5:L5:2557:G:H1	5:L5:2570:U:H3	1.67	0.42
7:L8:96:C:H5''	40:Lh:66:LYS:HD2	2.01	0.42
8:LA:234:LYS:HG2	8:LA:238:ILE:HG12	2.01	0.42
9:LB:77:THR:HG21	9:LB:337:VAL:HG22	2.01	0.42
42:Lj:54:LYS:O	42:Lj:58:THR:HB	2.19	0.42
54:Nm:459:LYS:HB2	54:Nm:459:LYS:HE2	1.79	0.42
55:S2:1007:C:H2'	55:S2:1008:A:C8	2.55	0.42
55:S2:1228:A:H2'	55:S2:1229:G:H8	1.81	0.42
57:SB:85:LYS:HB3	57:SB:101:HIS:HB3	2.01	0.42
61:SF:87:LEU:HD22	72:SQ:46:THR:HB	2.01	0.42
5:L5:3610:A:H2'	5:L5:3611:A:H8	1.84	0.42
5:L5:3641:U:H5	5:L5:3646:A:N7	2.17	0.42
5:L5:4507:A:H2'	5:L5:4508:C:C6	2.55	0.42
34:Lb:40:LEU:HD12	34:Lb:40:LEU:HA	1.85	0.42
55:S2:329:G:H2'	55:S2:330:G:C8	2.53	0.42
58:SC:184:VAL:HG23	58:SC:195:LEU:HB2	2.02	0.42
3:CR:291:PHE:O	3:CR:294:ILE:HG22	2.19	0.42
4:CZ:200:VAL:HG21	22:LP:133:HIS:HB3	2.01	0.42
5:L5:1175:A:H2	5:L5:1185:G:H22	1.67	0.42
5:L5:1339:U:H2'	5:L5:1340:C:C6	2.55	0.42
5:L5:3748:A:H5''	8:LA:243:THR:HB	2.01	0.42
7:L8:82:A:H62	7:L8:84:A:H3'	1.84	0.42
33:La:116:LYS:HB2	33:La:116:LYS:HE2	1.87	0.42
50:Ls:161:ILE:HD11	50:Ls:171:GLU:HB3	2.01	0.42
54:Nm:353:LEU:HB3	54:Nm:397:PHE:HZ	1.83	0.42
55:S2:686:U:OP1	78:SW:32:LYS:HG3	2.20	0.42
56:SA:121:LEU:HD12	56:SA:143:PRO:HB2	2.00	0.42
63:SH:60:ILE:HB	63:SH:92:VAL:HG22	2.01	0.42
75:ST:94:ARG:H	75:ST:94:ARG:HG2	1.70	0.42
81:SZ:69:THR:HB	81:SZ:72:VAL:HG22	2.02	0.42
5:L5:3722:G:H2'	5:L5:3723:A:H8	1.84	0.42
5:L5:3726:A:H2'	5:L5:3727:A:C8	2.54	0.42
5:L5:4178:A:H2'	5:L5:4179:G:C8	2.55	0.42
5:L5:4460:U:H2'	5:L5:4461:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:4870:G:H5''	19:LM:91:TRP:CE2	2.55	0.42
24:LR:19:LYS:HB2	24:LR:19:LYS:HE2	1.88	0.42
31:LY:22:PRO:O	31:LY:26:ARG:HB2	2.19	0.42
37:Le:32:LYS:HB3	37:Le:32:LYS:HE2	1.66	0.42
52:NA:103:LEU:HD22	52:NA:131:LEU:HD21	2.01	0.42
55:S2:1298:G:H5''	71:SP:102:PHE:CZ	2.53	0.42
55:S2:1736:G:H2'	55:S2:1737:G:C8	2.55	0.42
57:SB:124:HIS:HA	57:SB:137:LEU:O	2.20	0.42
58:SC:252:THR:HG22	58:SC:254:ASP:H	1.84	0.42
61:SF:41:VAL:HG11	61:SF:68:ILE:H	1.84	0.42
76:SU:66:ARG:HA	76:SU:66:ARG:HD2	1.90	0.42
4:CZ:213:LYS:HE3	5:L5:3908:A:C5	2.55	0.42
5:L5:4927:G:H5'	5:L5:4928:C:C5	2.53	0.42
27:LU:80:LYS:HD2	27:LU:108:GLU:HA	2.00	0.42
37:Le:19:LYS:HE3	37:Le:19:LYS:HB3	1.90	0.42
49:Lr:63:VAL:HG22	49:Lr:79:ARG:HG2	2.02	0.42
62:SG:12:CYS:HB3	62:SG:124:LEU:HA	2.01	0.42
62:SG:32:MET:HB2	62:SG:100:CYS:HB2	2.02	0.42
74:SS:84:LEU:HD12	74:SS:95:TYR:HB3	2.00	0.42
5:L5:1366:G:N2	18:LL:33:ILE:HD13	2.35	0.42
5:L5:2521:G:H4'	39:Lg:26:PRO:HD2	2.01	0.42
5:L5:4291:G:H5'	5:L5:4293:U:C6	2.54	0.42
5:L5:4743:G:H2'	5:L5:4744:A:C8	2.54	0.42
8:LA:28:ARG:HD2	8:LA:123:ARG:HG3	2.02	0.42
26:LT:71:ALA:HA	26:LT:92:ARG:HA	2.00	0.42
35:Lc:13:SER:O	35:Lc:17:ARG:HG3	2.20	0.42
54:Nm:338:LEU:HD12	54:Nm:385:PHE:HB3	2.00	0.42
55:S2:388:U:H2'	55:S2:389:A:C8	2.53	0.42
73:SR:34:VAL:O	73:SR:38:ILE:HG13	2.19	0.42
79:SX:108:LYS:H	79:SX:108:LYS:HD2	1.84	0.42
2:CP:10:G:O6	2:CP:24:U:O2	2.38	0.42
3:CR:310:LYS:NZ	3:CR:314:MET:HB2	2.35	0.42
5:L5:1468:C:H2'	5:L5:1469:C:H6	1.84	0.42
5:L5:4088:C:H2'	5:L5:4089:G:H8	1.85	0.42
6:L7:27:G:H2'	6:L7:28:C:C6	2.55	0.42
9:LB:223:THR:HG22	9:LB:338:VAL:HB	2.02	0.42
54:Nm:201:LEU:HD21	54:Nm:247:PHE:HE2	1.84	0.42
55:S2:1407:U:H2'	55:S2:1408:U:C6	2.55	0.42
55:S2:1798:C:H2'	55:S2:1799:G:O4'	2.20	0.42
87:Sf:107:LYS:HB2	87:Sf:107:LYS:HE2	1.71	0.42
5:L5:1317:U:H2'	5:L5:1318:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:1443:A:N6	5:L5:2104:G:N2	2.63	0.42
5:L5:4389:C:H2'	5:L5:4390:A:H8	1.84	0.42
7:L8:106:G:H4'	7:L8:137:A:H5'	2.01	0.42
9:LB:57:VAL:HA	9:LB:72:VAL:O	2.20	0.42
9:LB:201:LEU:HD12	9:LB:201:LEU:HA	1.92	0.42
15:LH:28:LYS:HE3	15:LH:28:LYS:HB3	1.84	0.42
16:LI:69:ARG:HA	16:LI:136:MET:HE1	2.02	0.42
18:LL:46:ILE:HD11	18:LL:51:ALA:HA	2.01	0.42
40:Lh:52:LYS:HA	40:Lh:52:LYS:HD3	1.80	0.42
55:S2:1365:G:H2'	55:S2:1366:G:C8	2.55	0.42
82:Sa:13:LYS:HA	82:Sa:13:LYS:HD3	1.86	0.42
82:Sa:40:VAL:HB	82:Sa:69:VAL:HG22	2.01	0.42
5:L5:2765:A:H2'	5:L5:2766:A:H8	1.84	0.42
5:L5:3848:U:H2'	5:L5:3849:A:C8	2.55	0.42
5:L5:4219:A:H2'	5:L5:4220:A:C8	2.55	0.42
5:L5:4258:C:H2'	5:L5:4259:C:H6	1.84	0.42
5:L5:4906:C:H2'	5:L5:4907:G:H8	1.85	0.42
21:LO:186:GLU:O	21:LO:190:ASP:HB3	2.20	0.42
51:Lt:80:LEU:HB3	51:Lt:112:ILE:HG12	2.01	0.42
54:Nm:204:PRO:HD2	54:Nm:370:GLU:HG2	2.01	0.42
55:S2:952:G:H2'	55:S2:953:C:C6	2.55	0.42
60:SE:29:PRO:HG2	60:SE:46:ILE:HG22	2.02	0.42
60:SE:80:ILE:HD12	60:SE:80:ILE:HA	1.82	0.42
65:SJ:134:HIS:CE1	65:SJ:164:PRO:HD2	2.55	0.42
74:SS:46:ARG:HG2	75:ST:35:ASP:HB3	2.01	0.42
5:L5:3599:A:H2'	5:L5:3600:G:C8	2.55	0.41
5:L5:3910:C:H2'	5:L5:3911:C:C6	2.54	0.41
5:L5:5018:C:H2'	5:L5:5019:A:H8	1.85	0.41
43:Lk:58:GLN:H	43:Lk:58:GLN:HG2	1.71	0.41
55:S2:441:C:H2'	55:S2:442:C:C6	2.55	0.41
55:S2:735:C:H5'	55:S2:736:C:H5	1.86	0.41
55:S2:1356:G:H2'	55:S2:1357:A:C8	2.55	0.41
55:S2:1623:A:O5'	74:SS:133:GLY:HA3	2.19	0.41
59:SD:18:LYS:HB2	59:SD:18:LYS:HE2	1.83	0.41
71:SP:56:LEU:HD13	71:SP:78:THR:HG21	2.02	0.41
71:SP:83:MET:HB3	71:SP:116:LEU:HD12	2.02	0.41
88:Sg:212:LYS:HA	88:Sg:235:ILE:HD12	2.00	0.41
5:L5:318:A:H2'	5:L5:319:A:H8	1.85	0.41
5:L5:2467:U:H4'	5:L5:2468:U:H5'	2.02	0.41
5:L5:3619:G:H22	5:L5:3624:A:H1'	1.84	0.41
5:L5:5057:C:H2'	5:L5:5058:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L8:14:U:H5'	22:LP:123:PRO:HD3	2.02	0.41
12:LE:119:GLU:HG3	37:Le:7:LEU:HD22	2.02	0.41
15:LH:43:VAL:HG12	15:LH:59:LYS:HD3	2.01	0.41
18:LL:5:ARG:H	18:LL:5:ARG:HG2	1.74	0.41
18:LL:19:GLN:HA	18:LL:22:VAL:HG23	2.02	0.41
23:LQ:12:LYS:HB3	23:LQ:14:ARG:HD3	2.03	0.41
24:LR:97:ARG:O	24:LR:101:ILE:HG13	2.20	0.41
47:Lo:51:GLN:HG2	47:Lo:55:ILE:HD11	2.02	0.41
51:Lt:108:GLU:HA	51:Lt:111:ASN:ND2	2.35	0.41
55:S2:433:A:H2'	55:S2:434:G:C8	2.55	0.41
55:S2:931:C:H2'	55:S2:932:G:C8	2.55	0.41
55:S2:1232:U:H2'	55:S2:1233:G:H8	1.85	0.41
66:SK:49:MET:HG2	66:SK:69:TRP:CD2	2.55	0.41
78:SW:42:MET:HE2	78:SW:42:MET:HB3	1.84	0.41
5:L5:2705:G:H22	5:L5:2710:C:H5	1.67	0.41
10:LC:150:LEU:HD12	10:LC:150:LEU:HA	1.85	0.41
11:LD:84:PRO:HG3	11:LD:89:LYS:HA	2.02	0.41
13:LF:208:LEU:HD23	13:LF:208:LEU:HA	1.91	0.41
13:LF:226:HIS:HA	13:LF:233:ALA:HB3	2.03	0.41
55:S2:38:A:OP1	65:SJ:5:ARG:HG3	2.20	0.41
55:S2:525:A:H2'	55:S2:526:A:C8	2.55	0.41
55:S2:1513:C:H2'	55:S2:1514:G:C8	2.54	0.41
58:SC:166:ARG:HH12	58:SC:252:THR:HG21	1.83	0.41
68:SM:93:LYS:HG2	68:SM:101:ARG:HH22	1.85	0.41
72:SQ:58:LEU:HD11	72:SQ:112:LEU:HD11	2.02	0.41
3:CR:324:GLU:HG3	3:CR:391:ILE:HG22	2.03	0.41
3:CR:404:LYS:HA	3:CR:404:LYS:HD2	1.90	0.41
5:L5:2744:A:H2'	5:L5:2745:A:C8	2.55	0.41
5:L5:4208:U:H2'	5:L5:4209:G:C8	2.54	0.41
5:L5:4524:G:N3	9:LB:252:ALA:HB1	2.35	0.41
6:L7:92:C:H2'	6:L7:93:G:H8	1.84	0.41
9:LB:82:PRO:HG3	9:LB:171:LEU:HD21	2.02	0.41
15:LH:34:LEU:HD11	15:LH:150:ASP:HB2	2.02	0.41
18:LL:106:SER:HB3	18:LL:109:SER:OG	2.20	0.41
36:Ld:24:GLU:O	36:Ld:119:THR:HA	2.20	0.41
49:Lr:16:PHE:HB3	49:Lr:27:THR:H	1.84	0.41
55:S2:1497:G:C6	66:SK:25:LYS:HD2	2.55	0.41
58:SC:108:LYS:HD3	58:SC:110:MET:HB3	2.00	0.41
60:SE:168:LYS:HE3	60:SE:168:LYS:HB3	1.91	0.41
63:SH:101:LEU:HD12	63:SH:120:ARG:HB3	2.02	0.41
72:SQ:41:MET:HE3	72:SQ:41:MET:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CZ:216:PRO:HA	4:CZ:217:PRO:HD3	1.78	0.41
5:L5:1364:U:H5''	18:LL:36:ARG:HH22	1.86	0.41
5:L5:2897:G:H4'	24:LR:101:ILE:HD13	2.02	0.41
5:L5:4991:U:H2'	5:L5:4992:G:H8	1.86	0.41
9:LB:358:ARG:HA	9:LB:358:ARG:HD3	1.87	0.41
23:LQ:178:ARG:N	33:La:51:GLY:HA2	2.35	0.41
50:Ls:98:ILE:O	50:Ls:102:LEU:HB2	2.21	0.41
51:Lt:154:ASP:HB3	51:Lt:159:ALA:HB3	2.03	0.41
54:NM:132:VAL:HG22	54:NM:482:LYS:HE3	2.03	0.41
54:NM:203:PRO:HG3	54:NM:229:ILE:HB	2.02	0.41
55:S2:17:C:H2'	55:S2:18:C:C6	2.56	0.41
55:S2:525:A:H2'	55:S2:526:A:H8	1.85	0.41
55:S2:1606:G:H5''	75:ST:86:GLY:C	2.45	0.41
61:SF:112:LEU:O	61:SF:116:ILE:HG12	2.20	0.41
62:SG:135:PRO:HG2	62:SG:141:ILE:HG12	2.02	0.41
78:SW:90:GLN:HA	78:SW:102:ILE:HD11	2.02	0.41
81:SZ:69:THR:HG22	81:SZ:71:ALA:H	1.85	0.41
3:CR:372:MET:HA	3:CR:373:PRO:HD3	1.71	0.41
5:L5:4169:G:H4'	5:L5:4171:C:C2	2.55	0.41
5:L5:4321:U:H2'	5:L5:4322:G:C8	2.55	0.41
10:LC:339:THR:O	10:LC:343:GLN:HG3	2.21	0.41
21:LO:9:LEU:HD23	21:LO:118:MET:HB2	2.01	0.41
31:LY:66:GLN:CD	31:LY:66:GLN:H	2.29	0.41
36:Ld:117:LEU:HD23	36:Ld:117:LEU:HA	1.89	0.41
40:Lh:13:LYS:H	40:Lh:13:LYS:HD2	1.86	0.41
43:Lk:70:LYS:HA	43:Lk:70:LYS:HD3	1.80	0.41
55:S2:66:G:N2	55:S2:82:G:H21	2.19	0.41
55:S2:582:U:H1'	80:SY:33:ALA:HB2	2.03	0.41
55:S2:867:G:H5''	67:SL:149:ALA:HB2	2.03	0.41
55:S2:1113:A:H62	55:S2:1120:U:H3	1.67	0.41
69:SN:40:LEU:HB3	69:SN:45:LEU:HD12	2.02	0.41
76:SU:31:SER:O	76:SU:35:VAL:HG23	2.20	0.41
78:SW:46:TYR:HB3	78:SW:69:LEU:HD13	2.02	0.41
78:SW:111:MET:HE2	78:SW:111:MET:HB3	1.80	0.41
3:CR:296:GLN:OE1	3:CR:298:THR:HB	2.20	0.41
5:L5:4934:A:H2'	5:L5:4935:C:C6	2.55	0.41
5:L5:4991:U:H2'	5:L5:4992:G:C8	2.55	0.41
10:LC:137:VAL:HG21	10:LC:150:LEU:HD21	2.03	0.41
16:LI:91:LEU:HD12	16:LI:135:ILE:HG23	2.01	0.41
26:LT:128:LEU:HD23	26:LT:128:LEU:HA	1.85	0.41
54:NM:366:MET:HE1	54:NM:370:GLU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SJ:151:LEU:HD12	65:SJ:151:LEU:HA	1.86	0.41
66:SK:49:MET:HE2	66:SK:49:MET:HB2	1.87	0.41
68:SM:42:LEU:HD12	68:SM:68:LEU:HD12	2.02	0.41
88:Sg:32:LEU:HD21	88:Sg:92:LEU:HD21	2.03	0.41
88:Sg:87:LEU:HD21	88:Sg:111:VAL:HG11	2.03	0.41
5:L5:1577:G:O2'	5:L5:1612:G:H4'	2.21	0.41
5:L5:4251:A:H5''	17:LJ:108:GLY:HA3	2.02	0.41
5:L5:4260:U:H2'	5:L5:4261:C:H6	1.85	0.41
5:L5:4344:U:H2'	5:L5:4345:C:C6	2.55	0.41
6:L7:4:U:H2'	6:L7:5:A:H8	1.84	0.41
11:LD:118:ILE:H	11:LD:118:ILE:HG13	1.64	0.41
18:LL:58:ILE:HG12	18:LL:157:VAL:HG13	2.02	0.41
23:LQ:110:ARG:HG3	23:LQ:120:ILE:HD12	2.03	0.41
38:Lf:36:ARG:HB2	38:Lf:80:ASN:HA	2.02	0.41
43:Lk:57:LYS:HB2	43:Lk:57:LYS:HE3	1.72	0.41
54:NM:152:LEU:HD11	54:NM:158:TRP:CD1	2.55	0.41
55:S2:1232:U:H2'	55:S2:1233:G:C8	2.56	0.41
60:SE:121:TYR:HA	60:SE:163:ASP:HA	2.03	0.41
3:CR:322:VAL:O	3:CR:391:ILE:HA	2.20	0.41
5:L5:287:U:H2'	5:L5:288:G:C8	2.55	0.41
5:L5:1978:C:H5'	51:Lt:100:HIS:HE1	1.86	0.41
5:L5:2029:A:H2'	5:L5:2030:A:C8	2.56	0.41
5:L5:2412:A:H2'	5:L5:2413:U:C6	2.56	0.41
5:L5:2640:G:H2'	5:L5:2641:A:C8	2.56	0.41
5:L5:3907:G:H5'	5:L5:4448:G:H5'	2.02	0.41
5:L5:3923:A:H2'	5:L5:3924:C:C6	2.56	0.41
5:L5:4155:C:H2'	5:L5:4156:G:O4'	2.21	0.41
5:L5:4543:G:H2'	5:L5:4544:A:C8	2.56	0.41
11:LD:99:TYR:HE2	11:LD:164:LYS:HG3	1.86	0.41
14:LG:190:LEU:HD23	14:LG:190:LEU:HA	1.91	0.41
15:LH:52:LYS:HD3	15:LH:52:LYS:HA	1.90	0.41
35:Lc:53:PRO:HG2	35:Lc:56:ARG:HB3	2.02	0.41
43:Lk:35:LYS:HA	43:Lk:43:TYR:O	2.20	0.41
54:NM:191:ASP:HB3	54:NM:404:PRO:HB2	2.02	0.41
55:S2:29:G:H2'	55:S2:30:C:C6	2.56	0.41
55:S2:382:C:H2'	55:S2:383:G:H8	1.86	0.41
55:S2:1124:C:H5''	57:SB:150:ILE:HG12	2.03	0.41
55:S2:1670:C:H2'	55:S2:1671:G:C8	2.55	0.41
60:SE:6:LYS:HD3	60:SE:6:LYS:HA	1.87	0.41
61:SF:22:LYS:HG3	61:SF:23:TRP:N	2.35	0.41
61:SF:128:ILE:HD13	61:SF:128:ILE:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SG:223:LYS:HE2	62:SG:223:LYS:HB2	1.99	0.41
68:SM:36:ARG:HA	68:SM:36:ARG:HD2	1.87	0.41
68:SM:84:LYS:O	68:SM:88:TRP:HB2	2.21	0.41
4:CZ:134:MET:HE1	4:CZ:139:ILE:HB	2.01	0.41
5:L5:172:C:H4'	5:L5:173:C:H5'	2.03	0.41
5:L5:5006:U:H4'	5:L5:5007:A:H5'	2.02	0.41
11:LD:125:VAL:HG23	11:LD:126:THR:H	1.86	0.41
16:LI:99:ILE:HG22	16:LI:123:GLN:HB2	2.03	0.41
33:La:146:LEU:HB2	41:Li:5:TYR:HB3	2.03	0.41
43:Lk:24:LYS:HA	43:Lk:67:LYS:O	2.21	0.41
50:Ls:106:LYS:HA	50:Ls:106:LYS:HD2	1.95	0.41
54:NM:349:VAL:HG22	54:NM:397:PHE:CD2	2.55	0.41
55:S2:1648:G:N7	72:SQ:17:LYS:HD3	2.36	0.41
55:S2:1845:A:H2'	55:S2:1846:G:H8	1.86	0.41
57:SB:60:ASP:HA	57:SB:63:LYS:HG3	2.03	0.41
71:SP:50:ARG:HD3	71:SP:50:ARG:HA	1.97	0.41
82:Sa:64:LEU:HD23	82:Sa:64:LEU:HA	1.92	0.41
88:Sg:129:ILE:H	88:Sg:142:VAL:HG22	1.86	0.41
5:L5:1097:C:H2'	5:L5:1098:G:H8	1.85	0.40
5:L5:1345:A:H2'	5:L5:1346:C:C6	2.56	0.40
5:L5:2020:U:H2'	5:L5:2021:G:H8	1.86	0.40
5:L5:4591:U:H2'	5:L5:4592:C:C6	2.56	0.40
9:LB:58:ARG:HD2	9:LB:363:ILE:HG23	2.03	0.40
12:LE:282:TYR:HA	12:LE:283:PRO:HD3	1.96	0.40
15:LH:92:MET:HE2	15:LH:179:ILE:HG22	2.02	0.40
16:LI:208:LYS:HA	16:LI:211:VAL:HG22	2.03	0.40
29:LW:105:ARG:HH22	62:SG:151:ASP:N	2.19	0.40
42:Lj:67:LEU:HD23	42:Lj:67:LEU:HA	1.88	0.40
54:NM:289:LYS:HA	54:NM:290:PRO:HD3	1.97	0.40
54:NM:376:TYR:HA	54:NM:377:PRO:HD3	1.96	0.40
55:S2:385:G:H3'	67:SL:136:LYS:HB2	2.03	0.40
59:SD:163:PRO:HA	59:SD:166:TYR:CE1	2.56	0.40
5:L5:395:A:C5'	52:NA:71:ARG:HH12	2.33	0.40
5:L5:400:A:H5''	22:LP:16:LYS:HG3	2.02	0.40
5:L5:475:G:H2'	5:L5:476:G:C8	2.56	0.40
5:L5:737:C:C5	5:L5:739:G:H5''	2.56	0.40
5:L5:1278:C:H2'	5:L5:1279:A:O4'	2.21	0.40
5:L5:1855:G:OP1	34:Lb:4:SER:HB2	2.21	0.40
55:S2:212:C:H2'	55:S2:213:G:C8	2.56	0.40
55:S2:1863:A:H8	82:Sa:79:ILE:HG21	1.86	0.40
59:SD:64:ARG:O	59:SD:68:GLU:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SQ:72:VAL:HG12	72:SQ:80:GLN:OE1	2.20	0.40
72:SQ:113:ILE:HD13	72:SQ:113:ILE:HA	1.94	0.40
79:SX:128:VAL:HG13	79:SX:133:LEU:HD11	2.03	0.40
5:L5:433:A:C2	5:L5:3867:A:H4'	2.56	0.40
5:L5:1867:A:H2'	5:L5:1868:A:C8	2.56	0.40
7:L8:40:A:H2'	7:L8:41:A:C8	2.56	0.40
9:LB:231:VAL:HG11	9:LB:251:VAL:HG23	2.04	0.40
10:LC:230:LEU:HD12	10:LC:230:LEU:HA	1.96	0.40
12:LE:147:GLY:HA2	12:LE:203:ILE:HG13	2.04	0.40
18:LL:146:LEU:HD11	40:Lh:122:LYS:HG2	2.02	0.40
19:LM:3:PHE:H	25:LS:175:PHE:HZ	1.69	0.40
23:LQ:128:LEU:HD23	23:LQ:128:LEU:HA	1.91	0.40
36:Ld:92:ARG:HA	36:Ld:102:LEU:HD23	2.04	0.40
55:S2:51:U:H2'	55:S2:52:G:C8	2.57	0.40
55:S2:367:U:H4'	55:S2:371:A:C8	2.57	0.40
55:S2:1844:U:H2'	55:S2:1845:A:C8	2.56	0.40
70:SO:78:ALA:HB3	70:SO:118:ALA:HB3	2.03	0.40
86:Se:28:LYS:H	86:Se:28:LYS:HG3	1.69	0.40
88:Sg:286:CYS:HB2	88:Sg:302:TYR:CZ	2.57	0.40
5:L5:1834:U:C2	26:LT:128:LEU:HD12	2.56	0.40
5:L5:2570:U:H2'	5:L5:2571:C:C6	2.57	0.40
5:L5:3861:A:H2'	5:L5:3862:A:C8	2.56	0.40
5:L5:4301:U:H4'	26:LT:54:HIS:CD2	2.57	0.40
5:L5:5024:C:N4	5:L5:5028:G:H21	2.20	0.40
23:LQ:75:ARG:HA	23:LQ:78:LYS:HD2	2.04	0.40
32:LZ:3:LYS:H	32:LZ:3:LYS:HG3	1.73	0.40
32:LZ:109:LYS:HE3	32:LZ:109:LYS:HB2	1.89	0.40
34:Lb:13:SER:HA	34:Lb:16:TRP:NE1	2.37	0.40
38:Lf:43:LEU:HD12	38:Lf:43:LEU:HA	1.95	0.40
54:Nm:443:LYS:HA	54:Nm:443:LYS:HD2	1.77	0.40
55:S2:1656:G:H1	55:S2:1668:U:H3	1.70	0.40
59:SD:131:ALA:HA	59:SD:191:PRO:HD3	2.03	0.40
65:SJ:87:LEU:HD23	65:SJ:87:LEU:HA	1.95	0.40
72:SQ:8:GLN:HG2	72:SQ:99:TYR:CD1	2.56	0.40
3:CR:89:PRO:HA	3:CR:90:PRO:HD3	1.95	0.40
4:CZ:122:LEU:HB2	4:CZ:172:TRP:HZ3	1.86	0.40
5:L5:1306:C:H2'	5:L5:1307:A:H8	1.86	0.40
5:L5:1327:C:H2'	5:L5:1328:G:C8	2.57	0.40
5:L5:4459:U:H2'	5:L5:4460:U:C6	2.56	0.40
7:L8:28:C:H4'	10:LC:51:PRO:HG2	2.04	0.40
10:LC:300:ARG:HH21	10:LC:300:ARG:HD2	1.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:199:LYS:H	13:LF:199:LYS:HG3	1.62	0.40
24:LR:25:ASP:HB3	24:LR:28:GLU:HB2	2.03	0.40
55:S2:1653:U:H2'	55:S2:1654:G:C8	2.55	0.40
63:SH:130:LEU:HD13	63:SH:177:TYR:CD2	2.57	0.40
68:SM:36:ARG:HA	68:SM:36:ARG:HH11	1.87	0.40
74:SS:103:LEU:HD12	74:SS:103:LEU:HA	1.94	0.40
86:Se:12:VAL:HA	86:Se:15:GLN:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CR	411/437 (94%)	397 (97%)	14 (3%)	0	100	100
4	CZ	200/217 (92%)	190 (95%)	10 (5%)	0	100	100
8	LA	246/257 (96%)	230 (94%)	16 (6%)	0	100	100
9	LB	393/403 (98%)	378 (96%)	15 (4%)	0	100	100
10	LC	362/427 (85%)	336 (93%)	26 (7%)	0	100	100
11	LD	291/297 (98%)	275 (94%)	16 (6%)	0	100	100
12	LE	213/288 (74%)	194 (91%)	19 (9%)	0	100	100
13	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
14	LG	225/266 (85%)	210 (93%)	15 (7%)	0	100	100
15	LH	188/192 (98%)	179 (95%)	9 (5%)	0	100	100
16	LI	203/214 (95%)	191 (94%)	12 (6%)	0	100	100
17	LJ	167/178 (94%)	162 (97%)	5 (3%)	0	100	100
18	LL	203/211 (96%)	192 (95%)	11 (5%)	0	100	100
19	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
21	LO	198/203 (98%)	194 (98%)	4 (2%)	0	100	100
22	LP	151/184 (82%)	142 (94%)	8 (5%)	1 (1%)	18	34
23	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
24	LR	174/196 (89%)	173 (99%)	1 (1%)	0	100	100
25	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
26	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
27	LU	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
28	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
29	LW	111/157 (71%)	103 (93%)	8 (7%)	0	100	100
30	LX	118/156 (76%)	114 (97%)	4 (3%)	0	100	100
31	LY	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
32	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
33	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
34	Lb	73/159 (46%)	69 (94%)	4 (6%)	0	100	100
35	Lc	95/115 (83%)	91 (96%)	4 (4%)	0	100	100
36	Ld	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
37	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
38	Lf	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
39	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
40	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
41	Li	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
42	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
43	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
44	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
45	Lm	50/128 (39%)	50 (100%)	0	0	100	100
46	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
48	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
49	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
50	Ls	210/317 (66%)	204 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	Lt	158/165 (96%)	154 (98%)	4 (2%)	0	100	100
52	NA	71/215 (33%)	70 (99%)	1 (1%)	0	100	100
53	NB	123/162 (76%)	123 (100%)	0	0	100	100
54	NM	381/496 (77%)	365 (96%)	16 (4%)	0	100	100
56	SA	214/295 (72%)	201 (94%)	11 (5%)	2 (1%)	14	28
57	SB	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
58	SC	217/293 (74%)	208 (96%)	9 (4%)	0	100	100
59	SD	219/243 (90%)	209 (95%)	10 (5%)	0	100	100
60	SE	260/263 (99%)	254 (98%)	6 (2%)	0	100	100
61	SF	177/204 (87%)	170 (96%)	6 (3%)	1 (1%)	21	38
62	SG	229/249 (92%)	211 (92%)	18 (8%)	0	100	100
63	SH	179/194 (92%)	170 (95%)	9 (5%)	0	100	100
64	SI	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
65	SJ	177/194 (91%)	173 (98%)	4 (2%)	0	100	100
66	SK	94/165 (57%)	88 (94%)	6 (6%)	0	100	100
67	SL	140/158 (89%)	130 (93%)	10 (7%)	0	100	100
68	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
69	SN	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
70	SO	132/151 (87%)	118 (89%)	14 (11%)	0	100	100
71	SP	127/145 (88%)	117 (92%)	10 (8%)	0	100	100
72	SQ	140/146 (96%)	129 (92%)	11 (8%)	0	100	100
73	SR	129/135 (96%)	118 (92%)	11 (8%)	0	100	100
74	SS	139/152 (91%)	120 (86%)	19 (14%)	0	100	100
75	ST	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
76	SU	99/119 (83%)	92 (93%)	7 (7%)	0	100	100
77	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
78	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
79	SX	139/143 (97%)	127 (91%)	12 (9%)	0	100	100
80	SY	121/133 (91%)	115 (95%)	6 (5%)	0	100	100
81	SZ	73/125 (58%)	69 (94%)	4 (6%)	0	100	100
82	Sa	97/115 (84%)	90 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	Sb	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
84	Sc	61/69 (88%)	54 (88%)	7 (12%)	0	100	100
85	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
86	Se	53/133 (40%)	52 (98%)	1 (2%)	0	100	100
87	Sf	61/156 (39%)	55 (90%)	6 (10%)	0	100	100
88	Sg	304/317 (96%)	275 (90%)	29 (10%)	0	100	100
All	All	12679/14770 (86%)	12037 (95%)	638 (5%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
56	SA	196	GLU
61	SF	80	GLY
22	LP	20	SER
56	SA	11	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CR	356/375 (95%)	346 (97%)	10 (3%)	38	61
4	CZ	139/189 (74%)	139 (100%)	0	100	100
8	LA	190/199 (96%)	181 (95%)	9 (5%)	23	45
9	LB	343/349 (98%)	337 (98%)	6 (2%)	53	71
10	LC	299/348 (86%)	294 (98%)	5 (2%)	53	71
11	LD	241/250 (96%)	237 (98%)	4 (2%)	53	71
12	LE	191/252 (76%)	185 (97%)	6 (3%)	35	59
13	LF	194/215 (90%)	191 (98%)	3 (2%)	57	74
14	LG	188/223 (84%)	184 (98%)	4 (2%)	47	67
15	LH	167/171 (98%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	LI	174/181 (96%)	174 (100%)	0	100	100
17	LJ	136/149 (91%)	135 (99%)	1 (1%)	76	86
18	LL	164/177 (93%)	160 (98%)	4 (2%)	43	65
19	LM	114/161 (71%)	111 (97%)	3 (3%)	40	63
20	LN	171/172 (99%)	167 (98%)	4 (2%)	44	66
21	LO	170/174 (98%)	169 (99%)	1 (1%)	78	88
22	LP	132/163 (81%)	129 (98%)	3 (2%)	44	66
23	LQ	161/165 (98%)	158 (98%)	3 (2%)	50	70
24	LR	150/175 (86%)	148 (99%)	2 (1%)	61	76
25	LS	156/157 (99%)	153 (98%)	3 (2%)	50	70
26	LT	135/140 (96%)	133 (98%)	2 (2%)	57	74
27	LU	86/115 (75%)	85 (99%)	1 (1%)	63	78
28	LV	99/107 (92%)	99 (100%)	0	100	100
29	LW	61/126 (48%)	61 (100%)	0	100	100
30	LX	107/133 (80%)	106 (99%)	1 (1%)	70	82
31	LY	123/135 (91%)	121 (98%)	2 (2%)	55	73
32	LZ	117/118 (99%)	115 (98%)	2 (2%)	53	71
33	La	118/121 (98%)	116 (98%)	2 (2%)	53	71
34	Lb	59/126 (47%)	56 (95%)	3 (5%)	21	40
35	Lc	79/97 (81%)	74 (94%)	5 (6%)	16	30
36	Ld	94/110 (86%)	91 (97%)	3 (3%)	34	58
37	Le	113/121 (93%)	112 (99%)	1 (1%)	70	82
38	Lf	87/89 (98%)	85 (98%)	2 (2%)	44	66
39	Lg	93/100 (93%)	92 (99%)	1 (1%)	65	79
40	Lh	108/110 (98%)	106 (98%)	2 (2%)	50	70
41	Li	81/89 (91%)	78 (96%)	3 (4%)	30	54
42	Lj	73/80 (91%)	70 (96%)	3 (4%)	27	49
43	Lk	57/65 (88%)	56 (98%)	1 (2%)	51	71
44	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	47
45	Lm	47/116 (40%)	44 (94%)	3 (6%)	16	29
46	Ln	23/24 (96%)	22 (96%)	1 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Lo	93/94 (99%)	88 (95%)	5 (5%)	20	38
48	Lp	71/74 (96%)	69 (97%)	2 (3%)	38	61
49	Lr	107/121 (88%)	102 (95%)	5 (5%)	23	45
50	Ls	180/258 (70%)	175 (97%)	5 (3%)	38	61
51	Lt	132/137 (96%)	130 (98%)	2 (2%)	57	74
52	NA	64/183 (35%)	64 (100%)	0	100	100
53	NB	107/136 (79%)	106 (99%)	1 (1%)	70	82
54	NM	345/443 (78%)	340 (99%)	5 (1%)	59	75
56	SA	170/243 (70%)	163 (96%)	7 (4%)	27	49
57	SB	191/231 (83%)	189 (99%)	2 (1%)	68	81
58	SC	175/225 (78%)	169 (97%)	6 (3%)	32	57
59	SD	148/202 (73%)	145 (98%)	3 (2%)	48	69
60	SE	196/225 (87%)	189 (96%)	7 (4%)	31	55
61	SF	142/170 (84%)	139 (98%)	3 (2%)	47	67
62	SG	138/218 (63%)	132 (96%)	6 (4%)	26	47
63	SH	109/174 (63%)	106 (97%)	3 (3%)	38	61
64	SI	149/180 (83%)	149 (100%)	0	100	100
65	SJ	143/168 (85%)	142 (99%)	1 (1%)	76	86
66	SK	65/136 (48%)	64 (98%)	1 (2%)	57	74
67	SL	121/142 (85%)	118 (98%)	3 (2%)	42	64
68	SM	104/108 (96%)	100 (96%)	4 (4%)	29	52
69	SN	123/131 (94%)	122 (99%)	1 (1%)	73	84
70	SO	95/119 (80%)	94 (99%)	1 (1%)	65	79
71	SP	98/130 (75%)	96 (98%)	2 (2%)	48	69
72	SQ	103/121 (85%)	101 (98%)	2 (2%)	50	70
73	SR	84/122 (69%)	79 (94%)	5 (6%)	17	32
74	SS	112/132 (85%)	107 (96%)	5 (4%)	24	46
75	ST	105/115 (91%)	103 (98%)	2 (2%)	50	70
76	SU	68/107 (64%)	64 (94%)	4 (6%)	18	33
77	SV	62/67 (92%)	59 (95%)	3 (5%)	23	44
78	SW	110/113 (97%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	SX	109/115 (95%)	104 (95%)	5 (5%)	24	45
80	SY	86/115 (75%)	83 (96%)	3 (4%)	32	56
81	SZ	56/103 (54%)	56 (100%)	0	100	100
82	Sa	83/98 (85%)	82 (99%)	1 (1%)	63	78
83	Sb	65/76 (86%)	64 (98%)	1 (2%)	57	74
84	Sc	51/62 (82%)	47 (92%)	4 (8%)	11	21
85	Sd	44/49 (90%)	43 (98%)	1 (2%)	44	66
86	Se	39/104 (38%)	37 (95%)	2 (5%)	21	40
87	Sf	56/140 (40%)	53 (95%)	3 (5%)	20	38
88	Sg	201/275 (73%)	193 (96%)	8 (4%)	28	50
All	All	10343/12577 (82%)	10108 (98%)	235 (2%)	44	66

All (235) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CR	34	MET
3	CR	43	ASP
3	CR	100	ILE
3	CR	124	LEU
3	CR	232	PHE
3	CR	274	VAL
3	CR	317	VAL
3	CR	324	GLU
3	CR	328	ILE
3	CR	409	ILE
8	LA	15	VAL
8	LA	32	VAL
8	LA	44	ILE
8	LA	92	LYS
8	LA	102	LEU
8	LA	128	ARG
8	LA	154	SER
8	LA	207	VAL
8	LA	249	THR
9	LB	2	SER
9	LB	159	VAL
9	LB	181	MET
9	LB	231	VAL

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Mol	Chain	Res	Type
9	LB	315	ASN
9	LB	360	LEU
10	LC	1	MET
10	LC	154	VAL
10	LC	290	SER
10	LC	297	GLU
10	LC	335	MET
11	LD	82	GLU
11	LD	118	ILE
11	LD	247	ILE
11	LD	271	MET
12	LE	49	VAL
12	LE	91	THR
12	LE	128	HIS
12	LE	145	THR
12	LE	184	VAL
12	LE	281	ILE
13	LF	41	MET
13	LF	83	VAL
13	LF	238	ASP
14	LG	55	VAL
14	LG	175	ARG
14	LG	222	ILE
14	LG	241	VAL
17	LJ	66	GLU
18	LL	70	VAL
18	LL	122	SER
18	LL	144	LEU
18	LL	164	GLU
19	LM	2	VAL
19	LM	25	VAL
19	LM	124	LYS
20	LN	15	GLN
20	LN	18	VAL
20	LN	89	VAL
20	LN	182	HIS
21	LO	127	VAL
22	LP	21	ASN
22	LP	57	CYS
22	LP	79	THR
23	LQ	98	LEU
23	LQ	160	HIS

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Mol	Chain	Res	Type
23	LQ	175	GLU
24	LR	3	MET
24	LR	144	LYS
25	LS	7	LEU
25	LS	124	ILE
25	LS	158	VAL
26	LT	43	LYS
26	LT	85	LEU
27	LU	60	VAL
30	LX	42	THR
31	LY	25	ILE
31	LY	111	LEU
32	LZ	26	VAL
32	LZ	100	VAL
33	La	134	GLU
33	La	140	VAL
34	Lb	11	ASN
34	Lb	22	LYS
34	Lb	30	GLU
35	Lc	28	VAL
35	Lc	42	LYS
35	Lc	44	LYS
35	Lc	80	GLU
35	Lc	93	THR
36	Ld	40	LYS
36	Ld	56	GLU
36	Ld	119	THR
37	Le	86	GLU
38	Lf	67	THR
38	Lf	105	LEU
39	Lg	2	VAL
40	Lh	44	LEU
40	Lh	116	LEU
41	Li	32	ARG
41	Li	81	ILE
41	Li	86	LYS
42	Lj	2	THR
42	Lj	55	ARG
42	Lj	83	THR
43	Lk	47	ILE
44	Ll	27	ILE
44	Ll	51	LEU

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Mol	Chain	Res	Type
45	Lm	103	LEU
45	Lm	120	ASN
45	Lm	127	VAL
46	Ln	10	MET
47	Lo	68	LEU
47	Lo	72	CYS
47	Lo	79	SER
47	Lo	83	LEU
47	Lo	103	VAL
48	Lp	26	VAL
48	Lp	36	LYS
49	Lr	27	THR
49	Lr	44	ILE
49	Lr	64	ILE
49	Lr	67	ARG
49	Lr	115	SER
50	Ls	35	VAL
50	Ls	53	VAL
50	Ls	107	VAL
50	Ls	188	VAL
50	Ls	214	ARG
51	Lt	28	LEU
51	Lt	133	LEU
53	NB	10	LYS
54	NM	240	LYS
54	NM	287	LEU
54	NM	296	TYR
54	NM	329	LEU
54	NM	456	MET
56	SA	5	LEU
56	SA	111	GLN
56	SA	112	ILE
56	SA	122	LEU
56	SA	141	ASN
56	SA	157	VAL
56	SA	197	VAL
57	SB	106	THR
57	SB	171	ILE
58	SC	83	LEU
58	SC	137	VAL
58	SC	184	VAL
58	SC	215	MET

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Mol	Chain	Res	Type
58	SC	248	TYR
58	SC	252	THR
59	SD	37	VAL
59	SD	59	LEU
59	SD	139	SER
60	SE	26	VAL
60	SE	46	ILE
60	SE	112	HIS
60	SE	168	LYS
60	SE	183	VAL
60	SE	248	ILE
60	SE	254	LYS
61	SF	39	ILE
61	SF	111	VAL
61	SF	128	ILE
62	SG	15	LEU
62	SG	36	VAL
62	SG	49	VAL
62	SG	129	VAL
62	SG	171	THR
62	SG	179	LEU
63	SH	62	ILE
63	SH	90	LYS
63	SH	139	ILE
65	SJ	161	LEU
66	SK	40	VAL
67	SL	35	ARG
67	SL	100	ASN
67	SL	104	LYS
68	SM	64	LEU
68	SM	85	LEU
68	SM	89	VAL
68	SM	109	VAL
69	SN	134	VAL
70	SO	51	GLU
71	SP	26	LEU
71	SP	37	TYR
72	SQ	27	ARG
72	SQ	34	VAL
73	SR	8	THR
73	SR	43	SER
73	SR	66	VAL

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Mol	Chain	Res	Type
73	SR	85	VAL
73	SR	126	MET
74	SS	46	ARG
74	SS	59	LEU
74	SS	83	PHE
74	SS	98	VAL
74	SS	116	LYS
75	ST	6	VAL
75	ST	87	VAL
76	SU	65	THR
76	SU	91	LEU
76	SU	98	VAL
76	SU	115	THR
77	SV	13	VAL
77	SV	32	ILE
77	SV	52	THR
79	SX	19	ASP
79	SX	57	VAL
79	SX	105	PHE
79	SX	123	VAL
79	SX	128	VAL
80	SY	5	VAL
80	SY	22	GLN
80	SY	27	VAL
82	Sa	45	VAL
83	Sb	44	THR
84	Sc	18	LEU
84	Sc	28	THR
84	Sc	50	VAL
84	Sc	57	THR
85	Sd	25	SER
86	Se	29	THR
86	Se	45	VAL
87	Sf	98	VAL
87	Sf	132	MET
87	Sf	148	TYR
88	Sg	14	HIS
88	Sg	18	VAL
88	Sg	105	THR
88	Sg	111	VAL
88	Sg	165	ILE
88	Sg	173	LEU

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Mol	Chain	Res	Type
88	Sg	241	PHE
88	Sg	287	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (114) such sidechains are listed below:

Mol	Chain	Res	Type
3	CR	199	HIS
4	CZ	95	ASN
8	LA	162	ASN
8	LA	205	ASN
9	LB	121	ASN
10	LC	21	ASN
10	LC	61	GLN
11	LD	111	ASN
11	LD	131	ASN
11	LD	202	GLN
11	LD	229	ASN
11	LD	250	ASN
12	LE	167	GLN
12	LE	205	ASN
14	LG	82	GLN
14	LG	141	ASN
14	LG	153	GLN
15	LH	98	HIS
15	LH	140	GLN
16	LI	147	HIS
17	LJ	65	ASN
18	LL	19	GLN
18	LL	40	GLN
18	LL	115	GLN
19	LM	125	ASN
20	LN	32	GLN
21	LO	46	ASN
21	LO	63	ASN
21	LO	180	GLN
22	LP	25	HIS
22	LP	56	GLN
22	LP	93	HIS
22	LP	133	HIS
23	LQ	21	GLN
24	LR	34	ASN
24	LR	40	GLN

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Mol	Chain	Res	Type
24	LR	141	HIS
26	LT	131	GLN
27	LU	44	GLN
27	LU	116	GLN
28	LV	27	ASN
29	LW	50	ASN
31	LY	18	HIS
32	LZ	97	ASN
33	La	19	HIS
33	La	34	ASN
34	Lb	6	ASN
35	Lc	40	GLN
35	Lc	73	HIS
37	Le	52	GLN
38	Lf	21	GLN
38	Lf	80	ASN
40	Lh	107	GLN
40	Lh	108	GLN
42	Lj	30	GLN
42	Lj	48	ASN
44	Ll	4	HIS
47	Lo	102	GLN
49	Lr	41	ASN
50	Ls	159	GLN
50	Ls	200	ASN
51	Lt	95	GLN
51	Lt	100	HIS
51	Lt	103	ASN
51	Lt	142	ASN
53	NB	8	GLN
53	NB	55	ASN
53	NB	63	ASN
53	NB	109	GLN
54	NM	211	HIS
54	NM	232	ASN
54	NM	317	ASN
56	SA	111	GLN
56	SA	141	ASN
57	SB	75	GLN
57	SB	95	ASN
59	SD	159	HIS
59	SD	226	GLN

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Mol	Chain	Res	Type
60	SE	17	HIS
60	SE	36	HIS
60	SE	98	ASN
60	SE	157	ASN
61	SF	74	ASN
61	SF	79	HIS
61	SF	95	HIS
62	SG	4	ASN
62	SG	177	GLN
62	SG	186	GLN
64	SI	7	ASN
64	SI	35	ASN
64	SI	52	ASN
65	SJ	140	GLN
65	SJ	154	GLN
66	SK	66	HIS
67	SL	18	GLN
67	SL	94	HIS
68	SM	15	ASN
68	SM	46	GLN
69	SN	13	GLN
70	SO	32	HIS
72	SQ	8	GLN
72	SQ	80	GLN
73	SR	26	ASN
75	ST	83	GLN
77	SV	35	ASN
78	SW	90	GLN
79	SX	97	ASN
81	SZ	112	ASN
82	Sa	43	ASN
84	Sc	7	GLN
85	Sd	26	ASN
85	Sd	37	ASN
85	Sd	45	GLN
88	Sg	237	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CM	11/952 (1%)	2 (18%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CP	74/75 (98%)	21 (28%)	2 (2%)
5	L5	3633/5070 (71%)	772 (21%)	14 (0%)
55	S2	1704/1869 (91%)	465 (27%)	17 (0%)
6	L7	119/121 (98%)	11 (9%)	0
7	L8	155/157 (98%)	29 (18%)	1 (0%)
All	All	5696/8244 (69%)	1300 (22%)	34 (0%)

All (1300) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CM	804	C
1	CM	809	U
2	CP	2	G
2	CP	4	U
2	CP	6	G
2	CP	8	U
2	CP	9	G
2	CP	15	G
2	CP	16	G
2	CP	17	G
2	CP	19	U
2	CP	22	G
2	CP	46	U
2	CP	49	C
2	CP	50	G
2	CP	57	A
2	CP	58	A
2	CP	68	A
2	CP	69	G
2	CP	70	C
2	CP	72	C
2	CP	73	C
2	CP	75	A
5	L5	17	A
5	L5	21	G
5	L5	25	A
5	L5	30	C
5	L5	39	A
5	L5	42	A
5	L5	48	G
5	L5	56	A
5	L5	59	A

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Mol	Chain	Res	Type
5	L5	63	G
5	L5	64	A
5	L5	65	A
5	L5	66	A
5	L5	69	A
5	L5	72	C
5	L5	73	A
5	L5	76	A
5	L5	91	G
5	L5	104	G
5	L5	108	A
5	L5	109	G
5	L5	110	C
5	L5	119	G
5	L5	120	A
5	L5	133	C
5	L5	134	G
5	L5	135	G
5	L5	136	C
5	L5	137	G
5	L5	144	G
5	L5	152	U
5	L5	159	C
5	L5	165	A
5	L5	172	C
5	L5	180	C
5	L5	183	C
5	L5	184	U
5	L5	185	C
5	L5	188	G
5	L5	189	G
5	L5	200	U
5	L5	210	C
5	L5	216	C
5	L5	217	C
5	L5	218	A
5	L5	233	U
5	L5	234	G
5	L5	254	G
5	L5	255	C
5	L5	261	G
5	L5	266	C

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Mol	Chain	Res	Type
5	L5	267	G
5	L5	269	G
5	L5	275	C
5	L5	280	G
5	L5	297	U
5	L5	306	A
5	L5	315	G
5	L5	316	U
5	L5	340	C
5	L5	350	C
5	L5	387	G
5	L5	388	A
5	L5	407	A
5	L5	409	G
5	L5	410	A
5	L5	411	G
5	L5	412	G
5	L5	413	G
5	L5	414	C
5	L5	449	C
5	L5	450	G
5	L5	452	A
5	L5	453	G
5	L5	454	U
5	L5	456	C
5	L5	457	G
5	L5	461	G
5	L5	467	U
5	L5	474	C
5	L5	479	G
5	L5	485	C
5	L5	486	C
5	L5	489	C
5	L5	493	G
5	L5	494	U
5	L5	497	G
5	L5	498	C
5	L5	500	G
5	L5	501	C
5	L5	502	C
5	L5	503	C
5	L5	504	G

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Mol	Chain	Res	Type
5	L5	505	G
5	L5	509	A
5	L5	510	U
5	L5	512	U
5	L5	513	U
5	L5	514	U
5	L5	515	C
5	L5	517	C
5	L5	518	G
5	L5	643	C
5	L5	644	G
5	L5	646	G
5	L5	655	C
5	L5	656	C
5	L5	657	C
5	L5	658	C
5	L5	660	A
5	L5	666	G
5	L5	667	A
5	L5	668	C
5	L5	669	C
5	L5	673	C
5	L5	674	G
5	L5	675	C
5	L5	676	C
5	L5	686	A
5	L5	687	U
5	L5	688	U
5	L5	692	A
5	L5	696	C
5	L5	697	G
5	L5	703	G
5	L5	704	C
5	L5	706	C
5	L5	708	G
5	L5	730	G
5	L5	731	G
5	L5	738	C
5	L5	739	G
5	L5	742	G
5	L5	746	A
5	L5	758	G

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Mol	Chain	Res	Type
5	L5	760	G
5	L5	904	C
5	L5	905	C
5	L5	912	G
5	L5	913	U
5	L5	914	U
5	L5	915	A
5	L5	916	C
5	L5	917	A
5	L5	918	G
5	L5	923	C
5	L5	924	C
5	L5	926	G
5	L5	929	A
5	L5	932	A
5	L5	933	G
5	L5	934	C
5	L5	941	C
5	L5	945	U
5	L5	946	C
5	L5	956	A
5	L5	958	G
5	L5	959	G
5	L5	960	A
5	L5	961	G
5	L5	962	C
5	L5	965	G
5	L5	966	A
5	L5	967	C
5	L5	969	C
5	L5	970	G
5	L5	972	C
5	L5	977	C
5	L5	988	C
5	L5	989	U
5	L5	990	C
5	L5	991	C
5	L5	992	C
5	L5	993	G
5	L5	1069	G
5	L5	1070	G
5	L5	1075	G

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Mol	Chain	Res	Type
5	L5	1083	U
5	L5	1168	G
5	L5	1173	G
5	L5	1178	G
5	L5	1179	U
5	L5	1180	C
5	L5	1181	C
5	L5	1182	C
5	L5	1183	C
5	L5	1184	A
5	L5	1187	G
5	L5	1193	C
5	L5	1196	G
5	L5	1202	C
5	L5	1203	G
5	L5	1205	G
5	L5	1209	U
5	L5	1211	G
5	L5	1214	C
5	L5	1215	C
5	L5	1218	G
5	L5	1235	G
5	L5	1238	A
5	L5	1241	C
5	L5	1253	G
5	L5	1258	G
5	L5	1259	G
5	L5	1260	G
5	L5	1266	G
5	L5	1267	C
5	L5	1269	G
5	L5	1270	A
5	L5	1271	G
5	L5	1272	C
5	L5	1273	G
5	L5	1274	A
5	L5	1275	G
5	L5	1277	G
5	L5	1280	C
5	L5	1284	G
5	L5	1285	U
5	L5	1287	G

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Mol	Chain	Res	Type
5	L5	1293	G
5	L5	1294	A
5	L5	1295	C
5	L5	1296	G
5	L5	1301	C
5	L5	1303	A
5	L5	1304	C
5	L5	1312	A
5	L5	1326	A
5	L5	1337	A
5	L5	1344	C
5	L5	1354	A
5	L5	1358	G
5	L5	1359	G
5	L5	1365	C
5	L5	1366	G
5	L5	1379	C
5	L5	1387	A
5	L5	1393	G
5	L5	1394	G
5	L5	1397	A
5	L5	1403	G
5	L5	1404	G
5	L5	1405	C
5	L5	1408	G
5	L5	1410	U
5	L5	1411	C
5	L5	1420	A
5	L5	1435	G
5	L5	1437	C
5	L5	1439	C
5	L5	1441	C
5	L5	1442	C
5	L5	1443	A
5	L5	1444	G
5	L5	1447	C
5	L5	1454	G
5	L5	1457	G
5	L5	1466	G
5	L5	1480	C
5	L5	1483	C
5	L5	1497	A

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Mol	Chain	Res	Type
5	L5	1498	G
5	L5	1501	C
5	L5	1502	G
5	L5	1514	U
5	L5	1525	A
5	L5	1534	A
5	L5	1547	A
5	L5	1564	A
5	L5	1566	C
5	L5	1578	U
5	L5	1586	G
5	L5	1591	U
5	L5	1596	U
5	L5	1612	G
5	L5	1624	G
5	L5	1625	G
5	L5	1631	A
5	L5	1633	G
5	L5	1634	A
5	L5	1637	A
5	L5	1638	A
5	L5	1640	C
5	L5	1641	G
5	L5	1642	A
5	L5	1654	G
5	L5	1661	C
5	L5	1663	C
5	L5	1676	C
5	L5	1677	U
5	L5	1680	G
5	L5	1684	A
5	L5	1685	G
5	L5	1694	C
5	L5	1697	G
5	L5	1699	A
5	L5	1700	G
5	L5	1705	G
5	L5	1707	C
5	L5	1734	G
5	L5	1740	C
5	L5	1742	A
5	L5	1750	G

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Mol	Chain	Res	Type
5	L5	1756	U
5	L5	1758	G
5	L5	1760	G
5	L5	1765	A
5	L5	1767	A
5	L5	1785	C
5	L5	1787	A
5	L5	1797	G
5	L5	1803	G
5	L5	1804	A
5	L5	1806	G
5	L5	1810	G
5	L5	1815	G
5	L5	1820	C
5	L5	1821	G
5	L5	1822	U
5	L5	1834	U
5	L5	1836	G
5	L5	1837	A
5	L5	1842	G
5	L5	1855	G
5	L5	1869	G
5	L5	1882	U
5	L5	1891	A
5	L5	1897	A
5	L5	1912	G
5	L5	1916	G
5	L5	1918	U
5	L5	1919	G
5	L5	1920	C
5	L5	1921	C
5	L5	1922	G
5	L5	1930	U
5	L5	1931	C
5	L5	1932	A
5	L5	1936	C
5	L5	1940	G
5	L5	1945	G
5	L5	1948	G
5	L5	1961	G
5	L5	1962	A
5	L5	1976	G

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Mol	Chain	Res	Type
5	L5	1979	A
5	L5	1980	U
5	L5	1981	G
5	L5	1983	A
5	L5	1984	A
5	L5	1985	G
5	L5	1986	U
5	L5	1987	C
5	L5	1997	U
5	L5	2001	G
5	L5	2002	A
5	L5	2004	U
5	L5	2007	G
5	L5	2016	C
5	L5	2017	A
5	L5	2018	C
5	L5	2024	G
5	L5	2025	A
5	L5	2026	A
5	L5	2046	G
5	L5	2048	U
5	L5	2052	G
5	L5	2055	G
5	L5	2056	G
5	L5	2069	A
5	L5	2084	C
5	L5	2085	G
5	L5	2092	G
5	L5	2094	G
5	L5	2095	A
5	L5	2098	G
5	L5	2101	C
5	L5	2106	G
5	L5	2107	C
5	L5	2108	G
5	L5	2116	C
5	L5	2117	G
5	L5	2118	G
5	L5	2119	C
5	L5	2120	G
5	L5	2121	C
5	L5	2123	C

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Mol	Chain	Res	Type
5	L5	2250	C
5	L5	2252	G
5	L5	2253	A
5	L5	2254	G
5	L5	2255	C
5	L5	2256	C
5	L5	2257	C
5	L5	2258	C
5	L5	2269	C
5	L5	2289	C
5	L5	2300	A
5	L5	2301	G
5	L5	2306	G
5	L5	2313	A
5	L5	2331	G
5	L5	2332	A
5	L5	2333	G
5	L5	2345	G
5	L5	2348	G
5	L5	2351	C
5	L5	2360	A
5	L5	2364	G
5	L5	2395	A
5	L5	2397	G
5	L5	2417	A
5	L5	2421	G
5	L5	2422	C
5	L5	2424	G
5	L5	2425	U
5	L5	2441	C
5	L5	2450	G
5	L5	2453	A
5	L5	2464	C
5	L5	2465	C
5	L5	2469	C
5	L5	2475	G
5	L5	2483	G
5	L5	2484	A
5	L5	2487	G
5	L5	2488	C
5	L5	2489	C
5	L5	2490	U

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Mol	Chain	Res	Type
5	L5	2491	C
5	L5	2493	G
5	L5	2503	G
5	L5	2504	C
5	L5	2505	C
5	L5	2506	G
5	L5	2513	A
5	L5	2519	U
5	L5	2520	C
5	L5	2529	A
5	L5	2537	A
5	L5	2544	G
5	L5	2545	U
5	L5	2546	G
5	L5	2547	G
5	L5	2554	U
5	L5	2555	G
5	L5	2573	A
5	L5	2583	C
5	L5	2587	A
5	L5	2589	C
5	L5	2601	A
5	L5	2618	G
5	L5	2627	C
5	L5	2638	G
5	L5	2653	C
5	L5	2662	G
5	L5	2669	C
5	L5	2675	G
5	L5	2676	A
5	L5	2687	U
5	L5	2694	G
5	L5	2695	A
5	L5	2696	A
5	L5	2703	G
5	L5	2710	C
5	L5	2711	G
5	L5	2721	G
5	L5	2724	G
5	L5	2726	G
5	L5	2738	C
5	L5	2739	C

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Mol	Chain	Res	Type
5	L5	2742	G
5	L5	2743	A
5	L5	2746	A
5	L5	2754	G
5	L5	2761	U
5	L5	2763	U
5	L5	2764	A
5	L5	2769	U
5	L5	2770	C
5	L5	2788	U
5	L5	2790	U
5	L5	2814	C
5	L5	2815	A
5	L5	2826	U
5	L5	2827	G
5	L5	2835	A
5	L5	2838	G
5	L5	2842	G
5	L5	2848	G
5	L5	2850	A
5	L5	2855	G
5	L5	2856	C
5	L5	2876	G
5	L5	2877	G
5	L5	2890	C
5	L5	2891	U
5	L5	2892	C
5	L5	2894	A
5	L5	2897	G
5	L5	2900	U
5	L5	2902	G
5	L5	2903	G
5	L5	2904	U
5	L5	2905	C
5	L5	2906	G
5	L5	2907	G
5	L5	2908	U
5	L5	3585	G
5	L5	3586	G
5	L5	3588	C
5	L5	3591	C
5	L5	3593	C

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Mol	Chain	Res	Type
5	L5	3594	C
5	L5	3595	U
5	L5	3596	A
5	L5	3597	G
5	L5	3604	A
5	L5	3605	C
5	L5	3615	G
5	L5	3618	C
5	L5	3626	G
5	L5	3630	A
5	L5	3635	A
5	L5	3644	U
5	L5	3646	A
5	L5	3648	A
5	L5	3662	A
5	L5	3664	G
5	L5	3673	C
5	L5	3674	G
5	L5	3711	A
5	L5	3713	U
5	L5	3726	A
5	L5	3727	A
5	L5	3729	U
5	L5	3735	G
5	L5	3736	A
5	L5	3750	G
5	L5	3753	G
5	L5	3760	A
5	L5	3761	C
5	L5	3771	C
5	L5	3776	G
5	L5	3777	G
5	L5	3784	A
5	L5	3786	U
5	L5	3810	C
5	L5	3814	U
5	L5	3817	A
5	L5	3818	U
5	L5	3819	G
5	L5	3823	G
5	L5	3827	G
5	L5	3838	U

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Mol	Chain	Res	Type
5	L5	3839	G
5	L5	3840	U
5	L5	3867	A
5	L5	3869	C
5	L5	3877	A
5	L5	3878	C
5	L5	3879	G
5	L5	3885	G
5	L5	3892	U
5	L5	3897	G
5	L5	3901	A
5	L5	3905	A
5	L5	3906	A
5	L5	3907	G
5	L5	3908	A
5	L5	3915	U
5	L5	3926	C
5	L5	3930	U
5	L5	3942	A
5	L5	3943	A
5	L5	3947	A
5	L5	3949	A
5	L5	4064	C
5	L5	4065	G
5	L5	4069	U
5	L5	4076	G
5	L5	4084	G
5	L5	4097	G
5	L5	4099	G
5	L5	4102	C
5	L5	4104	G
5	L5	4107	G
5	L5	4113	U
5	L5	4114	C
5	L5	4115	G
5	L5	4116	C
5	L5	4119	C
5	L5	4122	G
5	L5	4128	A
5	L5	4131	G
5	L5	4135	G
5	L5	4137	C

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Mol	Chain	Res	Type
5	L5	4138	C
5	L5	4140	C
5	L5	4141	G
5	L5	4142	C
5	L5	4143	G
5	L5	4145	C
5	L5	4150	G
5	L5	4154	G
5	L5	4155	C
5	L5	4162	C
5	L5	4163	U
5	L5	4170	A
5	L5	4183	G
5	L5	4184	G
5	L5	4191	G
5	L5	4203	A
5	L5	4206	C
5	L5	4222	G
5	L5	4225	G
5	L5	4228	G
5	L5	4229	U
5	L5	4233	A
5	L5	4238	G
5	L5	4243	C
5	L5	4249	G
5	L5	4251	A
5	L5	4254	G
5	L5	4268	A
5	L5	4273	A
5	L5	4281	A
5	L5	4291	G
5	L5	4296	U
5	L5	4304	A
5	L5	4305	G
5	L5	4306	U
5	L5	4314	C
5	L5	4319	C
5	L5	4329	G
5	L5	4330	G
5	L5	4332	C
5	L5	4349	C
5	L5	4354	U

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Mol	Chain	Res	Type
5	L5	4373	G
5	L5	4376	A
5	L5	4377	G
5	L5	4378	A
5	L5	4379	A
5	L5	4387	C
5	L5	4391	G
5	L5	4394	A
5	L5	4422	A
5	L5	4426	C
5	L5	4436	U
5	L5	4438	U
5	L5	4444	C
5	L5	4448	G
5	L5	4449	A
5	L5	4452	U
5	L5	4453	C
5	L5	4464	A
5	L5	4466	C
5	L5	4475	G
5	L5	4500	U
5	L5	4512	U
5	L5	4513	A
5	L5	4518	A
5	L5	4519	C
5	L5	4524	G
5	L5	4525	C
5	L5	4528	G
5	L5	4532	U
5	L5	4548	A
5	L5	4549	G
5	L5	4554	G
5	L5	4560	C
5	L5	4567	G
5	L5	4570	G
5	L5	4573	G
5	L5	4575	G
5	L5	4584	A
5	L5	4590	A
5	L5	4600	G
5	L5	4601	U
5	L5	4608	G

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Mol	Chain	Res	Type
5	L5	4617	G
5	L5	4627	U
5	L5	4632	U
5	L5	4636	U
5	L5	4637	G
5	L5	4638	U
5	L5	4639	G
5	L5	4652	G
5	L5	4656	A
5	L5	4670	C
5	L5	4672	A
5	L5	4687	A
5	L5	4693	C
5	L5	4694	G
5	L5	4700	A
5	L5	4708	A
5	L5	4709	U
5	L5	4732	G
5	L5	4733	C
5	L5	4734	A
5	L5	4740	G
5	L5	4741	C
5	L5	4742	G
5	L5	4745	G
5	L5	4754	G
5	L5	4757	C
5	L5	4759	C
5	L5	4761	G
5	L5	4765	G
5	L5	4771	C
5	L5	4772	C
5	L5	4773	C
5	L5	4775	C
5	L5	4860	G
5	L5	4868	G
5	L5	4870	G
5	L5	4871	C
5	L5	4875	G
5	L5	4881	U
5	L5	4882	U
5	L5	4883	C
5	L5	4888	U

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Mol	Chain	Res	Type
5	L5	4889	G
5	L5	4894	A
5	L5	4895	C
5	L5	4896	G
5	L5	4900	C
5	L5	4901	G
5	L5	4910	G
5	L5	4912	G
5	L5	4914	C
5	L5	4925	U
5	L5	4927	G
5	L5	4928	C
5	L5	4931	G
5	L5	4934	A
5	L5	4937	C
5	L5	4940	C
5	L5	4941	G
5	L5	4943	A
5	L5	4944	C
5	L5	4949	G
5	L5	4955	A
5	L5	4960	G
5	L5	4963	G
5	L5	4966	A
5	L5	4976	U
5	L5	4979	A
5	L5	4988	U
5	L5	4989	U
5	L5	4990	C
5	L5	4991	U
5	L5	5007	A
5	L5	5014	A
5	L5	5017	G
5	L5	5022	U
5	L5	5023	C
5	L5	5024	C
5	L5	5025	C
5	L5	5026	U
5	L5	5028	G
5	L5	5029	C
5	L5	5030	U
5	L5	5031	G

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Mol	Chain	Res	Type
5	L5	5034	A
5	L5	5041	G
5	L5	5050	C
5	L5	5054	C
5	L5	5058	A
5	L5	5062	G
5	L5	5069	U
6	L7	23	A
6	L7	33	U
6	L7	53	U
6	L7	63	C
6	L7	64	G
6	L7	97	G
6	L7	100	A
6	L7	102	U
6	L7	110	G
6	L7	117	G
6	L7	120	U
7	L8	23	C
7	L8	34	U
7	L8	35	C
7	L8	39	G
7	L8	48	A
7	L8	59	A
7	L8	63	U
7	L8	80	A
7	L8	82	A
7	L8	83	C
7	L8	84	A
7	L8	86	U
7	L8	87	G
7	L8	88	A
7	L8	94	G
7	L8	103	A
7	L8	105	C
7	L8	110	U
7	L8	111	U
7	L8	112	G
7	L8	114	G
7	L8	124	U
7	L8	125	C
7	L8	126	C

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Mol	Chain	Res	Type
7	L8	127	U
7	L8	150	C
7	L8	151	G
7	L8	153	C
7	L8	155	C
55	S2	7	G
55	S2	33	G
55	S2	41	G
55	S2	44	U
55	S2	45	A
55	S2	46	A
55	S2	56	G
55	S2	58	C
55	S2	59	U
55	S2	62	G
55	S2	66	G
55	S2	67	C
55	S2	68	A
55	S2	71	G
55	S2	72	C
55	S2	73	C
55	S2	75	G
55	S2	76	U
55	S2	80	G
55	S2	84	A
55	S2	85	A
55	S2	86	C
55	S2	96	C
55	S2	97	U
55	S2	99	A
55	S2	101	U
55	S2	113	G
55	S2	114	G
55	S2	121	U
55	S2	126	G
55	S2	127	C
55	S2	128	U
55	S2	130	G
55	S2	143	U
55	S2	144	U
55	S2	149	A
55	S2	150	A

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Mol	Chain	Res	Type
55	S2	151	C
55	S2	155	G
55	S2	156	G
55	S2	161	U
55	S2	162	C
55	S2	163	U
55	S2	167	G
55	S2	168	C
55	S2	170	A
55	S2	171	A
55	S2	182	C
55	S2	193	C
55	S2	198	U
55	S2	202	G
55	S2	207	G
55	S2	210	U
55	S2	211	G
55	S2	214	U
55	S2	219	U
55	S2	290	U
55	S2	291	G
55	S2	295	C
55	S2	306	C
55	S2	308	G
55	S2	309	G
55	S2	311	C
55	S2	312	G
55	S2	313	A
55	S2	319	C
55	S2	322	C
55	S2	323	C
55	S2	324	C
55	S2	325	C
55	S2	326	C
55	S2	328	U
55	S2	329	G
55	S2	332	G
55	S2	340	C
55	S2	360	A
55	S2	362	C
55	S2	364	A
55	S2	368	U

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Mol	Chain	Res	Type
55	S2	370	G
55	S2	380	G
55	S2	381	C
55	S2	383	G
55	S2	385	G
55	S2	386	C
55	S2	398	A
55	S2	400	C
55	S2	409	C
55	S2	413	G
55	S2	434	G
55	S2	448	A
55	S2	449	A
55	S2	450	C
55	S2	452	G
55	S2	464	A
55	S2	465	A
55	S2	466	G
55	S2	468	A
55	S2	471	G
55	S2	472	C
55	S2	473	A
55	S2	474	G
55	S2	482	G
55	S2	483	C
55	S2	487	U
55	S2	488	U
55	S2	489	A
55	S2	492	C
55	S2	493	A
55	S2	496	C
55	S2	500	A
55	S2	502	C
55	S2	503	C
55	S2	506	G
55	S2	516	A
55	S2	517	C
55	S2	525	A
55	S2	531	A
55	S2	532	C
55	S2	536	A
55	S2	537	C

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Mol	Chain	Res	Type
55	S2	539	C
55	S2	540	U
55	S2	541	U
55	S2	542	U
55	S2	543	C
55	S2	544	G
55	S2	545	A
55	S2	547	G
55	S2	549	C
55	S2	551	U
55	S2	554	A
55	S2	555	A
55	S2	556	U
55	S2	559	G
55	S2	561	A
55	S2	563	G
55	S2	566	U
55	S2	567	C
55	S2	575	A
55	S2	576	A
55	S2	582	U
55	S2	583	A
55	S2	587	A
55	S2	589	G
55	S2	590	A
55	S2	591	U
55	S2	592	C
55	S2	593	C
55	S2	595	U
55	S2	596	U
55	S2	604	A
55	S2	605	A
55	S2	606	G
55	S2	607	U
55	S2	608	C
55	S2	613	G
55	S2	614	C
55	S2	617	G
55	S2	628	A
55	S2	631	U
55	S2	643	A
55	S2	648	A

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Mol	Chain	Res	Type
55	S2	650	A
55	S2	651	U
55	S2	652	U
55	S2	655	A
55	S2	660	C
55	S2	668	A
55	S2	669	A
55	S2	670	A
55	S2	671	A
55	S2	672	A
55	S2	673	G
55	S2	688	U
55	S2	689	U
55	S2	690	G
55	S2	692	G
55	S2	694	G
55	S2	696	G
55	S2	697	G
55	S2	732	U
55	S2	733	C
55	S2	734	C
55	S2	735	C
55	S2	736	C
55	S2	738	C
55	S2	739	C
55	S2	746	C
55	S2	747	U
55	S2	748	C
55	S2	749	U
55	S2	751	G
55	S2	752	G
55	S2	753	C
55	S2	790	C
55	S2	791	C
55	S2	795	A
55	S2	796	G
55	S2	797	C
55	S2	798	G
55	S2	799	U
55	S2	801	U
55	S2	807	G
55	S2	808	A

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Mol	Chain	Res	Type
55	S2	809	A
55	S2	810	A
55	S2	811	A
55	S2	812	A
55	S2	813	A
55	S2	818	A
55	S2	821	G
55	S2	830	A
55	S2	834	C
55	S2	835	C
55	S2	836	G
55	S2	837	A
55	S2	838	G
55	S2	839	C
55	S2	840	C
55	S2	841	G
55	S2	842	C
55	S2	847	A
55	S2	858	A
55	S2	859	G
55	S2	868	G
55	S2	869	A
55	S2	870	A
55	S2	872	A
55	S2	873	G
55	S2	874	G
55	S2	878	G
55	S2	880	G
55	S2	883	U
55	S2	888	U
55	S2	889	U
55	S2	890	U
55	S2	891	G
55	S2	892	U
55	S2	893	U
55	S2	894	G
55	S2	895	G
55	S2	896	U
55	S2	898	U
55	S2	900	C
55	S2	901	G
55	S2	902	G

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Mol	Chain	Res	Type
55	S2	903	A
55	S2	904	A
55	S2	905	C
55	S2	909	G
55	S2	912	C
55	S2	913	A
55	S2	920	A
55	S2	922	A
55	S2	926	A
55	S2	933	G
55	S2	934	G
55	S2	955	A
55	S2	958	G
55	S2	963	A
55	S2	970	G
55	S2	971	G
55	S2	972	A
55	S2	990	A
55	S2	992	A
55	S2	1001	A
55	S2	1017	U
55	S2	1019	C
55	S2	1021	U
55	S2	1023	A
55	S2	1027	A
55	S2	1060	A
55	S2	1061	U
55	S2	1062	A
55	S2	1078	C
55	S2	1080	A
55	S2	1083	A
55	S2	1084	A
55	S2	1085	C
55	S2	1089	G
55	S2	1090	C
55	S2	1096	G
55	S2	1099	G
55	S2	1100	A
55	S2	1101	U
55	S2	1102	G
55	S2	1105	G
55	S2	1106	C

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Mol	Chain	Res	Type
55	S2	1108	G
55	S2	1112	U
55	S2	1114	U
55	S2	1116	C
55	S2	1119	A
55	S2	1120	U
55	S2	1121	G
55	S2	1126	G
55	S2	1133	A
55	S2	1139	C
55	S2	1142	G
55	S2	1143	A
55	S2	1144	A
55	S2	1145	A
55	S2	1146	C
55	S2	1149	A
55	S2	1153	C
55	S2	1154	U
55	S2	1155	U
55	S2	1157	G
55	S2	1158	G
55	S2	1168	G
55	S2	1183	A
55	S2	1195	A
55	S2	1207	G
55	S2	1212	G
55	S2	1215	C
55	S2	1217	A
55	S2	1221	G
55	S2	1224	G
55	S2	1242	U
55	S2	1243	U
55	S2	1251	A
55	S2	1253	A
55	S2	1256	G
55	S2	1257	G
55	S2	1259	A
55	S2	1260	A
55	S2	1265	A
55	S2	1268	C
55	S2	1271	C
55	S2	1272	C

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Mol	Chain	Res	Type
55	S2	1273	C
55	S2	1274	G
55	S2	1275	G
55	S2	1276	A
55	S2	1281	G
55	S2	1282	A
55	S2	1283	C
55	S2	1285	G
55	S2	1286	G
55	S2	1297	U
55	S2	1298	G
55	S2	1299	A
55	S2	1301	A
55	S2	1302	G
55	S2	1303	C
55	S2	1306	U
55	S2	1308	U
55	S2	1313	A
55	S2	1314	U
55	S2	1321	G
55	S2	1326	U
55	S2	1332	A
55	S2	1342	U
55	S2	1348	G
55	S2	1371	U
55	S2	1372	U
55	S2	1378	A
55	S2	1384	C
55	S2	1396	A
55	S2	1397	U
55	S2	1402	A
55	S2	1404	U
55	S2	1408	U
55	S2	1415	C
55	S2	1419	C
55	S2	1420	G
55	S2	1421	A
55	S2	1422	G
55	S2	1423	C
55	S2	1428	G
55	S2	1438	A
55	S2	1449	G

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Mol	Chain	Res	Type
55	S2	1450	G
55	S2	1452	A
55	S2	1454	A
55	S2	1462	U
55	S2	1463	U
55	S2	1475	G
55	S2	1477	U
55	S2	1487	A
55	S2	1489	A
55	S2	1490	G
55	S2	1495	G
55	S2	1497	G
55	S2	1498	A
55	S2	1505	U
55	S2	1506	A
55	S2	1508	A
55	S2	1510	G
55	S2	1519	U
55	S2	1520	G
55	S2	1521	C
55	S2	1522	A
55	S2	1527	C
55	S2	1528	G
55	S2	1533	A
55	S2	1546	G
55	S2	1548	G
55	S2	1552	G
55	S2	1553	C
55	S2	1555	U
55	S2	1556	A
55	S2	1563	G
55	S2	1567	G
55	S2	1570	G
55	S2	1580	A
55	S2	1585	U
55	S2	1586	U
55	S2	1587	G
55	S2	1588	A
55	S2	1589	A
55	S2	1599	U
55	S2	1601	A
55	S2	1602	U

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Mol	Chain	Res	Type
55	S2	1613	G
55	S2	1614	A
55	S2	1621	U
55	S2	1623	A
55	S2	1624	U
55	S2	1639	G
55	S2	1644	C
55	S2	1646	C
55	S2	1648	G
55	S2	1654	G
55	S2	1663	A
55	S2	1664	A
55	S2	1665	G
55	S2	1678	A
55	S2	1694	U
55	S2	1695	A
55	S2	1719	A
55	S2	1721	U
55	S2	1722	G
55	S2	1743	G
55	S2	1744	G
55	S2	1745	A
55	S2	1748	G
55	S2	1753	C
55	S2	1754	G
55	S2	1755	C
55	S2	1773	C
55	S2	1781	A
55	S2	1782	G
55	S2	1783	C
55	S2	1784	G
55	S2	1786	U
55	S2	1813	A
55	S2	1824	A
55	S2	1825	A
55	S2	1826	G
55	S2	1829	G
55	S2	1831	A
55	S2	1835	A
55	S2	1837	G
55	S2	1838	U
55	S2	1849	G

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Mol	Chain	Res	Type
55	S2	1850	A
55	S2	1851	A
55	S2	1852	C
55	S2	1861	G
55	S2	1862	G
55	S2	1863	A
55	S2	1865	C
55	S2	1868	U

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	CP	3	C
2	CP	21	U
5	L5	406	C
5	L5	504	G
5	L5	914	U
5	L5	1082	C
5	L5	1633	G
5	L5	2117	G
5	L5	2416	G
5	L5	2675	G
5	L5	2760	G
5	L5	3614	G
5	L5	3673	C
5	L5	4600	G
5	L5	4699	U
5	L5	4913	G
7	L8	87	G
55	S2	85	A
55	S2	143	U
55	S2	150	A
55	S2	213	G
55	S2	465	A
55	S2	604	A
55	S2	688	U
55	S2	912	C
55	S2	971	G
55	S2	1120	U
55	S2	1145	A
55	S2	1273	C
55	S2	1519	U

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Mol	Chain	Res	Type
55	S2	1585	U
55	S2	1601	A
55	S2	1664	A
55	S2	1860	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	LYO	CR	63	3	7,9,10	0.80	0	7,10,12	1.05	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LYO	CR	63	3	-	2/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	CR	63	LYO	N-CA-CB-CG
3	CR	63	LYO	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 200 ligands modelled in this entry, 199 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
90	G3D	CZ	301	-	33,34,34	3.26	15 (45%)	52,54,54	1.90	11 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
90	G3D	CZ	301	-	-	2/21/37/37	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	CZ	301	G3D	C3'-C4'	-8.34	1.31	1.52
90	CZ	301	G3D	O4'-C4'	7.85	1.62	1.45
90	CZ	301	G3D	C4-N3	6.63	1.49	1.34
90	CZ	301	G3D	C2-N3	5.44	1.46	1.33
90	CZ	301	G3D	PA-O3A	5.16	1.65	1.59
90	CZ	301	G3D	C2-N2	4.90	1.45	1.34
90	CZ	301	G3D	O4'-C1'	-4.75	1.31	1.42
90	CZ	301	G3D	P1-O3'	3.25	1.65	1.59
90	CZ	301	G3D	C2-N1	2.94	1.44	1.37
90	CZ	301	G3D	O2'-C2'	-2.80	1.36	1.43
90	CZ	301	G3D	C6-N1	2.55	1.43	1.38
90	CZ	301	G3D	C5-C6	2.54	1.53	1.44
90	CZ	301	G3D	C5-N7	-2.53	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	CZ	301	G3D	O6-C6	-2.51	1.18	1.23
90	CZ	301	G3D	C4-N9	-2.22	1.32	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	CZ	301	G3D	C1'-N9-C8	-5.83	110.17	126.73
90	CZ	301	G3D	C5-C4-N3	-4.52	121.19	128.39
90	CZ	301	G3D	C2-N3-C4	4.31	119.73	112.30
90	CZ	301	G3D	C1'-N9-C4	4.23	139.00	126.49
90	CZ	301	G3D	N9-C8-N7	-4.10	105.80	113.40
90	CZ	301	G3D	N9-C4-N3	3.15	132.25	125.95
90	CZ	301	G3D	C2-N1-C6	-2.86	119.93	125.11
90	CZ	301	G3D	C5-C6-N1	2.65	120.00	113.25
90	CZ	301	G3D	C8-N9-C4	2.57	110.83	106.03
90	CZ	301	G3D	C8-N7-C5	2.55	108.79	104.26
90	CZ	301	G3D	O6-C6-C5	-2.45	120.06	126.53

There are no chirality outliers.

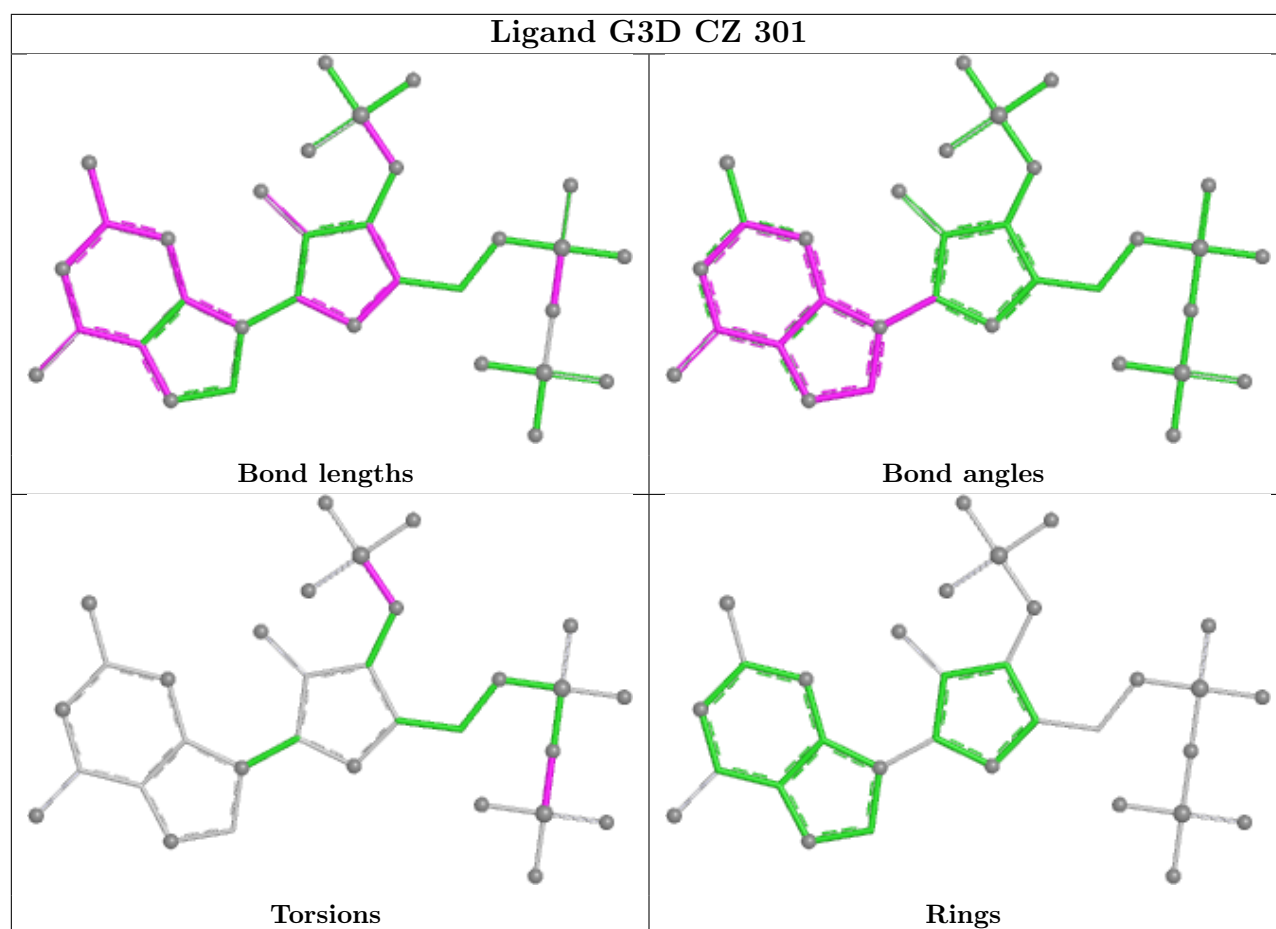
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	CZ	301	G3D	PA-O3A-PB-O1B
90	CZ	301	G3D	C3'-O3'-P1-O5P

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

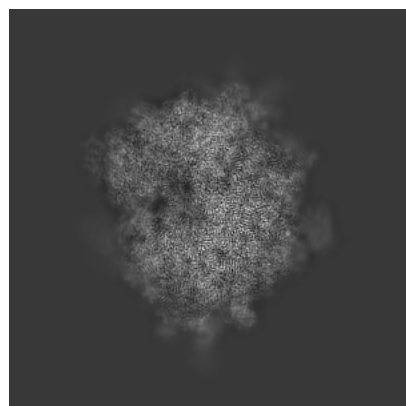
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53231. These allow visual inspection of the internal detail of the map and identification of artifacts.

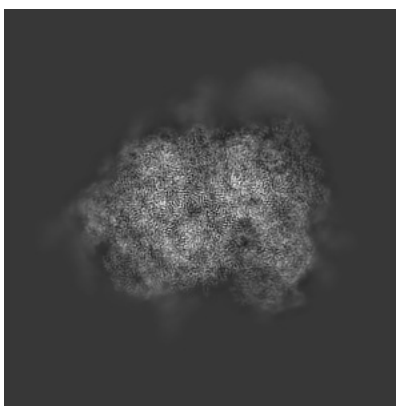
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

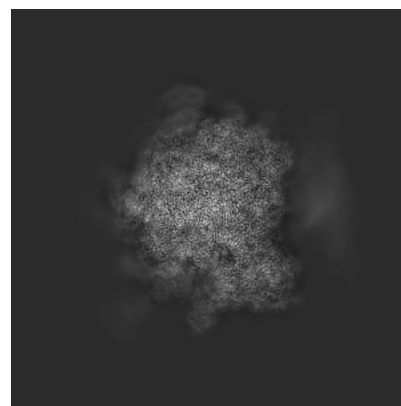
6.1.1 Primary map



X

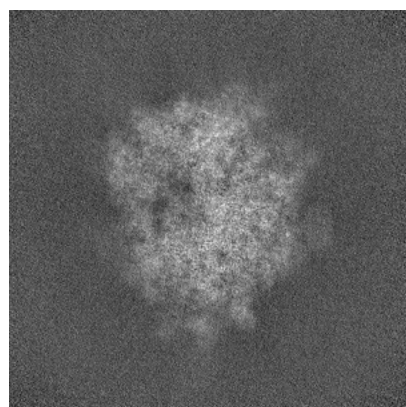


Y

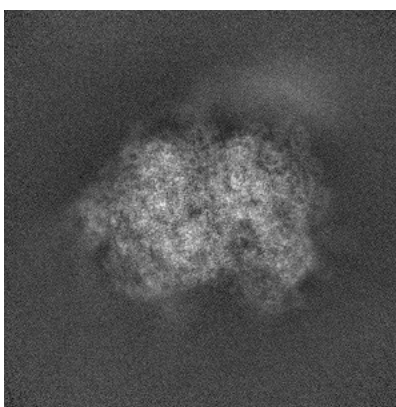


Z

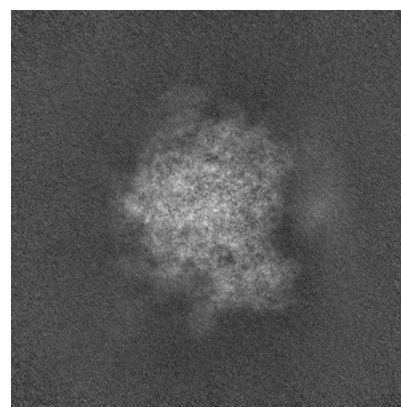
6.1.2 Raw map



X



Y

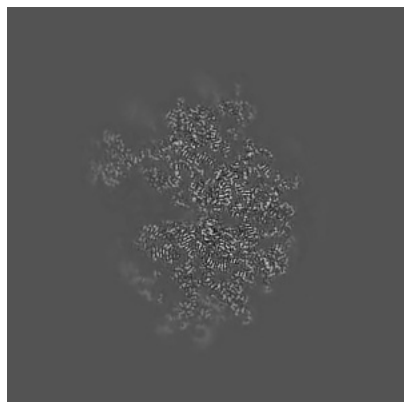


Z

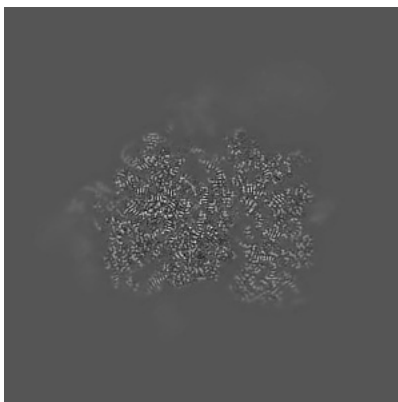
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

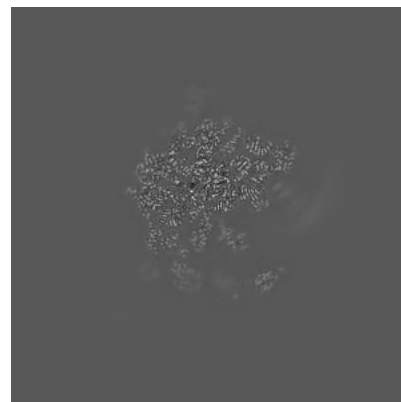
6.2.1 Primary map



X Index: 320

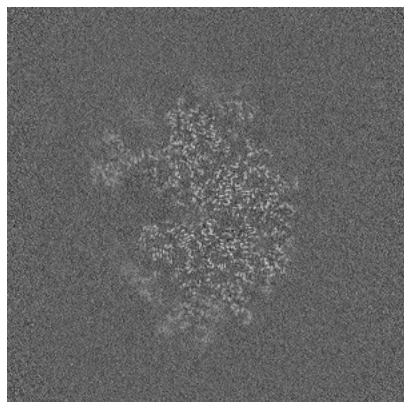


Y Index: 320

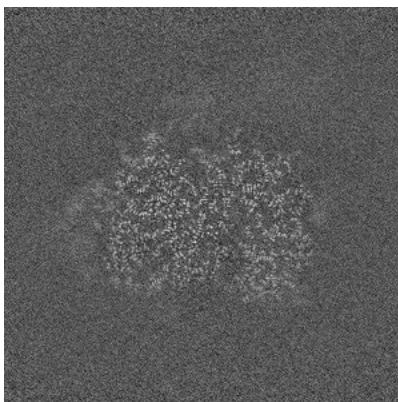


Z Index: 320

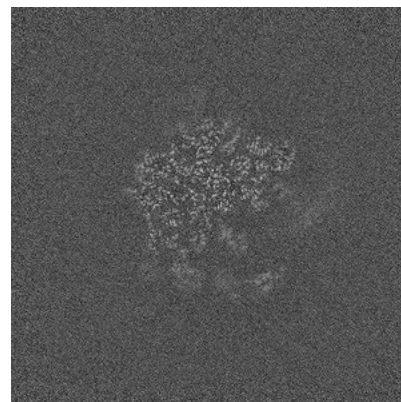
6.2.2 Raw map



X Index: 320



Y Index: 320

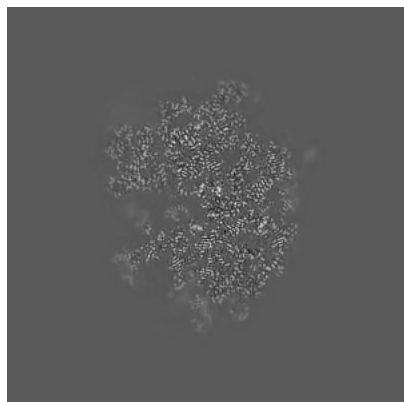


Z Index: 320

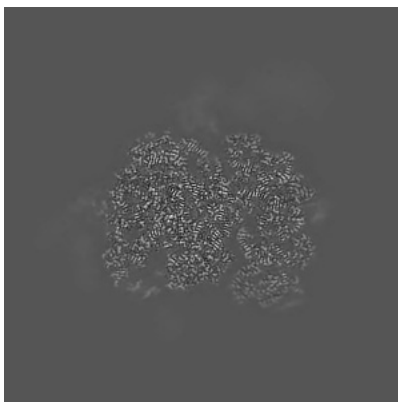
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

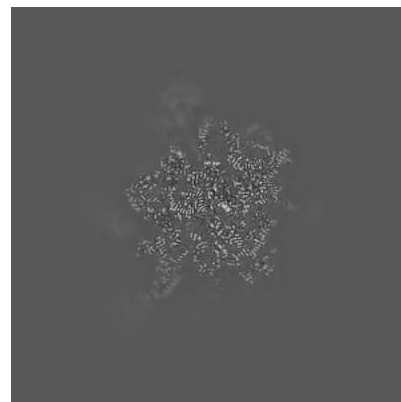
6.3.1 Primary map



X Index: 344

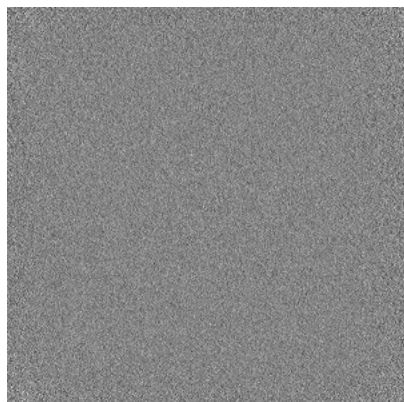


Y Index: 329

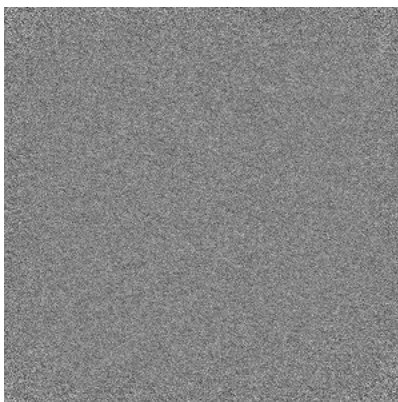


Z Index: 267

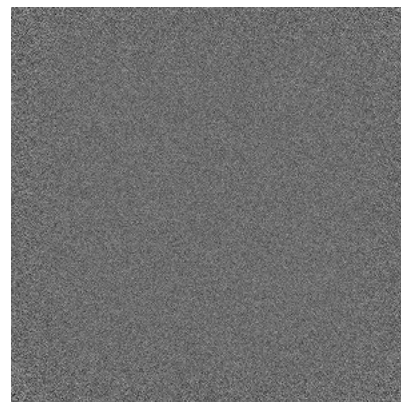
6.3.2 Raw map



X Index: 0



Y Index: 0

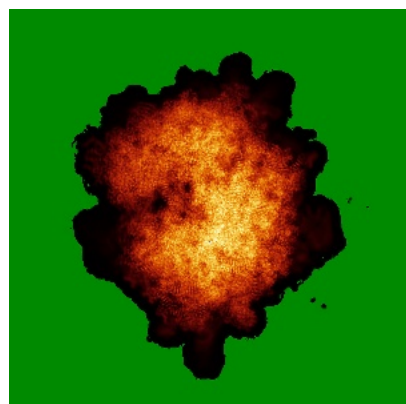


Z Index: 0

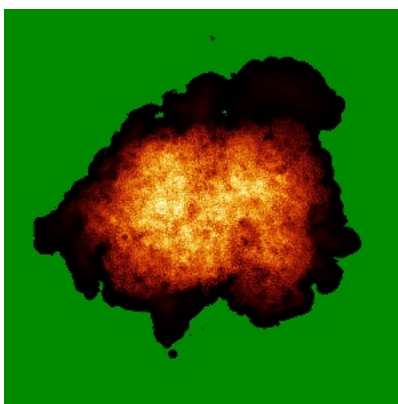
The images above show the largest variance slices of the map in three orthogonal directions.

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

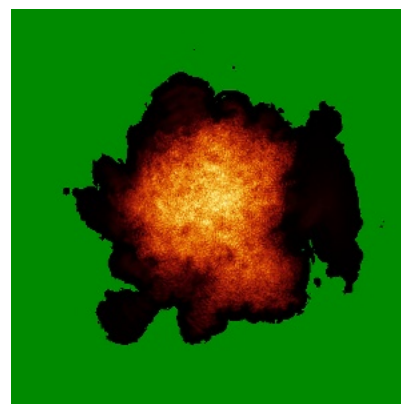
6.4.1 Primary map



X

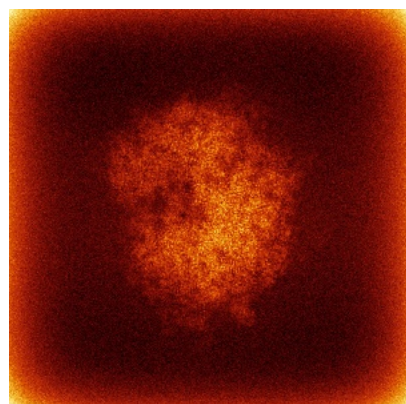


Y

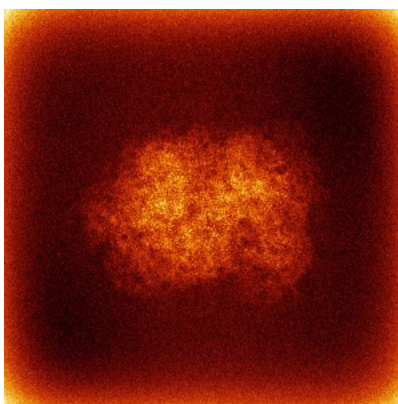


Z

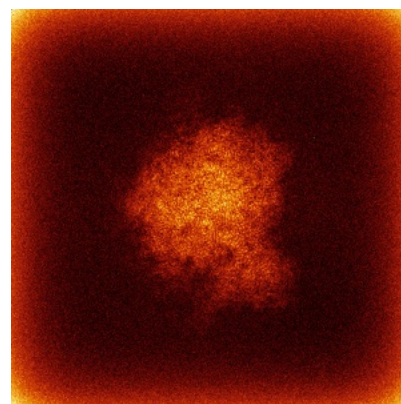
6.4.2 Raw map



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 [i](#)

6.5.1 Primary map



X



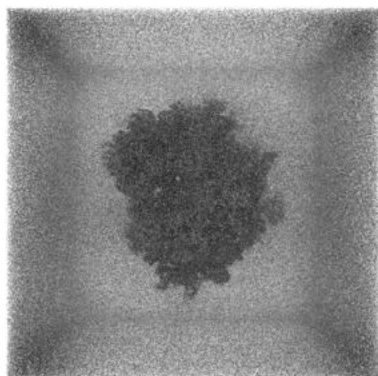
Y



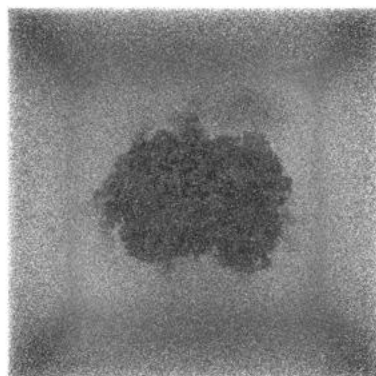
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

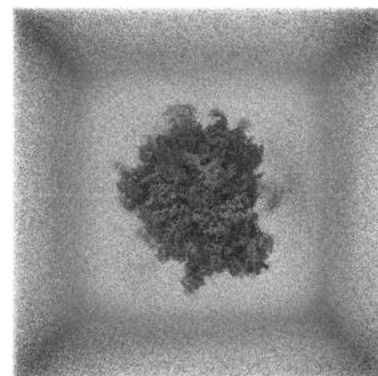
6.5.2 Raw map



X



Y



Z

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

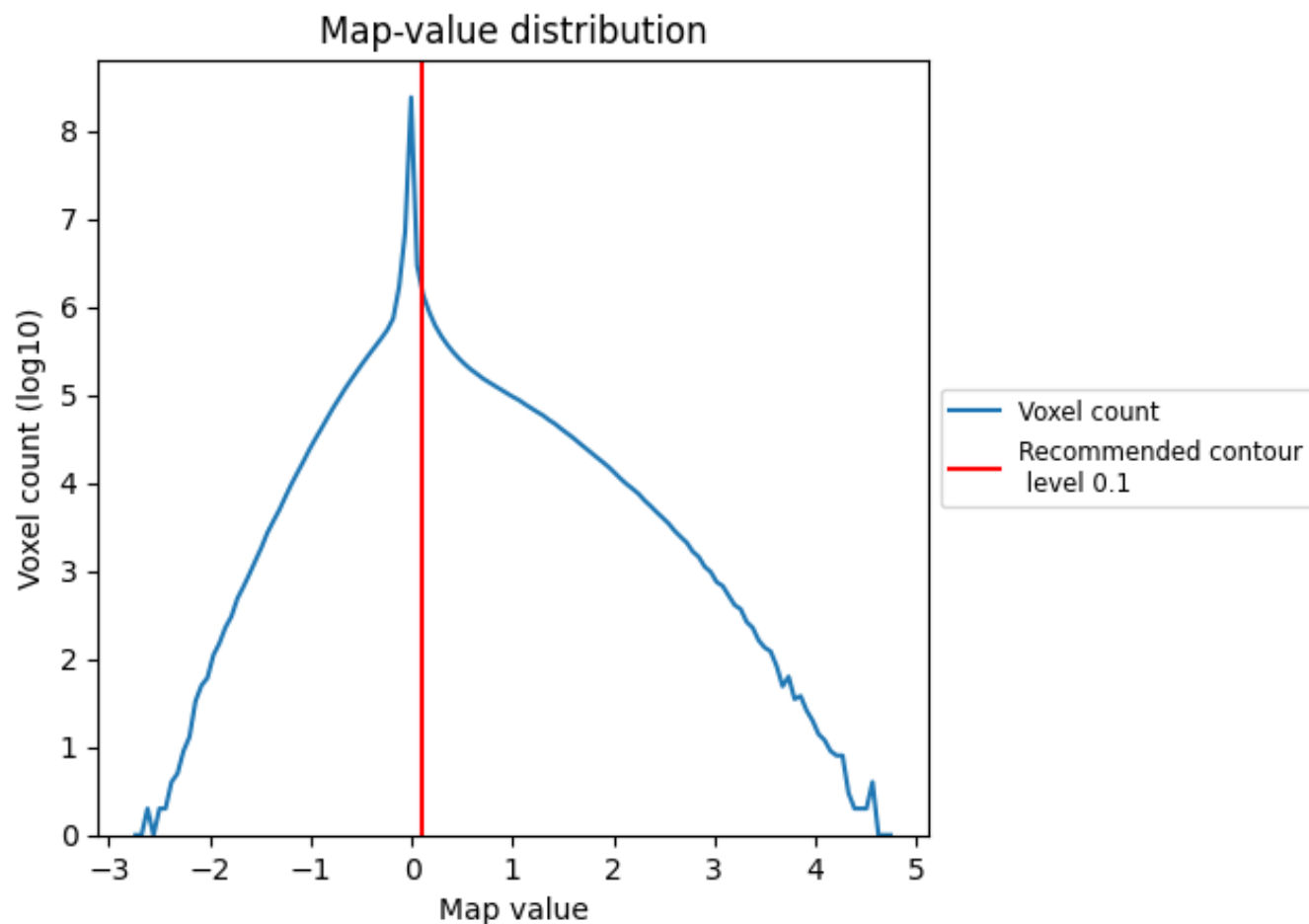
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

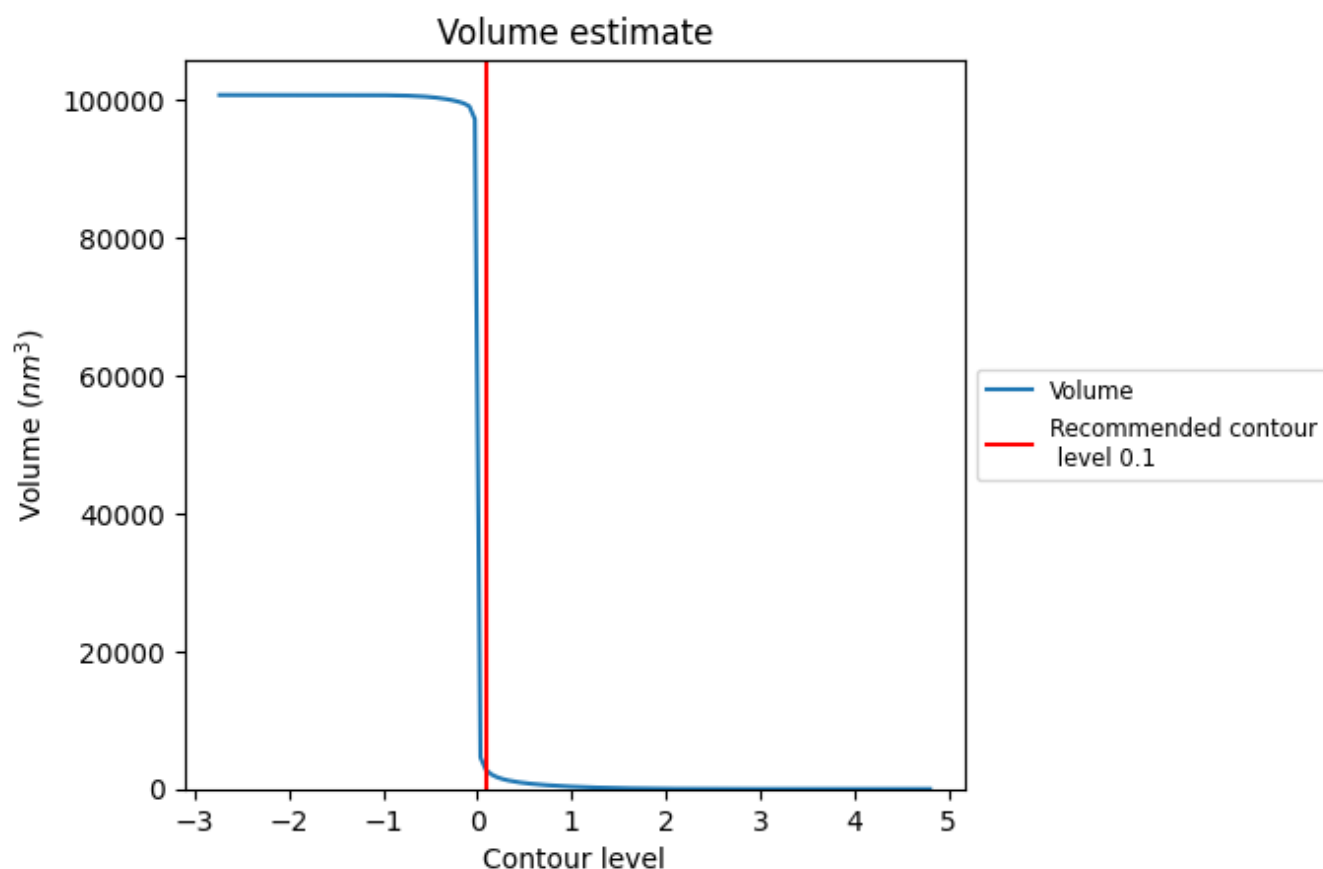
This section contains the results of statistical analysis of the map.

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.

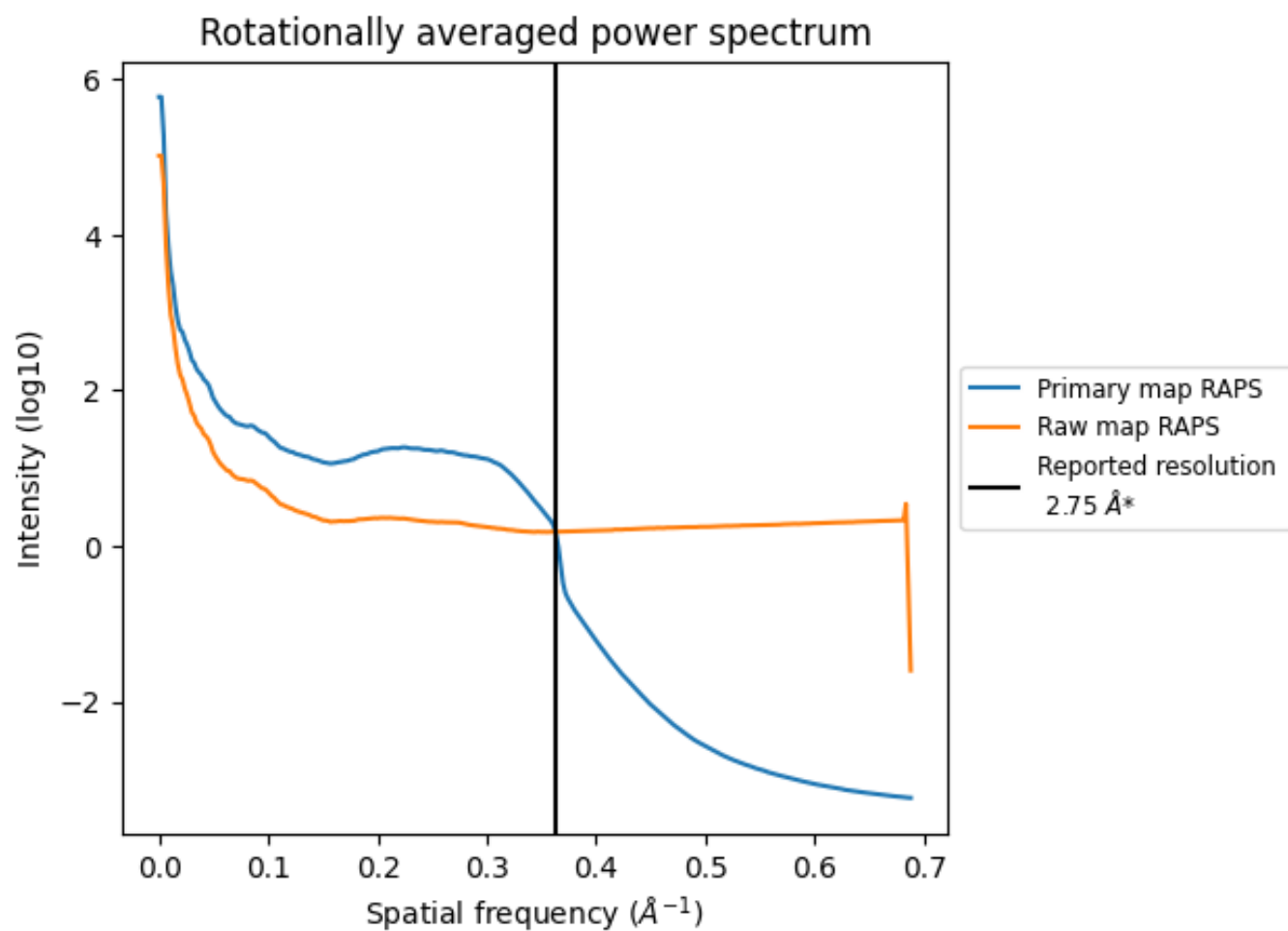
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2667 nm^3 ; this corresponds to an approximate mass of 2409 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 [i](#)

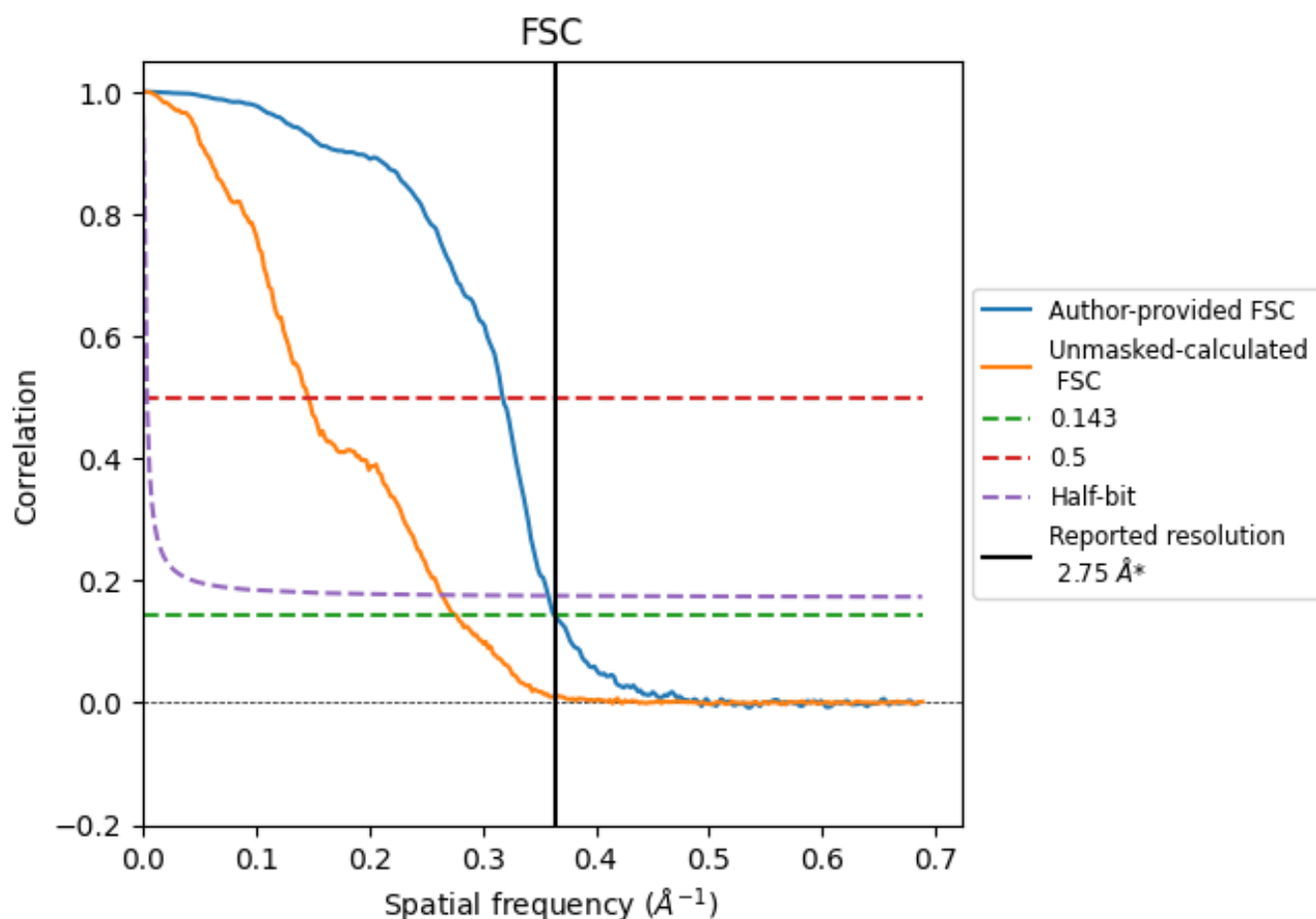


*Reported resolution corresponds to spatial frequency of 0.364 \AA^{-1}

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 0.364 \AA^{-1}

8.2 Resolution estimates [i](#)

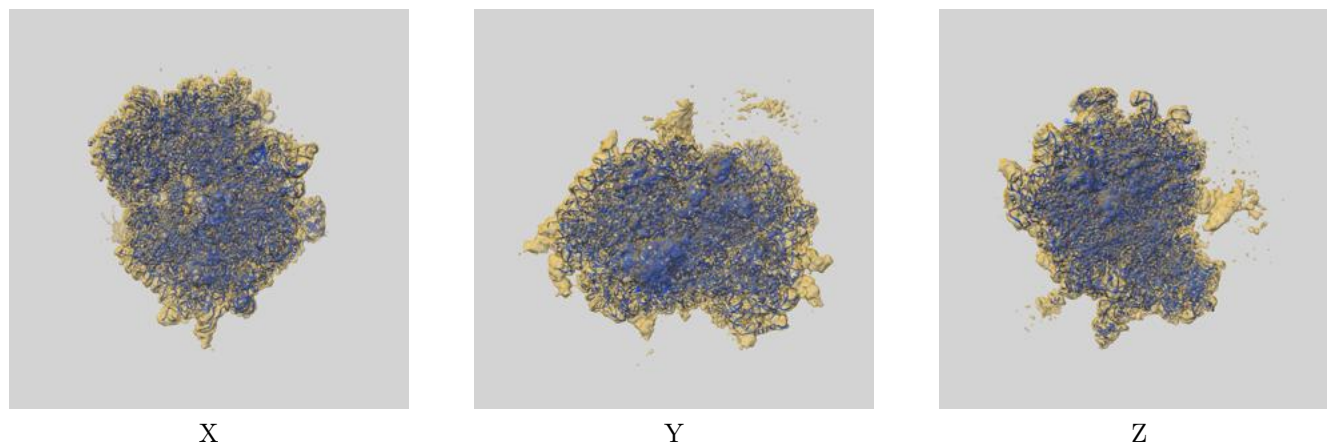
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	2.75	3.15	2.79
Unmasked-calculated*	3.61	6.84	3.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.61 differs from the reported value 2.75 by more than 10 %

9 Map-model fit [i](#)

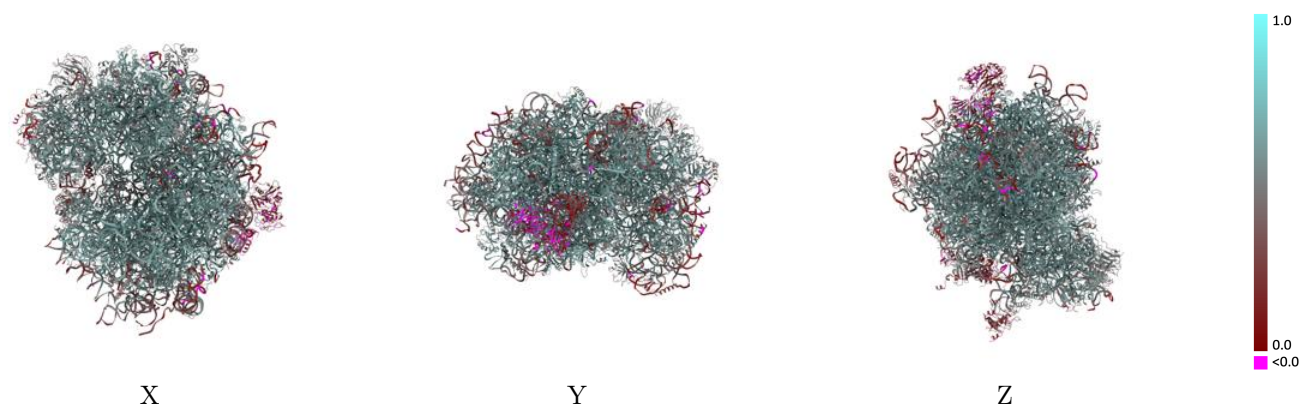
This section contains information regarding the fit between EMDB map EMD-53231 and PDB model 9QLP. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



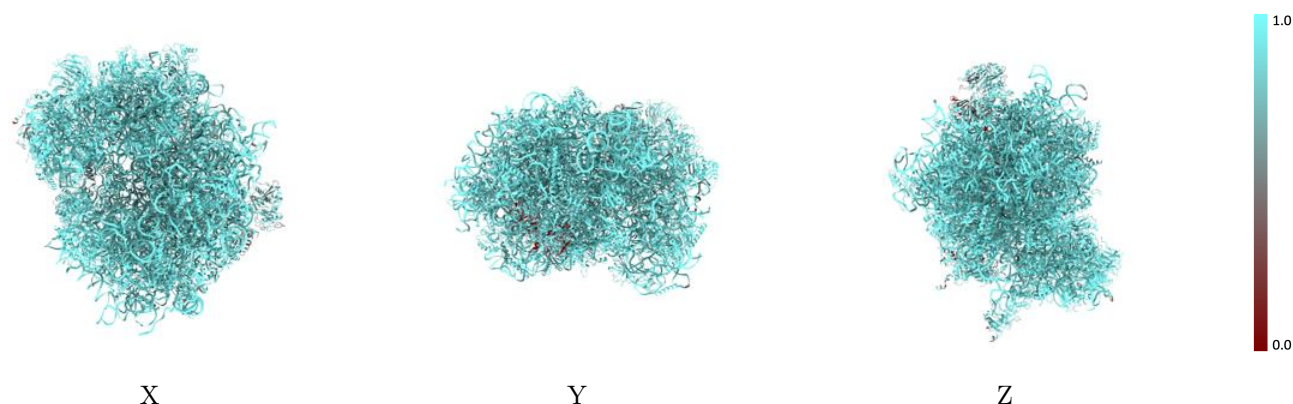
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



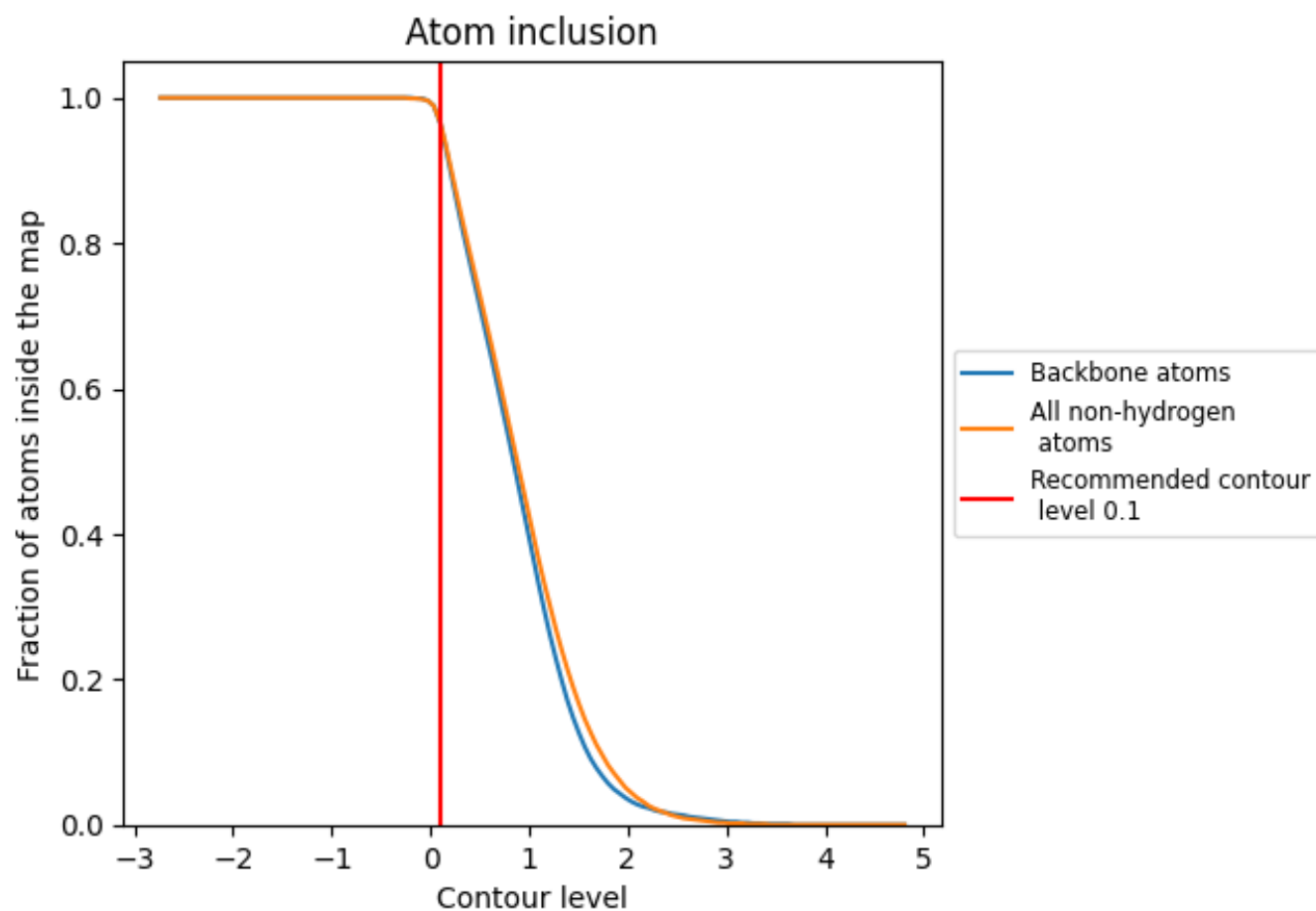
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9660	 0.5500
CM	 0.9600	 0.5400
CP	 0.9580	 0.5000
CR	 0.8870	 0.4450
CZ	 0.5950	 0.0830
L5	 0.9840	 0.5660
L7	 0.9960	 0.6220
L8	 0.9850	 0.5880
LA	 0.9900	 0.6370
LB	 0.9840	 0.6200
LC	 0.9850	 0.6150
LD	 0.9760	 0.5690
LE	 0.9770	 0.5590
LF	 0.9830	 0.6180
LG	 0.9640	 0.5550
LH	 0.9790	 0.5830
LI	 0.9710	 0.5900
LJ	 0.9660	 0.5570
LL	 0.9710	 0.5840
LM	 0.9910	 0.5920
LN	 0.9960	 0.6440
LO	 0.9850	 0.6270
LP	 0.9850	 0.6250
LQ	 0.9910	 0.6310
LR	 0.9860	 0.6050
LS	 0.9890	 0.6250
LT	 0.9680	 0.5830
LU	 0.9570	 0.4950
LV	 0.9870	 0.6230
LW	 0.9570	 0.4840
LX	 0.9650	 0.5950
LY	 0.9830	 0.5940
LZ	 0.9820	 0.5930
La	 0.9910	 0.6320
Lb	 0.9480	 0.5450



























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Chain	Atom inclusion	Q-score
Lc	 0.9810	 0.6040
Ld	 0.9830	 0.6020
Le	 0.9940	 0.6340
Lf	 0.9830	 0.6340
Lg	 0.9740	 0.6050
Lh	 0.9750	 0.5900
Li	 0.9800	 0.5790
Lj	 0.9840	 0.6290
Lk	 0.9340	 0.5230
Ll	 0.9810	 0.6110
Lm	 0.9730	 0.6000
Ln	 0.9950	 0.6330
Lo	 0.9860	 0.6150
Lp	 0.9910	 0.6330
Lr	 0.9810	 0.6050
Ls	 0.7980	 0.2570
Lt	 0.8740	 0.2670
NA	 0.3350	 0.0570
NB	 0.4800	 0.1730
NM	 0.8000	 0.1440
S2	 0.9790	 0.5500
SA	 0.9800	 0.5800
SB	 0.9660	 0.5800
SC	 0.9840	 0.5970
SD	 0.9640	 0.5370
SE	 0.9810	 0.5650
SF	 0.9560	 0.5520
SG	 0.9680	 0.4910
SH	 0.9690	 0.5130
SI	 0.9820	 0.5770
SJ	 0.9830	 0.5730
SK	 0.9610	 0.5090
SL	 0.9850	 0.6070
SM	 0.8110	 0.2230
SN	 0.9800	 0.6080
SO	 0.9760	 0.5930
SP	 0.9670	 0.5180
SQ	 0.9530	 0.5560
SR	 0.9440	 0.5150
SS	 0.9630	 0.5360
ST	 0.9670	 0.5550
SU	 0.9610	 0.4940

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Chain	Atom inclusion	Q-score
SV	 0.9820	 0.5790
SW	 0.9800	 0.6150
SX	 0.9780	 0.5940
SY	 0.9800	 0.5360
SZ	 0.9560	 0.5330
Sa	 0.9680	 0.5830
Sb	 0.9600	 0.5420
Sc	 0.9300	 0.5040
Sd	 0.9760	 0.5810
Se	 0.9630	 0.5500
Sf	 0.8150	 0.2630
Sg	 0.9520	 0.4780