



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 05:19 AM UTC

PDB ID : 9FQZ / pdb_00009fqz
EMDB ID : EMD-50673
Title : CRYO-EM STRUCTURE OF HCT15 POLYSOMES BOUND TO EEF2,
EBP1, AND SERBP1
Authors : Rajan, K.S.; Yonath, A.
Deposited on : 2024-06-17
Resolution : 2.85 Å(reported)

This is a wwPDB EM Validation Summary 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:

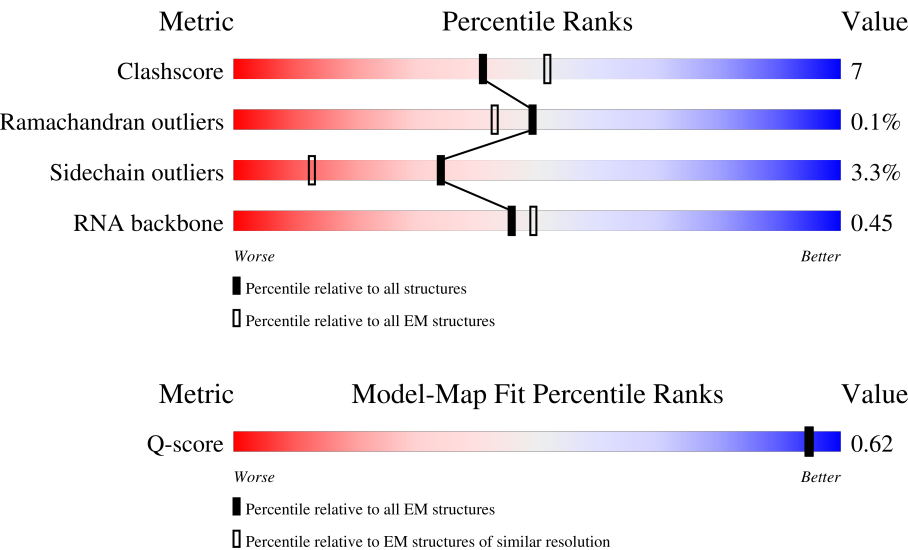
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 2.85 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.











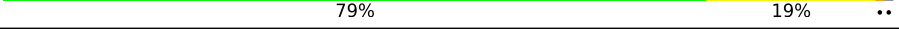

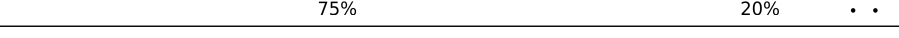
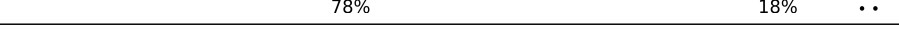

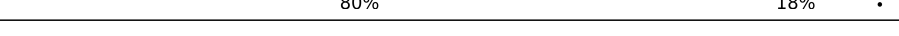


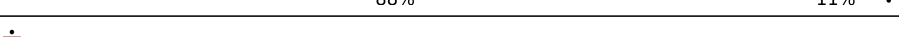

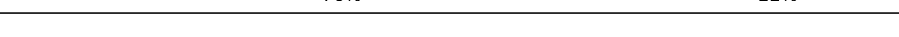






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11965 (2.35 - 3.35)

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	CB	858	
2	CC	85	
3	CD	402	













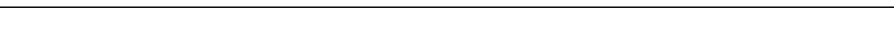

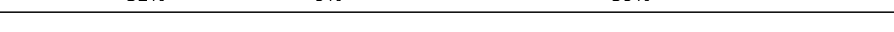

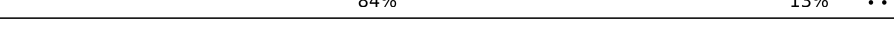








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Mol	Chain	Length	Quality of chain
4	L8	156	
5	LA	257	
6	LB	403	
7	LC	427	
8	LD	297	
9	LE	288	
10	LF	248	
11	LG	266	
12	LH	192	
13	LI	214	
14	LJ	178	
15	LL	211	
16	LM	215	
17	LN	204	
18	LO	203	
19	LP	184	
20	LQ	188	
21	LR	196	
22	LS	176	
23	LT	160	
24	LU	128	
25	LV	140	
26	LW	157	
27	LX	156	
28	LY	145	





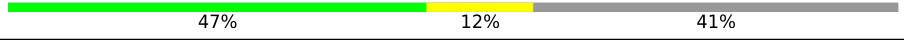

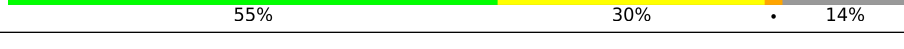
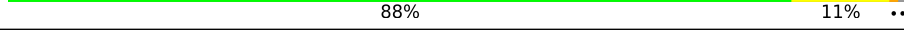
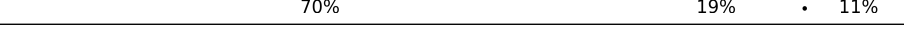
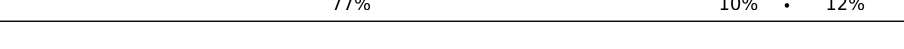
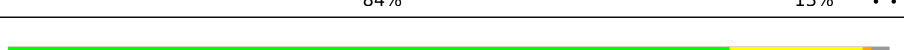

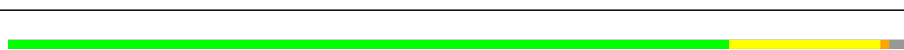

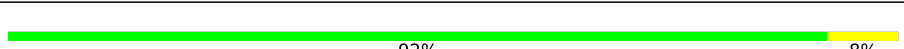



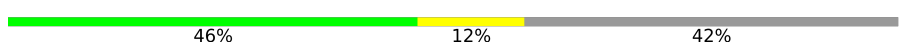

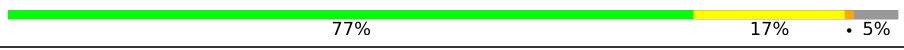
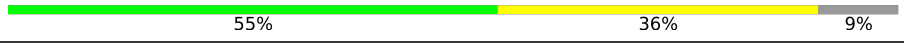



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Mol	Chain	Length	Quality of chain
29	LZ	136	
30	La	148	
31	Lb	159	
32	Lc	115	
33	Ld	125	
34	Le	135	
35	Lf	110	
36	Lg	117	
37	Lh	123	
38	Li	105	
39	Lj	97	
40	Lk	70	
41	Ll	51	
42	Lm	128	
43	Ln	25	
44	Lo	106	
45	Lp	92	
46	Lr	137	
47	S2	1871	
48	SA	295	
49	SB	264	
50	SC	293	
51	SD	243	
52	SE	263	
53	SF	204	

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Mol	Chain	Length	Quality of chain
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SM	132	
61	SN	151	
62	SO	151	
63	SP	145	
64	SQ	146	
65	SR	135	
66	SS	152	
67	ST	145	
68	SU	119	
69	SV	83	
70	SW	130	
71	SX	143	
72	SY	133	
73	SZ	125	
74	Sa	115	
75	Sb	84	
76	Sc	69	
77	Sd	56	
78	Se	133	

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Mol	Chain	Length	Quality of chain
79	Sf	156	
80	Sg	317	
81	L5	5069	
82	L7	120	
83	Lq	317	
84	CA	394	

2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 216008 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 protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CB	819	Total	C	N	O	S	0	0
			6379	4059	1091	1186	43		

- Molecule 2 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CC	22	Total	C	N	O	P	0	0
			470	210	84	154	22		

- Molecule 3 is a protein called Isoform 2 of SERPINE1 mRNA-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CD	72	Total	C	N	O	S	0	0
			585	352	114	118	1		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	155	Total	C	N	O	P	0	0
			3296	1473	583	1086	154		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LA	247	Total	C	N	O	S	1	0
			1896	1188	389	313	6		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LB	399	Total	C	N	O	S	0	0
			3220	2050	605	551	14		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LC	364	Total	C	N	O	S	0	0
			2895	1822	578	480	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD	292	Total	C	N	O	S	0	0
			2375	1501	434	426	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LE	225	Total	C	N	O	S	0	0
			1800	1159	342	295	4		

- Molecule 10 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LF	225	Total	C	N	O	S	1	0
			1880	1208	362	301	9		

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LG	227	Total	C	N	O	S	0	0
			1838	1173	354	307	4		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 13 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LI	203	Total	C	N	O	S	0	0
			1642	1042	315	270	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	49	CYS	GLY	conflict	UNP Q96L21

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LJ	170	Total	C	N	O	S	0	0
			1367	864	254	243	6		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LL	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LM	137	Total	C	N	O	S	0	0
			1125	722	216	180	7		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LN	203	Total	C	N	O	S	0	0
			1700	1072	359	265	4		

- Molecule 18 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LO	201	Total	C	N	O	S	0	0
			1649	1063	321	260	5		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LP	158	Total	C	N	O	S	0	0
			1282	803	248	222	9		

- Molecule 20 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LQ	187	Total	C	N	O	S	0	0
			1512	944	314	249	5		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LT	158	Total	C	N	O	S	0	0
			1292	820	251	215	6		

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LV	130	Total	C	N	O	S	0	0
			972	615	183	169	5		

- Molecule 26 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LW	113	Total	C	N	O	S	1	0
			935	586	192	152	5		

- Molecule 27 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LX	120	Total	C	N	O	S	1	0
			994	636	188	169	1		

- Molecule 28 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LZ	135	Total	C	N	O	S	0	0
			1106	714	208	181	3		

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	La	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lb	105	Total	C	N	O	S	0	0
			853	529	187	133	4		

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 34 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 35 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lf	110	Total	C	N	O	S	0	0
			881	558	175	145	3		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lg	113	Total	C	N	O	S	0	0
			897	560	185	146	6		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Li	102	Total	C	N	O	S	1	0
			843	527	181	130	5		

- Molecule 39 is a protein called 60S ribosomal protein L37.

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

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lk	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

- Molecule 41 is a protein called 60S ribosomal protein L39.

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

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lm	52	Total	C	N	O	S	0	0
			425	263	89	67	6		

- Molecule 43 is a protein called 60S ribosomal protein L41.

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

- Molecule 44 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lo	104	Total	C	N	O	S	1	0
			861	539	177	139	6		

- Molecule 45 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lp	91	Total	C	N	O	S	0	0
			704	443	135	119	7		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lr	126	Total	C	N	O	S	0	0
			1007	625	208	169	5		

- Molecule 47 is a RNA chain called SSU rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1598	Total	C	N	O	P	0	0
			34174	15280	6142	11155	1597		

- Molecule 48 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	215	Total	C	N	O	S	0	0
			1700	1080	298	314	8		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	220	Total	C	N	O	S	0	0
			1707	1104	293	300	10		

- Molecule 51 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	226	Total	C	N	O	S	0	0
			1757	1120	316	314	7		

- Molecule 52 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	260	Total	C	N	O	S	0	0
			2065	1319	384	354	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	184	Total	C	N	O	S	0	0
			1463	915	276	265	7		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG	235	Total	C	N	O	S	0	0
			1909	1191	385	326	7		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	SH	185	Total	C	N	O		
			1466	936	273	257	0	0

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SI	205	Total	C	N	O	S		
			1678	1053	330	290	5	0	0

- Molecule 57 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SJ	180	Total	C	N	O	S	
			1499	955	300	242	2	0

- Molecule 58 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	SK	97	Total	C	N	O	S	
			816	533	144	133	6	0

- Molecule 59 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	SL	145	Total	C	N	O	S	
			1189	759	223	201	6	0

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	SM	113	Total	C	N	O	S	
			864	545	149	163	7	0

- Molecule 61 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SN	150	Total	C	N	O	S	
			1208	773	229	205	1	0

- Molecule 62 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SO	135	Total	C	N	O	S	0	0
			1007	617	198	186	6		

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SP	128	Total	C	N	O	S	0	0
			1054	669	200	178	7		

- Molecule 64 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SQ	142	Total	C	N	O	S	0	0
			1117	712	210	192	3		

- Molecule 65 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 66 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 67 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	ST	142	Total	C	N	O	S	0	0
			1103	691	212	197	3		

- Molecule 68 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 69 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 70 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SW	129	Total	C	N	O	S	0	0
			1033	659	193	175	6		

- Molecule 71 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SX	141	Total	C	N	O	S	0	0
			1094	691	218	182	3		

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SY	123	Total	C	N	O	S	0	0
			1006	637	197	167	5		

- Molecule 73 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SZ	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	101	Total	C	N	O	S	1	0
			813	504	171	133	5		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sb	80	Total	C	N	O	S	0	0
			634	398	118	112	6		

- Molecule 76 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	63	Total	C	N	O	S	0	0
			495	302	98	93	2		

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sd	55	Total	C	N	O	S	0	0
			454	285	94	72	3		

- Molecule 78 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	52	Total	C	N	O	S	0	0
			414	253	93	67	1		

- Molecule 79 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sf	65	Total	C	N	O	S	0	0
			528	333	100	89	6		

- Molecule 80 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sg	313	Total	C	N	O	S	0	0
			2434	1535	424	465	10		

- Molecule 81 is a RNA chain called LSU rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	L5	3475	Total	C	N	O	P	0	0
			74592	33254	13663	24201	3474		

- Molecule 82 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	L7	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

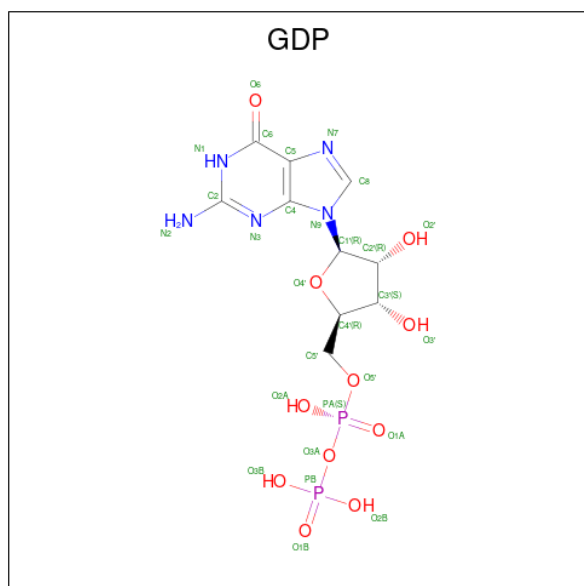
- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Lq	199	Total	C	N	O	S	0	0
			1529	973	266	281	9		

- Molecule 84 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CA	15	Total	C	N	O	S	1	0
			115	72	22	19	2		

- Molecule 85 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
85	CB	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	CB	1	Total	Mg	0
			1	1	
86	L8	2	Total	Mg	0
			2	2	
86	LB	1	Total	Mg	0
			1	1	
86	LC	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	LI	1	Total 1	Mg 1	0
86	Lg	1	Total 1	Mg 1	0
86	Lj	1	Total 1	Mg 1	0
86	S2	60	Total 60	Mg 60	0
86	SX	1	Total 1	Mg 1	0
86	Sd	1	Total 1	Mg 1	0
86	L5	198	Total 198	Mg 198	0
86	L7	3	Total 3	Mg 3	0

- Molecule 87 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
87	L8	3	Total 3	K 3	0
87	LA	1	Total 1	K 1	0
87	LI	1	Total 1	K 1	0
87	LN	1	Total 1	K 1	0
87	LP	1	Total 1	K 1	0
87	LV	1	Total 1	K 1	0
87	Le	1	Total 1	K 1	0
87	Lf	1	Total 1	K 1	0
87	S2	17	Total 17	K 17	0
87	Sa	1	Total 1	K 1	0
87	L5	74	Total 74	K 74	0

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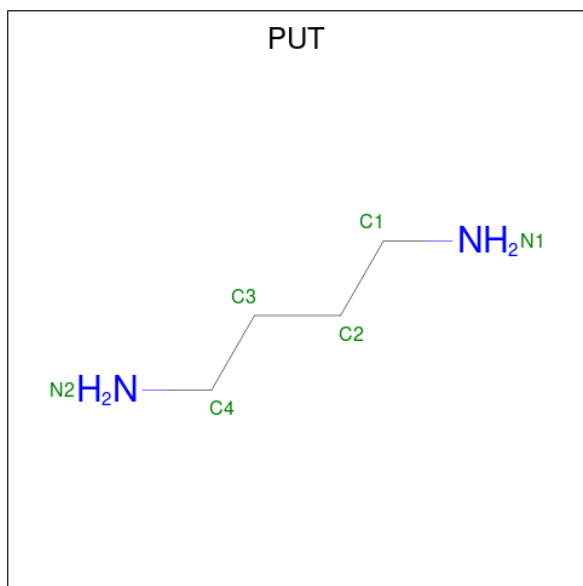
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Mol	Chain	Residues	Atoms		AltConf
87	L7	2	Total	K	0
			2	2	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

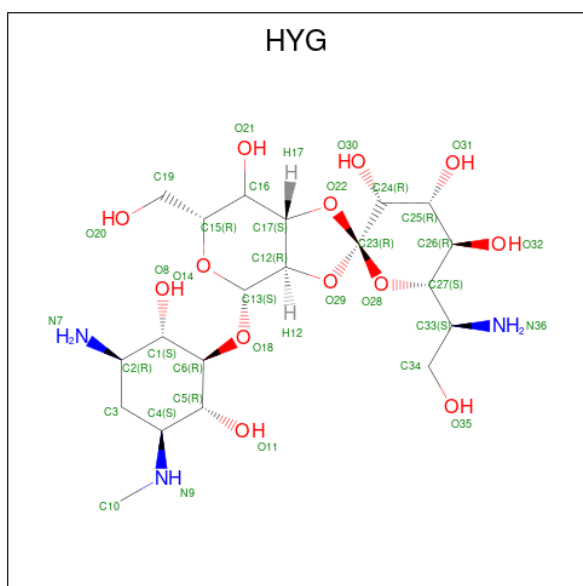
Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total	Zn	0
			1	1	
88	Lj	1	Total	Zn	0
			1	1	
88	Lm	1	Total	Zn	0
			1	1	
88	Lo	1	Total	Zn	0
			1	1	
88	Lp	1	Total	Zn	0
			1	1	
88	Sa	1	Total	Zn	0
			1	1	
88	Sd	1	Total	Zn	0
			1	1	
88	Sf	1	Total	Zn	0
			1	1	

- Molecule 89 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



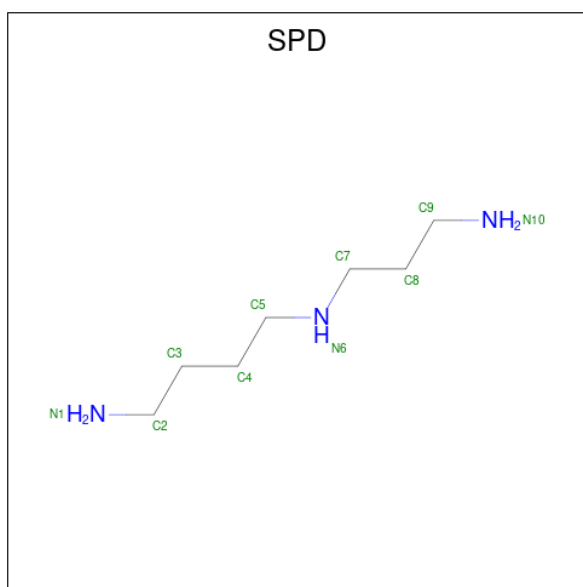
Mol	Chain	Residues	Atoms			AltConf
89	S2	1	Total	C	N	0
			6	4	2	
89	L5	1	Total	C	N	0
			6	4	2	
89	L5	1	Total	C	N	0
			6	4	2	
89	L5	1	Total	C	N	0
			6	4	2	
89	L5	1	Total	C	N	0
			6	4	2	
89	L5	1	Total	C	N	0
			6	4	2	

- Molecule 90 is HYGROMYCIN B (CCD ID: HYG) (formula: $C_{20}H_{37}N_3O_{13}$).



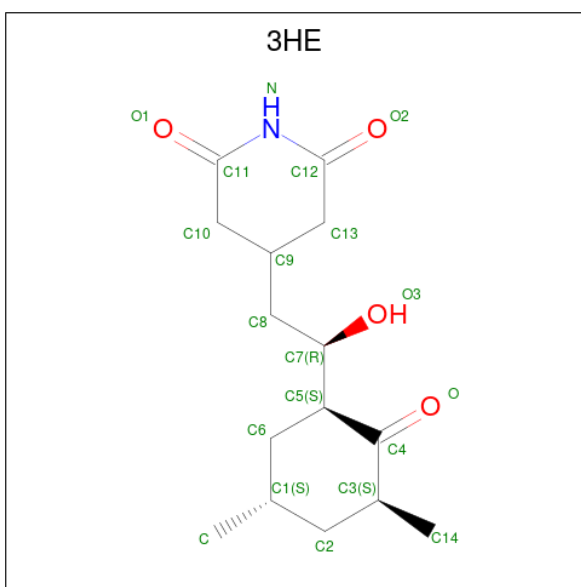
Mol	Chain	Residues	Atoms				AltConf
90	S2	1	Total	C	N	O	0
			36	20	3	13	

- Molecule 91 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



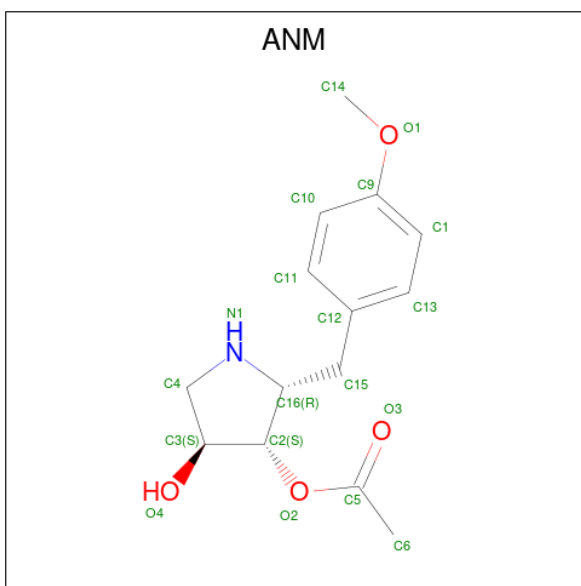
Mol	Chain	Residues	Atoms			AltConf
91	L5	1	Total	C	N	0
			10	7	3	
91	L5	1	Total	C	N	0
			10	7	3	
91	L5	1	Total	C	N	0
			10	7	3	
91	L5	1	Total	C	N	0
			10	7	3	
91	L5	1	Total	C	N	0
			10	7	3	
91	L5	1	Total	C	N	0
			10	7	3	

- Molecule 92 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).



Mol	Chain	Residues	Atoms				AltConf
92	L5	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 93 is ANISOMYCIN (CCD ID: ANM) (formula: $C_{14}H_{19}NO_4$).



Mol	Chain	Residues	Atoms				AltConf
93	L5	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 94 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
94	L5	1	Total	Na	0
			1	1	

- Molecule 95 is water.

Mol	Chain	Residues	Atoms		AltConf
95	CB	1	Total	O	0
			1	1	
95	L8	7	Total	O	0
			7	7	
95	LA	6	Total	O	0
			6	6	
95	LB	5	Total	O	0
			5	5	
95	LC	4	Total	O	0
			4	4	
95	LF	2	Total	O	0
			2	2	
95	LH	1	Total	O	0
			1	1	
95	LN	3	Total	O	0
			3	3	
95	LO	1	Total	O	0
			1	1	
95	LP	2	Total	O	0
			2	2	
95	LQ	1	Total	O	0
			1	1	
95	LS	1	Total	O	0
			1	1	
95	LT	1	Total	O	0
			1	1	
95	LV	1	Total	O	0
			1	1	
95	La	2	Total	O	0
			2	2	
95	Lc	1	Total	O	0
			1	1	
95	Le	5	Total	O	0
			5	5	
95	Lf	2	Total	O	0
			2	2	
95	Lg	1	Total	O	0
			1	1	

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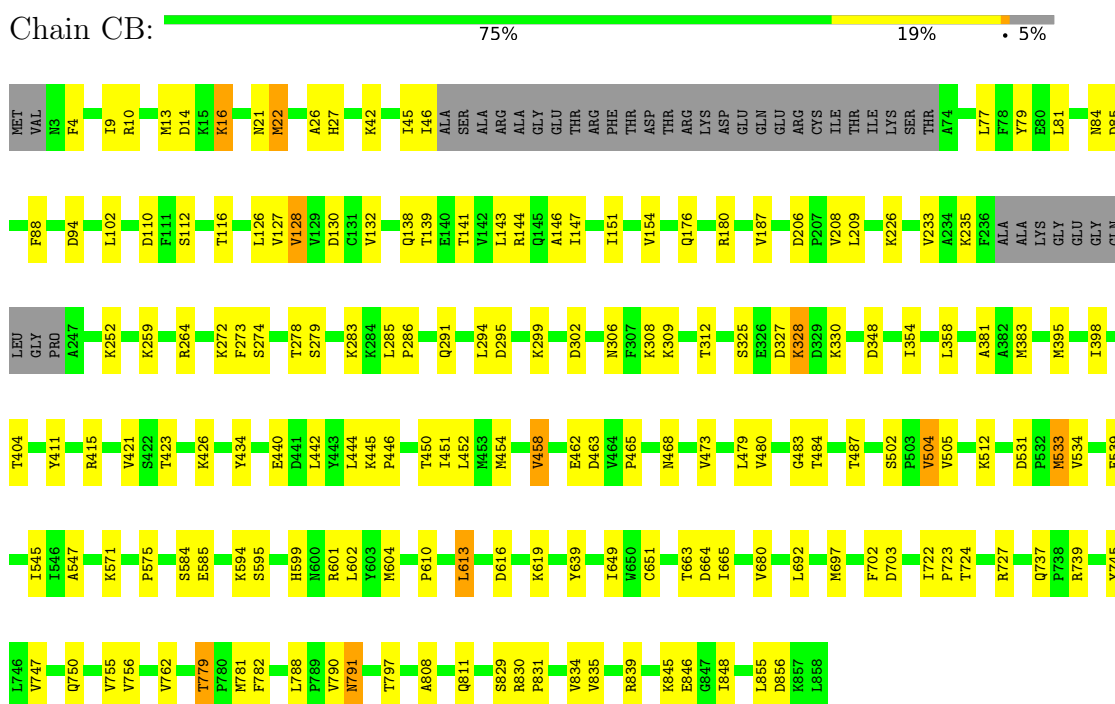
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Mol	Chain	Residues	Atoms		AltConf
95	Lj	1	Total 1	O 1	0
95	Lo	1	Total 1	O 1	0
95	Lp	3	Total 3	O 3	0
95	S2	78	Total 78	O 78	0
95	SF	1	Total 1	O 1	0
95	SL	1	Total 1	O 1	0
95	SN	1	Total 1	O 1	0
95	L5	263	Total 263	O 263	0
95	L7	2	Total 2	O 2	0

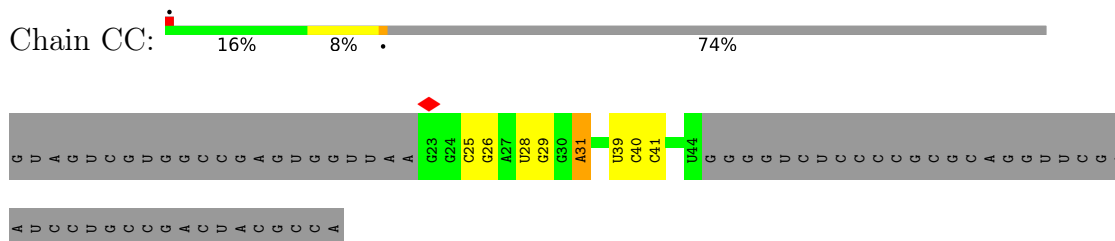
3 Residue-property plots [i](#)

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.

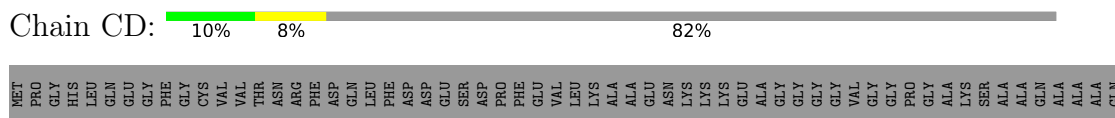
• Molecule 1: Elongation factor 2

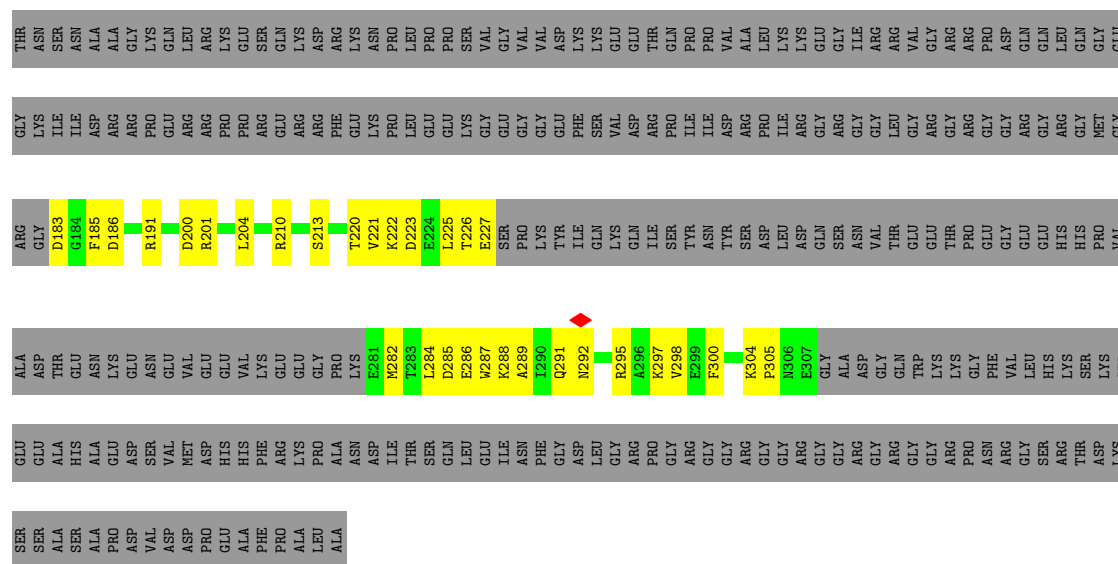


• Molecule 2: tRNA

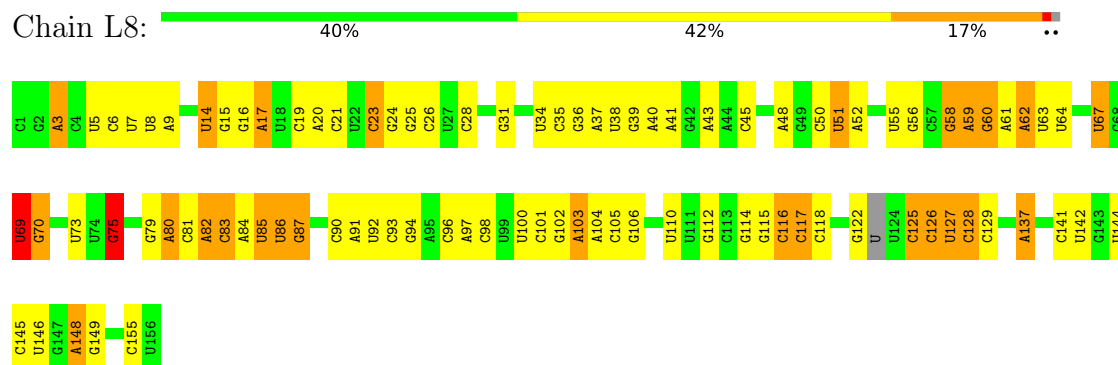


• Molecule 3: Isoform 2 of SERPINE1 mRNA-binding protein 1

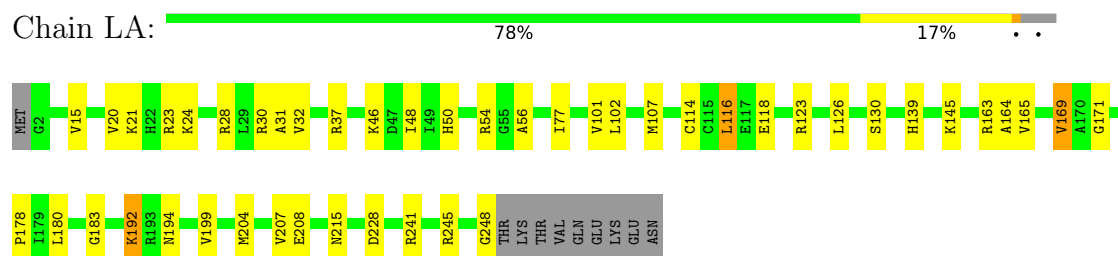




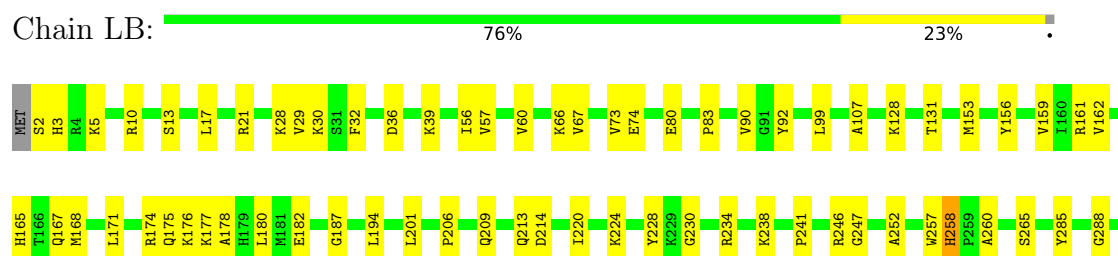
• Molecule 4: 5.8S rRNA



• Molecule 5: 60S ribosomal protein L8

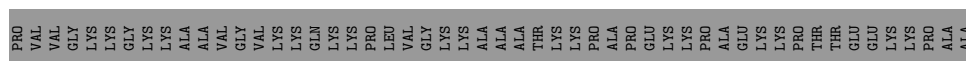
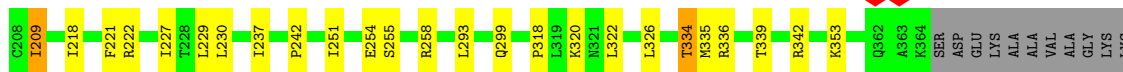


• Molecule 6: 60S ribosomal protein L3




- Molecule 7: 60S ribosomal protein L4

Chain LC:  72% 13% 15%



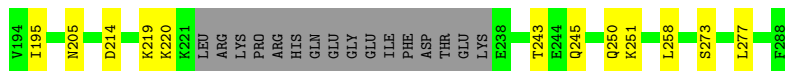
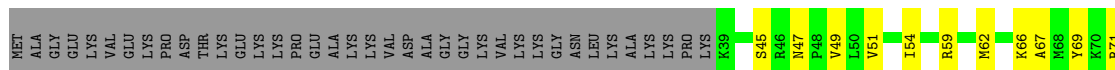
- Molecule 8: 60S ribosomal protein L5

Chain LD: 



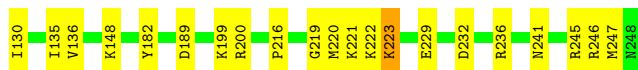
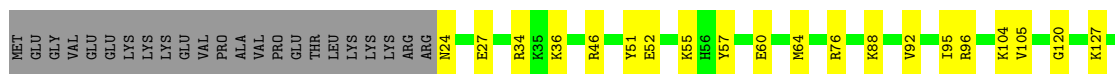
- Molecule 9: 60S ribosomal protein L6

Chain LE:



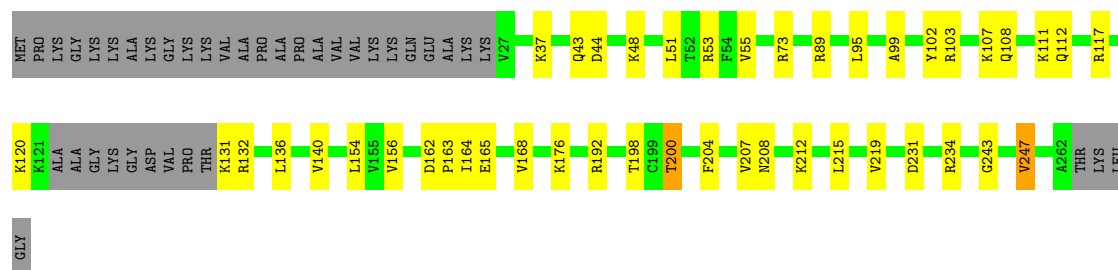
- Molecule 10: Large ribosomal subunit protein uL30

Chain LF:




- Molecule 11: 60S ribosomal protein L7a

Chain LG:  69% 16% 15%




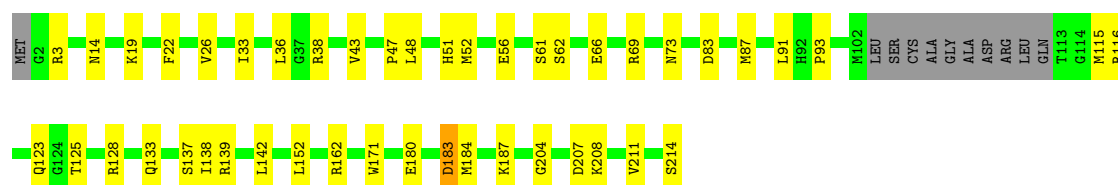
- Molecule 12: 60S ribosomal protein L9

Chain LH:  79% 19% ..




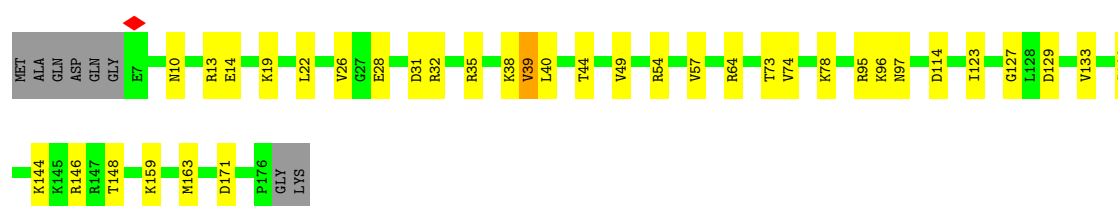
- Molecule 13: 60S ribosomal protein L10-like

Chain LI:  74% 21% 5%




- Molecule 14: 60S ribosomal protein L11

Chain LJ:  75% 20% ..



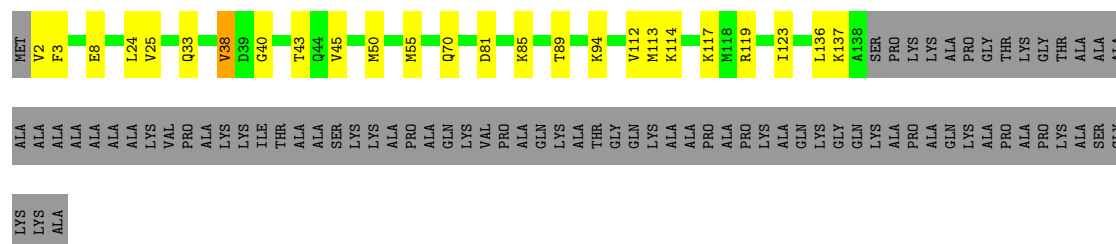
- Molecule 15: 60S ribosomal protein L13

Chain LL:  78% 18% ..

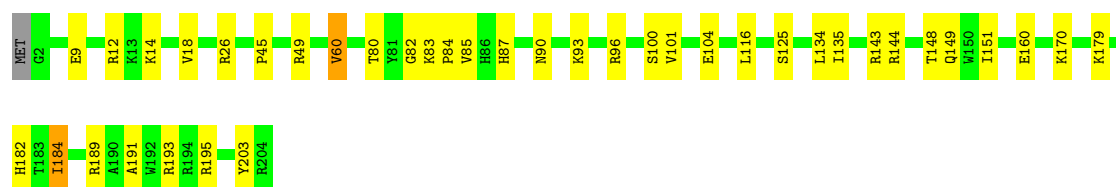
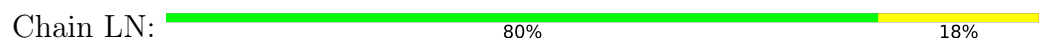




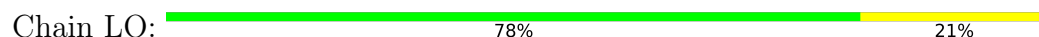
- Molecule 16: 60S ribosomal protein L14



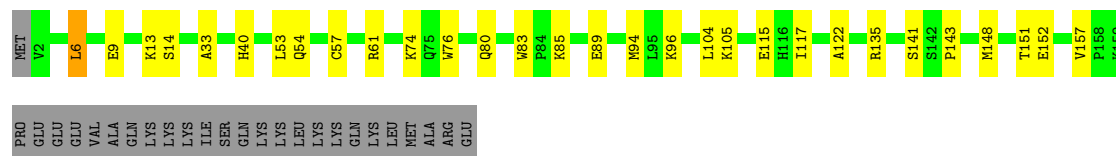
- Molecule 17: 60S ribosomal protein L15



- Molecule 18: 60S ribosomal protein L13a



- Molecule 19: 60S ribosomal protein L17



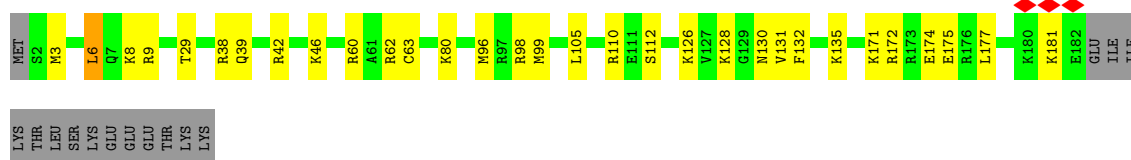
- Molecule 20: 60S ribosomal protein L18





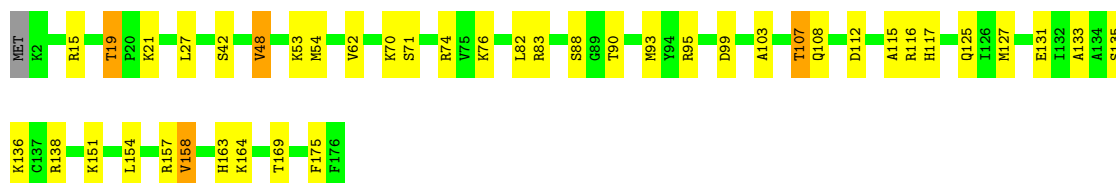
- Molecule 21: 60S ribosomal protein L19

Chain LR: 77% 15% 8%



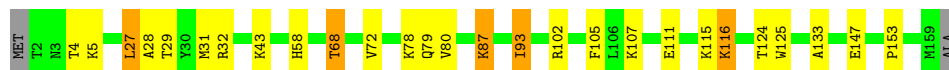
- Molecule 22: 60S ribosomal protein L18a

Chain LS: 76% 22% ..



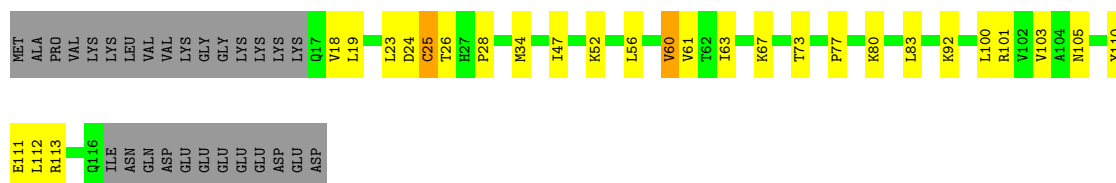
- Molecule 23: 60S ribosomal protein L21

Chain LT: 82% 14% ..



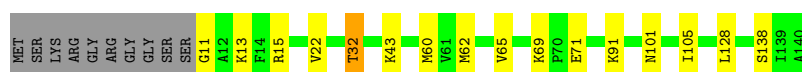
- Molecule 24: 60S ribosomal protein L22

Chain LU: 56% 20% 22%



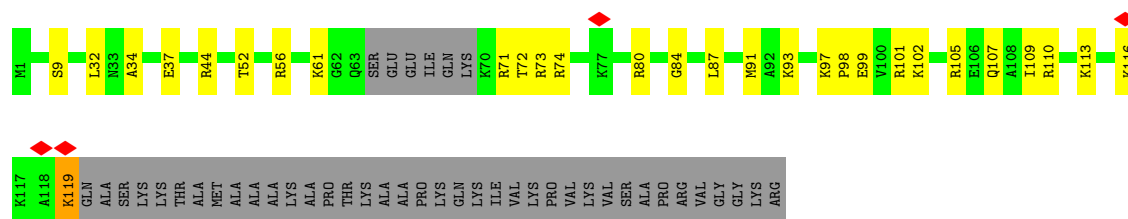
- Molecule 25: 60S ribosomal protein L23

Chain LV: 81% 11% 7%



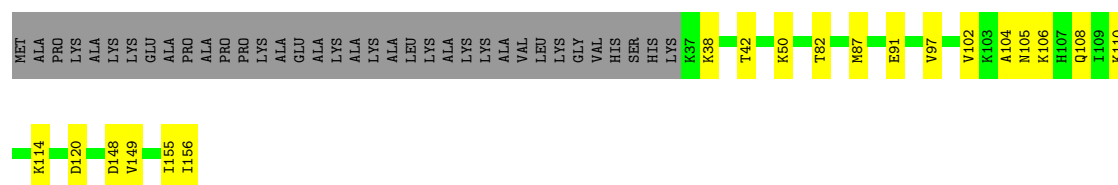
- Molecule 26: 60S ribosomal protein L24

Chain LW: 



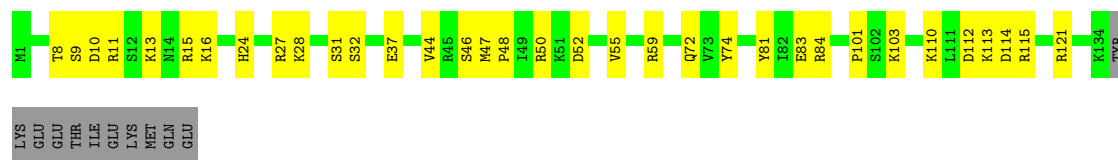
- Molecule 27: 60S ribosomal protein L23a

Chain LX: 




- Molecule 28: 60S ribosomal protein L26

Chain LY: 




- Molecule 29: 60S ribosomal protein L27

Chain LZ: 



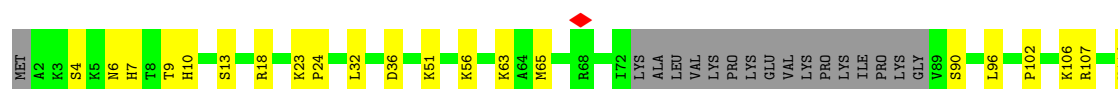
- Molecule 30: 60S ribosomal protein L27a

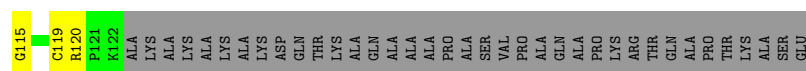
Chain La: 



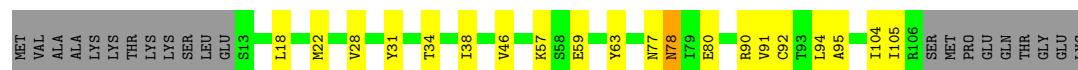
- Molecule 31: 60S ribosomal protein L29

Chain Lb: 

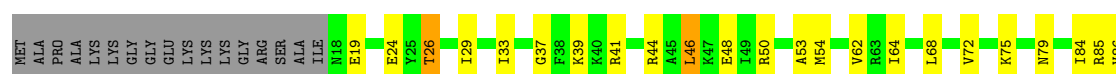




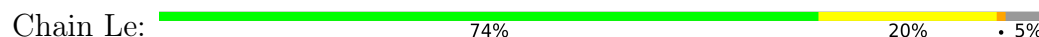
- Molecule 32: 60S ribosomal protein L30



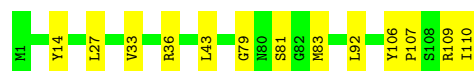
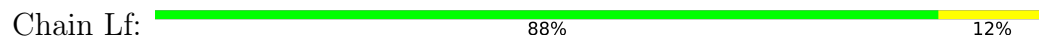
- Molecule 33: 60S ribosomal protein L31



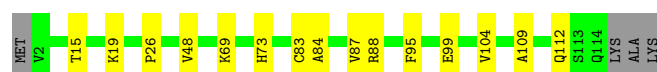
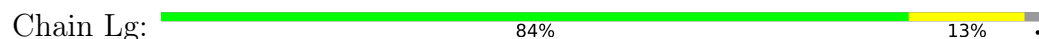
- Molecule 34: 60S ribosomal protein L32



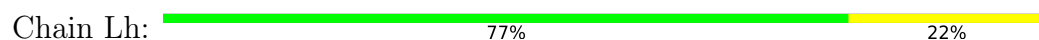
- Molecule 35: 60S ribosomal protein L35a




- Molecule 36: 60S ribosomal protein L34

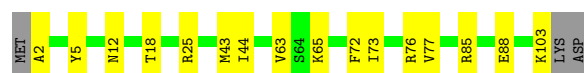


- Molecule 37: 60S ribosomal protein L35




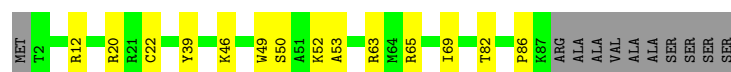
- Molecule 38: 60S ribosomal protein L36

Chain Li:  82% 15% .



- Molecule 39: 60S ribosomal protein L37

Chain Lj:  74% 14% 11%




- Molecule 40: 60S ribosomal protein L38

Chain Lk:  66% 29% . .




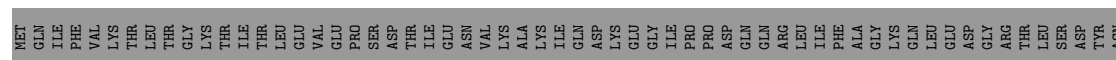
- Molecule 41: 60S ribosomal protein L39

Chain Ll:  86% 12% .




- Molecule 42: Ubiquitin-60S ribosomal protein L40

Chain Lm:  32% 9% 59%




- Molecule 43: 60S ribosomal protein L41

Chain Ln:  76% 20% .



- Molecule 44: 60S ribosomal protein L36a

Chain Lo:  84% 13% . .



- [illegible]





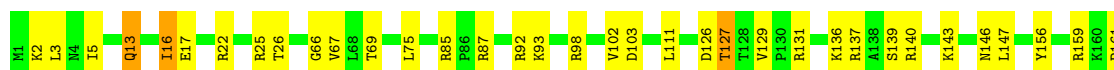
- Molecule 53: 40S ribosomal protein S5

Chain SF: 70% 20% 10%



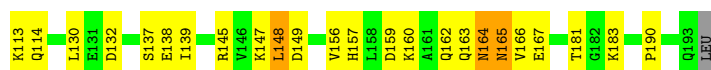
- Molecule 54: 40S ribosomal protein S6

Chain SG: 74% 19% 6%



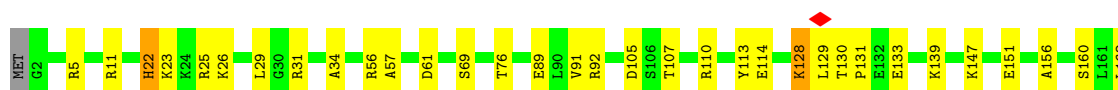
- Molecule 55: 40S ribosomal protein S7

Chain SH: 69% 25% 5%



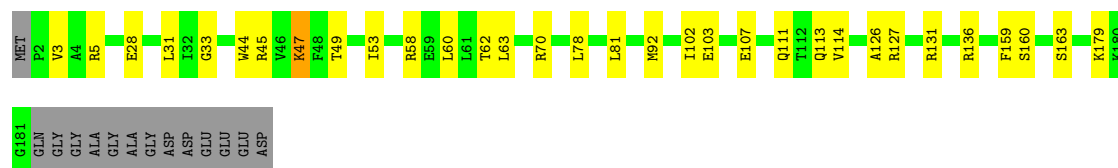
- Molecule 56: 40S ribosomal protein S8

Chain SI: 75% 23% 2%

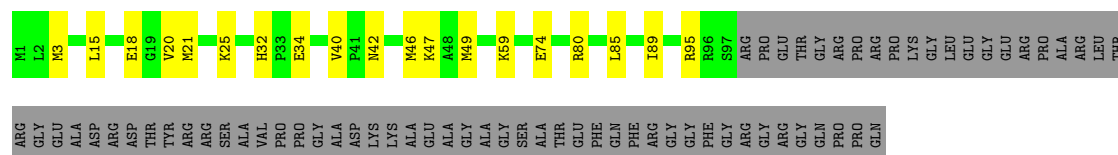


- Molecule 57: 40S ribosomal protein S9

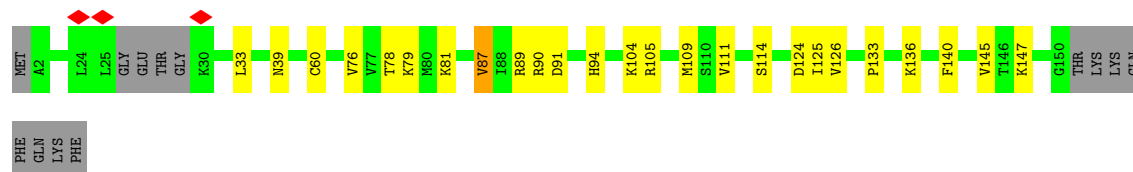
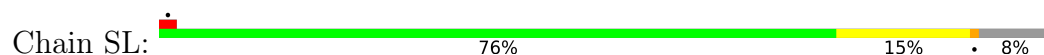
Chain SJ: 76% 16% 7%



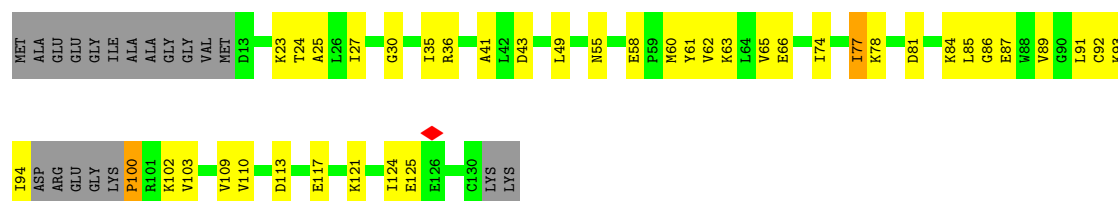
- Molecule 58: 40S ribosomal protein S10



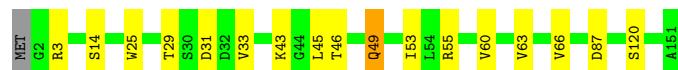
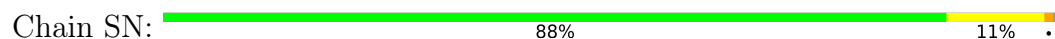
- Molecule 59: 40S ribosomal protein S11



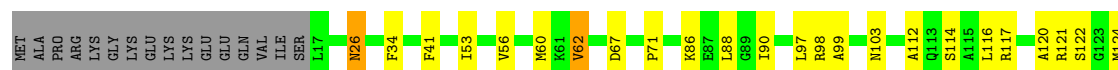
- Molecule 60: 40S ribosomal protein S12

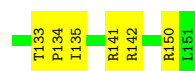


- Molecule 61: 40S ribosomal protein S13



- Molecule 62: 40S ribosomal protein S14





- Molecule 63: 40S ribosomal protein S15

Chain SP: 77% 10% 12%



- Molecule 64: 40S ribosomal protein S16

Chain SQ: 84% 13% 3%



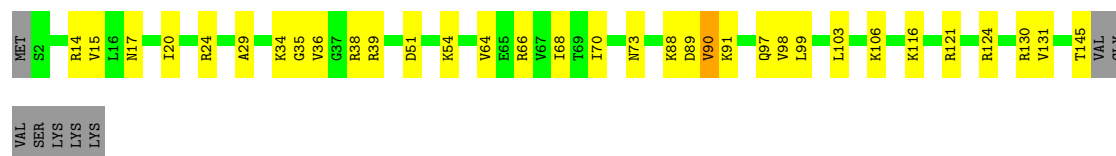
- Molecule 65: 40S ribosomal protein S17

Chain SR: 81% 15% 4%



- Molecule 66: 40S ribosomal protein S18

Chain SS: 73% 21% 6%



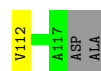
- Molecule 67: 40S ribosomal protein S19

Chain ST: 81% 17% 2%



- Molecule 68: 40S ribosomal protein S20

Chain SU: 62% 22% 16%




- Molecule 75: 40S ribosomal protein S27

MET
P2
K21
K22
R23
S30
Y31
F32
P38
G39
C40
Y41
K42
K43
T44
H49
L65
CYS
VAL
GLY
C59
S60
K70
E75
K82
Q83
H84

- Chain Sc:  55% 36% 9%



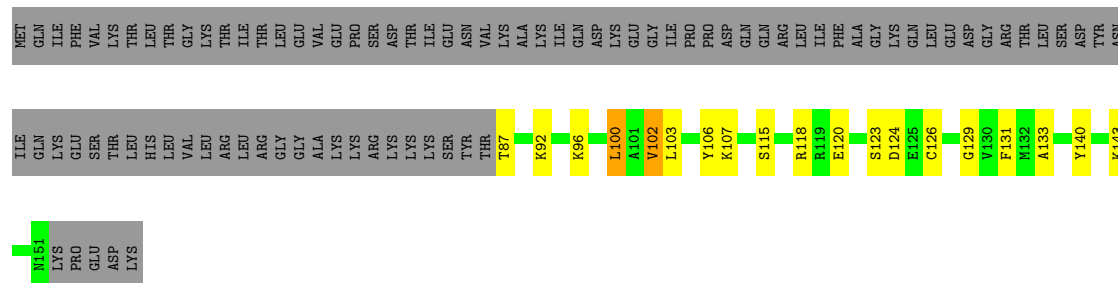
- Chain Sd:  84% 14%



- Chain Se:  35% 5% 61%

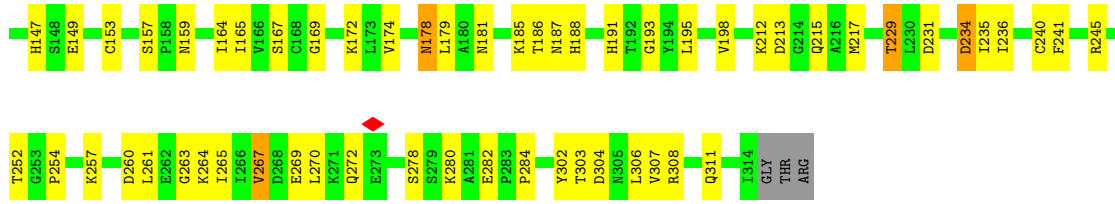


- Chain Sf: 29% 11% 58%



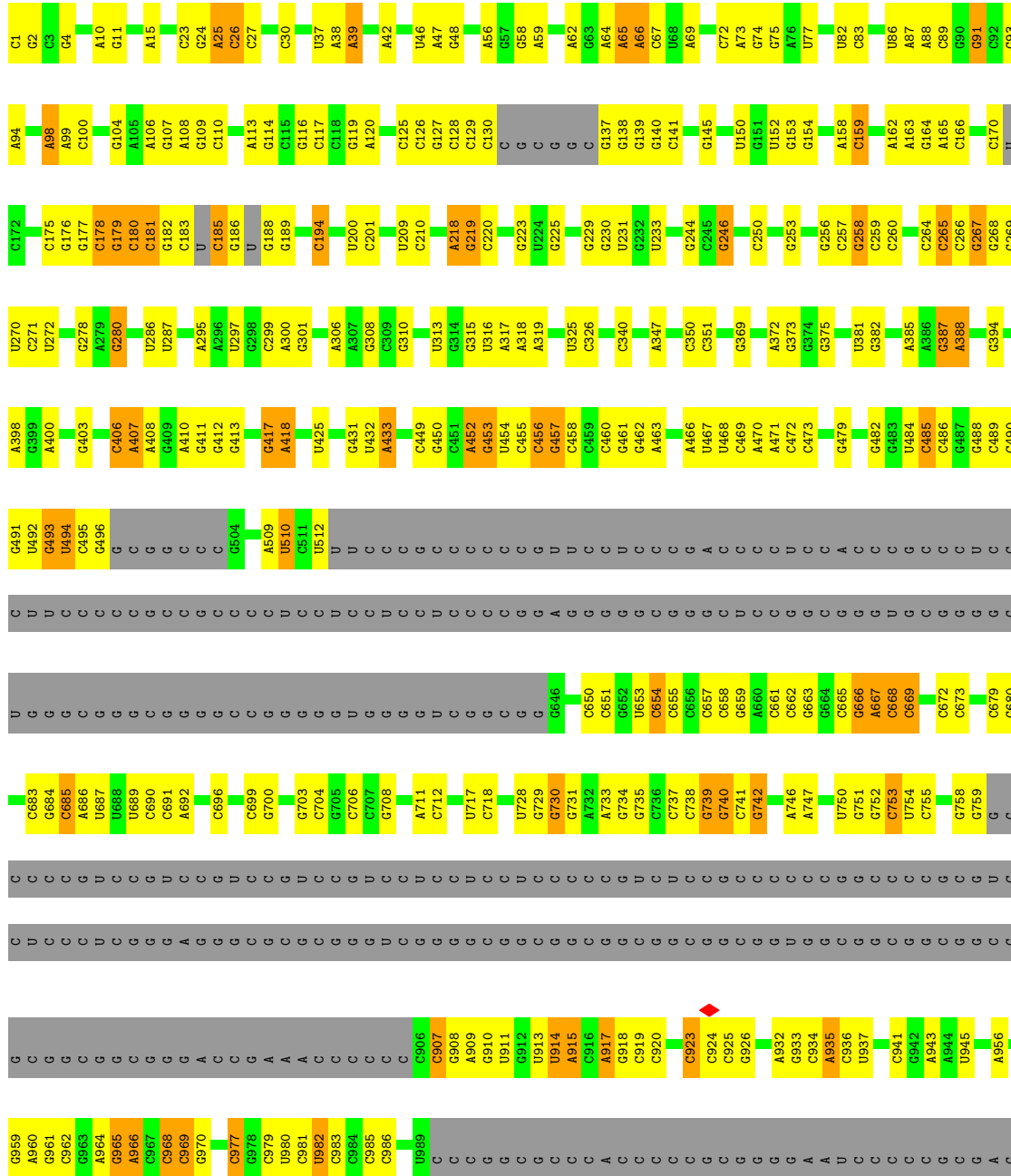
- Chain Sg: 70% 28% ..





• Molecule 81: LSU rRNA

Chain L5: 38% 24% 6% 31%







G4975	U4881	G4647	C4560	G4478	A4376	A4281	C4177	C4096	G	G	G3897	C3809
U4976	U4882	A4648	C4563	G4479	G4377	A4281	G4183	G4097	C	C	A3901	C3810
A4979	C4883	G4649	U4563	U4481	A4378	G4291	G4184	A4098	C	C	A3906	G3811
C4980	C4889	U4657	A4564	U4482	A4379	U4293	C	G	U	G	A3907	C3812
A4982	C	A4656	G4567	C4486	C4387	U4293	G4187	C	C	A	A3908	A3813
U4985	C	G4681	A4568	A4487	A4388	U4299	U4188	C	C	G	A3909	U3814
C4986	C	C4670	U4569	A4488	C4389	U4300	U4189	C	C	G	C3910	A3817
C4987	C	C4671	G4570	G4489	G4390	U4301	U4190	G	G	G	C3911	U3818
U4988	C	C4672	A4571	G4490	G4391	U4302	G4191	A	C	C	U3912	C3819
C	C	U4673	G4575	G4494	G4392	A4303	U4194	G	C	C	G3915	G3823
U	C	U4674	U4576	U4498	A4394	A4304	U4195	G4107	C	C	U3918	A3824
A4991	C	C4675	U4577	U4499	A4397	G4305	G4196	G4108	C	C	A3919	A3825
U4992	C	G4680	G4578	U4500	C4398	U4306	G4197	G4109	C	C	U3920	A3830
G4993	C	A4681	U4579	U4501	U4399	U4312	U4202	U4111	C	C	G3918	G3834
G4994	C	G4682	U4580	U4502	G4400	A4313	U4208	U4112	C	C	A3923	U3838
U4995	C	U4683	A4584	C4504	G4401	C4314	U4209	U4113	C	C	C3924	G3839
U5001	C	U4684	U4585	C4505	G4402	G4322	A4214	U4114	C	C	U3925	U3840
U5002	C	U4685	A4586	C4506	U4403	G4322	A4215	U4115	C	C	A3928	A3845
U5003	C	A4687	C4507	C4507	U4404	A4325	A4219	U4116	C	C	G3929	C3846
U5004	C	C4688	A4508	C4508	G4405	A4326	A4220	U4117	C	C	U3930	U3847
G5005	C	U4689	U4590	U4509	U4406	G4327	A4221	U4118	C	C	C3931	C3841
U5006	C	G4690	C4592	U4512	G4407	G4328	G4222	U4119	C	C	A3932	A3846
U5007	C	A4691	C4592	A4513	G4407	G4329	G4222	C	C	C	U3933	A3847
A5008	C	A4692	A4602	G4514	C4413	G4330	G4225	A4127	C	C	A3934	A3848
U5009	C	U4693	A4602	G4515	A4414	G4331	G4226	G4135	C	C	A3935	U3851
U5010	C	U4694	A4602	G4516	C4421	C4332	U4227	G4136	C	C	A3936	A3856
A5011	C	U4695	A4611	G4517	U4422	C4333	G4228	C	C	C	C3937	G3857
G5012	C	A4700	C4612	A4518	U4423	U4334	U4229	C	C	C	G3938	C3858
C5013	C	A4701	C4612	C4519	U4423	G4335	U4229	C	C	C	A3942	A3861
A5014	C	C4711	C4617	G4520	C4426	C4337	A4233	C	C	C	A3943	A3862
G5015	C	C4712	C4618	A4523	U4431	C4338	A4233	C	C	C	G3944	A3867
A5016	C	A4717	U4619	G4524	U4432	U4339	G4236	A3945	C	C	A3945	G3868
U5017	C	G4718	U4620	C4525	C4434	U4340	G4237	G3946	C	C	A	C3869
U5022	C	G4719	A4622	U4530	U4442	C4341	A4239	C	C	C	A	C3870
C5023	C	C4723	G4623	U4531	U4443	C4342	G4240	C	C	C	A	G3873
C5024	C	A4724	C4625	U4532	G4448	U4344	A4251	G4150	C	C	A	G3874
C5025	C	U4725	U4627	U4533	U4449	U4346	C4254	C4159	C	C	A	A3877
C5026	C	A4726	U4628	C4536	C4456	G4347	A4257	C4160	C	C	A	C3878
C5027	C	C4730	U4629	G4537	U4457	A4348	C4258	G4161	C	C	A	C3879
G5028	C	G4731	G4630	U4538	U4458	C4349	C4259	C4162	C	C	A	C3880
C5029	C	C4732	G4631	U4539	U4459	C4350	U4260	U4163	C	C	A	G3881
U5030	C	A4733	U4632	G4541	U4460	U4353	A4261	C4164	C	C	A	U3884
G5031	C	C4734	G4633	G4541	C4461	U4361	C4261	C4165	C	C	A	G3885
C5032	C	G4735	U4634	A4544	C4461	U4361	C4261	C4165	C	C	A	G3886
G5033	C	C4736	A4635	G4545	C4462	U4361	C4261	C4165	C	C	A	C3887
A5034	C	C4737	U4636	G4546	U4463	U4361	C4261	C4165	C	C	A	U3889
G5041	C	C4738	U4637	C4547	U4464	U4361	C4261	C4165	C	C	A	C3892
A5042	C	C4739	G4637	C4548	C4465	U4361	C4261	C4165	C	C	A	C3893
G5043	C	G4740	U4638	G4549	C4466	U4361	C4261	C4165	C	C	A	A
A5044	C	C4741	G4639	U4550	C4467	U4361	C4261	C4165	C	C	A	A
U5045	C	C4742	U4640	G4551	U4471	U4361	C4261	C4165	C	C	A	A
C5046	C	G4743	U4641	U4552	C4472	U4361	C4261	C4165	C	C	A	A
U5047	C	A4744	G4642	U4553	C4473	U4361	C4261	C4165	C	C	A	A
C5048	C	G4745	C4643	U4554	U4474	U4361	C4261	C4165	C	C	A	A
G5050	C	C4746	C4644	U4557	G4475	C4375	G4275	C4176	C	C	A	A

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	546553	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.157	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	395.76, 395.76, 395.76	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8245, 0.8245, 0.8245	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, OMU, PSU, K, UY1, PUT, ANM, OMC, A2M, OMG, 6MZ, 5MC, 4AC, B8N, NA, 3HE, MG, ZN, MA6, UR3, HYG, SPD

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	CB	0.24	0/6505	0.38	0/8787
2	CC	0.12	0/525	0.23	0/816
3	CD	0.18	0/594	0.31	0/788
4	L8	0.26	0/3608	0.36	0/5619
5	LA	0.23	0/1934	0.42	0/2593
6	LB	0.20	0/3288	0.37	0/4400
7	LC	0.21	0/2949	0.36	0/3960
8	LD	0.17	0/2420	0.32	0/3240
9	LE	0.18	0/1834	0.36	0/2460
10	LF	0.21	0/1915	0.34	0/2553
11	LG	0.19	0/1869	0.36	0/2515
12	LH	0.20	0/1537	0.36	0/2066
13	LI	0.19	0/1681	0.32	0/2246
14	LJ	0.17	0/1390	0.37	0/1859
15	LL	0.25	0/1695	0.54	1/2270 (0.0%)
16	LM	0.19	0/1147	0.35	0/1534
17	LN	0.22	0/1745	0.36	0/2338
18	LO	0.22	0/1681	0.36	0/2250
19	LP	0.20	0/1309	0.37	0/1757
20	LQ	0.21	0/1536	0.35	0/2052
21	LR	0.19	0/1533	0.33	0/2025
22	LS	0.21	0/1492	0.37	0/2003
23	LT	0.19	0/1320	0.35	0/1763
24	LU	0.16	0/831	0.40	0/1115
25	LV	0.21	0/986	0.35	0/1324
26	LW	0.18	0/949	0.39	0/1256
27	LX	0.19	0/1012	0.35	0/1360
28	LY	0.19	0/1132	0.35	0/1504
29	LZ	0.18	0/1129	0.31	0/1507
30	La	0.20	0/1190	0.31	0/1591
31	Lb	0.19	0/866	0.36	0/1143

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lc	0.21	0/742	0.36	0/996
33	Ld	0.19	0/903	0.36	0/1216
34	Le	0.22	0/1071	0.35	0/1429
35	Lf	0.21	0/900	0.34	0/1205
36	Lg	0.19	0/907	0.32	0/1209
37	Lh	0.18	0/1023	0.33	0/1351
38	Li	0.17	0/854	0.32	0/1129
39	Lj	0.22	0/720	0.40	0/952
40	Lk	0.19	0/565	0.31	0/750
41	Ll	0.20	0/454	0.35	0/599
42	Lm	0.17	0/431	0.32	0/571
43	Ln	0.27	0/231	0.50	0/294
44	Lo	0.20	0/875	0.34	0/1155
45	Lp	0.24	0/714	0.36	0/948
46	Lr	0.20	0/1022	0.33	0/1371
47	S2	0.27	1/36887 (0.0%)	0.34	1/57466 (0.0%)
48	SA	0.16	0/1737	0.32	0/2360
49	SB	0.17	0/1756	0.32	0/2350
50	SC	0.18	0/1744	0.35	0/2357
51	SD	0.21	0/1785	0.37	0/2404
52	SE	0.17	0/2107	0.33	0/2836
53	SF	0.18	0/1484	0.38	0/1994
54	SG	0.16	0/1932	0.34	0/2571
55	SH	0.42	1/1488 (0.1%)	0.73	4/1995 (0.2%)
56	SI	0.19	0/1707	0.35	0/2278
57	SJ	0.16	0/1524	0.30	0/2035
58	SK	0.17	0/840	0.38	0/1133
59	SL	0.17	0/1209	0.28	0/1617
60	SM	0.21	0/873	0.50	1/1175 (0.1%)
61	SN	0.19	0/1232	0.31	0/1656
62	SO	0.18	0/1020	0.34	0/1368
63	SP	0.19	0/1074	0.33	0/1434
64	SQ	0.17	0/1135	0.36	0/1522
65	SR	0.19	0/1082	0.36	0/1452
66	SS	0.16	0/1208	0.33	0/1618
67	ST	0.17	0/1122	0.34	0/1504
68	SU	0.17	0/805	0.37	0/1081
69	SV	0.15	0/643	0.25	0/860
70	SW	0.19	0/1050	0.34	0/1405
71	SX	0.20	0/1112	0.34	0/1485
72	SY	0.16	0/1023	0.33	0/1359
73	SZ	0.15	0/580	0.30	0/780
74	Sa	0.20	0/826	0.39	0/1107

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sb	0.16	0/647	0.38	0/865
76	Sc	0.18	0/497	0.35	0/666
77	Sd	0.19	0/465	0.34	0/617
78	Se	0.20	0/417	0.39	0/545
79	Sf	0.17	0/539	0.41	0/716
80	Sg	0.16	0/2491	0.37	0/3392
81	L5	0.27	1/81104 (0.0%)	0.34	0/126490
82	L7	0.24	0/2839	0.28	0/4425
83	Lq	0.15	0/1553	0.36	0/2097
84	CA	0.19	0/115	0.42	0/151
All	All	0.24	3/226666 (0.0%)	0.35	7/331035 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	SH	11	PRO	CG-CD	-13.57	1.04	1.50
81	L5	3785	A2M	O3'-P	5.21	1.61	1.56
47	S2	27	A2M	O3'-P	5.20	1.61	1.56

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	SH	11	PRO	N-CD-CG	-19.56	73.86	103.20
55	SH	11	PRO	CA-CB-CG	-17.10	72.02	104.50
15	LL	134	PRO	CA-N-CD	-12.75	94.15	112.00
55	SH	11	PRO	N-CA-CB	-11.10	95.10	102.65
60	SM	100	PRO	N-CD-CG	-7.57	91.85	103.20

There are no chirality outliers.

There are no planarity outliers.

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	CB	6379	0	6451	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	CC	470	0	237	5	0
3	CD	585	0	547	22	0
4	L8	3296	0	1677	56	0
5	LA	1896	0	1987	34	0
6	LB	3220	0	3362	59	0
7	LC	2895	0	3076	36	0
8	LD	2375	0	2409	37	0
9	LE	1800	0	1960	39	0
10	LF	1880	0	2008	30	0
11	LG	1838	0	1979	32	0
12	LH	1518	0	1601	26	0
13	LI	1642	0	1680	28	0
14	LJ	1367	0	1402	20	0
15	LL	1664	0	1773	33	0
16	LM	1125	0	1192	17	0
17	LN	1700	0	1749	27	0
18	LO	1649	0	1794	25	0
19	LP	1282	0	1317	17	0
20	LQ	1512	0	1628	16	0
21	LR	1517	0	1670	20	0
22	LS	1452	0	1490	24	0
23	LT	1292	0	1361	19	0
24	LU	817	0	839	19	0
25	LV	972	0	1034	10	0
26	LW	935	0	995	21	0
27	LX	994	0	1072	12	0
28	LY	1115	0	1205	21	0
29	LZ	1106	0	1182	18	0
30	La	1161	0	1213	19	0
31	Lb	853	0	921	20	0
32	Lc	732	0	769	10	0
33	Ld	888	0	930	16	0
34	Le	1053	0	1147	19	0
35	Lf	881	0	917	6	0
36	Lg	897	0	985	10	0
37	Lh	1015	0	1148	17	0
38	Li	843	0	929	12	0
39	Lj	705	0	737	10	0
40	Lk	559	0	624	15	0
41	Ll	444	0	483	4	0
42	Lm	425	0	454	7	0
43	Ln	230	0	276	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lo	861	0	926	11	0
45	Lp	704	0	750	9	0
46	Lr	1007	0	1073	11	0
47	S2	34174	0	17301	419	0
48	SA	1700	0	1701	29	0
49	SB	1729	0	1803	19	0
50	SC	1707	0	1791	22	0
51	SD	1757	0	1853	36	0
52	SE	2065	0	2169	32	0
53	SF	1463	0	1511	24	0
54	SG	1909	0	2073	39	0
55	SH	1466	0	1532	36	0
56	SI	1678	0	1758	34	0
57	SJ	1499	0	1618	18	0
58	SK	816	0	841	15	0
59	SL	1189	0	1262	15	0
60	SM	864	0	879	28	0
61	SN	1208	0	1294	14	0
62	SO	1007	0	1032	20	0
63	SP	1054	0	1108	14	0
64	SQ	1117	0	1180	15	0
65	SR	1068	0	1121	15	0
66	SS	1190	0	1249	22	0
67	ST	1103	0	1133	20	0
68	SU	795	0	862	18	0
69	SV	636	0	637	4	0
70	SW	1033	0	1077	9	0
71	SX	1094	0	1161	9	0
72	SY	1006	0	1078	15	0
73	SZ	574	0	627	8	0
74	Sa	813	0	857	26	0
75	Sb	634	0	652	12	0
76	Sc	495	0	523	13	0
77	Sd	454	0	442	7	0
78	Se	414	0	454	5	0
79	Sf	528	0	533	13	0
80	Sg	2434	0	2387	52	0
81	L5	74592	0	37762	813	0
82	L7	2541	0	1285	11	0
83	Lq	1529	0	1584	39	0
84	CA	115	0	124	2	0
85	CB	28	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	CB	1	0	0	0	0
86	L5	198	0	0	0	0
86	L7	3	0	0	0	0
86	L8	2	0	0	0	0
86	LB	1	0	0	0	0
86	LC	1	0	0	0	0
86	LI	1	0	0	0	0
86	Lg	1	0	0	0	0
86	Lj	1	0	0	0	0
86	S2	60	0	0	0	0
86	SX	1	0	0	0	0
86	Sd	1	0	0	0	0
87	L5	74	0	0	0	0
87	L7	2	0	0	0	0
87	L8	3	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LN	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lf	1	0	0	0	0
87	S2	17	0	0	0	0
87	Sa	1	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
89	L5	36	0	72	5	0
89	S2	6	0	12	1	0
90	S2	36	0	37	0	0
91	L5	80	0	152	4	0
92	L5	20	0	23	2	0
93	L5	19	0	19	1	0
94	L5	1	0	0	0	0
95	CB	1	0	0	0	0
95	L5	263	0	0	2	0
95	L7	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
95	L8	7	0	0	0	0
95	LA	6	0	0	1	0
95	LB	5	0	0	0	0
95	LC	4	0	0	0	0
95	LF	2	0	0	0	0
95	LH	1	0	0	0	0
95	LN	3	0	0	0	0
95	LO	1	0	0	0	0
95	LP	2	0	0	0	0
95	LQ	1	0	0	0	0
95	LS	1	0	0	0	0
95	LT	1	0	0	0	0
95	LV	1	0	0	0	0
95	La	2	0	0	0	0
95	Lc	1	0	0	0	0
95	Le	5	0	0	0	0
95	Lf	2	0	0	0	0
95	Lg	1	0	0	0	0
95	Lj	1	0	0	0	0
95	Lo	1	0	0	0	0
95	Lp	3	0	0	0	0
95	S2	78	0	0	0	0
95	SF	1	0	0	0	0
95	SL	1	0	0	0	0
95	SN	1	0	0	0	0
All	All	216008	0	163540	2571	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 7.

The worst 5 of 2571 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:SH:10:LYS:HZ3	55:SH:20:GLU:HB3	1.33	0.93
81:L5:181:C:H2'	81:L5:182:G:H8	1.35	0.89
81:L5:181:C:H2'	81:L5:182:G:C8	2.08	0.89
81:L5:4894:A:H3'	81:L5:4895:C:H5'	1.56	0.87
47:S2:563:G:H1	47:S2:592:C:H5	1.24	0.86

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CB	813/858 (95%)	794 (98%)	19 (2%)	0	100	100
3	CD	68/402 (17%)	63 (93%)	5 (7%)	0	100	100
5	LA	246/257 (96%)	237 (96%)	9 (4%)	0	100	100
6	LB	397/403 (98%)	382 (96%)	15 (4%)	0	100	100
7	LC	362/427 (85%)	344 (95%)	18 (5%)	0	100	100
8	LD	290/297 (98%)	278 (96%)	12 (4%)	0	100	100
9	LE	219/288 (76%)	204 (93%)	15 (7%)	0	100	100
10	LF	224/248 (90%)	217 (97%)	7 (3%)	0	100	100
11	LG	223/266 (84%)	216 (97%)	7 (3%)	0	100	100
12	LH	188/192 (98%)	175 (93%)	12 (6%)	1 (0%)	24	42
13	LI	199/214 (93%)	195 (98%)	4 (2%)	0	100	100
14	LJ	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
15	LL	204/211 (97%)	195 (96%)	8 (4%)	1 (0%)	24	42
16	LM	135/215 (63%)	129 (96%)	6 (4%)	0	100	100
17	LN	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
18	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
19	LP	156/184 (85%)	148 (95%)	8 (5%)	0	100	100
20	LQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
21	LR	179/196 (91%)	174 (97%)	5 (3%)	0	100	100
22	LS	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
23	LT	156/160 (98%)	151 (97%)	4 (3%)	1 (1%)	21	38
24	LU	98/128 (77%)	94 (96%)	3 (3%)	1 (1%)	12	25
25	LV	128/140 (91%)	123 (96%)	5 (4%)	0	100	100
26	LW	109/157 (69%)	107 (98%)	2 (2%)	0	100	100
27	LX	119/156 (76%)	117 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LY	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
29	LZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
30	La	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
31	Lb	101/159 (64%)	97 (96%)	4 (4%)	0	100	100
32	Lc	92/115 (80%)	90 (98%)	2 (2%)	0	100	100
33	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
34	Le	126/135 (93%)	122 (97%)	4 (3%)	0	100	100
35	Lf	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
36	Lg	111/117 (95%)	111 (100%)	0	0	100	100
37	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
38	Li	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
39	Lj	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
40	Lk	66/70 (94%)	66 (100%)	0	0	100	100
41	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
42	Lm	50/128 (39%)	50 (100%)	0	0	100	100
43	Ln	22/25 (88%)	22 (100%)	0	0	100	100
44	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
45	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
46	Lr	124/137 (90%)	119 (96%)	5 (4%)	0	100	100
48	SA	213/295 (72%)	205 (96%)	8 (4%)	0	100	100
49	SB	211/264 (80%)	205 (97%)	6 (3%)	0	100	100
50	SC	218/293 (74%)	209 (96%)	9 (4%)	0	100	100
51	SD	224/243 (92%)	221 (99%)	2 (1%)	1 (0%)	30	48
52	SE	258/263 (98%)	249 (96%)	9 (4%)	0	100	100
53	SF	180/204 (88%)	170 (94%)	10 (6%)	0	100	100
54	SG	233/249 (94%)	228 (98%)	4 (2%)	1 (0%)	30	48
55	SH	181/194 (93%)	172 (95%)	8 (4%)	1 (1%)	21	38
56	SI	203/208 (98%)	193 (95%)	10 (5%)	0	100	100
57	SJ	178/194 (92%)	173 (97%)	5 (3%)	0	100	100
58	SK	95/165 (58%)	89 (94%)	6 (6%)	0	100	100
59	SL	141/158 (89%)	137 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	SM	109/132 (83%)	102 (94%)	7 (6%)	0	100	100
61	SN	148/151 (98%)	148 (100%)	0	0	100	100
62	SO	133/151 (88%)	127 (96%)	6 (4%)	0	100	100
63	SP	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
64	SQ	140/146 (96%)	134 (96%)	6 (4%)	0	100	100
65	SR	130/135 (96%)	123 (95%)	7 (5%)	0	100	100
66	SS	142/152 (93%)	134 (94%)	8 (6%)	0	100	100
67	ST	140/145 (97%)	137 (98%)	3 (2%)	0	100	100
68	SU	98/119 (82%)	93 (95%)	5 (5%)	0	100	100
69	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
70	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
71	SX	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
72	SY	121/133 (91%)	120 (99%)	1 (1%)	0	100	100
73	SZ	70/125 (56%)	64 (91%)	5 (7%)	1 (1%)	9	19
74	Sa	100/115 (87%)	96 (96%)	4 (4%)	0	100	100
75	Sb	76/84 (90%)	70 (92%)	6 (8%)	0	100	100
76	Sc	61/69 (88%)	59 (97%)	2 (3%)	0	100	100
77	Sd	53/56 (95%)	53 (100%)	0	0	100	100
78	Se	48/133 (36%)	46 (96%)	2 (4%)	0	100	100
79	Sf	63/156 (40%)	60 (95%)	3 (5%)	0	100	100
80	Sg	311/317 (98%)	288 (93%)	23 (7%)	0	100	100
83	Lq	197/317 (62%)	184 (93%)	12 (6%)	1 (0%)	24	42
84	CA	13/394 (3%)	13 (100%)	0	0	100	100
All	All	12260/14733 (83%)	11805 (96%)	446 (4%)	9 (0%)	49	68

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	SH	148	LEU
54	SG	127	THR
73	SZ	103	HIS
24	LU	67	LYS
23	LT	80	VAL

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	
1	CB	697/730 (96%)	669 (96%)	28 (4%)	28	53
3	CD	62/322 (19%)	60 (97%)	2 (3%)	34	59
5	LA	189/199 (95%)	180 (95%)	9 (5%)	23	46
6	LB	347/349 (99%)	337 (97%)	10 (3%)	37	61
7	LC	302/348 (87%)	295 (98%)	7 (2%)	44	68
8	LD	246/250 (98%)	233 (95%)	13 (5%)	20	42
9	LE	197/252 (78%)	189 (96%)	8 (4%)	27	52
10	LF	195/215 (91%)	191 (98%)	4 (2%)	47	70
11	LG	196/223 (88%)	191 (97%)	5 (3%)	40	65
12	LH	169/171 (99%)	167 (99%)	2 (1%)	63	80
13	LI	174/182 (96%)	166 (95%)	8 (5%)	24	48
14	LJ	144/149 (97%)	135 (94%)	9 (6%)	16	34
15	LL	172/177 (97%)	169 (98%)	3 (2%)	53	75
16	LM	116/161 (72%)	111 (96%)	5 (4%)	26	50
17	LN	171/172 (99%)	165 (96%)	6 (4%)	32	57
18	LO	173/174 (99%)	166 (96%)	7 (4%)	28	53
19	LP	139/163 (85%)	132 (95%)	7 (5%)	22	44
20	LQ	164/165 (99%)	161 (98%)	3 (2%)	51	73
21	LR	160/175 (91%)	153 (96%)	7 (4%)	25	49
22	LS	156/157 (99%)	143 (92%)	13 (8%)	10	22
23	LT	139/140 (99%)	129 (93%)	10 (7%)	13	28
24	LU	90/115 (78%)	87 (97%)	3 (3%)	33	58
25	LV	100/107 (94%)	94 (94%)	6 (6%)	17	36
26	LW	94/126 (75%)	93 (99%)	1 (1%)	65	81
27	LX	109/133 (82%)	106 (97%)	3 (3%)	38	62
28	LY	124/135 (92%)	118 (95%)	6 (5%)	23	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	LZ	117/118 (99%)	114 (97%)	3 (3%)	40	65
30	La	120/121 (99%)	113 (94%)	7 (6%)	18	38
31	Lb	86/126 (68%)	82 (95%)	4 (5%)	23	47
32	Lc	79/97 (81%)	74 (94%)	5 (6%)	16	34
33	Ld	98/110 (89%)	93 (95%)	5 (5%)	21	43
34	Le	114/121 (94%)	110 (96%)	4 (4%)	32	57
35	Lf	88/89 (99%)	86 (98%)	2 (2%)	44	68
36	Lg	97/100 (97%)	95 (98%)	2 (2%)	47	70
37	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	84
38	Li	87/89 (98%)	84 (97%)	3 (3%)	32	58
39	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	78
40	Lk	63/65 (97%)	60 (95%)	3 (5%)	23	46
41	Ll	47/48 (98%)	47 (100%)	0	100	100
42	Lm	47/116 (40%)	47 (100%)	0	100	100
43	Ln	23/24 (96%)	23 (100%)	0	100	100
44	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	81
45	Lp	73/75 (97%)	70 (96%)	3 (4%)	27	52
46	Lr	109/121 (90%)	107 (98%)	2 (2%)	51	73
48	SA	180/243 (74%)	177 (98%)	3 (2%)	53	75
49	SB	194/231 (84%)	189 (97%)	5 (3%)	40	65
50	SC	186/225 (83%)	177 (95%)	9 (5%)	23	46
51	SD	189/202 (94%)	184 (97%)	5 (3%)	40	65
52	SE	223/225 (99%)	220 (99%)	3 (1%)	61	79
53	SF	157/170 (92%)	152 (97%)	5 (3%)	34	59
54	SG	205/218 (94%)	197 (96%)	8 (4%)	28	54
55	SH	157/174 (90%)	152 (97%)	5 (3%)	34	59
56	SI	177/180 (98%)	171 (97%)	6 (3%)	32	58
57	SJ	160/168 (95%)	156 (98%)	4 (2%)	42	66
58	SK	88/136 (65%)	86 (98%)	2 (2%)	44	68
59	SL	131/142 (92%)	129 (98%)	2 (2%)	57	77
60	SM	93/108 (86%)	90 (97%)	3 (3%)	34	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	SN	130/131 (99%)	126 (97%)	4 (3%)	35	60
62	SO	104/119 (87%)	100 (96%)	4 (4%)	29	54
63	SP	114/130 (88%)	111 (97%)	3 (3%)	40	65
64	SQ	115/121 (95%)	112 (97%)	3 (3%)	40	65
65	SR	119/122 (98%)	116 (98%)	3 (2%)	42	66
66	SS	125/132 (95%)	122 (98%)	3 (2%)	43	67
67	ST	112/115 (97%)	109 (97%)	3 (3%)	39	63
68	SU	92/107 (86%)	89 (97%)	3 (3%)	33	58
69	SV	67/67 (100%)	66 (98%)	1 (2%)	57	77
70	SW	111/113 (98%)	107 (96%)	4 (4%)	31	56
71	SX	112/115 (97%)	111 (99%)	1 (1%)	70	84
72	SY	107/115 (93%)	106 (99%)	1 (1%)	70	84
73	SZ	64/103 (62%)	61 (95%)	3 (5%)	23	47
74	Sa	87/98 (89%)	86 (99%)	1 (1%)	65	81
75	Sb	73/76 (96%)	71 (97%)	2 (3%)	39	63
76	Sc	56/62 (90%)	51 (91%)	5 (9%)	9	20
77	Sd	45/49 (92%)	44 (98%)	1 (2%)	45	69
78	Se	42/104 (40%)	41 (98%)	1 (2%)	43	67
79	Sf	57/140 (41%)	54 (95%)	3 (5%)	20	42
80	Sg	270/275 (98%)	260 (96%)	10 (4%)	30	55
83	Lq	167/258 (65%)	163 (98%)	4 (2%)	43	67
84	CA	12/336 (4%)	12 (100%)	0	100	100
All	All	10669/12504 (85%)	10315 (97%)	354 (3%)	34	58

5 of 354 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	SA	54	THR
59	SL	39	ASN
49	SB	154	SER
53	SF	202	SER
63	SP	112	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 118 such sidechains are listed below:

Mol	Chain	Res	Type
30	La	19	HIS
77	Sd	5	GLN
46	Lr	41	ASN
75	Sb	65	GLN
63	SP	41	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CC	21/85 (24%)	4 (19%)	0
4	L8	153/156 (98%)	52 (33%)	3 (1%)
47	S2	1579/1871 (84%)	403 (25%)	4 (0%)
81	L5	3447/5069 (68%)	752 (21%)	17 (0%)
82	L7	118/120 (98%)	14 (11%)	0
All	All	5318/7301 (72%)	1225 (23%)	24 (0%)

5 of 1225 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CC	25	C
2	CC	26	G
2	CC	31	A
2	CC	41	C
4	L8	3	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	L5	2675	G
81	L5	3614	G
81	L5	3597	G
81	L5	3673	C
47	S2	970	G

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

154 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
81	OMG	L5	4370	81	23,26,27	2.34	9 (39%)	32,38,41	2.35	11 (34%)
47	PSU	S2	406	47	18,21,22	4.53	7 (38%)	21,30,33	2.00	5 (23%)
81	PSU	L5	4628	81	18,21,22	4.45	7 (38%)	21,30,33	1.95	6 (28%)
47	OMU	S2	172	47	19,22,23	3.06	8 (42%)	25,31,34	1.83	4 (16%)
47	6MZ	S2	1871	86	26,26,26	2.30	4 (15%)	36,39,39	2.01	11 (30%)
47	A2M	S2	590	47	22,25,26	3.49	9 (40%)	30,36,39	2.56	12 (40%)
81	PSU	L5	1781	81	18,21,22	4.60	7 (38%)	21,30,33	1.89	4 (19%)
81	UR3	L5	4530	81	19,22,23	2.81	6 (31%)	26,32,35	1.86	5 (19%)
81	UY1	L5	3818	86	19,22,23	4.02	7 (36%)	21,31,34	1.89	6 (28%)
81	PSU	L5	4552	81	18,21,22	4.53	7 (38%)	21,30,33	1.96	5 (23%)
47	B8N	S2	1870	-	25,29,30	3.33	9 (36%)	28,42,45	2.10	7 (25%)
81	PSU	L5	3639	81	18,21,22	4.51	7 (38%)	21,30,33	2.03	5 (23%)
47	A2M	S2	576	47	22,25,26	3.54	9 (40%)	30,36,39	2.30	11 (36%)
47	PSU	S2	1177	47	18,21,22	4.46	7 (38%)	21,30,33	2.07	5 (23%)
81	PSU	L5	1862	81	18,21,22	4.55	7 (38%)	21,30,33	2.05	5 (23%)
4	OMG	L8	75	4	23,26,27	2.35	8 (34%)	32,38,41	2.41	10 (31%)
81	OMG	L5	3792	81	23,26,27	2.34	8 (34%)	32,38,41	2.41	8 (25%)
4	PSU	L8	69	4	18,21,22	4.59	8 (44%)	21,30,33	2.17	5 (23%)
81	OMG	L5	1316	81	23,26,27	2.31	8 (34%)	32,38,41	2.36	12 (37%)
81	OMU	L5	4498	81	19,22,23	2.98	8 (42%)	25,31,34	1.80	4 (16%)
47	A2M	S2	99	47,86	22,25,26	3.58	9 (40%)	30,36,39	2.30	11 (36%)
47	A2M	S2	27	47,86	22,25,26	3.40	9 (40%)	30,36,39	2.80	14 (46%)
81	A2M	L5	400	81	22,25,26	3.57	9 (40%)	30,36,39	2.31	10 (33%)
47	PSU	S2	1238	47	18,21,22	4.59	7 (38%)	21,30,33	2.05	5 (23%)
81	A2M	L5	3718	81	22,25,26	3.53	9 (40%)	30,36,39	2.29	12 (40%)
4	OMU	L8	14	81,4	19,22,23	2.98	8 (42%)	25,31,34	1.83	4 (16%)
47	4AC	S2	1842	47	21,24,25	3.10	10 (47%)	28,34,37	1.72	5 (17%)
81	A2M	L5	2787	81	22,25,26	3.52	9 (40%)	30,36,39	2.28	10 (33%)
47	OMG	S2	436	47	23,26,27	2.33	9 (39%)	32,38,41	2.31	11 (34%)
81	PSU	L5	4312	81	18,21,22	4.54	7 (38%)	21,30,33	1.99	5 (23%)
81	PSU	L5	4576	81	18,21,22	4.57	7 (38%)	21,30,33	1.96	5 (23%)
81	PSU	L5	5001	81	18,21,22	4.54	7 (38%)	21,30,33	1.96	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
81	PSU	L5	4403	81	18,21,22	4.45	7 (38%)	21,30,33	2.10	6 (28%)
81	PSU	L5	4579	81	18,21,22	4.52	7 (38%)	21,30,33	1.95	5 (23%)
47	PSU	S2	1232	47	18,21,22	4.58	7 (38%)	21,30,33	1.94	5 (23%)
81	OMG	L5	4623	81	23,26,27	2.30	8 (34%)	32,38,41	2.32	10 (31%)
81	OMG	L5	4499	81	23,26,27	2.37	8 (34%)	32,38,41	2.46	9 (28%)
81	OMC	L5	1340	81	19,22,23	2.91	8 (42%)	25,31,34	0.83	0
47	PSU	S2	109	47	18,21,22	4.55	7 (38%)	21,30,33	2.04	6 (28%)
47	OMC	S2	517	47	19,22,23	2.98	8 (42%)	25,31,34	0.76	1 (4%)
47	MA6	S2	1851	47	23,26,27	1.45	4 (17%)	33,38,41	2.99	12 (36%)
81	A2M	L5	1871	81	22,25,26	3.61	9 (40%)	30,36,39	2.46	12 (40%)
47	A2M	S2	468	47	22,25,26	3.57	9 (40%)	30,36,39	2.36	11 (36%)
81	OMG	L5	1625	81	23,26,27	2.35	8 (34%)	32,38,41	2.51	9 (28%)
47	OMC	S2	1391	47	19,22,23	2.93	8 (42%)	25,31,34	0.80	1 (4%)
47	PSU	S2	93	47	18,21,22	4.59	7 (38%)	21,30,33	1.89	4 (19%)
47	A2M	S2	166	47	22,25,26	3.54	9 (40%)	30,36,39	2.33	10 (33%)
81	A2M	L5	2401	81	22,25,26	3.54	9 (40%)	30,36,39	2.36	11 (36%)
81	OMG	L5	4637	81	23,26,27	2.34	8 (34%)	32,38,41	2.49	10 (31%)
47	OMU	S2	354	47	19,22,23	3.01	8 (42%)	25,31,34	1.78	4 (16%)
47	A2M	S2	1678	47	22,25,26	3.62	9 (40%)	30,36,39	2.36	11 (36%)
81	OMG	L5	2876	81	23,26,27	2.30	8 (34%)	32,38,41	2.53	10 (31%)
81	5MC	L5	3782	81,86	19,22,23	3.68	8 (42%)	26,32,35	1.24	3 (11%)
81	A2M	L5	1534	81,86	22,25,26	3.49	9 (40%)	30,36,39	2.38	11 (36%)
47	PSU	S2	1643	47,86	18,21,22	4.55	7 (38%)	21,30,33	1.94	5 (23%)
81	OMG	L5	2424	81	23,26,27	2.39	8 (34%)	32,38,41	2.59	9 (28%)
47	4AC	S2	1337	47	21,24,25	2.92	9 (42%)	28,34,37	1.62	6 (21%)
81	PSU	L5	4471	81	18,21,22	4.56	7 (38%)	21,30,33	2.02	5 (23%)
47	OMU	S2	121	47	19,22,23	3.01	8 (42%)	25,31,34	1.76	4 (16%)
81	OMC	L5	2351	81	19,22,23	2.88	8 (42%)	25,31,34	0.82	1 (4%)
81	OMU	L5	4620	81	19,22,23	2.99	8 (42%)	25,31,34	1.75	4 (16%)
81	A2M	L5	3724	81	22,25,26	3.54	9 (40%)	30,36,39	2.30	12 (40%)
81	A2M	L5	3825	81	22,25,26	3.56	9 (40%)	30,36,39	2.35	10 (33%)
81	OMC	L5	2804	81	19,22,23	2.89	8 (42%)	25,31,34	0.85	1 (4%)
47	OMG	S2	644	47	23,26,27	2.35	8 (34%)	32,38,41	2.45	10 (31%)
81	PSU	L5	5010	81	18,21,22	4.60	7 (38%)	21,30,33	1.94	5 (23%)
81	OMC	L5	3887	81	19,22,23	2.96	8 (42%)	25,31,34	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	OMC	S2	174	47	19,22,23	3.01	8 (42%)	25,31,34	0.83	0
81	OMU	L5	2415	81	19,22,23	3.05	8 (42%)	25,31,34	1.82	5 (20%)
81	OMG	L5	2364	81	23,26,27	2.31	9 (39%)	32,38,41	2.31	11 (34%)
81	A2M	L5	4590	81	22,25,26	3.56	9 (40%)	30,36,39	2.32	10 (33%)
81	PSU	L5	2839	81	18,21,22	4.47	7 (38%)	21,30,33	1.86	5 (23%)
81	PSU	L5	3884	81	18,21,22	4.49	7 (38%)	21,30,33	1.87	4 (19%)
47	OMG	S2	1328	87,47	23,26,27	2.30	8 (34%)	32,38,41	2.34	9 (28%)
47	PSU	S2	681	47	18,21,22	4.56	7 (38%)	21,30,33	1.93	5 (23%)
47	PSU	S2	34	47	18,21,22	4.59	7 (38%)	21,30,33	2.00	5 (23%)
81	PSU	L5	4569	81	18,21,22	4.51	7 (38%)	21,30,33	1.95	5 (23%)
81	A2M	L5	4523	81,86	22,25,26	3.53	9 (40%)	30,36,39	2.35	11 (36%)
47	OMG	S2	1490	47,86	23,26,27	2.33	8 (34%)	32,38,41	2.13	7 (21%)
47	A2M	S2	512	47	22,25,26	3.55	9 (40%)	30,36,39	2.31	10 (33%)
47	PSU	S2	1056	47	18,21,22	4.63	7 (38%)	21,30,33	1.97	5 (23%)
81	OMC	L5	2365	81,86	19,22,23	2.92	8 (42%)	25,31,34	0.83	0
81	PSU	L5	4457	81	18,21,22	4.48	7 (38%)	21,30,33	1.98	6 (28%)
81	PSU	L5	4972	81	18,21,22	4.56	7 (38%)	21,30,33	1.98	5 (23%)
47	MA6	S2	1850	47	23,26,27	1.48	5 (21%)	33,38,41	2.87	12 (36%)
47	PSU	S2	651	47	18,21,22	4.57	7 (38%)	21,30,33	2.00	5 (23%)
81	PSU	L5	4532	81	18,21,22	4.51	7 (38%)	21,30,33	1.87	4 (19%)
47	OMU	S2	116	47	19,22,23	3.06	8 (42%)	25,31,34	1.77	4 (16%)
81	PSU	L5	3770	81	18,21,22	4.50	7 (38%)	21,30,33	2.06	5 (23%)
47	OMC	S2	1703	47	19,22,23	3.03	8 (42%)	25,31,34	1.25	2 (8%)
81	PSU	L5	3637	81	18,21,22	4.47	7 (38%)	21,30,33	1.82	4 (19%)
81	PSU	L5	4353	81	18,21,22	4.53	7 (38%)	21,30,33	2.00	5 (23%)
47	PSU	S2	649	47	18,21,22	4.56	7 (38%)	21,30,33	1.98	5 (23%)
81	OMG	L5	4618	81	23,26,27	2.32	9 (39%)	32,38,41	2.31	11 (34%)
81	OMC	L5	1881	81,87	19,22,23	2.91	8 (42%)	25,31,34	0.82	0
47	OMG	S2	601	47	23,26,27	2.34	9 (39%)	32,38,41	2.44	10 (31%)
81	OMU	L5	2837	81	19,22,23	3.02	8 (42%)	25,31,34	1.81	4 (16%)
81	A2M	L5	3785	81	22,25,26	3.44	9 (40%)	30,36,39	2.48	13 (43%)
47	A2M	S2	1031	47	22,25,26	3.56	9 (40%)	30,36,39	2.33	10 (33%)
47	PSU	S2	1692	47	18,21,22	4.53	7 (38%)	21,30,33	2.03	5 (23%)
81	PSU	L5	4442	81	18,21,22	4.49	8 (44%)	21,30,33	2.13	6 (28%)
81	OMG	L5	4228	81	23,26,27	2.32	9 (39%)	32,38,41	2.25	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	A2M	S2	1383	47	22,25,26	3.53	9 (40%)	30,36,39	2.35	12 (40%)
81	PSU	L5	3695	81	18,21,22	4.44	7 (38%)	21,30,33	2.10	5 (23%)
47	OMG	S2	683	47	23,26,27	2.35	9 (39%)	32,38,41	2.36	11 (34%)
81	OMG	L5	1522	81	23,26,27	2.32	8 (34%)	32,38,41	2.36	11 (34%)
81	A2M	L5	1524	81	22,25,26	3.52	9 (40%)	30,36,39	2.47	13 (43%)
81	A2M	L5	3830	81	22,25,26	3.50	9 (40%)	30,36,39	2.34	10 (33%)
81	OMU	L5	4306	81	19,22,23	3.01	8 (42%)	25,31,34	1.76	4 (16%)
47	A2M	S2	484	47	22,25,26	3.51	9 (40%)	30,36,39	2.31	10 (33%)
47	PSU	S2	686	47	18,21,22	4.53	7 (38%)	21,30,33	1.96	5 (23%)
81	PSU	L5	4361	81	18,21,22	4.53	7 (38%)	21,30,33	1.97	5 (23%)
47	OMG	S2	1447	47	23,26,27	2.36	9 (39%)	32,38,41	2.42	9 (28%)
81	PSU	L5	2632	81	18,21,22	4.57	7 (38%)	21,30,33	1.93	5 (23%)
81	OMC	L5	3808	81	19,22,23	2.90	8 (42%)	25,31,34	0.78	1 (4%)
81	A2M	L5	2363	81,86	22,25,26	3.58	9 (40%)	30,36,39	2.33	10 (33%)
81	OMG	L5	3744	81	23,26,27	0.31	0	32,38,41	0.43	0
47	OMU	S2	1442	47,86	19,22,23	3.09	8 (42%)	25,31,34	1.93	7 (28%)
81	OMC	L5	3869	81	19,22,23	2.95	8 (42%)	25,31,34	0.80	0
81	OMU	L5	3925	81	19,22,23	3.01	8 (42%)	25,31,34	1.83	4 (16%)
81	OMC	L5	2824	81	19,22,23	2.94	8 (42%)	25,31,34	0.84	1 (4%)
81	PSU	L5	4431	81	18,21,22	4.55	7 (38%)	21,30,33	1.95	4 (19%)
81	A2M	L5	4571	81	22,25,26	3.62	9 (40%)	30,36,39	2.30	11 (36%)
81	PSU	L5	3851	81	18,21,22	4.50	7 (38%)	21,30,33	2.01	5 (23%)
47	PSU	S2	1244	47	18,21,22	4.53	7 (38%)	21,30,33	1.98	5 (23%)
47	OMU	S2	1288	47	19,22,23	3.05	8 (42%)	25,31,34	1.73	4 (16%)
47	PSU	S2	1445	47	18,21,22	4.58	7 (38%)	21,30,33	1.97	4 (19%)
81	6MZ	L5	4220	-	26,26,26	2.26	5 (19%)	36,39,39	2.04	11 (30%)
81	OMU	L5	4227	81	19,22,23	3.03	8 (42%)	25,31,34	1.76	4 (16%)
81	A2M	L5	3867	81	22,25,26	3.55	9 (40%)	30,36,39	2.33	11 (36%)
81	OMC	L5	2861	81	19,22,23	2.97	8 (42%)	25,31,34	0.78	1 (4%)
81	PSU	L5	1683	81	18,21,22	4.53	7 (38%)	21,30,33	1.92	5 (23%)
81	OMC	L5	4456	81	19,22,23	2.92	8 (42%)	25,31,34	0.84	1 (4%)
81	PSU	L5	4689	81	18,21,22	4.54	7 (38%)	21,30,33	1.97	5 (23%)
81	OMC	L5	3701	81,87,86	19,22,23	0.38	0	25,31,34	0.60	0
81	OMG	L5	4494	81	23,26,27	2.33	9 (39%)	32,38,41	2.36	9 (28%)
81	OMG	L5	4392	81	23,26,27	2.31	8 (34%)	32,38,41	2.33	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
81	PSU	L5	3758	81	18,21,22	4.48	7 (38%)	21,30,33	2.01	5 (23%)
81	A2M	L5	398	81	22,25,26	3.55	9 (40%)	30,36,39	2.32	10 (33%)
47	A2M	S2	159	47	22,25,26	3.53	9 (40%)	30,36,39	2.36	12 (40%)
47	PSU	S2	36	47	18,21,22	4.56	7 (38%)	21,30,33	1.99	5 (23%)
81	OMC	L5	2422	81,86	19,22,23	2.91	8 (42%)	25,31,34	0.84	1 (4%)
81	PSU	L5	1782	81	18,21,22	4.54	7 (38%)	21,30,33	1.96	5 (23%)
81	PSU	L5	3920	81,86	18,21,22	4.47	7 (38%)	21,30,33	1.96	5 (23%)
81	PSU	L5	4423	81	18,21,22	4.59	7 (38%)	21,30,33	2.01	5 (23%)
81	A2M	L5	2815	81	22,25,26	3.52	9 (40%)	30,36,39	2.34	11 (36%)
81	PSU	L5	1779	81	18,21,22	4.55	7 (38%)	21,30,33	1.94	5 (23%)
81	A2M	L5	1326	81	22,25,26	3.54	9 (40%)	30,36,39	2.33	9 (30%)
81	PSU	L5	4299	81	18,21,22	4.54	7 (38%)	21,30,33	1.99	5 (23%)
81	OMC	L5	4536	81	19,22,23	2.91	8 (42%)	25,31,34	0.82	1 (4%)
81	OMC	L5	3841	81	19,22,23	2.95	8 (42%)	25,31,34	1.43	3 (12%)
47	OMU	S2	428	47	19,22,23	3.03	8 (42%)	25,31,34	1.81	4 (16%)
47	OMG	S2	509	47	23,26,27	2.32	8 (34%)	32,38,41	2.39	9 (28%)
81	OMG	L5	3627	81	23,26,27	2.27	8 (34%)	32,38,41	2.26	10 (31%)

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
81	OMG	L5	4370	81	-	0/9/27/28	0/3/3/3
47	PSU	S2	406	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	4628	81	-	0/7/25/26	0/2/2/2
47	OMU	S2	172	47	-	0/9/27/28	0/2/2/2
47	6MZ	S2	1871	86	-	2/12/28/28	0/3/3/3
47	A2M	S2	590	47	-	1/9/27/28	0/3/3/3
81	PSU	L5	1781	81	-	1/7/25/26	0/2/2/2
81	UR3	L5	4530	81	-	2/7/25/26	0/2/2/2
81	UY1	L5	3818	86	-	5/9/27/28	0/2/2/2
81	PSU	L5	4552	81	-	0/7/25/26	0/2/2/2
47	B8N	S2	1870	-	-	8/16/34/35	0/2/2/2
81	PSU	L5	3639	81	-	0/7/25/26	0/2/2/2
47	A2M	S2	576	47	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	PSU	S2	1177	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	1862	81	-	0/7/25/26	0/2/2/2
4	OMG	L8	75	4	-	2/9/27/28	0/3/3/3
81	OMG	L5	3792	81	-	0/9/27/28	0/3/3/3
4	PSU	L8	69	4	-	2/7/25/26	0/2/2/2
81	OMG	L5	1316	81	-	0/9/27/28	0/3/3/3
81	OMU	L5	4498	81	-	0/9/27/28	0/2/2/2
47	A2M	S2	99	47,86	-	2/9/27/28	0/3/3/3
47	A2M	S2	27	47,86	-	3/9/27/28	0/3/3/3
81	A2M	L5	400	81	-	0/9/27/28	0/3/3/3
47	PSU	S2	1238	47	-	0/7/25/26	0/2/2/2
81	A2M	L5	3718	81	-	0/9/27/28	0/3/3/3
4	OMU	L8	14	81,4	-	1/9/27/28	0/2/2/2
47	4AC	S2	1842	47	-	2/11/29/30	0/2/2/2
81	A2M	L5	2787	81	-	5/9/27/28	0/3/3/3
47	OMG	S2	436	47	-	0/9/27/28	0/3/3/3
81	PSU	L5	4312	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	4576	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	5001	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	4403	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	4579	81	-	0/7/25/26	0/2/2/2
47	PSU	S2	1232	47	-	0/7/25/26	0/2/2/2
81	OMG	L5	4623	81	-	0/9/27/28	0/3/3/3
81	OMG	L5	4499	81	-	0/9/27/28	0/3/3/3
81	OMC	L5	1340	81	-	0/9/27/28	0/2/2/2
47	PSU	S2	109	47	-	0/7/25/26	0/2/2/2
47	OMC	S2	517	47	-	0/9/27/28	0/2/2/2
47	MA6	S2	1851	47	-	1/11/29/30	0/3/3/3
81	A2M	L5	1871	81	-	2/9/27/28	0/3/3/3
47	A2M	S2	468	47	-	0/9/27/28	0/3/3/3
81	OMG	L5	1625	81	-	0/9/27/28	0/3/3/3
47	OMC	S2	1391	47	-	0/9/27/28	0/2/2/2
47	PSU	S2	93	47	-	0/7/25/26	0/2/2/2
47	A2M	S2	166	47	-	0/9/27/28	0/3/3/3
81	A2M	L5	2401	81	-	0/9/27/28	0/3/3/3
81	OMG	L5	4637	81	-	1/9/27/28	0/3/3/3
47	OMU	S2	354	47	-	0/9/27/28	0/2/2/2
47	A2M	S2	1678	47	-	1/9/27/28	0/3/3/3
81	OMG	L5	2876	81	-	2/9/27/28	0/3/3/3
81	5MC	L5	3782	81,86	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	A2M	L5	1534	81,86	-	2/9/27/28	0/3/3/3
47	PSU	S2	1643	47,86	-	0/7/25/26	0/2/2/2
81	OMG	L5	2424	81	-	2/9/27/28	0/3/3/3
47	4AC	S2	1337	47	-	2/11/29/30	0/2/2/2
81	PSU	L5	4471	81	-	2/7/25/26	0/2/2/2
47	OMU	S2	121	47	-	1/9/27/28	0/2/2/2
81	OMC	L5	2351	81	-	4/9/27/28	0/2/2/2
81	OMU	L5	4620	81	-	0/9/27/28	0/2/2/2
81	A2M	L5	3724	81	-	0/9/27/28	0/3/3/3
81	A2M	L5	3825	81	-	0/9/27/28	0/3/3/3
81	OMC	L5	2804	81	-	0/9/27/28	0/2/2/2
47	OMG	S2	644	47	-	3/9/27/28	0/3/3/3
81	PSU	L5	5010	81	-	0/7/25/26	0/2/2/2
81	OMC	L5	3887	81	-	2/9/27/28	0/2/2/2
47	OMC	S2	174	47	-	0/9/27/28	0/2/2/2
81	OMU	L5	2415	81	-	1/9/27/28	0/2/2/2
81	OMG	L5	2364	81	-	2/9/27/28	0/3/3/3
81	A2M	L5	4590	81	-	1/9/27/28	0/3/3/3
81	PSU	L5	2839	81	-	4/7/25/26	0/2/2/2
81	PSU	L5	3884	81	-	0/7/25/26	0/2/2/2
47	OMG	S2	1328	87,47	-	0/9/27/28	0/3/3/3
47	PSU	S2	681	47	-	0/7/25/26	0/2/2/2
47	PSU	S2	34	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	4569	81	-	2/7/25/26	0/2/2/2
81	A2M	L5	4523	81,86	-	1/9/27/28	0/3/3/3
47	OMG	S2	1490	47,86	-	1/9/27/28	0/3/3/3
47	A2M	S2	512	47	-	2/9/27/28	0/3/3/3
47	PSU	S2	1056	47	-	0/7/25/26	0/2/2/2
81	OMC	L5	2365	81,86	-	0/9/27/28	0/2/2/2
81	PSU	L5	4457	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	4972	81	-	0/7/25/26	0/2/2/2
47	MA6	S2	1850	47	-	0/11/29/30	0/3/3/3
47	PSU	S2	651	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	4532	81	-	2/7/25/26	0/2/2/2
47	OMU	S2	116	47	-	3/9/27/28	0/2/2/2
81	PSU	L5	3770	81	-	0/7/25/26	0/2/2/2
47	OMC	S2	1703	47	-	4/9/27/28	0/2/2/2
81	PSU	L5	3637	81	-	3/7/25/26	0/2/2/2
81	PSU	L5	4353	81	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	PSU	S2	649	47	-	0/7/25/26	0/2/2/2
81	OMG	L5	4618	81	-	2/9/27/28	0/3/3/3
81	OMC	L5	1881	81,87	-	0/9/27/28	0/2/2/2
47	OMG	S2	601	47	-	0/9/27/28	0/3/3/3
81	OMU	L5	2837	81	-	0/9/27/28	0/2/2/2
81	A2M	L5	3785	81	-	3/9/27/28	0/3/3/3
47	A2M	S2	1031	47	-	0/9/27/28	0/3/3/3
47	PSU	S2	1692	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	4442	81	-	0/7/25/26	0/2/2/2
81	OMG	L5	4228	81	-	2/9/27/28	0/3/3/3
47	A2M	S2	1383	47	-	0/9/27/28	0/3/3/3
81	PSU	L5	3695	81	-	0/7/25/26	0/2/2/2
47	OMG	S2	683	47	-	2/9/27/28	0/3/3/3
81	OMG	L5	1522	81	-	0/9/27/28	0/3/3/3
81	A2M	L5	1524	81	-	0/9/27/28	0/3/3/3
81	A2M	L5	3830	81	-	0/9/27/28	0/3/3/3
81	OMU	L5	4306	81	-	2/9/27/28	0/2/2/2
47	A2M	S2	484	47	-	0/9/27/28	0/3/3/3
47	PSU	S2	686	47	-	0/7/25/26	0/2/2/2
81	PSU	L5	4361	81	-	0/7/25/26	0/2/2/2
47	OMG	S2	1447	47	-	3/9/27/28	0/3/3/3
81	PSU	L5	2632	81	-	0/7/25/26	0/2/2/2
81	OMC	L5	3808	81	-	0/9/27/28	0/2/2/2
81	A2M	L5	2363	81,86	-	0/9/27/28	0/3/3/3
81	OMG	L5	3744	81	-	0/9/27/28	0/3/3/3
47	OMU	S2	1442	47,86	-	4/9/27/28	0/2/2/2
81	OMC	L5	3869	81	-	0/9/27/28	0/2/2/2
81	OMU	L5	3925	81	-	1/9/27/28	0/2/2/2
81	OMC	L5	2824	81	-	0/9/27/28	0/2/2/2
81	PSU	L5	4431	81	-	0/7/25/26	0/2/2/2
81	A2M	L5	4571	81	-	0/9/27/28	0/3/3/3
81	PSU	L5	3851	81	-	2/7/25/26	0/2/2/2
47	PSU	S2	1244	47	-	0/7/25/26	0/2/2/2
47	OMU	S2	1288	47	-	0/9/27/28	0/2/2/2
47	PSU	S2	1445	47	-	1/7/25/26	0/2/2/2
81	6MZ	L5	4220	-	-	5/12/28/28	0/3/3/3
81	OMU	L5	4227	81	-	2/9/27/28	0/2/2/2
81	A2M	L5	3867	81	-	3/9/27/28	0/3/3/3
81	OMC	L5	2861	81	-	0/9/27/28	0/2/2/2
81	PSU	L5	1683	81	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	OMC	L5	4456	81	-	0/9/27/28	0/2/2/2
81	PSU	L5	4689	81	-	0/7/25/26	0/2/2/2
81	OMC	L5	3701	81,87,86	-	5/9/27/28	0/2/2/2
81	OMG	L5	4494	81	-	0/9/27/28	0/3/3/3
81	OMG	L5	4392	81	-	0/9/27/28	0/3/3/3
81	PSU	L5	3758	81	-	0/7/25/26	0/2/2/2
81	A2M	L5	398	81	-	1/9/27/28	0/3/3/3
47	A2M	S2	159	47	-	2/9/27/28	0/3/3/3
47	PSU	S2	36	47	-	0/7/25/26	0/2/2/2
81	OMC	L5	2422	81,86	-	2/9/27/28	0/2/2/2
81	PSU	L5	1782	81	-	0/7/25/26	0/2/2/2
81	PSU	L5	3920	81,86	-	0/7/25/26	0/2/2/2
81	PSU	L5	4423	81	-	0/7/25/26	0/2/2/2
81	A2M	L5	2815	81	-	2/9/27/28	0/3/3/3
81	PSU	L5	1779	81	-	0/7/25/26	0/2/2/2
81	A2M	L5	1326	81	-	3/9/27/28	0/3/3/3
81	PSU	L5	4299	81	-	0/7/25/26	0/2/2/2
81	OMC	L5	4536	81	-	0/9/27/28	0/2/2/2
81	OMC	L5	3841	81	-	2/9/27/28	0/2/2/2
47	OMU	S2	428	47	-	6/9/27/28	0/2/2/2
47	OMG	S2	509	47	-	0/9/27/28	0/3/3/3
81	OMG	L5	3627	81	-	1/9/27/28	0/3/3/3

The worst 5 of 1192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	L5	1781	PSU	C6-C5	12.27	1.48	1.35
81	L5	5010	PSU	C6-C5	12.23	1.48	1.35
47	S2	93	PSU	C6-C5	12.18	1.48	1.35
47	S2	1445	PSU	C6-C5	12.13	1.48	1.35
81	L5	4552	PSU	C6-C5	12.12	1.48	1.35

The worst 5 of 1004 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	1851	MA6	N1-C6-N6	-10.68	103.84	116.86
47	S2	1850	MA6	N1-C6-N6	-9.85	104.86	116.86
81	L5	2876	OMG	C1'-N9-C8	-8.29	103.17	126.73
81	L5	2424	OMG	C1'-N9-C8	-8.23	103.35	126.73
81	L5	3792	OMG	C1'-N9-C8	-7.83	104.47	126.73

There are no chirality outliers.

5 of 147 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L8	14	OMU	C1'-C2'-O2'-CM2
4	L8	75	OMG	O4'-C4'-C5'-O5'
47	S2	116	OMU	C1'-C2'-O2'-CM2
47	S2	116	OMU	O4'-C4'-C5'-O5'
47	S2	159	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

76 monomers are involved in 115 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	L5	4370	OMG	3	0
81	L5	4628	PSU	1	0
47	S2	1871	6MZ	3	0
81	L5	3818	UY1	2	0
81	L5	4552	PSU	1	0
47	S2	576	A2M	3	0
47	S2	1177	PSU	1	0
4	L8	75	OMG	1	0
4	L8	69	PSU	1	0
81	L5	1316	OMG	2	0
47	S2	27	A2M	3	0
47	S2	1238	PSU	1	0
81	L5	3718	A2M	4	0
4	L8	14	OMU	1	0
47	S2	1842	4AC	2	0
81	L5	5001	PSU	1	0
81	L5	4579	PSU	2	0
47	S2	1232	PSU	1	0
81	L5	4623	OMG	1	0
81	L5	1340	OMC	1	0
47	S2	109	PSU	1	0
47	S2	468	A2M	1	0
81	L5	1625	OMG	1	0
47	S2	1391	OMC	1	0
47	S2	93	PSU	1	0
81	L5	4637	OMG	1	0
47	S2	1678	A2M	2	0
47	S2	1337	4AC	1	0
81	L5	2351	OMC	3	0
81	L5	4620	OMU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	L5	3724	A2M	2	0
81	L5	2804	OMC	1	0
81	L5	5010	PSU	1	0
81	L5	2415	OMU	3	0
81	L5	2364	OMG	1	0
81	L5	2839	PSU	1	0
47	S2	1328	OMG	3	0
81	L5	4523	A2M	1	0
47	S2	512	A2M	1	0
81	L5	4457	PSU	1	0
47	S2	1850	MA6	1	0
47	S2	116	OMU	2	0
47	S2	1703	OMC	2	0
81	L5	4618	OMG	2	0
47	S2	601	OMG	2	0
81	L5	3785	A2M	2	0
81	L5	4442	PSU	1	0
81	L5	4228	OMG	1	0
47	S2	1383	A2M	1	0
47	S2	683	OMG	1	0
81	L5	1522	OMG	1	0
47	S2	484	A2M	2	0
81	L5	4361	PSU	1	0
47	S2	1447	OMG	2	0
81	L5	2632	PSU	1	0
81	L5	3808	OMC	1	0
81	L5	2363	A2M	1	0
47	S2	1442	OMU	1	0
81	L5	3925	OMU	1	0
81	L5	4431	PSU	1	0
47	S2	1445	PSU	3	0
81	L5	4220	6MZ	2	0
81	L5	4227	OMU	2	0
81	L5	3867	A2M	1	0
81	L5	1683	PSU	2	0
81	L5	4456	OMC	1	0
81	L5	4392	OMG	3	0
47	S2	159	A2M	4	0
81	L5	2815	A2M	2	0
81	L5	1779	PSU	1	0
81	L5	1326	A2M	2	0
81	L5	4536	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	L5	3841	OMC	2	0
47	S2	428	OMU	1	0
47	S2	509	OMG	2	0
81	L5	3627	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 403 ligands modelled in this entry, 384 are monoatomic - leaving 19 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	$\# Z > 2$
91	SPD	L5	5108	-	9,9,9	0.30	0	8,8,8	0.76	0
89	PUT	L5	5386	-	5,5,5	0.10	0	4,4,4	0.11	0
85	GDP	CB	901	-	29,30,30	0.45	0	45,47,47	0.47	0
90	HYG	S2	1979	-	36,39,39	0.77	1 (2%)	44,60,60	1.35	6 (13%)
91	SPD	L5	5104	-	9,9,9	0.32	0	8,8,8	0.76	0
92	3HE	L5	5109	-	21,21,21	0.10	0	23,30,30	0.23	0
89	PUT	L5	5382	-	5,5,5	0.09	0	4,4,4	0.12	0
89	PUT	L5	5384	-	5,5,5	0.11	0	4,4,4	0.12	0
91	SPD	L5	5106	-	9,9,9	0.33	0	8,8,8	0.84	0
91	SPD	L5	5107	-	9,9,9	0.32	0	8,8,8	0.88	0
91	SPD	L5	5102	-	9,9,9	0.31	0	8,8,8	0.80	0
89	PUT	L5	5387	-	5,5,5	0.07	0	4,4,4	0.14	0
91	SPD	L5	5103	-	9,9,9	0.32	0	8,8,8	0.90	0
89	PUT	L5	5383	-	5,5,5	0.09	0	4,4,4	0.14	0
89	PUT	S2	1939	-	5,5,5	0.08	0	4,4,4	0.14	0
91	SPD	L5	5101	-	9,9,9	0.31	0	8,8,8	0.78	0
89	PUT	L5	5385	-	5,5,5	0.09	0	4,4,4	0.15	0
93	ANM	L5	5388	-	20,20,20	0.58	0	24,27,27	0.44	0
91	SPD	L5	5105	-	9,9,9	0.31	0	8,8,8	0.88	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
91	SPD	L5	5108	-	-	1/7/7/7	-
89	PUT	L5	5386	-	-	1/3/3/3	-
85	GDP	CB	901	-	-	6/16/32/32	0/3/3/3
90	HYG	S2	1979	-	-	2/12/87/87	0/4/4/4
91	SPD	L5	5104	-	-	2/7/7/7	-
92	3HE	L5	5109	-	-	0/8/36/36	0/2/2/2
89	PUT	L5	5382	-	-	0/3/3/3	-
89	PUT	L5	5384	-	-	0/3/3/3	-
91	SPD	L5	5106	-	-	1/7/7/7	-
91	SPD	L5	5107	-	-	5/7/7/7	-
91	SPD	L5	5102	-	-	1/7/7/7	-
89	PUT	L5	5387	-	-	1/3/3/3	-
91	SPD	L5	5103	-	-	4/7/7/7	-
89	PUT	L5	5383	-	-	0/3/3/3	-
89	PUT	S2	1939	-	-	0/3/3/3	-
91	SPD	L5	5101	-	-	0/7/7/7	-
89	PUT	L5	5385	-	-	0/3/3/3	-
93	ANM	L5	5388	-	-	0/10/23/23	0/2/2/2
91	SPD	L5	5105	-	-	1/7/7/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	S2	1979	HYG	C4-N9	2.62	1.50	1.47

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	S2	1979	HYG	O22-C17-C16	4.19	121.21	111.22
90	S2	1979	HYG	C16-C17-C12	-4.13	103.64	113.50
90	S2	1979	HYG	O14-C13-C12	-3.18	103.30	109.49
90	S2	1979	HYG	O11-C5-C4	-3.02	103.13	109.40
90	S2	1979	HYG	O29-C12-C13	2.28	116.70	110.89

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

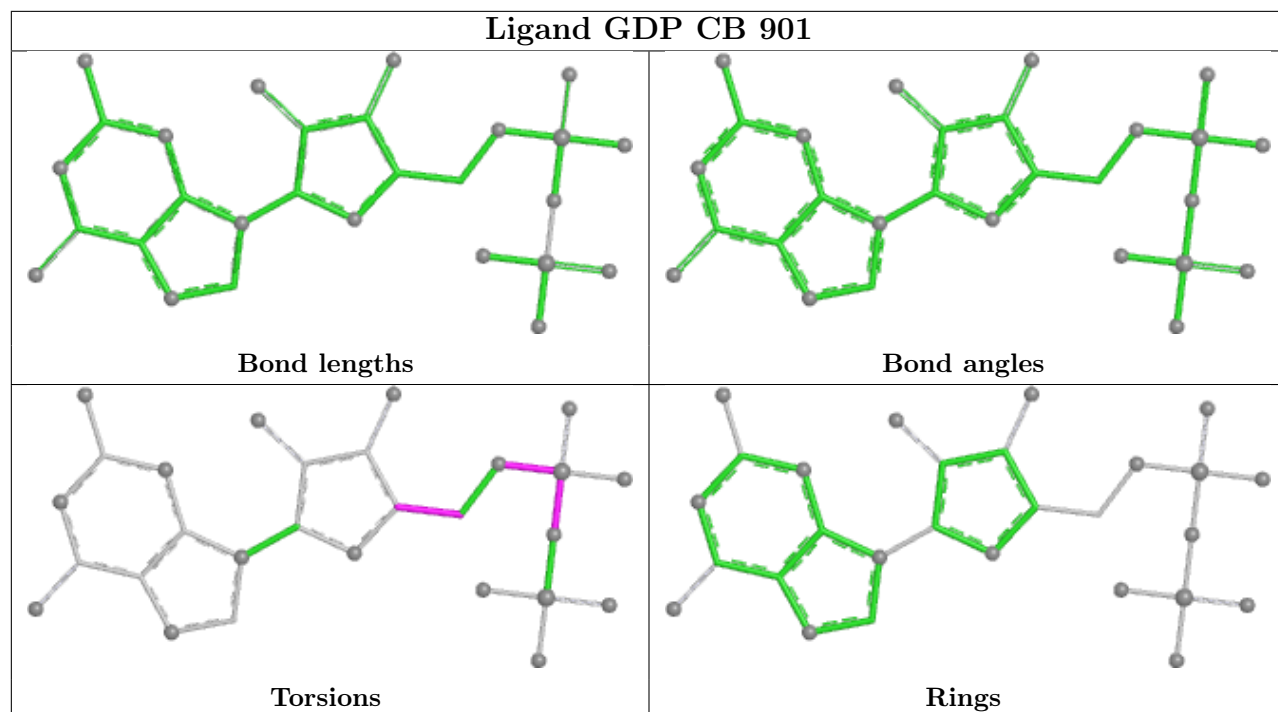
Mol	Chain	Res	Type	Atoms
85	CB	901	GDP	C5'-O5'-PA-O3A
85	CB	901	GDP	O4'-C4'-C5'-O5'
85	CB	901	GDP	C3'-C4'-C5'-O5'
90	S2	1979	HYG	O14-C13-O18-C6
91	L5	5107	SPD	C3-C4-C5-N6

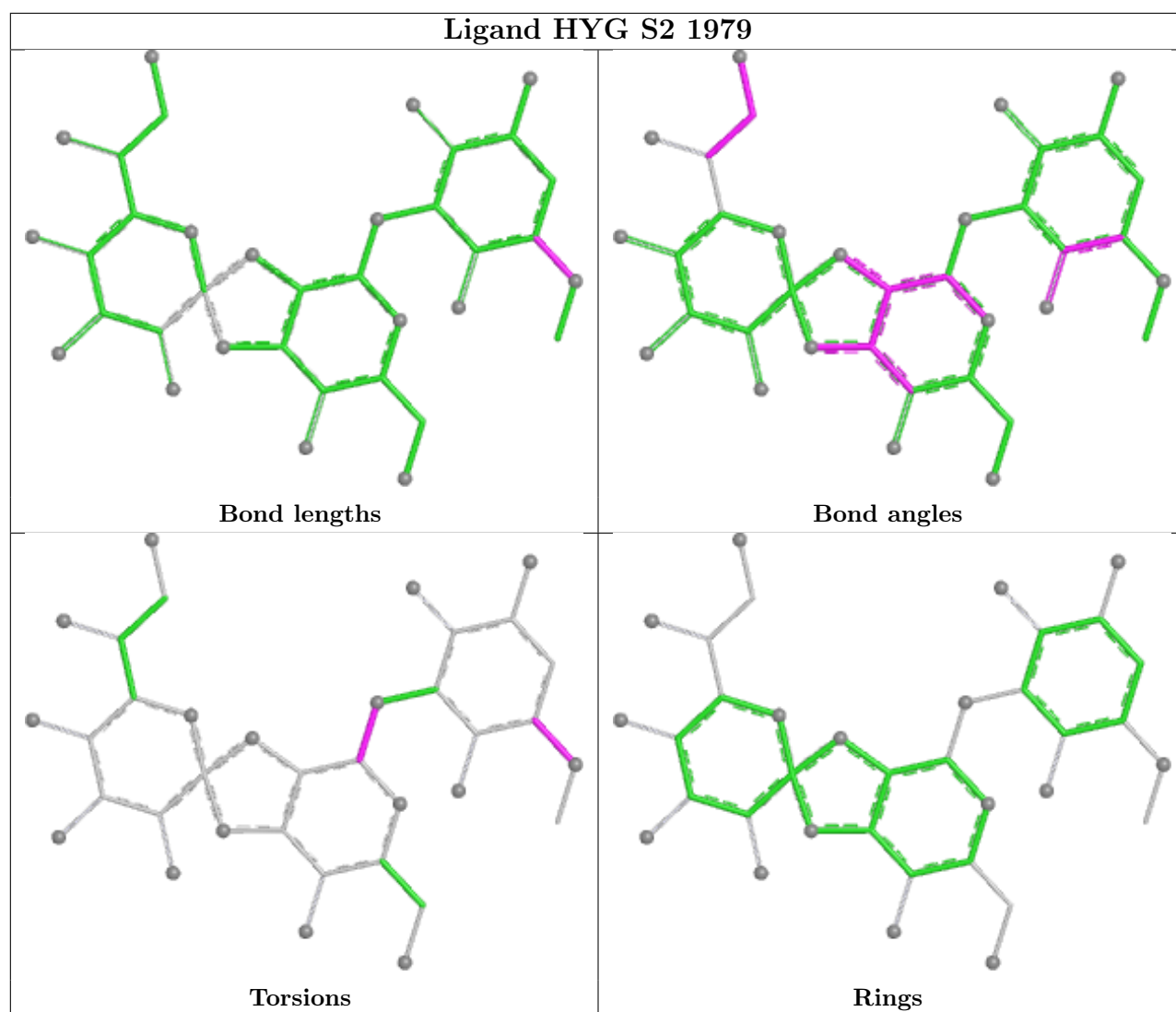
There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
92	L5	5109	3HE	2	0
89	L5	5382	PUT	1	0
91	L5	5107	SPD	1	0
91	L5	5102	SPD	1	0
89	L5	5387	PUT	2	0
89	S2	1939	PUT	1	0
91	L5	5101	SPD	1	0
89	L5	5385	PUT	2	0
93	L5	5388	ANM	1	0
91	L5	5105	SPD	1	0

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
81	L5	4
47	S2	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	1869:A	O3'	1870:B8N	P	61.81
1	S2	1870:B8N	O3'	1871:6MZ	P	34.71
1	L5	4219:A	O3'	4220:6MZ	P	4.27
1	L5	3817:A	O3'	3818:UY1	P	2.93
1	L5	3818:UY1	O3'	3819:G	P	2.92

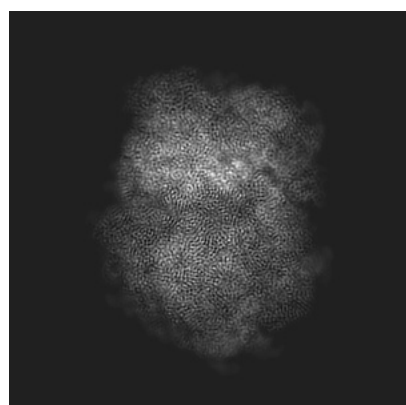
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50673. These allow visual inspection of the internal detail of the map and identification of artifacts.

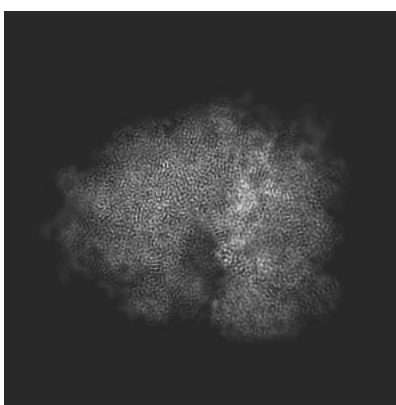
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

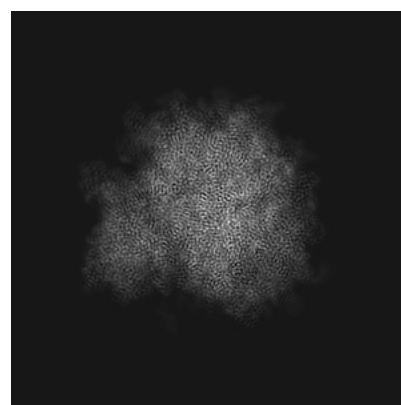
6.1.1 Primary map



X



Y

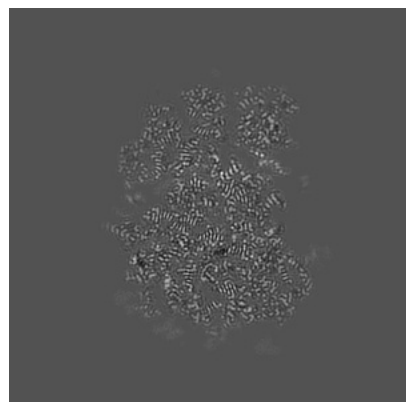


Z

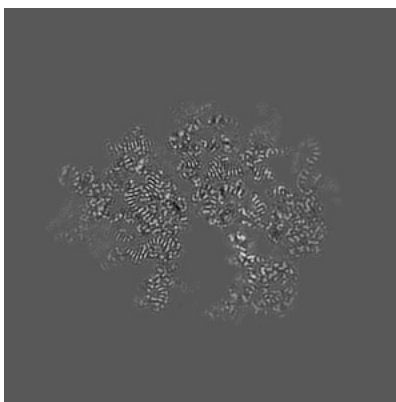
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

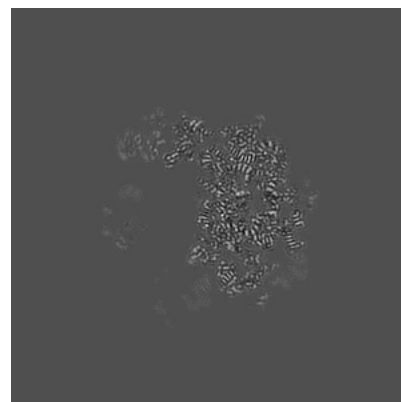
6.2.1 Primary map



X Index: 240



Y Index: 240

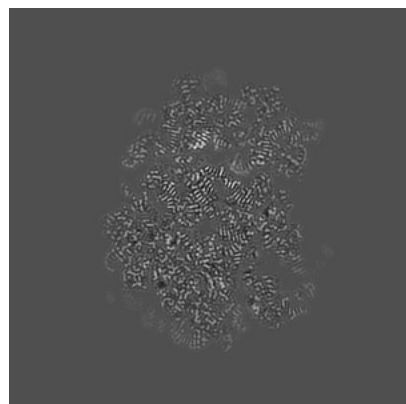


Z Index: 240

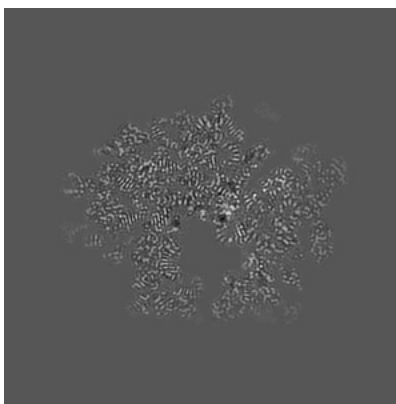
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

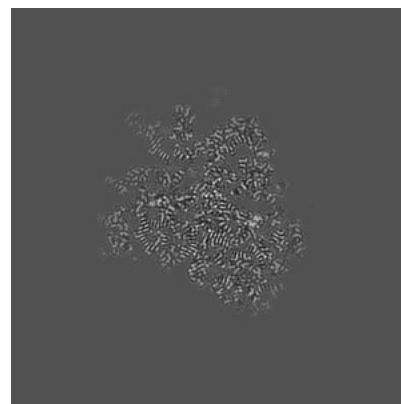
6.3.1 Primary map



X Index: 261



Y Index: 223

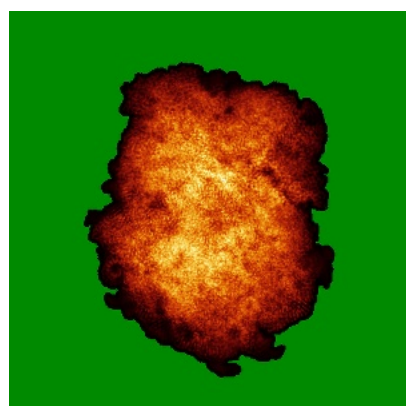


Z Index: 196

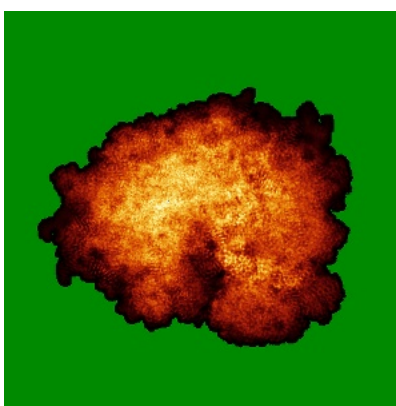
The images above show the largest variance slices of the map in three orthogonal directions.

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

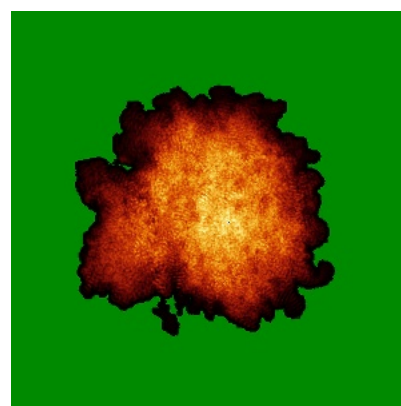
6.4.1 Primary map



X



Y

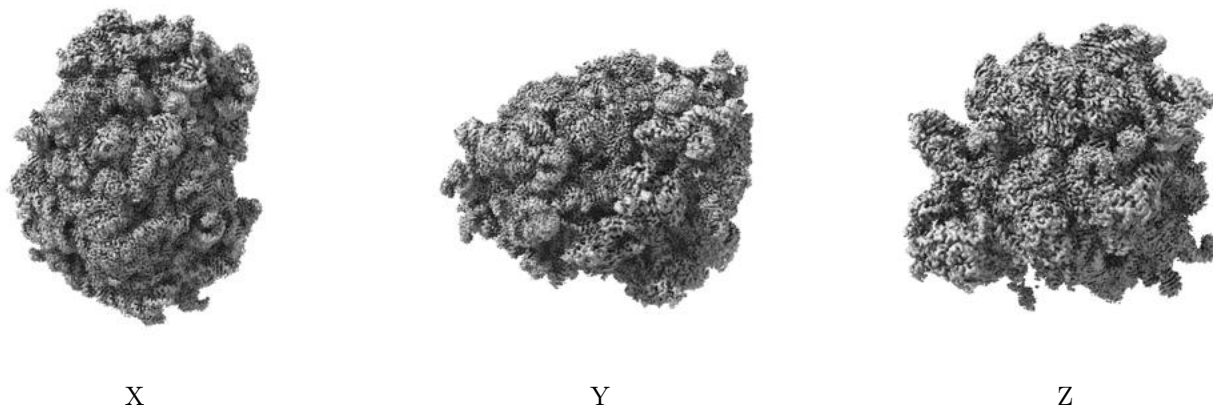


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

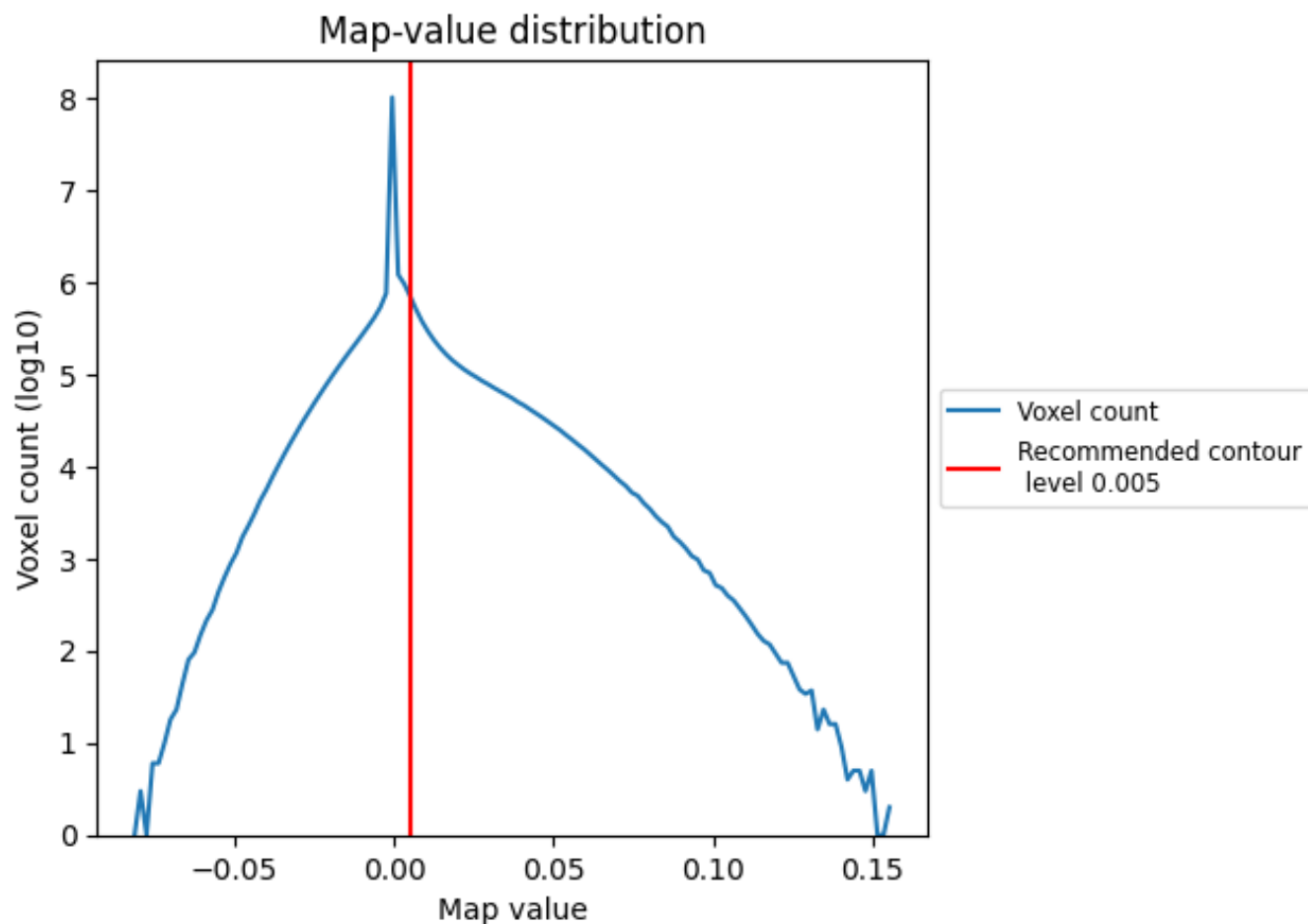
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

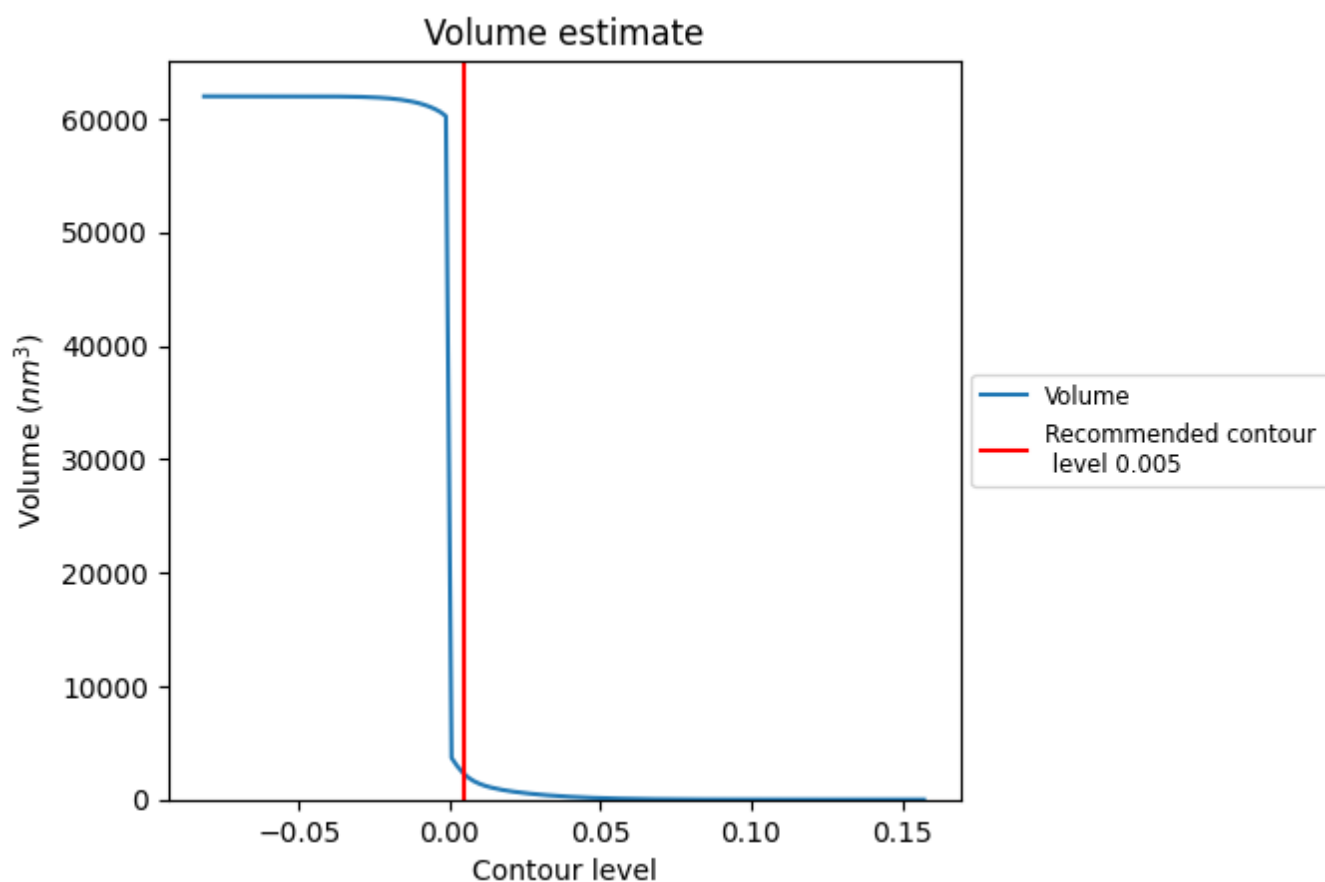
This section contains the results of statistical analysis of the map.

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.

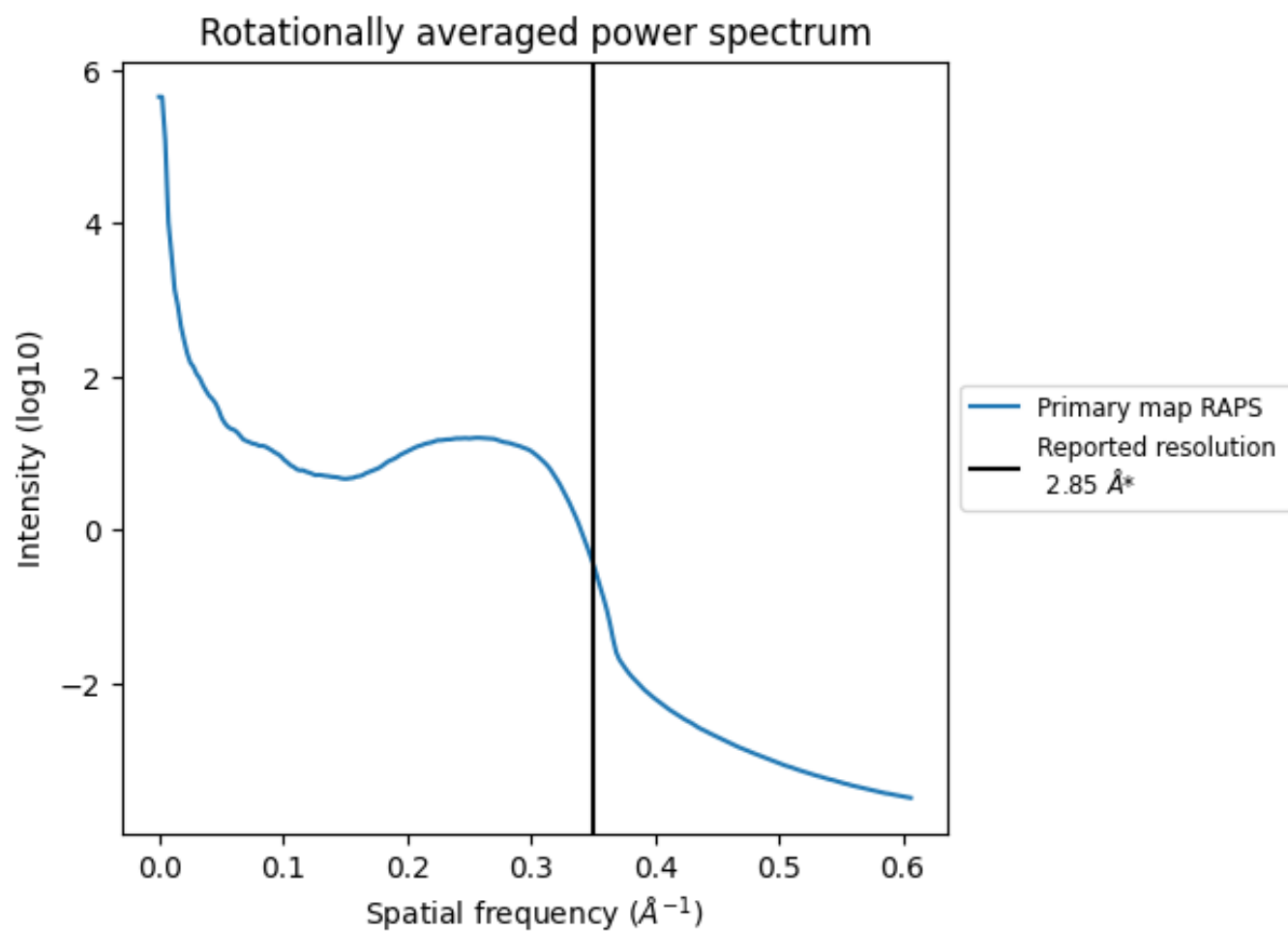
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2225 nm³; this corresponds to an approximate mass of 2010 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

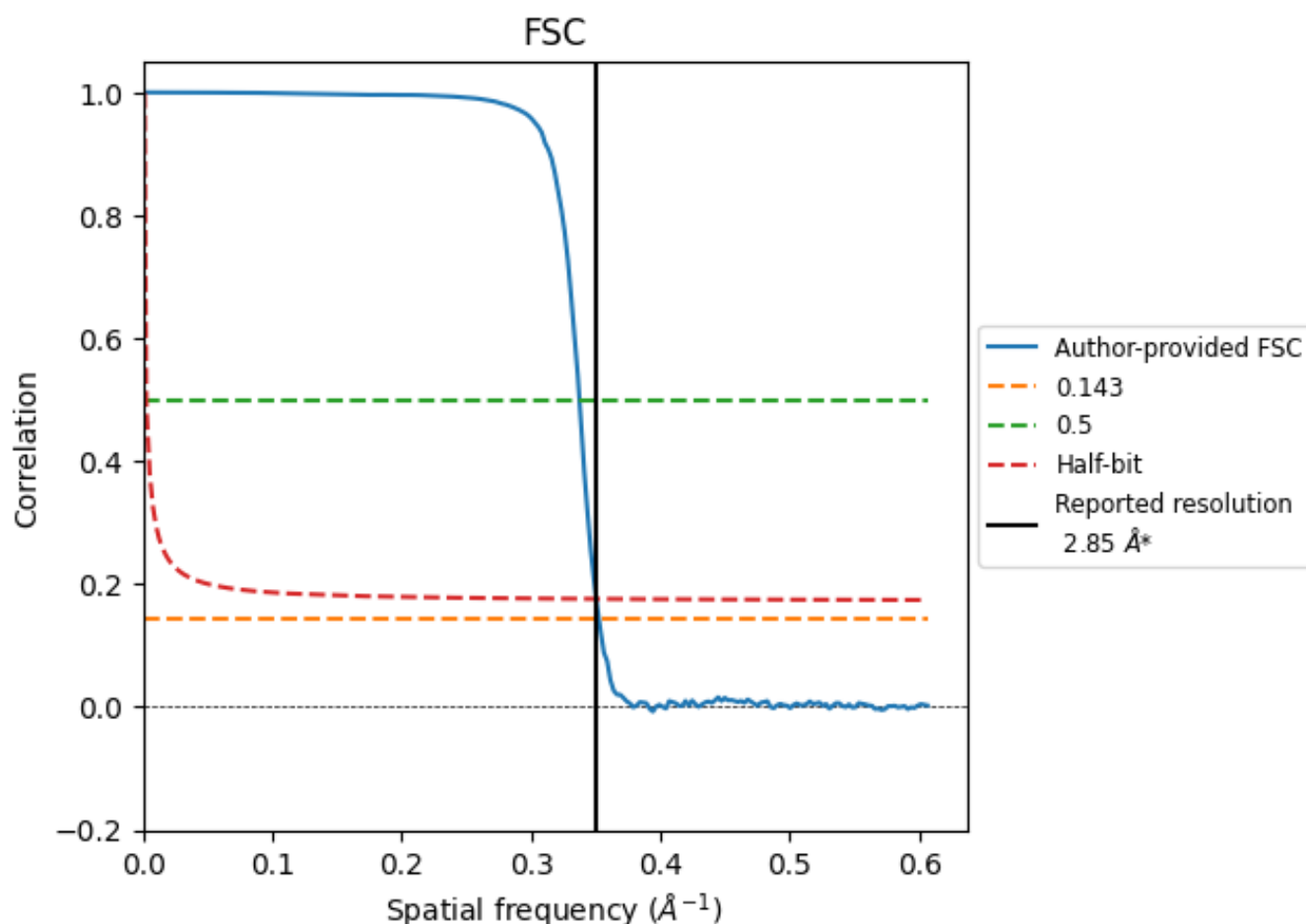


*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

8.2 Resolution estimates [i](#)

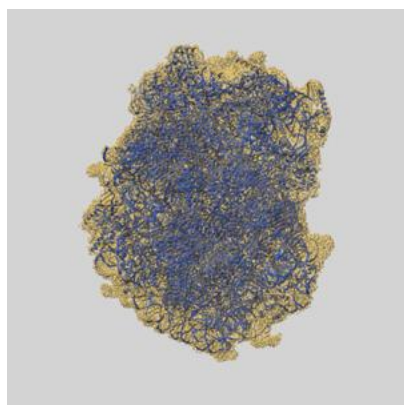
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.84	2.96	2.85
Unmasked-calculated*	-	-	-

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

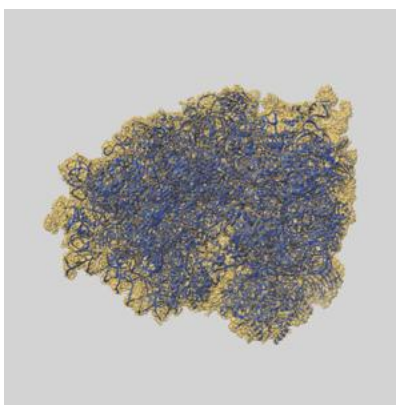
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50673 and PDB model 9FQZ. Per-residue inclusion information can be found in [section 3](#) on [page 27](#).

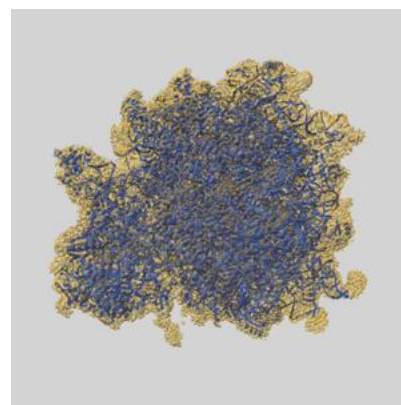
9.1 Map-model overlay [i](#)



X



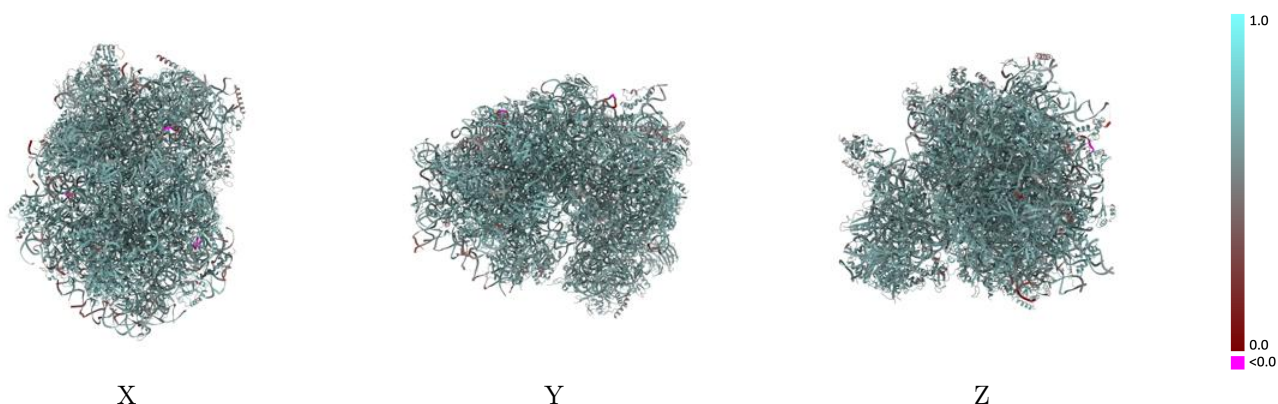
Y



Z

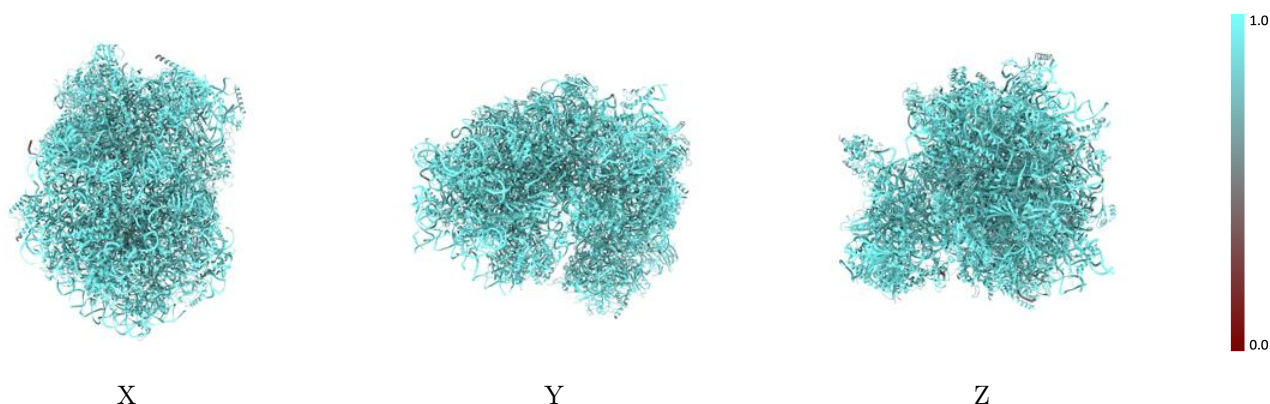
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



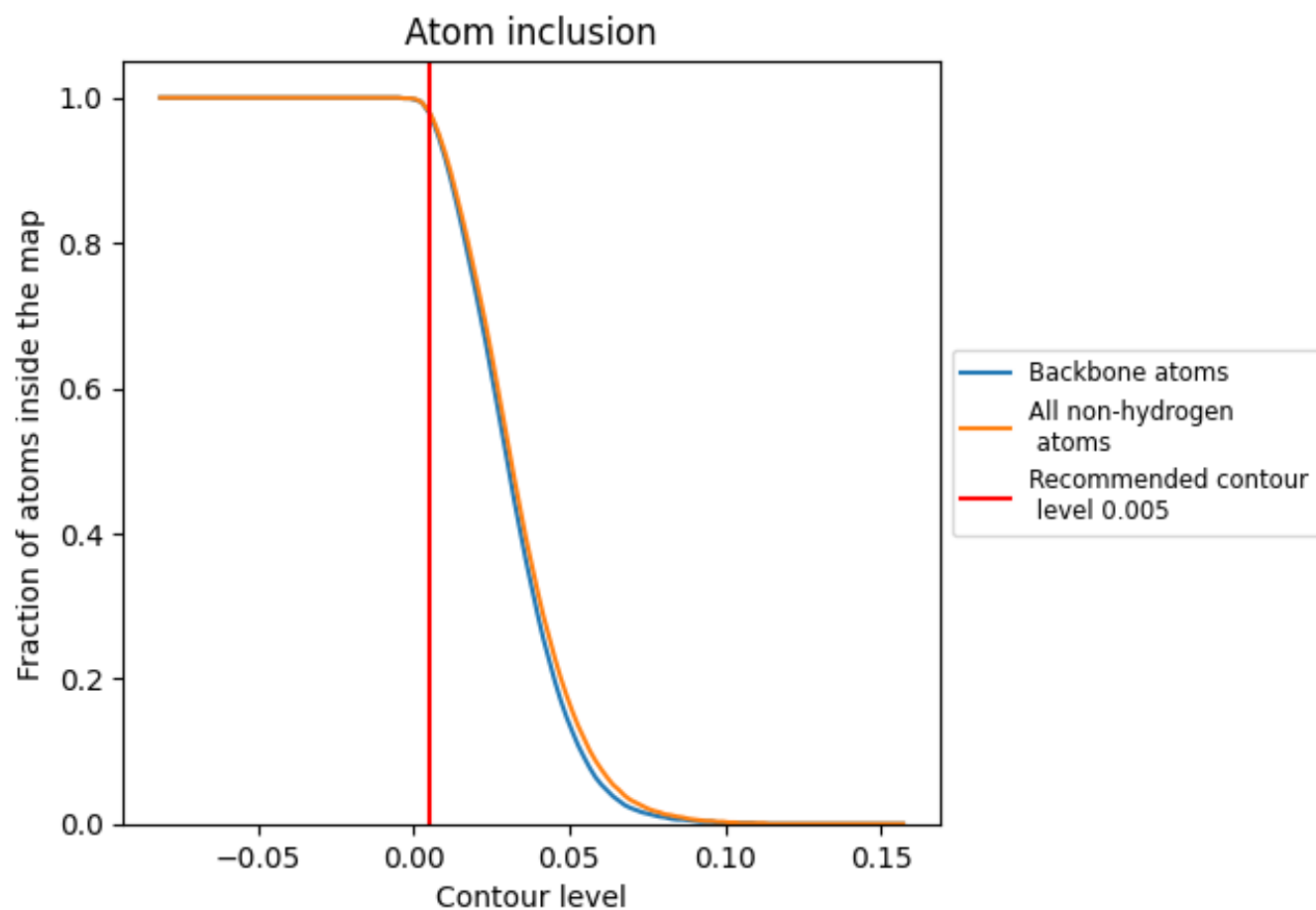
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9810	 0.6200
CA	 0.7170	 0.5430
CB	 0.9720	 0.5870
CC	 0.7510	 0.4660
CD	 0.8800	 0.5550
L5	 0.9860	 0.6180
L7	 1.0000	 0.6470
L8	 0.9800	 0.6060
LA	 0.9930	 0.6530
LB	 0.9850	 0.6490
LC	 0.9850	 0.6450
LD	 0.9760	 0.6350
LE	 0.9790	 0.6270
LF	 0.9920	 0.6490
LG	 0.9770	 0.6250
LH	 0.9820	 0.6380
LI	 0.9860	 0.6450
LJ	 0.9670	 0.6160
LL	 0.9750	 0.6290
LM	 0.9890	 0.6420
LN	 0.9960	 0.6600
LO	 0.9920	 0.6490
LP	 0.9870	 0.6490
LQ	 0.9970	 0.6580
LR	 0.9630	 0.6160
LS	 0.9930	 0.6560
LT	 0.9840	 0.6370
LU	 0.9590	 0.5960
LV	 0.9970	 0.6530
LW	 0.8900	 0.5530
LX	 0.9840	 0.6400
LY	 0.9790	 0.6450
LZ	 0.9890	 0.6410
La	 0.9940	 0.6600
Lb	 0.9700	 0.6170



















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Chain	Atom inclusion	Q-score
Lc	 0.9920	 0.6330
Ld	 0.9670	 0.6250
Le	 0.9920	 0.6540
Lf	 0.9910	 0.6590
Lg	 0.9760	 0.6380
Lh	 0.9870	 0.6420
Li	 0.9880	 0.6320
Lj	 0.9880	 0.6470
Lk	 0.9650	 0.6290
Ll	 0.9950	 0.6470
Lm	 0.9980	 0.6480
Ln	 0.9950	 0.6460
Lo	 0.9830	 0.6410
Lp	 1.0000	 0.6480
Lq	 0.9100	 0.5580
Lr	 0.9910	 0.6500
S2	 0.9910	 0.6160
SA	 0.9620	 0.6200
SB	 0.9870	 0.6260
SC	 0.9880	 0.6350
SD	 0.9690	 0.6040
SE	 0.9840	 0.6360
SF	 0.9780	 0.6090
SG	 0.9540	 0.5930
SH	 0.9190	 0.5740
SI	 0.9670	 0.6080
SJ	 0.9830	 0.6260
SK	 0.9670	 0.6100
SL	 0.9660	 0.6280
SM	 0.8990	 0.5550
SN	 0.9900	 0.6270
SO	 0.9740	 0.6250
SP	 0.9740	 0.6050
SQ	 0.9790	 0.6220
SR	 0.9360	 0.5990
SS	 0.9710	 0.6130
ST	 0.9750	 0.6170
SU	 0.9480	 0.5910
SV	 0.9820	 0.6330
SW	 0.9840	 0.6350
SX	 0.9930	 0.6370
SY	 0.9830	 0.6290

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Chain	Atom inclusion	Q-score
SZ	 0.9660	 0.6130
Sa	 0.9730	 0.6190
Sb	 0.9530	 0.6050
Sc	 0.9620	 0.5780
Sd	 0.9840	 0.6280
Se	 0.9750	 0.6140
Sf	 0.9360	 0.5660
Sg	 0.9520	 0.5980