



# wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 10:06 am BST

PDB ID : 6Y0G  
EMDB ID : EMD-10668  
Title : Structure of human ribosome in classical-PRE state  
Authors : Bhaskar, V.; Schenk, A.D.; Cavadini, S.; von Loeffelholz, O.; Natchiar, S.K.;  
Klaholz, B.P.; Chao, J.A.  
Deposited on : 2020-02-07  
Resolution : 3.20 Å(reported)  
Based on initial models : 5AJ0, 5LKS, 6QZP

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

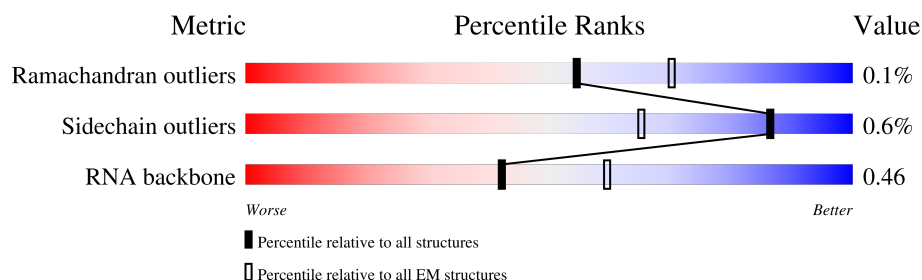
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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.



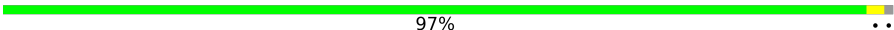

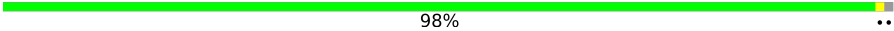



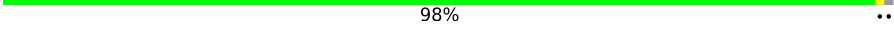
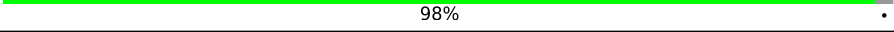
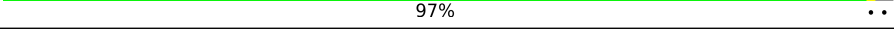
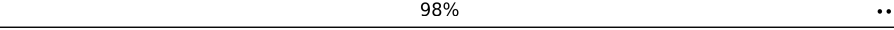

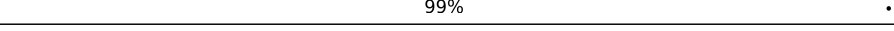
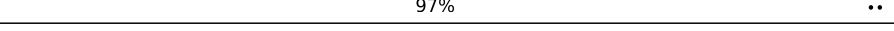

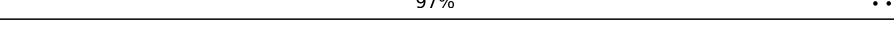

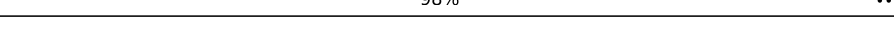
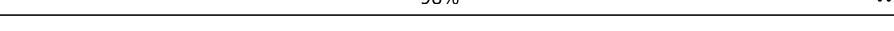

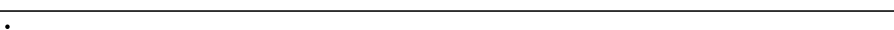

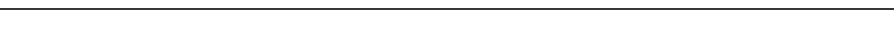
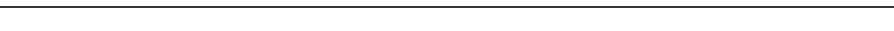


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A4	28	
2	B4	76	
2	D4	76	
3	C4	2	
4	L5	5070	
5	L7	120	
6	L8	156	
7	LA	257	




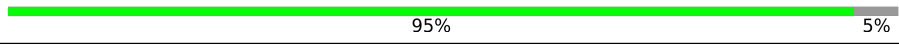
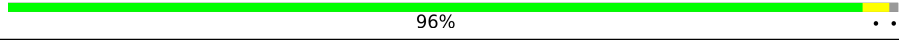
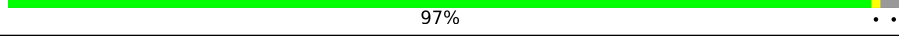
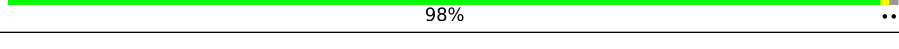
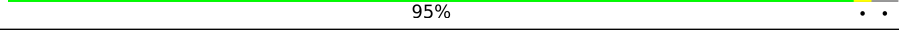
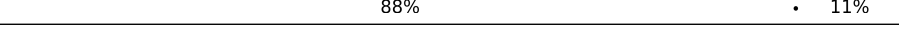
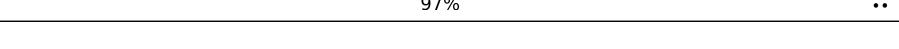
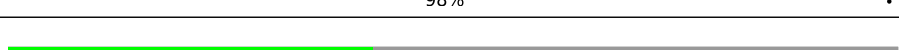

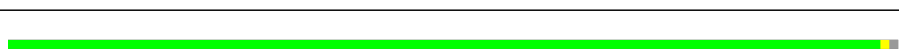
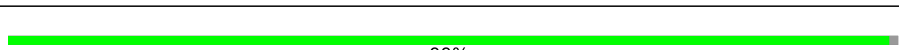
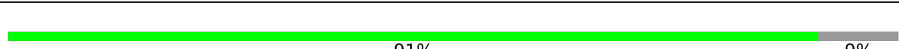





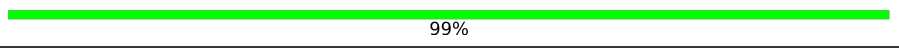
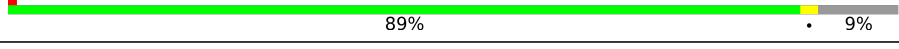
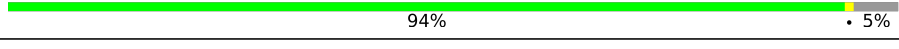
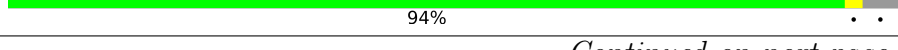

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Mol	Chain	Length	Quality of chain
8	LB	403	 97% ..
9	LC	427	 84% . 15%
10	LD	297	 98% ..
11	LE	288	 76% . 23%
12	LF	248	 90% . 9%
13	LG	266	 85% . 15%
14	LH	192	 98% ..
15	LI	214	 98% .
16	LJ	178	 97% ..
17	LL	211	 98% ..
18	LM	215	 63% 37%
19	LN	204	 99% .
20	LO	203	 97% ..
21	LP	184	 82% . 17%
22	LQ	188	 97% ..
23	LR	196	 92% 8%
24	LS	176	 98% ..
25	LT	160	 98% ..
26	LU	128	 79% 21%
27	LV	140	 94% 6%
28	LW	157	 72% . 27%
29	LX	156	 77% 23%
30	LY	145	 92% . 8%
31	LZ	136	 99% .
32	La	148	 99% ..

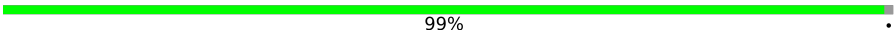











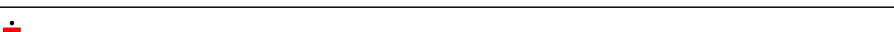

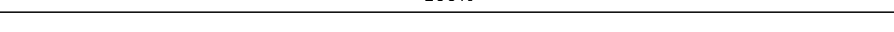
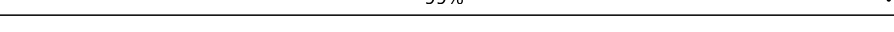
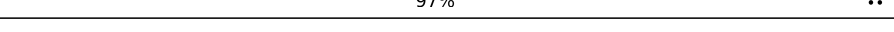



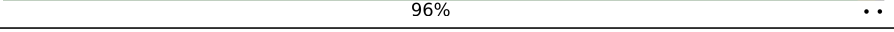

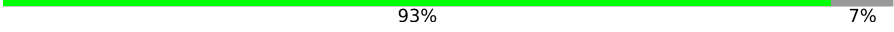
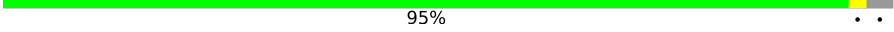

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Mol	Chain	Length	Quality of chain
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SC	293	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	

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Mol	Chain	Length	Quality of chain
58	SI	208	 99% .
59	SJ	194	 94% 6%
60	SK	165	 57% . 42%
61	SL	158	 93% . 6%
62	SM	132	 14% 76% . 21%
63	SN	151	 99% ..
64	SO	151	 88% . 11%
65	SP	145	 92% . 8%
66	SQ	146	 95% . .
67	SR	135	 95% . .
68	SS	152	 94% . 5%
69	ST	145	 97% . .
70	SU	119	 84% . 14%
71	SV	83	 100%
72	SW	130	 99% .
73	SX	143	 97% ..
74	SY	133	 91% . 8%
75	SZ	125	 68% . 31%
76	Sa	115	 86% 14%
77	Sb	84	 96% ..
78	Sc	69	 90% . 9%
79	Sd	56	 93% 7%
80	Se	59	 95% . .
81	Sf	156	 42% . 57%
82	Sg	317	 97% ..

## 2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 215032 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A4	17	Total	C	N	O	P	0	0
			340	153	34	136	17		

- Molecule 2 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B4	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
2	D4	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 3 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C4	2	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 4 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3644	Total	C	N	O	P	0	0
			78119	34786	14297	25393	3643		

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

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

- Molecule 6 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LA	247	Total	C	N	O	S	0	0
			1891	1185	388	312	6		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	398	Total	C	N	O	S	0	0
			3211	2045	604	548	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	365	Total	C	N	O	S	0	0
			2897	1823	579	480	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2379	1506	434	425	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	222	Total	C	N	O	S	0	0
			1785	1148	338	295	4		

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

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

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	227	Total	C	N	O	S	0	0
			1832	1168	352	308	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

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

- Molecule 15 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	209	Total	C	N	O	S	0	0
			1681	1065	325	278	13		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	208	Total	C	N	O	S	0	0
			1682	1052	348	278	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.



Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	200	Total	C	N	O	S	0	0
			1641	1058	320	258	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			821	526	143	150	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	115	Total	C	N	O	S	0	0
			914	571	186	153	4		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			981	628	185	167	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

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

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	75	Total	C	N	O	S	0	0
			601	370	129	99	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

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

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 41 is a protein called 60S ribosomal protein L37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

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

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1697	Total	C	N	O	P	0	0
			36223	16169	6504	11854	1696		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	215	Total	C	N	O	S	0	0
			1695	1077	297	313	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 52 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	219	Total	C	N	O	S	0	0
			1692	1096	291	295	10		

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SD	218	Total	C	N	O	S	0	0
			1689	1075	307	300	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	262	Total	C	N	O	S	0	0
			2070	1321	383	358	8		

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	186	Total	C	N	O	S	0	0
			1447	907	269	264	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	237	Total	C	N	O	S	0	0
			1917	1197	384	329	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH	187	Total	C	N	O	S	0	0
			1510	963	278	268	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI	206	Total	C	N	O	S	0	0
			1674	1049	329	291	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ	182	Total	C	N	O	S	0	0
			1506	959	300	245	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	148	Total	C	N	O	S	0	0
			1203	766	226	205	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM	104	Total	C	N	O	S	0	0
			796	497	146	147	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SP	134	Total	C	N	O	S	0	0
			1103	703	208	185	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SR	130	Total	C	N	O	S	0	0
			1051	661	196	189	5		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	144	Total	C	N	O	S	0	0
			1169	731	236	201	1		

- Molecule 69 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ST	141	Total	C	N	O	S	0	0
			1096	686	211	196	3		

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SU	102	Total	C	N	O	S	0	0
			799	501	153	141	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

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

- Molecule 72 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.



Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	123	Total	C	N	O	S	0	0
			1002	634	196	167	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ	86	Total	C	N	O	S	0	0
			680	436	127	116	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sb	83	Total	C	N	O	S	0	0
			643	402	119	115	7		

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sc	63	Total	C	N	O	S	0	0
			480	293	92	93	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sd	52	Total	C	N	O	S	0	0
			432	271	87	69	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Se	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 81 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sf	67	Total	C	N	O	S	0	0
			537	338	102	90	7		

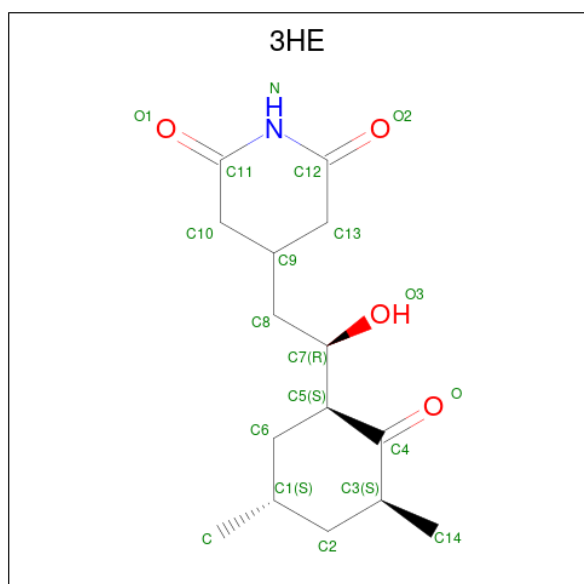
- Molecule 82 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	A4	1	Total	Mg	0
			1	1	
83	L5	36	Total	Mg	0
			36	36	
83	L7	2	Total	Mg	0
			2	2	
83	L8	4	Total	Mg	0
			4	4	
83	LI	1	Total	Mg	0
			1	1	
83	S2	28	Total	Mg	0
			28	28	

- Molecule 84 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: C<sub>15</sub>H<sub>23</sub>NO<sub>4</sub>).



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

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 86 is water.

Mol	Chain	Residues	Atoms		AltConf
86	L5	2	Total	O	0
			2	2	
86	L8	1	Total	O	0
			1	1	
86	LC	1	Total	O	0
			1	1	
86	LI	1	Total	O	0
			1	1	
86	LP	1	Total	O	0
			1	1	
86	LV	1	Total	O	0
			1	1	
86	S2	4	Total	O	0
			4	4	
86	SN	1	Total	O	0
			1	1	

### 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.

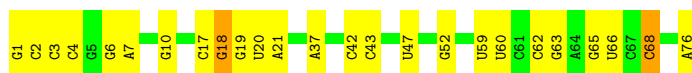
- Molecule 1: mRNA

Chain A4: 



- Molecule 2: tRNA

Chain B4: 








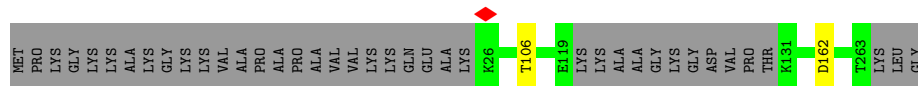






- Molecule 13: 60S ribosomal protein L7a

Chain LG:  85% 15%



- Molecule 14: 60S ribosomal protein L9

Chain LH:  98% ..



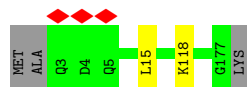
- Molecule 15: 60S ribosomal protein L10-like

Chain LI:  98% .

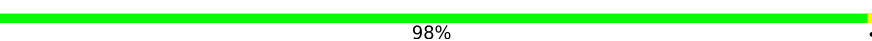


- Molecule 16: 60S ribosomal protein L11

Chain LJ:  97% ..



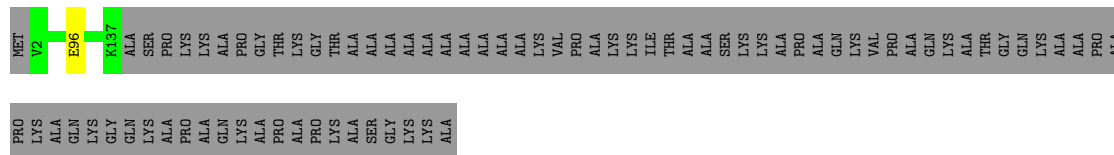
- Molecule 17: 60S ribosomal protein L13

Chain LL:  98% ..



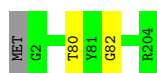
- Molecule 18: 60S ribosomal protein L14

Chain LM:  63% 37%



- Molecule 19: 60S ribosomal protein L15

Chain LN:  99% .



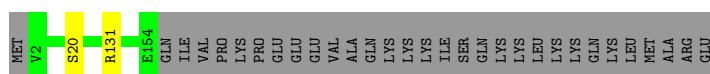
- Molecule 20: 60S ribosomal protein L13a

Chain LO: 97%



- Molecule 21: 60S ribosomal protein L17

Chain LP: 82%



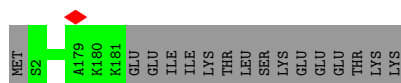
- Molecule 22: 60S ribosomal protein L18

Chain LQ: 97%



- Molecule 23: 60S ribosomal protein L19

Chain LR: 92%



- Molecule 24: 60S ribosomal protein L18a

Chain LS: 98%



- Molecule 25: 60S ribosomal protein L21

Chain LT: 98%

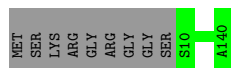


- Molecule 26: 60S ribosomal protein L22

Chain LU: 79%

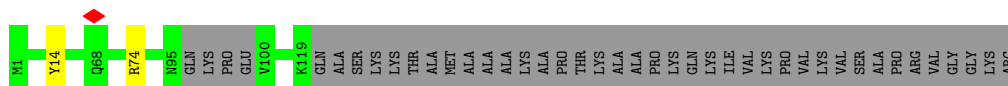
- Molecule 27: 60S ribosomal protein L23

Chain LV:  94% 6%




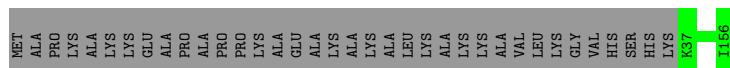
- Molecule 28: 60S ribosomal protein L24

Chain LW:  72% 27%



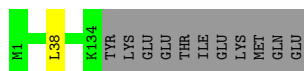
- Molecule 29: 60S ribosomal protein L23a

Chain LX:  77% 23%



- Molecule 30: 60S ribosomal protein L26

Chain LY:  92% • 8%



- Molecule 31: 60S ribosomal protein L27

Chain LZ:  99%



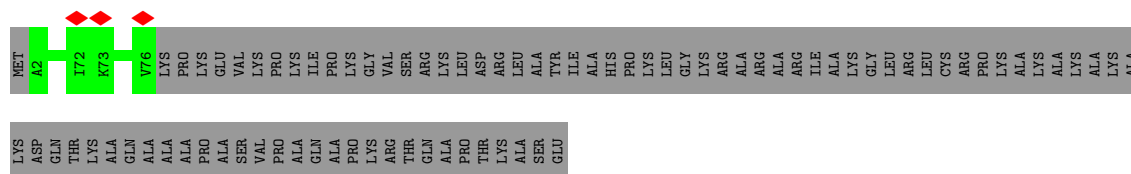
- Molecule 32: 60S ribosomal protein L27a

Chain La:  99%

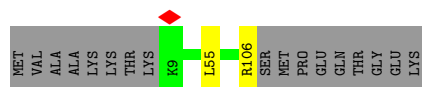
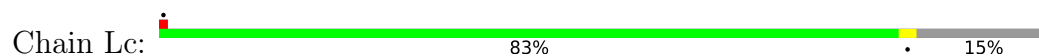


- Molecule 33: 60S ribosomal protein L29

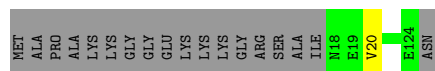
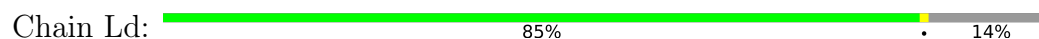
Chain Lb:  47% 53%



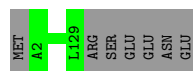
- Molecule 34: 60S ribosomal protein L30



- Molecule 35: 60S ribosomal protein L31



- Molecule 36: 60S ribosomal protein L32



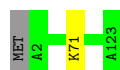
- Molecule 37: 60S ribosomal protein L35a



- Molecule 38: 60S ribosomal protein L34



- Molecule 39: 60S ribosomal protein L35




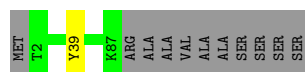
- Molecule 40: 60S ribosomal protein L36

Chain Li:  95% ..



- Molecule 41: 60S ribosomal protein L37

Chain Lj:  88% 11%



- Molecule 42: 60S ribosomal protein L38

Chain Lk:  97% ..



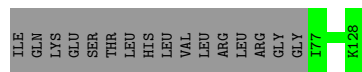
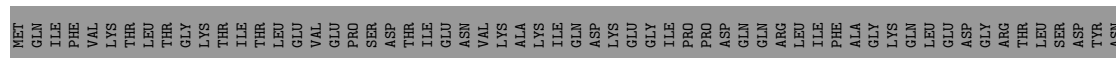
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  98% .



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  41% 59%



- Molecule 45: 60S ribosomal protein L41

Chain Ln:  96% .



- Molecule 46: 60S ribosomal protein L36a

Chain Lo:  98% ..



- Molecule 47: 60S ribosomal protein L37a

Chain Lp:  99%



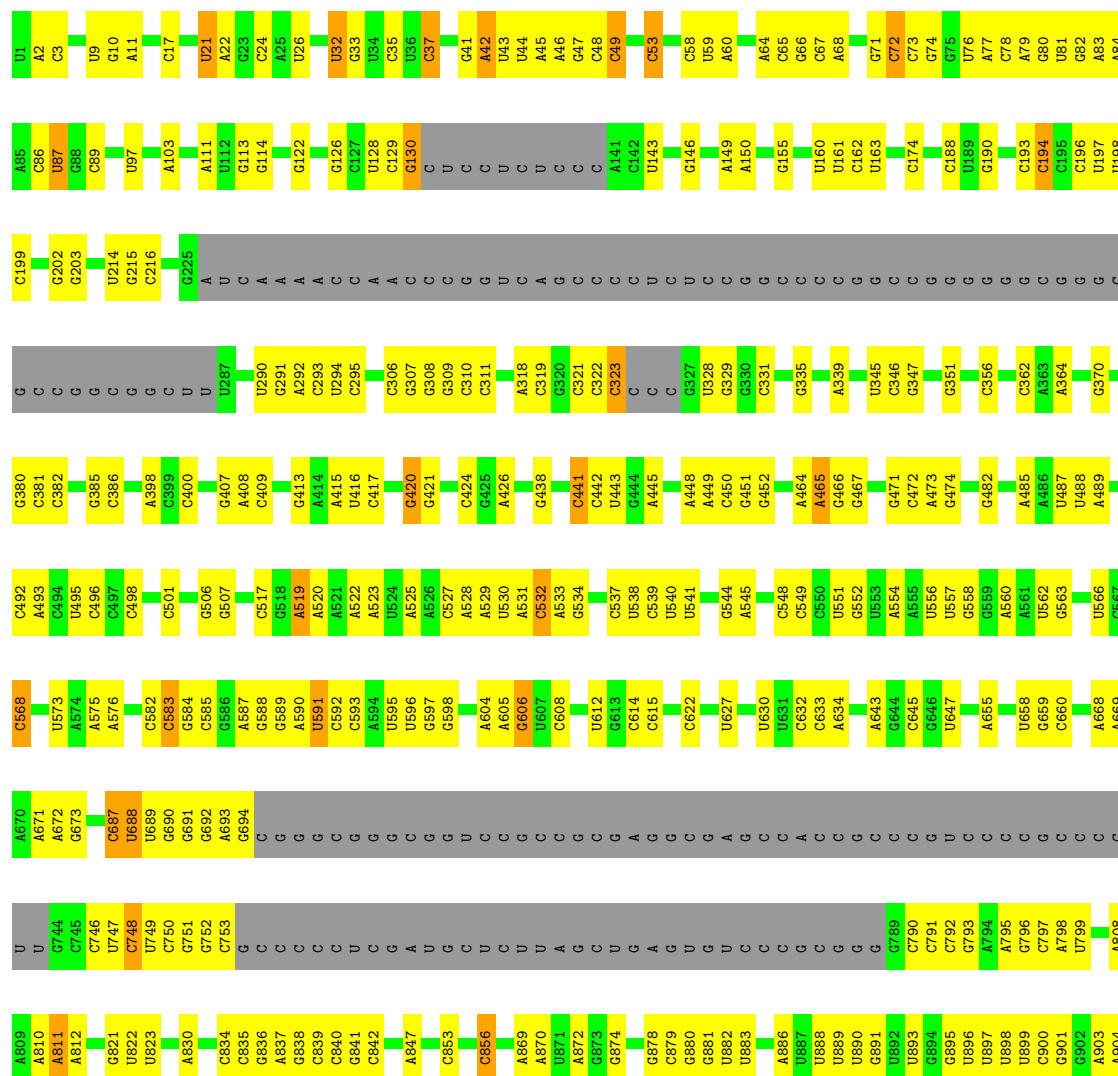
- Molecule 48: 60S ribosomal protein L28

Chain Lr:  91%

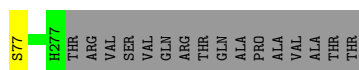
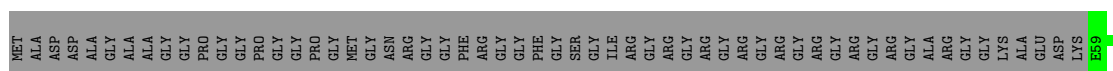


- Molecule 49: 18S ribosomal RNA

Chain S2:  60%

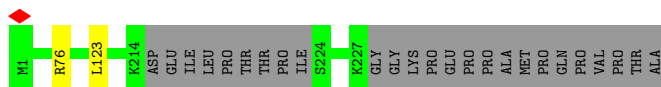






- Molecule 53: 40S ribosomal protein S3

Chain SD: 89% • 10%



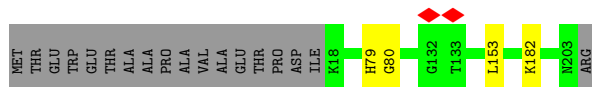
- Molecule 54: 40S ribosomal protein S4, X isoform

Chain SE: 99%



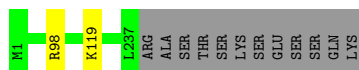
- Molecule 55: 40S ribosomal protein S5

Chain SF: 89% • 9%



- Molecule 56: 40S ribosomal protein S6

Chain SG: 94% • 5%



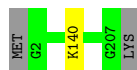
- Molecule 57: 40S ribosomal protein S7

Chain SH: 94% • •



- Molecule 58: 40S ribosomal protein S8

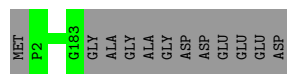
Chain SI: 99% •





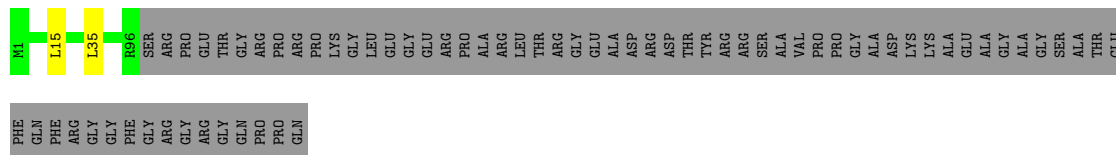
- Molecule 59: 40S ribosomal protein S9

Chain SJ:  94% 6%



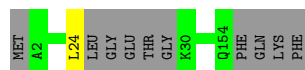
- Molecule 60: 40S ribosomal protein S10

Chain SK:  57% 42%




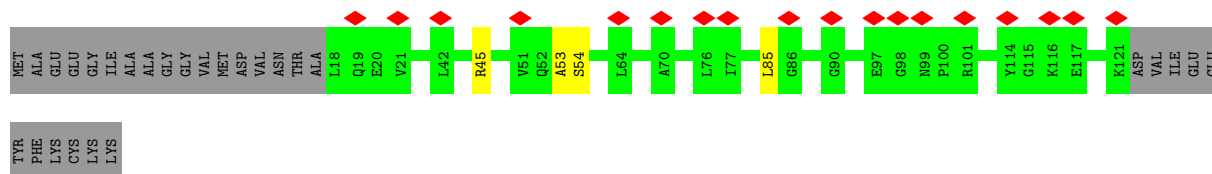
- Molecule 61: 40S ribosomal protein S11

Chain SL:  93% 6%



- Molecule 62: 40S ribosomal protein S12

Chain SM:  14% 76% 21%



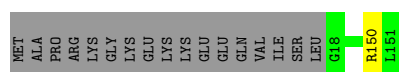
- Molecule 63: 40S ribosomal protein S13

Chain SN:  99% ..



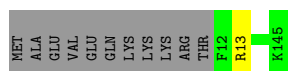
- Molecule 64: 40S ribosomal protein S14

Chain SO:  88% 11%



- Molecule 65: 40S ribosomal protein S15

Chain SP:  92% • 8%



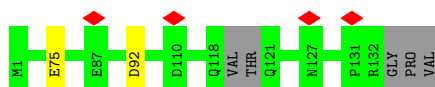
- Molecule 66: 40S ribosomal protein S16

Chain SQ:  95% • •



- Molecule 67: 40S ribosomal protein S17

Chain SR:  95% • •



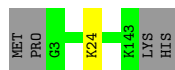
- Molecule 68: 40S ribosomal protein S18

Chain SS:  94% • 5%



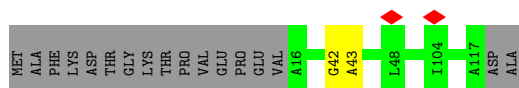
- Molecule 69: 40S ribosomal protein S19

Chain ST:  97% • •



- Molecule 70: 40S ribosomal protein S20

Chain SU:  84% • 14%



- Molecule 71: 40S ribosomal protein S21

Chain SV:  100%

There are no outlier residues recorded for this chain.

- Molecule 72: 40S ribosomal protein S15a

Chain SW:  99% •



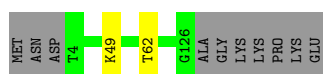
- Molecule 73: 40S ribosomal protein S23

Chain SX: 97%



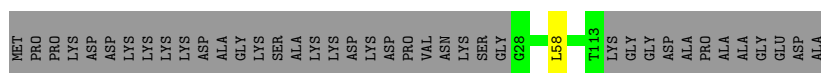
- Molecule 74: 40S ribosomal protein S24

Chain SY: 91%



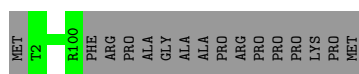
- Molecule 75: 40S ribosomal protein S25

Chain SZ: 68%



- Molecule 76: 40S ribosomal protein S26

Chain Sa: 86%



- Molecule 77: 40S ribosomal protein S27

Chain Sb: 96%



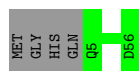
- Molecule 78: 40S ribosomal protein S28

Chain Sc: 90%



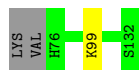
- Molecule 79: 40S ribosomal protein S29

Chain Sd: 93%



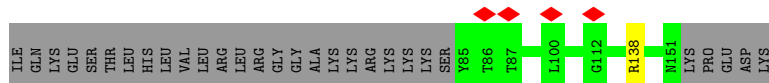
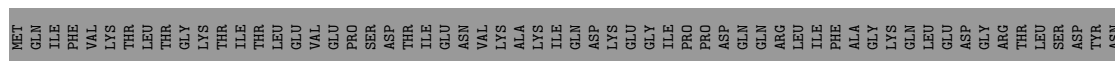
- Molecule 80: 40S ribosomal protein S30

Chain Se: 95%



- Molecule 81: Ubiquitin-40S ribosomal protein S27a

Chain Sf: 42%



- Molecule 82: Receptor of activated protein C kinase 1

Chain Sg: 97%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21820	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 ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0092	Depositor
Map size (Å)	473.0, 473.0, 473.0	wwPDB
Map dimensions	550, 550, 550	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A4	0.48	0/373	1.05	1/574 (0.2%)
2	B4	0.56	1/1813 (0.1%)	1.08	11/2823 (0.4%)
2	D4	0.56	1/1813 (0.1%)	1.13	16/2823 (0.6%)
4	L5	0.76	0/87379	0.98	164/136294 (0.1%)
5	L7	0.70	0/2858	0.97	2/4455 (0.0%)
6	L8	0.78	0/3701	0.98	6/5766 (0.1%)
7	LA	0.46	1/1929 (0.1%)	0.61	0/2586
8	LB	0.42	0/3279	0.59	2/4388 (0.0%)
9	LC	0.42	0/2951	0.57	1/3963 (0.0%)
10	LD	0.39	0/2425	0.55	0/3248
11	LE	0.38	0/1819	0.61	0/2439
12	LF	0.42	0/1905	0.53	0/2539
13	LG	0.38	0/1863	0.55	0/2510
14	LH	0.38	0/1537	0.58	0/2066
15	LI	0.39	0/1720	0.53	0/2298
16	LJ	0.35	0/1424	0.60	1/1904 (0.1%)
17	LL	0.41	0/1713	0.55	0/2293
18	LM	0.39	0/1142	0.57	0/1527
19	LN	0.48	1/1746 (0.1%)	0.52	0/2338
20	LO	0.41	0/1673	0.51	0/2238
21	LP	0.43	0/1268	0.51	0/1701
22	LQ	0.42	0/1537	0.55	0/2052
23	LR	0.35	0/1524	0.53	0/2013
24	LS	0.43	0/1493	0.52	0/2003
25	LT	0.40	0/1326	0.49	0/1770
26	LU	0.35	0/835	0.57	0/1122
27	LV	0.41	0/993	0.57	0/1332
28	LW	0.36	0/927	0.51	0/1232
29	LX	0.39	0/998	0.56	0/1340
30	LY	0.41	0/1132	0.59	1/1504 (0.1%)
31	LZ	0.42	0/1130	0.51	0/1507
32	La	0.43	0/1191	0.57	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Lb	0.34	0/611	0.49	0/808
34	Lc	0.40	0/774	0.54	0/1038
35	Ld	0.40	0/903	0.52	0/1216
36	Le	0.44	0/1071	0.52	0/1429
37	Lf	0.45	0/895	0.62	0/1198
38	Lg	0.39	0/916	0.56	0/1220
39	Lh	0.38	0/1023	0.48	0/1351
40	Li	0.38	0/843	0.52	0/1115
41	Lj	0.46	0/720	0.54	0/952
42	Lk	0.38	0/575	0.53	0/761
43	Ll	0.40	0/454	0.51	0/599
44	Lm	0.39	0/435	0.54	0/575
45	Ln	0.33	0/231	0.43	0/294
46	Lo	0.42	0/876	0.59	1/1156 (0.1%)
47	Lp	0.43	0/718	0.57	0/953
48	Lr	0.41	0/1017	0.54	0/1364
49	S2	0.65	0/40504	1.07	199/63126 (0.3%)
50	SA	0.35	0/1732	0.59	0/2355
51	SB	0.32	0/1765	0.56	0/2362
52	SC	0.37	0/1729	0.61	0/2337
53	SD	0.35	0/1714	0.59	0/2304
54	SE	0.35	0/2112	0.55	0/2842
55	SF	0.32	0/1468	0.55	0/1977
56	SG	0.32	0/1940	0.53	0/2583
57	SH	0.33	0/1533	0.65	1/2053 (0.0%)
58	SI	0.35	0/1703	0.53	0/2275
59	SJ	0.33	0/1531	0.56	0/2045
60	SK	0.34	0/834	0.57	2/1125 (0.2%)
61	SL	0.39	0/1223	0.59	1/1637 (0.1%)
62	SM	0.31	0/804	0.68	0/1081
63	SN	0.33	0/1232	0.56	1/1656 (0.1%)
64	SO	0.35	0/1015	0.57	0/1361
65	SP	0.35	0/1126	0.54	0/1505
66	SQ	0.34	0/1146	0.64	1/1534 (0.1%)
67	SR	0.31	0/1064	0.63	0/1425
68	SS	0.33	0/1187	0.59	1/1593 (0.1%)
69	ST	0.33	0/1114	0.56	0/1493
70	SU	0.33	0/809	0.67	0/1087
71	SV	0.37	0/643	0.59	0/860
72	SW	0.36	0/1051	0.59	0/1406
73	SX	0.38	0/1116	0.53	0/1490
74	SY	0.32	0/1019	0.54	0/1355
75	SZ	0.31	0/688	0.65	1/921 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Sa	0.37	0/805	0.52	0/1079
77	Sb	0.36	0/657	0.61	0/883
78	Sc	0.31	0/482	0.66	0/648
79	Sd	0.37	0/442	0.56	0/586
80	Se	0.31	0/458	0.47	0/602
81	Sf	0.30	0/548	0.57	0/728
82	Sg	0.33	0/2493	0.68	1/3394 (0.0%)
All	All	0.61	4/231166 (0.0%)	0.88	414/339976 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	LA	0	2
8	LB	0	1
9	LC	0	2
10	LD	0	1
11	LE	0	1
12	LF	0	2
13	LG	0	1
17	LL	0	1
18	LM	0	1
21	LP	0	2
22	LQ	0	1
24	LS	0	1
25	LT	0	1
28	LW	0	1
37	Lf	0	1
38	Lg	0	1
40	Li	0	1
41	Lj	0	1
51	SB	0	2
52	SC	0	1
55	SF	0	1
62	SM	0	1
70	SU	0	2
82	Sg	0	2
All	All	0	31

All (4) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B4	1	G	OP3-P	-10.75	1.48	1.61
2	D4	1	G	OP3-P	-10.66	1.48	1.61
19	LN	82	GLY	C-N	-5.27	1.22	1.34
7	LA	207	VAL	CB-CG1	-5.05	1.42	1.52

The worst 5 of 414 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	S2	1568	C	N1-C2-O2	14.65	127.69	118.90
49	S2	1453	C	N1-C2-O2	13.19	126.81	118.90
49	S2	1568	C	C2-N1-C1'	12.93	133.02	118.80
49	S2	293	C	N1-C2-O2	12.60	126.46	118.90
49	S2	293	C	C2-N1-C1'	12.16	132.17	118.80

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LA	205	ASN	Peptide
7	LA	239	ALA	Peptide
8	LB	258	HIS	Peptide
9	LC	279	LEU	Peptide
9	LC	70	GLY	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	LA	245/257 (95%)	223 (91%)	22 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	LB	396/403 (98%)	360 (91%)	35 (9%)	1 (0%)	41	74
9	LC	363/427 (85%)	338 (93%)	25 (7%)	0	100	100
10	LD	291/297 (98%)	267 (92%)	24 (8%)	0	100	100
11	LE	216/288 (75%)	182 (84%)	34 (16%)	0	100	100
12	LF	223/248 (90%)	208 (93%)	15 (7%)	0	100	100
13	LG	223/266 (84%)	208 (93%)	14 (6%)	1 (0%)	34	69
14	LH	188/192 (98%)	167 (89%)	21 (11%)	0	100	100
15	LI	205/214 (96%)	185 (90%)	20 (10%)	0	100	100
16	LJ	173/178 (97%)	158 (91%)	14 (8%)	1 (1%)	25	64
17	LL	206/211 (98%)	187 (91%)	18 (9%)	1 (0%)	29	67
18	LM	134/215 (62%)	119 (89%)	15 (11%)	0	100	100
19	LN	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
20	LO	198/203 (98%)	190 (96%)	8 (4%)	0	100	100
21	LP	151/184 (82%)	137 (91%)	14 (9%)	0	100	100
22	LQ	185/188 (98%)	173 (94%)	12 (6%)	0	100	100
23	LR	178/196 (91%)	175 (98%)	3 (2%)	0	100	100
24	LS	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
25	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
26	LU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
27	LV	129/140 (92%)	118 (92%)	11 (8%)	0	100	100
28	LW	111/157 (71%)	103 (93%)	8 (7%)	0	100	100
29	LX	118/156 (76%)	106 (90%)	12 (10%)	0	100	100
30	LY	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
31	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
32	La	145/148 (98%)	129 (89%)	16 (11%)	0	100	100
33	Lb	73/159 (46%)	66 (90%)	7 (10%)	0	100	100
34	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
35	Ld	105/125 (84%)	95 (90%)	10 (10%)	0	100	100
36	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
37	Lf	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
38	Lg	112/117 (96%)	102 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
40	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
41	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
42	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
43	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
44	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	103/106 (97%)	95 (92%)	8 (8%)	0	100	100
47	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
48	Lr	123/137 (90%)	113 (92%)	10 (8%)	0	100	100
50	SA	213/295 (72%)	201 (94%)	12 (6%)	0	100	100
51	SB	212/264 (80%)	192 (91%)	19 (9%)	1 (0%)	29	67
52	SC	217/293 (74%)	204 (94%)	13 (6%)	0	100	100
53	SD	214/243 (88%)	189 (88%)	25 (12%)	0	100	100
54	SE	260/263 (99%)	247 (95%)	13 (5%)	0	100	100
55	SF	184/204 (90%)	153 (83%)	30 (16%)	1 (0%)	29	67
56	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
57	SH	185/194 (95%)	161 (87%)	24 (13%)	0	100	100
58	SI	204/208 (98%)	186 (91%)	18 (9%)	0	100	100
59	SJ	180/194 (93%)	168 (93%)	12 (7%)	0	100	100
60	SK	94/165 (57%)	89 (95%)	5 (5%)	0	100	100
61	SL	144/158 (91%)	127 (88%)	17 (12%)	0	100	100
62	SM	102/132 (77%)	76 (74%)	25 (24%)	1 (1%)	15	54
63	SN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
64	SO	132/151 (87%)	117 (89%)	15 (11%)	0	100	100
65	SP	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
66	SQ	140/146 (96%)	119 (85%)	21 (15%)	0	100	100
67	SR	126/135 (93%)	110 (87%)	16 (13%)	0	100	100
68	SS	142/152 (93%)	123 (87%)	19 (13%)	0	100	100
69	ST	139/145 (96%)	123 (88%)	16 (12%)	0	100	100
70	SU	100/119 (84%)	86 (86%)	14 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	SV	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
72	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
73	SX	139/143 (97%)	136 (98%)	2 (1%)	1 (1%)	22	61
74	SY	121/133 (91%)	118 (98%)	3 (2%)	0	100	100
75	SZ	84/125 (67%)	75 (89%)	9 (11%)	0	100	100
76	Sa	97/115 (84%)	86 (89%)	11 (11%)	0	100	100
77	Sb	81/84 (96%)	67 (83%)	13 (16%)	1 (1%)	13	49
78	Sc	61/69 (88%)	47 (77%)	14 (23%)	0	100	100
79	Sd	50/56 (89%)	49 (98%)	1 (2%)	0	100	100
80	Se	55/59 (93%)	50 (91%)	5 (9%)	0	100	100
81	Sf	65/156 (42%)	60 (92%)	5 (8%)	0	100	100
82	Sg	311/317 (98%)	254 (82%)	56 (18%)	1 (0%)	41	74
All	All	11173/12688 (88%)	10187 (91%)	976 (9%)	10 (0%)	54	83

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	LL	48	PRO
55	SF	80	GLY
77	Sb	39	GLY
8	LB	393	LYS
82	Sg	283	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LA	189/199 (95%)	188 (100%)	1 (0%)	88	95
8	LB	346/349 (99%)	343 (99%)	3 (1%)	78	91
9	LC	302/348 (87%)	300 (99%)	2 (1%)	84	94
10	LD	245/250 (98%)	244 (100%)	1 (0%)	91	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LE	196/252 (78%)	194 (99%)	2 (1%)	76	90
12	LF	194/215 (90%)	193 (100%)	1 (0%)	88	95
13	LG	195/223 (87%)	195 (100%)	0	100	100
14	LH	169/171 (99%)	168 (99%)	1 (1%)	86	94
15	LI	175/181 (97%)	175 (100%)	0	100	100
16	LJ	147/149 (99%)	147 (100%)	0	100	100
17	LL	174/177 (98%)	174 (100%)	0	100	100
18	LM	116/161 (72%)	116 (100%)	0	100	100
19	LN	171/172 (99%)	170 (99%)	1 (1%)	86	94
20	LO	172/174 (99%)	169 (98%)	3 (2%)	60	83
21	LP	134/163 (82%)	134 (100%)	0	100	100
22	LQ	164/165 (99%)	161 (98%)	3 (2%)	59	82
23	LR	159/175 (91%)	159 (100%)	0	100	100
24	LS	156/157 (99%)	155 (99%)	1 (1%)	86	94
25	LT	139/140 (99%)	138 (99%)	1 (1%)	84	94
26	LU	90/115 (78%)	90 (100%)	0	100	100
27	LV	101/107 (94%)	101 (100%)	0	100	100
28	LW	88/126 (70%)	87 (99%)	1 (1%)	73	88
29	LX	107/133 (80%)	107 (100%)	0	100	100
30	LY	124/135 (92%)	124 (100%)	0	100	100
31	LZ	117/118 (99%)	117 (100%)	0	100	100
32	La	120/121 (99%)	119 (99%)	1 (1%)	81	93
33	Lb	60/126 (48%)	60 (100%)	0	100	100
34	Lc	83/97 (86%)	81 (98%)	2 (2%)	49	77
35	Ld	98/110 (89%)	97 (99%)	1 (1%)	76	90
36	Le	114/121 (94%)	114 (100%)	0	100	100
37	Lf	88/89 (99%)	86 (98%)	2 (2%)	50	78
38	Lg	98/100 (98%)	98 (100%)	0	100	100
39	Lh	109/110 (99%)	108 (99%)	1 (1%)	78	91
40	Li	86/89 (97%)	85 (99%)	1 (1%)	71	88
41	Lj	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Lk	64/65 (98%)	63 (98%)	1 (2%)	62	84
43	Ll	47/48 (98%)	47 (100%)	0	100	100
44	Lm	48/116 (41%)	48 (100%)	0	100	100
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	93/94 (99%)	93 (100%)	0	100	100
47	Lp	74/75 (99%)	74 (100%)	0	100	100
48	Lr	109/121 (90%)	109 (100%)	0	100	100
50	SA	178/243 (73%)	178 (100%)	0	100	100
51	SB	195/231 (84%)	195 (100%)	0	100	100
52	SC	183/225 (81%)	183 (100%)	0	100	100
53	SD	179/202 (89%)	177 (99%)	2 (1%)	73	88
54	SE	223/225 (99%)	222 (100%)	1 (0%)	91	95
55	SF	152/170 (89%)	150 (99%)	2 (1%)	69	87
56	SG	206/218 (94%)	204 (99%)	2 (1%)	76	90
57	SH	168/174 (97%)	165 (98%)	3 (2%)	59	82
58	SI	175/180 (97%)	174 (99%)	1 (1%)	86	94
59	SJ	160/168 (95%)	160 (100%)	0	100	100
60	SK	87/136 (64%)	87 (100%)	0	100	100
61	SL	131/142 (92%)	131 (100%)	0	100	100
62	SM	85/108 (79%)	83 (98%)	2 (2%)	49	77
63	SN	130/131 (99%)	130 (100%)	0	100	100
64	SO	104/119 (87%)	103 (99%)	1 (1%)	76	90
65	SP	120/130 (92%)	119 (99%)	1 (1%)	81	93
66	SQ	117/121 (97%)	114 (97%)	3 (3%)	46	76
67	SR	116/122 (95%)	114 (98%)	2 (2%)	60	83
68	SS	119/132 (90%)	119 (100%)	0	100	100
69	ST	111/115 (96%)	110 (99%)	1 (1%)	78	91
70	SU	89/107 (83%)	89 (100%)	0	100	100
71	SV	67/67 (100%)	67 (100%)	0	100	100
72	SW	112/113 (99%)	112 (100%)	0	100	100
73	SX	113/115 (98%)	112 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	SY	106/115 (92%)	104 (98%)	2 (2%)	57	81
75	SZ	73/103 (71%)	73 (100%)	0	100	100
76	Sa	86/98 (88%)	86 (100%)	0	100	100
77	Sb	73/76 (96%)	72 (99%)	1 (1%)	67	86
78	Sc	53/62 (86%)	52 (98%)	1 (2%)	57	81
79	Sd	45/49 (92%)	45 (100%)	0	100	100
80	Se	46/48 (96%)	45 (98%)	1 (2%)	52	79
81	Sf	57/140 (41%)	56 (98%)	1 (2%)	59	82
82	Sg	272/275 (99%)	270 (99%)	2 (1%)	84	94
All	All	9688/10801 (90%)	9628 (99%)	60 (1%)	86	94

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	Li	29	ARG
78	Sc	55	VAL
56	SG	98	ARG
77	Sb	33	MET
82	Sg	245	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
44	Lm	104	HIS
82	Sg	64	HIS
54	SE	179	ASN
80	Se	88	GLN
71	SV	49	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A4	16/28 (57%)	6 (37%)	0
2	B4	75/76 (98%)	20 (26%)	0
2	D4	75/76 (98%)	19 (25%)	0
4	L5	3626/5070 (71%)	885 (24%)	14 (0%)
49	S2	1688/1869 (90%)	532 (31%)	17 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	L7	119/120 (99%)	20 (16%)	0
6	L8	155/156 (99%)	34 (21%)	1 (0%)
All	All	5754/7395 (77%)	1516 (26%)	32 (0%)

5 of 1516 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A4	49	U
1	A4	53	U
1	A4	54	U
1	A4	55	U
1	A4	57	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S2	1606	G
49	S2	1622	U
4	L5	4699	U
4	L5	3673	C
49	S2	1664	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 80 ligands modelled in this entry, 79 are monoatomic - leaving 1 for Mogul analysis.

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



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
84	3HE	L5	5101	-	21,21,21	0.90	2 (9%)	19,30,30	2.12	6 (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
84	3HE	L5	5101	-	-	6/8/36/36	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	L5	5101	3HE	C12-N	-2.58	1.33	1.37
84	L5	5101	3HE	C11-N	-2.47	1.33	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	L5	5101	3HE	C10-C11-N	4.93	121.99	115.95
84	L5	5101	3HE	C13-C12-N	3.87	120.69	115.95
84	L5	5101	3HE	C11-N-C12	-3.49	121.55	125.78
84	L5	5101	3HE	C9-C8-C7	-3.02	109.36	116.82
84	L5	5101	3HE	C14-C3-C4	-2.33	110.08	112.53

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

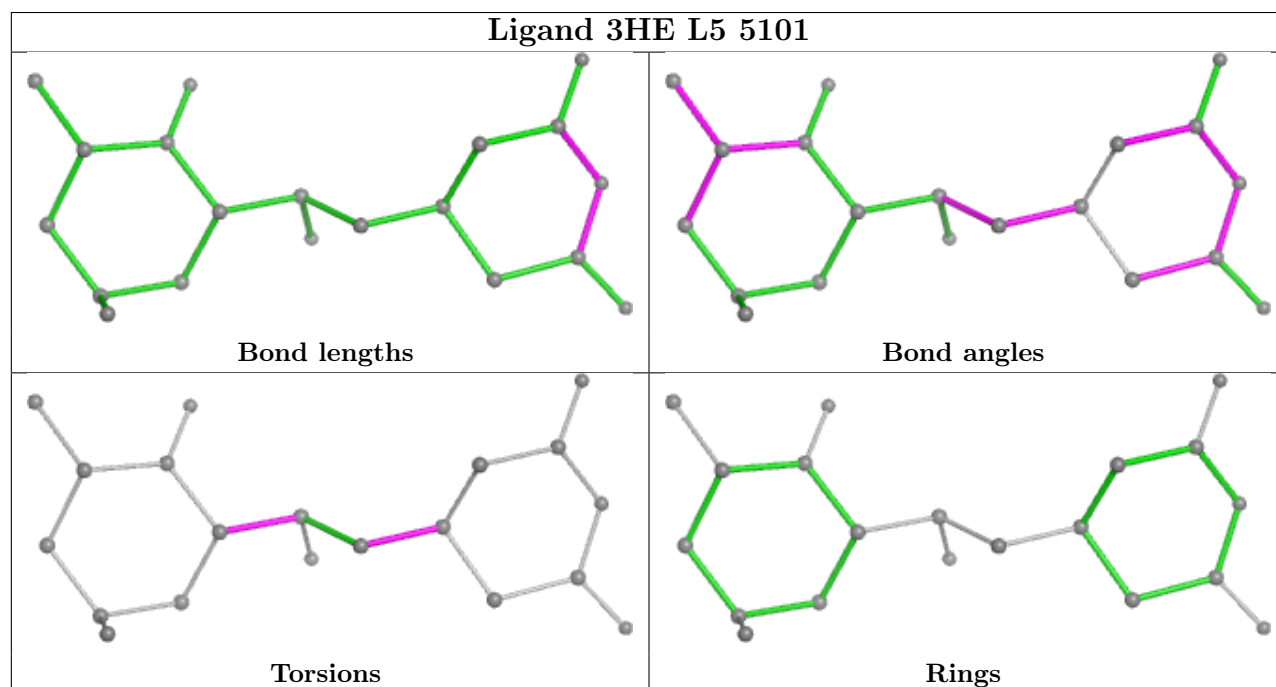
Mol	Chain	Res	Type	Atoms
84	L5	5101	3HE	C4-C5-C7-C8
84	L5	5101	3HE	C4-C5-C7-O3
84	L5	5101	3HE	C6-C5-C7-C8
84	L5	5101	3HE	C6-C5-C7-O3
84	L5	5101	3HE	C7-C8-C9-C10

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

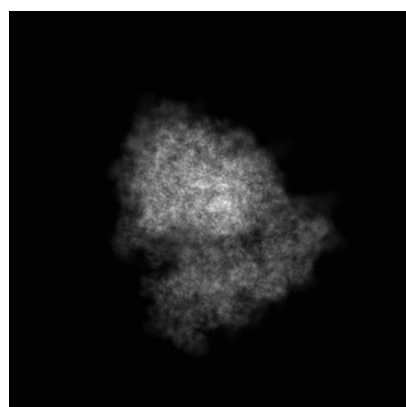
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10668. These allow visual inspection of the internal detail of the map and identification of artifacts.

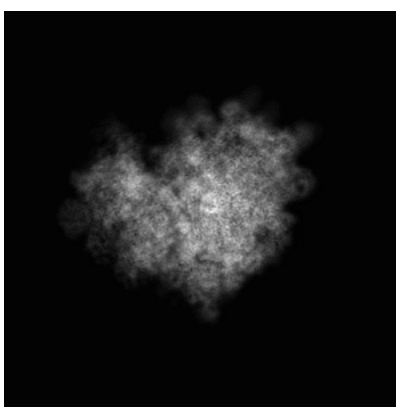
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

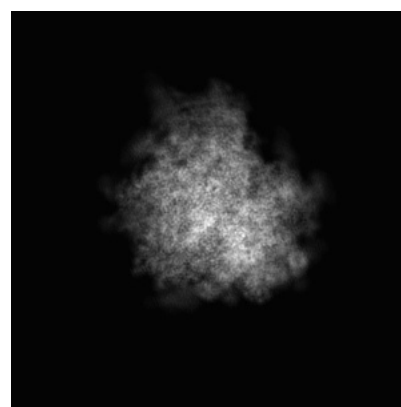
#### 6.1.1 Primary map



X



Y

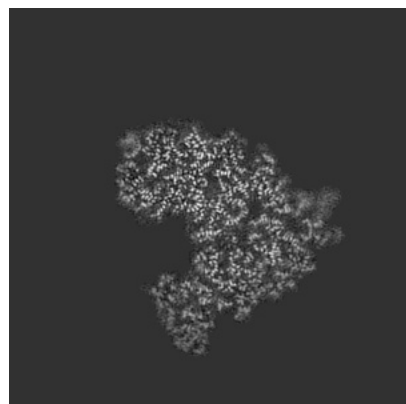


Z

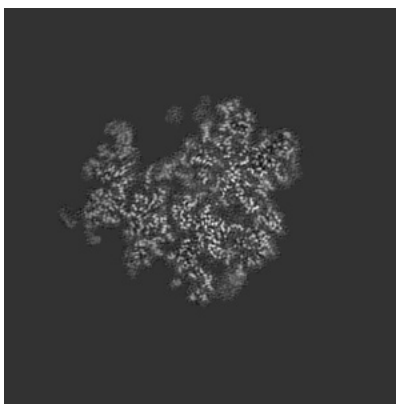
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

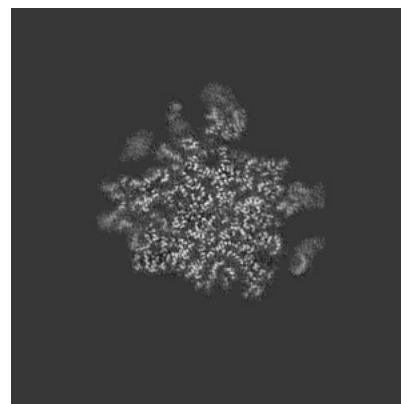
#### 6.2.1 Primary map



X Index: 275



Y Index: 275

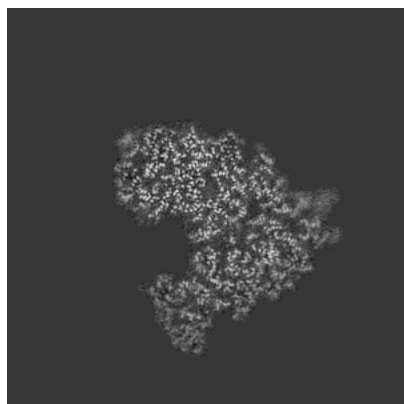


Z Index: 275

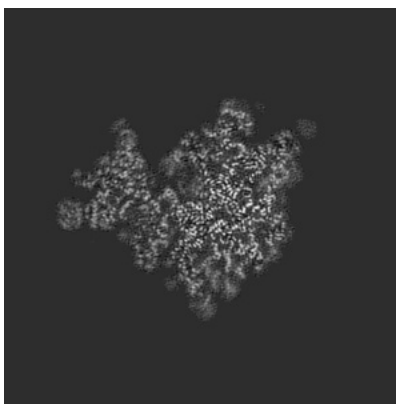
The images above show central slices of the map in three orthogonal directions.

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

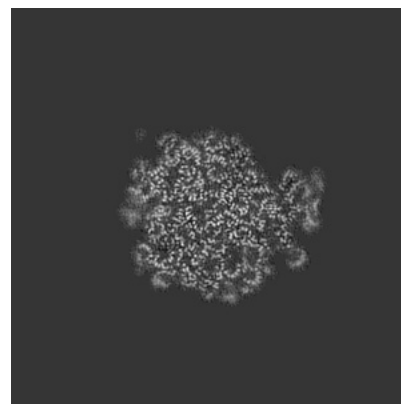
### 6.3.1 Primary map



X Index: 276



Y Index: 265

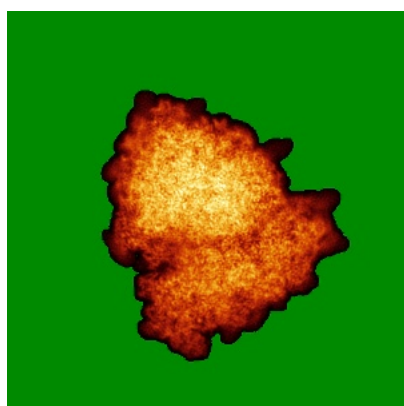


Z Index: 308

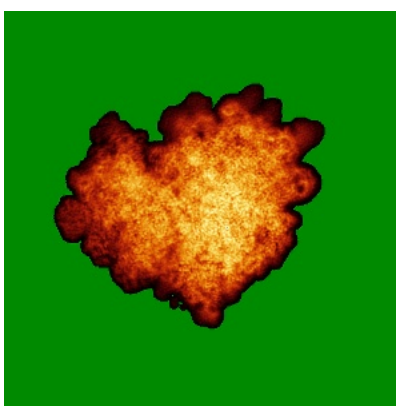
The images above show the largest variance slices of the map in three orthogonal directions.

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

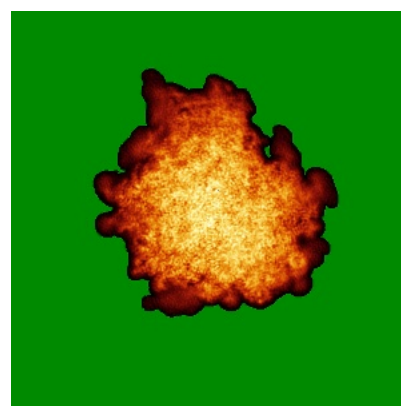
### 6.4.1 Primary map



X



Y

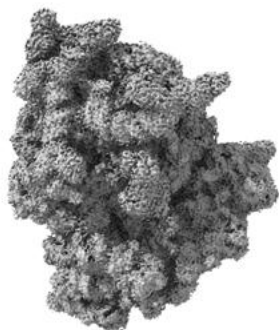


Z

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](#)

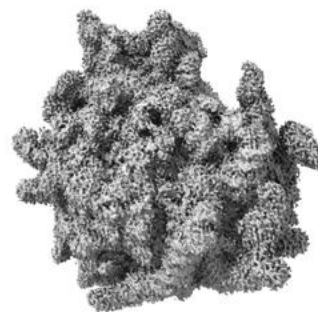
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0092. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

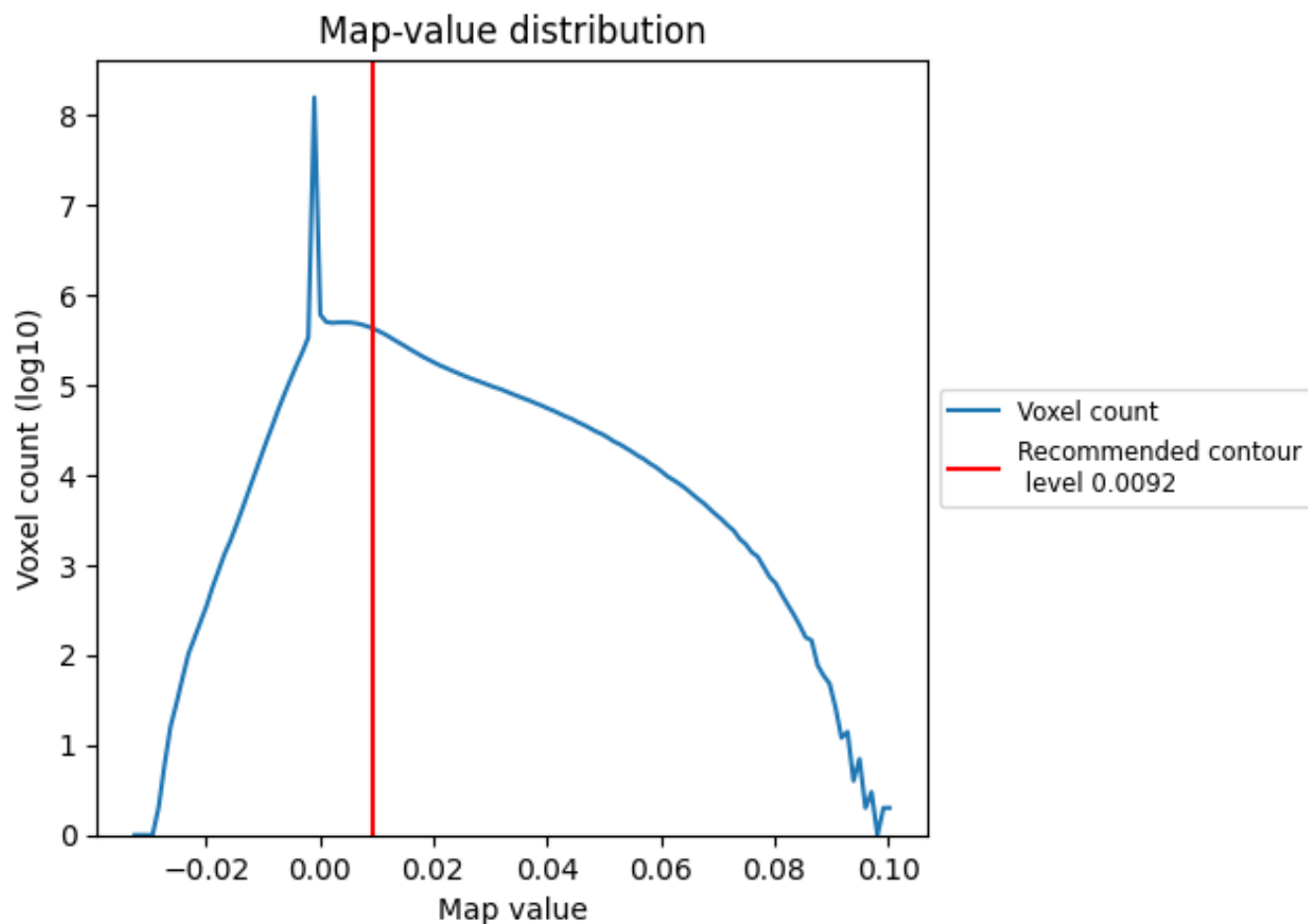
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

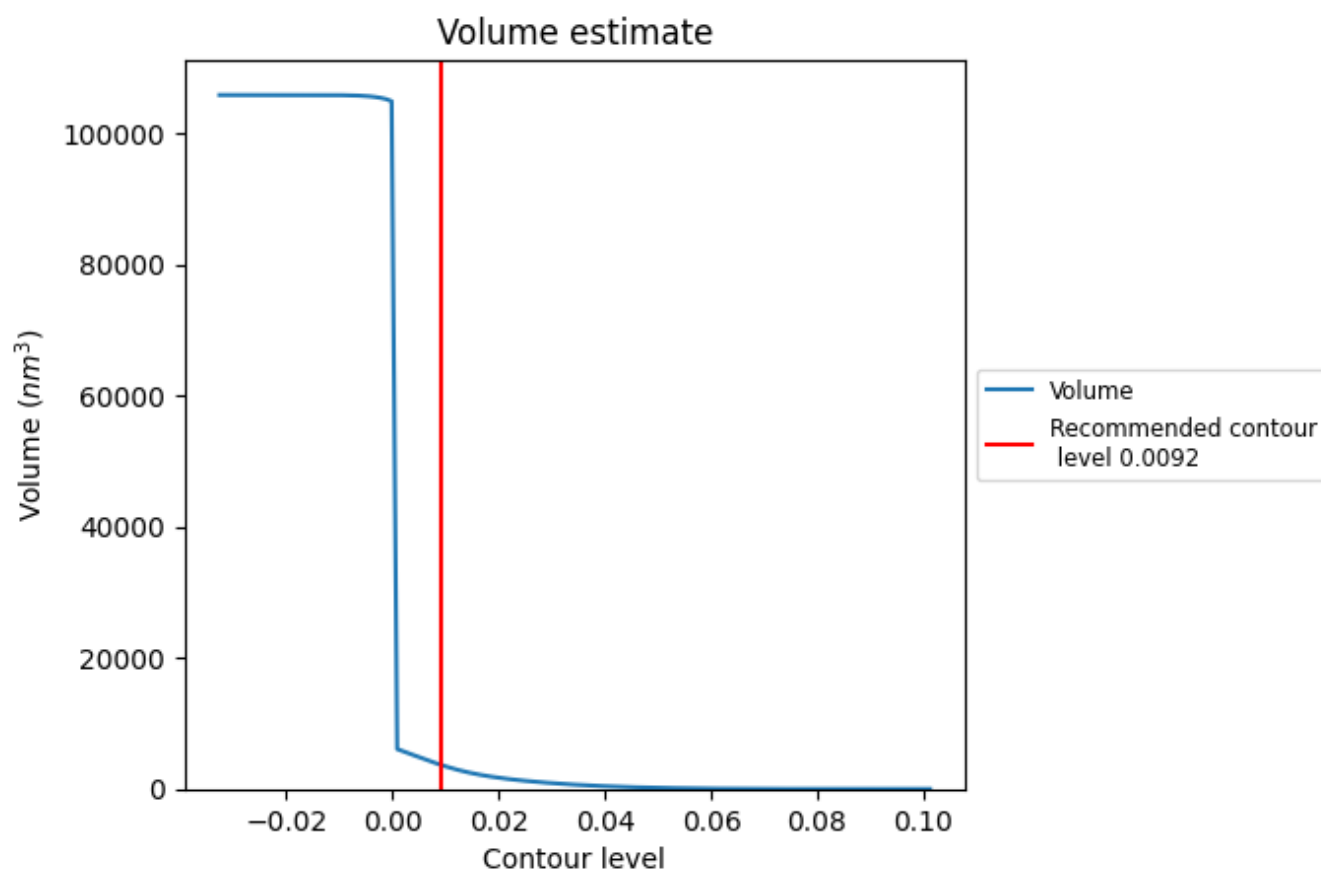
This section contains the results of statistical analysis of the map.

### 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.

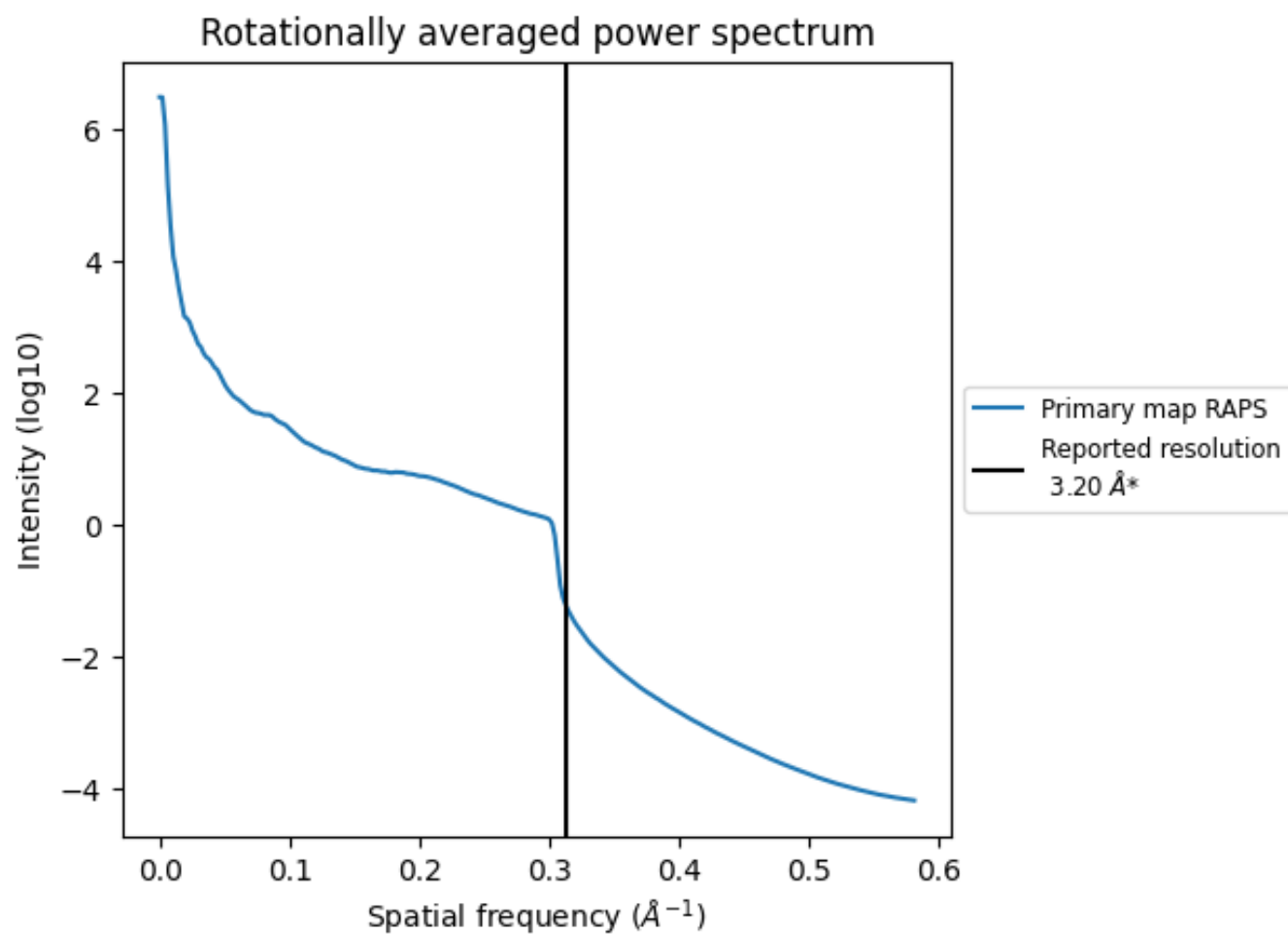
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3664  $\text{nm}^3$ ; this corresponds to an approximate mass of 3310 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 0.312 Å<sup>-1</sup>



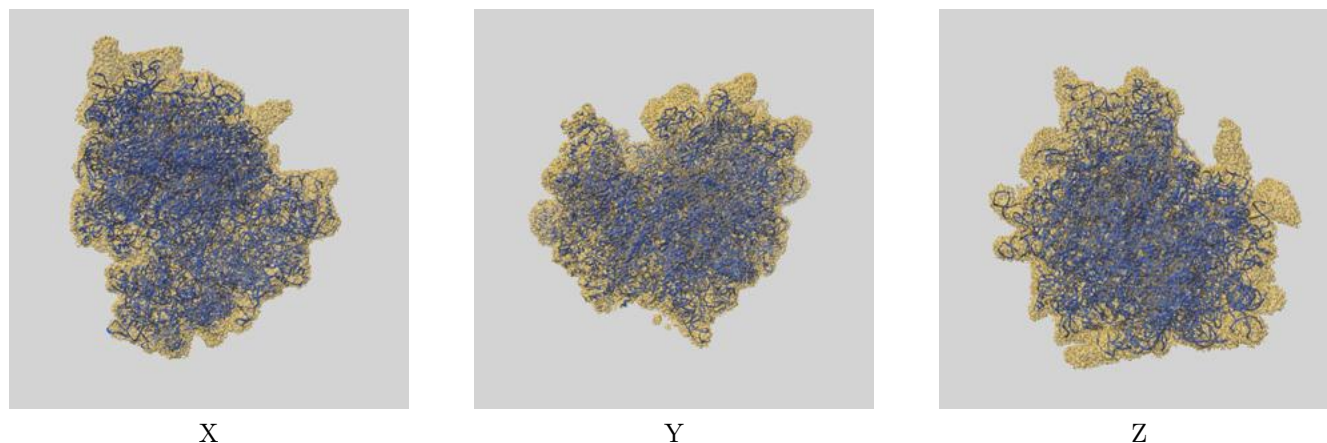
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

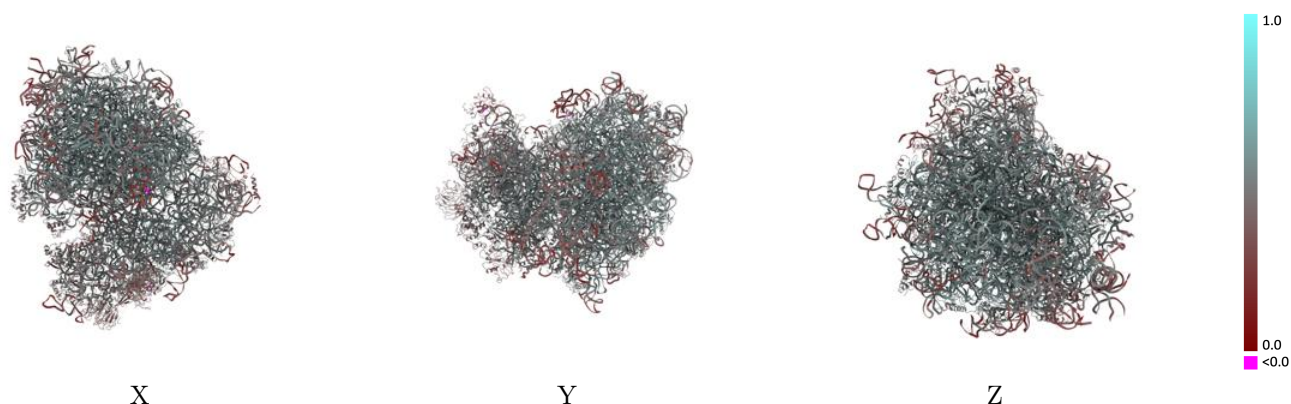
This section contains information regarding the fit between EMDB map EMD-10668 and PDB model 6Y0G. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

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



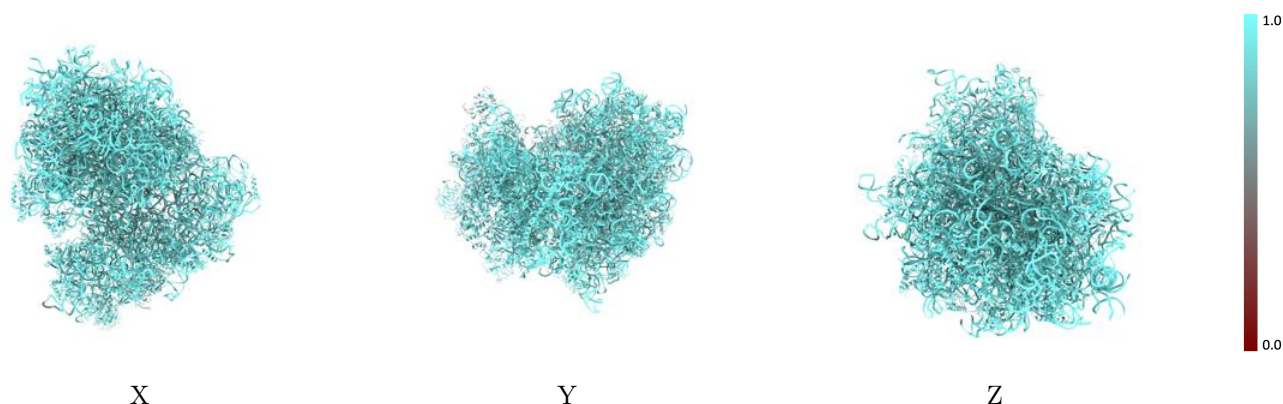
The images above show the 3D surface view of the map at the recommended contour level 0.0092 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



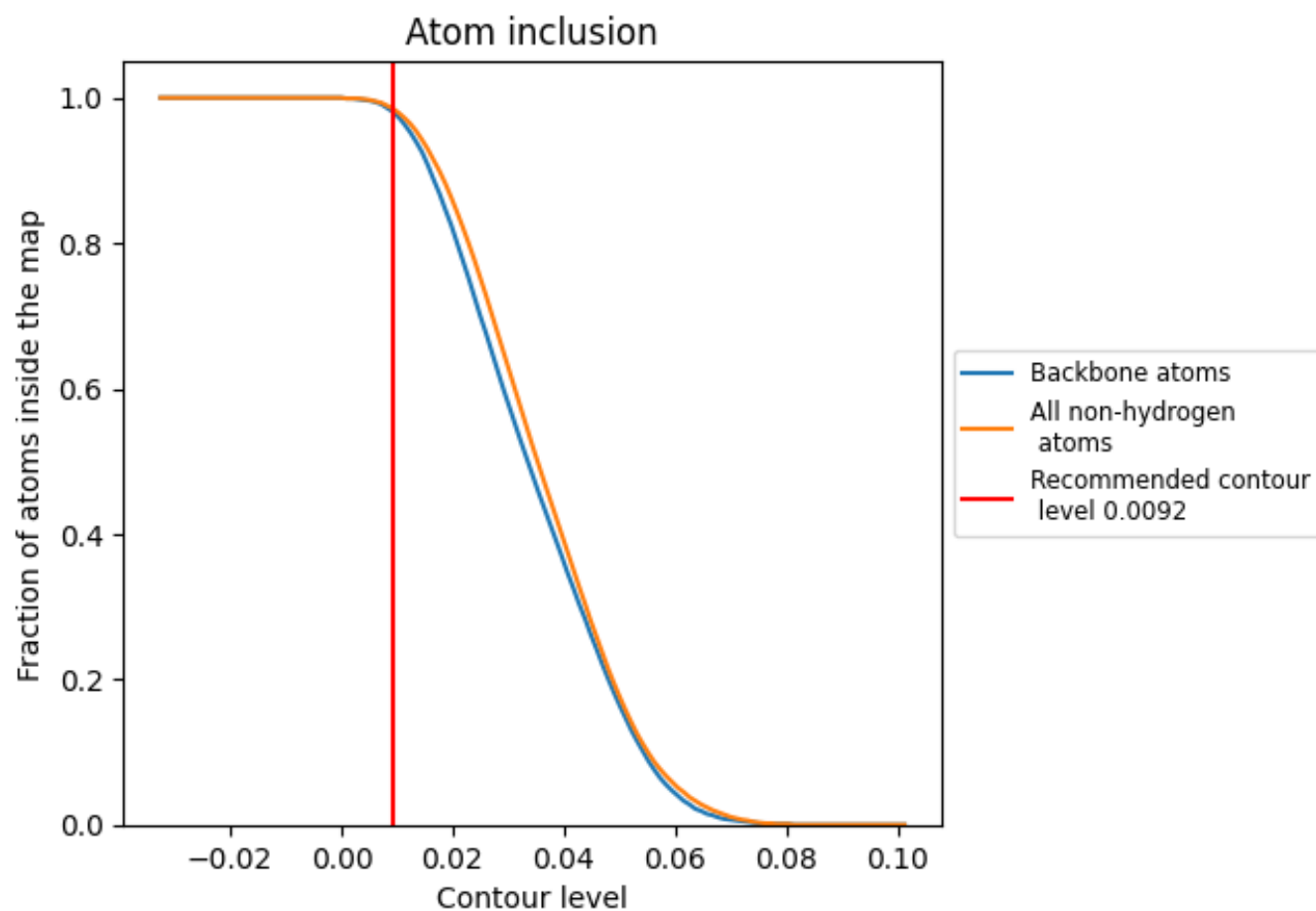
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0092).







































































## 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 (0.0092) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.4880
A4	 0.9910	 0.4220
B4	 0.9910	 0.4330
C4	 0.9000	 0.0840
D4	 0.9890	 0.4320
L5	 0.9960	 0.4950
L7	 0.9990	 0.5120
L8	 0.9970	 0.5200
LA	 0.9960	 0.5530
LB	 0.9890	 0.5280
LC	 0.9960	 0.5420
LD	 0.9900	 0.4850
LE	 0.9950	 0.5000
LF	 0.9960	 0.5360
LG	 0.9810	 0.5040
LH	 0.9930	 0.5030
LI	 0.9890	 0.5150
LJ	 0.9660	 0.4420
LL	 0.9860	 0.5230
LM	 0.9880	 0.5130
LN	 0.9950	 0.5600
LO	 0.9890	 0.5290
LP	 0.9970	 0.5470
LQ	 0.9950	 0.5490
LR	 0.9780	 0.5110
LS	 0.9960	 0.5400
LT	 0.9910	 0.5270
LU	 0.9930	 0.4750
LV	 0.9840	 0.5360
LW	 0.9600	 0.4340
LX	 0.9910	 0.5230
LY	 0.9970	 0.5310
LZ	 0.9900	 0.5080
La	 0.9930	 0.5480
Lb	 0.9640	 0.5000

















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Chain	Atom inclusion	Q-score
Lc	 0.9710	 0.4960
Ld	 0.9910	 0.5280
Le	 0.9960	 0.5550
Lf	 0.9940	 0.5560
Lg	 0.9830	 0.5210
Lh	 0.9830	 0.5170
Li	 0.9880	 0.5050
Lj	 1.0000	 0.5580
Lk	 0.9840	 0.4890
Ll	 0.9950	 0.5460
Lm	 0.9900	 0.5280
Ln	 0.9900	 0.5330
Lo	 0.9900	 0.5240
Lp	 0.9870	 0.5320
Lr	 0.9960	 0.5420
S2	 0.9930	 0.4690
SA	 0.9330	 0.4480
SB	 0.9690	 0.4310
SC	 0.9730	 0.4920
SD	 0.9630	 0.4510
SE	 0.9820	 0.4890
SF	 0.9630	 0.4350
SG	 0.9790	 0.4410
SH	 0.9020	 0.4010
SI	 0.9860	 0.4780
SJ	 0.9800	 0.4660
SK	 0.9670	 0.4400
SL	 0.9800	 0.5010
SM	 0.6590	 0.3060
SN	 0.9750	 0.4770
SO	 0.9710	 0.4380
SP	 0.9840	 0.4580
SQ	 0.9550	 0.4430
SR	 0.8870	 0.4100
SS	 0.9720	 0.4510
ST	 0.9790	 0.4450
SU	 0.9180	 0.4310
SV	 0.9570	 0.4570
SW	 0.9730	 0.5050
SX	 0.9920	 0.5330
SY	 0.9820	 0.4540
SZ	 0.9370	 0.4160

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Chain	Atom inclusion	Q-score
Sa	 0.9910	 0.4880
Sb	 0.9560	 0.4540
Sc	 0.9510	 0.4420
Sd	 0.9830	 0.4850
Se	 0.9840	 0.4910
Sf	 0.7530	 0.3380
Sg	 0.9180	 0.3600