



# wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 12:36 pm BST

PDB ID : 6Y57  
EMDB ID : EMD-10690  
Title : Structure of human ribosome in hybrid-PRE state  
Authors : Bhaskar, V.; Schenk, A.D.; Cavadini, S.; von Loeffelholz, O.; Natchiar, S.K.; Klaholz, B.P.; Chao, J.A.  
Deposited on : 2020-02-25  
Resolution : 3.50 Å(reported)  
Based on initial models : 5LKS, 6QZP, 3J7R, 5AJ0

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  
MolProbity : 4.02b-467  
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

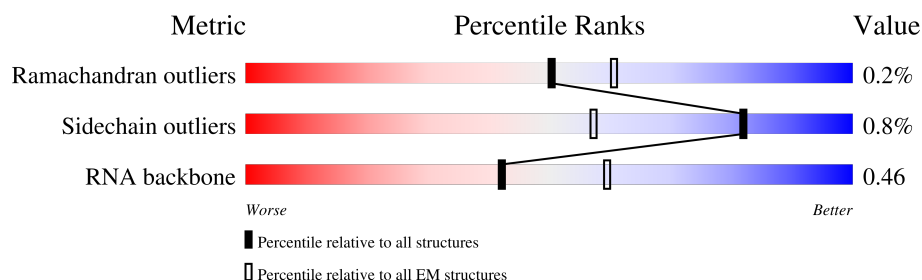
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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.




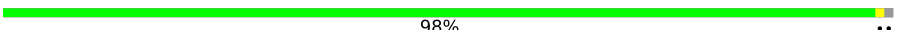








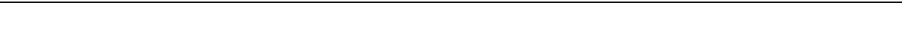

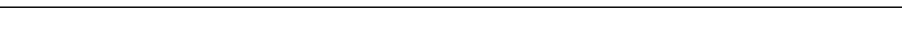
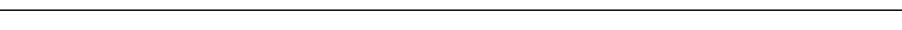
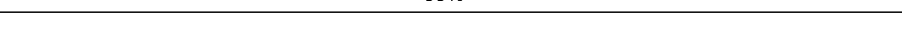

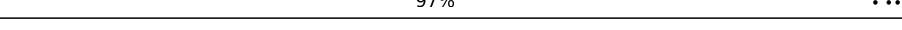
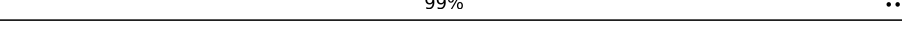





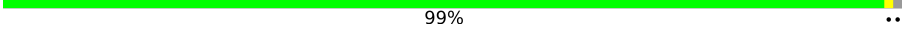
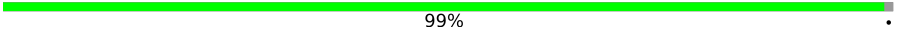
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	16	
2	B4	75	
3	D4	76	
4	L5	5070	
5	L7	120	
6	L8	156	
7	LA	257	
8	LB	403	



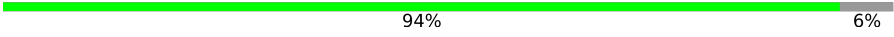
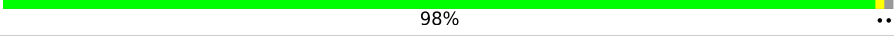
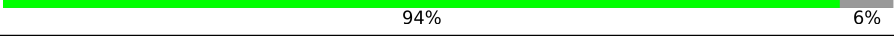
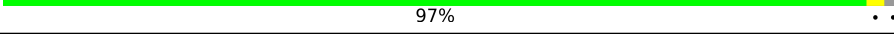
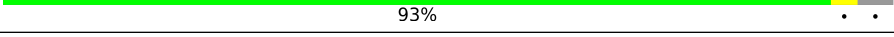

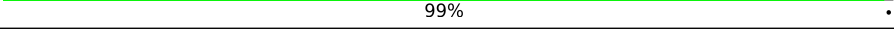
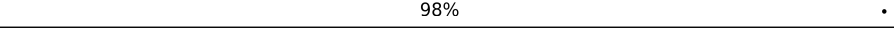
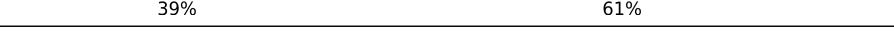
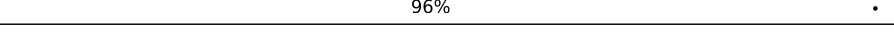
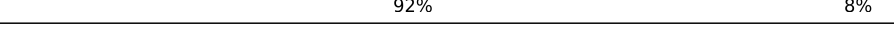
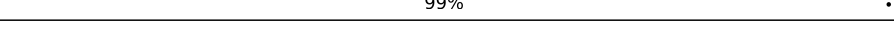


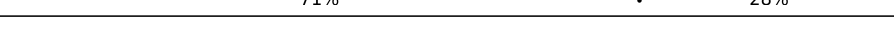

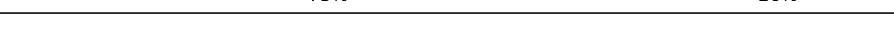






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Mol	Chain	Length	Quality of chain
9	LC	427	 84% 15%
10	LD	297	 98% ..
11	LE	288	 75% 24%
12	LF	248	 89% 9%
13	LG	266	 85% 14%
14	LH	192	 98% ..
15	LI	214	 95% 5%
16	LJ	178	 93% 6%
17	LL	211	 96% ..
18	LM	215	 62% 37%
19	LN	204	 98% .
20	LO	203	 99% .
21	LP	184	 83% 17%
22	LQ	188	 99% ..
23	LR	196	 89% 11%
24	LS	176	 97% ...
25	LT	160	 99% ..
26	LU	128	 78% 21%
27	LV	140	 91% 6%
28	LW	157	 73% 27%
29	LX	156	 76% 23%
30	LY	145	 91% 8%
31	LZ	136	 99% ..
32	La	148	 99% .
33	Lb	159	 40% 60%




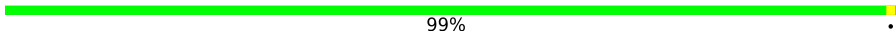


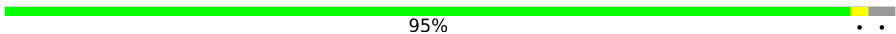


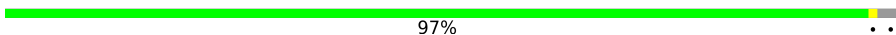


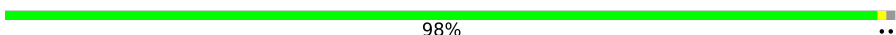
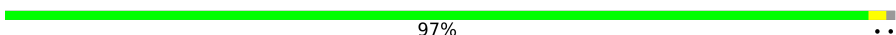



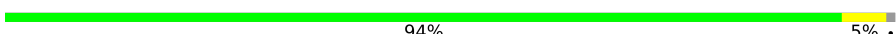






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Mol	Chain	Length	Quality of chain
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SC	293	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	

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Mol	Chain	Length	Quality of chain
59	SJ	194	 89% 9%
60	SK	165	 58% 42%
61	SL	158	 89% 11%
62	SN	151	 99% ..
63	SO	151	 86% 11%
64	SP	145	 85% 12%
65	SQ	146	 95% ..
66	SR	135	 89% .. 7%
67	SS	152	 91% 9%
68	ST	145	 97% ..
69	SU	119	 83% 16%
70	SV	83	 100%
71	SW	130	 98% ..
72	SX	143	 97% ..
73	SY	133	 85% 15%
74	SZ	125	 55% 44%
75	Sa	115	 85% 14%
76	Sb	84	 94% 5%
77	Sc	69	 87% 12%
78	Sd	56	 89% 7%
79	Se	59	 86% 14%
80	Sf	132	 5% 58% 41%
81	Sg	317	 87% 11%
82	sh	156	 26% 74%

## 2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 206539 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	13	Total	C	N	O	P	0	0
			260	117	26	104	13		

- Molecule 2 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B4	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 3 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D4	73	Total	C	N	O	P	0	0
			1559	696	283	508	72		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3574	Total	C	N	O	P	0	0
			76607	34114	14012	24908	3573		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

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

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	248	Total	C	N	O	S	0	0
			1886	1183	386	311	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	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
			2894	1819	578	482	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
			2287	1455	426	392	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	220	Total	C	N	O	S	0	0
			1713	1104	326	279	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
			1844	1189	355	291	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	229	Total	C	N	O	S	0	0
			1733	1106	335	288	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	204	Total	C	N	O	S	0	0
			1580	992	335	249	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
			1097	705	211	174	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
			1693	1068	359	262	4		

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



Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	201	Total	C	N	O	S	0	0
			1613	1042	318	248	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
			1203	754	238	202	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
			1493	931	311	246	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	175	Total	C	N	O	S	0	0
			1412	874	312	218	8		

- 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
			1436	915	281	230	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
			1268	805	249	209	5		

- 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
			768	497	136	133	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
			954	604	180	165	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
			784	493	154	135	2		

- 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
			950	611	182	156	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
			1084	681	220	180	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
			1082	703	207	169	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	93	Total	C	N	O	S	0	0
			716	456	125	129	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
			856	546	168	140	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	127	Total	C	N	O	S	0	0
			1045	661	215	164	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
			864	547	173	141	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	101	Total	C	N	O	S	0	0
			797	500	170	122	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
			701	431	154	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
			528	339	99	89	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
			440	278	97	64	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	50	Total	C	N	O	S	0	0
			393	244	82	61	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	98	Total	C	N	O	S	0	0
			774	488	159	121	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
			689	436	132	114	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
			982	609	205	164	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1658	Total	C	N	O	P	0	0
			35397	15801	6361	11578	1657		

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	212	Total	C	N	O	S	0	0
			1575	1016	285	266	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
			1627	1041	296	277	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SD	215	Total	C	N	O	S	0	0
			1475	950	267	251	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	212	Total	C	N	O	S	0	0
			1544	968	312	258	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH	176	Total	C	N	O	S	0	0
			1342	871	249	221	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI	187	Total	C	N	O	S	0	0
			1450	910	286	249	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		

- Molecule 62 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SN	150	Total	C	N	O	S	0	0
			1199	766	229	203	1		

- Molecule 63 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		

- Molecule 64 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST	141	Total	C	N	O	S	0	0
			993	624	195	172	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU	100	Total	C	N	O	S	0	0
			749	470	143	134	2		

- Molecule 70 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		

- Molecule 71 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		

- Molecule 72 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		

- Molecule 73 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY	113	Total	C	N	O	S	0	0
			855	544	164	143	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ	70	Total	C	N	O	S	0	0
			487	311	90	85	1		

- Molecule 75 is a protein called 40S ribosomal protein S26.



Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sa	99	Total	C	N	O	S	0	0
			762	478	157	122	5		

- Molecule 76 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		

- Molecule 77 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		

- Molecule 78 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	51	Total	C	N	O	S	0	0
			386	240	83	62	1		

- Molecule 80 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 81 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sg	283	Total	C	N	O	S	0	0
			1952	1243	341	359	9		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	sh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

- 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	91	Total	Mg	0
			91	91	
83	L7	2	Total	Mg	0
			2	2	
83	L8	5	Total	Mg	0
			5	5	
83	LQ	1	Total	Mg	0
			1	1	
83	LV	1	Total	Mg	0
			1	1	
83	Le	1	Total	Mg	0
			1	1	
83	Lg	1	Total	Mg	0
			1	1	
83	S2	57	Total	Mg	0
			57	57	

- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

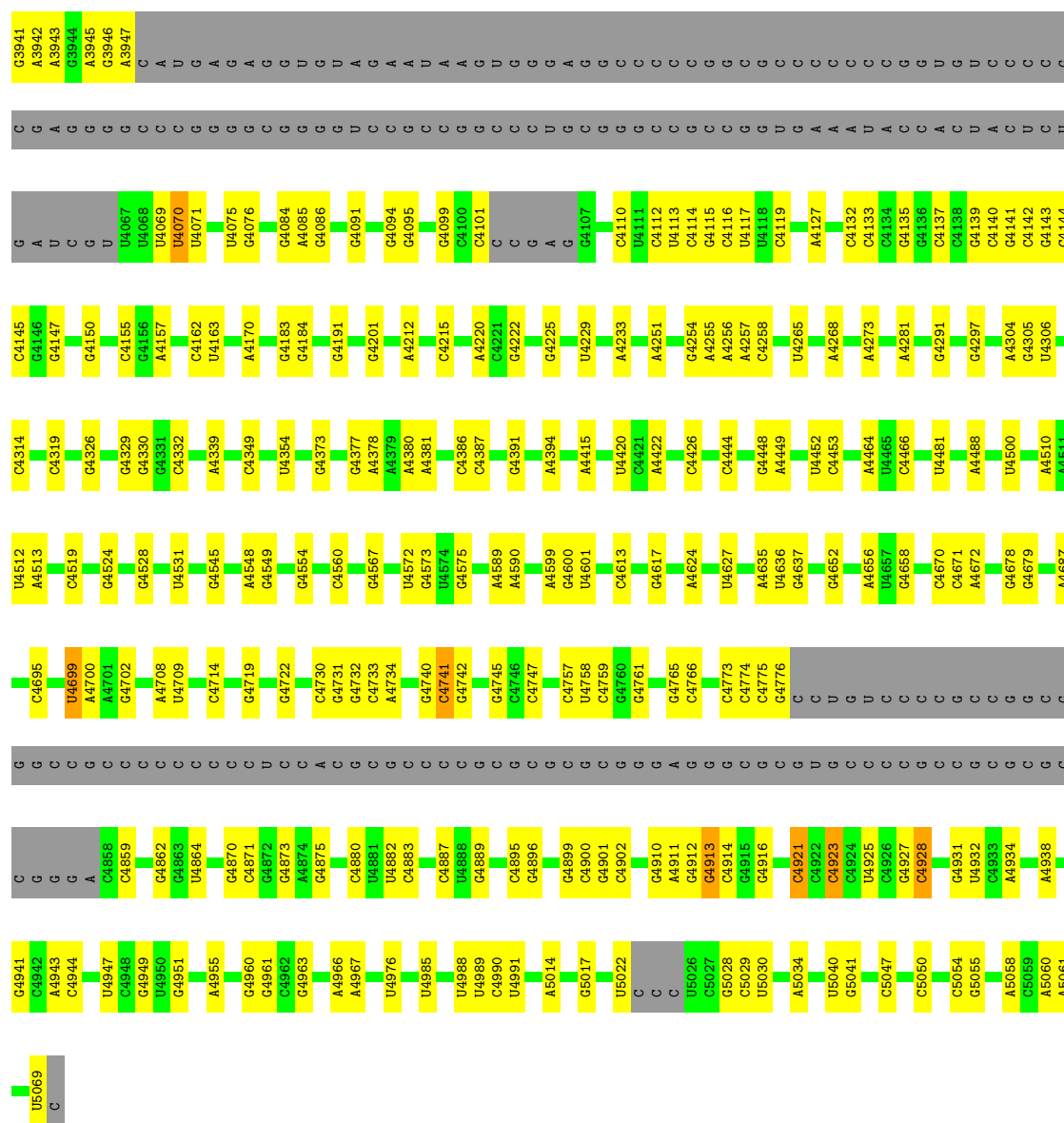
- Molecule 85 is water.

Mol	Chain	Residues	Atoms		AltConf
85	L5	10	Total 10	O 10	0
85	LH	1	Total 1	O 1	0
85	LI	1	Total 1	O 1	0
85	LP	1	Total 1	O 1	0
85	La	1	Total 1	O 1	0
85	S2	3	Total 3	O 3	0
85	SB	1	Total 1	O 1	0
85	SF	1	Total 1	O 1	0









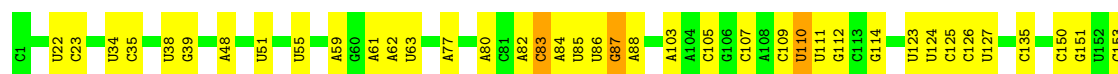
- Molecule 5: 5S ribosomal RNA

Chain L7:




- Molecule 6: 5.8S ribosomal RNA

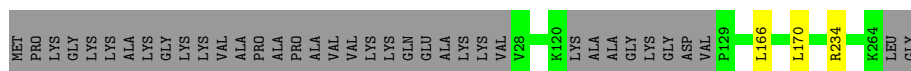
Chain L8:



- Molecule 13: 60S ribosomal protein L7a

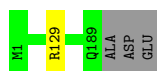


Chain LG:  85% 14%



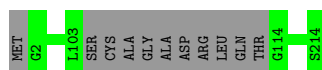
- Molecule 14: 60S ribosomal protein L9

Chain LH:  98%



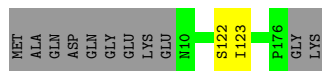
- Molecule 15: 60S ribosomal protein L10-like

Chain LI:  95% 5%



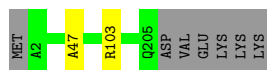
- Molecule 16: 60S ribosomal protein L11

Chain LJ:  93% 6%



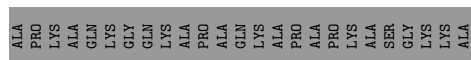
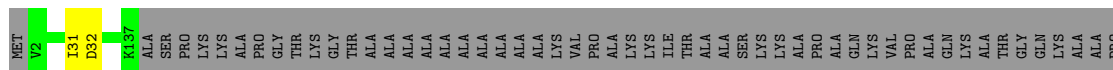
- Molecule 17: 60S ribosomal protein L13

Chain LL:  96%



- Molecule 18: 60S ribosomal protein L14

Chain LM:  62% 37%



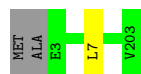
- Molecule 19: 60S ribosomal protein L15

Chain LN:  98%




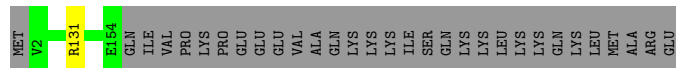
- Molecule 20: 60S ribosomal protein L13a

Chain LO:  99%



- Molecule 21: 60S ribosomal protein L17

Chain LP:  83% 17%



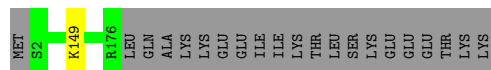
- Molecule 22: 60S ribosomal protein L18

Chain LQ:  99%



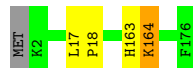
- Molecule 23: 60S ribosomal protein L19

Chain LR:  89% 11%



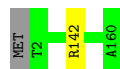
- Molecule 24: 60S ribosomal protein L18a

Chain LS:  97%




- Molecule 25: 60S ribosomal protein L21

Chain LT:  99%



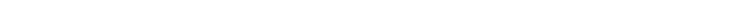
- Molecule 26: 60S ribosomal protein L22

Chain LU:  78% 21%

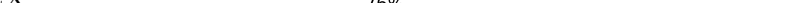


- Molecule 27: 60S ribosomal protein L23

MET SER LYS ARG GLY ARG GLY GLY SER S10 R48 R90 K109 A140

- Chain LW:  73% 27%

[illegible]

- Chain LX:  76% : 23%

MET	ALA	PRO	LYS	LYS	GLU	ALA	PRO	ALA	PRO	PRO	LYS	ALA	GLU	ALA	LYS	ALA	LYS	ALA	LEU	LYS	ALA	LYS	LYS	ALA	ALA	VAL	LEU	LYS	GLY	VAL	HIS	SER	HIS	LYS	K37	K38	K39	T156
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- Chain LY:  91% • 8%

Sequence logo for the 13th position. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows the amino acid sequence: TYR, LYS, GLU, GLU, THR, ILE, GLU, LYS, MET, GLN, GLU. The positions are color-coded: M1 (green), V79 (yellow), H96 (yellow), and K134 (green). The logo shows that the 13th position is highly conserved, with a peak of approximately 1.4 bits for the 'K' (Lysine) position.

- Chain LZ:  99%

MET G2 Y77 F136

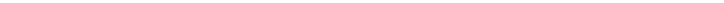
- Chain La:  99%

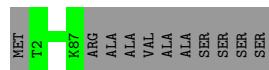
**MET** **P2** **T95** **GLY** **A97** **A148**

- Chain Lb: 

PRO	LYS	ALA	LYS	LYS	ALA	LYS	LYS	ASP	GLN	THR	LYS	LYS	ALA	GLN	ALA	ALA	PRO	PRO	GLN	ALA	LYS	LYS	LYS	ARG	THR	GLN	ALA	ALA	PRO	THR	LYS	ALA	ALA	SER	GLU																			
MET	A2	A64	MET	SER	ALA	ARG	ALA	GLU	ILE	LYS	ALA	LEU	VAL	LYS	LYS	PRO	LYS	ILE	PRO	LYS	GLY	VAL	SER	ARG	LYS	LEU	ASP	ARG	LEU	ALA	ALA	TYR	ILE	ALA	HLA	PRO	LYS	LYS	GLY	LEU	LYS	ARG	ALA	ARG	ALA	ARG	ILE	ALA	LYS	GLY	LEU	ARG	LEU	CYS

- Molecule 41: 60S ribosomal protein L37

Chain Lj:  89% 11%



- Molecule 42: 60S ribosomal protein L38

Chain Lk:  99%



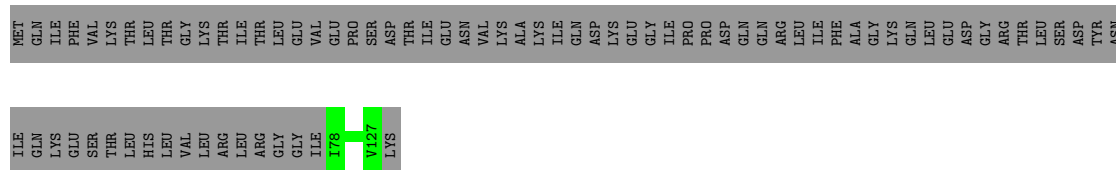
- Molecule 43: 60S ribosomal protein L39

Chain L1:  98%



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  39% 61%



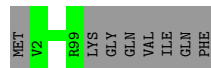
- Molecule 45: 60S ribosomal protein L41

Chain Ln:  96%



- Molecule 46: 60S ribosomal protein L36a

Chain Lo:  92% 8%

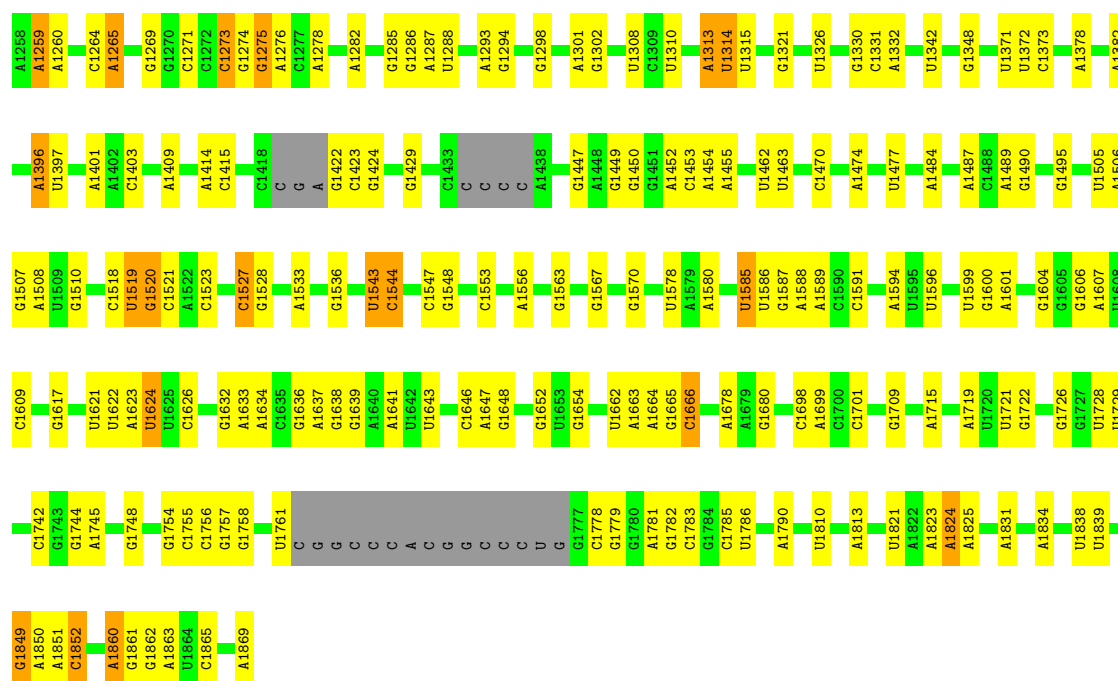


- Molecule 47: 60S ribosomal protein L37a

Chain Lp:  99%

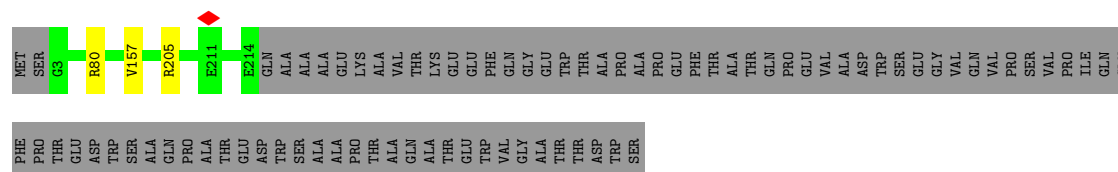






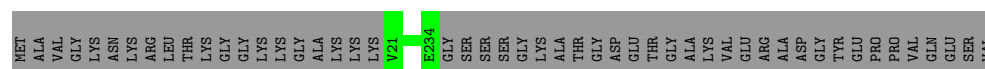
• Molecule 50: 40S ribosomal protein SA

Chain SA: 71% 28%



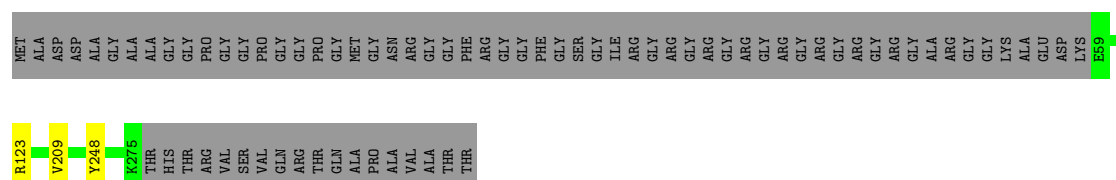
• Molecule 51: 40S ribosomal protein S3a

Chain SB: 81% 19%



• Molecule 52: 40S ribosomal protein S2

Chain SC: 73% 26%

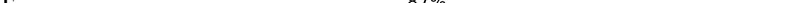


• Molecule 53: 40S ribosomal protein S3


[illegible]

- Chain SE:  97%

MET A2 V126 A258 LYS GLN SER SER GLY

- Chain SF:  87% • 12%

MET	THR	GLU	TRP	GLU	THR	ALA	ALA	PRO	PRO	ALA	ALA	VAL	VAL	ALA	THR	THR	PRO	ASP	ILE	R18	R122	R127	ILE	GLY	ARG	ALA	ALA	GLY	THR	VAL	R135	L173	R204
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- Chain SG: 

W1	V18	ASP	E21	L41	GLY	E43	R98	D126	T128	V129	P130	ARG	R132	M163	GLU	GLY	K167	A220	GLU	LYS	ARG	GLN	GLU	GLM	ILE	ALA	LYS	ARG	ARG	ARG	LEU	SER	SER	LEU	ARG	ALA	SER	THR	SER	LYS	SER	GLU	SER	SER	GLM
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- Chain SH:  90% : 9%

MET PHE SER SER SER ALA LYS LYS ILE V9 G13 GLU LYS P16 T33 T38 A38 V53 GLY GLY GLY R57 V64 K107 SER ARG THR LYS M12 H157 Q193 LEU

- Chain SI:  90% 10%

MET	G2	L121	GLY	ARG	LYS	LYS	GLY	ALA	LYS	LEU	THR	PRO	GLU	GLU	GLU	GLU	ILE	L137	K203	ALA	ARG	LYS	GLY	LYS
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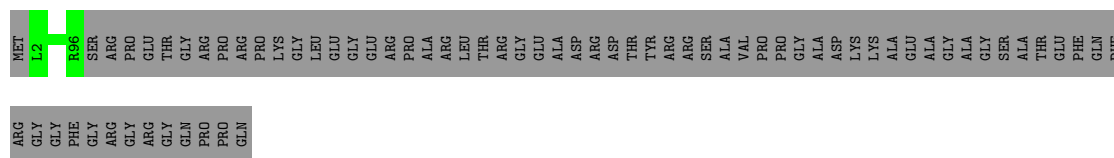
- Chain SJ:  89% • 9%

MET	P2	R17	K66	R108	R109	L110	N177	ALA	LYS	LYS	GLY	GLN	GLY	GLY	ALA	ALA	ALA	GLY	GLY	ASP	ASP	GLU	GLU	GLU	ASP
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- 



Chain SK:  58% 42%



- Molecule 61: 40S ribosomal protein S11

Chain SL:  89% 11%




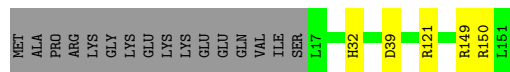
- Molecule 62: 40S ribosomal protein S13

Chain SN:  99% ..




- Molecule 63: 40S ribosomal protein S14

Chain SO:  86% . 11%



- Molecule 64: 40S ribosomal protein S15

Chain SP:  85% .. 12%



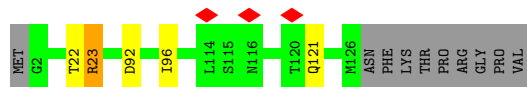
- Molecule 65: 40S ribosomal protein S16

Chain SQ:  95% ..



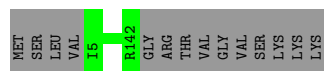
- Molecule 66: 40S ribosomal protein S17

Chain SR:  89% .. 7%



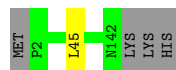
- Molecule 67: 40S ribosomal protein S18

Chain SS:  91% 9%




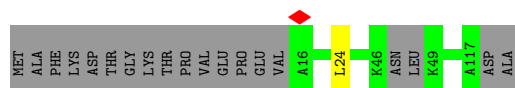
- Molecule 68: 40S ribosomal protein S19

Chain ST:  97% ..



- Molecule 69: 40S ribosomal protein S20

Chain SU:  83% 16%



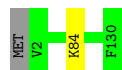
- Molecule 70: 40S ribosomal protein S21

Chain SV:  100%

There are no outlier residues recorded for this chain.

- Molecule 71: 40S ribosomal protein S15a

Chain SW:  98% ..




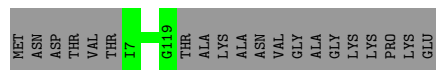
- Molecule 72: 40S ribosomal protein S23

Chain SX:  97% ..



- Molecule 73: 40S ribosomal protein S24

Chain SY:  85% 15%



- Molecule 74: 40S ribosomal protein S25

MET	PRO	PRO	LYS	ASP	ASP	LYS	LYS	LYS	ASP	ALA	GLY	LYS	SER	LYS	ALA	LYS	LYS	ASP	ASP	PRO	VAL	ASN	LYS	SER	GLY	GLY	LYS	ALA	LYS	LYS	LYS	LYS	TRP	SER	LYS	LYS	GLY	LYS	VAL	ARG	ASP	LYS	L44	I68	T113	LYS	GLY	GLY	ASP	ALA	PRO	ALA	ALA	GLY	GLU	ASP	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain Sa:  85% . 14%

MET
T2
V40
R100
PHE
ARG
PRO
ALA
GLY
ALA
ALA
PRO
ARG
PRO
PRO
PRO
LYS
PRO
MET

- Chain Sb:  94% 5%




Diagram illustrating the structure of the P2 domain of the P22 bacteriophage tail. The structure is shown as a yellow ribbon model. The P2 domain is highlighted in yellow, and the MET domain is highlighted in grey. The P2 domain is labeled with residues K20, K21, G39, T52, and H84.

- Chain Sc: 

MET  
ASP  
THR  
SER  
ARG  
VAL  
GLN  
P8  
L59  
L68  
ARG

- Chain Sd:  89% 7%

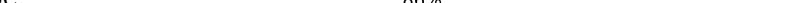
MET  
GLY  
HIS  
GLN

Q5

C24

D49

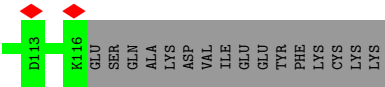
D56

- Chain Se:  86% 14%

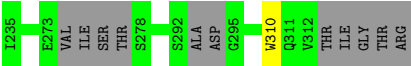
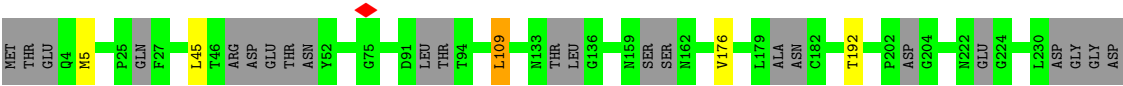
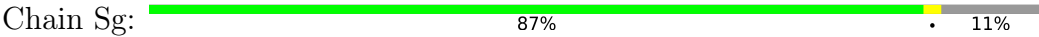
LYS
VAL
H76
P120
THR
PHE
GLY
LYS
LYS
K126
N131
SER

- Chain Sf: 

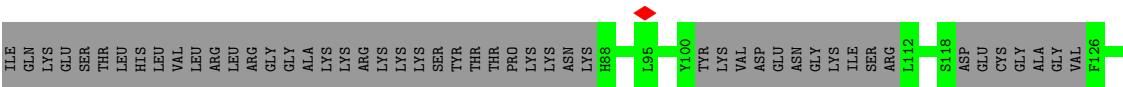
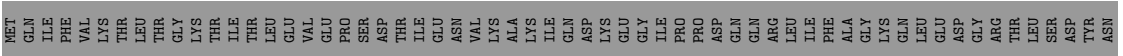
Amino Acid	Percentage
MET	10%
ALA	10%
GLU	10%
GLY	10%
ILE	10%
ALA	10%
ALA	10%
GLY	10%
GLY	10%
VAL	10%
MET	10%
ASP	10%
VAL	10%
ASN	10%
T16	10%
R33	20%
K40	30%
A41	30%
LEU	30%
ASP	30%
LYS	30%
ARG	30%
Q46	30%
C50	40%
N55	40%
E71	40%
HIS	40%
GLN	40%
ILE	40%
ASN	40%
LEU	40%
ILE	40%
K78	40%
L85	40%
GLY	40%
GLU	40%
W88	40%
L91	40%
CYS	40%
LYS	40%
ILE	40%
ASP	40%
ASP	40%
GLU	40%
GLY	40%
LYS	40%
PRO	40%
ARG	40%
LYS	40%
V103	40%
V104	40%



• Molecule 81: Receptor of activated protein C kinase 1



• Molecule 82: Ubiquitin-40S ribosomal protein S27a



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12694	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	0.098	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.009	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: 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	0.55	0/285	1.86	15/438 (3.4%)
2	B4	0.45	0/1795	0.98	1/2798 (0.0%)
3	D4	0.41	0/1741	1.19	19/2709 (0.7%)
4	L5	0.71	0/85684	0.98	163/133644 (0.1%)
5	L7	0.69	0/2858	0.90	1/4455 (0.0%)
6	L8	0.72	0/3701	0.98	10/5766 (0.2%)
7	LA	0.47	1/1924 (0.1%)	0.63	1/2581 (0.0%)
8	LB	0.42	0/3168	0.57	1/4253 (0.0%)
9	LC	0.40	0/2948	0.57	1/3960 (0.0%)
10	LD	0.39	0/2333	0.57	0/3139
11	LE	0.38	0/1747	0.60	0/2354
12	LF	0.43	0/1879	0.61	3/2507 (0.1%)
13	LG	0.38	0/1765	0.60	2/2400 (0.1%)
14	LH	0.37	0/1458	0.59	0/1973
15	LI	0.38	0/1619	0.53	0/2170
16	LJ	0.36	0/1249	0.57	0/1690
17	LL	0.39	0/1611	0.57	0/2167
18	LM	0.39	0/1119	0.54	0/1501
19	LN	0.47	0/1738	0.59	2/2328 (0.1%)
20	LO	0.42	0/1645	0.54	1/2205 (0.0%)
21	LP	0.42	0/1229	0.53	0/1655
22	LQ	0.42	0/1517	0.55	0/2030
23	LR	0.35	0/1428	0.53	0/1897
24	LS	0.41	0/1476	0.57	1/1983 (0.1%)
25	LT	0.42	0/1296	0.54	0/1734
26	LU	0.35	0/782	0.61	0/1057
27	LV	0.42	0/968	0.54	0/1303
28	LW	0.35	0/798	0.51	0/1081
29	LX	0.38	0/967	0.56	0/1304
30	LY	0.40	0/1101	0.52	0/1469
31	LZ	0.39	0/1105	0.48	0/1475
32	La	0.43	0/1173	0.55	0/1568

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Lb	0.34	0/509	0.43	0/675
34	Lc	0.41	0/726	0.61	1/977 (0.1%)
35	Ld	0.38	0/871	0.56	0/1176
36	Le	0.39	0/1063	0.50	0/1418
37	Lf	0.46	0/883	0.66	1/1185 (0.1%)
38	Lg	0.40	0/861	0.56	0/1153
39	Lh	0.35	0/983	0.52	1/1304 (0.1%)
40	Li	0.36	0/808	0.53	0/1074
41	Lj	0.42	0/716	0.52	0/948
42	Lk	0.38	0/534	0.55	0/712
43	Ll	0.38	0/450	0.55	0/595
44	Lm	0.37	0/399	0.58	0/532
45	Ln	0.32	0/231	0.51	0/294
46	Lo	0.41	0/787	0.54	0/1042
47	Lp	0.43	0/699	0.57	0/931
48	Lr	0.41	0/997	0.55	1/1341 (0.1%)
49	S2	0.59	0/39578	1.01	116/61671 (0.2%)
50	SA	0.36	0/1612	0.58	0/2203
51	SB	0.35	0/1654	0.54	0/2227
52	SC	0.37	0/1626	0.58	0/2211
53	SD	0.35	0/1499	0.58	1/2041 (0.0%)
54	SE	0.35	0/1933	0.57	0/2623
55	SF	0.33	0/1385	0.51	0/1870
56	SG	0.31	0/1562	0.57	0/2099
57	SH	0.34	0/1362	0.57	0/1831
58	SI	0.34	0/1477	0.54	0/1990
59	SJ	0.32	0/1432	0.57	0/1926
60	SK	0.32	0/759	0.53	0/1036
61	SL	0.40	0/1159	0.57	0/1555
62	SN	0.34	0/1223	0.58	1/1644 (0.1%)
63	SO	0.37	0/1016	0.61	0/1363
64	SP	0.35	0/1020	0.58	0/1369
65	SQ	0.34	0/1096	0.60	0/1473
66	SR	0.35	0/890	0.62	0/1207
67	SS	0.34	0/1098	0.58	0/1480
68	ST	0.32	0/1012	0.58	1/1371 (0.1%)
69	SU	0.31	0/758	0.60	1/1023 (0.1%)
70	SV	0.34	0/596	0.52	0/800
71	SW	0.40	0/1044	0.55	0/1398
72	SX	0.36	0/1066	0.67	0/1434
73	SY	0.32	0/871	0.54	0/1169
74	SZ	0.34	0/493	0.71	1/672 (0.1%)
75	Sa	0.38	0/775	0.54	0/1042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Sb	0.34	0/631	0.67	0/853
77	Sc	0.32	0/432	0.70	0/582
78	Sd	0.40	0/430	0.54	0/573
79	Se	0.29	0/390	0.50	0/515
80	Sf	0.27	0/485	0.56	0/661
81	Sg	0.33	0/1993	0.68	2/2730 (0.1%)
82	sh	0.27	0/270	0.55	0/359
All	All	0.57	1/222251 (0.0%)	0.87	348/327952 (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	1
10	LD	0	1
11	LE	0	2
16	LJ	0	1
17	LL	0	1
18	LM	0	1
21	LP	0	1
24	LS	0	2
27	LV	0	1
29	LX	0	1
64	SP	0	2
65	SQ	0	1
66	SR	0	5
72	SX	0	2
76	Sb	0	1
77	Sc	0	1
81	Sg	0	2
All	All	0	26

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	LA	118	GLU	C-N	-5.98	1.20	1.34

The worst 5 of 348 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A4	52	U	C2-N1-C1'	11.69	131.73	117.70
1	A4	52	U	N1-C2-O2	10.74	130.32	122.80
49	S2	1453	C	N1-C2-O2	10.59	125.25	118.90
49	S2	1453	C	C2-N1-C1'	10.55	130.41	118.80
1	A4	52	U	N3-C2-O2	-10.45	114.88	122.20

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LA	247	ARG	Peptide
10	LD	231	VAL	Peptide
11	LE	98	GLY	Peptide
11	LE	99	ASP	Peptide
16	LJ	122	SER	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	246/257 (96%)	212 (86%)	32 (13%)	2 (1%)	19	58
8	LB	389/403 (96%)	360 (92%)	29 (8%)	0	100	100
9	LC	363/427 (85%)	337 (93%)	25 (7%)	1 (0%)	41	75
10	LD	291/297 (98%)	271 (93%)	18 (6%)	2 (1%)	22	61
11	LE	214/288 (74%)	188 (88%)	25 (12%)	1 (0%)	29	68
12	LF	223/248 (90%)	208 (93%)	15 (7%)	0	100	100
13	LG	225/266 (85%)	201 (89%)	24 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	LH	187/192 (97%)	171 (91%)	16 (9%)	0	100	100
15	LI	199/214 (93%)	179 (90%)	20 (10%)	0	100	100
16	LJ	165/178 (93%)	153 (93%)	11 (7%)	1 (1%)	25	64
17	LL	202/211 (96%)	181 (90%)	21 (10%)	0	100	100
18	LM	134/215 (62%)	121 (90%)	12 (9%)	1 (1%)	22	61
19	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
20	LO	199/203 (98%)	194 (98%)	5 (2%)	0	100	100
21	LP	151/184 (82%)	138 (91%)	13 (9%)	0	100	100
22	LQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
23	LR	173/196 (88%)	168 (97%)	5 (3%)	0	100	100
24	LS	173/176 (98%)	154 (89%)	17 (10%)	2 (1%)	13	50
25	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
26	LU	99/128 (77%)	93 (94%)	6 (6%)	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%)	105 (89%)	13 (11%)	0	100	100
30	LY	132/145 (91%)	119 (90%)	13 (10%)	0	100	100
31	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
32	La	142/148 (96%)	131 (92%)	11 (8%)	0	100	100
33	Lb	61/159 (38%)	57 (93%)	4 (7%)	0	100	100
34	Lc	91/115 (79%)	86 (94%)	5 (6%)	0	100	100
35	Ld	105/125 (84%)	96 (91%)	9 (9%)	0	100	100
36	Le	125/135 (93%)	119 (95%)	6 (5%)	0	100	100
37	Lf	107/110 (97%)	95 (89%)	12 (11%)	0	100	100
38	Lg	108/117 (92%)	97 (90%)	11 (10%)	0	100	100
39	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
40	Li	99/105 (94%)	97 (98%)	2 (2%)	0	100	100
41	Lj	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
42	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
43	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
44	Lm	48/128 (38%)	45 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	96/106 (91%)	87 (91%)	9 (9%)	0	100	100
47	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
48	Lr	123/137 (90%)	113 (92%)	10 (8%)	0	100	100
50	SA	210/295 (71%)	191 (91%)	19 (9%)	0	100	100
51	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
52	SC	215/293 (73%)	206 (96%)	9 (4%)	0	100	100
53	SD	207/243 (85%)	188 (91%)	18 (9%)	1 (0%)	29	68
54	SE	255/263 (97%)	225 (88%)	30 (12%)	0	100	100
55	SF	176/204 (86%)	167 (95%)	9 (5%)	0	100	100
56	SG	200/249 (80%)	186 (93%)	14 (7%)	0	100	100
57	SH	168/194 (87%)	149 (89%)	19 (11%)	0	100	100
58	SI	183/208 (88%)	165 (90%)	18 (10%)	0	100	100
59	SJ	174/194 (90%)	163 (94%)	9 (5%)	2 (1%)	14	52
60	SK	93/165 (56%)	83 (89%)	10 (11%)	0	100	100
61	SL	136/158 (86%)	123 (90%)	13 (10%)	0	100	100
62	SN	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
63	SO	133/151 (88%)	118 (89%)	15 (11%)	0	100	100
64	SP	123/145 (85%)	109 (89%)	12 (10%)	2 (2%)	9	43
65	SQ	139/146 (95%)	133 (96%)	6 (4%)	0	100	100
66	SR	123/135 (91%)	102 (83%)	20 (16%)	1 (1%)	19	58
67	SS	136/152 (90%)	118 (87%)	18 (13%)	0	100	100
68	ST	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
69	SU	96/119 (81%)	87 (91%)	9 (9%)	0	100	100
70	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
71	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
72	SX	139/143 (97%)	120 (86%)	18 (13%)	1 (1%)	22	61
73	SY	111/133 (84%)	104 (94%)	7 (6%)	0	100	100
74	SZ	68/125 (54%)	61 (90%)	7 (10%)	0	100	100
75	Sa	97/115 (84%)	83 (86%)	14 (14%)	0	100	100
76	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	5	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	Sc	59/69 (86%)	49 (83%)	10 (17%)	0	100	100
78	Sd	50/56 (89%)	46 (92%)	4 (8%)	0	100	100
79	Se	47/59 (80%)	41 (87%)	6 (13%)	0	100	100
80	Sf	68/132 (52%)	59 (87%)	9 (13%)	0	100	100
81	Sg	259/317 (82%)	216 (83%)	43 (17%)	0	100	100
82	sh	35/156 (22%)	30 (86%)	5 (14%)	0	100	100
All	All	10821/12688 (85%)	9894 (91%)	908 (8%)	19 (0%)	50	81

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	LC	111	TRP
24	LS	164	LYS
64	SP	38	SER
66	SR	23	ARG
72	SX	10	ALA

### 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	187/199 (94%)	185 (99%)	2 (1%)	73	88
8	LB	324/349 (93%)	322 (99%)	2 (1%)	86	94
9	LC	301/348 (86%)	296 (98%)	5 (2%)	60	82
10	LD	218/250 (87%)	217 (100%)	1 (0%)	88	94
11	LE	179/252 (71%)	177 (99%)	2 (1%)	73	88
12	LF	187/215 (87%)	185 (99%)	2 (1%)	73	88
13	LG	167/223 (75%)	166 (99%)	1 (1%)	86	94
14	LH	150/171 (88%)	149 (99%)	1 (1%)	84	93
15	LI	156/181 (86%)	156 (100%)	0	100	100
16	LJ	113/149 (76%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LL	152/177 (86%)	151 (99%)	1 (1%)	84	93
18	LM	110/161 (68%)	110 (100%)	0	100	100
19	LN	169/172 (98%)	168 (99%)	1 (1%)	86	94
20	LO	163/174 (94%)	163 (100%)	0	100	100
21	LP	124/163 (76%)	124 (100%)	0	100	100
22	LQ	159/165 (96%)	158 (99%)	1 (1%)	86	94
23	LR	141/175 (81%)	140 (99%)	1 (1%)	84	93
24	LS	151/157 (96%)	151 (100%)	0	100	100
25	LT	130/140 (93%)	129 (99%)	1 (1%)	81	91
26	LU	77/115 (67%)	76 (99%)	1 (1%)	69	86
27	LV	94/107 (88%)	92 (98%)	2 (2%)	53	79
28	LW	54/126 (43%)	53 (98%)	1 (2%)	57	80
29	LX	98/133 (74%)	98 (100%)	0	100	100
30	LY	116/135 (86%)	114 (98%)	2 (2%)	60	82
31	LZ	109/118 (92%)	108 (99%)	1 (1%)	78	90
32	La	116/121 (96%)	116 (100%)	0	100	100
33	Lb	49/126 (39%)	49 (100%)	0	100	100
34	Lc	76/97 (78%)	74 (97%)	2 (3%)	46	74
35	Ld	88/110 (80%)	88 (100%)	0	100	100
36	Le	113/121 (93%)	113 (100%)	0	100	100
37	Lf	85/89 (96%)	85 (100%)	0	100	100
38	Lg	88/100 (88%)	88 (100%)	0	100	100
39	Lh	100/110 (91%)	99 (99%)	1 (1%)	76	88
40	Li	79/89 (89%)	76 (96%)	3 (4%)	33	65
41	Lj	72/80 (90%)	72 (100%)	0	100	100
42	Lk	52/65 (80%)	52 (100%)	0	100	100
43	Ll	46/48 (96%)	46 (100%)	0	100	100
44	Lm	42/116 (36%)	42 (100%)	0	100	100
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	79/94 (84%)	79 (100%)	0	100	100
47	Lp	70/75 (93%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	Lr	103/121 (85%)	102 (99%)	1 (1%)	76	88
50	SA	147/243 (60%)	144 (98%)	3 (2%)	55	79
51	SB	162/231 (70%)	162 (100%)	0	100	100
52	SC	155/225 (69%)	152 (98%)	3 (2%)	57	80
53	SD	126/202 (62%)	124 (98%)	2 (2%)	62	83
54	SE	176/225 (78%)	175 (99%)	1 (1%)	86	94
55	SF	133/170 (78%)	131 (98%)	2 (2%)	65	84
56	SG	136/218 (62%)	135 (99%)	1 (1%)	84	93
57	SH	134/174 (77%)	132 (98%)	2 (2%)	65	84
58	SI	141/180 (78%)	141 (100%)	0	100	100
59	SJ	140/168 (83%)	138 (99%)	2 (1%)	67	85
60	SK	68/136 (50%)	68 (100%)	0	100	100
61	SL	124/142 (87%)	124 (100%)	0	100	100
62	SN	127/131 (97%)	127 (100%)	0	100	100
63	SO	103/119 (87%)	98 (95%)	5 (5%)	25	59
64	SP	103/130 (79%)	102 (99%)	1 (1%)	76	88
65	SQ	105/121 (87%)	103 (98%)	2 (2%)	57	80
66	SR	77/122 (63%)	77 (100%)	0	100	100
67	SS	103/132 (78%)	103 (100%)	0	100	100
68	ST	82/115 (71%)	82 (100%)	0	100	100
69	SU	78/107 (73%)	78 (100%)	0	100	100
70	SV	53/67 (79%)	53 (100%)	0	100	100
71	SW	110/113 (97%)	109 (99%)	1 (1%)	78	90
72	SX	101/115 (88%)	101 (100%)	0	100	100
73	SY	79/115 (69%)	79 (100%)	0	100	100
74	SZ	40/103 (39%)	40 (100%)	0	100	100
75	Sa	79/98 (81%)	78 (99%)	1 (1%)	69	86
76	Sb	64/76 (84%)	63 (98%)	1 (2%)	62	83
77	Sc	41/62 (66%)	41 (100%)	0	100	100
78	Sd	42/49 (86%)	40 (95%)	2 (5%)	25	60
79	Se	37/48 (77%)	37 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Sf	30/108 (28%)	29 (97%)	1 (3%)	38	68
81	Sg	167/275 (61%)	164 (98%)	3 (2%)	59	81
82	sh	17/140 (12%)	17 (100%)	0	100	100
All	All	8390/10801 (78%)	8322 (99%)	68 (1%)	82	91

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	SQ	20	THR
71	SW	84	LYS
81	Sg	5	MET
28	LW	78	PHE
27	LV	90	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
43	Ll	20	ASN
52	SC	136	HIS
43	Ll	38	ASN
48	Lr	85	ASN
54	SE	179	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A4	12/16 (75%)	8 (66%)	1 (8%)
2	B4	74/75 (98%)	17 (22%)	0
3	D4	70/76 (92%)	29 (41%)	2 (2%)
4	L5	3555/5070 (70%)	895 (25%)	13 (0%)
49	S2	1644/1869 (87%)	505 (30%)	10 (0%)
5	L7	119/120 (99%)	20 (16%)	0
6	L8	155/156 (99%)	37 (23%)	2 (1%)
All	All	5629/7382 (76%)	1511 (26%)	28 (0%)

5 of 1511 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A4	43	U

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Mol	Chain	Res	Type
1	A4	46	U
1	A4	48	U
1	A4	50	U
1	A4	51	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L5	4699	U
49	S2	1860	A
6	L8	87	G
49	S2	1585	U
6	L8	86	U

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 167 ligands modelled in this entry, 167 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.



## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	LA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	LA	118:GLU	C	119:LYS	N	1.20

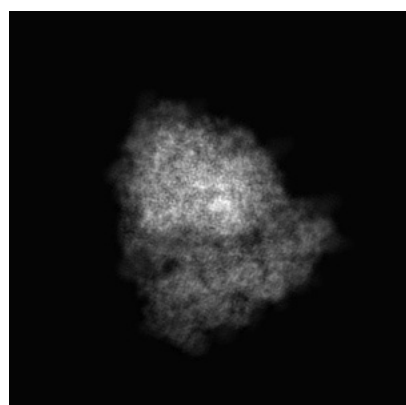
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10690. These allow visual inspection of the internal detail of the map and identification of artifacts.

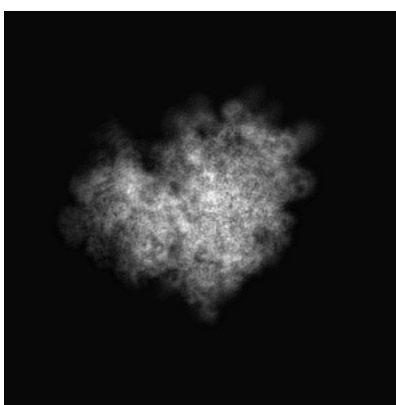
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

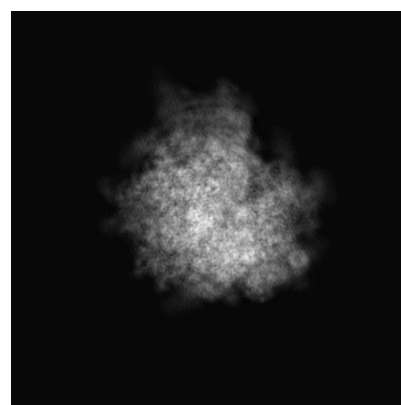
#### 6.1.1 Primary map



X



Y

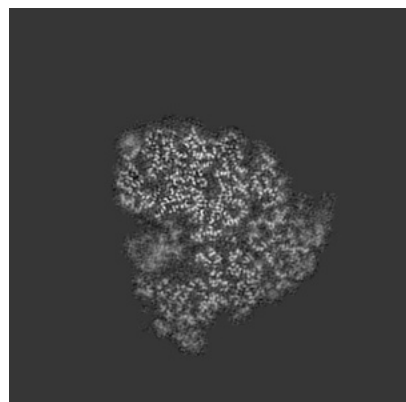


Z

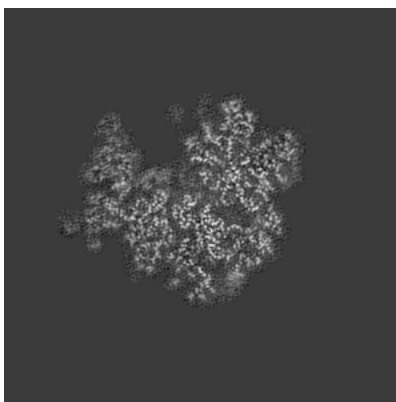
The images above show the map projected in three orthogonal directions.

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

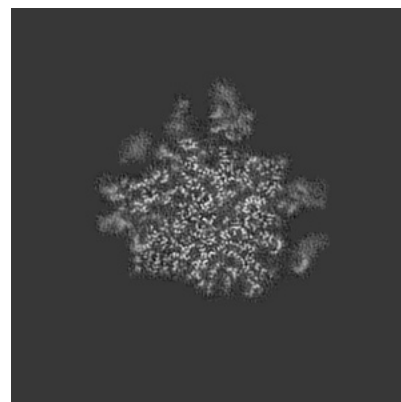
#### 6.2.1 Primary map



X Index: 275



Y Index: 275

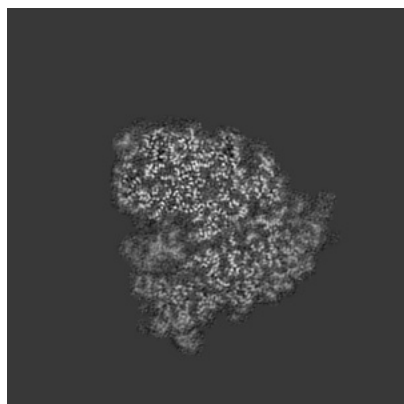


Z Index: 275

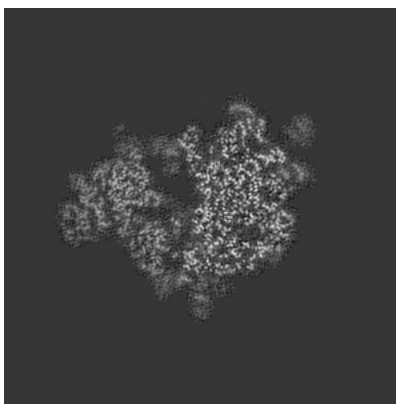
The images above show central slices of the map in three orthogonal directions.

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

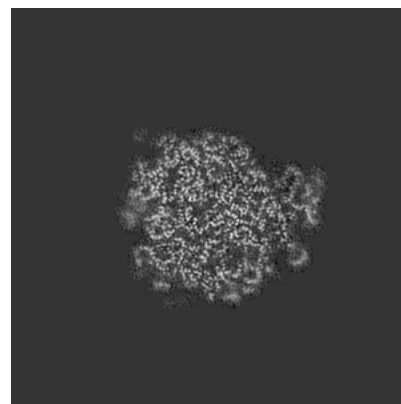
### 6.3.1 Primary map



X Index: 277



Y Index: 244

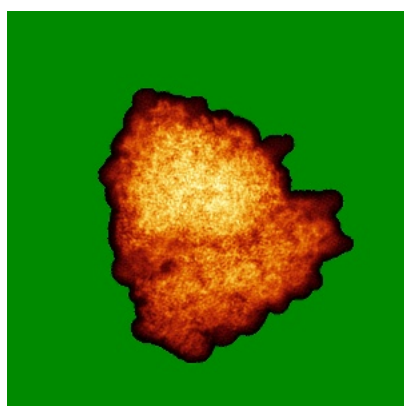


Z Index: 308

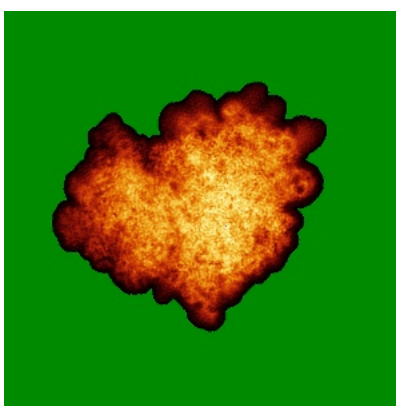
The images above show the largest variance slices of the map in three orthogonal directions.

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

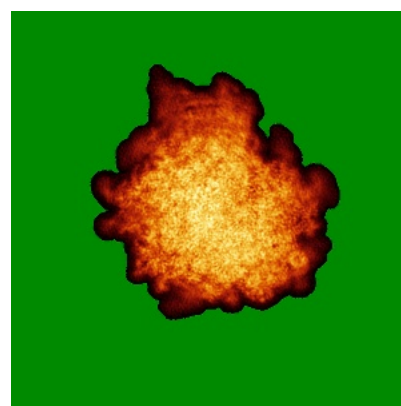
### 6.4.1 Primary map



X



Y



Z

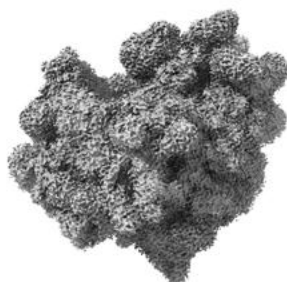
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

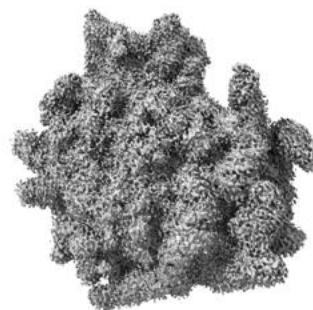
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

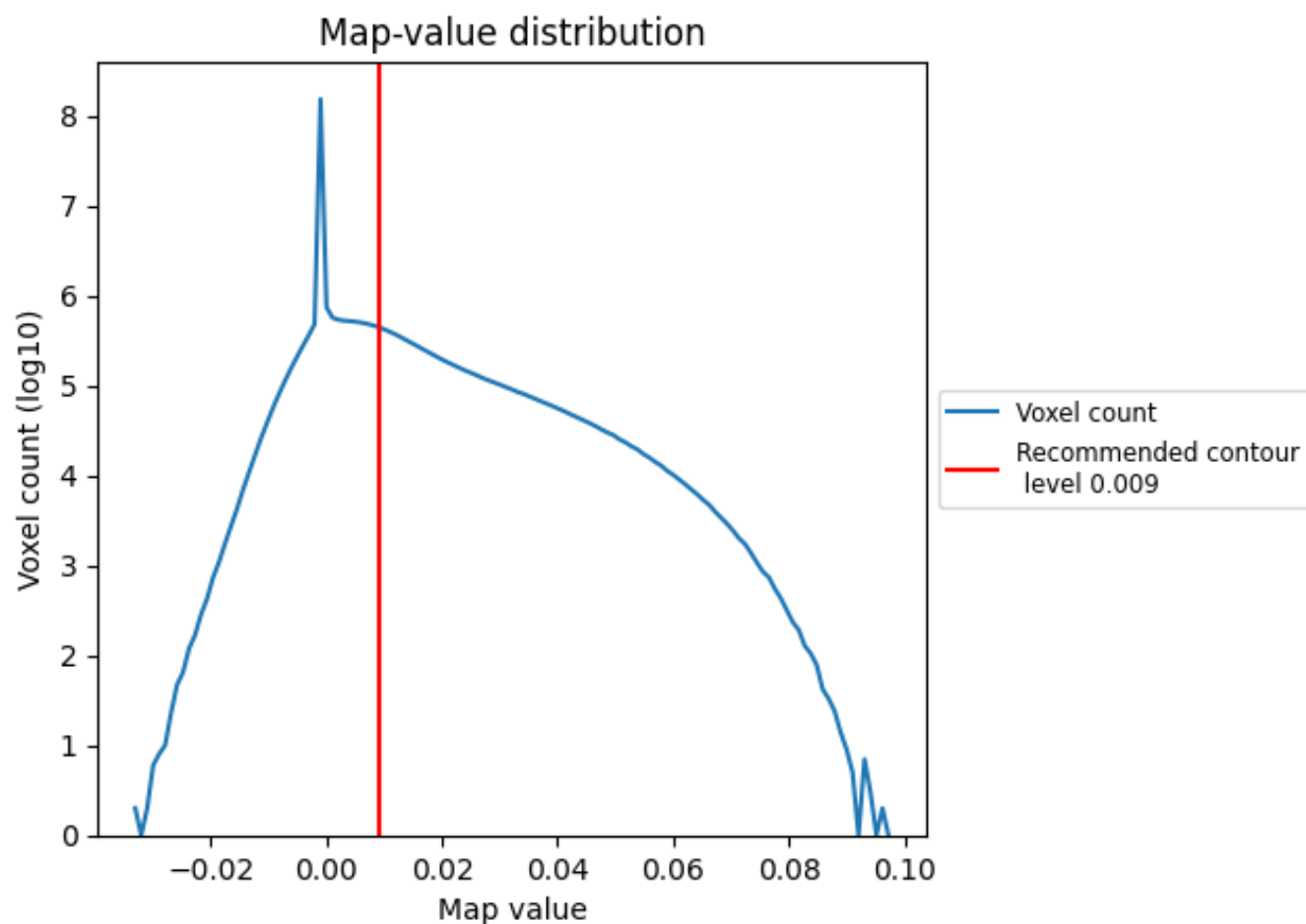
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

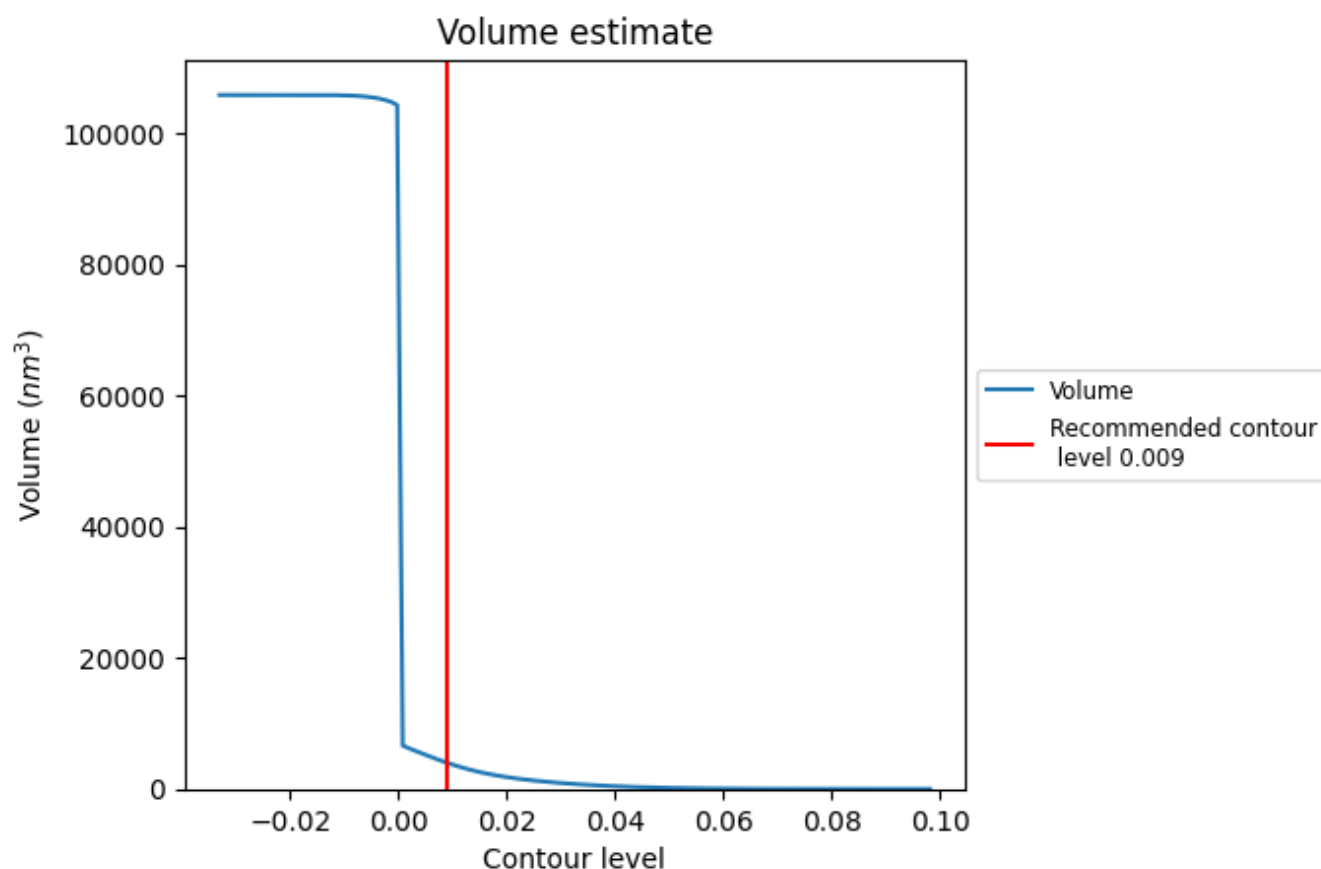
This section contains the results of statistical analysis of the map.

### 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.

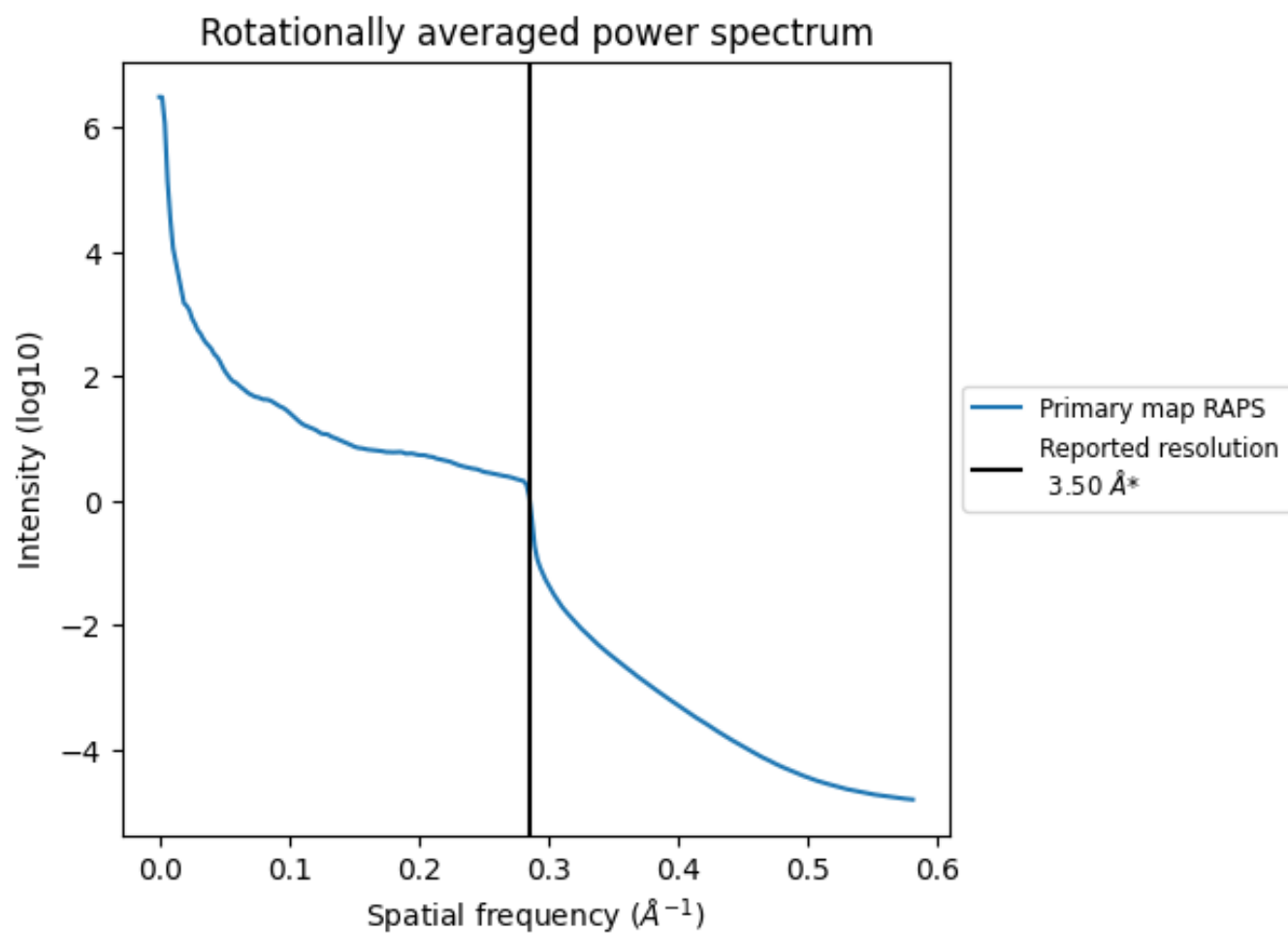
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4003  $\text{nm}^3$ ; this corresponds to an approximate mass of 3616 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 0.286 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

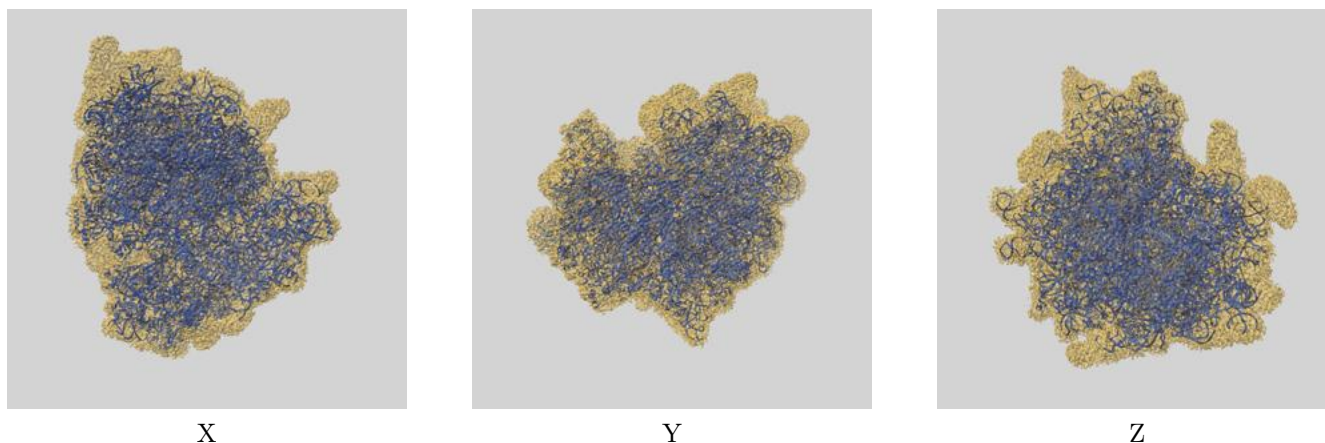
This section was not generated. No FSC curve or half-maps provided.



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

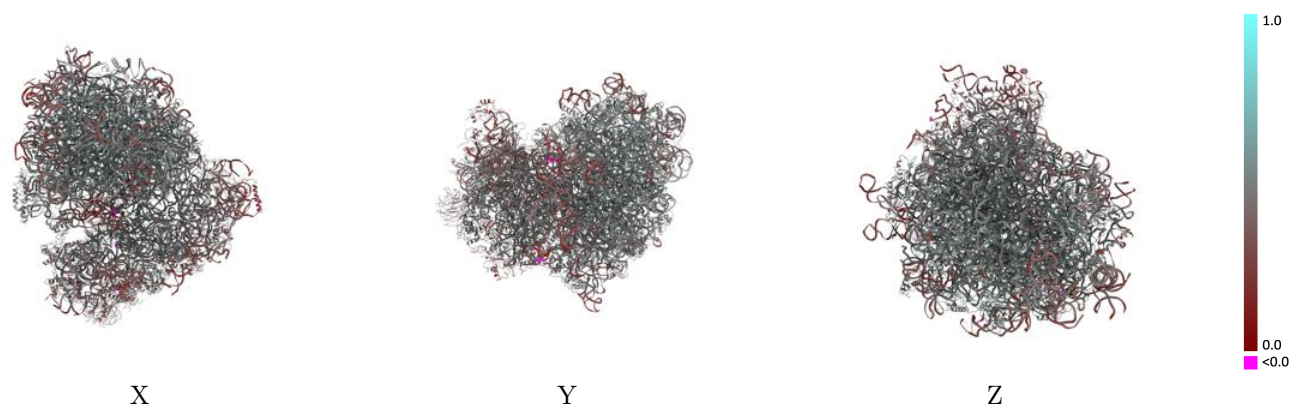
This section contains information regarding the fit between EMDB map EMD-10690 and PDB model 6Y57. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

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



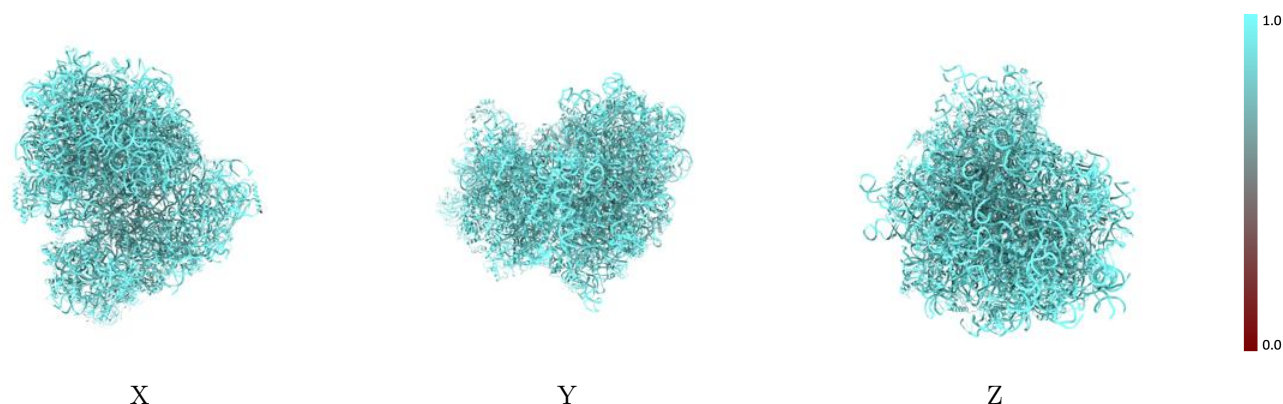
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



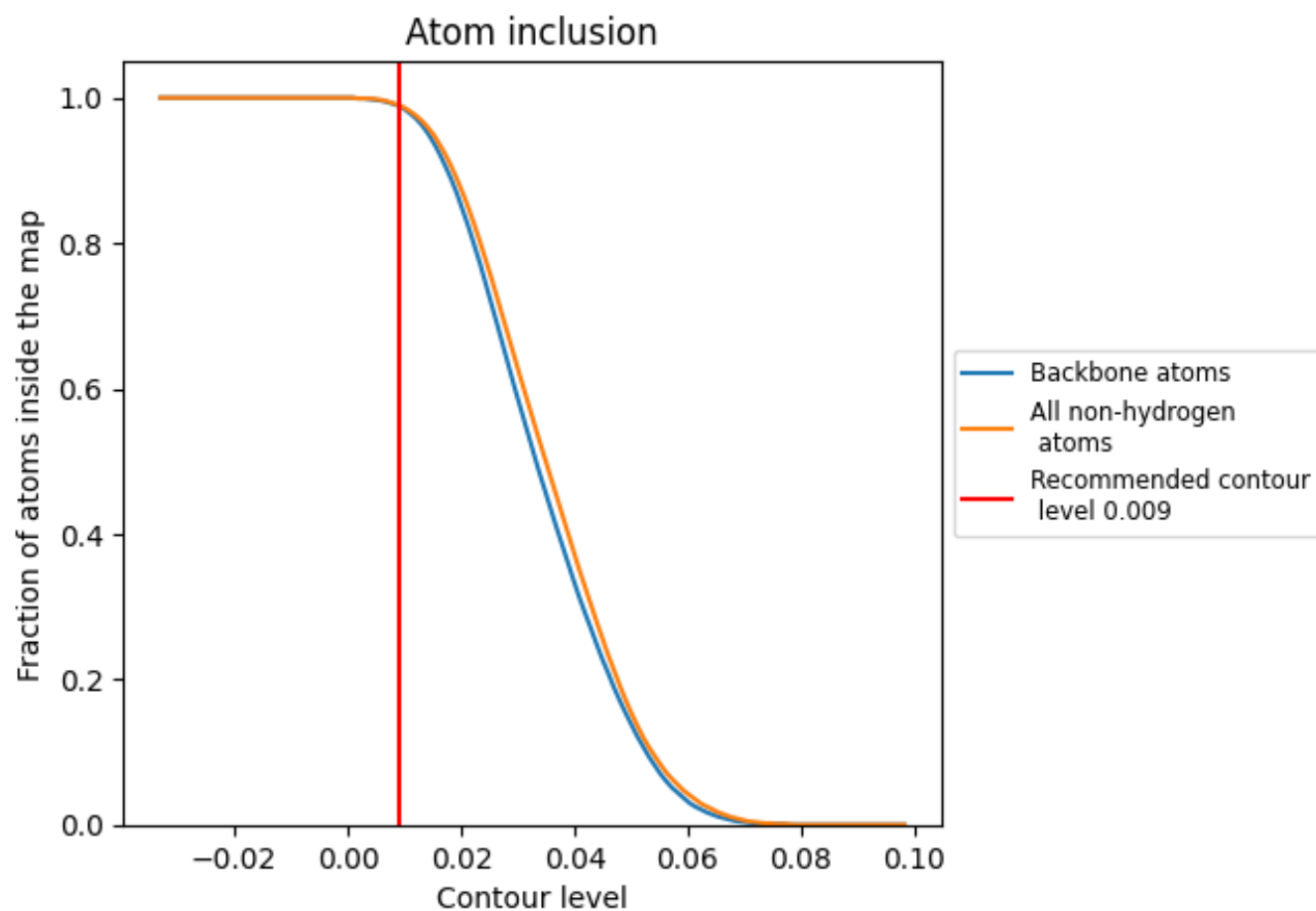
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.009).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9900	 0.4620
A4	 0.9810	 0.4280
B4	 0.9960	 0.3380
D4	 0.8410	 0.2300
L5	 0.9960	 0.4640
L7	 0.9990	 0.4870
L8	 0.9940	 0.4760
LA	 0.9950	 0.5260
LB	 0.9900	 0.5090
LC	 0.9950	 0.5220
LD	 0.9930	 0.4790
LE	 0.9950	 0.4900
LF	 0.9920	 0.5110
LG	 0.9890	 0.4780
LH	 0.9880	 0.4890
LI	 0.9900	 0.5120
LJ	 0.9960	 0.4710
LL	 0.9950	 0.5110
LM	 0.9980	 0.4990
LN	 0.9960	 0.5370
LO	 0.9940	 0.5100
LP	 0.9970	 0.5280
LQ	 0.9970	 0.5240
LR	 0.9930	 0.4950
LS	 0.9950	 0.5140
LT	 0.9900	 0.5010
LU	 0.9960	 0.4520
LV	 0.9940	 0.5170
LW	 0.9620	 0.4180
LX	 0.9910	 0.5020
LY	 0.9920	 0.5110
LZ	 0.9920	 0.5090
La	 0.9930	 0.5370
Lb	 1.0000	 0.5000
Lc	 0.9860	 0.4910















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Chain	Atom inclusion	Q-score
Ld	 0.9950	 0.5080
Le	 0.9990	 0.5320
Lf	 0.9960	 0.5320
Lg	 0.9850	 0.5060
Lh	 0.9930	 0.5060
Li	 0.9900	 0.4900
Lj	 0.9990	 0.5350
Lk	 0.9850	 0.4720
Ll	 0.9980	 0.5300
Lm	 0.9970	 0.5140
Ln	 0.9810	 0.5040
Lo	 1.0000	 0.5270
Lp	 0.9960	 0.5200
Lr	 0.9990	 0.5220
S2	 0.9960	 0.4310
SA	 0.9680	 0.4580
SB	 0.9890	 0.4730
SC	 0.9870	 0.4790
SD	 0.9720	 0.4260
SE	 0.9910	 0.4220
SF	 0.9820	 0.4580
SG	 0.9920	 0.4130
SH	 0.9420	 0.4160
SI	 0.9930	 0.4310
SJ	 0.9920	 0.4060
SK	 0.9800	 0.4150
SL	 0.9830	 0.4660
SN	 0.9860	 0.4720
SO	 0.9820	 0.4650
SP	 0.9870	 0.4430
SQ	 0.9750	 0.4270
SR	 0.9260	 0.4140
SS	 0.9820	 0.4440
ST	 0.9890	 0.4450
SU	 0.9730	 0.4130
SV	 0.9840	 0.4640
SW	 0.9870	 0.4950
SX	 0.9810	 0.4580
SY	 0.9920	 0.4010
SZ	 0.9560	 0.3770
Sa	 0.9910	 0.4960
Sb	 0.9750	 0.4490

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Chain	Atom inclusion	Q-score
Sc	 0.9790	 0.4400
Sd	 0.9880	 0.4710
Se	 0.9950	 0.4200
Sf	 0.8140	 0.3190
Sg	 0.9640	 0.3780
sh	 0.9010	 0.3040