



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:51 AM UTC

PDB ID : 9R9P / pdb_00009r9p
EMDB ID : EMD-53861
Title : Yeast 80S with nascent chain in complex with Ssb1-ADP in the S2 state
Authors : Grundmann, L.; Zhang, Y.; Grishkovskaya, I.; Rospert, S.; Haselbach, D.
Deposited on : 2025-05-20
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

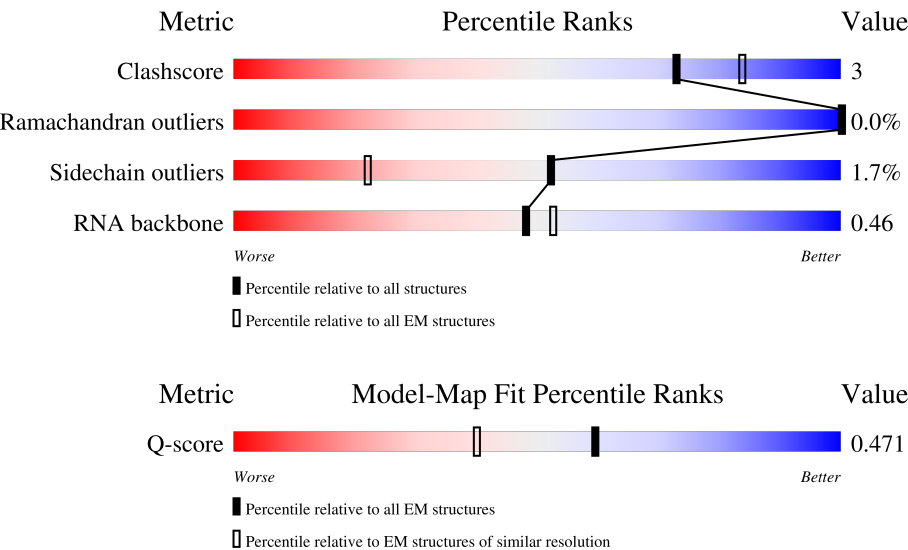
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



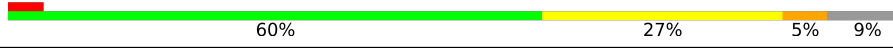
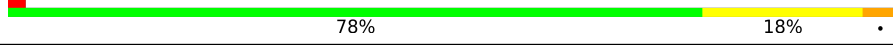
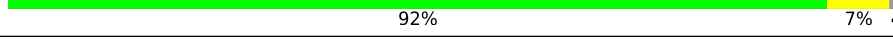
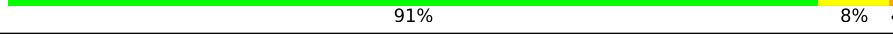
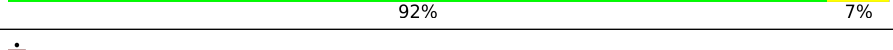
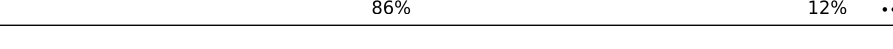
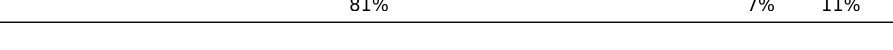
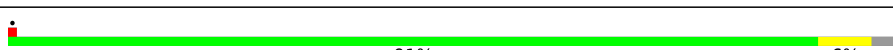
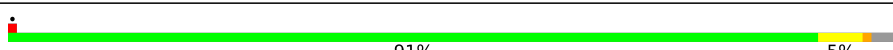
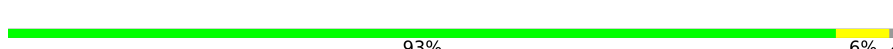
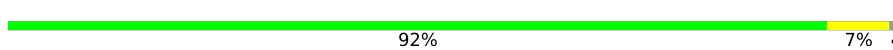
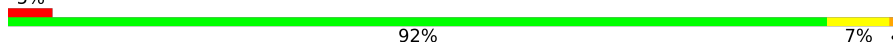
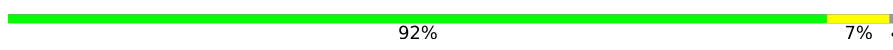
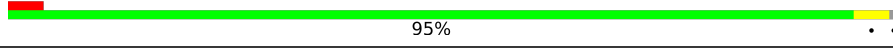
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	5	234	97%
2	6	76	8% 58% 36% 7%
3	A	613	12% 33% 65%

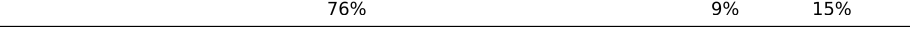
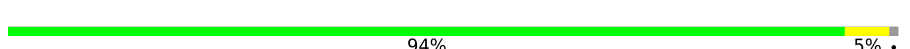
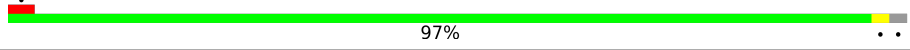
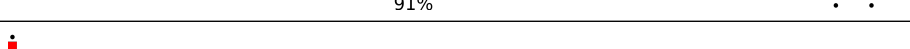
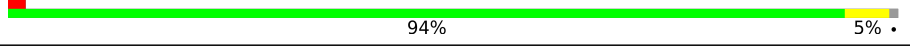
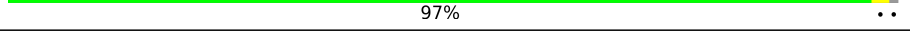
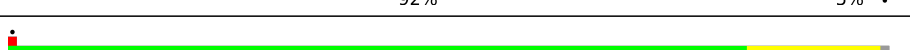
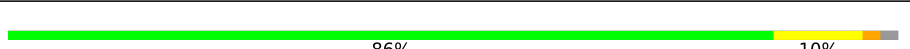
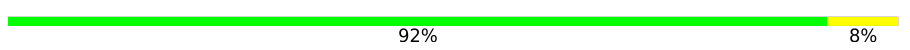
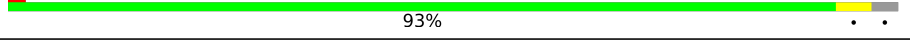
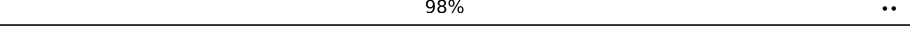
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Mol	Chain	Length	Quality of chain
4	B	78	
5	C1	3396	
6	C2	1800	
7	C3	158	
8	C4	121	
9	LA	254	
10	LB	387	
11	LC	362	
12	LD	297	
13	LE	176	
14	LF	244	
15	LG	256	
16	LH	191	
17	LI	221	
18	LJ	174	
19	LL	199	
20	LM	138	
21	LN	204	
22	LO	199	
23	LP	184	
24	LQ	186	
25	LR	189	
26	LS	172	
27	LT	160	
28	LU	121	

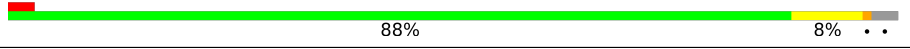
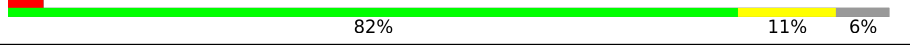
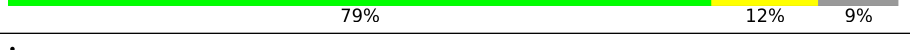
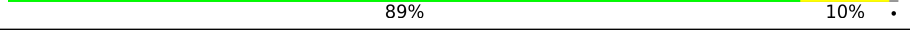
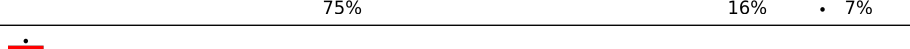
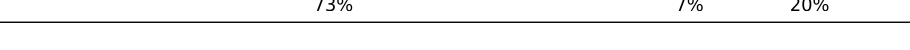
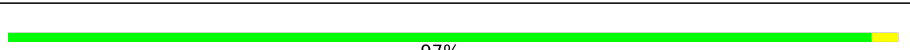
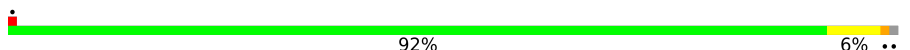
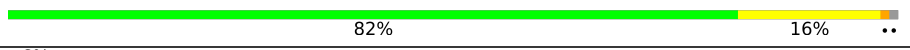
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Mol	Chain	Length	Quality of chain
29	LV	137	
30	LW	155	
31	LX	142	
32	LY	127	
33	LZ	136	
34	La	149	
35	Lb	59	
36	Lc	105	
37	Ld	113	
38	Le	130	
39	Lf	107	
40	Lg	121	
41	Lh	120	
42	Li	100	
43	Lj	88	
44	Lk	78	
45	Ll	51	
46	Ln	25	
47	Lo	106	
48	Lp	92	
49	SA	252	
50	SB	255	
51	SC	254	
52	SD	240	
53	SE	261	

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Mol	Chain	Length	Quality of chain
54	SF	225	
55	SG	236	
56	SH	190	
57	SI	200	
58	SJ	197	
59	SK	105	
60	SL	156	
61	SN	151	
62	SO	137	
63	SP	142	
64	SQ	143	
65	SR	136	
66	SS	146	
67	ST	144	
68	SU	121	
69	SV	87	
70	SW	130	
71	SX	145	
72	SY	135	
73	SZ	108	
74	Sa	119	
75	Sb	82	
76	Sc	67	
77	Sd	56	
78	Se	63	

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Mol	Chain	Length	Quality of chain
79	Sg	319	 A horizontal bar chart showing the quality of chain 79 (Sg, length 319). The bar is divided into three segments: a small red segment at the beginning, a large green segment labeled '86%', and a small yellow segment at the end labeled '12%'. A small grey dot is visible at the far right end of the bar.

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 339215 atoms, of which 144425 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_Flag-Pgk-1-70.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	5	7	Total	C	H	N	O	P	0	0
			229	68	76	29	49	7		

- Molecule 2 is a RNA chain called tRNA Methionin elongator.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	6	76	Total	C	H	N	O	P	0	0
			2440	724	820	292	528	76		

- Molecule 3 is a protein called Ribosome-associated molecular chaperone SSB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A	214	Total	C	H	N	O	S	0	0
			2293	788	999	247	258	1		

- Molecule 4 is a protein called Phosphoglycerate kinase.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	17	Total	C	H	N	O	S	0	0
			283	89	143	29	19	3		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P00560
B	2	ASP	-	expression tag	UNP P00560
B	3	TYR	-	expression tag	UNP P00560
B	4	LYS	-	expression tag	UNP P00560
B	5	ASP	-	expression tag	UNP P00560
B	6	ASP	-	expression tag	UNP P00560
B	7	ASP	-	expression tag	UNP P00560
B	8	ASP	-	expression tag	UNP P00560
B	9	LYS	-	expression tag	UNP P00560

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Chain	Residue	Modelled	Actual	Comment	Reference
B	10	GLU	-	expression tag	UNP P00560
B	76	MET	-	expression tag	UNP P00560
B	77	MET	-	expression tag	UNP P00560
B	78	MET	-	expression tag	UNP P00560

- Molecule 5 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C1	3063	Total	C	H	N	O	P	0	0
			98461	29271	32927	11830	21370	3063		

- Molecule 6 is a RNA chain called RNA (1642-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
6	C2	1642	Total	C	H	N	O	P	0	0
			52622	15656	17607	6227	11490	1642		

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	C3	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C4	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 9 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	LA	251	Total	C	H	N	O	S	0	0
			3858	1182	1959	385	331	1		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	LB	386	Total	C	H	N	O	S	0	0
			6241	1954	3162	584	533	8		

- Molecule 11 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	LC	361	Total	C	H	N	O	S	0	0
			5613	1730	2864	522	494	3		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	LD	294	Total	C	H	N	O	S	0	0
			4646	1484	2295	410	455	2		

- Molecule 13 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	LE	156	Total	C	H	N	O		0	0
			2565	802	1324	222	217			

- Molecule 14 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	LF	222	Total	C	H	N	O	S	0	0
			3648	1151	1864	324	308	1		

- Molecule 15 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	LG	229	Total	C	H	N	O	S	0	0
			3638	1138	1859	319	319	3		

- Molecule 16 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	LH	191	Total	C	H	N	O	S	0	0
			3082	957	1574	274	273	4		

- Molecule 17 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	LI	208	Total	C	H	N	O	S	0	0
			3429	1076	1734	321	293	5		

- Molecule 18 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	LJ	169	Total	C	H	N	O	S	0	0
			2733	846	1383	253	247	4		

- Molecule 19 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	LL	193	Total	C	H	N	O		0	0
			3152	962	1609	315	266			

- Molecule 20 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	LM	136	Total	C	H	N	O	S	0	0
			2203	675	1150	199	177	2		

- Molecule 21 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	LN	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 22 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	LO	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 23 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	LP	183	Total	C	H	N	O		0	0
			2850	879	1434	284	253			

- Molecule 24 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	LQ	185	Total	C	H	N	O	S	0	0
			2986	908	1545	290	241	2		

- Molecule 25 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	188	Total	C	H	N	O	0	0
			3122	932	1607	323	260		

- Molecule 26 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	LS	171	Total	C	H	N	O	S	0	0
			2914	925	1477	266	243	3		

- Molecule 27 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	LT	159	Total	C	H	N	O	S	0	0
			2600	805	1324	246	221	4		

- Molecule 28 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	100	Total	C	H	N	O	0	0
			1609	516	813	131	149		

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	LV	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 30 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace	
30	LW	63	Total	C	H	N	O	S	0	0
			1058	332	541	102	82	1		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	LX	121	Total	C	H	N	O	S	0	0
			1992	620	1027	169	174	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	125	Total	C	H	N	O	0	0
			2060	620	1076	191	173		

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	H	N	O	0	0
			2248	710	1156	202	180		

- Molecule 34 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	La	148	Total	C	H	N	O	S	0	0
			2391	749	1218	231	190	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	58	Total	C	H	N	O	0	0
			956	289	494	100	73		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	Lc	96	Total	C	H	N	O	S	0	0
			1530	476	793	123	137	1		

- Molecule 37 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Ld	108	Total	C	H	N	O	S	0	0
			1782	553	911	166	151	1		

- Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Le	127	Total	C	H	N	O	S	0	0
			2101	644	1084	205	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	Lf	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 40 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	Lg	112	Total	C	H	N	O	S	0	0
			1827	545	947	179	152	4		

- Molecule 41 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	Lh	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 42 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	Li	99	Total	C	H	N	O	S	0	0
			1611	478	845	154	132	2		

- Molecule 43 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	Lj	85	Total	C	H	N	O	S	0	0
			1350	408	680	146	111	5		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	Lk	77	Total	C	H	N	O		0	0
			1295	391	683	115	106			

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	Ll	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 46 is a protein called Large ribosomal subunit protein eL41B.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	Ln	25	Total	C	H	N	O	S	0	0
			502	139	273	62	27	1		

- Molecule 47 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	Lo	103	Total	C	H	N	O	S	0	0
			1718	517	894	167	135	5		

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	Lp	91	Total	C	H	N	O	S	0	0
			1433	429	739	138	121	6		

- Molecule 49 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	SA	206	Total	C	H	N	O	S	0	0
			3214	1030	1611	284	287	2		

- Molecule 50 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	SB	226	Total	C	H	N	O	S	0	0
			3690	1139	1892	330	325	4		

- Molecule 51 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	SC	216	Total	C	H	N	O	S	0	0
			3343	1042	1717	287	295	2		

- Molecule 52 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	SD	222	Total	C	H	N	O	S	0	0
			3543	1098	1814	312	313	6		

- Molecule 53 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	SE	258	Total	C	H	N	O	S	0	0
			4200	1308	2144	387	358	3		

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	SF	205	Total	C	H	N	O	S	0	0
			3256	996	1662	298	297	3		

- Molecule 55 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	SG	228	Total	C	H	N	O	S	0	0
			3709	1138	1894	351	323	3		

- Molecule 56 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	SH	184	Total	C	H	N	O		0	0
			3029	946	1556	263	264			

- Molecule 57 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	SI	187	Total	C	H	N	O	S	0	0
			2980	916	1504	295	263	2		

- Molecule 58 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	SJ	184	Total	C	H	N	O	S	0	0
			3035	935	1556	285	258	1		

- Molecule 59 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	SK	80	Total	C	H	N	O	S	0	0
			1363	446	678	109	128	2		

- Molecule 60 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	SL	142	Total	C	H	N	O	S	0	0
			2360	735	1214	217	191	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
61	SN	150	Total	C	H	N	O	S	0	0
			2448	759	1256	224	207	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
62	SO	127	Total	C	H	N	O	S	0	0
			1877	569	951	185	169	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
63	SP	114	Total	C	H	N	O	S	0	0
			1817	571	922	168	150	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
64	SQ	141	Total	C	H	N	O	S	0	0
			2273	708	1168	203	194			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
65	SR	121	Total	C	H	N	O	S	0	0
			1940	596	992	179	171	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
66	SS	145	Total	C	H	N	O	S	0	0
			2415	743	1223	237	210	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
67	ST	143	Total	C	H	N	O	S	0	0
			2237	694	1125	208	208	2		

- Molecule 68 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	SU	100	Total	C	H	N	O	S	0	0
			1661	506	864	144	146	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
69	SV	87	Total	C	H	N	O	S	0	0
			1335	415	662	125	131	2		

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	SW	129	Total	C	H	N	O	S	0	0
			2082	650	1061	188	180	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
71	SX	144	Total	C	H	N	O	S	0	0
			2319	708	1198	220	191	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
72	SY	133	Total	C	H	N	O		0	0
			2195	673	1128	207	187			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
73	SZ	67	Total	C	H	N	O		0	0
			1124	346	585	98	95			

- Molecule 74 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Sa	97	Total	C	H	N	O	S	0	0
			1587	475	818	160	129	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
75	Sb	81	Total	C	H	N	O	S	0	0
			1245	382	635	110	113	5		

- Molecule 76 is a protein called Small ribosomal subunit protein eS28B.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	Sc	63	Total	C	H	N	O	S	0	0
			1016	303	525	96	91	1		

- Molecule 77 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	Sd	45	Total	C	H	N	O	S	0	0
			749	227	378	80	60	4		

- Molecule 78 is a protein called 40S ribosomal protein S30-A.

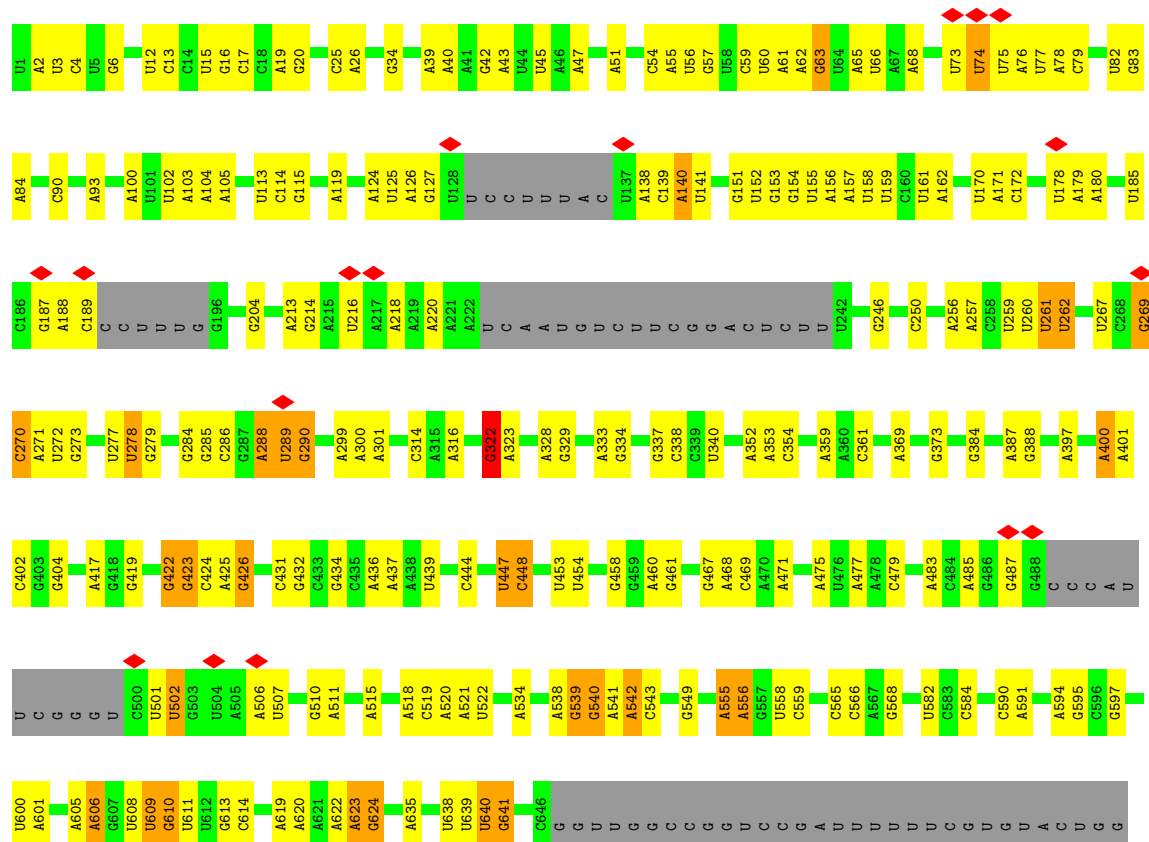
Mol	Chain	Residues	Atoms						AltConf	Trace
78	Se	60	Total	C	H	N	O	S	0	0
			994	298	522	97	76	1		

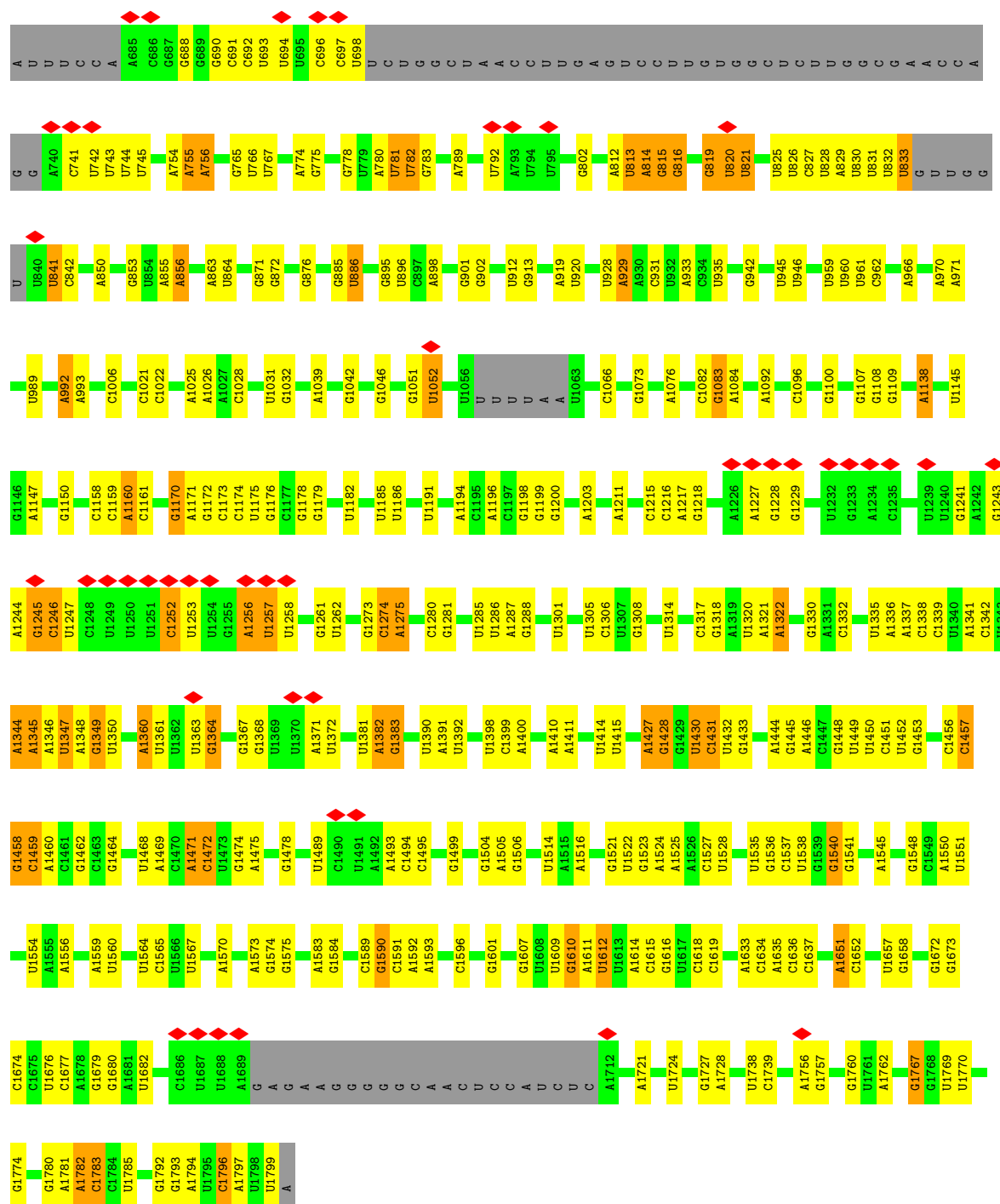
- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	Sg	312	Total	C	H	N	O	S	0	0
			4718	1514	2335	409	452	8		



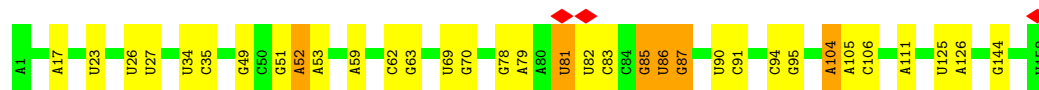
- Molecule 6: RNA (1642-MER)





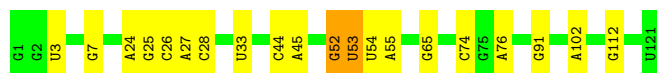
• Molecule 7: 5.8S ribosomal RNA

Chain C3:



• Molecule 8: 5S ribosomal RNA

Chain C4:  83% 15% .



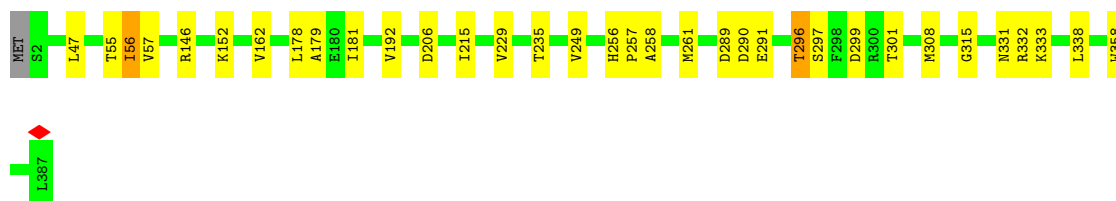
- Molecule 9: 60S ribosomal protein L2-A

Chain LA:  92% 7% .



- Molecule 10: 60S ribosomal protein L3

Chain LB:  91% 8% .



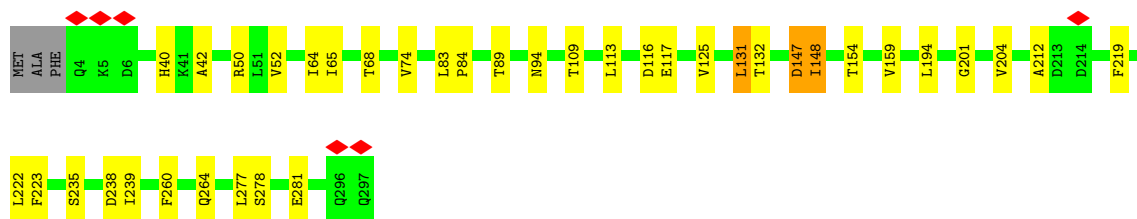
- Molecule 11: 60S ribosomal protein L4-A

Chain LC:  92% 7%



- Molecule 12: 60S ribosomal protein L5

Chain LD:  86% 12% ..



- Molecule 13: 60S ribosomal protein L6-B

Chain LE:  81% 7% 11%



- Molecule 14: 60S ribosomal protein L7-A

Chain LF:  82% 9% 9%

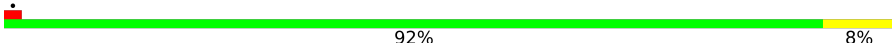


- Molecule 15: 60S ribosomal protein L8-A

Chain LG:  86% 11%



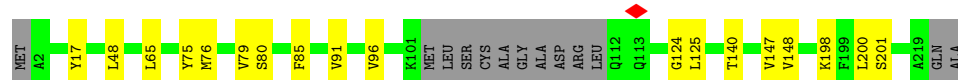
- Molecule 16: 60S ribosomal protein L9-A

Chain LH:  92% 8%



- Molecule 17: 60S ribosomal protein L10

Chain LI:  86% 8% 6%



- Molecule 18: 60S ribosomal protein L11-A

Chain LJ:  91% 6%

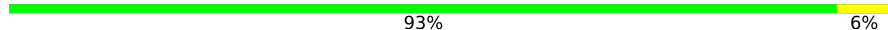


- Molecule 19: 60S ribosomal protein L13-A

Chain LL:  91% 5%



- Molecule 20: 60S ribosomal protein L14-A

Chain LM:  93% 6%



- Molecule 21: 60S ribosomal protein L15-A

Chain LN: 93% 6%



- Molecule 22: 60S ribosomal protein L16-A

Chain LO: 92% 7%



- Molecule 23: 60S ribosomal protein L17-A

Chain LP: 5% 92% 7%



- Molecule 24: 60S ribosomal protein L18-A

Chain LQ: 92% 7%



- Molecule 25: 60S ribosomal protein L19-A

Chain LR: 95%



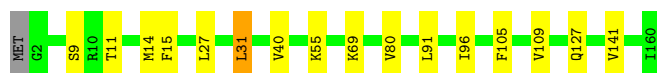
- Molecule 26: 60S ribosomal protein L20-A

Chain LS: 85% 13%



- Molecule 27: 60S ribosomal protein L21-A

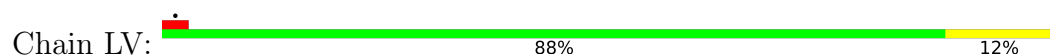
Chain LT: 89% 9%



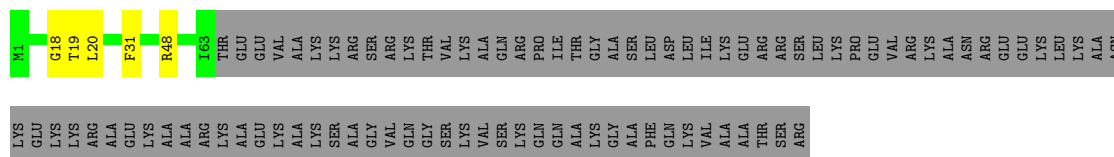
- Molecule 28: 60S ribosomal protein L22-A



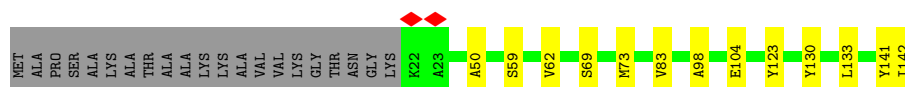
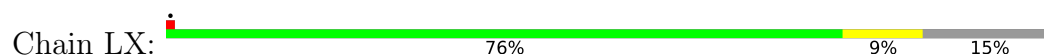
- Molecule 29: 60S ribosomal protein L23-A



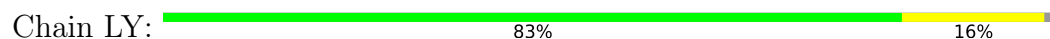
- Molecule 30: Large ribosomal subunit protein eL24B



- Molecule 31: 60S ribosomal protein L25



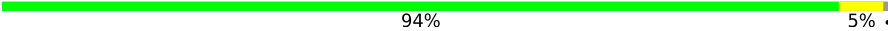
- Molecule 32: 60S ribosomal protein L26-A



- Molecule 33: 60S ribosomal protein L27-A



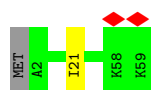
- Molecule 34: 60S ribosomal protein L28

Chain La:  94% 5%



- Molecule 35: 60S ribosomal protein L29

Chain Lb:  97%



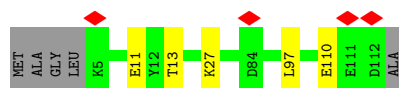
- Molecule 36: 60S ribosomal protein L30

Chain Lc:  86% 6% 9%

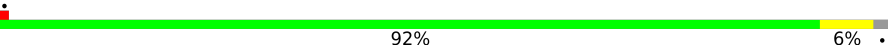


- Molecule 37: 60S ribosomal protein L31-A

Chain Ld:  91%



- Molecule 38: 60S ribosomal protein L32

Chain Le:  92% 6%



- Molecule 39: 60S ribosomal protein L33-A

Chain Lf:  92% 7%

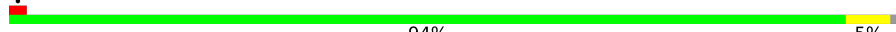


- Molecule 40: 60S ribosomal protein L34-A

Chain Lg:  84% 8% 7%



- Molecule 41: 60S ribosomal protein L35-A

Chain Lh:  94% 5%



- Molecule 42: 60S ribosomal protein L36-A

Chain Li:  97%



- Molecule 43: 60S ribosomal protein L37-A

Chain Lj:  92% 5%



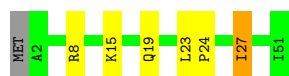
- Molecule 44: 60S ribosomal protein L38

Chain Lk:  83% 15%

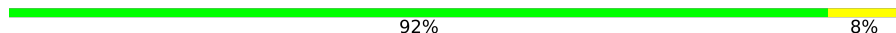


- Molecule 45: 60S ribosomal protein L39

Chain Ll:  86% 10%



- Molecule 46: Large ribosomal subunit protein eL41B

Chain Ln:  92% 8%

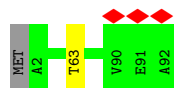


- Molecule 47: 60S ribosomal protein L42-A

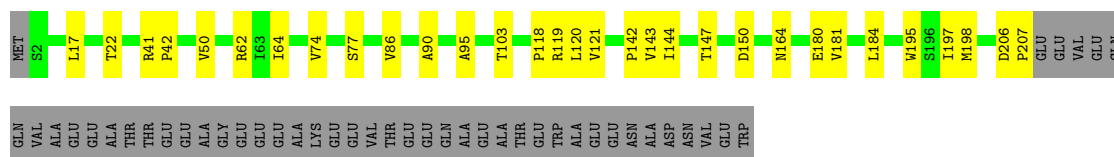
Chain Lo:  93%



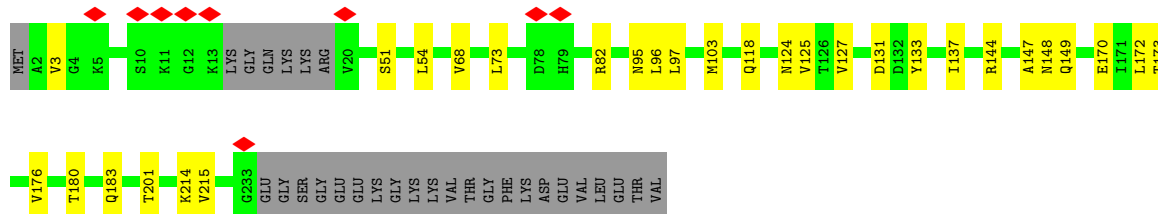
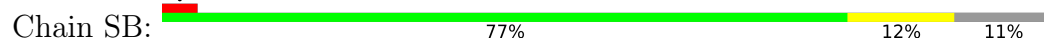
- Molecule 48: 60S ribosomal protein L43-A



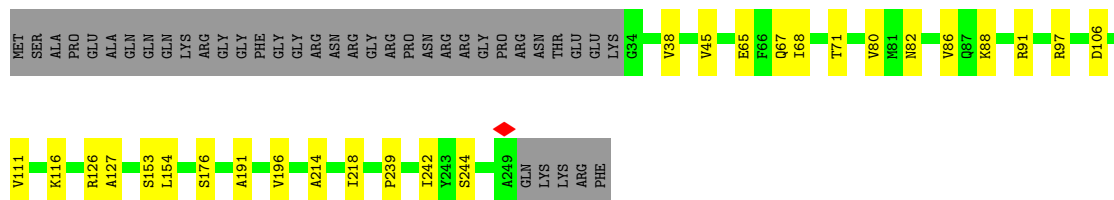
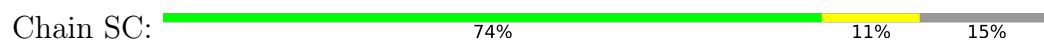
- Molecule 49: 40S ribosomal protein S0-A



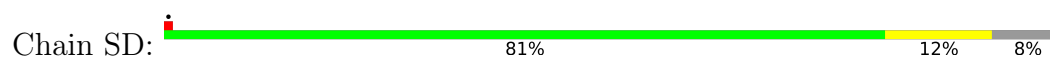
- Molecule 50: 40S ribosomal protein S1-A

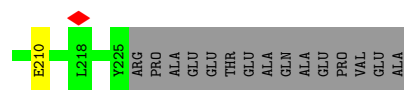


- Molecule 51: 40S ribosomal protein S2



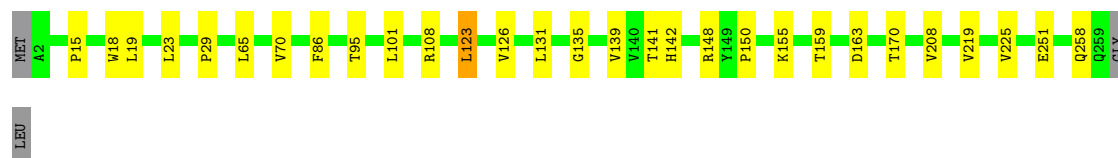
- Molecule 52: Small ribosomal subunit protein uS3





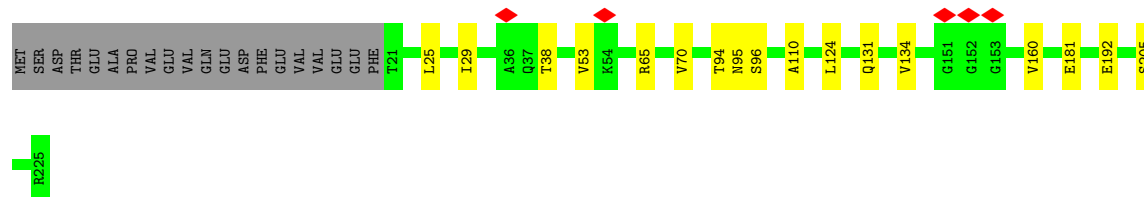
- Molecule 53: 40S ribosomal protein S4-A

Chain SE: 88% 11% .



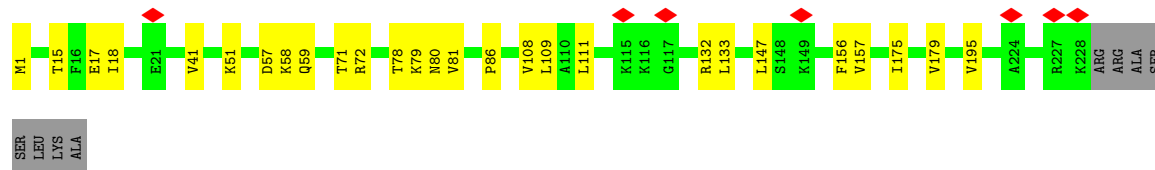
- Molecule 54: 40S ribosomal protein S5

Chain SF: 84% 8% 9%



- Molecule 55: 40S ribosomal protein S6-A

Chain SG: 85% 11% .



- Molecule 56: 40S ribosomal protein S7-A

Chain SH: 88% 8% . .



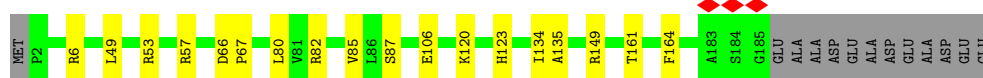
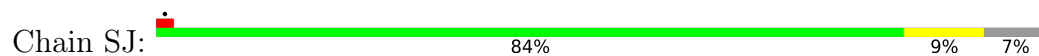
- Molecule 57: 40S ribosomal protein S8-A

Chain SI: 82% 11% 6%

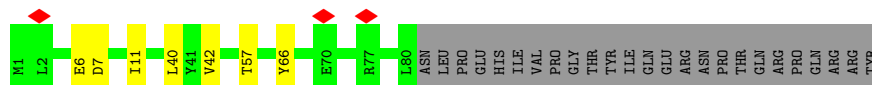




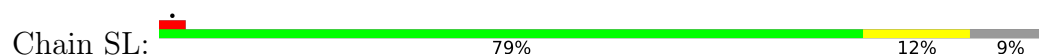
- Molecule 58: 40S ribosomal protein S9-A



- Molecule 59: 40S ribosomal protein S10-A



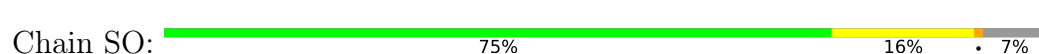
- Molecule 60: 40S ribosomal protein S11-A



- Molecule 61: 40S ribosomal protein S13



- Molecule 62: 40S ribosomal protein S14-A



- Molecule 63: 40S ribosomal protein S15



- Molecule 64: 40S ribosomal protein S16-A

Chain SQ:  83% 15% .



- Molecule 65: 40S ribosomal protein S17-B

Chain SR:  76% 13% 11%



- Molecule 66: 40S ribosomal protein S18-A

Chain SS:  85% 13% ..



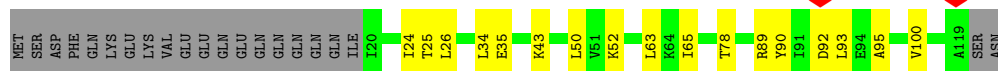
- Molecule 67: 40S ribosomal protein S19-A

Chain ST:  91% 8% .

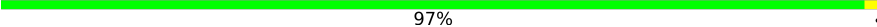


- Molecule 68: Small ribosomal subunit protein uS10

Chain SU:  69% 14% 17%



- Molecule 69: 40S ribosomal protein S21-A

Chain SV:  97% .

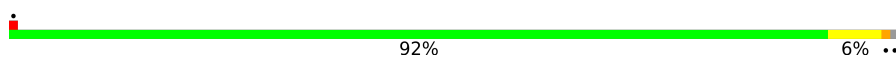


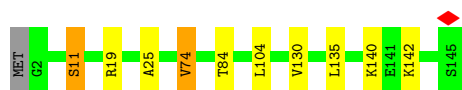
- Molecule 70: 40S ribosomal protein S22-A

Chain SW:  85% 13% ..



- Molecule 71: 40S ribosomal protein S23-A

Chain SX:  92% 6% ..



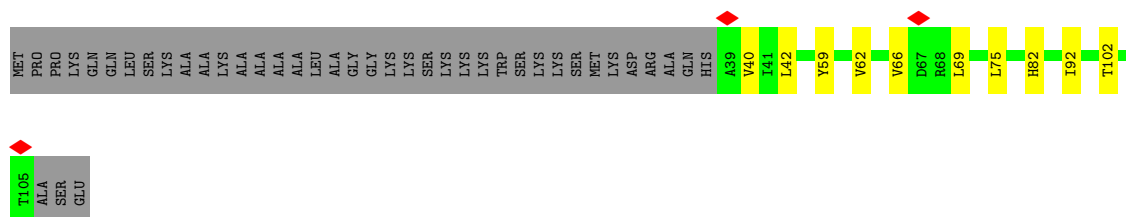
- Molecule 72: 40S ribosomal protein S24-A

Chain SY:  89% 10% .



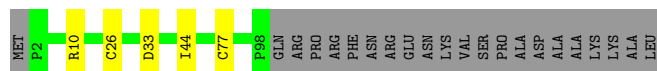
- Molecule 73: 40S ribosomal protein S25-A

Chain SZ:  53% 9% 38%



- Molecule 74: Small ribosomal subunit protein eS26A

Chain Sa:  77% 18%



- Molecule 75: 40S ribosomal protein S27-A

Chain Sb:  82% 16% ..

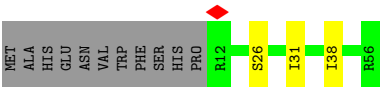
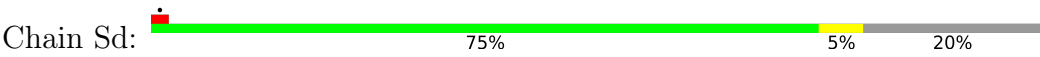


- Molecule 76: Small ribosomal subunit protein eS28B

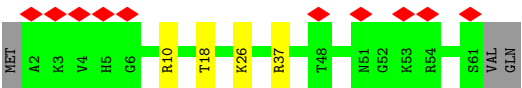
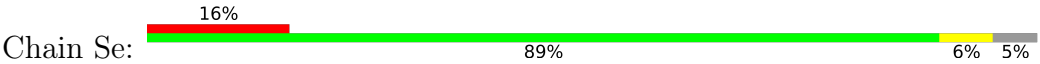
Chain Sc:  6% 81% 13% 6%



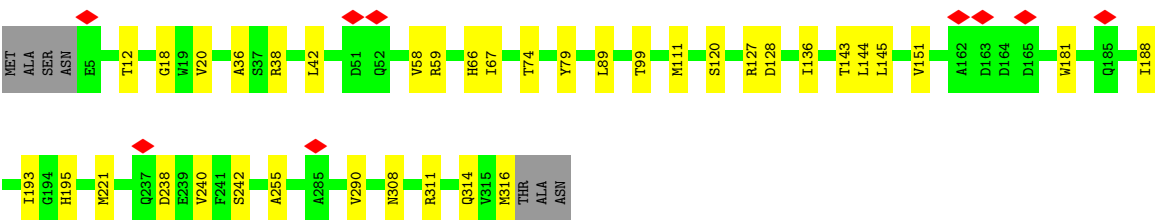
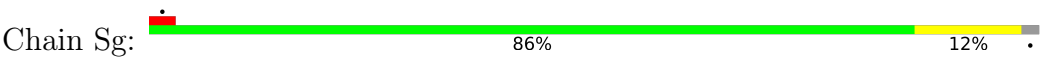
- Molecule 77: Small ribosomal subunit protein uS14A



• Molecule 78: 40S ribosomal protein S30-A



• Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14049	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.504	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.050	Depositor
Recommended contour level	0.0241	Depositor
Map size ($\text{\AA}$)	476.00003, 476.00003, 476.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.19, 1.19, 1.19	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	5	0.49	0/171	1.07	1/265 (0.4%)
2	6	0.27	0/1811	0.35	0/2820
3	A	0.13	0/1305	0.25	0/1785
4	B	0.26	0/144	0.46	0/192
5	C1	0.49	0/73353	0.37	0/114350
6	C2	0.45	0/39167	0.37	1/61016 (0.0%)
7	C3	0.50	0/3746	0.38	0/5832
8	C4	0.47	0/2883	0.34	0/4491
9	LA	0.44	0/1933	0.37	0/2598
10	LB	0.41	0/3150	0.36	0/4236
11	LC	0.42	0/2801	0.36	0/3792
12	LD	0.35	0/2400	0.34	0/3239
13	LE	0.36	0/1263	0.36	0/1703
14	LF	0.46	0/1821	0.35	0/2451
15	LG	0.39	0/1811	0.34	0/2447
16	LH	0.26	0/1529	0.29	0/2060
17	LI	0.34	0/1731	0.33	0/2321
18	LJ	0.29	0/1371	0.31	0/1838
19	LL	0.41	0/1568	0.33	0/2106
20	LM	0.38	0/1068	0.34	0/1438
21	LN	0.46	0/1757	0.36	0/2354
22	LO	0.45	0/1585	0.36	0/2128
23	LP	0.41	0/1439	0.36	0/1938
24	LQ	0.42	0/1465	0.37	0/1965
25	LR	0.38	0/1532	0.31	0/2043
26	LS	0.43	0/1473	0.36	0/1980
27	LT	0.40	0/1300	0.34	0/1743
28	LU	0.31	0/812	0.35	0/1099
29	LV	0.38	0/1018	0.39	0/1369
30	LW	0.46	0/529	0.37	0/702
31	LX	0.42	0/980	0.38	0/1321
32	LY	0.38	0/995	0.37	0/1329
33	LZ	0.37	0/1118	0.32	0/1497
34	La	0.46	0/1204	0.37	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Lb	0.36	0/473	0.35	0/629
36	Lc	0.42	0/745	0.32	0/1001
37	Ld	0.40	0/885	0.31	0/1189
38	Le	0.44	0/1038	0.35	0/1390
39	Lf	0.44	0/868	0.38	0/1168
40	Lg	0.41	0/890	0.38	0/1189
41	Lh	0.39	0/978	0.33	0/1301
42	Li	0.38	0/772	0.35	0/1026
43	Lj	0.46	0/685	0.36	0/908
44	Lk	0.31	0/618	0.33	0/826
45	Ll	0.45	0/443	0.32	0/588
46	Ln	0.40	0/230	0.38	0/296
47	Lo	0.39	0/836	0.35	0/1104
48	Lp	0.41	0/701	0.37	0/934
49	SA	0.39	0/1644	0.36	0/2249
50	SB	0.34	0/1823	0.34	0/2447
51	SC	0.39	0/1656	0.35	0/2251
52	SD	0.29	0/1754	0.32	0/2361
53	SE	0.35	0/2097	0.34	0/2823
54	SF	0.32	0/1613	0.36	0/2181
55	SG	0.25	0/1839	0.32	0/2460
56	SH	0.28	0/1498	0.32	0/2019
57	SI	0.38	0/1501	0.35	0/2006
58	SJ	0.34	0/1504	0.35	0/2016
59	SK	0.21	0/701	0.26	0/944
60	SL	0.40	0/1172	0.33	0/1580
61	SN	0.38	0/1215	0.35	0/1638
62	SO	0.37	0/937	0.43	0/1261
63	SP	0.22	0/914	0.28	0/1228
64	SQ	0.33	0/1125	0.33	0/1510
65	SR	0.32	0/957	0.33	0/1283
66	SS	0.25	0/1211	0.30	0/1628
67	ST	0.29	0/1130	0.32	0/1517
68	SU	0.26	0/807	0.31	0/1091
69	SV	0.38	0/682	0.31	0/921
70	SW	0.46	0/1038	0.37	0/1395
71	SX	0.37	0/1139	0.36	0/1518
72	SY	0.30	0/1081	0.30	0/1441
73	SZ	0.25	0/546	0.32	0/734
74	Sa	0.40	0/782	0.38	0/1047
75	Sb	0.36	0/620	0.34	0/838
76	Sc	0.33	0/493	0.35	0/663
77	Sd	0.36	0/376	0.32	0/495

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Se	0.30	0/480	0.33	0/639
79	Sg	0.22	0/2436	0.30	0/3318
All	All	0.44	0/209166	0.36	2/307111 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	0	3
62	SO	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	42	G	OP1-P-O3'	5.75	125.26	108.00
6	C2	322	G	C2'-C3'-O3'	5.09	117.14	109.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	568	ARG	Sidechain
3	A	596	ARG	Sidechain
3	A	613	ARG	Sidechain
62	SO	124	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	153	76	76	0	0
2	6	1620	820	820	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1294	999	998	8	0
4	B	140	143	142	5	0
5	C1	65534	32927	32937	211	0
6	C2	35015	17607	17617	241	0
7	C3	3353	1695	1695	12	0
8	C4	2579	1304	1304	8	0
9	LA	1899	1959	1957	9	0
10	LB	3079	3162	3158	24	0
11	LC	2749	2864	2863	19	0
12	LD	2351	2295	2294	22	0
13	LE	1241	1324	1322	8	0
14	LF	1784	1864	1862	12	0
15	LG	1779	1859	1858	7	0
16	LH	1508	1574	1572	10	0
17	LI	1695	1734	1732	15	0
18	LJ	1350	1383	1381	7	0
19	LL	1543	1609	1608	6	0
20	LM	1053	1150	1149	6	0
21	LN	1720	1780	1779	8	0
22	LO	1555	1661	1659	8	0
23	LP	1416	1434	1433	7	0
24	LQ	1441	1545	1543	9	0
25	LR	1515	1607	1606	6	0
26	LS	1437	1477	1475	17	0
27	LT	1276	1324	1323	14	0
28	LU	796	813	812	14	0
29	LV	1003	1049	1048	11	0
30	LW	517	541	540	3	0
31	LX	965	1027	1025	15	0
32	LY	984	1076	1075	14	0
33	LZ	1092	1156	1155	8	0
34	La	1173	1218	1215	8	0
35	Lb	462	494	491	1	0
36	Lc	737	793	792	3	0
37	Ld	871	911	910	2	0
38	Le	1017	1084	1081	5	0
39	Lf	850	881	880	4	0
40	Lg	880	947	945	8	0
41	Lh	969	1079	1078	5	0
42	Li	766	845	844	1	0
43	Lj	670	680	677	4	0
44	Lk	612	683	682	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	Ll	436	476	475	5	0
46	Ln	229	273	273	1	0
47	Lo	824	894	892	2	0
48	Lp	694	739	738	0	0
49	SA	1603	1611	1610	22	0
50	SB	1798	1892	1890	30	0
51	SC	1626	1717	1715	13	0
52	SD	1729	1814	1812	13	0
53	SE	2056	2144	2140	17	0
54	SF	1594	1662	1660	12	0
55	SG	1815	1894	1894	21	0
56	SH	1473	1556	1555	10	0
57	SI	1476	1504	1501	17	0
58	SJ	1479	1556	1556	13	0
59	SK	685	678	677	4	0
60	SL	1146	1214	1213	10	0
61	SN	1192	1256	1255	11	0
62	SO	926	951	950	17	0
63	SP	895	922	919	7	0
64	SQ	1105	1168	1166	16	0
65	SR	948	992	990	14	0
66	SS	1192	1223	1222	17	0
67	ST	1112	1125	1124	8	0
68	SU	797	864	863	15	0
69	SV	673	662	662	2	0
70	SW	1021	1061	1060	9	0
71	SX	1121	1198	1196	8	0
72	SY	1067	1128	1127	10	0
73	SZ	539	585	583	12	0
74	Sa	769	818	818	3	0
75	Sb	610	635	633	11	0
76	Sc	491	525	524	7	0
77	Sd	371	378	377	3	0
78	Se	472	522	521	5	0
79	Sg	2383	2335	2332	24	0
All	All	194790	144425	144336	1100	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 1100 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C2:40:A:H62	6:C2:467:G:N2	1.36	1.23
6:C2:40:A:N6	6:C2:467:G:H21	1.44	1.16
27:LT:40:VAL:HG21	27:LT:96:ILE:HD11	1.47	0.95
6:C2:819:G:C6	6:C2:853:G:C2	2.58	0.91
64:SQ:89:LEU:HD21	64:SQ:105:LEU:HD13	1.57	0.86

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	212/613 (35%)	208 (98%)	4 (2%)	0	100	100
4	B	15/78 (19%)	10 (67%)	4 (27%)	1 (7%)	1	5
9	LA	249/254 (98%)	231 (93%)	18 (7%)	0	100	100
10	LB	384/387 (99%)	361 (94%)	23 (6%)	0	100	100
11	LC	359/362 (99%)	341 (95%)	18 (5%)	0	100	100
12	LD	292/297 (98%)	278 (95%)	14 (5%)	0	100	100
13	LE	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
14	LF	220/244 (90%)	210 (96%)	9 (4%)	1 (0%)	24	60
15	LG	227/256 (89%)	221 (97%)	6 (3%)	0	100	100
16	LH	189/191 (99%)	179 (95%)	10 (5%)	0	100	100
17	LI	204/221 (92%)	191 (94%)	13 (6%)	0	100	100
18	LJ	167/174 (96%)	163 (98%)	4 (2%)	0	100	100
19	LL	191/199 (96%)	184 (96%)	6 (3%)	1 (0%)	24	60
20	LM	134/138 (97%)	132 (98%)	2 (2%)	0	100	100
21	LN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
22	LO	195/199 (98%)	188 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	LP	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
24	LQ	183/186 (98%)	170 (93%)	13 (7%)	0	100	100
25	LR	186/189 (98%)	183 (98%)	3 (2%)	0	100	100
26	LS	169/172 (98%)	159 (94%)	10 (6%)	0	100	100
27	LT	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
28	LU	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
29	LV	134/137 (98%)	127 (95%)	7 (5%)	0	100	100
30	LW	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
31	LX	119/142 (84%)	115 (97%)	4 (3%)	0	100	100
32	LY	123/127 (97%)	117 (95%)	6 (5%)	0	100	100
33	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
34	La	146/149 (98%)	129 (88%)	17 (12%)	0	100	100
35	Lb	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
36	Lc	94/105 (90%)	92 (98%)	2 (2%)	0	100	100
37	Ld	106/113 (94%)	104 (98%)	2 (2%)	0	100	100
38	Le	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
39	Lf	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
40	Lg	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
41	Lh	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
42	Li	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
43	Lj	83/88 (94%)	77 (93%)	6 (7%)	0	100	100
44	Lk	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
45	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
46	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
47	Lo	101/106 (95%)	92 (91%)	9 (9%)	0	100	100
48	Lp	89/92 (97%)	79 (89%)	10 (11%)	0	100	100
49	SA	204/252 (81%)	194 (95%)	10 (5%)	0	100	100
50	SB	222/255 (87%)	211 (95%)	11 (5%)	0	100	100
51	SC	214/254 (84%)	209 (98%)	5 (2%)	0	100	100
52	SD	220/240 (92%)	213 (97%)	7 (3%)	0	100	100
53	SE	256/261 (98%)	243 (95%)	13 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	SF	203/225 (90%)	198 (98%)	5 (2%)	0	100	100
55	SG	226/236 (96%)	214 (95%)	12 (5%)	0	100	100
56	SH	182/190 (96%)	172 (94%)	10 (6%)	0	100	100
57	SI	183/200 (92%)	177 (97%)	6 (3%)	0	100	100
58	SJ	182/197 (92%)	174 (96%)	8 (4%)	0	100	100
59	SK	78/105 (74%)	76 (97%)	2 (3%)	0	100	100
60	SL	140/156 (90%)	135 (96%)	5 (4%)	0	100	100
61	SN	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
62	SO	125/137 (91%)	119 (95%)	6 (5%)	0	100	100
63	SP	110/142 (78%)	107 (97%)	3 (3%)	0	100	100
64	SQ	139/143 (97%)	138 (99%)	1 (1%)	0	100	100
65	SR	117/136 (86%)	114 (97%)	3 (3%)	0	100	100
66	SS	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
67	ST	141/144 (98%)	134 (95%)	7 (5%)	0	100	100
68	SU	98/121 (81%)	90 (92%)	8 (8%)	0	100	100
69	SV	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
70	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
71	SX	142/145 (98%)	139 (98%)	3 (2%)	0	100	100
72	SY	131/135 (97%)	126 (96%)	5 (4%)	0	100	100
73	SZ	65/108 (60%)	64 (98%)	1 (2%)	0	100	100
74	Sa	95/119 (80%)	90 (95%)	5 (5%)	0	100	100
75	Sb	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
76	Sc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
77	Sd	43/56 (77%)	41 (95%)	2 (5%)	0	100	100
78	Se	58/63 (92%)	53 (91%)	5 (9%)	0	100	100
79	Sg	310/319 (97%)	294 (95%)	16 (5%)	0	100	100
All	All	10836/12148 (89%)	10352 (96%)	481 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	70	ALA
19	LL	61	PRO

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Mol	Chain	Res	Type
14	LF	191	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	75/509 (15%)	75 (100%)	0	100	100
4	B	15/73 (20%)	15 (100%)	0	100	100
9	LA	190/196 (97%)	185 (97%)	5 (3%)	40	72
10	LB	321/323 (99%)	318 (99%)	3 (1%)	70	85
11	LC	288/289 (100%)	281 (98%)	7 (2%)	43	73
12	LD	241/245 (98%)	235 (98%)	6 (2%)	42	72
13	LE	135/155 (87%)	133 (98%)	2 (2%)	57	80
14	LF	186/205 (91%)	181 (97%)	5 (3%)	39	71
15	LG	184/208 (88%)	183 (100%)	1 (0%)	81	89
16	LH	168/171 (98%)	164 (98%)	4 (2%)	43	73
17	LI	178/187 (95%)	176 (99%)	2 (1%)	65	83
18	LJ	146/150 (97%)	143 (98%)	3 (2%)	47	75
19	LL	154/159 (97%)	151 (98%)	3 (2%)	50	76
20	LM	107/109 (98%)	105 (98%)	2 (2%)	50	76
21	LN	175/176 (99%)	173 (99%)	2 (1%)	65	83
22	LO	160/162 (99%)	157 (98%)	3 (2%)	50	76
23	LP	138/146 (94%)	134 (97%)	4 (3%)	37	70
24	LQ	150/151 (99%)	149 (99%)	1 (1%)	76	86
25	LR	152/154 (99%)	152 (100%)	0	100	100
26	LS	155/156 (99%)	149 (96%)	6 (4%)	28	62
27	LT	136/137 (99%)	134 (98%)	2 (2%)	57	80
28	LU	87/107 (81%)	84 (97%)	3 (3%)	32	66
29	LV	104/105 (99%)	102 (98%)	2 (2%)	50	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	LW	54/128 (42%)	54 (100%)	0	100	100
31	LX	104/118 (88%)	104 (100%)	0	100	100
32	LY	108/110 (98%)	106 (98%)	2 (2%)	50	76
33	LZ	115/116 (99%)	114 (99%)	1 (1%)	70	85
34	La	118/119 (99%)	117 (99%)	1 (1%)	73	86
35	Lb	46/47 (98%)	46 (100%)	0	100	100
36	Lc	81/88 (92%)	81 (100%)	0	100	100
37	Ld	92/97 (95%)	89 (97%)	3 (3%)	33	67
38	Le	108/111 (97%)	106 (98%)	2 (2%)	50	76
39	Lf	90/91 (99%)	88 (98%)	2 (2%)	45	74
40	Lg	95/103 (92%)	91 (96%)	4 (4%)	26	61
41	Lh	104/105 (99%)	103 (99%)	1 (1%)	68	84
42	Li	80/82 (98%)	79 (99%)	1 (1%)	61	81
43	Lj	69/71 (97%)	69 (100%)	0	100	100
44	Lk	68/69 (99%)	67 (98%)	1 (2%)	57	80
45	Ll	45/46 (98%)	44 (98%)	1 (2%)	45	74
46	Ln	22/23 (96%)	22 (100%)	0	100	100
47	Lo	87/91 (96%)	86 (99%)	1 (1%)	65	83
48	Lp	71/72 (99%)	70 (99%)	1 (1%)	59	80
49	SA	170/210 (81%)	168 (99%)	2 (1%)	63	82
50	SB	200/224 (89%)	196 (98%)	4 (2%)	48	76
51	SC	175/205 (85%)	170 (97%)	5 (3%)	37	70
52	SD	182/195 (93%)	175 (96%)	7 (4%)	29	63
53	SE	220/222 (99%)	215 (98%)	5 (2%)	44	74
54	SF	171/191 (90%)	167 (98%)	4 (2%)	44	74
55	SG	189/201 (94%)	187 (99%)	2 (1%)	65	83
56	SH	163/170 (96%)	159 (98%)	4 (2%)	42	72
57	SI	148/161 (92%)	146 (99%)	2 (1%)	59	80
58	SJ	156/166 (94%)	155 (99%)	1 (1%)	78	88
59	SK	74/98 (76%)	74 (100%)	0	100	100
60	SL	127/137 (93%)	121 (95%)	6 (5%)	23	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	SN	127/128 (99%)	126 (99%)	1 (1%)	73	86
62	SO	91/105 (87%)	87 (96%)	4 (4%)	25	60
63	SP	92/118 (78%)	91 (99%)	1 (1%)	65	83
64	SQ	117/119 (98%)	117 (100%)	0	100	100
65	SR	101/124 (82%)	101 (100%)	0	100	100
66	SS	128/129 (99%)	125 (98%)	3 (2%)	44	74
67	ST	115/116 (99%)	115 (100%)	0	100	100
68	SU	93/114 (82%)	91 (98%)	2 (2%)	45	74
69	SV	71/74 (96%)	69 (97%)	2 (3%)	38	70
70	SW	110/111 (99%)	107 (97%)	3 (3%)	39	71
71	SX	119/120 (99%)	116 (98%)	3 (2%)	42	72
72	SY	111/113 (98%)	110 (99%)	1 (1%)	70	85
73	SZ	59/89 (66%)	59 (100%)	0	100	100
74	Sa	83/101 (82%)	82 (99%)	1 (1%)	63	82
75	Sb	70/71 (99%)	69 (99%)	1 (1%)	59	80
76	Sc	55/60 (92%)	55 (100%)	0	100	100
77	Sd	39/49 (80%)	38 (97%)	1 (3%)	40	72
78	Se	50/54 (93%)	50 (100%)	0	100	100
79	Sg	250/262 (95%)	247 (99%)	3 (1%)	63	82
All	All	9058/10197 (89%)	8903 (98%)	155 (2%)	52	78

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	SG	111	LEU
70	SW	104	LEU
56	SH	184	GLU
62	SO	54	GLU
75	Sb	3	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
51	SC	59	HIS

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Mol	Chain	Res	Type
61	SN	105	ASN
53	SE	50	ASN
55	SG	13	GLN
66	SS	127	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	7/234 (2%)	2 (28%)	1 (14%)
2	6	75/76 (98%)	16 (21%)	1 (1%)
5	C1	3052/3396 (89%)	462 (15%)	29 (0%)
6	C2	1632/1800 (90%)	333 (20%)	33 (2%)
7	C3	157/158 (99%)	24 (15%)	1 (0%)
8	C4	120/121 (99%)	12 (10%)	1 (0%)
All	All	5043/5785 (87%)	849 (16%)	66 (1%)

5 of 849 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	43	A
1	5	46	A
2	6	7	G
2	6	9	A
2	6	17	A

5 of 66 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	C2	1382	A
6	C2	1427	A
8	C4	52	G
5	C1	3218	A
5	C1	3103	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

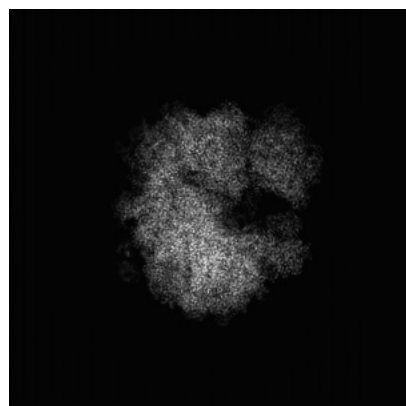
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53861. These allow visual inspection of the internal detail of the map and identification of artifacts.

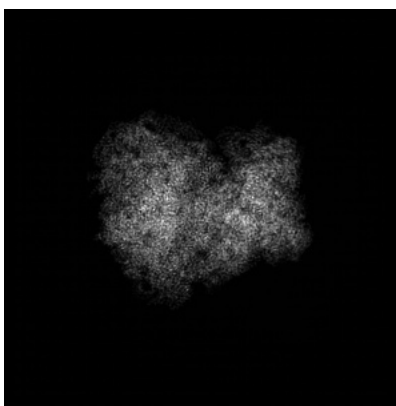
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

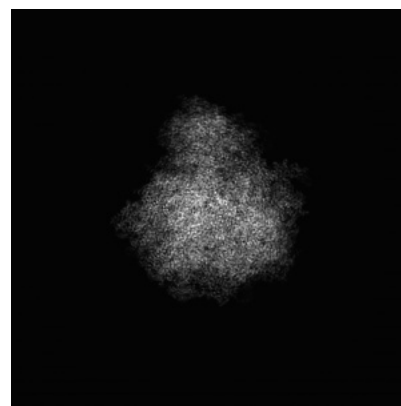
6.1.1 Primary map



X

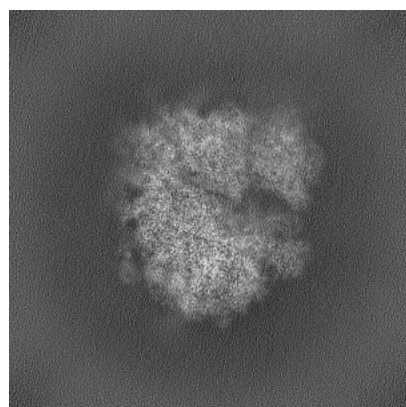


Y

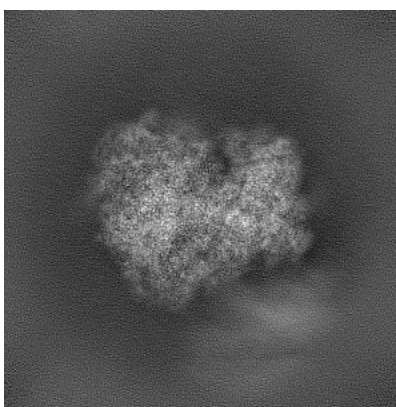


Z

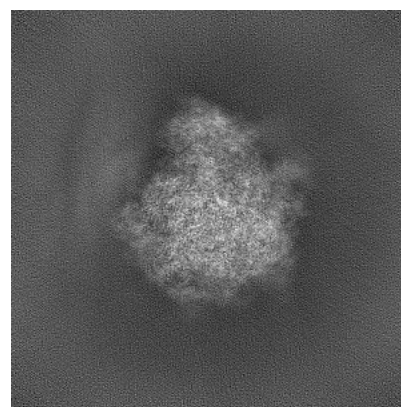
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200

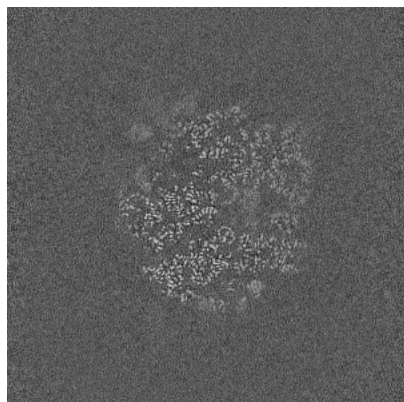


Y Index: 200

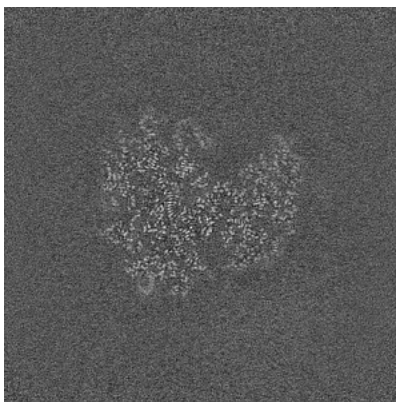


Z Index: 200

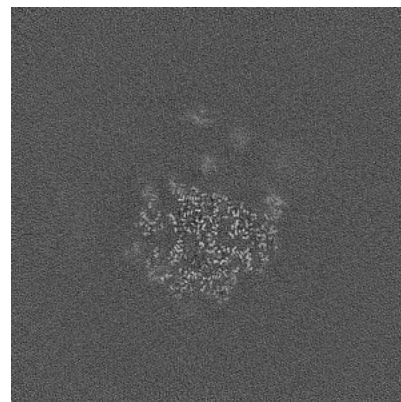
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

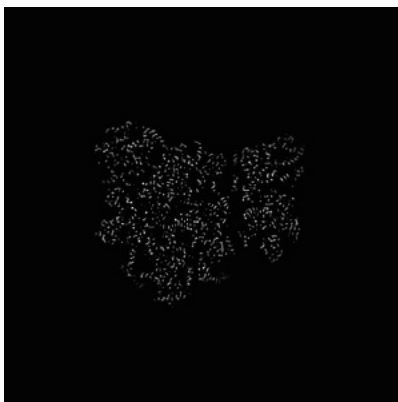
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 189

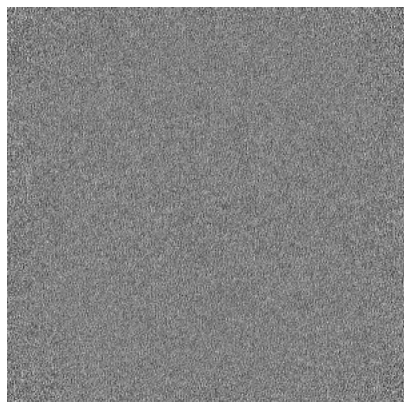


Y Index: 183

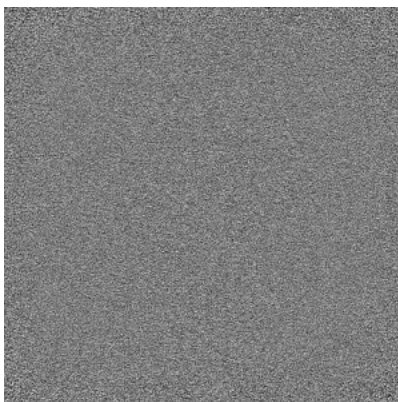


Z Index: 153

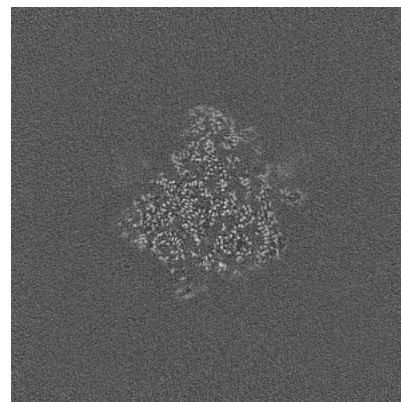
6.3.2 Raw map



X Index: 0



Y Index: 0

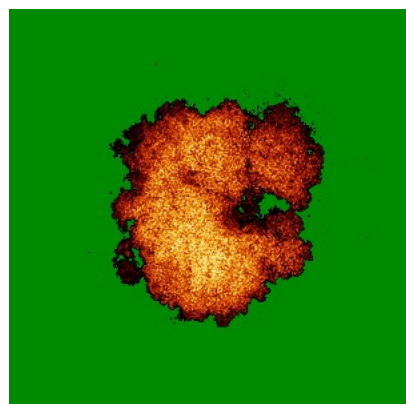


Z Index: 160

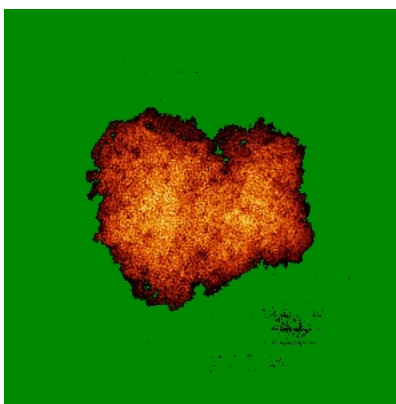
The images above show the largest variance slices of the map in three orthogonal directions.

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

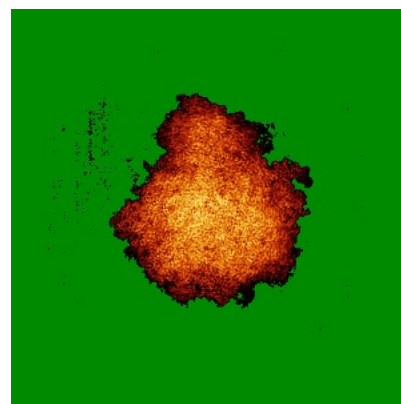
6.4.1 Primary map



X

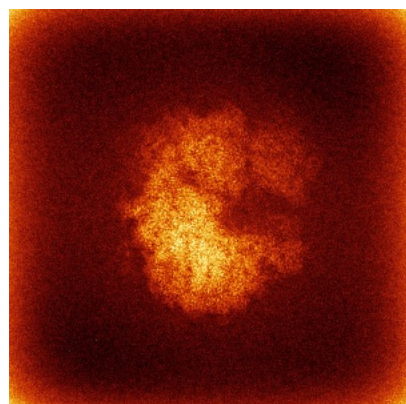


Y

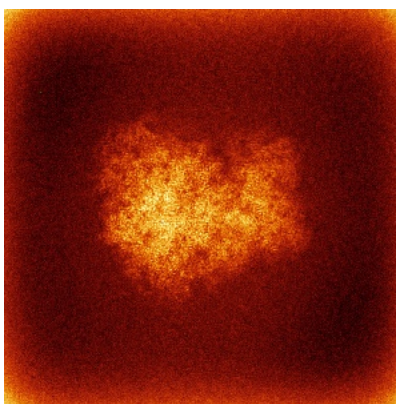


Z

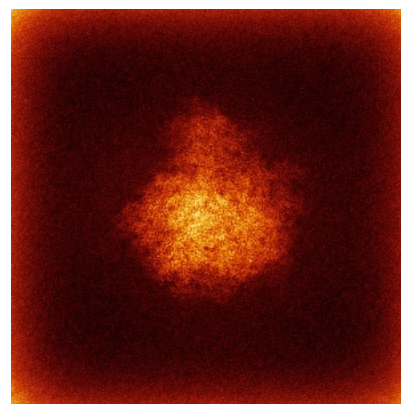
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

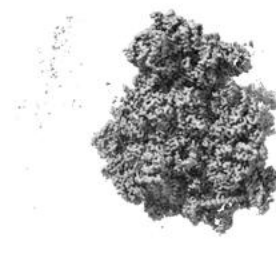
6.5.1 Primary map



X



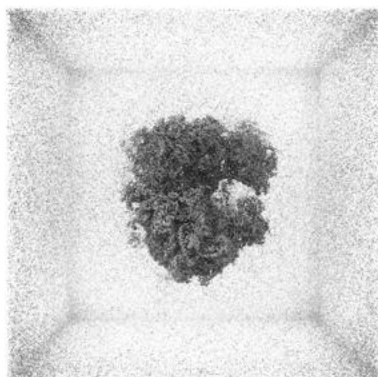
Y



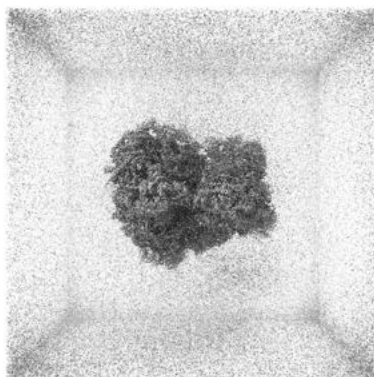
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0241. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

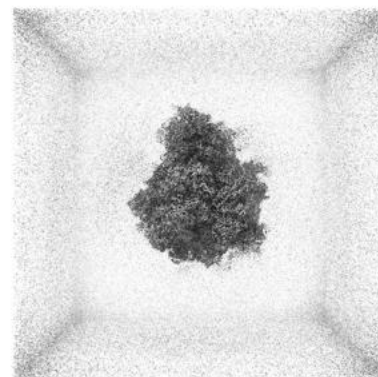
6.5.2 Raw map



X



Y



Z

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

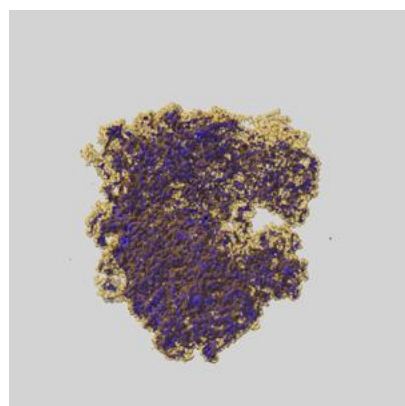
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

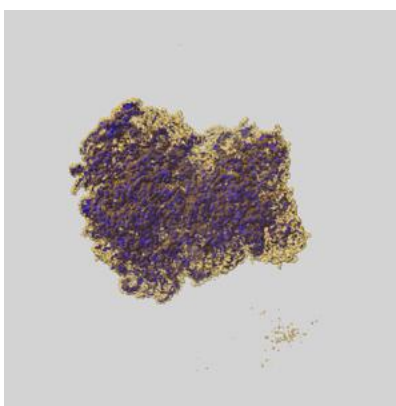
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

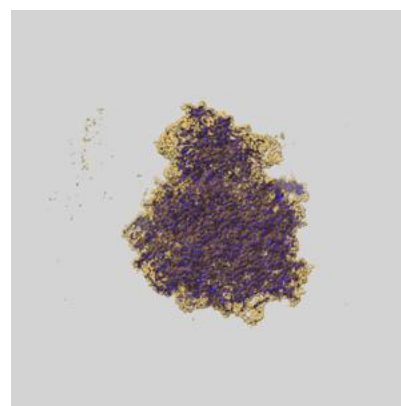
6.6.1 emd_53861_msk_1.map [i](#)



X



Y

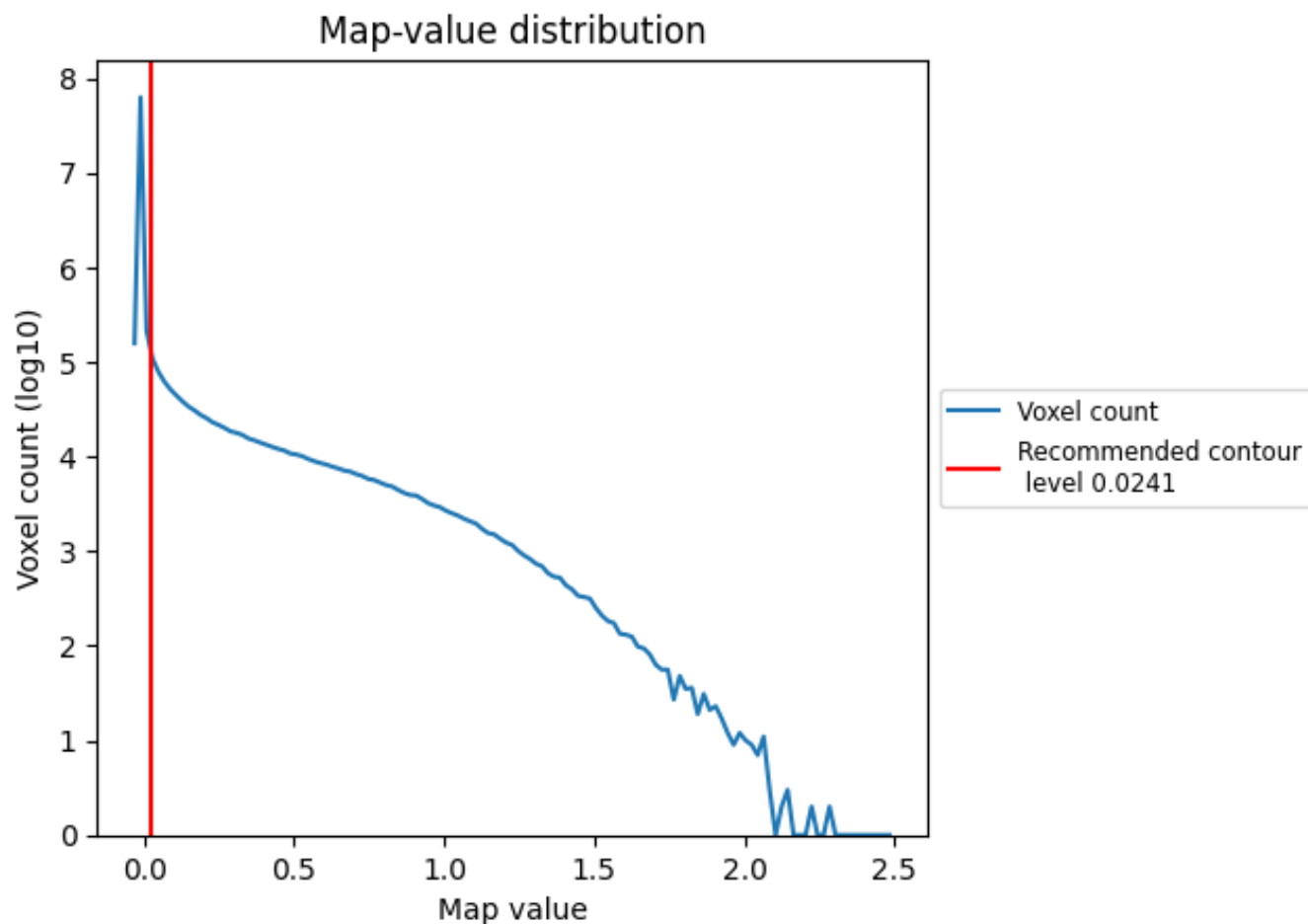


Z

7 Map analysis [i](#)

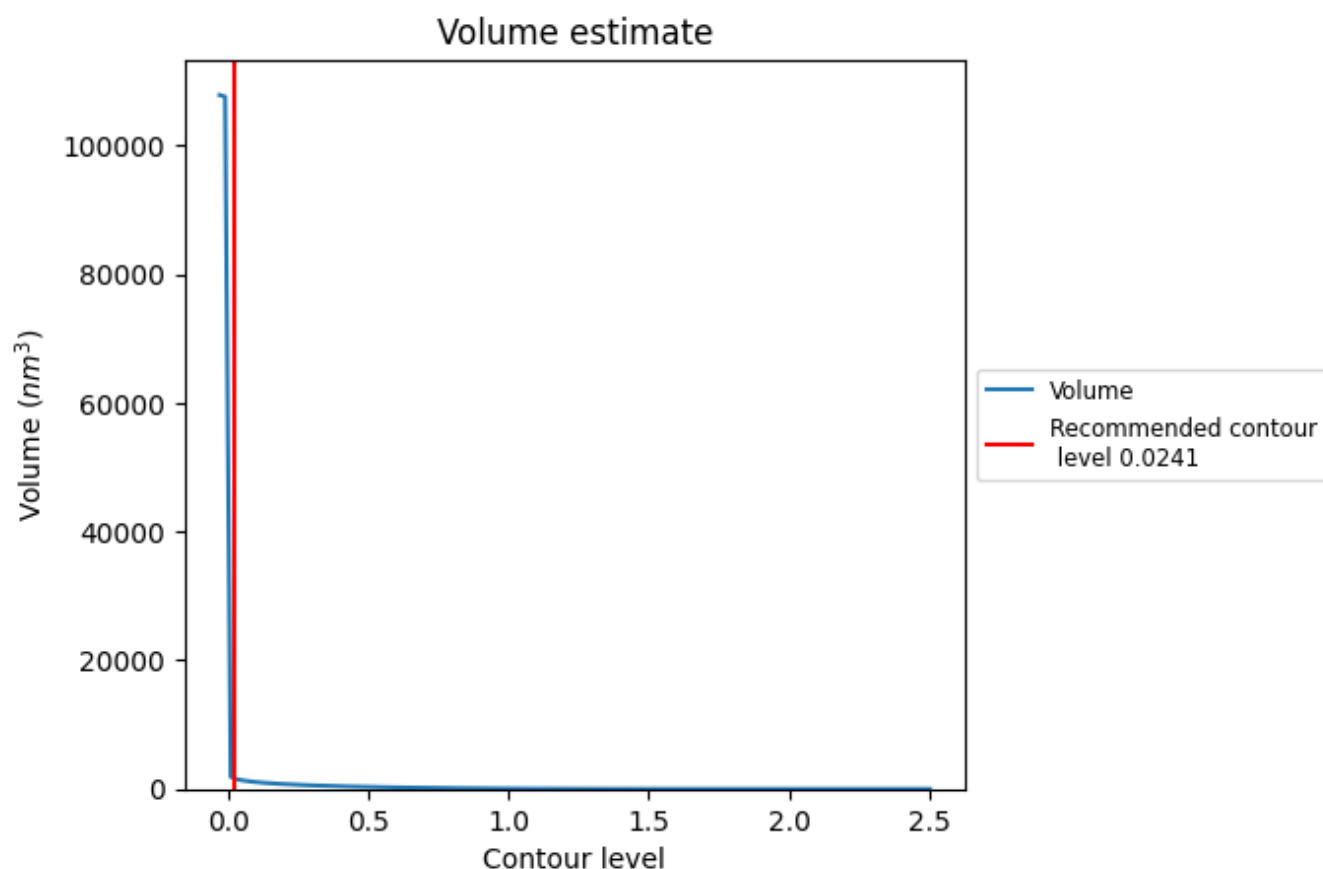
This section contains the results of statistical analysis of the map.

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.

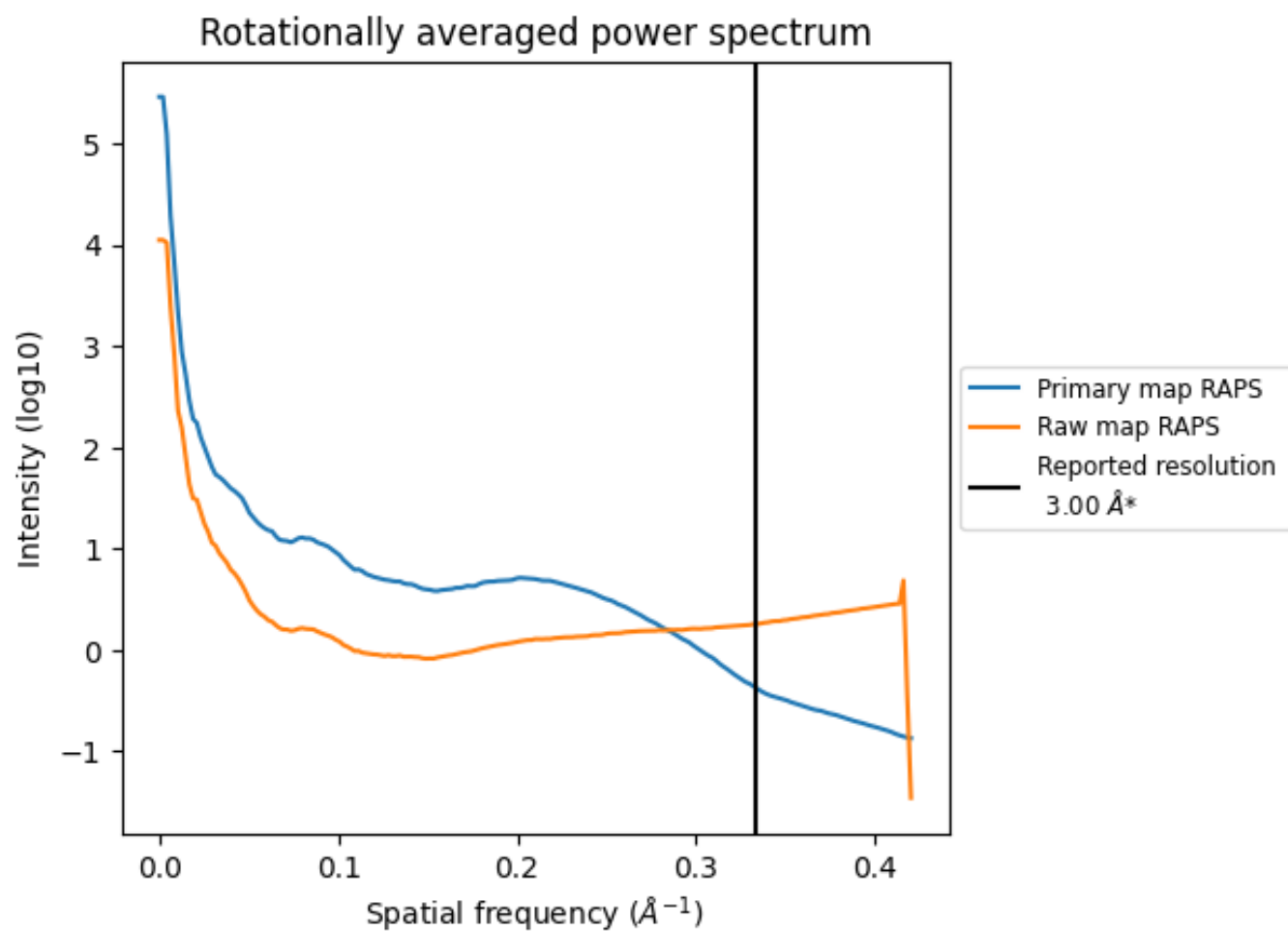
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1616 nm^3 ; this corresponds to an approximate mass of 1459 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 ⓘ

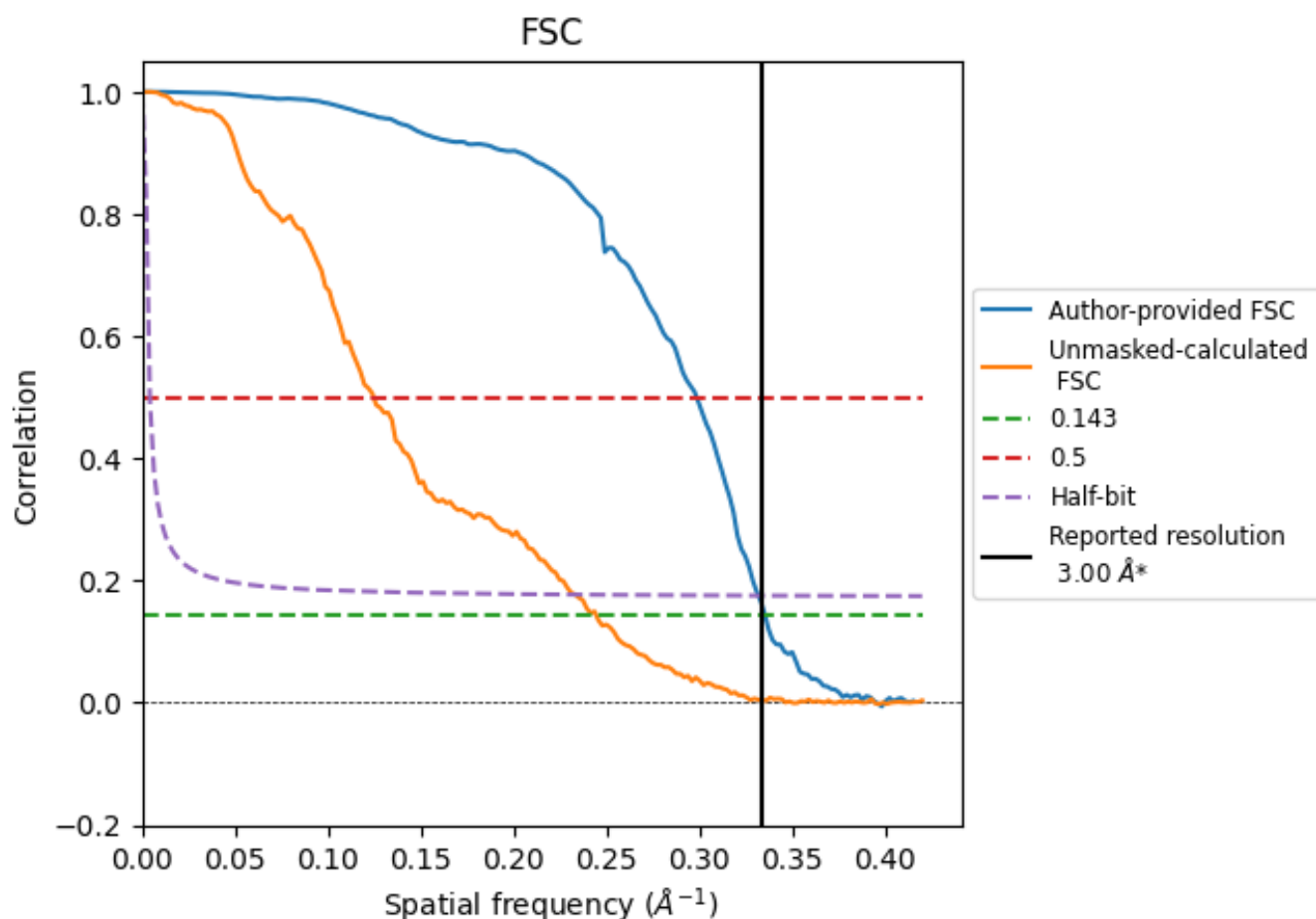


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

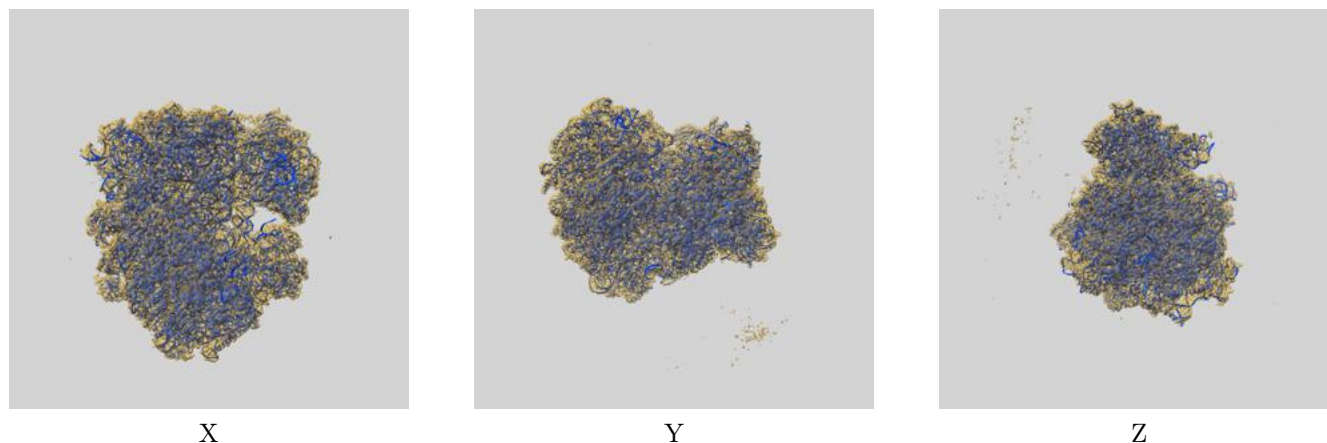
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.98	3.35	3.01
Unmasked-calculated*	4.09	8.02	4.28

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.09 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

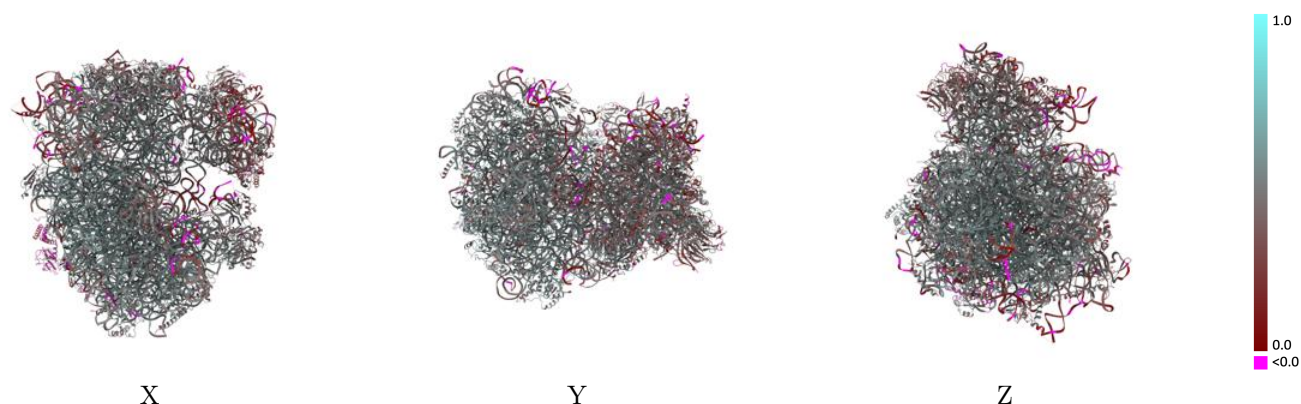
This section contains information regarding the fit between EMDB map EMD-53861 and PDB model 9R9P. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



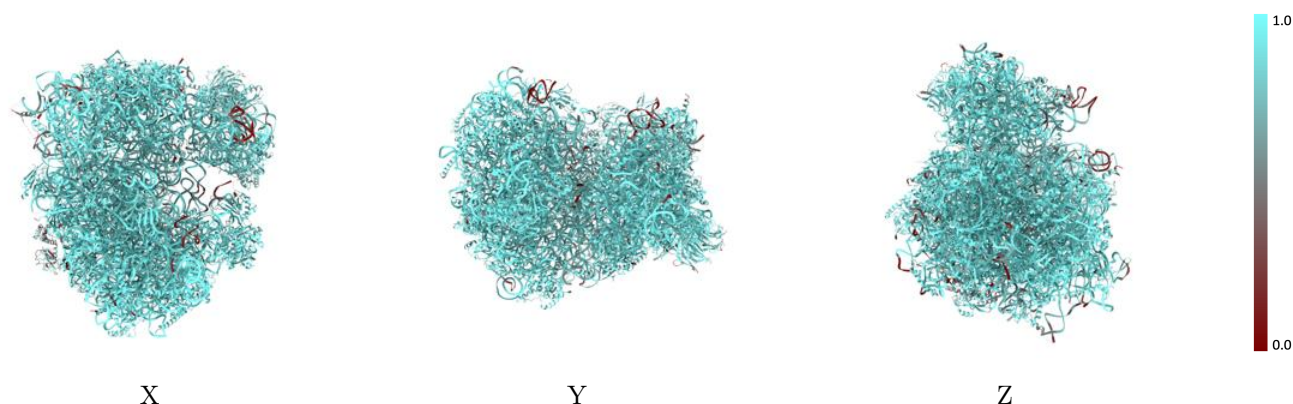
The images above show the 3D surface view of the map at the recommended contour level 0.0241 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



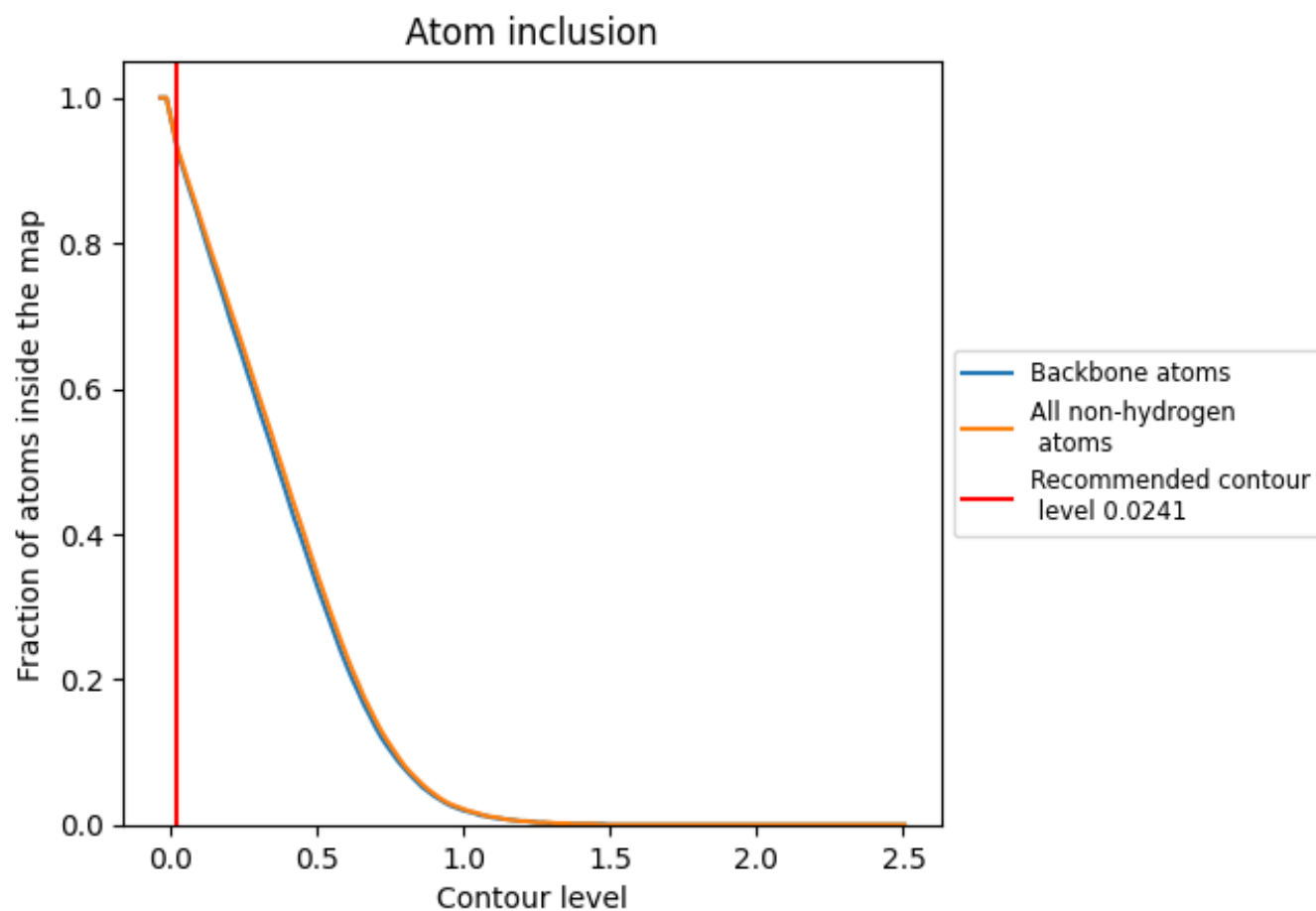
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0241).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.0241) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.4710
5	 0.9480	 0.4600
6	 0.7890	 0.2920
A	 0.5760	 0.1010
B	 0.7260	 0.3160
C1	 0.9540	 0.4940
C2	 0.9200	 0.4330
C3	 0.9620	 0.5280
C4	 0.9850	 0.4960
LA	 0.9790	 0.5540
LB	 0.9770	 0.5340
LC	 0.9730	 0.5460
LD	 0.9100	 0.4510
LE	 0.9390	 0.5010
LF	 0.9650	 0.5260
LG	 0.9430	 0.5110
LH	 0.8850	 0.4120
LI	 0.9270	 0.4600
LJ	 0.8910	 0.4190
LL	 0.9540	 0.5280
LM	 0.9610	 0.4980
LN	 0.9840	 0.5720
LO	 0.9760	 0.5300
LP	 0.9400	 0.5150
LQ	 0.9720	 0.5400
LR	 0.9130	 0.4880
LS	 0.9600	 0.4980
LT	 0.9540	 0.5130
LU	 0.9120	 0.4480
LV	 0.9410	 0.5100
LW	 0.9680	 0.5240
LX	 0.9500	 0.5320
LY	 0.9660	 0.5480
LZ	 0.9300	 0.4950
La	 0.9770	 0.5490



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Chain	Atom inclusion	Q-score
Lb	 0.9140	 0.4680
Lc	 0.9640	 0.5130
Ld	 0.9390	 0.5230
Le	 0.9700	 0.5490
Lf	 0.9830	 0.5370
Lg	 0.9290	 0.5150
Lh	 0.9520	 0.5330
Li	 0.9390	 0.4960
Lj	 0.9890	 0.5550
Lk	 0.9100	 0.4740
Ll	 0.9830	 0.5560
Ln	 0.9520	 0.5020
Lo	 0.9290	 0.5090
Lp	 0.9310	 0.5100
SA	 0.9660	 0.4850
SB	 0.8960	 0.4530
SC	 0.9670	 0.4940
SD	 0.8820	 0.3870
SE	 0.9500	 0.4770
SF	 0.9000	 0.4200
SG	 0.8590	 0.3700
SH	 0.8350	 0.3720
SI	 0.9280	 0.4910
SJ	 0.9210	 0.4350
SK	 0.7690	 0.2670
SL	 0.9320	 0.5000
SN	 0.9520	 0.4990
SO	 0.9650	 0.5000
SP	 0.8250	 0.3190
SQ	 0.9290	 0.4240
SR	 0.9080	 0.4400
SS	 0.8400	 0.3490
ST	 0.8880	 0.3780
SU	 0.8670	 0.3660
SV	 0.9680	 0.4950
SW	 0.9720	 0.5170
SX	 0.9440	 0.4910
SY	 0.8940	 0.4040
SZ	 0.8280	 0.3480
Sa	 0.9650	 0.5040
Sb	 0.9400	 0.4820
Sc	 0.8730	 0.4160

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Chain	Atom inclusion	Q-score
Sd	 0.9490	 0.4460
Se	 0.7890	 0.3770
Sg	 0.8470	 0.3460