



wwPDB EM Validation Summary Report ⓘ

May 19, 2025 – 06:27 PM EDT

PDB ID : 9BUQ / pdb_00009buq
EMDB ID : EMD-44916
Title : Single particle cryoEM structure of the Pf80S ribosome in the POST state (nrt with P- and E-site tRNA)
Authors : Anton, L.; Haile, M.; Ho, C.M.
Deposited on : 2024-05-17
Resolution : 2.30 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

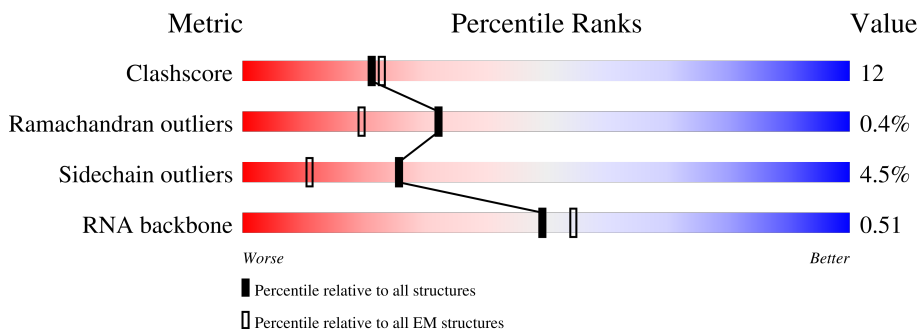
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	S1	133	
2	S2	105	
3	S3	107	
4	S4	82	
5	S5	67	
6	S6	58	
7	S7	74	

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Mol	Chain	Length	Quality of chain
8	SA	2092	
9	SB	262	
10	SC	263	
11	SD	221	
12	SE	189	
13	SF	261	
14	SG	272	
15	SH	306	
16	SI	195	
17	SJ	194	
18	SK	130	
19	SL	218	
20	SM	144	
21	SN	118	
22	SO	137	
23	SP	151	
24	SQ	145	
25	SR	141	
26	SS	156	
27	ST	54	
28	SU	151	
29	SV	161	
30	SW	137	
31	SX	145	
32	SY	170	

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Mol	Chain	Length	Quality of chain
33	SZ	82	
34	AA	3788	
35	AC	159	
36	AB	119	
37	AL	215	
38	A1	146	
39	A2	127	
40	A4	67	
41	A6	108	
42	A7	120	
43	AN	165	
44	A8	131	
45	A9	140	
46	Aa	150	
47	Ab	112	
48	Ad	87	
49	Ae	51	
50	Af	128	
51	AP	205	
52	Ah	96	
53	Ai	104	
54	AI	221	
55	AJ	283	
56	Ac	92	
57	AK	202	

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Mol	Chain	Length	Quality of chain
58	AM	139	
59	AS	187	
60	AO	148	
61	AQ	219	
62	AR	294	
63	AW	173	
64	AY	190	
65	AT	182	
66	AZ	126	
67	A3	124	
68	A5	257	
69	AD	260	
70	AE	386	
71	AF	411	
72	AG	173	
73	AU	184	
74	AH	190	
75	AV	161	
76	Ag	39	
77	AX	139	
78	A0	162	
79	S9	76	
80	mR	7	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 194758 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S1	120	Total	C	N	O	S	0	0
			985	632	189	162	2		

- Molecule 2 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	S2	41	Total	C	N	O	0	0
			320	208	56	56		

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S3	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 5 is a protein called 40S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S5	59	Total	C	N	O	S	0	0
			465	290	94	80	1		

- Molecule 6 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	S6	43	Total	C	N	O	0	0
			345	213	75	57		

- Molecule 7 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 8 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	1608	Total	C	N	O	P	0	0
			34208	15346	6106	11170	1586		

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SB	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 10 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SC	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SD	157	Total	C	N	O	S	0	0
			1228	782	225	214	7		

- Molecule 12 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SE	185	Total	C	N	O	S	0	0
			1514	962	290	260	2		

- Molecule 13 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SF	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SG	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SH	204	Total	C	N	O	S	0	0
			1651	1046	316	283	6		

- Molecule 16 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SI	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SJ	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 18 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SK	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SL	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 20 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SM	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 21 is a protein called 40S ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SN	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 22 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SO	79	Total	C	N	O	S	0	0
			686	450	116	118	2		

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SP	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 24 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SQ	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SR	98	Total	C	N	O	S	0	0
			746	474	123	145	4		

- Molecule 26 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SS	128	Total	C	N	O	S	0	0
			1046	657	205	180	4		

- Molecule 27 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	ST	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 28 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SU	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SV	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 30 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SW	95	Total	C	N	O	S	0	0
			785	498	149	135	3		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SX	96	Total	C	N	O	S	0	0
			776	497	137	138	4		

- Molecule 32 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SY	154	Total	C	N	O	S	0	0
			1266	811	239	214	2		

- Molecule 33 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SZ	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12053	22224	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2517	1126	457	817	117		

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	105	Total	C	N	O	S	0	0
			837	534	152	148	3		

- Molecule 40 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 42 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 43 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	147	Total	C	N	O	S	0	0
			1210	787	212	205	6		

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 45 is a protein called 60S ribosomal protein L35ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 46 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 47 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Ab	95	Total	C	N	O	0	0
			756	477	150	129		

- Molecule 48 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 49 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 51 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 54 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			709	441	150	113	5		

- Molecule 57 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 58 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 62 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2049	1301	385	357	6		

- Molecule 63 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 65 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 67 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 68 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 70 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 71 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 72 is a protein called 60S ribosomal protein L11a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1475	950	264	255	6		

- Molecule 75 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 79 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	S9	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

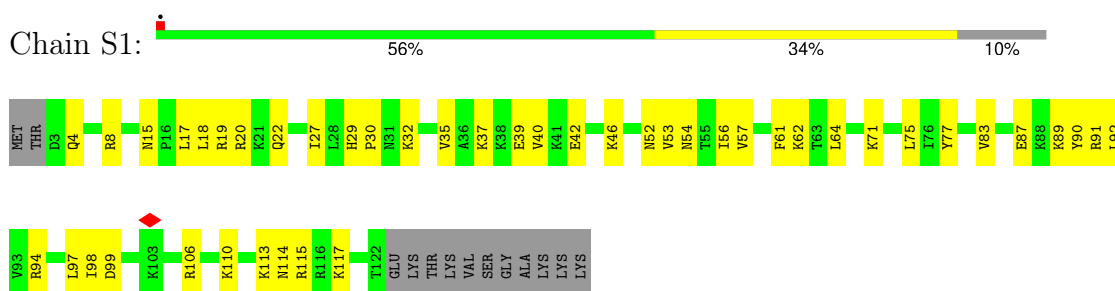
- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	mR	7	Total	C	N	O	P	0	0
			145	65	21	52	7		

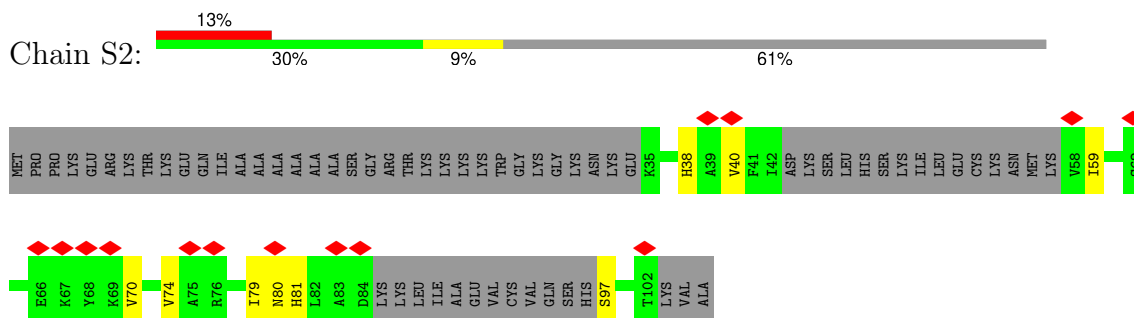
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

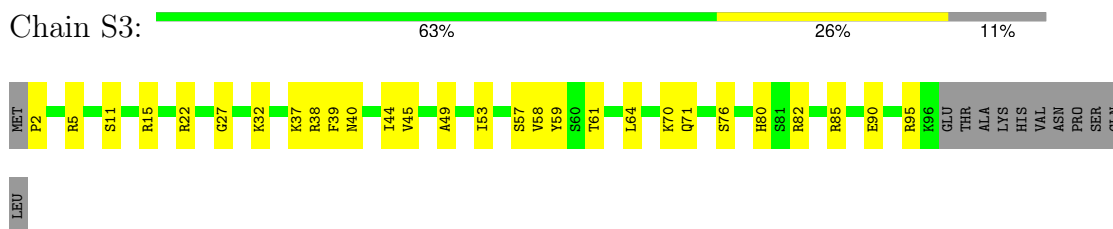
- Molecule 1: 40S ribosomal protein S24



- Molecule 2: 40S ribosomal protein S25



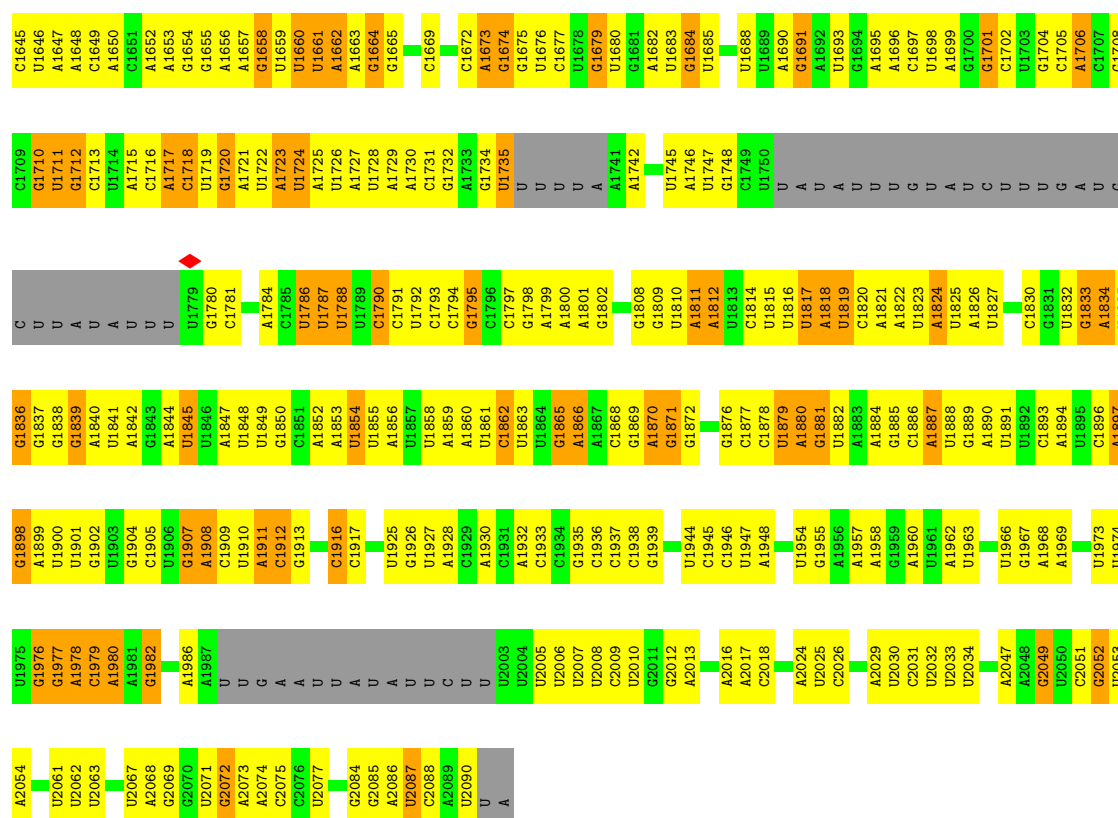
- Molecule 3: 40S ribosomal protein S26



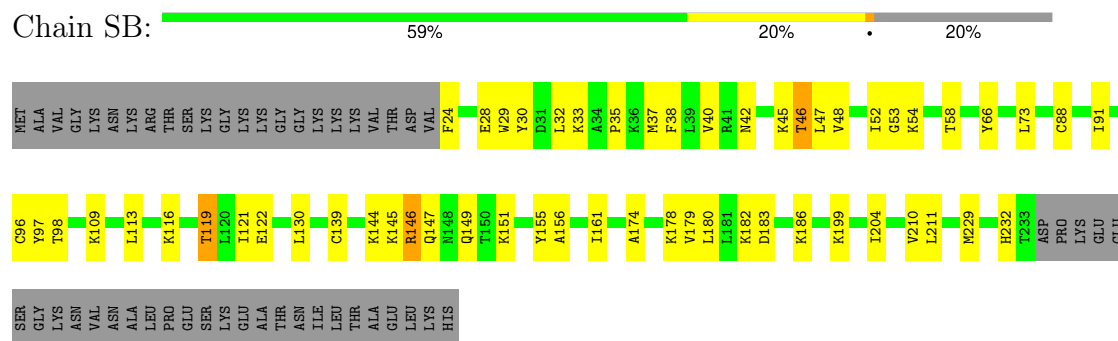
- Molecule 4: 40S ribosomal protein S27



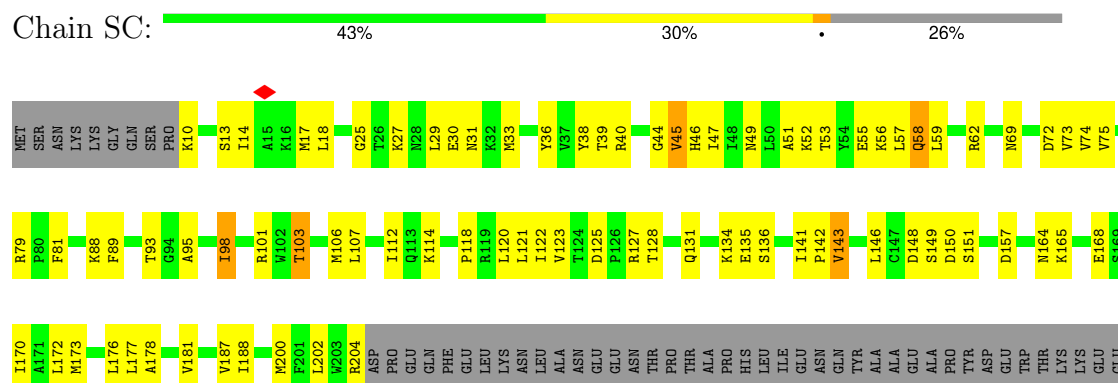




• Molecule 9: 40S ribosomal protein S3a



• Molecule 10: 40S ribosomal protein SA



TRP
ASN
SER
ASP
ASN
THR
ASN
GLU
ASP
TRP
LYS
ASN
PRO
ILE
ALA
GLU
GLU
TRP

• Molecule 11: 40S ribosomal protein S3

Chain SD: 

MET SER ALA P4 K7 K8 R9 K10 N13 V16 E23 F24 R27 I28 V39 ARG VAL THR PRO ILE ARG GLU ILE ILE ARG ALA THR THR ARG THR ARG GLU VAL LEU GLY LYS ASP GLY R65 R68 R76 F77 F78 ASN LYS SER THR ASN K152 VAL

GLU LEU PHE ALA GLU ARG VAL HIS ARG GLY L97 C98 A99 M100 A101 E104 S105 L106 K109 VAL L110 THR K111 PRO K112 ILE G113 L114 R117 G120 Y121 G122 V123 L124 THR R125 ARG THR R126 THR I127 R128 A132 GLY LYS G134 C135 E136 V137 I138 V139 K142 L143 F144 A145 Q146 R147 M151 K152 F153

R154 Y157 L158 T161 K166 R167 F169 M170 T171 Q177 L178 K179 Q180 L183 G184 I185 K188 I189 M190 T193 ALA ILE ASP THR ARG GLY LEU THR S207 D211 N212 I213 S214 V215 L216 GLU PRO LYS THR ASP THR VAL ASP LEU

• Molecule 12: 40S ribosomal protein S9

Chain SE: 

MET P2 Y5 S9 K16 E22 K29 G32 G35 L36 K37 N38 K39 R40 E41 I42 I43 R44 R45 Q46 L49 I52 R53 R57 Y58 L59 L60 T61 E64 K65 Q72 G73 E74 L76 L77 R78 R82 L86 E90 E91 K92 V96

L99 Q110 G117 L118 A119 V122 H123 R126 V127 L128 I129 R130 Q131 R132 H133 I134 R135 V136 G137 M140 V141 I143 V148 R149 V150 E153 K154 H155 I156 D157 F158 A159 S162 R168 R171 V172 S176 L177 Q180 K181 E185 A186 GLU ALA GLU

• Molecule 13: 40S ribosomal protein S4

Chain SF: 

MET G2 K6 K10 W18 M19 N20 L21 K22 Q26 Y27 K30 P35 H36 K37 E40 S41 I42 P43 L44 L45 L46 L47 L48 R51 T57 V61 K62 R63 I64 L65 I66 V70 N74 K75 R76 R77 T78 D79 F82 P83 S196 S197 I198 M201 T204

R100 L101 D104 K106 G107 R108 Y121 K122 L123 G124 K125 V126 K127 L131 R135 L136 S137 H142 I44 R145 S146 I147 V148 P149 I150 K155 T159 L164 H172 L173 K174 L180 V181 S188 V189 G190 R191 V192 G193 V194 S196 S197 I198 M201 T204

Y205 I208 H209 V210 K211 D212 S213 R214 V225 F226 V227 D230 N231 L238 P239 R240 E241 K242 K245 L246 D247 I248 L249 E250 E251 R252 R253 N254 K257 A258 LEU ASN ASN

• Molecule 14: 40S ribosomal protein S5

Chain SG: 

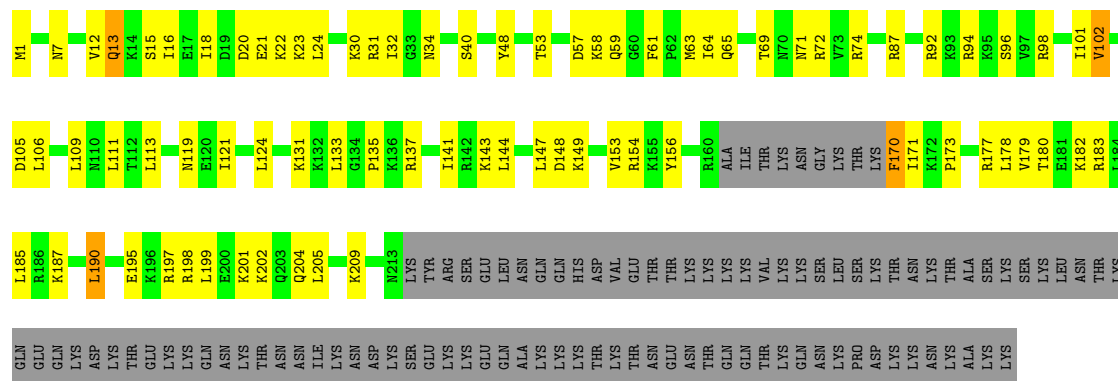
MET GLU ASP ARG GLY PHE SER ARG GLY PHE GLY ARG VAL ARG GLY THR ARG GLY ARG GLY GLY ARG GLY SER ALA GLU ASP ASP LEU K39 M40 V41 V42 P43 V44 T45 G43 G49 L50 I56 I59 E60 E61 I62 D76 Y77

Q80 E83 L88 D91 V92 V93 K94 T95 M96 P97 V98 Q99 K100 Q101 R107 T108 K111 V114 A115 I116 H122 C123 G124 R138 I142 S147 L148 T149 V150 V151 G154 I160 G161 D162 P167 M168 K169 V170 S171 G172 K173 V177 R178 V182 P183



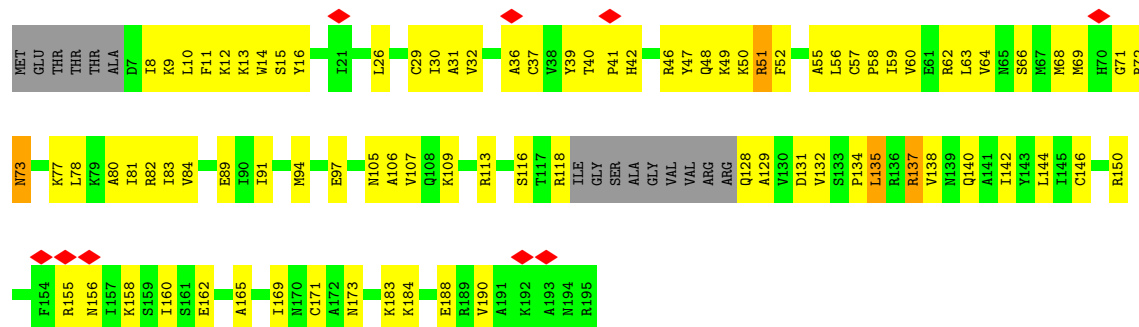
• Molecule 15: 40S ribosomal protein S6

Chain SH: 41% 25% 33%



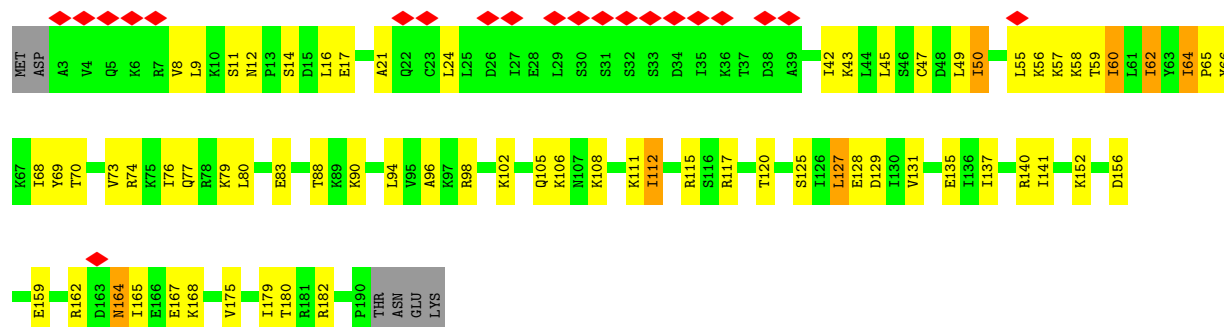
• Molecule 16: 40S ribosomal protein S5

Chain SI: 5% 48% 42% 8%



• Molecule 17: 40S ribosomal protein S7

Chain SJ: 11% 61% 32%



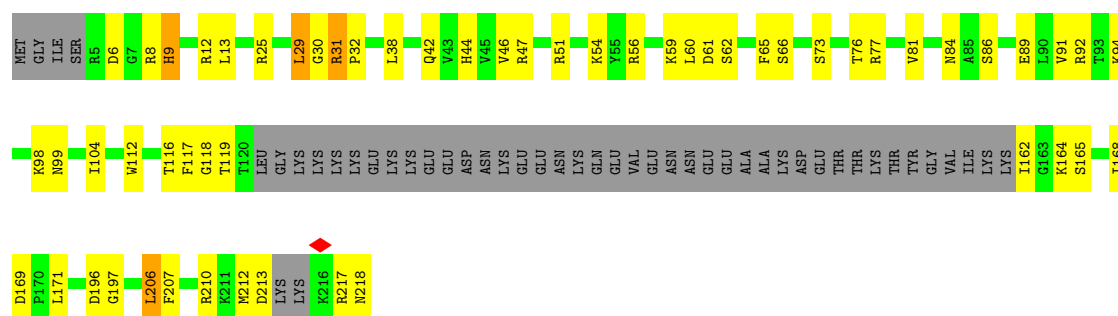
• Molecule 18: 40S ribosomal protein S15A

Chain SK: 



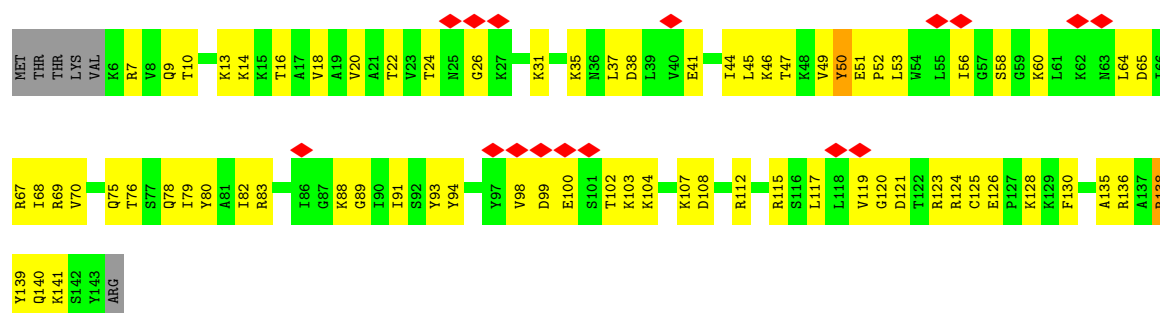
• Molecule 19: 40S ribosomal protein S8

Chain SL: 



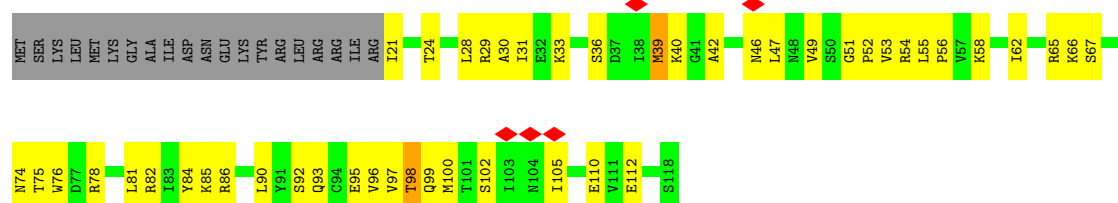
• Molecule 20: 40S ribosomal protein S16

Chain SM: 



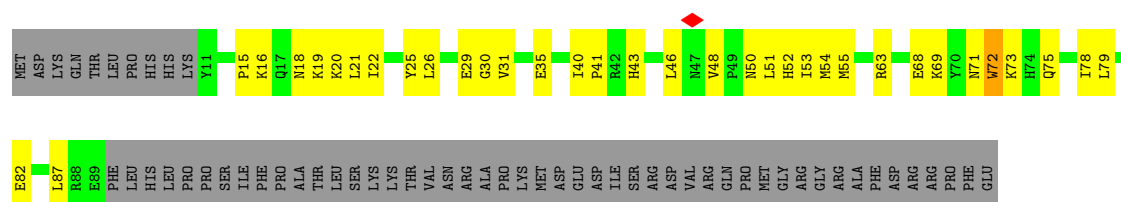
• Molecule 21: 40S ribosomal protein S20e

Chain SN: 

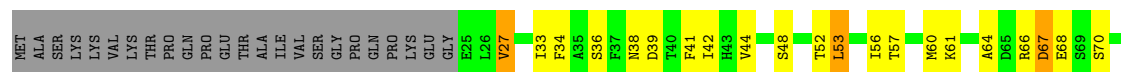


• Molecule 22: 40S ribosomal protein S10

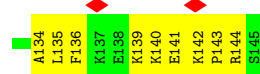
Chain SO: 



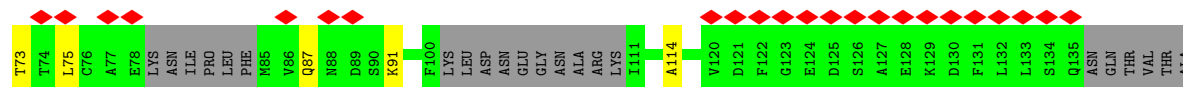
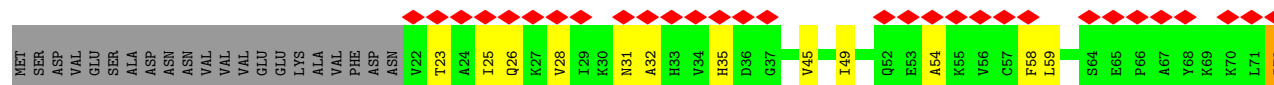
- Molecule 23: 40S ribosomal protein S11



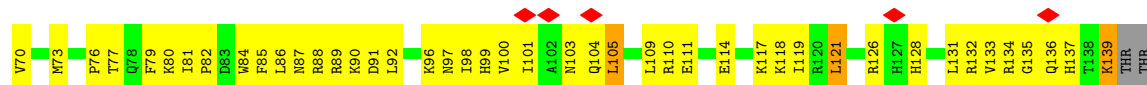
- Molecule 24: 40S ribosomal protein S23



- Molecule 25: 40S ribosomal protein S12



- Molecule 26: 40S ribosomal protein S18



GLY
ARG
ARG
GLY
CYS
ILE
LEU
THR
VAL
GLY
VAL
ALA
LYS
LYS
GLY
ALA

• Molecule 27: 40S ribosomal protein S29



MET GLY ARG CYS ILE LEU THR VAL GLY VAL ALA LYS LYS GLY ALA
V7 H8 P9 K10 K11 Y12 G13 S16 R17 Q18 C19 R20 V21 H26 A27 I28 I29 R30 K31 I36 C37 R38 Q39 C40 E43 R44 F50 K51 R52 Y53 R54

• Molecule 28: 40S ribosomal protein S15



MET GLY R3 K9 S14 T15 R20 K21 Q22 L26 K27 Q28 E32 I33 I37 K42 K43 G44 Q45 T46 Q49 I50 L54 P61 T67 G68 N69 K70 I71 L72 R73 I74 D87 M98 R99 L102 D108 K112 F113 R114 E119 S120
K121 R124 K130 K139 W139 R140 Q142 T145 I150 A151

• Molecule 29: 40S ribosomal protein S11



MET ALA THR LEU P6 V7 Q8 R11 A12 Y13 Q14 K15 Q16 A19 S20 N23 N24 K25 LYS ILE LYS GLY SER LYS TYR R36 R37 L43 T47 E50 A51 K52 V55 V56 V57 D58 C61 N66 G76 K82 I89 Y100 N101
R102 K105 K108 N109 T110 P111 C114 S115 P116 C117 D124 I125 V126 T127 V138 V142 V145 E146 K147 S153 K156 Q157 F161

• Molecule 30: 40S ribosomal protein S17

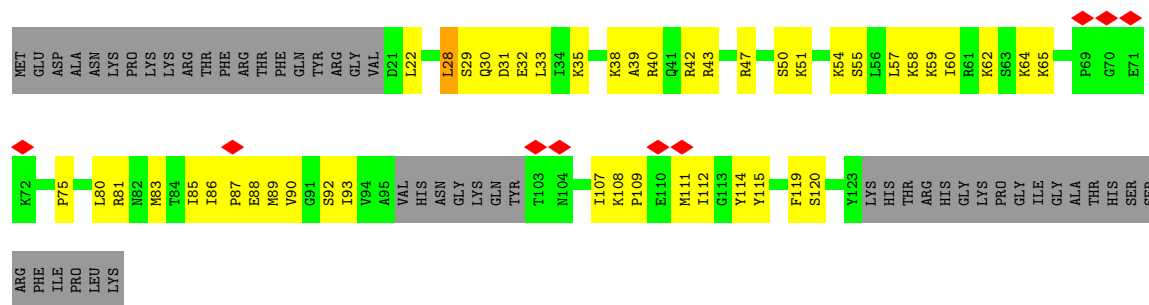


MET GLY R3 V4 R5 T6 K7 T8 T9 K10 R11 A12 Q15 I16 V17 E18 K19 A22 K23 L26 D27 F28 Q29 I30 N31 K32 K33 I34 T35 E36 A39 I40 I41 M46 K47 M48 K49 V50 A51 G52 F53 V54 T55 H56 L57 H58 K59 R60 I61 Q62 K63 I69 S70 L71
Q74 E77 R78 E79 L82 D83 PHE VAL PRO GLU LYS SER GLN ILE ASP VAL SER VAL ILE Y97 V98 E99 P100 R104 M105 I106 K107 S108 K109 G110 ILE ASN ILE SER ASN MET LYS VAL HIS ASN PRO MET ILE ASN THR ASN GLN GLN LYS GLN ASN ARG MET ASN ASN GLN

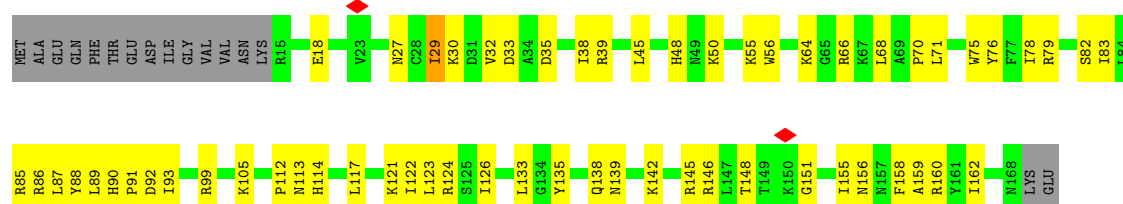
PHE

• Molecule 31: 40S ribosomal protein S19

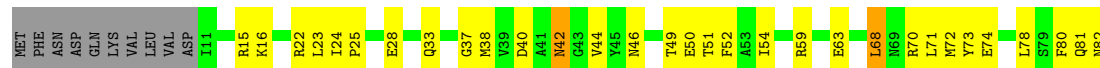




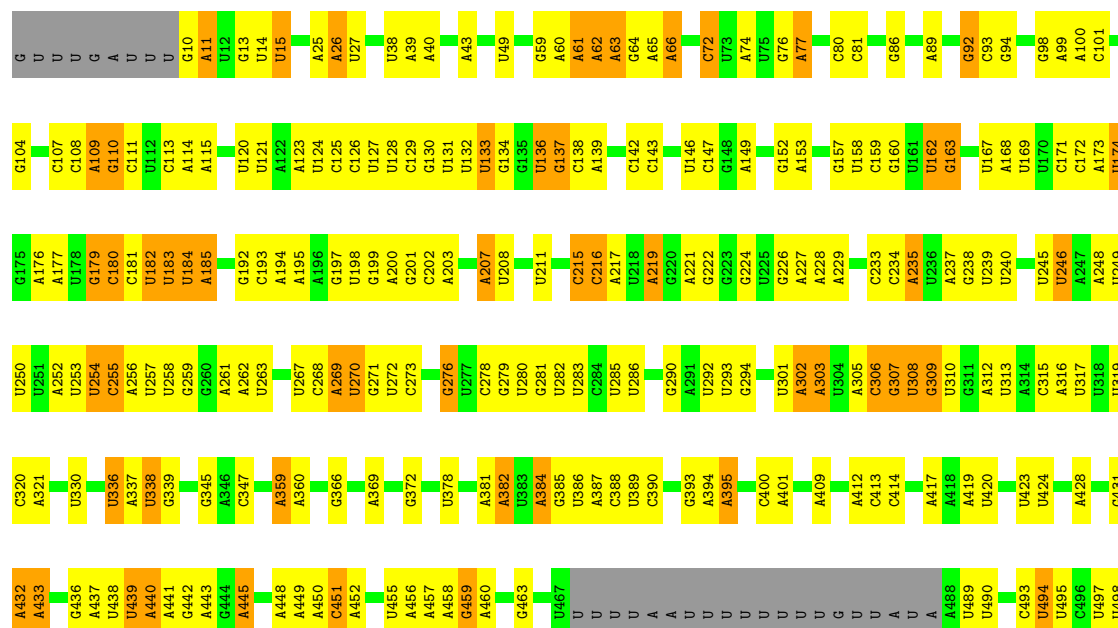
• Molecule 32: 40S ribosomal protein S19



• Molecule 33: 40S ribosomal protein S21

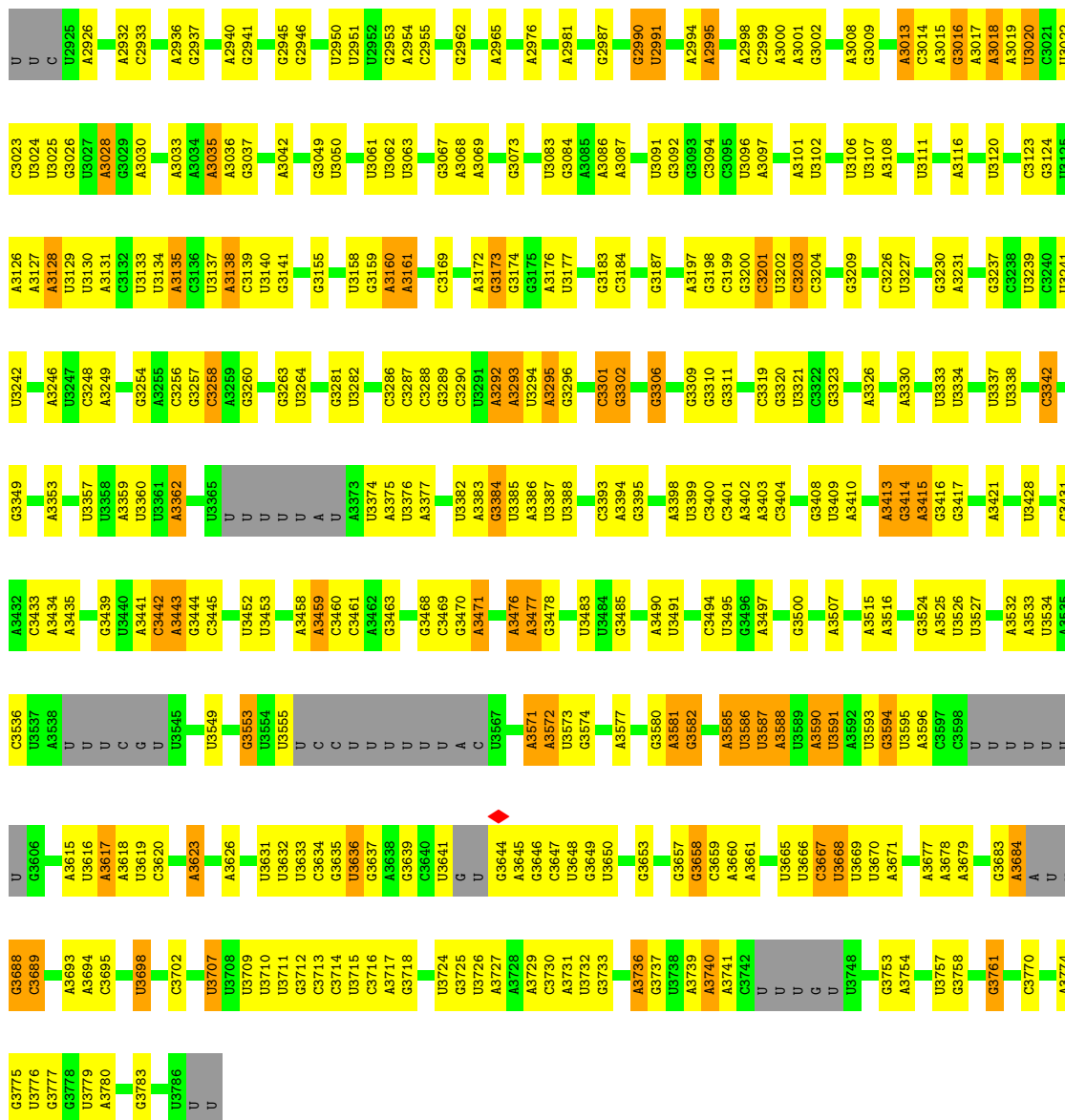


• Molecule 34: 28S ribosomal RNA



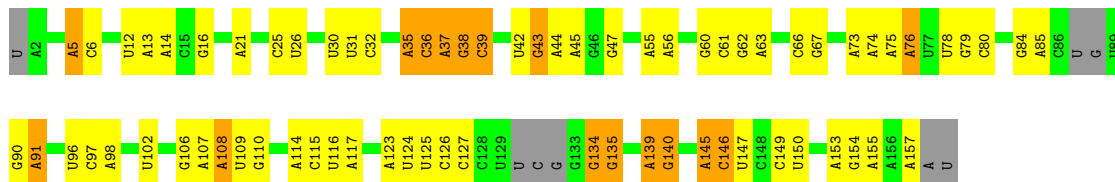






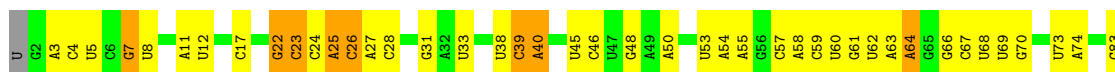
• Molecule 35: 5.8S ribosomal RNA

Chain AC: 50% 35% 10% 5%



• Molecule 36: 5S ribosomal RNA

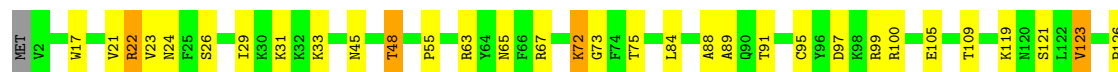
Chain AB: 57% 34% 8%





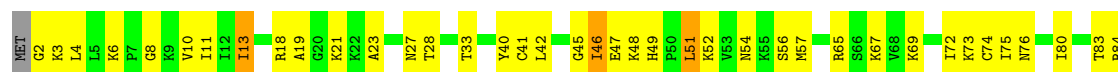
• Molecule 37: 60S ribosomal protein L13

Chain AL: 74% 21% • •



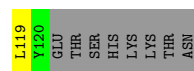
• Molecule 38: 60S ribosomal protein L27

Chain A1: 59% 34% • •



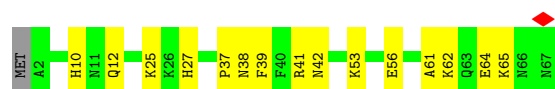
• Molecule 39: 60S ribosomal protein L28

Chain A2: 61% 20% 17%



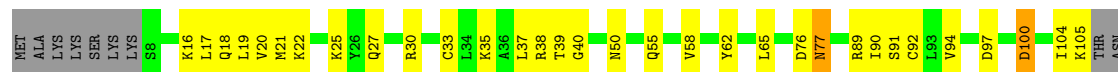
• Molecule 40: 60S ribosomal protein L29

Chain A4: 76% 22% •



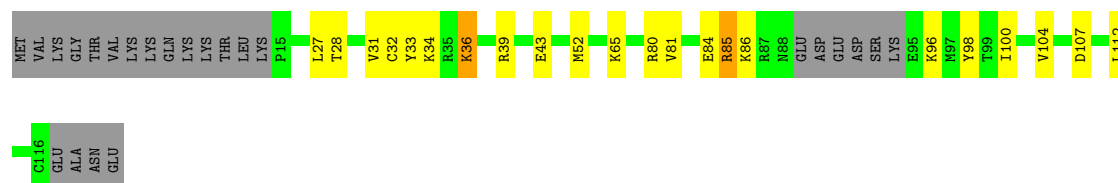
• Molecule 41: 60S ribosomal protein L30e

Chain A6: 61% 28% 9%



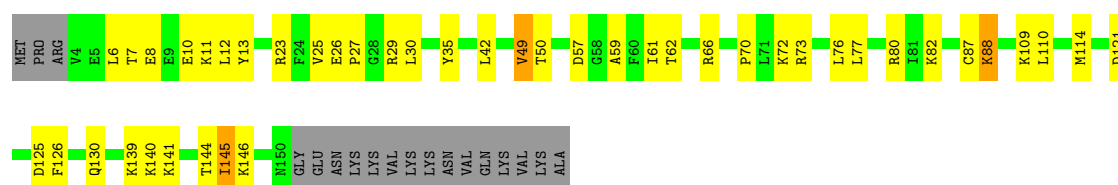
- Molecule 42: 60S ribosomal protein L31

Chain A7: 



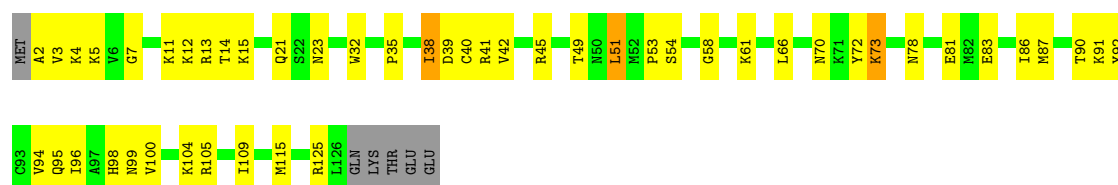
- Molecule 43: 60S ribosomal protein L14

Chain AN: 



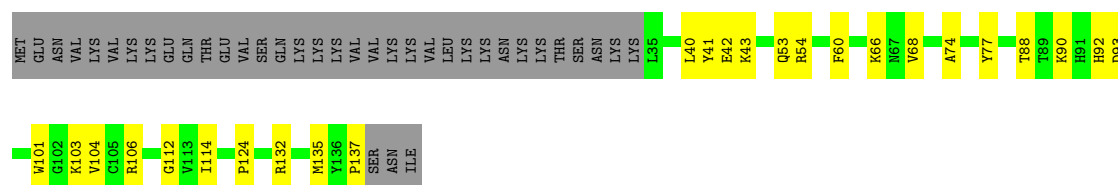
- Molecule 44: 60S ribosomal protein L32

Chain A8: 



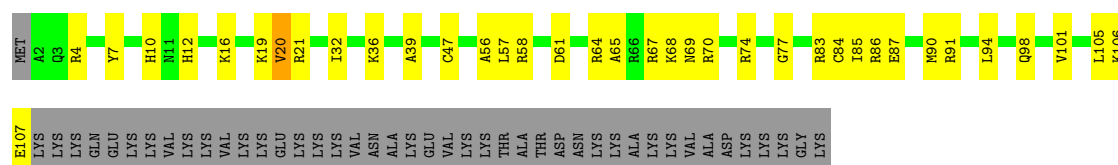
- Molecule 45: 60S ribosomal protein L35ae

Chain A9: 




- Molecule 46: 60S ribosomal protein L34

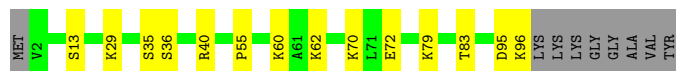
Chain Aa: 



- | MET |
|-----|
| S2 |
| R3 |
| R4 |
| T5 |
| V8 |
| T11 |
| G19 |
| I26 |
| I29 |
| E30 |
| L31 |
| M32 |
| L38 |
| T47 |
| K48 |
| G51 |
| V52 |
| G53 |
| F54 |
| C57 |
| V64 |
| C65 |
| A78 |
| A79 |
| T82 |
| I83 |
| I84 |
| R85 |
| L86 |
| ARG |
| LYS |
| GLN |
| LYS |
| GLU |
| GLU |
| ALA |
| GLN |
| LYS |
| P89 |

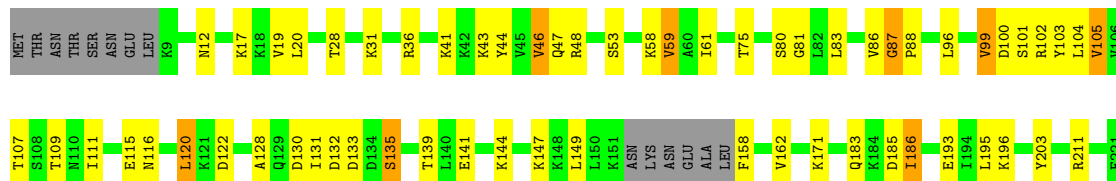
- Molecule 53: Large ribosomal subunit protein eL42

Chain Ai: 



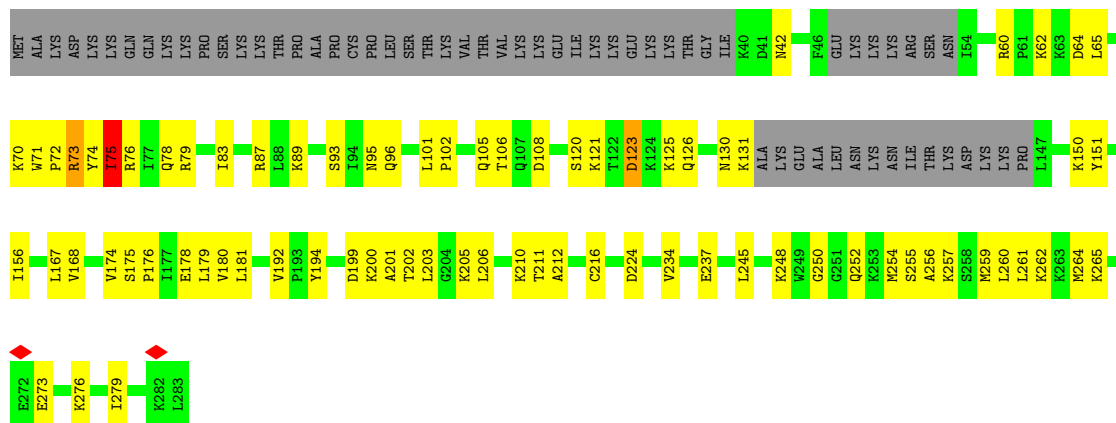
- Molecule 54: 60S ribosomal protein L6

Chain AI: 



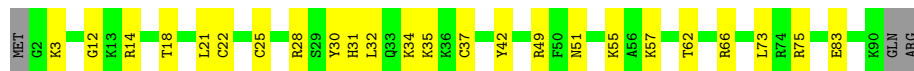
- Molecule 55: 60S ribosomal protein L7a

Chain AJ: 




- Molecule 56: Ribosomal protein L37

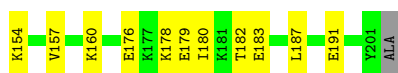
Chain Ac: 



- Molecule 57: 60S ribosomal protein L13

Chain AK: 





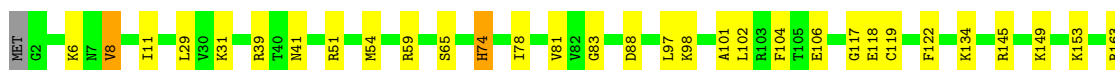
- Molecule 58: 60S ribosomal protein L23, putative

Chain AM: 66% 27% 5%



- Molecule 59: 60S ribosomal protein L18-2

Chain AS: 78% 20% ..



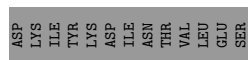
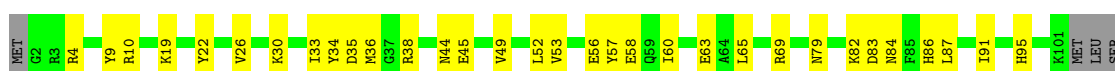
- Molecule 60: 60S ribosomal protein L27a

Chain AO: 81% 16% ..



- Molecule 61: 60S ribosomal protein L10

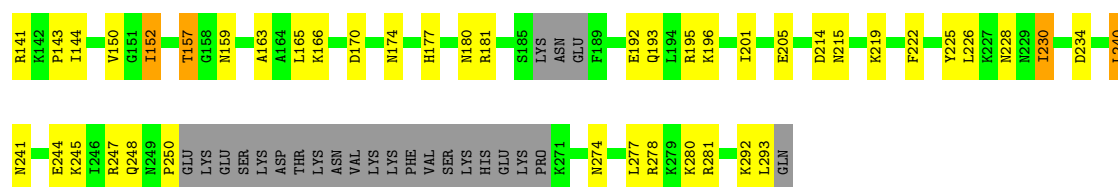
Chain AQ: 59% 27% 14%



- Molecule 62: 60S ribosomal protein L5

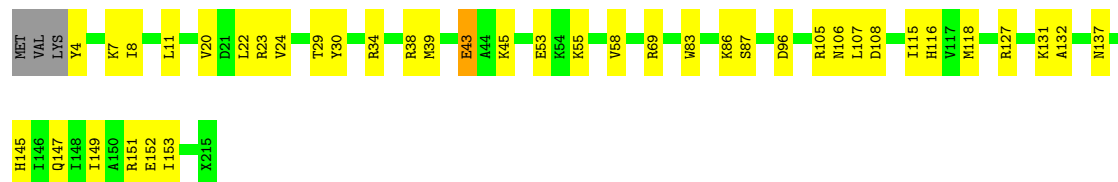
Chain AR: 63% 21% 14%





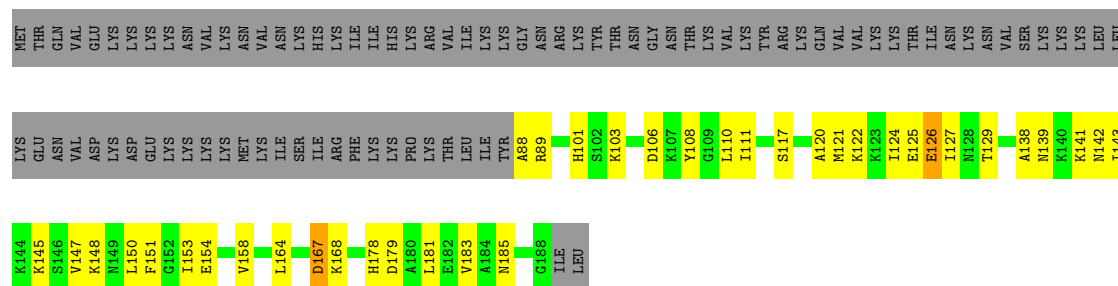
- Molecule 63: 60S ribosomal protein L17

Chain AW: 75% 23% ..



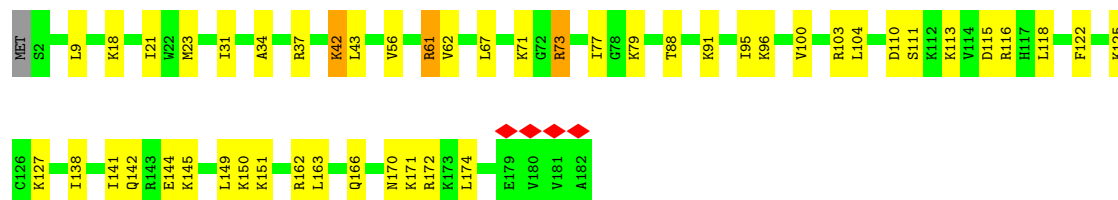
- Molecule 64: 60S ribosomal protein L23

Chain AY: 33% 19% 47%



- Molecule 65: 60S ribosomal protein L19

Chain AT: 73% 25% ..

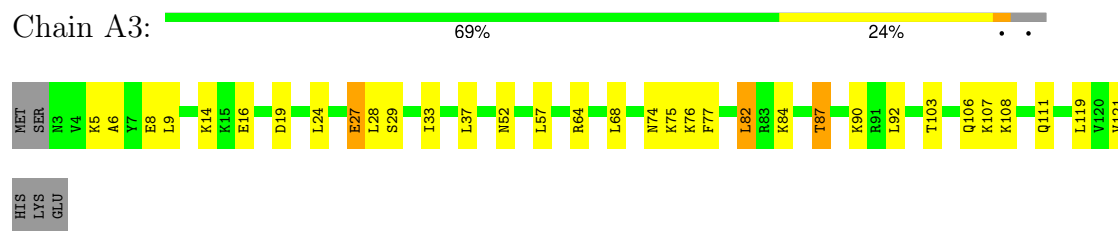


- Molecule 66: 60S ribosomal protein L26

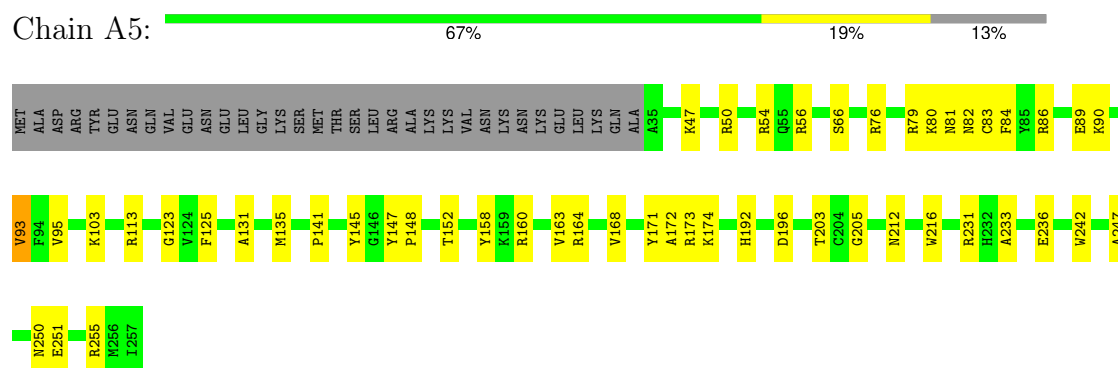
Chain AZ: 67% 26%



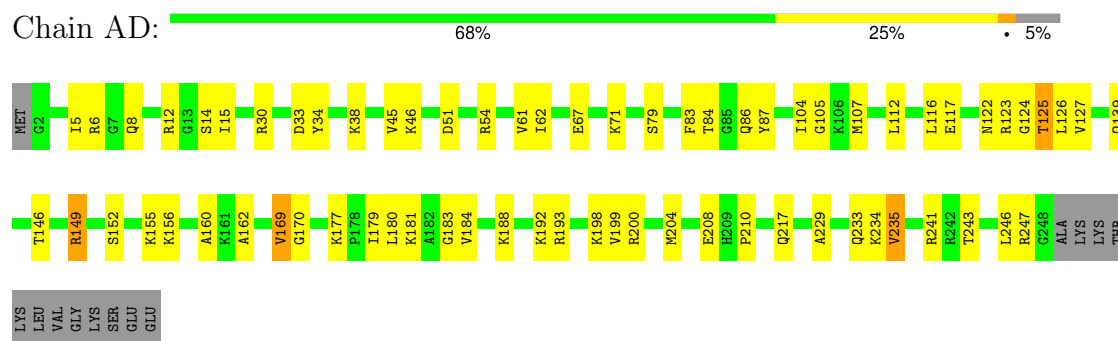
- Molecule 67: 60S ribosomal protein L35



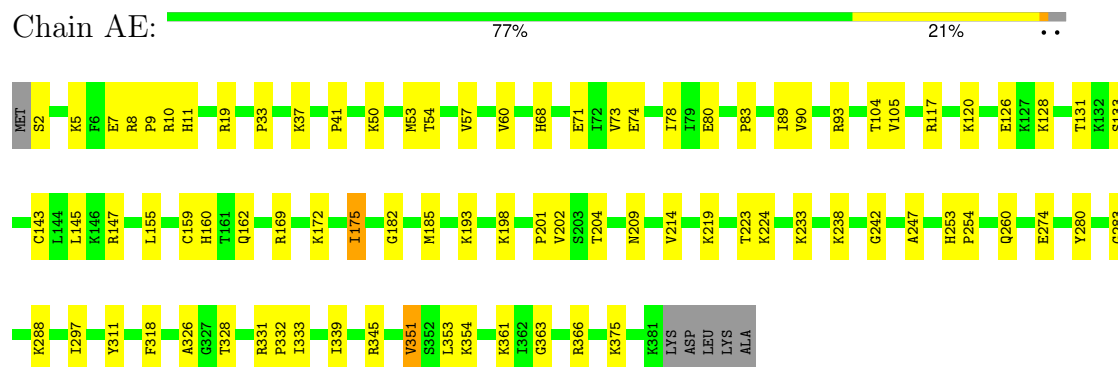
- Molecule 68: 60S ribosomal protein L7




- Molecule 69: 60S ribosomal protein L2

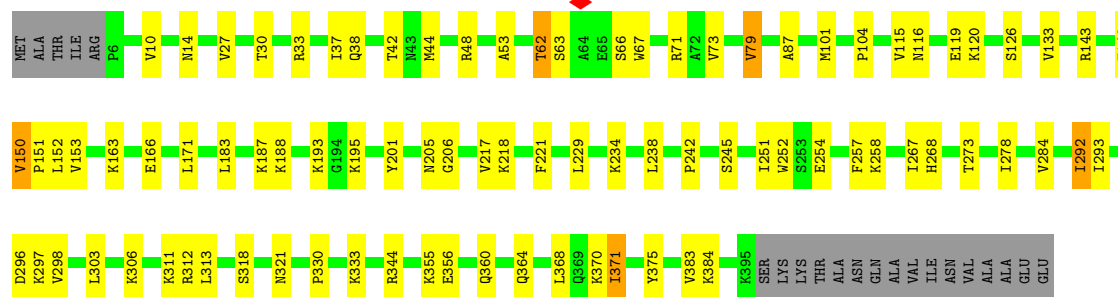


- Molecule 70: 60S ribosomal protein L3



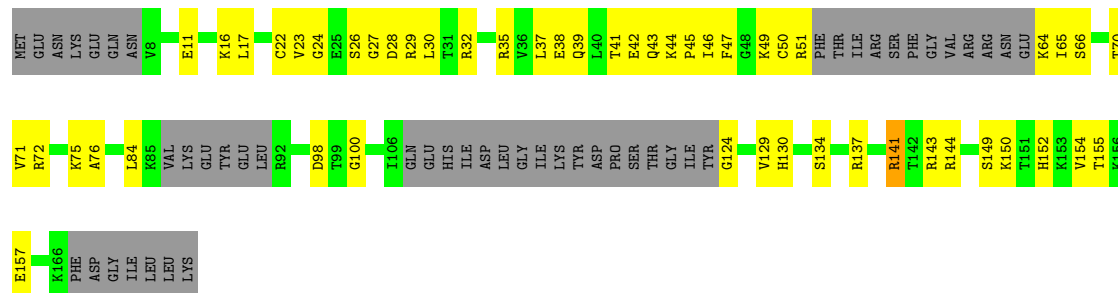
- Molecule 71: 60S ribosomal protein L4

Chain AF:  74% 20% 5%



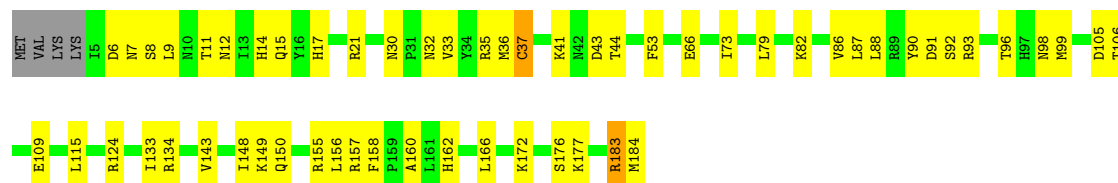
- Molecule 72: 60S ribosomal protein L11a

Chain AG:  42% 29% 28%



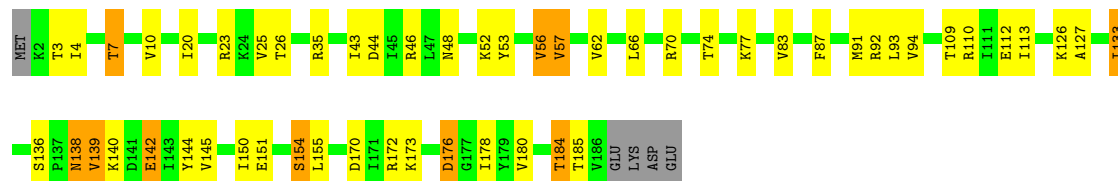
- Molecule 73: 60S ribosomal protein L18a

Chain AU:  67% 30% 2%



- Molecule 74: 60S ribosomal protein L6

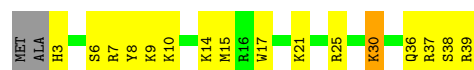
Chain AH:  69% 23% 5%



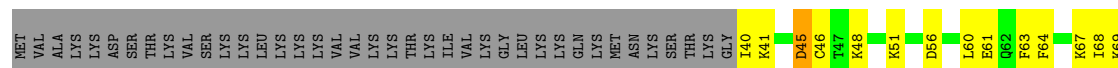
- Molecule 75: 60S ribosomal protein L21

Chain AV:  67% 28% 2%

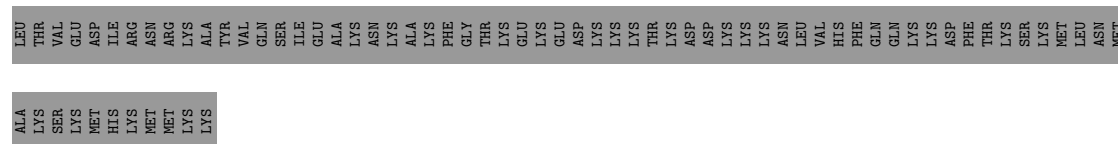
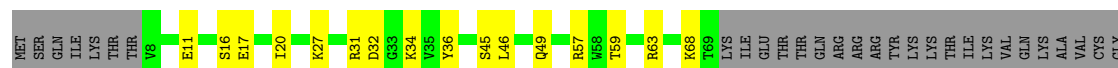
- Molecule 76: 60S ribosomal protein L41



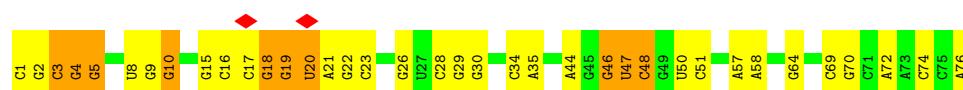
- Molecule 77: 60S ribosomal protein L22



- Molecule 78: 60S ribosomal protein L24



- Molecule 79: P-site tRNA



- Molecule 80: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	261029	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.083	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00404	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	S1	0.17	0/998	0.37	0/1321
2	S2	0.12	0/323	0.27	0/435
3	S3	0.21	0/793	0.37	0/1055
4	S4	0.17	0/597	0.45	0/801
5	S5	0.13	0/466	0.38	0/616
6	S6	0.16	0/348	0.51	0/458
7	S7	0.14	0/1754	0.23	0/2732
8	SA	0.20	0/38276	0.29	0/59598
9	SB	0.24	0/1737	0.51	1/2321 (0.0%)
10	SC	0.19	0/1569	0.47	0/2129
11	SD	0.14	0/1240	0.38	0/1652
12	SE	0.20	0/1538	0.45	0/2055
13	SF	0.20	0/2097	0.40	0/2819
14	SG	0.22	0/1799	0.42	0/2429
15	SH	0.16	0/1668	0.42	0/2214
16	SI	0.16	0/1443	0.42	0/1936
17	SJ	0.17	0/1544	0.44	0/2064
18	SK	0.23	0/1054	0.45	0/1411
19	SL	0.22	0/1407	0.44	0/1879
20	SM	0.14	0/1113	0.38	0/1487
21	SN	0.15	0/780	0.41	0/1053
22	SO	0.15	0/705	0.46	0/950
23	SP	0.22	0/966	0.44	0/1295
24	SQ	0.20	0/1149	0.39	0/1532
25	SR	0.09	0/754	0.25	0/1013
26	SS	0.15	0/1062	0.49	0/1425
27	ST	0.14	0/412	0.28	0/544
28	SU	0.24	0/1223	0.39	0/1634
29	SV	0.22	0/1233	0.39	0/1645
30	SW	0.17	0/792	0.50	0/1053
31	SX	0.13	0/787	0.40	0/1050
32	SY	0.15	0/1294	0.38	0/1742
33	SZ	0.20	0/565	0.38	0/758
34	AA	0.27	0/75947	0.32	0/118255

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.26	0/3599	0.31	0/5603
36	AB	0.24	0/2816	0.28	0/4388
37	AL	0.22	0/1793	0.39	0/2387
38	A1	0.21	0/1151	0.40	0/1531
39	A2	0.22	0/846	0.42	0/1124
40	A4	0.20	0/564	0.37	0/737
41	A6	0.23	0/748	0.37	0/1001
42	A7	0.21	0/805	0.33	0/1073
43	AN	0.21	0/1226	0.36	0/1632
44	A8	0.25	0/1053	0.45	0/1399
45	A9	0.28	0/864	0.46	0/1160
46	Aa	0.24	0/871	0.32	0/1161
47	Ab	0.21	0/762	0.44	0/1008
48	Ad	0.21	0/611	0.42	0/812
49	Ae	0.22	0/396	0.29	0/521
50	Af	0.23	0/418	0.38	0/556
51	AP	0.26	0/1735	0.46	1/2320 (0.0%)
52	Ah	0.22	0/667	0.34	0/887
53	Ai	0.22	0/788	0.33	0/1032
54	AI	0.22	0/1708	0.41	0/2274
55	AJ	0.22	0/1840	0.47	0/2456
56	Ac	0.25	0/722	0.44	0/951
57	AK	0.23	0/1689	0.34	0/2260
58	AM	0.25	0/1012	0.42	0/1363
59	AS	0.23	0/1531	0.37	0/2040
60	AO	0.24	0/1199	0.37	0/1597
61	AQ	0.19	0/1579	0.34	0/2113
62	AR	0.20	0/2078	0.34	0/2776
63	AW	0.23	0/1244	0.40	0/1663
64	AY	0.22	0/805	0.40	0/1074
65	AT	0.23	0/1525	0.41	0/2016
66	AZ	0.22	0/1012	0.48	0/1339
67	A3	0.21	0/1004	0.35	0/1329
68	A5	0.23	0/1917	0.42	0/2562
69	AD	0.25	0/1901	0.40	0/2544
70	AE	0.23	0/3129	0.33	0/4195
71	AF	0.22	0/3144	0.36	0/4205
72	AG	0.22	0/1020	0.44	0/1349
73	AU	0.23	0/1527	0.35	0/2043
74	AH	0.22	0/1500	0.38	0/2025
75	AV	0.23	0/1300	0.41	0/1732
76	Ag	0.22	0/348	0.44	0/448
77	AX	0.22	0/841	0.50	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A0	0.22	0/533	0.45	0/711
79	S9	0.13	0/1810	0.26	0/2821
80	mR	0.12	0/160	0.22	0/246
All	All	0.23	0/209224	0.35	2/306950 (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
9	SB	0	1
29	SV	0	1
54	AI	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	SB	54	LYS	N-CA-C	-9.08	104.27	114.62
51	AP	156	VAL	N-CA-C	-6.95	106.45	113.47

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
54	AI	87	GLY	Peptide
9	SB	53	GLY	Peptide
29	SV	12	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S1	985	0	1076	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	S2	320	0	338	6	0
3	S3	781	0	820	25	0
4	S4	586	0	604	20	0
5	S5	465	0	505	18	0
6	S6	345	0	381	12	0
7	S7	1571	0	797	43	0
8	SA	34208	0	17266	768	0
9	SB	1713	0	1838	32	0
10	SC	1538	0	1600	62	0
11	SD	1228	0	1311	50	0
12	SE	1514	0	1605	49	0
13	SF	2061	0	2200	70	0
14	SG	1757	0	1811	47	0
15	SH	1651	0	1807	70	0
16	SI	1424	0	1471	86	0
17	SJ	1528	0	1680	51	0
18	SK	1037	0	1099	28	0
19	SL	1383	0	1434	39	0
20	SM	1098	0	1183	56	0
21	SN	772	0	813	47	0
22	SO	686	0	695	27	0
23	SP	954	0	997	40	0
24	SQ	1129	0	1196	30	0
25	SR	746	0	754	9	0
26	SS	1046	0	1101	63	0
27	ST	405	0	419	30	0
28	SU	1202	0	1299	41	0
29	SV	1206	0	1239	35	0
30	SW	785	0	858	53	0
31	SX	776	0	832	38	0
32	SY	1266	0	1316	53	0
33	SZ	557	0	558	25	0
34	AA	67884	0	34243	1041	0
35	AC	3215	0	1633	53	0
36	AB	2517	0	1275	44	0
37	AL	1761	0	1896	45	0
38	A1	1134	0	1245	45	0
39	A2	837	0	896	18	0
40	A4	555	0	599	10	0
41	A6	740	0	763	26	0
42	A7	793	0	869	17	0
43	AN	1210	0	1329	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	A8	1036	0	1139	39	0
45	A9	844	0	886	23	0
46	Aa	858	0	912	28	0
47	Ab	756	0	842	19	0
48	Ad	603	0	686	21	0
49	Ae	388	0	421	4	0
50	Af	413	0	452	9	0
51	AP	1697	0	1802	50	0
52	Ah	658	0	727	17	0
53	Ai	778	0	859	10	0
54	AI	1685	0	1849	39	0
55	AJ	1813	0	1985	65	0
56	Ac	709	0	761	21	0
57	AK	1659	0	1782	34	0
58	AM	996	0	1044	25	0
59	AS	1503	0	1636	26	0
60	AO	1172	0	1230	25	0
61	AQ	1544	0	1582	35	0
62	AR	2049	0	2145	50	0
63	AW	1319	0	1303	27	0
64	AY	796	0	850	29	0
65	AT	1509	0	1682	36	0
66	AZ	1000	0	1099	29	0
67	A3	994	0	1121	21	0
68	A5	1879	0	2005	36	0
69	AD	1866	0	1964	52	0
70	AE	3061	0	3205	61	0
71	AF	3094	0	3333	67	0
72	AG	1010	0	1073	37	0
73	AU	1497	0	1556	48	0
74	AH	1475	0	1574	37	0
75	AV	1275	0	1355	31	0
76	Ag	343	0	388	14	0
77	AX	824	0	882	35	0
78	A0	521	0	539	13	0
79	S9	1620	0	827	28	0
80	mR	145	0	74	1	0
All	All	194758	0	145221	3875	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 12.

The worst 5 of 3875 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)
34:AA:11:A:N6	35:AC:154:G:H1	1.40	1.20
50:Af:10:ALA:O	50:Af:14:ASN:HB2	1.57	1.02
34:AA:3636:U:H3	34:AA:3649:G:H1	1.02	1.00
7:S7:8:U:H3	7:S7:14:A:H62	1.06	0.99
34:AA:3641:U:H3	34:AA:3644:G:H1	1.02	0.98

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	
1	S1	118/133 (89%)	116 (98%)	2 (2%)	0	100	100
2	S2	35/105 (33%)	35 (100%)	0	0	100	100
3	S3	93/107 (87%)	84 (90%)	9 (10%)	0	100	100
4	S4	74/82 (90%)	62 (84%)	12 (16%)	0	100	100
5	S5	55/67 (82%)	45 (82%)	9 (16%)	1 (2%)	7	6
6	S6	41/58 (71%)	38 (93%)	2 (5%)	1 (2%)	5	4
9	SB	208/262 (79%)	198 (95%)	9 (4%)	1 (0%)	25	32
10	SC	193/263 (73%)	179 (93%)	13 (7%)	1 (0%)	25	32
11	SD	149/221 (67%)	147 (99%)	2 (1%)	0	100	100
12	SE	183/189 (97%)	172 (94%)	11 (6%)	0	100	100
13	SF	255/261 (98%)	237 (93%)	17 (7%)	1 (0%)	30	39
14	SG	222/272 (82%)	211 (95%)	11 (5%)	0	100	100
15	SH	200/306 (65%)	189 (94%)	11 (6%)	0	100	100
16	SI	176/195 (90%)	165 (94%)	11 (6%)	0	100	100
17	SJ	186/194 (96%)	169 (91%)	16 (9%)	1 (0%)	25	32
18	SK	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	16	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	SL	165/218 (76%)	151 (92%)	13 (8%)	1 (1%)	22	27
20	SM	136/144 (94%)	130 (96%)	5 (4%)	1 (1%)	19	23
21	SN	96/118 (81%)	92 (96%)	4 (4%)	0	100	100
22	SO	77/137 (56%)	71 (92%)	5 (6%)	1 (1%)	10	11
23	SP	125/151 (83%)	115 (92%)	10 (8%)	0	100	100
24	SQ	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
25	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
26	SS	126/156 (81%)	110 (87%)	14 (11%)	2 (2%)	8	7
27	ST	46/54 (85%)	45 (98%)	1 (2%)	0	100	100
28	SU	147/151 (97%)	137 (93%)	10 (7%)	0	100	100
29	SV	142/161 (88%)	135 (95%)	6 (4%)	1 (1%)	19	23
30	SW	91/137 (66%)	79 (87%)	9 (10%)	3 (3%)	3	2
31	SX	92/145 (63%)	84 (91%)	8 (9%)	0	100	100
32	SY	152/170 (89%)	146 (96%)	6 (4%)	0	100	100
33	SZ	70/82 (85%)	66 (94%)	4 (6%)	0	100	100
37	AL	209/215 (97%)	202 (97%)	7 (3%)	0	100	100
38	A1	136/146 (93%)	124 (91%)	11 (8%)	1 (1%)	19	23
39	A2	97/127 (76%)	93 (96%)	3 (3%)	1 (1%)	13	15
40	A4	64/67 (96%)	60 (94%)	4 (6%)	0	100	100
41	A6	96/108 (89%)	92 (96%)	4 (4%)	0	100	100
42	A7	92/120 (77%)	91 (99%)	1 (1%)	0	100	100
43	AN	145/165 (88%)	135 (93%)	10 (7%)	0	100	100
44	A8	123/131 (94%)	113 (92%)	10 (8%)	0	100	100
45	A9	101/140 (72%)	91 (90%)	10 (10%)	0	100	100
46	Aa	104/150 (69%)	98 (94%)	6 (6%)	0	100	100
47	Ab	91/112 (81%)	83 (91%)	7 (8%)	1 (1%)	12	13
48	Ad	68/87 (78%)	67 (98%)	1 (2%)	0	100	100
49	Ae	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
50	Af	49/128 (38%)	45 (92%)	4 (8%)	0	100	100
51	AP	202/205 (98%)	182 (90%)	18 (9%)	2 (1%)	13	15
52	Ah	83/96 (86%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Ai	93/104 (89%)	87 (94%)	6 (6%)	0	100	100
54	AI	203/221 (92%)	190 (94%)	12 (6%)	1 (0%)	25	32
55	AJ	216/283 (76%)	209 (97%)	6 (3%)	1 (0%)	25	32
56	Ac	87/92 (95%)	80 (92%)	7 (8%)	0	100	100
57	AK	199/202 (98%)	194 (98%)	4 (2%)	1 (0%)	25	32
58	AM	130/139 (94%)	124 (95%)	5 (4%)	1 (1%)	16	20
59	AS	184/187 (98%)	177 (96%)	6 (3%)	1 (0%)	25	32
60	AO	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
61	AQ	185/219 (84%)	174 (94%)	9 (5%)	2 (1%)	12	13
62	AR	244/294 (83%)	236 (97%)	7 (3%)	1 (0%)	30	39
63	AW	149/173 (86%)	143 (96%)	6 (4%)	0	100	100
64	AY	99/190 (52%)	96 (97%)	3 (3%)	0	100	100
65	AT	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
66	AZ	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
67	A3	117/124 (94%)	109 (93%)	8 (7%)	0	100	100
68	A5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
69	AD	245/260 (94%)	231 (94%)	12 (5%)	2 (1%)	16	20
70	AE	378/386 (98%)	364 (96%)	13 (3%)	1 (0%)	37	47
71	AF	388/411 (94%)	373 (96%)	14 (4%)	1 (0%)	37	47
72	AG	116/173 (67%)	106 (91%)	8 (7%)	2 (2%)	7	7
73	AU	178/184 (97%)	171 (96%)	6 (3%)	1 (1%)	22	27
74	AH	183/190 (96%)	169 (92%)	14 (8%)	0	100	100
75	AV	153/161 (95%)	148 (97%)	5 (3%)	0	100	100
76	Ag	35/39 (90%)	28 (80%)	7 (20%)	0	100	100
77	AX	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
78	A0	60/162 (37%)	58 (97%)	2 (3%)	0	100	100
All	All	10114/12049 (84%)	9533 (94%)	545 (5%)	36 (0%)	32	39

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SB	146	ARG
17	SJ	112	ILE

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Mol	Chain	Res	Type
19	SL	168	ILE
20	SM	41	GLU
26	SS	101	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S1	104/115 (90%)	102 (98%)	2 (2%)	52	69
2	S2	35/88 (40%)	35 (100%)	0	100	100
3	S3	87/98 (89%)	84 (97%)	3 (3%)	32	47
4	S4	70/76 (92%)	67 (96%)	3 (4%)	25	36
5	S5	48/54 (89%)	47 (98%)	1 (2%)	48	66
6	S6	36/47 (77%)	34 (94%)	2 (6%)	17	26
9	SB	195/238 (82%)	184 (94%)	11 (6%)	17	26
10	SC	167/227 (74%)	160 (96%)	7 (4%)	25	37
11	SD	132/188 (70%)	122 (92%)	10 (8%)	11	14
12	SE	161/167 (96%)	152 (94%)	9 (6%)	17	26
13	SF	233/237 (98%)	219 (94%)	14 (6%)	16	23
14	SG	191/222 (86%)	180 (94%)	11 (6%)	17	24
15	SH	182/279 (65%)	175 (96%)	7 (4%)	28	42
16	SI	154/165 (93%)	148 (96%)	6 (4%)	27	41
17	SJ	177/183 (97%)	167 (94%)	10 (6%)	17	26
18	SK	115/116 (99%)	106 (92%)	9 (8%)	10	14
19	SL	151/193 (78%)	142 (94%)	9 (6%)	16	23
20	SM	116/122 (95%)	112 (97%)	4 (3%)	32	47
21	SN	91/109 (84%)	88 (97%)	3 (3%)	33	48
22	SO	76/129 (59%)	71 (93%)	5 (7%)	14	19
23	SP	99/119 (83%)	94 (95%)	5 (5%)	20	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	SQ	120/121 (99%)	117 (98%)	3 (2%)	42	60
25	SR	83/121 (69%)	80 (96%)	3 (4%)	30	44
26	SS	114/136 (84%)	102 (90%)	12 (10%)	5	6
27	ST	43/48 (90%)	42 (98%)	1 (2%)	45	63
28	SU	132/133 (99%)	128 (97%)	4 (3%)	36	52
29	SV	131/144 (91%)	125 (95%)	6 (5%)	23	33
30	SW	86/127 (68%)	84 (98%)	2 (2%)	45	63
31	SX	88/130 (68%)	86 (98%)	2 (2%)	45	63
32	SY	137/151 (91%)	130 (95%)	7 (5%)	20	29
33	SZ	60/70 (86%)	55 (92%)	5 (8%)	9	12
37	AL	190/194 (98%)	184 (97%)	6 (3%)	34	50
38	A1	127/132 (96%)	120 (94%)	7 (6%)	18	26
39	A2	98/118 (83%)	95 (97%)	3 (3%)	35	51
40	A4	60/61 (98%)	60 (100%)	0	100	100
41	A6	83/92 (90%)	79 (95%)	4 (5%)	21	32
42	A7	90/112 (80%)	87 (97%)	3 (3%)	33	48
43	AN	136/152 (90%)	131 (96%)	5 (4%)	29	43
44	A8	114/120 (95%)	107 (94%)	7 (6%)	15	22
45	A9	90/127 (71%)	87 (97%)	3 (3%)	33	48
46	Aa	89/128 (70%)	84 (94%)	5 (6%)	17	26
47	Ab	82/97 (84%)	78 (95%)	4 (5%)	21	31
48	Ad	69/83 (83%)	66 (96%)	3 (4%)	25	36
49	Ae	40/48 (83%)	40 (100%)	0	100	100
50	Af	45/114 (40%)	44 (98%)	1 (2%)	47	65
51	AP	179/180 (99%)	170 (95%)	9 (5%)	20	30
52	Ah	70/80 (88%)	65 (93%)	5 (7%)	12	17
53	Ai	87/93 (94%)	85 (98%)	2 (2%)	45	63
54	AI	189/203 (93%)	177 (94%)	12 (6%)	15	21
55	AJ	204/260 (78%)	197 (97%)	7 (3%)	32	47
56	Ac	74/77 (96%)	73 (99%)	1 (1%)	62	77
57	AK	181/182 (100%)	175 (97%)	6 (3%)	33	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AM	106/110 (96%)	100 (94%)	6 (6%)	17	25
59	AS	158/159 (99%)	152 (96%)	6 (4%)	28	42
60	AO	121/122 (99%)	118 (98%)	3 (2%)	42	60
61	AQ	165/190 (87%)	161 (98%)	4 (2%)	44	61
62	AR	215/254 (85%)	207 (96%)	8 (4%)	29	43
63	AW	128/131 (98%)	123 (96%)	5 (4%)	27	41
64	AY	90/177 (51%)	83 (92%)	7 (8%)	10	14
65	AT	162/163 (99%)	152 (94%)	10 (6%)	15	22
66	AZ	111/115 (96%)	105 (95%)	6 (5%)	18	27
67	A3	110/115 (96%)	106 (96%)	4 (4%)	30	44
68	A5	201/231 (87%)	196 (98%)	5 (2%)	42	60
69	AD	191/202 (95%)	185 (97%)	6 (3%)	35	51
70	AE	335/340 (98%)	325 (97%)	10 (3%)	36	52
71	AF	336/352 (96%)	325 (97%)	11 (3%)	33	48
72	AG	110/155 (71%)	104 (94%)	6 (6%)	18	26
73	AU	162/166 (98%)	156 (96%)	6 (4%)	29	43
74	AH	168/173 (97%)	153 (91%)	15 (9%)	8	10
75	AV	140/144 (97%)	130 (93%)	10 (7%)	12	17
76	Ag	34/35 (97%)	31 (91%)	3 (9%)	8	10
77	AX	92/131 (70%)	83 (90%)	9 (10%)	6	8
78	A0	53/146 (36%)	52 (98%)	1 (2%)	52	69
All	All	9099/10617 (86%)	8689 (96%)	410 (4%)	26	34

5 of 410 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	AP	80	VAL
61	AQ	126	VAL
76	Ag	38	SER
52	Ah	47	THR
55	AJ	192	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
55	AJ	240	ASN
62	AR	114	ASN
56	Ac	31	HIS
59	AS	18	HIS
65	AT	170	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	AA	3163/3788 (83%)	607 (19%)	69 (2%)
35	AC	148/159 (93%)	31 (20%)	5 (3%)
36	AB	117/119 (98%)	20 (17%)	3 (2%)
7	S7	73/74 (98%)	24 (32%)	0
79	S9	75/76 (98%)	15 (20%)	2 (2%)
8	SA	1588/2092 (75%)	355 (22%)	28 (1%)
80	mR	6/7 (85%)	1 (16%)	0
All	All	5170/6315 (81%)	1053 (20%)	107 (2%)

5 of 1053 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	S7	8	U
7	S7	9	G
7	S7	10	G
7	S7	16	U
7	S7	17	U

5 of 107 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	721	U
34	AA	1841	U
35	AC	134	G
34	AA	859	C
34	AA	1222	U

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	31.42

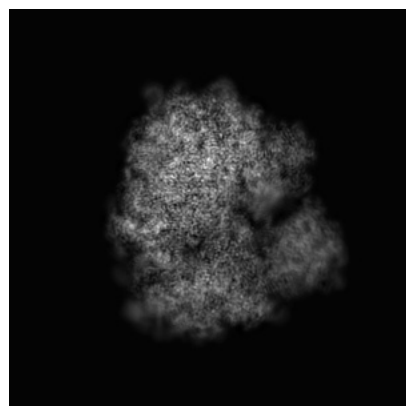
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44916. These allow visual inspection of the internal detail of the map and identification of artifacts.

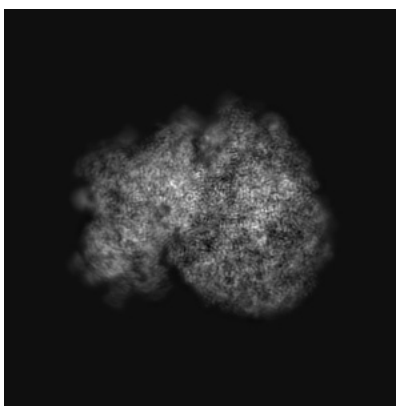
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

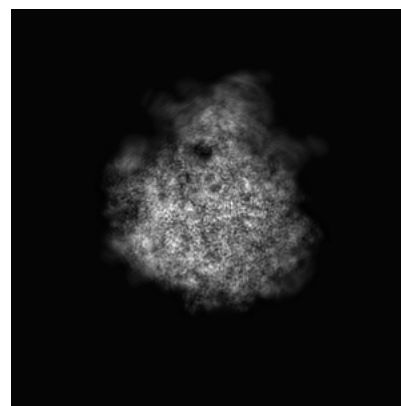
6.1.1 Primary map



X

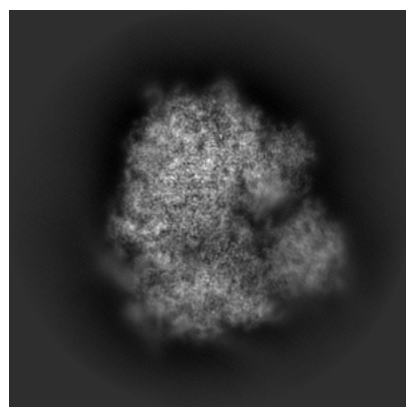


Y

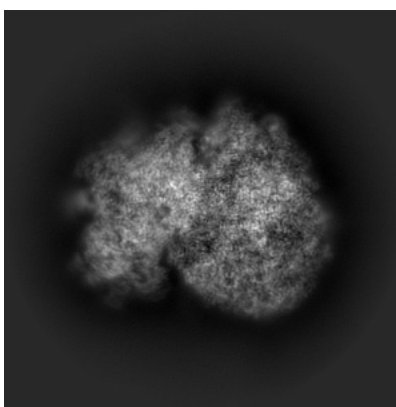


Z

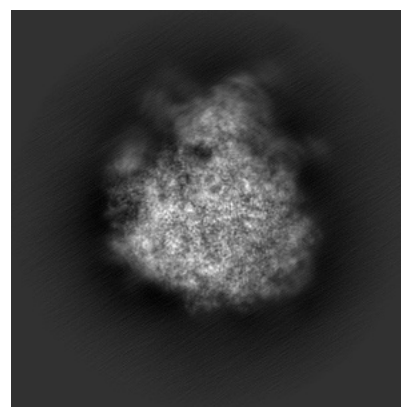
6.1.2 Raw map



X



Y

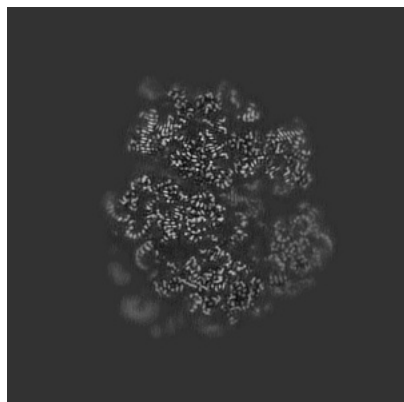


Z

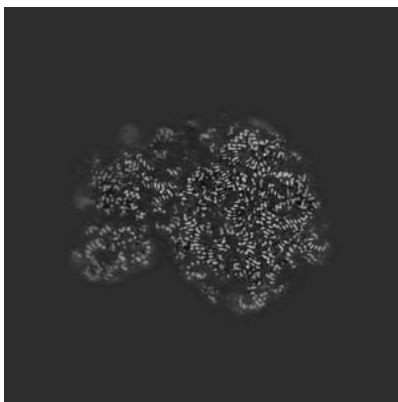
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

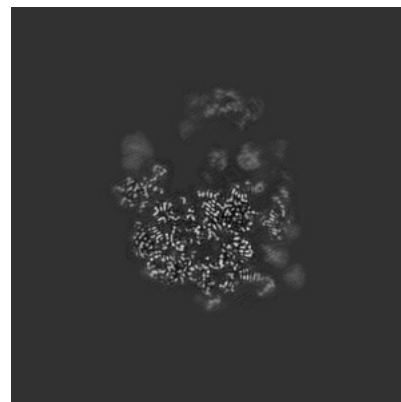
6.2.1 Primary map



X Index: 250

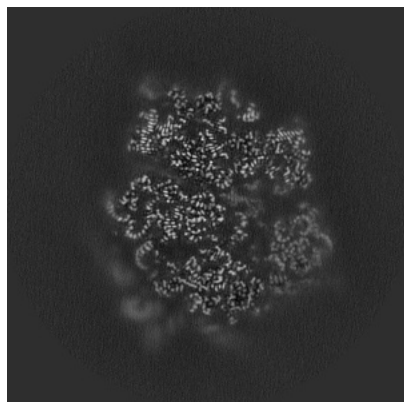


Y Index: 250

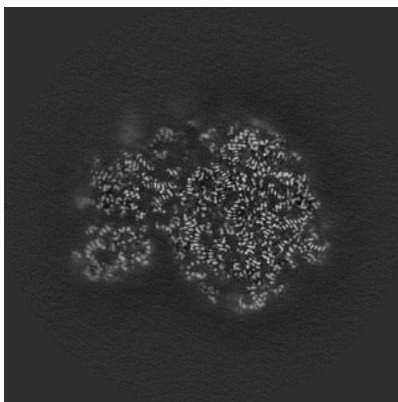


Z Index: 250

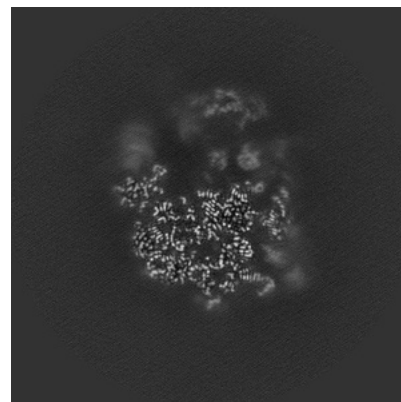
6.2.2 Raw map



X Index: 250



Y Index: 250

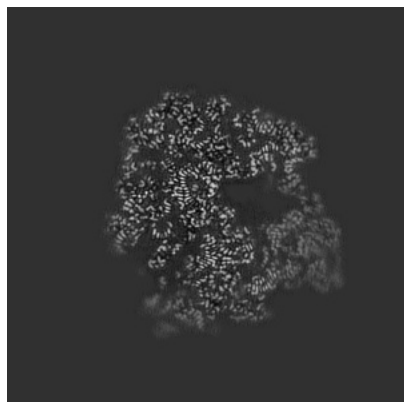


Z Index: 250

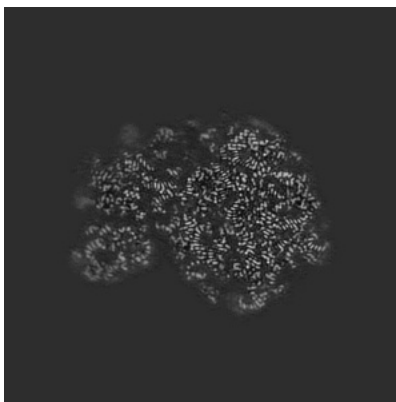
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

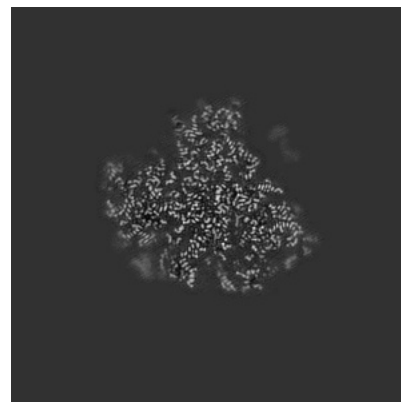
6.3.1 Primary map



X Index: 275

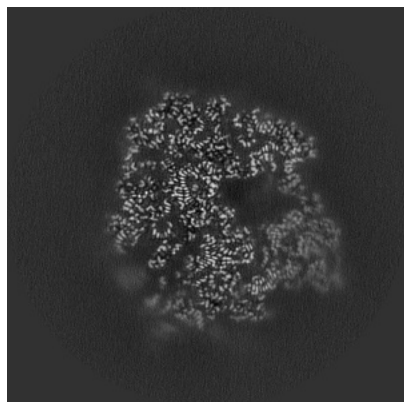


Y Index: 250

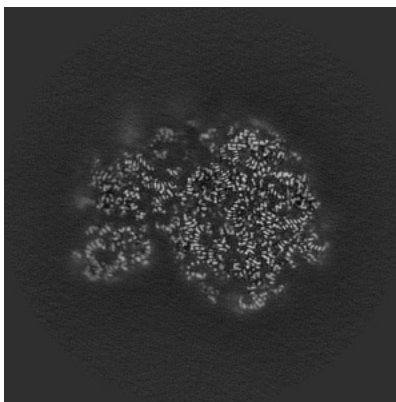


Z Index: 310

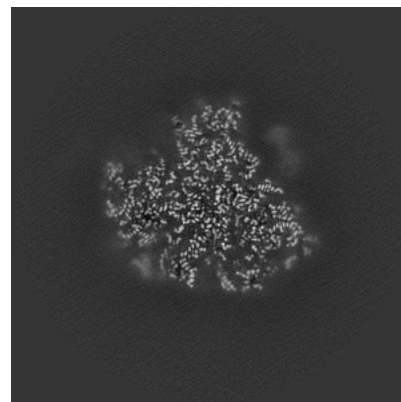
6.3.2 Raw map



X Index: 275



Y Index: 250

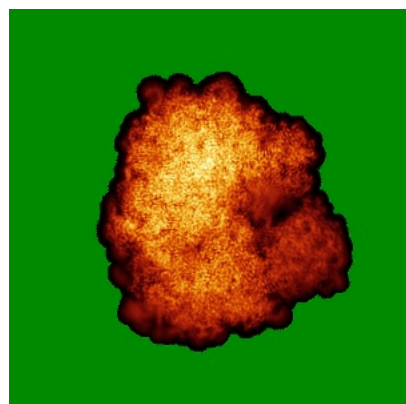


Z Index: 310

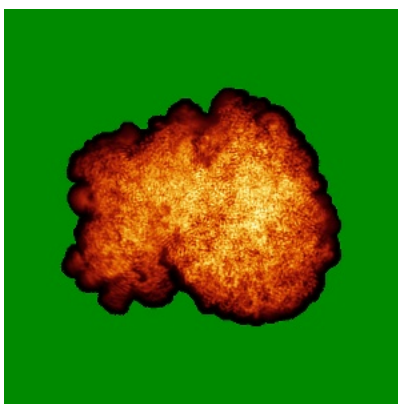
The images above show the largest variance slices of the map in three orthogonal directions.

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

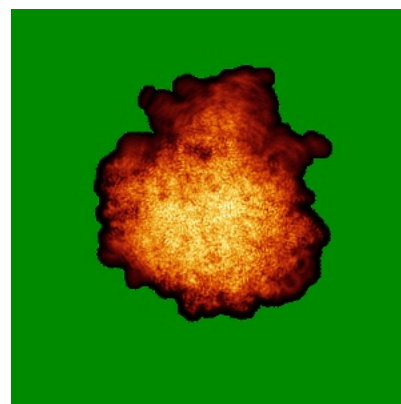
6.4.1 Primary map



X

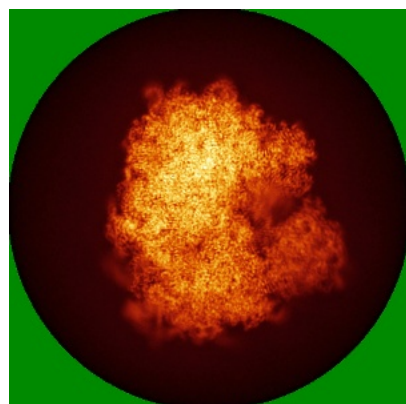


Y

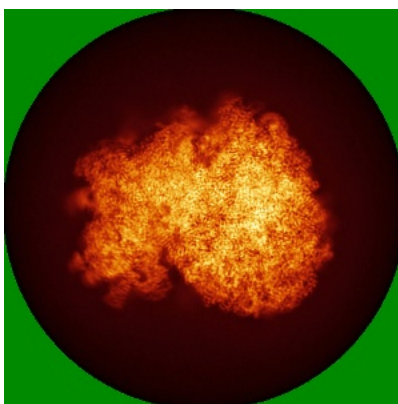


Z

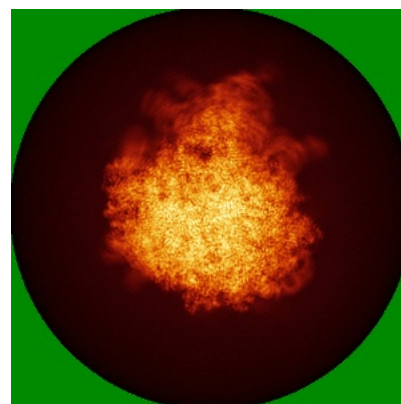
6.4.2 Raw map



X



Y

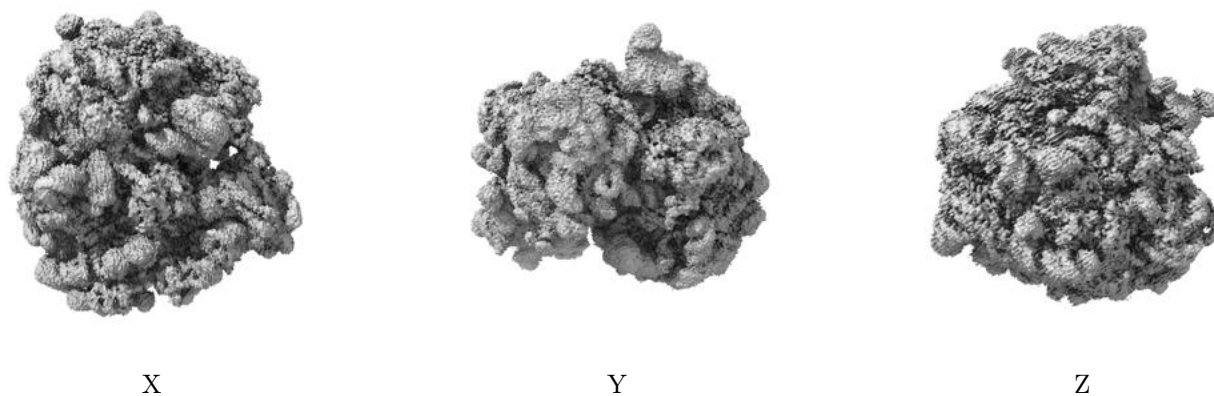


Z

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.

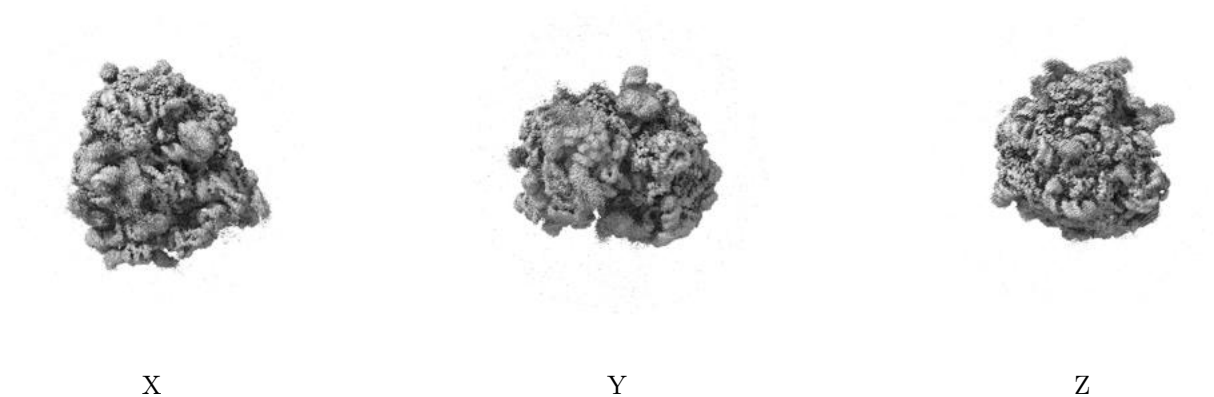
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00404. 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



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

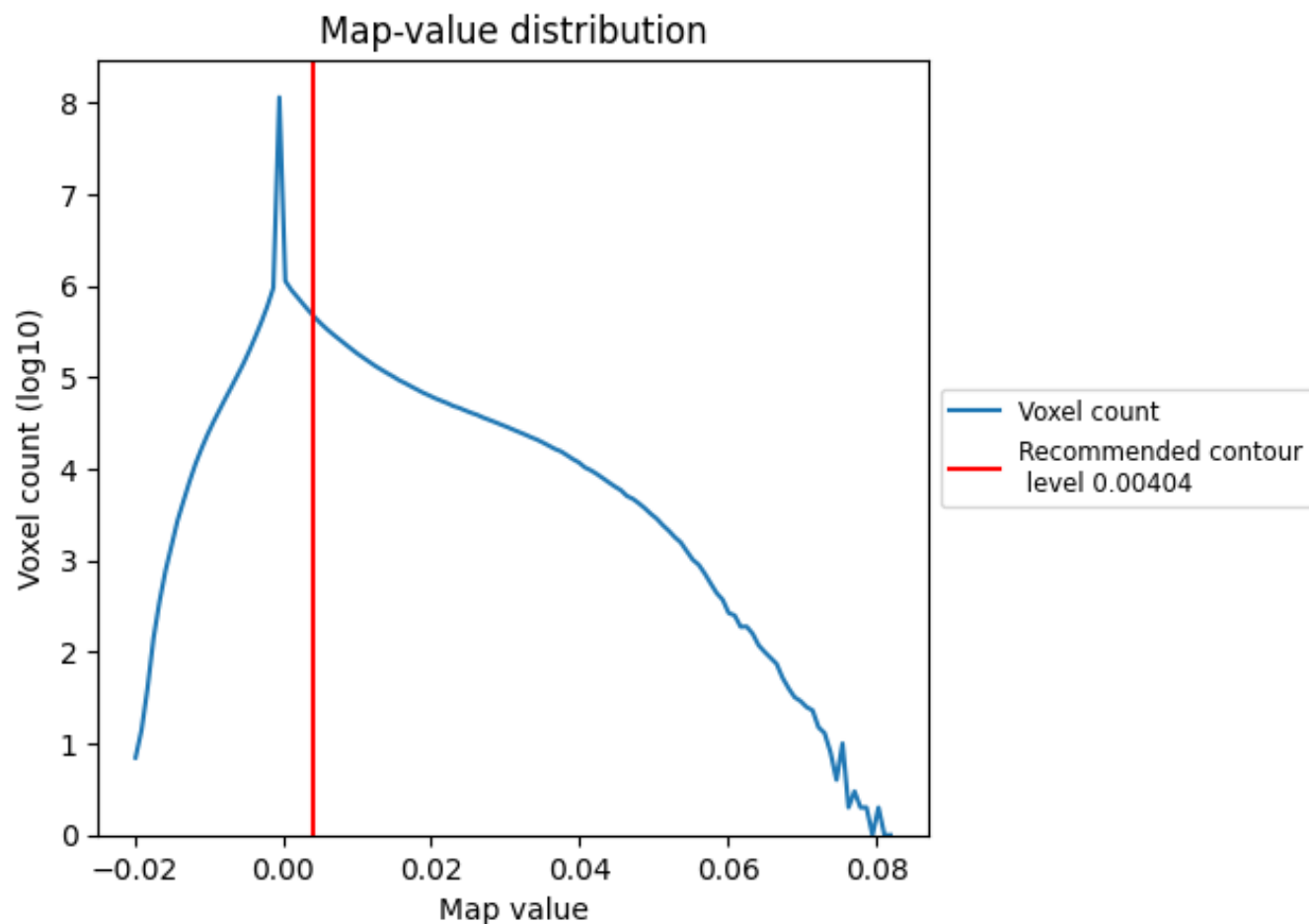
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

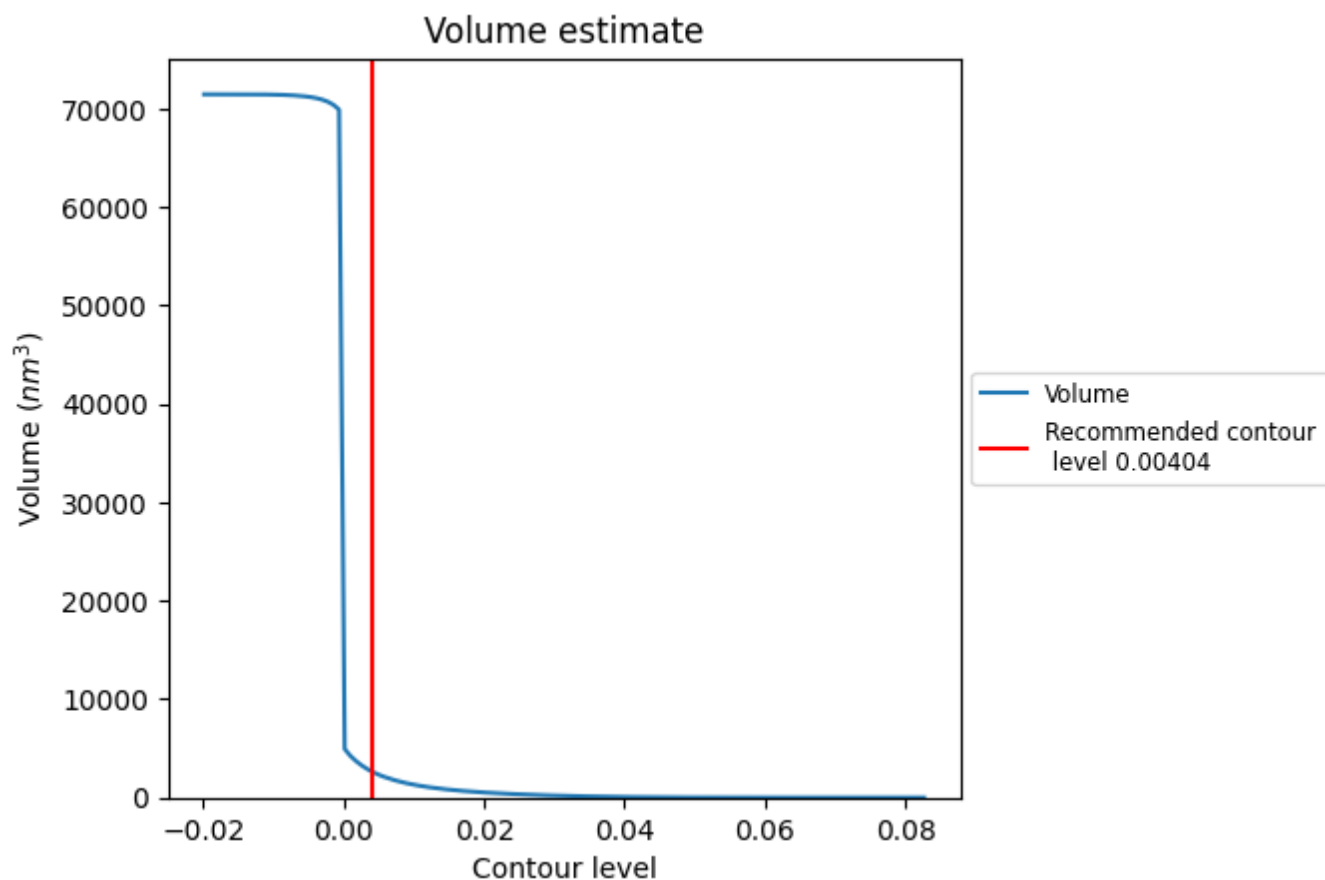
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

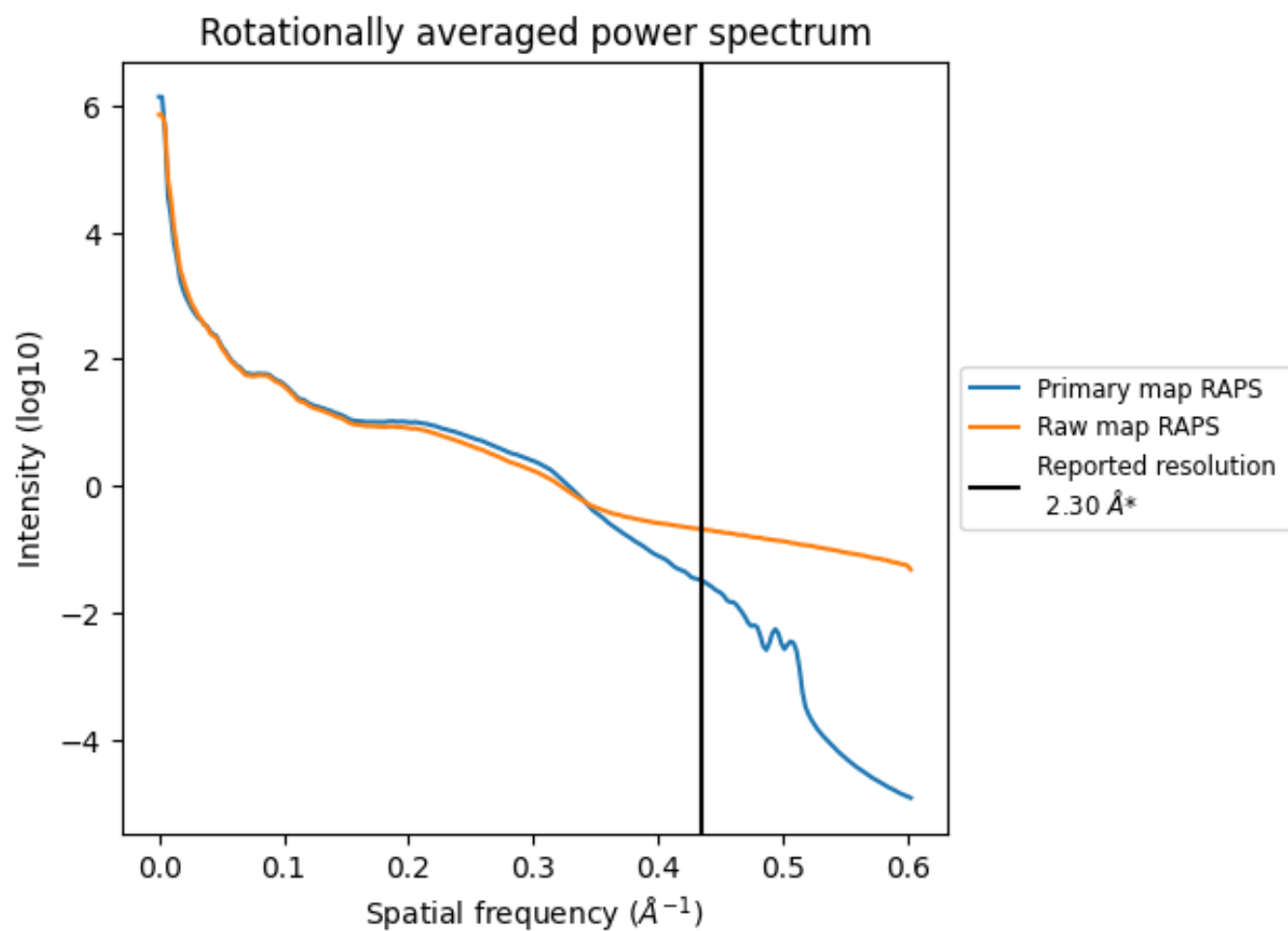
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2655 nm³; this corresponds to an approximate mass of 2399 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 ⓘ

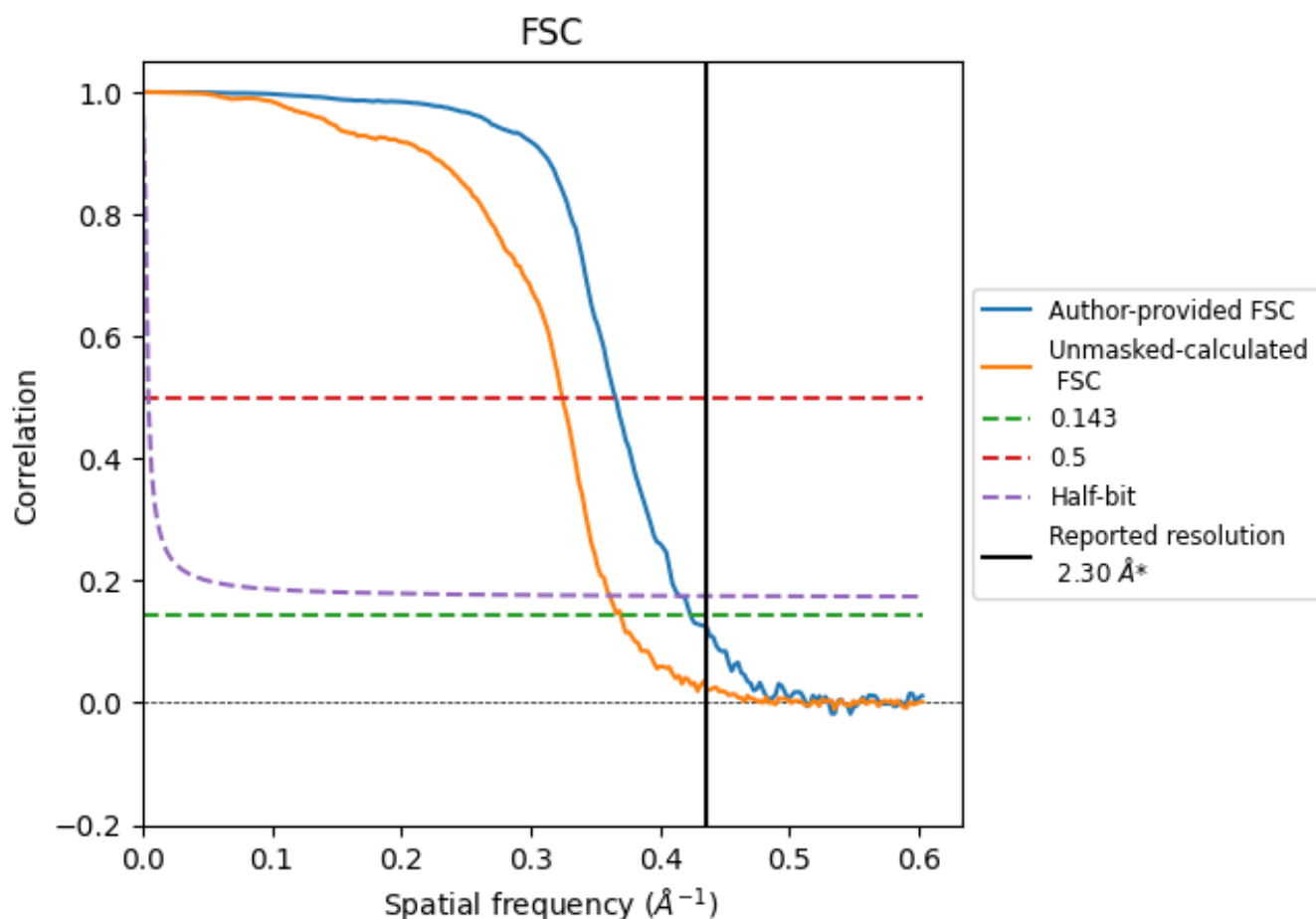


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

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 0.435 Å⁻¹

8.2 Resolution estimates [i](#)

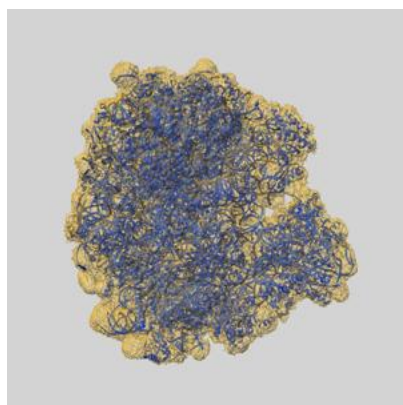
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.36	2.74	2.41
Unmasked-calculated*	2.71	3.08	2.77

*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 2.71 differs from the reported value 2.3 by more than 10 %

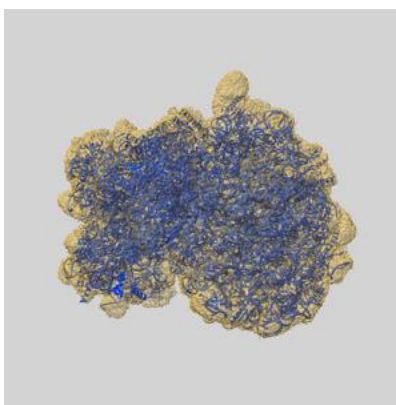
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44916 and PDB model 9BUQ. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

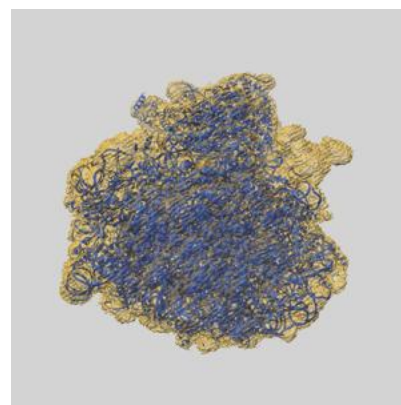
9.1 Map-model overlay [i](#)



X



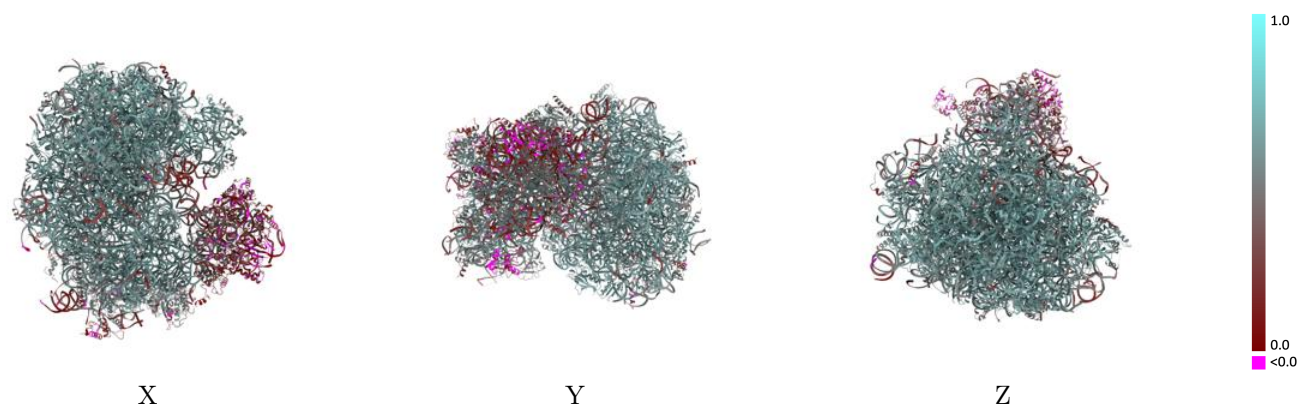
Y



Z

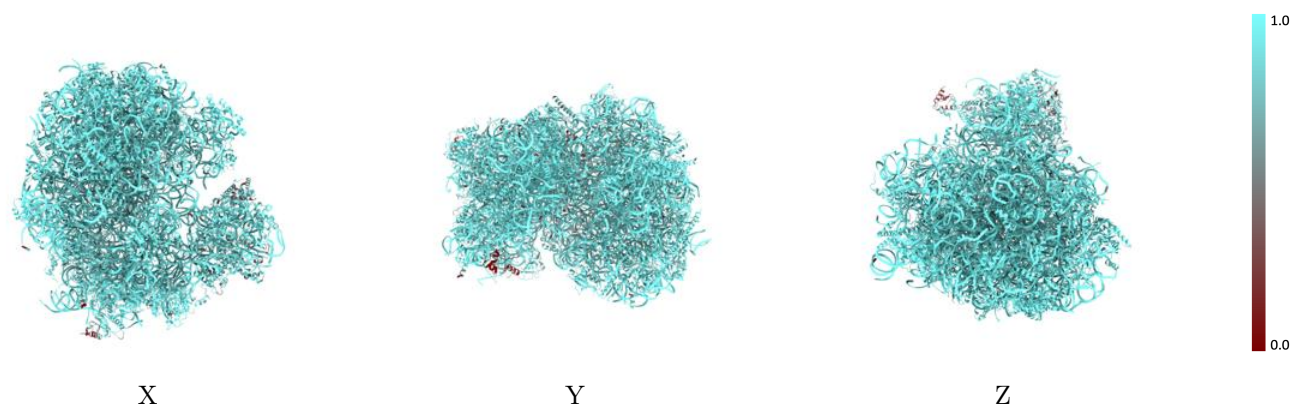
The images above show the 3D surface view of the map at the recommended contour level 0.00404 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



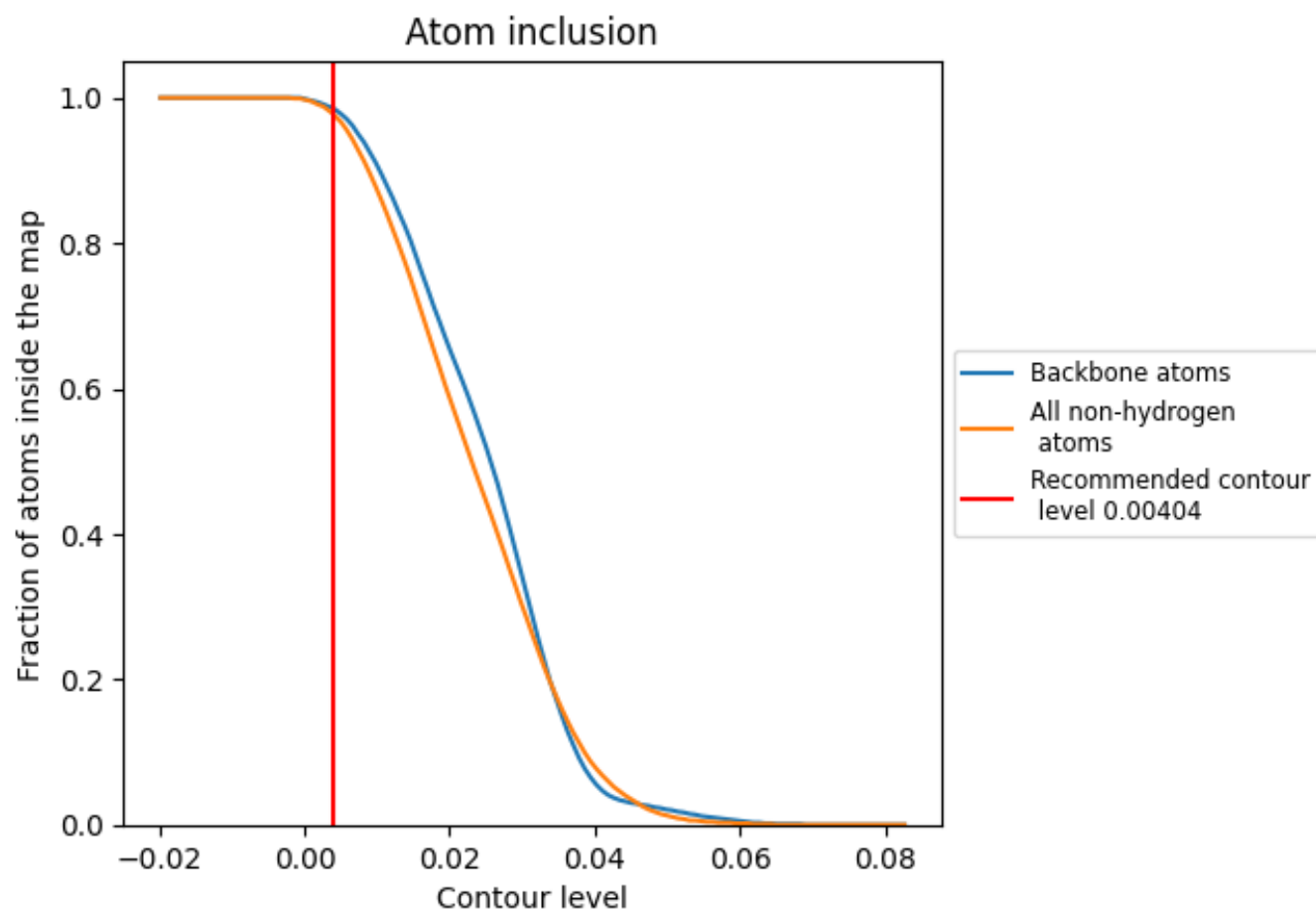
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00404).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.00404) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9770	 0.5580
A0	 0.9600	 0.6110
A1	 0.9770	 0.5460
A2	 0.9840	 0.6020
A3	 0.9960	 0.6080
A4	 0.9620	 0.5600
A5	 0.9890	 0.6300
A6	 0.9730	 0.5860
A7	 0.9920	 0.6330
A8	 0.9880	 0.6410
A9	 0.9930	 0.6540
AA	 0.9950	 0.6100
AB	 0.9970	 0.6150
AC	 0.9980	 0.6200
AD	 0.9890	 0.6500
AE	 0.9940	 0.6460
AF	 0.9620	 0.5960
AG	 0.9870	 0.5470
AH	 0.9960	 0.6160
AI	 0.9890	 0.5940
AJ	 0.9560	 0.5310
AK	 0.9930	 0.6440
AL	 0.9920	 0.6240
AM	 0.9820	 0.6390
AN	 0.9870	 0.5930
AO	 0.9950	 0.6570
AP	 0.9900	 0.6510
AQ	 0.9750	 0.5940
AR	 0.9850	 0.5810
AS	 0.9950	 0.6530
AT	 0.9400	 0.5790
AU	 0.9930	 0.6350
AV	 0.9900	 0.6180
AW	 0.9930	 0.6440
AX	 0.9630	 0.5210










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Chain	Atom inclusion	Q-score
AY	 0.9820	 0.5860
AZ	 0.9890	 0.5920
Aa	 0.9760	 0.6150
Ab	 0.9890	 0.6000
Ac	 0.9930	 0.6390
Ad	 0.9850	 0.5620
Ae	 0.9860	 0.6320
Af	 0.9930	 0.6280
Ag	 0.9620	 0.6160
Ah	 0.9880	 0.6460
Ai	 0.9840	 0.6400
S1	 0.9660	 0.4950
S2	 0.5820	 0.1060
S3	 0.9870	 0.6130
S4	 0.8810	 0.3830
S5	 0.7520	 0.2300
S6	 0.9100	 0.4730
S7	 0.9750	 0.3090
S9	 0.9400	 0.4860
SA	 0.9890	 0.5010
SB	 0.9700	 0.5590
SC	 0.9610	 0.5010
SD	 0.9150	 0.3340
SE	 0.9560	 0.5340
SF	 0.9760	 0.5690
SG	 0.9610	 0.5290
SH	 0.9690	 0.4530
SI	 0.8830	 0.2630
SJ	 0.8390	 0.3860
SK	 0.9750	 0.6040
SL	 0.9720	 0.5770
SM	 0.8330	 0.1780
SN	 0.8620	 0.2100
SO	 0.9180	 0.2230
SP	 0.9670	 0.5650
SQ	 0.9570	 0.5770
SR	 0.4270	 0.0410
SS	 0.8260	 0.2140
ST	 0.8710	 0.3580
SU	 0.9540	 0.5720
SV	 0.9520	 0.5820
SW	 0.8740	 0.2480

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Chain	Atom inclusion	Q-score
SX	 0.8520	 0.2540
SY	 0.9450	 0.2580
SZ	 0.9760	 0.5510
mR	 0.9310	 0.5090