



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:09 AM UTC

PDB ID : 9BUU / pdb_00009buu
EMDB ID : EMD-44920
Title : Single particle CryoEM structure of the Pf80S ribosome in rotated state with E-site tRNA
Authors : Anton, L.; Haile, M.; Ho, C.M.
Deposited on : 2024-05-17
Resolution : 2.80 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

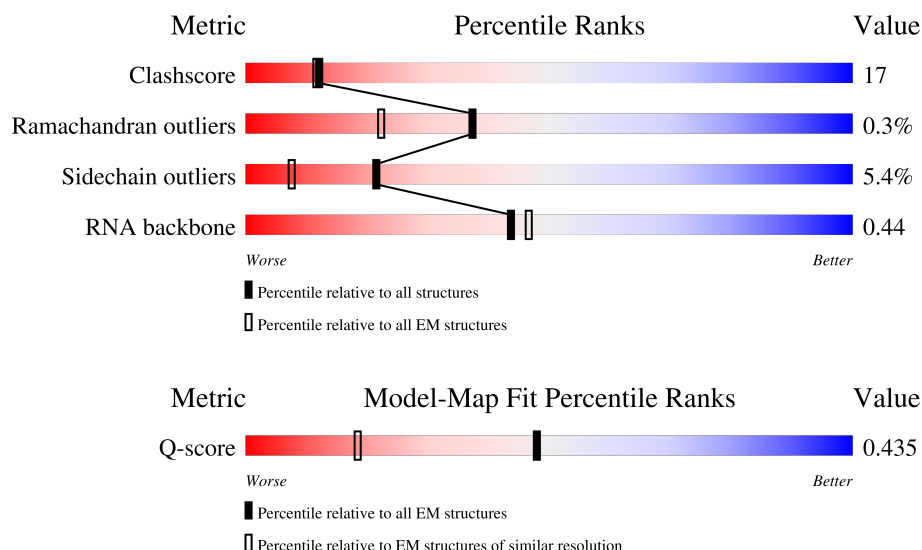
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



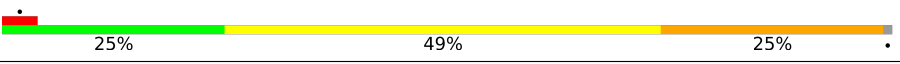
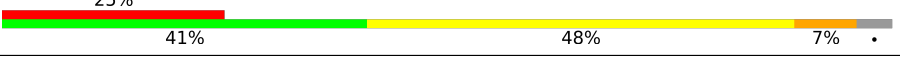
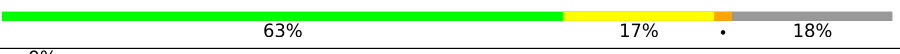
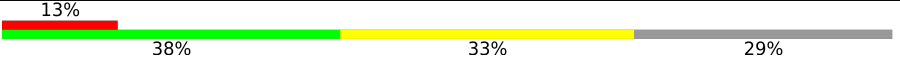
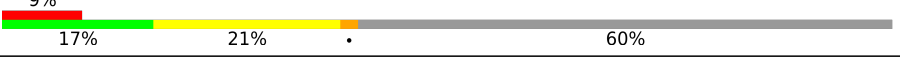
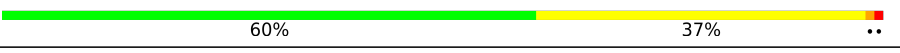
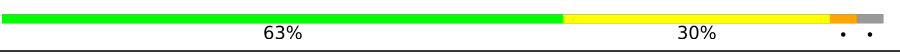
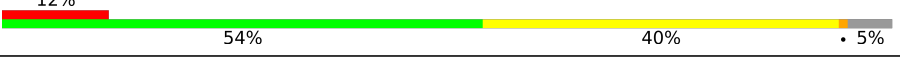
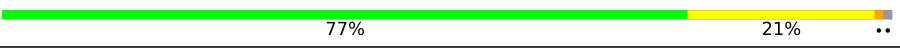
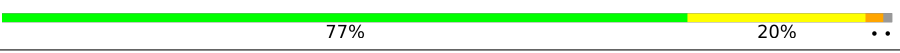
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	S7	76	
2	AA	3788	
3	AC	159	

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Mol	Chain	Length	Quality of chain
4	AB	119	
5	AL	215	
6	A1	146	
7	A2	127	
8	A4	67	
9	A6	108	
10	A7	120	
11	AN	165	
12	A8	131	
13	A9	140	
14	Aa	150	
15	Ab	112	
16	Ad	87	
17	Ae	51	
18	Af	128	
19	AP	205	
20	Ah	96	
21	Ai	104	
22	AI	221	
23	AJ	283	
24	Ac	92	
25	AK	202	
26	AM	139	
27	AS	187	
28	AO	148	

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Mol	Chain	Length	Quality of chain
29	AQ	219	
30	AR	294	
31	AW	173	
32	AY	190	
33	AT	182	
34	AZ	126	
35	A3	124	
36	A5	257	
37	AD	260	
38	AE	386	
39	AF	411	
40	AG	173	
41	AU	184	
42	AH	190	
43	AV	161	
44	Ag	39	
45	AX	139	
46	A0	162	
47	S1	133	
48	S2	105	
49	S3	107	
50	S4	82	
51	S5	67	
52	S6	58	
53	SA	2092	

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Mol	Chain	Length	Quality of chain
54	SB	262	
55	SC	263	
56	SD	221	
57	SE	189	
58	SF	261	
59	SG	272	
60	SH	306	
61	SI	195	
62	SJ	194	
63	SK	130	
64	SL	218	
65	SM	144	
66	SN	118	
67	SO	137	
68	SP	151	
69	SQ	145	
70	SR	141	
71	SS	156	
72	ST	54	
73	SU	151	
74	SV	161	
75	SW	137	
76	SX	145	
77	SY	170	
78	SZ	82	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193035 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S7	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

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

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 5 is a protein called 60S ribosomal protein L13.

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

- Molecule 6 is a protein called 60S ribosomal protein L27.

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

- Molecule 7 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A2	104	Total	C	N	O	S	0	0
			830	529	151	147	3		

- Molecule 8 is a protein called 60S ribosomal protein L29.

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

- Molecule 9 is a protein called 60S ribosomal protein L30e.

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

- Molecule 10 is a protein called 60S ribosomal protein L31.

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

- Molecule 11 is a protein called 60S ribosomal protein L14.

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

- Molecule 12 is a protein called 60S ribosomal protein L32.

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

- Molecule 13 is a protein called 60S ribosomal protein L35ae.

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

- Molecule 14 is a protein called 60S ribosomal protein L34.

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

- Molecule 15 is a protein called 60S ribosomal protein L36.

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

- Molecule 16 is a protein called 60S ribosomal protein L38.

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

- Molecule 17 is a protein called 60S ribosomal protein L39.

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

- Molecule 18 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 19 is a protein called Ribosomal protein L15.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 21 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 22 is a protein called 60S ribosomal protein L6.

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

- Molecule 23 is a protein called 60S ribosomal protein L7a.

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

- Molecule 24 is a protein called Ribosomal protein L37.

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

- Molecule 25 is a protein called 60S ribosomal protein L13.

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

- Molecule 26 is a protein called 60S ribosomal protein L23.

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

- Molecule 27 is a protein called 60S ribosomal protein L18-2.

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

- Molecule 28 is a protein called 60S ribosomal protein L27a.

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

- Molecule 29 is a protein called 60S ribosomal protein L10.

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

- Molecule 30 is a protein called 60S ribosomal protein L5.

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

- Molecule 31 is a protein called 60S ribosomal protein L17.

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

- Molecule 32 is a protein called 60S ribosomal protein L23.

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

- Molecule 33 is a protein called 60S ribosomal protein L19.

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

- Molecule 34 is a protein called 60S ribosomal protein L26.

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

- Molecule 35 is a protein called 60S ribosomal protein L35.

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

- Molecule 36 is a protein called 60S ribosomal protein L7.

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

- Molecule 37 is a protein called 60S ribosomal protein L2.

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

- Molecule 38 is a protein called 60S ribosomal protein L3.

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

- Molecule 39 is a protein called 60S ribosomal protein L4.

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

- Molecule 40 is a protein called 60S ribosomal protein L11a.

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

- Molecule 41 is a protein called 60S ribosomal protein L18a.

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

- Molecule 42 is a protein called 60S ribosomal protein L6.

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

- Molecule 43 is a protein called 60S ribosomal protein L21.

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

- Molecule 44 is a protein called 60S ribosomal protein L41.

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

- Molecule 45 is a protein called 60S ribosomal protein L22.

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

- Molecule 46 is a protein called 60S ribosomal protein L24.

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

- Molecule 47 is a protein called 40S ribosomal protein S24.

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

- Molecule 48 is a protein called 40S ribosomal protein S25.

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

- Molecule 49 is a protein called 40S ribosomal protein S26.

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

- Molecule 50 is a protein called 40S ribosomal protein S27.

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

- Molecule 51 is a protein called 40S ribosomal protein S28e.

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

- Molecule 52 is a protein called 40S ribosomal protein S30.

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

- Molecule 53 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 54 is a protein called 40S ribosomal protein S3a.

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

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

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

- Molecule 56 is a protein called 40S ribosomal protein S3.

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

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

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

- Molecule 58 is a protein called 40S ribosomal protein S4.

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

- Molecule 59 is a protein called 40S ribosomal protein S5.

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

- Molecule 60 is a protein called 40S ribosomal protein S6.

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

- Molecule 61 is a protein called 40S ribosomal protein S5.

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

- Molecule 62 is a protein called 40S ribosomal protein S7.

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

- Molecule 63 is a protein called 40S ribosomal protein S15A.

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

- Molecule 64 is a protein called 40S ribosomal protein S8.

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

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

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

- Molecule 66 is a protein called 40S ribosomal protein S20e.

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

- Molecule 67 is a protein called 40S ribosomal protein S10.

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

- Molecule 68 is a protein called 40S ribosomal protein S11.

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

- Molecule 69 is a protein called 40S ribosomal protein S23.

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

- Molecule 70 is a protein called 40S ribosomal protein S12.

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

- Molecule 71 is a protein called 40S ribosomal protein S18.

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

- Molecule 72 is a protein called 40S ribosomal protein S29.

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

- Molecule 73 is a protein called 40S ribosomal protein S15.

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

- Molecule 74 is a protein called 40S ribosomal protein S11.

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

- Molecule 75 is a protein called 40S ribosomal protein S17.

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

- Molecule 76 is a protein called 40S ribosomal protein S19.

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

- Molecule 77 is a protein called 40S ribosomal protein S19.

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

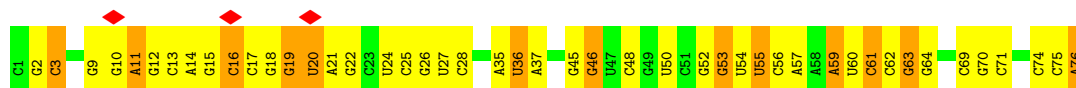
- Molecule 78 is a protein called 40S ribosomal protein S21.

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

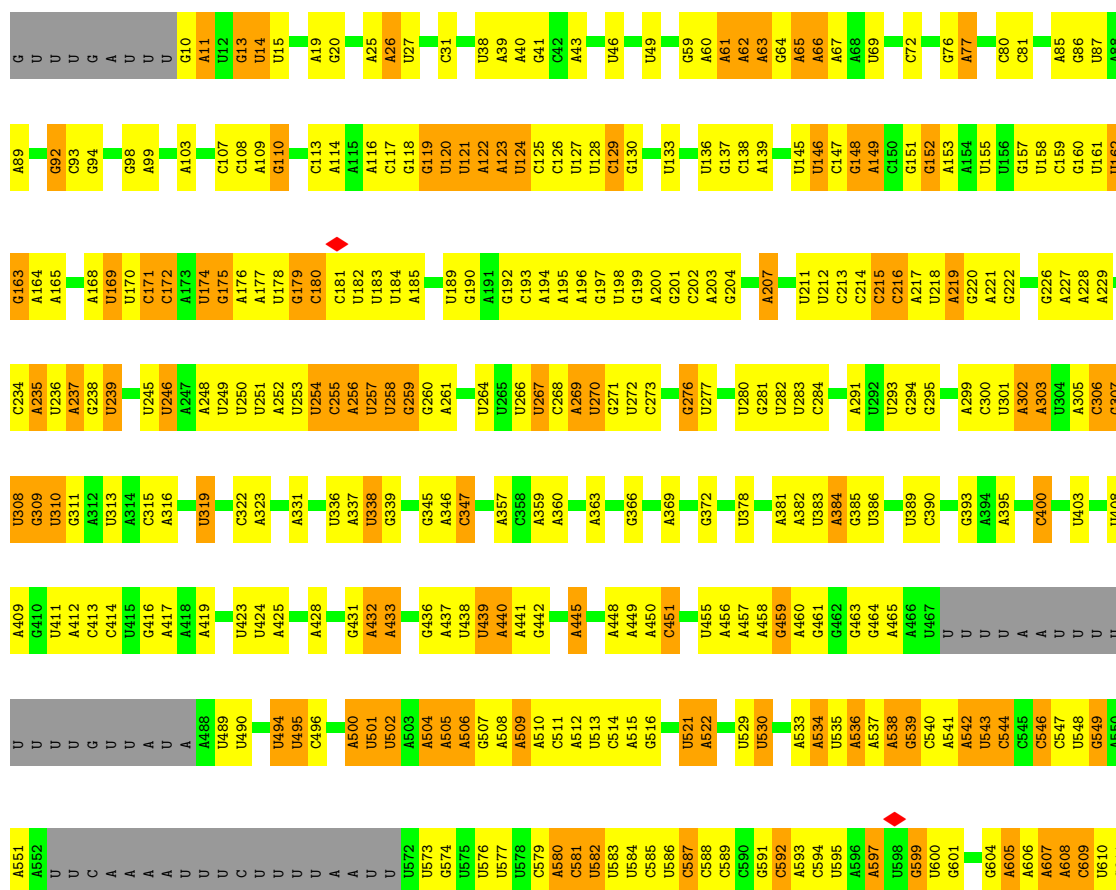
3 Residue-property plots

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: tRNA



• Molecule 2: 28S ribosomal RNA

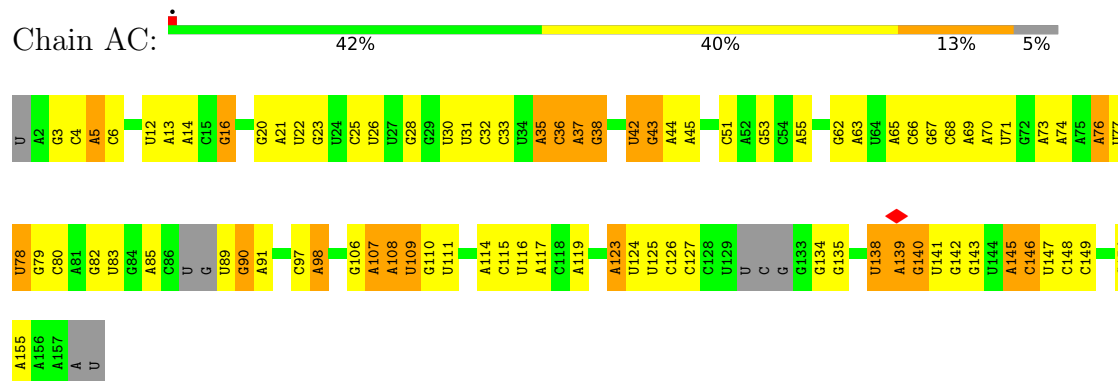




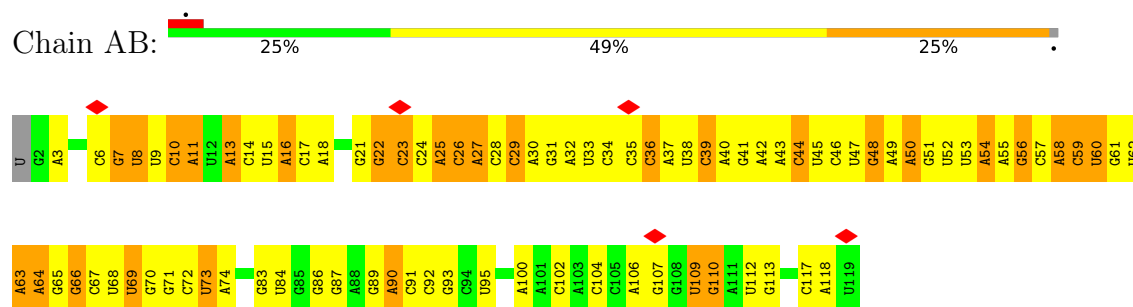




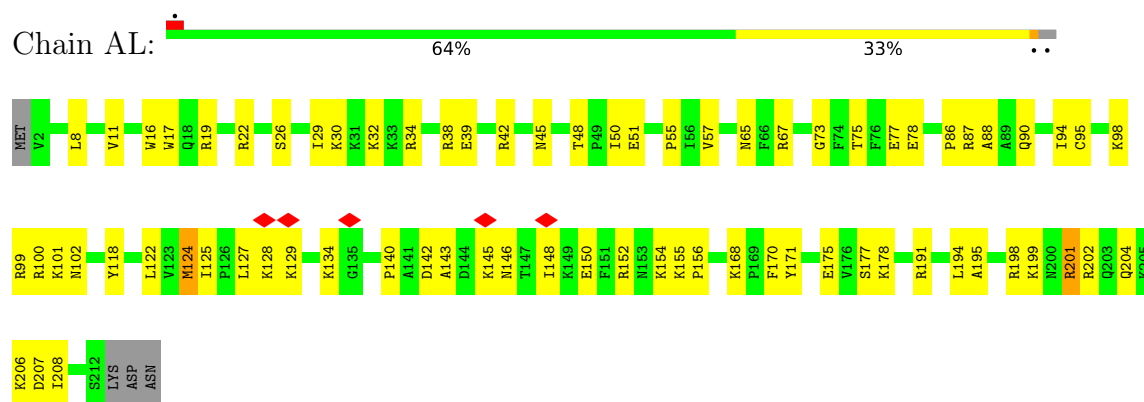
- Molecule 3: 5.8S ribosomal RNA



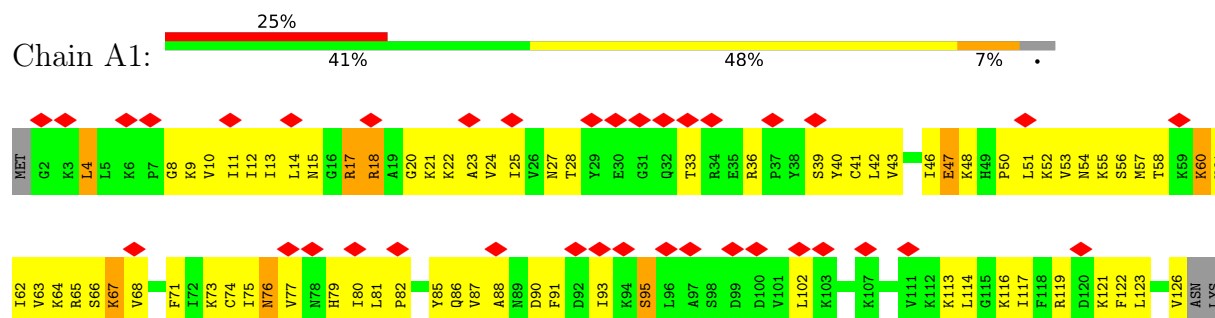
- Molecule 4: 5S ribosomal RNA



- Molecule 5: 60S ribosomal protein L13



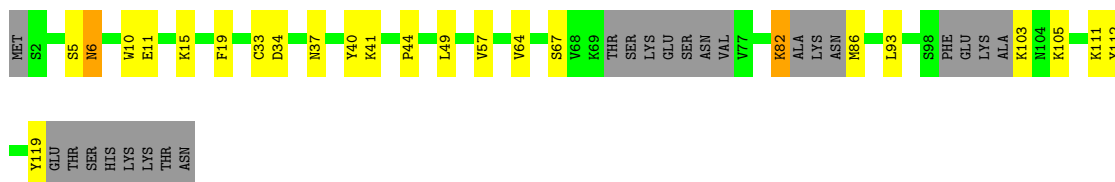
- Molecule 6: 60S ribosomal protein L27





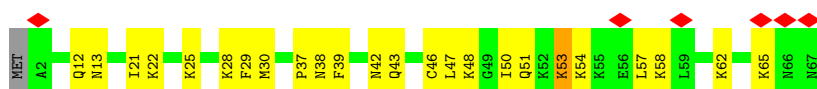
• Molecule 7: 60S ribosomal protein L28

Chain A2: 63% 17% 18%



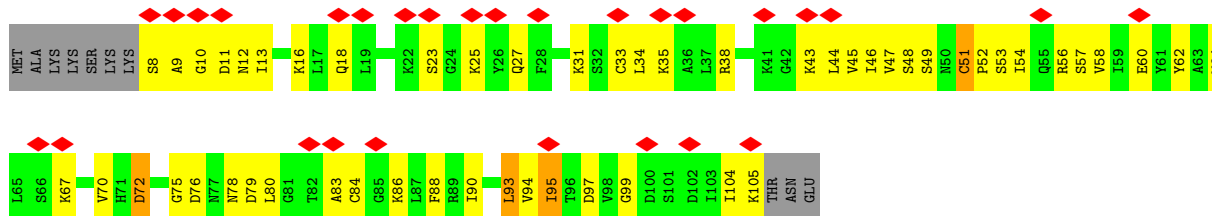
• Molecule 8: 60S ribosomal protein L29

Chain A4: 9% 63% 34%



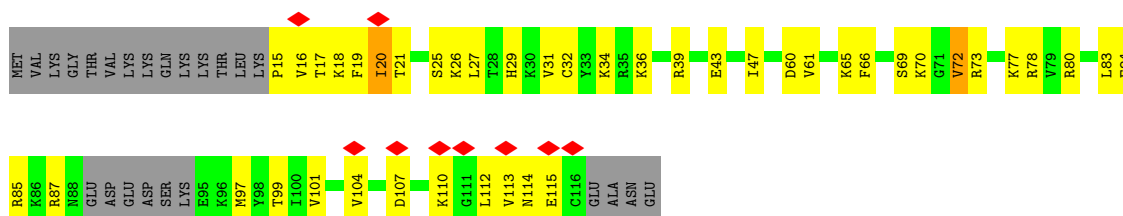
• Molecule 9: 60S ribosomal protein L30e

Chain A6: 26% 42% 45% 9%



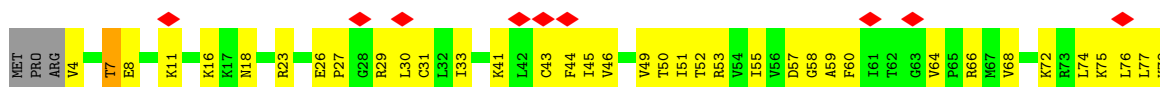
• Molecule 10: 60S ribosomal protein L31

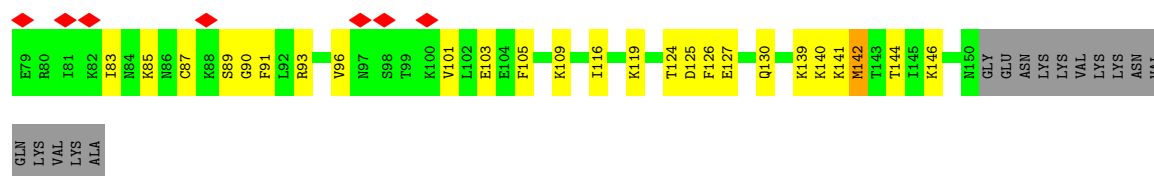
Chain A7: 8% 44% 34% 20%



• Molecule 11: 60S ribosomal protein L14

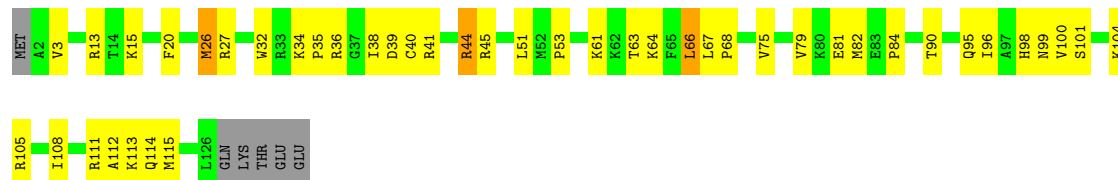
Chain AN: 10% 52% 36% 11%





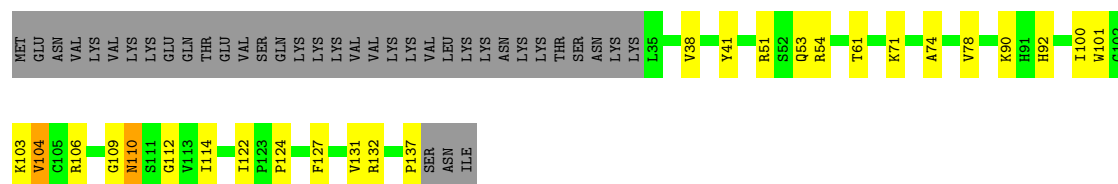
• Molecule 12: 60S ribosomal protein L32

Chain A8: 62% 31% 5%



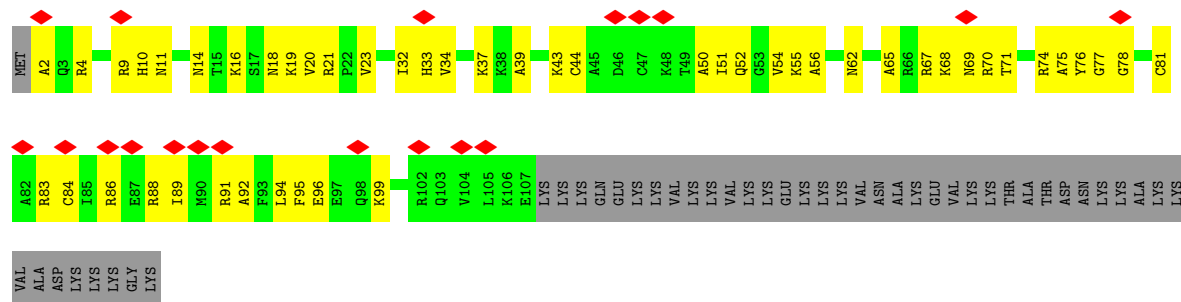
• Molecule 13: 60S ribosomal protein L35ae

Chain A9: 55% 17% 26%



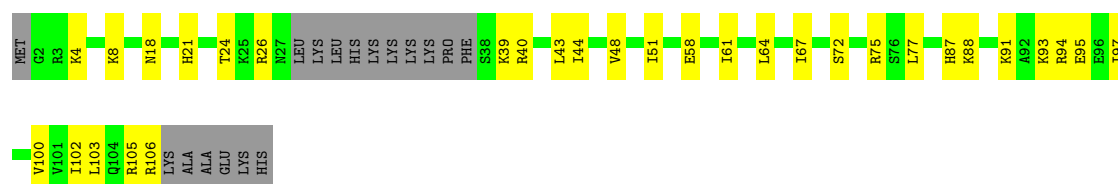
• Molecule 14: 60S ribosomal protein L34

Chain Aa: 13% 38% 33% 29%

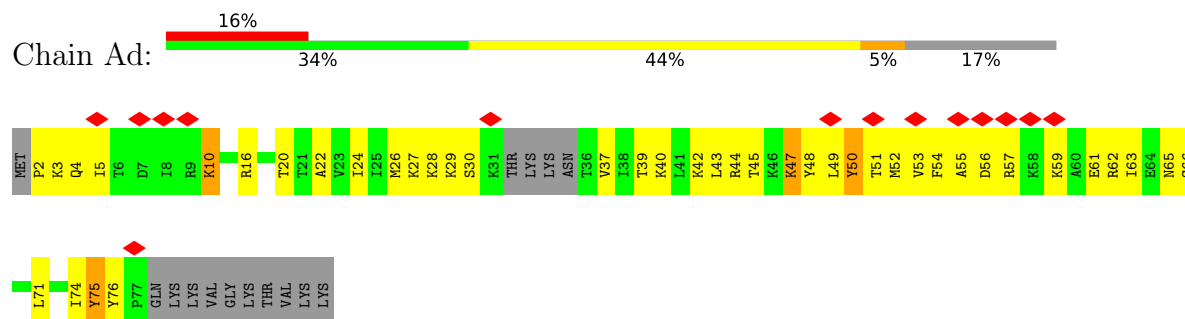


• Molecule 15: 60S ribosomal protein L36

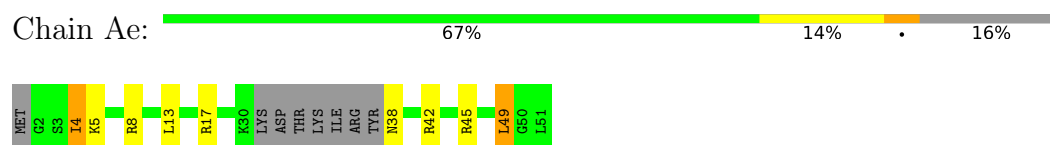
Chain Ab: 57% 28% 15%



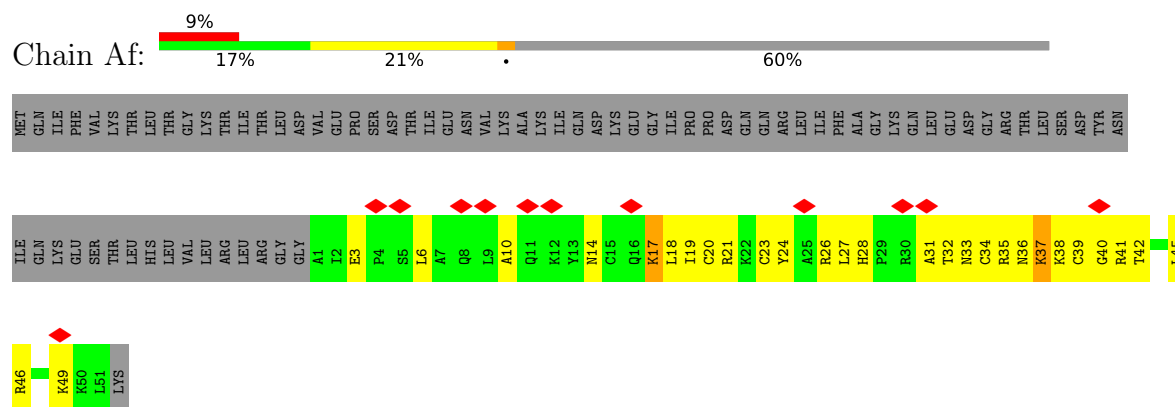
- Molecule 16: 60S ribosomal protein L38



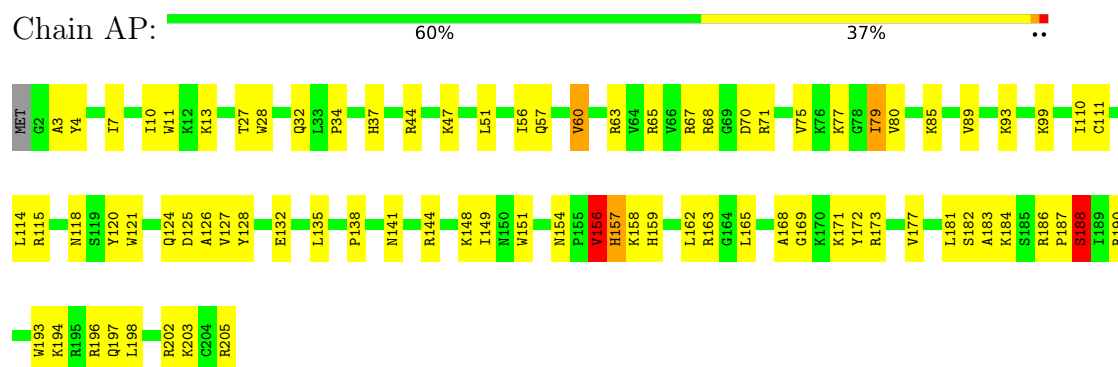
- Molecule 17: 60S ribosomal protein L39



- Molecule 18: Ubiquitin-60S ribosomal protein L40

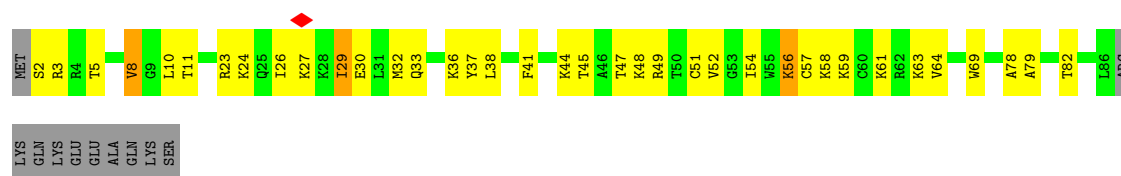


- Molecule 19: Ribosomal protein L15



- Molecule 20: Large ribosomal subunit protein eL43





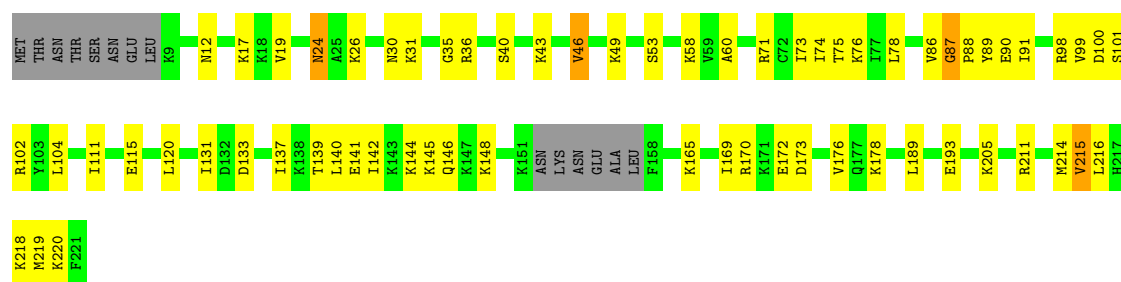
- Molecule 21: Large ribosomal subunit protein eL42

Chain Ai: 63% 27% 9%



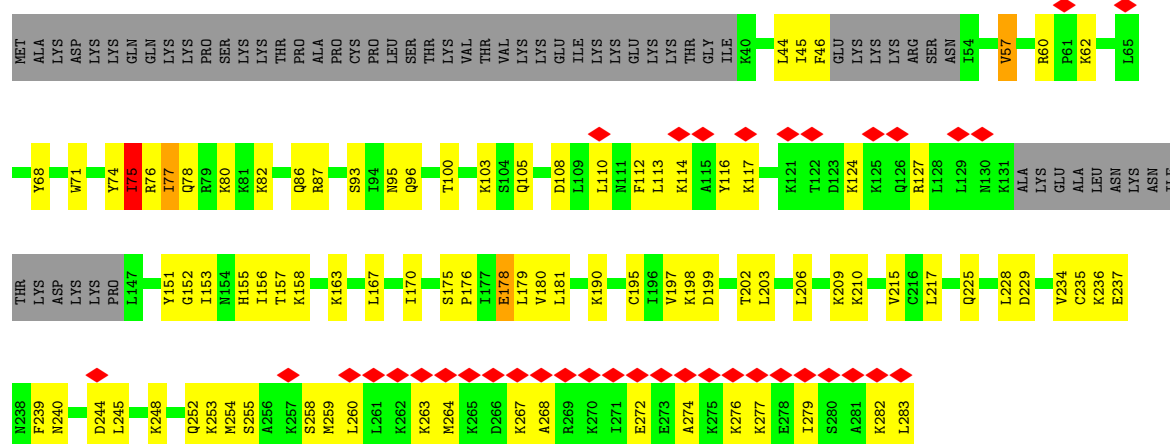
- Molecule 22: 60S ribosomal protein L6

Chain AI: 64% 28% 6%



- Molecule 23: 60S ribosomal protein L7a

Chain AJ: 13% 47% 30% 22%

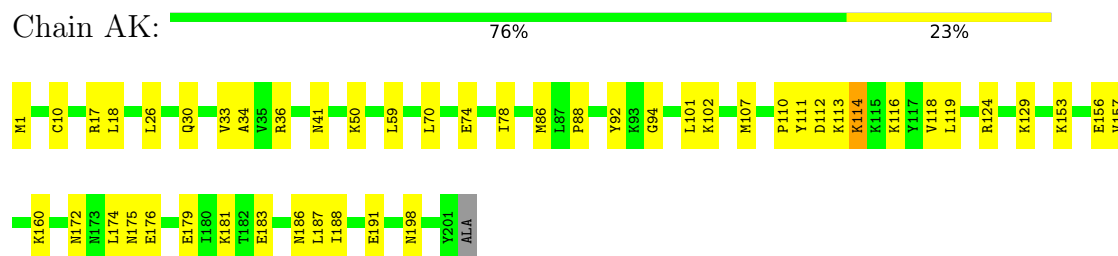


- Molecule 24: Ribosomal protein L37

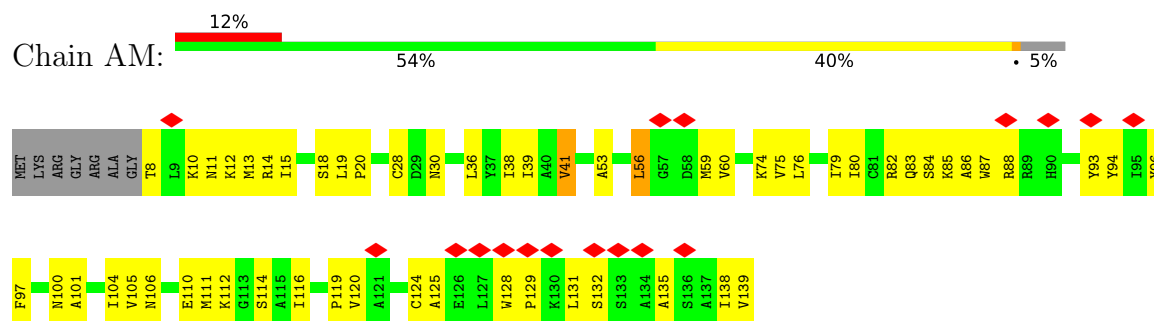
Chain Ac: 63% 30%



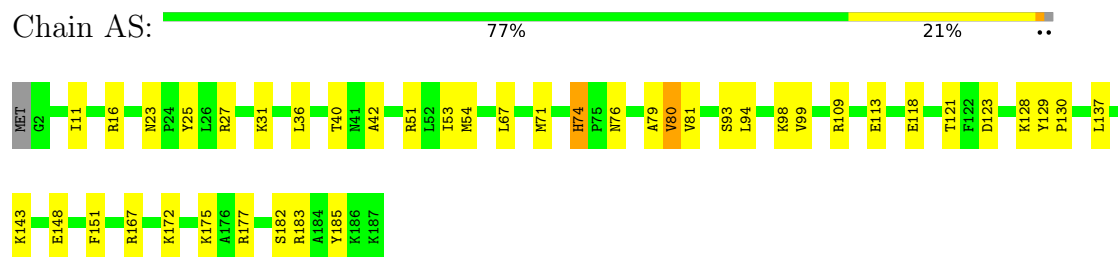
- Molecule 25: 60S ribosomal protein L13



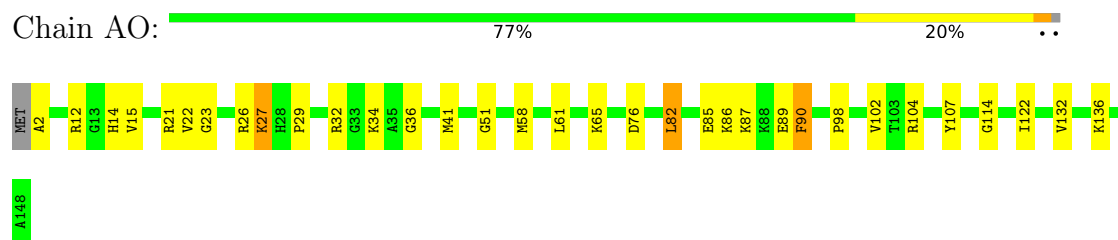
- Molecule 26: 60S ribosomal protein L23



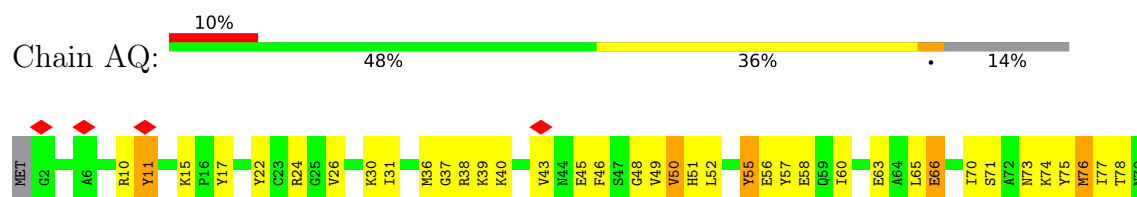
- Molecule 27: 60S ribosomal protein L18-2

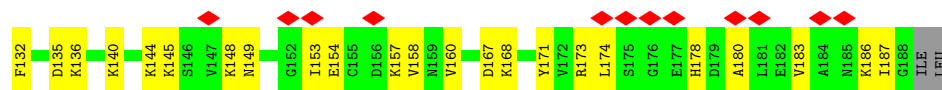


- Molecule 28: 60S ribosomal protein L27a

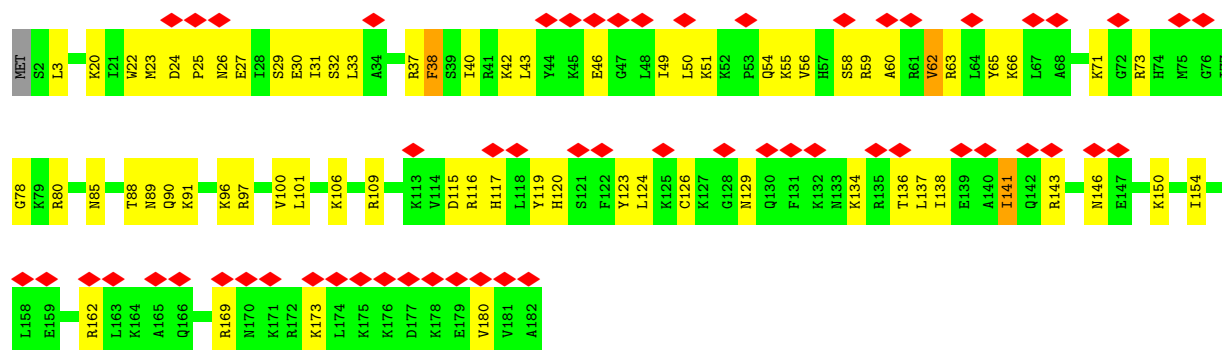


- Molecule 29: 60S ribosomal protein L10

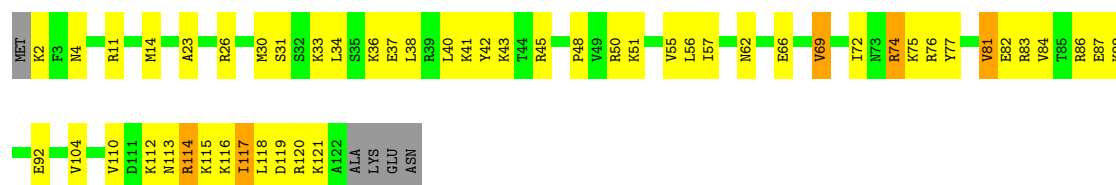




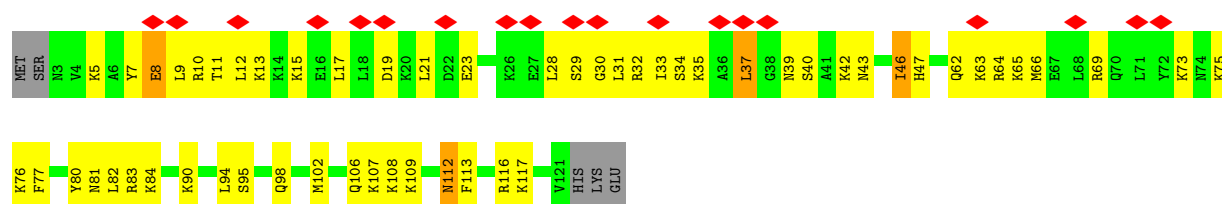
• Molecule 33: 60S ribosomal protein L19



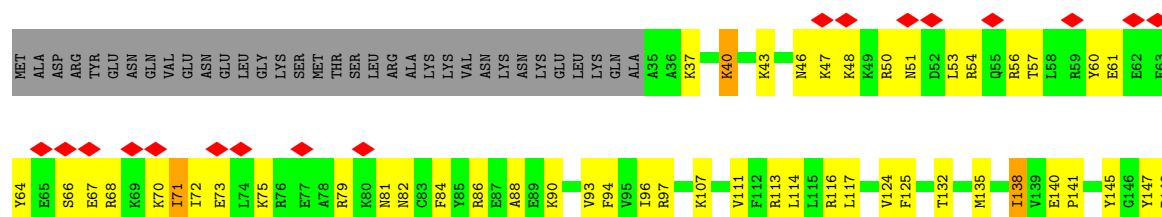
• Molecule 34: 60S ribosomal protein L26

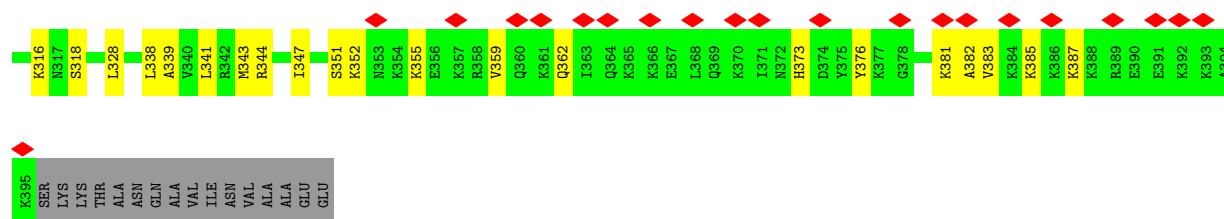


• Molecule 35: 60S ribosomal protein L35

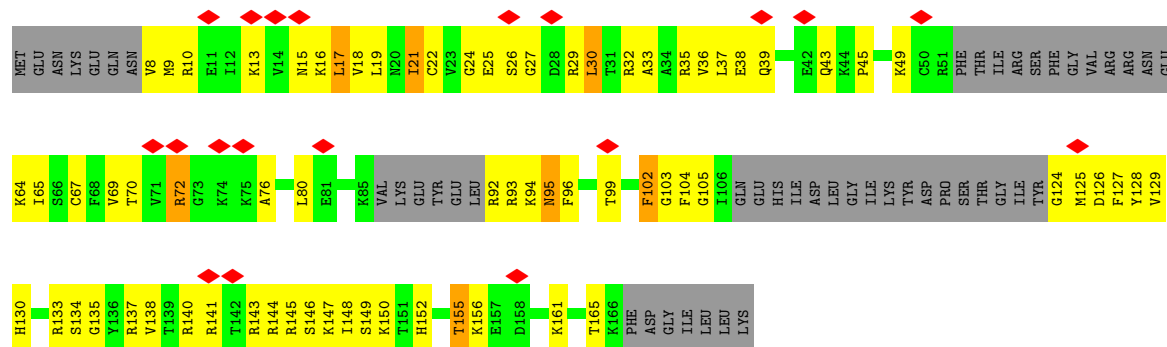


• Molecule 36: 60S ribosomal protein L7

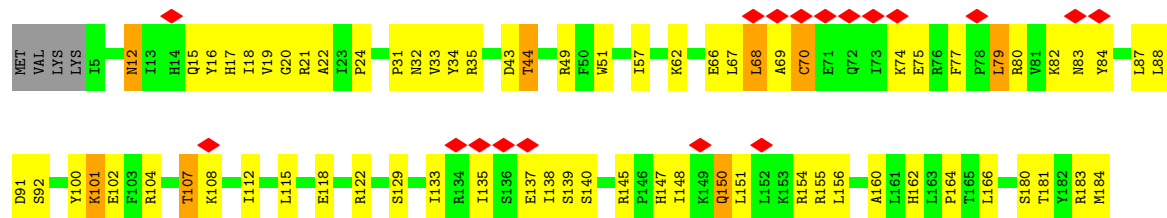




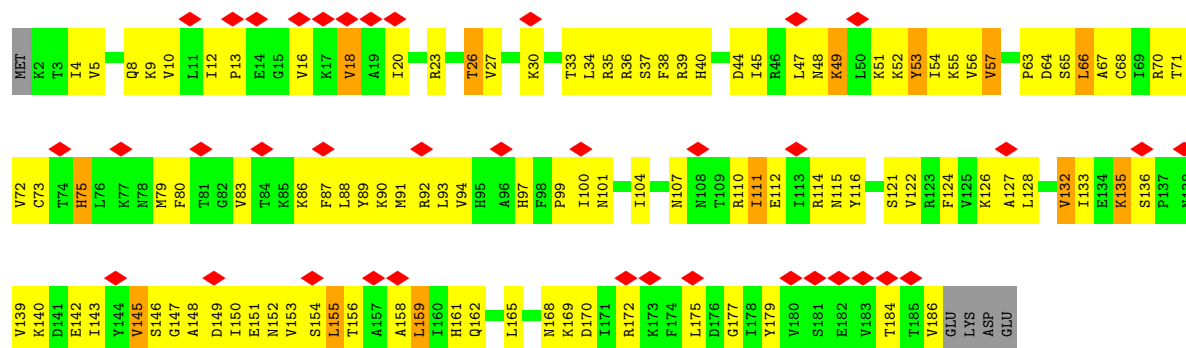
• Molecule 40: 60S ribosomal protein L11a



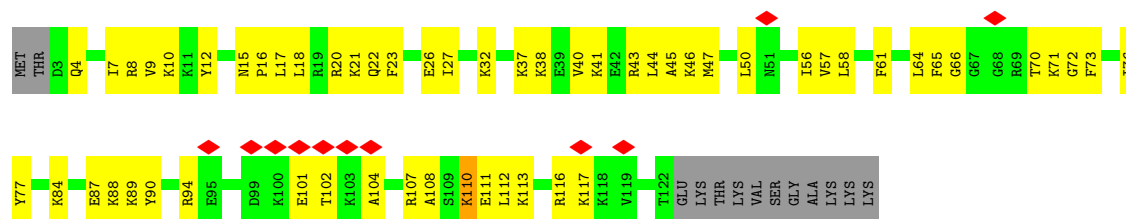
• Molecule 41: 60S ribosomal protein L18a



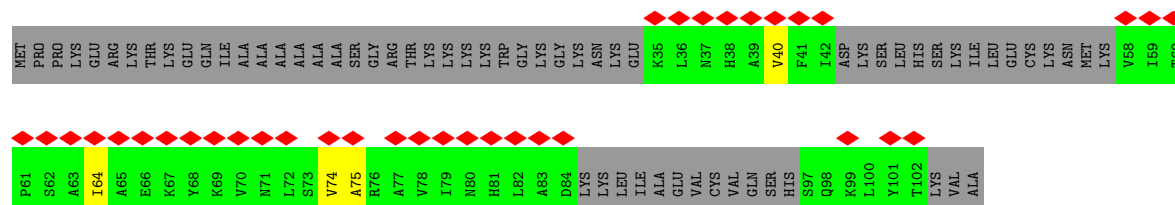
• Molecule 42: 60S ribosomal protein L6



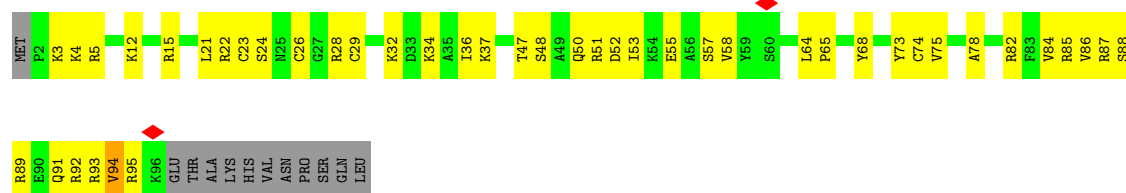
• Molecule 43: 60S ribosomal protein L21



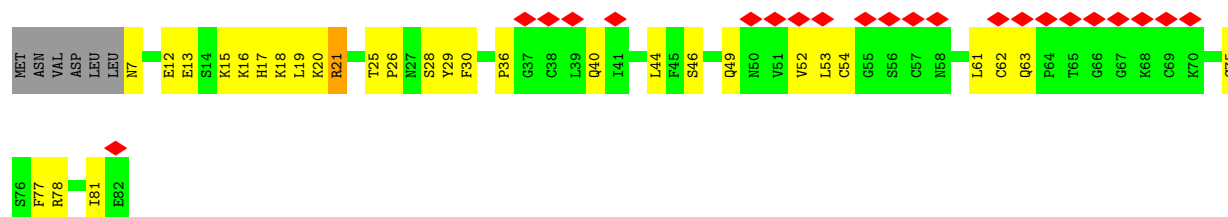
- Molecule 48: 40S ribosomal protein S25



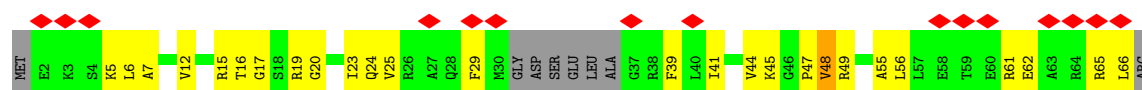
- Molecule 49: 40S ribosomal protein S26



- Molecule 50: 40S ribosomal protein S27



- Molecule 51: 40S ribosomal protein S28e

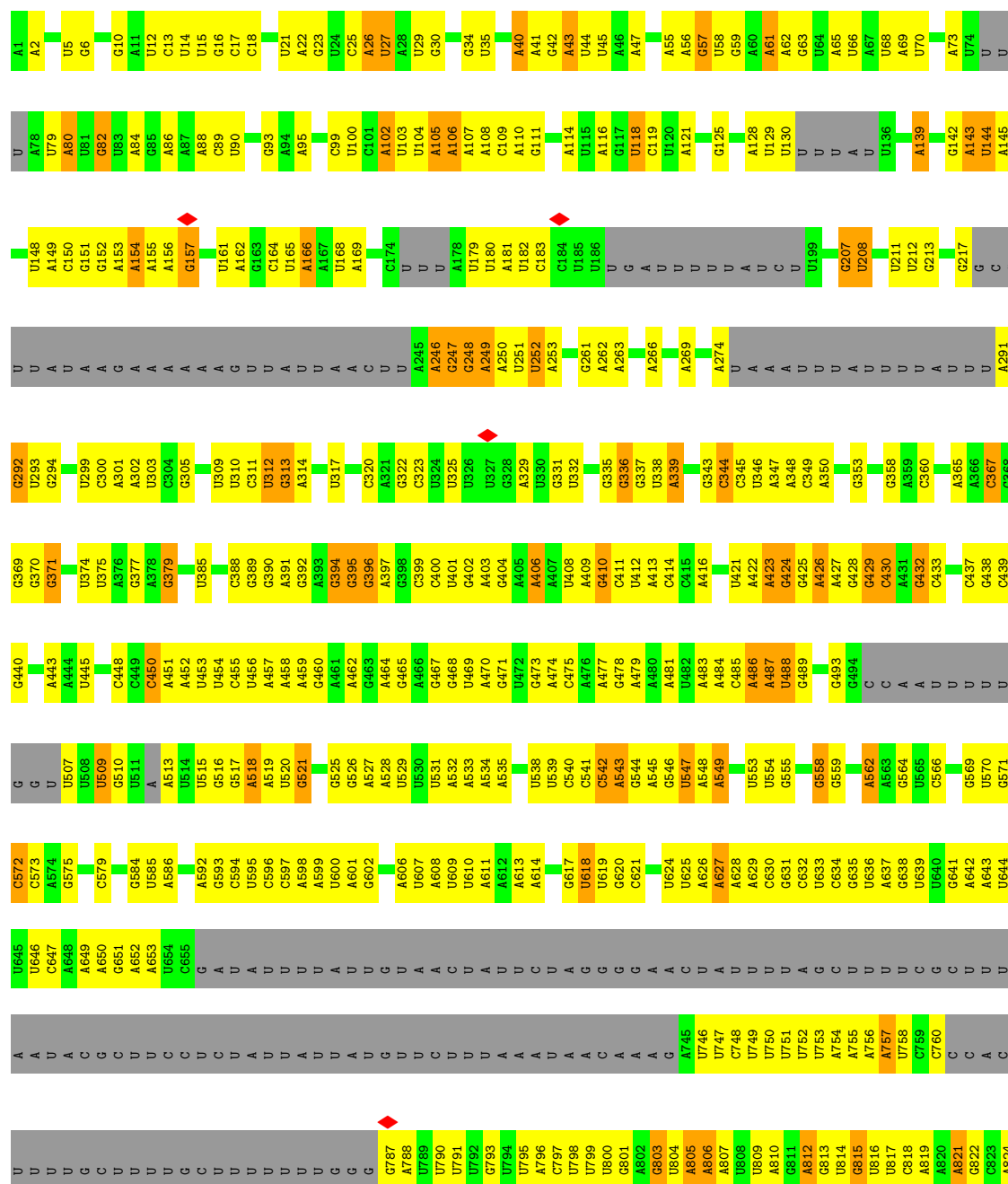


- Molecule 52: 40S ribosomal protein S30

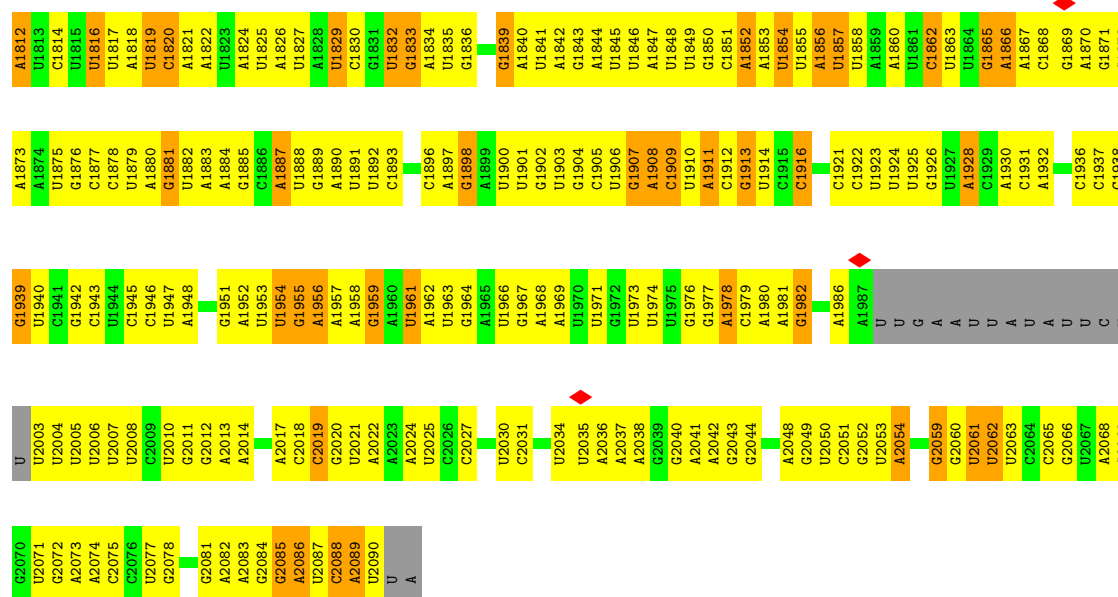
Chain S6:



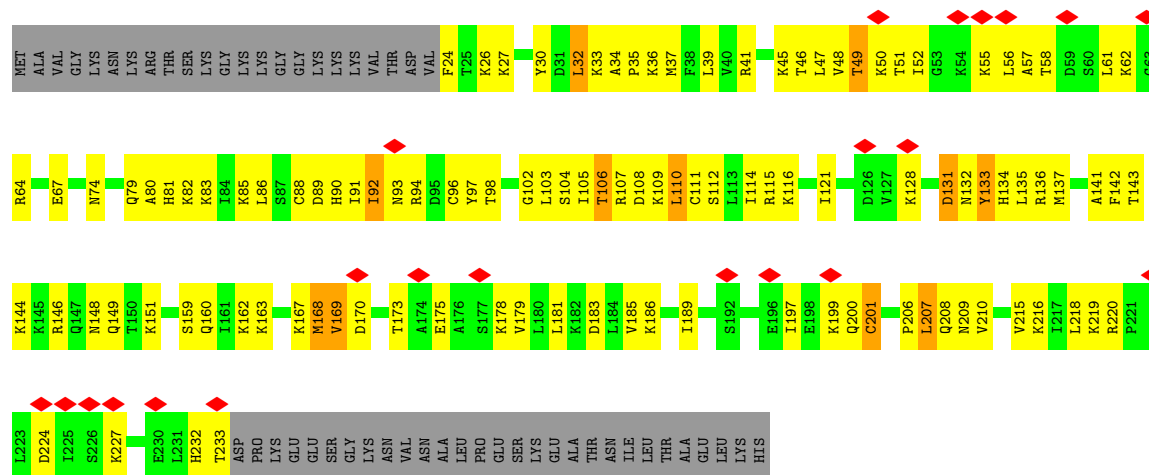
Chain SA:



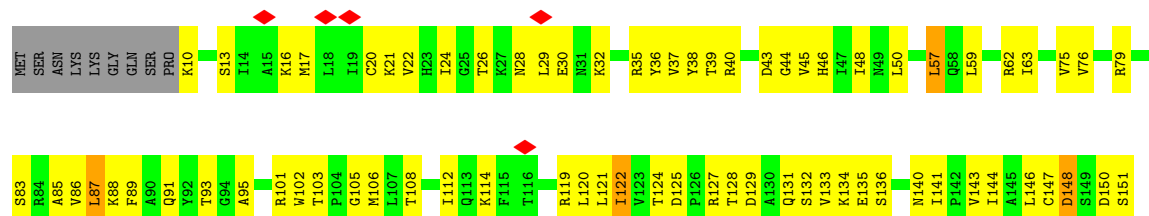




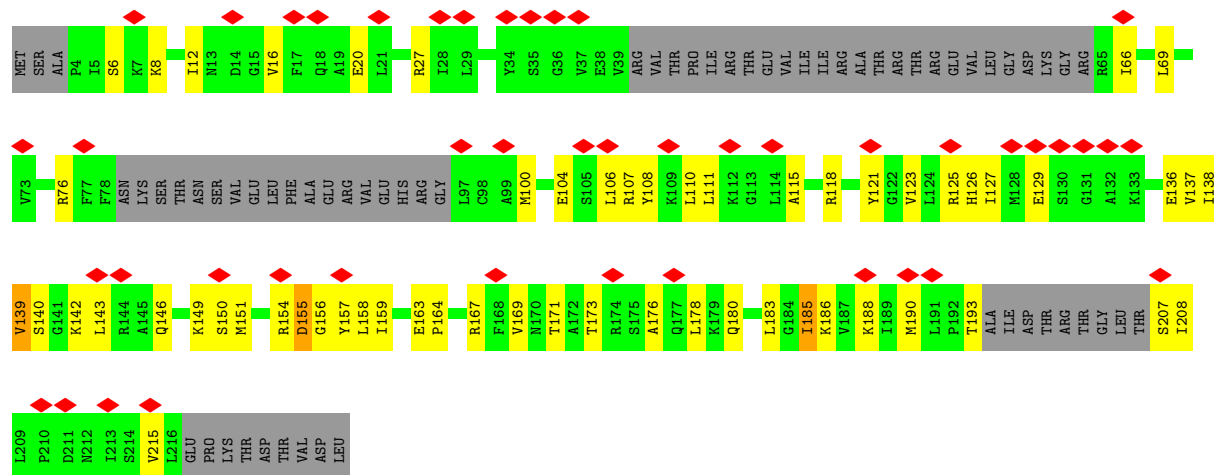
• Molecule 54: 40S ribosomal protein S3a



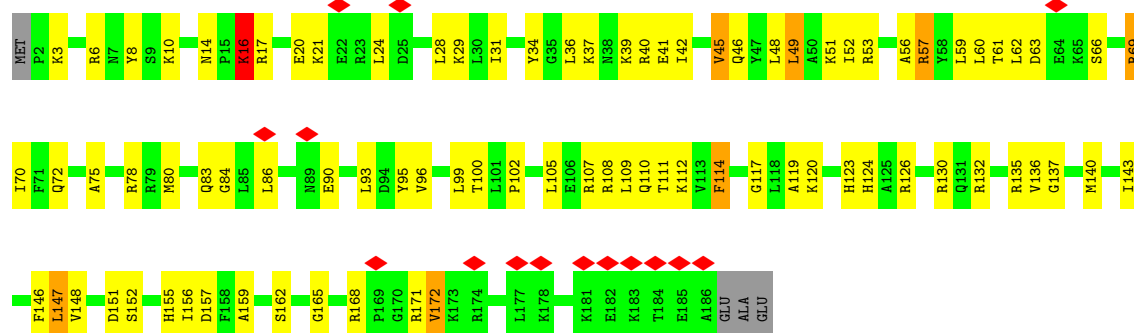
• Molecule 55: 40S ribosomal protein SA



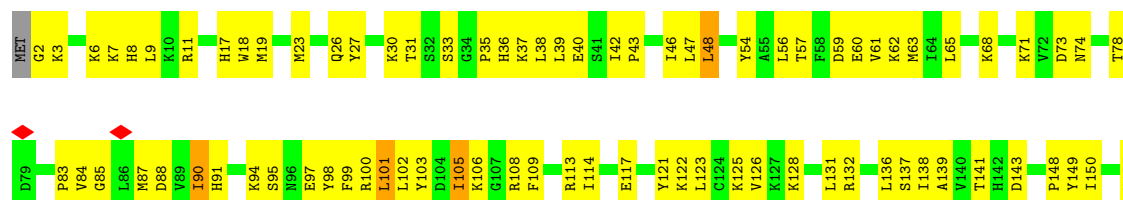
- Molecule 56: 40S ribosomal protein S3



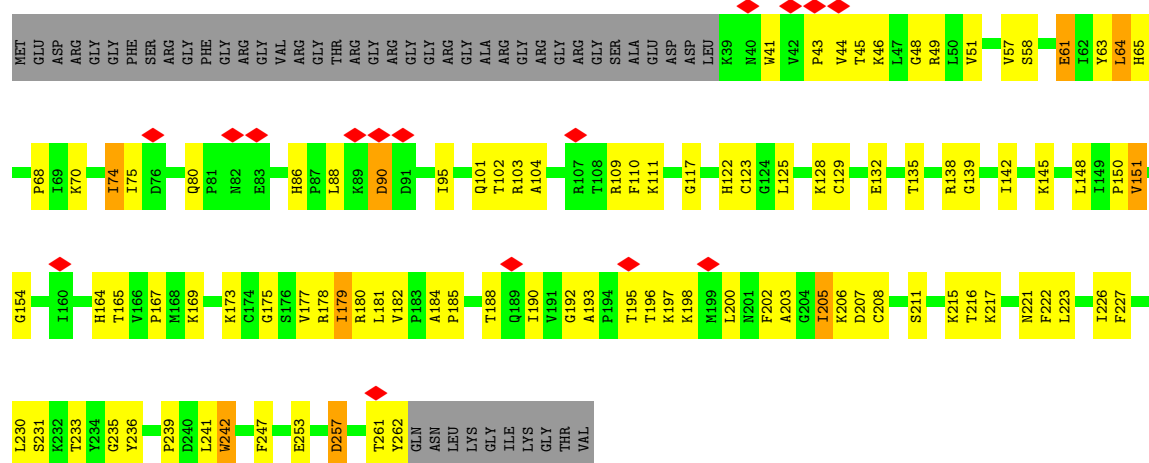
- Molecule 57: 40S ribosomal protein S9



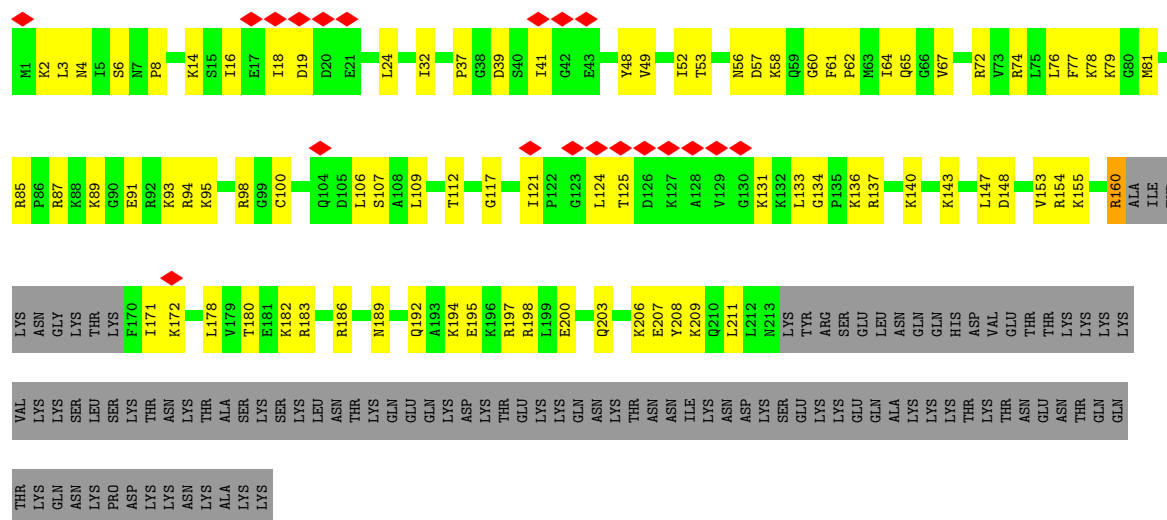
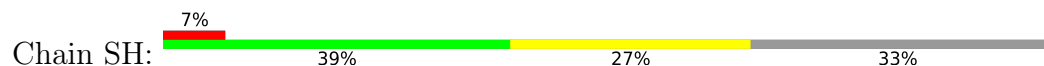
- Molecule 58: 40S ribosomal protein S4



- Molecule 59: 40S ribosomal protein S5

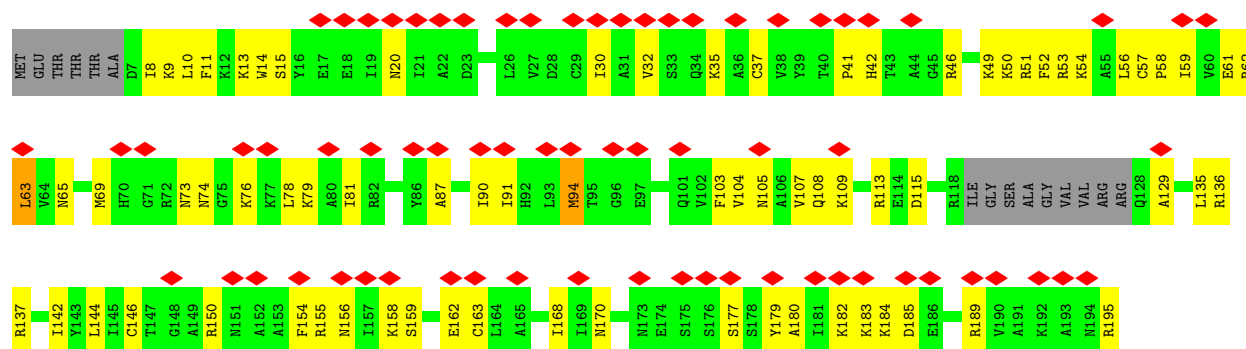


- Molecule 60: 40S ribosomal protein S6

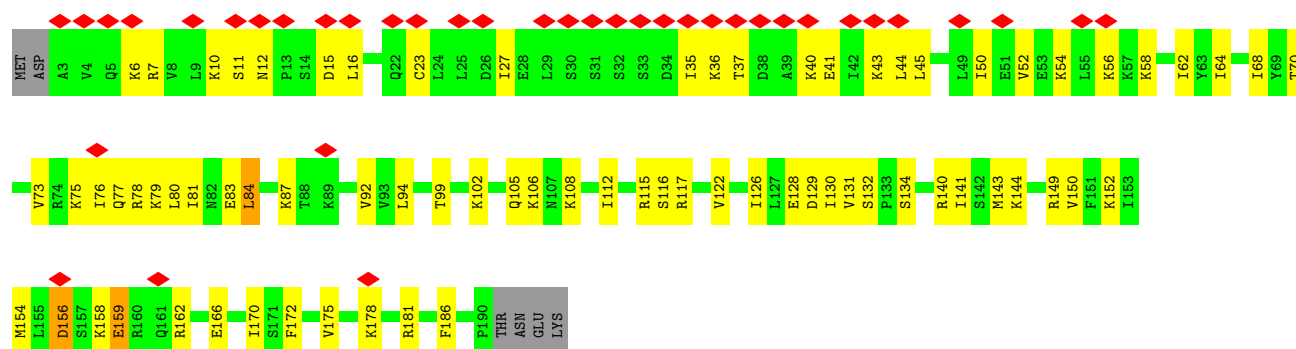


- Molecule 61: 40S ribosomal protein S5

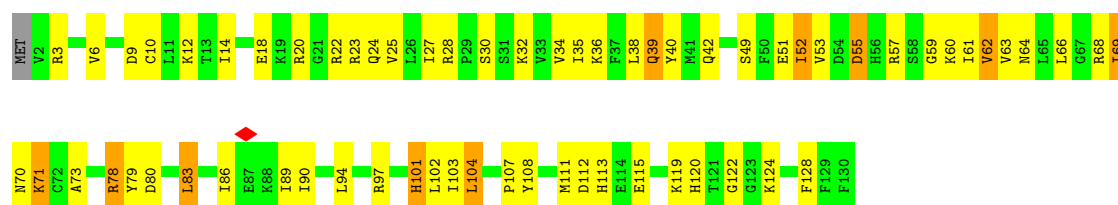




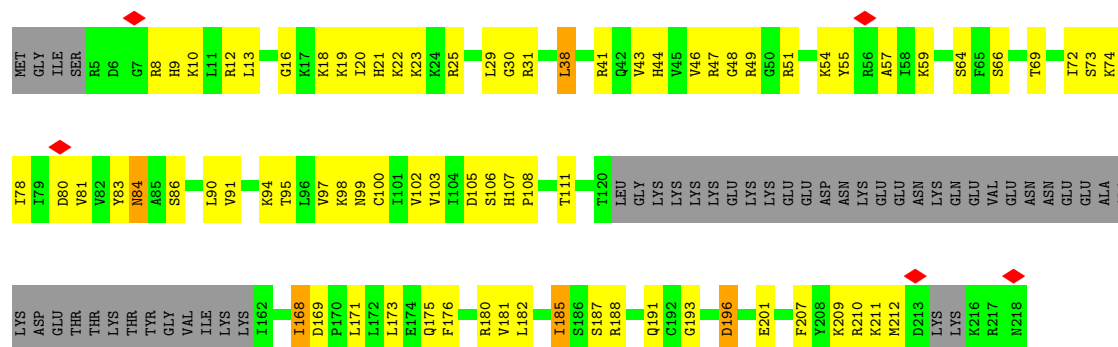
• Molecule 62: 40S ribosomal protein S7



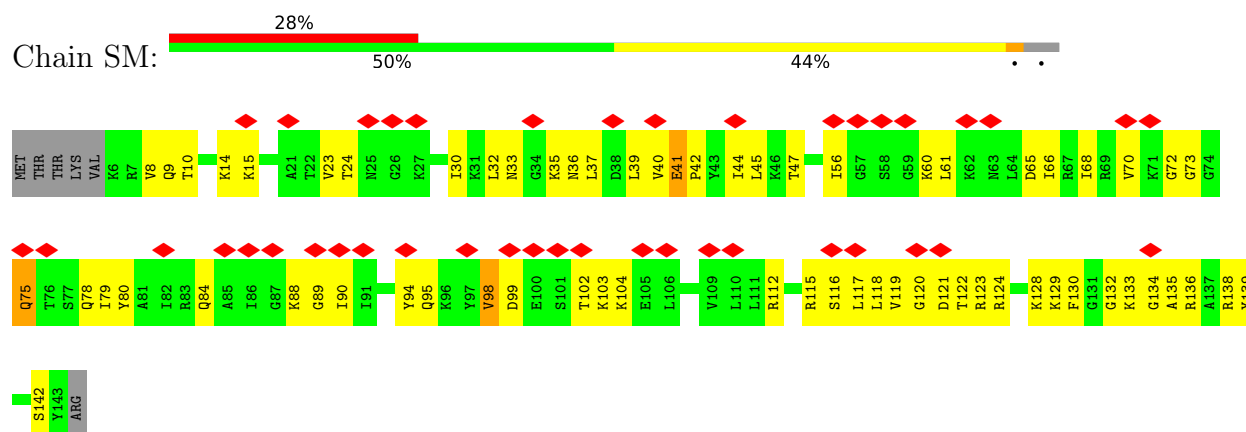
• Molecule 63: 40S ribosomal protein S15A



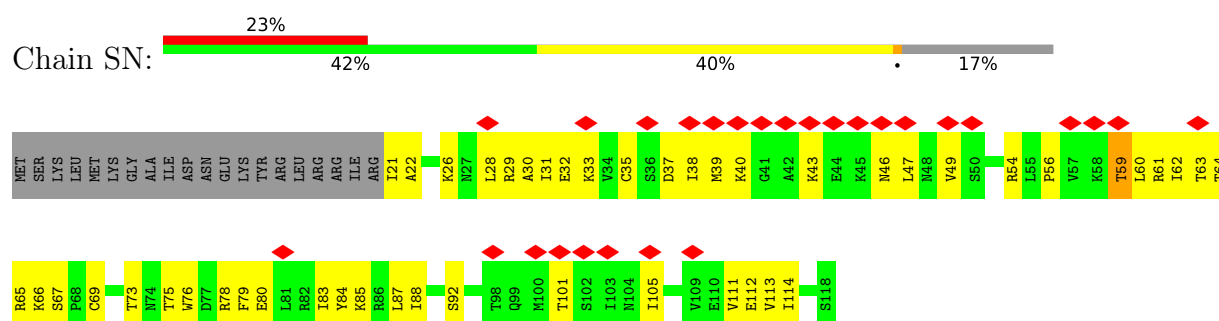
• Molecule 64: 40S ribosomal protein S8



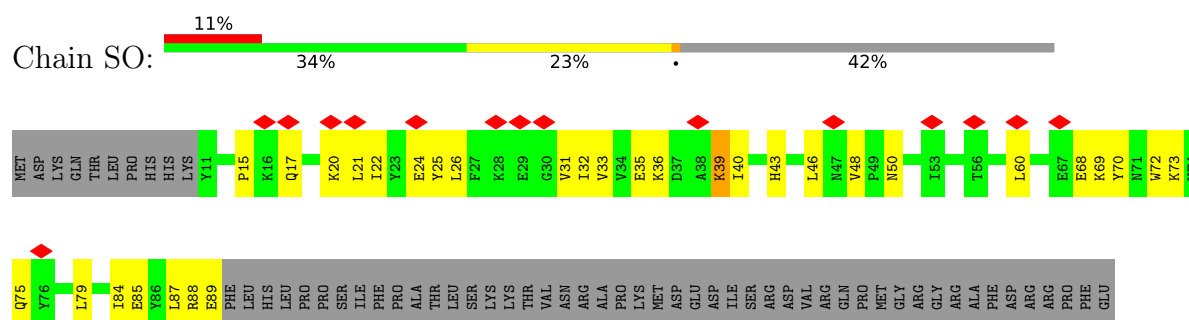
- Molecule 65: 40S ribosomal protein S16



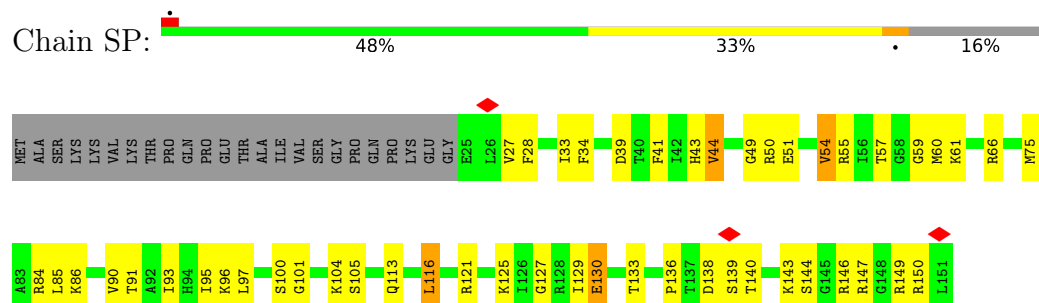
- Molecule 66: 40S ribosomal protein S20e



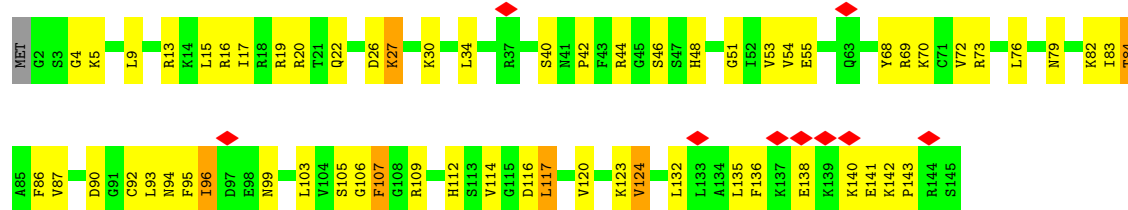
- Molecule 67: 40S ribosomal protein S10



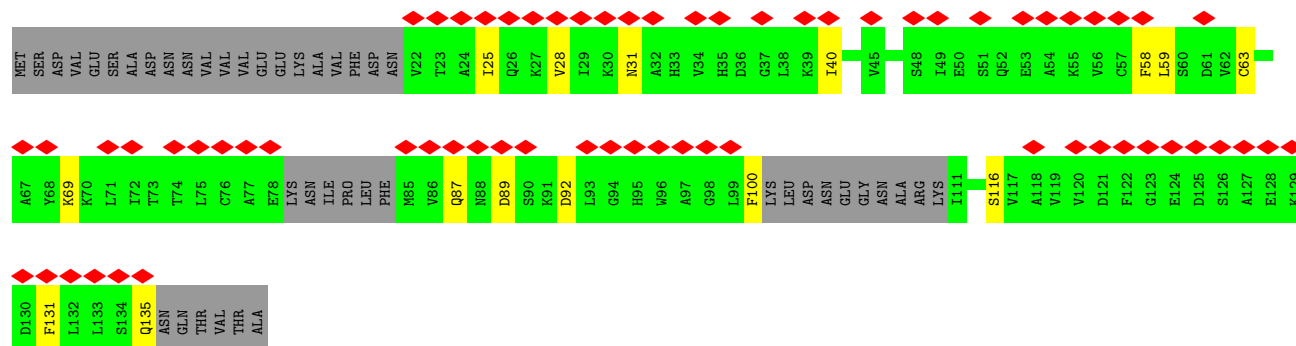
- Molecule 68: 40S ribosomal protein S11



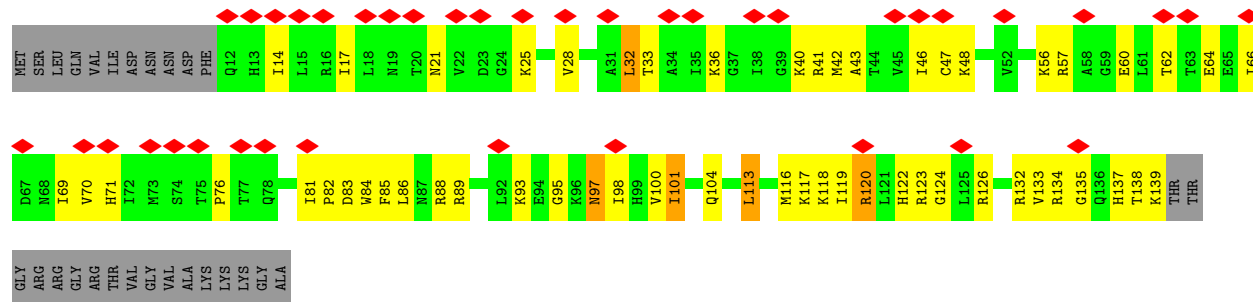
- Molecule 69: 40S ribosomal protein S23



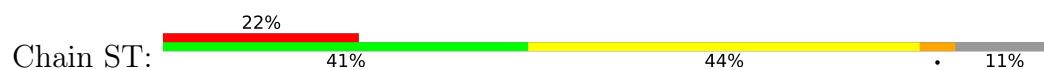
• Molecule 70: 40S ribosomal protein S12



• Molecule 71: 40S ribosomal protein S18

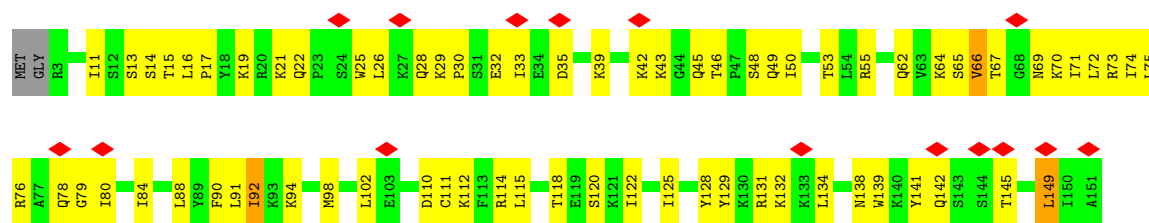


• Molecule 72: 40S ribosomal protein S29

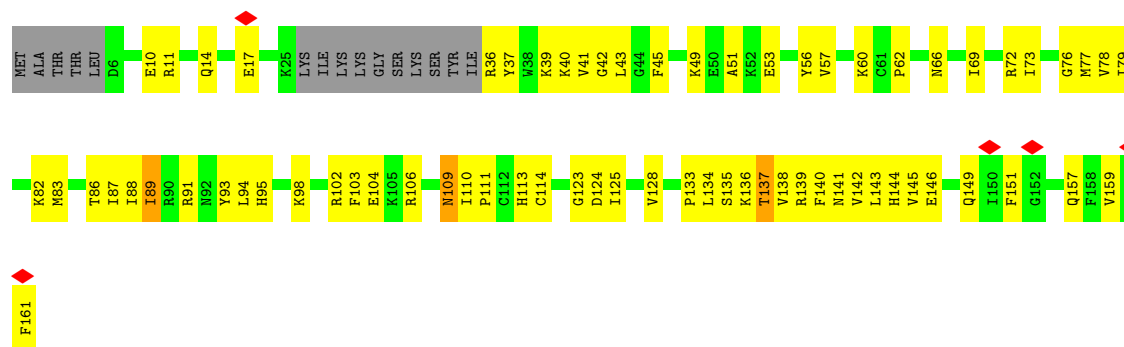


• Molecule 73: 40S ribosomal protein S15

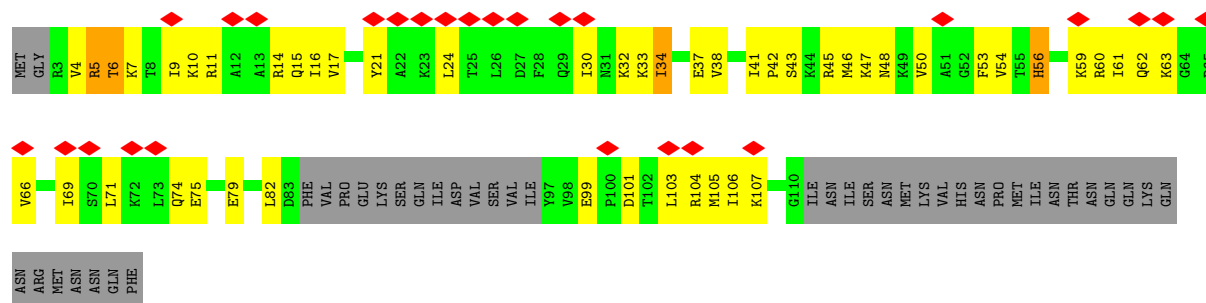




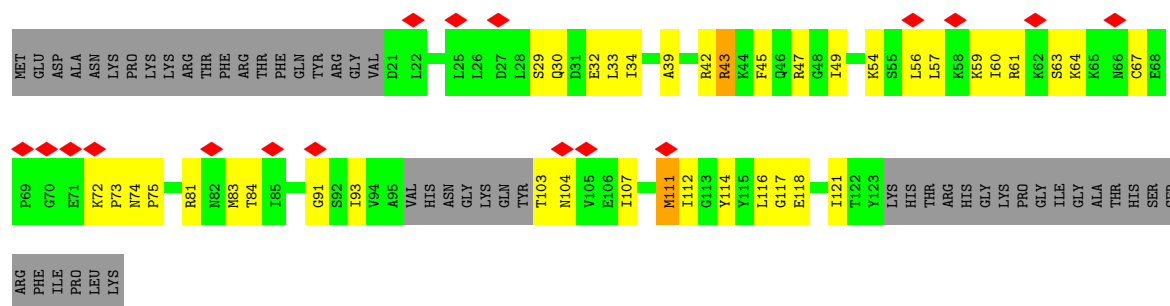
• Molecule 74: 40S ribosomal protein S11



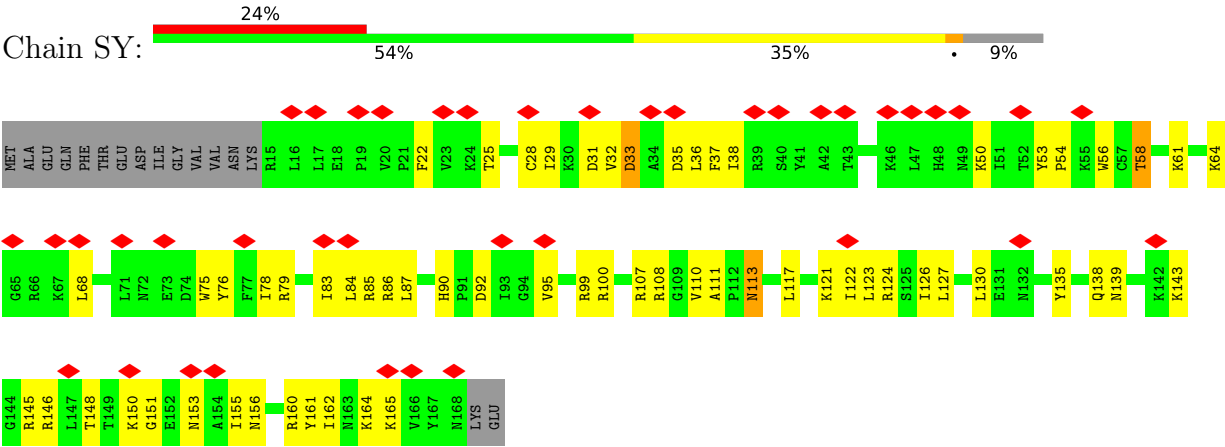
• Molecule 75: 40S ribosomal protein S17



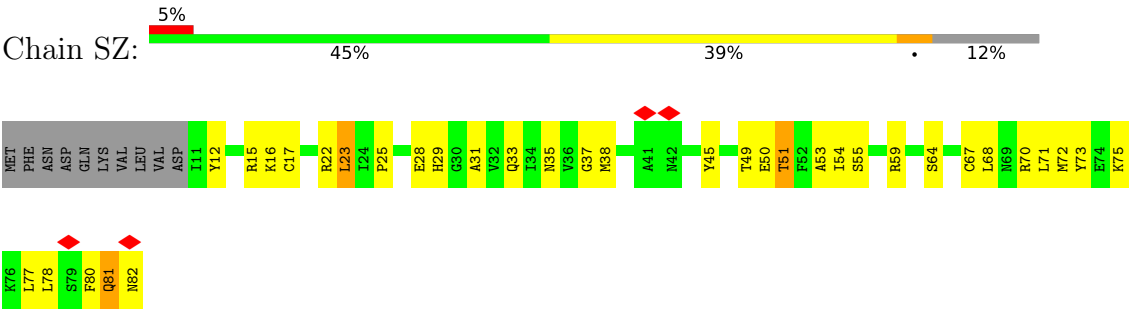
• Molecule 76: 40S ribosomal protein S19



• Molecule 77: 40S ribosomal protein S19



• Molecule 78: 40S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	104647	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	0.070	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00567	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	S7	0.13	0/1810	0.28	0/2821
2	AA	0.20	0/75947	0.33	0/118255
3	AC	0.19	0/3599	0.29	0/5603
4	AB	0.21	0/2816	0.42	0/4388
5	AL	0.19	0/1793	0.40	0/2387
6	A1	0.19	0/1151	0.45	0/1531
7	A2	0.17	0/839	0.33	0/1114
8	A4	0.18	0/564	0.37	0/737
9	A6	0.19	0/748	0.49	0/1001
10	A7	0.22	0/805	0.45	0/1073
11	AN	0.20	0/1226	0.54	1/1632 (0.1%)
12	A8	0.21	0/1053	0.42	0/1399
13	A9	0.20	0/864	0.38	0/1160
14	Aa	0.22	0/871	0.51	0/1161
15	Ab	0.18	0/762	0.43	0/1008
16	Ad	0.17	0/611	0.48	0/812
17	Ae	0.17	0/396	0.29	0/521
18	Af	0.23	0/418	0.57	0/556
19	AP	0.21	0/1735	0.47	0/2320
20	Ah	0.23	0/667	0.51	0/887
21	Ai	0.17	0/788	0.36	0/1032
22	AI	0.18	0/1708	0.37	0/2274
23	AJ	0.18	0/1840	0.44	1/2456 (0.0%)
24	Ac	0.21	0/722	0.41	0/951
25	AK	0.20	0/1689	0.39	0/2260
26	AM	0.21	0/1012	0.47	0/1363
27	AS	0.19	0/1531	0.40	0/2040
28	AO	0.19	0/1199	0.36	0/1597
29	AQ	0.20	0/1579	0.46	0/2113
30	AR	0.19	0/2078	0.46	0/2776
31	AW	0.20	0/1244	0.41	0/1663
32	AY	0.21	0/805	0.47	0/1074
33	AT	0.18	0/1525	0.47	0/2016
34	AZ	0.17	0/1012	0.39	0/1339

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	A3	0.23	0/1004	0.54	0/1329
36	A5	0.23	0/1917	0.49	1/2562 (0.0%)
37	AD	0.20	0/1901	0.38	0/2544
38	AE	0.20	0/3129	0.44	0/4195
39	AF	0.18	0/3144	0.37	0/4205
40	AG	0.18	0/1020	0.45	0/1349
41	AU	0.21	0/1527	0.49	0/2043
42	AH	0.23	0/1500	0.57	1/2025 (0.0%)
43	AV	0.25	0/1300	0.47	0/1732
44	Ag	0.16	0/348	0.51	0/448
45	AX	0.15	0/841	0.38	0/1125
46	A0	0.16	0/533	0.40	0/711
47	S1	0.13	0/998	0.34	0/1321
48	S2	0.10	0/323	0.33	0/435
49	S3	0.15	0/793	0.41	0/1055
50	S4	0.17	0/597	0.43	0/801
51	S5	0.13	0/466	0.39	0/616
52	S6	0.12	0/348	0.46	0/458
53	SA	0.12	0/38276	0.27	0/59598
54	SB	0.15	0/1737	0.43	0/2321
55	SC	0.17	0/1569	0.49	0/2129
56	SD	0.13	0/1240	0.37	0/1652
57	SE	0.16	0/1538	0.43	0/2055
58	SF	0.15	0/2097	0.39	0/2819
59	SG	0.16	0/1799	0.42	0/2429
60	SH	0.15	0/1668	0.42	0/2214
61	SI	0.13	0/1443	0.37	0/1936
62	SJ	0.16	0/1544	0.38	0/2064
63	SK	0.17	0/1054	0.47	0/1411
64	SL	0.18	0/1407	0.43	0/1879
65	SM	0.13	0/1113	0.37	0/1487
66	SN	0.17	0/780	0.39	0/1053
67	SO	0.14	0/705	0.37	0/950
68	SP	0.17	0/966	0.47	0/1295
69	SQ	0.27	0/1149	0.46	0/1532
70	SR	0.10	0/754	0.29	0/1013
71	SS	0.13	0/1062	0.40	0/1425
72	ST	0.14	0/412	0.34	0/544
73	SU	0.17	0/1223	0.44	0/1634
74	SV	0.16	0/1233	0.41	0/1645
75	SW	0.17	0/792	0.50	0/1053
76	SX	0.12	0/787	0.37	0/1050
77	SY	0.12	0/1294	0.36	0/1742

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	SZ	0.14	0/565	0.40	0/758
All	All	0.18	0/207303	0.36	4/303962 (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
22	AI	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AN	7	THR	CB-CA-C	-6.39	108.54	117.23
23	AJ	57	VAL	N-CA-C	-6.34	105.16	111.88
36	A5	246	GLU	CB-CA-C	-5.17	110.59	116.54
42	AH	155	LEU	CA-CB-CG	5.02	133.88	116.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	AI	87	GLY	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	S7	1620	0	827	24	0
2	AA	67884	0	34243	1628	0
3	AC	3215	0	1633	75	0
4	AB	2517	0	1275	135	0
5	AL	1761	0	1896	61	0
6	A1	1134	0	1245	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A2	830	0	887	19	0
8	A4	555	0	599	23	0
9	A6	740	0	763	48	0
10	A7	793	0	869	35	0
11	AN	1210	0	1329	63	0
12	A8	1036	0	1139	40	0
13	A9	844	0	886	19	0
14	Aa	858	0	912	55	0
15	Ab	756	0	842	20	0
16	Ad	603	0	686	45	0
17	Ae	388	0	421	8	0
18	Af	413	0	452	43	0
19	AP	1697	0	1802	62	0
20	Ah	658	0	727	38	0
21	Ai	778	0	861	22	0
22	AI	1685	0	1849	48	0
23	AJ	1813	0	1985	74	0
24	Ac	709	0	761	31	0
25	AK	1659	0	1782	37	0
26	AM	996	0	1044	54	0
27	AS	1503	0	1636	31	0
28	AO	1172	0	1230	28	0
29	AQ	1544	0	1582	69	0
30	AR	2049	0	2145	145	0
31	AW	1319	0	1303	35	0
32	AY	796	0	850	36	0
33	AT	1509	0	1682	60	0
34	AZ	1000	0	1099	48	0
35	A3	994	0	1121	61	0
36	A5	1879	0	2005	72	0
37	AD	1866	0	1964	49	0
38	AE	3061	0	3205	141	0
39	AF	3094	0	3333	103	0
40	AG	1010	0	1073	75	0
41	AU	1497	0	1556	76	0
42	AH	1475	0	1574	98	0
43	AV	1275	0	1355	50	0
44	Ag	343	0	388	18	0
45	AX	824	0	882	38	0
46	A0	521	0	539	19	0
47	S1	985	0	1076	60	0
48	S2	320	0	338	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	S3	781	0	820	47	0
50	S4	586	0	604	22	0
51	S5	465	0	505	23	0
52	S6	345	0	381	20	0
53	SA	34208	0	17266	1052	0
54	SB	1713	0	1838	95	0
55	SC	1538	0	1600	77	0
56	SD	1228	0	1311	47	0
57	SE	1514	0	1605	89	0
58	SF	2061	0	2200	109	0
59	SG	1757	0	1811	90	0
60	SH	1651	0	1807	74	0
61	SI	1424	0	1471	70	0
62	SJ	1528	0	1680	59	0
63	SK	1037	0	1099	56	0
64	SL	1383	0	1434	72	0
65	SM	1098	0	1183	55	0
66	SN	772	0	813	52	0
67	SO	686	0	695	21	0
68	SP	954	0	997	57	0
69	SQ	1129	0	1196	53	0
70	SR	746	0	754	9	0
71	SS	1046	0	1101	49	0
72	ST	405	0	419	32	0
73	SU	1202	0	1299	76	0
74	SV	1206	0	1239	54	0
75	SW	785	0	858	45	0
76	SX	776	0	832	30	0
77	SY	1266	0	1316	58	0
78	SZ	557	0	558	35	0
All	All	193035	0	144343	5696	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 17.

The worst 5 of 5696 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)
2:AA:3490:A:N6	2:AA:3513:G:H21	1.34	1.26
2:AA:3490:A:H62	2:AA:3513:G:N2	1.34	1.23
2:AA:965:A:H61	53:SA:1041:G:N2	1.42	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:3410:A:H62	2:AA:3417:G:N2	1.42	1.14
2:AA:3725:G:N2	2:AA:3762:A:H62	1.44	1.13

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	
5	AL	209/215 (97%)	195 (93%)	14 (7%)	0	100	100
6	A1	136/146 (93%)	125 (92%)	11 (8%)	0	100	100
7	A2	96/127 (76%)	90 (94%)	6 (6%)	0	100	100
8	A4	64/67 (96%)	59 (92%)	5 (8%)	0	100	100
9	A6	96/108 (89%)	89 (93%)	7 (7%)	0	100	100
10	A7	92/120 (77%)	90 (98%)	2 (2%)	0	100	100
11	AN	145/165 (88%)	134 (92%)	11 (8%)	0	100	100
12	A8	123/131 (94%)	110 (89%)	13 (11%)	0	100	100
13	A9	101/140 (72%)	93 (92%)	8 (8%)	0	100	100
14	Aa	104/150 (69%)	93 (89%)	10 (10%)	1 (1%)	12	38
15	Ab	91/112 (81%)	83 (91%)	8 (9%)	0	100	100
16	Ad	68/87 (78%)	64 (94%)	4 (6%)	0	100	100
17	Ae	39/51 (76%)	39 (100%)	0	0	100	100
18	Af	49/128 (38%)	41 (84%)	8 (16%)	0	100	100
19	AP	202/205 (98%)	179 (89%)	19 (9%)	4 (2%)	6	21
20	Ah	83/96 (86%)	75 (90%)	8 (10%)	0	100	100
21	Ai	93/104 (89%)	88 (95%)	5 (5%)	0	100	100
22	AI	203/221 (92%)	192 (95%)	9 (4%)	2 (1%)	12	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	AJ	216/283 (76%)	208 (96%)	7 (3%)	1 (0%)	24	55
24	Ac	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
25	AK	199/202 (98%)	192 (96%)	7 (4%)	0	100	100
26	AM	130/139 (94%)	123 (95%)	7 (5%)	0	100	100
27	AS	184/187 (98%)	176 (96%)	8 (4%)	0	100	100
28	AO	145/148 (98%)	138 (95%)	6 (4%)	1 (1%)	18	47
29	AQ	185/219 (84%)	163 (88%)	20 (11%)	2 (1%)	11	36
30	AR	244/294 (83%)	226 (93%)	17 (7%)	1 (0%)	30	60
31	AW	149/173 (86%)	141 (95%)	8 (5%)	0	100	100
32	AY	99/190 (52%)	93 (94%)	6 (6%)	0	100	100
33	AT	179/182 (98%)	169 (94%)	10 (6%)	0	100	100
34	AZ	119/126 (94%)	112 (94%)	7 (6%)	0	100	100
35	A3	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
36	A5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
37	AD	245/260 (94%)	236 (96%)	7 (3%)	2 (1%)	16	44
38	AE	378/386 (98%)	352 (93%)	26 (7%)	0	100	100
39	AF	388/411 (94%)	367 (95%)	21 (5%)	0	100	100
40	AG	116/173 (67%)	98 (84%)	17 (15%)	1 (1%)	14	41
41	AU	178/184 (97%)	162 (91%)	16 (9%)	0	100	100
42	AH	183/190 (96%)	166 (91%)	16 (9%)	1 (0%)	24	55
43	AV	153/161 (95%)	147 (96%)	6 (4%)	0	100	100
44	Ag	35/39 (90%)	29 (83%)	6 (17%)	0	100	100
45	AX	95/139 (68%)	89 (94%)	6 (6%)	0	100	100
46	A0	60/162 (37%)	55 (92%)	5 (8%)	0	100	100
47	S1	118/133 (89%)	115 (98%)	3 (2%)	0	100	100
48	S2	35/105 (33%)	34 (97%)	1 (3%)	0	100	100
49	S3	93/107 (87%)	85 (91%)	8 (9%)	0	100	100
50	S4	74/82 (90%)	63 (85%)	11 (15%)	0	100	100
51	S5	55/67 (82%)	54 (98%)	1 (2%)	0	100	100
52	S6	41/58 (71%)	36 (88%)	5 (12%)	0	100	100
54	SB	208/262 (79%)	192 (92%)	15 (7%)	1 (0%)	24	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	SC	193/263 (73%)	176 (91%)	15 (8%)	2 (1%)	12	38
56	SD	149/221 (67%)	146 (98%)	3 (2%)	0	100	100
57	SE	183/189 (97%)	170 (93%)	12 (7%)	1 (0%)	24	55
58	SF	255/261 (98%)	235 (92%)	19 (8%)	1 (0%)	30	60
59	SG	222/272 (82%)	205 (92%)	17 (8%)	0	100	100
60	SH	200/306 (65%)	188 (94%)	11 (6%)	1 (0%)	24	55
61	SI	176/195 (90%)	164 (93%)	12 (7%)	0	100	100
62	SJ	186/194 (96%)	172 (92%)	13 (7%)	1 (0%)	24	55
63	SK	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
64	SL	165/218 (76%)	149 (90%)	15 (9%)	1 (1%)	21	51
65	SM	136/144 (94%)	127 (93%)	8 (6%)	1 (1%)	18	47
66	SN	96/118 (81%)	90 (94%)	6 (6%)	0	100	100
67	SO	77/137 (56%)	75 (97%)	1 (1%)	1 (1%)	9	31
68	SP	125/151 (83%)	116 (93%)	9 (7%)	0	100	100
69	SQ	142/145 (98%)	133 (94%)	9 (6%)	0	100	100
70	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
71	SS	126/156 (81%)	111 (88%)	13 (10%)	2 (2%)	7	27
72	ST	46/54 (85%)	44 (96%)	2 (4%)	0	100	100
73	SU	147/151 (97%)	140 (95%)	7 (5%)	0	100	100
74	SV	142/161 (88%)	131 (92%)	10 (7%)	1 (1%)	18	47
75	SW	91/137 (66%)	82 (90%)	7 (8%)	2 (2%)	5	19
76	SX	92/145 (63%)	85 (92%)	7 (8%)	0	100	100
77	SY	152/170 (89%)	147 (97%)	5 (3%)	0	100	100
78	SZ	70/82 (85%)	68 (97%)	1 (1%)	1 (1%)	9	30
All	All	10113/12049 (84%)	9408 (93%)	673 (7%)	32 (0%)	37	66

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	AP	156	VAL
42	AH	53	TYR
54	SB	146	ARG
62	SJ	112	ILE
65	SM	41	GLU

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	
5	AL	190/194 (98%)	181 (95%)	9 (5%)	23	57
6	A1	127/132 (96%)	114 (90%)	13 (10%)	7	23
7	A2	97/118 (82%)	93 (96%)	4 (4%)	27	62
8	A4	60/61 (98%)	59 (98%)	1 (2%)	53	83
9	A6	83/92 (90%)	77 (93%)	6 (7%)	13	39
10	A7	90/112 (80%)	86 (96%)	4 (4%)	25	59
11	AN	136/152 (90%)	132 (97%)	4 (3%)	37	73
12	A8	114/120 (95%)	108 (95%)	6 (5%)	20	52
13	A9	90/127 (71%)	83 (92%)	7 (8%)	11	35
14	Aa	89/128 (70%)	86 (97%)	3 (3%)	32	68
15	Ab	82/97 (84%)	77 (94%)	5 (6%)	17	46
16	Ad	69/83 (83%)	61 (88%)	8 (12%)	5	18
17	Ae	40/48 (83%)	37 (92%)	3 (8%)	12	37
18	Af	45/114 (40%)	42 (93%)	3 (7%)	15	42
19	AP	179/180 (99%)	165 (92%)	14 (8%)	11	35
20	Ah	70/80 (88%)	67 (96%)	3 (4%)	26	60
21	Ai	87/93 (94%)	83 (95%)	4 (5%)	24	58
22	AI	189/203 (93%)	184 (97%)	5 (3%)	40	75
23	AJ	204/260 (78%)	198 (97%)	6 (3%)	37	73
24	Ac	74/77 (96%)	69 (93%)	5 (7%)	14	42
25	AK	181/182 (100%)	175 (97%)	6 (3%)	33	69
26	AM	106/110 (96%)	100 (94%)	6 (6%)	18	49
27	AS	158/159 (99%)	152 (96%)	6 (4%)	29	64
28	AO	121/122 (99%)	116 (96%)	5 (4%)	27	62
29	AQ	165/190 (87%)	154 (93%)	11 (7%)	15	42
30	AR	215/254 (85%)	198 (92%)	17 (8%)	11	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	AW	128/131 (98%)	120 (94%)	8 (6%)	16	45
32	AY	90/177 (51%)	86 (96%)	4 (4%)	25	59
33	AT	162/163 (99%)	154 (95%)	8 (5%)	22	55
34	AZ	111/115 (96%)	100 (90%)	11 (10%)	7	24
35	A3	110/115 (96%)	106 (96%)	4 (4%)	31	66
36	A5	201/231 (87%)	192 (96%)	9 (4%)	24	58
37	AD	191/202 (95%)	182 (95%)	9 (5%)	23	57
38	AE	335/340 (98%)	314 (94%)	21 (6%)	16	45
39	AF	336/352 (96%)	326 (97%)	10 (3%)	36	72
40	AG	110/155 (71%)	101 (92%)	9 (8%)	10	33
41	AU	162/166 (98%)	147 (91%)	15 (9%)	8	27
42	AH	168/173 (97%)	153 (91%)	15 (9%)	9	29
43	AV	140/144 (97%)	125 (89%)	15 (11%)	6	21
44	Ag	34/35 (97%)	32 (94%)	2 (6%)	18	48
45	AX	92/131 (70%)	81 (88%)	11 (12%)	5	17
46	A0	53/146 (36%)	52 (98%)	1 (2%)	50	81
47	S1	104/115 (90%)	102 (98%)	2 (2%)	50	81
48	S2	35/88 (40%)	35 (100%)	0	100	100
49	S3	87/98 (89%)	84 (97%)	3 (3%)	32	68
50	S4	70/76 (92%)	65 (93%)	5 (7%)	13	39
51	S5	48/54 (89%)	46 (96%)	2 (4%)	26	61
52	S6	36/47 (77%)	35 (97%)	1 (3%)	38	73
54	SB	195/238 (82%)	182 (93%)	13 (7%)	15	42
55	SC	167/227 (74%)	156 (93%)	11 (7%)	15	43
56	SD	132/188 (70%)	126 (96%)	6 (4%)	24	58
57	SE	161/167 (96%)	153 (95%)	8 (5%)	22	54
58	SF	233/237 (98%)	222 (95%)	11 (5%)	23	57
59	SG	191/222 (86%)	175 (92%)	16 (8%)	10	32
60	SH	182/279 (65%)	180 (99%)	2 (1%)	65	87
61	SI	154/165 (93%)	151 (98%)	3 (2%)	50	81
62	SJ	177/183 (97%)	171 (97%)	6 (3%)	32	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	SK	115/116 (99%)	101 (88%)	14 (12%)	5	16
64	SL	151/193 (78%)	142 (94%)	9 (6%)	17	47
65	SM	116/122 (95%)	113 (97%)	3 (3%)	40	75
66	SN	91/109 (84%)	87 (96%)	4 (4%)	25	59
67	SO	76/129 (59%)	72 (95%)	4 (5%)	20	52
68	SP	99/119 (83%)	91 (92%)	8 (8%)	11	33
69	SQ	120/121 (99%)	111 (92%)	9 (8%)	12	37
70	SR	83/121 (69%)	82 (99%)	1 (1%)	63	87
71	SS	114/136 (84%)	107 (94%)	7 (6%)	17	46
72	ST	43/48 (90%)	41 (95%)	2 (5%)	23	57
73	SU	132/133 (99%)	128 (97%)	4 (3%)	36	72
74	SV	131/144 (91%)	123 (94%)	8 (6%)	17	46
75	SW	86/127 (68%)	82 (95%)	4 (5%)	23	57
76	SX	88/130 (68%)	84 (96%)	4 (4%)	24	58
77	SY	137/151 (91%)	134 (98%)	3 (2%)	45	78
78	SZ	60/70 (86%)	57 (95%)	3 (5%)	22	54
All	All	9098/10617 (86%)	8606 (95%)	492 (5%)	21	51

5 of 492 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	AE	226	VAL
68	SP	104	LYS
42	AH	161	HIS
67	SO	89	GLU
74	SV	93	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
50	S4	63	GLN
61	SI	101	GLN
54	SB	147	GLN
59	SG	80	GLN
64	SL	191	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S7	75/76 (98%)	27 (36%)	2 (2%)
2	AA	3162/3788 (83%)	782 (24%)	59 (1%)
3	AC	148/159 (93%)	33 (22%)	5 (3%)
4	AB	117/119 (98%)	39 (33%)	1 (0%)
53	SA	1587/2092 (75%)	370 (23%)	25 (1%)
All	All	5089/6234 (81%)	1251 (24%)	92 (1%)

5 of 1251 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S7	3	C
1	S7	9	G
1	S7	11	A
1	S7	12	G
1	S7	13	C

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AA	3587	U
53	SA	423	A
2	AA	3658	G
3	AC	145	A
53	SA	844	G

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

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

5.5 Carbohydrates [i](#)

There are no 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
31	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	32.89

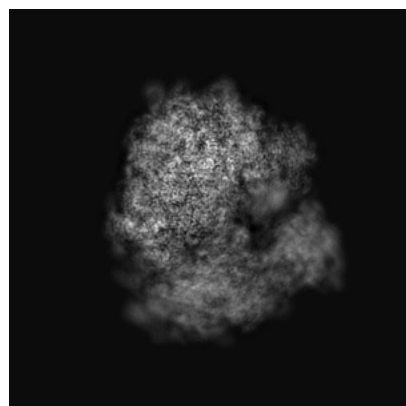
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44920. These allow visual inspection of the internal detail of the map and identification of artifacts.

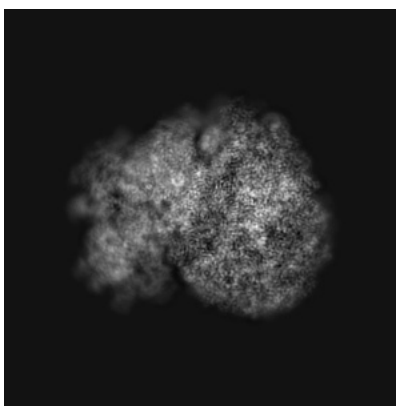
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

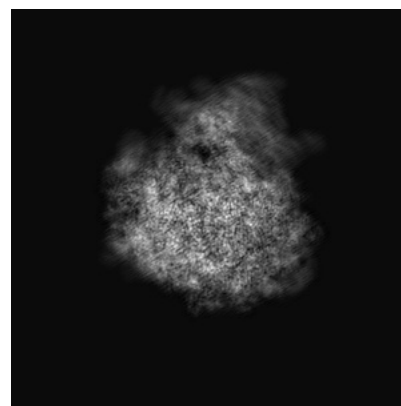
6.1.1 Primary map



X

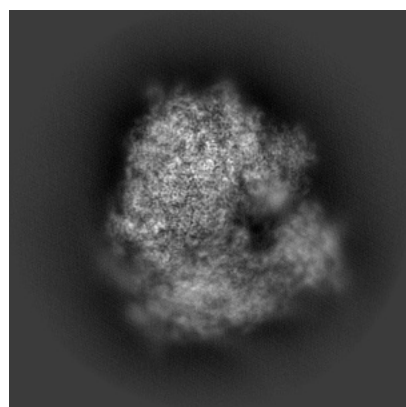


Y

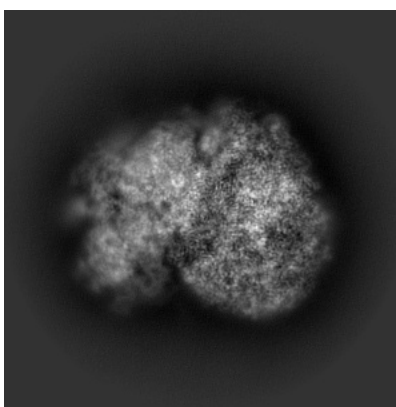


Z

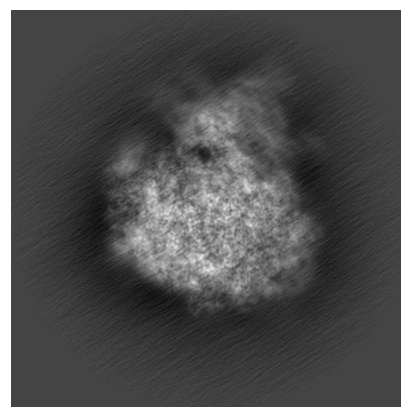
6.1.2 Raw map



X



Y

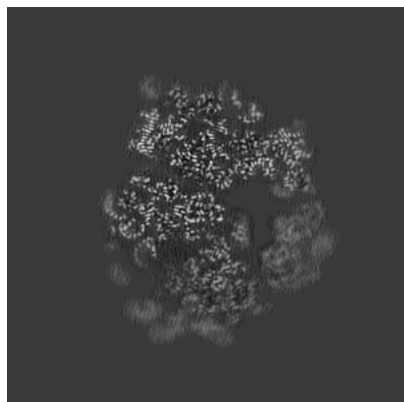


Z

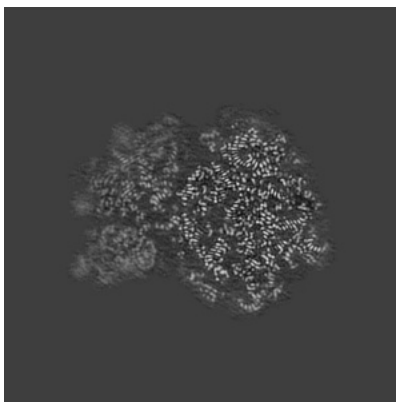
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

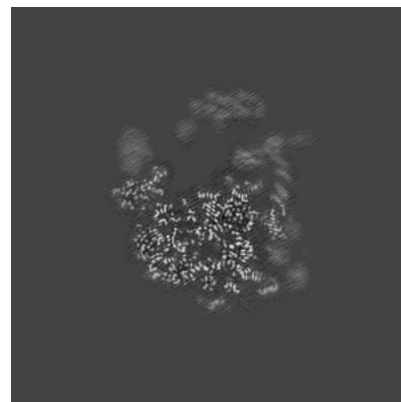
6.2.1 Primary map



X Index: 250

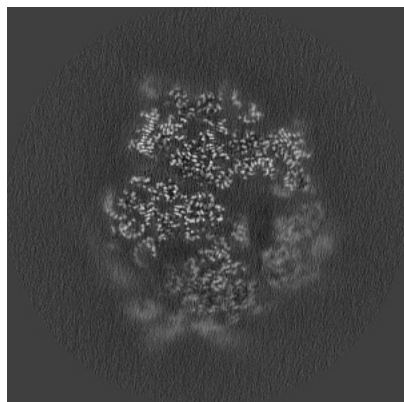


Y Index: 250

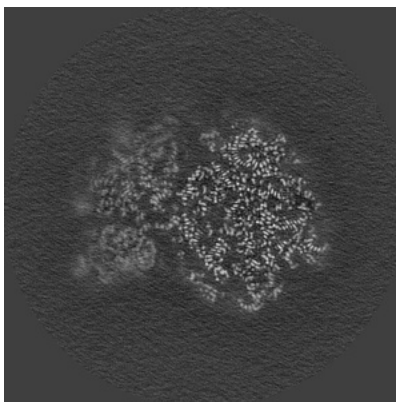


Z Index: 250

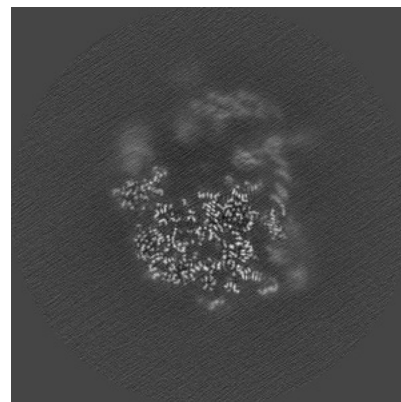
6.2.2 Raw map



X Index: 250



Y Index: 250

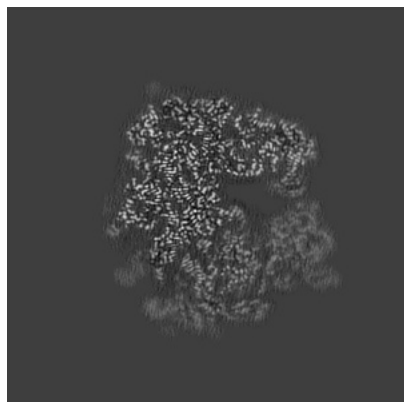


Z Index: 250

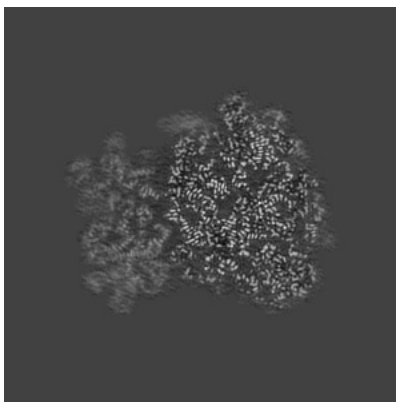
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

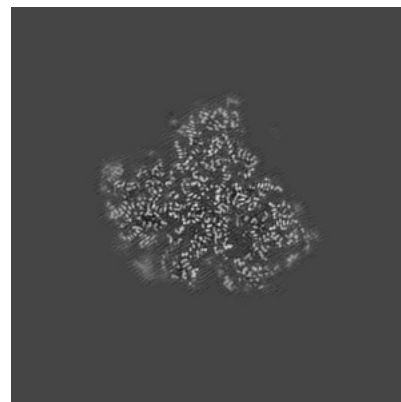
6.3.1 Primary map



X Index: 269

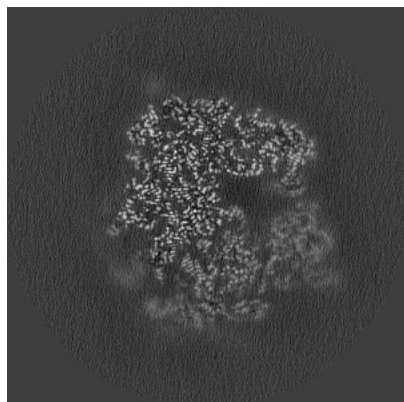


Y Index: 223

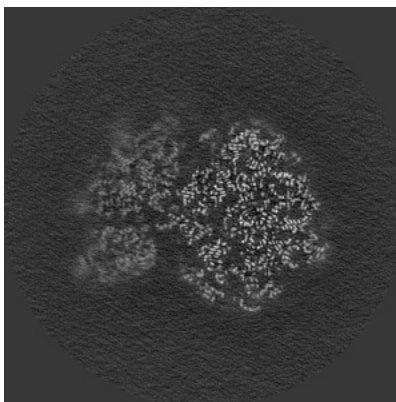


Z Index: 310

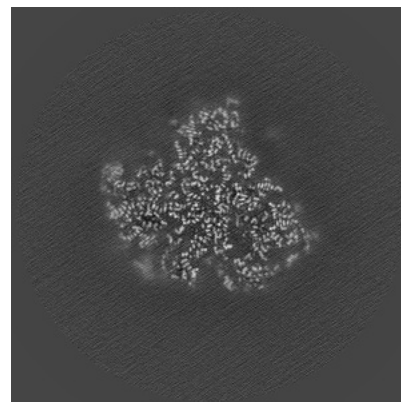
6.3.2 Raw map



X Index: 269



Y Index: 252

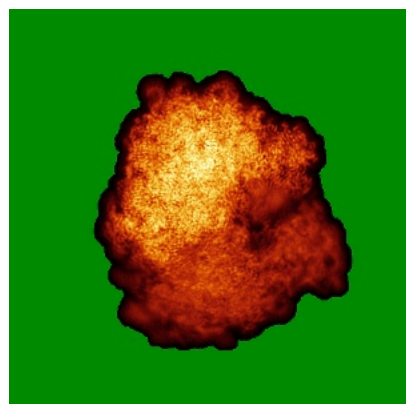


Z Index: 310

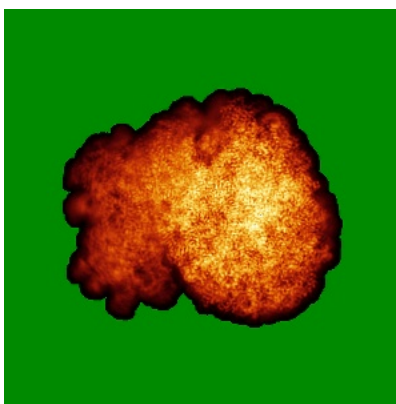
The images above show the largest variance slices of the map in three orthogonal directions.

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

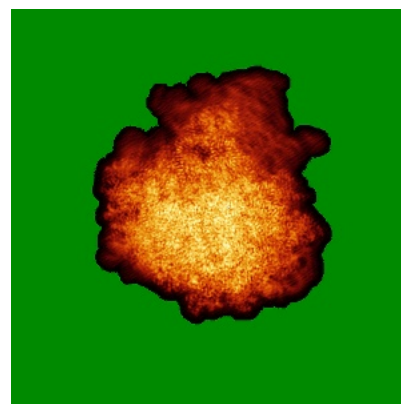
6.4.1 Primary map



X

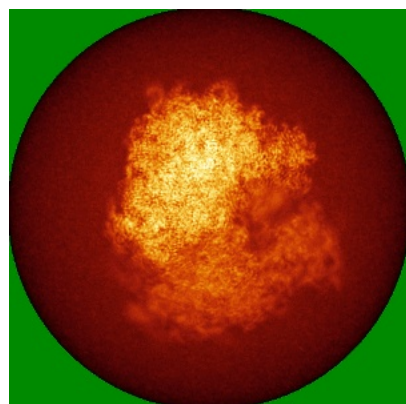


Y

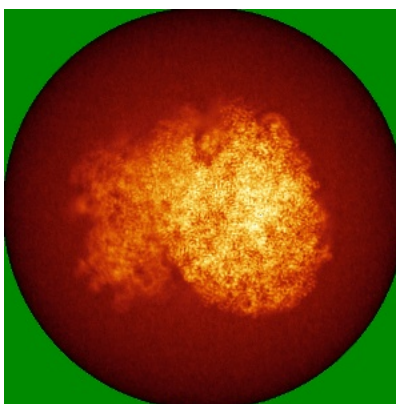


Z

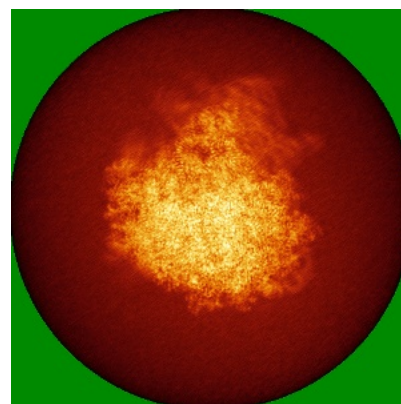
6.4.2 Raw map



X



Y

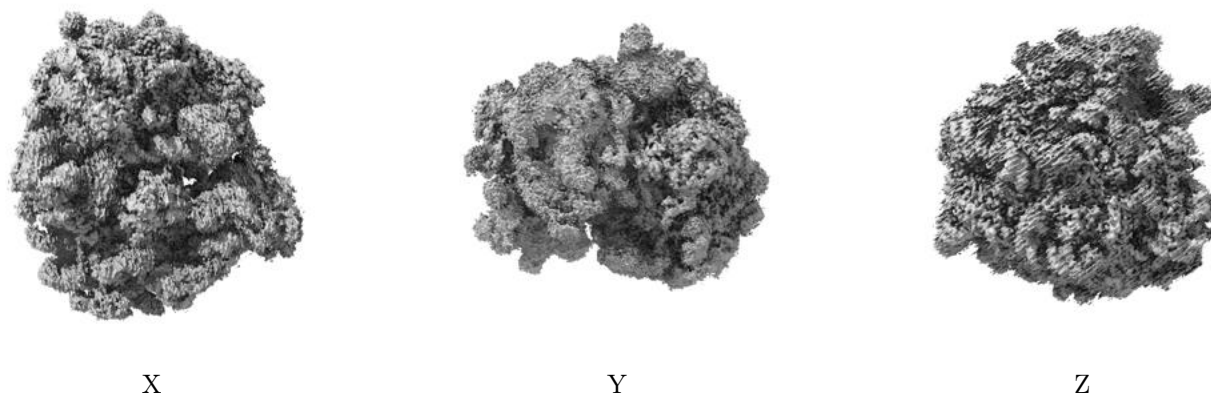


Z

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.

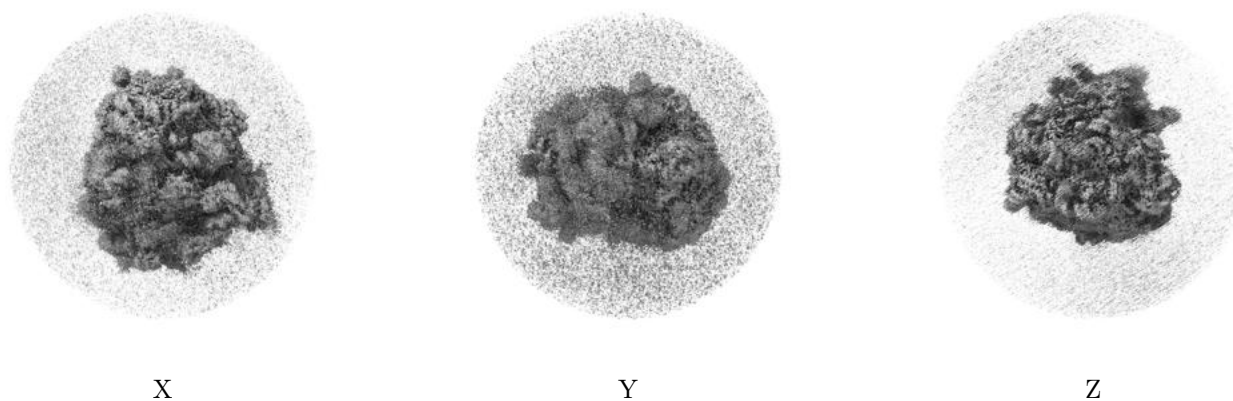
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00567. 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.

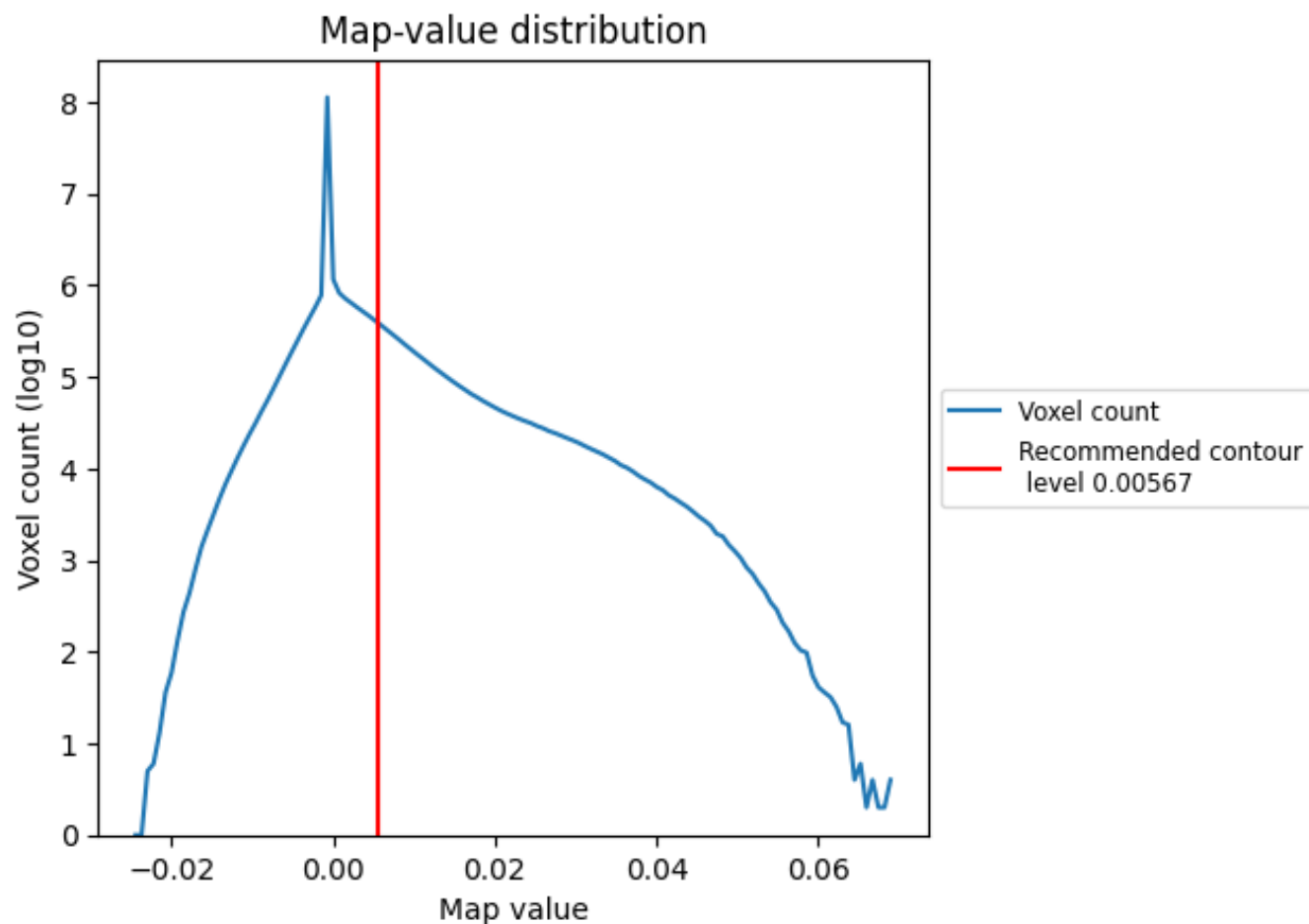
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

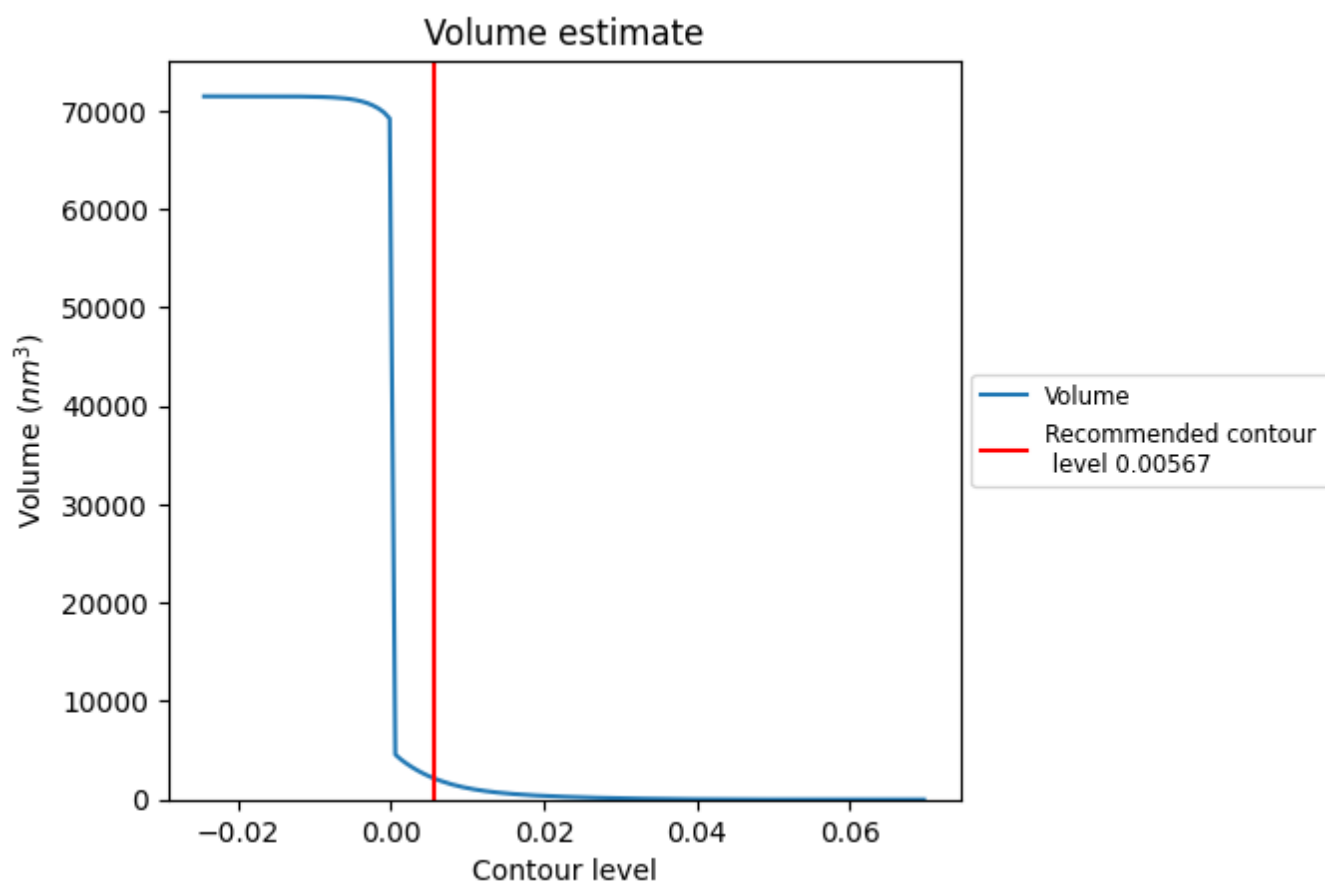
This section contains the results of statistical analysis of the map.

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.

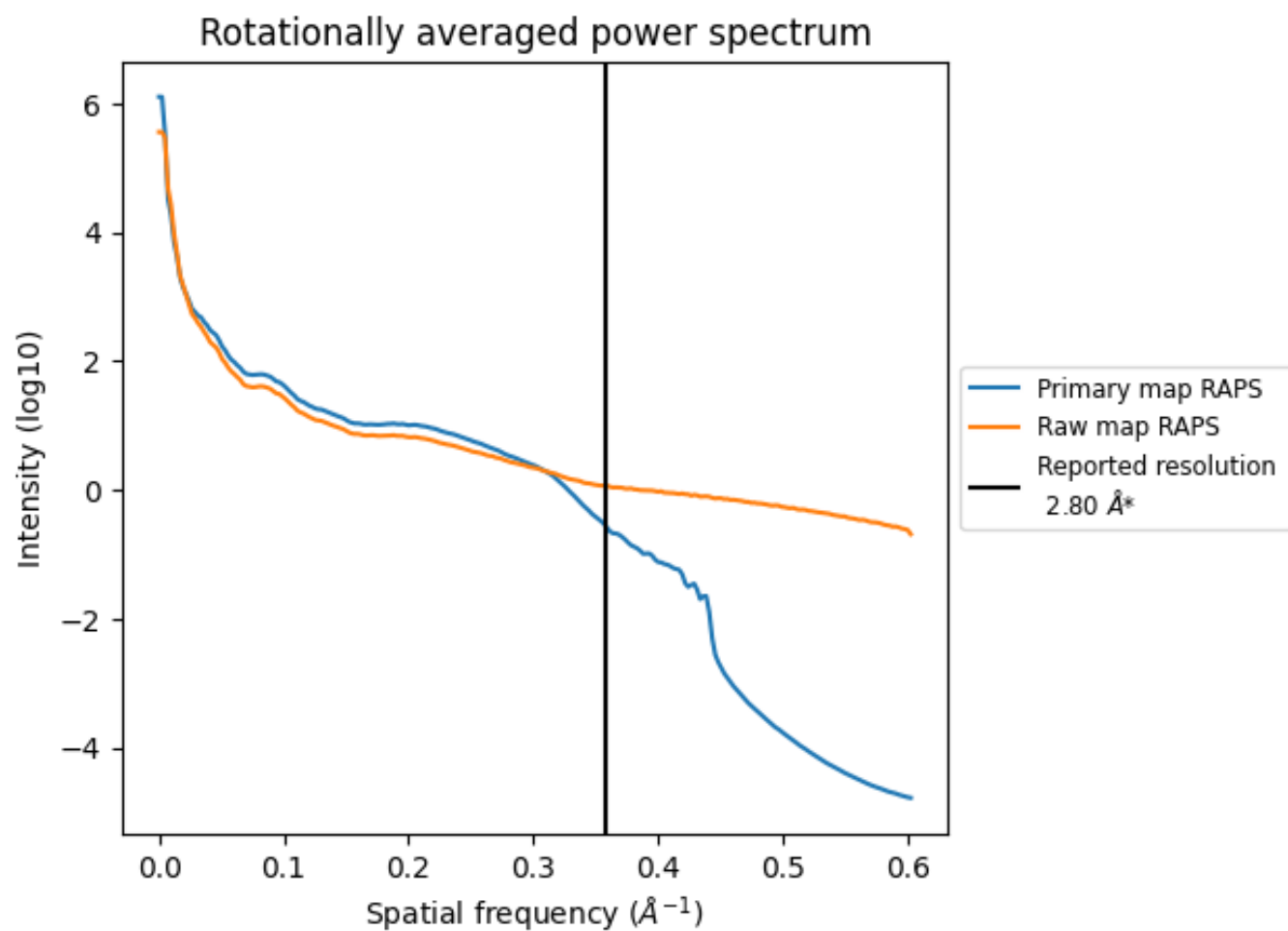
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2146 nm³; this corresponds to an approximate mass of 1938 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 ⓘ

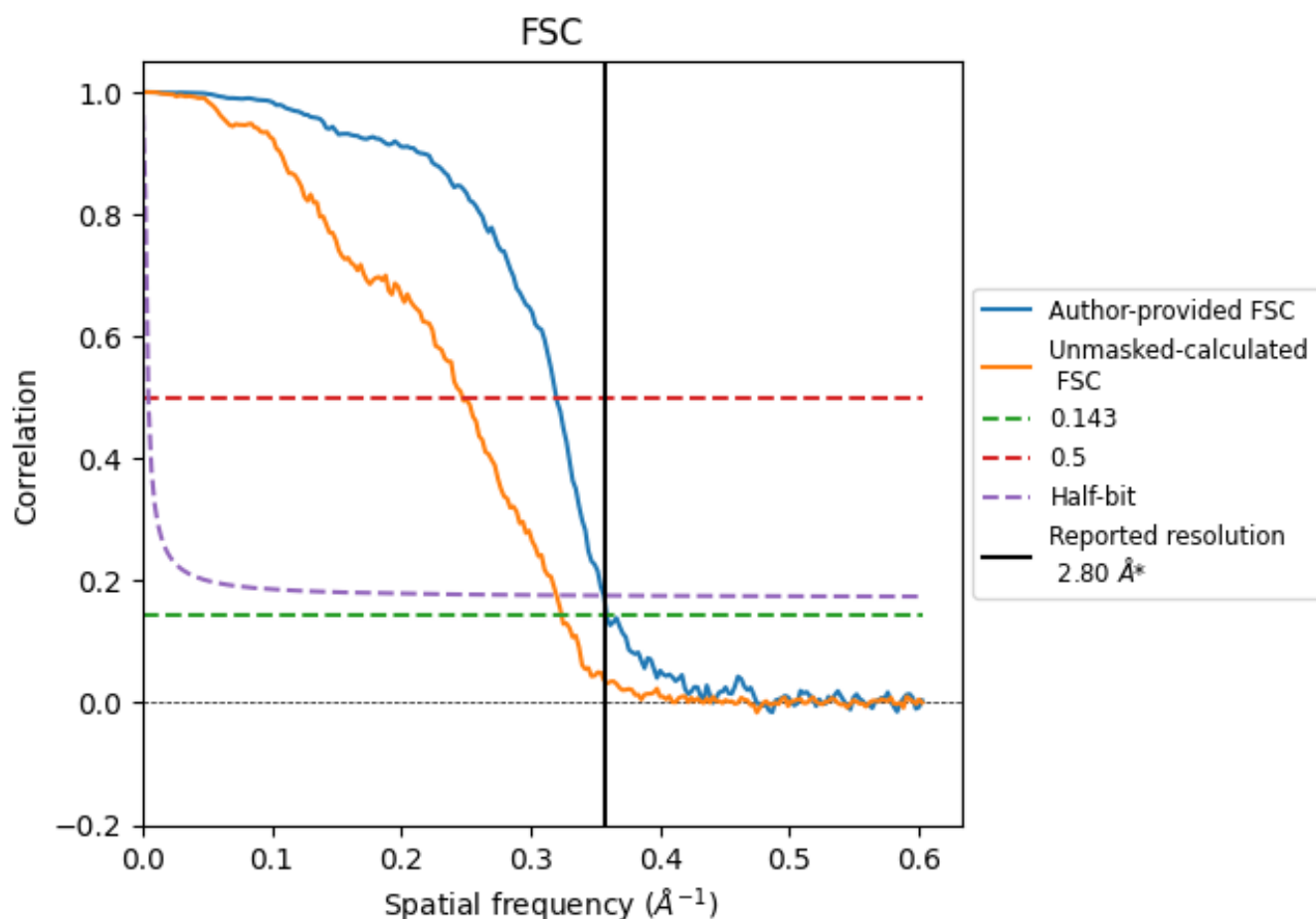


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

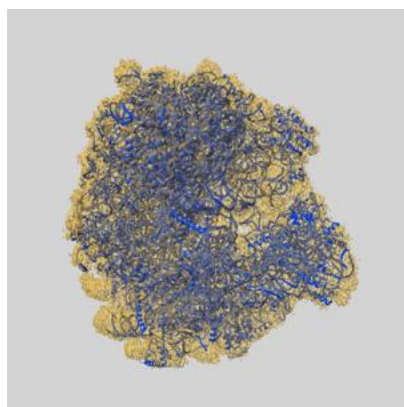
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.79	3.13	2.80
Unmasked-calculated*	3.09	4.04	3.12

*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 3.09 differs from the reported value 2.8 by more than 10 %

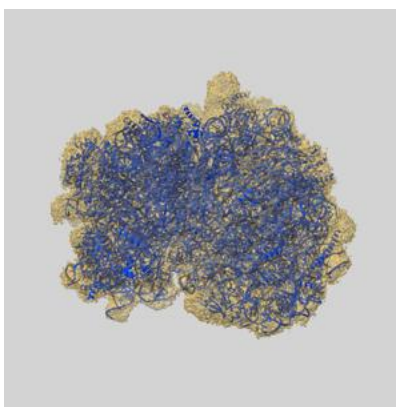
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44920 and PDB model 9BUU. Per-residue inclusion information can be found in section [3](#) on page [18](#).

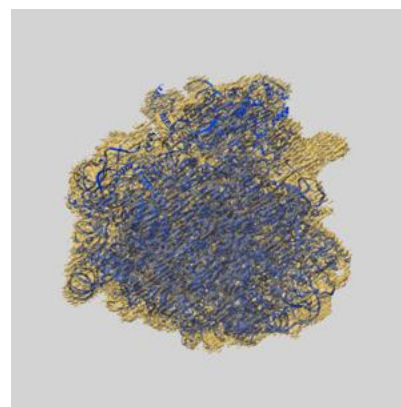
9.1 Map-model overlay [i](#)



X



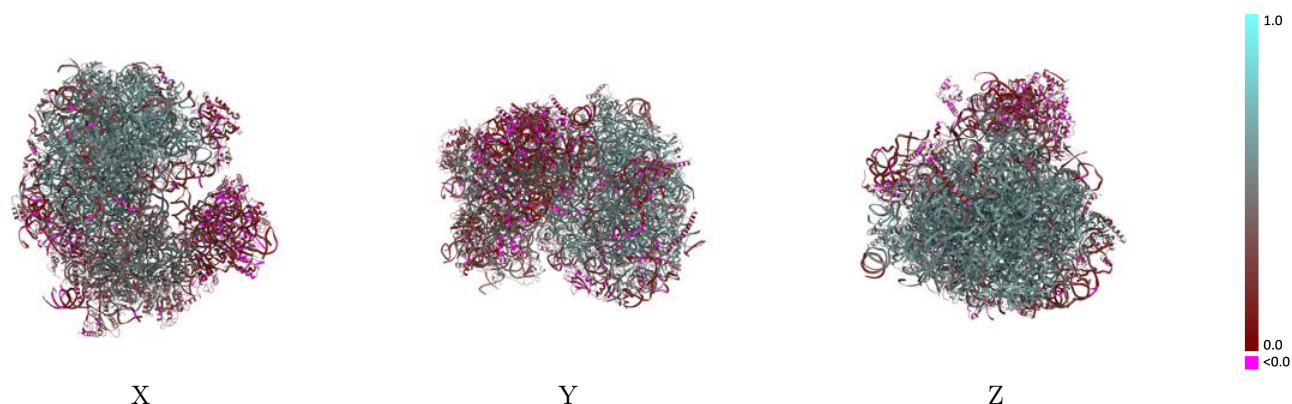
Y



Z

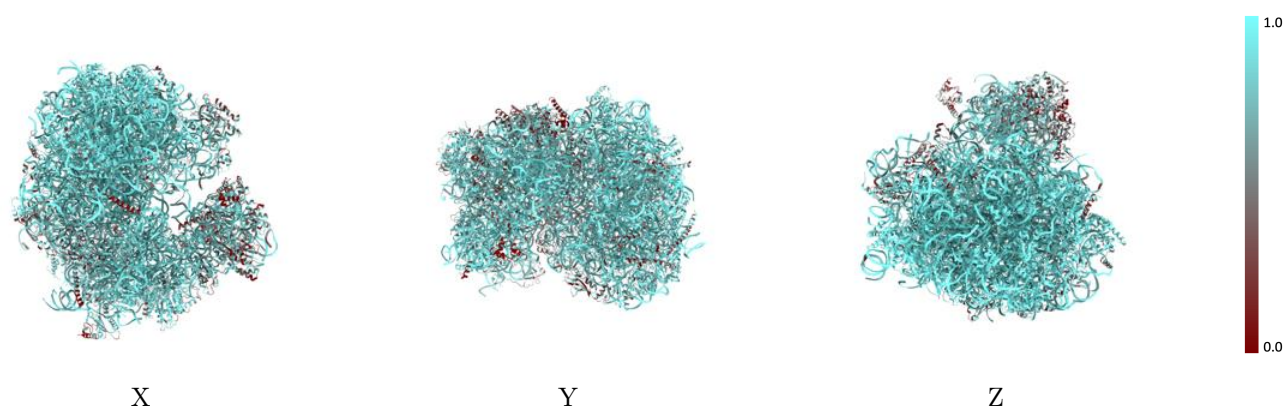
The images above show the 3D surface view of the map at the recommended contour level 0.00567 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



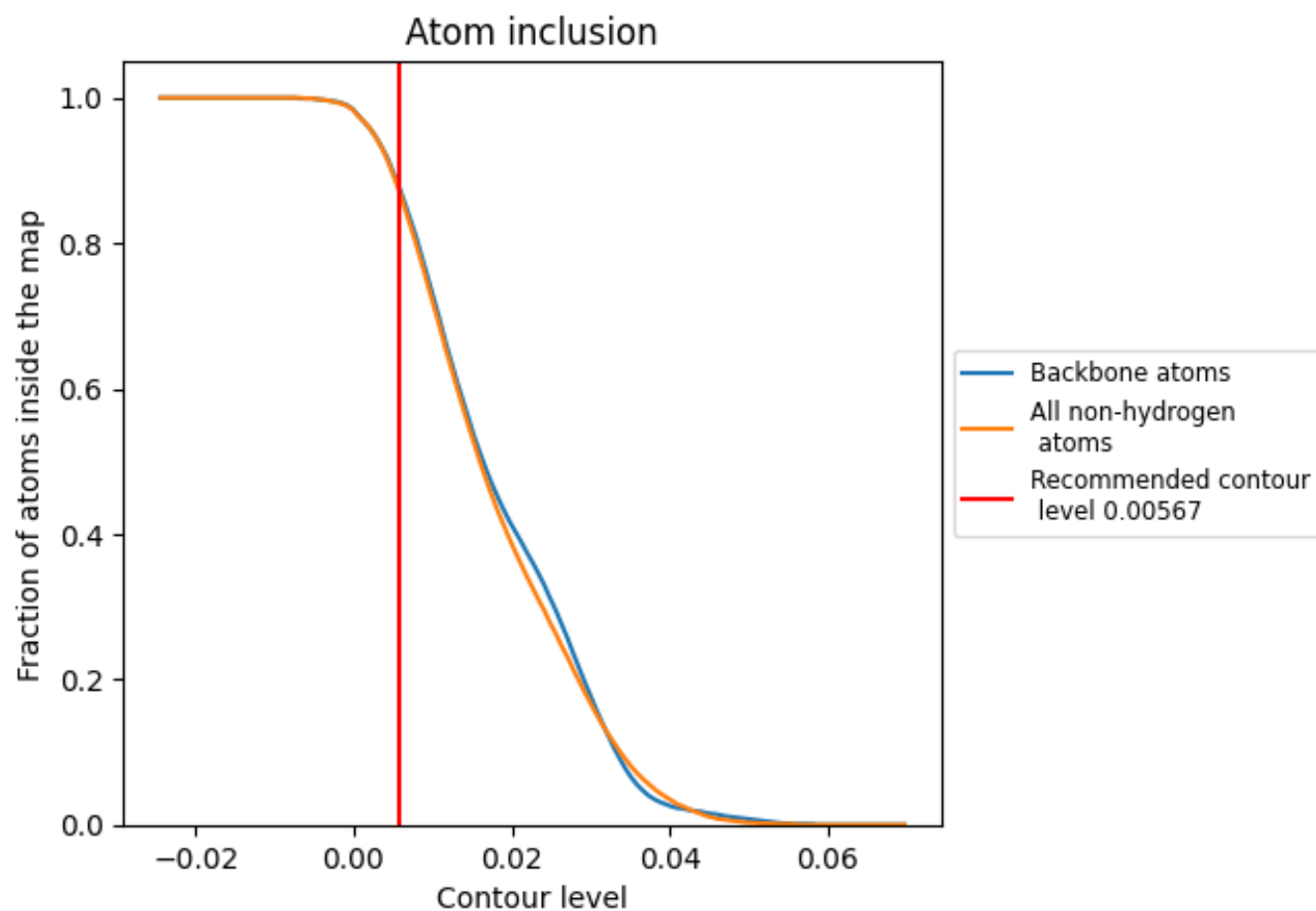
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00567).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.00567) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.4350
A0	 0.4680	 0.1690
A1	 0.6300	 0.1920
A2	 0.9540	 0.5790
A3	 0.7720	 0.3560
A4	 0.8390	 0.4850
A5	 0.8740	 0.4790
A6	 0.6210	 0.2170
A7	 0.8740	 0.4740
A8	 0.9570	 0.6090
A9	 0.9840	 0.6290
AA	 0.9470	 0.5220
AB	 0.8240	 0.3030
AC	 0.9710	 0.5470
AD	 0.9560	 0.6160
AE	 0.8320	 0.4630
AF	 0.8970	 0.5360
AG	 0.7550	 0.2630
AH	 0.6750	 0.2440
AI	 0.9670	 0.5720
AJ	 0.7640	 0.4070
AK	 0.9700	 0.6010
AL	 0.9290	 0.5450
AM	 0.7970	 0.4380
AN	 0.8290	 0.3920
AO	 0.9790	 0.6200
AP	 0.9720	 0.6130
AQ	 0.7640	 0.3760
AR	 0.6370	 0.2040
AS	 0.9700	 0.6200
AT	 0.6200	 0.2990
AU	 0.8040	 0.4060
AV	 0.8900	 0.5170
AW	 0.9800	 0.6090
AX	 0.5330	 0.2020



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Chain	Atom inclusion	Q-score
AY	 0.7470	 0.3620
AZ	 0.9470	 0.5370
Aa	 0.7360	 0.3480
Ab	 0.9540	 0.5670
Ac	 0.9650	 0.6090
Ad	 0.6850	 0.2520
Ae	 0.9610	 0.5980
Af	 0.6820	 0.2610
Ag	 0.6920	 0.4030
Ah	 0.8610	 0.5020
Ai	 0.9590	 0.6110
S1	 0.7980	 0.2960
S2	 0.0760	 0.0180
S3	 0.8700	 0.4400
S4	 0.6110	 0.2730
S5	 0.5840	 0.2500
S6	 0.6690	 0.2520
S7	 0.8490	 0.2930
SA	 0.9230	 0.3630
SB	 0.7490	 0.3710
SC	 0.8240	 0.3410
SD	 0.5640	 0.1820
SE	 0.7910	 0.3410
SF	 0.8590	 0.3790
SG	 0.8220	 0.4000
SH	 0.7890	 0.2990
SI	 0.5330	 0.1420
SJ	 0.6810	 0.2960
SK	 0.8820	 0.4900
SL	 0.8350	 0.3710
SM	 0.5680	 0.1330
SN	 0.6150	 0.1290
SO	 0.7020	 0.1620
SP	 0.8450	 0.3860
SQ	 0.7980	 0.4450
SR	 0.2840	 0.0600
SS	 0.5980	 0.1680
ST	 0.6570	 0.2150
SU	 0.7560	 0.4200
SV	 0.8350	 0.4280
SW	 0.6350	 0.1760
SX	 0.7060	 0.1920

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Chain	Atom inclusion	Q-score
SY	 0.6180	 0.1280
SZ	 0.8460	 0.4170