



# wwPDB EM Validation Summary Report ⓘ

Oct 6, 2025 – 08:51 PM JST

PDB ID : 9V24 / pdb\_00009v24  
EMDB ID : EMD-64716  
Title : Cryo- EM structure of 75S ribosome with A/P- & P/E- tRNAs from Entamoeba histolytica  
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.  
Deposited on : 2025-05-19  
Resolution : 3.10 Å(reported)  
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

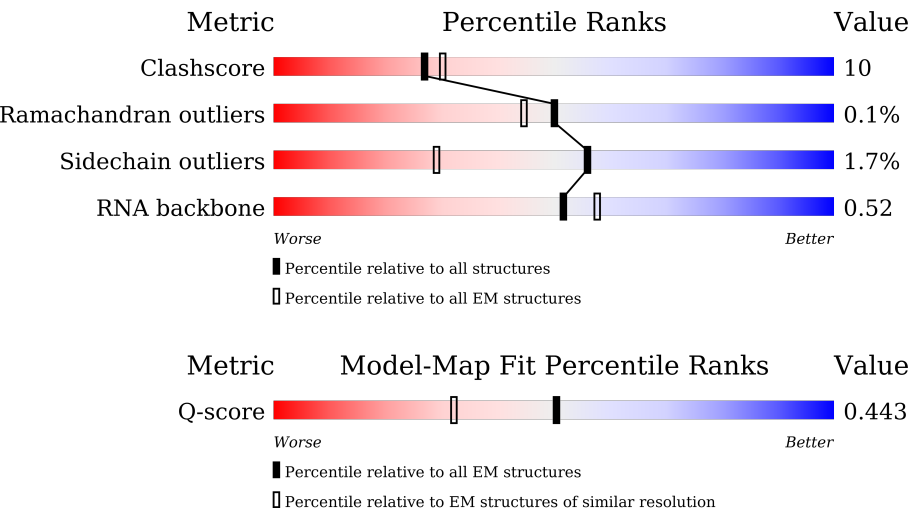
EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 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.













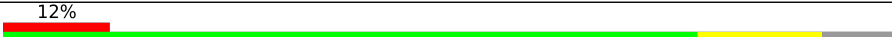


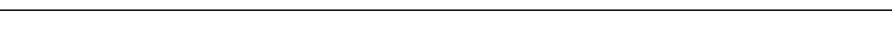
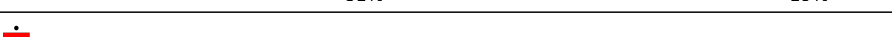
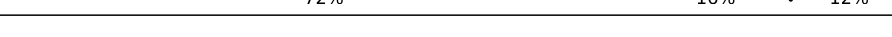



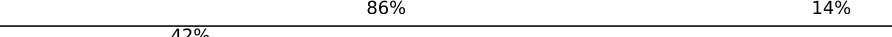





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14724 ( 2.60 - 3.60 )

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

Mol	Chain	Length	Quality of chain
1	1A	3503	<div><div></div><div>46%37%7%10%</div></div>
2	1B	155	<div><div></div><div>47%41%5%6%</div></div>
3	1C	117	<div><div></div><div>26%64%10%</div></div>













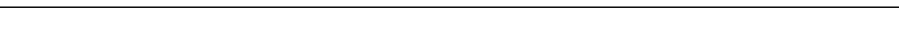

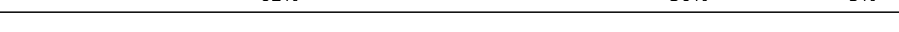

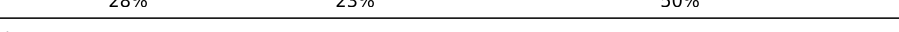







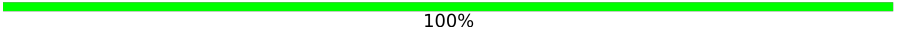
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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	77	
41	lo	51	
42	lp	56	
43	lq	98	
44	sA	137	
45	sB	144	
46	sC	84	
47	sD	69	
48	sE	56	
49	sH	4	
50	sI	76	
51	sJ	77	
52	sK	10	
53	sa	1947	

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Mol	Chain	Length	Quality of chain
54	sb	254	
55	sc	255	
56	sd	244	
57	se	256	
58	sf	326	
59	sg	206	
60	sh	266	
61	si	201	
62	sj	237	
63	sk	185	
64	sl	127	
65	sm	156	
66	so	151	
67	sp	146	
68	sq	144	
69	sr	130	
70	ss	158	
71	st	117	
72	su	155	
73	sv	155	
74	sw	118	
75	sx	86	
76	sy	141	
77	sz	140	

## 2 Entry composition

There are 77 unique types of molecules in this entry. The entry contains 185725 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	lA	3145	Total	C	N	O	P	0	0
			67215	30134	12203	21733	3145		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	lB	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	lC	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	lD	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	lE	387	Total	C	N	O	S	0	0
			3076	1956	578	527	15		

- Molecule 6 is a protein called 60S ribosomal protein L4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	lF	424	Total	C	N	O	S	0	0
			3253	2069	619	551	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	282	Total	C	N	O	S	0	0
			2245	1434	405	398	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	213	Total	C	N	O	S	0	0
			1727	1114	317	291	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	200	Total	C	N	O	S	0	0
			1597	1017	302	264	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	267	Total	C	N	O	S	0	0
			2122	1352	410	352	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1020	654	188	174	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	158	Total	C	N	O	S	0	0
			1232	779	238	210	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1316	832	257	218	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			761	491	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	103	Total	C	N	O	S	0	0
			768	486	131	149	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	146	Total	C	N	O	S	0	0
			1184	759	219	200	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	129	Total	C	N	O	S	0	0
			1058	672	209	172	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38 putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	sA	69	Total	C	N	O	S	0	0
			548	356	92	96	4		

- Molecule 45 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 46 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sC	33	Total	C	N	O	S	0	0
			257	167	43	46	1		

- Molecule 47 is a protein called 40S ribosomal protein S28, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sD	60	Total	C	N	O	S	0	0
			468	289	93	84	2		

- Molecule 48 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sE	55	Total	C	N	O	S	0	0
			442	273	90	75	4		

- Molecule 49 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	sH	2	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 50 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	sI	72	Total	C	N	O	P	0	0
			1533	685	278	499	71		

- Molecule 51 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	sJ	77	Total	C	N	O	P	0	0
			1630	728	282	543	77		

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	sK	10	Total	C	N	O	P	0	0
			215	97	41	67	10		

- Molecule 53 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	sa	1434	Total	C	N	O	P	0	0
			30685	13734	5586	9931	1434		

- Molecule 54 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	sb	205	Total	C	N	O	S	0	0
			1626	1029	286	296	15		

- Molecule 55 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	sc	215	Total	C	N	O	S	0	0
			1642	1052	291	291	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
56	sd	219	Total	C	N	O	S	0	0
			1696	1072	310	303	11		

- Molecule 57 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	se	163	Total	C	N	O	S	0	0
			1329	853	237	232	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	sf	256	Total	C	N	O	S	0	0
			2031	1297	378	345	11		

- Molecule 59 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	sg	181	Total	C	N	O	S	0	0
			1440	908	261	260	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	sh	119	Total	C	N	O	S	0	0
			944	588	194	157	5		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	si	110	Total	C	N	O	S	0	0
			854	559	152	142	1		

- Molecule 62 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	sj	127	Total	C	N	O	S	0	0
			990	611	198	177	4		

- Molecule 63 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	sk	162	Total	C	N	O	S	0	0
			1323	845	251	221	6		

- Molecule 64 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sl	91	Total	C	N	O	S	0	0
			729	475	122	123	9		

- Molecule 65 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sm	141	Total	C	N	O	S	0	0
			1161	735	224	196	6		

- Molecule 66 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	so	76	Total	C	N	O	S	0	0
			644	410	123	108	3		

- Molecule 67 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	sp	133	Total	C	N	O	S	0	0
			999	615	192	186	6		

- Molecule 68 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sq	105	Total	C	N	O	S	0	0
			842	543	150	144	5		

- Molecule 69 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 70 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	ss	141	Total	C	N	O	S	0	0
			1104	713	198	189	4		

- Molecule 71 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	st	81	Total	C	N	O	S	0	0
			676	424	135	116	1		

- Molecule 72 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	su	135	Total	C	N	O	S	0	0
			1096	681	224	185	6		

- Molecule 73 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	sv	151	Total	C	N	O	S	0	0
			1214	777	218	212	7		

- Molecule 74 is a protein called 40S ribosomal protein S20, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	sw	98	Total	C	N	O	S	0	0
			766	486	133	142	5		

- Molecule 75 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sx	83	Total	C	N	O	S	0	0
			651	412	117	119	3		

- Molecule 76 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sy	106	Total	C	N	O	S	0	0
			836	522	169	142	3		

- Molecule 77 is a protein called 40S ribosomal protein S24, putative.

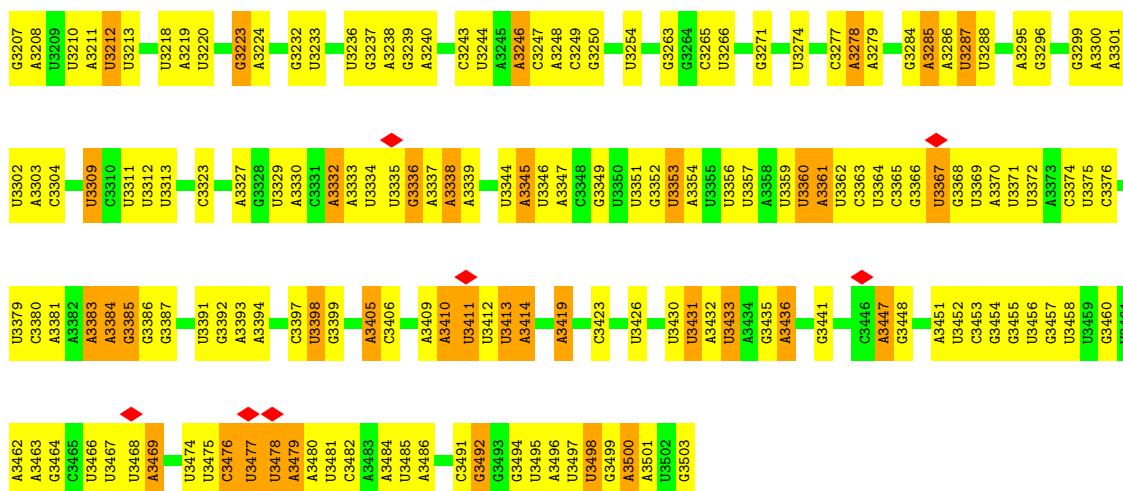


Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	56	Total	C	N	O	S	0	0
			438	288	74	75	1		

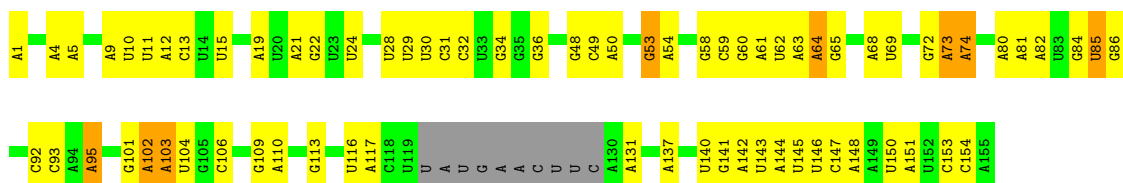


U1935	A1848	U	A1605	G1512	G1430	A1254	C1156	A965	A871	A802
A1936	A1849	G	A1606	A1513	G1431	A1255	A1157	A966	A872	U803
G1938	U1850	A	U1611	A1514	A1432	G1256	U1158	A967	U873	U804
A1939	G1855	U	C1612	C1516	U1433	A1261	C1159	C968	A874	C968
A1940	G1856	U	A1618	A1517	G1434	C1266	A1165	U969	C875	G805
A1941	A1857	A	C1619	A1518	A1437	A1267	A1166	U974	A876	A806
C1944	A1858	A	A1622	A1519	A1440	U1269	A1167	G809	G851	C809
A1946	G1859	A	A1623	A1520	U1441	A1275	C1168	C882	C882	G810
A	U1860	C	A1624	G1522	A1442	A1278	U1169	A883	A883	A811
A	U1861	U	A1625	U1523	A1443	A1279	G1172	U981	A884	A812
U	U1862	A	G1626	A1524	A1447	A1284	A1177	U982	U885	U813
U	U1869	G	G1627	A1527	A1450	A1284	A1178	A988	C887	G816
A	U1870	A	A1631	A1528	A1451	A1284	A1178	U993	A889	A817
U	C1871	A	A1632	U1533	A1452	A1292	A1181	A994	A889	A818
A	U1872	U	G1633	U1534	U1453	U1293	A1182	A995	C892	U819
A	U1873	A	G1634	A1535	A1454	A1303	G1183	A996	A896	A820
U	U1876	U	U1636	A1536	A1455	A1306	A1184	C997	A897	G821
U1965	A1877	A	U1637	G1537	U1456	A1307	G1186	G999	U898	C822
A1968	A1878	G	U1639	G1538	A1457	A1308	G1186	A904	U899	A823
U1969	A1882	U	A1640	A1541	U1466	A1309	G1194	A1003	A905	G824
G1961	A1883	A	A1641	U1544	U1467	A1310	G1195	A1006	G906	A826
U1965	A1886	A	A1642	A1545	A1468	A1311	U1198	C1007	U907	A827
U	U1887	U	U1648	A1546	A1469	A1312	U1203	A1007	A908	A828
U1969	A1888	C	U1649	U1549	A1470	A1313	U1204	A1013	A909	G829
A	U1890	C	U1650	U1551	A1471	A1314	C1205	G1019	U910	A832
C1991	A1891	A	G1661	A1552	A1472	A1315	A1206	A1121	G918	A834
G1973	A1892	U	G1664	C1553	A1473	A1316	C1207	U1122	G919	A835
A1974	A1893	A	A1670	U1554	A1474	A1326	U1208	G1027	A920	C836
G1975	A1897	A	A1670	U1555	U1480	A1326	C1210	G1028	U837	U838
U1978	A1898	A	U1674	G1556	U1481	A1327	A1211	C1030	A925	G839
U1979	U1904	A	A1675	U1561	A1482	A1328	A1219	A1033	A926	A840
C1980	C1905	U	A1676	G1562	U1483	A1328	A1220	A1034	U933	A841
U1982	A1906	U	U1677	G1568	A1484	A1328	A1221	A1035	G934	G842
A1984	A1907	C	U1678	A1569	A1485	U1335	U1222	A1036	A935	A843
A1985	U1912	A	A1680	U1570	C1486	C1340	U1235	G1042	A936	A846
A1986	G1913	U	C1681	C1571	U1490	A1341	G1236	G1043	U940	A847
A1992	A1921	U	A1682	A1580	A1491	A1342	U1236	U1047	A941	A848
G1993	U1922	A	G1686	U1581	G1494	A1343	C1240	A1048	C942	C849
G1994	U1923	U	G1687	U1582	A1495	A1344	G1241	U1049	U943	A853
G1995	U1924	A	A1688	G1583	A1496	U1345	G1242	G1053	A944	A854
U1998	A1925	U	A1689	G1584	G1499	U1346	C1243	U1057	C948	A855
C	U1926	A	U1691	A1593	A1502	A1347	C1244	G1056	G949	C856
U	G1927	U	A1701	G1595	A1503	A1349	G1247	C1057	U953	U857
U	G1928	A	U	A1596	U1504	A1352	U1248	C1063	G954	U858
U	C1930	U	A	A1597	G1505	G1353	C1249	A1071	G957	G860
A	U1931	U	U	A1602	U1508	A1354	U1250	A1072	G960	G866
C	U1932	U	A	A1603	U1509	G1354	G1251	U1073	U960	U867
A	G1934	A	U	A1604	U1509	A	U1252	A1074	G964	A868
U		A	U			C				G869
						G				A870

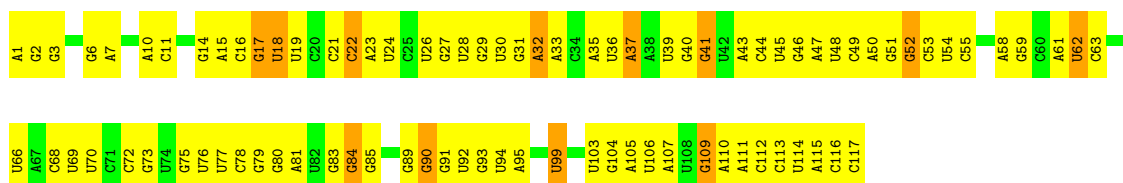
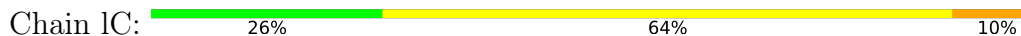




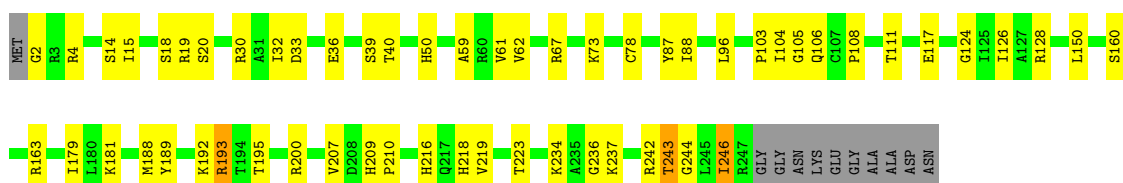
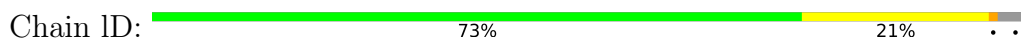
- Molecule 2: 5.8S rRNA



- Molecule 3: 5S rRNA

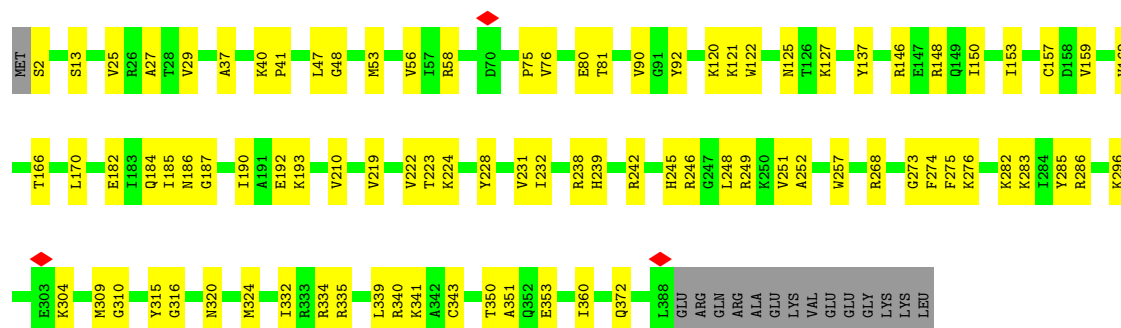


- Molecule 4: Large ribosomal subunit protein uL2



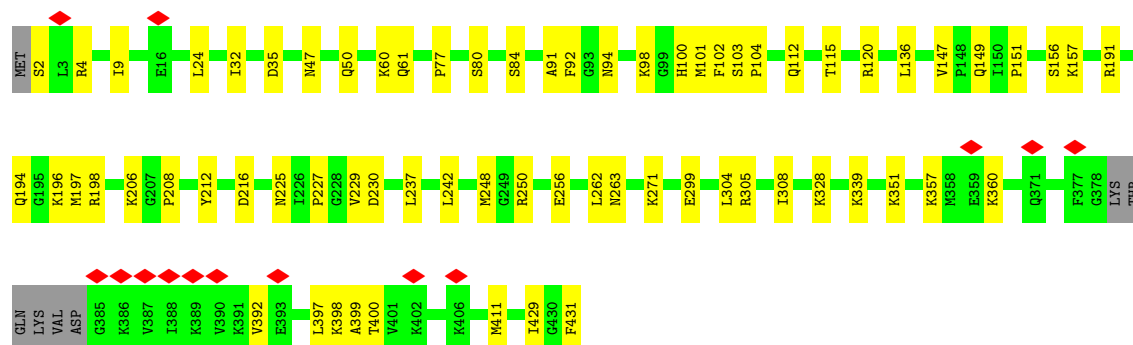
- Molecule 5: 60S ribosomal protein L3, putative





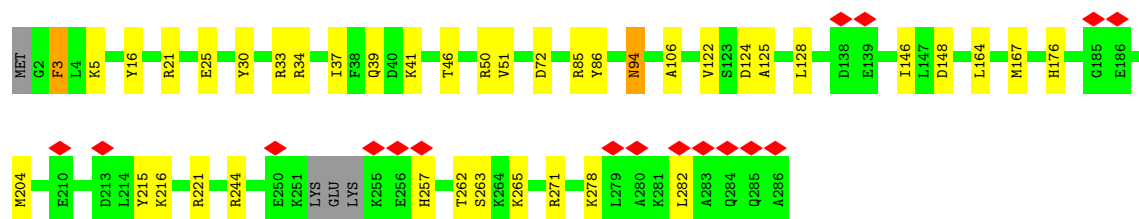
- Molecule 6: 60S ribosomal protein L4, putative

Chain 1F: 82% 16%



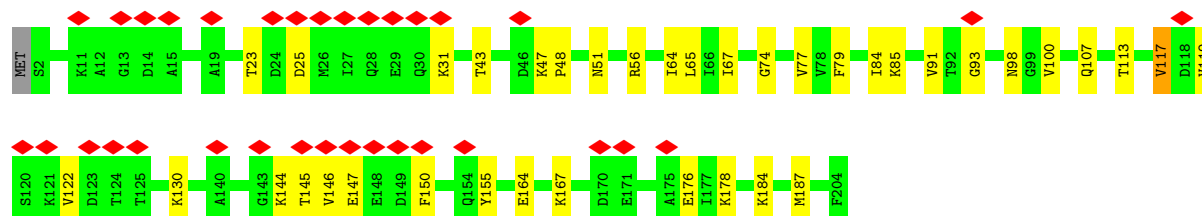
- Molecule 7: 60S ribosomal protein L5, putative

Chain 1G: 6% 85% 13%




- Molecule 8: Large ribosomal subunit protein eL6

Chain 1H: 16% 81% 18%



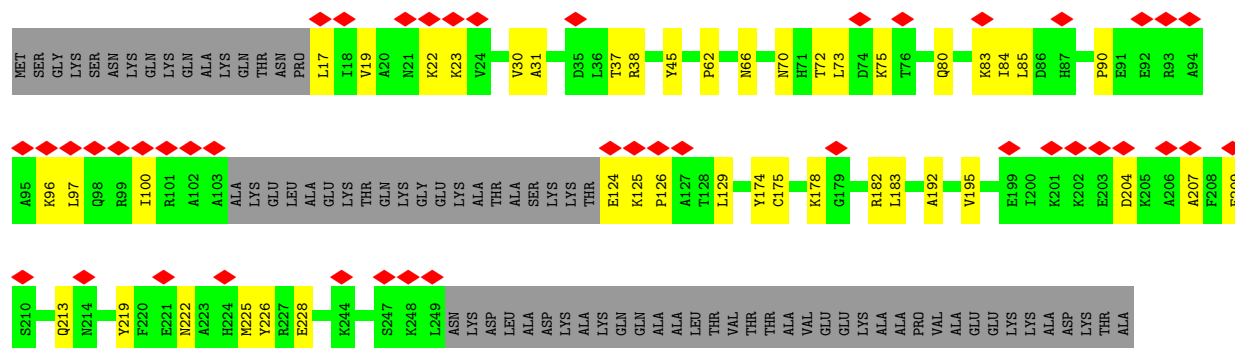
- Molecule 9: 60S ribosomal protein L7, putative

Chain II: 



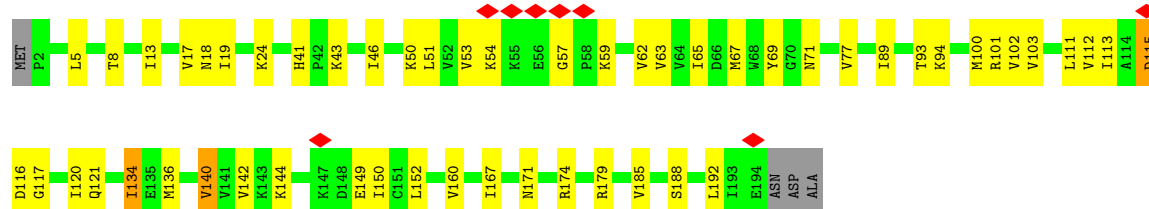
- Molecule 10: 60S ribosomal protein L7a

Chain IJ: 




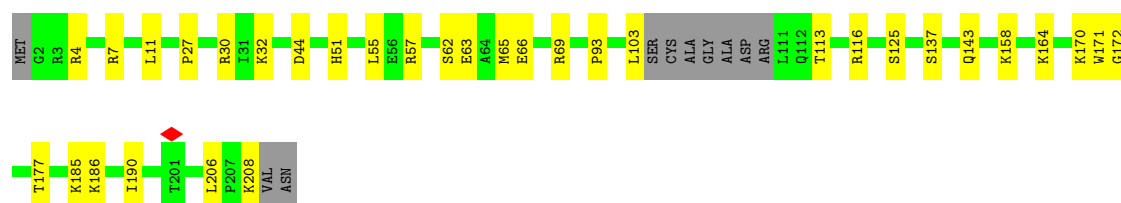
- Molecule 11: 60S ribosomal protein L9, putative

Chain IK: 




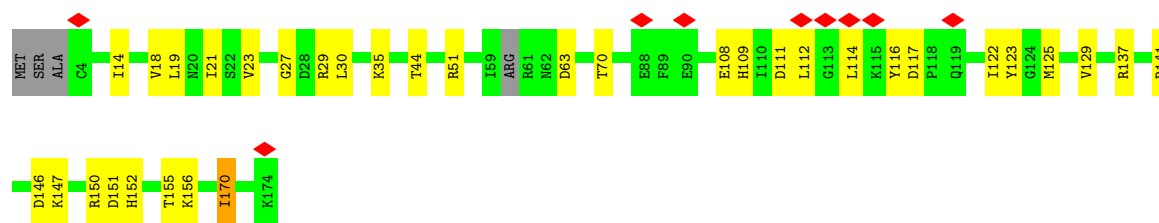
- Molecule 12: Ribosomal protein L10, putative

Chain IL: 

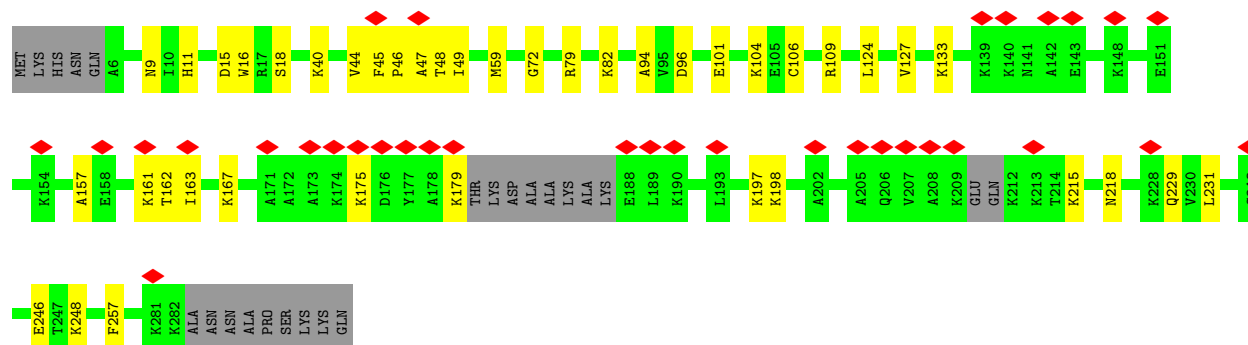
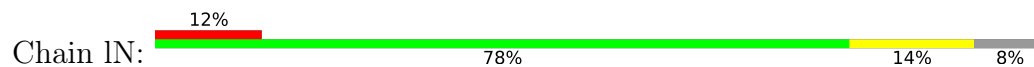


- Molecule 13: 60S ribosomal protein L11, putative

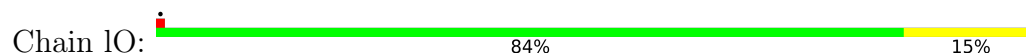
Chain IM: 



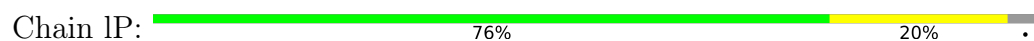
- Molecule 14: 60S ribosomal protein L13, putative



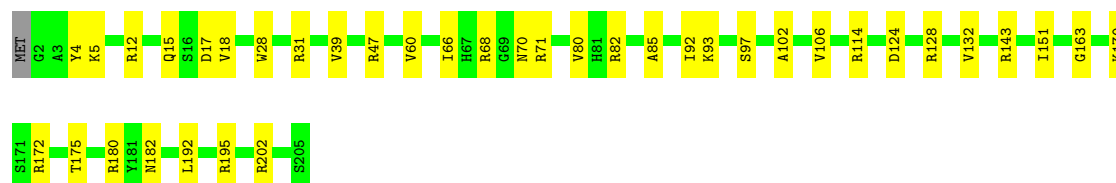
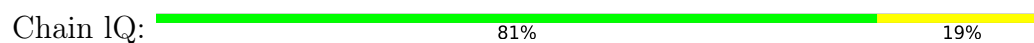
- Molecule 15: 60S ribosomal protein L13, putative



- Molecule 16: 60S ribosomal protein L14, putative



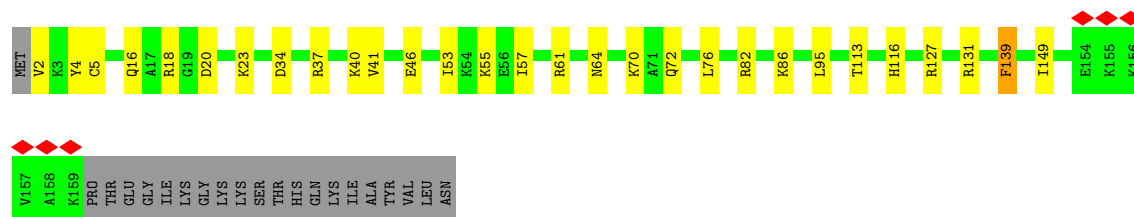
- Molecule 17: Ribosomal protein L15



- Molecule 18: 60S ribosomal protein L17, putative







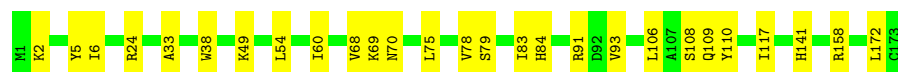
- Molecule 19: 60S ribosomal protein L18, putative

Chain IS:    ..



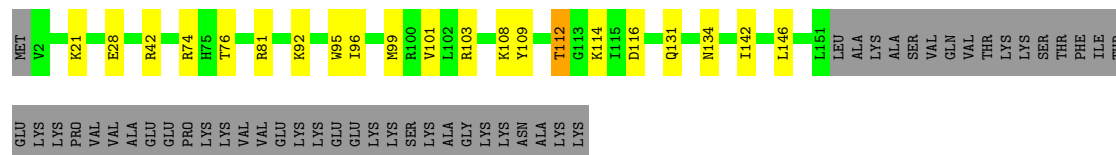
- Molecule 20: 60S ribosomal protein L18a

Chain IT:



- Molecule 21: Ribosomal protein L19

Chain IU:    .



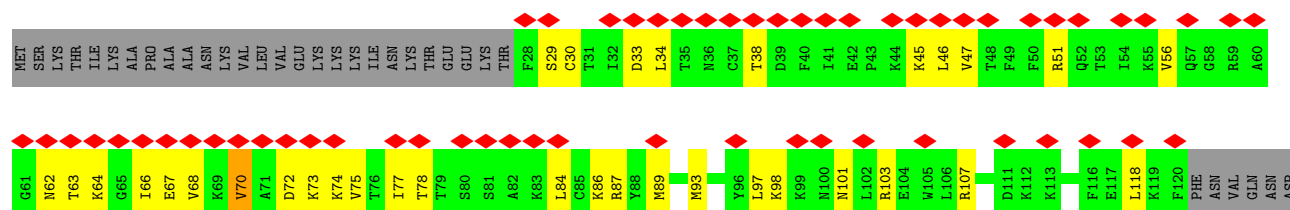
- Molecule 22: 60S ribosomal protein L21, putative

Chain IV:   .



- Molecule 23: Large ribosomal subunit protein eL22

Chain IW:     .



GLU  
GLU  
GLU  
VAL  
ARG  
ALA  
GLU  
GLU  
THR  
ASN  
ALA  
GLN

- Molecule 24: 60S ribosomal protein L23, putative

Chain IX: 79% 16% 5%

MET PRO GLY ARG GLY ALA GLY G8 R15 V16 T17 C18 N21 N22 K71 A23 S24 I40 S41 V42 K43 L52 F53 R54 M60 V61 R83 Q84 R85 R86 T87 R88 R89 Y97 M108 T118 K123 V140

- Molecule 25: Ribosomal protein L23A, putative

Chain IY: 83% 12% . .

MET ALA GLY THR LYS R6 K17 R27 D57 A69 N70 K71 T72 K75 K76 G83 V84 K85 V86 L95 K99 D108 V109 E110 A111 M112 E113 K117 L120 F121

- Molecule 26: 60S ribosomal protein L24, putative

Chain IZ: 29% 6% 65%

MET SER ILE THR Q6 S11 R21 R25 F31 T54 A55 I56 Q59 L60 N61 K62 LYS GLY GLN ASN GLU LEU VAL GLU LYS LYS THR ARG VAL ILE LYS VAL ASN ARG GLY TYR SER ILE SER ALA GLU LEU ILE ALA LYS ARG HIS GLN THR

PHE  
ASN  
SER  
ARG

- Molecule 27: 60S ribosomal protein L26, putative

Chain Ia: 80% 18% .

M1 K2 A21 N22 R26 S31 A32 R33 K36 E37 L38 Y42 P48 D52 K59 Q60 K63 K67 R73 S74 K75 Y76 V77 D81 K82 K85 T86 K87 A88 N89 I95 L109 R113 E114 S123 V145 N150 I153 T162

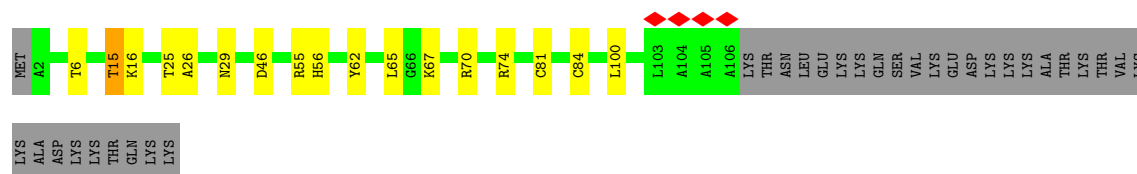
E163 K164 M174 A175 E176 K177 L178 K181 P182 R185 H194 A205 A206 L207 A208 K209 K210 ILE ALA LYS

- Molecule 28: 60S ribosomal protein L27, putative

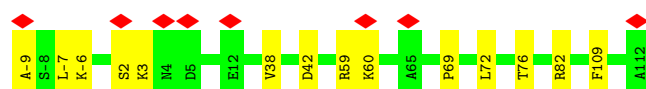
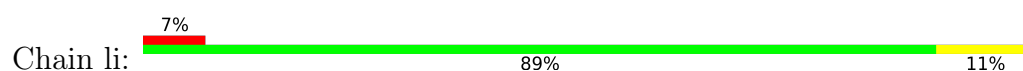
Chain Ib: 19% 74% 24% . .

MET SER K3 V10 V11 R17 G20 A23 T33 K34 D35 R36 K37 Y38 V43 V46 E47 R48 A49 P50 T53 T54 R55 K56 A59 K60 V61 Q62 E63 M64 V68 K69 N78 P82 T83 N88 L89 E90 Q91 F92 N93 L94 I95 K96 Q97 V98 K99

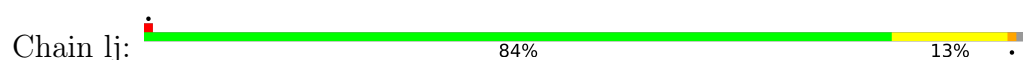




• Molecule 35: uL29



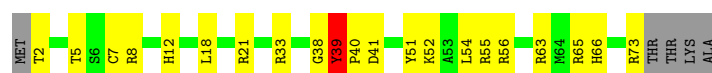
• Molecule 36: 60S ribosomal protein L35a, putative



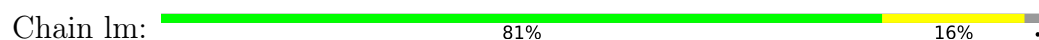
• Molecule 37: 60S ribosomal protein L36, putative



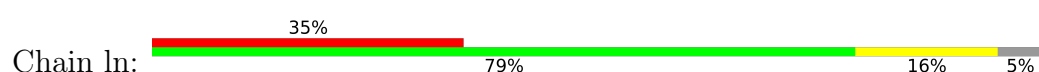
• Molecule 38: 60S ribosomal protein L37-A, putative

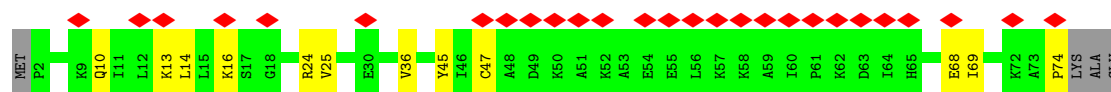


• Molecule 39: 60S ribosomal protein L37a, putative



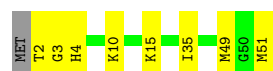
• Molecule 40: 60S ribosomal protein L38 putative





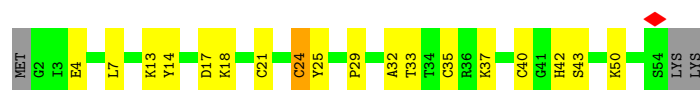
- Molecule 41: Ribosomal protein L39, putative

Chain lo: 82% 16%



- Molecule 42: 60S ribosomal protein L40, putative

Chain lp: 62% 30% 5%



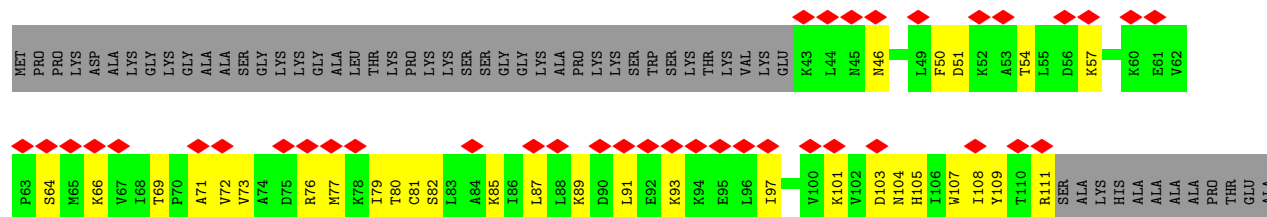
- Molecule 43: 60S ribosomal protein L44, putative

Chain lq: 79% 15% 6%



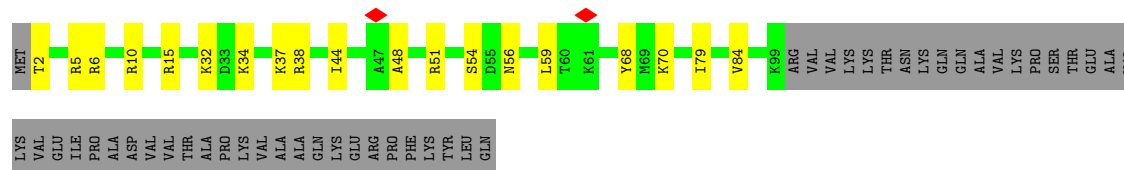
- Molecule 44: 40S ribosomal protein S25

Chain sA: 28% 23% 50%

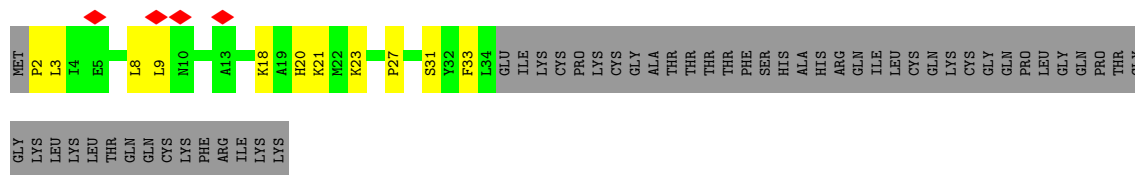


- Molecule 45: 40S ribosomal protein S26

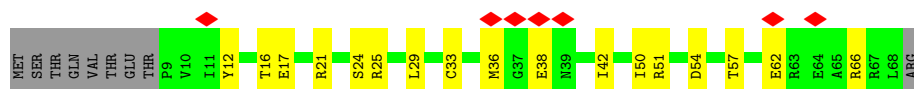
Chain sB: 55% 13% 32%



- Molecule 46: Small ribosomal subunit protein eS27



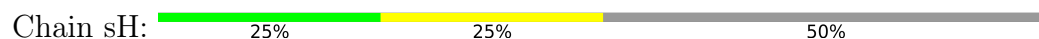
- Molecule 47: 40S ribosomal protein S28, putative



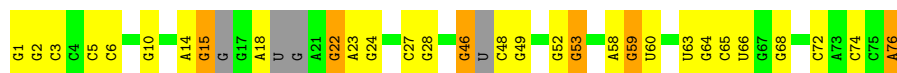
- Molecule 48: Ribosomal protein S29, putative



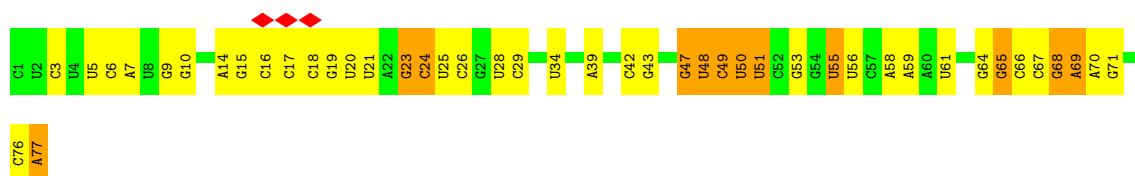
- Molecule 49: Unknown peptide



- Molecule 50: A/P-tRNA



- Molecule 51: P/E-tRNA

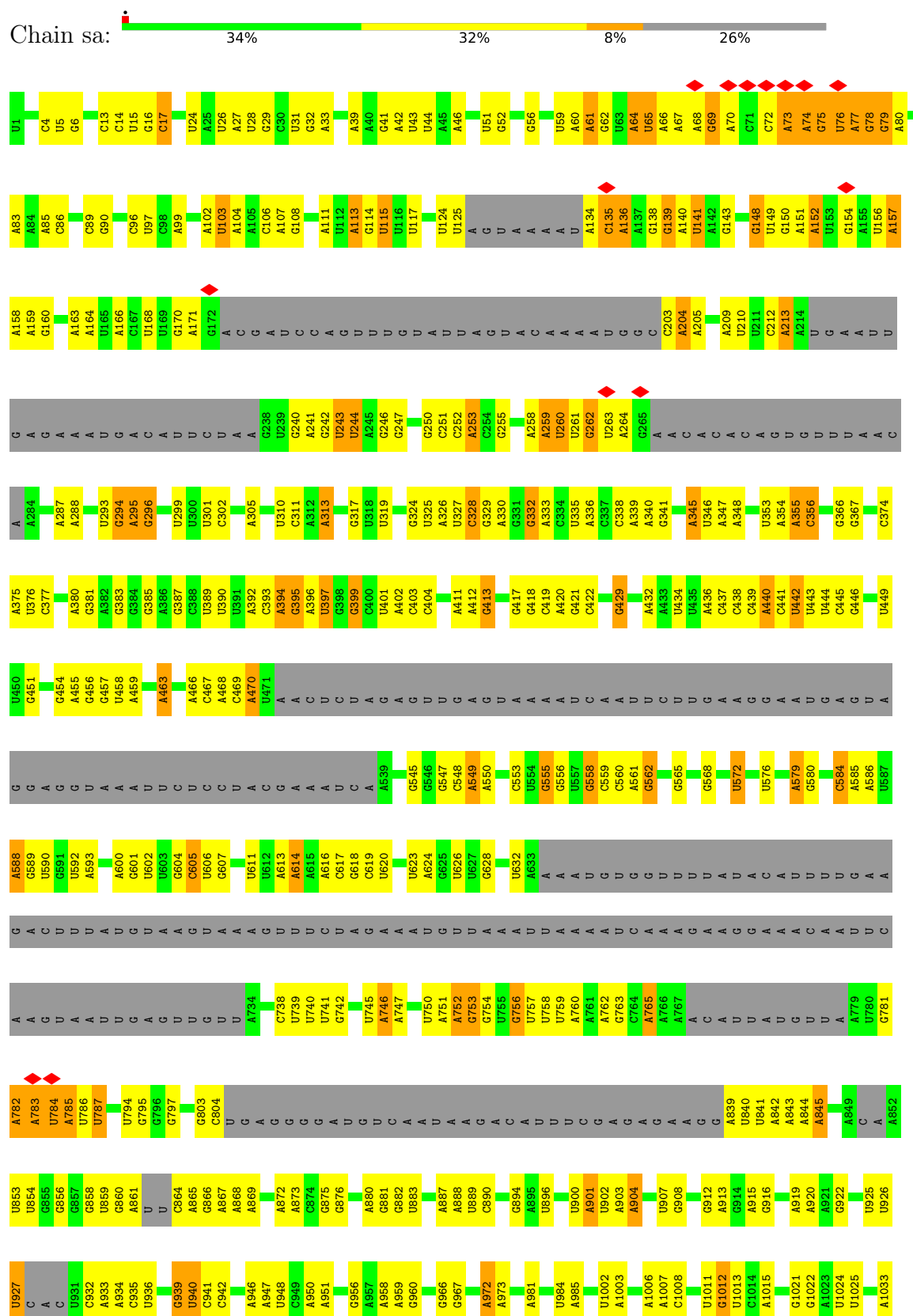


- Molecule 52: mRNA



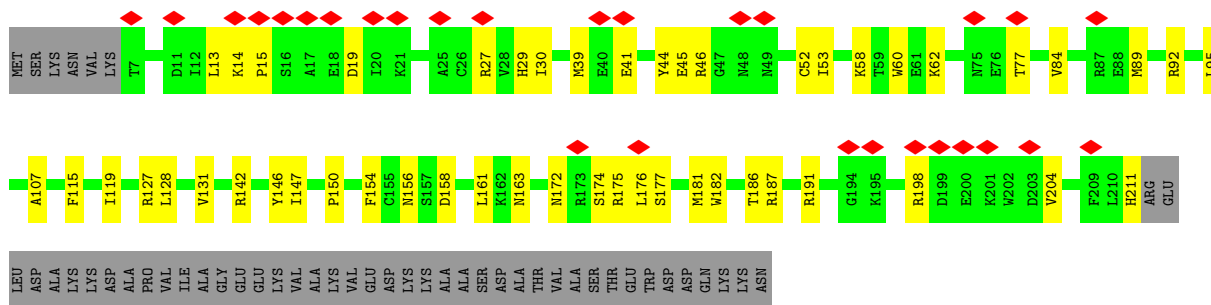
There are no outlier residues recorded for this chain.

• Molecule 53: 17S rRNA

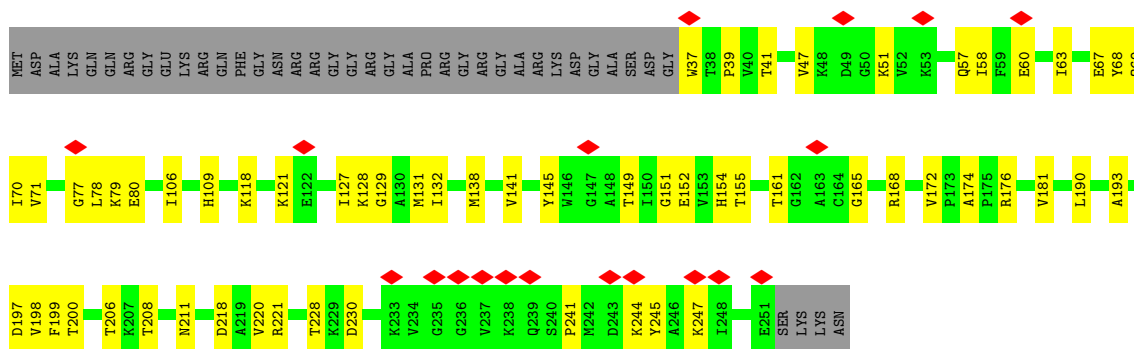




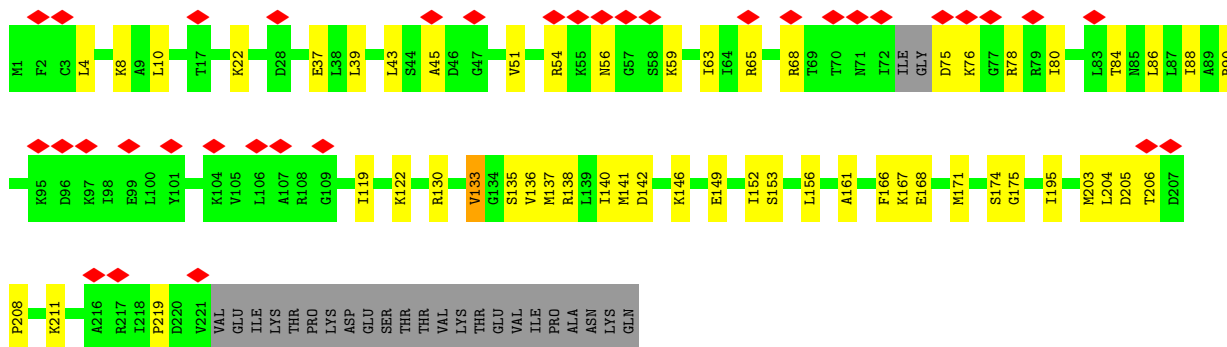




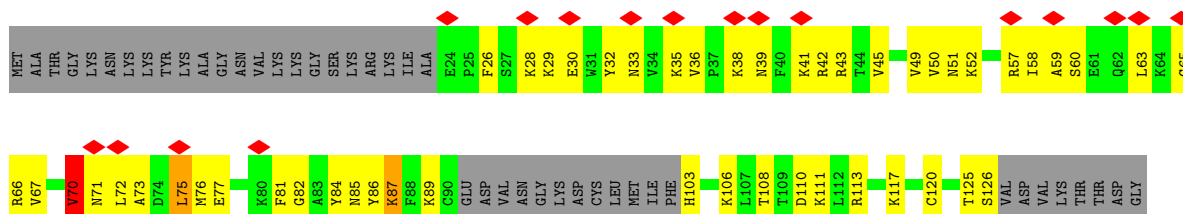
- Molecule 55: Small ribosomal subunit protein uS5



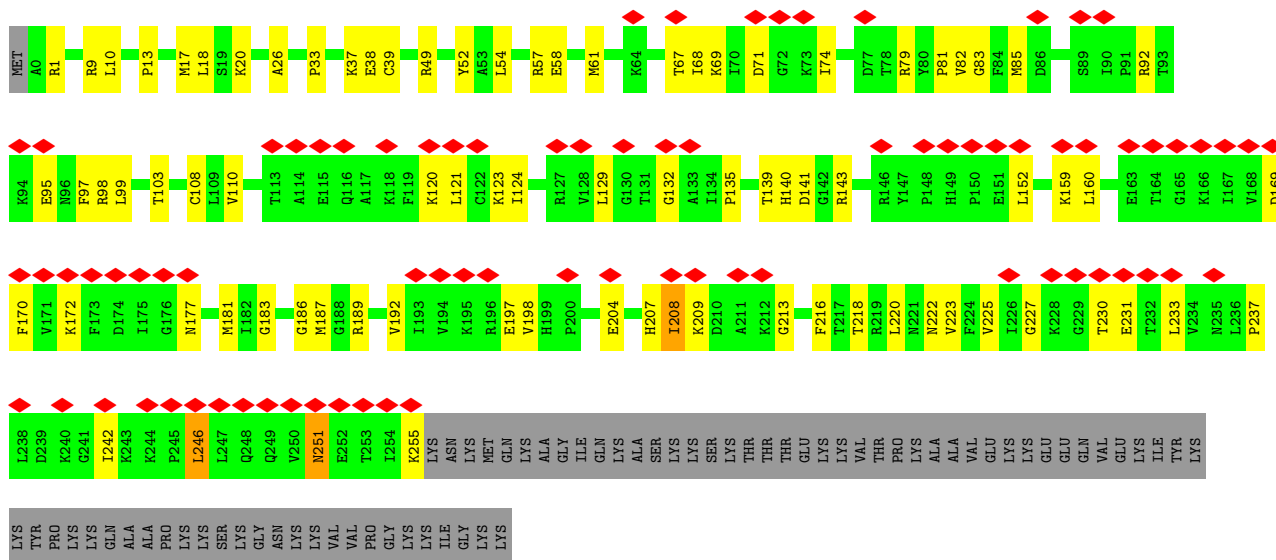
- Molecule 56: 40S ribosomal protein S3



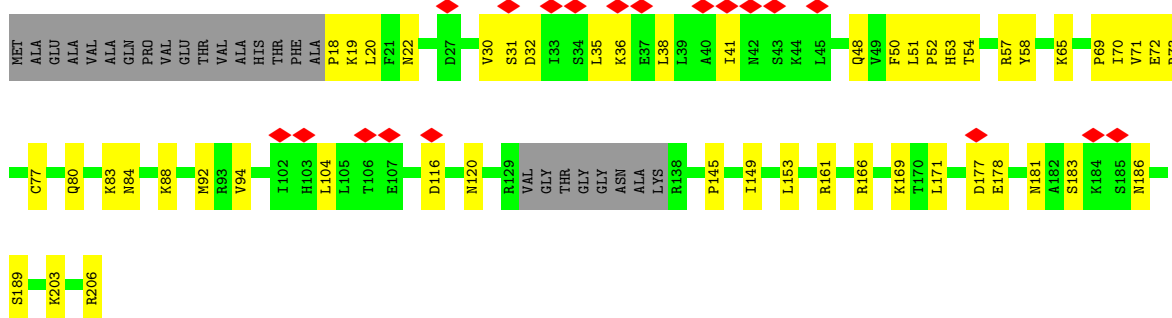
- Molecule 57: Small ribosomal subunit protein eS1



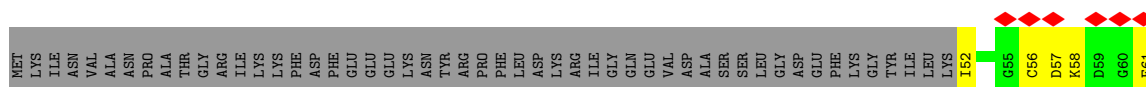
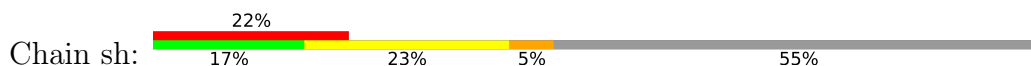
- Molecule 58: 40S ribosomal protein S4, putative

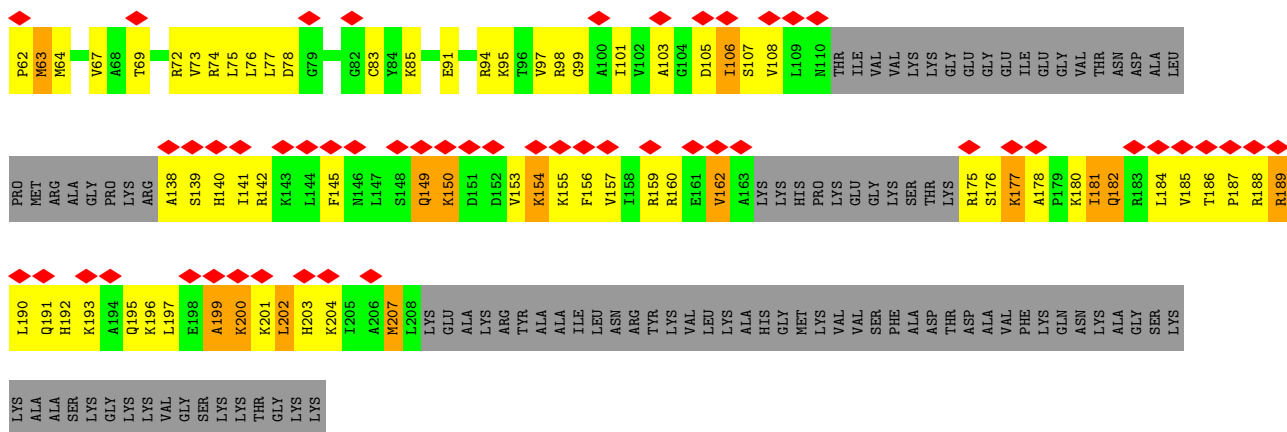


- Molecule 59: Small ribosomal subunit protein uS7

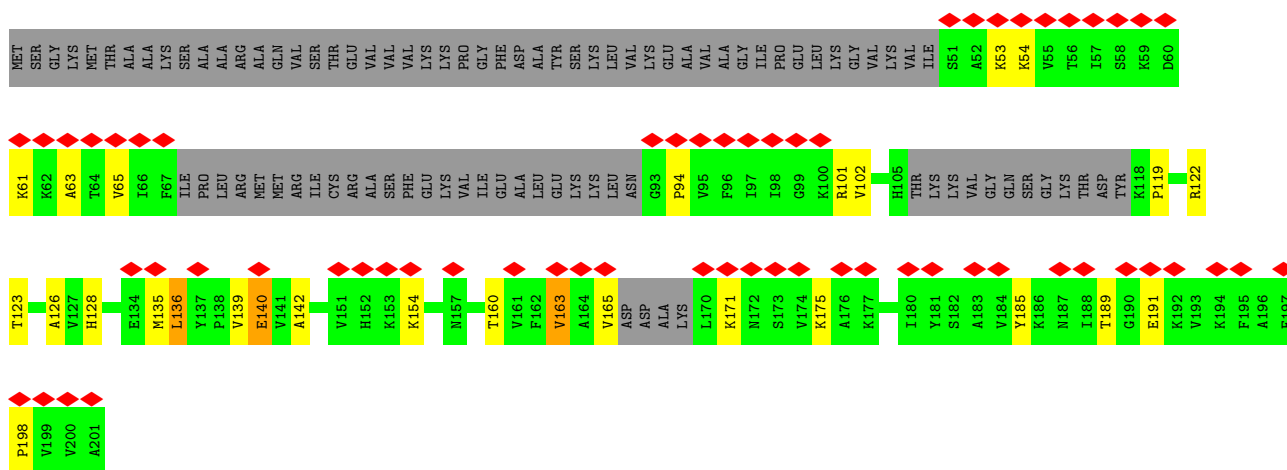


- Molecule 60: 40S ribosomal protein S6

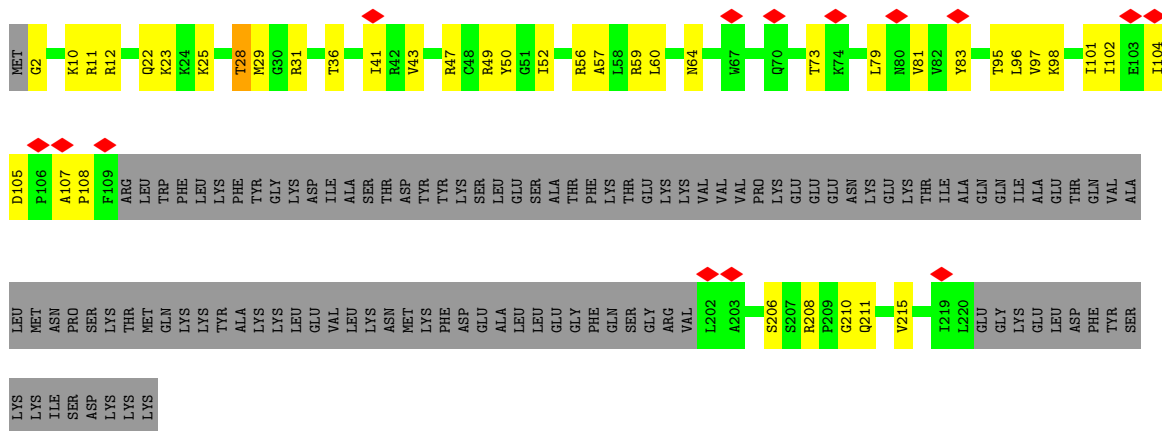
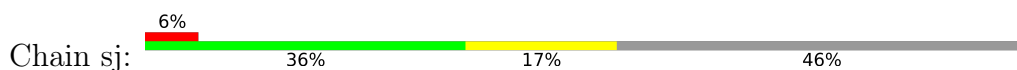




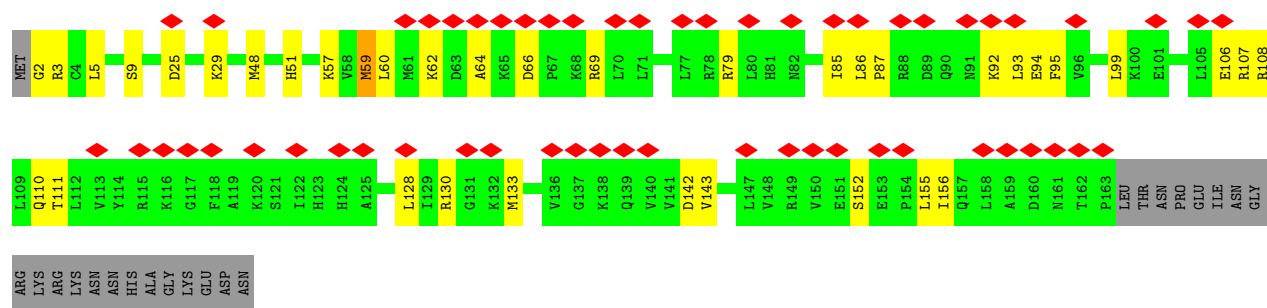
• Molecule 61: 40S ribosomal protein S7



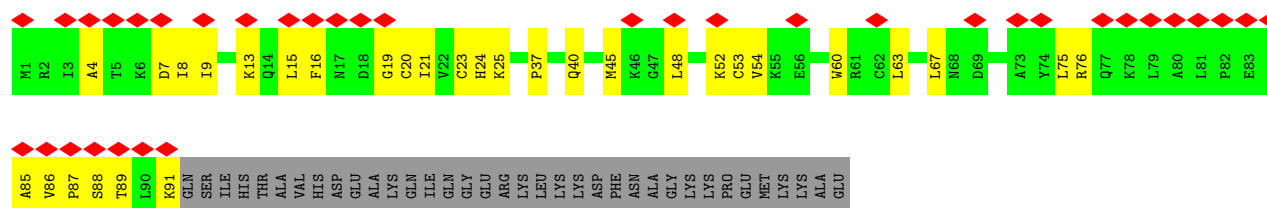
• Molecule 62: 40S ribosomal protein S8



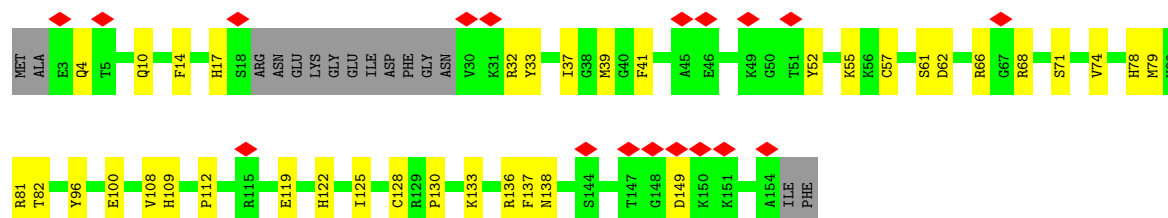
• Molecule 63: Small ribosomal subunit protein uS4



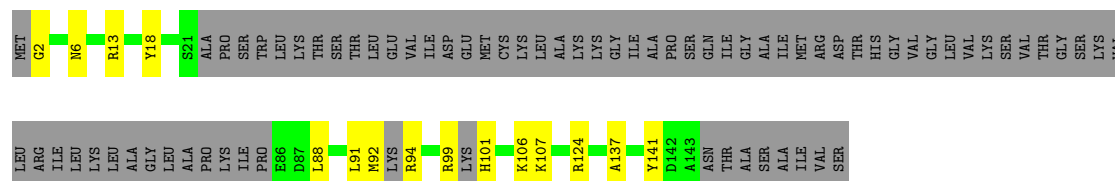
- Molecule 64: 40S ribosomal protein S10, putative



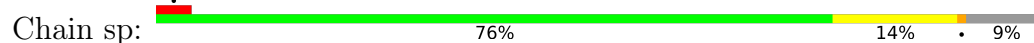
- Molecule 65: 40S ribosomal protein S11, putative

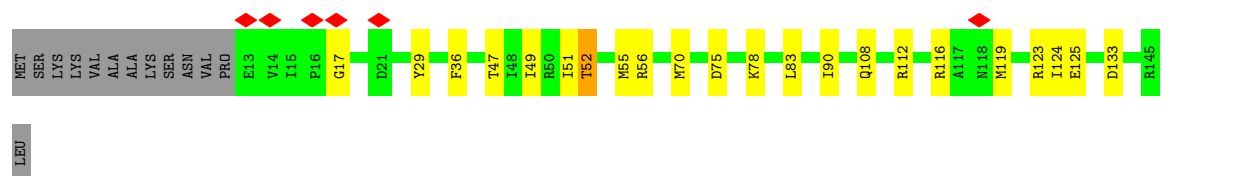


- Molecule 66: 40S ribosomal protein S13, putative

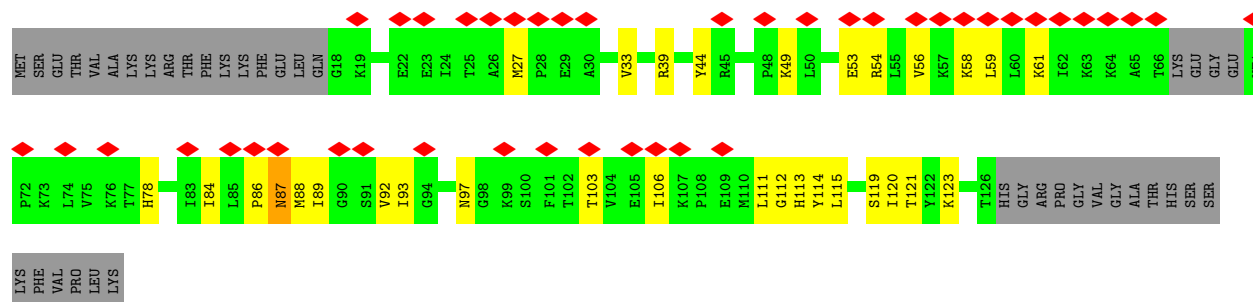


- Molecule 67: Ribosomal protein S14, putative

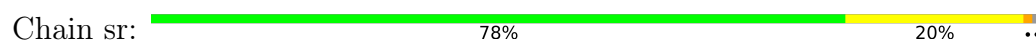




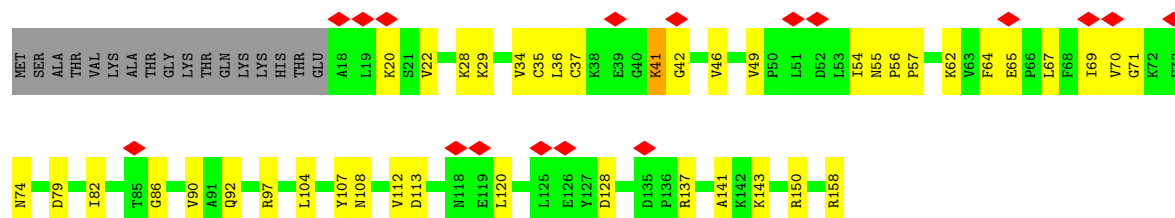
- Molecule 68: 40S ribosomal protein S15, putative



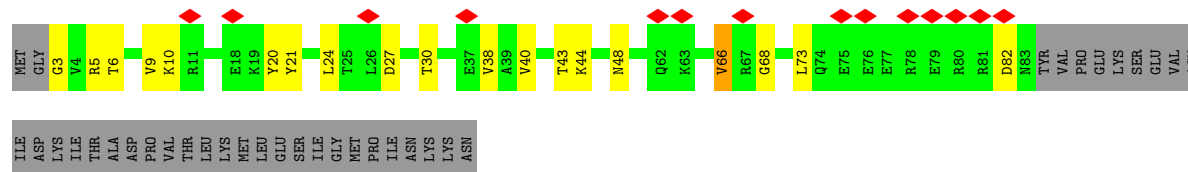
- Molecule 69: 40S ribosomal protein S15a, putative



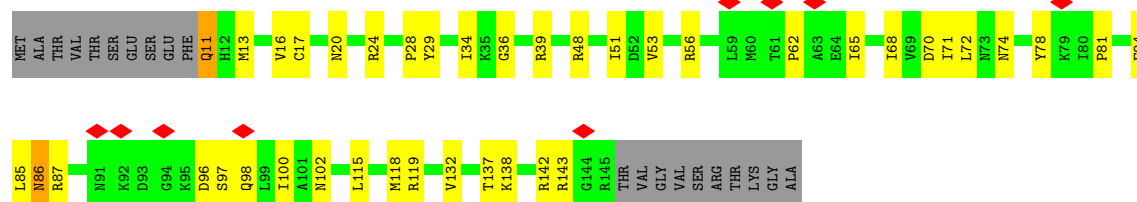
- Molecule 70: 40S ribosomal protein S16, putative



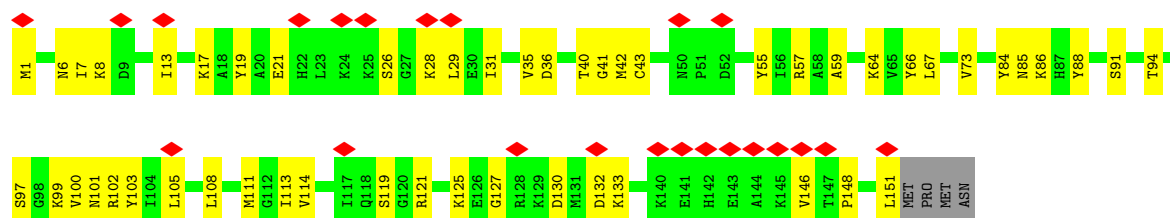
- Molecule 71: 40S ribosomal protein S17, putative



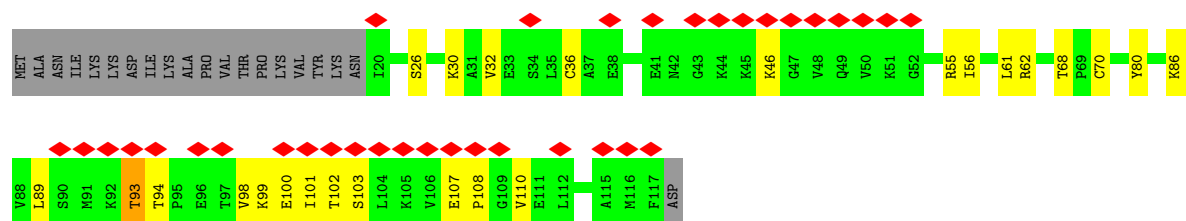
- Molecule 72: Small ribosomal subunit protein uS13



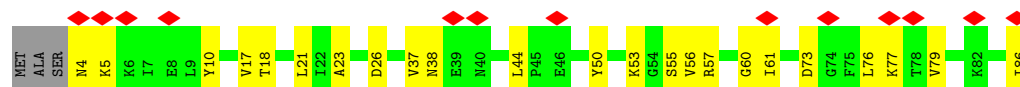
- Molecule 73: Small ribosomal subunit protein eS19



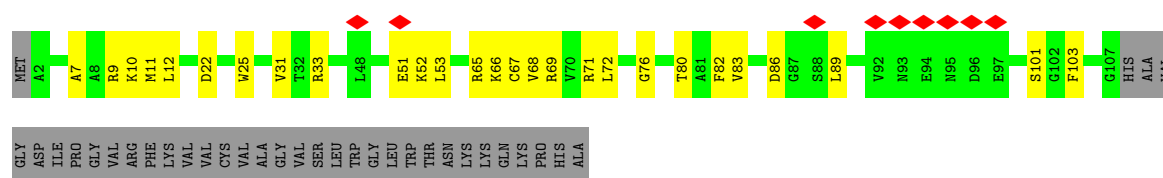
- Molecule 74: 40S ribosomal protein S20, putative



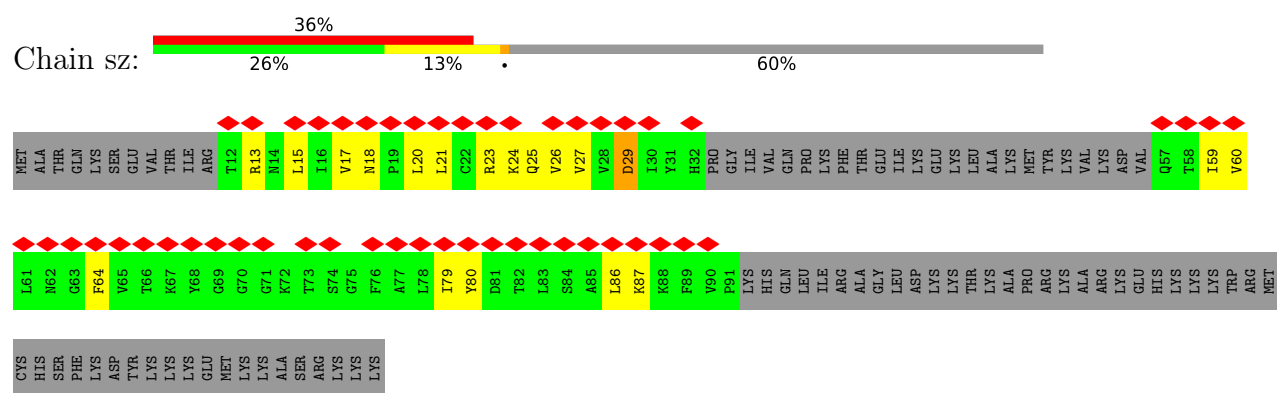
- Molecule 75: 40S ribosomal protein S21



- Molecule 76: 40S ribosomal protein S23, putative



- Molecule 77: 40S ribosomal protein S24, putative



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39958	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	18.910	Depositor
Minimum map value	-5.957	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	1A	0.12	0/75319	0.28	0/117329
2	1B	0.11	0/3470	0.27	0/5401
3	1C	0.12	0/2765	0.35	2/4303 (0.0%)
4	1D	0.10	0/1920	0.25	0/2582
5	1E	0.09	0/3140	0.25	0/4216
6	1F	0.09	0/3311	0.26	0/4446
7	1G	0.10	0/2284	0.26	0/3059
8	1H	0.09	0/1640	0.27	0/2204
9	1I	0.08	0/1680	0.23	0/2252
10	1J	0.09	0/1757	0.26	0/2360
11	1K	0.07	0/1562	0.21	0/2103
12	1L	0.09	0/1633	0.23	0/2184
13	1M	0.08	0/1369	0.23	0/1834
14	1N	0.09	0/2150	0.23	0/2867
15	1O	0.09	0/1646	0.23	0/2209
16	1P	0.08	0/1032	0.21	0/1388
17	1Q	0.09	0/1707	0.22	0/2276
18	1R	0.08	0/1251	0.23	0/1675
19	1S	0.09	0/1337	0.23	0/1789
20	1T	0.09	0/1445	0.26	0/1946
21	1U	0.09	0/1253	0.23	0/1666
22	1V	0.10	0/1351	0.25	0/1819
23	1W	0.12	0/772	0.29	0/1028
24	1X	0.09	0/1030	0.23	0/1384
25	1Y	0.08	0/941	0.21	0/1262
26	1Z	0.09	0/492	0.23	0/656
27	1a	0.08	0/1673	0.23	0/2236
28	1b	0.09	0/1112	0.26	0/1489
29	1c	0.09	0/1223	0.23	0/1636
30	1d	0.10	0/485	0.25	0/639
31	1e	0.08	0/776	0.29	0/1044
32	1f	0.10	0/1205	0.25	0/1609
33	1g	0.09	0/1075	0.23	0/1434
34	1h	0.09	0/833	0.22	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	li	0.07	0/984	0.21	0/1310
36	lj	0.11	0/862	0.25	0/1163
37	lk	0.07	0/721	0.20	0/955
38	ll	0.11	0/602	0.28	0/797
39	lm	0.09	0/696	0.23	0/928
40	ln	0.10	0/592	0.27	0/789
41	lo	0.09	0/444	0.20	0/587
42	lp	0.13	0/425	0.42	1/563 (0.2%)
43	lq	0.09	0/770	0.22	0/1019
44	sA	0.13	0/555	0.37	0/749
45	sB	0.09	0/797	0.23	0/1062
46	sC	0.08	0/263	0.25	0/357
47	sD	0.10	0/470	0.25	0/630
48	sE	0.15	0/449	0.37	0/595
50	sI	0.13	0/1710	0.28	0/2657
51	sJ	0.09	0/1818	0.24	0/2827
52	sK	0.07	0/241	0.20	0/373
53	sa	0.11	0/34364	0.28	0/53526
54	sb	0.08	0/1659	0.22	0/2243
55	sc	0.11	0/1673	0.29	0/2257
56	sd	0.08	0/1716	0.24	0/2297
57	se	0.41	0/1346	0.95	6/1793 (0.3%)
58	sf	0.10	0/2072	0.28	0/2792
59	sg	0.08	0/1460	0.25	0/1960
60	sh	0.19	0/952	0.54	0/1265
61	si	0.11	0/868	0.30	0/1166
62	sj	0.08	0/1002	0.22	0/1341
63	sk	0.07	0/1344	0.22	0/1800
64	sl	0.08	0/745	0.24	0/1007
65	sm	0.08	0/1187	0.24	0/1586
66	so	0.07	0/654	0.20	0/866
67	sp	0.09	0/1013	0.22	0/1361
68	sq	0.11	0/856	0.37	0/1143
69	sr	0.10	0/1040	0.28	0/1404
70	ss	0.08	0/1121	0.23	0/1503
71	st	0.10	0/684	0.30	0/914
72	su	0.13	0/1113	0.37	0/1491
73	sv	0.09	0/1239	0.23	0/1665
74	sw	0.10	0/776	0.31	0/1044
75	sx	0.10	0/663	0.28	0/898
76	sy	0.07	0/848	0.24	0/1131
77	sz	0.09	0/445	0.24	0/601
All	All	0.11	0/199878	0.28	9/293855 (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
38	ll	0	1
48	sE	0	1
57	se	0	2
60	sh	0	2
68	sq	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	se	70	VAL	N-CA-C	-21.55	81.78	109.58
3	lC	62	U	OP2-P-O3'	-8.82	81.54	108.00
3	lC	62	U	OP1-P-O3'	-8.48	82.56	108.00
57	se	39	ASN	CA-C-N	-6.54	110.65	122.54
57	se	39	ASN	C-N-CA	-6.54	110.65	122.54

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	ll	39	TYR	Peptide
48	sE	15	GLY	Peptide
57	se	176	LYS	Peptide
57	se	195	LEU	Peptide
60	sh	199	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	lA	67215	0	33720	1093	0
2	lB	3097	0	1552	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	lC	2477	0	1252	87	0
4	lD	1881	0	1928	43	0
5	lE	3076	0	3209	60	0
6	lF	3253	0	3444	56	0
7	lG	2245	0	2325	33	0
8	lH	1608	0	1728	29	0
9	lI	1658	0	1802	21	0
10	lJ	1727	0	1849	27	0
11	lK	1538	0	1598	39	0
12	lL	1597	0	1654	21	0
13	lM	1350	0	1390	25	0
14	lN	2122	0	2316	32	0
15	lO	1616	0	1700	19	0
16	lP	1020	0	1104	19	0
17	lQ	1676	0	1777	33	0
18	lR	1232	0	1307	22	0
19	lS	1316	0	1420	23	0
20	lT	1413	0	1479	18	0
21	lU	1235	0	1369	18	0
22	lV	1320	0	1406	18	0
23	lW	761	0	811	23	0
24	lX	1015	0	1054	17	0
25	lY	926	0	997	12	0
26	lZ	481	0	518	7	0
27	la	1651	0	1822	26	0
28	lb	1094	0	1174	24	0
29	lc	1192	0	1205	19	0
30	ld	478	0	507	15	0
31	le	768	0	810	15	0
32	lf	1184	0	1270	22	0
33	lg	1058	0	1140	15	0
34	lh	820	0	864	15	0
35	li	974	0	1093	8	0
36	lj	841	0	878	11	0
37	lk	712	0	755	19	0
38	ll	591	0	617	16	0
39	lm	688	0	726	12	0
40	ln	584	0	643	8	0
41	lo	432	0	444	8	0
42	lp	420	0	450	19	0
43	lq	756	0	821	12	0
44	sA	548	0	604	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	sB	787	0	833	16	0
46	sC	257	0	270	9	0
47	sD	468	0	500	14	0
48	sE	442	0	444	17	0
49	sH	9	0	4	1	0
50	sI	1533	0	785	22	0
51	sJ	1630	0	829	31	0
52	sK	215	0	108	0	0
53	sa	30685	0	15419	589	0
54	sb	1626	0	1627	30	0
55	sc	1642	0	1721	39	0
56	sd	1696	0	1794	41	0
57	se	1329	0	1420	54	0
58	sf	2031	0	2145	59	0
59	sg	1440	0	1506	32	0
60	sh	944	0	1023	81	0
61	si	854	0	928	20	0
62	sj	990	0	1031	34	0
63	sk	1323	0	1420	31	0
64	sl	729	0	760	24	0
65	sm	1161	0	1181	35	0
66	so	644	0	664	13	0
67	sp	999	0	1024	18	0
68	sq	842	0	913	22	0
69	sr	1022	0	1051	20	0
70	ss	1104	0	1185	33	0
71	st	676	0	718	14	0
72	su	1096	0	1143	30	0
73	sv	1214	0	1254	41	0
74	sw	766	0	829	20	0
75	sx	651	0	668	16	0
76	sy	836	0	885	19	0
77	sz	438	0	465	11	0
All	All	185725	0	137079	3057	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 10.

The worst 5 of 3057 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)
1:1A:511:A:H62	1:1A:561:G:H21	1.01	0.95
53:sa:389:U:H3	53:sa:396:A:H62	1.07	0.95
3:1C:27:G:H1	3:1C:50:A:H61	1.12	0.94
57:se:72:LEU:HB3	57:se:81:PHE:HB3	1.52	0.91
3:1C:79:G:H1	3:1C:95:A:H2	1.13	0.91

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	
4	ID	244/257 (95%)	233 (96%)	11 (4%)	0	100	100
5	IE	385/402 (96%)	378 (98%)	7 (2%)	0	100	100
6	IF	420/431 (97%)	400 (95%)	20 (5%)	0	100	100
7	IG	278/286 (97%)	261 (94%)	17 (6%)	0	100	100
8	IH	201/204 (98%)	181 (90%)	19 (10%)	1 (0%)	25	58
9	II	208/230 (90%)	203 (98%)	5 (2%)	0	100	100
10	IJ	209/286 (73%)	199 (95%)	10 (5%)	0	100	100
11	IK	191/197 (97%)	185 (97%)	5 (3%)	1 (0%)	25	58
12	IL	196/210 (93%)	187 (95%)	9 (5%)	0	100	100
13	IM	166/174 (95%)	160 (96%)	6 (4%)	0	100	100
14	IN	261/291 (90%)	252 (97%)	9 (3%)	0	100	100
15	IO	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
16	IP	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
17	IQ	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
18	IR	156/179 (87%)	153 (98%)	3 (2%)	0	100	100
19	IS	165/168 (98%)	152 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	IT	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
21	IU	148/198 (75%)	146 (99%)	2 (1%)	0	100	100
22	IV	163/166 (98%)	158 (97%)	5 (3%)	0	100	100
23	IW	91/137 (66%)	84 (92%)	7 (8%)	0	100	100
24	IX	131/140 (94%)	126 (96%)	5 (4%)	0	100	100
25	IY	114/121 (94%)	111 (97%)	3 (3%)	0	100	100
26	IZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	202 (97%)	6 (3%)	0	100	100
28	lb	135/139 (97%)	134 (99%)	1 (1%)	0	100	100
29	lc	146/149 (98%)	141 (97%)	5 (3%)	0	100	100
30	ld	58/64 (91%)	54 (93%)	4 (7%)	0	100	100
31	le	101/109 (93%)	92 (91%)	9 (9%)	0	100	100
32	lf	144/150 (96%)	137 (95%)	7 (5%)	0	100	100
33	lg	127/134 (95%)	120 (94%)	7 (6%)	0	100	100
34	lh	103/137 (75%)	100 (97%)	3 (3%)	0	100	100
35	li	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	48
36	lj	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
37	lk	83/104 (80%)	83 (100%)	0	0	100	100
38	ll	70/77 (91%)	64 (91%)	4 (6%)	2 (3%)	3	20
39	lm	88/93 (95%)	83 (94%)	5 (6%)	0	100	100
40	ln	71/77 (92%)	67 (94%)	4 (6%)	0	100	100
41	lo	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
42	lp	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
43	lq	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
44	sA	67/137 (49%)	62 (92%)	5 (8%)	0	100	100
45	sB	96/144 (67%)	94 (98%)	2 (2%)	0	100	100
46	sC	31/84 (37%)	30 (97%)	1 (3%)	0	100	100
47	sD	58/69 (84%)	54 (93%)	4 (7%)	0	100	100
48	sE	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
54	sb	203/254 (80%)	193 (95%)	10 (5%)	0	100	100
55	sc	213/255 (84%)	205 (96%)	7 (3%)	1 (0%)	25	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	sd	215/244 (88%)	202 (94%)	13 (6%)	0	100	100
57	se	155/256 (60%)	127 (82%)	27 (17%)	1 (1%)	22	53
58	sf	254/326 (78%)	243 (96%)	11 (4%)	0	100	100
59	sg	177/206 (86%)	168 (95%)	9 (5%)	0	100	100
60	sh	113/266 (42%)	88 (78%)	22 (20%)	3 (3%)	4	21
61	si	102/201 (51%)	96 (94%)	5 (5%)	1 (1%)	13	42
62	sj	123/237 (52%)	120 (98%)	3 (2%)	0	100	100
63	sk	160/185 (86%)	158 (99%)	2 (1%)	0	100	100
64	sl	89/127 (70%)	87 (98%)	2 (2%)	0	100	100
65	sm	137/156 (88%)	126 (92%)	11 (8%)	0	100	100
66	so	68/151 (45%)	68 (100%)	0	0	100	100
67	sp	131/146 (90%)	125 (95%)	6 (5%)	0	100	100
68	sq	101/144 (70%)	90 (89%)	10 (10%)	1 (1%)	13	42
69	sr	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
70	ss	139/158 (88%)	134 (96%)	5 (4%)	0	100	100
71	st	79/117 (68%)	79 (100%)	0	0	100	100
72	su	133/155 (86%)	121 (91%)	12 (9%)	0	100	100
73	sv	149/155 (96%)	144 (97%)	5 (3%)	0	100	100
74	sw	96/118 (81%)	93 (97%)	1 (1%)	2 (2%)	5	25
75	sx	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
76	sy	104/141 (74%)	99 (95%)	5 (5%)	0	100	100
77	sz	52/140 (37%)	49 (94%)	3 (6%)	0	100	100
All	All	9738/11683 (83%)	9285 (95%)	439 (4%)	14 (0%)	50	79

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	ll	40	PRO
60	sh	107	SER
60	sh	149	GLN
60	sh	202	LEU
74	sw	93	THR



### 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	
4	ID	195/201 (97%)	190 (97%)	5 (3%)	41	68
5	IE	330/343 (96%)	327 (99%)	3 (1%)	75	88
6	IF	332/345 (96%)	332 (100%)	0	100	100
7	IG	227/231 (98%)	225 (99%)	2 (1%)	75	88
8	IH	172/173 (99%)	169 (98%)	3 (2%)	56	78
9	II	178/195 (91%)	176 (99%)	2 (1%)	70	84
10	IJ	186/242 (77%)	182 (98%)	4 (2%)	47	71
11	IK	171/174 (98%)	165 (96%)	6 (4%)	31	61
12	IL	169/176 (96%)	168 (99%)	1 (1%)	84	91
13	IM	144/147 (98%)	141 (98%)	3 (2%)	48	72
14	IN	222/243 (91%)	221 (100%)	1 (0%)	86	92
15	IO	167/168 (99%)	164 (98%)	3 (2%)	54	76
16	IP	113/118 (96%)	112 (99%)	1 (1%)	75	88
17	IQ	171/172 (99%)	170 (99%)	1 (1%)	84	91
18	IR	129/147 (88%)	128 (99%)	1 (1%)	79	89
19	IS	141/143 (99%)	138 (98%)	3 (2%)	48	72
20	IT	156/156 (100%)	155 (99%)	1 (1%)	84	91
21	IU	132/174 (76%)	130 (98%)	2 (2%)	60	80
22	IV	144/145 (99%)	142 (99%)	2 (1%)	62	81
23	IW	85/125 (68%)	84 (99%)	1 (1%)	67	83
24	IX	109/113 (96%)	108 (99%)	1 (1%)	75	88
25	IY	99/102 (97%)	97 (98%)	2 (2%)	50	74
26	IZ	52/137 (38%)	52 (100%)	0	100	100
27	la	177/179 (99%)	173 (98%)	4 (2%)	45	70
28	lb	121/123 (98%)	120 (99%)	1 (1%)	79	89
29	lc	120/121 (99%)	119 (99%)	1 (1%)	79	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	ld	50/54 (93%)	50 (100%)	0	100	100
31	le	86/92 (94%)	85 (99%)	1 (1%)	67	83
32	lf	125/128 (98%)	124 (99%)	1 (1%)	79	89
33	lg	112/116 (97%)	110 (98%)	2 (2%)	54	76
34	lh	86/116 (74%)	83 (96%)	3 (4%)	31	61
35	li	103/103 (100%)	102 (99%)	1 (1%)	73	86
36	lj	89/91 (98%)	87 (98%)	2 (2%)	47	71
37	lk	71/82 (87%)	71 (100%)	0	100	100
38	ll	60/64 (94%)	60 (100%)	0	100	100
39	lm	72/75 (96%)	72 (100%)	0	100	100
40	ln	63/66 (96%)	62 (98%)	1 (2%)	58	79
41	lo	44/45 (98%)	44 (100%)	0	100	100
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	67	83
44	sA	64/112 (57%)	64 (100%)	0	100	100
45	sB	87/127 (68%)	86 (99%)	1 (1%)	70	84
46	sC	29/73 (40%)	28 (97%)	1 (3%)	32	62
47	sD	50/59 (85%)	49 (98%)	1 (2%)	50	74
48	sE	45/46 (98%)	44 (98%)	1 (2%)	47	71
54	sb	178/218 (82%)	177 (99%)	1 (1%)	84	91
55	sc	172/199 (86%)	170 (99%)	2 (1%)	67	83
56	sd	183/206 (89%)	178 (97%)	5 (3%)	40	67
57	se	149/225 (66%)	140 (94%)	9 (6%)	16	44
58	sf	223/283 (79%)	218 (98%)	5 (2%)	47	71
59	sg	162/178 (91%)	159 (98%)	3 (2%)	52	75
60	sh	101/220 (46%)	87 (86%)	14 (14%)	3	12
61	si	93/167 (56%)	90 (97%)	3 (3%)	34	63
62	sj	106/205 (52%)	103 (97%)	3 (3%)	38	66
63	sk	144/164 (88%)	142 (99%)	2 (1%)	62	81
64	sl	81/111 (73%)	80 (99%)	1 (1%)	67	83
65	sm	126/138 (91%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	so	68/129 (53%)	68 (100%)	0	100	100
67	sp	103/114 (90%)	99 (96%)	4 (4%)	27	58
68	sq	94/127 (74%)	93 (99%)	1 (1%)	70	84
69	sr	112/113 (99%)	110 (98%)	2 (2%)	54	76
70	ss	114/128 (89%)	112 (98%)	2 (2%)	54	76
71	st	73/106 (69%)	70 (96%)	3 (4%)	26	57
72	su	114/130 (88%)	111 (97%)	3 (3%)	41	68
73	sv	128/132 (97%)	126 (98%)	2 (2%)	58	79
74	sw	89/107 (83%)	89 (100%)	0	100	100
75	sx	75/77 (97%)	73 (97%)	2 (3%)	40	67
76	sy	86/114 (75%)	85 (99%)	1 (1%)	67	83
77	sz	49/125 (39%)	46 (94%)	3 (6%)	15	43
All	All	8431/9897 (85%)	8290 (98%)	141 (2%)	56	78

5 of 141 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
63	sk	59	MET
67	sp	75	ASP
72	su	11	GLN
27	la	36	LYS
25	lY	120	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
27	la	198	ASN
64	sl	40	GLN
36	lj	76	HIS
58	sf	221	ASN
71	st	31	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3131/3503 (89%)	564 (18%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	lB	143/155 (92%)	30 (20%)	0
3	lC	116/117 (99%)	19 (16%)	0
50	sI	68/76 (89%)	11 (16%)	0
51	sJ	76/77 (98%)	23 (30%)	0
52	sK	9/10 (90%)	0	0
53	sa	1417/1947 (72%)	308 (21%)	0
All	All	4960/5885 (84%)	955 (19%)	0

5 of 955 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A

There are no RNA pucker outliers to report.

## 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](#)

There are no chain breaks in this entry.

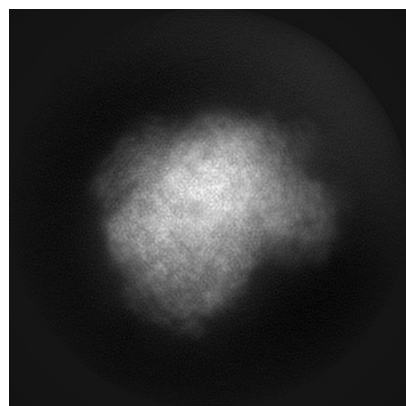
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64716. These allow visual inspection of the internal detail of the map and identification of artifacts.

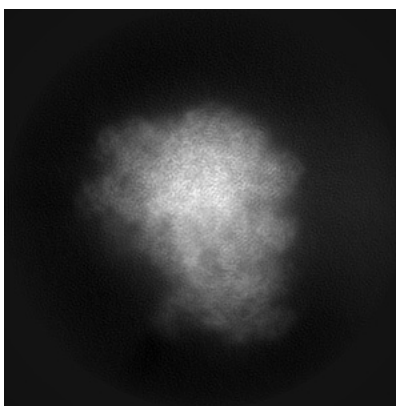
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

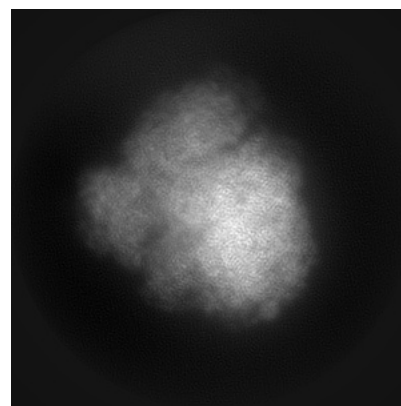
#### 6.1.1 Primary map



X

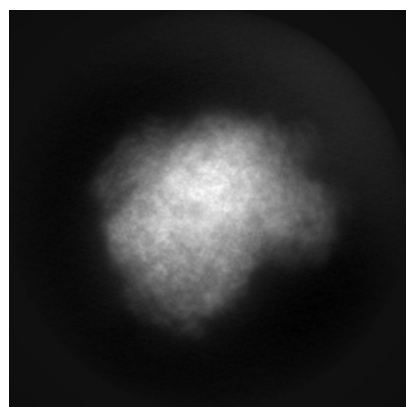


Y

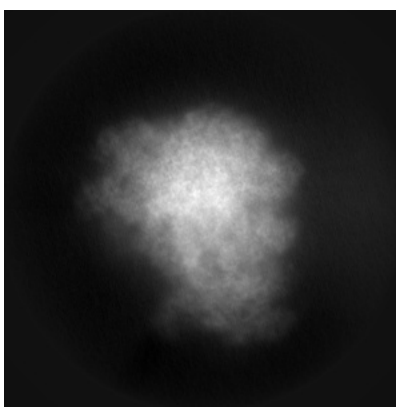


Z

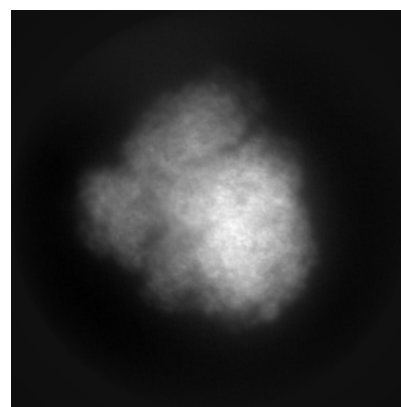
#### 6.1.2 Raw map



X



Y

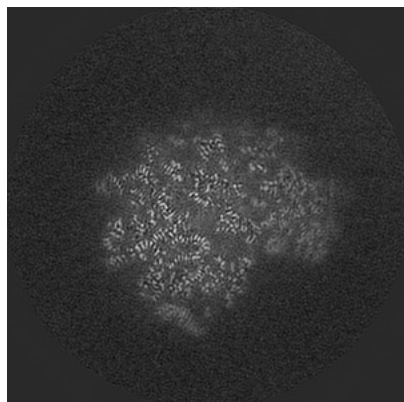


Z

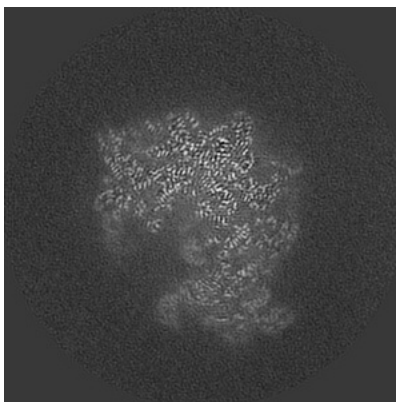
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

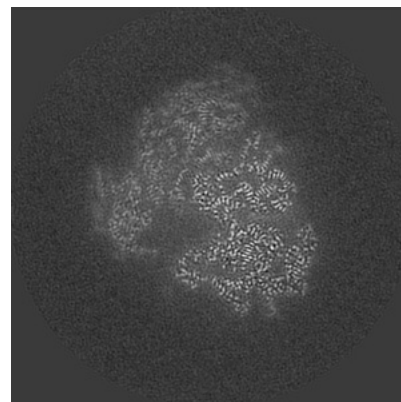
### 6.2.1 Primary map



X Index: 200

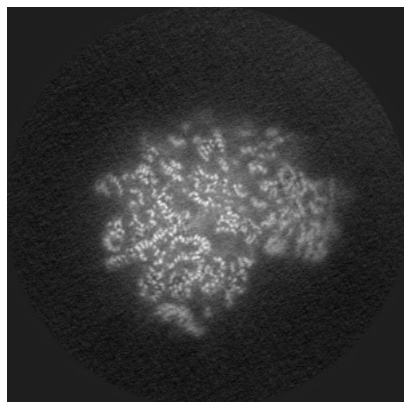


Y Index: 200

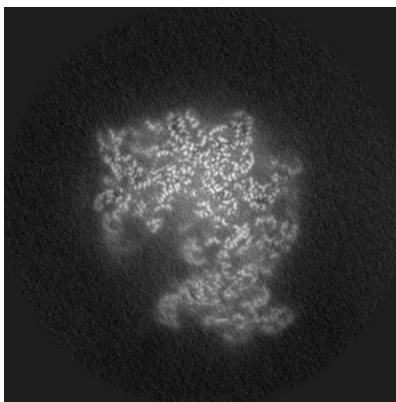


Z Index: 200

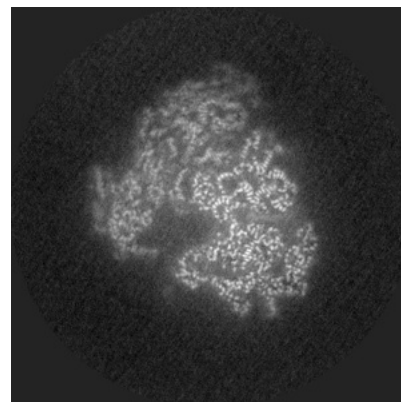
### 6.2.2 Raw map



X Index: 200



Y Index: 200



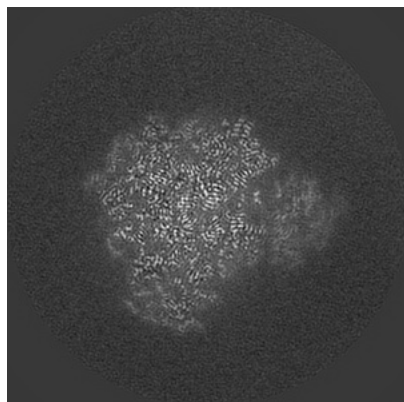
Z Index: 200

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

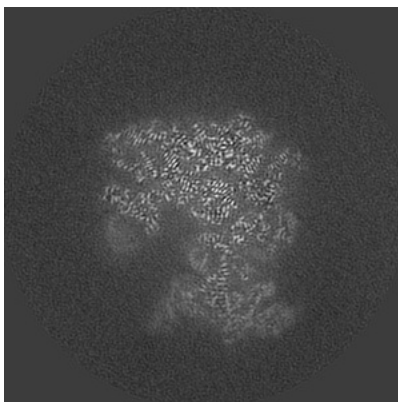


## 6.3 Largest variance slices [i](#)

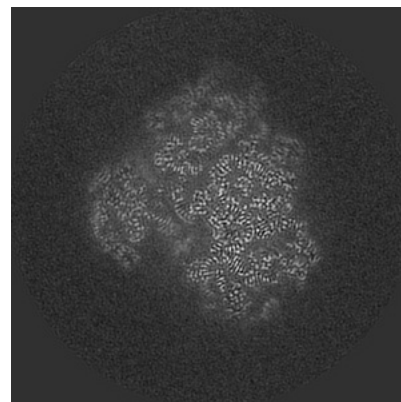
### 6.3.1 Primary map



X Index: 221

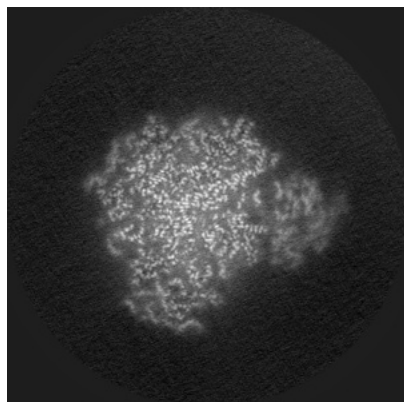


Y Index: 208

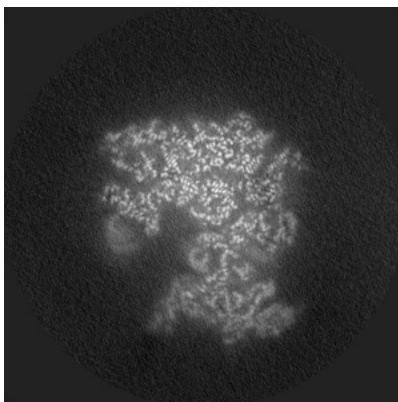


Z Index: 213

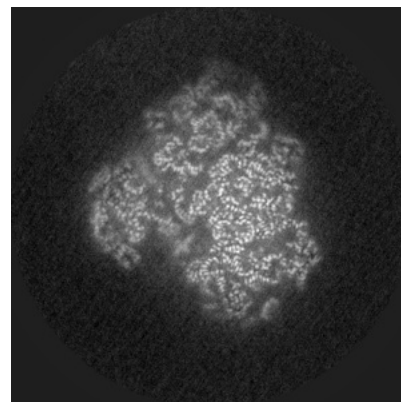
### 6.3.2 Raw map



X Index: 220



Y Index: 208

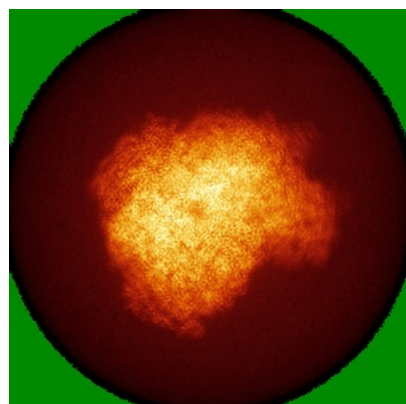


Z Index: 213

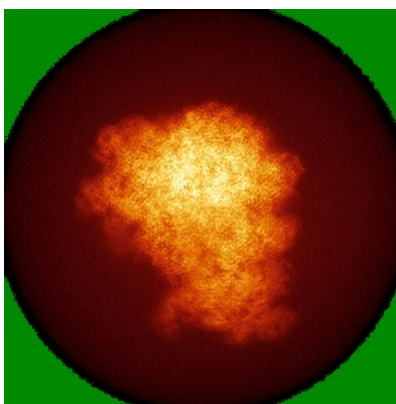
The images above show the largest variance slices of the map in three orthogonal directions.

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

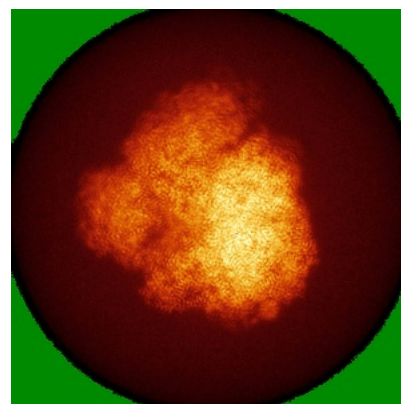
### 6.4.1 Primary map



X

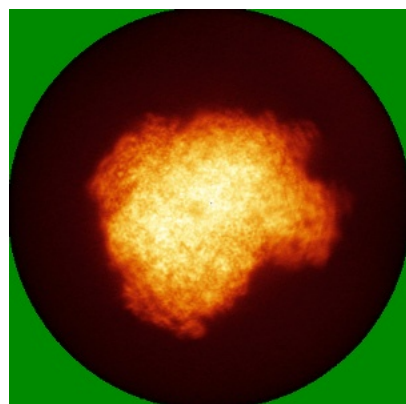


Y

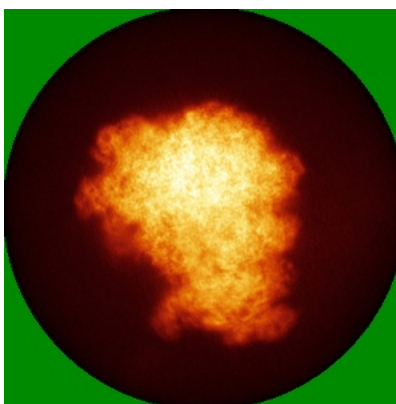


Z

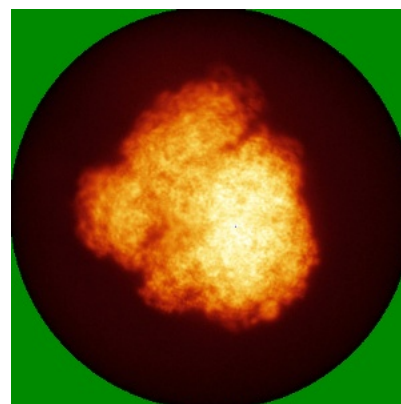
### 6.4.2 Raw map



X



Y



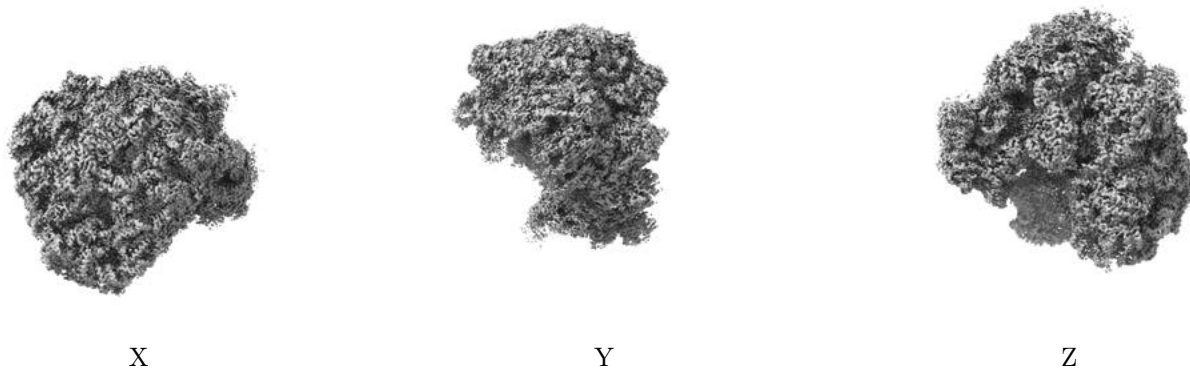
Z

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 2.8. 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.

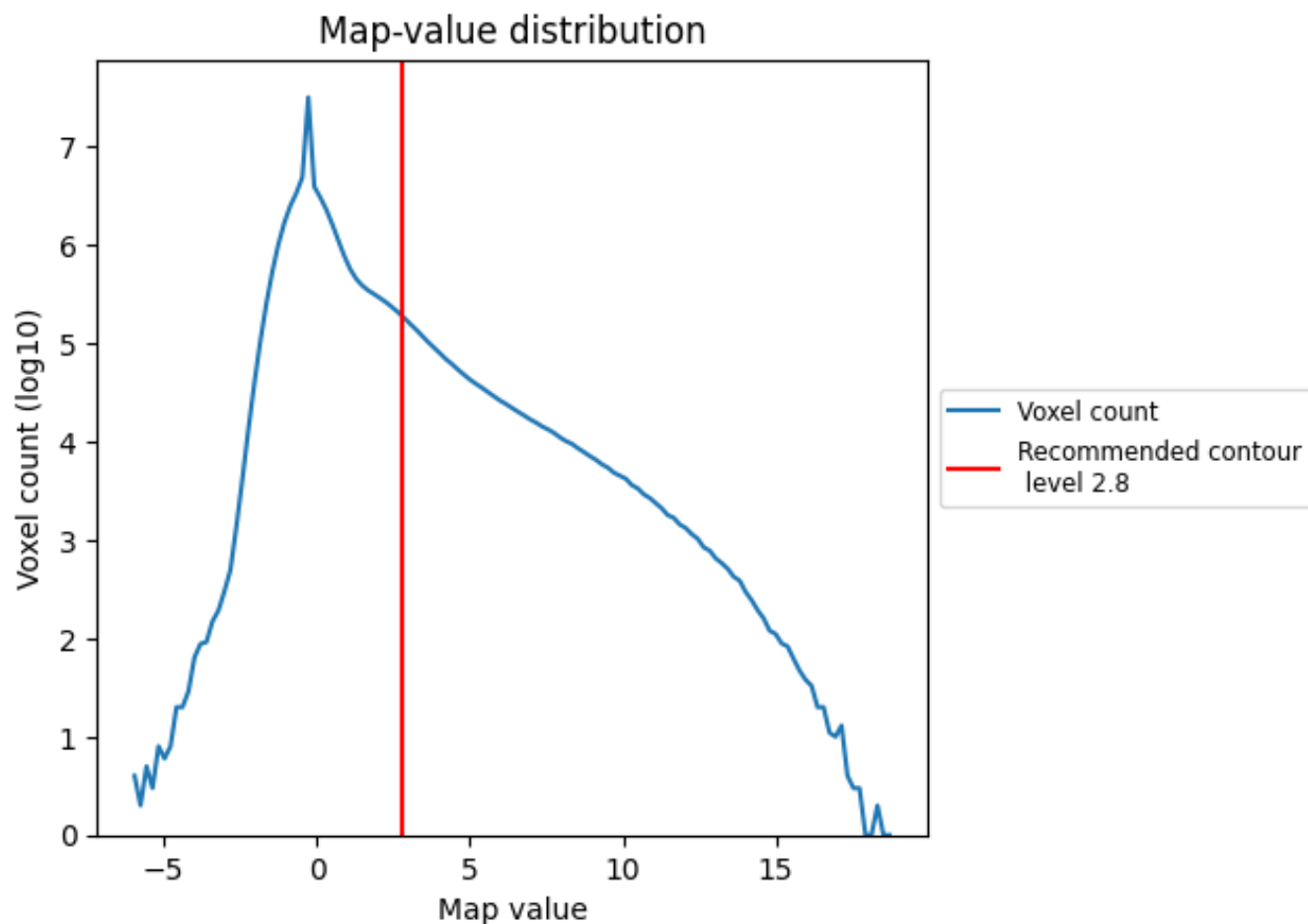
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

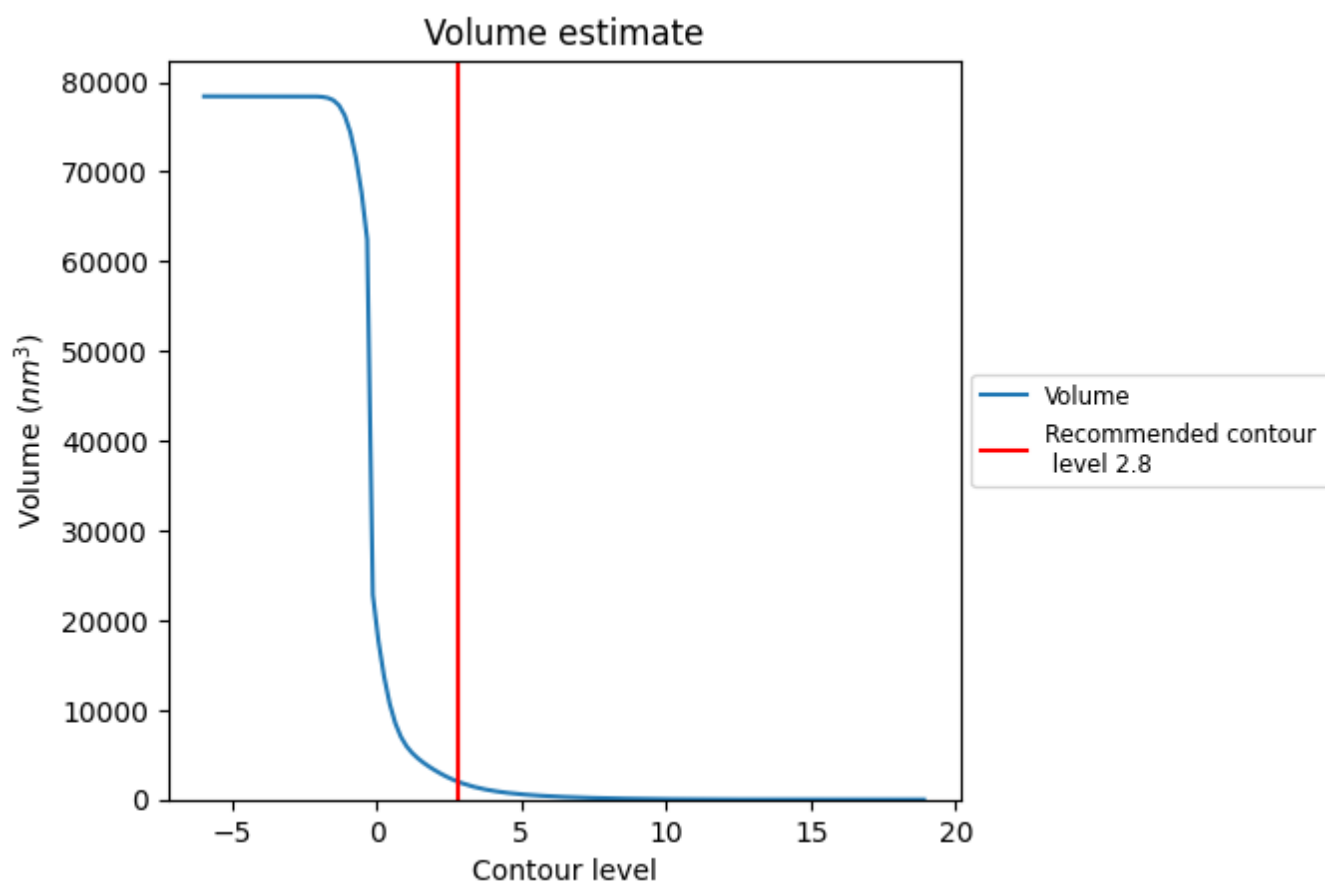
This section contains the results of statistical analysis of the map.

### 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.

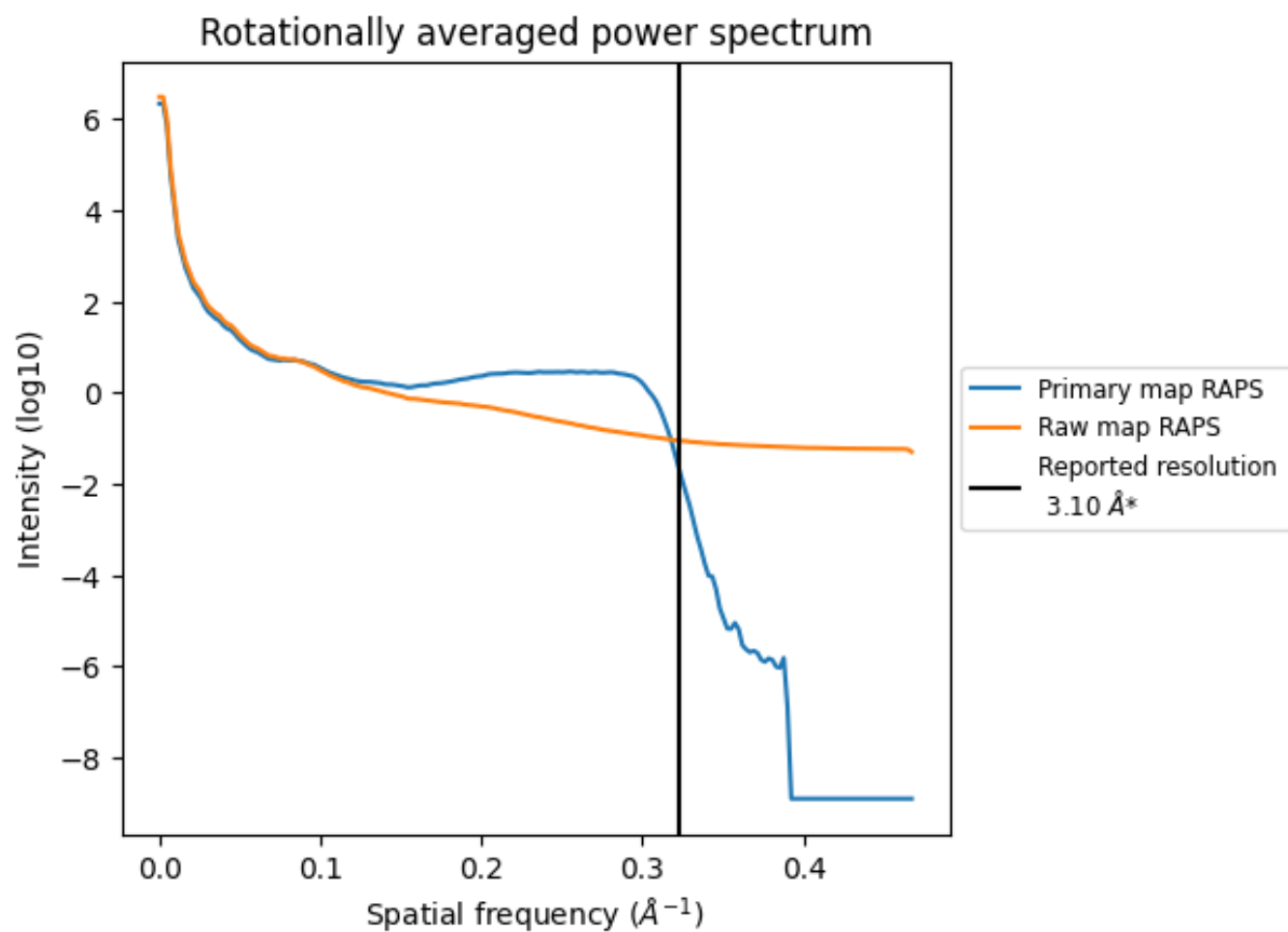
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2011 nm<sup>3</sup>; this corresponds to an approximate mass of 1817 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 ⓘ

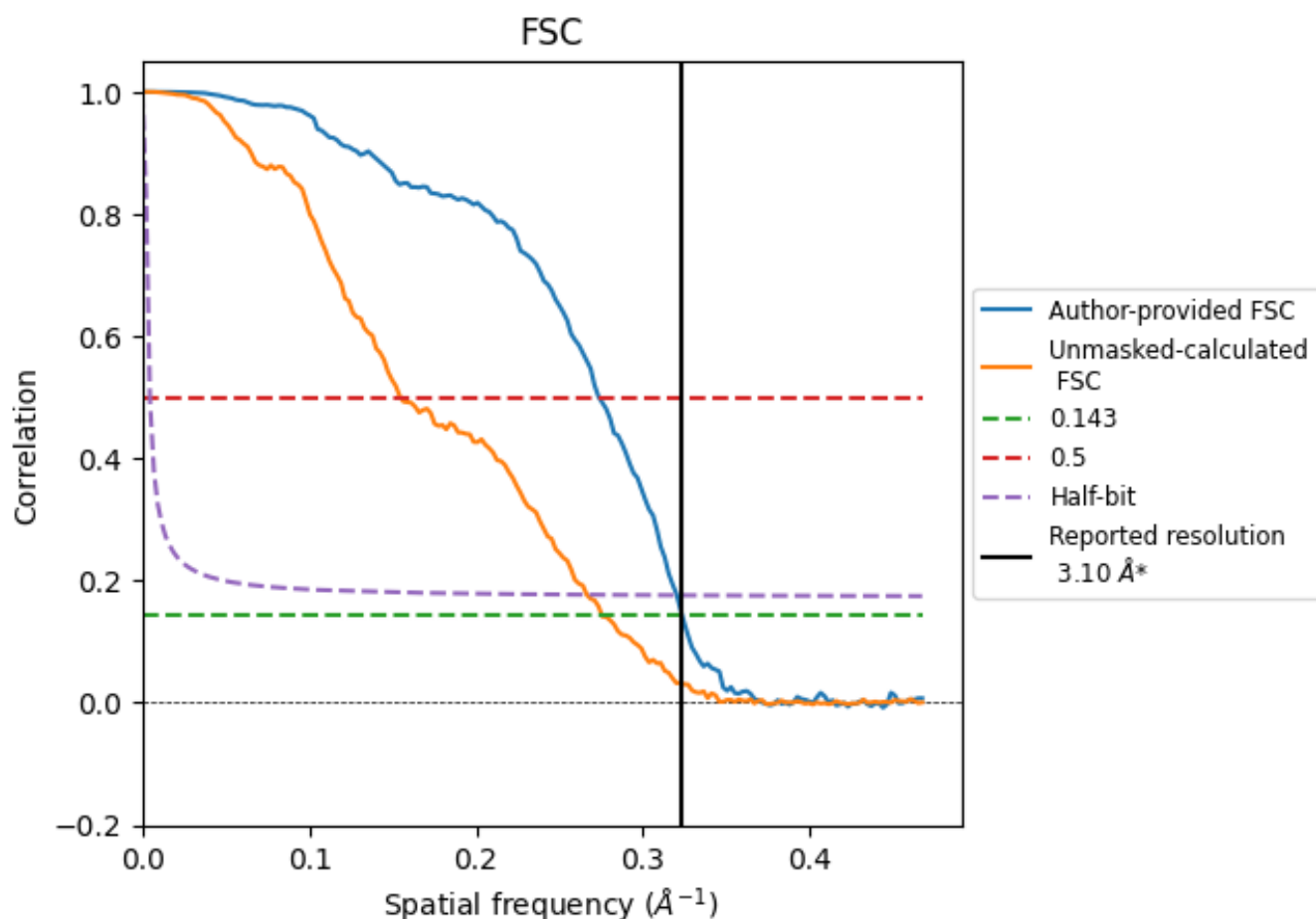


\*Reported resolution corresponds to spatial frequency of  $0.323 \text{ \AA}^{-1}$

## 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  $0.323 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

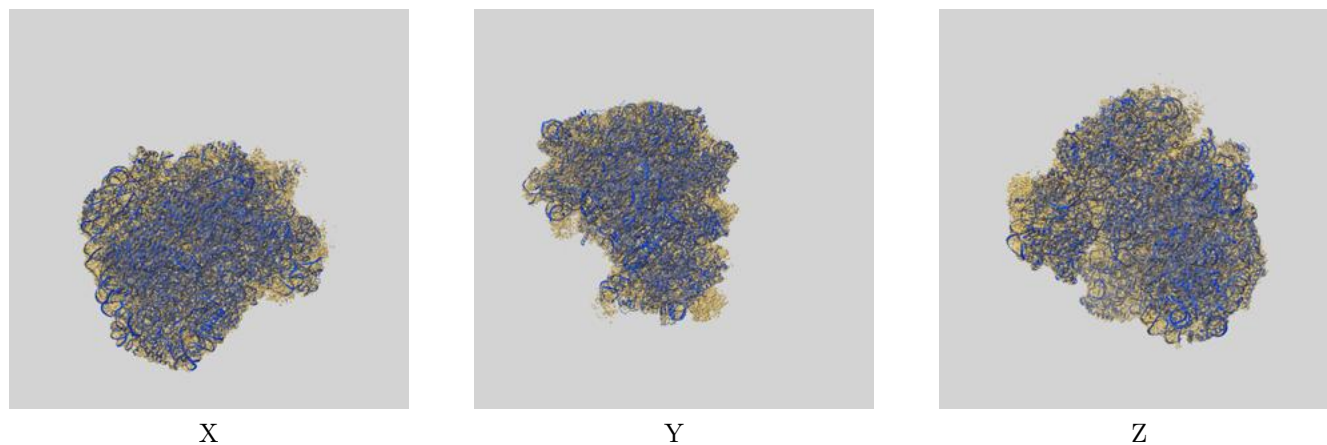
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.65	3.12
Unmasked-calculated*	3.63	6.46	3.76

\*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 3.63 differs from the reported value 3.1 by more than 10 %

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

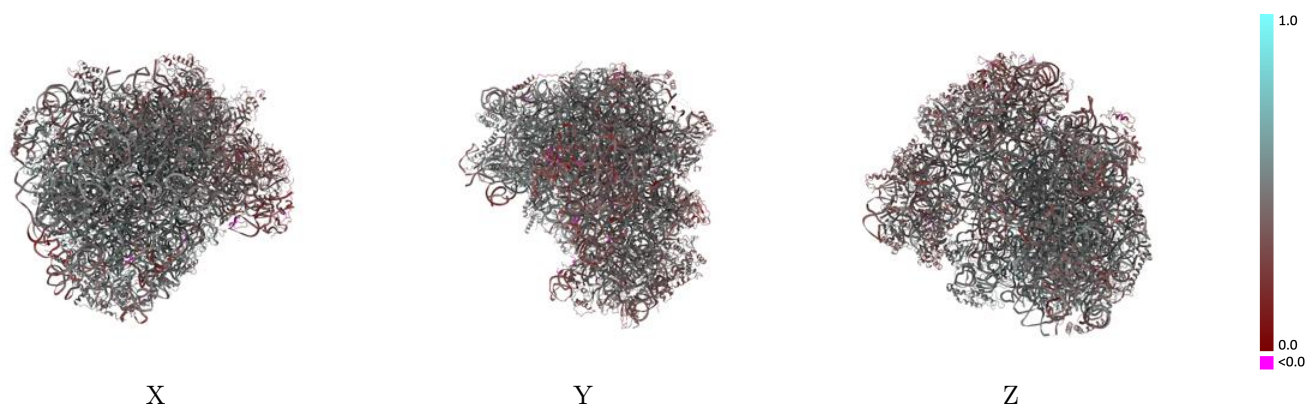
This section contains information regarding the fit between EMDB map EMD-64716 and PDB model 9V24. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

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



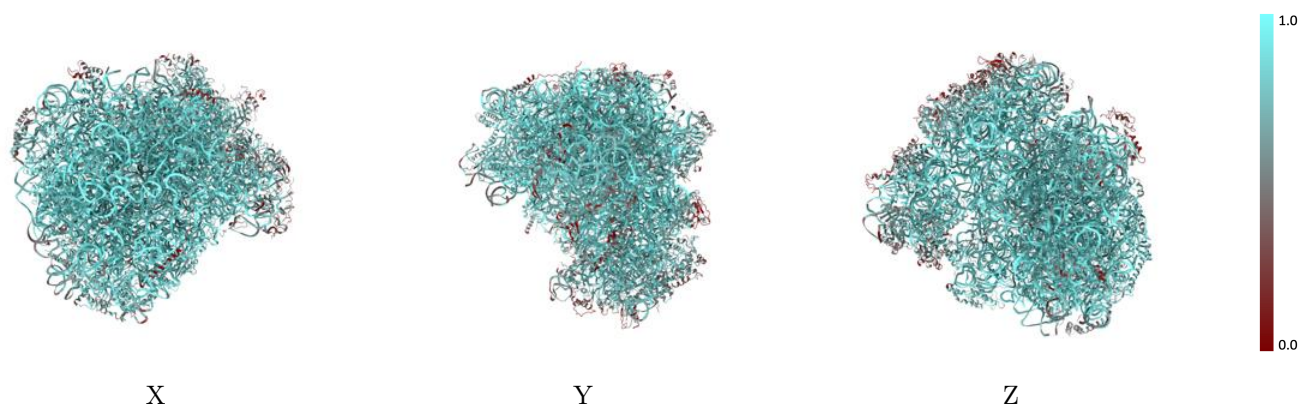
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

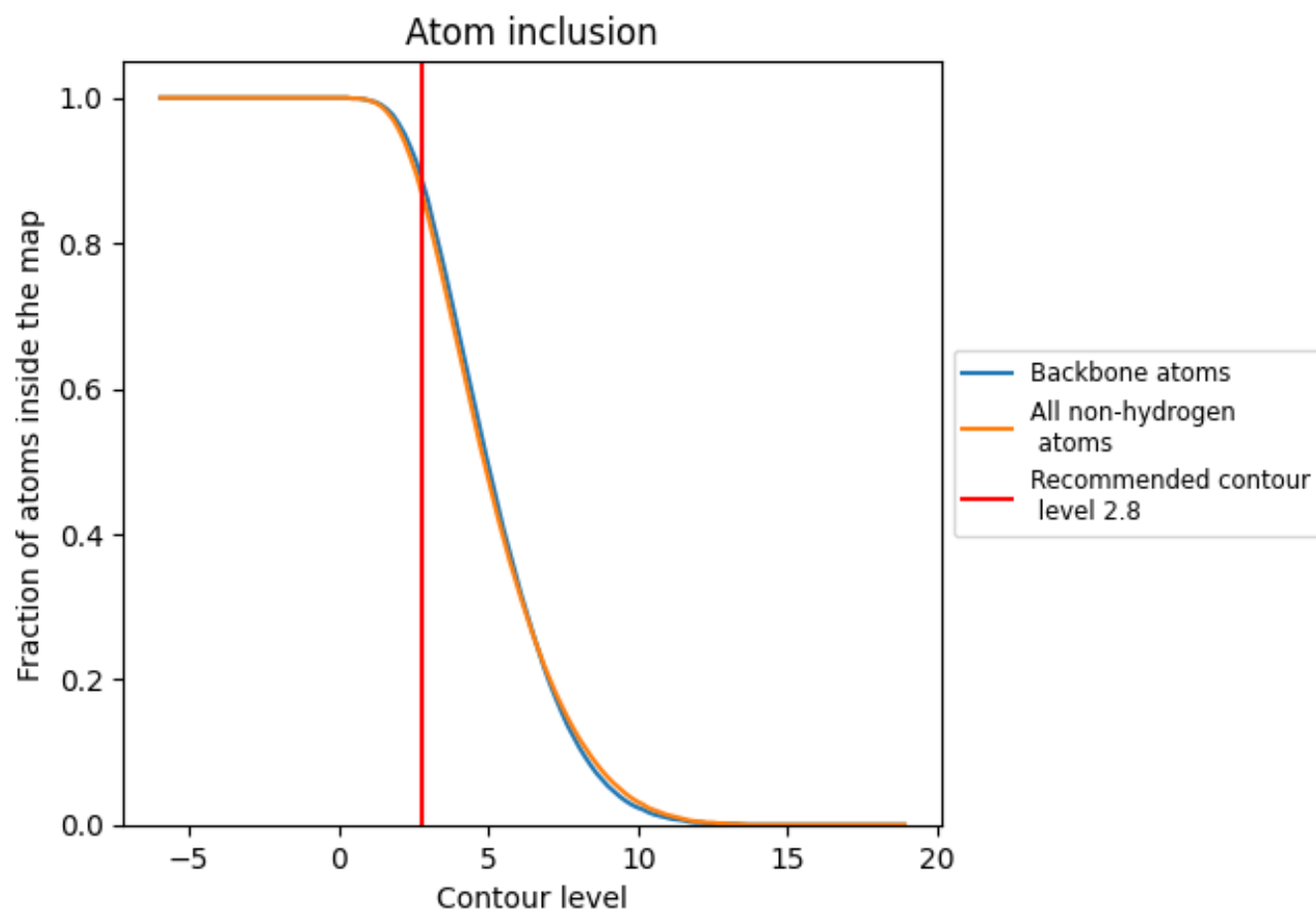
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.8).








































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8650	 0.4430
1A	 0.9340	 0.4630
1B	 0.9440	 0.4660
1C	 0.9550	 0.4640
1D	 0.9470	 0.4750
1E	 0.9000	 0.4810
1F	 0.8670	 0.4890
1G	 0.8040	 0.4900
1H	 0.6910	 0.4490
1I	 0.9180	 0.5080
1J	 0.6770	 0.4250
1K	 0.8130	 0.4780
1L	 0.9350	 0.4840
1M	 0.8100	 0.4610
1N	 0.7580	 0.4590
1O	 0.9010	 0.4930
1P	 0.8480	 0.4950
1Q	 0.9590	 0.4940
1R	 0.8950	 0.4630
1S	 0.9520	 0.5010
1T	 0.9370	 0.5120
1U	 0.8670	 0.4430
1V	 0.9220	 0.5130
1W	 0.3630	 0.2860
1X	 0.9450	 0.4770
1Y	 0.8070	 0.4380
1Z	 0.9190	 0.4670
1a	 0.8150	 0.4580
1b	 0.6130	 0.3670
1c	 0.9460	 0.5100
1d	 0.9550	 0.5110
1e	 0.7030	 0.4170
1f	 0.6710	 0.3970
1g	 0.8870	 0.4830
1h	 0.8750	 0.4510





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Chain	Atom inclusion	Q-score
li	 0.8010	 0.4450
lj	 0.9310	 0.5040
lk	 0.8620	 0.4760
ll	 0.9820	 0.4880
lm	 0.9320	 0.4580
ln	 0.5160	 0.3580
lo	 0.9830	 0.4880
lp	 0.9060	 0.4860
lq	 0.9580	 0.5010
sA	 0.4060	 0.3350
sB	 0.8830	 0.4620
sC	 0.7240	 0.4080
sD	 0.6730	 0.3820
sE	 0.8740	 0.4390
sH	 0.8890	 0.2080
sI	 0.9460	 0.3250
sJ	 0.9100	 0.3970
sK	 0.9810	 0.4740
sa	 0.9060	 0.4150
sb	 0.6630	 0.4110
sc	 0.7930	 0.4550
sd	 0.6500	 0.4050
se	 0.6980	 0.3690
sf	 0.5440	 0.3320
sg	 0.7250	 0.4120
sh	 0.4340	 0.2000
si	 0.3500	 0.3040
sj	 0.7580	 0.3860
sk	 0.5370	 0.3630
sl	 0.5290	 0.3930
sm	 0.7510	 0.3760
so	 0.8490	 0.4170
sp	 0.8470	 0.4580
sq	 0.4960	 0.2260
sr	 0.8450	 0.4470
ss	 0.6830	 0.4280
st	 0.6570	 0.3770
su	 0.7660	 0.4450
sv	 0.6680	 0.4240
sw	 0.5580	 0.3530
sx	 0.6760	 0.4200
sy	 0.7580	 0.4080

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*Continued from previous page...*

Chain	Atom inclusion	Q-score
SZ	 0.1580	 0.2410