wwPDB EM Validation Summary Report

Nov 9, 2026 – 11:08 AM EST

PDB ID	:	37KM / pdb_000037km
EMDB ID	:	EMD-78242
Title	:	5MP1(eIF1S) 48S complex - open head conformation
Authors	:	Zottig, X.; Huang, C.-Y.; Seraj, Z.; Grigorieff, N.; Korostelev, A.A.
Deposited on	:	2026-07-24
Resolution	:	2.70 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:

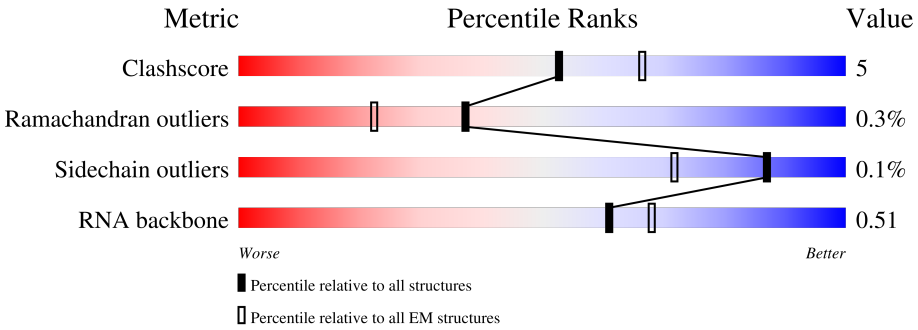
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

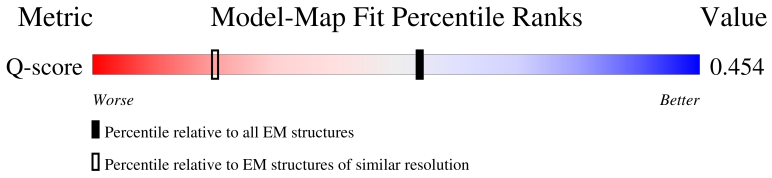
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

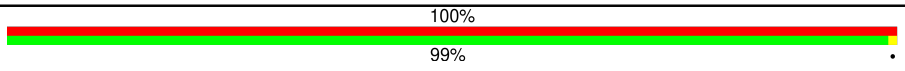
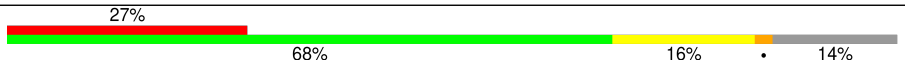
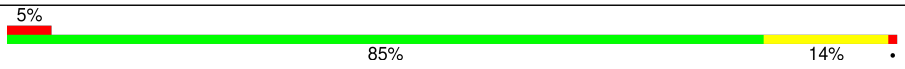
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





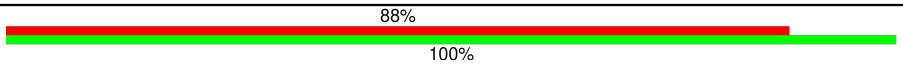
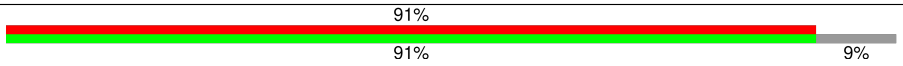
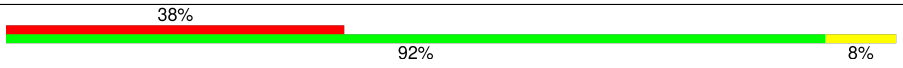
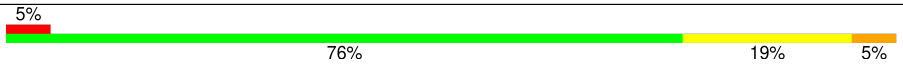
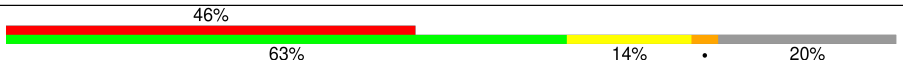
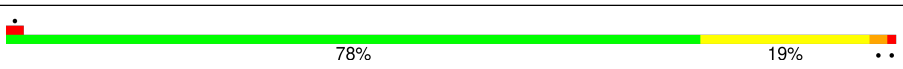
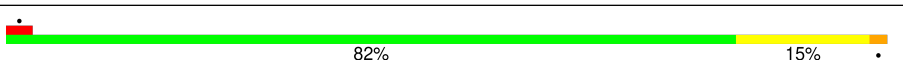
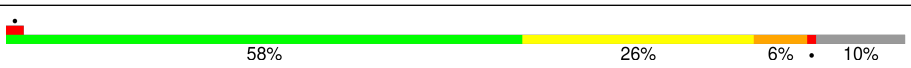
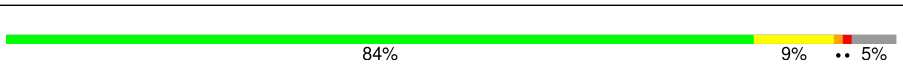
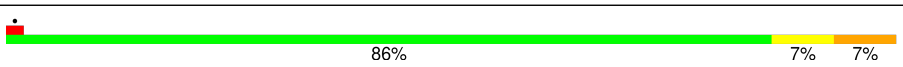
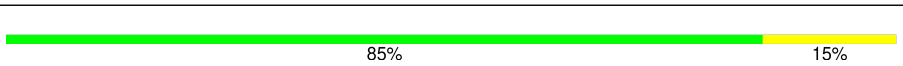
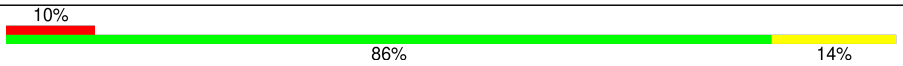
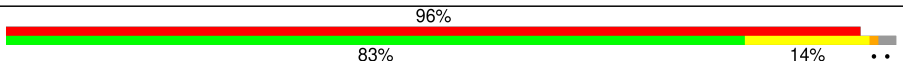
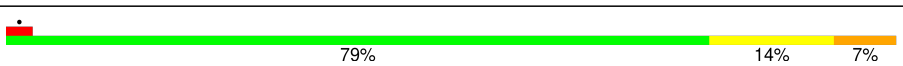
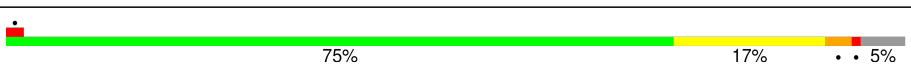
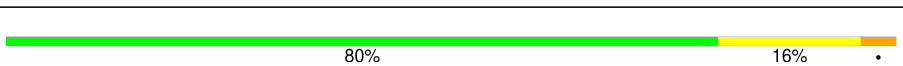
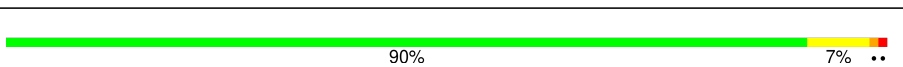
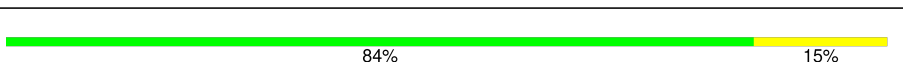
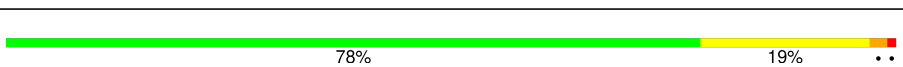
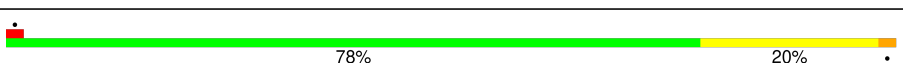
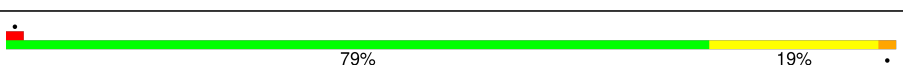
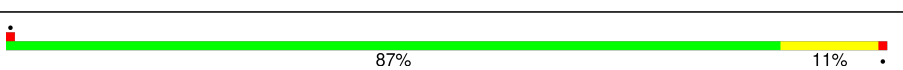
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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 <=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	0	156	
2	1	835	
3	3	110	

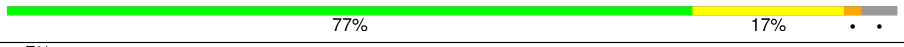
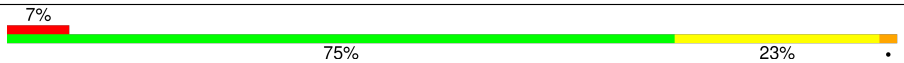
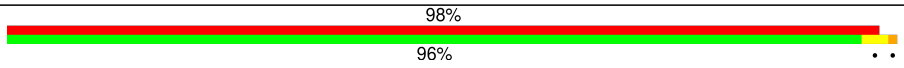
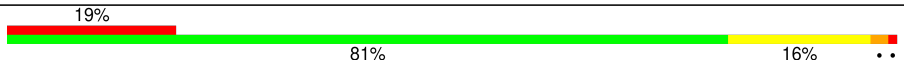
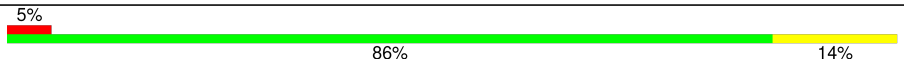
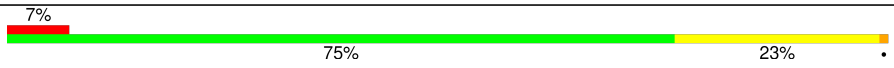
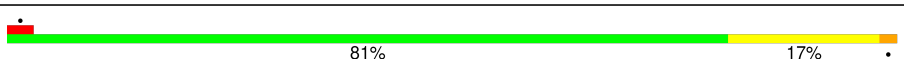
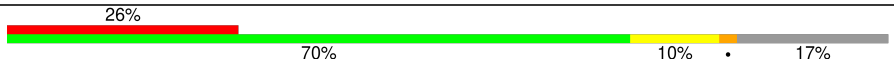
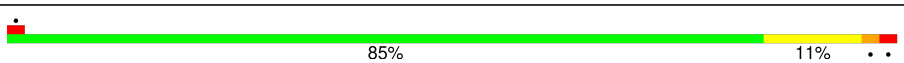
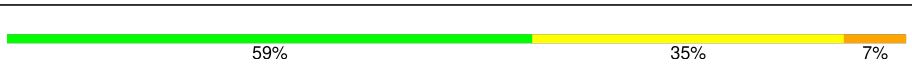
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	5	420	
5	6	55	
6	7	77	
7	8	119	
8	9	21	
9	A	716	
10	B	158	
11	C	405	
12	D	1869	
13	E	150	
14	F	59	
15	G	86	
16	H	29	
17	I	442	
18	J	102	
19	L	187	
20	M	81	
21	N	81	
22	O	220	
23	P	211	
24	Q	214	
25	S	230	
26	T	127	
27	U	131	
28	V	150	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	W	206	
30	Y	256	
31	Z	177	
32	a	140	
33	b	128	
34	c	129	
35	e	125	
36	f	189	
37	g	141	
38	h	227	
39	i	99	
40	j	56	
41	k	313	
42	l	142	
43	m	73	
44	n	142	
45	o	595	
46	q	122	
47	r	271	
48	s	76	
49	t	440	
50	w	103	
51	x	509	
52	y	61	
53	z	75	

2 Entry composition (i)

There are 54 unique types of molecules in this entry. The entry contains 114380 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	156	1171	736	208	220	7	0	0

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	718	5879	3694	1059	1089	37	0	0

- Molecule 3 is a protein called SUI1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	110	830	524	150	154	2	0	0

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	5	420	2091	1250	420	421	0	0

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	6	50	250	149	50	51	0	0

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	7	77	617	389	111	117	0	0

- Molecule 7 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	8	80	Total	C	N	O	0	0
			398	237	80	81		

- Molecule 8 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	21	Total	C	N	O	S	0	0
			205	125	55	22	3		

- Molecule 9 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	575	Total	C	N	O	S	0	0
			4568	2880	819	847	22		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	MET	LEU	conflict	UNP G1SMZ5
A	433	ASN	SER	conflict	UNP G1SMZ5
A	444	SER	ALA	conflict	UNP G1SMZ5

- Molecule 10 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	158	Total	C	N	O	S	0	0
			1281	809	237	226	9		

- Molecule 11 is a protein called eIF5-mimic protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	405	Total	C	N	O	S	0	0
			3283	2107	555	608	13		

- Molecule 12 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	1691	Total	C	N	O	P	0	0
			36103	16115	6485	11813	1690		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	142	Total	C	N	O	S	0	0
			1167	743	218	200	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 15 is a protein called Eukaryotic translation initiation factor 4C.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	86	Total	C	N	O	S	0	0
			701	445	125	127	4		

- Molecule 16 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	29	Total	C	N	O	P	0	0
			437	195	34	179	29		

- Molecule 17 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	435	Total	C	N	O	S	0	0
			3536	2272	615	632	17		

- Molecule 18 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	102	Total	C	N	O	S	0	0
			819	511	168	133	7		

- Molecule 19 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	178	Total	C	N	O	S	0	0
			1440	923	262	254	1		

- Molecule 20 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	81	Total	C	N	O	S	0	0
			632	397	116	112	7		

- Molecule 21 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	81	Total	C	N	O	S	0	0
			619	379	114	121	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	220	Total	C	N	O	S	0	0
			1704	1100	293	301	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	190	SER	-	insertion	UNP G1SWM1

- Molecule 23 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	211	Total	C	N	O	S	0	0
			1716	1088	307	307	14		

- Molecule 24 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	214	Total	C	N	O	S	0	0
			1696	1077	297	314	8		

- Molecule 25 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	230	Total	C	N	O	S	0	0
			1863	1164	371	321	7		

- Molecule 26 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	127	Total	C	N	O	S	0	0
			957	585	189	177	6		

- Molecule 27 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	131	Total	C	N	O	S	0	0
			1065	668	198	195	4		

- Molecule 28 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 29 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	198	Total	C	N	O	S	0	0
			1622	1017	319	281	5		

- Molecule 30 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	256	Total	C	N	O	S	0	0
			2034	1300	376	349	9		

- Molecule 31 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	177	Total	C	N	O	S	0	0
			1478	941	295	240	2		

- Molecule 32 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	140	Total	C	N	O	S	0	0
			1088	687	215	183	3		

- Molecule 33 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	128	Total	C	N	O	S	0	0
			1048	664	197	180	7		

- Molecule 34 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 35 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	125	Total	C	N	O	S	0	0
			1016	642	199	170	5		

- Molecule 36 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 37 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 38 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	227	Total	C	N	O	S	0	0
			1765	1124	317	316	8		

- Molecule 39 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	99	Total	C	N	O	S	0	0
			835	544	149	136	6		

- Molecule 40 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	56	Total	C	N	O	S	0	0
			467	291	95	75	6		

- Molecule 41 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	313	Total	C	N	O	S	0	0
			2437	1535	424	466	12		

- Molecule 42 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	142	Total	C	N	O	S	0	0
			1117	703	214	197	3		

- Molecule 43 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	73	Total	C	N	O	S	0	0
			586	374	108	103	1		

- Molecule 44 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	142	Total	C	N	O	S	0	0
			1177	737	239	200	1		

- Molecule 45 is a protein called ATP-binding cassette sub-family E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	595	Total	C	N	O	S	0	0
			4693	2995	802	865	31		

- Molecule 46 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	271	Total	C	N	O	S	0	0
			2018	1269	360	381	8		

- Molecule 48 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	76	Total	C	N	O	S	0	0
			620	390	119	104	7		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	440	Total	C	N	O	S	0	0
			3353	2131	588	617	17		

- Molecule 50 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	423	Total	C	N	O	S	0	0
			2847	1756	523	558	10		

- Molecule 52 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	61	Total	C	N	O	S	0	0
			477	290	93	92	2		

- Molecule 53 is a RNA chain called Initiator methionyl-tRNA.

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

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
54	J	1	Total Zn 1 1	0
54	j	1	Total Zn 1 1	0
54	s	1	Total Zn 1 1	0

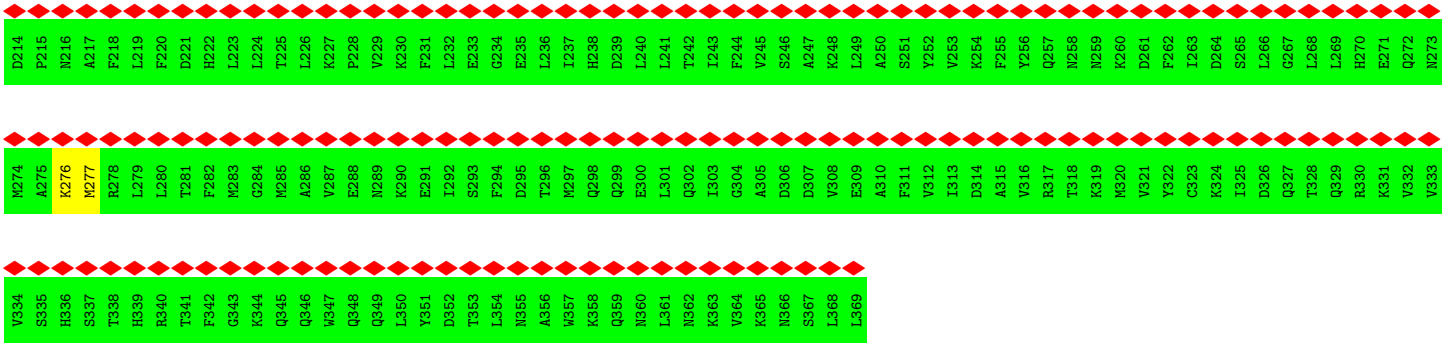
3 Residue-property plots (i)

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: Eukaryotic translation initiation factor 3 subunit M

Chain 0:

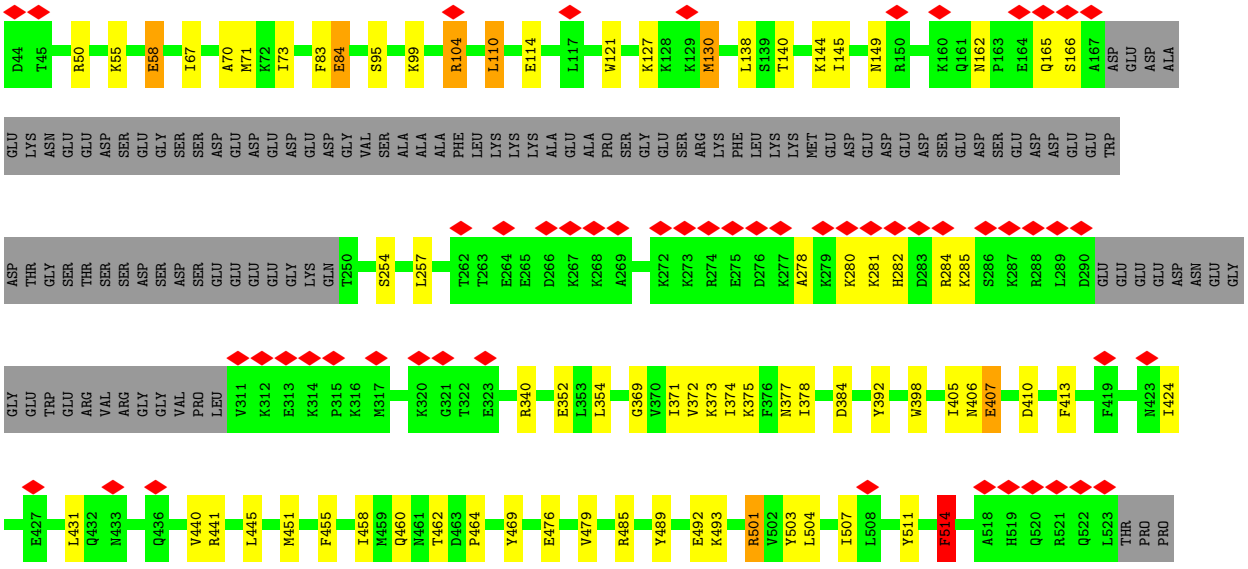


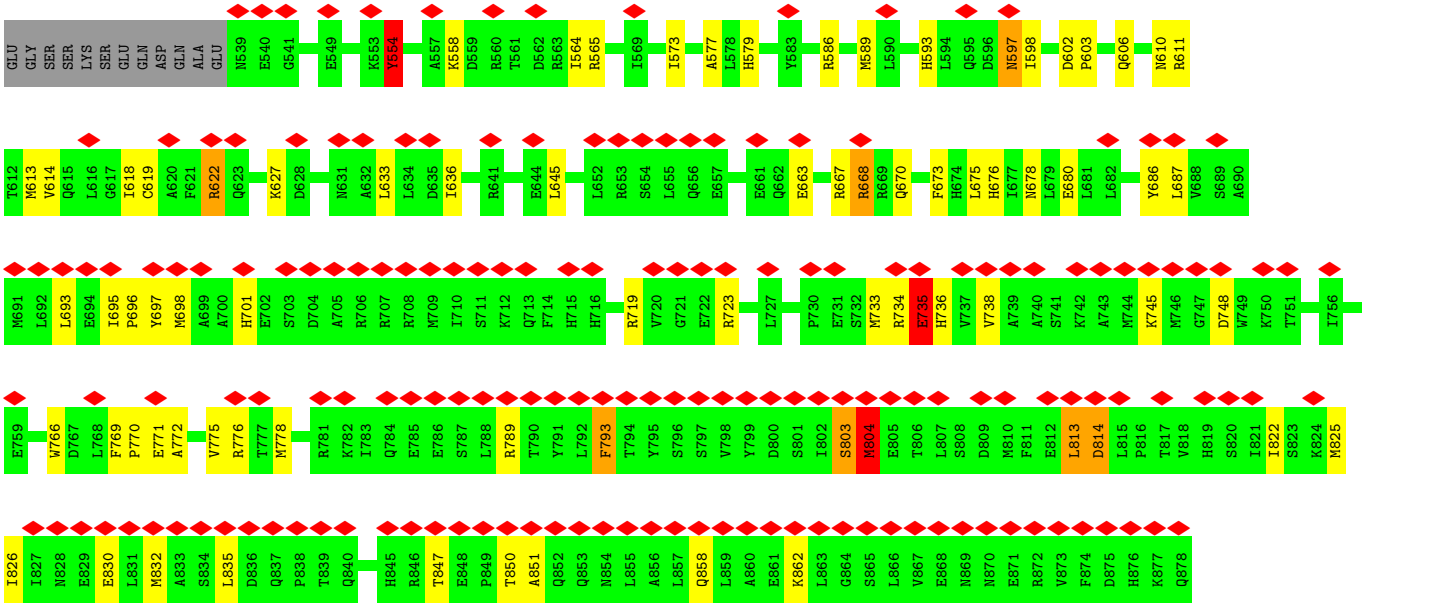


• Molecule 2: Eukaryotic translation initiation factor 3 subunit C

Chain 1:



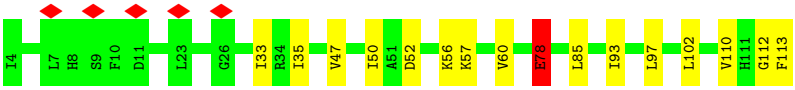




• Molecule 3: SUI1 domain-containing protein

Chain 3:

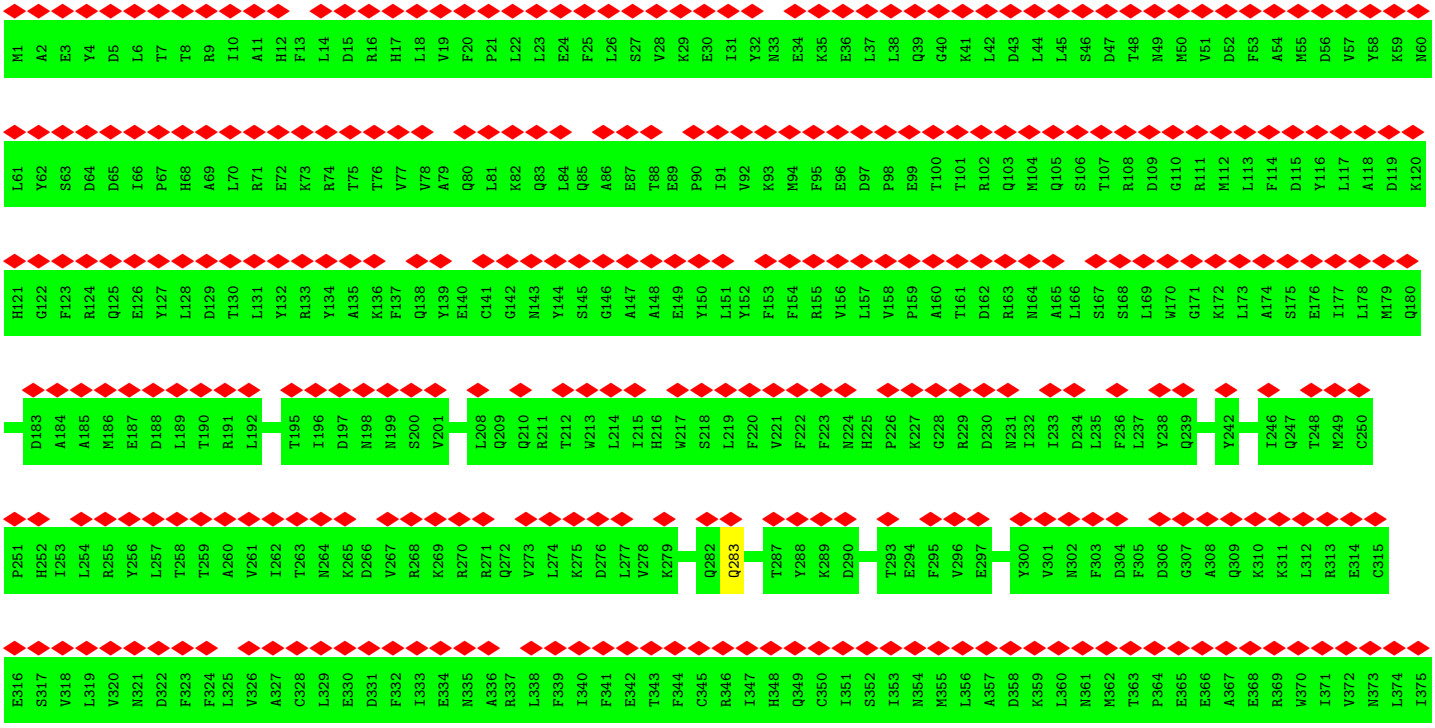


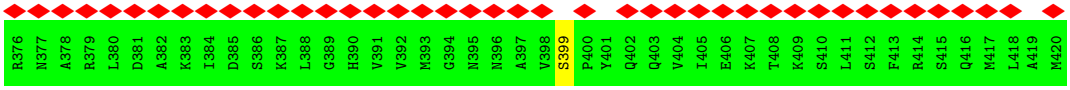


• Molecule 4: Eukaryotic translation initiation factor 3 subunit E

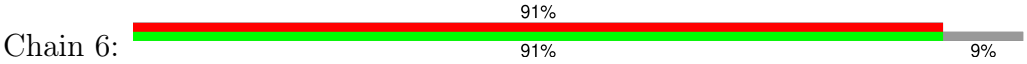
Chain 5:

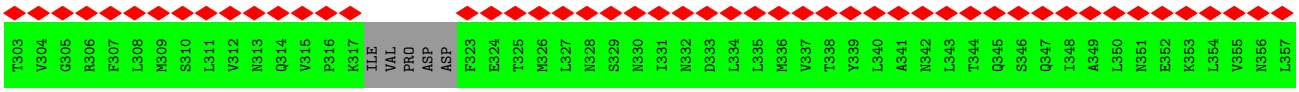




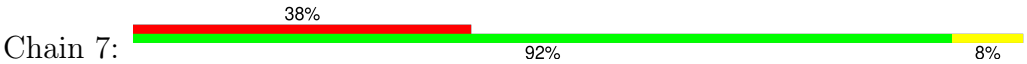


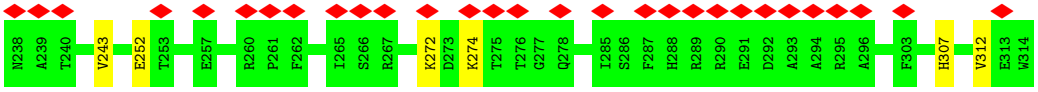
• Molecule 5: Eukaryotic translation initiation factor 3 subunit F





• Molecule 6: Eukaryotic translation initiation factor 3 subunit G





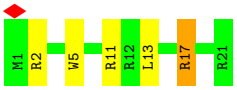
• Molecule 7: Eukaryotic translation initiation factor 3 subunit H





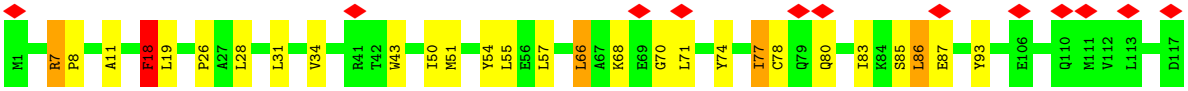
• Molecule 8: Small ribosomal subunit protein eS32

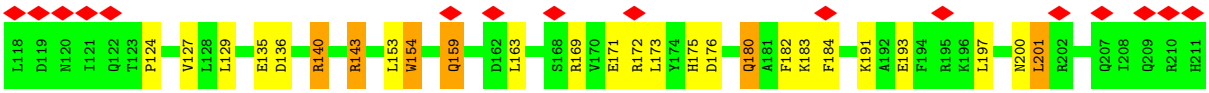


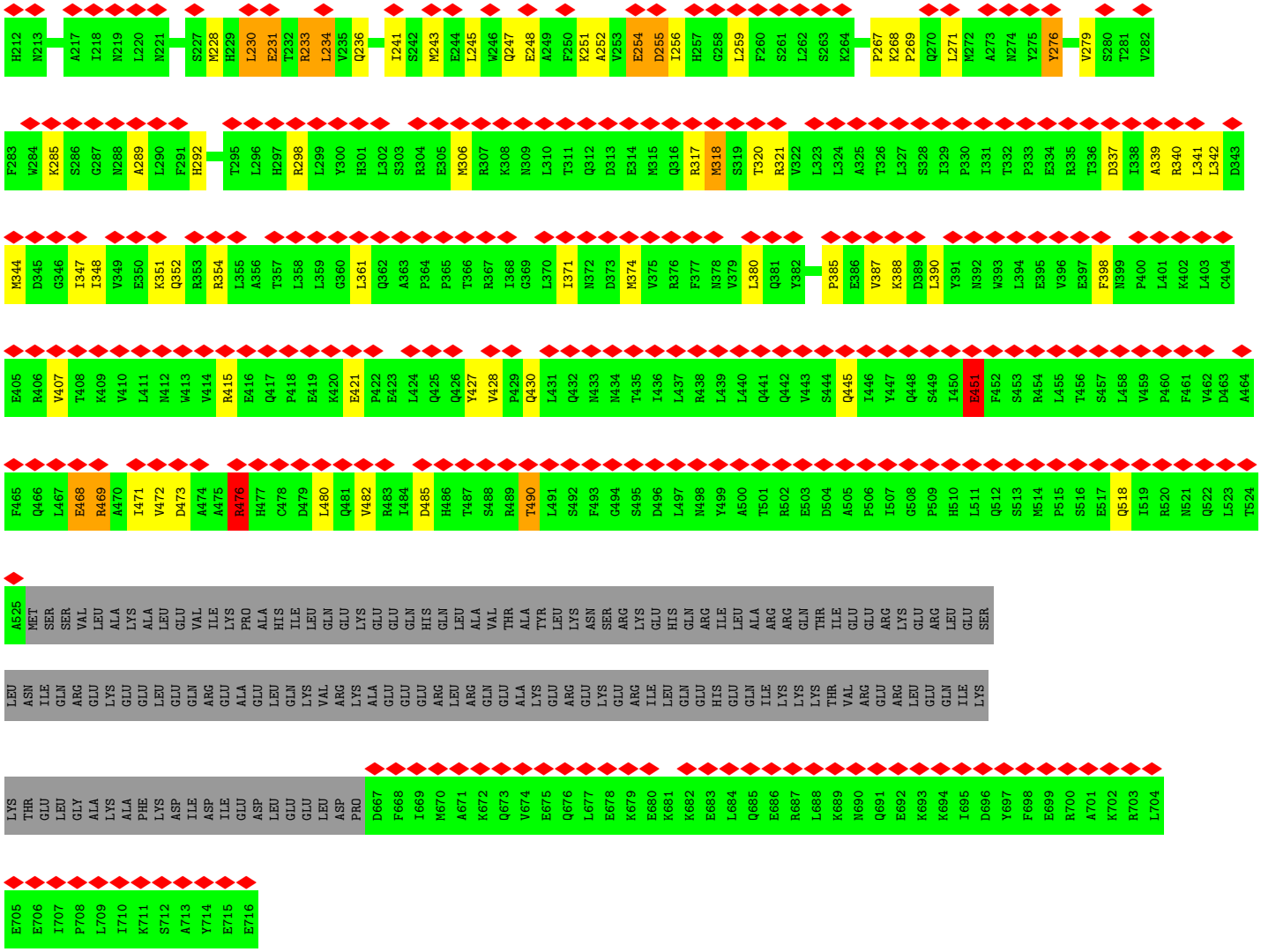


• Molecule 9: Eukaryotic translation initiation factor 3 subunit A





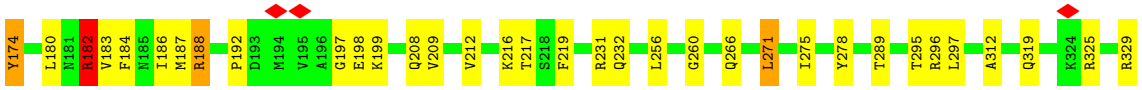




• Molecule 10: Eukaryotic translation initiation factor 2 subunit 2

Chain B:



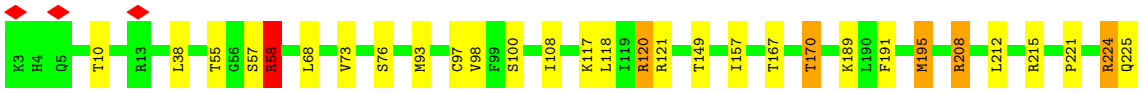


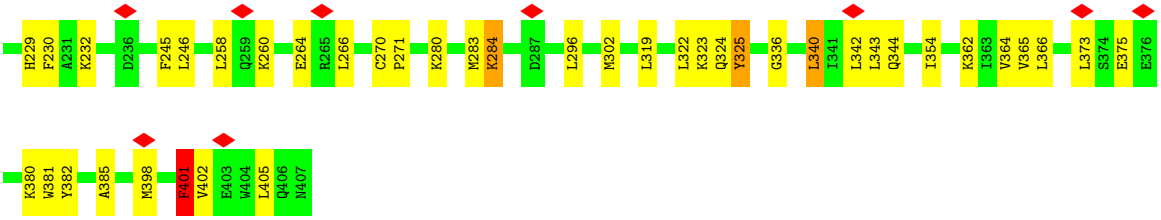


• Molecule 11: eIF5-mimic protein 1

Chain C:



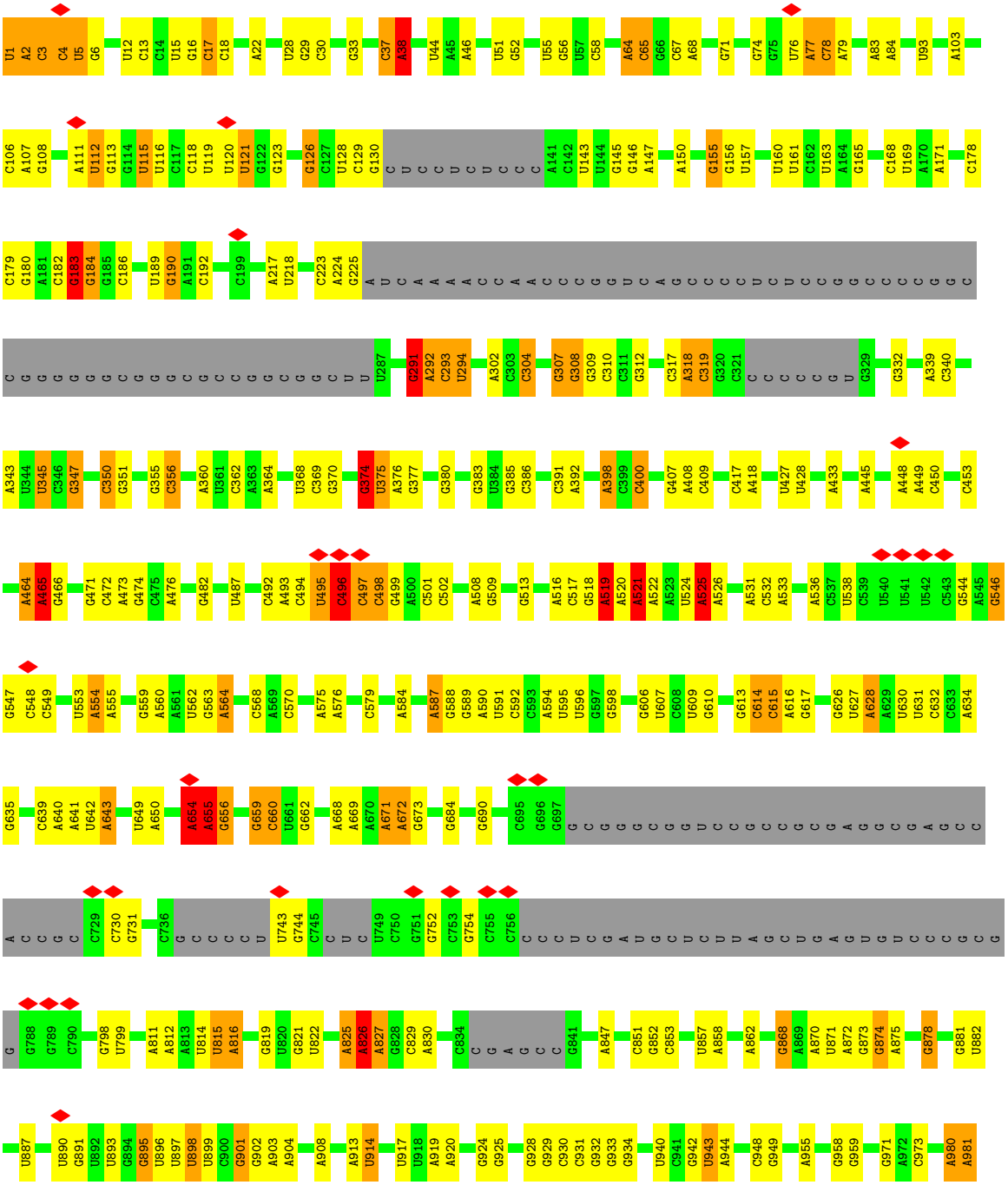


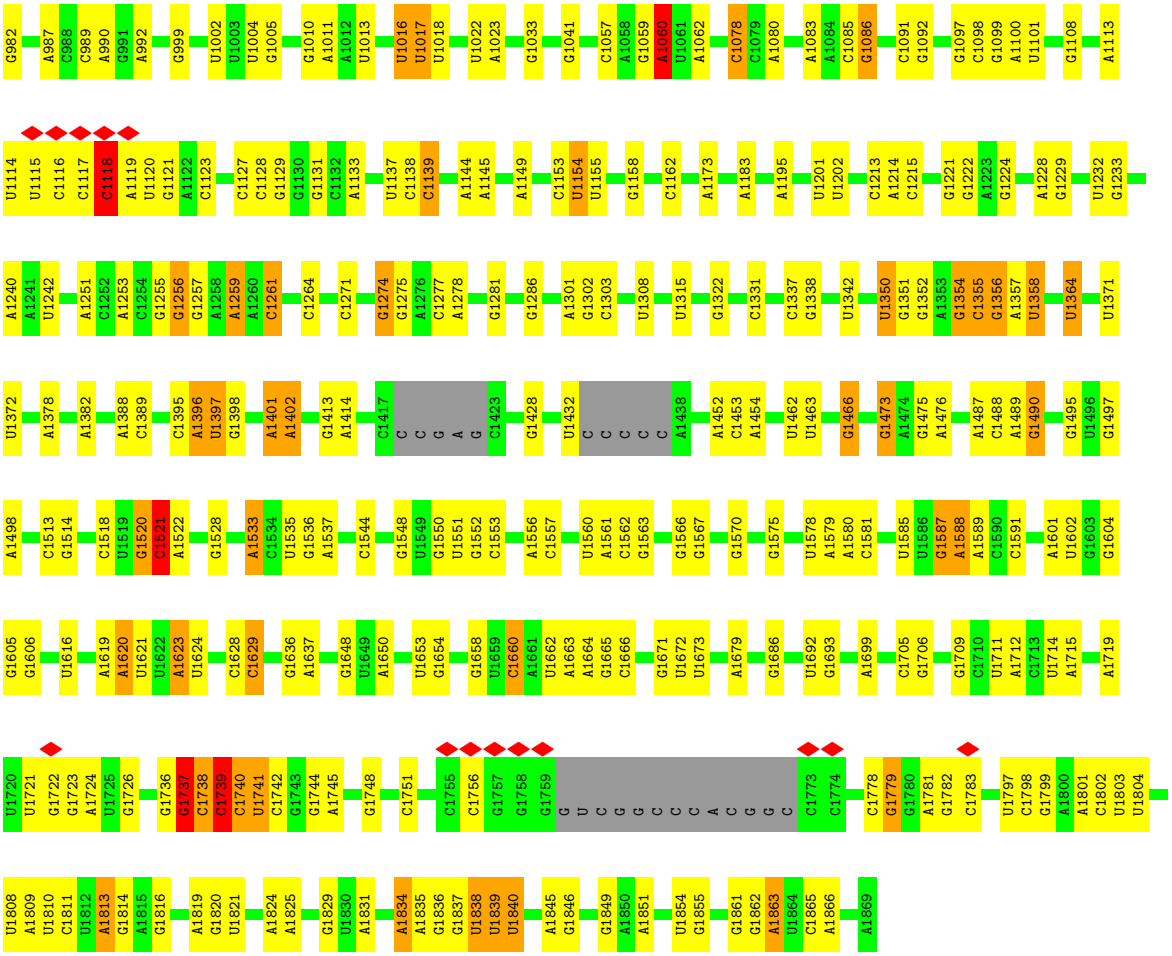


• Molecule 12: 18S ribosomal RNA

Chain D:







• Molecule 13: Small ribosomal subunit protein uS17

Chain E:

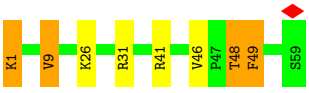




• Molecule 14: Small ribosomal subunit protein eS30

Chain F:





• Molecule 15: Eukaryotic translation initiation factor 4C

Chain G:

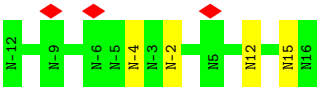




• Molecule 16: mRNA

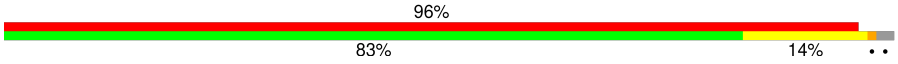
Chain H:

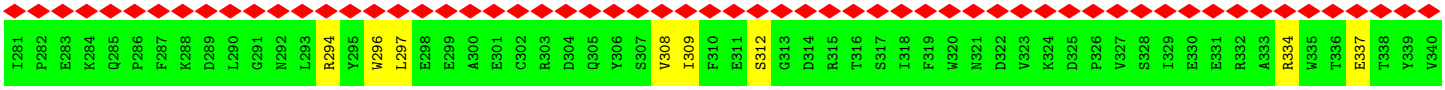


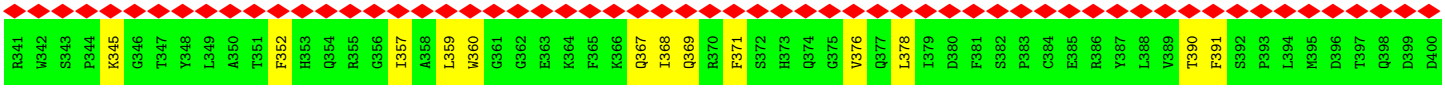


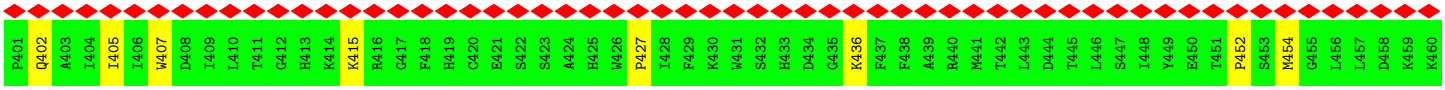
• Molecule 17: Eukaryotic translation initiation factor 3 subunit B

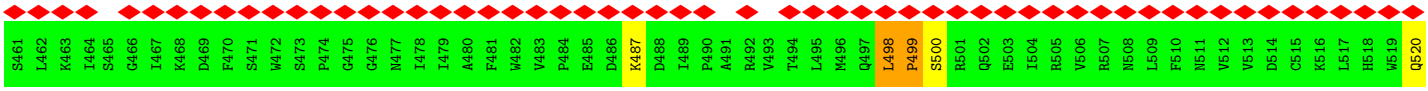
Chain I:

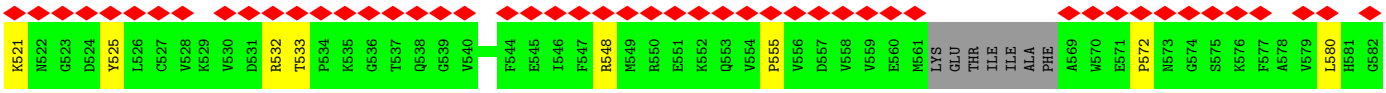


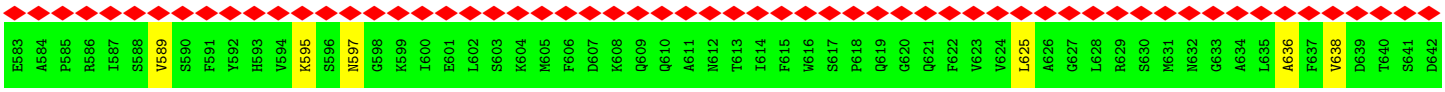


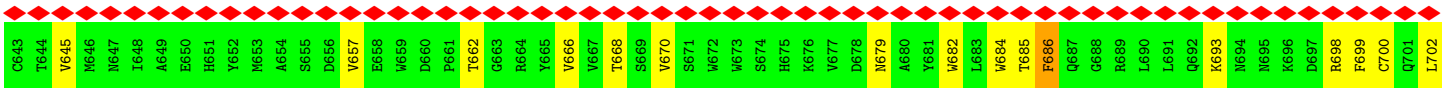


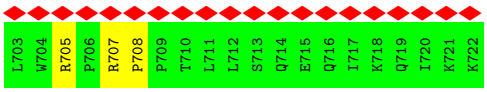








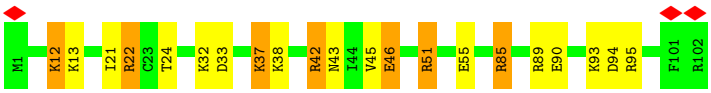




• Molecule 18: Small ribosomal subunit protein eS26

Chain J:

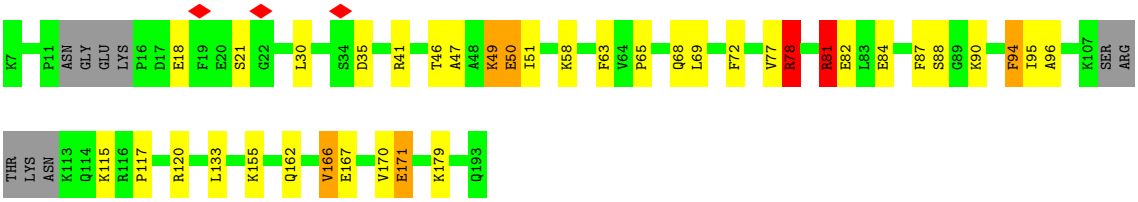




• Molecule 19: Small ribosomal subunit protein eS7

Chain L:





• Molecule 20: Small ribosomal subunit protein eS27

Chain M:





• Molecule 21: Small ribosomal subunit protein eS21

Chain N:

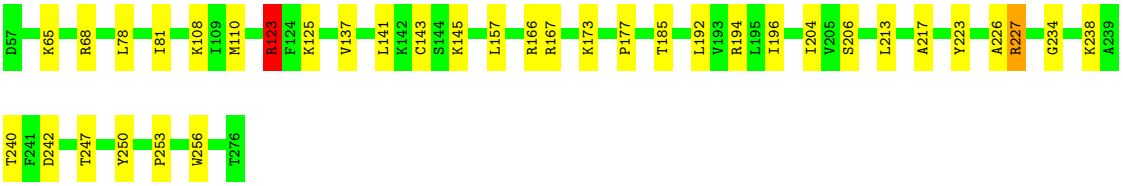




• Molecule 22: Small ribosomal subunit protein uS5

Chain O:

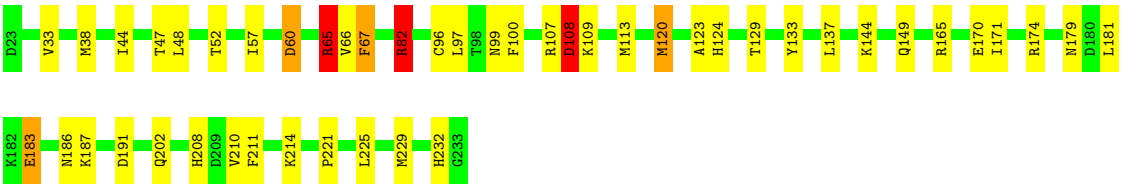




• Molecule 23: 40S ribosomal protein S3a

Chain P:



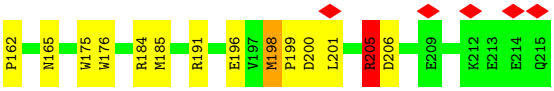


• Molecule 24: Small ribosomal subunit protein uS2

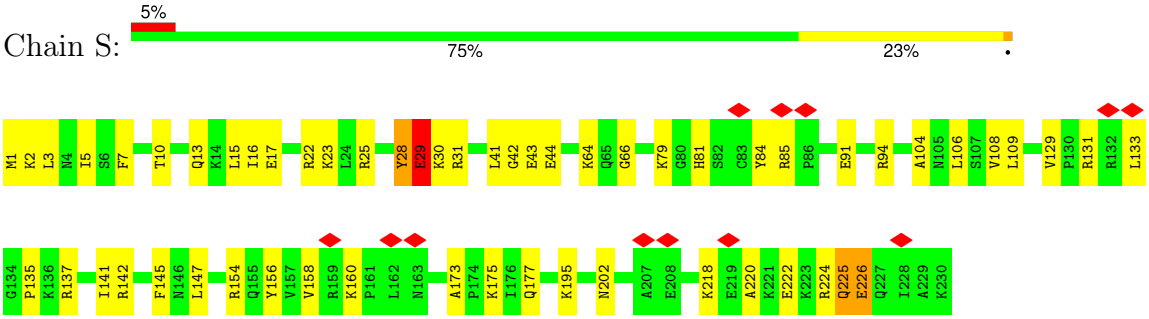
Chain Q:



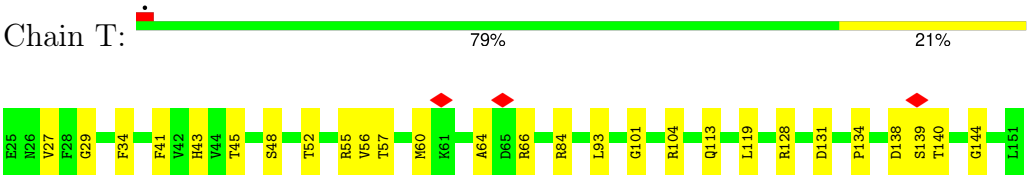




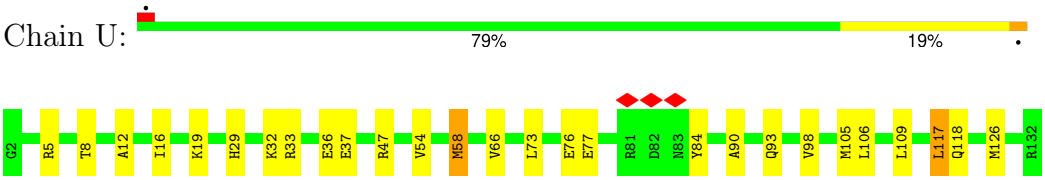
• Molecule 25: Small ribosomal subunit protein eS6



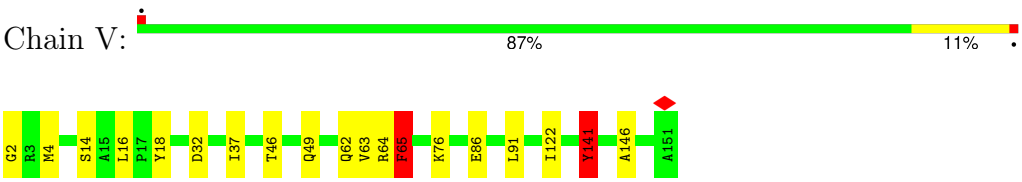
• Molecule 26: Small ribosomal subunit protein uS11



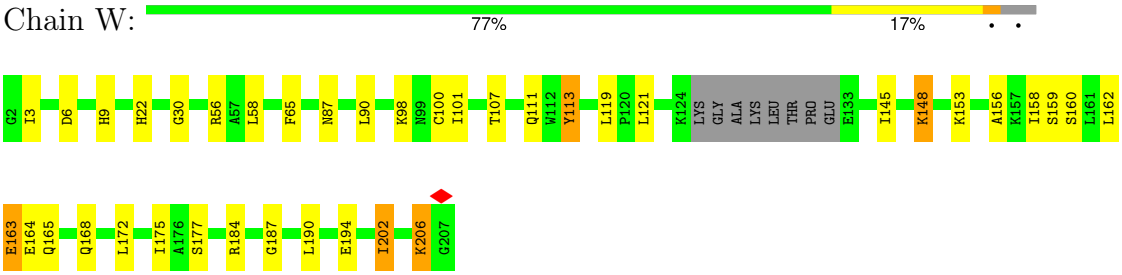
• Molecule 27: Small ribosomal subunit protein eS17



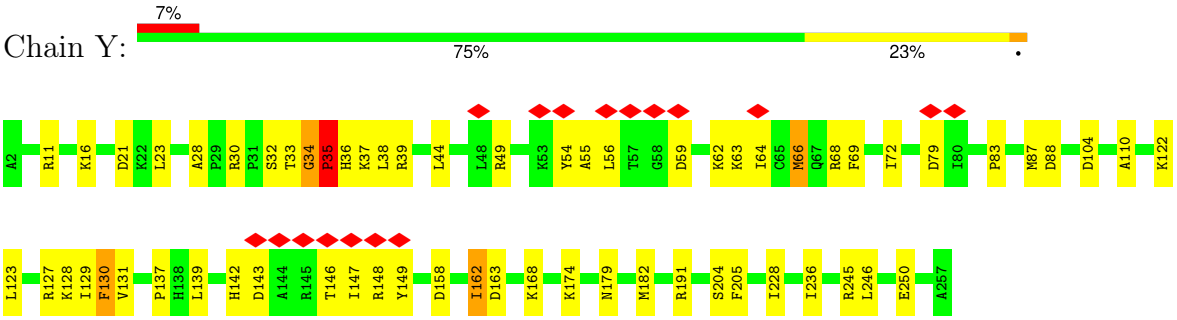
• Molecule 28: Small ribosomal subunit protein uS15



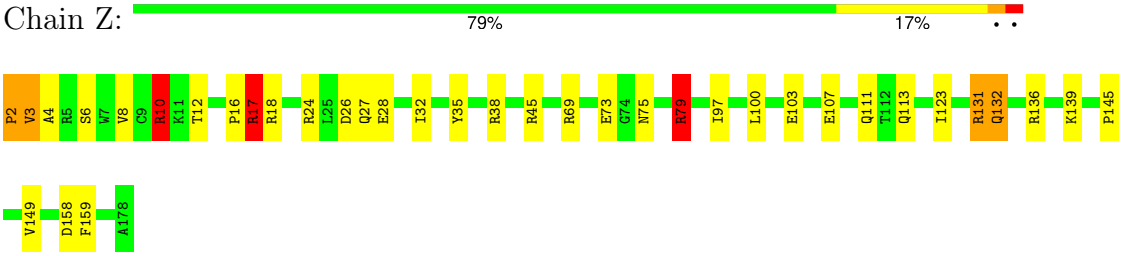
• Molecule 29: Small ribosomal subunit protein eS8



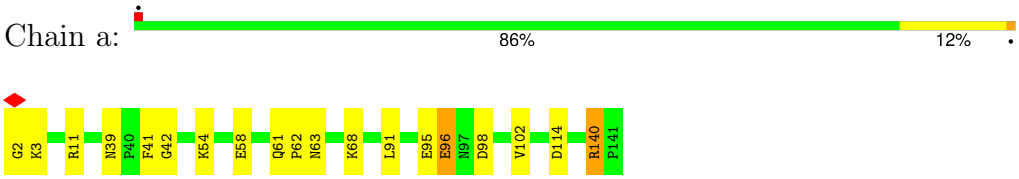
• Molecule 30: Small ribosomal subunit protein eS4



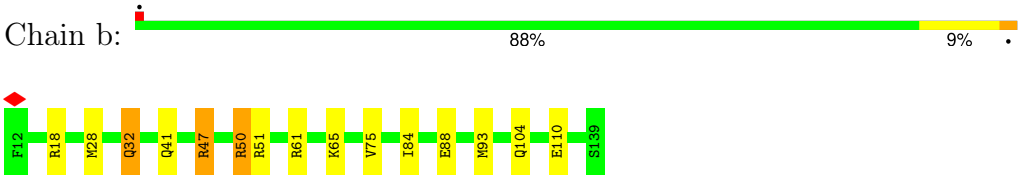
• Molecule 31: Small ribosomal subunit protein uS4



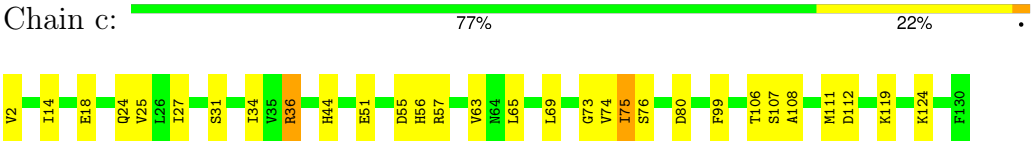
• Molecule 32: Small ribosomal subunit protein uS12



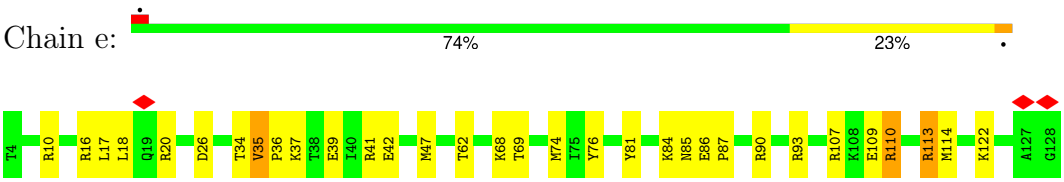
• Molecule 33: Small ribosomal subunit protein uS19



• Molecule 34: 40S ribosomal protein S15a

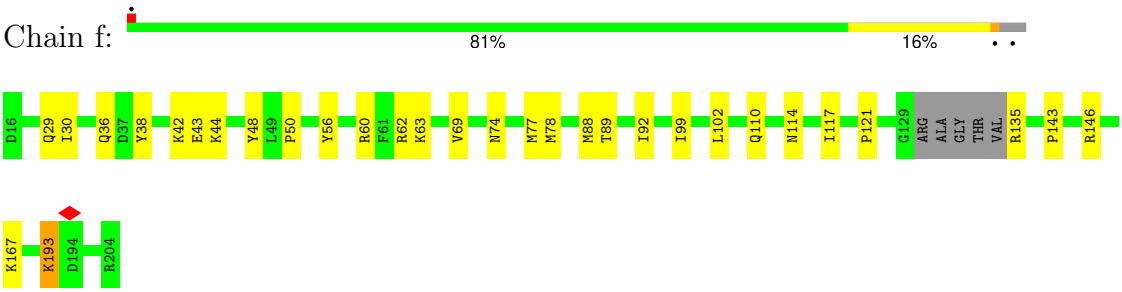


• Molecule 35: 40S ribosomal protein S24



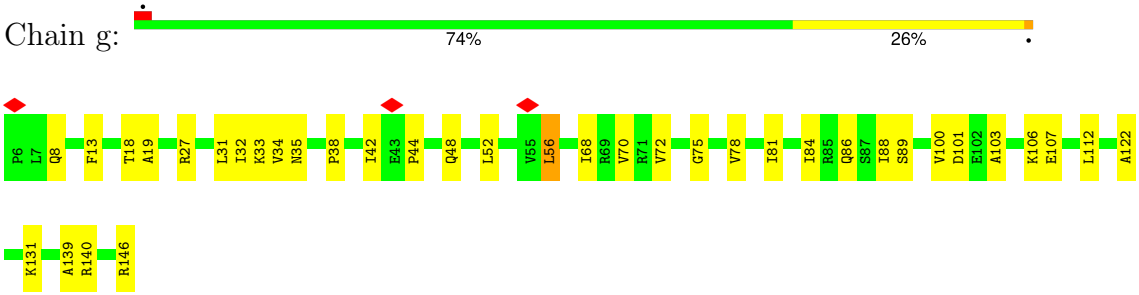
• Molecule 36: Small ribosomal subunit protein uS7

Chain f:



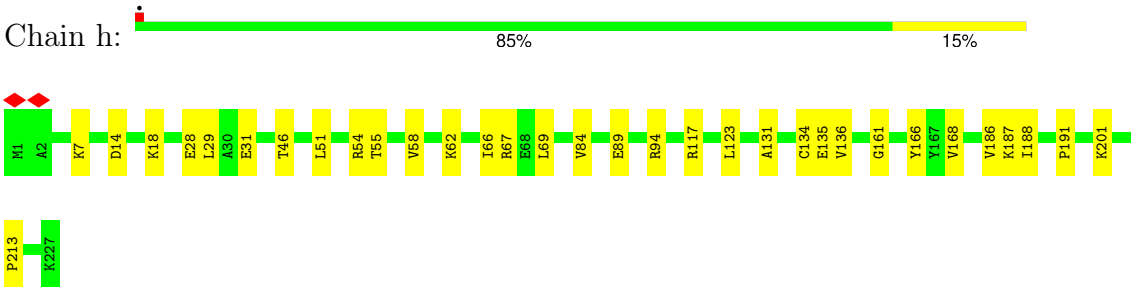
• Molecule 37: Small ribosomal subunit protein uS9

Chain g:



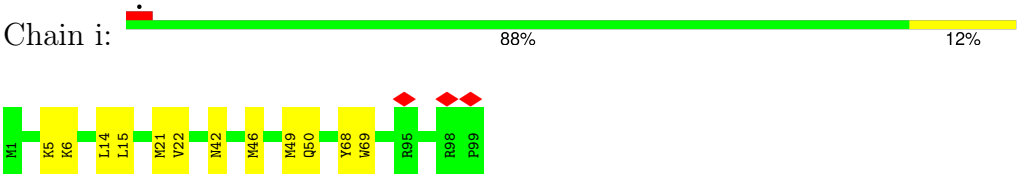
• Molecule 38: Small ribosomal subunit protein uS3

Chain h:



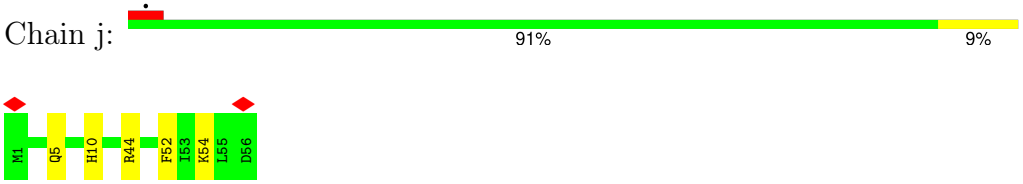
• Molecule 39: Small ribosomal subunit protein eS10

Chain i:



• Molecule 40: uS14

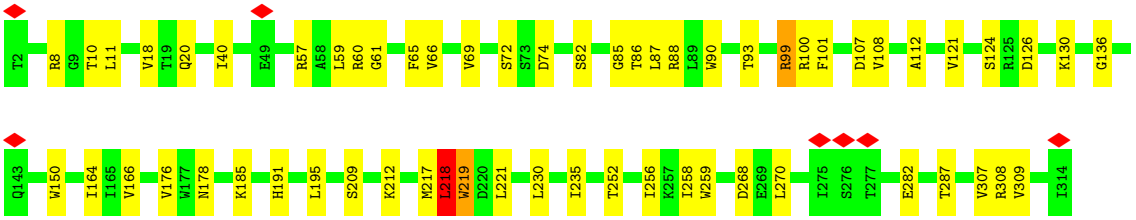
Chain j:



• Molecule 41: Receptor of activated protein C kinase 1

Chain k:

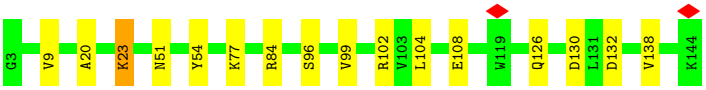




• Molecule 42: Small ribosomal subunit protein eS19

Chain l:

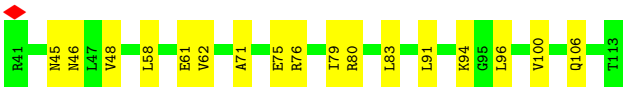




• Molecule 43: Small ribosomal subunit protein eS25

Chain m:

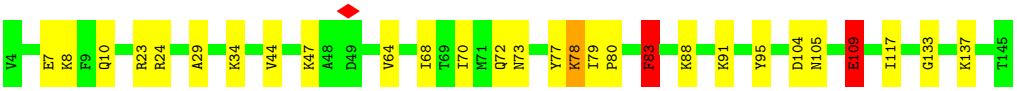




• Molecule 44: Small ribosomal subunit protein uS13

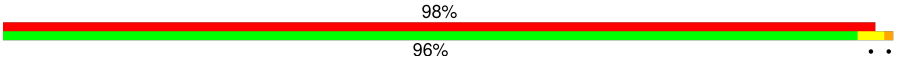
Chain n:

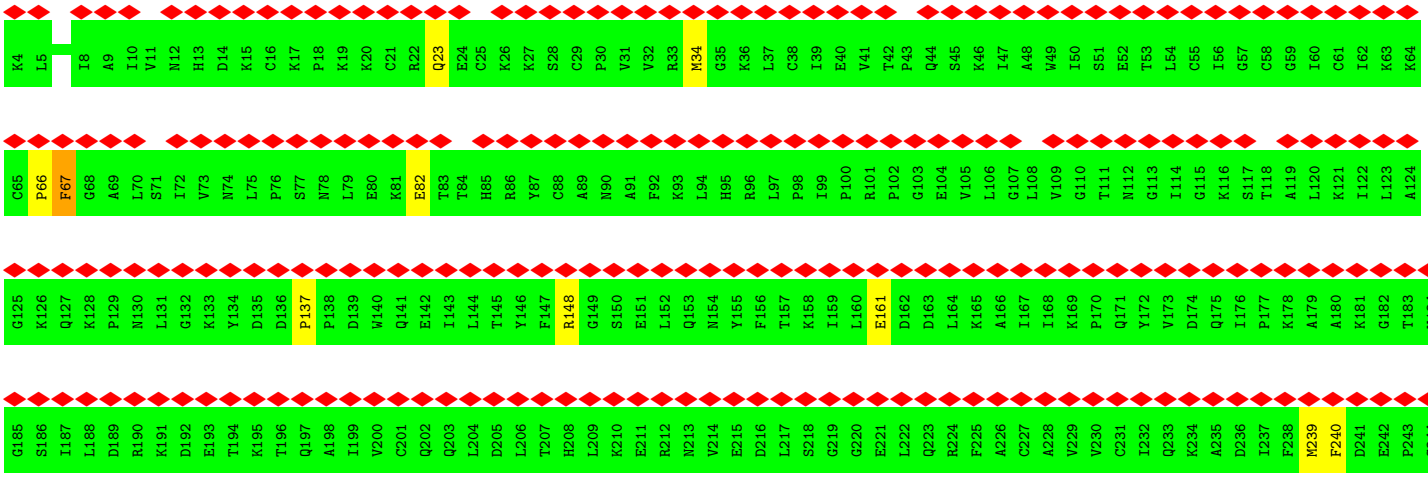


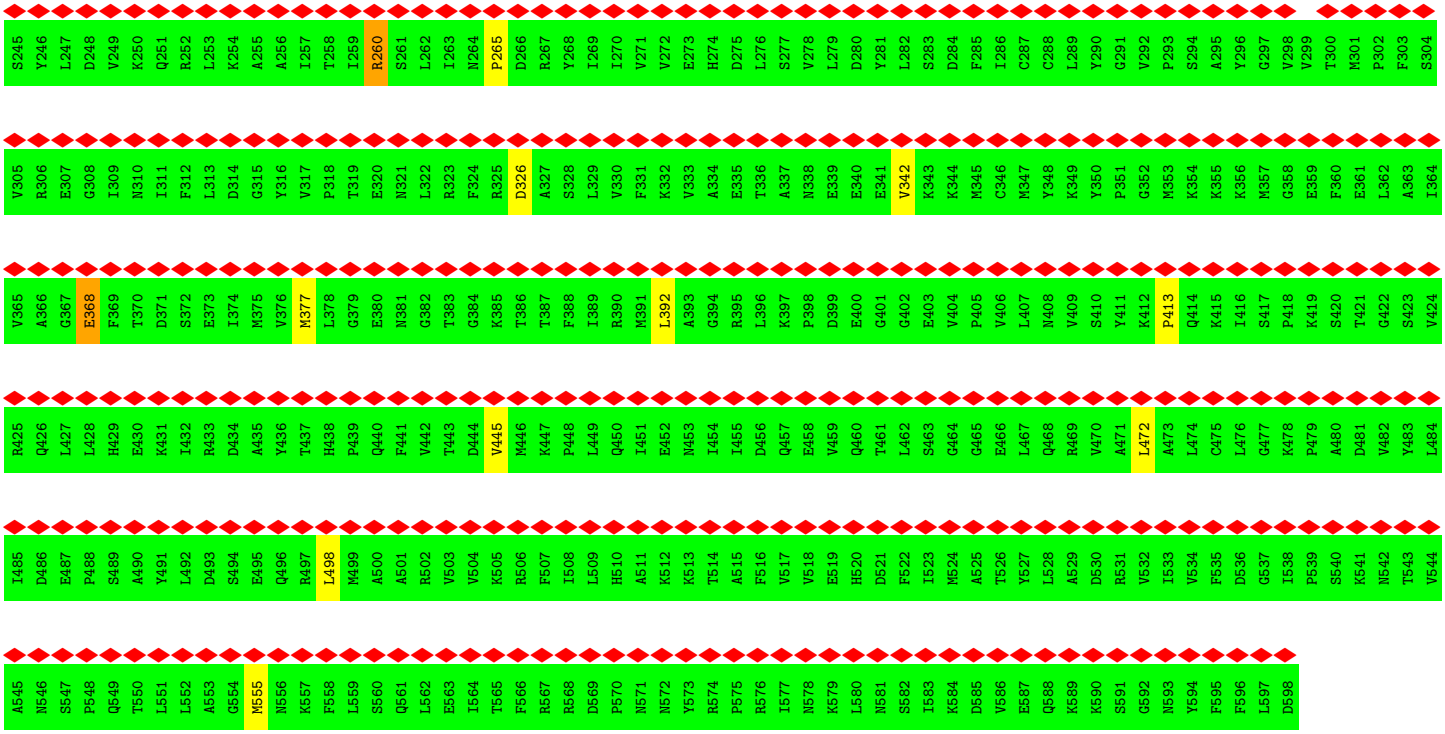


• Molecule 45: ATP-binding cassette sub-family E member 1

Chain o:



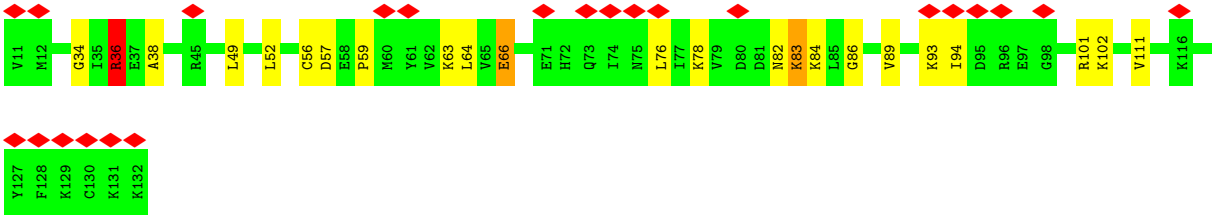




• Molecule 46: Small ribosomal subunit protein eS12

Chain q:

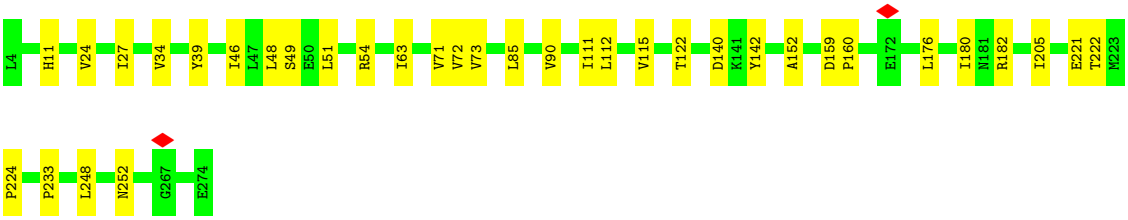




• Molecule 47: Eukaryotic translation initiation factor 2 subunit 1

Chain r:

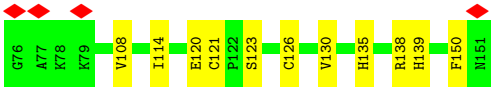




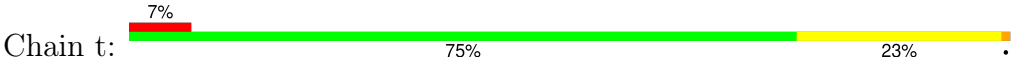
• Molecule 48: Ubiquitin-ribosomal protein eS31 fusion protein

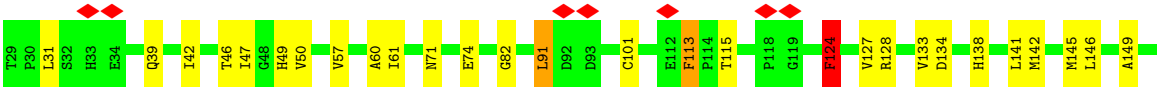
Chain s:



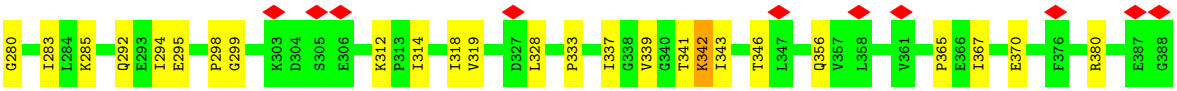


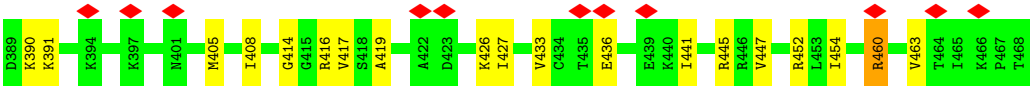
• Molecule 49: Eukaryotic translation initiation factor 2 subunit 3



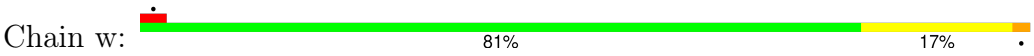


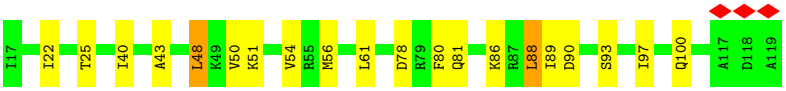






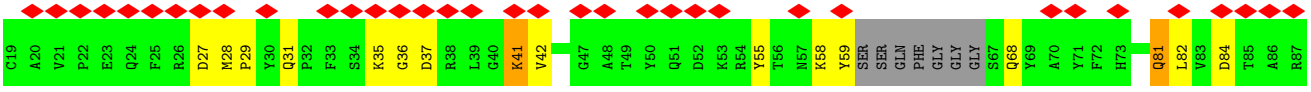
• Molecule 50: Small ribosomal subunit protein uS10

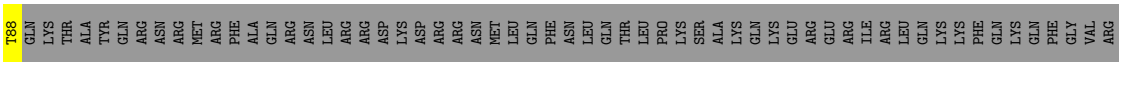


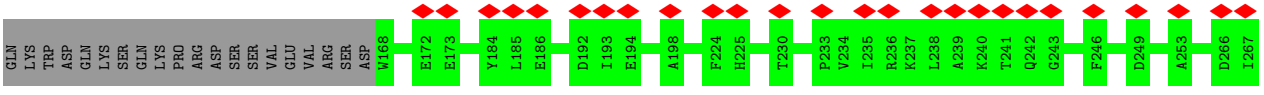


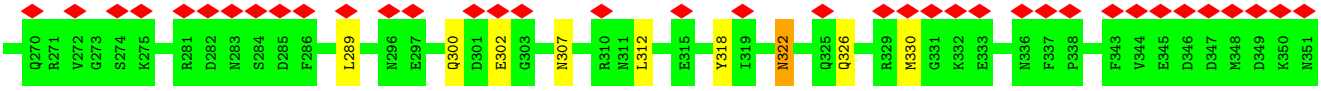
• Molecule 51: Eukaryotic translation initiation factor 3 subunit D

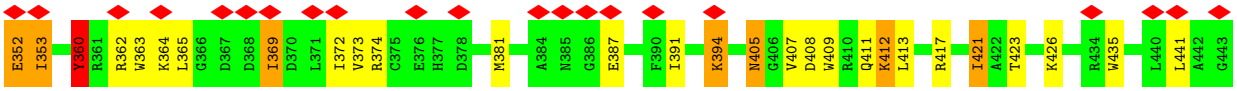


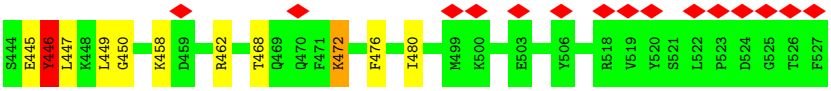








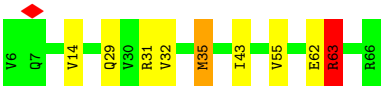




• Molecule 52: Small ribosomal subunit protein eS28

Chain y:





• Molecule 53: Initiator methionyl-tRNA

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112959	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 ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	15.276	Depositor
Minimum map value	-7.409	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.446	Depositor
Recommended contour level	1.35	Depositor
Map size (Å)	464.8, 464.8, 464.8	wwPDB
Map dimensions	560, 560, 560	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)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0	0.26	0/1187	0.71	8/1602 (0.5%)
2	1	0.47	5/5972 (0.1%)	0.90	42/8021 (0.5%)
3	3	0.65	2/843 (0.2%)	0.88	5/1134 (0.4%)
4	5	0.10	0/2090	0.28	0/2917
5	6	0.13	0/248	0.23	0/342
6	7	0.18	0/629	0.52	0/846
7	8	0.15	0/396	0.27	0/548
8	9	0.40	0/206	1.02	2/260 (0.8%)
9	A	0.41	4/4651 (0.1%)	0.99	55/6301 (0.9%)
10	B	0.46	1/1302 (0.1%)	1.08	12/1746 (0.7%)
11	C	0.42	2/3342 (0.1%)	0.86	19/4493 (0.4%)
12	D	0.61	0/40369	0.98	179/62910 (0.3%)
13	E	0.54	1/1187 (0.1%)	0.74	4/1585 (0.3%)
14	F	0.46	1/478 (0.2%)	1.11	8/628 (1.3%)
15	G	0.48	0/710	0.73	0/947
17	I	0.25	0/3640	0.52	2/4937 (0.0%)
18	J	0.86	4/833 (0.5%)	1.96	27/1116 (2.4%)
19	L	0.51	0/1461	1.24	25/1953 (1.3%)
20	M	0.69	2/645 (0.3%)	1.09	5/864 (0.6%)
21	N	0.51	0/625	0.80	5/835 (0.6%)
22	O	0.49	0/1738	0.60	2/2345 (0.1%)
23	P	0.47	1/1743 (0.1%)	0.89	13/2330 (0.6%)
24	Q	0.54	1/1733 (0.1%)	0.86	10/2353 (0.4%)
25	S	0.47	1/1886 (0.1%)	1.21	26/2510 (1.0%)
26	T	0.41	1/969 (0.1%)	0.88	4/1298 (0.3%)
27	U	0.43	0/1079	1.04	10/1447 (0.7%)
28	V	0.46	1/1232 (0.1%)	0.63	4/1656 (0.2%)
29	W	0.56	0/1649	0.95	14/2196 (0.6%)
30	Y	0.41	0/2075	0.76	6/2790 (0.2%)
31	Z	0.51	4/1503 (0.3%)	1.04	16/2008 (0.8%)
32	a	0.40	0/1106	0.74	3/1476 (0.2%)
33	b	0.45	0/1069	0.87	6/1427 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
34	c	0.48	0/1051	0.74	0/1406
35	e	0.50	1/1033 (0.1%)	1.01	7/1371 (0.5%)
36	f	0.37	0/1481	0.57	2/1988 (0.1%)
37	g	0.50	1/1142 (0.1%)	0.71	1/1528 (0.1%)
38	h	0.33	0/1793	0.52	3/2412 (0.1%)
39	i	0.52	0/860	0.75	5/1159 (0.4%)
40	j	0.50	0/478	0.53	0/633
41	k	0.43	0/2494	0.87	15/3394 (0.4%)
42	l	0.39	0/1137	0.54	1/1522 (0.1%)
43	m	0.57	0/592	0.96	5/794 (0.6%)
44	n	0.54	1/1195 (0.1%)	1.23	15/1599 (0.9%)
45	o	0.33	0/4780	0.77	19/6452 (0.3%)
46	q	0.50	1/960 (0.1%)	1.19	9/1286 (0.7%)
47	r	0.39	0/2047	0.55	1/2775 (0.0%)
48	s	0.51	0/632	0.64	1/834 (0.1%)
49	t	0.38	1/3409 (0.0%)	0.92	22/4609 (0.5%)
50	w	0.32	0/827	0.92	6/1110 (0.5%)
51	x	0.55	5/2890 (0.2%)	1.16	38/3946 (1.0%)
52	y	0.63	1/479 (0.2%)	1.55	10/641 (1.6%)
53	z	0.53	0/1795	0.95	5/2798 (0.2%)
All	All	0.51	42/119671 (0.0%)	0.92	677/170078 (0.4%)

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
2	1	0	14
3	3	0	1
8	9	0	1
9	A	0	8
10	B	0	2
11	C	0	6
13	E	0	2
14	F	0	2
17	I	0	2
18	J	0	6
19	L	0	6
20	M	0	2
21	N	0	2
22	O	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
23	P	0	6
24	Q	0	3
25	S	0	5
26	T	0	2
28	V	0	3
29	W	0	1
30	Y	0	4
31	Z	0	4
32	a	0	2
33	b	0	3
34	c	0	1
35	e	0	3
36	f	0	1
37	g	0	1
41	k	0	1
42	l	0	1
43	m	0	2
44	n	0	3
45	o	0	5
46	q	0	1
49	t	0	5
51	x	0	4
52	y	0	2
All	All	0	121

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	407	GLU	CG-CD	-8.80	1.30	1.52
2	1	804	MET	CB-CG	-8.54	1.26	1.52
18	J	85	ARG	CB-CG	-7.46	1.30	1.52
11	C	58	ARG	CB-CG	-7.10	1.31	1.52
25	S	17	GLU	CG-CD	-6.91	1.34	1.52

The worst 5 of 677 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
52	y	63	ARG	CB-CG-CD	22.05	162.03	111.30
51	x	462	ARG	CA-CB-CG	20.88	155.86	114.10
41	k	99	ARG	CG-CD-NE	20.58	157.27	112.00
2	1	407	GLU	CA-CB-CG	18.32	150.73	114.10
12	D	1839	U	O4'-C1'-N1	18.25	121.28	108.50

There are no chirality outliers.

5 of 121 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	104	ARG	Sidechain
2	1	407	GLU	Sidechain
2	1	501	ARG	Sidechain
2	1	514	PHE	Sidechain
2	1	84	GLU	Sidechain

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	0	1171	0	1079	0	0
2	1	5879	0	5975	89	0
3	3	830	0	793	7	0
4	5	2091	0	918	1	0
5	6	250	0	104	0	0
6	7	617	0	600	4	0
7	8	398	0	176	0	0
8	9	205	0	250	3	0
9	A	4568	0	4470	73	0
10	B	1281	0	1329	20	0
11	C	3283	0	3346	43	0
12	D	36103	0	18234	268	0
13	E	1167	0	1233	12	0
14	F	473	0	527	8	0
15	G	701	0	719	9	0
16	H	437	0	222	3	0
17	I	3536	0	3404	35	0
18	J	819	0	871	9	0
19	L	1440	0	1533	19	0
20	M	632	0	657	12	0
21	N	619	0	617	6	0
22	O	1704	0	1798	22	0
23	P	1716	0	1785	29	0
24	Q	1696	0	1696	30	0
25	S	1863	0	2018	29	0
26	T	957	0	982	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	U	1065	0	1118	17	0
28	V	1208	0	1294	18	0
29	W	1622	0	1696	25	0
30	Y	2034	0	2132	50	0
31	Z	1478	0	1589	24	0
32	a	1088	0	1154	14	0
33	b	1048	0	1091	7	0
34	c	1034	0	1080	20	0
35	e	1016	0	1086	24	0
36	f	1461	0	1511	23	0
37	g	1124	0	1193	23	0
38	h	1765	0	1863	19	0
39	i	835	0	861	5	0
40	j	467	0	460	5	0
41	k	2437	0	2393	37	0
42	l	1117	0	1152	9	0
43	m	586	0	640	9	0
44	n	1177	0	1233	18	0
45	o	4693	0	4826	3	0
46	q	950	0	987	15	0
47	r	2018	0	1884	25	0
48	s	620	0	642	7	0
49	t	3353	0	3505	64	0
50	w	817	0	882	14	0
51	x	2847	0	2220	44	0
52	y	477	0	499	7	0
53	z	1604	0	816	9	0
54	J	1	0	0	0	0
54	j	1	0	0	0	0
54	s	1	0	0	0	0
All	All	114380	0	95143	1108	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 5.

The worst 5 of 1108 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)
2:1:804:MET:HE1	2:1:822:ILE:HD13	1.43	0.99
12:D:925:G:H1	12:D:1017:U:H3	1.14	0.94
47:r:221:GLU:O	47:r:222:THR:HG22	1.67	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:1033:G:H1	12:D:1080:A:HO2'	1.24	0.85
32:a:98:ASP:OD2	32:a:140:ARG:NH2	2.09	0.84

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	0	154/156 (99%)	149 (97%)	5 (3%)	0	100 100
2	1	710/835 (85%)	696 (98%)	14 (2%)	0	100 100
3	3	108/110 (98%)	93 (86%)	13 (12%)	2 (2%)	6 17
4	5	418/420 (100%)	406 (97%)	11 (3%)	1 (0%)	43 68
5	6	46/55 (84%)	45 (98%)	1 (2%)	0	100 100
6	7	75/77 (97%)	71 (95%)	4 (5%)	0	100 100
7	8	76/119 (64%)	75 (99%)	1 (1%)	0	100 100
8	9	19/21 (90%)	19 (100%)	0	0	100 100
9	A	571/716 (80%)	554 (97%)	17 (3%)	0	100 100
10	B	156/158 (99%)	151 (97%)	4 (3%)	1 (1%)	21 44
11	C	403/405 (100%)	391 (97%)	11 (3%)	1 (0%)	43 68
13	E	138/150 (92%)	131 (95%)	7 (5%)	0	100 100
14	F	57/59 (97%)	50 (88%)	6 (10%)	1 (2%)	6 18
15	G	84/86 (98%)	74 (88%)	10 (12%)	0	100 100
17	I	431/442 (98%)	397 (92%)	30 (7%)	4 (1%)	14 35
18	J	100/102 (98%)	97 (97%)	3 (3%)	0	100 100
19	L	172/187 (92%)	164 (95%)	8 (5%)	0	100 100
20	M	79/81 (98%)	74 (94%)	5 (6%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	N	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
22	O	218/220 (99%)	213 (98%)	5 (2%)	0	100	100
23	P	209/211 (99%)	201 (96%)	8 (4%)	0	100	100
24	Q	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
25	S	228/230 (99%)	206 (90%)	21 (9%)	1 (0%)	30	54
26	T	125/127 (98%)	109 (87%)	14 (11%)	2 (2%)	7	20
27	U	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
28	V	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
29	W	194/206 (94%)	188 (97%)	6 (3%)	0	100	100
30	Y	254/256 (99%)	217 (85%)	33 (13%)	4 (2%)	7	20
31	Z	175/177 (99%)	164 (94%)	9 (5%)	2 (1%)	11	29
32	a	138/140 (99%)	129 (94%)	8 (6%)	1 (1%)	18	41
33	b	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
34	c	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	7	20
35	e	123/125 (98%)	113 (92%)	9 (7%)	1 (1%)	16	37
36	f	180/189 (95%)	174 (97%)	6 (3%)	0	100	100
37	g	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
38	h	225/227 (99%)	223 (99%)	2 (1%)	0	100	100
39	i	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
40	j	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
41	k	311/313 (99%)	296 (95%)	15 (5%)	0	100	100
42	l	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
43	m	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
44	n	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
45	o	593/595 (100%)	522 (88%)	67 (11%)	4 (1%)	18	41
46	q	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
47	r	269/271 (99%)	260 (97%)	8 (3%)	1 (0%)	30	54
48	s	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
49	t	438/440 (100%)	419 (96%)	19 (4%)	0	100	100
50	w	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
51	x	417/509 (82%)	384 (92%)	31 (7%)	2 (0%)	24	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
52	y	59/61 (97%)	51 (86%)	8 (14%)	0	100 100
All	All	9710/10263 (95%)	9188 (95%)	492 (5%)	30 (0%)	37 60

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	78	GLU
10	B	198	GLU
17	I	427	PRO
17	I	452	PRO
17	I	499	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	0	111/142 (78%)	111 (100%)	0	100 100
2	1	647/747 (87%)	646 (100%)	1 (0%)	87 95
3	3	79/94 (84%)	79 (100%)	0	100 100
6	7	64/64 (100%)	64 (100%)	0	100 100
8	9	20/20 (100%)	20 (100%)	0	100 100
9	A	484/660 (73%)	484 (100%)	0	100 100
10	B	143/143 (100%)	143 (100%)	0	100 100
11	C	356/356 (100%)	356 (100%)	0	100 100
13	E	129/135 (96%)	129 (100%)	0	100 100
14	F	49/49 (100%)	49 (100%)	0	100 100
15	G	73/73 (100%)	73 (100%)	0	100 100
17	I	377/397 (95%)	377 (100%)	0	100 100
18	J	90/90 (100%)	90 (100%)	0	100 100
19	L	160/168 (95%)	160 (100%)	0	100 100
20	M	73/73 (100%)	73 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	N	66/66 (100%)	66 (100%)	0	100	100
22	O	185/185 (100%)	185 (100%)	0	100	100
23	P	192/192 (100%)	191 (100%)	1 (0%)	81	92
24	Q	180/180 (100%)	180 (100%)	0	100	100
25	S	200/200 (100%)	199 (100%)	1 (0%)	81	92
26	T	100/100 (100%)	100 (100%)	0	100	100
27	U	119/119 (100%)	119 (100%)	0	100	100
28	V	130/130 (100%)	130 (100%)	0	100	100
29	W	171/177 (97%)	170 (99%)	1 (1%)	78	91
30	Y	219/220 (100%)	219 (100%)	0	100	100
31	Z	158/158 (100%)	158 (100%)	0	100	100
32	a	112/112 (100%)	112 (100%)	0	100	100
33	b	114/114 (100%)	114 (100%)	0	100	100
34	c	112/112 (100%)	112 (100%)	0	100	100
35	e	107/107 (100%)	107 (100%)	0	100	100
36	f	156/159 (98%)	156 (100%)	0	100	100
37	g	117/117 (100%)	117 (100%)	0	100	100
38	h	190/190 (100%)	190 (100%)	0	100	100
39	i	90/90 (100%)	90 (100%)	0	100	100
40	j	49/49 (100%)	49 (100%)	0	100	100
41	k	272/272 (100%)	272 (100%)	0	100	100
42	l	113/113 (100%)	113 (100%)	0	100	100
43	m	65/65 (100%)	65 (100%)	0	100	100
44	n	123/123 (100%)	123 (100%)	0	100	100
45	o	523/523 (100%)	523 (100%)	0	100	100
46	q	104/104 (100%)	104 (100%)	0	100	100
47	r	192/243 (79%)	192 (100%)	0	100	100
48	s	67/67 (100%)	67 (100%)	0	100	100
49	t	371/371 (100%)	371 (100%)	0	100	100
50	w	94/94 (100%)	94 (100%)	0	100	100
51	x	208/458 (45%)	207 (100%)	1 (0%)	81	92

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	y	54/54 (100%)	54 (100%)	0	100 100
All	All	7808/8475 (92%)	7803 (100%)	5 (0%)	87 96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1	597	ASN
23	P	202	GLN
25	S	225	GLN
29	W	202	ILE
51	x	405	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
41	k	159	ASN
45	o	112	ASN
49	t	401	ASN
11	C	355	HIS
11	C	161	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	D	1680/1869 (89%)	323 (19%)	30 (1%)
16	H	0/29	-	-
53	z	74/75 (98%)	20 (27%)	0
All	All	1754/1973 (88%)	343 (19%)	30 (1%)

5 of 343 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	D	2	A
12	D	3	C
12	D	4	C
12	D	5	U
12	D	17	C

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	D	615	C
12	D	1813	A
12	D	655	A
12	D	1839	U
12	D	1737	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)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

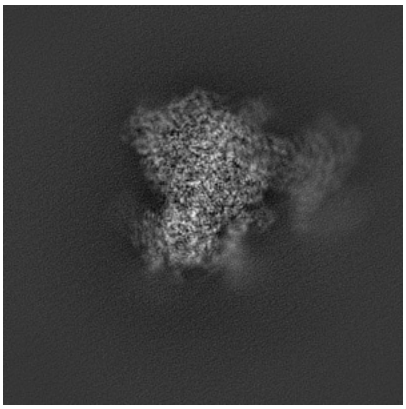
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-78242. These allow visual inspection of the internal detail of the map and identification of artifacts.

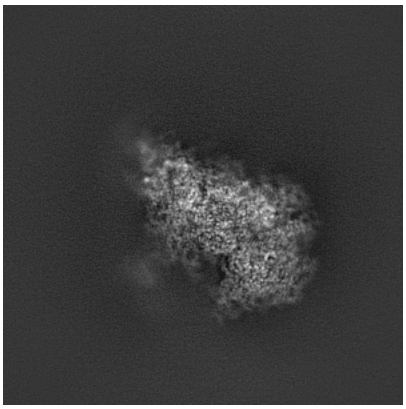
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

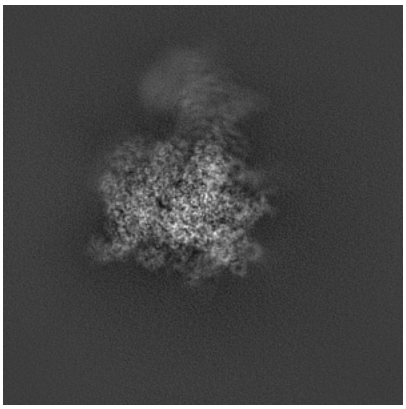
6.1.1 Primary map



X

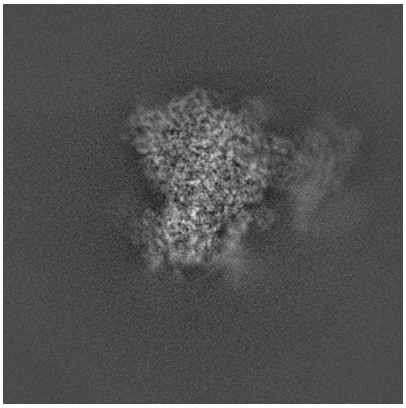


Y

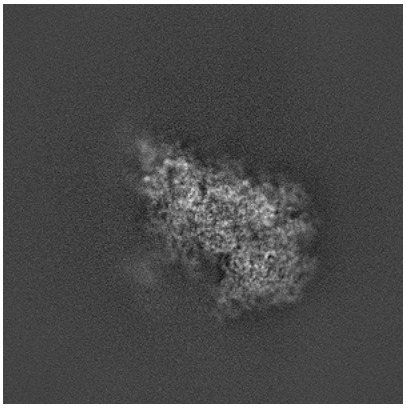


Z

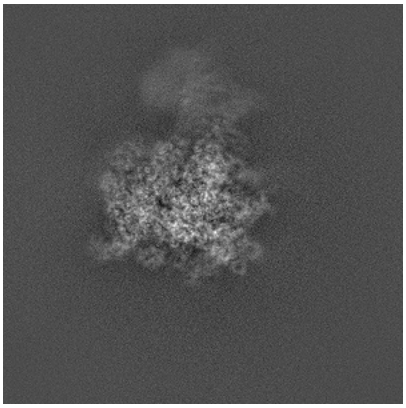
6.1.2 Raw map



X



Y

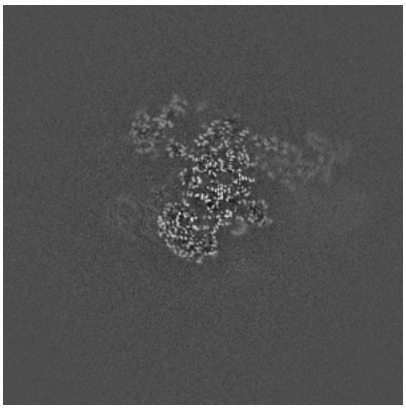


Z

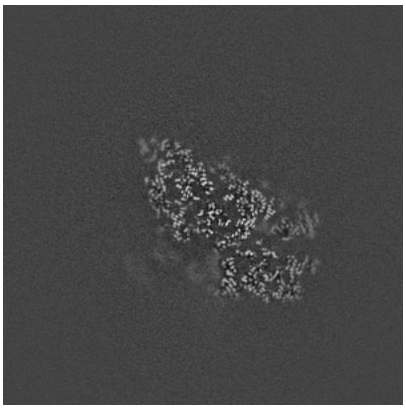
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

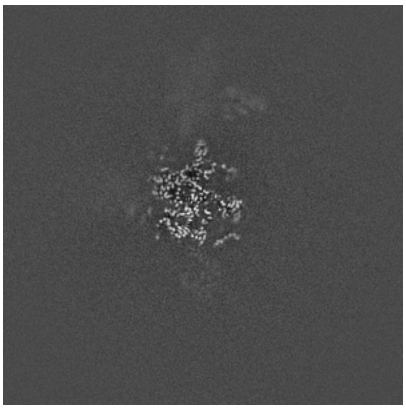
6.2.1 Primary map



X Index: 280

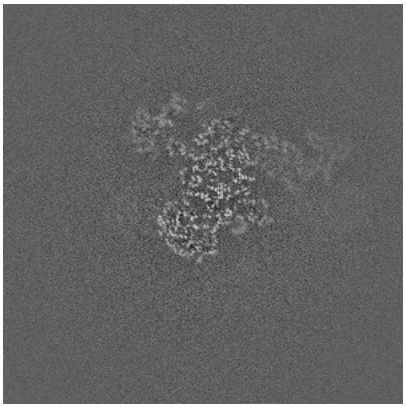


Y Index: 280

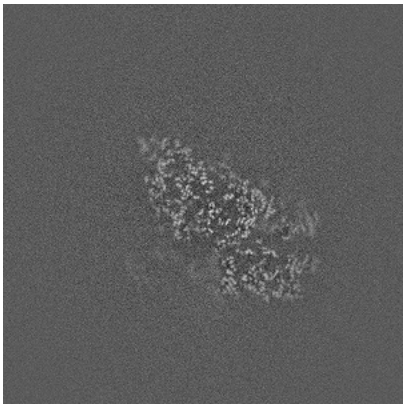


Z Index: 280

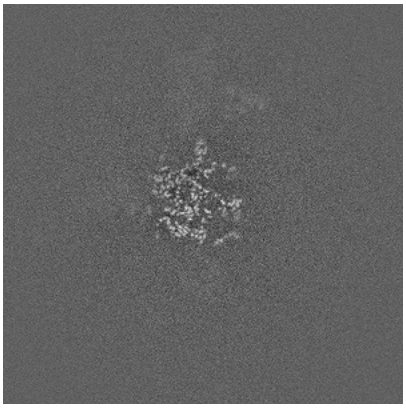
6.2.2 Raw map



X Index: 280



Y Index: 280

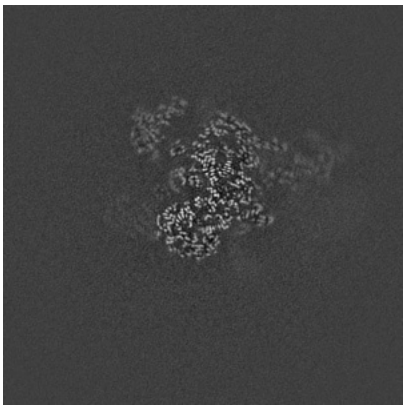


Z Index: 280

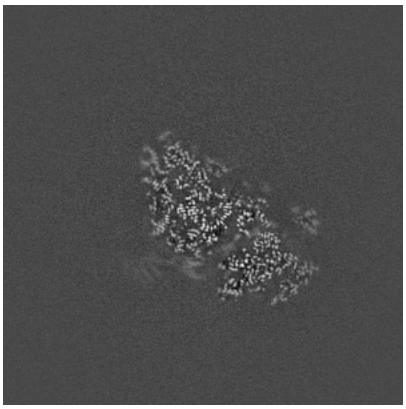
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

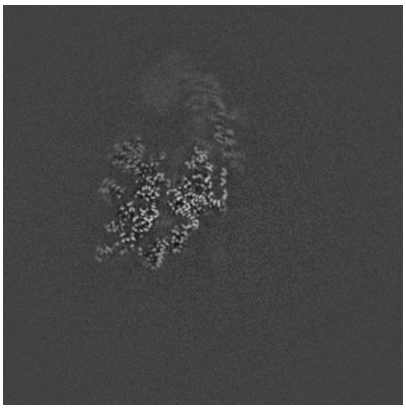
6.3.1 Primary map



X Index: 284

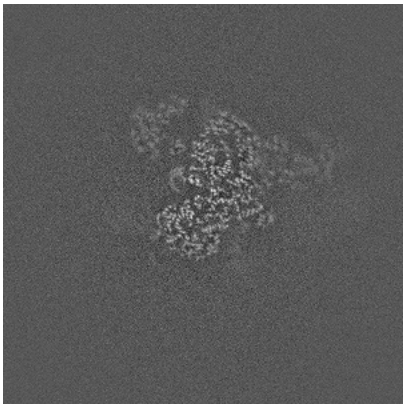


Y Index: 267

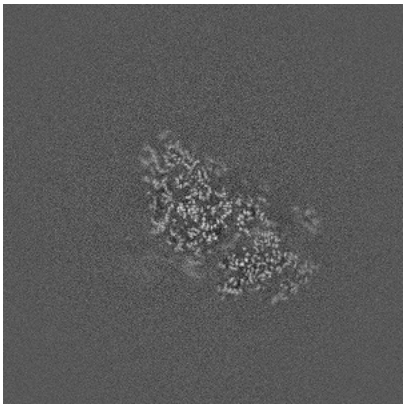


Z Index: 336

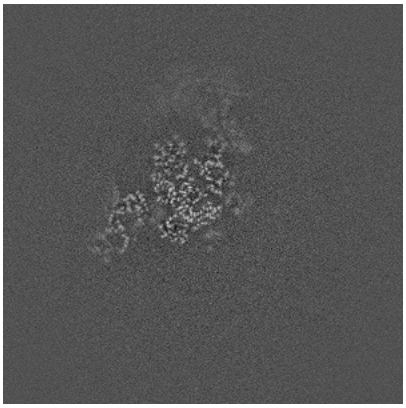
6.3.2 Raw map



X Index: 285



Y Index: 267

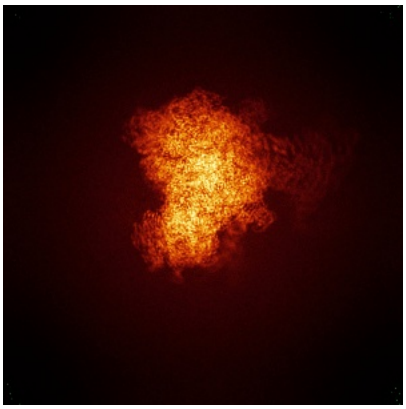


Z Index: 311

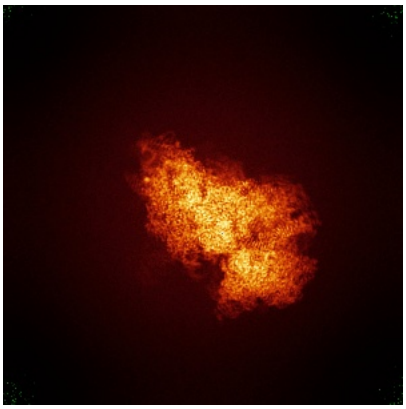
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

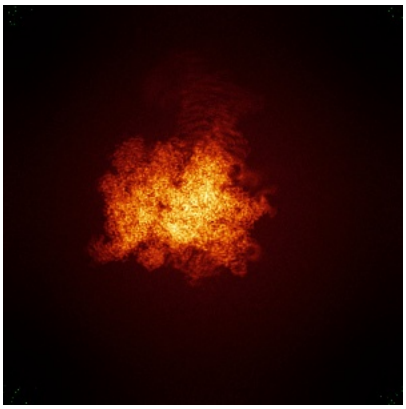
6.4.1 Primary map



X

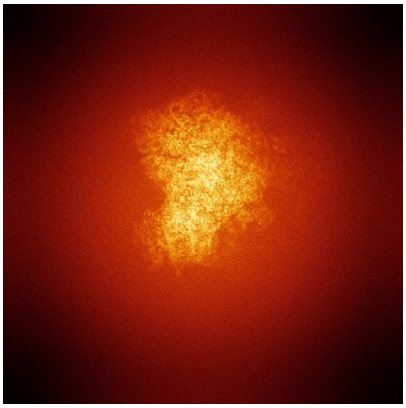


Y

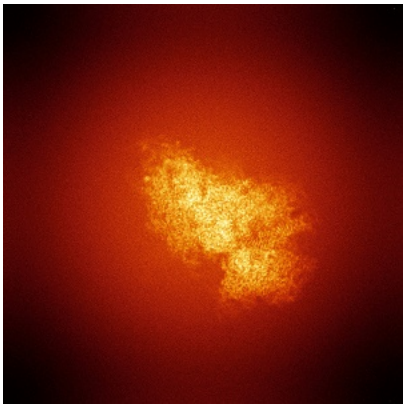


Z

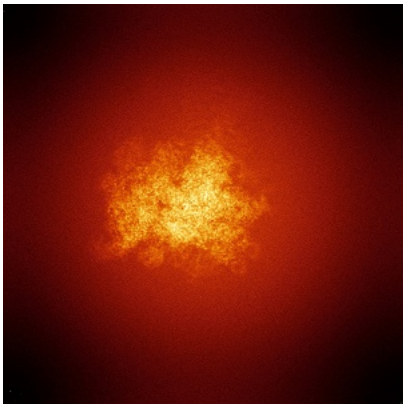
6.4.2 Raw map



X



Y

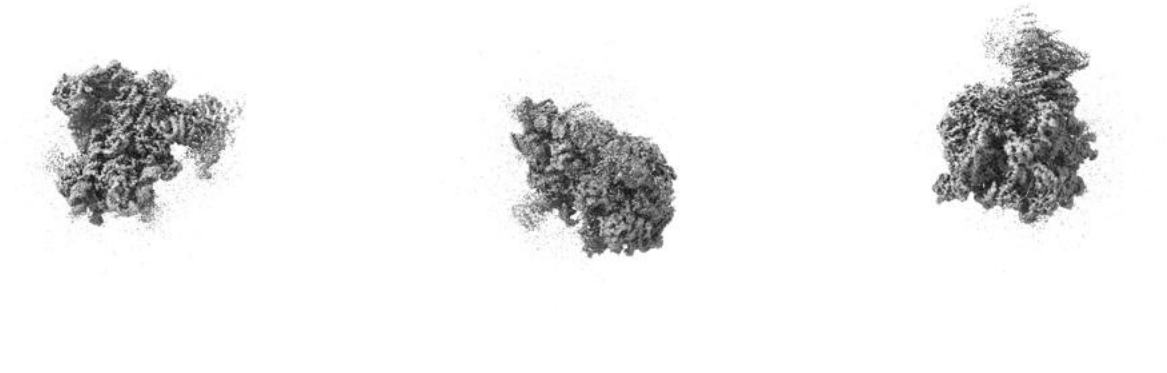


Z

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

6.5 Orthogonal surface views (i)

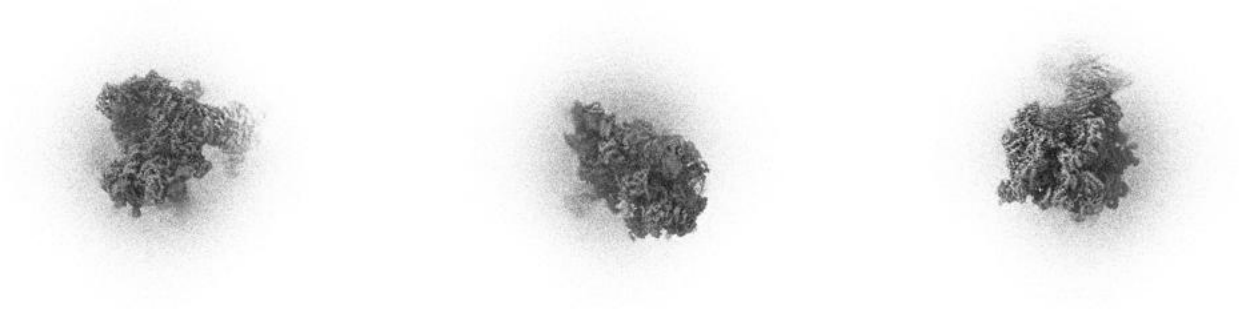
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

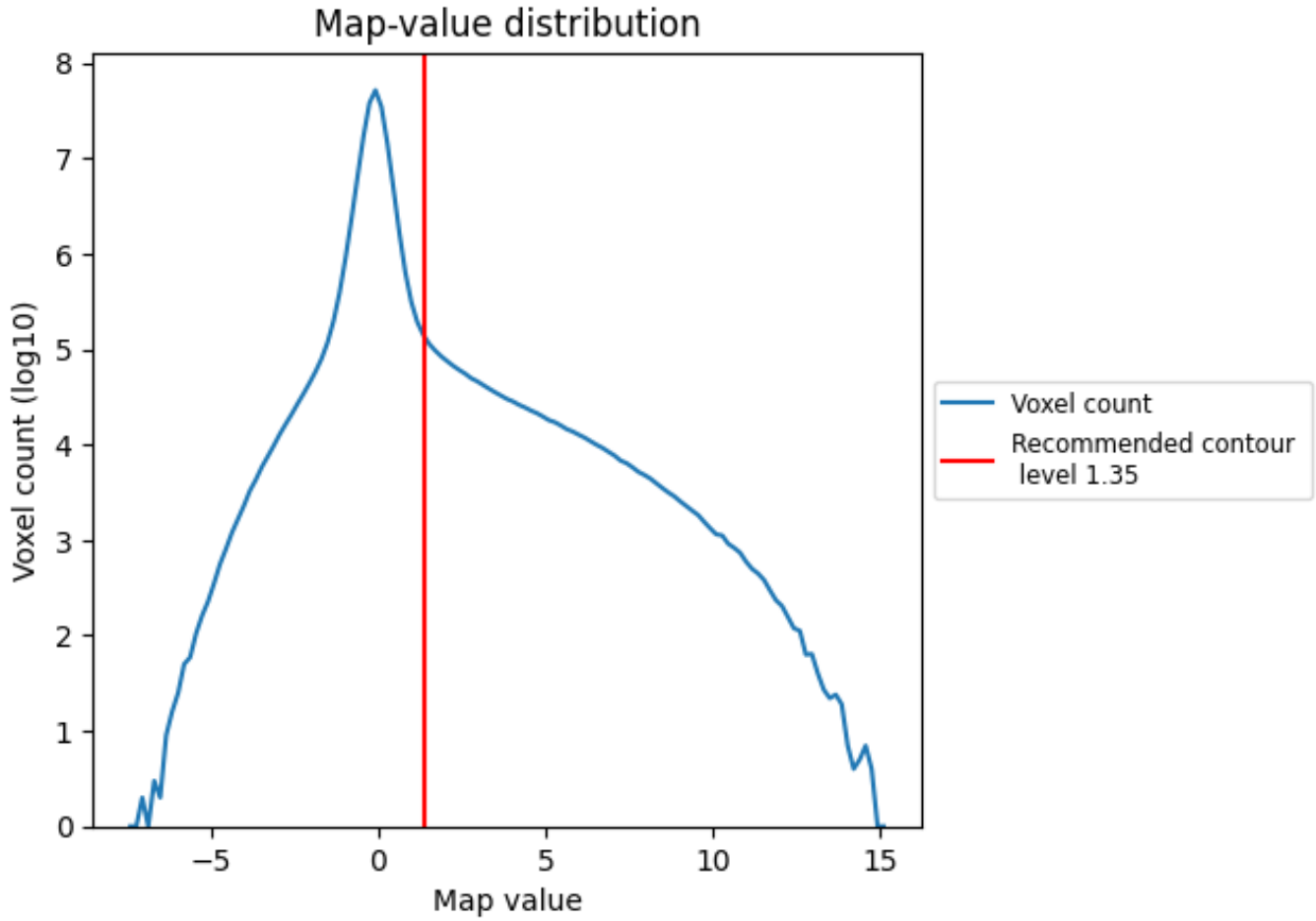
6.6 Mask visualisation (i)

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

7 Map analysis

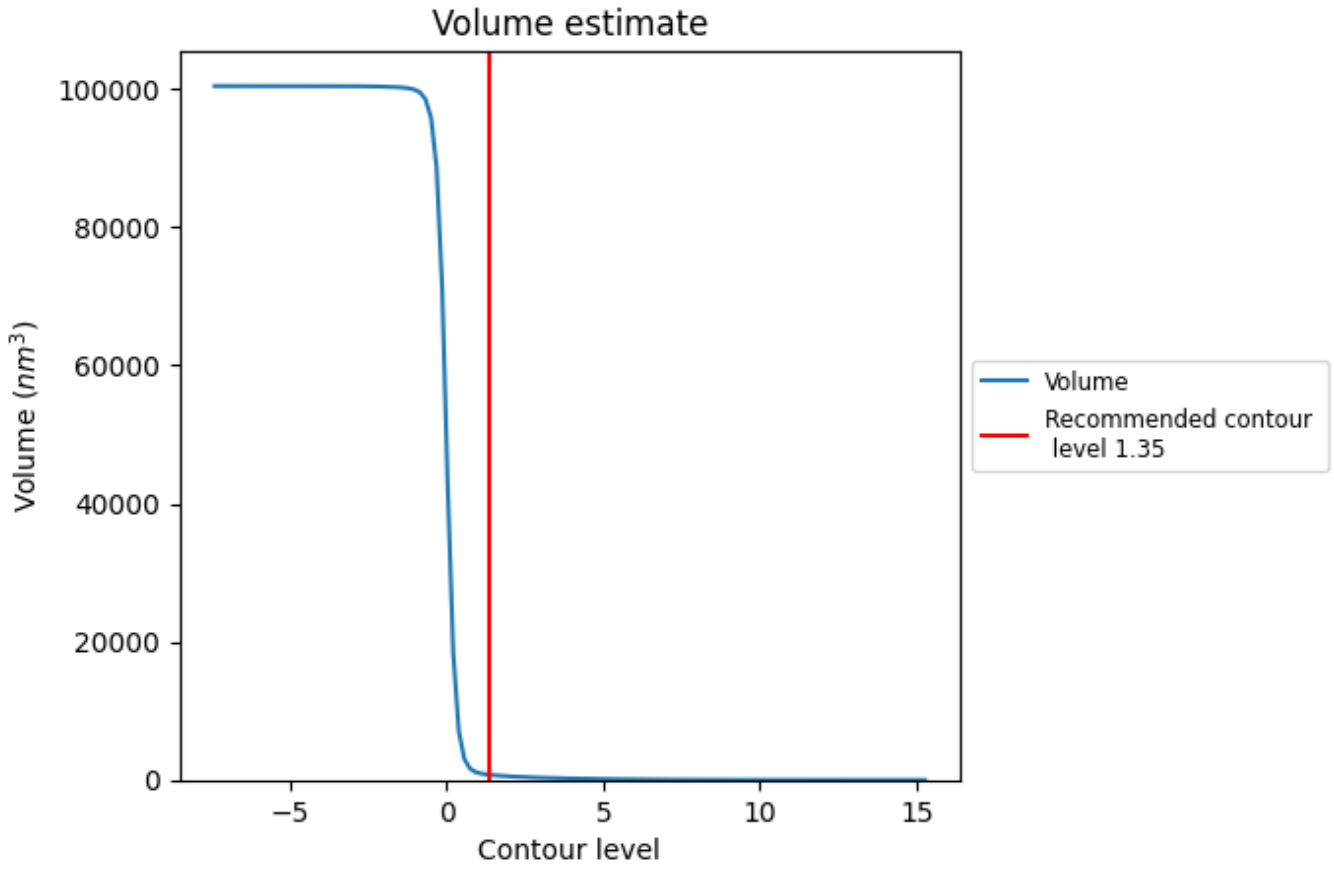
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

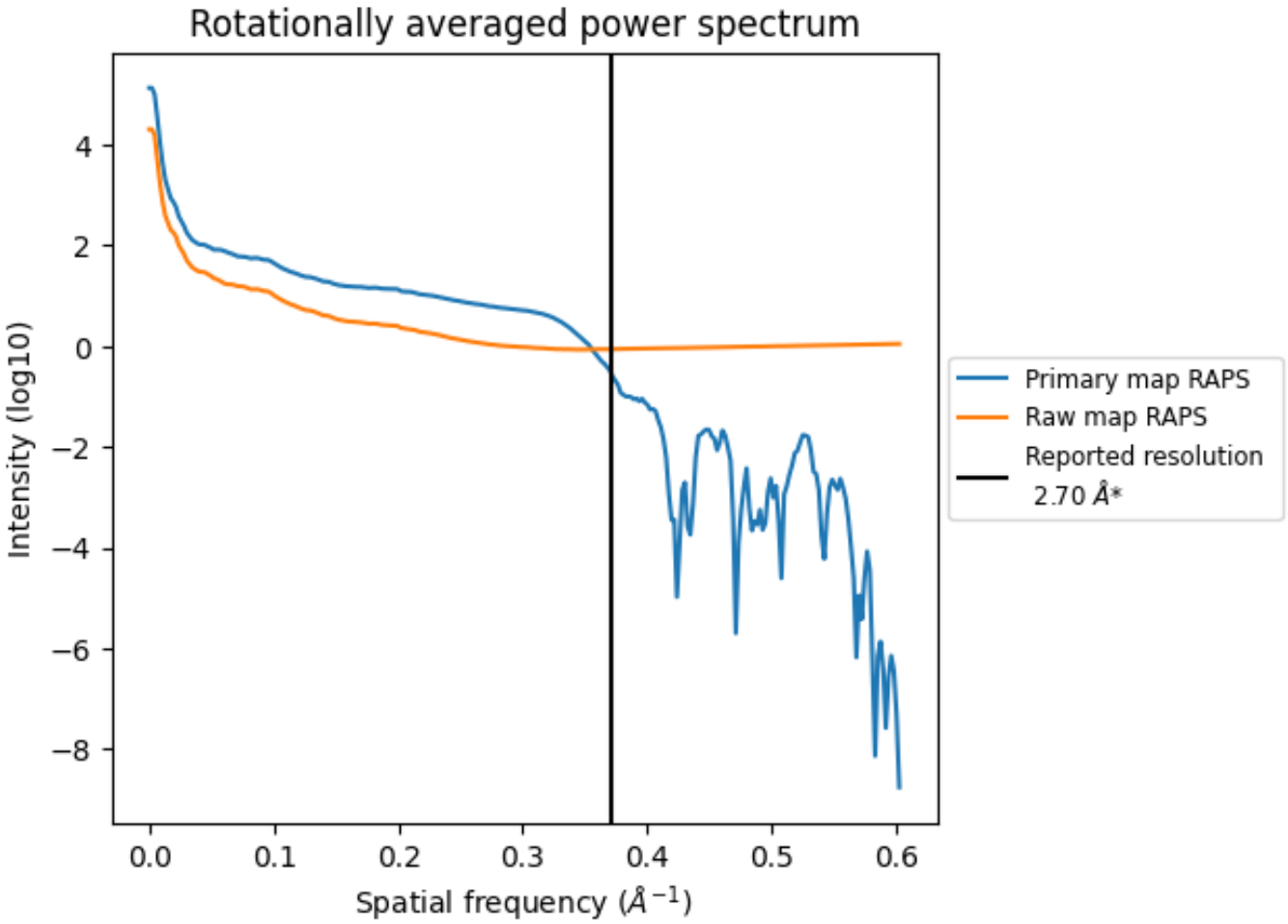
7.2 Volume estimate (i)



The volume at the recommended contour level is 759 nm^3; this corresponds to an approximate mass of 686 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 (i)

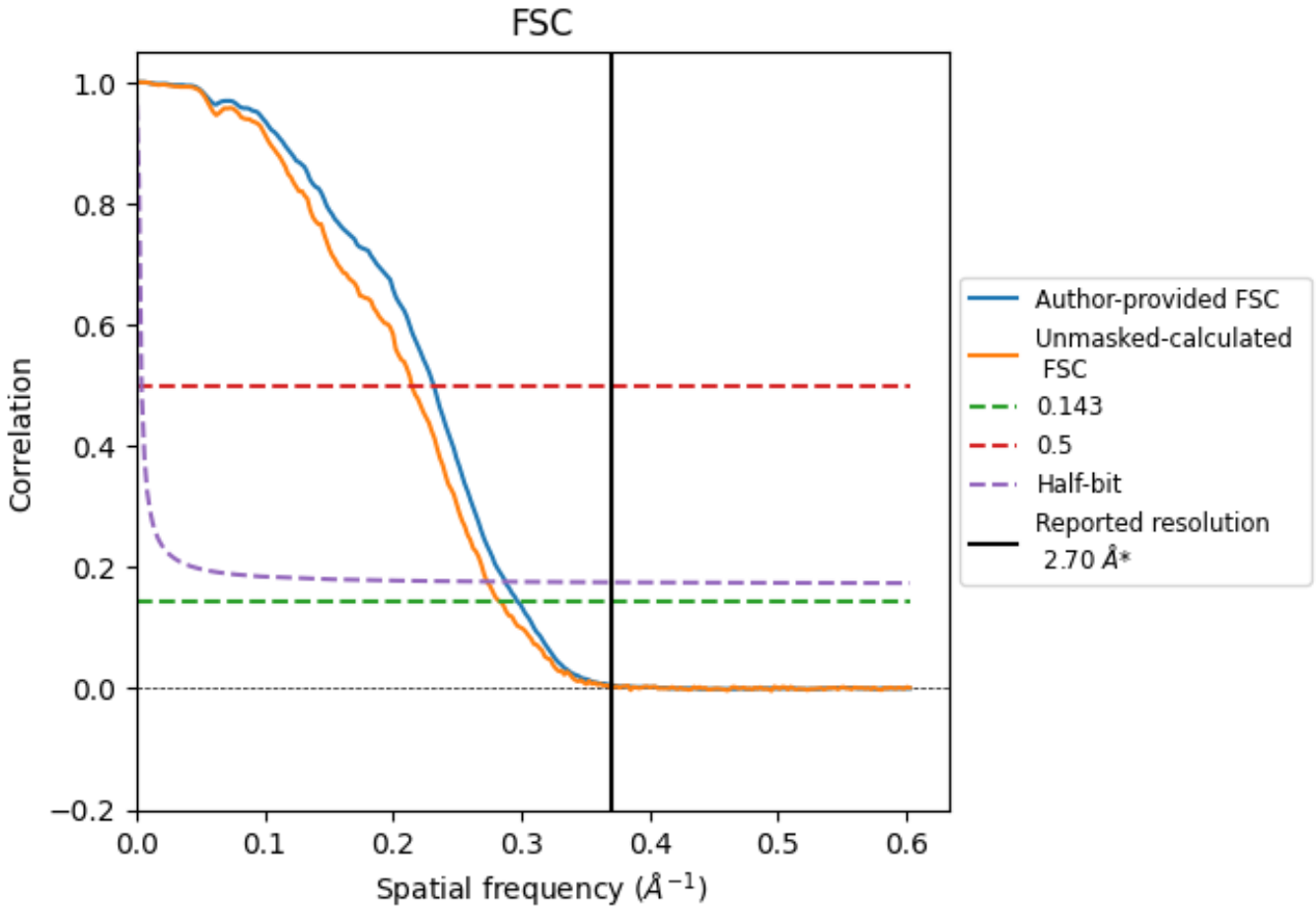


*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	3.36	4.32	3.48
Unmasked-calculated*	3.52	4.66	3.66

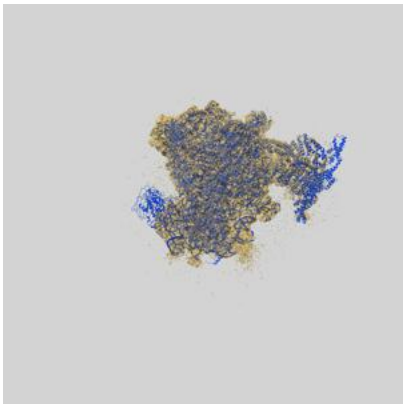
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.36 differs from the reported value 2.7 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.52 differs from the reported value 2.7 by more than 10 %

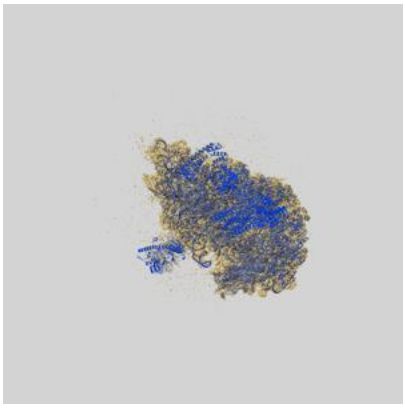
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-78242 and PDB model 37KM. Per-residue inclusion information can be found in section 3 on page 14.

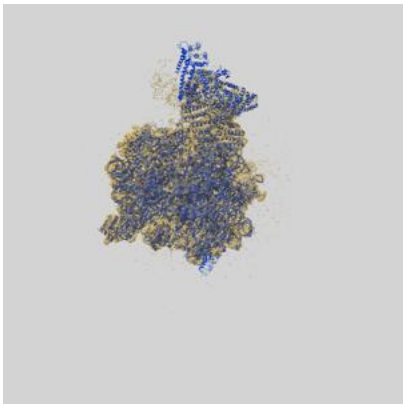
9.1 Map-model overlay



X



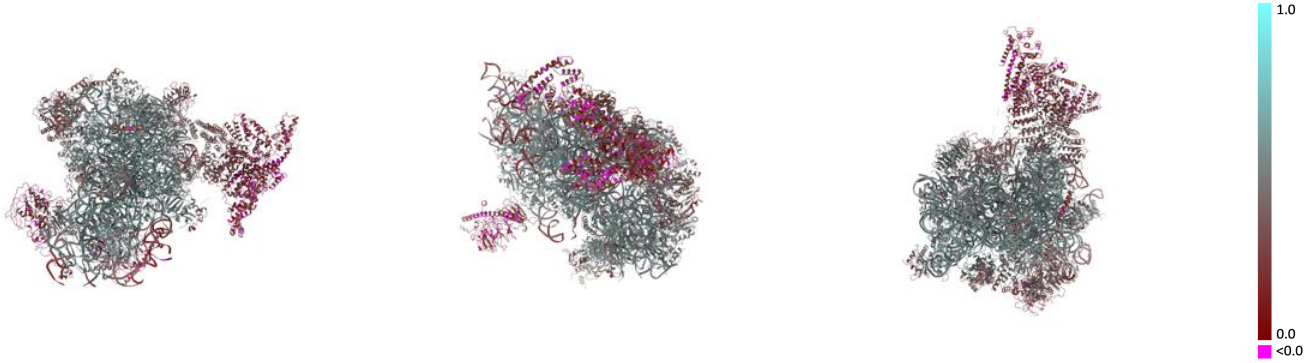
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.35 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.

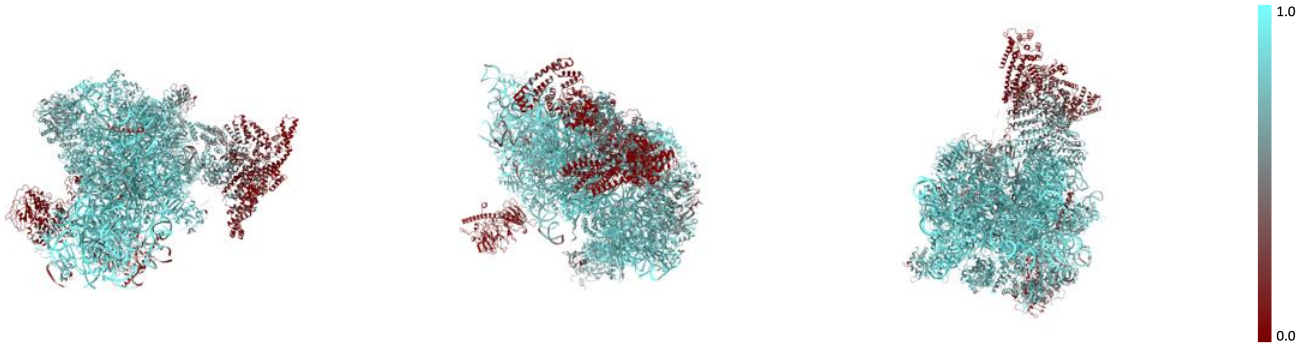
9.2 Q-score mapped to coordinate model



X Y Z

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.

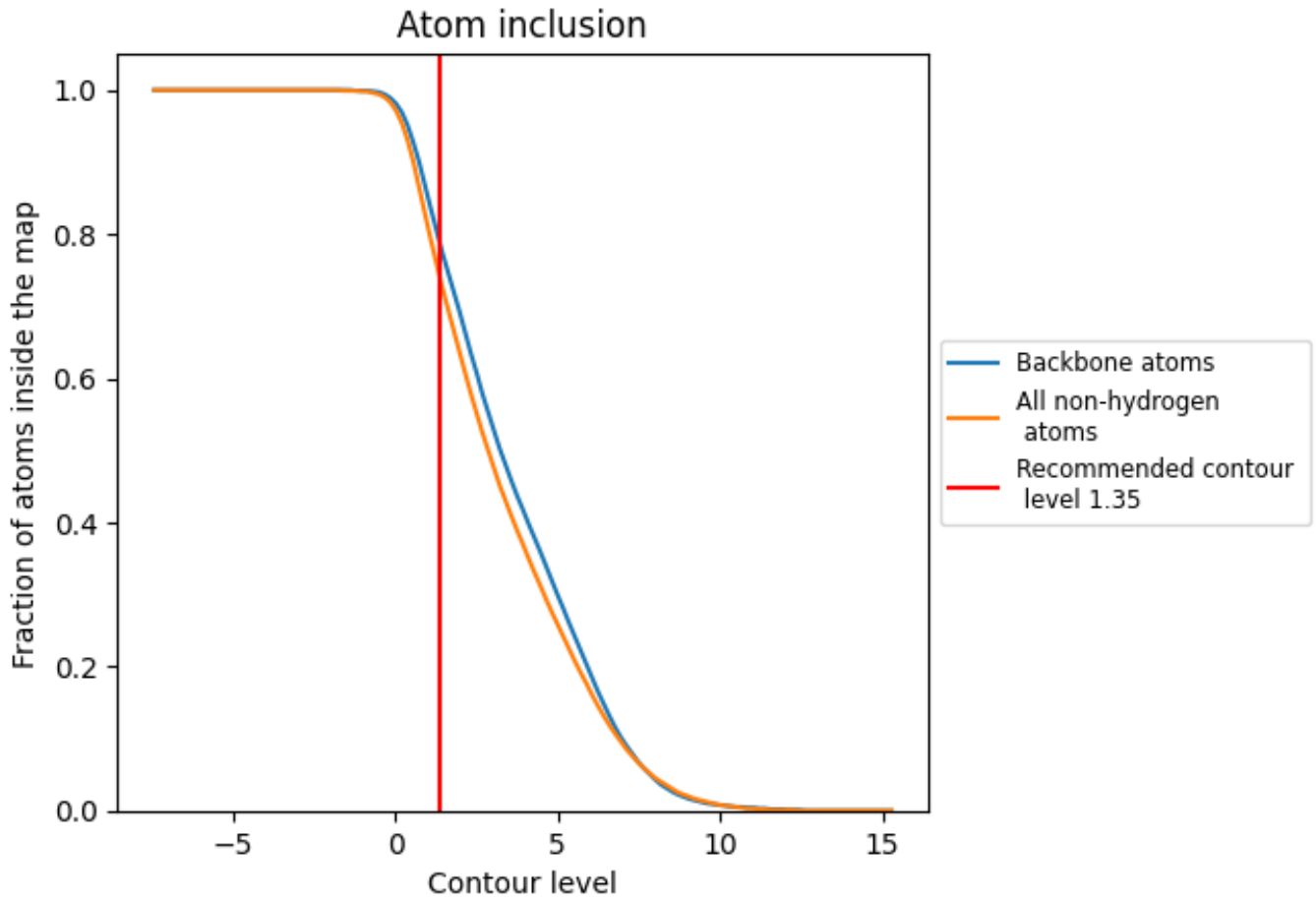
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (1.35).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 74% 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 (1.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7450	0.4540
0	0.0150	0.1710
1	0.5200	0.3290
3	0.8430	0.5130
5	0.1780	0.2070
6	0.0360	0.1760
7	0.5020	0.3620
8	0.0650	0.1100
9	0.9030	0.5440
A	0.3650	0.2680
B	0.8440	0.4910
C	0.7650	0.4490
D	0.9440	0.5300
E	0.9230	0.5600
F	0.8510	0.5210
G	0.8960	0.5420
H	0.6590	0.3360
I	0.0480	0.1440
J	0.8590	0.5280
L	0.8360	0.4830
M	0.8840	0.5240
N	0.9020	0.5460
O	0.9200	0.5570
P	0.8600	0.5220
Q	0.8720	0.5210
S	0.7990	0.4270
T	0.8570	0.5100
U	0.8400	0.4960
V	0.9010	0.5470
W	0.8960	0.5300
Y	0.8160	0.4590
Z	0.8960	0.5340
a	0.9380	0.5790
b	0.8660	0.5370
c	0.9420	0.5740



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	0.8470	0.4740
f	0.8610	0.5460
g	0.8520	0.5280
h	0.8730	0.5370
i	0.8760	0.5420
j	0.9330	0.5900
k	0.8000	0.4840
l	0.8440	0.5270
m	0.7760	0.4980
n	0.8400	0.5220
o	0.0480	0.2450
q	0.5910	0.3630
r	0.7930	0.4550
s	0.7380	0.4720
t	0.6720	0.3800
w	0.8050	0.5090
x	0.5400	0.3380
y	0.8130	0.4940
z	0.9680	0.5380