



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:53 PM UTC

PDB ID : 5OA3 / pdb\_00005oa3  
EMDB ID : EMD-3770  
Title : Human 40S-eIF2D-re-initiation complex  
Authors : Weisser, M.; Schaefer, T.; Leibundgut, M.; Boehringer, D.; Aylett, C.H.S.;  
Ban, N.  
Deposited on : 2017-06-20  
Resolution : 4.20 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](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:

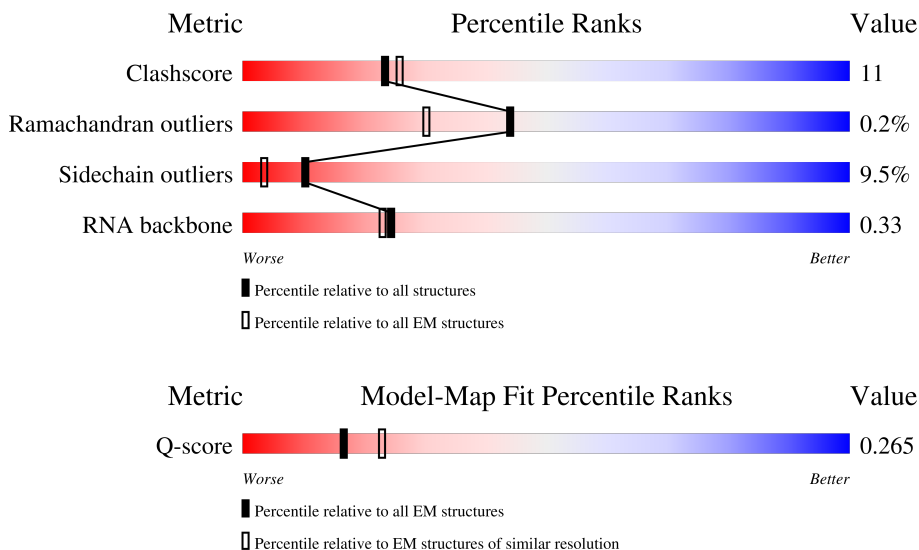
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.20 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	5410 ( 3.70 - 4.70 )

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	0	584	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">60%</div> </div>
2	1	75	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">32%</div> </div>
3	2	1868	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">39%</div> </div>


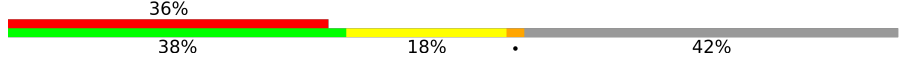

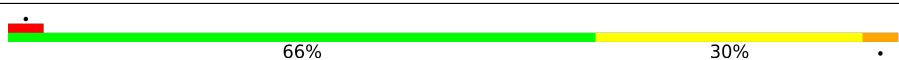
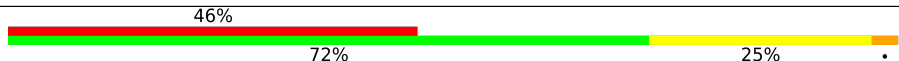
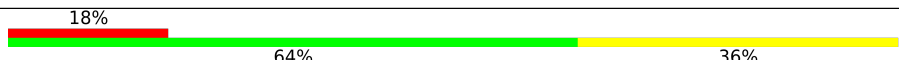
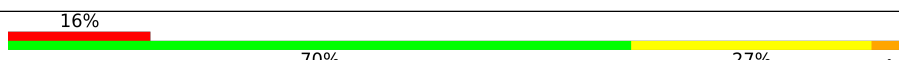

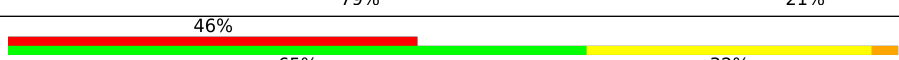
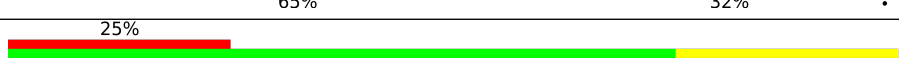
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Mol	Chain	Length	Quality of chain
4	3	275	
5	A	295	
6	B	264	
7	C	293	
8	D	243	
9	E	263	
10	F	204	
11	G	249	
12	H	194	
13	I	208	
14	J	194	
15	K	165	
16	L	158	
17	M	132	
18	N	151	
19	O	151	
20	P	145	
21	Q	146	
22	R	135	
23	S	152	
24	T	145	
25	U	119	
26	V	83	
27	W	130	
28	X	143	

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Mol	Chain	Length	Quality of chain
29	Y	130	
30	Z	125	
31	a	101	
32	b	82	
33	c	61	
34	d	55	
35	e	56	
36	f	72	
37	g	315	
38	h	24	

## 2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 83675 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 2D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	479	3740	2392	643	684	21	0	0

- Molecule 2 is a RNA chain called initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	75	1608	716	297	520	75	0	0

- Molecule 3 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	1661	35466	15831	6370	11604	1661	0	0

- Molecule 4 is a RNA chain called IRES mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	3	186	3976	1770	713	1307	186	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	216	1705	1083	299	315	8	0	0

- Molecule 6 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	213	1729	1098	309	308	14	0	0

- Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	218	1690	1094	289	297	10	0	0

- Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	D	225	1752	1117	315	313	7	0	0

- Molecule 9 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	262	2076	1324	386	358	8	0	0

- Molecule 10 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	F	189	1495	934	284	270	7	0	0

- Molecule 11 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	G	230	1862	1164	371	320	7	0	0

- Molecule 12 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	H	186	1501	957	276	267	1	0	0

- Molecule 13 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	I	205	1675	1053	328	289	5	0	0

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	J	180	1499	955	300	242	2	0	0

- Molecule 15 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	K	95	800	522	142	131	5	0	0

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	L	151	1229	782	230	211	6	0	0

- Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	M	123	953	598	169	177	9	0	0

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	N	149	1202	770	228	203	1	0	0

- Molecule 19 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	O	135	1010	618	198	188	6	0	0

- Molecule 20 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	P	120	984	625	184	168	7	0	0

- Molecule 21 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	Q	139	1109	704	210	192	3	0	0

- Molecule 22 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	R	132	1068	670	199	195	4	0	0

- Molecule 23 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	S	143	1184	743	240	200	1	0	0

- Molecule 24 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	T	144	1122	703	217	199	3	0	0

- Molecule 25 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	U	101	803	504	153	142	4	0	0

- Molecule 26 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	V	82	625	384	116	120	5	0	0

- Molecule 27 is a protein called 40S ribosomal protein S15a.

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

- Molecule 28 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 29 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 30 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 31 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 32 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 34 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 35 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 36 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	72	Total	C	N	O	S	0	0
			585	366	114	97	8		

- Molecule 37 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 38 is a protein called RIBOSOMAL PROTEIN EL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

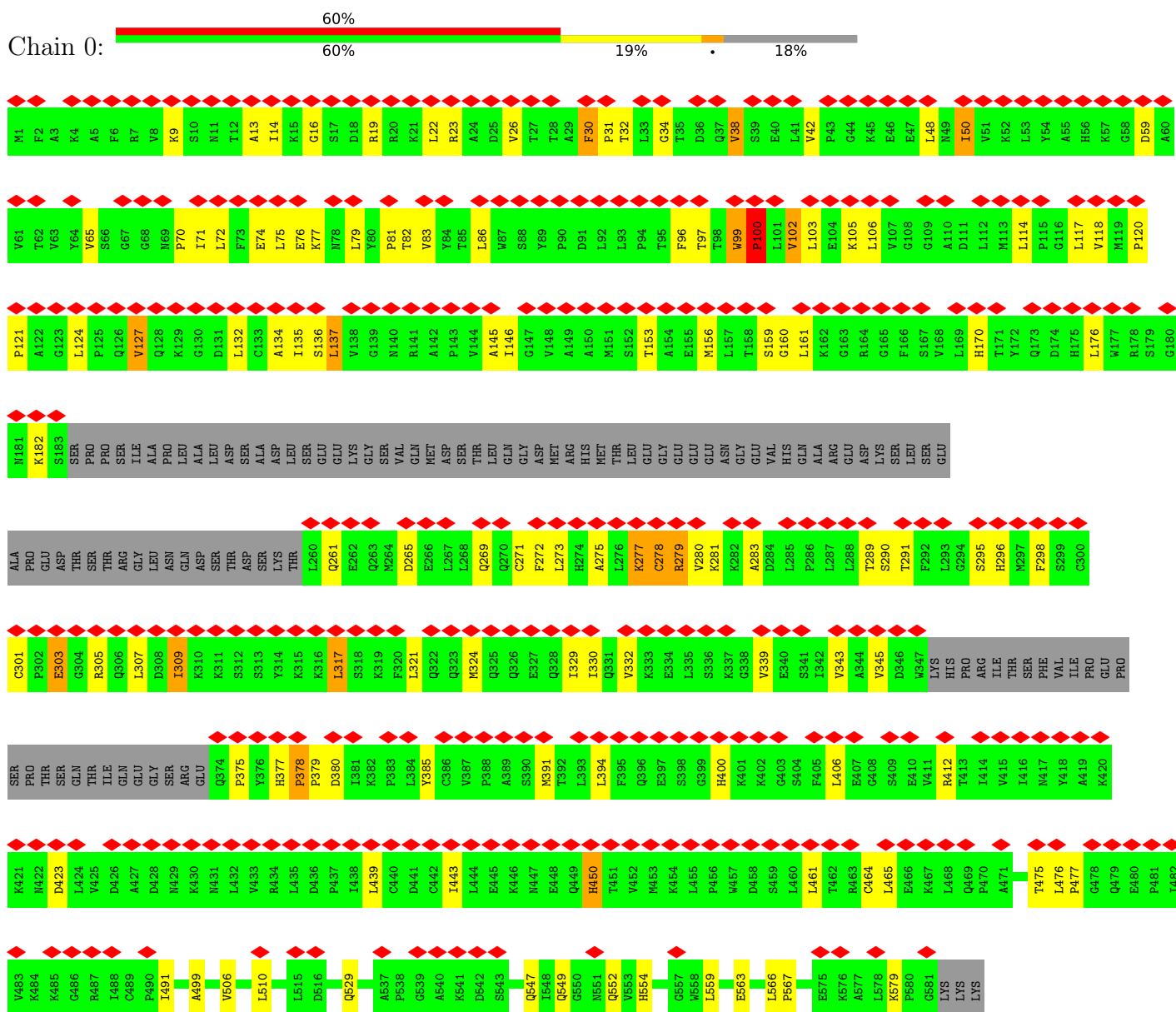
- Molecule 39 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
39	a	1	Total	Zn	0
			1	1	
39	d	1	Total	Zn	0
			1	1	
39	f	1	Total	Zn	0
			1	1	

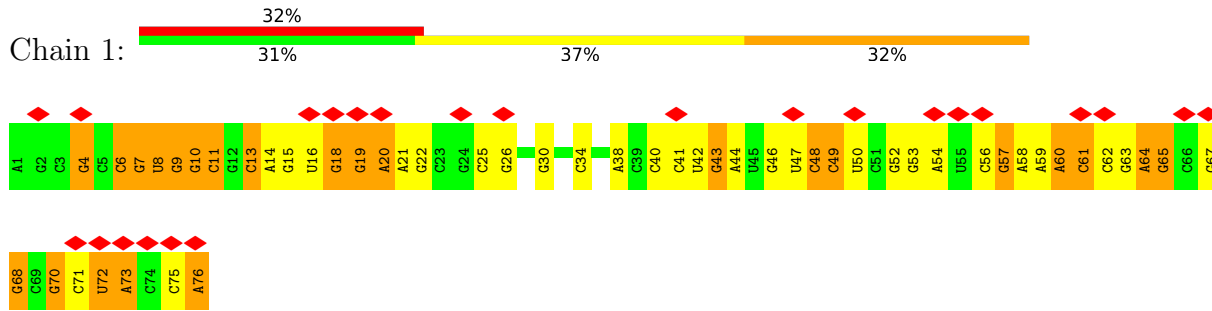
### 3 Residue-property plots

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

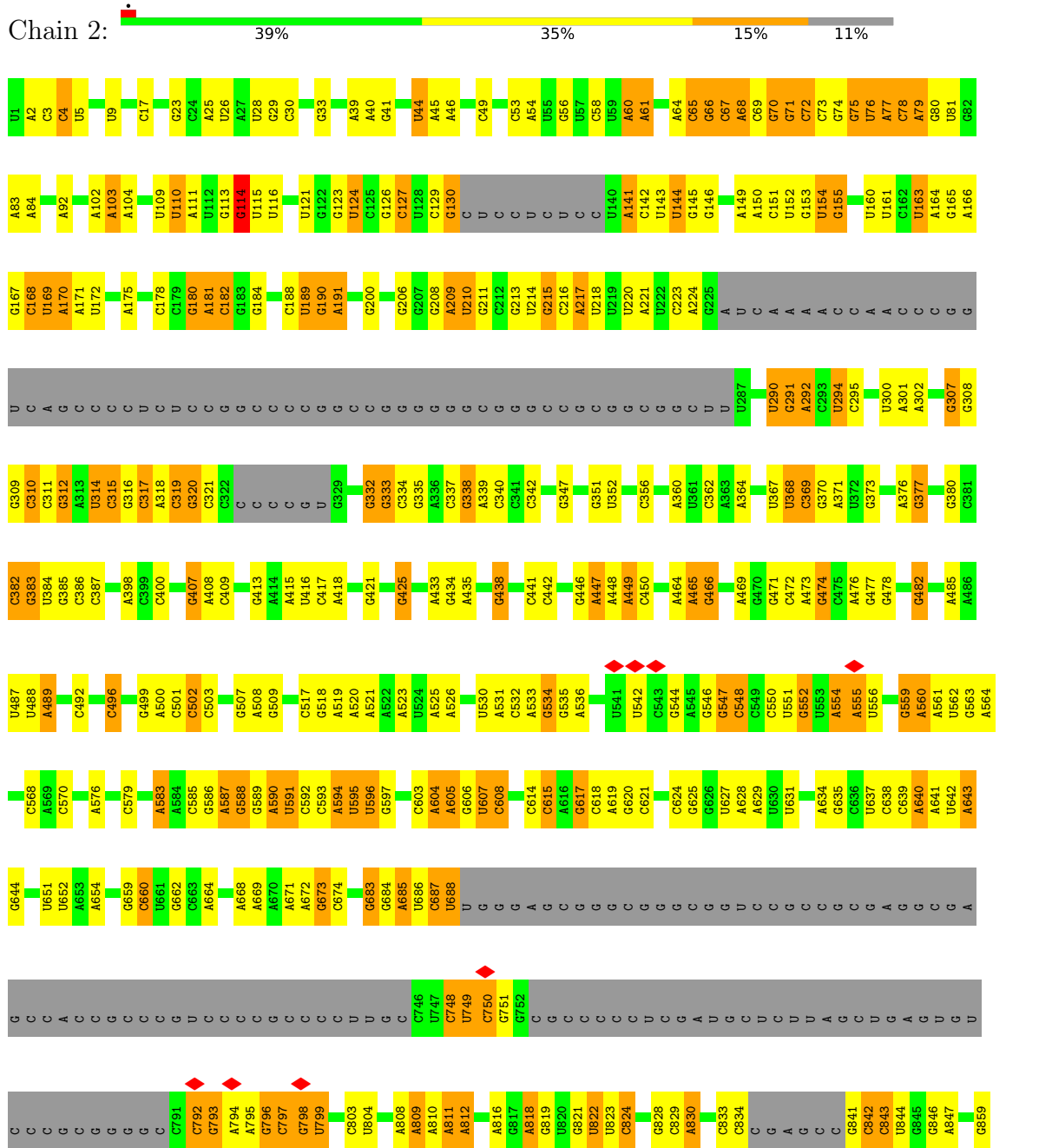
- Molecule 1: Eukaryotic translation initiation factor 2D

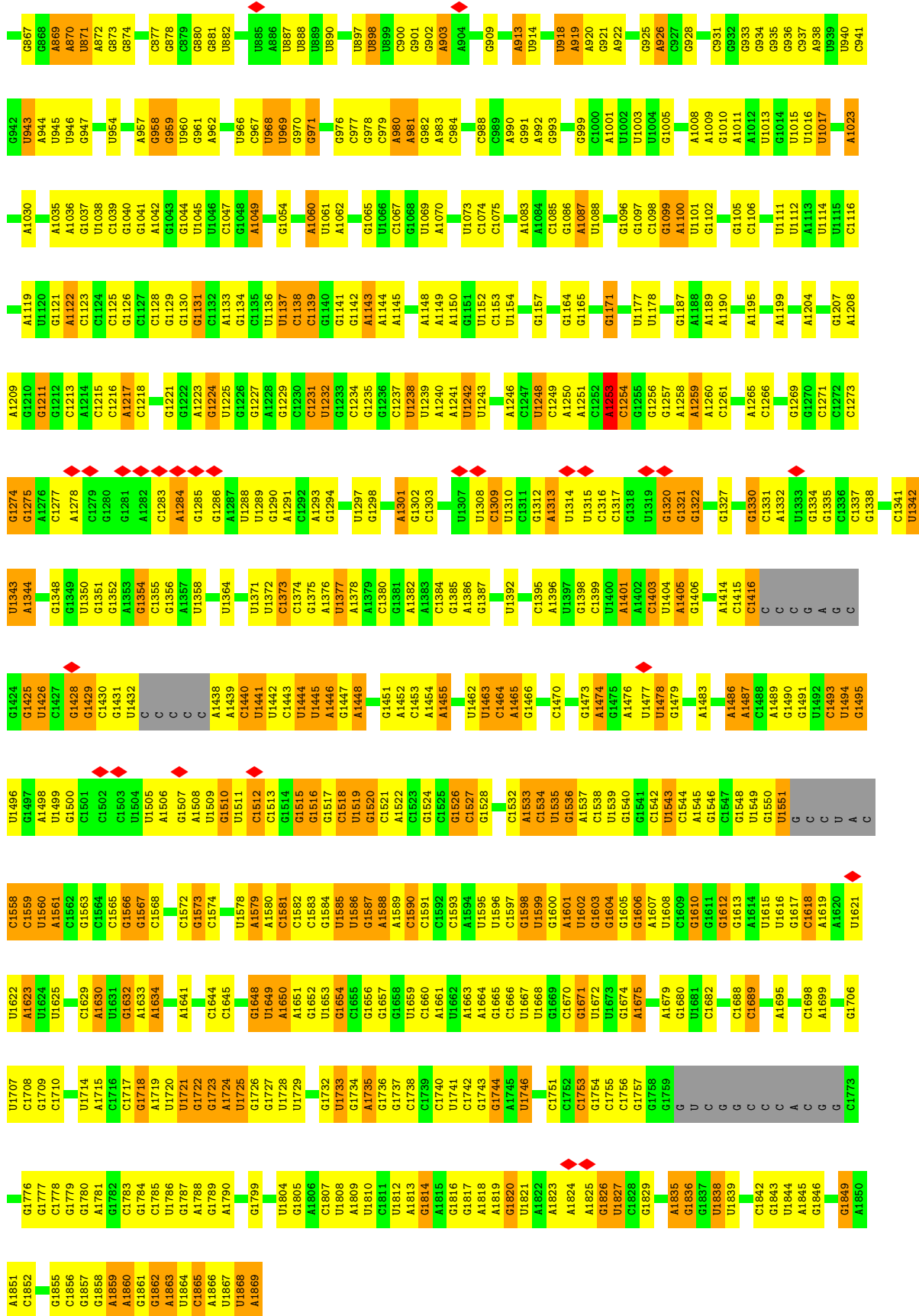


- Molecule 2: initiator Met-tRNA-i

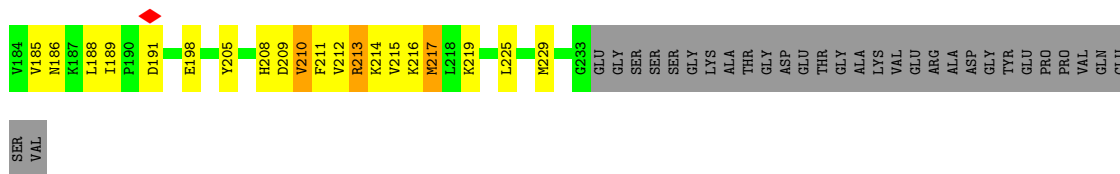


• Molecule 3: 18S ribosomal RNA

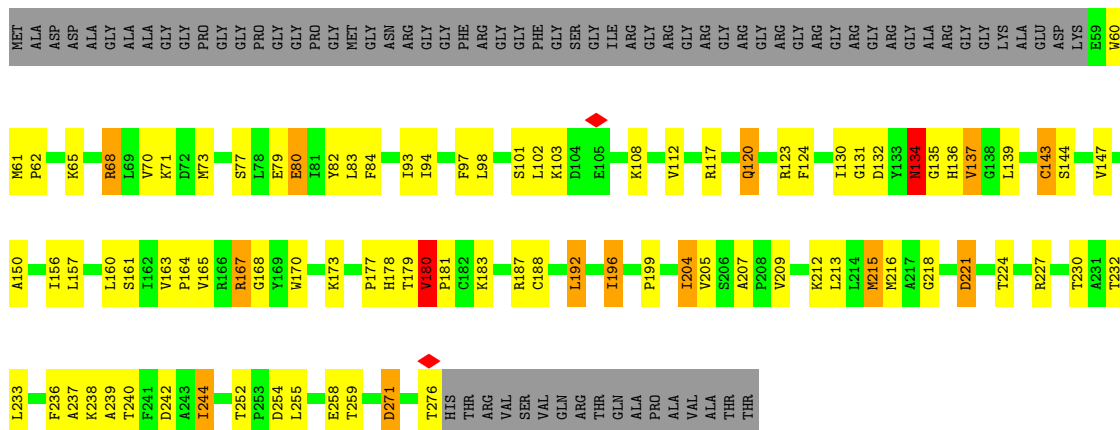




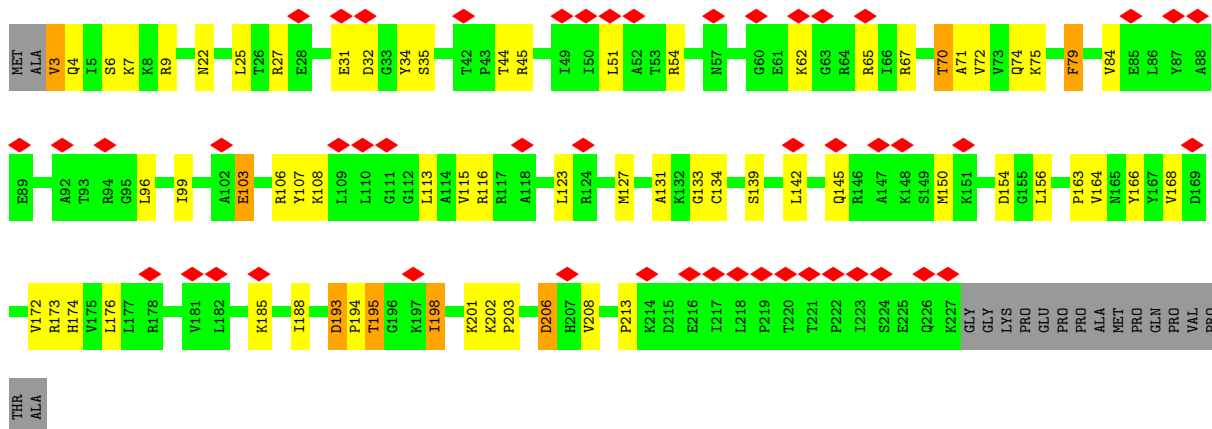




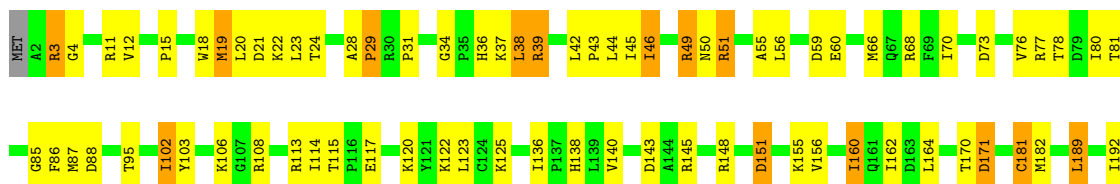
• Molecule 7: 40S ribosomal protein S2



• Molecule 8: 40S ribosomal protein S3

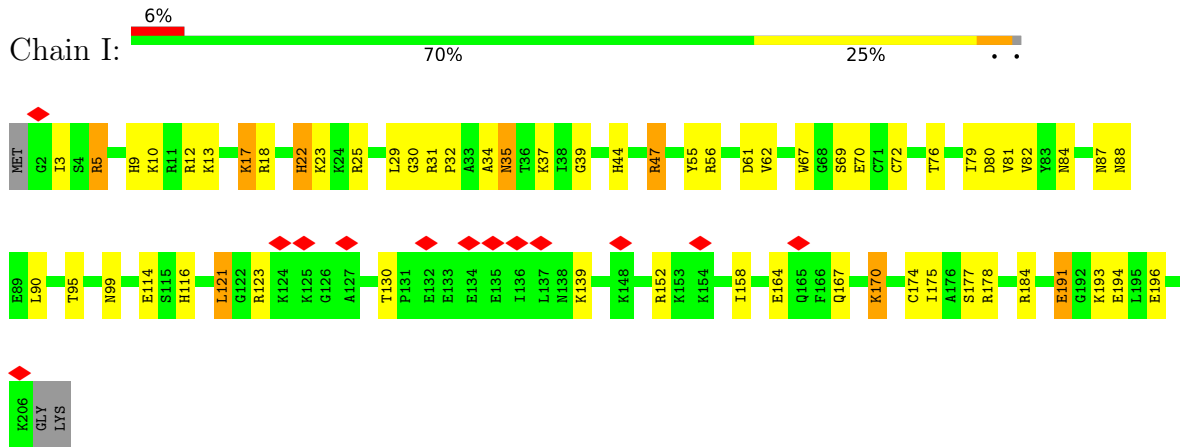


• Molecule 9: 40S ribosomal protein S4, X isoform

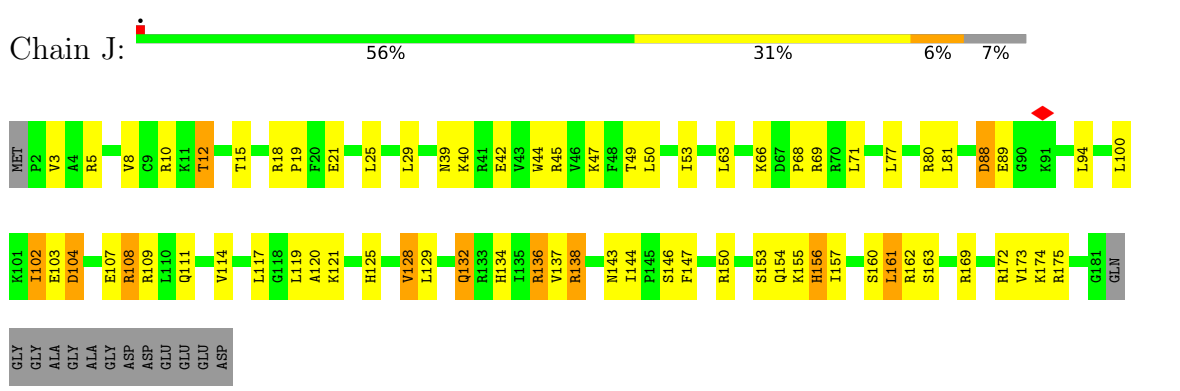




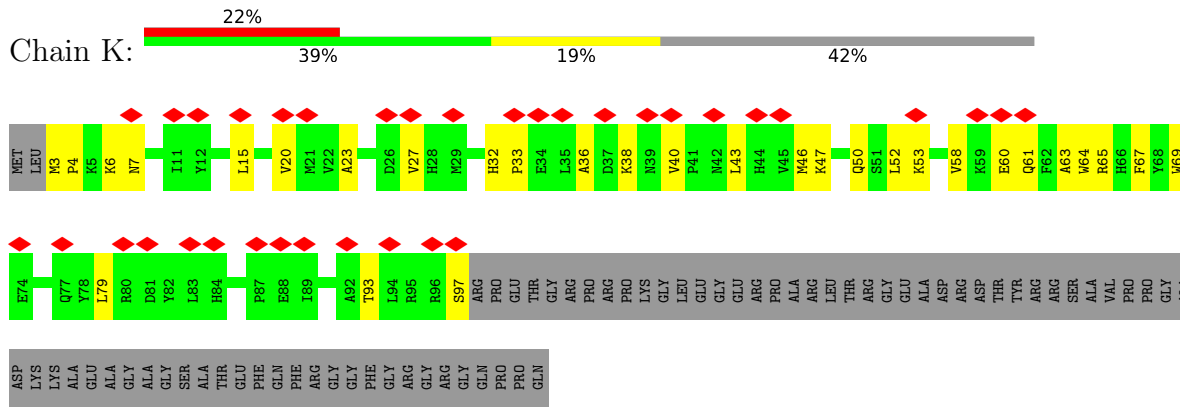
• Molecule 13: 40S ribosomal protein S8



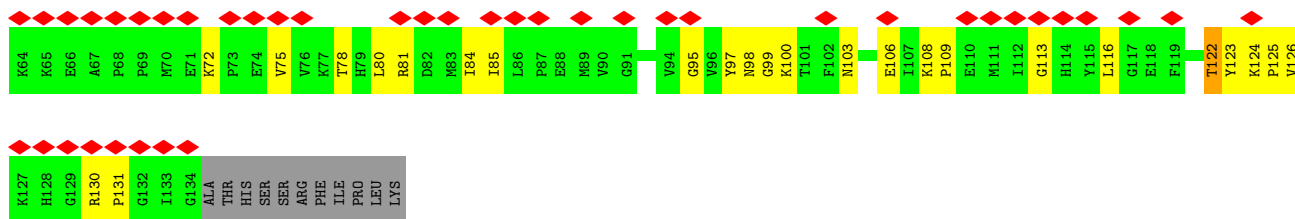
• Molecule 14: 40S ribosomal protein S9



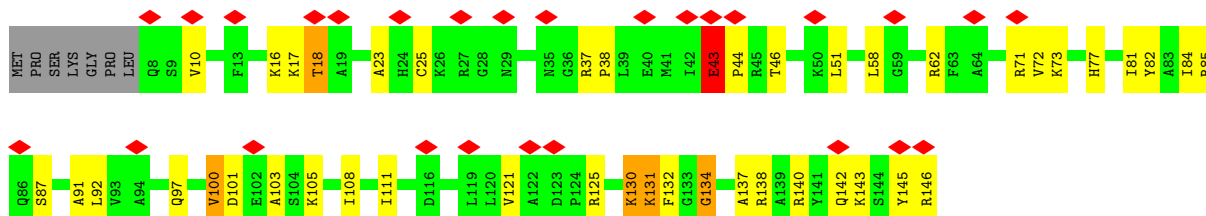
• Molecule 15: 40S ribosomal protein S10



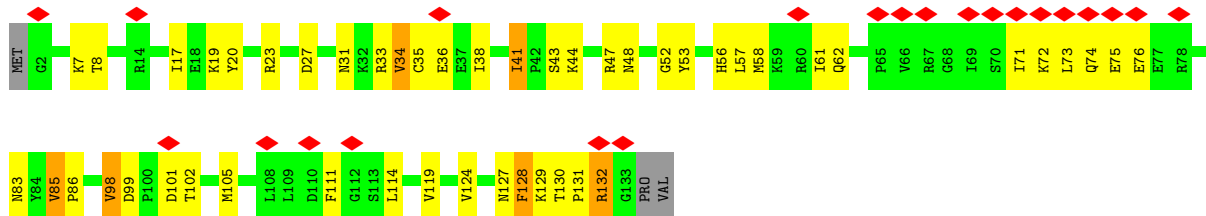




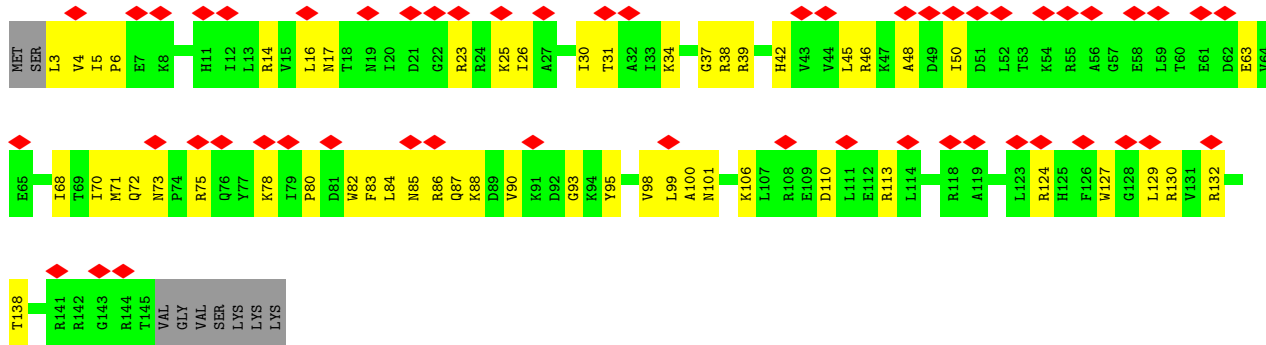
• Molecule 21: 40S ribosomal protein S16



• Molecule 22: 40S ribosomal protein S17

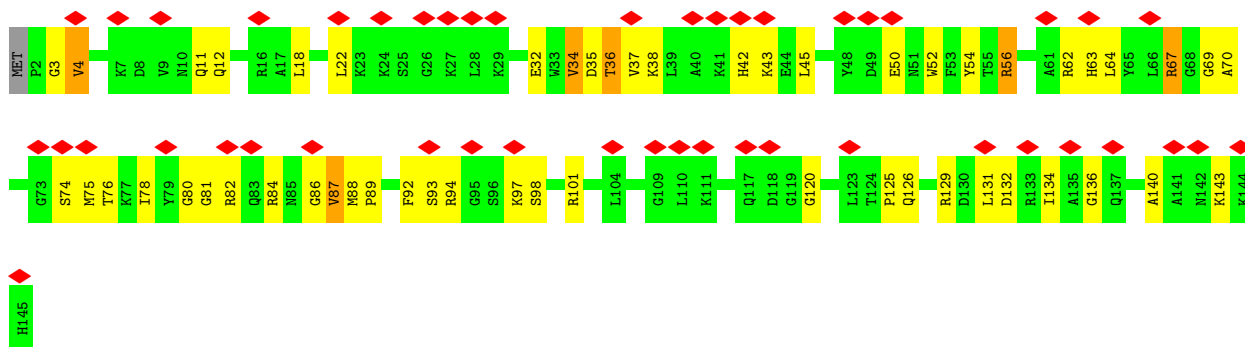


• Molecule 23: 40S ribosomal protein S18

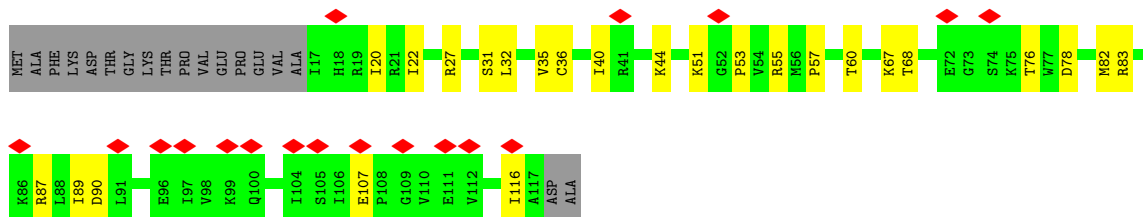


• Molecule 24: 40S ribosomal protein S19

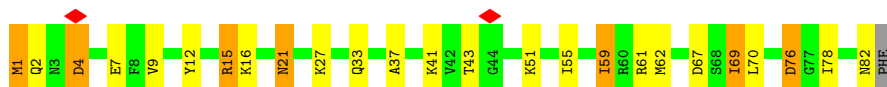




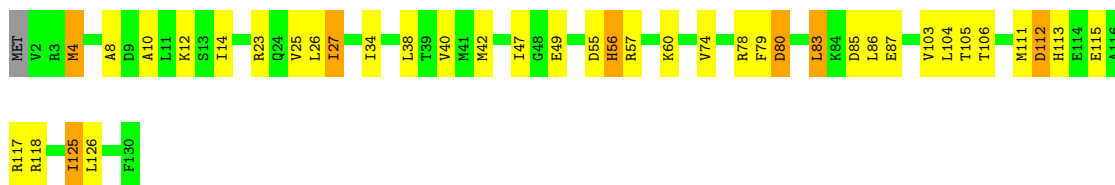
• Molecule 25: 40S ribosomal protein S20



• Molecule 26: 40S ribosomal protein S21



• Molecule 27: 40S ribosomal protein S15a

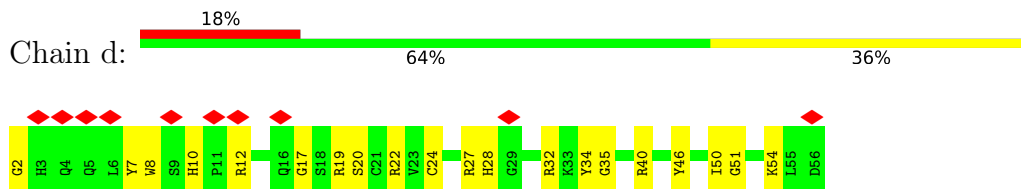


• Molecule 28: 40S ribosomal protein S23

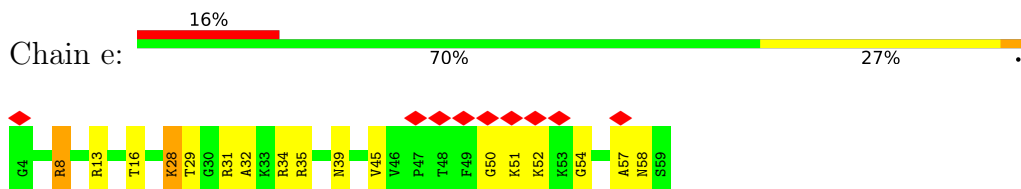




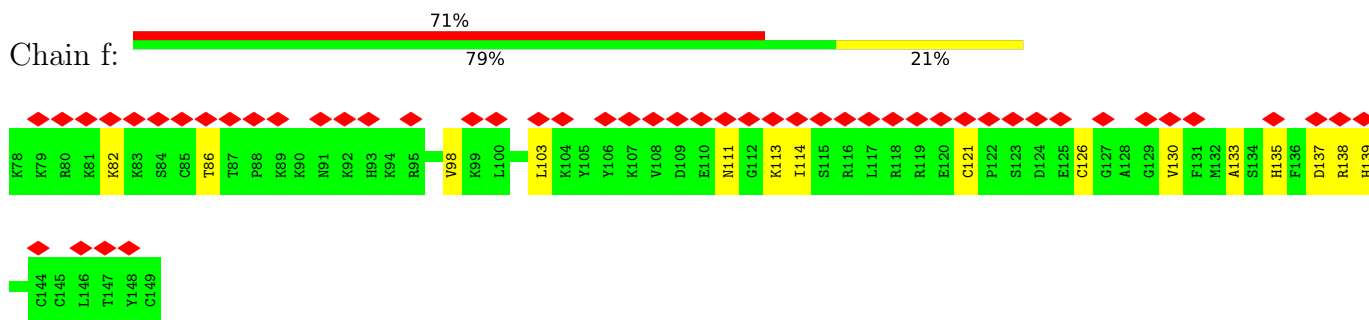
• Molecule 34: 40S ribosomal protein S29



• Molecule 35: 40S ribosomal protein S30



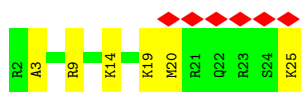
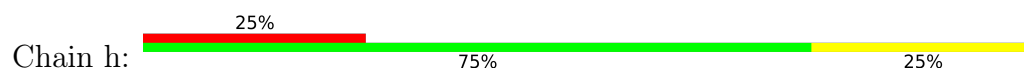
• Molecule 36: Ribosomal protein S27a



• Molecule 37: Receptor of activated protein C kinase 1



• Molecule 38: RIBOSOMAL PROTEIN EL41



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	62177	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.881	Depositor
Minimum map value	-0.648	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	274.4, 274.4, 274.4	wwPDB
Map dimensions	196, 196, 196	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	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	0.85	5/3816 (0.1%)	1.14	24/5171 (0.5%)
2	1	0.18	0/1798	0.41	0/2801
3	2	0.22	0/39659	0.41	4/61804 (0.0%)
4	3	0.16	0/4440	0.36	0/6916
5	A	0.44	0/1742	0.86	2/2367 (0.1%)
6	B	0.39	0/1756	0.83	1/2350 (0.0%)
7	C	0.48	0/1726	0.90	7/2332 (0.3%)
8	D	0.36	0/1780	0.82	2/2397 (0.1%)
9	E	0.41	0/2118	0.91	8/2849 (0.3%)
10	F	0.43	0/1516	0.85	1/2037 (0.0%)
11	G	0.39	0/1885	0.87	8/2510 (0.3%)
12	H	0.42	0/1524	0.91	3/2042 (0.1%)
13	I	0.39	0/1704	0.86	1/2274 (0.0%)
14	J	0.40	0/1524	0.89	4/2035 (0.2%)
15	K	0.33	0/824	0.79	0/1112
16	L	0.45	0/1250	0.95	5/1673 (0.3%)
17	M	0.36	0/963	0.76	0/1291
18	N	0.44	0/1226	0.91	4/1649 (0.2%)
19	O	0.42	0/1023	0.95	0/1372
20	P	0.35	0/1003	0.78	2/1341 (0.1%)
21	Q	0.36	0/1126	0.93	4/1506 (0.3%)
22	R	0.58	2/1081 (0.2%)	0.98	4/1449 (0.3%)
23	S	0.33	0/1202	0.77	2/1610 (0.1%)
24	T	0.36	0/1142	0.82	0/1530
25	U	0.37	0/813	0.81	0/1092
26	V	0.42	0/631	0.82	0/844
27	W	0.51	0/1051	0.90	1/1406 (0.1%)
28	X	0.48	0/1116	0.94	2/1490 (0.1%)
29	Y	0.40	0/1031	0.83	1/1370 (0.1%)
30	Z	0.42	0/580	0.77	0/780
31	a	0.44	0/828	0.90	0/1109
32	b	0.42	0/653	0.87	1/876 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.42	0/481	0.81	1/643 (0.2%)
34	d	0.35	0/469	0.87	1/623 (0.2%)
35	e	0.40	0/447	0.84	0/587
36	f	0.32	0/595	0.81	2/785 (0.3%)
37	g	0.36	0/2497	0.80	2/3399 (0.1%)
38	h	0.35	0/232	0.79	0/295
All	All	0.36	7/89252 (0.0%)	0.67	97/129717 (0.1%)

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
8	D	0	1
28	X	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	277	LYS	CA-C	8.82	1.60	1.52
1	0	120	PRO	CA-C	8.22	1.59	1.52
1	0	301	CYS	C-O	-6.33	1.18	1.24
22	R	71	ILE	C-O	-6.30	1.14	1.23
1	0	278	CYS	C-O	-5.28	1.17	1.24

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	377	HIS	CA-C-N	12.32	133.06	120.38
1	0	377	HIS	C-N-CA	12.32	133.06	120.38
1	0	378	PRO	N-CA-C	9.58	122.39	110.70
16	L	41	GLY	N-CA-C	9.17	123.73	112.73
1	0	160	GLY	N-CA-C	-8.87	102.42	115.63

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	D	193	ASP	Peptide

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Mol	Chain	Res	Type	Group
28	X	107	ARG	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	0	3740	0	3855	79	0
2	1	1608	0	816	24	0
3	2	35466	0	17905	622	0
4	3	3976	0	2013	47	0
5	A	1705	0	1706	60	0
6	B	1729	0	1803	59	0
7	C	1690	0	1777	47	0
8	D	1752	0	1848	47	0
9	E	2076	0	2177	55	0
10	F	1495	0	1549	44	0
11	G	1862	0	2018	79	0
12	H	1501	0	1593	37	0
13	I	1675	0	1755	36	0
14	J	1499	0	1618	48	0
15	K	800	0	818	22	0
16	L	1229	0	1302	44	0
17	M	953	0	990	25	0
18	N	1202	0	1289	31	0
19	O	1010	0	1034	47	0
20	P	984	0	1028	33	0
21	Q	1109	0	1174	34	0
22	R	1068	0	1120	34	0
23	S	1184	0	1244	47	0
24	T	1122	0	1153	53	0
25	U	803	0	873	20	0
26	V	625	0	628	18	0
27	W	1034	0	1080	20	0
28	X	1098	0	1167	33	0
29	Y	1014	0	1082	28	0
30	Z	574	0	627	20	0
31	a	814	0	863	29	0
32	b	640	0	665	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	c	479	0	507	15	0
34	d	458	0	448	15	0
35	e	442	0	487	10	0
36	f	585	0	615	10	0
37	g	2440	0	2396	61	0
38	h	231	0	277	3	0
39	a	1	0	0	0	0
39	d	1	0	0	0	0
39	f	1	0	0	0	0
All	All	83675	0	65300	1627	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 11.

The worst 5 of 1627 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)
1:0:9:LYS:NZ	3:2:966:U:OP1	1.92	1.02
7:C:60:TRP:O	7:C:71:LYS:NZ	1.93	1.01
3:2:615:C:O2'	35:e:8:ARG:NH1	1.94	0.99
37:g:245:ARG:HH12	37:g:312:VAL:HG11	1.29	0.93
9:E:11:ARG:NH1	9:E:24:THR:OG1	2.03	0.92

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	473/584 (81%)	451 (95%)	20 (4%)	2 (0%)	30 66
5	A	214/295 (72%)	202 (94%)	11 (5%)	1 (0%)	24 62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	B	211/264 (80%)	200 (95%)	11 (5%)	0	100	100
7	C	216/293 (74%)	215 (100%)	1 (0%)	0	100	100
8	D	223/243 (92%)	214 (96%)	8 (4%)	1 (0%)	30	66
9	E	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
10	F	187/204 (92%)	172 (92%)	13 (7%)	2 (1%)	11	45
11	G	228/249 (92%)	218 (96%)	10 (4%)	0	100	100
12	H	184/194 (95%)	174 (95%)	9 (5%)	1 (0%)	24	62
13	I	203/208 (98%)	196 (97%)	7 (3%)	0	100	100
14	J	178/194 (92%)	173 (97%)	4 (2%)	1 (1%)	21	58
15	K	93/165 (56%)	89 (96%)	4 (4%)	0	100	100
16	L	149/158 (94%)	145 (97%)	4 (3%)	0	100	100
17	M	121/132 (92%)	111 (92%)	10 (8%)	0	100	100
18	N	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
19	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
20	P	118/145 (81%)	117 (99%)	1 (1%)	0	100	100
21	Q	137/146 (94%)	131 (96%)	6 (4%)	0	100	100
22	R	128/135 (95%)	121 (94%)	7 (6%)	0	100	100
23	S	141/152 (93%)	136 (96%)	5 (4%)	0	100	100
24	T	142/145 (98%)	137 (96%)	4 (3%)	1 (1%)	18	54
25	U	99/119 (83%)	94 (95%)	5 (5%)	0	100	100
26	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
27	W	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
28	X	139/143 (97%)	131 (94%)	7 (5%)	1 (1%)	18	54
29	Y	122/130 (94%)	118 (97%)	4 (3%)	0	100	100
30	Z	70/125 (56%)	65 (93%)	5 (7%)	0	100	100
31	a	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
32	b	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
33	c	59/61 (97%)	56 (95%)	3 (5%)	0	100	100
34	d	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
35	e	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
36	f	70/72 (97%)	65 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	312/315 (99%)	295 (95%)	16 (5%)	1 (0%)	36	71
38	h	22/24 (92%)	22 (100%)	0	0	100	100
All	All	5272/5967 (88%)	5046 (96%)	215 (4%)	11 (0%)	44	77

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	189	ILE
12	H	170	VAL
14	J	161	LEU
28	X	108	LYS
37	g	145	GLU

### 5.3.2 Protein sidechains [i](#)

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	417/511 (82%)	402 (96%)	15 (4%)	31	52
5	A	180/243 (74%)	155 (86%)	25 (14%)	3	16
6	B	194/231 (84%)	173 (89%)	21 (11%)	6	22
7	C	184/225 (82%)	148 (80%)	36 (20%)	1	9
8	D	189/202 (94%)	180 (95%)	9 (5%)	23	45
9	E	224/225 (100%)	195 (87%)	29 (13%)	4	18
10	F	159/170 (94%)	149 (94%)	10 (6%)	16	39
11	G	200/218 (92%)	186 (93%)	14 (7%)	14	37
12	H	167/174 (96%)	153 (92%)	14 (8%)	10	31
13	I	176/180 (98%)	155 (88%)	21 (12%)	5	20
14	J	160/168 (95%)	138 (86%)	22 (14%)	3	16
15	K	86/136 (63%)	84 (98%)	2 (2%)	44	64
16	L	135/142 (95%)	107 (79%)	28 (21%)	1	7
17	M	104/108 (96%)	95 (91%)	9 (9%)	9	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	N	130/131 (99%)	116 (89%)	14 (11%)	6	22
19	O	105/119 (88%)	95 (90%)	10 (10%)	8	26
20	P	107/130 (82%)	104 (97%)	3 (3%)	38	59
21	Q	115/121 (95%)	107 (93%)	8 (7%)	14	37
22	R	119/122 (98%)	105 (88%)	14 (12%)	5	20
23	S	124/132 (94%)	119 (96%)	5 (4%)	28	49
24	T	114/115 (99%)	107 (94%)	7 (6%)	17	40
25	U	93/107 (87%)	90 (97%)	3 (3%)	34	56
26	V	66/67 (98%)	54 (82%)	12 (18%)	2	11
27	W	112/113 (99%)	93 (83%)	19 (17%)	2	12
28	X	113/115 (98%)	105 (93%)	8 (7%)	13	36
29	Y	108/112 (96%)	97 (90%)	11 (10%)	7	24
30	Z	64/103 (62%)	59 (92%)	5 (8%)	11	33
31	a	88/88 (100%)	73 (83%)	15 (17%)	2	12
32	b	74/74 (100%)	64 (86%)	10 (14%)	4	17
33	c	54/54 (100%)	51 (94%)	3 (6%)	19	42
34	d	48/48 (100%)	45 (94%)	3 (6%)	16	39
35	e	45/45 (100%)	39 (87%)	6 (13%)	4	17
36	f	65/65 (100%)	63 (97%)	2 (3%)	35	56
37	g	272/273 (100%)	250 (92%)	22 (8%)	11	32
38	h	23/23 (100%)	21 (91%)	2 (9%)	9	30
All	All	4614/5090 (91%)	4177 (90%)	437 (10%)	10	26

5 of 437 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	L	69	ARG
21	Q	100	VAL
33	c	26	GLN
16	L	85	THR
18	N	80	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
23	S	87	GLN
35	e	37	GLN
23	S	101	ASN
29	Y	15	ASN
37	g	51	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	74/75 (98%)	47 (63%)	4 (5%)
3	2	1652/1868 (88%)	558 (33%)	62 (3%)
4	3	183/275 (66%)	98 (53%)	18 (9%)
All	All	1909/2218 (86%)	703 (36%)	84 (4%)

5 of 703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	4	G
2	1	6	C
2	1	7	G
2	1	8	U
2	1	9	G

5 of 84 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	1585	U
4	3	230	G
3	2	1601	A
3	2	1838	U
4	3	252	A

## 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
22	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	72:LYS	C	73:LEU	N	4.52

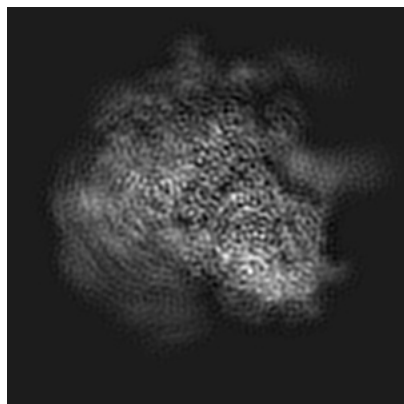
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3770. These allow visual inspection of the internal detail of the map and identification of artifacts.

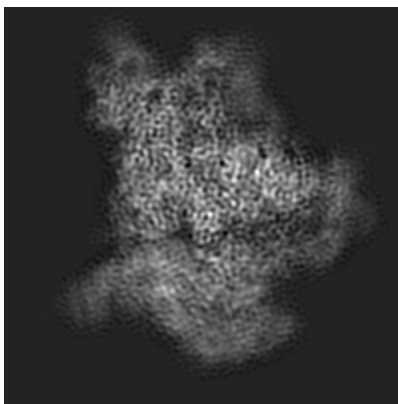
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

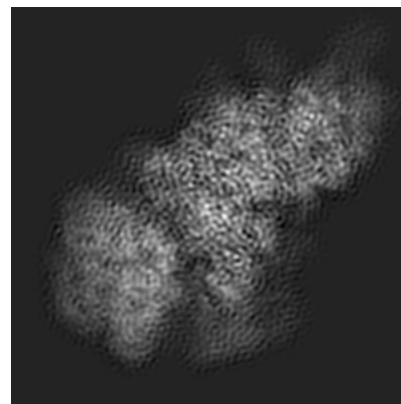
#### 6.1.1 Primary map



X

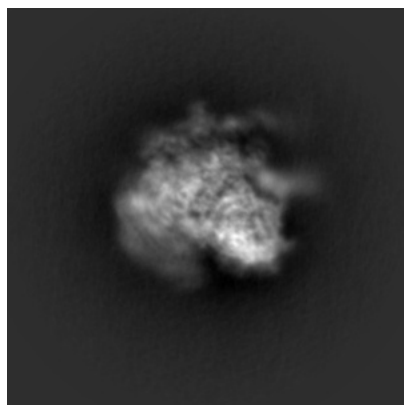


Y

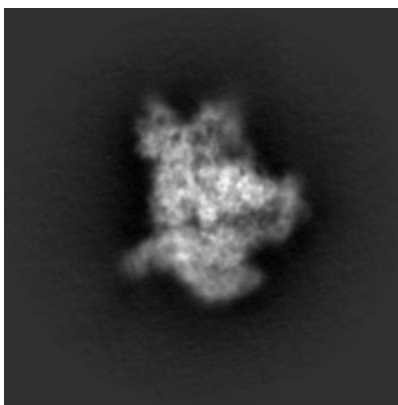


Z

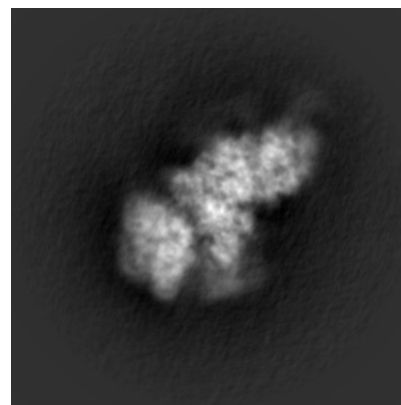
#### 6.1.2 Raw map



X



Y

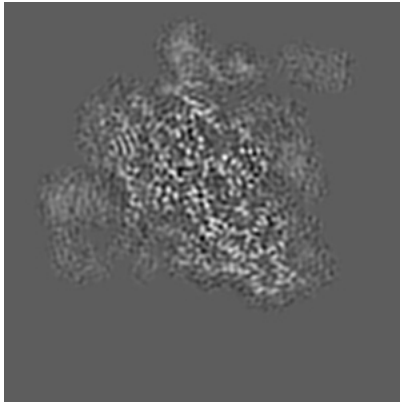


Z

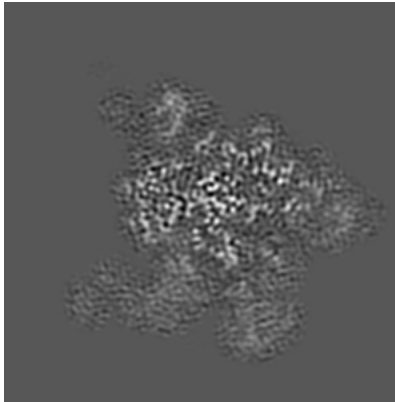
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

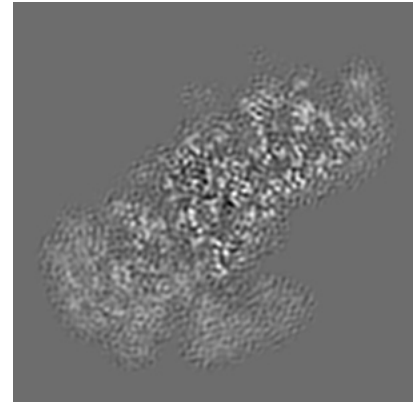
### 6.2.1 Primary map



X Index: 98

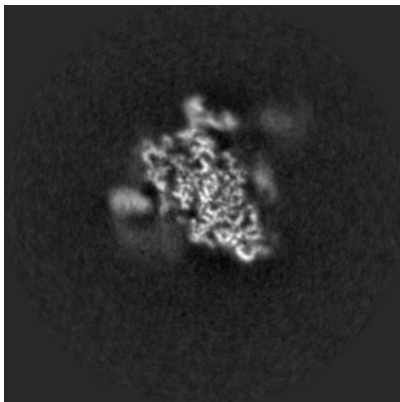


Y Index: 98

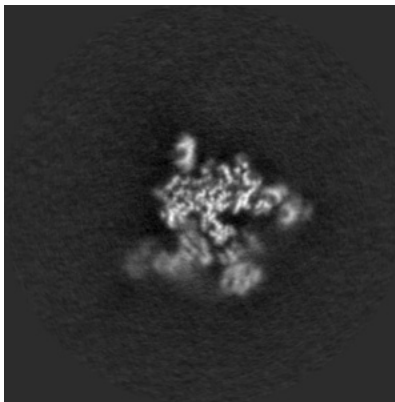


Z Index: 98

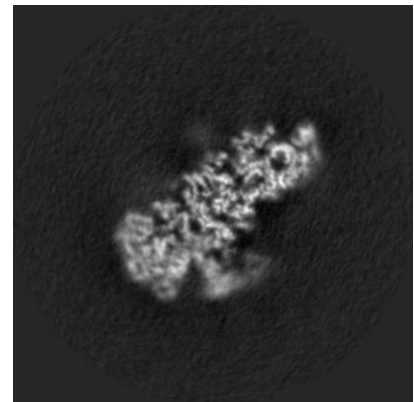
### 6.2.2 Raw map



X Index: 160



Y Index: 160

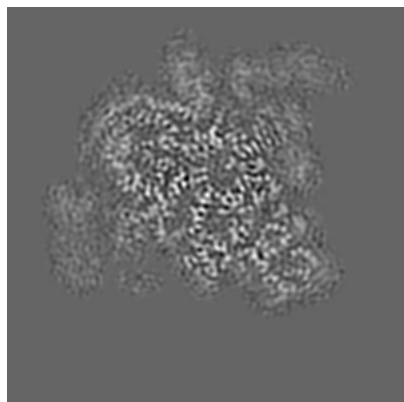


Z Index: 160

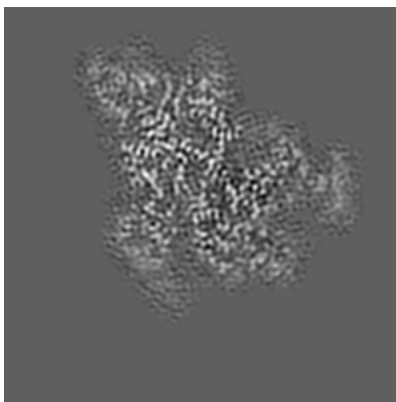
The images above show central slices of the map in three orthogonal directions.

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

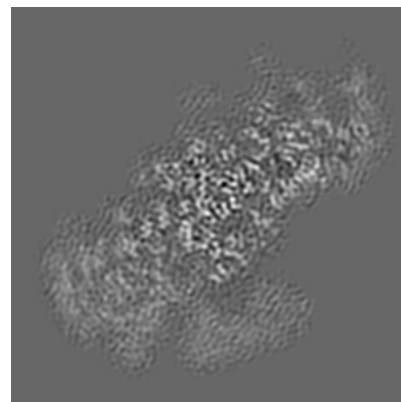
### 6.3.1 Primary map



X Index: 105

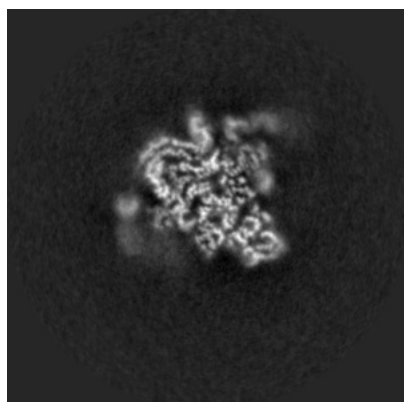


Y Index: 117

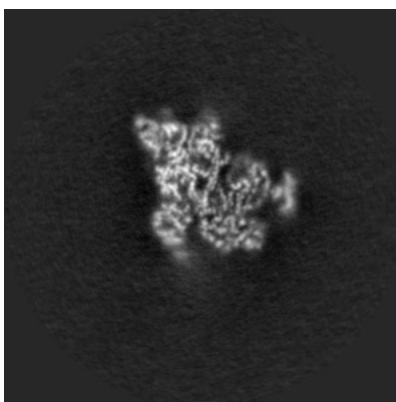


Z Index: 101

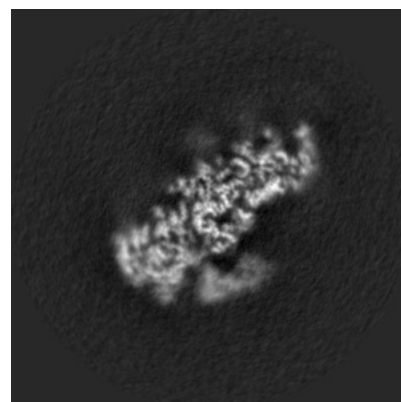
### 6.3.2 Raw map



X Index: 169



Y Index: 181

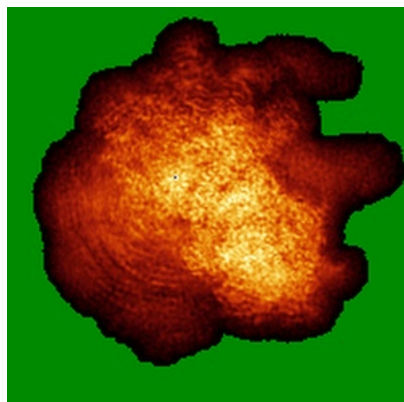


Z Index: 165

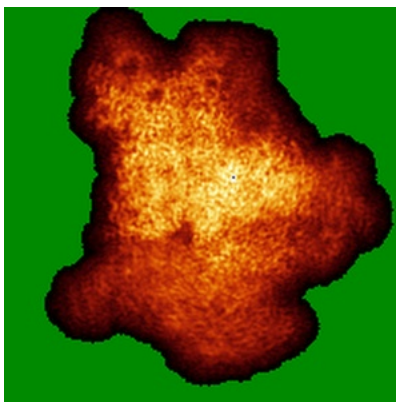
The images above show the largest variance slices of the map in three orthogonal directions.

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

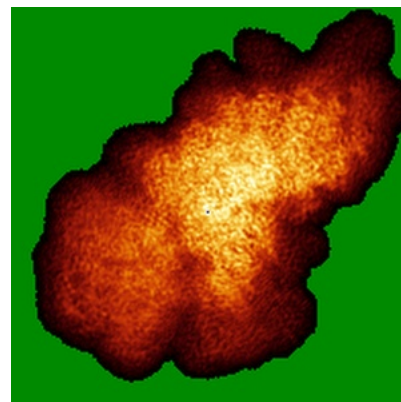
### 6.4.1 Primary map



X

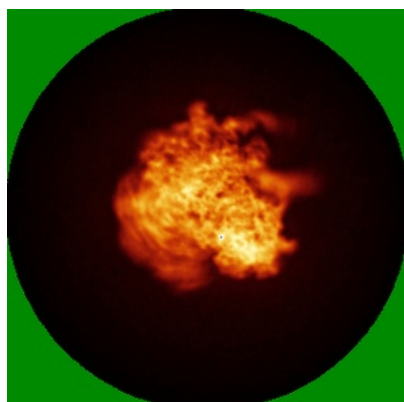


Y

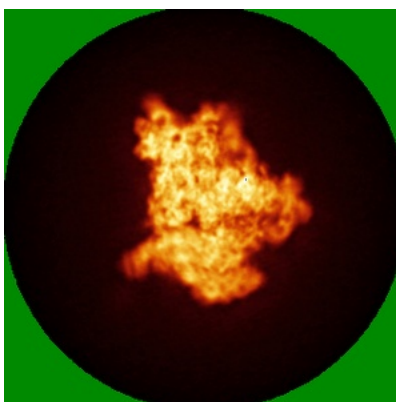


Z

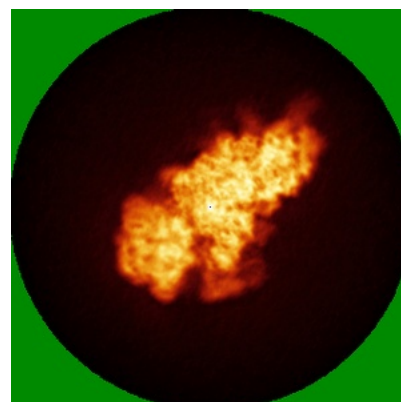
### 6.4.2 Raw map



X



Y

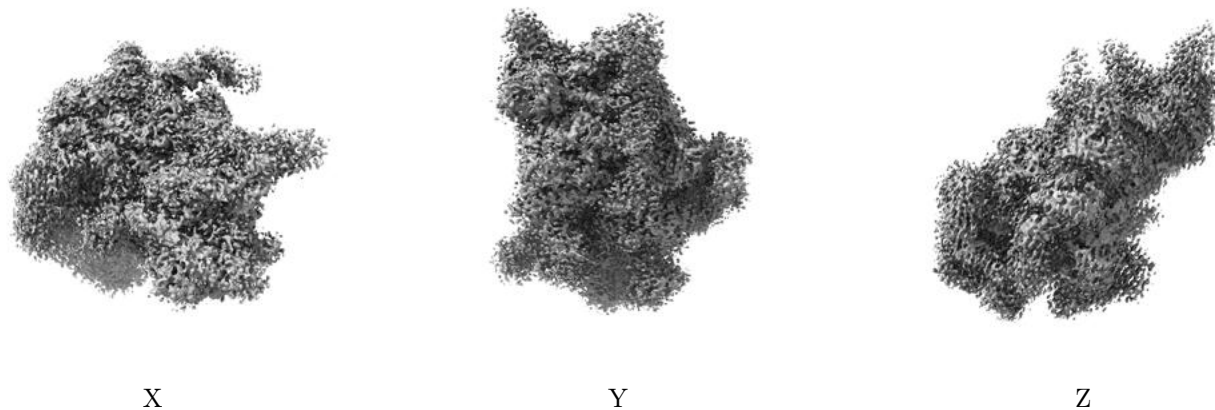


Z

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

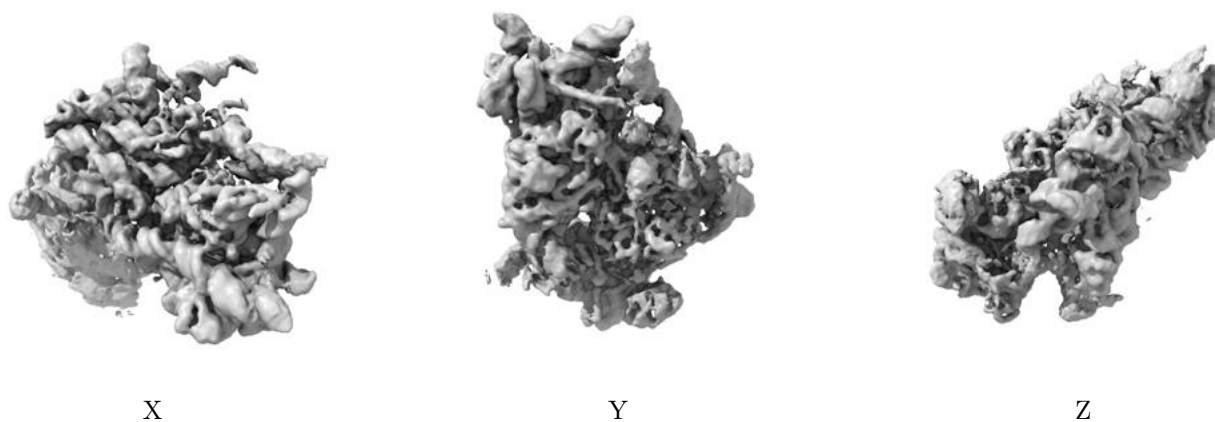
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. 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.

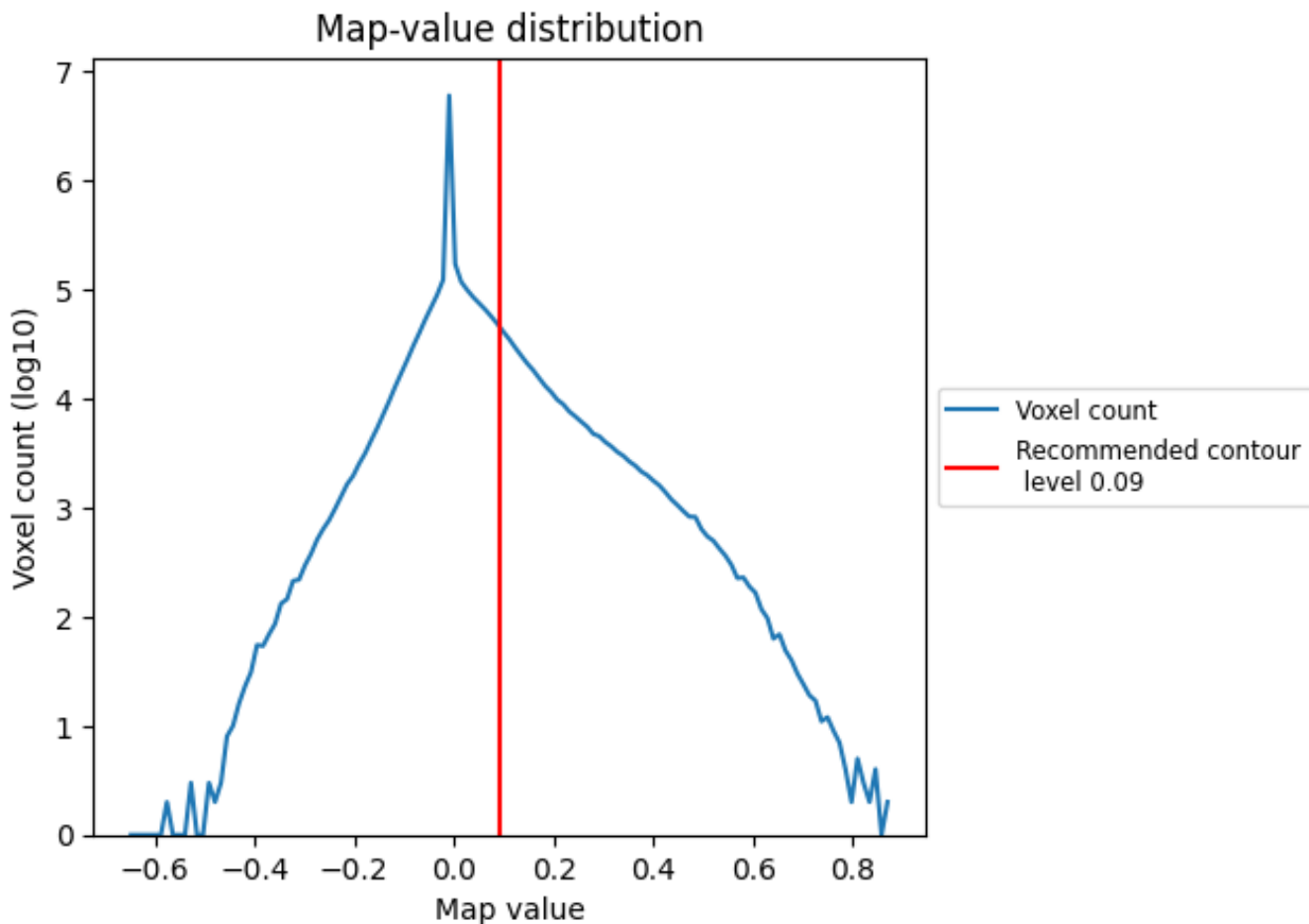
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

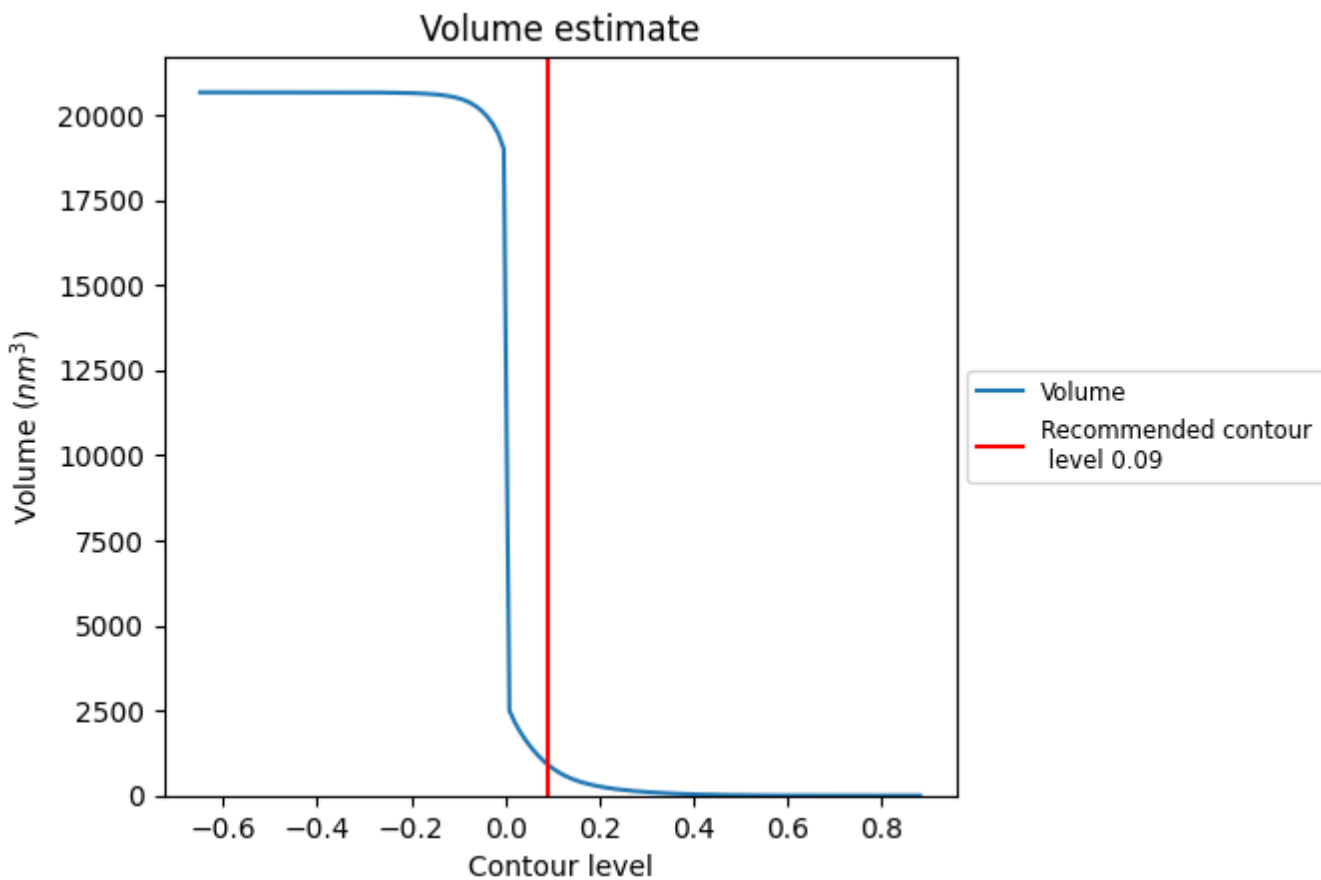
This section contains the results of statistical analysis of the map.

### 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.

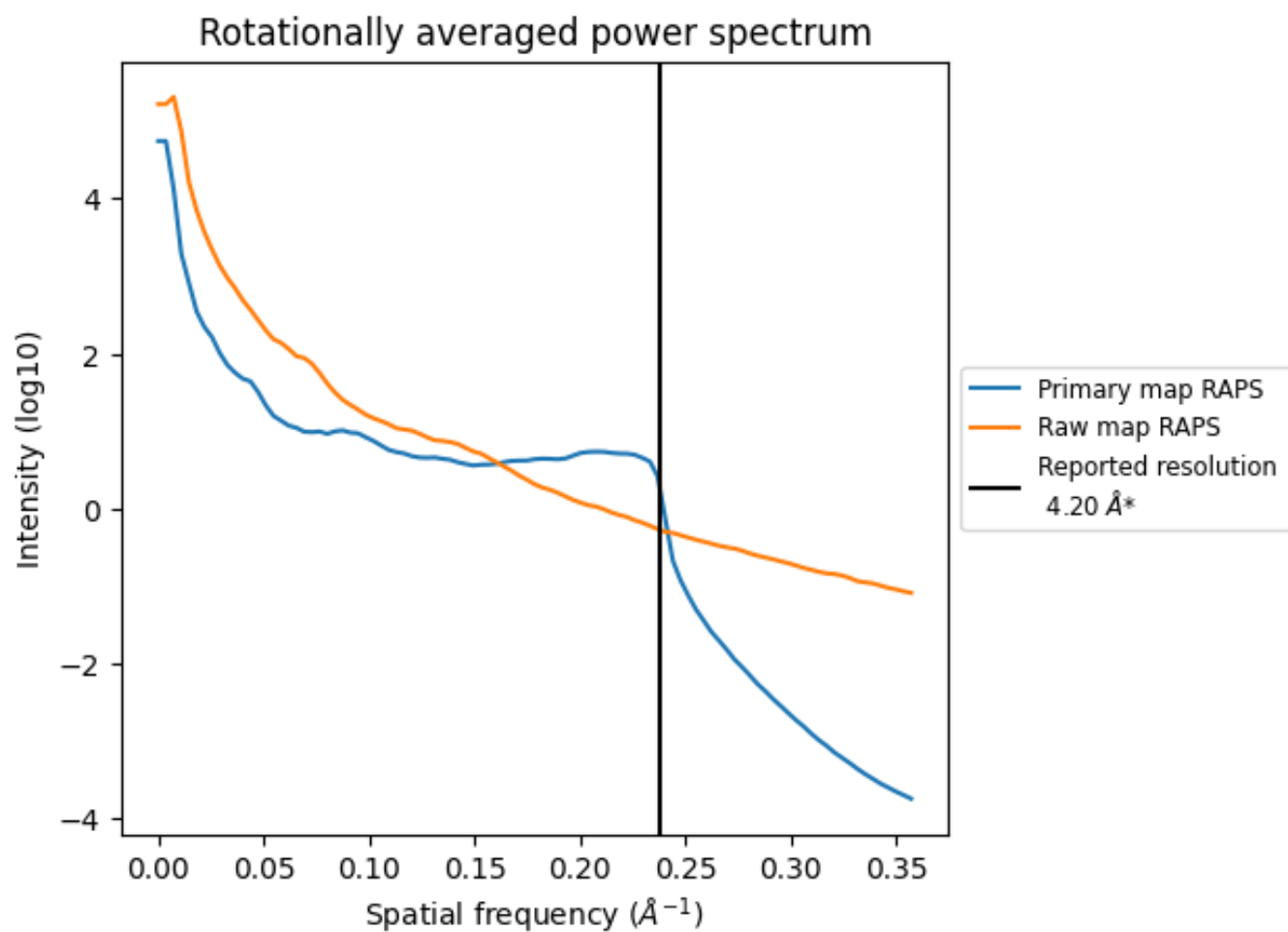
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 916 nm<sup>3</sup>; this corresponds to an approximate mass of 827 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](#)

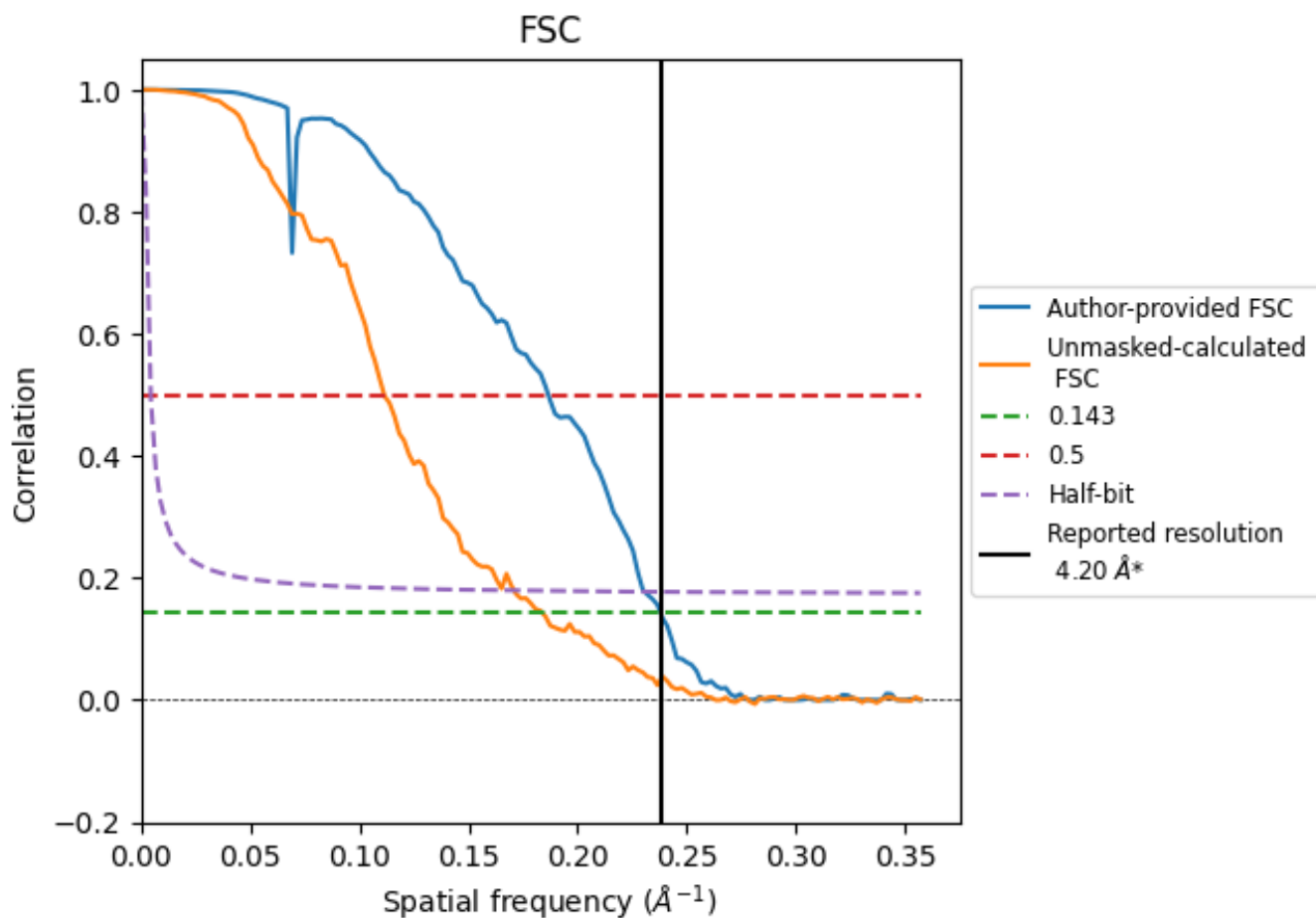


\*Reported resolution corresponds to spatial frequency of 0.238 Å<sup>-1</sup>

## 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 0.238 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.20	5.36	4.33
Unmasked-calculated*	5.44	8.98	5.85

\*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 5.44 differs from the reported value 4.2 by more than 10 %

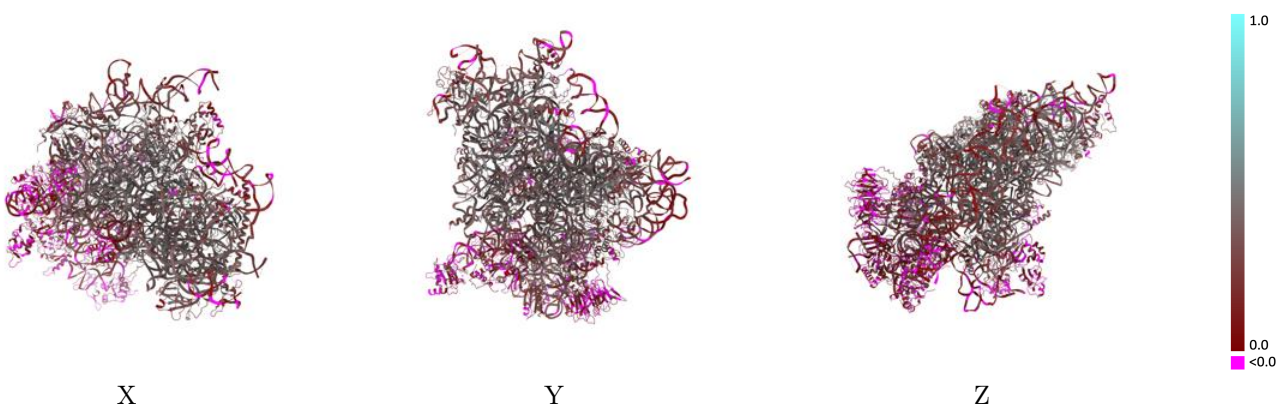
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3770 and PDB model 5OA3. Per-residue inclusion information can be found in section 3 on page 11.

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

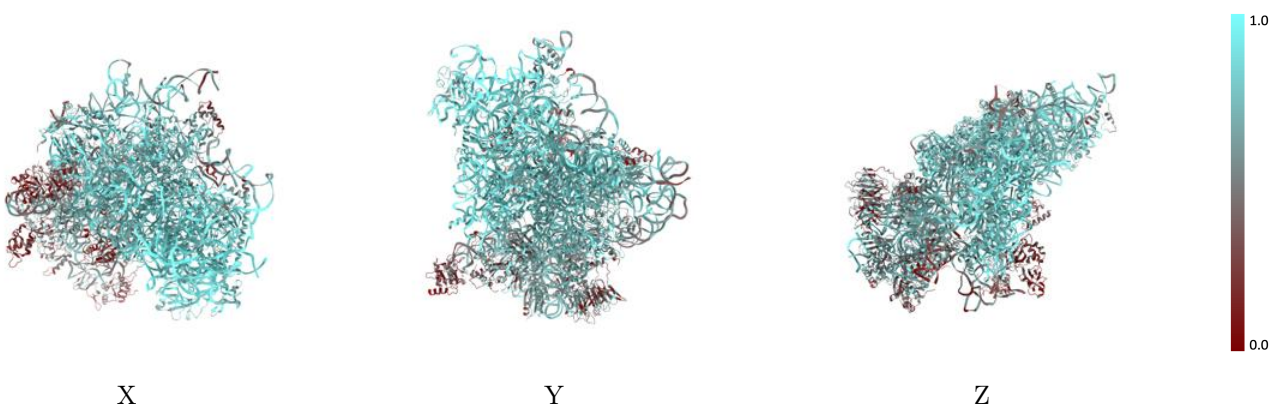
This section was not generated.

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



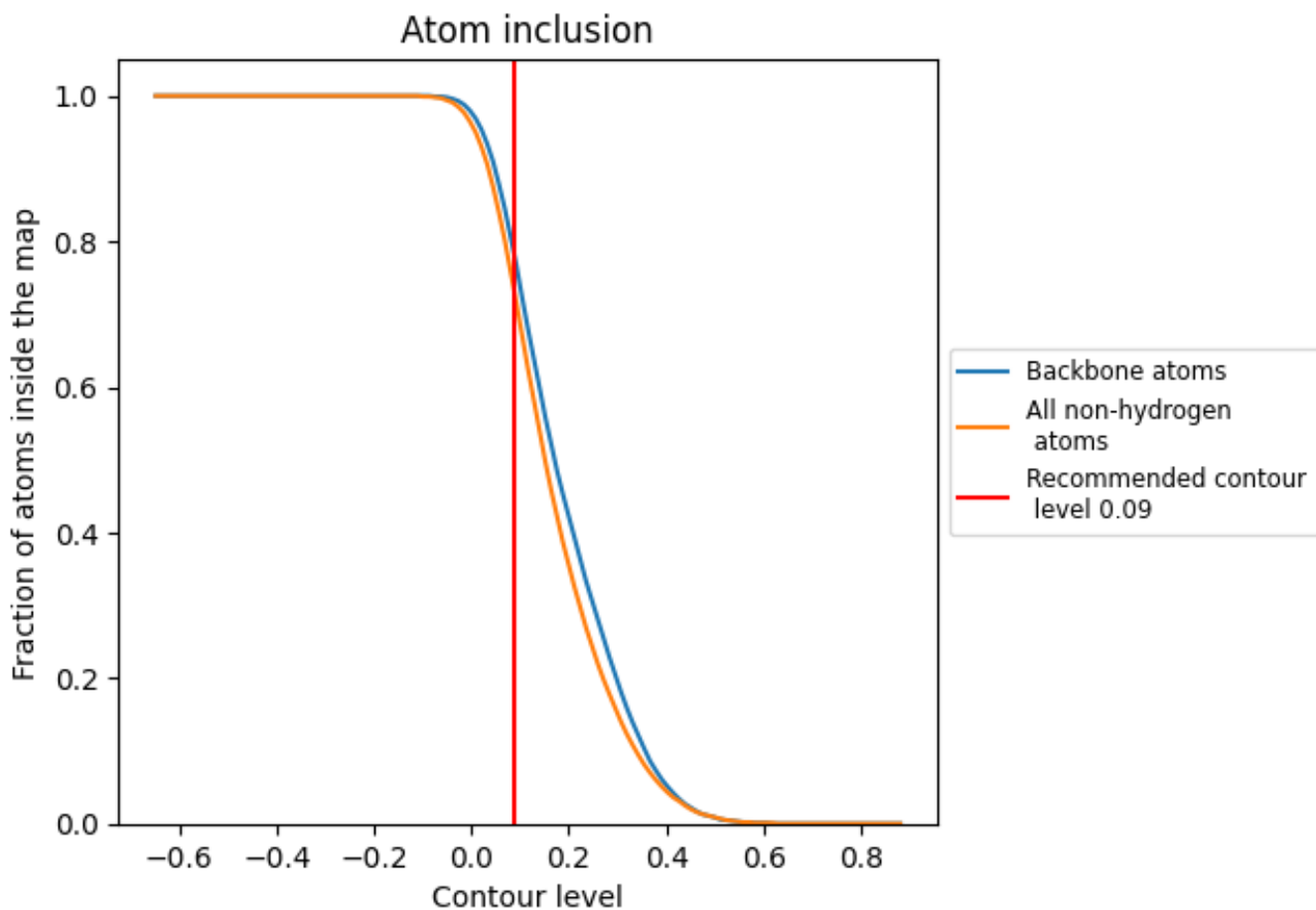
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary









The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.2650
0	 0.2800	 0.0960
1	 0.4910	 0.0950
2	 0.8640	 0.3120
3	 0.6250	 0.1520
A	 0.7840	 0.3440
B	 0.7810	 0.3450
C	 0.7940	 0.3880
D	 0.5830	 0.1790
E	 0.8270	 0.3970
F	 0.4720	 0.1010
G	 0.7870	 0.3110
H	 0.6180	 0.2840
I	 0.7680	 0.3290
J	 0.8270	 0.3810
K	 0.4880	 0.1030
L	 0.7680	 0.3780
M	 0.2180	 0.0450
N	 0.8140	 0.3700
O	 0.7490	 0.3300
P	 0.3980	 0.0540
Q	 0.5910	 0.1510
R	 0.6040	 0.2430
S	 0.4960	 0.0970
T	 0.5170	 0.1010
U	 0.6220	 0.2370
V	 0.8000	 0.3710
W	 0.8200	 0.4260
X	 0.8250	 0.4100
Y	 0.8350	 0.3600
Z	 0.3740	 0.0470
a	 0.7760	 0.3810
b	 0.7710	 0.3450
c	 0.4140	 0.1040
d	 0.6120	 0.1920



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*Continued from previous page...*

Chain	Atom inclusion	Q-score
e	 0.6860	 0.3280
f	 0.2580	 0.0210
g	 0.4360	 0.0400
h	 0.6860	 0.3190