



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 12:23 AM UTC

PDB ID : 9F58 / pdb_00009f58
EMDB ID : EMD-50188
Title : Gen2 dimer bound to the 60S ribosomal subunit
Authors : Paternoga, H.; Dimitrova-Paternoga, L.; Wilson, D.N.
Deposited on : 2024-04-28
Resolution : 3.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

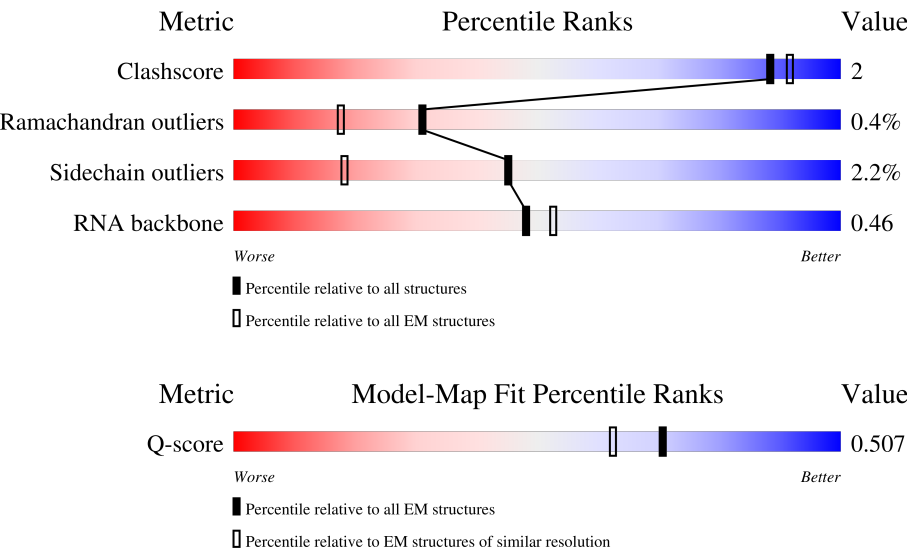
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	A	1659	19% 19% 81%
1	C	1659	16% 15% 84%
1	D	1659	29% 24% 71%

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Mol	Chain	Length	Quality of chain
1	E	1659	
1	H	1659	
1	I	1659	
2	P	25	
3	4	158	
4	b	121	
5	d	387	
6	e	297	
7	f	176	
8	g	244	
9	h	256	
10	i	191	
11	j	221	
12	k	174	
13	m	199	
14	n	138	
15	o	204	
16	p	199	
17	q	184	
18	r	186	
19	s	189	
20	t	172	
21	u	160	
22	v	121	
23	w	137	

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Mol	Chain	Length	Quality of chain
24	y	155	
25	z	142	
26	J	127	
27	K	136	
28	L	149	
29	M	59	
30	N	105	
31	O	113	
32	Q	130	
33	R	107	
34	T	120	
35	U	100	
36	V	88	
37	W	78	
38	X	51	
39	Y	128	
40	Z	106	
41	0	92	
42	3	362	
43	S	121	
44	c	254	
45	a	3396	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 135896 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 eIF-2-alpha kinase GCN2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	322	Total	C	N	O	S	0	0
			2590	1683	417	477	13		
1	H	104	Total	C	N	O	S	2	0
			845	531	150	160	4		
1	I	108	Total	C	N	O	S	0	0
			864	543	155	164	2		
1	C	259	Total	C	N	O	S	0	0
			2125	1358	366	392	9		
1	D	474	Total	C	N	O	S	0	0
			3796	2430	637	720	9		
1	E	473	Total	C	N	O	S	0	0
			3790	2429	634	718	9		

- Molecule 2 is a protein called Large ribosomal subunit protein eL41B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	15	Total	C	N	O	S	0	0
			144	89	38	16	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	d	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	e	291	Total	C	N	O	S	0	0
			2333	1474	407	450	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	g	218	Total	C	N	O	S	0	0
			1754	1133	319	301	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	h	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	i	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	j	210	Total	C	N	O	S	0	0
			1700	1080	321	293	6		

- Molecule 12 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	k	166	Total	C	N	O	S	0	0
			1327	832	247	244	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	s	155	Total	C	N	O		
			1249	776	264	209	0	0

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	170	Total	C	N	O	S		
			1432	922	265	242	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	159	Total	C	N	O	S		
			1276	805	246	221	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	v	100	Total	C	N	O		
			796	516	131	149	0	0

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	136	Total	C	N	O	S		
			1003	628	189	179	7	0	0

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S		
			521	336	102	82	1	0	0

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	121	Total	C	N	O	S		
			964	620	169	173	2	0	0

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	J	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	K	129	Total	C	N	O	0	0
			1046	684	193	169		

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	M	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Q	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	R	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	T	117	Total	C	N	O	S	0	0
			960	610	184	165	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	U	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	V	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	W	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	X	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 39 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 40 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	0	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	3	356	Total	C	N	O	S	0	0
			2714	1710	516	485	3		

- Molecule 43 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 44 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	c	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 45 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	3134	Total	C	N	O	P	0	0
			67031	29941	12080	21876	3134		

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	V	1	Total	Zn	0
			1	1	
46	Y	1	Total	Zn	0
			1	1	
46	Z	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
46	0	1	Total 1	Zn 1	0
46	S	1	Total 1	Zn 1	0





ARG	S1622	F1623	F1624	T1625	S1626	T1627	T1628	M1629	M1630	L1631	S1632	K1633	E1634	A1635	H1636	K1637	G1638	M1639	R1640	V1641	A1642	T1643	L1644	V1645	G1646	H1647	T1648	T1649	K1650	K1651	S1652	S1653	V1654	T1655	D1656	L1657	Q1658	R1659
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Chain I: 7%
6% 93%

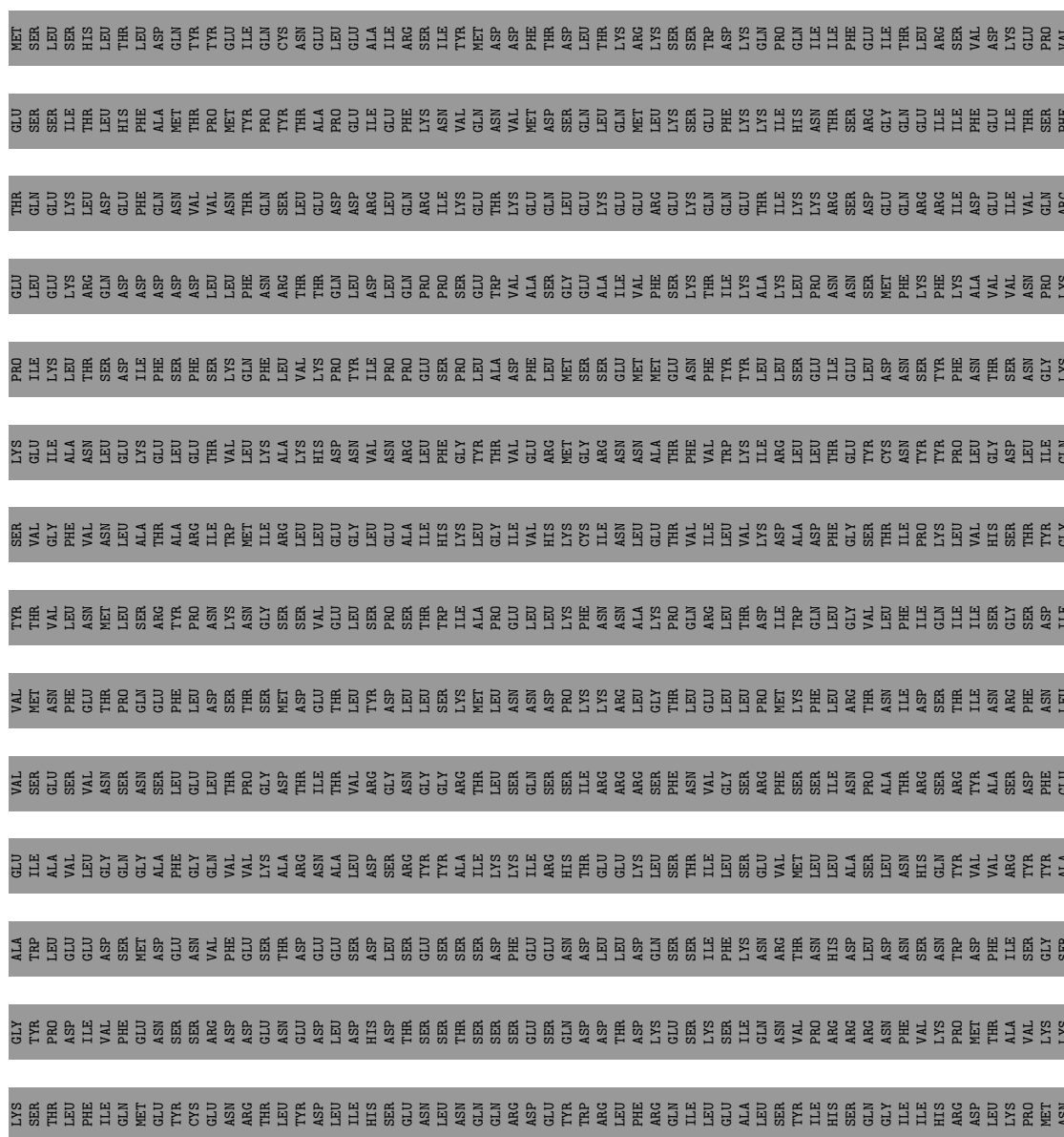
[illegible]

- Molecule 1: eIF-2-alpha kinase GCN2



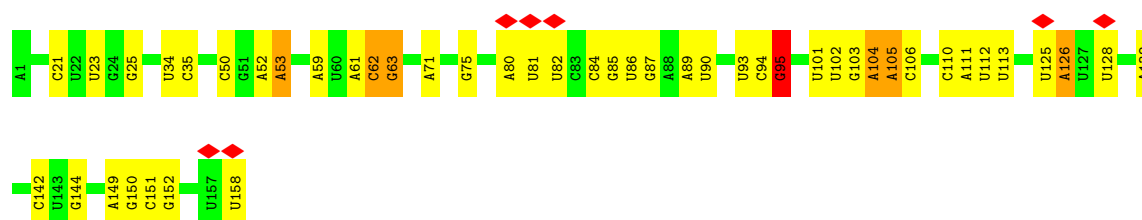




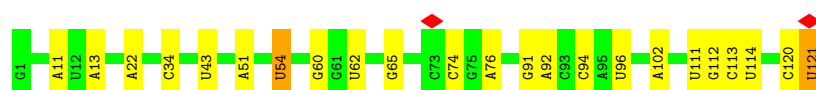
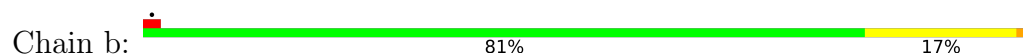




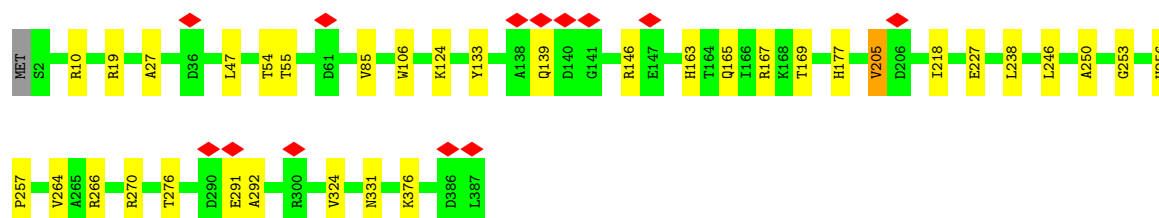
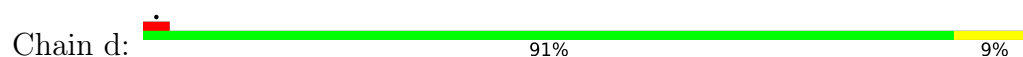
• Molecule 3: 5.8S rRNA



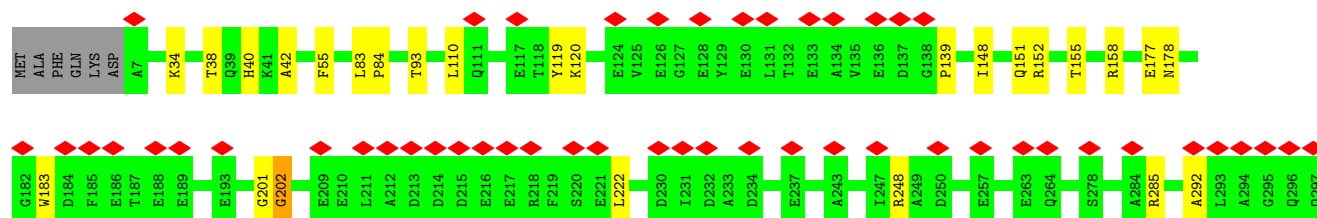
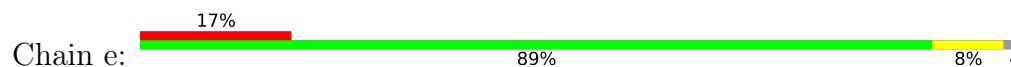
• Molecule 4: 5S rRNA



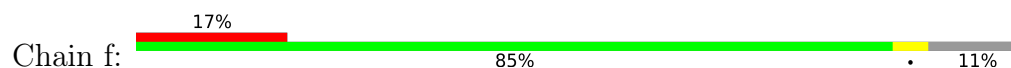
• Molecule 5: 60S ribosomal protein L3

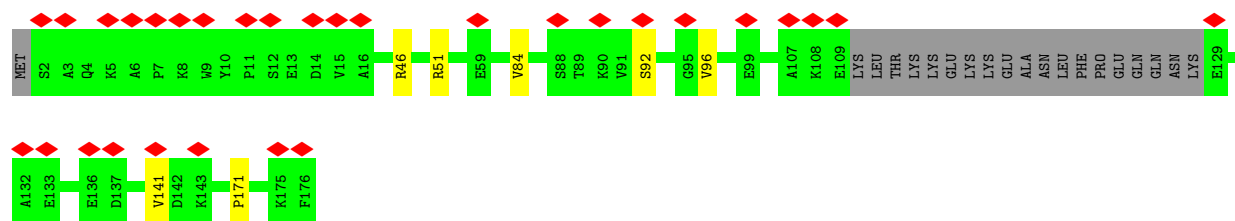


• Molecule 6: 60S ribosomal protein L5

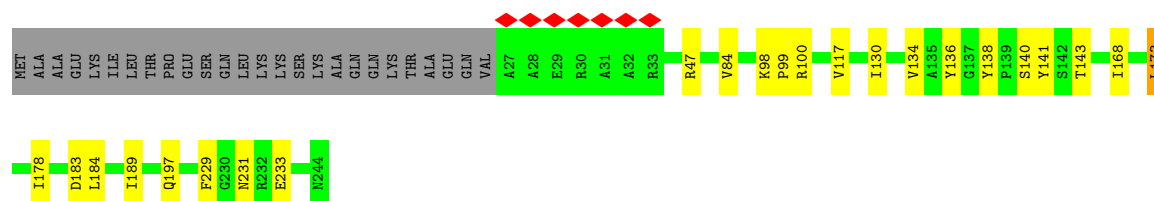
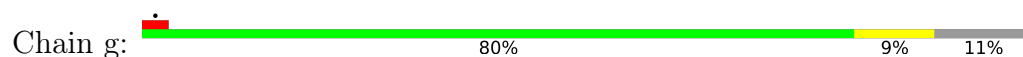


• Molecule 7: 60S ribosomal protein L6-A

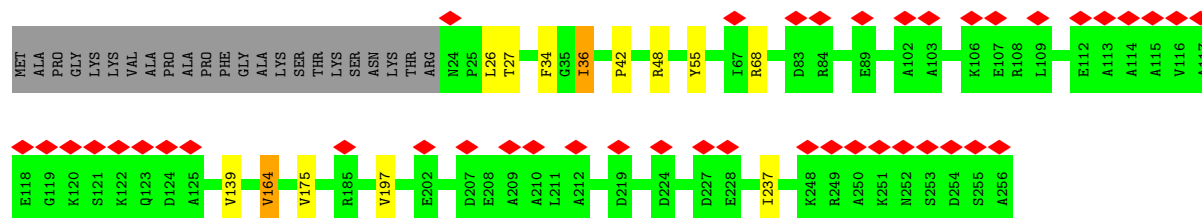
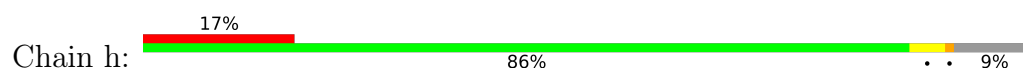




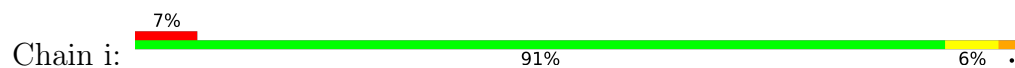
- Molecule 8: 60S ribosomal protein L7-A



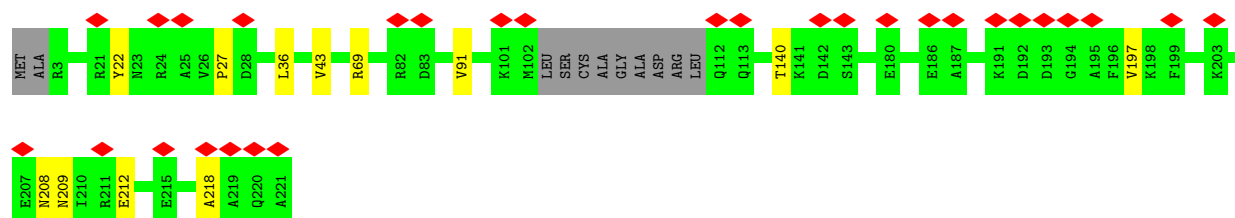
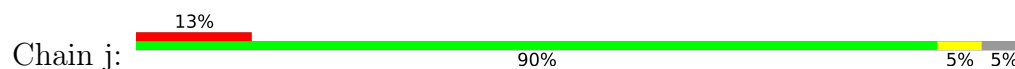
- Molecule 9: 60S ribosomal protein L8-A



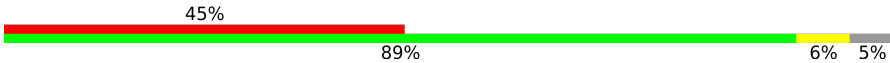
- Molecule 10: 60S ribosomal protein L9-A

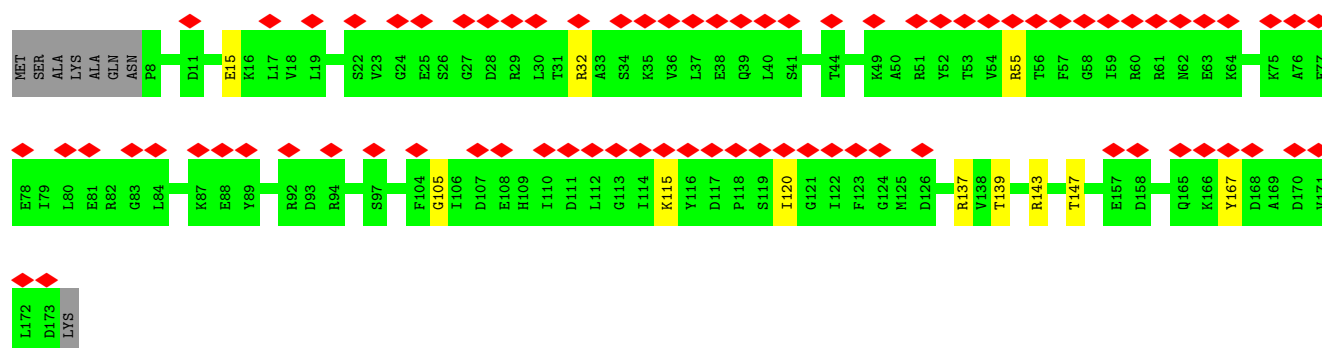


- Molecule 11: 60S ribosomal protein L10

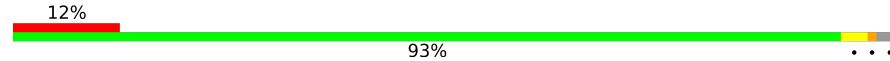


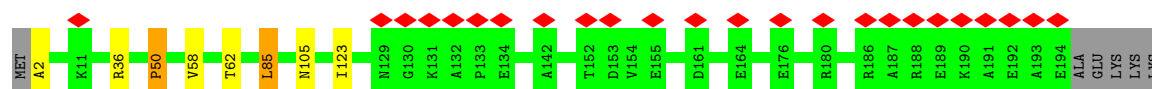
- Molecule 12: 60S ribosomal protein L11-A

Chain k: 

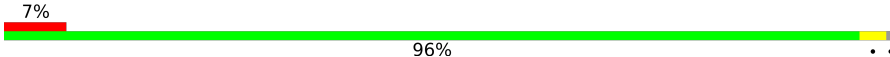


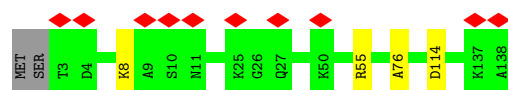
- Molecule 13: 60S ribosomal protein L13-A

Chain m: 

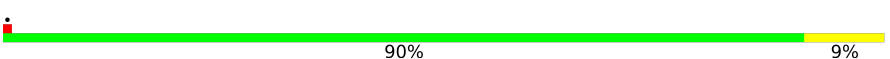


- Molecule 14: 60S ribosomal protein L14-A

Chain n: 



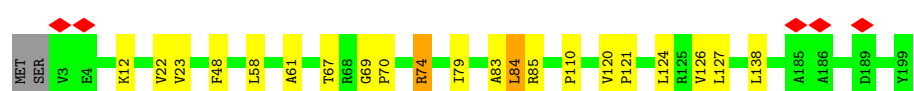
- Molecule 15: 60S ribosomal protein L15-A

Chain o: 

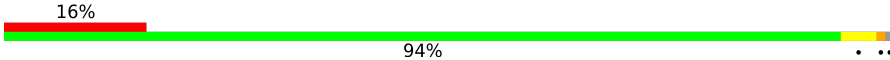


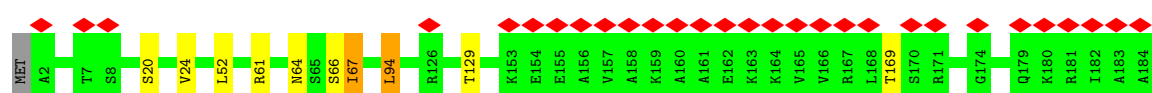
- Molecule 16: 60S ribosomal protein L16-A

Chain p: 

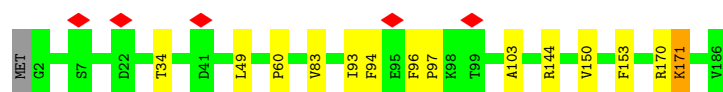
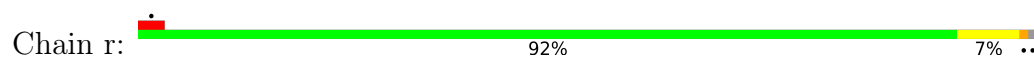


- Molecule 17: 60S ribosomal protein L17-A

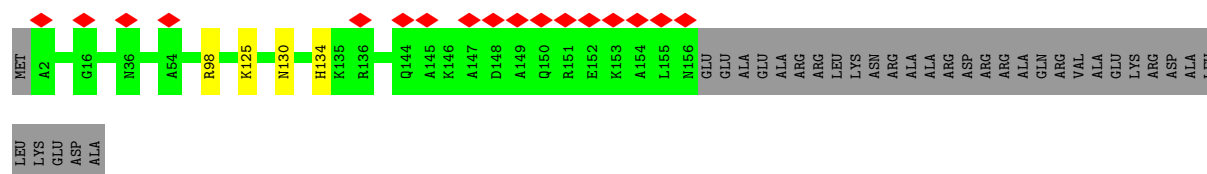
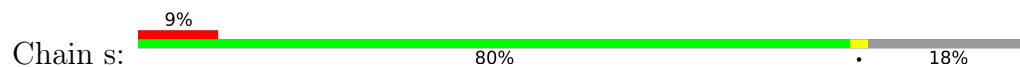
Chain q: 



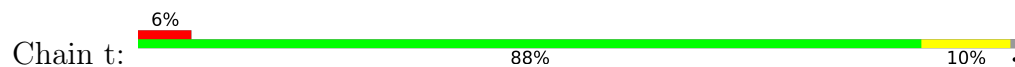
- Molecule 18: 60S ribosomal protein L18-A



- Molecule 19: 60S ribosomal protein L19-A



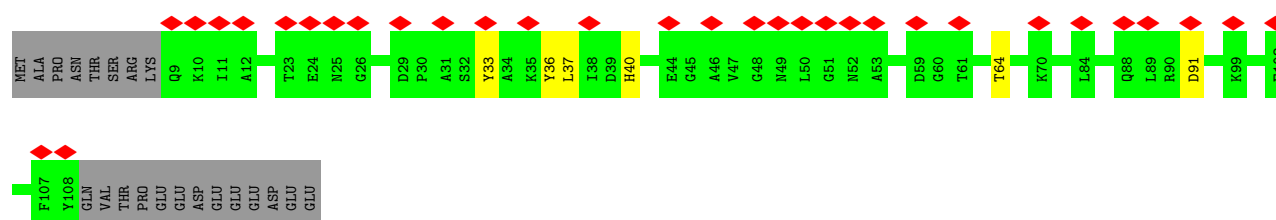
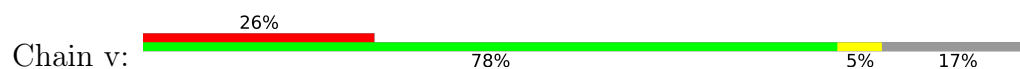
- Molecule 20: 60S ribosomal protein L20-A



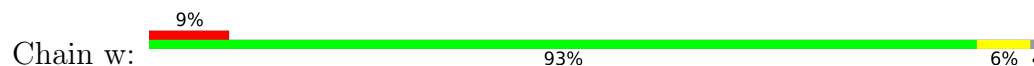
- Molecule 21: 60S ribosomal protein L21-A

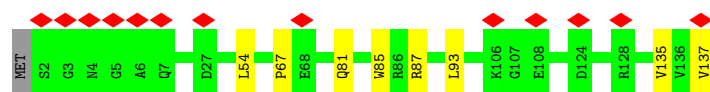


- Molecule 22: 60S ribosomal protein L22-A

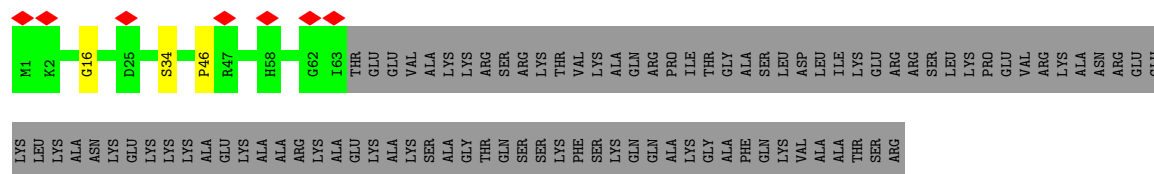


- Molecule 23: 60S ribosomal protein L23-A

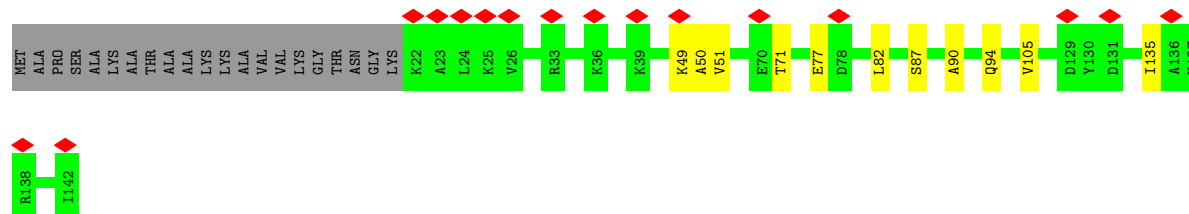
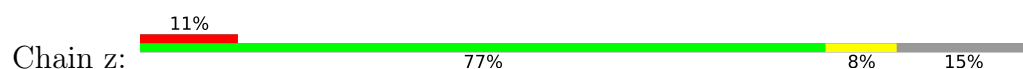




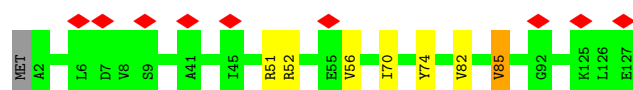
- Molecule 24: 60S ribosomal protein L24-A



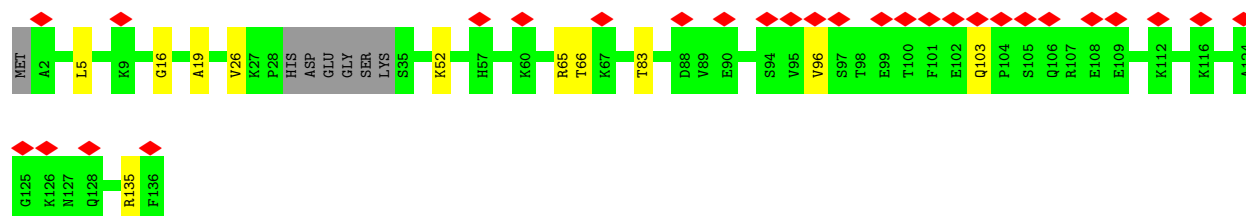
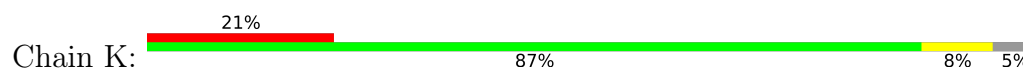
- Molecule 25: 60S ribosomal protein L25



- Molecule 26: 60S ribosomal protein L26-A



- Molecule 27: 60S ribosomal protein L27-A

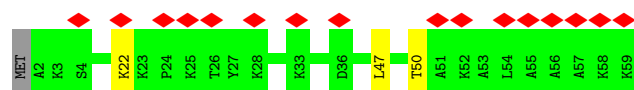


- Molecule 28: 60S ribosomal protein L28

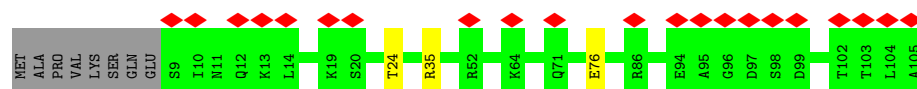




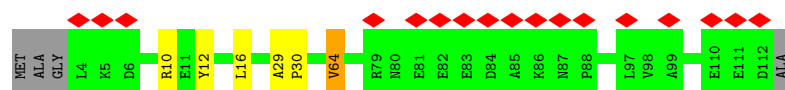
- Molecule 29: 60S ribosomal protein L29



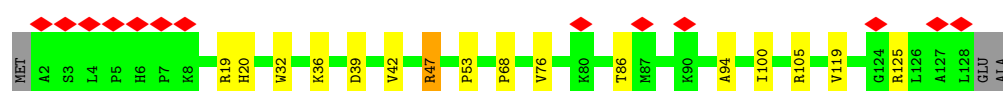
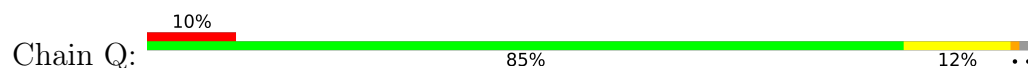
- Molecule 30: 60S ribosomal protein L30



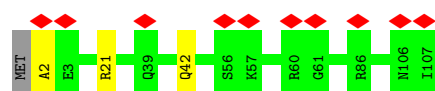
- Molecule 31: 60S ribosomal protein L31-A



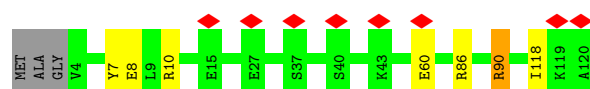
- Molecule 32: 60S ribosomal protein L32



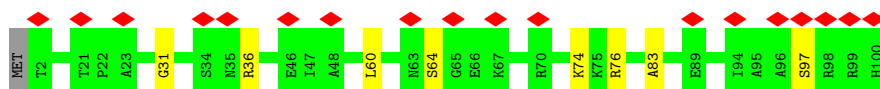
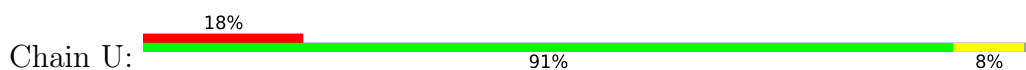
- Molecule 33: 60S ribosomal protein L33-A



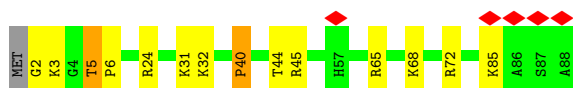
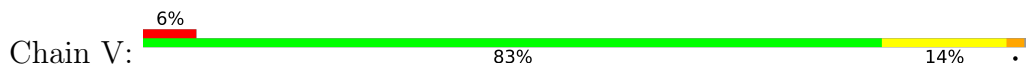
- Molecule 34: 60S ribosomal protein L35-A



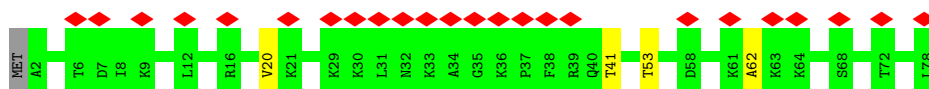
- Molecule 35: 60S ribosomal protein L36-A



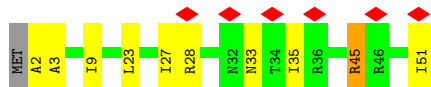
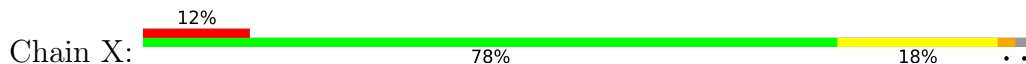
- Molecule 36: 60S ribosomal protein L37-A



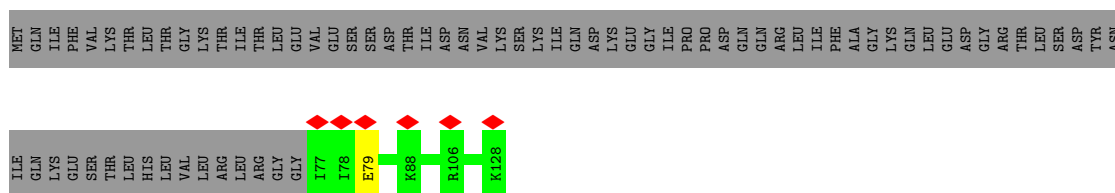
- Molecule 37: 60S ribosomal protein L38



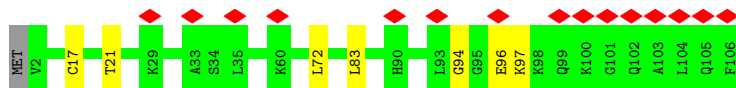
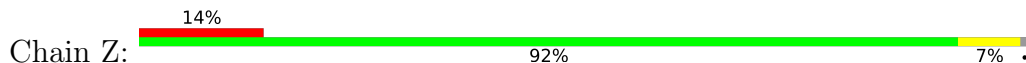
- Molecule 38: 60S ribosomal protein L39



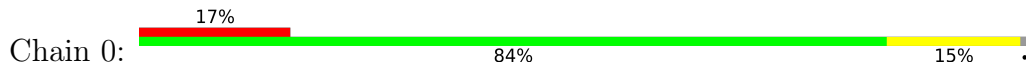
- Molecule 39: Ubiquitin-60S ribosomal protein L40

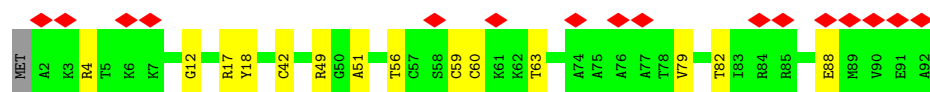


- Molecule 40: 60S ribosomal protein L42-A



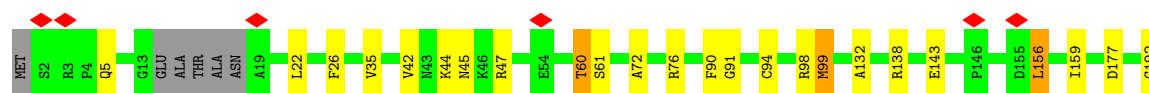
- Molecule 41: 60S ribosomal protein L43-A





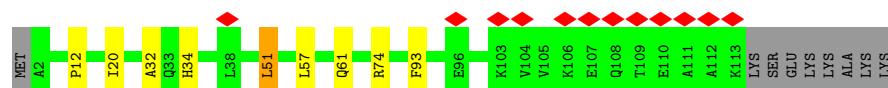
- Molecule 42: 60S ribosomal protein L4-A

Chain 3: 87% 9% ..



- Molecule 43: 60S ribosomal protein L34-A

Chain S: 10% 85% 7% 7%



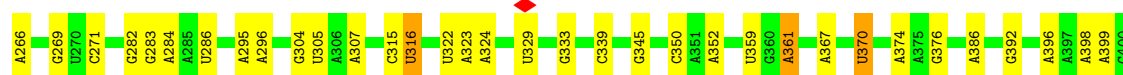
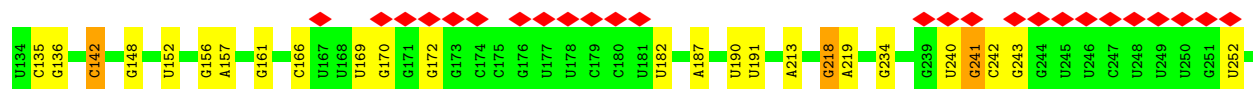
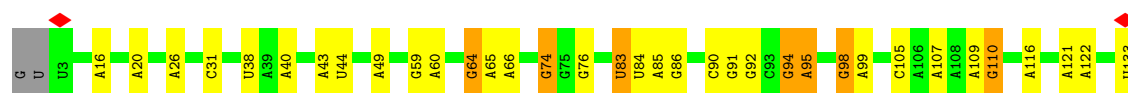
- Molecule 44: 60S ribosomal protein L2-A

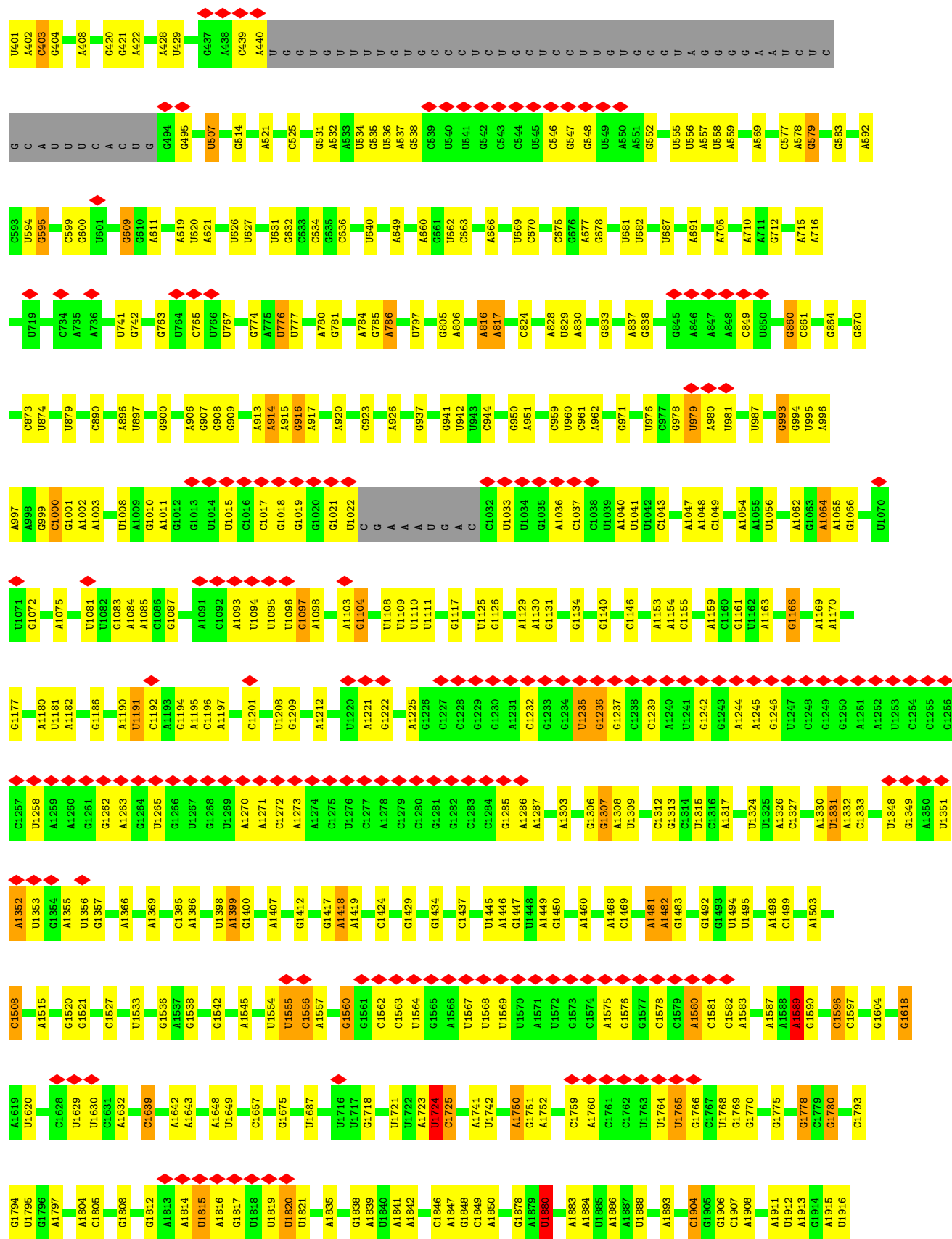
Chain c: 84% 13% .

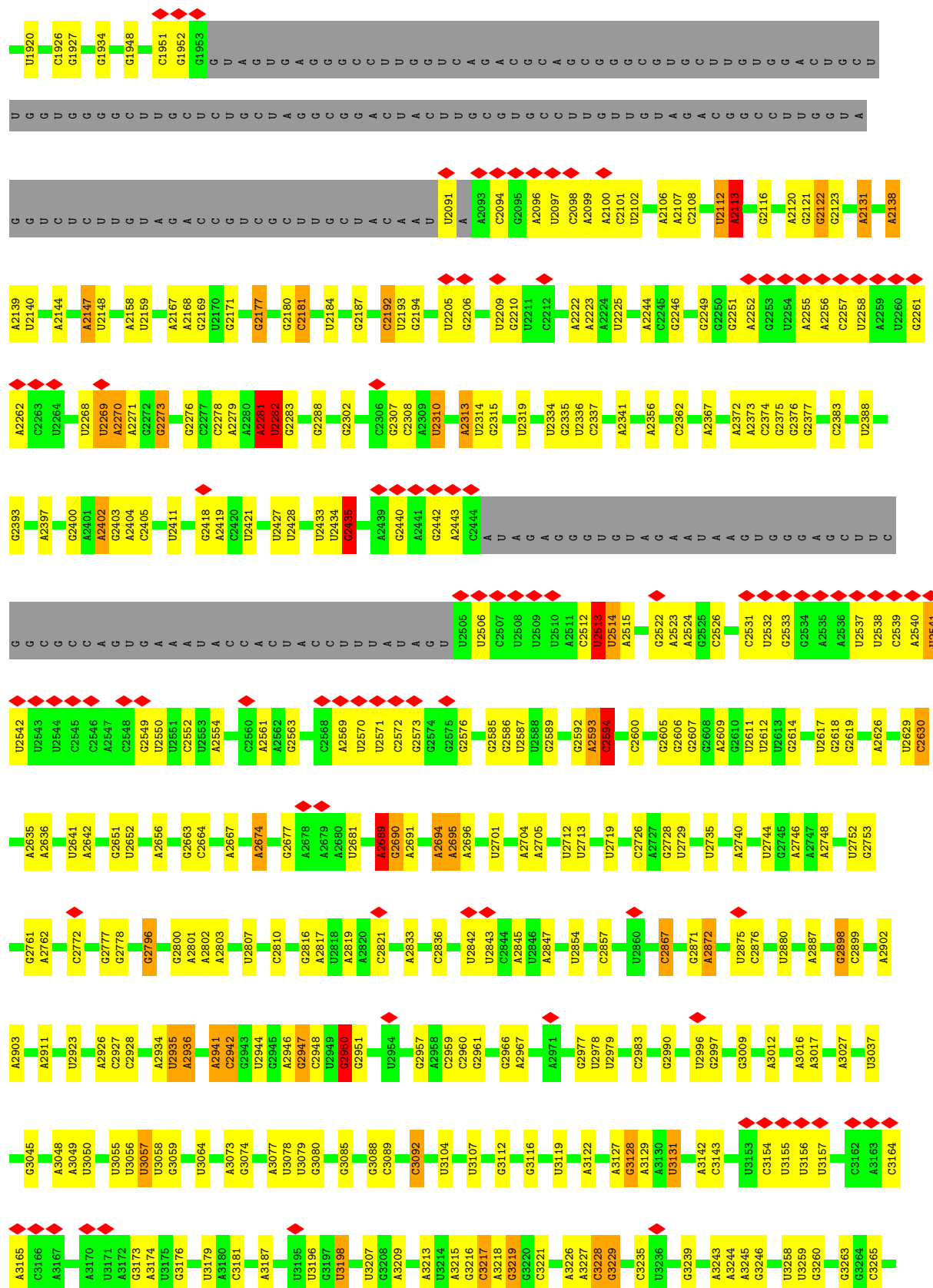


- Molecule 45: 25S rRNA

Chain a: 10% 66% 23% 8%









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14552	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)	400	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.174	Depositor
Minimum map value	-0.101	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0279	Depositor
Map size ($\text{\AA}$)	395.52, 395.52, 395.52	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.03, 1.03, 1.03	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.66	0/2649	0.90	3/3588 (0.1%)
1	C	0.68	0/2165	0.95	2/2916 (0.1%)
1	D	0.63	0/3873	0.97	4/5234 (0.1%)
1	E	0.63	0/3868	0.94	4/5228 (0.1%)
1	H	0.60	0/858	0.97	0/1157
1	I	0.60	0/880	0.97	0/1190
2	P	0.57	0/145	0.98	0/186
3	4	0.55	0/3747	0.97	9/5832 (0.2%)
4	b	0.57	0/2884	0.96	9/4491 (0.2%)
5	d	0.63	0/3146	0.96	2/4228 (0.0%)
6	e	0.56	0/2382	0.98	0/3214
7	f	0.58	0/1260	0.92	0/1694
8	g	0.60	0/1791	0.97	1/2410 (0.0%)
9	h	0.57	0/1836	0.98	1/2481 (0.0%)
10	i	0.58	0/1539	0.93	1/2073 (0.0%)
11	j	0.60	0/1736	0.94	0/2328
12	k	0.56	0/1348	0.98	0/1807
13	m	0.59	0/1568	1.00	1/2106 (0.0%)
14	n	0.57	0/1068	0.98	0/1438
15	o	0.61	0/1757	1.00	1/2354 (0.0%)
16	p	0.64	0/1585	1.02	3/2128 (0.1%)
17	q	0.63	0/1443	0.95	0/1944
18	r	0.62	0/1465	0.98	1/1965 (0.1%)
19	s	0.61	0/1266	1.01	0/1690
20	t	0.61	0/1468	0.98	2/1973 (0.1%)
21	u	0.60	0/1300	0.91	1/1743 (0.1%)
22	v	0.53	0/812	0.94	0/1099
23	w	0.64	0/1018	0.98	0/1369
24	y	0.62	0/533	0.89	0/707
25	z	0.56	0/979	0.97	0/1321
26	J	0.60	0/1004	0.99	0/1341
27	K	0.58	0/1070	0.93	0/1432

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	L	0.65	0/1204	0.94	0/1612
29	M	0.66	0/473	0.98	0/629
30	N	0.57	0/751	0.93	0/1008
31	O	0.56	0/890	0.96	1/1196 (0.1%)
32	Q	0.61	0/1041	0.96	1/1394 (0.1%)
33	R	0.61	0/868	0.87	0/1168
34	T	0.58	0/969	1.01	0/1289
35	U	0.61	0/778	0.95	0/1034
36	V	0.68	0/696	1.02	2/923 (0.2%)
37	W	0.59	0/618	0.95	0/826
38	X	0.58	0/443	0.96	0/588
39	Y	0.63	0/423	1.00	0/562
40	Z	0.60	0/860	0.93	0/1136
41	0	0.63	0/701	1.05	0/934
42	3	0.62	0/2765	1.02	4/3740 (0.1%)
43	S	0.63	0/890	0.99	1/1189 (0.1%)
44	c	0.66	0/1908	0.96	0/2564
45	a	0.57	0/75028	0.99	211/116969 (0.2%)
All	All	0.59	0/145749	0.98	265/213428 (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
5	d	0	1
14	n	0	1
15	o	0	1
16	p	0	1
20	t	0	1
35	U	0	1
45	a	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 265 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	a	420	G	O3'-P-O5'	-10.02	88.97	104.00
42	3	317	PRO	N-CA-C	-9.12	97.73	111.41
45	a	873	C	C2'-C3'-O3'	-9.10	100.05	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	a	2313	A	O3'-P-O5'	-8.73	90.91	104.00
45	a	1417	G	O3'-P-O5'	-8.71	90.94	104.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	d	253	GLY	Peptide
14	n	8	LYS	Peptide
15	o	127	TYR	Peptide
16	p	74	ARG	Sidechain
20	t	153	PRO	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	A	2590	0	2636	1	0
1	C	2125	0	2127	21	0
1	D	3796	0	3812	66	0
1	E	3790	0	3805	56	0
1	H	845	0	844	6	0
1	I	864	0	860	3	0
2	P	144	0	174	0	0
3	4	3354	0	1695	14	0
4	b	2580	0	1304	3	0
5	d	3075	0	3142	17	0
6	e	2333	0	2286	11	0
7	f	1239	0	1326	3	0
8	g	1754	0	1834	10	0
9	h	1804	0	1877	10	0
10	i	1518	0	1587	7	0
11	j	1700	0	1731	5	0
12	k	1327	0	1357	3	0
13	m	1543	0	1608	5	0
14	n	1053	0	1149	2	0
15	o	1720	0	1779	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	p	1555	0	1659	12	0
17	q	1420	0	1437	3	0
18	r	1441	0	1543	9	0
19	s	1249	0	1336	2	0
20	t	1432	0	1470	6	0
21	u	1276	0	1323	5	0
22	v	796	0	812	2	0
23	w	1003	0	1048	3	0
24	y	521	0	551	2	0
25	z	964	0	1025	4	0
26	J	993	0	1081	5	0
27	K	1046	0	1116	7	0
28	L	1173	0	1215	5	0
29	M	462	0	491	1	0
30	N	743	0	797	2	0
31	O	876	0	912	2	0
32	Q	1020	0	1090	7	0
33	R	850	0	880	3	0
34	T	960	0	1070	5	0
35	U	771	0	849	3	0
36	V	681	0	683	8	0
37	W	612	0	682	1	0
38	X	436	0	475	9	0
39	Y	417	0	455	0	0
40	Z	847	0	914	2	0
41	0	694	0	734	8	0
42	3	2714	0	2829	15	0
43	S	880	0	941	5	0
44	c	1874	0	1943	17	0
45	a	67031	0	33688	167	0
46	0	1	0	0	0	0
46	S	1	0	0	0	0
46	V	1	0	0	0	0
46	Y	1	0	0	0	0
46	Z	1	0	0	0	0
All	All	135896	0	101982	450	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 2.

The worst 5 of 450 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:D:1000:PRO:HA	1:D:1005:GLN:OE1	1.36	1.25
1:E:1000:PRO:HA	1:E:1005:GLN:OE1	1.36	1.20
1:D:989:VAL:HG11	1:E:989:VAL:HG11	1.36	1.07
1:D:1004:TRP:CZ3	1:E:990:ILE:HG23	1.89	1.07
1:D:990:ILE:HG23	1:E:1004:TRP:CZ3	1.97	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	320/1659 (19%)	314 (98%)	6 (2%)	0	100	100
1	C	253/1659 (15%)	245 (97%)	7 (3%)	1 (0%)	30	61
1	D	468/1659 (28%)	440 (94%)	26 (6%)	2 (0%)	30	61
1	E	467/1659 (28%)	459 (98%)	8 (2%)	0	100	100
1	H	100/1659 (6%)	100 (100%)	0	0	100	100
1	I	104/1659 (6%)	104 (100%)	0	0	100	100
2	P	13/25 (52%)	13 (100%)	0	0	100	100
5	d	384/387 (99%)	362 (94%)	21 (6%)	1 (0%)	36	67
6	e	289/297 (97%)	273 (94%)	14 (5%)	2 (1%)	18	49
7	f	152/176 (86%)	143 (94%)	9 (6%)	0	100	100
8	g	216/244 (88%)	210 (97%)	6 (3%)	0	100	100
9	h	231/256 (90%)	219 (95%)	12 (5%)	0	100	100
10	i	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
11	j	206/221 (93%)	193 (94%)	12 (6%)	1 (0%)	24	57
12	k	164/174 (94%)	155 (94%)	7 (4%)	2 (1%)	10	37
13	m	191/199 (96%)	178 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	n	134/138 (97%)	126 (94%)	8 (6%)	0	100	100
15	o	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
16	p	195/199 (98%)	187 (96%)	8 (4%)	0	100	100
17	q	181/184 (98%)	166 (92%)	14 (8%)	1 (1%)	21	52
18	r	183/186 (98%)	170 (93%)	12 (7%)	1 (0%)	24	57
19	s	153/189 (81%)	148 (97%)	5 (3%)	0	100	100
20	t	168/172 (98%)	156 (93%)	11 (6%)	1 (1%)	21	52
21	u	157/160 (98%)	147 (94%)	9 (6%)	1 (1%)	21	52
22	v	98/121 (81%)	88 (90%)	10 (10%)	0	100	100
23	w	134/137 (98%)	129 (96%)	5 (4%)	0	100	100
24	y	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
25	z	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	16	47
26	J	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
27	K	125/136 (92%)	118 (94%)	6 (5%)	1 (1%)	16	47
28	L	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
29	M	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
30	N	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
31	O	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
32	Q	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
33	R	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
34	T	115/120 (96%)	109 (95%)	6 (5%)	0	100	100
35	U	97/100 (97%)	87 (90%)	9 (9%)	1 (1%)	12	41
36	V	85/88 (97%)	78 (92%)	6 (7%)	1 (1%)	10	37
37	W	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
38	X	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	5	25
39	Y	50/128 (39%)	47 (94%)	2 (4%)	1 (2%)	6	25
40	Z	103/106 (97%)	92 (89%)	8 (8%)	3 (3%)	3	19
41	0	89/92 (97%)	81 (91%)	5 (6%)	3 (3%)	3	16
42	3	352/362 (97%)	324 (92%)	24 (7%)	4 (1%)	11	39
43	S	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
44	c	244/254 (96%)	224 (92%)	17 (7%)	3 (1%)	10	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7781/16537 (47%)	7361 (95%)	388 (5%)	32 (0%)	31	61

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	e	202	GLY
18	r	171	LYS
36	V	85	LYS
12	k	55	ARG
17	q	66	SER

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	A	294/1520 (19%)	291 (99%)	3 (1%)	68	79
1	C	232/1520 (15%)	230 (99%)	2 (1%)	70	80
1	D	429/1520 (28%)	424 (99%)	5 (1%)	63	78
1	E	428/1520 (28%)	427 (100%)	1 (0%)	87	89
1	H	94/1520 (6%)	90 (96%)	4 (4%)	26	57
1	I	96/1520 (6%)	87 (91%)	9 (9%)	8	31
2	P	14/23 (61%)	14 (100%)	0	100	100
5	d	320/323 (99%)	312 (98%)	8 (2%)	42	69
6	e	240/245 (98%)	233 (97%)	7 (3%)	37	66
7	f	134/153 (88%)	131 (98%)	3 (2%)	45	71
8	g	183/205 (89%)	179 (98%)	4 (2%)	45	71
9	h	187/208 (90%)	184 (98%)	3 (2%)	55	75
10	i	171/171 (100%)	163 (95%)	8 (5%)	23	55
11	j	177/187 (95%)	174 (98%)	3 (2%)	53	74
12	k	144/150 (96%)	140 (97%)	4 (3%)	38	66
13	m	154/159 (97%)	150 (97%)	4 (3%)	40	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	n	107/109 (98%)	107 (100%)	0	100	100
15	o	175/176 (99%)	174 (99%)	1 (1%)	78	83
16	p	160/162 (99%)	158 (99%)	2 (1%)	61	77
17	q	140/146 (96%)	133 (95%)	7 (5%)	22	53
18	r	150/151 (99%)	150 (100%)	0	100	100
19	s	128/154 (83%)	127 (99%)	1 (1%)	73	81
20	t	155/156 (99%)	151 (97%)	4 (3%)	40	68
21	u	136/137 (99%)	135 (99%)	1 (1%)	76	82
22	v	87/107 (81%)	85 (98%)	2 (2%)	44	70
23	w	104/105 (99%)	100 (96%)	4 (4%)	29	60
24	y	55/129 (43%)	54 (98%)	1 (2%)	51	73
25	z	104/118 (88%)	101 (97%)	3 (3%)	37	66
26	J	109/110 (99%)	106 (97%)	3 (3%)	38	66
27	K	110/116 (95%)	110 (100%)	0	100	100
28	L	118/119 (99%)	115 (98%)	3 (2%)	42	69
29	M	46/47 (98%)	45 (98%)	1 (2%)	45	71
30	N	81/88 (92%)	80 (99%)	1 (1%)	63	78
31	O	92/97 (95%)	90 (98%)	2 (2%)	45	71
32	Q	109/111 (98%)	103 (94%)	6 (6%)	19	50
33	R	90/91 (99%)	90 (100%)	0	100	100
34	T	104/105 (99%)	103 (99%)	1 (1%)	68	79
35	U	81/82 (99%)	80 (99%)	1 (1%)	63	78
36	V	70/71 (99%)	66 (94%)	4 (6%)	18	49
37	W	68/69 (99%)	66 (97%)	2 (3%)	37	66
38	X	45/46 (98%)	44 (98%)	1 (2%)	45	71
39	Y	47/116 (40%)	47 (100%)	0	100	100
40	Z	90/91 (99%)	88 (98%)	2 (2%)	45	71
41	0	71/72 (99%)	69 (97%)	2 (3%)	38	66
42	3	285/289 (99%)	274 (96%)	11 (4%)	28	60
43	S	95/103 (92%)	93 (98%)	2 (2%)	47	71
44	c	189/196 (96%)	181 (96%)	8 (4%)	26	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	6698/14613 (46%)	6554 (98%)	144 (2%)	45 71

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	V	68	LYS
44	c	207	VAL
40	Z	21	THR
42	3	230	VAL
9	h	175	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
34	T	59	ASN
44	c	144	ASN
36	V	79	GLN
42	3	48	GLN
12	k	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	4	157/158 (99%)	30 (19%)	4 (2%)
4	b	120/121 (99%)	12 (10%)	0
45	a	3129/3396 (92%)	582 (18%)	0
All	All	3406/3675 (92%)	624 (18%)	4 (0%)

5 of 624 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	4	21	C
3	4	23	U
3	4	34	U
3	4	35	C
3	4	50	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	4	84	C
3	4	85	G
3	4	90	U
3	4	105	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 5 ligands modelled in this entry, 5 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.

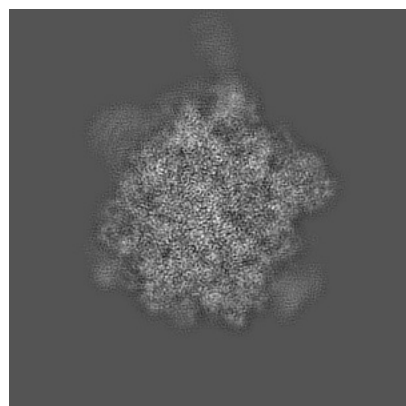
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50188. These allow visual inspection of the internal detail of the map and identification of artifacts.

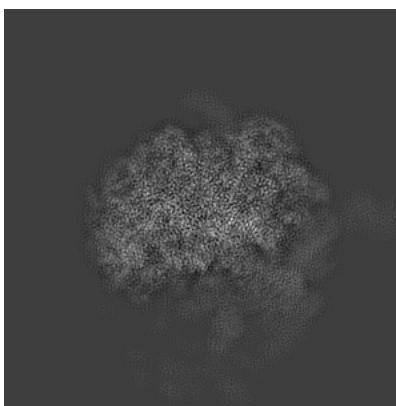
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

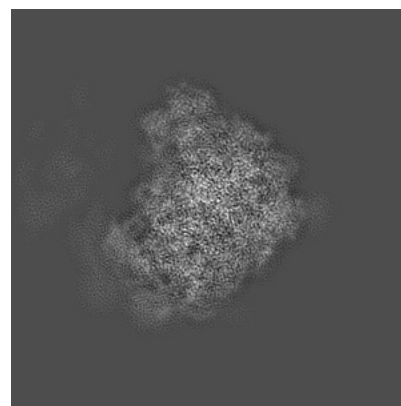
6.1.1 Primary map



X

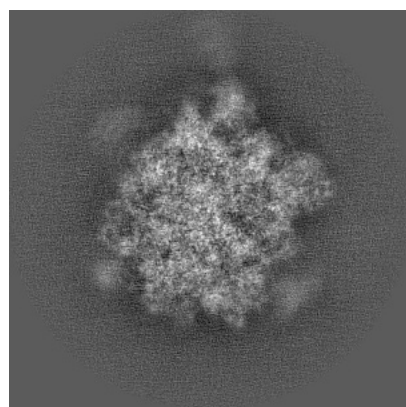


Y

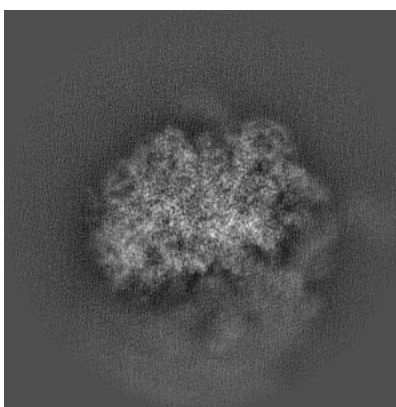


Z

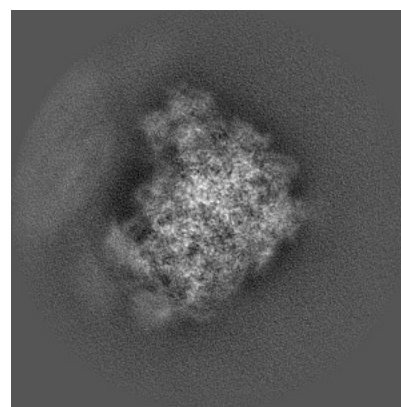
6.1.2 Raw map



X



Y

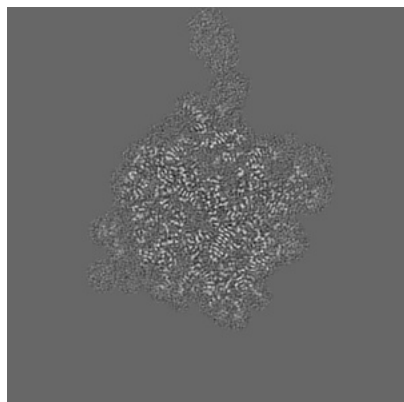


Z

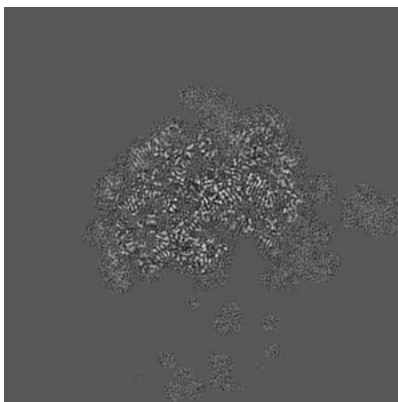
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

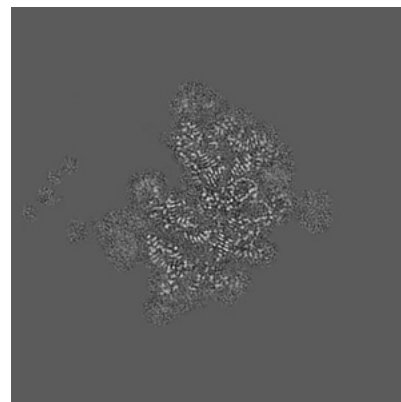
6.2.1 Primary map



X Index: 192

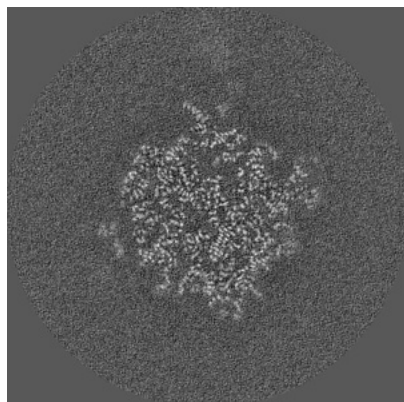


Y Index: 192

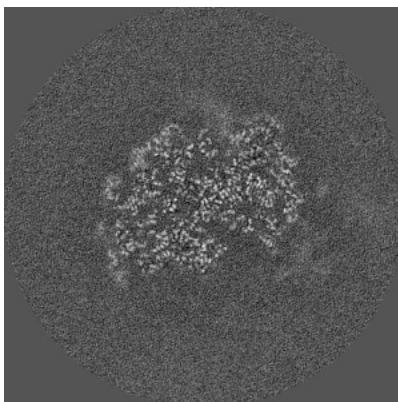


Z Index: 192

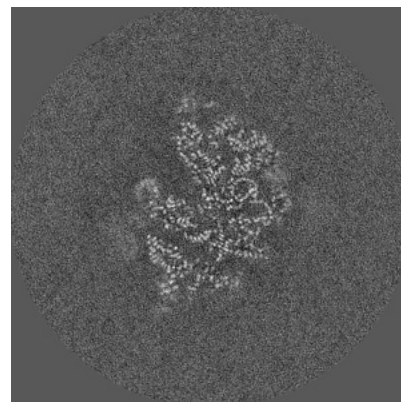
6.2.2 Raw map



X Index: 192



Y Index: 192

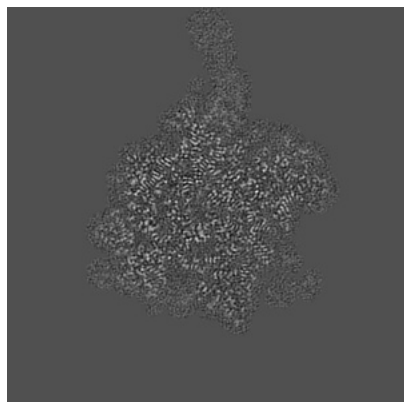


Z Index: 192

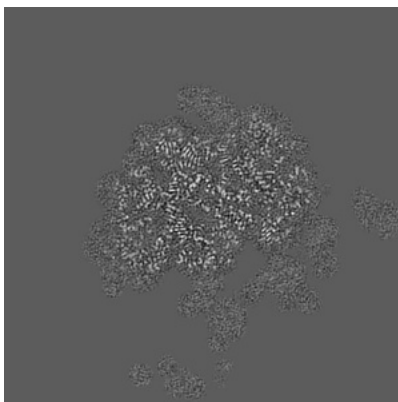
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

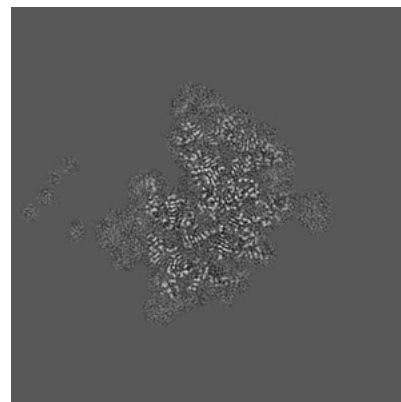
6.3.1 Primary map



X Index: 179

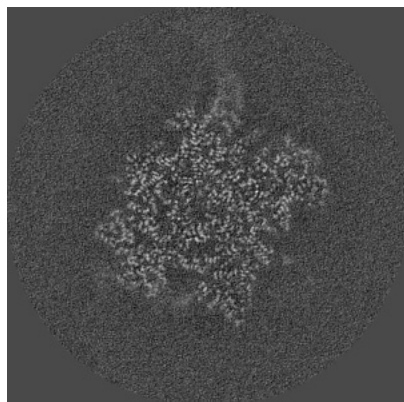


Y Index: 183

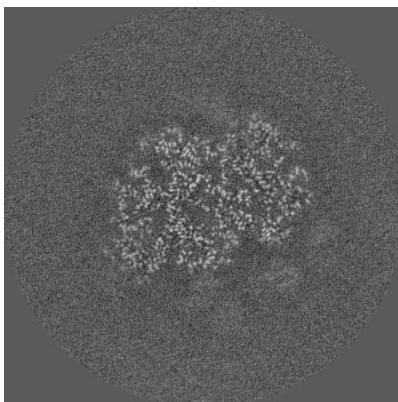


Z Index: 191

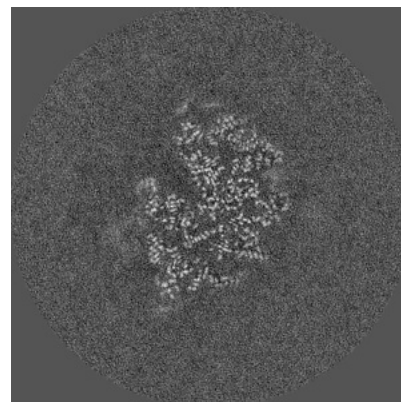
6.3.2 Raw map



X Index: 179



Y Index: 183

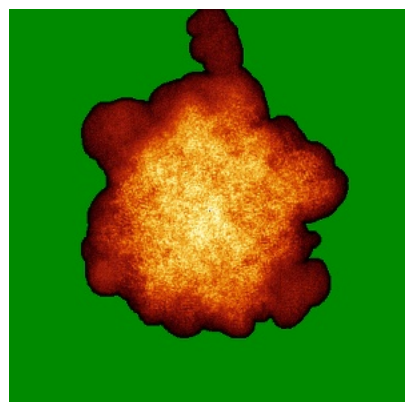


Z Index: 191

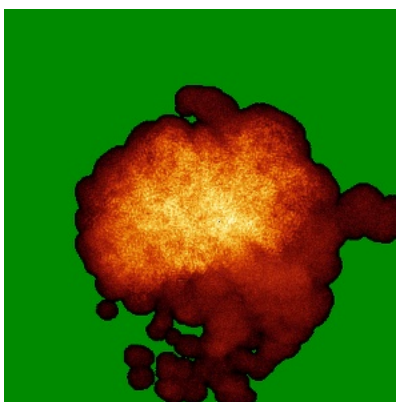
The images above show the largest variance slices of the map in three orthogonal directions.

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

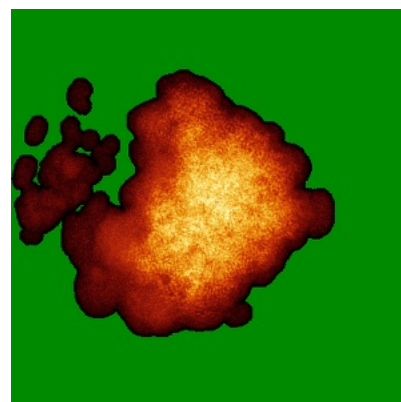
6.4.1 Primary map



X

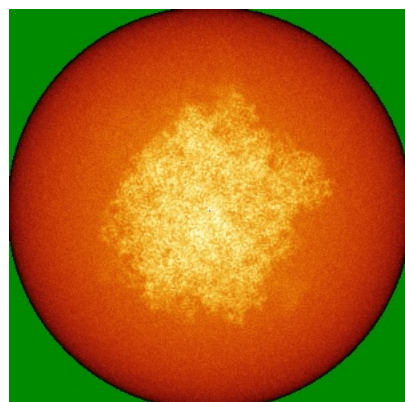


Y

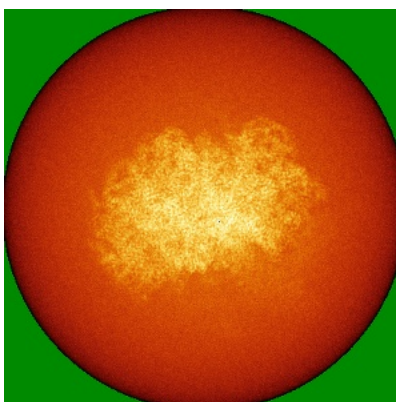


Z

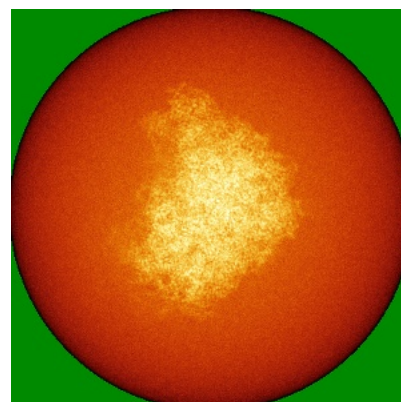
6.4.2 Raw map



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.

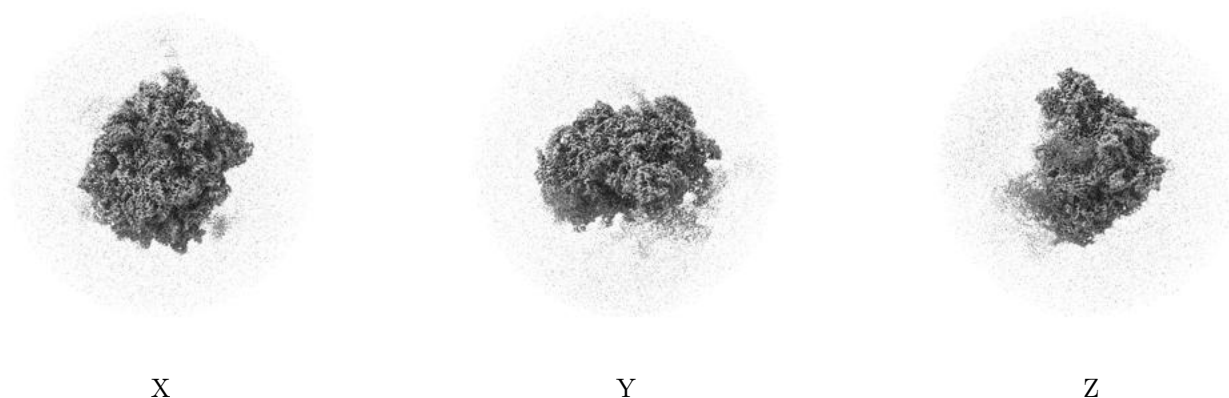
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0279. 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.

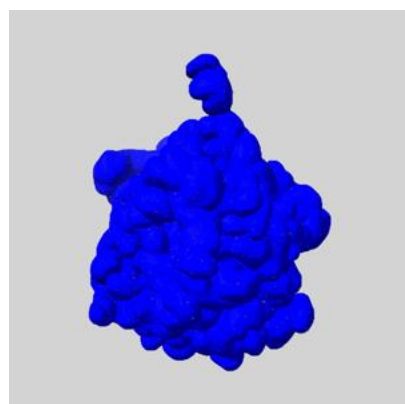
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

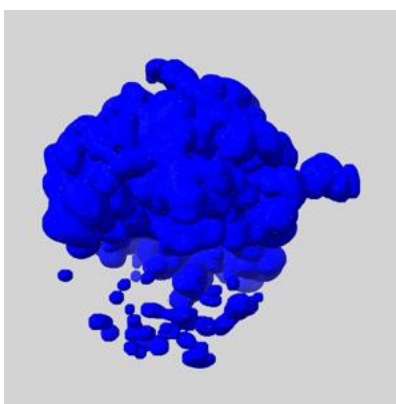
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

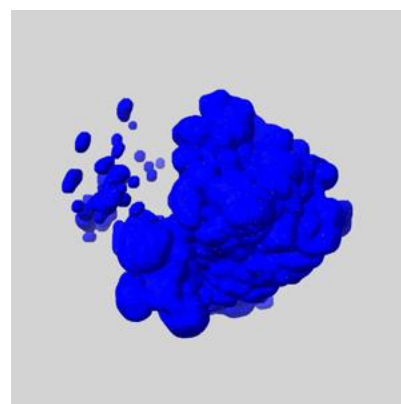
6.6.1 emd_50188_msk_1.map [i](#)



X



Y

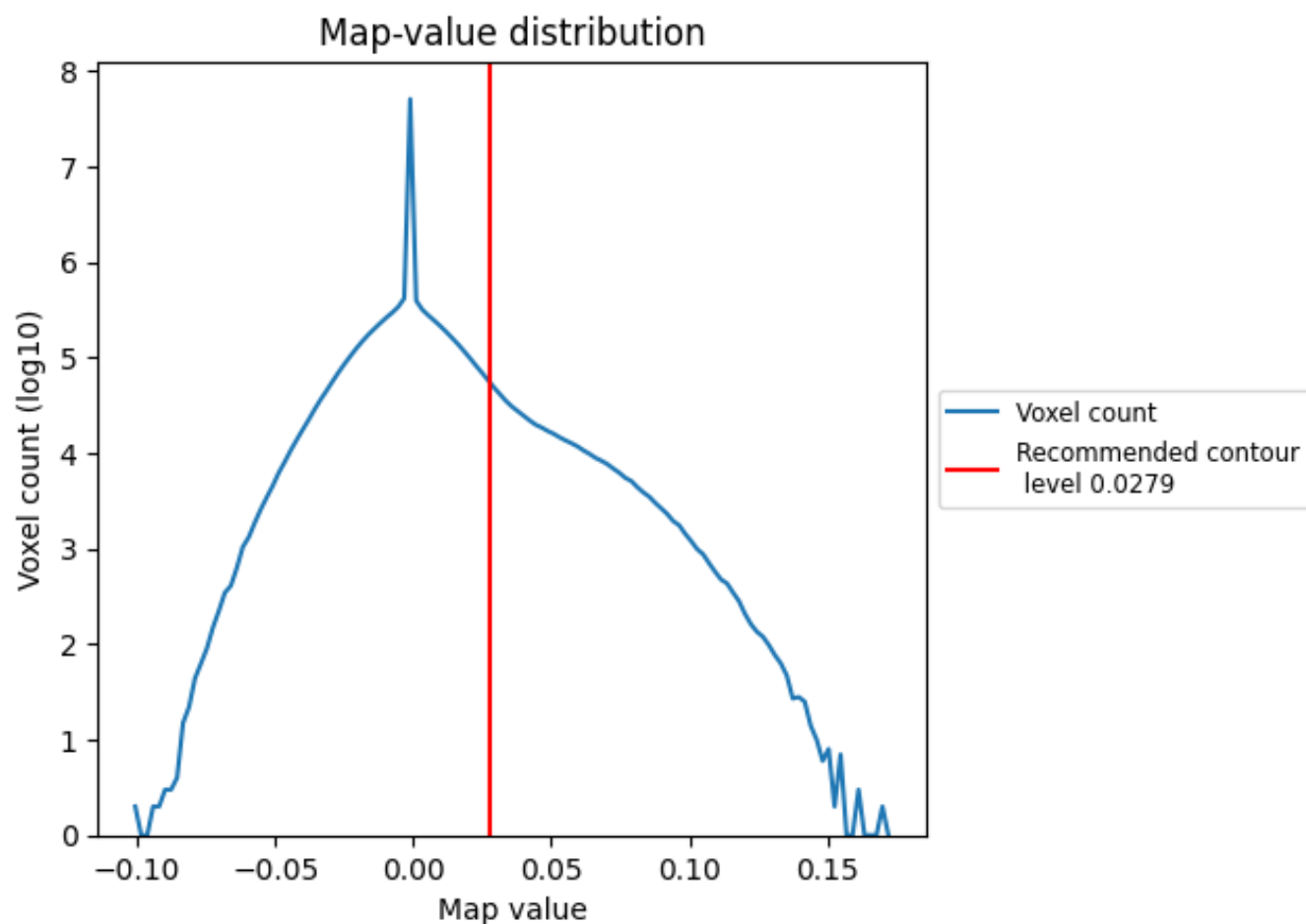


Z

7 Map analysis [i](#)

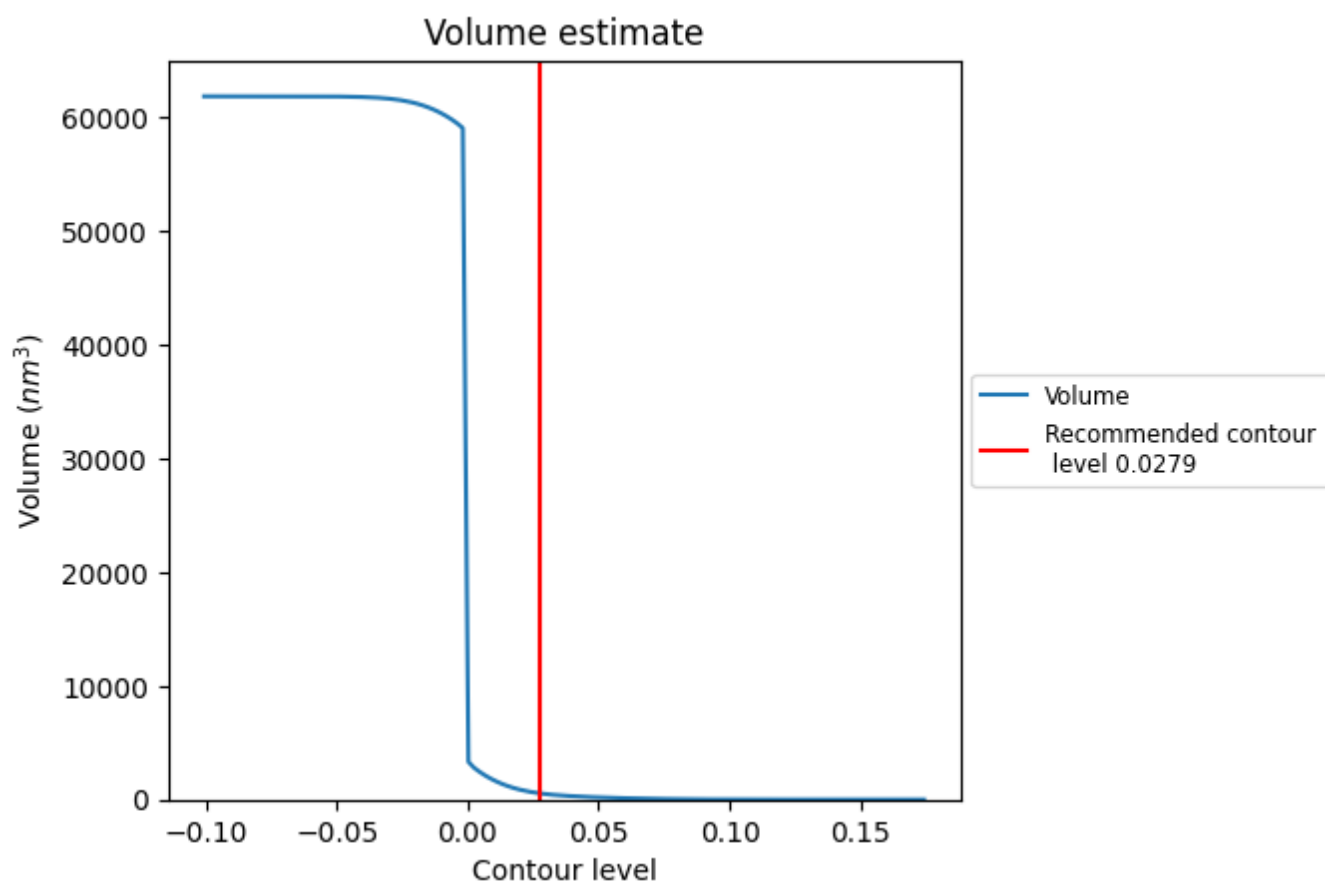
This section contains the results of statistical analysis of the map.

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.

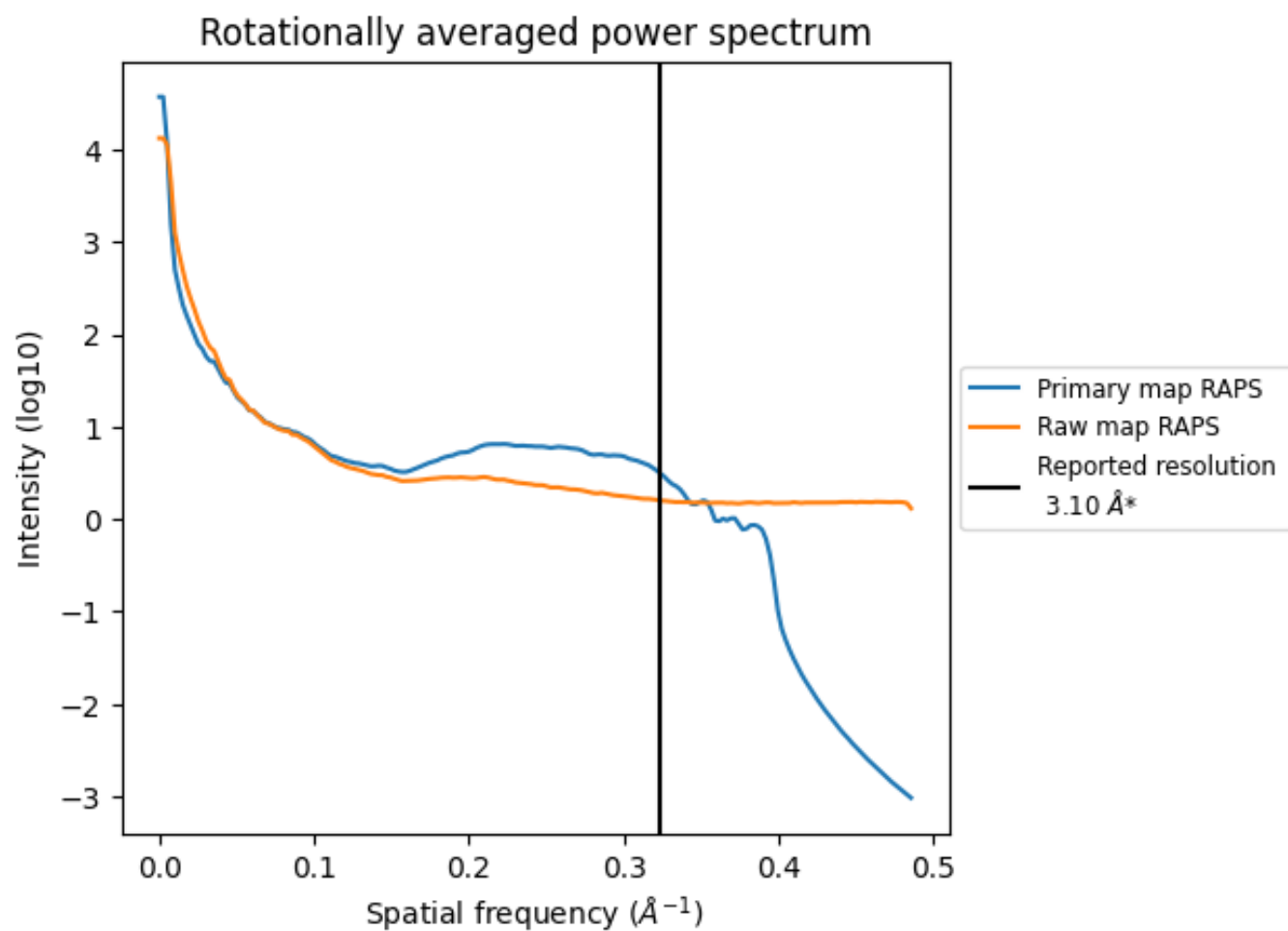
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 536 nm³; this corresponds to an approximate mass of 485 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

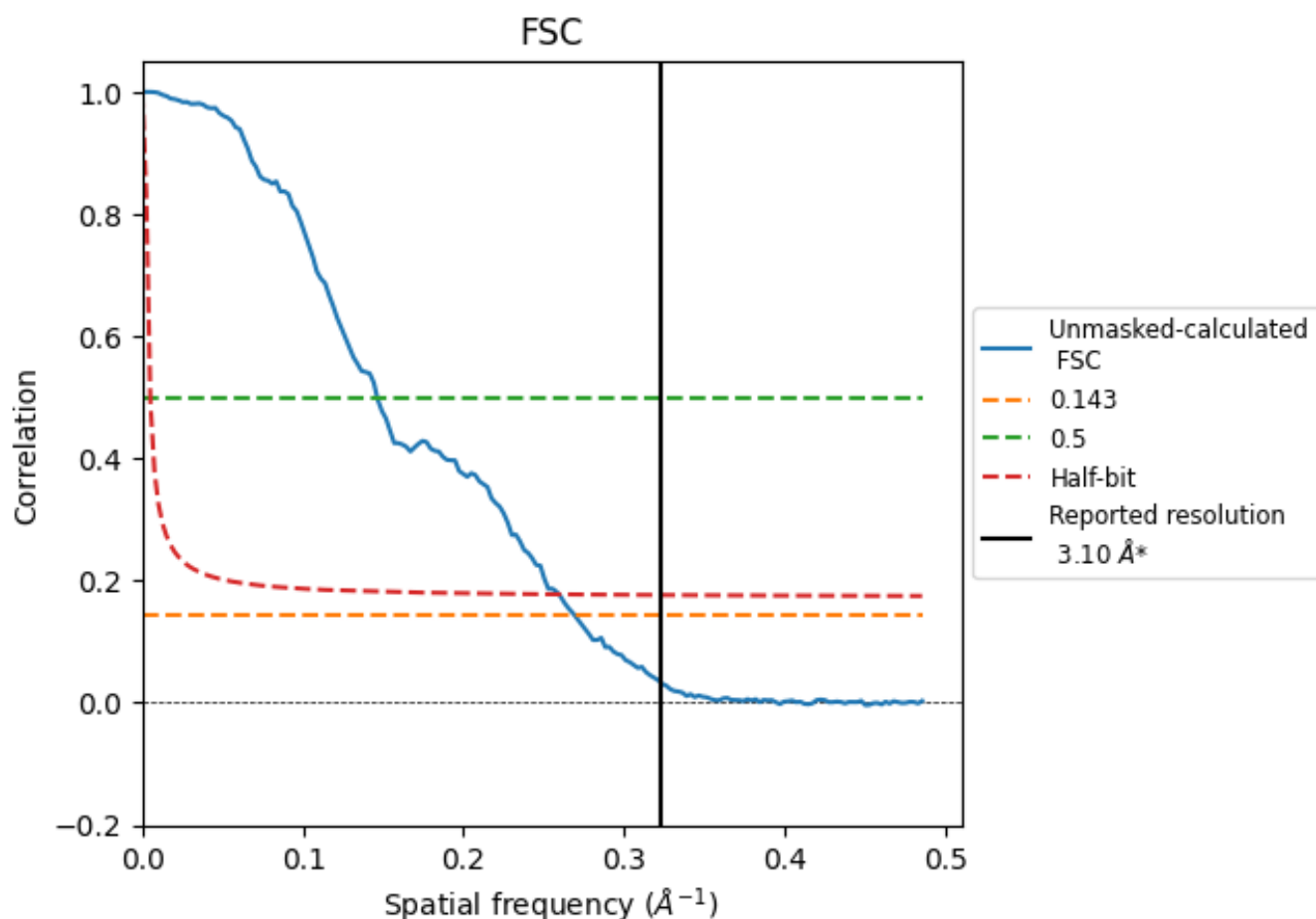


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

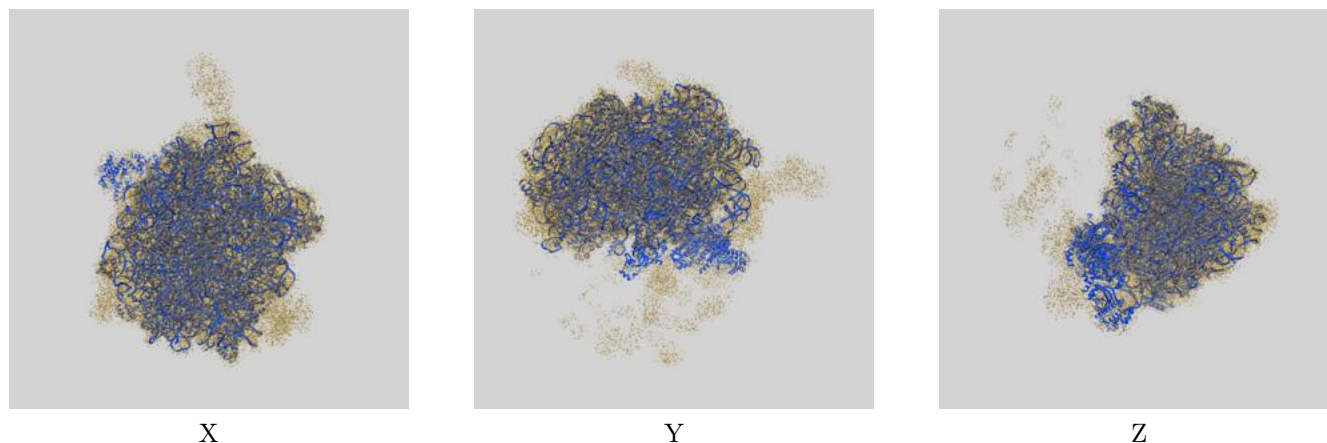
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.72	6.84	3.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.72 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

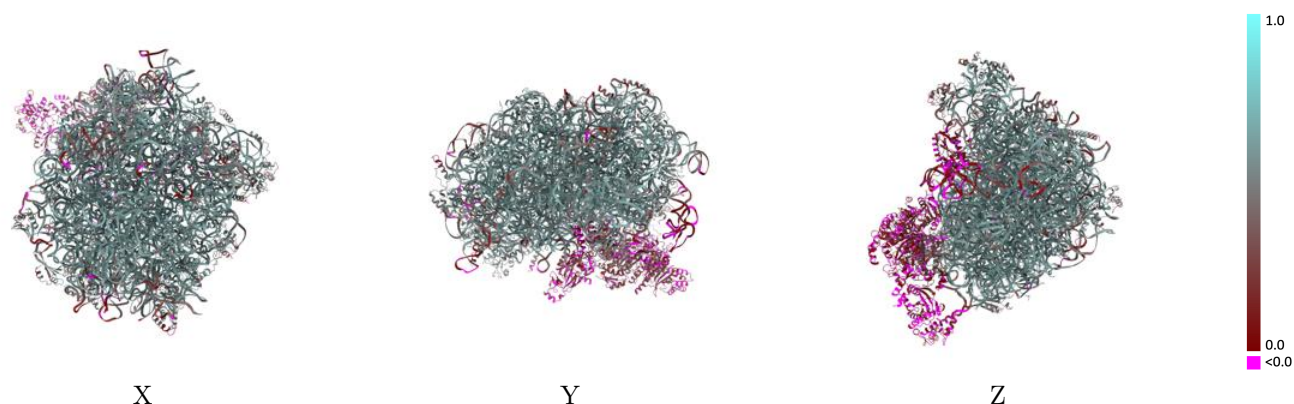
This section contains information regarding the fit between EMDB map EMD-50188 and PDB model 9F58. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



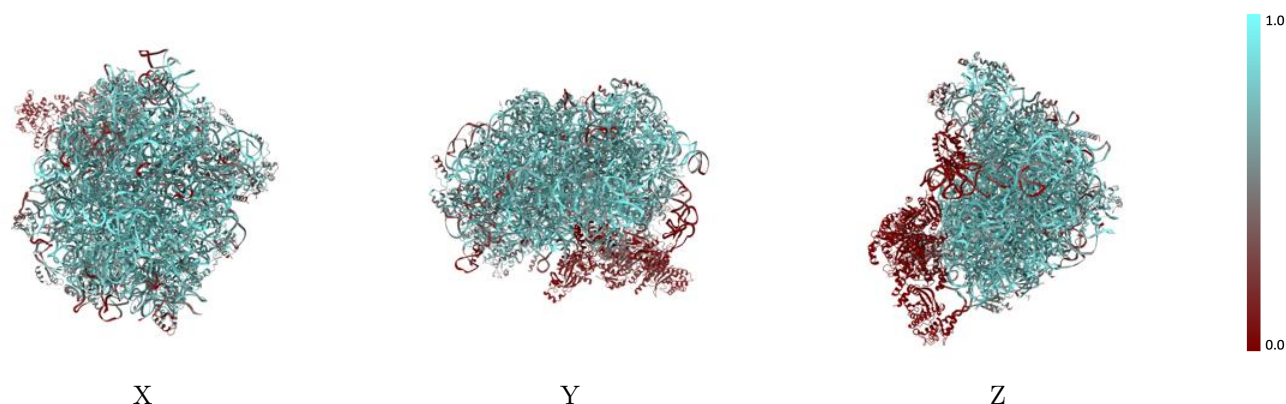
The images above show the 3D surface view of the map at the recommended contour level 0.0279 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



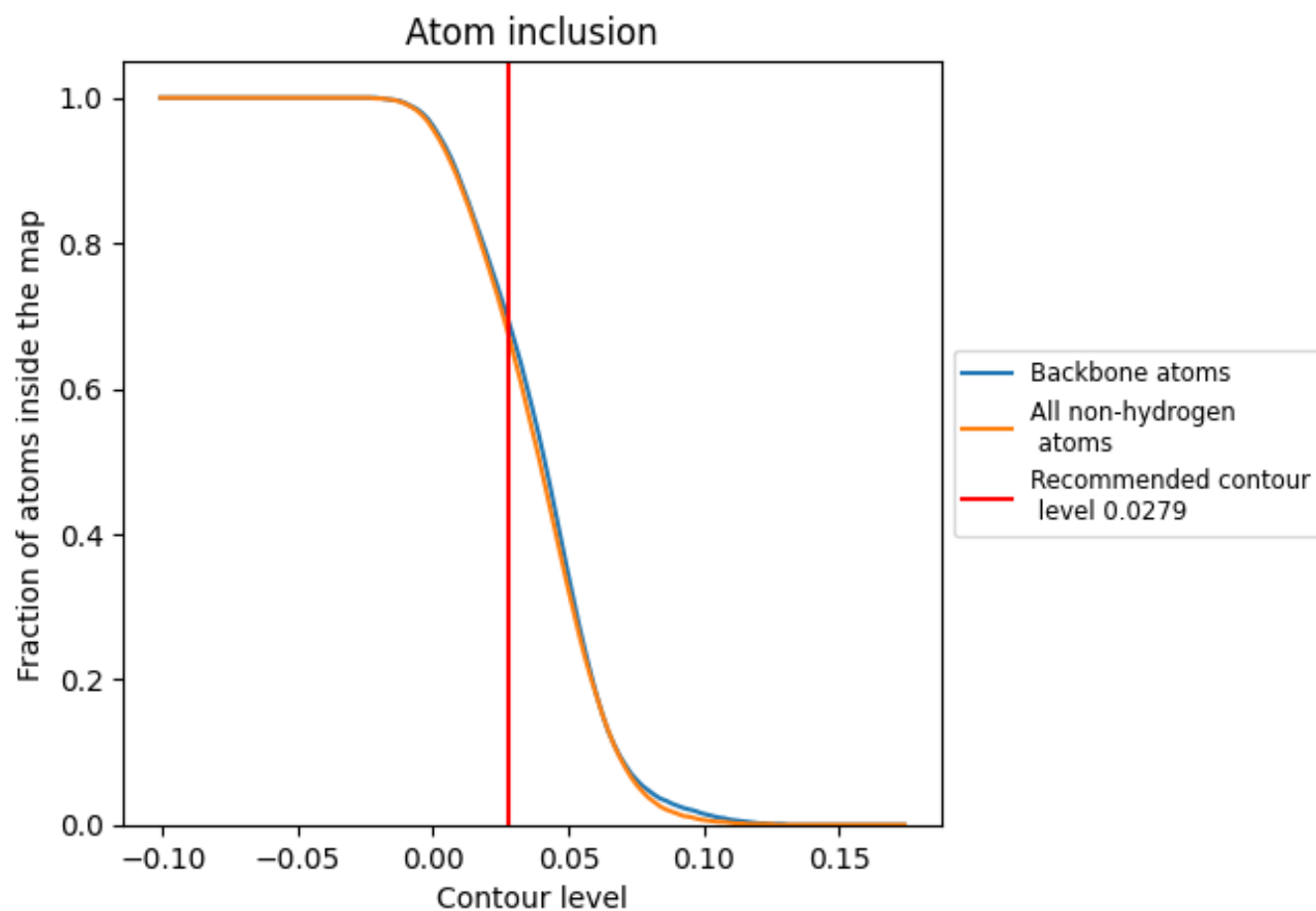
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0279).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 67% 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 (0.0279) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6740	 0.5070
0	 0.6580	 0.5420
3	 0.7200	 0.5700
4	 0.8140	 0.5780
A	 0.0210	 0.0720
C	 0.0100	 0.0320
D	 0.0420	 0.1130
E	 0.0860	 0.1820
H	 0.0160	 0.0960
I	 0.0150	 0.0320
J	 0.7000	 0.5700
K	 0.5930	 0.5090
L	 0.7560	 0.5910
M	 0.5890	 0.5080
N	 0.5750	 0.5140
O	 0.6630	 0.5420
P	 0.0760	 0.3490
Q	 0.6870	 0.5670
R	 0.7600	 0.5900
S	 0.6800	 0.5600
T	 0.6780	 0.5430
U	 0.6050	 0.4980
V	 0.7940	 0.6040
W	 0.5290	 0.4750
X	 0.6990	 0.5620
Y	 0.7180	 0.5500
Z	 0.6140	 0.5140
a	 0.7820	 0.5530
b	 0.8280	 0.5860
c	 0.7750	 0.6050
d	 0.7790	 0.5970
e	 0.6210	 0.5140
f	 0.6190	 0.5150
g	 0.7630	 0.5810
h	 0.6080	 0.5000



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Chain	Atom inclusion	Q-score
i	 0.6930	 0.5470
j	 0.6490	 0.5330
k	 0.4380	 0.4170
m	 0.6870	 0.5470
n	 0.7140	 0.5710
o	 0.7930	 0.6070
p	 0.7900	 0.5970
q	 0.6910	 0.5490
r	 0.7320	 0.5760
s	 0.6830	 0.5430
t	 0.7560	 0.5830
u	 0.6980	 0.5530
v	 0.5130	 0.4450
w	 0.7150	 0.5730
y	 0.7090	 0.5660
z	 0.6660	 0.5440