



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:09 AM UTC

PDB ID : 3JAM / pdb_00003jam
EMDB ID : EMD-3047
Title : CryoEM structure of 40S-eIF1A-eIF1 complex from yeast
Authors : Llacer, J.L.; Hussain, T.; Ramakrishnan, V.
Deposited on : 2015-06-17
Resolution : 3.46 Å (reported)
Based on initial model : 3J80

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:

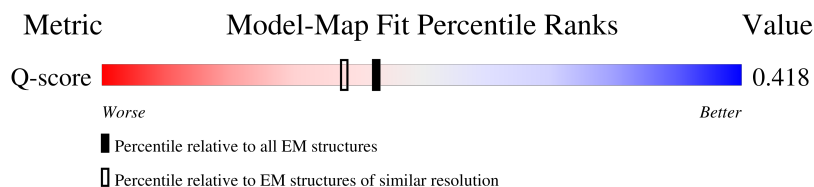
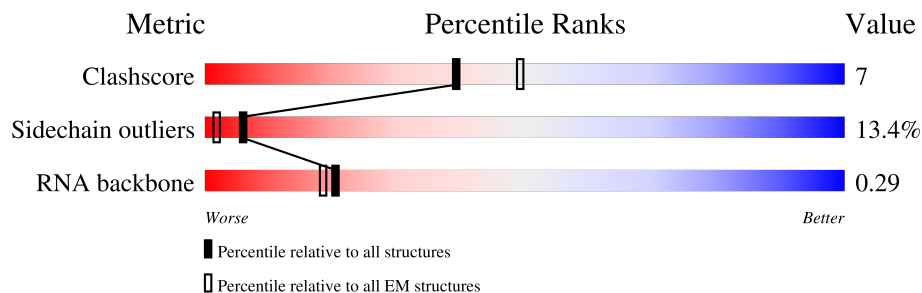
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.46 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13788 (2.96 - 3.96)

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	2	1799	
2	A	254	
3	B	255	
4	C	259	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	D	237	9% 71% 19% 6%
6	E	261	75% 21%
7	F	227	15% 69% 21% 9%
8	G	236	77% 18%
9	H	190	5% 74% 21%
10	I	201	6% 76% 14% 6%
11	J	188	69% 24%
12	K	106	14% 65% 23% 9%
13	L	156	11% 81% 16%
14	M	134	66% 70% 15% 6% 9%
15	N	151	80% 19%
16	O	137	73% 19% 7%
17	P	142	30% 65% 20% 13%
18	Q	143	70% 24% 5%
19	R	136	68% 19% 8%
20	S	146	39% 68% 28%
21	T	144	9% 73% 24%
22	U	117	16% 68% 21% 9%
23	V	87	79% 18%
24	W	130	71% 25%
25	X	145	78% 16% 6%
26	Y	135	76% 21%
27	Z	108	60% 48% 17% 35%
28	a	119	66% 14% 18%
29	b	82	79% 18%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	c	67	
31	d	56	
32	e	63	
33	f	150	
34	g	326	
35	h	25	
36	i	153	
37	j	108	

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 77850 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1780	37797	16892	6658	12467	1780	0	0

- Molecule 2 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	208	1626	1040	286	298	2	0	0

- Molecule 3 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	223	1774	1120	325	326	3	0	0

- Molecule 4 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	217	1629	1041	287	297	4	0	0

- Molecule 5 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	223	1744	1108	313	318	5	0	0

- Molecule 6 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	260	2078	1322	393	359	4	0	0

- Molecule 7 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	206	1609	1008	298	300	3	0	0

- Molecule 8 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	226	1812	1134	348	326	4	0	0

- Molecule 9 is a protein called eS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	H	184	1483	950	270	263	0	0

- Molecule 10 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	188	1489	923	300	265	1	0	0

- Molecule 11 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	182	1471	929	287	254	1	0	0

- Molecule 12 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	96	809	533	129	146	1	0	0

- Molecule 13 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	155	1248	798	237	210	3	0	0

- Molecule 14 is a protein called eS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	M	122	Total	C	N	O	0	0
			922	575	167	180		

- Molecule 15 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 16 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 17 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	123	Total	C	N	O	S	0	0
			980	628	179	168	5		

- Molecule 18 is a protein called uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	141	Total	C	N	O	0	0
			1105	709	204	192		

- Molecule 19 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	125	Total	C	N	O	S	0	0
			991	619	182	187	3		

- Molecule 20 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 21 is a protein called eS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	143	Total	C	N	O	0	0
			1110	693	210	207		

- Molecule 22 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 23 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 24 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 25 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 26 is a protein called eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Y	134	Total	C	N	O	0	0
			1061	665	207	189		

- Molecule 27 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 28 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	98	Total	C	N	O	S	0	0
			779	480	165	129	5		

- Molecule 29 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 30 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 31 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 32 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	53	Total	C	N	O	S	0	0
			428	268	87	72	1		

- Molecule 33 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	69	Total	C	N	O	S	0	0
			549	352	102	91	4		

- Molecule 34 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 35 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	h	25	233	142	63	27	1	0	0

- Molecule 36 is a protein called eIF1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	i	96	778	482	144	147	5	0	0

- Molecule 37 is a protein called eIF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	j	86	695	439	128	124	4	0	0

- Molecule 38 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
38	2	78	78	78	0
38	J	1	1	1	0
38	f	1	1	1	0

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

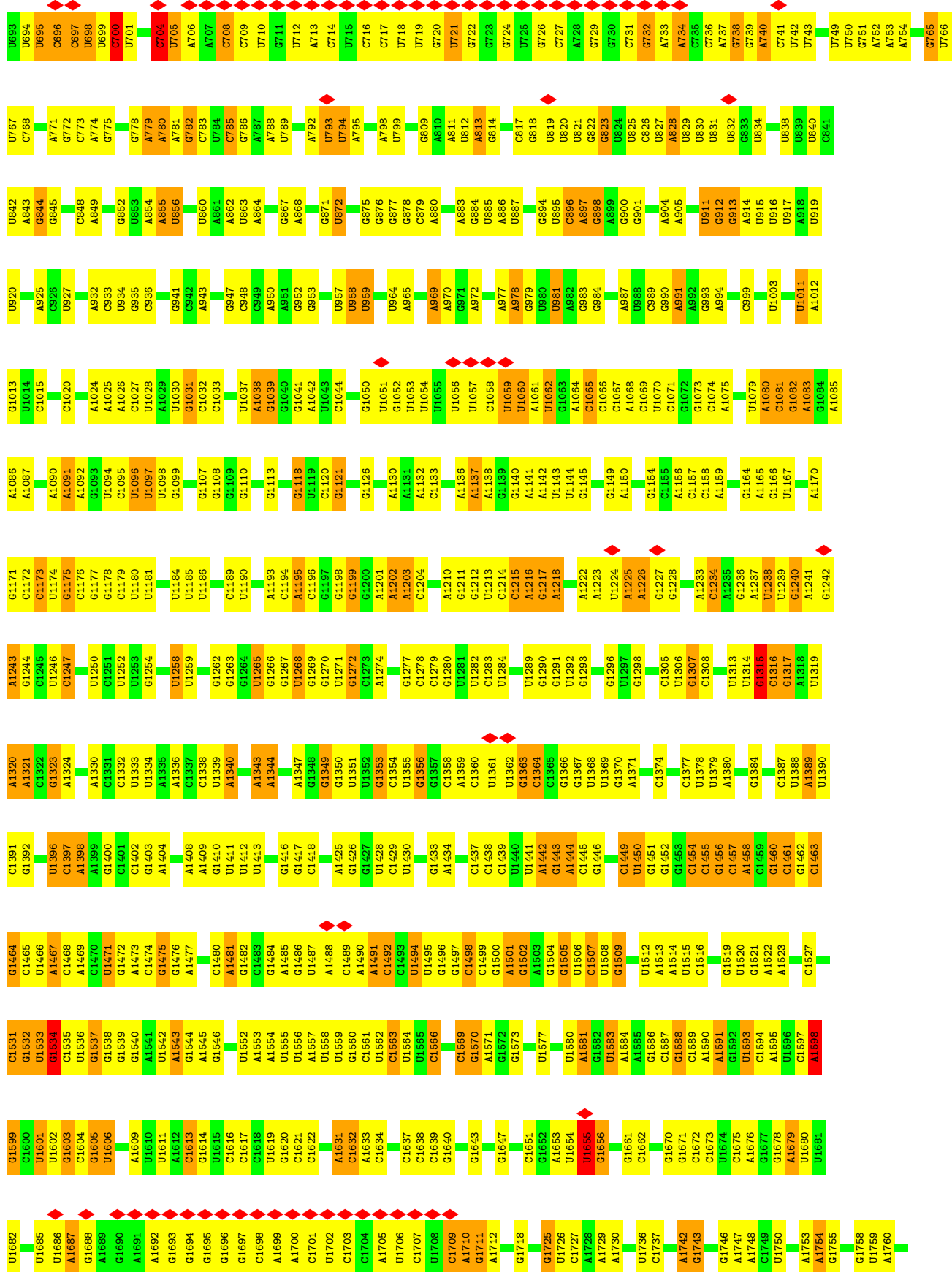
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
39	a	1	1	1	0
39	b	1	1	1	0
39	f	1	1	1	0

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.

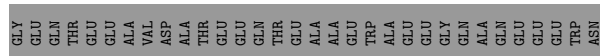
• Molecule 1: 18S rRNA



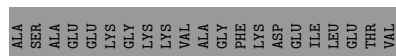
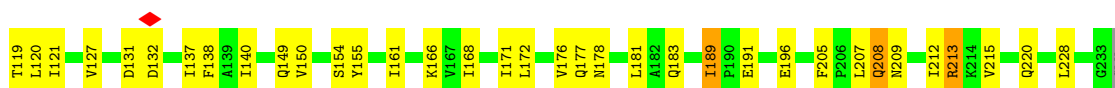
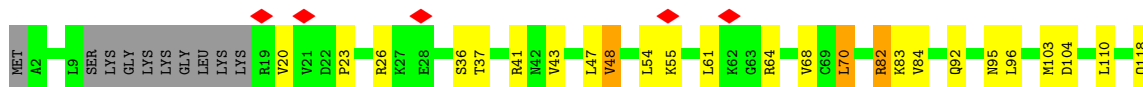




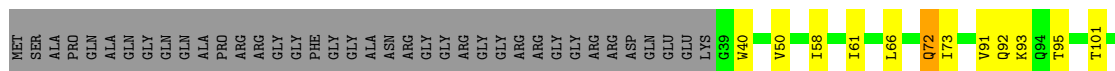
• Molecule 2: uS2



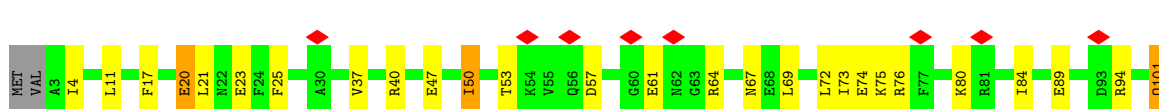
• Molecule 3: eS1

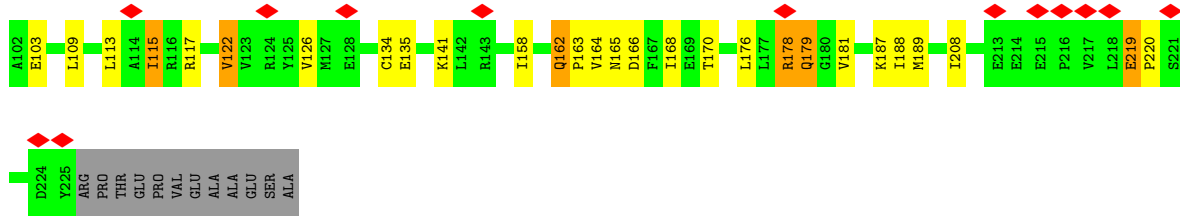


• Molecule 4: uS5

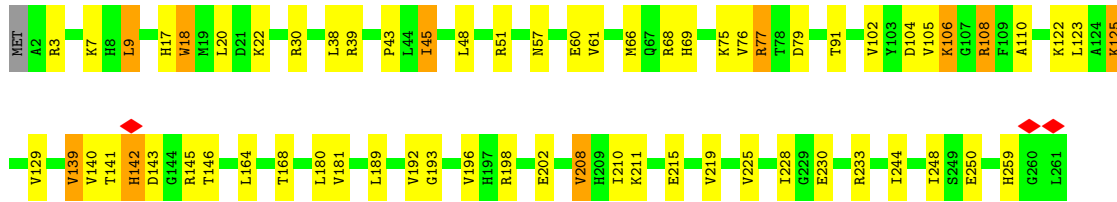
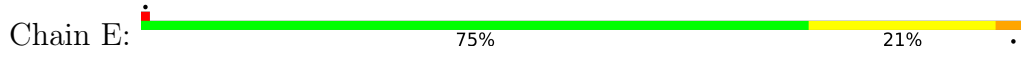


• Molecule 5: uS3

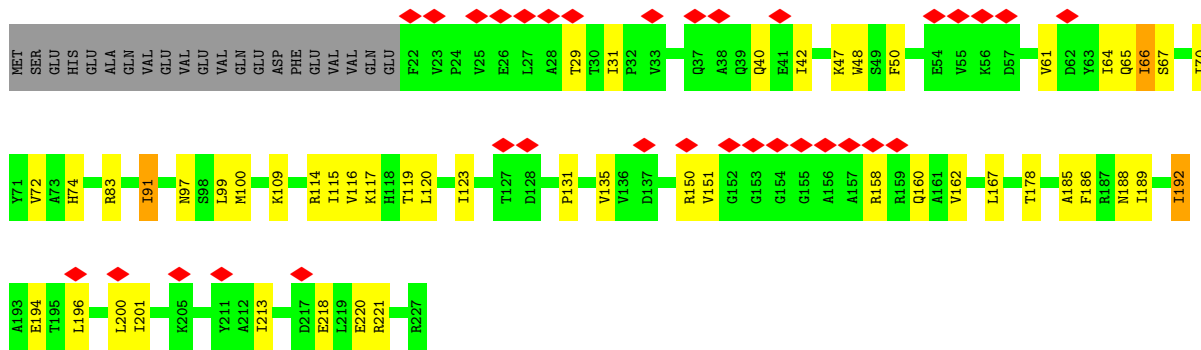




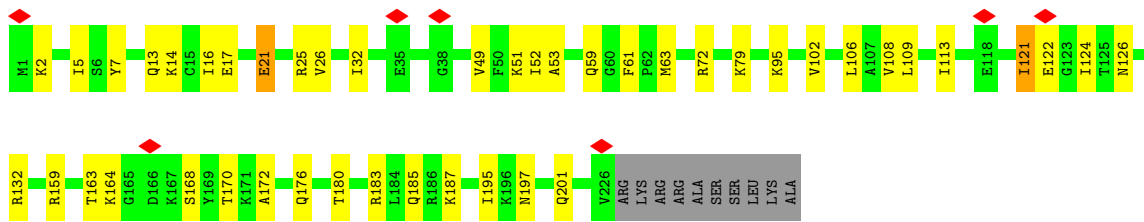
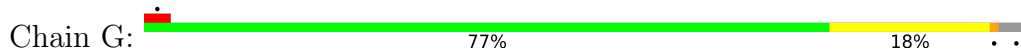
• Molecule 6: eS4



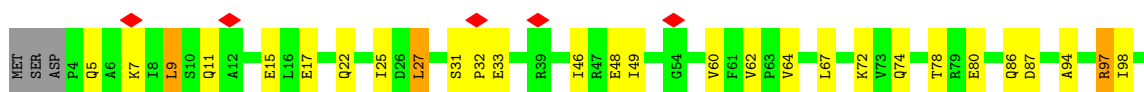
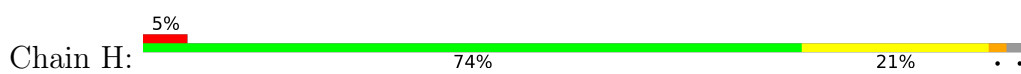
• Molecule 7: uS7



• Molecule 8: eS6

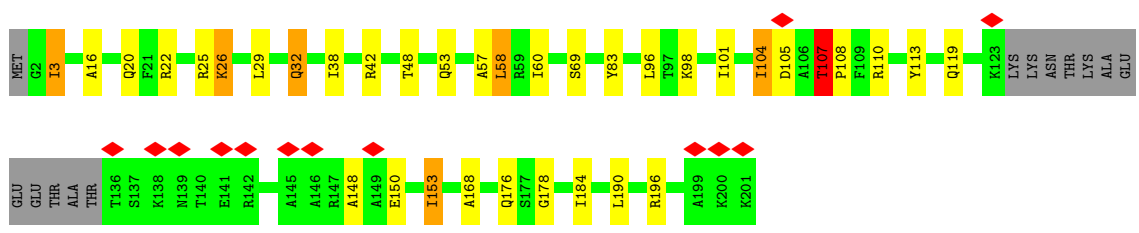
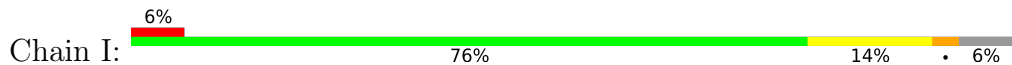


• Molecule 9: eS7

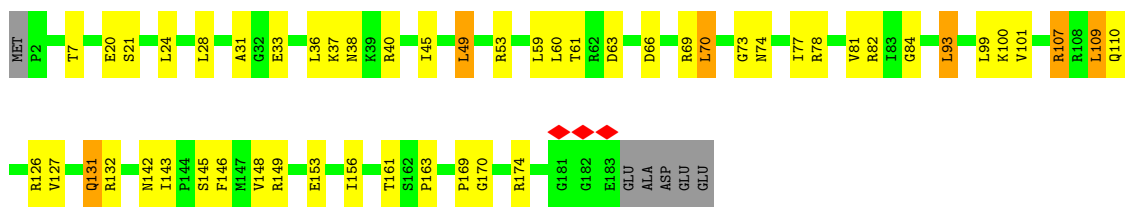




• Molecule 10: eS8



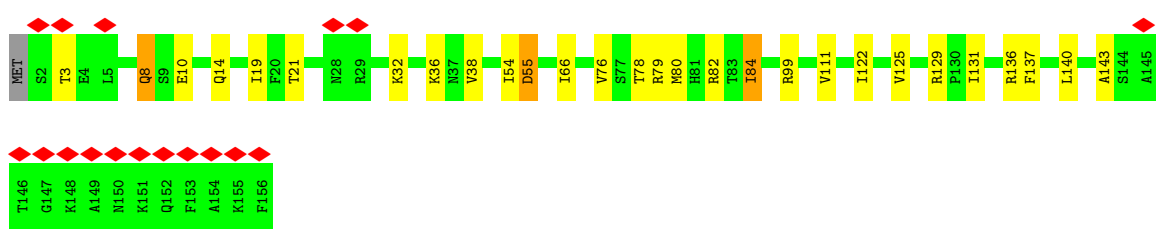
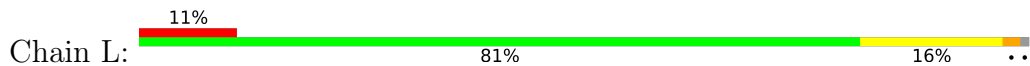
• Molecule 11: uS4



• Molecule 12: eS10

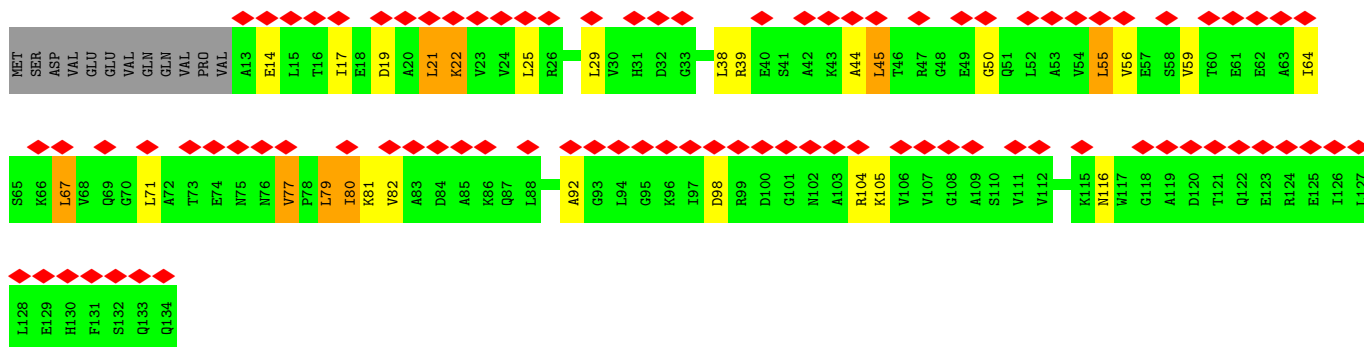


• Molecule 13: uS17

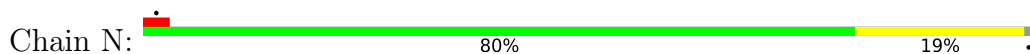


• Molecule 14: eS12





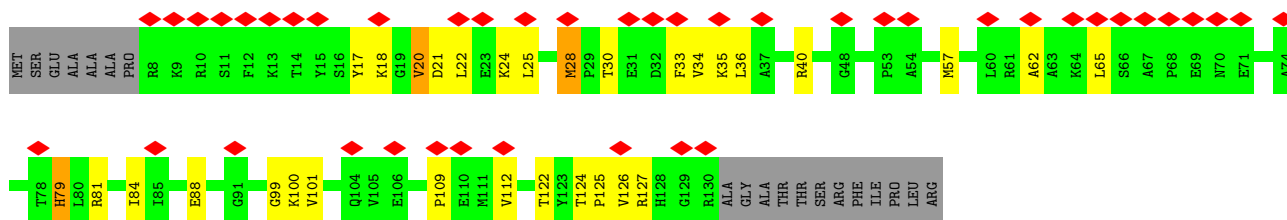
• Molecule 15: uS15



• Molecule 16: uS11



• Molecule 17: uS19

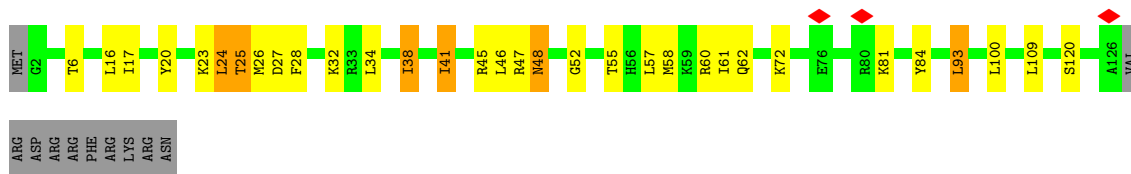


• Molecule 18: uS9

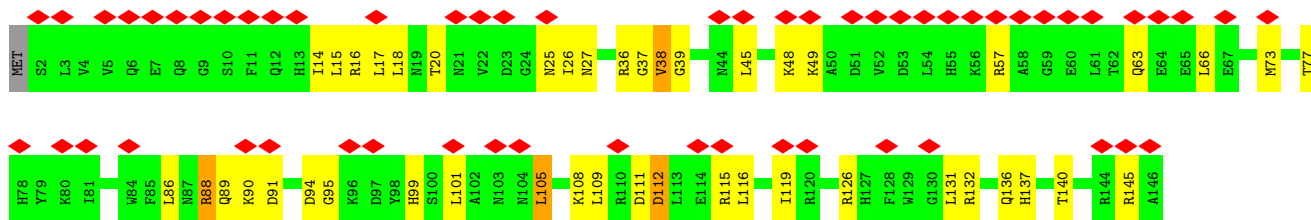
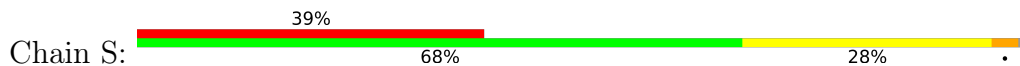


• Molecule 19: eS17

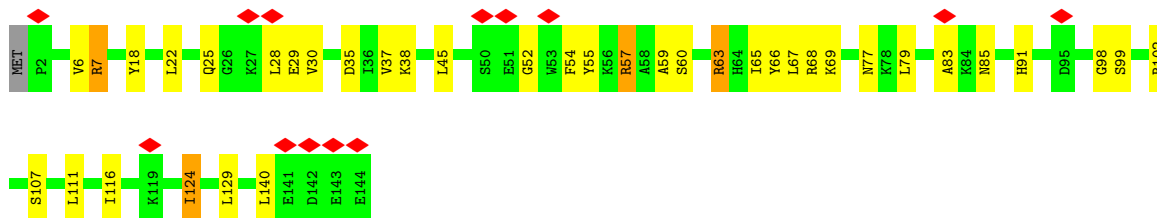




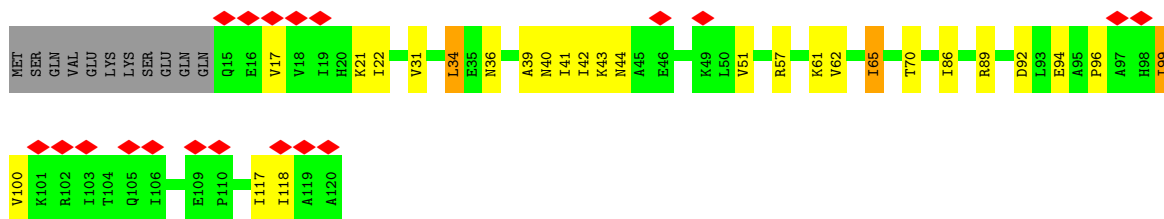
• Molecule 20: uS13



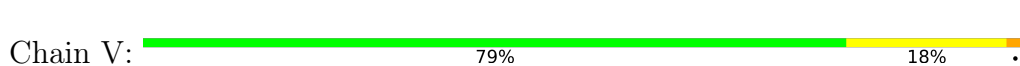
• Molecule 21: eS19



• Molecule 22: uS10

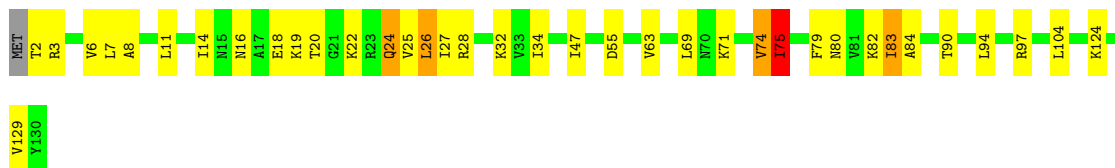


• Molecule 23: eS21

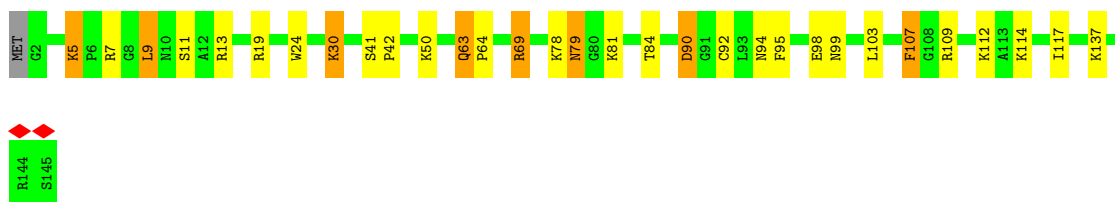
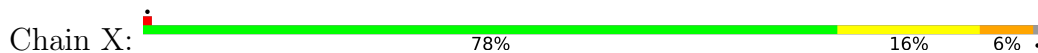


• Molecule 24: uS8

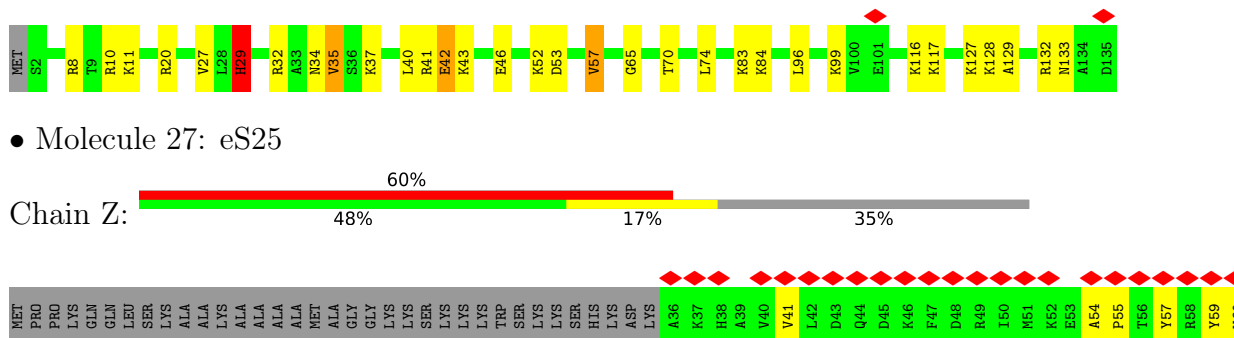




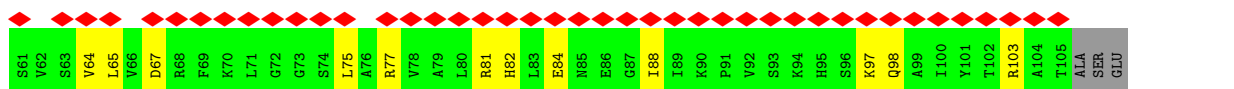
• Molecule 25: uS12



• Molecule 26: eS24



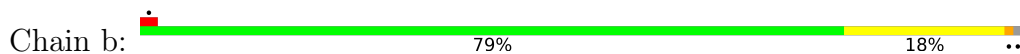
• Molecule 27: eS25



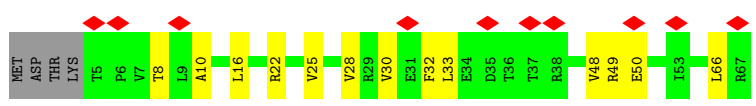
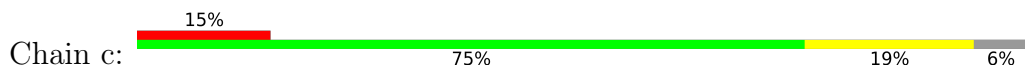
• Molecule 28: eS26



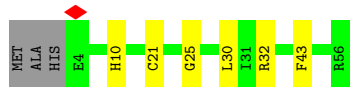
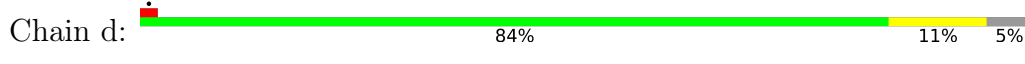
• Molecule 29: eS27



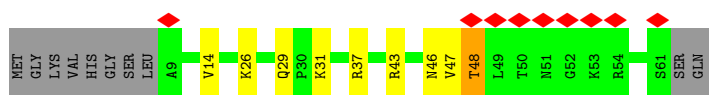
• Molecule 30: eS28



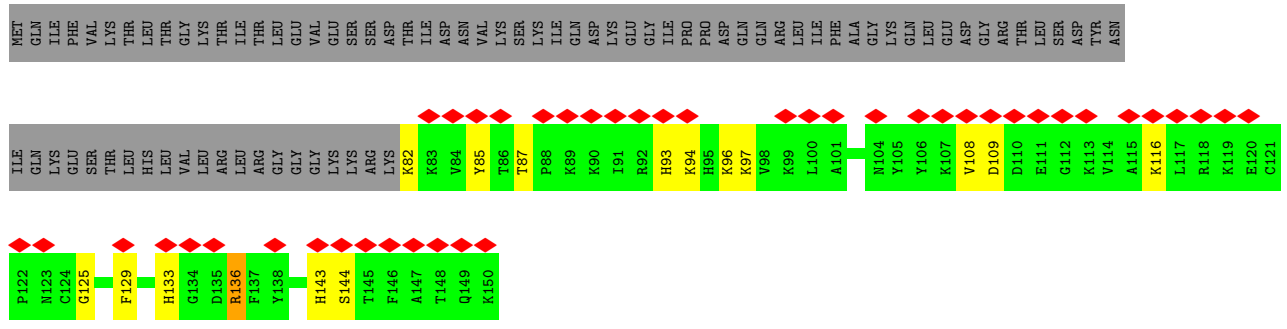
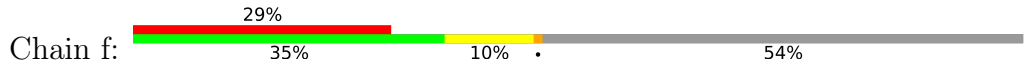
• Molecule 31: uS14



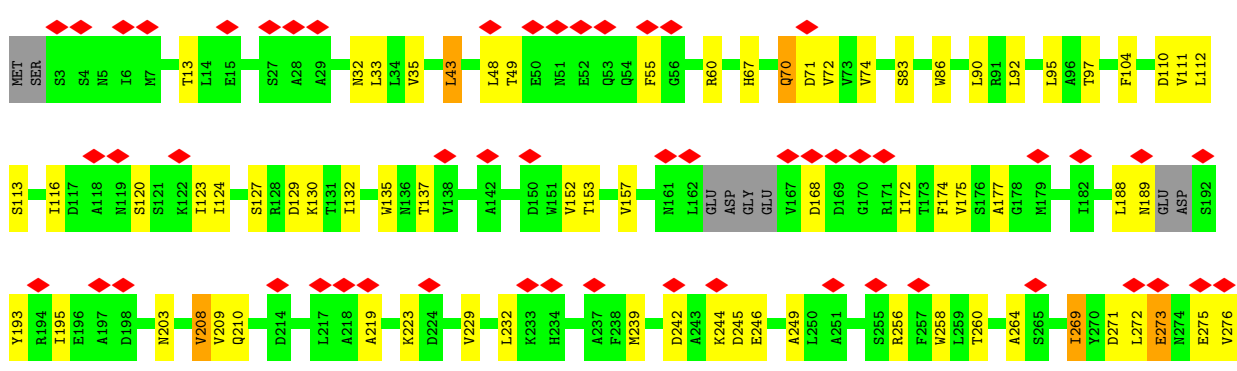
• Molecule 32: eS30

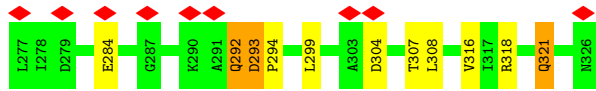


• Molecule 33: eS31

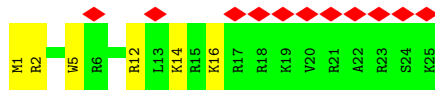
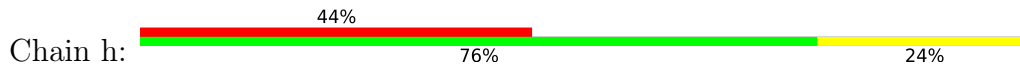


• Molecule 34: RACK1

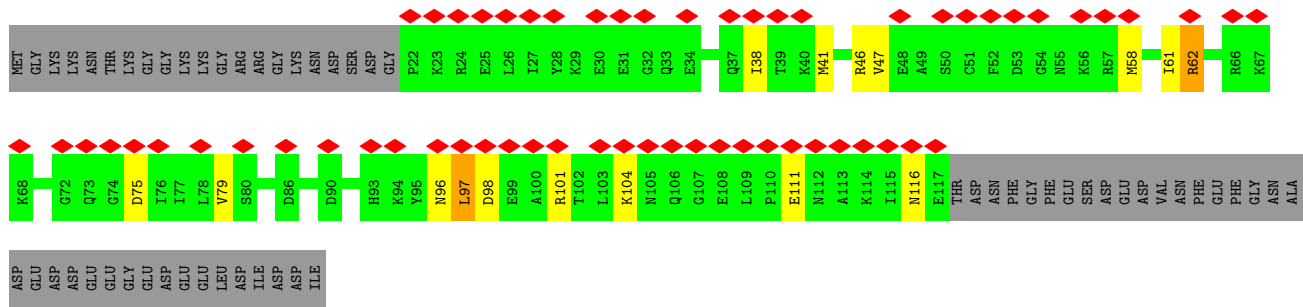




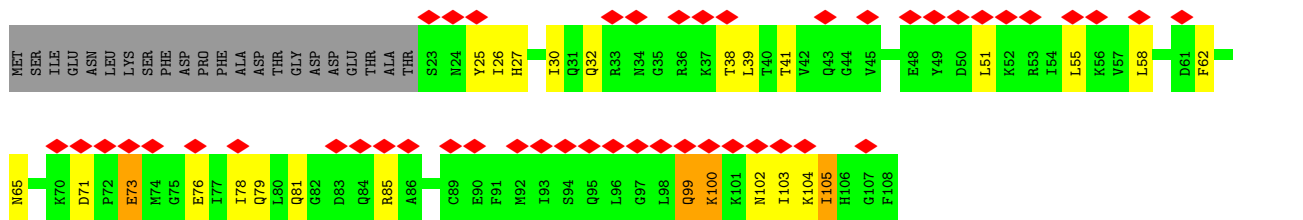
• Molecule 35: eL41



• Molecule 36: eIF1A



• Molecule 37: eIF1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86055	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.016	Depositor
Minimum map value	-0.605	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.1	Depositor
Map size (\AA)	402.0, 402.0, 402.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	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: MG, 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	2	0.39	0/42269	0.75	37/65862 (0.1%)
2	A	0.59	0/1666	1.16	5/2279 (0.2%)
3	B	0.56	1/1798 (0.1%)	1.01	2/2421 (0.1%)
4	C	0.57	0/1659	1.09	1/2252 (0.0%)
5	D	0.60	0/1769	1.06	2/2378 (0.1%)
6	E	0.53	0/2122	0.93	1/2861 (0.0%)
7	F	0.61	0/1628	1.15	0/2198
8	G	0.57	0/1835	0.97	1/2451 (0.0%)
9	H	0.63	0/1507	1.07	2/2028 (0.1%)
10	I	0.53	0/1515	1.04	1/2029 (0.0%)
11	J	0.57	0/1495	1.17	3/2001 (0.1%)
12	K	0.60	0/831	1.15	2/1123 (0.2%)
13	L	0.55	0/1276	0.92	1/1718 (0.1%)
14	M	0.67	0/929	1.15	1/1255 (0.1%)
15	N	0.56	0/1210	1.18	0/1628
16	O	0.58	0/953	1.06	2/1279 (0.2%)
17	P	0.65	0/1000	1.14	2/1343 (0.1%)
18	Q	0.60	0/1125	1.09	0/1510
19	R	0.59	0/1002	1.17	1/1346 (0.1%)
20	S	0.58	0/1212	1.08	0/1629
21	T	0.61	0/1129	1.15	0/1520
22	U	0.58	0/857	1.00	0/1158
23	V	0.54	0/696	0.99	0/938
24	W	0.50	0/1039	1.10	4/1399 (0.3%)
25	X	0.54	0/1137	1.01	2/1516 (0.1%)
26	Y	0.51	0/1075	1.08	2/1433 (0.1%)
27	Z	0.70	0/567	1.07	1/762 (0.1%)
28	a	0.56	0/791	1.01	0/1059
29	b	0.54	0/619	0.90	0/837
30	c	0.65	0/496	0.92	1/666 (0.2%)
31	d	0.53	0/457	0.94	0/607
32	e	0.54	0/435	1.03	1/579 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.71	0/562	1.06	2/751 (0.3%)
34	g	0.60	0/2521	0.86	2/3431 (0.1%)
35	h	0.56	0/234	1.27	1/300 (0.3%)
36	i	0.54	0/788	0.86	0/1051
37	j	0.58	0/703	1.01	3/938 (0.3%)
All	All	0.49	1/82907 (0.0%)	0.90	83/120536 (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
12	K	0	1
17	P	0	1
18	Q	0	1
25	X	0	1
26	Y	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	189	ILE	CA-CB	5.98	1.57	1.54

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1534	G	C2'-C3'-O3'	9.36	123.53	109.50
1	2	828	A	C2'-C3'-O3'	8.69	122.53	109.50
1	2	277	U	C2'-C3'-O3'	8.30	121.96	109.50
5	D	219	GLU	CA-C-N	7.92	129.75	119.84
5	D	219	GLU	C-N-CA	7.92	129.75	119.84

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	K	87	PHE	Peptide
17	P	28	MET	Peptide
18	Q	40	GLN	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
25	X	63	GLN	Peptide
26	Y	29	HIS	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	2	37797	0	19016	584	0
2	A	1626	0	1633	26	0
3	B	1774	0	1834	19	0
4	C	1629	0	1710	18	0
5	D	1744	0	1826	18	0
6	E	2078	0	2157	21	0
7	F	1609	0	1679	23	0
8	G	1812	0	1911	21	0
9	H	1483	0	1579	16	0
10	I	1489	0	1504	17	0
11	J	1471	0	1554	22	0
12	K	809	0	810	12	0
13	L	1248	0	1311	15	0
14	M	922	0	953	10	0
15	N	1187	0	1251	6	0
16	O	942	0	979	11	0
17	P	980	0	1026	16	0
18	Q	1105	0	1170	23	0
19	R	991	0	1039	16	0
20	S	1193	0	1217	22	0
21	T	1110	0	1124	19	0
22	U	845	0	913	10	0
23	V	687	0	682	12	0
24	W	1021	0	1056	21	0
25	X	1119	0	1198	14	0
26	Y	1061	0	1111	11	0
27	Z	558	0	585	6	0
28	a	779	0	828	10	0
29	b	609	0	631	7	0
30	c	494	0	534	5	0
31	d	446	0	436	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	e	428	0	468	3	0
33	f	549	0	564	5	0
34	g	2466	0	2406	28	0
35	h	233	0	284	5	0
36	i	778	0	779	7	0
37	j	695	0	729	10	0
38	2	78	0	0	0	0
38	J	1	0	0	0	0
38	f	1	0	0	0	0
39	a	1	0	0	0	0
39	b	1	0	0	0	0
39	f	1	0	0	0	0
All	All	77850	0	60487	979	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 7.

The worst 5 of 979 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)
1:2:51:A:N6	1:2:439:U:H3	1.05	1.41
1:2:1593:U:H3	1:2:1598:A:N6	1.13	1.40
1:2:480:A:N1	1:2:506:U:O4	1.62	1.33
1:2:628:U:N3	1:2:969:A:N6	1.77	1.32
1:2:1079:U:O4	1:2:1090:A:N1	1.66	1.25

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	
2	A	174/211 (82%)	139 (80%)	35 (20%)	1	7
3	B	198/228 (87%)	169 (85%)	29 (15%)	3	17
4	C	176/203 (87%)	157 (89%)	19 (11%)	6	27
5	D	185/196 (94%)	153 (83%)	32 (17%)	2	12
6	E	223/224 (100%)	185 (83%)	38 (17%)	2	12
7	F	174/194 (90%)	148 (85%)	26 (15%)	3	17
8	G	192/200 (96%)	176 (92%)	16 (8%)	10	35
9	H	164/170 (96%)	142 (87%)	22 (13%)	4	20
10	I	147/159 (92%)	128 (87%)	19 (13%)	4	21
11	J	153/158 (97%)	133 (87%)	20 (13%)	4	21
12	K	88/96 (92%)	78 (89%)	10 (11%)	5	25
13	L	136/137 (99%)	125 (92%)	11 (8%)	11	36
14	M	97/109 (89%)	79 (81%)	18 (19%)	1	9
15	N	127/128 (99%)	107 (84%)	20 (16%)	2	15
16	O	96/104 (92%)	82 (85%)	14 (15%)	3	17
17	P	105/119 (88%)	96 (91%)	9 (9%)	10	34
18	Q	117/119 (98%)	99 (85%)	18 (15%)	2	16
19	R	112/124 (90%)	97 (87%)	15 (13%)	4	20
20	S	128/129 (99%)	107 (84%)	21 (16%)	2	14
21	T	117/118 (99%)	103 (88%)	14 (12%)	5	23
22	U	96/107 (90%)	80 (83%)	16 (17%)	2	13
23	V	73/73 (100%)	67 (92%)	6 (8%)	10	35
24	W	110/111 (99%)	96 (87%)	14 (13%)	4	22
25	X	119/120 (99%)	106 (89%)	13 (11%)	6	27
26	Y	108/109 (99%)	93 (86%)	15 (14%)	3	19
27	Z	60/88 (68%)	53 (88%)	7 (12%)	5	25
28	a	83/100 (83%)	73 (88%)	10 (12%)	5	23
29	b	71/72 (99%)	63 (89%)	8 (11%)	5	25
30	c	55/59 (93%)	49 (89%)	6 (11%)	6	27
31	d	46/48 (96%)	44 (96%)	2 (4%)	26	52

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	e	47/55 (86%)	42 (89%)	5 (11%)	6	27
33	f	58/133 (44%)	48 (83%)	10 (17%)	2	12
34	g	265/272 (97%)	227 (86%)	38 (14%)	3	18
35	h	23/23 (100%)	21 (91%)	2 (9%)	9	34
36	i	83/130 (64%)	76 (92%)	7 (8%)	10	35
37	j	77/96 (80%)	66 (86%)	11 (14%)	3	18
All	All	4283/4722 (91%)	3707 (87%)	576 (13%)	6	20

5 of 576 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Y	70	THR
37	j	100	LYS
27	Z	98	GLN
26	Y	57	VAL
34	g	49	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
16	O	29	HIS
34	g	292	GLN
20	S	89	GLN
34	g	234	HIS
36	i	112	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1778/1799 (98%)	684 (38%)	113 (6%)

5 of 684 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	2	26	A

5 of 113 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	779	A
1	2	1778	G
1	2	1098	U
1	2	1766	G
1	2	1580	U

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 83 ligands modelled in this entry, 83 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.

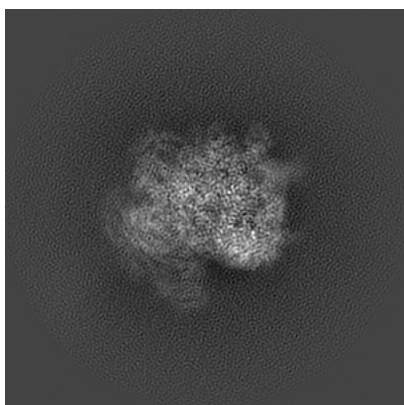
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3047. These allow visual inspection of the internal detail of the map and identification of artifacts.

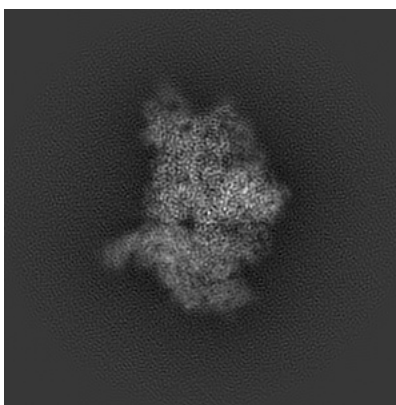
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

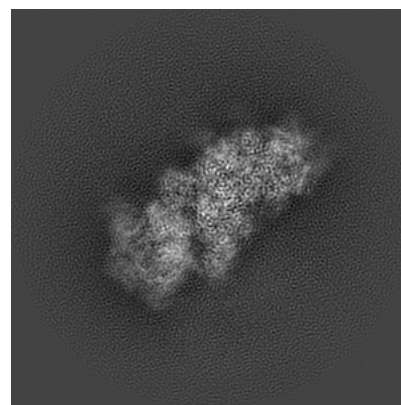
6.1.1 Primary map



X



Y

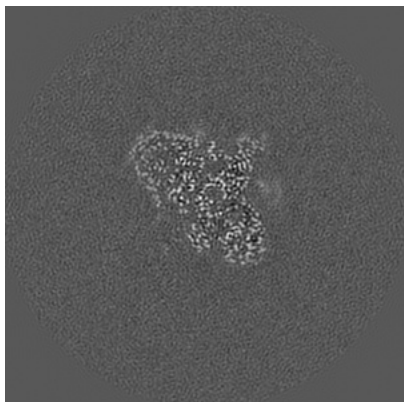


Z

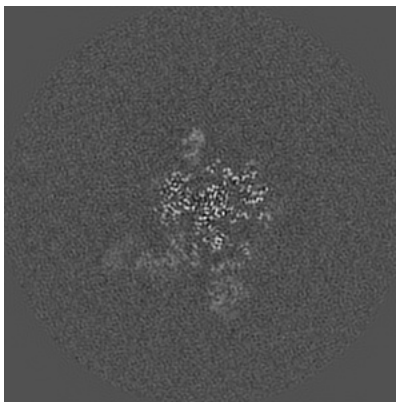
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

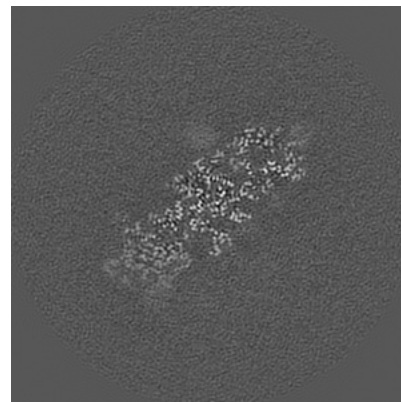
6.2.1 Primary map



X Index: 150



Y Index: 150

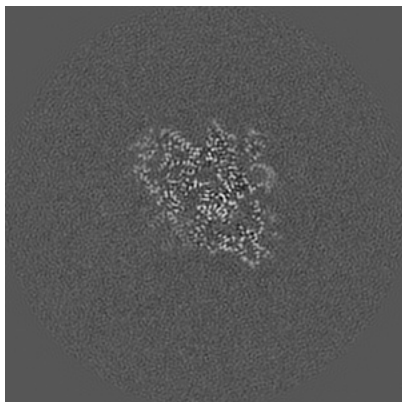


Z Index: 150

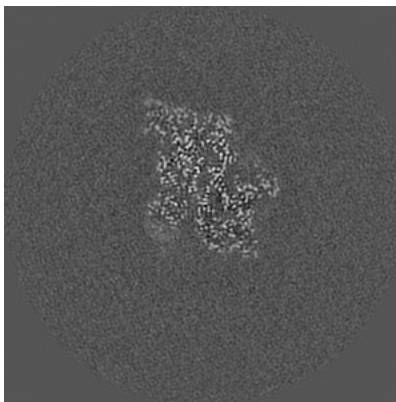
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

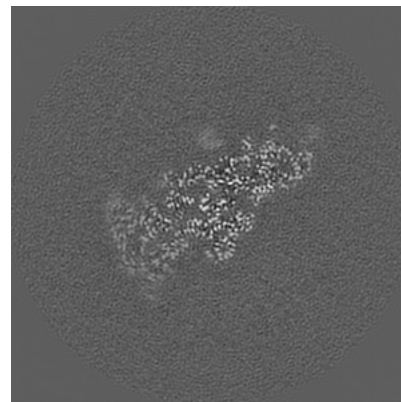
6.3.1 Primary map



X Index: 157



Y Index: 170

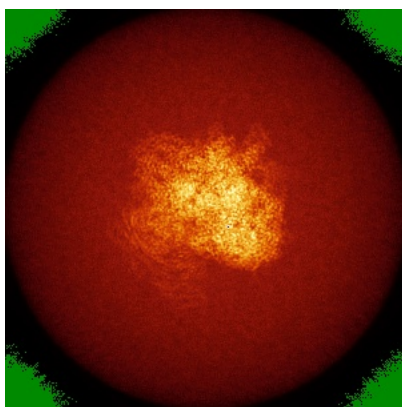


Z Index: 161

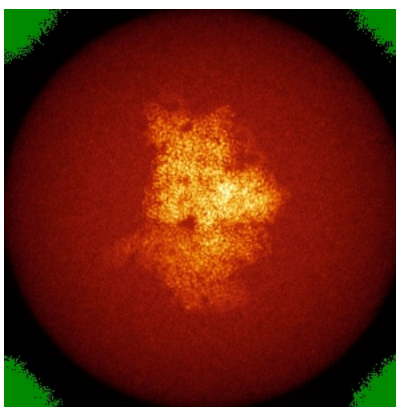
The images above show the largest variance slices of the map in three orthogonal directions.

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

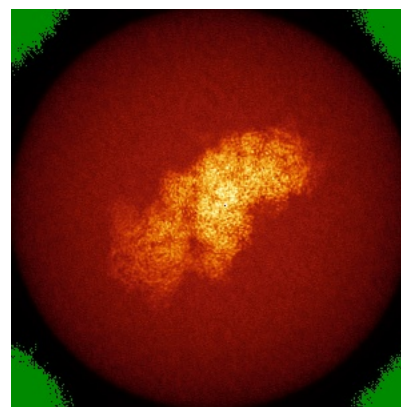
6.4.1 Primary map



X



Y

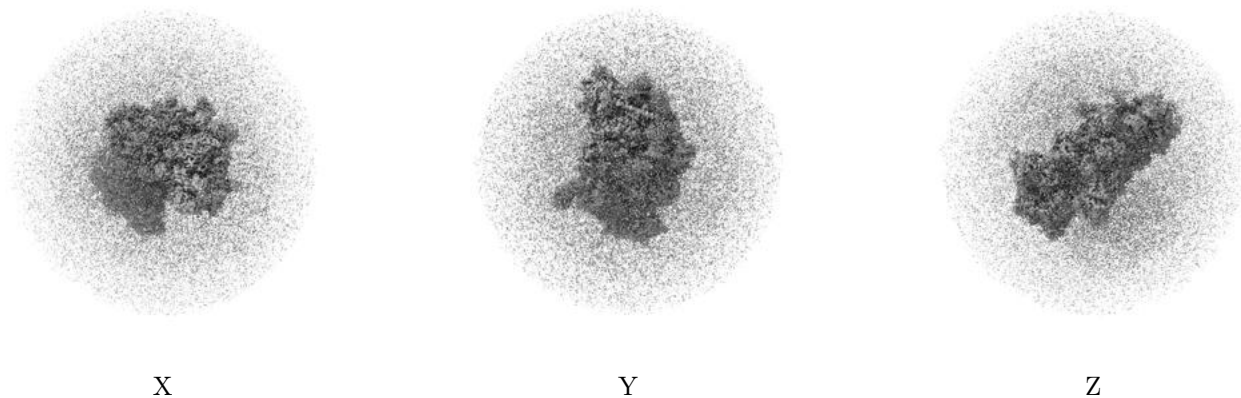


Z

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 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

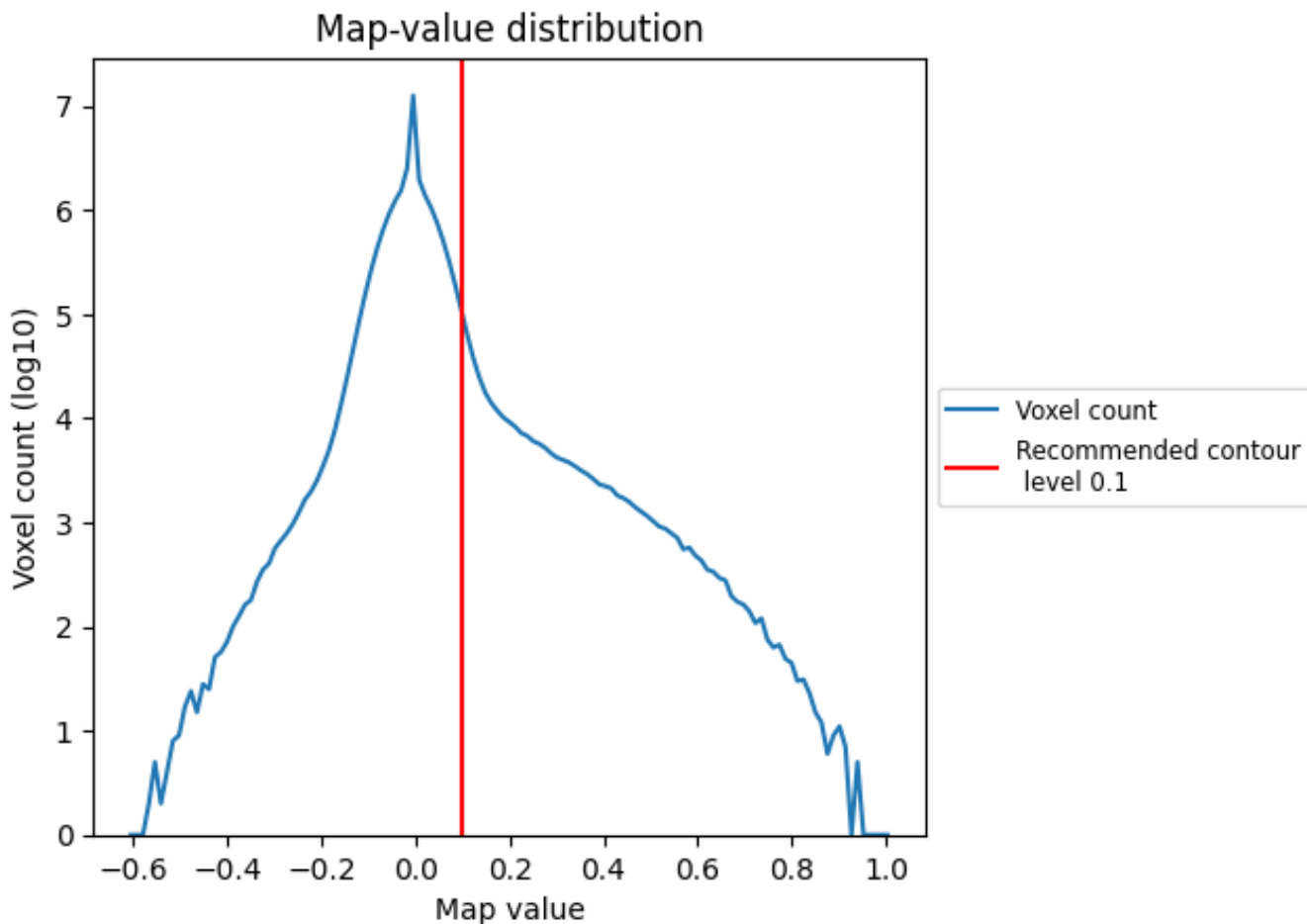
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

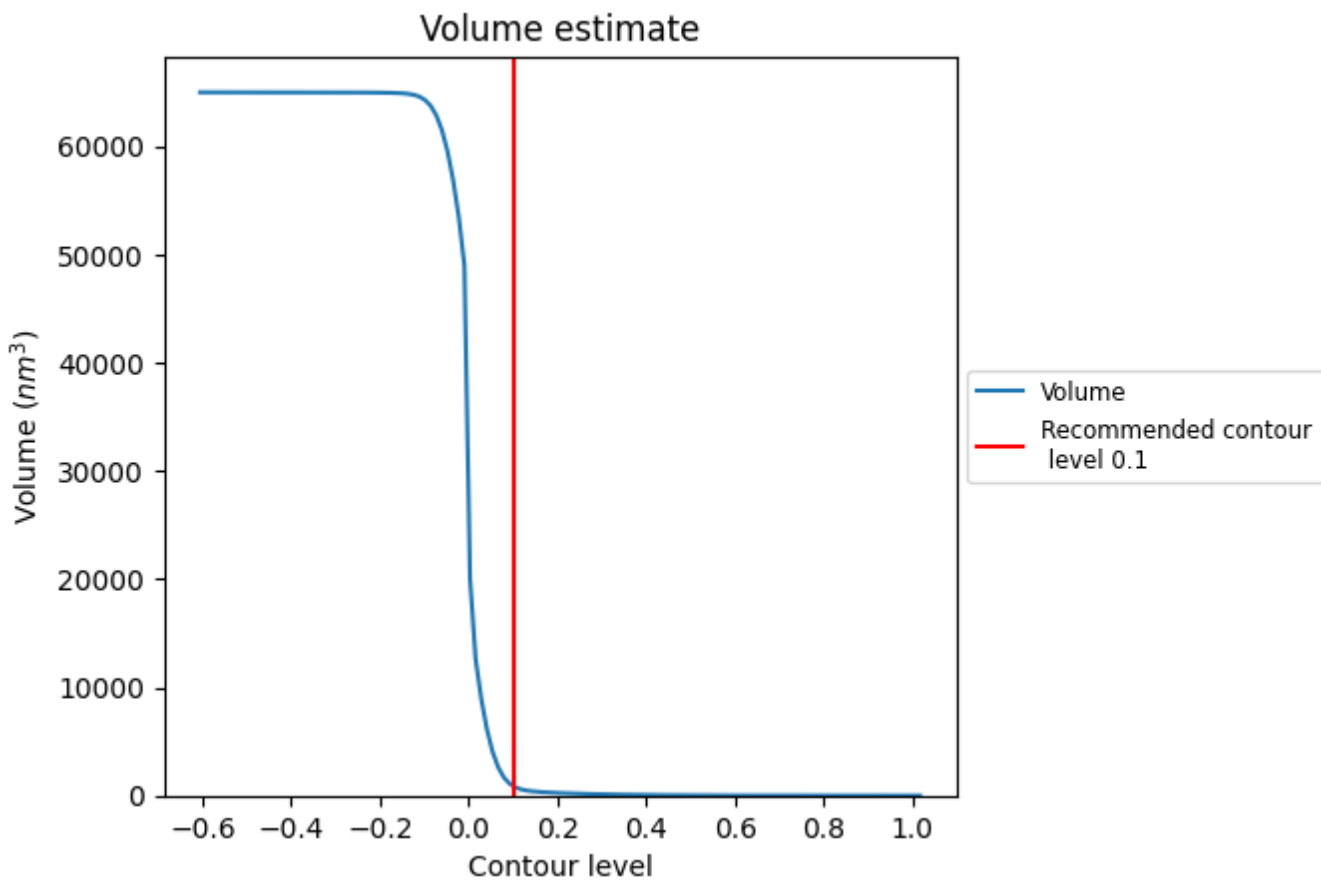
This section contains the results of statistical analysis of the map.

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.

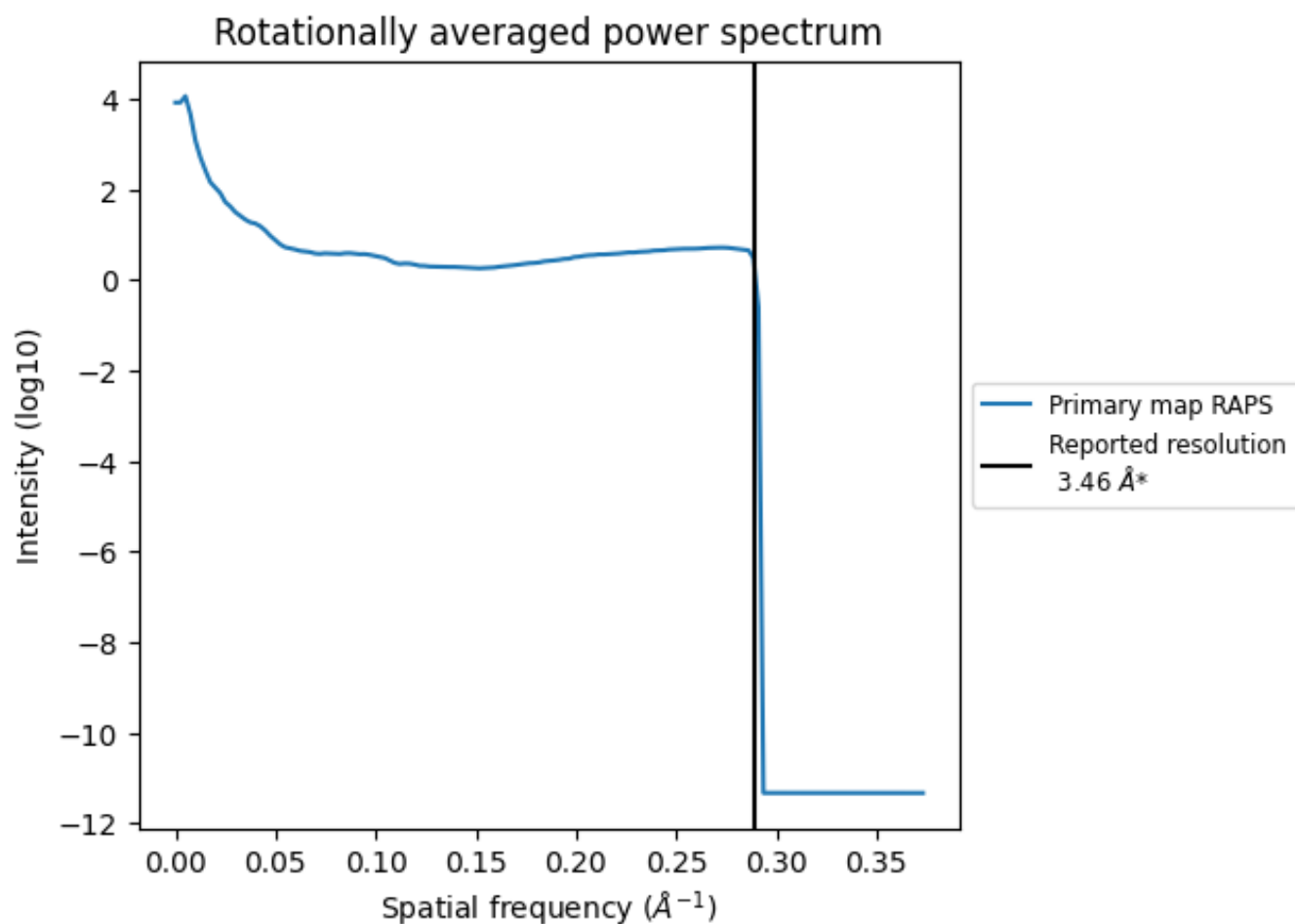
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 894 nm³; this corresponds to an approximate mass of 808 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 [\(i\)](#)

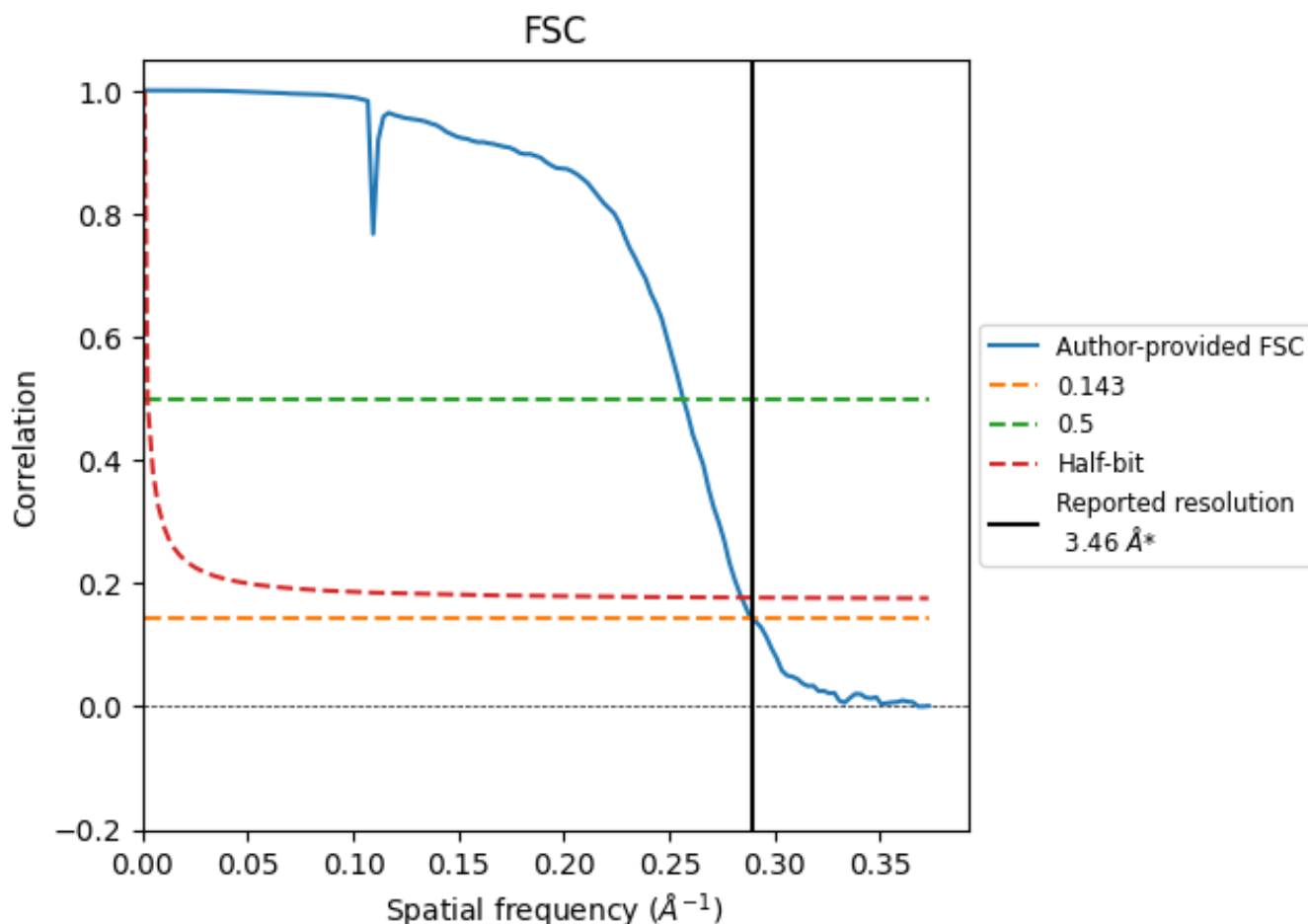


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 \AA^{-1}

8.2 Resolution estimates [i](#)

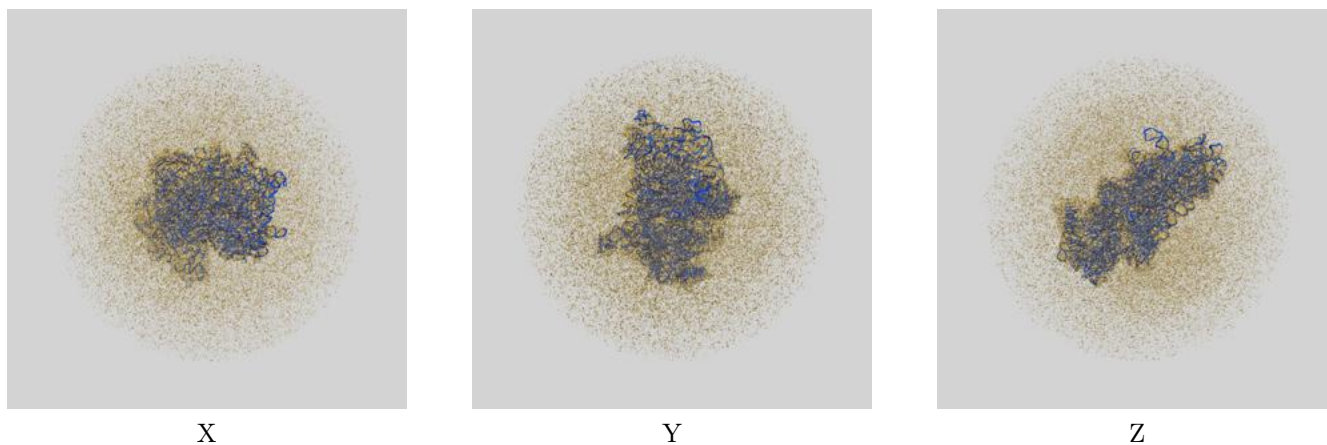
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	3.90	3.52
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

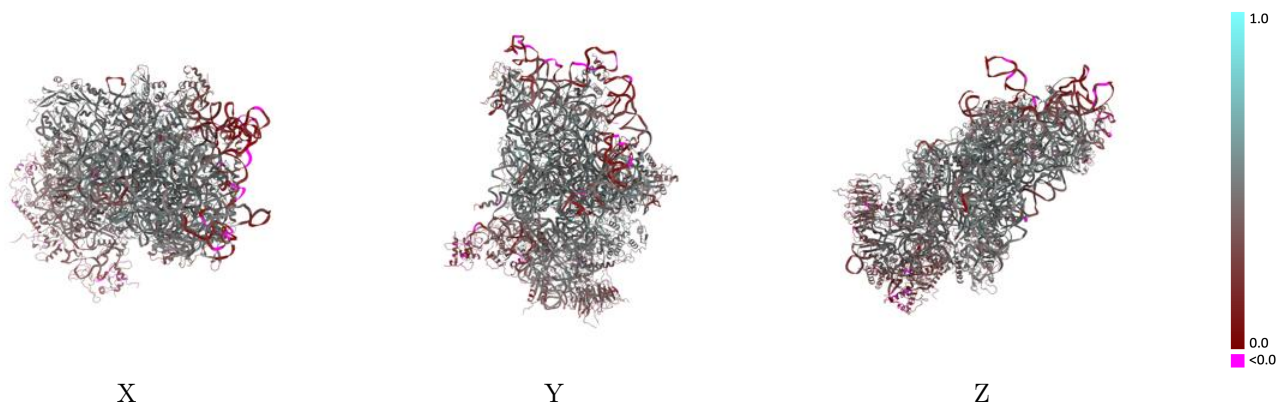
This section contains information regarding the fit between EMDB map EMD-3047 and PDB model 3JAM. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

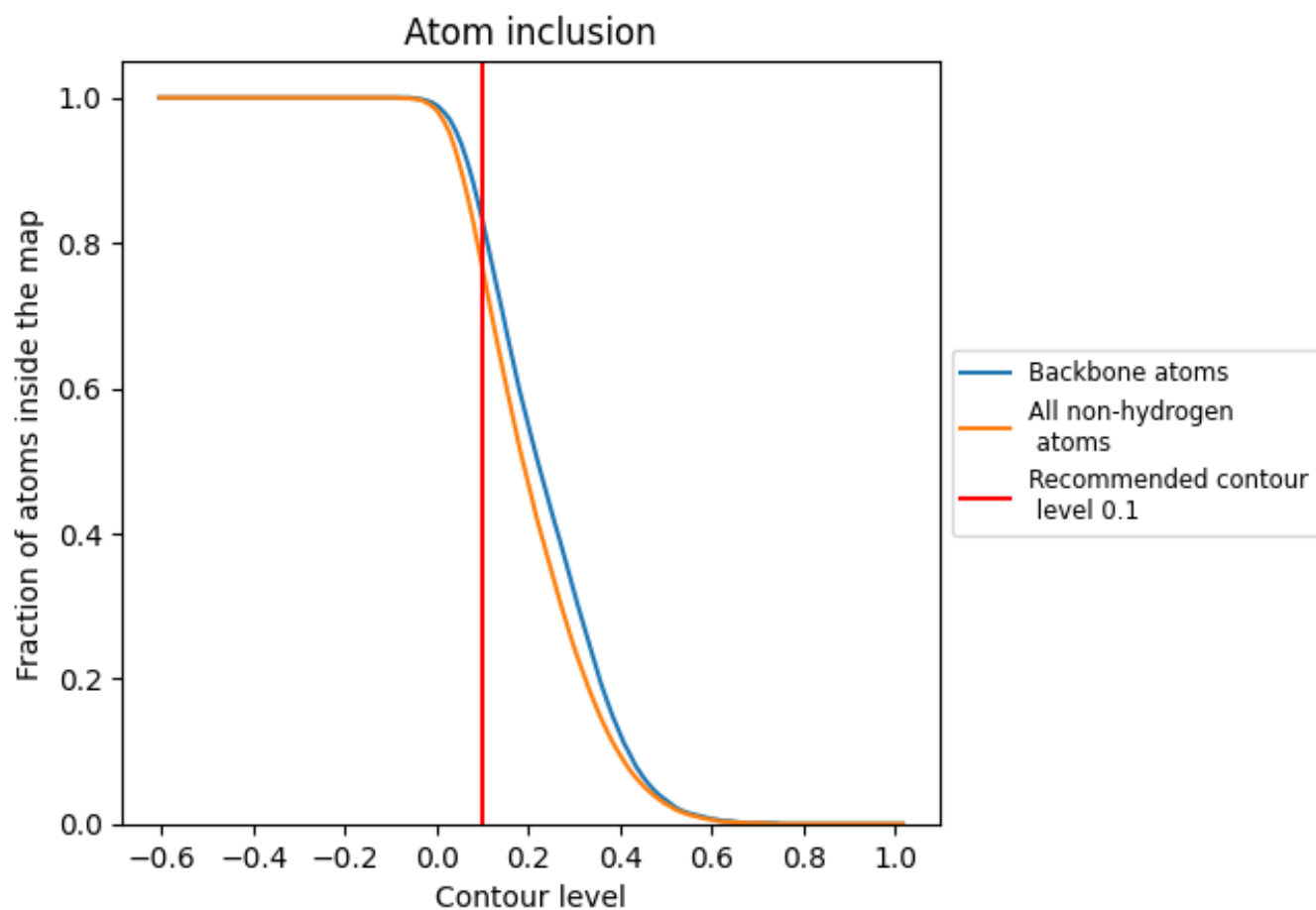


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 76% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7650	 0.4180
2	 0.8310	 0.4190
A	 0.8380	 0.4840
B	 0.7800	 0.4680
C	 0.8130	 0.4990
D	 0.6630	 0.3870
E	 0.8270	 0.4990
F	 0.6190	 0.3510
G	 0.7540	 0.4320
H	 0.7480	 0.4370
I	 0.7940	 0.4730
J	 0.8190	 0.4900
K	 0.6360	 0.3370
L	 0.7630	 0.4730
M	 0.2560	 0.1520
N	 0.8160	 0.4800
O	 0.8270	 0.4730
P	 0.4830	 0.2740
Q	 0.7460	 0.4350
R	 0.7500	 0.4360
S	 0.4800	 0.2520
T	 0.6870	 0.3690
U	 0.6370	 0.3810
V	 0.8320	 0.4880
W	 0.8560	 0.5210
X	 0.8530	 0.5200
Y	 0.8240	 0.4810
Z	 0.1160	 0.1420
a	 0.8530	 0.5060
b	 0.8160	 0.4720
c	 0.5950	 0.3680
d	 0.7960	 0.4530
e	 0.7100	 0.4570
f	 0.3350	 0.2010
g	 0.6200	 0.3420



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.4620	 0.3630
i	 0.3580	 0.3720
j	 0.3810	 0.3470