



wwPDB EM Validation Summary Report ⓘ

Dec 8, 2025 – 01:11 PM JST

PDB ID : 9KKF / pdb_00009kkf
EMDB ID : EMD-62386
Title : Structure of the human 40S ribosome complexed with HCV IRES and eIF3
Authors : Iwasaki, W.; Kashiwagi, K.; Sakamoto, A.; Nishimoto, M.; Takahashi, M.;
Machida, K.; Imataka, H.; Matsumoto, A.; Shichino, Y.; Iwasaki, S.; Imami,
K.; Ito, T.
Deposited on : 2024-11-13
Resolution : 3.30 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.47

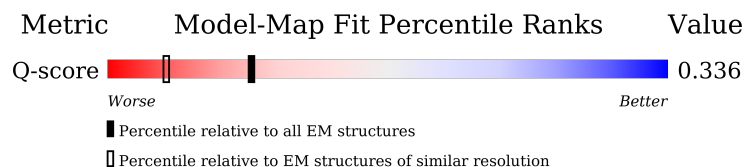
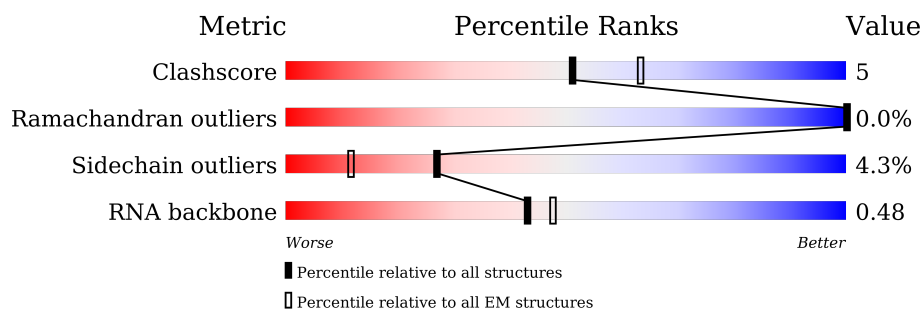
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

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










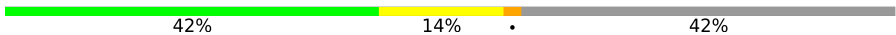














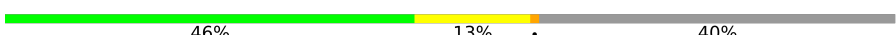


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	SA	295	
2	SB	264	
3	SC	293	

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Mol	Chain	Length	Quality of chain
4	SD	243	
5	SE	263	
6	SF	204	
7	SG	249	
8	SH	194	
9	SI	208	
10	SJ	194	
11	SK	165	
12	SL	158	
13	Sf	132	
14	SN	151	
15	SO	151	
16	SP	145	
17	SQ	146	
18	SR	135	
19	SS	152	
20	ST	145	
21	SU	119	
22	SV	83	
23	SW	130	
24	SX	143	
25	SY	133	
26	SZ	125	
27	Sa	115	
28	Sb	84	

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Mol	Chain	Length	Quality of chain
29	Sc	69	
30	Sd	56	
31	Se	59	
32	sh	156	
33	Sg	317	
34	Ln	25	
35	S2	1869	
36	zz	332	
37	3m	374	
38	3f	357	
39	3a	1382	
40	3e	445	
41	3c	913	
42	3h	352	
43	3d	548	
44	3k	218	
45	3l	564	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 108043 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 Small ribosomal subunit protein uS2.

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

- Molecule 2 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 3 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SC	219	Total	C	N	O	S	0	0
			1700	1100	292	298	10		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	260	Total	C	N	O	S	0	0
			2065	1319	384	354	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	192	Total	C	N	O	S	0	0
			1518	948	287	276	7		

- Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 8 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SH	187	Total	C	N	O	S	0	0
			1506	961	277	267	1		

- Molecule 9 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SI	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 10 is a protein called 40S ribosomal protein S9.

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

- Molecule 11 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 12 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SL	150	Total	C	N	O	S	0	0
			1220	776	228	210	6		

- Molecule 13 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Sf	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 14 is a protein called 40S ribosomal protein S13.

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

- Molecule 15 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SO	135	Total	C	N	O	S	0	0
			1007	617	198	186	6		

- Molecule 16 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SP	119	Total	C	N	O	S	0	0
			984	625	187	165	7		

- Molecule 17 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SQ	140	Total	C	N	O	S	0	0
			1116	710	211	192	3		

- Molecule 18 is a protein called 40S ribosomal protein S17.

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

- Molecule 19 is a protein called 40S ribosomal protein S18.

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

- Molecule 20 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ST	142	Total	C	N	O	S	0	0
			1103	691	212	197	3		

- Molecule 21 is a protein called 40S ribosomal protein S20.

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

- Molecule 22 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 23 is a protein called 40S ribosomal protein S15a.

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

- Molecule 24 is a protein called 40S ribosomal protein S23.

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

- Molecule 25 is a protein called 40S ribosomal protein S24.

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

- Molecule 26 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SZ	75	Total	C	N	O	S	0	0
			601	385	111	104	1		

- Molecule 27 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Sa	100	Total	C	N	O	S	0	0
			803	501	166	131	5		

- Molecule 28 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 29 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 30 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 31 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Se	52	Total	C	N	O	S	0	0
			417	259	92	65	1		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	sh	64	Total	C	N	O	S	0	0
			522	329	99	87	7		

- Molecule 33 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 34 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 35 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	S2	1759	Total	C	N	O	P	6	0
			37669	16814	6767	12324	1764		

- Molecule 36 is a RNA chain called HCV-IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	zz	302	Total	C	N	O	P	0	0
			6443	2871	1148	2122	302		

- Molecule 37 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	3m	363	Total	C	N	O	S	0	0
			2639	1666	450	511	12		

- Molecule 38 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	3f	269	Total	C	N	O	S	0	0
			2063	1303	354	394	12		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3a	592	Total	C	N	O	S	0	0
			4497	2849	805	822	21		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	3e	430	Total	C	N	O	S	0	0
			3224	2053	561	594	16		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	3c	543	Total	C	N	O	S	0	0
			3924	2463	721	716	24		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	3h	318	Total	C	N	O	S	0	0
			2520	1599	431	475	15		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	3d	55	Total	C	N	O	S	0	0
			347	222	65	59	1		

- Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	3k	215	Total	C	N	O	S	0	0
			1475	932	251	282	10		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 3 subunit L.


Mol	Chain	Residues	Atoms					AltConf	Trace
45	3l	520	Total	C	N	O	S	0	0
			4335	2808	715	793	19		

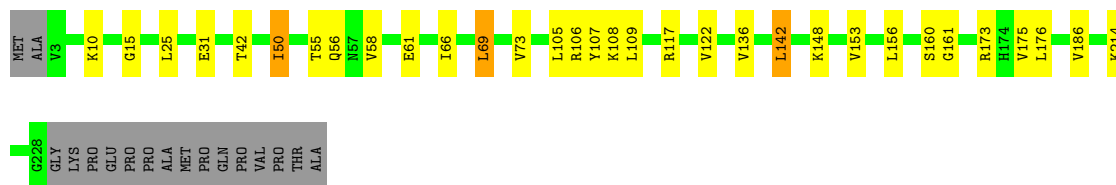
- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
46	Sa	1	Total	Zn	0
			1	1	
46	sh	1	Total	Zn	0
			1	1	


- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
47	S2	8	Total	Mg	0
			8	8	

Chain SD:  80% 12% 7%




- Molecule 5: 40S ribosomal protein S4, X isoform

Chain SE:  86% 13% 1%




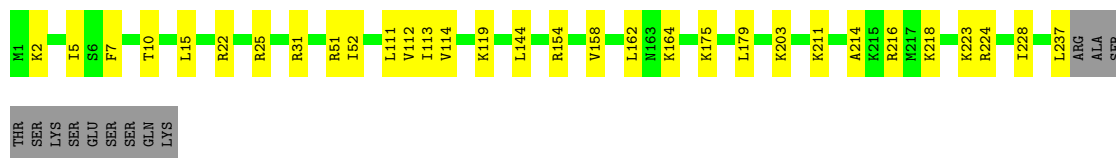
- Molecule 6: 40S ribosomal protein S5

Chain SF:  84% 9% 6%




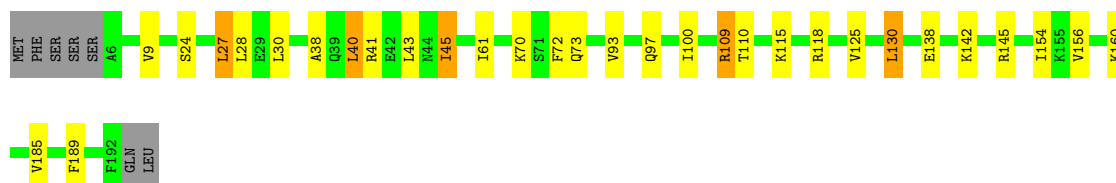
- Molecule 7: 40S ribosomal protein S6

Chain SG:  83% 12% 5%




- Molecule 8: 40S ribosomal protein S7

Chain SH:  80% 13% 7%



- Molecule 9: 40S ribosomal protein S8

Chain SI:  86% 12% 2%



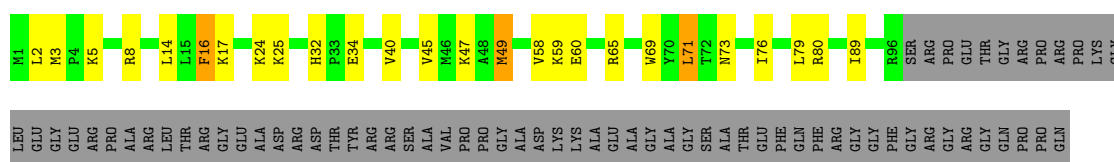
- Molecule 10: 40S ribosomal protein S9

Chain SJ: 82% 11% 7%



- Molecule 11: 40S ribosomal protein S10

Chain SK: 42% 14% 42%



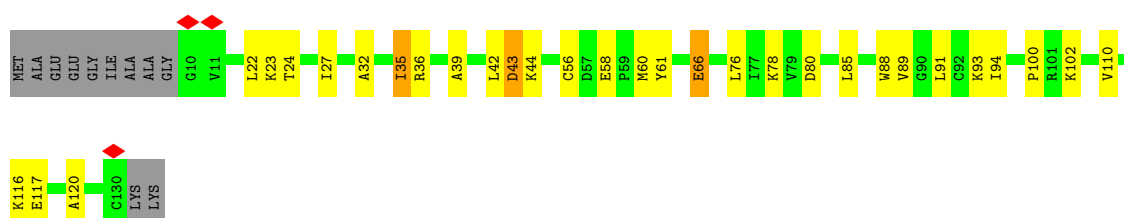
- Molecule 12: 40S ribosomal protein S11

Chain SL: 83% 11% 5%



- Molecule 13: 40S ribosomal protein S12

Chain Sf: 68% 21% 8%



- Molecule 14: 40S ribosomal protein S13

Chain SN: 88% 11% 1%

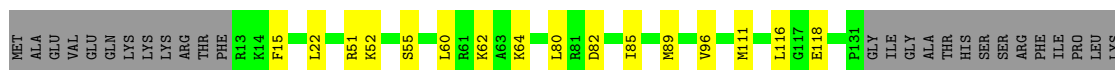


- Molecule 15: 40S ribosomal protein S14

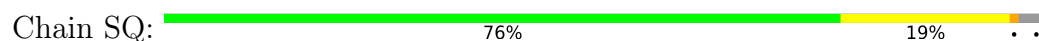
Chain SO: 74% 15% 11%



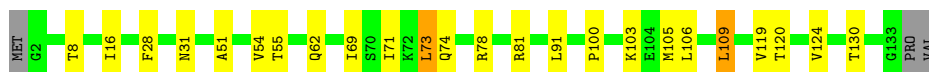
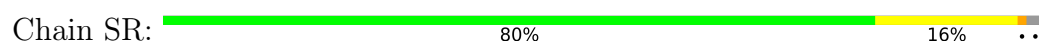
- Molecule 16: 40S ribosomal protein S15



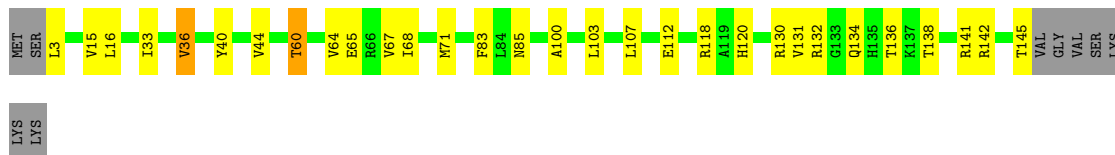
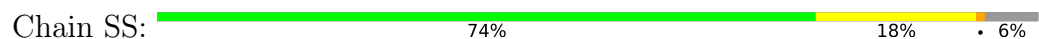
- Molecule 17: 40S ribosomal protein S16



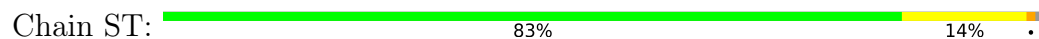
- Molecule 18: 40S ribosomal protein S17



- Molecule 19: 40S ribosomal protein S18




- Molecule 20: 40S ribosomal protein S19



- Molecule 21: 40S ribosomal protein S20



- Molecule 22: 40S ribosomal protein S21

Chain SV:  87% 13%




- Molecule 23: 40S ribosomal protein S15a

Chain SW:  91% 8% ..




- Molecule 24: 40S ribosomal protein S23

Chain SX:  81% 17% ..



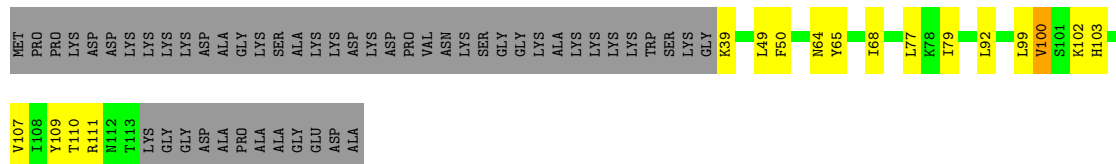
- Molecule 25: 40S ribosomal protein S24

Chain SY:  81% 11% • 7%




- Molecule 26: 40S ribosomal protein S25

Chain SZ:  46% 13% • 40%




- Molecule 27: 40S ribosomal protein S26

Chain Sa:  80% 7% 13%



- Molecule 28: 40S ribosomal protein S27

Chain Sb:  85% 14% •




- Molecule 29: 40S ribosomal protein S28

Chain Sc:  70% 20% 10%




- Molecule 30: 40S ribosomal protein S29

Chain Sd:  80% 18%



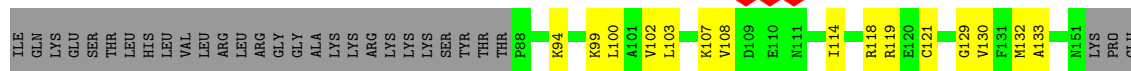
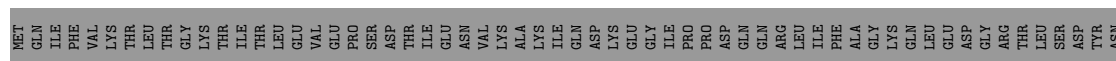
- Molecule 31: 40S ribosomal protein S30

Chain Se:  76% 12% 12%




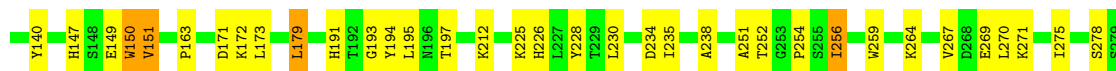
- Molecule 32: Ubiquitin-40S ribosomal protein S27a

Chain sh:  31% 10% 59%



- Molecule 33: Receptor of activated protein C kinase 1

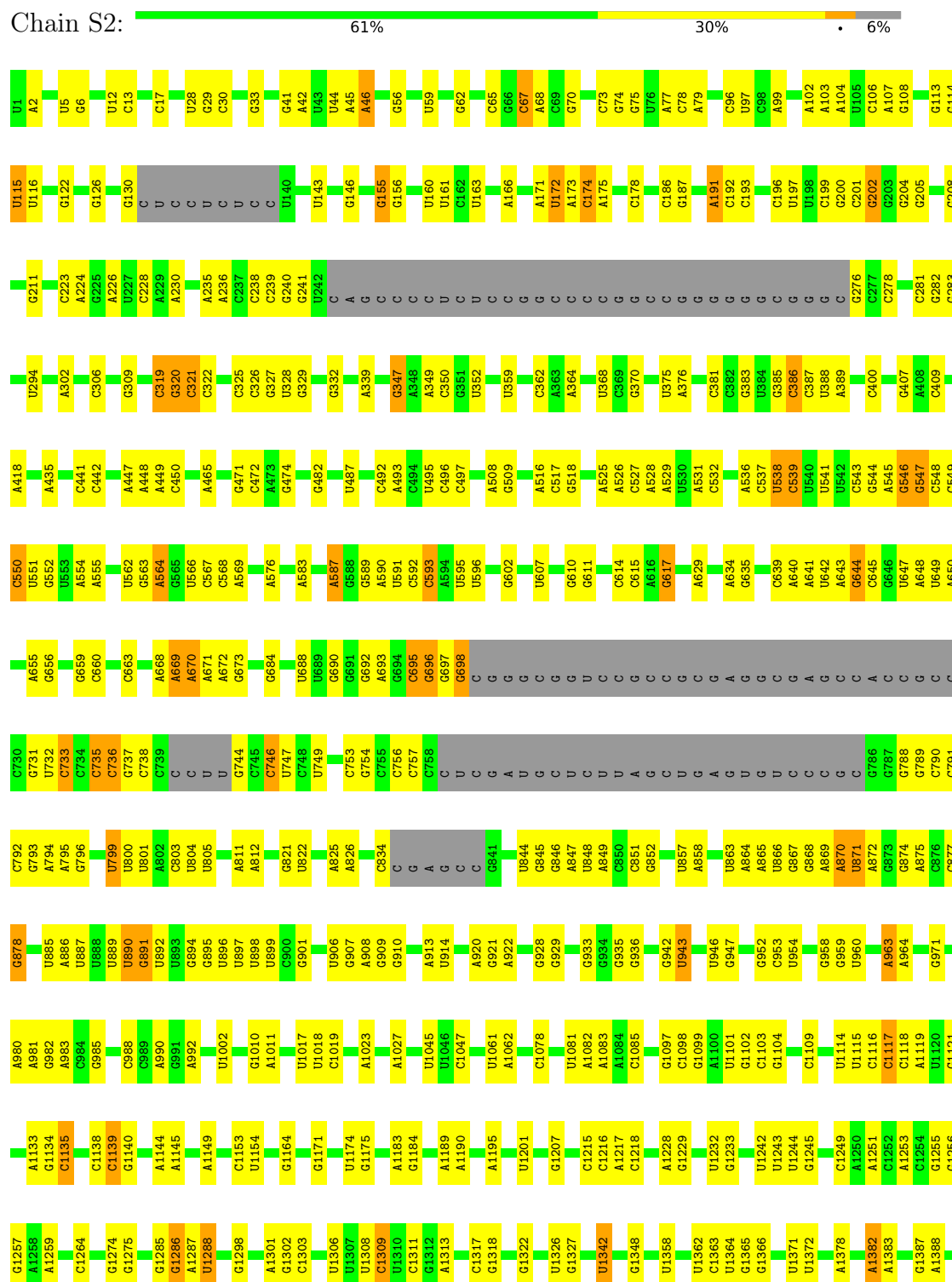
Chain Sg:  75% 22%

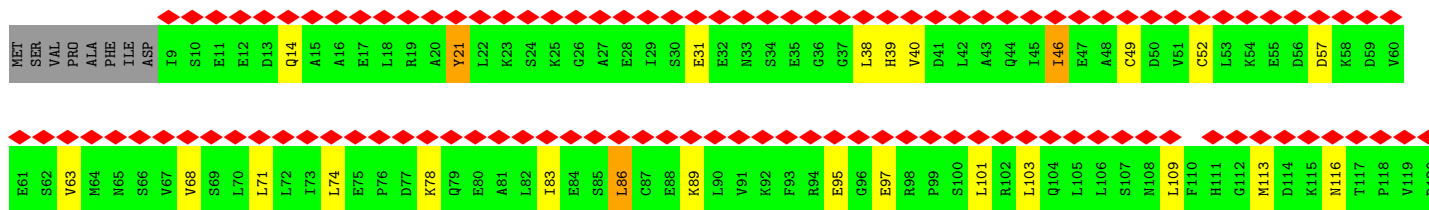


- Molecule 34: 60S ribosomal protein L41

Chain Ln:  88% 8%

- Molecule 35: 18S ribosomal RNA

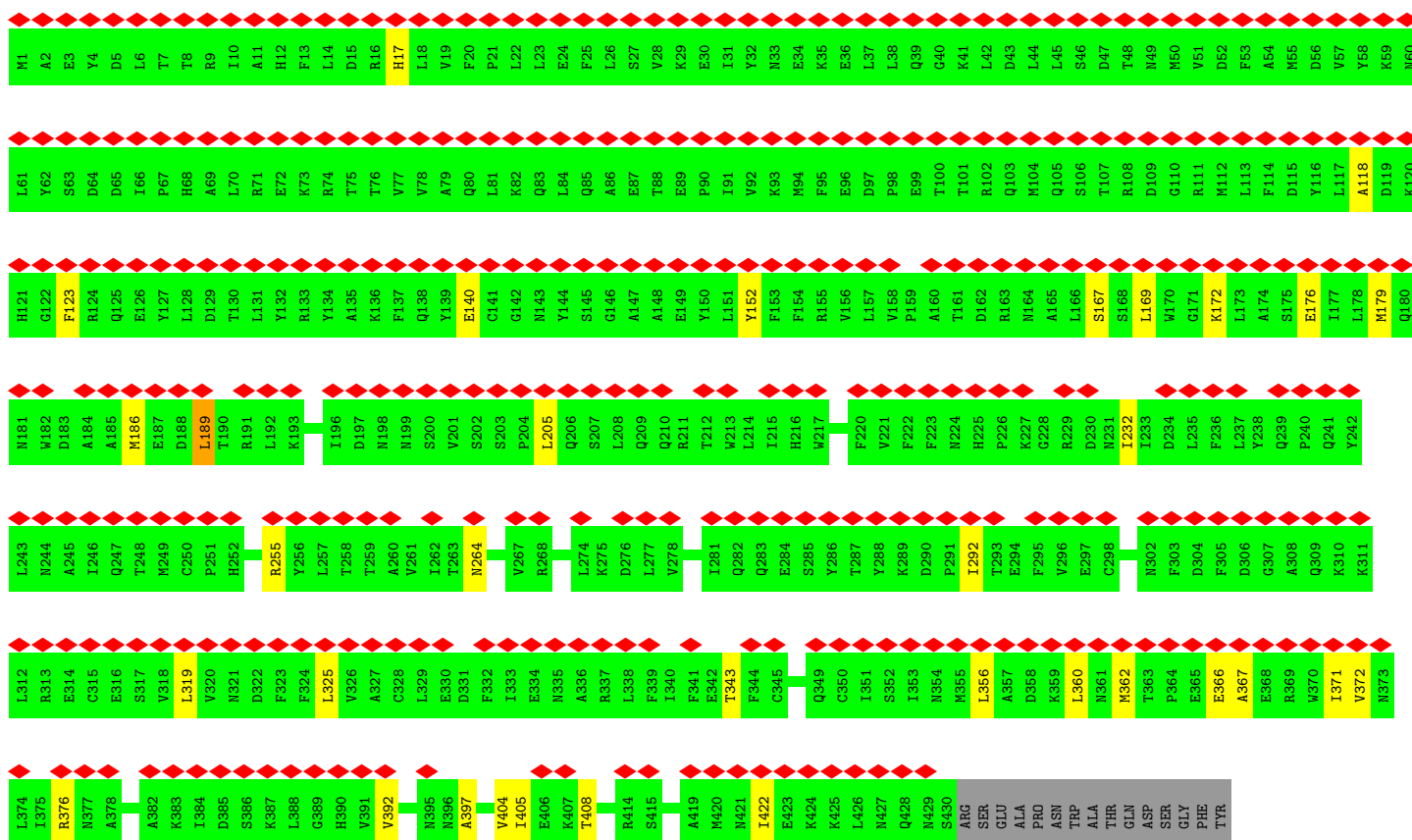
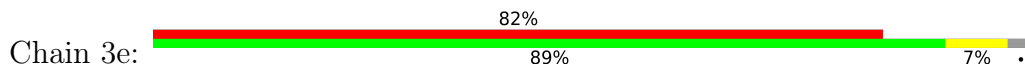




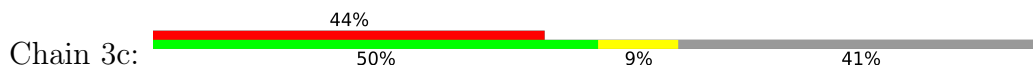


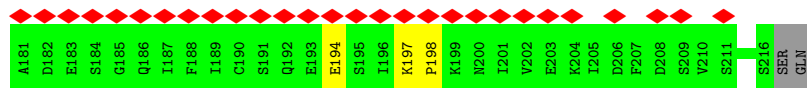
[illegible]

- Molecule 40: Eukaryotic translation initiation factor 3 subunit E

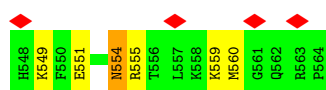
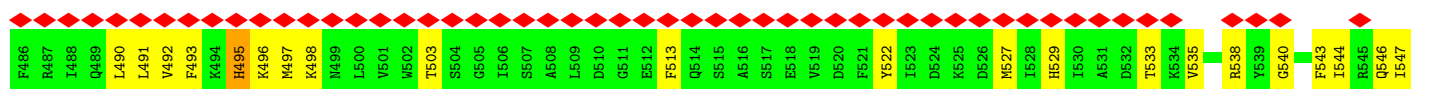
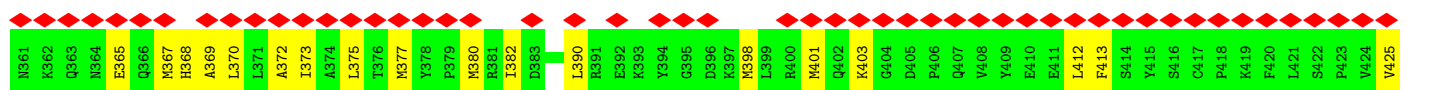
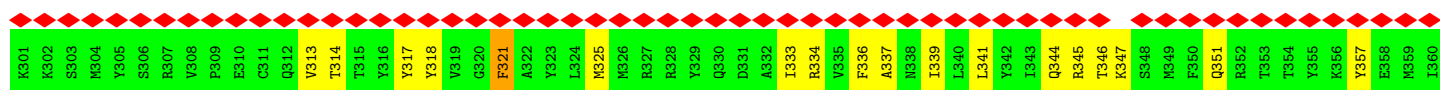
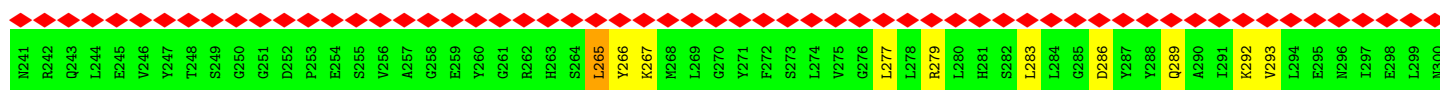
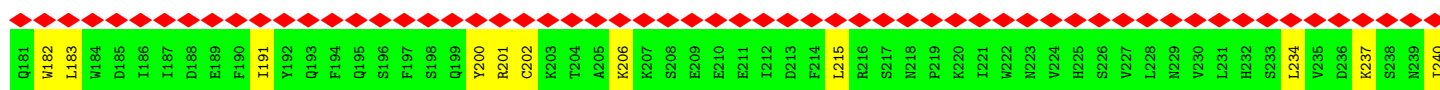
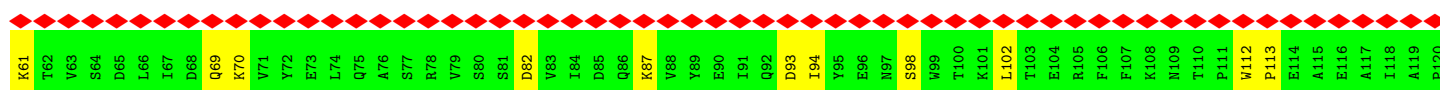
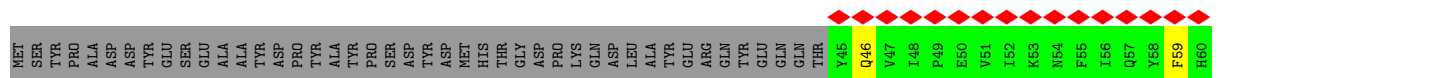
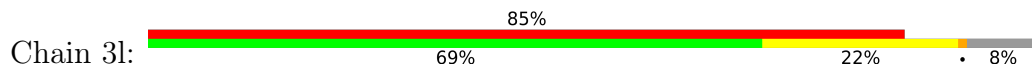


- Molecule 41: Eukaryotic translation initiation factor 3 subunit C

[illegible]



• Molecule 45: Eukaryotic translation initiation factor 3 subunit L



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24675	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (\AA)	636.0, 636.0, 636.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.272, 1.272, 1.272	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, MG

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	SA	0.22	0/1742	0.37	0/2367
2	SB	0.21	0/1749	0.43	0/2340
3	SC	0.23	0/1737	0.40	0/2347
4	SD	0.17	0/1784	0.34	0/2402
5	SE	0.23	0/2107	0.43	1/2836 (0.0%)
6	SF	0.23	0/1540	0.50	2/2071 (0.1%)
7	SG	0.17	0/1946	0.34	0/2590
8	SH	0.20	0/1529	0.43	0/2048
9	SI	0.20	0/1711	0.35	0/2282
10	SJ	0.22	0/1524	0.38	0/2035
11	SK	0.19	0/834	0.49	0/1125
12	SL	0.24	0/1241	0.38	0/1662
13	Sf	0.19	0/945	0.53	0/1269
14	SN	0.24	0/1226	0.45	0/1649
15	SO	0.22	0/1020	0.38	0/1368
16	SP	0.19	0/1003	0.49	0/1340
17	SQ	0.23	0/1133	0.51	0/1517
18	SR	0.21	0/1082	0.48	0/1452
19	SS	0.17	0/1202	0.41	0/1610
20	ST	0.18	0/1122	0.37	0/1504
21	SU	0.19	0/813	0.47	0/1092
22	SV	0.22	0/643	0.50	0/860
23	SW	0.25	0/1051	0.36	0/1406
24	SX	0.24	0/1116	0.44	0/1490
25	SY	0.20	0/1031	0.37	0/1370
26	SZ	0.22	0/607	0.52	0/815
27	Sa	0.23	0/817	0.35	0/1095
28	Sb	0.21	0/665	0.41	0/891
29	Sc	0.22	0/490	0.49	0/656
30	Sd	0.22	0/470	0.47	0/623
31	Se	0.21	0/422	0.42	0/555
32	sh	0.18	0/533	0.45	0/706

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sg	0.17	0/2493	0.40	0/3394
34	Ln	0.22	0/231	0.59	0/294
35	S2	0.22	0/42121	0.31	0/65651
36	zz	0.16	0/7199	0.33	0/11223
37	3m	0.12	0/2676	0.36	0/3635
38	3f	0.12	0/2099	0.35	0/2856
39	3a	0.14	0/4583	0.40	0/6237
40	3e	0.12	0/3288	0.33	0/4475
41	3c	0.14	0/3990	0.39	1/5424 (0.0%)
42	3h	0.13	0/2571	0.37	0/3484
43	3d	0.11	0/358	0.30	0/493
44	3k	0.13	0/1502	0.34	0/2052
45	3l	0.13	0/4446	0.35	0/6013
All	All	0.20	0/114392	0.36	4/164604 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	3c	424	ILE	N-CA-C	6.65	113.33	106.21
5	SE	19	MET	CB-CG-SD	-5.60	95.90	112.70
6	SF	78	MET	CA-C-N	5.37	130.47	122.74
6	SF	78	MET	C-N-CA	5.37	130.47	122.74

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	SA	1705	0	1706	23	0
2	SB	1722	0	1794	15	0
3	SC	1700	0	1784	24	0
4	SD	1756	0	1851	20	0
5	SE	2065	0	2169	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	SF	1518	0	1569	13	0
7	SG	1923	0	2089	21	0
8	SH	1506	0	1603	19	0
9	SI	1682	0	1769	16	0
10	SJ	1499	0	1618	7	0
11	SK	810	0	836	15	0
12	SL	1220	0	1289	9	0
13	Sf	935	0	964	18	0
14	SN	1202	0	1289	7	0
15	SO	1007	0	1032	13	0
16	SP	984	0	1033	10	0
17	SQ	1116	0	1185	17	0
18	SR	1068	0	1121	11	0
19	SS	1184	0	1244	14	0
20	ST	1103	0	1133	11	0
21	SU	803	0	873	9	0
22	SV	636	0	637	7	0
23	SW	1034	0	1080	6	0
24	SX	1098	0	1167	12	0
25	SY	1014	0	1082	11	0
26	SZ	601	0	662	9	0
27	Sa	803	0	850	4	0
28	Sb	651	0	672	6	0
29	Sc	488	0	514	9	0
30	Sd	459	0	452	7	0
31	Se	417	0	463	3	0
32	sh	522	0	530	9	0
33	Sg	2436	0	2393	45	0
34	Ln	230	0	276	2	0
35	S2	37669	0	19037	276	0
36	zz	6443	0	3259	82	0
37	3m	2639	0	2442	32	0
38	3f	2063	0	2054	28	0
39	3a	4497	0	4224	64	0
40	3e	3224	0	2925	18	0
41	3c	3924	0	3512	51	0
42	3h	2520	0	2445	46	0
43	3d	347	0	259	2	0
44	3k	1475	0	1239	10	0
45	3l	4335	0	4272	76	0
46	Sa	1	0	0	0	0
46	sh	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	S2	8	0	0	0	0
All	All	108043	0	86397	1035	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1035 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)
36:zz:61:U:H3	36:zz:107:G:H1	1.12	0.94
36:zz:145:G:H1	36:zz:248:U:H3	1.11	0.93
35:S2:172:U:H3	35:S2:174:C:H41	1.18	0.90
36:zz:52:G:N2	36:zz:111:C:O2	2.06	0.88
41:3c:573:ILE:HD13	41:3c:589:MET:HE3	1.60	0.82

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	SA	214/295 (72%)	207 (97%)	7 (3%)	0	100	100
2	SB	210/264 (80%)	204 (97%)	6 (3%)	0	100	100
3	SC	217/293 (74%)	209 (96%)	8 (4%)	0	100	100
4	SD	224/243 (92%)	222 (99%)	2 (1%)	0	100	100
5	SE	258/263 (98%)	243 (94%)	15 (6%)	0	100	100
6	SF	190/204 (93%)	181 (95%)	9 (5%)	0	100	100
7	SG	235/249 (94%)	230 (98%)	5 (2%)	0	100	100
8	SH	185/194 (95%)	175 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	SI	203/208 (98%)	195 (96%)	8 (4%)	0	100	100
10	SJ	178/194 (92%)	174 (98%)	4 (2%)	0	100	100
11	SK	94/165 (57%)	87 (93%)	7 (7%)	0	100	100
12	SL	148/158 (94%)	143 (97%)	5 (3%)	0	100	100
13	Sf	119/132 (90%)	114 (96%)	5 (4%)	0	100	100
14	SN	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
15	SO	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
16	SP	117/145 (81%)	115 (98%)	2 (2%)	0	100	100
17	SQ	138/146 (94%)	133 (96%)	5 (4%)	0	100	100
18	SR	130/135 (96%)	124 (95%)	6 (5%)	0	100	100
19	SS	141/152 (93%)	134 (95%)	7 (5%)	0	100	100
20	ST	140/145 (97%)	137 (98%)	3 (2%)	0	100	100
21	SU	99/119 (83%)	98 (99%)	1 (1%)	0	100	100
22	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
23	SW	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
24	SX	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
25	SY	122/133 (92%)	120 (98%)	2 (2%)	0	100	100
26	SZ	73/125 (58%)	69 (94%)	4 (6%)	0	100	100
27	Sa	98/115 (85%)	95 (97%)	3 (3%)	0	100	100
28	Sb	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
29	Sc	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
30	Sd	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
31	Se	50/59 (85%)	49 (98%)	1 (2%)	0	100	100
32	sh	62/156 (40%)	56 (90%)	6 (10%)	0	100	100
33	Sg	311/317 (98%)	296 (95%)	15 (5%)	0	100	100
34	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100	100
37	3m	361/374 (96%)	347 (96%)	14 (4%)	0	100	100
38	3f	267/357 (75%)	261 (98%)	6 (2%)	0	100	100
39	3a	590/1382 (43%)	567 (96%)	23 (4%)	0	100	100
40	3e	428/445 (96%)	419 (98%)	8 (2%)	1 (0%)	44	71
41	3c	537/913 (59%)	522 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	3h	316/352 (90%)	306 (97%)	10 (3%)	0	100	100
43	3d	53/548 (10%)	49 (92%)	4 (8%)	0	100	100
44	3k	213/218 (98%)	210 (99%)	3 (1%)	0	100	100
45	3l	518/564 (92%)	506 (98%)	12 (2%)	0	100	100
All	All	8082/10654 (76%)	7808 (97%)	273 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
40	3e	264	ASN

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	SA	180/243 (74%)	172 (96%)	8 (4%)	24	52
2	SB	193/231 (84%)	187 (97%)	6 (3%)	35	61
3	SC	185/225 (82%)	177 (96%)	8 (4%)	25	53
4	SD	189/202 (94%)	180 (95%)	9 (5%)	21	50
5	SE	223/225 (99%)	215 (96%)	8 (4%)	30	57
6	SF	162/170 (95%)	155 (96%)	7 (4%)	25	53
7	SG	207/218 (95%)	202 (98%)	5 (2%)	44	68
8	SH	167/174 (96%)	159 (95%)	8 (5%)	21	50
9	SI	178/180 (99%)	173 (97%)	5 (3%)	38	64
10	SJ	160/168 (95%)	151 (94%)	9 (6%)	17	45
11	SK	87/136 (64%)	79 (91%)	8 (9%)	7	26
12	SL	134/142 (94%)	127 (95%)	7 (5%)	19	47
13	Sf	102/108 (94%)	97 (95%)	5 (5%)	21	49
14	SN	130/131 (99%)	125 (96%)	5 (4%)	28	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	SO	104/119 (87%)	99 (95%)	5 (5%)	21	50
16	SP	107/130 (82%)	106 (99%)	1 (1%)	75	85
17	SQ	116/121 (96%)	109 (94%)	7 (6%)	16	42
18	SR	119/122 (98%)	110 (92%)	9 (8%)	11	34
19	SS	124/132 (94%)	110 (89%)	14 (11%)	4	18
20	ST	112/115 (97%)	106 (95%)	6 (5%)	18	46
21	SU	93/107 (87%)	89 (96%)	4 (4%)	25	53
22	SV	67/67 (100%)	65 (97%)	2 (3%)	36	62
23	SW	112/113 (99%)	109 (97%)	3 (3%)	40	65
24	SX	113/115 (98%)	104 (92%)	9 (8%)	10	32
25	SY	108/115 (94%)	104 (96%)	4 (4%)	29	56
26	SZ	67/103 (65%)	62 (92%)	5 (8%)	11	34
27	Sa	87/98 (89%)	84 (97%)	3 (3%)	32	59
28	Sb	75/76 (99%)	71 (95%)	4 (5%)	19	47
29	Sc	55/62 (89%)	53 (96%)	2 (4%)	30	57
30	Sd	48/49 (98%)	47 (98%)	1 (2%)	48	70
31	Se	42/48 (88%)	39 (93%)	3 (7%)	12	37
32	sh	57/140 (41%)	54 (95%)	3 (5%)	19	47
33	Sg	272/275 (99%)	256 (94%)	16 (6%)	16	43
34	Ln	23/24 (96%)	23 (100%)	0	100	100
37	3m	252/335 (75%)	237 (94%)	15 (6%)	16	42
38	3f	229/289 (79%)	221 (96%)	8 (4%)	31	58
39	3a	439/1259 (35%)	422 (96%)	17 (4%)	27	55
40	3e	302/406 (74%)	296 (98%)	6 (2%)	50	71
41	3c	347/811 (43%)	338 (97%)	9 (3%)	41	66
42	3h	272/310 (88%)	267 (98%)	5 (2%)	54	74
43	3d	20/494 (4%)	19 (95%)	1 (5%)	20	48
44	3k	121/193 (63%)	118 (98%)	3 (2%)	42	67
45	3l	475/515 (92%)	451 (95%)	24 (5%)	20	48
All	All	6655/9296 (72%)	6368 (96%)	287 (4%)	27	53

5 of 287 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	3a	341	LEU
45	3l	554	ASN
39	3a	535	GLU
44	3k	128	LEU
14	SN	118	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
31	Se	37	GLN
45	3l	229	ASN
39	3a	180	GLN
45	3l	225	HIS
45	3l	546	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	S2	1746/1869 (93%)	325 (18%)	6 (0%)
36	zz	301/332 (90%)	117 (38%)	0
All	All	2047/2201 (93%)	442 (21%)	6 (0%)

5 of 442 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	S2	2	A
35	S2	17	C
35	S2	33	G
35	S2	41	G
35	S2	42	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	S2	871	U
35	S2	1326	U
35	S2	1434	C
35	S2	517	C
35	S2	174	C

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 10 ligands modelled in this entry, 10 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.

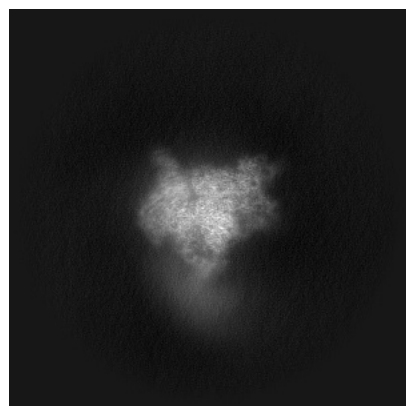
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62386. These allow visual inspection of the internal detail of the map and identification of artifacts.

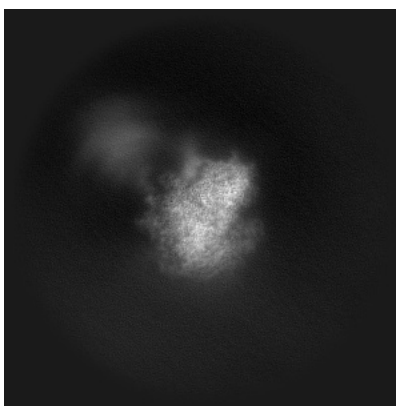
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

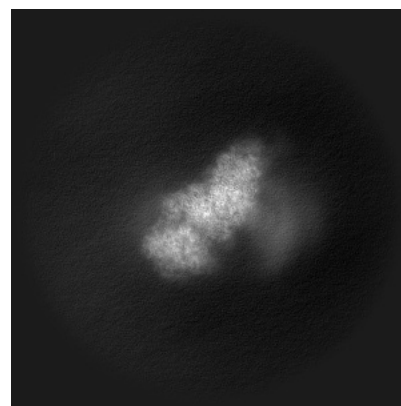
6.1.1 Primary map



X

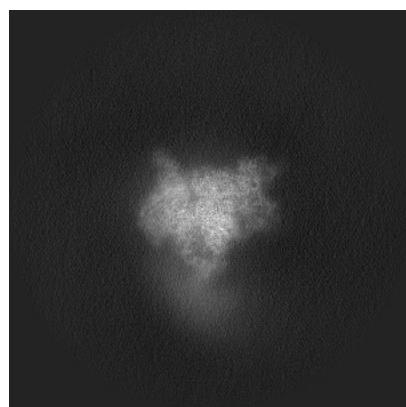


Y

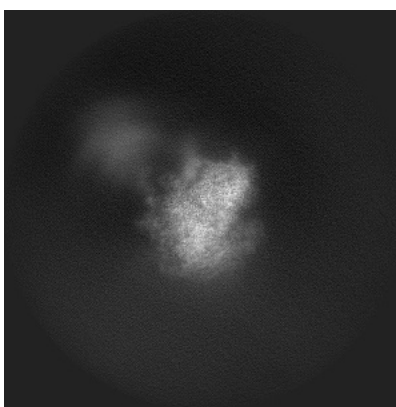


Z

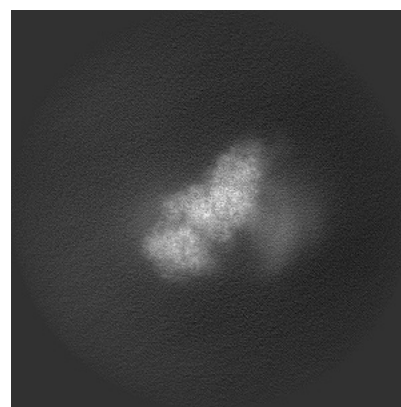
6.1.2 Raw map



X



Y

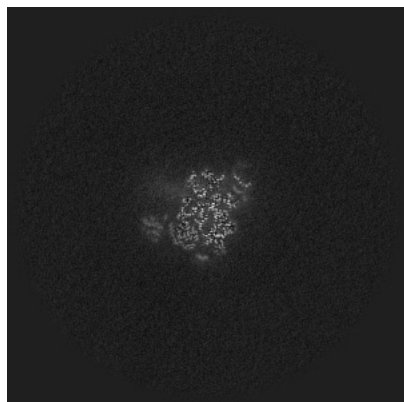


Z

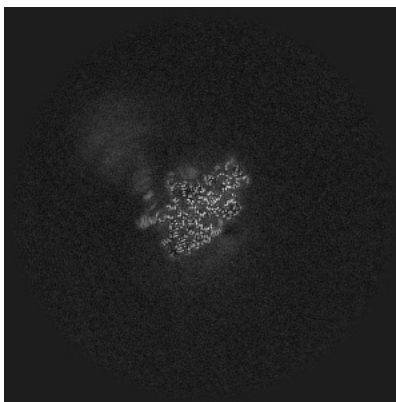
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

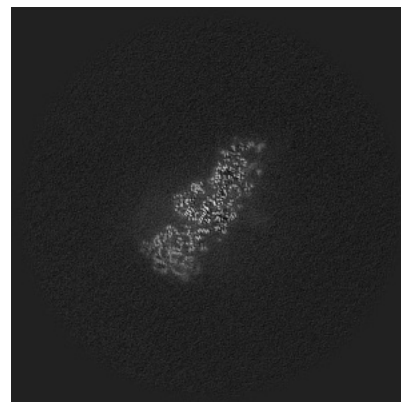
6.2.1 Primary map



X Index: 250

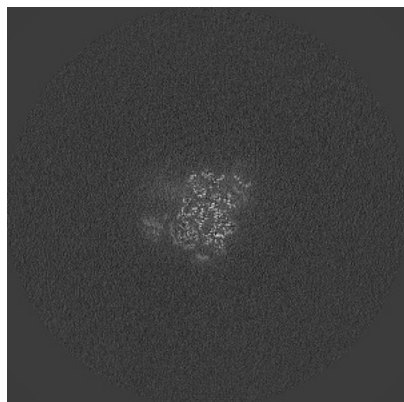


Y Index: 250

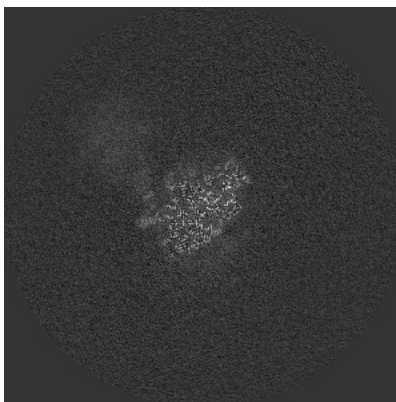


Z Index: 250

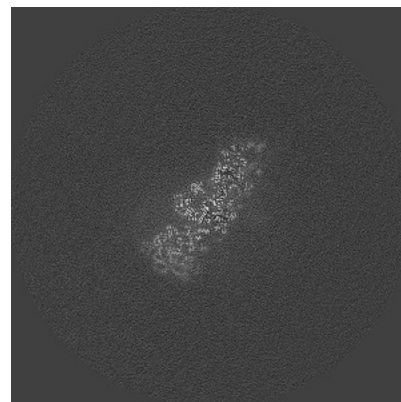
6.2.2 Raw map



X Index: 250



Y Index: 250

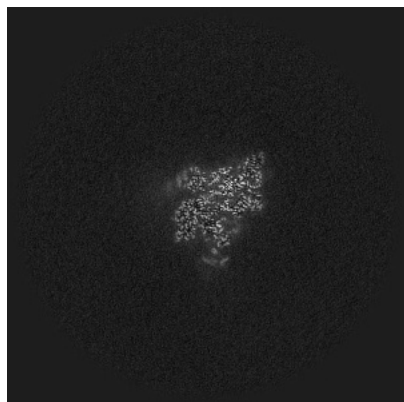


Z Index: 250

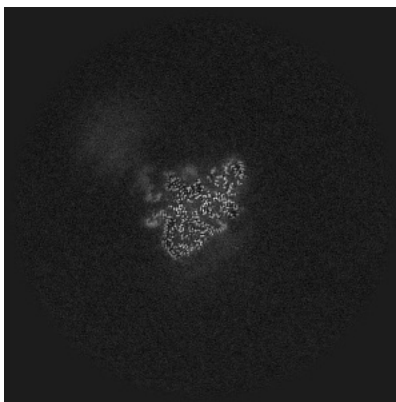
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

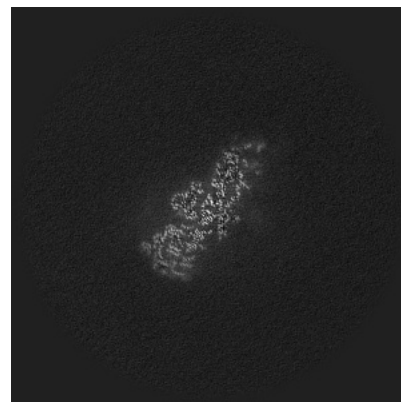
6.3.1 Primary map



X Index: 267

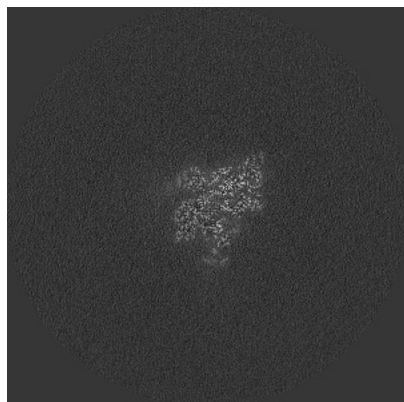


Y Index: 255

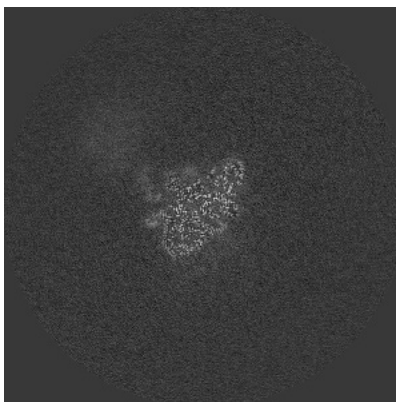


Z Index: 248

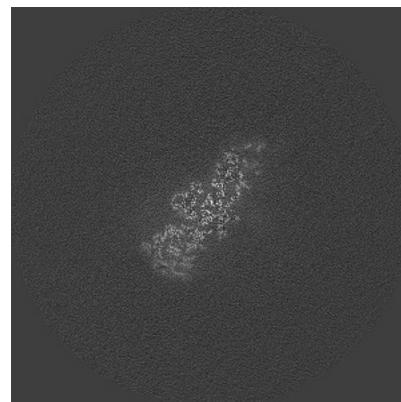
6.3.2 Raw map



X Index: 267



Y Index: 255

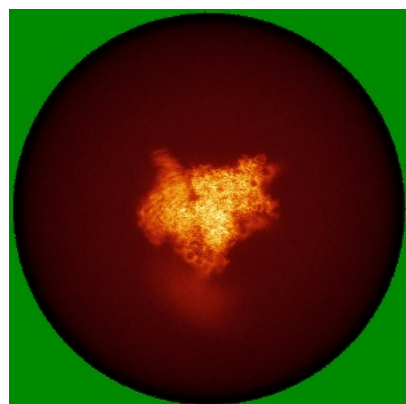


Z Index: 248

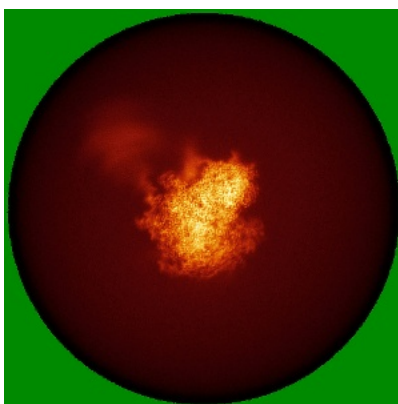
The images above show the largest variance slices of the map in three orthogonal directions.

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

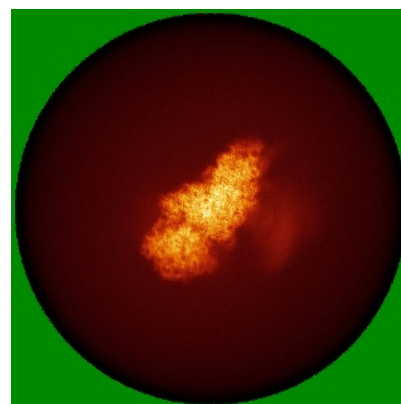
6.4.1 Primary map



X

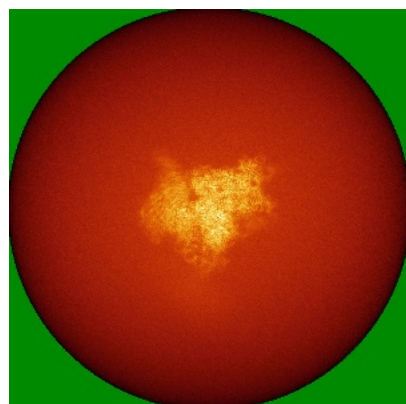


Y

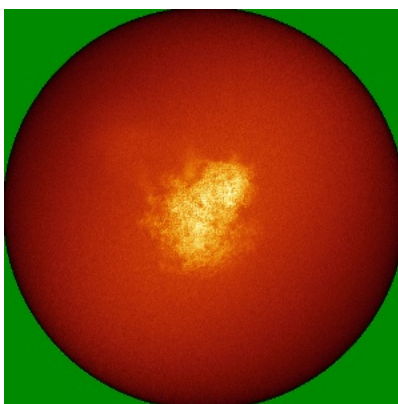


Z

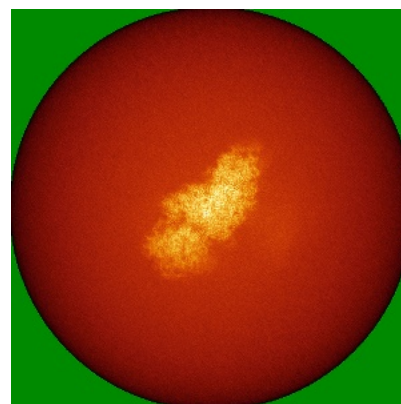
6.4.2 Raw map



X



Y

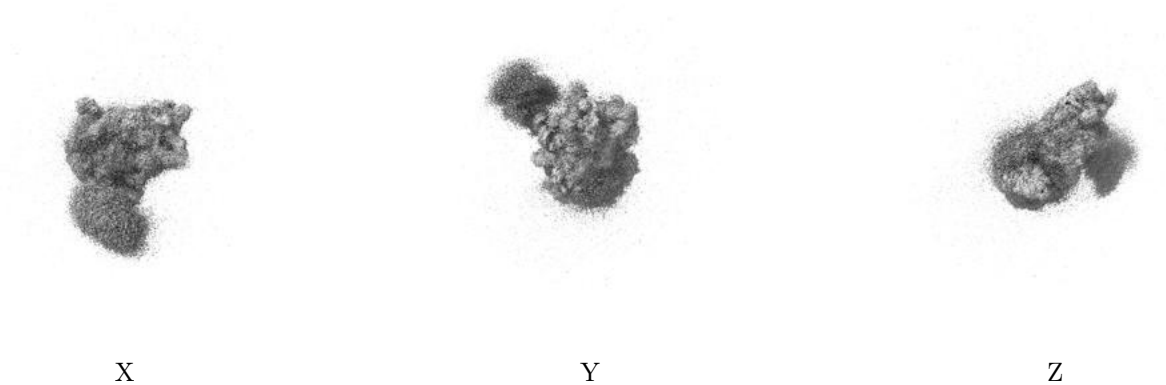


Z

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.

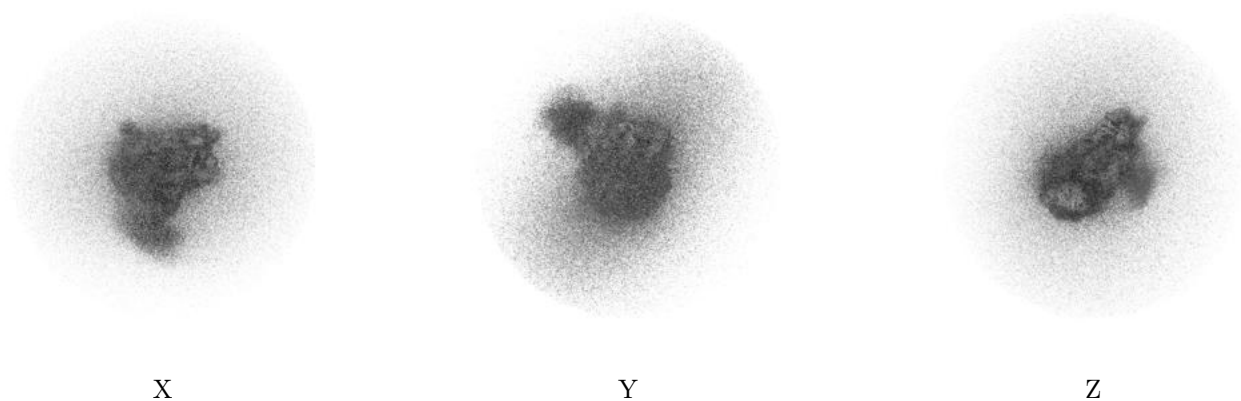
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

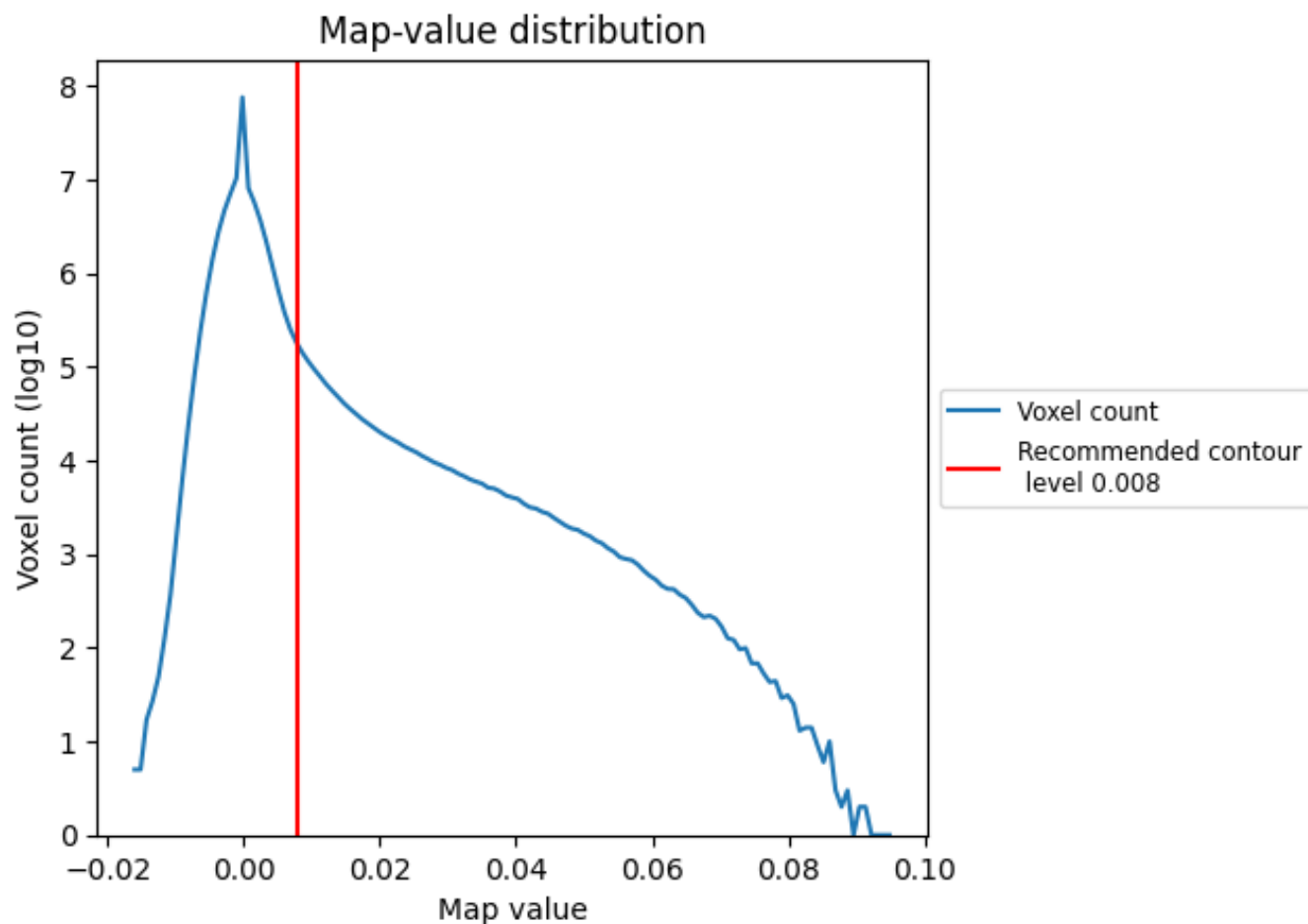
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

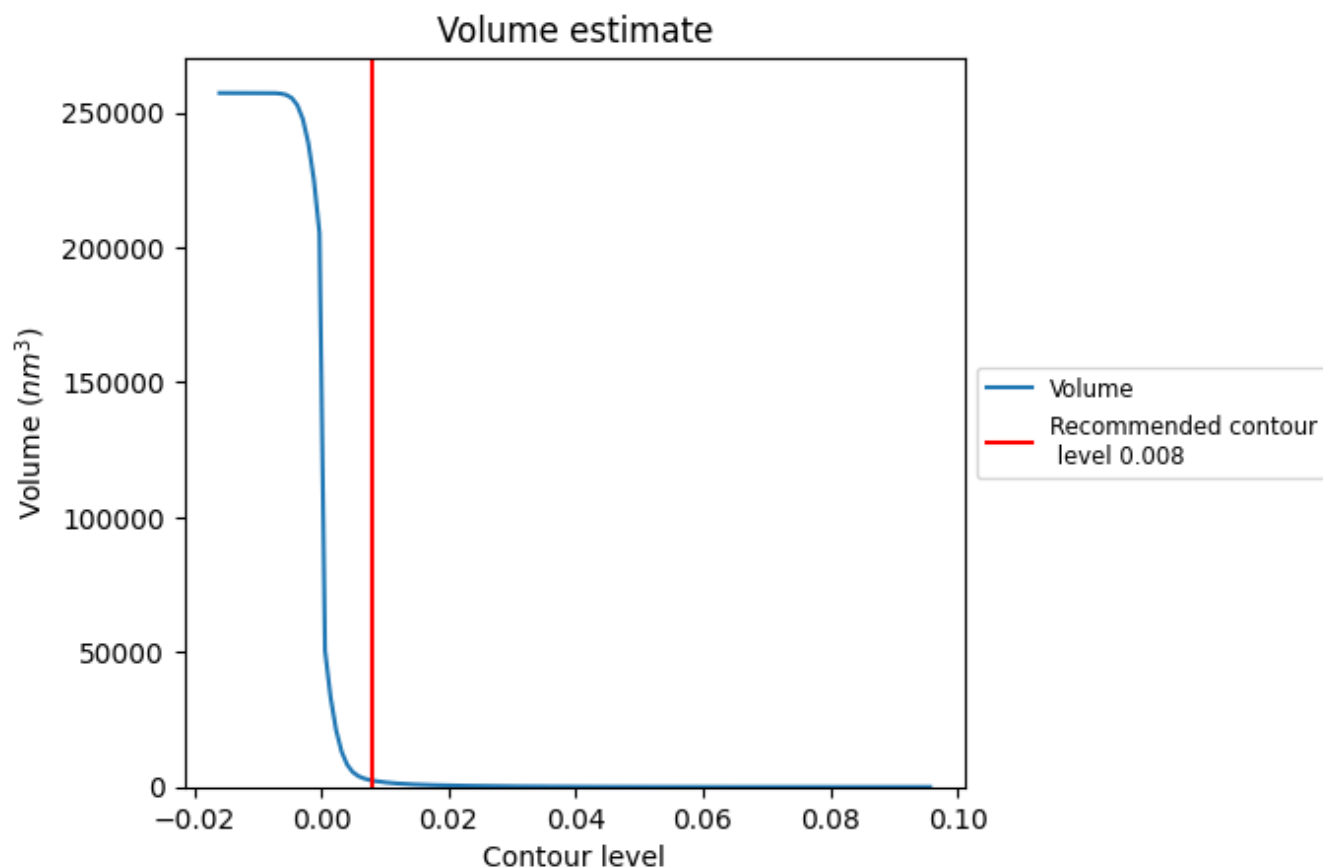
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

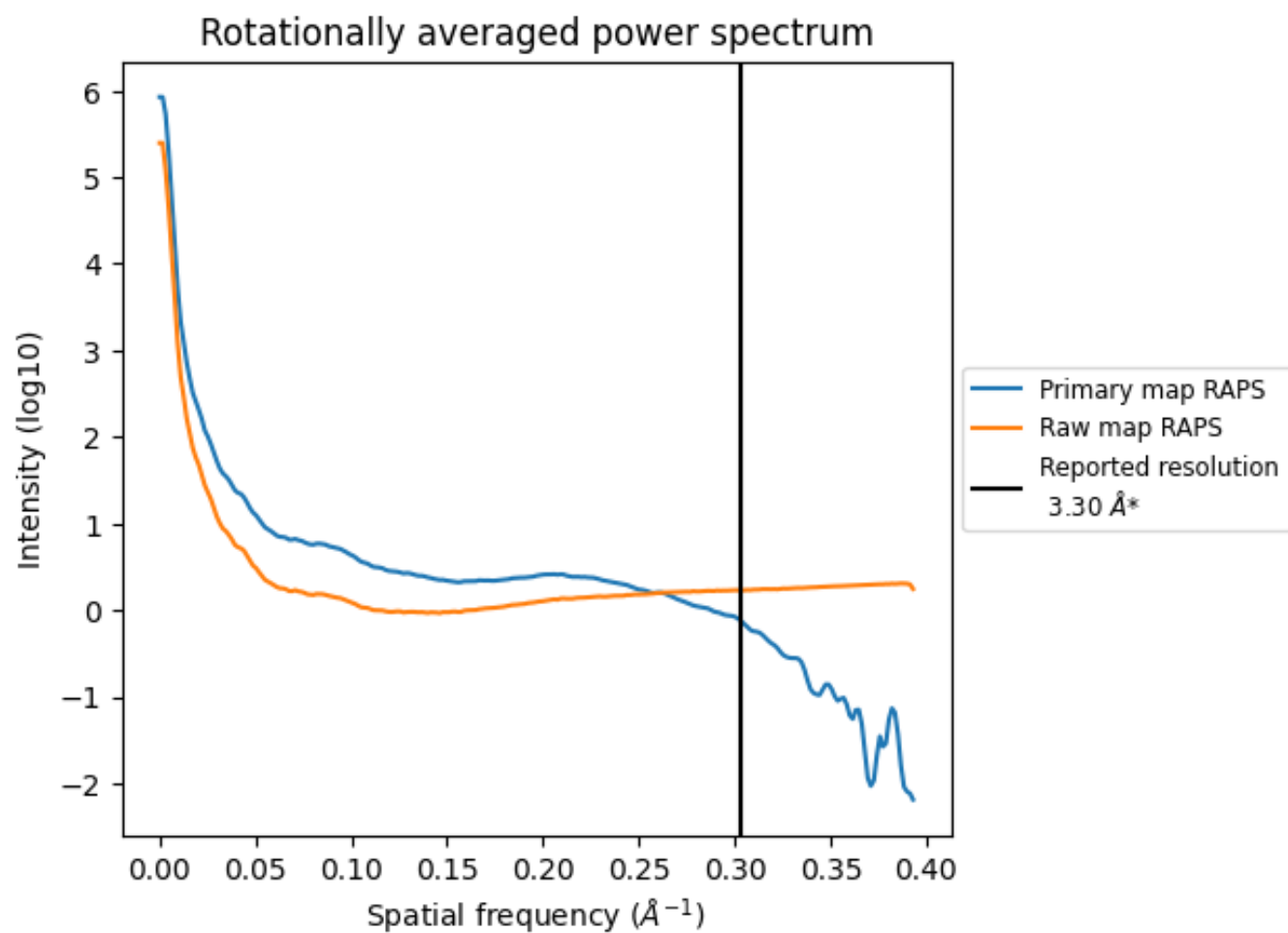
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2406 nm^3 ; this corresponds to an approximate mass of 2173 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 ⓘ

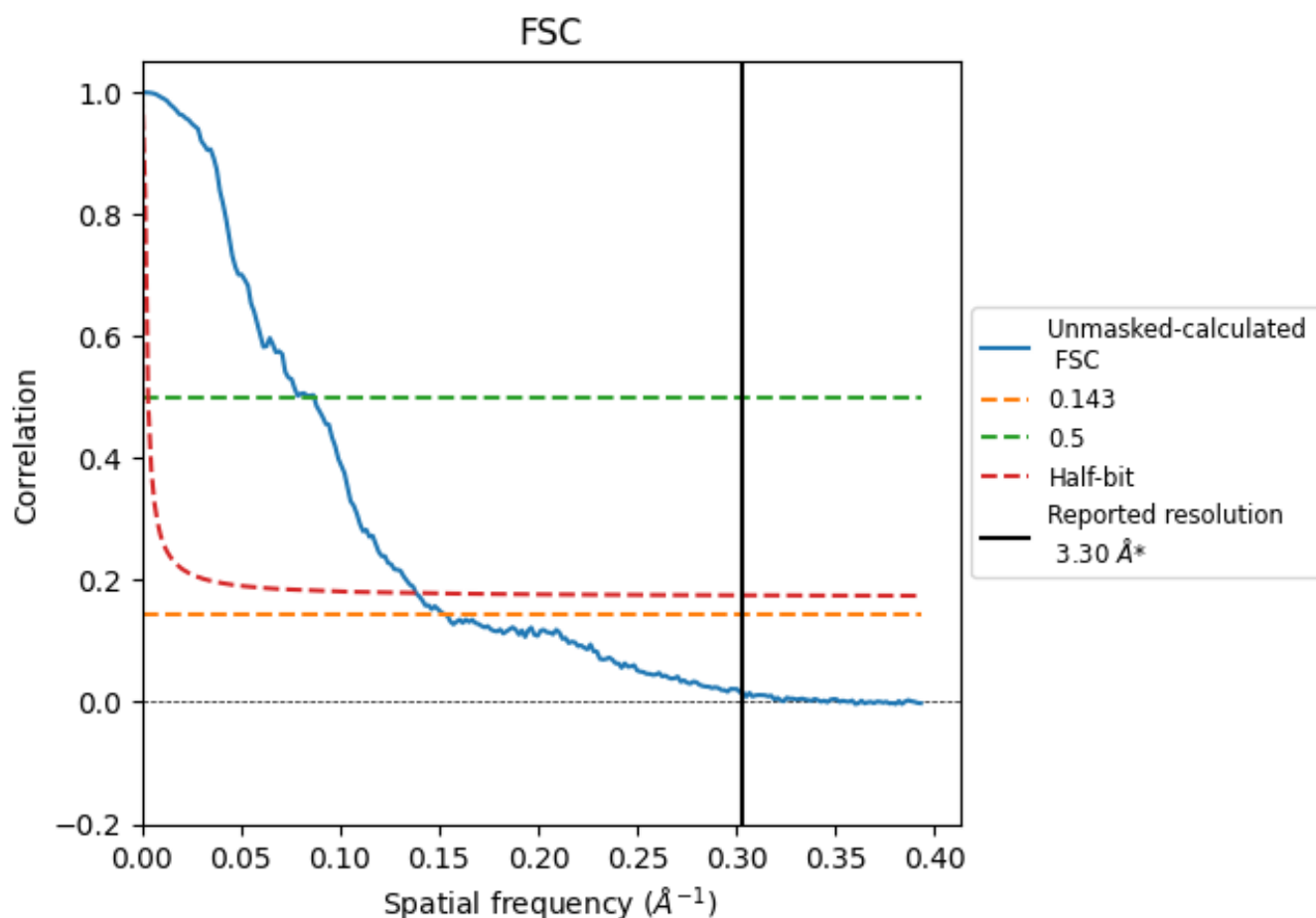


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

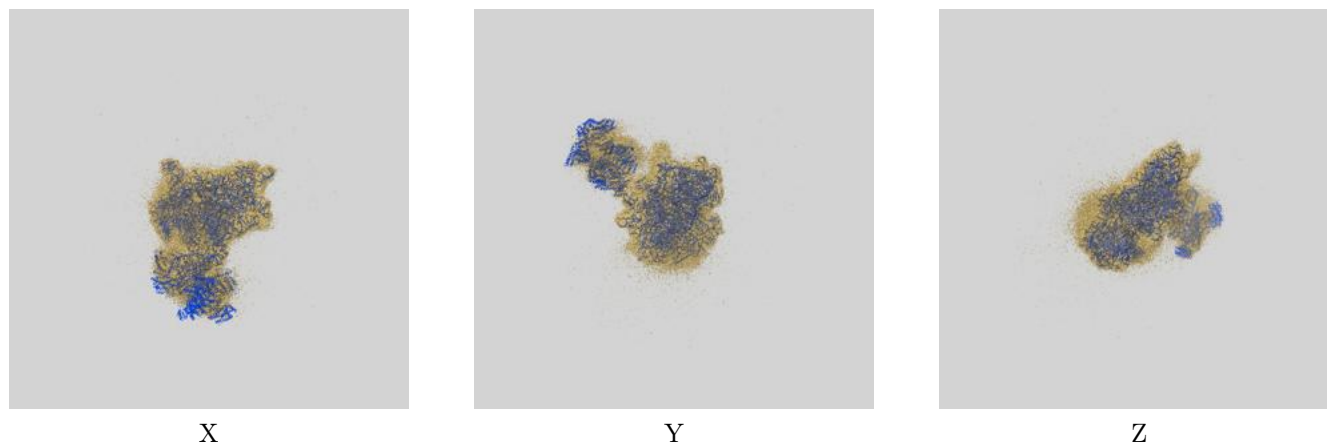
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.53	11.53	7.23

*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 6.53 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

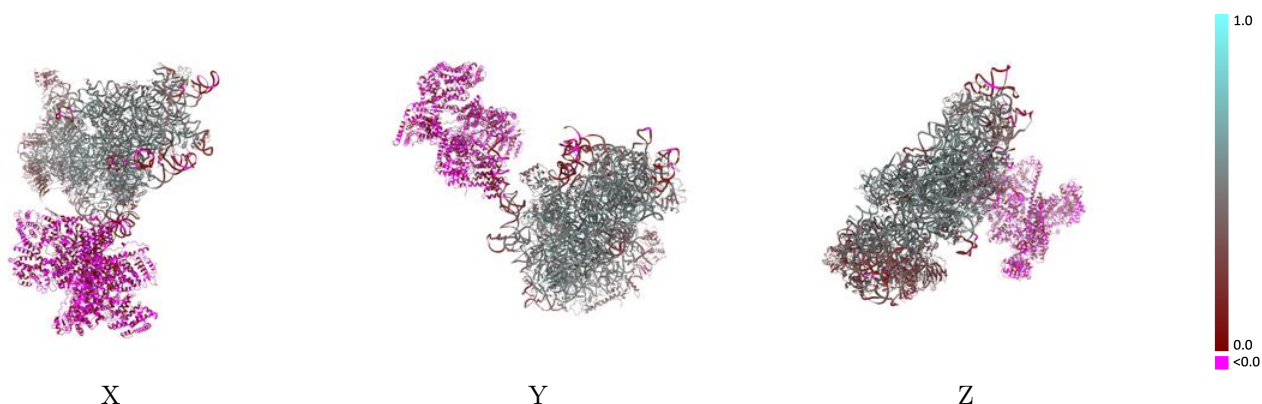
This section contains information regarding the fit between EMDB map EMD-62386 and PDB model 9KKF. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



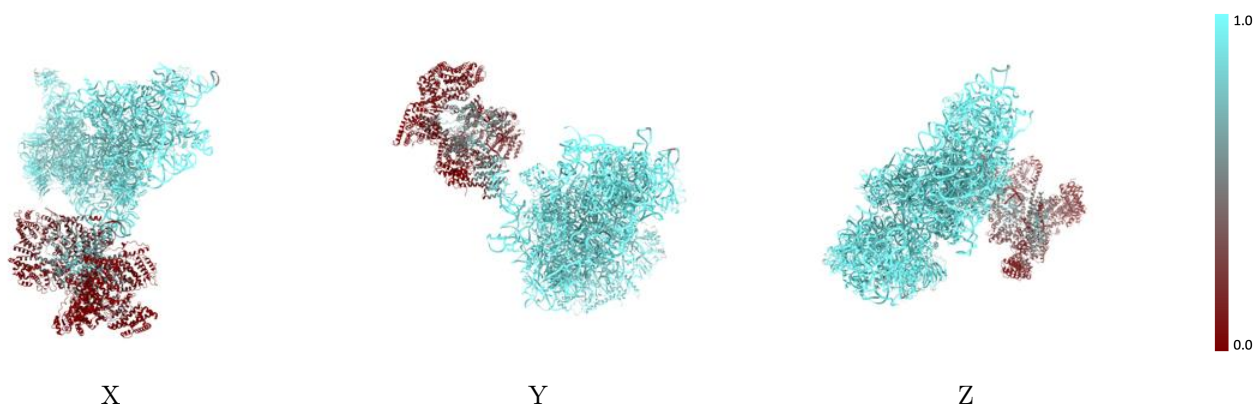
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



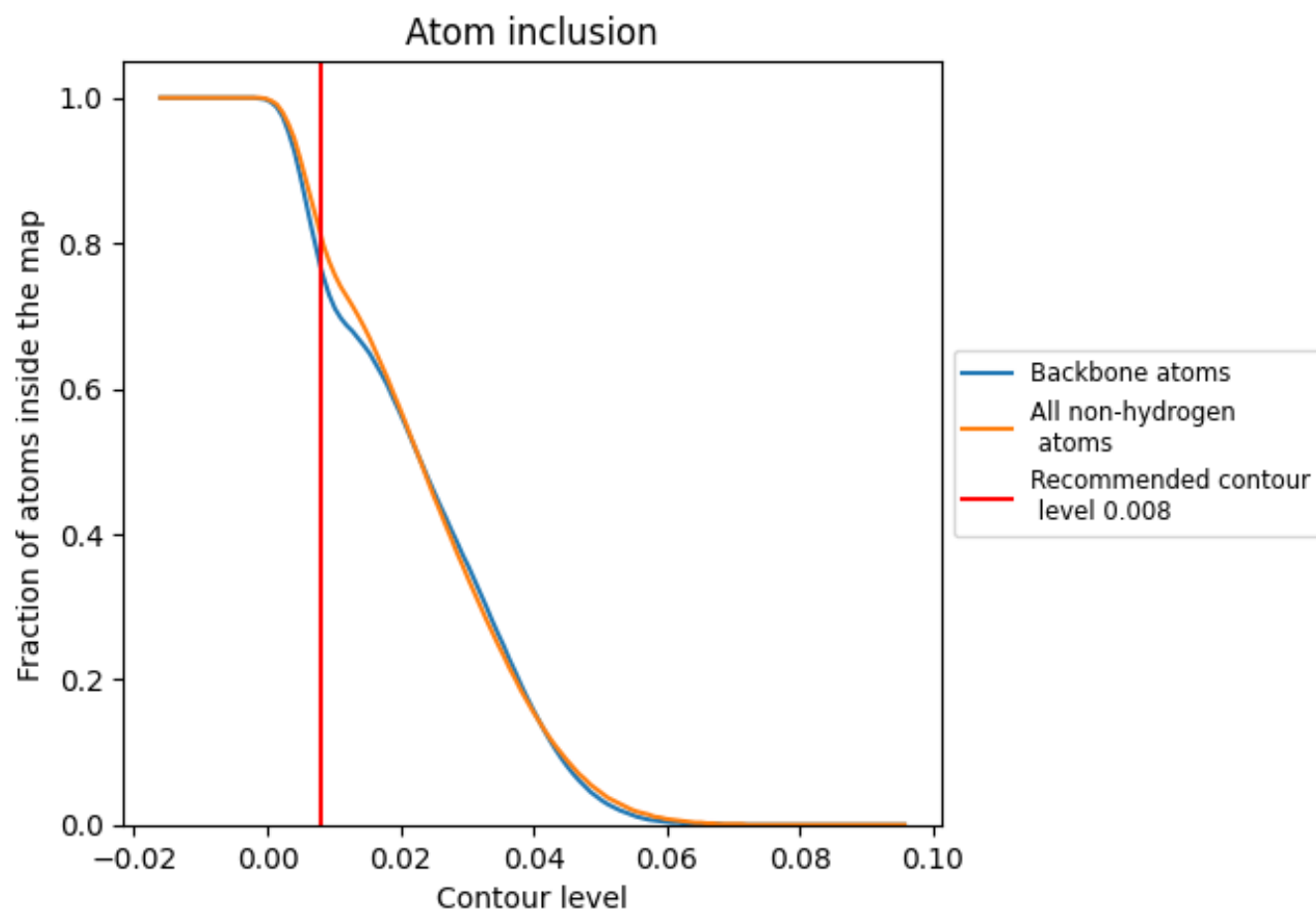
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 81% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8110	 0.3360
3a	 0.3820	 0.0180
3c	 0.2760	 -0.0020
3d	 0.2020	 0.0300
3e	 0.1760	 0.0030
3f	 0.3100	 0.0060
3h	 0.4350	 0.0140
3k	 0.0380	 -0.0160
3l	 0.0860	 -0.0050
3m	 0.0720	 -0.0110
Ln	 1.0000	 0.5090
S2	 0.9960	 0.4550
SA	 0.9950	 0.5030
SB	 0.9880	 0.5000
SC	 0.9960	 0.5170
SD	 0.9940	 0.4090
SE	 0.9950	 0.4970
SF	 0.9960	 0.4770
SG	 0.9790	 0.4050
SH	 0.9870	 0.4450
SI	 0.9880	 0.4930
SJ	 0.9950	 0.5060
SK	 0.9920	 0.3470
SL	 0.9940	 0.5010
SN	 0.9950	 0.4950
SO	 0.9960	 0.5260
SP	 0.9780	 0.3210
SQ	 0.9950	 0.4310
SR	 0.9830	 0.4480
SS	 0.9750	 0.3650
ST	 0.9910	 0.3840
SU	 0.9940	 0.3800
SV	 0.9890	 0.5010
SW	 1.0000	 0.5040
SX	 0.9980	 0.5080



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Chain	Atom inclusion	Q-score
SY	 0.9880	 0.4480
SZ	 0.9980	 0.4390
Sa	 1.0000	 0.5340
Sb	 0.9950	 0.5070
Sc	 1.0000	 0.5000
Sd	 0.9980	 0.4190
Se	 0.9950	 0.4710
Sf	 0.8830	 0.2190
Sg	 0.9770	 0.3200
sh	 0.9060	 0.2140
zz	 0.9130	 0.2920