



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 10:25 PM UTC

PDB ID : 6R7H / pdb_00006r7h
EMDB ID : EMD-4741
Title : Structural basis of Cullin-2 RING E3 ligase regulation by the COP9 signalosome
Authors : Faull, S.V.; Lau, A.M.C.; Beuron, F.; Cronin, N.B.; Morris, E.P.; Politis, A.
Deposited on : 2019-03-28
Resolution : 8.80 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:

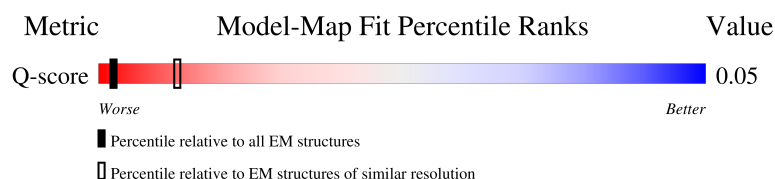
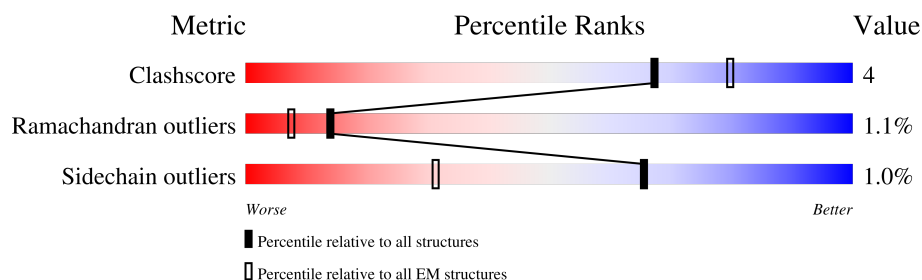
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 8.80 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.



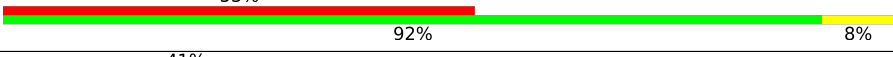
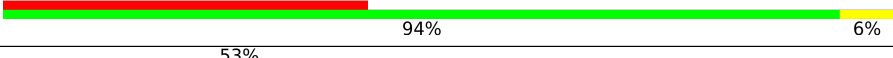
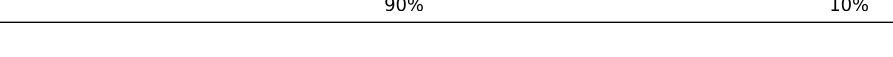
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	265 (8.30 - 9.30)

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	433	
2	Q	112	
3	O	654	
4	R	90	

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Mol	Chain	Length	Quality of chain
5	B	414	
6	C	403	
7	D	406	
8	E	311	
9	F	288	
10	G	208	
11	H	199	
12	P	104	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 28843 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 COP9 signalosome complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	433	Total	C	N	O	S	0	0
			3450	2174	605	649	22		

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	112	Total	C	N	O	S	0	0
			873	553	139	173	8		

- Molecule 3 is a protein called Cullin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	O	654	Total	C	N	O	S	0	0
			5364	3419	899	1006	40		

- Molecule 4 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	90	Total	C	N	O	S	0	0
			746	472	137	128	9		

- Molecule 5 is a protein called COP9 signalosome complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	414	Total	C	N	O	S	0	0
			3386	2149	579	643	15		

- Molecule 6 is a protein called COP9 signalosome complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	403	Total	C	N	O	S	0	0
			3205	2040	537	601	27		

- Molecule 7 is a protein called COP9 signalosome complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	406	Total	C	N	O	S	0	0
			3251	2047	566	622	16		

- Molecule 8 is a protein called COP9 signalosome complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	311	Total	C	N	O	S	0	0
			2472	1575	412	471	14		

- Molecule 9 is a protein called COP9 signalosome complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	288	Total	C	N	O	S	0	0
			2280	1452	379	434	15		

- Molecule 10 is a protein called COP9 signalosome complex subunit 7b.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	208	Total	C	N	O	S	0	0
			1645	1039	279	321	6		

- Molecule 11 is a protein called COP9 signalosome complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	169	Total	C	N	O	S	0	0
			1349	864	234	247	4		

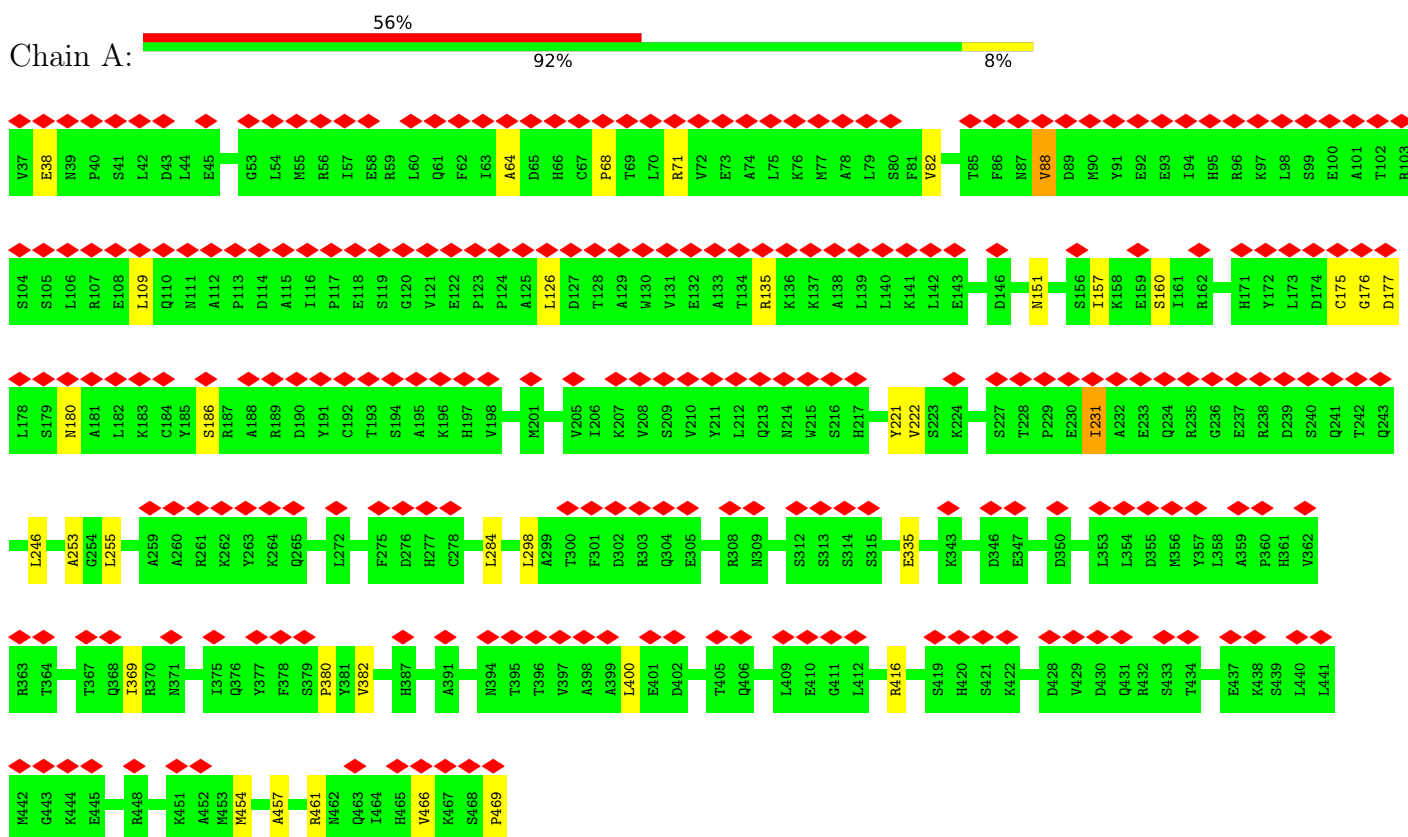
- Molecule 12 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	104	Total	C	N	O	S	0	0
			822	520	138	159	5		

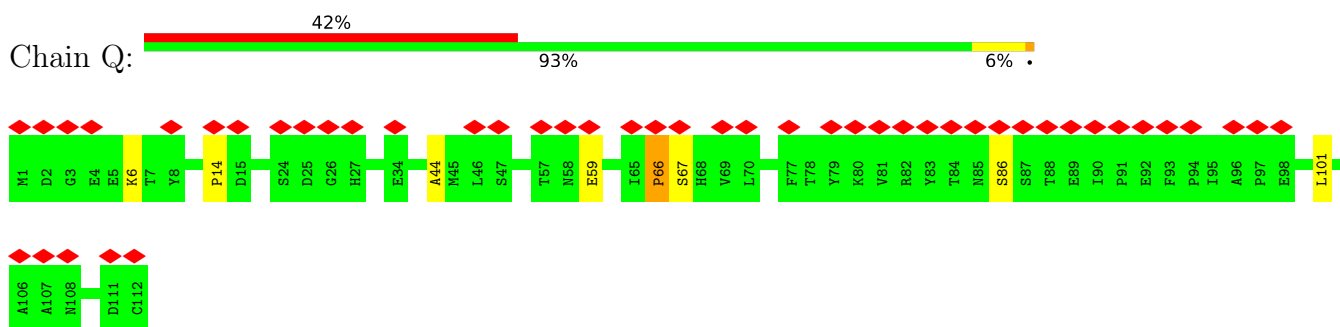
3 Residue-property plots

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.

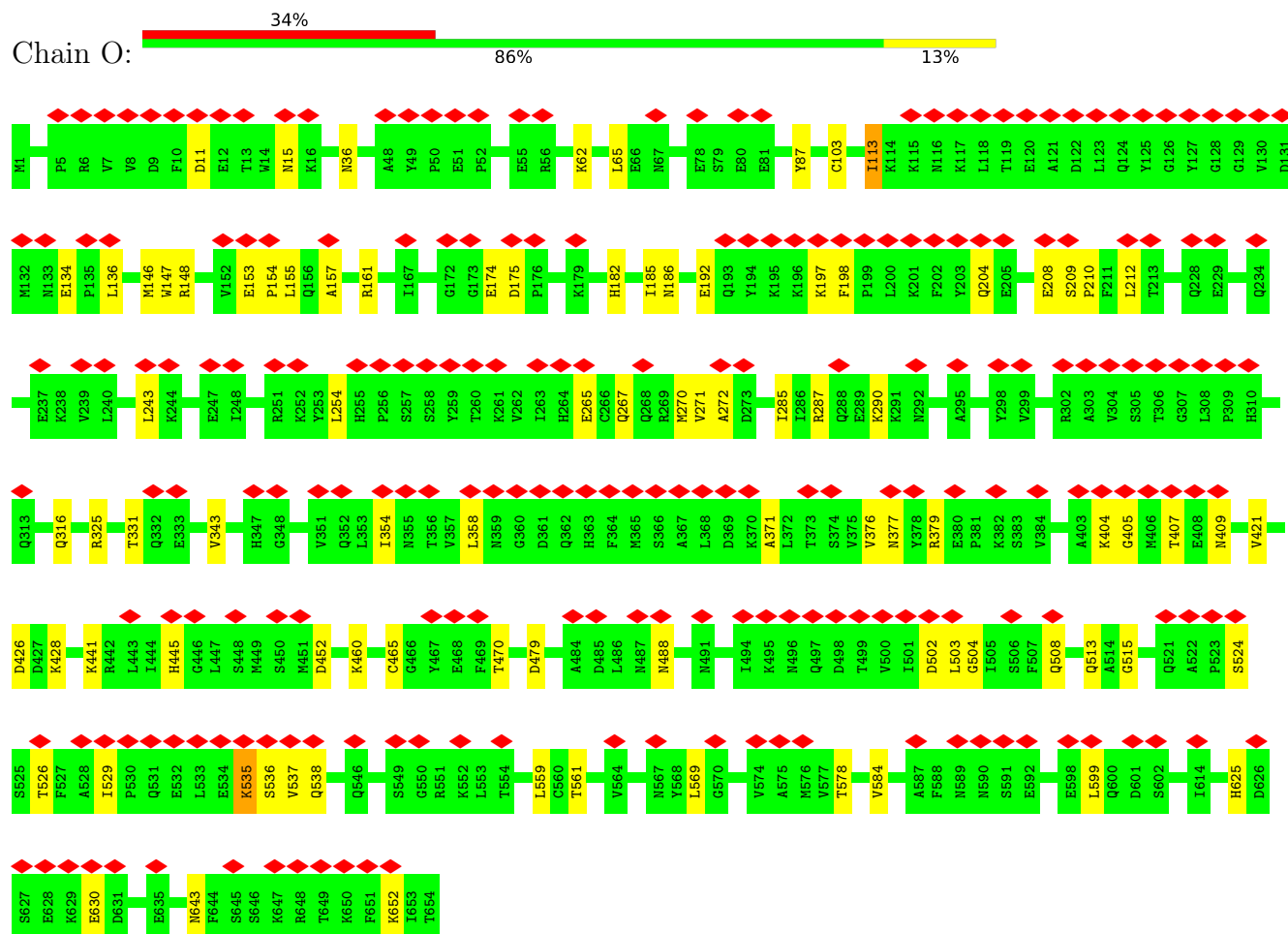
• Molecule 1: COP9 signalosome complex subunit 1



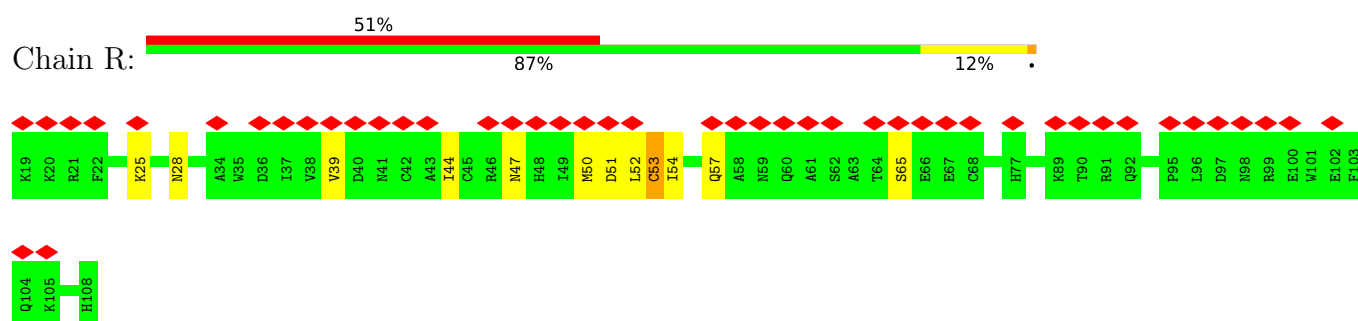
• Molecule 2: Elongin-C



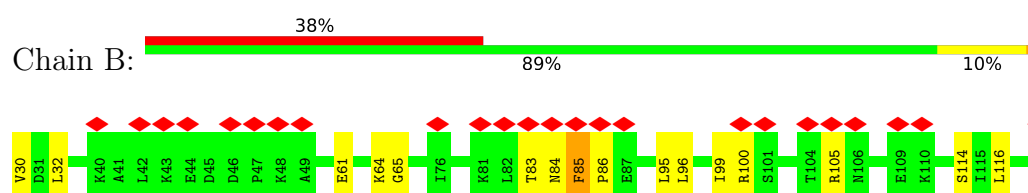
- Molecule 3: Cullin-2

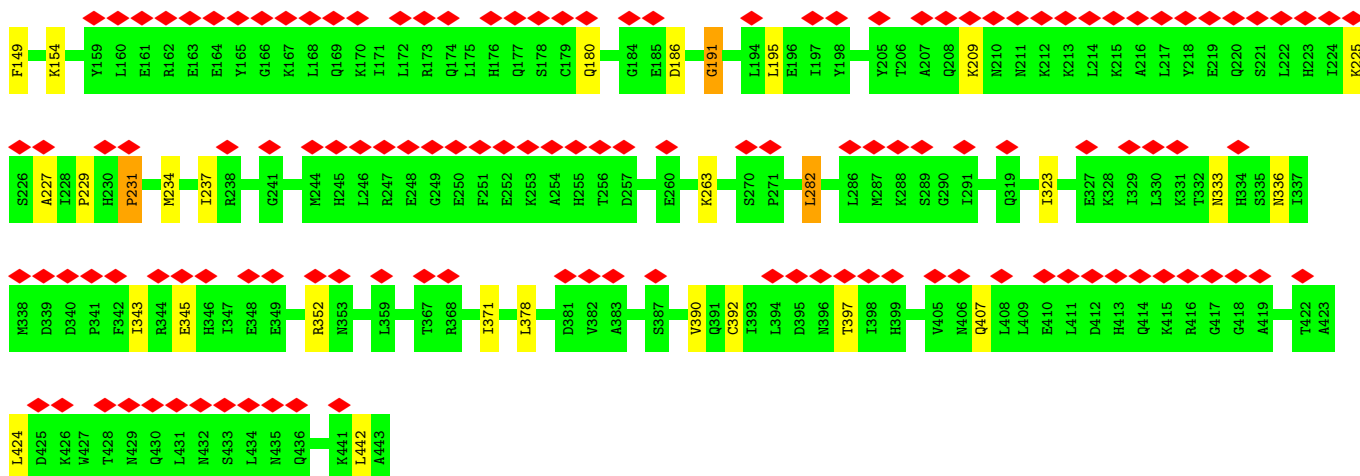


- Molecule 4: E3 ubiquitin-protein ligase RBX1

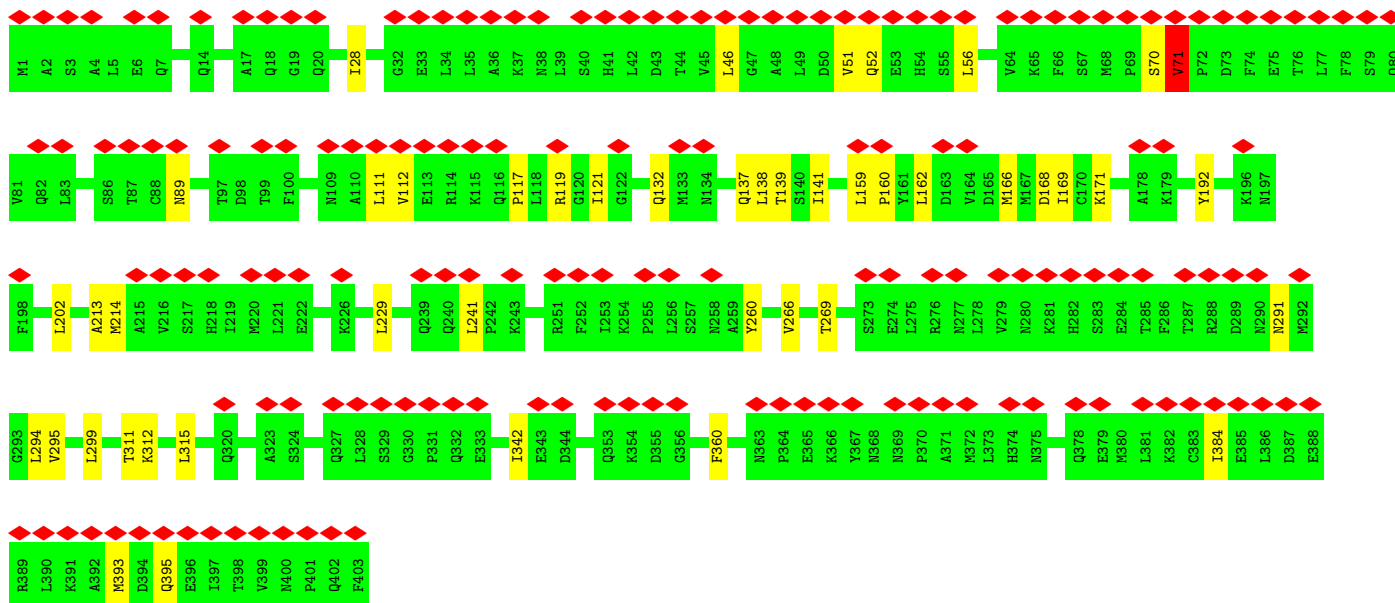
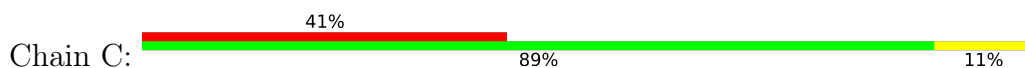


- Molecule 5: COP9 signalosome complex subunit 2

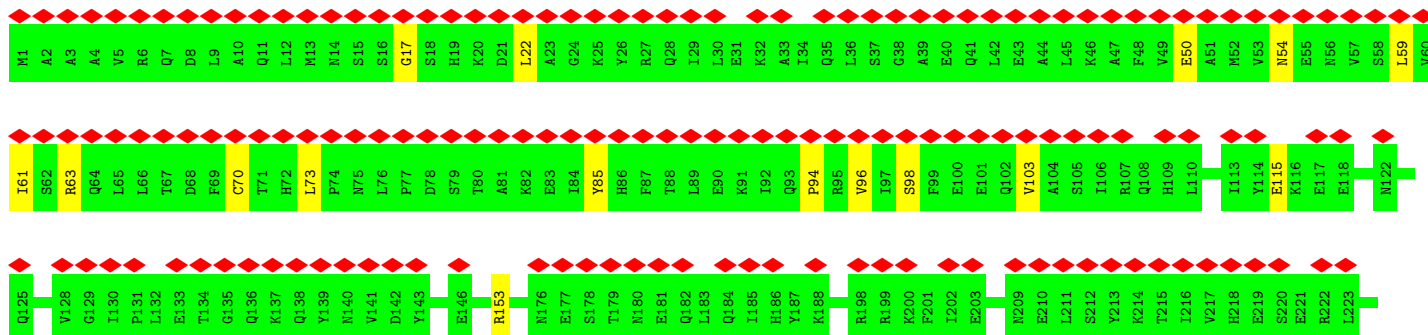
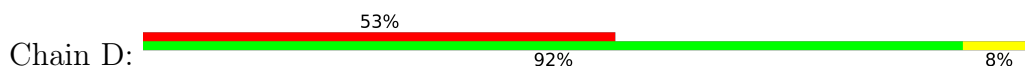


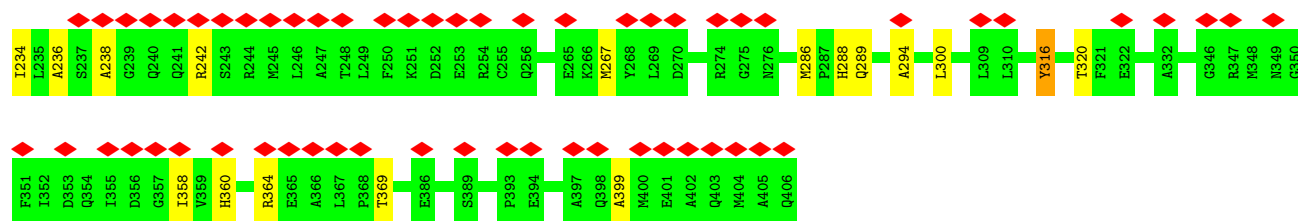


• Molecule 6: COP9 signalosome complex subunit 3

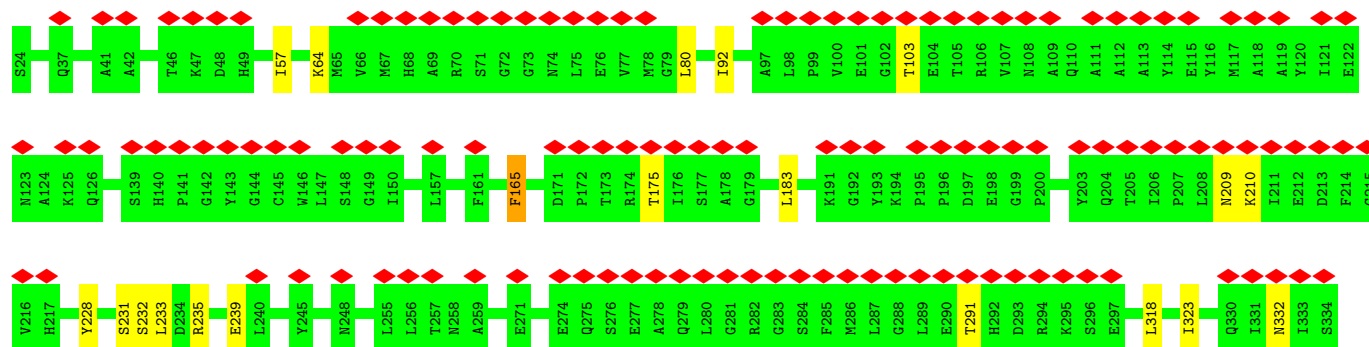
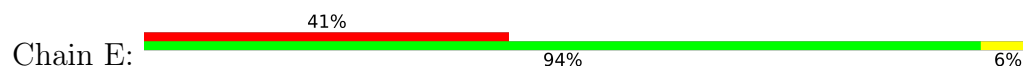


• Molecule 7: COP9 signalosome complex subunit 4

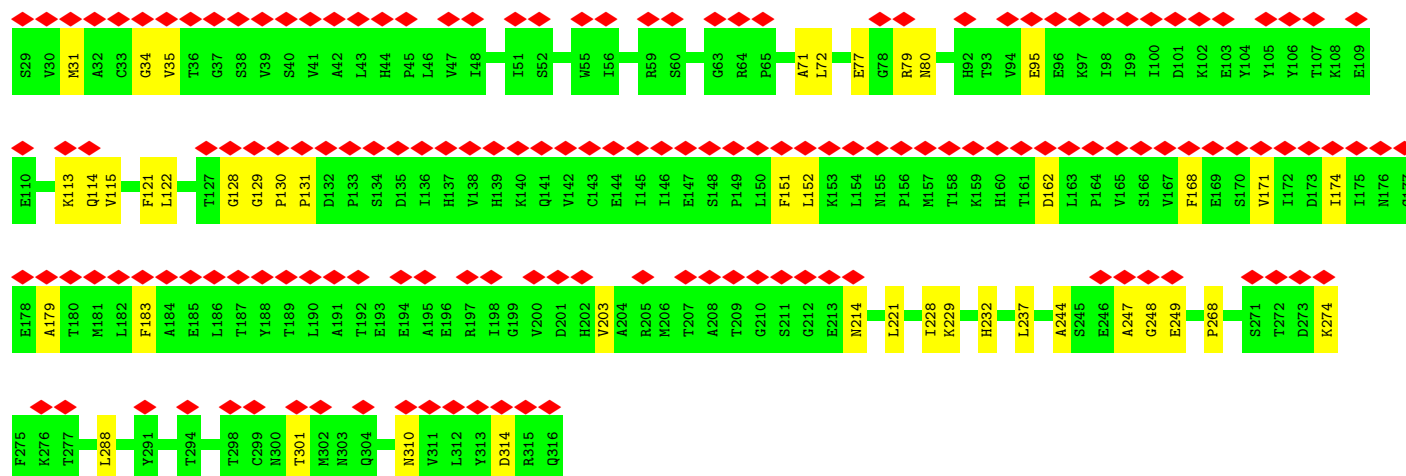
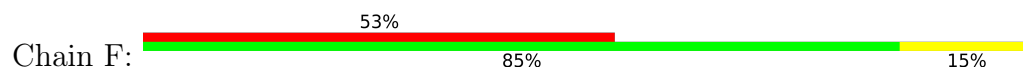




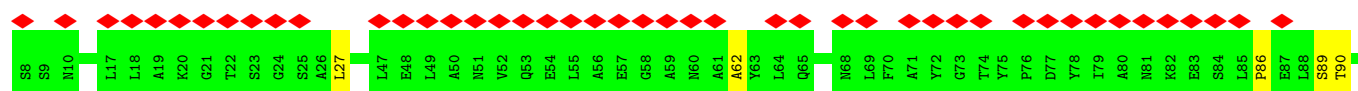
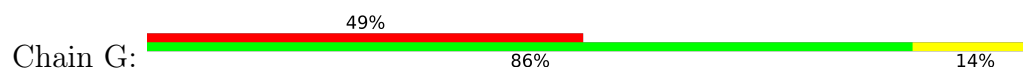
• Molecule 8: COP9 signalosome complex subunit 5

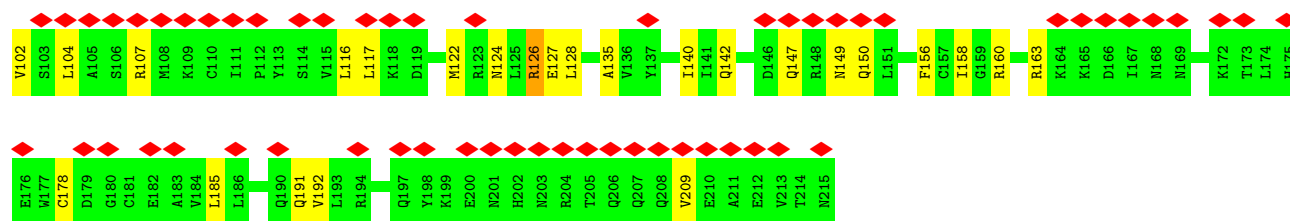


• Molecule 9: COP9 signalosome complex subunit 6

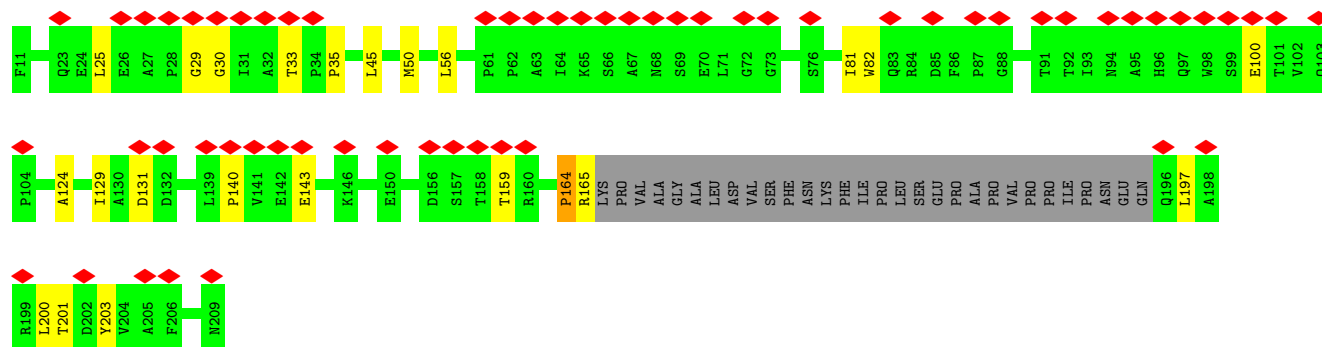
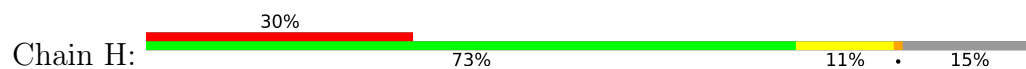


• Molecule 10: COP9 signalosome complex subunit 7b

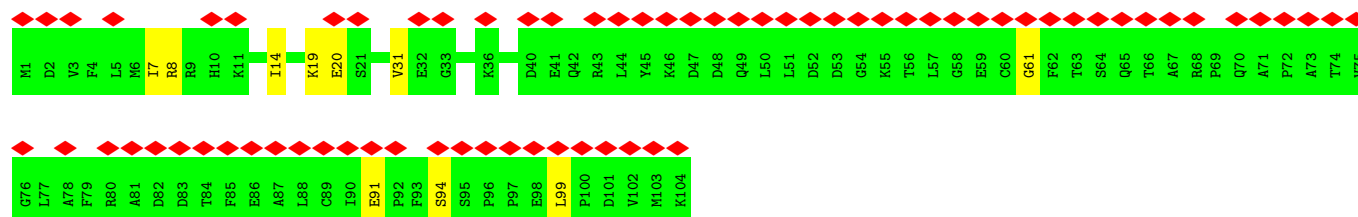
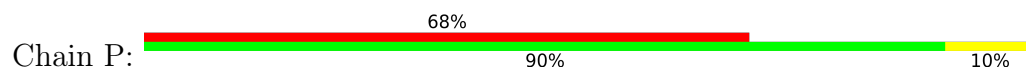




• Molecule 11: COP9 signalosome complex subunit 8



• Molecule 12: Elongin-B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17191	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 ($e^-/\text{\AA}^2$)	83	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	10.037	Depositor
Minimum map value	-1.471	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	6	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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	0.08	0/3509	0.24	0/4733
2	Q	0.09	0/892	0.24	0/1204
3	O	0.07	0/5475	0.22	0/7379
4	R	0.09	0/767	0.26	0/1037
5	B	0.08	0/3444	0.23	0/4634
6	C	0.07	0/3264	0.22	0/4407
7	D	0.72	6/3303 (0.2%)	0.22	0/4460
8	E	0.08	0/2526	0.22	0/3411
9	F	0.07	0/2327	0.20	0/3153
10	G	1.38	1/1665 (0.1%)	0.35	2/2253 (0.1%)
11	H	0.11	0/1381	0.28	0/1877
12	P	0.07	0/838	0.22	0/1132
All	All	0.42	7/29391 (0.0%)	0.24	2/39680 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	G	126	ARG	CG-CD	56.29	3.21	1.52
7	D	316	TYR	CD2-CE2	20.19	1.99	1.38
7	D	316	TYR	CD1-CE1	20.17	1.99	1.38
7	D	316	TYR	CE1-CZ	15.88	1.76	1.38
7	D	316	TYR	CE2-CZ	15.80	1.76	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	G	126	ARG	CB-CG-CD	9.37	132.85	111.30
10	G	126	ARG	CG-CD-NE	6.10	125.43	112.00

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	A	3450	0	3482	22	0
2	Q	873	0	845	8	0
3	O	5364	0	5334	48	0
4	R	746	0	706	13	0
5	B	3386	0	3424	28	0
6	C	3205	0	3225	26	0
7	D	3251	0	3253	47	0
8	E	2472	0	2444	12	0
9	F	2280	0	2263	24	0
10	G	1645	0	1667	42	0
11	H	1349	0	1332	13	0
12	P	822	0	824	6	0
All	All	28843	0	28799	219	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 4.

The worst 5 of 219 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)
7:D:316:TYR:CZ	7:D:316:TYR:CE2	1.76	1.71
7:D:316:TYR:CZ	7:D:316:TYR:CE1	1.76	1.70
7:D:316:TYR:CE2	7:D:316:TYR:CD2	1.99	1.49
7:D:316:TYR:CE1	7:D:316:TYR:CD1	1.99	1.48
7:D:316:TYR:CZ	10:G:126:ARG:CG	2.36	1.09

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	431/433 (100%)	396 (92%)	33 (8%)	2 (0%)	24	63
2	Q	110/112 (98%)	101 (92%)	7 (6%)	2 (2%)	6	34
3	O	652/654 (100%)	592 (91%)	54 (8%)	6 (1%)	14	51
4	R	87/90 (97%)	68 (78%)	18 (21%)	1 (1%)	11	46
5	B	412/414 (100%)	378 (92%)	27 (7%)	7 (2%)	7	36
6	C	401/403 (100%)	364 (91%)	34 (8%)	3 (1%)	18	56
7	D	404/406 (100%)	392 (97%)	9 (2%)	3 (1%)	18	56
8	E	309/311 (99%)	280 (91%)	26 (8%)	3 (1%)	12	49
9	F	286/288 (99%)	254 (89%)	26 (9%)	6 (2%)	5	30
10	G	206/208 (99%)	197 (96%)	8 (4%)	1 (0%)	24	63
11	H	165/199 (83%)	152 (92%)	9 (6%)	4 (2%)	4	27
12	P	102/104 (98%)	91 (89%)	10 (10%)	1 (1%)	12	49
All	All	3565/3622 (98%)	3265 (92%)	261 (7%)	39 (1%)	14	46

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	229	PRO
5	B	231	PRO
11	H	164	PRO
2	Q	66	PRO
3	O	524	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	377/377 (100%)	372 (99%)	5 (1%)	61	74
2	Q	96/96 (100%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	O	599/599 (100%)	594 (99%)	5 (1%)	73	80
4	R	79/79 (100%)	78 (99%)	1 (1%)	61	74
5	B	376/376 (100%)	373 (99%)	3 (1%)	73	80
6	C	359/359 (100%)	351 (98%)	8 (2%)	45	64
7	D	347/347 (100%)	346 (100%)	1 (0%)	86	86
8	E	267/267 (100%)	264 (99%)	3 (1%)	65	76
9	F	255/255 (100%)	253 (99%)	2 (1%)	73	80
10	G	181/181 (100%)	179 (99%)	2 (1%)	65	76
11	H	140/166 (84%)	138 (99%)	2 (1%)	59	72
12	P	92/92 (100%)	91 (99%)	1 (1%)	65	76
All	All	3168/3194 (99%)	3135 (99%)	33 (1%)	65	78

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	G	27	LEU
10	G	185	LEU
12	P	31	VAL
5	B	95	LEU
5	B	83	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
6	C	291	ASN
7	D	354	GLN
11	H	51	ASN
6	C	395	GLN
7	D	102	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	107:GLY	C	108:HIS	N	3.75

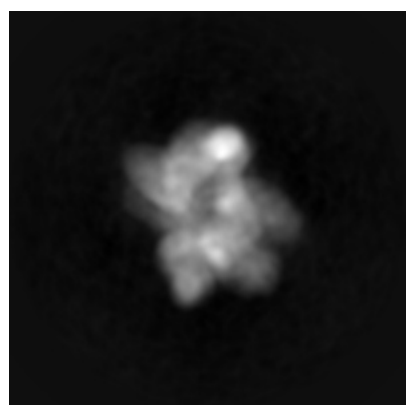
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4741. These allow visual inspection of the internal detail of the map and identification of artifacts.

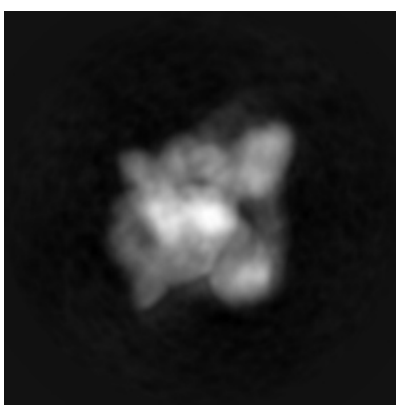
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

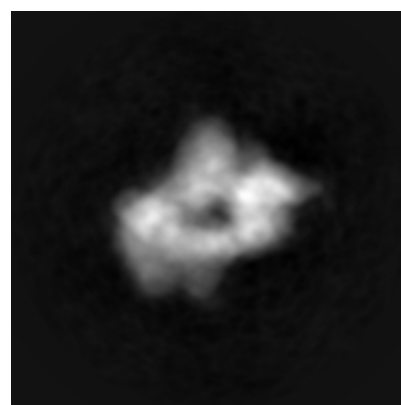
6.1.1 Primary map



X



Y

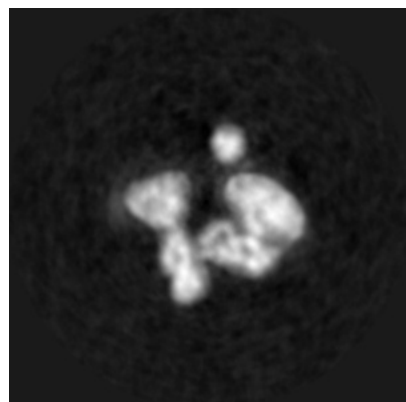


Z

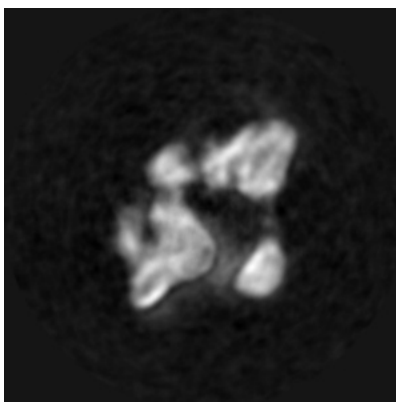
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

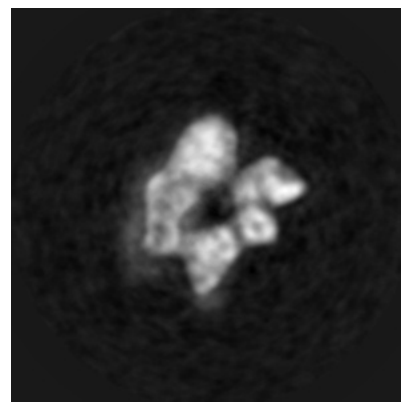
6.2.1 Primary map



X Index: 150



Y Index: 150

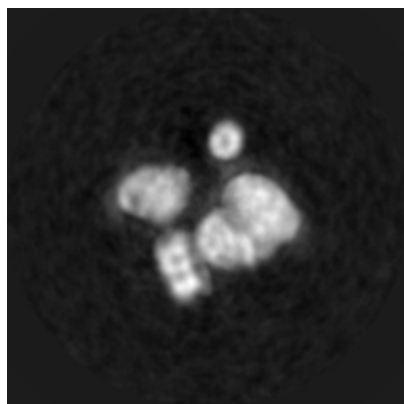


Z Index: 150

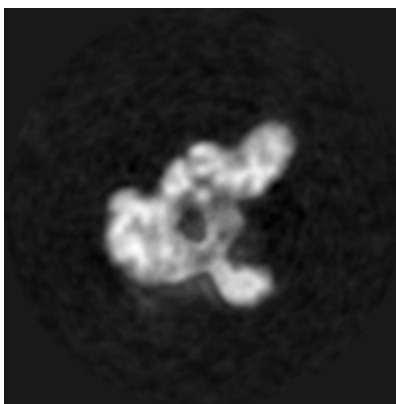
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

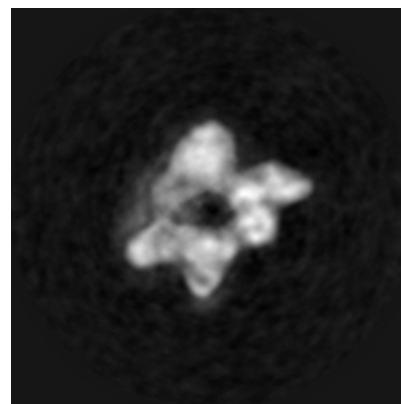
6.3.1 Primary map



X Index: 142



Y Index: 132

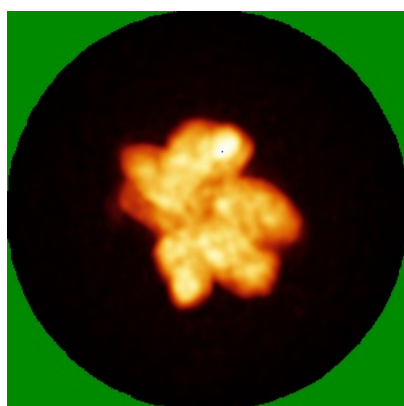


Z Index: 156

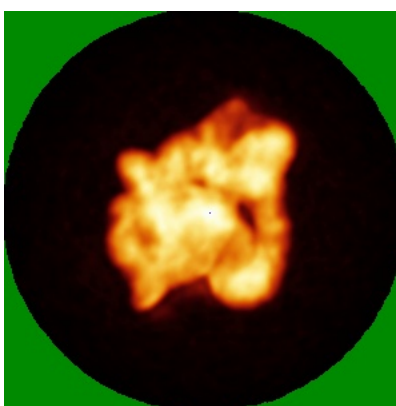
The images above show the largest variance slices of the map in three orthogonal directions.

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

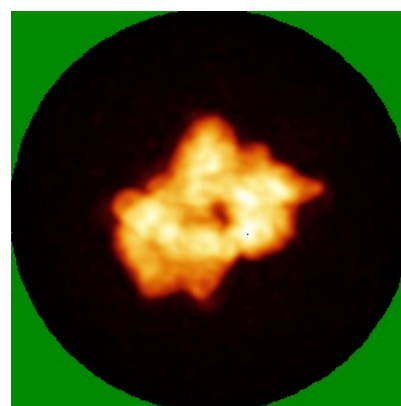
6.4.1 Primary map



X



Y

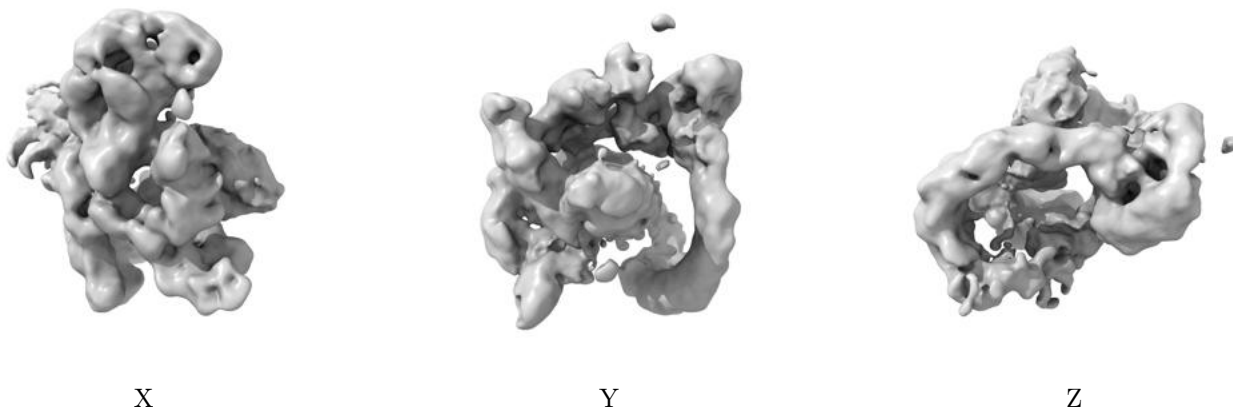


Z

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

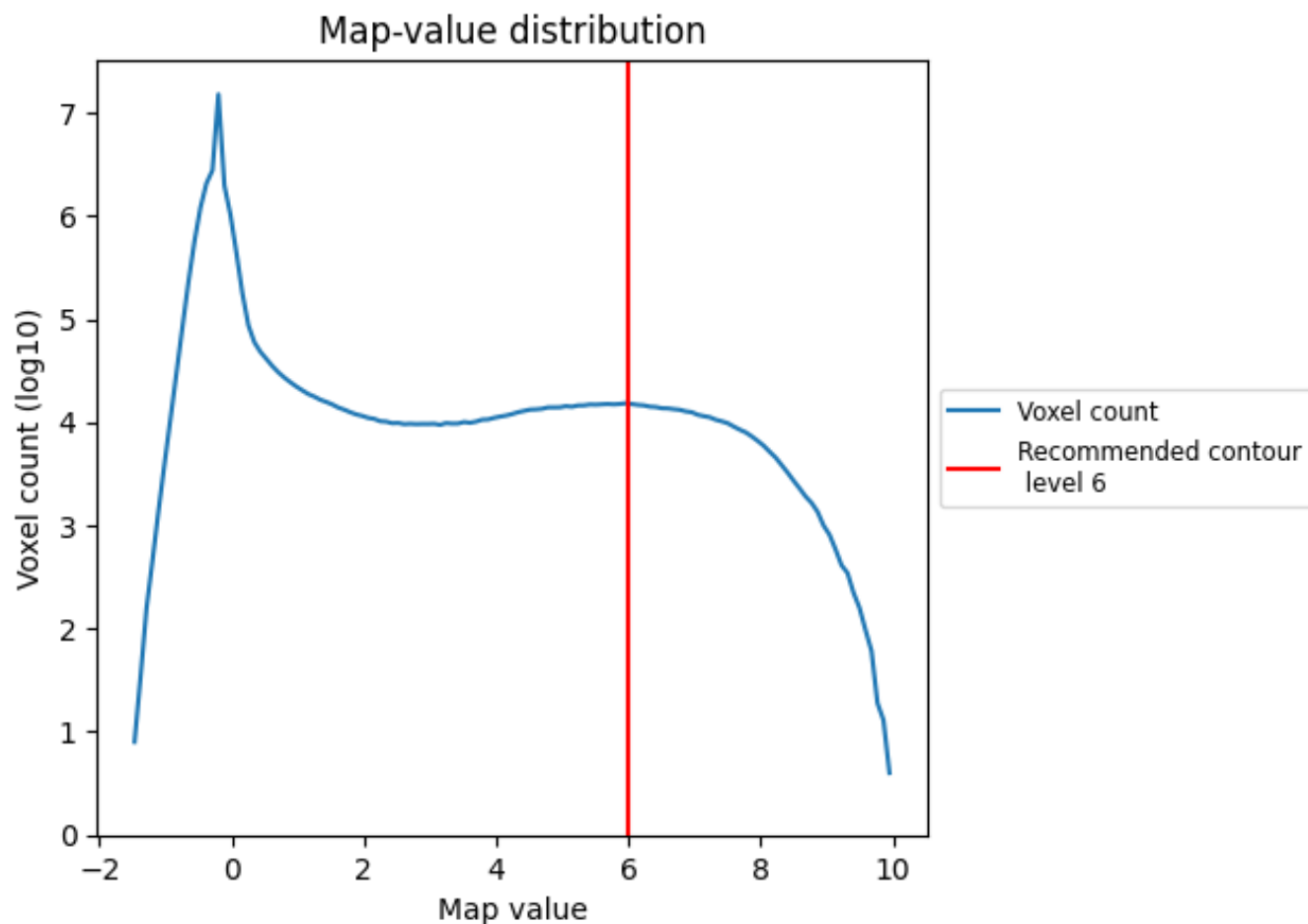
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

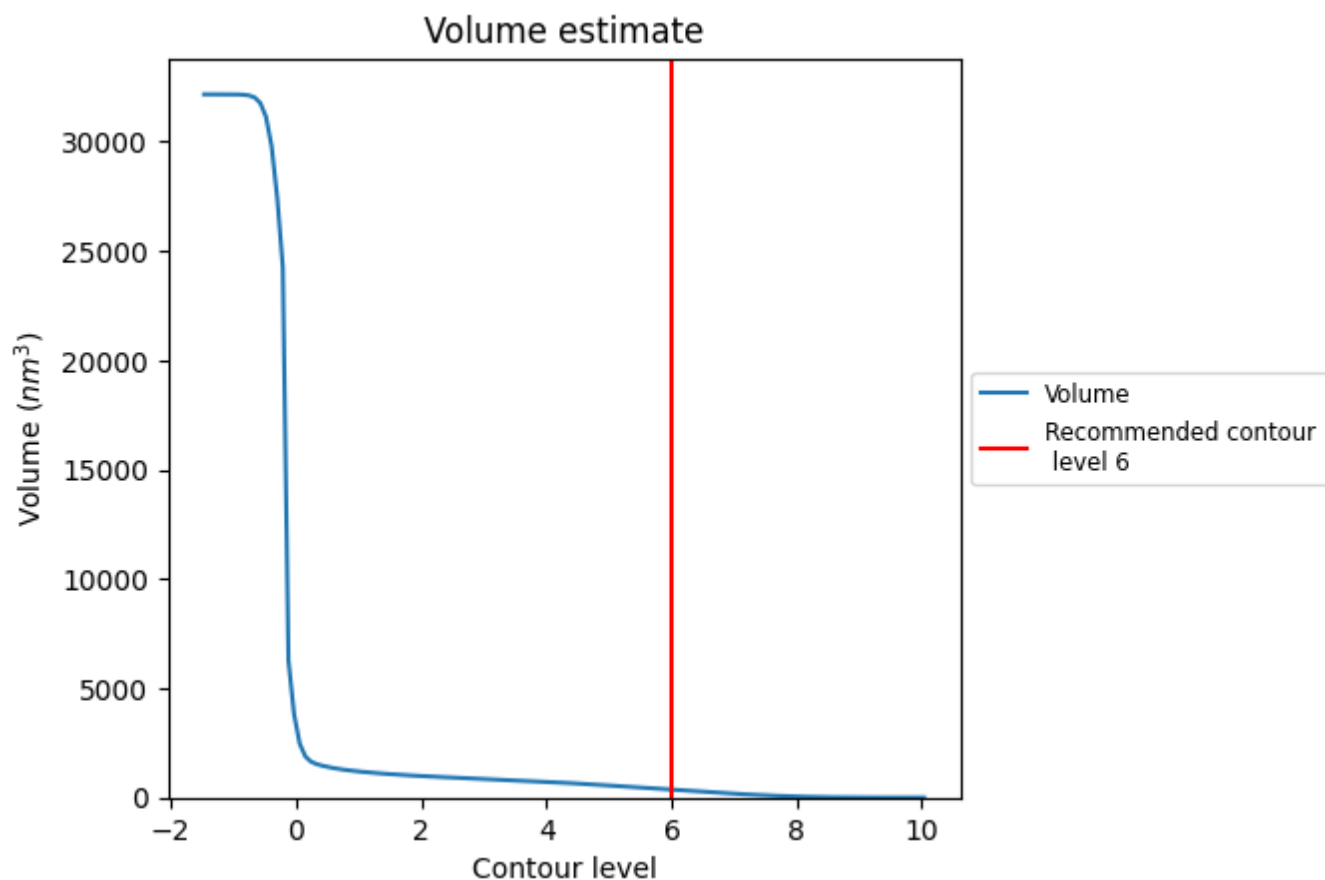
This section contains the results of statistical analysis of the map.

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.

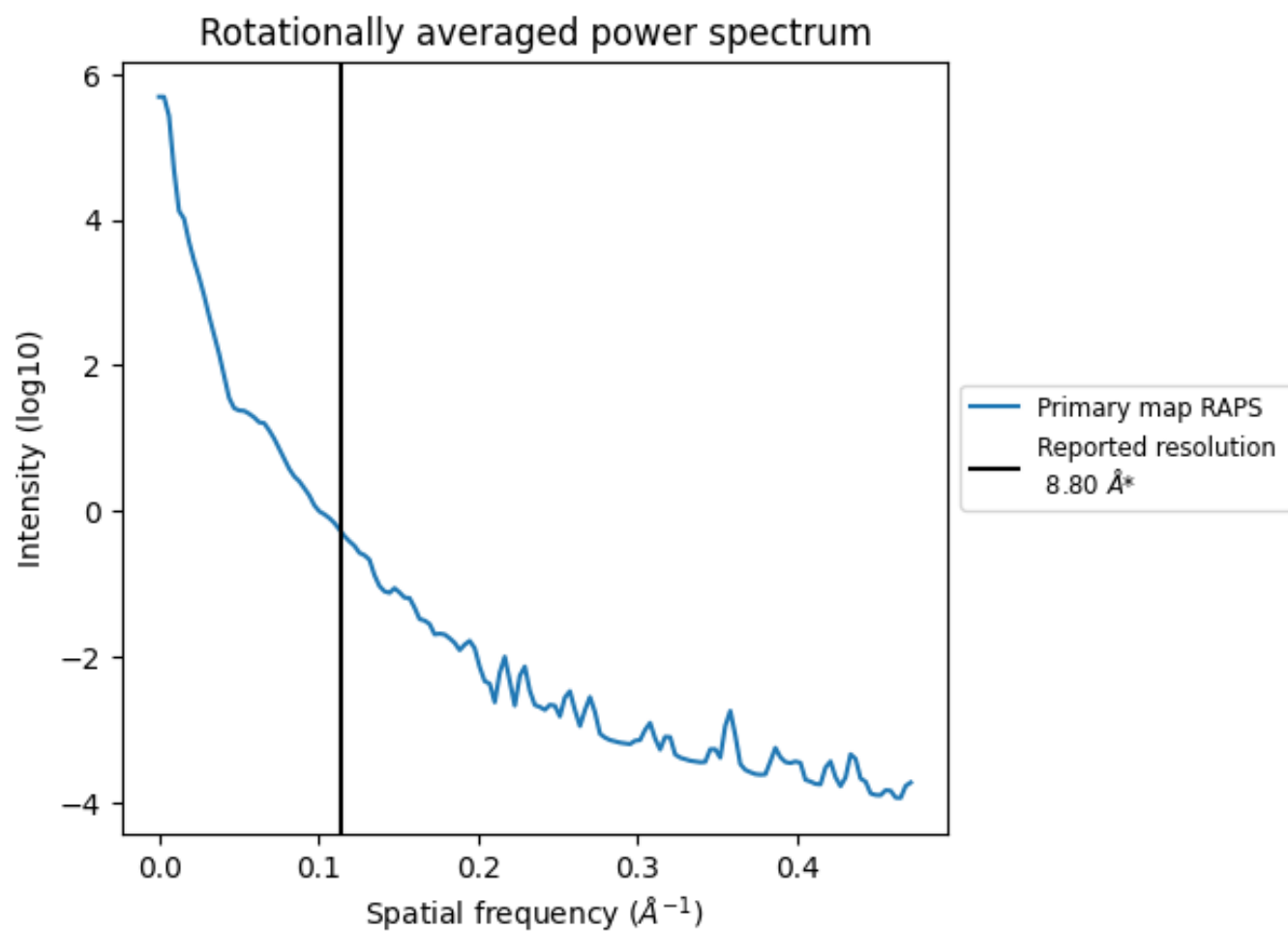
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 359 nm³; this corresponds to an approximate mass of 324 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 0.114 Å⁻¹

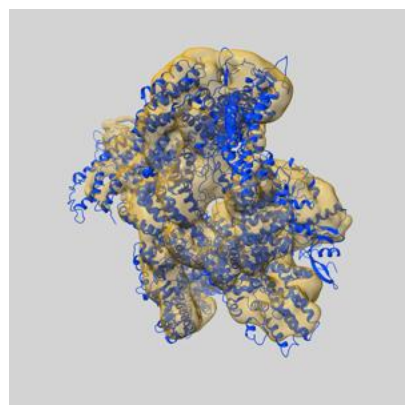
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

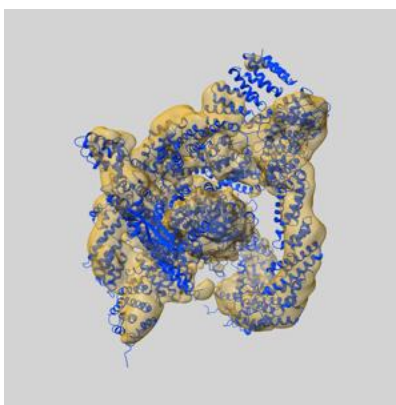
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4741 and PDB model 6R7H. Per-residue inclusion information can be found in section [3](#) on page [6](#).

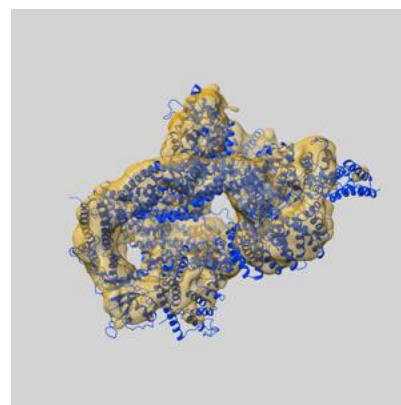
9.1 Map-model overlay [i](#)



X



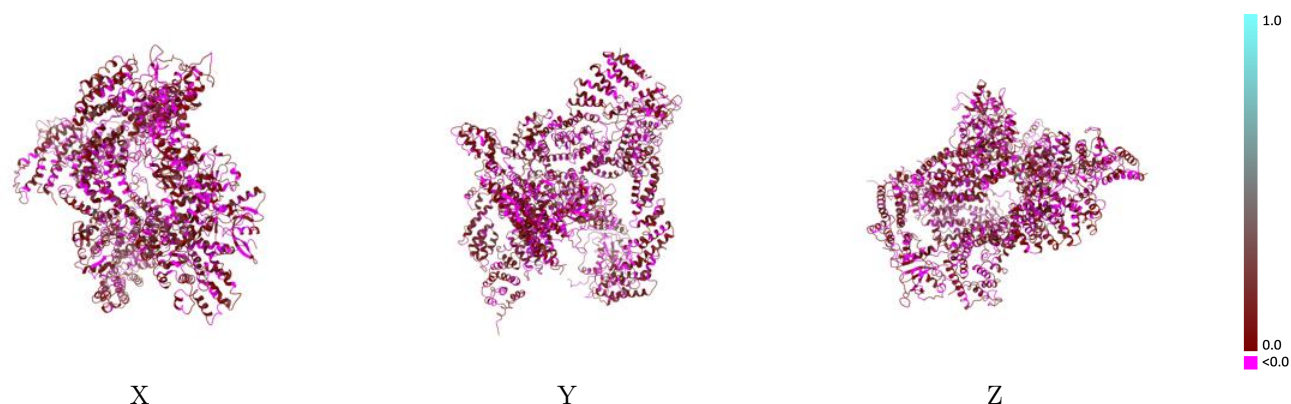
Y



Z

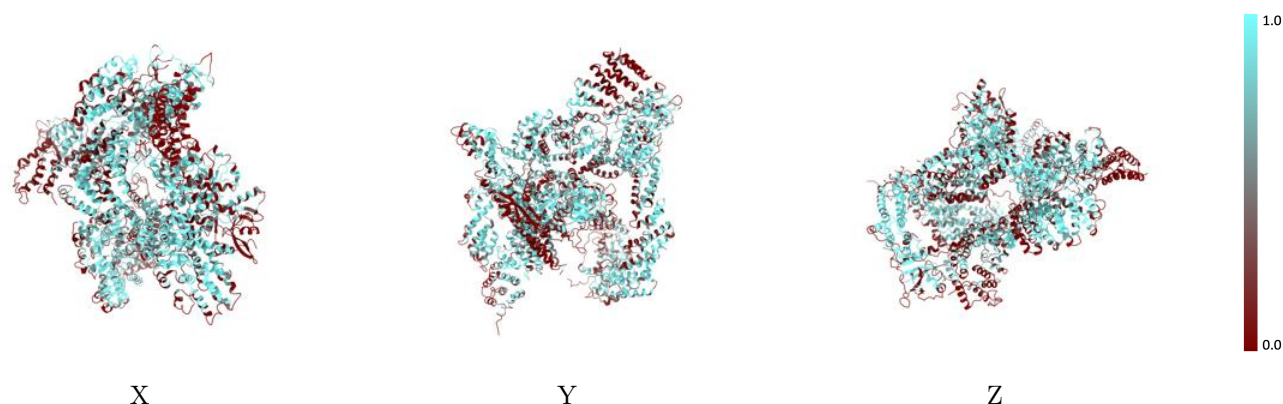
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



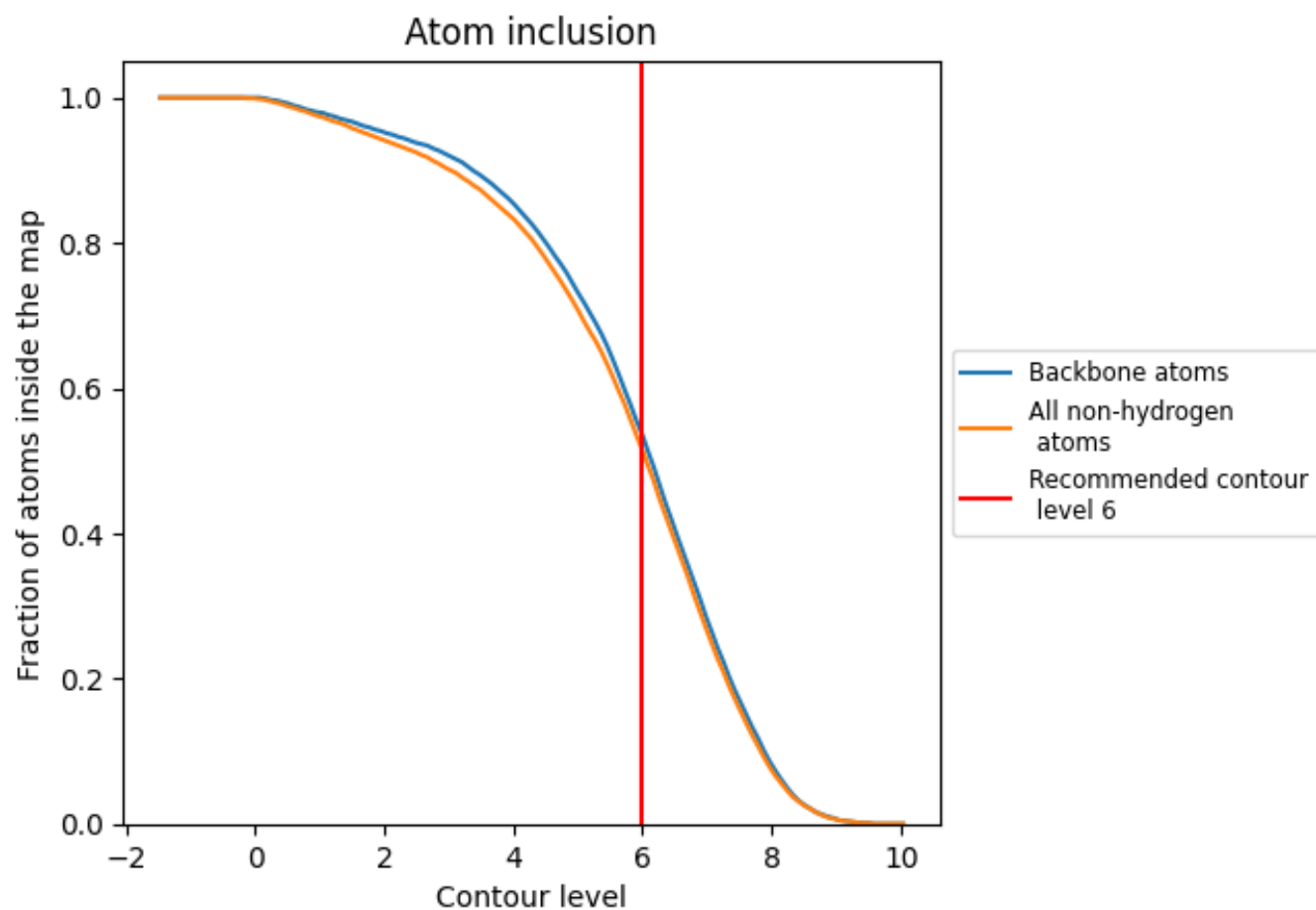
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 51% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5140	0.0500
A	0.3980	0.0520
B	0.5710	0.0450
C	0.5420	0.0590
D	0.4320	0.0550
E	0.5580	0.0360
F	0.4390	0.0210
G	0.4770	0.0460
H	0.6240	0.0750
O	0.6100	0.0620
P	0.2950	0.0380
Q	0.5440	0.0510
R	0.4990	0.0090

1.0

0.0

<0.0