



wwPDB EM Validation Summary Report ⓘ

Mar 13, 2026 – 10:25 AM UTC

PDB ID : 6Q6H / pdb_00006q6h
EMDB ID : EMD-4466
Title : Cryo-EM structure of the APC/C-Cdc20-Cdk2-cyclinA2-Cks2 complex, the D2 box class
Authors : Zhang, S.; Barford, D.
Deposited on : 2018-12-11
Resolution : 3.20 Å(reported)

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

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

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:

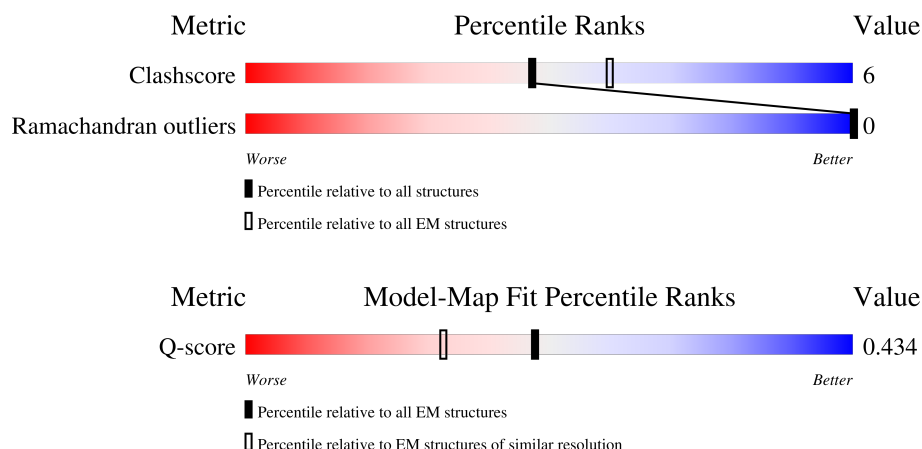
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	L	185	
2	D	121	
3	A	1855	
4	N	822	
5	I	808	

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Mol	Chain	Length	Quality of chain
6	O	755	
7	K	620	
7	Q	620	
8	C	84	
9	G	85	
9	W	85	
10	M	74	
11	H	110	
12	J	824	
12	P	824	
13	Y	599	
13	Z	599	
14	U	597	
14	V	597	
15	R	499	
16	S	394	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 67944 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 Anaphase-promoting complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	179	Total	C	N	O	S	0	0
			1446	906	263	270	7		

- Molecule 2 is a protein called Anaphase-promoting complex subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	56	Total	C	N	O	S	1	0
			470	299	81	89	1		

- Molecule 3 is a protein called Apc1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1551	Total	C	N	O	S	0	0
			12131	7785	2041	2222	83		

- Molecule 4 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	653	Total	C	N	O	S	0	0
			5238	3337	932	944	25		

- Molecule 5 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	729	Total	C	N	O	S	0	0
			5752	3685	956	1077	34		

- Molecule 6 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	O	703	Total	C	N	O	S	0	0
			5532	3529	963	1011	29		

- Molecule 7 is a protein called Cell division cycle protein 16 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	518	Total	C	N	O	S	0	0
			4187	2694	704	764	25		
7	Q	504	Total	C	N	O	S	0	0
			4055	2606	684	741	24		

- Molecule 8 is a protein called Anaphase-promoting complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	84	Total	C	N	O	S	0	0
			657	418	120	103	16		

- Molecule 9 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	27	Total	C	N	O	S	0	0
			226	142	42	41	1		
9	W	26	Total	C	N	O	S	0	0
			225	142	42	40	1		

- Molecule 10 is a protein called Anaphase-promoting complex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	61	Total	C	N	O	S	0	0
			499	314	81	102	2		

- Molecule 11 is a protein called Anaphase-promoting complex subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	57	Total	C	N	O	S	0	0
			459	296	75	86	2		

- Molecule 12 is a protein called Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	496	Total	C	N	O	S	0	0
			3964	2547	668	723	26		
12	P	484	Total	C	N	O	S	0	0
			3883	2497	653	707	26		

- Molecule 13 is a protein called Anaphase-promoting complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	499	Total	C	N	O	S	1	0
			3911	2474	682	728	27		
13	Z	486	Total	C	N	O	S	1	0
			3807	2413	664	705	25		

- Molecule 14 is a protein called Cell division cycle protein 23 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	515	Total	C	N	O	S	0	0
			4160	2678	700	758	24		
14	V	530	Total	C	N	O	S	0	0
			4311	2778	720	789	24		

- Molecule 15 is a protein called Cell division cycle protein 20 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	375	Total	C	N	O	S	2	0
			2897	1818	529	538	12		

- Molecule 16 is a protein called Cyclin-A2.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	S	17	Total	C	N	O	0	0
			134	83	22	29		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	?	-	ASN	deletion	UNP P20248
S	?	-	PRO	deletion	UNP P20248
S	?	-	GLU	deletion	UNP P20248
S	?	-	LYS	deletion	UNP P20248
S	?	-	ALA	deletion	UNP P20248
S	?	-	ALA	deletion	UNP P20248
S	?	-	PRO	deletion	UNP P20248
S	?	-	VAL	deletion	UNP P20248
S	?	-	GLN	deletion	UNP P20248
S	?	-	GLN	deletion	UNP P20248
S	?	-	PRO	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248
S	?	-	THR	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248
S	?	-	ALA	deletion	UNP P20248

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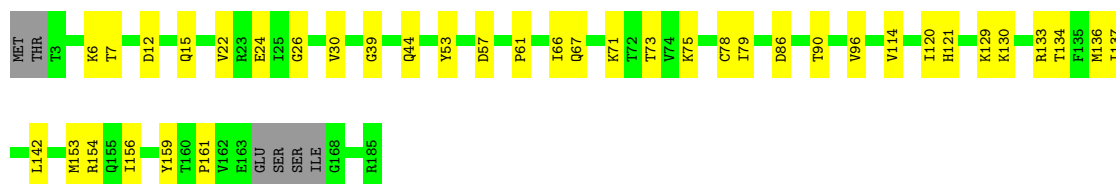
Chain	Residue	Modelled	Actual	Comment	Reference
S	?	-	ALA	deletion	UNP P20248
S	?	-	LEU	deletion	UNP P20248
S	?	-	ALA	deletion	UNP P20248
S	?	-	VAL	deletion	UNP P20248
S	?	-	LEU	deletion	UNP P20248
S	?	-	LYS	deletion	UNP P20248
S	?	-	SER	deletion	UNP P20248
S	?	-	GLY	deletion	UNP P20248
S	?	-	ASN	deletion	UNP P20248
S	?	-	PRO	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248
S	?	-	GLY	deletion	UNP P20248
S	?	-	LEU	deletion	UNP P20248
S	?	-	ALA	deletion	UNP P20248
S	?	-	GLN	deletion	UNP P20248
S	?	-	GLN	deletion	UNP P20248
S	?	-	GLN	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248
S	?	-	PRO	deletion	UNP P20248
S	?	-	LYS	deletion	UNP P20248
S	?	-	THR	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248
S	?	-	ARG	deletion	UNP P20248

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.

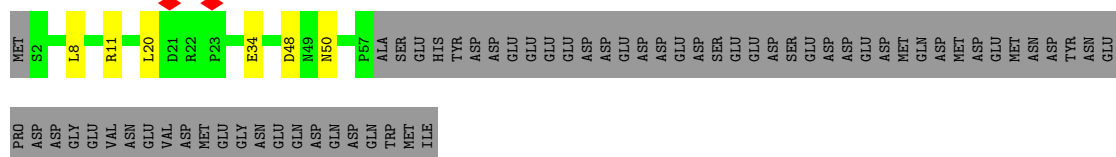
• Molecule 1: Anaphase-promoting complex subunit 10

Chain L: 



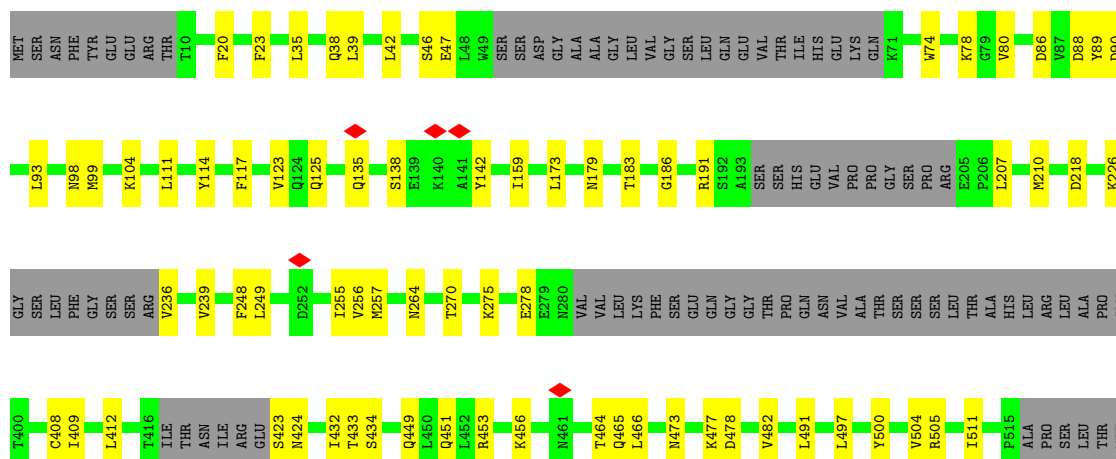
• Molecule 2: Anaphase-promoting complex subunit 15

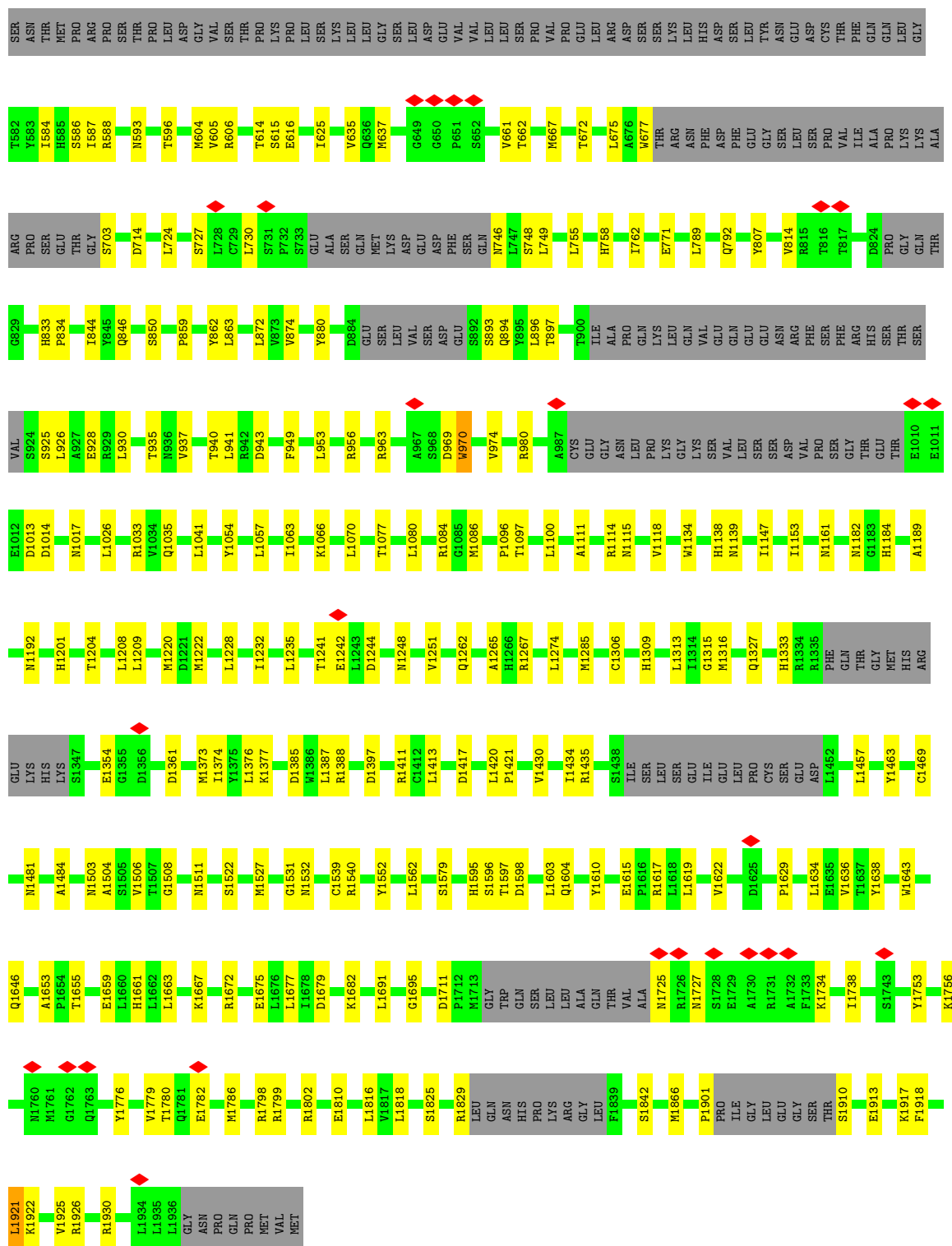
Chain D: 



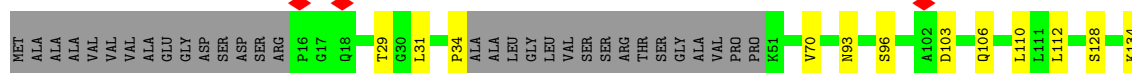
• Molecule 3: Apc1

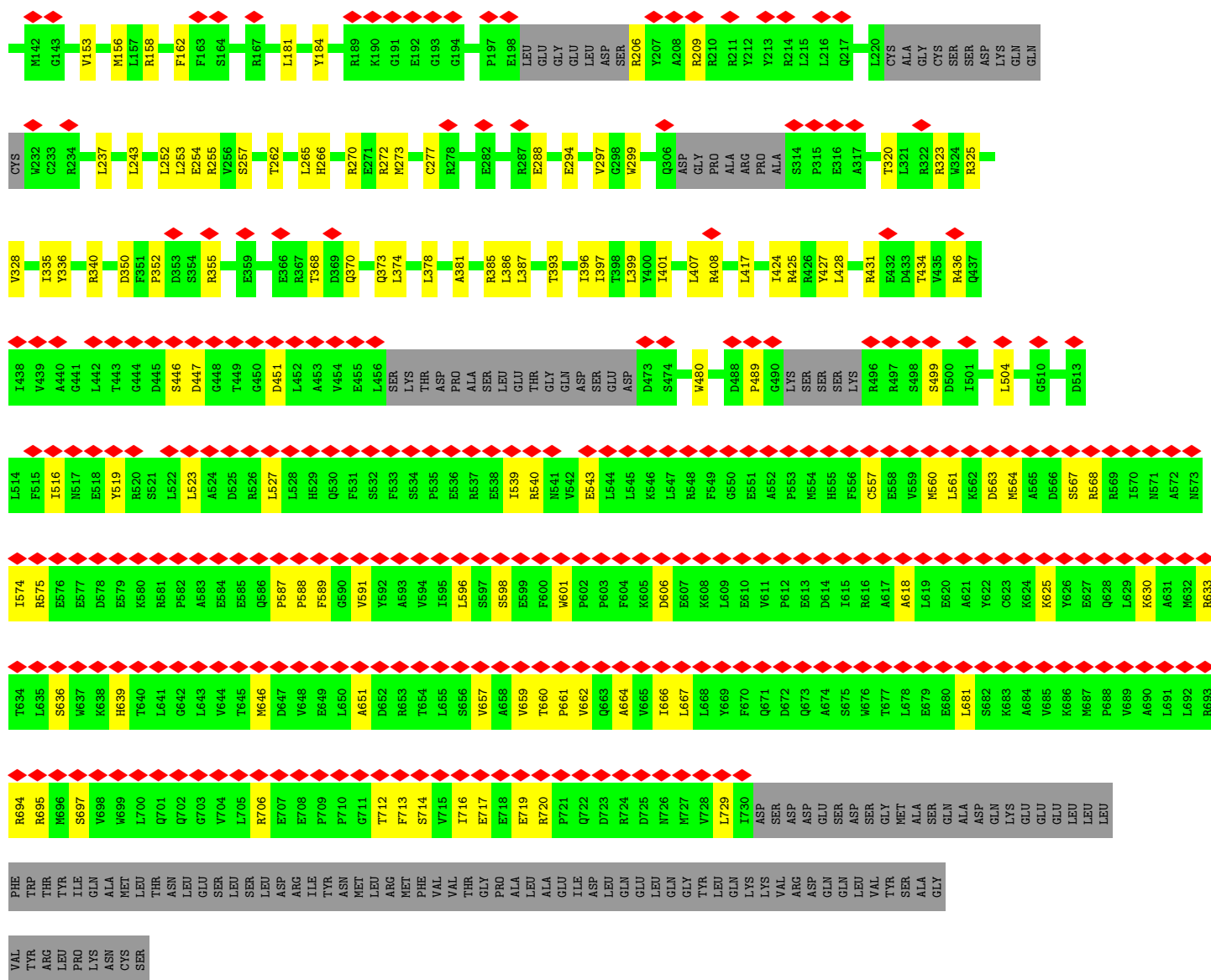
Chain A: 



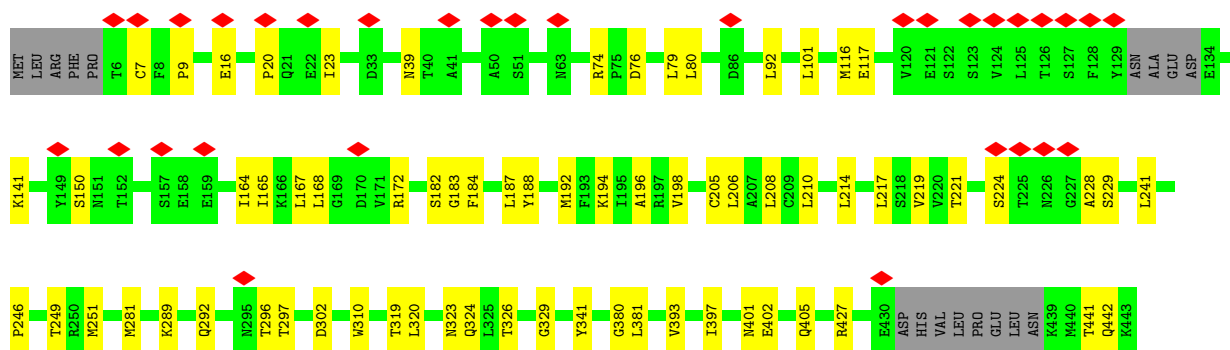
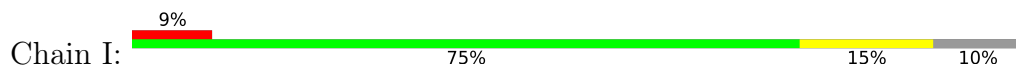


• Molecule 4: Anaphase-promoting complex subunit 2

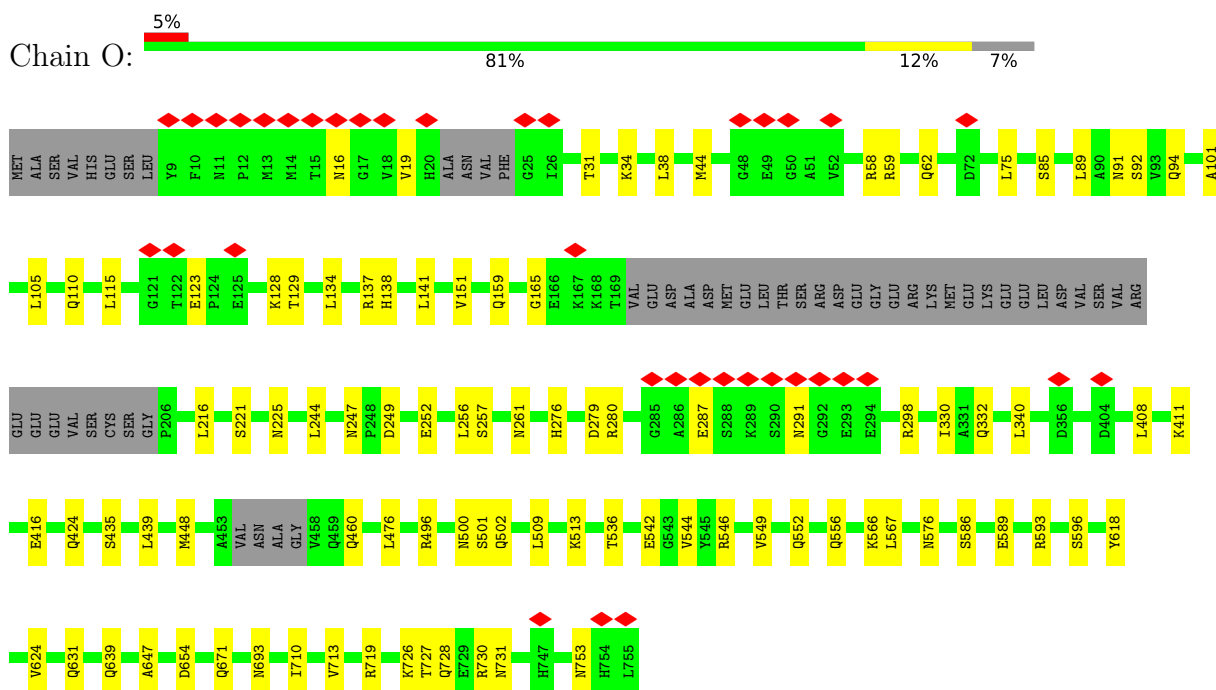




• Molecule 5: Anaphase-promoting complex subunit 4

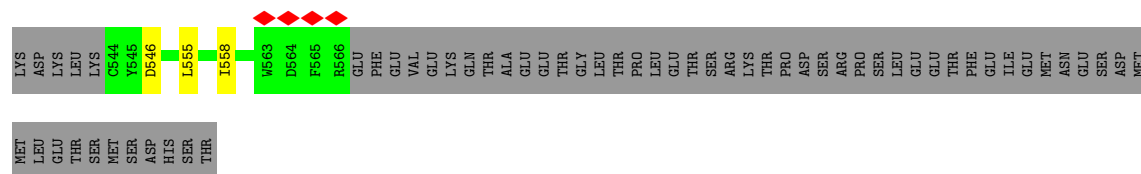


- Molecule 6: Anaphase-promoting complex subunit 5



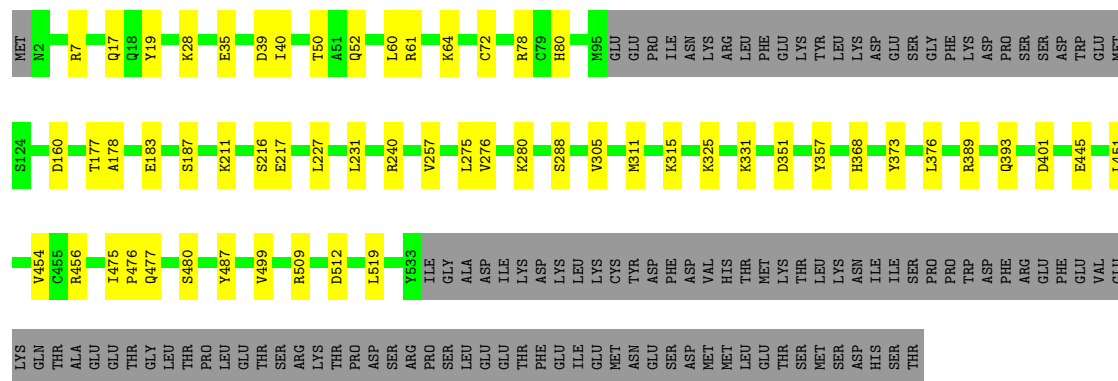
- Molecule 7: Cell division cycle protein 16 homolog





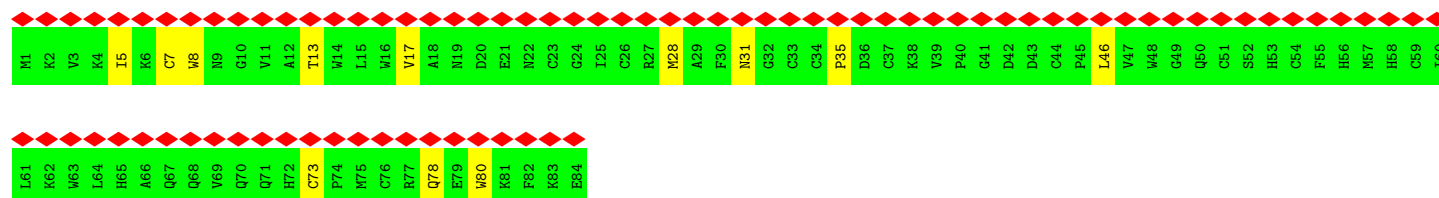
• Molecule 7: Cell division cycle protein 16 homolog

Chain Q: 72% 9% 19%



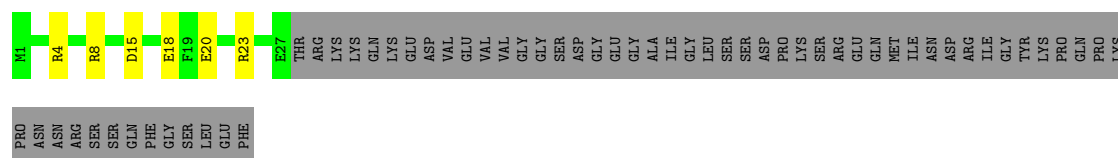
• Molecule 8: Anaphase-promoting complex subunit 11

Chain C: 100% 86% 14%



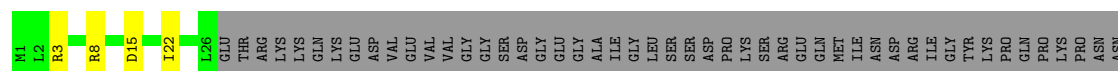
• Molecule 9: Anaphase-promoting complex subunit CDC26

Chain G: 25% 7% 68%

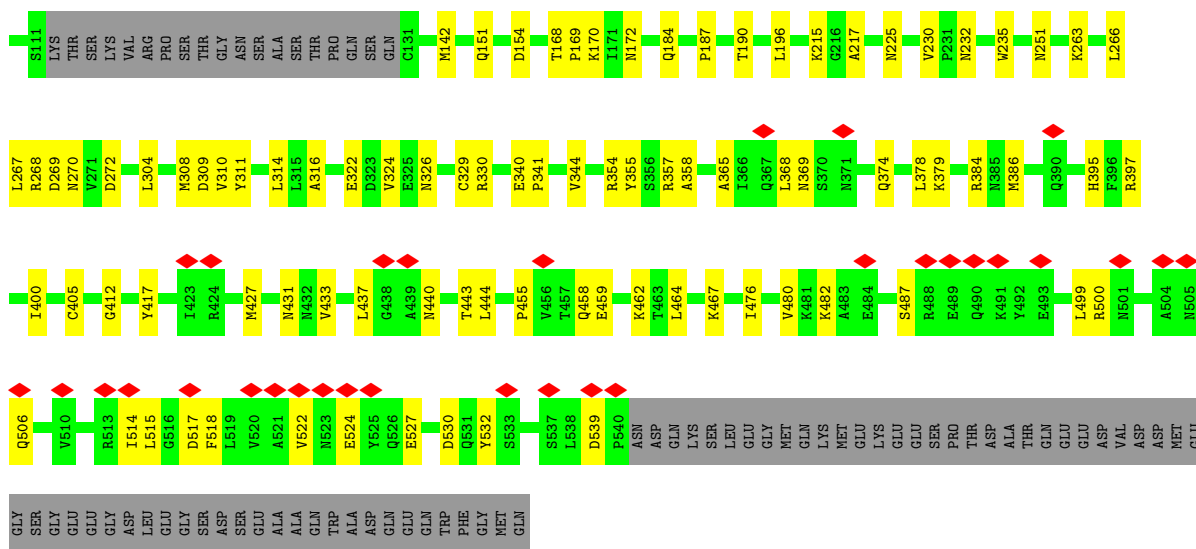


• Molecule 9: Anaphase-promoting complex subunit CDC26

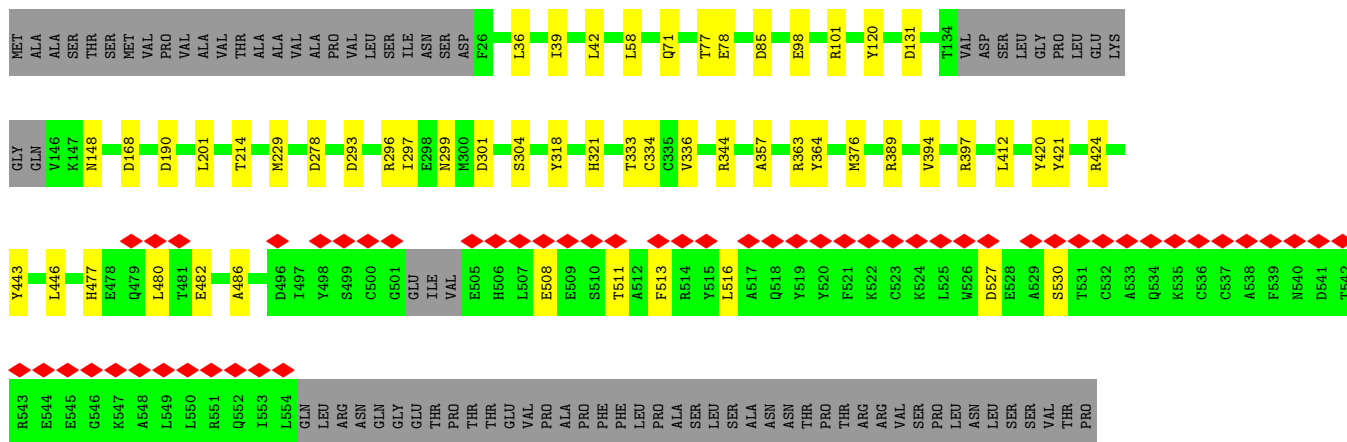
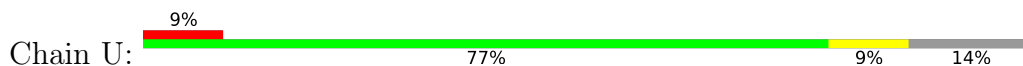
Chain W: 26% 5% 69%



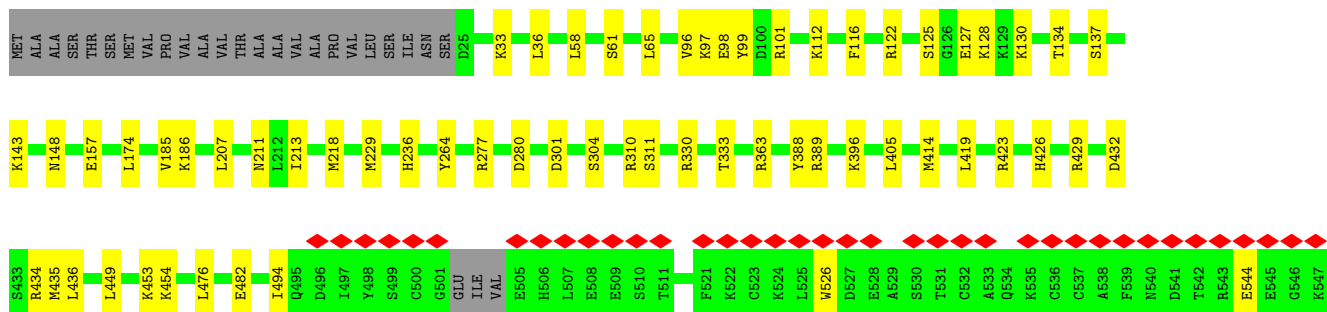
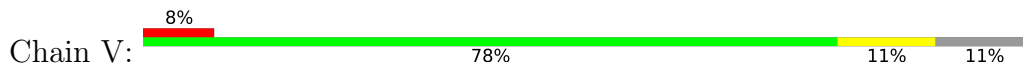




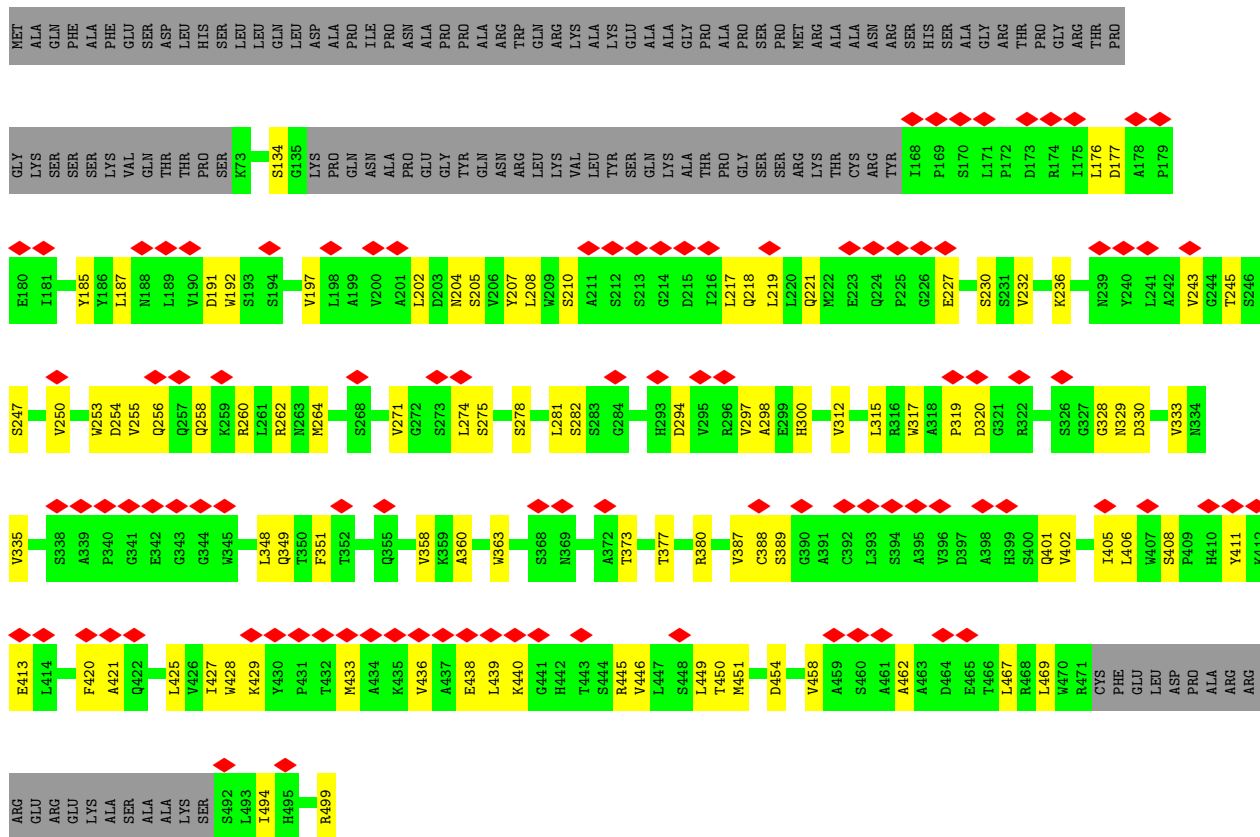
• Molecule 14: Cell division cycle protein 23 homolog



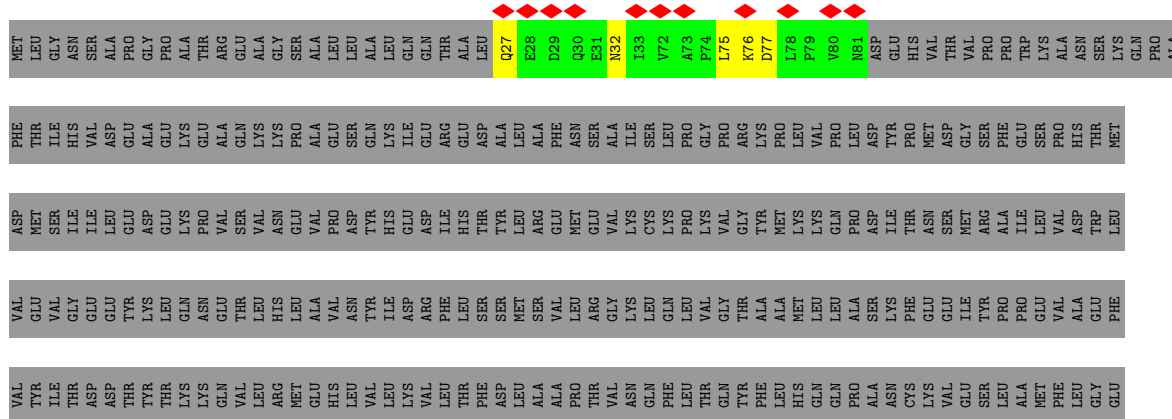
• Molecule 14: Cell division cycle protein 23 homolog



Chain R:



Chain S: 96%



LEU SER LEU ILE ASP ALA ASP PRO TYR LYS TYR LEU PRO SER VAL ILE ALA GLY ALA PHE HIS LEU ALA LEU TYR THR VAL THR GLY GLN SER TRP PRO GLU SER LEU ILE ARG LYS THR TYR THR LEU GLU SER LEU LYS PRO CYS MET ASP LEU HIS GLN THR TYR

LEU LYS ALA PRO GLN HIS ALA GLN GLN SER ARG GLU LYS TYR LYS ASN SER LYS TYR HIS GLY VAL SER LEU LEU ASN PRO VAL GLU THR LEU ASN LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	117044	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.042	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 (Å)	418.80002, 418.80002, 418.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.047, 1.047, 1.047	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	L	0.33	0/1480	0.52	0/2005
2	D	0.30	0/485	0.52	0/662
3	A	0.32	0/12411	0.56	6/16877 (0.0%)
4	N	0.22	0/5343	0.56	0/7236
5	I	0.24	0/5871	0.48	0/7954
6	O	0.31	0/5634	0.50	0/7612
7	K	0.31	0/4291	0.50	2/5812 (0.0%)
7	Q	0.35	0/4154	0.51	0/5627
8	C	0.21	0/680	0.54	0/921
9	G	0.32	0/227	0.53	0/302
9	W	0.29	0/226	0.53	0/299
10	M	0.33	0/508	0.51	0/689
11	H	0.32	0/468	0.46	0/631
12	J	0.34	0/4058	0.47	0/5485
12	P	0.36	0/3975	0.46	0/5371
13	Y	0.28	0/3974	0.52	0/5369
13	Z	0.27	0/3870	0.54	0/5233
14	U	0.30	0/4255	0.47	0/5753
14	V	0.34	0/4409	0.49	0/5958
15	R	0.24	0/2969	0.55	0/4038
16	S	0.27	0/134	0.75	0/181
All	All	0.30	0/69422	0.51	8/94015 (0.0%)

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
3	A	0	2
4	N	0	1
6	O	0	1
15	R	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
16	S	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	758	HIS	CA-C-N	6.52	124.35	120.24
3	A	758	HIS	C-N-CA	6.52	124.35	120.24
3	A	1596	SER	CA-C-N	5.72	136.58	126.45
3	A	1596	SER	C-N-CA	5.72	136.58	126.45
7	K	62	SER	CA-C-N	5.24	131.55	121.54

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	969	ASP	Peptide
3	A	970	TRP	Peptide
4	N	630	LYS	Peptide
6	O	123	GLU	Peptide
15	R	202	LEU	Peptide

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	L	1446	0	1423	24	0
2	D	470	0	458	6	0
3	A	12131	0	12060	185	0
4	N	5238	0	5220	80	0
5	I	5752	0	5680	80	0
6	O	5532	0	5570	65	0
7	K	4187	0	4099	48	0
7	Q	4055	0	3959	41	0
8	C	657	0	611	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	G	226	0	233	5	0
9	W	225	0	242	6	0
10	M	499	0	469	4	0
11	H	459	0	449	7	0
12	J	3964	0	3903	38	0
12	P	3883	0	3836	30	0
13	Y	3911	0	3986	54	0
13	Z	3807	0	3885	70	0
14	U	4160	0	4038	35	0
14	V	4311	0	4237	45	0
15	R	2897	0	2789	64	0
16	S	134	0	129	4	0
All	All	67944	0	67276	813	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 6.

The worst 5 of 813 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:K:205:PHE:O	7:K:209:LEU:HB2	1.85	0.77
4:N:273:MET:O	4:N:277:CYS:HB2	1.88	0.71
13:Y:66:ASN:HD21	13:Z:269:ASP:H	1.38	0.71
3:A:1638:TYR:O	3:A:1646:GLN:HA	1.93	0.69
15:R:208:LEU:HB3	15:R:217:LEU:HB2	1.75	0.67

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	L	175/185 (95%)	163 (93%)	12 (7%)	0	100	100
2	D	55/121 (46%)	50 (91%)	5 (9%)	0	100	100
3	A	780/1855 (42%)	729 (94%)	51 (6%)	0	100	100
6	O	599/755 (79%)	582 (97%)	17 (3%)	0	100	100
7	K	512/620 (83%)	497 (97%)	15 (3%)	0	100	100
7	Q	500/620 (81%)	482 (96%)	18 (4%)	0	100	100
8	C	82/84 (98%)	74 (90%)	8 (10%)	0	100	100
9	G	25/85 (29%)	25 (100%)	0	0	100	100
9	W	24/85 (28%)	24 (100%)	0	0	100	100
10	M	50/74 (68%)	49 (98%)	1 (2%)	0	100	100
12	P	291/824 (35%)	284 (98%)	7 (2%)	0	100	100
13	Y	496/599 (83%)	485 (98%)	11 (2%)	0	100	100
13	Z	483/599 (81%)	475 (98%)	8 (2%)	0	100	100
14	U	509/597 (85%)	488 (96%)	21 (4%)	0	100	100
14	V	526/597 (88%)	508 (97%)	18 (3%)	0	100	100
15	R	371/499 (74%)	348 (94%)	23 (6%)	0	100	100
16	S	13/394 (3%)	10 (77%)	3 (23%)	0	100	100
All	All	5491/8593 (64%)	5273 (96%)	218 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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
16	S	1
15	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S	33:ILE	C	72:VAL	N	27.52
1	R	388[A]:CYS	C	389:SER	N	3.12

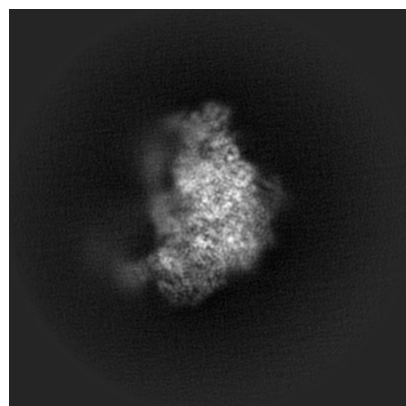
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4466. These allow visual inspection of the internal detail of the map and identification of artifacts.

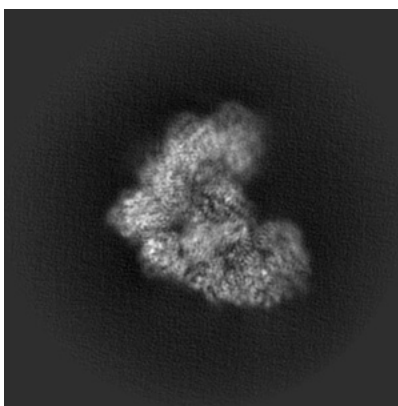
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

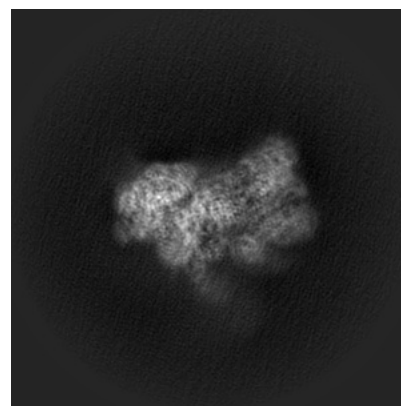
6.1.1 Primary map



X

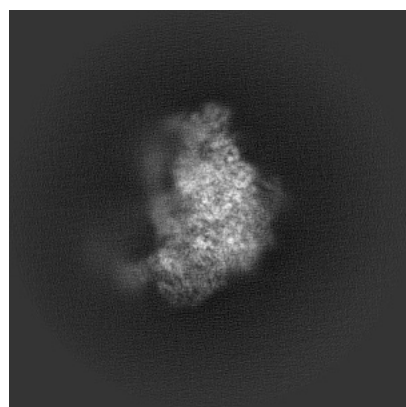


Y

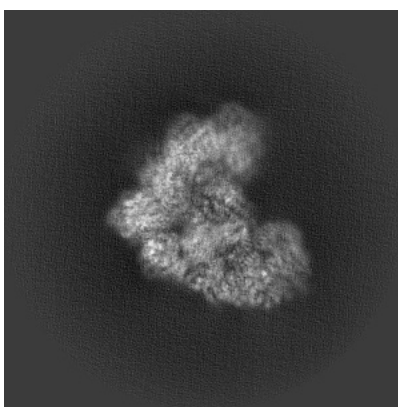


Z

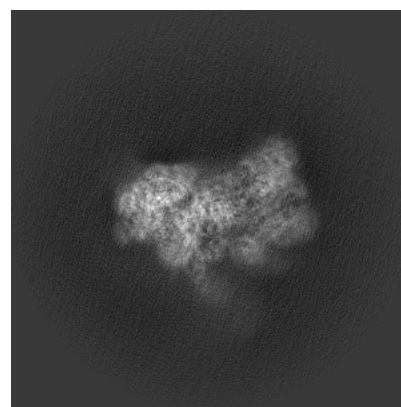
6.1.2 Raw map



X



Y

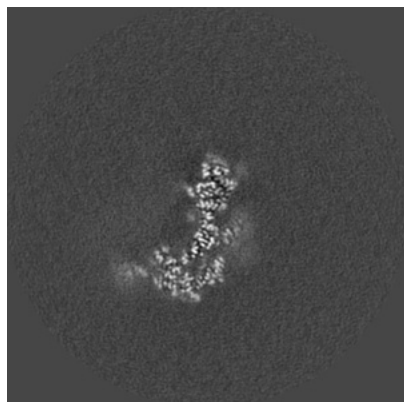


Z

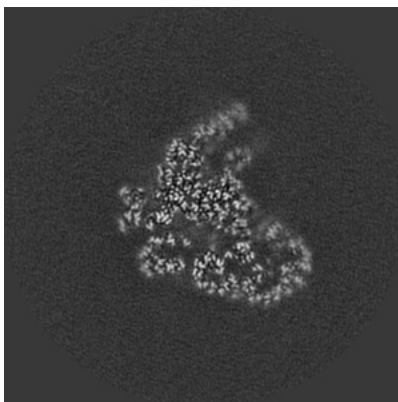
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

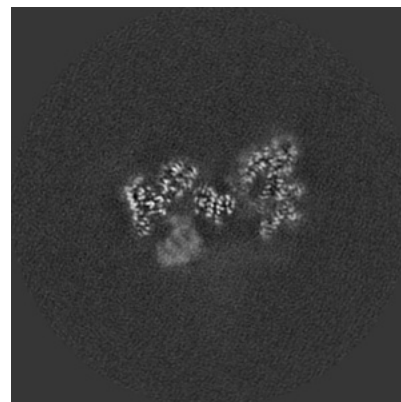
6.2.1 Primary map



X Index: 200

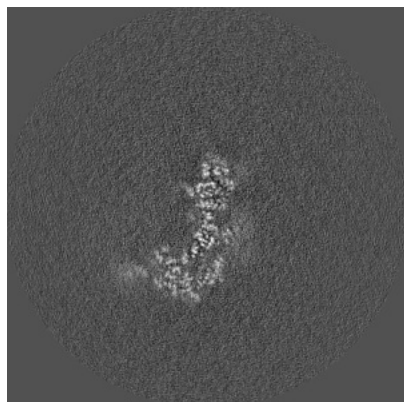


Y Index: 200

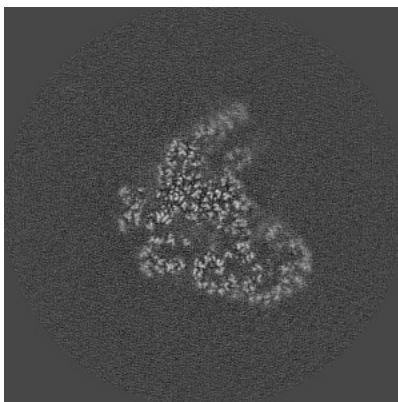


Z Index: 200

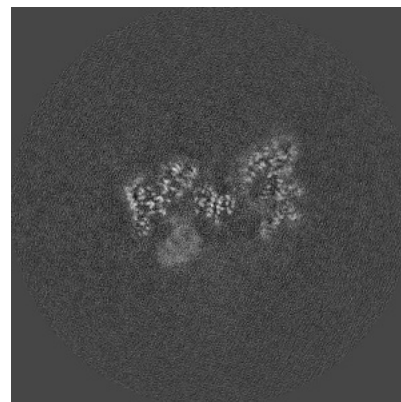
6.2.2 Raw map



X Index: 200



Y Index: 200

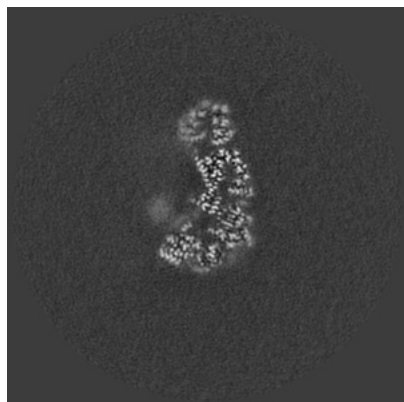


Z Index: 200

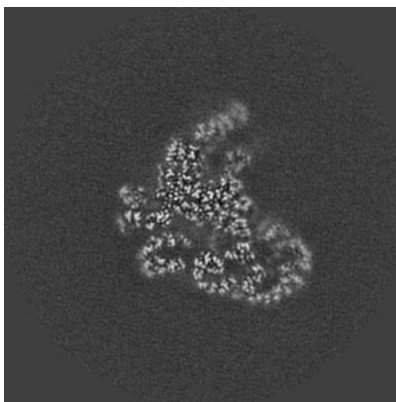
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 150

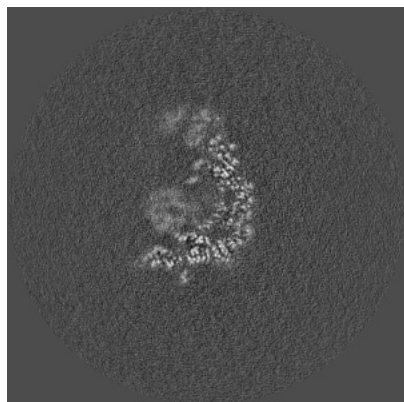


Y Index: 199

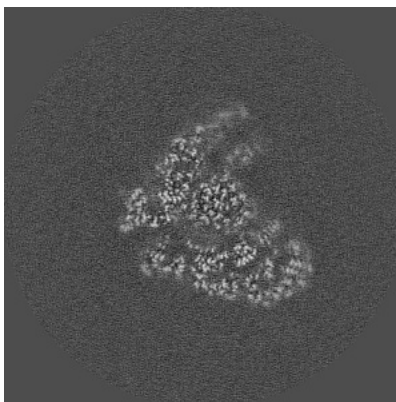


Z Index: 166

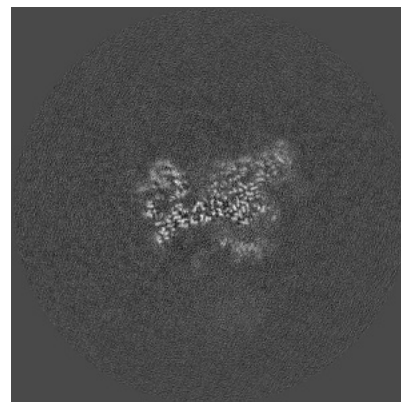
6.3.2 Raw map



X Index: 165



Y Index: 203

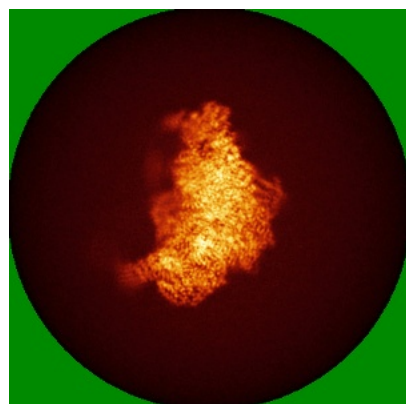


Z Index: 164

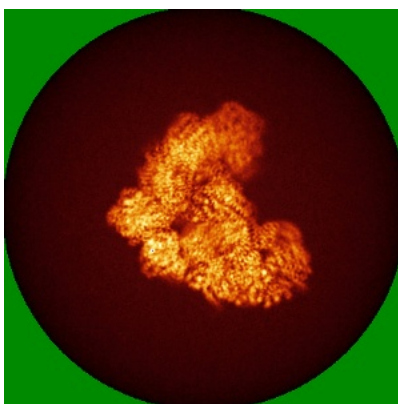
The images above show the largest variance slices of the map in three orthogonal directions.

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

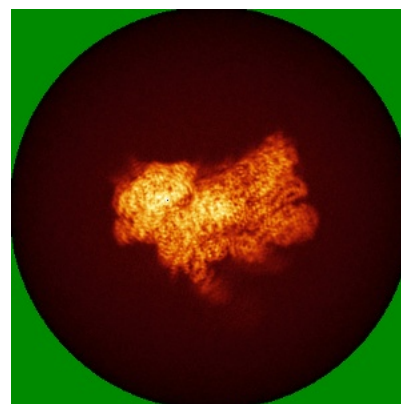
6.4.1 Primary map



X

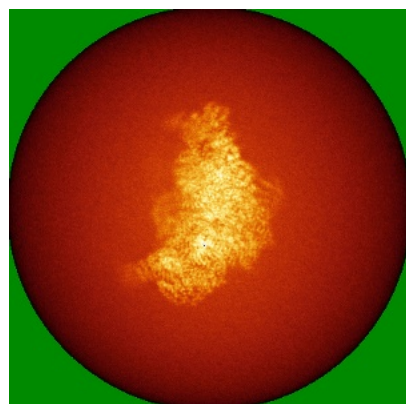


Y

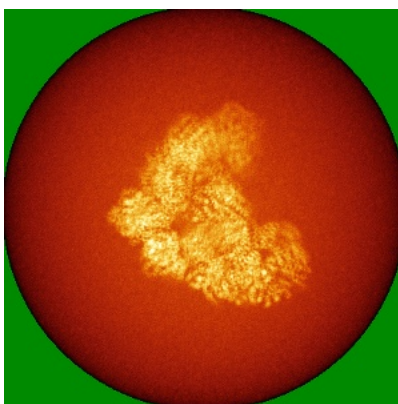


Z

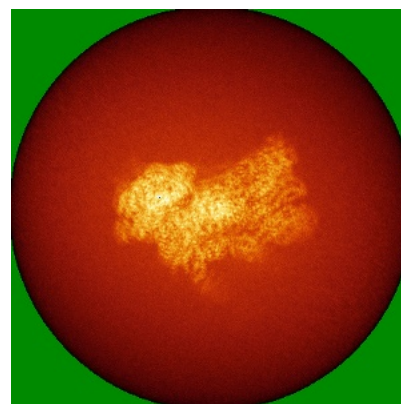
6.4.2 Raw map



X



Y

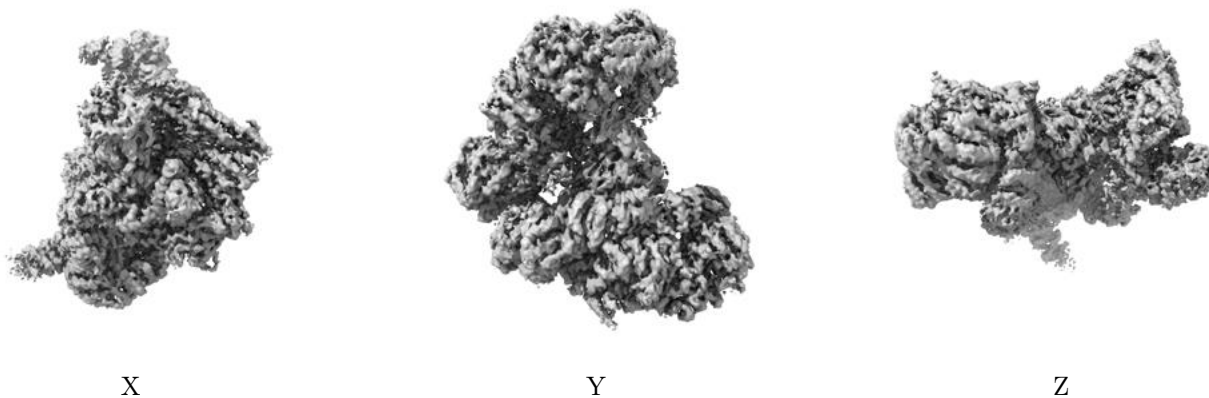


Z

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.

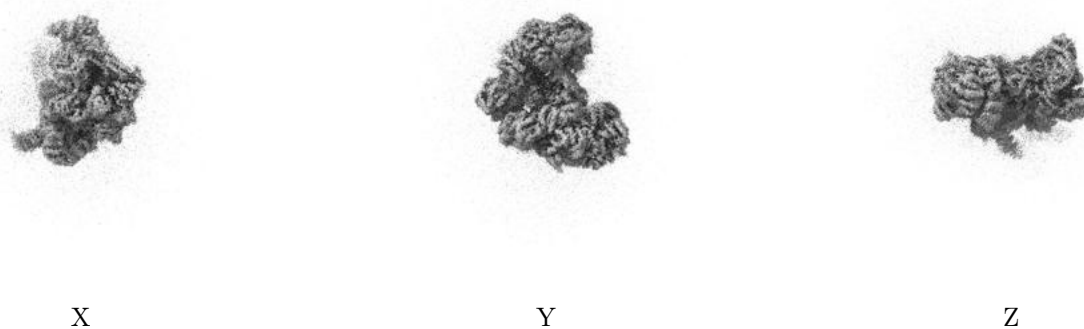
6.5 Orthogonal surface views [i](#)

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.

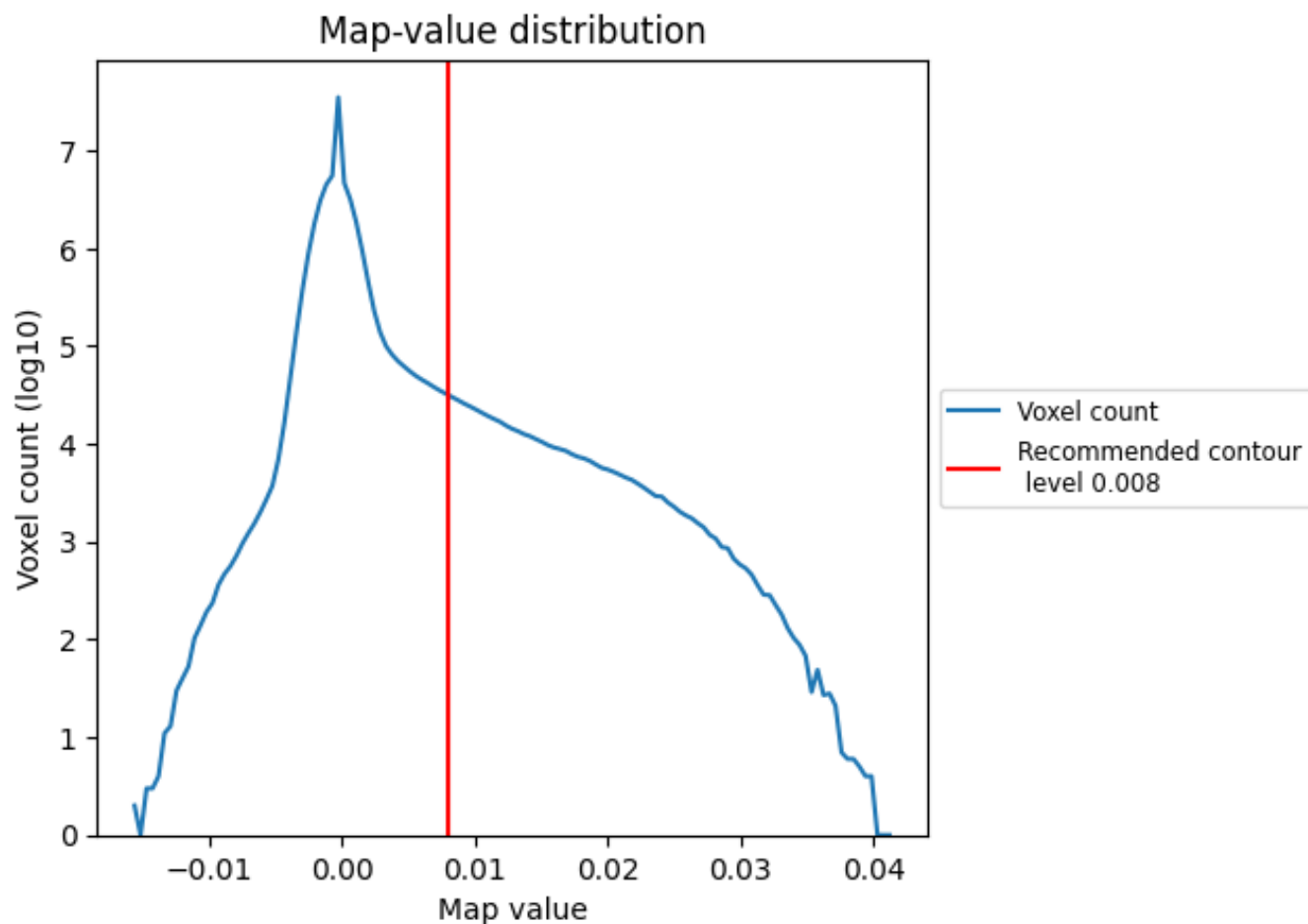
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

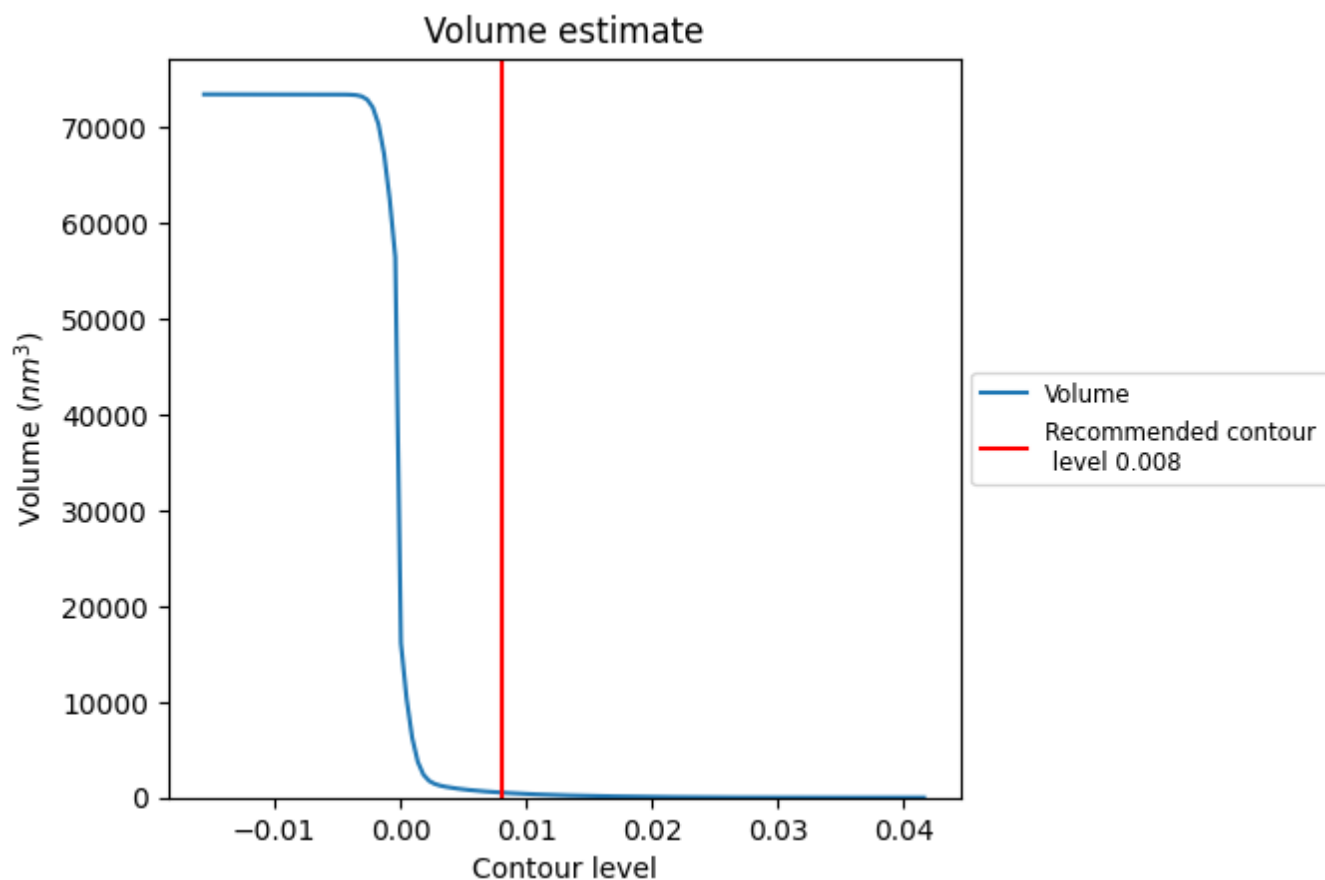
This section contains the results of statistical analysis of the map.

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.

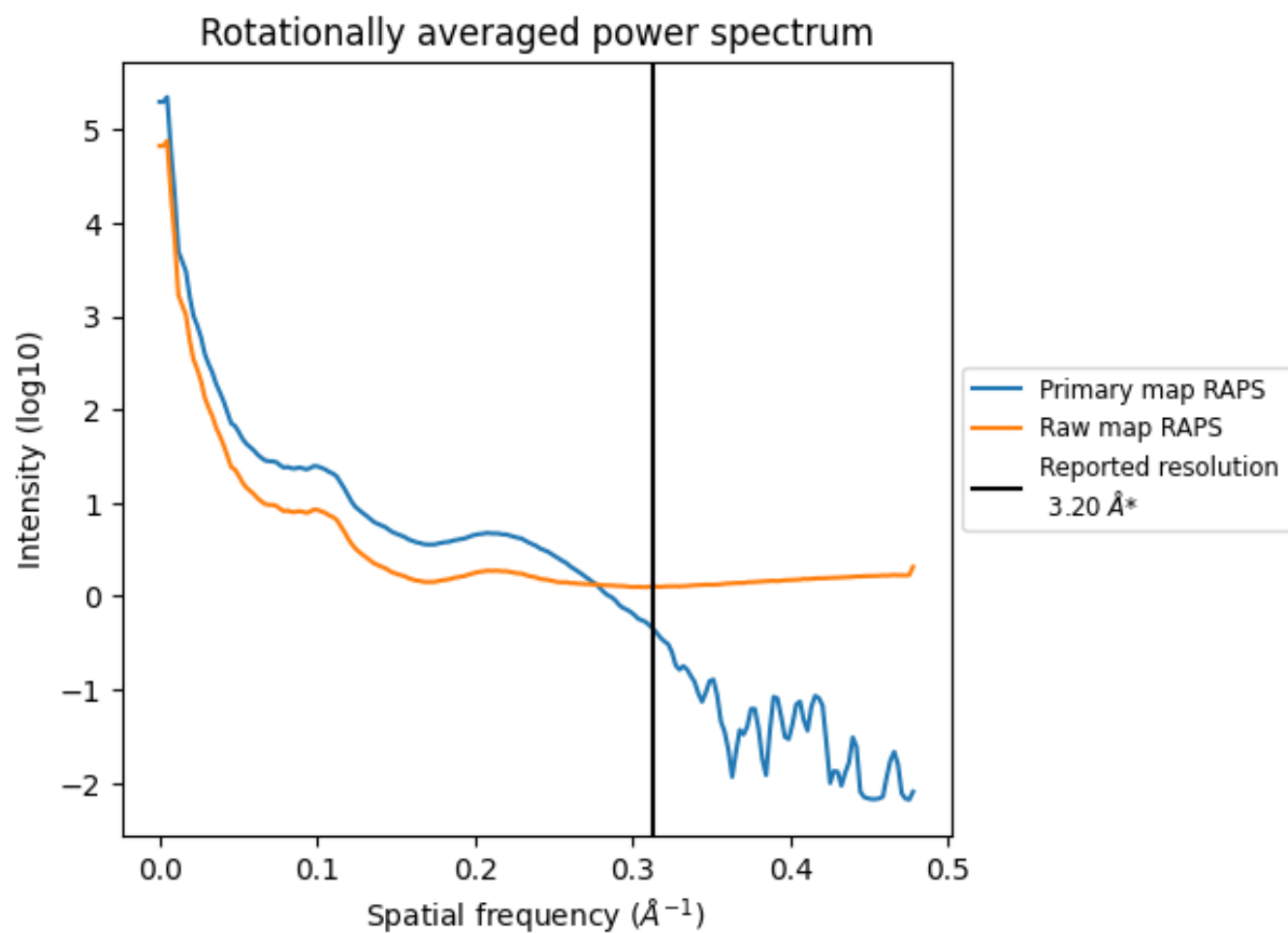
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 522 nm³; this corresponds to an approximate mass of 471 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 ⓘ

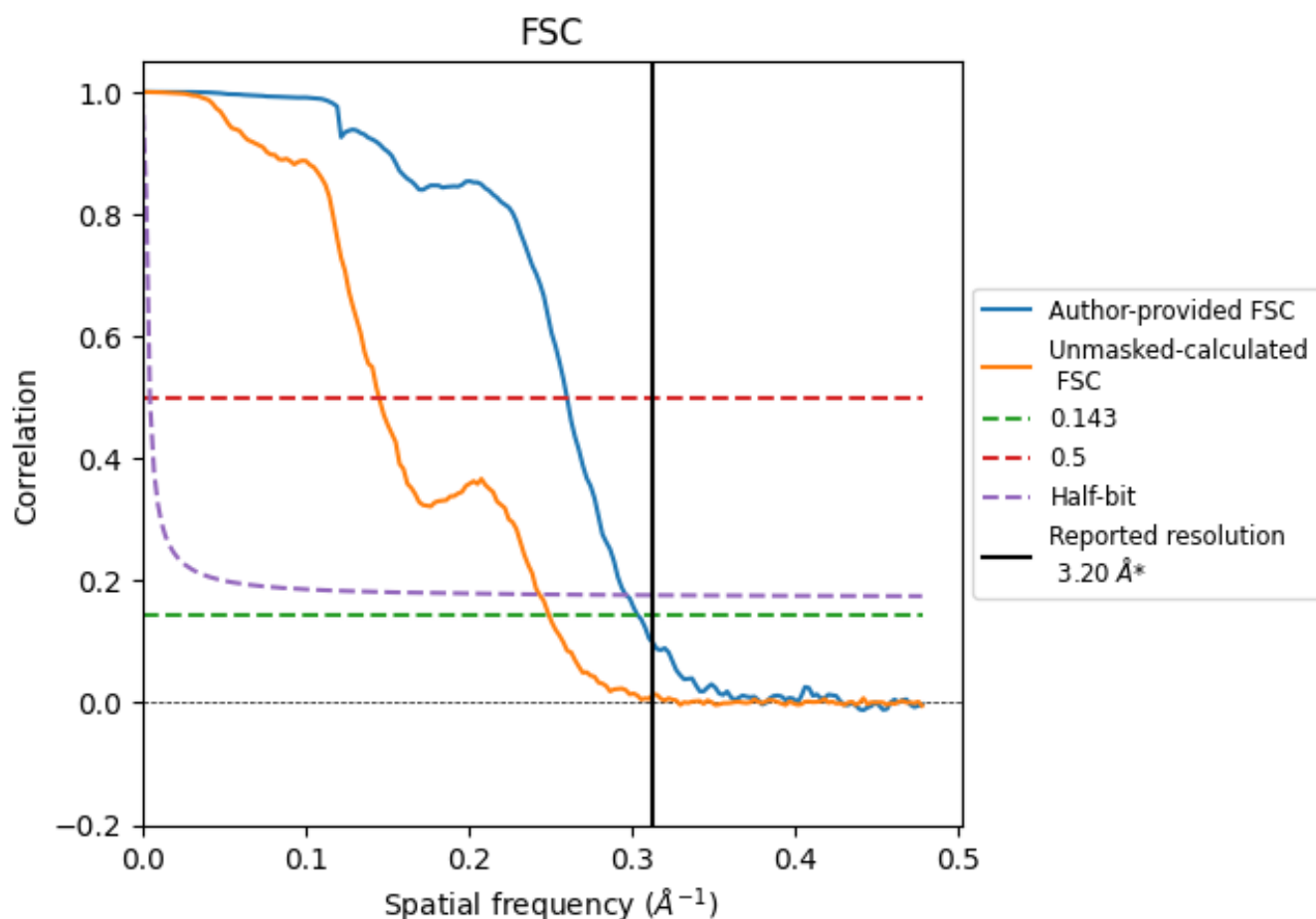


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

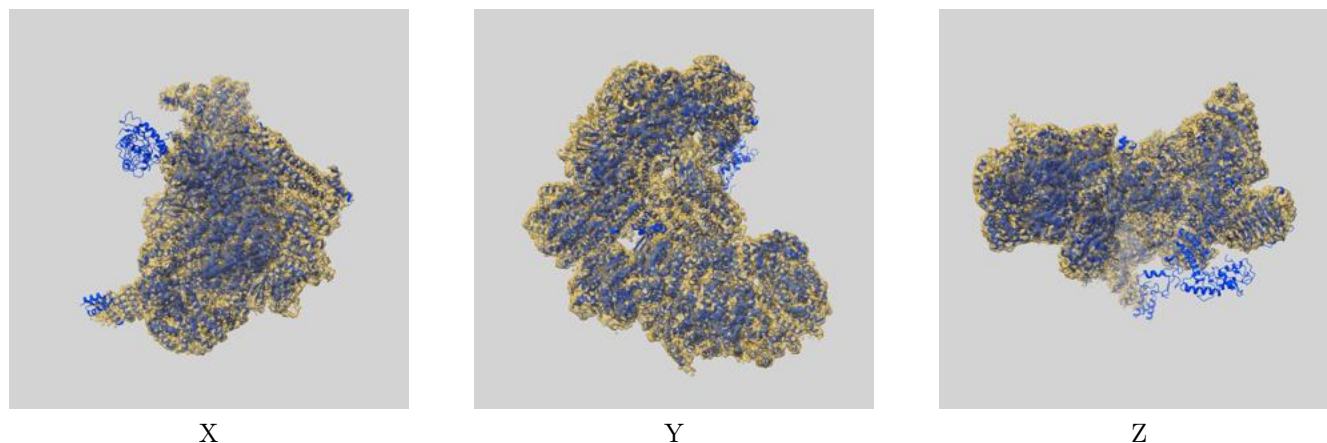
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.29	3.84	3.38
Unmasked-calculated*	4.01	6.90	4.11

*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 4.01 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

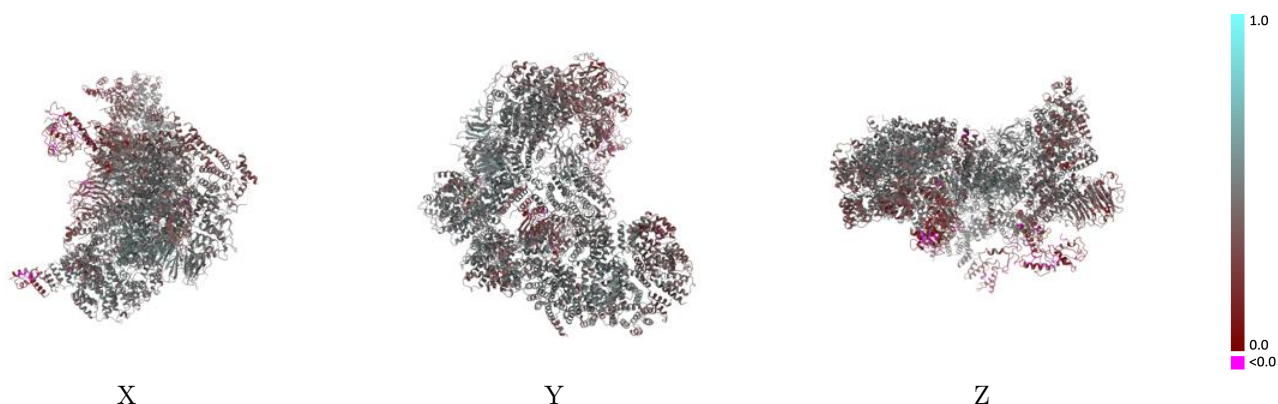
This section contains information regarding the fit between EMDB map EMD-4466 and PDB model 6Q6H. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



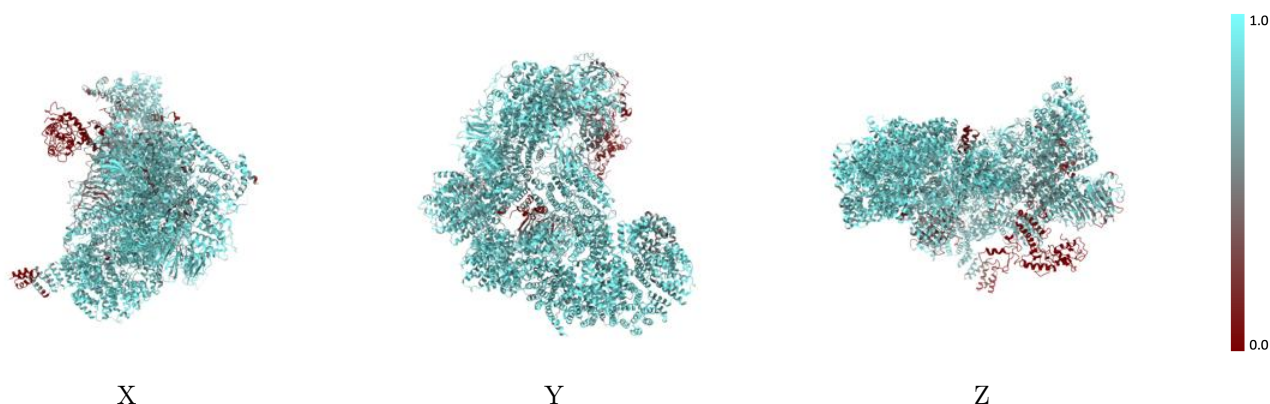
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



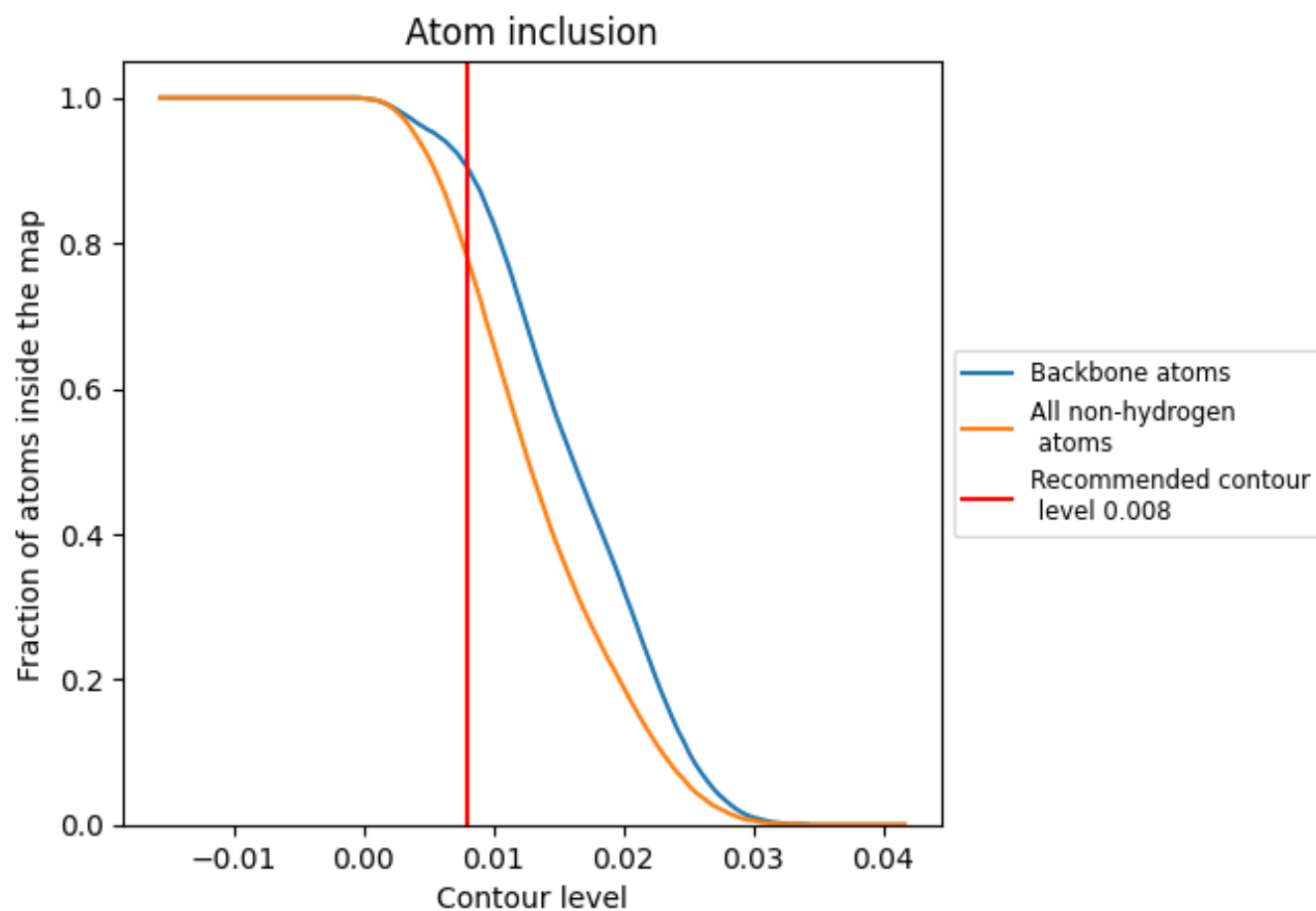
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% of all backbone atoms, 78% 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	 0.7790	 0.4340
A	 0.8380	 0.4710
C	 0.0000	 0.2030
D	 0.7780	 0.4920
G	 0.8300	 0.4860
H	 0.8740	 0.4810
I	 0.7310	 0.4020
J	 0.8680	 0.4890
K	 0.8600	 0.4600
L	 0.8470	 0.4490
M	 0.7770	 0.4970
N	 0.4380	 0.3090
O	 0.8160	 0.4750
P	 0.8940	 0.4950
Q	 0.8910	 0.4880
R	 0.6170	 0.2570
S	 0.3280	 0.2700
U	 0.8000	 0.4460
V	 0.8030	 0.4660
W	 0.7880	 0.4600
Y	 0.8440	 0.4350
Z	 0.7830	 0.3680

