



## wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 08:00 pm GMT

PDB ID : 8A3T  
EMDB ID : EMD-15123  
Title : S. cerevisiae APC/C-Cdh1 complex  
Authors : Barford, D.; Vazquez-Fernandez, E.; Zhang, Z.; Yang, J.  
Deposited on : 2022-06-09  
Resolution : 3.50 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

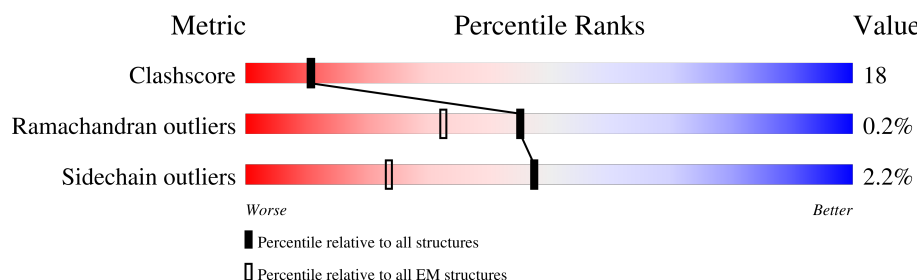
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	F	758	<div> <div>6%</div> <div>44%</div> <div>22%</div> <div>34%</div> </div>
1	H	758	<div> <div>29%</div> <div>41%</div> <div>24%</div> <div>33%</div> </div>
2	J	850	<div> <div>40%</div> <div>19%</div> <div>40%</div> </div>
2	K	850	<div> <div>7%</div> <div>35%</div> <div>23%</div> <div>41%</div> </div>
3	G	124	<div> <div>9%</div> <div>15%</div> <div>13%</div> <div>72%</div> </div>
3	W	124	<div> <div>20%</div> <div>21%</div> <div>9%</div> <div>70%</div> </div>
4	E	265	<div> <div>24%</div> <div>31%</div> <div>18%</div> <div>51%</div> </div>
5	A	250	<div> <div>33%</div> <div>50%</div> <div>37%</div> <div>12%</div> </div>

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Mol	Chain	Length	Quality of chain
6	B	566	
7	S	1518	
8	C	1748	
9	O	685	
10	D	626	
10	P	626	
11	I	170	
12	N	368	
13	Q	652	
14	T	853	
15	U	165	

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 61351 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 CDC27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	502	Total	C	N	O	S	0	0
			3991	2569	656	739	27		
1	H	505	Total	C	N	O	S	0	0
			4031	2593	664	747	27		

- Molecule 2 is a protein called Anaphase-promoting complex subunit CDC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	509	Total	C	N	O	S	0	0
			4128	2661	675	769	23		
2	K	505	Total	C	N	O	S	0	0
			4102	2642	673	764	23		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	841	LYS	-	expression tag	UNP P09798
J	842	SER	-	expression tag	UNP P09798
J	843	SER	-	expression tag	UNP P09798
J	844	ILE	-	expression tag	UNP P09798
J	845	PRO	-	expression tag	UNP P09798
J	846	GLU	-	expression tag	UNP P09798
J	847	ASN	-	expression tag	UNP P09798
J	848	LEU	-	expression tag	UNP P09798
J	849	TYR	-	expression tag	UNP P09798
J	850	PHE	-	expression tag	UNP P09798
K	841	LYS	-	expression tag	UNP P09798
K	842	SER	-	expression tag	UNP P09798
K	843	SER	-	expression tag	UNP P09798
K	844	ILE	-	expression tag	UNP P09798
K	845	PRO	-	expression tag	UNP P09798
K	846	GLU	-	expression tag	UNP P09798
K	847	ASN	-	expression tag	UNP P09798

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Chain	Residue	Modelled	Actual	Comment	Reference
K	848	LEU	-	expression tag	UNP P09798
K	849	TYR	-	expression tag	UNP P09798
K	850	PHE	-	expression tag	UNP P09798

- Molecule 3 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	35	Total	C	N	O	S	0	0
			284	174	51	58	1		
3	W	37	Total	C	N	O	S	0	0
			300	184	54	61	1		

- Molecule 4 is a protein called Anaphase-promoting complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	130	Total	C	N	O	S	0	0
			1091	678	201	205	7		

- Molecule 5 is a protein called Anaphase-promoting complex subunit DOC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	219	Total	C	N	O	S	0	0
			1743	1118	304	311	10		

- Molecule 6 is a protein called CDH1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	440	Total	C	N	O	S	0	0
			3418	2143	602	660	13		

- Molecule 7 is a protein called HSL1 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	S	6	Total	C	N	O	0	0
			45	27	7	11		

- Molecule 8 is a protein called Anaphase-promoting complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	1410	Total	C	N	O	S	0	0
			10863	7023	1756	2038	46		

- Molecule 9 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	658	Total	C	N	O	S	0	0
			5288	3402	869	990	27		

- Molecule 10 is a protein called Anaphase-promoting complex subunit CDC23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	560	Total	C	N	O	S	0	0
			4524	2925	729	844	26		
10	P	556	Total	C	N	O	S	0	0
			4518	2922	738	831	27		

- Molecule 11 is a protein called Anaphase-promoting complex subunit SWM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	111	Total	C	N	O	S	0	0
			906	568	158	176	4		

- Molecule 12 is a protein called Anaphase-promoting complex subunit MND2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	96	Total	C	N	O	S	0	0
			784	504	138	139	3		

- Molecule 13 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	623	Total	C	N	O	S	0	0
			5083	3278	842	950	13		

- Molecule 14 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	645	Total	C	N	O	S	0	0
			5337	3466	871	976	24		

- Molecule 15 is a protein called Anaphase-promoting complex subunit 11.

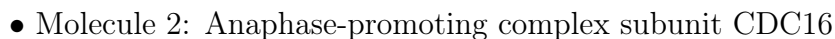
Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	114	Total	C	N	O	S	0	0
			912	574	164	162	12		

- Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

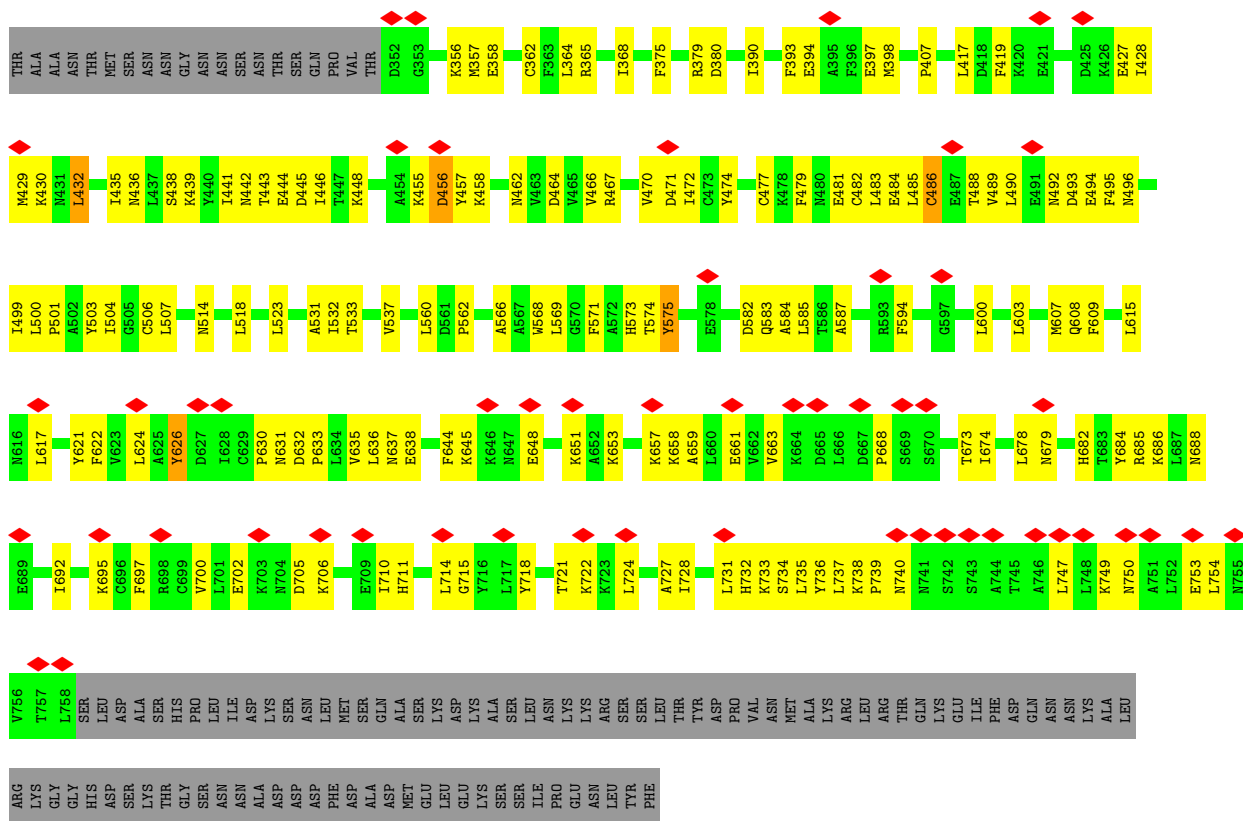
Mol	Chain	Residues	Atoms		AltConf
16	U	3	Total 3	Zn 3	0



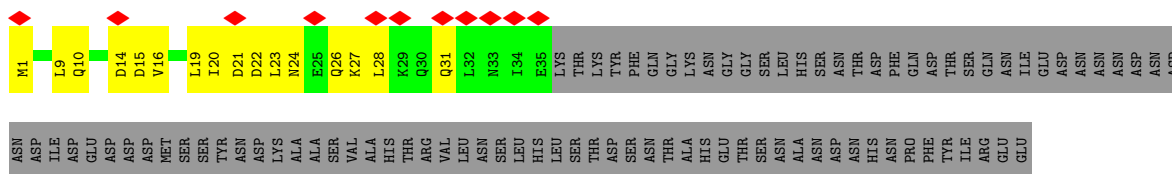




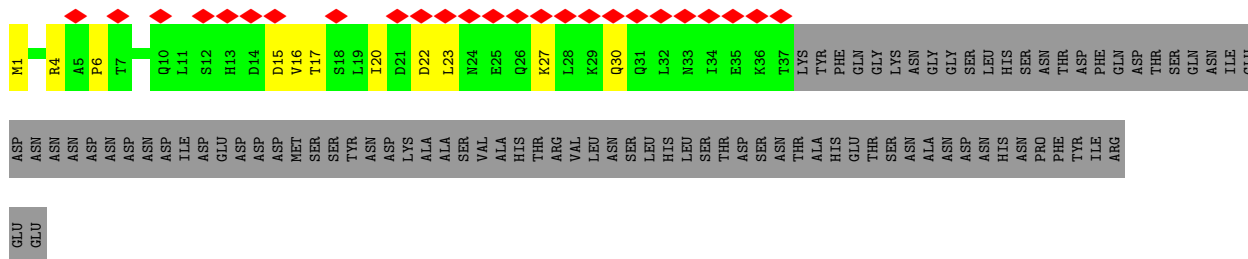




- Molecule 3: Anaphase-promoting complex subunit CDC26

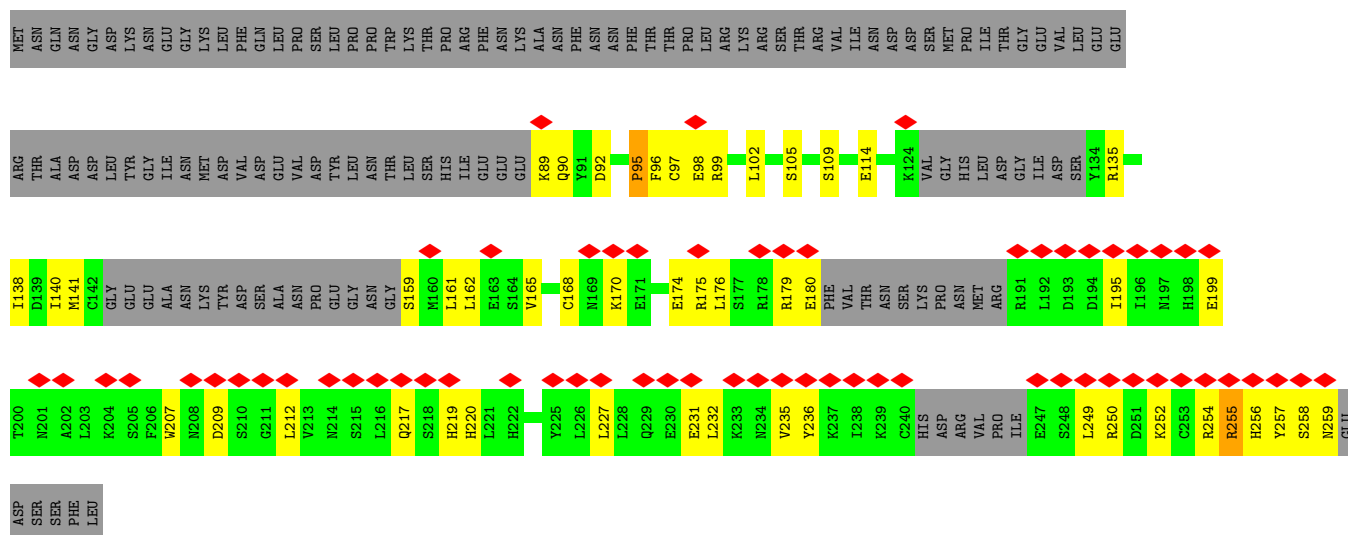


- Molecule 3: Anaphase-promoting complex subunit CDC26



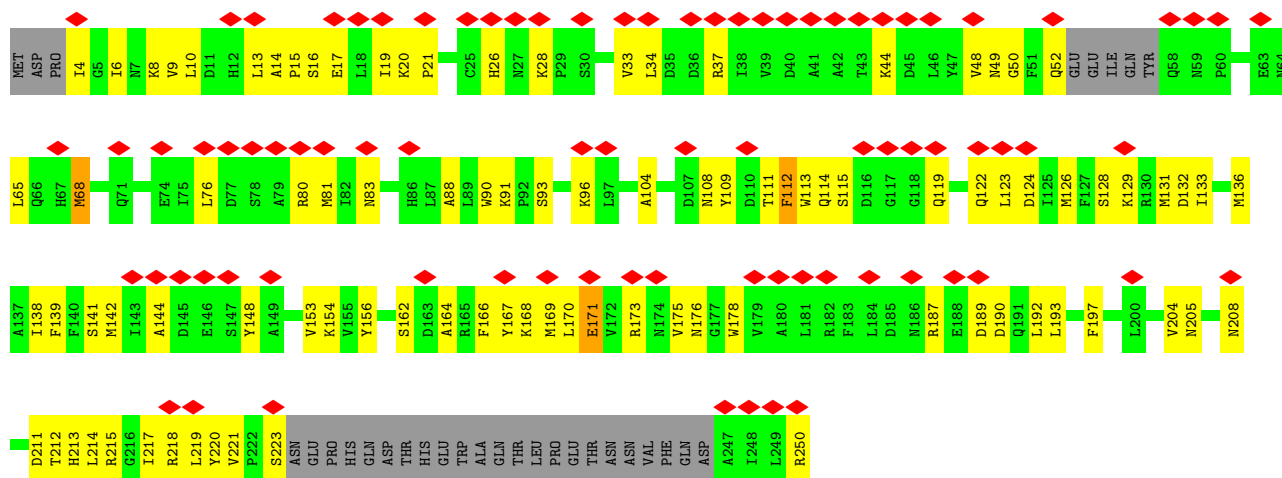
- Molecule 4: Anaphase-promoting complex subunit 9





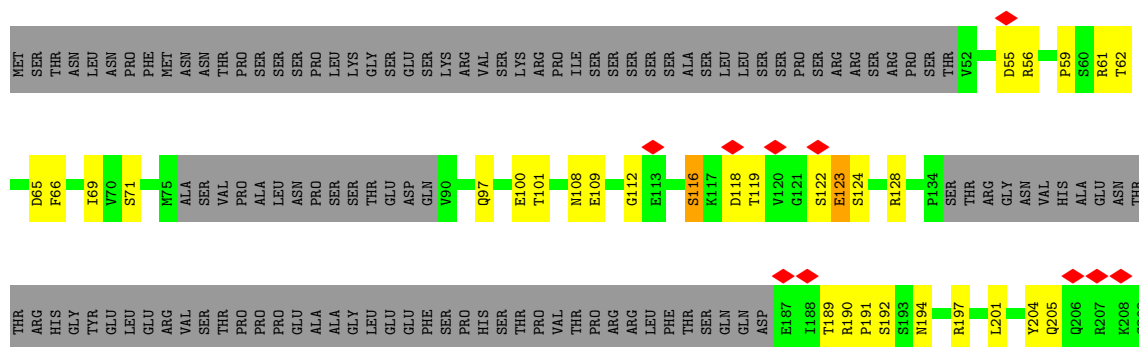
• Molecule 5: Anaphase-promoting complex subunit DOC1

Chain A: 33% 50% 37% 12%



• Molecule 6: CDH1 isoform 1

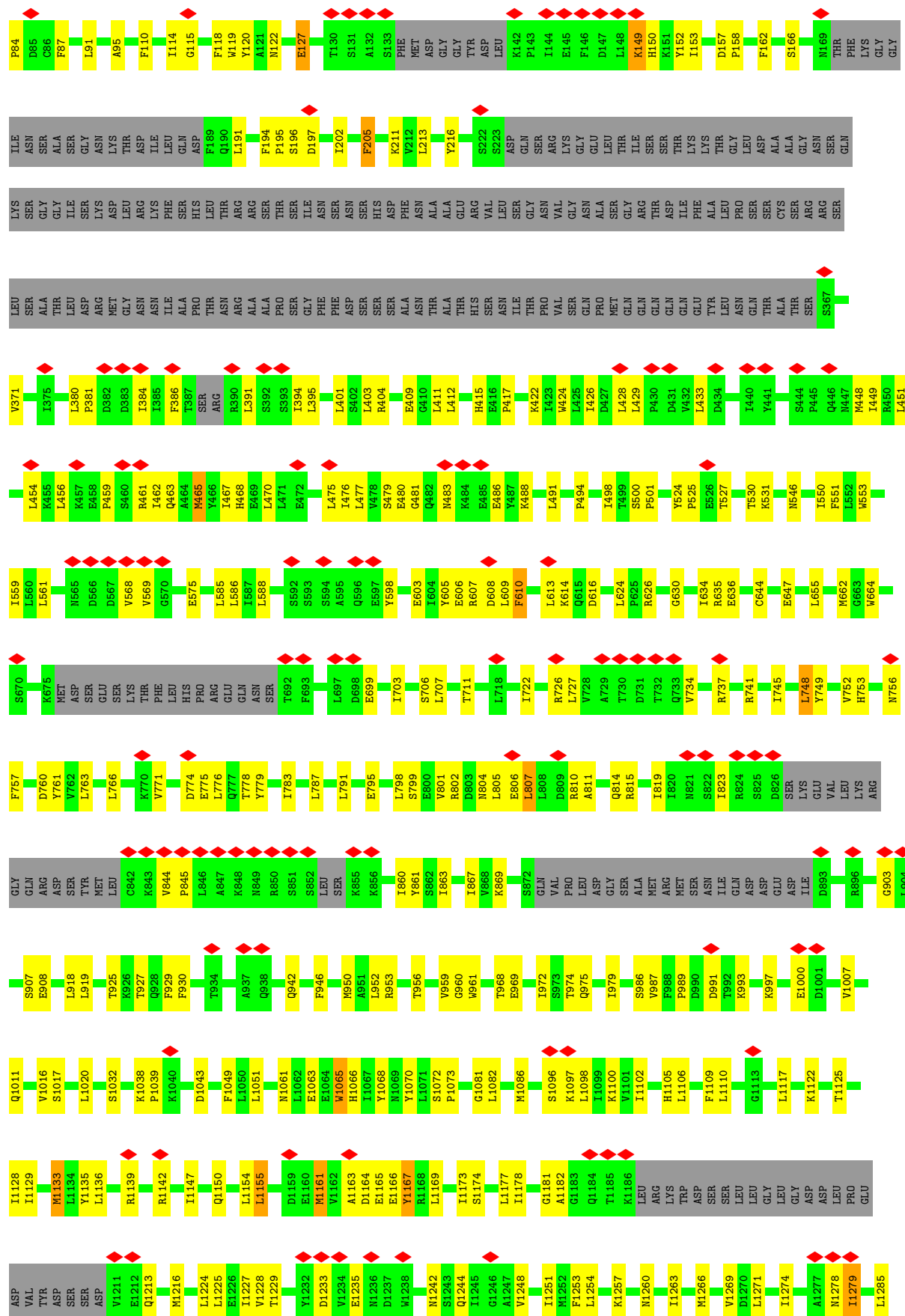
Chain B: 49% 46% 31% 22%





- Molecule 8: Anaphase-promoting complex subunit 1

MET	THR	SER	LYS	PRO	SER	THR	ARG	ASN	ASP	TYR	LEU	PRO	ARG	GLU	THR	HIS	ASN	GLY	GLU	TYR	THR	GLY	ASP	SER	PRO	E27	I32	N33	I34	T35	I38	G39	S48	R49	D50	V54	I58	E59	R64	Y68	I72	A75	G76	Y77	I78	D79	F80	E81	K82
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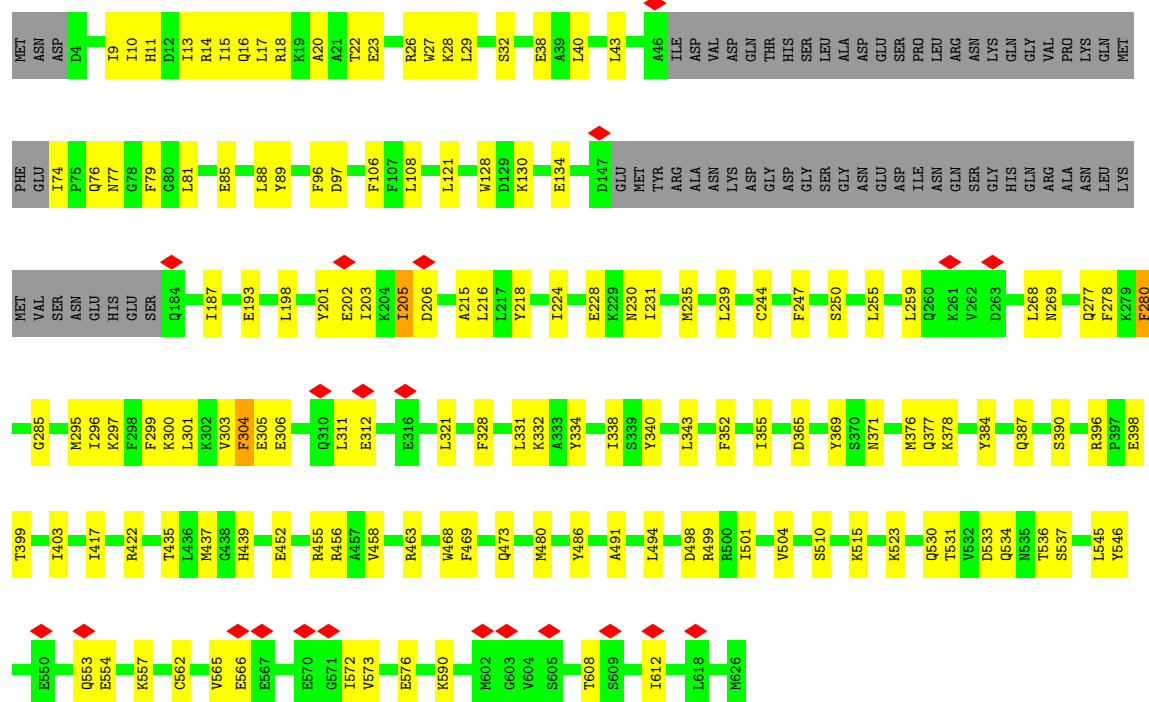






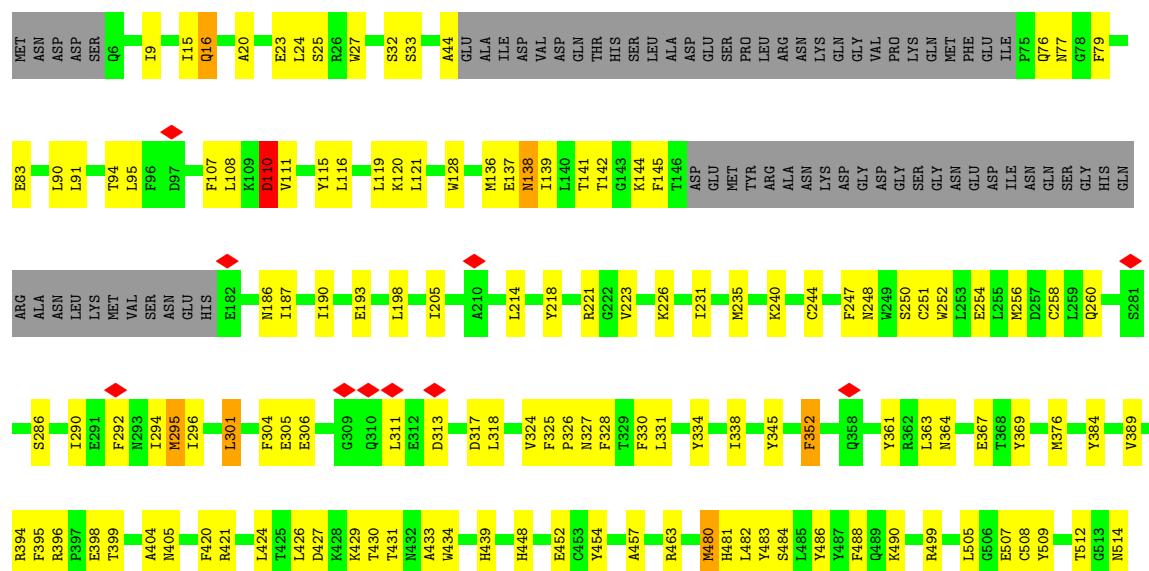
• Molecule 10: Anaphase-promoting complex subunit CDC23

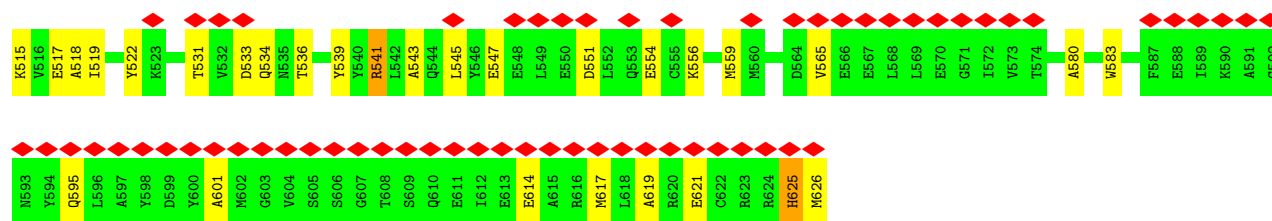
Chain D: 67% 22% 11%



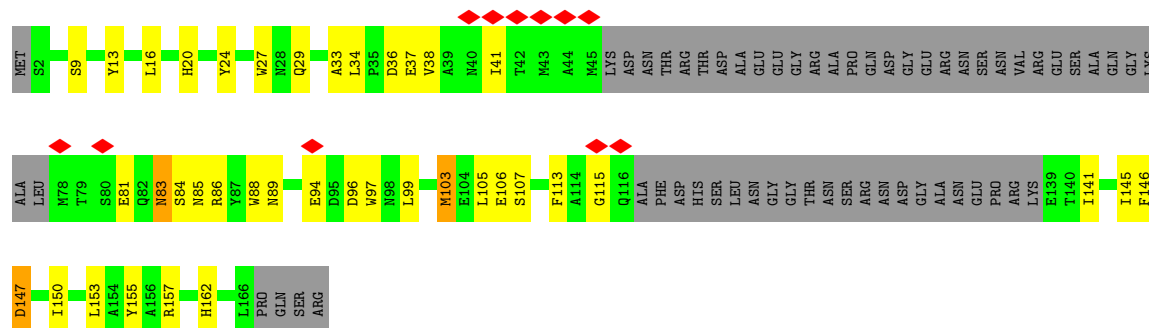
• Molecule 10: Anaphase-promoting complex subunit CDC23

Chain P: 12% 63% 24% 1%

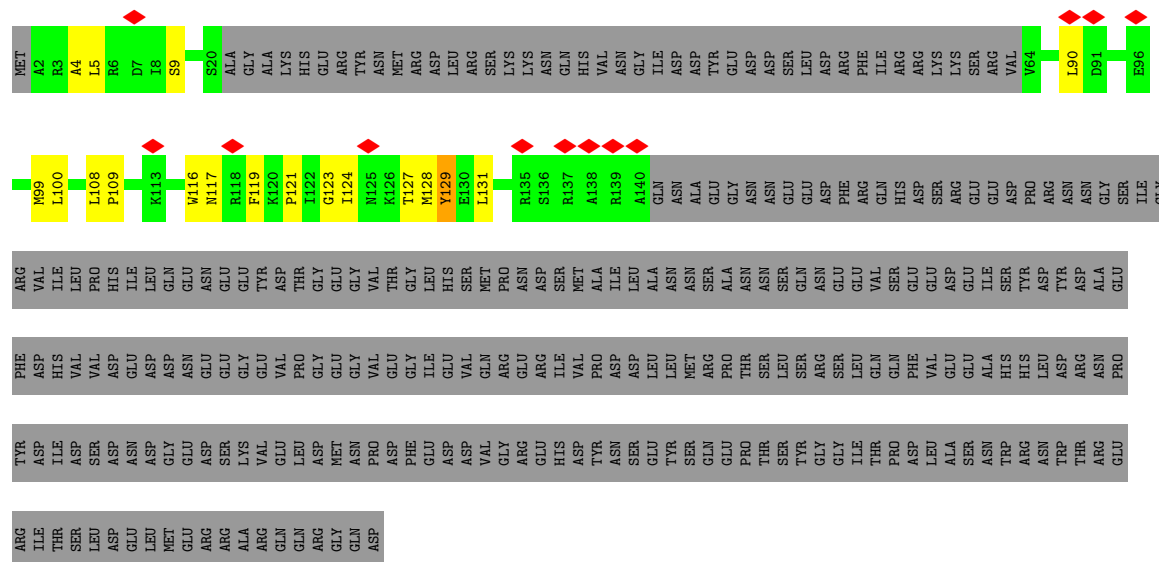




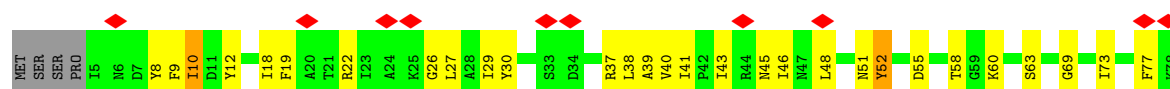
• Molecule 11: Anaphase-promoting complex subunit SWM1

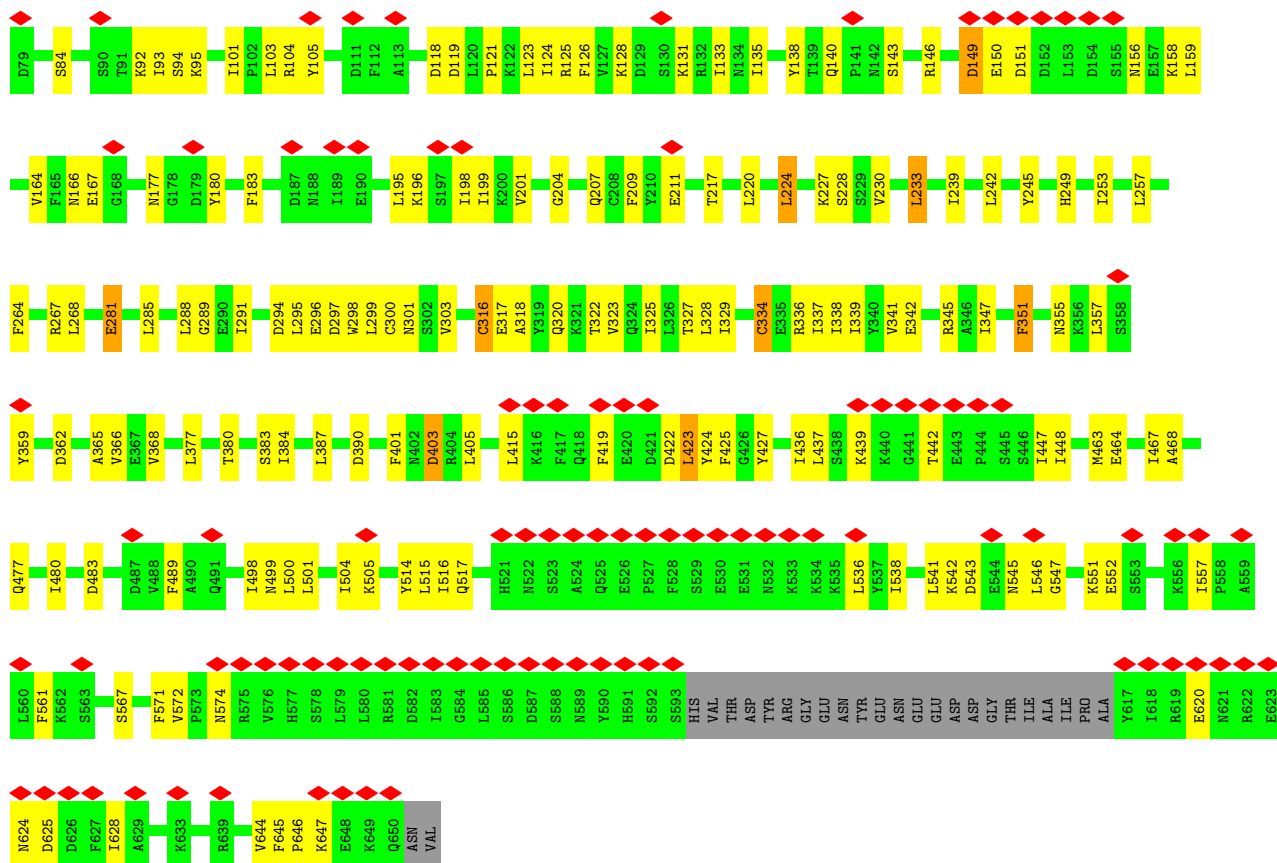


• Molecule 12: Anaphase-promoting complex subunit MND2

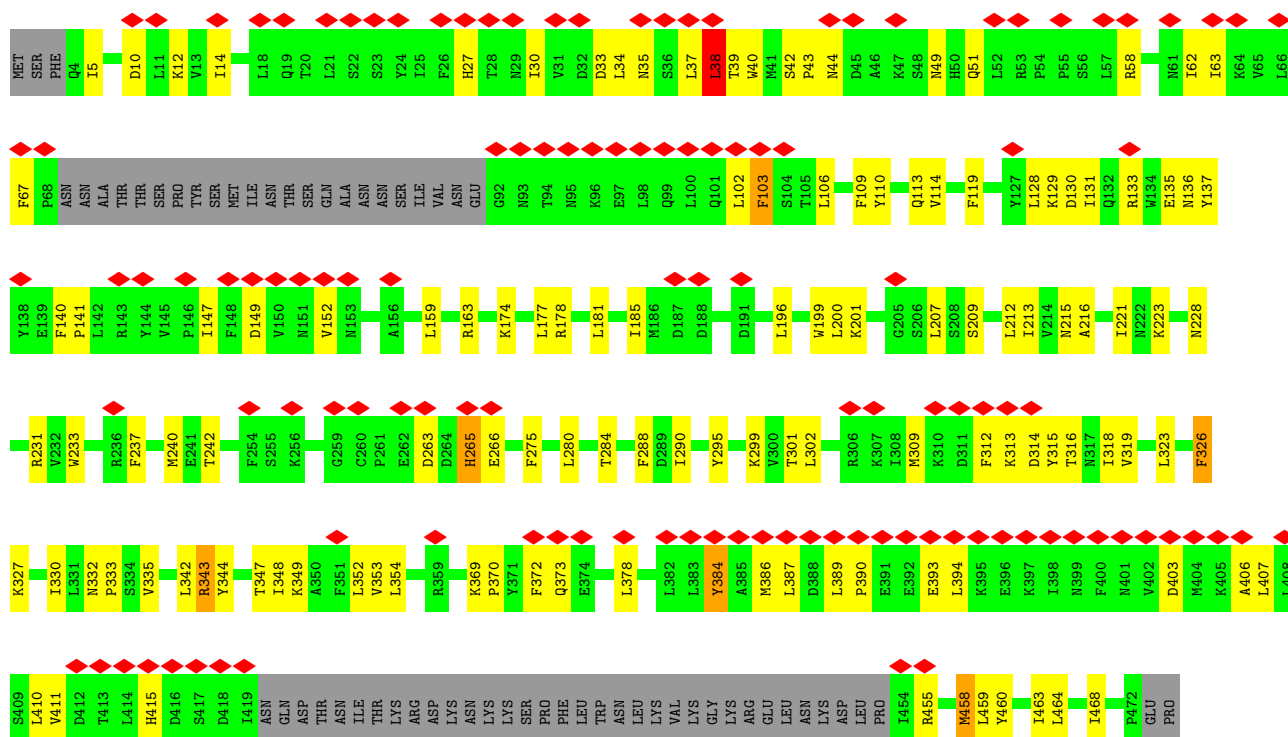
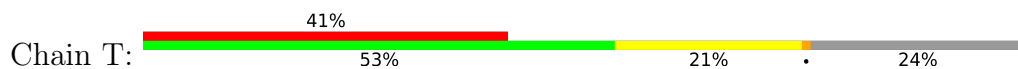


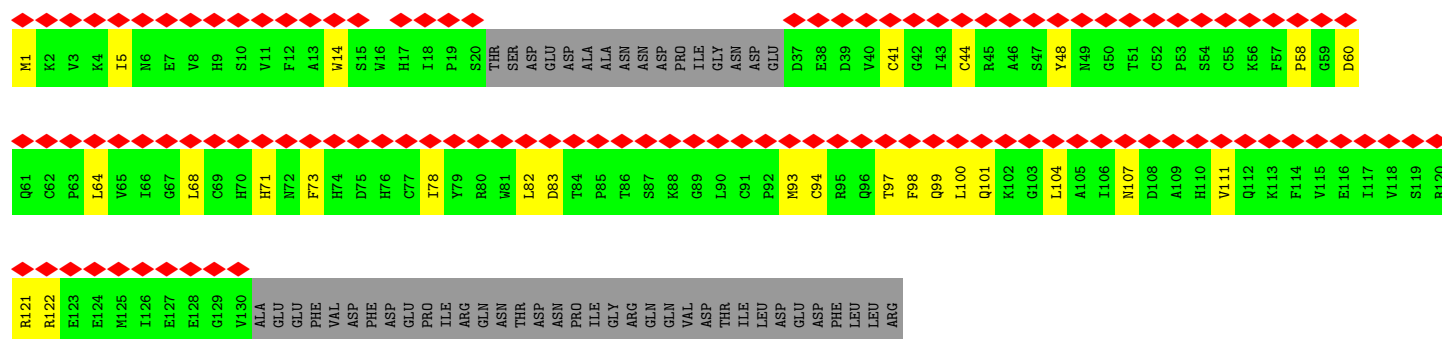
• Molecule 13: Anaphase-promoting complex subunit 4





• Molecule 14: Anaphase-promoting complex subunit 2





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	249193	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	59	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.287	Depositor
Minimum map value	-0.161	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size ( $\text{\AA}$ )	353.28, 353.28, 353.28	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.38, 1.38, 1.38	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	F	0.27	0/4079	0.53	1/5525 (0.0%)
1	H	0.27	0/4118	0.50	0/5574
2	J	0.28	0/4214	0.51	0/5692
2	K	0.30	0/4188	0.52	0/5657
3	G	0.28	0/285	0.68	0/384
3	W	0.25	0/301	0.59	0/405
4	E	0.75	1/1108 (0.1%)	0.73	2/1481 (0.1%)
5	A	0.25	0/1785	0.55	1/2418 (0.0%)
6	B	0.27	0/3487	0.53	0/4730
7	S	0.21	0/44	0.39	0/59
8	C	0.26	0/11088	0.50	3/15080 (0.0%)
9	O	0.27	0/5387	0.47	0/7291
10	D	0.26	0/4621	0.44	0/6243
10	P	0.28	0/4616	0.50	2/6228 (0.0%)
11	I	0.29	0/930	0.64	1/1263 (0.1%)
12	N	0.28	0/800	0.55	0/1076
13	Q	0.25	0/5190	0.49	0/7020
14	T	0.32	2/5455 (0.0%)	0.61	5/7387 (0.1%)
15	U	0.25	0/936	0.49	0/1265
All	All	0.29	3/62632 (0.0%)	0.52	15/84778 (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
1	H	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	95	PRO	N-CD	23.35	1.80	1.47
14	T	650	PRO	CB-CG	-11.48	0.92	1.50
14	T	650	PRO	CG-CD	-6.54	1.29	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	T	650	PRO	CB-CG-CD	18.83	179.94	106.50
14	T	650	PRO	N-CD-CG	-18.79	75.01	103.20
4	E	95	PRO	CA-N-CD	-16.35	88.61	111.50
14	T	650	PRO	CA-CB-CG	-15.95	73.70	104.00
14	T	650	PRO	CA-N-CD	-9.06	98.81	111.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	635	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3991	0	3947	171	0
1	H	4031	0	4003	204	0
2	J	4128	0	4096	176	0
2	K	4102	0	4065	230	0
3	G	284	0	293	20	0
3	W	300	0	313	17	0
4	E	1091	0	1058	67	0
5	A	1743	0	1714	82	0
6	B	3418	0	3307	184	0
7	S	45	0	43	1	0
8	C	10863	0	10672	373	0
9	O	5288	0	5299	176	0
10	D	4524	0	4391	132	0
10	P	4518	0	4410	189	0
11	I	906	0	813	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	N	784	0	784	20	0
13	Q	5083	0	5093	155	0
14	T	5337	0	5314	226	0
15	U	912	0	873	28	0
16	U	3	0	0	0	0
All	All	61351	0	60488	2228	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 18.

The worst 5 of 2228 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)
9:O:431:LEU:HD13	9:O:472:TYR:CZ	1.16	1.65
6:B:190:ARG:HB2	11:I:97:TRP:CZ3	1.32	1.62
10:P:27:TRP:CH2	10:P:115:TYR:CE1	1.85	1.61
9:O:170:TRP:CZ3	9:O:174:GLN:HG3	1.32	1.61
10:P:301:LEU:HD22	10:P:334:TYR:CE2	1.33	1.57

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	F	496/758 (65%)	475 (96%)	21 (4%)	0	100	100
1	H	499/758 (66%)	481 (96%)	16 (3%)	2 (0%)	30	64
2	J	505/850 (59%)	487 (96%)	18 (4%)	0	100	100
2	K	501/850 (59%)	488 (97%)	13 (3%)	0	100	100
3	G	33/124 (27%)	32 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	W	35/124 (28%)	35 (100%)	0	0	100	100
4	E	120/265 (45%)	119 (99%)	1 (1%)	0	100	100
5	A	213/250 (85%)	201 (94%)	11 (5%)	1 (0%)	25	59
6	B	432/566 (76%)	404 (94%)	27 (6%)	1 (0%)	44	75
7	S	4/1518 (0%)	3 (75%)	1 (25%)	0	100	100
8	C	1384/1748 (79%)	1299 (94%)	81 (6%)	4 (0%)	37	68
9	O	654/685 (96%)	625 (96%)	25 (4%)	4 (1%)	22	56
10	D	554/626 (88%)	540 (98%)	13 (2%)	1 (0%)	44	75
10	P	550/626 (88%)	530 (96%)	20 (4%)	0	100	100
11	I	105/170 (62%)	98 (93%)	7 (7%)	0	100	100
12	N	92/368 (25%)	89 (97%)	3 (3%)	0	100	100
13	Q	619/652 (95%)	596 (96%)	22 (4%)	1 (0%)	44	75
14	T	631/853 (74%)	620 (98%)	11 (2%)	0	100	100
15	U	110/165 (67%)	107 (97%)	3 (3%)	0	100	100
All	All	7537/11956 (63%)	7229 (96%)	294 (4%)	14 (0%)	45	75

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	C	844	VAL
8	C	1279	ILE
9	O	193	VAL
10	D	205	ILE
1	H	507	LYS

### 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	F	433/684 (63%)	429 (99%)	4 (1%)	75	86
1	H	439/684 (64%)	428 (98%)	11 (2%)	42	67

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	451/760 (59%)	443 (98%)	8 (2%)	54	74
2	K	448/760 (59%)	434 (97%)	14 (3%)	35	63
3	G	34/115 (30%)	33 (97%)	1 (3%)	37	64
3	W	36/115 (31%)	35 (97%)	1 (3%)	38	65
4	E	123/246 (50%)	120 (98%)	3 (2%)	44	68
5	A	190/226 (84%)	185 (97%)	5 (3%)	41	66
6	B	375/503 (75%)	362 (96%)	13 (4%)	31	59
7	S	6/1389 (0%)	6 (100%)	0	100	100
8	C	1180/1568 (75%)	1161 (98%)	19 (2%)	58	76
9	O	598/643 (93%)	583 (98%)	15 (2%)	42	67
10	D	477/560 (85%)	473 (99%)	4 (1%)	79	88
10	P	476/560 (85%)	464 (98%)	12 (2%)	42	67
11	I	95/144 (66%)	91 (96%)	4 (4%)	25	54
12	N	83/332 (25%)	82 (99%)	1 (1%)	67	82
13	Q	571/598 (96%)	555 (97%)	16 (3%)	38	65
14	T	605/804 (75%)	589 (97%)	16 (3%)	41	66
15	U	103/149 (69%)	103 (100%)	0	100	100
All	All	6723/10840 (62%)	6576 (98%)	147 (2%)	47	70

5 of 147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	Q	52	TYR
14	T	492	PHE
13	Q	281	GLU
13	Q	546	LEU
6	B	222	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
8	C	1543	HIS
10	D	77	ASN
13	Q	355	ASN
9	O	372	ASN

*Continued on next page...*

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Mol	Chain	Res	Type
10	D	371	ASN

### 5.3.3 RNA [i](#)

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](#)

Of 3 ligands modelled in this entry, 3 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.

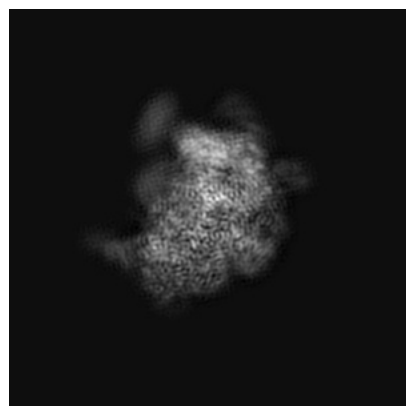
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15123. These allow visual inspection of the internal detail of the map and identification of artifacts.

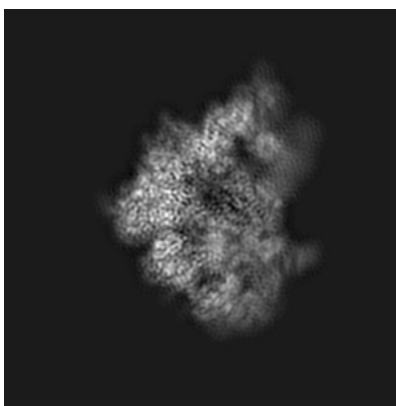
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

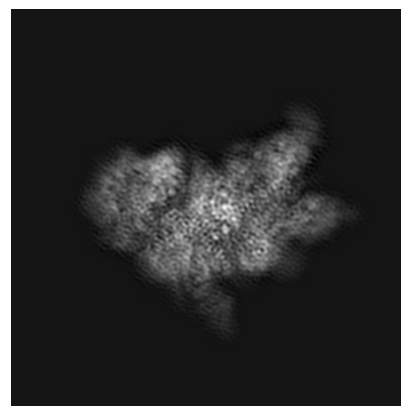
#### 6.1.1 Primary map



X

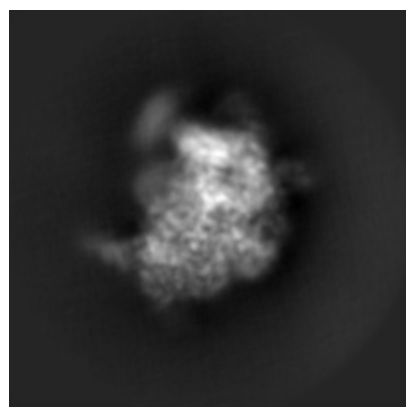


Y

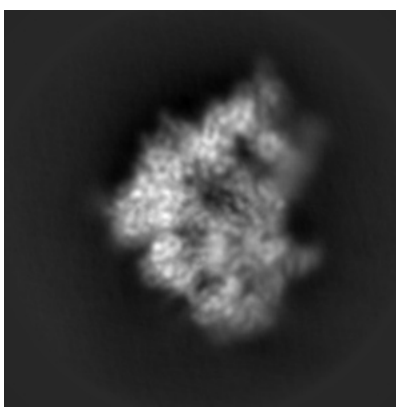


Z

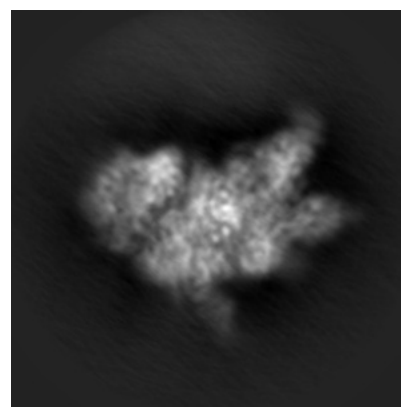
#### 6.1.2 Raw map



X



Y

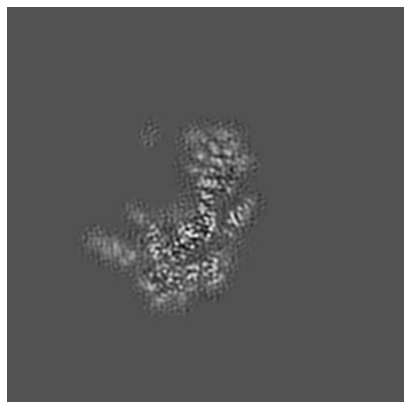


Z

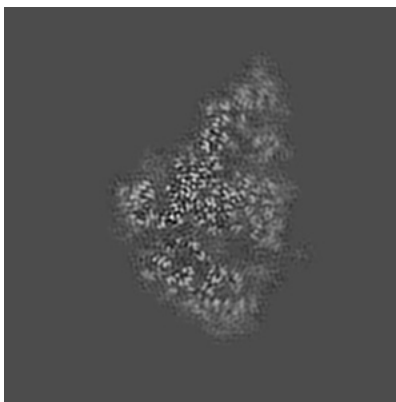
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

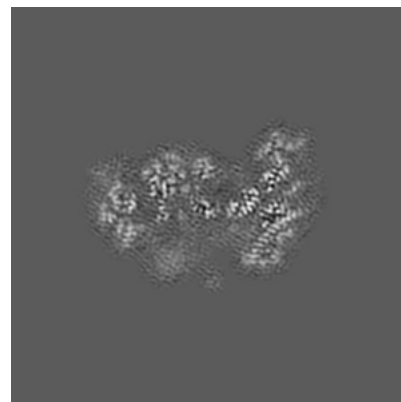
### 6.2.1 Primary map



X Index: 128

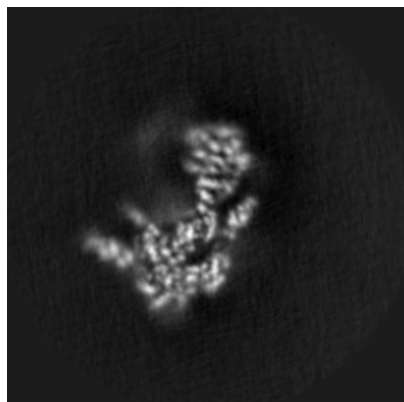


Y Index: 128

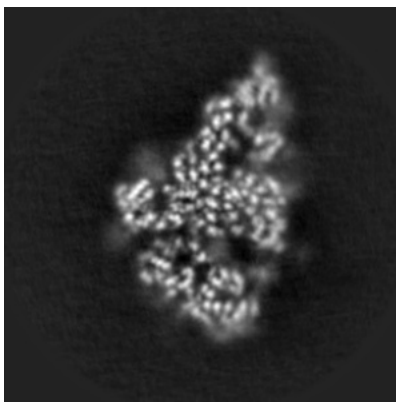


Z Index: 128

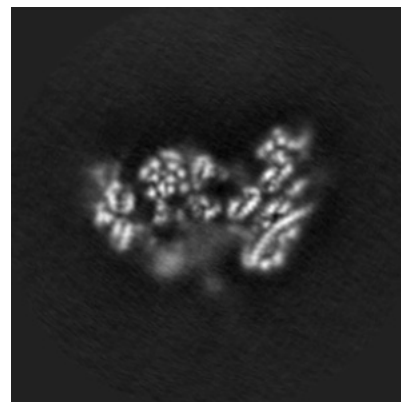
### 6.2.2 Raw map



X Index: 128



Y Index: 128

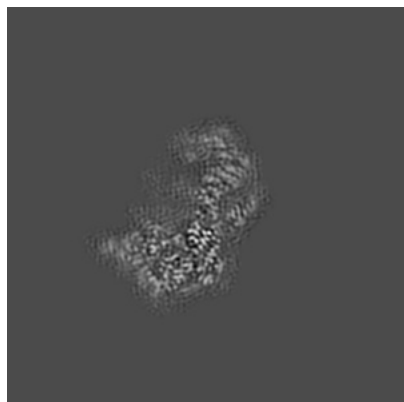


Z Index: 128

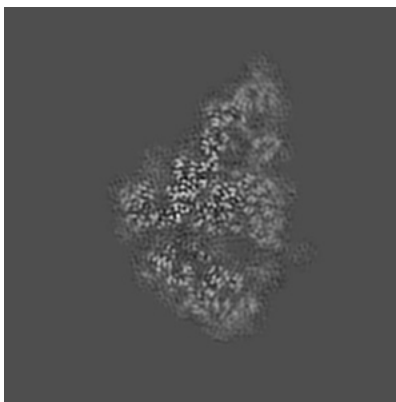
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

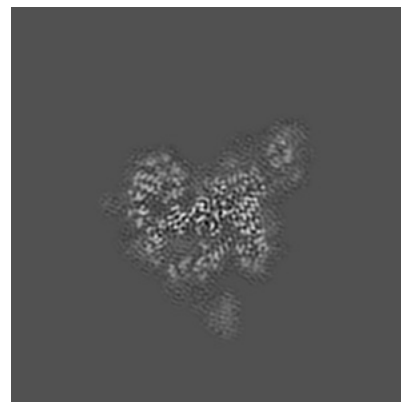
### 6.3.1 Primary map



X Index: 122

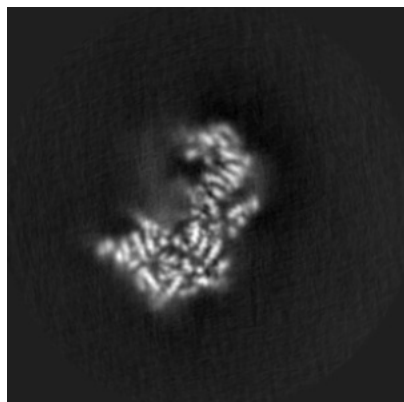


Y Index: 129

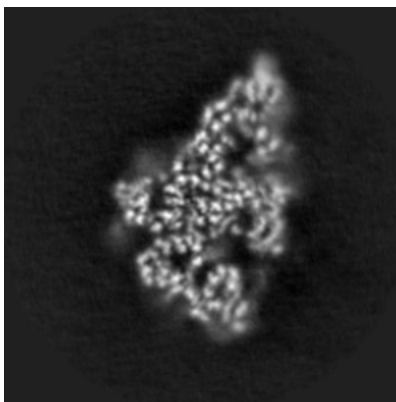


Z Index: 111

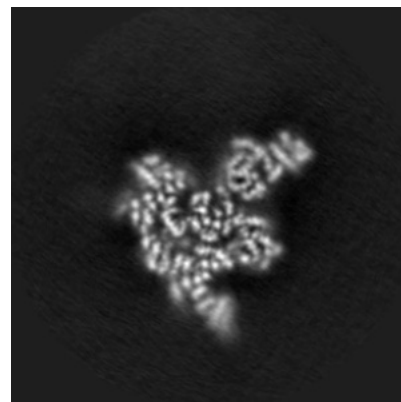
### 6.3.2 Raw map



X Index: 123



Y Index: 125

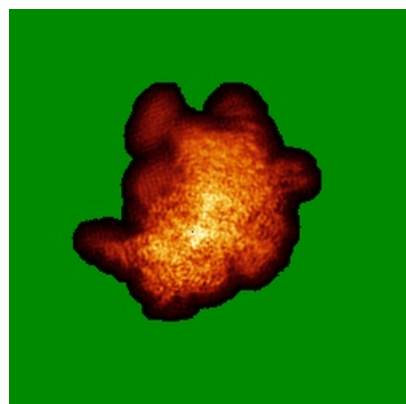


Z Index: 104

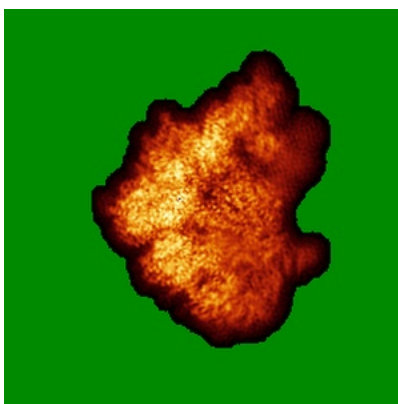
The images above show the largest variance slices of the map in three orthogonal directions.

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

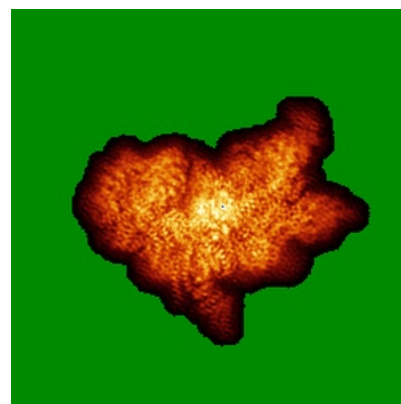
### 6.4.1 Primary map



X

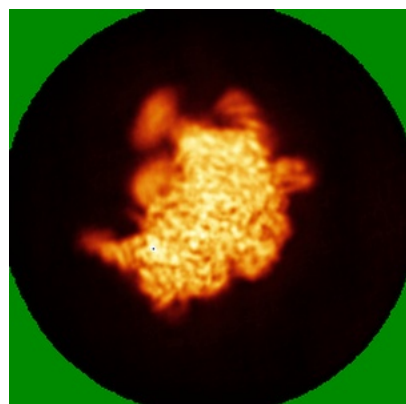


Y

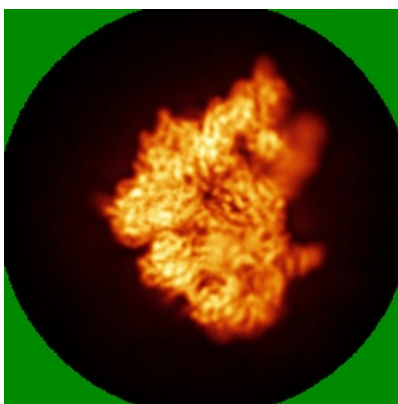


Z

### 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.

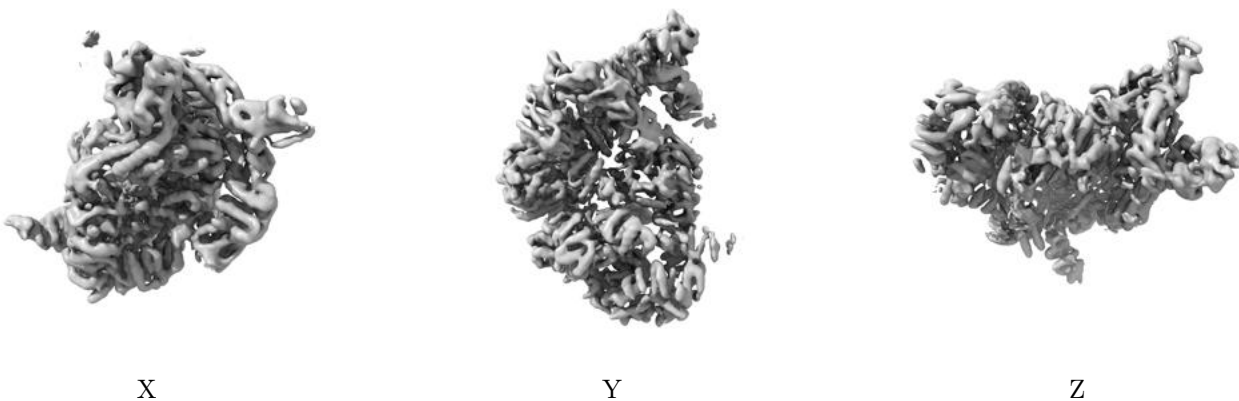
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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](#)

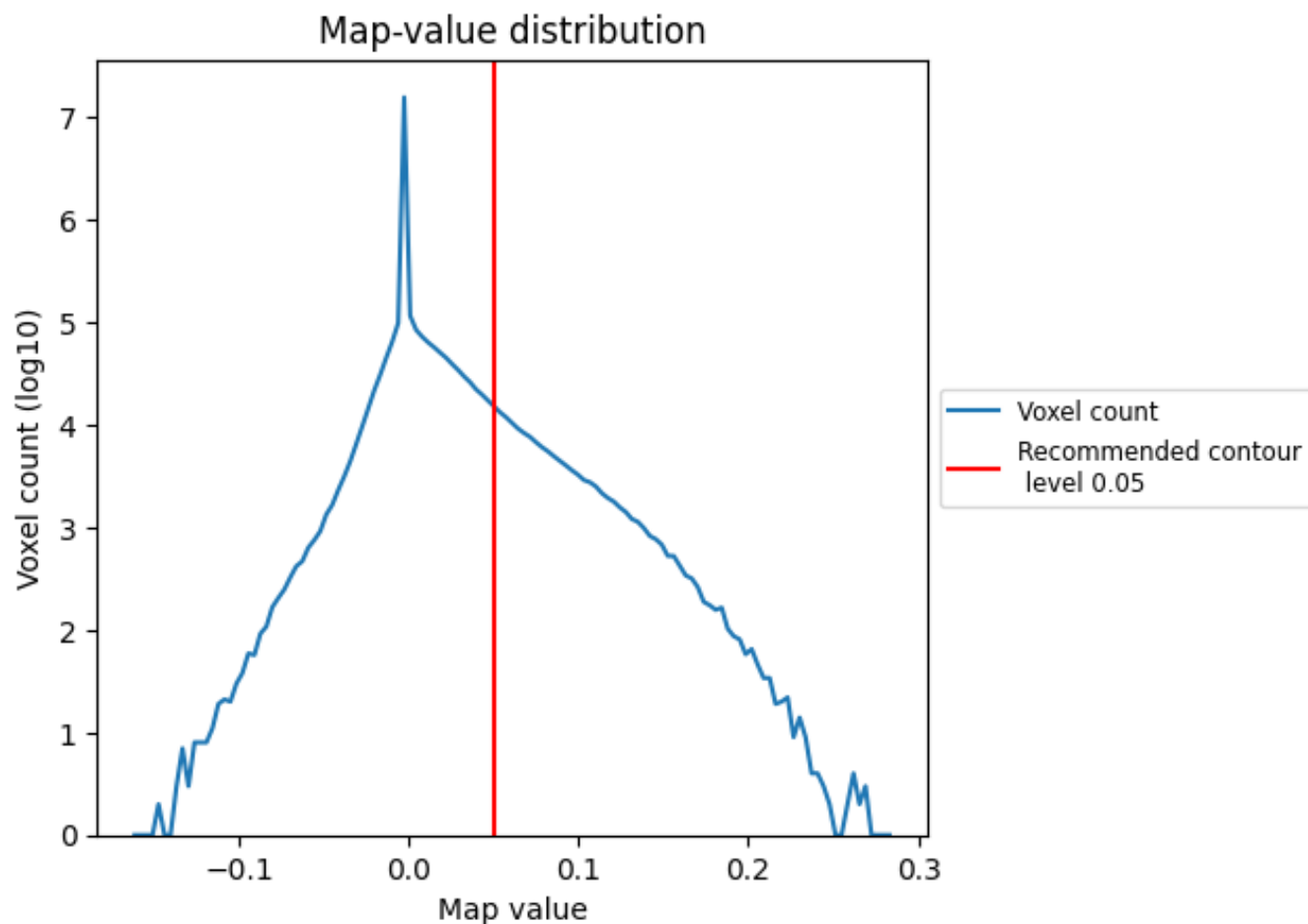
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

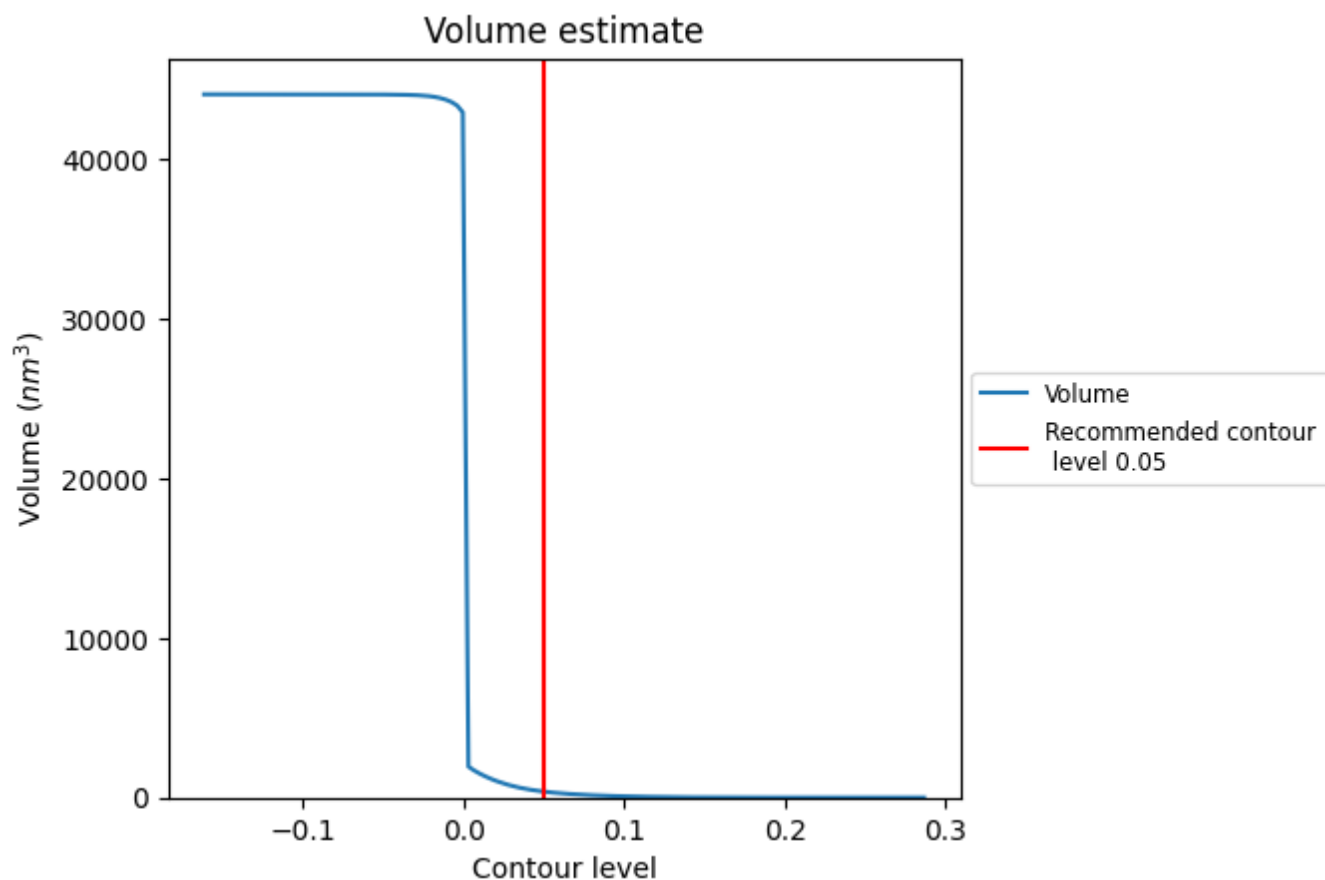
This section contains the results of statistical analysis of the map.

### 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.

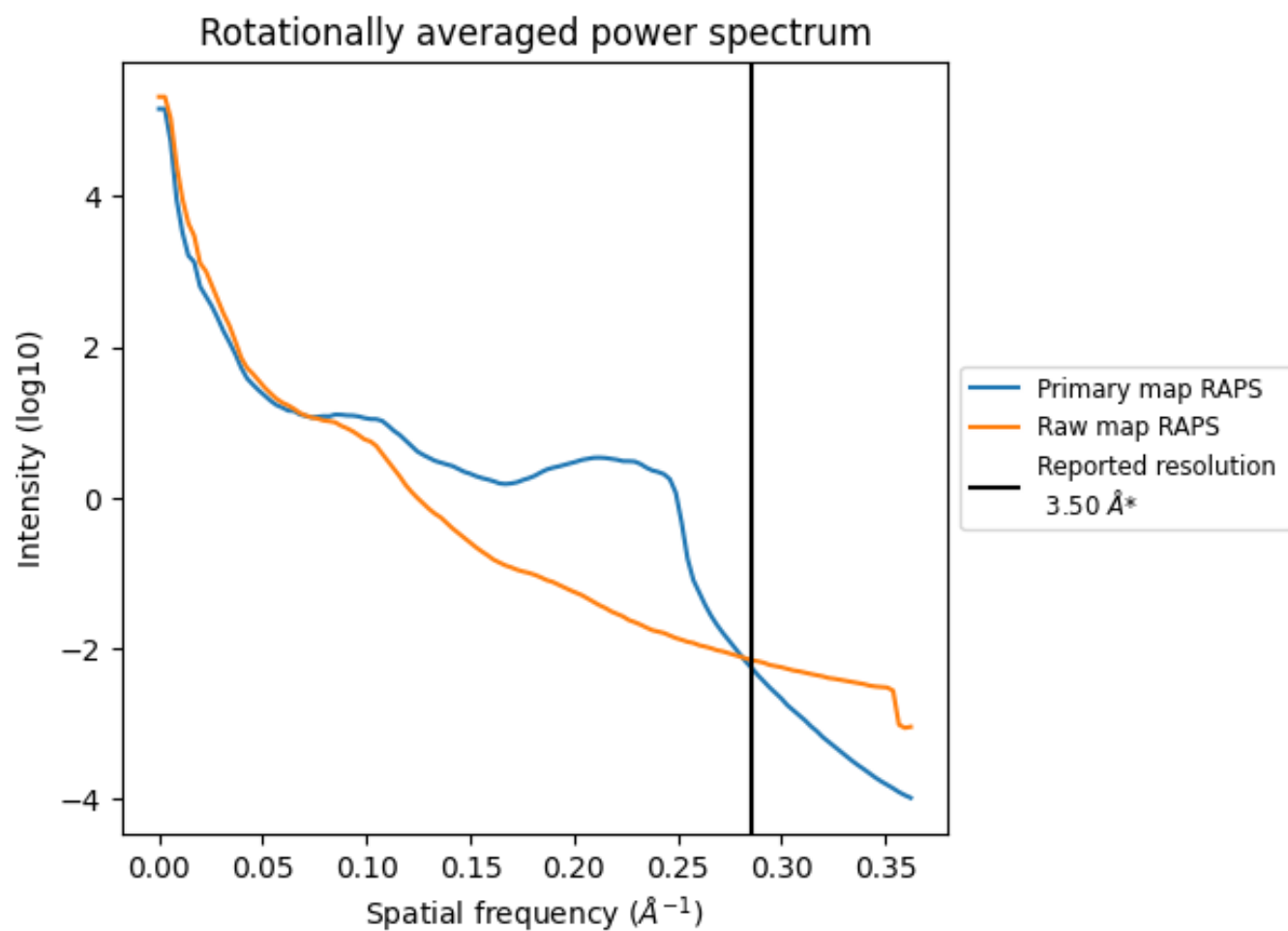
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 376 nm<sup>3</sup>; this corresponds to an approximate mass of 339 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 ⓘ

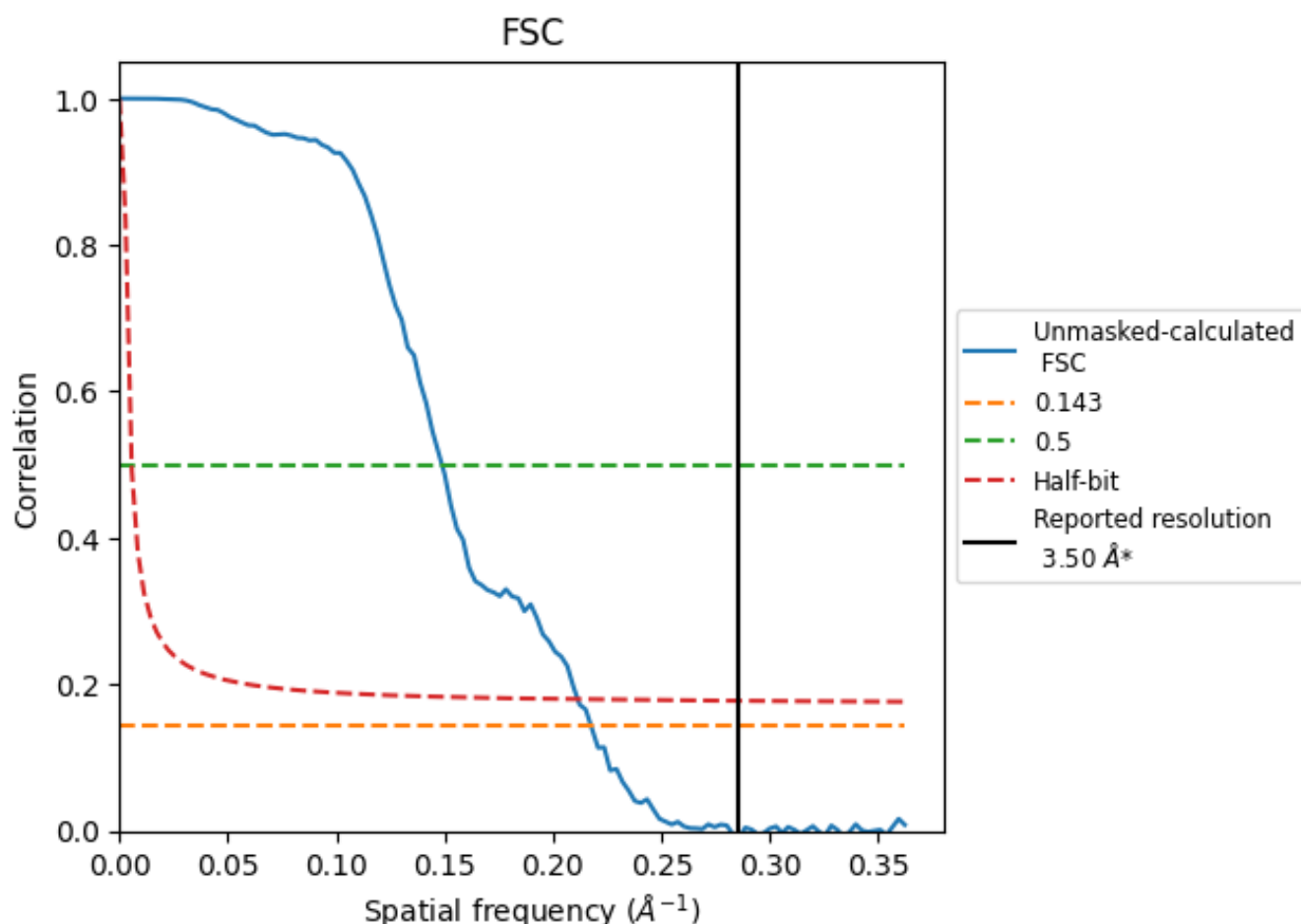


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

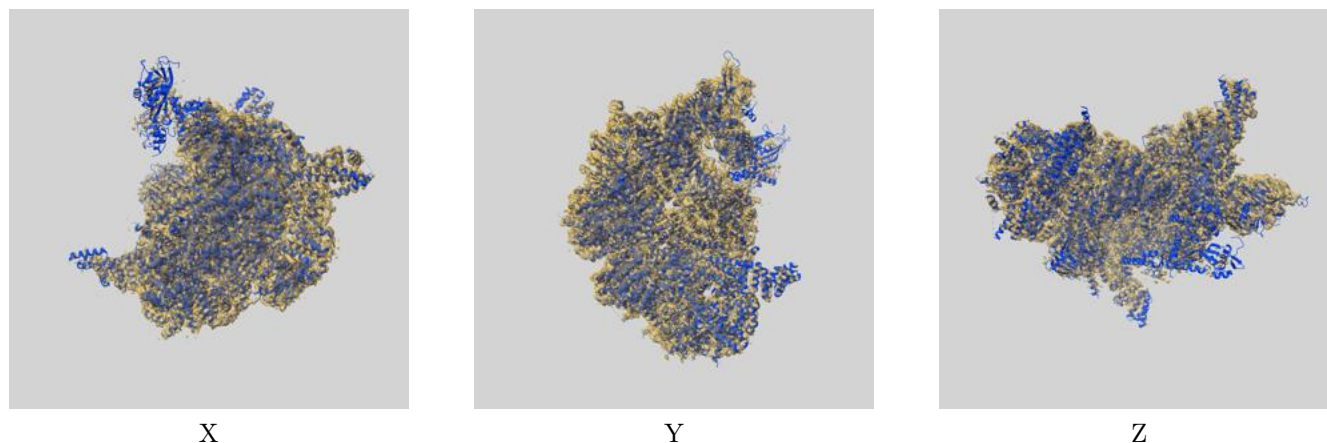
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.60	6.72	4.73

\*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 4.60 differs from the reported value 3.5 by more than 10 %

## 9 Map-model fit [i](#)

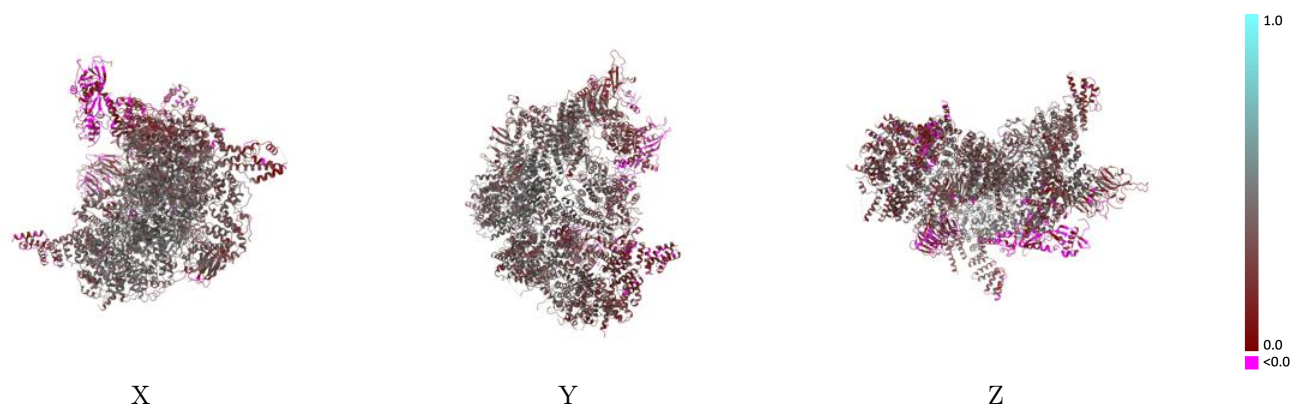
This section contains information regarding the fit between EMDB map EMD-15123 and PDB model 8A3T. Per-residue inclusion information can be found in section [3](#) on page [8](#).

### 9.1 Map-model overlay [i](#)



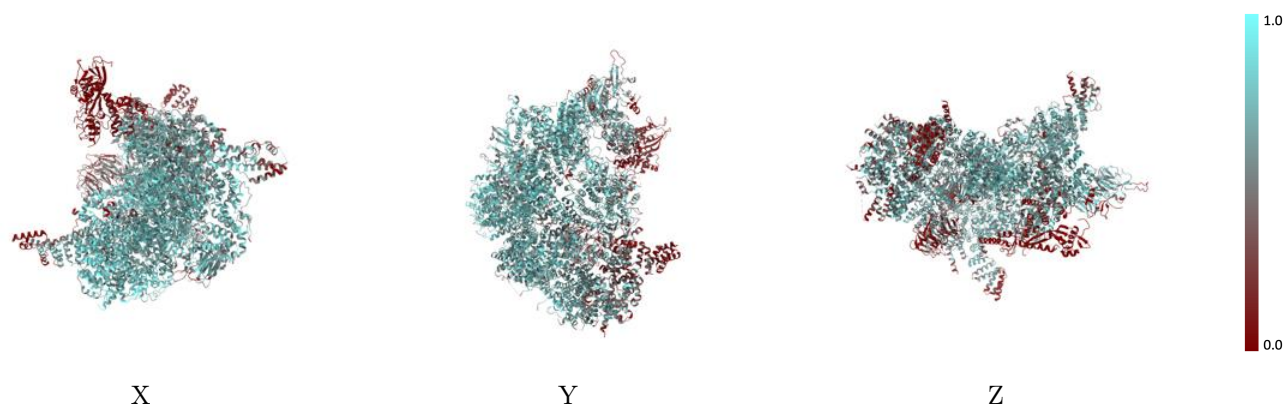
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



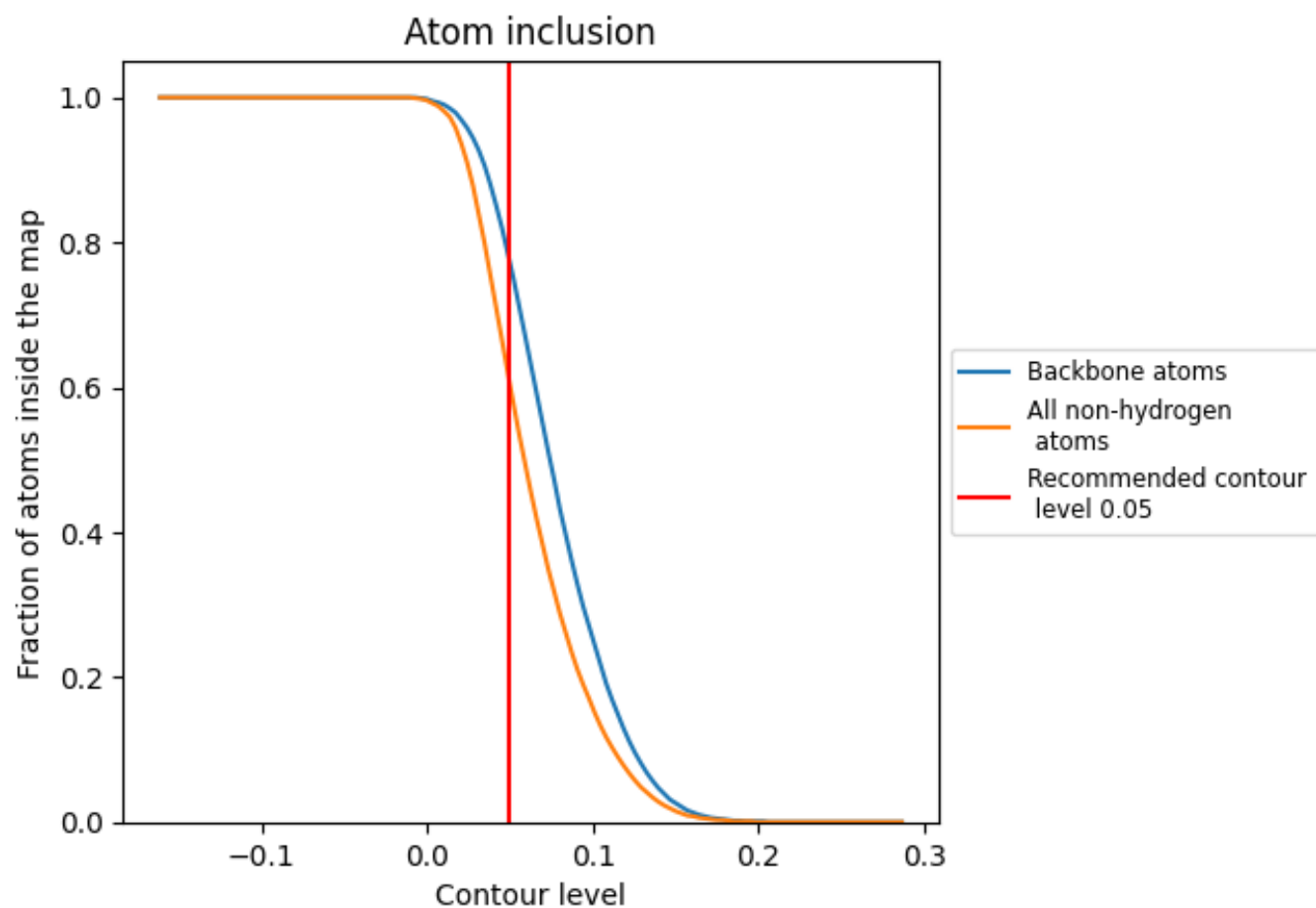
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

## 9.4 Atom inclusion [i](#)











































At the recommended contour level, 77% of all backbone atoms, 60% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6040	 0.3360
A	 0.4920	 0.2640
B	 0.3380	 0.2250
C	 0.6640	 0.3690
D	 0.7720	 0.4350
E	 0.4390	 0.3050
F	 0.6580	 0.3470
G	 0.5860	 0.3150
H	 0.4310	 0.2530
I	 0.7310	 0.4370
J	 0.7380	 0.3990
K	 0.6630	 0.3650
N	 0.7000	 0.4200
O	 0.7470	 0.4260
P	 0.7050	 0.3710
Q	 0.6150	 0.3270
S	 0.4890	 0.3190
T	 0.3620	 0.1900
U	 0.0230	 0.0240
W	 0.3110	 0.2370

