



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 07:46 pm BST

PDB ID : 8S4G
EMDB ID : EMD-19711
Title : Cryo-EM structure of the Anaphase-promoting complex/cyclosome (APC/C) bound to co-activator Cdh1 at 3.2 Angstrom resolution
Authors : Hoefler, A.; Yu, J.; Chang, L.; Zhang, Z.; Yang, J.; Boland, A.; Barford, D.
Deposited on : 2024-02-21
Resolution : 3.20 Å(reported)
Based on initial model : 4UI9

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

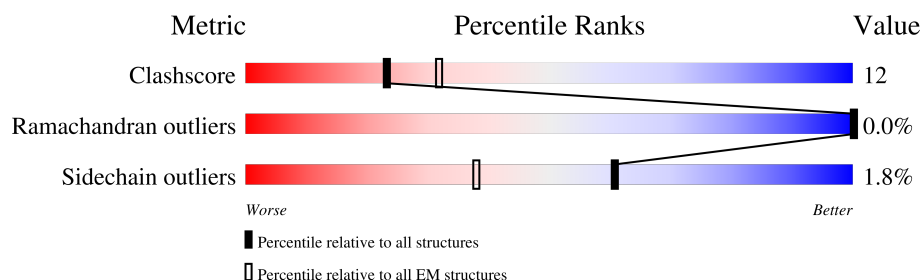
1 Overall quality at a glance

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	<div> <div>12%</div> <div>76%</div> <div>22%</div> <div>..</div> </div>
2	D	121	<div> <div>9%</div> <div>26%</div> <div>19%</div> <div>54%</div> </div>
3	A	1944	<div> <div>11%</div> <div>59%</div> <div>26%</div> <div>15%</div> </div>
4	N	822	<div> <div>36%</div> <div>56%</div> <div>26%</div> <div>17%</div> </div>
5	I	814	<div> <div>26%</div> <div>65%</div> <div>26%</div> <div>9%</div> </div>
6	O	755	<div> <div>8%</div> <div>68%</div> <div>24%</div> <div>6%</div> </div>
7	S	447	<div> <div>15%</div> <div>11%</div> <div>9%</div> <div>79%</div> </div>
8	K	620	<div> <div>7%</div> <div>65%</div> <div>20%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
8	Q	620	
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	496	
16	C	84	

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 71291 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	183	Total	C	N	O	S	0	0
			1479	926	268	278	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 Anaphase-promoting complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1648	Total	C	N	O	S	0	0
			12968	8284	2191	2407	86		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	682	Total	C	N	O	S	0	0
			5505	3484	973	1021	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	742	Total	C	N	O	S	0	0
			5925	3793	989	1109	34		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	809	GLU	-	expression tag	UNP Q9UJX5
I	810	ASN	-	expression tag	UNP Q9UJX5
I	811	LEU	-	expression tag	UNP Q9UJX5

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Chain	Residue	Modelled	Actual	Comment	Reference
I	812	TYR	-	expression tag	UNP Q9UJX5
I	813	PHE	-	expression tag	UNP Q9UJX5
I	814	GLN	-	expression tag	UNP Q9UJX5

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	O	707	Total	C	N	O	S	0	0
			5593	3567	972	1024	30		

- Molecule 7 is a protein called F-box only protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	94	Total	C	N	O	S	0	0
			751	463	145	135	8		

- Molecule 8 is a protein called Cell division cycle protein 16 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	531	Total	C	N	O	S	0	0
			4323	2775	726	794	28		
8	Q	506	Total	C	N	O	S	1	0
			4103	2630	694	754	25		

- 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
			233	146	43	43	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	68	Total	C	N	O	S	0	0
			553	342	91	118	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	58	Total	C	N	O	S	0	0
			475	304	79	90	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	512	Total	C	N	O	S	1	0
			4121	2646	697	752	26		
12	P	496	Total	C	N	O	S	0	0
			3994	2569	671	728	26		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	502	Total	C	N	O	S	0	0
			3922	2480	682	731	29		
13	Z	488	Total	C	N	O	S	1	0
			3830	2426	664	714	26		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	540	Total	C	N	O	S	0	0
			4442	2859	747	810	26		
14	V	534	Total	C	N	O	S	1	0
			4380	2817	732	805	26		

- Molecule 15 is a protein called Fizzy-related protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	432	Total	C	N	O	S	0	0
			3375	2120	612	632	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	83	Total	C	N	O	S	0	0
			618	393	109	102	14		

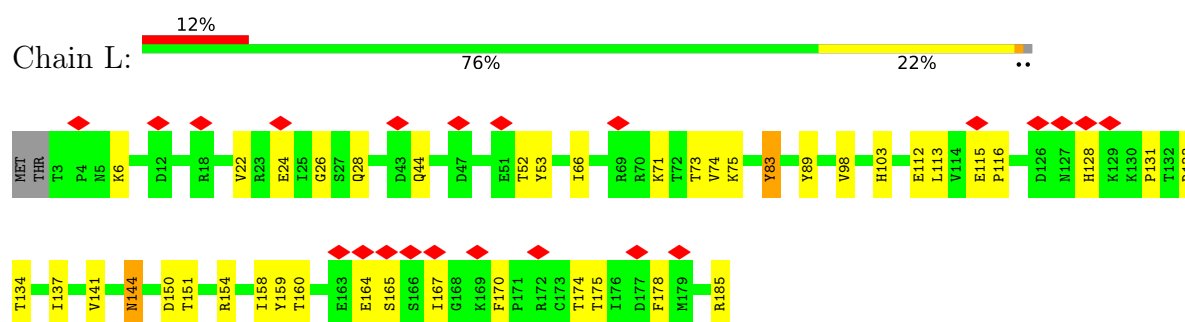
- Molecule 17 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
17	N	1	Total 1	Zn 1	0
17	S	2	Total 2	Zn 2	0
17	C	3	Total 3	Zn 3	0

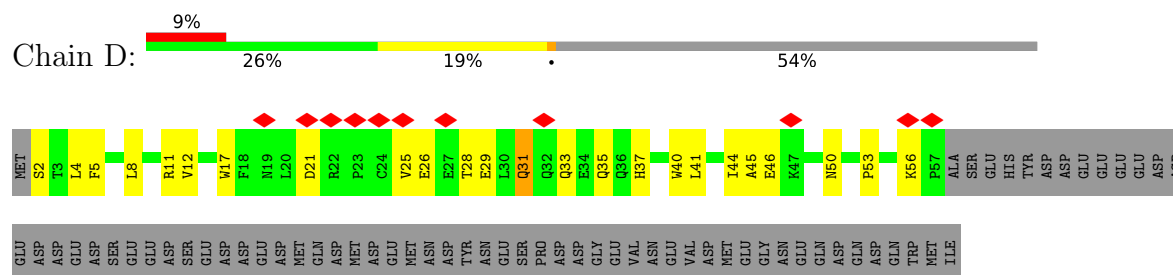
3 Residue-property plots [i](#)

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.

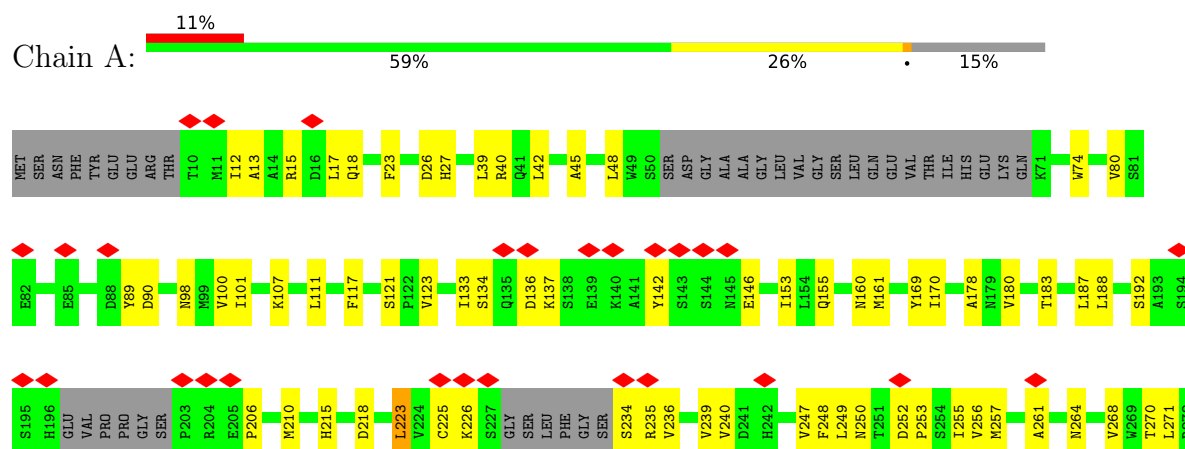
- Molecule 1: Anaphase-promoting complex subunit 10

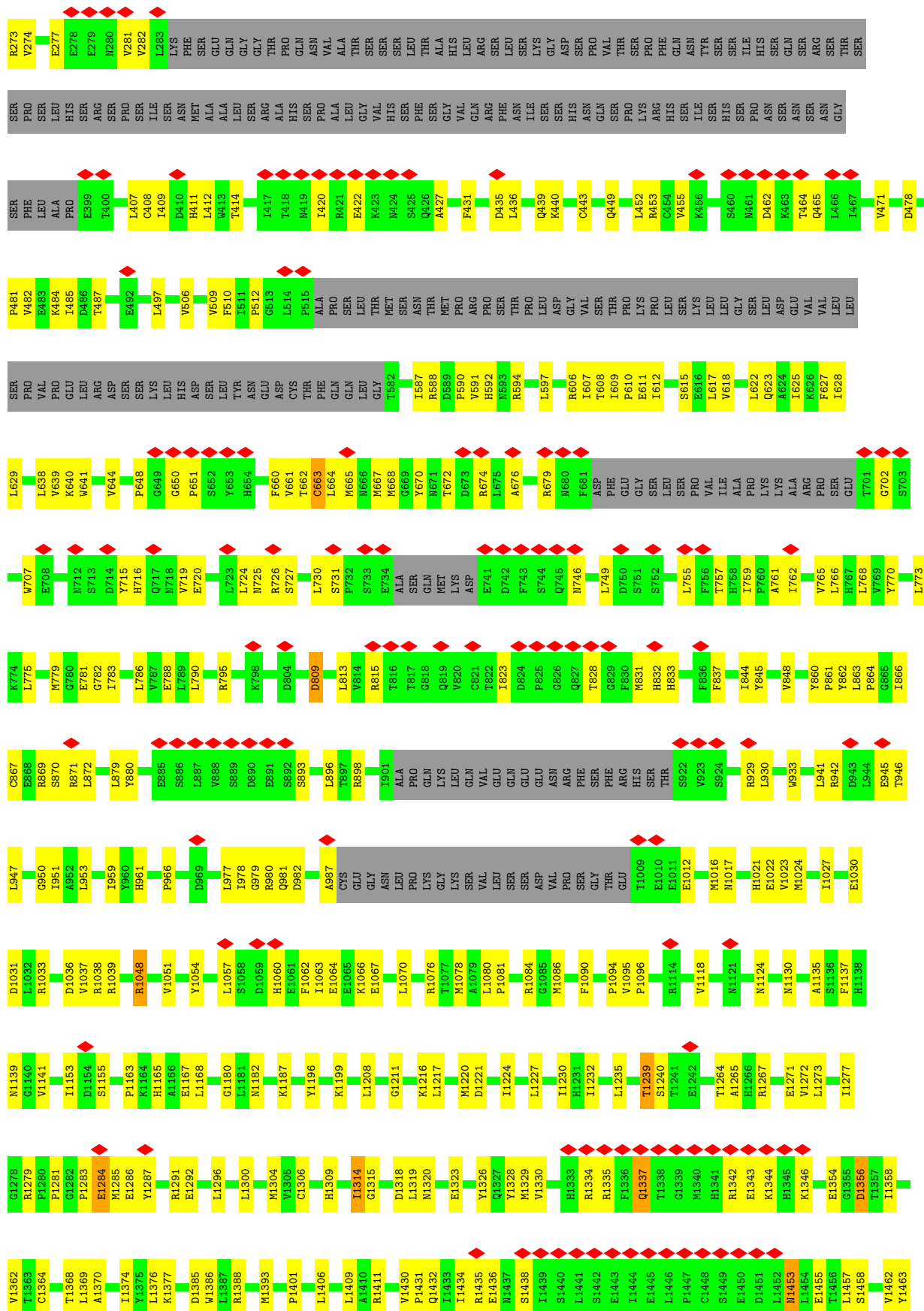


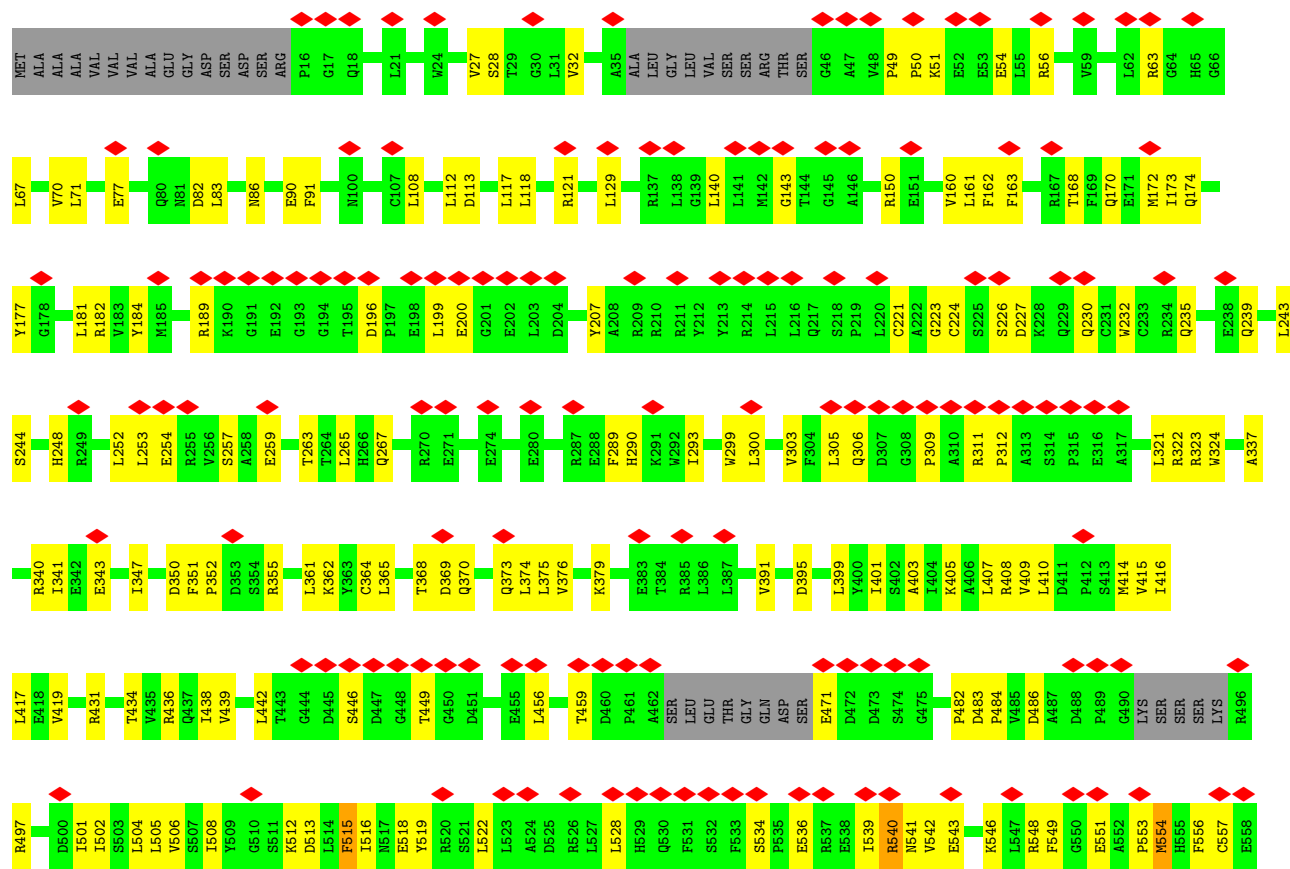
- Molecule 2: Anaphase-promoting complex subunit 15

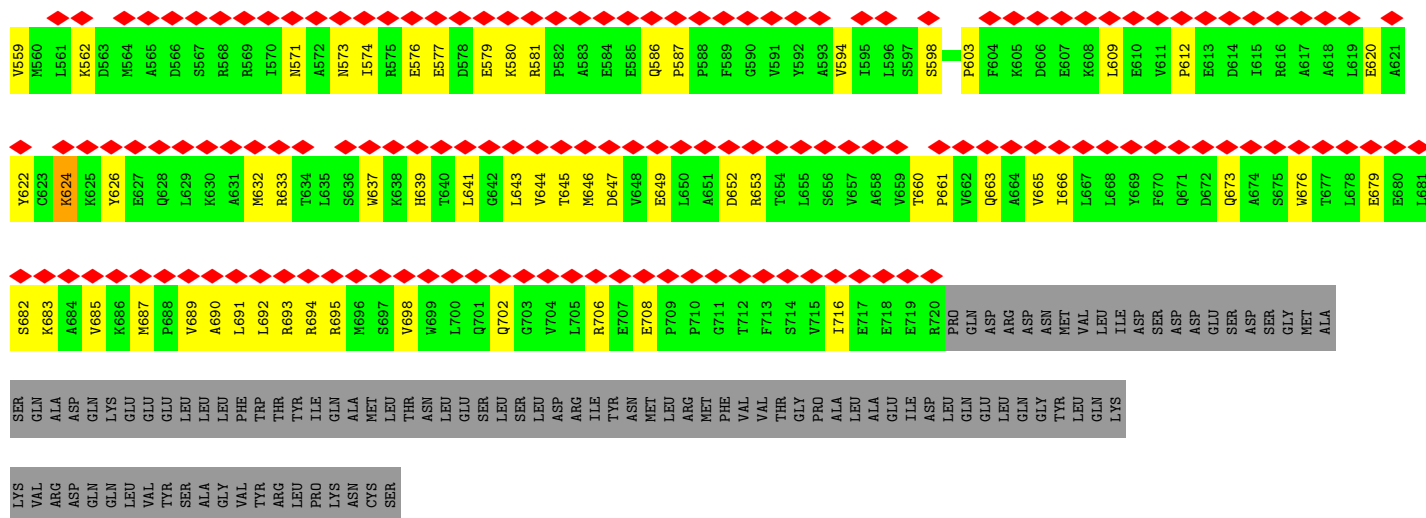


- Molecule 3: Anaphase-promoting complex subunit 1

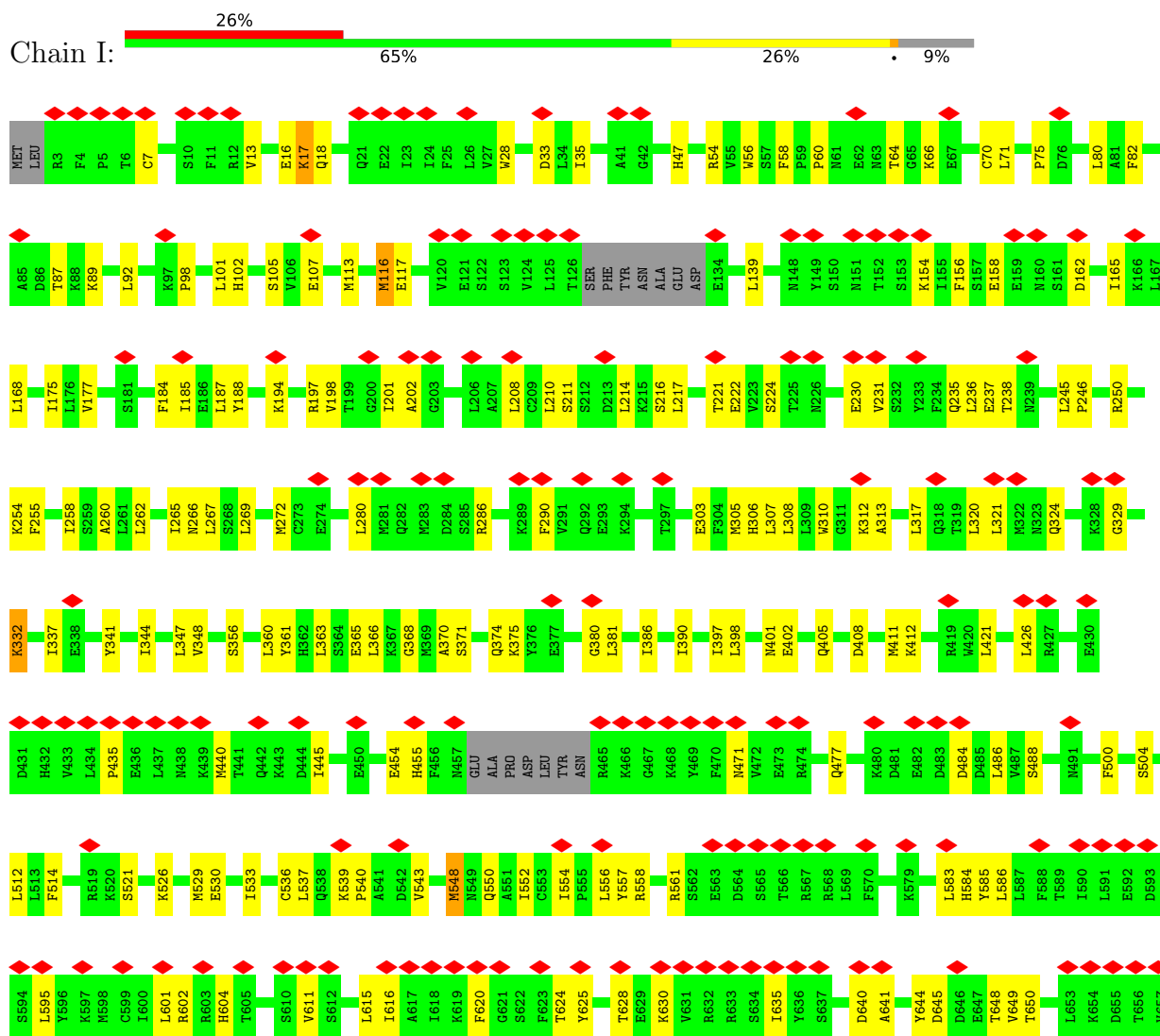


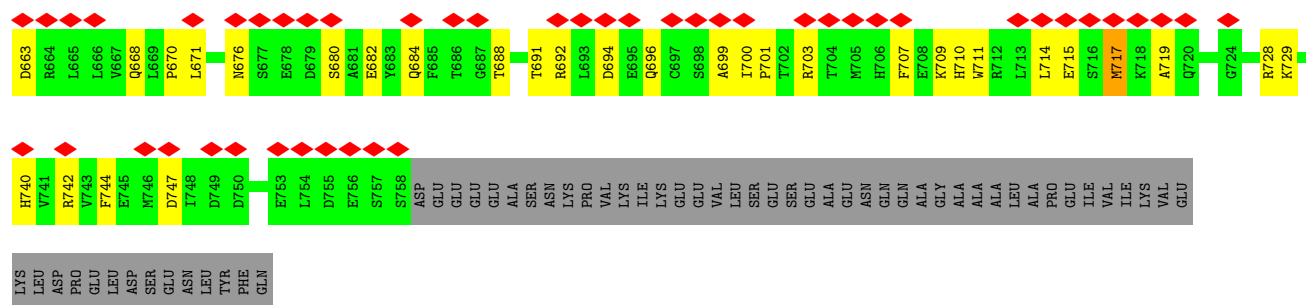




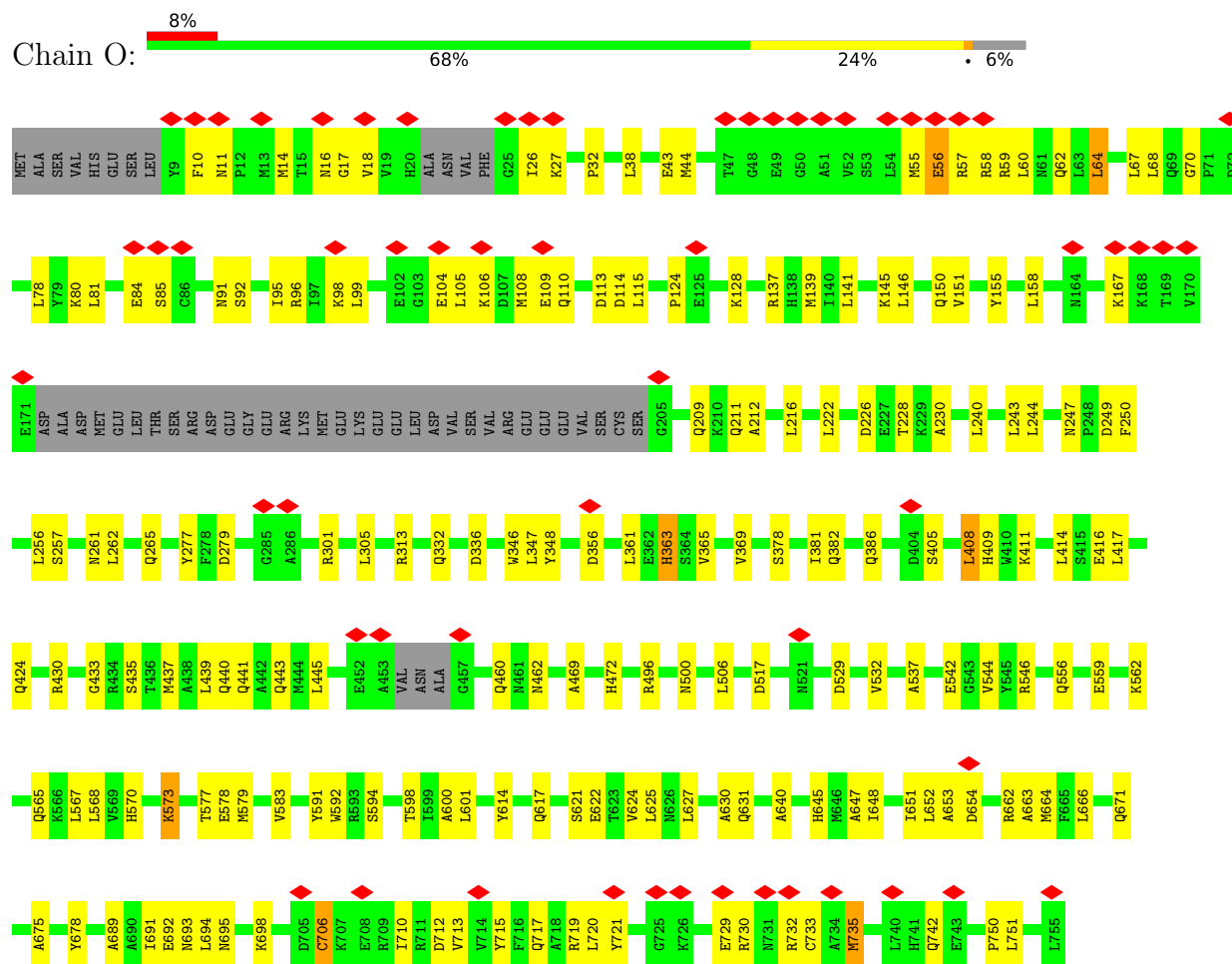


• Molecule 5: Anaphase-promoting complex subunit 4

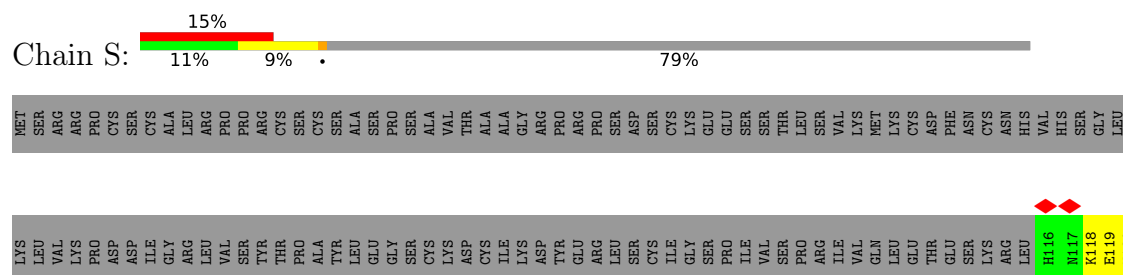


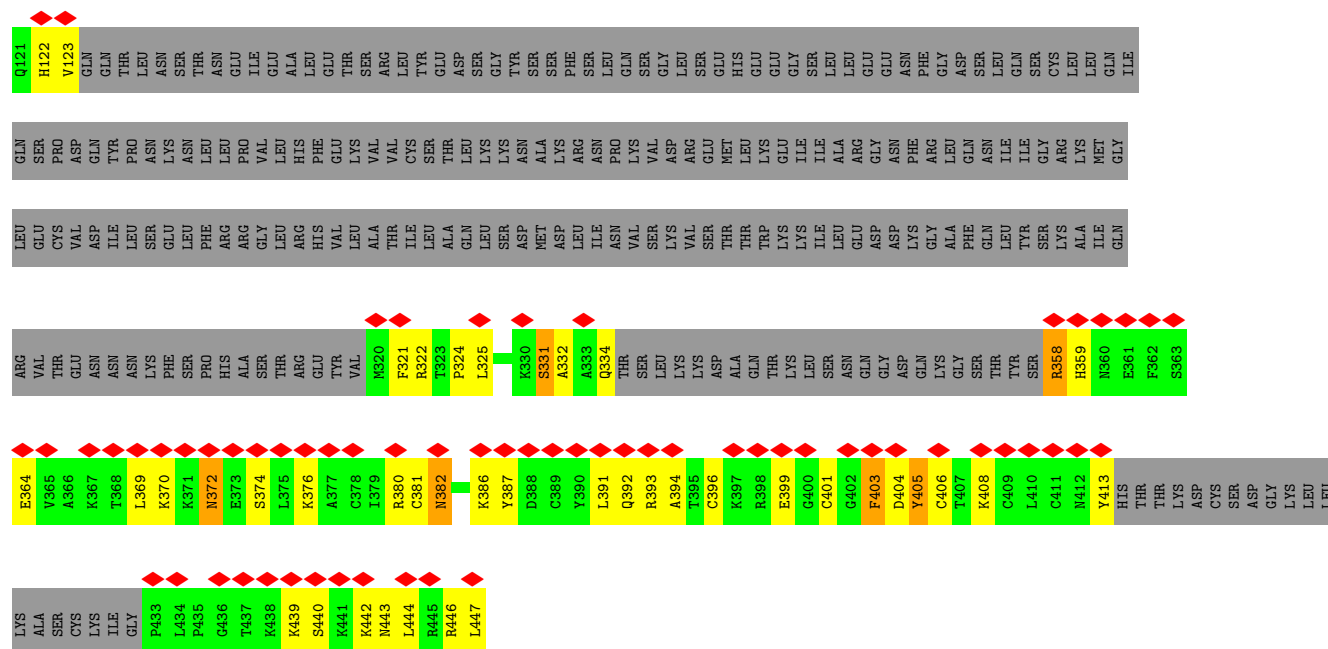


• Molecule 6: Anaphase-promoting complex subunit 5

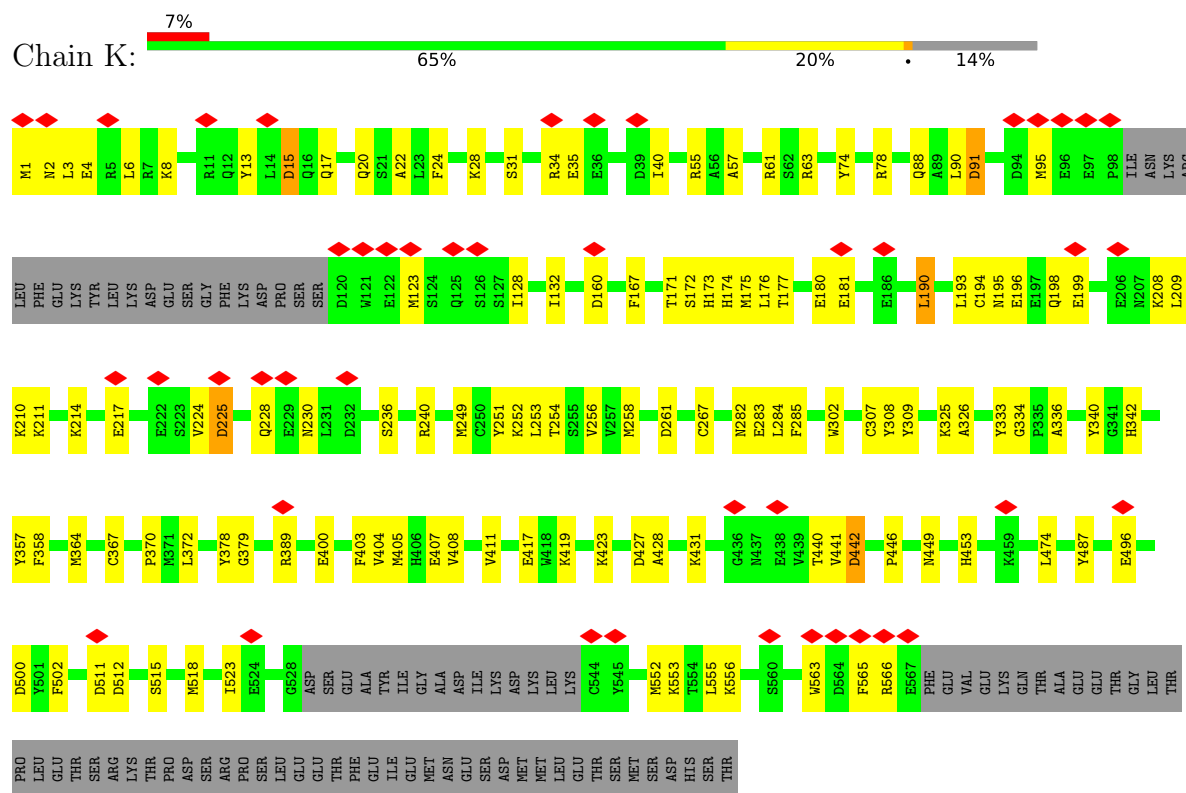


• Molecule 7: F-box only protein 5



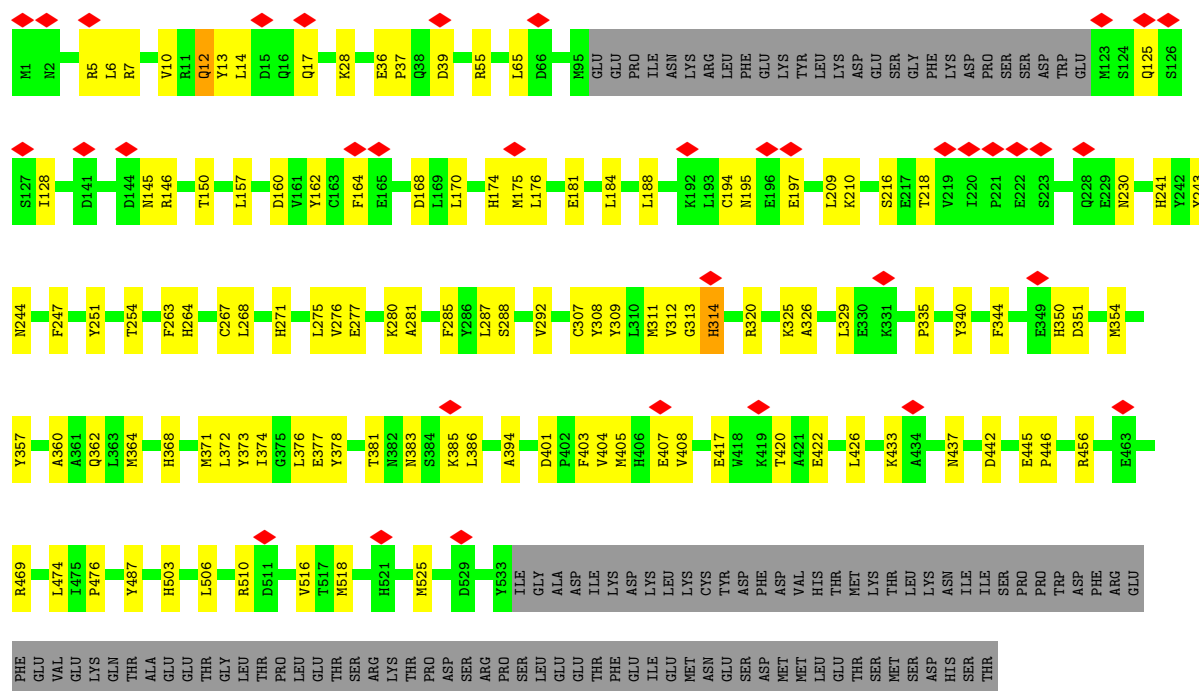


• Molecule 8: Cell division cycle protein 16 homolog



• Molecule 8: Cell division cycle protein 16 homolog





- Molecule 9: Anaphase-promoting complex subunit CDC26



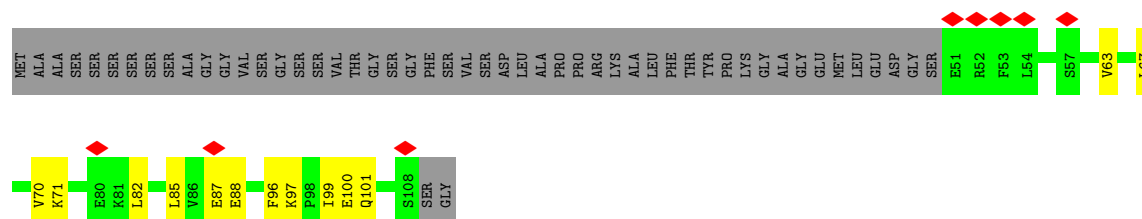
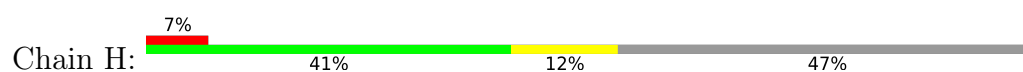
- Molecule 9: Anaphase-promoting complex subunit CDC26



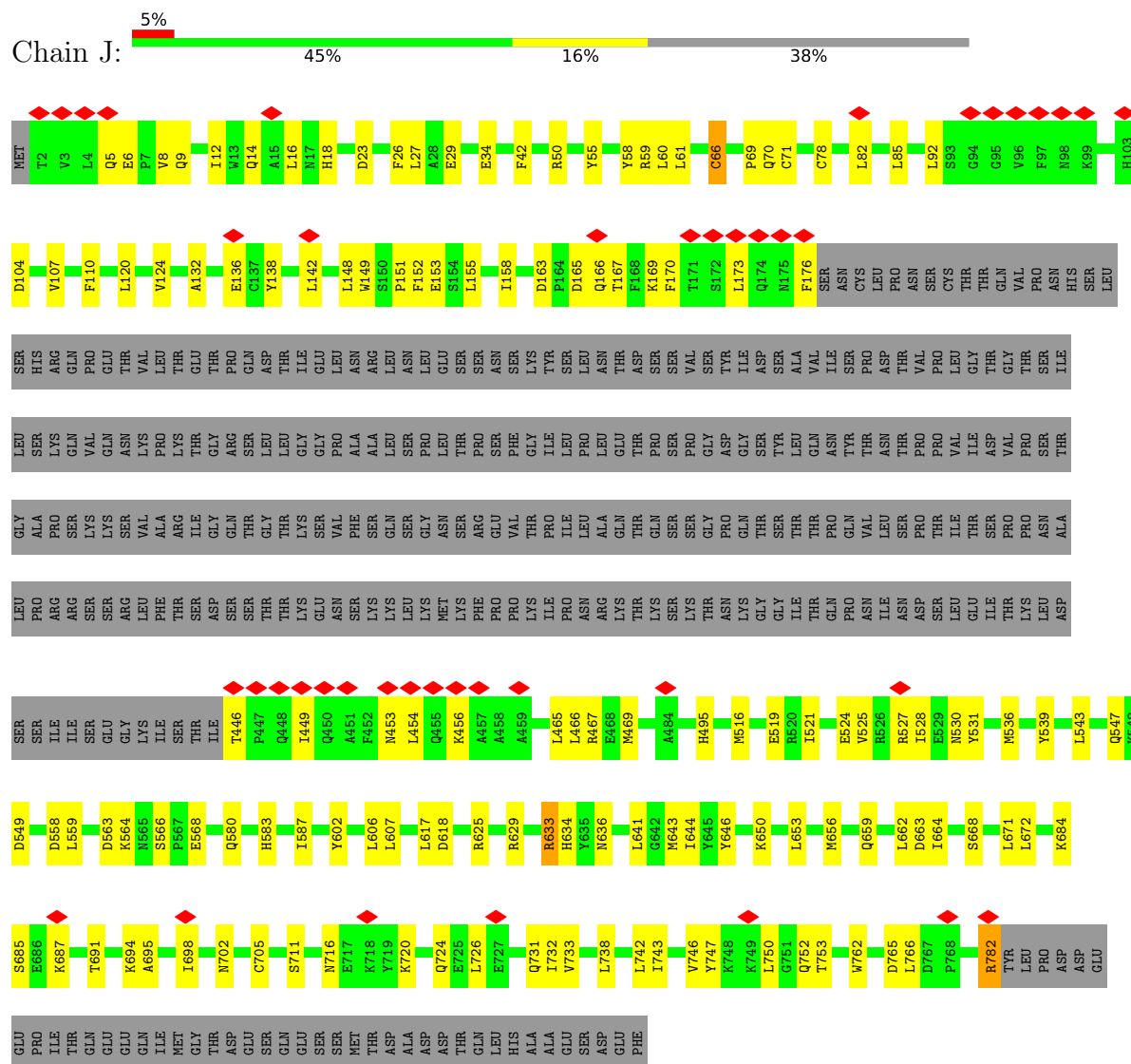
- Molecule 10: Anaphase-promoting complex subunit 13



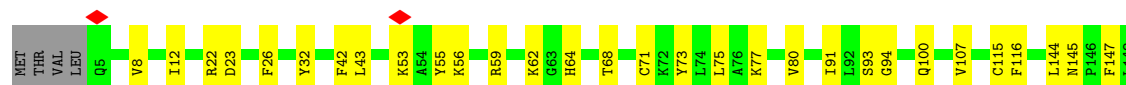
- Molecule 11: Anaphase-promoting complex subunit 16

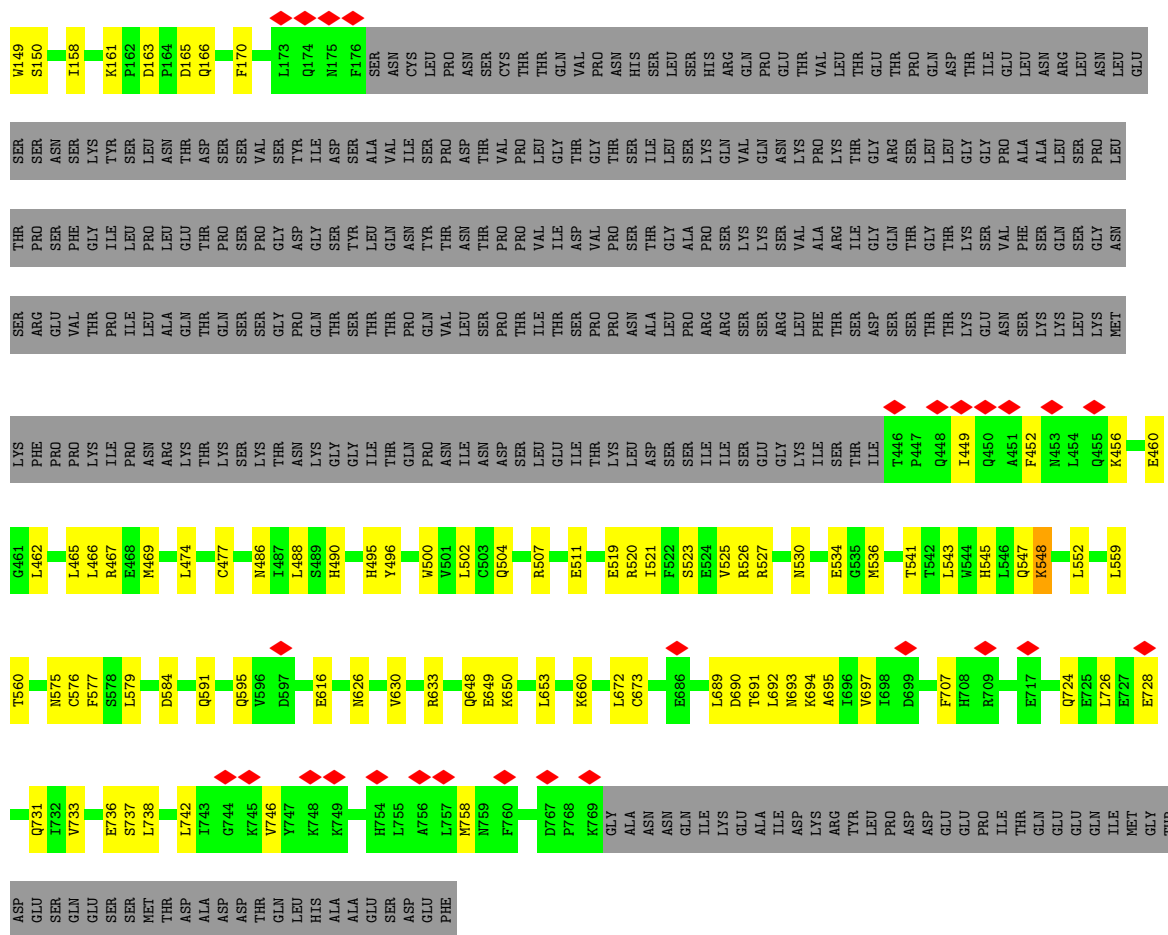


- Molecule 12: Cell division cycle protein 27 homolog

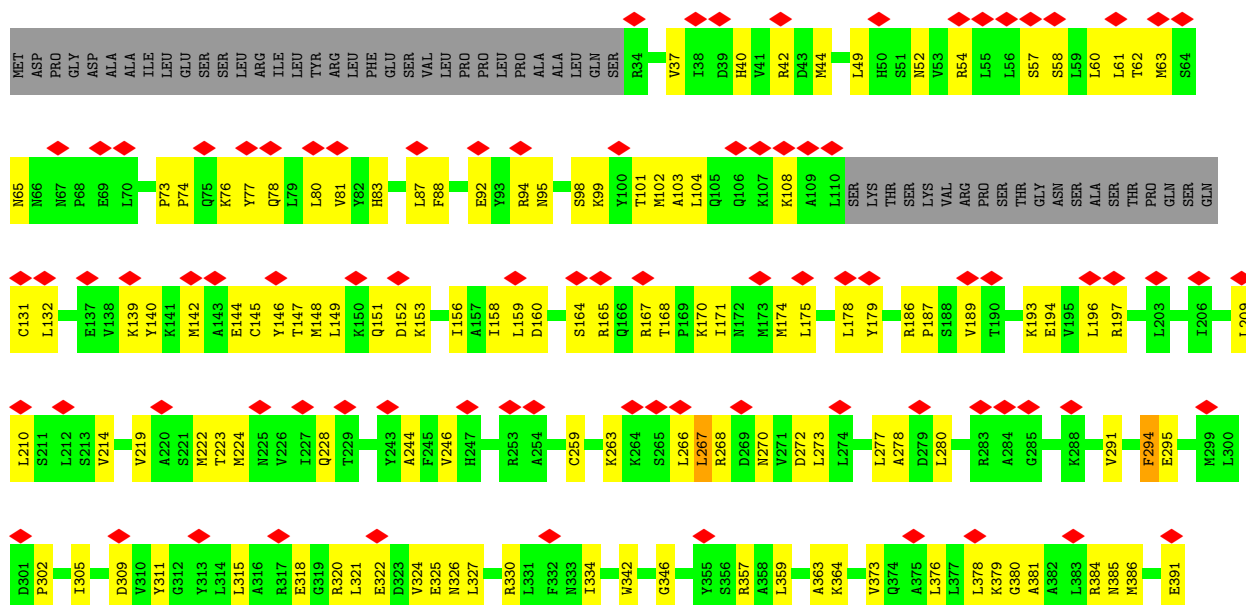


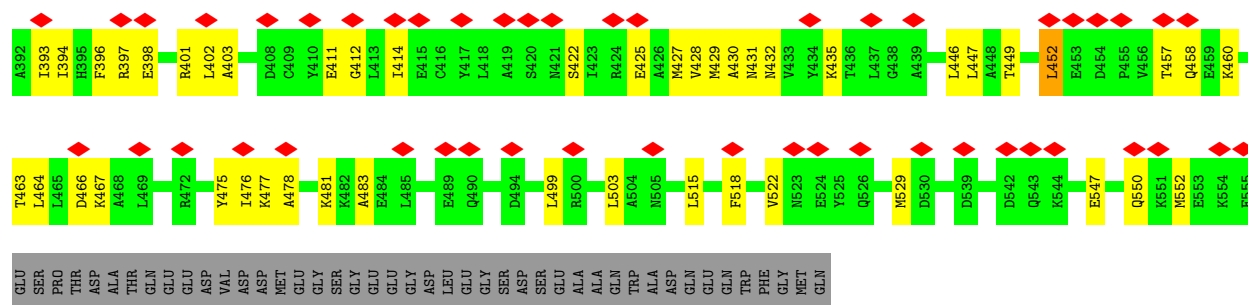
- Molecule 12: Cell division cycle protein 27 homolog



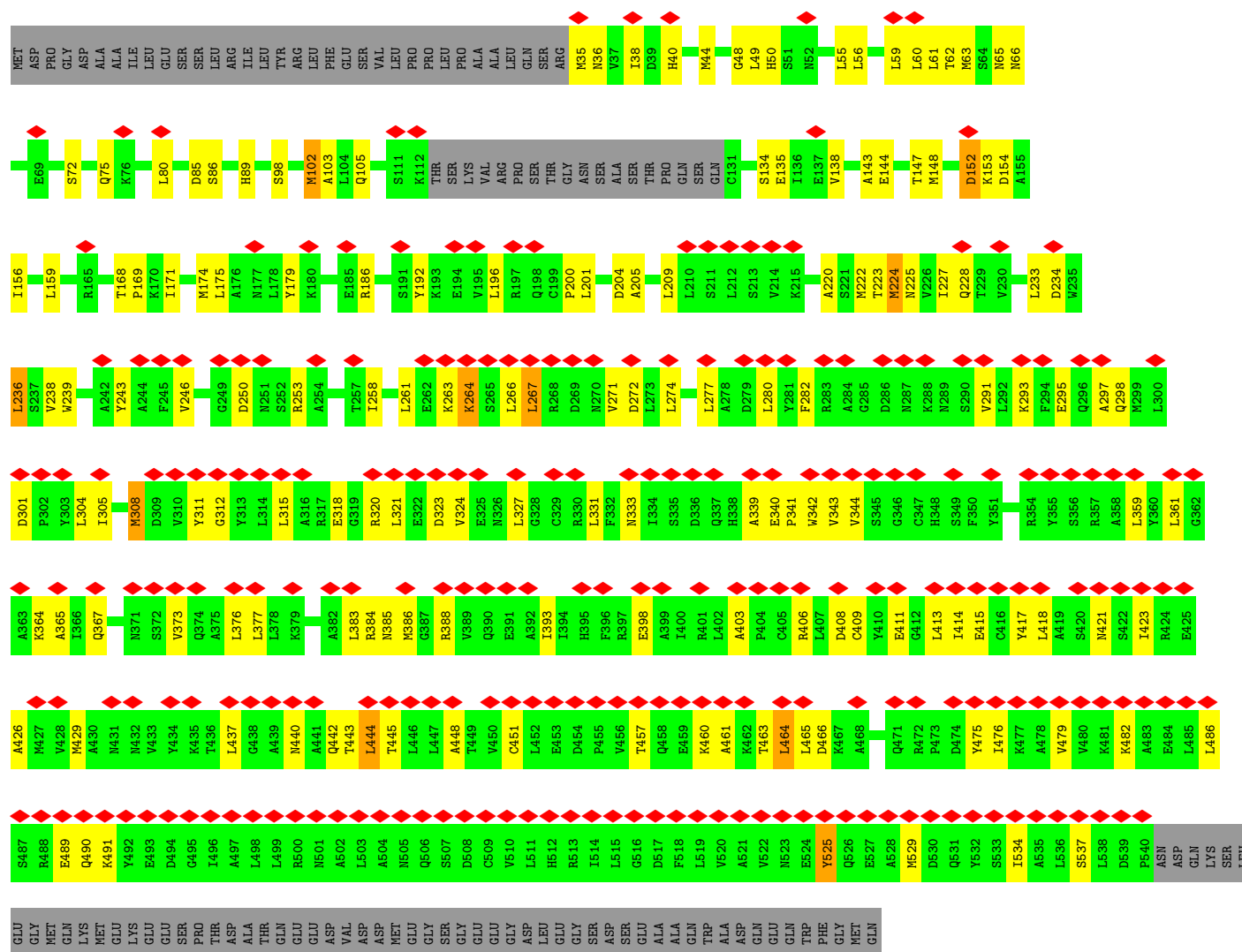
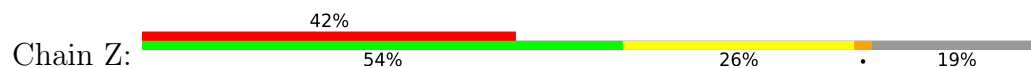


• Molecule 13: Anaphase-promoting complex subunit 7



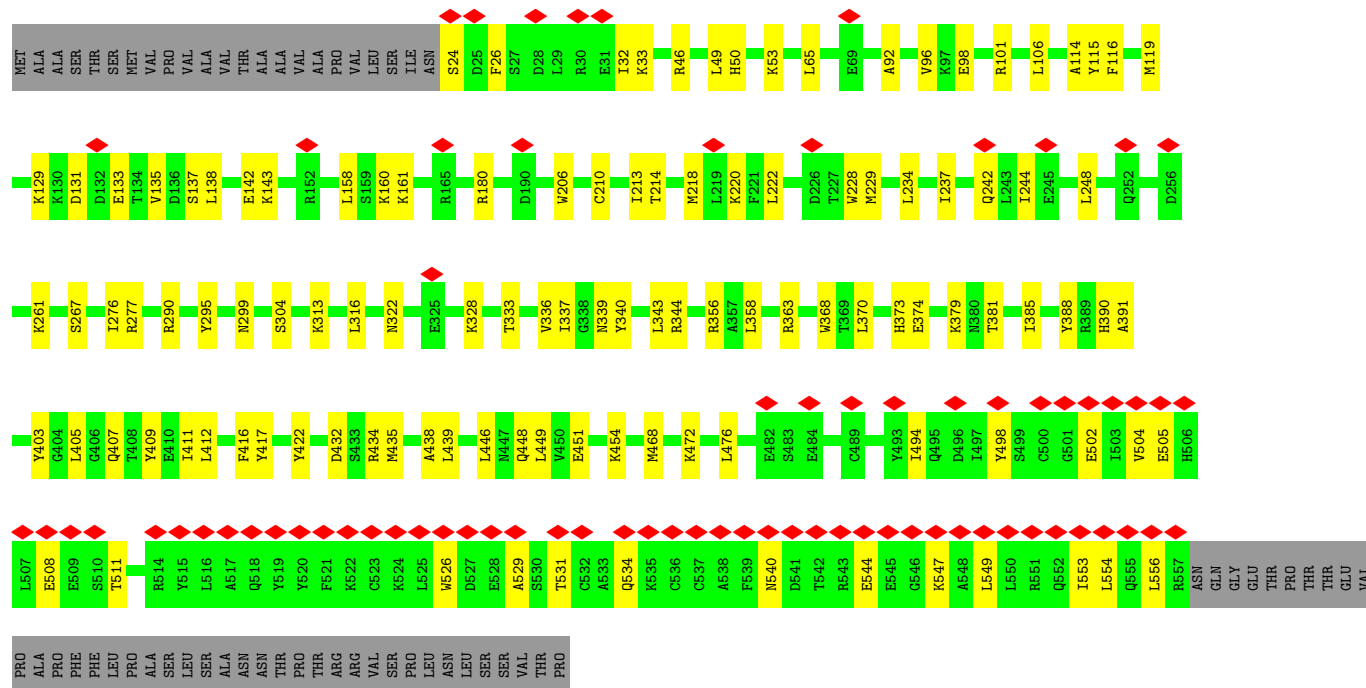


• Molecule 13: Anaphase-promoting complex subunit 7

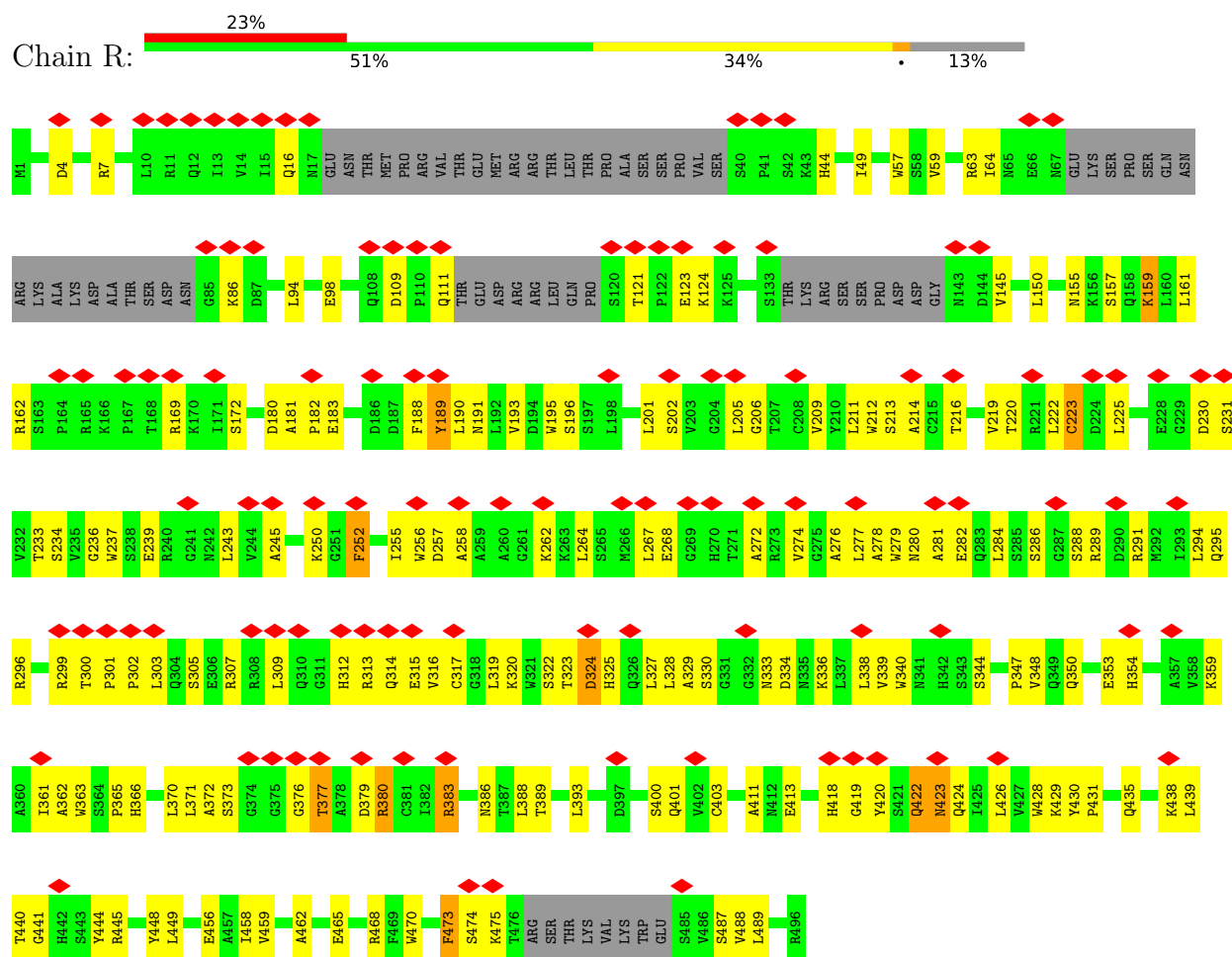


• Molecule 14: Cell division cycle protein 23 homolog

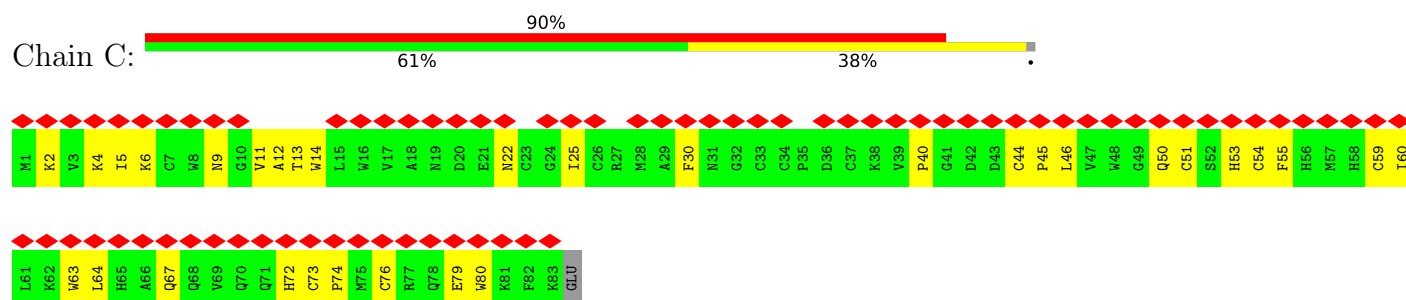




- Molecule 15: Fizzy-related protein homolog



- Molecule 16: Anaphase-promoting complex subunit 11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54395	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.019	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	385.2, 385.2, 385.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.29	0/1514	0.56	0/2051
2	D	0.30	0/485	0.62	0/662
3	A	0.28	0/13269	0.49	0/18041
4	N	0.26	0/5618	0.53	0/7605
5	I	0.26	0/6050	0.49	0/8188
6	O	0.27	0/5697	0.47	0/7694
7	S	0.32	0/761	0.63	0/1010
8	K	0.27	0/4431	0.45	0/5998
8	Q	0.28	0/4205	0.47	0/5691
9	G	0.31	0/234	0.76	0/310
9	W	0.28	0/226	0.56	0/299
10	M	0.30	0/563	0.58	0/765
11	H	0.31	0/484	0.56	0/651
12	J	0.28	0/4220	0.47	0/5702
12	P	0.28	0/4090	0.44	0/5527
13	Y	0.25	0/3982	0.51	0/5380
13	Z	0.27	0/3893	0.54	0/5262
14	U	0.27	0/4544	0.47	0/6133
14	V	0.28	0/4483	0.45	0/6056
15	R	0.30	0/3446	0.55	0/4670
16	C	0.30	0/639	0.47	0/874
All	All	0.27	0/72834	0.50	0/98569

There are no bond length outliers.

There are no bond angle outliers.

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	L	1479	0	1462	32	0
2	D	470	0	458	21	0
3	A	12968	0	12918	348	0
4	N	5505	0	5487	170	0
5	I	5925	0	5902	146	0
6	O	5593	0	5659	139	0
7	S	751	0	752	53	0
8	K	4323	0	4229	100	0
8	Q	4103	0	4026	91	0
9	G	233	0	246	20	0
9	W	225	0	242	9	0
10	M	553	0	516	23	0
11	H	475	0	469	13	0
12	J	4121	0	4088	101	0
12	P	3994	0	3955	91	0
13	Y	3922	0	3989	134	0
13	Z	3830	0	3909	121	0
14	U	4442	0	4409	98	0
14	V	4380	0	4326	81	0
15	R	3375	0	3341	139	0
16	C	618	0	542	31	0
17	C	3	0	0	0	0
17	N	1	0	0	0	0
17	S	2	0	0	0	0
All	All	71291	0	70925	1754	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 12.

The worst 5 of 1754 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)
16:C:53:HIS:HE1	16:C:76:CYS:SG	1.82	1.01
8:Q:360:ALA:O	8:Q:364:MET:HB2	1.65	0.97
3:A:788:GLU:HG2	3:A:813:LEU:HD21	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:O:38:LEU:HD21	6:O:139:MET:HG3	1.53	0.90
7:S:325:LEU:HD23	15:R:219:VAL:HG22	1.55	0.89

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	181/185 (98%)	173 (96%)	8 (4%)	0	100	100
2	D	55/121 (46%)	52 (94%)	3 (6%)	0	100	100
3	A	1628/1944 (84%)	1558 (96%)	68 (4%)	2 (0%)	51	83
4	N	674/822 (82%)	651 (97%)	23 (3%)	0	100	100
5	I	736/814 (90%)	709 (96%)	27 (4%)	0	100	100
6	O	699/755 (93%)	683 (98%)	16 (2%)	0	100	100
7	S	86/447 (19%)	77 (90%)	9 (10%)	0	100	100
8	K	525/620 (85%)	512 (98%)	13 (2%)	0	100	100
8	Q	503/620 (81%)	489 (97%)	14 (3%)	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	66/74 (89%)	60 (91%)	6 (9%)	0	100	100
11	H	56/110 (51%)	56 (100%)	0	0	100	100
12	J	509/824 (62%)	494 (97%)	15 (3%)	0	100	100
12	P	492/824 (60%)	480 (98%)	12 (2%)	0	100	100
13	Y	498/599 (83%)	489 (98%)	9 (2%)	0	100	100
13	Z	485/599 (81%)	473 (98%)	12 (2%)	0	100	100
14	U	534/597 (89%)	510 (96%)	24 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	V	533/597 (89%)	521 (98%)	12 (2%)	0	100	100
15	R	420/496 (85%)	388 (92%)	32 (8%)	0	100	100
16	C	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
All	All	8810/11302 (78%)	8499 (96%)	309 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	1284	GLU
3	A	1314	ILE

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	L	168/170 (99%)	165 (98%)	3 (2%)	59	82
2	D	54/115 (47%)	51 (94%)	3 (6%)	21	57
3	A	1450/1720 (84%)	1429 (99%)	21 (1%)	67	86
4	N	600/724 (83%)	591 (98%)	9 (2%)	65	85
5	I	663/736 (90%)	653 (98%)	10 (2%)	65	85
6	O	604/650 (93%)	592 (98%)	12 (2%)	55	80
7	S	83/403 (21%)	75 (90%)	8 (10%)	8	32
8	K	463/548 (84%)	453 (98%)	10 (2%)	52	79
8	Q	437/548 (80%)	434 (99%)	3 (1%)	84	94
9	G	26/77 (34%)	23 (88%)	3 (12%)	5	24
9	W	25/77 (32%)	24 (96%)	1 (4%)	31	66
10	M	61/67 (91%)	59 (97%)	2 (3%)	38	71
11	H	52/89 (58%)	52 (100%)	0	100	100
12	J	442/727 (61%)	435 (98%)	7 (2%)	62	84
12	P	429/727 (59%)	426 (99%)	3 (1%)	84	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	Y	425/513 (83%)	417 (98%)	8 (2%)	57	81
13	Z	417/513 (81%)	400 (96%)	17 (4%)	30	66
14	U	471/520 (91%)	468 (99%)	3 (1%)	86	94
14	V	463/520 (89%)	459 (99%)	4 (1%)	78	91
15	R	370/431 (86%)	354 (96%)	16 (4%)	29	64
16	C	62/75 (83%)	61 (98%)	1 (2%)	62	84
All	All	7765/9950 (78%)	7621 (98%)	144 (2%)	61	81

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	Z	224	MET
16	C	14	TRP
13	Z	267	LEU
15	R	205	LEU
6	O	64	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
15	R	401	GLN
16	C	50	GLN
16	C	71	GLN
15	R	423	ASN
8	K	198	GLN

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

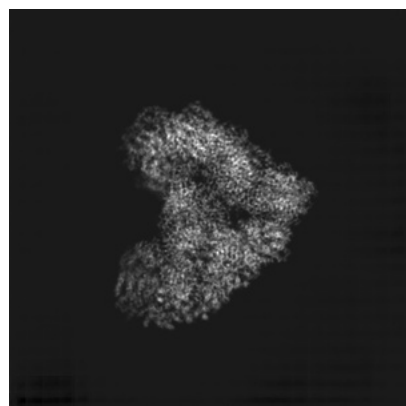
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19711. These allow visual inspection of the internal detail of the map and identification of artifacts.

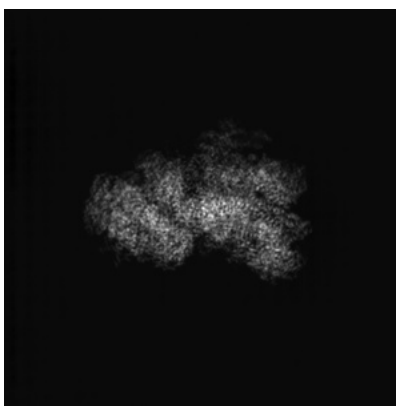
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

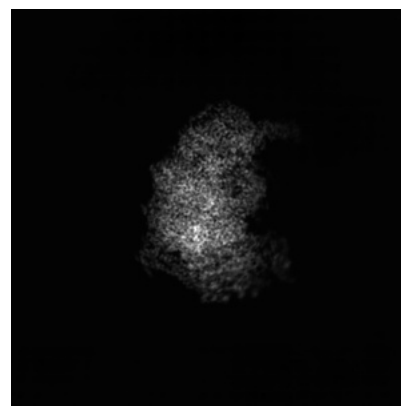
6.1.1 Primary map



X

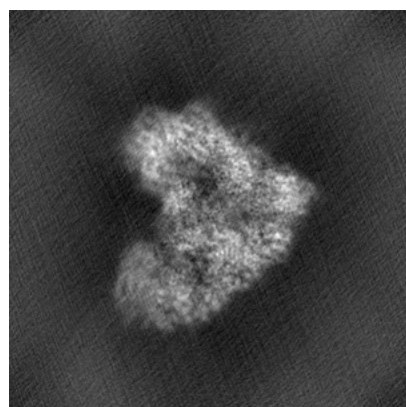


Y

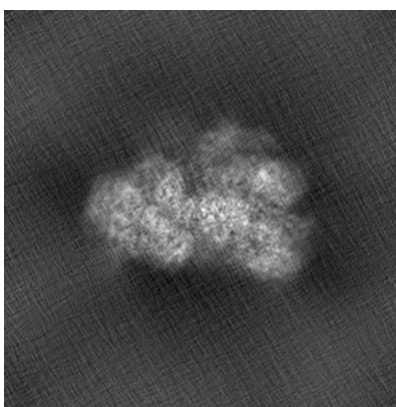


Z

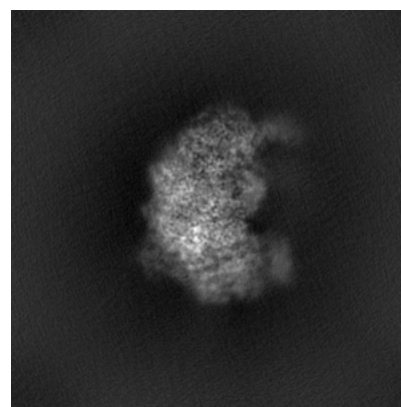
6.1.2 Raw map



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: 180

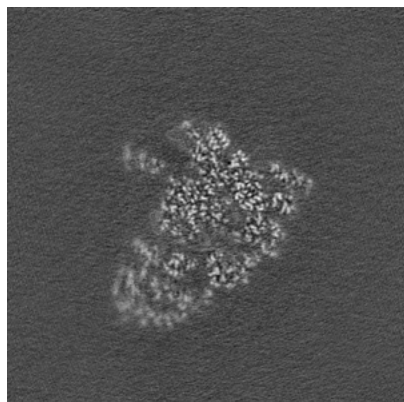


Y Index: 180

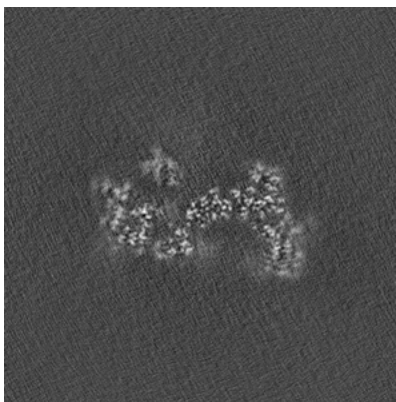


Z Index: 180

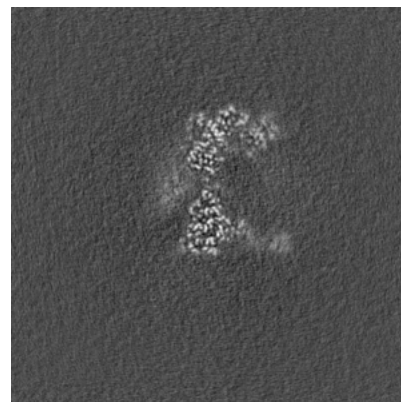
6.2.2 Raw map



X Index: 180



Y Index: 180



Z Index: 180

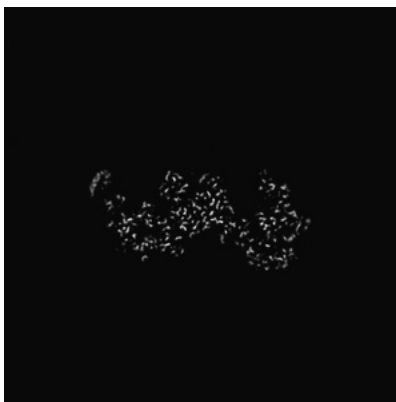
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

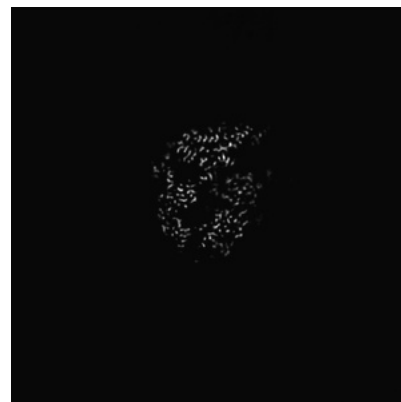
6.3.1 Primary map



X Index: 175

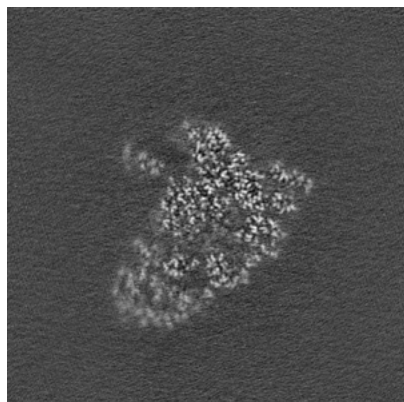


Y Index: 163

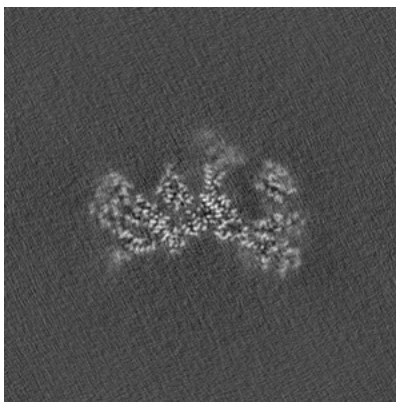


Z Index: 155

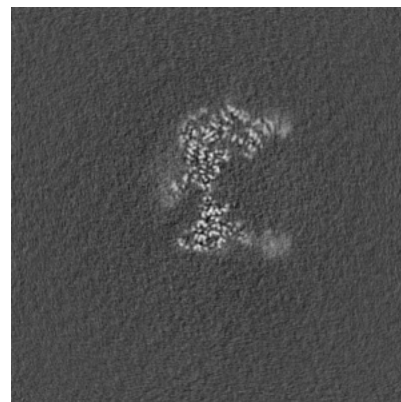
6.3.2 Raw map



X Index: 179



Y Index: 155

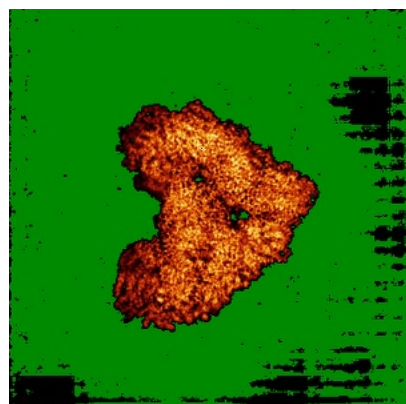


Z Index: 187

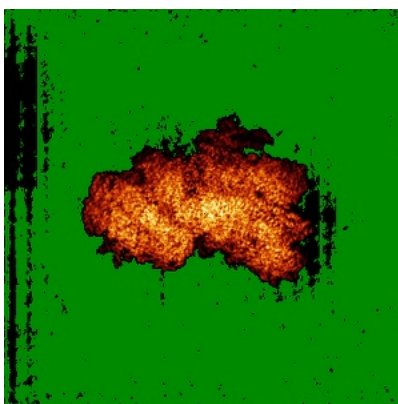
The images above show the largest variance slices of the map in three orthogonal directions.

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

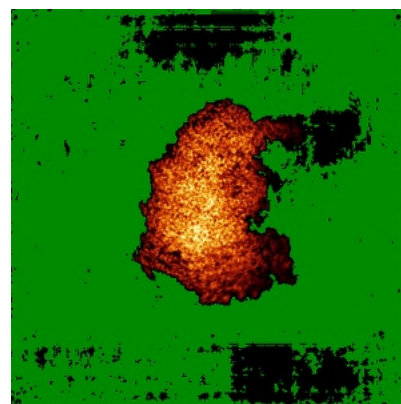
6.4.1 Primary map



X

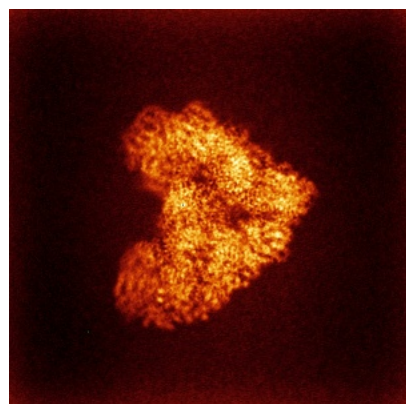


Y

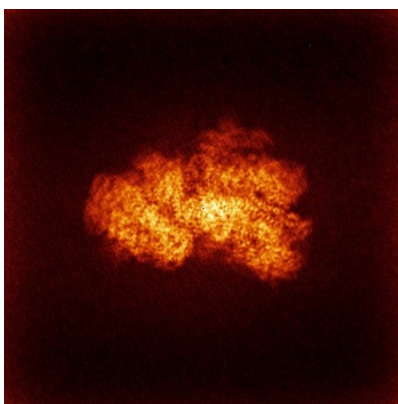


Z

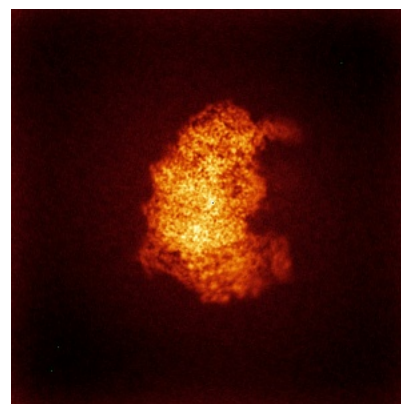
6.4.2 Raw map



X



Y

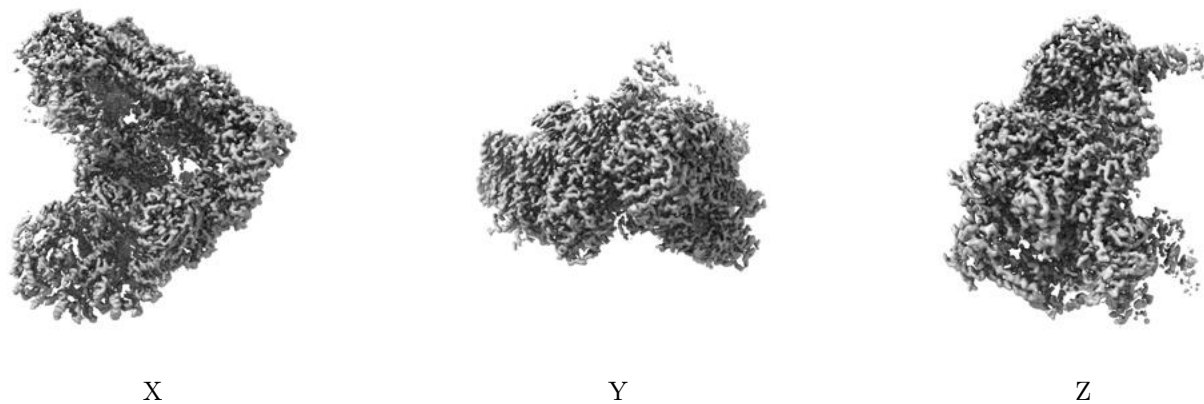


Z

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.

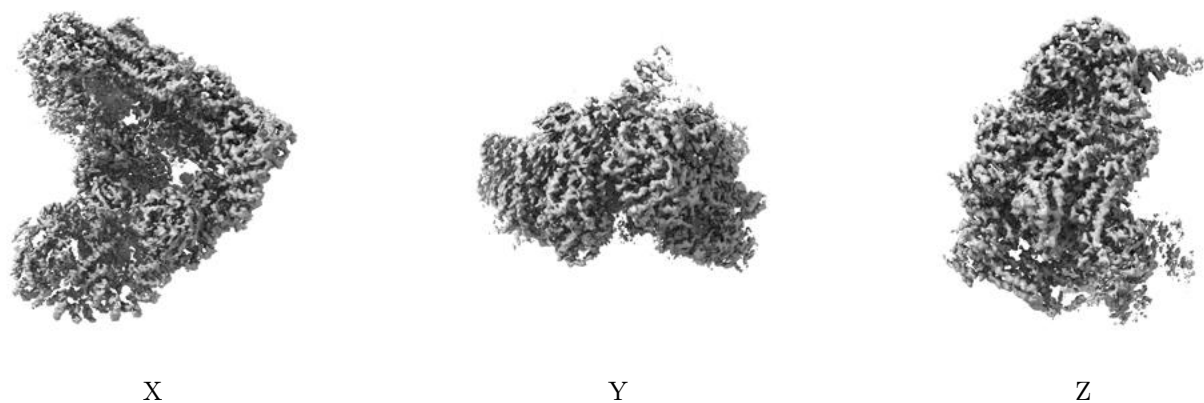
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. 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.

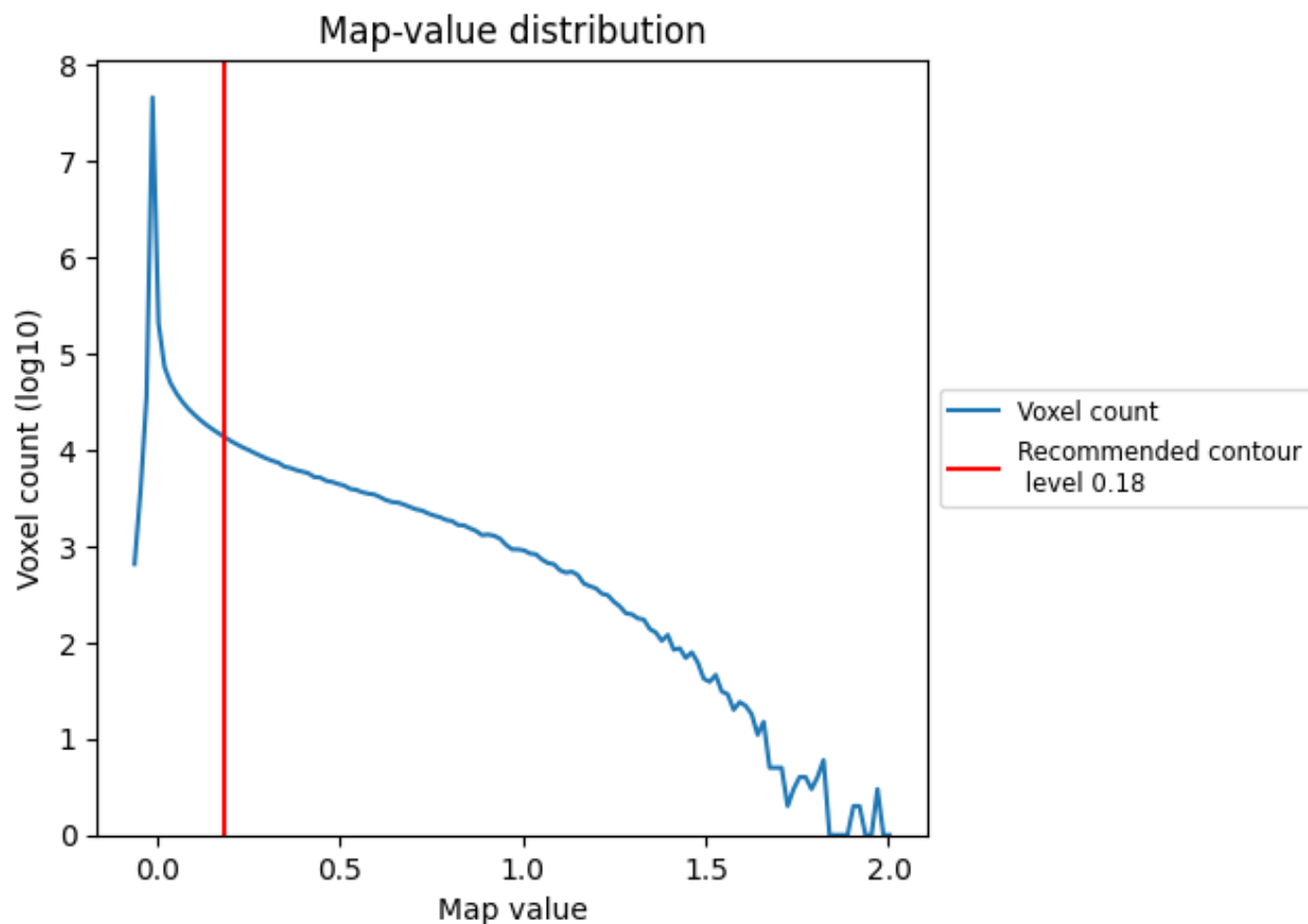
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

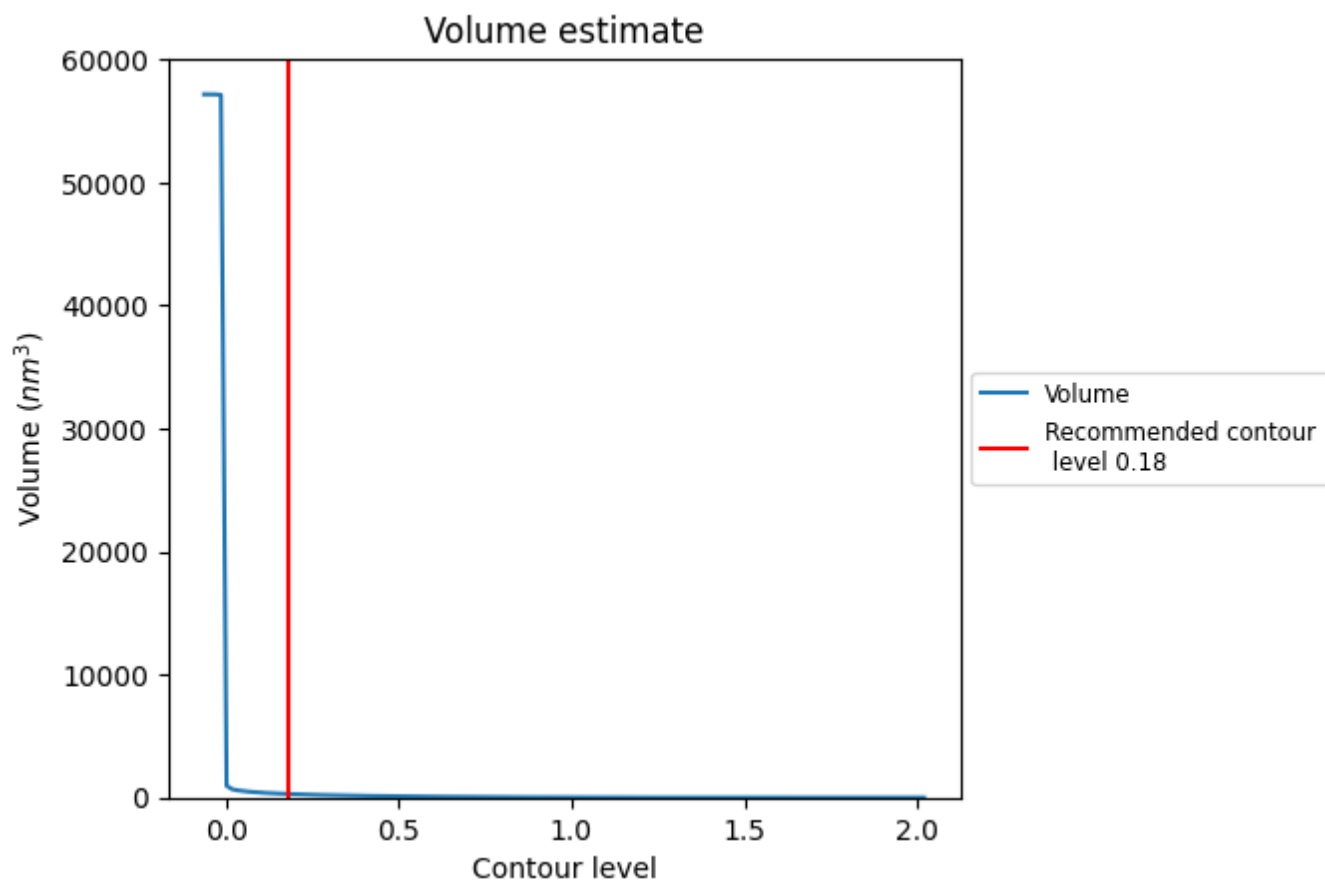
This section contains the results of statistical analysis of the map.

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.

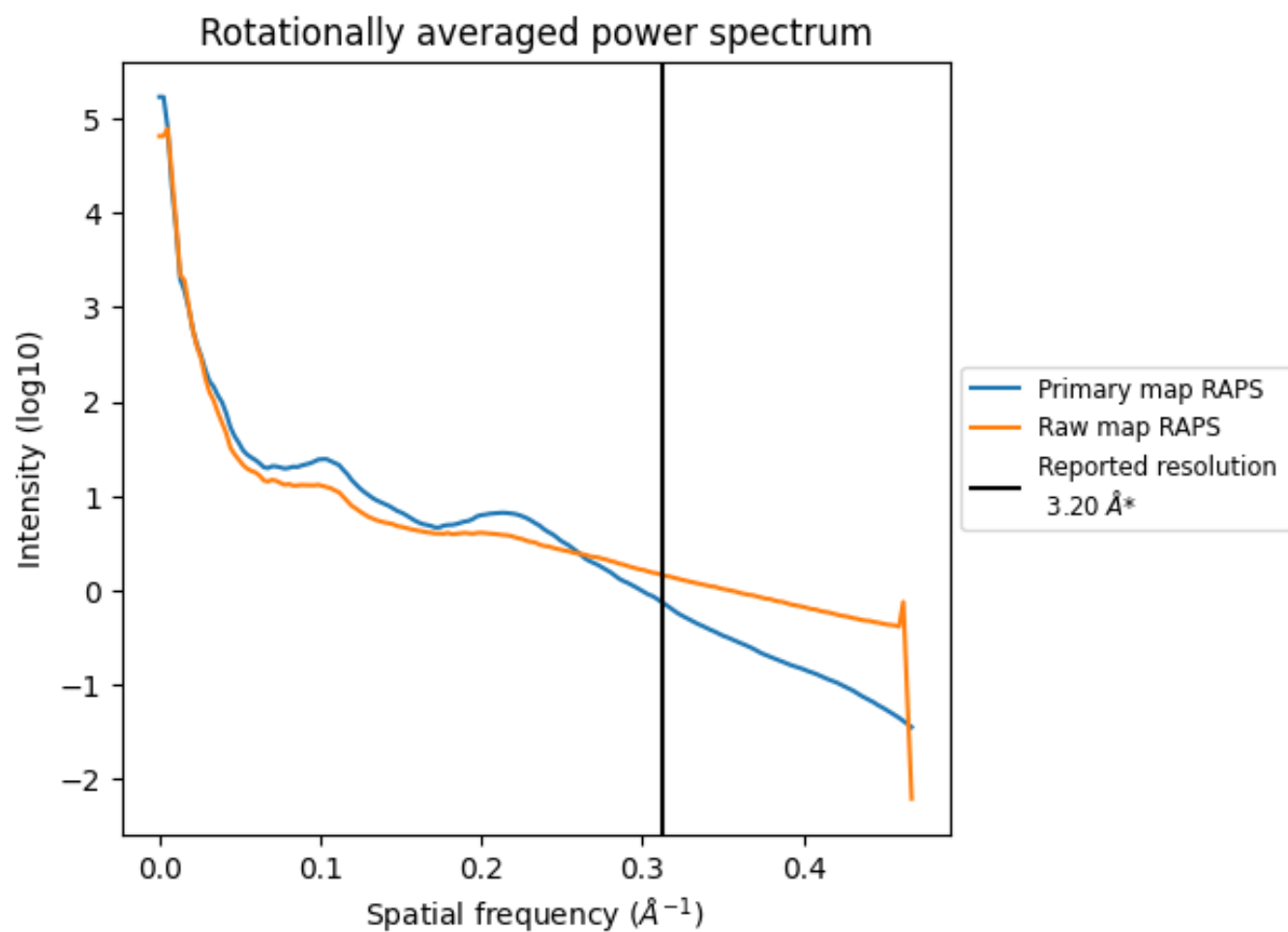
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 291 nm³; this corresponds to an approximate mass of 263 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 ⓘ

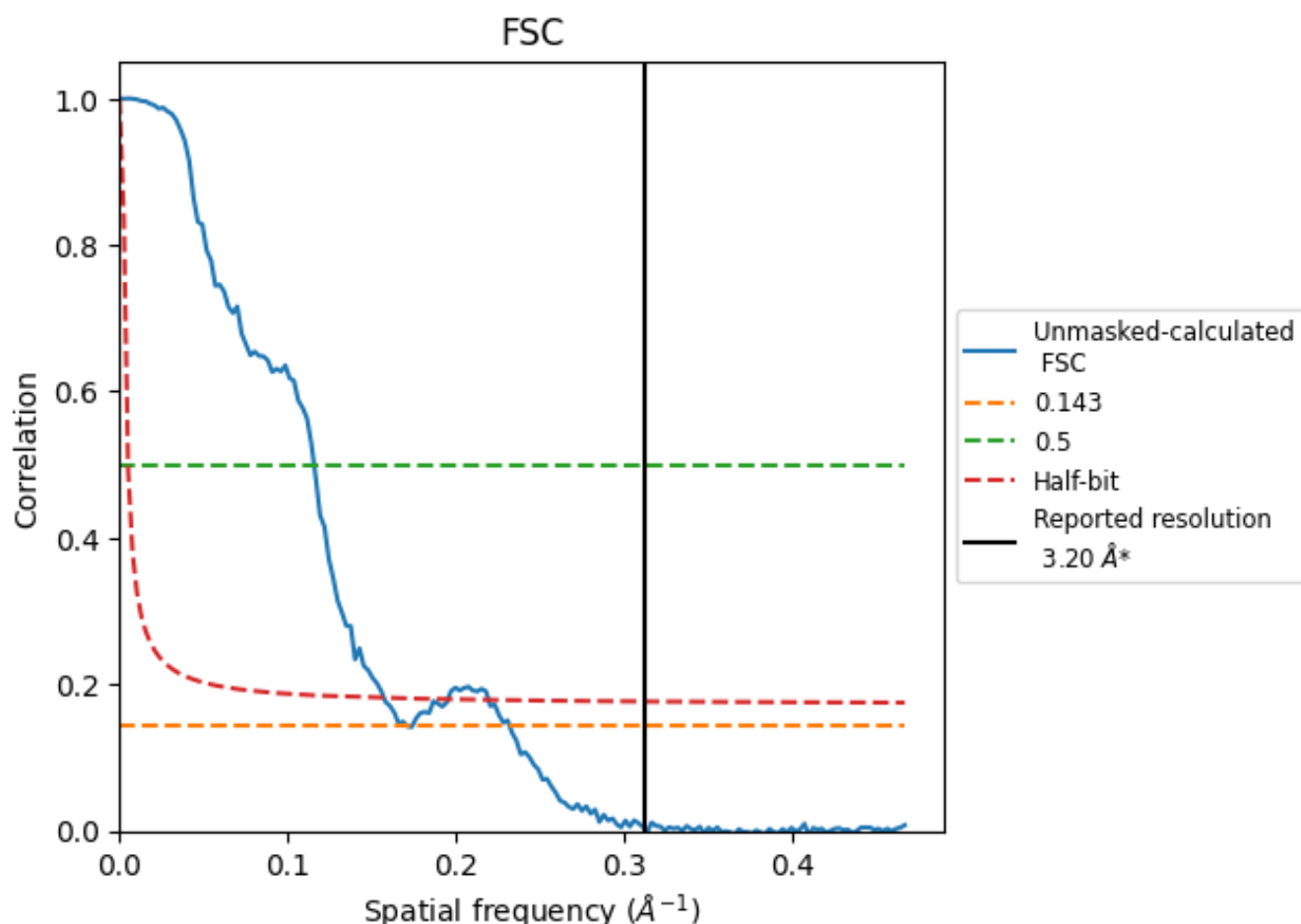


*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}

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 Å⁻¹

8.2 Resolution estimates [i](#)

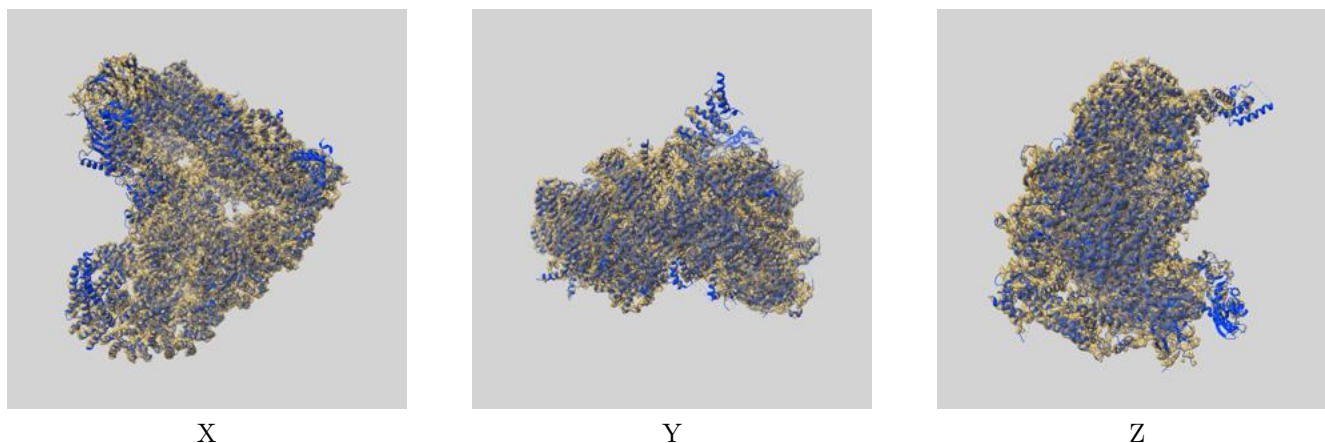
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.84	8.64	6.35

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

9 Map-model fit [i](#)

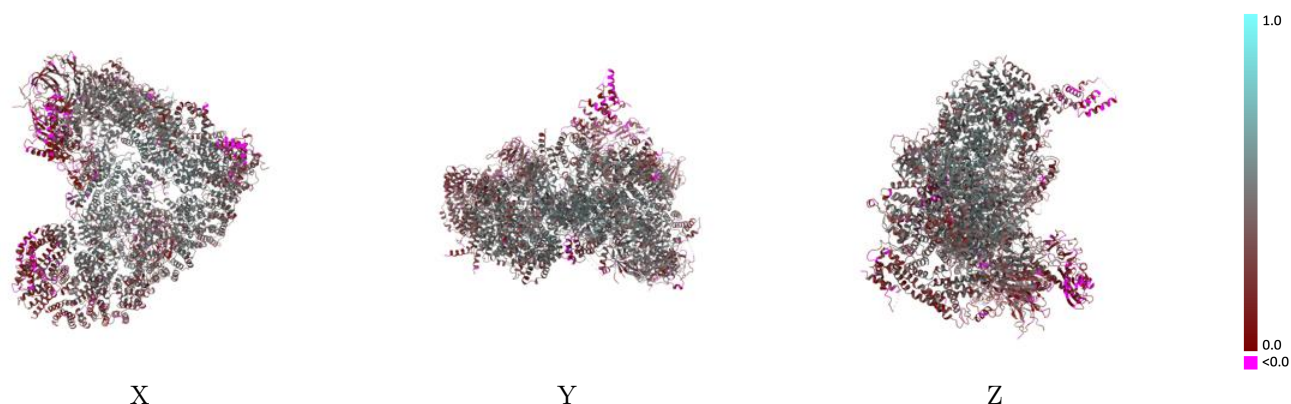
This section contains information regarding the fit between EMDB map EMD-19711 and PDB model 8S4G. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



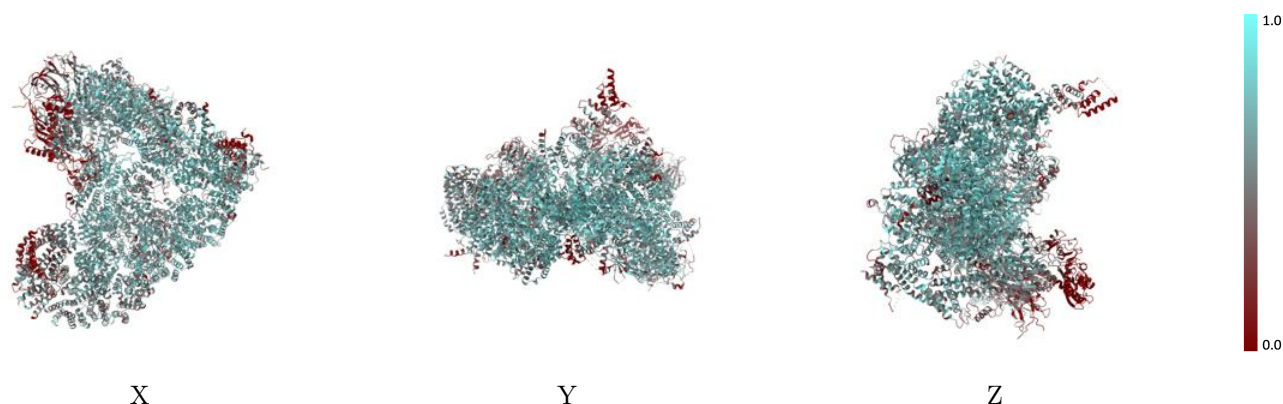
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



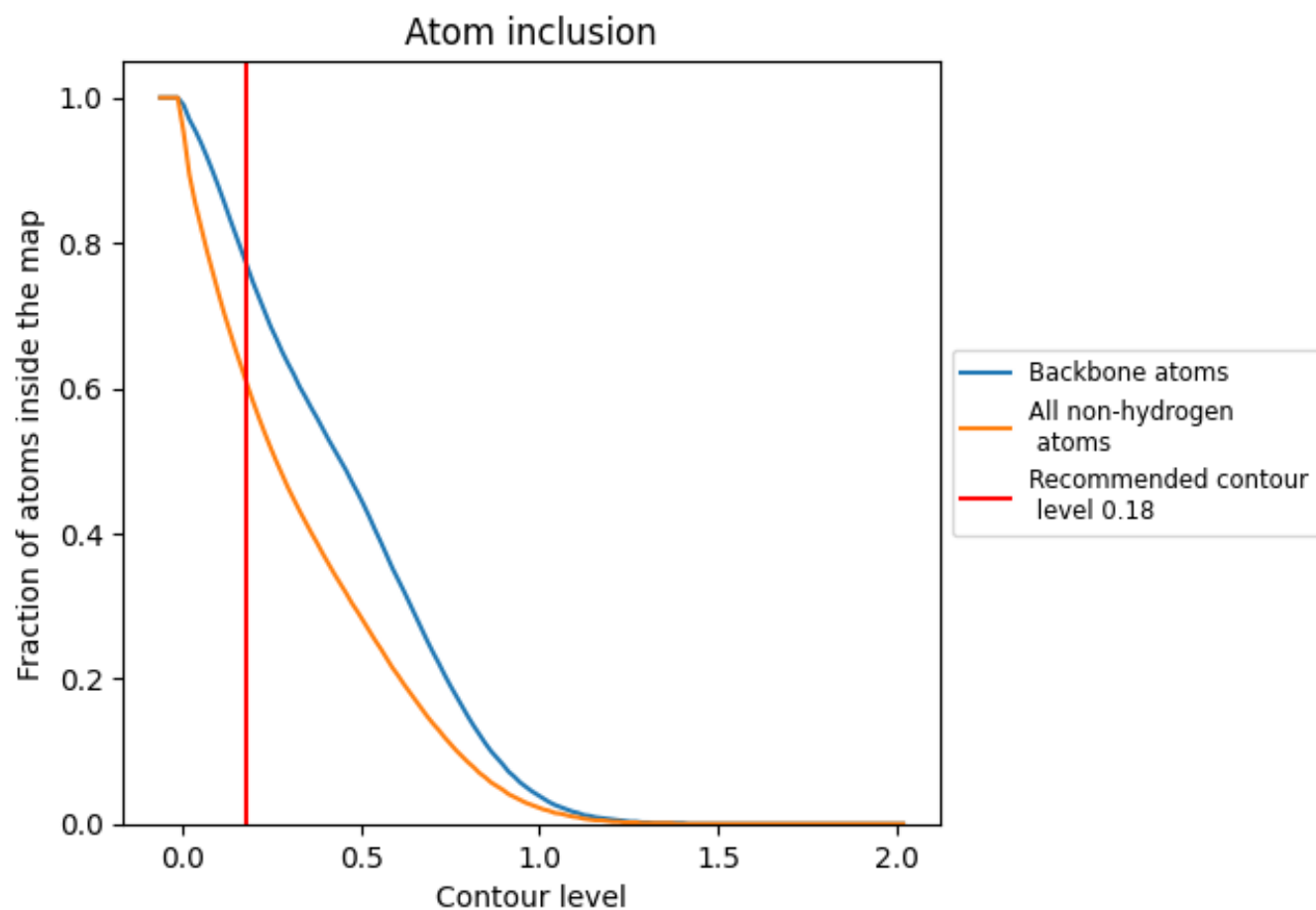
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 61% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.3710
A	 0.6640	 0.4160
C	 0.1140	 0.1570
D	 0.6320	 0.4260
G	 0.5820	 0.3730
H	 0.6490	 0.3680
I	 0.5310	 0.3410
J	 0.6950	 0.4060
K	 0.6990	 0.4500
L	 0.6770	 0.4380
M	 0.6390	 0.4100
N	 0.4240	 0.2390
O	 0.7010	 0.4380
P	 0.6980	 0.4320
Q	 0.7070	 0.4400
R	 0.5420	 0.3240
S	 0.2920	 0.2160
U	 0.5890	 0.3590
V	 0.6750	 0.4330
W	 0.6130	 0.4670
Y	 0.5360	 0.2670
Z	 0.4040	 0.2070

