



wwPDB EM Validation Summary Report ⓘ

Apr 29, 2024 – 10:33 pm BST

PDB ID : 5L9T
EMDB ID : EMD-3433
Title : Model of human Anaphase-promoting complex/Cyclosome (APC/C-CDH1) with E2 UBE2S poised for polyubiquitination where UBE2S, APC2, and APC11 are modeled into low resolution density
Authors : Brown, N.G.; VanderLinden, R.; Dube, P.; Haselbach, D.; Peters, J.M.; Stark, H.; Schulman, B.A.
Deposited on : 2016-06-11
Resolution : 6.40 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:

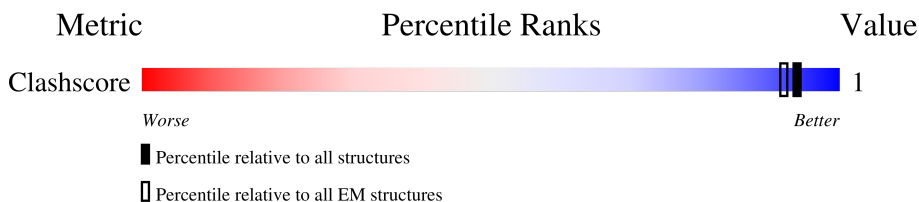
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance i

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


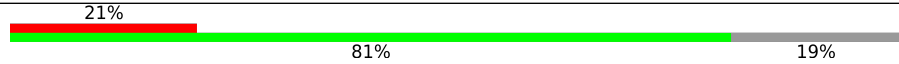
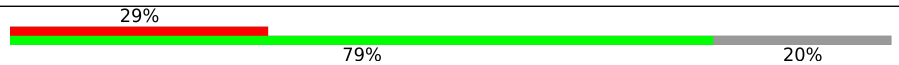

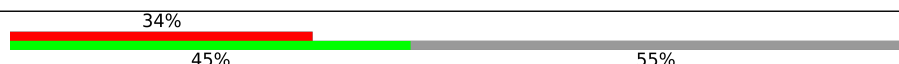
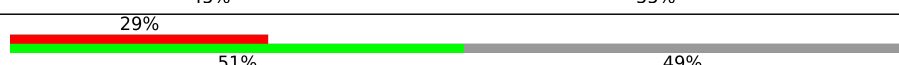

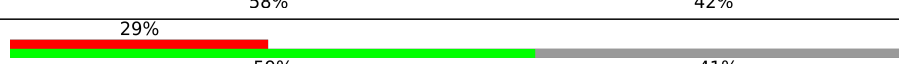


The reported resolution of this entry is 6.40 Å.

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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1944	
2	B	84	
3	C	597	
3	P	597	
4	D	121	
5	E	110	
6	F	824	
6	H	824	
7	G	85	
7	W	85	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	I	818	
9	J	620	
9	K	620	
10	L	185	
11	M	74	
12	N	822	
13	O	755	
14	R	493	
15	S	108	
16	T	185	
17	X	565	
17	Y	565	

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 8038 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 1.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	1380	Total C 1380 1380	0	1380

- Molecule 2 is a protein called Anaphase-promoting complex subunit 11.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	68	Total C 68 68	0	68

- Molecule 3 is a protein called Cell division cycle protein 23 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	C	475	Total C 475 475	0	475
3	P	443	Total C 443 443	0	443

- Molecule 4 is a protein called Anaphase-promoting complex subunit 15.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	D	55	Total C 55 55	0	55

- Molecule 5 is a protein called Anaphase-promoting complex subunit 16.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	E	56	Total C 56 56	0	56

- Molecule 6 is a protein called Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	F	482	Total 482	C 482	0	482
6	H	483	Total 483	C 483	0	483

- Molecule 7 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	G	25	Total 25	C 25	0	25
7	W	25	Total 25	C 25	0	25

- Molecule 8 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	I	727	Total 727	C 727	0	727

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	809	GLY	-	expression tag	UNP Q9UJX5
I	810	GLY	-	expression tag	UNP Q9UJX5
I	811	SER	-	expression tag	UNP Q9UJX5
I	812	LEU	-	expression tag	UNP Q9UJX5
I	813	GLU	-	expression tag	UNP Q9UJX5
I	814	VAL	-	expression tag	UNP Q9UJX5
I	815	LEU	-	expression tag	UNP Q9UJX5
I	816	PHE	-	expression tag	UNP Q9UJX5
I	817	GLN	-	expression tag	UNP Q9UJX5
I	818	GLY	-	expression tag	UNP Q9UJX5

- Molecule 9 is a protein called Cell division cycle protein 16 homolog.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	J	504	Total 504	C 504	0	504
9	K	493	Total 493	C 493	0	493

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

Mol	Chain	Residues	Atoms		AltConf	Trace
10	L	170	Total	C	0	170
			170	170		

- Molecule 11 is a protein called Anaphase-promoting complex subunit 13.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	M	42	Total	C	0	42
			42	42		

- Molecule 12 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	N	546	Total	C	0	546
			546	546		

- Molecule 13 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	O	685	Total	C	0	685
			685	685		

- Molecule 14 is a protein called Fizzy-related protein homolog.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	R	385	Total	C	0	385
			385	385		

- Molecule 15 is a protein called Ubiquitin_variant-Hsl1(substrate) fusion.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	S	84	Total	C	0	84
			84	84		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-4	GLY	-	expression tag	UNP P0CG47
S	-3	SER	-	expression tag	UNP P0CG47
S	-2	GLY	-	expression tag	UNP P0CG47
S	-1	GLY	-	expression tag	UNP P0CG47
S	0	SER	-	expression tag	UNP P0CG47
S	4	LEU	PHE	engineered mutation	UNP P0CG47

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
S	8	PRO	LEU	engineered mutation	UNP P0CG47
S	9	ARG	THR	engineered mutation	UNP P0CG47
S	11	CYS	LYS	engineered mutation	UNP P0CG47
S	42	ILE	ARG	engineered mutation	UNP P0CG47
S	44	PHE	ILE	engineered mutation	UNP P0CG47
S	47	VAL	GLY	engineered mutation	UNP P0CG47
S	49	ARG	GLN	engineered mutation	UNP P0CG47
S	64	LYS	GLU	engineered mutation	UNP P0CG47
S	66	SER	THR	engineered mutation	UNP P0CG47
S	68	LEU	HIS	engineered mutation	UNP P0CG47
S	70	ALA	VAL	engineered mutation	UNP P0CG47
S	71	MET	LEU	engineered mutation	UNP P0CG47
S	73	VAL	LEU	engineered mutation	UNP P0CG47
S	74	PRO	ARG	engineered mutation	UNP P0CG47
S	815	LYS	GLY	engineered mutation	UNP P0CG47
S	817	LYS	-	linker	UNP P0CG47

- Molecule 16 is a protein called Ubiquitin-conjugating enzyme E2 S.

Mol	Chain	Residues	Atoms	AltConf	Trace
16	T	97	Total C 97 97	0	97

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-3	GLY	-	expression tag	UNP Q16763
T	-2	PRO	-	expression tag	UNP Q16763
T	-1	GLY	-	expression tag	UNP Q16763
T	0	SER	-	expression tag	UNP Q16763
T	118	PHE	CYS	conflict	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ARG	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ARG	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
T	?	-	LEU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	THR	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	THR	deletion	UNP Q16763
T	?	-	ASP	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	MET	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	LYS	deletion	UNP Q16763
T	?	-	LYS	deletion	UNP Q16763
T	?	-	HIS	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763

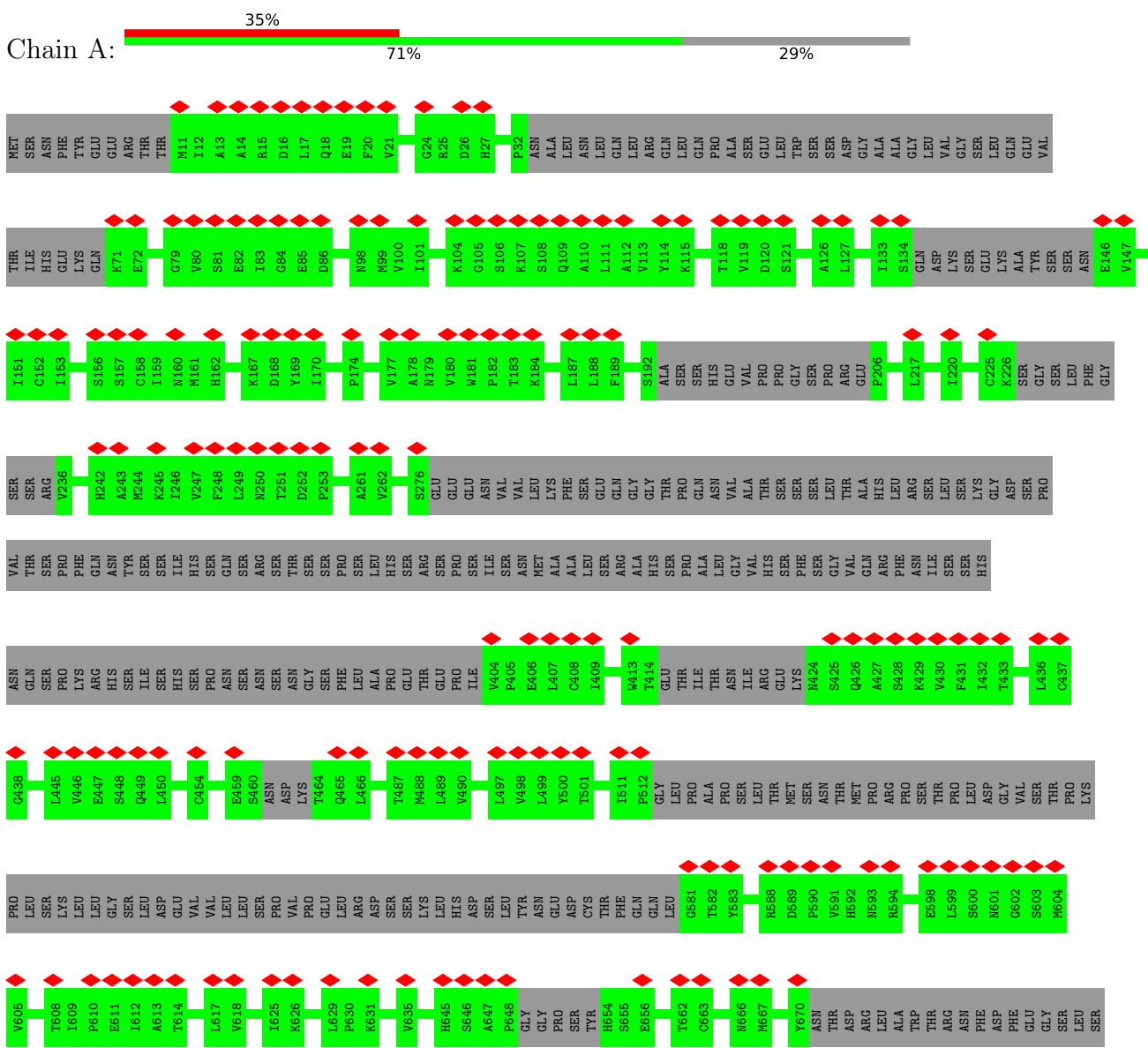
- Molecule 17 is a protein called Anaphase-promoting complex subunit 7.

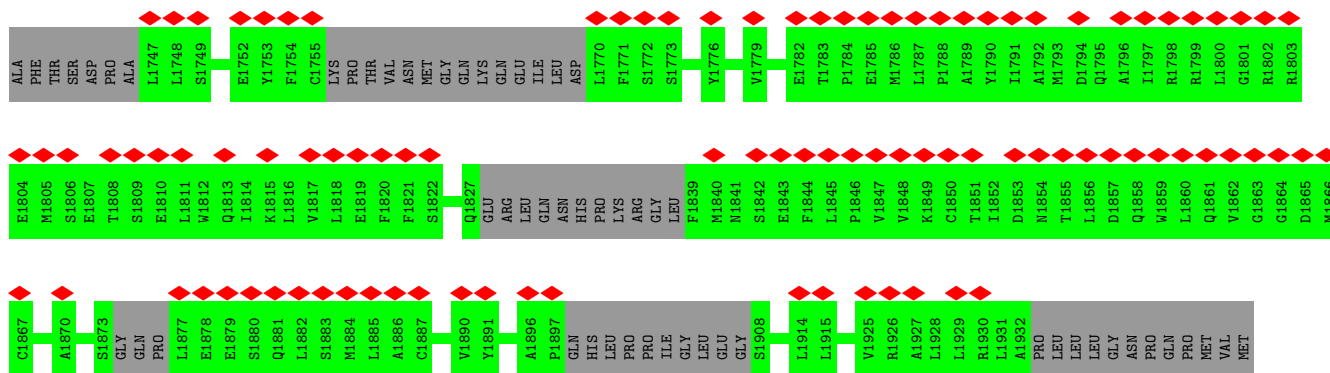
Mol	Chain	Residues	Atoms	AltConf	Trace
17	X	397	Total C 397 397	0	397
17	Y	416	Total C 416 416	0	416

3 Residue-property plots

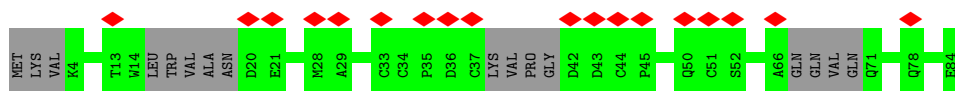
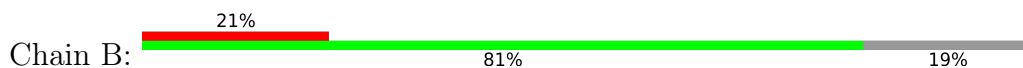
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 1

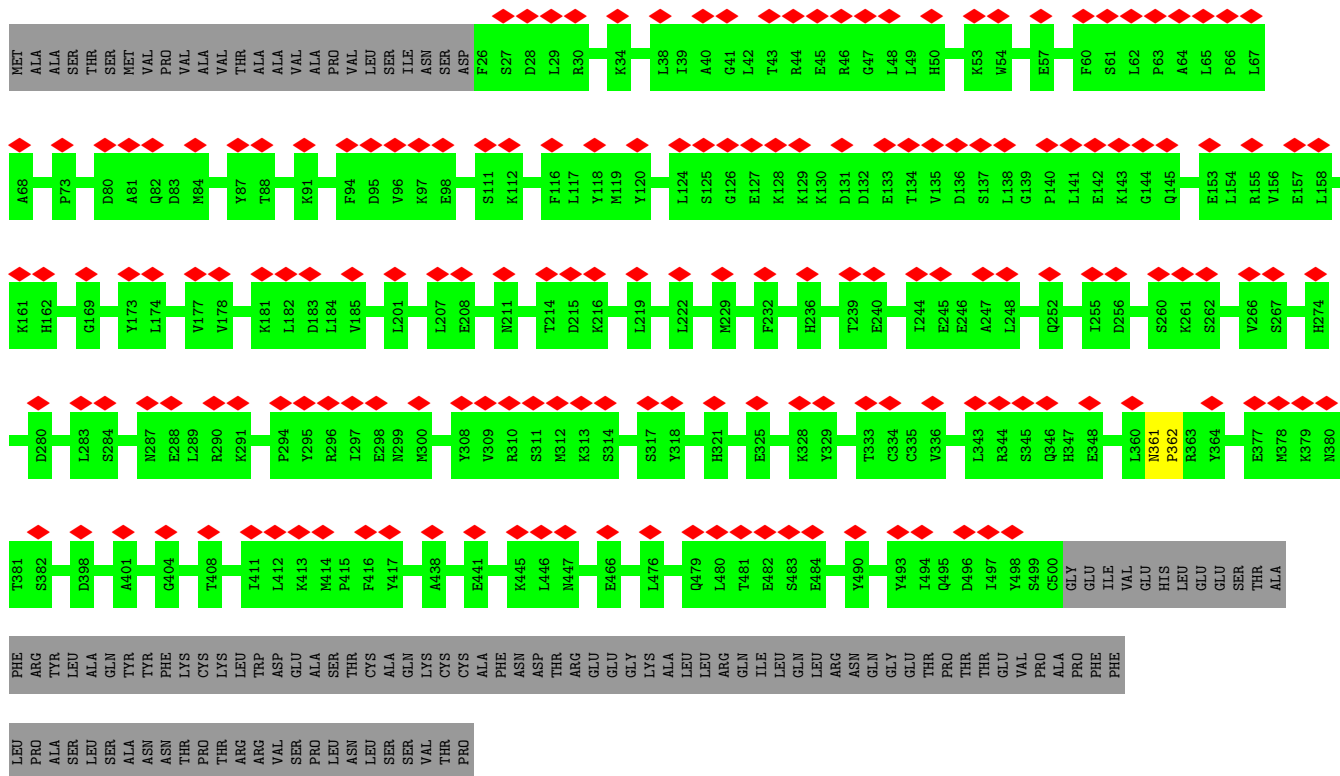
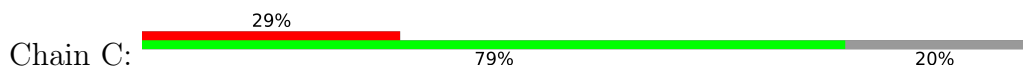




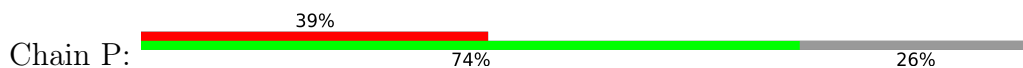
- Molecule 2: Anaphase-promoting complex subunit 11

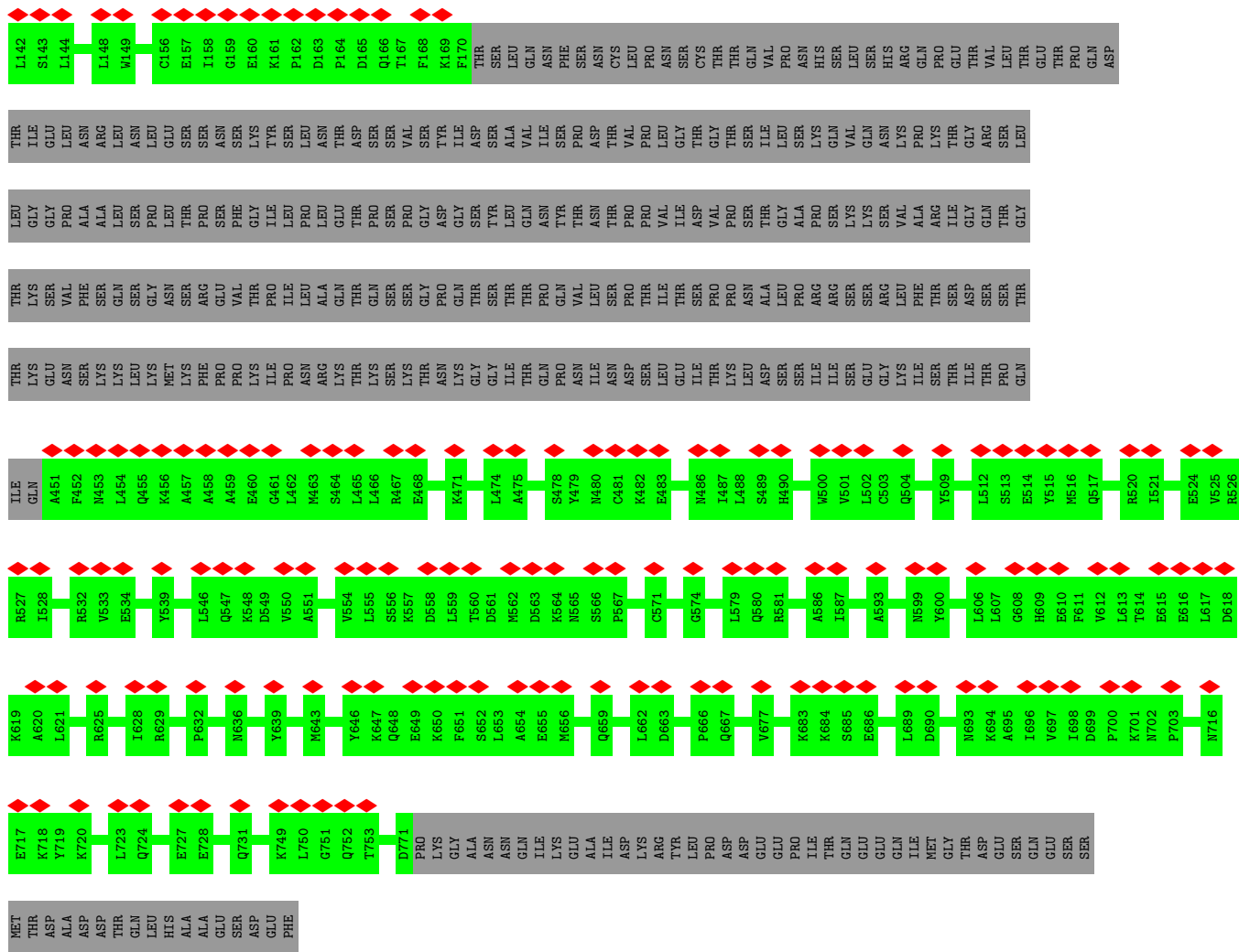


- Molecule 3: Cell division cycle protein 23 homolog

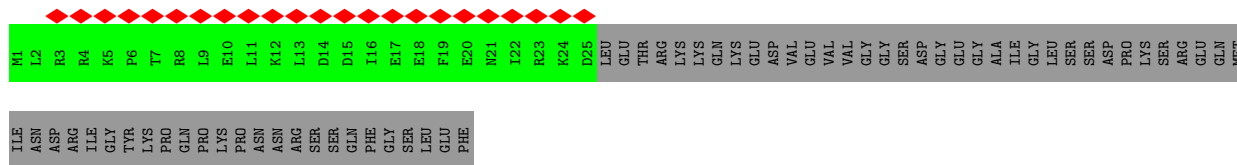


- Molecule 3: Cell division cycle protein 23 homolog

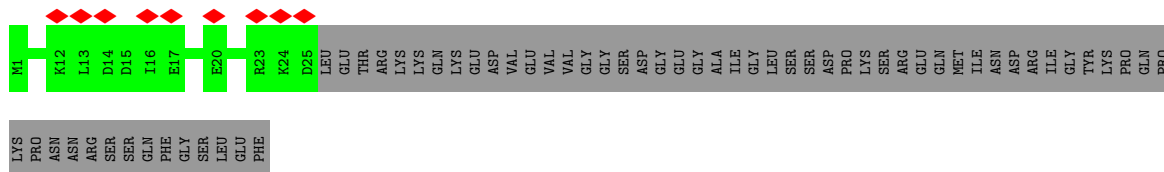


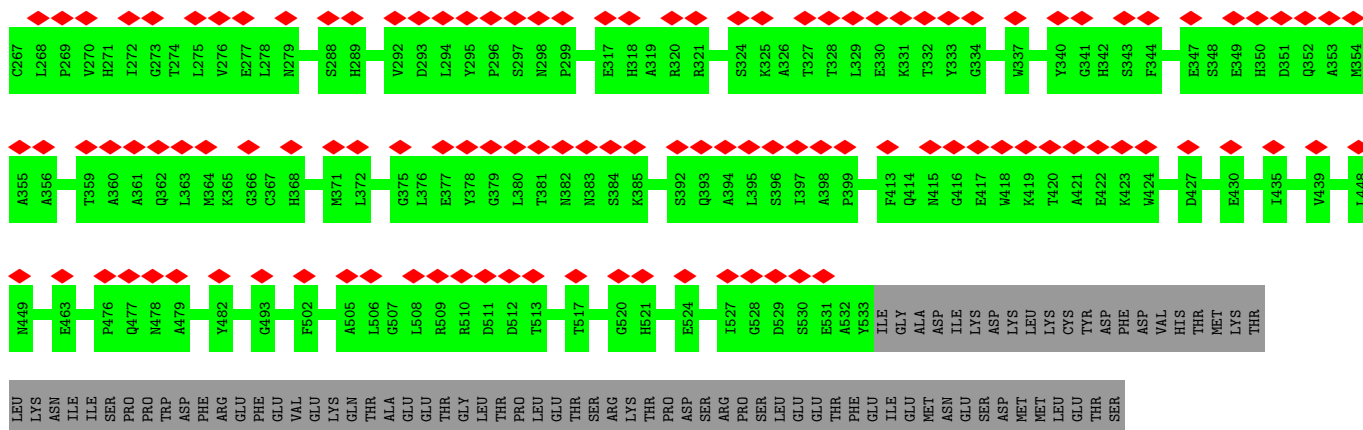


- Molecule 7: Anaphase-promoting complex subunit CDC26

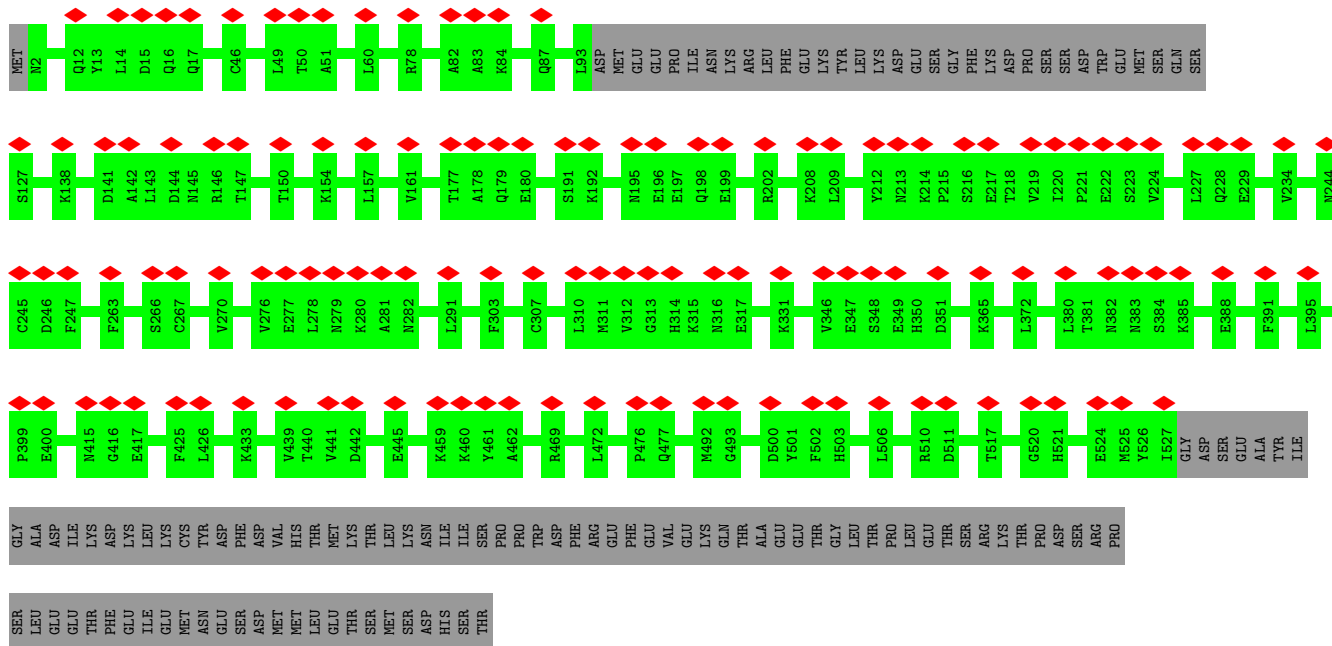
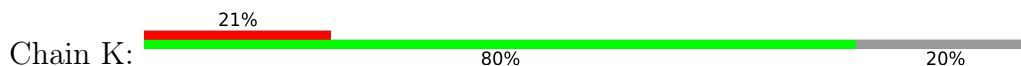


- Molecule 7: Anaphase-promoting complex subunit CDC26

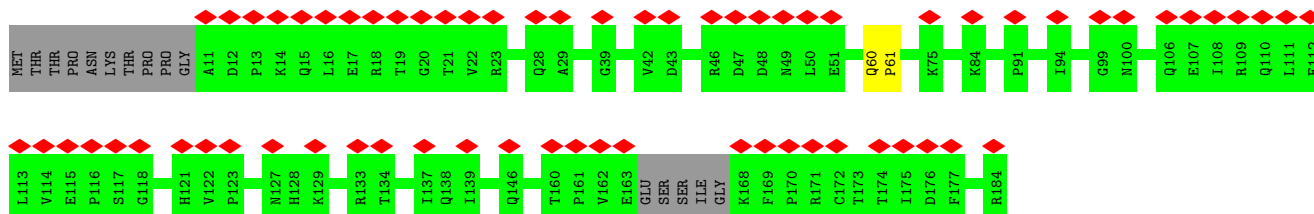
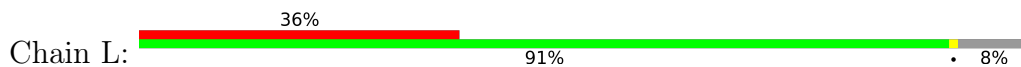




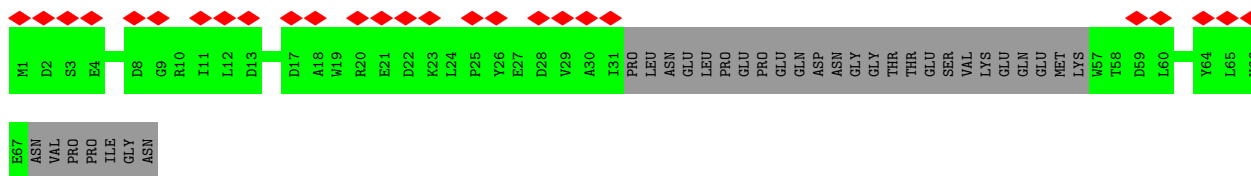
● Molecule 9: Cell division cycle protein 16 homolog



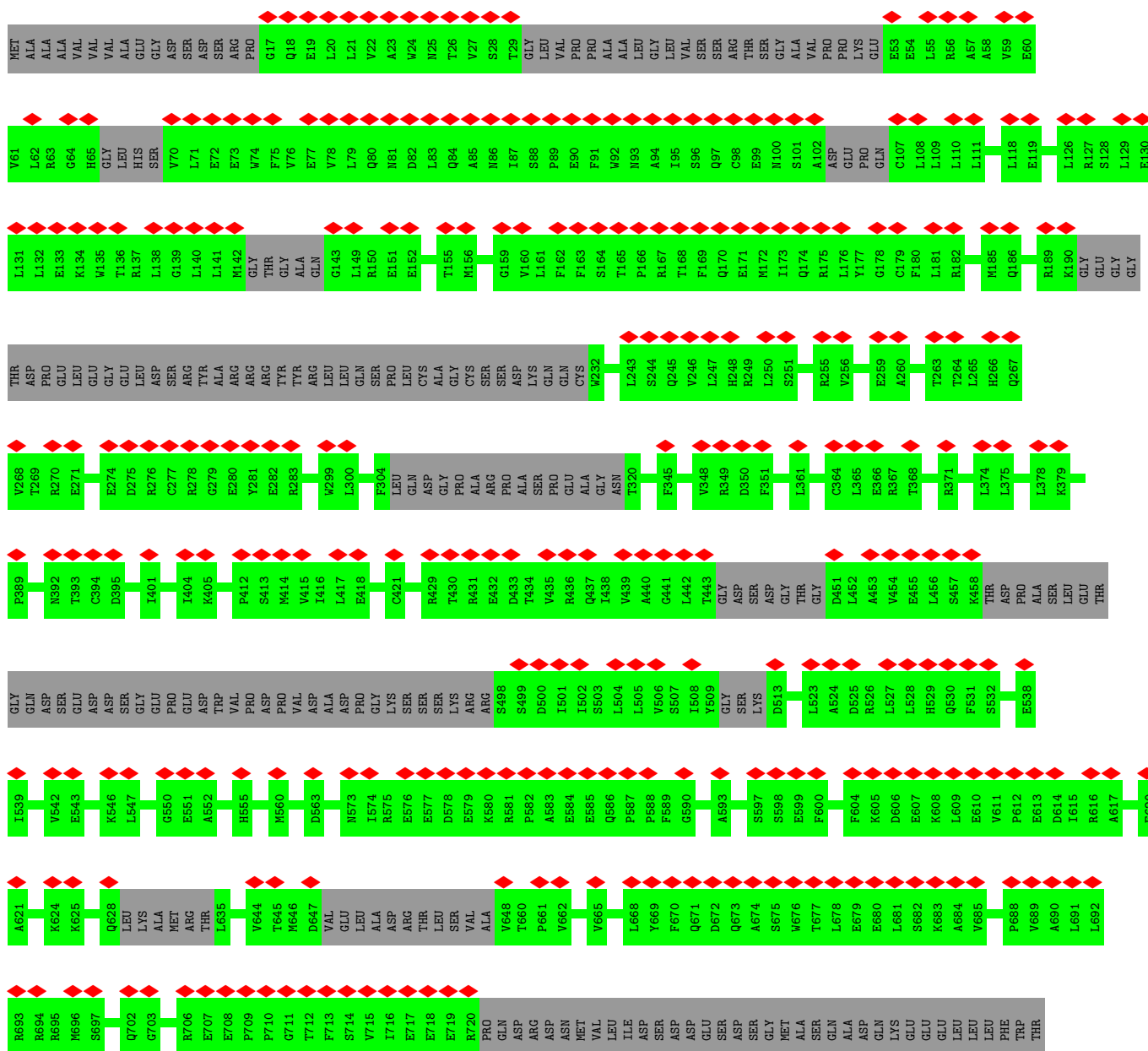
● Molecule 10: Anaphase-promoting complex subunit 10



• Molecule 11: Anaphase-promoting complex subunit 13



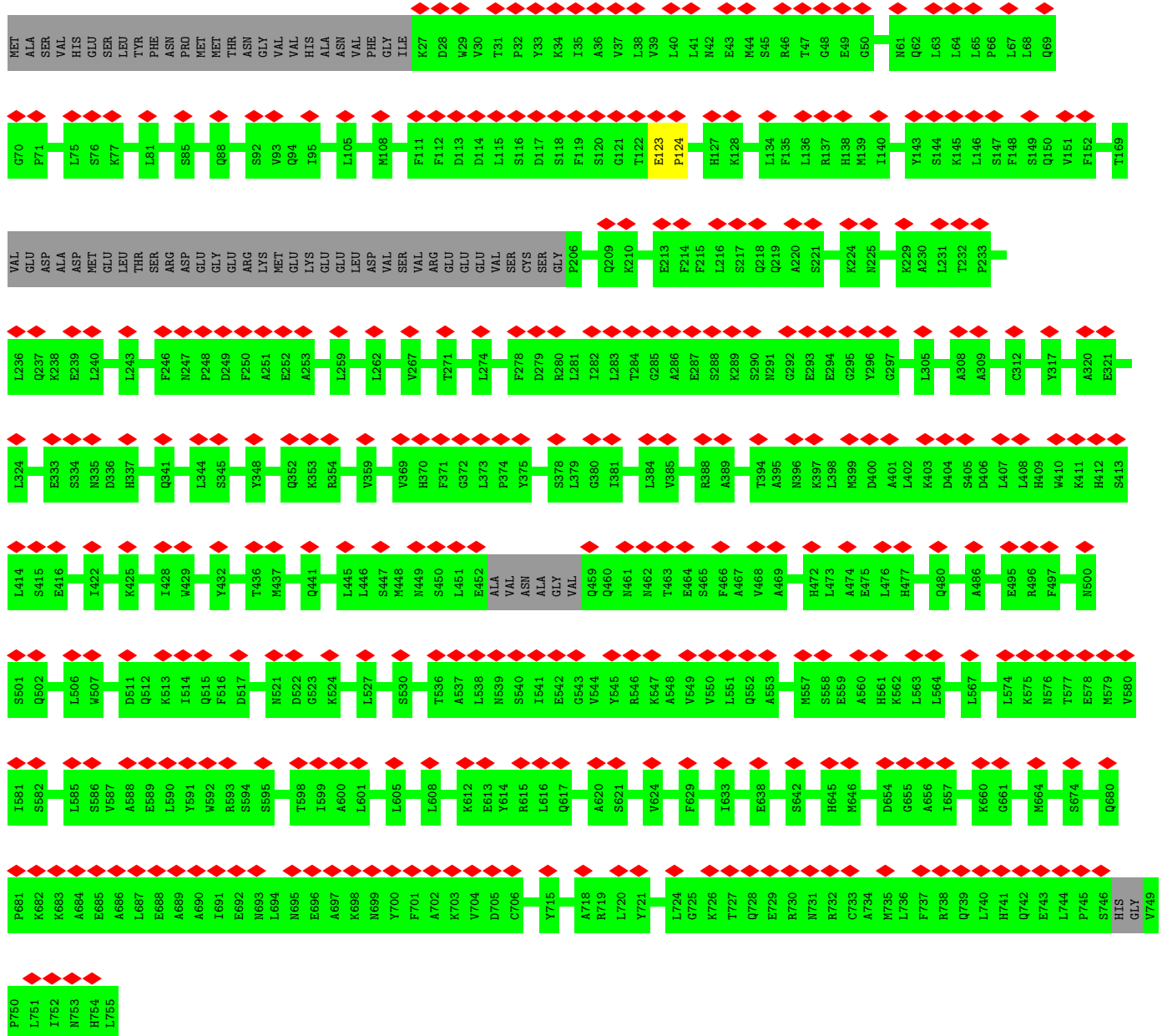
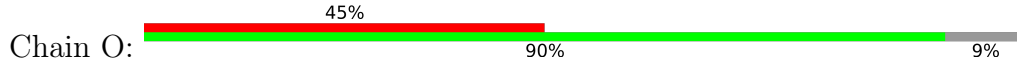
• Molecule 12: Anaphase-promoting complex subunit 2



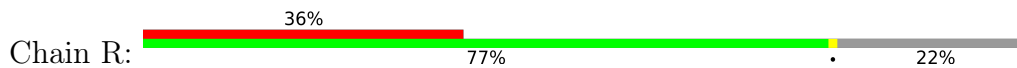
TYR
ILE
GLN
ALA
MET
LEU
THR
ASN
LEU
GLU
SER
ASN
LEU
SER
MET
LEU
ASP
PHE
ILE
TYR
GLY
VAL
ASN
MET
LEU
ARG
MET
PHE
GLY
VAL
VAL
THR
GLY
GLN
ALA
LEU
ALA
LEU
GLU
ASP
ASP
GLN
GLN
GLY
TYR
LEU
GLN
LYS
VAL
ARG
ASP
GLN
GLN
VAL
VAL
TYR
SER
SER
ALA
GLY
VAL
TYR
ARG

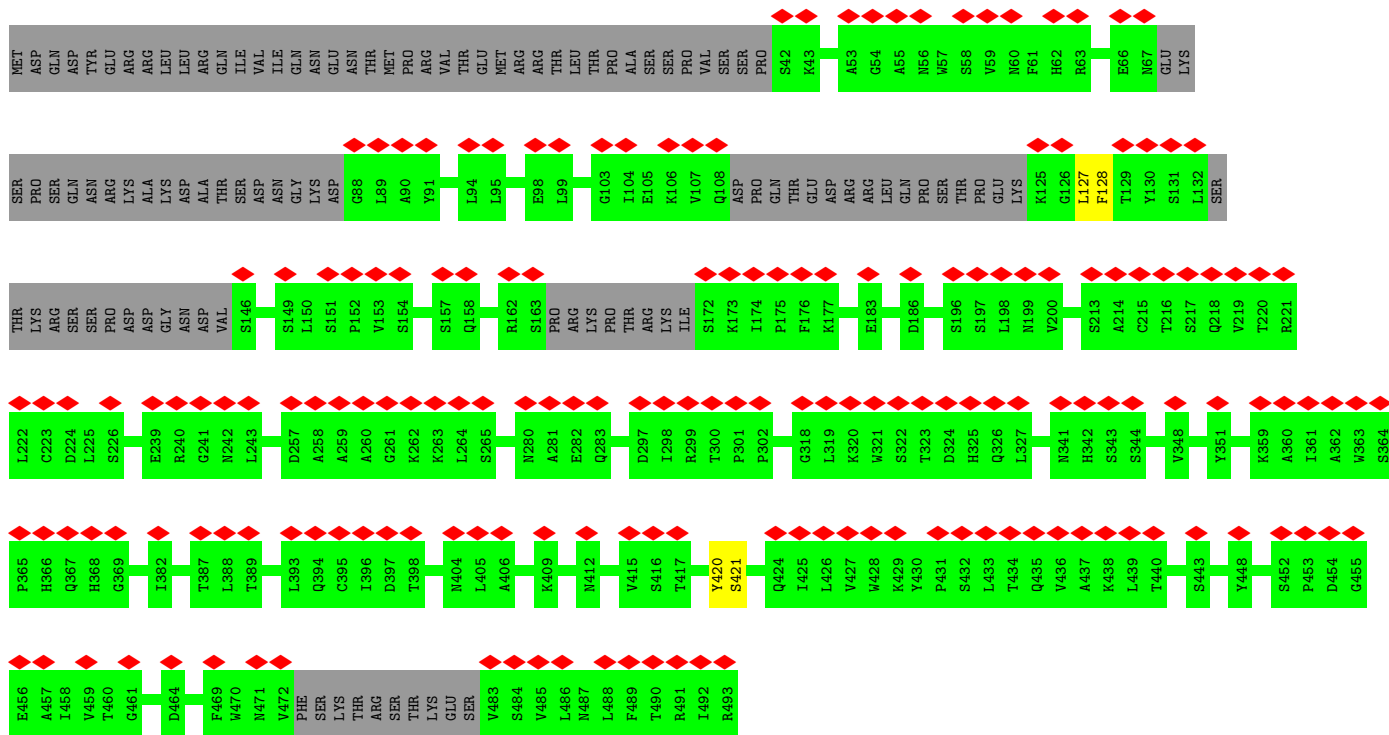
LEU
PRO
LYS
ASN
CYS
SER

● Molecule 13: Anaphase-promoting complex subunit 5

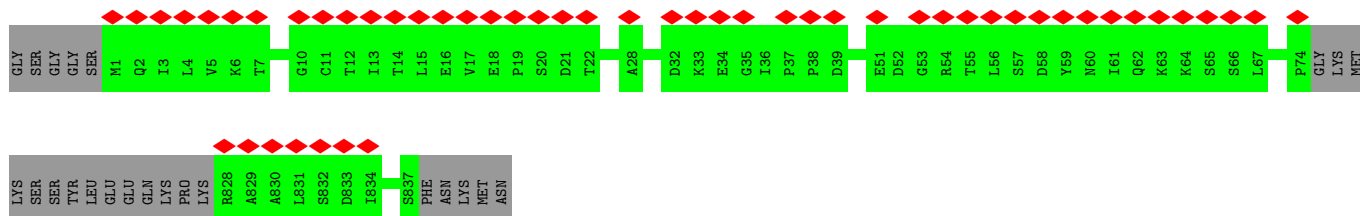
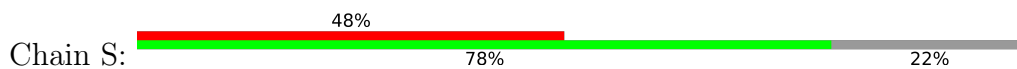


● Molecule 14: Fizzy-related protein homolog

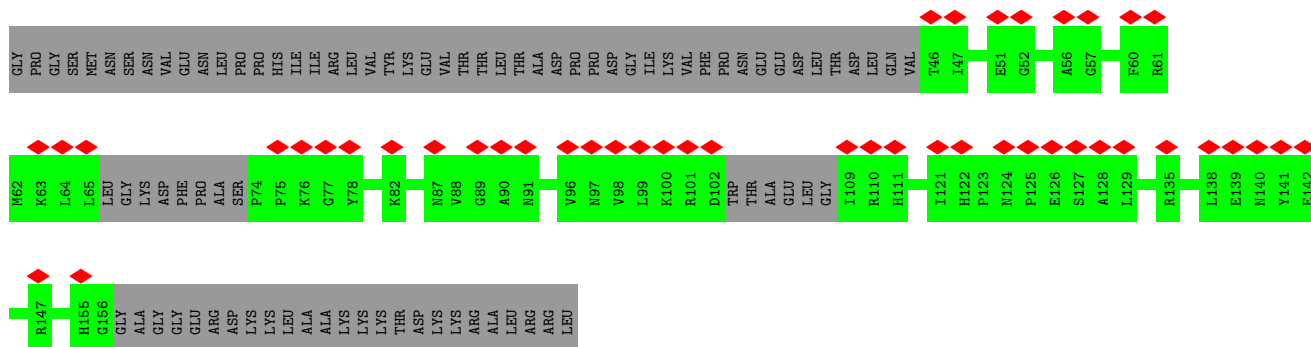




• Molecule 15: Ubiquitin_variant-Hsl1(substrate) fusion



• Molecule 16: Ubiquitin-conjugating enzyme E2 S



• Molecule 17: Anaphase-promoting complex subunit 7

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

PRO
THR
ASP
ALA
THR
GLN
GLU
ASP
VAL
ASP
MET
GLU
GLY
SER
SER
GLY
GLU
GLY
GLY
ASP
LEU
GLU
GLY
SER
ASP
SER
GLU
ALA
ALA
GLN
TRP
ALA
ASP
GLN
TYR
GLU
GLN
TRP
PHE
GLY
MET
GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135578	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.206	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	401.92, 401.92, 401.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.57, 1.57, 1.57	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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 [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	A	1380	0	0	3	0
2	B	68	0	0	0	0
3	C	475	0	0	1	0
3	P	443	0	0	1	0
4	D	55	0	0	0	0
5	E	56	0	0	0	0
6	F	482	0	0	0	0
6	H	483	0	0	0	0
7	G	25	0	0	0	0
7	W	25	0	0	0	0
8	I	727	0	0	1	0
9	J	504	0	0	0	0
9	K	493	0	0	0	0
10	L	170	0	0	1	0
11	M	42	0	0	0	0
12	N	546	0	0	0	0
13	O	685	0	0	1	0
14	R	385	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	S	84	0	0	0	0
16	T	97	0	0	0	0
17	X	397	0	0	0	0
17	Y	416	0	0	0	0
All	All	8038	0	0	10	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 1.

The worst 5 of 10 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)
14:R:420:TYR:CA	14:R:421:SER:CA	2.81	0.59
1:A:1670:GLY:CA	1:A:1671:PRO:CA	2.84	0.54
14:R:127:LEU:CA	14:R:128:PHE:CA	2.92	0.48
3:P:361:ASN:CA	3:P:362:PRO:CA	2.92	0.47
1:A:1100:LEU:CA	1:A:1101:PRO:CA	2.93	0.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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 monosaccharides 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](#)

There are no chain breaks in this entry.

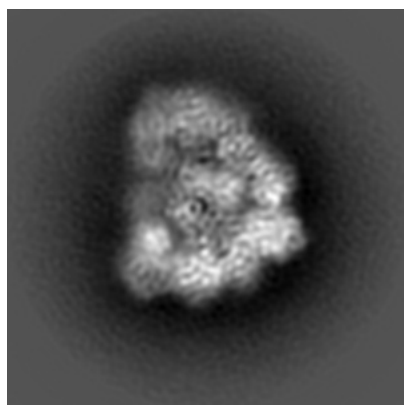
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3433. These allow visual inspection of the internal detail of the map and identification of artifacts.

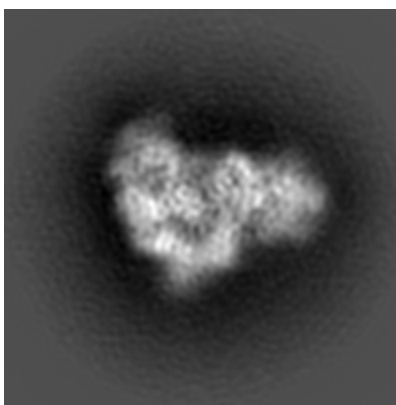
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

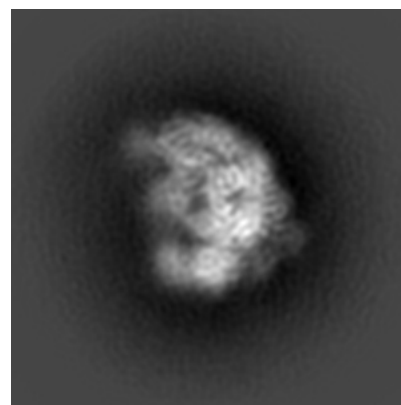
6.1.1 Primary map



X



Y

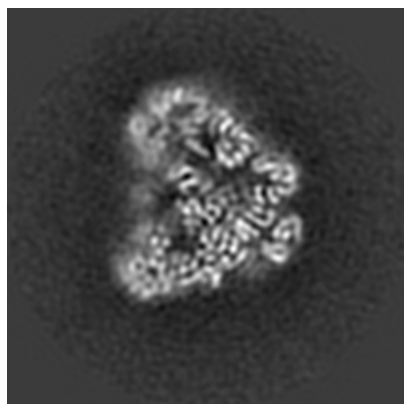


Z

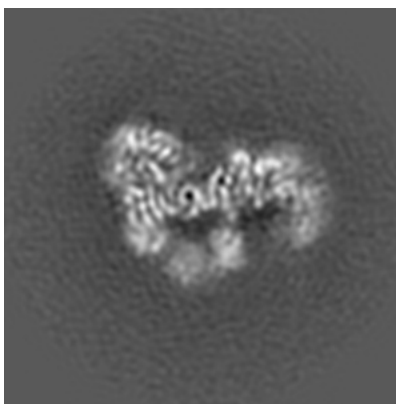
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

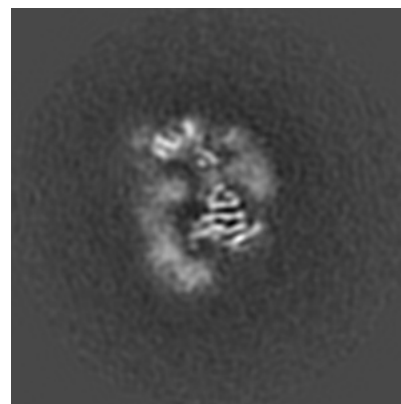
6.2.1 Primary map



X Index: 128



Y Index: 128

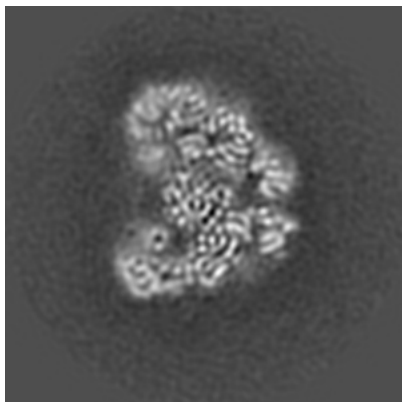


Z Index: 128

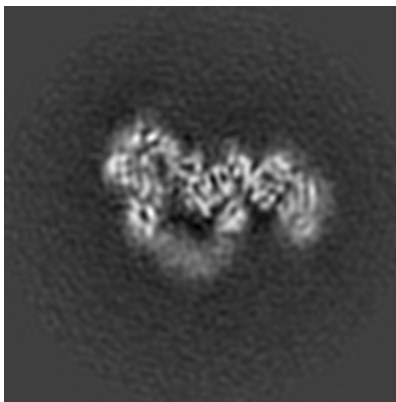
The images above show central slices of the map in three orthogonal directions.

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

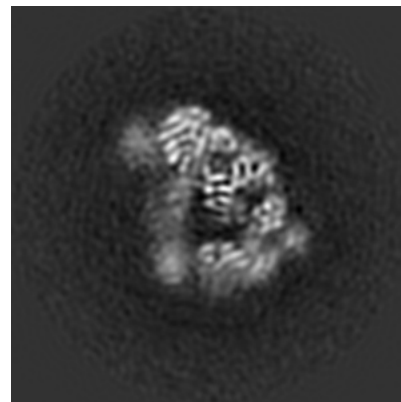
6.3.1 Primary map



X Index: 134



Y Index: 121

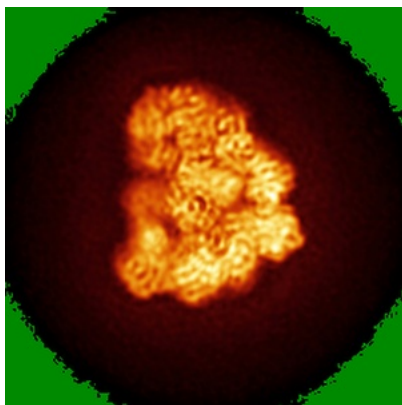


Z Index: 104

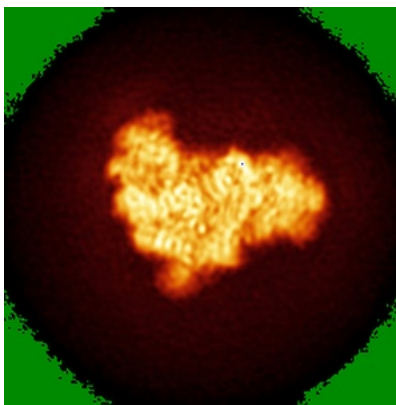
The images above show the largest variance slices of the map in three orthogonal directions.

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

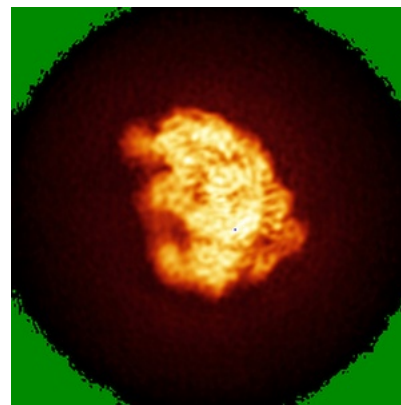
6.4.1 Primary map



X



Y

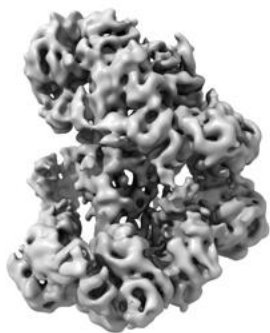


Z

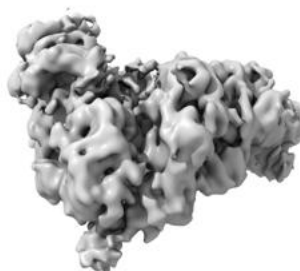
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

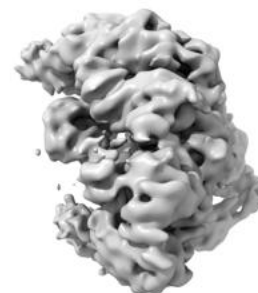
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

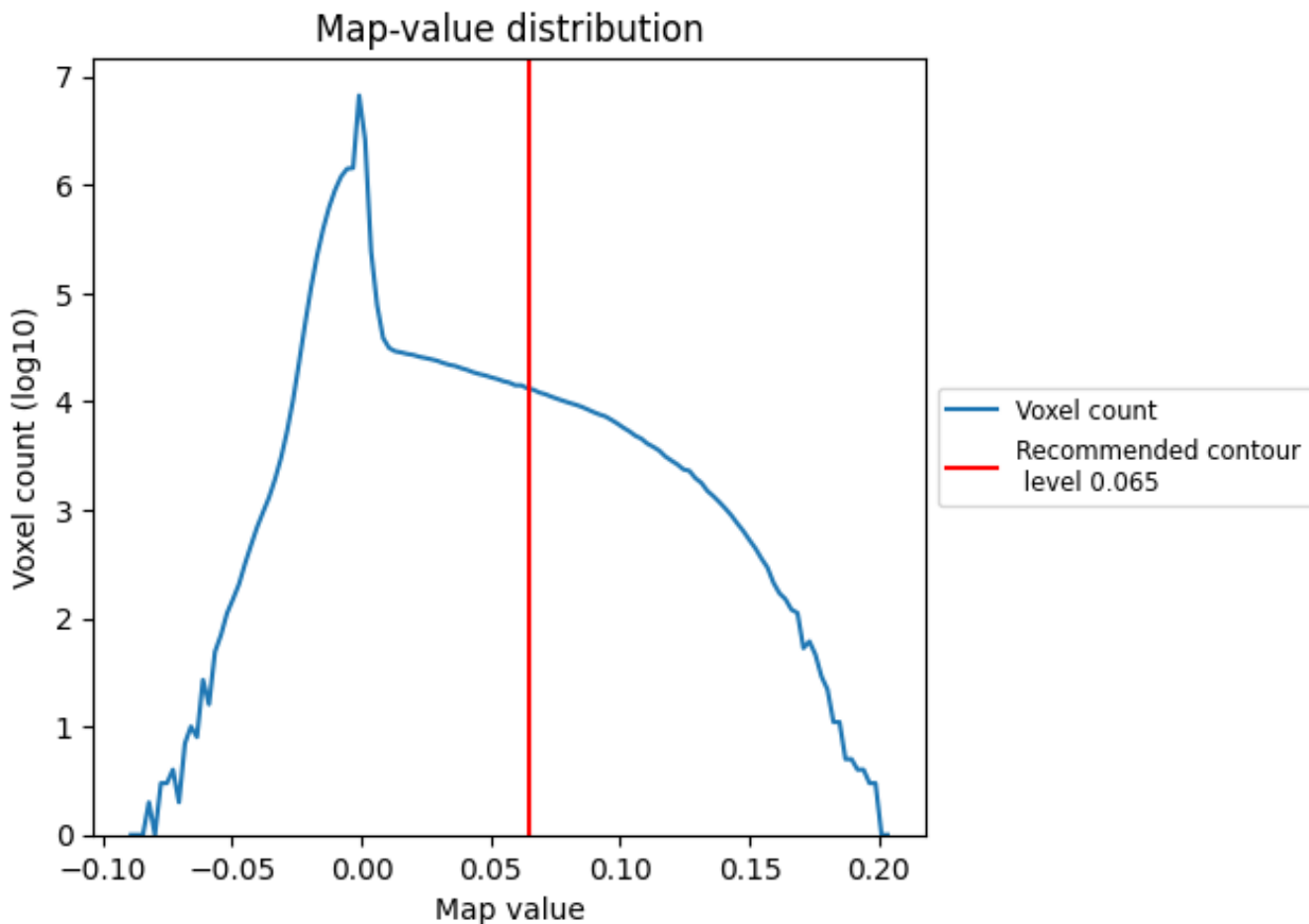
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

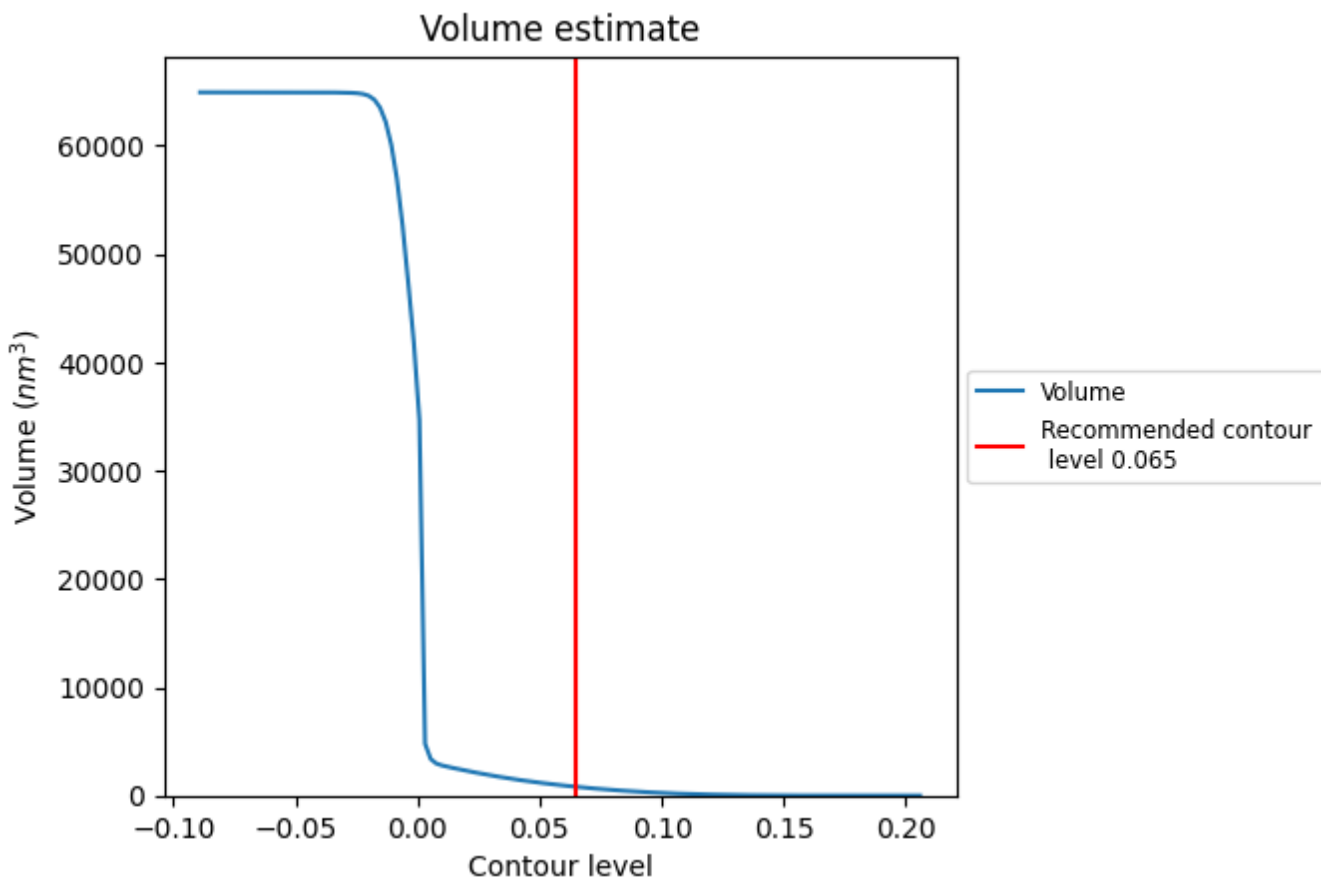
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

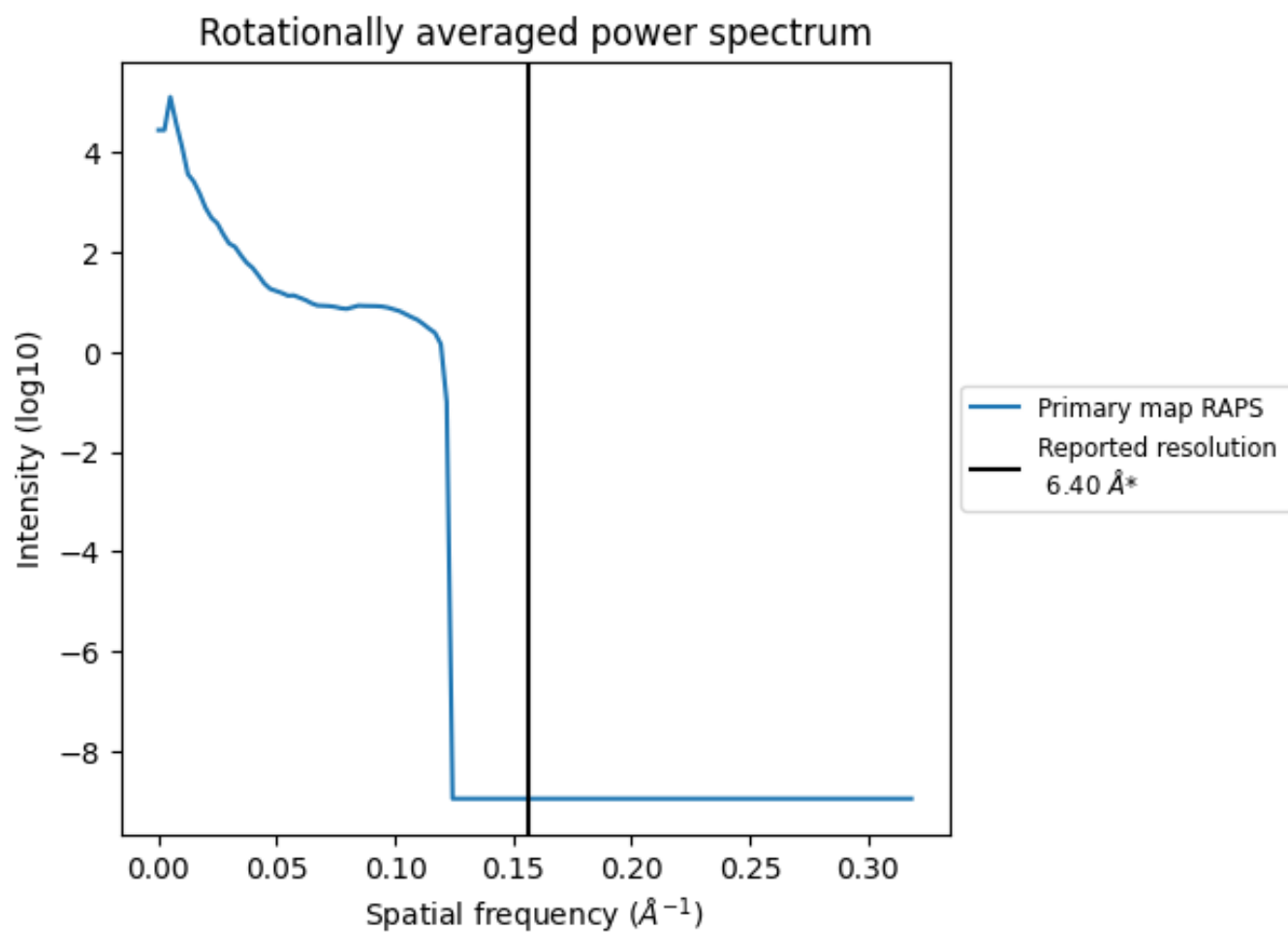
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 807 nm³; this corresponds to an approximate mass of 729 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.156\AA^{-1}

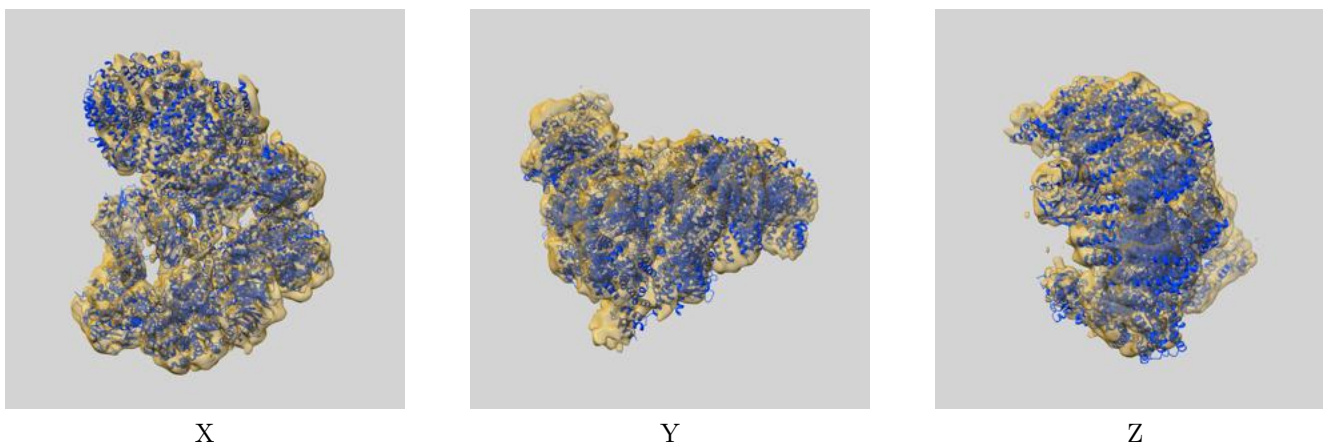
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

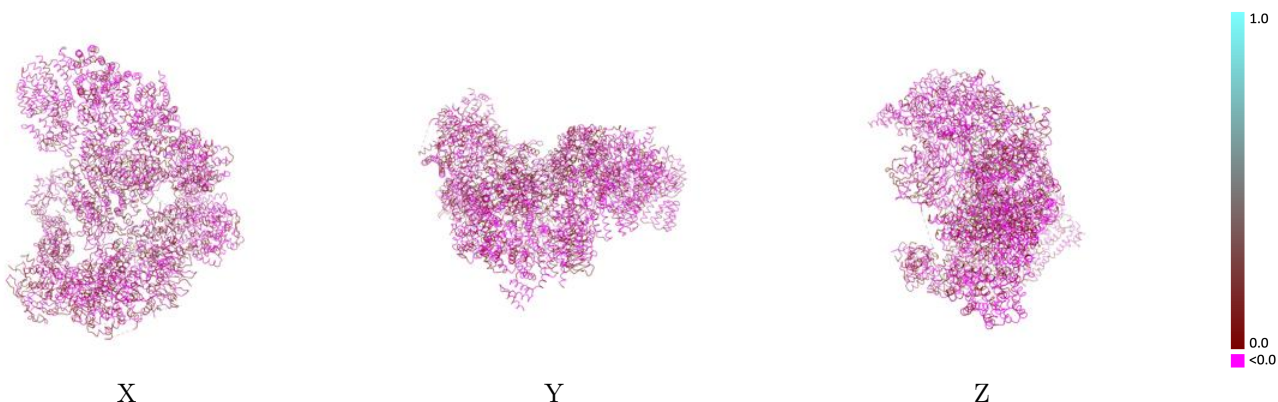
This section contains information regarding the fit between EMDB map EMD-3433 and PDB model 5L9T. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



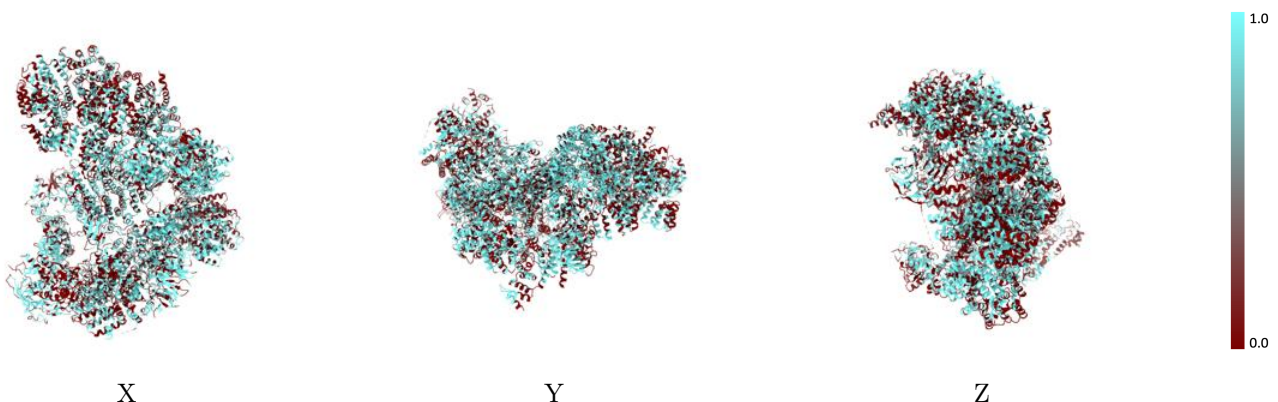
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



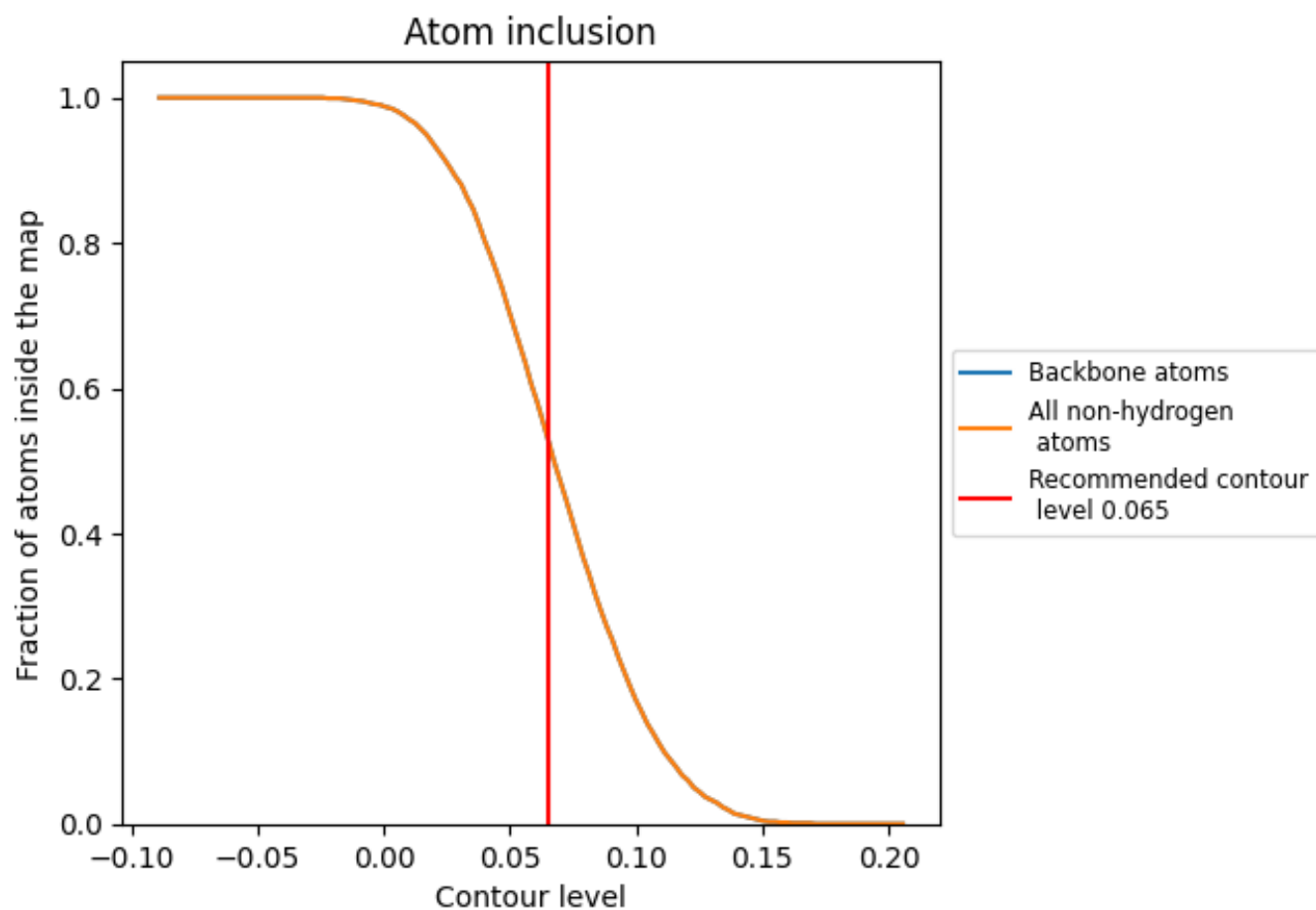
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 53% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5300	 0.0200
A	 0.5030	 0.0460
B	 0.7350	 0.0960
C	 0.6290	 0.0360
D	 0.2550	 0.0010
E	 0.4290	 -0.0170
F	 0.5210	 -0.0290
G	 0.0800	 -0.1230
H	 0.5050	 -0.0140
I	 0.5520	 0.0420
J	 0.5690	 -0.0200
K	 0.7380	 0.0700
L	 0.6060	 0.0710
M	 0.3810	 0.0660
N	 0.4380	 0.0370
O	 0.5040	 0.0180
P	 0.4810	 -0.0420
R	 0.5400	 0.0320
S	 0.3810	 0.0450
T	 0.5260	 0.0410
W	 0.6400	 0.1460
X	 0.4560	 -0.0220
Y	 0.5430	 -0.0000

