



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 04:18 AM UTC

PDB ID : 6VKL / pdb_00006vkl
EMDB ID : EMD-21226
Title : Negative stain reconstruction of the yeast exocyst octameric complex.
Authors : Frost, A.; Munson, M.
Deposited on : 2020-01-21
Resolution : 15.00 Å(reported)
Based on initial model : 5YFP

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

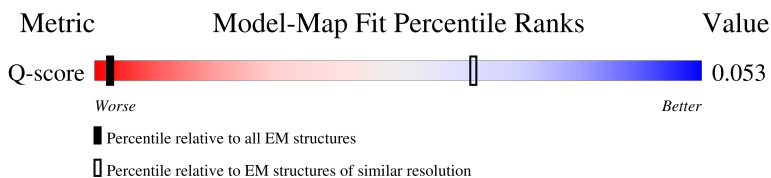
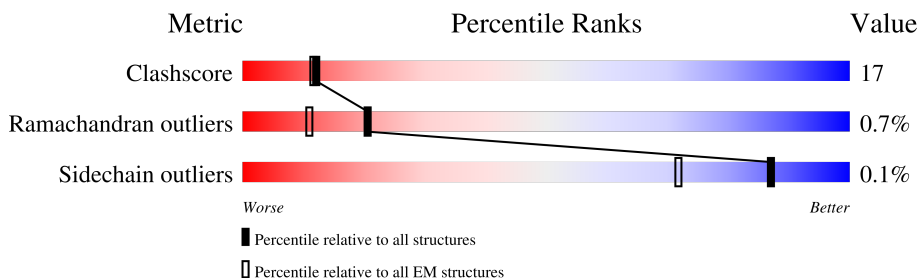
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 15.00 Å.

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



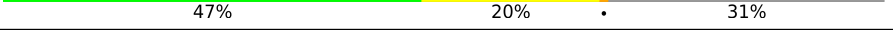
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	37 (14.50 - 15.50)

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	1336	11% 39% 11% 50%
2	B	971	19% 74% 20% • •
3	C	805	43% 67% 31% •
4	D	1065	9% 68% 20% • 10%

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Mol	Chain	Length	Quality of chain
5	E	871	 63% 25% 11% 5%
6	F	910	 61% 18% 20% 5%
7	G	623	 58% 40% 44%
8	H	753	 47% 20% 31% 5%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 33096 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 Exocyst complex component SEC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	672	Total	C	N	O	0	0
			3345	2001	672	672		

- Molecule 2 is a protein called Exocyst complex component SEC5.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	928	Total	C	N	O	0	0
			4610	2755	927	928		

- Molecule 3 is a protein called Exocyst complex component SEC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	794	Total	C	N	O	S	0	0
			4994	3097	892	989	16		

- Molecule 4 is a protein called Exocyst complex component SEC8.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	954	Total	C	N	O	0	0
			4739	2831	954	954		

- Molecule 5 is a protein called Exocyst complex component SEC10.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	776	Total	C	N	O	0	0
			3860	2308	776	776		

- Molecule 6 is a protein called Exocyst complex component SEC15.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	725	Total	C	N	O	0	0
			3612	2162	725	725		

- Molecule 7 is a protein called Exocyst complex component EXO70.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	615	Total	C	N	O	S	0	0
			4696	2968	809	902	17		

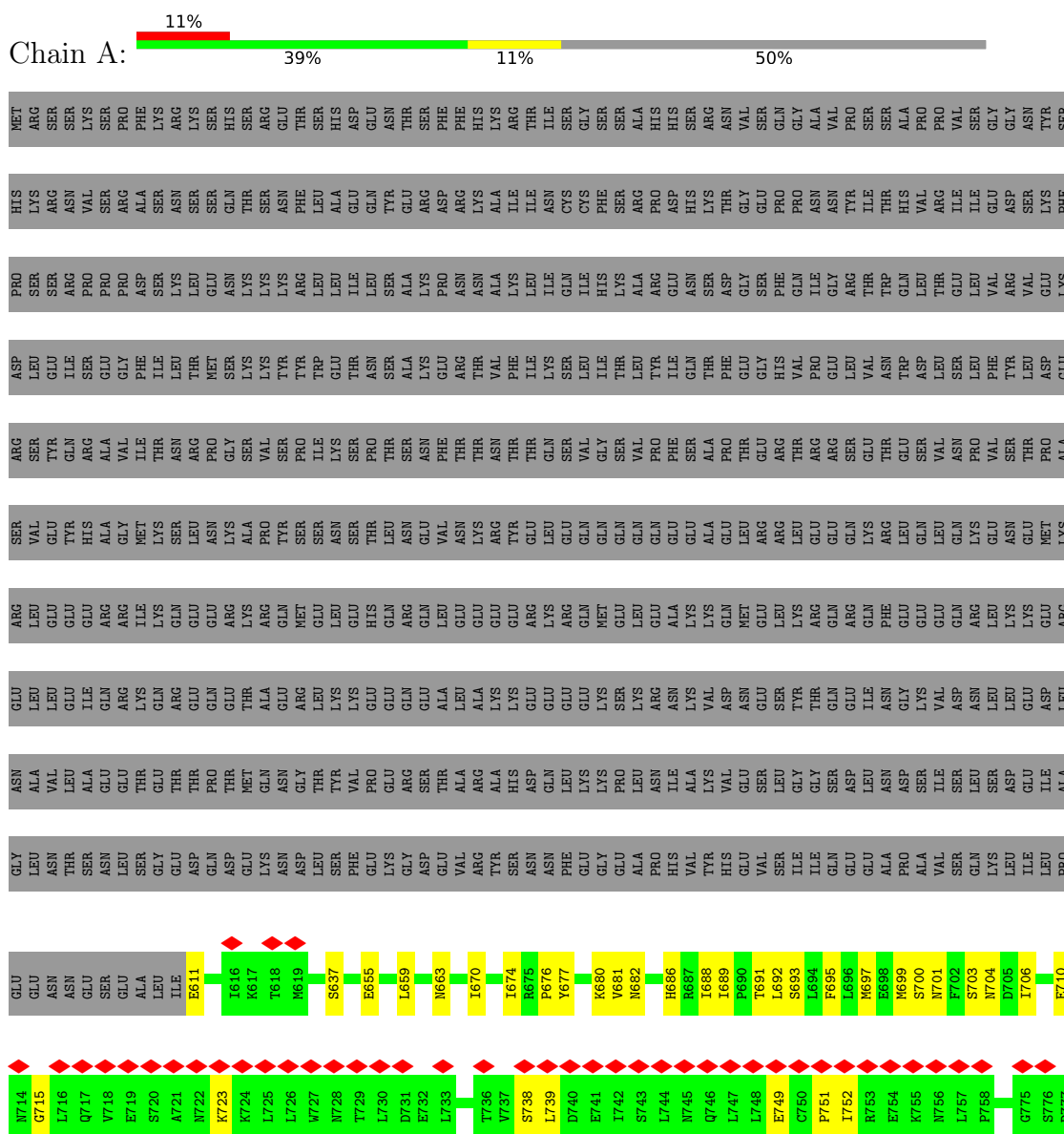
- Molecule 8 is a protein called Exocyst complex component EXO84.

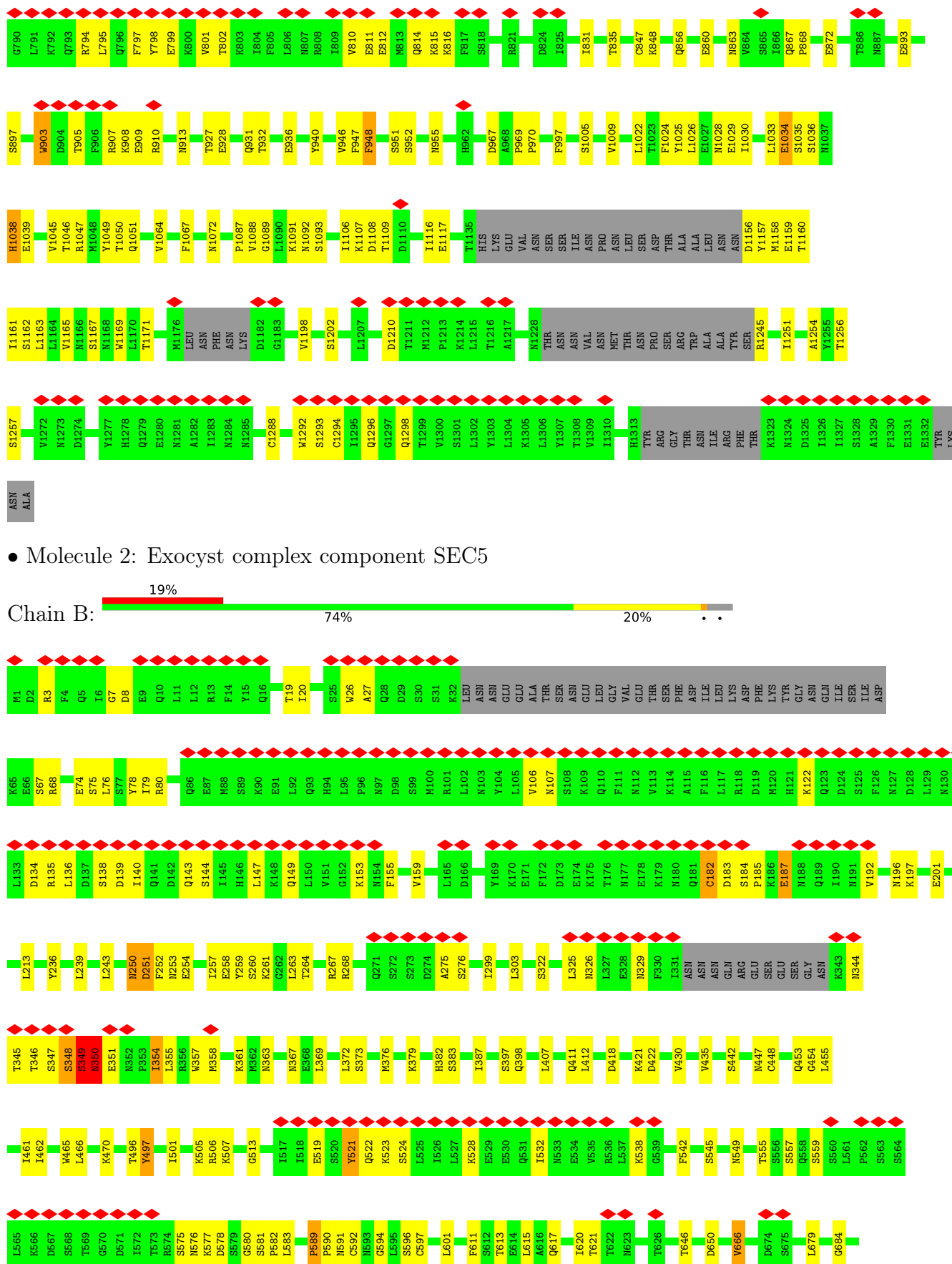
Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	518	Total	C	N	O	S	0	0
			3240	2002	591	643	4		

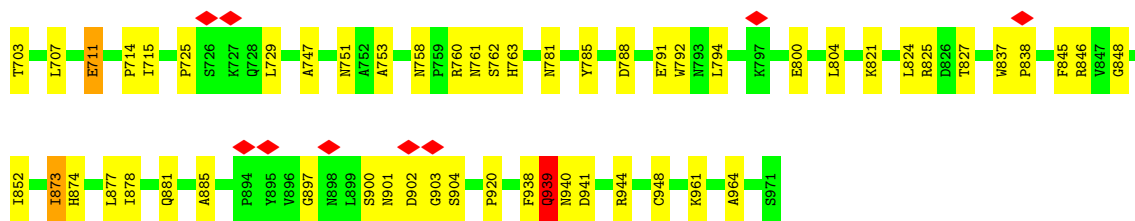
3 Residue-property plots

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.

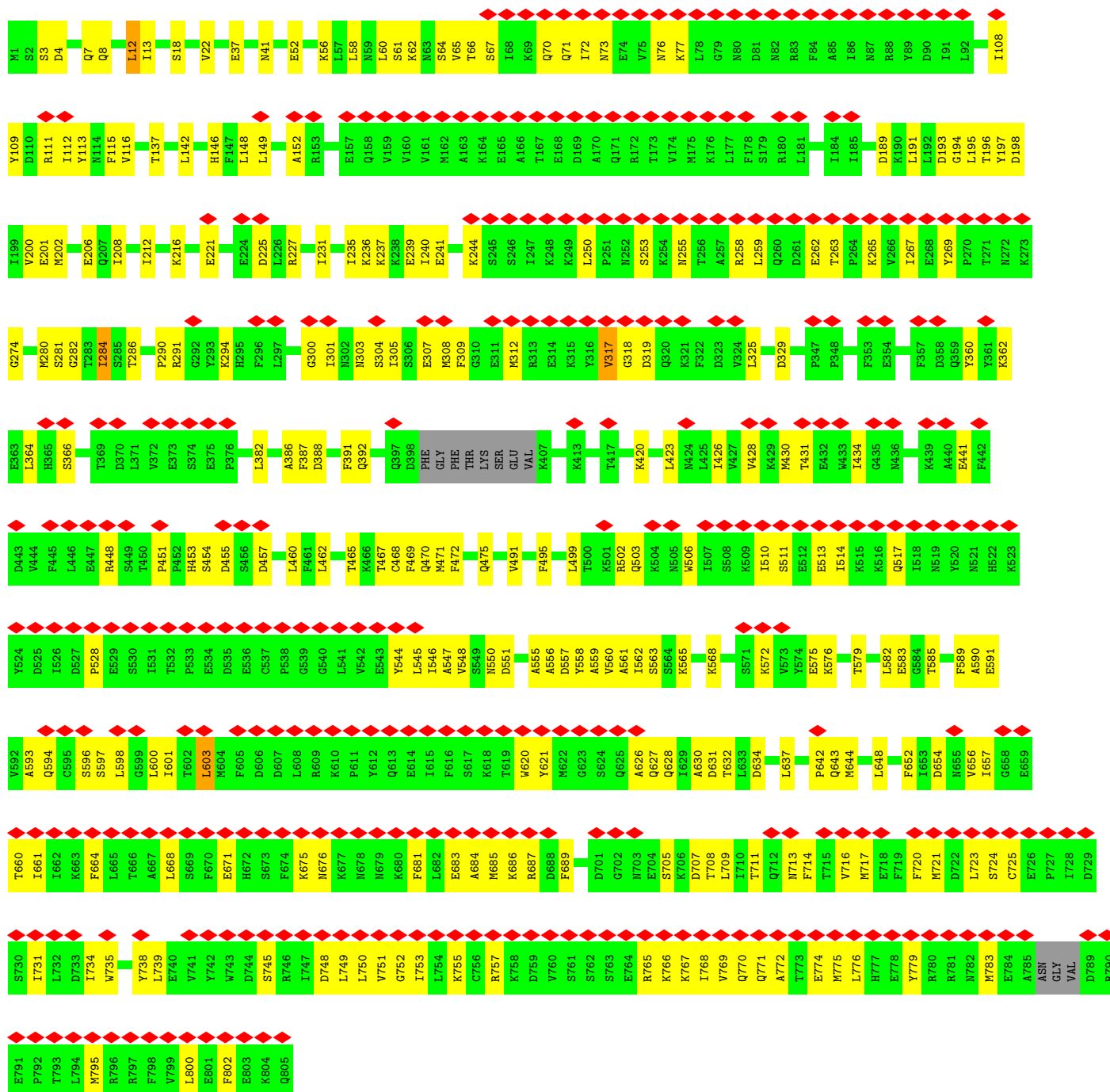
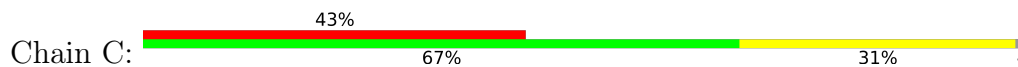
- Molecule 1: Exocyst complex component SEC3



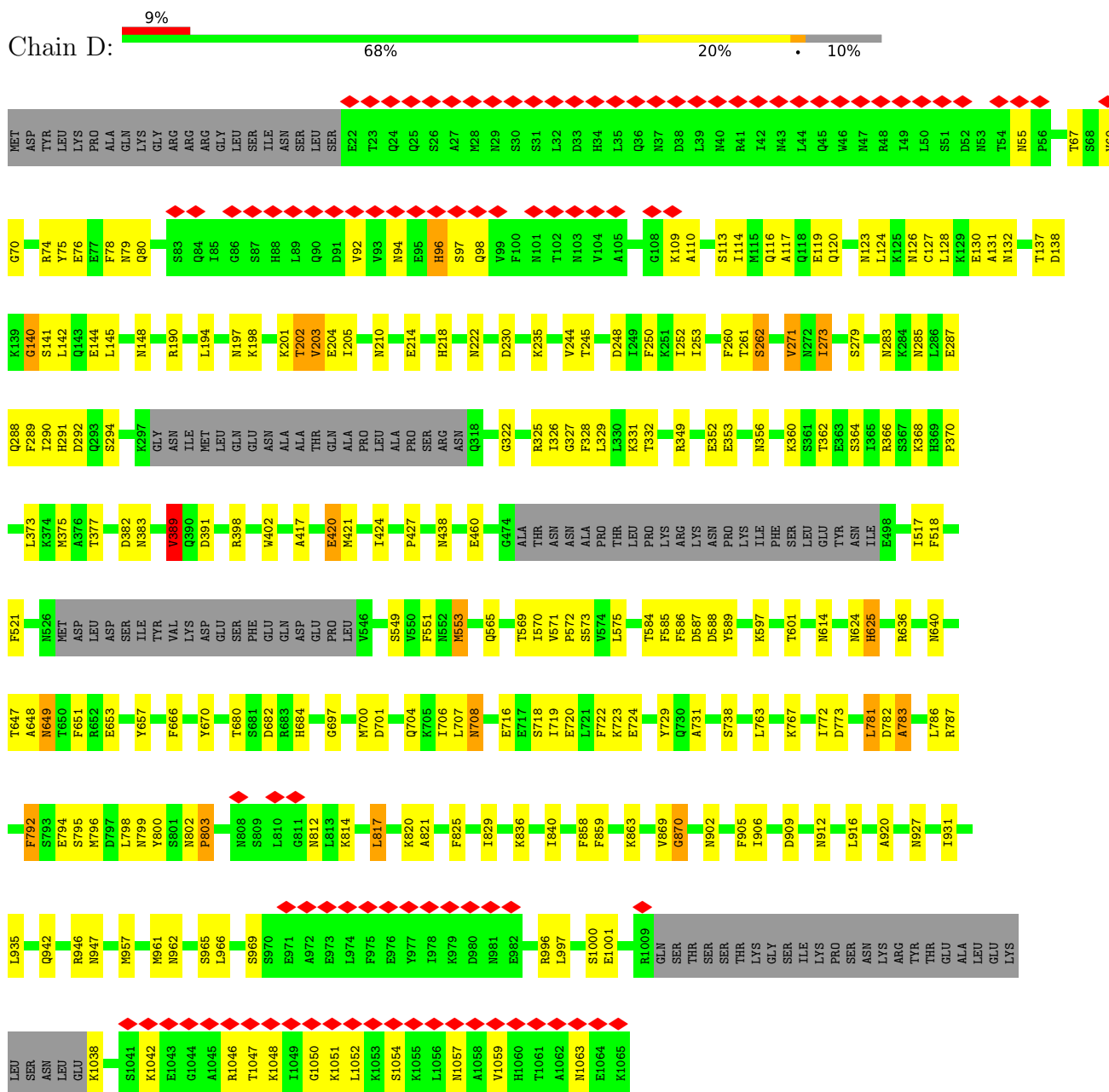




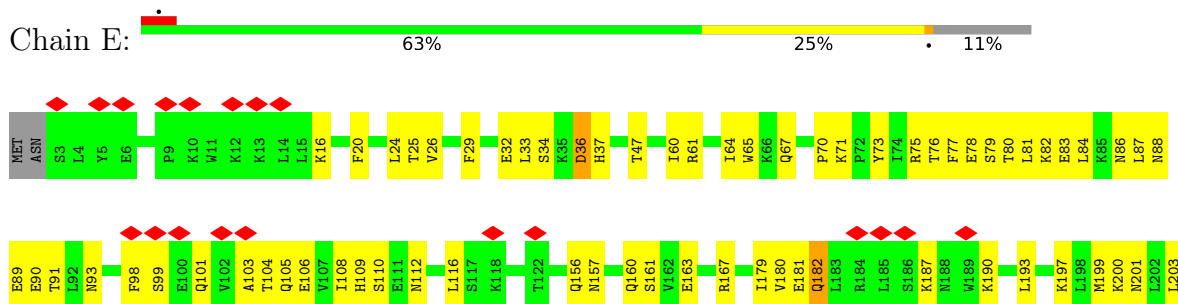
• Molecule 3: Exocyst complex component SEC6

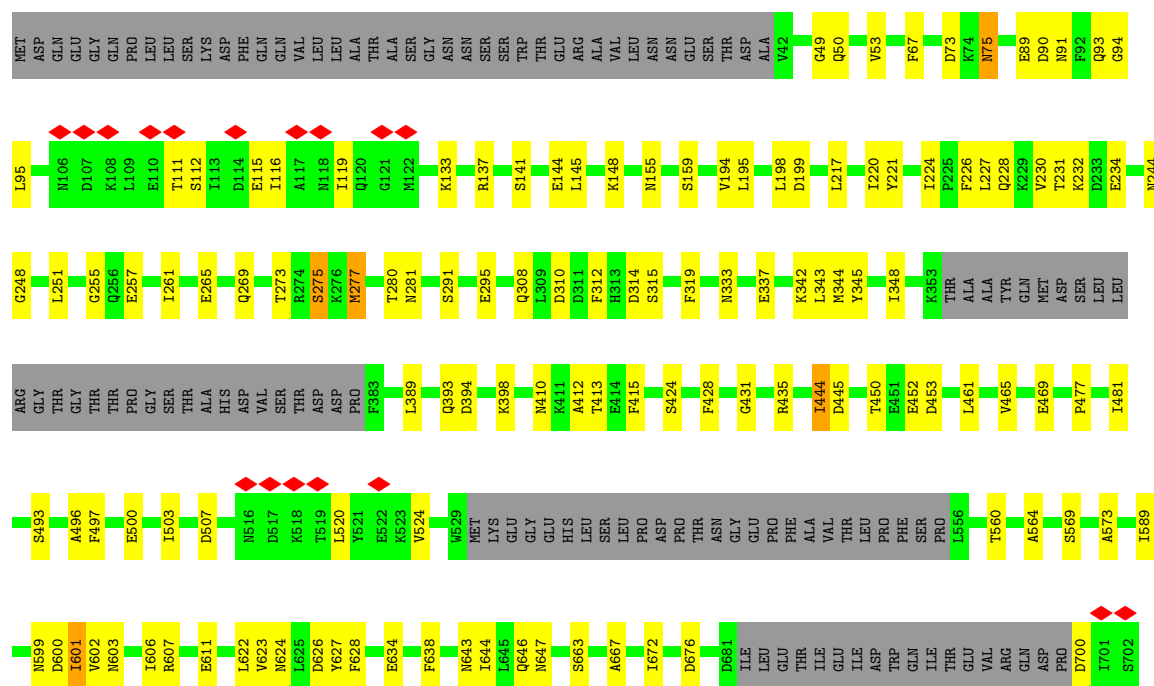


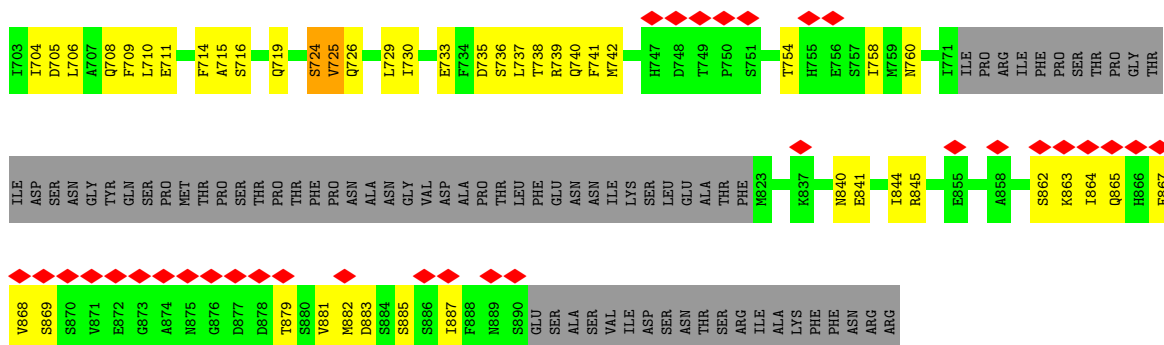
• Molecule 4: Exocyst complex component SEC8



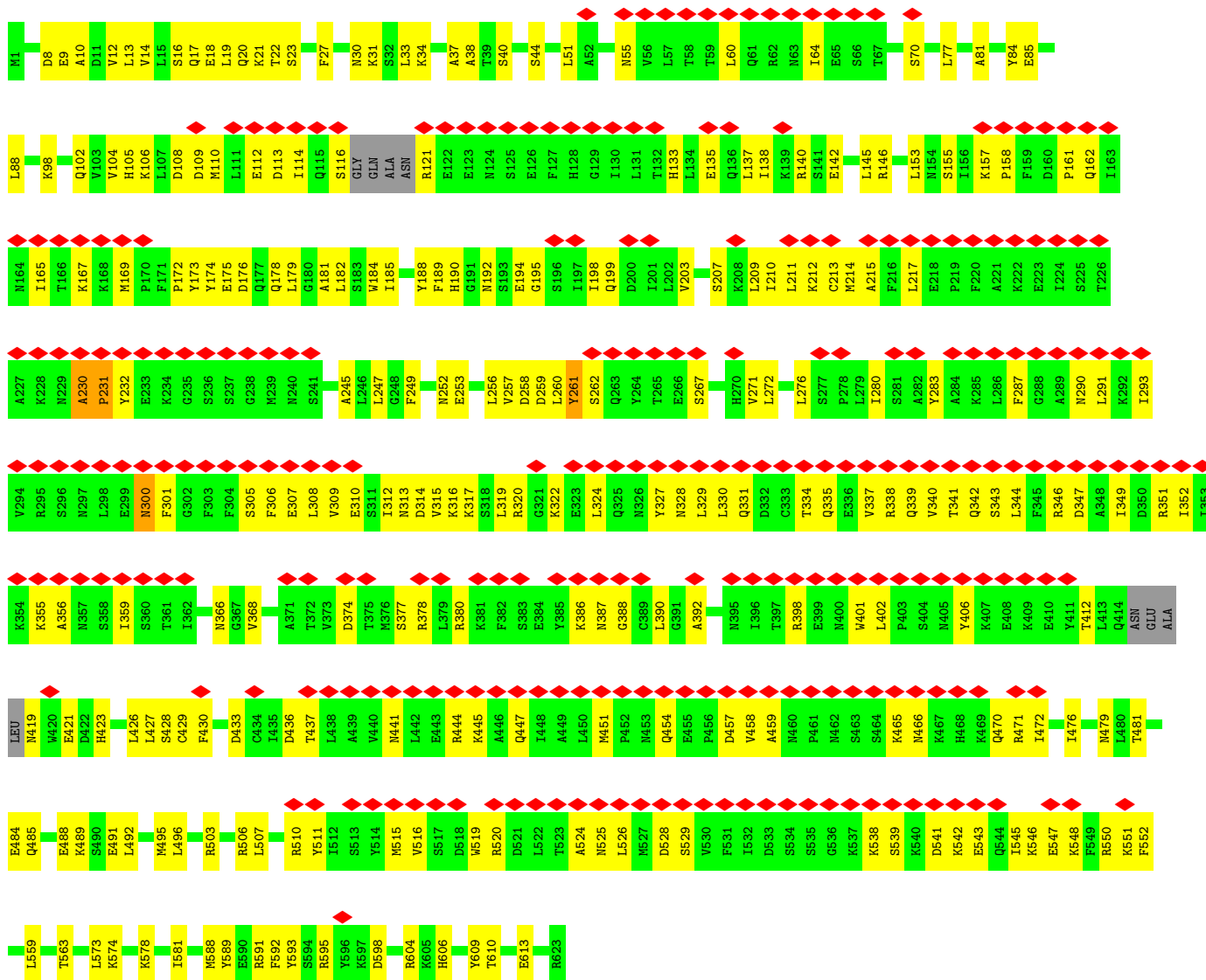
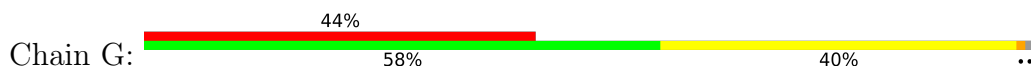
• Molecule 5: Exocyst complex component SEC10



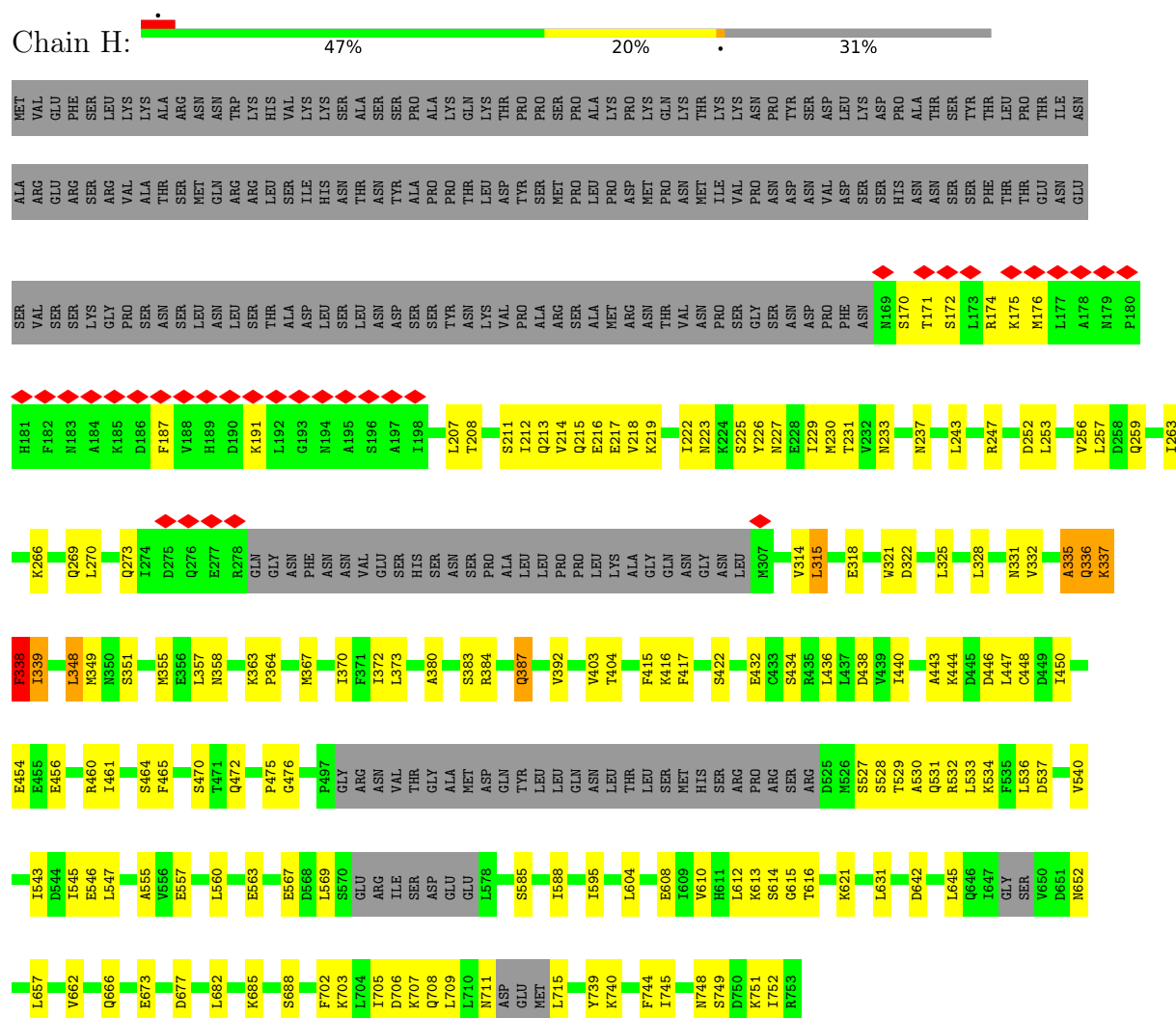




• Molecule 7: Exocyst complex component EXO70



• Molecule 8: Exocyst complex component EXO84



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	67509, 67509	Depositor
Resolution determination method	FSC 0.5 CUT-OFF, FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.00	Depositor
Minimum defocus (nm)	2000.00	Depositor
Maximum defocus (nm)	3000.00	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.402	Depositor
Minimum map value	-2.171	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.405	Depositor
Recommended contour level	4.1	Depositor
Map size (Å)	734.976, 734.976, 734.976	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.871, 2.871, 2.871	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.30	0/3340	0.90	24/4659 (0.5%)
2	B	0.37	0/4607	1.02	53/6427 (0.8%)
3	C	0.29	0/5043	0.77	20/6885 (0.3%)
4	D	0.38	0/4734	1.06	61/6601 (0.9%)
5	E	0.27	0/3857	0.78	17/5383 (0.3%)
6	F	0.31	0/3607	0.85	15/5034 (0.3%)
7	G	0.32	0/4768	0.74	4/6443 (0.1%)
8	H	0.39	0/3253	0.81	9/4443 (0.2%)
All	All	0.33	0/33209	0.88	203/45875 (0.4%)

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	A	0	11
2	B	0	41
3	C	0	8
4	D	0	43
5	E	0	6
6	F	0	13
7	G	0	9
8	H	0	12
All	All	0	143

There are no bond length outliers.

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	758	ASN	CA-C-N	11.84	155.41	127.00
2	B	758	ASN	C-N-CA	11.84	155.41	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1116	ILE	CA-C-N	10.77	141.08	121.70
1	A	1116	ILE	C-N-CA	10.77	141.08	121.70
6	F	444	ILE	CA-C-N	10.01	139.72	121.70

There are no chirality outliers.

5 of 143 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	749	GLU	Peptide
1	A	780	GLU	Peptide
1	A	946	VAL	Peptide
1	A	947	PHE	Peptide
1	A	948	PHE	Peptide

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	3345	0	1403	70	0
2	B	4610	0	1926	82	0
3	C	4994	0	3576	173	0
4	D	4739	0	2011	90	0
5	E	3860	0	1635	124	0
6	F	3612	0	1508	85	0
7	G	4696	0	4483	192	0
8	H	3240	0	2433	88	0
All	All	33096	0	18975	894	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 17.

The worst 5 of 894 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)
3:C:506:TRP:O	3:C:510:ILE:HB	1.54	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:714:PHE:CD2	3:C:714:PHE:CZ	2.38	1.04
3:C:544:TYR:CG	3:C:544:TYR:CE2	2.40	1.02
3:C:558:TYR:O	3:C:562:ILE:HB	1.60	1.00
3:C:557:ASP:O	3:C:561:ALA:HB3	1.66	0.95

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	A	662/1336 (50%)	517 (78%)	144 (22%)	1 (0%)	43	78
2	B	922/971 (95%)	708 (77%)	201 (22%)	13 (1%)	9	40
3	C	788/805 (98%)	674 (86%)	113 (14%)	1 (0%)	48	83
4	D	944/1065 (89%)	717 (76%)	214 (23%)	13 (1%)	9	40
5	E	770/871 (88%)	639 (83%)	129 (17%)	2 (0%)	36	72
6	F	715/910 (79%)	577 (81%)	131 (18%)	7 (1%)	12	49
7	G	609/623 (98%)	555 (91%)	52 (8%)	2 (0%)	36	72
8	H	506/753 (67%)	431 (85%)	73 (14%)	2 (0%)	30	67
All	All	5916/7334 (81%)	4818 (81%)	1057 (18%)	41 (1%)	20	56

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	349	SER
2	B	350	ASN
2	B	590	PRO
2	B	762	SER
4	D	97	SER

5.3.2 Protein sidechains [i](#)

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	
3	C	297/740 (40%)	297 (100%)	0	100	100
7	G	480/570 (84%)	480 (100%)	0	100	100
8	H	202/697 (29%)	201 (100%)	1 (0%)	81	83
All	All	979/2007 (49%)	978 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	545	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
7	G	366	ASN
7	G	470	GLN
7	G	468	HIS
7	G	544	GLN
3	C	655	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](#)

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-21226. These allow visual inspection of the internal detail of the map and identification of artifacts.

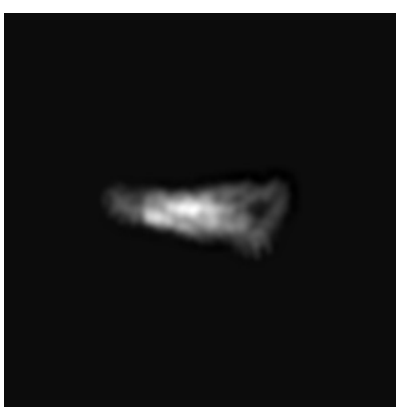
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

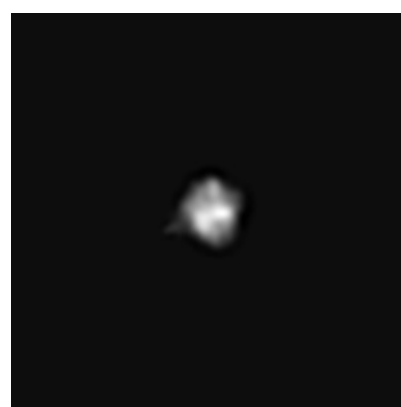
6.1.1 Primary map



X



Y

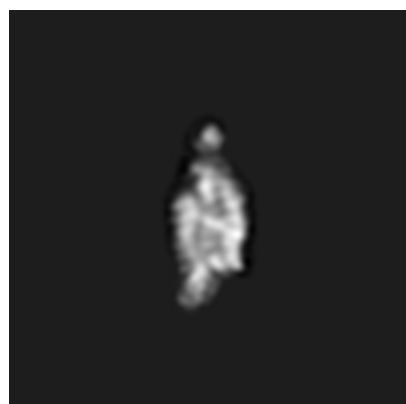


Z

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

6.2 Central slices [i](#)

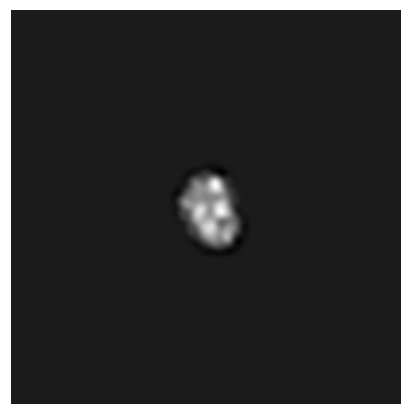
6.2.1 Primary map



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](#)

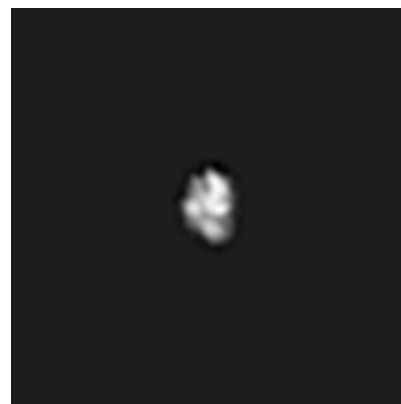
6.3.1 Primary map



X Index: 129



Y Index: 127

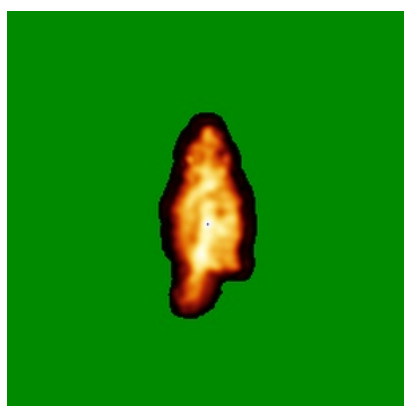


Z Index: 119

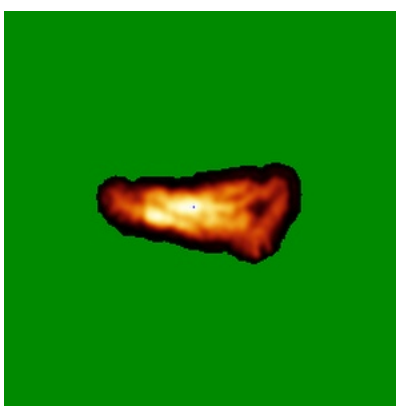
The images above show the largest variance slices of the map in three orthogonal directions.

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

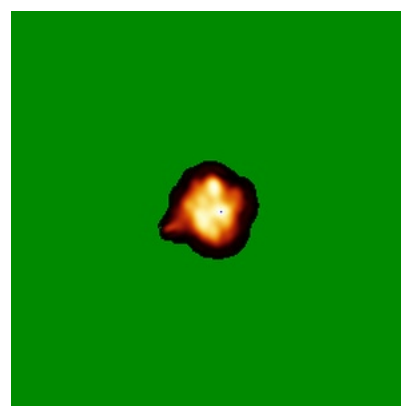
6.4.1 Primary map



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

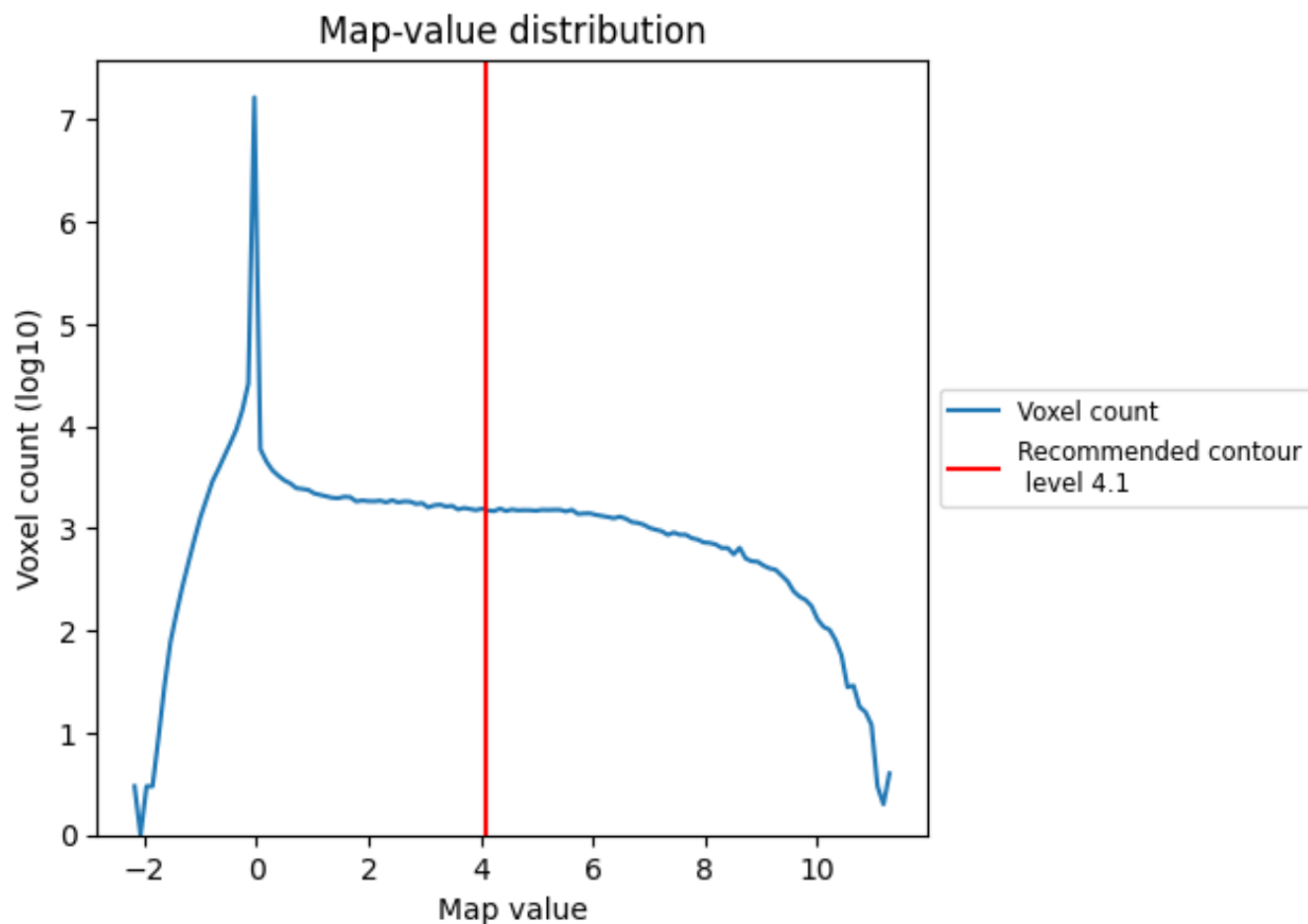
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

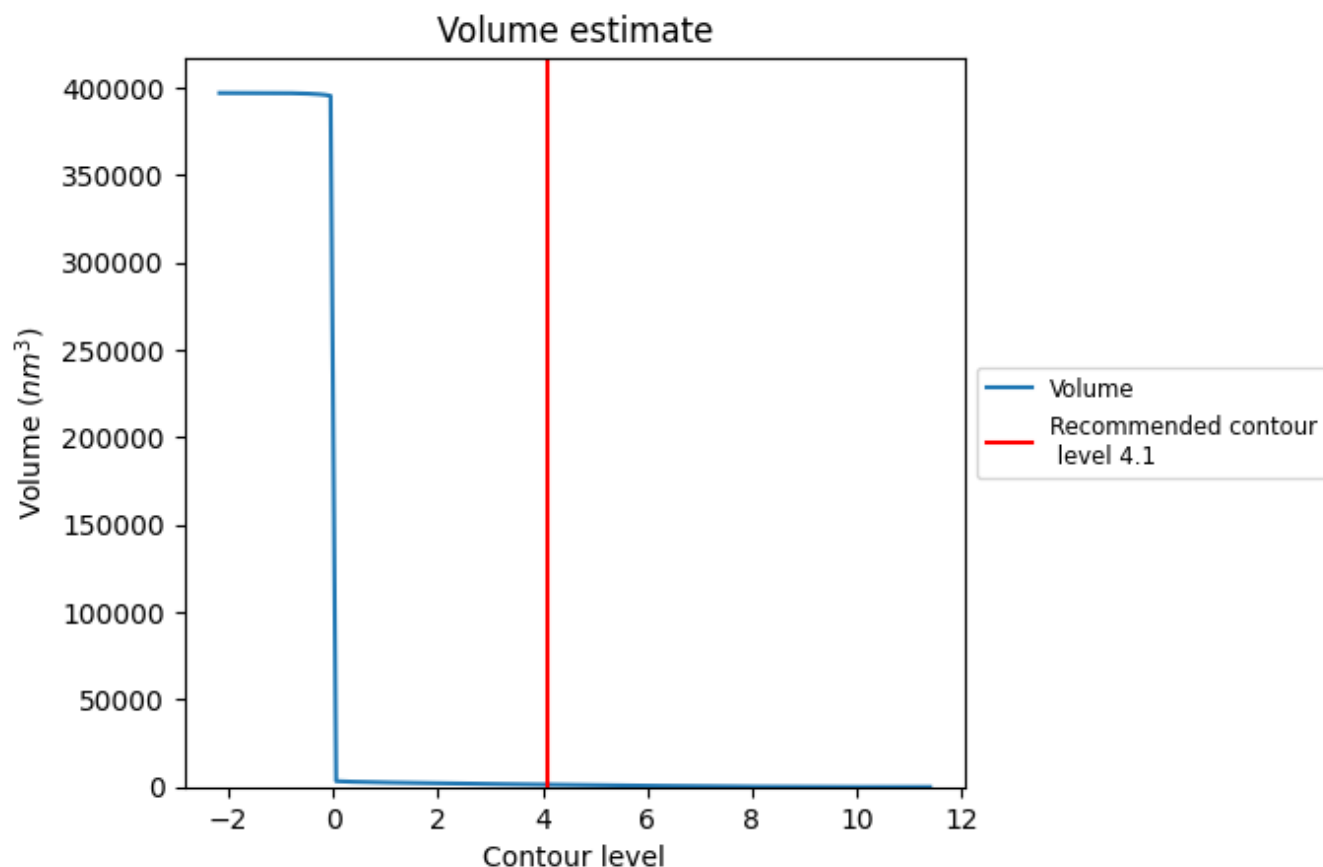
This section contains the results of statistical analysis of the map.

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.

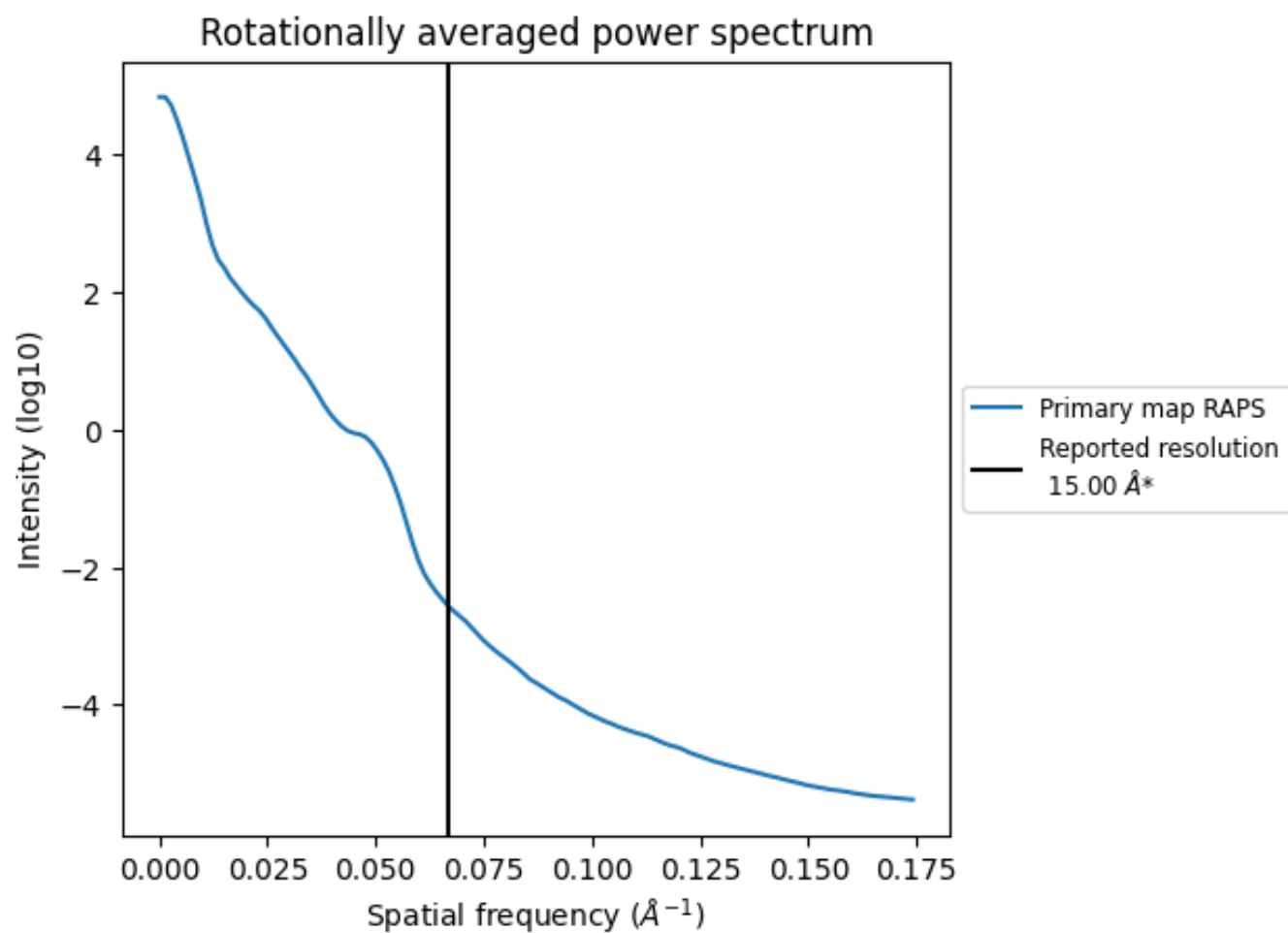
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1324 nm^3 ; this corresponds to an approximate mass of 1196 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 0.067 Å⁻¹

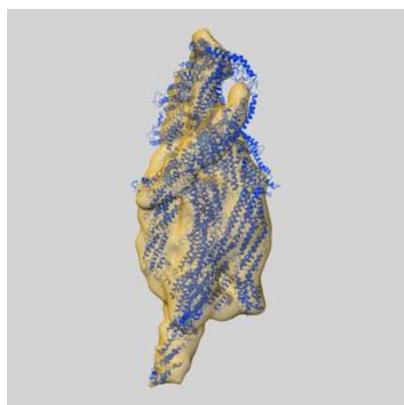
8 Fourier-Shell correlation

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

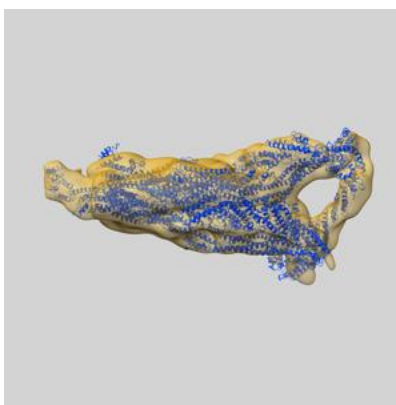
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21226 and PDB model 6VKL. Per-residue inclusion information can be found in section [3](#) on page [6](#).

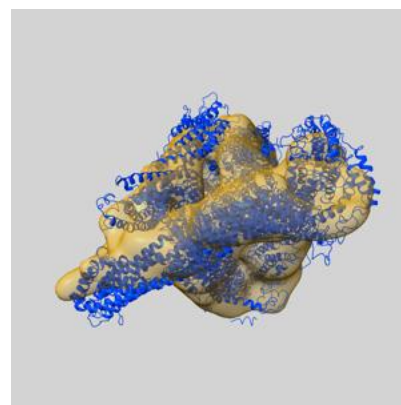
9.1 Map-model overlay [i](#)



X



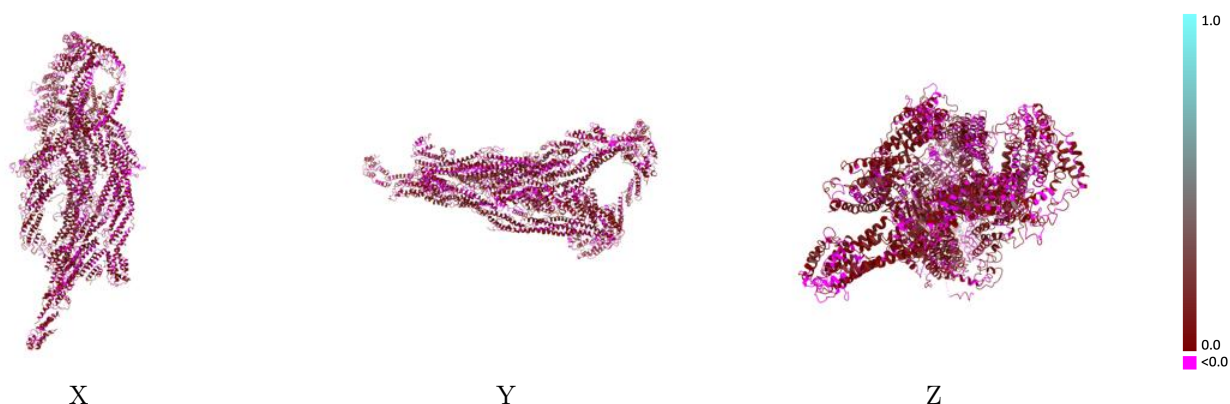
Y



Z

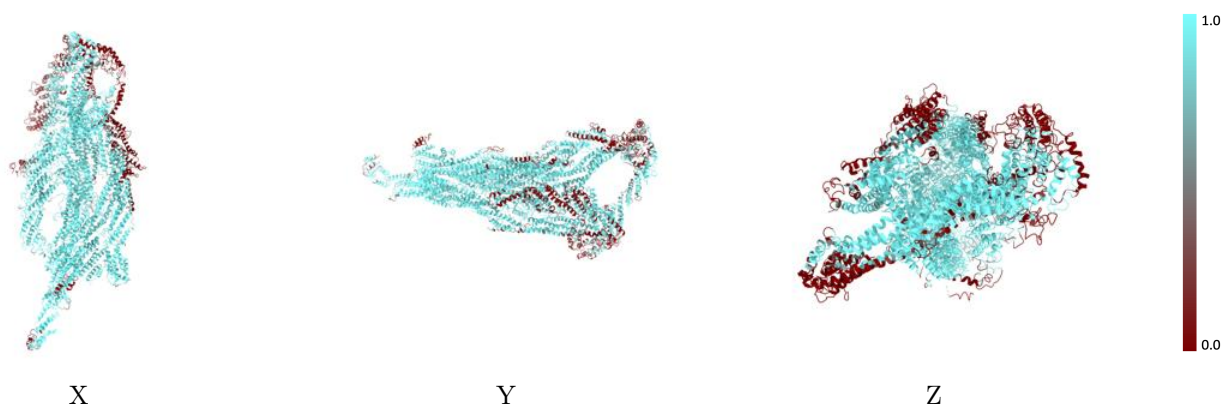
The images above show the 3D surface view of the map at the recommended contour level 4.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



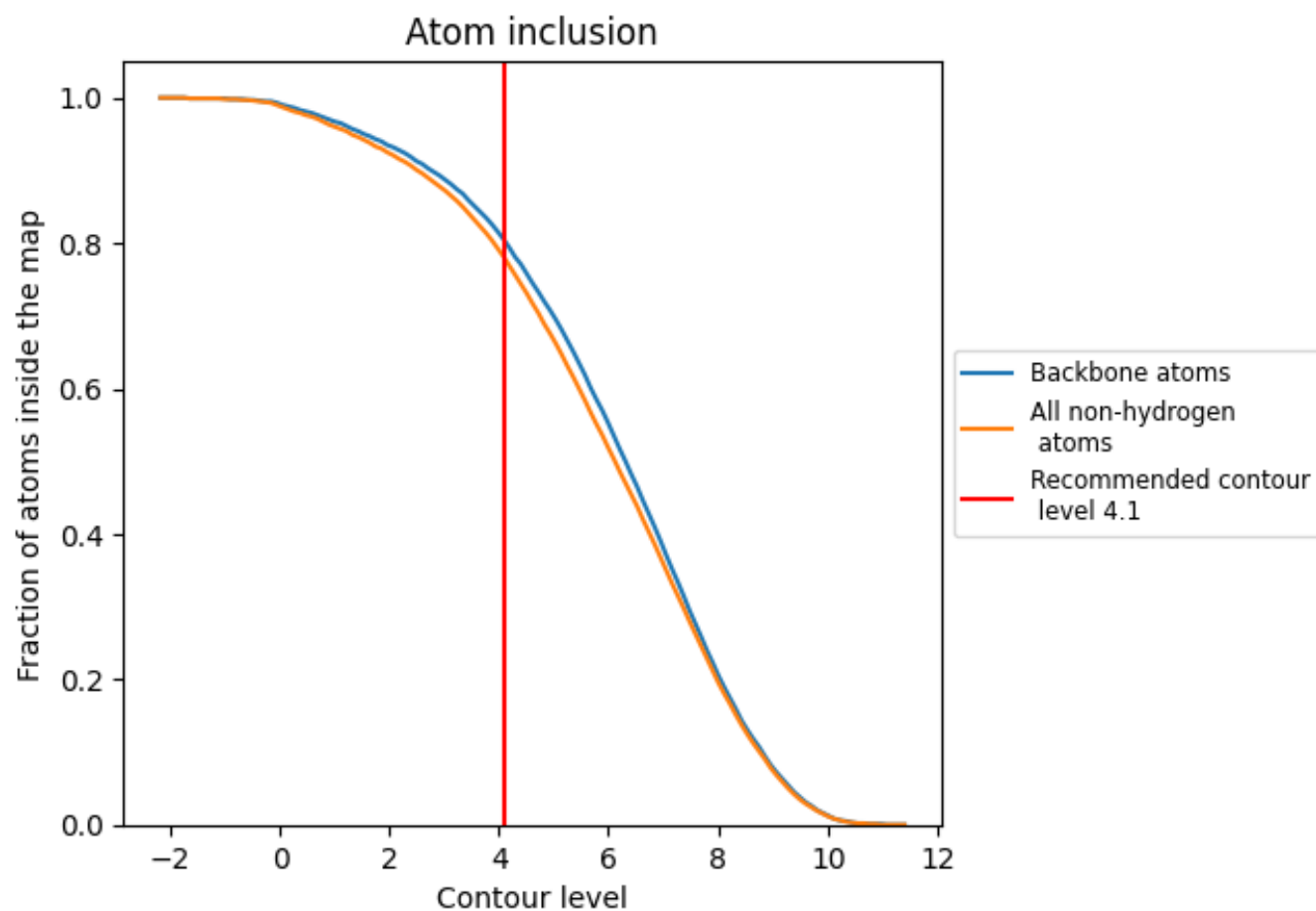
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (4.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7800	0.0530
A	0.7820	0.0630
B	0.8010	0.0490
C	0.5240	0.0400
D	0.8920	0.0530
E	0.9520	0.0710
F	0.9310	0.0620
G	0.5410	0.0330
H	0.9480	0.0670

1.0

0.0

<0.0