



## wwPDB EM Validation Summary Report ⓘ

Feb 12, 2024 – 02:23 PM EST

PDB ID : 3J99  
EMDB ID : EMD-6209  
Title : Structure of 20S supercomplex determined by single particle cryoelectron microscopy (State IIIb)  
Authors : Zhao, M.; Wu, S.; Cheng, Y.; Brunger, A.T.  
Deposited on : 2014-12-05  
Resolution : 8.20 Å (reported)  
Based on initial models : 1QCS, 1N7S, 1NSF

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.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

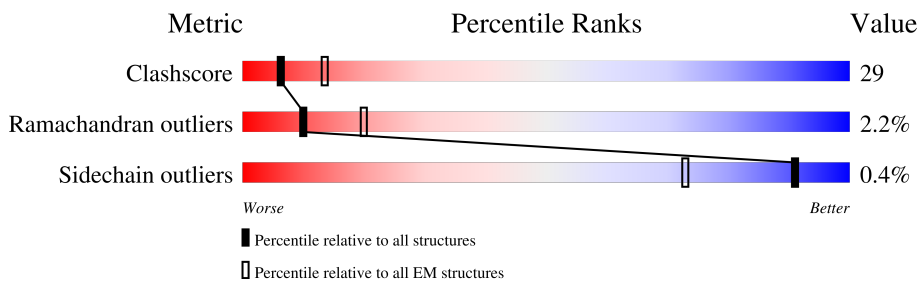
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.20 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.



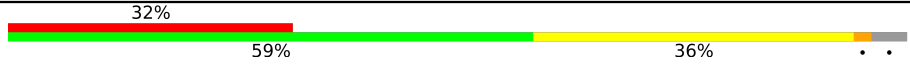

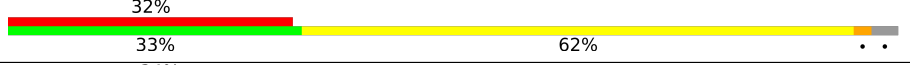
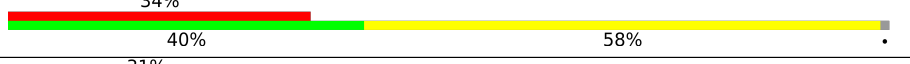
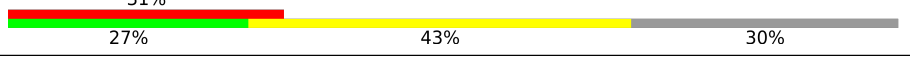
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	A	747	
1	B	747	
1	C	747	
1	D	747	
1	E	747	
1	F	747	
2	G	297	
2	H	297	

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Mol	Chain	Length	Quality of chain
2	I	297	
2	J	297	
3	K	63	
4	L	67	
5	M	188	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 40976 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 Vesicle-fusing ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	678	5039	3197	876	943	23	0	0
1	B	672	4995	3168	863	940	24	0	0
1	C	676	5027	3186	871	947	23	0	0
1	D	673	4976	3157	856	939	24	0	0
1	E	670	4992	3171	860	938	23	0	0
1	F	654	4903	3112	849	918	24	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P18708
A	-1	ALA	-	expression tag	UNP P18708
A	0	HIS	-	expression tag	UNP P18708
B	-2	GLY	-	expression tag	UNP P18708
B	-1	ALA	-	expression tag	UNP P18708
B	0	HIS	-	expression tag	UNP P18708
C	-2	GLY	-	expression tag	UNP P18708
C	-1	ALA	-	expression tag	UNP P18708
C	0	HIS	-	expression tag	UNP P18708
D	-2	GLY	-	expression tag	UNP P18708
D	-1	ALA	-	expression tag	UNP P18708
D	0	HIS	-	expression tag	UNP P18708
E	-2	GLY	-	expression tag	UNP P18708
E	-1	ALA	-	expression tag	UNP P18708
E	0	HIS	-	expression tag	UNP P18708
F	-2	GLY	-	expression tag	UNP P18708
F	-1	ALA	-	expression tag	UNP P18708
F	0	HIS	-	expression tag	UNP P18708

- Molecule 2 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	286	2246	1415	373	441	17	0	0
2	I	286	2249	1418	373	441	17	0	0
2	J	286	2255	1424	373	441	17	0	0
2	G	286	2249	1421	370	441	17	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	GLY	-	expression tag	UNP P54921
H	0	SER	-	expression tag	UNP P54921
I	-1	GLY	-	expression tag	UNP P54921
I	0	SER	-	expression tag	UNP P54921
J	-1	GLY	-	expression tag	UNP P54921
J	0	SER	-	expression tag	UNP P54921
G	-1	GLY	-	expression tag	UNP P54921
G	0	SER	-	expression tag	UNP P54921

- Molecule 3 is a protein called Vesicle-associated membrane protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	K	61	480	293	89	97	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	27	GLY	-	expression tag	UNP P63045

- Molecule 4 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L	66	523	320	89	109	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	MET	-	expression tag	UNP P32851

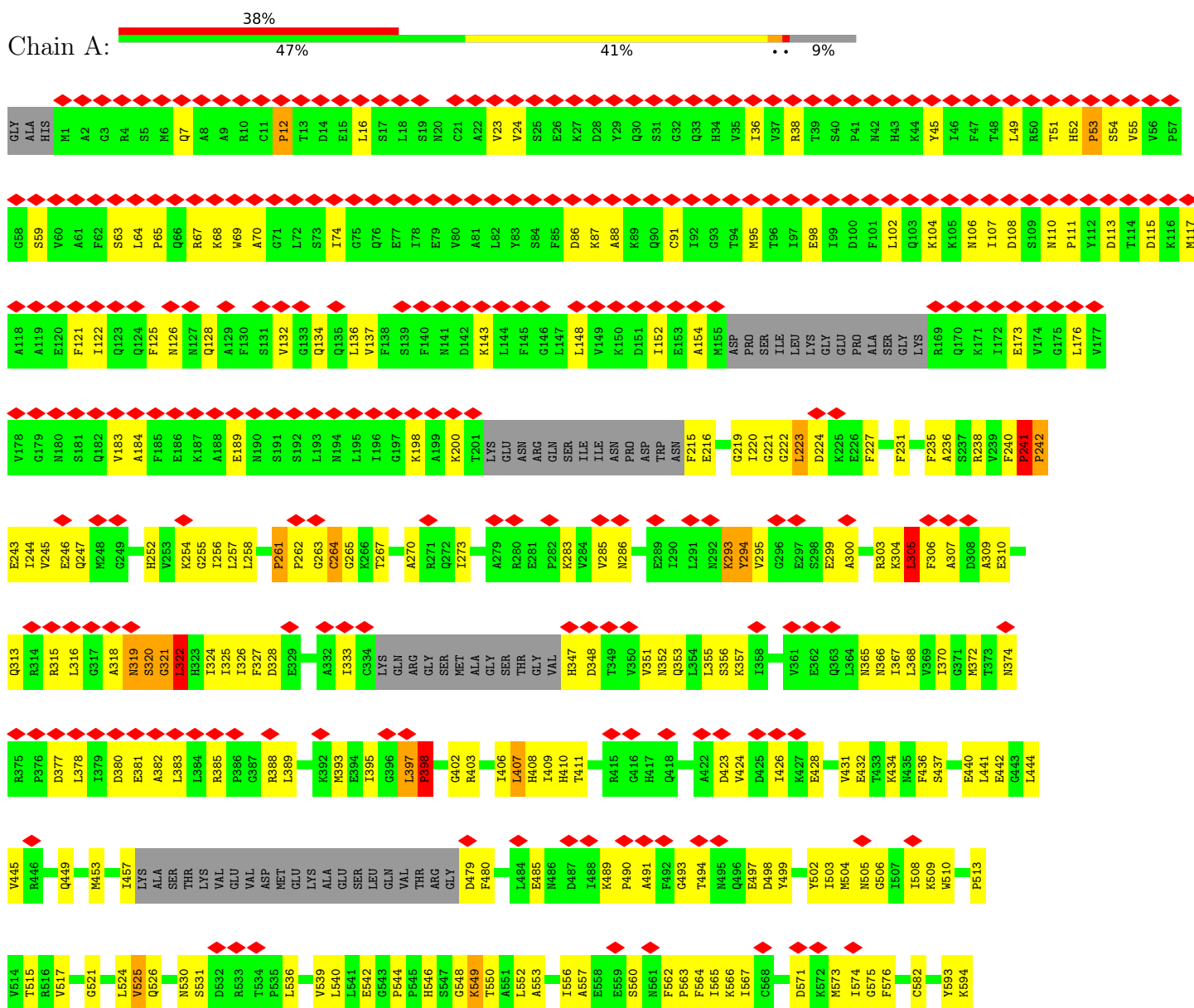
- Molecule 5 is a protein called Synaptosomal-associated protein 25.

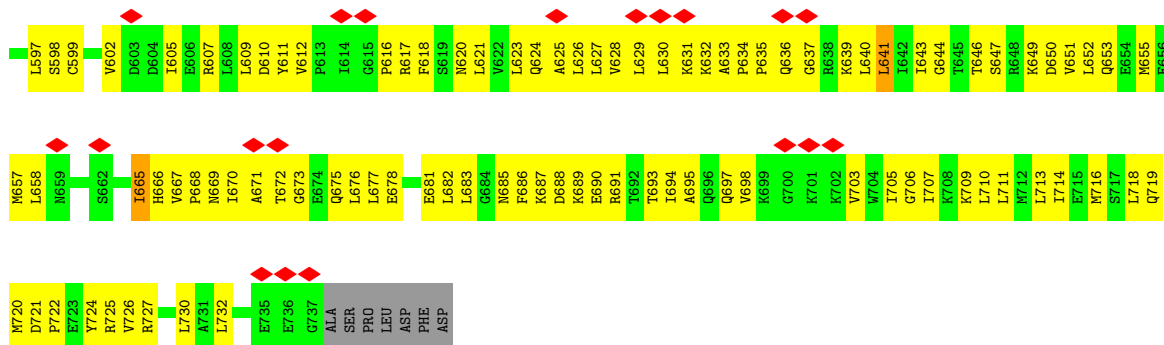
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	M	131	1042	617	195	221	9	0	0

### 3 Residue-property plots

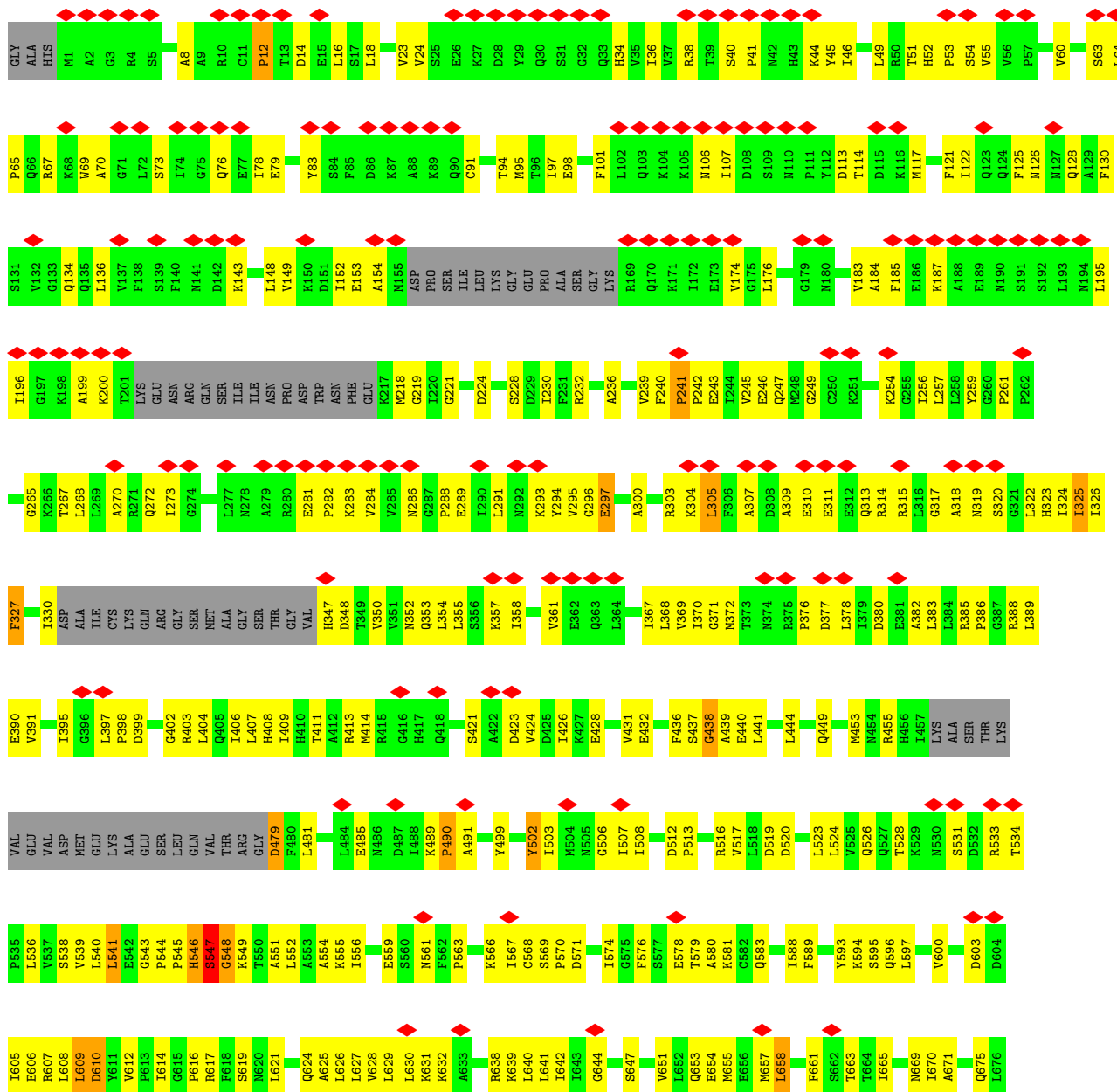
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





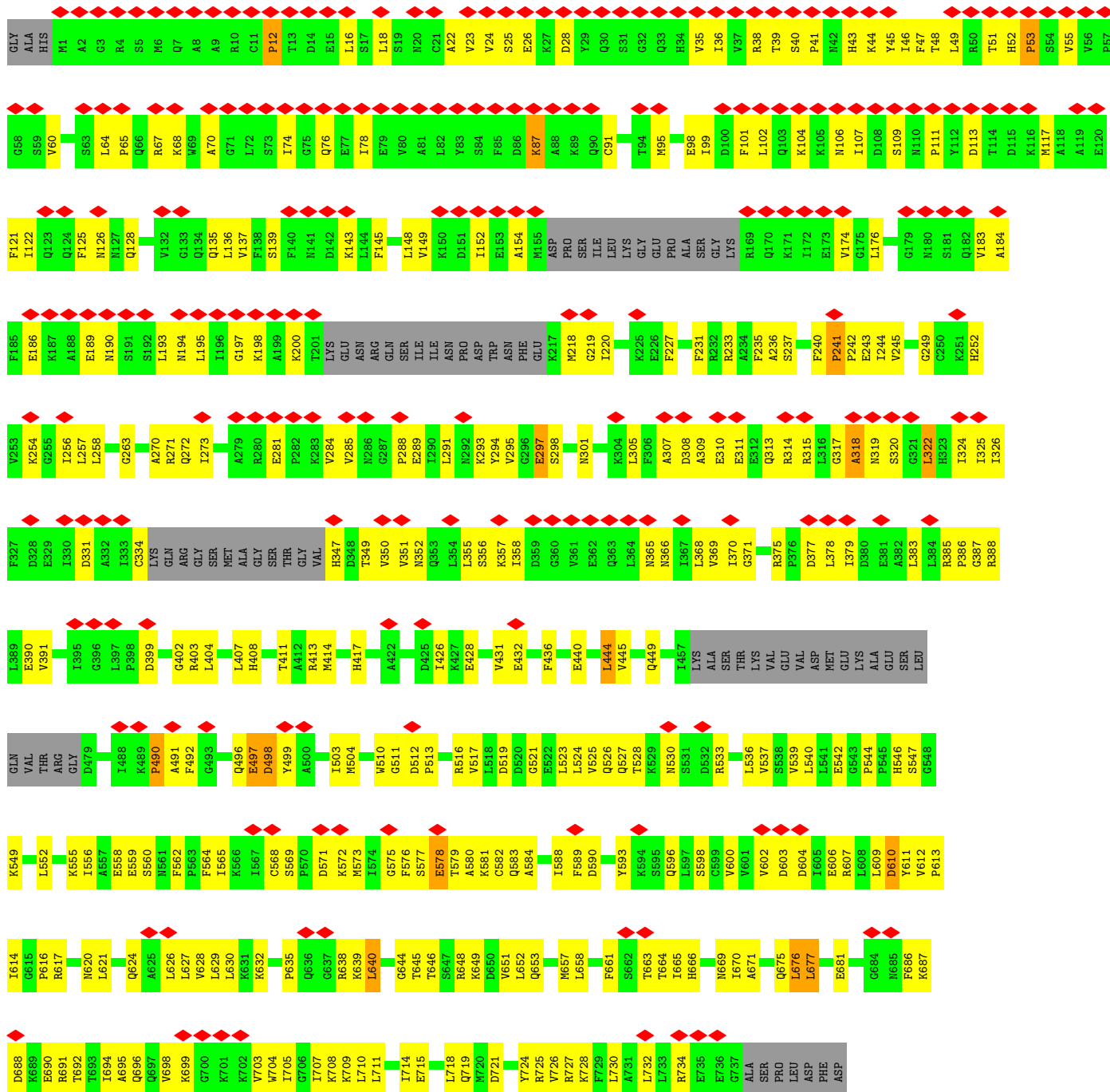
• Molecule 1: Vesicle-fusing ATPase





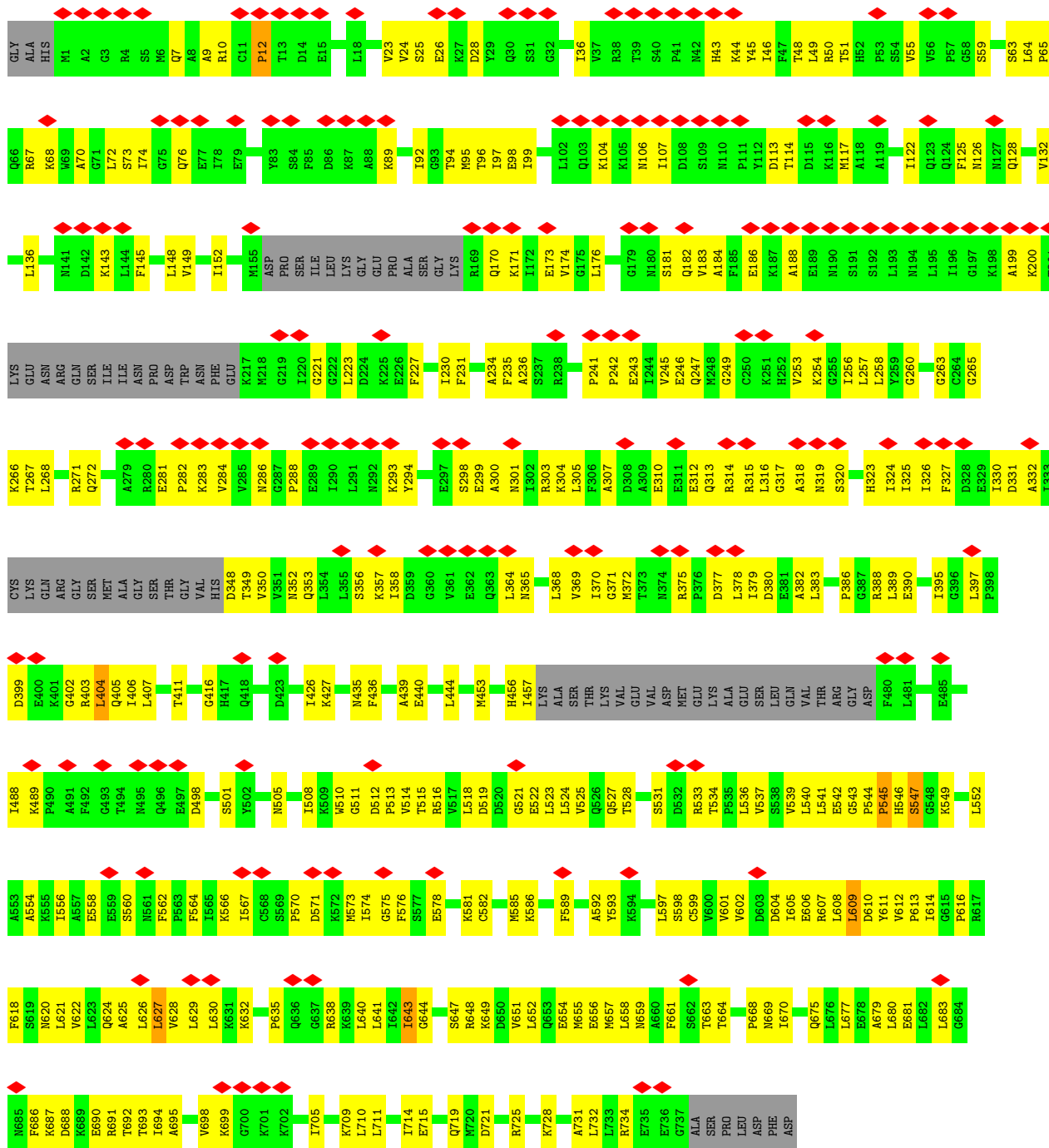


• Molecule 1: Vesicle-fusing ATPase

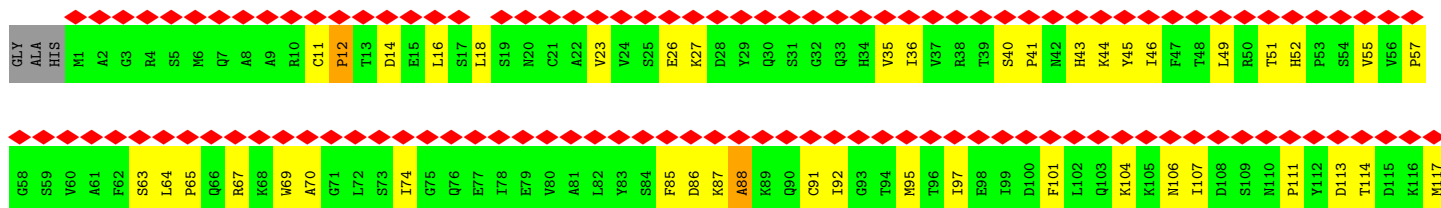
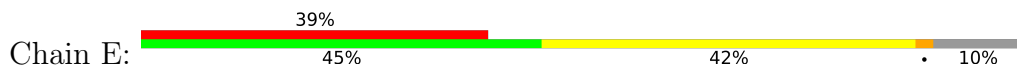


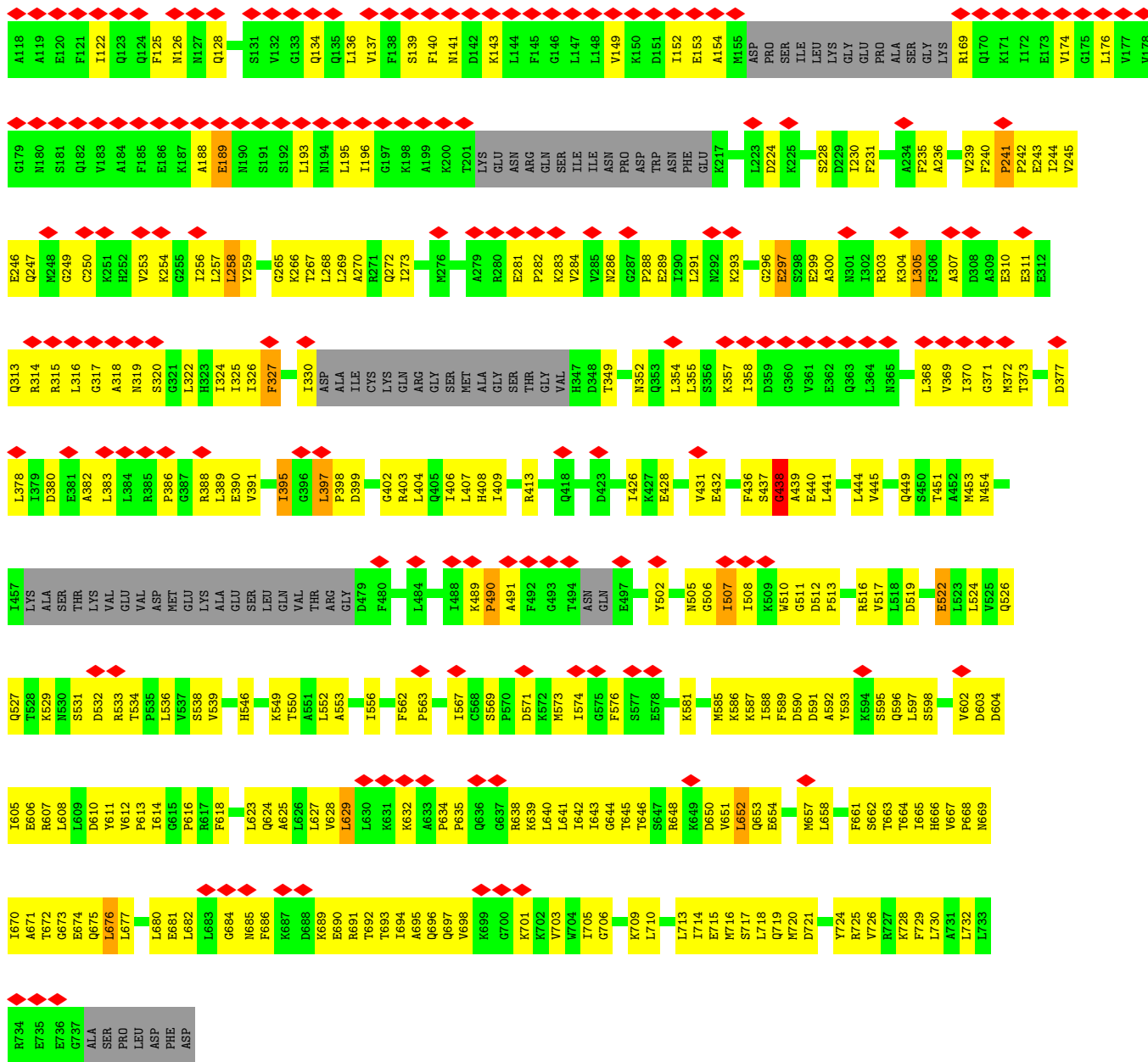
• Molecule 1: Vesicle-fusing ATPase



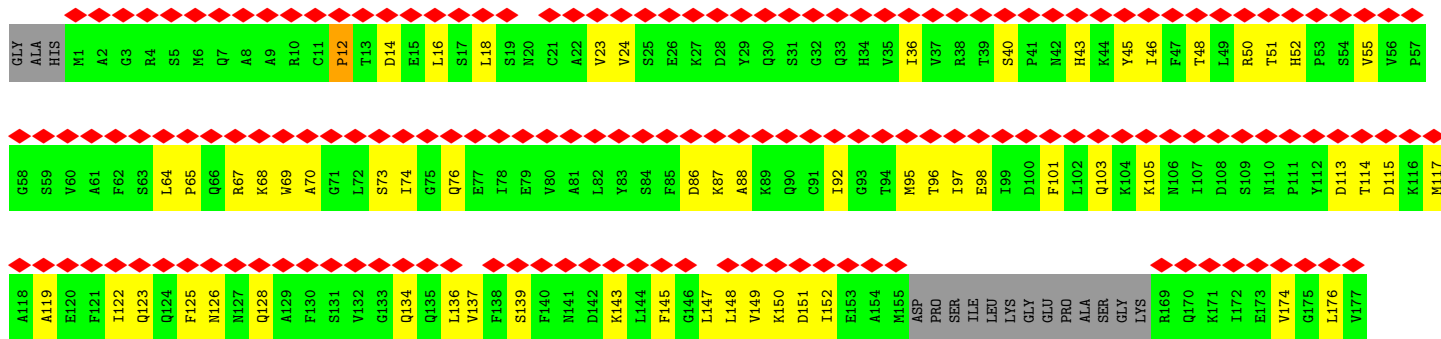
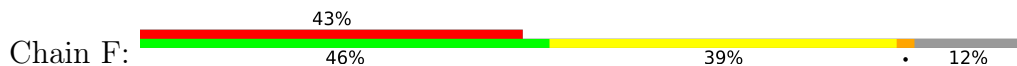


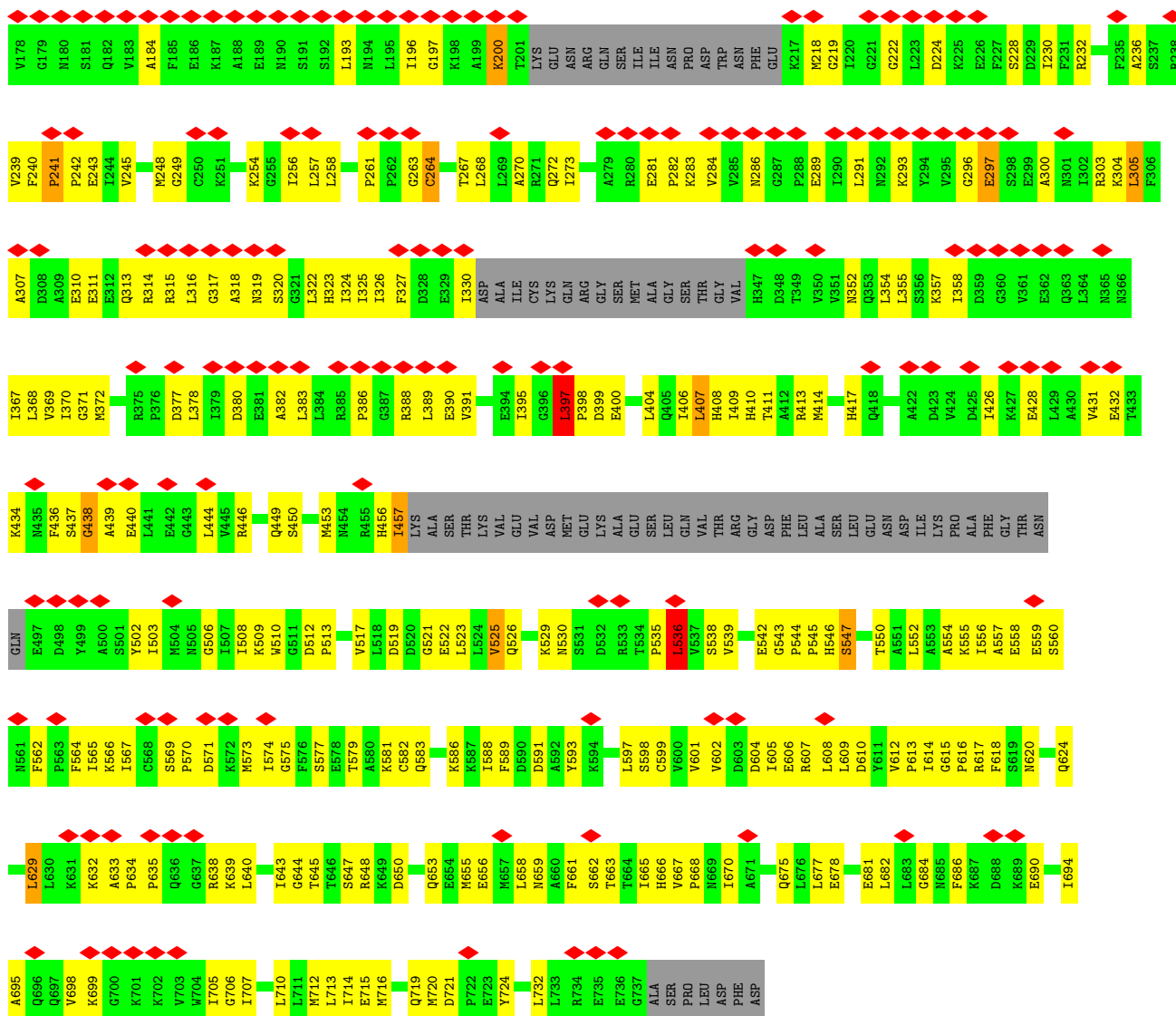
● Molecule 1: Vesicle-fusing ATPase



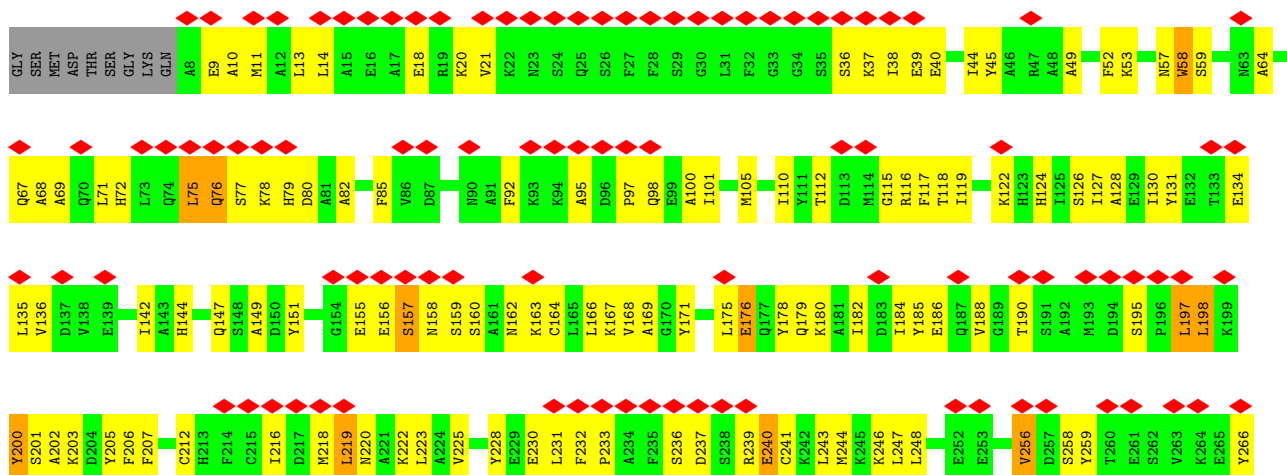
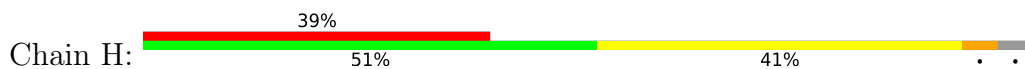


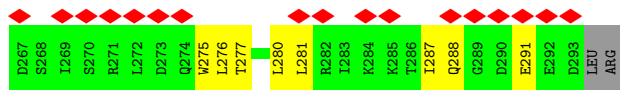
● Molecule 1: Vesicle-fusing ATPase





● Molecule 2: Alpha-soluble NSF attachment protein

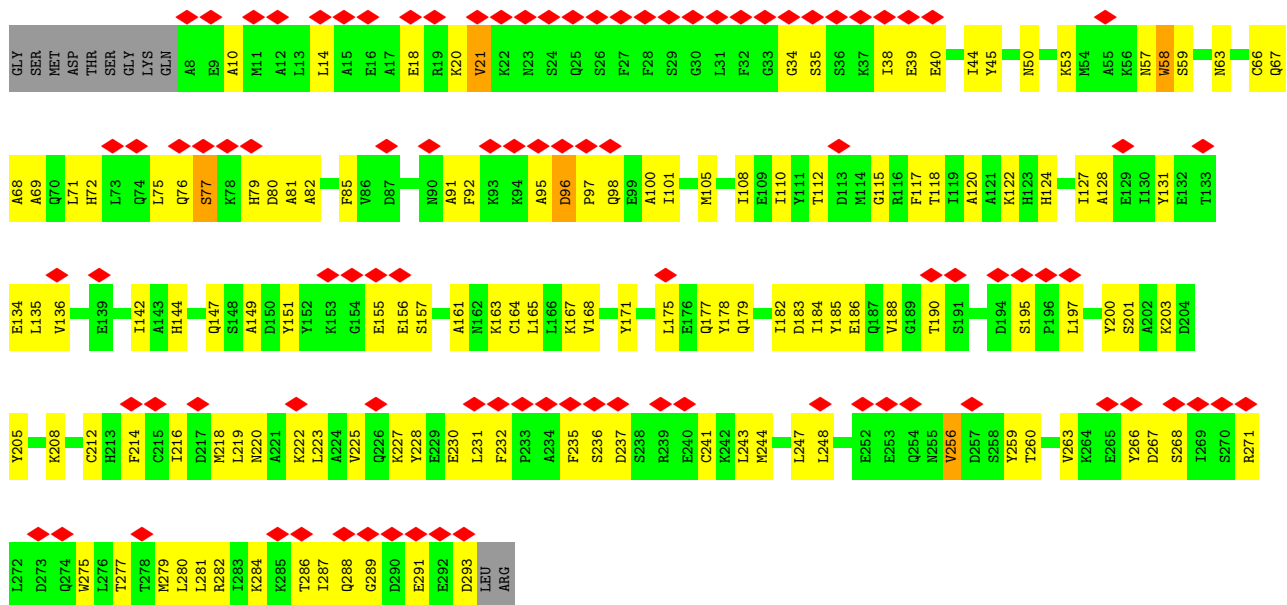




• Molecule 2: Alpha-soluble NSF attachment protein

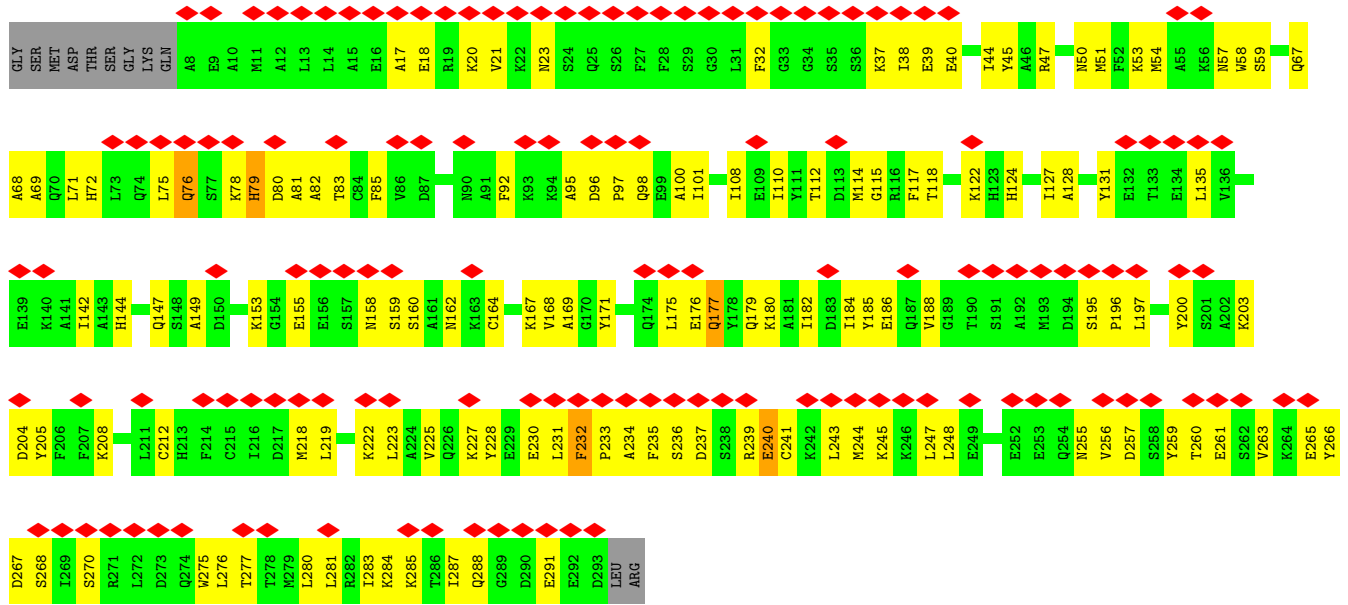


• Molecule 2: Alpha-soluble NSF attachment protein



• Molecule 2: Alpha-soluble NSF attachment protein

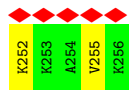
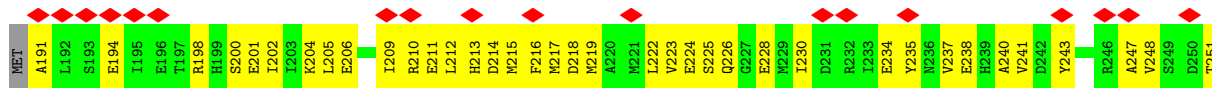




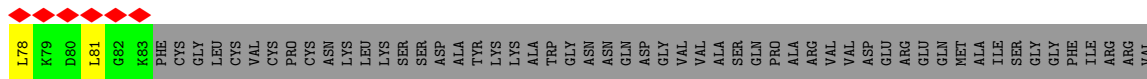
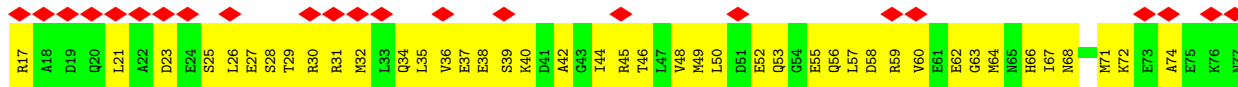
• Molecule 3: Vesicle-associated membrane protein 2

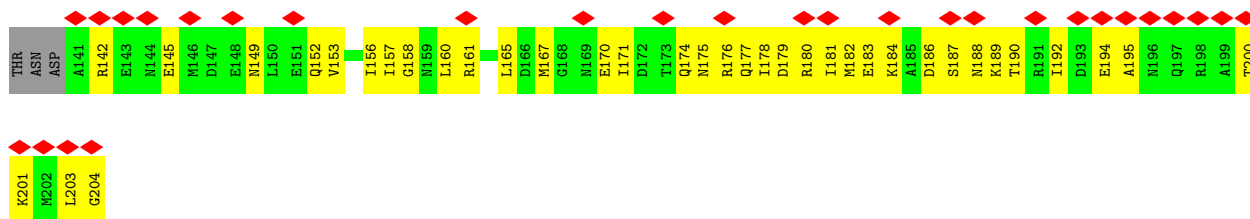


• Molecule 4: Syntaxin-1A



• Molecule 5: Synaptosomal-associated protein 25





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14991	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	44	Depositor
Minimum defocus (nm)	-1800	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	10.964	Depositor
Minimum map value	-5.319	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.0	Depositor
Map size ( $\text{\AA}$ )	311.1936, 311.1936, 311.1936	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.4312, 2.4312, 2.4312	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	0.48	0/5116	0.85	14/6925 (0.2%)
1	B	0.41	1/5069 (0.0%)	0.77	11/6863 (0.2%)
1	C	0.40	0/5102	0.74	6/6905 (0.1%)
1	D	0.42	0/5050	0.75	7/6840 (0.1%)
1	E	0.44	0/5068	0.81	9/6859 (0.1%)
1	F	0.43	1/4977 (0.0%)	0.79	12/6730 (0.2%)
2	G	0.35	0/2289	0.61	0/3079
2	H	0.38	0/2285	0.63	4/3073 (0.1%)
2	I	0.34	0/2288	0.59	1/3077 (0.0%)
2	J	0.36	0/2295	0.57	0/3086
3	K	0.25	0/483	0.42	0/648
4	L	0.23	0/527	0.42	0/704
5	M	0.22	0/1042	0.43	0/1385
All	All	0.41	2/41591 (0.0%)	0.74	64/56174 (0.1%)

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	2
1	B	0	1
1	E	0	1
1	F	0	1
2	H	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	264	CYS	CB-SG	-5.77	1.72	1.81
1	B	547	SER	C-O	5.69	1.34	1.23

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	319	ASN	N-CA-C	-9.95	84.15	111.00
1	F	397	LEU	CA-CB-CG	9.06	136.15	115.30
1	E	629	LEU	CB-CG-CD1	-8.90	95.87	111.00
1	D	547	SER	C-N-CA	-8.85	103.72	122.30
1	C	322	LEU	CA-CB-CG	8.20	134.15	115.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	A	321	GLY	Peptide
1	B	438	GLY	Peptide
1	E	438	GLY	Peptide
1	F	438	GLY	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	5039	0	4945	309	0
1	B	4995	0	4920	281	0
1	C	5027	0	4945	329	0
1	D	4976	0	4880	318	0
1	E	4992	0	4910	318	0
1	F	4903	0	4853	308	0
2	G	2249	0	2188	114	0
2	H	2246	0	2183	128	0
2	I	2249	0	2192	99	0
2	J	2255	0	2199	129	0
3	K	480	0	465	73	0
4	L	523	0	497	52	0
5	M	1042	0	1022	118	0
All	All	40976	0	40199	2329	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 29.

The worst 5 of 2329 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)
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.46	0.93
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.50	0.92
1:C:386:PRO:HA	1:C:390:GLU:HA	1.54	0.90
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.51	0.90
1:F:545:PRO:HA	1:F:547:SER:H	1.38	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	A	668/747 (89%)	614 (92%)	37 (6%)	17 (2%)	5	32
1	B	662/747 (89%)	593 (90%)	55 (8%)	14 (2%)	7	36
1	C	666/747 (89%)	615 (92%)	39 (6%)	12 (2%)	8	40
1	D	663/747 (89%)	607 (92%)	47 (7%)	9 (1%)	11	46
1	E	658/747 (88%)	603 (92%)	41 (6%)	14 (2%)	7	36
1	F	644/747 (86%)	587 (91%)	44 (7%)	13 (2%)	7	38
2	G	284/297 (96%)	230 (81%)	43 (15%)	11 (4%)	3	23
2	H	284/297 (96%)	229 (81%)	46 (16%)	9 (3%)	4	26
2	I	284/297 (96%)	227 (80%)	48 (17%)	9 (3%)	4	26
2	J	284/297 (96%)	232 (82%)	41 (14%)	11 (4%)	3	23
3	K	59/63 (94%)	56 (95%)	2 (3%)	1 (2%)	9	42
4	L	64/67 (96%)	56 (88%)	8 (12%)	0	100	100
5	M	127/188 (68%)	124 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5347/5988 (89%)	4773 (89%)	454 (8%)	120 (2%)	10	35

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	293	LYS
1	A	294	TYR
1	A	318	ALA
1	A	320	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	
1	A	511/638 (80%)	509 (100%)	2 (0%)	91	94
1	B	512/638 (80%)	508 (99%)	4 (1%)	81	89
1	C	513/638 (80%)	512 (100%)	1 (0%)	93	96
1	D	506/638 (79%)	505 (100%)	1 (0%)	93	96
1	E	511/638 (80%)	508 (99%)	3 (1%)	86	92
1	F	505/638 (79%)	501 (99%)	4 (1%)	81	89
2	G	234/244 (96%)	234 (100%)	0	100	100
2	H	233/244 (96%)	233 (100%)	0	100	100
2	I	234/244 (96%)	233 (100%)	1 (0%)	91	94
2	J	235/244 (96%)	234 (100%)	1 (0%)	91	94
3	K	49/54 (91%)	49 (100%)	0	100	100
4	L	56/61 (92%)	56 (100%)	0	100	100
5	M	114/161 (71%)	114 (100%)	0	100	100
All	All	4213/5080 (83%)	4196 (100%)	17 (0%)	91	94

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	536	LEU
2	J	183	ASP
1	D	305	LEU
1	E	305	LEU
1	E	322	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	252	HIS
2	G	50	ASN
2	H	72	HIS
2	J	50	ASN
3	K	38	GLN

### 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.

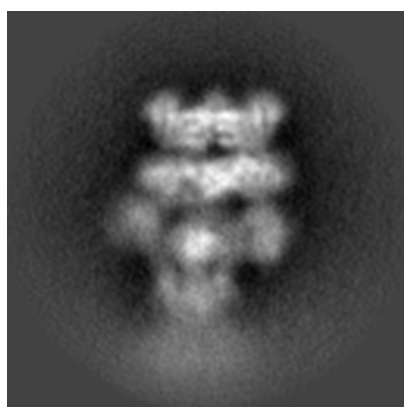
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6209. These allow visual inspection of the internal detail of the map and identification of artifacts.

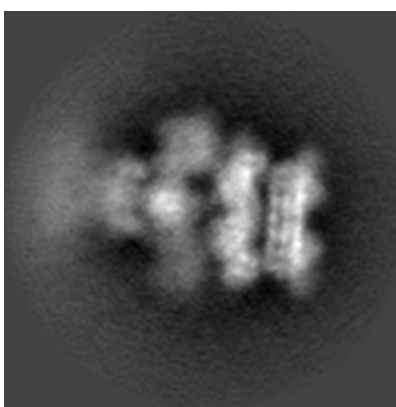
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

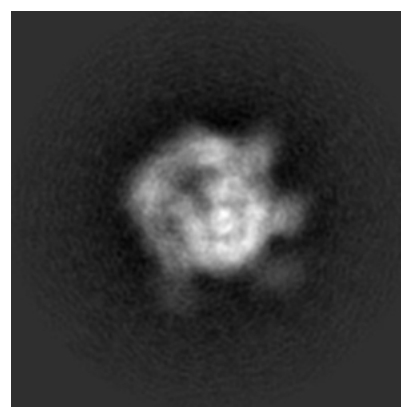
#### 6.1.1 Primary map



X



Y

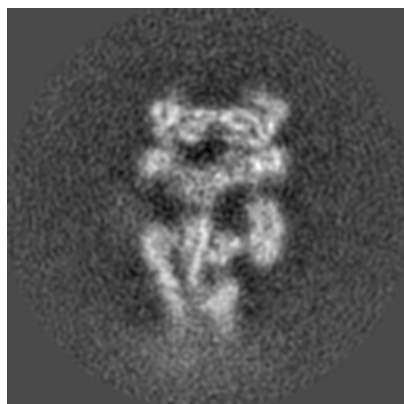


Z

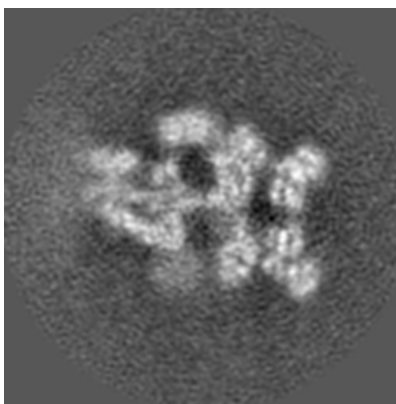
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

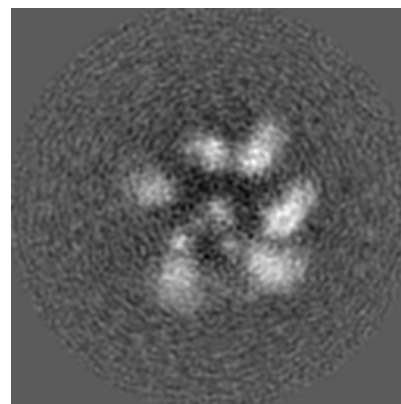
#### 6.2.1 Primary map



X Index: 64



Y Index: 64

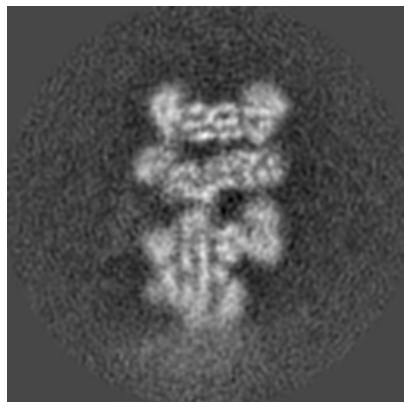


Z Index: 64

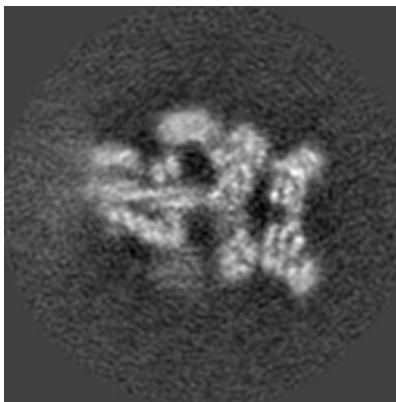
The images above show central slices of the map in three orthogonal directions.

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

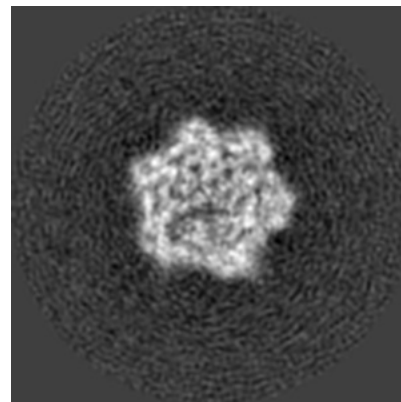
### 6.3.1 Primary map



X Index: 67



Y Index: 63

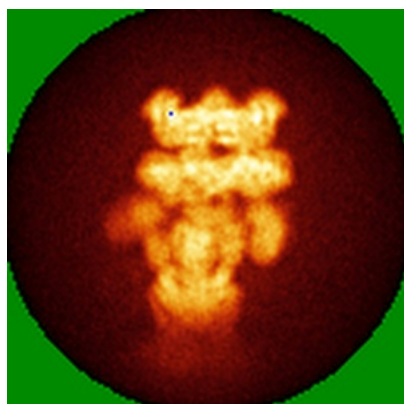


Z Index: 76

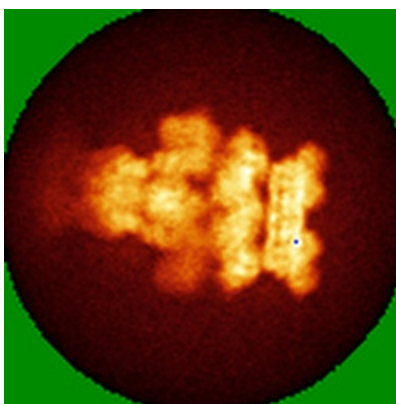
The images above show the largest variance slices of the map in three orthogonal directions.

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

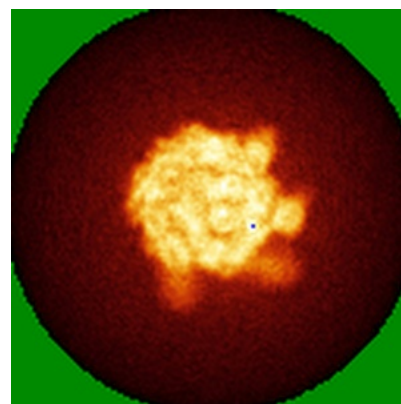
### 6.4.1 Primary map



X



Y

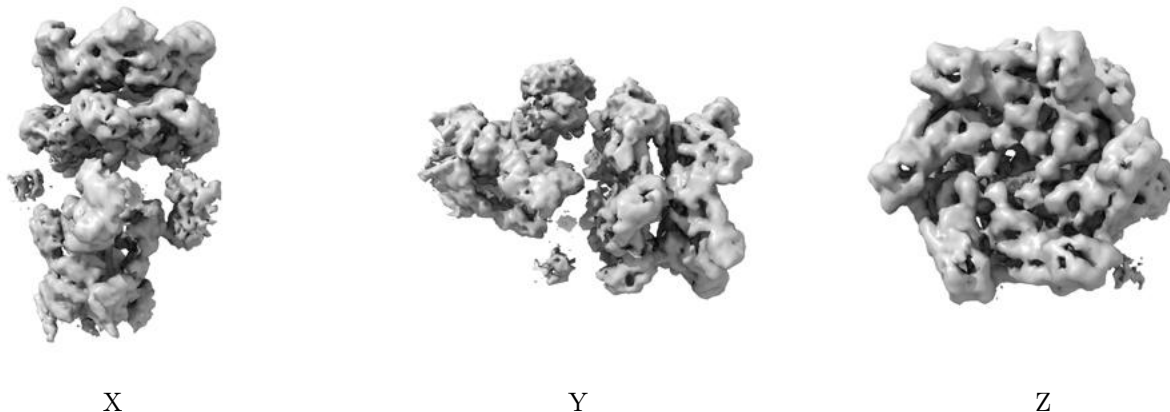


Z

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



The images above show the 3D surface view of the map at the recommended contour level 5.0. 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](#)

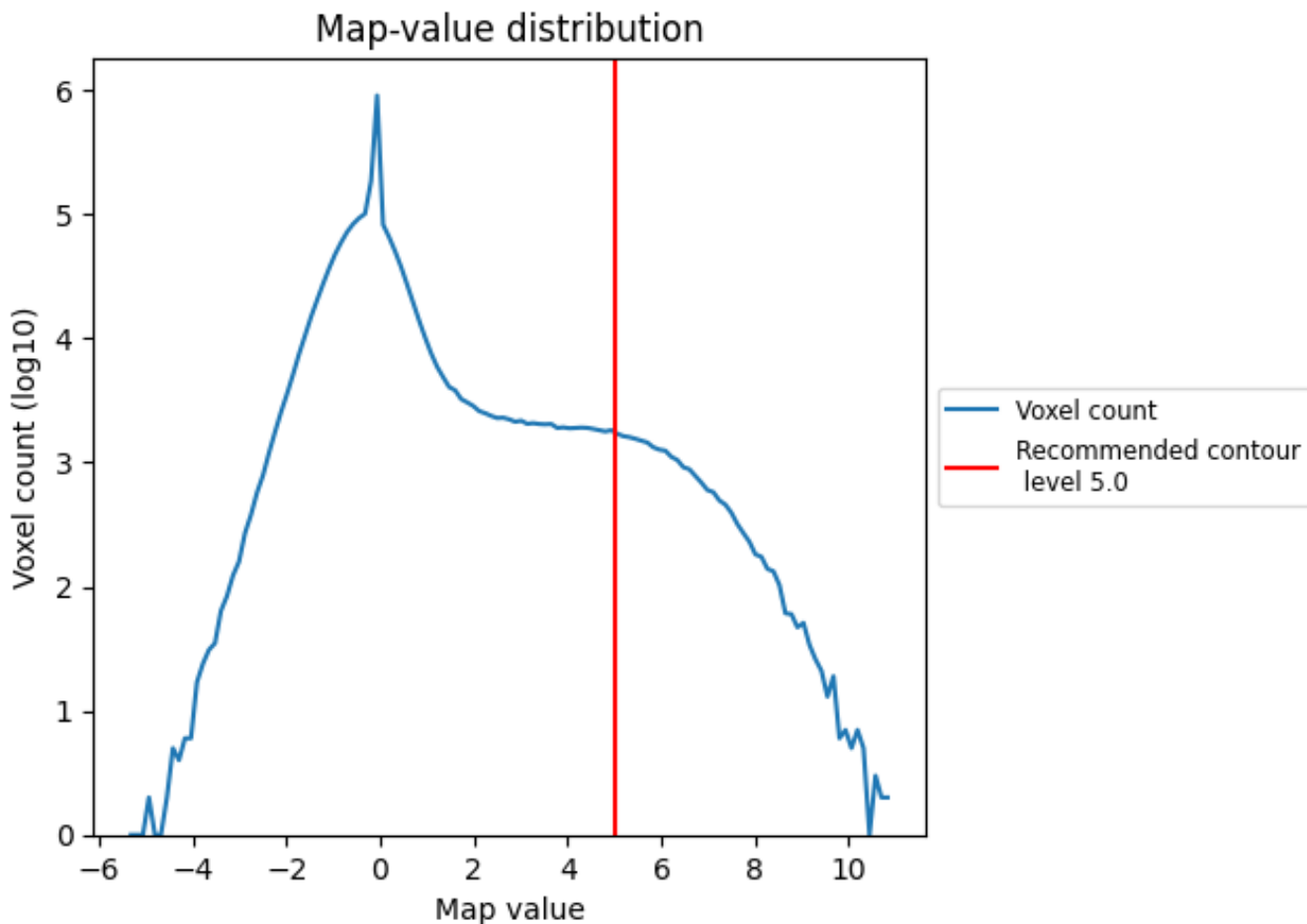
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

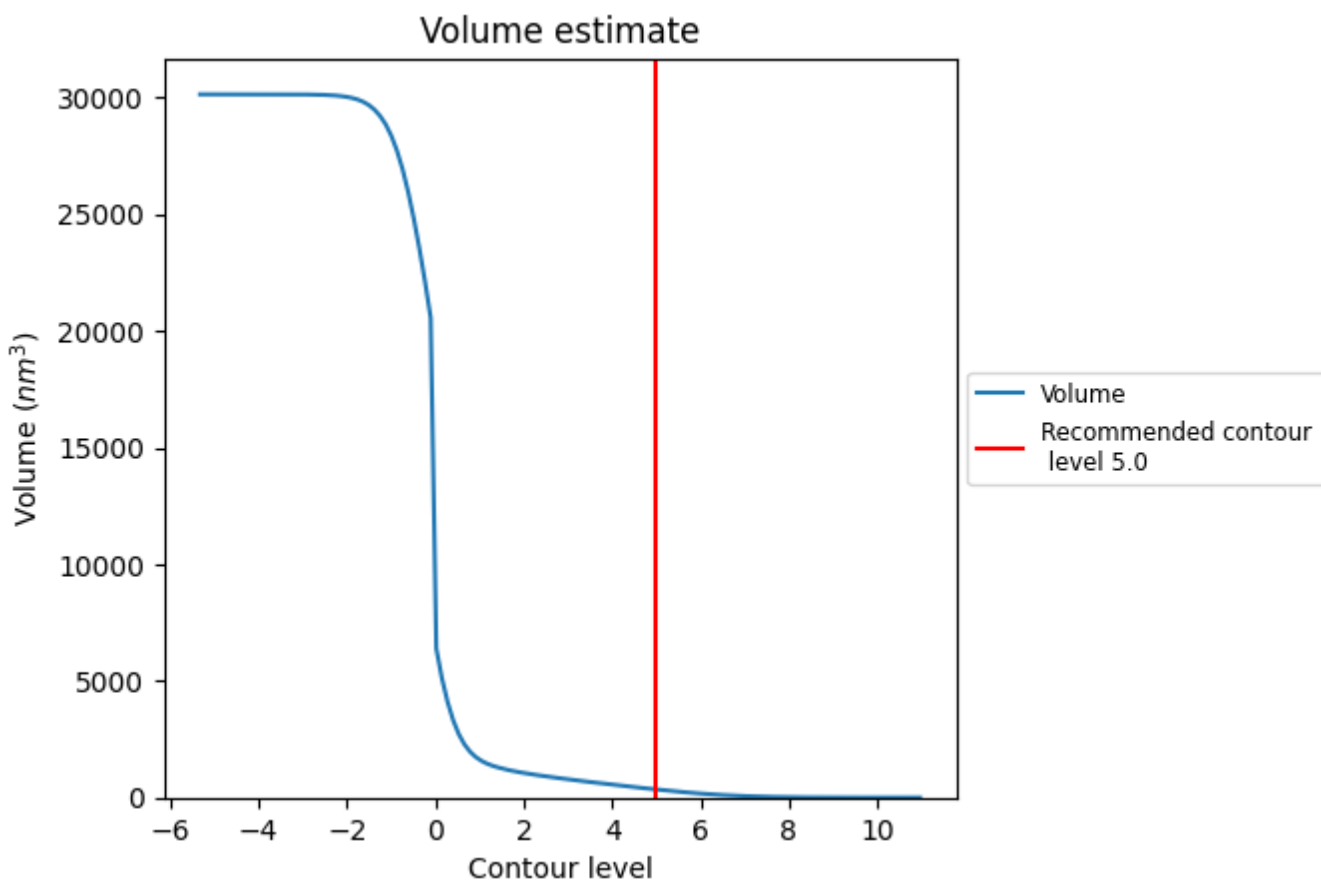
This section contains the results of statistical analysis of the map.

### 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.

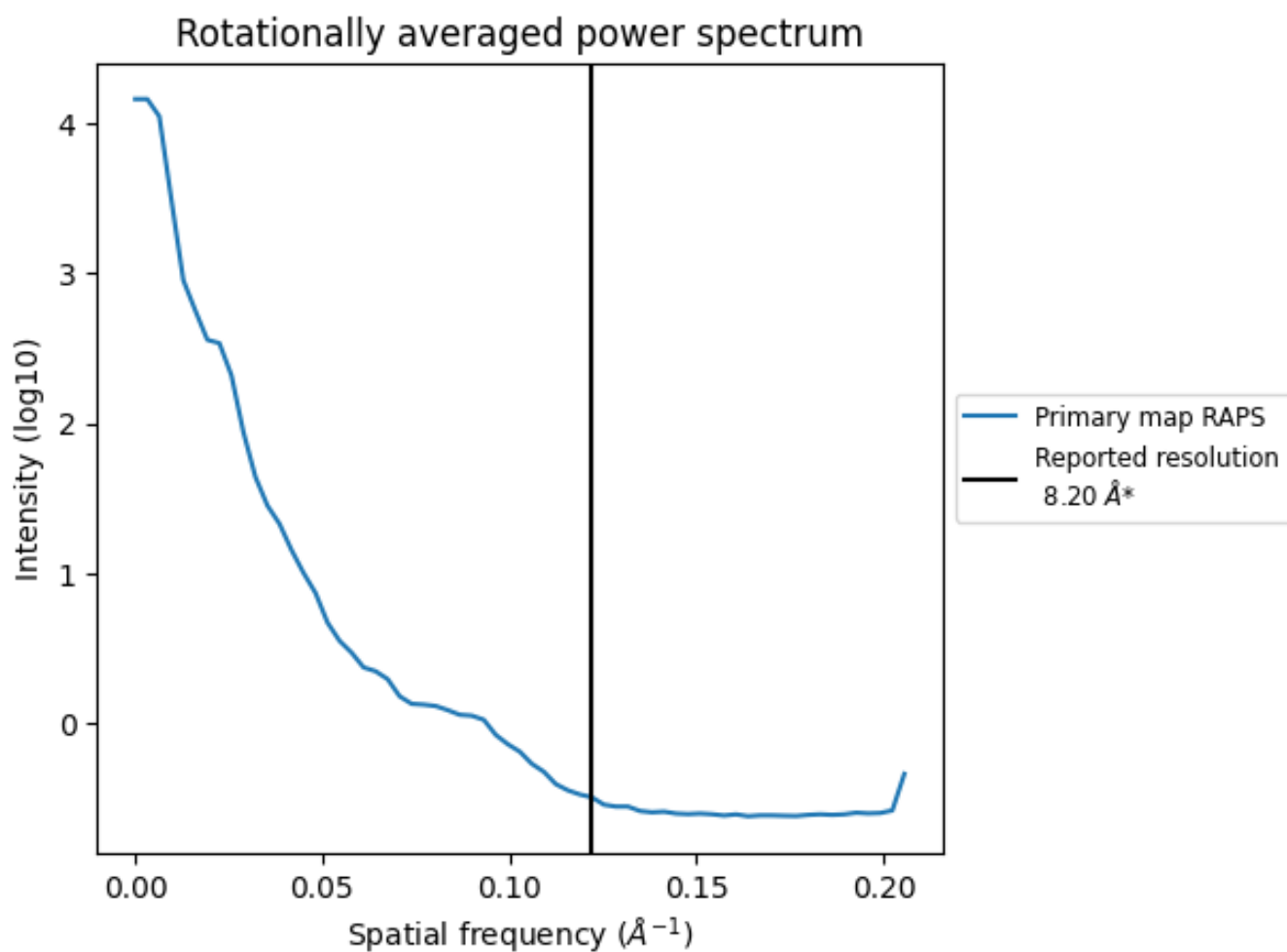
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 346 nm<sup>3</sup>; this corresponds to an approximate mass of 313 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 0.122 Å<sup>-1</sup>

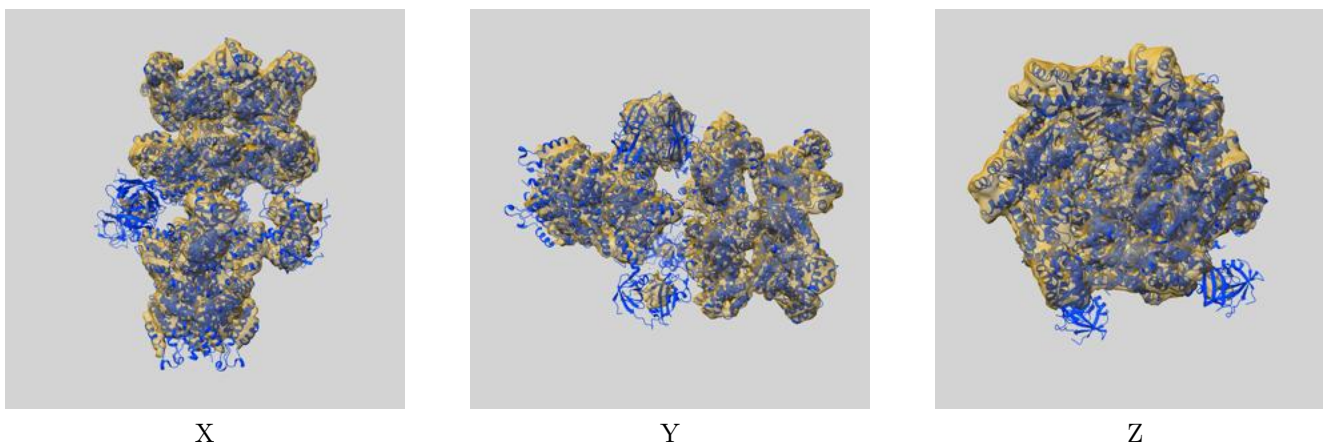
## 8 Fourier-Shell correlation

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

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

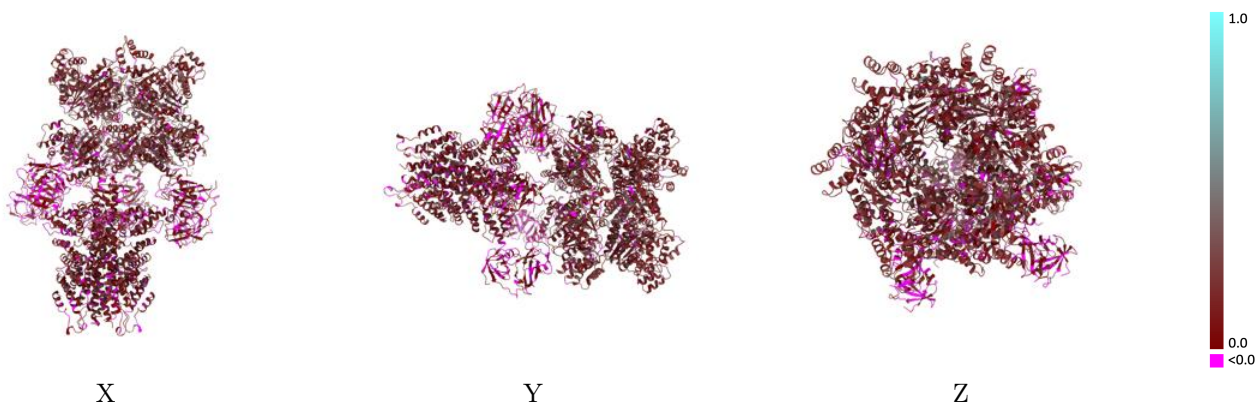
This section contains information regarding the fit between EMDB map EMD-6209 and PDB model 3J99. Per-residue inclusion information can be found in section 3 on page 7.

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



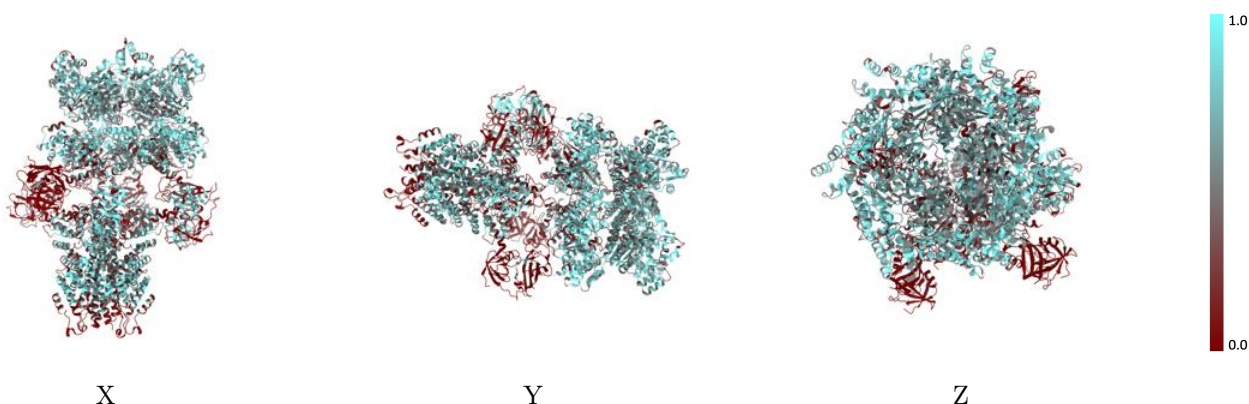
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



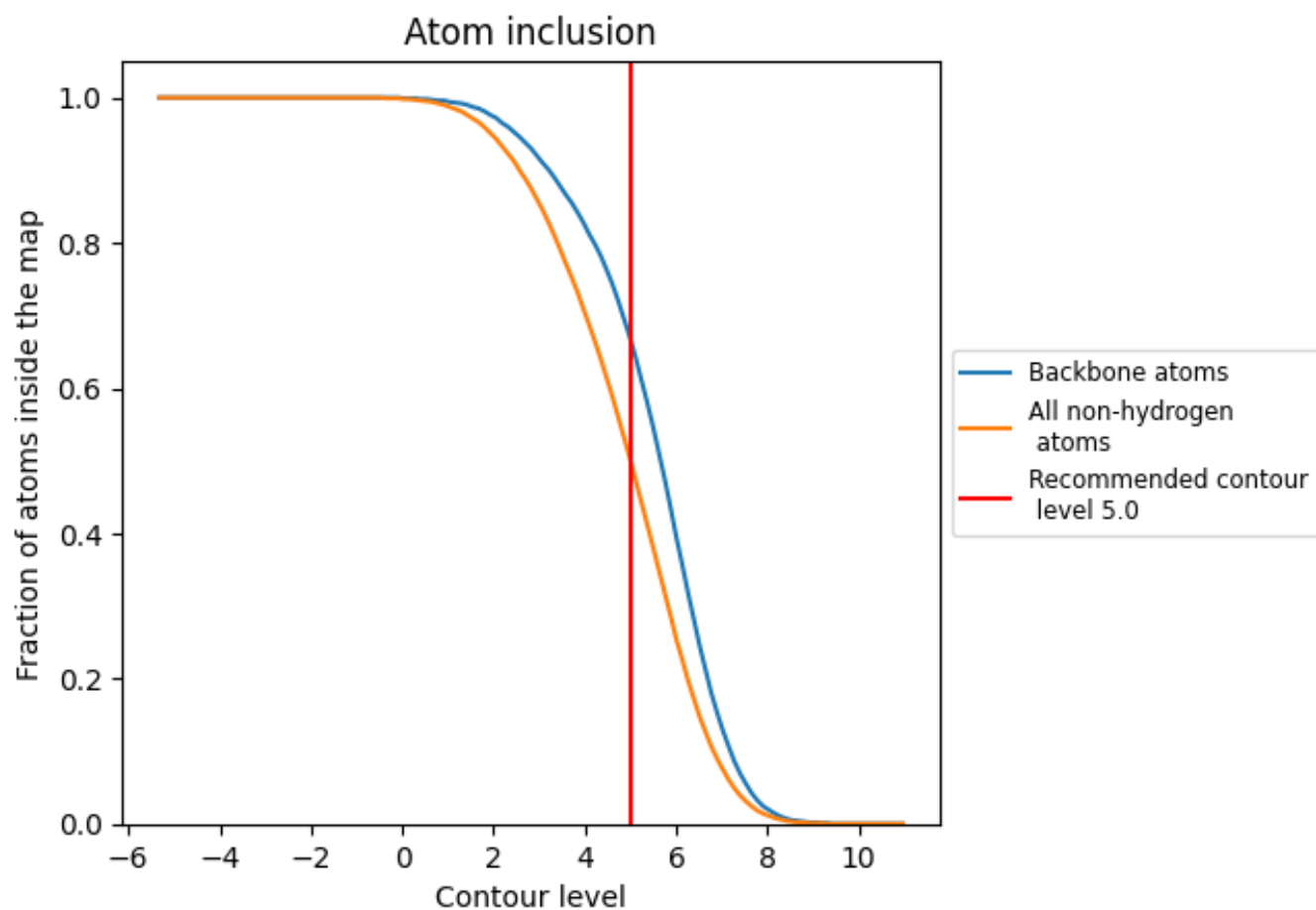
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.0).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (5.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5000	0.1330
A	0.4580	0.1250
B	0.5980	0.1550
C	0.5120	0.1420
D	0.6030	0.1590
E	0.4490	0.1270
F	0.4060	0.1150
G	0.4300	0.1110
H	0.4870	0.1190
I	0.5260	0.1270
J	0.5350	0.1230
K	0.4870	0.1240
L	0.4870	0.1580
M	0.4190	0.1200

