



## wwPDB EM Validation Summary Report ⓘ

Aug 17, 2024 – 12:31 pm BST

PDB ID : 8QBE  
EMDB ID : EMD-18311  
Title : Compact state - Pill in native eisosome lattice bound to plasma membrane microdomain  
Authors : Kefauver, J.M.; Zou, L.; Desfosses, A.; Loewith, R.J.  
Deposited on : 2023-08-24  
Resolution : 3.67 Å(reported)  
Based on initial model : .

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:

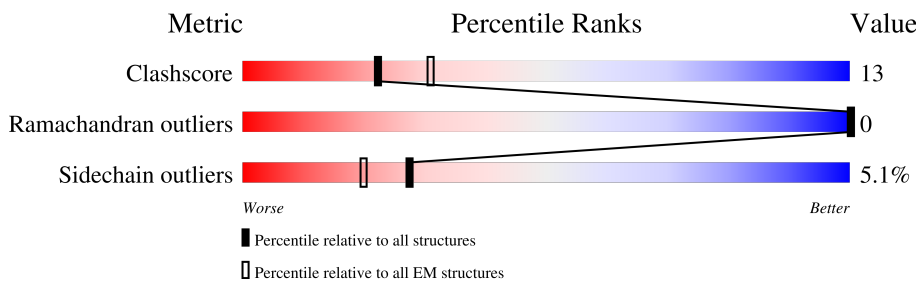
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

# 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 3.67 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	339	6% (poor fit), 54% (0 outliers), 25% (1 outlier), 20% (2+ outliers)
1	B	339	6% (poor fit), 56% (0 outliers), 22% (1 outlier), 20% (2+ outliers)
1	C	339	19% (poor fit), 55% (0 outliers), 23% (1 outlier), 20% (2+ outliers)
1	D	339	42% (poor fit), 55% (0 outliers), 24% (1 outlier), 20% (2+ outliers)
1	E	339	67% (poor fit), 56% (0 outliers), 23% (1 outlier), 20% (2+ outliers)
1	F	339	24% (poor fit), 55% (0 outliers), 24% (1 outlier), 20% (2+ outliers)
1	G	339	32% (poor fit), 56% (0 outliers), 22% (1 outlier), 20% (2+ outliers)
1	H	339	51% (poor fit), 55% (0 outliers), 24% (1 outlier), 20% (2+ outliers)

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Mol	Chain	Length	Quality of chain
1	I	339	<p>26% 55% 24% • 20%</p>
1	J	339	<p>33% 55% 23% • 20%</p>
1	K	339	<p>56% 56% 22% • 20%</p>
1	L	339	<p>17% 55% 24% • 20%</p>
1	M	339	<p>47% 55% 24% • 20%</p>
1	N	339	<p>69% 56% 23% • 20%</p>

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 30058 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.

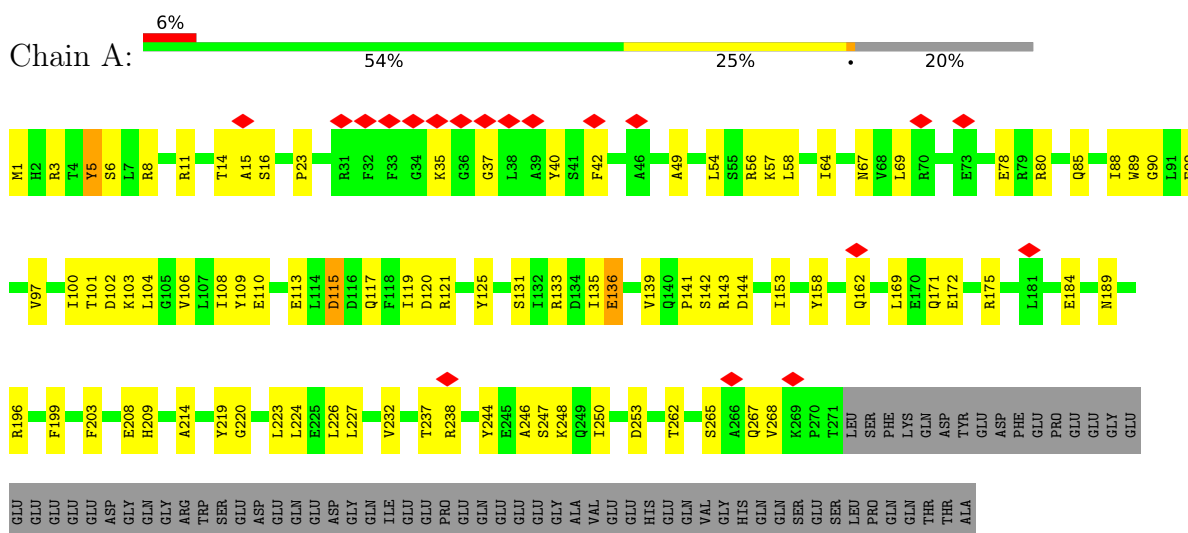
- Molecule 1 is a protein called Sphingolipid long chain base-responsive protein PIL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	271	2147	1346	374	425	2	0	0
1	B	271	2147	1346	374	425	2	0	0
1	C	271	2147	1346	374	425	2	0	0
1	I	271	2147	1346	374	425	2	0	0
1	D	271	2147	1346	374	425	2	0	0
1	J	271	2147	1346	374	425	2	0	0
1	E	271	2147	1346	374	425	2	0	0
1	K	271	2147	1346	374	425	2	0	0
1	F	271	2147	1346	374	425	2	0	0
1	L	271	2147	1346	374	425	2	0	0
1	G	271	2147	1346	374	425	2	0	0
1	M	271	2147	1346	374	425	2	0	0
1	H	271	2147	1346	374	425	2	0	0
1	N	271	2147	1346	374	425	2	0	0

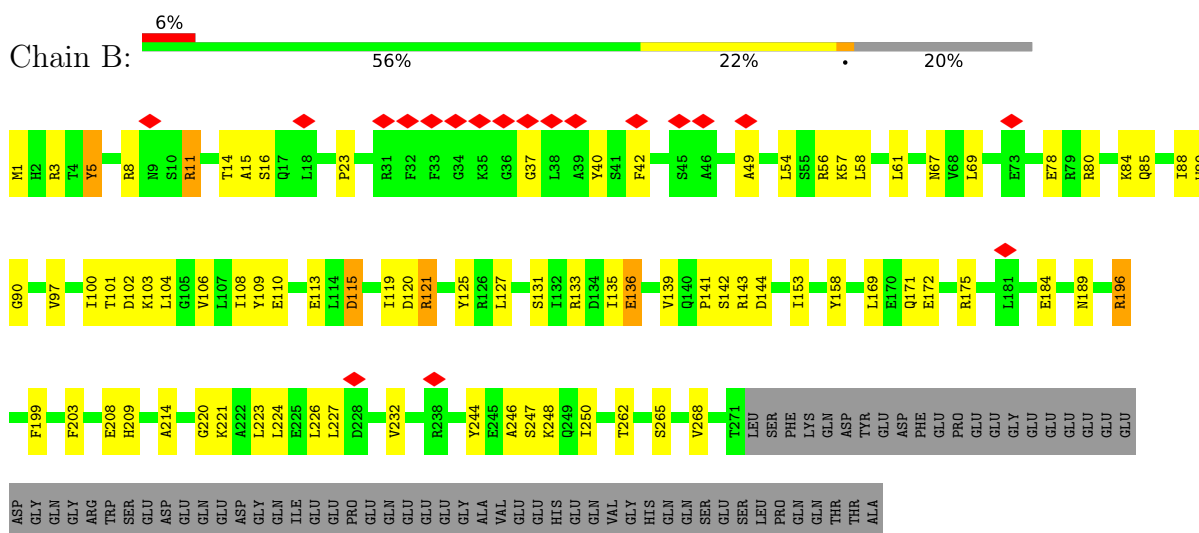
### 3 Residue-property plots [i](#)

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: Spingolipid long chain base-responsive protein PIL1

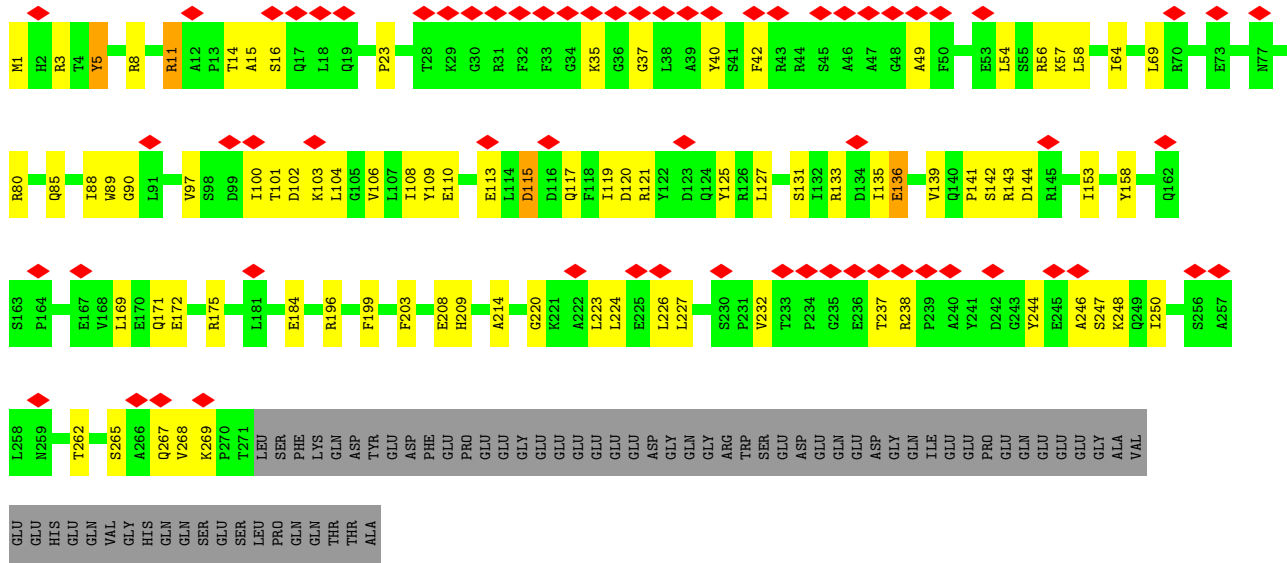


- Molecule 1: Spingolipid long chain base-responsive protein PIL1

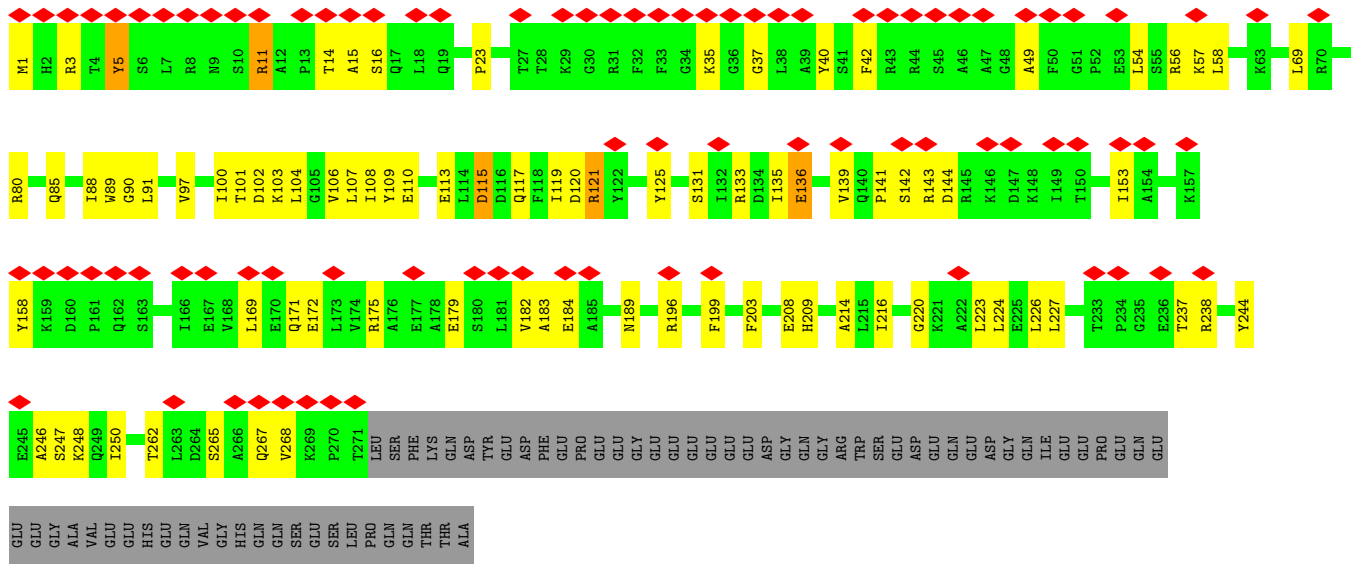


- Molecule 1: Spingolipid long chain base-responsive protein PIL1

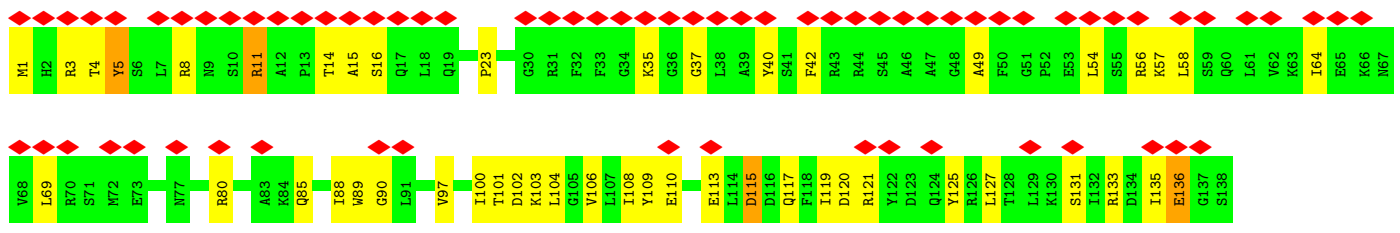
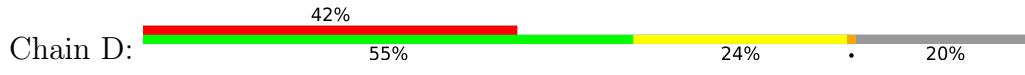


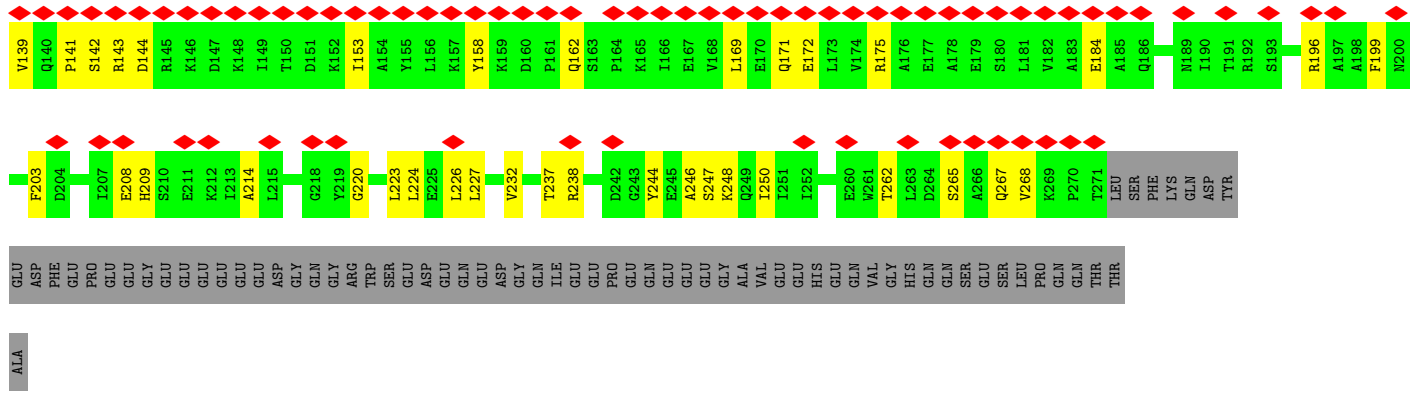


• Molecule 1: Spingolipid long chain base-responsive protein PIL1

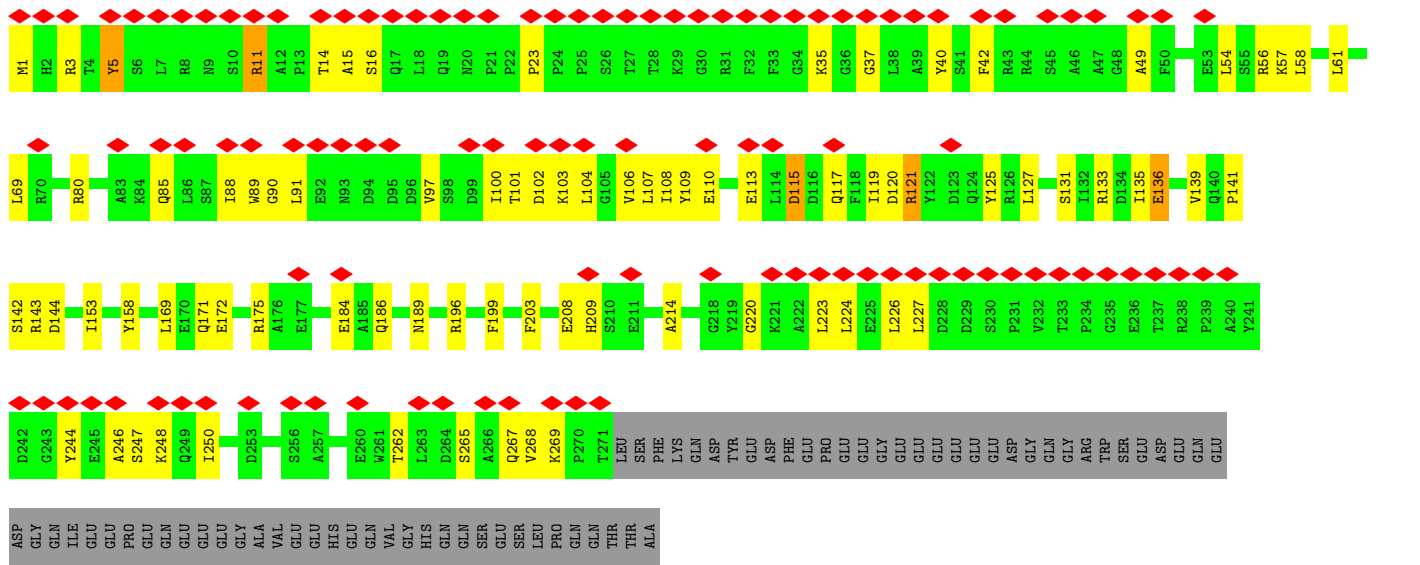


• Molecule 1: Spingolipid long chain base-responsive protein PIL1

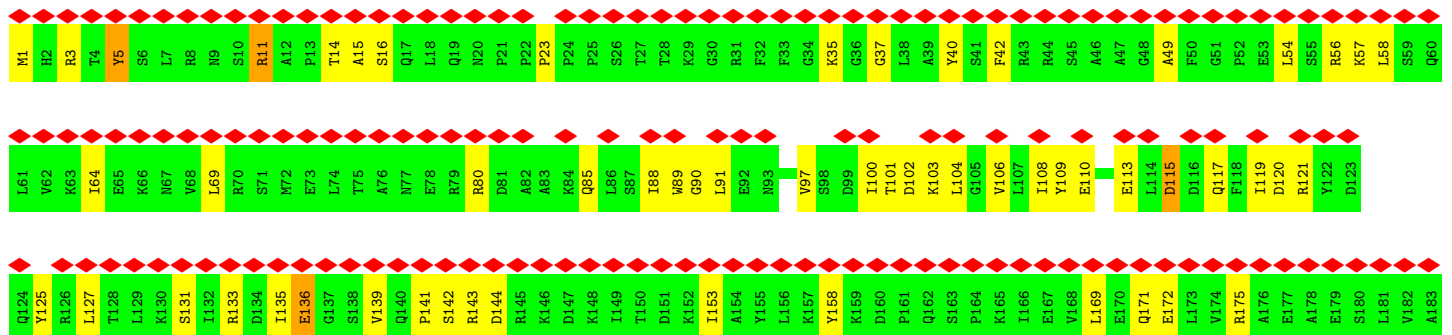


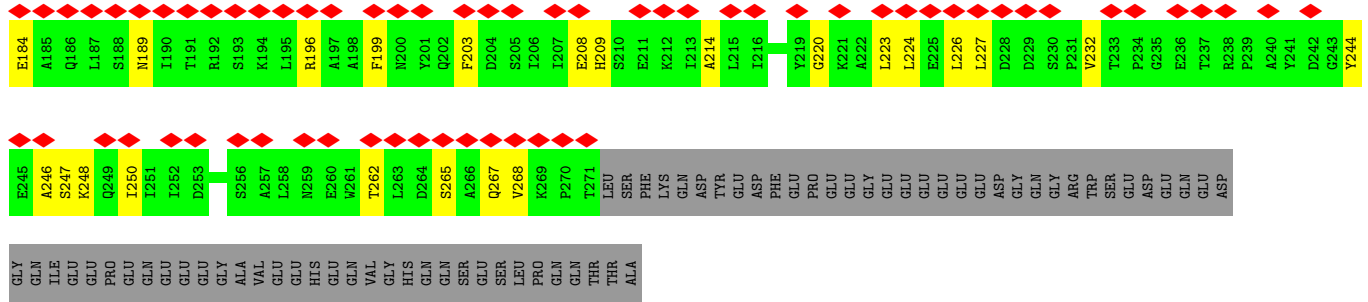


• Molecule 1: Spingolipid long chain base-responsive protein PIL1

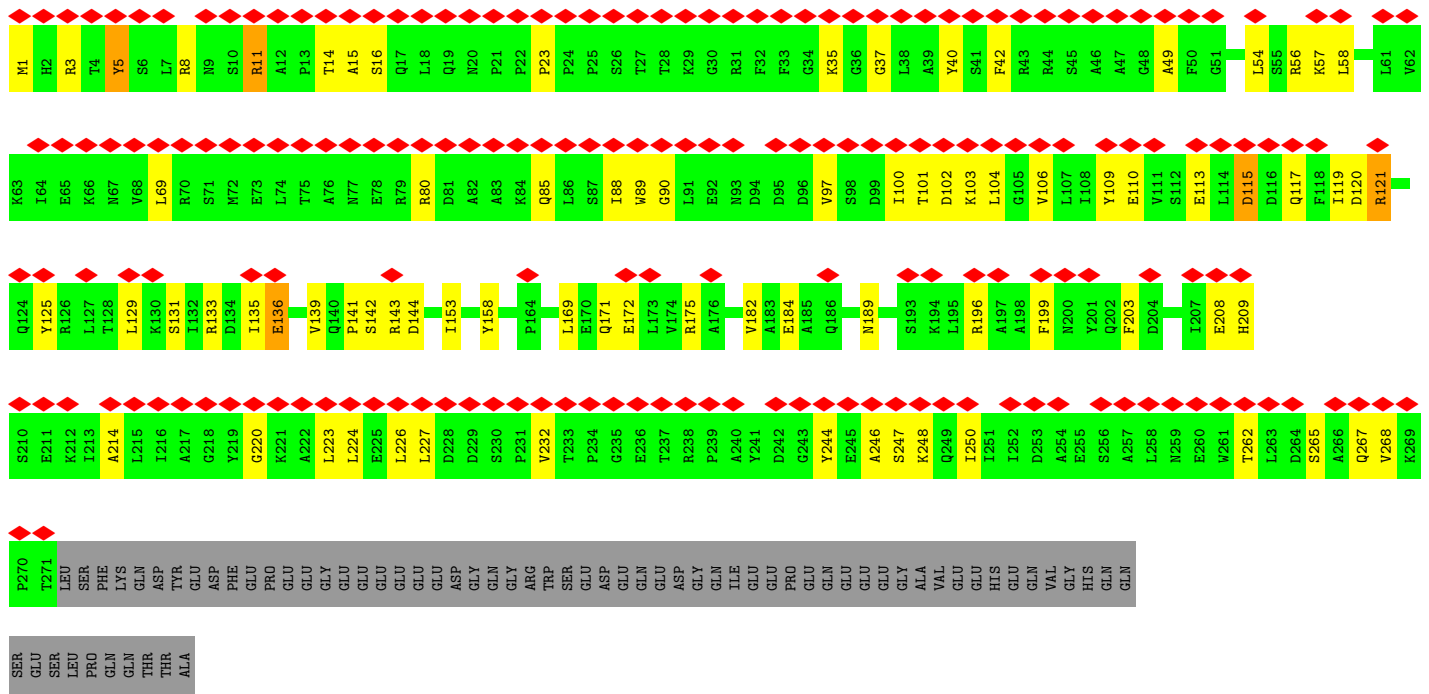


• Molecule 1: Spingolipid long chain base-responsive protein PIL1

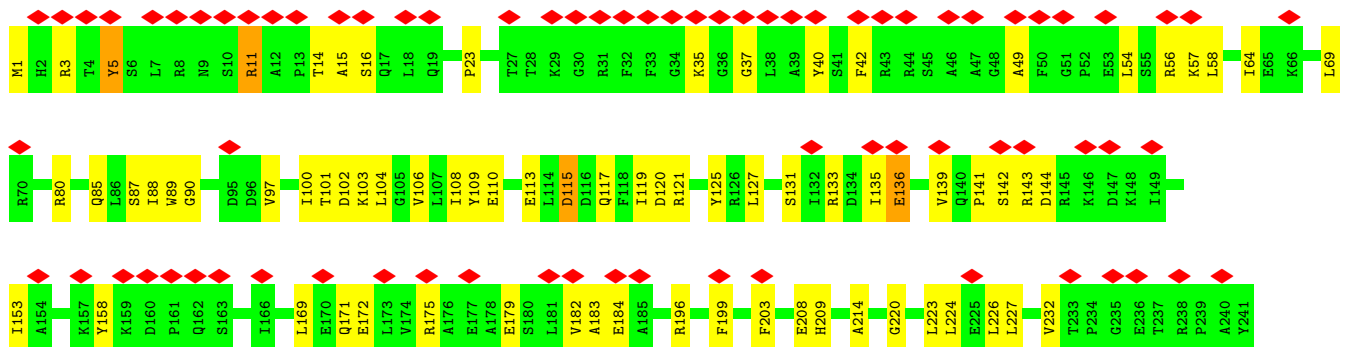




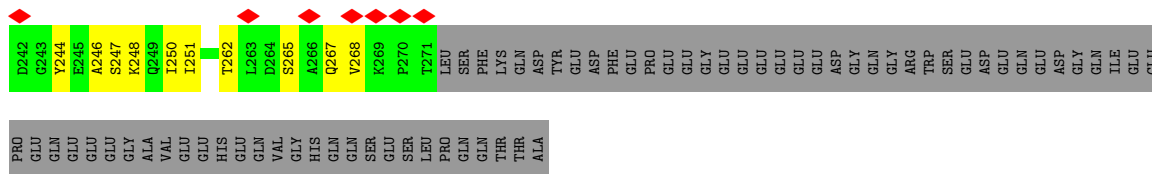
• Molecule 1: Spingolipid long chain base-responsive protein PIL1



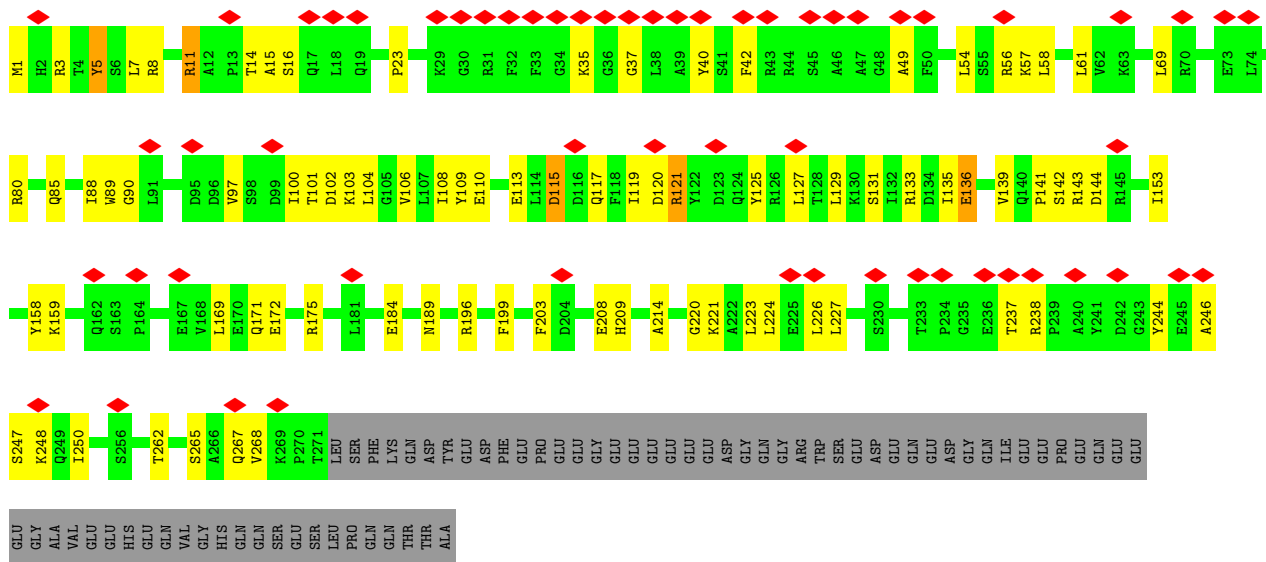
• Molecule 1: Spingolipid long chain base-responsive protein PIL1



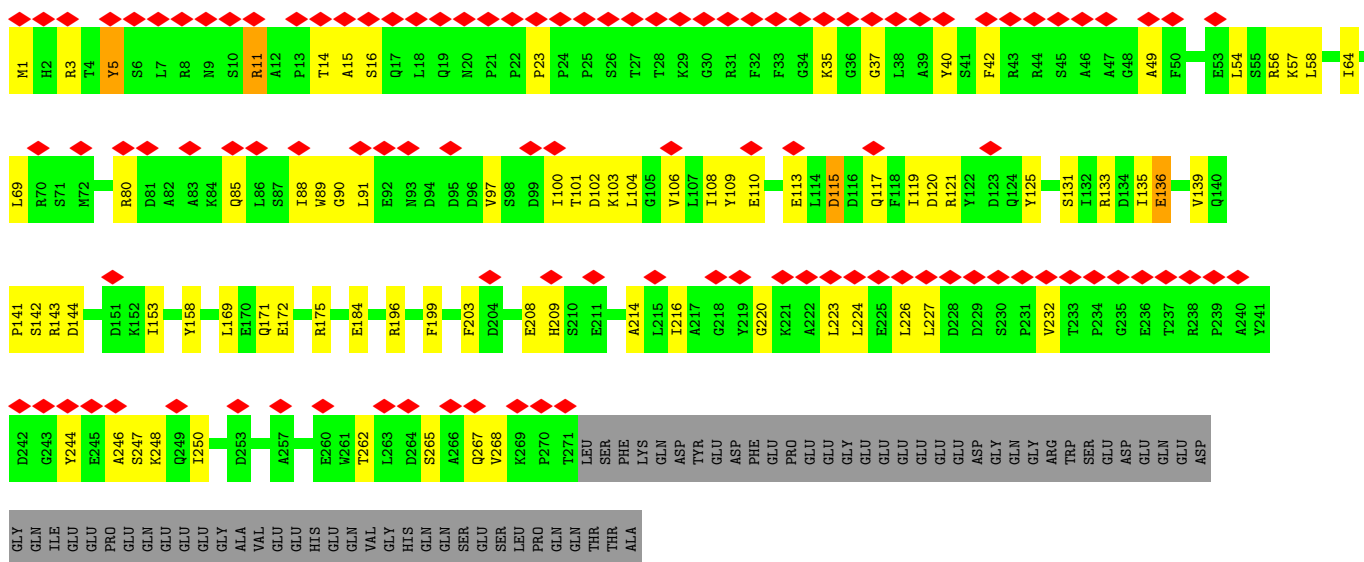




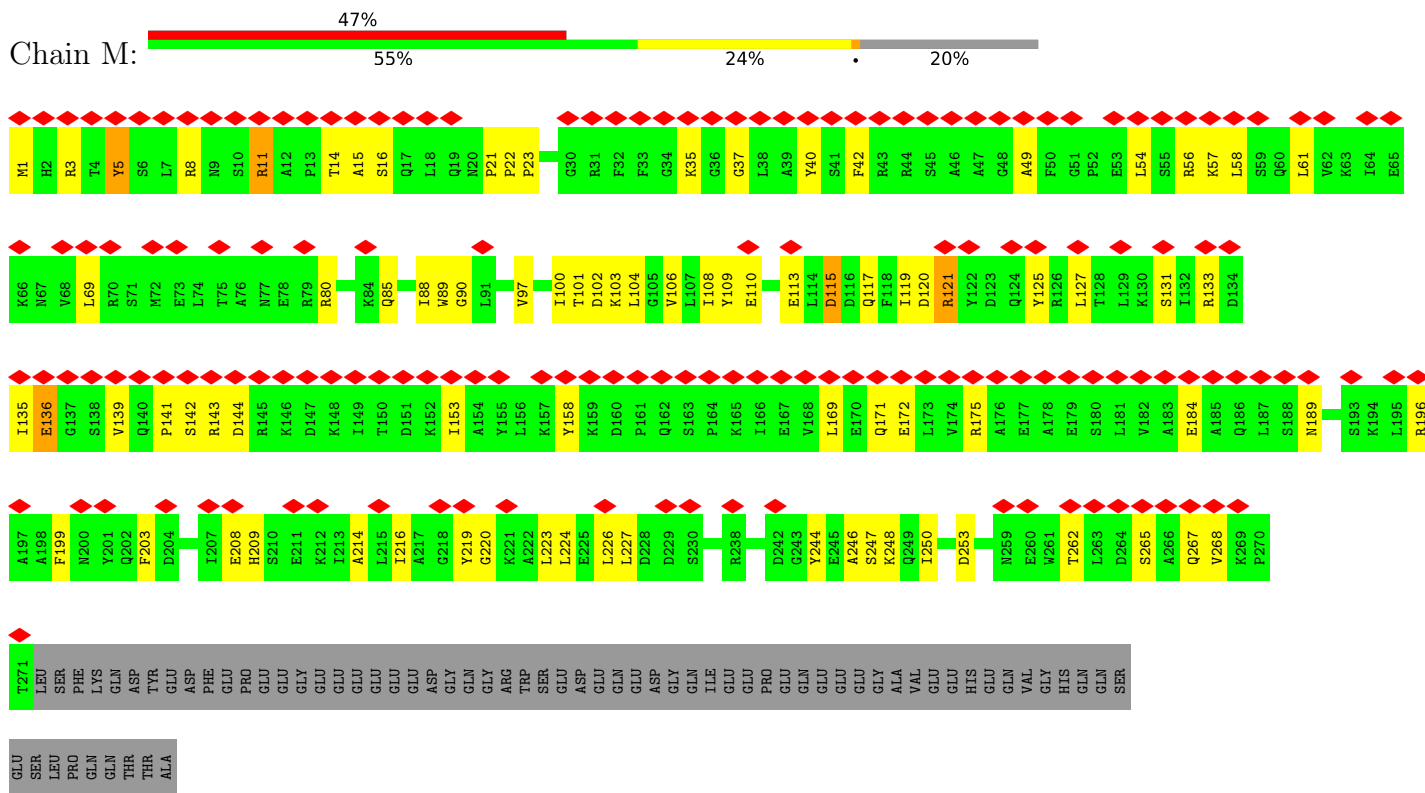
• Molecule 1: Spingolipid long chain base-responsive protein PIL1



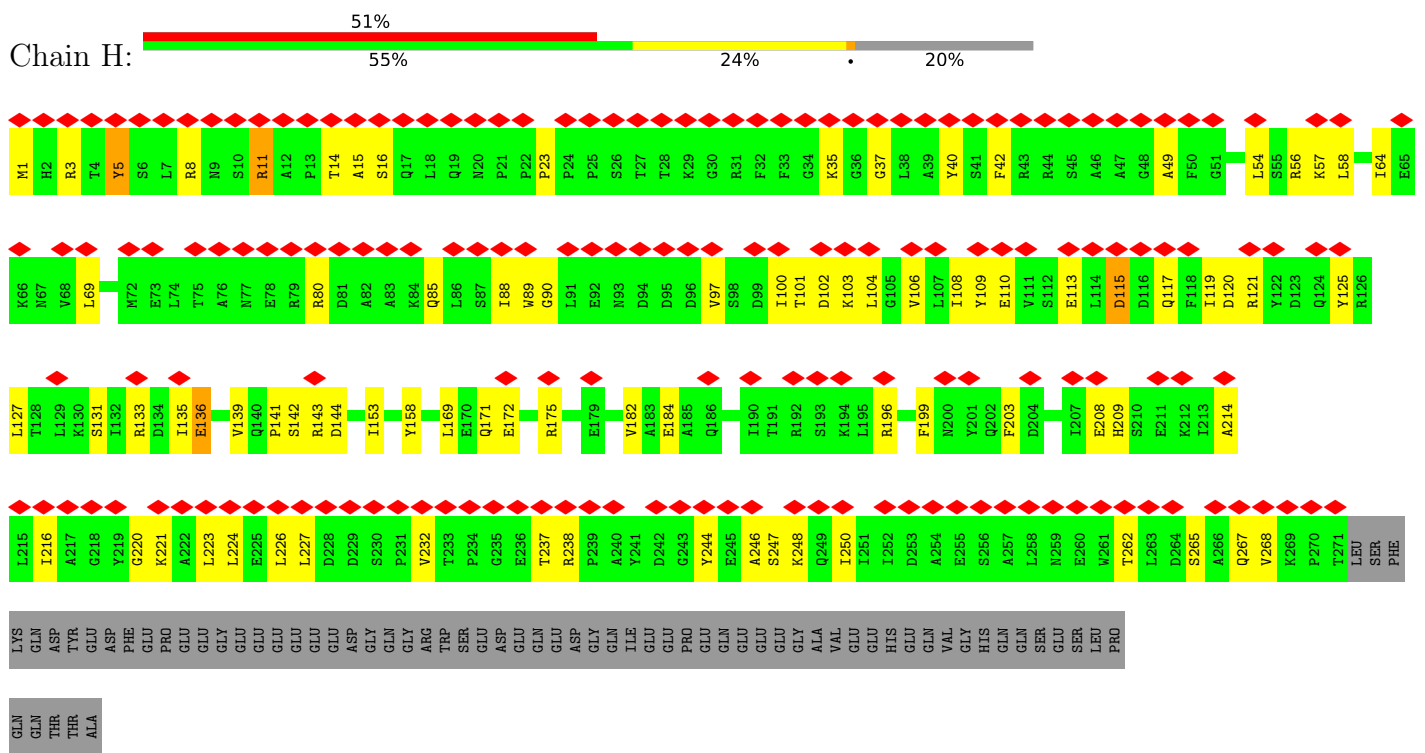
• Molecule 1: Spingolipid long chain base-responsive protein PIL1



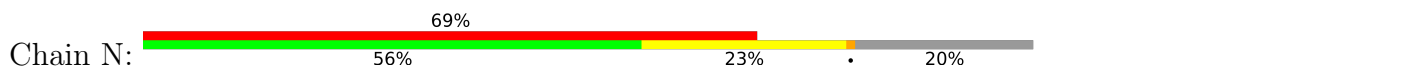
• Molecule 1: Spingolipid long chain base-responsive protein PIL1



• Molecule 1: Spingolipid long chain base-responsive protein PIL1



• Molecule 1: Spingolipid long chain base-responsive protein PIL1



M1	H2	R3	T4	Y5	L7	H8	N9	S10	R11	A12	P13	T14	A15	S16	Q17	L18	Q19	N20	P21	P22	P23	P24	P25	S26	T27	T28	K29	G30	R31	F32	F33	G34	K35	G36	G37	L38	A39	Y40	S41	F42	R43	R44	S45	A46	A47	O48	A49	F50	G51	P52	E53	L54	S55	R56	K57	L58	S59	O60
L61	V62	K63	I64	E65	K66	N67	V68	L69	R70	S71	M72	E73	L74	T75	A76	M77	E78	R79	B80	D81	A82	A83	Q84	Q85	L86	S87	I88	W89	G90	L91	E92	M93	V97	S98	D99	I100	T101	D102	K103	L104	G105	V106	L107	I108	Y109	E110	E113	L114	D115	D116	Q117	F118	I119	D120	R121	Y122	D123	
Q124	Y125	R126	L127	L128	K130	S131	I132	R133	D134	I135	E136	G137	S138	V139	Q140	P141	S142	R143	D144	R145	K146	D147	K148	I149	T150	D151	K152	I153	A154	Y155	L156	K157	Y158	K159	D160	P161	Q162	S163	P164	K165	I166	E167	V168	E170	Q171	E172	L173	V174	R175	A176	E177	A178	E179	S180	L181	V182	A183	
E184	A185	Q186	L187	S188	M189	T190	T191	R192	S193	K194	L195	R196	A197	A198	F199	N200	Y201	Q202	F203	D204	S205	I206	I207	E208	H209	S210	E211	K212	I213	A214	L215	I216	A217	G218	Y219	G220	K221	A222	L223	L224	E225	L226	L227	D228	D229	S230	T233	P234	G235	E236	T237	R238	P239	A240	Y241	D242	G243	Y244
E245	A246	S247	K248	Q249	I250	I251	I252	D253	S256	A257	L258	N259	E260	W261	T262	L263	D264	S265	A266	Q267	V268	K269	P270	T271	LEU	SER	PHE	LYS	GLN	ASP	TYR	GLU	GLY	GLU	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLY	GLN	GLY	GLY	TRP	SER	GLU	ASP	GLU	GLN	GLU	ASP			
GLY	GLN	ILE	GLU	PRO	GLN	GLU	GLU	GLY	ALA	VAL	GLU	HIS	GLU	GLN	VAL	GLY	HIS	GLN	GLN	SER	GLU	LEU	SER	PRO	GLN	THR	THR	ALA																														

## 4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63118	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)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	3.476	Depositor
Minimum map value	-2.576	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	339.712, 339.712, 339.712	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.327, 1.327, 1.327	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	0.27	0/2184	0.52	0/2952
1	B	0.27	0/2184	0.52	0/2952
1	C	0.27	0/2184	0.52	0/2952
1	D	0.27	0/2184	0.52	0/2952
1	E	0.27	0/2184	0.52	0/2952
1	F	0.27	0/2184	0.52	0/2952
1	G	0.27	0/2184	0.52	0/2952
1	H	0.27	0/2184	0.52	0/2952
1	I	0.27	0/2184	0.52	0/2952
1	J	0.27	0/2184	0.52	0/2952
1	K	0.27	0/2184	0.52	0/2952
1	L	0.27	0/2184	0.52	0/2952
1	M	0.27	0/2184	0.52	0/2952
1	N	0.27	0/2184	0.52	0/2952
All	All	0.27	0/30576	0.52	0/41328

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	2147	0	2150	79	0
1	B	2147	0	2150	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2147	0	2150	63	0
1	D	2147	0	2150	63	0
1	E	2147	0	2150	60	0
1	F	2147	0	2150	73	0
1	G	2147	0	2150	60	0
1	H	2147	0	2150	79	0
1	I	2147	0	2150	79	0
1	J	2147	0	2150	68	0
1	K	2147	0	2150	77	0
1	L	2147	0	2150	71	0
1	M	2147	0	2150	65	0
1	N	2147	0	2150	65	0
All	All	30058	0	30100	763	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 13.

The worst 5 of 763 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:88:ILE:HA	1:L:8:ARG:HH12	1.21	1.04
1:J:88:ILE:HA	1:K:8:ARG:HH12	1.36	0.89
1:M:8:ARG:NH1	1:N:91:LEU:HB2	1.91	0.85
1:I:183:ALA:HA	1:H:175:ARG:HH21	1.44	0.82
1:I:175:ARG:CZ	1:H:182:VAL:HG13	2.12	0.80

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	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	B	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	C	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	D	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	E	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	F	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	G	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	H	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	I	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	J	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	K	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	L	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
1	M	269/339 (79%)	263 (98%)	6 (2%)	0	100	100
1	N	269/339 (79%)	264 (98%)	5 (2%)	0	100	100
All	All	3766/4746 (79%)	3690 (98%)	76 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	B	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	C	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	D	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	E	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	F	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	G	234/294 (80%)	222 (95%)	12 (5%)	24	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	I	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	J	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	K	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	L	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	M	234/294 (80%)	222 (95%)	12 (5%)	24	55
1	N	234/294 (80%)	222 (95%)	12 (5%)	24	55
All	All	3276/4116 (80%)	3108 (95%)	168 (5%)	27	55

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	136	GLU
1	M	208	GLU
1	L	208	GLU
1	G	196	ARG
1	H	125	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	67	ASN
1	H	117	GLN
1	F	60	GLN
1	H	85	GLN
1	N	117	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.

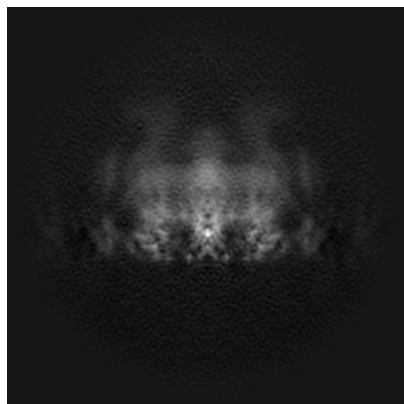
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18311. These allow visual inspection of the internal detail of the map and identification of artifacts.

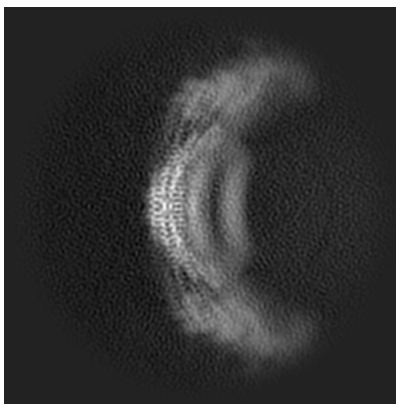
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

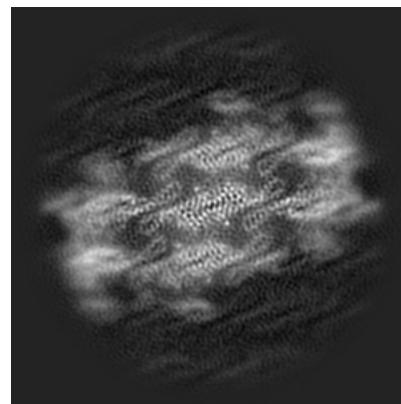
#### 6.1.1 Primary map



X

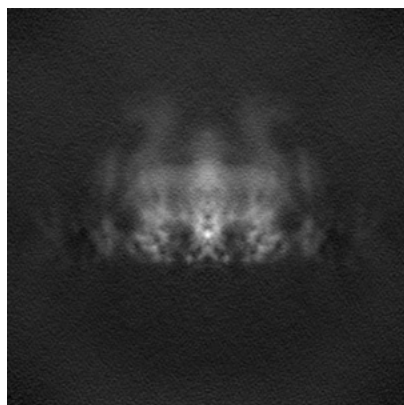


Y

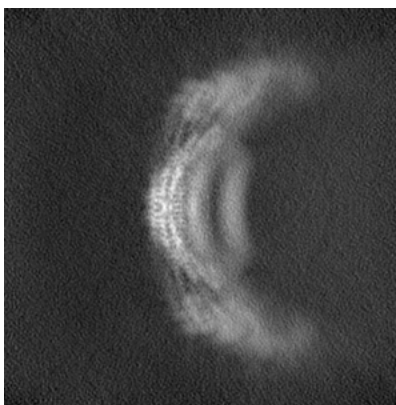


Z

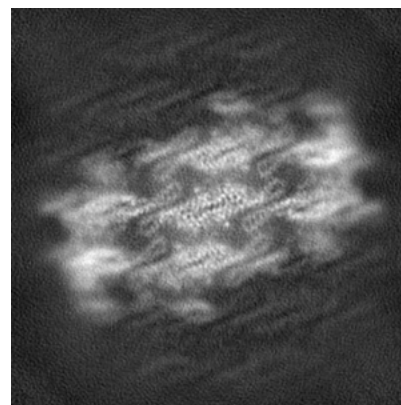
#### 6.1.2 Raw map



X



Y

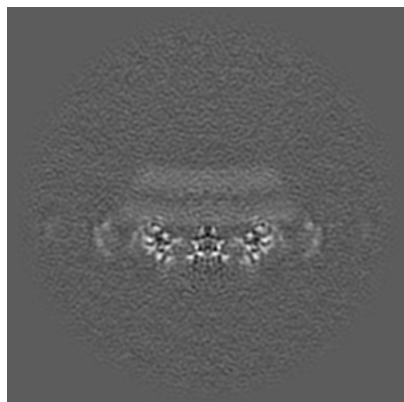


Z

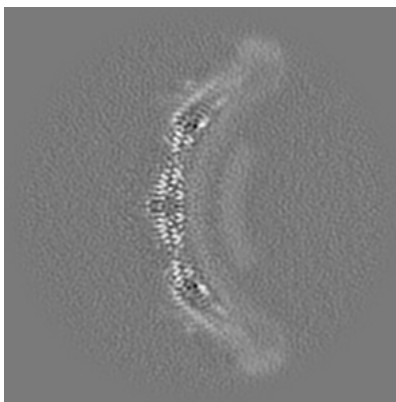
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

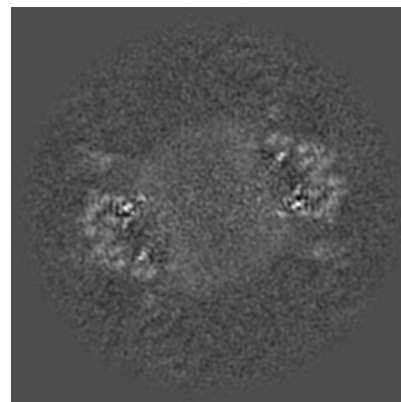
### 6.2.1 Primary map



X Index: 128

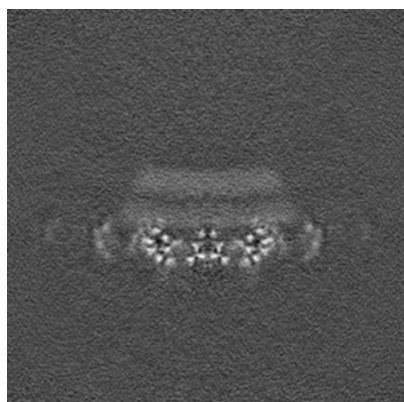


Y Index: 128

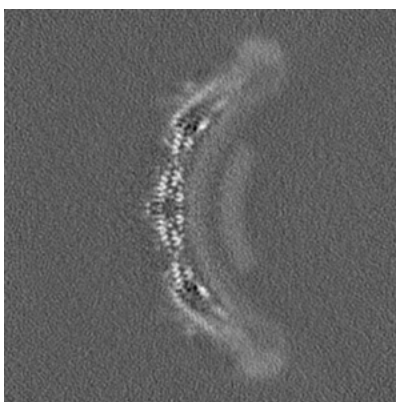


Z Index: 128

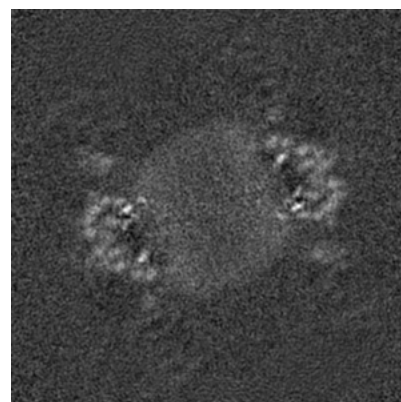
### 6.2.2 Raw map



X Index: 128



Y Index: 128

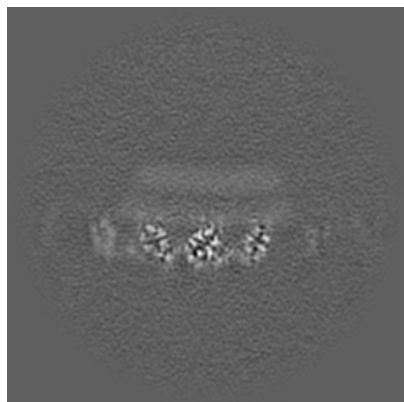


Z Index: 128

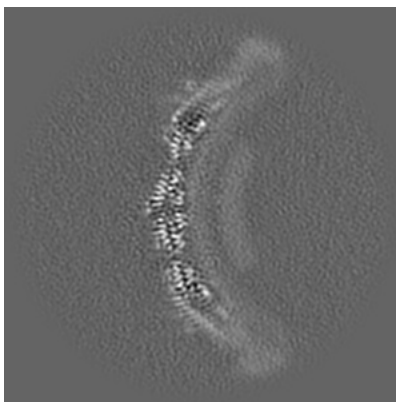
The images above show central slices of the map in three orthogonal directions.

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

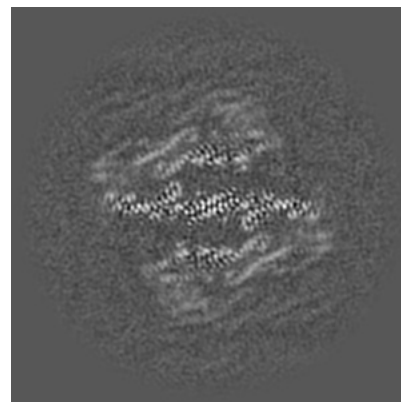
### 6.3.1 Primary map



X Index: 123

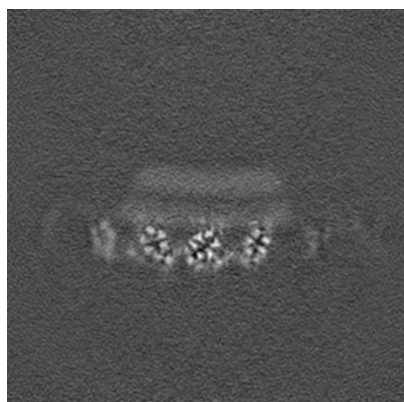


Y Index: 127

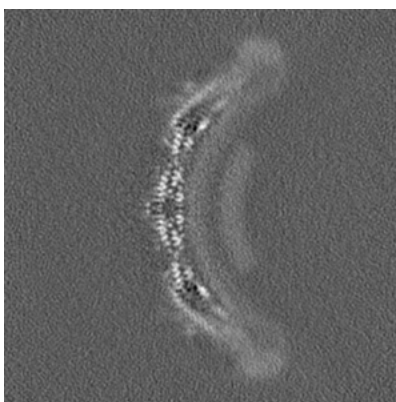


Z Index: 111

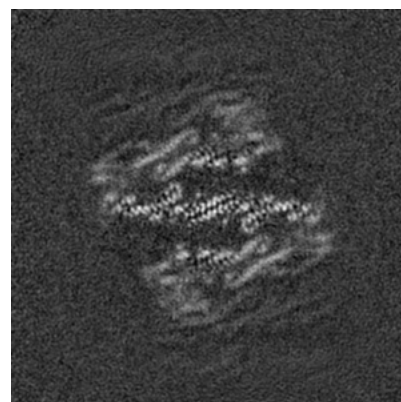
### 6.3.2 Raw map



X Index: 123



Y Index: 128

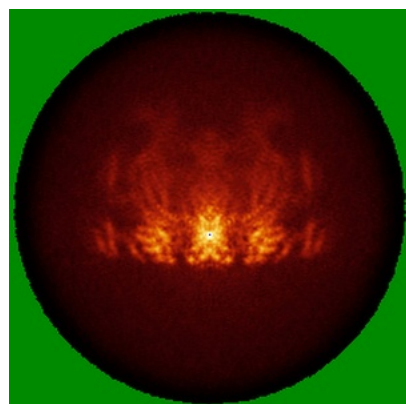


Z Index: 111

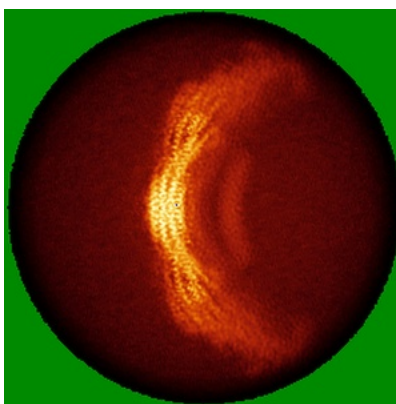
The images above show the largest variance slices of the map in three orthogonal directions.

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

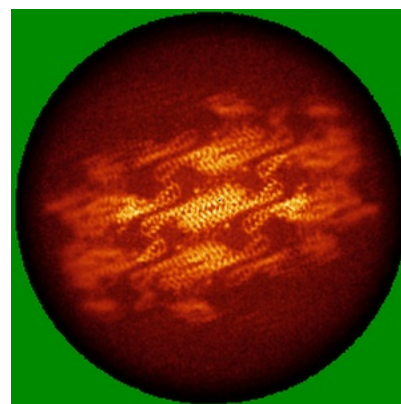
### 6.4.1 Primary map



X

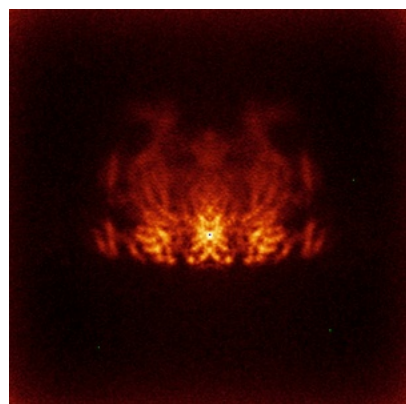


Y

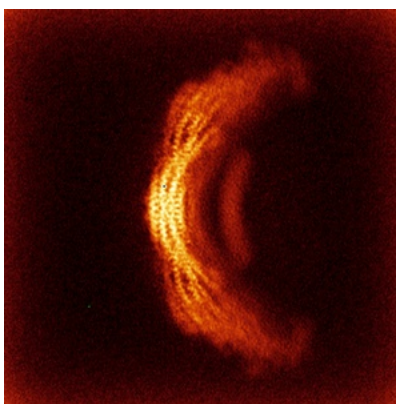


Z

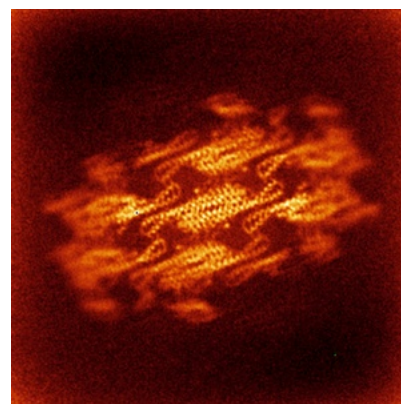
### 6.4.2 Raw map



X



Y

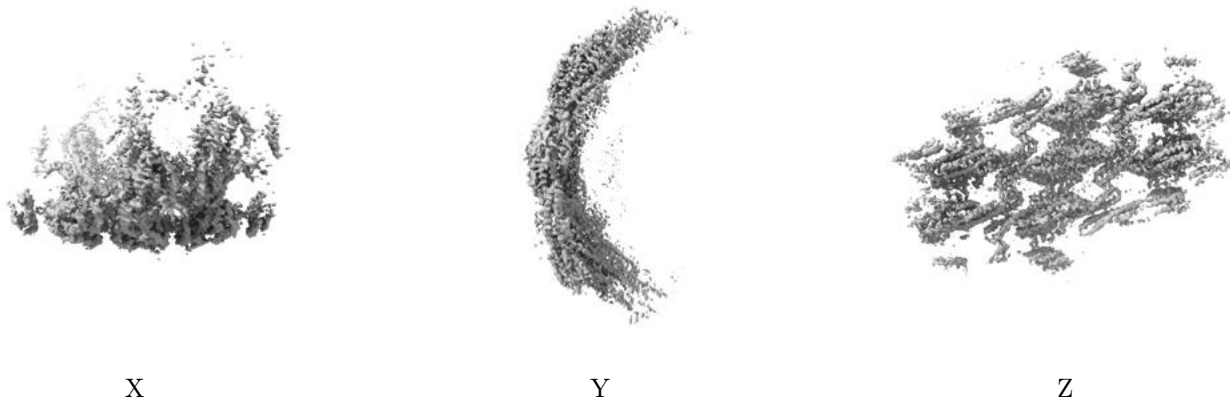


Z

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.

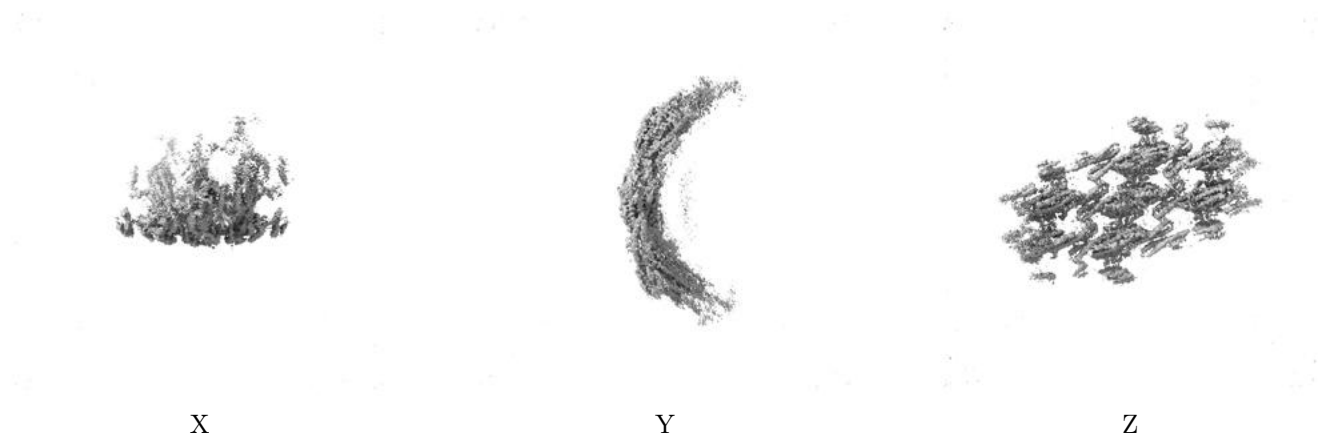
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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.

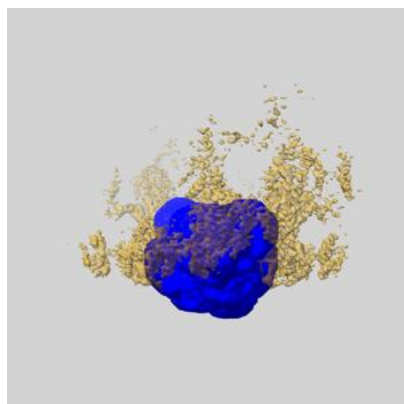
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

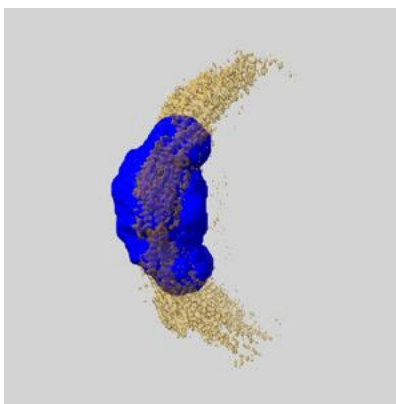
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

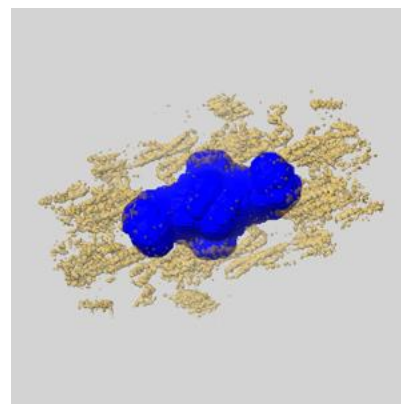
### 6.6.1 emd\_18311\_msk\_1.map [i](#)



X



Y

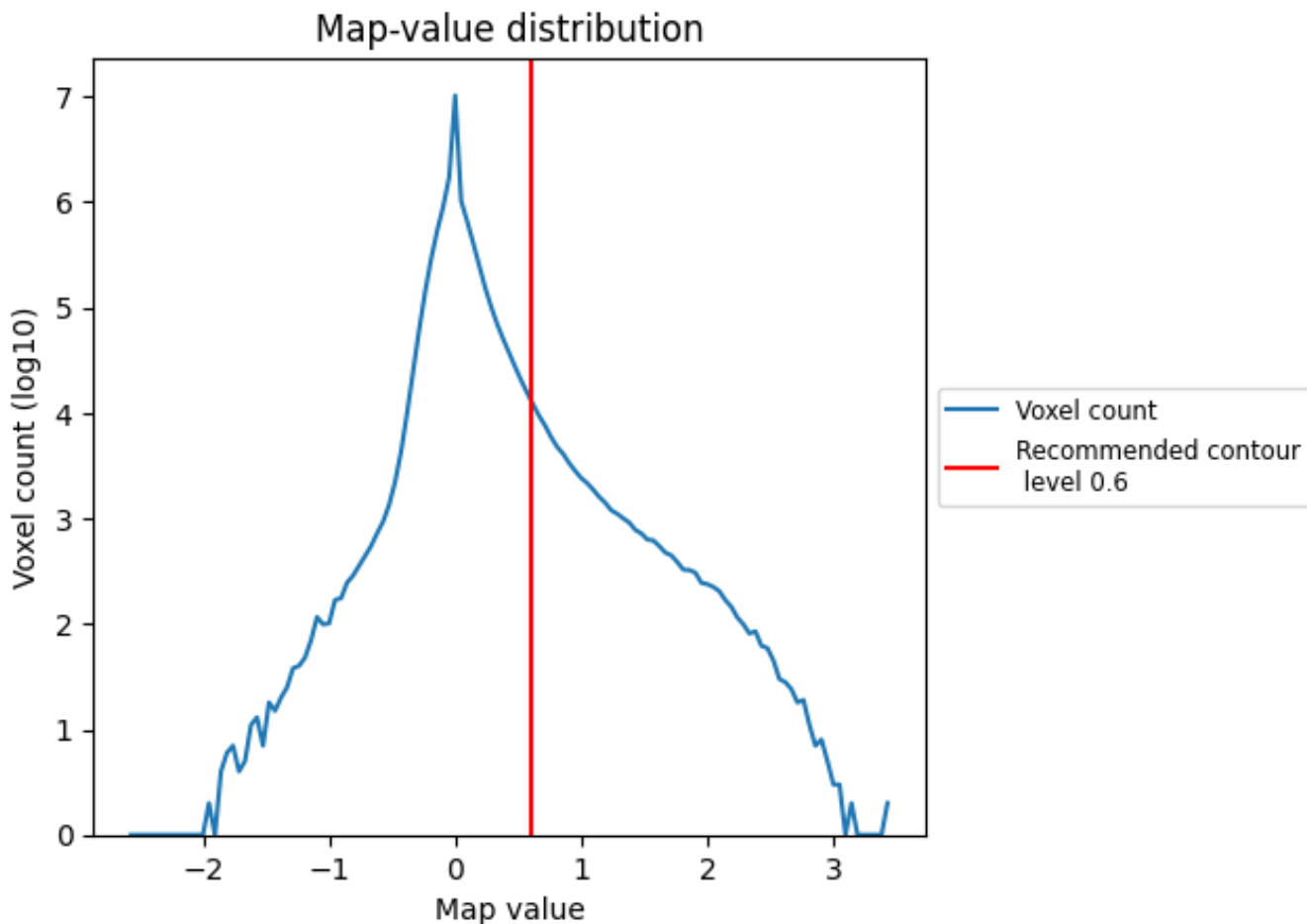


Z

## 7 Map analysis [i](#)

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

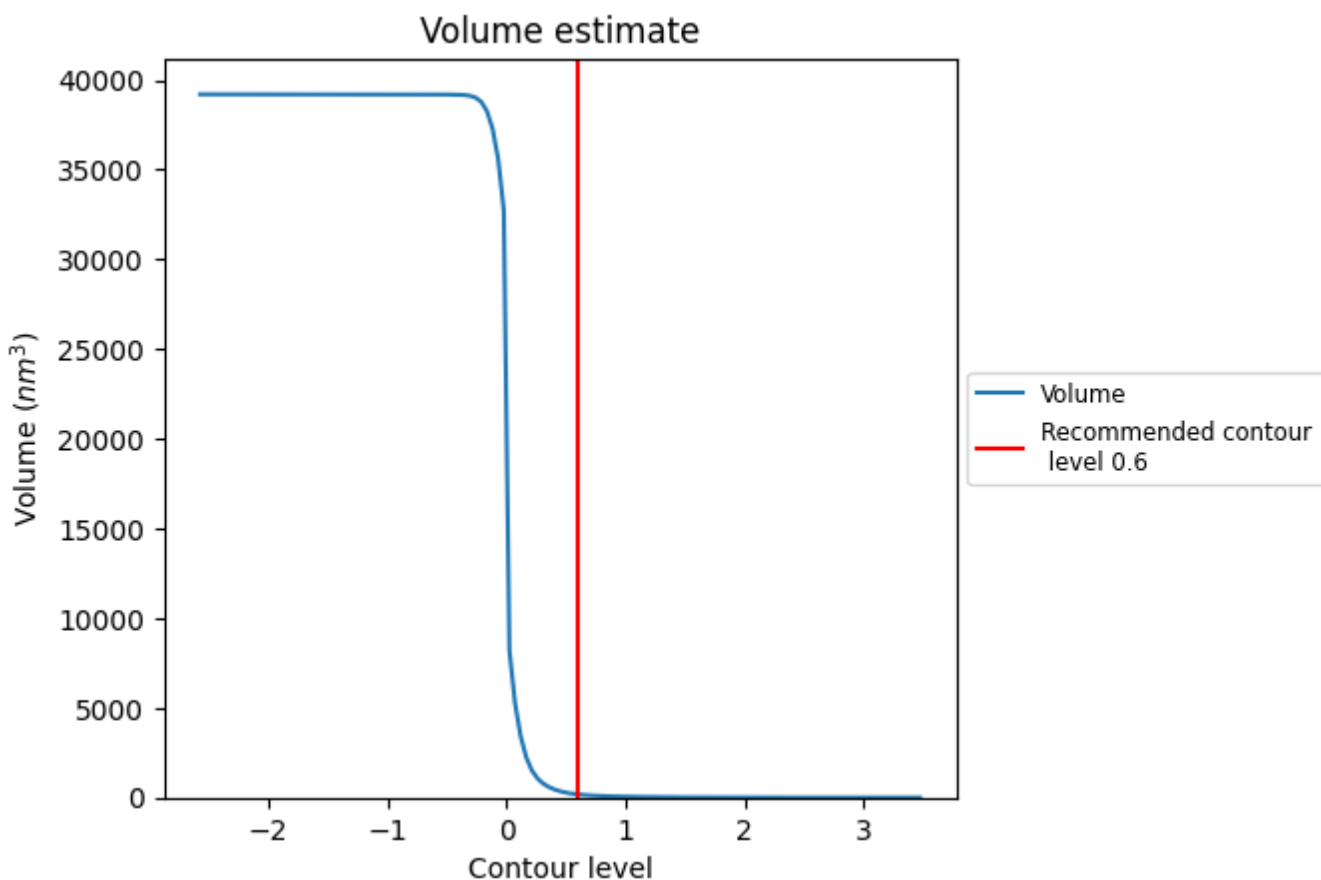
### 7.1 Map-value distribution [i](#)



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.



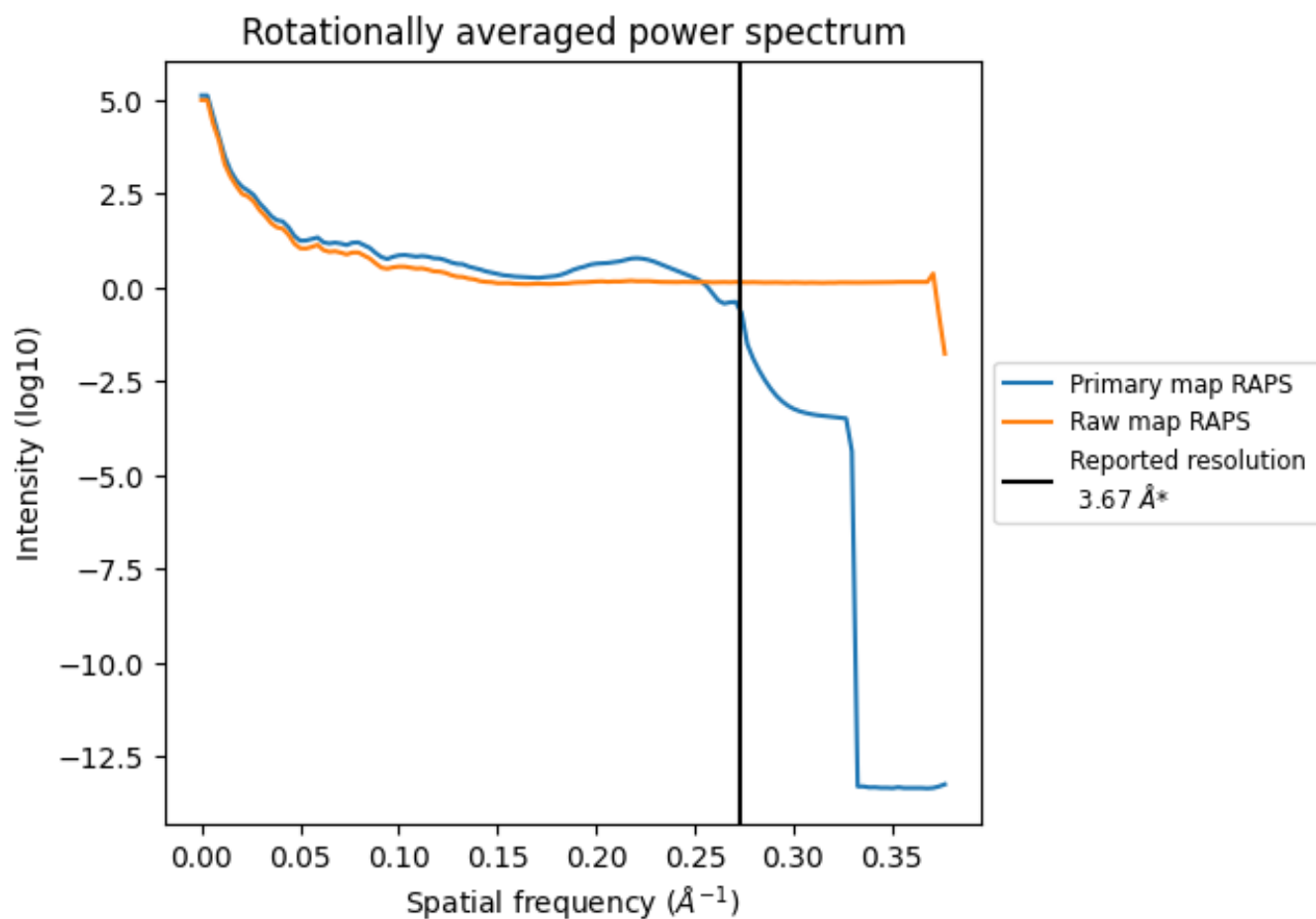
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 178 nm<sup>3</sup>; this corresponds to an approximate mass of 161 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](#)

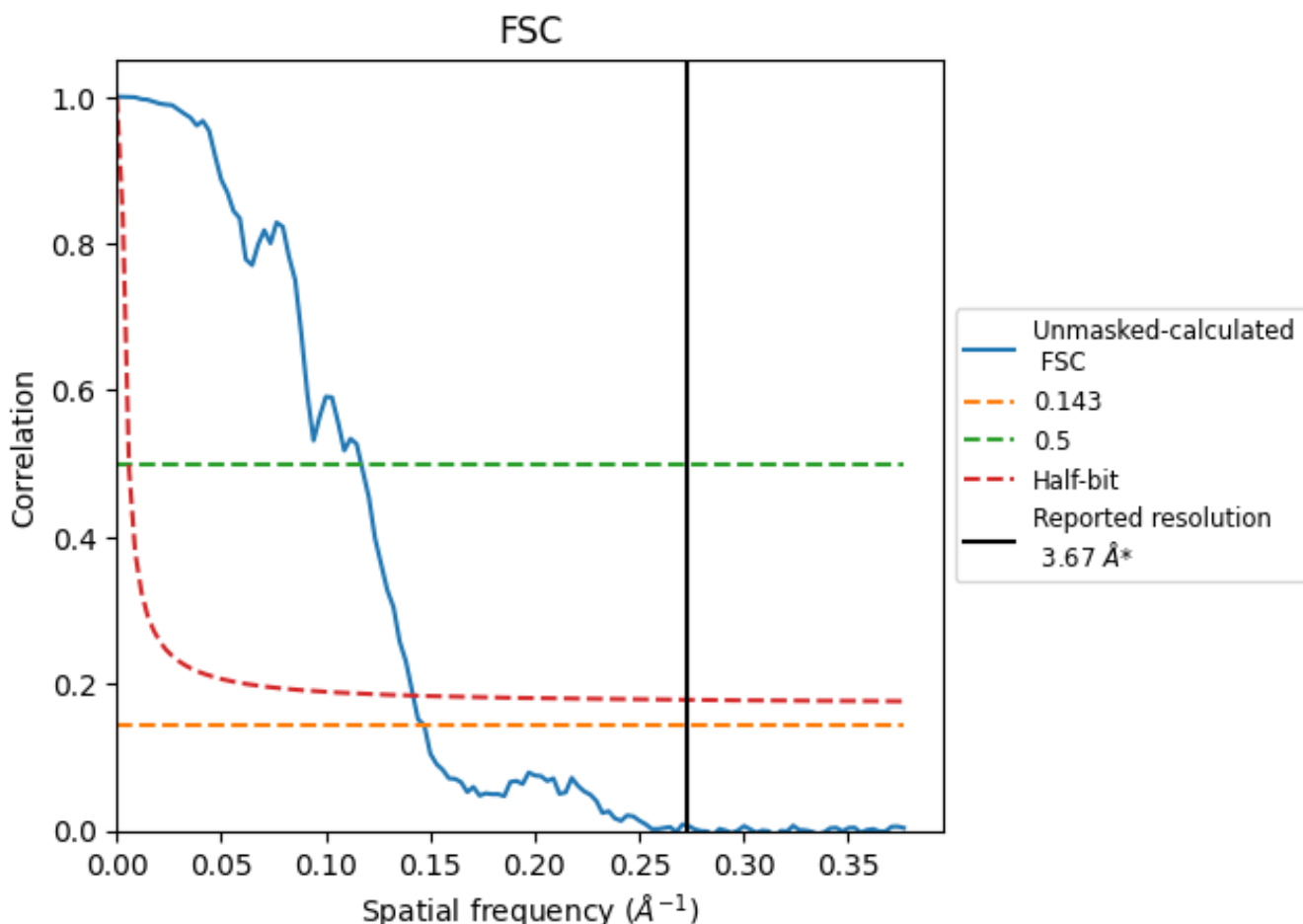


\*Reported resolution corresponds to spatial frequency of 0.272 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.272  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

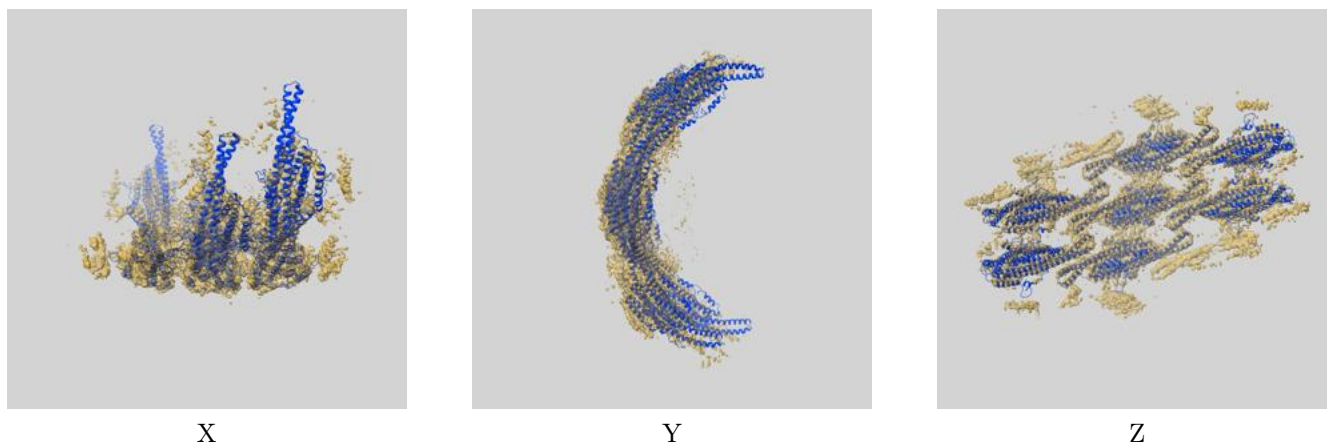
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.67	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.79	8.55	7.05

\*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 6.79 differs from the reported value 3.67 by more than 10 %

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

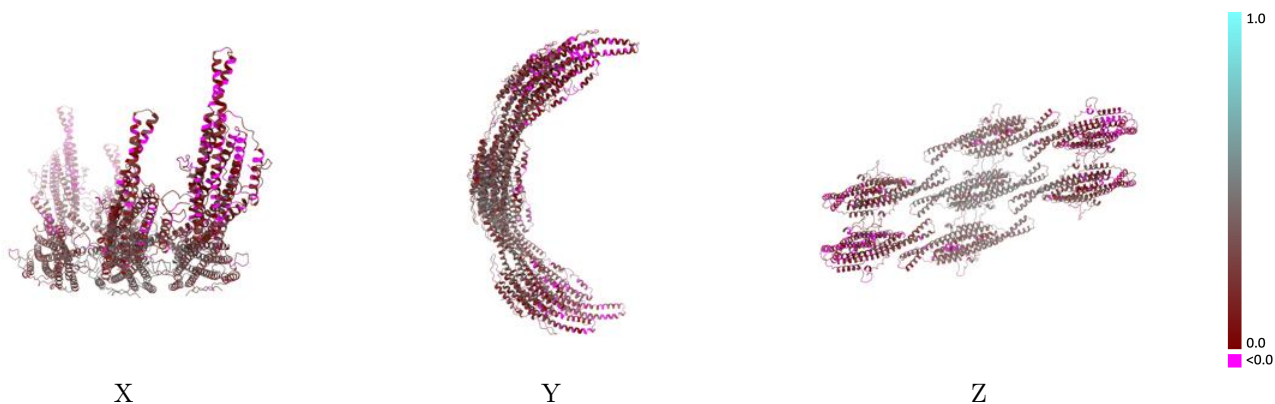
This section contains information regarding the fit between EMDB map EMD-18311 and PDB model 8QBE. Per-residue inclusion information can be found in section 3 on page 5.

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



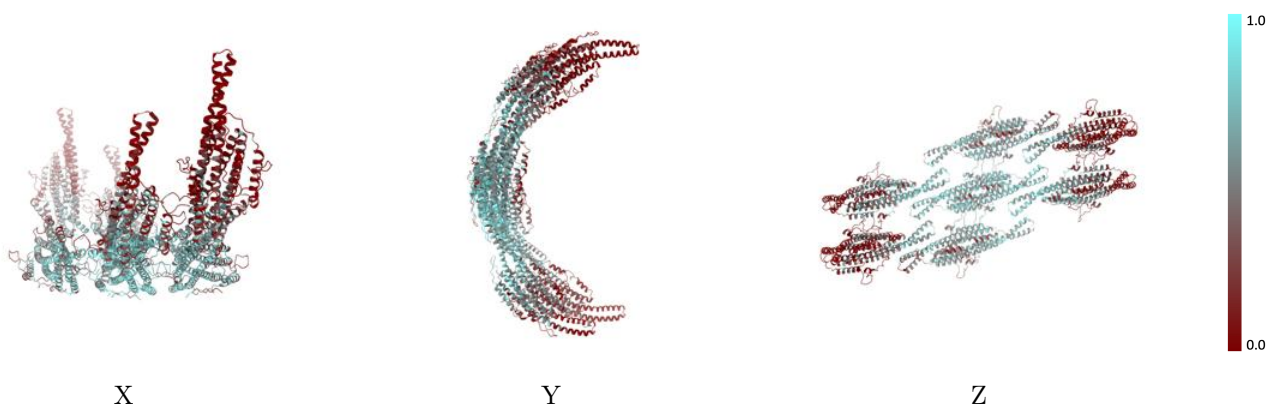
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



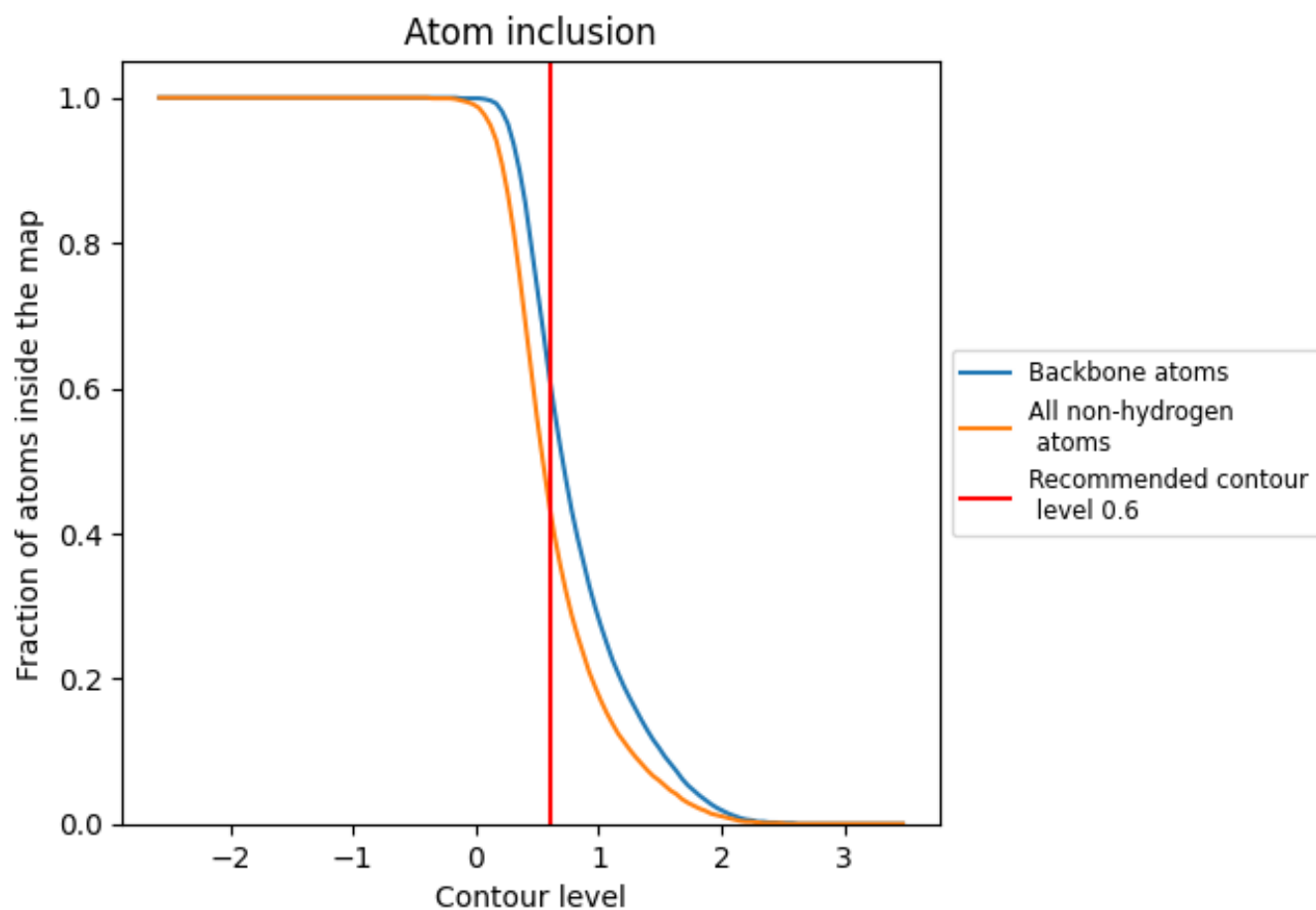
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 44% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4370	 0.2280
A	 0.7200	 0.3950
B	 0.7090	 0.3800
C	 0.5650	 0.2870
D	 0.3580	 0.1970
E	 0.1640	 0.1070
F	 0.5180	 0.2690
G	 0.4680	 0.2340
H	 0.2890	 0.1340
I	 0.5120	 0.2550
J	 0.4690	 0.2320
K	 0.2780	 0.1460
L	 0.5770	 0.2890
M	 0.3440	 0.1700
N	 0.1480	 0.0980

