



wwPDB EM Validation Summary Report ⓘ

May 4, 2025 – 07:19 PM EDT

PDB ID : 6O81 / pdb_00006o81
EMDB ID : EMD-0649
Title : Electron cryo-microscopy of the eukaryotic translation initiation factor 2B bound to translation initiation factor 2 from Homo sapiens
Authors : Nguyen, H.; Kenner, L.; Frost, A.
Deposited on : 2019-03-08
Resolution : 3.21 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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

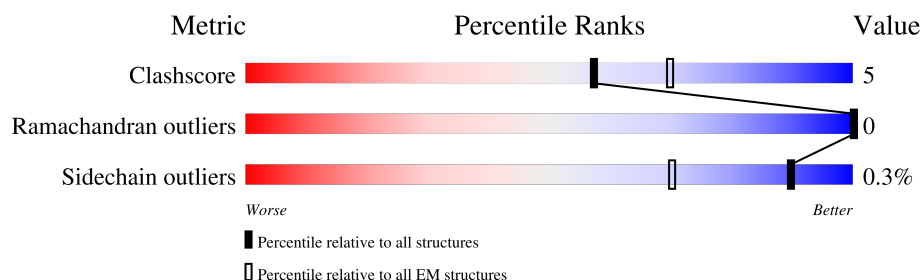
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.21 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	721	<div> <div>22%</div> <div>74%</div> <div>8%</div> <div>18%</div> </div>
1	B	721	<div> <div>22%</div> <div>74%</div> <div>7%</div> <div>18%</div> </div>
2	C	368	<div> <div>6%</div> <div>69%</div> <div>17%</div> <div>14%</div> </div>
2	D	368	<div> <div>5%</div> <div>69%</div> <div>17%</div> <div>14%</div> </div>
3	E	523	<div> <div>58%</div> <div>10%</div> <div>32%</div> </div>
3	F	523	<div> <div>54%</div> <div>14%</div> <div>32%</div> </div>
4	G	305	<div> <div>81%</div> <div>12%</div> <div>7%</div> </div>
4	H	305	<div> <div>81%</div> <div>12%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
5	I	452	
5	J	452	
6	L	315	
6	M	315	
7	S	472	
7	T	472	
8	d	14	
8	e	14	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 33693 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 Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	590	Total	C	N	O	S	0	0
			4055	2541	735	764	15		
1	B	590	Total	C	N	O	S	0	0
			4055	2541	735	764	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	563	LYS	ARG	conflict	UNP Q13144
A	678	GLY	GLU	conflict	UNP Q13144
B	563	LYS	ARG	conflict	UNP Q13144
B	678	GLY	GLU	conflict	UNP Q13144

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	317	Total	C	N	O	S	0	0
			2462	1559	434	454	15		
2	D	318	Total	C	N	O	S	0	0
			2472	1565	437	455	15		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	MET	-	initiating methionine	UNP P49770
C	-15	HIS	-	expression tag	UNP P49770
C	-14	HIS	-	expression tag	UNP P49770
C	-13	HIS	-	expression tag	UNP P49770
C	-12	HIS	-	expression tag	UNP P49770
C	-11	HIS	-	expression tag	UNP P49770
C	-10	HIS	-	expression tag	UNP P49770
C	-9	GLY	-	expression tag	UNP P49770
C	-8	GLY	-	expression tag	UNP P49770

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	GLY	-	expression tag	UNP P49770
C	-6	SER	-	expression tag	UNP P49770
C	-5	GLU	-	expression tag	UNP P49770
C	-4	ASN	-	expression tag	UNP P49770
C	-3	LEU	-	expression tag	UNP P49770
C	-2	TYR	-	expression tag	UNP P49770
C	-1	PHE	-	expression tag	UNP P49770
C	0	GLN	-	expression tag	UNP P49770
C	1	SER	-	expression tag	UNP P49770
D	-16	MET	-	initiating methionine	UNP P49770
D	-15	HIS	-	expression tag	UNP P49770
D	-14	HIS	-	expression tag	UNP P49770
D	-13	HIS	-	expression tag	UNP P49770
D	-12	HIS	-	expression tag	UNP P49770
D	-11	HIS	-	expression tag	UNP P49770
D	-10	HIS	-	expression tag	UNP P49770
D	-9	GLY	-	expression tag	UNP P49770
D	-8	GLY	-	expression tag	UNP P49770
D	-7	GLY	-	expression tag	UNP P49770
D	-6	SER	-	expression tag	UNP P49770
D	-5	GLU	-	expression tag	UNP P49770
D	-4	ASN	-	expression tag	UNP P49770
D	-3	LEU	-	expression tag	UNP P49770
D	-2	TYR	-	expression tag	UNP P49770
D	-1	PHE	-	expression tag	UNP P49770
D	0	GLN	-	expression tag	UNP P49770
D	1	SER	-	expression tag	UNP P49770

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	357	Total	C	N	O	S	0	0
			2775	1754	495	512	14		
3	F	357	Total	C	N	O	S	0	0
			2776	1755	495	512	14		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	285	Total	C	N	O	S	0	0
			2051	1324	344	375	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	285	Total	C	N	O	S	0	0
			2051	1324	344	375	8		

- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	240	Total	C	N	O	S	0	0
			1634	1054	279	293	8		
5	J	240	Total	C	N	O	S	0	0
			1634	1054	279	293	8		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	275	Total	C	N	O	S	0	0
			1651	1047	307	294	3		
6	M	275	Total	C	N	O	S	0	0
			1651	1047	307	294	3		

- Molecule 7 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	410	Total	C	N	O	S	0	0
			2113	1266	435	411	1		
7	T	410	Total	C	N	O	S	0	0
			2113	1266	435	411	1		

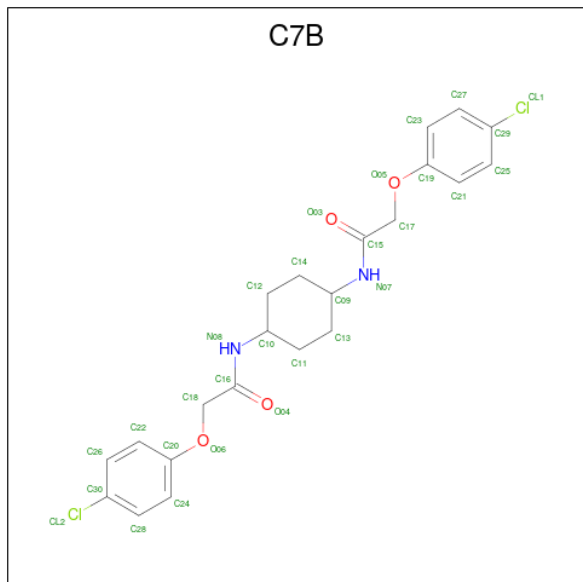
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	304	ALA	ASP	conflict	UNP P41091
S	314	LYS	ILE	conflict	UNP P41091
T	304	ALA	ASP	conflict	UNP P41091
T	314	LYS	ILE	conflict	UNP P41091

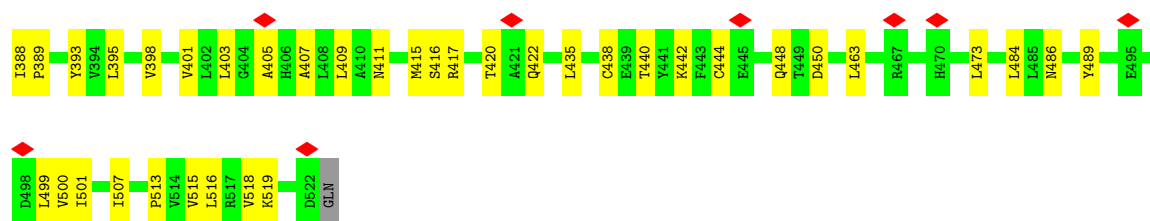
- Molecule 8 is a protein called Translation initiation factor eiF2 beta-subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	d	14	Total	C	N	O	0	0
			70	42	14	14		
8	e	14	Total	C	N	O	0	0
			70	42	14	14		

- Molecule 9 is 2-(4-chloranylphenoxy)- {N}-[4-[2-(4-chloranylphenoxy)ethanoylamino]cyclohexyl]ethanamide (CCD ID: C7B) (formula: $C_{22}H_{24}Cl_2N_2O_4$).

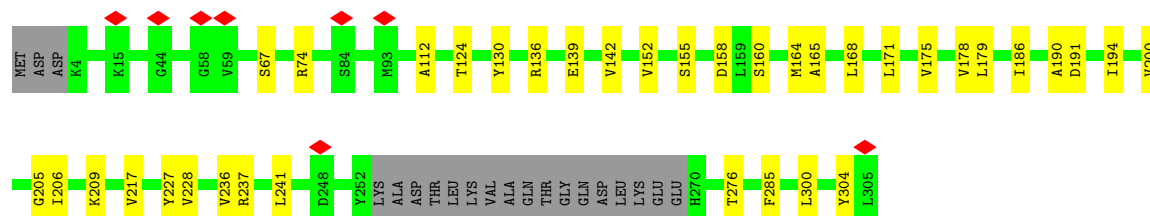


Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
9	C	1	60	44	4	4	8	1



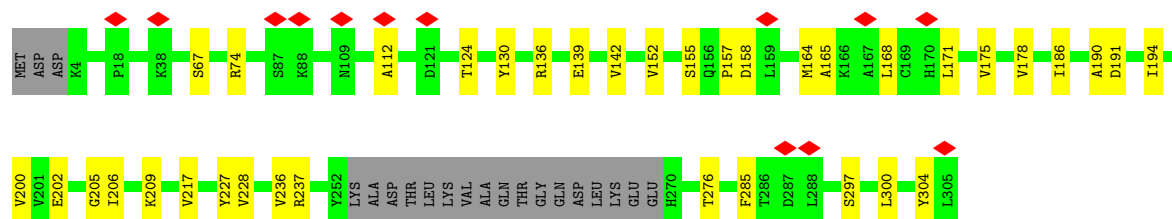
- Molecule 4: Translation initiation factor eIF-2B subunit alpha

Chain G: 81% 12% 7%



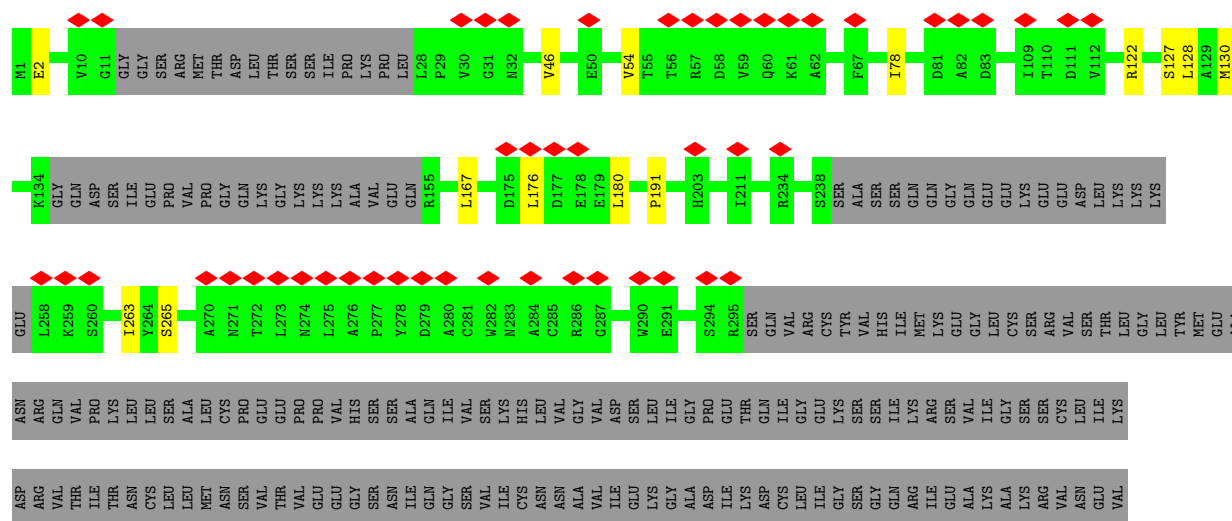
- Molecule 4: Translation initiation factor eIF-2B subunit alpha

Chain H: 81% 12% 7%



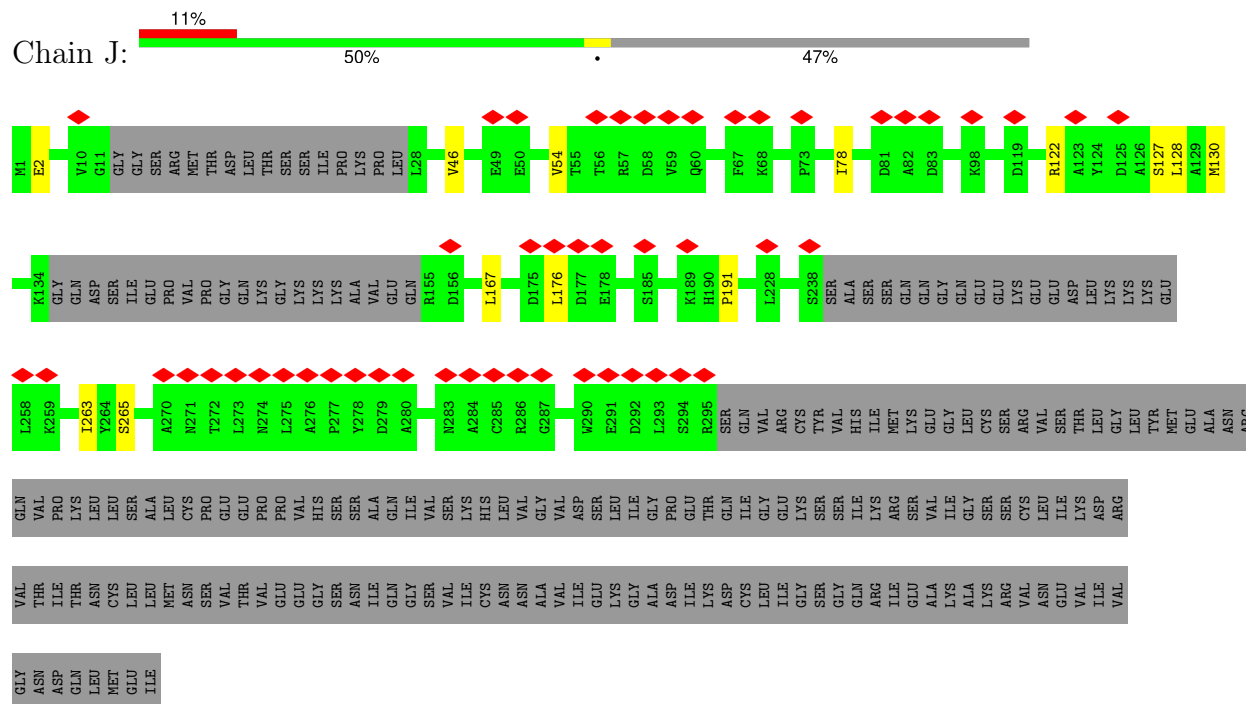
- Molecule 5: Translation initiation factor eIF-2B subunit gamma

Chain I: 11% 50% 47%

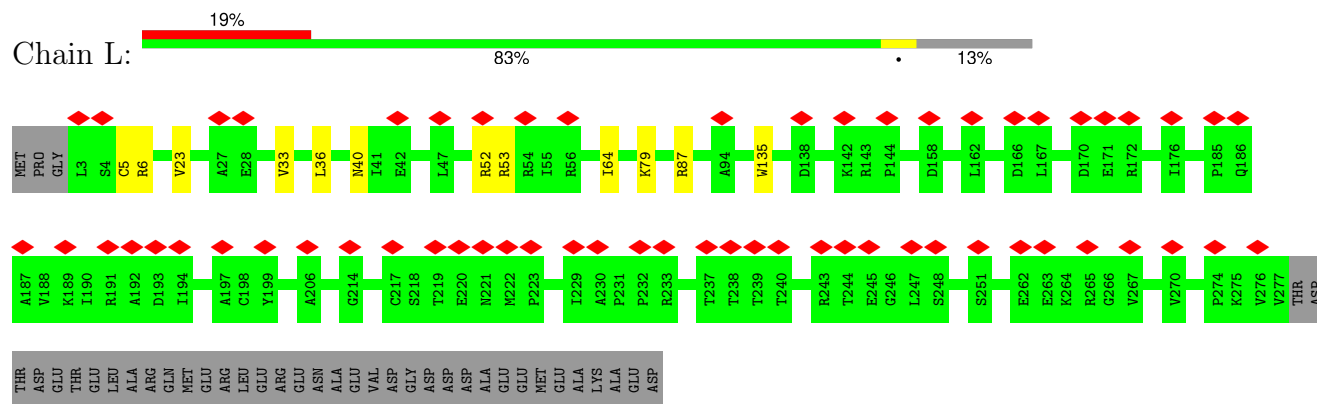


ILE
VAL
GLY
ASN
ASP
GLN
LEU
MET
GLU
ILE

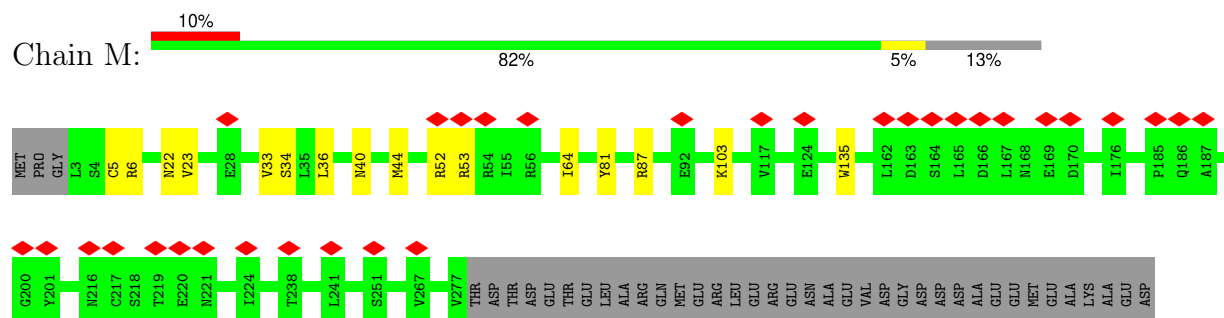
• Molecule 5: Translation initiation factor eIF-2B subunit gamma



• Molecule 6: Eukaryotic translation initiation factor 2 subunit 1



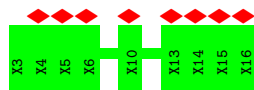
• Molecule 6: Eukaryotic translation initiation factor 2 subunit 1



• Molecule 7: Eukaryotic translation initiation factor 2 subunit 3

- Molecule 8: Translation initiation factor eiF2 beta-subunit

Chain e:  57% 100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11640	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.908	Depositor
Minimum map value	-0.822	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.327	Depositor
Map size (\AA)	411.0, 411.0, 411.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.822, 0.822, 0.822	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C7B

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	0.15	0/4123	0.43	0/5650
1	B	0.15	0/4123	0.43	0/5650
2	C	0.18	0/2508	0.46	0/3393
2	D	0.17	0/2519	0.42	0/3408
3	E	0.17	0/2827	0.42	0/3841
3	F	0.18	0/2828	0.45	0/3843
4	G	0.17	0/2087	0.44	0/2842
4	H	0.17	0/2087	0.44	0/2842
5	I	0.13	0/1656	0.36	0/2260
5	J	0.13	0/1656	0.36	0/2260
6	L	0.20	0/1670	0.45	2/2282 (0.1%)
6	M	0.20	0/1670	0.45	2/2282 (0.1%)
7	S	0.11	0/2119	0.34	0/2925
7	T	0.11	0/2119	0.34	0/2925
All	All	0.16	0/33992	0.42	4/46403 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	135	TRP	CD2-CE3-CZ3	8.37	129.49	118.60
6	M	135	TRP	CD2-CE3-CZ3	8.32	129.41	118.60
6	M	135	TRP	CE2-CD2-CE3	6.03	124.83	118.80
6	L	135	TRP	CE2-CD2-CE3	5.96	124.76	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4055	0	3505	34	0
1	B	4055	0	3505	33	0
2	C	2462	0	2479	43	0
2	D	2472	0	2486	42	0
3	E	2775	0	2835	33	0
3	F	2776	0	2836	48	0
4	G	2051	0	1951	24	0
4	H	2051	0	1951	24	0
5	I	1634	0	1423	8	0
5	J	1634	0	1423	7	0
6	L	1651	0	1123	8	0
6	M	1651	0	1123	11	0
7	S	2113	0	1064	3	0
7	T	2113	0	1064	5	0
8	d	70	0	16	0	0
8	e	70	0	16	0	0
9	C	60	0	0	0	0
All	All	33693	0	28800	286	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 5.

The worst 5 of 286 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)
2:D:231:LYS:HG3	2:D:264:PRO:HG2	1.76	0.68
4:G:206:ILE:HG21	4:G:228:VAL:HG11	1.82	0.61
4:H:206:ILE:HG21	4:H:228:VAL:HG11	1.82	0.60
2:D:135:GLU:OE2	6:M:53:ARG:NH1	2.36	0.59
3:E:407:ALA:HB3	3:E:415:MET:HB3	1.85	0.59

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	584/721 (81%)	550 (94%)	34 (6%)	0	100	100
1	B	584/721 (81%)	550 (94%)	34 (6%)	0	100	100
2	C	313/368 (85%)	302 (96%)	11 (4%)	0	100	100
2	D	314/368 (85%)	305 (97%)	9 (3%)	0	100	100
3	E	355/523 (68%)	345 (97%)	10 (3%)	0	100	100
3	F	355/523 (68%)	341 (96%)	14 (4%)	0	100	100
4	G	281/305 (92%)	268 (95%)	13 (5%)	0	100	100
4	H	281/305 (92%)	268 (95%)	13 (5%)	0	100	100
5	I	232/452 (51%)	225 (97%)	7 (3%)	0	100	100
5	J	232/452 (51%)	225 (97%)	7 (3%)	0	100	100
6	L	273/315 (87%)	261 (96%)	12 (4%)	0	100	100
6	M	273/315 (87%)	261 (96%)	12 (4%)	0	100	100
7	S	402/472 (85%)	380 (94%)	22 (6%)	0	100	100
7	T	402/472 (85%)	379 (94%)	23 (6%)	0	100	100
All	All	4881/6312 (77%)	4660 (96%)	221 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/625 (56%)	347 (100%)	1 (0%)	91	95
1	B	348/625 (56%)	347 (100%)	1 (0%)	91	95
2	C	265/312 (85%)	265 (100%)	0	100	100
2	D	266/312 (85%)	265 (100%)	1 (0%)	89	93
3	E	312/444 (70%)	312 (100%)	0	100	100
3	F	312/444 (70%)	312 (100%)	0	100	100
4	G	193/260 (74%)	193 (100%)	0	100	100
4	H	193/260 (74%)	193 (100%)	0	100	100
5	I	128/398 (32%)	125 (98%)	3 (2%)	45	70
5	J	128/398 (32%)	125 (98%)	3 (2%)	45	70
6	L	75/280 (27%)	75 (100%)	0	100	100
6	M	75/280 (27%)	75 (100%)	0	100	100
7	S	16/396 (4%)	16 (100%)	0	100	100
7	T	16/396 (4%)	16 (100%)	0	100	100
All	All	2675/5430 (49%)	2666 (100%)	9 (0%)	90	95

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	J	127	SER
5	J	176	LEU
5	I	46	VAL
5	I	127	SER
5	I	176	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	216	GLN
4	G	156	GLN
3	F	254	ASN
3	F	431	ASN
4	H	156	GLN

5.3.3 RNA ⓘ

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	C7B	C	401[A]	-	32,32,32	1.73	4 (12%)	42,42,42	0.93	2 (4%)
9	C7B	C	401[B]	-	32,32,32	1.72	4 (12%)	42,42,42	0.92	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	C7B	C	401[A]	-	-	6/18/28/28	0/3/3/3
9	C7B	C	401[B]	-	-	5/18/28/28	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	401[A]	C7B	C16-N08	6.04	1.46	1.34
9	C	401[B]	C7B	C16-N08	5.99	1.46	1.34
9	C	401[A]	C7B	C15-N07	5.58	1.45	1.34
9	C	401[B]	C7B	C15-N07	5.53	1.45	1.34
9	C	401[A]	C7B	O03-C15	-2.23	1.18	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	401[B]	C7B	C10-N08-C16	2.69	126.86	122.88
9	C	401[A]	C7B	C10-N08-C16	2.69	126.86	122.88
9	C	401[A]	C7B	C17-C15-N07	2.03	119.91	116.41

There are no chirality outliers.

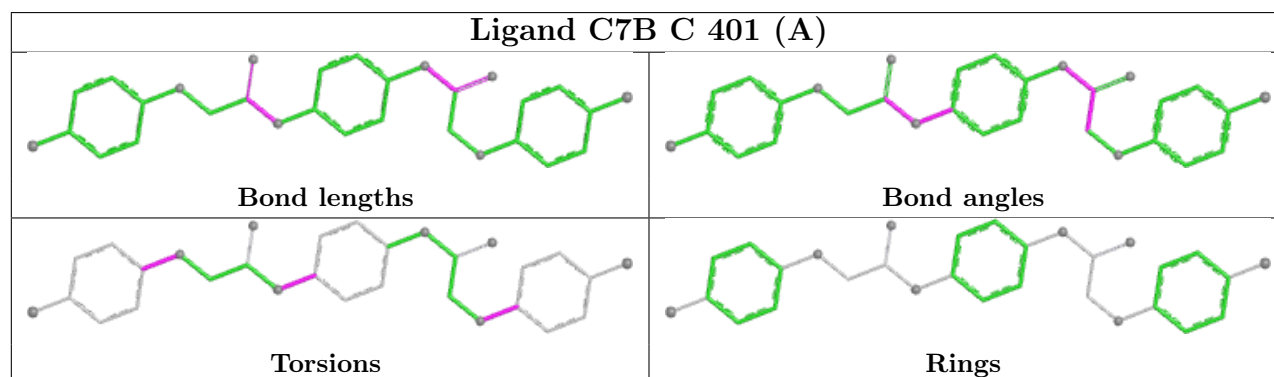
5 of 11 torsion outliers are listed below:

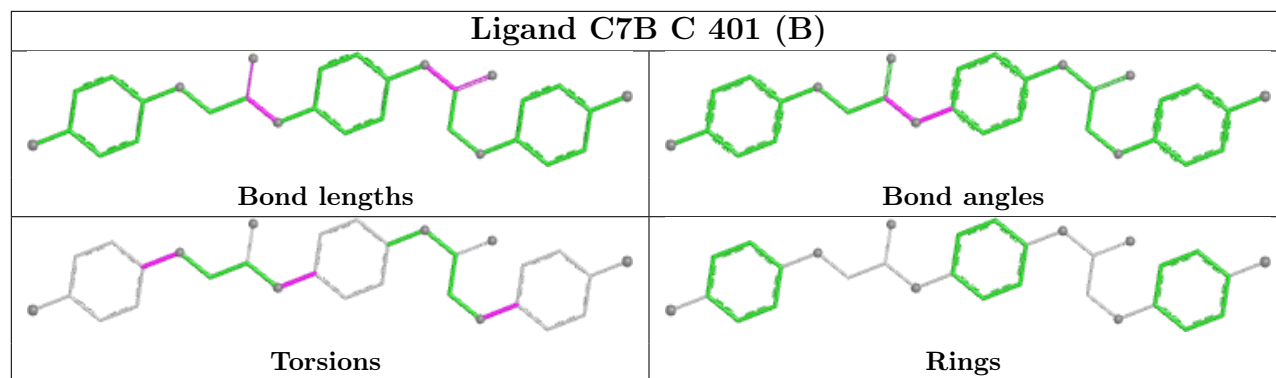
Mol	Chain	Res	Type	Atoms
9	C	401[A]	C7B	C22-C20-O06-C18
9	C	401[A]	C7B	C24-C20-O06-C18
9	C	401[B]	C7B	C22-C20-O06-C18
9	C	401[B]	C7B	C24-C20-O06-C18
9	C	401[A]	C7B	C21-C19-O05-C17

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

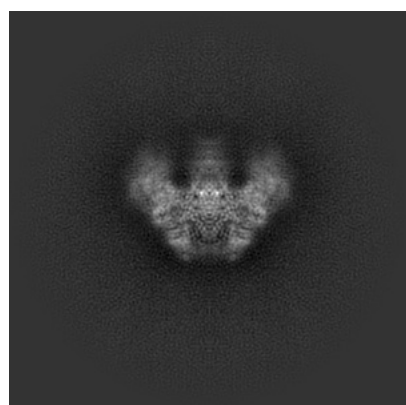
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0649. These allow visual inspection of the internal detail of the map and identification of artifacts.

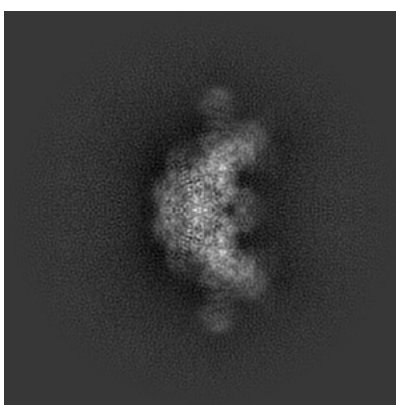
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

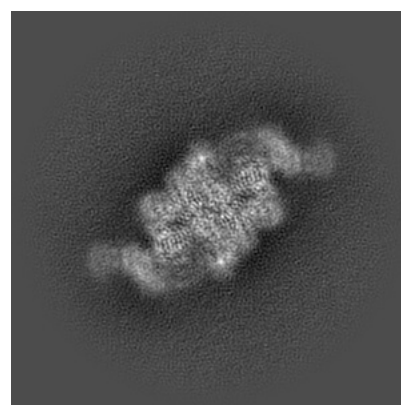
6.1.1 Primary map



X



Y

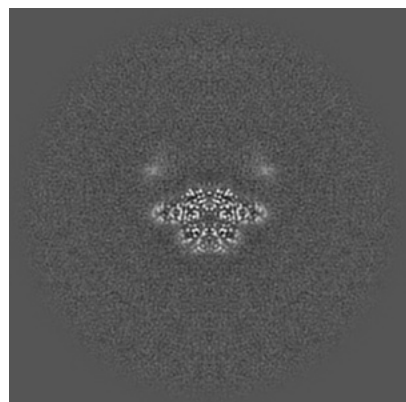


Z

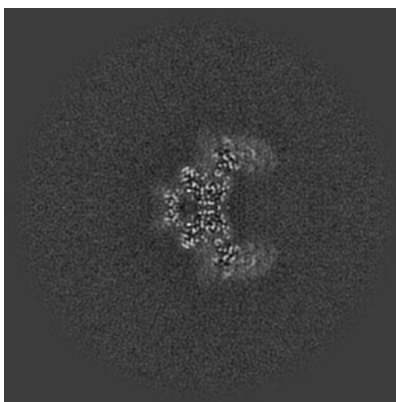
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

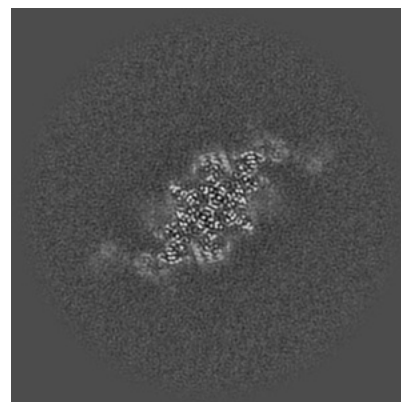
6.2.1 Primary map



X Index: 250



Y Index: 250

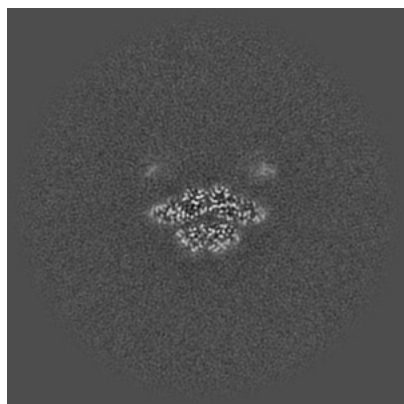


Z Index: 250

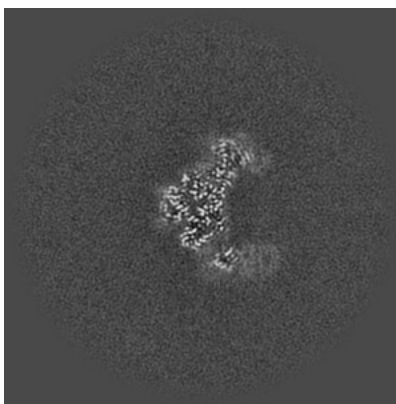
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

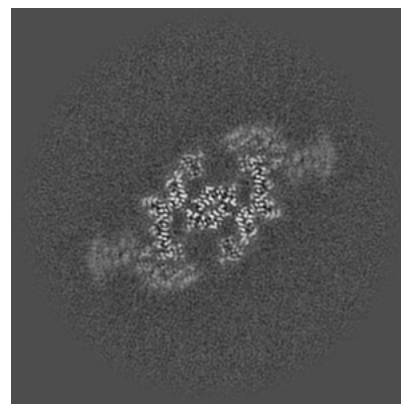
6.3.1 Primary map



X Index: 248



Y Index: 243

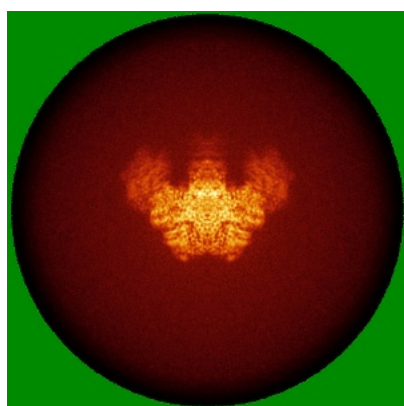


Z Index: 271

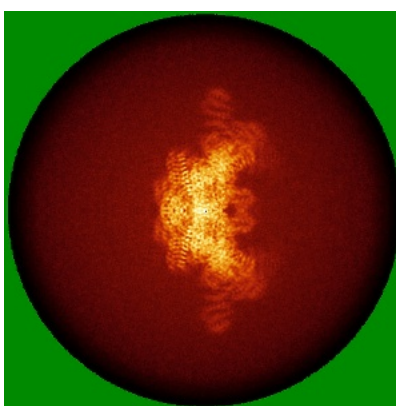
The images above show the largest variance slices of the map in three orthogonal directions.

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

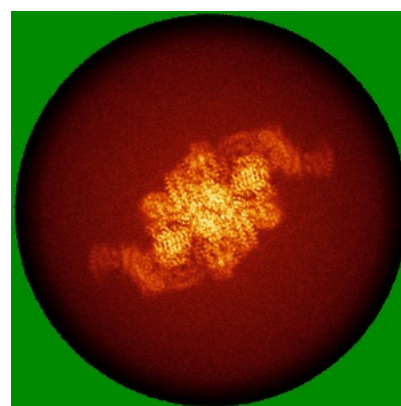
6.4.1 Primary map



X



Y

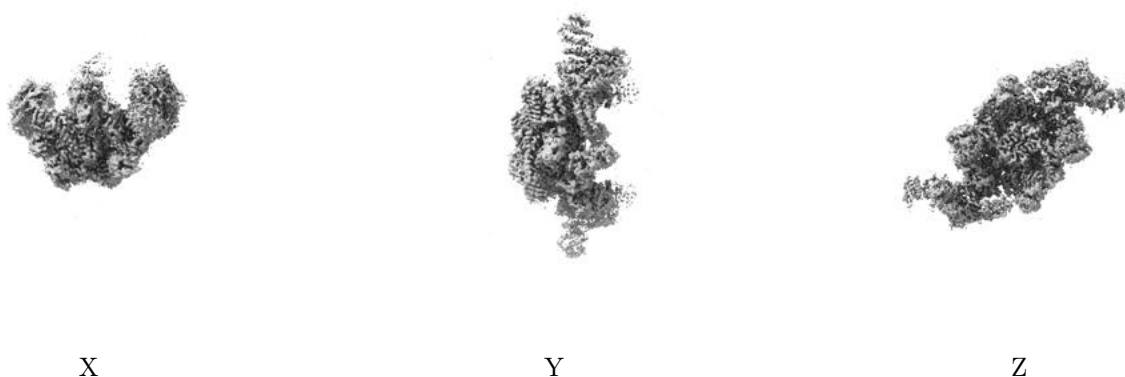


Z

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

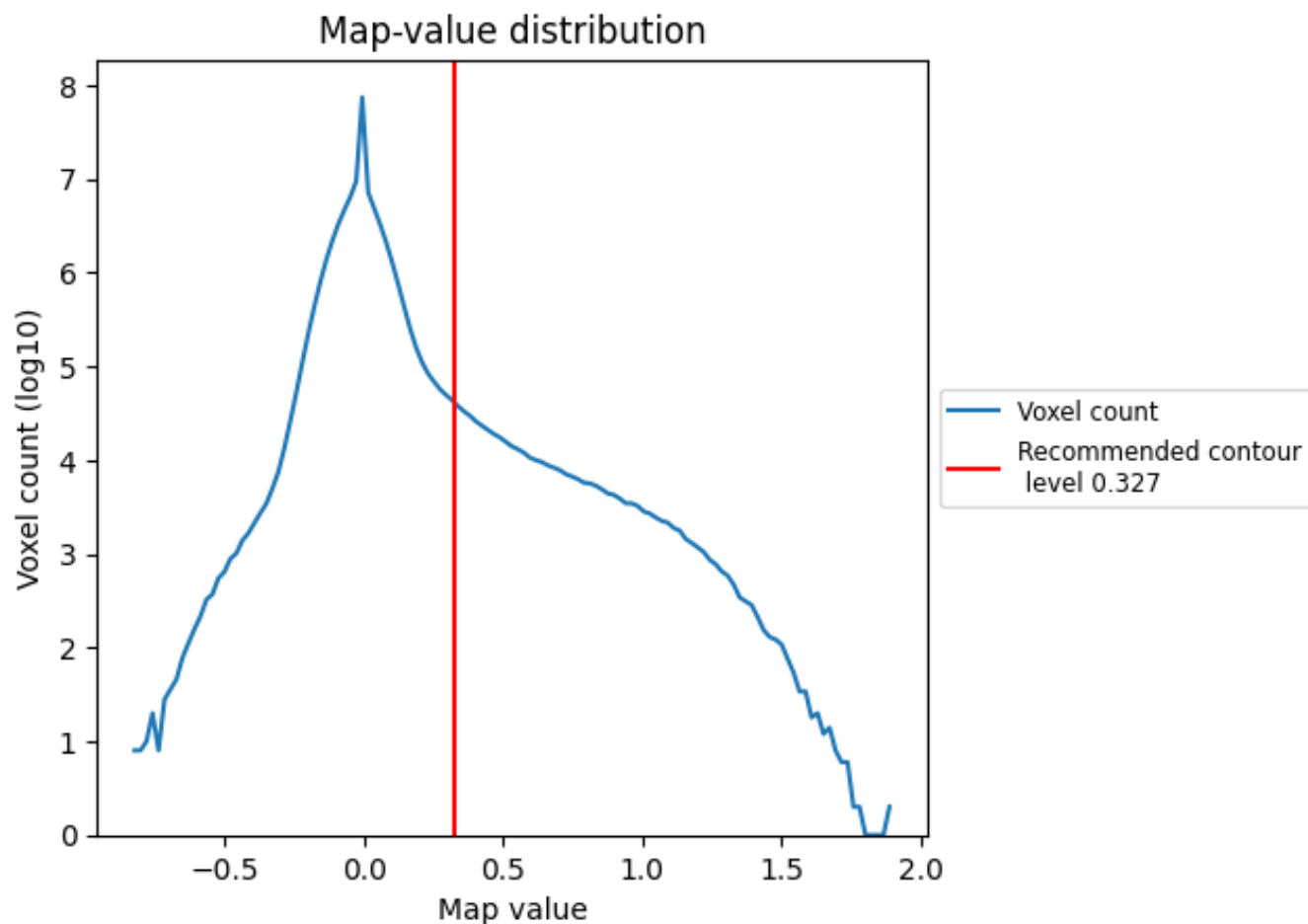
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

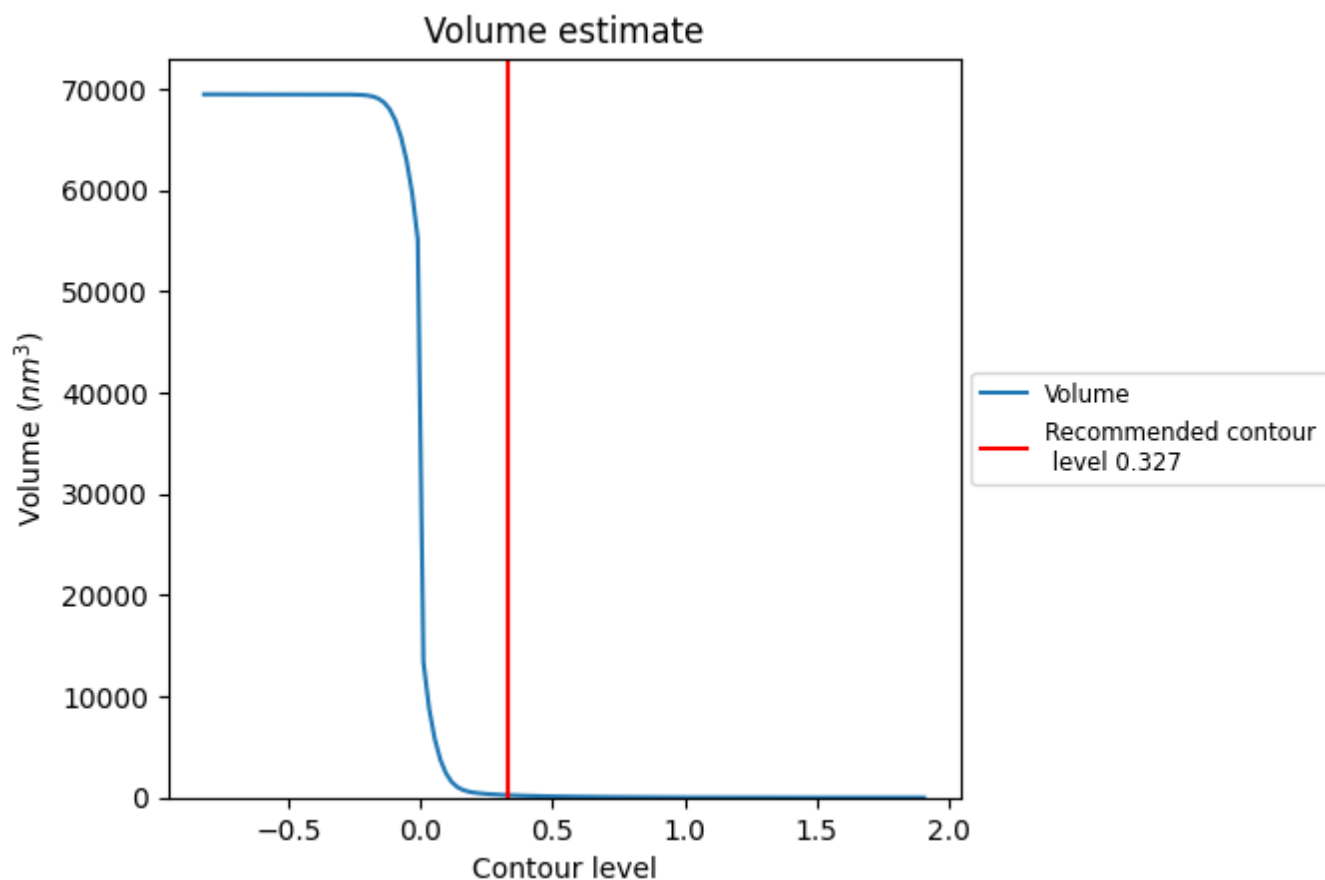
This section contains the results of statistical analysis of the map.

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.

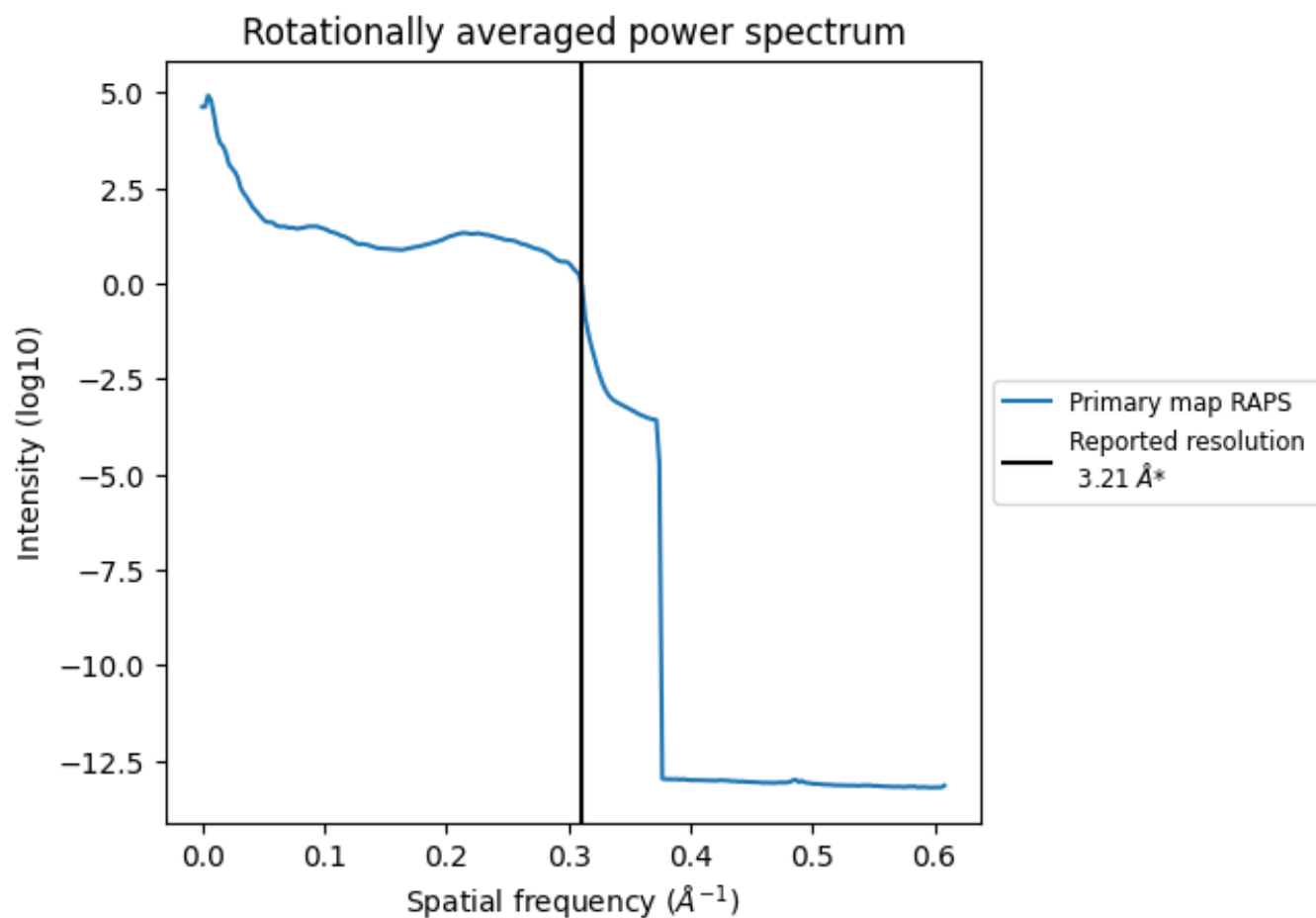
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 240 nm^3 ; this corresponds to an approximate mass of 217 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

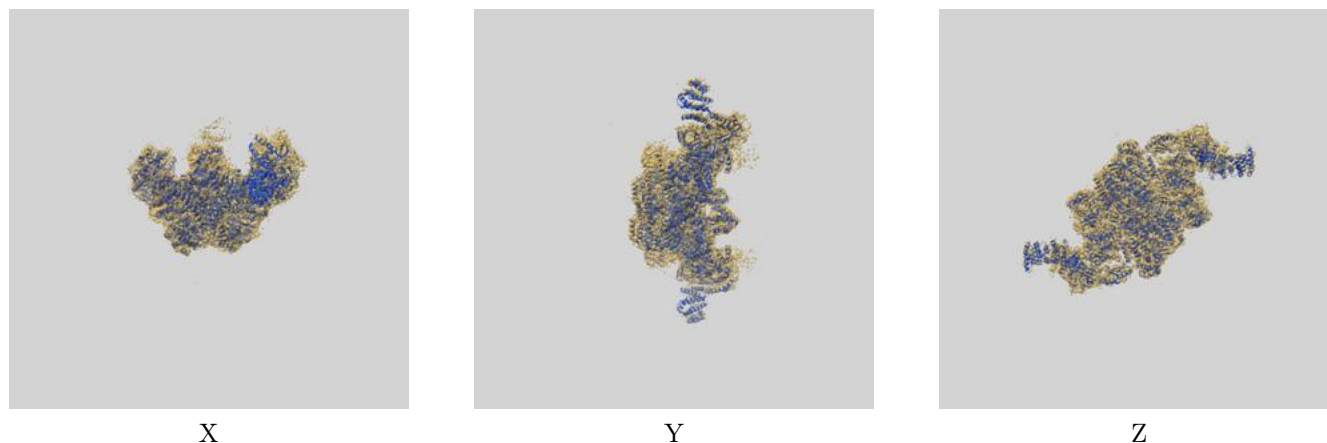
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

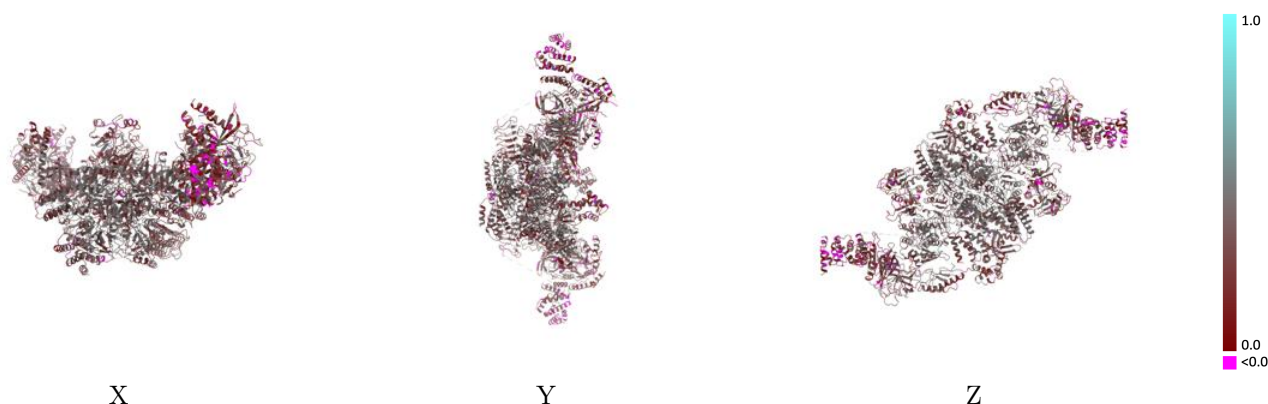
This section contains information regarding the fit between EMDB map EMD-0649 and PDB model 6O81. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



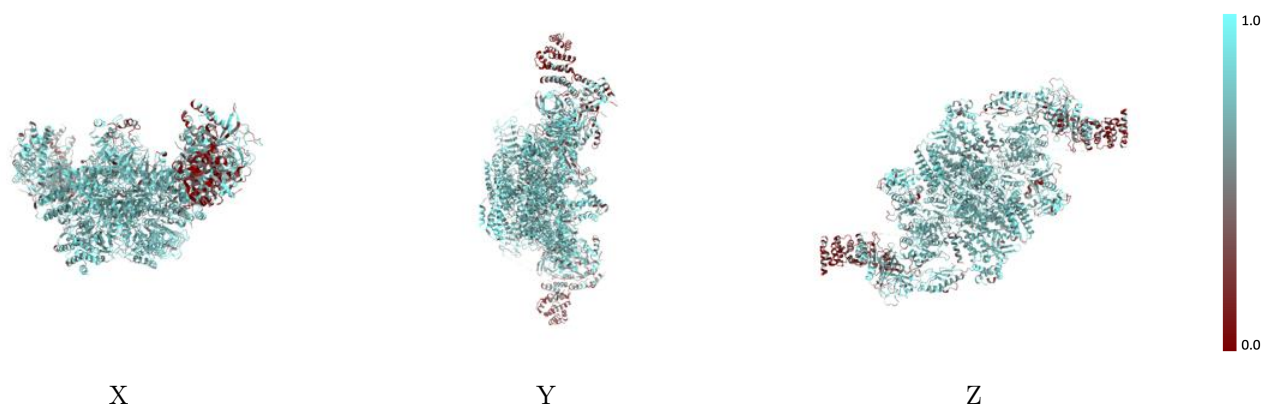
The images above show the 3D surface view of the map at the recommended contour level 0.327 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



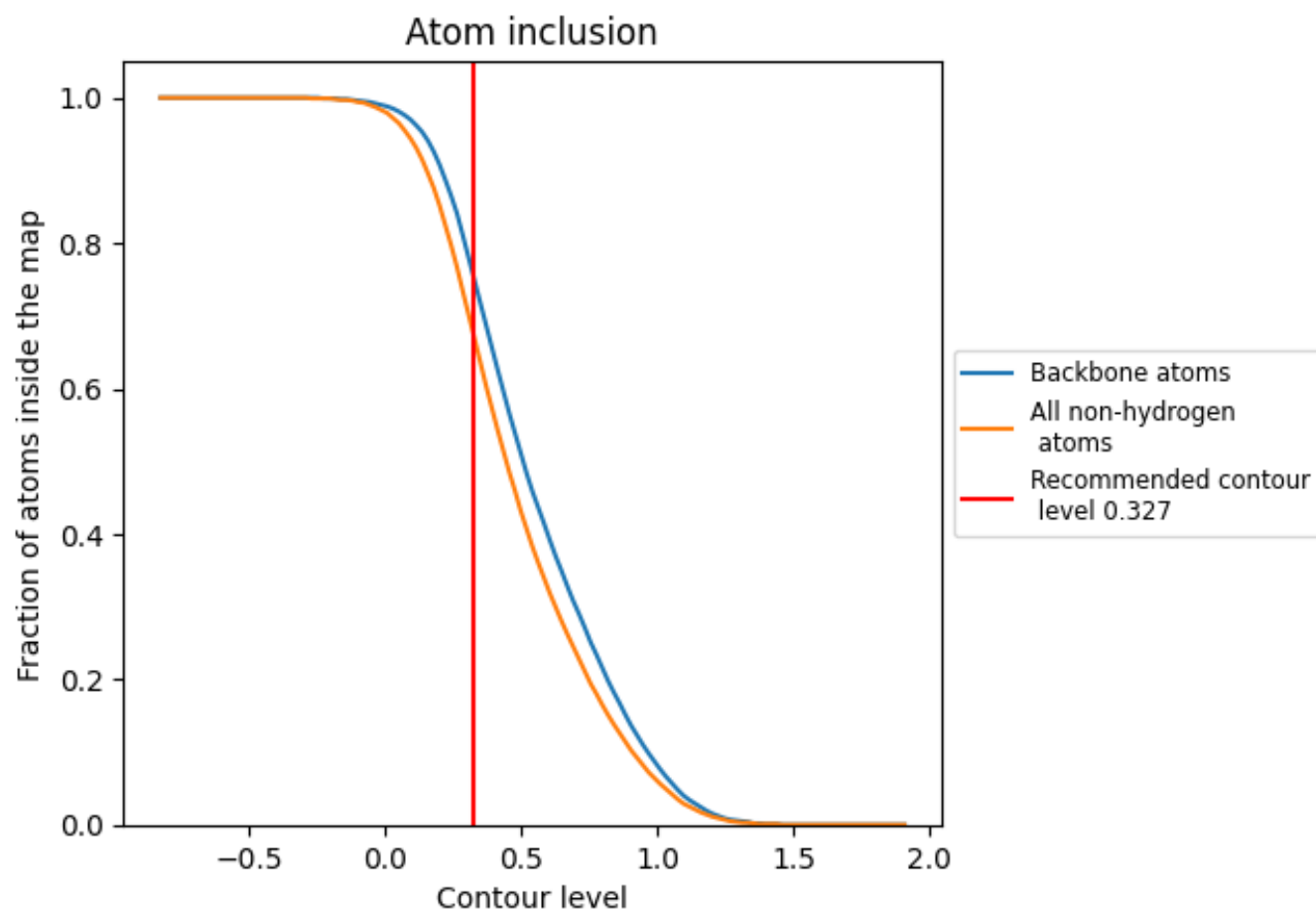
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.327).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (0.327) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6740	 0.3240
A	 0.6370	 0.3260
B	 0.6220	 0.3030
C	 0.7130	 0.3430
D	 0.7300	 0.3650
E	 0.7460	 0.3670
F	 0.7470	 0.3710
G	 0.7580	 0.3630
H	 0.7400	 0.3330
I	 0.6730	 0.2960
J	 0.6400	 0.2860
L	 0.6410	 0.2690
M	 0.6900	 0.3290
S	 0.5650	 0.2800
T	 0.5590	 0.2680
d	 0.4860	 0.1120
e	 0.5000	 0.1510

