



wwPDB EM Validation Summary Report ⓘ

Sep 24, 2026 – 04:31 PM EDT

PDB ID : 9P7P / pdb_00009p7p
EMDB ID : EMD-71350
Title : LPS transport bridge LptBFGCADE from Escherichia coli in complex with lipopolysaccharide
Authors : Taylor, R.J.; Pahil, K.S.; Walsh Jr., R.M.; Kahne, D.E.
Deposited on : 2025-06-20
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

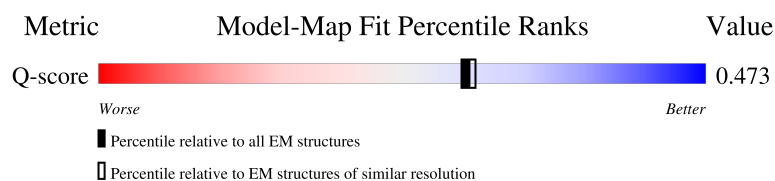
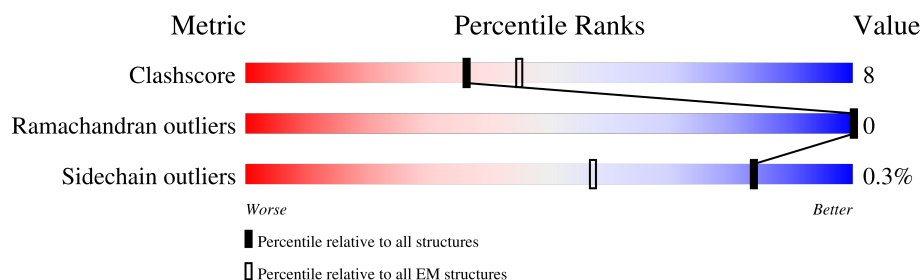
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	B	239	 86% 14%
1	H	239	 78% 22%
2	C	383	 62% 9% 29%
3	D	759	 89% 10%

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Mol	Chain	Length	Quality of chain
4	E	151	 79% 21%
5	F	366	 56% 10% 34%
6	G	358	 58% 12% 30%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 33115 atoms, of which 16303 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 Lipopolysaccharide export system ATP-binding protein LptB.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	238	Total	C	H	N	O	S	0	0
			3736	1162	1879	338	352	5		
1	H	239	Total	C	H	N	O	S	0	0
			3759	1168	1891	342	353	5		

- Molecule 2 is a protein called Lipopolysaccharide export system protein LptC,Lipopolysaccharide export system protein LptA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	273	Total	C	H	N	O	S	0	0
			3437	1119	1597	332	385	4		

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	194	LEU	-	linker	UNP P0ADV9
C	195	VAL	-	linker	UNP P0ADV9
C	196	PRO	-	linker	UNP P0ADV9
C	197	GLY	-	linker	UNP P0ADV9
C	198	GLY	-	linker	UNP P0ADV9
C	199	SER	-	linker	UNP P0ADV9
C	200	GLY	-	linker	UNP P0ADV9
C	201	GLY	-	linker	UNP P0ADV9
C	202	GLY	-	linker	UNP P0ADV9
C	203	GLY	-	linker	UNP P0ADV9
C	204	SER	-	linker	UNP P0ADV9
C	205	GLY	-	linker	UNP P0ADV9
C	206	GLY	-	linker	UNP P0ADV9
C	207	GLY	-	linker	UNP P0ADV9
C	208	GLY	-	linker	UNP P0ADV9
C	209	SER	-	linker	UNP P0ADV9
C	210	GLY	-	linker	UNP P0ADV9
C	211	GLY	-	linker	UNP P0ADV9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	212	GLY	-	linker	UNP P0ADV9
C	213	GLY	-	linker	UNP P0ADV9
C	214	SER	-	linker	UNP P0ADV9
C	373	LEU	-	expression tag	UNP P0ADV1
C	374	VAL	-	expression tag	UNP P0ADV1
C	375	PRO	-	expression tag	UNP P0ADV1
C	376	ARG	-	expression tag	UNP P0ADV1
C	377	GLY	-	expression tag	UNP P0ADV1
C	378	SER	-	expression tag	UNP P0ADV1
C	379	HIS	-	expression tag	UNP P0ADV1
C	380	HIS	-	expression tag	UNP P0ADV1
C	381	HIS	-	expression tag	UNP P0ADV1
C	382	HIS	-	expression tag	UNP P0ADV1
C	383	HIS	-	expression tag	UNP P0ADV1
C	384	HIS	-	expression tag	UNP P0ADV1
C	385	HIS	-	expression tag	UNP P0ADV1

- Molecule 3 is a protein called LPS-assembly protein LptD.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	752	Total	C	H	N	O	S	0	0
			11782	3836	5679	1047	1200	20		

- Molecule 4 is a protein called LPS-assembly lipoprotein LptE.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	151	Total	C	H	N	O	S	0	0
			2407	740	1220	216	223	8		

- Molecule 5 is a protein called Lipopolysaccharide export system permease protein LptF.

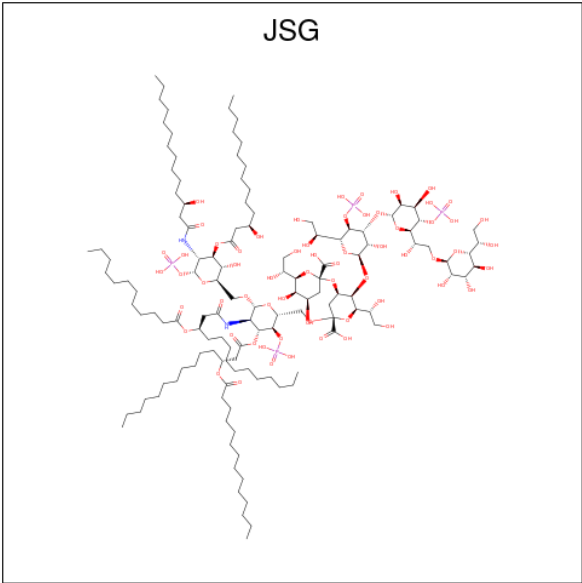
Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	242	Total	C	H	N	O	S	0	0
			3905	1251	2014	307	318	15		

- Molecule 6 is a protein called Lipopolysaccharide export system permease protein LptG.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	G	250	Total	C	H	N	O	S	0	0
			3951	1280	2023	307	323	18		

- Molecule 7 is (2 {R},4 {R},5 {R},6 {R})-6-[(1 {R})-1,2-bis(oxidanyl)ethyl]-2-[(2 {R},4 {R}

,5 {R},6 {R})-6-[(1 {R})-1,2-bis(oxidanyl)ethyl]-5-[(2 {S},3 {S},4 {R},5 {R},6 {R})-6-[(1 {S})-1,2-bis(oxidanyl)ethyl]-4-[(2 {R},3 {S},4 {R},5 {S},6 {R})-6-[(1 {S})-2-[(2 {S},3 {S},4 {S},5 {S},6 {R})-6-[(1 {S})-1,2-bis(oxidanyl)ethyl]-3,4,5-tris(oxidanyl)oxan-2-yl]oxy-1-oxidanyl-ethyl]-3,4-bis(oxidanyl)-5-phosphonooxy-oxan-2-yl]oxy-3-oxidanyl-5-phosphonooxy-oxan-2-yl]oxy-2-carboxy-2-[[[(2 {R},3 {S},4 {R},5 {R},6 {R})-5-[[[(3 {R})-3-dodecanoyloxytetradecanoyl]amino]-6-[[[(2 {R},3 {S},4 {R},5 {R},6 {R})-3-oxidanyl-5-[[[(3 {R})-3-oxidanyltetradecanoyl]amino]-4-[(3 {R})-3-oxidanyltetradecanoyl]oxy-6-phosphonooxy-oxan-2-yl]methoxy]-3-phosphonooxy-4-[(3 {R})-3-tetradecanoyloxytetradecanoyl]oxy-oxan-2-yl]methoxy]oxan-4-yl]oxy-4,5-bis(oxidanyl)oxane-2-carboxylic acid (CCD ID: JSG) (formula: C₁₃₁H₂₄₀N₂O₆₃P₄) (labeled as "Ligand of Interest" by depositor).

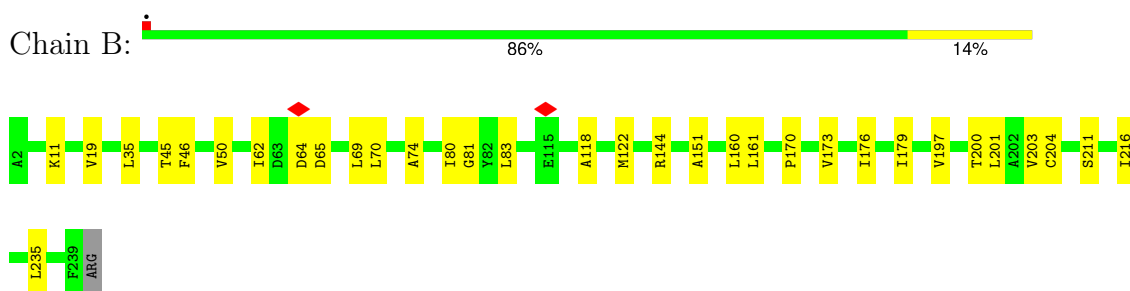


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
7	F	1	138	102	2	32	2	0

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.

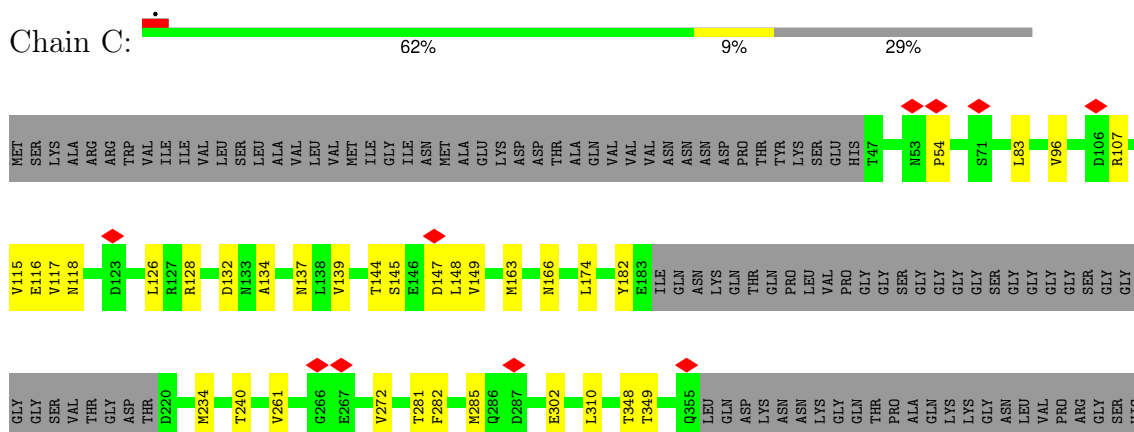
- Molecule 1: Lipopolysaccharide export system ATP-binding protein LptB

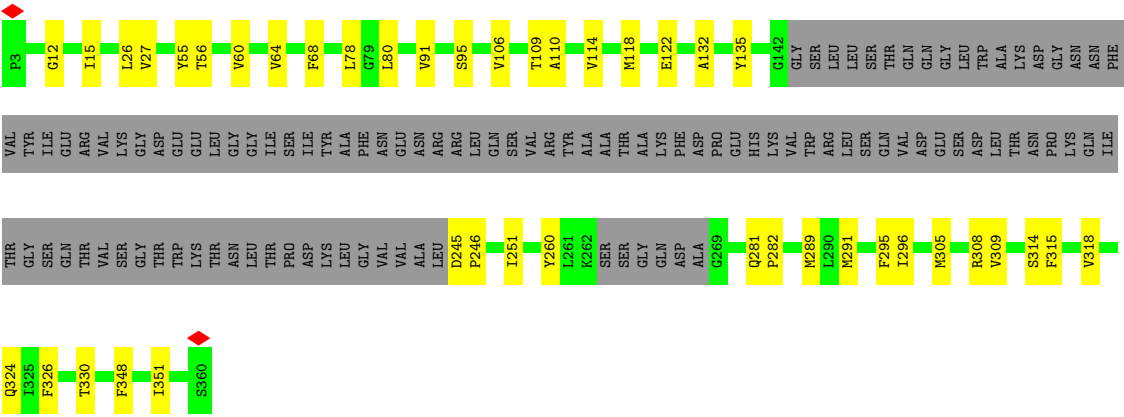


- Molecule 1: Lipopolysaccharide export system ATP-binding protein LptB



- Molecule 2: Lipopolysaccharide export system protein LptC, Lipopolysaccharide export system protein LptA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	157094	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.512	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0417	Depositor
Map size (Å)	498.0, 498.0, 498.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	B	0.13	0/1884	0.26	0/2548
1	H	0.12	0/1895	0.26	0/2562
2	C	0.14	0/1864	0.33	0/2520
3	D	0.17	0/6260	0.32	0/8517
4	E	0.15	0/1204	0.26	0/1625
5	F	0.17	0/1927	0.29	0/2624
6	G	0.15	0/1971	0.27	0/2664
All	All	0.15	0/17005	0.30	0/23060

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	B	1857	1879	1875	32	0
1	H	1868	1891	1888	46	0
2	C	1840	1597	1549	25	0
3	D	6103	5679	5707	67	0
4	E	1187	1220	1217	19	0
5	F	1891	2014	2026	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	1928	2023	2030	33	0
7	F	138	0	0	16	0
All	All	16812	16303	16292	254	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 8.

The worst 5 of 254 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)
5:F:303:MET:HE1	7:F:402:JSG:CFX	1.19	1.57
5:F:303:MET:HE1	7:F:402:JSG:CFW	1.48	1.40
5:F:303:MET:CE	7:F:402:JSG:CFW	2.11	1.29
5:F:29:GLN:NE2	7:F:402:JSG:CGD	1.99	1.23
5:F:303:MET:CE	7:F:402:JSG:CFX	2.15	1.23

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	B	236/239 (99%)	226 (96%)	10 (4%)	0	100	100
1	H	237/239 (99%)	226 (95%)	11 (5%)	0	100	100
2	C	269/383 (70%)	251 (93%)	18 (7%)	0	100	100
3	D	744/759 (98%)	701 (94%)	43 (6%)	0	100	100
4	E	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
5	F	238/366 (65%)	227 (95%)	11 (5%)	0	100	100
6	G	244/358 (68%)	239 (98%)	5 (2%)	0	100	100
All	All	2117/2495 (85%)	2017 (95%)	100 (5%)	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	B	199/200 (100%)	199 (100%)	0	100	100
1	H	200/200 (100%)	200 (100%)	0	100	100
2	C	165/327 (50%)	164 (99%)	1 (1%)	78	80
3	D	658/662 (99%)	657 (100%)	1 (0%)	87	85
4	E	132/132 (100%)	132 (100%)	0	100	100
5	F	208/307 (68%)	207 (100%)	1 (0%)	81	81
6	G	207/298 (70%)	205 (99%)	2 (1%)	68	75
All	All	1769/2126 (83%)	1764 (100%)	5 (0%)	84	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	240	THR
3	D	599	ASN
5	F	272	LEU
6	G	68	PHE
6	G	260	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	98	ASN
1	H	229	HIS
3	D	737	ASN
4	E	131	GLN
5	F	29	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
7	JSG	F	402	-	139,140,206	0.97	9 (6%)	166,176,278	2.26	42 (25%)

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
7	JSG	F	402	-	-	21/140/199/333	0/3/3/7

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	F	402	JSG	OBD-CBC	3.80	1.51	1.43
7	F	402	JSG	OBH-CBG	3.63	1.49	1.44
7	F	402	JSG	O6-CBA	3.51	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	F	402	JSG	CBI-CBG	2.52	1.58	1.52
7	F	402	JSG	CAP-CAN	2.38	1.56	1.53

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	402	JSG	CEW-OFJ-CGB	7.29	135.25	117.80
7	F	402	JSG	OFZ-CFM-CFL	7.12	121.94	106.72
7	F	402	JSG	CFM-OFZ-CGN	7.05	134.67	117.80
7	F	402	JSG	CAP-OAQ-CEE	6.74	128.56	117.59
7	F	402	JSG	CAP-CAN-NAO	6.60	121.43	110.91

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

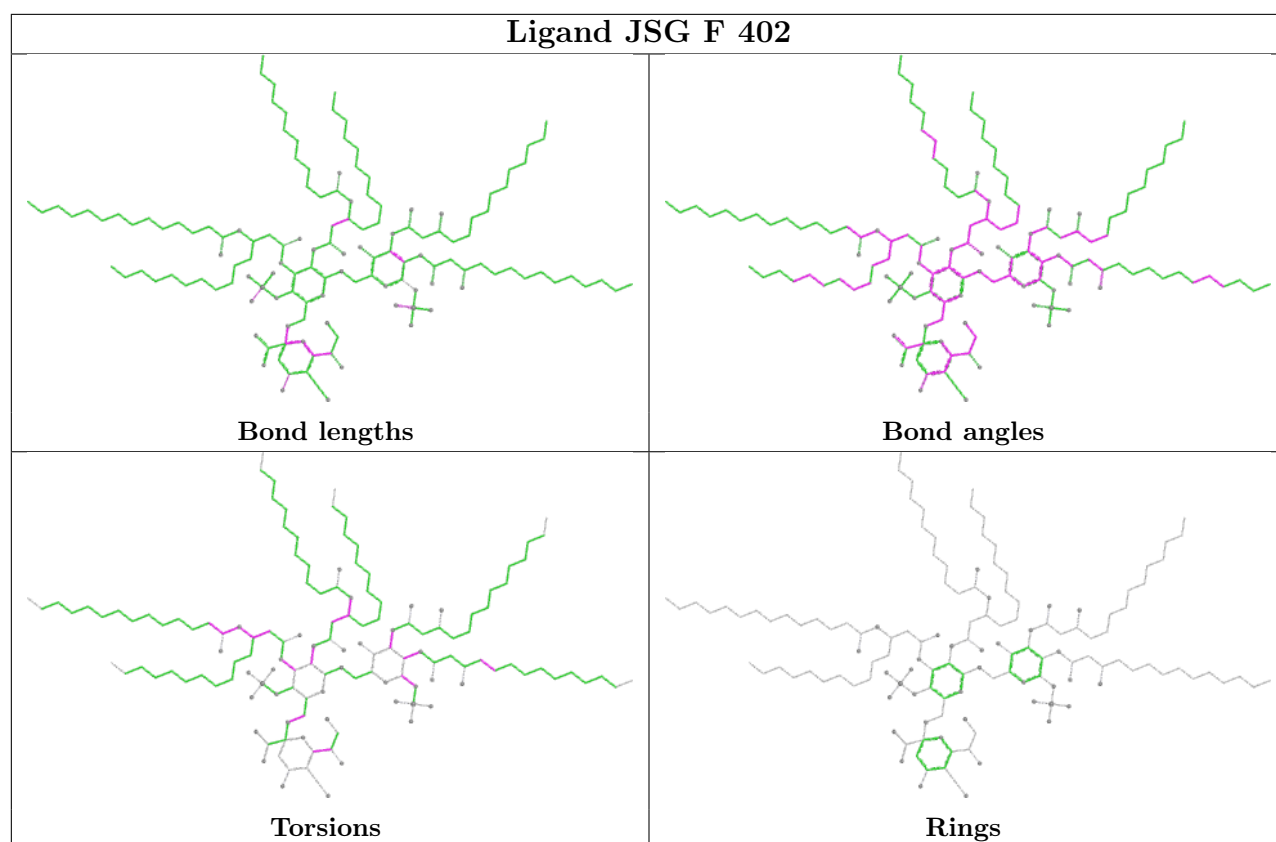
Mol	Chain	Res	Type	Atoms
7	F	402	JSG	C7-C8-CEW-CEX
7	F	402	JSG	OAU-CAL-OAM-PHG
7	F	402	JSG	CBE-CBG-CBI-CBK
7	F	402	JSG	CBE-CBG-CBI-OBJ
7	F	402	JSG	CFL-CFM-OFZ-CGN

There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	402	JSG	16	0

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.

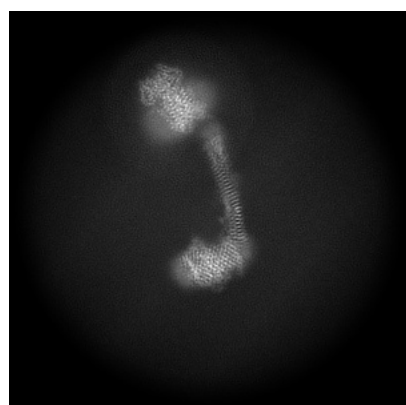
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71350. These allow visual inspection of the internal detail of the map and identification of artifacts.

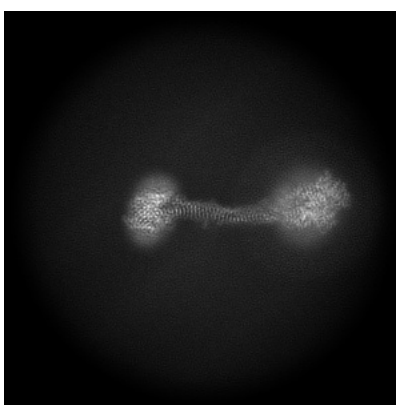
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

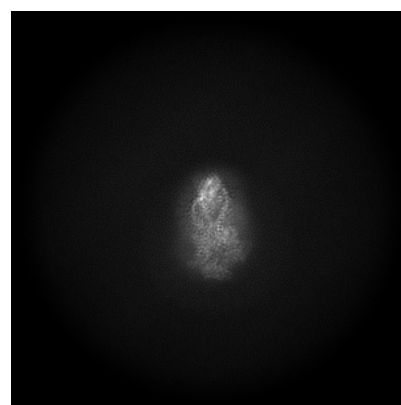
6.1.1 Primary map



X



Y



Z

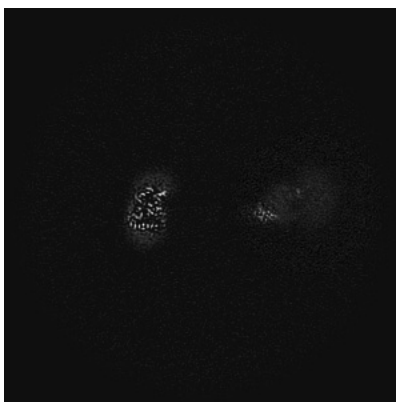
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 300



Y Index: 300

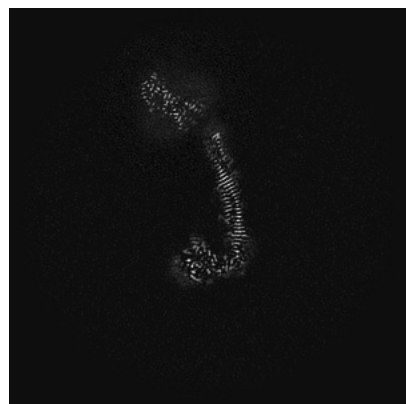


Z Index: 300

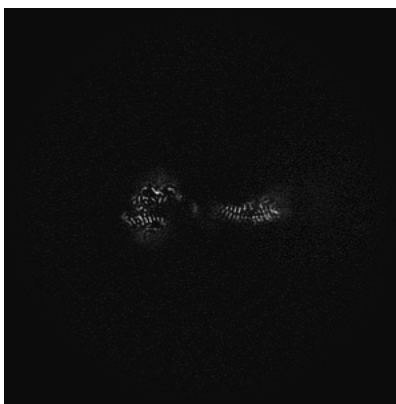
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

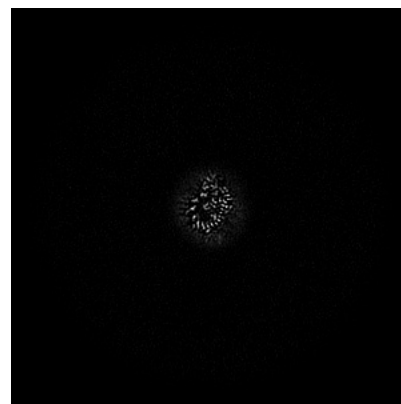
6.3.1 Primary map



X Index: 299



Y Index: 316

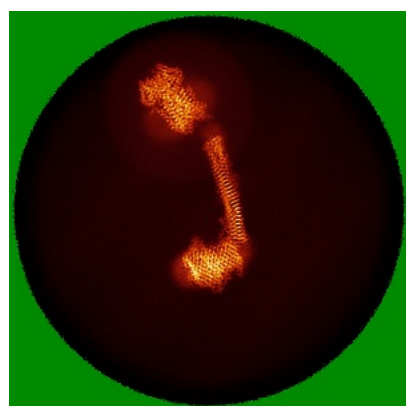


Z Index: 216

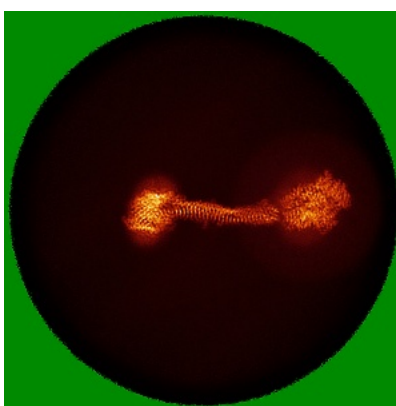
The images above show the largest variance slices of the map in three orthogonal directions.

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

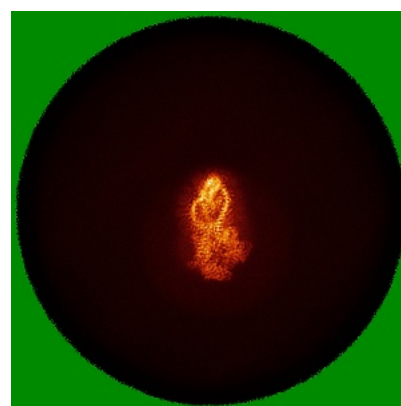
6.4.1 Primary map



X



Y

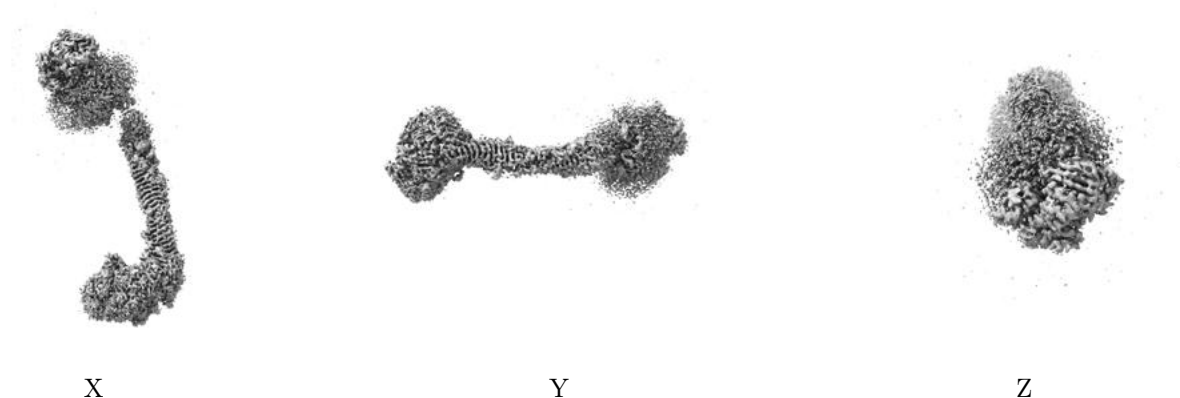


Z

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 0.0417. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

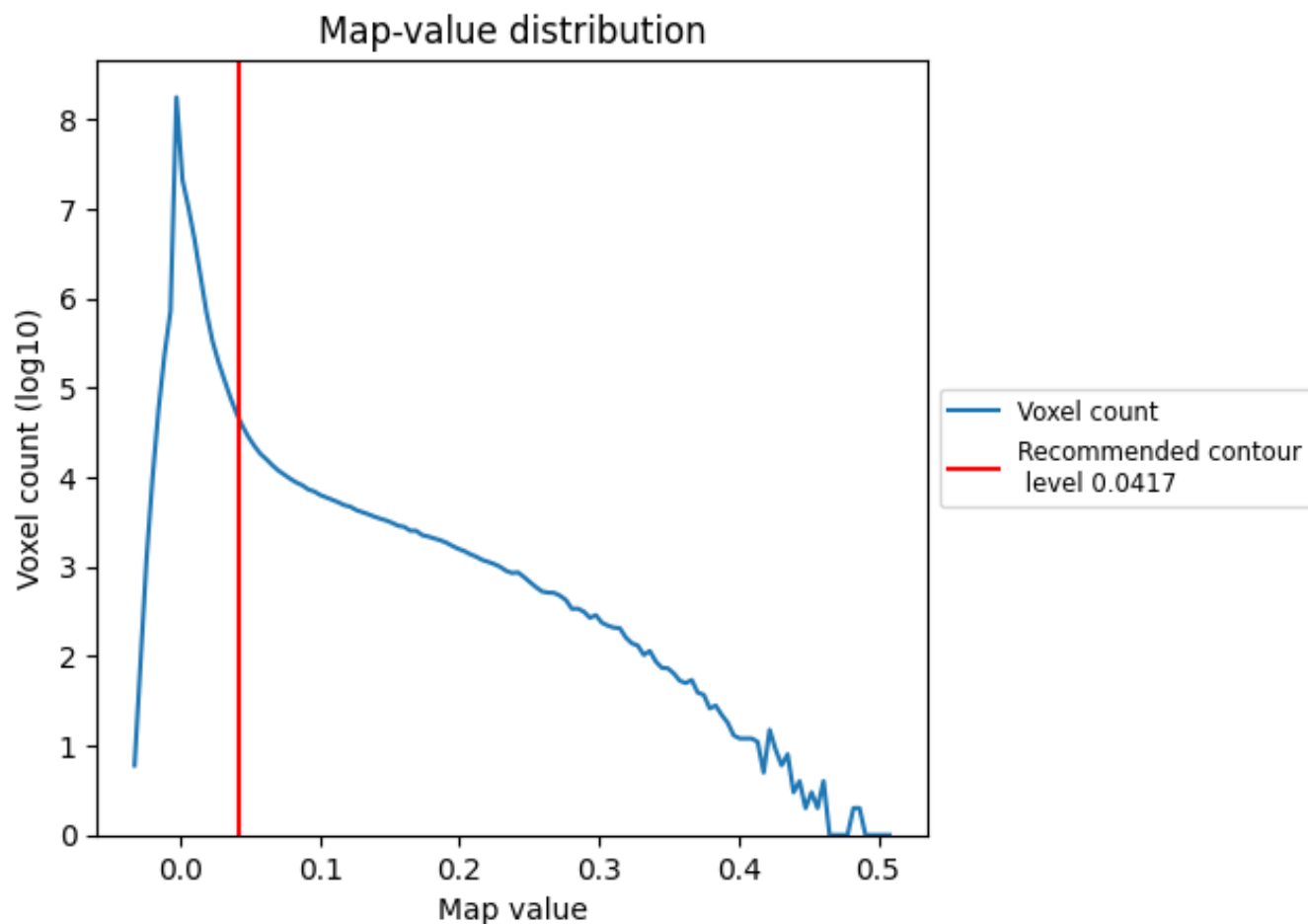
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

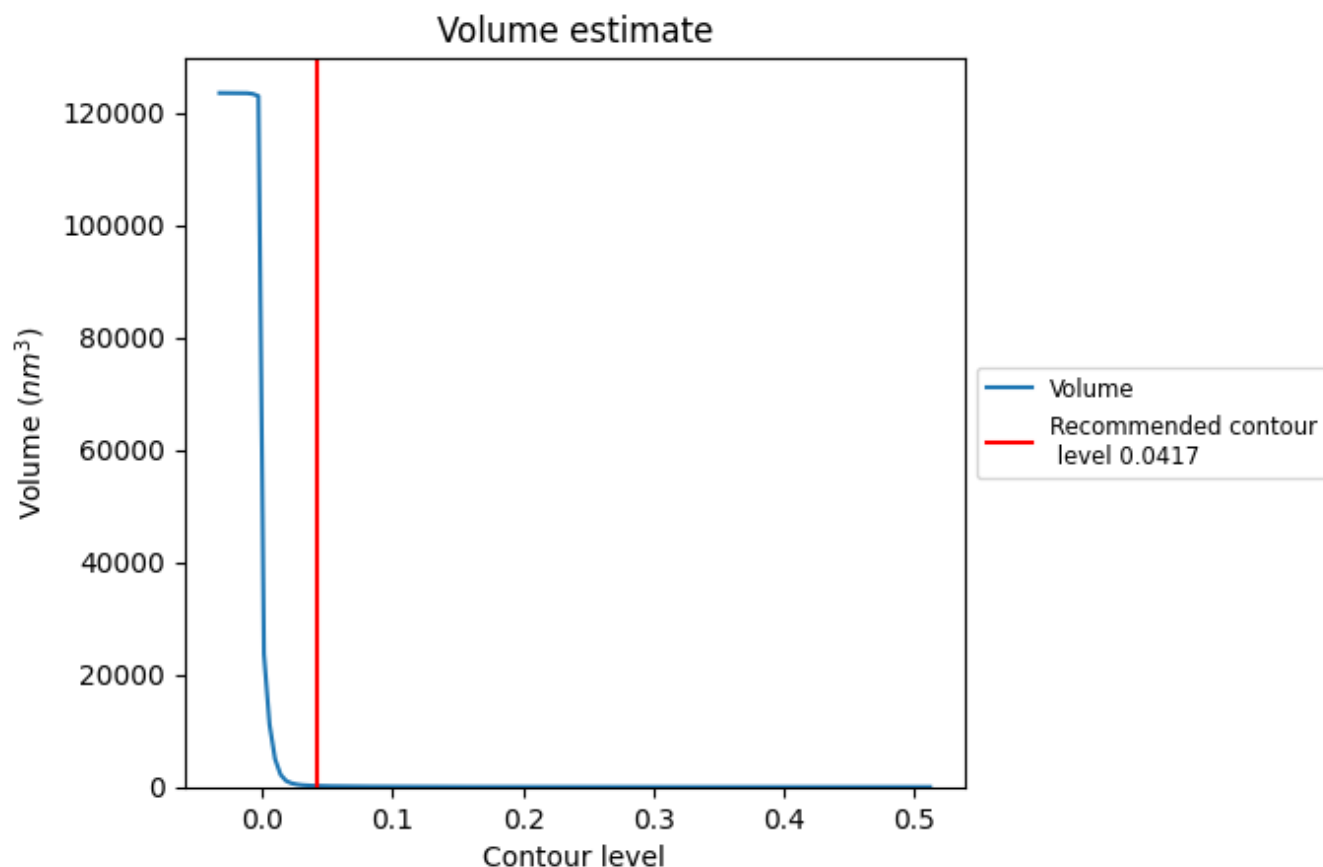
This section contains the results of statistical analysis of the map.

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.

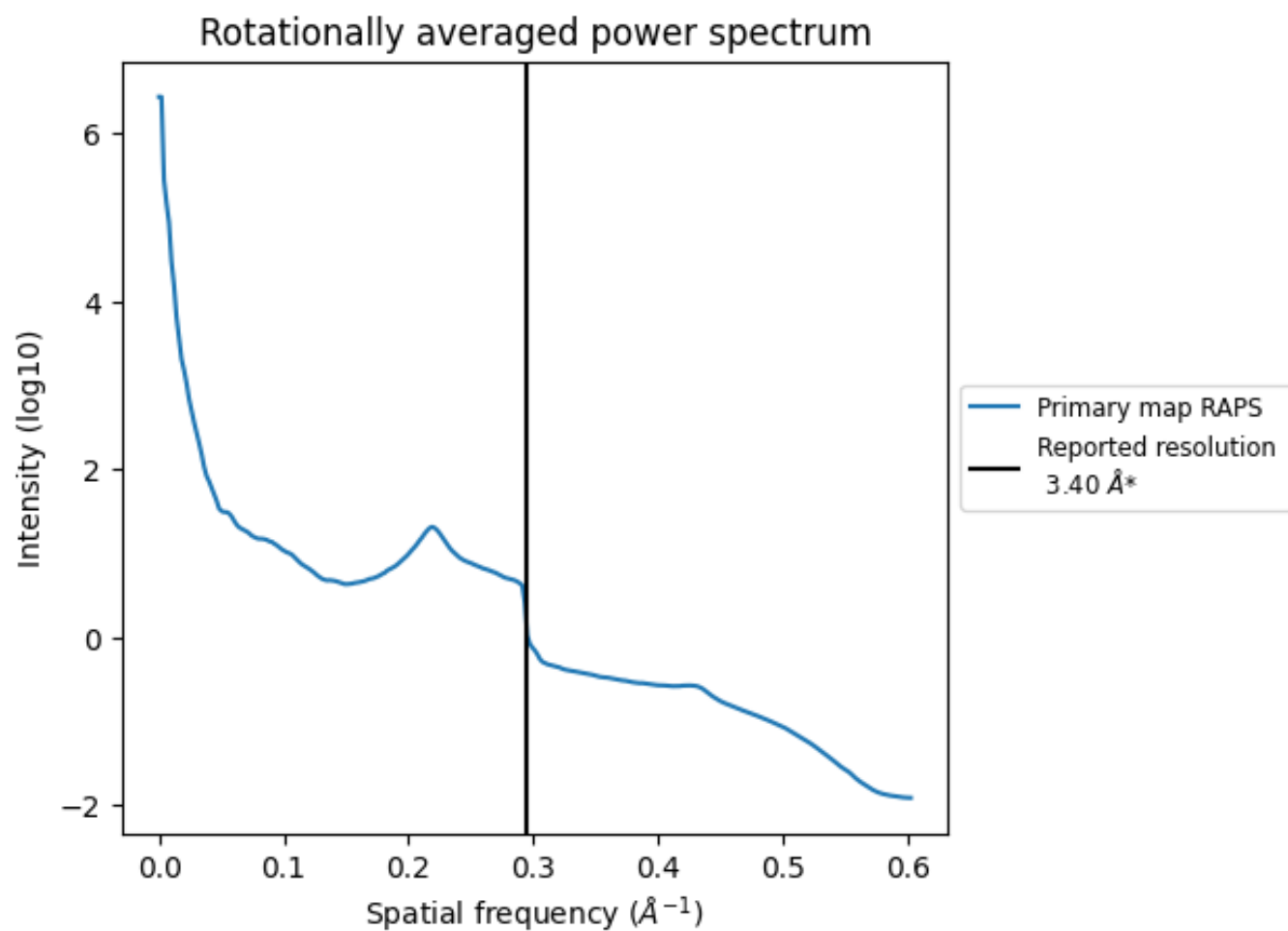
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 191 nm^3 ; this corresponds to an approximate mass of 172 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 0.294 Å⁻¹

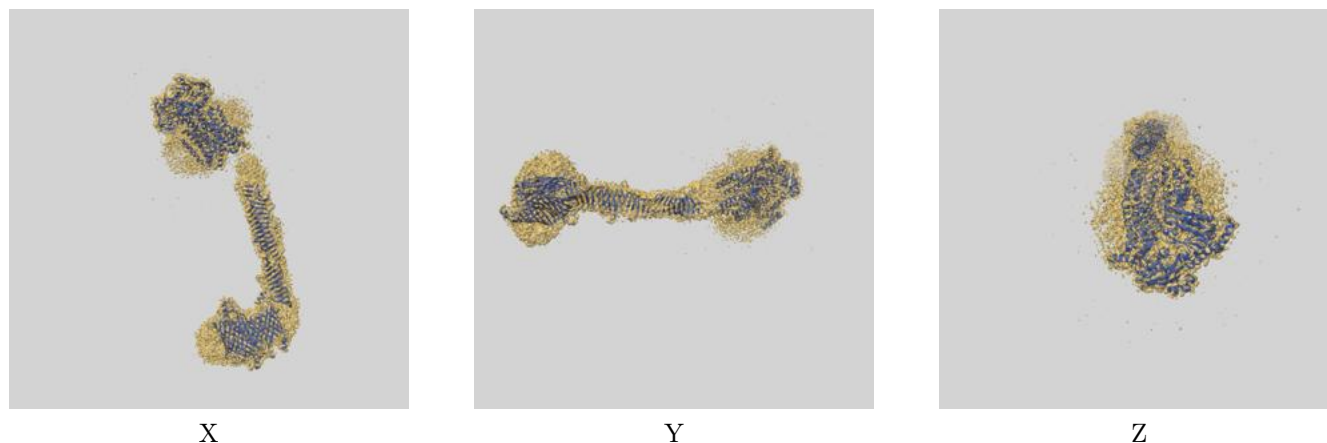
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

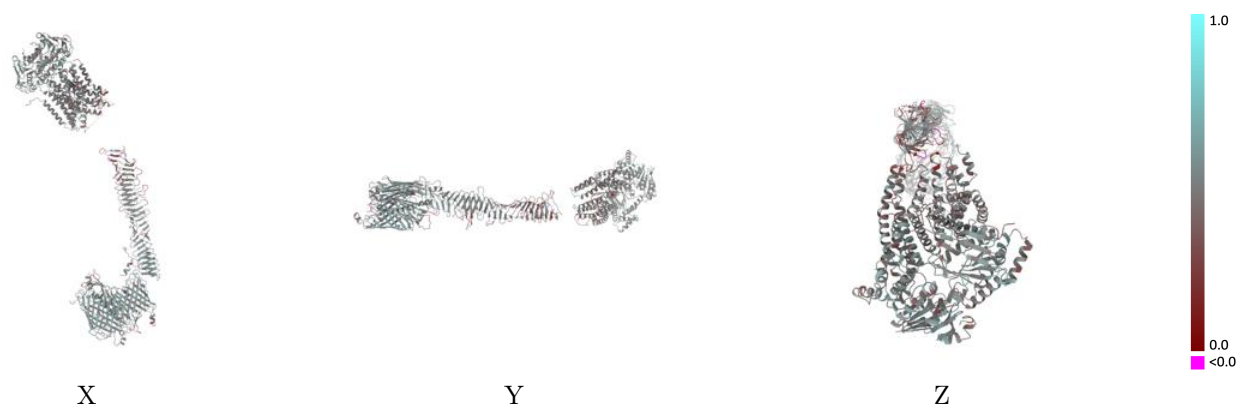
This section contains information regarding the fit between EMDB map EMD-71350 and PDB model 9P7P. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



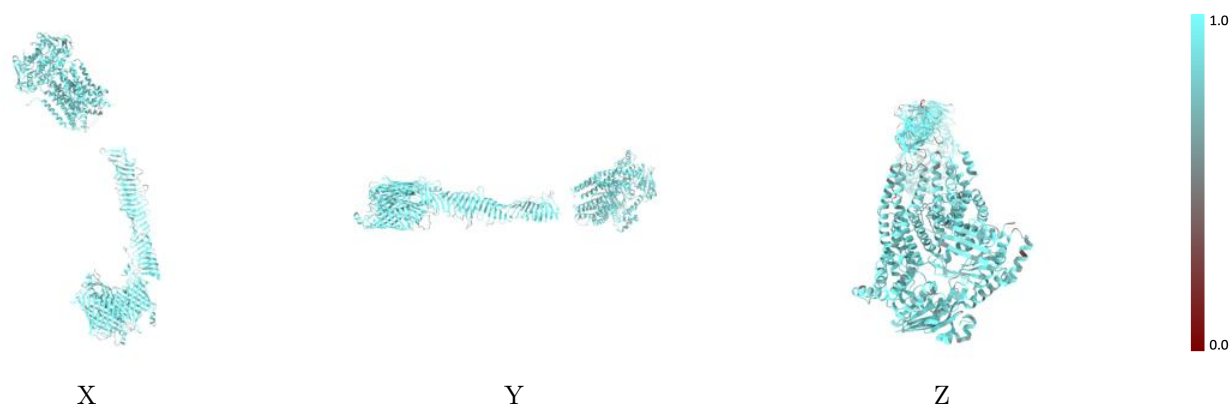
The images above show the 3D surface view of the map at the recommended contour level 0.0417 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



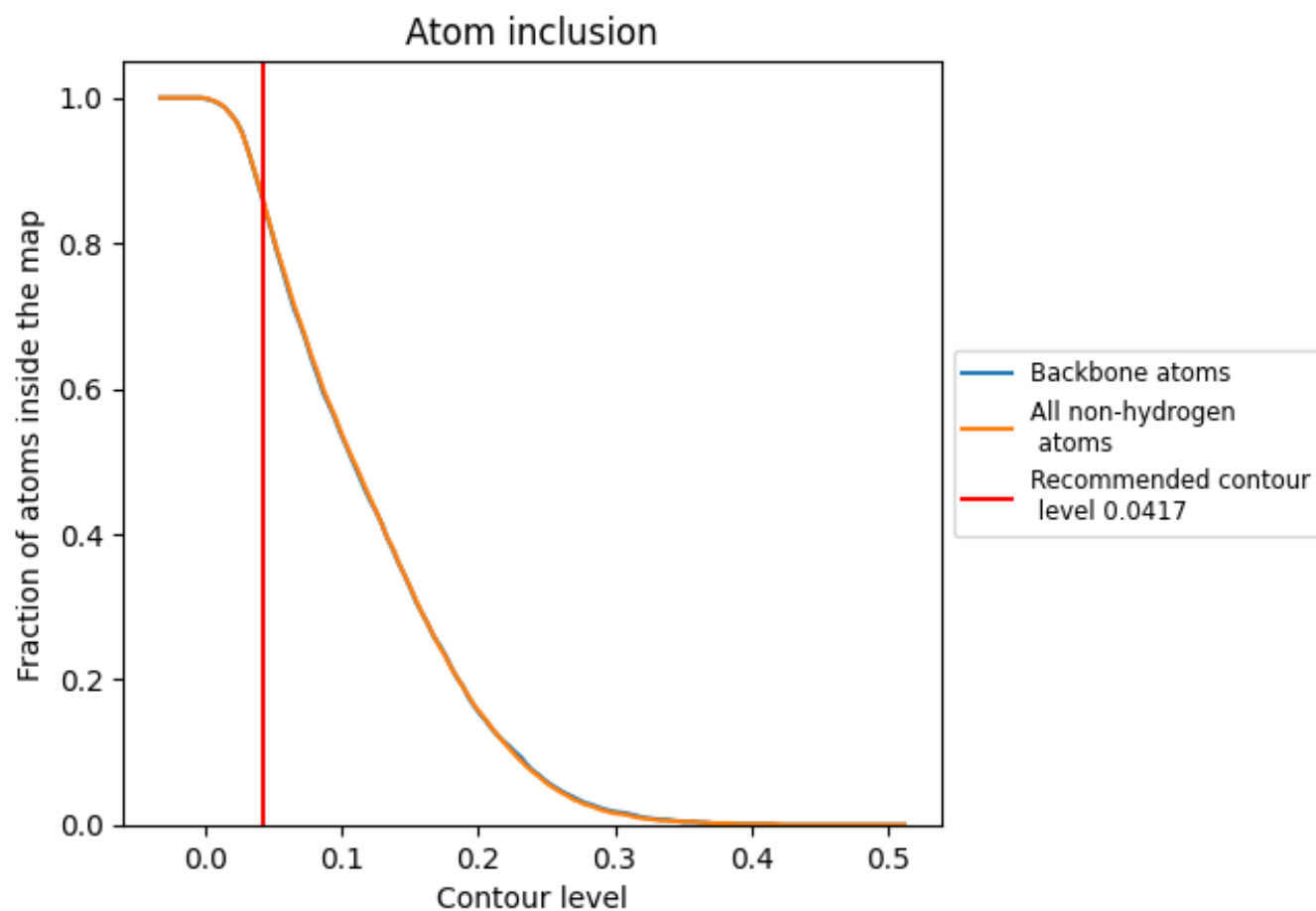
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0417).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.0417) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8640	0.4730
B	0.8610	0.4940
C	0.8380	0.4010
D	0.8860	0.4960
E	0.8580	0.4720
F	0.8480	0.4520
G	0.8570	0.4600
H	0.8450	0.4900

1.0

0.0

<0.0