



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:40 PM UTC

PDB ID : 7TD3 / pdb_00007td3
EMDB ID : EMD-25822
Title : Sphingosine-1-phosphate receptor 1-Gi complex bound to S1P
Authors : Liu, S.; Paknejad, N.; Zhu, L.; Kihara, Y.; Ray, D.; Chun, J.; Liu, W.; Hite, R.K.; Huang, X.Y.
Deposited on : 2021-12-30
Resolution : 3.00 Å(reported)

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

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A user guide is available at

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

The types of validation reports are described at

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

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

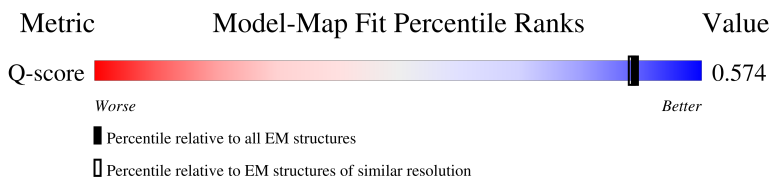
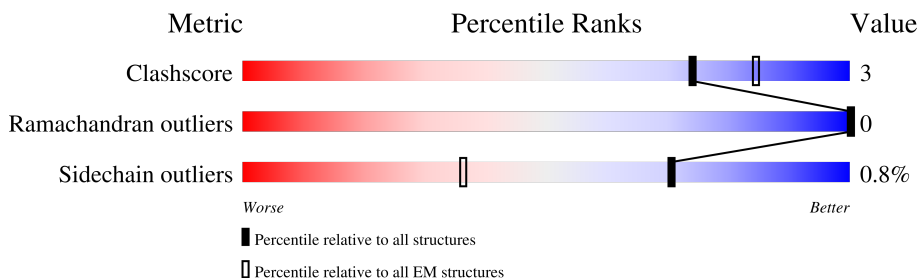
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

1 Overall quality at a glance

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

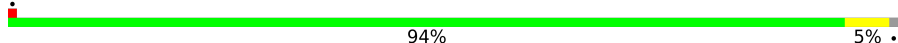
The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	340	
2	A	379	
3	G	71	
4	R	392	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7035 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 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	338	Total	C	N	O	S	0	0
			2556	1580	458	497	21		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	223	Total	C	N	O	S	0	0
			1759	1124	294	328	13		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP B2RSH2
A	-23	GLY	-	expression tag	UNP B2RSH2
A	-22	SER	-	expression tag	UNP B2RSH2
A	-21	SER	-	expression tag	UNP B2RSH2
A	-20	HIS	-	expression tag	UNP B2RSH2
A	-19	HIS	-	expression tag	UNP B2RSH2
A	-18	HIS	-	expression tag	UNP B2RSH2
A	-17	HIS	-	expression tag	UNP B2RSH2
A	-16	HIS	-	expression tag	UNP B2RSH2
A	-15	HIS	-	expression tag	UNP B2RSH2
A	-14	SER	-	expression tag	UNP B2RSH2
A	-13	SER	-	expression tag	UNP B2RSH2
A	-12	GLY	-	expression tag	UNP B2RSH2
A	-11	LEU	-	expression tag	UNP B2RSH2
A	-10	GLU	-	expression tag	UNP B2RSH2
A	-9	VAL	-	expression tag	UNP B2RSH2
A	-8	LEU	-	expression tag	UNP B2RSH2
A	-7	PHE	-	expression tag	UNP B2RSH2
A	-6	GLN	-	expression tag	UNP B2RSH2
A	-5	GLY	-	expression tag	UNP B2RSH2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	PRO	-	expression tag	UNP B2RSH2
A	-3	HIS	-	expression tag	UNP B2RSH2
A	-2	MET	-	expression tag	UNP B2RSH2
A	-1	ALA	-	expression tag	UNP B2RSH2
A	0	SER	-	expression tag	UNP B2RSH2
A	203	ALA	GLY	engineered mutation	UNP B2RSH2

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	56	Total	C	N	O	S	0	0
			405	257	73	72	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	68	SER	CYS	engineered mutation	UNP P63212

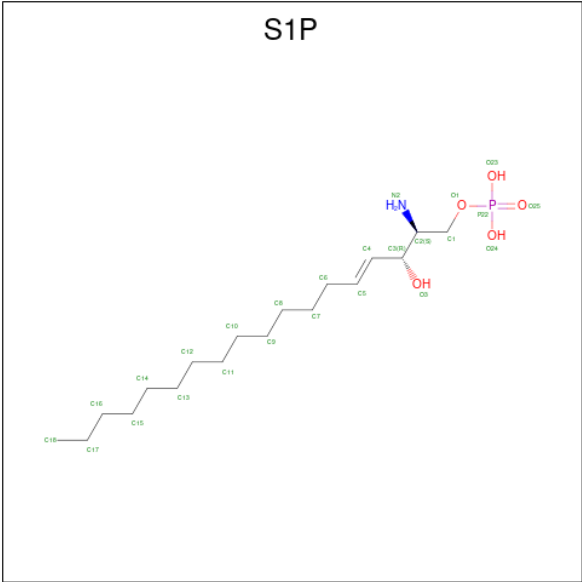
- Molecule 4 is a protein called Sphingosine 1-phosphate receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	292	Total	C	N	O	S	0	0
			2276	1516	366	378	16		

There are 11 discrepancies between the modelled and reference sequences:

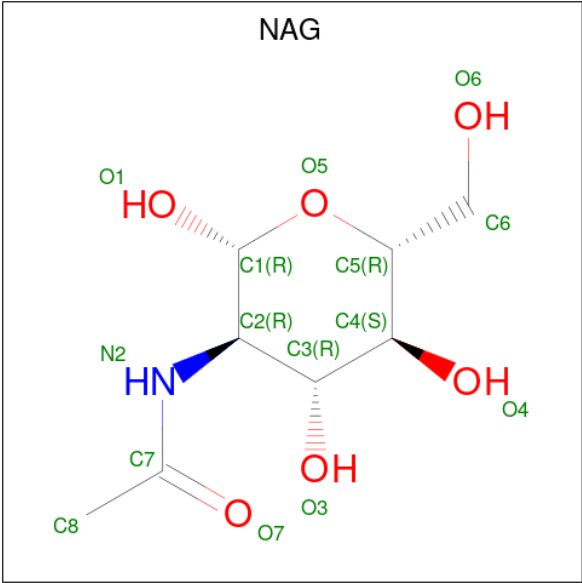
Chain	Residue	Modelled	Actual	Comment	Reference
R	-9	ASP	-	expression tag	UNP P21453
R	-8	TYR	-	expression tag	UNP P21453
R	-7	LYS	-	expression tag	UNP P21453
R	-6	ASP	-	expression tag	UNP P21453
R	-5	ASP	-	expression tag	UNP P21453
R	-4	ASP	-	expression tag	UNP P21453
R	-3	ASP	-	expression tag	UNP P21453
R	-2	LYS	-	expression tag	UNP P21453
R	-1	ALA	-	expression tag	UNP P21453
R	0	ALA	-	expression tag	UNP P21453
R	1	ALA	-	expression tag	UNP P21453

- Molecule 5 is (2S,3R,4E)-2-amino-3-hydroxyoctadec-4-en-1-yl dihydrogen phosphate (CCD ID: S1P) (formula: C₁₈H₃₈NO₅P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	R	1	Total	C	N	O	P	0
			25	18	1	5	1	

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total	C	N	O	0
			14	8	1	5	

L92	L93	A94	G95	V96	T99	A127	V132	T145	M146	L147	K148	M149	K150	L151	R159	L162	L177	W182	S192	T193	I203	L213	L227	K239	ASN	ILE	SER	LYS	ALA	SER	ARG	S248	K263	V284	Y295	V298	I323	ARG	ILE	MET	SER				
CYS	CYS	LYS	CYS	PRO	SER	GLY	ASP	SER	ALA	GLY	LYS	PHE	LYS	ARG	PRO	ILE	ALA	GLY	MET	GLU	PHE	SER	ARG	SER	LYS	ASP	ASN	ASN	PRO	PRO	GLU	GLU	THR	ILE	MET	SER	SER	GLY	ASN	VAL	ASN	SER	SER	SER	SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	449331	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 ($e^-/\text{\AA}^2$)	24.65	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	62.165	Depositor
Minimum map value	-34.994	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.975	Depositor
Recommended contour level	2	Depositor
Map size (Å)	277.248, 277.248, 277.248	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, S1P

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	0.23	0/2603	0.33	0/3534
2	A	0.32	1/1789 (0.1%)	0.39	0/2404
3	G	0.17	0/411	0.29	0/558
4	R	0.54	4/2326 (0.2%)	0.73	4/3170 (0.1%)
All	All	0.37	5/7129 (0.1%)	0.51	4/9666 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	145	THR	C-O	-6.27	1.16	1.24
4	R	146	MET	C-O	-6.20	1.16	1.24
4	R	192	SER	CA-CB	-5.30	1.45	1.53
4	R	79	PRO	C-O	-5.25	1.17	1.24
2	A	351	CYS	C-O	-5.11	1.17	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	65	PHE	CB-CA-C	-6.53	100.63	110.88
4	R	145	THR	CB-CA-C	-5.94	101.56	110.88
4	R	193	THR	CA-CB-OG1	-5.75	100.98	109.60
4	R	145	THR	CA-CB-OG1	-5.51	101.33	109.60

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	B	2556	0	2435	13	0
2	A	1759	0	1734	9	0
3	G	405	0	402	2	0
4	R	2276	0	2330	25	0
5	R	25	0	36	0	0
6	R	14	0	13	0	0
All	All	7035	0	6950	45	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 3.

All (45) 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:333:ASP:O	1:B:334:SER:OG	2.06	0.74
4:R:60:ILE:O	4:R:64:ILE:HG12	1.90	0.71
4:R:149:MET:O	4:R:149:MET:HG3	1.99	0.62
1:B:225:HIS:CG	1:B:245:SER:HG	2.18	0.62
2:A:251:ASP:OD1	2:A:255:ASN:ND2	2.34	0.61
2:A:254:CYS:O	2:A:317:LYS:NZ	2.34	0.61
4:R:162:LEU:HD23	4:R:162:LEU:O	2.04	0.56
4:R:162:LEU:HD23	4:R:162:LEU:C	2.31	0.54
1:B:86:THR:O	1:B:87:THR:OG1	2.19	0.53
4:R:32:THR:HA	4:R:284:VAL:CG1	2.40	0.52
4:R:192:SER:OG	4:R:203:ILE:CD1	2.57	0.52
4:R:70:ILE:HA	4:R:76:PHE:HD2	1.75	0.51
1:B:225:HIS:CE1	1:B:245:SER:HG	2.29	0.51
1:B:196:THR:HG22	1:B:196:THR:O	2.11	0.51
4:R:74:LYS:HA	4:R:77:HIS:CE1	2.47	0.49
2:A:34:VAL:HG22	4:R:151:LEU:HD21	1.94	0.49
4:R:132:VAL:HG12	4:R:213:LEU:HD23	1.95	0.48
4:R:32:THR:HA	4:R:284:VAL:HG13	1.96	0.48
4:R:147:LEU:HD13	4:R:227:LEU:HD11	1.95	0.48
4:R:20:VAL:HG12	4:R:20:VAL:O	2.13	0.48
2:A:247:MET:HE1	2:A:287:TYR:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:60:ILE:HG23	4:R:92:LEU:CD1	2.45	0.47
4:R:60:ILE:HG23	4:R:92:LEU:HD13	1.98	0.46
1:B:88:ASN:HB2	2:A:16:SER:HB2	1.97	0.46
4:R:295:TYR:O	4:R:298:VAL:HG12	2.16	0.45
4:R:62:GLU:O	4:R:65:PHE:HB2	2.17	0.44
4:R:148:LYS:HD3	4:R:148:LYS:HA	1.60	0.44
4:R:177:LEU:HD23	4:R:182:TRP:CZ3	2.53	0.44
1:B:48:ARG:NH2	3:G:62:ARG:HD2	2.33	0.43
4:R:76:PHE:CD1	4:R:76:PHE:N	2.86	0.43
1:B:160:SER:HB3	1:B:190:LEU:HD23	2.00	0.43
2:A:247:MET:HE1	2:A:287:TYR:HE1	1.82	0.43
2:A:201:VAL:HG22	2:A:201:VAL:O	2.19	0.43
2:A:353:LEU:HD23	2:A:353:LEU:HA	1.85	0.42
4:R:79:PRO:HA	4:R:82:TYR:CD2	2.55	0.42
4:R:94:ALA:HA	4:R:127:ALA:HB1	2.01	0.42
1:B:292:PHE:CD1	1:B:292:PHE:N	2.86	0.41
4:R:76:PHE:N	4:R:76:PHE:HD1	2.17	0.41
1:B:256:ARG:NH2	3:G:36:ASP:OD2	2.54	0.41
1:B:333:ASP:C	1:B:334:SER:HG	2.19	0.41
4:R:96:VAL:O	4:R:99:THR:OG1	2.33	0.40
4:R:162:LEU:O	4:R:162:LEU:CD2	2.69	0.40
1:B:102:THR:HG22	1:B:103:CYS:N	2.36	0.40
1:B:298:ASP:O	1:B:301:LYS:O	2.38	0.40
2:A:247:MET:HE1	2:A:287:TYR:OH	2.21	0.40

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	336/340 (99%)	319 (95%)	17 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	219/379 (58%)	207 (94%)	12 (6%)	0	100	100
3	G	54/71 (76%)	54 (100%)	0	0	100	100
4	R	286/392 (73%)	277 (97%)	9 (3%)	0	100	100
All	All	895/1182 (76%)	857 (96%)	38 (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	B	270/283 (95%)	269 (100%)	1 (0%)	84	90
2	A	187/326 (57%)	185 (99%)	2 (1%)	65	83
3	G	38/58 (66%)	38 (100%)	0	100	100
4	R	243/349 (70%)	240 (99%)	3 (1%)	63	82
All	All	738/1016 (73%)	732 (99%)	6 (1%)	70	86

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	234	PHE
2	A	271	LYS
2	A	298	GLU
4	R	148	LYS
4	R	159	ARG
4	R	283	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	241	ASN
4	R	77	HIS

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Mol	Chain	Res	Type
4	R	157	ASN
4	R	199	HIS
4	R	315	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
5	S1P	R	401	-	23,24,24	1.75	4 (17%)	22,28,28	1.71	5 (22%)
6	NAG	R	402	4	14,14,15	1.05	1 (7%)	17,19,21	1.54	4 (23%)

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
5	S1P	R	401	-	-	6/25/25/25	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	R	402	4	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	401	S1P	P22-O1	6.72	1.81	1.60
5	R	401	S1P	C1-C2	2.74	1.57	1.51
5	R	401	S1P	O1-C1	-2.65	1.34	1.44
6	R	402	NAG	O7-C7	-2.47	1.17	1.23
5	R	401	S1P	O3-C3	-2.09	1.39	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	401	S1P	O1-P22-O25	-4.27	94.91	106.44
5	R	401	S1P	O3-C3-C2	3.62	113.40	107.31
5	R	401	S1P	O24-P22-O23	3.50	120.94	107.80
6	R	402	NAG	C8-C7-N2	2.56	120.36	116.12
6	R	402	NAG	O5-C1-C2	-2.54	107.36	111.29
6	R	402	NAG	C2-N2-C7	-2.35	119.74	122.90
6	R	402	NAG	O7-C7-C8	-2.10	118.31	122.05
5	R	401	S1P	C3-C4-C5	-2.10	120.33	124.69
5	R	401	S1P	O23-P22-O1	-2.08	101.25	106.67

There are no chirality outliers.

All (6) torsion outliers are listed below:

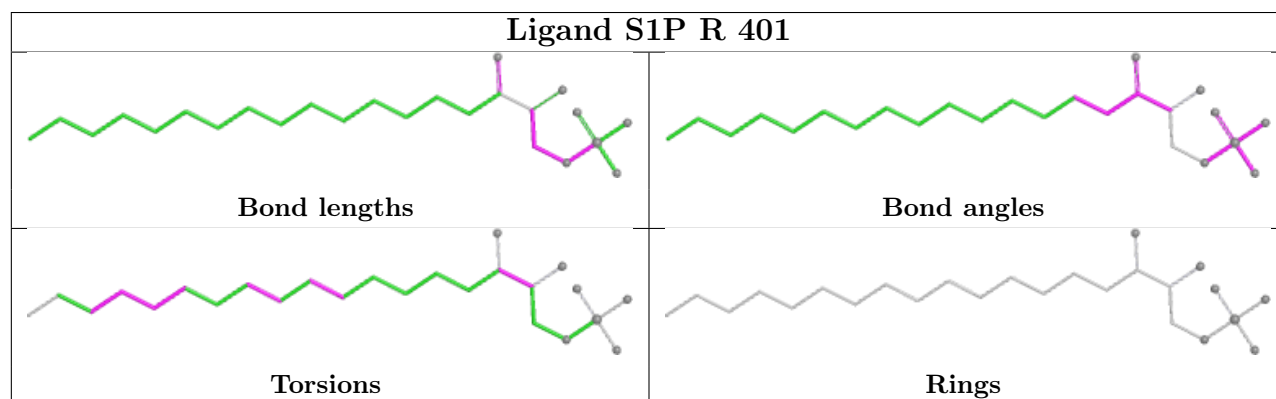
Mol	Chain	Res	Type	Atoms
5	R	401	S1P	C9-C10-C11-C12
5	R	401	S1P	C1-C2-C3-C4
5	R	401	S1P	C13-C14-C15-C16
5	R	401	S1P	C7-C8-C9-C10
5	R	401	S1P	C14-C15-C16-C17
5	R	401	S1P	C12-C13-C14-C15

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.

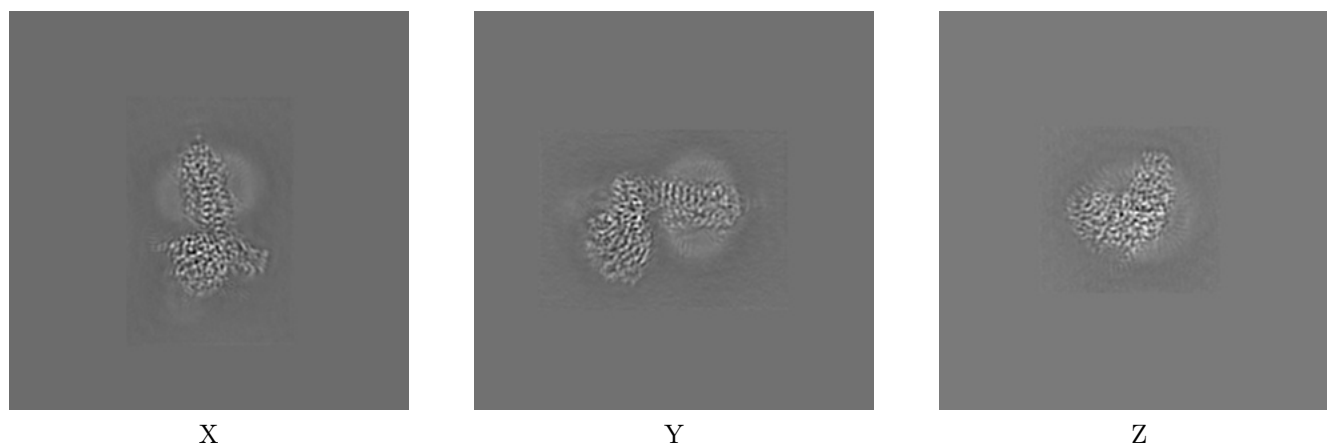
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25822. 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](#)

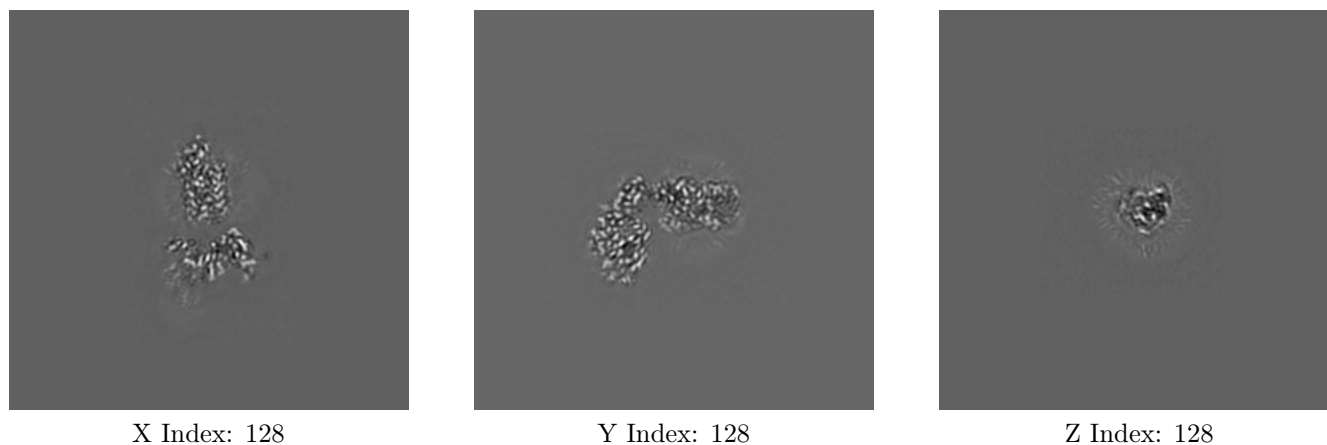
6.1.1 Primary map



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

6.2 Central slices [i](#)

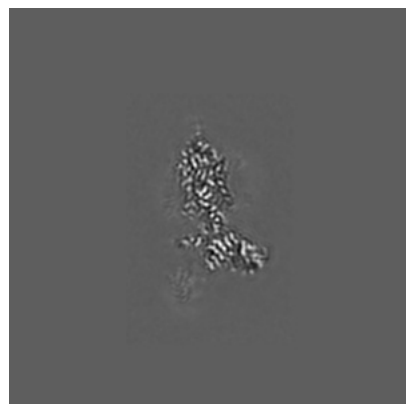
6.2.1 Primary map



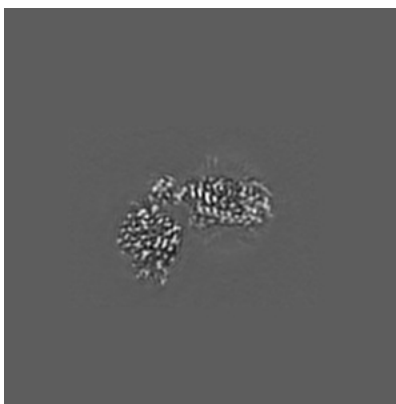
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 133



Y Index: 126

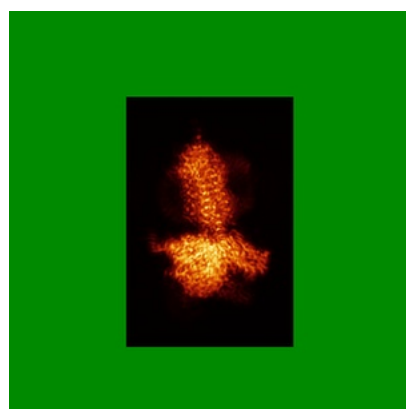


Z Index: 103

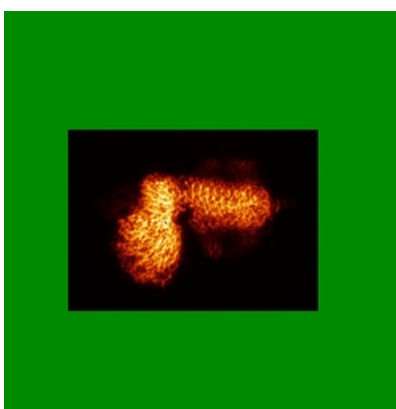
The images above show the largest variance slices of the map in three orthogonal directions.

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

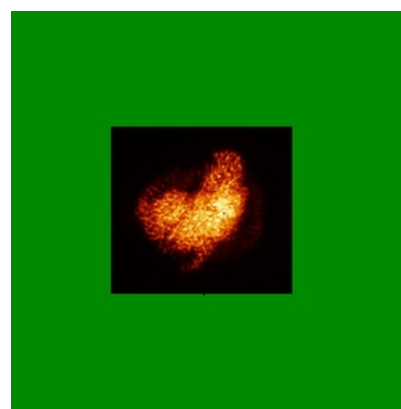
6.4.1 Primary map



X



Y

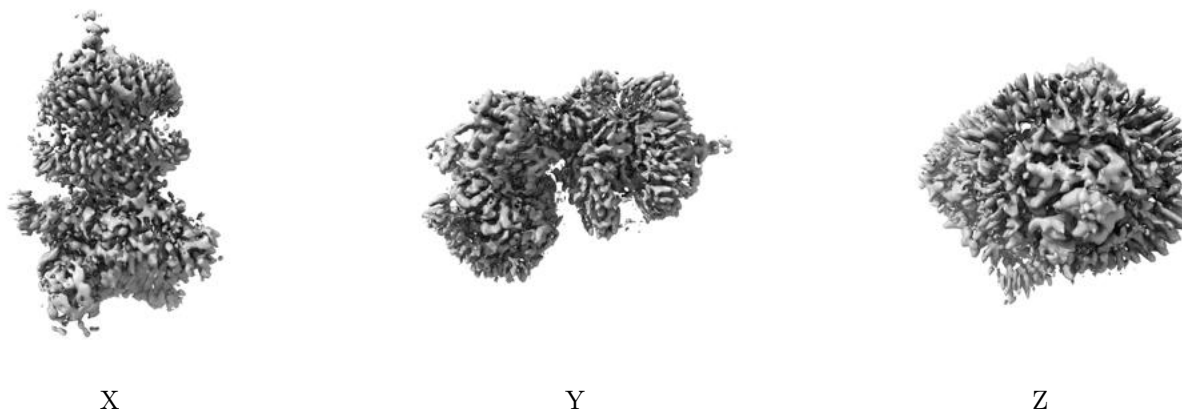


Z

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

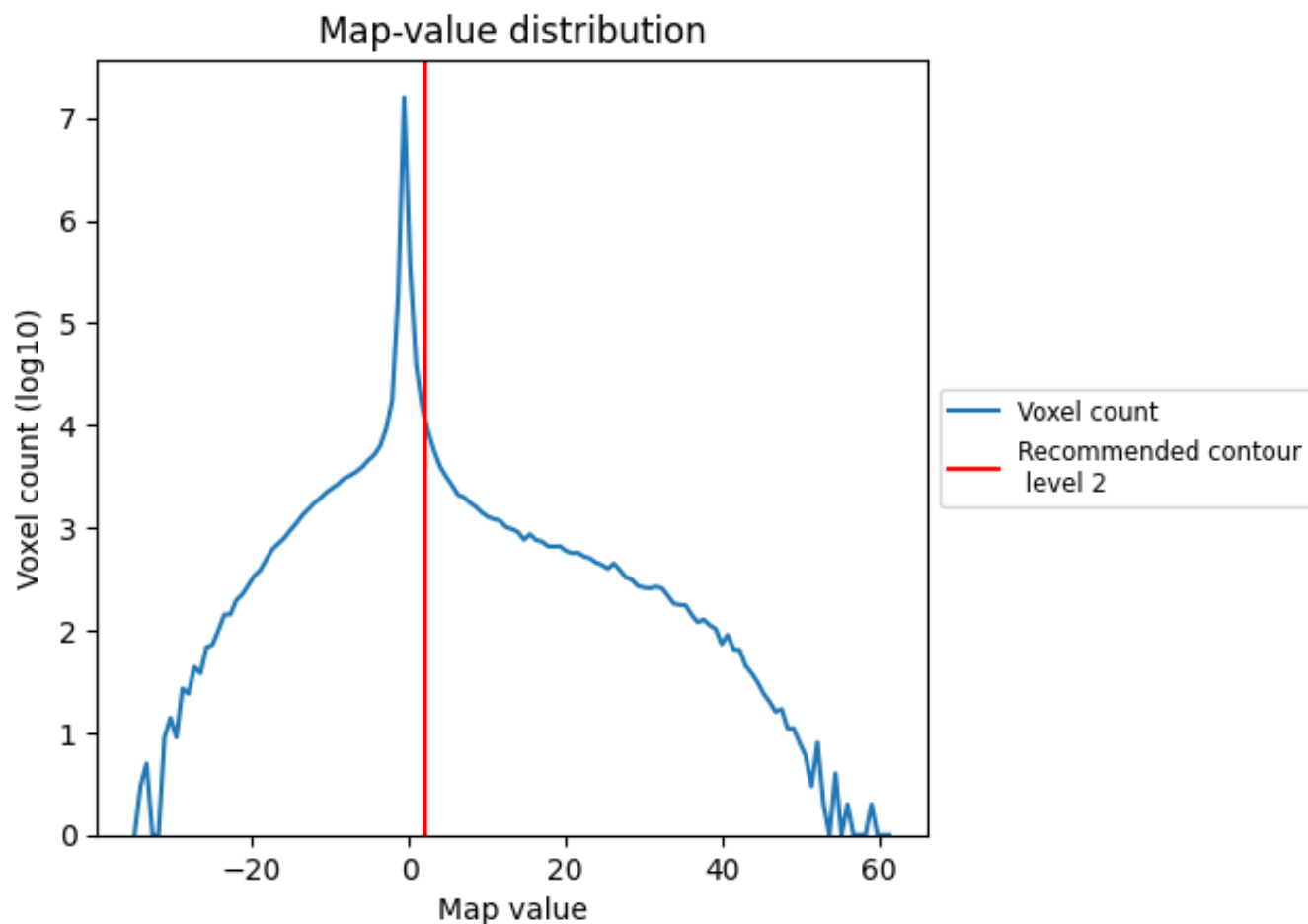
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

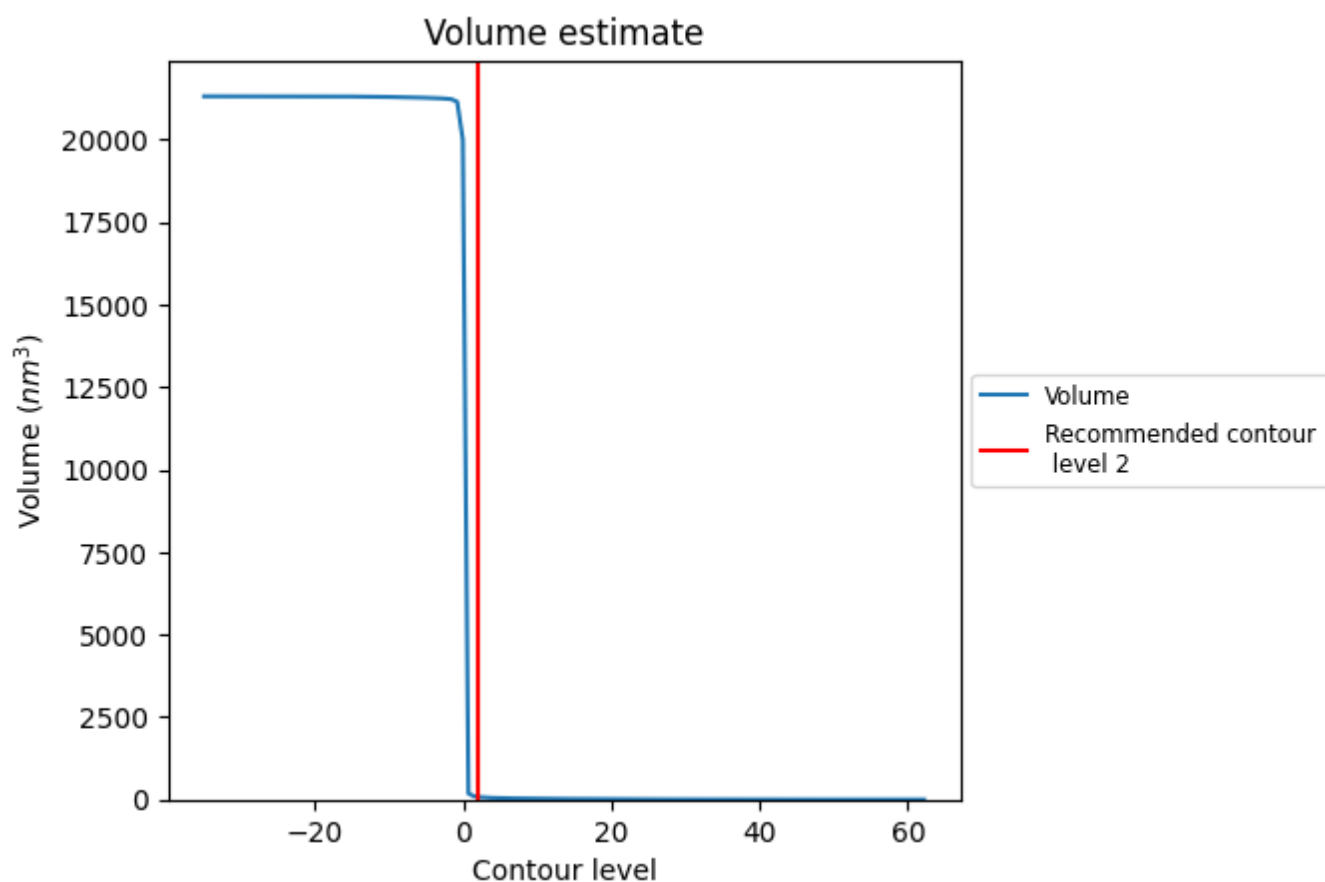
This section contains the results of statistical analysis of the map.

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.

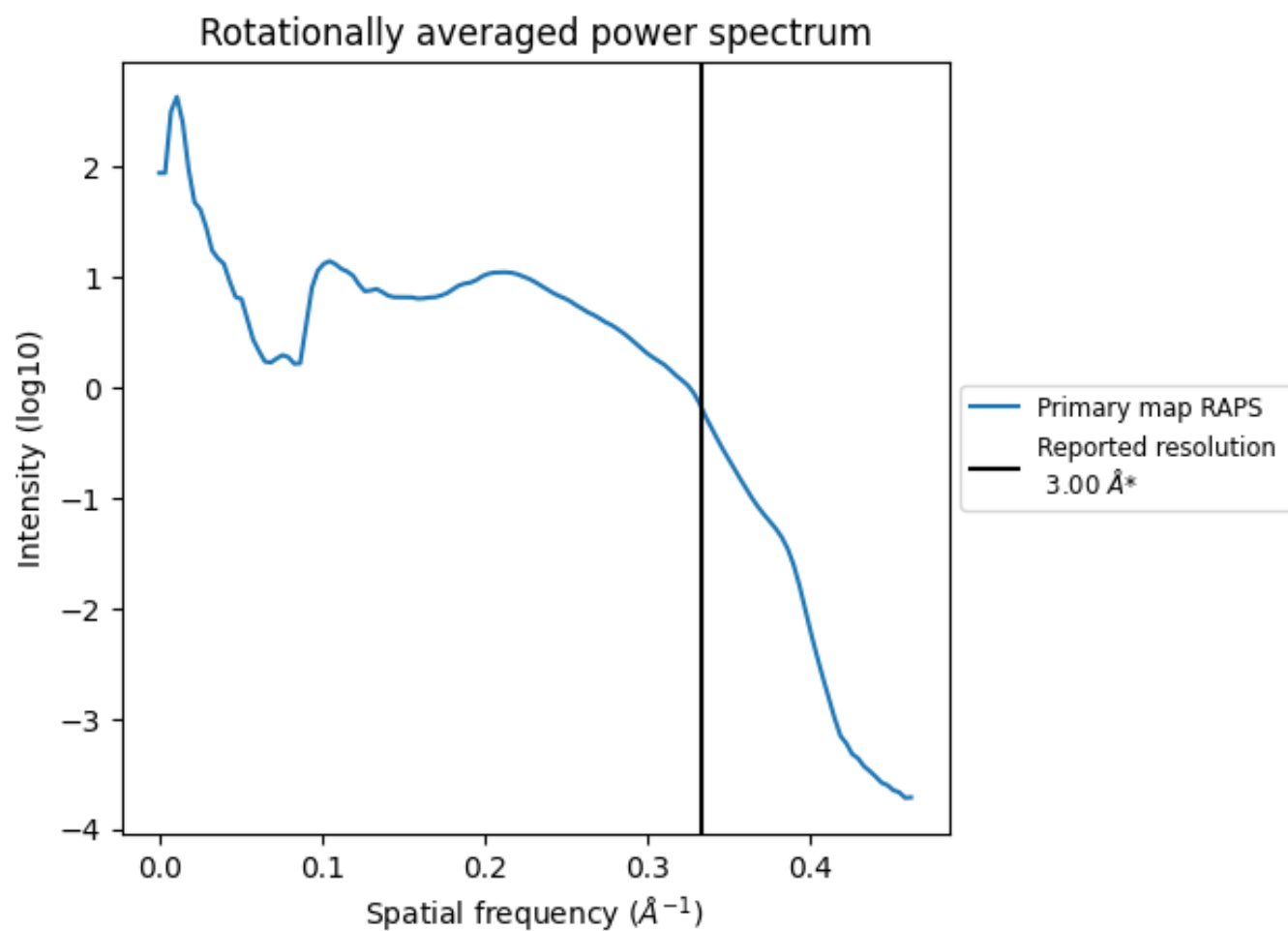
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 81 nm^3 ; this corresponds to an approximate mass of 73 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 0.333 Å⁻¹

8 Fourier-Shell correlation

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

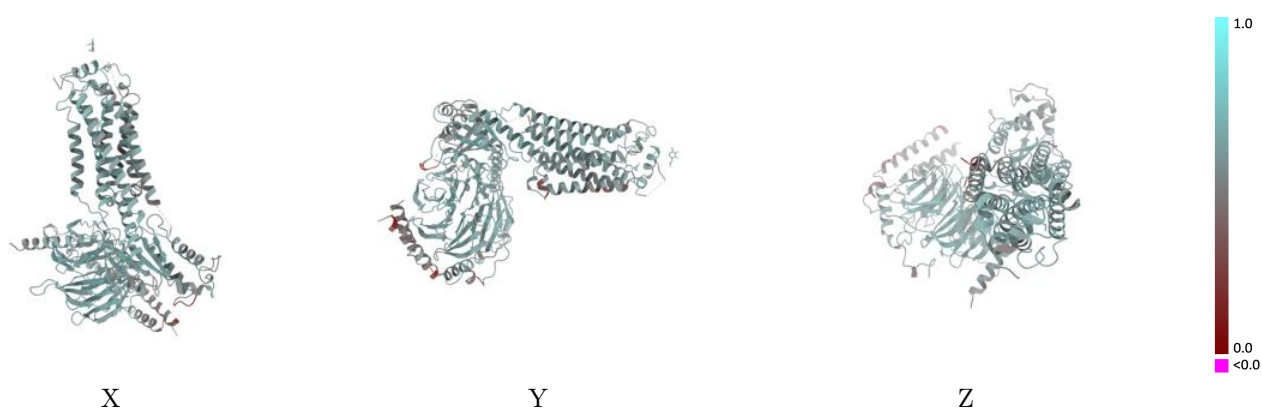
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-25822 and PDB model 7TD3. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

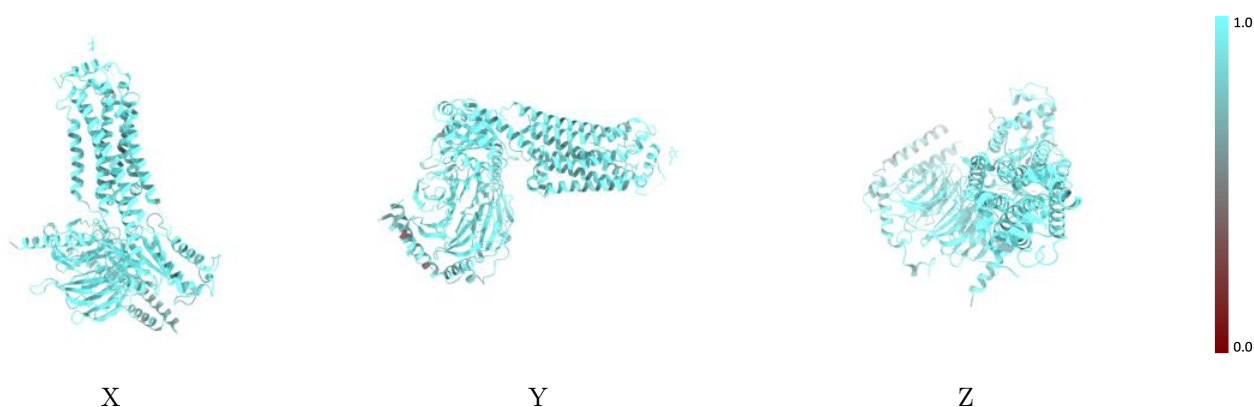
This section was not generated.

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



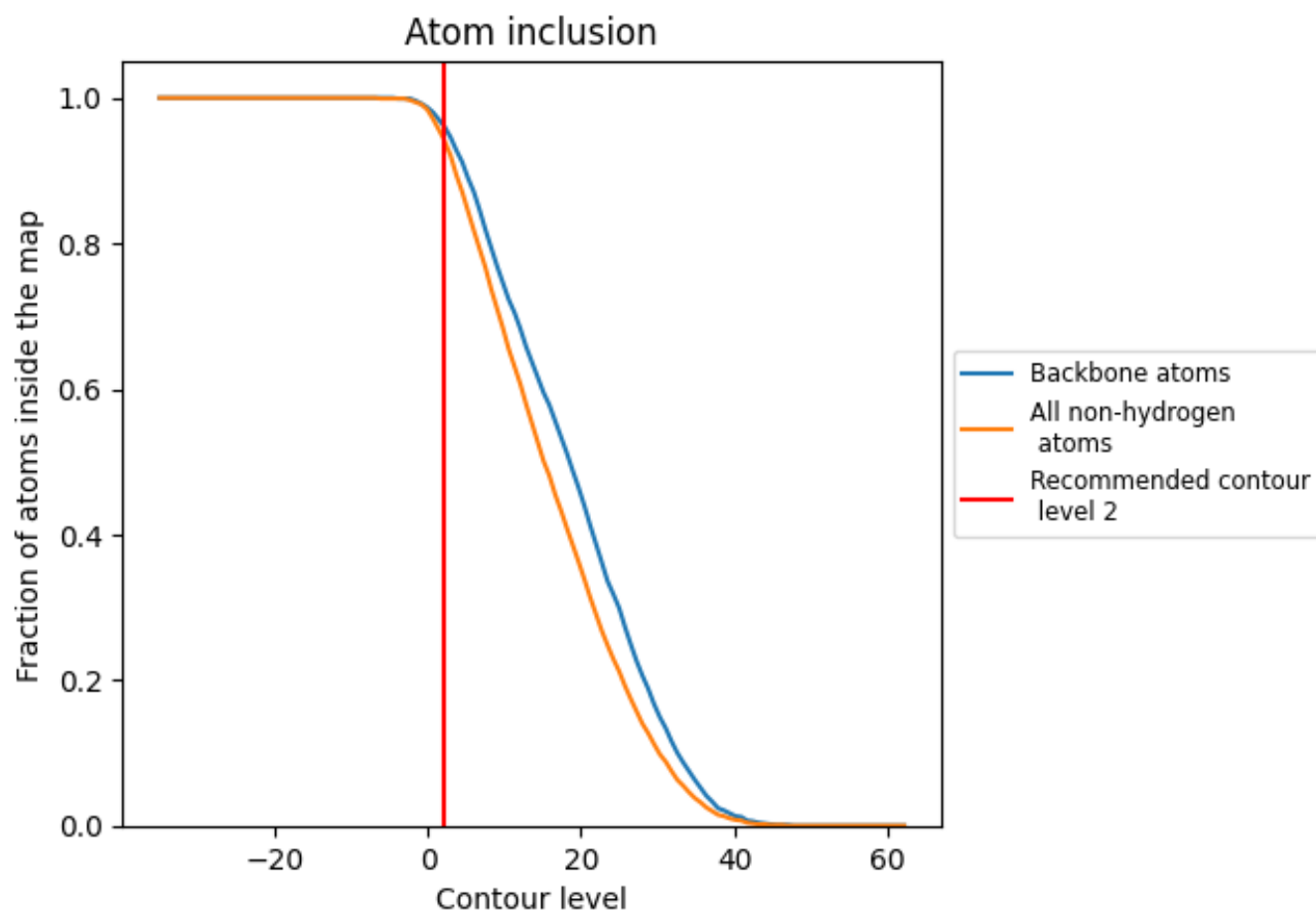
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9450	0.5740
A	0.9510	0.5690
B	0.9490	0.5930
G	0.8720	0.5280
R	0.9480	0.5660

