



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:17 PM UTC

PDB ID : 7S1X / pdb_00007s1x
EMDB ID : EMD-24807
Title : Cryo-EM structure of human NKCC1 K289NA492EL671C bound with bumetanide
Authors : Zhao, Y.X.; Cao, E.H.
Deposited on : 2021-09-02
Resolution : 2.90 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.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

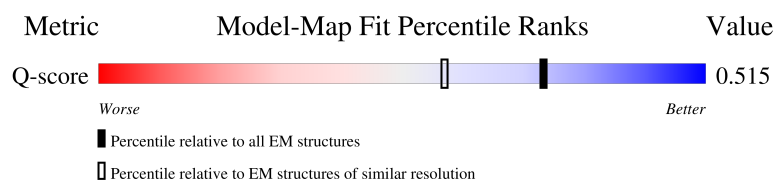
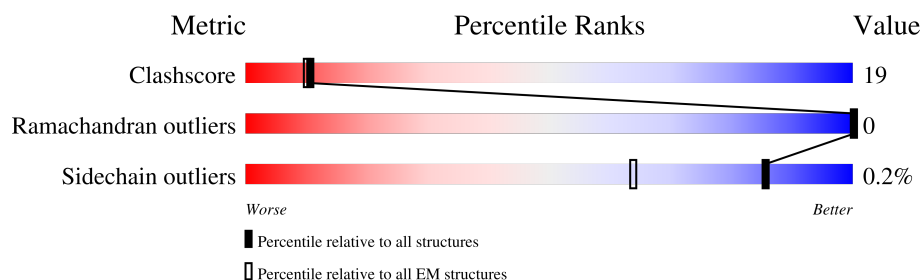
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	1216	 46% 26% 28%
1	B	1216	 46% 25% 28%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	A	1303	-	-	X	-
4	CL	B	1303	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12658 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.

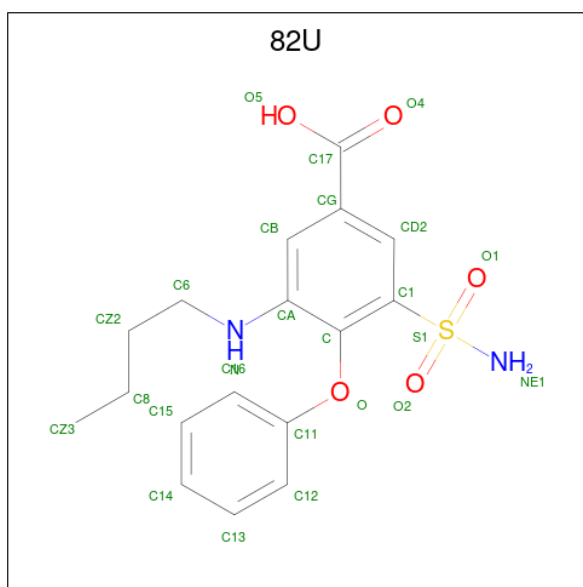
- Molecule 1 is a protein called Solute carrier family 12 member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	871	Total	C	N	O	S	0	0
			6302	4115	1063	1088	36		
1	A	871	Total	C	N	O	S	0	0
			6302	4115	1063	1088	36		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P55011
B	-2	ALA	-	expression tag	UNP P55011
B	-1	MET	-	expression tag	UNP P55011
B	0	GLY	-	expression tag	UNP P55011
B	1	SER	-	expression tag	UNP P55011
B	289	ASN	LYS	engineered mutation	UNP P55011
B	492	GLU	ALA	engineered mutation	UNP P55011
B	671	CYS	LEU	engineered mutation	UNP P55011
A	-3	GLY	-	expression tag	UNP P55011
A	-2	ALA	-	expression tag	UNP P55011
A	-1	MET	-	expression tag	UNP P55011
A	0	GLY	-	expression tag	UNP P55011
A	1	SER	-	expression tag	UNP P55011
A	289	ASN	LYS	engineered mutation	UNP P55011
A	492	GLU	ALA	engineered mutation	UNP P55011
A	671	CYS	LEU	engineered mutation	UNP P55011

- Molecule 2 is 3-(butylamino)-4-phenoxy-5-sulfamoylbenzoic acid (CCD ID: 82U) (formula: C₁₇H₂₀N₂O₅S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total	C	N	O	S	0
			25	17	2	5	1	
2	A	1	Total	C	N	O	S	0
			25	17	2	5	1	

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	K	0
			1	1	
3	A	1	Total	K	0
			1	1	

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total	Cl	0
			1	1	
4	A	1	Total	Cl	0
			1	1	



L722	C723	C724	I725	V726	M727	I730	M731	W732	W733	A734	A735	L736	L737	V740	I741	Y746	W758	G759	A764	L765	T766	Y767	L771	Q772	H773	S774	I775	S778	G779	V780	K785	M786	F787	Q790	C791	L792	V793	M794	A797	S800	A803	L804	L805	V808	F811									
L817	C820	V918	V919	R828	M832	M835	D838	Y842	L846	M851	F854	P857	V858	H859	A860	D861	D862	L863	R864	E865	G866	A867	L870	M871	Q872	A873	A874	G875	L876	G877	R878	M879	K880	L884	V885	L886	G887	F888	M897	R898	D899	V900	D901	M902	Y903	I904								
F907	H908	V918	V919	R828	M832	M835	D838	Y842	L846	M851	F854	P857	V858	H859	A860	D861	D862	L863	R864	E865	G866	A867	L870	M871	Q872	A873	A874	G875	L876	G877	R878	M879	K880	L884	V885	L886	G887	F888	M897	R898	D899	V900	D901	M902	Y903	I904								
L920	R921	E924	G925	L926	ASP	ILE	SER	SER	HIS	LEU	GLN	GLY	GLN	GLU	LEU	SER	PRO	GLN	LYS	SER	PRO	GLY	THR	LYS	ASP	VAL	VAL	SER	GLN	VAL	GLU	TVR	SER	LYS	LYS	SER	ASP	LEU	ASP	LYS	PRO	LEU	SER	GLU	LYS	PRO	ILE	THR	HIS					
LYS	VAL	GLU	GLU	ASP	GLY	LYS	THR	ALA	THR	GLN	PRO	LEU	LYS	LYS	GLN	SER	GLY	PRO	ILE	VAL	PRO	LEU	ASN	VAL	ALA	ASP	GLN	LYS	LEU	LEU	ALA	SER	THR	GLN	PHE	GLN	LYS	LYS	GLN	GLY	LYS	N1022	T1023	I1024	D1025	V1026	W1027	W1028	D1032	G1033	G1034	L1035	T1036	L1037
L1038	I1039	P1040	Y1041	L1042	L1043	T1044	W1049	C1052	K1053	I1054	R1055	V1056	F1057	M1072	L1076	F1079	R1080	F1083	L1089	G1090	D1091	T1094	K1095	P1096	K1097	K1098	I1101	I1102	A1103	I1107	I1108	Y1111	R1112	L1113	H1114	D1117	K1118	E1119	Q1120	D1121	I1122	K1125	E1130	P1131	W1132									
M1137	E1140	L1141	Y1142	K1143	T1144	K1145	T1146	Y1147	R1148	Q1149	I1150	R1151	L1152	N1153	E1154	L1155	L1156	A1163	V1167	M1168	S1169	L1170	R1174	A1177	V1178	L1182	Y1183	M1184	A1185	W1186	A1189	L1190	S1191	K1192	D1193	L1194	L1199	V1200	R1201	G1202	Q1205	S1206	V1207	F1210	Y1211	S1212								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	504481	Depositor
Resolution determination method	DIFFRACTION PATTERN/LAYERLINES	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.175	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.478	Depositor
Minimum map value	-3.239	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.6	Depositor
Map size ($\text{\AA}$)	271.36, 271.36, 271.36	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, K, 82U

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	0.23	0/6451	0.47	0/8796
1	B	0.23	0/6451	0.47	0/8796
All	All	0.23	0/12902	0.47	0/17592

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

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	6302	0	6014	245	0
1	B	6302	0	6014	241	0
2	A	25	0	0	0	0
2	B	25	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	2	0
4	B	1	0	0	2	0
All	All	12658	0	12028	461	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 19.

The worst 5 of 461 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:686:TYR:OH	4:B:1303:CL:CL	2.06	1.10
1:A:686:TYR:OH	4:A:1303:CL:CL	2.06	1.07
1:B:1079:PHE:O	1:A:705:ARG:NH1	2.05	0.88
1:B:705:ARG:NH1	1:A:1079:PHE:O	2.05	0.88
1:B:476:ASN:HA	1:B:546:ARG:HH12	1.42	0.83

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	865/1216 (71%)	779 (90%)	86 (10%)	0	100	100
1	B	865/1216 (71%)	780 (90%)	85 (10%)	0	100	100
All	All	1730/2432 (71%)	1559 (90%)	171 (10%)	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	592/985 (60%)	591 (100%)	1 (0%)	87	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	592/985 (60%)	591 (100%)	1 (0%)	87	96
All	All	1184/1970 (60%)	1182 (100%)	2 (0%)	85	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	298	ASN
1	A	298	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	849	ASN
1	A	843	GLN
1	B	1153	ASN
1	B	849	ASN
1	A	515	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
2	82U	A	1301	3	26,26,26	1.50	5 (19%)	36,36,36	1.34	1 (2%)
2	82U	B	1301	3	26,26,26	1.50	5 (19%)	36,36,36	1.33	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
2	82U	A	1301	3	-	1/19/19/19	0/2/2/2
2	82U	B	1301	3	-	1/19/19/19	0/2/2/2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1301	82U	S1-NE1	5.38	1.70	1.60
2	A	1301	82U	S1-NE1	5.34	1.70	1.60
2	A	1301	82U	CA-N	2.74	1.44	1.37
2	B	1301	82U	CA-N	2.71	1.44	1.37
2	B	1301	82U	O4-C17	2.44	1.29	1.22

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	82U	O2-S1-O1	-6.21	109.25	118.80
2	B	1301	82U	O2-S1-O1	-6.21	109.25	118.80

There are no chirality outliers.

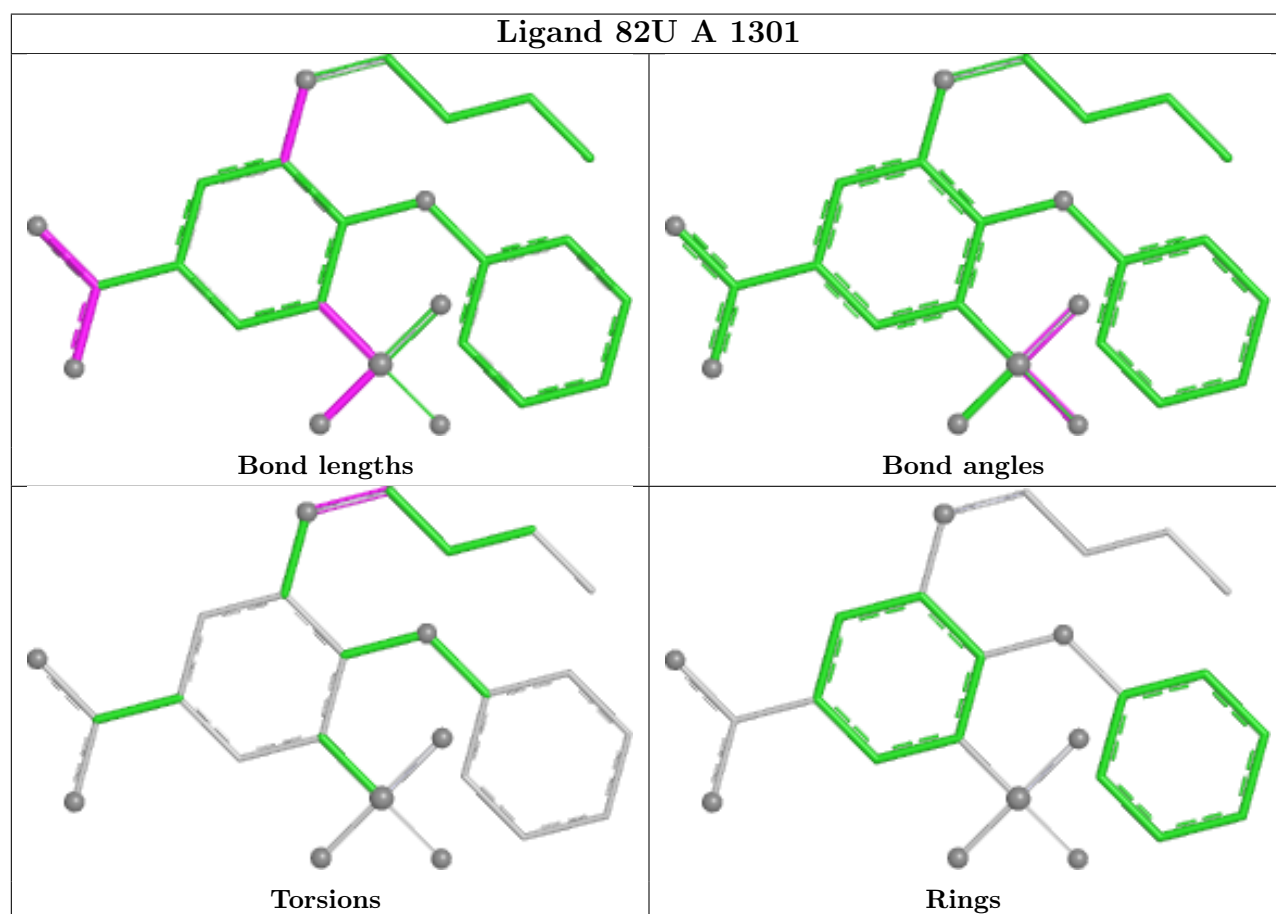
All (2) torsion outliers are listed below:

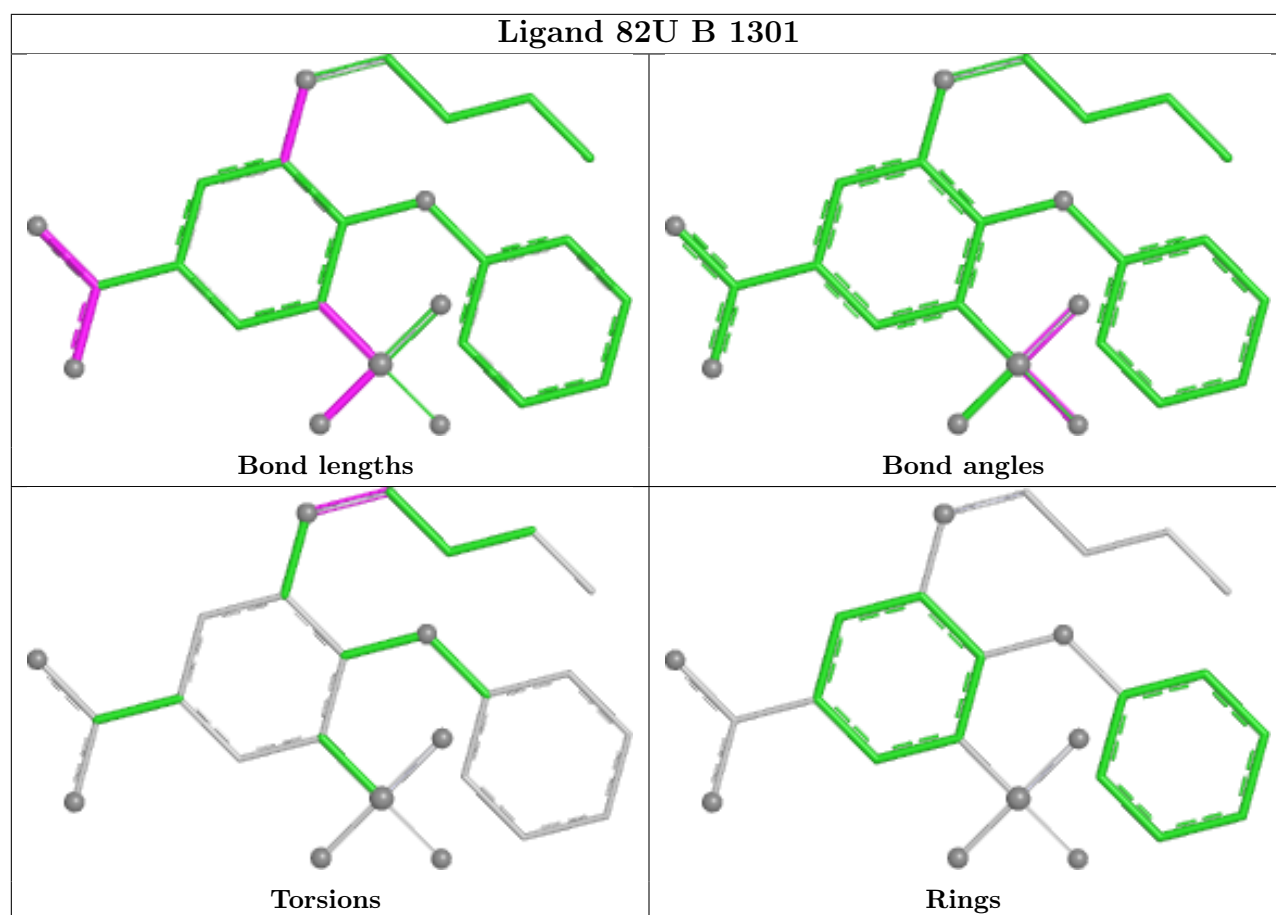
Mol	Chain	Res	Type	Atoms
2	B	1301	82U	CZ2-C6-N-CA
2	A	1301	82U	CZ2-C6-N-CA

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.

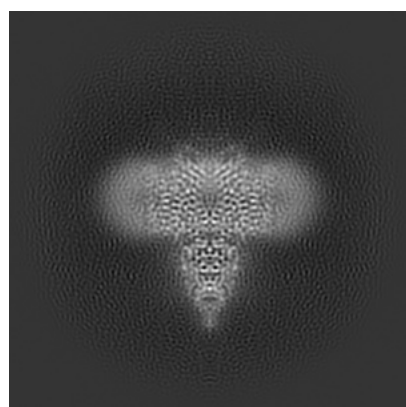
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24807. These allow visual inspection of the internal detail of the map and identification of artifacts.

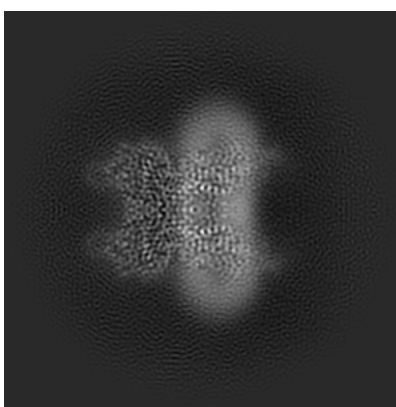
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

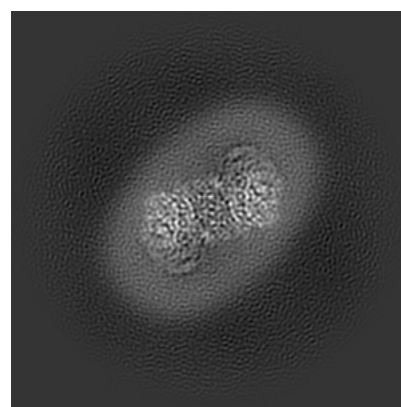
6.1.1 Primary map



X



Y

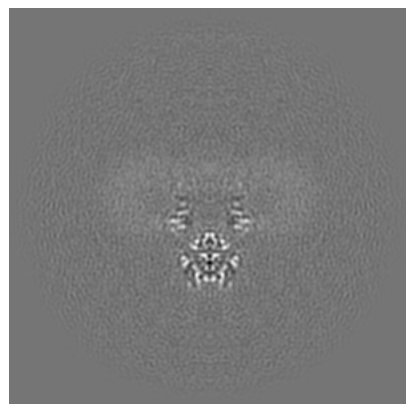


Z

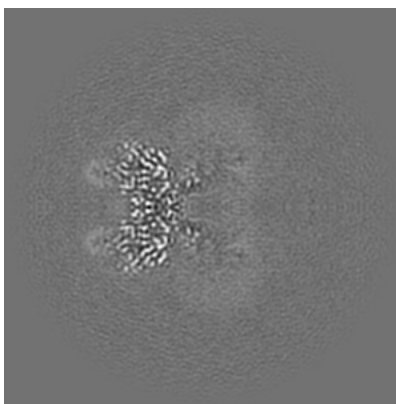
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

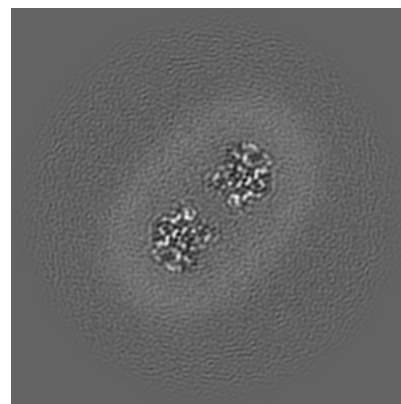
6.2.1 Primary map



X Index: 128



Y Index: 128

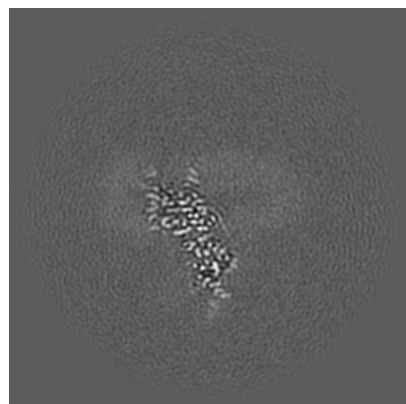


Z Index: 128

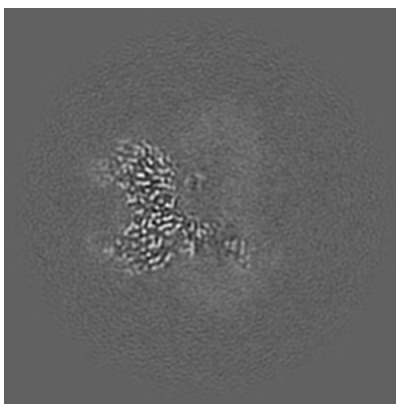
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

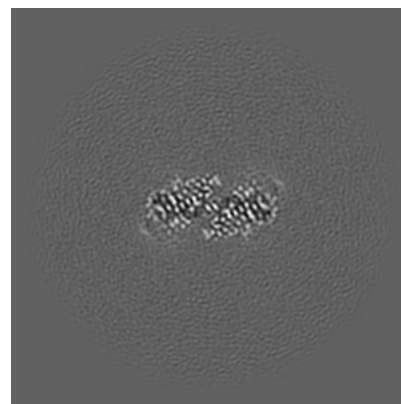
6.3.1 Primary map



X Index: 113



Y Index: 124

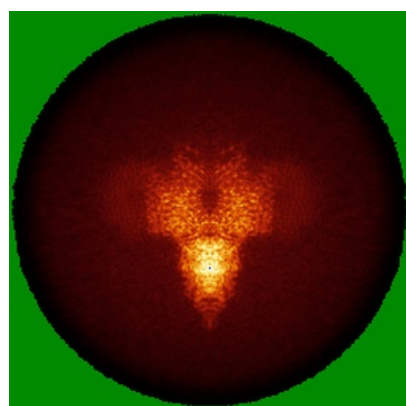


Z Index: 91

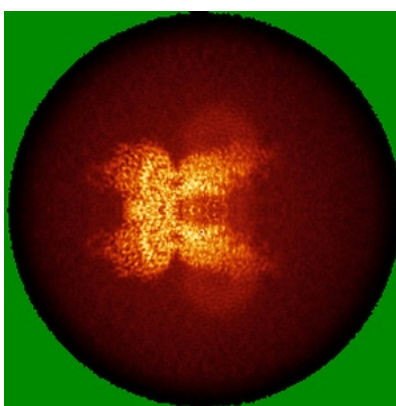
The images above show the largest variance slices of the map in three orthogonal directions.

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

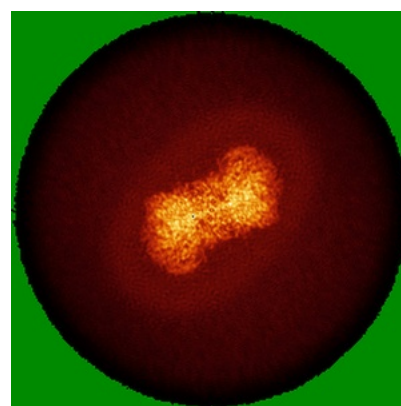
6.4.1 Primary map



X



Y

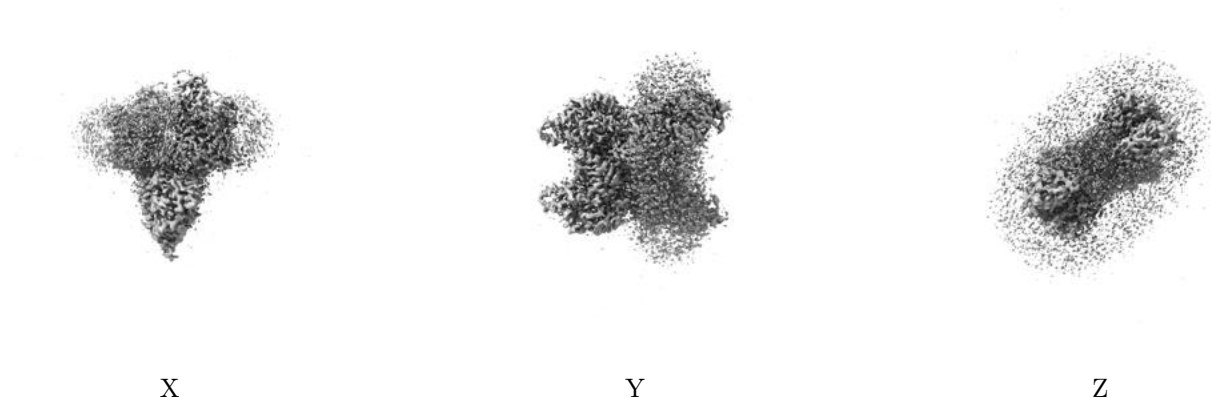


Z

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

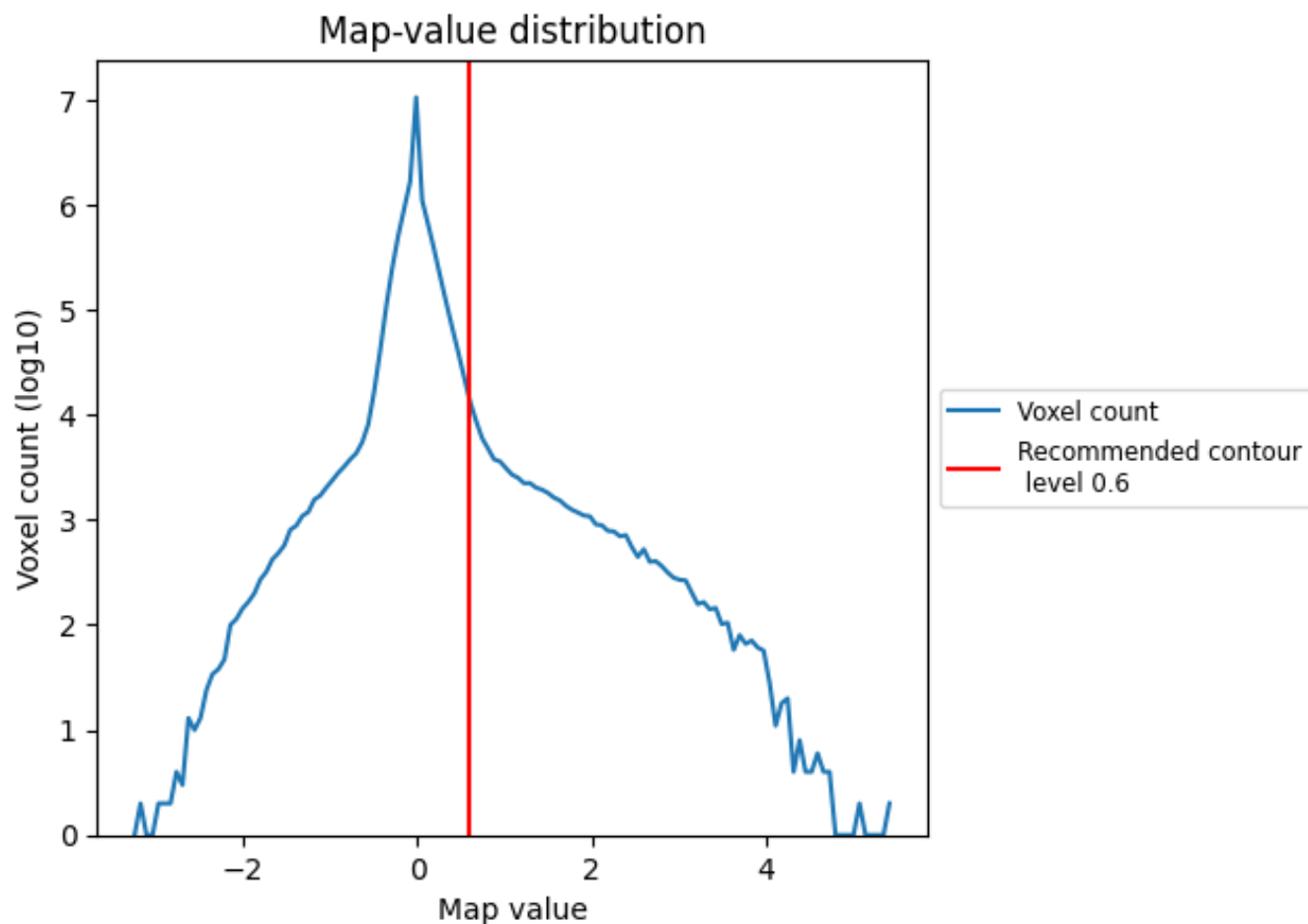
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

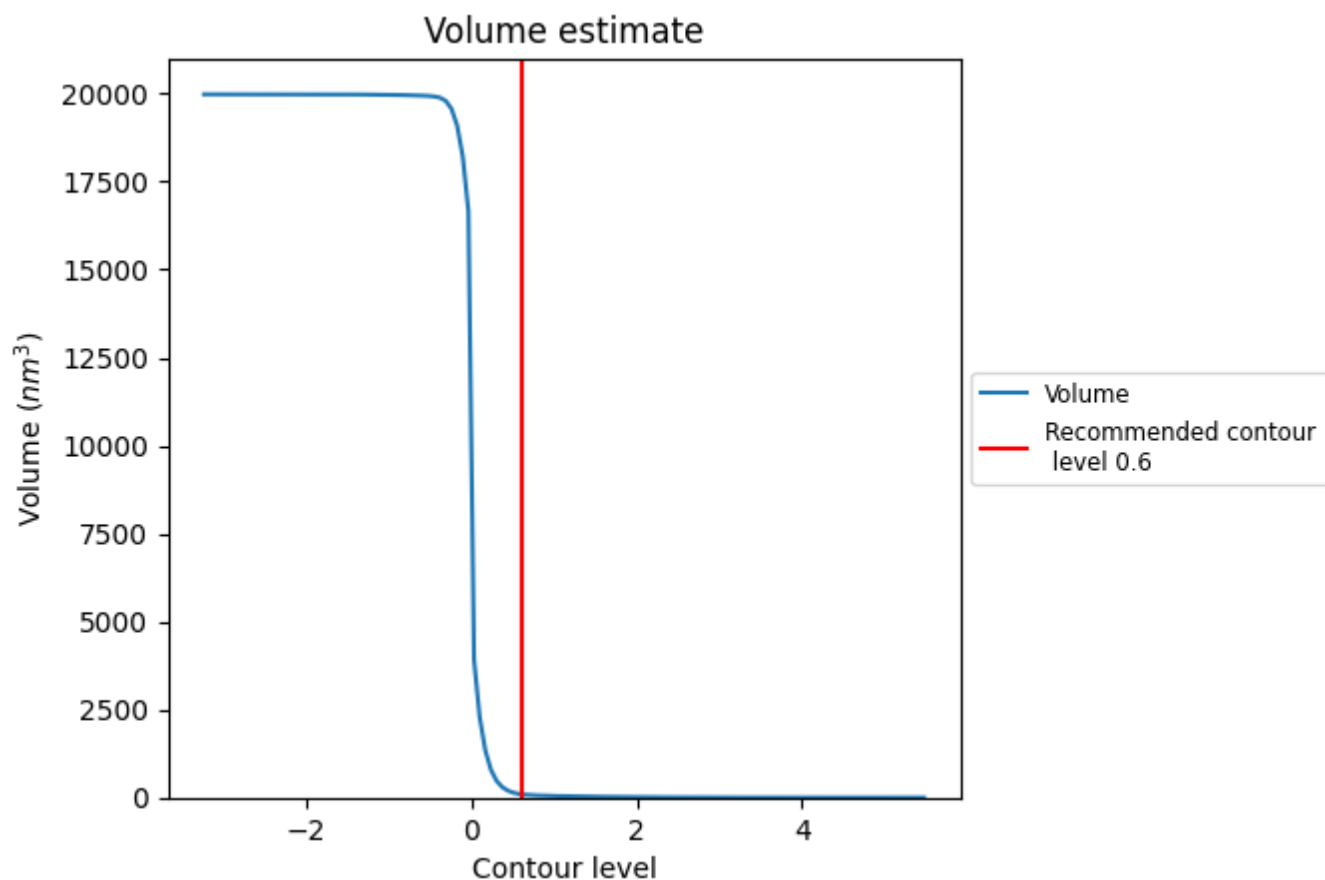
This section contains the results of statistical analysis of the map.

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.

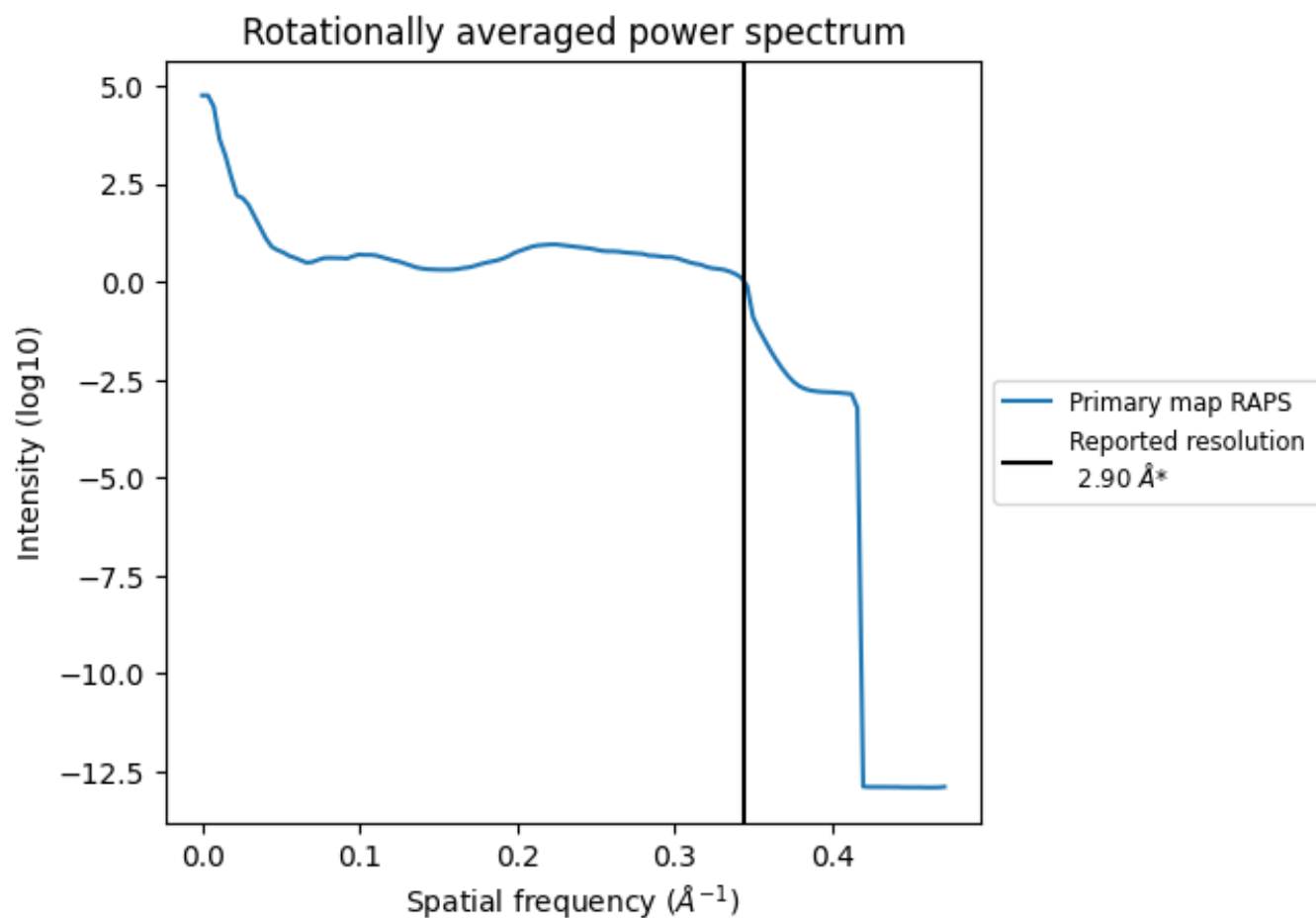
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 96 nm³; this corresponds to an approximate mass of 87 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 0.345 Å⁻¹

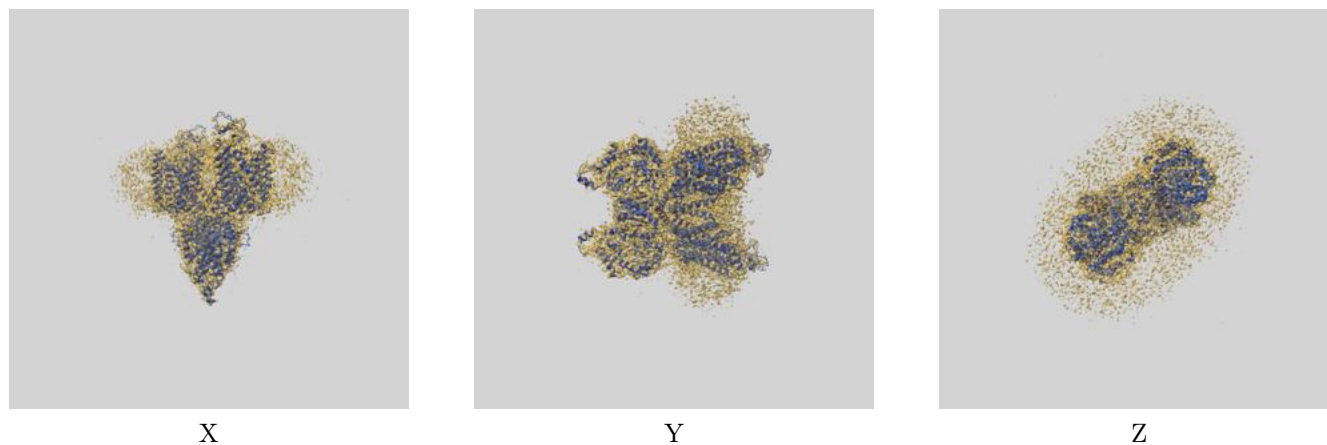
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

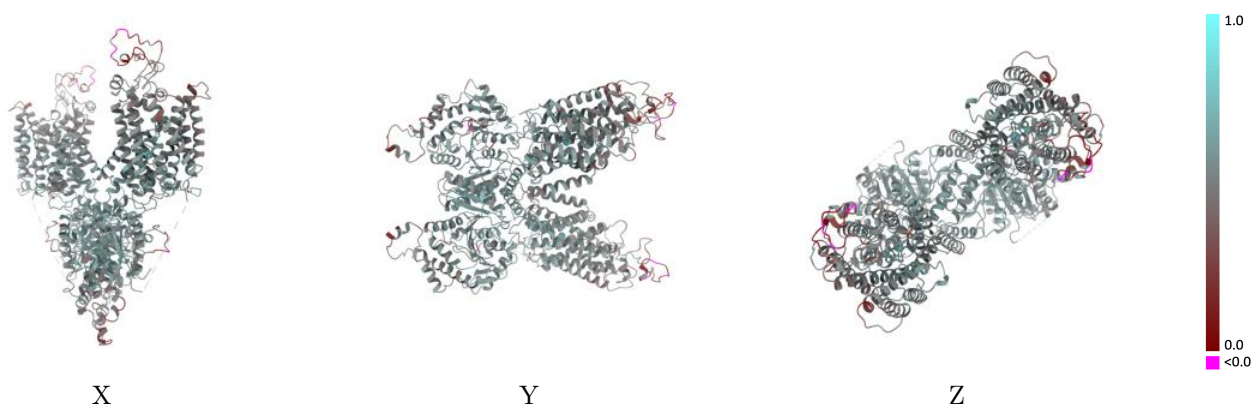
This section contains information regarding the fit between EMDB map EMD-24807 and PDB model 7S1X. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



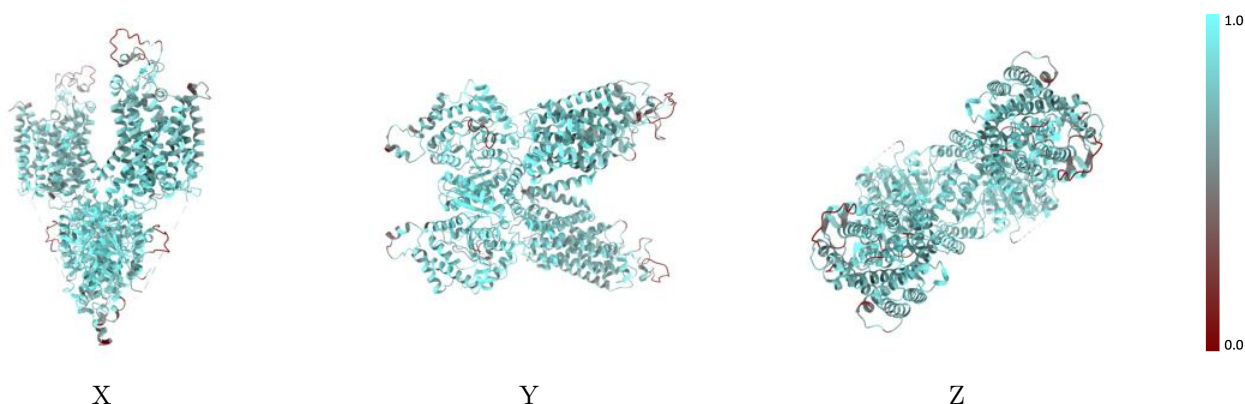
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



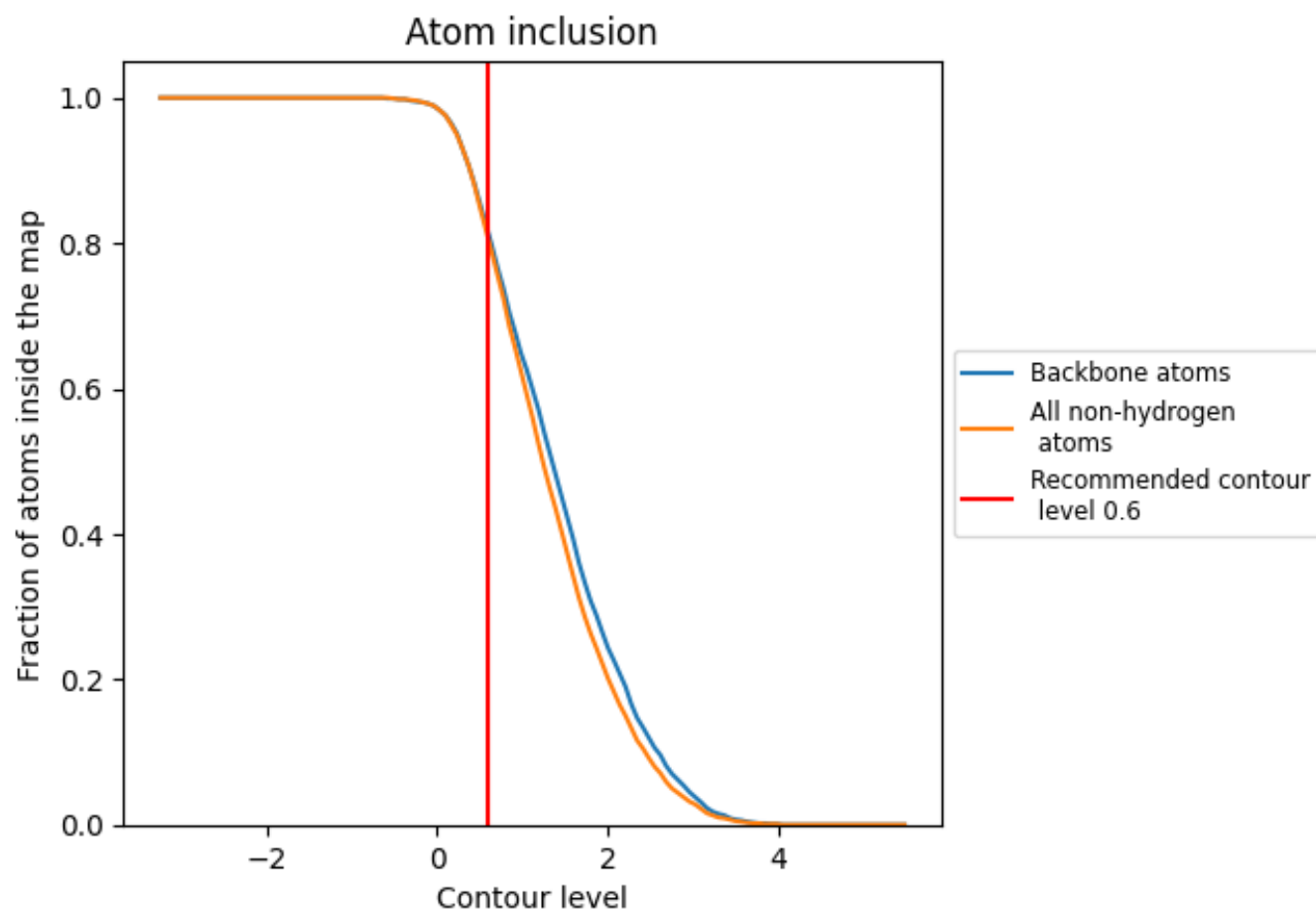
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 82% of all backbone atoms, 81% 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	0.8060	0.5150
A	0.8060	0.5150
B	0.8060	0.5150

