



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:14 PM UTC

PDB ID : 8TYQ / pdb_00008tyq
EMDB ID : EMD-41728
Title : Structure of the C-terminal half of LRRK2 bound to GZD-824 (G2019S mutant)
Authors : Villagran-Suarez, A.; Sanz-Murillo, M.; Alegrio-Louro, J.; Leschziner, A.
Deposited on : 2023-08-25
Resolution : 2.99 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

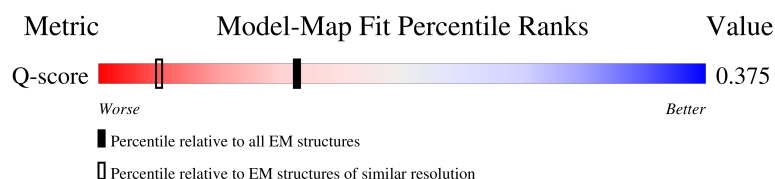
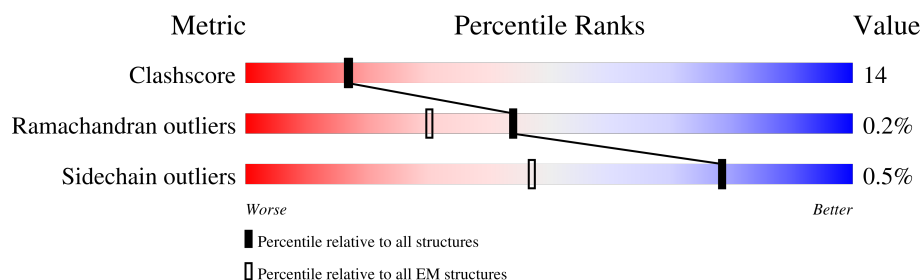
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

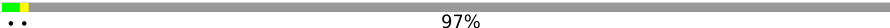
The reported resolution of this entry is 2.99 Å.

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	13287 (2.49 - 3.49)

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	1406	 .. 97%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8529 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 Leucine-rich repeat serine/threonine-protein kinase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	957	Total	C	N	O	S	1	0
			7645	4914	1301	1382	48		

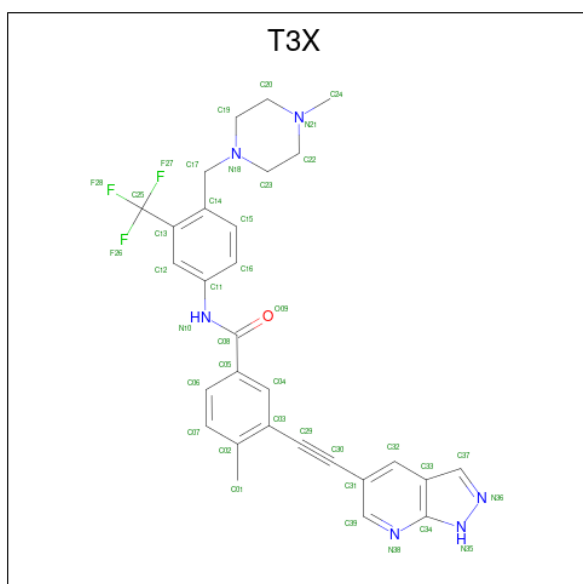
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2019	SER	GLY	engineered mutation	UNP Q5S007

- Molecule 2 is a protein called Designed Ankyrin Repeats Protein E11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	S	0	0
			845	541	142	161	1		

- Molecule 3 is 4-methyl-N-{4-[(4-methylpiperazin-1-yl)methyl]-3-(trifluoromethyl)phenyl}-3-[(1H-pyrazolo[3,4-b]pyridin-5-yl)ethynyl]benzamide (CCD ID: T3X) (formula: C₂₉H₂₇F₃N₆O) (labeled as "Ligand of Interest" by depositor).

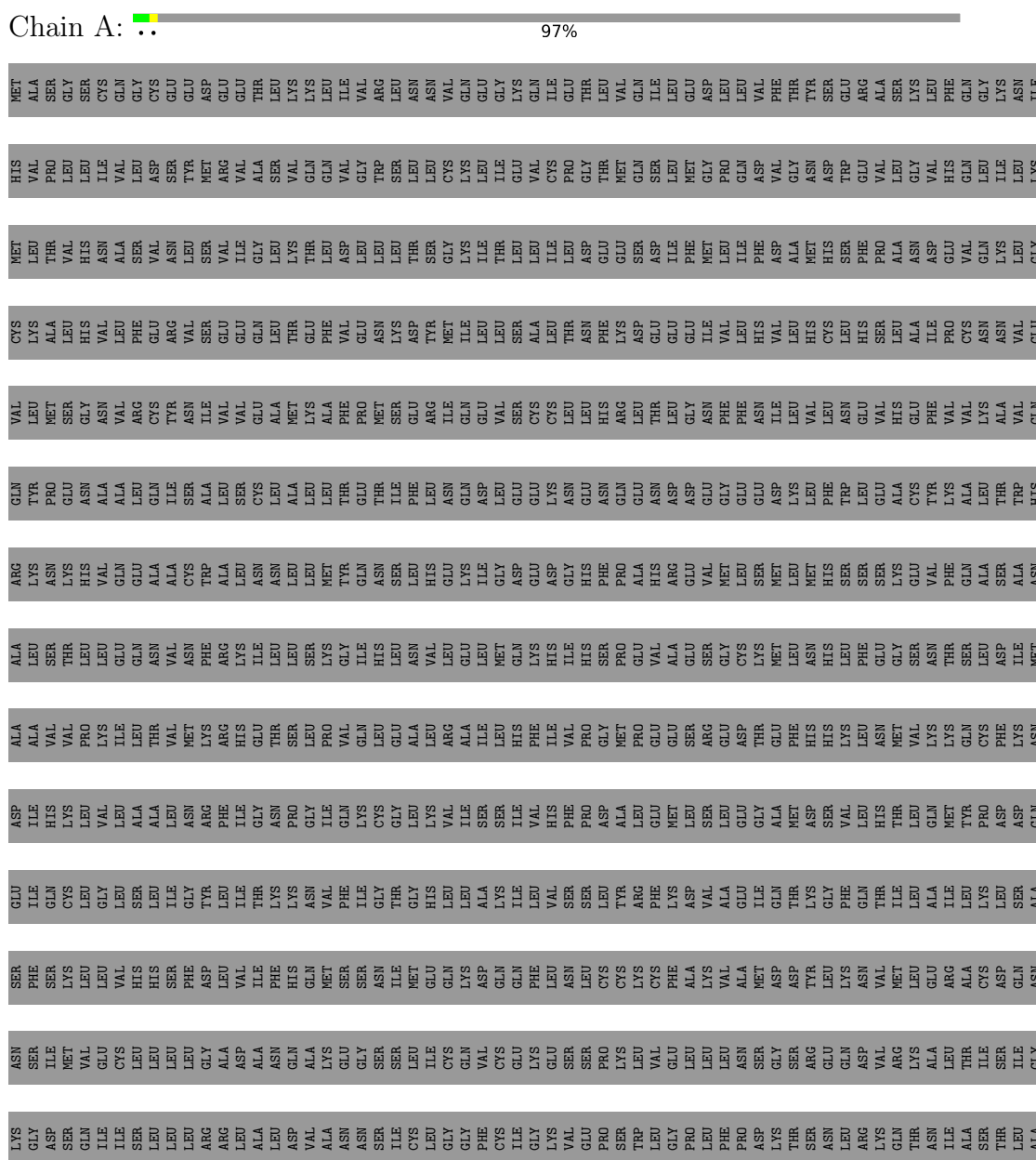


Mol	Chain	Residues	Atoms					AltConf
			Total	C	F	N	O	
3	A	1	39	29	3	6	1	0

3 Residue-property plots

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: Leucine-rich repeat serine/threonine-protein kinase 2



L1390	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG
W1393	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET
D1394	GLN	GLU	MET	SER	PRO	THR	LEU	VAL	LEU
F1395	GLN	ILE	SER	THR	THR	THR	THR	VAL	ILE
ALA	ARG	GLY	SER	SER	LEU	PHE	SER	LYS	TYR
GLY	LEU	CYS	ASN	ASN	LYS	PRO	HIS	LYS	GLN
ARG	LYS	LEU	ASP	ASN	PHE	GLN	MET	SER	GLN
E1399	LYS	GLU	ILE	PHE	ASN	THR	ASN	VAL	VAL
Y1402	ALA	ASN	GLN	LEU	LEU	LYS	HIS	GLY	GLU
SER	VAL	THR	TYR	GLU	ALA	THR	SER	VAL	GLU
THR	PRO	THR	PRO	LEU	THR	LEU	ASP	GLY	GLY
HIS	ASN	ASN	GLY	CYS	TYR	ASN	SER	VAL	GLU
PRO	ARG	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU
M1335	ARG	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU
K1336	VAL	VAL	ALA	VAL	LEU	LEU	SER	GLY	GLY
L1337	SER	TYR	HIS	GLU	SER	LYS	SER	PHE	THR
M1338	THR	THR	TRP	SER	PHE	LEU	LEU	TYR	ALA
I1339	LEU	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER
V1340	LEU	GLU	LEU	SER	PRO	HIS	SER	ASP	GLY
G1341	LEU	LEU	ASN	ARG	GLU	ASP	GLU	ALA	SER
M1342	ARG	ARG	LEU	MET	THR	LEU	THR	VAL	GLY
T1348	PHE	PRO	LEU	PHE	VAL	ASN	CYS	PHE	SER
L1351	ASN	ASN	LEU	ALA	VAL	LEU	THR	ARG	GLU
Q1352	GLU	GLU	PHE	ALA	GLU	ASP	LEU	VAL	ASP
G1353	MET	MET	SER	MET	LYS	THR	LEU	ASN	VAL
L1354	GLY	GLY	HIS	PRO	LEU	PHE	LEU	LEU	LEU
MET	LYS	LYS	ASN	PHE	GLU	SER	GLN	SER	SER
LYS	LEU	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS
THR	SER	SER	ILE	PRO	ILE	SER	ASN	HIS	PHE
LYS	LYS	LYS	SER	PRO	ILE	GLU	GLU	ASP	ASP
ILE	ILE	ILE	ILE	SER	LEU	TYR	LEU	ASN	GLU
SER	THR	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP
ASP	ASP	ASP	ASP	THR	LYS	GLY	LEU	LEU	THR
LEU	LEU	LEU	LEU	ILE	ASN	MET	GLY	GLY	THR
GLY	GLY	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE
MET	LEU	LEU	GLU	LYS	ILE	CYS	THR	ILE	PRO
GLN	GLN	ASP	LYS	LEU	SER	ILE	ALA	ILE	PRO
SER	ALA	GLU	TYR	GLN	ILE	ALA	ASN	PHE	SER
ALA	THR	HIS	LEU	ASN	CYS	LEU	GLN	HIS	SER
THR	VAL	LEU	TRP	LYS	SER	ASP	LYS	GLY	MET
G1370	ASN	ASN	SER	PHE	PRO	VAL	CYS	ASP	SER
I1371	PHE	ARG	ARG	SER	LEU	SER	ILE	LEU	SER
D1372	ASP	VAL	VAL	CYS	ARG	ARG	SER	VAL	VAL
I1378	PHE	GLU	LYS	ILE	LEU	ASN	VAL	ARG	ALA
GLN	HIS	LYS	LEU	PRO	LYS	ASP	HIS	LYS	GLN
ILE	GLN	ILE	LEU	ALA	GLU	ILE	GLY	ARG	SER
ARG	ILE	LEU	HIS	ALA	LEU	GLY	PRO	LYS	ASP
ASP	GLY	LEU	LEU	ILE	LEU	ILE	HIS	ILE	ASP
LYS	ASP	SER	LYS	LEU	ILE	SER	LEU	LEU	LYS
ARG	LYS	ALA	HIS	ASN	ASN	VAL	VAL	SER	ASP
LYS	ARG	LYS	ASN	LEU	ASN	VAL	LEU	SER	GLY
THR	LYS	LYS	LYS	PRO	LEU	ASP	LEU	ASP	GLY
ARG	LYS	ASP	LEU	HIS	SER	LYS	LEU	ASP	SER
ASP	ARG	ILE	LYS	LEU	LYS	PRO	THR	SER	LEU
I1388	ASP	ILE	LYS	GLU	ASN	THR	ASN	LEU	GLY
V1389	ILE	ARG	ILE	SER	ARG	VAL	GLN	ARG	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	261641	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.157	Depositor
Minimum map value	-1.097	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.124	Depositor
Map size (Å)	299.2, 299.2, 299.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93500006, 0.93500006, 0.93500006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: T3X

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	0.30	2/7779 (0.0%)	0.57	16/10498 (0.2%)
2	B	0.15	0/866	0.33	0/1187
All	All	0.29	2/8645 (0.0%)	0.55	16/11685 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2208	PRO	N-CD	-15.46	1.26	1.47
1	A	1695	TYR	C-N	-7.08	1.23	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1699	TYR	CB-CA-C	-15.56	79.48	109.66
1	A	1700	PHE	CA-C-N	9.74	132.02	119.84
1	A	1700	PHE	C-N-CA	9.74	132.02	119.84
1	A	1699	TYR	CA-C-O	-9.11	110.81	121.46
1	A	2208	PRO	N-CD-CG	7.05	113.78	103.20

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	7645	0	7826	224	0
2	B	845	0	808	19	0
3	A	39	0	0	3	0
All	All	8529	0	8634	238	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 14.

The worst 5 of 238 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:A:1902:GLU:HG2	1:A:1949:LEU:HD23	1.51	0.93
1:A:1699:TYR:O	1:A:1701:PRO:HD3	1.77	0.83
1:A:2216:VAL:HG12	1:A:2226:VAL:HG22	1.62	0.80
1:A:1866:ARG:HA	1:A:1869:MET:HE1	1.64	0.79
1:A:1730:ASN:HB3	1:A:1741:ASN:HB3	1.66	0.76

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	908/1406 (65%)	871 (96%)	35 (4%)	2 (0%)	43	76
2	B	-	105 (97%)	3 (3%)	0	100	100
All	All	1016/1406 (72%)	976 (96%)	38 (4%)	2 (0%)	44	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1701	PRO
1	A	1700	PHE

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	857/1278 (67%)	852 (99%)	5 (1%)	78	88
2	B	-	85 (100%)	0	100	100
All	All	942/1278 (74%)	937 (100%)	5 (0%)	78	89

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

Mol	Chain	Res	Type
1	A	1694	LEU
1	A	1697	MET
1	A	1810	LYS
1	A	1946	VAL
1	A	1949	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	80	HIS
2	B	109	ASN
1	A	2422	ASN
1	A	2433	HIS
1	A	2476	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	T3X	A	2601	-	43,43,43	3.82	17 (39%)	61,62,62	7.91	22 (36%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	T3X	A	2601	-	-	4/23/33/33	0/5/5/5

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2601	T3X	C37-N36	-8.87	1.26	1.32
3	A	2601	T3X	C34-N35	8.61	1.41	1.35
3	A	2601	T3X	N35-N36	-8.49	1.30	1.36
3	A	2601	T3X	C22-N21	-7.13	1.29	1.46
3	A	2601	T3X	C23-N18	-6.93	1.28	1.46

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2601	T3X	C34-N35-N36	47.28	122.32	111.26
3	A	2601	T3X	C37-N36-N35	-22.91	94.07	106.02
3	A	2601	T3X	C33-C37-N36	17.80	124.62	111.68
3	A	2601	T3X	C33-C34-N35	-15.30	100.56	107.21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2601	T3X	N35-C34-N38	12.32	136.67	125.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

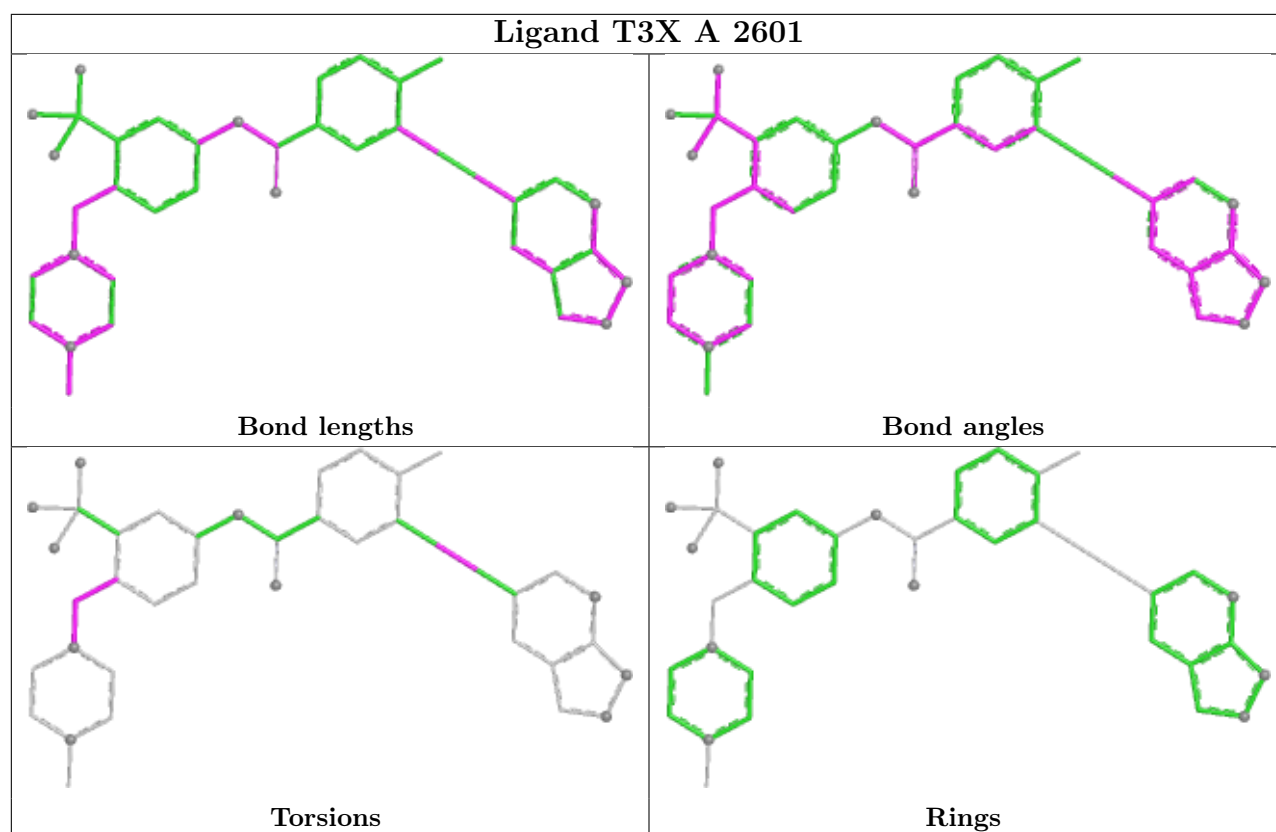
Mol	Chain	Res	Type	Atoms
3	A	2601	T3X	C14-C17-N18-C19
3	A	2601	T3X	C14-C17-N18-C23
3	A	2601	T3X	C03-C29-C30-C31
3	A	2601	T3X	C13-C14-C17-N18

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2601	T3X	3	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.

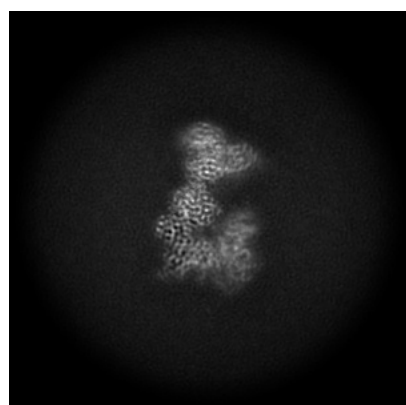
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41728. These allow visual inspection of the internal detail of the map and identification of artifacts.

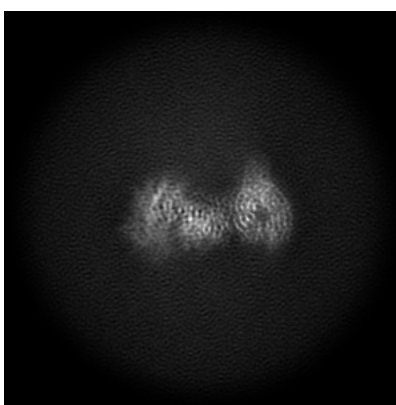
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

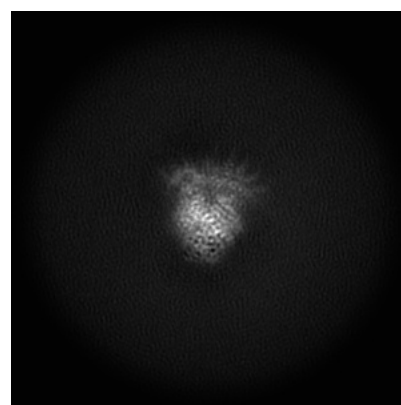
6.1.1 Primary map



X



Y

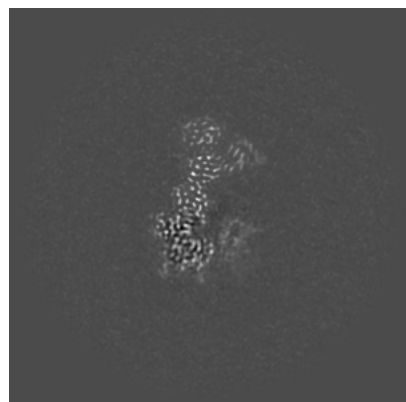


Z

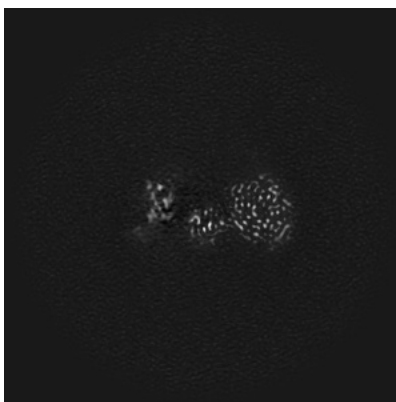
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

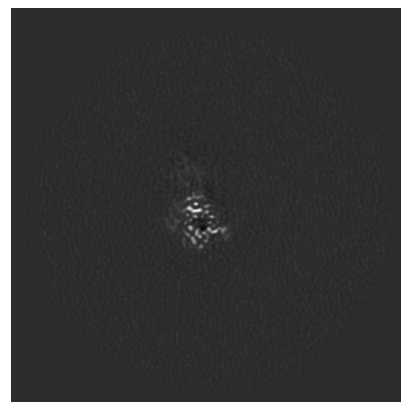
6.2.1 Primary map



X Index: 160



Y Index: 160

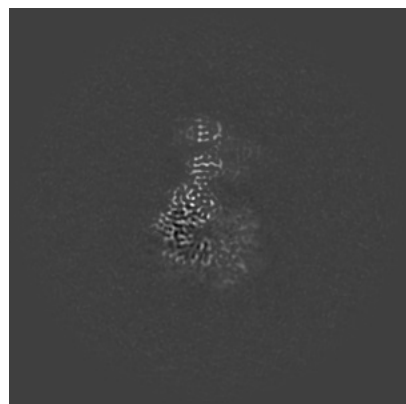


Z Index: 160

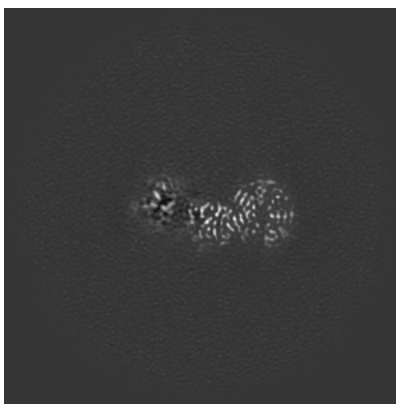
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

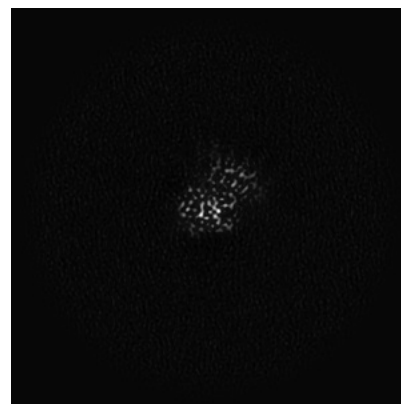
6.3.1 Primary map



X Index: 153



Y Index: 152

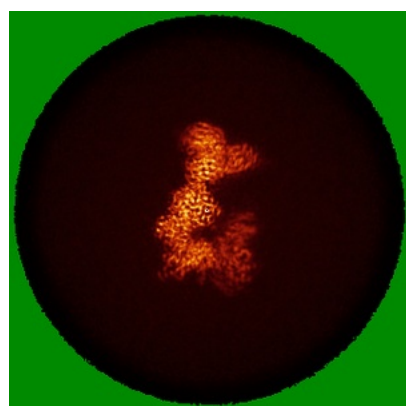


Z Index: 195

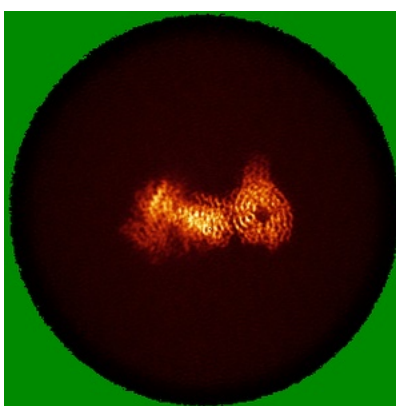
The images above show the largest variance slices of the map in three orthogonal directions.

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

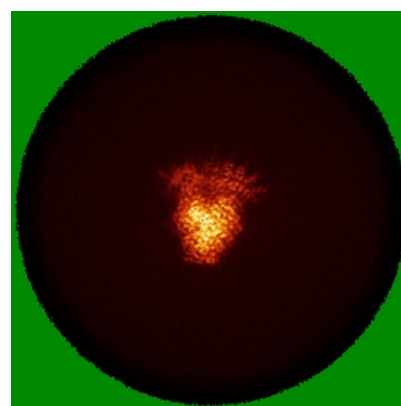
6.4.1 Primary map



X



Y

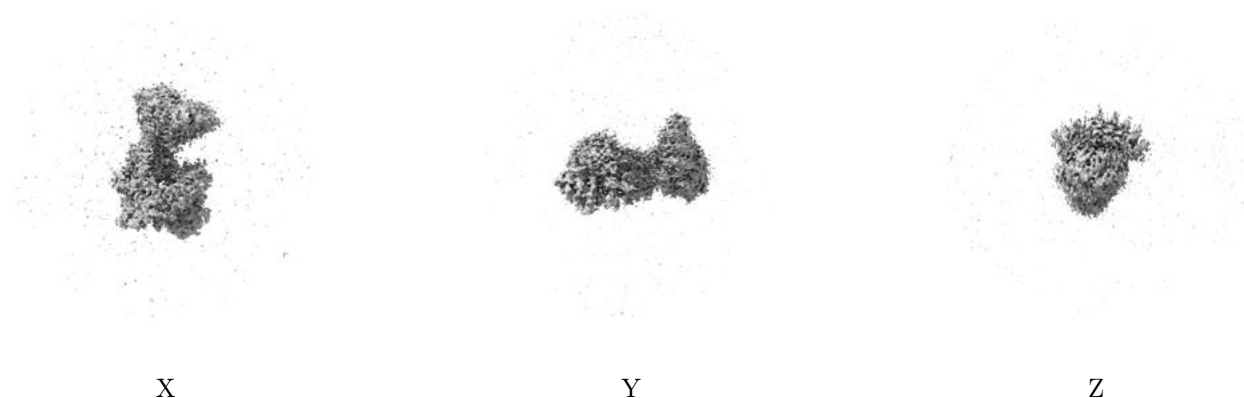


Z

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

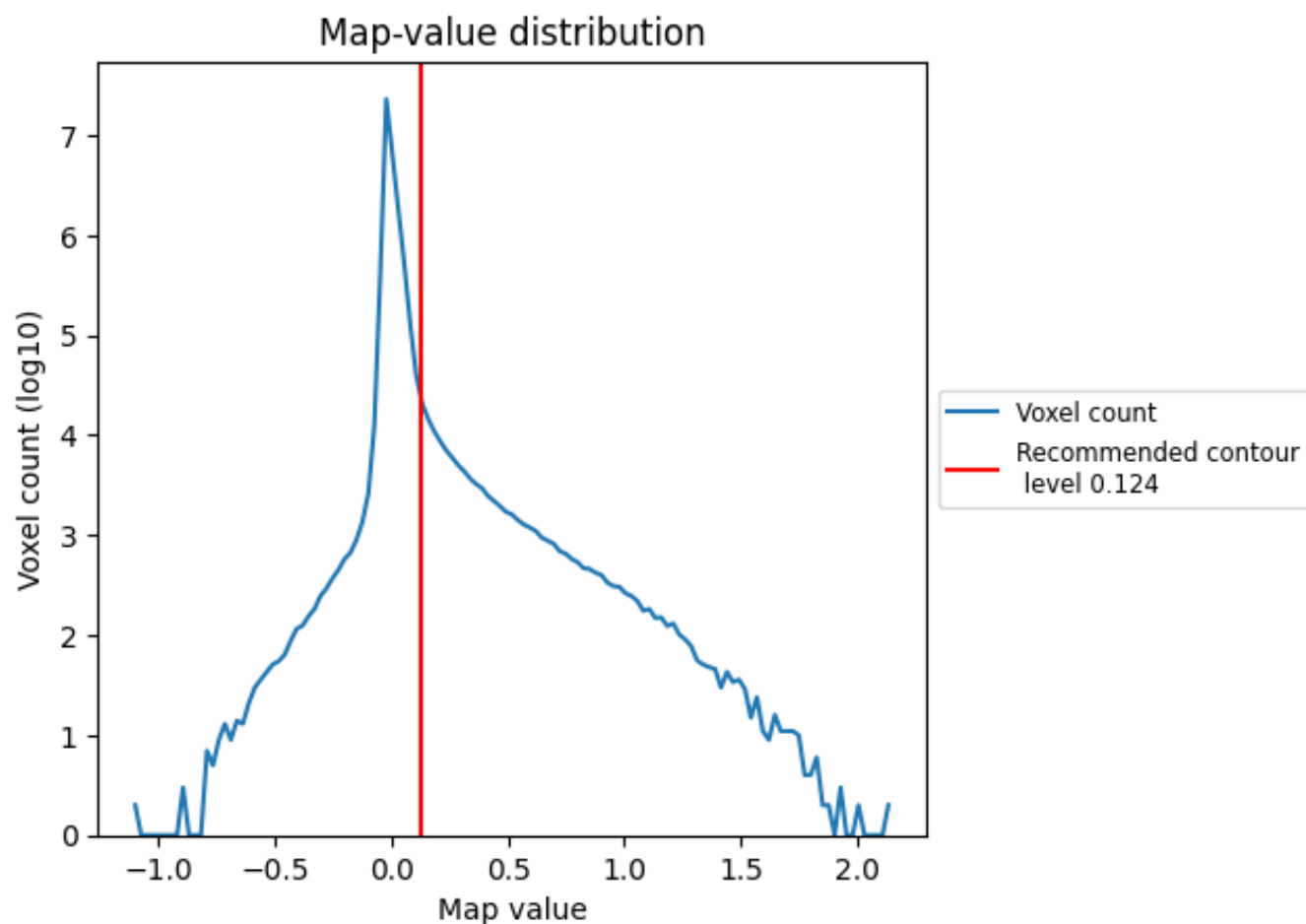
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

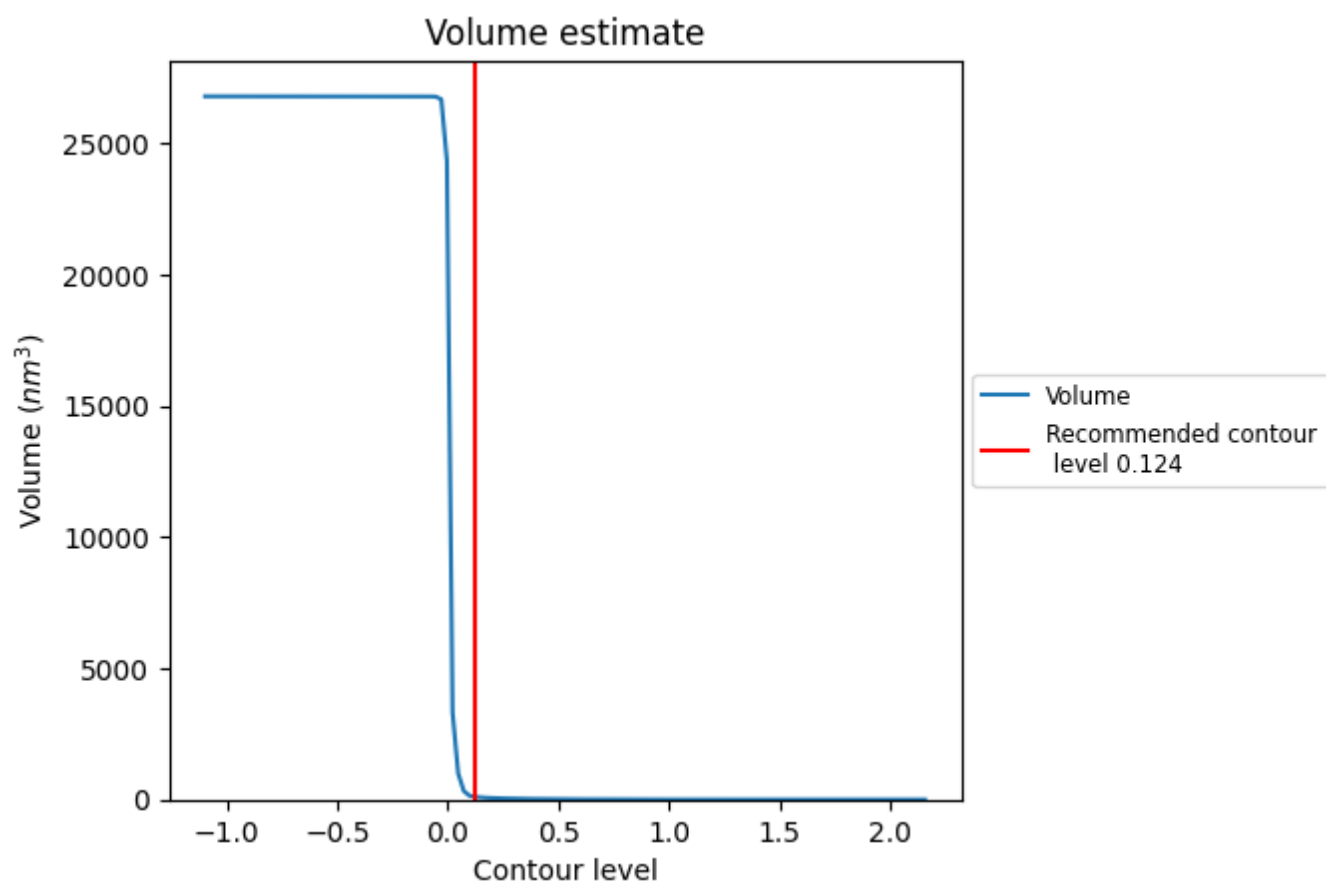
This section contains the results of statistical analysis of the map.

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.

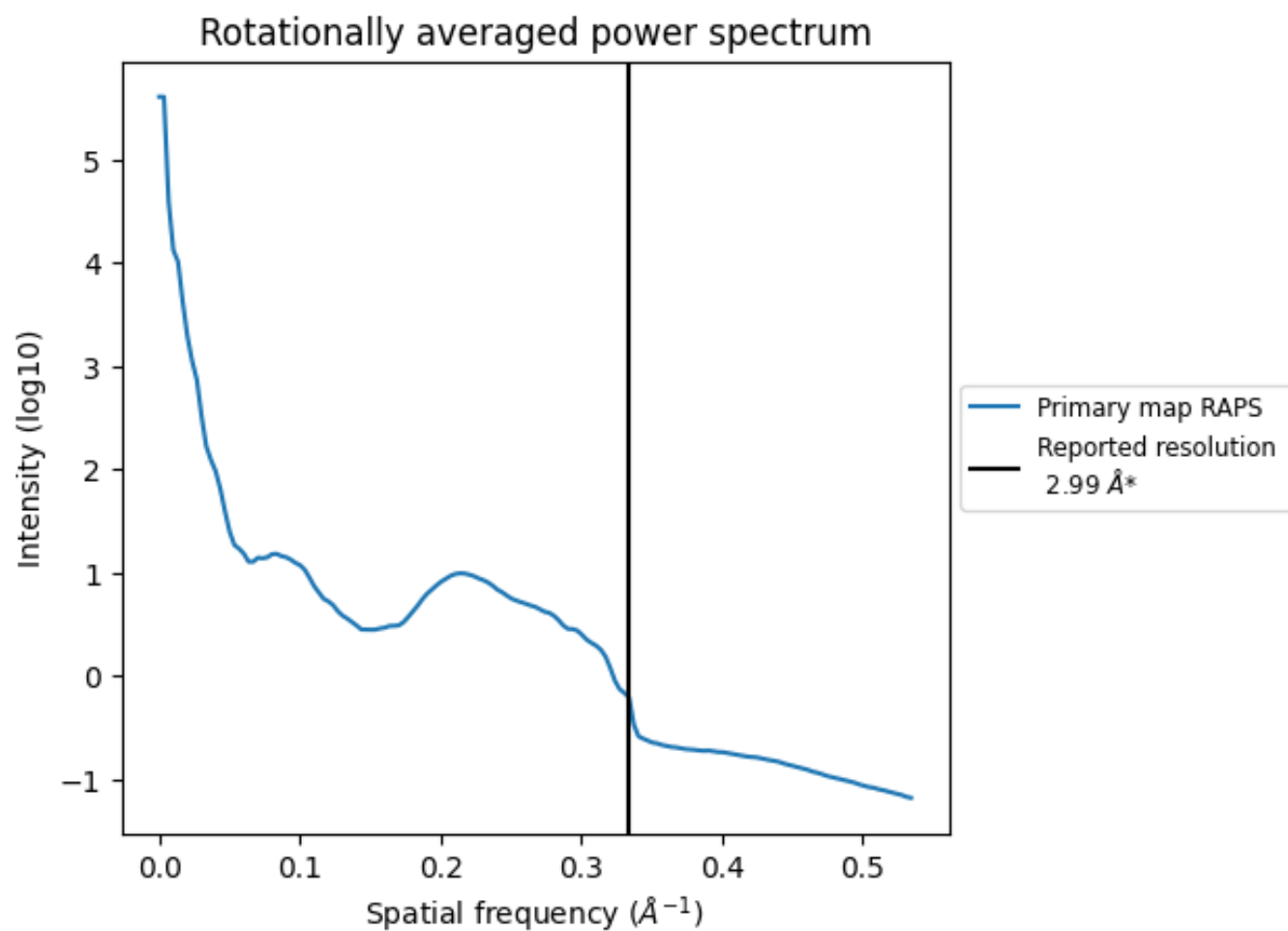
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 101 nm³; this corresponds to an approximate mass of 91 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 0.334 Å⁻¹

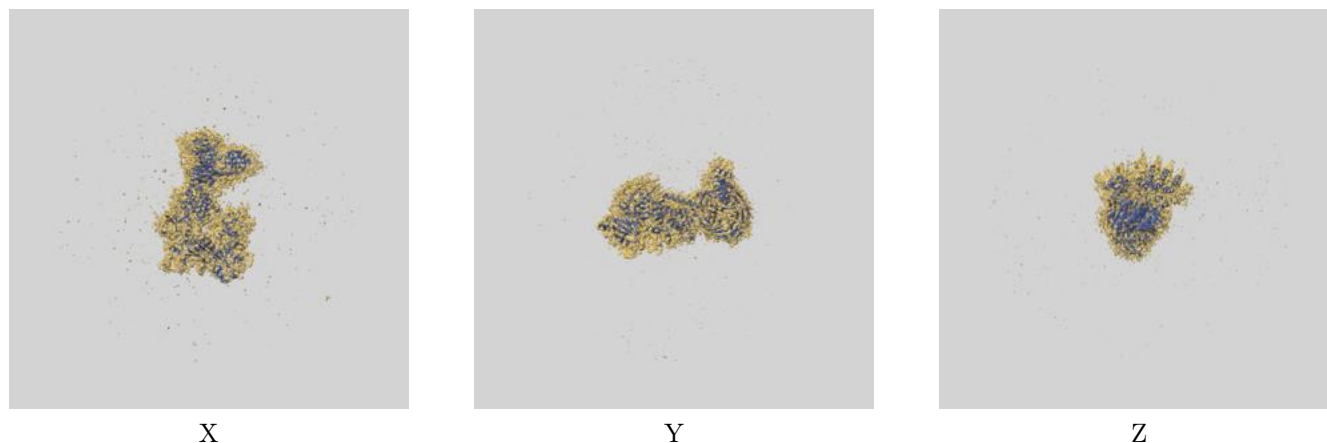
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

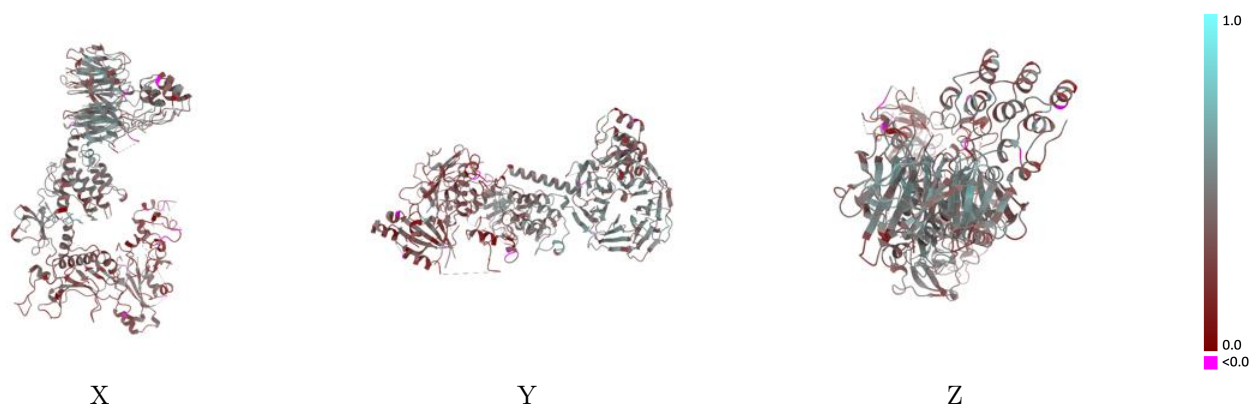
This section contains information regarding the fit between EMDB map EMD-41728 and PDB model 8TYQ. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



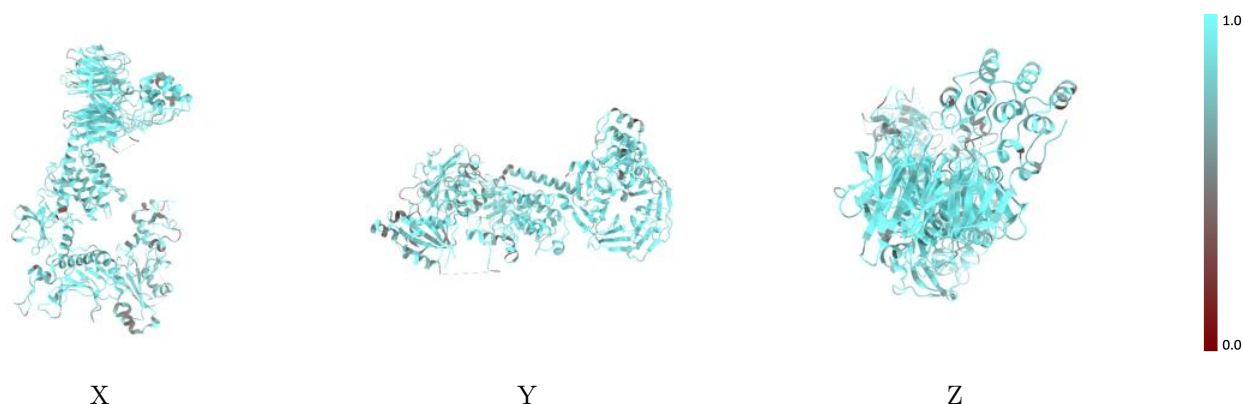
The images above show the 3D surface view of the map at the recommended contour level 0.124 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



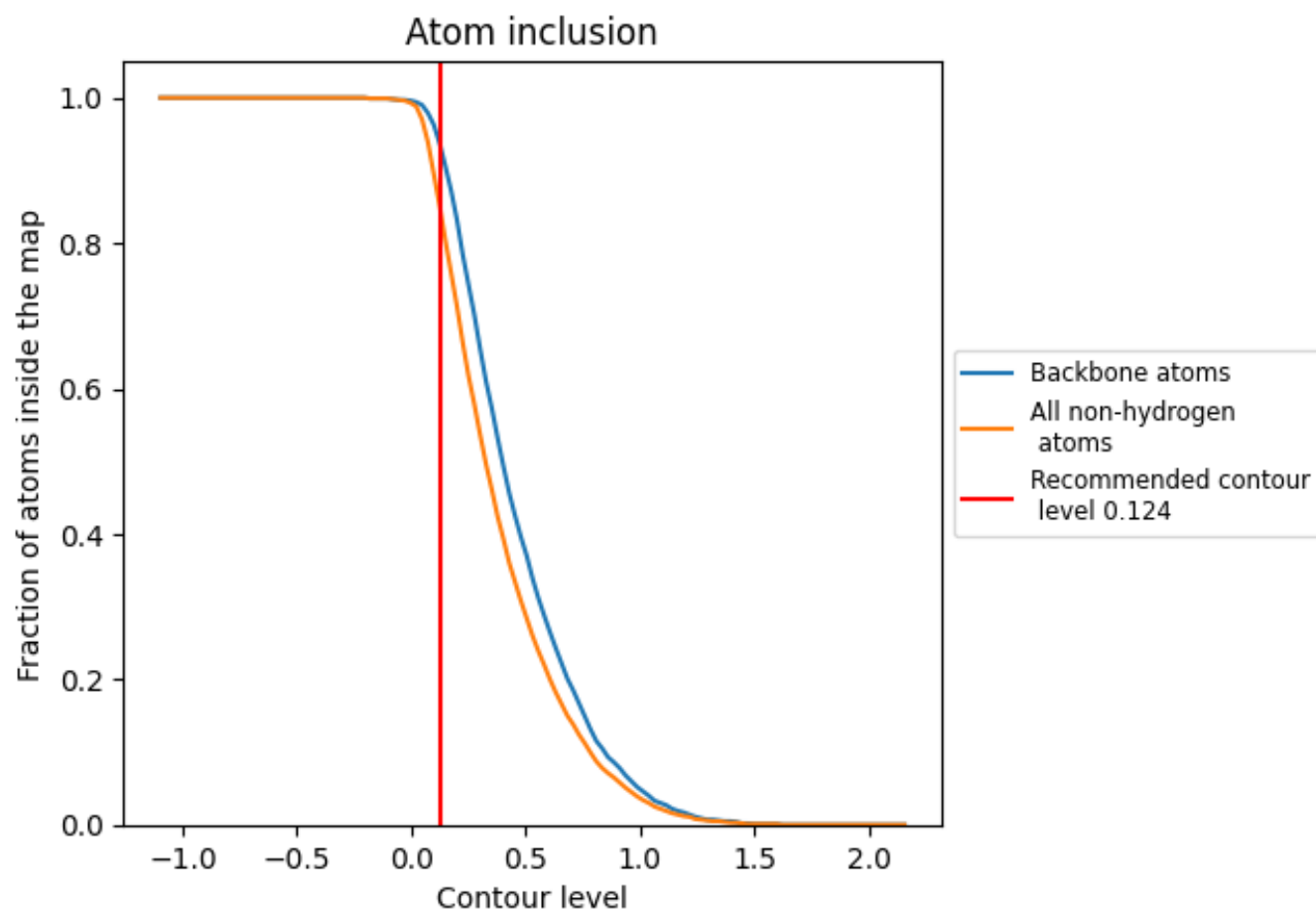
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.124).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% 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 (0.124) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.3750
A	0.8540	0.3730
B	0.8250	0.3850

