



## Full wwPDB EM Validation Report ⓘ

Apr 22, 2024 – 09:47 pm BST

PDB ID : 7BL1  
EMDB ID : EMD-12214  
Title : human complex II-BATS bound to membrane-attached Rab5a-GTP  
Authors : Tremel, S.; Morado, D.R.; Kovtun, O.; Williams, R.L.; Briggs, J.A.G.; Munro, S.; Ohashi, Y.; Bertram, J.; Perisic, O.  
Deposited on : 2021-01-17  
Resolution : 9.80 Å (reported)  
Based on initial models : 4DDP, 3MJH, 5DFZ, 3IHY

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

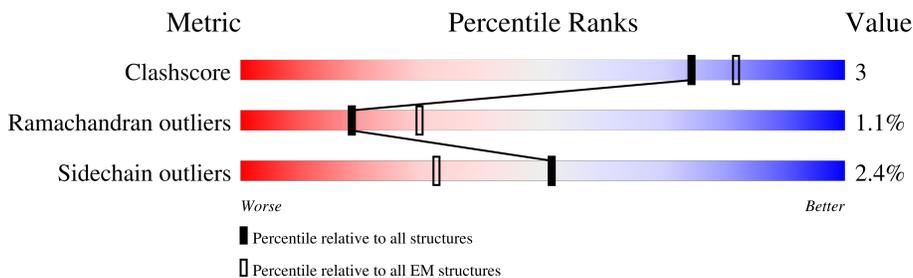
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	AAA	699	
2	BBB	887	
3	CCC	1371	
4	EEE	450	
5	FFF	22	
6	DDD	168	

## 2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 15071 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 UV radiation resistance-associated gene protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	AAA	380	1896	1136	380	380	0	0

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase catalytic subunit type 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	BBB	805	4062	2452	805	805	0	0

- Molecule 3 is a protein called Phosphoinositide 3-kinase regulatory subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	CCC	1189	6009	3631	1189	1189	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CCC	1359	SER	-	expression tag	UNP Q99570
CCC	1360	ARG	-	expression tag	UNP Q99570
CCC	1361	PRO	-	expression tag	UNP Q99570
CCC	1362	THR	-	expression tag	UNP Q99570
CCC	1363	THR	-	expression tag	UNP Q99570
CCC	1364	ALA	-	expression tag	UNP Q99570
CCC	1365	SER	-	expression tag	UNP Q99570
CCC	1366	GLU	-	expression tag	UNP Q99570
CCC	1367	ASN	-	expression tag	UNP Q99570
CCC	1368	LEU	-	expression tag	UNP Q99570
CCC	1369	TYR	-	expression tag	UNP Q99570
CCC	1370	PHE	-	expression tag	UNP Q99570
CCC	1371	GLN	-	expression tag	UNP Q99570

- Molecule 4 is a protein called Beclin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	EEE	337	1680	1006	337	337	0	0

- Molecule 5 is a protein called unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	FFF	14	70	42	14	14	0	0

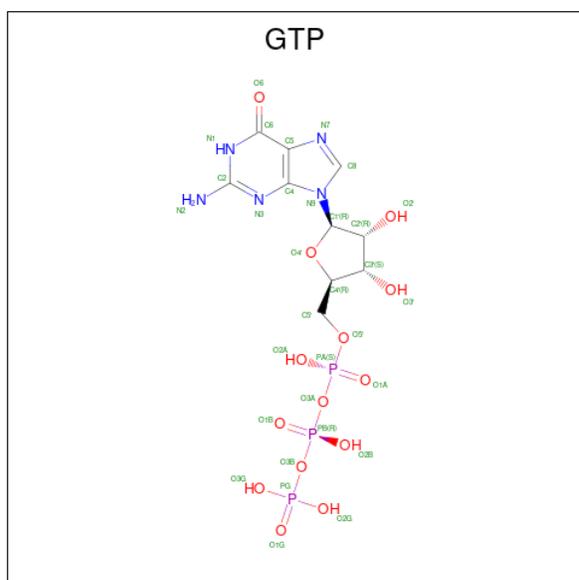
- Molecule 6 is a protein called Ras-related protein Rab-5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	DDD	168	1321	842	223	252	4	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DDD	19	SER	CYS	conflict	UNP P20339
DDD	63	SER	CYS	conflict	UNP P20339
DDD	79	LEU	GLN	conflict	UNP P20339

- Molecule 7 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



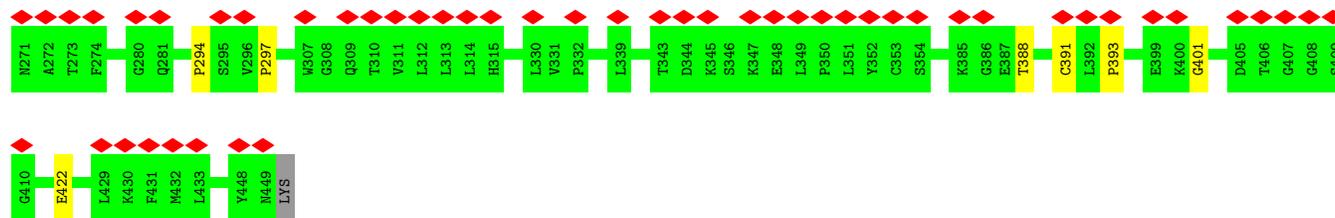
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
7	DDD	1	32	10	5	14	3	0

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
8	DDD	1	1	1	0



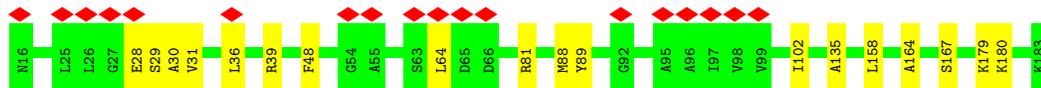




- Molecule 5: unknown peptide



- Molecule 6: Ras-related protein Rab-5A



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	26979	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 ( $e^-/\text{\AA}^2$ )	2.99	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	341.27997, 341.27997, 341.27997	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0665, 1.0665, 1.0665	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: GTP, MG

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	AAA	0.38	0/1902	0.82	0/2654
2	BBB	0.39	0/4097	0.83	0/5738
3	CCC	0.42	0/6065	0.90	0/8499
4	EEE	0.32	0/1685	0.72	0/2352
5	FFF	0.41	0/69	0.81	0/95
6	DDD	0.37	0/1344	0.72	0/1814
All	All	0.39	0/15162	0.84	0/21152

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	AAA	1896	0	866	3	0
2	BBB	4062	0	1959	20	0
3	CCC	6009	0	2982	41	0
4	EEE	1680	0	765	9	0
5	FFF	70	0	72	0	0
6	DDD	1321	0	1321	10	0
7	DDD	32	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	DDD	1	0	0	0	0
All	All	15071	0	7977	73	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 (73) 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)
3:CCC:1194:PRO:CD	3:CCC:1249:PRO:HA	1.53	1.35
3:CCC:1194:PRO:HD3	3:CCC:1249:PRO:CA	1.54	1.35
2:BBB:198:PHE:CB	6:DDD:88:MET:SD	2.32	1.18
3:CCC:699:LEU:O	3:CCC:701:PRO:HD3	1.52	1.09
2:BBB:199:ARG:HA	6:DDD:89:TYR:OH	1.66	0.94
3:CCC:1038:TYR:O	3:CCC:1084:PRO:HG3	1.75	0.86
4:EEE:294:PRO:HG3	4:EEE:422:GLU:HA	1.65	0.78
2:BBB:146:TRP:HA	2:BBB:151:ALA:HB3	1.69	0.73
3:CCC:1321:PRO:HD3	4:EEE:258:GLN:CB	2.18	0.72
3:CCC:266:ALA:HB1	3:CCC:272:PHE:HA	1.72	0.71
3:CCC:1038:TYR:O	3:CCC:1084:PRO:CG	2.39	0.70
3:CCC:1253:ASN:N	3:CCC:1254:PRO:HD2	2.07	0.69
3:CCC:429:SER:O	3:CCC:431:PRO:HD3	1.92	0.68
3:CCC:1281:GLY:O	3:CCC:1325:PRO:HG3	1.96	0.66
3:CCC:52:VAL:H	3:CCC:105:TYR:HA	1.65	0.60
3:CCC:1194:PRO:HD3	3:CCC:1249:PRO:C	2.21	0.58
3:CCC:1321:PRO:HG2	4:EEE:258:GLN:C	2.23	0.58
6:DDD:39:ARG:HD2	6:DDD:164:ALA:O	2.05	0.56
2:BBB:36:LYS:CB	2:BBB:55:SER:H	2.18	0.56
3:CCC:59:ASP:CB	3:CCC:60:PRO:HD3	2.34	0.56
2:BBB:616:LEU:C	2:BBB:618:PRO:HD3	2.26	0.56
3:CCC:1252:GLY:C	3:CCC:1254:PRO:HD2	2.26	0.56
2:BBB:199:ARG:CA	6:DDD:89:TYR:OH	2.48	0.56
3:CCC:1253:ASN:N	3:CCC:1254:PRO:CD	2.70	0.54
3:CCC:1252:GLY:C	3:CCC:1254:PRO:CD	2.77	0.53
4:EEE:294:PRO:CG	4:EEE:422:GLU:HA	2.35	0.53
2:BBB:18:ASN:CB	2:BBB:94:PRO:HA	2.40	0.52
6:DDD:158:LEU:HD21	6:DDD:180:LYS:HD2	1.92	0.51
2:BBB:667:LEU:O	2:BBB:669:PRO:HD3	2.12	0.50
3:CCC:462:TYR:HA	3:CCC:465:PRO:HG2	1.93	0.50
4:EEE:391:CYS:C	4:EEE:393:PRO:HD2	2.32	0.49
3:CCC:59:ASP:CB	3:CCC:60:PRO:CD	2.92	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BBB:616:LEU:CB	2:BBB:618:PRO:HD3	2.43	0.48
3:CCC:1281:GLY:C	3:CCC:1325:PRO:HG3	2.35	0.47
3:CCC:81:ALA:HA	3:CCC:86:PRO:HG2	1.95	0.47
2:BBB:114:TYR:HA	3:CCC:685:GLN:HA	1.95	0.47
3:CCC:95:SER:H	3:CCC:99:ALA:HA	1.79	0.47
3:CCC:81:ALA:HA	3:CCC:86:PRO:CG	2.44	0.47
1:AAA:57:ASN:HA	1:AAA:103:PRO:HB3	1.97	0.46
3:CCC:1192:MET:O	3:CCC:1249:PRO:HG3	2.15	0.46
3:CCC:1252:GLY:O	3:CCC:1254:PRO:HD3	2.16	0.46
3:CCC:759:CYS:N	3:CCC:760:PRO:CD	2.79	0.46
3:CCC:693:CYS:O	3:CCC:697:PRO:HD2	2.16	0.46
2:BBB:617:MET:N	2:BBB:618:PRO:CD	2.79	0.45
1:AAA:397:ASP:H	1:AAA:406:LYS:CB	2.29	0.45
3:CCC:1321:PRO:CD	4:EEE:258:GLN:CB	2.91	0.45
6:DDD:102:ILE:CD1	6:DDD:135:ALA:HA	2.48	0.44
3:CCC:761:PRO:O	3:CCC:765:PRO:HD2	2.17	0.44
4:EEE:127:SER:C	4:EEE:129:GLN:H	2.22	0.43
2:BBB:151:ALA:HB2	2:BBB:159:THR:CB	2.49	0.43
3:CCC:560:GLY:HA2	3:CCC:570:ARG:H	1.83	0.43
6:DDD:28:GLU:O	6:DDD:31:VAL:HG22	2.19	0.42
2:BBB:17:ILE:C	2:BBB:96:LYS:HA	2.39	0.42
2:BBB:507:GLN:HA	2:BBB:511:PRO:HD2	2.02	0.42
2:BBB:507:GLN:CB	2:BBB:514:HIS:CB	2.96	0.42
3:CCC:1194:PRO:O	3:CCC:1195:LEU:CB	2.68	0.42
3:CCC:1079:SER:N	3:CCC:1080:PRO:CD	2.81	0.42
2:BBB:64:PHE:CB	2:BBB:69:PRO:HA	2.50	0.42
3:CCC:974:PRO:HA	3:CCC:975:PRO:HD2	1.75	0.42
2:BBB:309:THR:CB	3:CCC:182:ASP:N	2.83	0.42
4:EEE:294:PRO:HG3	4:EEE:422:GLU:CA	2.43	0.41
2:BBB:309:THR:CB	3:CCC:180:PRO:O	2.68	0.41
3:CCC:1192:MET:O	3:CCC:1249:PRO:HD3	2.20	0.41
3:CCC:456:ILE:O	3:CCC:460:PRO:HD2	2.20	0.41
3:CCC:429:SER:O	3:CCC:431:PRO:CD	2.64	0.41
6:DDD:29:SER:OG	7:DDD:200:GTP:O1G	2.26	0.41
6:DDD:30:ALA:HA	7:DDD:200:GTP:H5'	2.03	0.41
3:CCC:1194:PRO:HG3	3:CCC:1249:PRO:C	2.41	0.41
2:BBB:146:TRP:CA	2:BBB:151:ALA:HB3	2.47	0.41
3:CCC:617:LYS:CB	3:CCC:618:PRO:HD3	2.52	0.40
2:BBB:199:ARG:HA	6:DDD:89:TYR:HH	1.80	0.40
1:AAA:99:PHE:CB	1:AAA:102:MET:H	2.34	0.40
4:EEE:391:CYS:O	4:EEE:393:PRO:HD2	2.22	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	AAA	376/699 (54%)	332 (88%)	40 (11%)	4 (1%)	14	52
2	BBB	799/887 (90%)	709 (89%)	79 (10%)	11 (1%)	11	46
3	CCC	1181/1371 (86%)	1019 (86%)	149 (13%)	13 (1%)	14	52
4	EEE	335/450 (74%)	302 (90%)	30 (9%)	3 (1%)	17	57
5	FFF	12/22 (54%)	12 (100%)	0	0	100	100
6	DDD	166/168 (99%)	163 (98%)	2 (1%)	1 (1%)	25	66
All	All	2869/3597 (80%)	2537 (88%)	300 (10%)	32 (1%)	18	52

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	BBB	147	PRO
2	BBB	149	VAL
2	BBB	306	LYS
2	BBB	159	THR
2	BBB	771	LYS
3	CCC	569	GLY
1	AAA	233	LEU
2	BBB	18	ASN
3	CCC	105	TYR
3	CCC	207	MET
3	CCC	1253	ASN
4	EEE	388	THR
1	AAA	63	ASP
1	AAA	399	ILE
2	BBB	214	PHE
2	BBB	215	MET
3	CCC	178	ASP

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Mol	Chain	Res	Type
3	CCC	1220	ARG
2	BBB	282	SER
3	CCC	96	GLU
3	CCC	223	VAL
4	EEE	297	PRO
6	DDD	167	SER
2	BBB	113	VAL
3	CCC	144	VAL
3	CCC	175	LEU
3	CCC	1249	PRO
4	EEE	401	GLY
2	BBB	123	GLY
3	CCC	176	PRO
3	CCC	719	VAL
1	AAA	133	VAL

### 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	AAA	8/607 (1%)	8 (100%)	0	100	100
2	BBB	38/799 (5%)	37 (97%)	1 (3%)	46	66
3	CCC	60/1213 (5%)	60 (100%)	0	100	100
4	EEE	6/405 (2%)	6 (100%)	0	100	100
6	DDD	141/141 (100%)	136 (96%)	5 (4%)	36	59
All	All	253/3165 (8%)	247 (98%)	6 (2%)	51	69

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

Mol	Chain	Res	Type
2	BBB	147	PRO
6	DDD	36	LEU
6	DDD	48	PHE
6	DDD	64	LEU

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Mol	Chain	Res	Type
6	DDD	81	ARG
6	DDD	179	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
7	GTP	DDD	200	8	26,34,34	0.95	1 (3%)	32,54,54	1.25	3 (9%)

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	GTP	DDD	200	8	-	2/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	DDD	200	GTP	C5-C6	-3.16	1.41	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	DDD	200	GTP	C2-N1-C6	-3.05	119.49	125.10
7	DDD	200	GTP	C8-N7-C5	2.91	108.54	102.99
7	DDD	200	GTP	C5-C6-N1	2.58	118.51	113.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

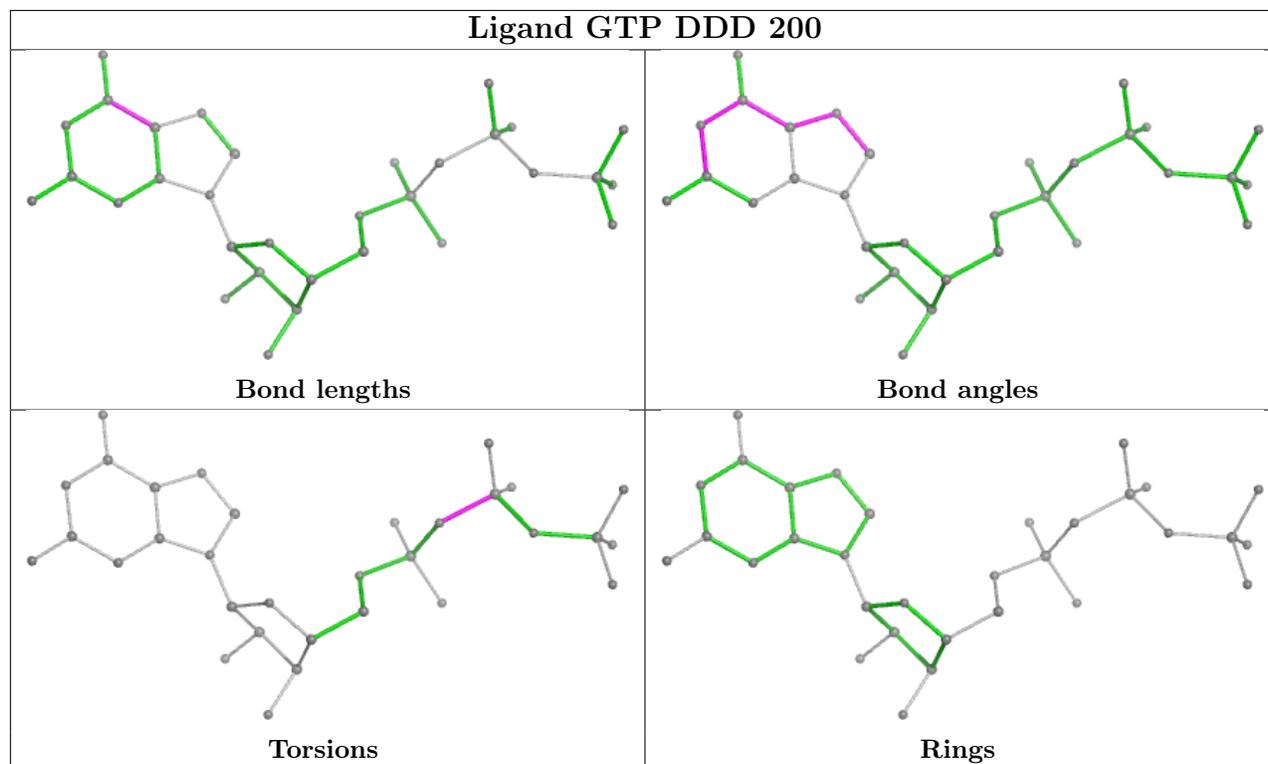
Mol	Chain	Res	Type	Atoms
7	DDD	200	GTP	PA-O3A-PB-O1B
7	DDD	200	GTP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	DDD	200	GTP	2	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-12214. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



X

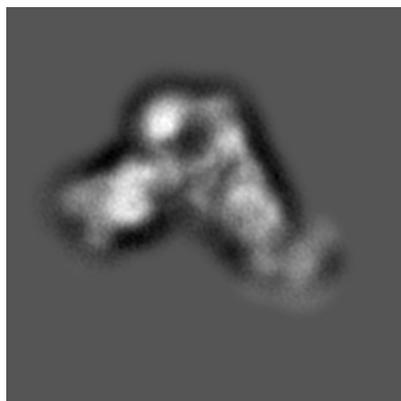


Y



Z

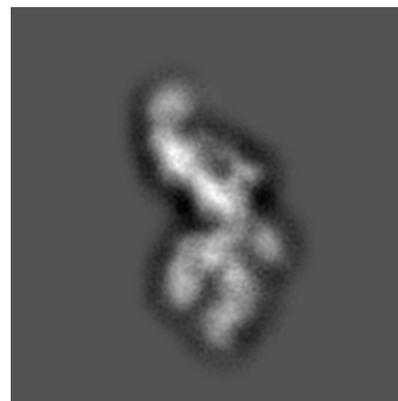
#### 6.1.2 Raw map



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

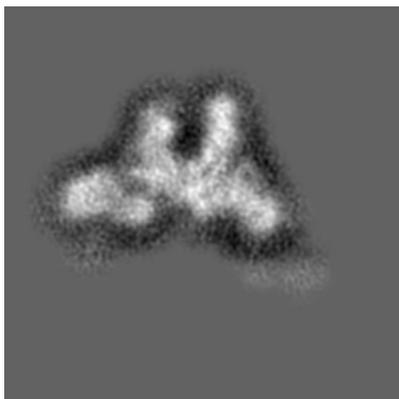


Y Index: 160

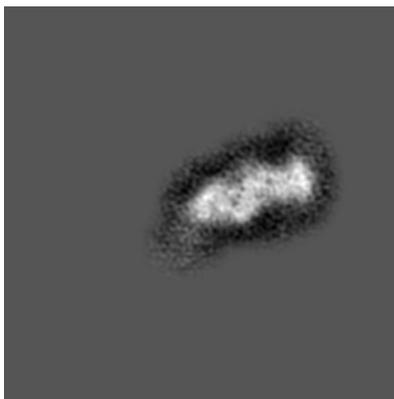


Z Index: 160

### 6.2.2 Raw map



X Index: 80



Y Index: 80

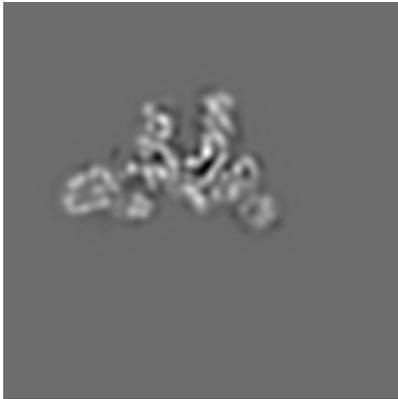


Z Index: 80

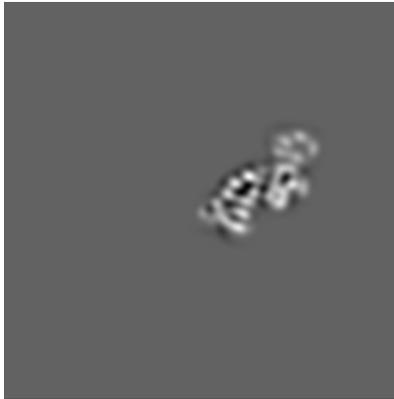
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 162

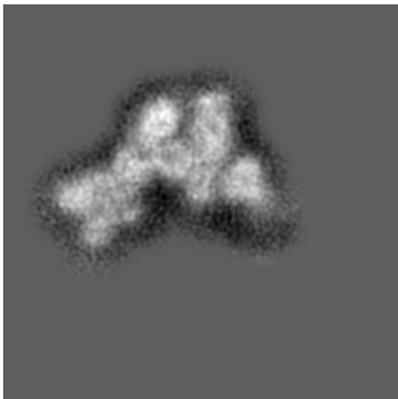


Y Index: 131

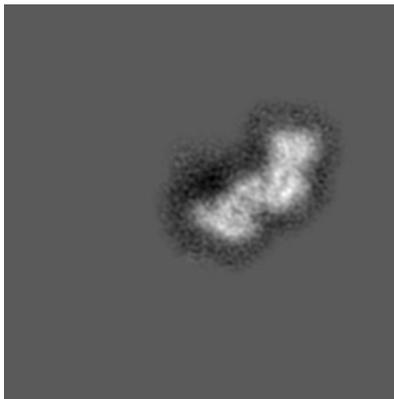


Z Index: 184

### 6.3.2 Raw map



X Index: 86



Y Index: 62

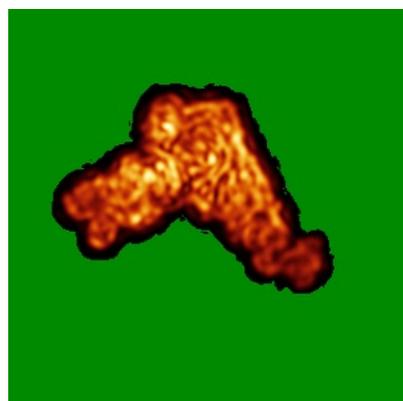


Z Index: 84

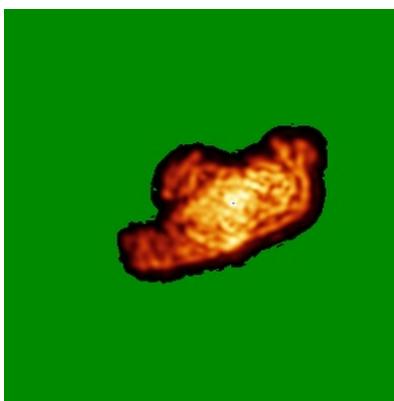
The images above show the largest variance slices of the map in three orthogonal directions.

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

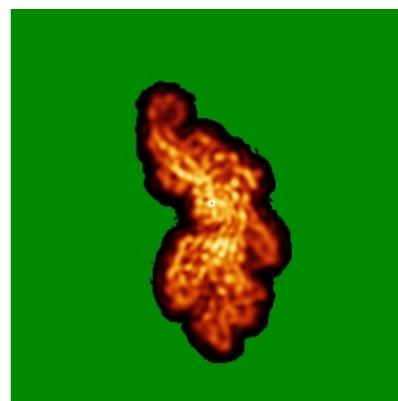
### 6.4.1 Primary map



X

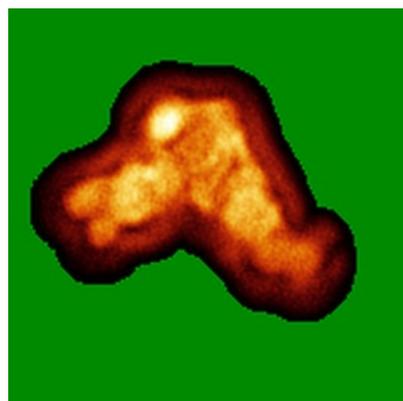


Y

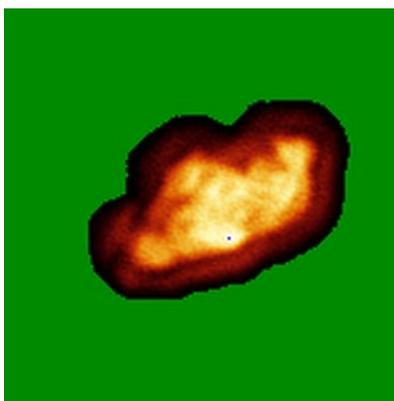


Z

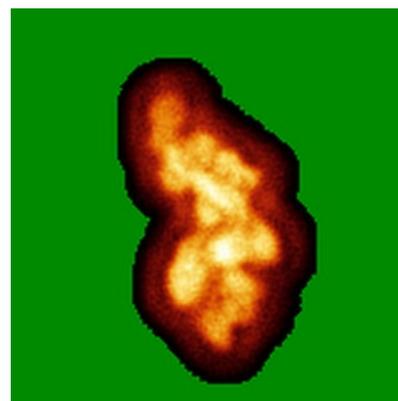
### 6.4.2 Raw map



X



Y

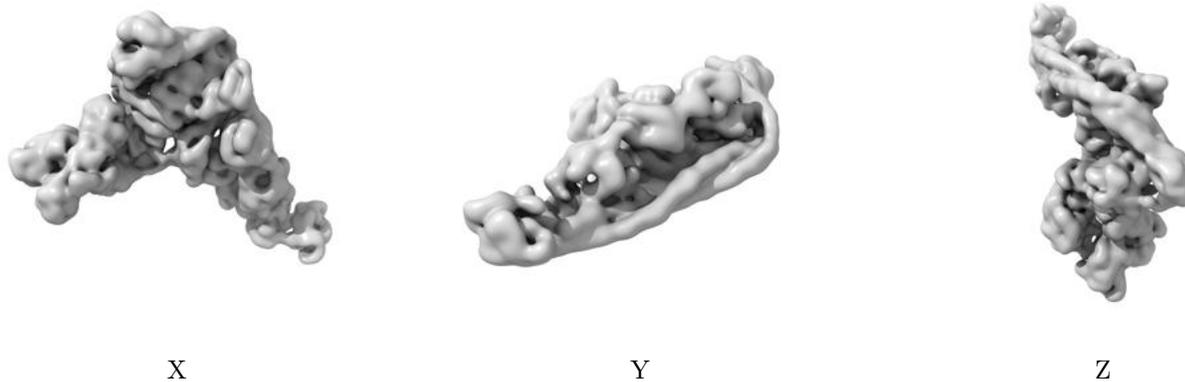


Z

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.

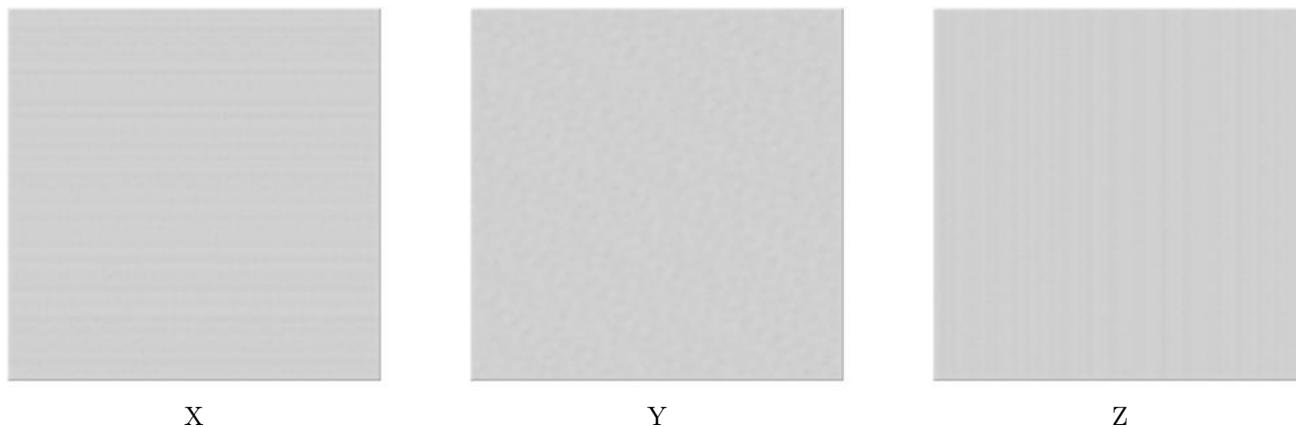
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

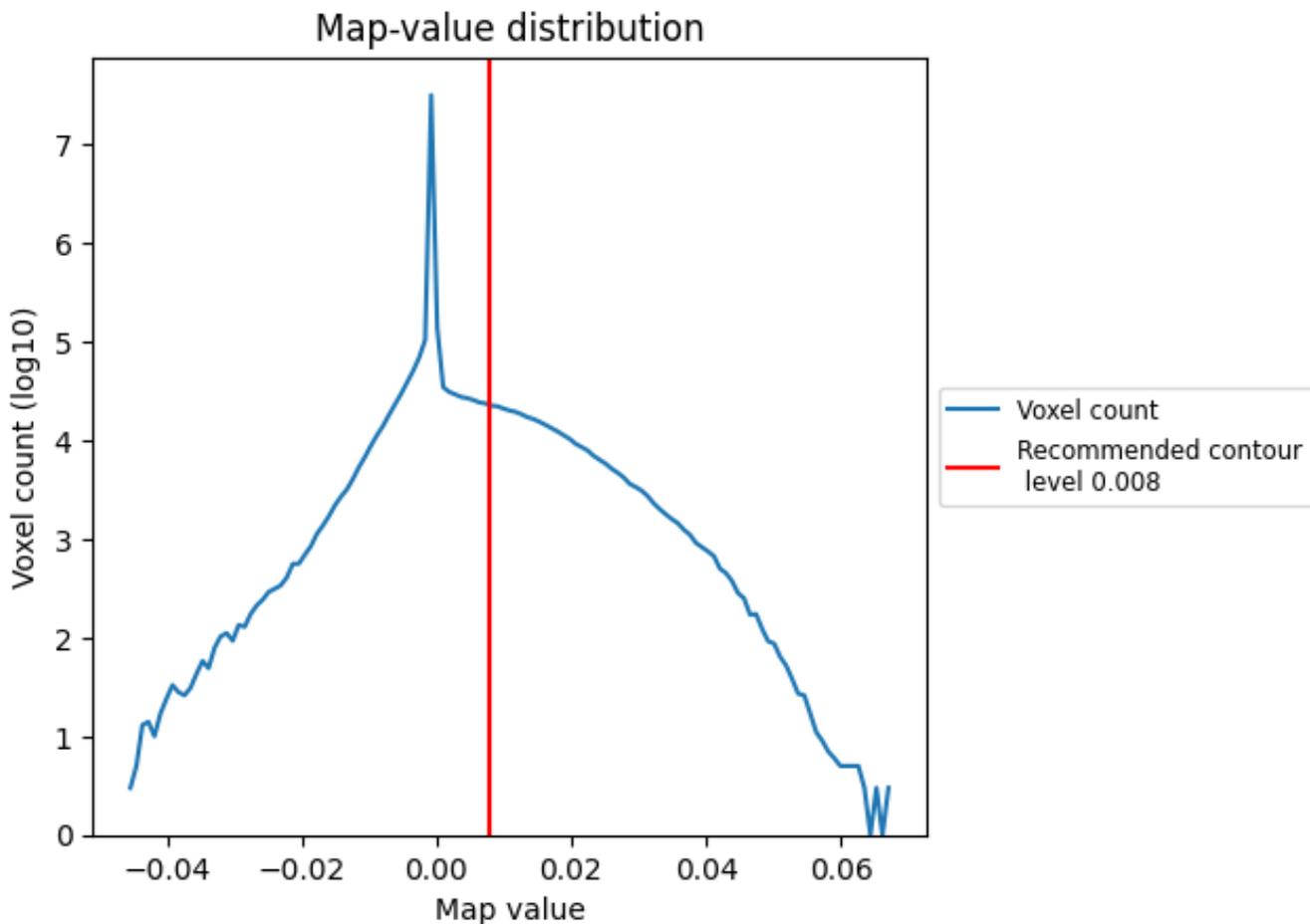
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

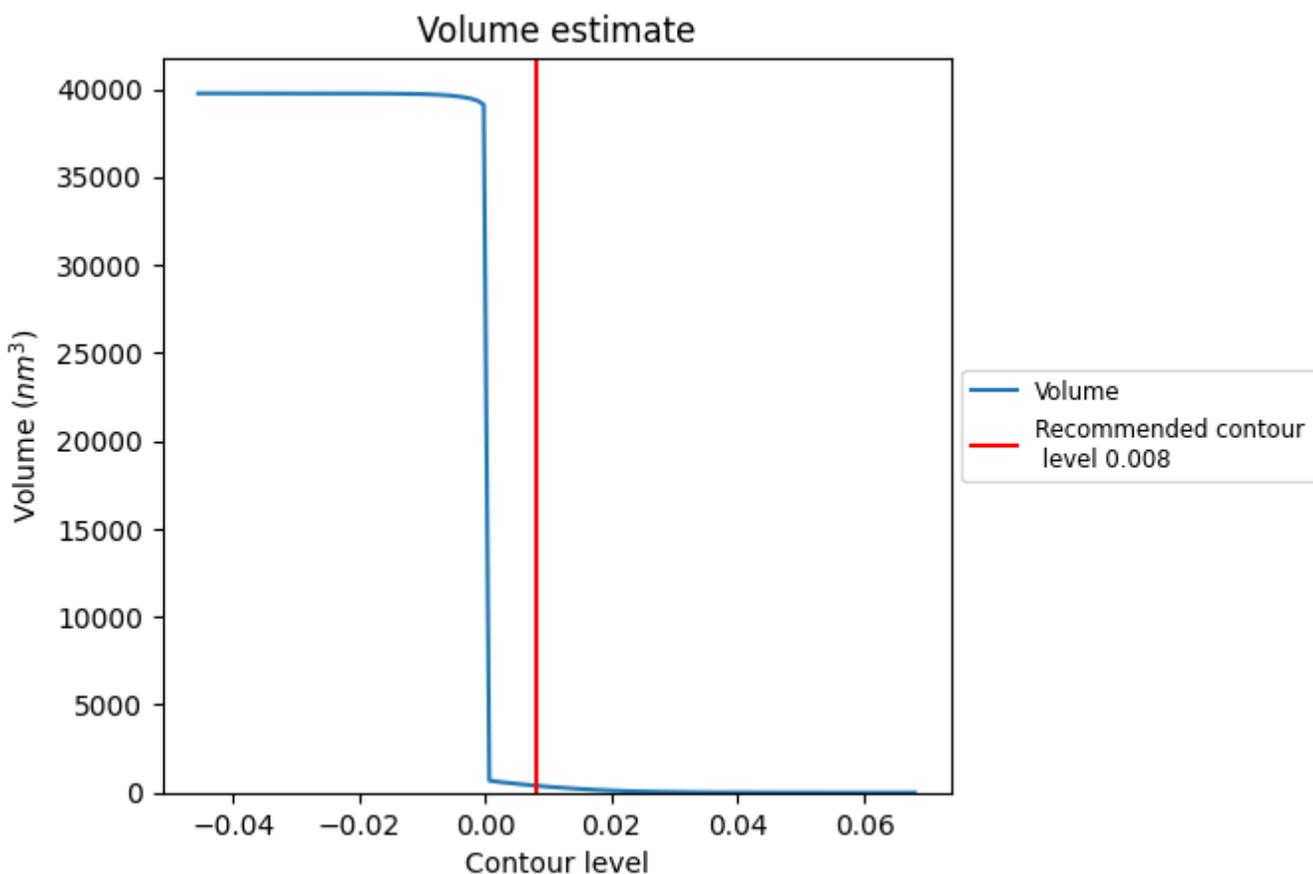
This section contains the results of statistical analysis of the map.

### 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.

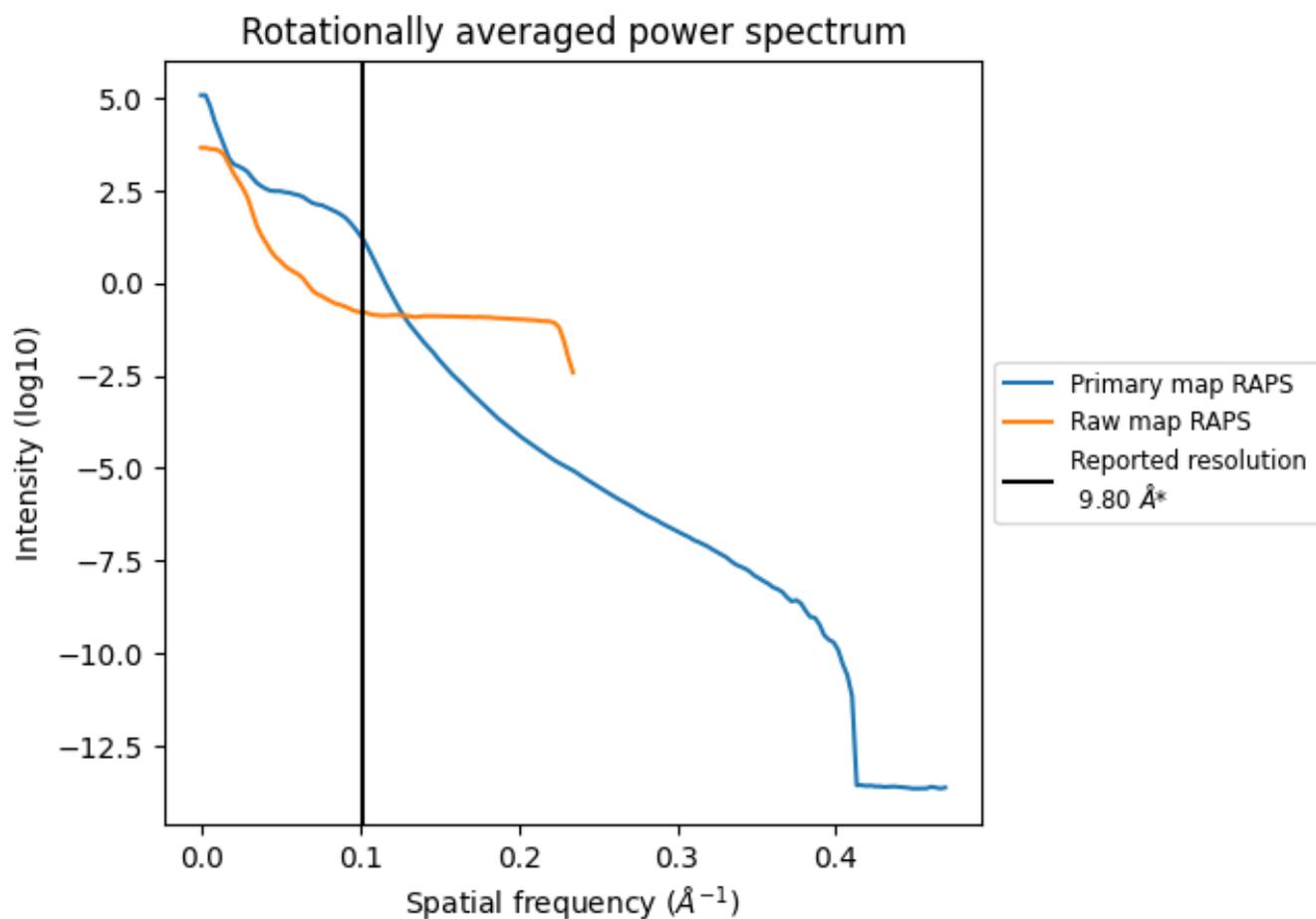
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 397 nm<sup>3</sup>; this corresponds to an approximate mass of 359 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

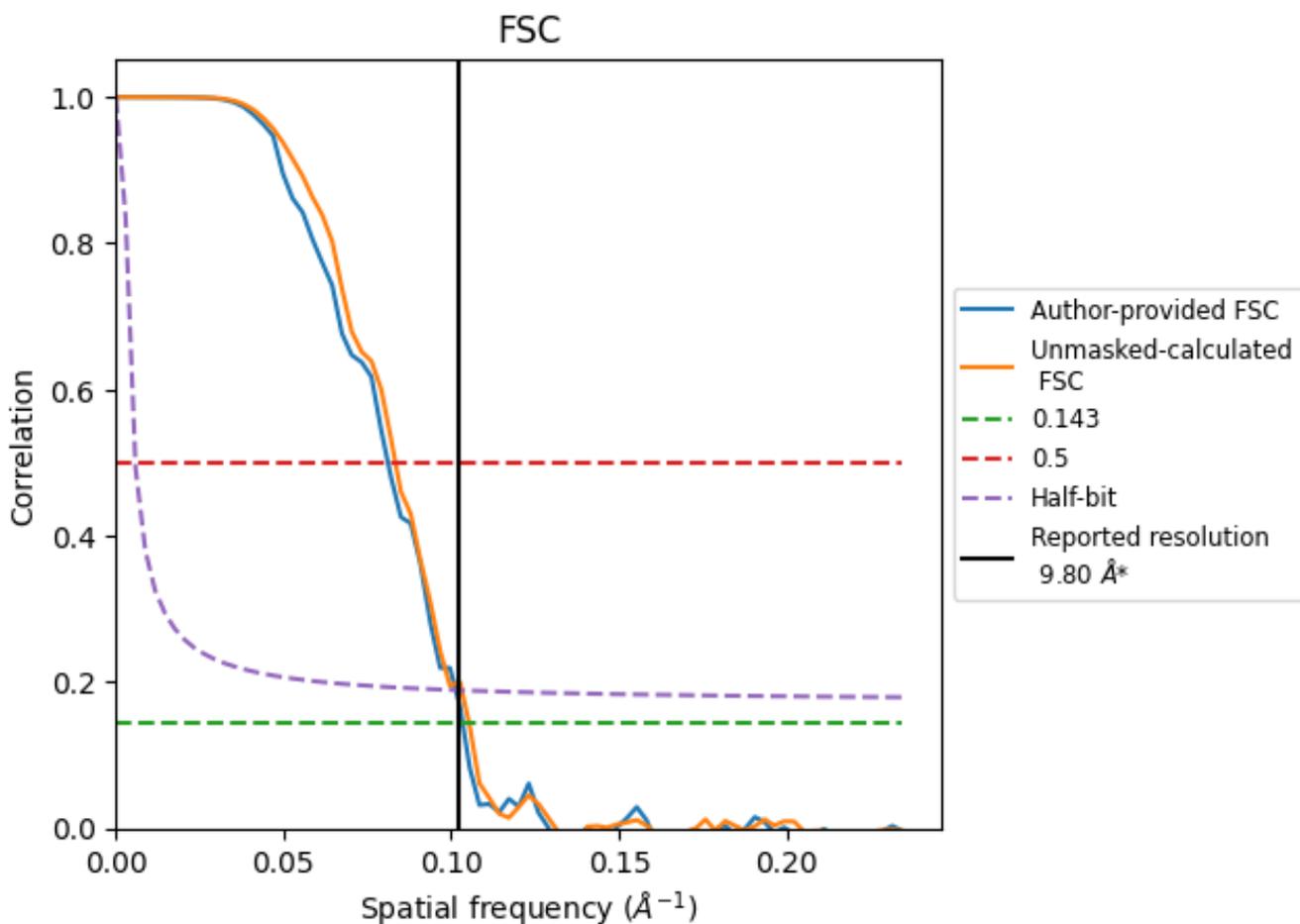


\*Reported resolution corresponds to spatial frequency of 0.102 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.102 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

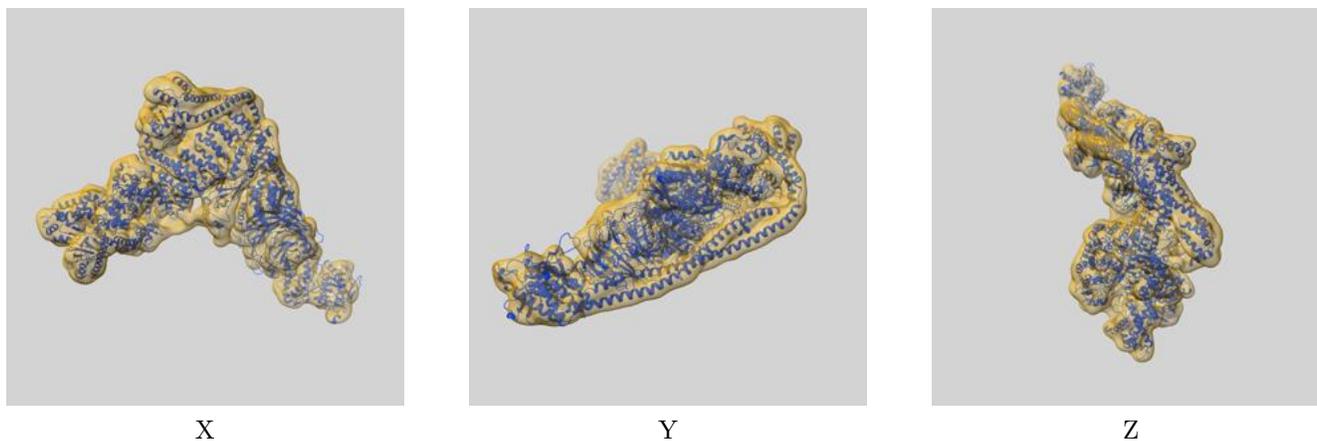
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.80	-	-
Author-provided FSC curve	9.67	12.32	9.87
Unmasked-calculated*	9.50	11.99	9.70

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

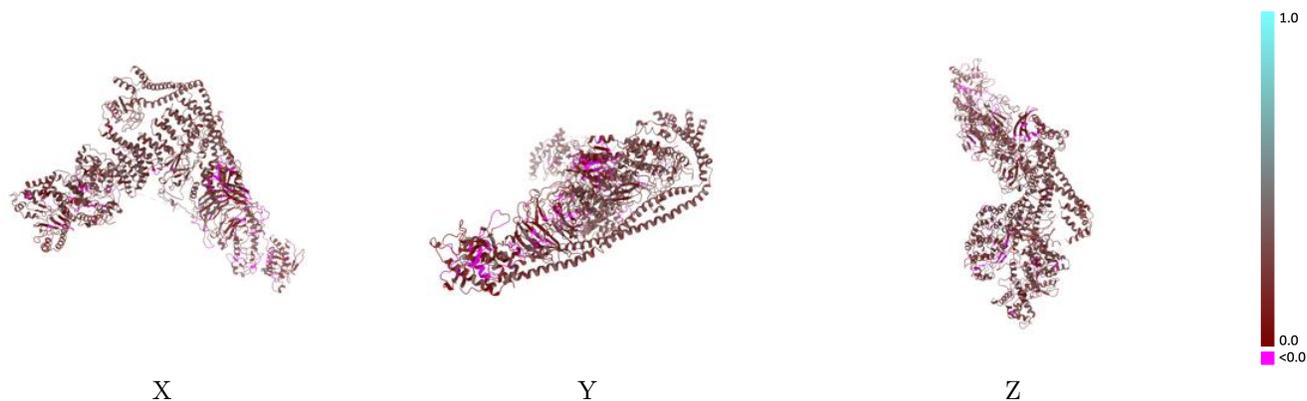
This section contains information regarding the fit between EMDB map EMD-12214 and PDB model 7BL1. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlay [i](#)



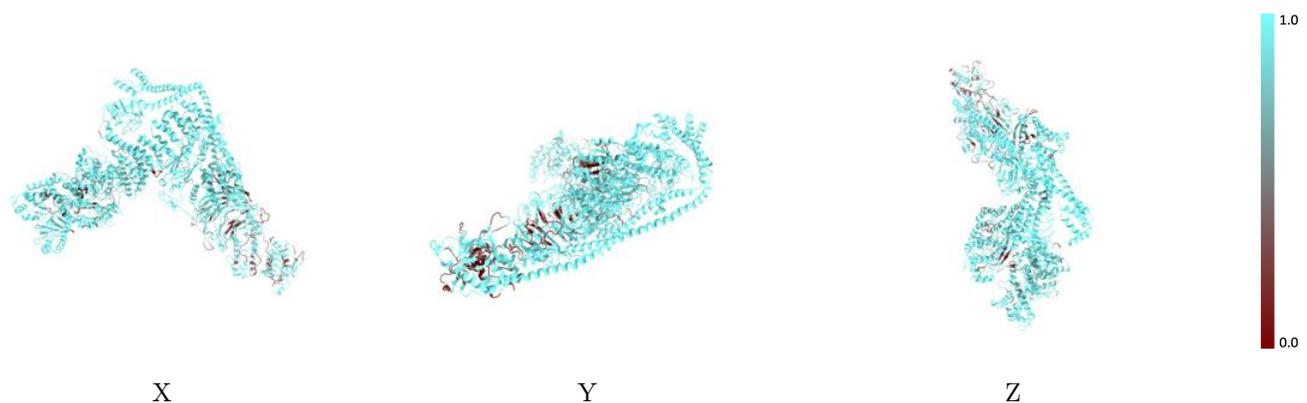
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



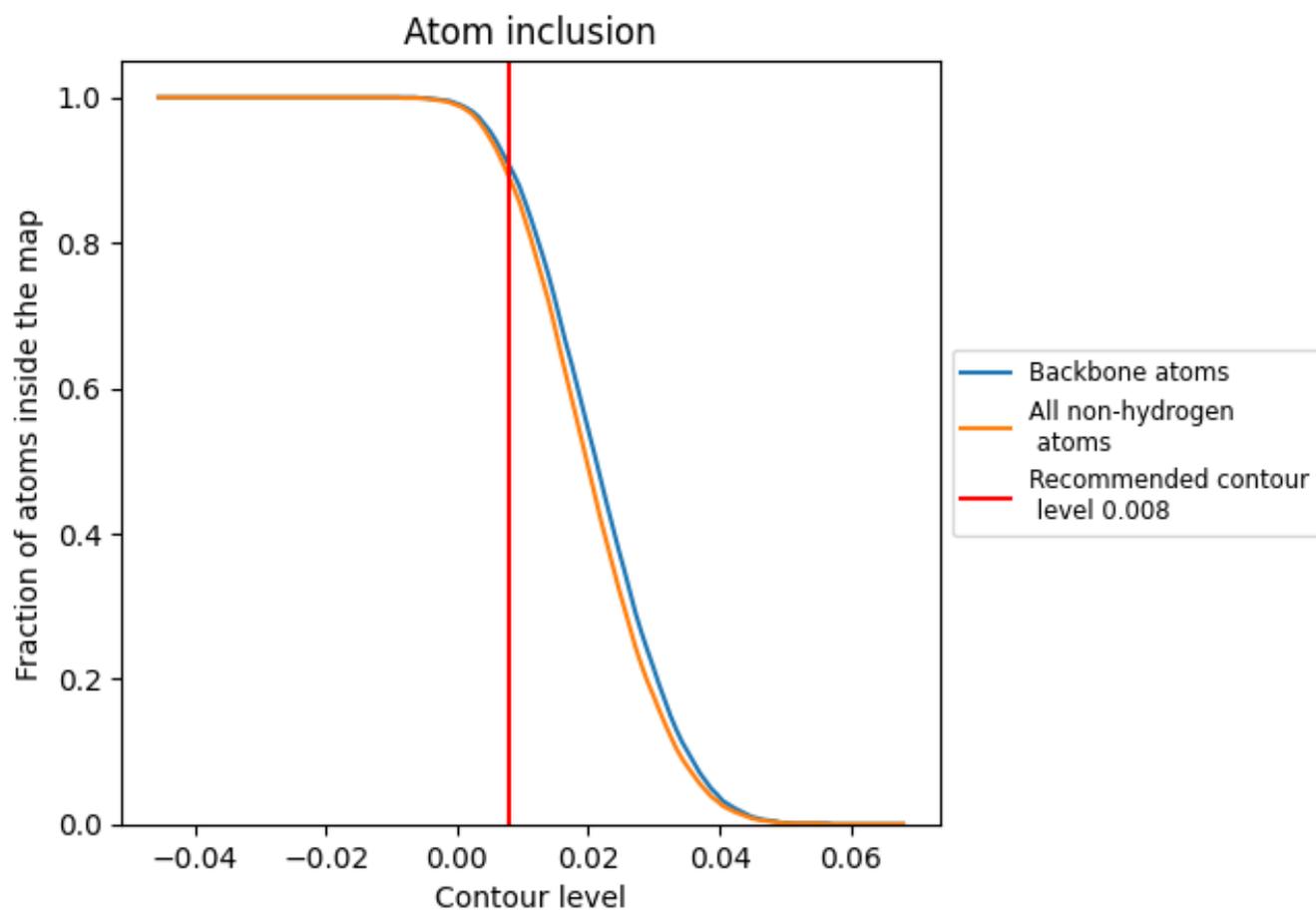
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.2040
AAA	 0.9130	 0.2260
BBB	 0.9230	 0.2240
CCC	 0.8870	 0.2040
DDD	 0.8070	 0.1090
EEE	 0.8420	 0.2000
FFF	 1.0000	 0.2640

