



## Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 07:59 PM JST

PDB ID : 7DGD  
EMDB ID : EMD-30671  
Title : apo state of class C GPCR  
Authors : Zhang, J.Y.; Wu, L.J.; Luo, F.; Hua, T.; Liu, Z.J.  
Deposited on : 2020-11-11  
Resolution : 3.96 Å (reported)

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>.

---

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

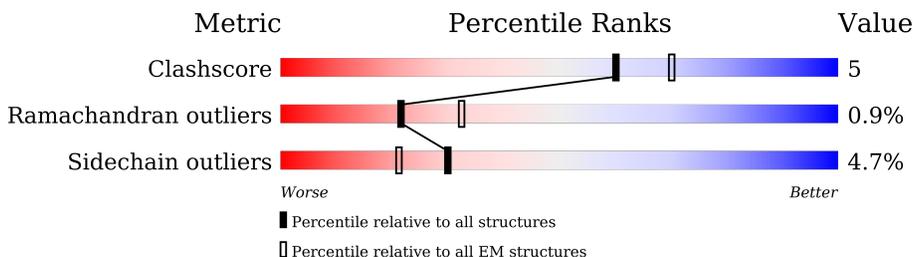
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.96 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	A	833	 80% 14% • 6%
1	B	833	 80% 14% • 6%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12381 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.

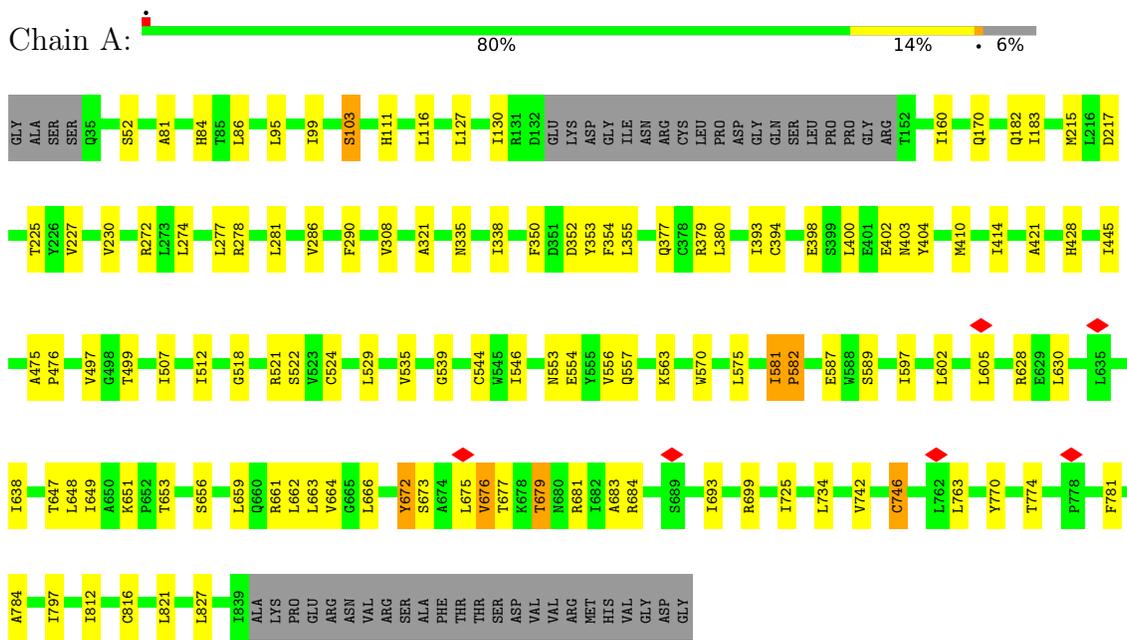
- Molecule 1 is a protein called Metabotropic glutamate receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	786	Total 6194	C 3982	N 1037	O 1126	S 49	0	0
1	B	786	Total 6187	C 3976	N 1037	O 1125	S 49	0	0

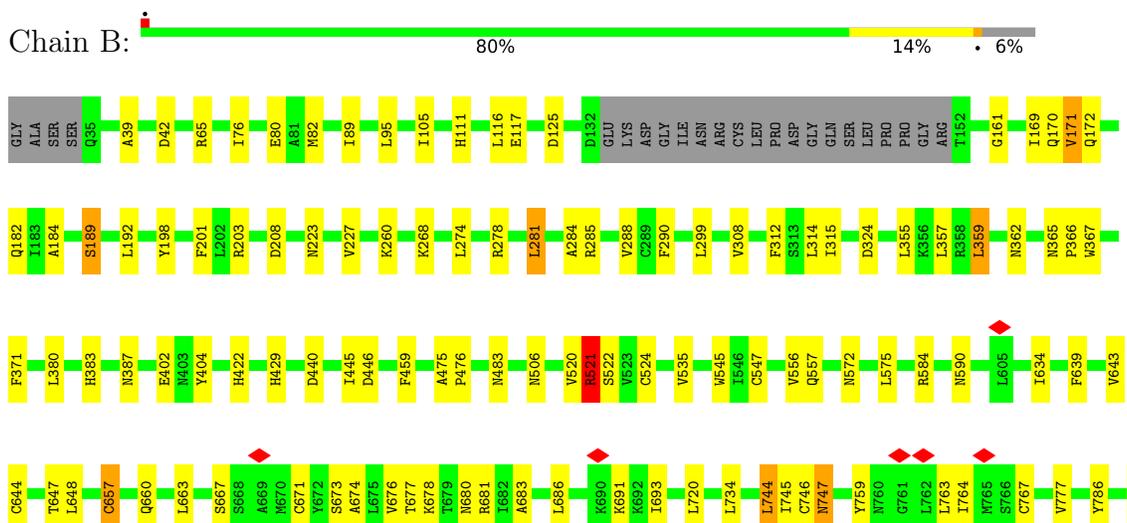
### 3 Residue-property plots

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: Metabotropic glutamate receptor 1



#### • Molecule 1: Metabotropic glutamate receptor 1



M791	N809	T815	C829	I839	ALA	LYS	PRO	GLU	ARG	ASN	VAL	ARG	SER	ALA	PHE	THR	SER	SER	ASP	VAL	VAL	ARG	MET	HIS	VAL	GLY	ASP	GLY
------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	134512	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 ( $e^-/\text{\AA}^2$ )	1.78	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	0.925	Depositor
Minimum map value	-0.767	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	304.56, 304.56, 304.56	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.41, 1.41, 1.41	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.71	0/6333	1.06	3/8591 (0.0%)
1	B	0.72	1/6325 (0.0%)	1.06	4/8580 (0.0%)
All	All	0.71	1/12658 (0.0%)	1.06	7/17171 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	2
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	80	GLU	CD-OE2	10.16	1.36	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	ASP	CB-CG-OD2	-6.97	112.03	118.30
1	B	208	ASP	CB-CG-OD1	6.68	124.31	118.30
1	A	272	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	A	535	VAL	CA-CB-CG1	5.16	118.64	110.90
1	A	746	CYS	CA-CB-SG	5.13	123.23	114.00
1	B	657	CYS	CA-CB-SG	5.10	123.18	114.00
1	B	643	VAL	CA-CB-CG1	5.01	118.42	110.90

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	353	TYR	Sidechain
1	A	499	THR	Peptide
1	A	589	SER	Peptide
1	A	672	TYR	Sidechain
1	B	161	GLY	Peptide
1	B	308	VAL	Peptide

## 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	A	6194	0	6226	53	0
1	B	6187	0	6221	65	0
All	All	12381	0	12447	116	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 5.

All (116) 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:281:LEU:O	1:B:285:ARG:HG2	1.42	1.17
1:B:281:LEU:O	1:B:285:ARG:CG	1.93	1.16
1:B:281:LEU:O	1:B:285:ARG:CD	2.08	1.02
1:B:647:THR:HG23	1:B:663:LEU:HD11	1.52	0.91
1:B:281:LEU:O	1:B:285:ARG:HD3	1.69	0.91
1:A:648:LEU:HD11	1:A:812:ILE:HD11	1.64	0.80
1:B:634:ILE:HD11	1:B:678:LYS:HB2	1.67	0.76
1:A:507:ILE:HD11	1:A:512:ILE:HD13	1.68	0.74
1:B:285:ARG:NH2	1:B:520:VAL:HB	2.09	0.67
1:B:676:VAL:HG21	1:B:763:LEU:HD22	1.77	0.67
1:A:81:ALA:HB1	1:A:414:ILE:HD11	1.79	0.64
1:B:720:LEU:HD22	1:B:759:TYR:CG	2.33	0.64
1:B:89:ILE:HD12	1:B:95:LEU:HD23	1.80	0.64
1:B:169:ILE:HG12	1:B:192:LEU:HD11	1.81	0.63
1:A:597:ILE:HD11	1:A:649:ILE:HG21	1.80	0.63
1:A:95:LEU:HD21	1:A:421:ALA:HB1	1.83	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:LEU:HD11	1:B:404:TYR:CD2	2.38	0.58
1:B:648:LEU:HD23	1:B:816:CYS:HB3	1.85	0.58
1:B:285:ARG:NH2	1:B:520:VAL:H	2.02	0.58
1:A:797:ILE:HG12	1:A:821:LEU:HD11	1.85	0.57
1:A:379:ARG:HH22	1:A:393:ILE:HD11	1.69	0.57
1:B:359:LEU:HD21	1:B:383:HIS:NE2	2.22	0.54
1:B:764:ILE:HD11	1:B:791:MET:HB2	1.88	0.54
1:A:554:GLU:O	1:A:575:LEU:HD13	2.08	0.54
1:A:127:LEU:HD13	1:B:117:GLU:HG2	1.90	0.54
1:A:393:ILE:H	1:A:393:ILE:HD12	1.73	0.53
1:B:535:VAL:HG13	1:B:545:TRP:CD1	2.44	0.53
1:A:116:LEU:HD21	1:A:170:GLN:O	2.08	0.53
1:B:184:ALA:HB3	1:B:203:ARG:HB3	1.91	0.53
1:B:475:ALA:HB1	1:B:476:PRO:HD2	1.91	0.52
1:B:281:LEU:C	1:B:285:ARG:HG2	2.25	0.52
1:A:648:LEU:HD23	1:A:816:CYS:HB3	1.92	0.52
1:A:673:SER:O	1:A:677:THR:HG23	2.09	0.52
1:B:357:LEU:HD21	1:B:362:ASN:HD22	1.75	0.51
1:A:338:ILE:HD11	1:A:512:ILE:HD11	1.92	0.51
1:A:661:ARG:HD3	1:A:725:ILE:HG12	1.93	0.51
1:A:227:VAL:HG12	1:A:286:VAL:HG23	1.92	0.51
1:A:676:VAL:HA	1:A:679:THR:HG22	1.92	0.50
1:B:790:THR:HG21	1:B:830:MET:HG2	1.93	0.50
1:A:400:LEU:H	1:A:400:LEU:HD12	1.77	0.50
1:A:693:ILE:HD12	1:B:693:ILE:HG13	1.92	0.50
1:B:680:ASN:HA	1:B:683:ALA:HB3	1.93	0.50
1:A:581:ILE:HD12	1:A:582:PRO:HD3	1.94	0.50
1:B:39:ALA:HB2	1:B:366:PRO:HD2	1.94	0.50
1:B:644:CYS:HA	1:B:663:LEU:HD22	1.94	0.49
1:B:445:ILE:H	1:B:445:ILE:HD12	1.77	0.49
1:B:189:SER:HB3	1:B:192:LEU:HD13	1.94	0.49
1:B:76:ILE:HD11	1:B:367:TRP:HB2	1.94	0.49
1:A:648:LEU:HD13	1:A:663:LEU:HD22	1.93	0.49
1:B:116:LEU:HD21	1:B:170:GLN:O	2.13	0.49
1:B:520:VAL:HG12	1:B:521:ARG:N	2.28	0.48
1:B:691:LYS:HD3	1:B:777:VAL:HG21	1.95	0.48
1:B:203:ARG:HH11	1:B:203:ARG:HG2	1.77	0.48
1:B:285:ARG:HH22	1:B:520:VAL:H	1.60	0.48
1:B:634:ILE:HD11	1:B:678:LYS:CB	2.41	0.47
1:A:653:THR:H	1:A:656:SER:HB3	1.79	0.47
1:A:99:ILE:HD11	1:A:428:HIS:CE1	2.50	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:LEU:HD11	1:A:404:TYR:CD2	2.49	0.47
1:A:647:THR:HB	1:A:659:LEU:HD21	1.97	0.47
1:A:278:ARG:HD2	1:A:308:VAL:HG11	1.96	0.47
1:A:475:ALA:HB1	1:A:476:PRO:HD2	1.96	0.46
1:A:529:LEU:H	1:A:529:LEU:HD23	1.80	0.46
1:B:284:ALA:HA	1:B:522:SER:HB3	1.97	0.46
1:A:570:TRP:HD1	1:A:581:ILE:HD13	1.80	0.46
1:B:285:ARG:HH22	1:B:520:VAL:HB	1.80	0.46
1:A:587:GLU:HG2	1:A:651:LYS:H	1.80	0.46
1:B:380:LEU:HD23	1:B:383:HIS:CD2	2.51	0.46
1:B:734:LEU:HD12	1:B:744:LEU:HD13	1.98	0.46
1:A:230:VAL:CG2	1:A:277:LEU:HD21	2.46	0.45
1:A:160:ILE:HD13	1:A:183:ILE:HD11	1.96	0.45
1:A:278:ARG:HA	1:A:281:LEU:HD21	1.98	0.45
1:A:380:LEU:HD21	1:A:394:CYS:SG	2.56	0.45
1:A:676:VAL:HG11	1:A:763:LEU:HD21	1.99	0.45
1:A:581:ILE:H	1:A:581:ILE:HG13	1.68	0.45
1:A:638:ILE:HG21	1:A:827:LEU:HD12	1.99	0.45
1:A:663:LEU:HD23	1:A:664:VAL:N	2.32	0.44
1:A:672:TYR:CE2	1:A:675:LEU:HD23	2.52	0.44
1:B:663:LEU:HA	1:B:667:SER:HB3	1.98	0.44
1:B:227:VAL:HG11	1:B:288:VAL:HG23	2.00	0.44
1:B:274:LEU:HD11	1:B:299:LEU:HD12	1.99	0.43
1:B:422:HIS:CD2	1:B:459:PHE:HB3	2.53	0.43
1:B:673:SER:O	1:B:677:THR:HG23	2.19	0.43
1:B:745:ILE:HG22	1:B:746:CYS:O	2.19	0.43
1:A:630:LEU:HD11	1:A:681:ARG:HD3	2.00	0.43
1:B:355:LEU:HD21	1:B:404:TYR:CG	2.54	0.43
1:B:535:VAL:HG22	1:B:545:TRP:NE1	2.33	0.43
1:A:497:VAL:O	1:A:507:ILE:HD12	2.19	0.43
1:B:535:VAL:HG13	1:B:545:TRP:CG	2.53	0.43
1:A:683:ALA:HB1	1:A:770:TYR:CD2	2.54	0.42
1:A:734:LEU:HD11	1:A:742:VAL:HG12	2.01	0.42
1:B:288:VAL:HG22	1:B:315:ILE:HD11	2.01	0.42
1:B:786:TYR:O	1:B:790:THR:HG23	2.18	0.42
1:B:817:PHE:CE2	1:B:821:LEU:HD11	2.54	0.42
1:A:225:THR:H	1:A:522:SER:CB	2.32	0.42
1:A:602:LEU:HD23	1:A:605:LEU:HD12	2.02	0.42
1:B:521:ARG:HD3	1:B:521:ARG:HA	1.43	0.42
1:A:662:LEU:HA	1:A:666:LEU:HD13	2.01	0.42
1:B:65:ARG:HH22	1:B:117:GLU:HB2	1.84	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:556:VAL:H	1:B:575:LEU:HB3	1.85	0.41
1:B:172:GLN:HE22	1:B:198:TYR:HA	1.84	0.41
1:B:192:LEU:HD23	1:B:201:PHE:CZ	2.55	0.41
1:B:790:THR:HG22	1:B:829:CYS:HB3	2.01	0.41
1:A:86:LEU:HD22	1:A:103:SER:HB3	2.01	0.41
1:A:350:PHE:CZ	1:A:354:PHE:HB2	2.56	0.41
1:A:774:THR:HB	1:A:784:ALA:HB1	2.03	0.41
1:A:127:LEU:HA	1:A:130:ILE:HG22	2.02	0.41
1:B:285:ARG:HB3	1:B:312:PHE:HB3	2.03	0.41
1:B:314:LEU:HD23	1:B:314:LEU:H	1.85	0.41
1:B:520:VAL:CG1	1:B:521:ARG:N	2.83	0.41
1:B:648:LEU:HD21	1:B:815:THR:OG1	2.20	0.41
1:B:105:ILE:N	1:B:105:ILE:HD12	2.36	0.41
1:B:634:ILE:HA	1:B:674:ALA:HB1	2.03	0.41
1:A:350:PHE:CG	1:A:410:MET:HE2	2.57	0.40
1:A:597:ILE:HD11	1:A:649:ILE:CG2	2.49	0.40
1:B:171:VAL:HG13	1:B:182:GLN:HE22	1.86	0.40
1:A:684:ARG:HE	1:A:699:ARG:HB3	1.87	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	782/833 (94%)	694 (89%)	78 (10%)	10 (1%)	<b>12</b> 47
1	B	782/833 (94%)	712 (91%)	66 (8%)	4 (0%)	29 <b>66</b>
All	All	1564/1666 (94%)	1406 (90%)	144 (9%)	14 (1%)	<b>21</b> 54

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	SER
1	A	539	GLY
1	A	781	PHE
1	A	518	GLY
1	A	546	ILE
1	B	402	GLU
1	B	521	ARG
1	B	747	ASN
1	A	402	GLU
1	A	521	ARG
1	A	321	ALA
1	B	744	LEU
1	A	556	VAL
1	A	582	PRO

### 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	685/723 (95%)	661 (96%)	24 (4%)	36	61
1	B	684/723 (95%)	644 (94%)	40 (6%)	20	48
All	All	1369/1446 (95%)	1305 (95%)	64 (5%)	30	53

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	HIS
1	A	103	SER
1	A	111	HIS
1	A	182	GLN
1	A	215	MET
1	A	217	ASP
1	A	274	LEU
1	A	290	PHE
1	A	335	ASN
1	A	352	ASP

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	377	GLN
1	A	398	GLU
1	A	403	ASN
1	A	445	ILE
1	A	524	CYS
1	A	544	CYS
1	A	553	ASN
1	A	557	GLN
1	A	563	LYS
1	A	581	ILE
1	A	628	ARG
1	A	676	VAL
1	A	679	THR
1	A	746	CYS
1	B	42	ASP
1	B	82	MET
1	B	111	HIS
1	B	125	ASP
1	B	171	VAL
1	B	189	SER
1	B	223	ASN
1	B	260	LYS
1	B	268	LYS
1	B	278	ARG
1	B	281	LEU
1	B	290	PHE
1	B	324	ASP
1	B	359	LEU
1	B	365	ASN
1	B	371	PHE
1	B	387	ASN
1	B	429	HIS
1	B	440	ASP
1	B	446	ASP
1	B	483	ASN
1	B	506	ASN
1	B	521	ARG
1	B	524	CYS
1	B	547	CYS
1	B	557	GLN
1	B	572	ASN
1	B	584	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	590	ASN
1	B	639	PHE
1	B	657	CYS
1	B	660	GLN
1	B	671	CYS
1	B	681	ARG
1	B	686	LEU
1	B	747	ASN
1	B	767	CYS
1	B	791	MET
1	B	809	ASN
1	B	810	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	173	ASN
1	A	231	HIS
1	A	250	GLN
1	A	365	ASN
1	A	387	ASN
1	B	77	GLN
1	B	172	GLN
1	B	173	ASN
1	B	182	GLN
1	B	223	ASN
1	B	362	ASN
1	B	365	ASN
1	B	557	GLN
1	B	572	ASN
1	B	590	ASN
1	B	660	GLN
1	B	680	ASN

### 5.3.3 RNA

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](#)

There are no ligands in this entry.

## 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.

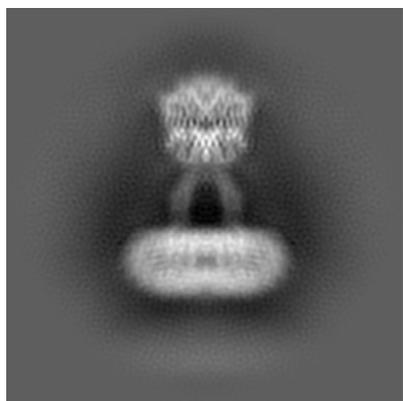
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30671. These allow visual inspection of the internal detail of the map and identification of artifacts.

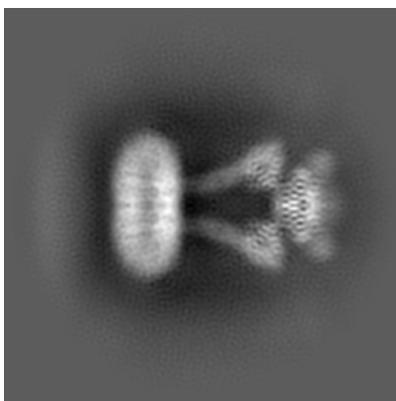
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

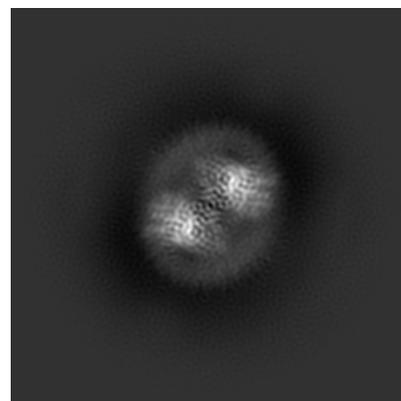
#### 6.1.1 Primary map



X



Y

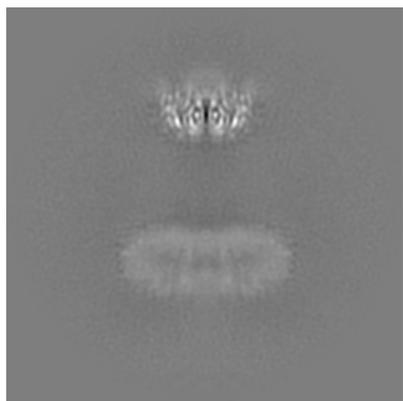


Z

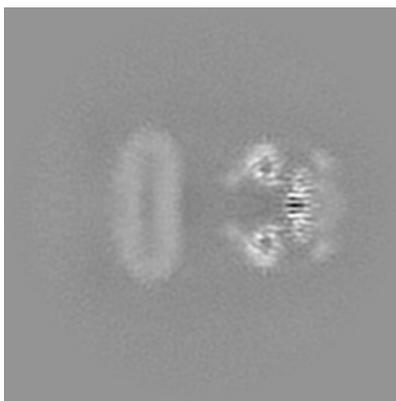
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

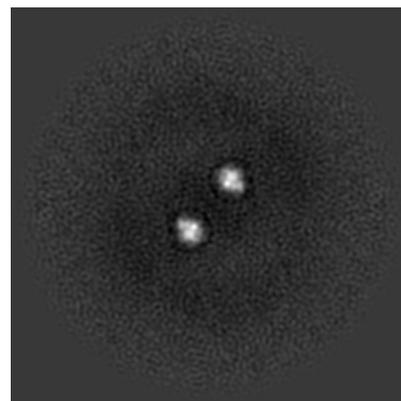
#### 6.2.1 Primary map



X Index: 108



Y Index: 108

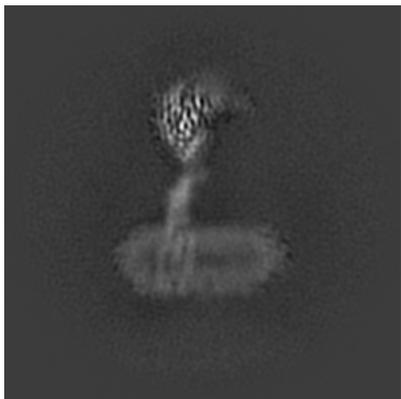


Z Index: 108

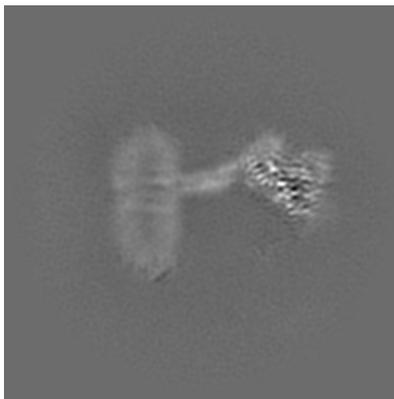
The images above show central slices of the map in three orthogonal directions.

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

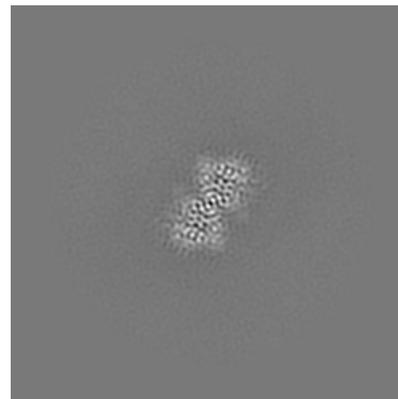
### 6.3.1 Primary map



X Index: 97



Y Index: 120



Z Index: 157

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

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

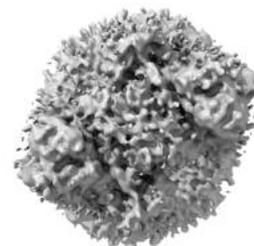
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

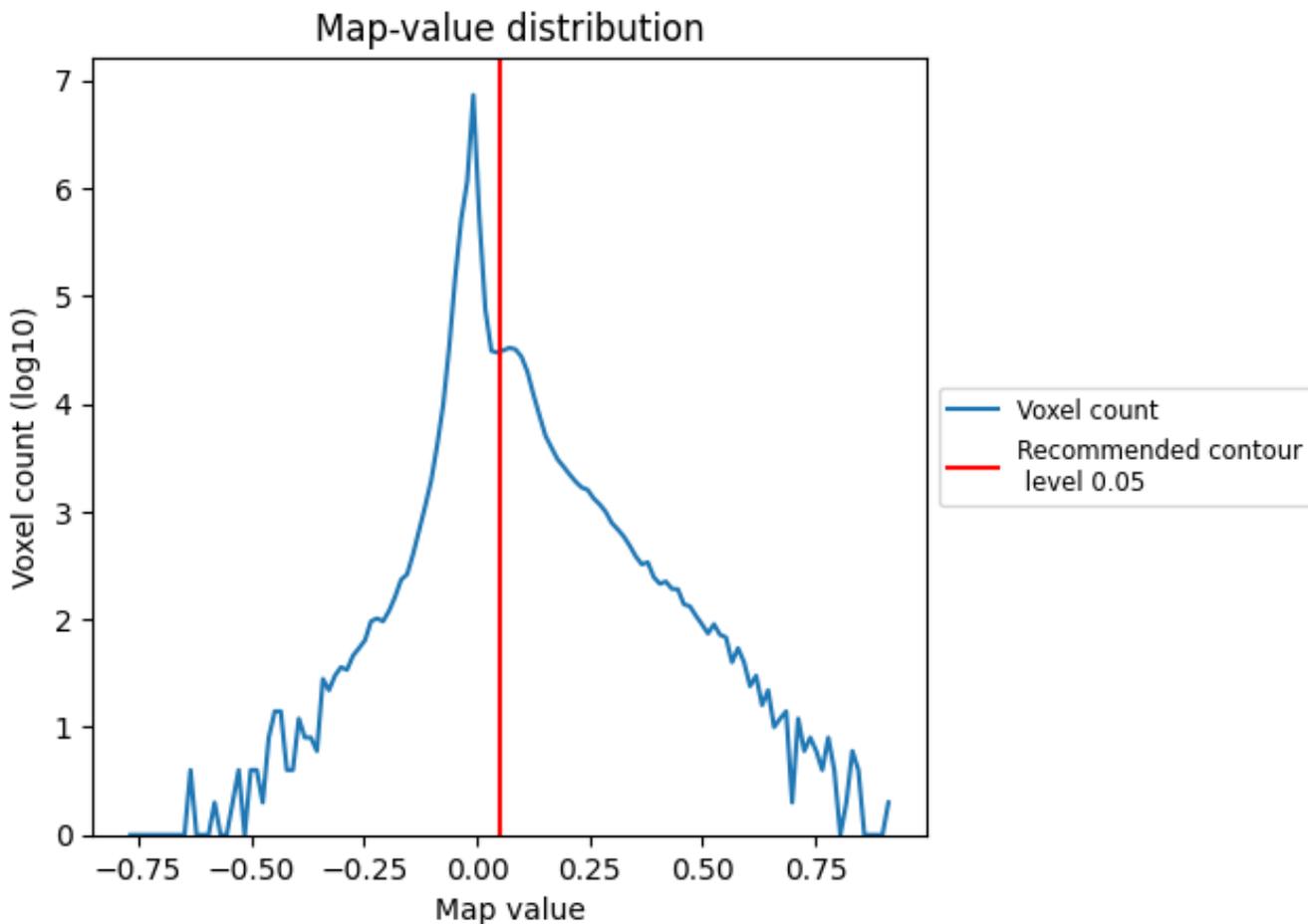
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

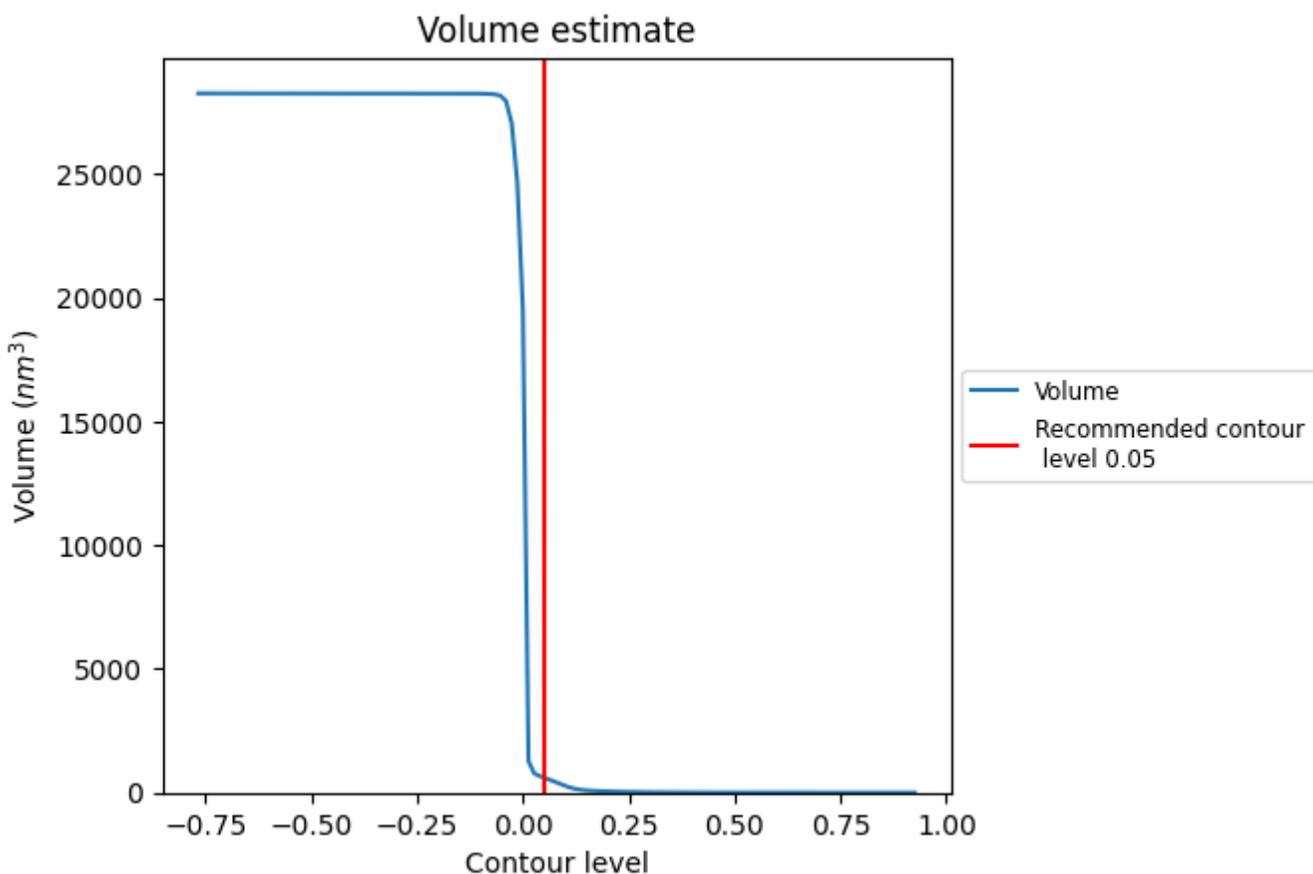
This section contains the results of statistical analysis of the map.

### 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.

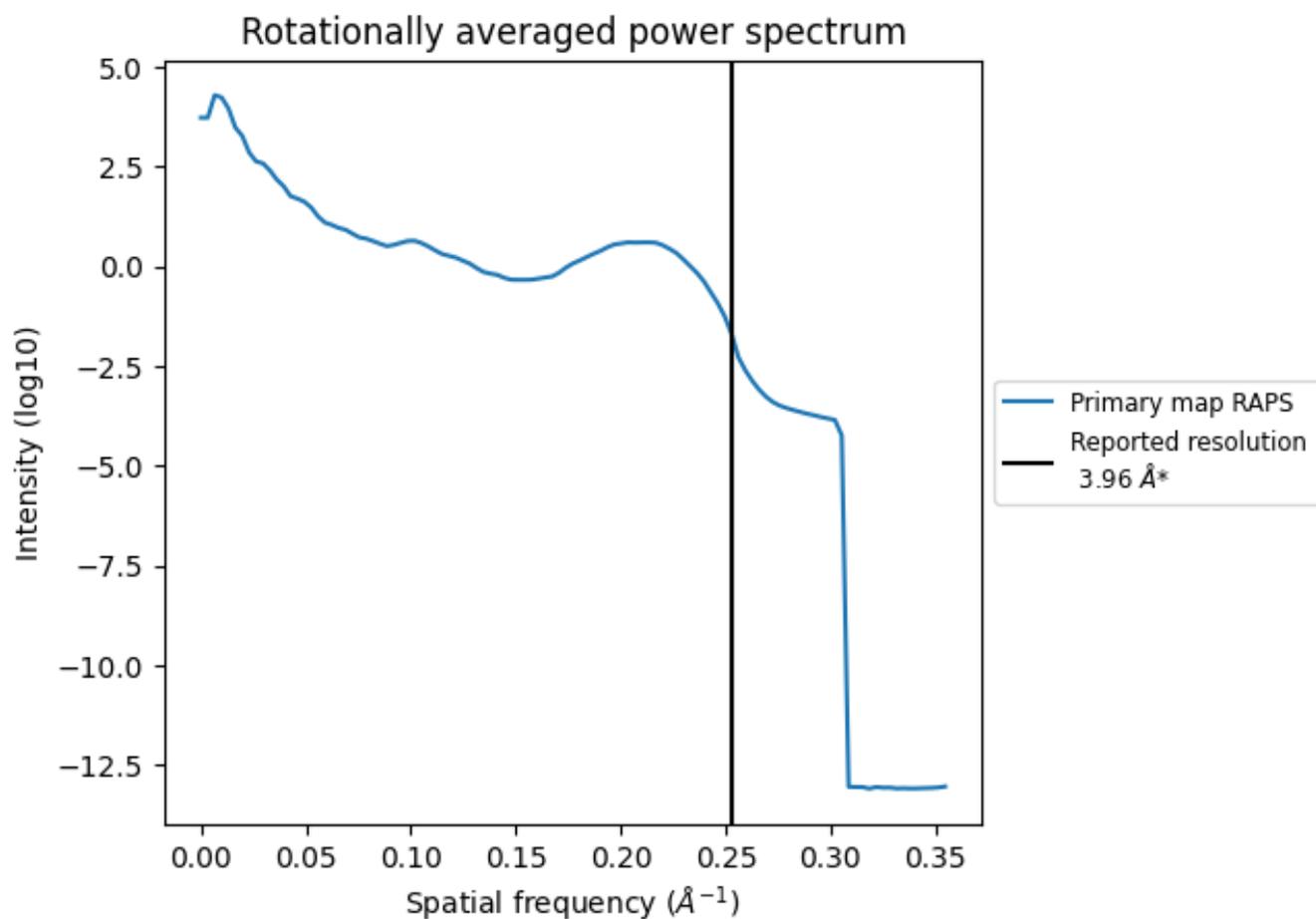
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 602 nm<sup>3</sup>; this corresponds to an approximate mass of 544 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 i



\*Reported resolution corresponds to spatial frequency of 0.253 Å<sup>-1</sup>

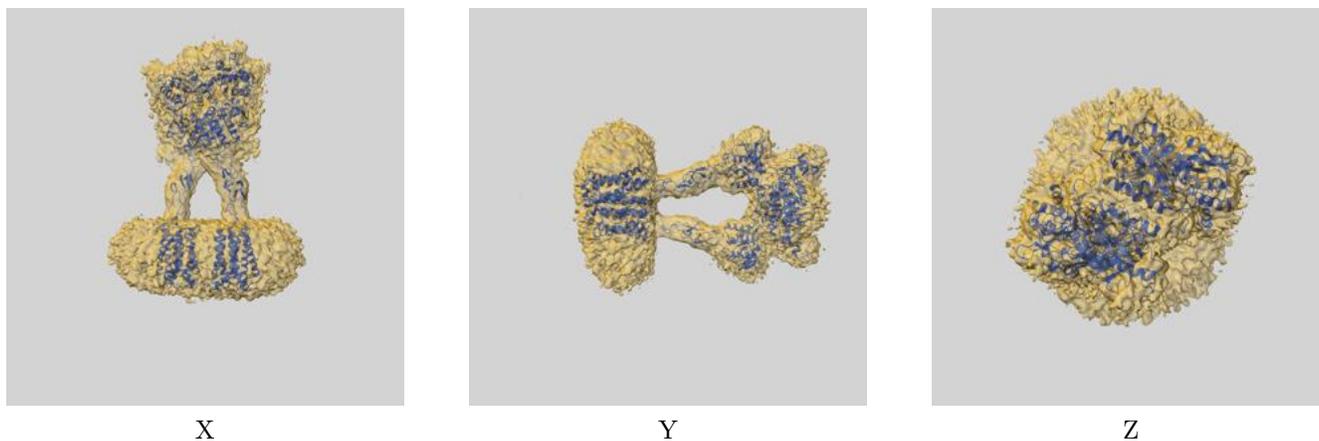
## 8 Fourier-Shell correlation

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

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

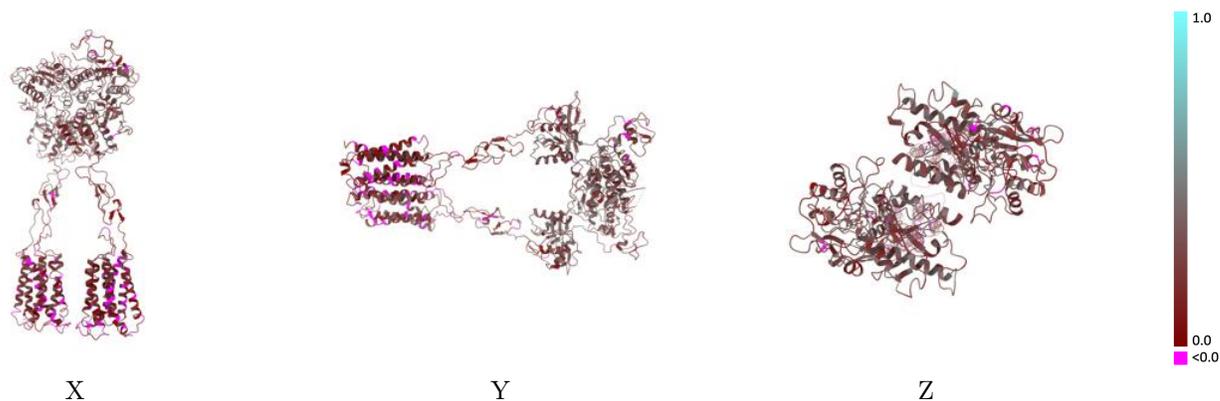
This section contains information regarding the fit between EMDB map EMD-30671 and PDB model 7DGD. Per-residue inclusion information can be found in section [3](#) on page [4](#).

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



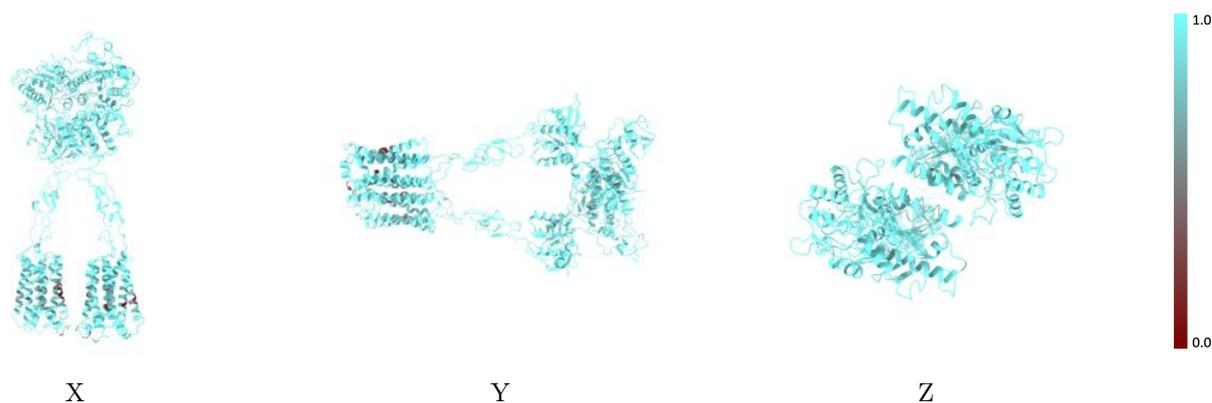
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



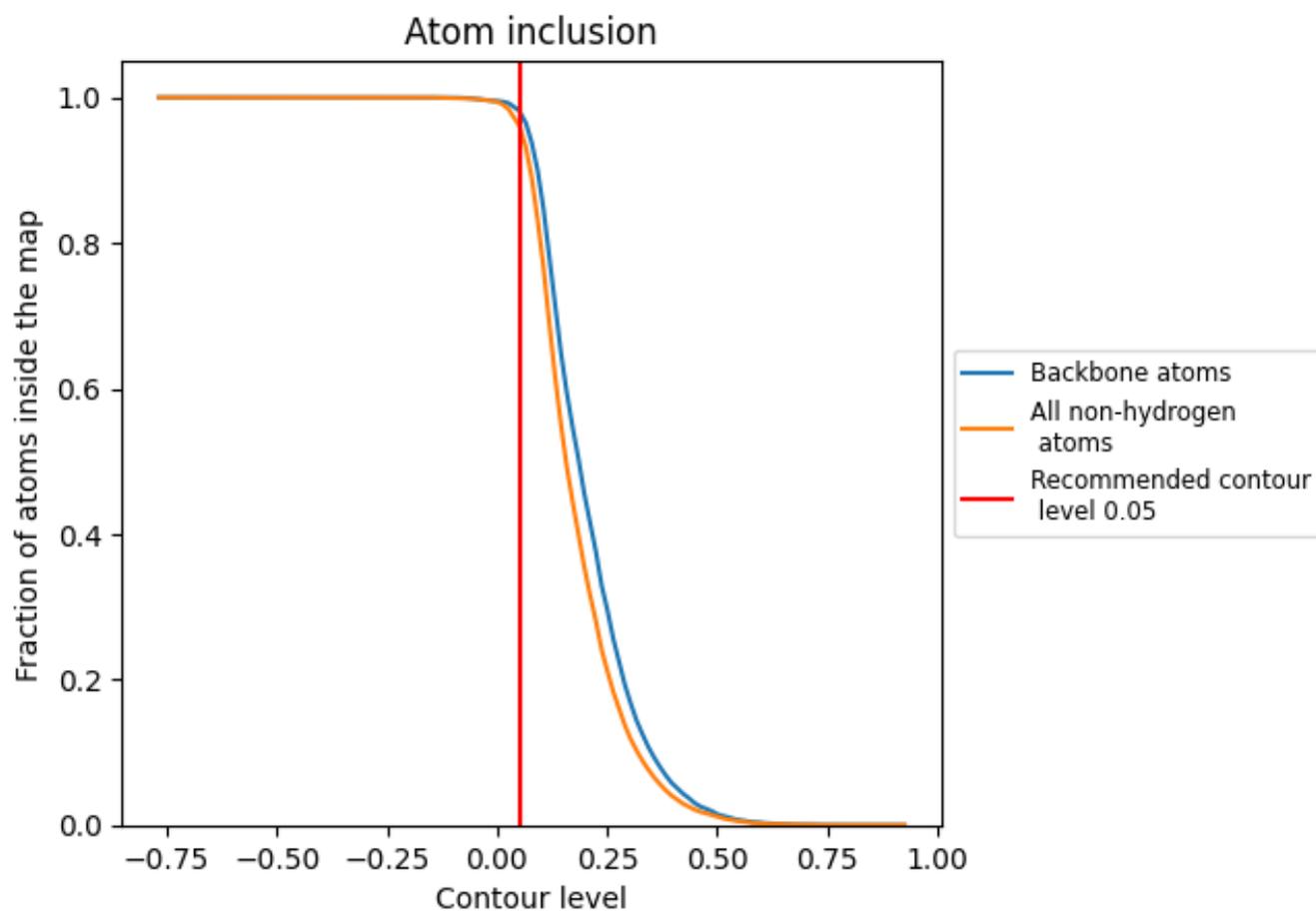
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9617	 0.2320
A	 0.9624	 0.2300
B	 0.9609	 0.2350

