



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 03:56 AM UTC

PDB ID : 7YOO / pdb_00007yoo
EMDB ID : EMD-33985
Title : Complex structure of Neuropeptide Y Y2 receptor in complex with NPY and Gi
Authors : Kang, H.; Park, C.; Kim, J.; Choi, H.-J.
Deposited on : 2022-08-01
Resolution : 3.11 Å (reported)
Based on initial models : 7DDZ, 7VGX

This is a Full wwPDB EM Validation 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:

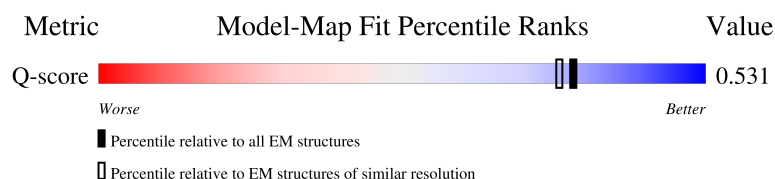
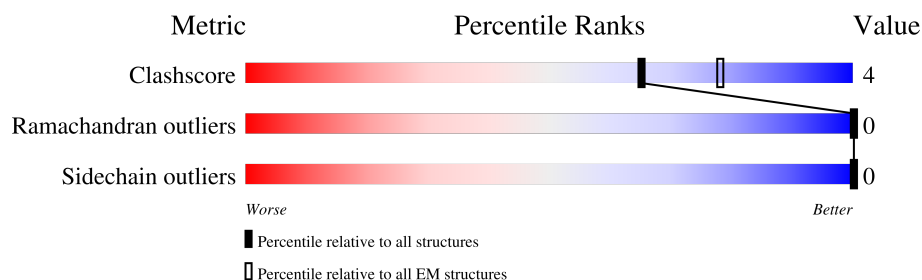
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.11 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	14465 (2.61 - 3.61)

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	354	
2	B	345	
3	G	71	
4	L	36	

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Mol	Chain	Length	Quality of chain
5	R	391	73%23%
6	S	259	75%15%10%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9188 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	216	Total	C	N	O	S	0	0
			1743	1109	291	331	12		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	335	Total	C	N	O	S	0	0
			2576	1589	464	502	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP P62873
B	-3	PRO	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	54	Total	C	N	O	S	0	0
			418	263	74	78	3		

- Molecule 4 is a protein called Neuropeptide Y.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	29	Total	C	N	O	S	0	0
			255	162	48	44	1		

- Molecule 5 is a protein called Neuropeptide Y receptor type 2.

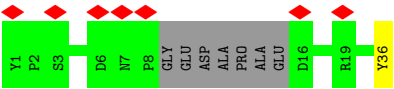
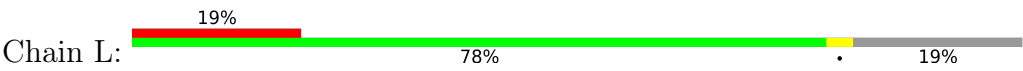
Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	302	Total	C	N	O	S	0	0
			2402	1595	385	408	14		

There are 13 discrepancies between the modelled and reference sequences:

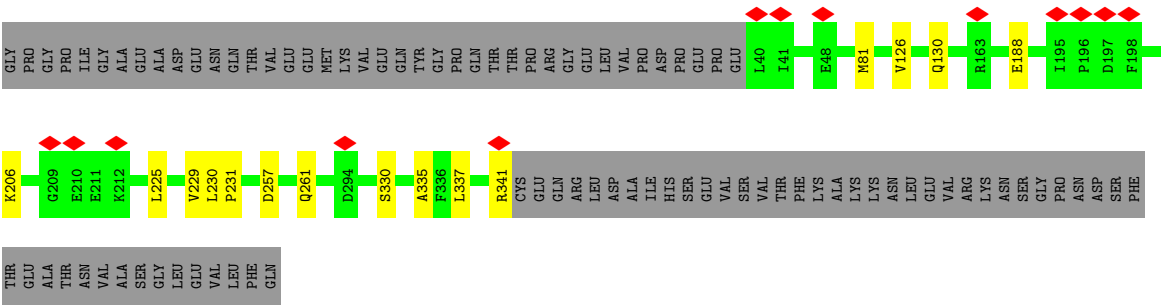
Chain	Residue	Modelled	Actual	Comment	Reference
R	0	GLY	-	expression tag	UNP P49146
R	1	PRO	-	expression tag	UNP P49146
R	149	TYR	HIS	engineered mutation	UNP P49146
R	280	CYS	SER	engineered mutation	UNP P49146
R	382	ALA	-	expression tag	UNP P49146
R	383	SER	-	expression tag	UNP P49146
R	384	GLY	-	expression tag	UNP P49146
R	385	LEU	-	expression tag	UNP P49146
R	386	GLU	-	expression tag	UNP P49146
R	387	VAL	-	expression tag	UNP P49146
R	388	LEU	-	expression tag	UNP P49146
R	389	PHE	-	expression tag	UNP P49146
R	390	GLN	-	expression tag	UNP P49146

- Molecule 6 is a protein called single-chain antibody Fv fragment (scFv16).

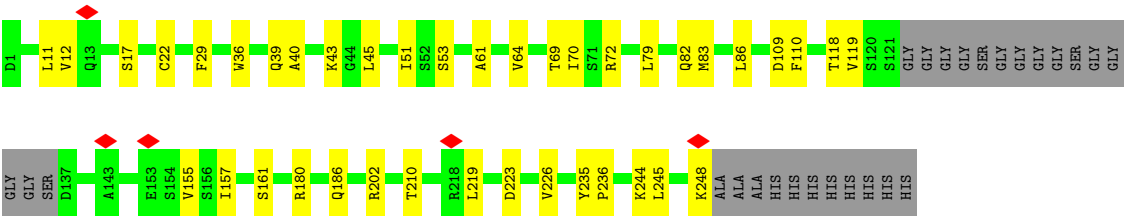
Mol	Chain	Residues	Atoms					AltConf	Trace
6	S	233	Total	C	N	O	S	0	0
			1794	1138	297	349	10		



• Molecule 5: Neuropeptide Y receptor type 2



• Molecule 6: single-chain antibody Fv fragment (scFv16)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	500366	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 ($e^-/\text{\AA}^2$)	66	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2250	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	7.615	Depositor
Minimum map value	-2.536	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.6	Depositor
Map size ($\text{\AA}$)	336.6, 336.6, 336.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.84150004, 0.84150004, 0.84150004	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: TYC

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	0.09	0/1772	0.23	0/2374
2	B	0.10	0/2623	0.25	0/3555
3	G	0.09	0/424	0.20	0/572
4	L	0.07	0/248	0.18	0/334
5	R	0.09	0/2460	0.21	0/3352
6	S	0.10	0/1838	0.26	0/2491
All	All	0.09	0/9365	0.24	0/12678

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	A	1743	0	1735	17	0
2	B	2576	0	2482	25	0
3	G	418	0	431	3	0
4	L	255	0	248	0	0
5	R	2402	0	2515	9	0
6	S	1794	0	1732	22	0
All	All	9188	0	9143	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 4.

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)
6:S:40:ALA:HB3	6:S:43:LYS:HB2	1.75	0.69
2:B:51:LEU:HB2	2:B:336:LEU:HB2	1.79	0.65
2:B:333:ASP:O	2:B:333:ASP:OD1	2.15	0.64
6:S:83:MET:HE2	6:S:86:LEU:HD21	1.80	0.62
1:A:352:GLY:HA2	5:R:330:SER:OG	2.01	0.61
6:S:29:PHE:O	6:S:72:ARG:NH2	2.34	0.60
2:B:49:ARG:HB2	2:B:338:ILE:HD13	1.82	0.60
1:A:227:LEU:HD13	1:A:268:LEU:HD12	1.84	0.59
2:B:286:LEU:HB3	2:B:318:LEU:HD11	1.85	0.58
6:S:202:ARG:NH2	6:S:223:ASP:OD2	2.36	0.58
2:B:285:LEU:HB3	2:B:297:TRP:HB2	1.86	0.58
6:S:39:GLN:HB2	6:S:45:LEU:HD23	1.85	0.58
2:B:229:ILE:HA	2:B:245:SER:HA	1.85	0.58
1:A:325:CYS:SG	1:A:326:ALA:N	2.78	0.57
5:R:81:MET:HE1	5:R:335:ALA:HB2	1.87	0.56
6:S:109:ASP:OD1	6:S:110:PHE:N	2.39	0.55
6:S:12:VAL:HB	6:S:119:VAL:HG22	1.87	0.55
1:A:262:THR:O	1:A:317:LYS:NZ	2.37	0.55
2:B:49:ARG:NH1	3:G:61:PHE:O	2.40	0.55
2:B:234:PHE:CE2	2:B:238:GLY:HA2	2.43	0.54
5:R:126:VAL:HG12	5:R:130:GLN:HE21	1.72	0.53
6:S:155:VAL:HG22	6:S:219:LEU:HD11	1.92	0.52
6:S:161:SER:HB3	6:S:210:THR:HG23	1.92	0.52
2:B:271:CYS:HB3	2:B:290:ASP:HB2	1.91	0.52
5:R:337:LEU:HB3	5:R:341:ARG:HH21	1.74	0.51
1:A:251:ASP:HB2	1:A:310:LEU:HD22	1.91	0.51
2:B:160:SER:HB3	2:B:190:LEU:HD23	1.91	0.51
6:S:11:LEU:HD23	6:S:118:THR:HB	1.92	0.51
1:A:48:THR:HA	1:A:51:LYS:HE3	1.93	0.50
1:A:327:THR:HG22	1:A:329:THR:HG22	1.92	0.49
6:S:180:ARG:NH1	6:S:186:GLN:OE1	2.44	0.49
6:S:226:VAL:HG22	6:S:244:LYS:HG2	1.94	0.49
6:S:157:ILE:HD11	6:S:245:LEU:HD11	1.96	0.48
1:A:52:GLN:NE2	1:A:328:ASP:OD1	2.46	0.47
1:A:226:ALA:HB3	1:A:229:ASP:HB2	1.97	0.47
3:G:26:ASP:OD1	3:G:26:ASP:N	2.48	0.47
1:A:36:LEU:HD23	1:A:222:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:22:CYS:N	6:S:79:LEU:O	2.48	0.46
6:S:235:TYR:HB3	6:S:236:PRO:HD3	1.96	0.46
2:B:155:ASN:ND2	2:B:170:ASP:OD1	2.49	0.46
2:B:222:PHE:HE1	2:B:258:ASP:HA	1.79	0.46
2:B:232:ILE:HG12	2:B:243:THR:HG22	1.96	0.46
6:S:17:SER:OG	6:S:83:MET:O	2.32	0.46
1:A:40:GLY:O	1:A:44:SER:OG	2.28	0.45
1:A:225:VAL:HG23	1:A:268:LEU:HD13	1.97	0.45
5:R:188:GLU:HG2	5:R:206:LYS:HB2	1.98	0.45
6:S:69:THR:HB	6:S:82:GLN:HB3	1.98	0.45
2:B:318:LEU:HB2	2:B:329:THR:HG22	1.99	0.45
1:A:229:ASP:HA	1:A:232:LEU:HD13	1.98	0.45
2:B:192:LEU:HD23	2:B:199:PHE:HB3	1.99	0.44
5:R:257:ASP:O	5:R:261:GLN:HG2	2.18	0.44
6:S:51:ILE:HG12	6:S:72:ARG:HG3	1.98	0.44
1:A:38:LEU:HD23	1:A:200:ASP:OD1	2.17	0.44
2:B:30:LEU:HD13	3:G:34:ALA:HB1	2.00	0.44
2:B:151:PHE:HA	2:B:157:ILE:HG13	1.99	0.43
5:R:225:LEU:HA	5:R:229:VAL:HB	2.01	0.43
2:B:211:TRP:CZ3	2:B:218:CYS:HB2	2.54	0.42
6:S:61:ALA:HB3	6:S:64:VAL:HG22	2.02	0.42
6:S:248:LYS:HE3	6:S:248:LYS:HB2	1.80	0.42
2:B:246:ASP:HA	2:B:272:GLY:HA3	2.01	0.42
2:B:253:PHE:CE1	2:B:260:GLU:HG2	2.54	0.42
2:B:188:MET:HE3	2:B:188:MET:HB3	1.83	0.42
2:B:64:GLY:HA2	2:B:105:TYR:CD2	2.55	0.42
2:B:108:SER:OG	2:B:154:ASP:OD1	2.33	0.42
5:R:230:LEU:HB3	5:R:231:PRO:HD3	2.02	0.41
6:S:53:SER:HA	6:S:72:ARG:NH1	2.35	0.41
2:B:169:TRP:HA	2:B:176:GLN:HA	2.03	0.41
1:A:45:GLY:HA3	1:A:270:LYS:HZ1	1.86	0.41
1:A:47:SER:O	1:A:51:LYS:HG2	2.20	0.41
2:B:202:GLY:HA3	2:B:229:ILE:HD11	2.01	0.40
5:R:188:GLU:HB3	5:R:206:LYS:HE3	2.02	0.40
6:S:36:TRP:HD1	6:S:70:ILE:HD12	1.86	0.40
1:A:247:MET:SD	1:A:287:TYR:OH	2.78	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	210/354 (59%)	204 (97%)	6 (3%)	0	100	100
2	B	333/345 (96%)	328 (98%)	5 (2%)	0	100	100
3	G	52/71 (73%)	52 (100%)	0	0	100	100
4	L	25/36 (69%)	25 (100%)	0	0	100	100
5	R	300/391 (77%)	297 (99%)	3 (1%)	0	100	100
6	S	229/259 (88%)	223 (97%)	6 (3%)	0	100	100
All	All	1149/1456 (79%)	1129 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/305 (63%)	192 (100%)	0	100	100
2	B	278/285 (98%)	278 (100%)	0	100	100
3	G	44/58 (76%)	44 (100%)	0	100	100
4	L	26/30 (87%)	26 (100%)	0	100	100
5	R	269/345 (78%)	269 (100%)	0	100	100
6	S	198/209 (95%)	198 (100%)	0	100	100
All	All	1007/1232 (82%)	1007 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	311	ASN
1	A	331	ASN
2	B	36	ASN
5	R	130	GLN
5	R	155	HIS
6	S	194	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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
4	TYC	L	36	4	13,13,13	1.74	2 (15%)	17,17,17	0.77	0

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
4	TYC	L	36	4	-	2/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	36	TYC	C-NXT	5.35	1.45	1.32
4	L	36	TYC	O-C	-2.75	1.18	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	36	TYC	O-C-CA-CB
4	L	36	TYC	NXT-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

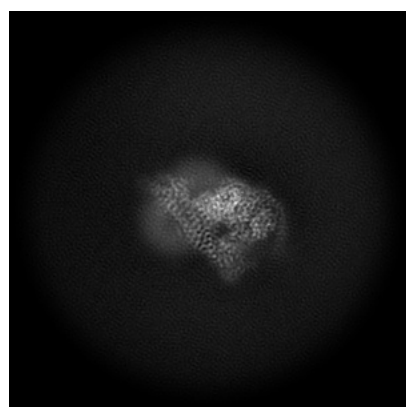
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33985. These allow visual inspection of the internal detail of the map and identification of artifacts.

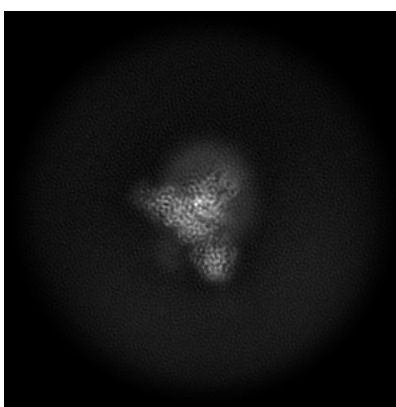
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

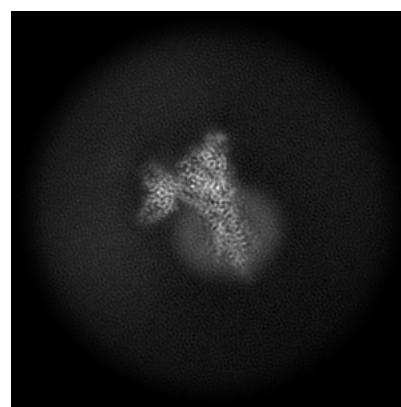
6.1.1 Primary map



X



Y

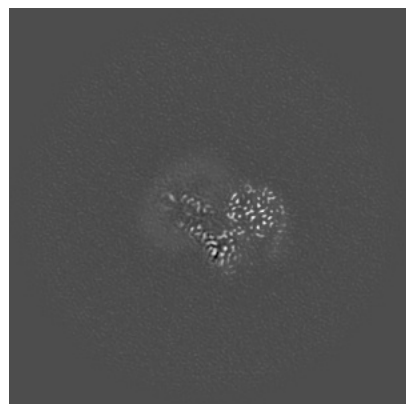


Z

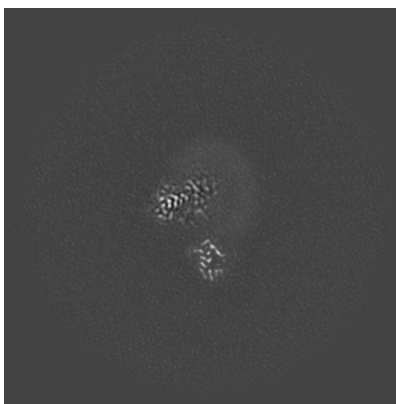
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

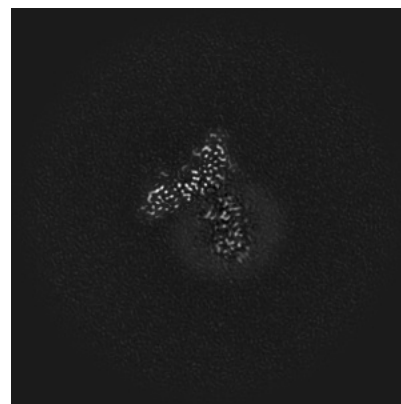
6.2.1 Primary map



X Index: 200



Y Index: 200

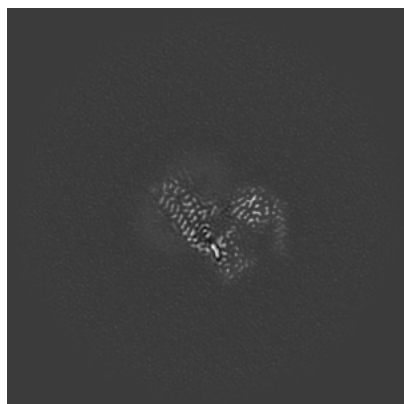


Z Index: 200

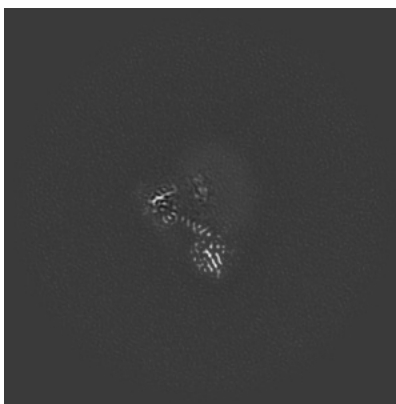
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

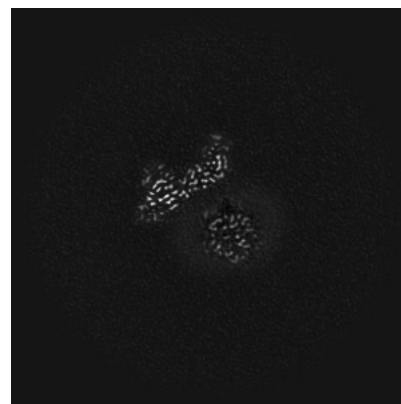
6.3.1 Primary map



X Index: 209



Y Index: 209

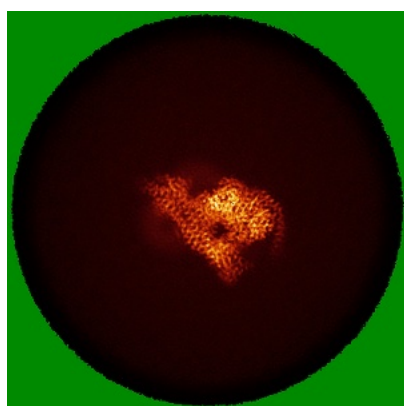


Z Index: 207

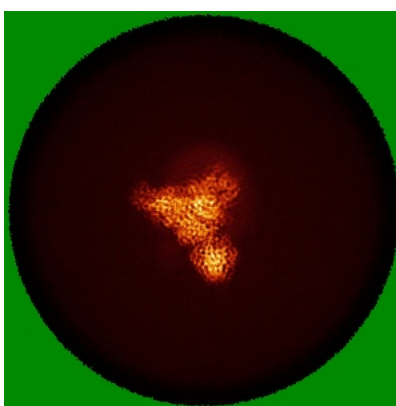
The images above show the largest variance slices of the map in three orthogonal directions.

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

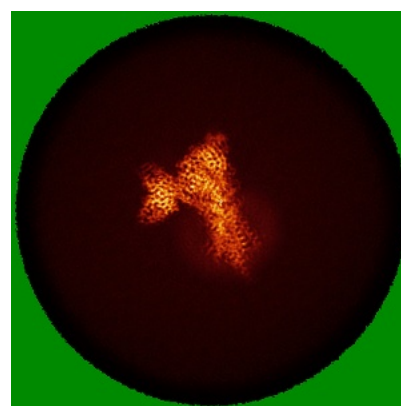
6.4.1 Primary map



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.

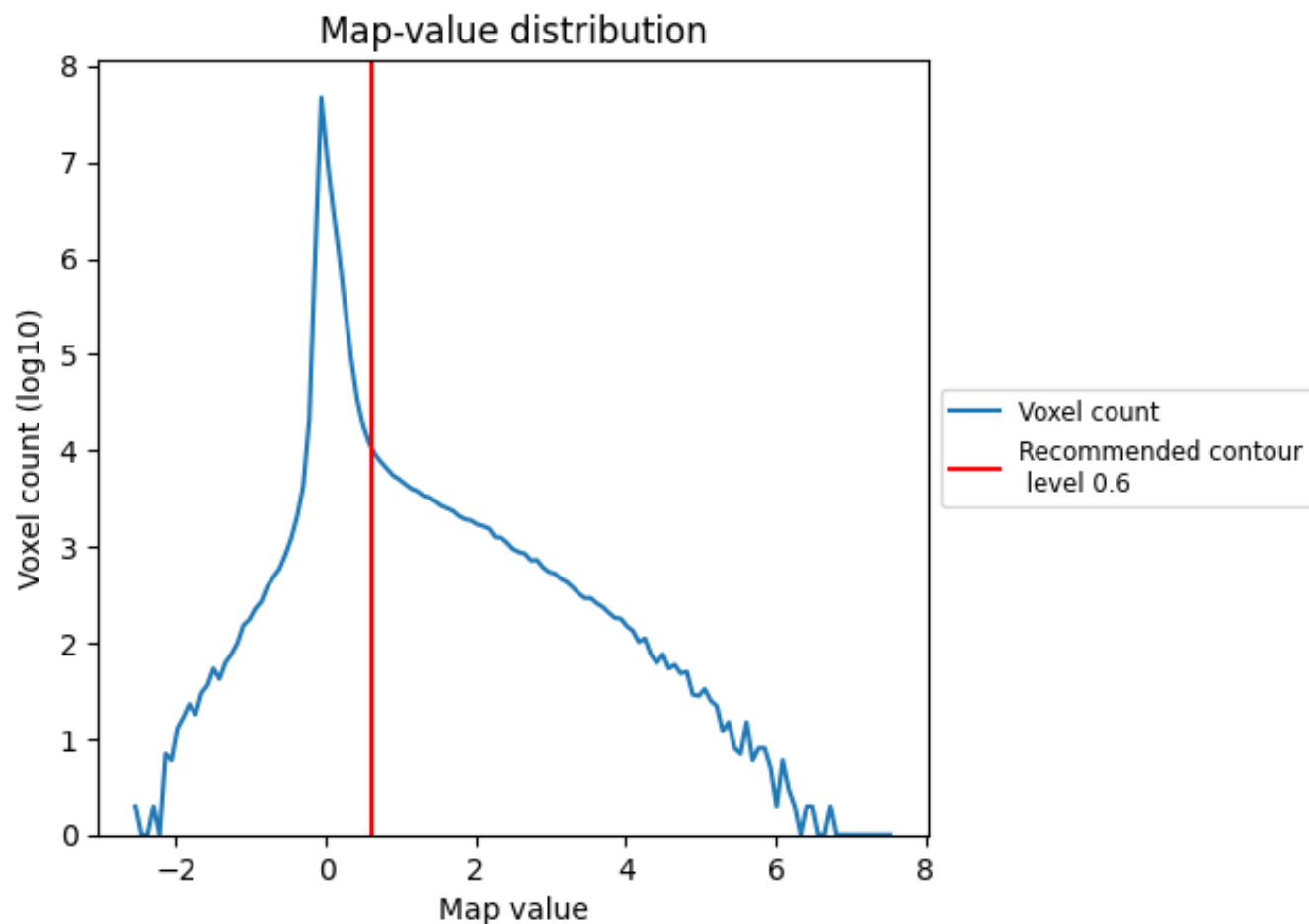
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

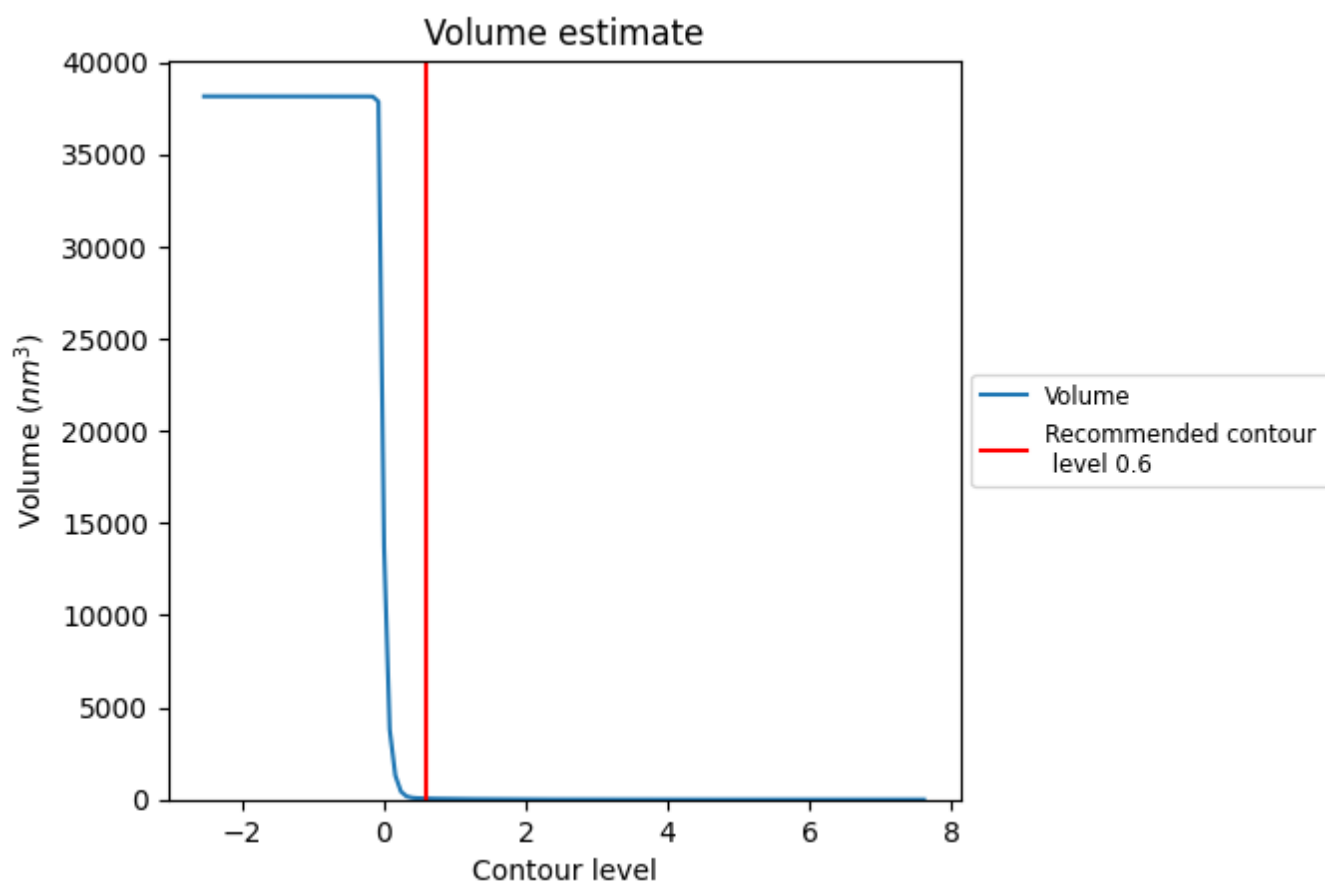
This section contains the results of statistical analysis of the map.

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.

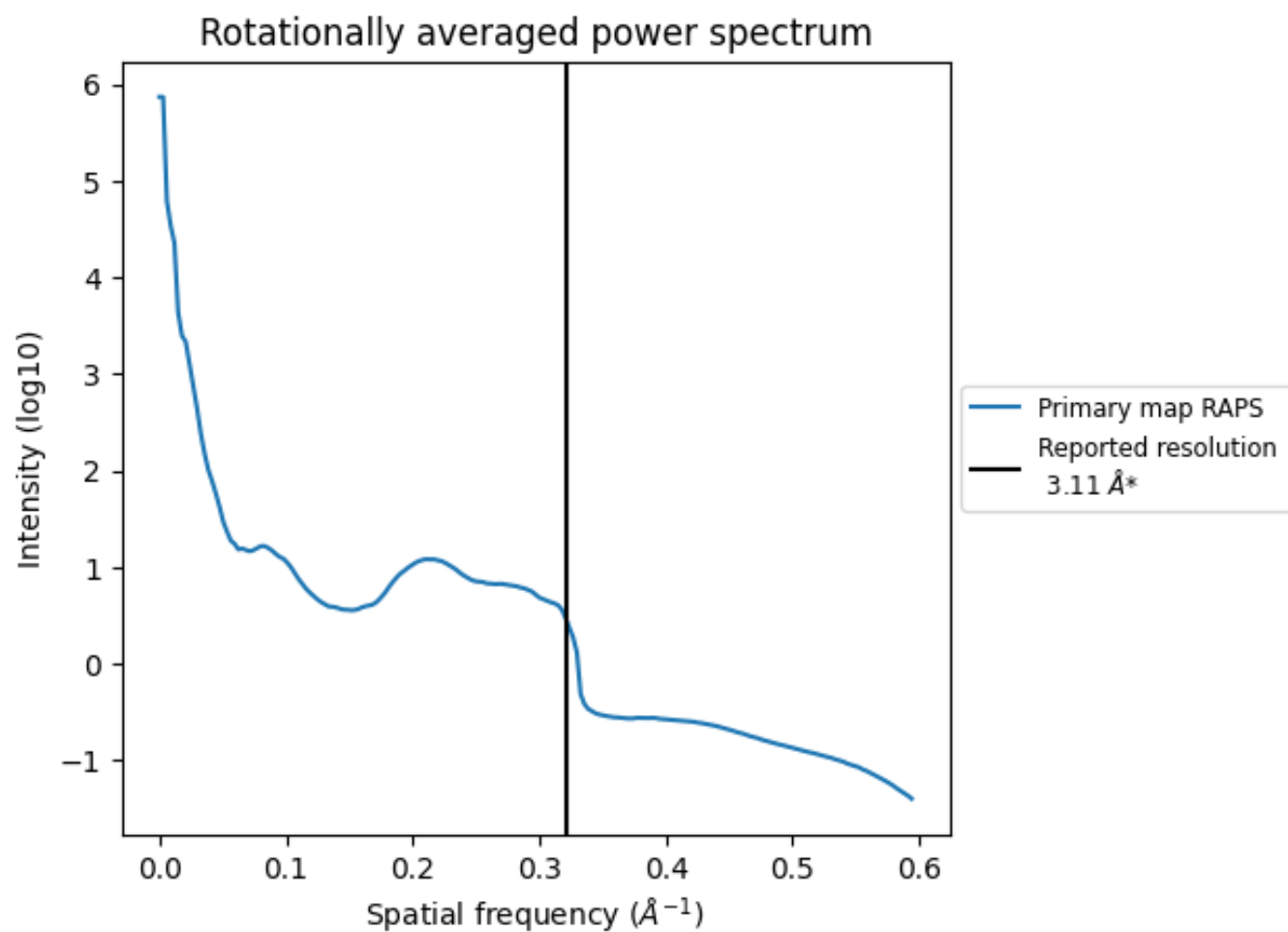
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 58 nm^3 ; this corresponds to an approximate mass of 52 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 0.322 Å⁻¹

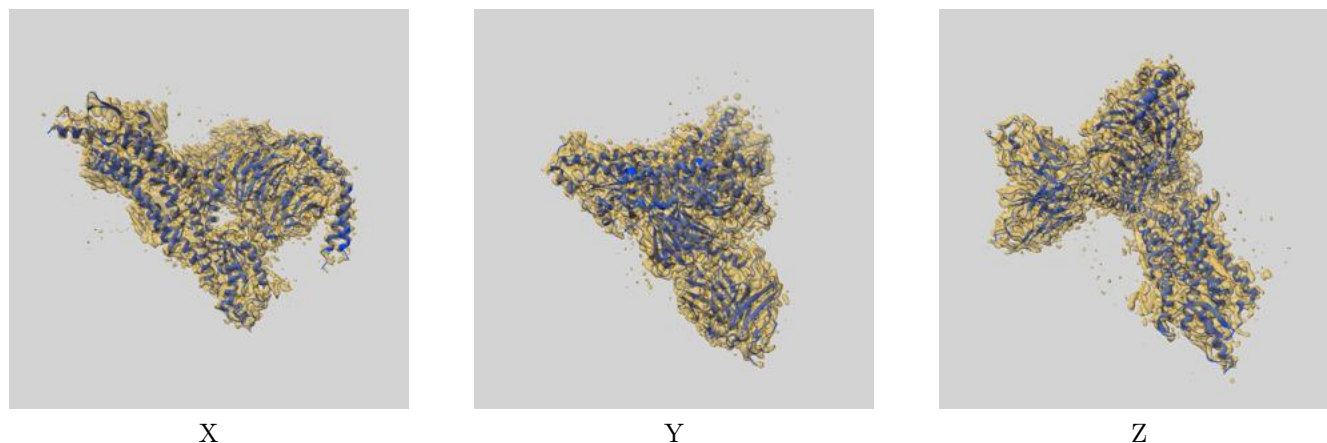
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

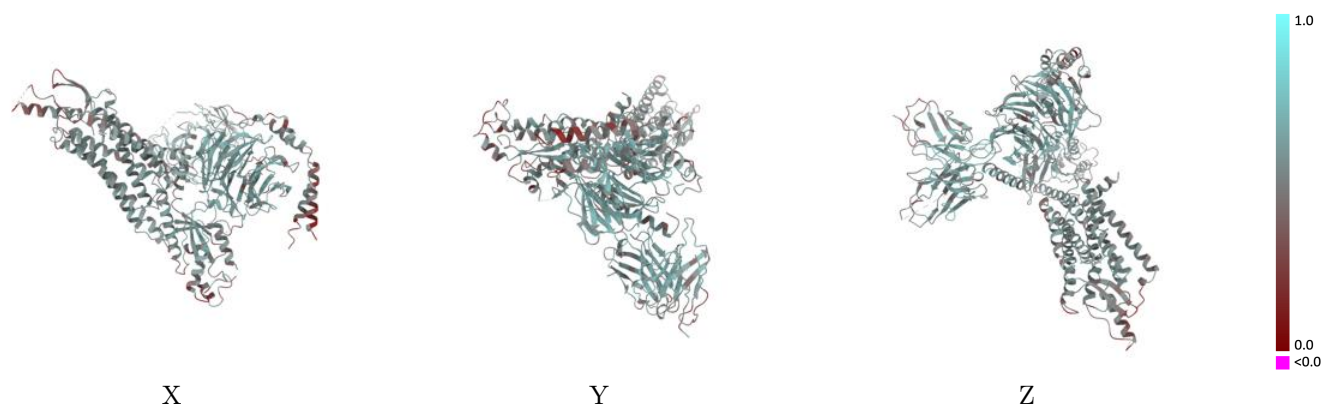
This section contains information regarding the fit between EMDB map EMD-33985 and PDB model 7YOO. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



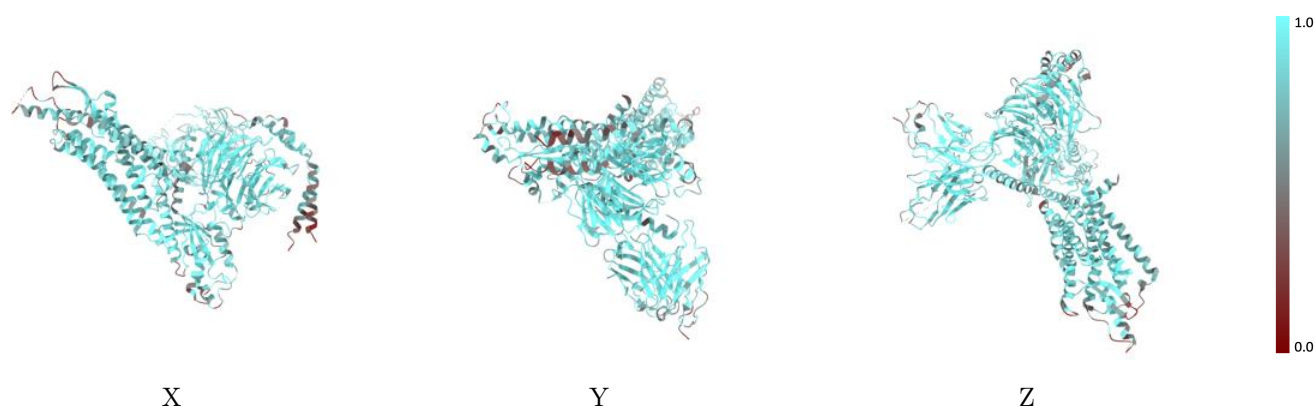
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



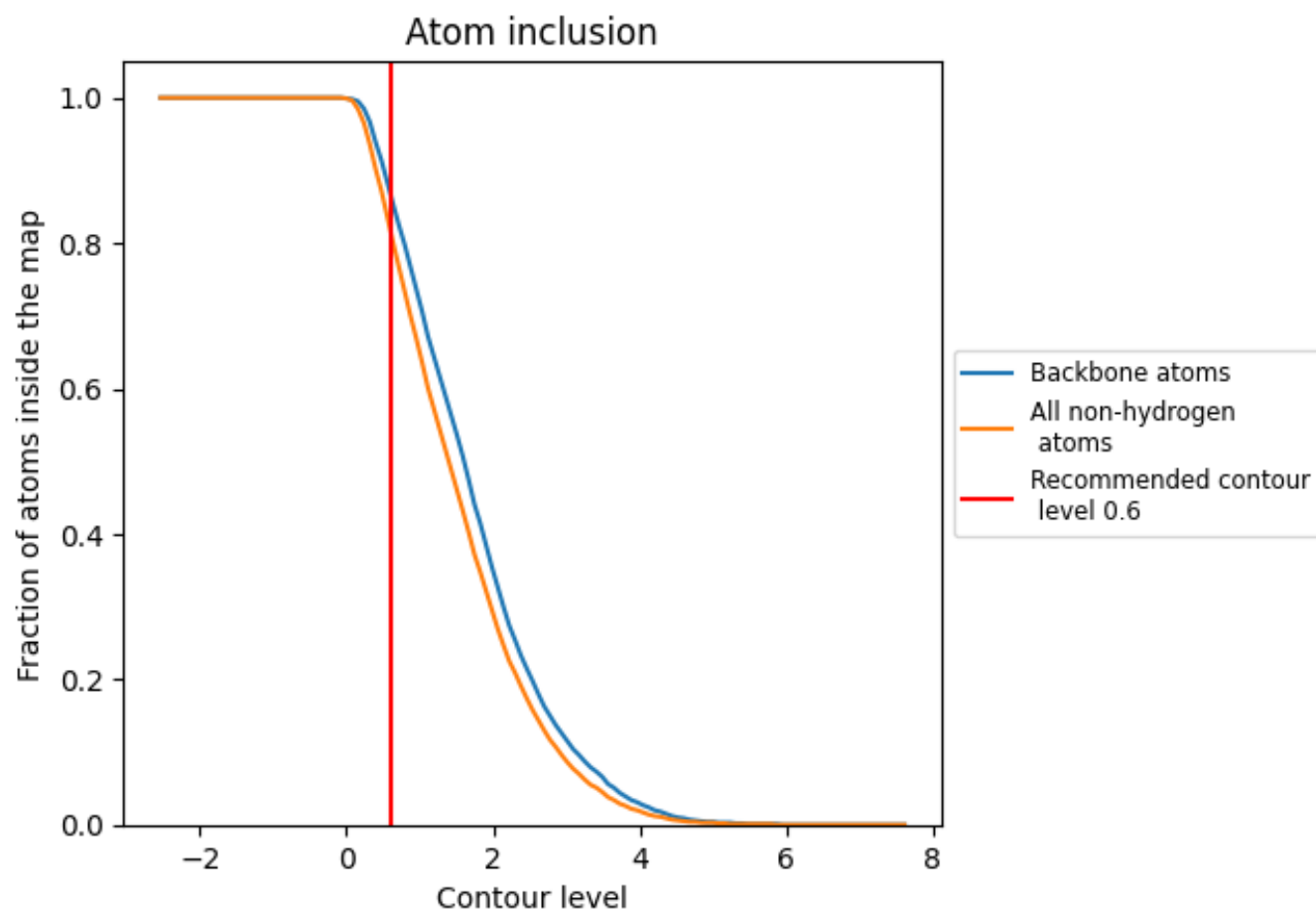
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 87% of all backbone atoms, 82% 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	0.8170	0.5310
A	0.7960	0.5120
B	0.8710	0.5650
G	0.6620	0.4750
L	0.6530	0.4580
R	0.7940	0.5080
S	0.8480	0.5530

1.0

0.0

<0.0