

Full wwPDB EM Validation Report (i)

Nov 29, 2022 – 08:42 PM JST

PDB ID : 7X1T

EMDB ID : EMD-32949

Title : Structure of Thyrotropin-Releasing Hormone Receptor bound with Taltirelin. Authors : Yang, F.; Zhang, H.H.; Meng, X.Y.; Li, Y.G.; Zhou, Y.X.; Ling, S.L.; Liu, L.;

Shi, P.; Tian, C.L.

Deposited on : 2022-02-24

Resolution : 3.26 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
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43

Mogul : 1.8.5 (274361), CSD as541be (2020)

MolProbity: 4.02b-467

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $MapQ \quad : \quad 1.9.9$

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

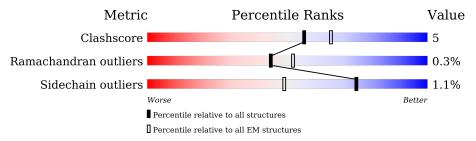
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.26 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 $(\# \mathrm{Entries})$	${ m EM\ structures} \ (\#{ m Entries})$
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 >=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 <=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				
	_			37%				
1	F	71		68%	•	31%		
2	Λ	398	9%					
	A	398		64%	•	32%		
9	D	0.46	16%					
3	В	246		76%		13%	11%	
		0.40	9%					
4	С	340		80%		16	% •	
			20%					
5	D	251		74%		10%	17%	
				40%				
6	E	5	20%	20%	60%			



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7488 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)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues		Ato	ms			AltConf	Trace
1	E	40	Total	С	N	О	S	0	0
1	Г	49	299	190	52	55	2	0	U

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	68	SER	CYS	conflict	UNP P63212

• Molecule 2 is a protein called Thyrotropin-releasing hormone receptor.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	A	272	Total 1958	C 1301	N 318	O 327	S 12	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	87	LEU	ILE	conflict	UNP P34981

• Molecule 3 is a protein called mini-G alpha q protein.

Mol	Chain	Residues		Ato	oms			AltConf	Trace
3	В	218	Total 1578	C 1010	N 280	O 282	S 6	0	0

• Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms				AltConf	Trace	
4	С	330	Total 2288	C 1436	N 393	O 441	S 18	0	0



 \bullet Molecule 5 is a protein called ScFv16.

Mol	Chain	Residues	Atoms				AltConf	Trace	
5	D	209	Total	С	N	О	S	0	0
9	ט	209	1336	836	232	263	5	0	U

 \bullet Molecule 6 is a protein called Taltirelin.

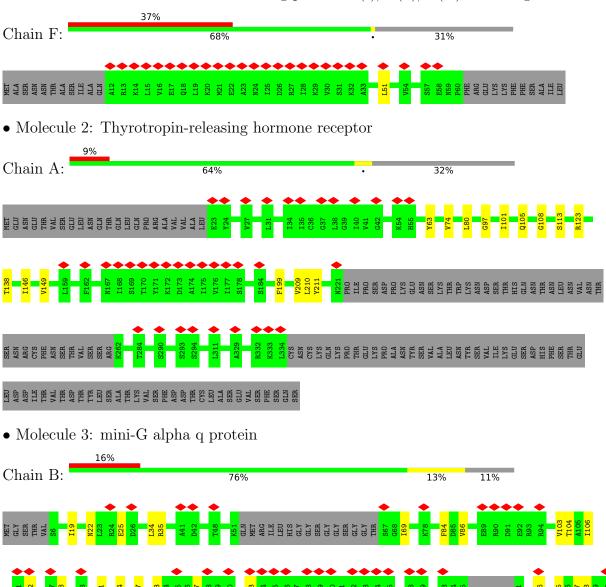
Mol	Chain	Residues	Atoms			AltConf	Trace	
6	E	7	Total	С	N	О	0	1
0	Ľ	9	29	17	7	5	U	1



3 Residue-property plots (i)

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: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2







• Molecule 6: Taltirelin

Chain E: 20% 20% 60%

RGI1 OD2 H3 P4 NH25



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	394270	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	55	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.714	Depositor
Minimum map value	-2.471	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.52	Depositor
Map size (Å)	214.00002, 214.00002, 214.00002	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: NH2, RGI

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	Bo	nd lengths	Во	ond angles
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	F	0.26	0/304	0.49	0/423
2	A	0.29	0/1998	0.54	0/2741
3	В	0.29	0/1604	0.50	0/2181
4	С	0.30	0/2331	0.59	2/3193 (0.1%)
5	D	0.32	0/1361	0.64	0/1870
6	Е	3.59	3/25 (12.0%)	1.94	1/33 (3.0%)
All	All	0.36	3/7623 (0.0%)	0.57	3/10441 (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 maintenain group or atoms of a sidechain that are expected to be planar.

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(ext{\AA})$
6	Е	4	PRO	N-CD	-8.74	1.35	1.47
6	Е	3	HIS	C-N	8.12	1.49	1.34
6	Е	2	ASP	C-N	6.49	1.49	1.34

All (3) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
	4	С	318	LEU	CA-CB-CG	5.41	127.75	115.30
ſ	4	С	336	LEU	CA-CB-CG	5.35	127.61	115.30



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
6	Ε	2	ASP	N-CA-CB	5.23	120.02	110.60

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	Е	3	HIS	CA
6	Е	4	PRO	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	80	LEU	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	F	299	0	243	1	0
2	A	1958	0	1881	9	0
3	В	1578	0	1421	20	0
4	С	2288	0	2040	33	0
5	D	1336	0	1043	15	0
6	Е	29	0	20	1	0
All	All	7488	0	6648	74	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 (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
2:A:123:ARG:NH1	2:A:211:TYR:OH	2.31	0.63
5:D:63:THR:HG23	5:D:64:VAL:HG23	1.81	0.62
4:C:320:VAL:HG22	4:C:327:VAL:HG22	1.86	0.58
4:C:157:ILE:HG23	4:C:169:TRP:HB2	1.86	0.57
3:B:19:ILE:HG23	4:C:92:ALA:HB2	1.87	0.56



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Continued from prev		Interatomic	Clash	
Atom-1	Atom-2	${\rm distance} \ (\mathring{\rm A})$	$-$ overlap (\mathring{A})	
4:C:276:VAL:HG13	4:C:285:LEU:HD11	1.87	0.56	
5:D:8:GLY:HA3	5:D:20:LEU:HD22	1.87	0.56	
4:C:79:LEU:HB3	4:C:93:ILE:HB	1.87	0.56	
5:D:6:GLU:HA	5:D:22:CYS:HA	1.87	0.55	
5:D:22:CYS:SG	5:D:23:SER:N	2.78	0.55	
4:C:129:ARG:O	5:D:2:VAL:N	2.39	0.55	
3:B:216:THR:OG1	3:B:226:ARG:NH2	2.40	0.54	
5:D:175:LEU:HD21	5:D:178:TYR:HB3	1.89	0.54	
4:C:211:TRP:HA	4:C:218:CYS:HA	1.90	0.54	
1:F:51:LEU:HD21	4:C:283:ARG:HB3	1.89	0.54	
4:C:166:CYS:HB2	4:C:180:PHE:HB2	1.91	0.51	
3:B:106:ILE:HD11	3:B:134:LEU:HD22	1.93	0.51	
4:C:290:ASP:OD1	4:C:314:ARG:NE	2.41	0.51	
3:B:143:LEU:HD21	3:B:197:PHE:HE2	1.76	0.50	
4:C:165:THR:HG22	4:C:181:THR:HG22	1.94	0.50	
4:C:227:SER:OG	4:C:228:ASP:N	2.45	0.49	
3:B:69:ILE:HG13	4:C:117:LEU:HB3	1.94	0.49	
4:C:187:VAL:HA	4:C:203:ALA:HA	1.93	0.48	
2:A:146:ILE:HA	2:A:149:VAL:HG12	1.96	0.48	
4:C:145:TYR:O	4:C:162:GLY:N	2.46	0.48	
4:C:121:CYS:HB3	4:C:139:LEU:HB2	1.95	0.48	
3:B:22:ASN:ND2	3:B:25:GLU:OE2	2.47	0.47	
5:D:62:ASP:N	5:D:62:ASP:OD1	2.47	0.47	
4:C:192:LEU:HD23	4:C:199:PHE:HB3	1.96	0.47	
4:C:275:SER:OG	4:C:316:SER:O	2.33	0.47	
4:C:161:SER:OG	4:C:162:GLY:N	2.47	0.47	
2:A:113:SER:OG	2:A:199:PHE:O	2.32	0.46	
3:B:35:ARG:HB2	3:B:103:VAL:HG23	1.98	0.46	
4:C:222:PHE:HE1	4:C:258:ASP:HA	1.80	0.46	
3:B:239:ASN:HA	3:B:242:GLU:HB3	1.98	0.45	
3:B:112:SER:HA	3:B:118:LEU:HD21	1.98	0.45	
2:A:105:GLN:HB3	6:E:4:PRO:HB2	1.97	0.45	
3:B:69:ILE:HD12	3:B:86:VAL:HG13	1.98	0.44	
3:B:153:VAL:HG11	3:B:186:VAL:HB	2.00	0.44	
4:C:58:ILE:O	4:C:316:SER:OG	2.25	0.44	
3:B:103:VAL:HG12	3:B:137:ILE:HD13	1.98	0.44	
4:C:163:ASP:N	4:C:163:ASP:OD1	2.50	0.44	
2:A:209:VAL:HG12	2:A:210:LEU:HD23	1.98	0.44	
5:D:161:TYR:HD2	5:D:221:LEU:HG	1.81	0.44	
4:C:186:ASP:H	4:C:204:CYS:HB3	1.83	0.44	
5:D:178:TYR:HD2	5:D:179:ARG:HG2	1.81	0.44	



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A J		Interatomic	Clash
Atom-1	Atom-2	${ m distance} \; ({ m \AA})$	overlap (Å)
4:C:160:SER:OG	4:C:187:VAL:O	2.36	0.44
2:A:113:SER:OG	2:A:113:SER:O	2.36	0.43
4:C:55:LEU:HD23	4:C:55:LEU:HA	1.88	0.43
4:C:230:ASN:OD1	4:C:230:ASN:N	2.52	0.43
4:C:210:LEU:O	4:C:219:ARG:N	2.52	0.43
3:B:35:ARG:HB3	3:B:84:PHE:HE2	1.84	0.43
3:B:238:MET:O	3:B:242:GLU:N	2.51	0.43
5:D:152:SER:HA	5:D:198:THR:HB	2.00	0.42
4:C:162:GLY:HA2	4:C:186:ASP:HB3	2.01	0.42
4:C:242:ALA:HA	4:C:252:LEU:HA	2.02	0.42
2:A:63:TYR:HA	2:A:146:ILE:HD11	2.02	0.42
3:B:195:LYS:HA	3:B:198:VAL:HG22	2.02	0.42
4:C:247:ASP:OD1	4:C:247:ASP:N	2.53	0.42
5:D:220:HIS:O	5:D:220:HIS:ND1	2.53	0.42
3:B:131:ASN:HD22	3:B:134:LEU:HD12	1.85	0.42
5:D:138:THR:HA	5:D:139:PRO:HD3	1.92	0.41
5:D:203:THR:O	5:D:203:THR:OG1	2.38	0.41
3:B:231:CYS:HA	3:B:234:ILE:HD12	2.03	0.41
3:B:147:ASP:N	3:B:147:ASP:OD1	2.44	0.41
5:D:70:ILE:HA	5:D:81:LEU:HA	2.02	0.41
4:C:83:ASP:N	4:C:88:ASN:O	2.44	0.41
4:C:271:CYS:HB3	4:C:290:ASP:HB2	2.03	0.41
3:B:214:HIS:CE1	3:B:226:ARG:HB3	2.56	0.40
5:D:7:SER:N	5:D:21:SER:O	2.54	0.40
3:B:34:LEU:HB3	3:B:104:THR:HG21	2.03	0.40
4:C:54:HIS:CE1	4:C:80:ILE:HD12	2.56	0.40
2:A:74:VAL:HB	2:A:108:GLY:HA3	2.04	0.40
2:A:97:GLY:O	2:A:101:ILE:N	2.45	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	Perce	ntiles
1	F	47/71 (66%)	42 (89%)	5 (11%)	0	100	100
2	A	268/398 (67%)	256 (96%)	12 (4%)	0	100	100
3	В	210/246 (85%)	197 (94%)	13 (6%)	0	100	100
4	С	328/340 (96%)	299 (91%)	29 (9%)	0	100	100
5	D	199/251 (79%)	164 (82%)	35 (18%)	0	100	100
6	Е	3/5 (60%)	0	0	3 (100%)	0	0
All	All	1055/1311 (80%)	958 (91%)	94 (9%)	3 (0%)	44	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	Е	2	ASP
6	Е	3	HIS
6	Е	4	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	Perce	ntiles
1	F	19/58~(33%)	19 (100%)	0	100	100
2	A	183/363 (50%)	182 (100%)	1 (0%)	88	93
3	В	139/213 (65%)	139 (100%)	0	100	100
4	С	210/283 (74%)	206 (98%)	4 (2%)	57	76
5	D	101/201 (50%)	101 (100%)	0	100	100
6	Е	3/3 (100%)	1 (33%)	2 (67%)	0	0
All	All	655/1121 (58%)	648 (99%)	7 (1%)	74	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	138	THR
4	С	134	ARG



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Mol	Chain	Res	Type
4	С	190	LEU
4	С	315	VAL
4	С	318	LEU
6	Е	2	ASP
6	Е	3	HIS

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

Mol	Chain	Res	Type
2	A	105	GLN
2	A	312	ASN
3	В	22	ASN
4	С	32	GLN
4	С	62	HIS
5	D	159	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	\mathbf{B}	ond leng	${ m gths}$	В	ond ang	gles
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	RGI	E	1	6	3,3,4	1.89	1 (33%)	2,2,4	0.25	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
6	RGI	Е	1	6	-	0/1/1/2	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
6	Ε	1	RGI	C-N	2.66	1.49	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.



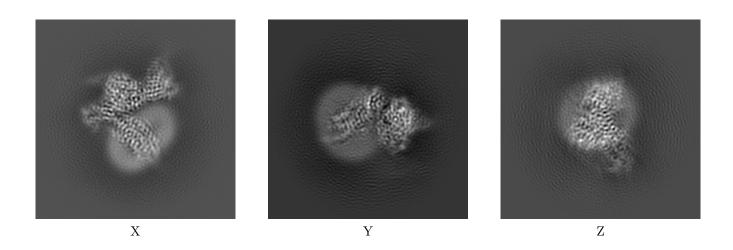
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-32949. 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)

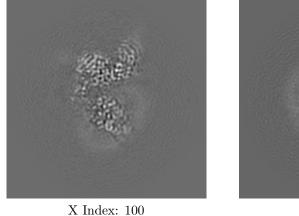
6.1.1 Primary map

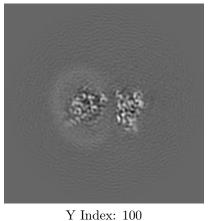


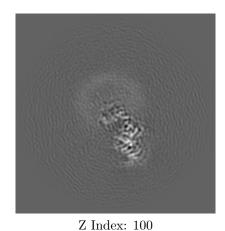
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map







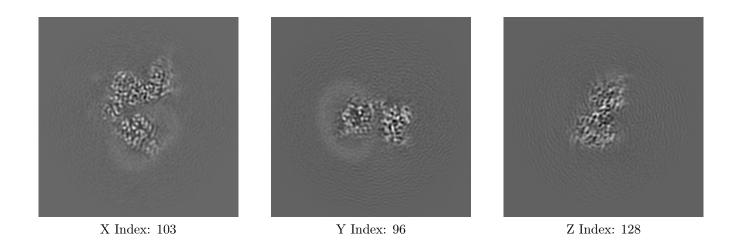
1d0X: 100



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

6.3 Largest variance slices (i)

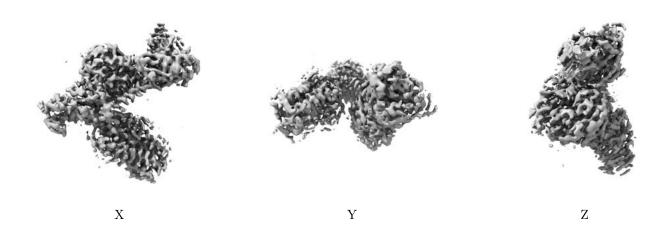
6.3.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.52. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



6.5 Mask visualisation (i)

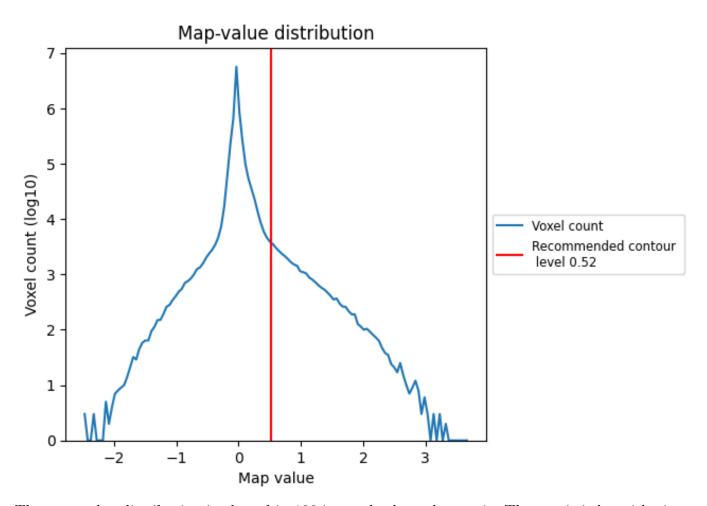
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

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

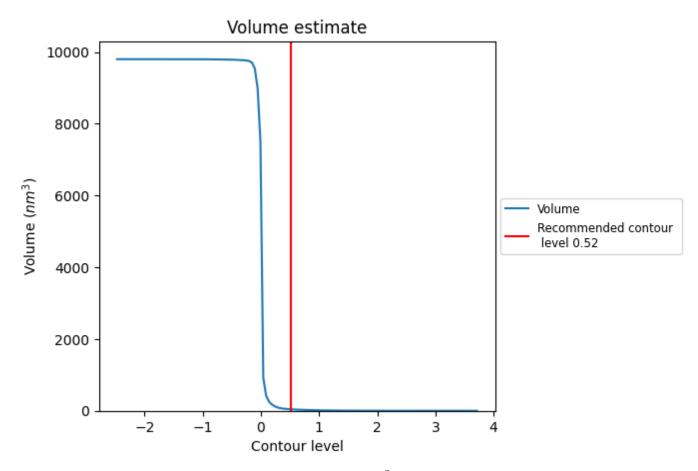
7.1 Map-value distribution (i)



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)

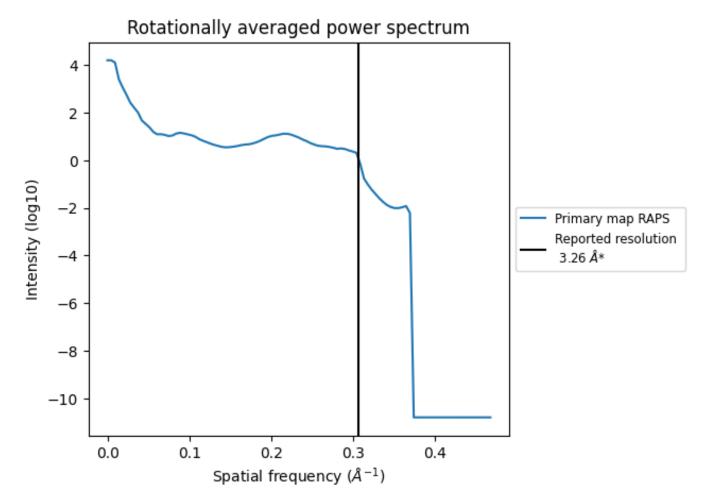


The volume at the recommended contour level is 42 nm^3 ; this corresponds to an approximate mass of 38 kDa.

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 0.307 $\rm \mathring{A}^{-1}$



8 Fourier-Shell correlation (i)

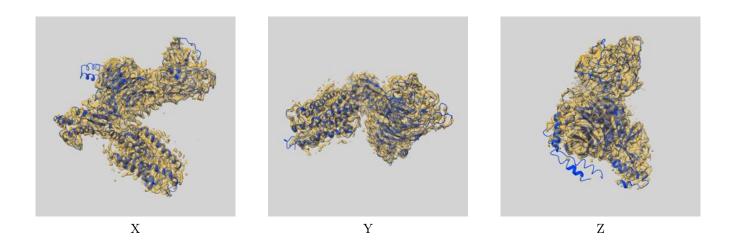
This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-32949 and PDB model 7X1T. Per-residue inclusion information can be found in section 3 on page 5.

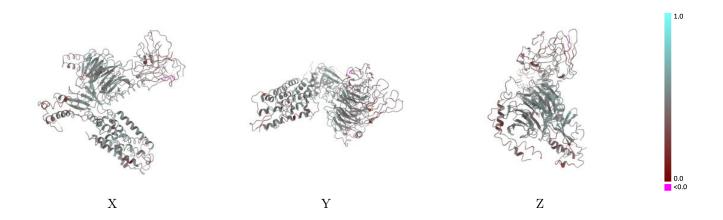
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.52 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.

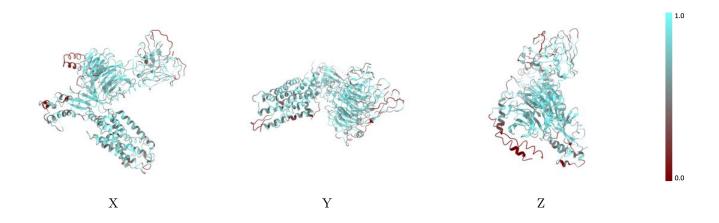


9.2 Q-score mapped to coordinate model (i)



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.

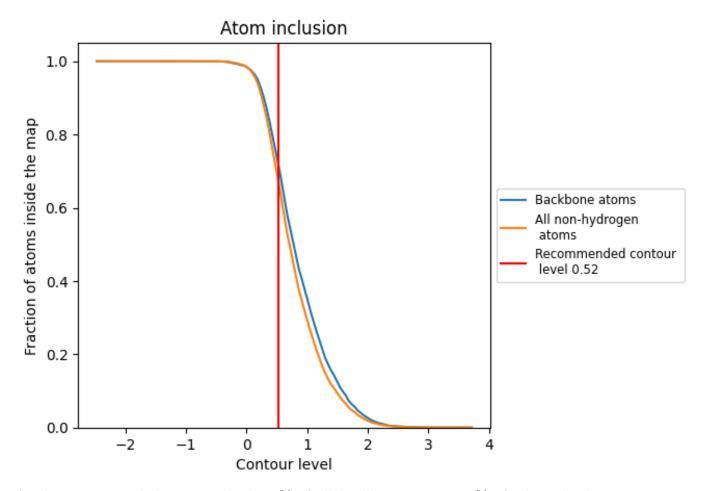
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.52).



9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.52) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6768	0.4620
A	0.6655	0.4750
В	0.6768	0.4680
С	0.7590	0.4940
D	0.6161	0.4000
E	0.7241	0.4210
F	0.3926	0.3930



