



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 09:34 PM UTC

PDB ID : 7TS0 / pdb_00007ts0
EMDB ID : EMD-26104
Title : Cryo-EM structure of corticotropin releasing factor receptor 2 bound to Urocortin 1 and coupled with heterotrimeric Go protein
Authors : Zhao, L.-H.; Lin, J.; Mao, C.; Zhou, X.E.; Ji, S.; Shen, D.; Xiao, P.; Melcher, K.; Zhang, Y.; Yu, X.; Xu, H.E.
Deposited on : 2022-01-31
Resolution : 2.80 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 ⓘ 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
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

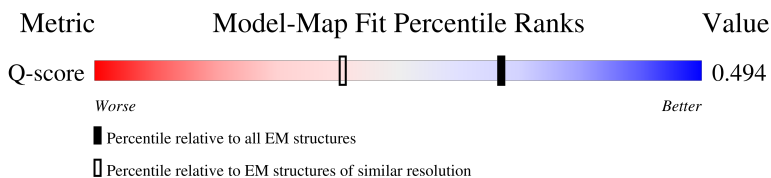
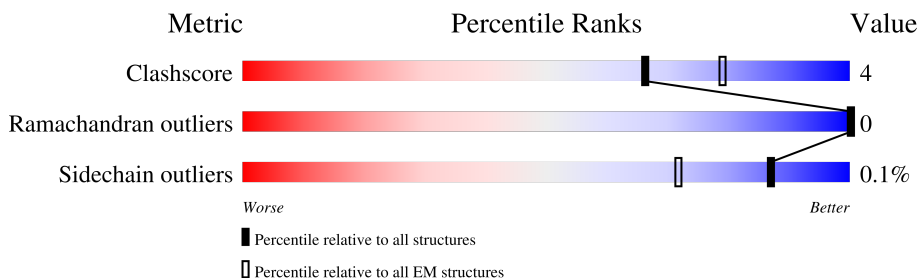
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

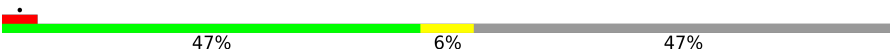
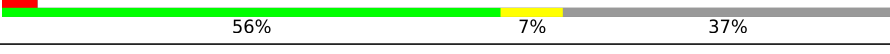
The reported resolution of this entry is 2.80 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	P	560	
2	U	40	
3	A	353	
4	B	400	

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Mol	Chain	Length	Quality of chain
5	G	71	 79%20%
6	H	247	 82%12%6%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9383 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 Corticotropin-releasing factor receptor 2,Corticotropin-releasing factor receptor 2,Corticotropin-releasing factor receptor 2,Corticotropin-releasing factor receptor 2,Human corticotropin releasing factor receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	P	296	Total	C	N	O	S	0	0
			2459	1644	403	395	17		

- Molecule 2 is a protein called Urocortin.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	U	36	Total	C	N	O	0	0
			301	188	58	55		

- Molecule 3 is a protein called Dominant negative Go alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	224	Total	C	N	O	S	0	0
			1788	1130	304	342	12		

- 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	B	341	Total	C	N	O	S	0	0
			2616	1612	470	513	21		

There are 61 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-33	MET	-	expression tag	UNP P54311
B	-32	HIS	-	expression tag	UNP P54311
B	-31	HIS	-	expression tag	UNP P54311
B	-30	HIS	-	expression tag	UNP P54311
B	-29	HIS	-	expression tag	UNP P54311
B	-28	HIS	-	expression tag	UNP P54311

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-27	HIS	-	expression tag	UNP P54311
B	-26	SER	-	expression tag	UNP P54311
B	-25	SER	-	expression tag	UNP P54311
B	-24	GLY	-	expression tag	UNP P54311
B	-23	LEU	-	expression tag	UNP P54311
B	-22	VAL	-	expression tag	UNP P54311
B	-21	PRO	-	expression tag	UNP P54311
B	-20	ARG	-	expression tag	UNP P54311
B	-19	GLY	-	expression tag	UNP P54311
B	-18	SER	-	expression tag	UNP P54311
B	-17	HIS	-	expression tag	UNP P54311
B	-16	MET	-	expression tag	UNP P54311
B	-15	ALA	-	expression tag	UNP P54311
B	-14	SER	-	expression tag	UNP P54311
B	-13	HIS	-	expression tag	UNP P54311
B	-12	HIS	-	expression tag	UNP P54311
B	-11	HIS	-	expression tag	UNP P54311
B	-10	HIS	-	expression tag	UNP P54311
B	-9	HIS	-	expression tag	UNP P54311
B	-8	HIS	-	expression tag	UNP P54311
B	-7	HIS	-	expression tag	UNP P54311
B	-6	HIS	-	expression tag	UNP P54311
B	-5	HIS	-	expression tag	UNP P54311
B	-4	HIS	-	expression tag	UNP P54311
B	-3	GLY	-	expression tag	UNP P54311
B	-2	SER	-	expression tag	UNP P54311
B	-1	LEU	-	expression tag	UNP P54311
B	0	LEU	-	expression tag	UNP P54311
B	1	GLN	-	expression tag	UNP P54311
B	341	GLY	-	expression tag	UNP P54311
B	342	SER	-	expression tag	UNP P54311
B	343	SER	-	expression tag	UNP P54311
B	344	GLY	-	expression tag	UNP P54311
B	345	GLY	-	expression tag	UNP P54311
B	346	GLY	-	expression tag	UNP P54311
B	347	GLY	-	expression tag	UNP P54311
B	348	SER	-	expression tag	UNP P54311
B	349	GLY	-	expression tag	UNP P54311
B	350	GLY	-	expression tag	UNP P54311
B	351	GLY	-	expression tag	UNP P54311
B	352	GLY	-	expression tag	UNP P54311
B	353	SER	-	expression tag	UNP P54311

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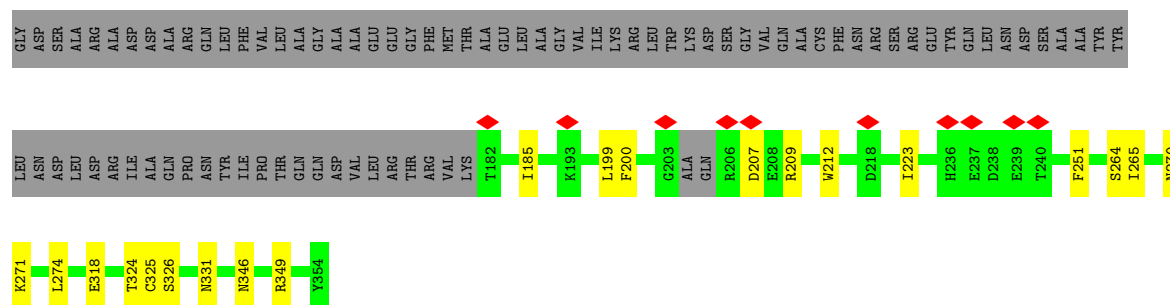
Chain	Residue	Modelled	Actual	Comment	Reference
B	354	SER	-	expression tag	UNP P54311
B	355	GLY	-	expression tag	UNP P54311
B	356	VAL	-	expression tag	UNP P54311
B	357	SER	-	expression tag	UNP P54311
B	358	GLY	-	expression tag	UNP P54311
B	359	TRP	-	expression tag	UNP P54311
B	360	ARG	-	expression tag	UNP P54311
B	361	LEU	-	expression tag	UNP P54311
B	362	PHE	-	expression tag	UNP P54311
B	363	LYS	-	expression tag	UNP P54311
B	364	LYS	-	expression tag	UNP P54311
B	365	ILE	-	expression tag	UNP P54311
B	366	SER	-	expression tag	UNP P54311

- Molecule 5 is a protein called G protein gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

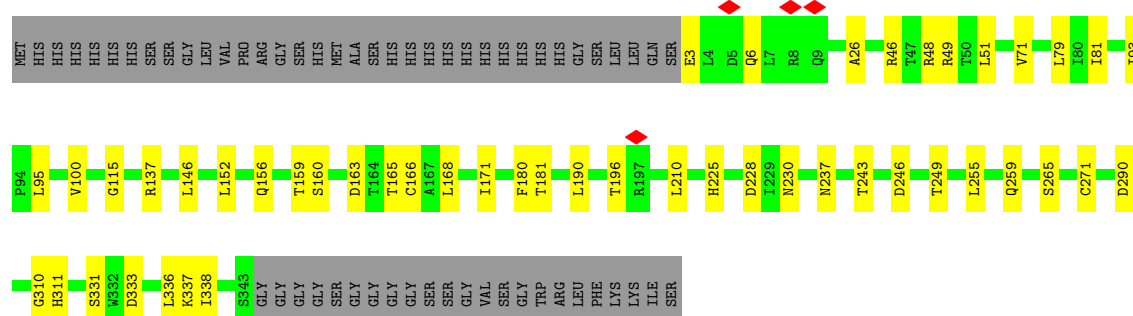
- Molecule 6 is a protein called scFV16.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	232	Total	C	N	O	S	1	0
			1783	1132	295	346	10		



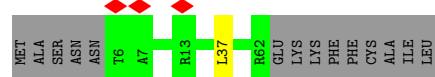
- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 73% 12% 15%



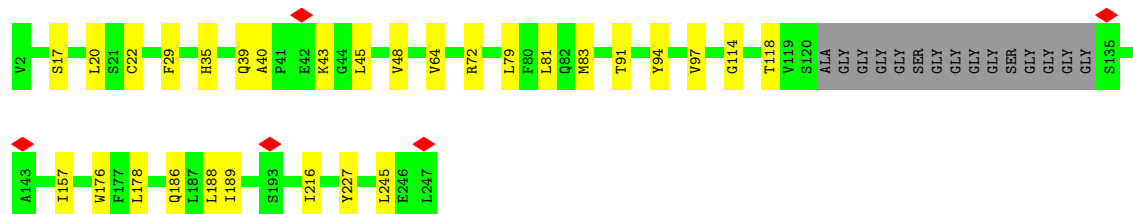
- Molecule 5: G protein gamma subunit

Chain G: 79% 20%



- Molecule 6: scFV16

Chain H: 82% 12% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	171435	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.119	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.018	Depositor
Map size ($\text{\AA}$)	227.13602, 227.13602, 227.13602	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.014, 1.014, 1.014	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	P	0.24	0/2535	0.56	0/3448
2	U	0.25	0/304	0.47	0/409
3	A	0.19	0/1816	0.47	0/2441
4	B	0.17	0/2663	0.46	0/3610
5	G	0.15	0/442	0.40	0/597
6	H	0.20	0/1830	0.54	0/2481
All	All	0.20	0/9590	0.50	0/12986

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	P	2459	0	2443	17	0
2	U	301	0	310	2	0
3	A	1788	0	1779	13	0
4	B	2616	0	2518	28	0
5	G	436	0	448	1	0
6	H	1783	0	1718	15	0
All	All	9383	0	9216	72	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 (72) 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:P:329:ASN:HD22	1:P:340:PHE:HB2	1.60	0.67
6:H:40:ALA:HB3	6:H:43:LYS:HB2	1.79	0.64
4:B:271:CYS:HB3	4:B:290:ASP:HB3	1.80	0.62
6:H:22:CYS:HB3	6:H:79:LEU:HB3	1.82	0.60
4:B:115:GLY:HA3	4:B:146:LEU:HD23	1.83	0.60
4:B:51:LEU:HB2	4:B:336:LEU:HB2	1.83	0.60
1:P:298:THR:O	1:P:304:GLN:NE2	2.34	0.59
3:A:18:MET:SD	3:A:21:ARG:NH1	2.73	0.58
3:A:52:GLN:OE1	3:A:331:ASN:ND2	2.37	0.58
1:P:162:ARG:HH11	1:P:198:ASN:HD22	1.52	0.56
4:B:166:CYS:HB2	4:B:180:PHE:HB2	1.86	0.56
3:A:271:LYS:HD2	3:A:274:LEU:HD12	1.87	0.55
6:H:91:THR:HG23	6:H:118:THR:HA	1.87	0.55
4:B:146:LEU:HD11	4:B:159:THR:HB	1.89	0.55
6:H:39:GLN:HB2	6:H:45:LEU:HD23	1.88	0.55
4:B:95:LEU:HD13	4:B:100:VAL:HG21	1.89	0.55
6:H:35:HIS:HB2	6:H:97:VAL:HB	1.89	0.54
1:P:358:PHE:HA	1:P:362:PHE:HD2	1.73	0.54
1:P:376:ARG:NH2	4:B:311:HIS:O	2.42	0.53
1:P:142:ARG:HG2	1:P:145:ARG:HH11	1.74	0.53
4:B:230:ASN:ND2	4:B:246:ASP:OD1	2.39	0.53
4:B:3:GLU:OE1	4:B:6:GLN:NE2	2.43	0.52
4:B:237:ASN:HD21	5:G:37:LEU:HD23	1.75	0.52
4:B:165:THR:HG22	4:B:181:THR:HG22	1.92	0.52
1:P:216:THR:OG1	1:P:223:ARG:NH2	2.43	0.52
4:B:331:SER:OG	4:B:333:ASP:OD1	2.27	0.52
4:B:49:ARG:HB2	4:B:338:ILE:HD12	1.92	0.52
1:P:181:GLU:OE1	1:P:183:TRP:NE1	2.42	0.51
1:P:148:ARG:NH1	1:P:205:GLU:OE2	2.43	0.51
4:B:225:HIS:NE2	4:B:243:THR:OG1	2.35	0.51
3:A:325:CYS:SG	3:A:326:SER:N	2.84	0.51
6:H:48:VAL:HG13	6:H:64:VAL:HG11	1.93	0.51
4:B:210:LEU:HD22	4:B:255:LEU:HD22	1.93	0.51
3:A:185:ILE:HD11	3:A:200:PHE:HB3	1.93	0.51
3:A:207:ASP:OD2	3:A:212:TRP:NE1	2.44	0.50
3:A:38:LEU:HB2	3:A:199:LEU:HD11	1.93	0.50
4:B:26:ALA:HB2	4:B:259:GLN:HE22	1.77	0.49
4:B:46:ARG:HB2	4:B:48:ARG:HH12	1.77	0.49
3:A:251:PHE:HE1	3:A:265:ILE:HG21	1.78	0.49
4:B:71:VAL:HG22	4:B:81:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:230:ILE:HA	1:P:234:ILE:HD12	1.95	0.48
1:P:242:TRP:HE1	1:P:265:ASP:HA	1.78	0.48
6:H:20:LEU:HD12	6:H:81:LEU:HD23	1.95	0.48
6:H:94:TYR:O	6:H:114:GLY:HA2	2.13	0.48
6:H:157:ILE:HD11	6:H:245:LEU:HD21	1.97	0.47
3:A:346:ASN:OD1	3:A:349:ARG:NH2	2.45	0.47
4:B:310:GLY:O	4:B:337:LYS:NZ	2.37	0.47
4:B:79:LEU:HB2	4:B:95:LEU:HD11	1.97	0.46
3:A:270:ASN:OD1	3:A:324:THR:OG1	2.31	0.46
6:H:216:ILE:HD11	6:H:227:TYR:HE2	1.81	0.46
1:P:196:VAL:HG22	1:P:272:ILE:HD11	1.97	0.46
1:P:200:PHE:HD2	1:P:235:PRO:HG3	1.82	0.45
6:H:17:SER:HA	6:H:83:MET:O	2.17	0.45
4:B:152:LEU:HD22	4:B:196:THR:HB	2.00	0.44
6:H:176:TRP:HB2	6:H:189:ILE:HB	2.00	0.44
4:B:79:LEU:HB3	4:B:93:ILE:HB	2.00	0.43
3:A:209:ARG:NH2	4:B:228:ASP:OD2	2.51	0.43
2:U:24:GLN:OE1	2:U:27:ARG:NH2	2.51	0.42
3:A:36:LEU:HD13	3:A:223:ILE:HD11	2.01	0.42
3:A:264:SER:OG	3:A:318:GLU:O	2.36	0.42
4:B:137:ARG:NE	4:B:171:ILE:O	2.52	0.42
4:B:160:SER:HB2	4:B:190:LEU:HD23	2.01	0.42
6:H:178:LEU:O	6:H:186:GLN:N	2.49	0.42
4:B:163:ASP:OD1	4:B:165:THR:OG1	2.33	0.41
6:H:178:LEU:HB2	6:H:188:LEU:HD11	2.02	0.41
1:P:358:PHE:O	1:P:362:PHE:HB2	2.20	0.41
1:P:120:ASN:OD1	1:P:349:SER:OG	2.34	0.41
1:P:326:PHE:O	2:U:6:SER:OG	2.38	0.41
4:B:156:GLN:HB3	4:B:168:LEU:HD11	2.03	0.41
6:H:29:PHE:O	6:H:72:ARG:NH2	2.52	0.40
4:B:249:THR:HG22	4:B:265:SER:HB2	2.03	0.40
1:P:180:ASN:HD21	1:P:252:GLU:HA	1.85	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	P	292/560 (52%)	285 (98%)	7 (2%)	0	100	100
2	U	34/40 (85%)	34 (100%)	0	0	100	100
3	A	218/353 (62%)	214 (98%)	4 (2%)	0	100	100
4	B	339/400 (85%)	335 (99%)	4 (1%)	0	100	100
5	G	55/71 (78%)	55 (100%)	0	0	100	100
6	H	229/247 (93%)	226 (99%)	3 (1%)	0	100	100
All	All	1167/1671 (70%)	1149 (98%)	18 (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	P	264/488 (54%)	263 (100%)	1 (0%)	84	94
2	U	34/38 (90%)	34 (100%)	0	100	100
3	A	199/303 (66%)	199 (100%)	0	100	100
4	B	283/328 (86%)	283 (100%)	0	100	100
5	G	46/58 (79%)	46 (100%)	0	100	100
6	H	196/198 (99%)	196 (100%)	0	100	100
All	All	1022/1413 (72%)	1021 (100%)	1 (0%)	87	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	171	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14)

such sidechains are listed below:

Mol	Chain	Res	Type
1	P	69	ASN
1	P	106	GLN
1	P	198	ASN
1	P	269	GLN
3	A	233	GLN
3	A	331	ASN
4	B	6	GLN
4	B	142	HIS
4	B	175	GLN
4	B	220	GLN
4	B	239	ASN
4	B	259	GLN
6	H	39	GLN
6	H	179	GLN

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 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.

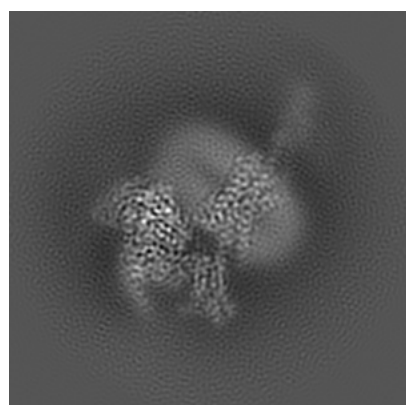
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26104. These allow visual inspection of the internal detail of the map and identification of artifacts.

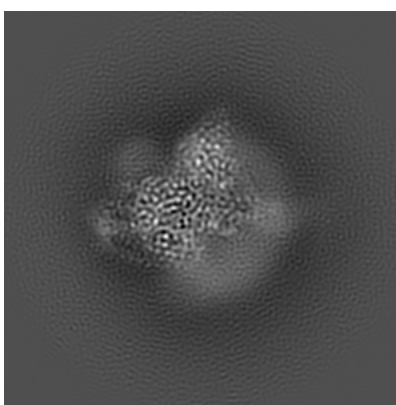
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

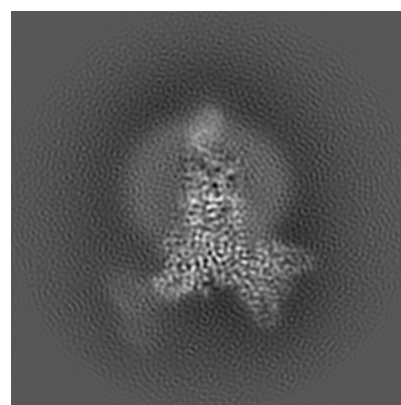
6.1.1 Primary map



X



Y

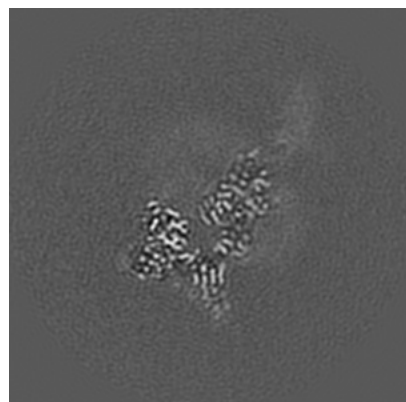


Z

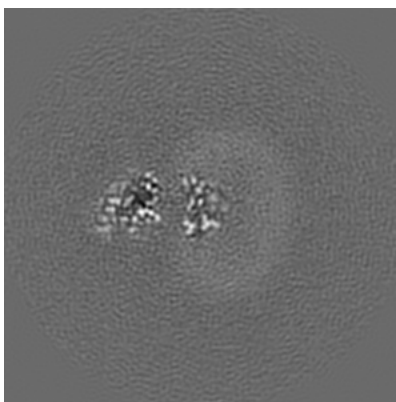
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

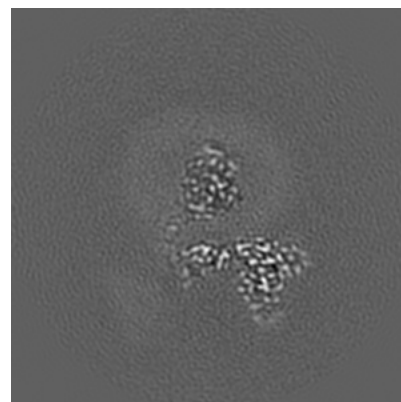
6.2.1 Primary map



X Index: 112



Y Index: 112

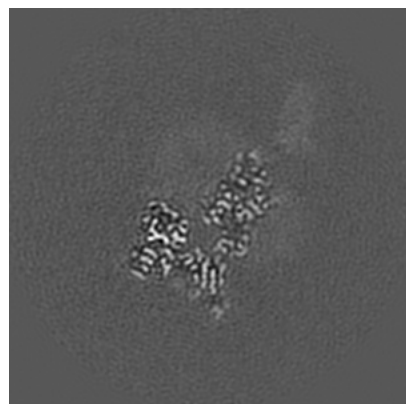


Z Index: 112

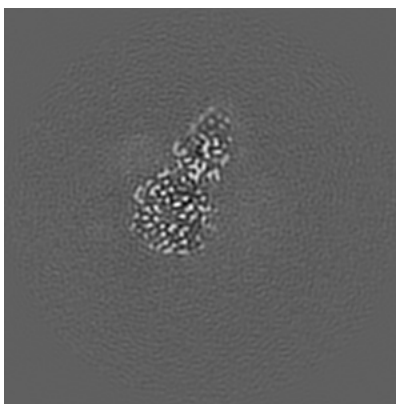
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

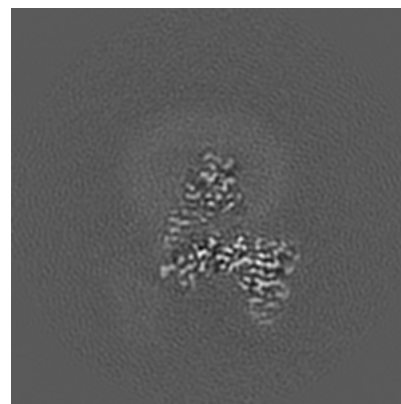
6.3.1 Primary map



X Index: 113



Y Index: 82

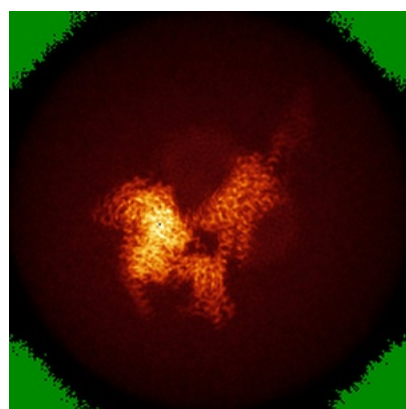


Z Index: 108

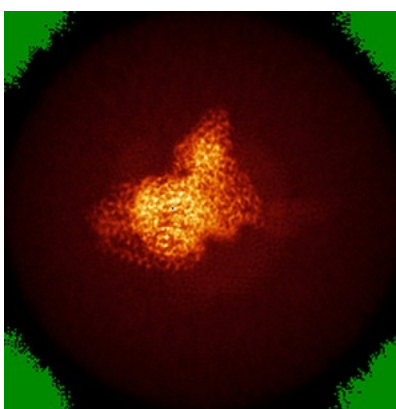
The images above show the largest variance slices of the map in three orthogonal directions.

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

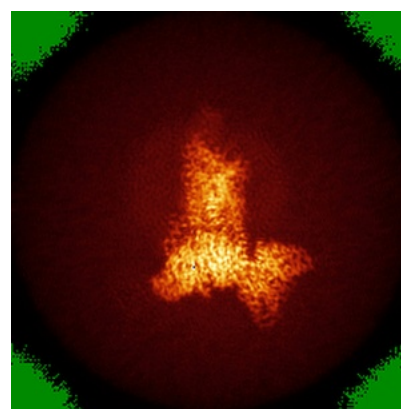
6.4.1 Primary map



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

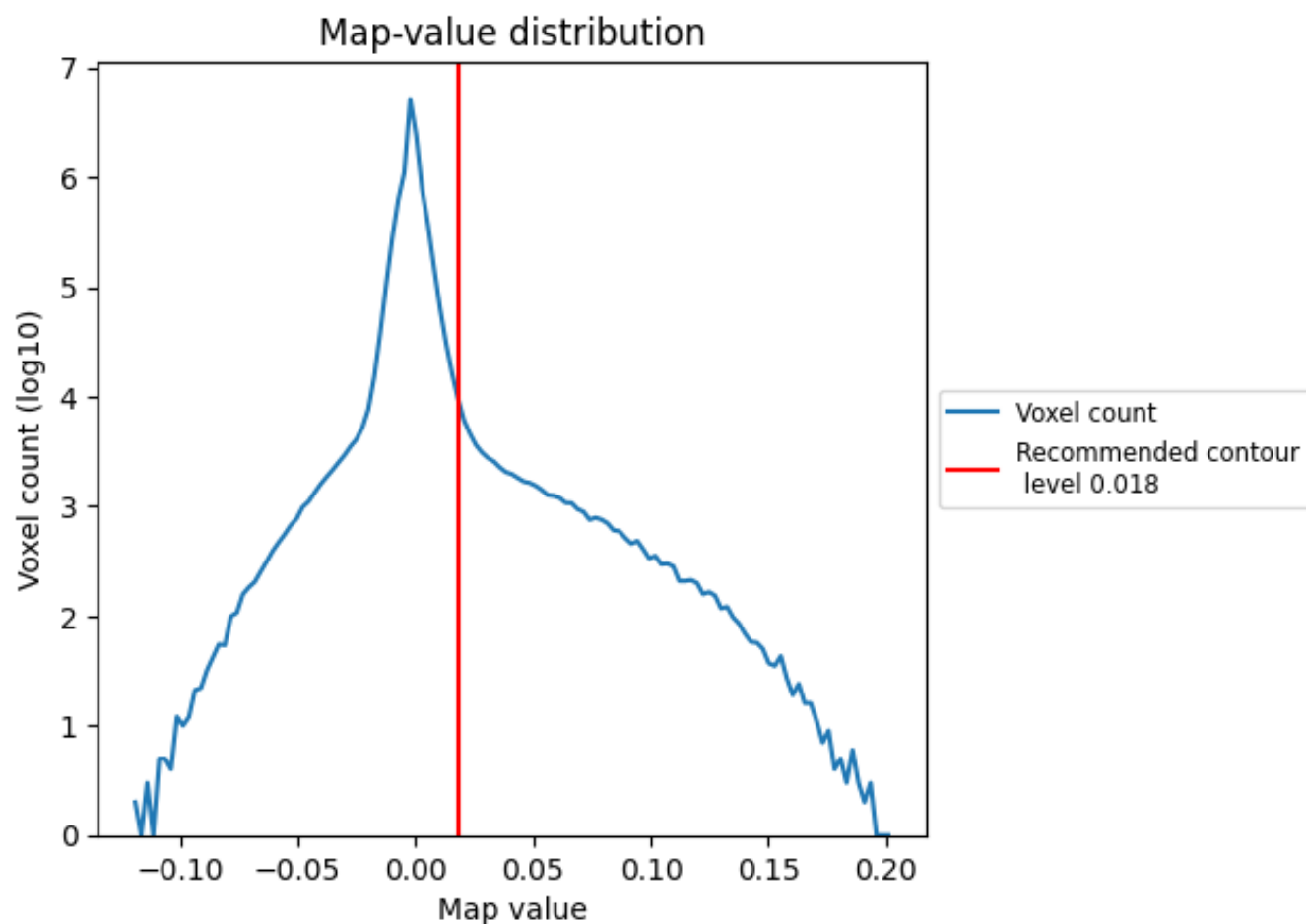
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

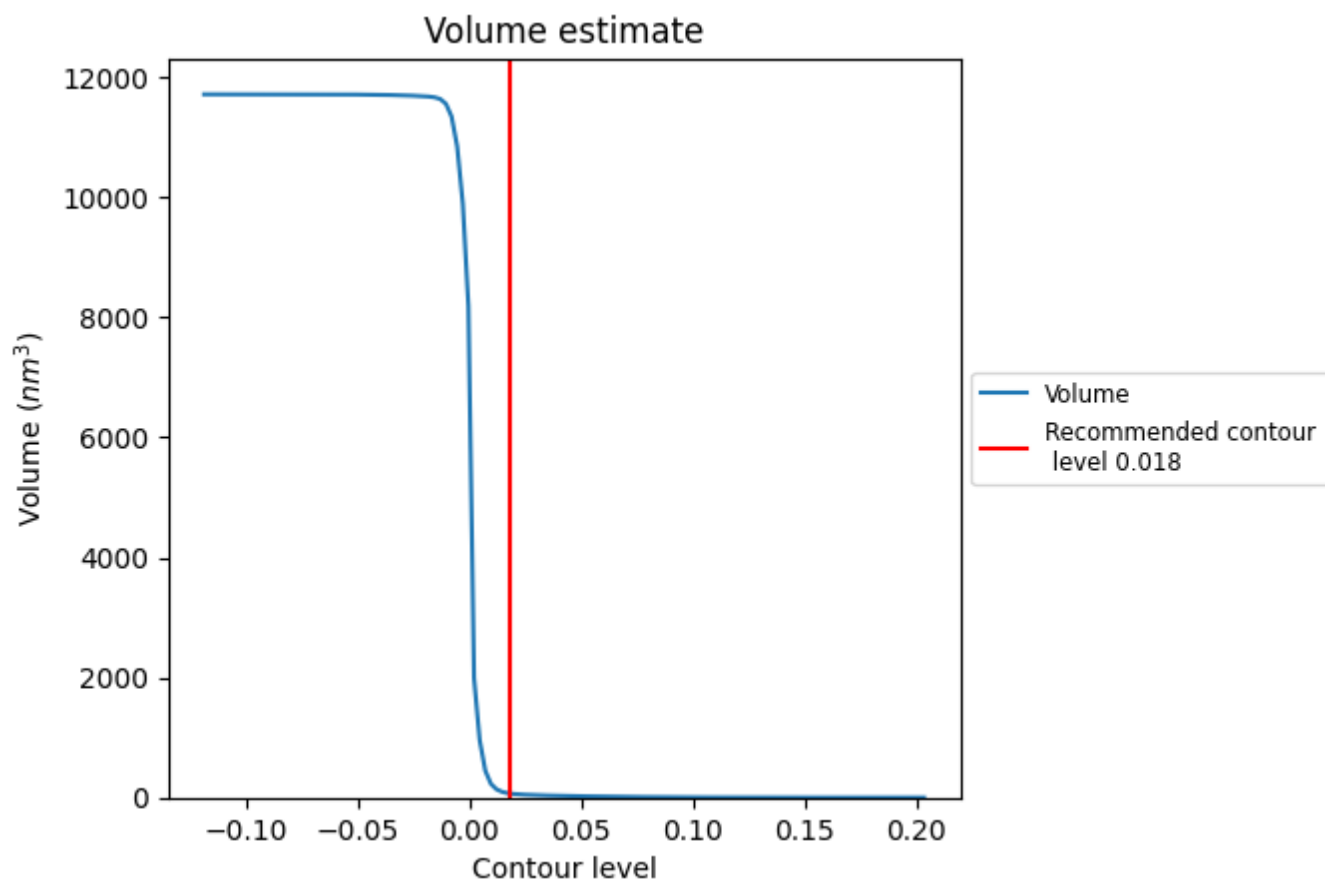
This section contains the results of statistical analysis of the map.

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.

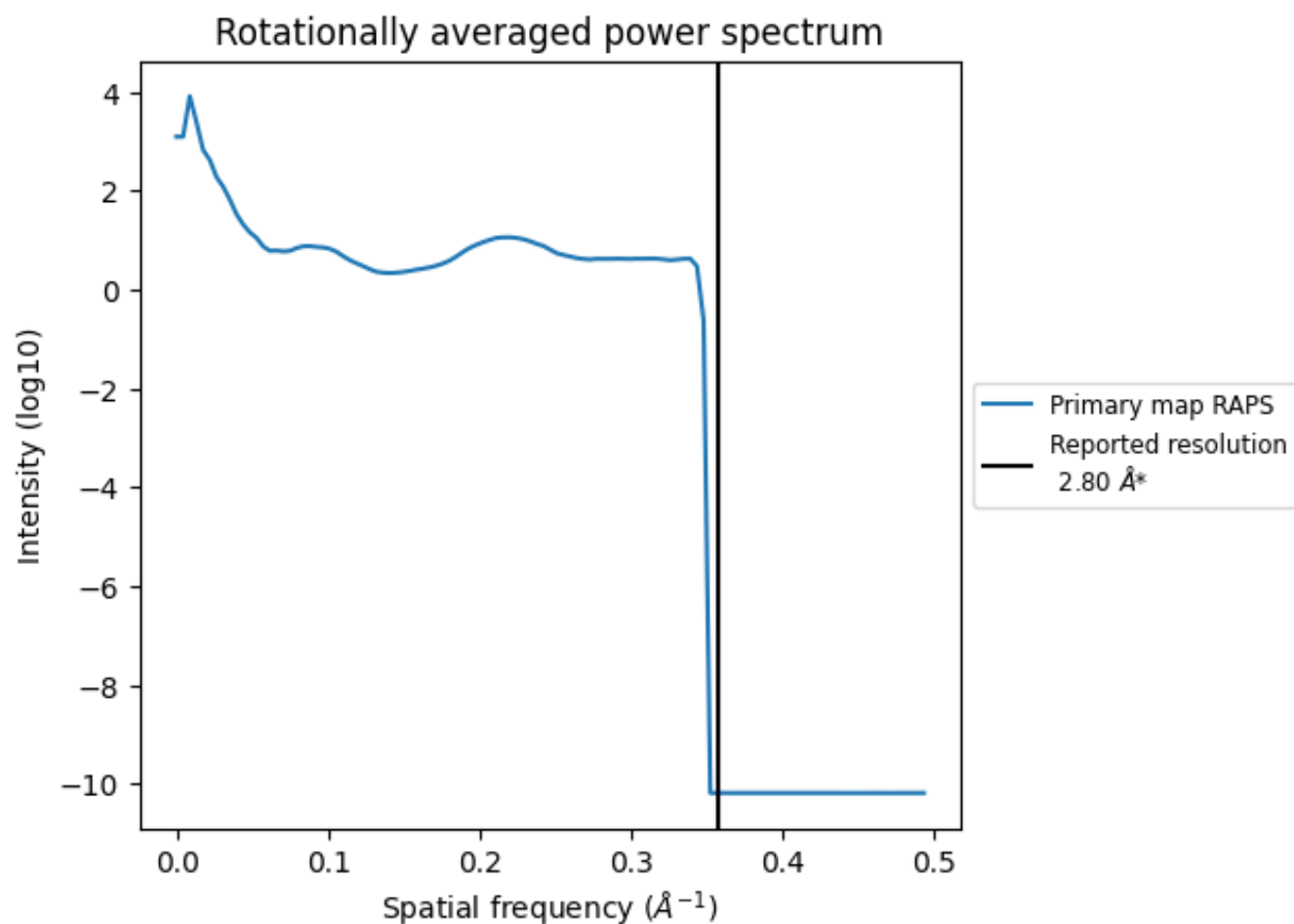
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68 nm³; this corresponds to an approximate mass of 62 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 0.357 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

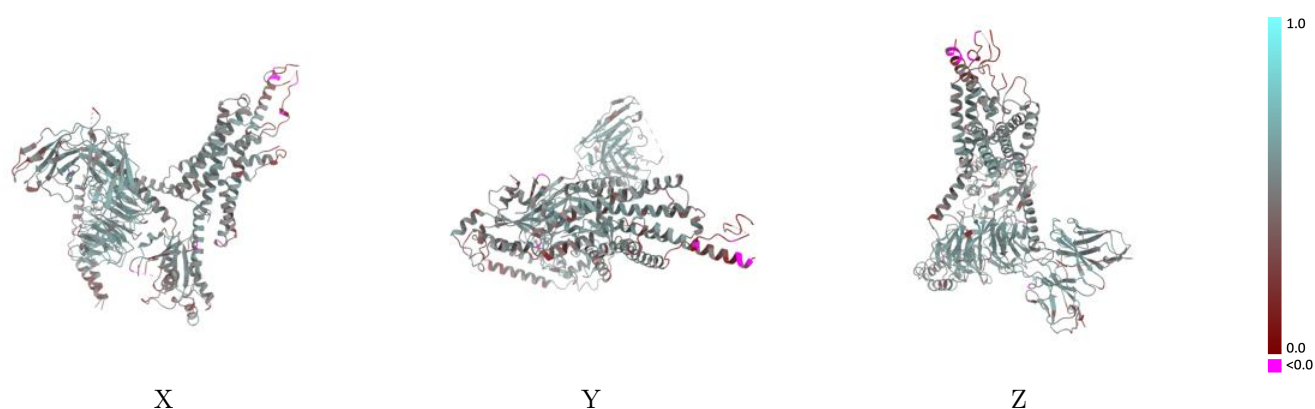
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26104 and PDB model 7TS0. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

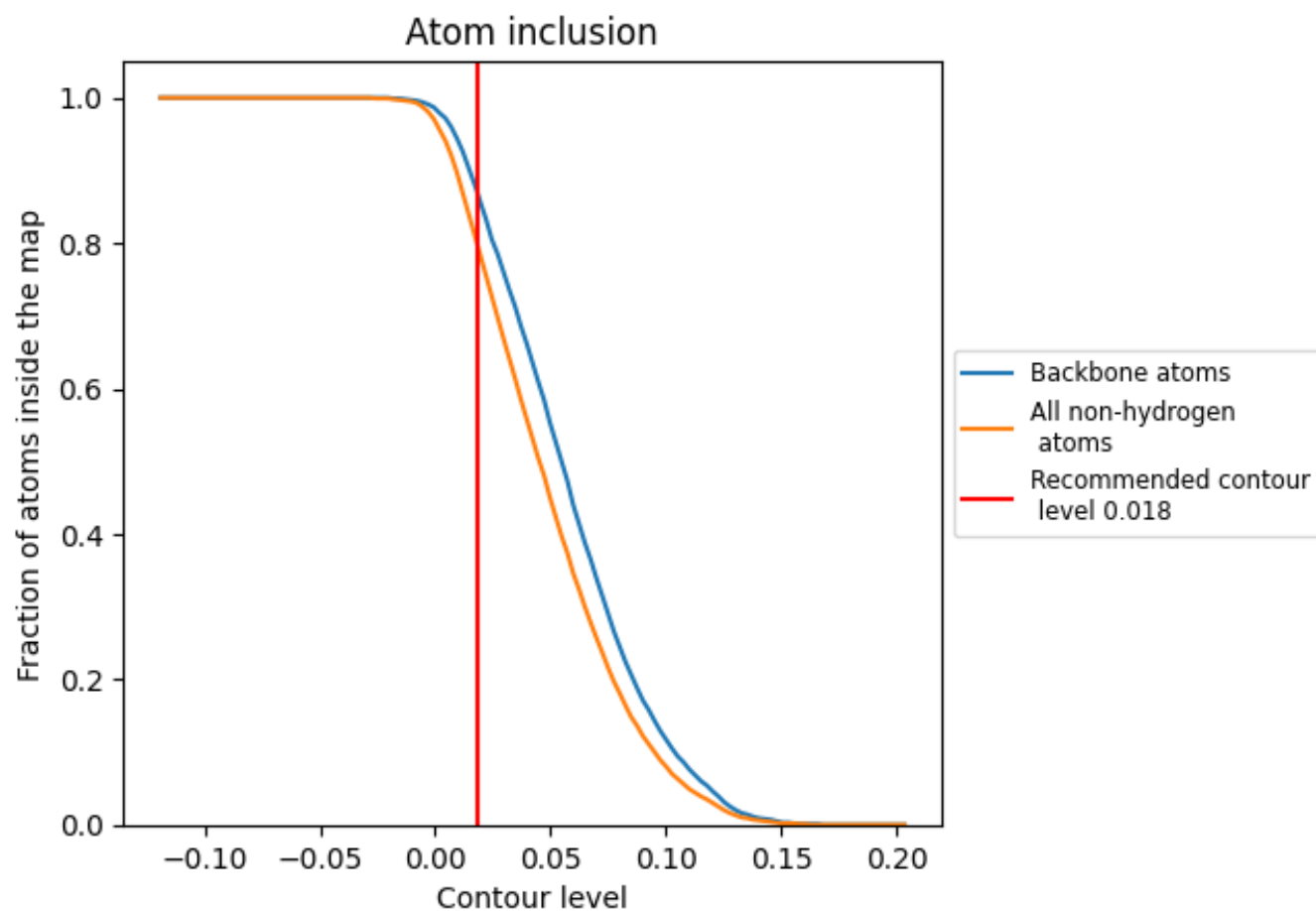


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 80% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8020	0.4940
A	0.7630	0.4680
B	0.8710	0.5430
G	0.7230	0.4440
H	0.8490	0.5260
P	0.7590	0.4610
U	0.6080	0.3740

1.0

0.0

<0.0