Full wwPDB EM Validation Report

Nov 22, 2022 – 09:48 PM JST

PDB ID	:	7F1R
EMDB ID	:	EMD-31423
Title	:	Cryo-EM structure of the chemokine receptor CCR5 in complex with RANTES and Gi
Authors	:	Zhang, H.; Chen, K.; Tan, Q.; Han, S.; Zhu, Y.; Zhao, Q.; Wu, B.
Deposited on	:	2021-06-09
Resolution	:	3.00 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:

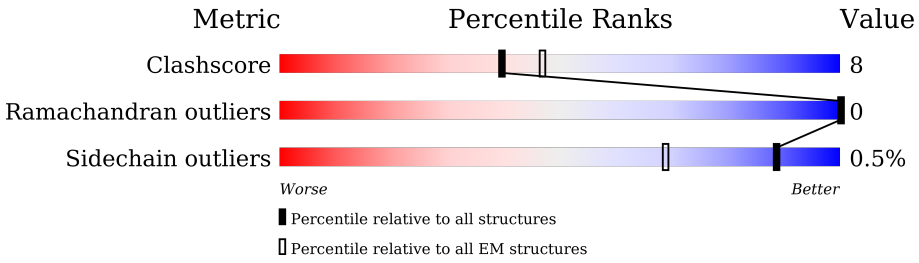
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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 >=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
1	R	462	15% 60% 11% 29%
2	A	354	53% 8% 39%
3	B	340	69% 24% 7%
4	C	71	42% 7% 51%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6621 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 C-C motif chemokine 5,C-C chemokine receptor type 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	R	327	2450	1634	391	407	18	0	0

There are 79 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	28	CYS	PHE	engineered mutation	UNP P13501
R	69	GLU	-	linker	UNP P13501
R	70	PHE	-	linker	UNP P13501
R	71	LEU	-	linker	UNP P13501
R	72	GLU	-	linker	UNP P13501
R	73	GLY	-	linker	UNP P13501
R	74	SER	-	linker	UNP P13501
R	75	GLY	-	linker	UNP P13501
R	76	SER	-	linker	UNP P13501
R	77	GLY	-	linker	UNP P13501
R	78	SER	-	linker	UNP P13501
R	79	GLY	-	linker	UNP P13501
R	80	SER	-	linker	UNP P13501
R	81	GLY	-	linker	UNP P13501
R	82	SER	-	linker	UNP P13501
R	83	GLY	-	linker	UNP P13501
R	84	SER	-	linker	UNP P13501
R	85	GLY	-	linker	UNP P13501
R	86	SER	-	linker	UNP P13501
R	87	GLY	-	linker	UNP P13501
R	88	SER	-	linker	UNP P13501
R	89	GLY	-	linker	UNP P13501
R	90	SER	-	linker	UNP P13501
R	91	GLY	-	linker	UNP P13501
R	92	SER	-	linker	UNP P13501
R	93	GLY	-	linker	UNP P13501
R	94	SER	-	linker	UNP P13501
R	95	GLY	-	linker	UNP P13501

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Chain	Residue	Modelled	Actual	Comment	Reference
R	96	SER	-	linker	UNP P13501
R	258	ASN	GLY	engineered mutation	UNP P51681
R	267	CYS	GLU	engineered mutation	UNP P51681
R	415	GLU	-	expression tag	UNP P51681
R	416	PHE	-	expression tag	UNP P51681
R	417	LEU	-	expression tag	UNP P51681
R	418	GLU	-	expression tag	UNP P51681
R	419	VAL	-	expression tag	UNP P51681
R	420	LEU	-	expression tag	UNP P51681
R	421	PHE	-	expression tag	UNP P51681
R	422	GLN	-	expression tag	UNP P51681
R	423	GLY	-	expression tag	UNP P51681
R	424	PRO	-	expression tag	UNP P51681
R	425	GLY	-	expression tag	UNP P51681
R	426	SER	-	expression tag	UNP P51681
R	427	TRP	-	expression tag	UNP P51681
R	428	SER	-	expression tag	UNP P51681
R	429	HIS	-	expression tag	UNP P51681
R	430	PRO	-	expression tag	UNP P51681
R	431	GLN	-	expression tag	UNP P51681
R	432	PHE	-	expression tag	UNP P51681
R	433	GLU	-	expression tag	UNP P51681
R	434	LYS	-	expression tag	UNP P51681
R	435	GLY	-	expression tag	UNP P51681
R	436	SER	-	expression tag	UNP P51681
R	437	GLY	-	expression tag	UNP P51681
R	438	ALA	-	expression tag	UNP P51681
R	439	GLY	-	expression tag	UNP P51681
R	440	ALA	-	expression tag	UNP P51681
R	441	SER	-	expression tag	UNP P51681
R	442	ALA	-	expression tag	UNP P51681
R	443	GLY	-	expression tag	UNP P51681
R	444	SER	-	expression tag	UNP P51681
R	445	TRP	-	expression tag	UNP P51681
R	446	SER	-	expression tag	UNP P51681
R	447	HIS	-	expression tag	UNP P51681
R	448	PRO	-	expression tag	UNP P51681
R	449	GLN	-	expression tag	UNP P51681
R	450	PHE	-	expression tag	UNP P51681
R	451	GLU	-	expression tag	UNP P51681
R	452	LYS	-	expression tag	UNP P51681
R	453	GLY	-	expression tag	UNP P51681

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Chain	Residue	Modelled	Actual	Comment	Reference
R	454	SER	-	expression tag	UNP P51681
R	455	ASP	-	expression tag	UNP P51681
R	456	TYR	-	expression tag	UNP P51681
R	457	LYS	-	expression tag	UNP P51681
R	458	ASP	-	expression tag	UNP P51681
R	459	ASP	-	expression tag	UNP P51681
R	460	ASP	-	expression tag	UNP P51681
R	461	ASP	-	expression tag	UNP P51681
R	462	LYS	-	expression tag	UNP P51681

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	216	Total	C	N	O	S	0	0
			1627	1047	281	287	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	CYS	SER	engineered mutation	UNP P63096
A	202	THR	GLY	engineered mutation	UNP P63096
A	203	ALA	GLY	engineered mutation	UNP P63096
A	245	ALA	GLU	engineered mutation	UNP P63096
A	326	SER	ALA	engineered mutation	UNP P63096

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	316	Total	C	N	O	S	0	0
			2305	1440	400	445	20		

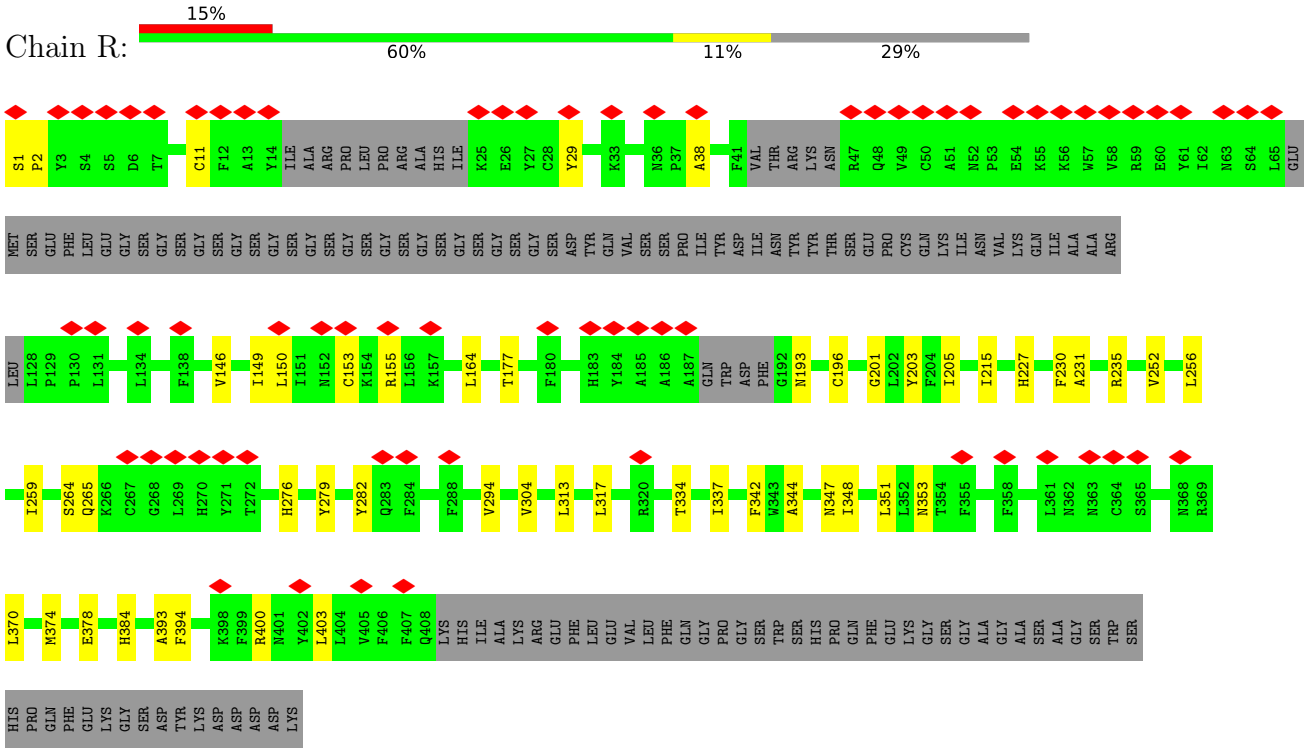
- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	35	Total	C	N	O	S	0	0
			239	153	38	46	2		

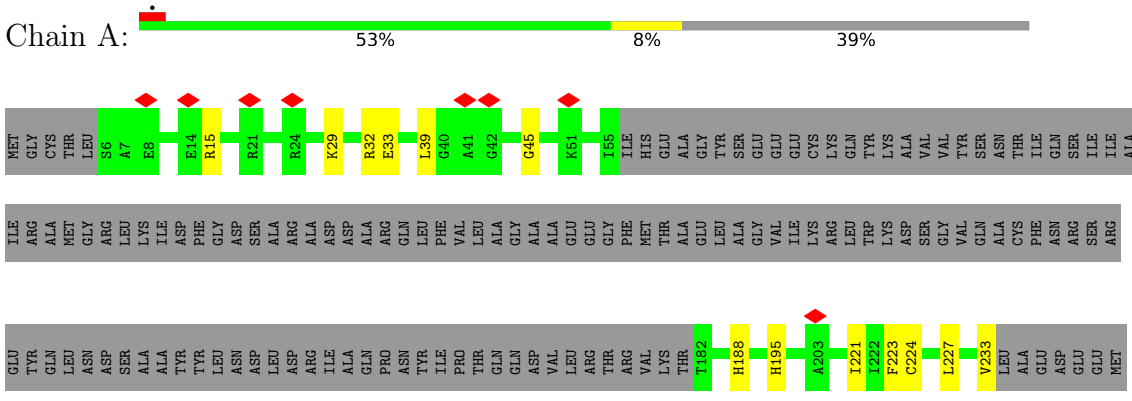
3 Residue-property plots (i)

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.

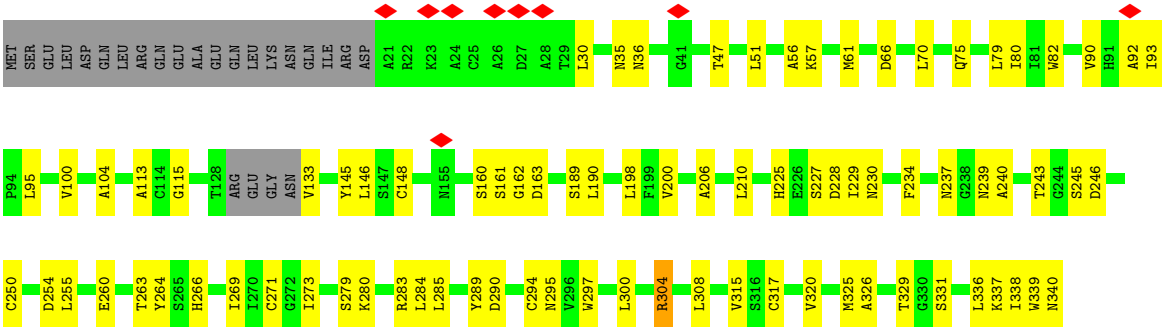
• Molecule 1: C-C motif chemokine 5,C-C chemokine receptor type 5



• Molecule 2: Guanine nucleotide-binding protein G(i) subunit alpha-1



• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1304062	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2.1875	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.200	Depositor
Minimum map value	-0.136	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	267.52, 267.52, 267.52	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

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	R	0.25	0/2511	0.39	0/3428
2	A	0.24	0/1655	0.39	0/2233
3	B	0.24	0/2351	0.43	0/3204
4	C	0.24	0/245	0.34	0/339
All	All	0.24	0/6762	0.41	0/9204

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

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	R	2450	0	2356	25	0
2	A	1627	0	1555	20	0
3	B	2305	0	2134	53	0
4	C	239	0	214	3	0
All	All	6621	0	6259	99	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 8.

All (99) 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:R:294:VAL:HG23	1:R:347:ASN:HB3	1.69	0.72
3:B:70:LEU:HB3	3:B:82:TRP:HB2	1.73	0.69
1:R:227:HIS:HB3	1:R:230:PHE:HB3	1.77	0.66
3:B:160:SER:HB2	3:B:190:LEU:HD23	1.77	0.65
2:A:308:GLU:HG3	2:A:319:ILE:HD11	1.81	0.62
3:B:250:CYS:HB2	3:B:264:TYR:HB2	1.82	0.61
1:R:279:TYR:HA	1:R:282:TYR:HB2	1.81	0.61
2:A:251:ASP:OD1	2:A:255:ASN:ND2	2.34	0.61
2:A:15:ARG:NH1	3:B:90:VAL:O	2.34	0.60
3:B:225:HIS:HE2	3:B:243:THR:HG1	1.50	0.58
1:R:153:CYS:O	1:R:155:ARG:NH2	2.36	0.58
3:B:61:MET:HG3	3:B:317:CYS:HB2	1.86	0.58
3:B:210:LEU:HD22	3:B:255:LEU:HD22	1.86	0.58
3:B:75:GLN:NE2	3:B:100:VAL:O	2.38	0.57
1:R:252:VAL:O	1:R:256:LEU:HG	2.06	0.56
1:R:149:ILE:HD12	1:R:403:LEU:HD13	1.88	0.56
2:A:254:CYS:O	2:A:317:LYS:NZ	2.32	0.56
3:B:104:ALA:HB3	3:B:113:ALA:HB3	1.89	0.55
1:R:193:ASN:HA	1:R:264:SER:HB2	1.89	0.54
3:B:240:ALA:HA	3:B:254:ASP:HA	1.88	0.54
1:R:394:PHE:O	1:R:400:ARG:NH1	2.40	0.54
3:B:198:LEU:HB3	3:B:210:LEU:HD11	1.88	0.54
3:B:237:ASN:HD21	3:B:239:ASN:HB2	1.74	0.53
3:B:161:SER:OG	3:B:163:ASP:OD1	2.26	0.53
3:B:295:ASN:ND2	3:B:304:ARG:HE	2.07	0.53
2:A:260:THR:HB	2:A:313:ARG:NH1	2.24	0.53
3:B:271:CYS:HB2	3:B:290:ASP:HB2	1.91	0.52
2:A:233:VAL:HA	2:A:241:ASN:HB3	1.92	0.52
1:R:177:THR:HG21	1:R:203:TYR:HB2	1.92	0.51
3:B:266:HIS:HB3	3:B:269:ILE:HG12	1.91	0.51
1:R:201:GLY:HA3	1:R:259:ILE:HD11	1.92	0.51
3:B:315:VAL:HA	3:B:331:SER:HA	1.93	0.51
3:B:325:MET:O	3:B:340:ASN:ND2	2.44	0.50
2:A:33:GLU:HG2	2:A:195:HIS:HB3	1.93	0.50
4:C:40:TYR:O	4:C:44:HIS:ND1	2.44	0.50
1:R:215:ILE:HG23	1:R:304:VAL:HG11	1.93	0.50
3:B:329:THR:HB	3:B:339:TRP:HZ3	1.76	0.50
3:B:30:LEU:HD21	3:B:300:LEU:HD13	1.93	0.50
2:A:227:LEU:HG	2:A:268:LEU:HD12	1.94	0.49
3:B:295:ASN:ND2	3:B:304:ARG:NE	2.60	0.48
2:A:313:ARG:HB2	2:A:316:THR:HB	1.95	0.48
1:R:11:CYS:HB2	1:R:38:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:353:ASN:HB3	1:R:370:LEU:HD13	1.96	0.48
3:B:230:ASN:ND2	3:B:246:ASP:OD1	2.47	0.47
2:A:29:LYS:HE2	2:A:32:ARG:HE	1.78	0.47
3:B:227:SER:OG	3:B:228:ASP:N	2.47	0.47
1:R:29:TYR:HB2	1:R:265:GLN:HG3	1.96	0.47
3:B:284:LEU:HD21	4:C:50:LEU:HB3	1.97	0.47
2:A:221:ILE:O	2:A:265:ILE:N	2.40	0.47
3:B:51:LEU:N	3:B:336:LEU:O	2.44	0.47
3:B:285:LEU:N	3:B:297:TRP:O	2.37	0.46
2:A:188:HIS:HB3	2:A:195:HIS:CE1	2.50	0.46
2:A:260:THR:CB	2:A:313:ARG:HH11	2.28	0.46
2:A:39:LEU:HD11	2:A:253:ILE:HD13	1.97	0.46
1:R:344:ALA:O	1:R:348:ILE:HG12	2.15	0.45
2:A:45:GLY:HA2	2:A:224:CYS:HB2	1.99	0.45
2:A:260:THR:HB	2:A:313:ARG:HH11	1.82	0.45
3:B:266:HIS:ND1	3:B:304:ARG:NH1	2.65	0.45
1:R:342:PHE:HB3	1:R:384:HIS:HB2	1.98	0.44
3:B:294:CYS:O	3:B:308:LEU:N	2.45	0.44
1:R:164:LEU:HD21	1:R:393:ALA:HB2	2.00	0.44
2:A:39:LEU:HD11	2:A:253:ILE:HG21	1.99	0.44
2:A:348:LEU:HG	2:A:353:LEU:HD12	1.98	0.44
3:B:279:SER:HA	3:B:320:VAL:HG11	2.00	0.44
2:A:295:THR:HG23	2:A:298:GLU:H	1.83	0.44
3:B:148:CYS:HB2	3:B:189:SER:HA	2.00	0.44
3:B:229:ILE:HA	3:B:245:SER:HA	1.99	0.43
3:B:273:ILE:HG12	3:B:289:TYR:CD2	2.53	0.43
3:B:225:HIS:CE1	3:B:243:THR:HG1	2.37	0.43
3:B:51:LEU:HB2	3:B:336:LEU:HB2	2.00	0.43
3:B:80:ILE:HG22	3:B:92:ALA:HA	2.00	0.43
3:B:326:ALA:HB1	3:B:338:ILE:HG23	2.01	0.43
3:B:115:GLY:HA3	3:B:146:LEU:HD23	2.01	0.42
3:B:206:ALA:HB1	3:B:225:HIS:HB2	2.01	0.42
1:R:231:ALA:HB1	1:R:235:ARG:HD3	2.02	0.42
3:B:254:ASP:OD1	3:B:254:ASP:N	2.52	0.42
1:R:146:VAL:O	1:R:150:LEU:HD13	2.20	0.42
3:B:56:ALA:HB1	3:B:75:GLN:HB2	2.01	0.42
3:B:93:ILE:HG12	3:B:133:VAL:HG11	2.02	0.42
3:B:260:GLU:OE2	3:B:263:THR:OG1	2.37	0.42
1:R:201:GLY:O	1:R:205:ILE:HG12	2.20	0.42
3:B:79:LEU:HB2	3:B:95:LEU:HD11	2.02	0.42
3:B:47:THR:HG23	3:B:337:LYS:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:334:THR:HA	1:R:337:ILE:HG12	2.03	0.41
3:B:35:ASN:OD1	3:B:36:ASN:N	2.54	0.41
3:B:146:LEU:HA	3:B:161:SER:HA	2.01	0.41
3:B:200:VAL:HG22	3:B:234:PHE:CE2	2.55	0.41
1:R:374:MET:O	1:R:378:GLU:HG3	2.20	0.41
3:B:66:ASP:OD1	3:B:66:ASP:N	2.48	0.41
3:B:280:LYS:HE3	3:B:280:LYS:HB3	1.98	0.41
3:B:329:THR:HB	3:B:339:TRP:CZ3	2.55	0.41
1:R:1:SER:N	1:R:2:PRO:HD2	2.36	0.41
1:R:313:LEU:O	1:R:317:LEU:HG	2.21	0.41
3:B:57:LYS:HE3	3:B:57:LYS:HB2	1.92	0.41
1:R:294:VAL:HG21	1:R:351:LEU:HD11	2.02	0.40
3:B:283:ARG:HD2	3:B:300:LEU:HD23	2.04	0.40
2:A:223:PHE:N	2:A:265:ILE:O	2.40	0.40
3:B:145:TYR:O	3:B:162:GLY:N	2.54	0.40
4:C:47:GLU:O	4:C:49:PRO:HD3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	317/462 (69%)	313 (99%)	4 (1%)	0	100	100
2	A	210/354 (59%)	207 (99%)	3 (1%)	0	100	100
3	B	312/340 (92%)	307 (98%)	5 (2%)	0	100	100
4	C	33/71 (46%)	32 (97%)	1 (3%)	0	100	100
All	All	872/1227 (71%)	859 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	R	242/403 (60%)	240 (99%)	2 (1%)	81 93
2	A	158/306 (52%)	158 (100%)	0	100 100
3	B	232/283 (82%)	231 (100%)	1 (0%)	91 97
4	C	22/58 (38%)	22 (100%)	0	100 100
All	All	654/1050 (62%)	651 (100%)	3 (0%)	89 96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	196	CYS
1	R	276	HIS
3	B	304	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	143	ASN
1	R	265	GLN
1	R	388	ASN
2	A	255	ASN
2	A	294	ASN
3	B	183	HIS
3	B	295	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)

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.

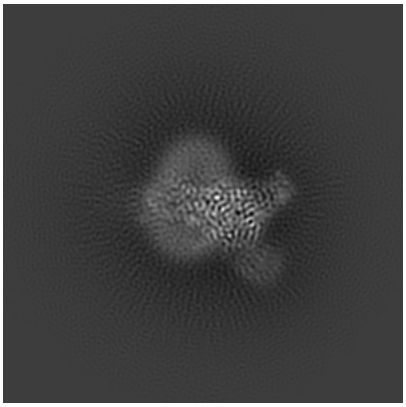
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31423. These allow visual inspection of the internal detail of the map and identification of artifacts.

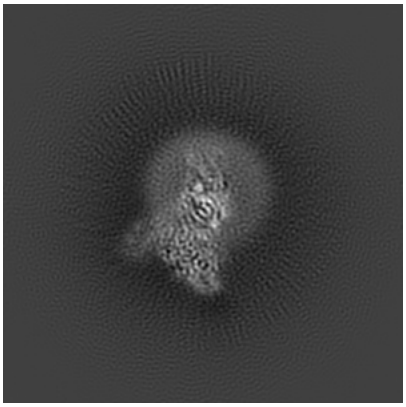
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

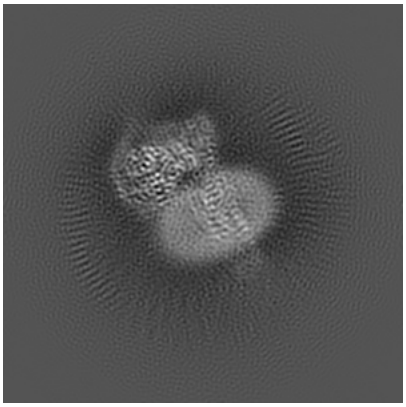
6.1.1 Primary map



X



Y

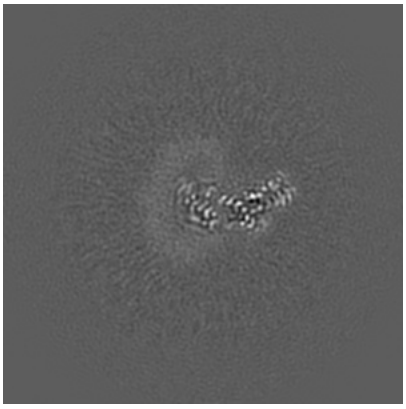


Z

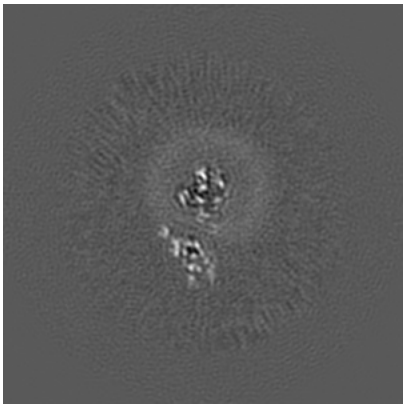
The images above show the map projected in three orthogonal directions.

6.2 Central slices

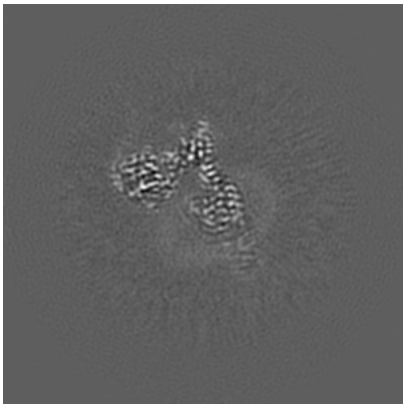
6.2.1 Primary map



X Index: 128



Y Index: 128

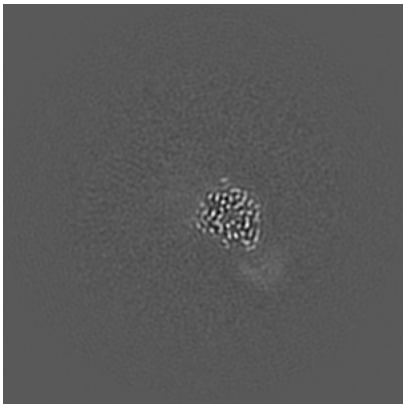


Z Index: 128

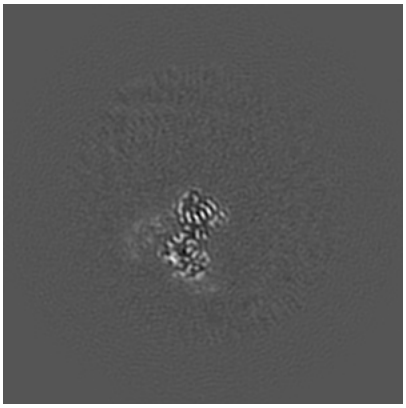
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

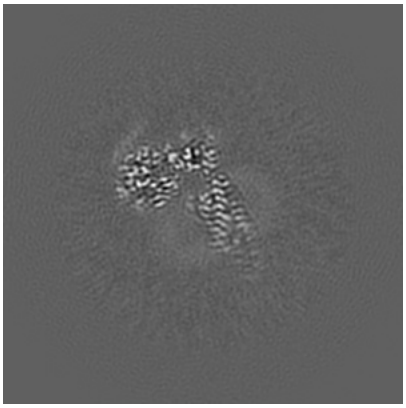
6.3.1 Primary map



X Index: 95



Y Index: 158



Z Index: 124

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

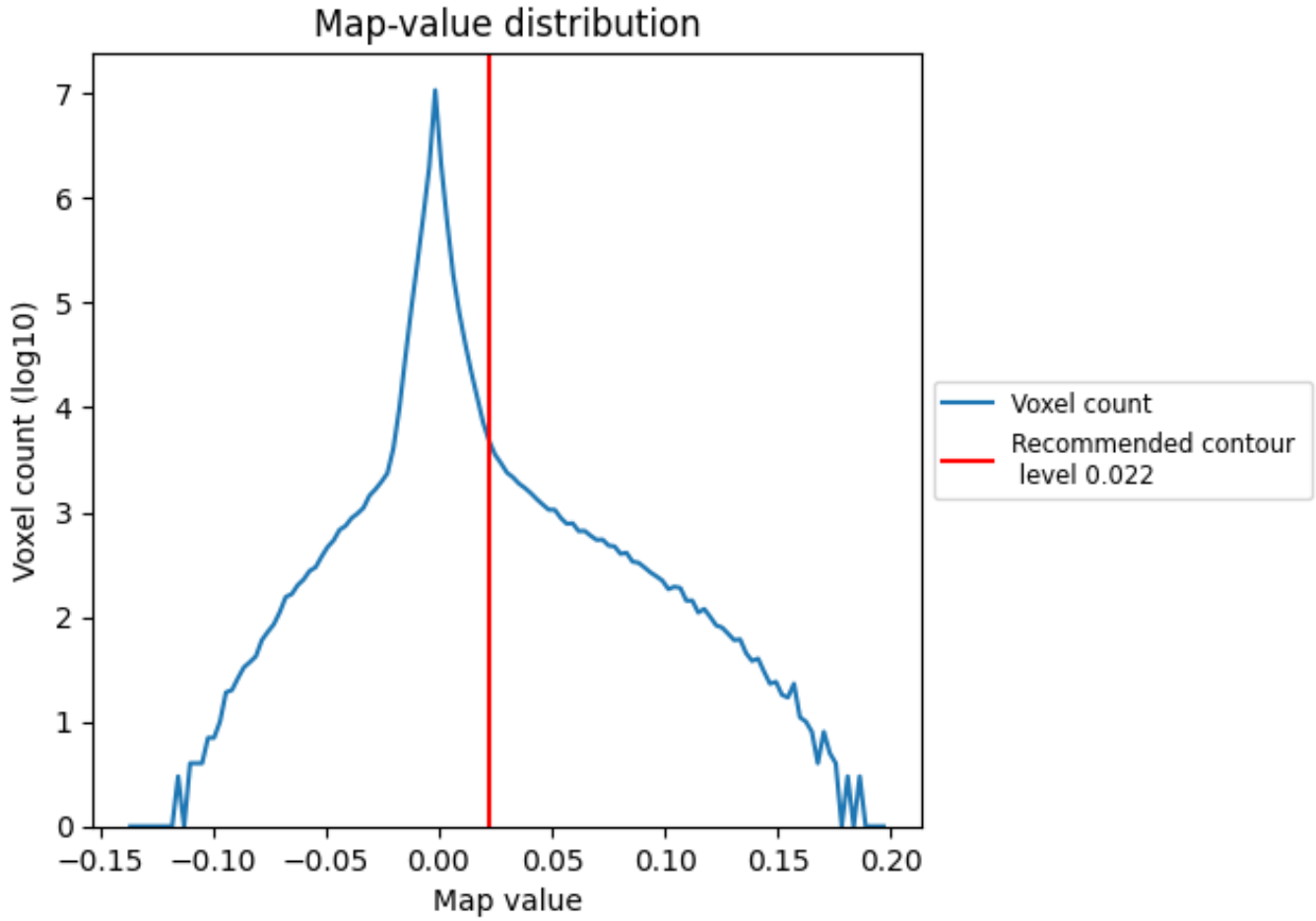
6.5 Mask visualisation (i)

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

7 Map analysis

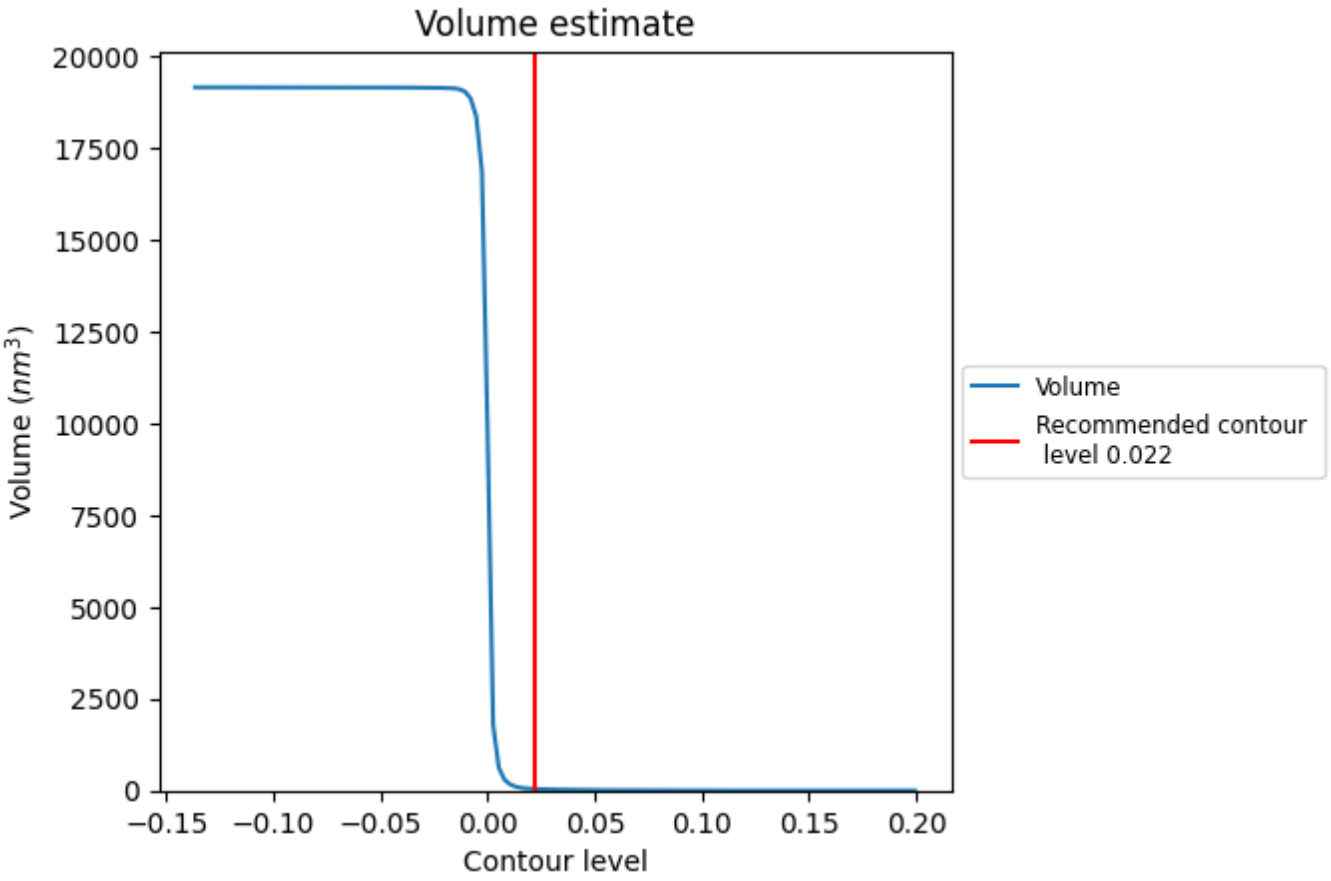
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

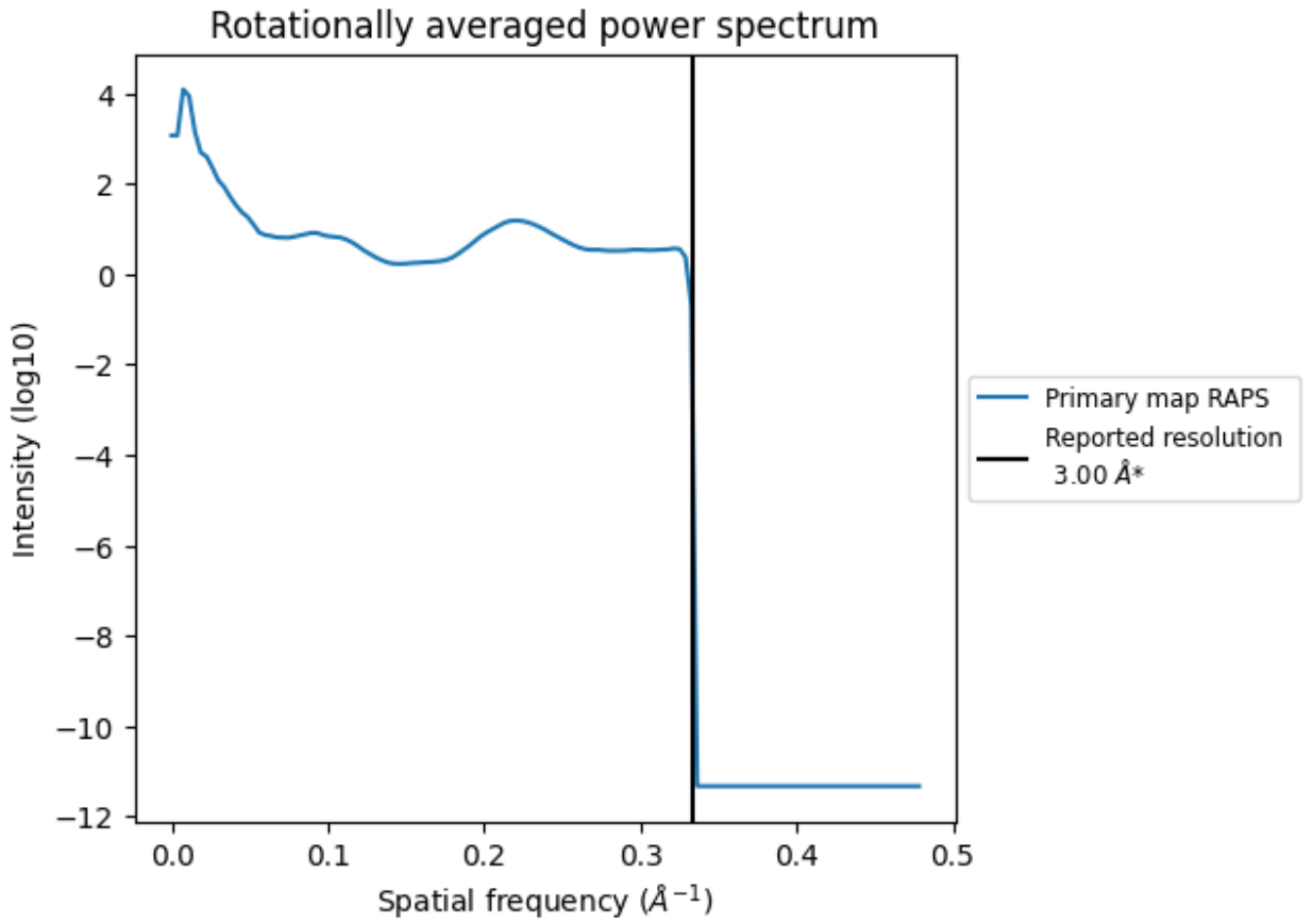
7.2 Volume estimate



The volume at the recommended contour level is 43 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 0.333 Å^{-1}

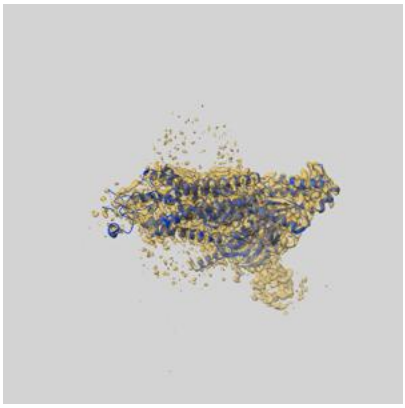
8 Fourier-Shell correlation (i)

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

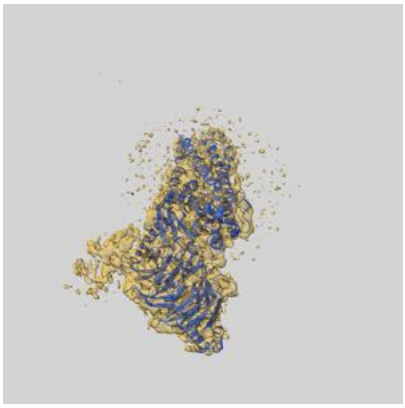
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31423 and PDB model 7F1R. Per-residue inclusion information can be found in section 3 on page 6.

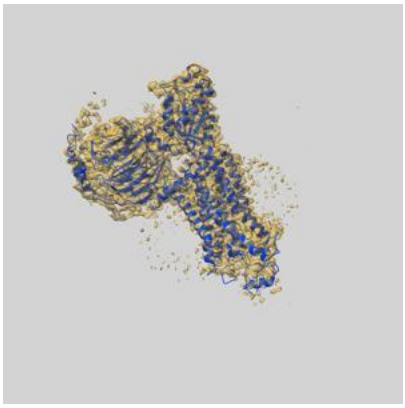
9.1 Map-model overlay



X



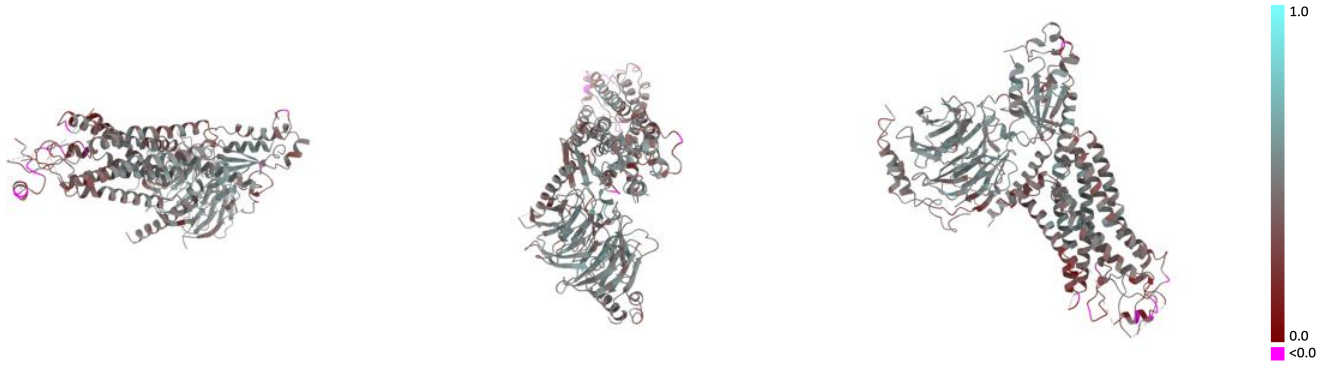
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.022 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.

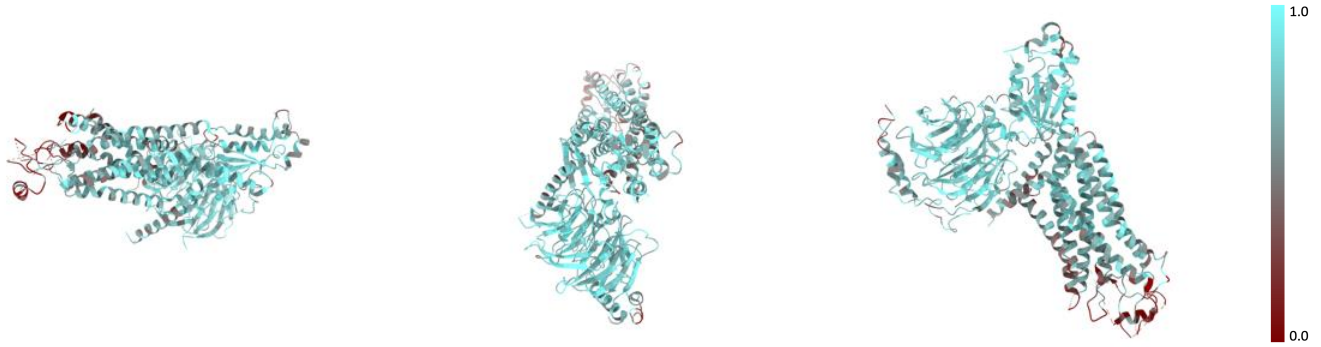
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

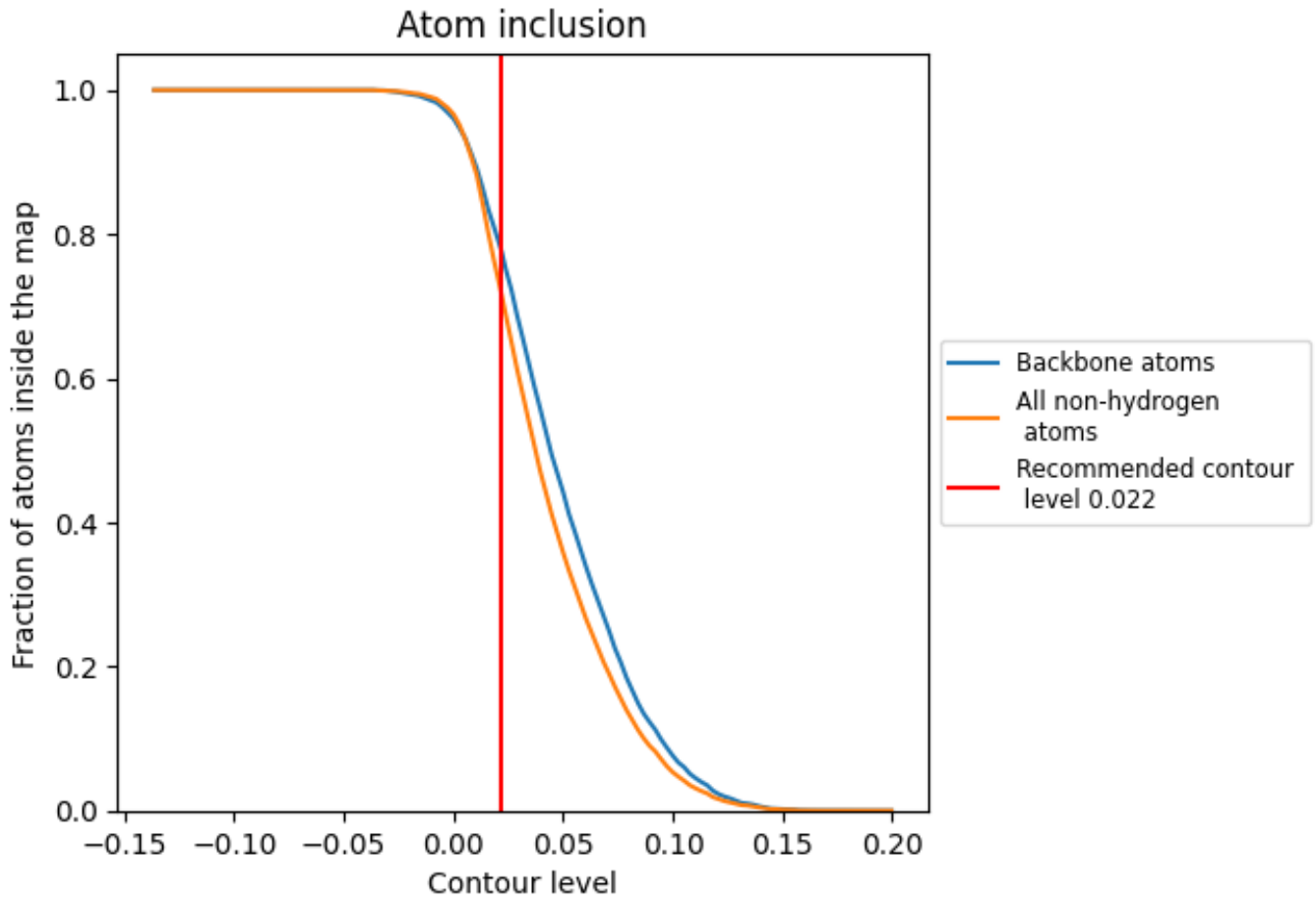
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.022).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 71% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7142	0.4390
A	0.7553	0.4600
B	0.7962	0.4760
C	0.7101	0.4250
R	0.6101	0.3920