



Full wwPDB EM Validation Report ⓘ

Jul 20, 2026 – 07:44 PM JST

PDB ID : 24IP / pdb_000024ip
EMDB ID : EMD-69549
Title : Cryo-EM structure of the dimeric WDR11-FAM91A1-C17orf75 complex
Authors : Liu, Z.M.; Zhang, Y.F.; Chen, Z.Y.; Chen, Z.G.; Ding, J.P.
Deposited on : 2026-03-04
Resolution : 3.07 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:

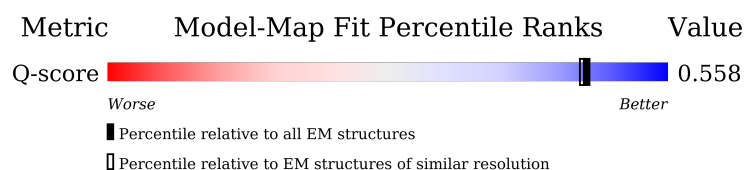
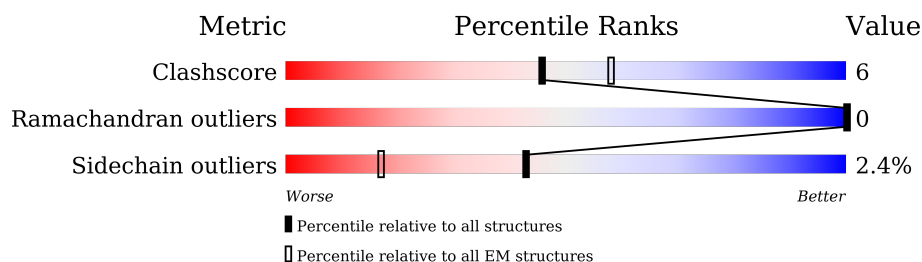
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.07 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	13977 (2.57 - 3.57)

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	1238	
1	D	1238	
2	C	410	
2	F	410	

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Mol	Chain	Length	Quality of chain
3	B	851	 39%6%55%
3	E	851	 36%7%57%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28209 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 WD repeat-containing protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	1100	Total	C	N	O	S	1	0
			8677	5523	1498	1606	50		
1	A	1103	Total	C	N	O	S	4	0
			8728	5552	1512	1614	50		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	MET	-	initiating methionine	UNP Q9BZH6
D	-12	ALA	-	expression tag	UNP Q9BZH6
D	-11	SER	-	expression tag	UNP Q9BZH6
D	-10	ASP	-	expression tag	UNP Q9BZH6
D	-9	TYR	-	expression tag	UNP Q9BZH6
D	-8	LYS	-	expression tag	UNP Q9BZH6
D	-7	ASP	-	expression tag	UNP Q9BZH6
D	-6	ASP	-	expression tag	UNP Q9BZH6
D	-5	ASP	-	expression tag	UNP Q9BZH6
D	-4	ASP	-	expression tag	UNP Q9BZH6
D	-3	LYS	-	expression tag	UNP Q9BZH6
D	-2	GLY	-	expression tag	UNP Q9BZH6
D	-1	SER	-	expression tag	UNP Q9BZH6
D	0	GLY	-	expression tag	UNP Q9BZH6
A	-13	MET	-	initiating methionine	UNP Q9BZH6
A	-12	ALA	-	expression tag	UNP Q9BZH6
A	-11	SER	-	expression tag	UNP Q9BZH6
A	-10	ASP	-	expression tag	UNP Q9BZH6
A	-9	TYR	-	expression tag	UNP Q9BZH6
A	-8	LYS	-	expression tag	UNP Q9BZH6
A	-7	ASP	-	expression tag	UNP Q9BZH6
A	-6	ASP	-	expression tag	UNP Q9BZH6
A	-5	ASP	-	expression tag	UNP Q9BZH6
A	-4	ASP	-	expression tag	UNP Q9BZH6
A	-3	LYS	-	expression tag	UNP Q9BZH6
A	-2	GLY	-	expression tag	UNP Q9BZH6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q9BZH6
A	0	GLY	-	expression tag	UNP Q9BZH6

- Molecule 2 is a protein called Protein Njmu-R1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	308	Total	C	N	O	S	0	0
			2466	1572	412	461	21		
2	F	307	Total	C	N	O	S	0	0
			2468	1572	416	459	21		

There are 28 discrepancies between the modelled and reference sequences:

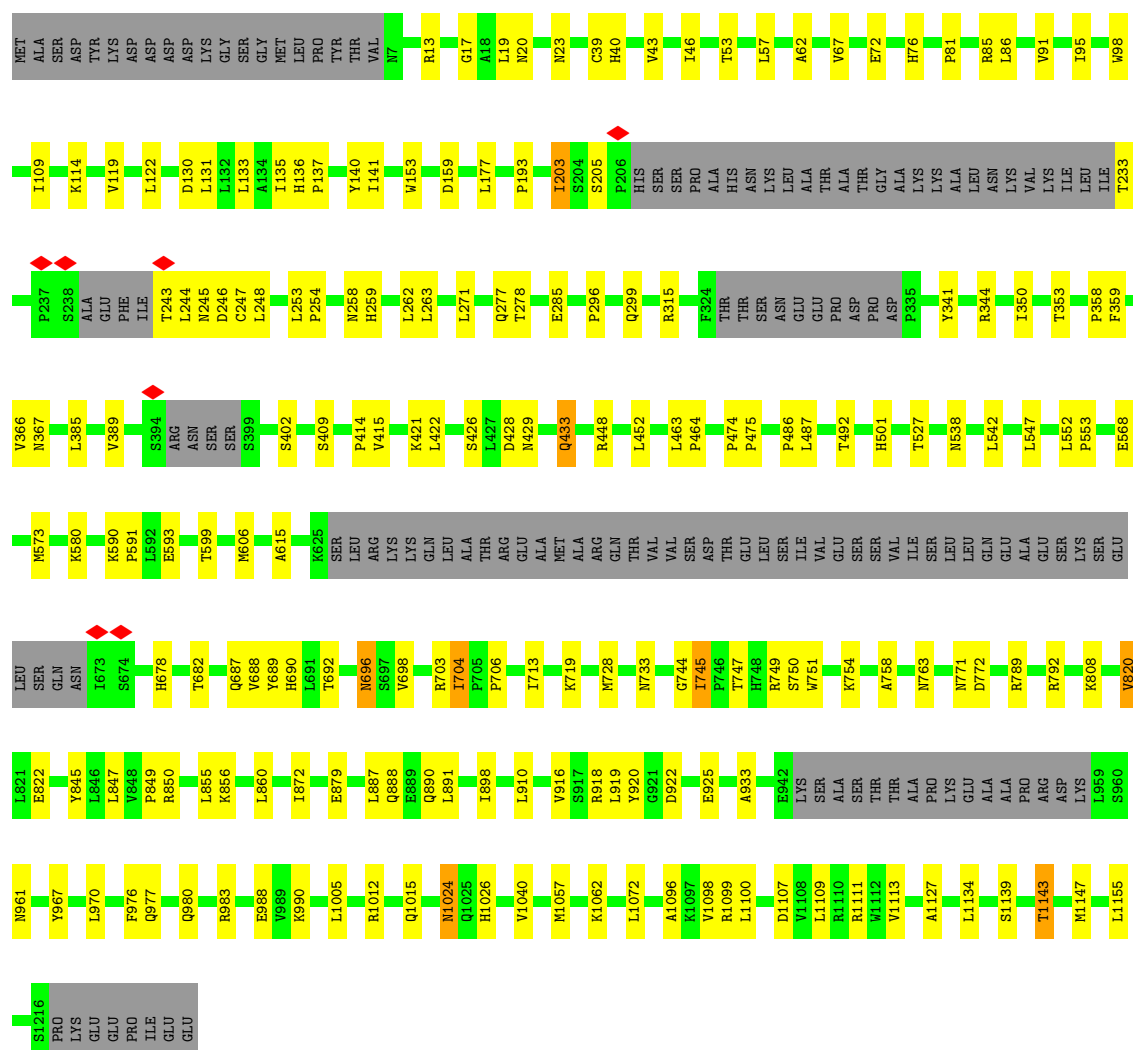
Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	MET	-	initiating methionine	UNP Q9HAS0
C	-12	ALA	-	expression tag	UNP Q9HAS0
C	-11	SER	-	expression tag	UNP Q9HAS0
C	-10	ASP	-	expression tag	UNP Q9HAS0
C	-9	TYR	-	expression tag	UNP Q9HAS0
C	-8	LYS	-	expression tag	UNP Q9HAS0
C	-7	ASP	-	expression tag	UNP Q9HAS0
C	-6	ASP	-	expression tag	UNP Q9HAS0
C	-5	ASP	-	expression tag	UNP Q9HAS0
C	-4	ASP	-	expression tag	UNP Q9HAS0
C	-3	LYS	-	expression tag	UNP Q9HAS0
C	-2	GLY	-	expression tag	UNP Q9HAS0
C	-1	SER	-	expression tag	UNP Q9HAS0
C	0	GLY	-	expression tag	UNP Q9HAS0
F	-13	MET	-	initiating methionine	UNP Q9HAS0
F	-12	ALA	-	expression tag	UNP Q9HAS0
F	-11	SER	-	expression tag	UNP Q9HAS0
F	-10	ASP	-	expression tag	UNP Q9HAS0
F	-9	TYR	-	expression tag	UNP Q9HAS0
F	-8	LYS	-	expression tag	UNP Q9HAS0
F	-7	ASP	-	expression tag	UNP Q9HAS0
F	-6	ASP	-	expression tag	UNP Q9HAS0
F	-5	ASP	-	expression tag	UNP Q9HAS0
F	-4	ASP	-	expression tag	UNP Q9HAS0
F	-3	LYS	-	expression tag	UNP Q9HAS0
F	-2	GLY	-	expression tag	UNP Q9HAS0
F	-1	SER	-	expression tag	UNP Q9HAS0
F	0	GLY	-	expression tag	UNP Q9HAS0

- Molecule 3 is a protein called Protein FAM91A1.

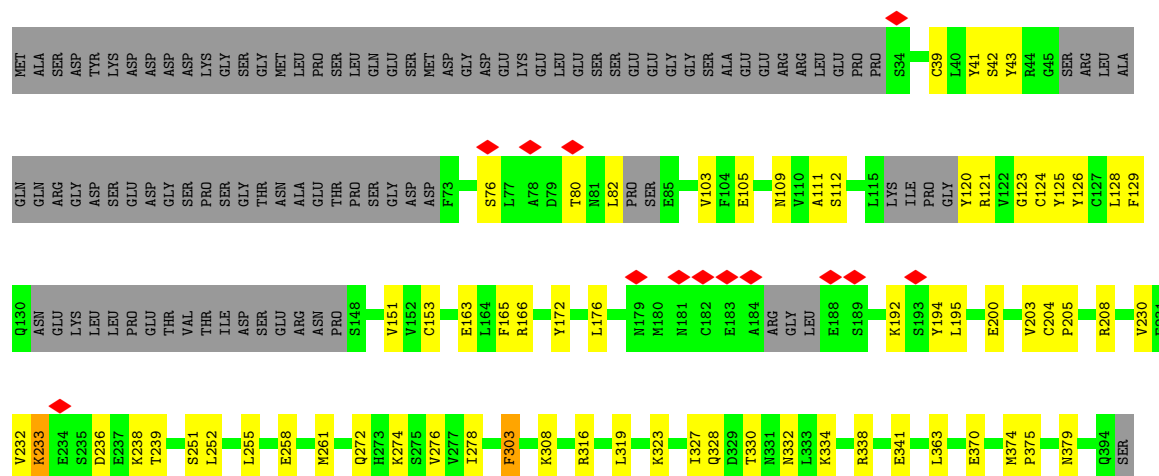
Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	380	Total	C	N	O	S	1	0
			2986	1906	522	543	15		
3	E	367	Total	C	N	O	S	1	0
			2884	1845	503	521	15		

There are 26 discrepancies between the modelled and reference sequences:

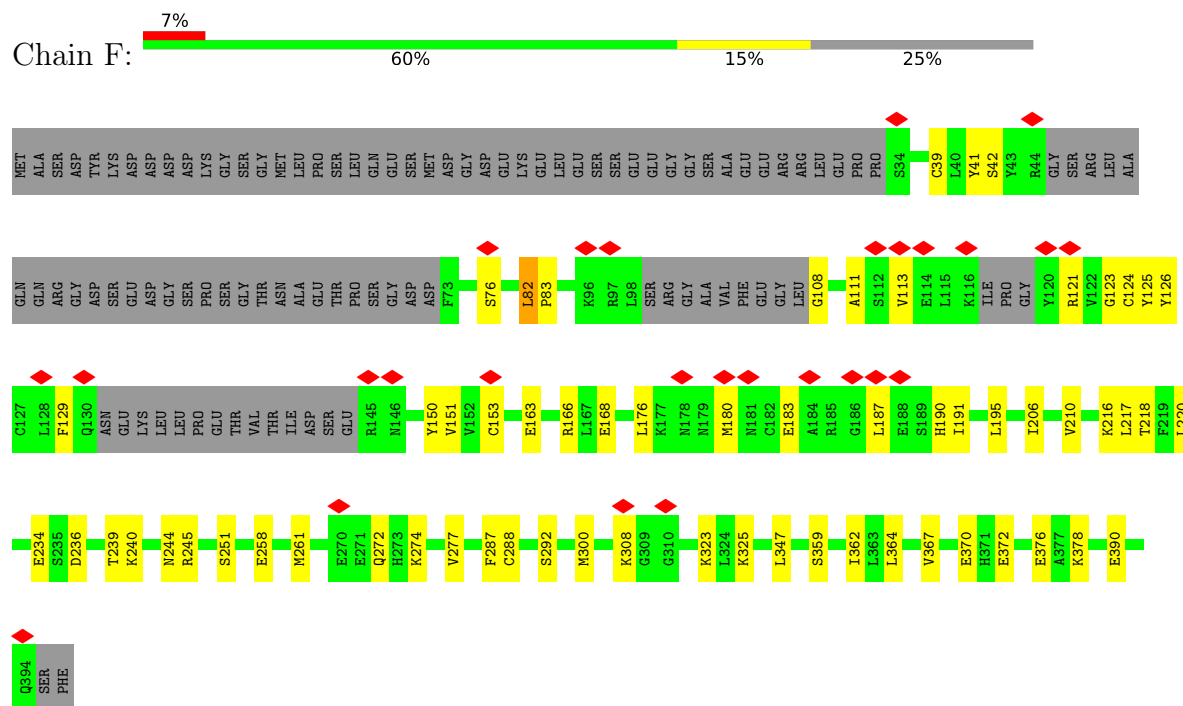
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	MET	-	initiating methionine	UNP Q658Y4
B	-11	GLY	-	expression tag	UNP Q658Y4
B	-10	TYR	-	expression tag	UNP Q658Y4
B	-9	PRO	-	expression tag	UNP Q658Y4
B	-8	TYR	-	expression tag	UNP Q658Y4
B	-7	ASP	-	expression tag	UNP Q658Y4
B	-6	VAL	-	expression tag	UNP Q658Y4
B	-5	PRO	-	expression tag	UNP Q658Y4
B	-4	ASP	-	expression tag	UNP Q658Y4
B	-3	TYR	-	expression tag	UNP Q658Y4
B	-2	ALA	-	expression tag	UNP Q658Y4
B	-1	GLY	-	expression tag	UNP Q658Y4
B	0	SER	-	expression tag	UNP Q658Y4
E	-12	MET	-	initiating methionine	UNP Q658Y4
E	-11	GLY	-	expression tag	UNP Q658Y4
E	-10	TYR	-	expression tag	UNP Q658Y4
E	-9	PRO	-	expression tag	UNP Q658Y4
E	-8	TYR	-	expression tag	UNP Q658Y4
E	-7	ASP	-	expression tag	UNP Q658Y4
E	-6	VAL	-	expression tag	UNP Q658Y4
E	-5	PRO	-	expression tag	UNP Q658Y4
E	-4	ASP	-	expression tag	UNP Q658Y4
E	-3	TYR	-	expression tag	UNP Q658Y4
E	-2	ALA	-	expression tag	UNP Q658Y4
E	-1	GLY	-	expression tag	UNP Q658Y4
E	0	SER	-	expression tag	UNP Q658Y4



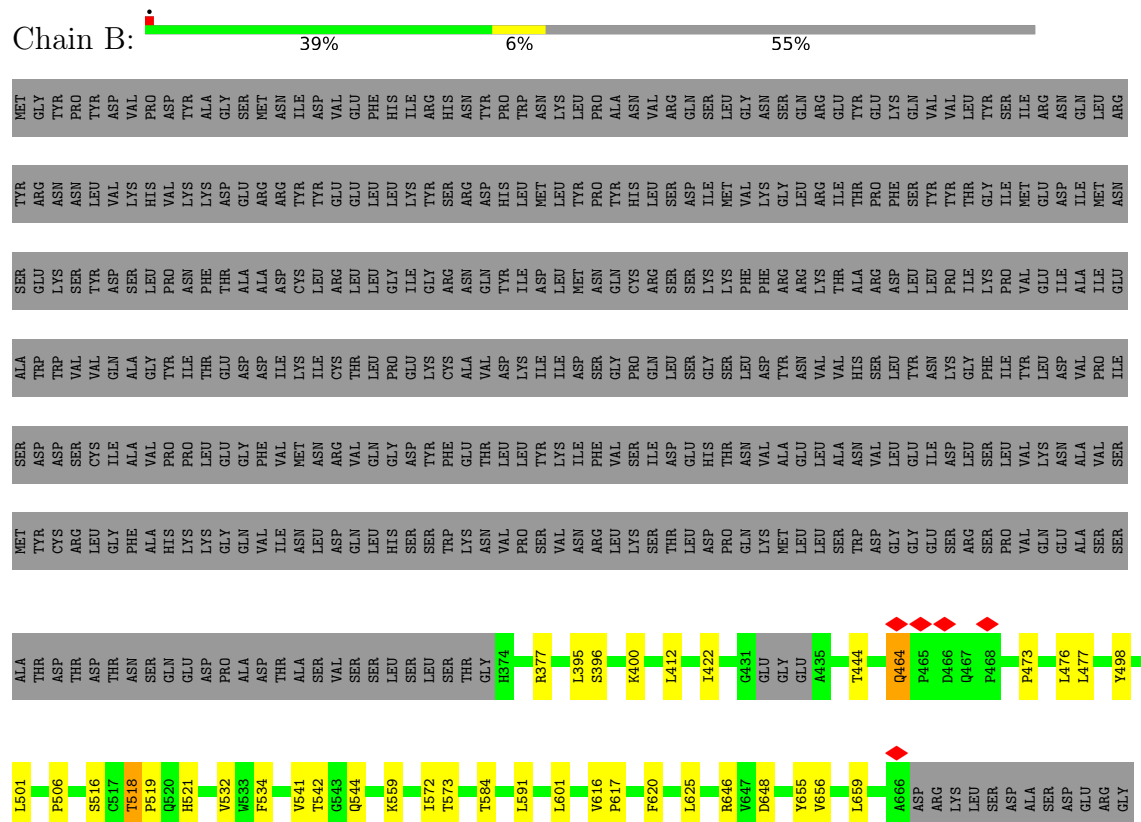
• Molecule 2: Protein Njmu-R1



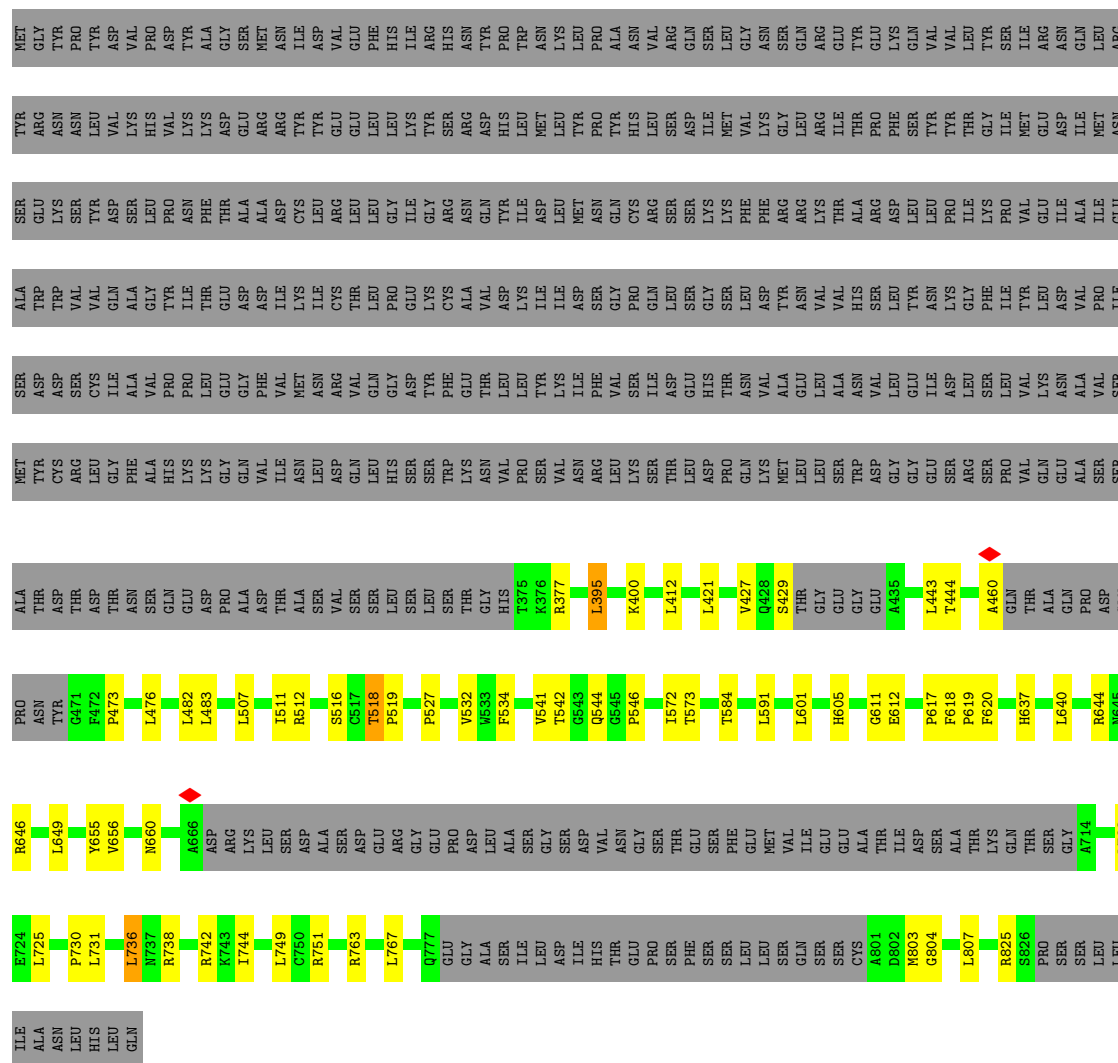
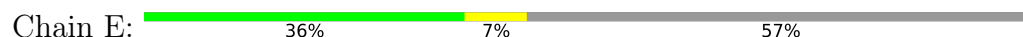
Chain F:



Chain B:



- Molecule 3: Protein FAM91A1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	190979	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	19.754	Depositor
Minimum map value	0.000	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.272	Depositor
Recommended contour level	1	Depositor
Map size (Å)	559.2, 559.2, 559.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93200004, 0.93200004, 0.93200004	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.08	0/8914	0.23	0/12101
1	D	0.08	0/8861	0.23	0/12030
2	C	0.08	0/2509	0.22	0/3367
2	F	0.08	0/2513	0.23	0/3375
3	B	0.08	0/3053	0.22	0/4144
3	E	0.08	0/2946	0.23	0/3994
All	All	0.08	0/28796	0.23	0/39011

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	8728	0	8744	109	0
1	D	8677	0	8697	114	0
2	C	2466	0	2430	34	0
2	F	2468	0	2442	32	0
3	B	2986	0	3008	29	0
3	E	2884	0	2921	35	0
All	All	28209	0	28242	348	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 6.

All (348) 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:A:205:SER:HG	1:A:233:THR:N	1.66	0.93
1:A:1024:ASN:HD22	1:A:1026:HIS:H	1.34	0.75
1:D:807:ASP:HA	1:D:823:MET:HE3	1.69	0.72
1:A:344:ARG:NH1	1:A:402:SER:O	2.23	0.72
1:D:860:LEU:HD13	1:D:1155:LEU:HD11	1.75	0.68
1:D:52:GLN:HE22	1:D:839:GLU:H	1.42	0.68
1:D:299:GLN:NE2	1:D:366:VAL:O	2.27	0.67
1:D:136:HIS:HB2	1:D:140:TYR:HB2	1.77	0.67
1:D:855:LEU:HB2	1:D:887:LEU:HD11	1.76	0.66
1:A:299:GLN:NE2	1:A:366:VAL:O	2.29	0.66
3:B:377:ARG:HG2	3:B:473:PRO:HG2	1.77	0.66
1:A:860:LEU:HD13	1:A:1155:LEU:HD11	1.78	0.66
1:D:850:ARG:NH1	1:D:879:GLU:OE2	2.29	0.65
2:F:191:ILE:HG22	2:F:195:LEU:HD12	1.79	0.65
1:A:976:PHE:O	1:A:980:GLN:NE2	2.29	0.65
2:F:217:LEU:HB2	2:F:300:MET:HG3	1.78	0.65
1:A:678:HIS:HB3	1:A:690[A]:HIS:HE1	1.63	0.64
3:E:656:VAL:HG22	3:E:725:LEU:HG	1.80	0.64
1:D:344:ARG:NH1	1:D:402:SER:O	2.30	0.63
1:D:1067:VAL:HG13	1:D:1079:ALA:HB1	1.81	0.63
3:B:444:THR:HG21	3:B:731:LEU:HA	1.79	0.63
2:C:39:CYS:N	2:C:153:CYS:SG	2.72	0.63
3:E:534:PHE:HE1	3:E:725:LEU:HB3	1.64	0.62
2:F:111:ALA:HB3	2:F:124:CYS:HB3	1.80	0.62
1:D:64:VAL:HA	1:D:90:ASP:HA	1.81	0.62
1:A:23:ASN:ND2	1:A:39:CYS:O	2.32	0.62
1:A:1096:ALA:HA	1:A:1100:LEU:HD13	1.81	0.62
1:D:114:LYS:HB3	1:D:137:PRO:HG2	1.81	0.62
1:D:153:TRP:HB2	1:D:193:PRO:HG3	1.81	0.62
1:D:62:ALA:HB1	1:D:91:VAL:HG12	1.80	0.62
1:D:268:ILE:HB	1:D:282:ILE:HB	1.81	0.62
1:D:1096:ALA:HA	1:D:1100:LEU:HD13	1.80	0.62
2:C:111:ALA:HB3	2:C:124:CYS:HB3	1.81	0.61
1:D:139:ASN:ND2	1:D:156:SER:OG	2.33	0.61
3:E:617:PRO:HA	3:E:655:TYR:HA	1.83	0.61
1:D:554:THR:HG23	3:E:807:LEU:HB2	1.81	0.61
1:A:687:GLN:NE2	1:A:689:TYR:OH	2.34	0.60
1:A:538:ASN:ND2	1:A:542:LEU:O	2.35	0.60
1:D:976:PHE:O	1:D:980:GLN:NE2	2.31	0.60
1:A:203:ILE:HD11	1:A:244:LEU:HD13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:750:SER:O	1:A:771:ASN:ND2	2.34	0.59
1:D:1113:VAL:HG13	1:D:1127:ALA:HB1	1.83	0.59
3:B:412:LEU:HD23	3:B:476:LEU:HD12	1.84	0.59
1:D:17:GLY:HA2	1:D:463:LEU:H	1.68	0.59
1:D:23:ASN:HD21	1:D:40:HIS:H	1.50	0.59
1:D:753:ARG:HD3	1:D:769:MET:HE2	1.85	0.59
2:C:163:GLU:OE1	2:C:166:ARG:NH1	2.36	0.59
2:C:112:SER:HA	2:C:123:GLY:HA2	1.85	0.58
2:C:251:SER:O	2:C:323:LYS:NZ	2.34	0.58
1:A:62:ALA:HB1	1:A:91:VAL:HG22	1.85	0.58
1:A:682:THR:HG21	1:A:713:ILE:HD12	1.85	0.58
3:B:541:VAL:HG13	3:B:646:ARG:HD3	1.85	0.58
1:A:855:LEU:HB2	1:A:887:LEU:HD11	1.84	0.58
1:D:545:ASN:ND2	1:D:569:SER:O	2.37	0.58
1:D:415:VAL:HG23	1:D:421:LYS:HE2	1.86	0.58
3:E:377:ARG:HG2	3:E:473:PRO:HG2	1.85	0.58
1:D:876:ASP:HB3	1:D:1194:GLN:HB2	1.86	0.57
2:C:375:PRO:O	2:C:379:ASN:ND2	2.37	0.57
1:A:409:SER:OG	1:A:961:ASN:ND2	2.32	0.57
1:D:95:ILE:HB	1:D:109:ILE:HB	1.86	0.57
1:A:136:HIS:HB2	1:A:140:TYR:HB2	1.85	0.57
1:D:847:LEU:HD11	1:D:890:GLN:HG3	1.86	0.57
2:F:187:LEU:HG	2:F:191:ILE:HD11	1.85	0.57
3:E:744:ILE:HG12	3:E:749:LEU:HD12	1.85	0.57
2:C:109:ASN:HB3	2:C:126:TYR:HB2	1.85	0.57
1:D:804:CYS:HB3	1:D:810:ILE:HD11	1.86	0.56
3:B:573:THR:HB	3:B:601:LEU:HB3	1.87	0.56
1:D:548:GLN:NE2	1:D:557:SER:OG	2.38	0.56
2:C:124:CYS:SG	2:C:125:TYR:N	2.78	0.56
1:A:85:ARG:NH1	1:A:130:ASP:OD1	2.35	0.56
2:F:251:SER:O	2:F:323:LYS:NZ	2.34	0.56
2:C:208:ARG:HE	2:C:238:LYS:HE2	1.70	0.56
1:A:114:LYS:HB3	1:A:137:PRO:HG2	1.86	0.56
2:F:124:CYS:SG	2:F:125:TYR:N	2.75	0.56
1:D:516:CYS:SG	1:D:517:GLU:N	2.78	0.56
1:A:153:TRP:HB2	1:A:193:PRO:HG3	1.88	0.56
3:E:573:THR:HB	3:E:601:LEU:HB3	1.88	0.56
1:A:245:ASN:ND2	1:A:246:ASP:OD1	2.39	0.56
2:C:233:LYS:NZ	2:C:278:ILE:O	2.37	0.56
1:A:850:ARG:NH1	1:A:879:GLU:OE2	2.38	0.56
2:F:180:MET:SD	2:F:190:HIS:NE2	2.79	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:ASN:O	1:A:696:ASN:ND2	2.37	0.55
1:D:547:LEU:HD12	1:D:561:ARG:HB2	1.88	0.55
3:E:444:THR:HG21	3:E:731:LEU:HA	1.89	0.55
1:D:561:ARG:NH1	1:D:568:GLU:OE2	2.40	0.55
1:D:898:ILE:HD13	1:D:919:LEU:HD21	1.87	0.55
1:A:415:VAL:HG23	1:A:421:LYS:HE2	1.89	0.55
1:A:789:ARG:HD2	1:A:792:ARG:HD2	1.88	0.55
3:E:395:LEU:HD13	3:E:395:LEU:H	1.71	0.55
1:A:1107:ASP:OD2	1:A:1111:ARG:NH1	2.40	0.55
3:E:541:VAL:HG13	3:E:646:ARG:HD3	1.88	0.55
1:A:606:MET:HE1	1:A:698:VAL:HG11	1.88	0.55
1:A:977:GLN:NE2	1:A:1098:VAL:O	2.40	0.55
1:A:43:VAL:HB	1:A:57:LEU:HB2	1.88	0.55
1:A:248:LEU:HB2	1:A:263:LEU:HD12	1.89	0.55
1:A:590:LYS:NZ	1:A:593:GLU:OE2	2.35	0.54
1:A:898:ILE:HD13	1:A:919:LEU:HD21	1.88	0.54
3:B:735:GLU:OE1	3:B:738:ARG:NH2	2.40	0.54
1:A:81:PRO:HB3	1:A:849:PRO:HB3	1.90	0.54
1:A:749:ARG:NH2	1:A:772:ASP:OD1	2.40	0.54
3:E:460:ALA:HB2	3:E:751:ARG:HH22	1.71	0.54
1:D:1182:ASP:OD1	1:D:1185:ARG:NH2	2.41	0.54
3:B:532:VAL:HG13	3:B:601:LEU:HD22	1.89	0.54
2:C:374:MET:SD	2:C:374:MET:N	2.80	0.54
1:A:20:ASN:OD1	1:A:23:ASN:ND2	2.41	0.54
1:D:1139:SER:O	1:D:1143:THR:OG1	2.25	0.54
1:A:808:LYS:NZ	1:A:822:GLU:OE2	2.41	0.54
2:F:163:GLU:OE1	2:F:166:ARG:NH1	2.41	0.54
3:E:572:ILE:HD12	3:E:591:LEU:HD21	1.89	0.54
1:A:464:PRO:HG2	1:A:492:THR:HG21	1.89	0.53
1:A:17:GLY:HA2	1:A:463:LEU:H	1.72	0.53
1:A:1139:SER:O	1:A:1143:THR:OG1	2.26	0.53
1:D:967:TYR:HB3	1:D:970:LEU:HB2	1.91	0.53
1:D:574:ILE:HB	1:D:583:LEU:HD11	1.91	0.53
2:C:230:VAL:HG22	2:C:276:VAL:HB	1.90	0.53
2:F:218:THR:OG1	2:F:292:SER:OG	2.27	0.53
1:D:534:THR:HG23	1:D:543:VAL:HG21	1.90	0.53
1:A:19:LEU:HD22	1:A:39:CYS:HA	1.91	0.53
1:A:203:ILE:O	1:A:243:THR:N	2.42	0.53
1:D:704:ILE:HG23	1:D:740:ARG:HH12	1.74	0.52
1:A:428:ASP:OD2	1:A:918:ARG:NH2	2.42	0.52
1:D:687:GLN:H	1:D:706:PRO:HG3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:988:GLU:OE1	1:A:1012:ARG:NH1	2.32	0.52
1:A:1113:VAL:HG13	1:A:1127:ALA:HB1	1.91	0.52
3:B:617:PRO:HA	3:B:655:TYR:HA	1.92	0.52
1:D:385:LEU:HD11	1:D:452:LEU:HB3	1.91	0.52
1:A:389:VAL:HG21	1:A:448:ARG:HH11	1.74	0.52
1:A:1143:THR:HG22	1:A:1147:MET:HE3	1.91	0.52
1:D:248:LEU:HB2	1:D:263:LEU:HD12	1.91	0.52
1:D:707:ASP:HB2	1:D:735:TRP:HZ2	1.75	0.52
2:F:258:GLU:HA	2:F:261:MET:HE2	1.92	0.52
1:D:389:VAL:HG21	1:D:448:ARG:HH21	1.75	0.52
1:D:135:ILE:HG12	1:D:141:ILE:HG22	1.90	0.51
3:E:730:PRO:HG2	3:E:736:LEU:HD22	1.91	0.51
1:D:790:SER:HB2	1:D:797:ARG:HG2	1.91	0.51
2:F:236:ASP:HB3	2:F:239:THR:HB	1.91	0.51
1:D:567:ASP:N	1:D:567:ASP:OD1	2.42	0.51
1:D:1005:LEU:HD22	1:D:1072:LEU:HD21	1.92	0.51
2:C:80:THR:OG1	2:C:192:LYS:NZ	2.43	0.51
2:F:372:GLU:OE1	2:F:378:LYS:NZ	2.41	0.51
1:D:750:SER:OG	1:D:772:ASP:OD2	2.29	0.51
1:D:786:SER:OG	1:D:823:MET:O	2.24	0.51
3:E:516:SER:HB3	3:E:519:PRO:HD2	1.92	0.51
1:D:139:ASN:OD1	1:D:139:ASN:N	2.44	0.51
1:D:409:SER:HA	1:D:414:PRO:HA	1.92	0.51
1:A:1098:VAL:HG12	1:A:1099:ARG:HG2	1.93	0.51
1:D:277:GLN:NE2	1:D:990:LYS:O	2.37	0.50
1:D:67:VAL:HG13	1:D:86:LEU:HD23	1.93	0.50
1:D:303:LEU:HB2	1:D:315:ARG:HB2	1.94	0.50
1:A:135:ILE:HG12	1:A:141:ILE:HG22	1.93	0.50
3:B:572:ILE:HD12	3:B:591:LEU:HD21	1.93	0.50
2:F:240:LYS:O	2:F:244:ASN:ND2	2.35	0.50
2:C:41:TYR:H	2:C:151:VAL:HB	1.77	0.50
1:A:409:SER:HA	1:A:414:PRO:HA	1.93	0.50
3:E:532:VAL:HG13	3:E:601:LEU:HD22	1.92	0.50
3:E:542:THR:HG23	3:E:544:GLN:H	1.77	0.50
3:B:542:THR:HG23	3:B:544:GLN:H	1.76	0.50
1:A:847:LEU:HD11	1:A:890:GLN:HG3	1.94	0.50
2:C:330:THR:HG22	2:C:334:LYS:HE3	1.93	0.50
1:D:155:LYS:HG3	1:D:194:PRO:HG2	1.94	0.50
2:F:376:GLU:OE2	3:E:763:ARG:NH2	2.40	0.50
1:D:55:GLN:HG2	1:D:832:MET:HG3	1.94	0.50
1:A:872:ILE:HG22	1:A:888:GLN:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:39:CYS:N	2:F:153:CYS:SG	2.85	0.49
1:A:1109:LEU:HD12	1:A:1134:LEU:HD21	1.94	0.49
1:D:1143:THR:HG22	1:D:1147:MET:HE3	1.94	0.49
1:A:967:TYR:HB3	1:A:970:LEU:HB2	1.94	0.49
3:B:506:PRO:HG3	3:B:732:PHE:HD2	1.77	0.49
1:A:1057:MET:HG2	1:A:1062:LYS:HB2	1.94	0.49
2:C:272:GLN:O	2:C:272:GLN:NE2	2.45	0.49
2:F:108:GLY:N	2:F:126:TYR:O	2.46	0.49
1:A:719:LYS:NZ	1:A:758:ALA:O	2.43	0.49
3:E:620:PHE:HD2	3:E:644:ARG:HD3	1.77	0.49
1:D:81:PRO:HB3	1:D:849:PRO:HB3	1.93	0.48
1:D:350:ILE:HD11	1:D:358:PRO:HG3	1.94	0.48
1:A:254:PRO:HD2	1:A:296:PRO:HB2	1.95	0.48
1:A:486:PRO:HD2	1:A:501:HIS:HE1	1.77	0.48
3:B:648:ASP:OD2	3:B:761:SER:OG	2.29	0.48
3:B:744:ILE:HG12	3:B:749:LEU:HD12	1.95	0.48
2:F:217:LEU:HD23	2:F:220:LEU:HD21	1.95	0.48
1:A:159:ASP:OD1	1:A:159:ASP:N	2.45	0.48
1:A:687:GLN:HG2	1:A:706:PRO:HD3	1.95	0.48
1:D:14:THR:HB	1:D:56:VAL:HG11	1.94	0.48
1:A:687:GLN:HE22	1:A:703:ARG:HH21	1.60	0.48
2:F:272:GLN:O	2:F:272:GLN:NE2	2.47	0.48
3:B:616:VAL:O	3:B:656:VAL:N	2.39	0.48
2:F:347:LEU:HG	3:E:767:LEU:HD21	1.96	0.48
3:E:618:PHE:CD2	3:E:619:PRO:HD3	2.49	0.48
1:D:789:ARG:HH11	1:D:792:ARG:HH21	1.61	0.48
1:D:43:VAL:HB	1:D:57:LEU:HB2	1.95	0.48
2:C:42:SER:OG	2:C:76:SER:OG	2.32	0.48
1:D:547:LEU:O	1:D:560:PHE:N	2.36	0.48
1:D:749:ARG:NH2	1:D:772:ASP:OD1	2.47	0.48
1:A:474:PRO:HG3	1:A:580:LYS:HE3	1.95	0.48
1:D:910:LEU:HD13	1:D:933:ALA:HA	1.94	0.48
1:A:95:ILE:HB	1:A:109:ILE:HB	1.96	0.48
1:D:464:PRO:HG2	1:D:492:THR:HG21	1.96	0.47
1:D:610:PHE:HE1	1:D:613:ILE:HD11	1.78	0.47
2:F:176:LEU:HG	2:F:195:LEU:HD21	1.96	0.47
1:D:1109:LEU:HD12	1:D:1134:LEU:HD21	1.95	0.47
1:A:527:THR:HB	1:A:553:PRO:HD3	1.96	0.47
1:A:350:ILE:HD11	1:A:358:PRO:HG3	1.97	0.47
1:A:262:LEU:HD13	1:A:271:LEU:HD13	1.96	0.47
1:D:839:GLU:HA	3:E:825:ARG:HH22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:VAL:HB	1:A:704:ILE:HG23	1.96	0.47
1:A:910:LEU:HD13	1:A:933:ALA:HA	1.96	0.47
1:D:254:PRO:HD2	1:D:296:PRO:HB2	1.96	0.47
1:D:977:GLN:NE2	1:D:1098:VAL:O	2.48	0.47
3:E:637:HIS:HB3	3:E:640:LEU:HD13	1.97	0.47
1:D:872:ILE:H	1:D:888:GLN:HE21	1.62	0.47
3:E:738:ARG:HG2	3:E:742:ARG:NE	2.30	0.47
2:C:328:GLN:O	2:C:332:ASN:ND2	2.34	0.46
1:A:76:HIS:ND1	1:A:922:ASP:OD1	2.48	0.46
1:D:13:ARG:H	1:D:820:VAL:HG13	1.81	0.46
3:B:412:LEU:HB3	3:B:476:LEU:HB2	1.97	0.46
2:F:41:TYR:H	2:F:151:VAL:HB	1.80	0.46
3:E:507:LEU:HD11	3:E:511:ILE:HD11	1.97	0.46
1:D:77:ASN:ND2	1:D:79:GLY:H	2.14	0.46
1:D:472:MET:N	1:D:802:ASP:OD2	2.48	0.46
1:A:922:ASP:HB3	1:A:925:GLU:HG2	1.97	0.46
3:E:518:THR:HG23	3:E:519:PRO:HD3	1.98	0.46
1:D:91:VAL:HG22	1:D:115:PRO:HG3	1.98	0.46
3:E:612:GLU:HB3	3:E:660:ASN:HB3	1.98	0.46
1:D:678:HIS:HB3	1:D:690:HIS:HE1	1.80	0.46
1:D:859:LEU:HD22	1:D:902:LEU:HD13	1.97	0.45
3:E:395:LEU:HD23	3:E:400:LYS:HB2	1.98	0.45
1:D:358:PRO:HB3	1:D:373:LEU:HD11	1.98	0.45
1:D:409:SER:HB3	1:D:961:ASN:HD21	1.81	0.45
1:A:855:LEU:HD11	1:A:891:LEU:HD21	1.99	0.45
3:B:659:LEU:HB2	3:B:723:LEU:HD12	1.98	0.45
1:A:315:ARG:HB3	1:A:341:TYR:HB3	1.99	0.45
1:A:733:ASN:HA	1:A:744:GLY:HA2	1.99	0.45
1:A:258:ASN:HB2	1:A:983:ARG:HH12	1.82	0.45
2:F:42:SER:OG	2:F:76:SER:OG	2.35	0.45
1:D:177:LEU:HD13	1:D:250:LEU:HD13	1.98	0.45
2:C:232:VAL:HG12	2:C:278:ILE:HB	1.98	0.45
2:F:113:VAL:H	2:F:123:GLY:HA2	1.82	0.45
2:C:128:LEU:HG	2:C:151:VAL:HA	1.99	0.44
3:B:620:PHE:HB3	3:B:625:LEU:HD21	1.99	0.44
3:E:644:ARG:HG2	3:E:649:LEU:HD12	1.98	0.44
2:C:200:GLU:HA	2:C:204:CYS:HB3	2.00	0.44
1:A:872:ILE:H	1:A:888:GLN:HE21	1.63	0.44
2:F:364:LEU:HA	2:F:367:VAL:HG22	1.98	0.44
1:A:244:LEU:HD12	1:A:247:CYS:HB3	1.99	0.44
1:A:253:LEU:HD12	1:A:259:HIS:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1035:CYS:O	1:D:1039:THR:OG1	2.28	0.44
1:A:414:PRO:HG3	1:A:961:ASN:HD22	1.82	0.44
3:B:395:LEU:HG	3:B:396:SER:H	1.83	0.44
3:B:501:LEU:HB2	3:B:521:HIS:HA	2.00	0.44
1:D:704:ILE:HD12	1:D:740:ARG:HH12	1.83	0.44
1:A:486:PRO:HD2	1:A:501:HIS:CE1	2.53	0.44
1:D:202:TYR:N	1:D:235:GLU:O	2.41	0.43
1:A:23:ASN:HD21	1:A:40:HIS:HA	1.81	0.43
2:C:303:PHE:HZ	2:C:319:LEU:HG	1.83	0.43
1:A:542:LEU:HB3	1:A:568:GLU:N	2.33	0.43
1:A:385:LEU:HD11	1:A:452:LEU:HB3	2.00	0.43
1:A:527:THR:HA	1:A:552:LEU:HD12	1.98	0.43
3:B:395:LEU:H	3:B:400:LYS:NZ	2.16	0.43
2:C:172:TYR:OH	2:C:194:TYR:O	2.37	0.43
2:C:105:GLU:HA	2:C:129:PHE:HA	2.00	0.43
2:C:258:GLU:HA	2:C:261:MET:HE2	2.01	0.43
3:B:518:THR:HG23	3:B:519:PRO:HD3	1.99	0.43
2:F:216:LYS:HB3	2:F:287:PHE:HE2	1.84	0.43
1:D:57:LEU:HD13	1:D:98:TRP:CD2	2.53	0.43
2:C:252:LEU:HG	2:C:255:LEU:HD12	2.00	0.43
2:F:359:SER:HB2	2:F:362:ILE:HD11	1.99	0.43
1:D:306:LEU:HD22	1:D:361:MET:HB2	2.01	0.43
1:A:67:VAL:HG13	1:A:86:LEU:HD21	2.01	0.43
1:D:855:LEU:HD11	1:D:891:LEU:HD21	2.00	0.43
2:C:41:TYR:HB2	2:C:151:VAL:HG21	2.01	0.43
1:D:1024:ASN:ND2	1:D:1026:HIS:H	2.17	0.43
3:B:534:PHE:HE1	3:B:725:LEU:HB3	1.83	0.43
3:B:617:PRO:HG2	3:B:743:LYS:NZ	2.34	0.43
1:A:13:ARG:H	1:A:820:VAL:HG13	1.84	0.42
1:A:177:LEU:HD11	1:A:244:LEU:HD11	2.01	0.42
1:A:433:GLN:HE21	1:A:433:GLN:HB3	1.64	0.42
3:B:422:ILE:HD12	3:B:422:ILE:HA	1.92	0.42
3:B:506:PRO:HD3	3:B:730:PRO:HA	2.01	0.42
1:A:205:SER:OG	1:A:233:THR:N	2.41	0.42
1:A:277:GLN:NE2	1:A:990:LYS:O	2.53	0.42
1:A:745:ILE:H	1:A:745:ILE:HG13	1.66	0.42
3:E:546:PRO:HG2	3:E:723:LEU:HD23	2.00	0.42
1:D:591:PRO:HB3	1:D:606:MET:HB2	2.01	0.42
1:D:798:ILE:HD12	1:D:811:LEU:HB3	2.01	0.42
2:F:82:LEU:HD13	2:F:83:PRO:HD2	2.02	0.42
1:D:872:ILE:HG12	1:D:887:LEU:HD23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:338:ARG:O	2:C:341:GLU:HG2	2.19	0.42
1:A:299:GLN:HE22	1:A:367:ASN:HA	1.84	0.42
2:F:168:GLU:OE1	2:F:245:ARG:NH1	2.53	0.42
2:F:277:VAL:HG23	2:F:288:CYS:HB2	2.01	0.42
1:D:299:GLN:NE2	1:D:918:ARG:HH12	2.18	0.42
1:A:845:TYR:OH	1:A:920:TYR:O	2.31	0.42
3:B:559:LYS:HE2	3:B:559:LYS:HB3	1.91	0.42
1:D:737:LEU:HD13	1:D:737:LEU:H	1.84	0.42
1:A:1005:LEU:HD22	1:A:1072:LEU:HD21	2.02	0.42
3:E:427:VAL:HG12	3:E:429:SER:H	1.84	0.42
1:D:317:ARG:HH11	1:D:434:SER:HB3	1.84	0.42
2:C:165:PHE:CE2	2:C:316:ARG:HG3	2.55	0.42
2:C:204:CYS:N	2:C:205:PRO:HD3	2.35	0.42
1:A:46:ILE:HG22	1:A:53:THR:HA	2.01	0.42
1:A:72:GLU:OE1	1:A:76:HIS:NE2	2.39	0.41
1:D:784:MET:SD	1:D:787:SER:HB2	2.60	0.41
2:C:255:LEU:HB3	2:C:327:ILE:HD11	2.02	0.41
1:D:486:PRO:HB2	1:D:502:LEU:HB2	2.02	0.41
3:B:516:SER:HB2	3:B:519:PRO:HD2	2.02	0.41
2:F:206:ILE:HG22	2:F:210:VAL:HG23	2.02	0.41
1:D:177:LEU:HD11	1:D:244:LEU:HD11	2.01	0.41
1:D:258:ASN:HB2	1:D:983:ARG:HH22	1.86	0.41
1:A:474:PRO:HA	1:A:475:PRO:HD3	1.96	0.41
1:D:143:LEU:HG	1:D:152:LEU:HD12	2.03	0.41
1:D:312:ILE:N	1:D:347:CYS:SG	2.85	0.41
1:A:19:LEU:HB2	1:A:359:PHE:HE1	1.85	0.41
1:A:285:GLU:CD	1:A:285:GLU:H	2.29	0.41
1:A:573:MET:HE1	1:A:615:ALA:HA	2.02	0.41
1:D:398:SER:OG	1:D:399:SER:N	2.54	0.41
1:A:299:GLN:NE2	1:A:918:ARG:HH12	2.18	0.41
1:A:678:HIS:ND1	1:A:692:THR:HG22	2.35	0.41
3:B:464:GLN:HE21	3:B:464:GLN:HB3	1.73	0.41
1:D:203:ILE:HD11	1:D:244:LEU:HD13	2.03	0.41
2:C:334:LYS:HE2	2:C:370:GLU:HG2	2.02	0.41
1:A:1040:VAL:HG21	1:A:1072:LEU:HB3	2.02	0.41
3:E:803:MET:HG3	3:E:804:GLY:H	1.84	0.41
1:D:532:PHE:HB3	1:D:547:LEU:HD23	2.03	0.41
2:C:236:ASP:HB3	2:C:239:THR:HB	2.02	0.41
1:A:57:LEU:HD13	1:A:98:TRP:CG	2.55	0.41
1:A:122:LEU:HD22	1:A:131:LEU:HD23	2.01	0.41
1:A:426:SER:OG	1:A:429:ASN:OD1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:591:PRO:HB2	1:A:606:MET:HB2	2.02	0.41
3:E:412:LEU:HD23	3:E:476:LEU:HD12	2.02	0.41
1:D:57:LEU:HB3	1:D:98:TRP:CZ3	2.56	0.41
1:D:474:PRO:HA	1:D:475:PRO:HD3	1.94	0.41
1:D:767:ILE:HD13	1:D:801:VAL:HB	2.03	0.41
1:D:813:SER:OG	1:D:819:ARG:NH2	2.54	0.41
1:A:872:ILE:HG12	1:A:887:LEU:HD23	2.03	0.41
3:E:605:HIS:CD2	3:E:611:GLY:H	2.39	0.41
1:D:838:THR:O	3:E:825:ARG:NH1	2.44	0.40
3:B:477:LEU:HD11	3:B:498:TYR:CZ	2.56	0.40
1:D:23:ASN:ND2	1:D:40:HIS:H	2.18	0.40
1:D:685:ASP:OD1	1:D:685:ASP:N	2.54	0.40
1:D:586:VAL:HG13	1:D:613:ILE:HB	2.04	0.40
2:C:176:LEU:HG	2:C:195:LEU:HD21	2.02	0.40
2:F:129:PHE:HZ	2:F:150:TYR:HB2	1.86	0.40
1:D:1007:LEU:HD23	1:D:1098:VAL:HG11	2.02	0.40
1:D:1151:ASP:OD1	1:D:1151:ASP:N	2.55	0.40
1:A:728:MET:HA	1:A:751:TRP:HA	2.02	0.40
2:F:183:GLU:HB2	2:F:190:HIS:HB2	2.03	0.40
3:E:512:ARG:HE	3:E:527:PRO:HG2	1.87	0.40
1:A:856:LYS:HG3	1:A:916:VAL:HG11	2.03	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	A	1093/1238 (88%)	1070 (98%)	23 (2%)	0	100	100
1	D	1087/1238 (88%)	1060 (98%)	27 (2%)	0	100	100
2	C	296/410 (72%)	288 (97%)	8 (3%)	0	100	100
2	F	297/410 (72%)	291 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	373/851 (44%)	364 (98%)	9 (2%)	0	100	100
3	E	358/851 (42%)	349 (98%)	9 (2%)	0	100	100
All	All	3504/4998 (70%)	3422 (98%)	82 (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	971/1084 (90%)	951 (98%)	20 (2%)	47	68
1	D	965/1084 (89%)	941 (98%)	24 (2%)	42	66
2	C	273/360 (76%)	262 (96%)	11 (4%)	28	56
2	F	275/360 (76%)	267 (97%)	8 (3%)	37	63
3	B	337/759 (44%)	332 (98%)	5 (2%)	57	73
3	E	326/759 (43%)	318 (98%)	8 (2%)	42	66
All	All	3147/4406 (71%)	3071 (98%)	76 (2%)	43	66

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	64	VAL
1	D	86	LEU
1	D	91	VAL
1	D	119	VAL
1	D	133	LEU
1	D	192	LYS
1	D	203	ILE
1	D	353	THR
1	D	422	LEU
1	D	433	GLN
1	D	443	ARG
1	D	487	LEU

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Mol	Chain	Res	Type
1	D	573	MET
1	D	625	LYS
1	D	737	LEU
1	D	745	ILE
1	D	763	ASN
1	D	820	VAL
1	D	862	GLN
1	D	981	LEU
1	D	1015	GLN
1	D	1039	THR
1	D	1143	THR
1	D	1210	LEU
2	C	43	TYR
2	C	82	LEU
2	C	103	VAL
2	C	120	TYR
2	C	121	ARG
2	C	203	VAL
2	C	233	LYS
2	C	274	LYS
2	C	303	PHE
2	C	308	LYS
2	C	363	LEU
1	A	119	VAL
1	A	133	LEU
1	A	203	ILE
1	A	278	THR
1	A	353	THR
1	A	422	LEU
1	A	433	GLN
1	A	487	LEU
1	A	547	LEU
1	A	599	THR
1	A	696	ASN
1	A	704	ILE
1	A	745	ILE
1	A	747	THR
1	A	754	LYS
1	A	763	ASN
1	A	820	VAL
1	A	1015	GLN
1	A	1024	ASN

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Mol	Chain	Res	Type
1	A	1143	THR
3	B	464	GLN
3	B	518	THR
3	B	584	THR
3	B	723	LEU
3	B	736	LEU
2	F	82	LEU
2	F	121	ARG
2	F	234	GLU
2	F	274	LYS
2	F	308	LYS
2	F	325	LYS
2	F	370	GLU
2	F	390	GLU
3	E	395	LEU
3	E	421	LEU
3	E	443	LEU
3	E	482	LEU
3	E	483	LEU
3	E	518	THR
3	E	584	THR
3	E	736	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	23	ASN
1	D	52	GLN
1	D	75	HIS
1	D	77	ASN
1	D	106	GLN
1	D	117	GLN
1	D	120	GLN
1	D	124	ASN
1	D	125	GLN
1	D	299	GLN
1	D	337	GLN
1	D	367	ASN
1	D	419	GLN
1	D	433	GLN
1	D	480	ASN
1	D	514	HIS

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Mol	Chain	Res	Type
1	D	548	GLN
1	D	581	GLN
1	D	623	ASN
1	D	690	HIS
1	D	696	ASN
1	D	763	ASN
1	D	835	GLN
1	D	867	GLN
1	D	888	GLN
1	D	941	GLN
1	D	961	ASN
1	D	977	GLN
1	D	1024	ASN
1	D	1145	HIS
2	C	109	ASN
2	C	222	HIS
2	C	253	GLN
2	C	257	HIS
2	C	272	GLN
2	C	301	GLN
2	C	328	GLN
1	A	23	ASN
1	A	75	HIS
1	A	120	GLN
1	A	124	ASN
1	A	125	GLN
1	A	245	ASN
1	A	276	ASN
1	A	321	ASN
1	A	337	GLN
1	A	367	ASN
1	A	433	GLN
1	A	485	GLN
1	A	501	HIS
1	A	514	HIS
1	A	548	GLN
1	A	581	GLN
1	A	687	GLN
1	A	764	GLN
1	A	835	GLN
1	A	867	GLN
1	A	874	HIS

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Mol	Chain	Res	Type
1	A	885	ASN
1	A	888	GLN
1	A	937	HIS
1	A	941	GLN
1	A	961	ASN
1	A	1003	GLN
1	A	1024	ASN
1	A	1060	ASN
3	B	436	GLN
3	B	441	HIS
3	B	461	GLN
3	B	464	GLN
3	B	592	ASN
3	B	626	GLN
3	B	641	GLN
3	B	645	ASN
3	B	756	GLN
2	F	37	HIS
2	F	81	ASN
2	F	178	ASN
2	F	272	GLN
2	F	317	GLN
2	F	328	GLN
2	F	344	HIS
3	E	436	GLN
3	E	454	HIS
3	E	592	ASN
3	E	605	HIS
3	E	626	GLN
3	E	664	GLN
3	E	756	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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.

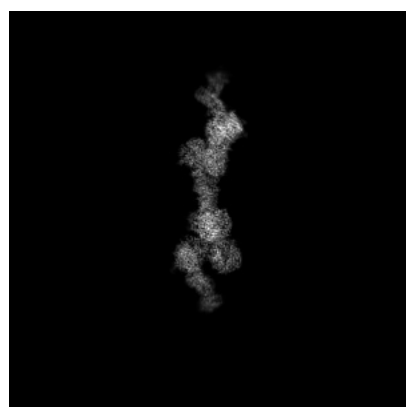
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-69549. These allow visual inspection of the internal detail of the map and identification of artifacts.

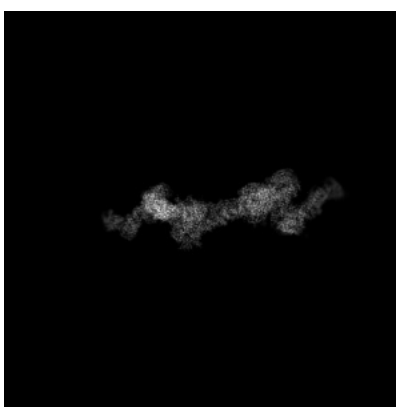
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

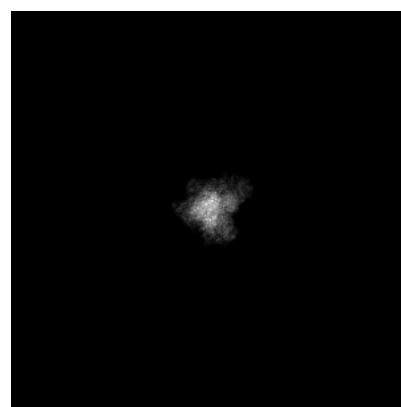
6.1.1 Primary map



X



Y

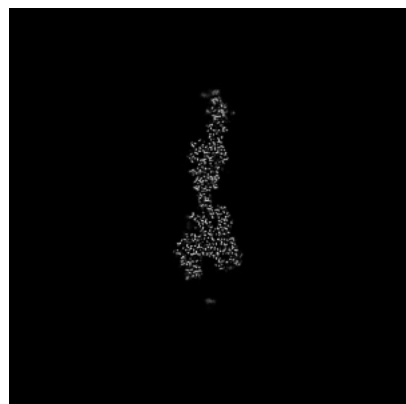


Z

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

6.2 Central slices [i](#)

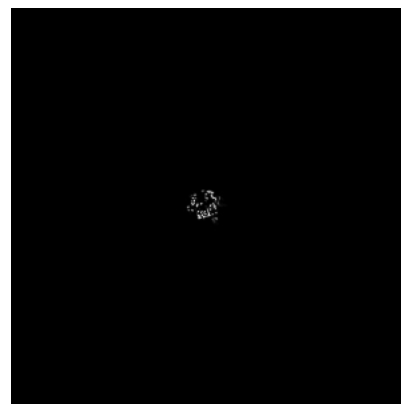
6.2.1 Primary map



X Index: 300



Y Index: 300

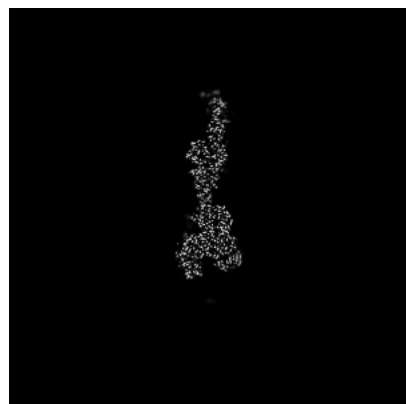


Z Index: 300

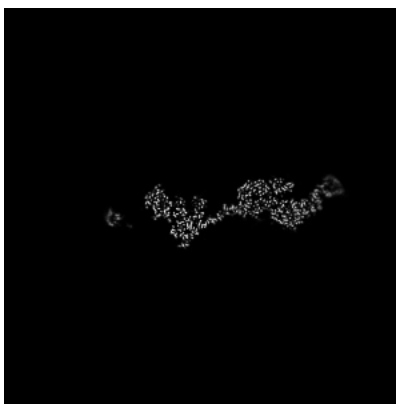
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

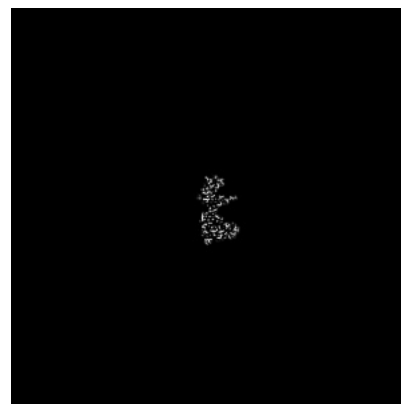
6.3.1 Primary map



X Index: 302



Y Index: 310

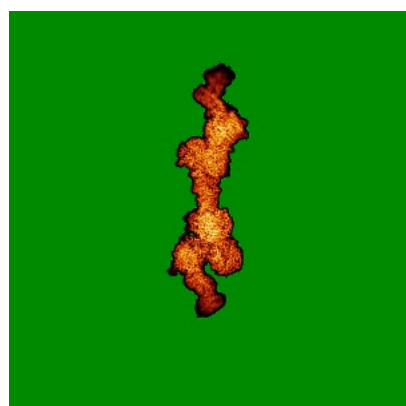


Z Index: 236

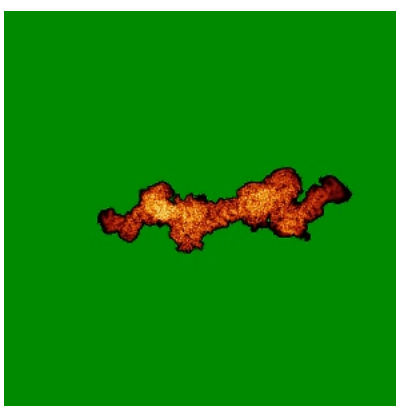
The images above show the largest variance slices of the map in three orthogonal directions.

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

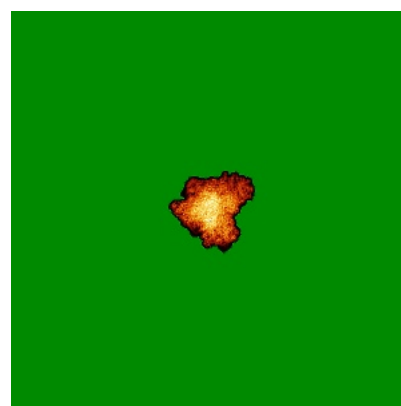
6.4.1 Primary map



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](#)

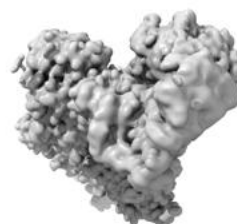
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

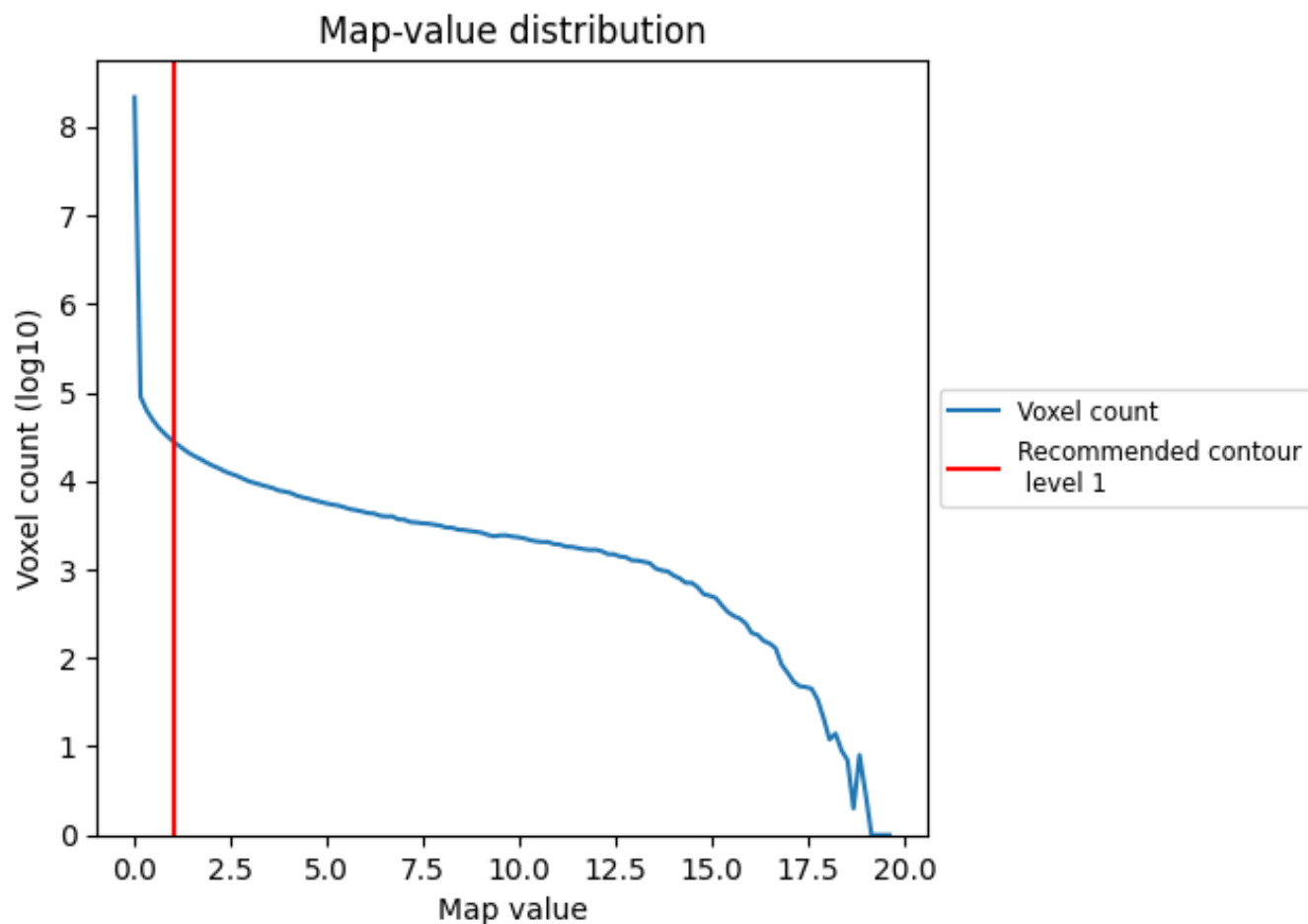
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

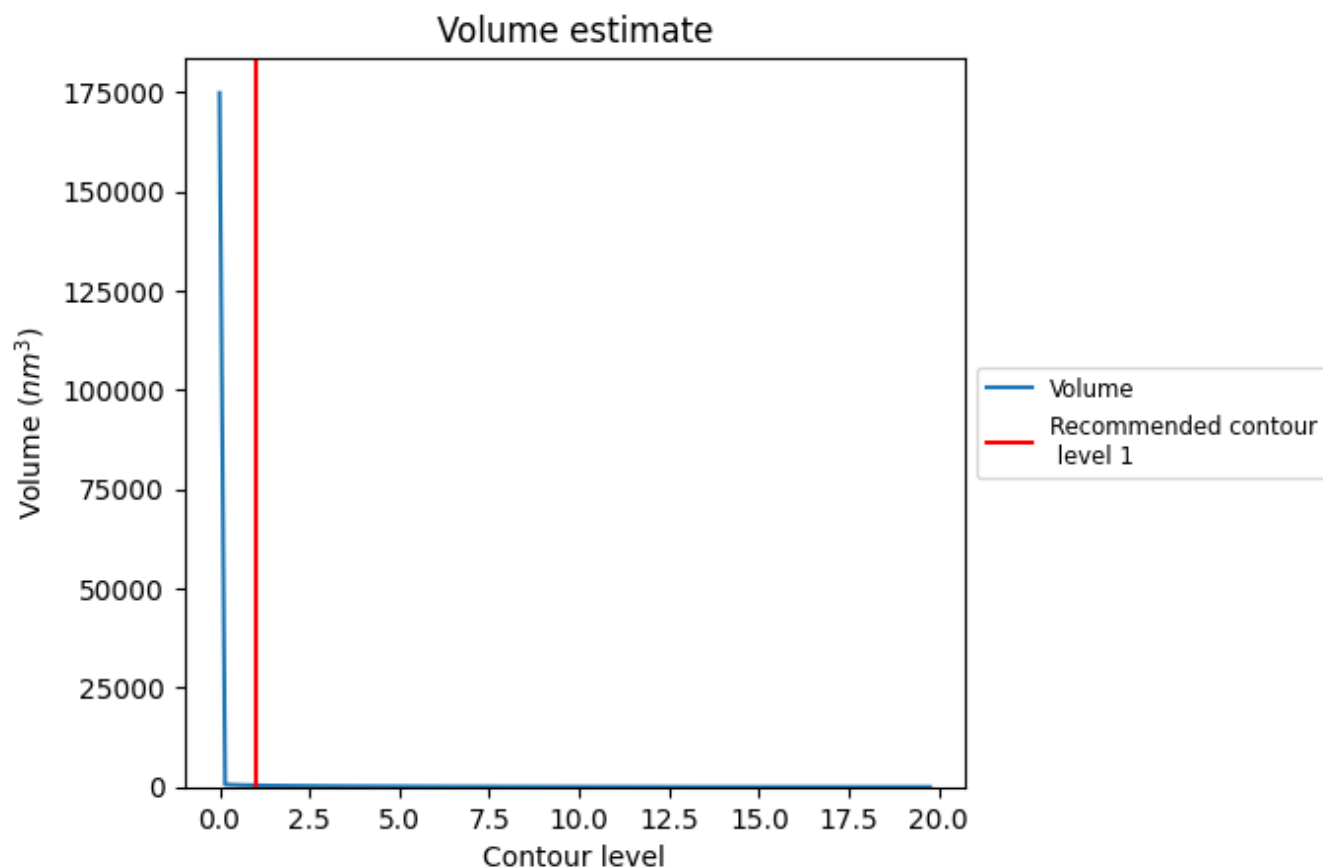
This section contains the results of statistical analysis of the map.

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.

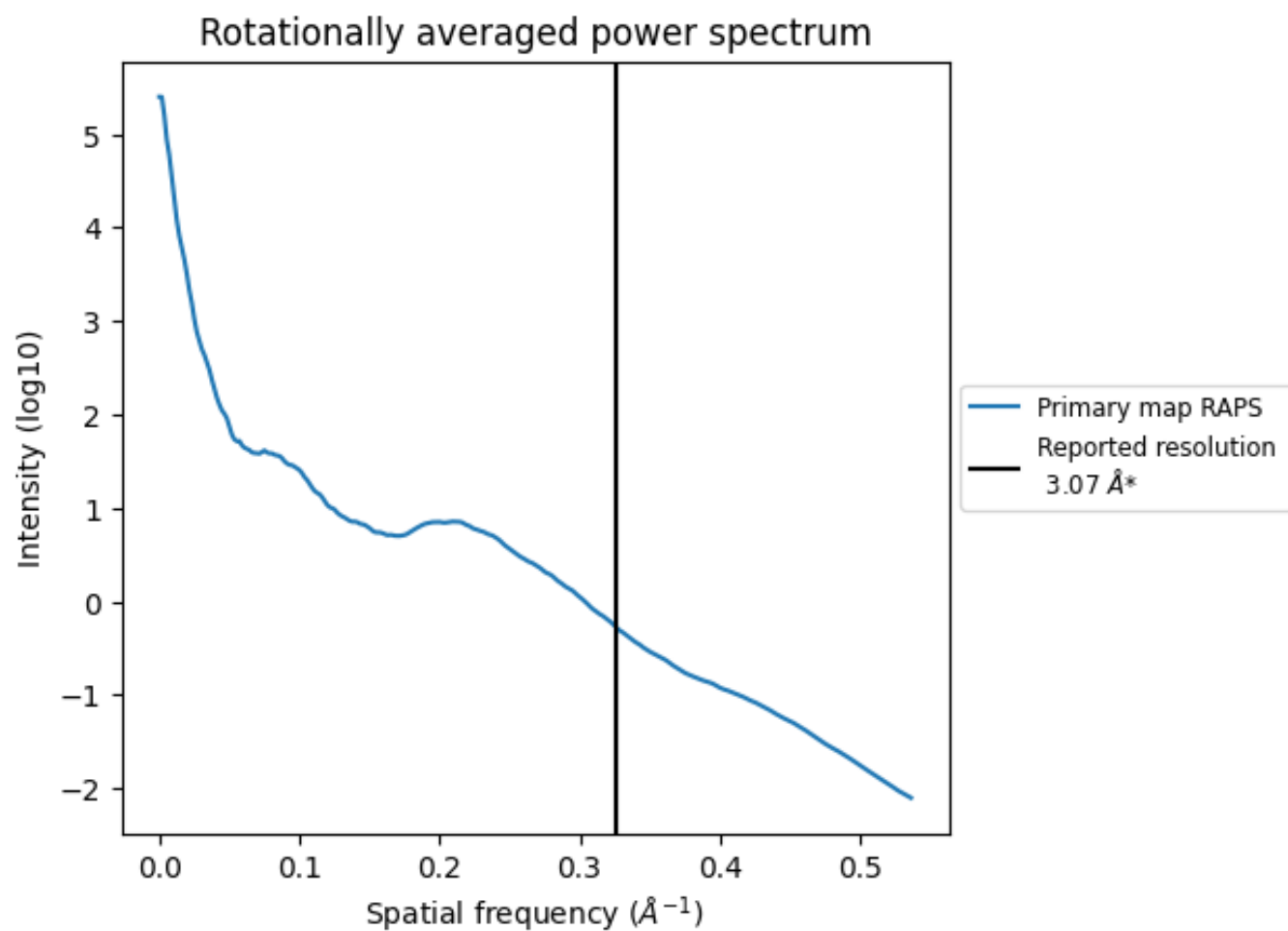
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 389 nm^3 ; this corresponds to an approximate mass of 351 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 0.326 $\text{\AA}^{-1}$

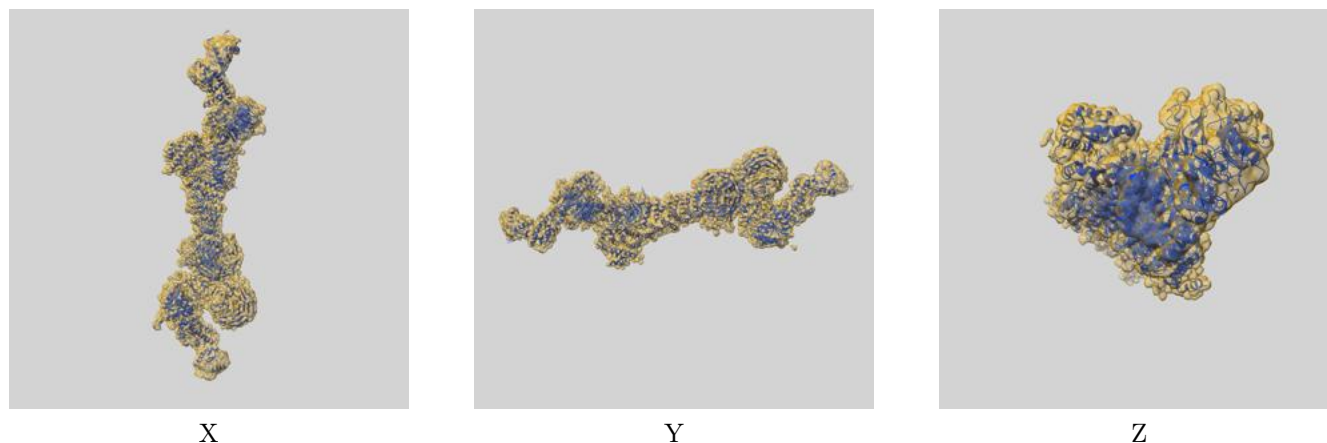
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

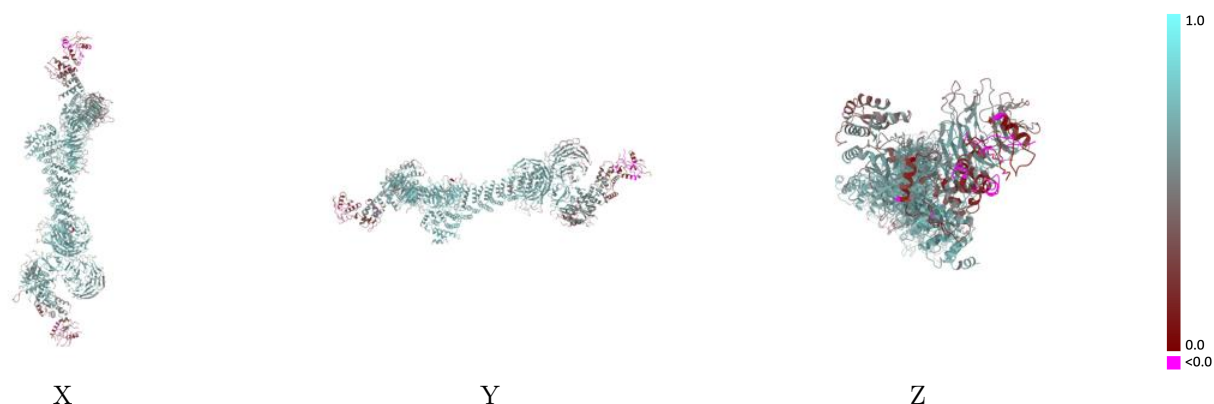
This section contains information regarding the fit between EMDB map EMD-69549 and PDB model 24IP. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



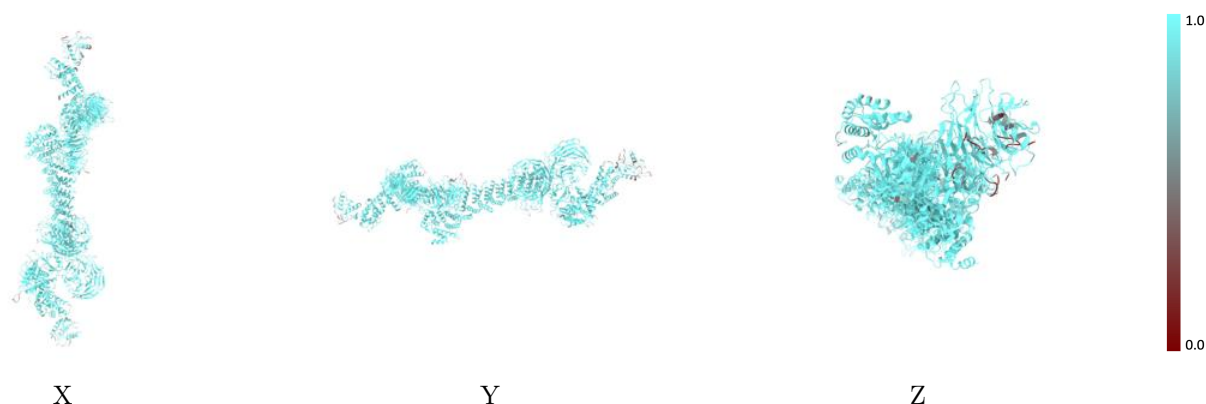
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



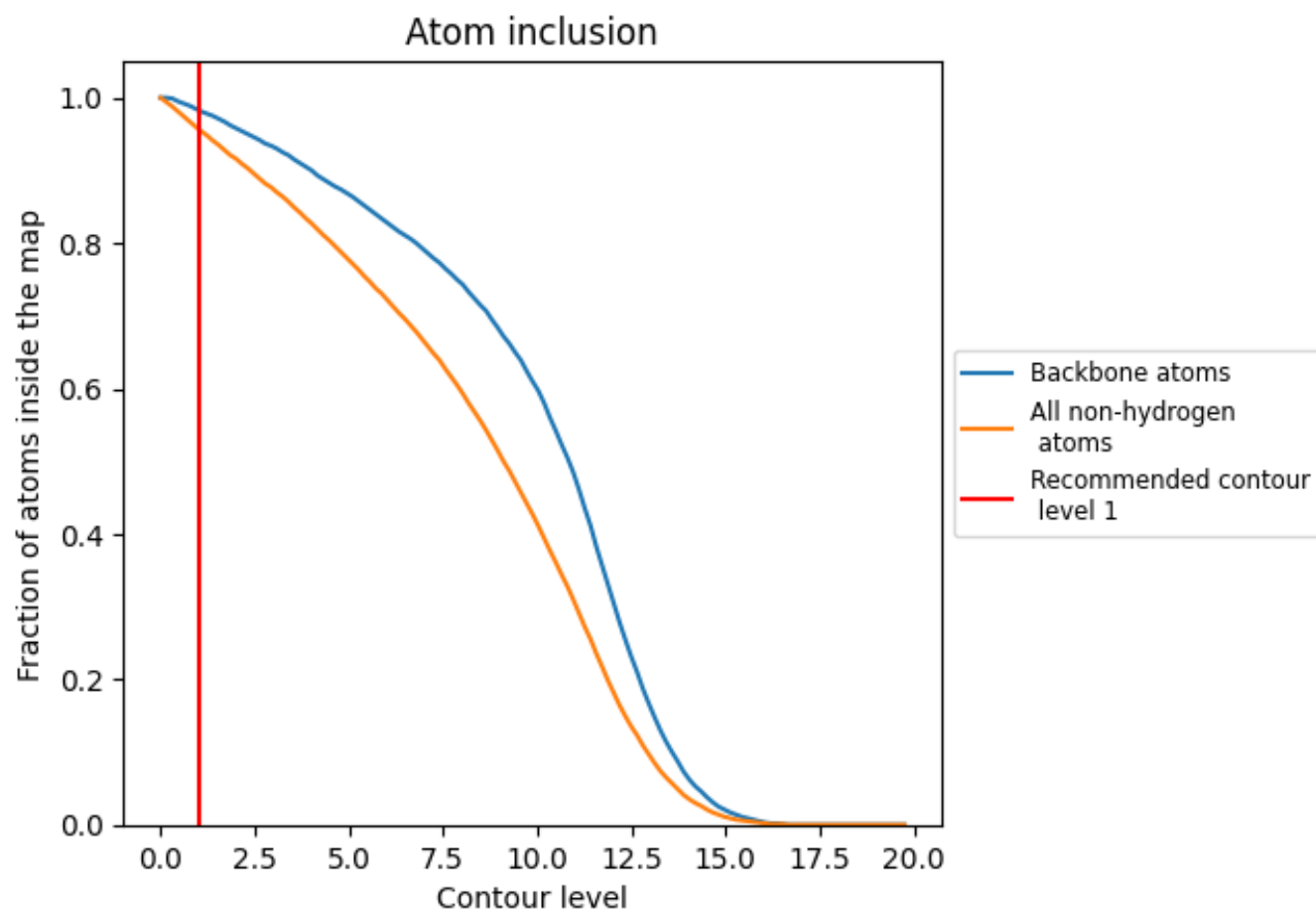
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9570	0.5580
A	0.9810	0.6390
B	0.9690	0.6080
C	0.8870	0.3530
D	0.9810	0.6060
E	0.9680	0.5430
F	0.8370	0.2670

1.0

0.0

<0.0