



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:47 PM UTC

PDB ID : 9O5A / pdb_00009o5a
EMDB ID : EMD-70135
Title : The KICSTOR-GATOR1 complex
Authors : Bayly-Jones, C.; Lupton, C.J.; Chang, Y.G.; Ellisdon, A.M.
Deposited on : 2025-04-09
Resolution : 3.20 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

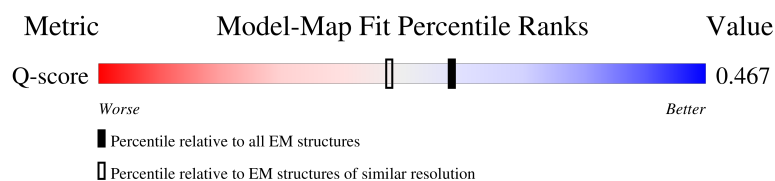
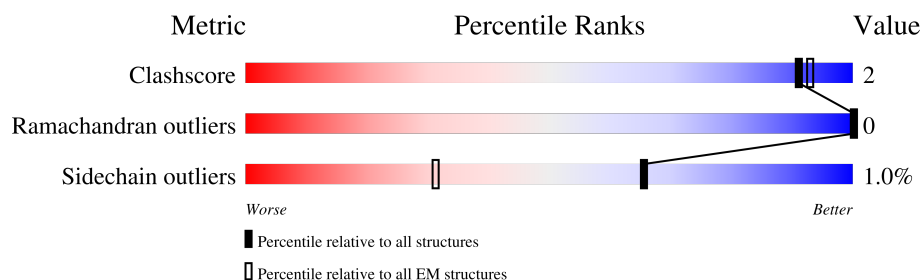
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	H	401	
2	B	1621	
3	D	3451	
4	E	457	

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Mol	Chain	Length	Quality of chain
5	F	466	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>77%20%</div></div>
6	G	466	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>78%6%16%</div></div>
7	C	590	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>75%22%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 42618 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 GATOR complex protein NPRL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	370	Total	C	N	O	S	0	0
			2993	1915	503	556	19		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-20	MET	-	expression tag	UNP Q8WTW4
H	-19	GLY	-	expression tag	UNP Q8WTW4
H	-18	TYR	-	expression tag	UNP Q8WTW4
H	-17	PRO	-	expression tag	UNP Q8WTW4
H	-16	TYR	-	expression tag	UNP Q8WTW4
H	-15	ASP	-	expression tag	UNP Q8WTW4
H	-14	VAL	-	expression tag	UNP Q8WTW4
H	-13	PRO	-	expression tag	UNP Q8WTW4
H	-12	ASP	-	expression tag	UNP Q8WTW4
H	-11	TYR	-	expression tag	UNP Q8WTW4
H	-10	ALA	-	expression tag	UNP Q8WTW4
H	-9	ASP	-	expression tag	UNP Q8WTW4
H	-8	LEU	-	expression tag	UNP Q8WTW4
H	-7	ASN	-	expression tag	UNP Q8WTW4
H	-6	GLY	-	expression tag	UNP Q8WTW4
H	-5	GLY	-	expression tag	UNP Q8WTW4
H	-4	GLY	-	expression tag	UNP Q8WTW4
H	-3	GLY	-	expression tag	UNP Q8WTW4
H	-2	GLY	-	expression tag	UNP Q8WTW4
H	-1	SER	-	expression tag	UNP Q8WTW4
H	0	THR	-	expression tag	UNP Q8WTW4

- Molecule 2 is a protein called GATOR1 complex protein DEPDC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1004	Total	C	N	O	S	0	0
			8226	5317	1358	1506	45		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	expression tag	UNP O75140
B	-16	GLY	-	expression tag	UNP O75140
B	-15	ASP	-	expression tag	UNP O75140
B	-14	TYR	-	expression tag	UNP O75140
B	-13	LYS	-	expression tag	UNP O75140
B	-12	ASP	-	expression tag	UNP O75140
B	-11	ASP	-	expression tag	UNP O75140
B	-10	ASP	-	expression tag	UNP O75140
B	-9	ASP	-	expression tag	UNP O75140
B	-8	LYS	-	expression tag	UNP O75140
B	-7	GLY	-	expression tag	UNP O75140
B	-6	GLY	-	expression tag	UNP O75140
B	-5	GLY	-	expression tag	UNP O75140
B	-4	GLY	-	expression tag	UNP O75140
B	-3	GLY	-	expression tag	UNP O75140
B	-2	ALA	-	expression tag	UNP O75140
B	-1	SER	-	expression tag	UNP O75140
B	0	THR	-	expression tag	UNP O75140

- Molecule 3 is a protein called KICSTOR complex protein SZT2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	2316	Total	C	N	O	S	0	0
			18448	11838	3246	3255	109		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	expression tag	UNP Q5T011
D	-19	GLU	-	expression tag	UNP Q5T011
D	-18	MET	-	expression tag	UNP Q5T011
D	-17	ASP	-	expression tag	UNP Q5T011
D	-16	TYR	-	expression tag	UNP Q5T011
D	-15	LYS	-	expression tag	UNP Q5T011
D	-14	ASP	-	expression tag	UNP Q5T011
D	-13	ASP	-	expression tag	UNP Q5T011
D	-12	ASP	-	expression tag	UNP Q5T011
D	-11	ASP	-	expression tag	UNP Q5T011
D	-10	LYS	-	expression tag	UNP Q5T011
D	-9	GLY	-	expression tag	UNP Q5T011
D	-8	GLY	-	expression tag	UNP Q5T011

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	GLY	-	expression tag	UNP Q5T011
D	-6	GLY	-	expression tag	UNP Q5T011
D	-5	GLY	-	expression tag	UNP Q5T011
D	-4	ALA	-	expression tag	UNP Q5T011
D	-3	SER	-	expression tag	UNP Q5T011
D	-2	THR	-	expression tag	UNP Q5T011

- Molecule 4 is a protein called KICSTOR complex protein kaptin.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	406	Total	C	N	O	S	0	0
			3185	2019	552	604	10		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-20	MET	-	initiating methionine	UNP Q9Y664
E	-19	GLY	-	expression tag	UNP Q9Y664
E	-18	TYR	-	expression tag	UNP Q9Y664
E	-17	PRO	-	expression tag	UNP Q9Y664
E	-16	TYR	-	expression tag	UNP Q9Y664
E	-15	ASP	-	expression tag	UNP Q9Y664
E	-14	VAL	-	expression tag	UNP Q9Y664
E	-13	PRO	-	expression tag	UNP Q9Y664
E	-12	ASP	-	expression tag	UNP Q9Y664
E	-11	TYR	-	expression tag	UNP Q9Y664
E	-10	ALA	-	expression tag	UNP Q9Y664
E	-9	ASP	-	expression tag	UNP Q9Y664
E	-8	LEU	-	expression tag	UNP Q9Y664
E	-7	ASN	-	expression tag	UNP Q9Y664
E	-6	GLY	-	expression tag	UNP Q9Y664
E	-5	GLY	-	expression tag	UNP Q9Y664
E	-4	GLY	-	expression tag	UNP Q9Y664
E	-3	GLY	-	expression tag	UNP Q9Y664
E	-2	GLY	-	expression tag	UNP Q9Y664
E	-1	SER	-	expression tag	UNP Q9Y664
E	0	THR	-	expression tag	UNP Q9Y664

- Molecule 5 is a protein called KICSTOR subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	373	Total	C	N	O	S	0	0
			3037	1971	509	546	11		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-20	MET	-	initiating methionine	UNP Q96MD2
F	-19	GLY	-	expression tag	UNP Q96MD2
F	-18	TYR	-	expression tag	UNP Q96MD2
F	-17	PRO	-	expression tag	UNP Q96MD2
F	-16	TYR	-	expression tag	UNP Q96MD2
F	-15	ASP	-	expression tag	UNP Q96MD2
F	-14	VAL	-	expression tag	UNP Q96MD2
F	-13	PRO	-	expression tag	UNP Q96MD2
F	-12	ASP	-	expression tag	UNP Q96MD2
F	-11	TYR	-	expression tag	UNP Q96MD2
F	-10	ALA	-	expression tag	UNP Q96MD2
F	-9	ASP	-	expression tag	UNP Q96MD2
F	-8	LEU	-	expression tag	UNP Q96MD2
F	-7	ASN	-	expression tag	UNP Q96MD2
F	-6	GLY	-	expression tag	UNP Q96MD2
F	-5	GLY	-	expression tag	UNP Q96MD2
F	-4	GLY	-	expression tag	UNP Q96MD2
F	-3	GLY	-	expression tag	UNP Q96MD2
F	-2	GLY	-	expression tag	UNP Q96MD2
F	-1	SER	-	expression tag	UNP Q96MD2
F	0	THR	-	expression tag	UNP Q96MD2
F	443	SER	ALA	variant	UNP Q96MD2

- Molecule 6 is a protein called KICSTOR complex protein ITFG2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	391	Total	C	N	O	S	0	0
			3066	1939	525	581	21		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-18	MET	-	initiating methionine	UNP Q969R8
G	-17	GLU	-	expression tag	UNP Q969R8
G	-16	GLN	-	expression tag	UNP Q969R8
G	-15	LYS	-	expression tag	UNP Q969R8
G	-14	LEU	-	expression tag	UNP Q969R8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-13	ILE	-	expression tag	UNP Q969R8
G	-12	SER	-	expression tag	UNP Q969R8
G	-11	GLU	-	expression tag	UNP Q969R8
G	-10	GLU	-	expression tag	UNP Q969R8
G	-9	ASP	-	expression tag	UNP Q969R8
G	-8	LEU	-	expression tag	UNP Q969R8
G	-7	ASN	-	expression tag	UNP Q969R8
G	-6	GLY	-	expression tag	UNP Q969R8
G	-5	GLY	-	expression tag	UNP Q969R8
G	-4	GLY	-	expression tag	UNP Q969R8
G	-3	GLY	-	expression tag	UNP Q969R8
G	-2	GLY	-	expression tag	UNP Q969R8
G	-1	SER	-	expression tag	UNP Q969R8
G	0	THR	-	expression tag	UNP Q969R8

- Molecule 7 is a protein called GATOR complex protein NPRL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	461	Total	C	N	O	S	0	0
			3663	2347	641	654	21		

There are 21 discrepancies between the modelled and reference sequences:

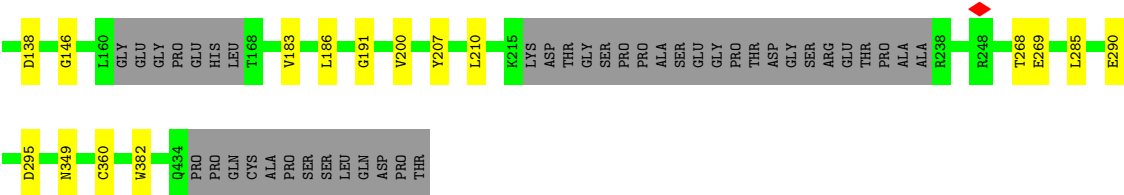
Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	expression tag	UNP Q12980
C	-19	GLY	-	expression tag	UNP Q12980
C	-18	TYR	-	expression tag	UNP Q12980
C	-17	PRO	-	expression tag	UNP Q12980
C	-16	TYR	-	expression tag	UNP Q12980
C	-15	ASP	-	expression tag	UNP Q12980
C	-14	VAL	-	expression tag	UNP Q12980
C	-13	PRO	-	expression tag	UNP Q12980
C	-12	ASP	-	expression tag	UNP Q12980
C	-11	TYR	-	expression tag	UNP Q12980
C	-10	ALA	-	expression tag	UNP Q12980
C	-9	ASP	-	expression tag	UNP Q12980
C	-8	LEU	-	expression tag	UNP Q12980
C	-7	ASN	-	expression tag	UNP Q12980
C	-6	GLY	-	expression tag	UNP Q12980
C	-5	GLY	-	expression tag	UNP Q12980
C	-4	GLY	-	expression tag	UNP Q12980
C	-3	GLY	-	expression tag	UNP Q12980

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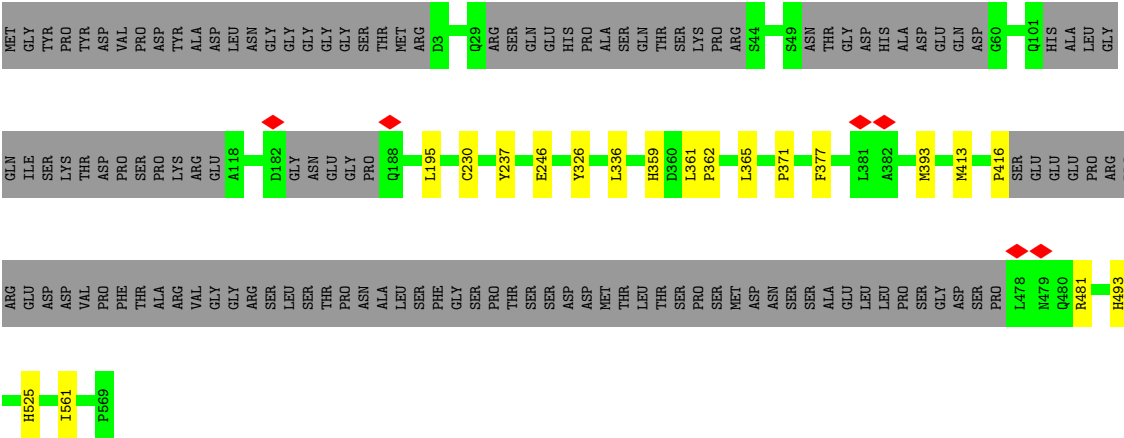
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q12980
C	-1	SER	-	expression tag	UNP Q12980
C	0	THR	-	expression tag	UNP Q12980





● Molecule 7: GATOR complex protein NPRL3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43700	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	20.188	Depositor
Minimum map value	0.000	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.385	Depositor
Recommended contour level	1.8	Depositor
Map size (Å)	480.0, 480.0, 480.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	H	0.32	0/3053	0.52	0/4136
2	B	0.33	0/8440	0.48	0/11443
3	D	0.22	0/18908	0.43	0/25693
4	E	0.26	0/3250	0.49	0/4410
5	F	0.22	0/3117	0.45	0/4210
6	G	0.25	0/3126	0.47	0/4241
7	C	0.31	0/3739	0.48	0/5073
All	All	0.26	0/43633	0.46	0/59206

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	H	2993	0	3036	9	0
2	B	8226	0	8017	31	0
3	D	18448	0	18505	56	0
4	E	3185	0	3155	9	0
5	F	3037	0	3018	7	0
6	G	3066	0	3031	17	0
7	C	3663	0	3738	11	0
All	All	42618	0	42500	134	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 2.

All (134) 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)
7:C:416:PRO:HA	7:C:493:HIS:CE1	2.28	0.67
6:G:360:CYS:HG	6:G:382:TRP:CD1	2.14	0.65
3:D:2384:ASP:OD2	3:D:2646:ARG:NH2	2.35	0.59
2:B:1205:PHE:CD1	2:B:1210:VAL:HG21	2.38	0.58
3:D:2923:TYR:CE2	3:D:2927:ILE:HD11	2.39	0.58
5:F:21:PHE:CD2	5:F:33:ALA:HB1	2.40	0.57
6:G:88:GLY:O	6:G:123:ILE:HD13	2.06	0.56
2:B:862:LYS:HE3	2:B:864:THR:HG21	1.88	0.56
3:D:744:LYS:NZ	3:D:864:THR:O	2.38	0.56
2:B:290:ALA:HB1	2:B:293:PHE:HB2	1.88	0.55
3:D:2923:TYR:CZ	3:D:2927:ILE:HD11	2.42	0.54
3:D:2550:SER:OG	4:E:247:ASP:OD1	2.20	0.54
6:G:268:THR:HG22	6:G:269:GLU:H	1.72	0.54
6:G:186:LEU:HD23	6:G:200:VAL:HG22	1.90	0.53
7:C:326:TYR:HH	7:C:525:HIS:CE1	2.27	0.53
2:B:171:VAL:HG22	2:B:332:MET:HE2	1.91	0.52
3:D:2386:ILE:HG21	3:D:2529:TRP:CZ2	2.45	0.52
4:E:116:TYR:CD2	4:E:134:CYS:HB3	2.46	0.51
3:D:131:LEU:HD21	3:D:172:LEU:HB3	1.92	0.51
1:H:73:HIS:HB3	1:H:76:TYR:CE2	2.47	0.50
5:F:27:ILE:HG22	5:F:27:ILE:O	2.09	0.50
6:G:268:THR:HG22	6:G:269:GLU:N	2.27	0.50
3:D:66:TRP:CH2	3:D:68:PRO:HA	2.47	0.49
3:D:2533:MET:HE3	3:D:2541:VAL:HG21	1.93	0.49
2:B:974:ARG:O	2:B:976:ASP:N	2.41	0.49
2:B:228:ALA:HB2	2:B:294:PRO:HG3	1.93	0.49
3:D:2558:LEU:HD22	3:D:2610:LEU:HD11	1.95	0.48
2:B:218:VAL:HG21	2:B:270:LEU:HD21	1.96	0.48
7:C:246:GLU:OE1	7:C:246:GLU:N	2.43	0.48
2:B:1548:TRP:C	2:B:1548:TRP:CD1	2.91	0.48
7:C:359:HIS:CD2	7:C:393:MET:HE1	2.48	0.48
3:D:875:HIS:O	3:D:903:ASN:N	2.39	0.48
3:D:2855:LEU:HD21	3:D:3081:HIS:CG	2.48	0.48
2:B:801:GLU:OE1	2:B:1366:ARG:NH1	2.47	0.47
3:D:129:GLY:HA3	3:D:341:TYR:CD2	2.49	0.47
7:C:416:PRO:HA	7:C:493:HIS:HE1	1.74	0.47
3:D:1416:SER:HA	3:D:1606:ARG:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:167:ASP:O	4:E:169:ALA:N	2.47	0.47
4:E:253:VAL:HA	4:E:276:LEU:O	2.14	0.47
7:C:326:TYR:OH	7:C:525:HIS:CE1	2.67	0.47
1:H:290:PRO:HB2	7:C:371:PRO:HD3	1.96	0.47
3:D:2801:LYS:HA	3:D:2801:LYS:HE2	1.97	0.47
3:D:2849:TYR:CE2	6:G:86:ALA:HB1	2.49	0.47
4:E:310:VAL:HG13	4:E:328:VAL:HG13	1.95	0.47
2:B:167:THR:HG22	2:B:749:THR:HG22	1.96	0.46
6:G:191:GLY:HA2	6:G:290:GLU:HG2	1.96	0.46
3:D:2396:LEU:O	3:D:2518:LEU:HD12	2.15	0.46
2:B:97:LEU:HD21	2:B:154:GLY:HA3	1.98	0.46
2:B:115:TRP:CZ2	2:B:119:LYS:HE3	2.51	0.46
3:D:2553:LEU:HD11	3:D:2689:ALA:HB2	1.97	0.46
2:B:805:GLN:HG3	2:B:925:ILE:HD11	1.98	0.46
2:B:978:ASP:N	2:B:978:ASP:OD1	2.49	0.46
6:G:45:VAL:HG11	6:G:81:LEU:HD21	1.99	0.45
2:B:115:TRP:CH2	2:B:119:LYS:HE3	2.51	0.45
3:D:2240:TYR:CE2	3:D:2646:ARG:HD3	2.51	0.45
2:B:172:TYR:CZ	2:B:316:VAL:HG11	2.51	0.45
2:B:1470:HIS:CD2	2:B:1470:HIS:C	2.94	0.45
3:D:453:GLY:H	3:D:454:PRO:HA	1.80	0.45
2:B:223:ARG:NH2	2:B:308:GLU:OE2	2.41	0.45
3:D:798:TRP:CH2	3:D:908:VAL:HG21	2.50	0.45
1:H:213:ALA:O	1:H:215:VAL:N	2.47	0.45
4:E:362:PHE:HZ	4:E:393:LEU:HD11	1.82	0.45
6:G:207:TYR:OH	6:G:295:ASP:OD2	2.31	0.45
3:D:1710:ARG:HH11	3:D:1918:TRP:CD1	2.35	0.44
3:D:2386:ILE:HG21	3:D:2529:TRP:CH2	2.52	0.44
1:H:290:PRO:HB2	7:C:371:PRO:CD	2.48	0.44
3:D:2358:ASP:OD1	3:D:2358:ASP:N	2.50	0.44
2:B:113:ASP:HB3	2:B:137:ILE:HD11	2.00	0.44
3:D:920:GLY:HA3	3:D:924:TRP:CH2	2.53	0.44
3:D:2292:LYS:O	3:D:2364:ASN:N	2.51	0.44
2:B:212:CYS:HB3	2:B:214:HIS:CD2	2.52	0.44
3:D:3148:SER:HB3	3:D:3162:ASP:HA	2.00	0.44
1:H:101:ILE:CD1	1:H:159:VAL:HG22	2.47	0.44
6:G:138:ASP:OD1	6:G:138:ASP:C	2.61	0.44
3:D:800:TRP:CD1	3:D:800:TRP:H	2.34	0.44
3:D:2856:PHE:CE2	3:D:3050:HIS:CD2	3.06	0.44
2:B:44:PRO:HA	2:B:86:TYR:CE2	2.51	0.44
4:E:118:ASP:OD1	4:E:119:TYR:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:389:VAL:HG12	5:F:389:VAL:O	2.18	0.43
3:D:131:LEU:HD21	3:D:172:LEU:CB	2.48	0.43
6:G:40:ASP:OD1	6:G:41:THR:N	2.52	0.43
2:B:145:TRP:CZ2	2:B:150:LYS:HE2	2.53	0.43
6:G:146:GLY:HA3	6:G:183:VAL:HG11	2.00	0.43
6:G:186:LEU:CD2	6:G:200:VAL:HG22	2.48	0.43
5:F:383:HIS:CD2	5:F:414:GLU:HA	2.53	0.43
4:E:193:GLU:HG3	4:E:217:SER:HB2	2.00	0.43
5:F:328:HIS:O	5:F:331:HIS:NE2	2.51	0.43
7:C:336:LEU:HD22	7:C:365:LEU:HD22	2.01	0.43
3:D:2829:THR:C	3:D:2830:MET:SD	3.02	0.43
1:H:36:LEU:O	1:H:40:VAL:HG22	2.19	0.43
2:B:234:PHE:CG	2:B:242:ILE:HD13	2.54	0.42
3:D:99:ASP:HB3	3:D:263:THR:HA	2.01	0.42
3:D:103:SER:O	3:D:106:ILE:HD12	2.17	0.42
3:D:152:GLN:HE22	3:D:243:GLN:HB3	1.84	0.42
2:B:133:GLU:HA	2:B:137:ILE:O	2.20	0.42
2:B:216:VAL:HB	2:B:267:TRP:CH2	2.54	0.42
3:D:169:GLY:HA2	3:D:251:LEU:HD22	2.01	0.42
3:D:2556:SER:OG	3:D:2788:ASP:OD2	2.38	0.42
6:G:90:PHE:N	6:G:121:GLN:O	2.49	0.42
1:H:277:SER:HG	1:H:280:ASP:CG	2.27	0.42
3:D:18:MET:HE3	3:D:89:ALA:HB2	2.02	0.42
7:C:326:TYR:CE1	7:C:561:ILE:HD12	2.54	0.42
3:D:106:ILE:HD11	3:D:306:HIS:HB3	2.02	0.42
3:D:2558:LEU:CD2	3:D:2610:LEU:HD11	2.49	0.42
6:G:69:GLY:HA3	6:G:130:MET:HE1	2.02	0.42
3:D:447:TRP:HA	3:D:448:PRO:C	2.44	0.42
3:D:2233:TRP:CH2	3:D:2386:ILE:HG12	2.54	0.42
1:H:226:ASN:OD1	2:B:421:PRO:HA	2.20	0.42
3:D:569:ASP:OD1	3:D:569:ASP:C	2.63	0.42
6:G:64:MET:O	6:G:86:ALA:N	2.47	0.42
3:D:659:ALA:HA	3:D:660:PRO:C	2.45	0.41
5:F:223:LEU:HD23	5:F:223:LEU:O	2.20	0.41
2:B:406:SER:HB2	2:B:742:VAL:HA	2.01	0.41
3:D:2573:SER:HB2	3:D:2615:PHE:CE2	2.54	0.41
3:D:455:ARG:HA	3:D:455:ARG:NE	2.36	0.41
2:B:1197:GLN:O	2:B:1198:LYS:C	2.63	0.41
6:G:200:VAL:HG21	6:G:210:LEU:HD11	2.02	0.41
1:H:328:LYS:HE2	1:H:379:TRP:CZ2	2.56	0.41
2:B:980:TRP:CZ2	2:B:1212:HIS:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:149:VAL:HG21	3:D:172:LEU:HD11	2.02	0.41
3:D:234:ASP:OD1	3:D:234:ASP:N	2.48	0.41
3:D:581:ARG:HA	3:D:664:LEU:O	2.21	0.41
3:D:2848:HIS:CG	3:D:2849:TYR:N	2.89	0.41
2:B:336:ILE:HG23	2:B:369:MET:HE3	2.04	0.40
3:D:106:ILE:HG22	3:D:107:VAL:N	2.37	0.40
3:D:302:CYS:O	3:D:303:SER:C	2.64	0.40
7:C:361:LEU:HB3	7:C:362:PRO:HD3	2.03	0.40
3:D:2554:LEU:HD21	3:D:2608:LEU:HD12	2.02	0.40
3:D:3428:TRP:CD2	5:F:277:LEU:HD21	2.56	0.40
4:E:316:THR:HG21	4:E:371:HIS:CG	2.55	0.40
3:D:3374:VAL:HG11	3:D:3419:VAL:HG11	2.03	0.40
2:B:10:VAL:O	2:B:68:SER:HA	2.21	0.40
3:D:1048:GLU:HA	3:D:1124:CYS:O	2.22	0.40
3:D:2314:TRP:CG	3:D:2315:PRO:HD2	2.57	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	H	366/401 (91%)	357 (98%)	9 (2%)	0	100	100
2	B	976/1621 (60%)	940 (96%)	36 (4%)	0	100	100
3	D	2250/3451 (65%)	2173 (97%)	77 (3%)	0	100	100
4	E	402/457 (88%)	381 (95%)	21 (5%)	0	100	100
5	F	363/466 (78%)	351 (97%)	12 (3%)	0	100	100
6	G	383/466 (82%)	364 (95%)	19 (5%)	0	100	100
7	C	449/590 (76%)	431 (96%)	18 (4%)	0	100	100
All	All	5189/7452 (70%)	4997 (96%)	192 (4%)	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	H	343/365 (94%)	339 (99%)	4 (1%)	63	79
2	B	905/1423 (64%)	899 (99%)	6 (1%)	76	83
3	D	2043/2970 (69%)	2024 (99%)	19 (1%)	70	81
4	E	353/384 (92%)	351 (99%)	2 (1%)	78	84
5	F	337/404 (83%)	332 (98%)	5 (2%)	57	76
6	G	343/401 (86%)	339 (99%)	4 (1%)	63	79
7	C	410/518 (79%)	404 (98%)	6 (2%)	57	76
All	All	4734/6465 (73%)	4688 (99%)	46 (1%)	65	80

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	9	CYS
1	H	190	ASP
1	H	254	LEU
1	H	366	ASP
2	B	148	ASN
2	B	260	GLN
2	B	275	LYS
2	B	980	TRP
2	B	1354	VAL
2	B	1470	HIS
3	D	149	VAL
3	D	276	GLU
3	D	300	TYR
3	D	388	LYS
3	D	406	ARG
3	D	590	THR
3	D	596	LEU
3	D	693	PHE

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Mol	Chain	Res	Type
3	D	739	LEU
3	D	800	TRP
3	D	818	LEU
3	D	835	CYS
3	D	904	LEU
3	D	1328	ASP
3	D	1576	ARG
3	D	1931	TYR
3	D	2358	ASP
3	D	2608	LEU
3	D	3372	CYS
4	E	357	LEU
4	E	412	VAL
5	F	30	TYR
5	F	189	LEU
5	F	216	LEU
5	F	264	MET
5	F	280	GLN
6	G	1	MET
6	G	123	ILE
6	G	285	LEU
6	G	349	ASN
7	C	195	LEU
7	C	230	CYS
7	C	237	TYR
7	C	377	PHE
7	C	413	MET
7	C	481	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	240	GLN
2	B	211	ASN
2	B	383	HIS
2	B	981	GLN
2	B	1455	HIS
3	D	38	HIS
3	D	152	GLN
3	D	597	HIS
3	D	875	HIS
3	D	903	ASN

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Mol	Chain	Res	Type
3	D	1001	GLN
3	D	1428	HIS
3	D	1446	HIS
3	D	1579	HIS
3	D	2035	HIS
3	D	2086	GLN
3	D	2212	GLN
3	D	2223	HIS
3	D	2282	ASN
3	D	2390	GLN
3	D	2816	ASN
3	D	3057	HIS
3	D	3095	GLN
4	E	399	GLN
5	F	124	HIS
5	F	201	GLN
5	F	224	GLN
5	F	274	HIS
5	F	326	GLN
5	F	328	HIS
6	G	431	HIS
7	C	143	HIS
7	C	259	HIS
7	C	359	HIS
7	C	493	HIS
7	C	525	HIS
7	C	565	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 ⓘ

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.

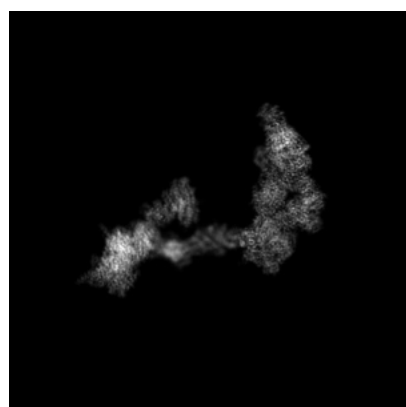
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70135. These allow visual inspection of the internal detail of the map and identification of artifacts.

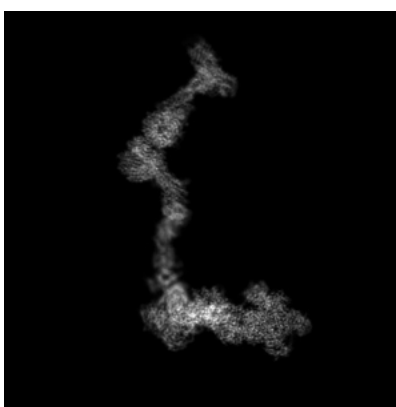
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

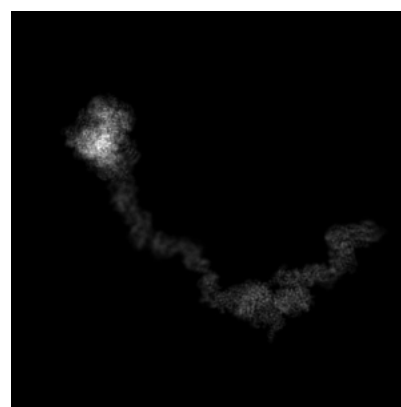
6.1.1 Primary map



X



Y

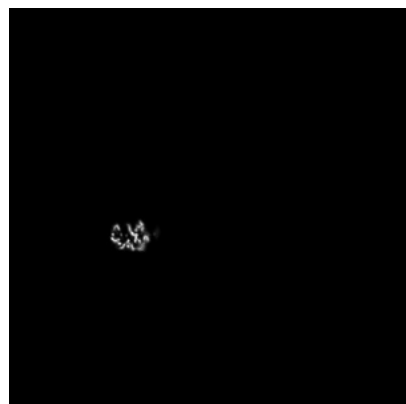


Z

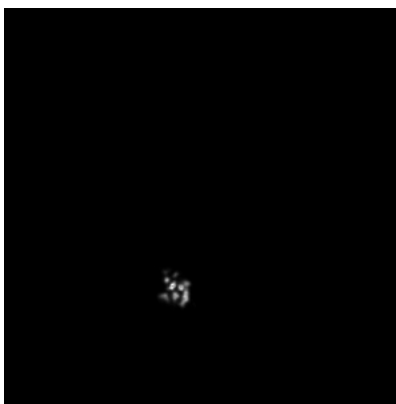
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240



Y Index: 240

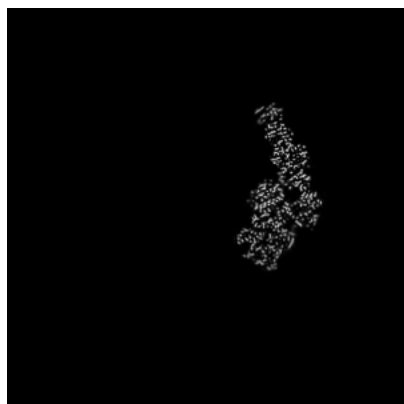


Z Index: 240

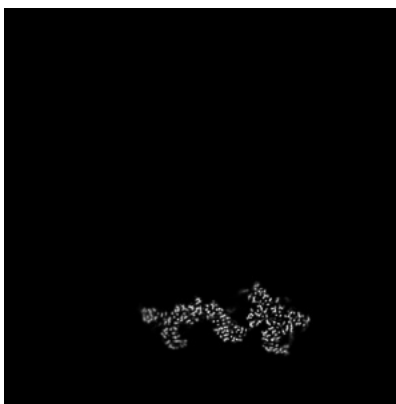
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

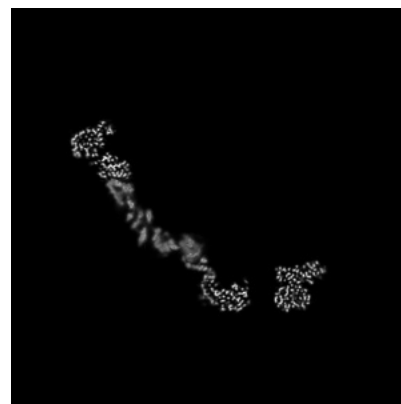
6.3.1 Primary map



X Index: 110



Y Index: 321

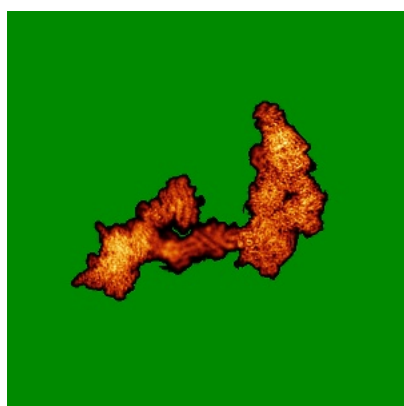


Z Index: 199

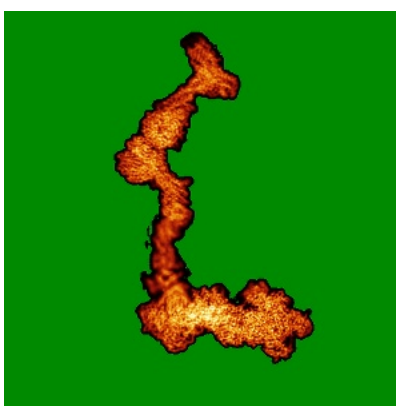
The images above show the largest variance slices of the map in three orthogonal directions.

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

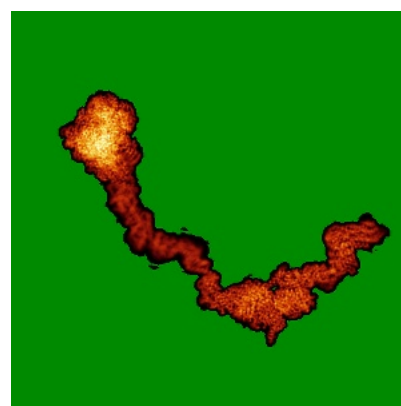
6.4.1 Primary map



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

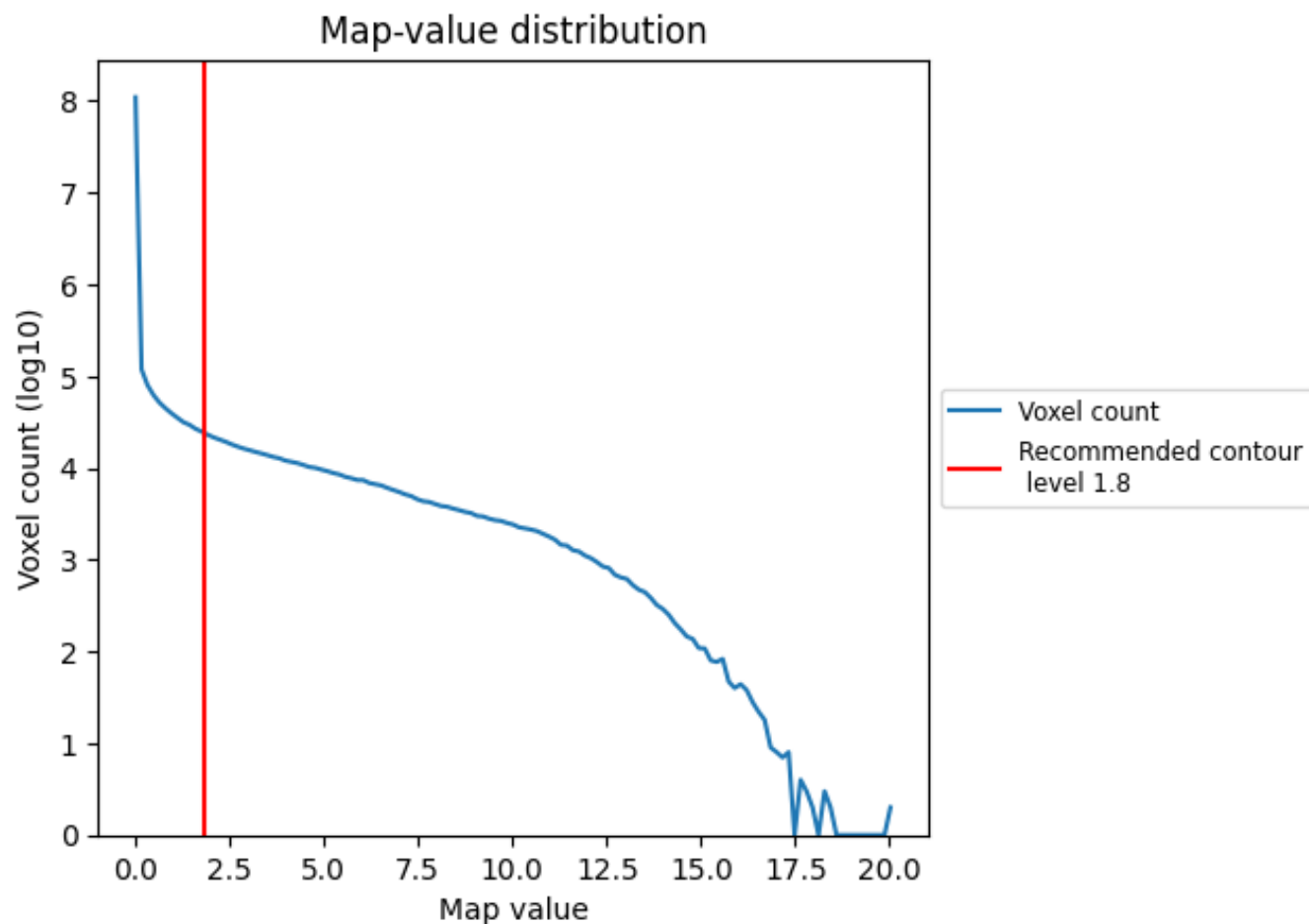
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

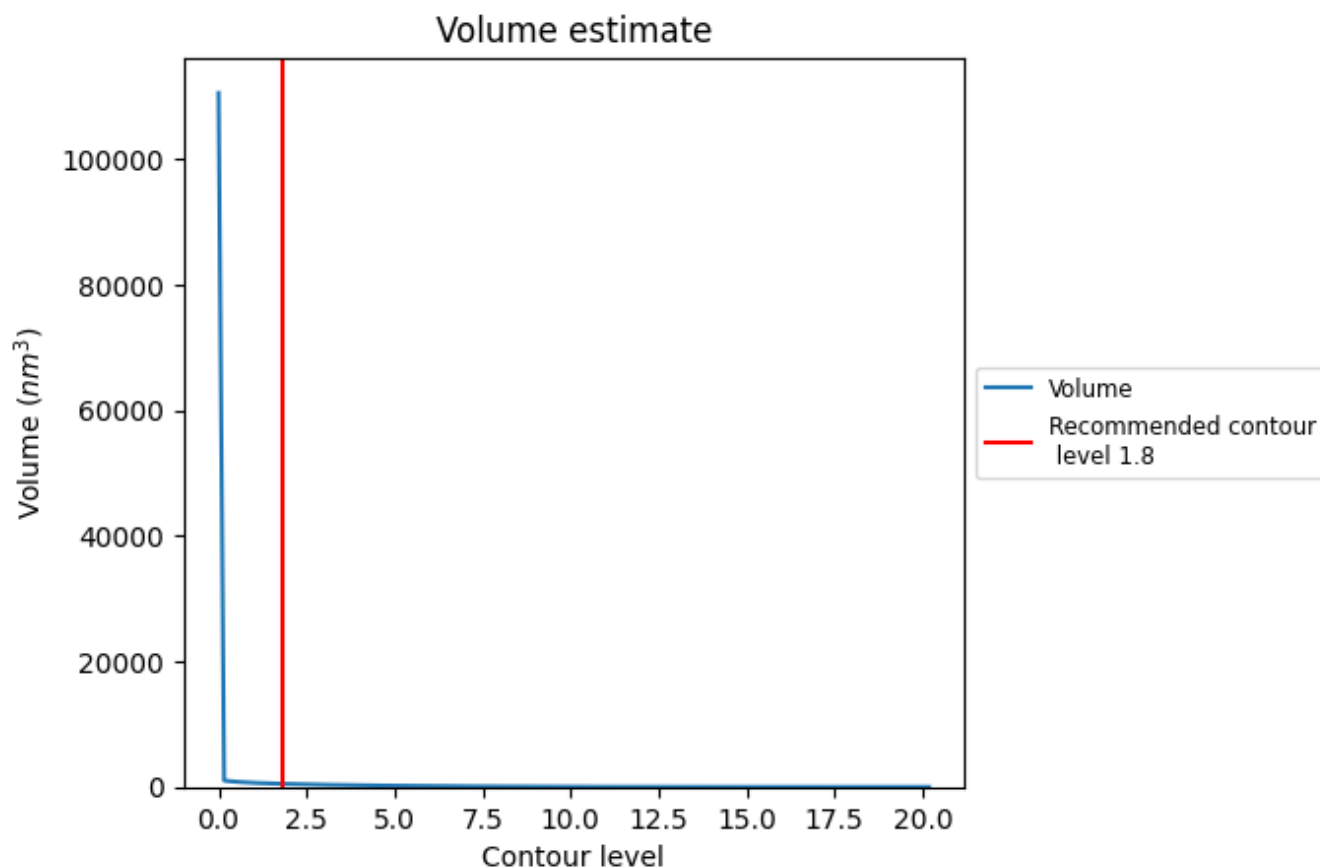
This section contains the results of statistical analysis of the map.

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.

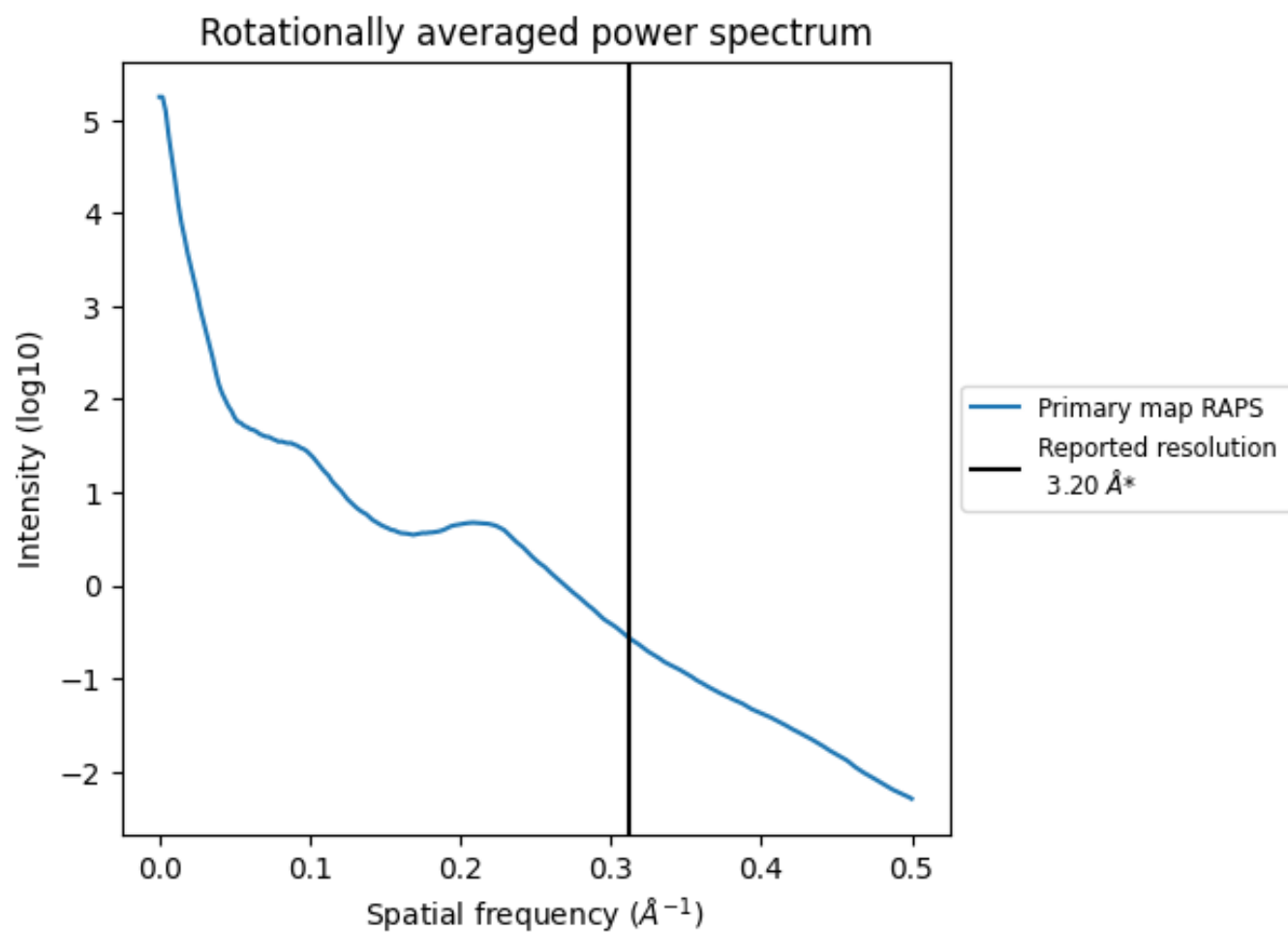
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 506 nm^3 ; this corresponds to an approximate mass of 457 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 0.312 Å⁻¹

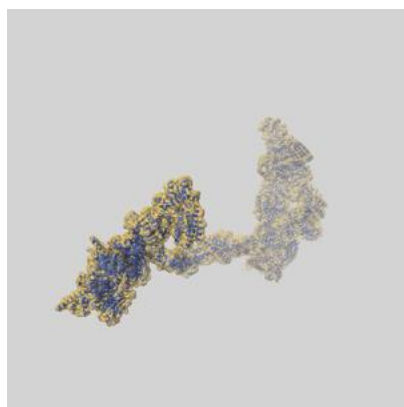
8 Fourier-Shell correlation ⓘ

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

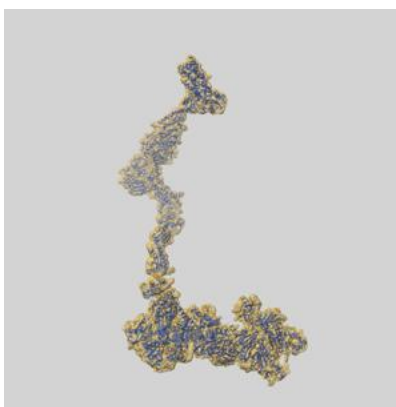
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70135 and PDB model 9O5A. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

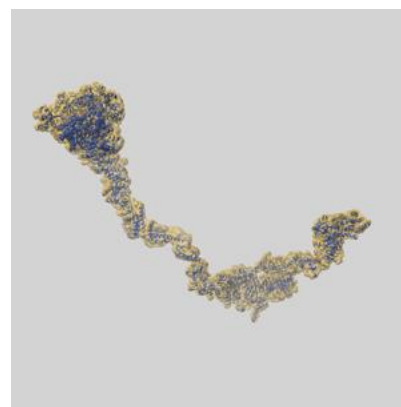
9.1 Map-model overlay [i](#)



X



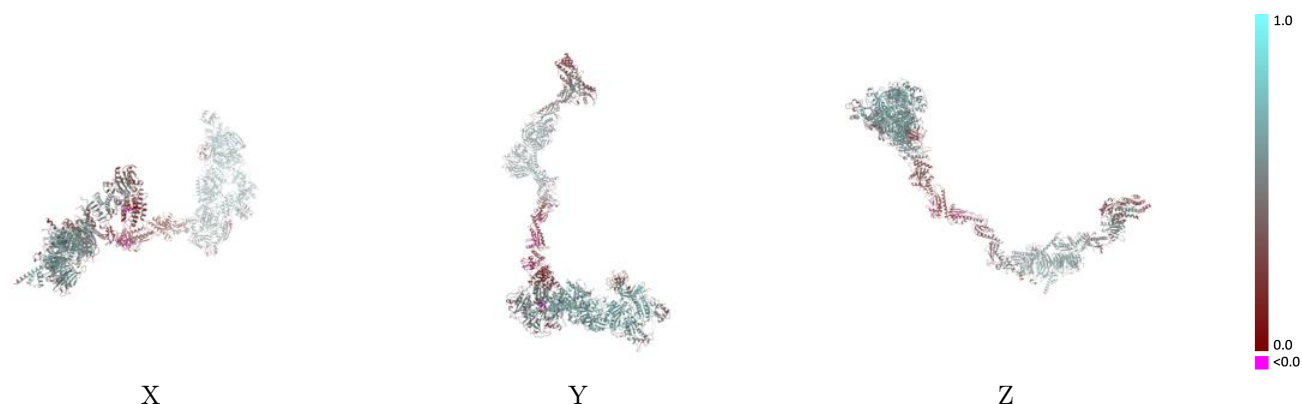
Y



Z

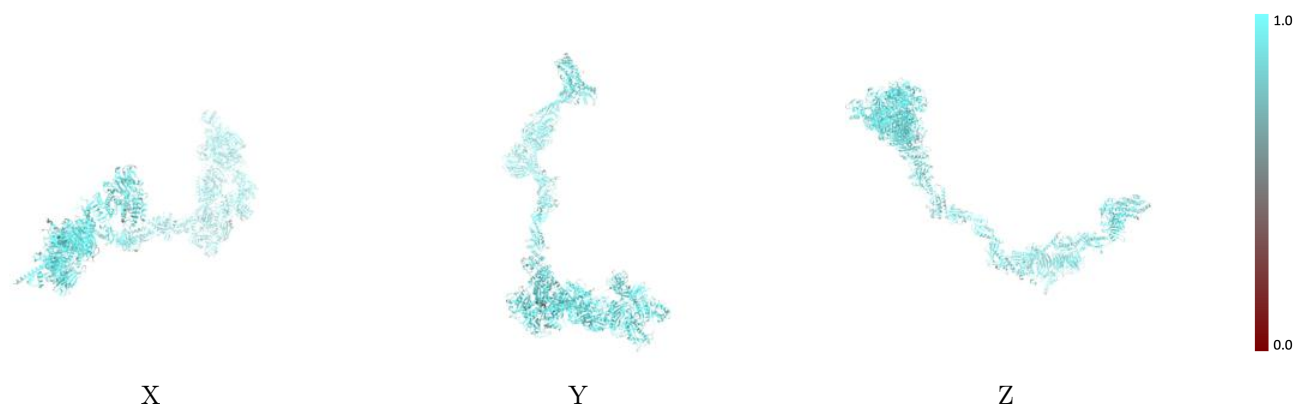
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



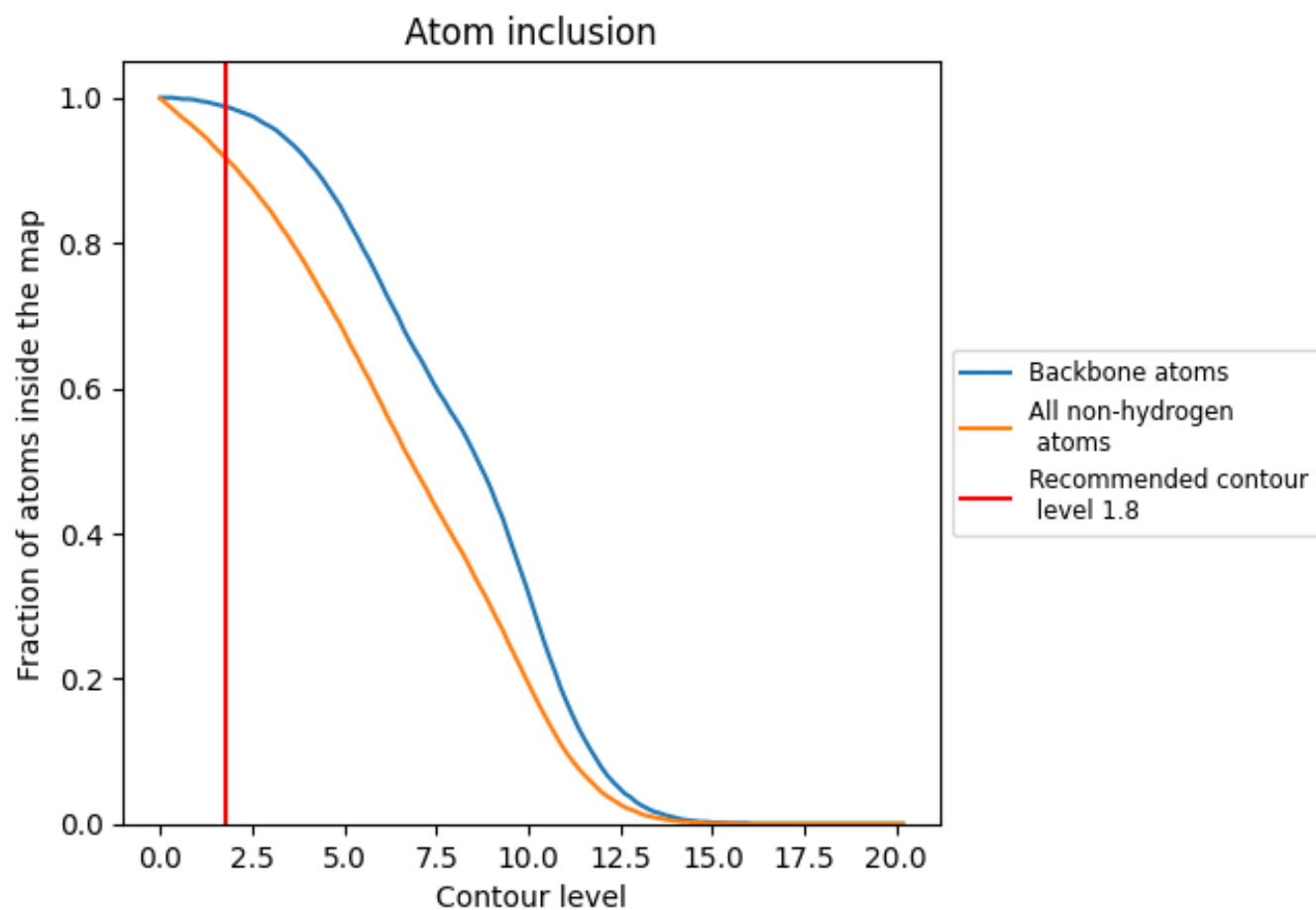
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 92% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.9160</div>	<div><div></div>0.4670</div>
B	<div><div></div>0.9230</div>	<div><div></div>0.5350</div>
C	<div><div></div>0.9580</div>	<div><div></div>0.5680</div>
D	<div><div></div>0.8970</div>	<div><div></div>0.3960</div>
E	<div><div></div>0.9390</div>	<div><div></div>0.5290</div>
F	<div><div></div>0.8590</div>	<div><div></div>0.3460</div>
G	<div><div></div>0.9370</div>	<div><div></div>0.5270</div>
H	<div><div></div>0.9700</div>	<div><div></div>0.5980</div>

1.0

0.0

<0.0