



wwPDB EM Validation Summary Report ⓘ

Oct 1, 2026 – 04:53 PM EDT

PDB ID : 38LP / pdb_000038lp
EMDB ID : EMD-78907
Title : Salmonella Flagellar Export Apparatus (FliPQR/FlhB/FlhA) in the context of the intact basal body with an asymmetric FlhA ring
Authors : Johnson, S.; Johnson, M.K.; Lea, S.M.
Deposited on : 2026-09-01
Resolution : 4.20 Å(reported)

This is a wwPDB EM Validation Summary 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:

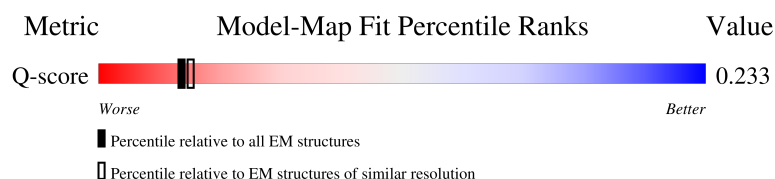
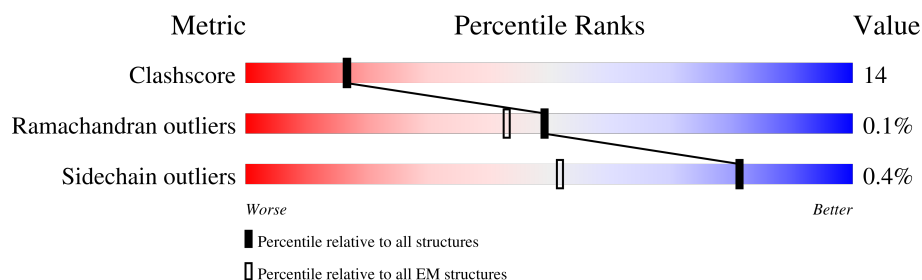
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 4.20 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	5410 (3.70 - 4.70)

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	A1	245	15% 58% 25% 15%
1	B1	245	14% 57% 28% 15%
1	C1	245	11% 61% 23% 15%
1	D1	245	10% 62% 22% 15%

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Mol	Chain	Length	Quality of chain
1	E1	245	
2	F1	264	
3	G1	89	
3	H1	89	
3	I1	89	
3	J1	89	
4	K1	383	
5	A2	692	
5	B2	692	
5	C2	692	
5	D2	692	
5	E2	692	
5	F2	692	
5	G2	692	
5	H2	692	
5	I2	692	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 35427 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 Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
1	B1	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
1	C1	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
1	D1	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
1	E1	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 2 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F1	250	Total	C	N	O	S	0	0
			1925	1293	304	313	15		

- Molecule 3 is a protein called Flagellar biosynthetic protein FliQ.

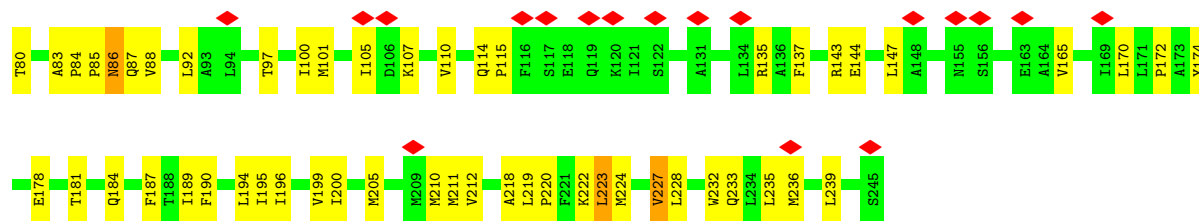
Mol	Chain	Residues	Atoms					AltConf	Trace
3	G1	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	H1	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	I1	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	J1	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 4 is a protein called Flagellar biosynthetic protein FlhB.

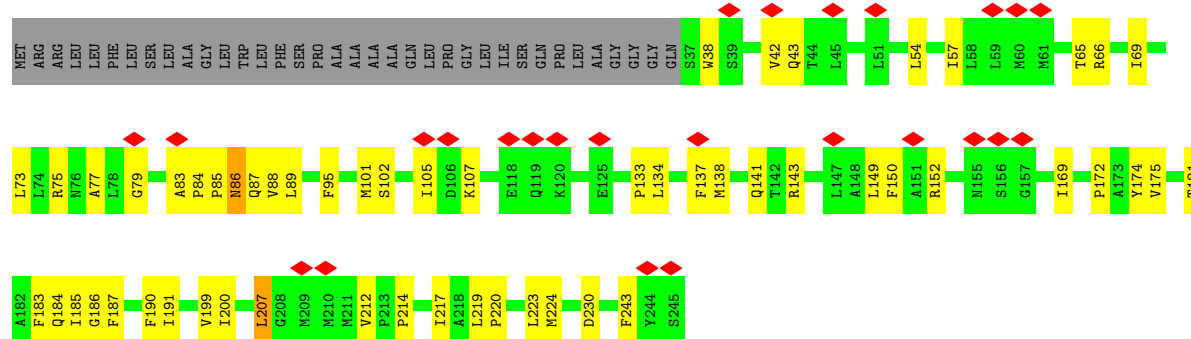
Mol	Chain	Residues	Atoms					AltConf	Trace
4	K1	249	Total	C	N	O	S	0	0
			1926	1245	333	331	17		

- Molecule 5 is a protein called Flagellar biosynthesis protein FlhA.

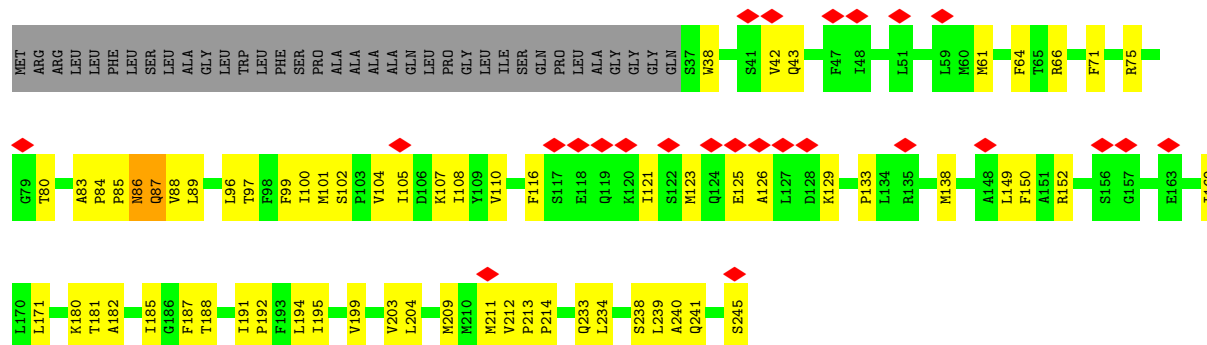
Mol	Chain	Residues	Atoms					AltConf	Trace
5	A2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	B2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	C2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	D2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	E2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	F2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	G2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	H2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		
5	I2	311	Total	C	N	O	S	0	0
			2309	1516	377	401	15		



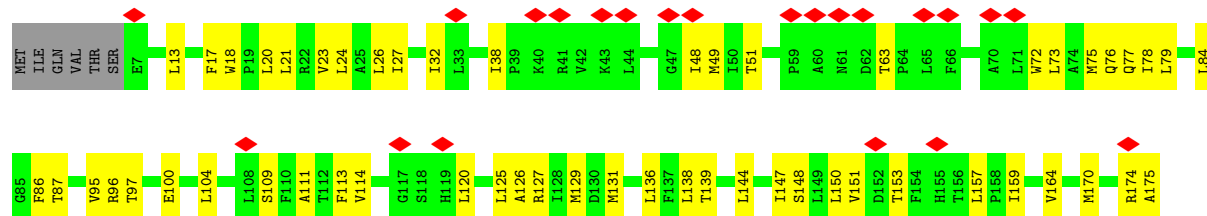
• Molecule 1: Flagellar biosynthetic protein Flp



• Molecule 1: Flagellar biosynthetic protein Flp



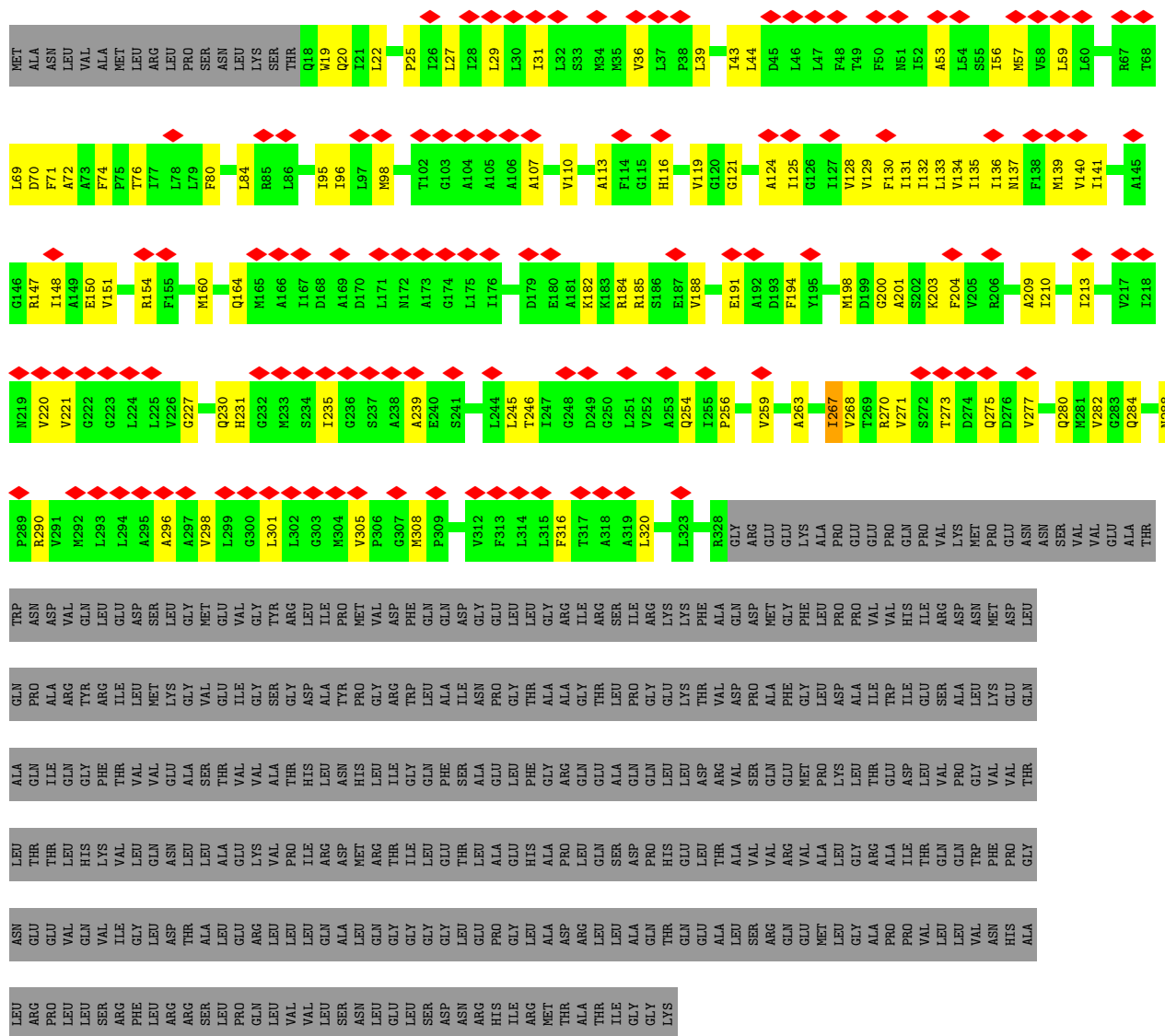
• Molecule 2: Flagellar biosynthetic protein Flr



PRO
GLU
ASN
LEU
PRO
VAL
MET
PRO
GLU
ALA
LEU
ASP
PHE
MET
ASN
GLU
LYS
ASN
THR
ASP
GLY

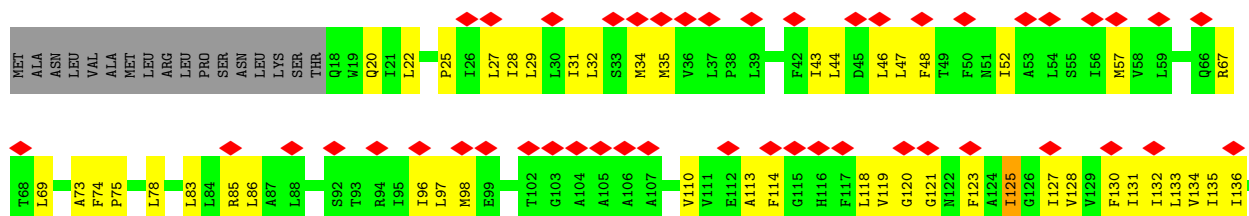
• Molecule 5: Flagellar biosynthesis protein FlhA

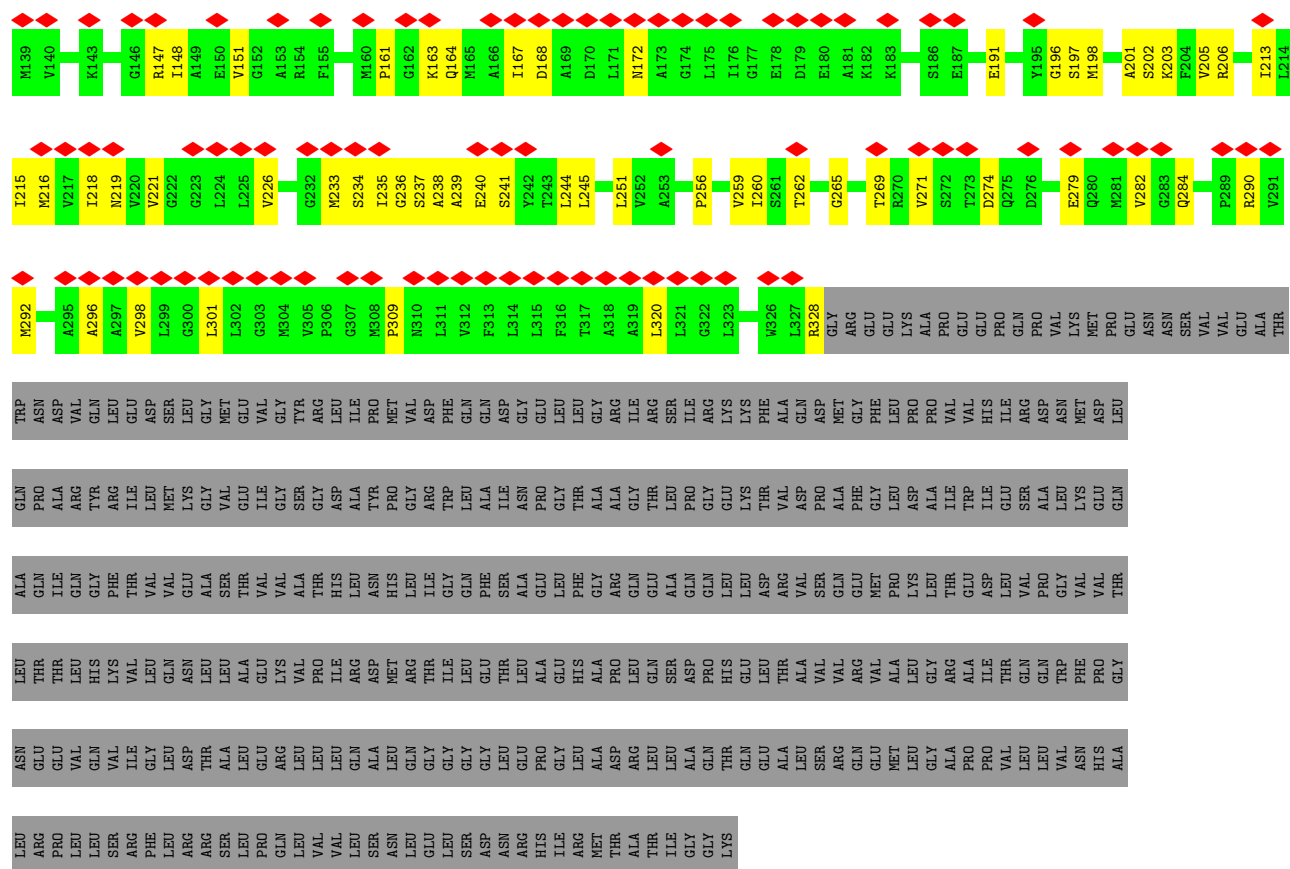
Chain A2: 



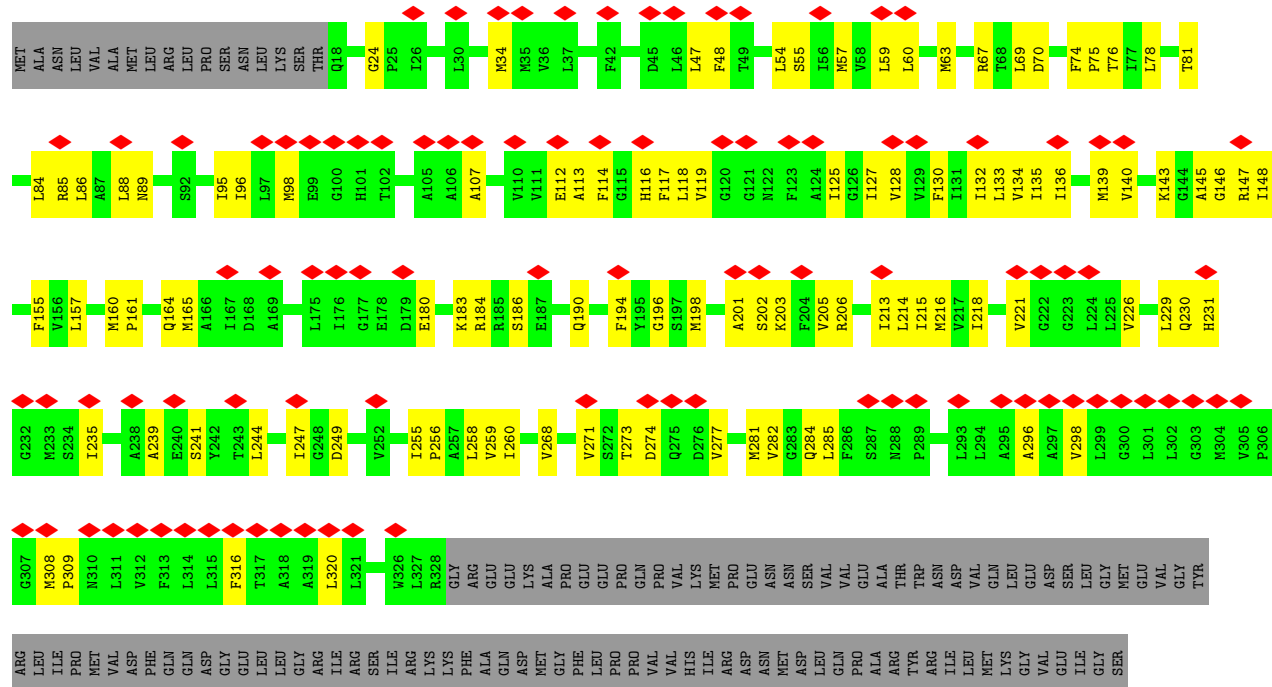
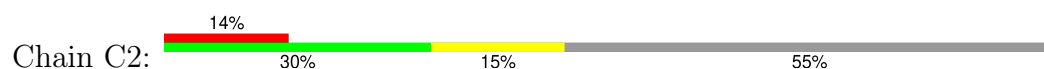
• Molecule 5: Flagellar biosynthesis protein FlhA

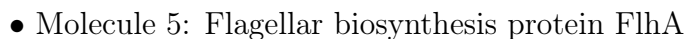
Chain B2: 

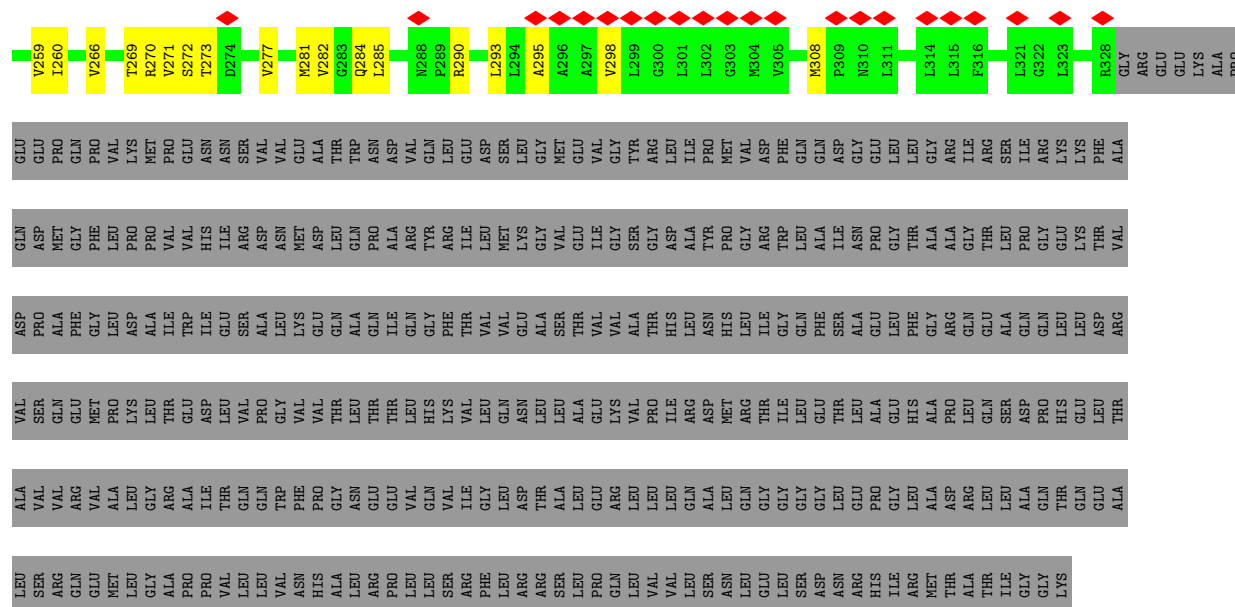




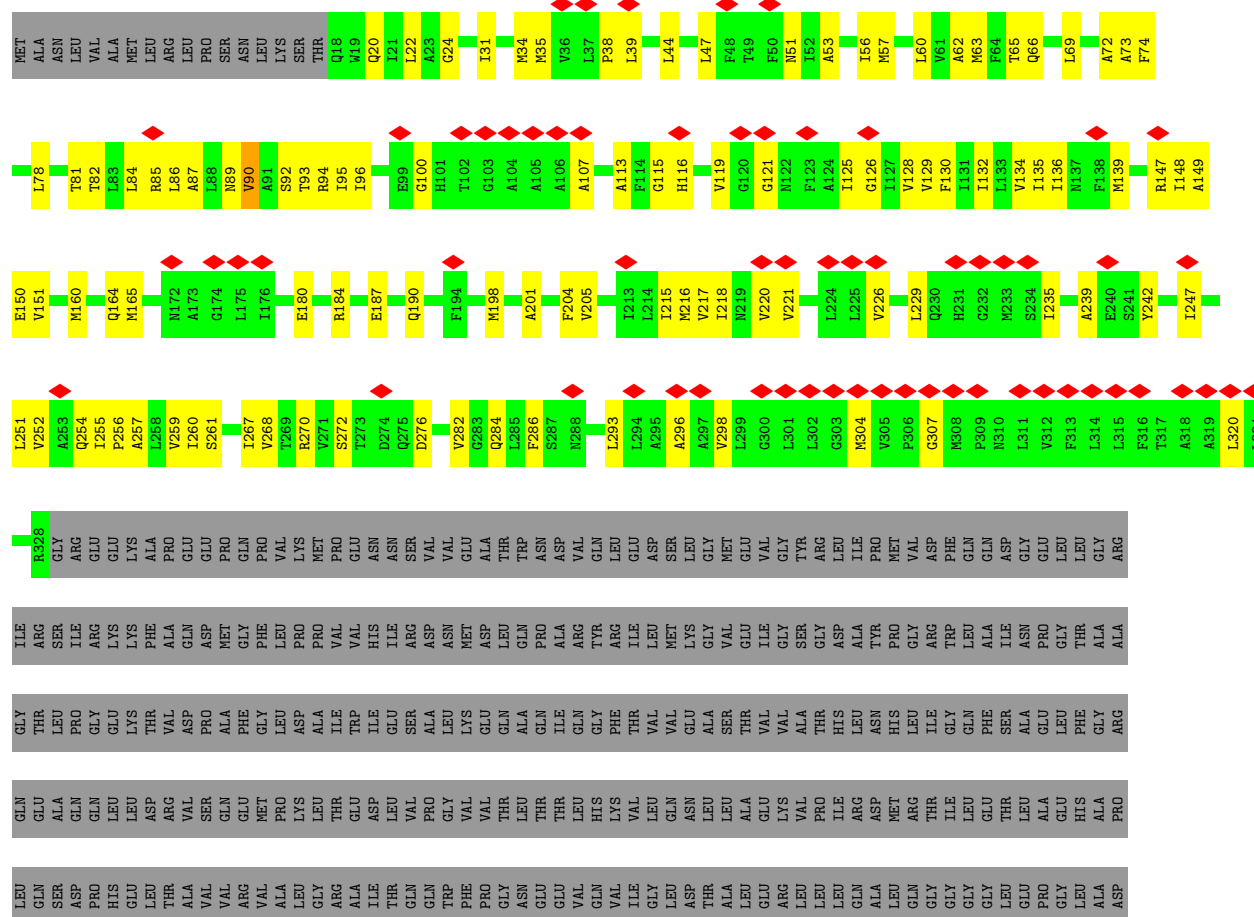
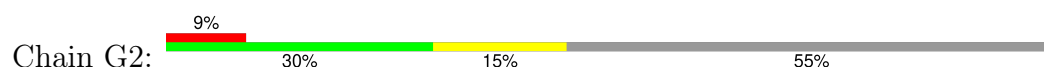
• Molecule 5: Flagellar biosynthesis protein FlhA

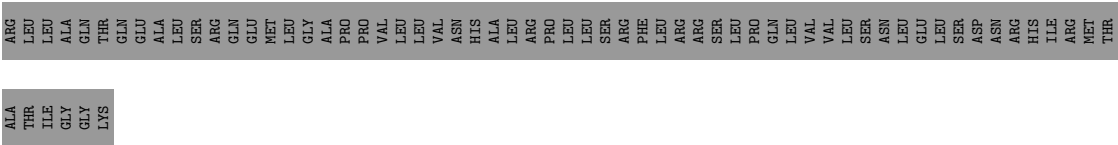




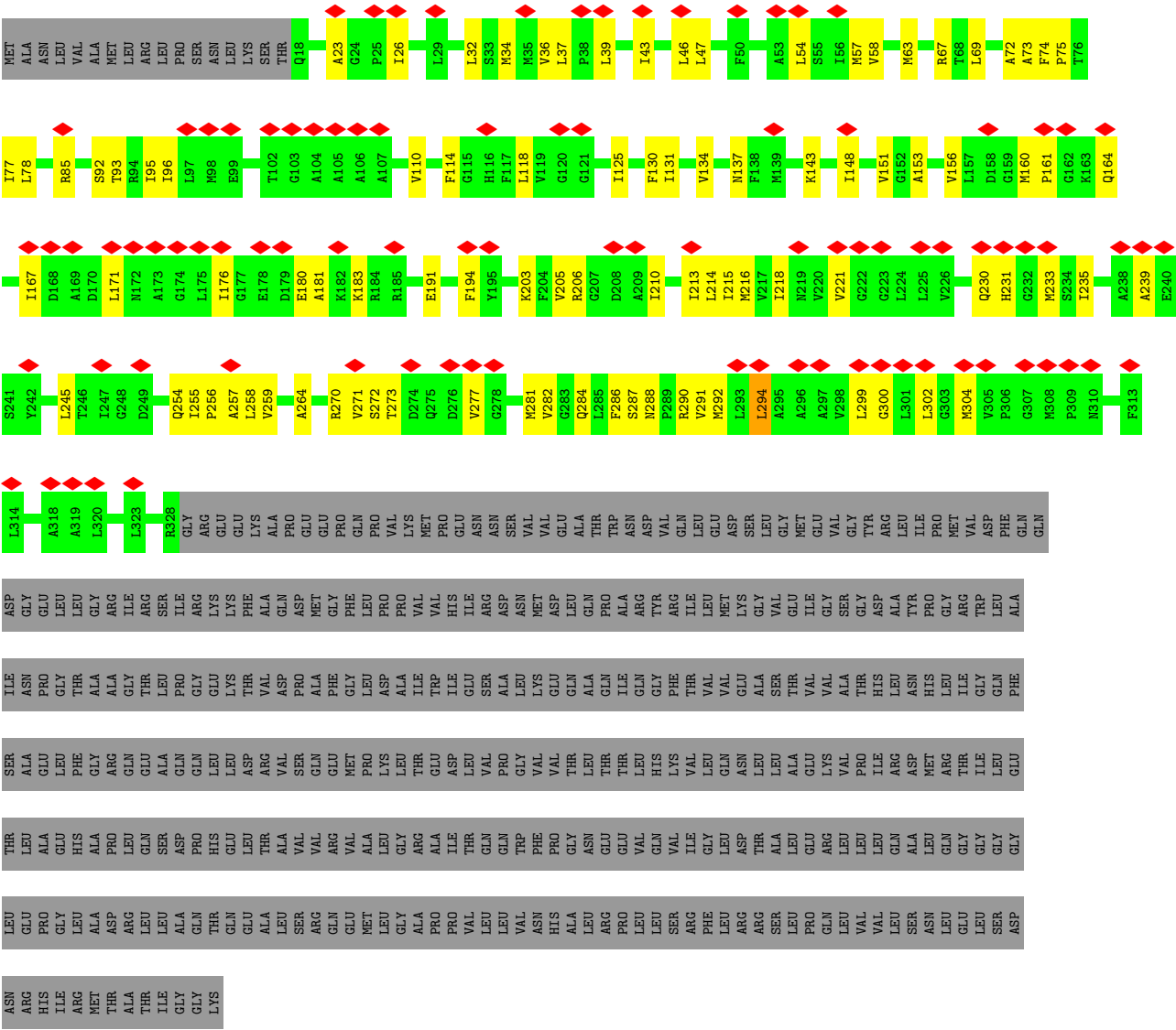
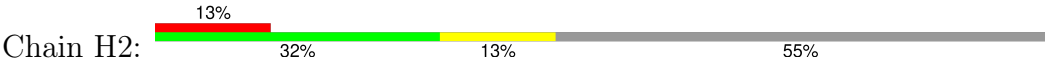


● Molecule 5: Flagellar biosynthesis protein FlhA

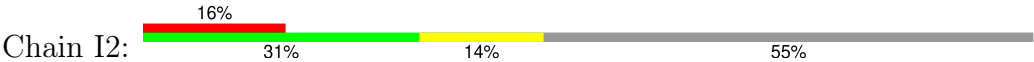




● Molecule 5: Flagellar biosynthesis protein FlhA



● Molecule 5: Flagellar biosynthesis protein FlhA



GLU	LEU	GLY	GLY	THR	THR	ILE	ARG	ASP	N310	V217	V140	A73
LEU	GLY	ILE	GLY	ILE	GLY	GLN	TRP	PHE	L311	I218	V140	F74
SER	GLY	LEU	GLN	LEU	GLN	GLN	LEU	GLN	V312	N219	R147	P75
ASP	GLY	GLU	PHE	GLU	PHE	ASP	ALA	ASP	F313	V220	I148	T76
ASN	LEU	THR	SER	LEU	THR	LEU	ILE	ASN	L314	V221	V151	I77
ARG	GLU	ALA	ASN	ALA	ASN	GLY	PRO	GLY	L315	G222	R154	L78
HIS	PRO	ALA	GLY	LEU	GLY	GLU	GLY	LEU	F316	G223	R155	L79
ILE	GLY	HIS	PHE	PHE	GLY	THR	THR	LEU	T317	L224	F156	F80
ARG	LEU	ALA	GLY	ARG	ALA	ALA	ALA	GLY	A318	L225	V157	T81
THR	GLN	GLN	GLY	THR	THR	THR	THR	ILE	A319	L228	L157	R85
LEU	GLN	ALA	LEU	LEU	ALA	ALA	LEU	ARG	L320	V228	L158	R85
SER	SER	SER	GLN	PRO	GLY	GLY	LEU	SER	R328	L229	D158	L88
ASP	ASP	ASP	GLN	PRO	GLY	GLY	PRO	ILE	GLY	Q230	G159	M89
PRO	PRO	PRO	GLN	GLY	GLY	GLY	GLY	GLY	ARG	H231	M160	V90
HIS	HIS	HIS	LEU	LEU	LEU	LEU	LEU	LYS	GLY	G232	P161	A91
LEU	LEU	LEU	ASP	ASP	THR	THR	THR	PHE	GLU	I235	G162	S92
ALA	ALA	ALA	ARG	ARG	VAL	VAL	VAL	ALA	GLU	I236	K163	T93
LEU	LEU	LEU	VAL	VAL	VAL	VAL	VAL	ALA	LYS	A239	Q164	R94
LEU	LEU	LEU	SER	SER	VAL	VAL	VAL	ASP	PRO	L245	M165	I95
ARG	ARG	ARG	GLN	GLN	GLN	GLN	GLN	ASP	ALA	D249	A166	I96
SER	SER	SER	VAL	VAL	VAL	VAL	VAL	MET	PRO	G250	I167	L97
GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLY	GLY	L251	D168	M98
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	PHE	GLU	P256	A169	E99
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	PRO	I260	D170	G100
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	GLN	V259	L171	H101
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	PRO	I260	N172	T102
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	V268	A173	G103
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	ILE	S272	G174	A104
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	GLY	T273	L175	A105
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	ASN	D274	K176	A106
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	ASN	Q275	E177	A107
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	Q280	E178	G108
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	M281	D179	K109
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	Q284	E180	V110
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	R290	A181	V111
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	M292	K182	E112
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	L293	G115	A113
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	A296	H116	F114
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	G121	F117	G115
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	N122	G121	H116
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	A124	N122	F117
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	I125	F123	G121
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	F194	A124	N122
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	Y195	I125	F123
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	D199	V129	A124
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	G200	F130	I125
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	A201	I131	G121
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	S202	I132	N122
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	K203	L133	F123
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	F204	V134	A124
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	V205	I135	I125
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	R206	I136	I125
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	I213	N137	G121
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	L214	F138	F123
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	I215	M139	A124
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU	VAL	N216		I125

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51079	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 ($e^-/\text{\AA}^2$)	58.5	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.397	Depositor
Minimum map value	-0.674	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	537.6, 537.6, 537.6	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	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	A1	0.14	0/1662	0.40	1/2263 (0.0%)
1	B1	0.15	0/1662	0.39	0/2263
1	C1	0.14	0/1662	0.41	0/2263
1	D1	0.15	0/1662	0.37	0/2263
1	E1	0.14	0/1662	0.37	0/2263
2	F1	0.13	0/1974	0.30	0/2696
3	G1	0.13	0/681	0.34	0/930
3	H1	0.14	0/681	0.42	0/930
3	I1	0.14	0/681	0.36	0/930
3	J1	0.13	0/681	0.36	0/930
4	K1	0.14	0/1963	0.36	0/2647
5	A2	0.13	0/2346	0.33	0/3187
5	B2	0.13	0/2346	0.37	0/3187
5	C2	0.14	0/2346	0.38	0/3187
5	D2	0.15	0/2346	0.39	0/3187
5	E2	0.14	0/2346	0.37	0/3187
5	F2	0.14	0/2346	0.36	0/3187
5	G2	0.15	0/2346	0.39	0/3187
5	H2	0.13	0/2346	0.34	0/3187
5	I2	0.14	0/2346	0.38	0/3187
All	All	0.14	0/36085	0.37	1/49061 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	1
1	B1	0	1
1	C1	0	1
1	D1	0	1
1	E1	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	B2	0	1
5	E2	0	1
5	F2	0	1
5	H2	0	1
5	I2	0	1
All	All	0	10

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	223	LEU	CA-CB-CG	5.09	134.10	116.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	86	ASN	Peptide
1	B1	86	ASN	Peptide
1	C1	86	ASN	Peptide
1	D1	86	ASN	Peptide
1	E1	86	ASN	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1623	0	1715	55	0
1	B1	1623	0	1715	63	0
1	C1	1623	0	1715	49	0
1	D1	1623	0	1715	57	0
1	E1	1623	0	1715	54	0
2	F1	1925	0	2042	71	0
3	G1	670	0	739	35	0
3	H1	670	0	739	27	0
3	I1	670	0	739	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J1	670	0	739	20	0
4	K1	1926	0	2031	52	0
5	A2	2309	0	2450	86	0
5	B2	2309	0	2450	81	0
5	C2	2309	0	2450	82	0
5	D2	2309	0	2450	84	0
5	E2	2309	0	2450	71	0
5	F2	2309	0	2450	78	0
5	G2	2309	0	2450	86	0
5	H2	2309	0	2450	70	0
5	I2	2309	0	2450	73	0
All	All	35427	0	37654	1023	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 14.

The worst 5 of 1023 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)
5:A2:147:ARG:HD3	5:I2:203:LYS:HD3	1.48	0.92
5:C2:89:ASN:HD21	5:C2:215:ILE:HG12	1.34	0.89
1:A1:87:GLN:HB3	1:B1:59:LEU:HD11	1.57	0.87
5:E2:137:ASN:HD21	5:E2:254:GLN:HE21	1.26	0.82
1:B1:118:GLU:HG3	1:B1:120:LYS:HG2	1.61	0.82

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	A1	207/245 (84%)	197 (95%)	9 (4%)	1 (0%)	24 62

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B1	207/245 (84%)	192 (93%)	14 (7%)	1 (0%)	24	62
1	C1	207/245 (84%)	195 (94%)	11 (5%)	1 (0%)	24	62
1	D1	207/245 (84%)	196 (95%)	10 (5%)	1 (0%)	24	62
1	E1	207/245 (84%)	194 (94%)	12 (6%)	1 (0%)	24	62
2	F1	248/264 (94%)	237 (96%)	10 (4%)	1 (0%)	30	66
3	G1	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
3	H1	87/89 (98%)	83 (95%)	4 (5%)	0	100	100
3	I1	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
3	J1	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
4	K1	247/383 (64%)	235 (95%)	12 (5%)	0	100	100
5	A2	309/692 (45%)	289 (94%)	20 (6%)	0	100	100
5	B2	309/692 (45%)	287 (93%)	22 (7%)	0	100	100
5	C2	309/692 (45%)	291 (94%)	18 (6%)	0	100	100
5	D2	309/692 (45%)	288 (93%)	21 (7%)	0	100	100
5	E2	309/692 (45%)	290 (94%)	19 (6%)	0	100	100
5	F2	309/692 (45%)	291 (94%)	18 (6%)	0	100	100
5	G2	309/692 (45%)	291 (94%)	18 (6%)	0	100	100
5	H2	309/692 (45%)	294 (95%)	15 (5%)	0	100	100
5	I2	309/692 (45%)	286 (93%)	23 (7%)	0	100	100
All	All	4659/8456 (55%)	4391 (94%)	262 (6%)	6 (0%)	49	82

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A1	87	GLN
1	B1	87	GLN
1	C1	87	GLN
1	D1	87	GLN
1	E1	87	GLN

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	A1	179/204 (88%)	177 (99%)	2 (1%)	65	73
1	B1	179/204 (88%)	179 (100%)	0	100	100
1	C1	179/204 (88%)	177 (99%)	2 (1%)	65	73
1	D1	179/204 (88%)	178 (99%)	1 (1%)	78	80
1	E1	179/204 (88%)	179 (100%)	0	100	100
2	F1	207/221 (94%)	207 (100%)	0	100	100
3	G1	74/74 (100%)	74 (100%)	0	100	100
3	H1	74/74 (100%)	74 (100%)	0	100	100
3	I1	74/74 (100%)	74 (100%)	0	100	100
3	J1	74/74 (100%)	74 (100%)	0	100	100
4	K1	210/316 (66%)	209 (100%)	1 (0%)	81	81
5	A2	241/561 (43%)	240 (100%)	1 (0%)	84	82
5	B2	241/561 (43%)	240 (100%)	1 (0%)	84	82
5	C2	241/561 (43%)	241 (100%)	0	100	100
5	D2	241/561 (43%)	241 (100%)	0	100	100
5	E2	241/561 (43%)	240 (100%)	1 (0%)	84	82
5	F2	241/561 (43%)	238 (99%)	3 (1%)	63	73
5	G2	241/561 (43%)	240 (100%)	1 (0%)	84	82
5	H2	241/561 (43%)	240 (100%)	1 (0%)	84	82
5	I2	241/561 (43%)	240 (100%)	1 (0%)	84	82
All	All	3777/6902 (55%)	3762 (100%)	15 (0%)	81	82

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B2	240	GLU
5	H2	294	LEU
5	E2	291	VAL
5	I2	245	LEU
5	F2	249	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
5	G2	284	GLN
5	H2	137	ASN
4	K1	66	HIS
3	J1	39	GLN
5	H2	284	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

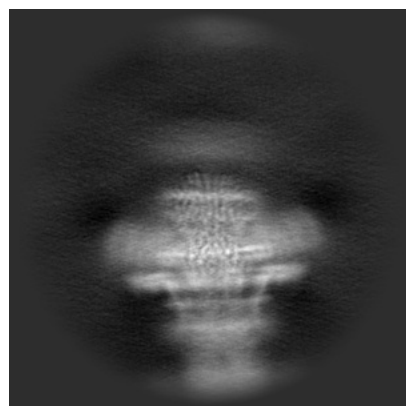
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-78907. These allow visual inspection of the internal detail of the map and identification of artifacts.

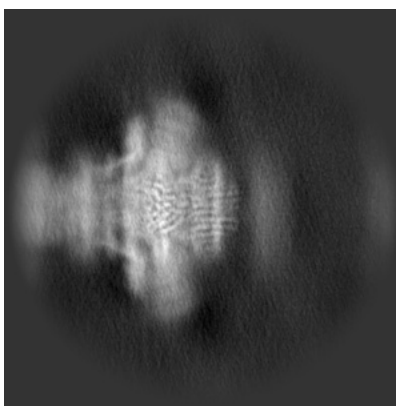
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

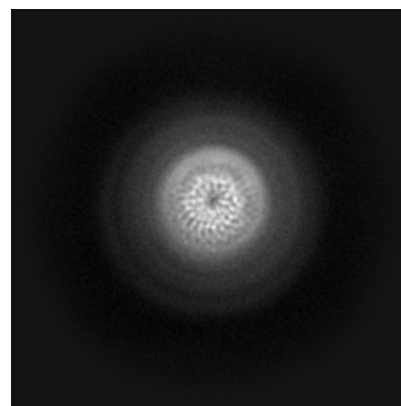
6.1.1 Primary map



X

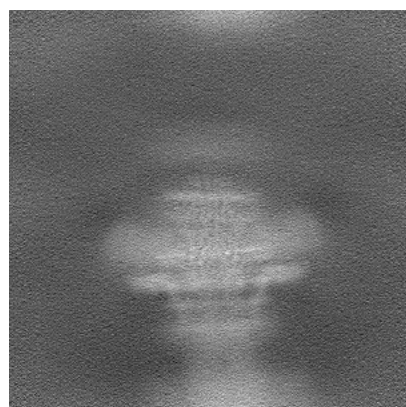


Y

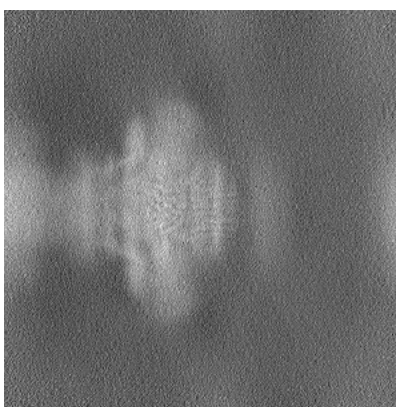


Z

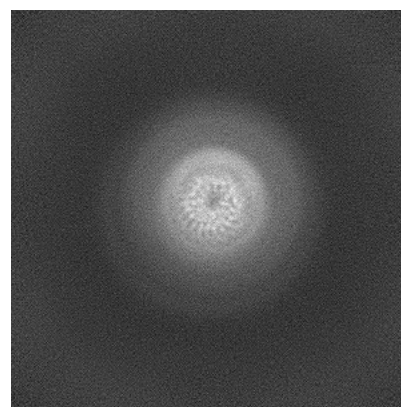
6.1.2 Raw map



X



Y

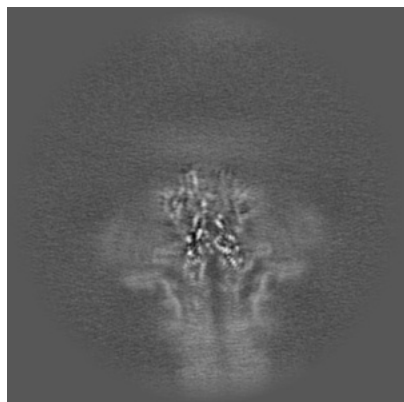


Z

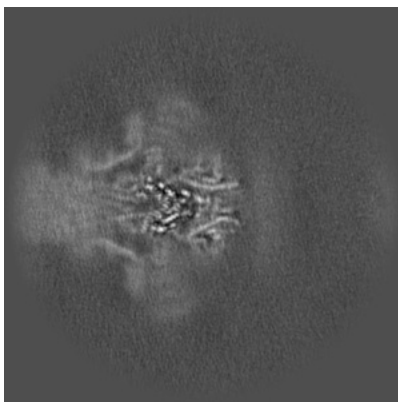
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

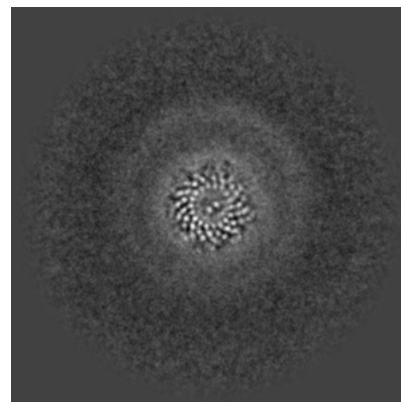
6.2.1 Primary map



X Index: 256

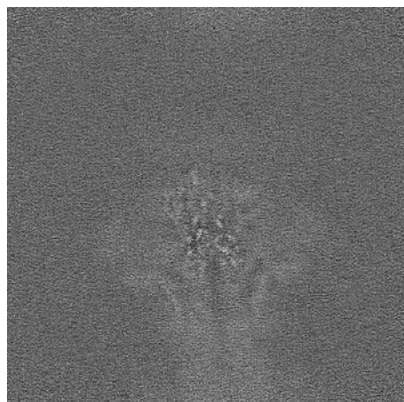


Y Index: 256

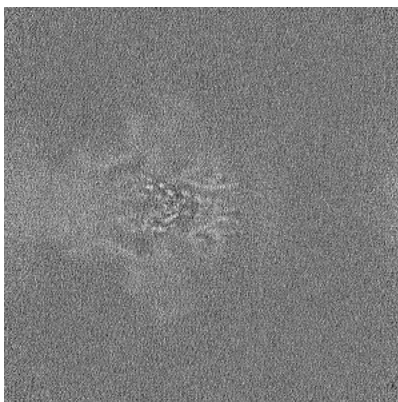


Z Index: 256

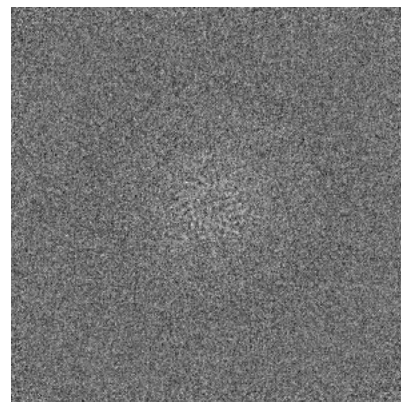
6.2.2 Raw map



X Index: 256



Y Index: 256

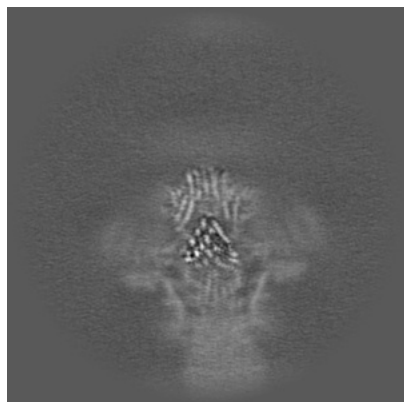


Z Index: 256

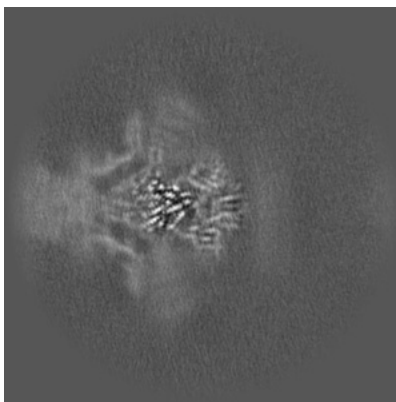
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

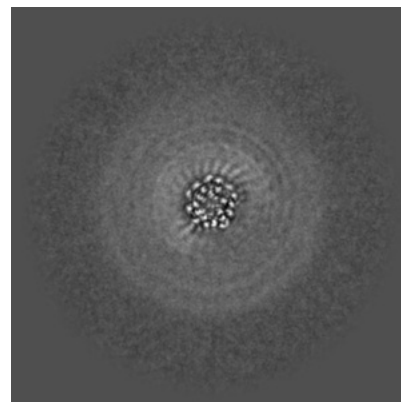
6.3.1 Primary map



X Index: 242

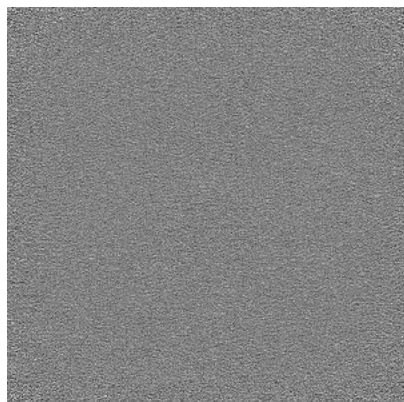


Y Index: 245

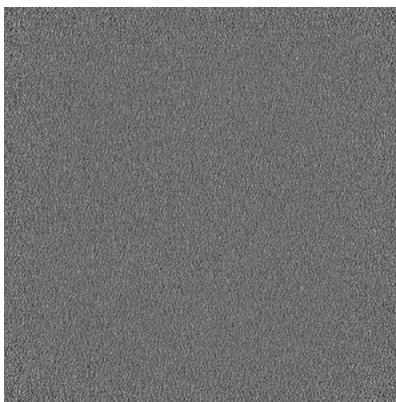


Z Index: 204

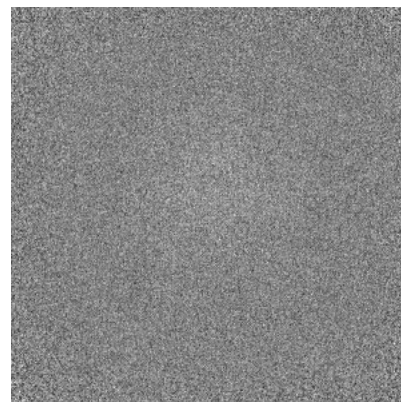
6.3.2 Raw map



X Index: 0



Y Index: 0

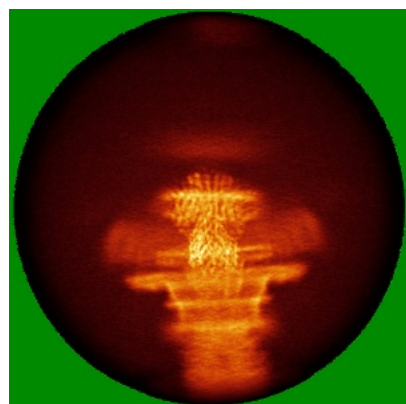


Z Index: 0

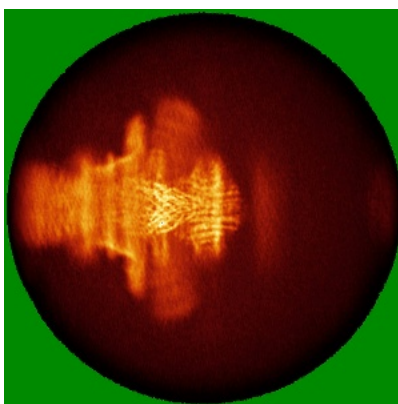
The images above show the largest variance slices of the map in three orthogonal directions.

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

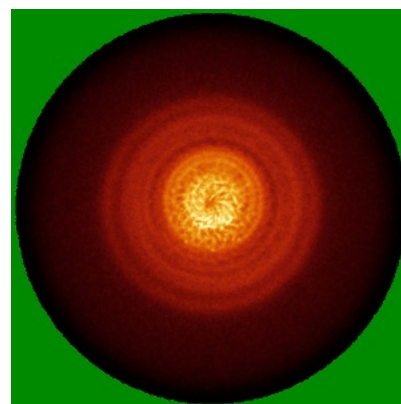
6.4.1 Primary map



X

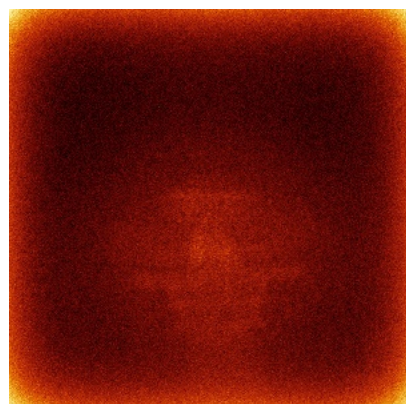


Y

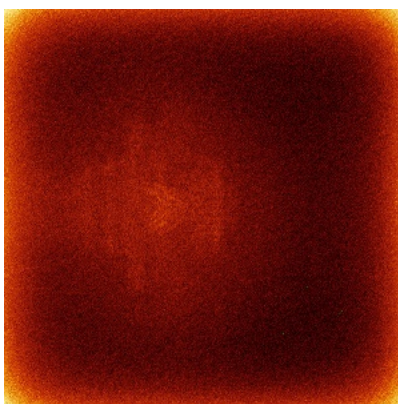


Z

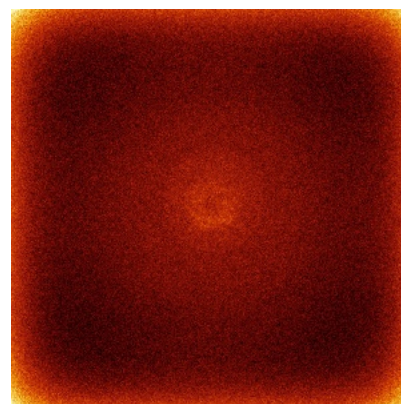
6.4.2 Raw map



X



Y

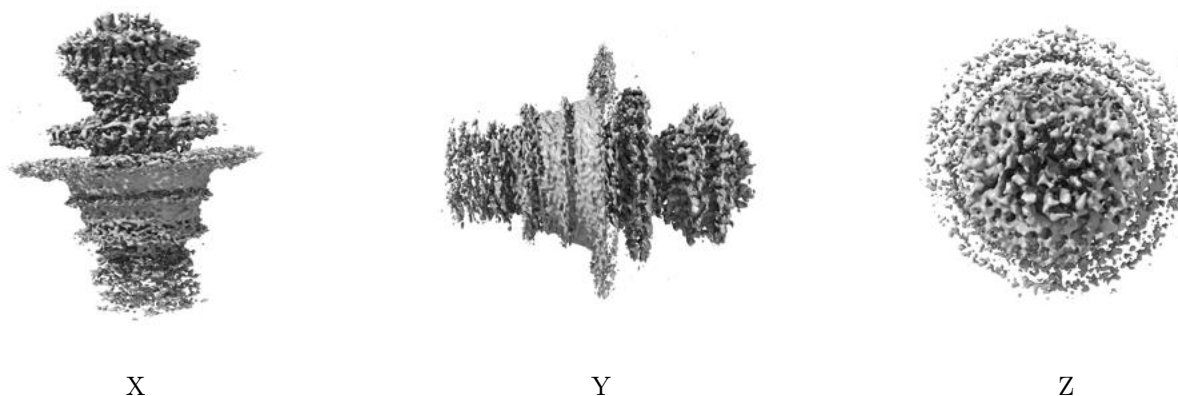


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

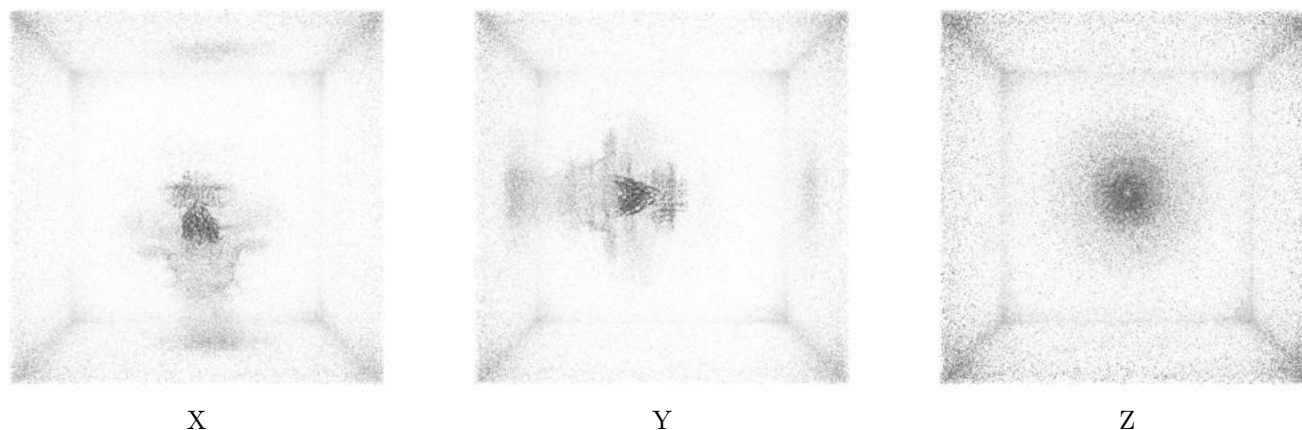
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

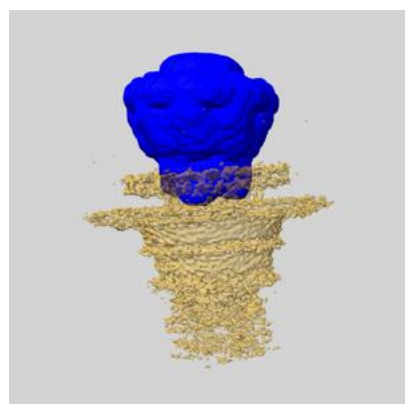
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

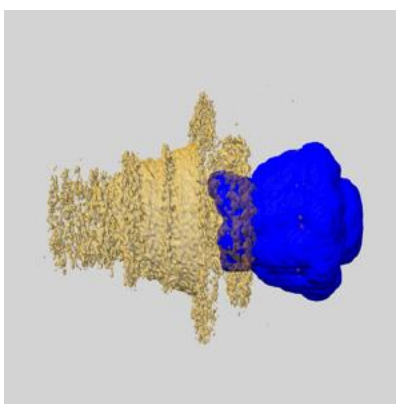
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

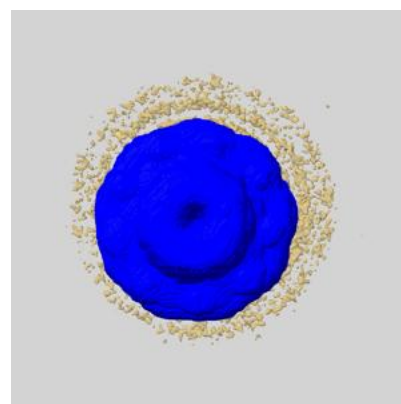
6.6.1 emd_78907_msk_1.map [i](#)



X



Y

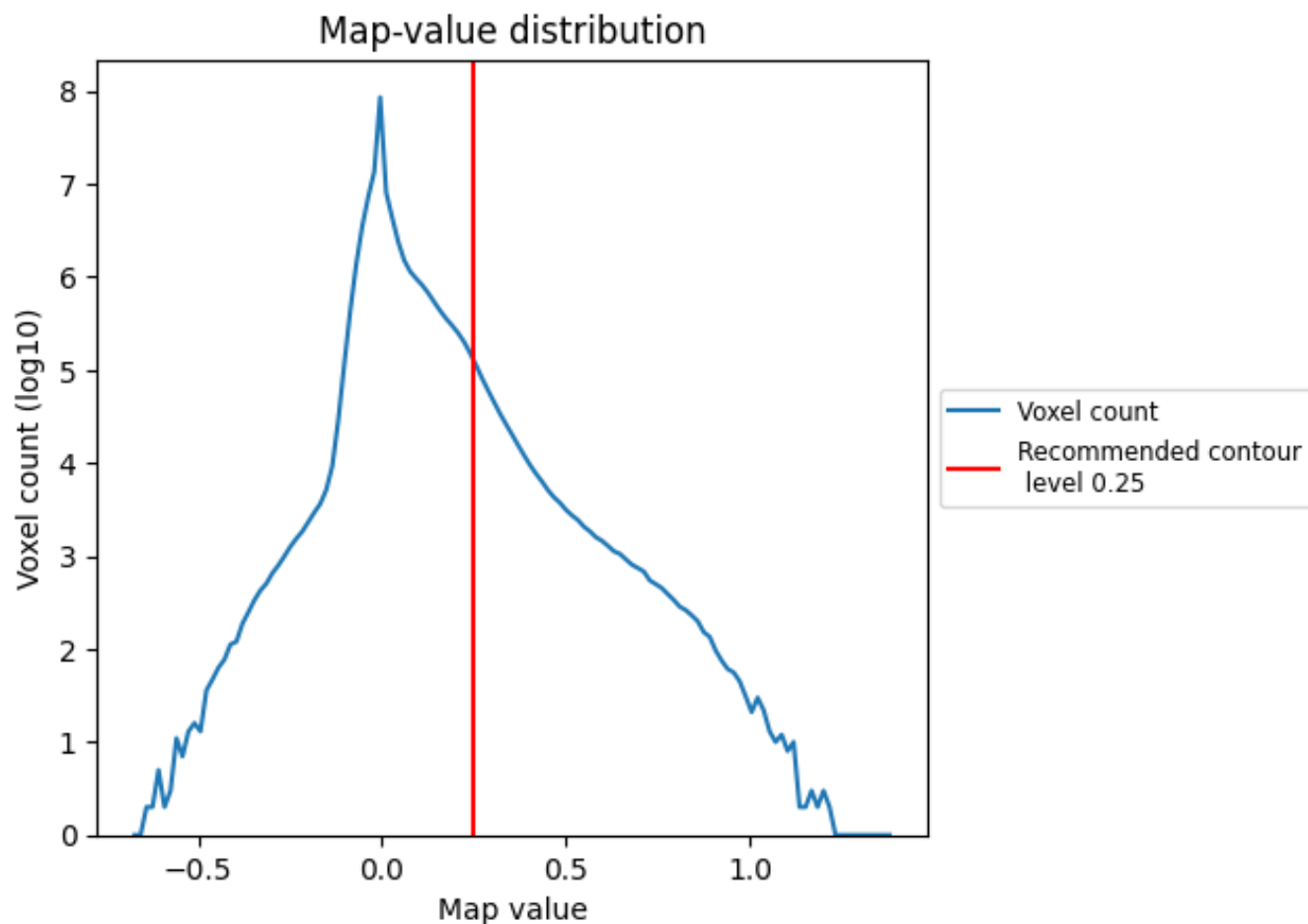


Z

7 Map analysis [i](#)

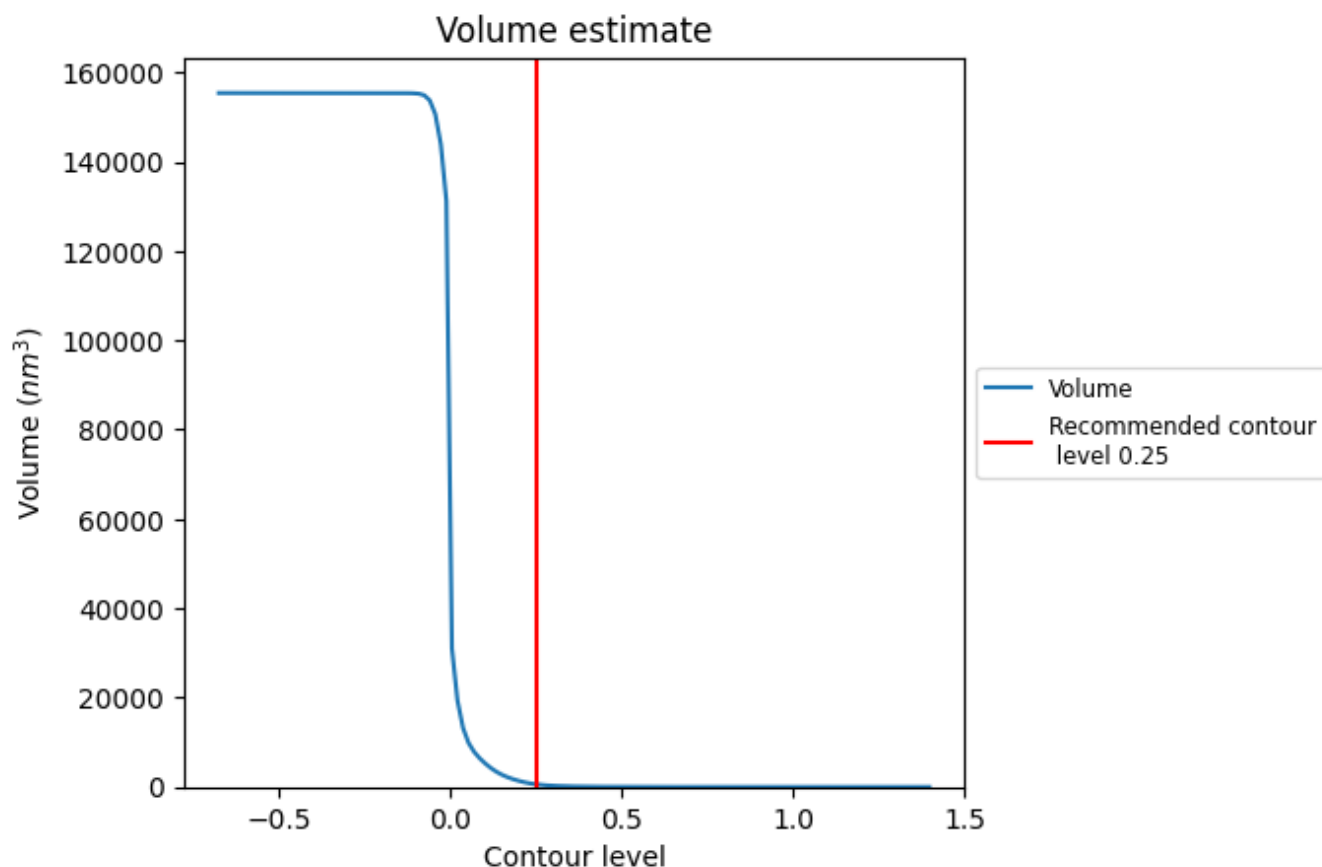
This section contains the results of statistical analysis of the map.

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.

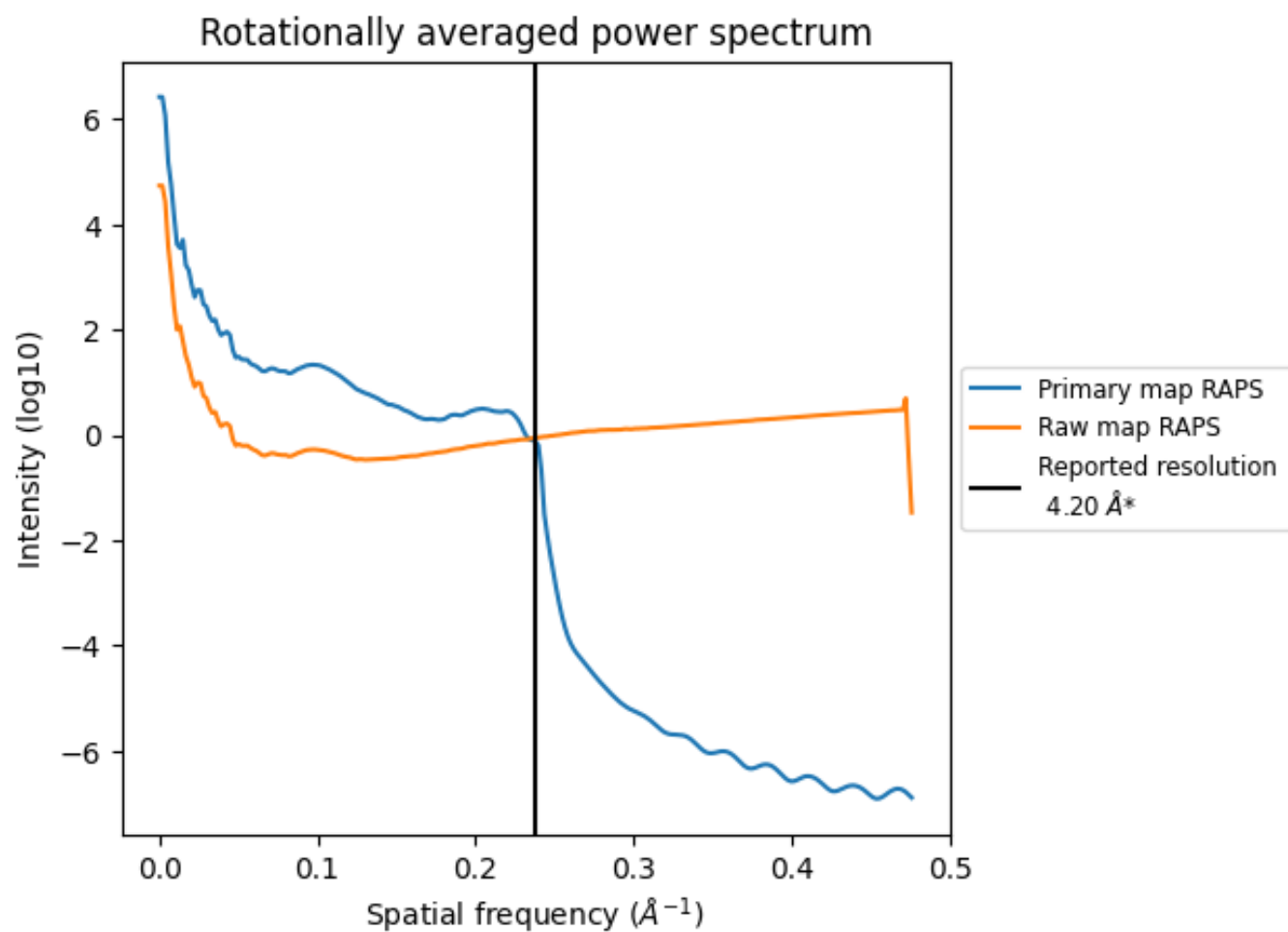
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 602 nm^3 ; this corresponds to an approximate mass of 544 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 ⓘ

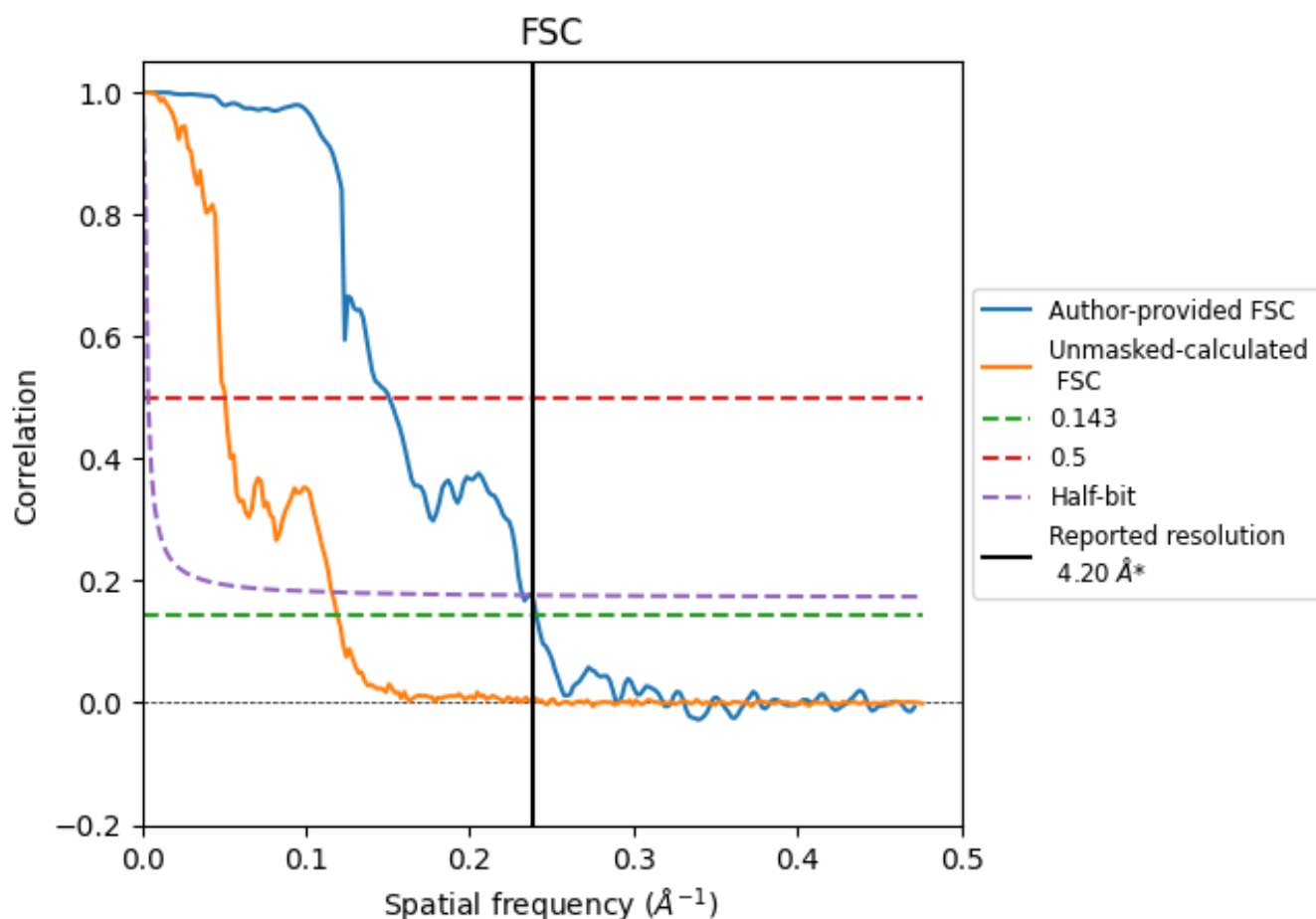


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

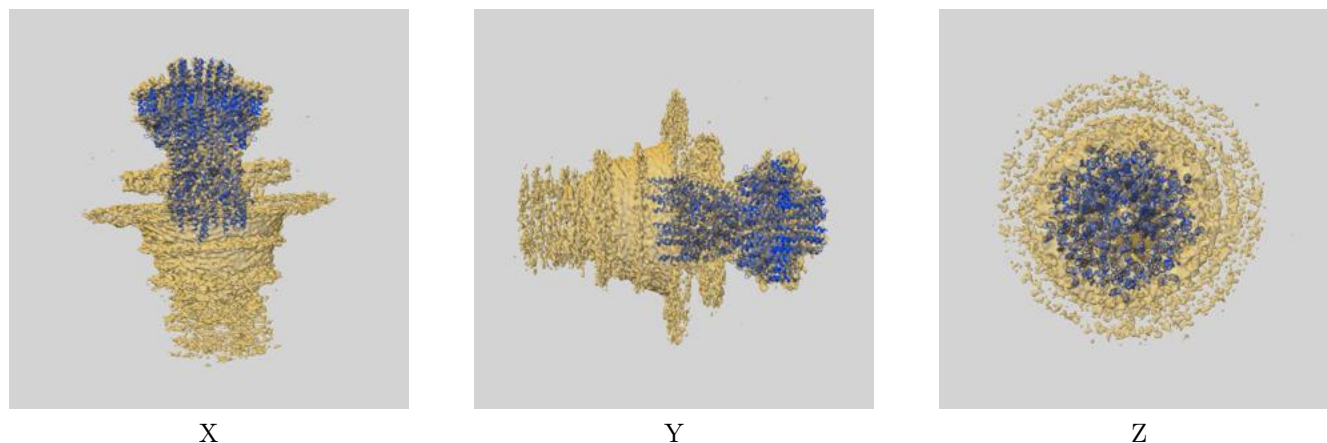
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.16	6.63	4.30
Unmasked-calculated*	8.40	19.80	8.64

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.40 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

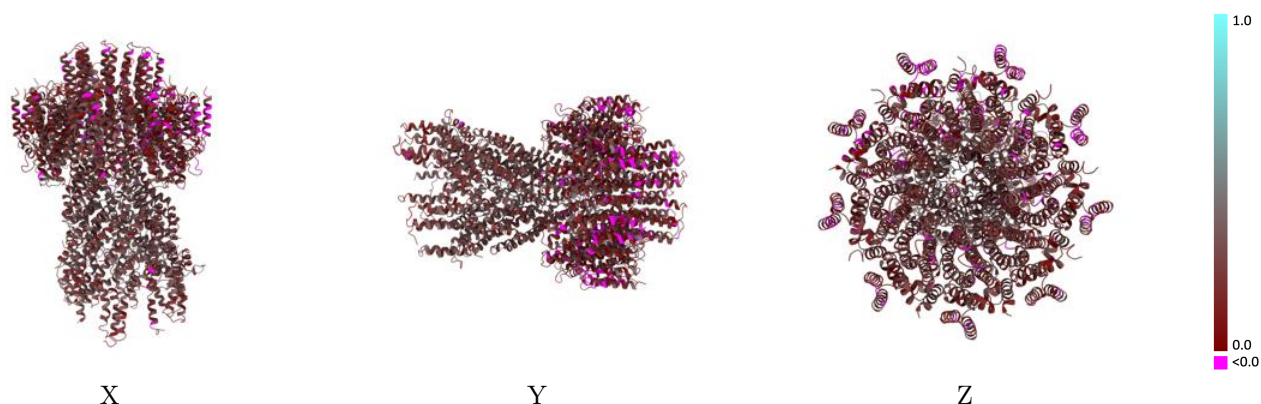
This section contains information regarding the fit between EMDB map EMD-78907 and PDB model 38LP. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



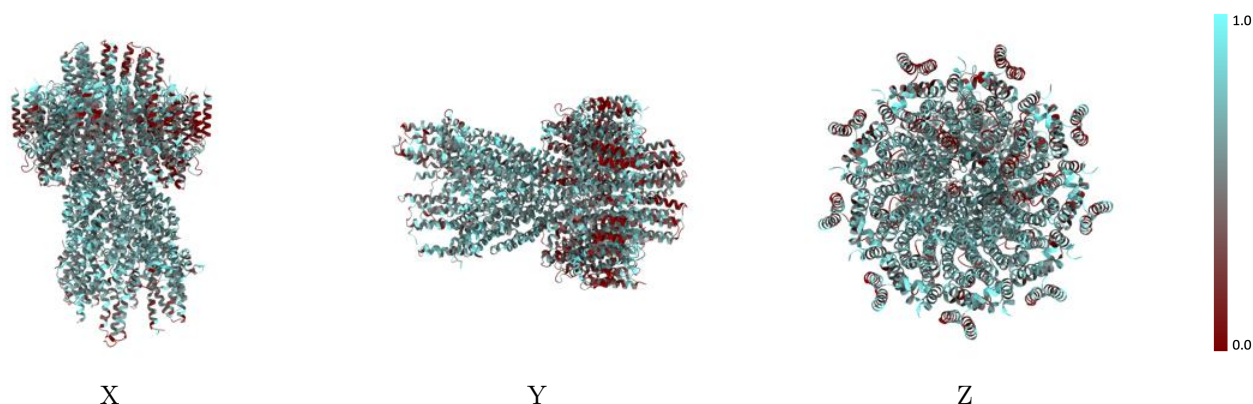
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



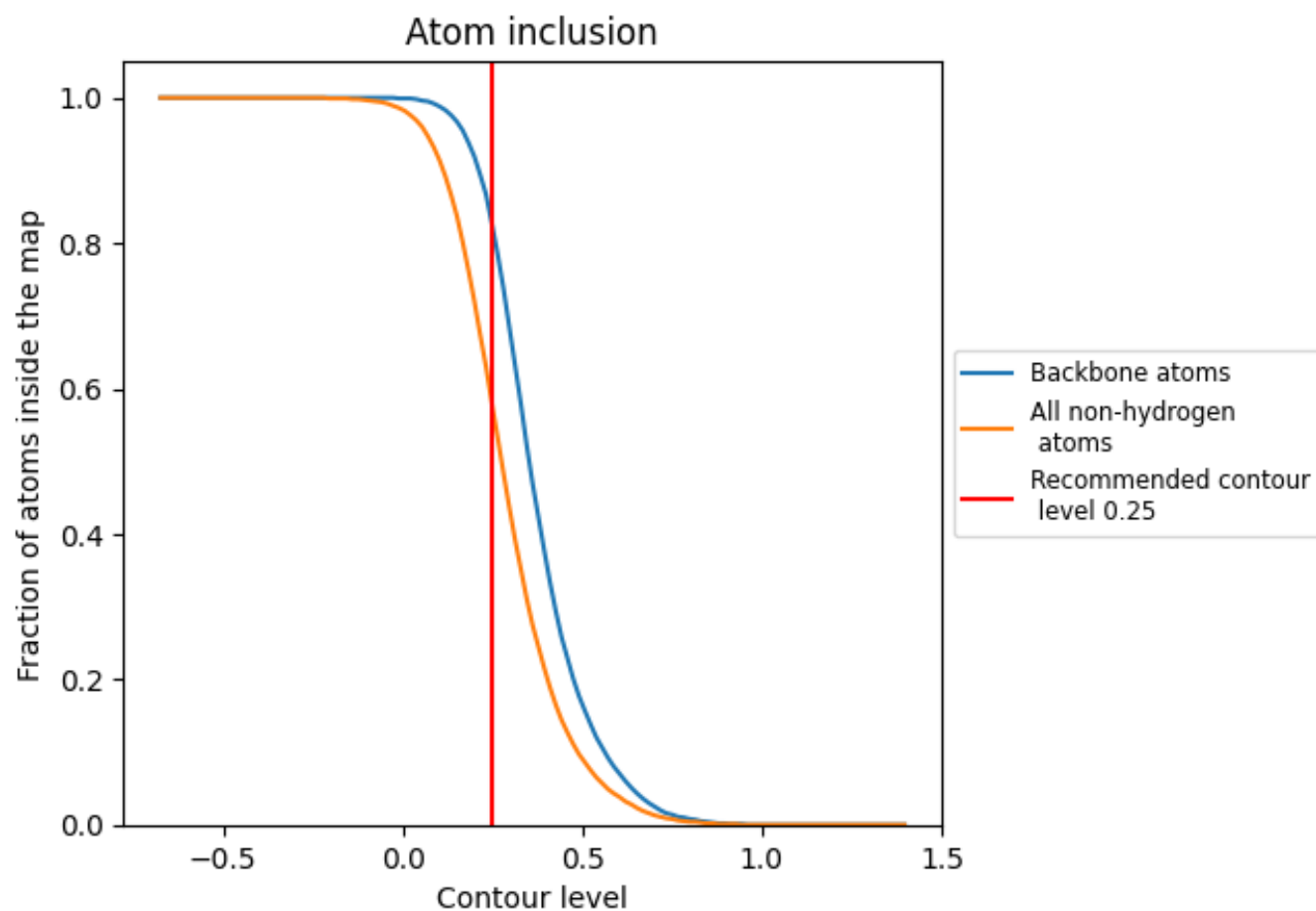
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 57% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5750	 0.2330
A1	 0.5740	 0.2890
A2	 0.5010	 0.1730
B1	 0.6100	 0.2860
B2	 0.4520	 0.1590
C1	 0.6380	 0.2930
C2	 0.5180	 0.1670
D1	 0.6480	 0.3110
D2	 0.5450	 0.1960
E1	 0.6360	 0.2960
E2	 0.5900	 0.2150
F1	 0.6130	 0.3090
F2	 0.5930	 0.2180
G1	 0.6260	 0.2890
G2	 0.5900	 0.2190
H1	 0.6450	 0.2760
H2	 0.5360	 0.2000
I1	 0.6380	 0.2750
I2	 0.5120	 0.1840
J1	 0.6500	 0.2800
K1	 0.6660	 0.2650

