



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:01 AM UTC

PDB ID : 6EJF / pdb_00006ejf
EMDB ID : EMD-3882
Title : Thermus thermophilus PilF ATPase (apoprotein form)
Authors : Derrick, J.P.; Collins, R.F.
Deposited on : 2017-09-21
Resolution : 8.00 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:

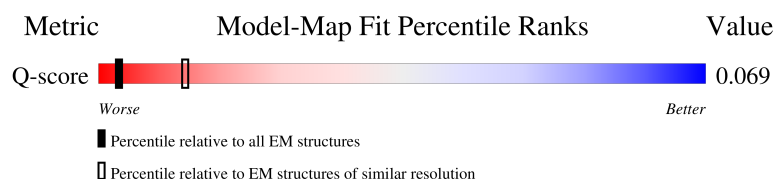
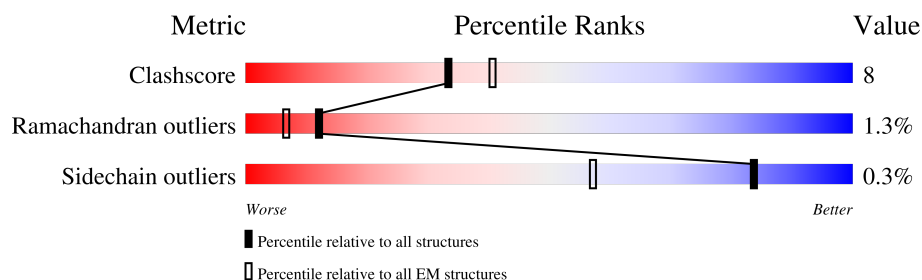
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	361 (7.50 - 8.50)

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	G	146	50% 85% 12% •
1	H	146	34% 74% 21% 5%
1	I	146	35% 73% 21% 5%
1	M	146	49% 79% 16% 5% •

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Mol	Chain	Length	Quality of chain
1	Q	146	
1	R	146	
2	J	137	
2	K	137	
2	L	137	
2	N	137	
2	O	137	
2	P	137	
3	A	409	
3	B	409	
3	C	409	
3	D	409	
3	E	409	
3	F	409	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 31260 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 Type IV pilus assembly protein PilF.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		
1	H	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		
1	I	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		
1	M	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		
1	Q	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		
1	R	146	Total	C	N	O	S	0	0
			1144	726	205	211	2		

- Molecule 2 is a protein called Type IV pilus assembly protein PilF.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	J	137	Total	C	N	O	0	0
			1091	699	190	202		
2	K	137	Total	C	N	O	0	0
			1091	699	190	202		
2	L	137	Total	C	N	O	0	0
			1091	699	190	202		
2	N	137	Total	C	N	O	0	0
			1091	699	190	202		
2	O	137	Total	C	N	O	0	0
			1091	699	190	202		
2	P	137	Total	C	N	O	0	0
			1091	699	190	202		

- Molecule 3 is a protein called Type IV pilus assembly protein PilF.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	384	Total	C	N	O	S	0	0
			2975	1874	535	556	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	383	Total	C	N	O	S	0	0
			2966	1868	534	554	10		
3	C	384	Total	C	N	O	S	0	0
			2975	1874	535	556	10		
3	D	384	Total	C	N	O	S	0	0
			2975	1874	535	556	10		
3	E	384	Total	C	N	O	S	0	0
			2975	1874	535	556	10		
3	F	385	Total	C	N	O	S	0	0
			2984	1879	536	559	10		

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	890	ALA	-	expression tag	UNP Q5SLC9
A	891	ALA	-	expression tag	UNP Q5SLC9
A	892	ALA	-	expression tag	UNP Q5SLC9
A	893	GLU	-	expression tag	UNP Q5SLC9
A	894	LEU	-	expression tag	UNP Q5SLC9
A	895	ALA	-	expression tag	UNP Q5SLC9
A	896	LEU	-	expression tag	UNP Q5SLC9
A	897	VAL	-	expression tag	UNP Q5SLC9
A	898	PRO	-	expression tag	UNP Q5SLC9
A	899	ARG	-	expression tag	UNP Q5SLC9
A	900	GLY	-	expression tag	UNP Q5SLC9
A	901	SER	-	expression tag	UNP Q5SLC9
A	902	SER	-	expression tag	UNP Q5SLC9
A	903	ALA	-	expression tag	UNP Q5SLC9
A	904	HIS	-	expression tag	UNP Q5SLC9
A	905	HIS	-	expression tag	UNP Q5SLC9
A	906	HIS	-	expression tag	UNP Q5SLC9
A	907	HIS	-	expression tag	UNP Q5SLC9
A	908	HIS	-	expression tag	UNP Q5SLC9
A	909	HIS	-	expression tag	UNP Q5SLC9
A	910	HIS	-	expression tag	UNP Q5SLC9
A	911	HIS	-	expression tag	UNP Q5SLC9
A	912	HIS	-	expression tag	UNP Q5SLC9
A	913	HIS	-	expression tag	UNP Q5SLC9
B	890	ALA	-	expression tag	UNP Q5SLC9
B	891	ALA	-	expression tag	UNP Q5SLC9
B	892	ALA	-	expression tag	UNP Q5SLC9
B	893	GLU	-	expression tag	UNP Q5SLC9
B	894	LEU	-	expression tag	UNP Q5SLC9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	895	ALA	-	expression tag	UNP Q5SLC9
B	896	LEU	-	expression tag	UNP Q5SLC9
B	897	VAL	-	expression tag	UNP Q5SLC9
B	898	PRO	-	expression tag	UNP Q5SLC9
B	899	ARG	-	expression tag	UNP Q5SLC9
B	900	GLY	-	expression tag	UNP Q5SLC9
B	901	SER	-	expression tag	UNP Q5SLC9
B	902	SER	-	expression tag	UNP Q5SLC9
B	903	ALA	-	expression tag	UNP Q5SLC9
B	904	HIS	-	expression tag	UNP Q5SLC9
B	905	HIS	-	expression tag	UNP Q5SLC9
B	906	HIS	-	expression tag	UNP Q5SLC9
B	907	HIS	-	expression tag	UNP Q5SLC9
B	908	HIS	-	expression tag	UNP Q5SLC9
B	909	HIS	-	expression tag	UNP Q5SLC9
B	910	HIS	-	expression tag	UNP Q5SLC9
B	911	HIS	-	expression tag	UNP Q5SLC9
B	912	HIS	-	expression tag	UNP Q5SLC9
B	913	HIS	-	expression tag	UNP Q5SLC9
C	890	ALA	-	expression tag	UNP Q5SLC9
C	891	ALA	-	expression tag	UNP Q5SLC9
C	892	ALA	-	expression tag	UNP Q5SLC9
C	893	GLU	-	expression tag	UNP Q5SLC9
C	894	LEU	-	expression tag	UNP Q5SLC9
C	895	ALA	-	expression tag	UNP Q5SLC9
C	896	LEU	-	expression tag	UNP Q5SLC9
C	897	VAL	-	expression tag	UNP Q5SLC9
C	898	PRO	-	expression tag	UNP Q5SLC9
C	899	ARG	-	expression tag	UNP Q5SLC9
C	900	GLY	-	expression tag	UNP Q5SLC9
C	901	SER	-	expression tag	UNP Q5SLC9
C	902	SER	-	expression tag	UNP Q5SLC9
C	903	ALA	-	expression tag	UNP Q5SLC9
C	904	HIS	-	expression tag	UNP Q5SLC9
C	905	HIS	-	expression tag	UNP Q5SLC9
C	906	HIS	-	expression tag	UNP Q5SLC9
C	907	HIS	-	expression tag	UNP Q5SLC9
C	908	HIS	-	expression tag	UNP Q5SLC9
C	909	HIS	-	expression tag	UNP Q5SLC9
C	910	HIS	-	expression tag	UNP Q5SLC9
C	911	HIS	-	expression tag	UNP Q5SLC9
C	912	HIS	-	expression tag	UNP Q5SLC9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	913	HIS	-	expression tag	UNP Q5SLC9
D	890	ALA	-	expression tag	UNP Q5SLC9
D	891	ALA	-	expression tag	UNP Q5SLC9
D	892	ALA	-	expression tag	UNP Q5SLC9
D	893	GLU	-	expression tag	UNP Q5SLC9
D	894	LEU	-	expression tag	UNP Q5SLC9
D	895	ALA	-	expression tag	UNP Q5SLC9
D	896	LEU	-	expression tag	UNP Q5SLC9
D	897	VAL	-	expression tag	UNP Q5SLC9
D	898	PRO	-	expression tag	UNP Q5SLC9
D	899	ARG	-	expression tag	UNP Q5SLC9
D	900	GLY	-	expression tag	UNP Q5SLC9
D	901	SER	-	expression tag	UNP Q5SLC9
D	902	SER	-	expression tag	UNP Q5SLC9
D	903	ALA	-	expression tag	UNP Q5SLC9
D	904	HIS	-	expression tag	UNP Q5SLC9
D	905	HIS	-	expression tag	UNP Q5SLC9
D	906	HIS	-	expression tag	UNP Q5SLC9
D	907	HIS	-	expression tag	UNP Q5SLC9
D	908	HIS	-	expression tag	UNP Q5SLC9
D	909	HIS	-	expression tag	UNP Q5SLC9
D	910	HIS	-	expression tag	UNP Q5SLC9
D	911	HIS	-	expression tag	UNP Q5SLC9
D	912	HIS	-	expression tag	UNP Q5SLC9
D	913	HIS	-	expression tag	UNP Q5SLC9
E	890	ALA	-	expression tag	UNP Q5SLC9
E	891	ALA	-	expression tag	UNP Q5SLC9
E	892	ALA	-	expression tag	UNP Q5SLC9
E	893	GLU	-	expression tag	UNP Q5SLC9
E	894	LEU	-	expression tag	UNP Q5SLC9
E	895	ALA	-	expression tag	UNP Q5SLC9
E	896	LEU	-	expression tag	UNP Q5SLC9
E	897	VAL	-	expression tag	UNP Q5SLC9
E	898	PRO	-	expression tag	UNP Q5SLC9
E	899	ARG	-	expression tag	UNP Q5SLC9
E	900	GLY	-	expression tag	UNP Q5SLC9
E	901	SER	-	expression tag	UNP Q5SLC9
E	902	SER	-	expression tag	UNP Q5SLC9
E	903	ALA	-	expression tag	UNP Q5SLC9
E	904	HIS	-	expression tag	UNP Q5SLC9
E	905	HIS	-	expression tag	UNP Q5SLC9
E	906	HIS	-	expression tag	UNP Q5SLC9

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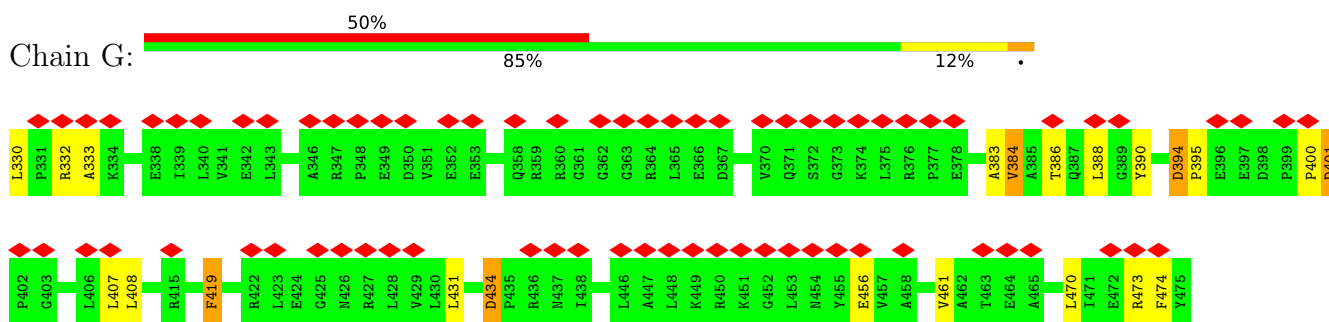
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Chain	Residue	Modelled	Actual	Comment	Reference
E	907	HIS	-	expression tag	UNP Q5SLC9
E	908	HIS	-	expression tag	UNP Q5SLC9
E	909	HIS	-	expression tag	UNP Q5SLC9
E	910	HIS	-	expression tag	UNP Q5SLC9
E	911	HIS	-	expression tag	UNP Q5SLC9
E	912	HIS	-	expression tag	UNP Q5SLC9
E	913	HIS	-	expression tag	UNP Q5SLC9
F	890	ALA	-	expression tag	UNP Q5SLC9
F	891	ALA	-	expression tag	UNP Q5SLC9
F	892	ALA	-	expression tag	UNP Q5SLC9
F	893	GLU	-	expression tag	UNP Q5SLC9
F	894	LEU	-	expression tag	UNP Q5SLC9
F	895	ALA	-	expression tag	UNP Q5SLC9
F	896	LEU	-	expression tag	UNP Q5SLC9
F	897	VAL	-	expression tag	UNP Q5SLC9
F	898	PRO	-	expression tag	UNP Q5SLC9
F	899	ARG	-	expression tag	UNP Q5SLC9
F	900	GLY	-	expression tag	UNP Q5SLC9
F	901	SER	-	expression tag	UNP Q5SLC9
F	902	SER	-	expression tag	UNP Q5SLC9
F	903	ALA	-	expression tag	UNP Q5SLC9
F	904	HIS	-	expression tag	UNP Q5SLC9
F	905	HIS	-	expression tag	UNP Q5SLC9
F	906	HIS	-	expression tag	UNP Q5SLC9
F	907	HIS	-	expression tag	UNP Q5SLC9
F	908	HIS	-	expression tag	UNP Q5SLC9
F	909	HIS	-	expression tag	UNP Q5SLC9
F	910	HIS	-	expression tag	UNP Q5SLC9
F	911	HIS	-	expression tag	UNP Q5SLC9
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F	913	HIS	-	expression tag	UNP Q5SLC9

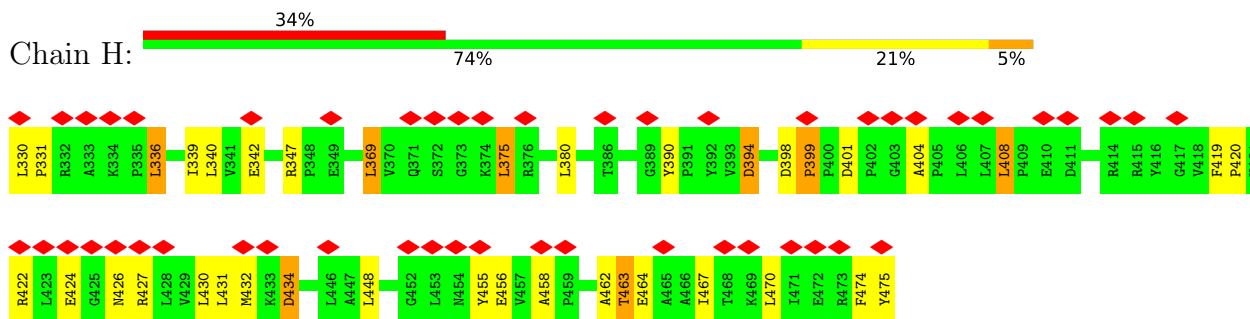
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

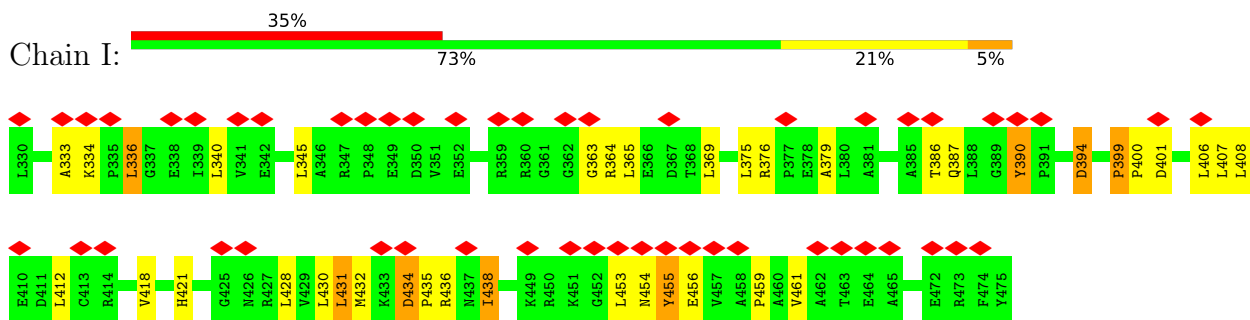
- Molecule 1: Type IV pilus assembly protein PilF



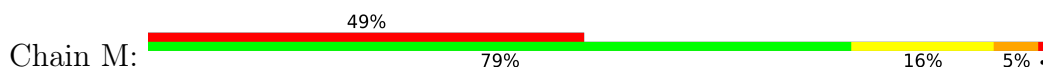
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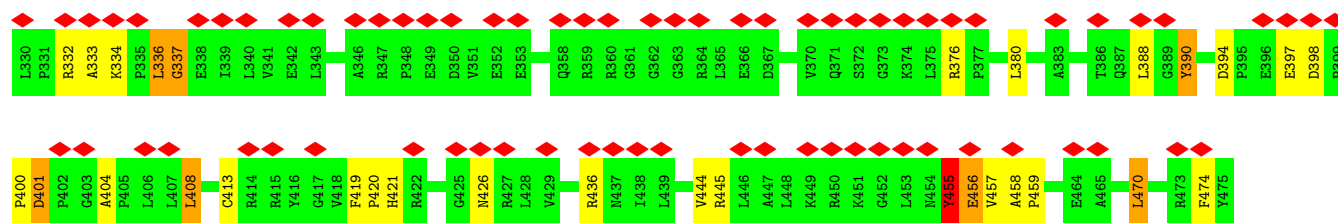


- Molecule 1: Type IV pilus assembly protein PilF

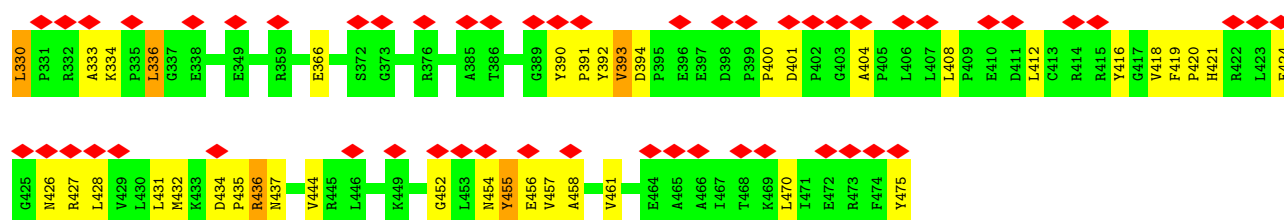
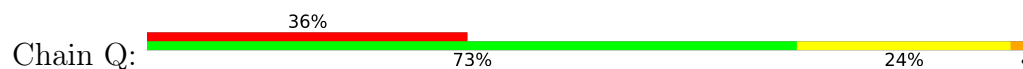


- Molecule 1: Type IV pilus assembly protein PilF

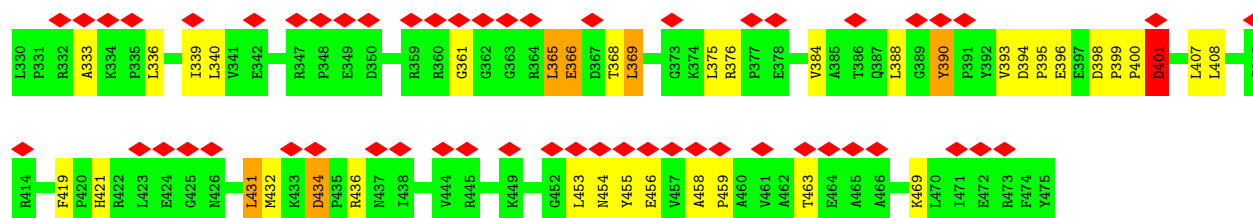
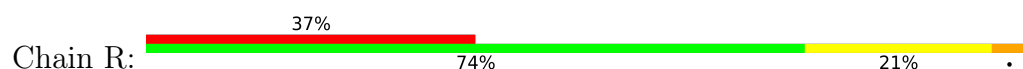




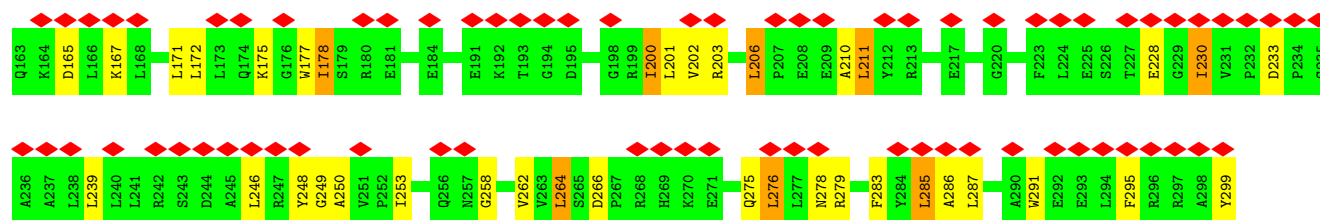
• Molecule 1: Type IV pilus assembly protein PilF



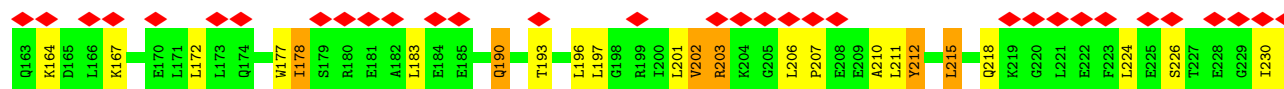
• Molecule 1: Type IV pilus assembly protein PilF

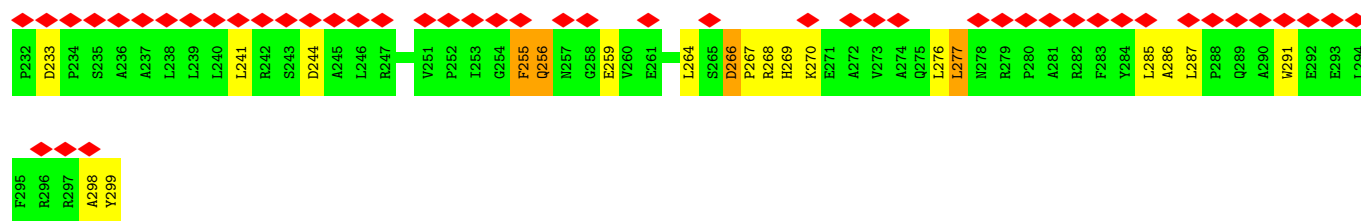


• Molecule 2: Type IV pilus assembly protein PilF

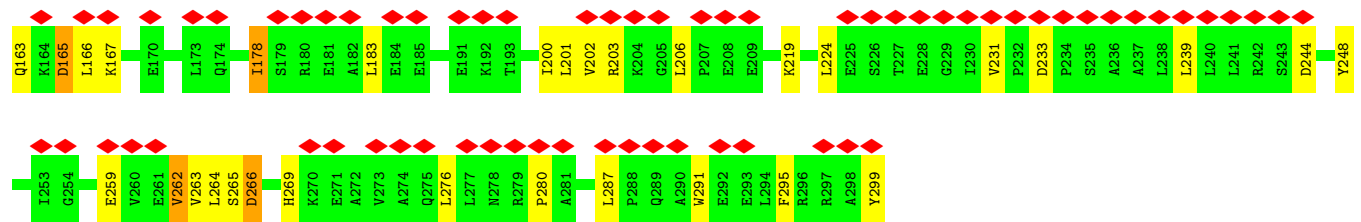
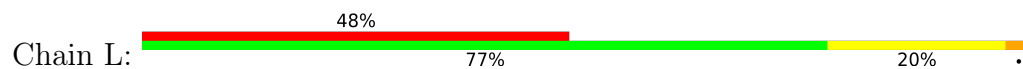


• Molecule 2: Type IV pilus assembly protein PilF

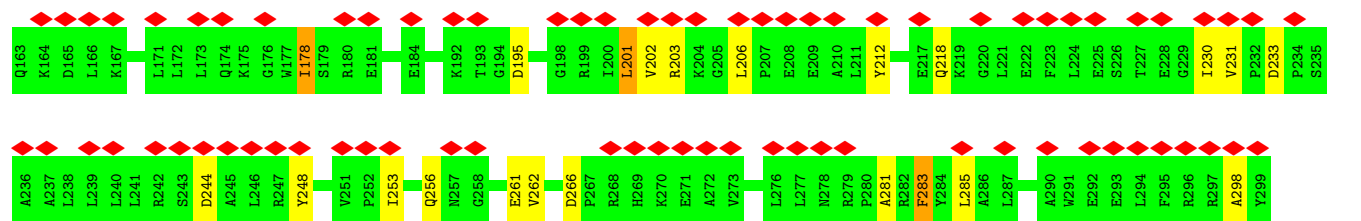
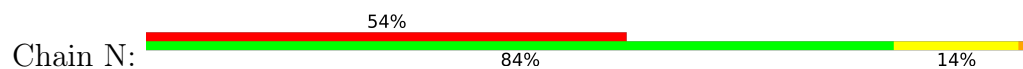




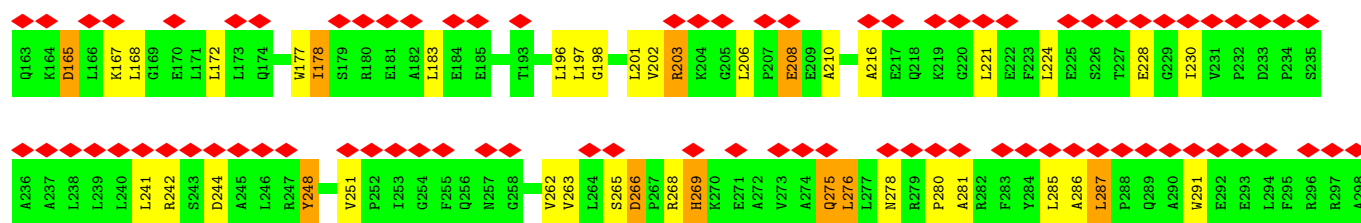
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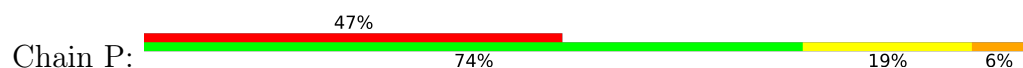
• Molecule 2: Type IV pilus assembly protein PilF



• Molecule 2: Type IV pilus assembly protein PilF

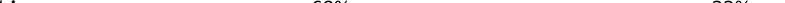


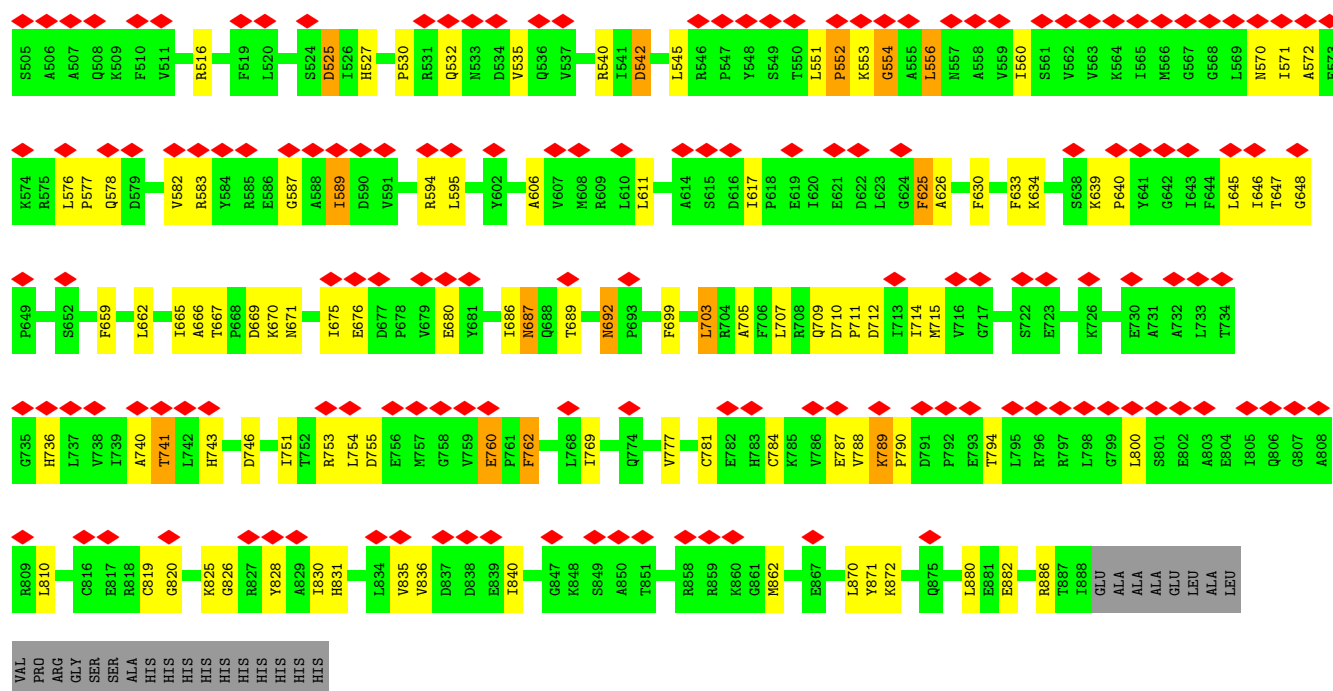
• Molecule 2: Type IV pilus assembly protein PilF



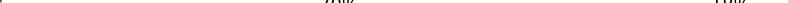


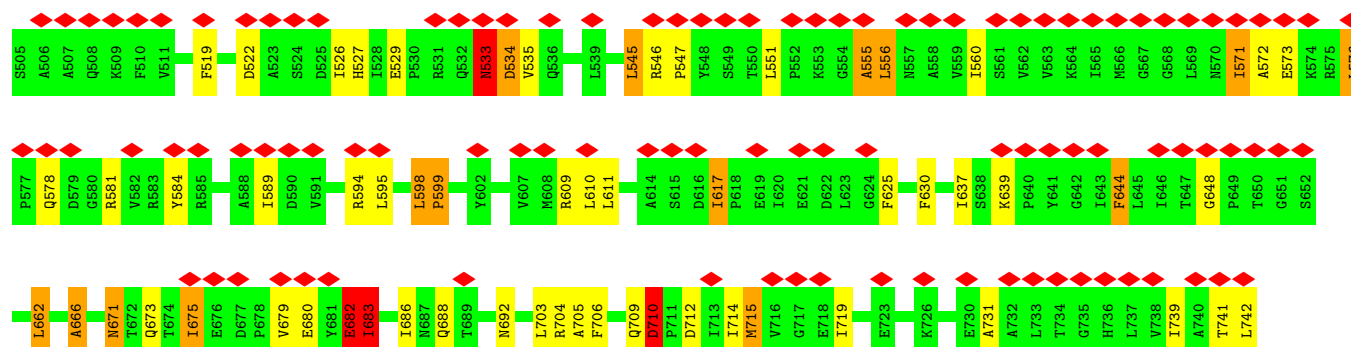
- Molecule 3: Type IV pilus assembly protein PilF

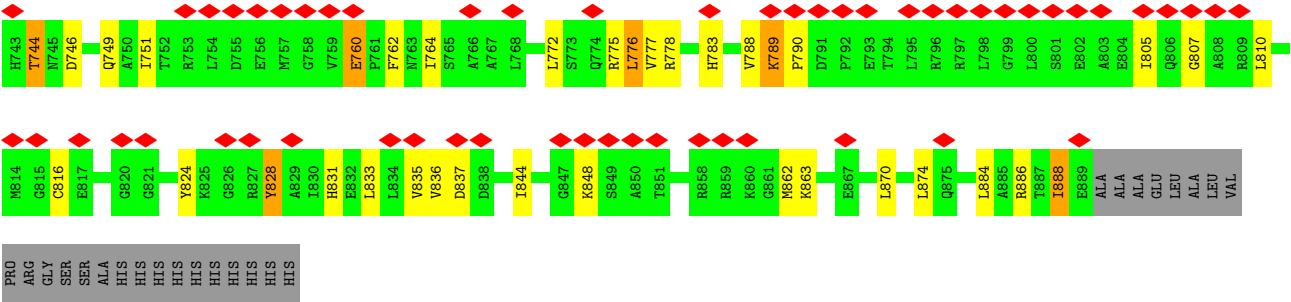
Chain E:  37% 68% 22% 6%



- Molecule 3: Type IV pilus assembly protein PilF

Chain F: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	6.449	Depositor
Minimum map value	-4.043	Depositor
Average map value	0.033	Depositor
Map value standard deviation	0.367	Depositor
Recommended contour level	1.9	Depositor
Map size (Å)	307.2, 307.2, 307.2	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6, 1.6, 1.6	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	G	1.26	4/1165 (0.3%)	1.55	21/1580 (1.3%)
1	H	1.38	8/1165 (0.7%)	1.61	25/1580 (1.6%)
1	I	1.33	5/1165 (0.4%)	1.57	29/1580 (1.8%)
1	M	1.25	2/1165 (0.2%)	1.48	20/1580 (1.3%)
1	Q	1.36	4/1165 (0.3%)	1.55	25/1580 (1.6%)
1	R	1.30	9/1165 (0.8%)	1.54	23/1580 (1.5%)
2	J	1.27	9/1110 (0.8%)	1.61	26/1499 (1.7%)
2	K	1.44	9/1110 (0.8%)	1.57	23/1499 (1.5%)
2	L	1.27	5/1110 (0.5%)	1.54	21/1499 (1.4%)
2	N	1.23	3/1110 (0.3%)	1.50	20/1499 (1.3%)
2	O	1.35	9/1110 (0.8%)	1.63	21/1499 (1.4%)
2	P	1.45	14/1110 (1.3%)	1.56	18/1499 (1.2%)
3	A	1.56	39/3017 (1.3%)	1.63	62/4073 (1.5%)
3	B	1.48	19/3008 (0.6%)	1.64	66/4061 (1.6%)
3	C	1.62	38/3017 (1.3%)	1.70	71/4073 (1.7%)
3	D	1.58	42/3017 (1.4%)	1.70	78/4073 (1.9%)
3	E	1.44	17/3017 (0.6%)	1.59	69/4073 (1.7%)
3	F	1.51	31/3026 (1.0%)	1.62	61/4085 (1.5%)
All	All	1.45	267/31752 (0.8%)	1.61	679/42912 (1.6%)

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	M	0	1
1	Q	0	1
2	P	0	1
3	C	0	4
3	D	0	8
3	E	0	2
3	F	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	23

The worst 5 of 267 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	556	LEU	CB-CG	-13.56	1.26	1.53
3	C	810	LEU	CB-CG	-13.52	1.26	1.53
2	P	285	LEU	CB-CG	-13.11	1.27	1.53
3	A	662	LEU	CB-CG	-10.52	1.32	1.53
3	D	775	ARG	CD-NE	-10.47	1.31	1.46

The worst 5 of 679 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	625	PHE	CA-CB-CG	14.00	127.80	113.80
3	E	576	LEU	CA-C-N	12.37	132.52	119.90
3	E	576	LEU	C-N-CA	12.37	132.52	119.90
3	C	712	ASP	N-CA-C	-12.05	98.06	113.12
1	H	426	ASN	CA-CB-CG	11.06	123.66	112.60

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	506	ALA	Mainchain,Peptide
3	C	684	PRO	Mainchain
1	M	455	TYR	Sidechain
2	P	212	TYR	Sidechain
1	Q	416	TYR	Sidechain

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	G	1144	0	1182	10	0
1	H	1144	0	1182	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	1144	0	1182	20	0
1	M	1144	0	1182	13	0
1	Q	1144	0	1182	23	0
1	R	1144	0	1182	14	0
2	J	1091	0	1117	22	0
2	K	1091	0	1117	28	0
2	L	1091	0	1117	22	0
2	N	1091	0	1117	10	0
2	O	1091	0	1117	31	0
2	P	1091	0	1117	19	0
3	A	2975	0	3080	55	0
3	B	2966	0	3066	43	0
3	C	2975	0	3080	69	0
3	D	2975	0	3080	54	0
3	E	2975	0	3080	41	0
3	F	2984	0	3084	43	0
All	All	31260	0	32264	526	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 526 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)
2:J:276:LEU:O	2:J:276:LEU:HD23	1.39	1.17
1:Q:393:VAL:O	1:Q:393:VAL:HG13	1.46	1.05
2:O:263:VAL:HG23	2:O:263:VAL:O	1.73	0.87
2:L:219:LYS:O	2:L:219:LYS:HG3	1.75	0.85
3:F:710:ASP:O	3:F:710:ASP:OD2	1.96	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	G	144/146 (99%)	135 (94%)	8 (6%)	1 (1%)	18	56
1	H	144/146 (99%)	132 (92%)	8 (6%)	4 (3%)	4	24
1	I	144/146 (99%)	131 (91%)	12 (8%)	1 (1%)	18	56
1	M	144/146 (99%)	132 (92%)	9 (6%)	3 (2%)	5	30
1	Q	144/146 (99%)	130 (90%)	8 (6%)	6 (4%)	2	17
1	R	144/146 (99%)	126 (88%)	13 (9%)	5 (4%)	3	20
2	J	135/137 (98%)	124 (92%)	9 (7%)	2 (2%)	8	40
2	K	135/137 (98%)	123 (91%)	9 (7%)	3 (2%)	5	29
2	L	135/137 (98%)	118 (87%)	15 (11%)	2 (2%)	8	40
2	N	135/137 (98%)	126 (93%)	9 (7%)	0	100	100
2	O	135/137 (98%)	124 (92%)	8 (6%)	3 (2%)	5	29
2	P	135/137 (98%)	122 (90%)	11 (8%)	2 (2%)	8	40
3	A	382/409 (93%)	365 (96%)	16 (4%)	1 (0%)	36	72
3	B	381/409 (93%)	363 (95%)	16 (4%)	2 (0%)	24	63
3	C	382/409 (93%)	363 (95%)	15 (4%)	4 (1%)	12	49
3	D	382/409 (93%)	361 (94%)	17 (4%)	4 (1%)	12	49
3	E	382/409 (93%)	363 (95%)	16 (4%)	3 (1%)	16	54
3	F	383/409 (94%)	362 (94%)	15 (4%)	6 (2%)	7	38
All	All	3966/4152 (96%)	3700 (93%)	214 (5%)	52 (1%)	12	42

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	456	GLU
2	K	203	ARG
1	H	399	PRO
1	H	422	ARG
1	H	455	TYR

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	G	120/120 (100%)	120 (100%)	0	100	100
1	H	120/120 (100%)	119 (99%)	1 (1%)	73	80
1	I	120/120 (100%)	118 (98%)	2 (2%)	53	69
1	M	120/120 (100%)	119 (99%)	1 (1%)	73	80
1	Q	120/120 (100%)	120 (100%)	0	100	100
1	R	120/120 (100%)	120 (100%)	0	100	100
2	J	112/112 (100%)	112 (100%)	0	100	100
2	K	112/112 (100%)	110 (98%)	2 (2%)	51	68
2	L	112/112 (100%)	112 (100%)	0	100	100
2	N	112/112 (100%)	112 (100%)	0	100	100
2	O	112/112 (100%)	111 (99%)	1 (1%)	70	79
2	P	112/112 (100%)	112 (100%)	0	100	100
3	A	317/336 (94%)	316 (100%)	1 (0%)	86	86
3	B	315/336 (94%)	315 (100%)	0	100	100
3	C	317/336 (94%)	316 (100%)	1 (0%)	86	86
3	D	317/336 (94%)	316 (100%)	1 (0%)	86	86
3	E	317/336 (94%)	317 (100%)	0	100	100
3	F	318/336 (95%)	318 (100%)	0	100	100
All	All	3293/3408 (97%)	3283 (100%)	10 (0%)	84	86

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	879	THR
3	C	519	PHE
3	D	551	LEU
1	I	336	LEU
1	I	438	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	745	ASN

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Mol	Chain	Res	Type
3	D	745	ASN
3	E	875	GLN
3	D	783	HIS
1	H	454	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

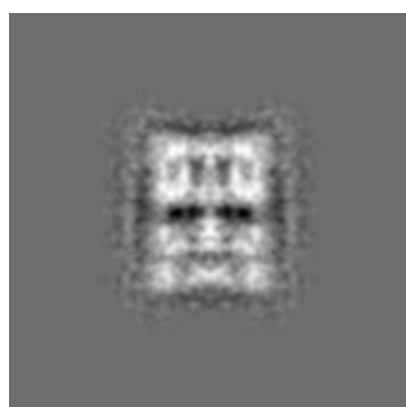
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3882. These allow visual inspection of the internal detail of the map and identification of artifacts.

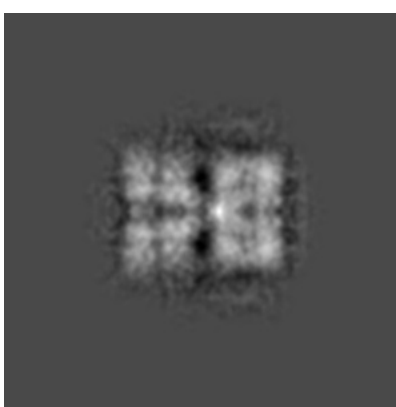
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

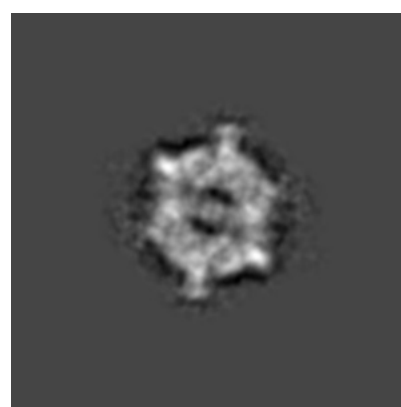
6.1.1 Primary map



X



Y

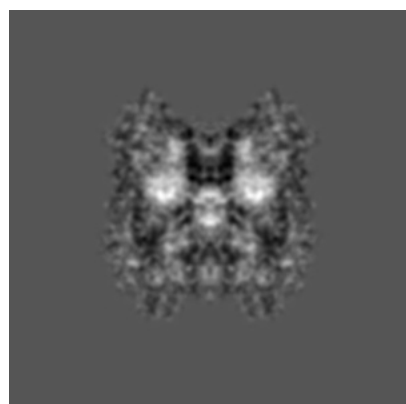


Z

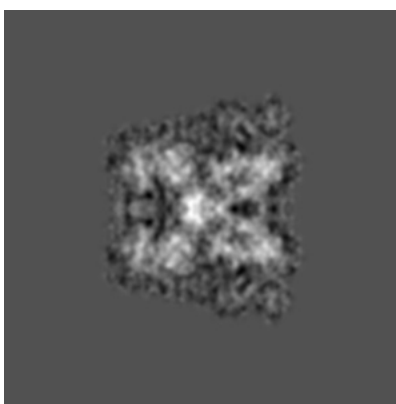
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

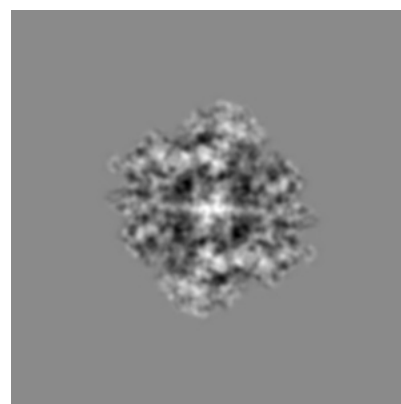
6.2.1 Primary map



X Index: 96



Y Index: 96

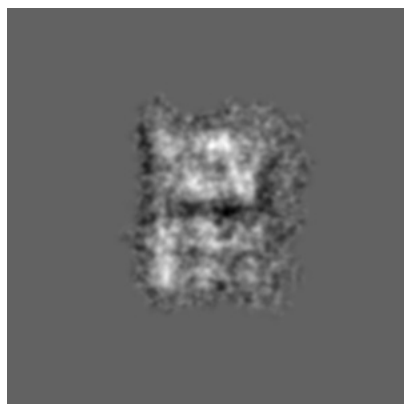


Z Index: 96

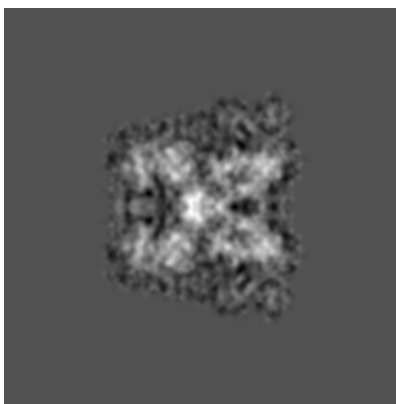
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

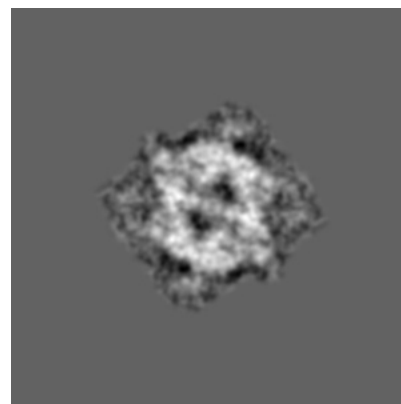
6.3.1 Primary map



X Index: 114



Y Index: 96

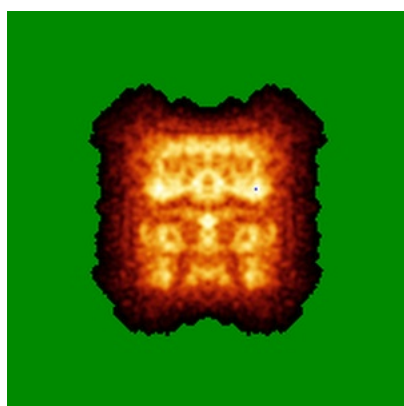


Z Index: 106

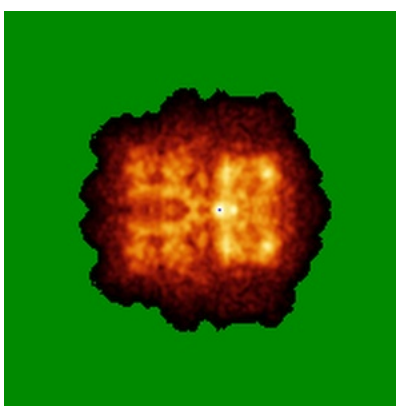
The images above show the largest variance slices of the map in three orthogonal directions.

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

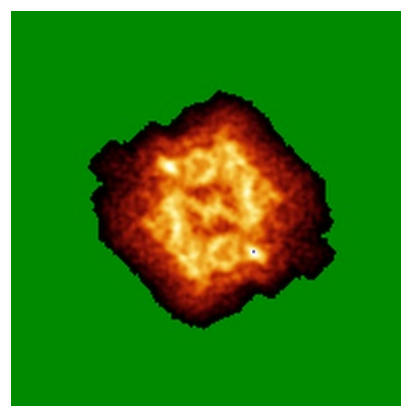
6.4.1 Primary map



X



Y

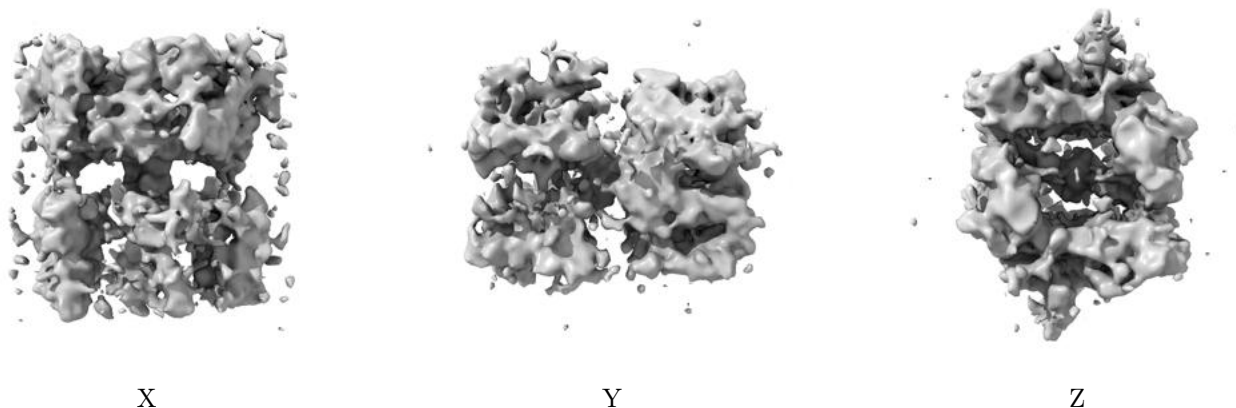


Z

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

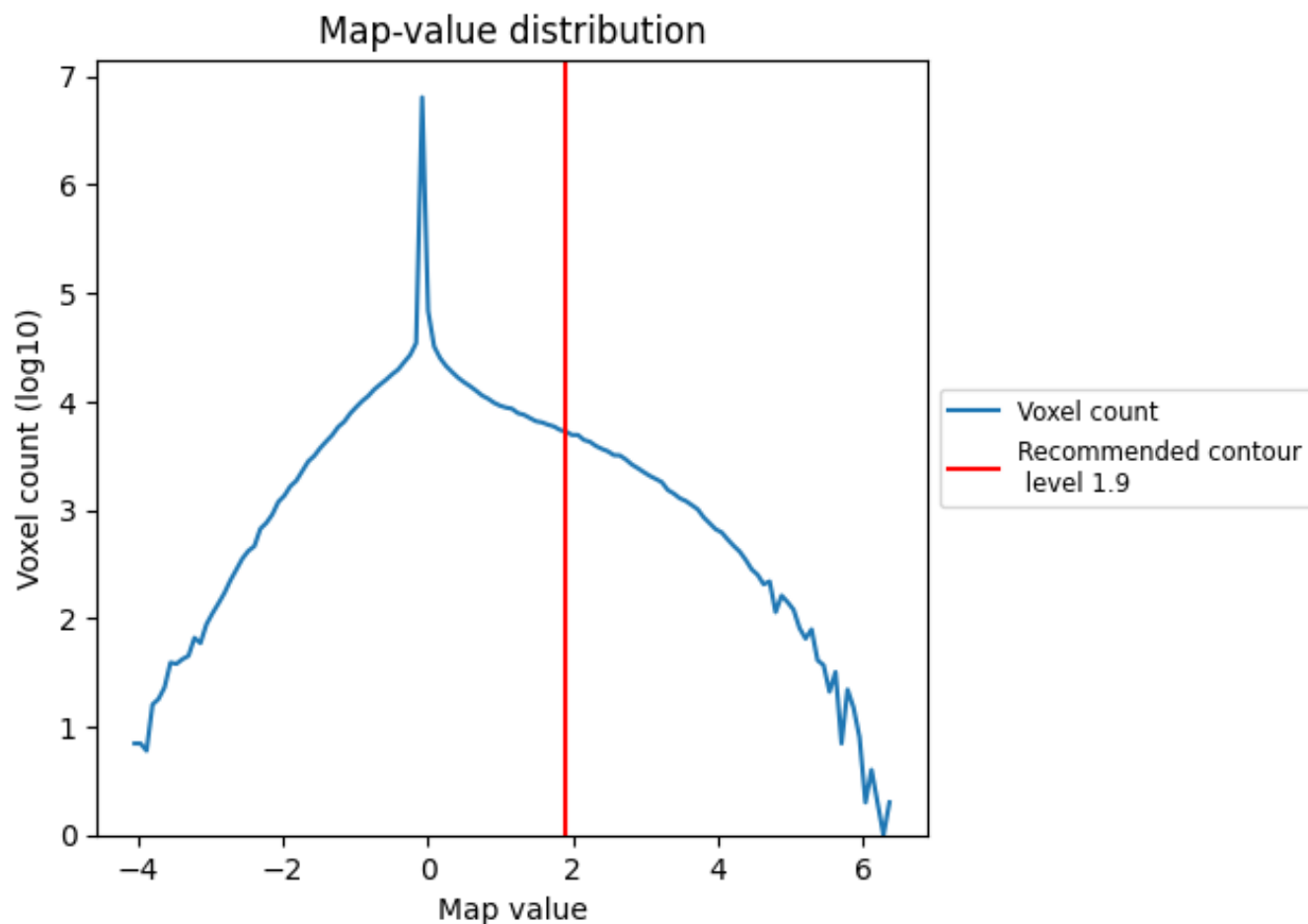
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

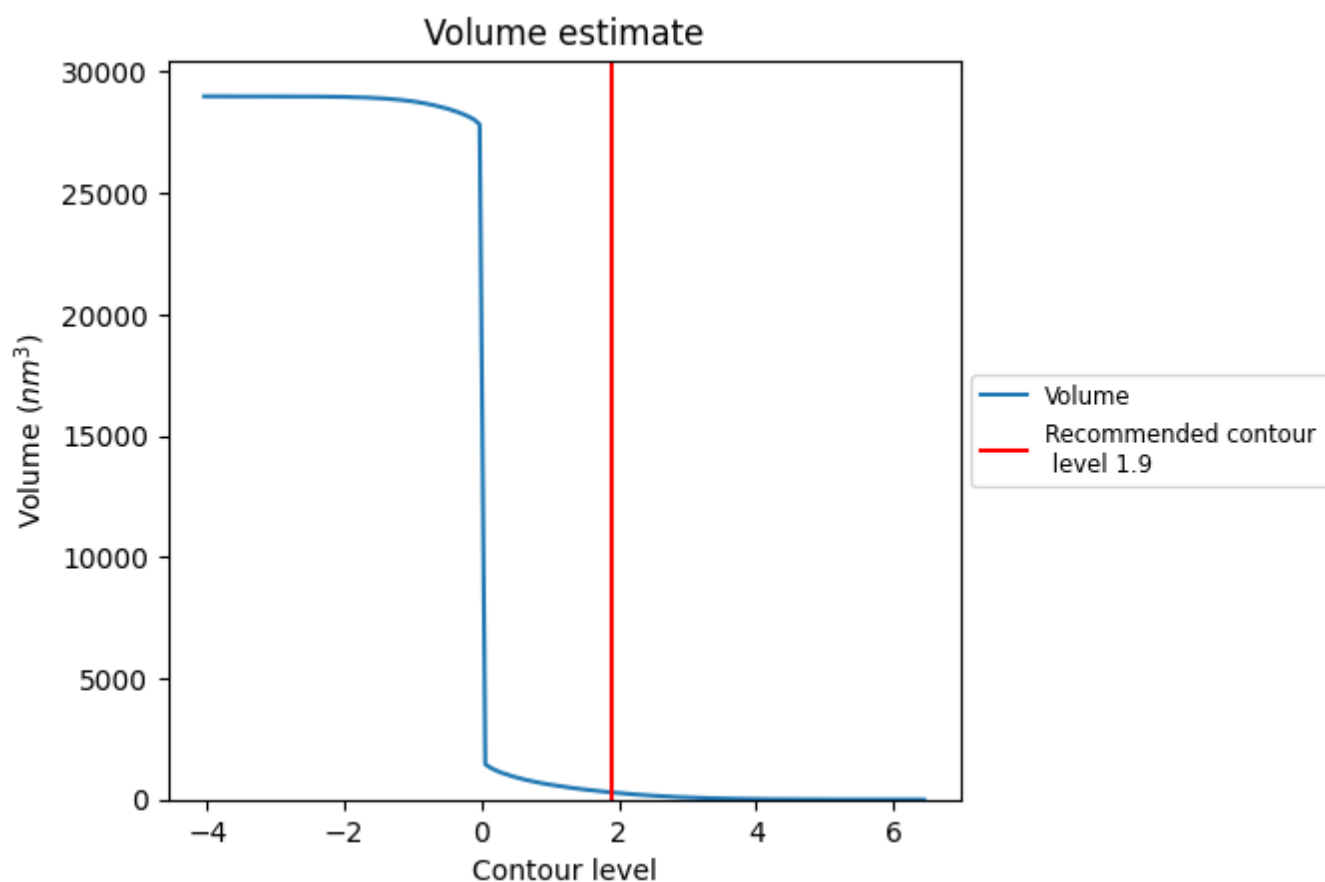
This section contains the results of statistical analysis of the map.

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.

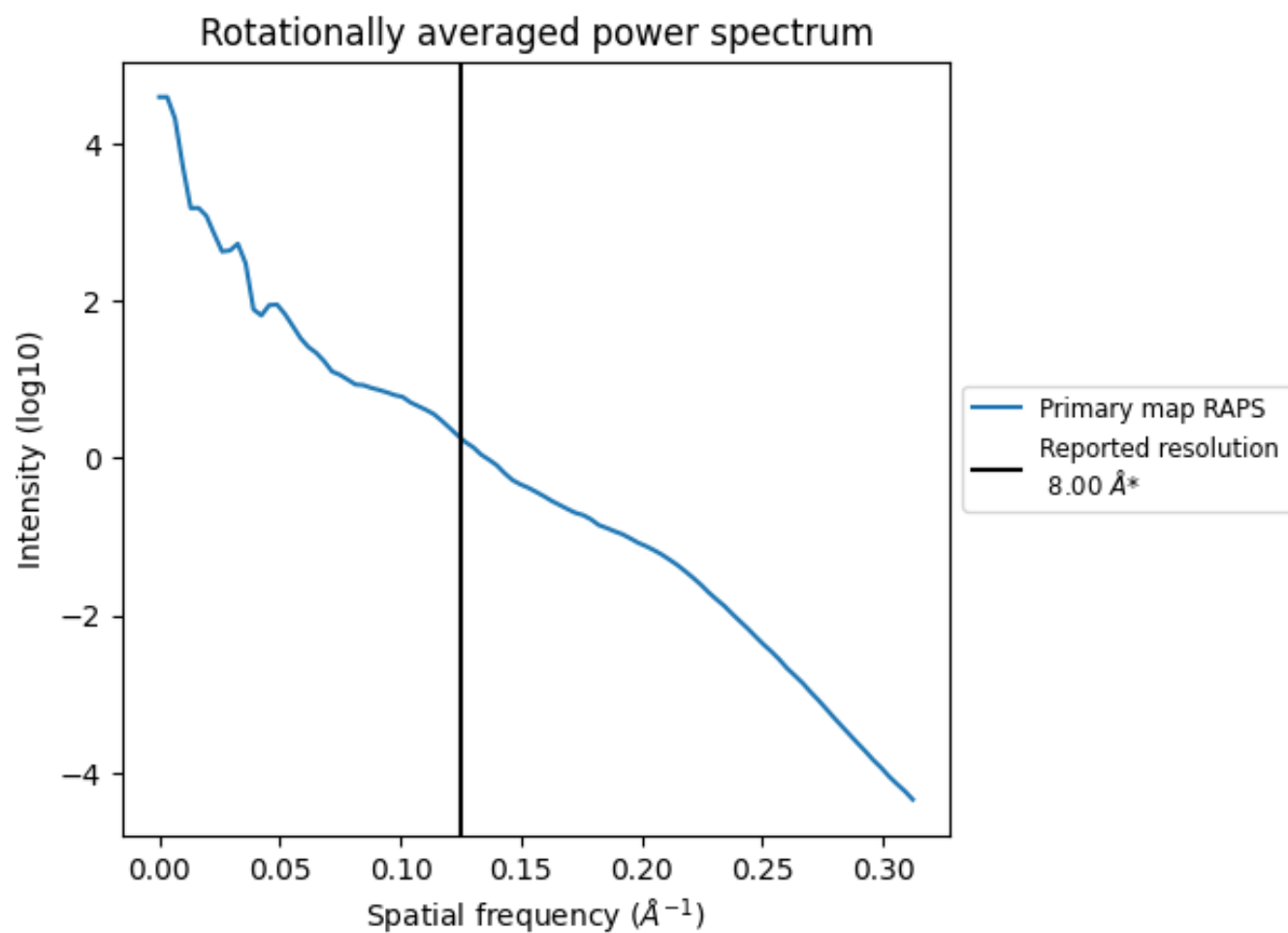
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 294 nm³; this corresponds to an approximate mass of 265 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 0.125 Å⁻¹

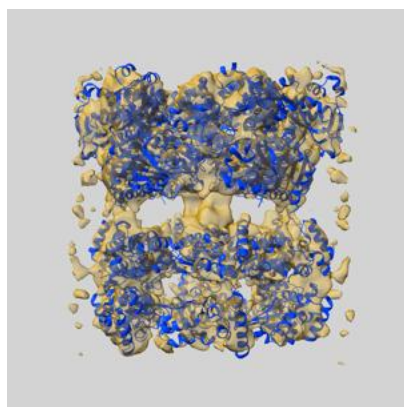
8 Fourier-Shell correlation

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

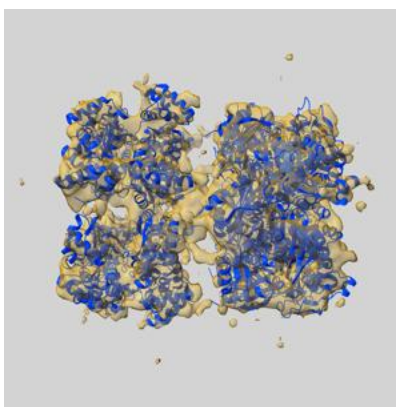
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3882 and PDB model 6EJF. Per-residue inclusion information can be found in section [3](#) on page [9](#).

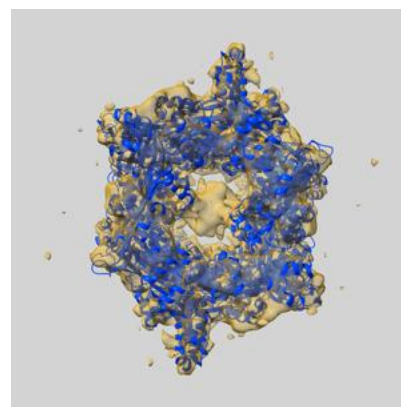
9.1 Map-model overlay [i](#)



X



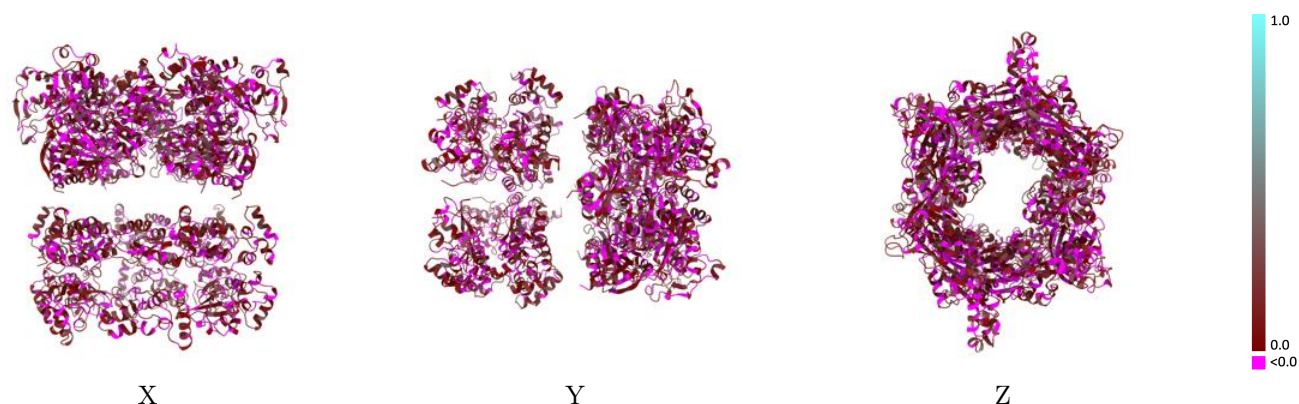
Y



Z

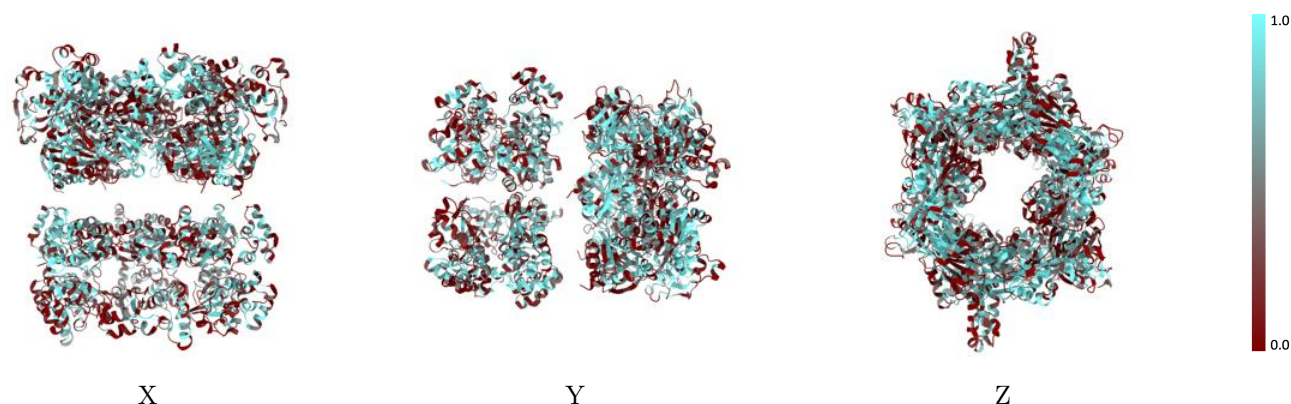
The images above show the 3D surface view of the map at the recommended contour level 1.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



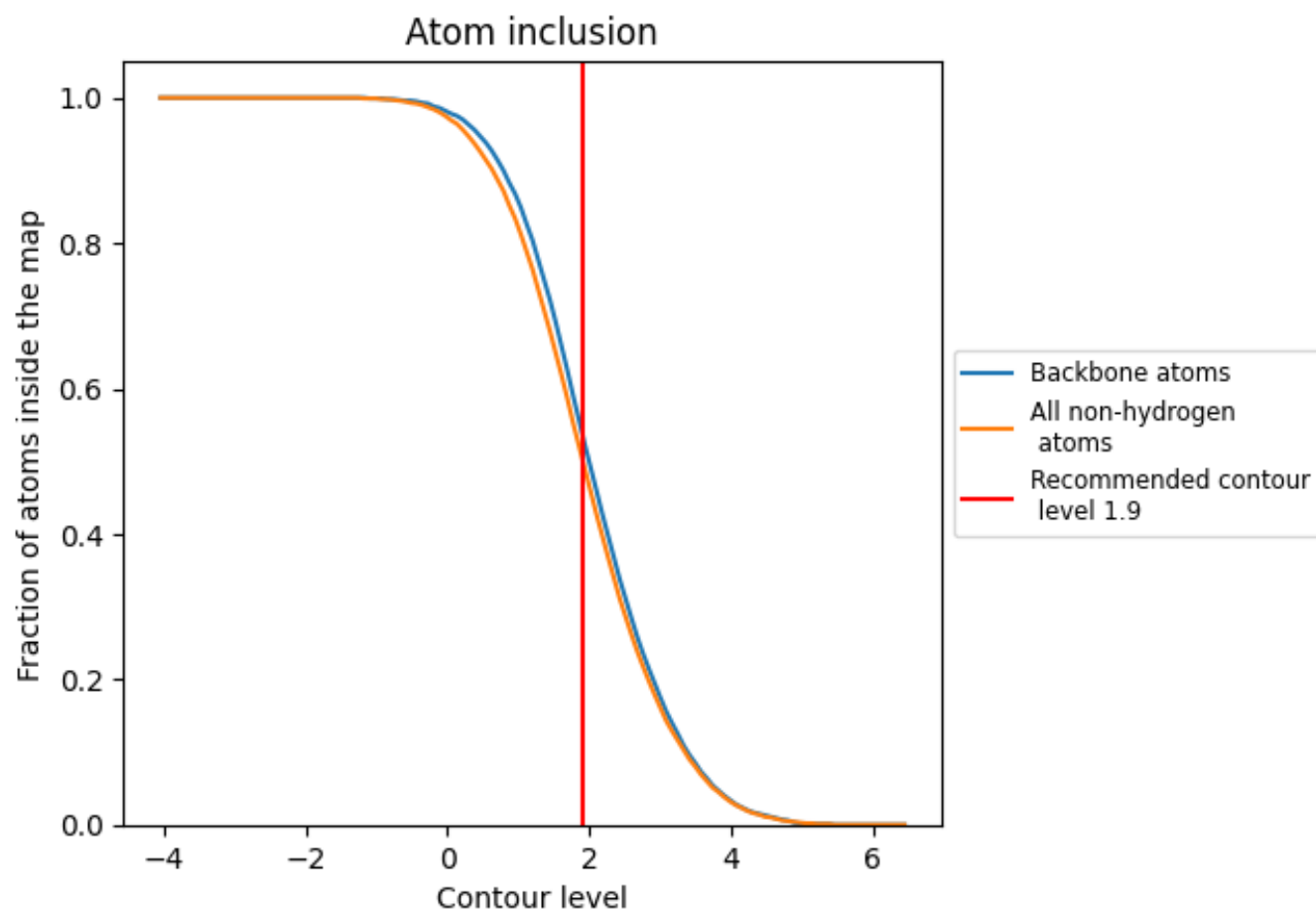
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 50% 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 (1.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5050	 0.0690
A	 0.5150	 0.0660
B	 0.5070	 0.0510
C	 0.5390	 0.0640
D	 0.5490	 0.0700
E	 0.5200	 0.0570
F	 0.5310	 0.0580
G	 0.4440	 0.0870
H	 0.5640	 0.0760
I	 0.5640	 0.0800
J	 0.3980	 0.0840
K	 0.3790	 0.0730
L	 0.4740	 0.0730
M	 0.4540	 0.0830
N	 0.4110	 0.0920
O	 0.3810	 0.0740
P	 0.4950	 0.0690
Q	 0.5590	 0.0800
R	 0.5630	 0.0730

