



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:30 AM UTC

PDB ID : 6N38 / pdb_00006n38
EMDB ID : EMD-9341
Title : Structure of the type VI secretion system TssK-TssF-TssG baseplate subcomplex revealed by cryo-electron microscopy - full map sharpened
Authors : Park, Y.J.; Lacourse, K.D.; Cambillau, C.; Seattle Structural Genomics Center for Infectious Disease (SSGCID); DiMaio, F.; Mougous, J.D.; Veesler, D.
Deposited on : 2018-11-14
Resolution : 3.70 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:

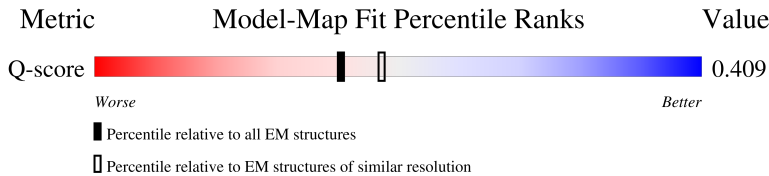
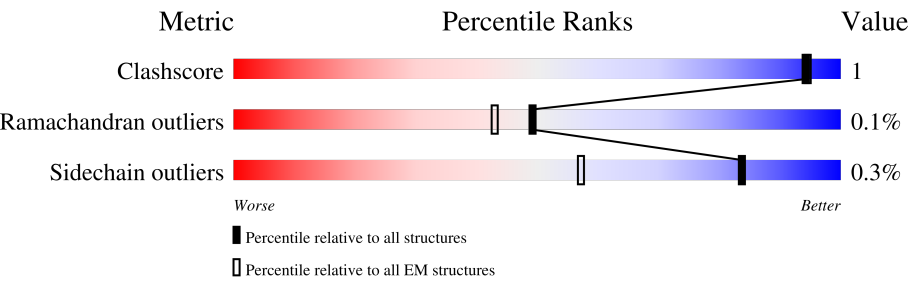
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 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	11569 (3.20 - 4.20)

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	587	35% 85% 5% 9%
1	I	587	40% 83% 6% 10%
2	G	303	13% 74% 5% 21%
3	K	21	95% 100%

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Mol	Chain	Length	Quality of chain
3	L	21	71% 86% 14%
4	A	322	5% 86% 6% 7%
4	B	322	5% 86% 7% 7%
4	C	322	5% 85% 7% 7%
4	D	322	5% 85% 7% 7%
4	E	322	5% 87% 6% 7%
4	F	322	5% 84% 8% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24456 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 Putative type VI secretion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	528	Total	C	N	O	S	0	0
			4047	2587	721	719	20		
1	H	532	Total	C	N	O	S	0	0
			4085	2621	729	715	20		

- Molecule 2 is a protein called Putative type VI secretion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	240	Total	C	N	O	S	0	0
			1903	1203	359	333	8		

- Molecule 3 is a protein called Unassigned protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	K	21	Total	C	N	O	0	0
			105	63	21	21		
3	L	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 4 is a protein called Putative type VI secretion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	299	Total	C	N	O	S	0	0
			2375	1504	432	429	10		
4	D	299	Total	C	N	O	S	0	0
			2376	1505	432	429	10		
4	B	300	Total	C	N	O	S	0	0
			2378	1507	433	427	11		
4	E	301	Total	C	N	O	S	0	0
			2374	1505	434	424	11		
4	C	299	Total	C	N	O	S	0	0
			2356	1495	430	421	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	300	Total	C	N	O	S	0	0
			2367	1501	433	423	10		

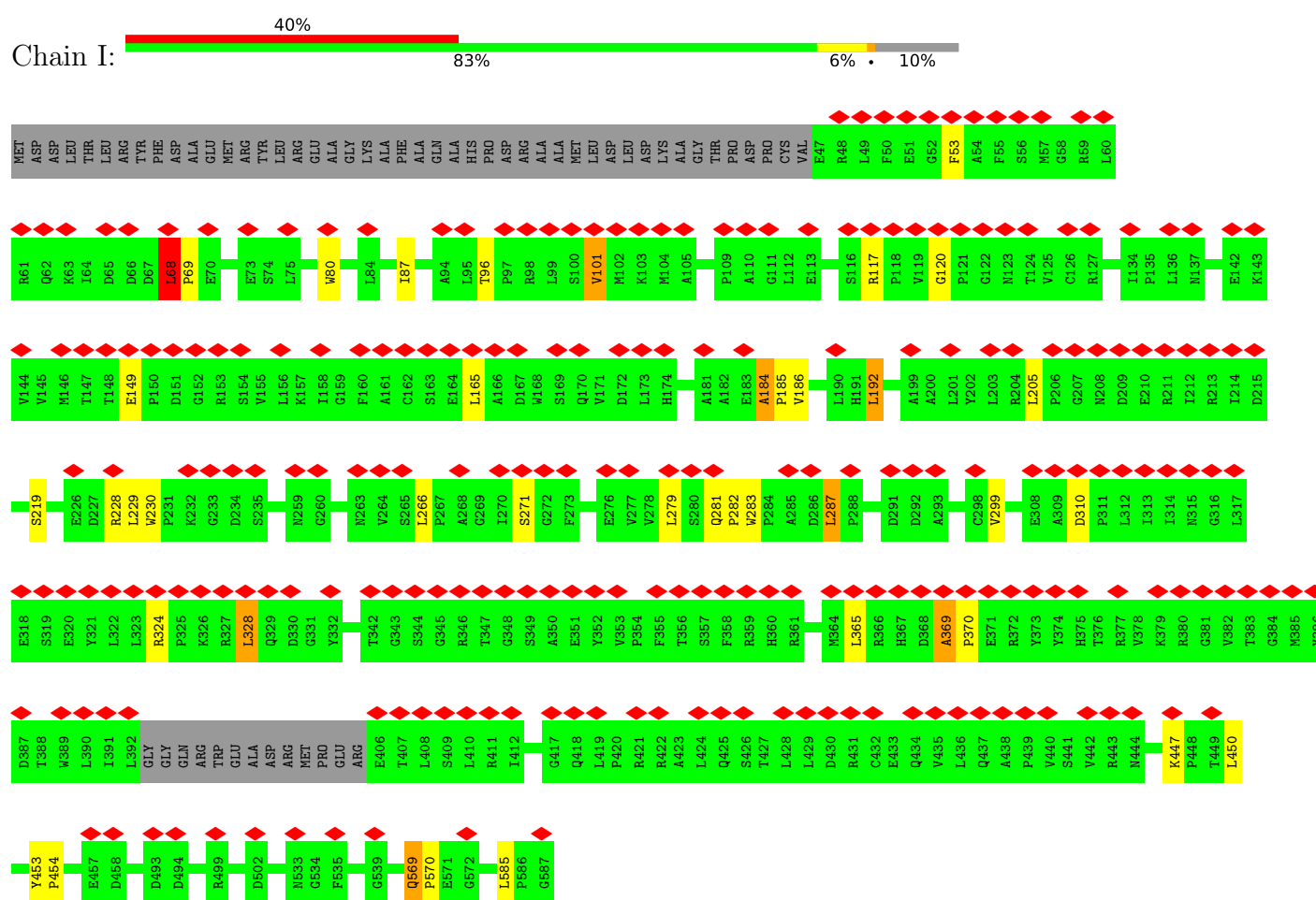
There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	317	HIS	-	expression tag	UNP D3GU39
A	318	HIS	-	expression tag	UNP D3GU39
A	319	HIS	-	expression tag	UNP D3GU39
A	320	HIS	-	expression tag	UNP D3GU39
A	321	HIS	-	expression tag	UNP D3GU39
A	322	HIS	-	expression tag	UNP D3GU39
D	317	HIS	-	expression tag	UNP D3GU39
D	318	HIS	-	expression tag	UNP D3GU39
D	319	HIS	-	expression tag	UNP D3GU39
D	320	HIS	-	expression tag	UNP D3GU39
D	321	HIS	-	expression tag	UNP D3GU39
D	322	HIS	-	expression tag	UNP D3GU39
B	317	HIS	-	expression tag	UNP D3GU39
B	318	HIS	-	expression tag	UNP D3GU39
B	319	HIS	-	expression tag	UNP D3GU39
B	320	HIS	-	expression tag	UNP D3GU39
B	321	HIS	-	expression tag	UNP D3GU39
B	322	HIS	-	expression tag	UNP D3GU39
E	317	HIS	-	expression tag	UNP D3GU39
E	318	HIS	-	expression tag	UNP D3GU39
E	319	HIS	-	expression tag	UNP D3GU39
E	320	HIS	-	expression tag	UNP D3GU39
E	321	HIS	-	expression tag	UNP D3GU39
E	322	HIS	-	expression tag	UNP D3GU39
C	317	HIS	-	expression tag	UNP D3GU39
C	318	HIS	-	expression tag	UNP D3GU39
C	319	HIS	-	expression tag	UNP D3GU39
C	320	HIS	-	expression tag	UNP D3GU39
C	321	HIS	-	expression tag	UNP D3GU39
C	322	HIS	-	expression tag	UNP D3GU39
F	317	HIS	-	expression tag	UNP D3GU39
F	318	HIS	-	expression tag	UNP D3GU39
F	319	HIS	-	expression tag	UNP D3GU39
F	320	HIS	-	expression tag	UNP D3GU39
F	321	HIS	-	expression tag	UNP D3GU39
F	322	HIS	-	expression tag	UNP D3GU39

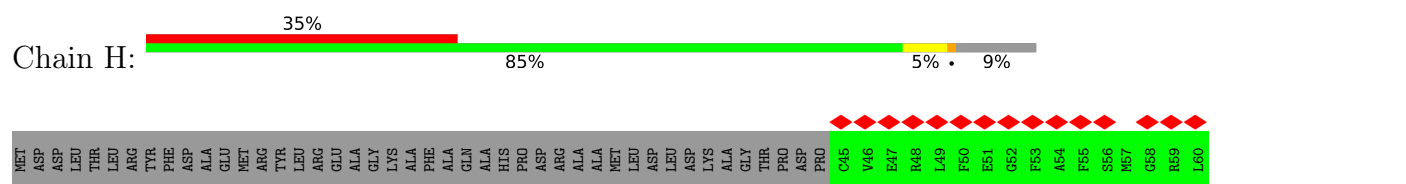
3 Residue-property plots

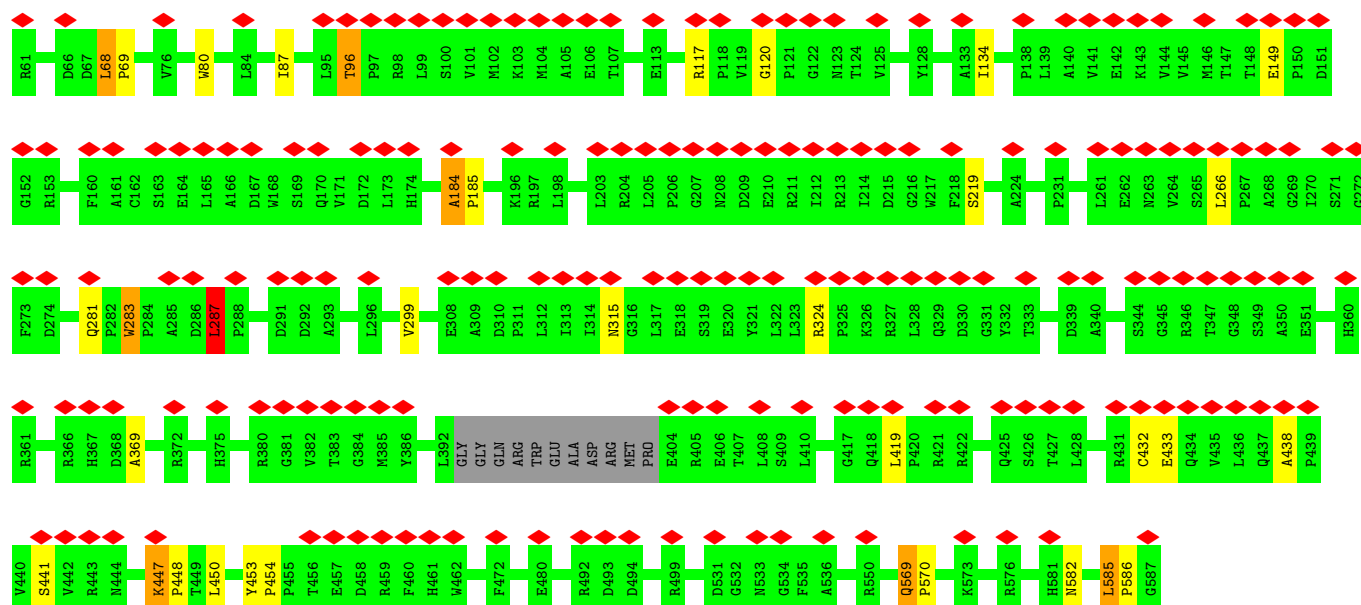
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Putative type VI secretion protein

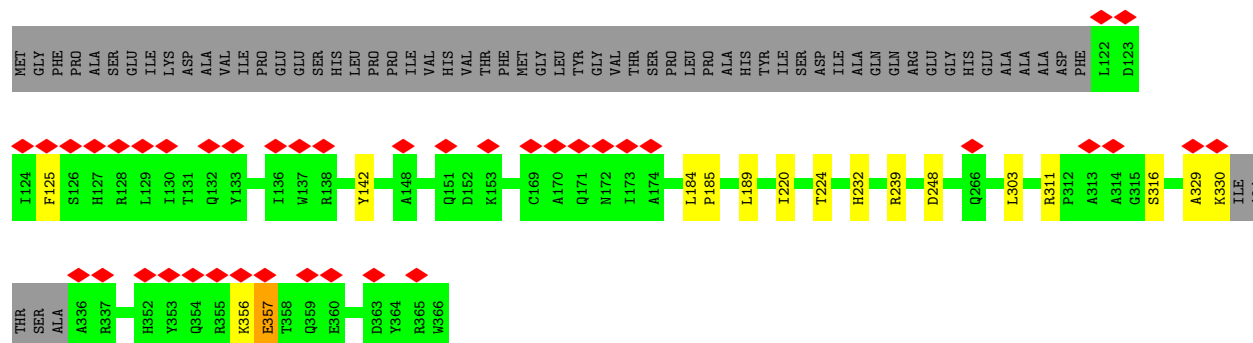
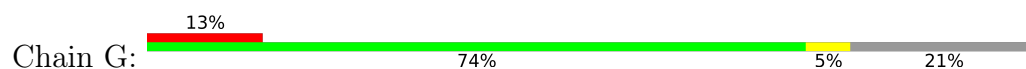


• Molecule 1: Putative type VI secretion protein

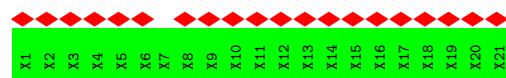




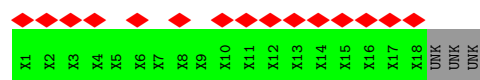
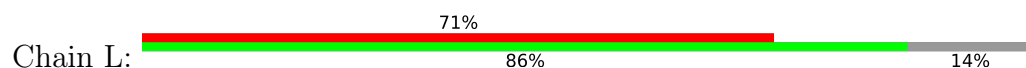
• Molecule 2: Putative type VI secretion protein



• Molecule 3: Unassigned protein

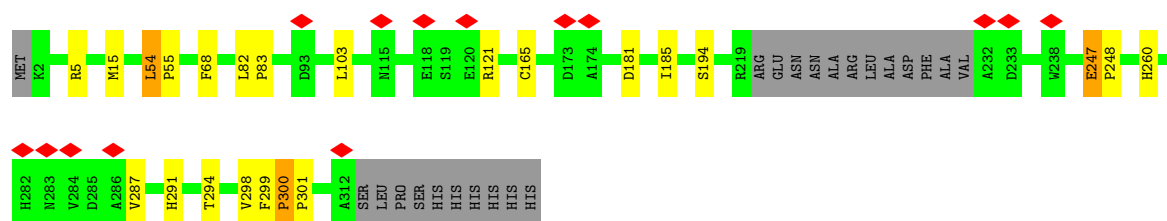


• Molecule 3: Unassigned protein



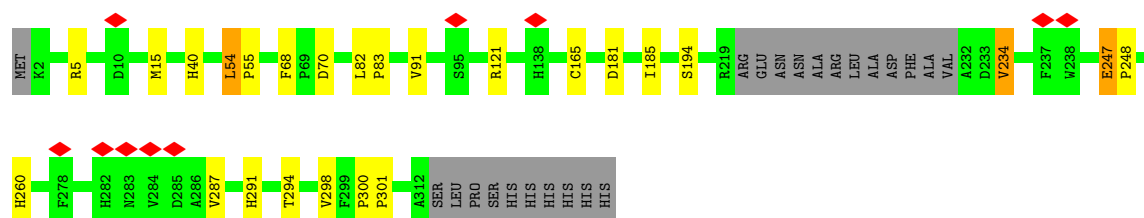
• Molecule 4: Putative type VI secretion protein

Chain A:  86% 6% • 7%



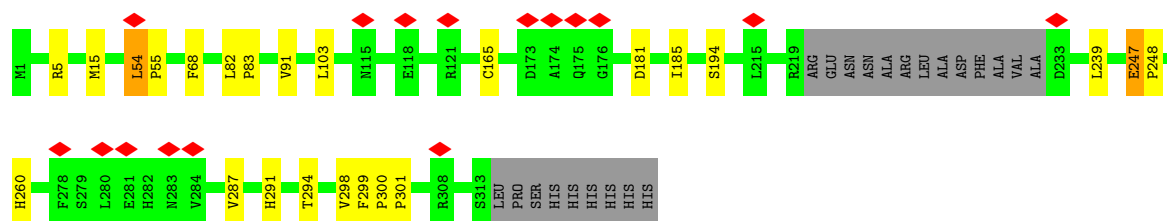
• Molecule 4: Putative type VI secretion protein

Chain D:  85% 7% • 7%



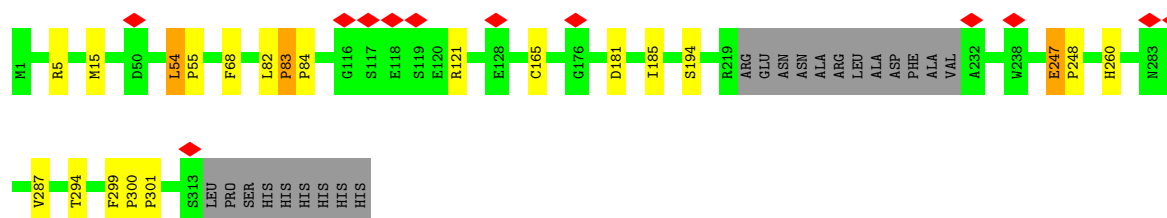
• Molecule 4: Putative type VI secretion protein

Chain B:  5% 86% 7% • 7%



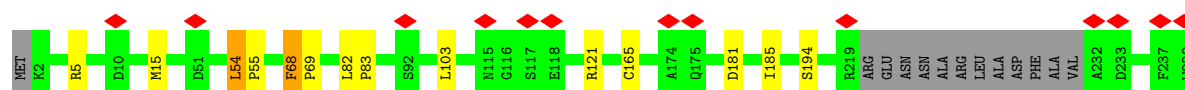
• Molecule 4: Putative type VI secretion protein

Chain E:  87% 6% • 7%



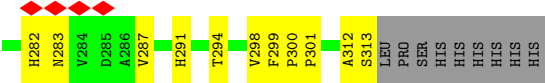
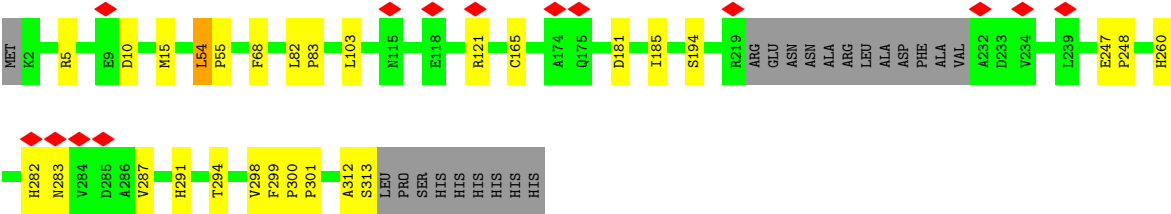
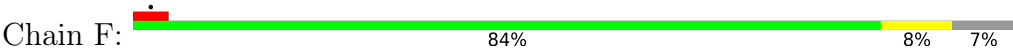
• Molecule 4: Putative type VI secretion protein

Chain C:  5% 85% 7% • 7%





• Molecule 4: Putative type VI secretion protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36496	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	394.56, 394.56, 394.56	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	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	0.71	0/4186	1.01	49/5703 (0.9%)
1	I	0.71	0/4148	1.05	52/5653 (0.9%)
2	G	0.69	0/1945	0.96	18/2639 (0.7%)
4	A	0.76	0/2431	0.98	34/3317 (1.0%)
4	B	0.74	0/2434	0.98	31/3320 (0.9%)
4	C	0.74	0/2412	0.95	32/3293 (1.0%)
4	D	0.76	0/2432	0.99	33/3318 (1.0%)
4	E	0.74	0/2430	0.95	30/3316 (0.9%)
4	F	0.76	0/2423	0.99	31/3307 (0.9%)
All	All	0.73	0/24841	0.99	310/33866 (0.9%)

There are no bond length outliers.

All (310) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	365	LEU	CD1-CG-CD2	10.07	132.96	110.80
1	I	101	VAL	CA-CB-CG2	10.06	127.50	110.40
1	I	165	LEU	CD1-CG-CD2	9.86	132.48	110.80
4	D	234	VAL	CA-CB-CG2	9.57	126.68	110.40
1	I	287	LEU	CD1-CG-CD2	9.55	131.81	110.80
1	H	287	LEU	CD1-CG-CD2	9.52	131.73	110.80
4	B	239	LEU	CD1-CG-CD2	9.47	131.63	110.80
1	I	192	LEU	CD1-CG-CD2	9.46	131.60	110.80
4	F	82	LEU	CA-C-N	9.20	126.28	119.66
4	F	82	LEU	C-N-CA	9.20	126.28	119.66
1	I	186	VAL	CG1-CB-CG2	9.16	130.95	110.80
1	I	328	LEU	CD1-CG-CD2	9.14	130.91	110.80
4	A	82	LEU	CA-C-N	9.02	126.15	119.66
4	A	82	LEU	C-N-CA	9.02	126.15	119.66
4	D	185	ILE	CA-C-N	8.75	126.04	119.66
4	D	185	ILE	C-N-CA	8.75	126.04	119.66
4	F	165	CYS	CA-C-N	7.86	127.92	119.90
4	F	165	CYS	C-N-CA	7.86	127.92	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	453	TYR	CA-C-N	7.77	125.25	119.66
1	I	453	TYR	C-N-CA	7.77	125.25	119.66
4	D	181	ASP	CA-C-N	7.38	127.09	119.56
4	D	181	ASP	C-N-CA	7.38	127.09	119.56
4	E	294	THR	CA-C-N	7.31	127.02	119.56
4	E	294	THR	C-N-CA	7.31	127.02	119.56
1	H	96	THR	CA-C-N	7.21	127.14	119.85
1	H	96	THR	C-N-CA	7.21	127.14	119.85
4	C	294	THR	CA-C-N	7.17	126.88	119.56
4	C	294	THR	C-N-CA	7.17	126.88	119.56
4	E	181	ASP	CA-C-N	7.16	126.86	119.56
4	E	181	ASP	C-N-CA	7.16	126.86	119.56
4	B	181	ASP	CA-C-N	7.15	126.85	119.56
4	B	181	ASP	C-N-CA	7.15	126.85	119.56
1	H	453	TYR	CA-C-N	7.13	124.87	119.66
1	H	453	TYR	C-N-CA	7.13	124.87	119.66
4	F	294	THR	CA-C-N	7.08	126.78	119.56
4	F	294	THR	C-N-CA	7.08	126.78	119.56
2	G	232	HIS	CA-C-N	7.08	127.00	119.85
2	G	232	HIS	C-N-CA	7.08	127.00	119.85
4	F	181	ASP	CA-C-N	7.06	126.76	119.56
4	F	181	ASP	C-N-CA	7.06	126.76	119.56
1	H	585	LEU	CA-C-N	7.04	126.74	119.56
1	H	585	LEU	C-N-CA	7.04	126.74	119.56
4	B	294	THR	CA-C-N	7.00	126.70	119.56
4	B	294	THR	C-N-CA	7.00	126.70	119.56
4	D	294	THR	CA-C-N	6.96	126.66	119.56
4	D	294	THR	C-N-CA	6.96	126.66	119.56
4	B	194	SER	CA-C-N	6.96	127.55	119.47
4	B	194	SER	C-N-CA	6.96	127.55	119.47
4	C	83	PRO	CA-C-N	6.94	126.93	119.78
4	C	83	PRO	C-N-CA	6.94	126.93	119.78
4	D	40	HIS	CA-C-N	6.93	126.63	119.56
4	D	40	HIS	C-N-CA	6.93	126.63	119.56
1	I	324	ARG	CA-C-N	6.92	127.09	120.31
1	I	324	ARG	C-N-CA	6.92	127.09	120.31
4	B	83	PRO	CA-C-N	6.87	126.86	119.78
4	B	83	PRO	C-N-CA	6.87	126.86	119.78
4	C	260	HIS	CA-C-N	6.85	127.41	119.47
4	C	260	HIS	C-N-CA	6.85	127.41	119.47
4	A	83	PRO	CA-C-N	6.84	126.87	119.89
4	A	83	PRO	C-N-CA	6.84	126.87	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	260	HIS	CA-C-N	6.83	127.40	119.47
4	A	260	HIS	C-N-CA	6.83	127.40	119.47
4	B	260	HIS	CA-C-N	6.83	127.39	119.47
4	B	260	HIS	C-N-CA	6.83	127.39	119.47
4	E	260	HIS	CA-C-N	6.81	127.37	119.47
4	E	260	HIS	C-N-CA	6.81	127.37	119.47
4	D	260	HIS	CA-C-N	6.79	126.48	119.56
4	D	260	HIS	C-N-CA	6.79	126.48	119.56
4	A	294	THR	CA-C-N	6.78	126.47	119.56
4	A	294	THR	C-N-CA	6.78	126.47	119.56
4	E	165	CYS	CA-C-N	6.76	126.79	119.90
4	E	165	CYS	C-N-CA	6.76	126.79	119.90
4	E	194	SER	CA-C-N	6.74	127.29	119.47
4	E	194	SER	C-N-CA	6.74	127.29	119.47
1	H	87	ILE	CA-C-N	6.72	126.68	120.03
1	H	87	ILE	C-N-CA	6.72	126.68	120.03
4	F	260	HIS	CA-C-N	6.71	127.26	119.47
4	F	260	HIS	C-N-CA	6.71	127.26	119.47
4	B	68	PHE	CA-C-N	6.71	128.23	119.84
4	B	68	PHE	C-N-CA	6.71	128.23	119.84
4	E	83	PRO	CA-C-N	6.71	126.73	119.89
4	E	83	PRO	C-N-CA	6.71	126.73	119.89
4	F	5	ARG	CA-C-N	6.69	126.61	119.85
4	F	5	ARG	C-N-CA	6.69	126.61	119.85
4	F	83	PRO	CA-C-N	6.63	127.01	119.92
4	F	83	PRO	C-N-CA	6.63	127.01	119.92
4	D	83	PRO	CA-C-N	6.62	126.64	119.89
4	D	83	PRO	C-N-CA	6.62	126.64	119.89
4	D	194	SER	CA-C-N	6.62	127.14	119.47
4	D	194	SER	C-N-CA	6.62	127.14	119.47
4	C	181	ASP	CA-C-N	6.59	126.73	119.87
4	C	181	ASP	C-N-CA	6.59	126.73	119.87
1	H	80	TRP	CA-C-N	6.57	126.26	119.56
1	H	80	TRP	C-N-CA	6.57	126.26	119.56
2	G	303	LEU	CA-C-N	6.56	126.53	120.03
2	G	303	LEU	C-N-CA	6.56	126.53	120.03
4	D	15	MET	CA-C-N	6.55	126.24	119.56
4	D	15	MET	C-N-CA	6.55	126.24	119.56
4	C	165	CYS	CA-C-N	6.55	126.58	119.90
4	C	165	CYS	C-N-CA	6.55	126.58	119.90
4	C	194	SER	CA-C-N	6.53	127.05	119.47
4	C	194	SER	C-N-CA	6.53	127.05	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	419	LEU	CA-C-N	6.53	126.56	119.90
1	H	419	LEU	C-N-CA	6.53	126.56	119.90
1	I	149	GLU	CA-C-N	6.53	126.22	119.56
1	I	149	GLU	C-N-CA	6.53	126.22	119.56
4	A	181	ASP	CA-C-N	6.52	126.66	119.87
4	A	181	ASP	C-N-CA	6.52	126.66	119.87
1	H	324	ARG	CA-C-N	6.51	126.49	119.78
1	H	324	ARG	C-N-CA	6.51	126.49	119.78
4	A	194	SER	CA-C-N	6.47	126.98	119.47
4	A	194	SER	C-N-CA	6.47	126.98	119.47
2	G	239	ARG	CA-C-N	6.46	126.43	120.03
2	G	239	ARG	C-N-CA	6.46	126.43	120.03
1	I	96	THR	CA-C-N	6.45	126.63	120.31
1	I	96	THR	C-N-CA	6.45	126.63	120.31
4	F	194	SER	CA-C-N	6.42	126.92	119.47
4	F	194	SER	C-N-CA	6.42	126.92	119.47
1	I	281	GLN	CA-C-N	6.42	127.86	119.84
1	I	281	GLN	C-N-CA	6.42	127.86	119.84
4	B	5	ARG	CA-C-N	6.42	126.33	119.85
4	B	5	ARG	C-N-CA	6.42	126.33	119.85
4	A	15	MET	CA-C-N	6.41	126.63	119.32
4	A	15	MET	C-N-CA	6.41	126.63	119.32
4	A	165	CYS	CA-C-N	6.39	126.42	119.90
4	A	165	CYS	C-N-CA	6.39	126.42	119.90
4	E	121	ARG	CA-C-N	6.39	126.30	119.85
4	E	121	ARG	C-N-CA	6.39	126.30	119.85
4	D	68	PHE	CA-C-N	6.35	127.78	119.84
4	D	68	PHE	C-N-CA	6.35	127.78	119.84
4	C	68	PHE	CA-C-N	6.35	127.77	119.84
4	C	68	PHE	C-N-CA	6.35	127.77	119.84
4	A	68	PHE	CA-C-N	6.30	127.71	119.84
4	A	68	PHE	C-N-CA	6.30	127.71	119.84
4	A	287	VAL	CA-C-N	6.29	126.21	119.85
4	A	287	VAL	C-N-CA	6.29	126.21	119.85
4	B	54	LEU	CA-C-N	6.29	125.99	119.82
4	B	54	LEU	C-N-CA	6.29	125.99	119.82
4	B	165	CYS	CA-C-N	6.29	126.32	119.90
4	B	165	CYS	C-N-CA	6.29	126.32	119.90
1	I	120	GLY	CA-C-N	6.29	126.24	119.76
1	I	120	GLY	C-N-CA	6.29	126.24	119.76
4	D	287	VAL	CA-C-N	6.29	126.25	120.03
4	D	287	VAL	C-N-CA	6.29	126.25	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	54	LEU	CA-C-N	6.27	125.96	119.82
4	C	54	LEU	C-N-CA	6.27	125.96	119.82
2	G	189	LEU	CA-C-N	6.26	125.83	119.19
2	G	189	LEU	C-N-CA	6.26	125.83	119.19
4	A	54	LEU	CA-C-N	6.26	125.94	119.56
4	A	54	LEU	C-N-CA	6.26	125.94	119.56
4	E	287	VAL	CA-C-N	6.21	126.12	119.85
4	E	287	VAL	C-N-CA	6.21	126.12	119.85
4	F	68	PHE	CA-C-N	6.19	127.57	119.84
4	F	68	PHE	C-N-CA	6.19	127.57	119.84
1	H	281	GLN	CA-C-N	6.15	126.07	119.85
1	H	281	GLN	C-N-CA	6.15	126.07	119.85
4	B	103	LEU	CA-C-N	6.13	126.15	119.90
4	B	103	LEU	C-N-CA	6.13	126.15	119.90
1	H	369	ALA	CA-C-N	6.10	126.29	120.31
1	H	369	ALA	C-N-CA	6.10	126.29	120.31
4	B	15	MET	CA-C-N	6.10	126.28	119.32
4	B	15	MET	C-N-CA	6.10	126.28	119.32
2	G	224	THR	CA-C-N	6.09	126.06	120.03
2	G	224	THR	C-N-CA	6.09	126.06	120.03
4	D	165	CYS	CA-C-N	6.08	126.11	119.90
4	D	165	CYS	C-N-CA	6.08	126.11	119.90
2	G	220	ILE	CA-C-N	6.05	126.01	119.78
2	G	220	ILE	C-N-CA	6.05	126.01	119.78
4	B	287	VAL	CA-C-N	6.03	125.94	119.85
4	B	287	VAL	C-N-CA	6.03	125.94	119.85
4	F	287	VAL	CA-C-N	6.03	125.94	119.85
4	F	287	VAL	C-N-CA	6.03	125.94	119.85
4	F	54	LEU	CA-C-N	6.03	125.71	119.56
4	F	54	LEU	C-N-CA	6.03	125.71	119.56
1	H	447	LYS	CA-C-N	6.02	125.96	119.76
1	H	447	LYS	C-N-CA	6.02	125.96	119.76
1	I	369	ALA	CA-C-N	6.01	125.71	119.82
1	I	369	ALA	C-N-CA	6.01	125.71	119.82
4	D	54	LEU	CA-C-N	6.01	125.71	119.82
4	D	54	LEU	C-N-CA	6.01	125.71	119.82
1	I	80	TRP	CA-C-N	6.01	125.69	119.56
1	I	80	TRP	C-N-CA	6.01	125.69	119.56
4	A	103	LEU	CA-C-N	6.01	126.03	119.90
4	A	103	LEU	C-N-CA	6.01	126.03	119.90
4	C	121	ARG	CA-C-N	6.00	125.91	119.85
4	C	121	ARG	C-N-CA	6.00	125.91	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	311	ARG	CA-C-N	5.98	125.95	120.03
2	G	311	ARG	C-N-CA	5.98	125.95	120.03
4	E	54	LEU	CA-C-N	5.97	125.65	119.56
4	E	54	LEU	C-N-CA	5.97	125.65	119.56
4	A	121	ARG	CA-C-N	5.90	125.66	119.76
4	A	121	ARG	C-N-CA	5.90	125.66	119.76
1	H	569	GLN	CA-C-N	5.89	125.57	119.56
1	H	569	GLN	C-N-CA	5.89	125.57	119.56
1	H	184	ALA	CA-C-N	5.88	125.56	119.56
1	H	184	ALA	C-N-CA	5.88	125.56	119.56
1	I	266	LEU	CA-C-N	5.87	125.77	119.85
1	I	266	LEU	C-N-CA	5.87	125.77	119.85
1	H	134	ILE	CA-C-N	5.85	125.79	119.76
1	H	134	ILE	C-N-CA	5.85	125.79	119.76
1	H	120	GLY	CA-C-N	5.85	125.79	119.76
1	H	120	GLY	C-N-CA	5.85	125.79	119.76
4	B	82	LEU	CA-C-N	5.83	126.39	120.38
4	B	82	LEU	C-N-CA	5.83	126.39	120.38
4	C	247	GLU	CA-C-N	5.80	125.48	119.56
4	C	247	GLU	C-N-CA	5.80	125.48	119.56
4	C	82	LEU	CA-C-N	5.78	126.33	120.38
4	C	82	LEU	C-N-CA	5.78	126.33	120.38
4	E	5	ARG	CA-C-N	5.76	125.67	119.85
4	E	5	ARG	C-N-CA	5.76	125.67	119.85
4	D	247	GLU	CA-C-N	5.75	125.42	119.56
4	D	247	GLU	C-N-CA	5.75	125.42	119.56
4	E	15	MET	CA-C-N	5.74	125.59	119.28
4	E	15	MET	C-N-CA	5.74	125.59	119.28
4	B	247	GLU	CA-C-N	5.74	125.41	119.56
4	B	247	GLU	C-N-CA	5.74	125.41	119.56
1	I	569	GLN	CA-C-N	5.72	125.40	119.56
1	I	569	GLN	C-N-CA	5.72	125.40	119.56
4	F	10	ASP	CB-CA-C	-5.72	109.96	116.54
1	I	454	PRO	CA-C-N	5.71	125.47	119.76
1	I	454	PRO	C-N-CA	5.71	125.47	119.76
4	C	15	MET	CA-C-N	5.71	125.57	119.28
4	C	15	MET	C-N-CA	5.71	125.57	119.28
4	C	5	ARG	CA-C-N	5.71	125.61	119.85
4	C	5	ARG	C-N-CA	5.71	125.61	119.85
1	H	299	VAL	CA-C-N	5.70	125.63	119.76
1	H	299	VAL	C-N-CA	5.70	125.63	119.76
4	A	300	PRO	CA-C-N	5.70	126.96	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	300	PRO	C-N-CA	5.70	126.96	119.84
1	I	87	ILE	CA-C-N	5.69	125.66	120.03
1	I	87	ILE	C-N-CA	5.69	125.66	120.03
4	C	287	VAL	CA-C-N	5.69	125.59	119.85
4	C	287	VAL	C-N-CA	5.69	125.59	119.85
4	A	247	GLU	CA-C-N	5.68	125.36	119.56
4	A	247	GLU	C-N-CA	5.68	125.36	119.56
1	H	68	LEU	CA-C-N	5.67	125.35	119.56
1	H	68	LEU	C-N-CA	5.67	125.35	119.56
4	F	15	MET	CA-C-N	5.66	125.33	119.56
4	F	15	MET	C-N-CA	5.66	125.33	119.56
4	A	5	ARG	CA-C-N	5.63	125.53	119.85
4	A	5	ARG	C-N-CA	5.63	125.53	119.85
1	I	447	LYS	CA-C-N	5.62	125.56	119.78
1	I	447	LYS	C-N-CA	5.62	125.56	119.78
1	I	299	VAL	CA-C-N	5.61	125.53	119.76
1	I	299	VAL	C-N-CA	5.61	125.53	119.76
4	E	82	LEU	CA-C-N	5.60	126.15	120.38
4	E	82	LEU	C-N-CA	5.60	126.15	120.38
4	D	121	ARG	CA-C-N	5.59	125.52	119.76
4	D	121	ARG	C-N-CA	5.59	125.52	119.76
4	D	5	ARG	CA-C-N	5.58	125.49	119.85
4	D	5	ARG	C-N-CA	5.58	125.49	119.85
1	H	266	LEU	CA-C-N	5.57	125.47	119.85
1	H	266	LEU	C-N-CA	5.57	125.47	119.85
4	D	82	LEU	CA-C-N	5.57	126.11	120.38
4	D	82	LEU	C-N-CA	5.57	126.11	120.38
1	I	117	ARG	CA-C-N	5.56	125.88	119.93
1	I	117	ARG	C-N-CA	5.56	125.88	119.93
1	H	219	SER	CA-C-N	5.55	125.48	119.76
1	H	219	SER	C-N-CA	5.55	125.48	119.76
1	H	149	GLU	CA-C-N	5.54	126.77	119.84
1	H	149	GLU	C-N-CA	5.54	126.77	119.84
1	H	438	ALA	CA-C-N	5.52	125.45	119.76
1	H	438	ALA	C-N-CA	5.52	125.45	119.76
4	C	185	ILE	CA-C-N	5.51	126.06	120.38
4	C	185	ILE	C-N-CA	5.51	126.06	120.38
1	H	117	ARG	CA-C-N	5.50	125.78	119.83
1	H	117	ARG	C-N-CA	5.50	125.78	119.83
1	H	454	PRO	CA-C-N	5.50	125.77	119.83
1	H	454	PRO	C-N-CA	5.50	125.77	119.83
4	F	103	LEU	CA-C-N	5.49	125.50	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	103	LEU	C-N-CA	5.49	125.50	119.90
4	F	121	ARG	CA-C-N	5.49	125.42	119.76
4	F	121	ARG	C-N-CA	5.49	125.42	119.76
1	I	310	ASP	CA-C-N	5.48	126.69	119.84
1	I	310	ASP	C-N-CA	5.48	126.69	119.84
4	E	247	GLU	CA-C-N	5.46	125.13	119.56
4	E	247	GLU	C-N-CA	5.46	125.13	119.56
4	B	185	ILE	CA-C-N	5.44	125.98	120.38
4	B	185	ILE	C-N-CA	5.44	125.98	120.38
1	I	450	LEU	CA-C-N	5.43	125.44	119.90
1	I	450	LEU	C-N-CA	5.43	125.44	119.90
1	I	585	LEU	CA-C-N	5.43	126.62	119.84
1	I	585	LEU	C-N-CA	5.43	126.62	119.84
1	I	219	SER	CA-C-N	5.39	125.30	119.85
1	I	219	SER	C-N-CA	5.39	125.30	119.85
4	A	185	ILE	CA-C-N	5.37	125.91	120.38
4	A	185	ILE	C-N-CA	5.37	125.91	120.38
1	H	450	LEU	CA-C-N	5.36	125.37	119.90
1	H	450	LEU	C-N-CA	5.36	125.37	119.90
1	I	287	LEU	CA-C-N	5.36	125.82	120.14
1	I	287	LEU	C-N-CA	5.36	125.82	120.14
1	I	68	LEU	N-CA-C	5.35	121.64	109.81
4	F	185	ILE	CA-C-N	5.35	125.89	120.38
4	F	185	ILE	C-N-CA	5.35	125.89	120.38
1	I	184	ALA	CA-C-N	5.34	125.01	119.56
1	I	184	ALA	C-N-CA	5.34	125.01	119.56
4	E	185	ILE	CA-C-N	5.20	125.74	120.38
4	E	185	ILE	C-N-CA	5.20	125.74	120.38
1	I	205	LEU	CA-C-N	5.20	125.11	119.76
1	I	205	LEU	C-N-CA	5.20	125.11	119.76
2	G	316	SER	CA-C-N	5.15	125.07	119.76
2	G	316	SER	C-N-CA	5.15	125.07	119.76
4	E	68	PHE	CA-C-N	5.13	126.25	119.84
4	E	68	PHE	C-N-CA	5.13	126.25	119.84
2	G	142	TYR	CA-C-N	5.13	125.17	119.32
2	G	142	TYR	C-N-CA	5.13	125.17	119.32
4	C	103	LEU	CA-C-N	5.11	125.11	119.90
4	C	103	LEU	C-N-CA	5.11	125.11	119.90
1	H	582	ASN	CA-C-N	5.01	124.92	119.76
1	H	582	ASN	C-N-CA	5.01	124.92	119.76

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	4085	0	4015	10	0
1	I	4047	0	3931	7	0
2	G	1903	0	1945	5	0
3	K	105	0	23	0	0
3	L	90	0	20	0	0
4	A	2375	0	2367	6	0
4	B	2378	0	2375	6	0
4	C	2356	0	2345	6	0
4	D	2376	0	2369	6	0
4	E	2374	0	2370	5	0
4	F	2367	0	2360	8	0
All	All	24456	0	24120	58	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 1.

All (58) 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)
4:E:54:LEU:N	4:E:55:PRO:CD	2.67	0.57
4:D:54:LEU:N	4:D:55:PRO:CD	2.68	0.57
4:A:54:LEU:N	4:A:55:PRO:CD	2.68	0.56
4:C:54:LEU:N	4:C:55:PRO:CD	2.68	0.56
1:H:96:THR:OG1	1:H:441:SER:OG	2.22	0.56
4:B:54:LEU:N	4:B:55:PRO:CD	2.68	0.55
4:F:54:LEU:N	4:F:55:PRO:CD	2.70	0.55
1:I:369:ALA:N	1:I:370:PRO:CD	2.72	0.53
2:G:329:ALA:O	2:G:330:LYS:C	2.53	0.51
1:H:68:LEU:N	1:H:69:PRO:CD	2.74	0.50
1:I:184:ALA:N	1:I:185:PRO:CD	2.75	0.50
4:A:300:PRO:HB2	4:A:301:PRO:HD3	1.93	0.49
1:I:569:GLN:N	1:I:570:PRO:CD	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:184:ALA:N	1:H:185:PRO:CD	2.76	0.49
4:B:91:VAL:HG12	4:B:91:VAL:O	2.13	0.49
4:F:282:HIS:CG	4:F:283:ASN:H	2.31	0.49
2:G:356:LYS:O	2:G:357:GLU:C	2.56	0.48
1:I:68:LEU:N	1:I:69:PRO:CD	2.77	0.48
1:H:585:LEU:N	1:H:586:PRO:CD	2.77	0.48
1:H:569:GLN:N	1:H:570:PRO:CD	2.78	0.47
4:A:291:HIS:H	4:A:298:VAL:HG21	1.80	0.46
4:D:91:VAL:HG12	4:D:91:VAL:O	2.15	0.46
1:I:53:PHE:CD1	2:G:125:PHE:CD2	3.04	0.46
1:H:283:TRP:CE3	1:H:287:LEU:HG	2.51	0.46
4:F:312:ALA:O	4:F:313:SER:C	2.59	0.44
4:E:247:GLU:N	4:E:248:PRO:CD	2.81	0.44
4:B:300:PRO:N	4:B:301:PRO:HD2	2.33	0.44
4:A:299:PHE:HB2	4:A:300:PRO:HD3	2.00	0.44
4:B:299:PHE:HB2	4:B:300:PRO:HD3	2.00	0.43
4:F:300:PRO:N	4:F:301:PRO:HD2	2.33	0.43
4:D:291:HIS:H	4:D:298:VAL:HG21	1.83	0.43
4:E:300:PRO:N	4:E:301:PRO:HD2	2.33	0.43
4:C:299:PHE:HB2	4:C:300:PRO:HD3	2.00	0.43
1:I:282:PRO:O	1:I:283:TRP:C	2.62	0.43
4:D:247:GLU:HB3	4:D:248:PRO:HD3	2.00	0.43
4:C:300:PRO:N	4:C:301:PRO:HD2	2.34	0.43
4:F:247:GLU:N	4:F:248:PRO:CD	2.82	0.43
4:B:291:HIS:H	4:B:298:VAL:HG21	1.84	0.42
4:A:247:GLU:N	4:A:248:PRO:CD	2.81	0.42
4:B:247:GLU:N	4:B:248:PRO:CD	2.82	0.42
4:E:299:PHE:HB2	4:E:300:PRO:HD3	2.01	0.42
2:G:184:LEU:N	2:G:185:PRO:CD	2.83	0.42
2:G:248:ASP:OD1	2:G:248:ASP:C	2.62	0.42
4:E:83:PRO:HA	4:E:84:PRO:HD3	1.91	0.42
4:D:300:PRO:HG2	4:D:301:PRO:HD3	2.01	0.41
1:H:68:LEU:HB3	1:H:69:PRO:HD3	2.03	0.41
4:C:291:HIS:H	4:C:298:VAL:HG21	1.86	0.41
1:H:447:LYS:HA	1:H:448:PRO:HD3	1.92	0.41
4:C:247:GLU:N	4:C:248:PRO:CD	2.83	0.41
4:A:300:PRO:N	4:A:301:PRO:CD	2.84	0.41
4:F:291:HIS:H	4:F:298:VAL:HG21	1.85	0.41
1:I:228:ARG:C	1:I:230:TRP:H	2.28	0.40
4:F:299:PHE:HB2	4:F:300:PRO:HD3	2.03	0.40
4:D:70:ASP:OD1	4:D:70:ASP:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:282:HIS:CG	4:F:283:ASN:N	2.89	0.40
1:H:432:CYS:O	1:H:433:GLU:C	2.63	0.40
4:C:68:PHE:HA	4:C:69:PRO:HD3	1.94	0.40
1:H:315:ASN:OD1	1:H:315:ASN:N	2.50	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	528/587 (90%)	513 (97%)	15 (3%)	0	100	100
1	I	524/587 (89%)	506 (97%)	15 (3%)	3 (1%)	21	52
2	G	236/303 (78%)	230 (98%)	5 (2%)	1 (0%)	30	60
4	A	295/322 (92%)	288 (98%)	7 (2%)	0	100	100
4	B	296/322 (92%)	289 (98%)	7 (2%)	0	100	100
4	C	295/322 (92%)	289 (98%)	6 (2%)	0	100	100
4	D	295/322 (92%)	284 (96%)	11 (4%)	0	100	100
4	E	297/322 (92%)	289 (97%)	8 (3%)	0	100	100
4	F	296/322 (92%)	287 (97%)	9 (3%)	0	100	100
All	All	3062/3409 (90%)	2975 (97%)	83 (3%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	357	GLU
1	I	68	LEU
1	I	229	LEU
1	I	271	SER

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	421/504 (84%)	419 (100%)	2 (0%)	81	80
1	I	416/504 (82%)	411 (99%)	5 (1%)	63	72
2	G	204/254 (80%)	204 (100%)	0	100	100
4	A	258/280 (92%)	258 (100%)	0	100	100
4	B	258/280 (92%)	258 (100%)	0	100	100
4	C	253/280 (90%)	253 (100%)	0	100	100
4	D	258/280 (92%)	257 (100%)	1 (0%)	84	81
4	E	256/280 (91%)	256 (100%)	0	100	100
4	F	255/280 (91%)	255 (100%)	0	100	100
All	All	2579/2942 (88%)	2571 (100%)	8 (0%)	84	83

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	101	VAL
1	I	192	LEU
1	I	279	LEU
1	I	287	LEU
1	I	328	LEU
1	H	283	TRP
1	H	287	LEU
4	D	234	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	461	HIS
1	I	549	ASN
1	I	563	GLN
1	I	580	ASN
1	I	581	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	281	GLN
1	H	375	HIS
1	H	549	ASN
4	A	140	GLN
4	A	282	HIS
4	D	22	GLN
4	D	177	GLN
4	B	131	ASN
4	B	241	ASN
4	E	241	ASN
4	C	148	HIS
4	F	22	GLN
4	F	213	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.

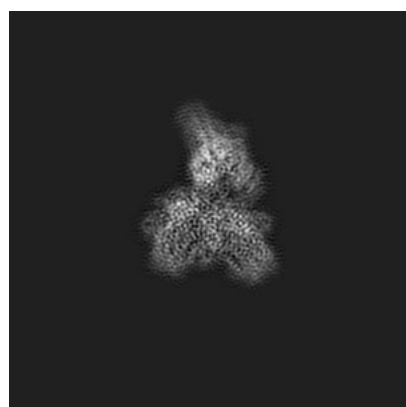
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9341. These allow visual inspection of the internal detail of the map and identification of artifacts.

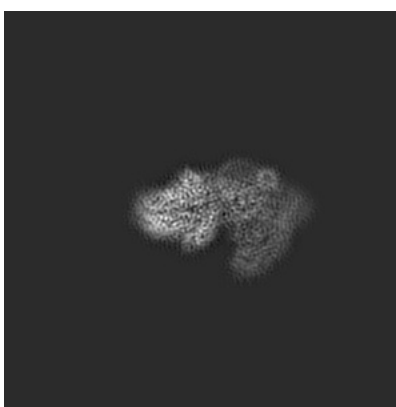
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

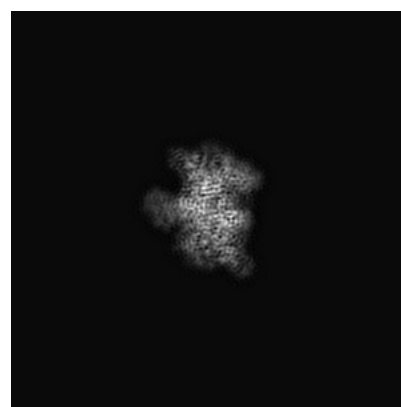
6.1.1 Primary map



X



Y

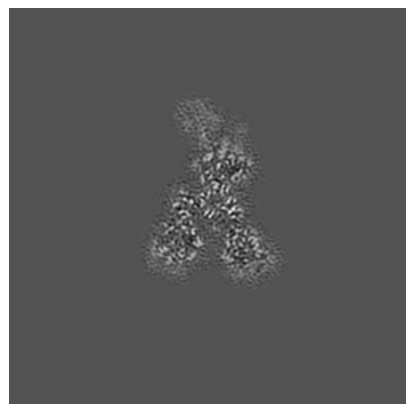


Z

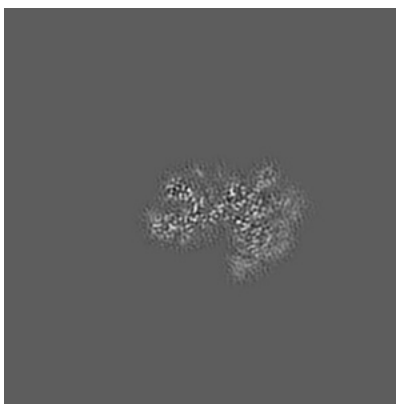
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

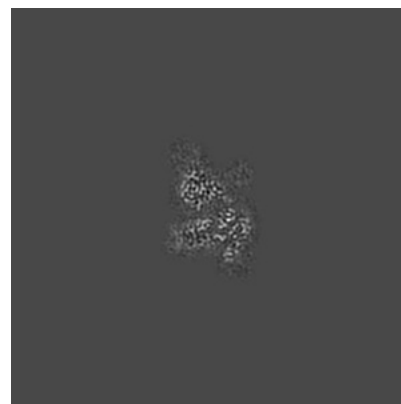
6.2.1 Primary map



X Index: 144



Y Index: 144



Z Index: 144

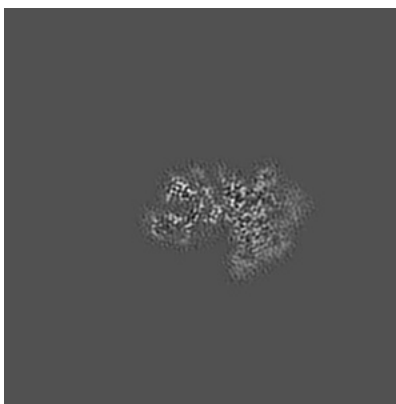
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

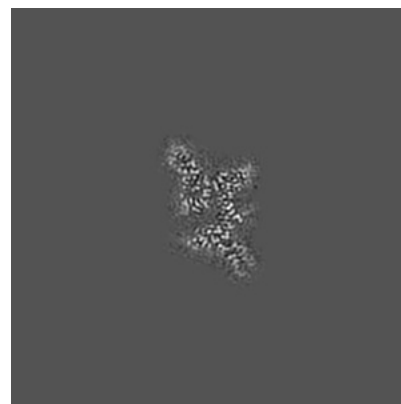
6.3.1 Primary map



X Index: 150



Y Index: 143

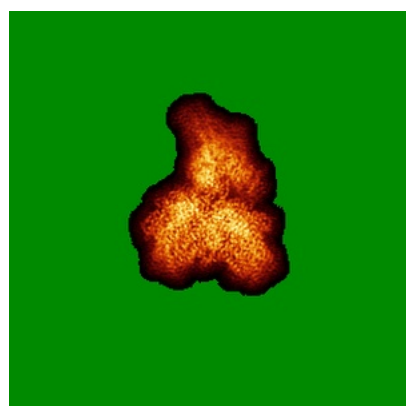


Z Index: 133

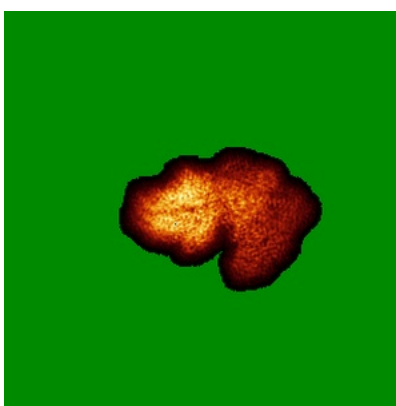
The images above show the largest variance slices of the map in three orthogonal directions.

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

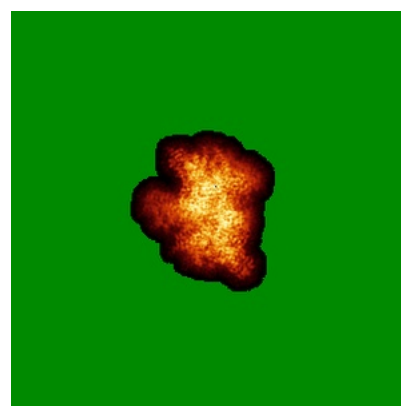
6.4.1 Primary map



X



Y

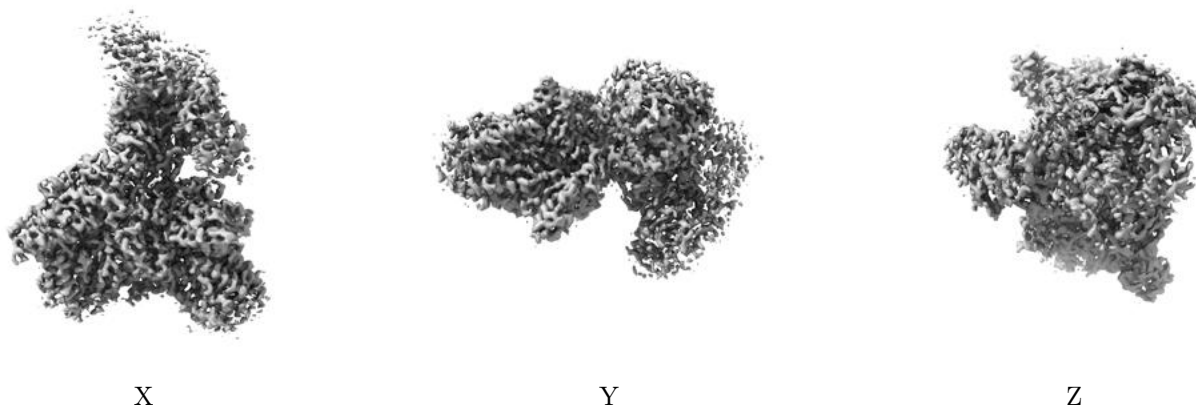


Z

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

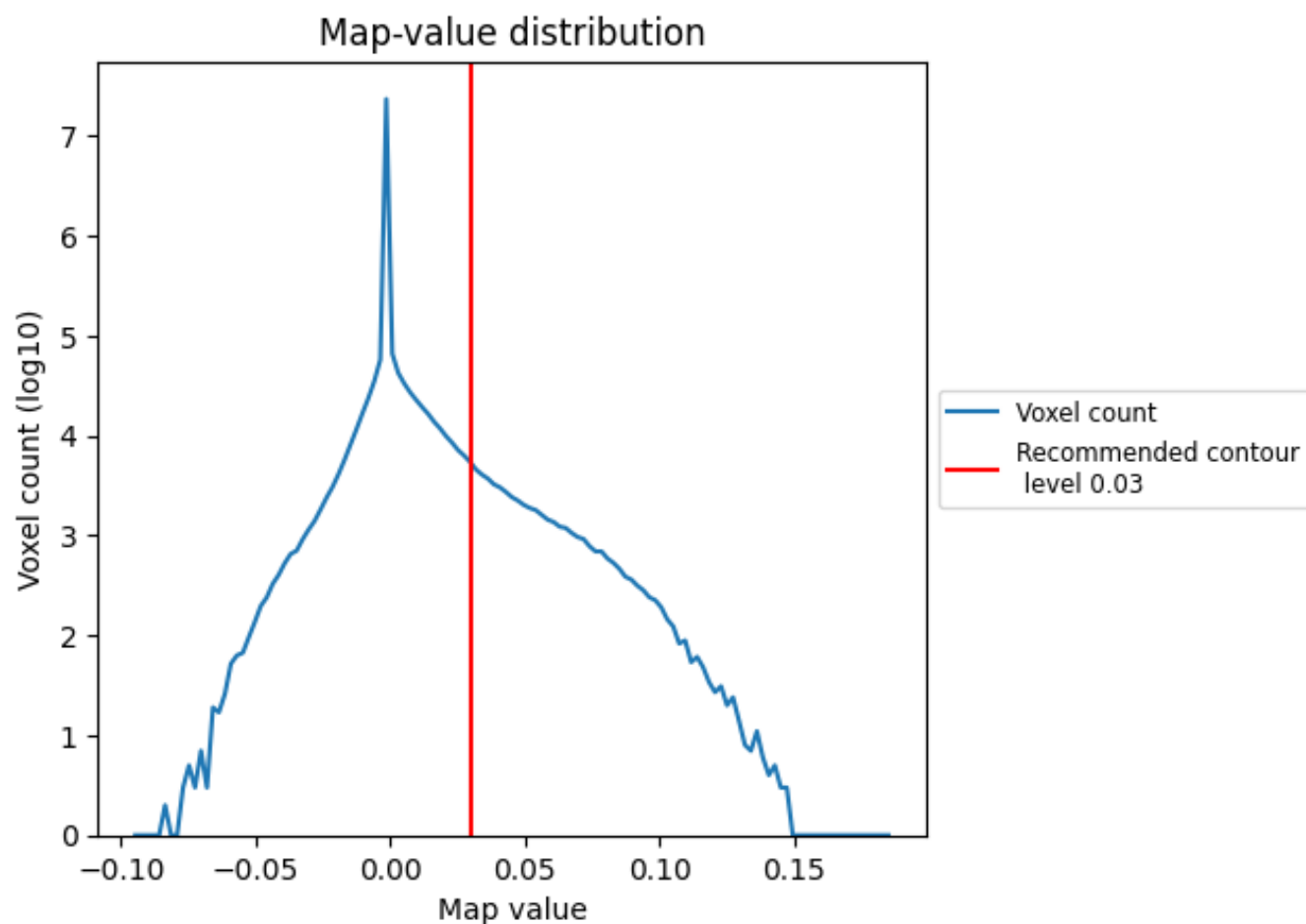
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

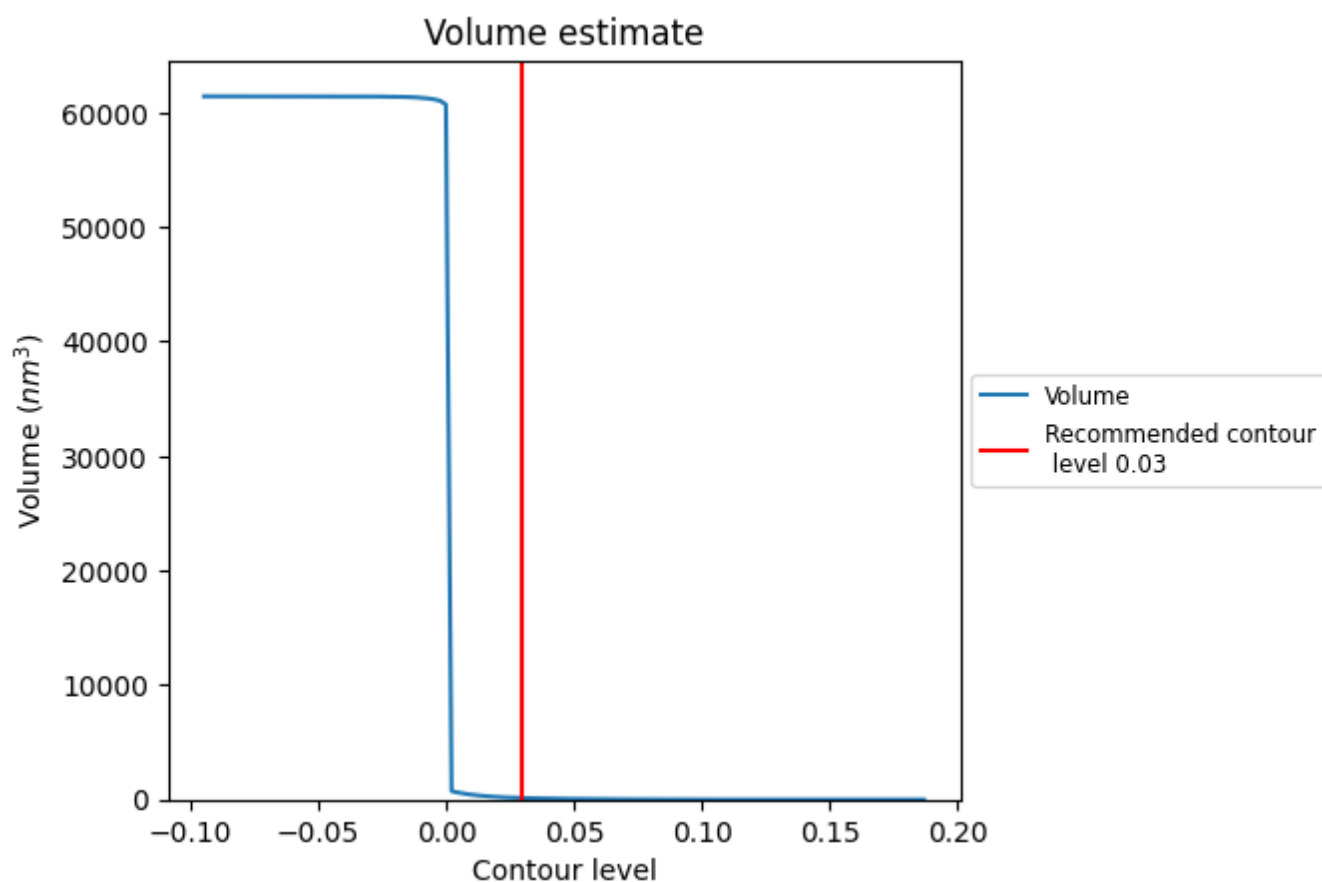
This section contains the results of statistical analysis of the map.

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.

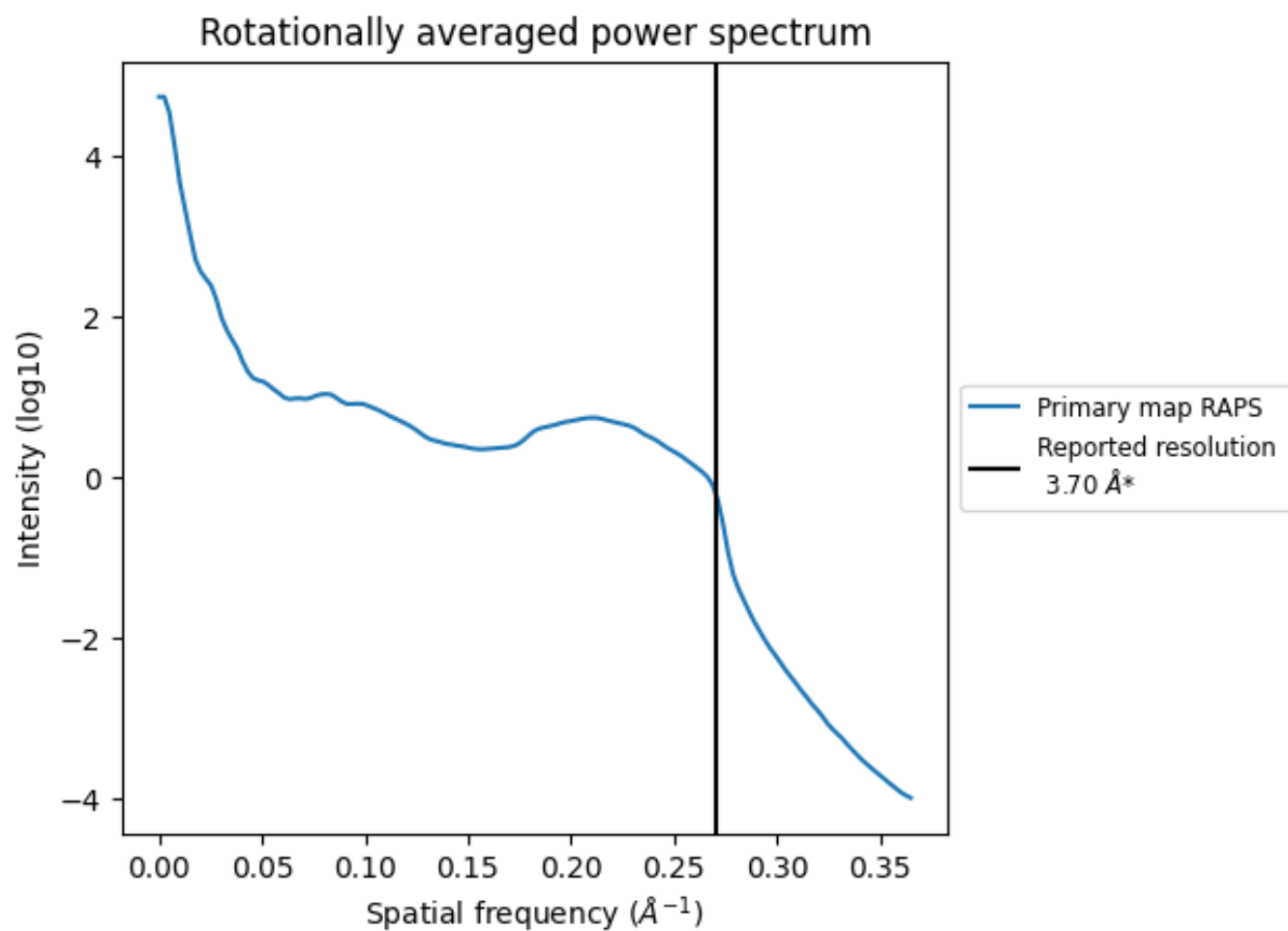
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 135 nm³; this corresponds to an approximate mass of 122 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 0.270 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

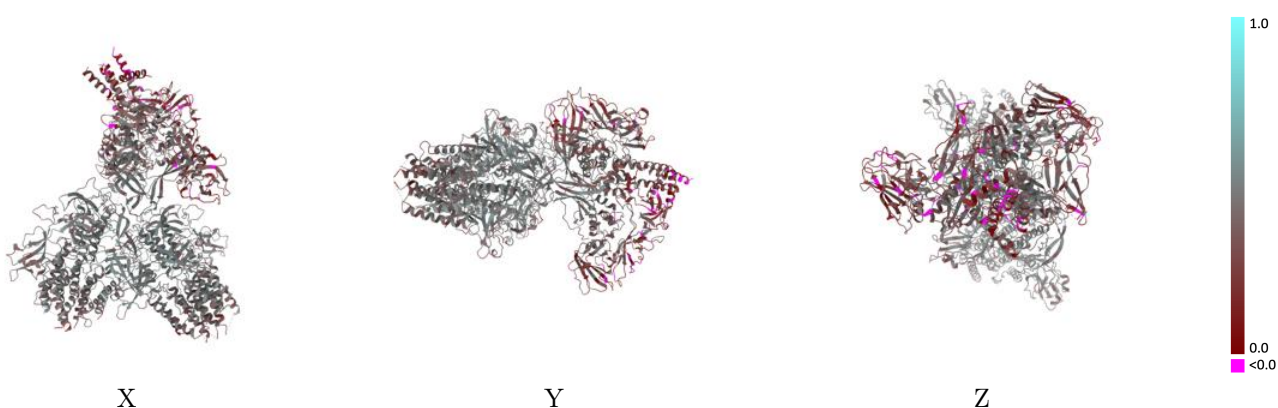
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9341 and PDB model 6N38. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

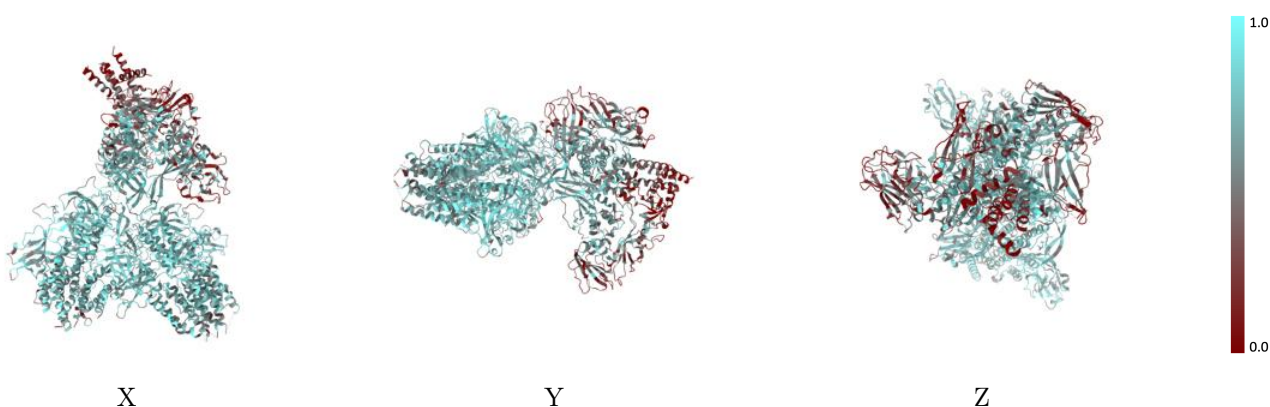
This section was not generated.

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



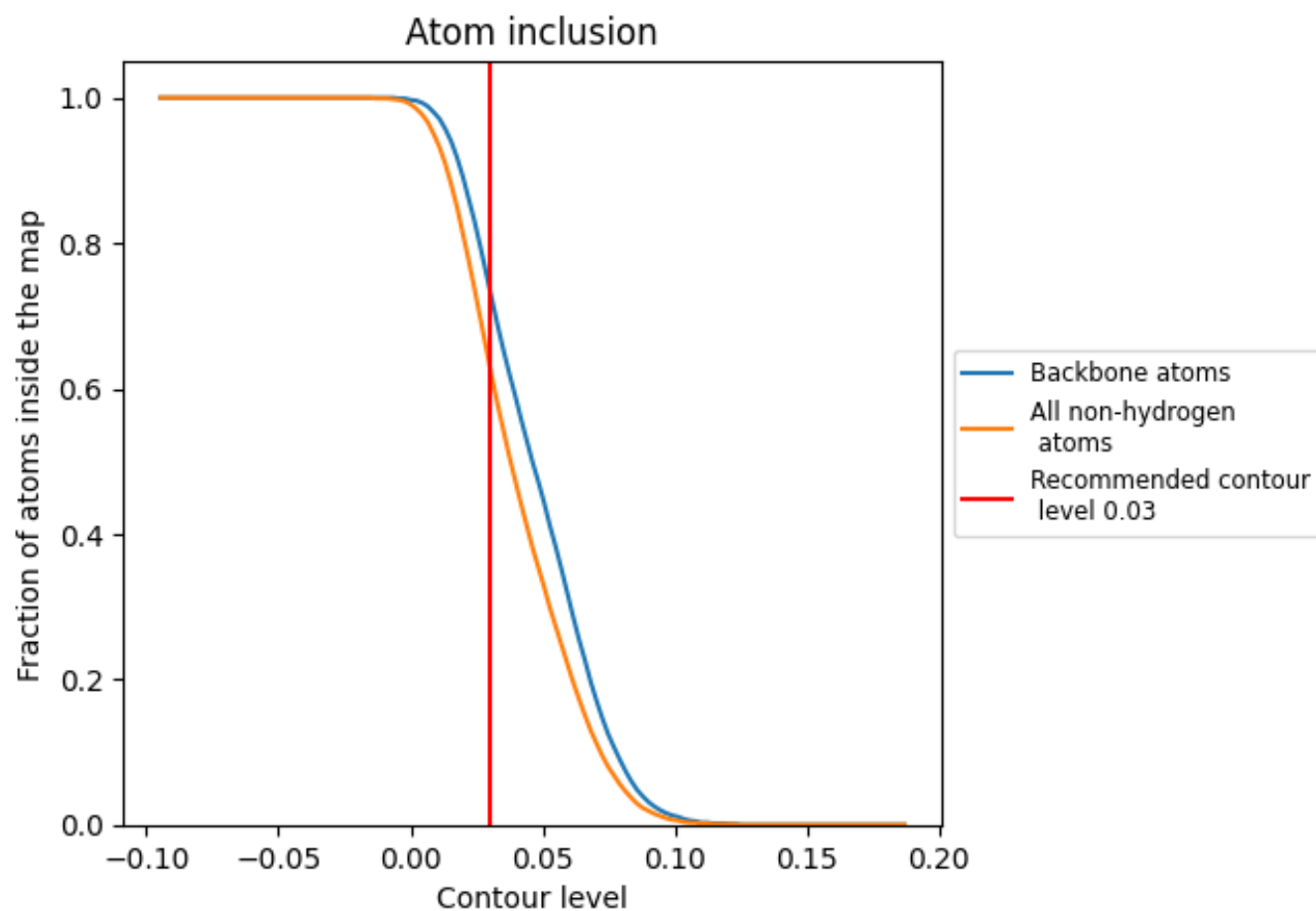
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 63% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6300	 0.4090
A	 0.7380	 0.4660
B	 0.7090	 0.4520
C	 0.7120	 0.4490
D	 0.7370	 0.4640
E	 0.7290	 0.4590
F	 0.7260	 0.4590
G	 0.6430	 0.4180
H	 0.4970	 0.3420
I	 0.4490	 0.3090
K	 0.1430	 0.1590
L	 0.2000	 0.2130

