



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:53 AM UTC

PDB ID : 7MUE / pdb_00007mue
EMDB ID : EMD-24006
Title : Legionella pneumophila Dot/Icm T4SS PR
Authors : Sheedlo, M.J.; Durie, C.L.; Swanson, M.; Lacy, D.B.; Ohi, M.D.
Deposited on : 2021-05-14
Resolution : 2.80 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

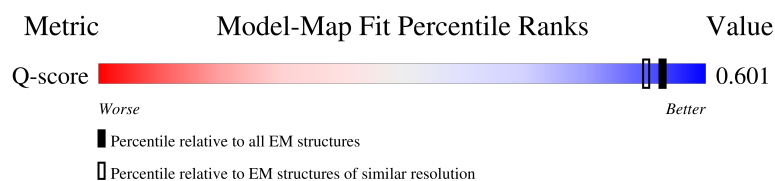
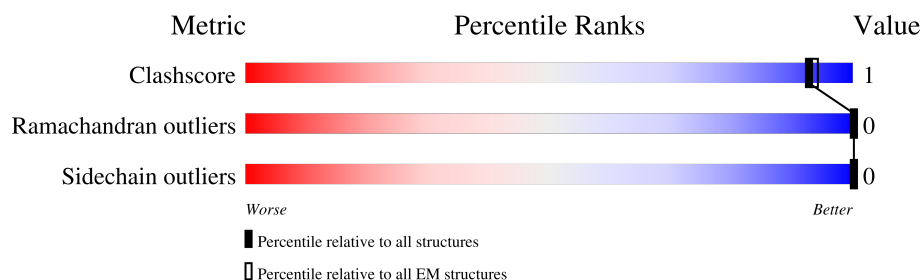
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	AF	269	
1	BF	269	
1	CF	269	
1	DF	269	

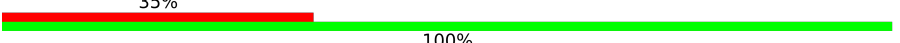
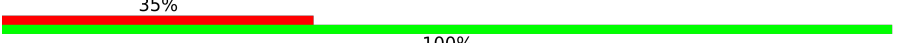
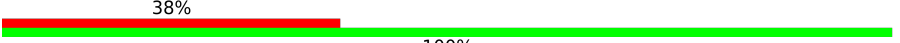
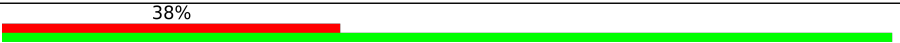
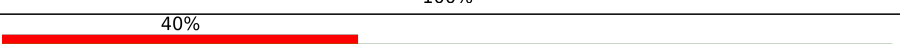
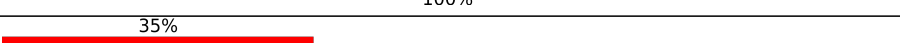
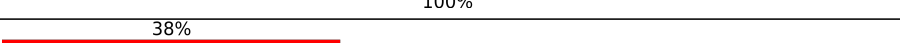
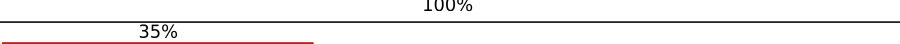
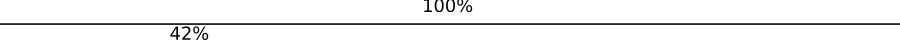
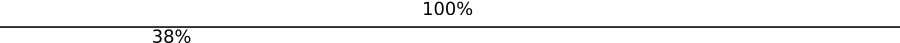
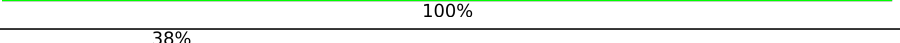
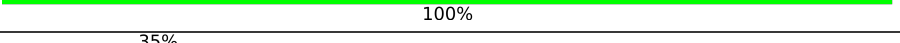
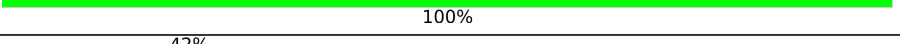
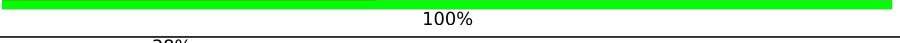
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Mol	Chain	Length	Quality of chain	
1	EF	269		
1	FF	269		
1	GF	269		
1	HF	269		
1	IF	269		
1	JF	269		
1	KF	269		
1	LF	269		
1	MF	269		
1	VF	269		
1	WF	269		
1	XF	269		
1	YF	269		
1	ZF	269		
2	AH	361		
2	BH	361		
2	CH	361		
2	DH	361		
2	EH	361		
2	FH	361		
2	GH	361		
2	HH	361		
2	IH	361		
2	JH	361		
2	KH	361		

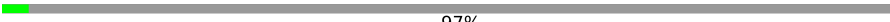
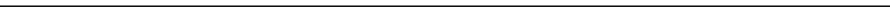
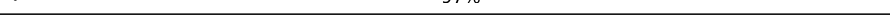
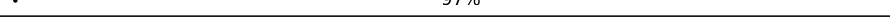
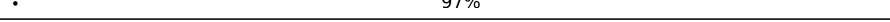
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Mol	Chain	Length	Quality of chain
2	LH	361	
2	MH	361	
2	VH	361	
2	WH	361	
2	XH	361	
2	YH	361	
2	ZH	361	
3	AX	48	
3	BX	48	
3	CX	48	
3	DX	48	
3	EX	48	
3	FX	48	
3	GX	48	
3	HX	48	
3	IX	48	
3	JX	48	
3	KX	48	
3	LX	48	
3	MX	48	
3	VX	48	
3	WX	48	
3	XX	48	
3	YX	48	
3	ZX	48	

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Mol	Chain	Length	Quality of chain
4	AG	1048	 97%
4	BG	1048	 97%
4	CG	1048	 97%
4	DG	1048	 97%
4	EG	1048	 97%
4	FG	1048	 97%
4	GG	1048	 97%
4	HG	1048	 97%
4	IG	1048	 97%
4	JG	1048	 97%
4	KG	1048	 97%
4	LG	1048	 97%
4	MG	1048	 97%
4	VG	1048	 97%
4	WG	1048	 97%
4	XG	1048	 97%
4	YG	1048	 97%
4	ZG	1048	 97%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 40266 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 DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	BF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	CF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	DF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	EF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	FF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	GF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	HF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	IF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	JF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	KF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	LF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	MF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	VF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	WF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	XF	63	Total 483	C 308	N 84	O 90	S 1	0	0
1	YF	63	Total 483	C 308	N 84	O 90	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ZF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

- Molecule 2 is a protein called Type IV secretion protein IcmK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	XH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	YH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	ZH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	AH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	BH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	CH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	DH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	EH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	FH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	GH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	HH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	IH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	JH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	KH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	LH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	MH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	VH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
2	WH	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		

- Molecule 3 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	AX	48	Total	C	N	O	0	0
			240	144	48	48		
3	BX	48	Total	C	N	O	0	0
			240	144	48	48		
3	CX	48	Total	C	N	O	0	0
			240	144	48	48		
3	DX	48	Total	C	N	O	0	0
			240	144	48	48		
3	EX	48	Total	C	N	O	0	0
			240	144	48	48		
3	FX	48	Total	C	N	O	0	0
			240	144	48	48		
3	GX	48	Total	C	N	O	0	0
			240	144	48	48		
3	HX	48	Total	C	N	O	0	0
			240	144	48	48		
3	IX	48	Total	C	N	O	0	0
			240	144	48	48		
3	JX	48	Total	C	N	O	0	0
			240	144	48	48		
3	KX	48	Total	C	N	O	0	0
			240	144	48	48		
3	LX	48	Total	C	N	O	0	0
			240	144	48	48		
3	MX	48	Total	C	N	O	0	0
			240	144	48	48		
3	VX	48	Total	C	N	O	0	0
			240	144	48	48		
3	WX	48	Total	C	N	O	0	0
			240	144	48	48		
3	XX	48	Total	C	N	O	0	0
			240	144	48	48		
3	YX	48	Total	C	N	O	0	0
			240	144	48	48		
3	ZX	48	Total	C	N	O	0	0
			240	144	48	48		

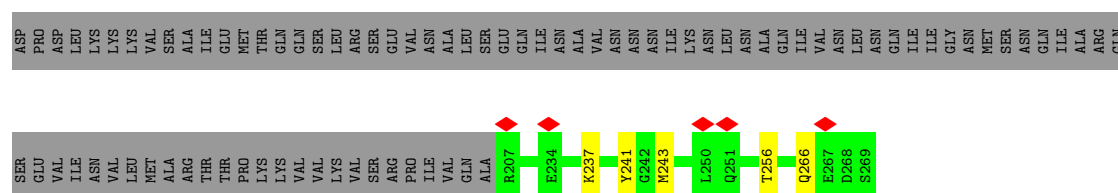
- Molecule 4 is a protein called IcmE protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	IG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

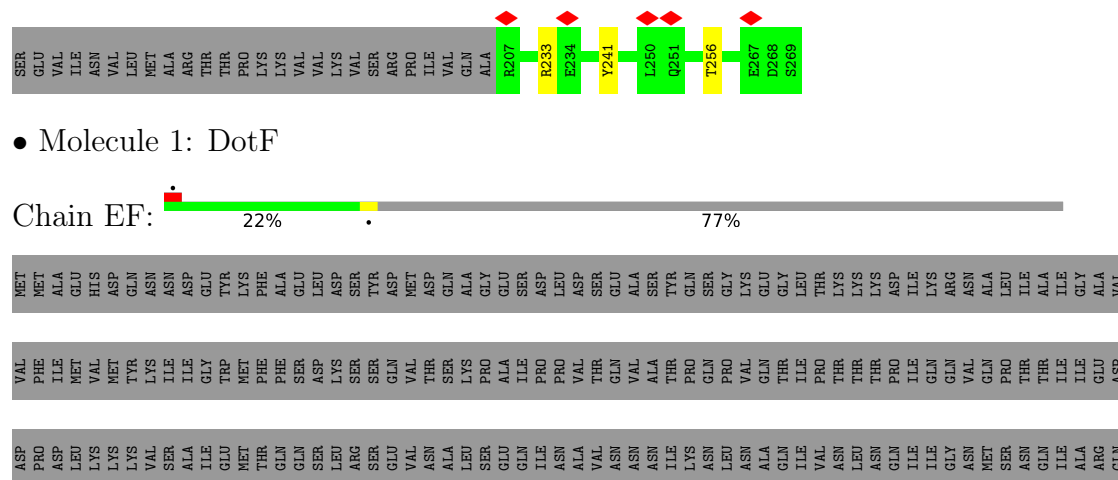
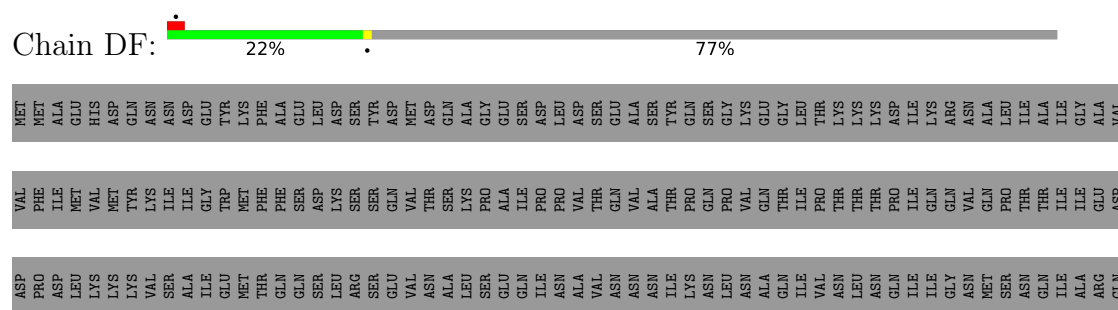
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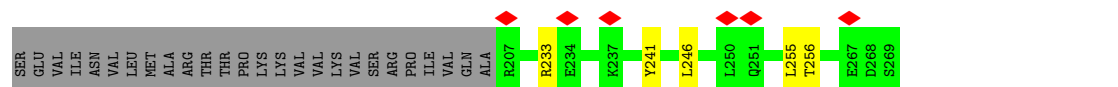
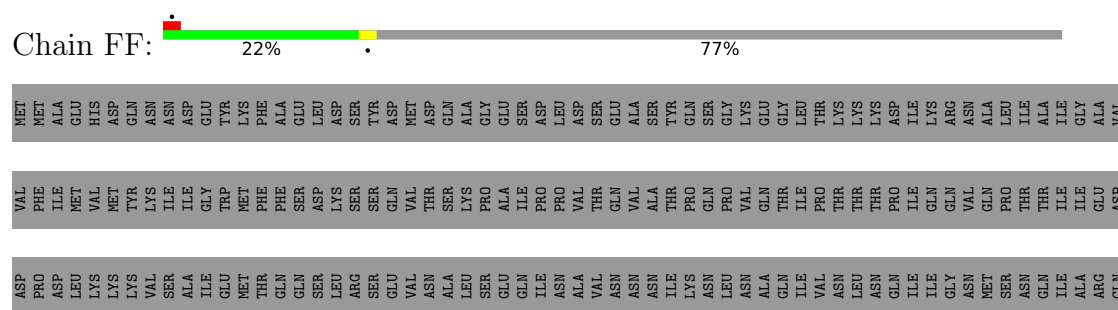
Mol	Chain	Residues	Atoms					AltConf	Trace
4	AG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	BG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	CG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	DG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	EG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	FG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	GG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	HG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	JG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	KG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	LG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	MG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	VG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	WG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	XG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	YG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
4	ZG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

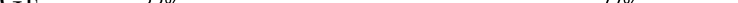


- Molecule 1: DotF



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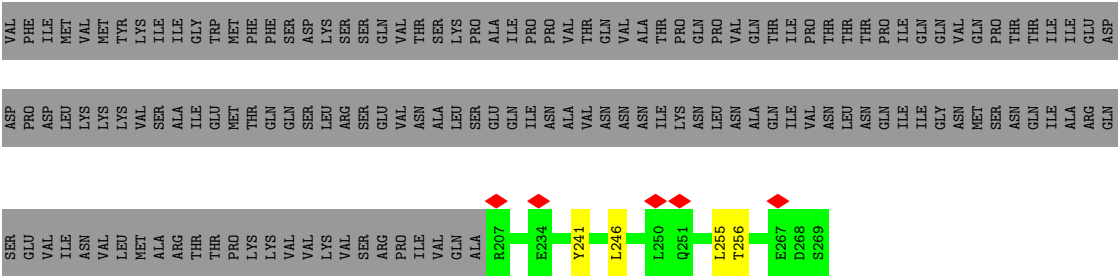


Chain GF:  22% 77%

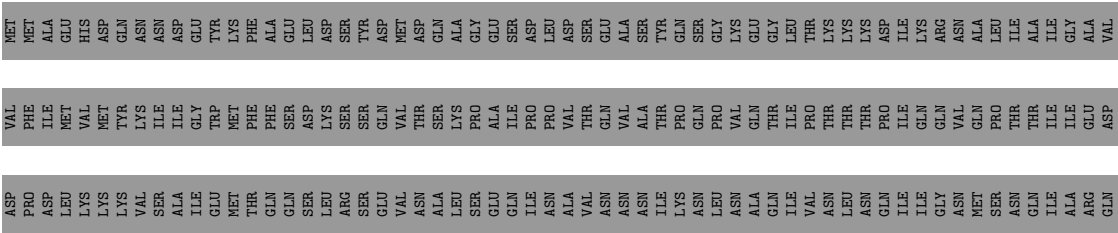
Chain HF:  21% 77%

Chain IF: 22% 77%

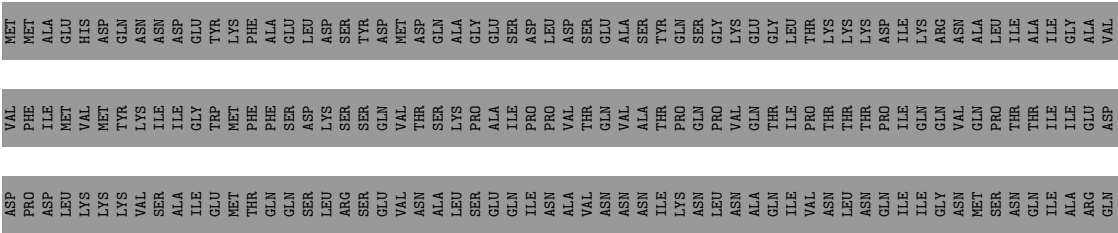
Chain JF: 22% 77%



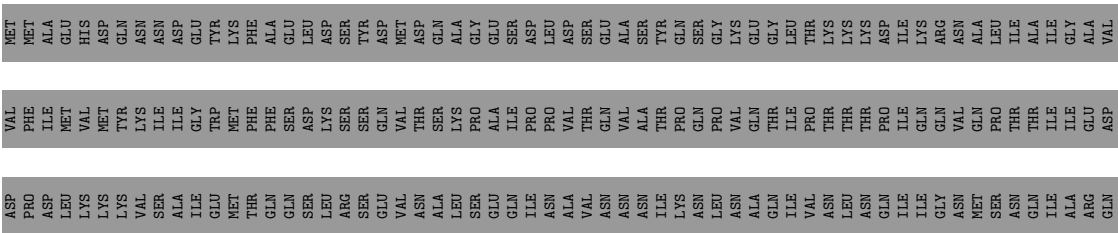
• Molecule 1: DotF

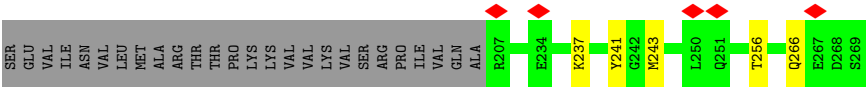


• Molecule 1: DotF

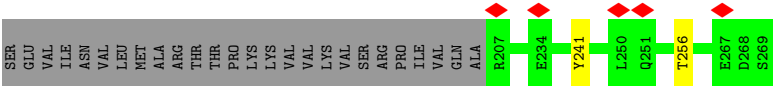
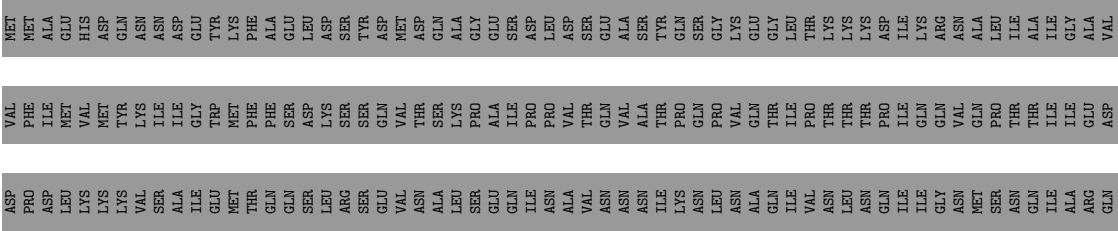


• Molecule 1: DotF

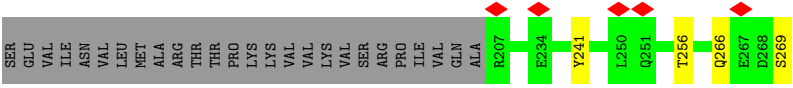
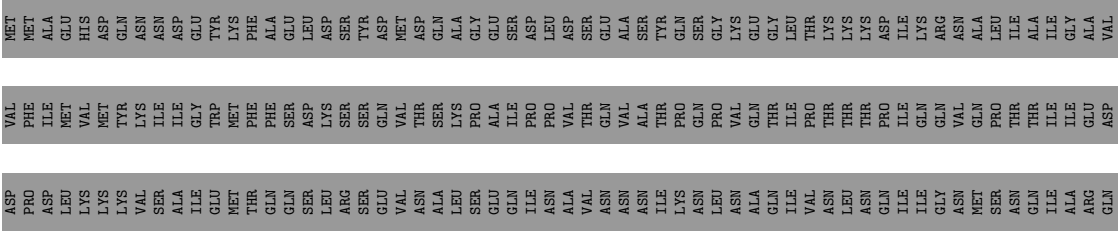




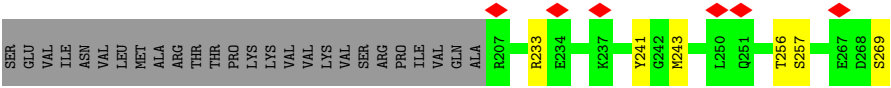
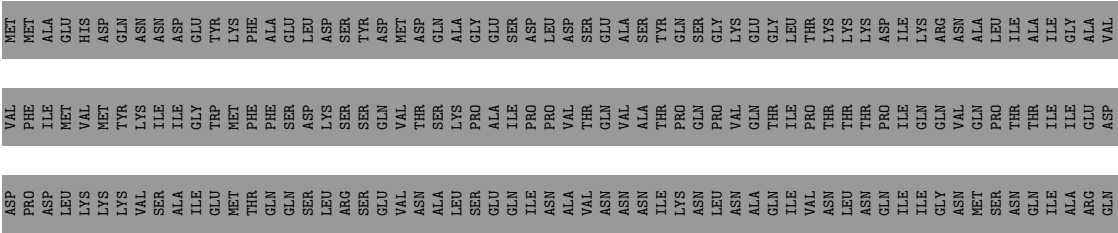
• Molecule 1: DotF



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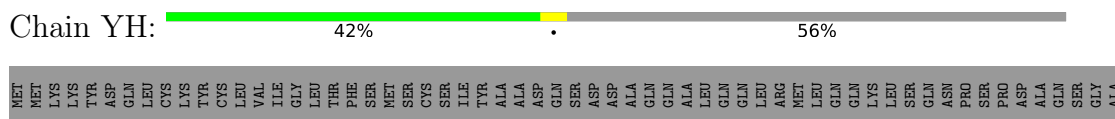


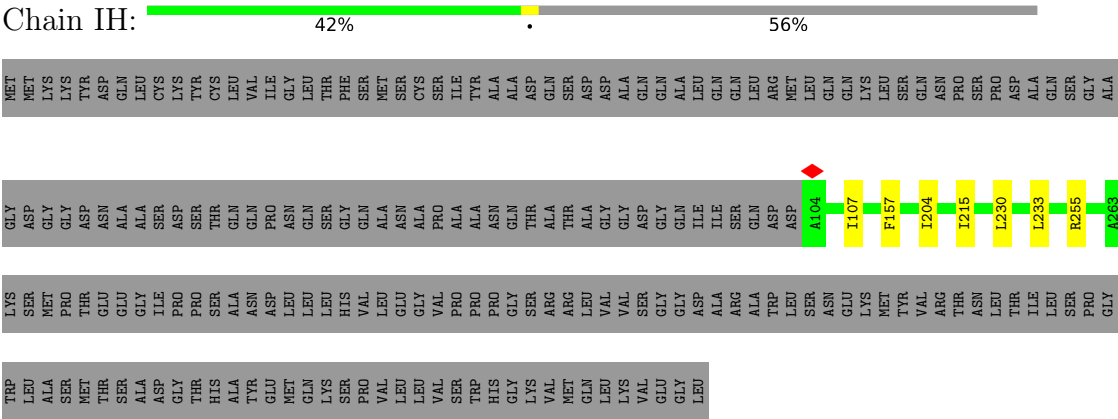
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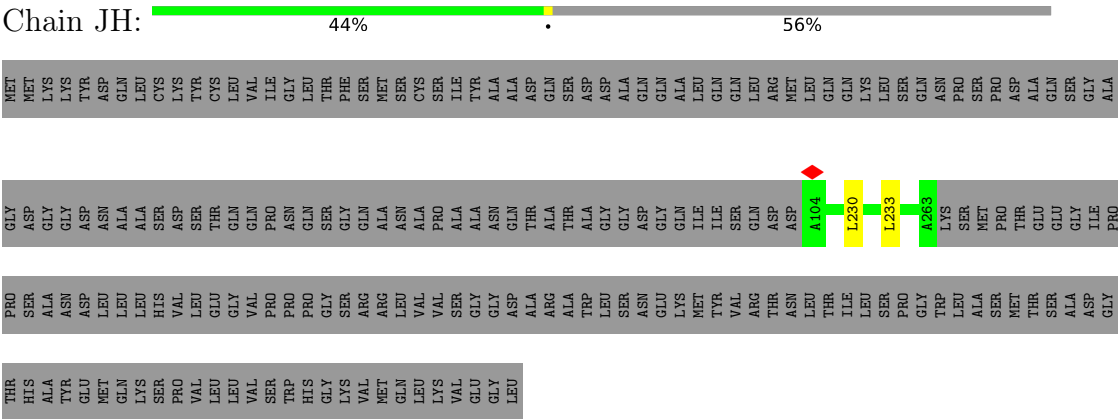
- Molecule 2: Type IV secretion protein IcmK

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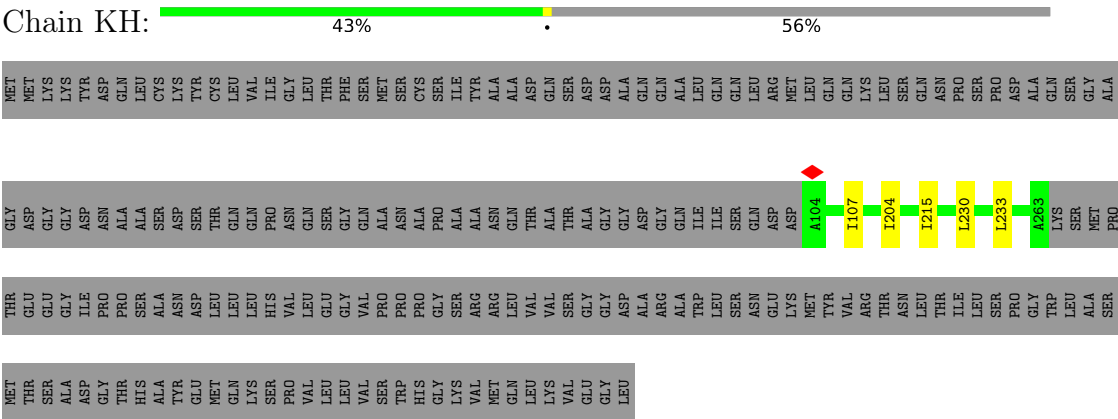




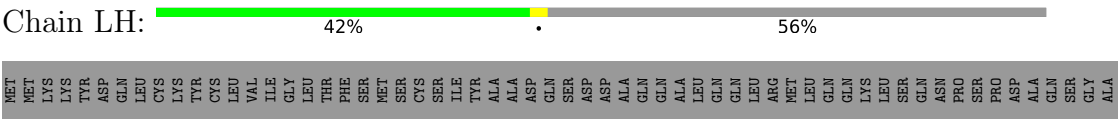
• Molecule 2: Type IV secretion protein IcmK

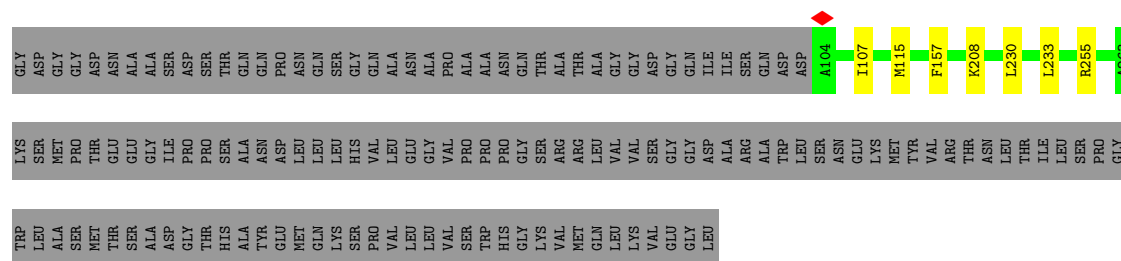


• Molecule 2: Type IV secretion protein IcmK

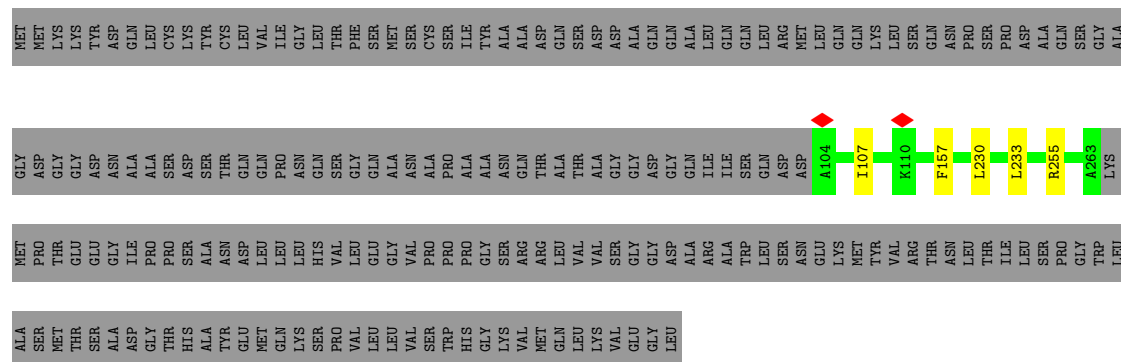


• Molecule 2: Type IV secretion protein IcmK

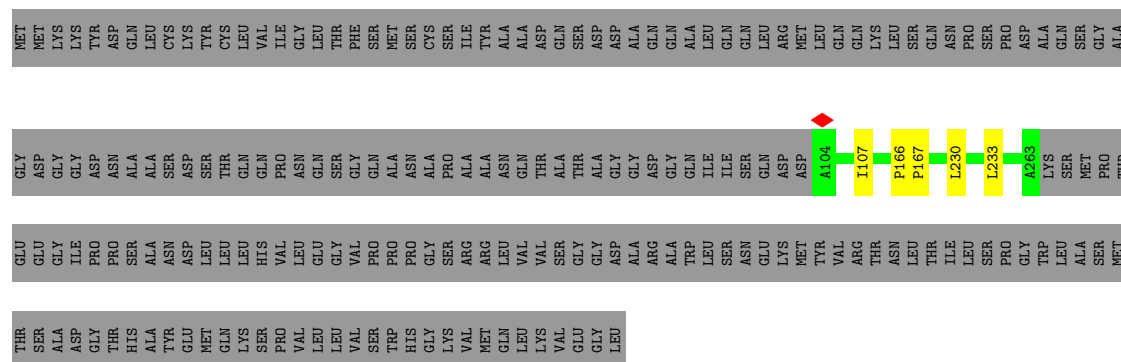




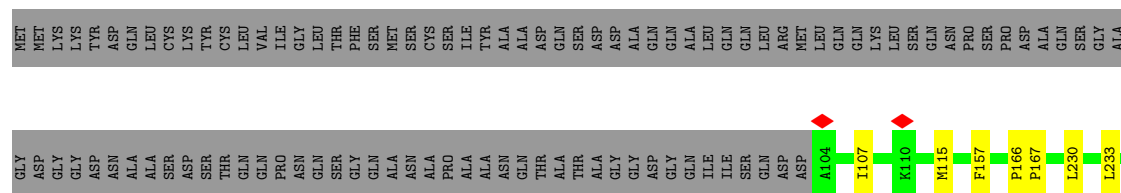
- Molecule 2: Type IV secretion protein IcmK

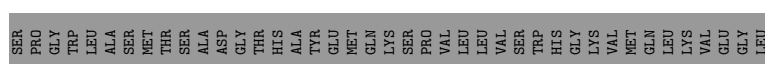
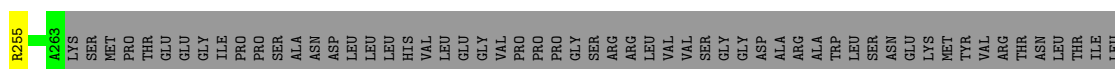


- Molecule 2: Type IV secretion protein IcmK

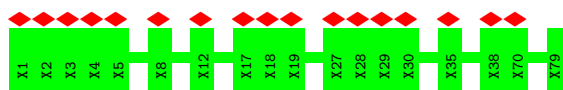


- Molecule 2: Type IV secretion protein IcmK

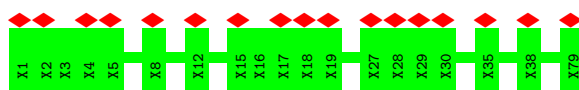




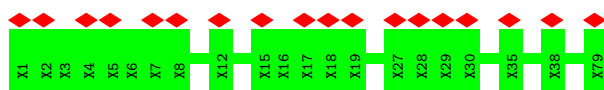
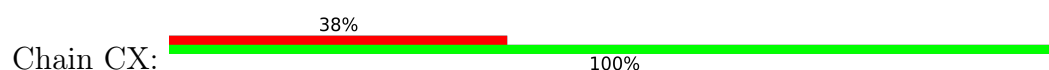
- Molecule 3: Unknown protein fragment



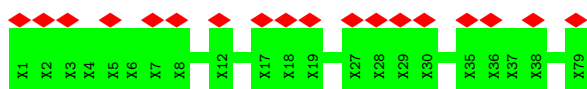
- Molecule 3: Unknown protein fragment



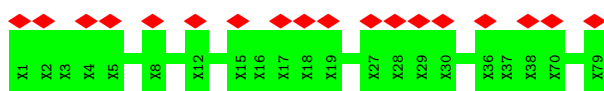
- Molecule 3: Unknown protein fragment



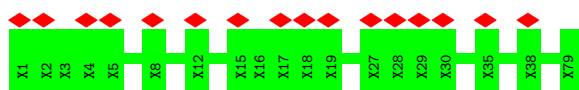
- Molecule 3: Unknown protein fragment



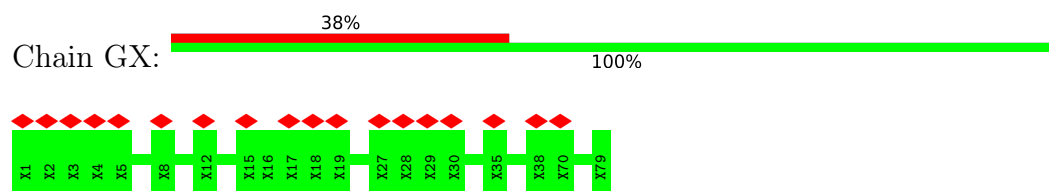
- Molecule 3: Unknown protein fragment



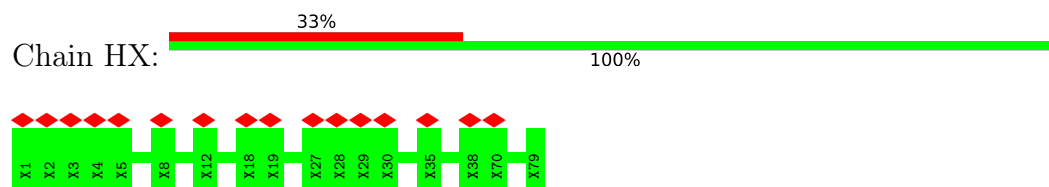
- Molecule 3: Unknown protein fragment



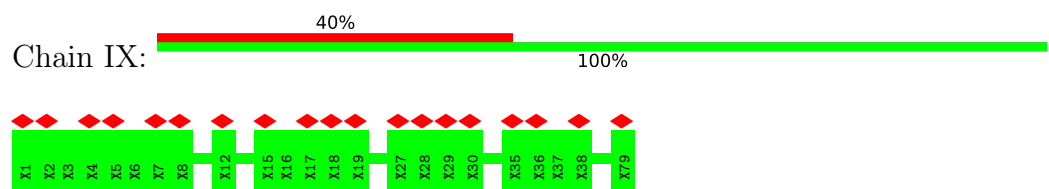
- Molecule 3: Unknown protein fragment



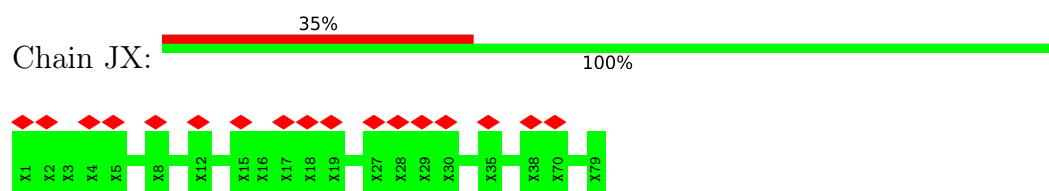
- Molecule 3: Unknown protein fragment



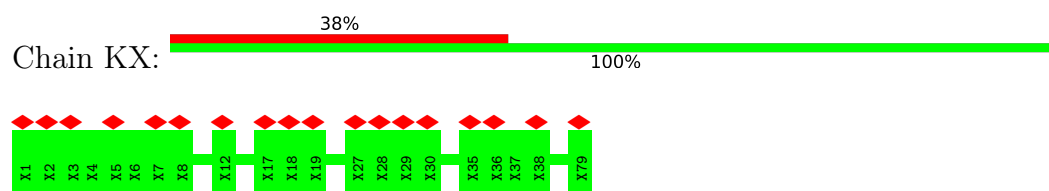
- Molecule 3: Unknown protein fragment



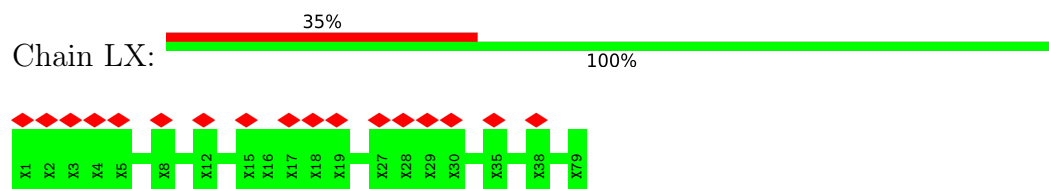
- Molecule 3: Unknown protein fragment



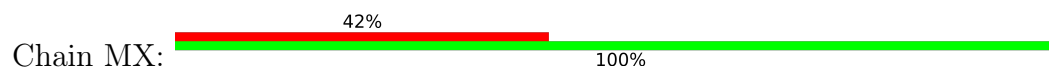
- Molecule 3: Unknown protein fragment

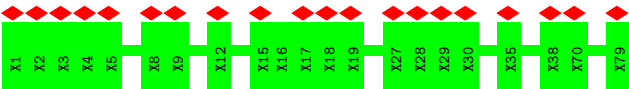


- Molecule 3: Unknown protein fragment

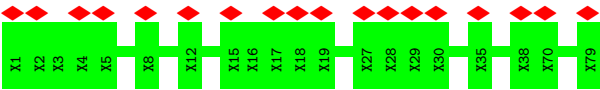


- Molecule 3: Unknown protein fragment

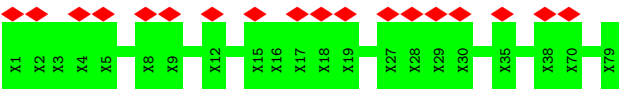




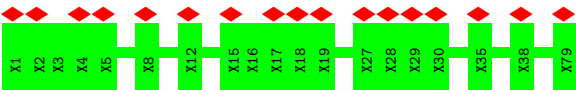
• Molecule 3: Unknown protein fragment



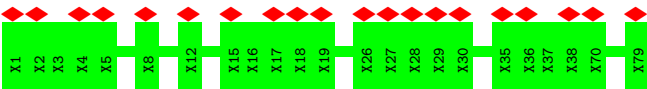
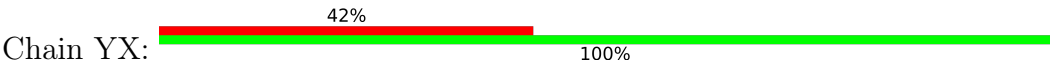
• Molecule 3: Unknown protein fragment



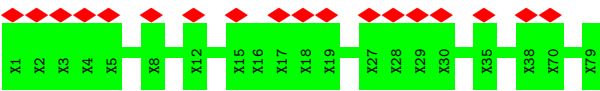
• Molecule 3: Unknown protein fragment



• Molecule 3: Unknown protein fragment



• Molecule 3: Unknown protein fragment



• Molecule 4: IcmE protein

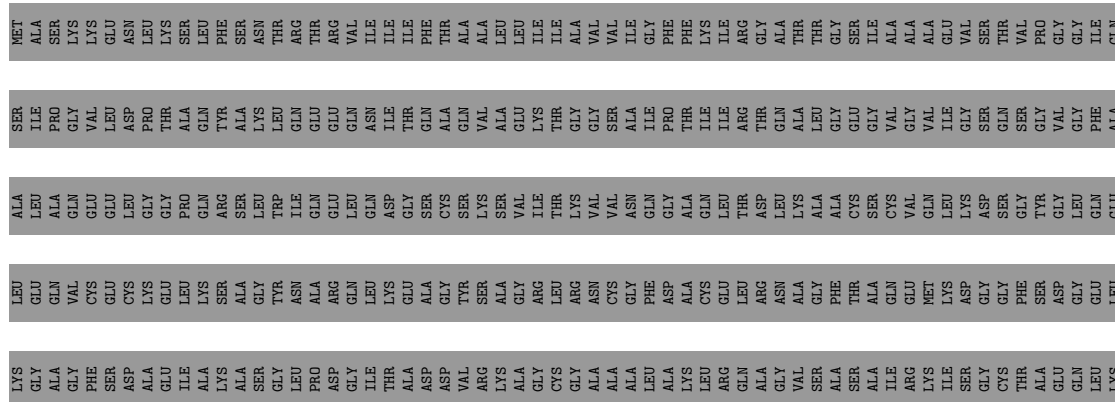


MET	ALA	SER	GLY	LYS	GLU	ASN	LEU	LYS	SER	PHE	THR	ASN	THR	ARG	THR	ARG	VAL	ILE	ILE	ILE	PHE	THR	ALA	ALA	LEU	LEU	ILE	ILE	ALA	VAL	VAL	VAL	ILE	GLY	GLY	ALA	THR	THR	GLY	SER	ILE	ALA	ALA	ALA	VAL	GLU	VAL	SER	THR	VAL	VAL	PRO	GLY	GLY	ILE	GLN
SER	ILE	PRO	GLY	VAL	LEU	ASP	PRO	THR	ALA	GLN	TYR	ALA	LYS	LEU	GLN	GLU	GLN	ASN	ILE	THR	THR	GLN	ALA	GLN	VAL	ALA	GLU	LYS	THR	THR	ILE	ILE	THR	ARG	THR	GLN	ALA	ALA	LEU	GLY	GLU	GLY	VAL	VAL	ILE	GLY	SER	GLN	SER	SER	GLY	VAL	VAL	GLY	PHE	ALA



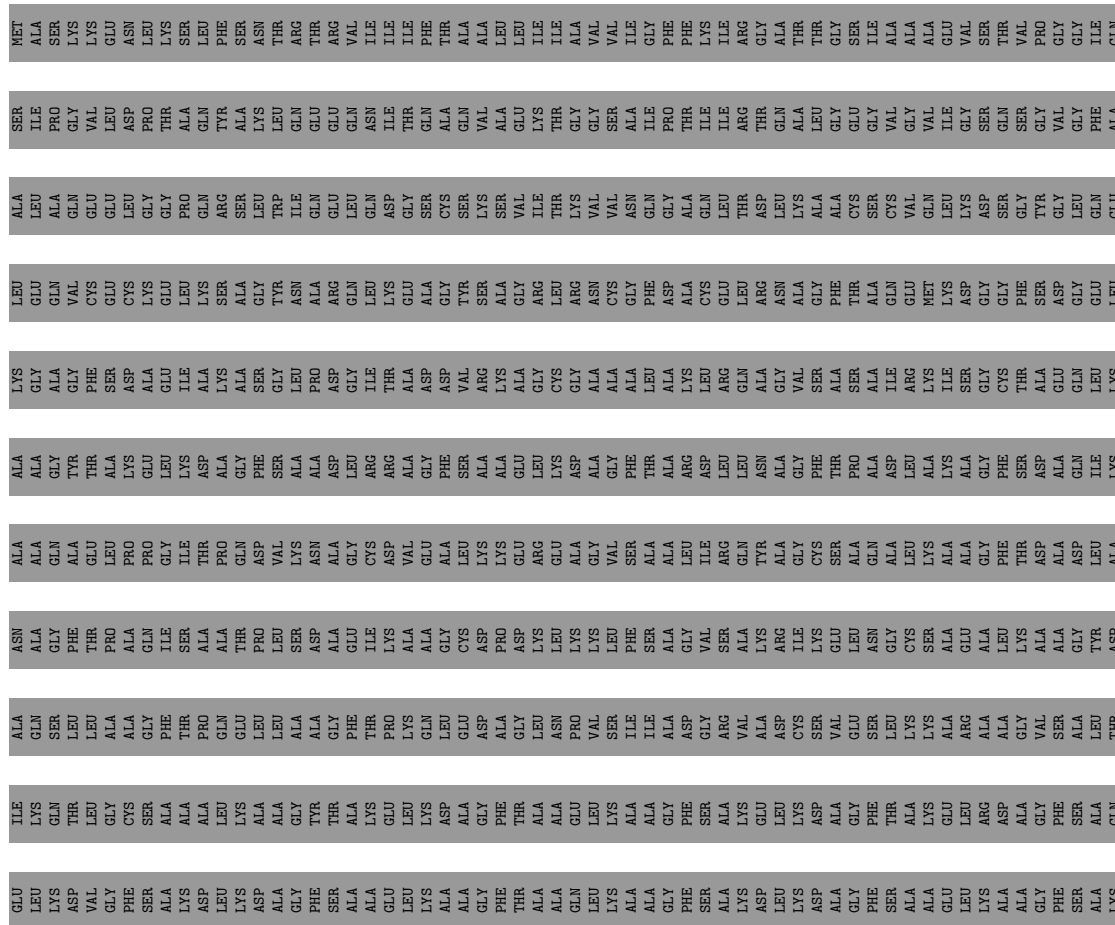
Chain EG: 97%





[illegible]







[illegible]

- Molecule 4: IcmE protein

Chain VG: 97%

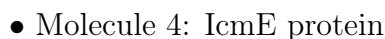
GLU	LEU	ARG	ASN	ALA	GLY	PHE	SER	PRO	GLN	GLU	SER	ALA	VAL	GLY	LEU	GLN	GLY	PRO	ASP	LEU	GLN	LEU	SER	ASP	GLY	THR	ILE	LEU	PRO	PRO	GLY	ALA	ALA	PRO	ARG	PRO	THR	THR	SER	ASP	ALA	ALA	SER	SER	ALA	ALA	GLU	GLN	LEU	GLN	LEU	LEU	GLN	YS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

GLN	ASN	GLU	GLN	LEU	ALA	GLU	GLN	LYS	TYR	Q791	Q792	E793	I794	T824	GLU	GLU	THR	LYS	THR	SER	GLY	GLY	THR	THR	GLY	THR	GLY	SER	ASN	ASN	GLN	PRO	VAL	ASP	GLN	GLY	ALA	VAL	SER	ALA	GLN	ASN	THR	THR	GLY	ASP
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- Molecule 4: IcmE protein

Chain WG: 97%

[illegible]



97%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43907	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.124	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	561.0, 561.0, 561.0	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	AF	0.15	0/490	0.42	0/660
1	BF	0.15	0/490	0.44	0/660
1	CF	0.16	0/490	0.43	0/660
1	DF	0.15	0/490	0.40	0/660
1	EF	0.15	0/490	0.40	0/660
1	FF	0.15	0/490	0.42	0/660
1	GF	0.15	0/490	0.39	0/660
1	HF	0.15	0/490	0.42	0/660
1	IF	0.15	0/490	0.39	0/660
1	JF	0.16	0/490	0.43	0/660
1	KF	0.15	0/490	0.40	0/660
1	LF	0.15	0/490	0.43	0/660
1	MF	0.16	0/490	0.41	0/660
1	VF	0.16	0/490	0.43	0/660
1	WF	0.16	0/490	0.41	0/660
1	XF	0.15	0/490	0.44	0/660
1	YF	0.15	0/490	0.41	0/660
1	ZF	0.15	0/490	0.39	0/660
2	AH	0.17	0/1269	0.43	0/1734
2	BH	0.16	0/1269	0.40	0/1734
2	CH	0.17	0/1269	0.42	0/1734
2	DH	0.15	0/1269	0.38	0/1734
2	EH	0.16	0/1269	0.41	0/1734
2	FH	0.16	0/1269	0.40	0/1734
2	GH	0.16	0/1269	0.41	0/1734
2	HH	0.16	0/1269	0.42	0/1734
2	IH	0.16	0/1269	0.40	0/1734
2	JH	0.15	0/1269	0.37	0/1734
2	KH	0.16	0/1269	0.39	0/1734
2	LH	0.16	0/1269	0.39	0/1734
2	MH	0.16	0/1269	0.40	0/1734
2	VH	0.15	0/1269	0.38	0/1734
2	WH	0.16	0/1269	0.39	0/1734
2	XH	0.16	0/1269	0.39	0/1734

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	YH	0.16	0/1269	0.41	0/1734
2	ZH	0.17	0/1269	0.43	0/1734
4	AG	0.12	0/278	0.33	0/377
4	BG	0.12	0/278	0.34	0/377
4	CG	0.13	0/278	0.35	0/377
4	DG	0.12	0/278	0.32	0/377
4	EG	0.10	0/278	0.29	0/377
4	FG	0.12	0/278	0.34	0/377
4	GG	0.13	0/278	0.34	0/377
4	HG	0.19	0/278	0.44	0/377
4	IG	0.15	0/278	0.39	0/377
4	JG	0.14	0/278	0.37	0/377
4	KG	0.12	0/278	0.32	0/377
4	LG	0.12	0/278	0.34	0/377
4	MG	0.16	0/278	0.38	0/377
4	VG	0.14	0/278	0.36	0/377
4	WG	0.14	0/278	0.36	0/377
4	XG	0.17	0/278	0.39	0/377
4	YG	0.11	0/278	0.30	0/377
4	ZG	0.12	0/278	0.34	0/377
All	All	0.15	0/36666	0.40	0/49878

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AF	483	0	502	1	0
1	BF	483	0	502	4	0
1	CF	483	0	502	3	0
1	DF	483	0	502	2	0
1	EF	483	0	502	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	FF	483	0	502	3	0
1	GF	483	0	502	3	0
1	HF	483	0	502	4	0
1	IF	483	0	502	2	0
1	JF	483	0	502	2	0
1	KF	483	0	502	1	0
1	LF	483	0	502	2	0
1	MF	483	0	502	3	0
1	VF	483	0	502	1	0
1	WF	483	0	502	3	0
1	XF	483	0	502	4	0
1	YF	483	0	502	2	0
1	ZF	483	0	502	1	0
2	AH	1238	0	1252	5	0
2	BH	1238	0	1252	5	0
2	CH	1238	0	1252	5	0
2	DH	1238	0	1252	5	0
2	EH	1238	0	1252	5	0
2	FH	1238	0	1252	6	0
2	GH	1238	0	1252	2	0
2	HH	1238	0	1252	6	0
2	IH	1238	0	1252	4	0
2	JH	1238	0	1252	1	0
2	KH	1238	0	1252	3	0
2	LH	1238	0	1252	5	0
2	MH	1238	0	1252	3	0
2	VH	1238	0	1252	3	0
2	WH	1238	0	1252	5	0
2	XH	1238	0	1252	3	0
2	YH	1238	0	1252	6	0
2	ZH	1238	0	1252	3	0
3	AX	240	0	55	0	0
3	BX	240	0	55	0	0
3	CX	240	0	55	0	0
3	DX	240	0	54	0	0
3	EX	240	0	54	0	0
3	FX	240	0	55	0	0
3	GX	240	0	55	0	0
3	HX	240	0	54	0	0
3	IX	240	0	54	0	0
3	JX	240	0	55	0	0
3	KX	240	0	55	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	LX	240	0	55	0	0
3	MX	240	0	55	0	0
3	VX	240	0	55	0	0
3	WX	240	0	54	0	0
3	XX	240	0	55	0	0
3	YX	240	0	54	0	0
3	ZX	240	0	55	0	0
4	AG	276	0	263	1	0
4	BG	276	0	263	2	0
4	CG	276	0	263	2	0
4	DG	276	0	263	2	0
4	EG	276	0	263	1	0
4	FG	276	0	263	1	0
4	GG	276	0	263	0	0
4	HG	276	0	263	1	0
4	IG	276	0	263	1	0
4	JG	276	0	263	1	0
4	KG	276	0	263	2	0
4	LG	276	0	263	1	0
4	MG	276	0	263	2	0
4	VG	276	0	263	1	0
4	WG	276	0	263	2	0
4	XG	276	0	263	0	0
4	YG	276	0	263	1	0
4	ZG	276	0	263	0	0
All	All	40266	0	37290	111	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.

The worst 5 of 111 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:DH:204:ILE:HG12	2:DH:215:ILE:HG12	1.81	0.63
2:KH:204:ILE:HG12	2:KH:215:ILE:HG12	1.81	0.62
2:CH:204:ILE:HG12	2:CH:215:ILE:HG12	1.83	0.61
2:IH:204:ILE:HG12	2:IH:215:ILE:HG12	1.83	0.60
2:YH:204:ILE:HG12	2:YH:215:ILE:HG12	1.84	0.60

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	AF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	BF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	CF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	DF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	EF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	FF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	GF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	HF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	IF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	JF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
1	KF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	LF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	MF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	VF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
1	WF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	XF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	YF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
1	ZF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
2	AH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	BH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	CH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	DH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	EH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	FH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	GH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	HH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	IH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	JH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	KH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	LH	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
2	MH	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
2	VH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	WH	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
2	XH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
2	YH	158/361 (44%)	153 (97%)	5 (3%)	0	100	100
2	ZH	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
4	AG	32/1048 (3%)	32 (100%)	0	0	100	100
4	BG	32/1048 (3%)	32 (100%)	0	0	100	100
4	CG	32/1048 (3%)	32 (100%)	0	0	100	100
4	DG	32/1048 (3%)	32 (100%)	0	0	100	100
4	EG	32/1048 (3%)	32 (100%)	0	0	100	100
4	FG	32/1048 (3%)	32 (100%)	0	0	100	100
4	GG	32/1048 (3%)	32 (100%)	0	0	100	100
4	HG	32/1048 (3%)	32 (100%)	0	0	100	100
4	IG	32/1048 (3%)	32 (100%)	0	0	100	100
4	JG	32/1048 (3%)	32 (100%)	0	0	100	100
4	KG	32/1048 (3%)	32 (100%)	0	0	100	100
4	LG	32/1048 (3%)	32 (100%)	0	0	100	100
4	MG	32/1048 (3%)	32 (100%)	0	0	100	100
4	VG	32/1048 (3%)	32 (100%)	0	0	100	100
4	WG	32/1048 (3%)	32 (100%)	0	0	100	100
4	XG	32/1048 (3%)	32 (100%)	0	0	100	100
4	YG	32/1048 (3%)	32 (100%)	0	0	100	100
4	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
All	All	4518/30204 (15%)	4378 (97%)	140 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AF	53/237 (22%)	53 (100%)	0	100	100
1	BF	53/237 (22%)	53 (100%)	0	100	100
1	CF	53/237 (22%)	53 (100%)	0	100	100
1	DF	53/237 (22%)	53 (100%)	0	100	100
1	EF	53/237 (22%)	53 (100%)	0	100	100
1	FF	53/237 (22%)	53 (100%)	0	100	100
1	GF	53/237 (22%)	53 (100%)	0	100	100
1	HF	53/237 (22%)	53 (100%)	0	100	100
1	IF	53/237 (22%)	53 (100%)	0	100	100
1	JF	53/237 (22%)	53 (100%)	0	100	100
1	KF	53/237 (22%)	53 (100%)	0	100	100
1	LF	53/237 (22%)	53 (100%)	0	100	100
1	MF	53/237 (22%)	53 (100%)	0	100	100
1	VF	53/237 (22%)	53 (100%)	0	100	100
1	WF	53/237 (22%)	53 (100%)	0	100	100
1	XF	53/237 (22%)	53 (100%)	0	100	100
1	YF	53/237 (22%)	53 (100%)	0	100	100
1	ZF	53/237 (22%)	53 (100%)	0	100	100
2	AH	137/300 (46%)	137 (100%)	0	100	100
2	BH	137/300 (46%)	137 (100%)	0	100	100
2	CH	137/300 (46%)	137 (100%)	0	100	100
2	DH	137/300 (46%)	137 (100%)	0	100	100
2	EH	137/300 (46%)	137 (100%)	0	100	100
2	FH	137/300 (46%)	137 (100%)	0	100	100
2	GH	137/300 (46%)	137 (100%)	0	100	100
2	HH	137/300 (46%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	IH	137/300 (46%)	137 (100%)	0	100	100
2	JH	137/300 (46%)	137 (100%)	0	100	100
2	KH	137/300 (46%)	137 (100%)	0	100	100
2	LH	137/300 (46%)	137 (100%)	0	100	100
2	MH	137/300 (46%)	137 (100%)	0	100	100
2	VH	137/300 (46%)	137 (100%)	0	100	100
2	WH	137/300 (46%)	137 (100%)	0	100	100
2	XH	137/300 (46%)	137 (100%)	0	100	100
2	YH	137/300 (46%)	137 (100%)	0	100	100
2	ZH	137/300 (46%)	137 (100%)	0	100	100
4	AG	31/765 (4%)	31 (100%)	0	100	100
4	BG	31/765 (4%)	31 (100%)	0	100	100
4	CG	31/765 (4%)	31 (100%)	0	100	100
4	DG	31/765 (4%)	31 (100%)	0	100	100
4	EG	31/765 (4%)	31 (100%)	0	100	100
4	FG	31/765 (4%)	31 (100%)	0	100	100
4	GG	31/765 (4%)	31 (100%)	0	100	100
4	HG	31/765 (4%)	31 (100%)	0	100	100
4	IG	31/765 (4%)	31 (100%)	0	100	100
4	JG	31/765 (4%)	31 (100%)	0	100	100
4	KG	31/765 (4%)	31 (100%)	0	100	100
4	LG	31/765 (4%)	31 (100%)	0	100	100
4	MG	31/765 (4%)	31 (100%)	0	100	100
4	VG	31/765 (4%)	31 (100%)	0	100	100
4	WG	31/765 (4%)	31 (100%)	0	100	100
4	XG	31/765 (4%)	31 (100%)	0	100	100
4	YG	31/765 (4%)	31 (100%)	0	100	100
4	ZG	31/765 (4%)	31 (100%)	0	100	100
All	All	3978/23436 (17%)	3978 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48

such sidechains are listed below:

Mol	Chain	Res	Type
4	ZG	807	GLN
2	EH	262	ASN
2	AH	118	ASN
2	CH	257	GLN
2	GH	203	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	ZX	1
3	GX	1
3	CX	1
3	KX	1
3	BX	1
3	HX	1

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Mol	Chain	Number of breaks
3	YX	1
3	MX	1
3	XX	1
3	IX	1
3	LX	1
3	WX	1
3	FX	1
3	AX	1
3	EX	1
3	DX	1
3	JX	1
3	VX	1

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	ZX	38:UNK	C	70:UNK	N	24.53
1	GX	38:UNK	C	70:UNK	N	24.52
1	CX	38:UNK	C	70:UNK	N	24.51
1	KX	38:UNK	C	70:UNK	N	24.51
1	BX	38:UNK	C	70:UNK	N	24.49

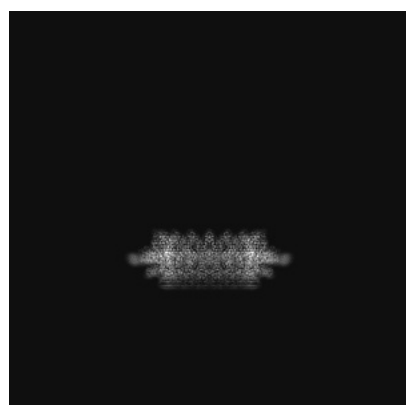
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24006. These allow visual inspection of the internal detail of the map and identification of artifacts.

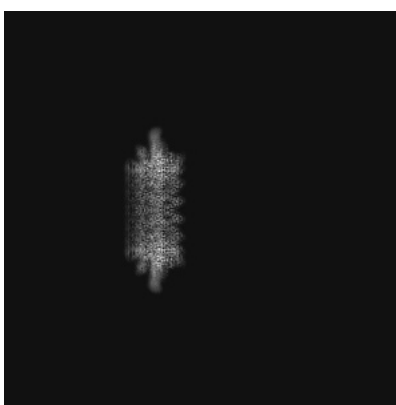
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

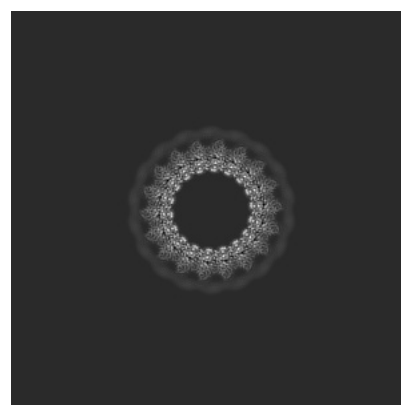
6.1.1 Primary map



X



Y

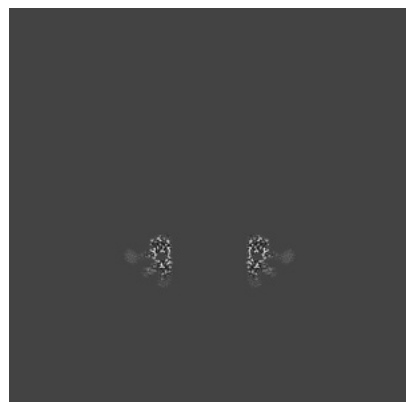


Z

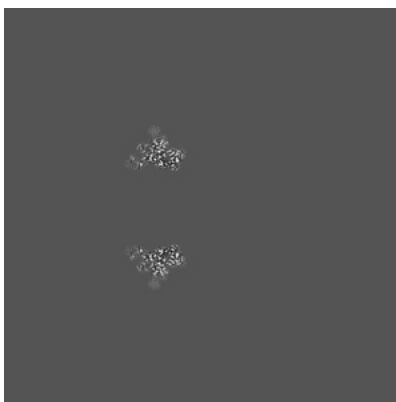
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

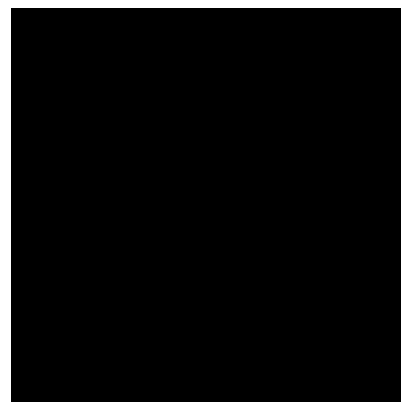
6.2.1 Primary map



X Index: 255



Y Index: 255



Z Index: 255

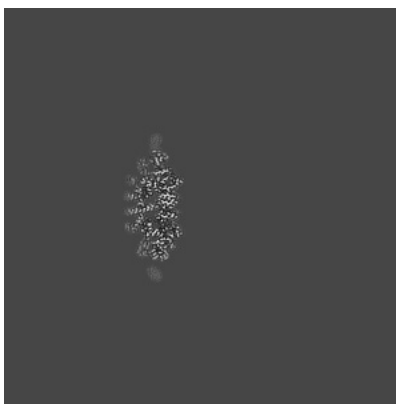
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

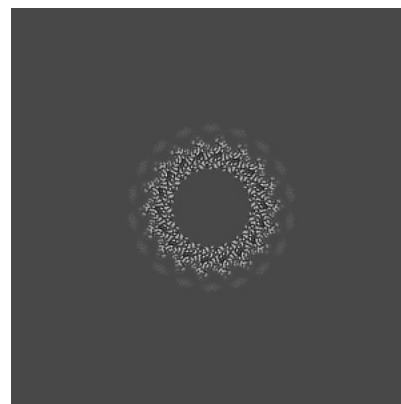
6.3.1 Primary map



X Index: 204



Y Index: 202

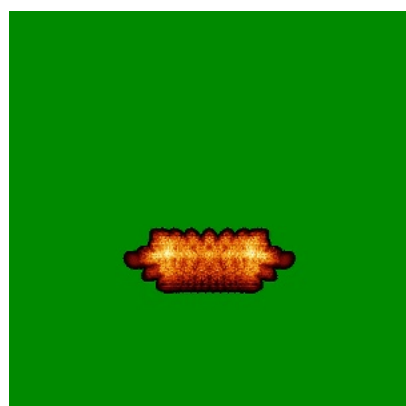


Z Index: 200

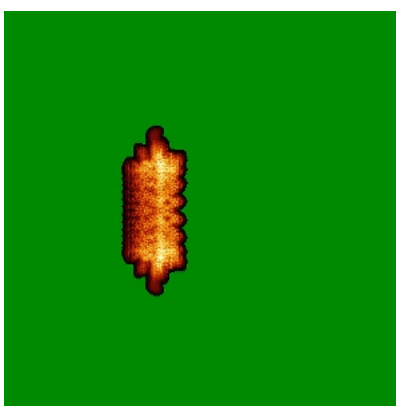
The images above show the largest variance slices of the map in three orthogonal directions.

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

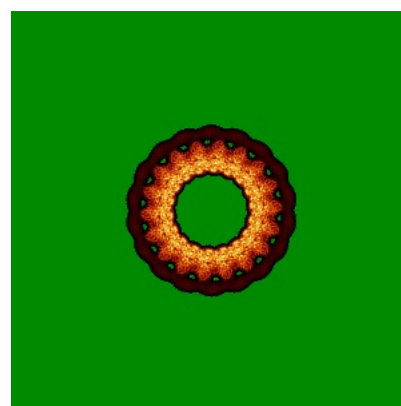
6.4.1 Primary map



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

This section was not generated.

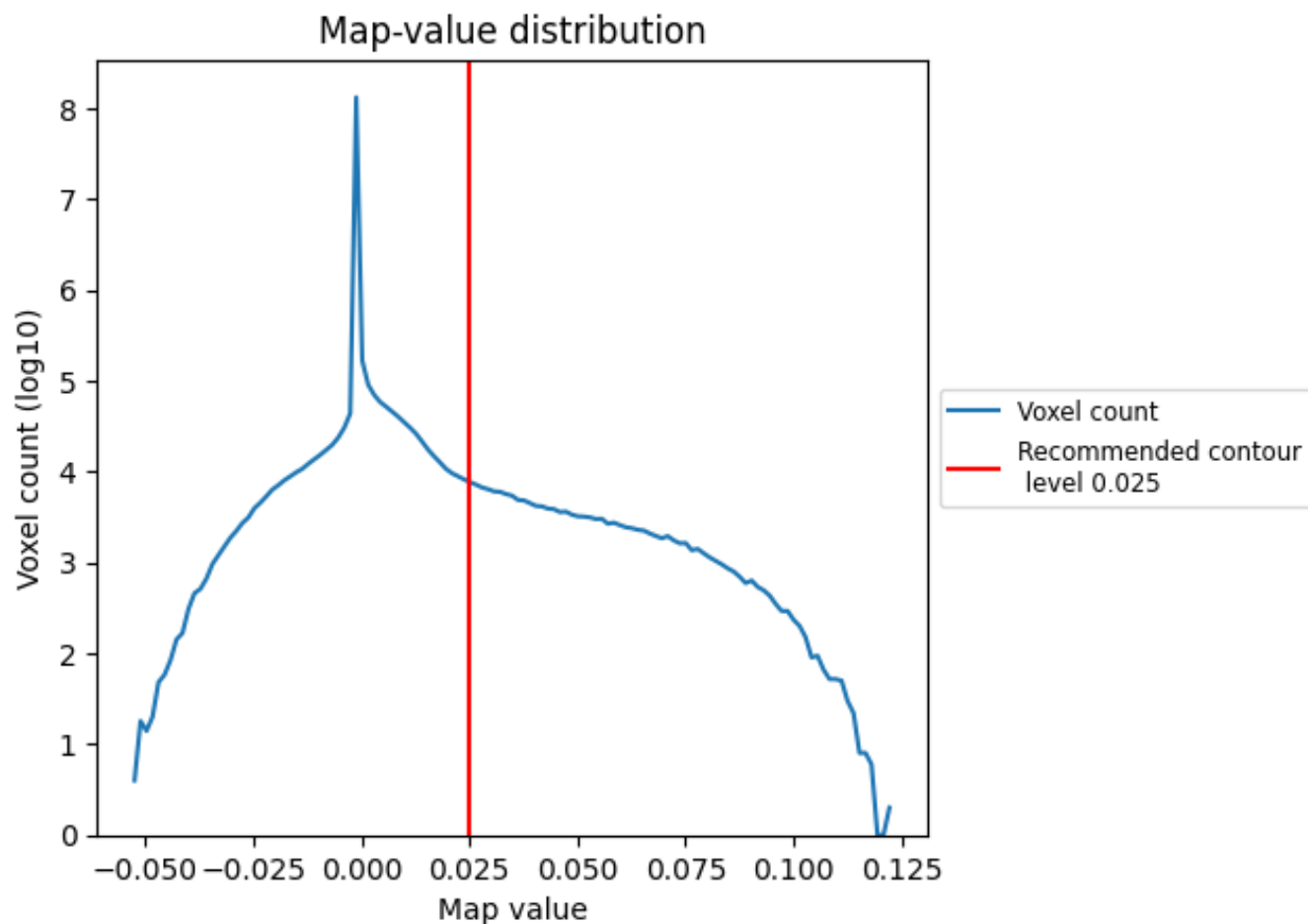
6.6 Mask visualisation

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

7 Map analysis [i](#)

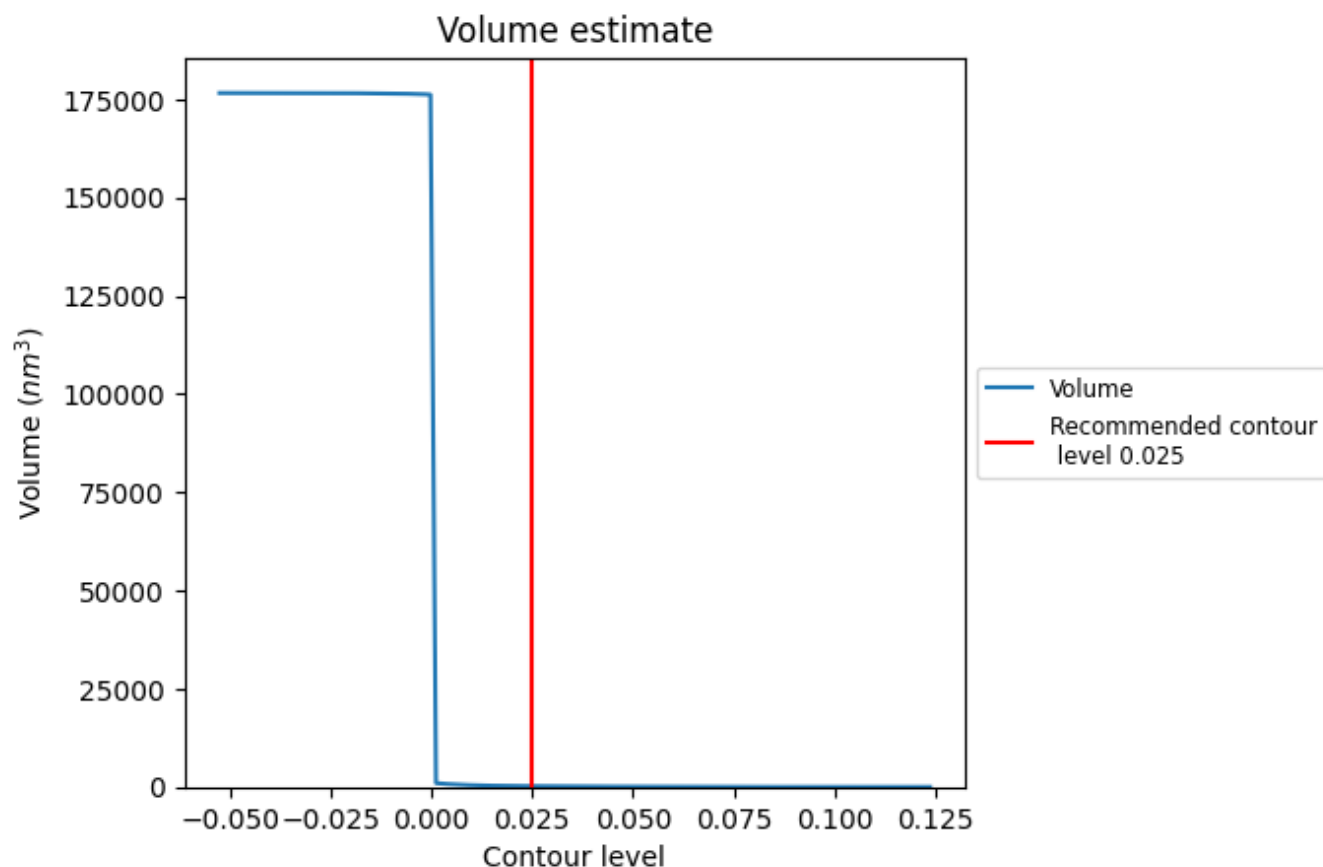
This section contains the results of statistical analysis of the map.

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.

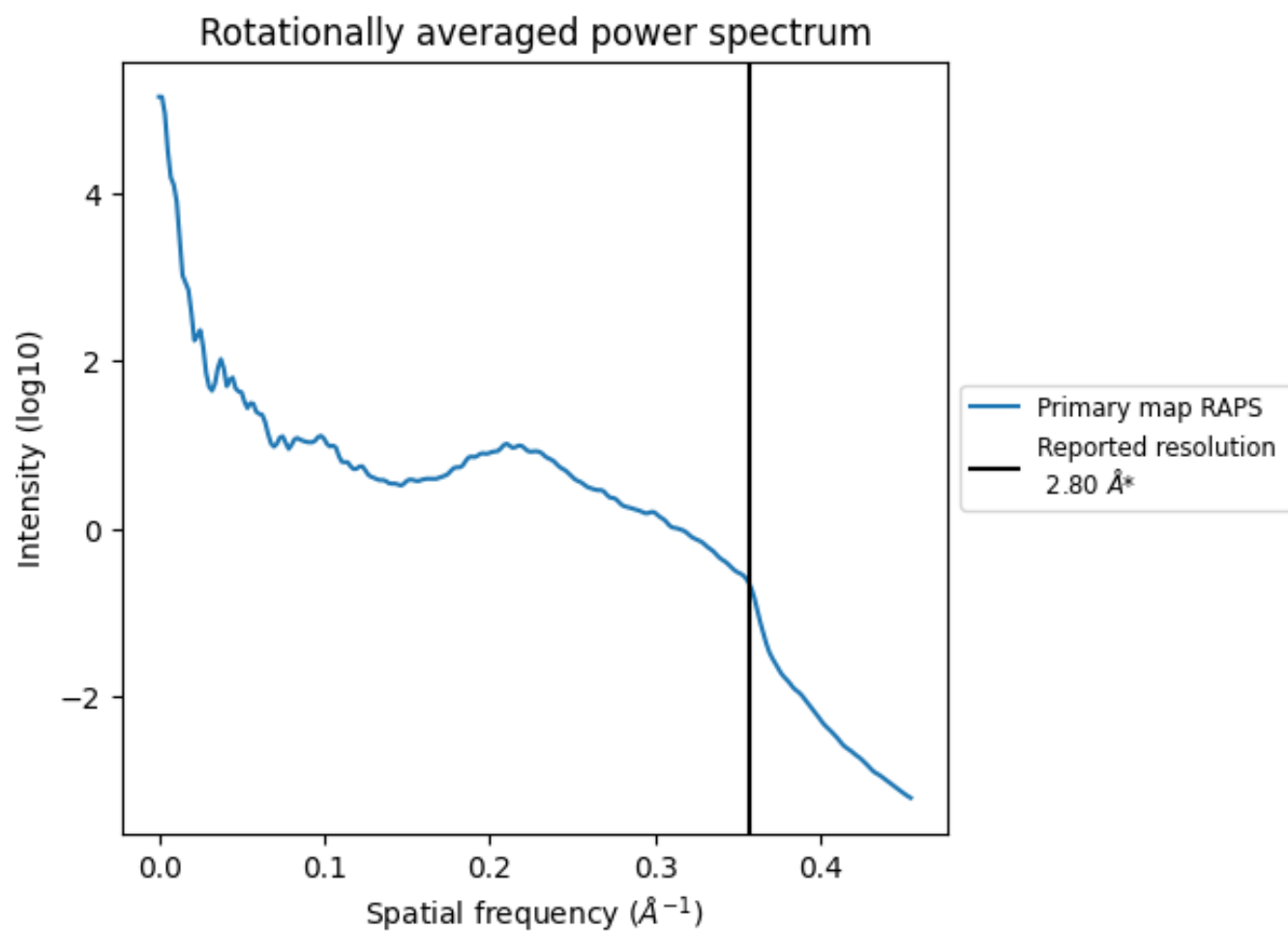
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 203 nm^3 ; this corresponds to an approximate mass of 184 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 0.357 Å⁻¹

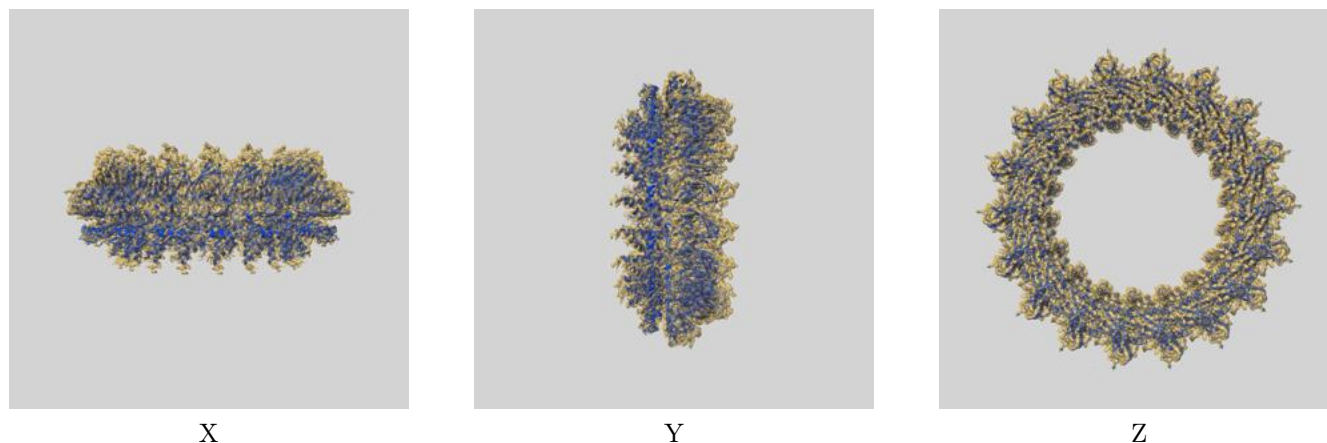
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

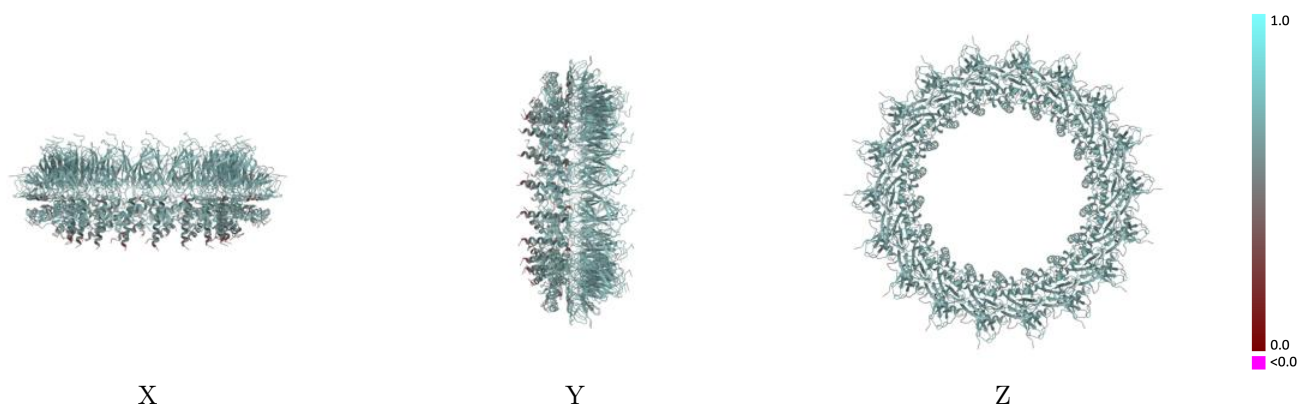
This section contains information regarding the fit between EMDB map EMD-24006 and PDB model 7MUE. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



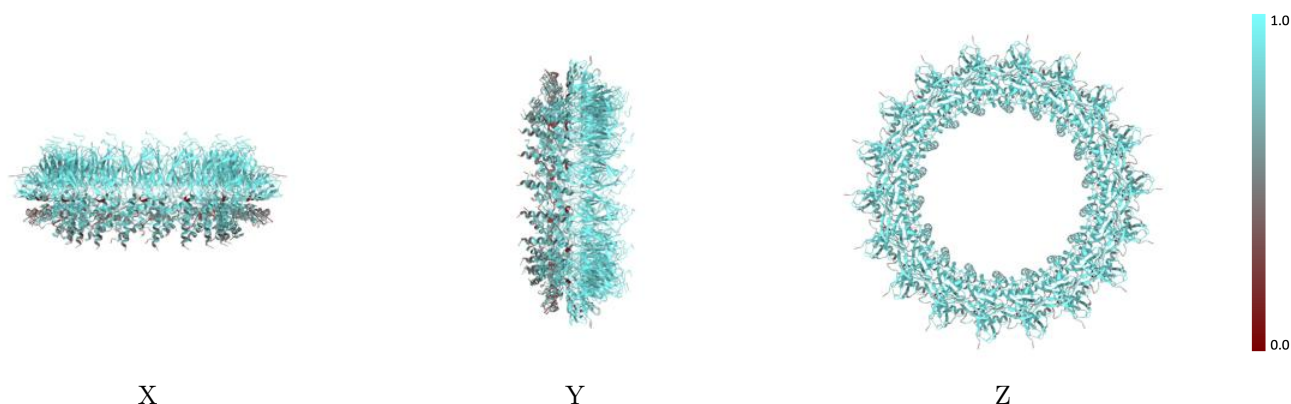
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



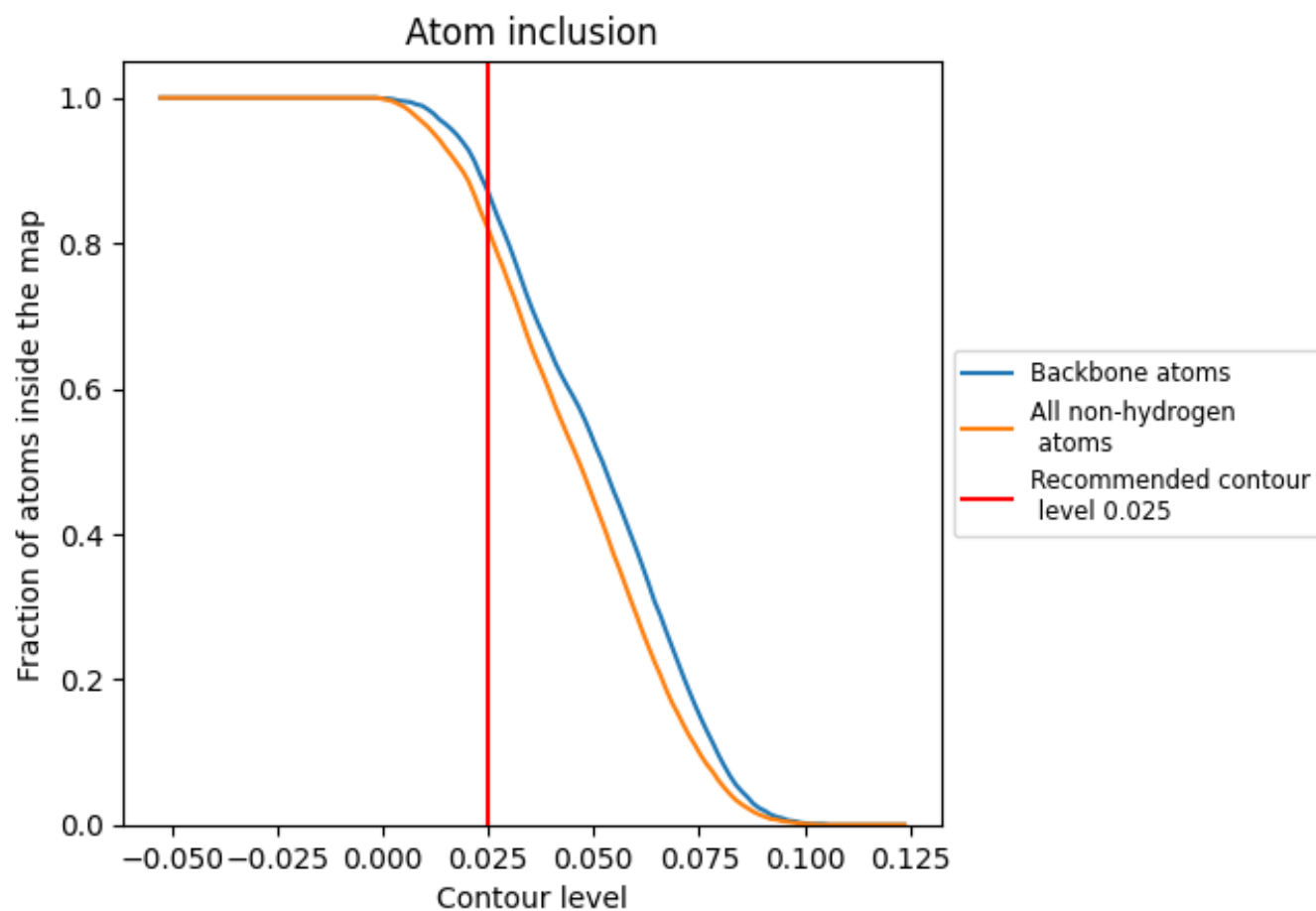
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.6010
AF	 0.7960	 0.5830
AG	 0.7610	 0.5780
AH	 0.8960	 0.6240
AX	 0.5330	 0.5540
BF	 0.7860	 0.5700
BG	 0.7650	 0.5760
BH	 0.9050	 0.6250
BX	 0.5370	 0.5530
CF	 0.7960	 0.5760
CG	 0.7720	 0.5800
CH	 0.9040	 0.6250
CX	 0.5250	 0.5520
DF	 0.7810	 0.5760
DG	 0.7650	 0.5770
DH	 0.8970	 0.6250
DX	 0.5250	 0.5530
EF	 0.7880	 0.5790
EG	 0.7790	 0.5810
EH	 0.9010	 0.6250
EX	 0.5250	 0.5520
FF	 0.7920	 0.5680
FG	 0.7680	 0.5800
FH	 0.8940	 0.6260
FX	 0.5460	 0.5500
GF	 0.8050	 0.5790
GG	 0.7760	 0.5880
GH	 0.8960	 0.6270
GX	 0.5460	 0.5560
HF	 0.7940	 0.5810
HG	 0.7650	 0.5860
HH	 0.8960	 0.6270
HX	 0.5370	 0.5530
IF	 0.7920	 0.5800
IG	 0.7720	 0.5830



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Chain	Atom inclusion	Q-score
IH	 0.9050	 0.6240
IX	 0.5210	 0.5550
JF	 0.7980	 0.5770
JG	 0.7680	 0.5820
JH	 0.8970	 0.6230
JX	 0.5500	 0.5530
KF	 0.7810	 0.5750
KG	 0.7680	 0.5800
KH	 0.8970	 0.6240
KX	 0.5330	 0.5550
LF	 0.7900	 0.5700
LG	 0.7650	 0.5850
LH	 0.8940	 0.6250
LX	 0.5420	 0.5540
MF	 0.7900	 0.5790
MG	 0.7610	 0.5840
MH	 0.8960	 0.6240
MX	 0.5290	 0.5560
VF	 0.8020	 0.5790
VG	 0.7680	 0.5730
VH	 0.8980	 0.6230
VX	 0.5460	 0.5480
WF	 0.7940	 0.5780
WG	 0.7610	 0.5840
WH	 0.8980	 0.6260
WX	 0.5370	 0.5520
XF	 0.7830	 0.5690
XG	 0.7610	 0.5690
XH	 0.9050	 0.6270
XX	 0.5330	 0.5530
YF	 0.7920	 0.5750
YG	 0.7830	 0.5760
YH	 0.9000	 0.6260
YX	 0.5250	 0.5540
ZF	 0.8020	 0.5780
ZG	 0.7790	 0.5820
ZH	 0.8970	 0.6240
ZX	 0.5460	 0.5570