



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:04 PM UTC

PDB ID : 7B9S / pdb_00007b9s
EMDB ID : EMD-12105
Title : Structure of the mycobacterial ESX-5 Type VII Secretion System hexameric pore complex
Authors : Chojnowski, G.; Ritter, C.; Beckham, K.S.H.; Mullapudi, E.; Rettel, M.; Savitski, M.M.; Mortensen, S.A.; Ziemianowicz, D.; Kosinski, J.; Wilmanns, M.
Deposited on : 2020-12-14
Resolution : 3.40 Å (reported)
Based on initial model : 7B9F

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:

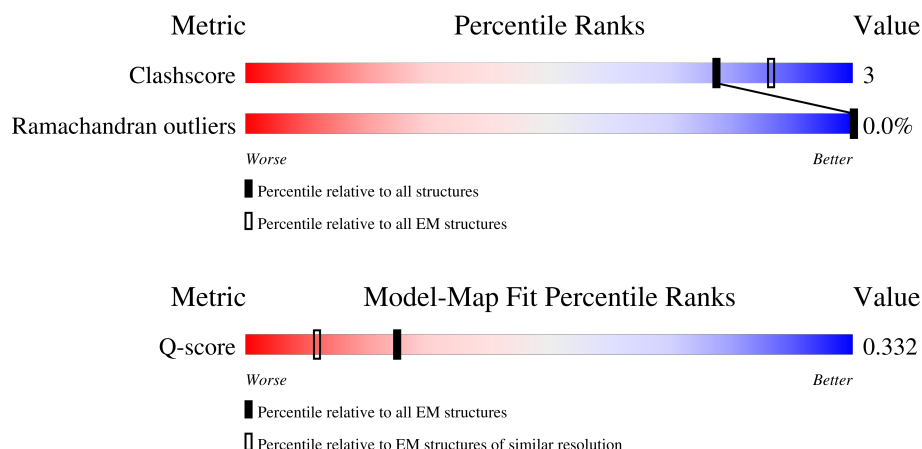
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 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	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	4	400	
1	E	400	
1	H	400	
1	M	400	
1	R	400	

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Mol	Chain	Length	Quality of chain
1	Y	400	
2	3	502	
2	5	502	
2	D	502	
2	G	502	
2	I	502	
2	L	502	
2	N	502	
2	Q	502	
2	S	502	
2	W	502	
2	X	502	
2	Z	502	
3	2	1392	
3	C	1392	
3	F	1392	
3	K	1392	
3	P	1392	
3	V	1392	
4	1	506	
4	A	506	
4	B	506	
4	J	506	
4	O	506	
4	T	506	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 72030 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 EccE5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		
1	H	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		
1	M	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		
1	R	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		
1	Y	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		
1	4	165	Total	C	N	O	S	0	0
			1305	814	249	240	2		

- Molecule 2 is a protein called EccD5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	D	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	I	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	G	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	N	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	L	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	S	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	Q	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	Z	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		

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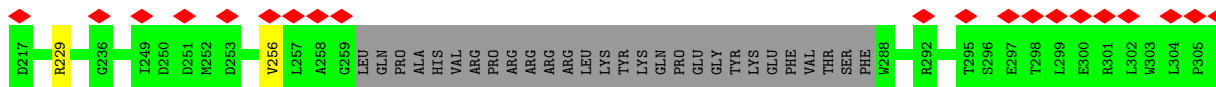
Mol	Chain	Residues	Atoms					AltConf	Trace
2	W	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		
2	5	462	Total	C	N	O	S	0	0
			3469	2272	598	581	18		
2	3	485	Total	C	N	O	S	0	0
			3644	2382	628	616	18		

- Molecule 3 is a protein called EccC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	F	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	K	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	P	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	V	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		
3	2	396	Total	C	N	O	S	0	0
			3107	1990	533	562	22		

- Molecule 4 is a protein called EccB5.

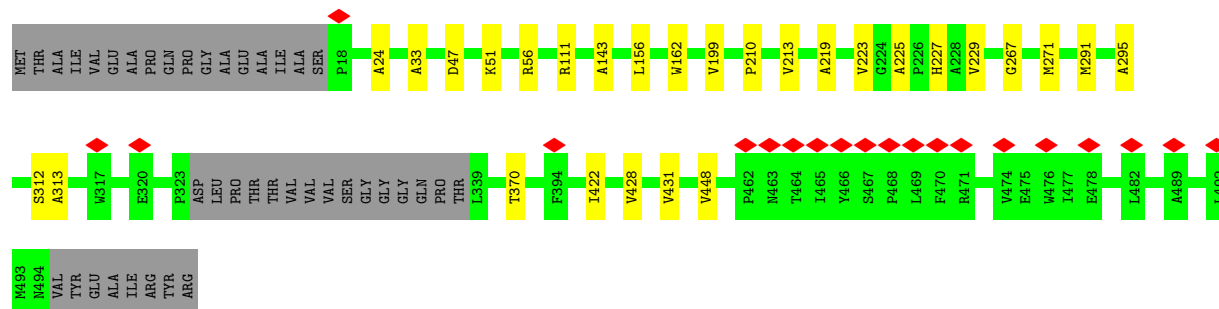
Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	A	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	J	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	O	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	T	63	Total	C	N	O	S	0	0
			480	304	92	81	3		
4	1	63	Total	C	N	O	S	0	0
			480	304	92	81	3		



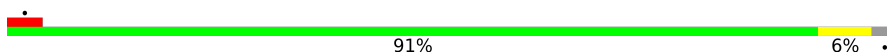
ALA
ARG
GLU
ILE
HIS
ASP
GLY
GLU
LEU
ALA
VAL
LEU
VAL
GLY
GLN
ALA
PRO
PRO
PRO
PRO
PRO
ALA
ALA
ARG

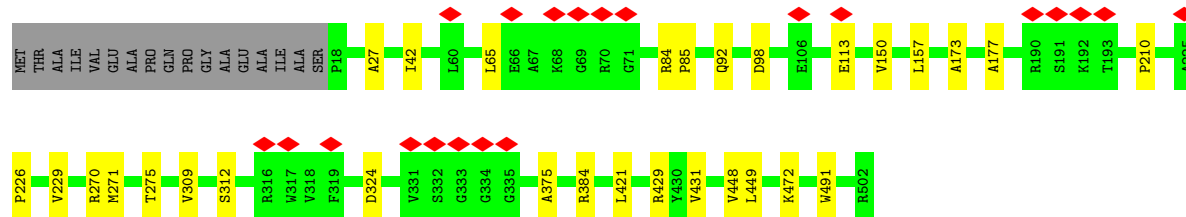
• Molecule 2: EccD5

Chain X:  86% 6% 8%



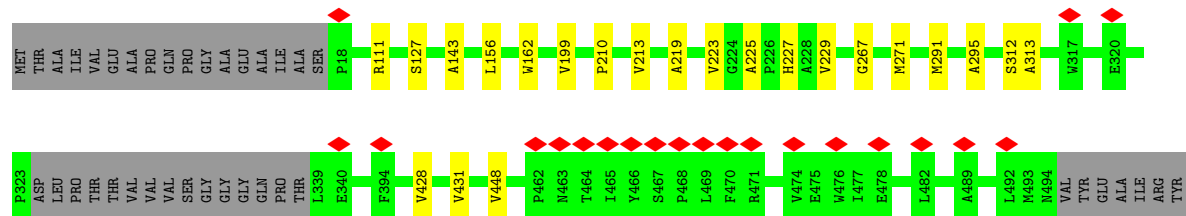
• Molecule 2: EccD5

Chain D:  91% 6% 3%

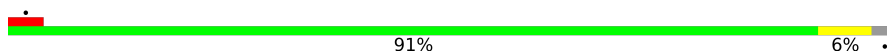


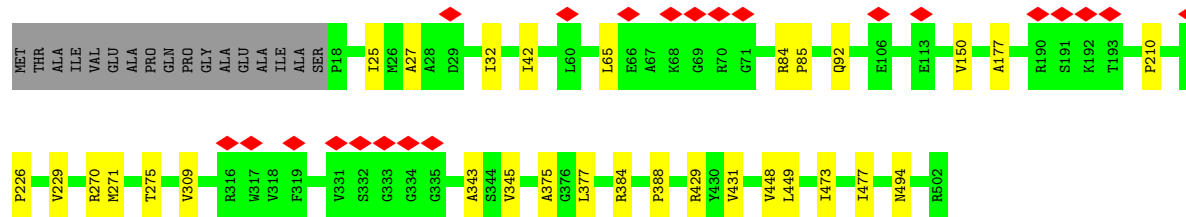
• Molecule 2: EccD5

Chain I:  88% 8% 4%



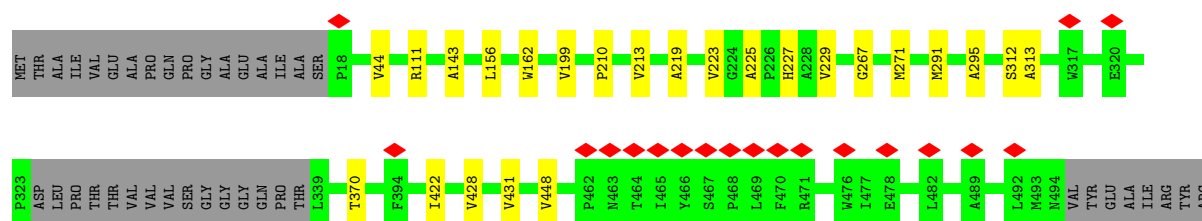
• Molecule 2: EccD5

Chain G:  91% 6% 3%

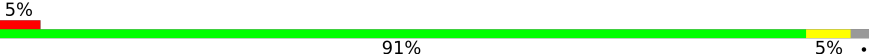


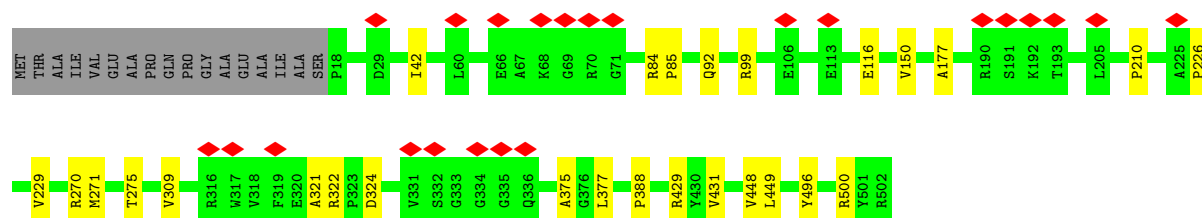
• Molecule 2: EccD5

Chain N:  87% 5% 8%



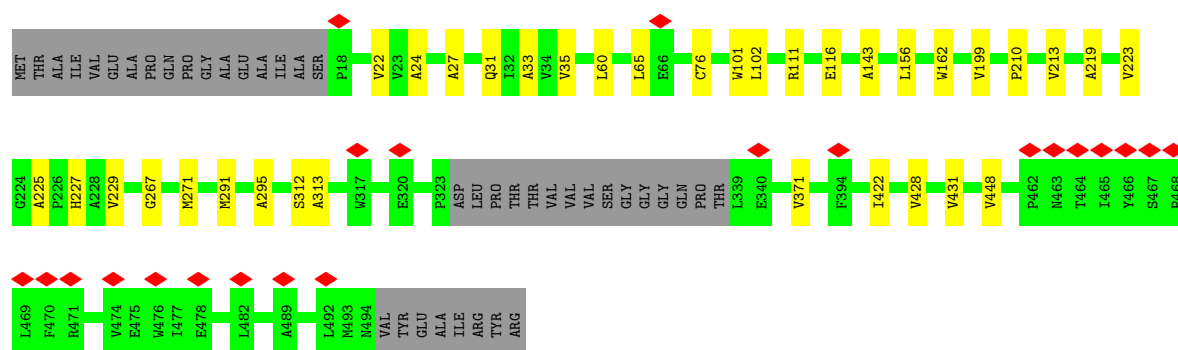
• Molecule 2: EccD5

Chain L:  91% 5% 5%



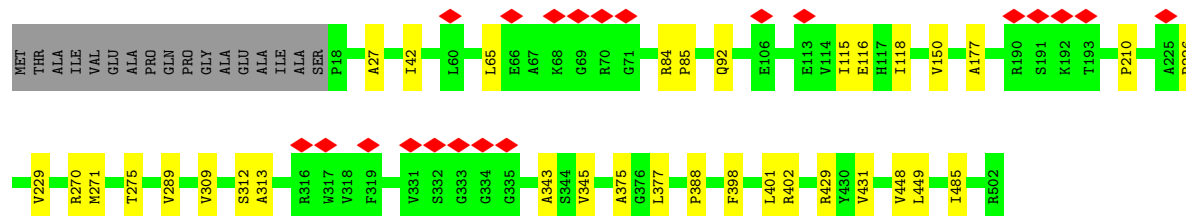
• Molecule 2: EccD5

Chain S:  85% 7% 8%



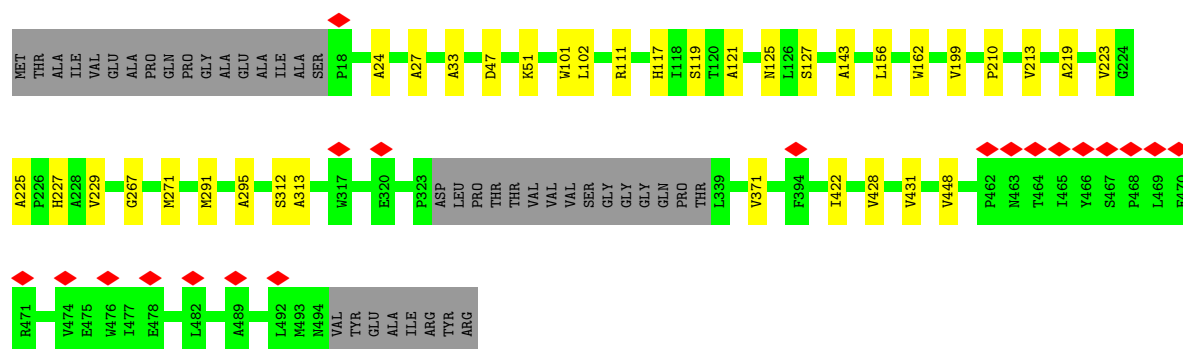
• Molecule 2: EccD5

Chain Q:  90% 7% 5%



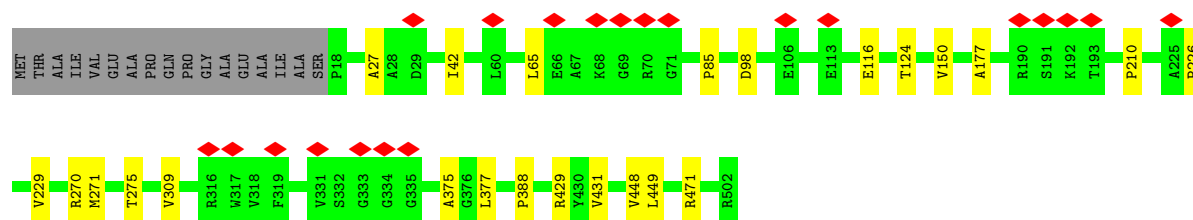
• Molecule 2: EccD5

Chain Z:  85% 7% 8%



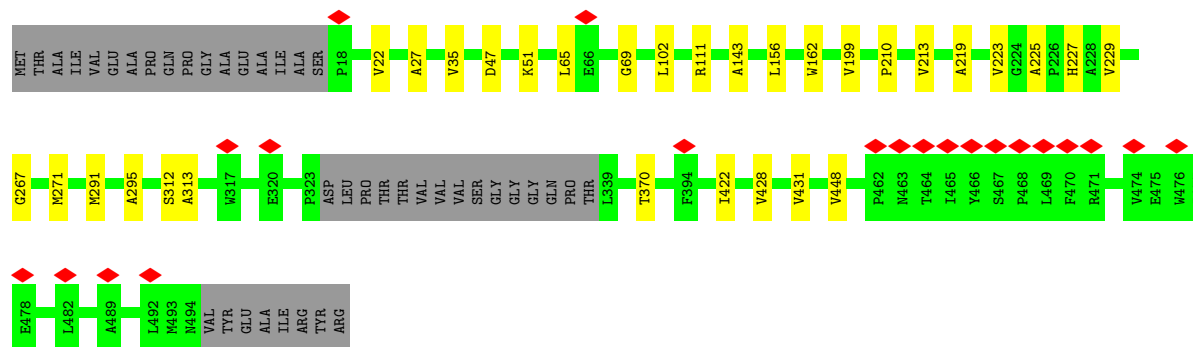
• Molecule 2: EccD5

Chain W: 92% 5%



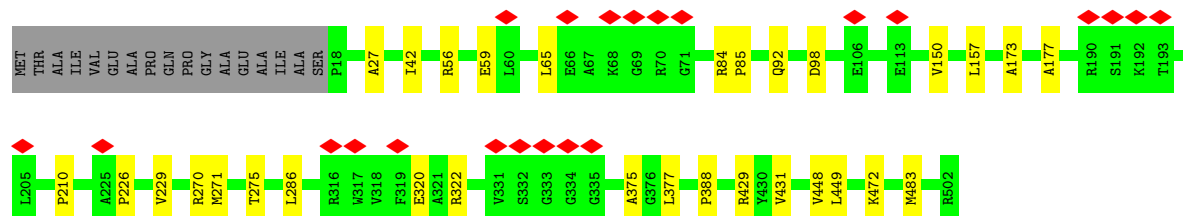
• Molecule 2: EccD5

Chain 5: 86% 6% 8%

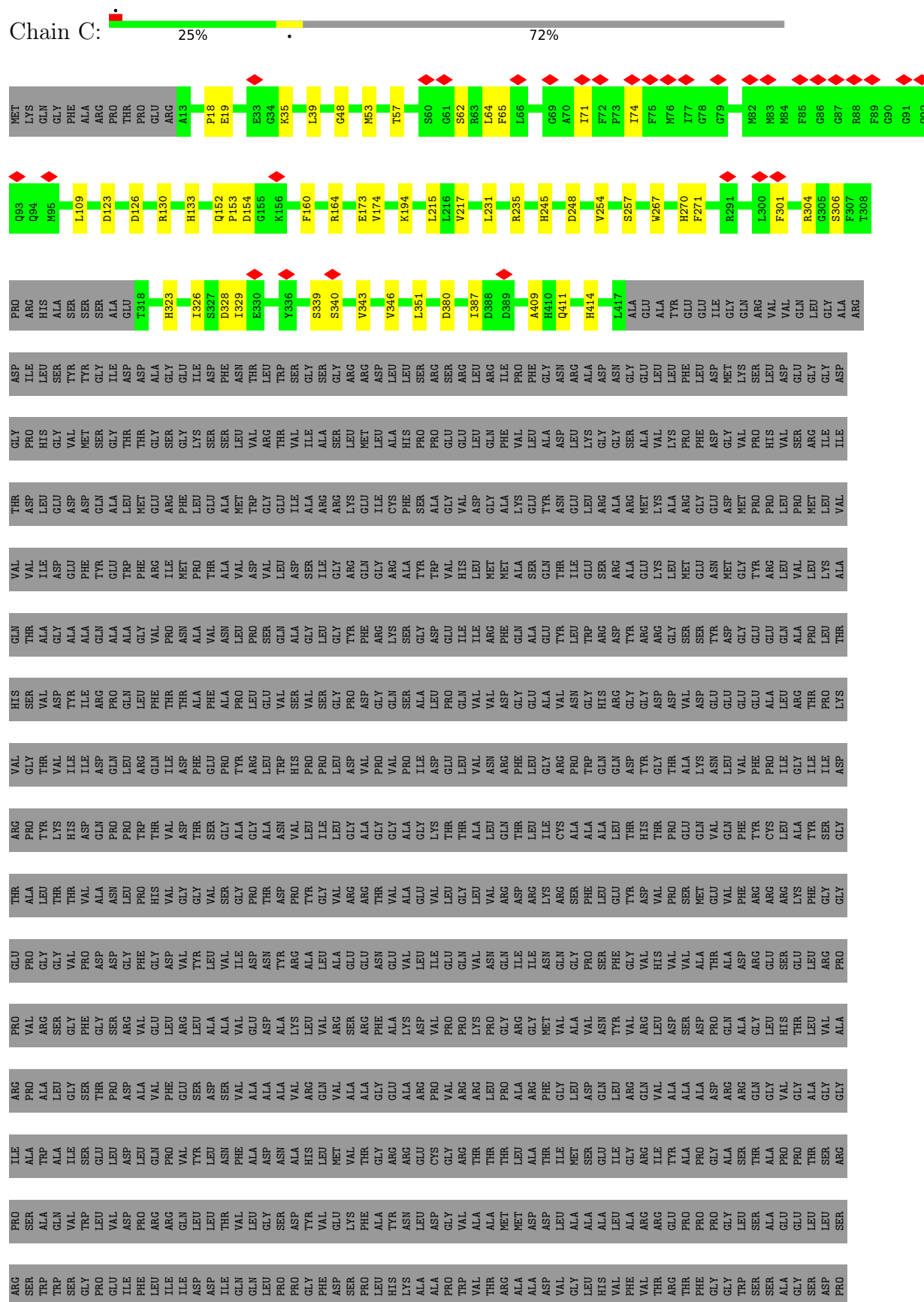


• Molecule 2: EccD5

Chain 3: 90% 6%



• Molecule 3: EccC5

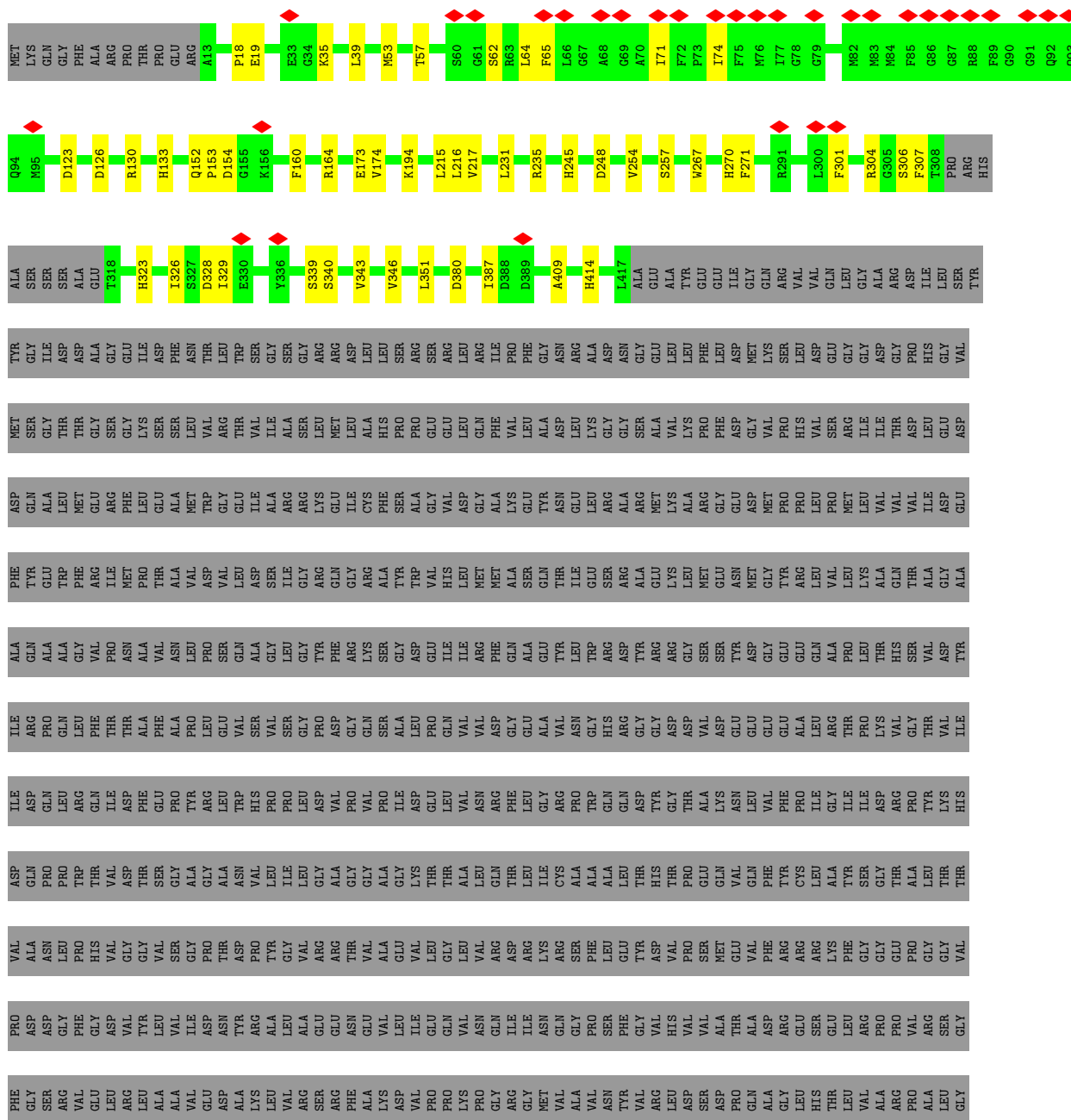


Chain F: 25% 72%



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

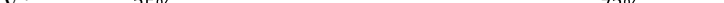
- Molecule 3: EccC5

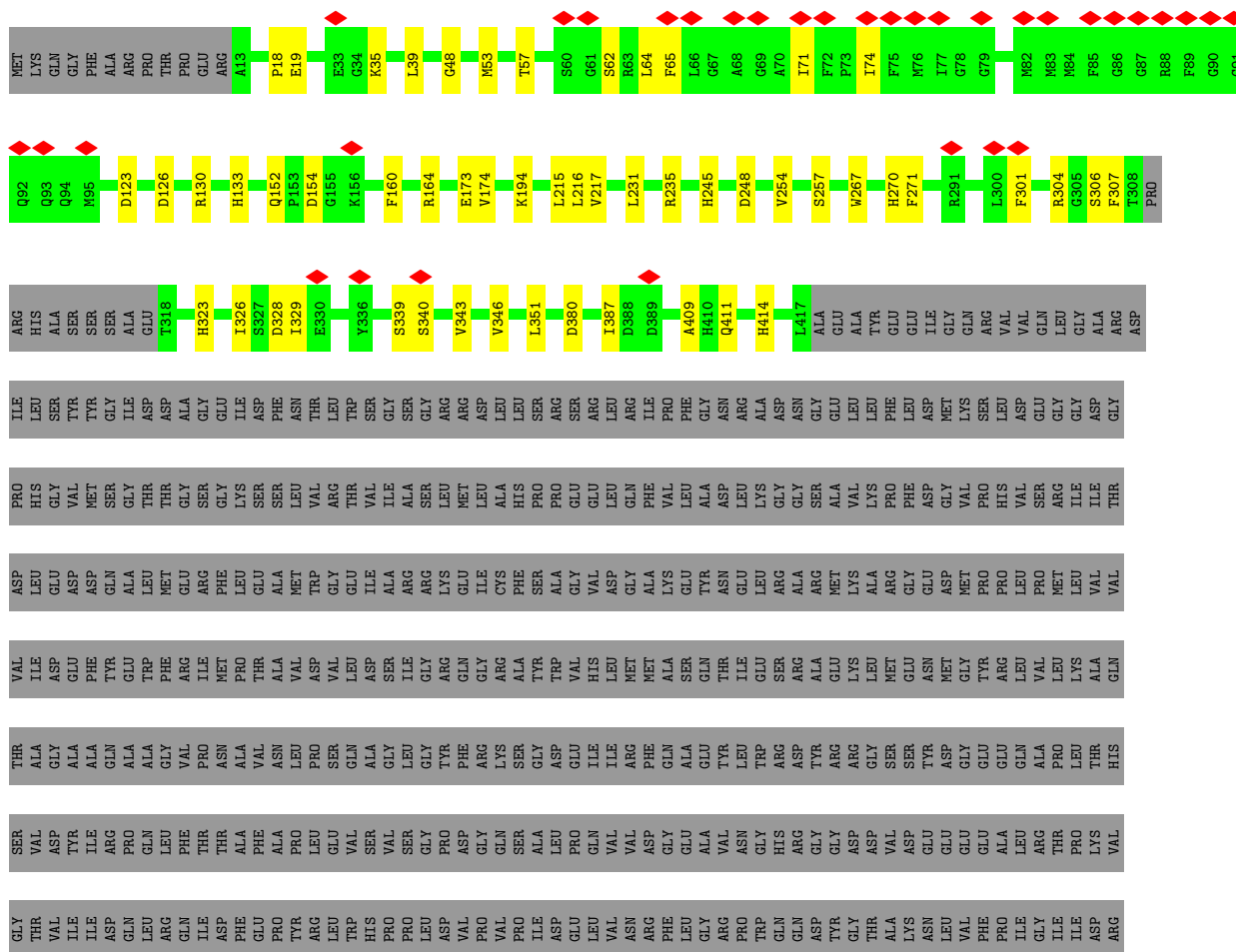




[illegible]

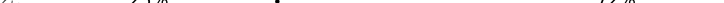
- Molecule 3: EccC5

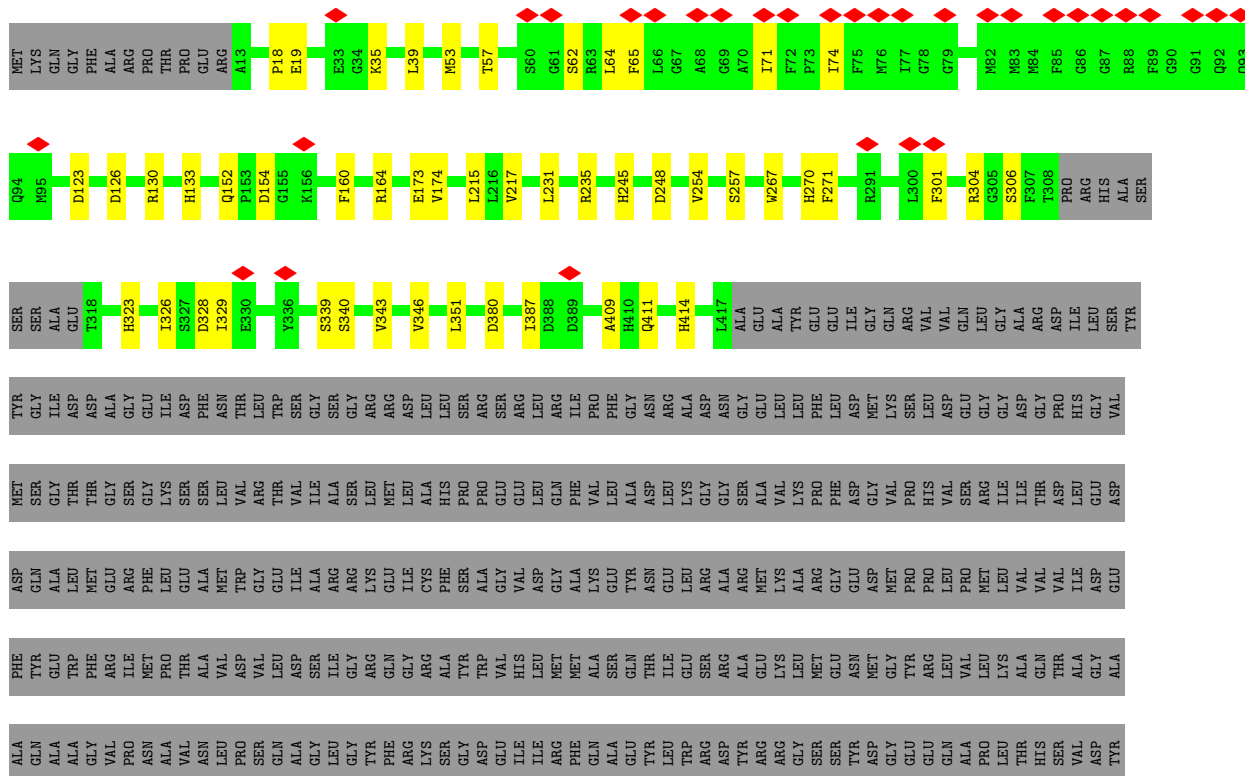
Chain V:  25% 72%



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

- Molecule 3: EccC5

Chain 2:  25% 72%



- Molecule 4: EccB5

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121974	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 ($e^-/\text{\AA}^2$)	49.34	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.687	Depositor
Minimum map value	-0.260	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	580.5, 580.5, 580.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.29, 1.29, 1.29	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	4	0.22	0/1330	0.61	0/1814
1	E	0.21	0/1330	0.61	0/1814
1	H	0.21	0/1330	0.61	0/1814
1	M	0.21	0/1330	0.61	0/1814
1	R	0.21	0/1330	0.61	0/1814
1	Y	0.21	0/1330	0.61	0/1814
2	3	0.30	0/3727	0.59	0/5110
2	5	0.28	0/3547	0.61	0/4862
2	D	0.30	0/3727	0.58	0/5110
2	G	0.31	0/3727	0.60	0/5110
2	I	0.28	0/3547	0.61	0/4862
2	L	0.32	0/3727	0.61	0/5110
2	N	0.28	0/3547	0.62	0/4862
2	Q	0.31	0/3727	0.60	0/5110
2	S	0.28	0/3547	0.61	0/4862
2	W	0.32	0/3727	0.61	0/5110
2	X	0.28	0/3547	0.61	0/4862
2	Z	0.28	0/3547	0.61	0/4862
3	2	0.25	0/3196	0.60	0/4355
3	C	0.25	0/3196	0.60	0/4355
3	F	0.25	0/3196	0.60	0/4355
3	K	0.25	0/3196	0.60	0/4355
3	P	0.25	0/3196	0.60	0/4355
3	V	0.25	0/3196	0.60	0/4355
4	1	0.41	0/487	0.70	0/659
4	A	0.41	0/487	0.70	0/659
4	B	0.41	0/487	0.70	0/659
4	J	0.41	0/487	0.70	0/659
4	O	0.41	0/487	0.70	0/659
4	T	0.41	0/487	0.70	0/659
All	All	0.28	0/73722	0.61	0/100800

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

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	4	1305	0	1283	5	0
1	E	1305	0	1283	8	0
1	H	1305	0	1283	8	0
1	M	1305	0	1283	8	0
1	R	1305	0	1283	9	0
1	Y	1305	0	1283	8	0
2	3	3644	0	3854	19	0
2	5	3469	0	3679	19	0
2	D	3644	0	3854	20	0
2	G	3644	0	3854	17	0
2	I	3469	0	3679	14	0
2	L	3644	0	3854	17	0
2	N	3469	0	3679	15	0
2	Q	3644	0	3854	23	0
2	S	3469	0	3679	22	0
2	W	3644	0	3854	16	0
2	X	3469	0	3679	18	0
2	Z	3469	0	3679	23	0
3	2	3107	0	3031	30	0
3	C	3107	0	3031	35	0
3	F	3107	0	3031	35	0
3	K	3107	0	3031	32	0
3	P	3107	0	3031	33	0
3	V	3107	0	3031	33	0
4	1	480	0	503	4	0
4	A	480	0	503	3	0
4	B	480	0	503	6	0
4	J	480	0	503	2	0
4	O	480	0	503	3	0
4	T	480	0	503	3	0
All	All	72030	0	74100	428	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 3.

The worst 5 of 428 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:Q:375:ALA:O	2:Q:429:ARG:NH1	2.27	0.68
2:W:375:ALA:O	2:W:429:ARG:NH1	2.29	0.66
2:G:375:ALA:O	2:G:429:ARG:NH1	2.28	0.66
4:J:43:ARG:NH1	2:Q:313:ALA:O	2.28	0.66
2:L:375:ALA:O	2:L:429:ARG:NH1	2.28	0.66

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	4	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	E	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	H	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
1	M	157/400 (39%)	146 (93%)	11 (7%)	0	100	100
1	R	157/400 (39%)	146 (93%)	11 (7%)	0	100	100
1	Y	157/400 (39%)	145 (92%)	12 (8%)	0	100	100
2	3	483/502 (96%)	466 (96%)	17 (4%)	0	100	100
2	5	458/502 (91%)	447 (98%)	10 (2%)	1 (0%)	43	71
2	D	483/502 (96%)	466 (96%)	17 (4%)	0	100	100
2	G	483/502 (96%)	465 (96%)	18 (4%)	0	100	100
2	I	458/502 (91%)	448 (98%)	10 (2%)	0	100	100
2	L	483/502 (96%)	468 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N	458/502 (91%)	449 (98%)	9 (2%)	0	100	100
2	Q	483/502 (96%)	463 (96%)	20 (4%)	0	100	100
2	S	458/502 (91%)	447 (98%)	11 (2%)	0	100	100
2	W	483/502 (96%)	464 (96%)	19 (4%)	0	100	100
2	X	458/502 (91%)	447 (98%)	11 (2%)	0	100	100
2	Z	458/502 (91%)	448 (98%)	10 (2%)	0	100	100
3	2	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	C	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	F	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	K	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	P	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
3	V	392/1392 (28%)	374 (95%)	18 (5%)	0	100	100
4	1	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	A	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	B	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	J	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	O	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
4	T	61/506 (12%)	60 (98%)	1 (2%)	0	100	100
All	All	9306/19812 (47%)	8954 (96%)	351 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	5	69	GLY

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

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.

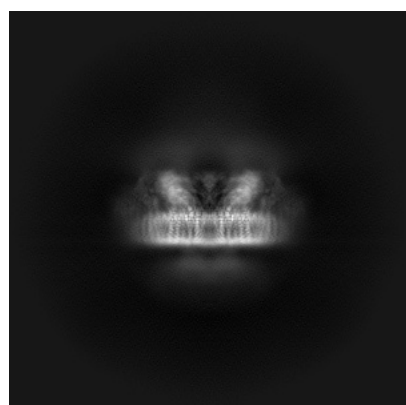
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12105. These allow visual inspection of the internal detail of the map and identification of artifacts.

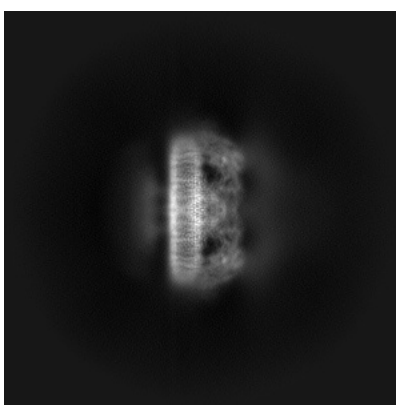
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

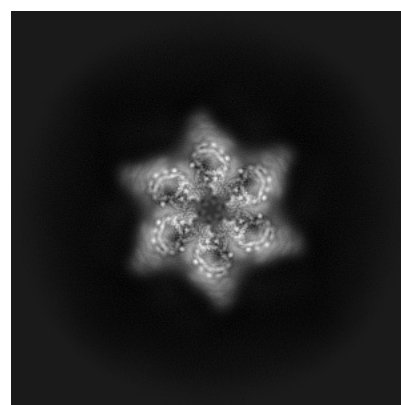
6.1.1 Primary map



X



Y

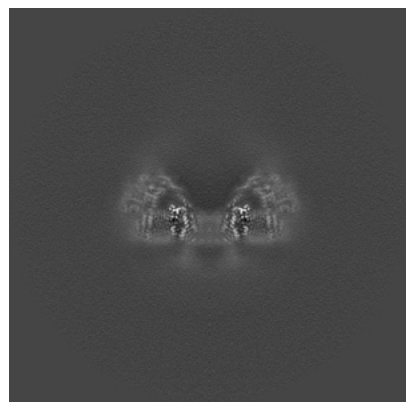


Z

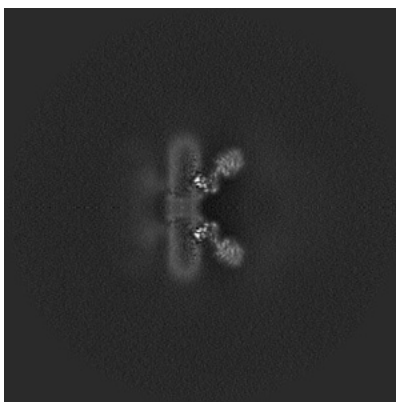
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

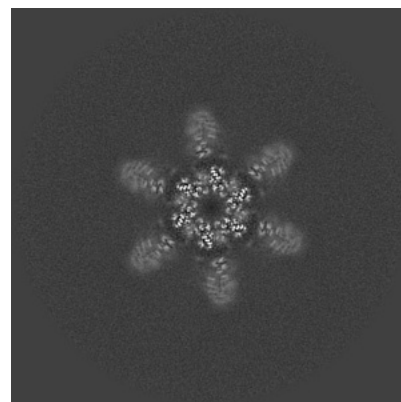
6.2.1 Primary map



X Index: 225



Y Index: 225

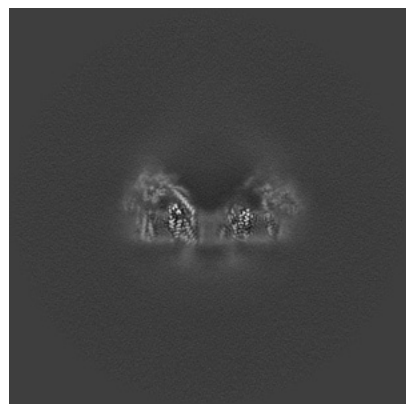


Z Index: 225

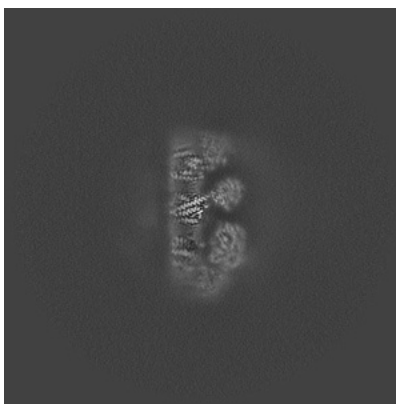
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

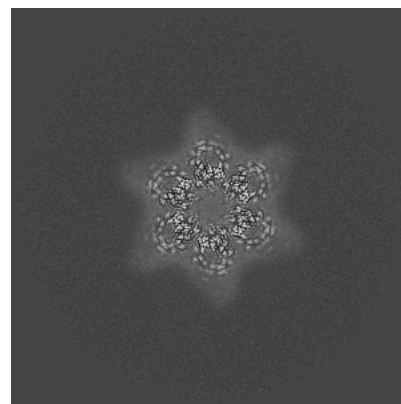
6.3.1 Primary map



X Index: 222



Y Index: 267

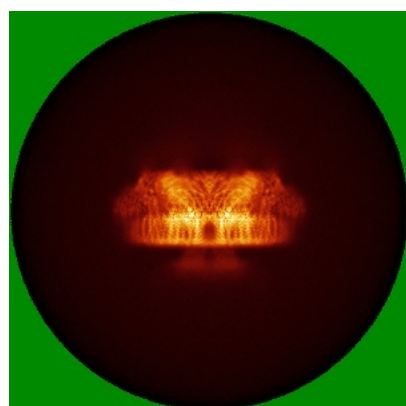


Z Index: 215

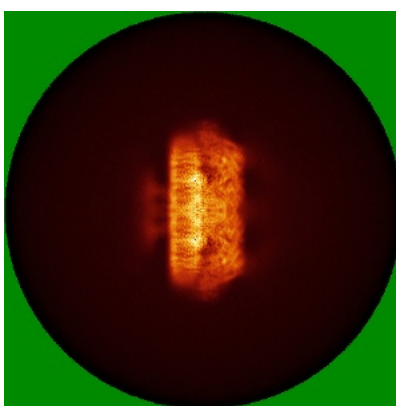
The images above show the largest variance slices of the map in three orthogonal directions.

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

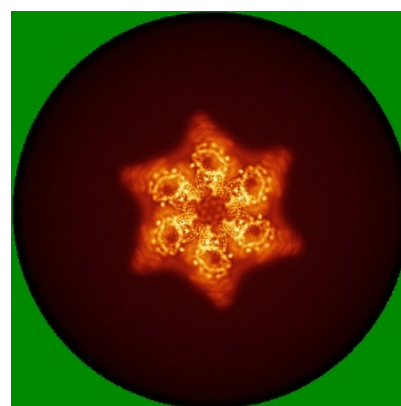
6.4.1 Primary map



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

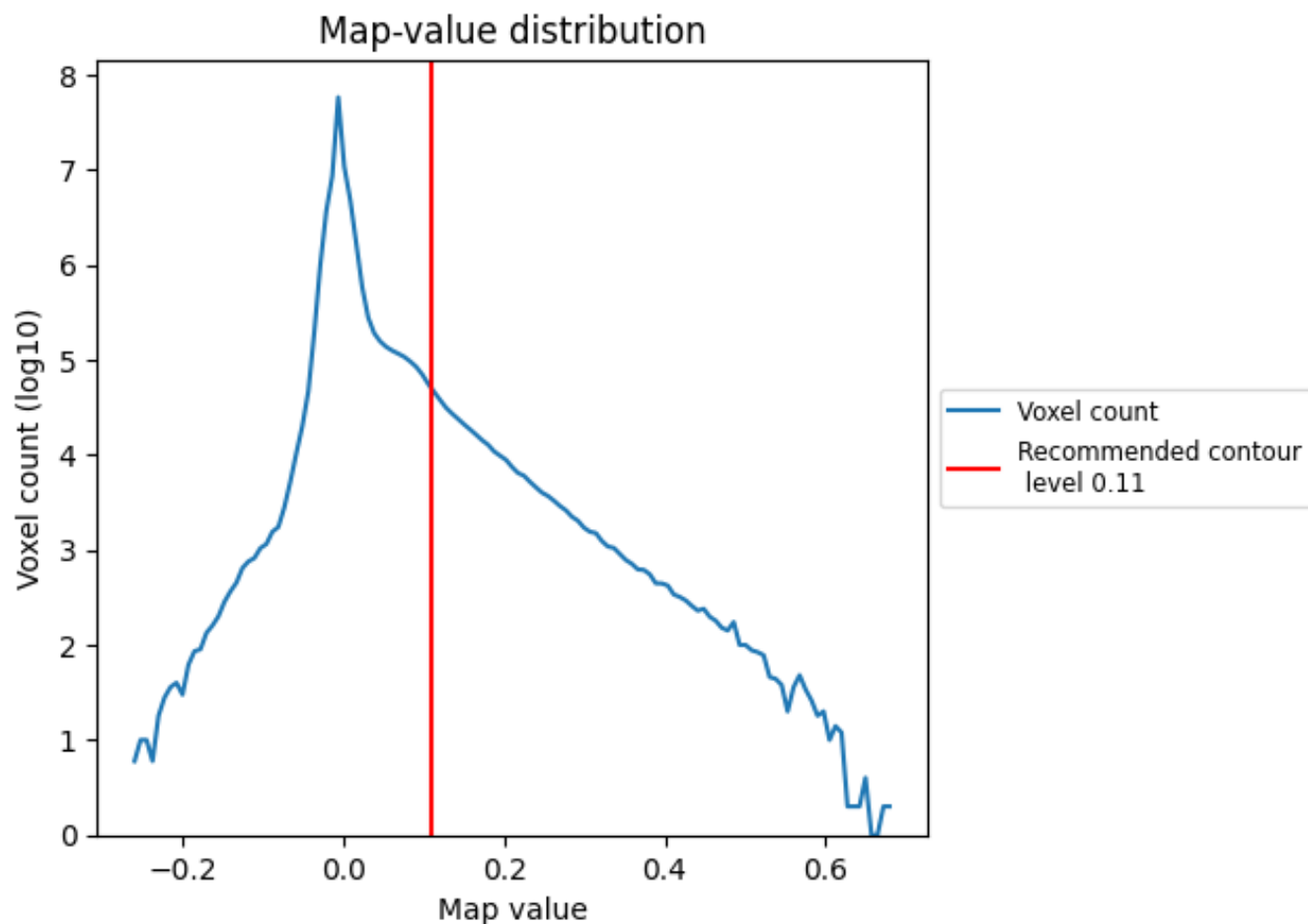
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

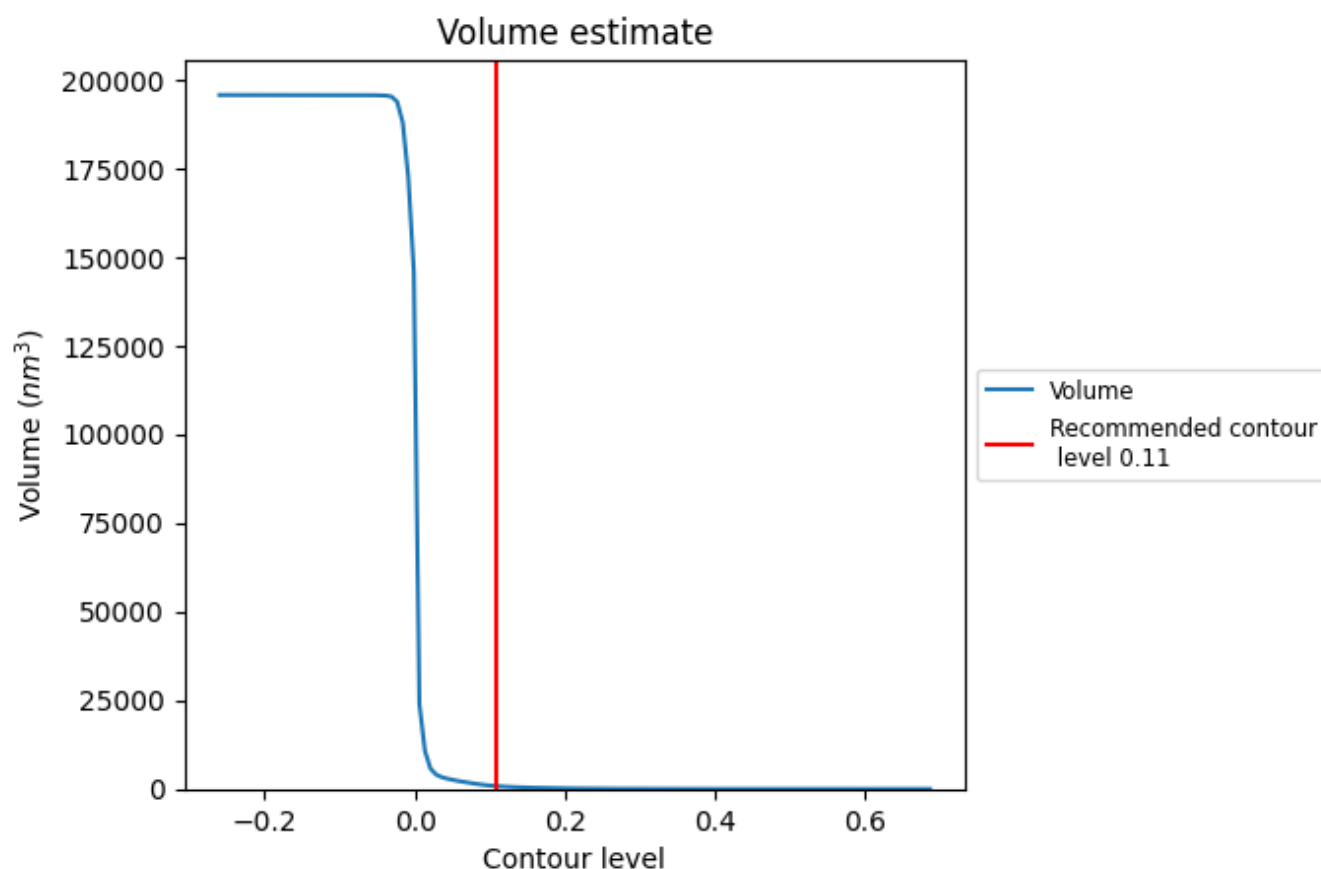
This section contains the results of statistical analysis of the map.

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.

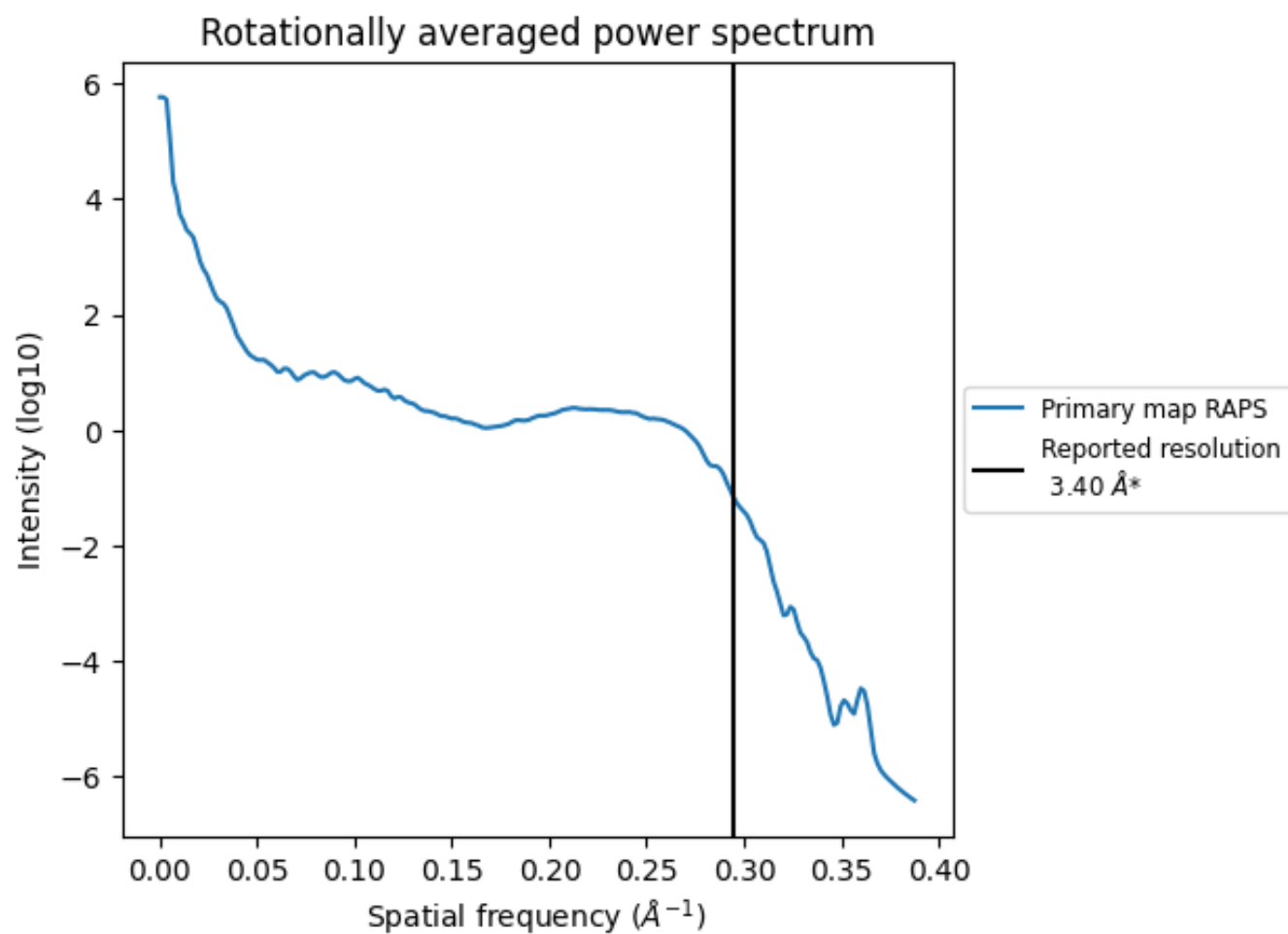
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 786 nm^3 ; this corresponds to an approximate mass of 710 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 0.294 Å⁻¹

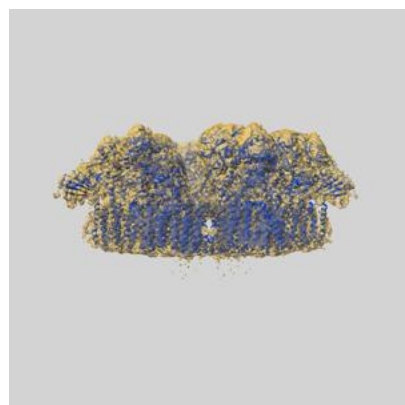
8 Fourier-Shell correlation

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

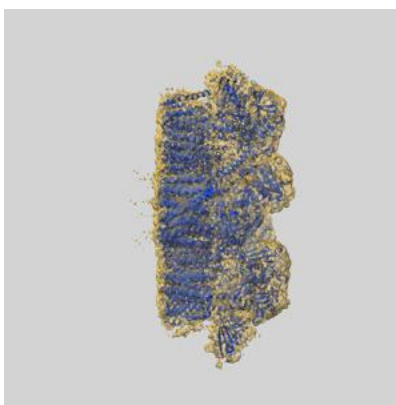
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12105 and PDB model 7B9S. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

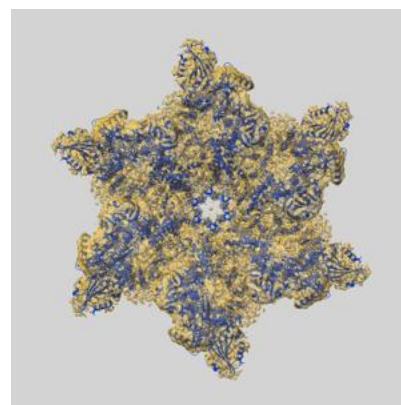
9.1 Map-model overlay [i](#)



X



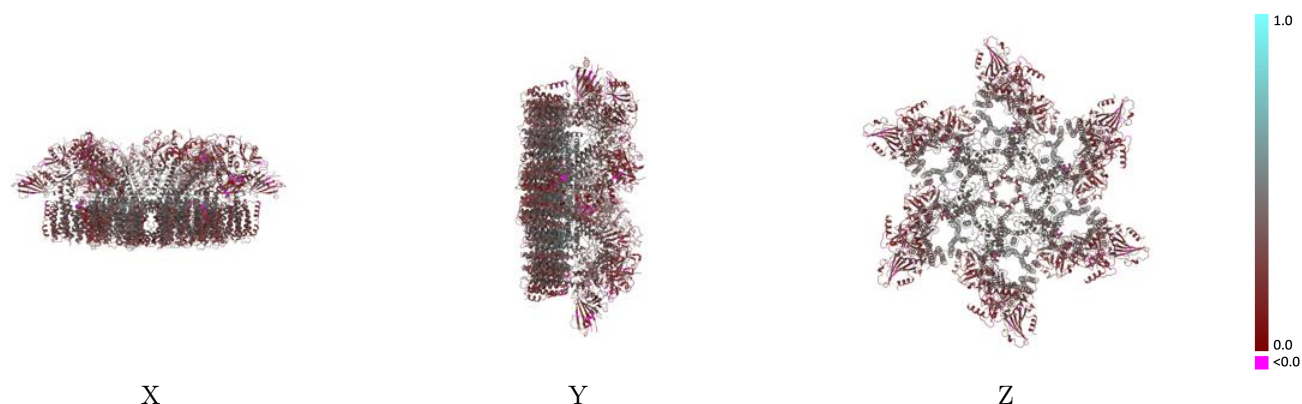
Y



Z

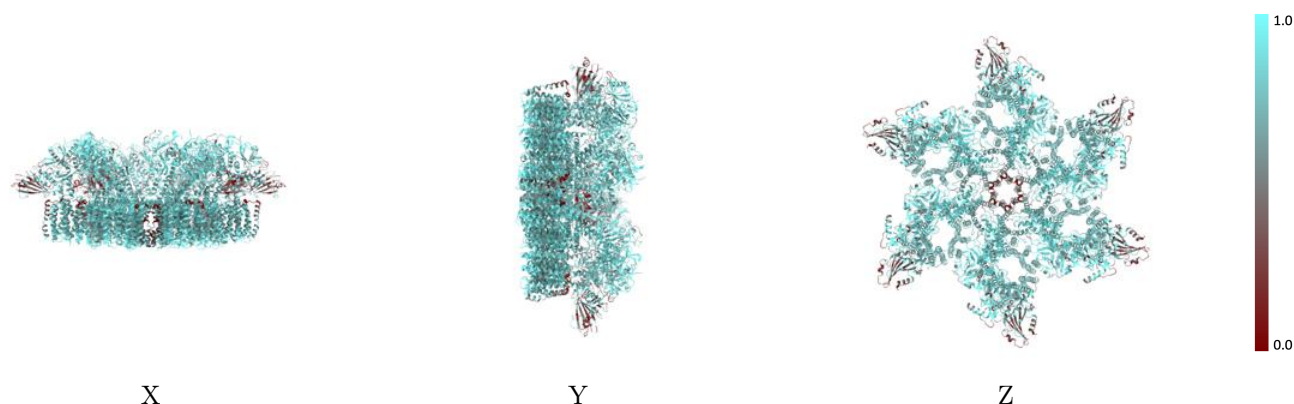
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



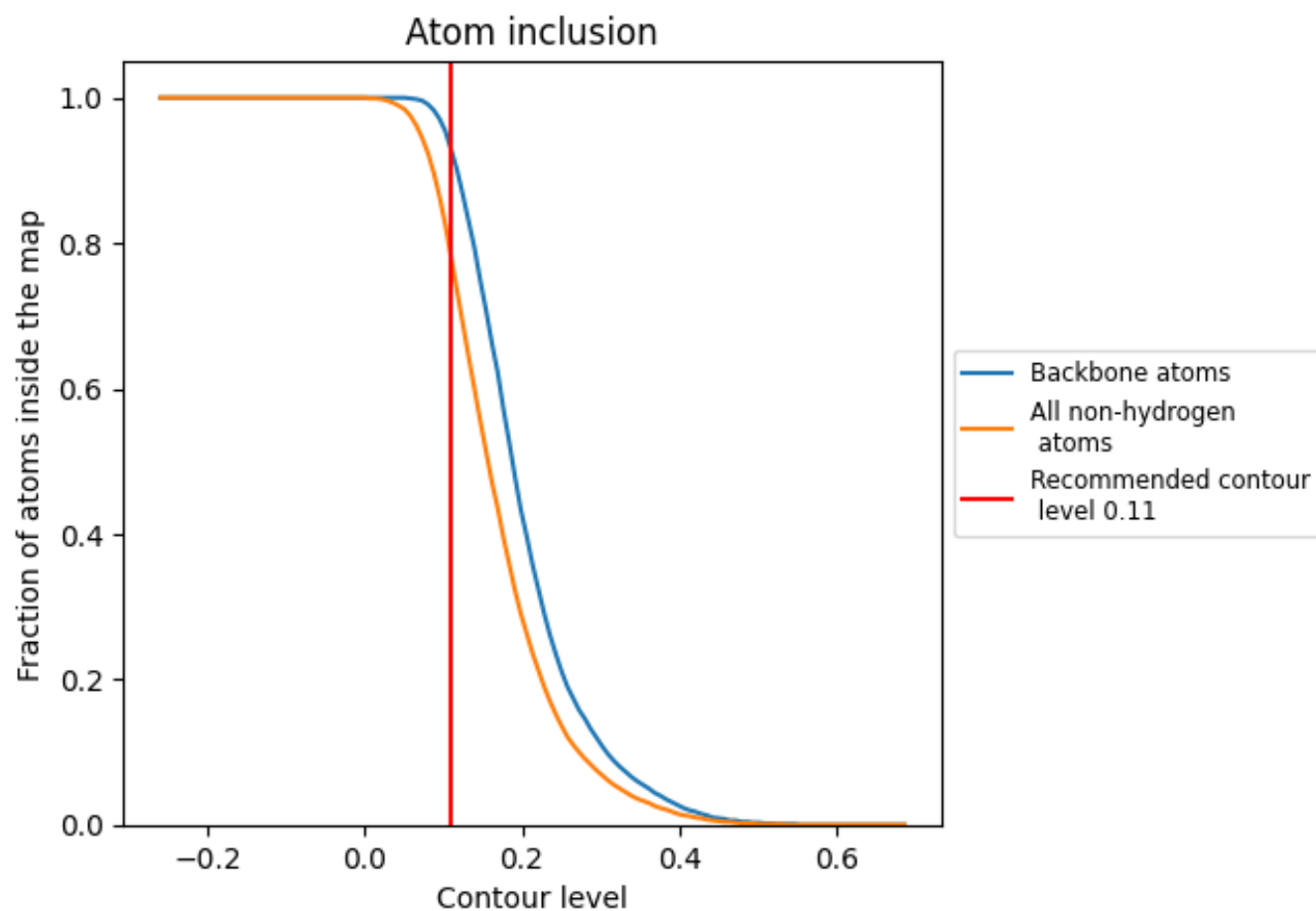
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 78% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.3320
1	 0.8850	 0.4460
2	 0.8080	 0.3130
3	 0.8250	 0.3550
4	 0.5700	 0.2620
5	 0.7750	 0.3340
A	 0.9000	 0.4490
B	 0.8700	 0.4440
C	 0.8070	 0.3130
D	 0.8240	 0.3570
E	 0.5660	 0.2660
F	 0.8060	 0.3140
G	 0.8250	 0.3550
H	 0.5660	 0.2630
I	 0.7780	 0.3340
J	 0.8780	 0.4300
K	 0.8070	 0.3140
L	 0.8220	 0.3540
M	 0.5620	 0.2630
N	 0.7770	 0.3350
O	 0.8870	 0.4410
P	 0.8070	 0.3150
Q	 0.8240	 0.3590
R	 0.5660	 0.2640
S	 0.7730	 0.3350
T	 0.8740	 0.4340
V	 0.8040	 0.3140
W	 0.8230	 0.3550
X	 0.7730	 0.3350
Y	 0.5670	 0.2630
Z	 0.7790	 0.3350

