



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:40 PM UTC

PDB ID : 6ZVS / pdb_00006zvs
EMDB ID : EMD-11469
Title : C12 symmetry: Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily.
Authors : Liu, J.; Tassinari, M.; Souza, D.P.; Naskar, S.; Noel, J.K.; Bohuszewicz, O.; Buck, M.; Williams, T.A.; Baum, B.; Low, H.H.
Deposited on : 2020-07-27
Resolution : 7.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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

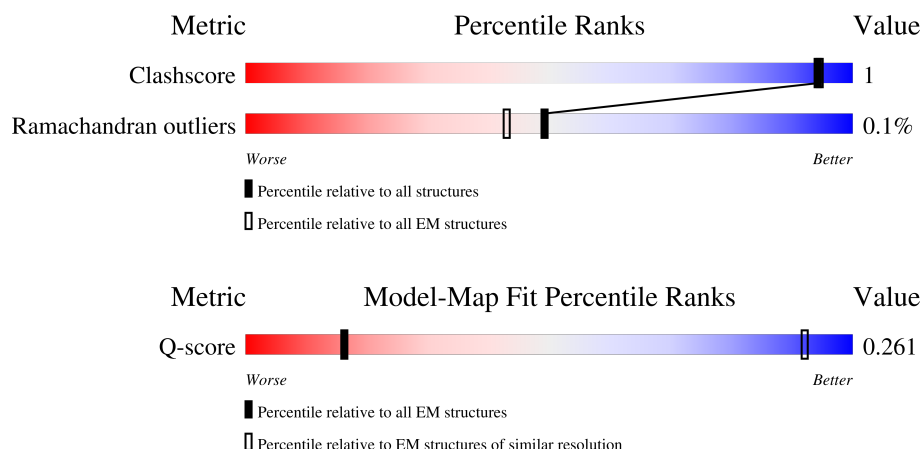
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	444 (6.70 - 7.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	258	33% 52% 48%
1	AA	258	16% 84% 15%
1	AB	258	84% 15%
1	B	258	16% 84% 15%
1	BA	258	83% 15%

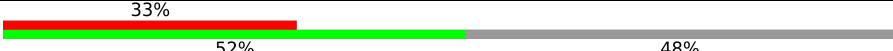
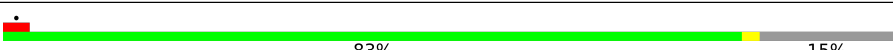
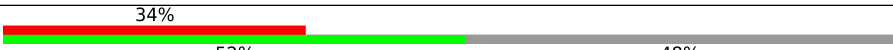
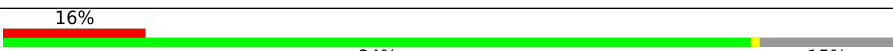
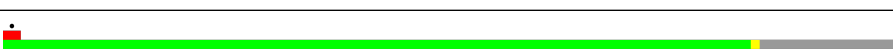
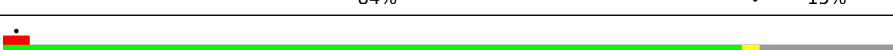
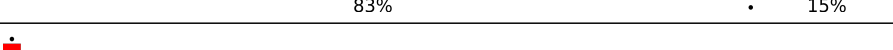
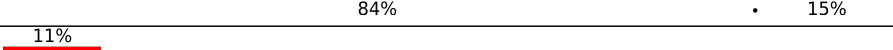
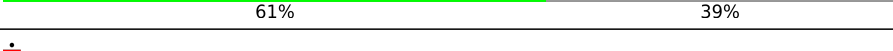
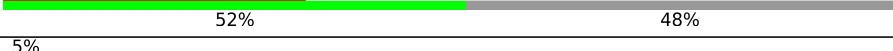
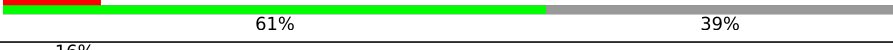
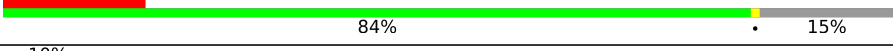
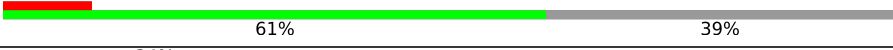
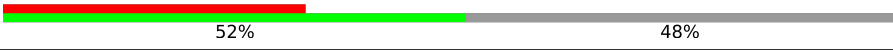
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Mol	Chain	Length	Quality of chain
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1	C	258	
1	CA	258	
1	CB	258	
1	D	258	
1	DA	258	
1	DB	258	
1	E	258	
1	EA	258	
1	EB	258	
1	F	258	
1	FA	258	
1	FB	258	
1	G	258	
1	GA	258	
1	GB	258	
1	H	258	
1	HA	258	
1	HB	258	
1	I	258	
1	IA	258	
1	IB	258	
1	J	258	
1	JA	258	
1	JB	258	

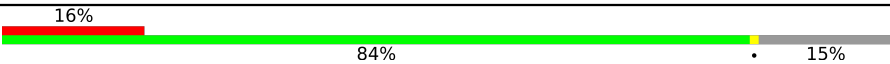
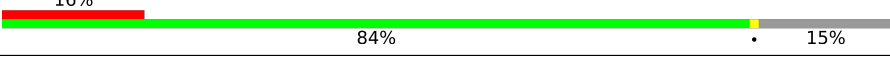
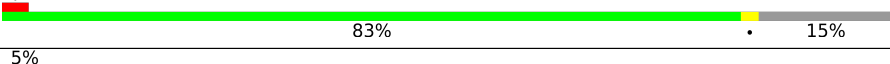
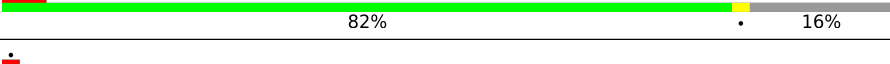
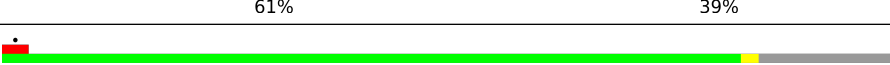
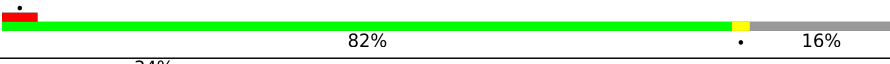
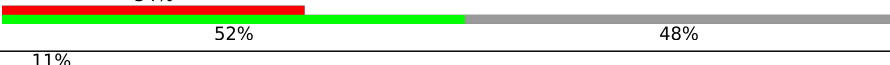
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Mol	Chain	Length	Quality of chain
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1	KA	258	
1	KB	258	
1	L	258	
1	LA	258	
1	LB	258	
1	M	258	
1	MA	258	
1	MB	258	
1	N	258	
1	NA	258	
1	NB	258	
1	O	258	
1	OA	258	
1	OB	258	
1	P	258	
1	PA	258	
1	PB	258	
1	Q	258	
1	QA	258	
1	QB	258	
1	R	258	
1	RA	258	
1	RB	258	
1	S	258	

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Mol	Chain	Length	Quality of chain
1	SA	258	
1	SB	258	
1	T	258	
1	TA	258	
1	TB	258	
1	UA	258	
1	UB	258	
1	V	258	
1	VA	258	
1	W	258	
1	WA	258	
1	X	258	
1	XA	258	
1	Y	258	
1	YA	258	
1	Z	258	
1	ZA	258	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 69420 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 Vip1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	133	Total 661	C 395	N 133	O 133	0	0
1	B	219	Total 1086	C 648	N 219	O 219	0	0
1	C	219	Total 1086	C 648	N 219	O 219	0	0
1	D	219	Total 1086	C 648	N 219	O 219	0	0
1	E	218	Total 1081	C 645	N 218	O 218	0	0
1	F	158	Total 785	C 469	N 158	O 158	0	0
1	G	133	Total 661	C 395	N 133	O 133	0	0
1	H	219	Total 1086	C 648	N 219	O 219	0	0
1	I	219	Total 1086	C 648	N 219	O 219	0	0
1	J	219	Total 1086	C 648	N 219	O 219	0	0
1	K	218	Total 1081	C 645	N 218	O 218	0	0
1	L	158	Total 785	C 469	N 158	O 158	0	0
1	M	133	Total 661	C 395	N 133	O 133	0	0
1	N	219	Total 1086	C 648	N 219	O 219	0	0
1	O	219	Total 1086	C 648	N 219	O 219	0	0
1	P	219	Total 1086	C 648	N 219	O 219	0	0
1	Q	218	Total 1081	C 645	N 218	O 218	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	158	Total 785	C 469	N 158	O 158	0	0
1	S	133	Total 661	C 395	N 133	O 133	0	0
1	T	219	Total 1086	C 648	N 219	O 219	0	0
1	V	219	Total 1086	C 648	N 219	O 219	0	0
1	W	219	Total 1086	C 648	N 219	O 219	0	0
1	X	218	Total 1081	C 645	N 218	O 218	0	0
1	Y	158	Total 785	C 469	N 158	O 158	0	0
1	Z	133	Total 661	C 395	N 133	O 133	0	0
1	AA	219	Total 1086	C 648	N 219	O 219	0	0
1	BA	219	Total 1086	C 648	N 219	O 219	0	0
1	CA	219	Total 1086	C 648	N 219	O 219	0	0
1	DA	218	Total 1081	C 645	N 218	O 218	0	0
1	EA	158	Total 785	C 469	N 158	O 158	0	0
1	FA	133	Total 661	C 395	N 133	O 133	0	0
1	GA	219	Total 1086	C 648	N 219	O 219	0	0
1	HA	219	Total 1086	C 648	N 219	O 219	0	0
1	IA	219	Total 1086	C 648	N 219	O 219	0	0
1	JA	218	Total 1081	C 645	N 218	O 218	0	0
1	KA	158	Total 785	C 469	N 158	O 158	0	0
1	LA	133	Total 661	C 395	N 133	O 133	0	0
1	MA	219	Total 1086	C 648	N 219	O 219	0	0

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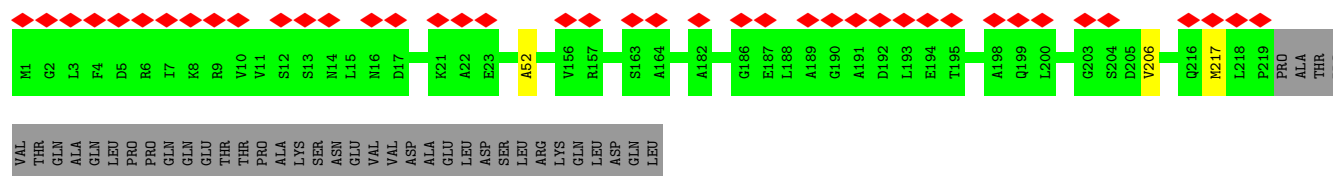
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	NA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	OA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	PA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	QA	158	Total	C	N	O	0	0
			785	469	158	158		
1	RA	133	Total	C	N	O	0	0
			661	395	133	133		
1	SA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	TA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	UA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	VA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	WA	158	Total	C	N	O	0	0
			785	469	158	158		
1	XA	133	Total	C	N	O	0	0
			661	395	133	133		
1	YA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	ZA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	AB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	BB	218	Total	C	N	O	0	0
			1081	645	218	218		
1	CB	158	Total	C	N	O	0	0
			785	469	158	158		
1	DB	133	Total	C	N	O	0	0
			661	395	133	133		
1	EB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	FB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	GB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	HB	218	Total	C	N	O	0	0
			1081	645	218	218		

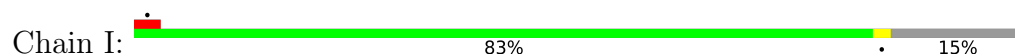
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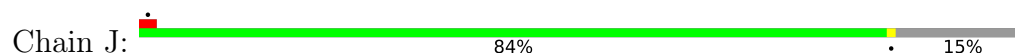
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1	JB	133	Total 661	C 395	N 133	O 133	0	0
1	KB	219	Total 1086	C 648	N 219	O 219	0	0
1	LB	219	Total 1086	C 648	N 219	O 219	0	0
1	MB	219	Total 1086	C 648	N 219	O 219	0	0
1	NB	218	Total 1081	C 645	N 218	O 218	0	0
1	OB	158	Total 785	C 469	N 158	O 158	0	0
1	PB	133	Total 661	C 395	N 133	O 133	0	0
1	QB	219	Total 1086	C 648	N 219	O 219	0	0
1	RB	219	Total 1086	C 648	N 219	O 219	0	0
1	SB	219	Total 1086	C 648	N 219	O 219	0	0
1	TB	218	Total 1081	C 645	N 218	O 218	0	0
1	UB	158	Total 785	C 469	N 158	O 158	0	0



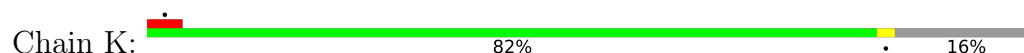
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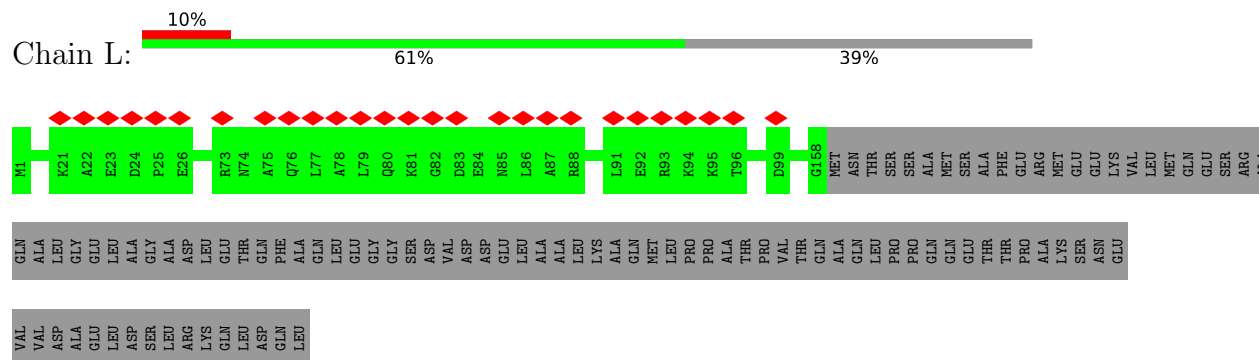
• Molecule 1: Vipp1



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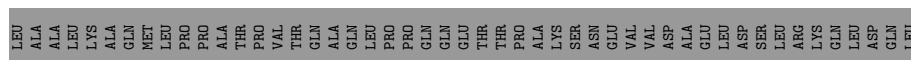
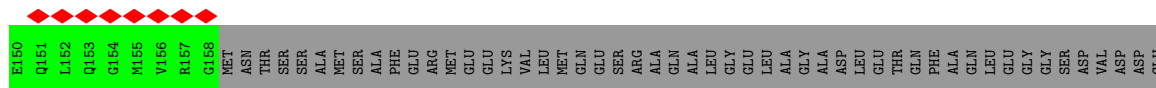
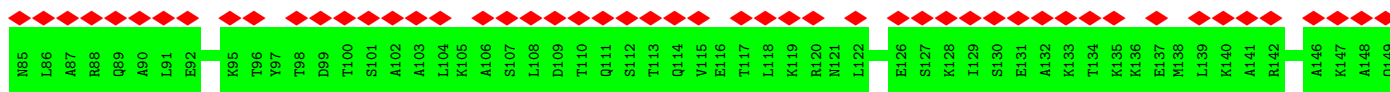


• Molecule 1: Vipp1

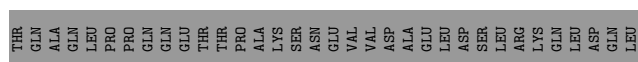
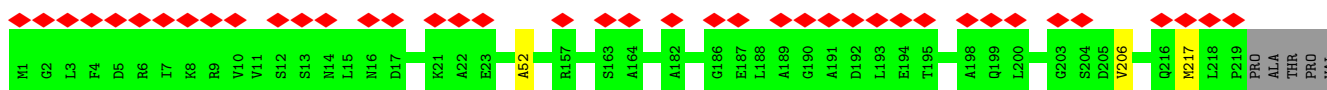
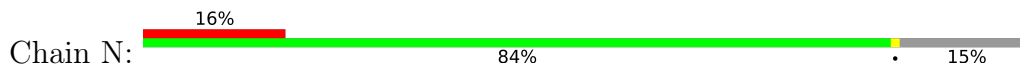


• Molecule 1: Vipp1

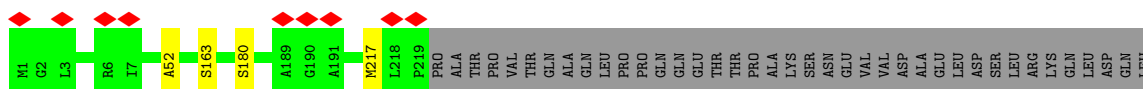
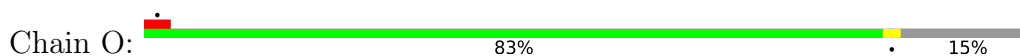




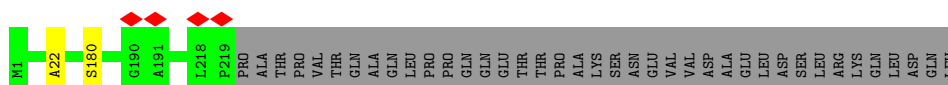
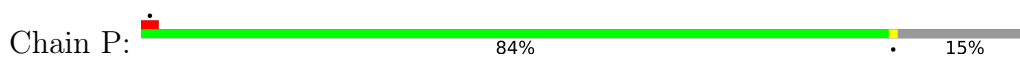
• Molecule 1: Vipp1



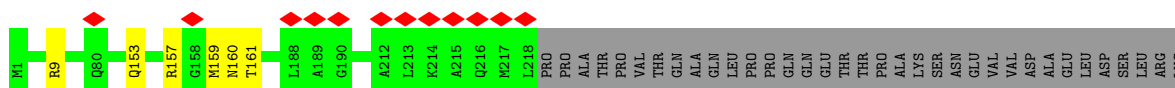
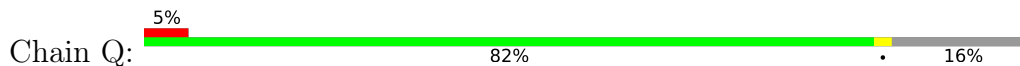
• Molecule 1: Vipp1



• Molecule 1: Vipp1

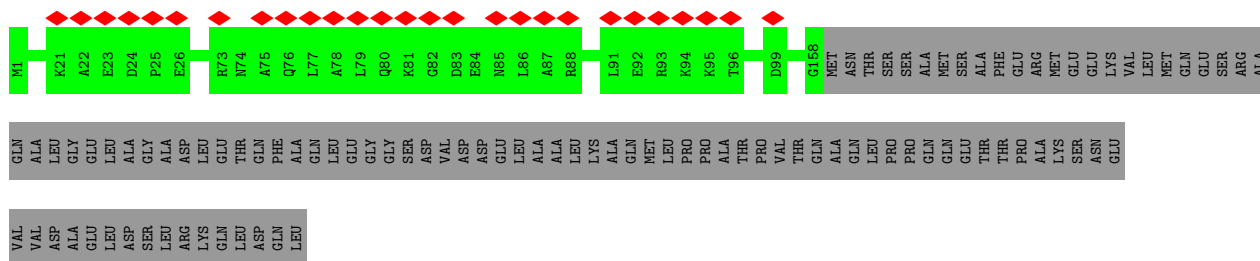


• Molecule 1: Vipp1

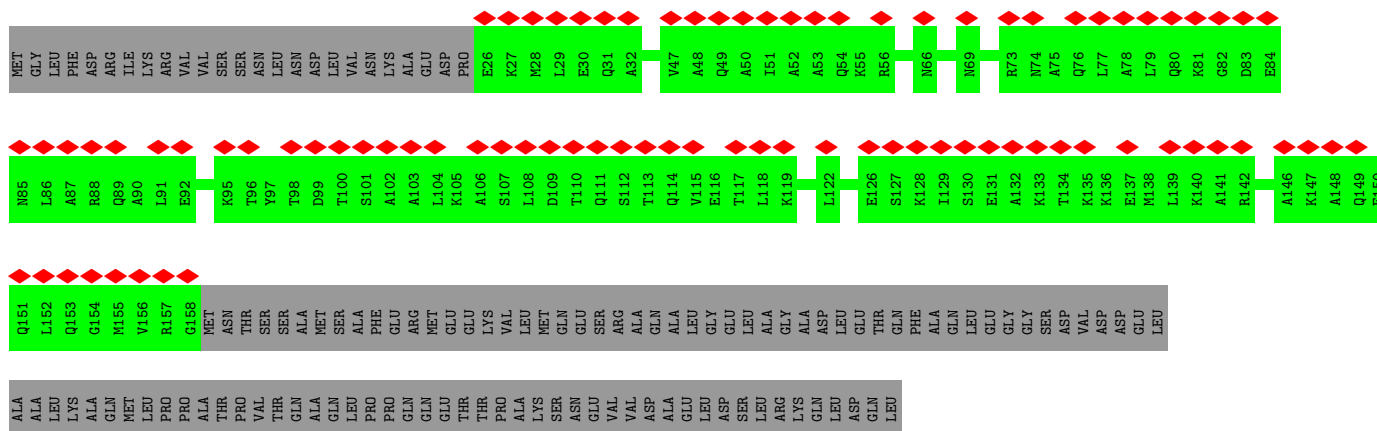


• Molecule 1: Vipp1

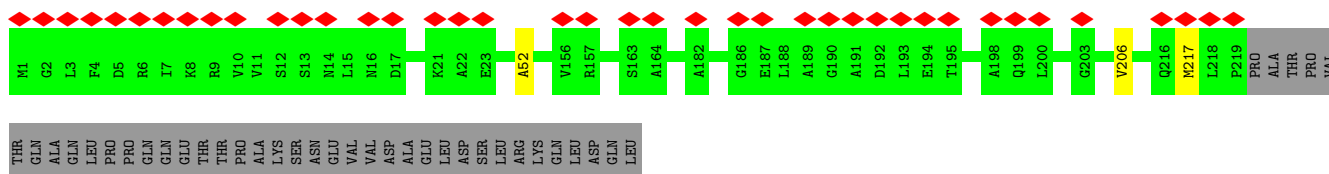
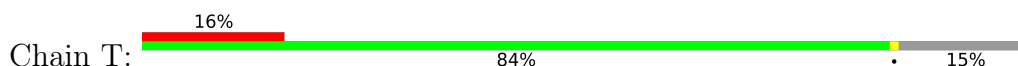




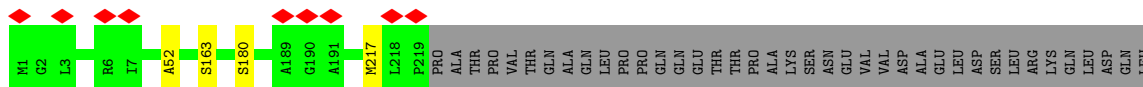
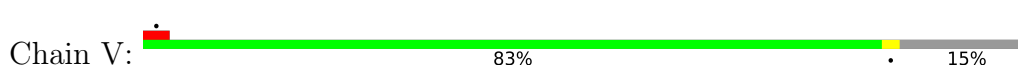
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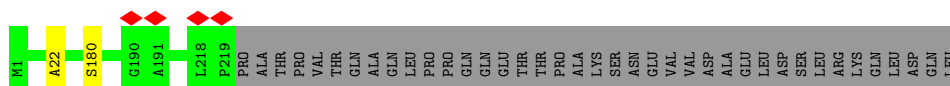
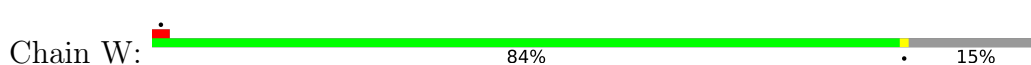
- Molecule 1: Vippp1

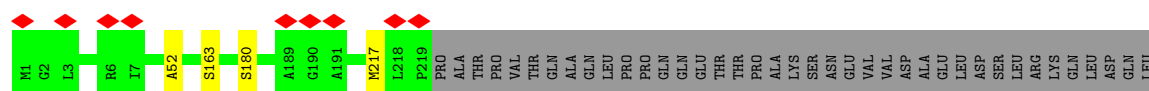


- Molecule 1: Vippp1

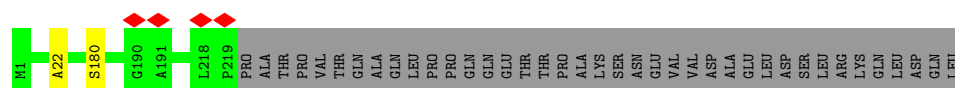


- Molecule 1: Vippp1

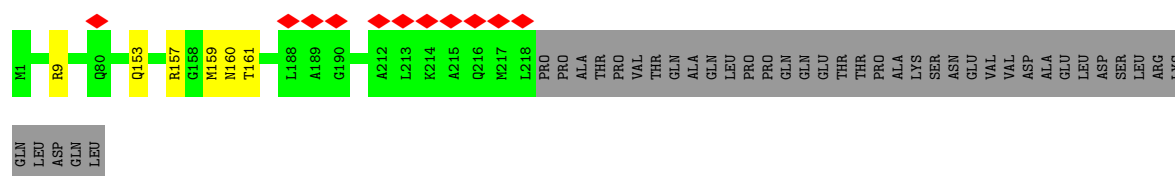


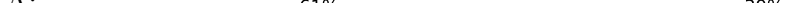


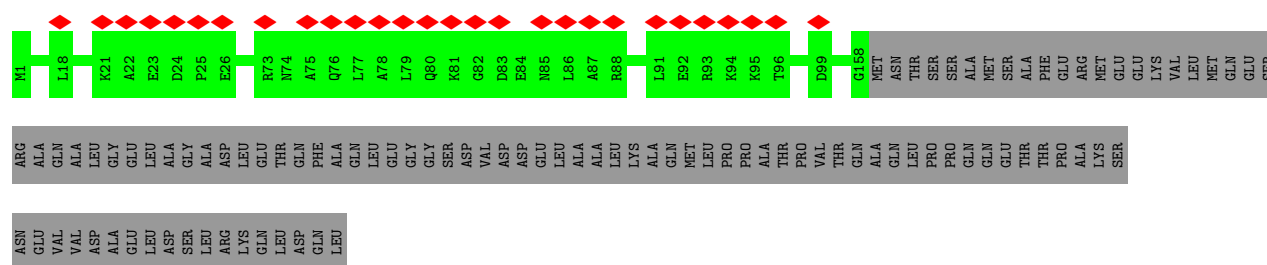
- Chain CA:  84% 15%

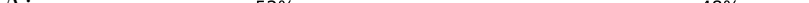


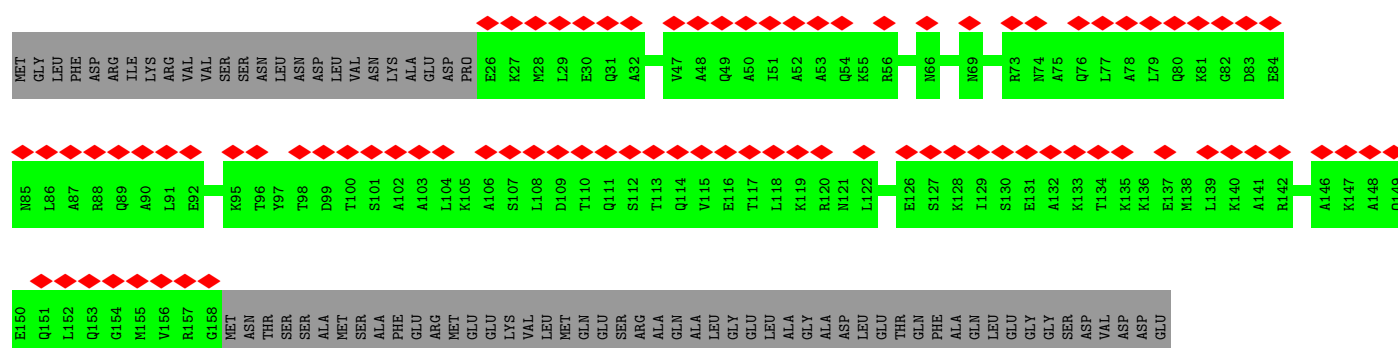
- Chain DA:  82% 16%



- Chain EA: 

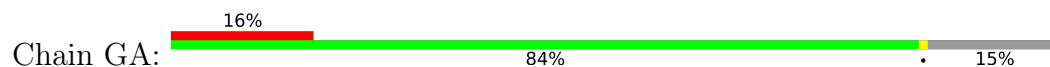


- Chain FA: 



LEU
ALA
ALA
LEU
LYS
ALA
GLN
MET
LEU
PRO
PRO
ALA
THR
PRO
VAL
GLN
ALA
GLN
LEU
PRO
GLN
GLN
GLU
THR
THR
PRO
ALA
LYS
SER
ASN
GLU
VAL
VAL
ASP
ALA
GLU
LEU
SER
SER
LEU
LYS
ARG
LYS
GLN
ASP
GLN
LEU

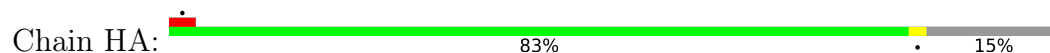
• Molecule 1: Vipp1



M1 G2 L3 F4 D5 R6 I7 K8 R9 V10 V11 S12 S13 N14 L15 N16 D17 K21 A22 E23 A52 R157 S163 A164 A182 G186 E187 L188 A189 G190 A191 D192 L193 E194 T195 A198 Q199 L200 G203 S204 D205 V206 Q216 M217 L218 P219 PRO ALA THR PRO VAL

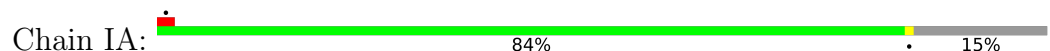
THR
GLN
ALA
GLN
LEU
PRO
PRO
GLN
THR
THR
PRO
ALA
LYS
SER
ASN
GLU
VAL
VAL
ASP
GLU
LEU
SER
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1



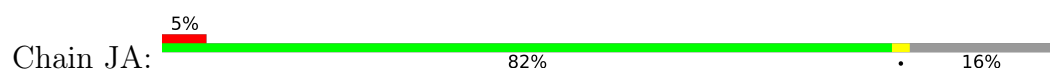
M1 G2 L3 R6 I7 A52 S163 S180 A189 G190 A191 M217 L218 P219 PRO THR PRO VAL THR GLN ALA GLN LEU PRO PRO GLN THR GLU THR PRO ALA LYS SER ASN GLU VAL VAL ASP ALA LEU ASP SER LEU ARG LYS GLN LEU ASP GLN LEU

• Molecule 1: Vipp1



M1 A22 S180 G190 A191 L218 P219 PRO ALA THR PRO VAL THR GLN ALA GLN LEU PRO PRO GLN THR THR ALA LYS SER ASN GLU VAL VAL ASP ALA LEU ASP SER LEU ARG LYS GLN LEU ASP GLN LEU

• Molecule 1: Vipp1



M1 R9 Q80 Q153 R157 G158 M159 N160 T161 L188 A189 G190 A212 L213 K214 A215 Q216 M217 L218 PRO PRO THR THR VAL THR GLN ALA GLN LEU PRO PRO GLN THR THR ALA LYS SER ASN GLU VAL VAL ASP ALA LEU ASP SER LEU ARG LYS

GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1



M1 K21 A22 E23 D24 P25 E26 R73 N74 A75 Q76 L77 A78 Q80 K81 G82 D83 A84 N85 L86 A87 R88 L91 E92 R93 K94 K95 T96 D99 G158 MET ASN THR SER SER MET SER ALA PHE GLU ARG MET GLU VAL LYS VAL MET GLN MET GLU ARG ALA

GLN
ALA
LEU
GLY
GLU
LEU
ALA
GLY
ASP
ARG
LYS
GLN
PHE
ALA
GLN
GLY
GLY
SER
ASP
VAL
ASP
GLU
ALA
ALA
LEU
LYS
ALA

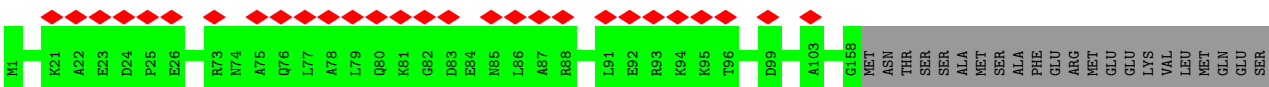
VAL
VAL
ASP
GLU
LEU
ASP
SER
LEU
ARG
GLN
LEU
ASP
GLN
LEU

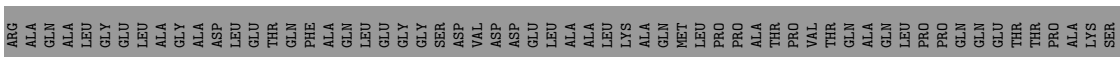
[illegible]

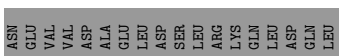
GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1

Chain QA: 

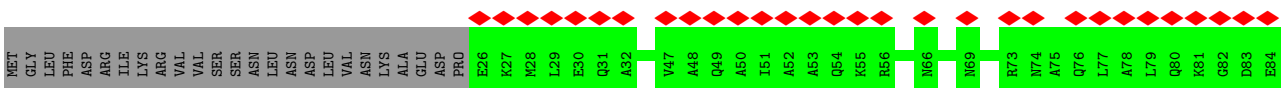


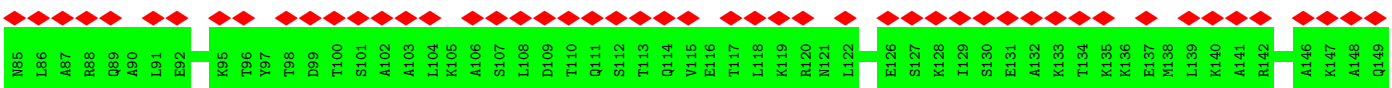


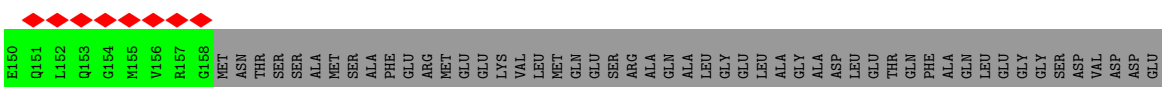


• Molecule 1: Vipp1

Chain RA: 



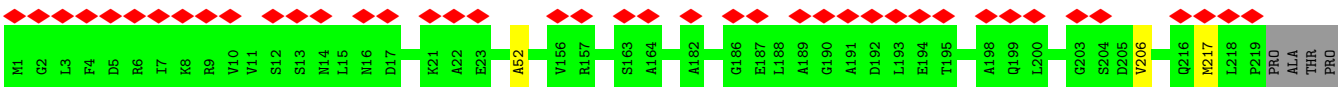






• Molecule 1: Vipp1

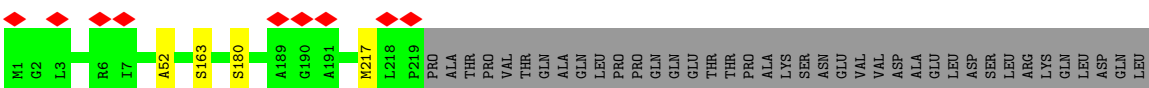
Chain SA: 



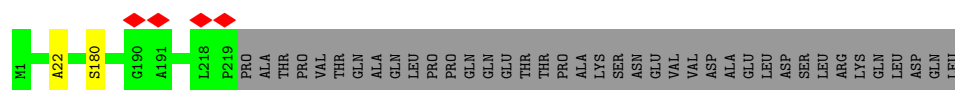
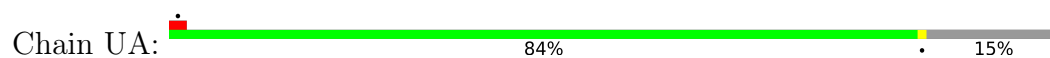


• Molecule 1: Vipp1

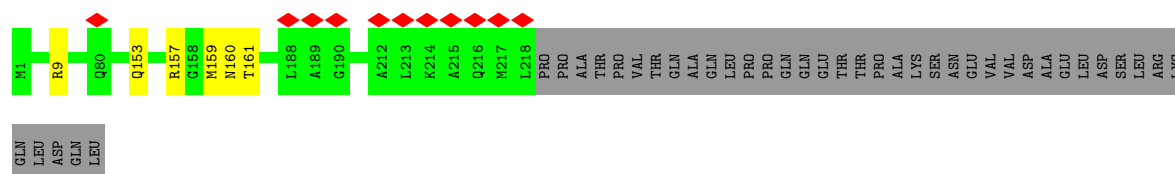
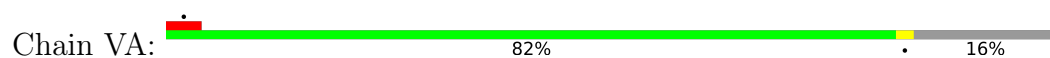
Chain TA: 



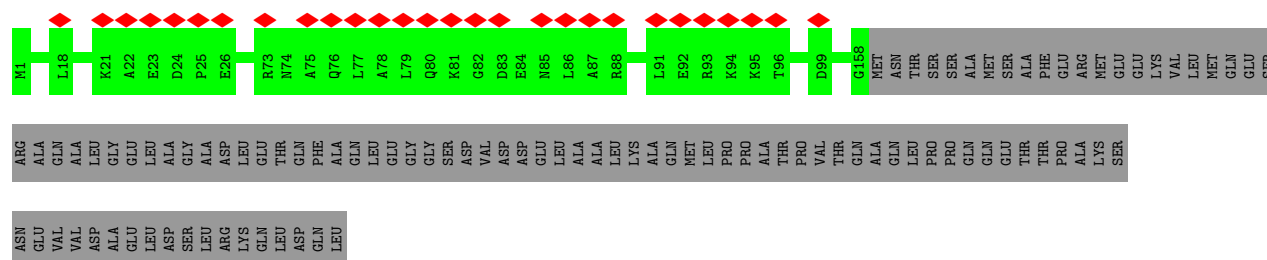
• Molecule 1: Vipp1



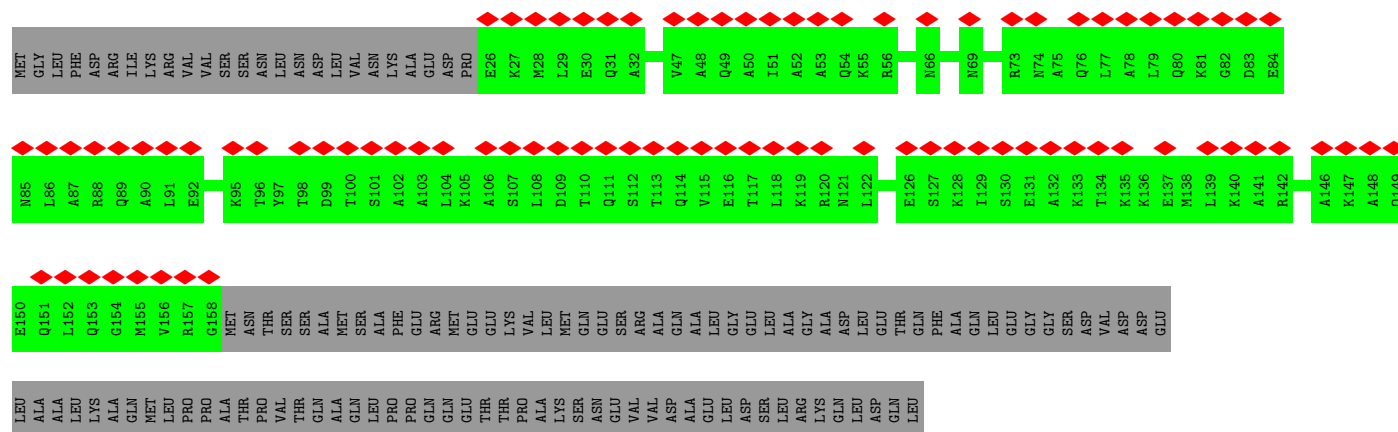
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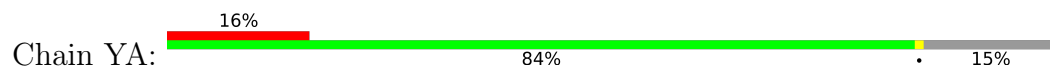
• Molecule 1: Vipp1

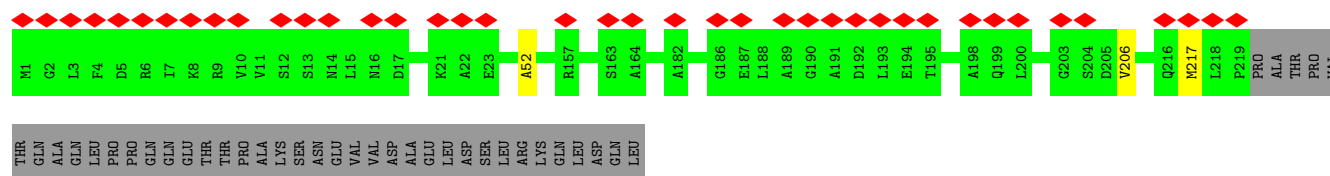


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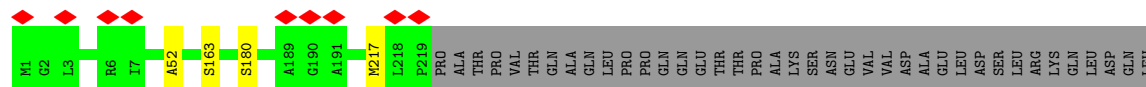
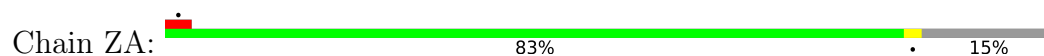


• Molecule 1: Vipp1

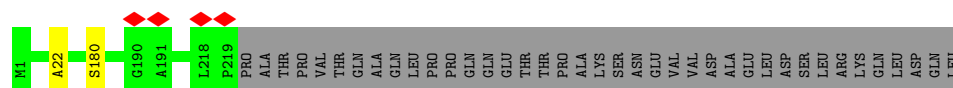
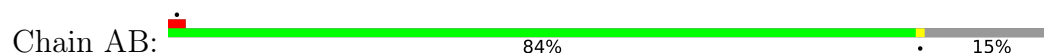




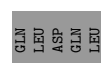
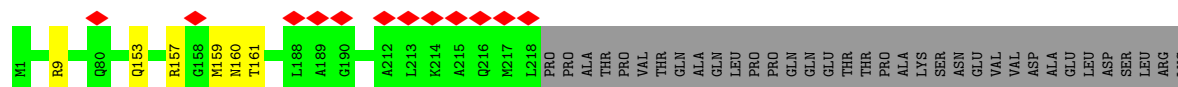
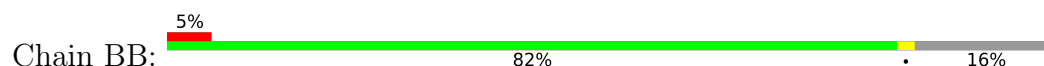
• Molecule 1: Vipp1



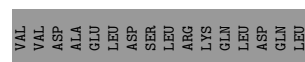
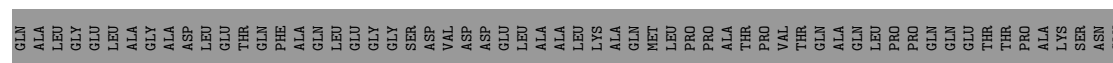
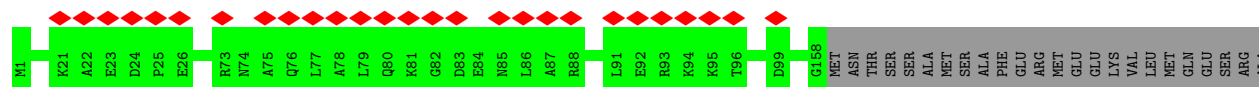
• Molecule 1: Vipp1



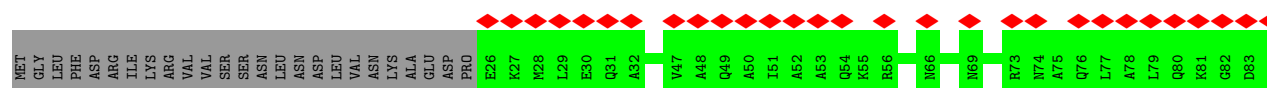
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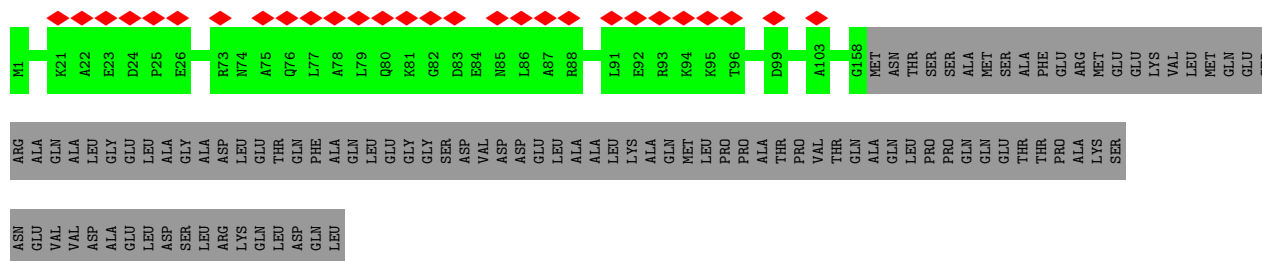


• Molecule 1: Vipp1

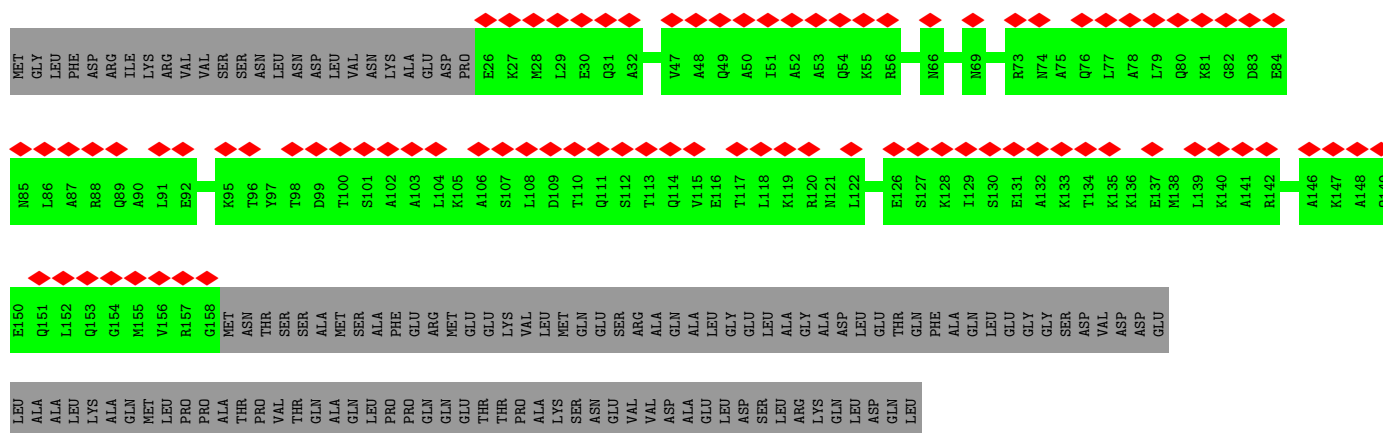


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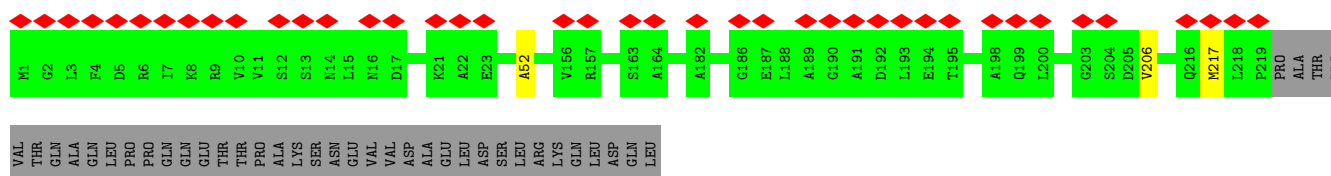
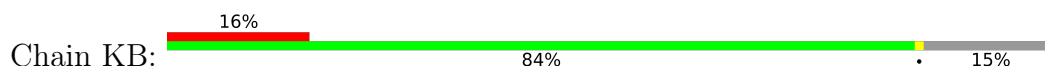




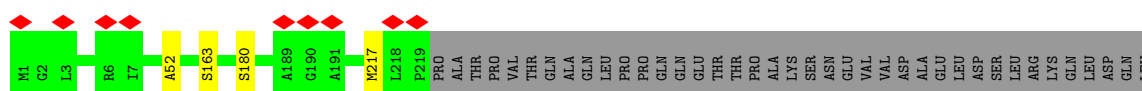
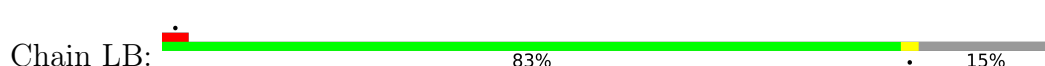
- Molecule 1: Vipp1



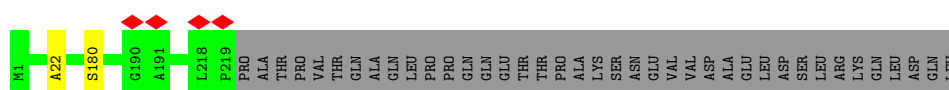
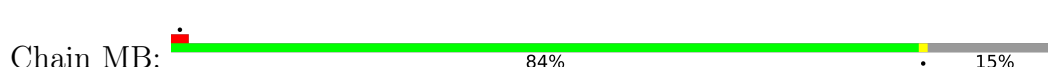
- Molecule 1: Vipp1



- Molecule 1: Vipp1

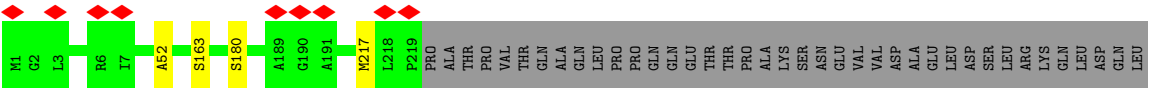
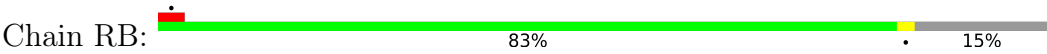


- Molecule 1: Vipp1

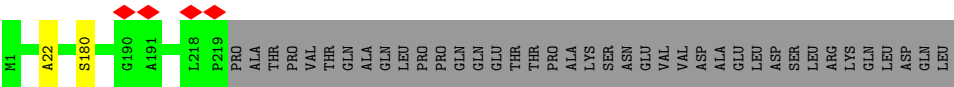
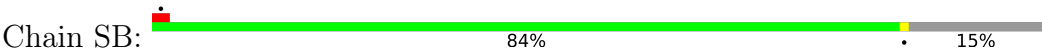


[illegible]

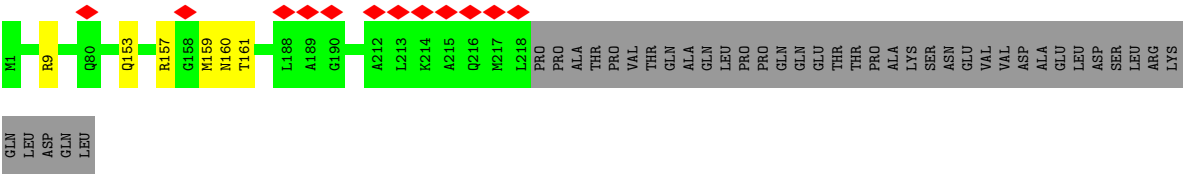
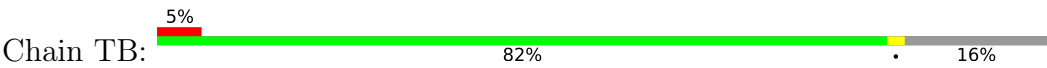
• Molecule 1: Vipp1



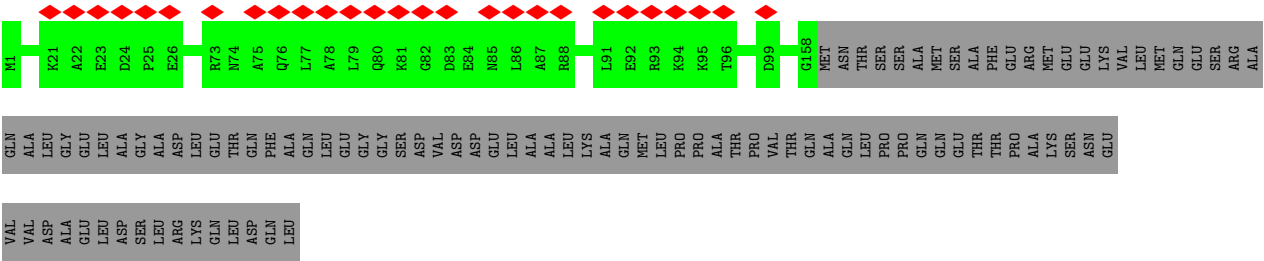
• Molecule 1: Vipp1



• Molecule 1: Vipp1



• Molecule 1: Vipp1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7433	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	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	0.051	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0178	Depositor
Map size ($\text{\AA}$)	467.04, 467.04, 467.04	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	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	A	0.34	0/660	0.86	0/920
1	AA	0.35	0/1085	0.92	2/1512 (0.1%)
1	AB	0.36	0/1085	0.93	0/1512
1	B	0.35	0/1085	0.92	2/1512 (0.1%)
1	BA	0.37	0/1085	0.95	2/1512 (0.1%)
1	BB	0.35	0/1080	0.96	0/1505
1	C	0.37	0/1085	0.95	2/1512 (0.1%)
1	CA	0.36	0/1085	0.93	0/1512
1	CB	0.34	0/784	0.92	0/1093
1	D	0.36	0/1085	0.93	0/1512
1	DA	0.35	0/1080	0.96	0/1505
1	DB	0.34	0/660	0.86	0/920
1	E	0.35	0/1080	0.96	0/1505
1	EA	0.34	0/784	0.92	0/1093
1	EB	0.35	0/1085	0.92	2/1512 (0.1%)
1	F	0.34	0/784	0.92	0/1093
1	FA	0.34	0/660	0.86	0/920
1	FB	0.37	0/1085	0.95	2/1512 (0.1%)
1	G	0.34	0/660	0.86	0/920
1	GA	0.35	0/1085	0.92	2/1512 (0.1%)
1	GB	0.36	0/1085	0.93	0/1512
1	H	0.35	0/1085	0.92	2/1512 (0.1%)
1	HA	0.37	0/1085	0.95	2/1512 (0.1%)
1	HB	0.35	0/1080	0.96	0/1505
1	I	0.37	0/1085	0.95	2/1512 (0.1%)
1	IA	0.36	0/1085	0.93	0/1512
1	IB	0.34	0/784	0.92	0/1093
1	J	0.36	0/1085	0.93	0/1512
1	JA	0.35	0/1080	0.96	0/1505
1	JB	0.34	0/660	0.86	0/920
1	K	0.35	0/1080	0.96	0/1505
1	KA	0.34	0/784	0.92	0/1093
1	KB	0.35	0/1085	0.92	2/1512 (0.1%)
1	L	0.34	0/784	0.92	0/1093

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	LA	0.34	0/660	0.86	0/920
1	LB	0.37	0/1085	0.95	2/1512 (0.1%)
1	M	0.34	0/660	0.86	0/920
1	MA	0.35	0/1085	0.92	2/1512 (0.1%)
1	MB	0.36	0/1085	0.93	0/1512
1	N	0.35	0/1085	0.92	2/1512 (0.1%)
1	NA	0.37	0/1085	0.95	2/1512 (0.1%)
1	NB	0.35	0/1080	0.96	0/1505
1	O	0.37	0/1085	0.95	2/1512 (0.1%)
1	OA	0.36	0/1085	0.93	0/1512
1	OB	0.34	0/784	0.92	0/1093
1	P	0.36	0/1085	0.93	0/1512
1	PA	0.35	0/1080	0.96	0/1505
1	PB	0.34	0/660	0.86	0/920
1	Q	0.35	0/1080	0.96	0/1505
1	QA	0.34	0/784	0.92	0/1093
1	QB	0.35	0/1085	0.92	2/1512 (0.1%)
1	R	0.34	0/784	0.92	0/1093
1	RA	0.34	0/660	0.86	0/920
1	RB	0.37	0/1085	0.95	2/1512 (0.1%)
1	S	0.34	0/660	0.86	0/920
1	SA	0.35	0/1085	0.92	2/1512 (0.1%)
1	SB	0.36	0/1085	0.93	0/1512
1	T	0.35	0/1085	0.92	2/1512 (0.1%)
1	TA	0.37	0/1085	0.95	2/1512 (0.1%)
1	TB	0.35	0/1080	0.96	0/1505
1	UA	0.36	0/1085	0.93	0/1512
1	UB	0.34	0/784	0.92	0/1093
1	V	0.37	0/1085	0.95	2/1512 (0.1%)
1	VA	0.35	0/1080	0.96	0/1505
1	W	0.36	0/1085	0.93	0/1512
1	WA	0.34	0/784	0.92	0/1093
1	X	0.35	0/1080	0.96	0/1505
1	XA	0.34	0/660	0.86	0/920
1	Y	0.34	0/784	0.92	0/1093
1	YA	0.35	0/1085	0.92	2/1512 (0.1%)
1	Z	0.34	0/660	0.86	0/920
1	ZA	0.36	0/1085	0.95	2/1512 (0.1%)
All	All	0.35	0/69348	0.93	48/96648 (0.0%)

There are no bond length outliers.

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KB	217	MET	N-CA-C	6.01	117.84	111.28
1	N	217	MET	N-CA-C	6.01	117.83	111.28
1	GA	217	MET	N-CA-C	6.00	117.82	111.28
1	H	217	MET	N-CA-C	5.99	117.81	111.28
1	B	217	MET	N-CA-C	5.97	117.79	111.28

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	A	661	0	320	0	0
1	AA	1086	0	531	3	0
1	AB	1086	0	531	4	0
1	B	1086	0	531	3	0
1	BA	1086	0	531	6	0
1	BB	1081	0	530	5	0
1	C	1086	0	531	6	0
1	CA	1086	0	531	4	0
1	CB	785	0	376	0	0
1	D	1086	0	531	4	0
1	DA	1081	0	530	4	0
1	DB	661	0	320	0	0
1	E	1081	0	530	5	0
1	EA	785	0	376	0	0
1	EB	1086	0	531	3	0
1	F	785	0	376	0	0
1	FA	661	0	320	0	0
1	FB	1086	0	531	6	0
1	G	661	0	320	0	0
1	GA	1086	0	531	3	0
1	GB	1086	0	531	4	0
1	H	1086	0	531	4	0
1	HA	1086	0	531	6	0
1	HB	1081	0	530	5	0
1	I	1086	0	531	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IA	1086	0	531	4	0
1	IB	785	0	376	0	0
1	J	1086	0	531	4	0
1	JA	1081	0	530	4	0
1	JB	661	0	320	0	0
1	K	1081	0	530	5	0
1	KA	785	0	376	0	0
1	KB	1086	0	531	3	0
1	L	785	0	376	0	0
1	LA	661	0	320	0	0
1	LB	1086	0	531	6	0
1	M	661	0	320	0	0
1	MA	1086	0	531	3	0
1	MB	1086	0	531	4	0
1	N	1086	0	531	3	0
1	NA	1086	0	531	6	0
1	NB	1081	0	530	4	0
1	O	1086	0	531	6	0
1	OA	1086	0	531	4	0
1	OB	785	0	376	0	0
1	P	1086	0	531	4	0
1	PA	1081	0	530	4	0
1	PB	661	0	320	0	0
1	Q	1081	0	530	5	0
1	QA	785	0	376	0	0
1	QB	1086	0	531	3	0
1	R	785	0	376	0	0
1	RA	661	0	320	0	0
1	RB	1086	0	531	6	0
1	S	661	0	320	0	0
1	SA	1086	0	531	3	0
1	SB	1086	0	531	4	0
1	T	1086	0	531	3	0
1	TA	1086	0	531	6	0
1	TB	1081	0	530	5	0
1	UA	1086	0	531	4	0
1	UB	785	0	376	0	0
1	V	1086	0	531	7	0
1	VA	1081	0	530	4	0
1	W	1086	0	531	4	0
1	WA	785	0	376	0	0
1	X	1081	0	530	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	XA	661	0	320	0	0
1	Y	785	0	376	0	0
1	YA	1086	0	531	3	0
1	Z	661	0	320	0	0
1	ZA	1086	0	531	6	0
All	All	69420	0	33828	128	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 128 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)
1:N:52:ALA:HB1	1:BA:180:SER:CB	1.30	1.61
1:AA:52:ALA:HB1	1:NA:180:SER:CB	1.30	1.61
1:T:52:ALA:HB1	1:HA:180:SER:CB	1.30	1.61
1:GA:52:ALA:HB1	1:TA:180:SER:CB	1.30	1.61
1:MA:52:ALA:HB1	1:ZA:180:SER:CB	1.30	1.61

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	A	131/258 (51%)	131 (100%)	0	0	100	100
1	AA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	AB	217/258 (84%)	217 (100%)	0	0	100	100
1	B	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	BA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BB	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	C	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CA	217/258 (84%)	217 (100%)	0	0	100	100
1	CB	156/258 (60%)	156 (100%)	0	0	100	100
1	D	217/258 (84%)	217 (100%)	0	0	100	100
1	DA	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	DB	131/258 (51%)	131 (100%)	0	0	100	100
1	E	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	EA	156/258 (60%)	156 (100%)	0	0	100	100
1	EB	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	F	156/258 (60%)	156 (100%)	0	0	100	100
1	FA	131/258 (51%)	131 (100%)	0	0	100	100
1	FB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	G	131/258 (51%)	131 (100%)	0	0	100	100
1	GA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	GB	217/258 (84%)	217 (100%)	0	0	100	100
1	H	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	HA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	HB	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	I	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	IA	217/258 (84%)	217 (100%)	0	0	100	100
1	IB	156/258 (60%)	156 (100%)	0	0	100	100
1	J	217/258 (84%)	217 (100%)	0	0	100	100
1	JA	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	JB	131/258 (51%)	131 (100%)	0	0	100	100
1	K	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	KA	156/258 (60%)	156 (100%)	0	0	100	100
1	KB	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	L	156/258 (60%)	156 (100%)	0	0	100	100
1	LA	131/258 (51%)	131 (100%)	0	0	100	100
1	LB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	131/258 (51%)	131 (100%)	0	0	100	100
1	MA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	MB	217/258 (84%)	217 (100%)	0	0	100	100
1	N	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	NA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	NB	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	O	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	OA	217/258 (84%)	217 (100%)	0	0	100	100
1	OB	156/258 (60%)	156 (100%)	0	0	100	100
1	P	217/258 (84%)	217 (100%)	0	0	100	100
1	PA	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	PB	131/258 (51%)	131 (100%)	0	0	100	100
1	Q	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	QA	156/258 (60%)	156 (100%)	0	0	100	100
1	QB	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	R	156/258 (60%)	156 (100%)	0	0	100	100
1	RA	131/258 (51%)	131 (100%)	0	0	100	100
1	RB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	S	131/258 (51%)	131 (100%)	0	0	100	100
1	SA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	SB	217/258 (84%)	217 (100%)	0	0	100	100
1	T	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	TA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	TB	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	UA	217/258 (84%)	217 (100%)	0	0	100	100
1	UB	156/258 (60%)	156 (100%)	0	0	100	100
1	V	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	VA	216/258 (84%)	215 (100%)	0	1 (0%)	24	63
1	W	217/258 (84%)	217 (100%)	0	0	100	100
1	WA	156/258 (60%)	156 (100%)	0	0	100	100
1	X	216/258 (84%)	215 (100%)	0	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	XA	131/258 (51%)	131 (100%)	0	0	100	100
1	Y	156/258 (60%)	156 (100%)	0	0	100	100
1	YA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	Z	131/258 (51%)	131 (100%)	0	0	100	100
1	ZA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
All	All	13848/18576 (74%)	13800 (100%)	36 (0%)	12 (0%)	49	83

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	160	ASN
1	K	160	ASN
1	Q	160	ASN
1	X	160	ASN
1	DA	160	ASN

5.3.2 Protein sidechains [i](#)

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

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.

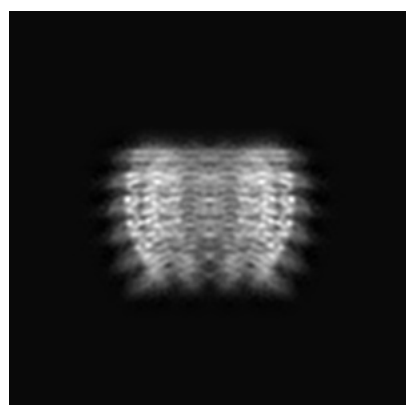
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11469. These allow visual inspection of the internal detail of the map and identification of artifacts.

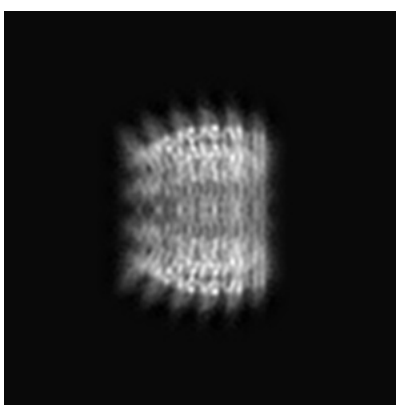
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 168



Y Index: 168



Z Index: 168

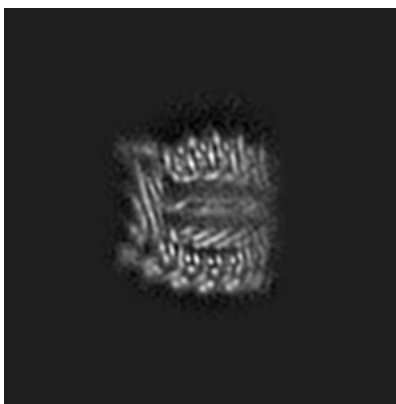
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 215



Y Index: 121

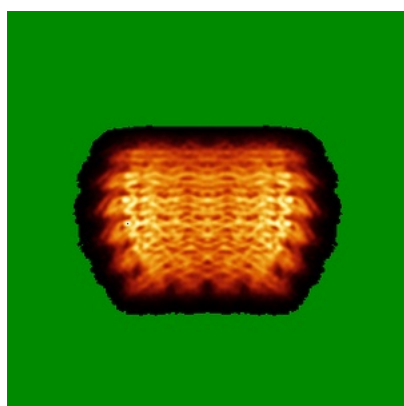


Z Index: 157

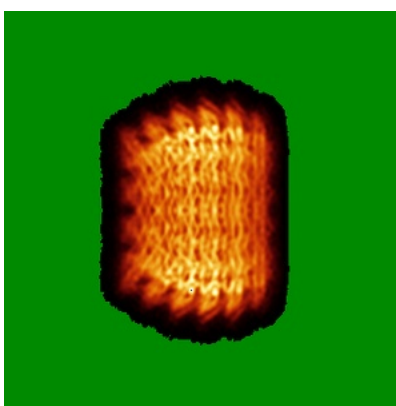
The images above show the largest variance slices of the map in three orthogonal directions.

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

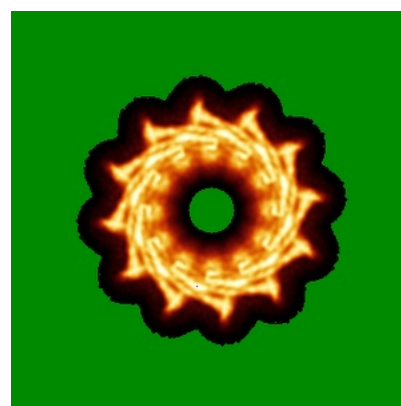
6.4.1 Primary map



X



Y

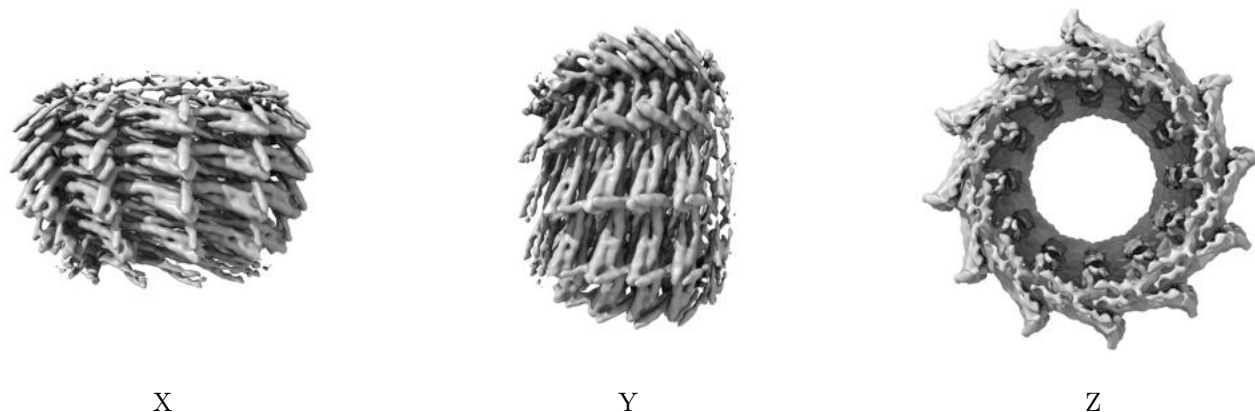


Z

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 0.0178. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

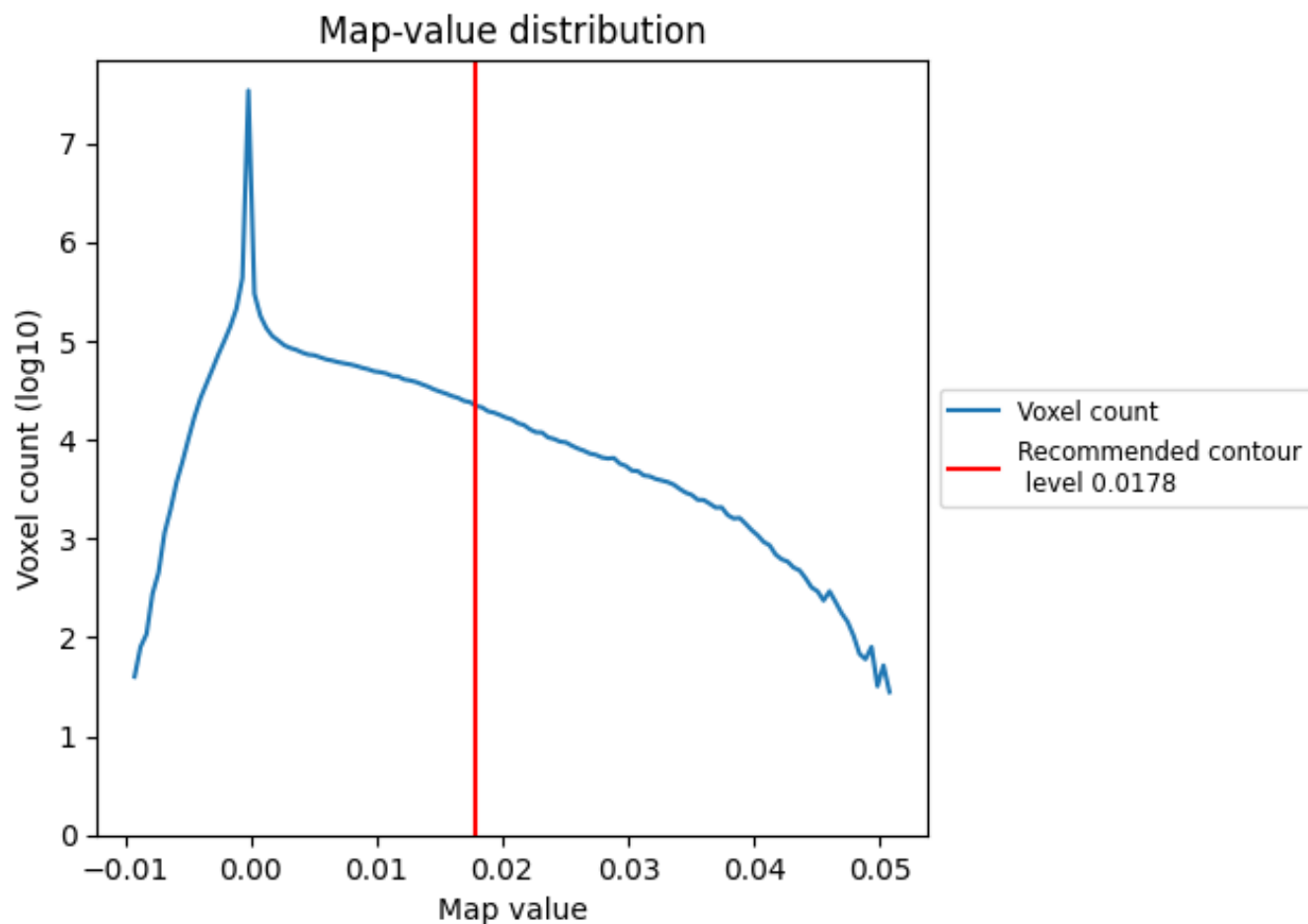
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

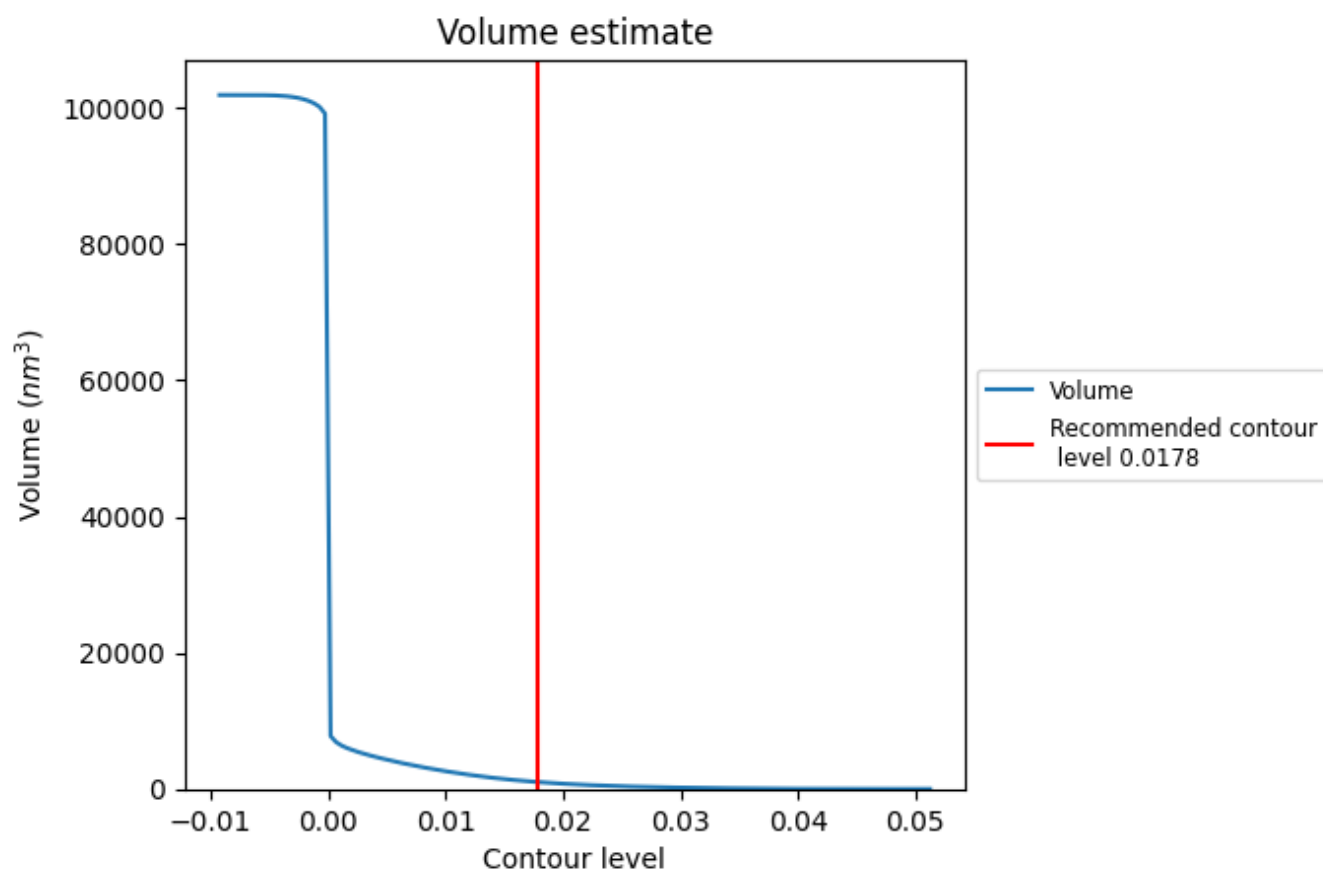
This section contains the results of statistical analysis of the map.

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.

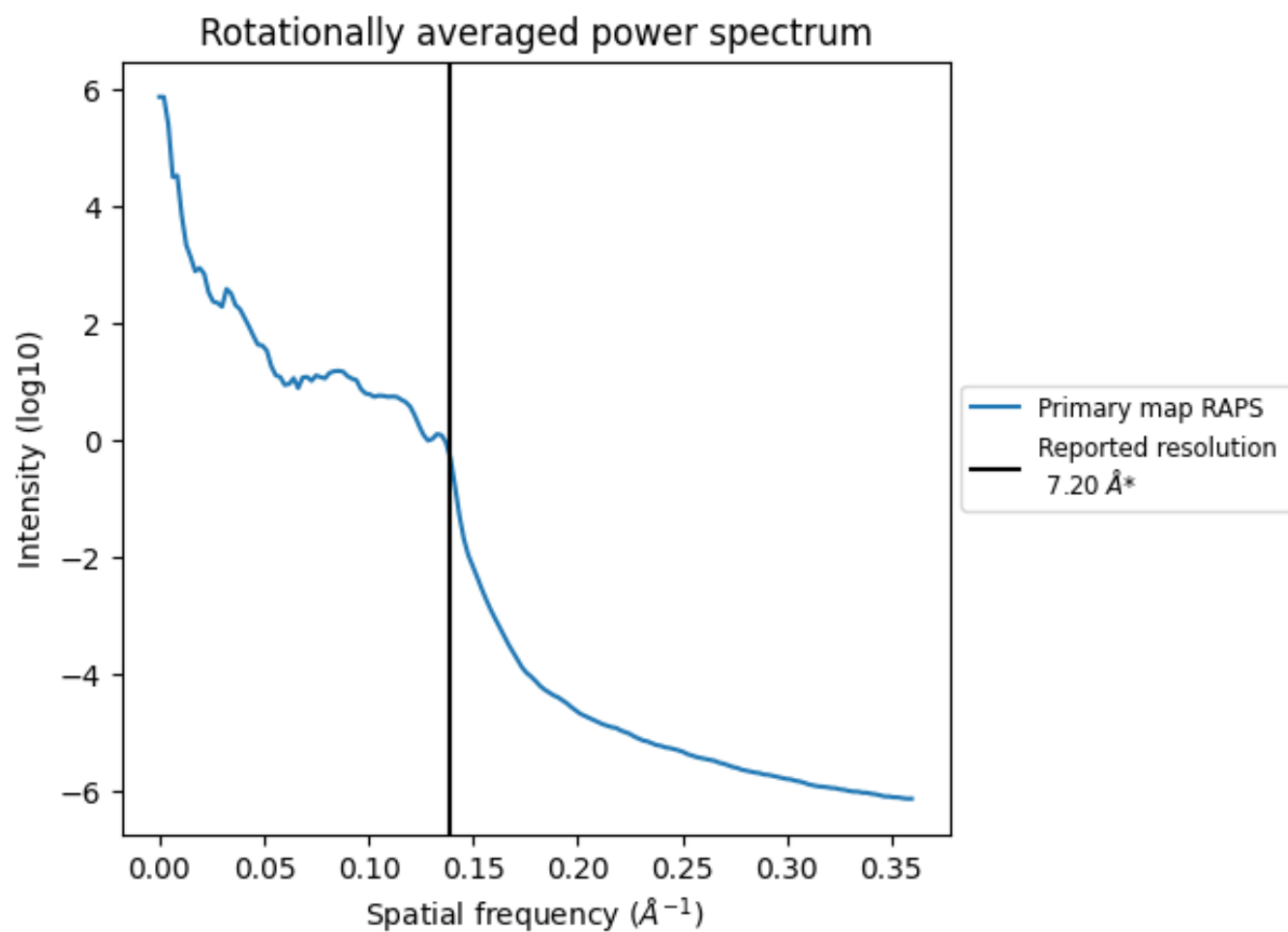
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1022 nm³; this corresponds to an approximate mass of 923 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 0.139 Å⁻¹

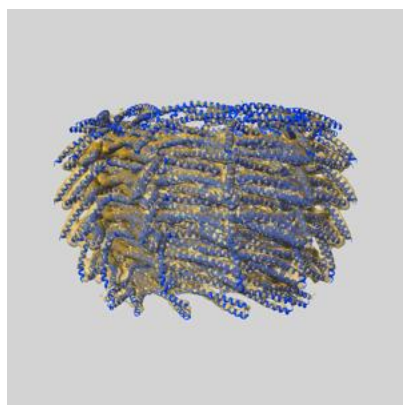
8 Fourier-Shell correlation

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

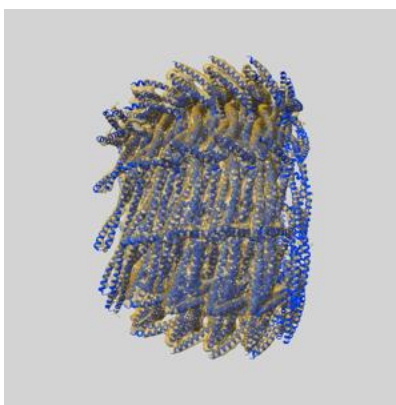
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11469 and PDB model 6ZVS. Per-residue inclusion information can be found in section [3](#) on page [10](#).

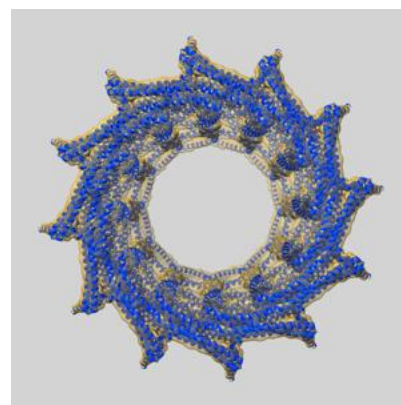
9.1 Map-model overlay [i](#)



X



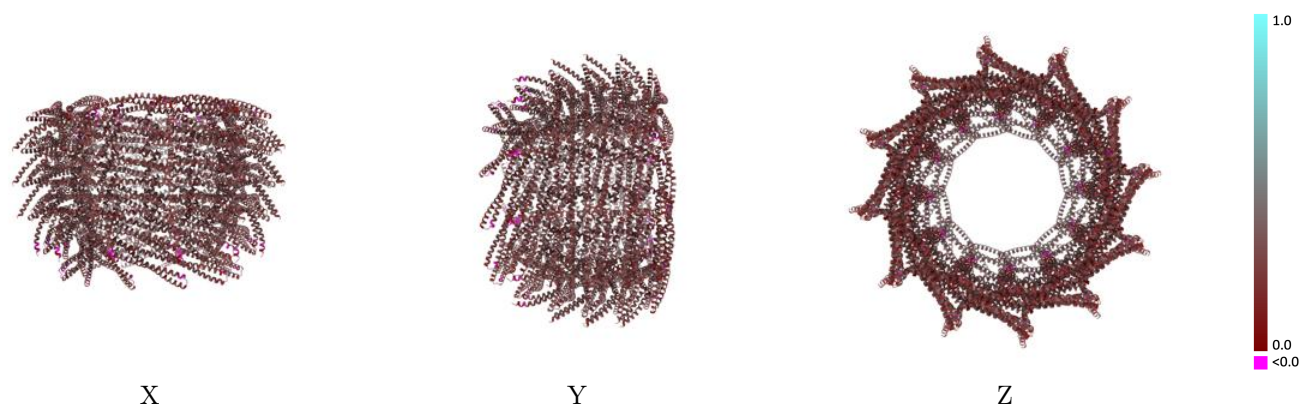
Y



Z

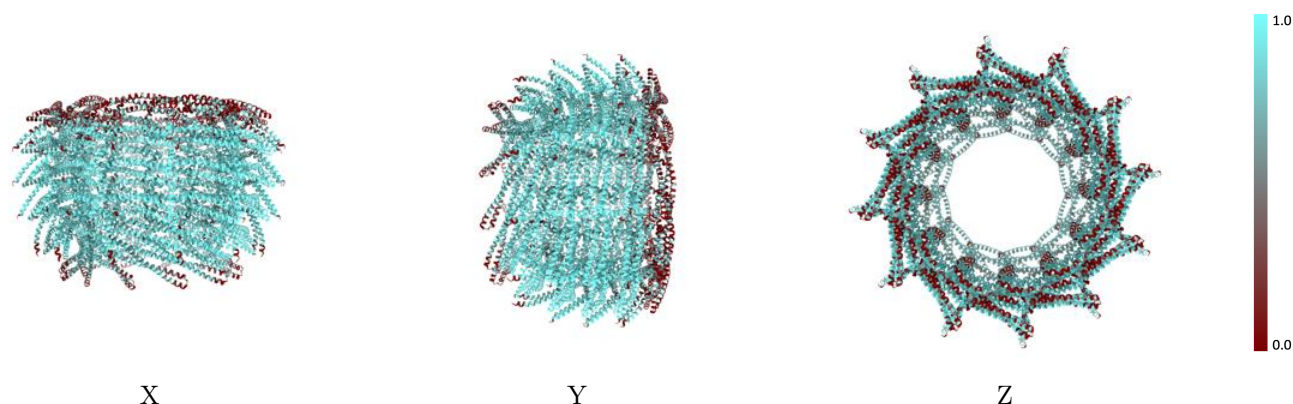
The images above show the 3D surface view of the map at the recommended contour level 0.0178 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



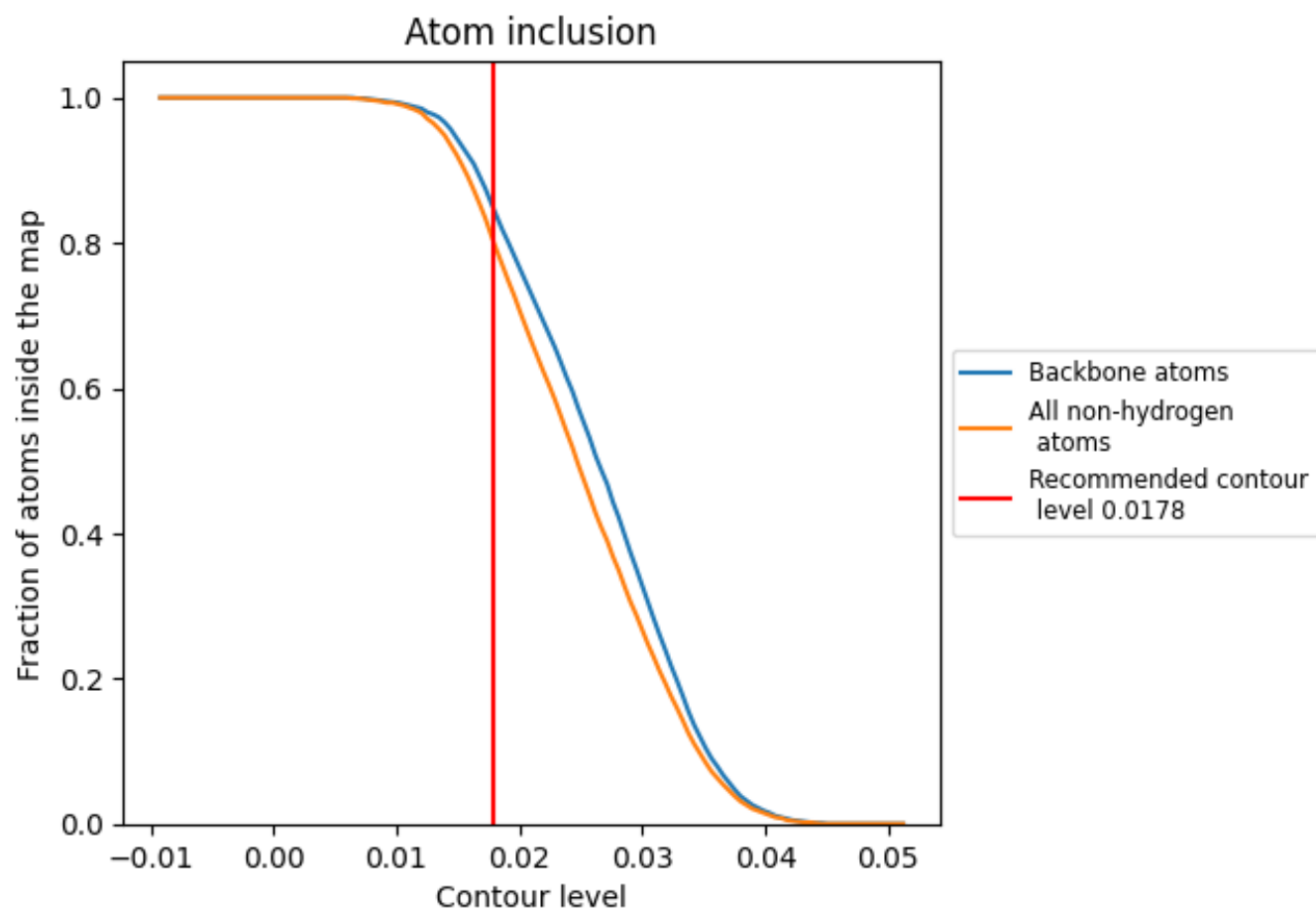
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0178).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 81% 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 (0.0178) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.2610
A	 0.3270	 0.2420
AA	 0.7760	 0.2490
AB	 0.9560	 0.2760
B	 0.7780	 0.2520
BA	 0.9240	 0.2680
BB	 0.8990	 0.2600
C	 0.9230	 0.2710
CA	 0.9550	 0.2740
CB	 0.7480	 0.2600
D	 0.9580	 0.2760
DA	 0.9020	 0.2580
DB	 0.3270	 0.2390
E	 0.9030	 0.2580
EA	 0.7470	 0.2580
EB	 0.7780	 0.2500
F	 0.7470	 0.2580
FA	 0.3210	 0.2410
FB	 0.9230	 0.2710
G	 0.3220	 0.2390
GA	 0.7790	 0.2520
GB	 0.9580	 0.2770
H	 0.7760	 0.2500
HA	 0.9240	 0.2730
HB	 0.9030	 0.2580
I	 0.9240	 0.2690
IA	 0.9560	 0.2770
IB	 0.7470	 0.2590
J	 0.9560	 0.2730
JA	 0.8990	 0.2610
JB	 0.3240	 0.2400
K	 0.9020	 0.2570
KA	 0.7480	 0.2600
KB	 0.7760	 0.2510
L	 0.7450	 0.2560



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Chain	Atom inclusion	Q-score
LA	 0.3270	 0.2400
LB	 0.9240	 0.2710
M	 0.3240	 0.2420
MA	 0.7780	 0.2510
MB	 0.9560	 0.2750
N	 0.7790	 0.2490
NA	 0.9230	 0.2710
NB	 0.9020	 0.2590
O	 0.9240	 0.2680
OA	 0.9580	 0.2780
OB	 0.7450	 0.2570
P	 0.9560	 0.2730
PA	 0.9030	 0.2600
PB	 0.3220	 0.2420
Q	 0.8990	 0.2590
QA	 0.7470	 0.2610
QB	 0.7780	 0.2520
R	 0.7480	 0.2580
RA	 0.3240	 0.2390
RB	 0.9240	 0.2710
S	 0.3270	 0.2410
SA	 0.7760	 0.2510
SB	 0.9560	 0.2740
T	 0.7780	 0.2490
TA	 0.9240	 0.2740
TB	 0.8990	 0.2580
UA	 0.9560	 0.2780
UB	 0.7480	 0.2580
V	 0.9230	 0.2690
VA	 0.9020	 0.2610
W	 0.9580	 0.2740
WA	 0.7450	 0.2600
X	 0.9030	 0.2580
XA	 0.3220	 0.2400
Y	 0.7470	 0.2600
YA	 0.7790	 0.2530
Z	 0.3240	 0.2390
ZA	 0.9240	 0.2720