



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:55 PM UTC

PDB ID : 6ZW4 / pdb_00006zw4
EMDB ID : EMD-11478
Title : C14 symmetry: Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily.
Authors : Liu, J.W.; 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 : 6.50 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:

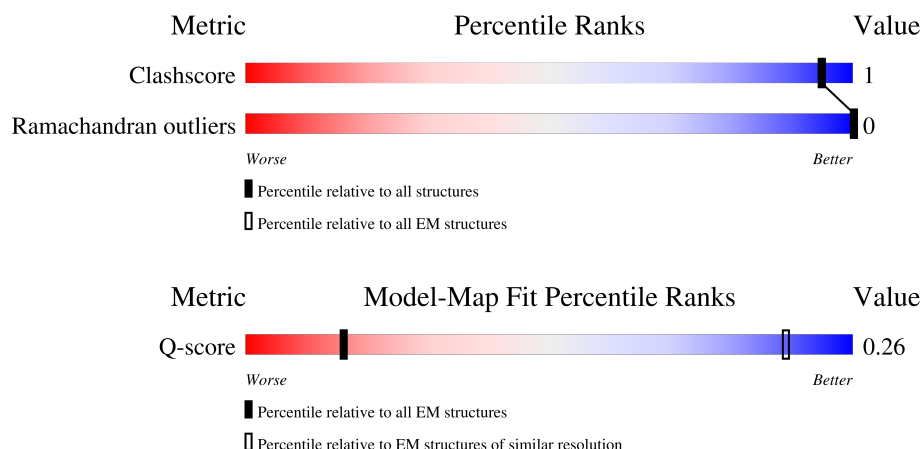
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 6.50 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	556 (6.00 - 7.00)

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	6% 52% 48%
1	AA	258	8% 84% 15%
1	AB	258	83% 15%
1	AC	258	21% 61% 39%
1	B	258	9% 83% 15%

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Mol	Chain	Length	Quality of chain
1	BA	258	
1	BB	258	
1	BC	258	
1	C	258	
1	CA	258	
1	CB	258	
1	CC	258	
1	D	258	
1	DA	258	
1	DB	258	
1	DC	258	
1	E	258	
1	EA	258	
1	EB	258	
1	EC	258	
1	F	258	
1	FA	258	
1	FB	258	
1	FC	258	
1	G	258	
1	GA	258	
1	GB	258	
1	GC	258	
1	H	258	
1	HA	258	

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Mol	Chain	Length	Quality of chain
1	HB	258	
1	I	258	
1	IA	258	
1	IB	258	
1	J	258	
1	JA	258	
1	JB	258	
1	K	258	
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	

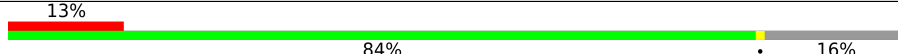
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Mol	Chain	Length	Quality of chain
1	Q	258	
1	QA	258	
1	QB	258	
1	R	258	
1	RA	258	
1	RB	258	
1	S	258	
1	SA	258	
1	SB	258	
1	T	258	
1	TA	258	
1	TB	258	
1	UA	258	
1	UB	258	
1	V	258	
1	VA	258	
1	VB	258	
1	W	258	
1	WA	258	
1	WB	258	
1	X	258	
1	XA	258	
1	XB	258	
1	Y	258	
1	YA	258	

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Mol	Chain	Length	Quality of chain
1	YB	258	 83% 15% 6%
1	Z	258	 52% 48% 6%
1	ZA	258	 82% 15% 13%
1	ZB	258	 84% 16% 13%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 80990 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 vipp1.

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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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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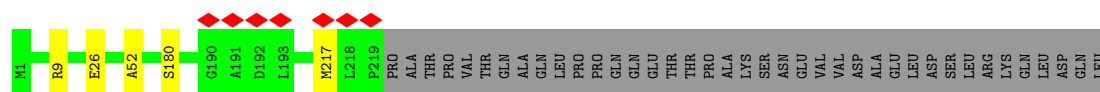
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	IB	158	Total 785	C 469	N 158	O 158	0	0
1	JB	133	Total 661	C 395	N 133	O 133	0	0
1	KB	219	Total 1086	C 648	N 219	O 219	0	0
1	LB	219	Total 1086	C 648	N 219	O 219	0	0
1	MB	219	Total 1086	C 648	N 219	O 219	0	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
1	VB	133	Total 661	C 395	N 133	O 133	0	0
1	WB	219	Total 1086	C 648	N 219	O 219	0	0
1	XB	219	Total 1086	C 648	N 219	O 219	0	0
1	YB	219	Total 1086	C 648	N 219	O 219	0	0
1	ZB	218	Total 1081	C 645	N 218	O 218	0	0
1	AC	158	Total 785	C 469	N 158	O 158	0	0
1	BC	133	Total 661	C 395	N 133	O 133	0	0
1	CC	219	Total 1086	C 648	N 219	O 219	0	0

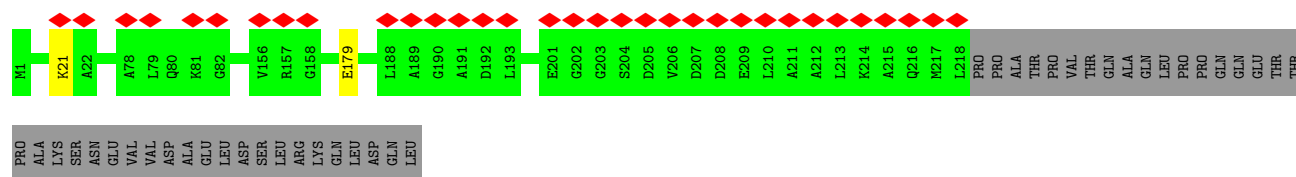
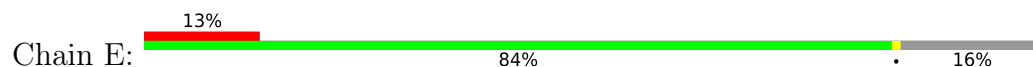
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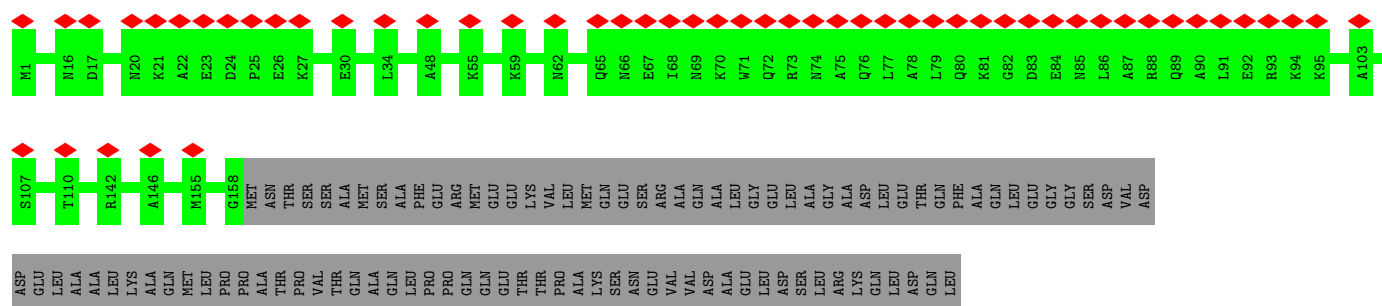
Mol	Chain	Residues	Atoms				AltConf	Trace
1	DC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	EC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	FC	218	Total	C	N	O	0	0
			1081	645	218	218		
1	GC	158	Total	C	N	O	0	0
			785	469	158	158		



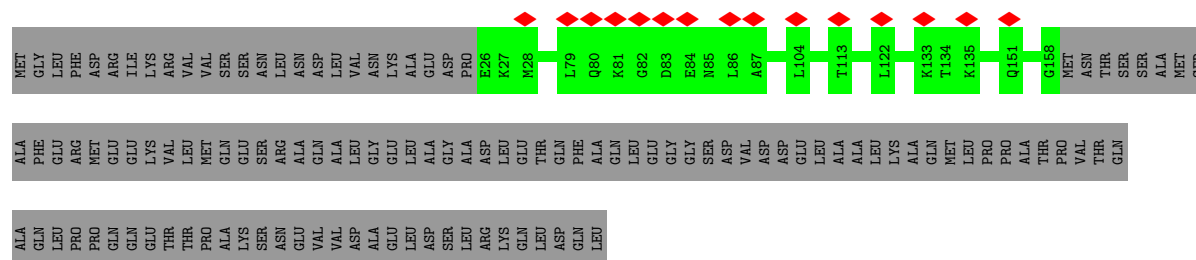
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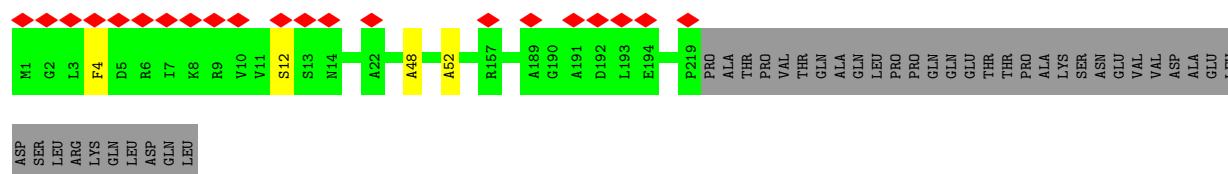
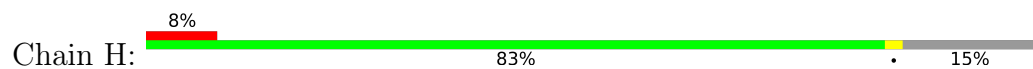
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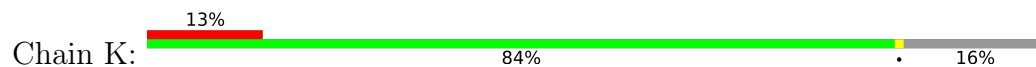
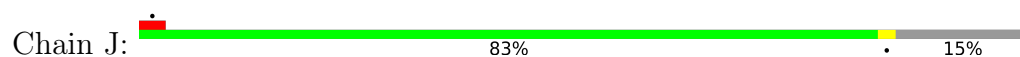
- Molecule 1: vipp1



- Molecule 1: vipp1

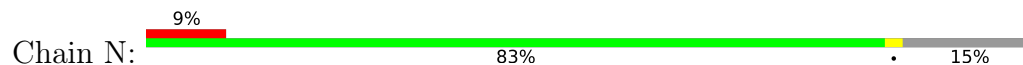


- Chain I:  82% 15%



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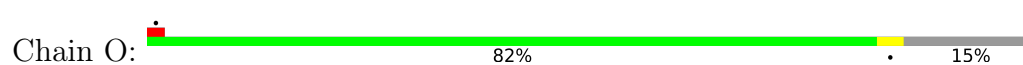
• Molecule 1: vippl



M1 G2 L3 F4 D5 R6 I7 K8 R9 V10 V11 S12 S13 N14 A22 A48 A52 R157 A189 G190 A191 D192 L193 E194 T195 P219 PRO ALA THR PRO VAL THR THR ALA GLN LEU PRO PRO GLN GLN GLU THR THR PRO ALA LYS SER ASN GLU VAL ASP GLU

LEU ASP SER LEU ARG LYS GLN LEU ASP GLN LEU

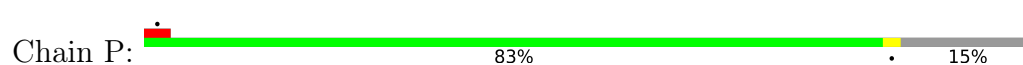
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M1 V19 A22 E23 A52 V156 R157 G158 S180 A184 A189 G190 A191 P219 PRO ALA THR PRO VAL THR GLN GLN LEU PRO PRO GLN GLN THR THR PRO ALA LYS SER ASN GLU VAL ASP ALA GLU LEU ASP SER LYS GLN ASP GLN

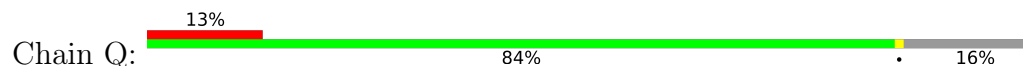
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• Molecule 1: vippl



M1 R9 E26 A52 S180 G190 D192 L193 K217 L218 P219 PRO THR THR VAL THR GLN ALA GLN LEU PRO PRO GLN GLN GLU THR THR PRO ALA LYS SER ASN GLU VAL ASP LEU SER LEU ARG LYS GLN ASP GLN

• Molecule 1: vippl



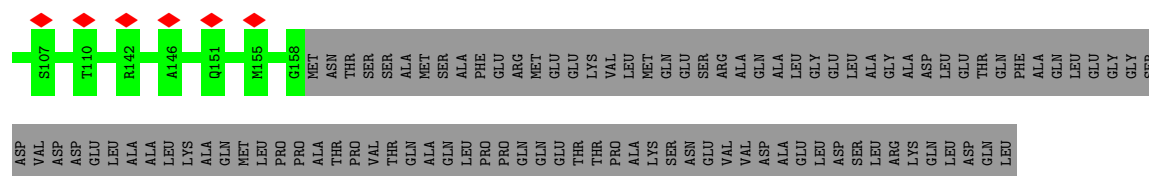
M1 K21 A22 A78 L79 Q80 K81 G82 V156 R157 G158 E179 L188 A189 G190 A191 D192 L193 E201 Q202 Q203 S204 D205 V206 D207 D208 E209 L210 A211 A212 L213 L214 K214 A215 Q216 M217 L218 PRO PRO ALA THR PRO VAL THR GLN GLN LEU PRO PRO GLN GLN THR

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

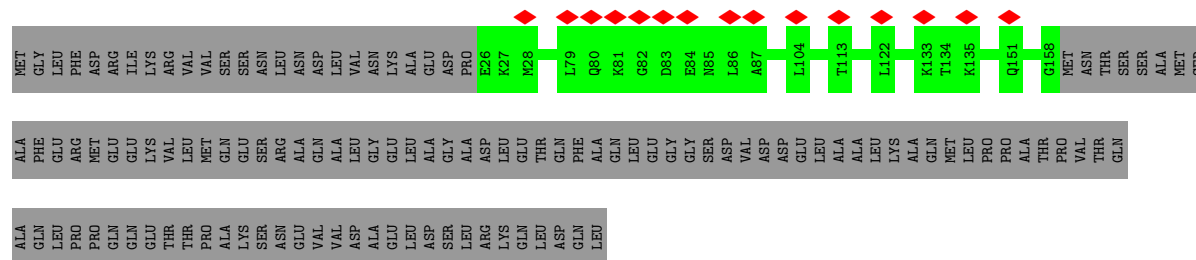
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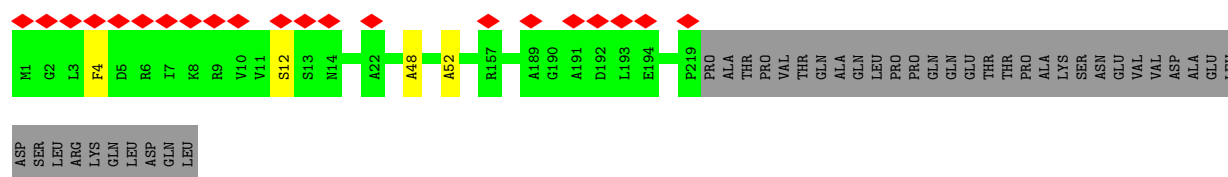
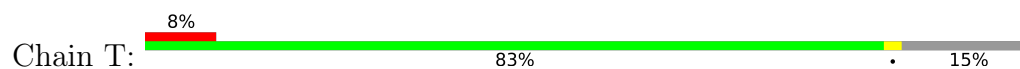
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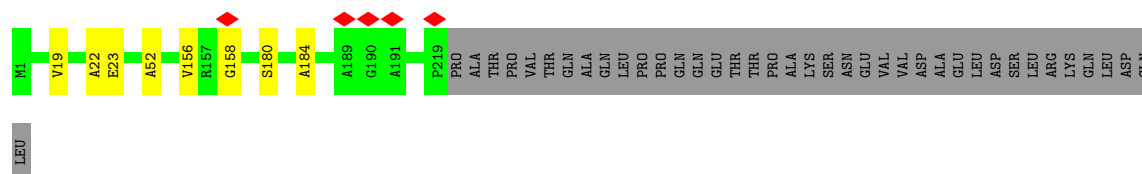
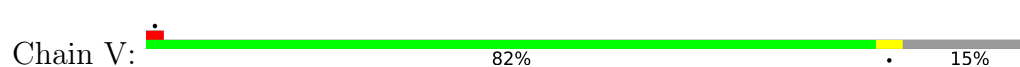
- Molecule 1: vipp1



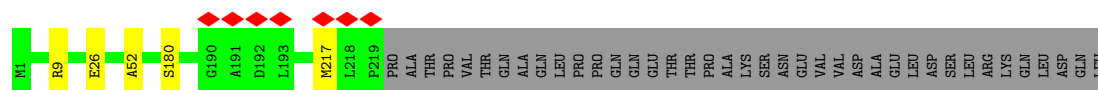
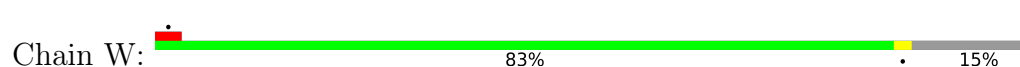
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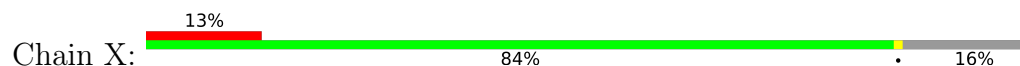
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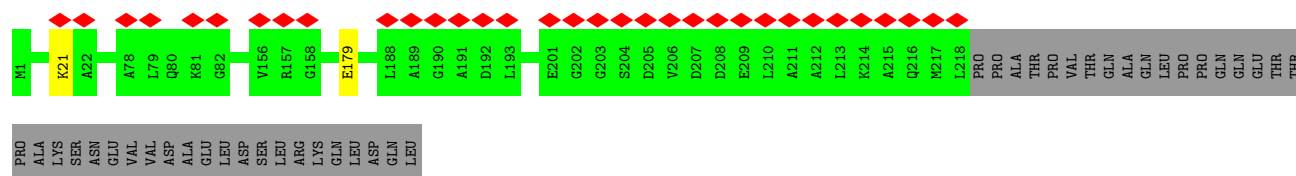


- Molecule 1: vipp1

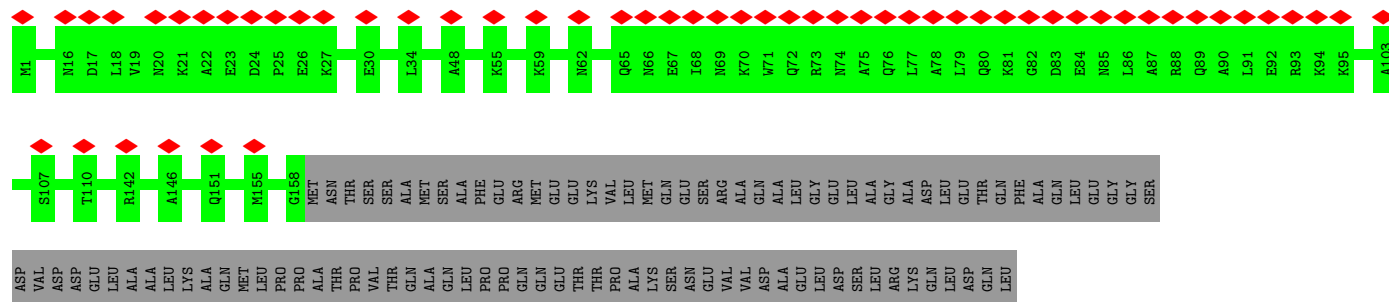


- Molecule 1: vipp1

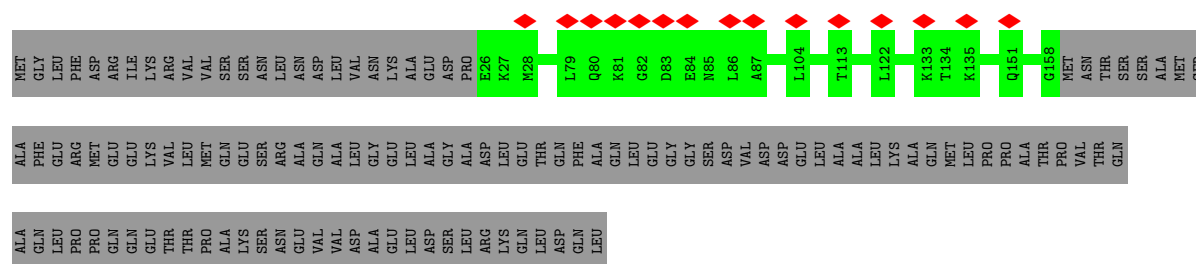




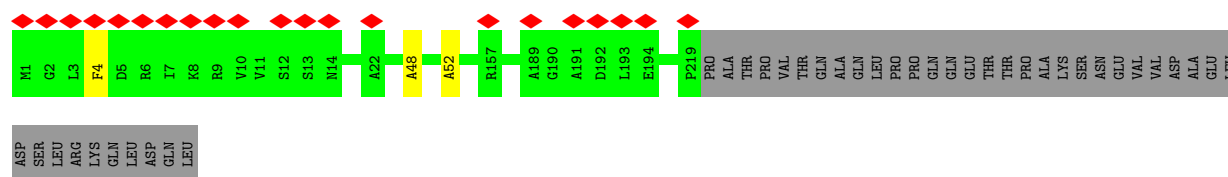
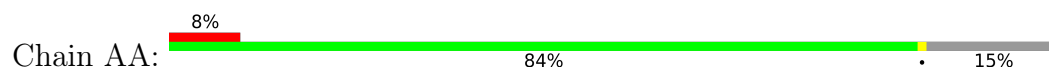
• Molecule 1: vippl



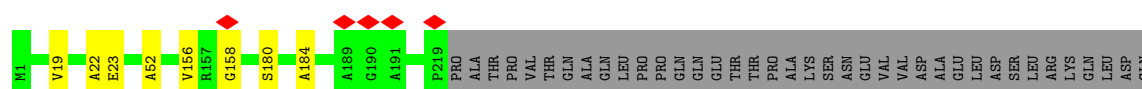
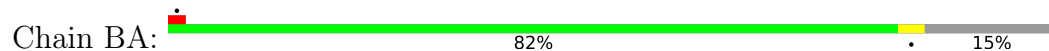
• Molecule 1: vippl



• Molecule 1: vippl



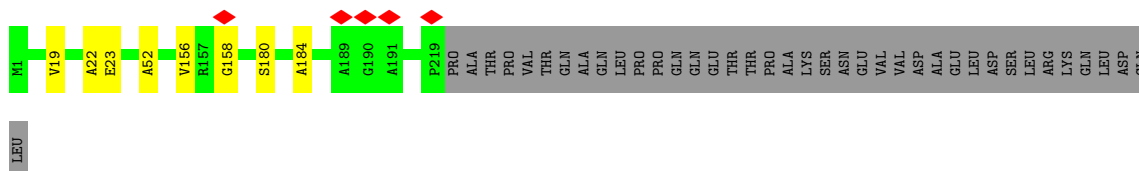
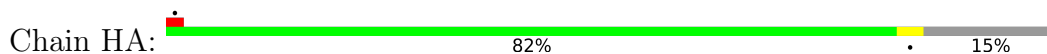
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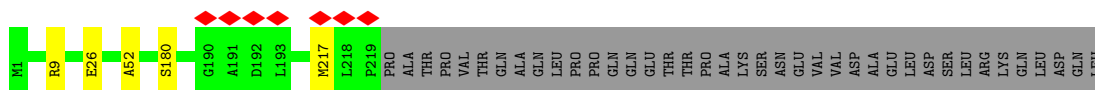
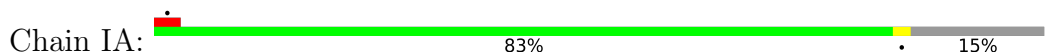
Chain GA: 



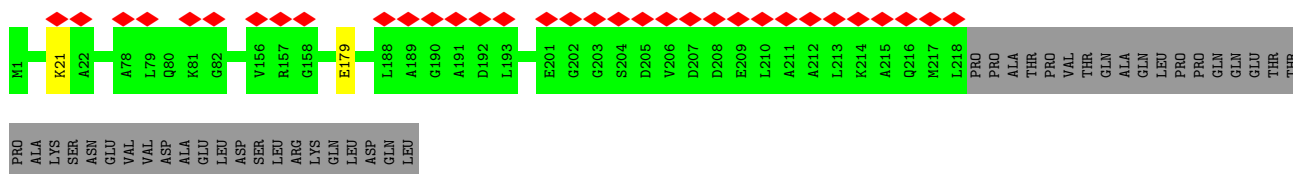
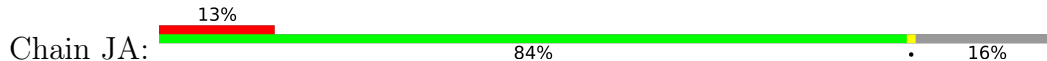
- Molecule 1: vipp1



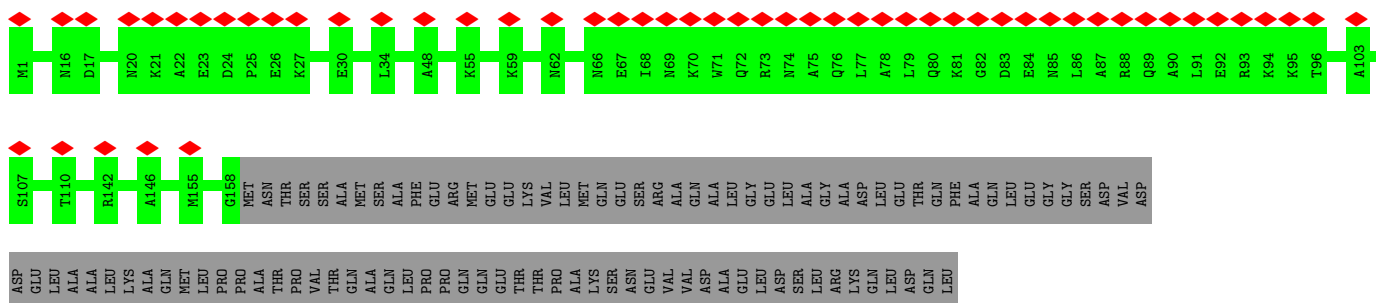
- Molecule 1: vipp1



- Molecule 1: vipp1

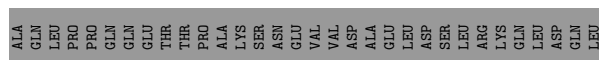
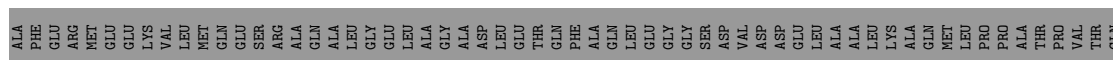
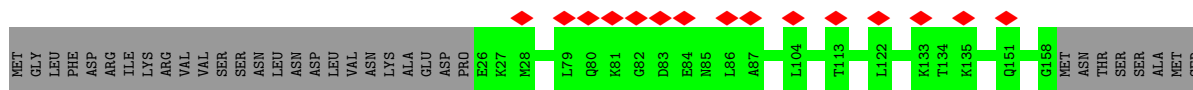


- Molecule 1: vipp1

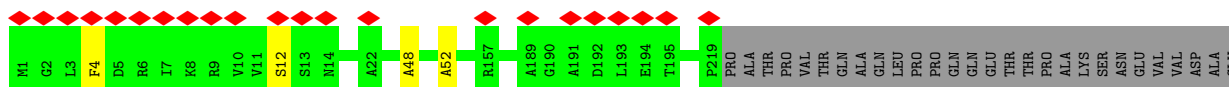
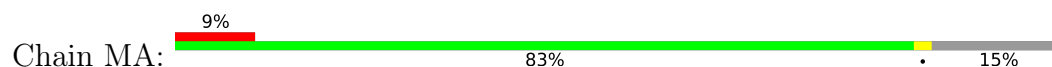


- Molecule 1: vipp1

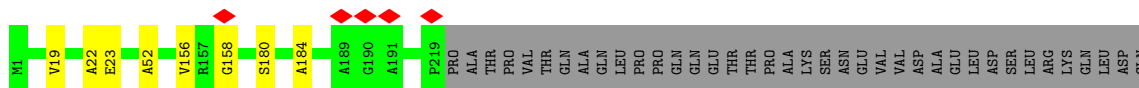
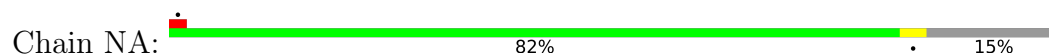




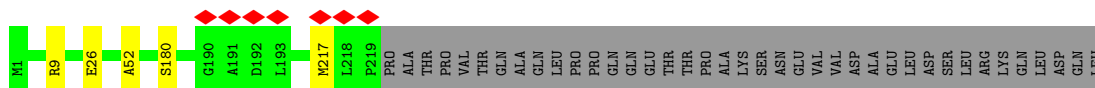
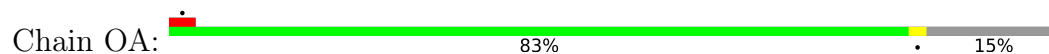
- Molecule 1: vipp1



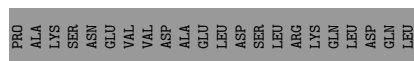
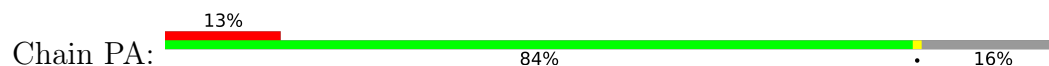
- Molecule 1: vipp1



- Molecule 1: vipp1

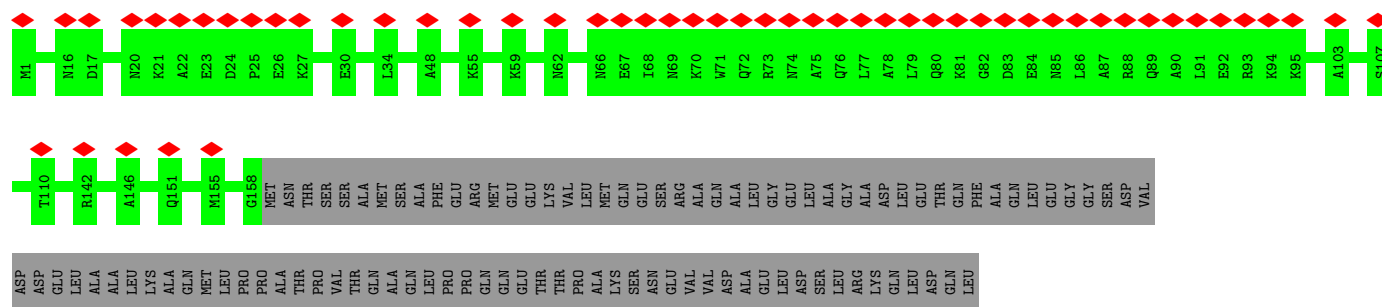


- Molecule 1: vipp1

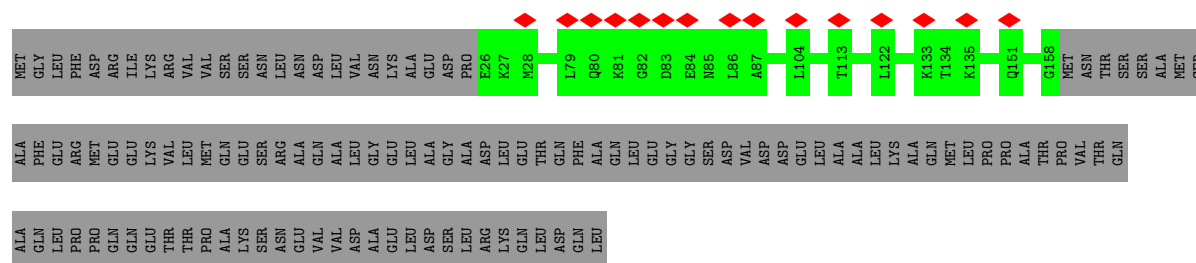


- Molecule 1: vipp1

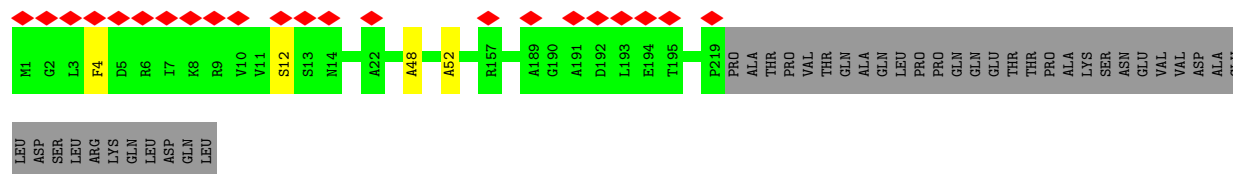
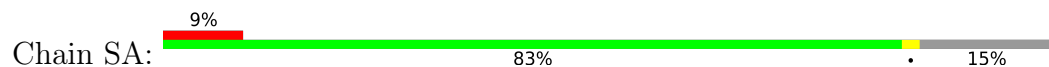




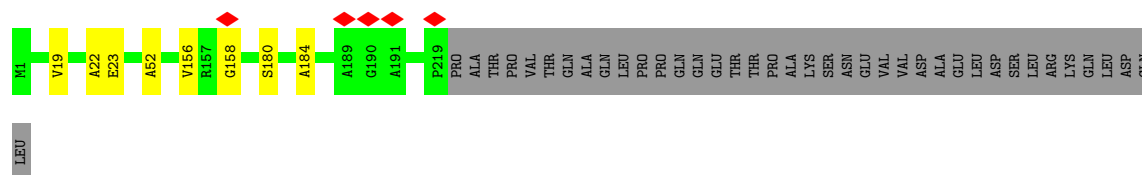
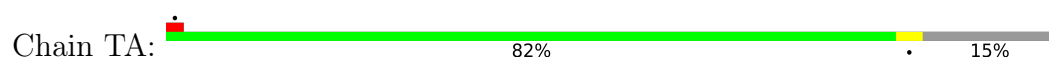
- Molecule 1: vippp1



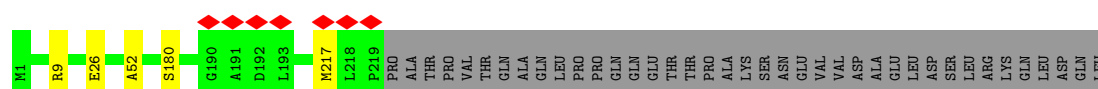
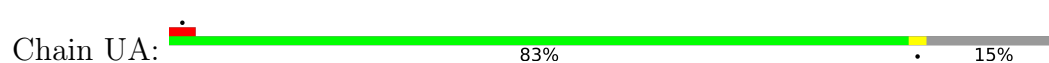
- Molecule 1: vippp1



- Molecule 1: vippp1



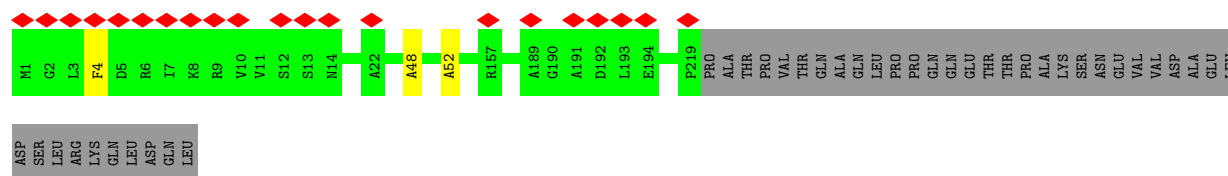
- Molecule 1: vippp1



Chain ZA: 82% 15%

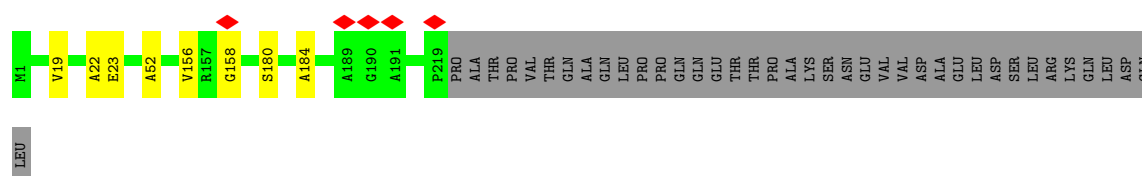
• Molecule 1: vipp1

Chain EB:  8% 84% 15%



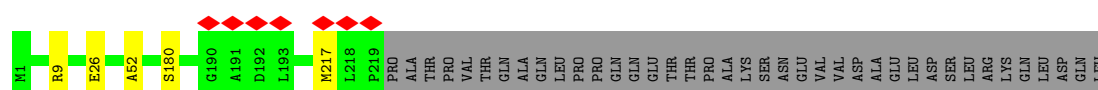
• Molecule 1: vipp1

Chain FB:  82% 15%



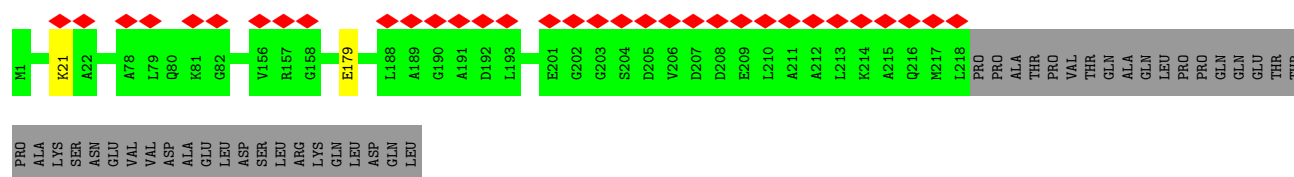
• Molecule 1: vipp1

Chain GB:  83% 15%



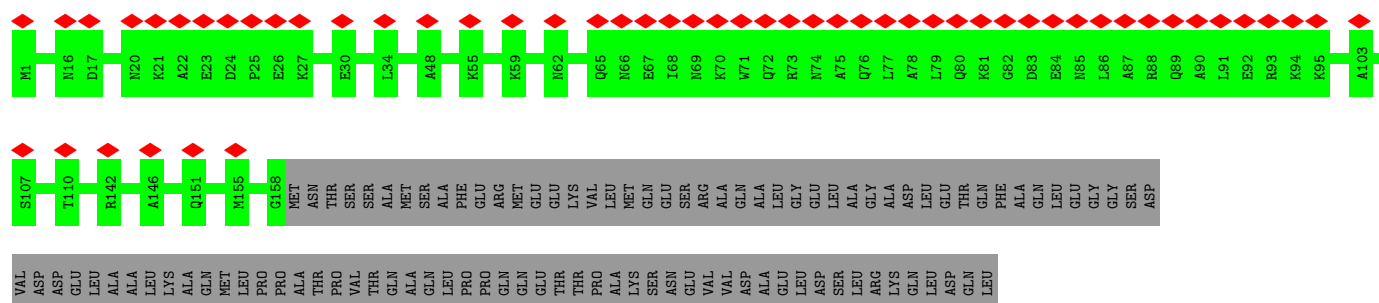
• Molecule 1: vipp1

Chain HB:  13% 84% 16%



• Molecule 1: vipp1

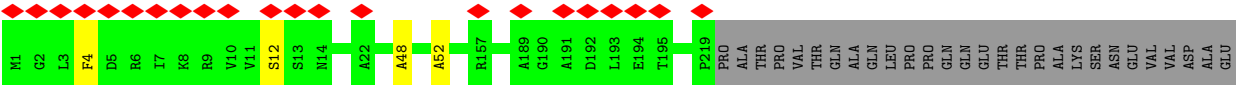
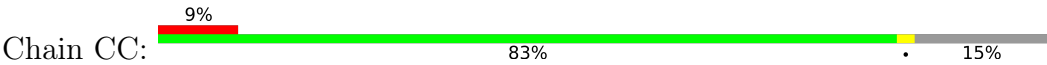
Chain IB:  21% 61% 39%



ALA	PHE	GLU	ARG	MET	GLU	GLU	VAL	LEU	MET	GLN	GLU	SER	ARG	LEU	ASN	ASP	GLN	ALA	LEU	GLY	GLU	ASP	ASP	ASP	VAL	ASP	ASP	GLU	LEU	ALA	LEU	LYS	ALA	GLN	THR	THR	GLN	PHE	ALA	GLN	LEU	GLU	GLY	SER	ASP	VAL	ASP	ASP	ASP	GLU	LEU	ALA	LEU	LYS	ALA	GLN	LEU	MET	LEU	PRO	PRO	ALA	THR	THR	VAL	THR	THR	GLN
MET	GLY	LEU	PHE	ASP	ARG	ILE	ARG	VAL	VAL	SER	SER	ASN	LEU	ASN	ASP	ASP	LEU	VAL	ASN	LYS	GLU	ASP	PRO	E26	M28	L79	Q90	K91	G92	D93	E94	N95	L86	A97	L104	T113	L122	K133	T134	K135	Q151	G158	MET	ASN	THR	SER	SER	SER	ALA	MET																		

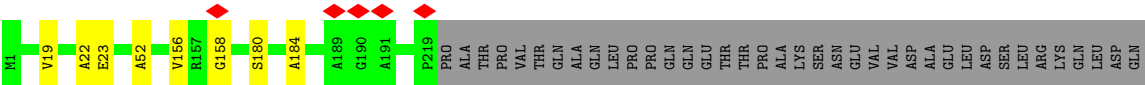
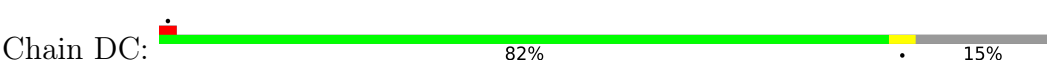
ALA
GLN
LEU
PRO
PRO
GLN
GLN
GLU
THR
THR
PRO
PRO
ALA
LYS
SER
ASN
GLU
VAL
VAL
ASP
ASP
ALA
GLU
LEU
LEU
ASP
SER
SER
LEU
ARG
LYS
GLN
LEU
LEU
ASP
GLN
LEU

• Molecule 1: vippl



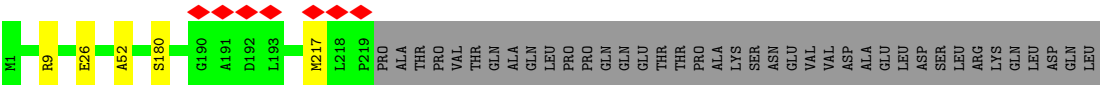
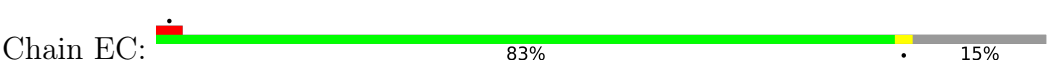
LEU
ASP
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: vippl

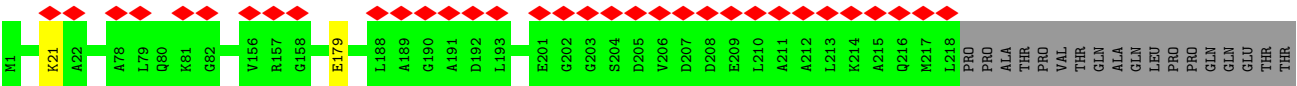
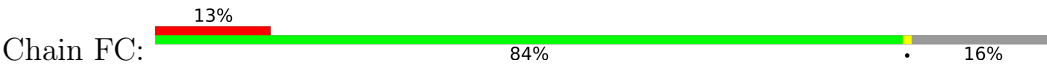


LEU

• Molecule 1: vippl

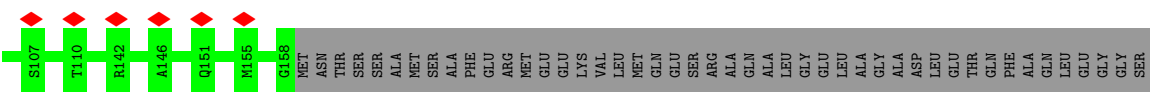
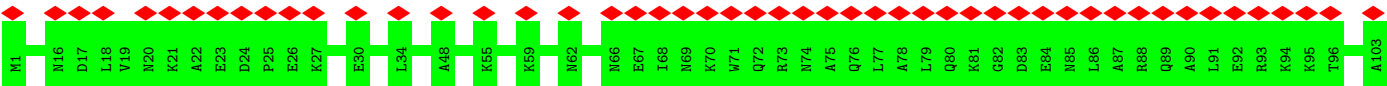


• Molecule 1: vippl



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

• Molecule 1: vippl



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

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17114	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	0.058	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0153	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	0.35	0/660	0.93	0/920
1	AA	0.67	0/1085	1.39	2/1512 (0.1%)
1	AB	0.36	0/1085	0.89	2/1512 (0.1%)
1	AC	0.34	0/784	0.92	0/1093
1	B	0.67	0/1085	1.39	3/1512 (0.2%)
1	BA	0.37	0/1085	0.98	4/1512 (0.3%)
1	BB	0.36	0/1080	0.97	1/1505 (0.1%)
1	BC	0.35	0/660	0.93	0/920
1	C	0.37	0/1085	0.98	4/1512 (0.3%)
1	CA	0.36	0/1085	0.89	2/1512 (0.1%)
1	CB	0.34	0/784	0.92	0/1093
1	CC	0.67	0/1085	1.39	3/1512 (0.2%)
1	D	0.36	0/1085	0.89	2/1512 (0.1%)
1	DA	0.36	0/1080	0.96	1/1505 (0.1%)
1	DB	0.35	0/660	0.93	0/920
1	DC	0.37	0/1085	0.98	4/1512 (0.3%)
1	E	0.36	0/1080	0.97	1/1505 (0.1%)
1	EA	0.34	0/784	0.92	0/1093
1	EB	0.67	0/1085	1.39	2/1512 (0.1%)
1	EC	0.36	0/1085	0.89	2/1512 (0.1%)
1	F	0.34	0/784	0.92	0/1093
1	FA	0.35	0/660	0.93	0/920
1	FB	0.37	0/1085	0.98	4/1512 (0.3%)
1	FC	0.36	0/1080	0.97	1/1505 (0.1%)
1	G	0.35	0/660	0.93	0/920
1	GA	0.67	0/1085	1.39	3/1512 (0.2%)
1	GB	0.36	0/1085	0.89	2/1512 (0.1%)
1	GC	0.34	0/784	0.92	0/1093
1	H	0.67	0/1085	1.39	3/1512 (0.2%)
1	HA	0.37	0/1085	0.98	4/1512 (0.3%)
1	HB	0.36	0/1080	0.97	1/1505 (0.1%)
1	I	0.37	0/1085	0.98	4/1512 (0.3%)
1	IA	0.36	0/1085	0.89	2/1512 (0.1%)
1	IB	0.34	0/784	0.92	0/1093

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	J	0.36	0/1085	0.89	2/1512 (0.1%)
1	JA	0.36	0/1080	0.96	1/1505 (0.1%)
1	JB	0.35	0/660	0.93	0/920
1	K	0.36	0/1080	0.97	1/1505 (0.1%)
1	KA	0.34	0/784	0.92	0/1093
1	KB	0.67	0/1085	1.39	3/1512 (0.2%)
1	L	0.34	0/784	0.92	0/1093
1	LA	0.35	0/660	0.93	0/920
1	LB	0.37	0/1085	0.98	4/1512 (0.3%)
1	M	0.35	0/660	0.93	0/920
1	MA	0.67	0/1085	1.39	3/1512 (0.2%)
1	MB	0.36	0/1085	0.89	2/1512 (0.1%)
1	N	0.67	0/1085	1.39	3/1512 (0.2%)
1	NA	0.37	0/1085	0.98	4/1512 (0.3%)
1	NB	0.36	0/1080	0.96	1/1505 (0.1%)
1	O	0.37	0/1085	0.98	4/1512 (0.3%)
1	OA	0.36	0/1085	0.89	2/1512 (0.1%)
1	OB	0.34	0/784	0.92	0/1093
1	P	0.36	0/1085	0.89	2/1512 (0.1%)
1	PA	0.36	0/1080	0.97	1/1505 (0.1%)
1	PB	0.35	0/660	0.93	0/920
1	Q	0.36	0/1080	0.97	1/1505 (0.1%)
1	QA	0.34	0/784	0.92	0/1093
1	QB	0.67	0/1085	1.39	2/1512 (0.1%)
1	R	0.34	0/784	0.92	0/1093
1	RA	0.35	0/660	0.93	0/920
1	RB	0.37	0/1085	0.98	4/1512 (0.3%)
1	S	0.35	0/660	0.93	0/920
1	SA	0.67	0/1085	1.39	3/1512 (0.2%)
1	SB	0.36	0/1085	0.89	2/1512 (0.1%)
1	T	0.67	0/1085	1.39	3/1512 (0.2%)
1	TA	0.37	0/1085	0.98	4/1512 (0.3%)
1	TB	0.36	0/1080	0.96	1/1505 (0.1%)
1	UA	0.36	0/1085	0.89	2/1512 (0.1%)
1	UB	0.34	0/784	0.92	0/1093
1	V	0.37	0/1085	0.98	4/1512 (0.3%)
1	VA	0.36	0/1080	0.97	1/1505 (0.1%)
1	VB	0.35	0/660	0.93	0/920
1	W	0.36	0/1085	0.89	2/1512 (0.1%)
1	WA	0.34	0/784	0.92	0/1093
1	WB	0.67	0/1085	1.39	3/1512 (0.2%)
1	X	0.36	0/1080	0.97	1/1505 (0.1%)
1	XA	0.35	0/660	0.93	0/920

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	XB	0.37	0/1085	0.98	4/1512 (0.3%)
1	Y	0.34	0/784	0.92	0/1093
1	YA	0.67	0/1085	1.39	3/1512 (0.2%)
1	YB	0.36	0/1085	0.89	2/1512 (0.1%)
1	Z	0.35	0/660	0.93	0/920
1	ZA	0.37	0/1085	0.98	4/1512 (0.3%)
1	ZB	0.36	0/1080	0.96	1/1505 (0.1%)
All	All	0.43	0/80906	1.04	137/112756 (0.1%)

There are no bond length outliers.

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	21	LYS	N-CA-C	6.35	118.29	111.36
1	K	21	LYS	N-CA-C	6.35	118.28	111.36
1	PA	21	LYS	N-CA-C	6.33	118.26	111.36
1	BB	21	LYS	N-CA-C	6.33	118.26	111.36
1	DA	21	LYS	N-CA-C	6.33	118.26	111.36

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	A	661	0	320	0	0
1	AA	1086	0	531	2	0
1	AB	1086	0	531	7	0
1	AC	785	0	376	0	0
1	B	1086	0	531	2	0
1	BA	1086	0	531	7	0
1	BB	1081	0	530	2	0
1	BC	661	0	320	0	0
1	C	1086	0	531	7	0
1	CA	1086	0	531	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CB	785	0	376	0	0
1	CC	1086	0	531	2	0
1	D	1086	0	531	7	0
1	DA	1081	0	530	2	0
1	DB	661	0	320	0	0
1	DC	1086	0	531	7	0
1	E	1081	0	530	2	0
1	EA	785	0	376	0	0
1	EB	1086	0	531	2	0
1	EC	1086	0	531	7	0
1	F	785	0	376	0	0
1	FA	661	0	320	0	0
1	FB	1086	0	531	7	0
1	FC	1081	0	530	2	0
1	G	661	0	320	0	0
1	GA	1086	0	531	2	0
1	GB	1086	0	531	7	0
1	GC	785	0	376	0	0
1	H	1086	0	531	2	0
1	HA	1086	0	531	7	0
1	HB	1081	0	530	2	0
1	I	1086	0	531	7	0
1	IA	1086	0	531	7	0
1	IB	785	0	376	0	0
1	J	1086	0	531	7	0
1	JA	1081	0	530	2	0
1	JB	661	0	320	0	0
1	K	1081	0	530	2	0
1	KA	785	0	376	0	0
1	KB	1086	0	531	2	0
1	L	785	0	376	0	0
1	LA	661	0	320	0	0
1	LB	1086	0	531	7	0
1	M	661	0	320	0	0
1	MA	1086	0	531	2	0
1	MB	1086	0	531	7	0
1	N	1086	0	531	2	0
1	NA	1086	0	531	7	0
1	NB	1081	0	530	2	0
1	O	1086	0	531	7	0
1	OA	1086	0	531	7	0
1	OB	785	0	376	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1086	0	531	7	0
1	PA	1081	0	530	2	0
1	PB	661	0	320	0	0
1	Q	1081	0	530	2	0
1	QA	785	0	376	0	0
1	QB	1086	0	531	2	0
1	R	785	0	376	0	0
1	RA	661	0	320	0	0
1	RB	1086	0	531	7	0
1	S	661	0	320	0	0
1	SA	1086	0	531	2	0
1	SB	1086	0	531	7	0
1	T	1086	0	531	2	0
1	TA	1086	0	531	7	0
1	TB	1081	0	530	2	0
1	UA	1086	0	531	7	0
1	UB	785	0	376	0	0
1	V	1086	0	531	7	0
1	VA	1081	0	530	2	0
1	VB	661	0	320	0	0
1	W	1086	0	531	7	0
1	WA	785	0	376	0	0
1	WB	1086	0	531	2	0
1	X	1081	0	530	2	0
1	XA	661	0	320	0	0
1	XB	1086	0	531	7	0
1	Y	785	0	376	0	0
1	YA	1086	0	531	2	0
1	YB	1086	0	531	7	0
1	Z	661	0	320	0	0
1	ZA	1086	0	531	7	0
1	ZB	1081	0	530	2	0
All	All	80990	0	39466	126	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 126 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:I:22:ALA:HB1	1:J:9:ARG:CB	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:22:ALA:HB1	1:P:9:ARG:CB	2.12	0.80
1:DC:22:ALA:HB1	1:EC:9:ARG:CB	2.12	0.80
1:LB:22:ALA:HB1	1:MB:9:ARG:CB	2.12	0.80
1:RB:22:ALA:HB1	1:SB:9:ARG:CB	2.12	0.80

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%)	213 (98%)	4 (2%)	0	100	100
1	AB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	AC	156/258 (60%)	156 (100%)	0	0	100	100
1	B	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	BA	217/258 (84%)	217 (100%)	0	0	100	100
1	BB	216/258 (84%)	216 (100%)	0	0	100	100
1	BC	131/258 (51%)	131 (100%)	0	0	100	100
1	C	217/258 (84%)	217 (100%)	0	0	100	100
1	CA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CB	156/258 (60%)	156 (100%)	0	0	100	100
1	CC	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	D	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	DA	216/258 (84%)	216 (100%)	0	0	100	100
1	DB	131/258 (51%)	131 (100%)	0	0	100	100
1	DC	217/258 (84%)	217 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	216/258 (84%)	216 (100%)	0	0	100	100
1	EA	156/258 (60%)	156 (100%)	0	0	100	100
1	EB	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	EC	217/258 (84%)	216 (100%)	1 (0%)	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%)	217 (100%)	0	0	100	100
1	FC	216/258 (84%)	216 (100%)	0	0	100	100
1	G	131/258 (51%)	131 (100%)	0	0	100	100
1	GA	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	GB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	GC	156/258 (60%)	156 (100%)	0	0	100	100
1	H	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	HA	217/258 (84%)	217 (100%)	0	0	100	100
1	HB	216/258 (84%)	216 (100%)	0	0	100	100
1	I	217/258 (84%)	217 (100%)	0	0	100	100
1	IA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	IB	156/258 (60%)	156 (100%)	0	0	100	100
1	J	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	JA	216/258 (84%)	216 (100%)	0	0	100	100
1	JB	131/258 (51%)	131 (100%)	0	0	100	100
1	K	216/258 (84%)	216 (100%)	0	0	100	100
1	KA	156/258 (60%)	156 (100%)	0	0	100	100
1	KB	217/258 (84%)	213 (98%)	4 (2%)	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%)	217 (100%)	0	0	100	100
1	M	131/258 (51%)	131 (100%)	0	0	100	100
1	MA	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	MB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	N	217/258 (84%)	213 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	NA	217/258 (84%)	217 (100%)	0	0	100	100
1	NB	216/258 (84%)	216 (100%)	0	0	100	100
1	O	217/258 (84%)	217 (100%)	0	0	100	100
1	OA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	OB	156/258 (60%)	156 (100%)	0	0	100	100
1	P	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	PA	216/258 (84%)	216 (100%)	0	0	100	100
1	PB	131/258 (51%)	131 (100%)	0	0	100	100
1	Q	216/258 (84%)	216 (100%)	0	0	100	100
1	QA	156/258 (60%)	156 (100%)	0	0	100	100
1	QB	217/258 (84%)	213 (98%)	4 (2%)	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%)	217 (100%)	0	0	100	100
1	S	131/258 (51%)	131 (100%)	0	0	100	100
1	SA	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	SB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	T	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	TA	217/258 (84%)	217 (100%)	0	0	100	100
1	TB	216/258 (84%)	216 (100%)	0	0	100	100
1	UA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	UB	156/258 (60%)	156 (100%)	0	0	100	100
1	V	217/258 (84%)	217 (100%)	0	0	100	100
1	VA	216/258 (84%)	216 (100%)	0	0	100	100
1	VB	131/258 (51%)	131 (100%)	0	0	100	100
1	W	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	WA	156/258 (60%)	156 (100%)	0	0	100	100
1	WB	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	X	216/258 (84%)	216 (100%)	0	0	100	100
1	XA	131/258 (51%)	131 (100%)	0	0	100	100
1	XB	217/258 (84%)	217 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	156/258 (60%)	156 (100%)	0	0	100	100
1	YA	217/258 (84%)	213 (98%)	4 (2%)	0	100	100
1	YB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	Z	131/258 (51%)	131 (100%)	0	0	100	100
1	ZA	217/258 (84%)	217 (100%)	0	0	100	100
1	ZB	216/258 (84%)	216 (100%)	0	0	100	100
All	All	16156/21672 (74%)	16086 (100%)	70 (0%)	0	100	100

There are no Ramachandran outliers to report.

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 ⓘ

There are no chain breaks in this entry.

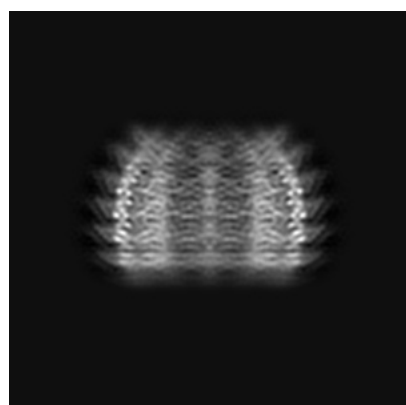
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11478. These allow visual inspection of the internal detail of the map and identification of artifacts.

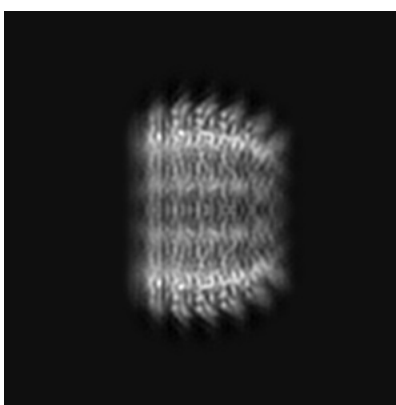
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

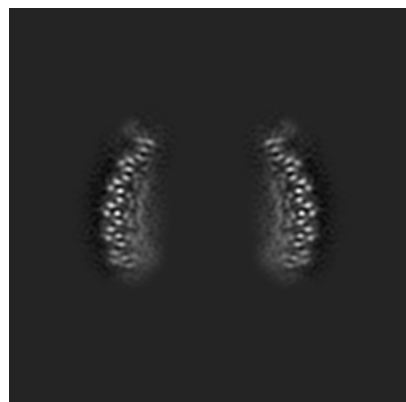


Z

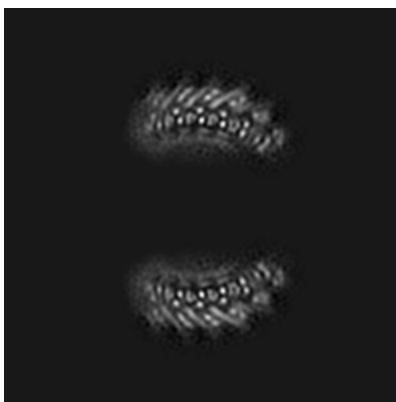
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 168



Y Index: 168



Z Index: 168

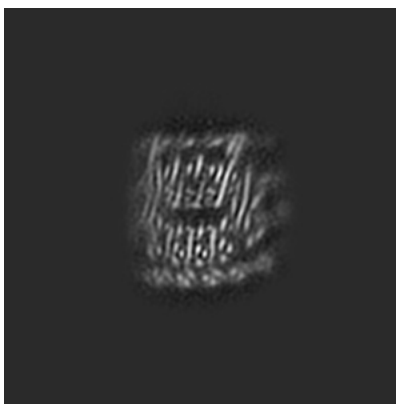
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

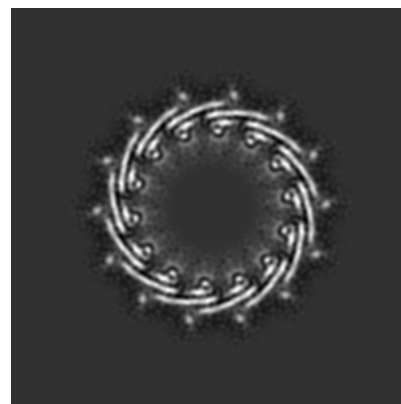
6.3.1 Primary map



X Index: 232



Y Index: 237

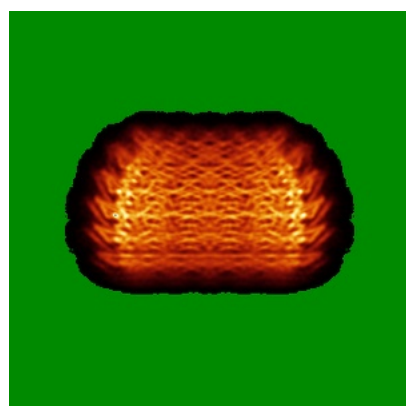


Z Index: 164

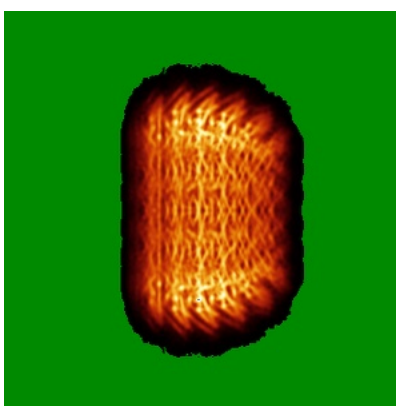
The images above show the largest variance slices of the map in three orthogonal directions.

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

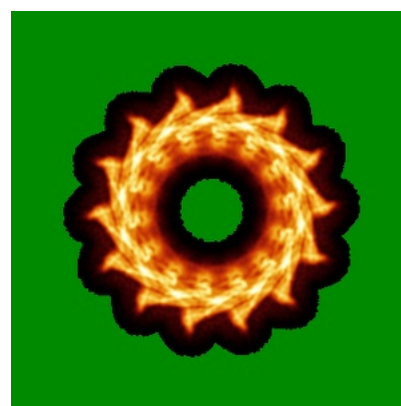
6.4.1 Primary map



X



Y

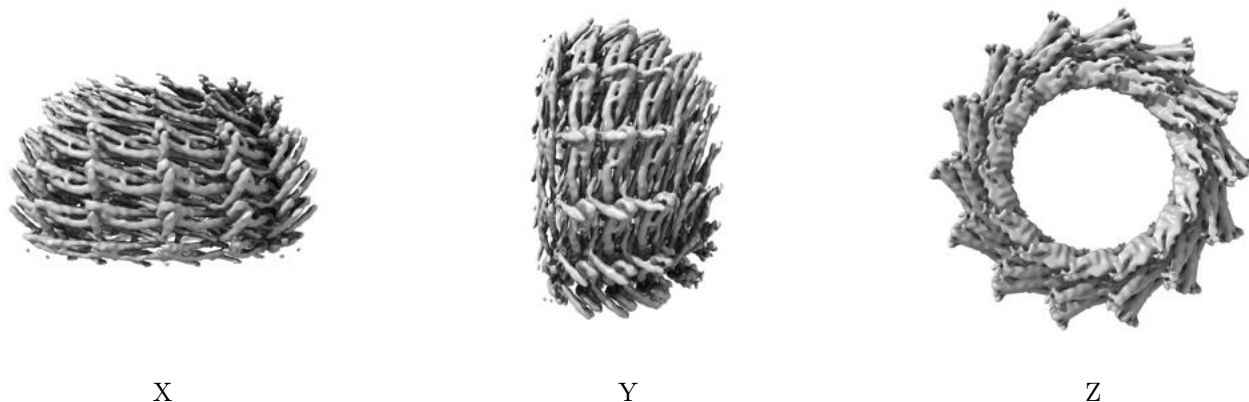


Z

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 0.0153. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

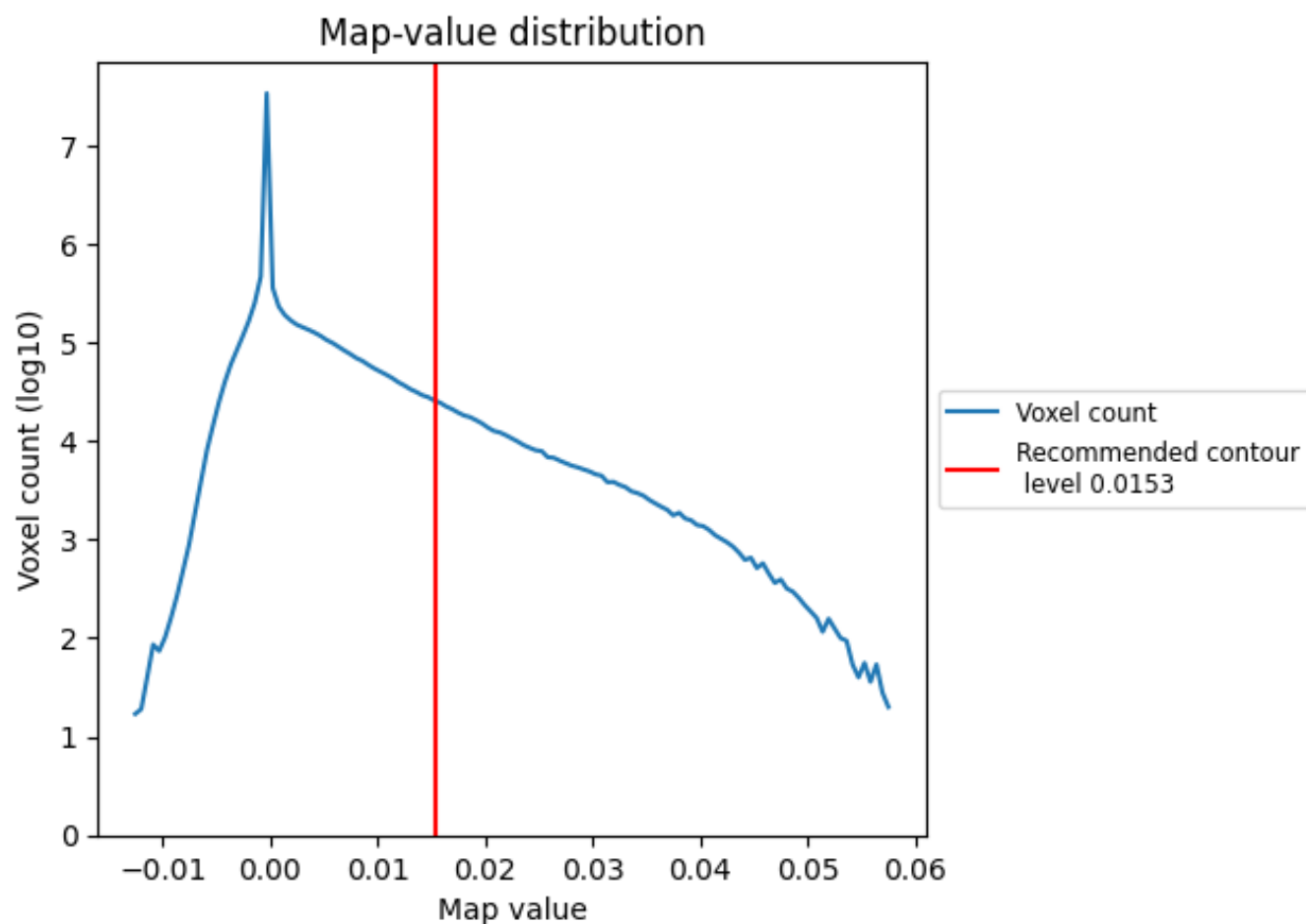
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

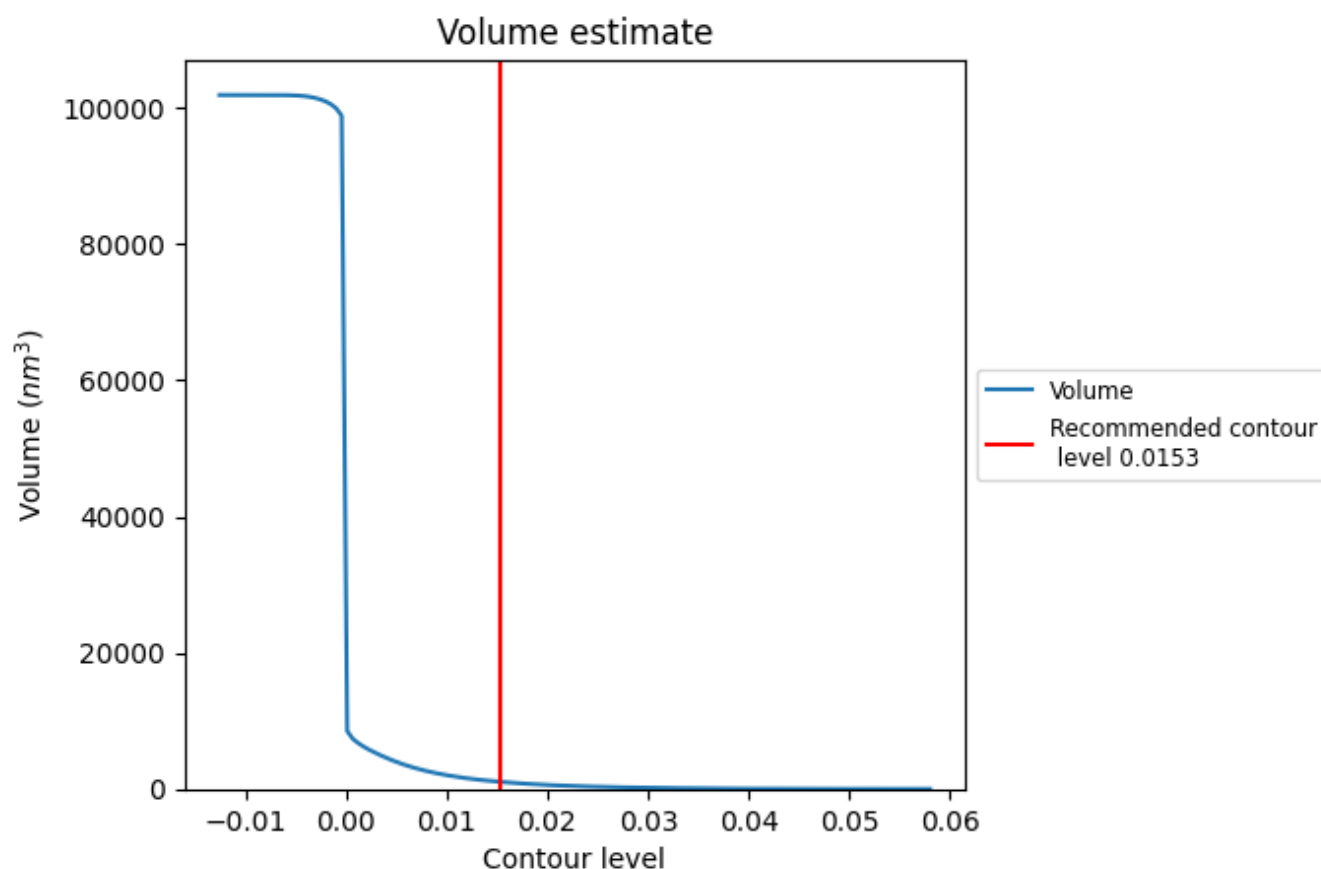
This section contains the results of statistical analysis of the map.

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.

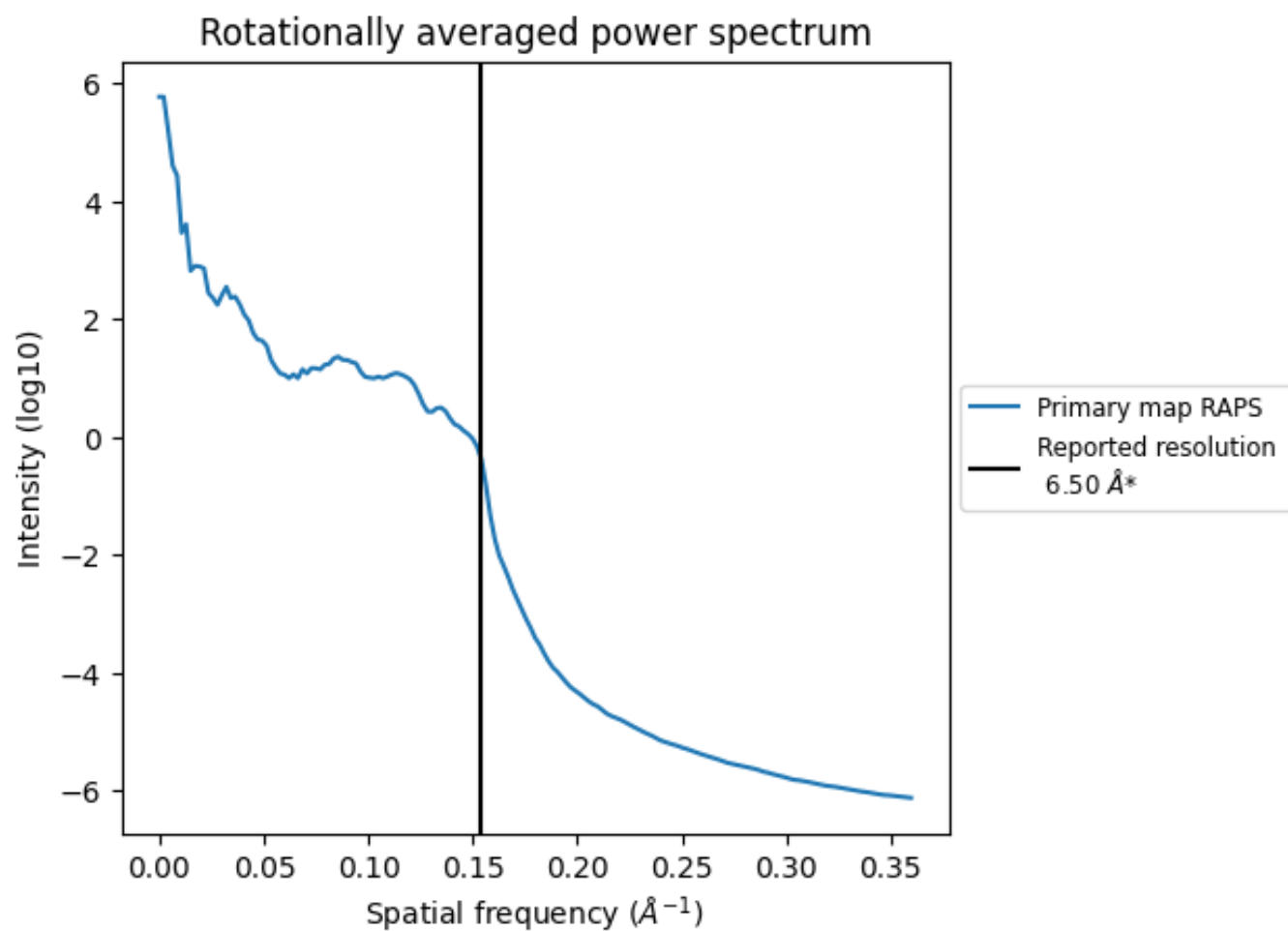
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1051 nm³; this corresponds to an approximate mass of 949 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 0.154 Å⁻¹

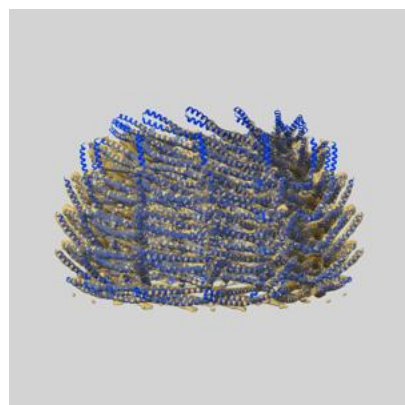
8 Fourier-Shell correlation

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

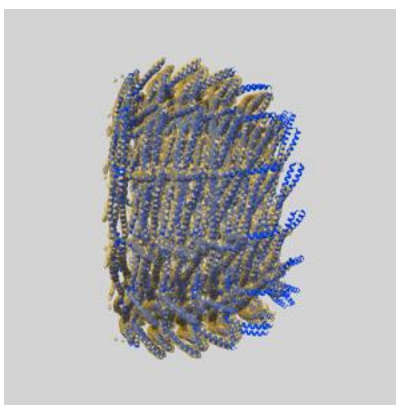
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11478 and PDB model 6ZW4. Per-residue inclusion information can be found in section 3 on page 12.

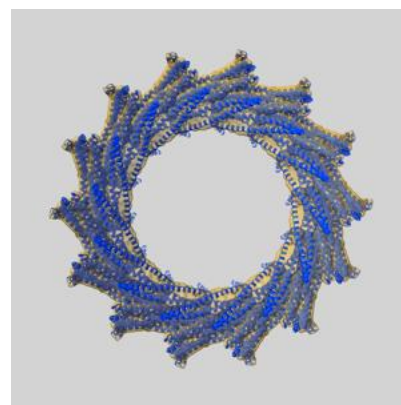
9.1 Map-model overlay [i](#)



X



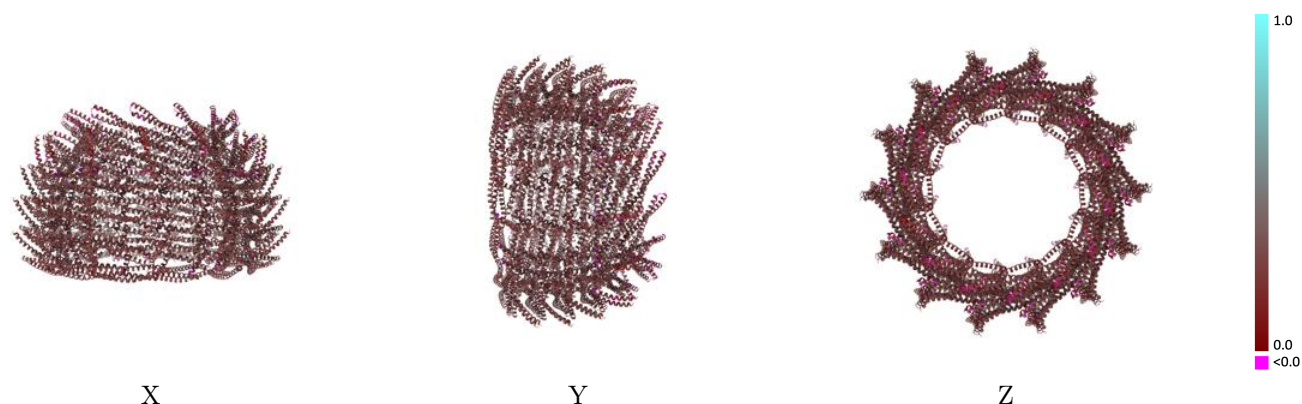
Y



Z

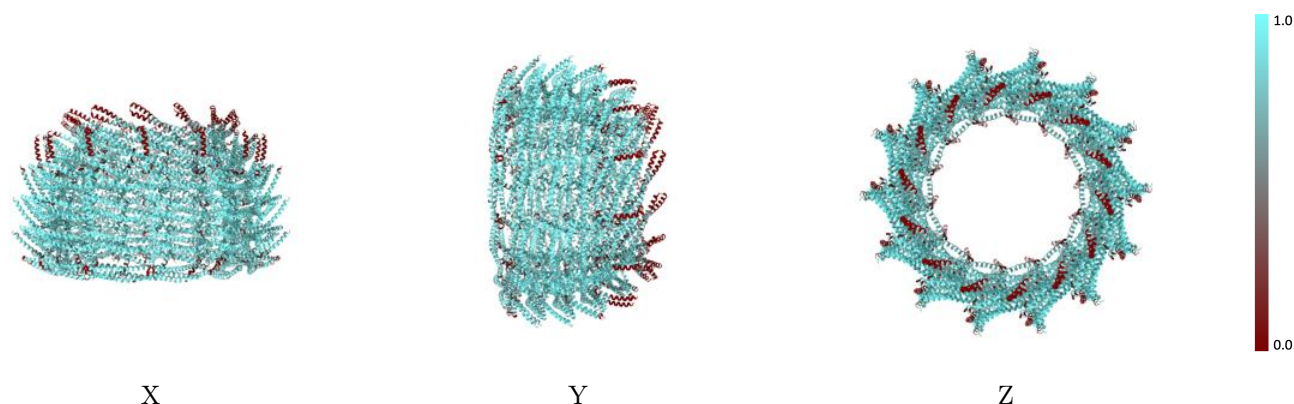
The images above show the 3D surface view of the map at the recommended contour level 0.0153 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



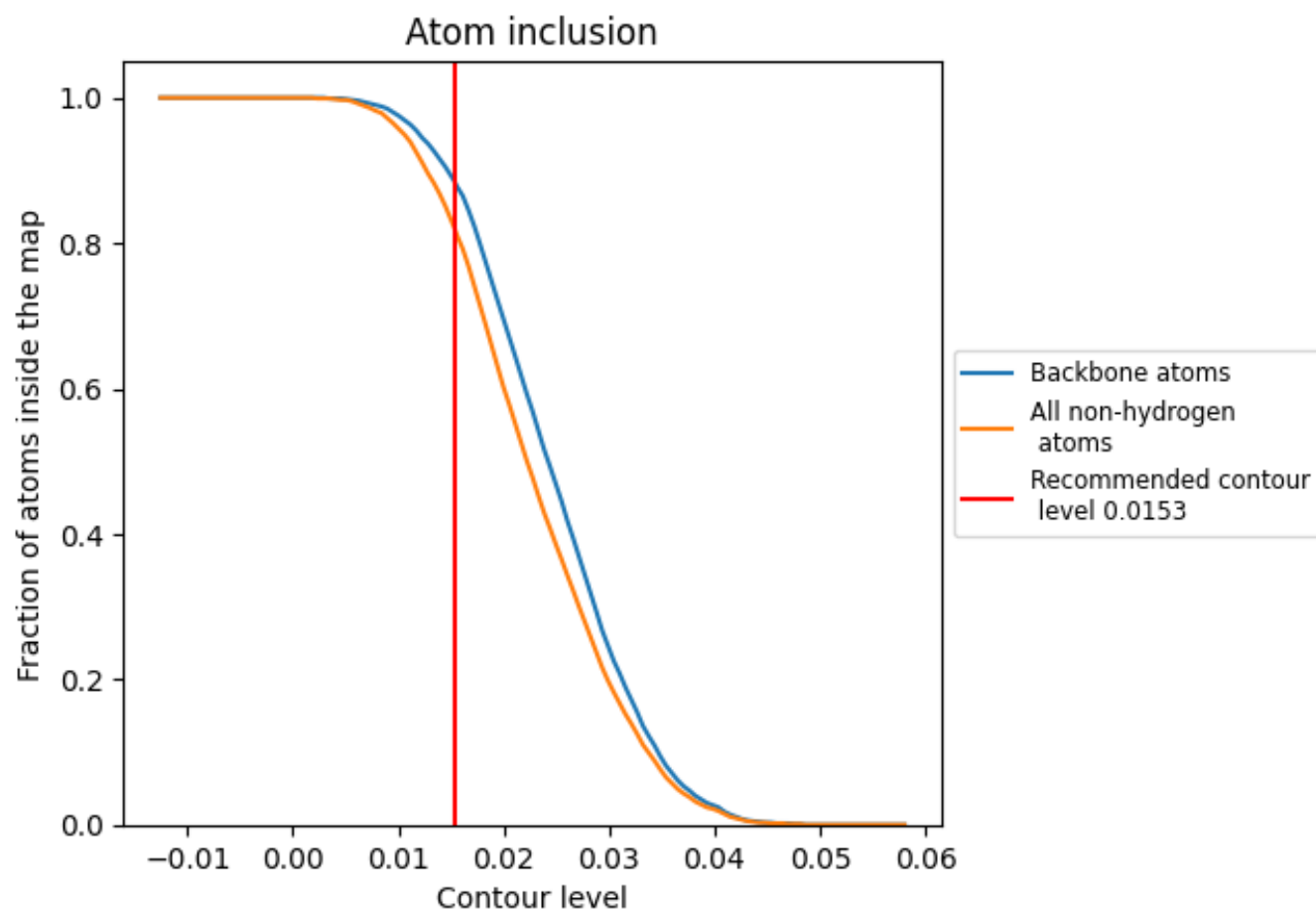
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0153).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% 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 (0.0153) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8220	 0.2600
A	 0.7900	 0.2640
AA	 0.8470	 0.2640
AB	 0.9160	 0.2680
AC	 0.6000	 0.2390
B	 0.8470	 0.2660
BA	 0.9280	 0.2680
BB	 0.7830	 0.2500
BC	 0.7880	 0.2670
C	 0.9280	 0.2670
CA	 0.9130	 0.2670
CB	 0.6010	 0.2400
CC	 0.8440	 0.2660
D	 0.9130	 0.2660
DA	 0.7790	 0.2520
DB	 0.7850	 0.2660
DC	 0.9270	 0.2680
E	 0.7810	 0.2480
EA	 0.6000	 0.2380
EB	 0.8500	 0.2670
EC	 0.9120	 0.2660
F	 0.6000	 0.2370
FA	 0.7850	 0.2650
FB	 0.9280	 0.2670
FC	 0.7820	 0.2500
G	 0.7900	 0.2640
GA	 0.8480	 0.2640
GB	 0.9160	 0.2670
GC	 0.5980	 0.2380
H	 0.8520	 0.2660
HA	 0.9290	 0.2660
HB	 0.7840	 0.2540
I	 0.9290	 0.2690
IA	 0.9150	 0.2660
IB	 0.6000	 0.2420



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Chain	Atom inclusion	Q-score
J	 0.9130	 0.2690
JA	 0.7790	 0.2490
JB	 0.7870	 0.2660
K	 0.7820	 0.2530
KA	 0.6000	 0.2390
KB	 0.8520	 0.2660
L	 0.6030	 0.2400
LA	 0.7880	 0.2670
LB	 0.9290	 0.2670
M	 0.7880	 0.2620
MA	 0.8440	 0.2680
MB	 0.9140	 0.2670
N	 0.8490	 0.2650
NA	 0.9270	 0.2690
NB	 0.7800	 0.2510
O	 0.9280	 0.2660
OA	 0.9120	 0.2670
OB	 0.5950	 0.2390
P	 0.9150	 0.2650
PA	 0.7800	 0.2500
PB	 0.7870	 0.2620
Q	 0.7830	 0.2490
QA	 0.6000	 0.2390
QB	 0.8490	 0.2650
R	 0.5980	 0.2380
RA	 0.7900	 0.2670
RB	 0.9300	 0.2650
S	 0.7850	 0.2640
SA	 0.8470	 0.2660
SB	 0.9140	 0.2640
T	 0.8510	 0.2650
TA	 0.9280	 0.2680
TB	 0.7810	 0.2490
UA	 0.9130	 0.2680
UB	 0.5960	 0.2390
V	 0.9300	 0.2670
VA	 0.7820	 0.2520
VB	 0.7870	 0.2630
W	 0.9160	 0.2650
WA	 0.6000	 0.2410
WB	 0.8470	 0.2650
X	 0.7790	 0.2500

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Chain	Atom inclusion	Q-score
XA	 0.7900	 0.2650
XB	 0.9290	 0.2650
Y	 0.5950	 0.2380
YA	 0.8510	 0.2660
YB	 0.9160	 0.2650
Z	 0.7880	 0.2640
ZA	 0.9300	 0.2670
ZB	 0.7790	 0.2490