



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:06 AM UTC

PDB ID : 6ZVR / pdb_00006zvr
EMDB ID : EMD-11468
Title : C11 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 : 8.20 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:

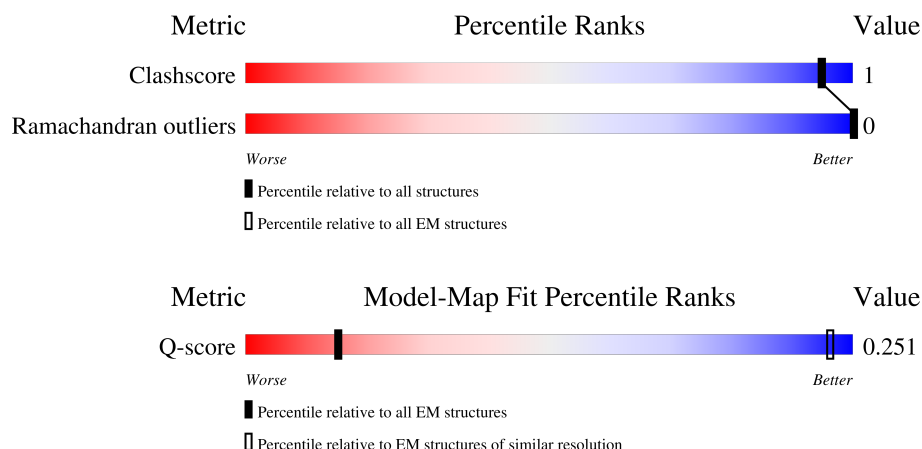
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.20 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.



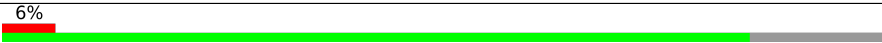
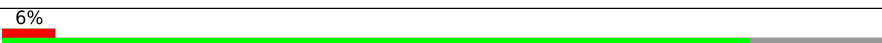
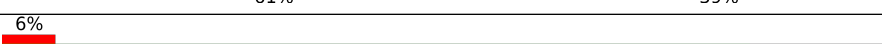
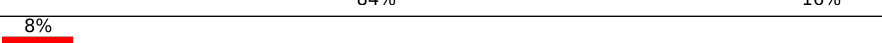
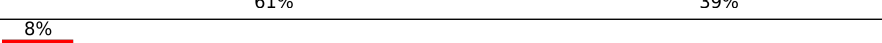
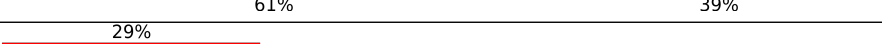
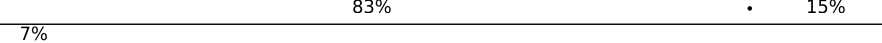
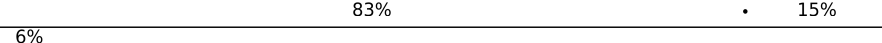
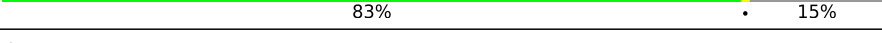
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	337 (7.70 - 8.70)

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	29% 83% 15%
1	AA	258	29% 83% 15%
1	AB	258	7% 83% 15%
1	B	258	29% 83% 15%
1	BA	258	7% 83% 15%

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Mol	Chain	Length	Quality of chain
1	BB	258	
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	F	258	
1	FA	258	
1	G	258	
1	GA	258	
1	H	258	
1	HA	258	
1	I	258	
1	IA	258	
1	J	258	
1	JA	258	
1	K	258	
1	KA	258	
1	L	258	
1	LA	258	
1	M	258	
1	MA	258	

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Mol	Chain	Length	Quality of chain
1	N	258	
1	NA	258	
1	O	258	
1	OA	258	
1	P	258	
1	PA	258	
1	Q	258	
1	QA	258	
1	R	258	
1	RA	258	
1	S	258	
1	SA	258	
1	T	258	
1	TA	258	
1	UA	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 56364 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	B	219	Total	C	N	O	0	0
			1086	648	219	219		
1	C	219	Total	C	N	O	0	0
			1086	648	219	219		
1	D	219	Total	C	N	O	0	0
			1086	648	219	219		
1	E	218	Total	C	N	O	0	0
			1081	645	218	218		
1	F	158	Total	C	N	O	0	0
			785	469	158	158		
1	A	219	Total	C	N	O	0	0
			1086	648	219	219		
1	G	219	Total	C	N	O	0	0
			1086	648	219	219		
1	H	219	Total	C	N	O	0	0
			1086	648	219	219		
1	I	218	Total	C	N	O	0	0
			1081	645	218	218		
1	J	158	Total	C	N	O	0	0
			785	469	158	158		
1	K	219	Total	C	N	O	0	0
			1086	648	219	219		
1	L	219	Total	C	N	O	0	0
			1086	648	219	219		
1	M	219	Total	C	N	O	0	0
			1086	648	219	219		
1	N	218	Total	C	N	O	0	0
			1081	645	218	218		
1	O	158	Total	C	N	O	0	0
			785	469	158	158		
1	P	219	Total	C	N	O	0	0
			1086	648	219	219		
1	Q	219	Total	C	N	O	0	0
			1086	648	219	219		

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

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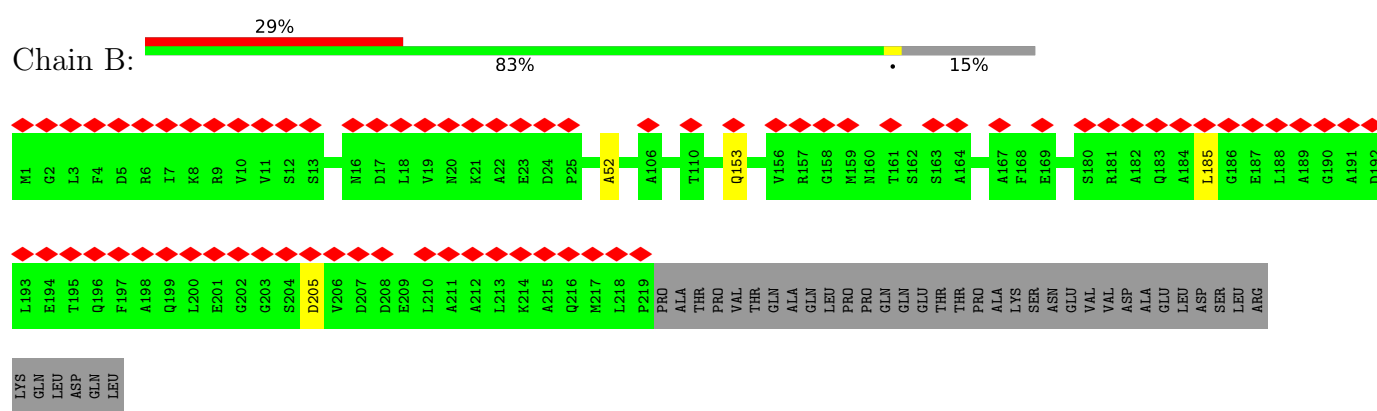
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	NA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	OA	158	Total	C	N	O	0	0
			785	469	158	158		
1	PA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	QA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	RA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	SA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	TA	158	Total	C	N	O	0	0
			785	469	158	158		
1	UA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	VA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	WA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	XA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	YA	158	Total	C	N	O	0	0
			785	469	158	158		
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	219	Total	C	N	O	0	0
			1086	648	219	219		
1	CB	218	Total	C	N	O	0	0
			1081	645	218	218		
1	DB	158	Total	C	N	O	0	0
			785	469	158	158		

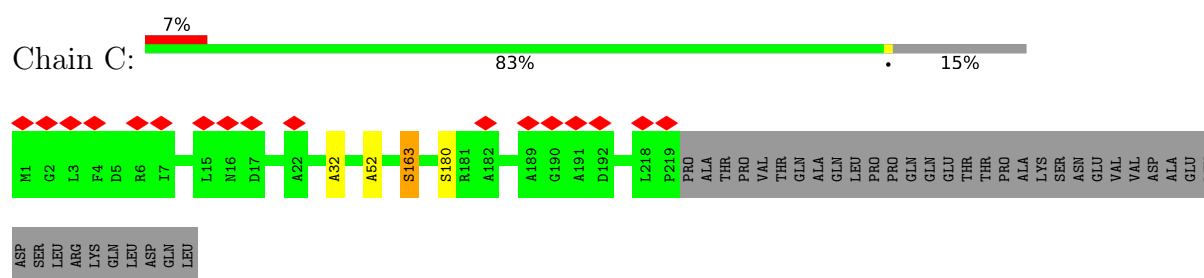
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

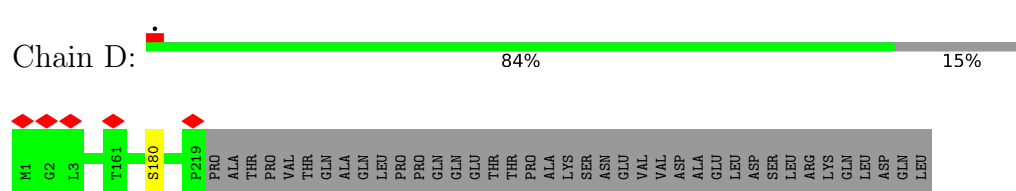
• Molecule 1: Vipp1



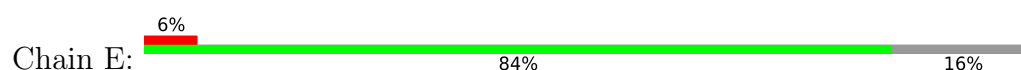
• Molecule 1: Vipp1

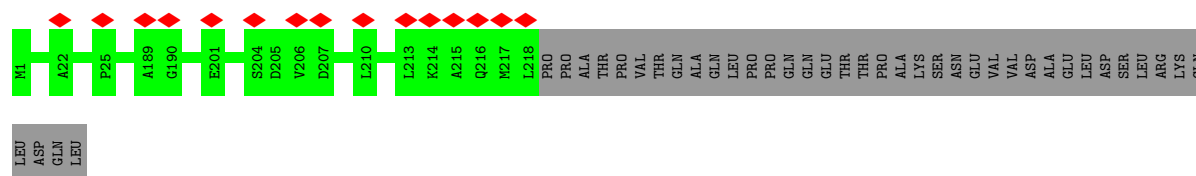


• Molecule 1: Vipp1

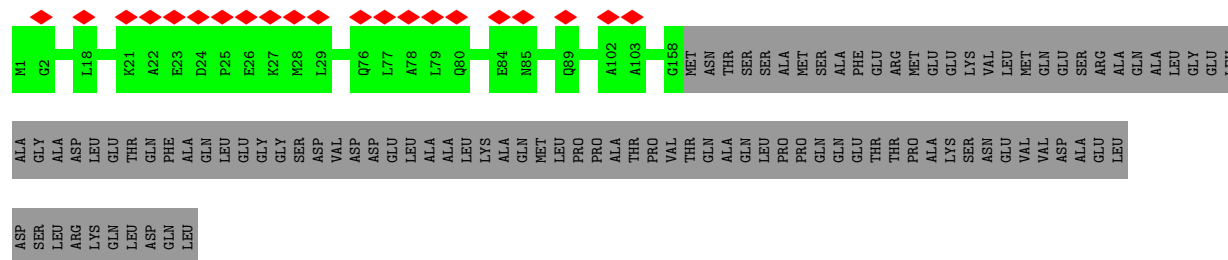


• Molecule 1: Vipp1

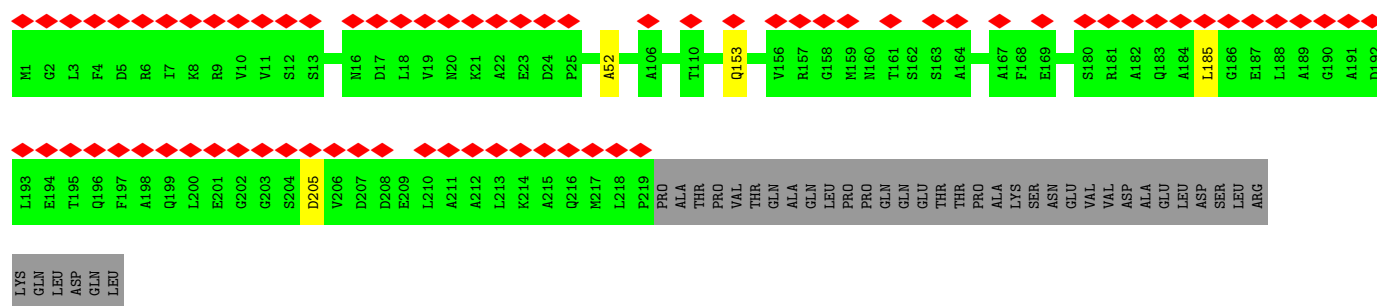
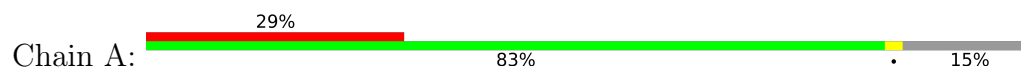




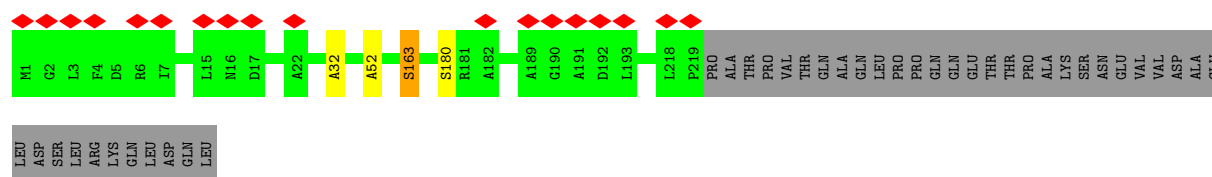
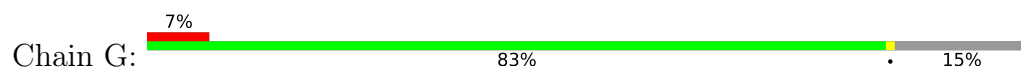
• Molecule 1: Vipp1



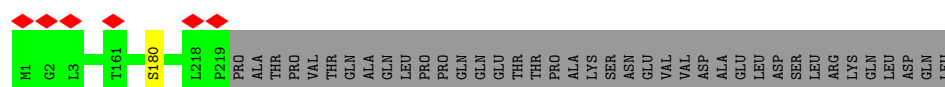
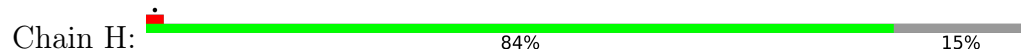
• Molecule 1: Vipp1



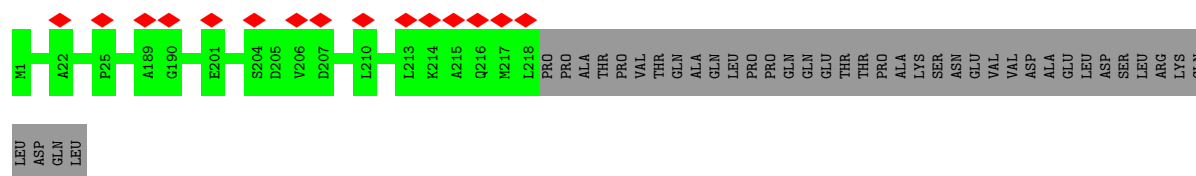
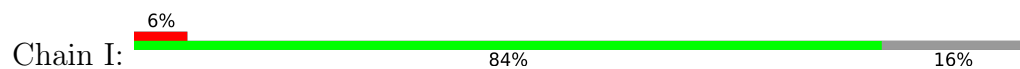
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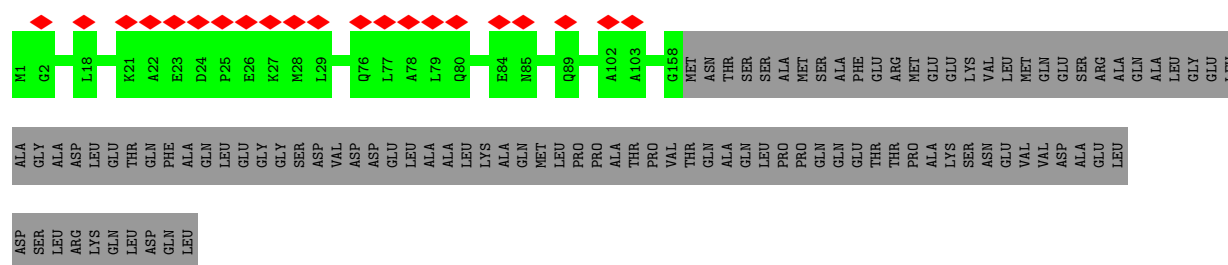
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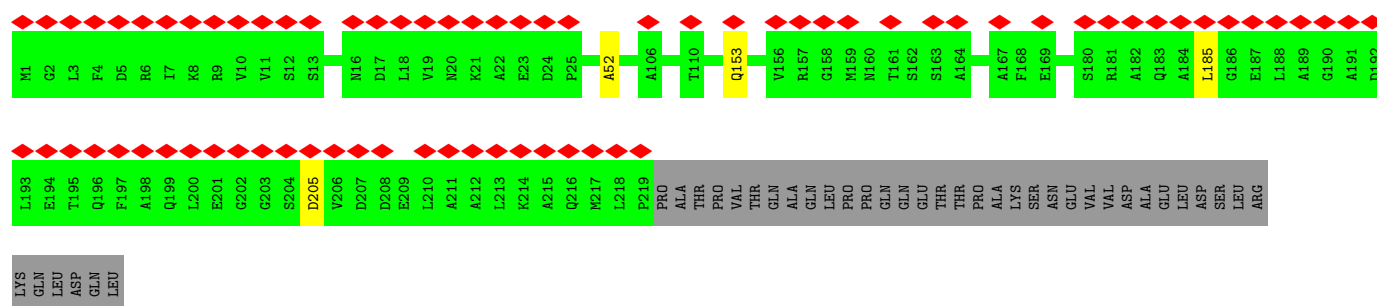
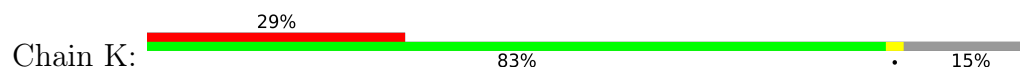
● Molecule 1: Vipp1



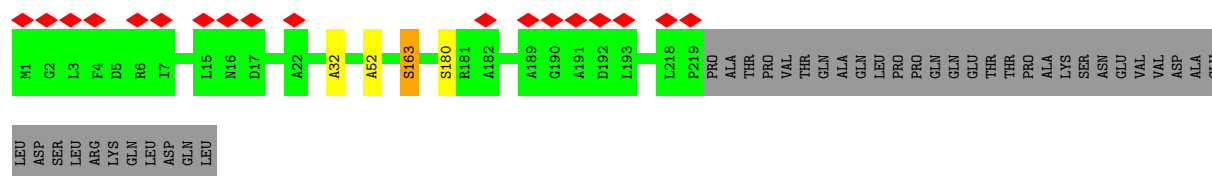
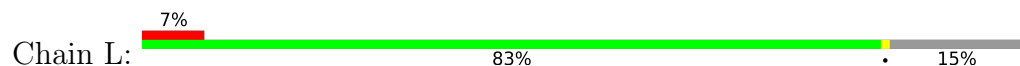
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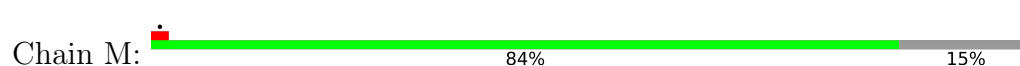
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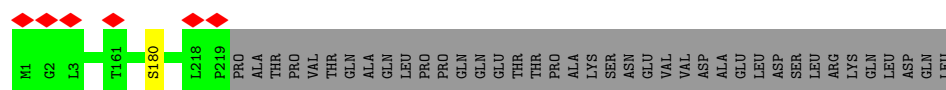


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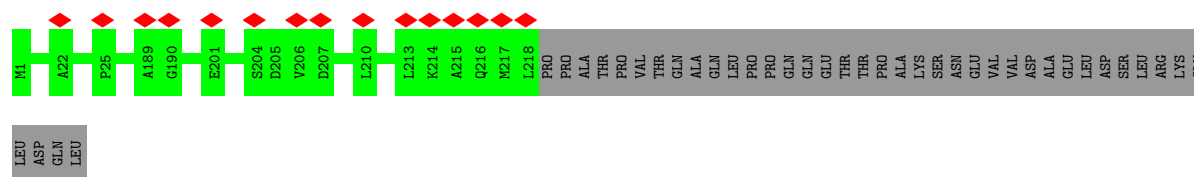
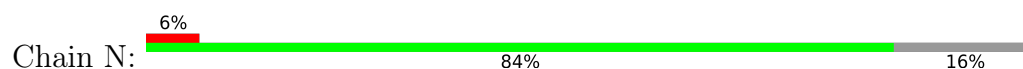


● Molecule 1: Vipp1

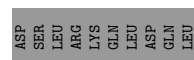
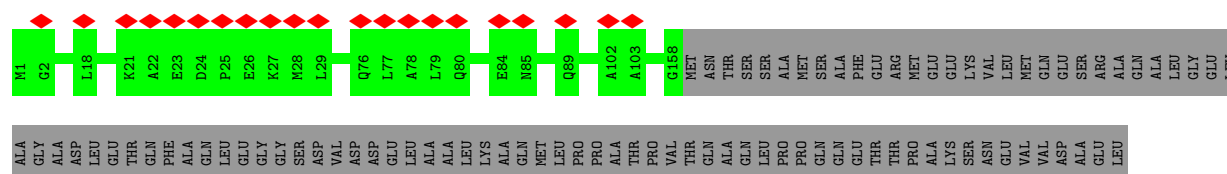




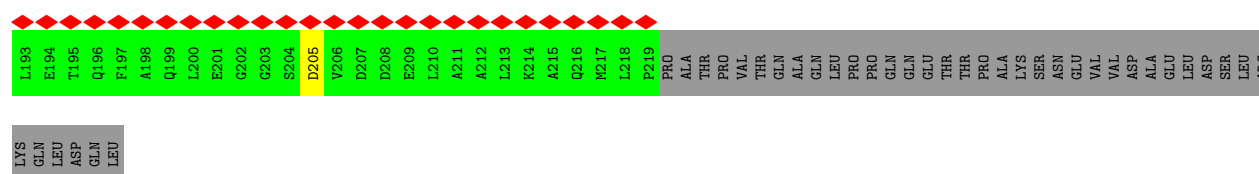
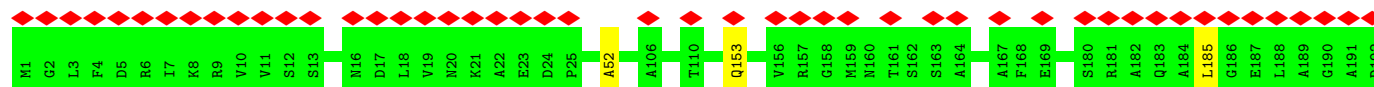
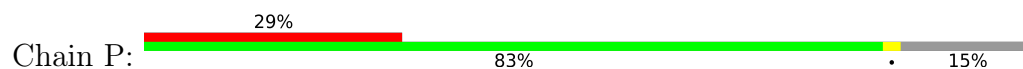
- Molecule 1: Vipp1



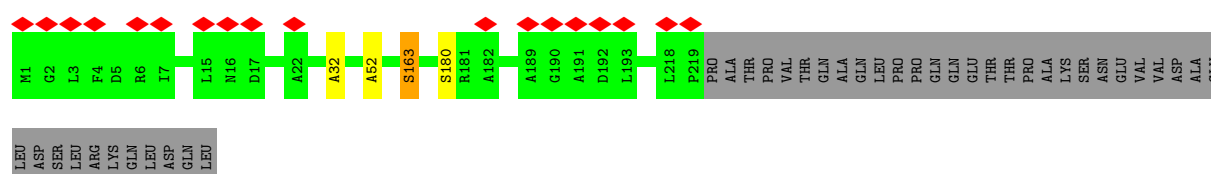
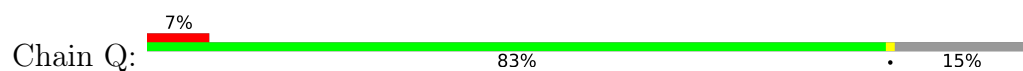
- Molecule 1: Vipp1



- Molecule 1: Vipp1

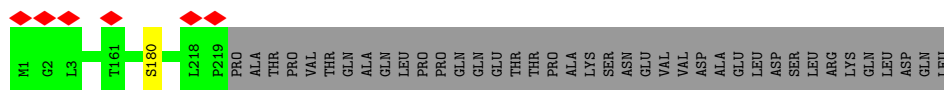


- Molecule 1: Vipp1



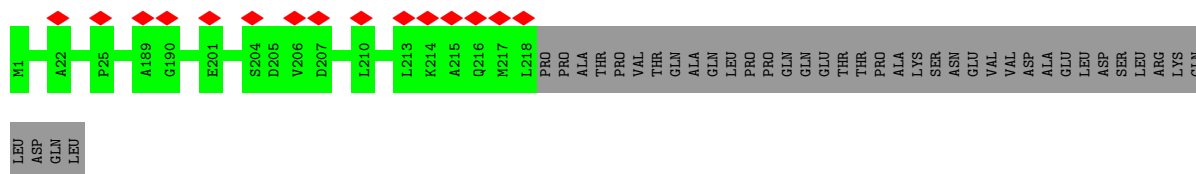
• Molecule 1: Vipp1

Chain R:  84% 15%



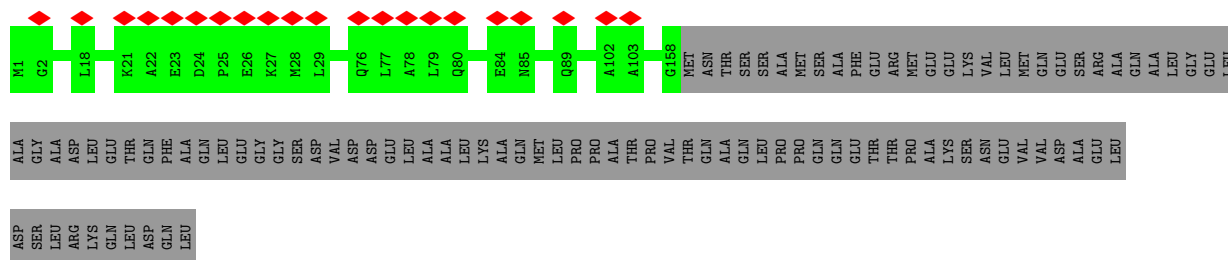
• Molecule 1: Vipp1

Chain S:  6% 84% 16%



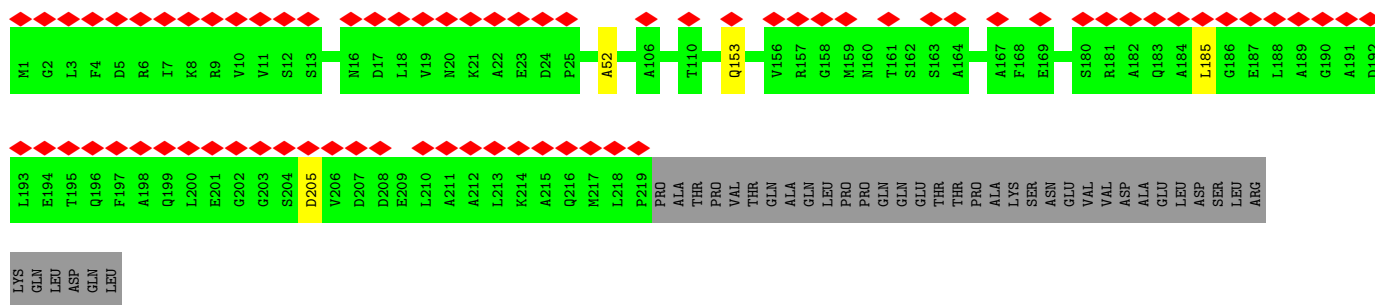
• Molecule 1: Vipp1

Chain T:  8% 61% 39%



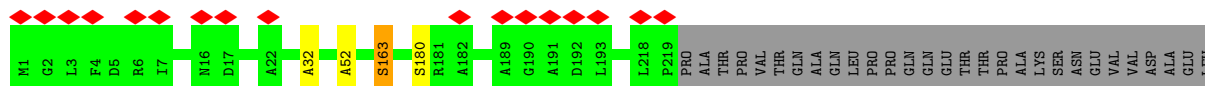
• Molecule 1: Vipp1

Chain V:  29% 83% 15%



• Molecule 1: Vipp1

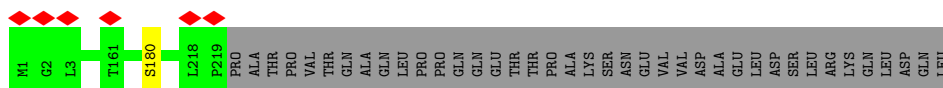
Chain W:  7% 83% 15%



ASP
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

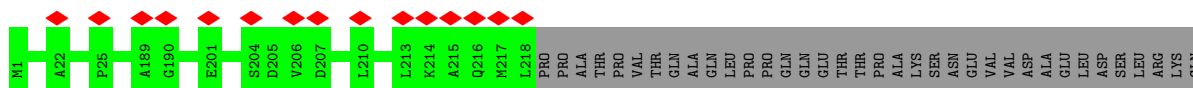
• Molecule 1: Vipp1

Chain X:  84% 15%



• Molecule 1: Vipp1

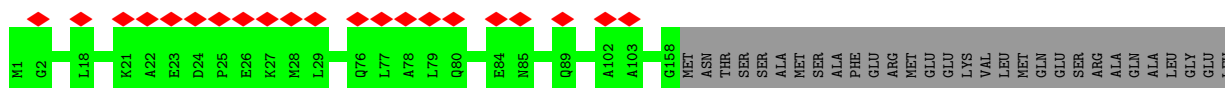
Chain Y:  6% 84% 16%



LEU
ASP
GLN
LEU

• Molecule 1: Vipp1

Chain Z:  8% 61% 39%

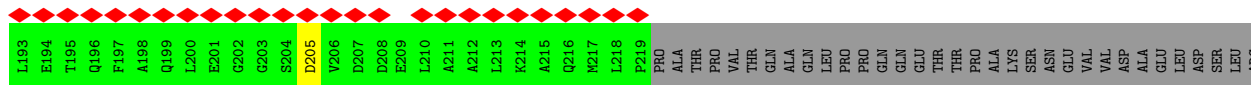
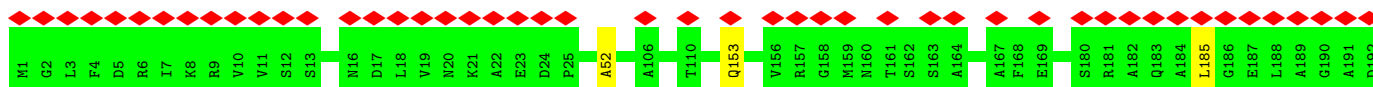


ALA
GLY
ALA
ASP
LEU
GLU
THR
GLN
PHE
ALA
GLN
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GLU
GLY
GLY
SER
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PRO
PRO
ALA
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GLN
LEU
PRO
PRO
GLN
GLN
GLU
THR
PRO
ALA
LYS
SER
ASN
GLU
VAL
VAL
ASP
ALA
LEU

ASP
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1

Chain AA:  29% 83% 15%



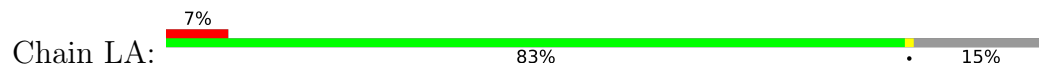
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1

Chain BA:  7% 83% 15%

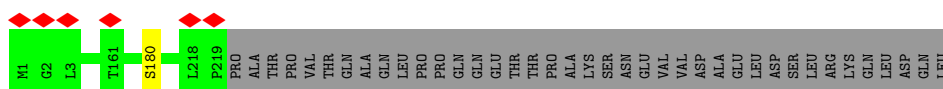
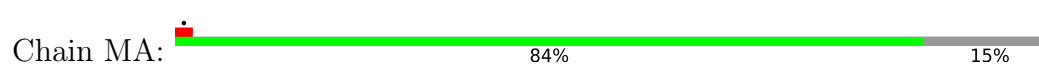
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: Vipp1

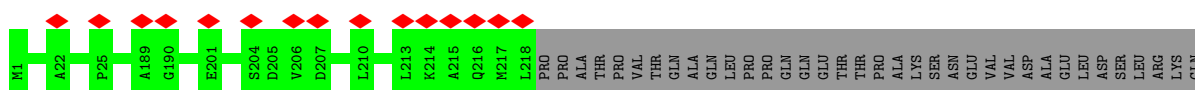
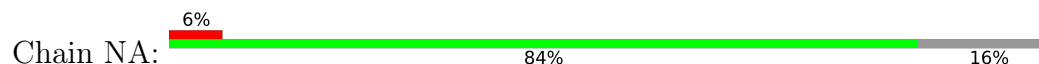


LEU
ASP
SER
LEU
ARG
LYS
GLN
LEU
ASP
LEU

• Molecule 1: Vipp1

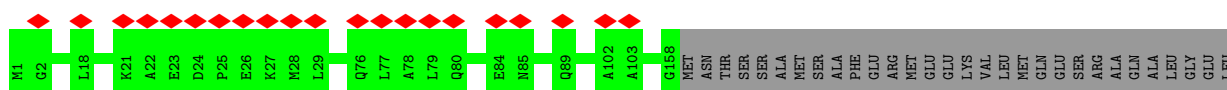


• Molecule 1: Vipp1



LEU
ASP
GLN
LEU

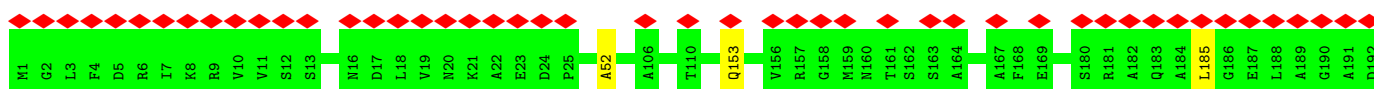
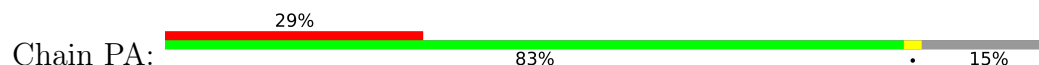
• Molecule 1: Vipp1

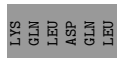


ALA
GLY
ALA
ASP
LEU
GLU
THR
GLN
PHE
GLN
ALA
LEU
GLU
GLY
GLY
SER
ASP
VAL
ASP
ASP
GLU
LEU
LEU
ALA
ALA
LEU
LYS
ALA
GLN
MET
LEU
PRO
PRO
ALA
THR
VAL
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ALA
GLN
LEU
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PRO
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GLU
PHE
THR
THR
PRO
MET
GLU
GLU
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ASN
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GLU
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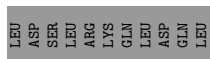
ASP
SER
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GLN
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ASP
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• Molecule 1: Vipp1

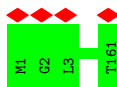




- Molecule 1: Vippp1



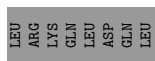
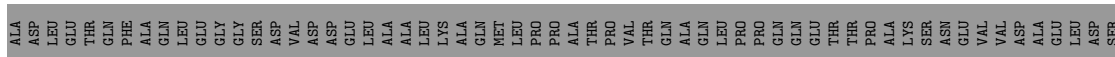
- Molecule 1: Vippp1



- Molecule 1: Vippp1

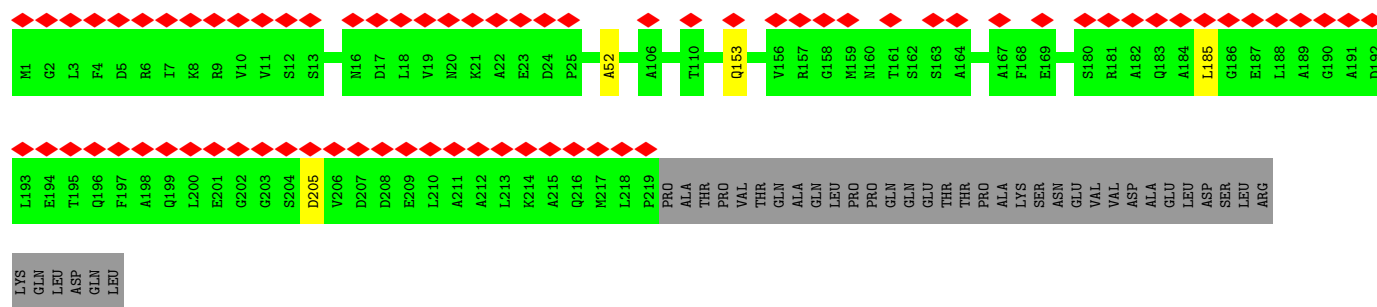


- Molecule 1: Vippp1

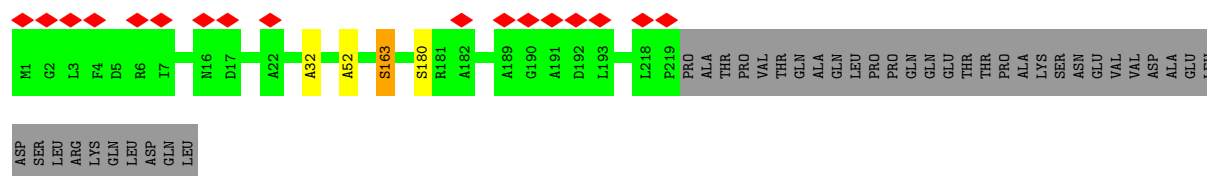
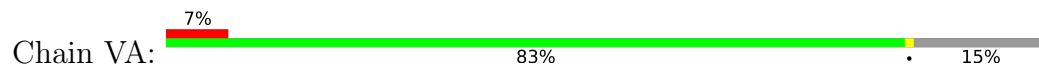


- Molecule 1: Vippp1

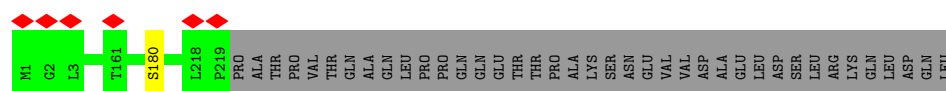
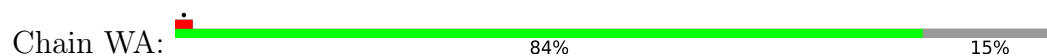




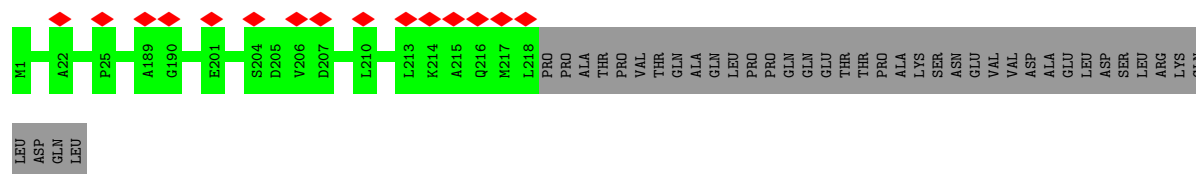
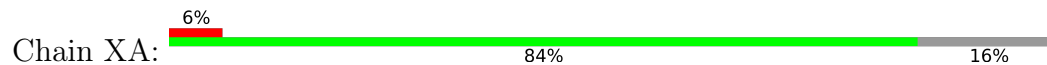
- Molecule 1: Vipp1



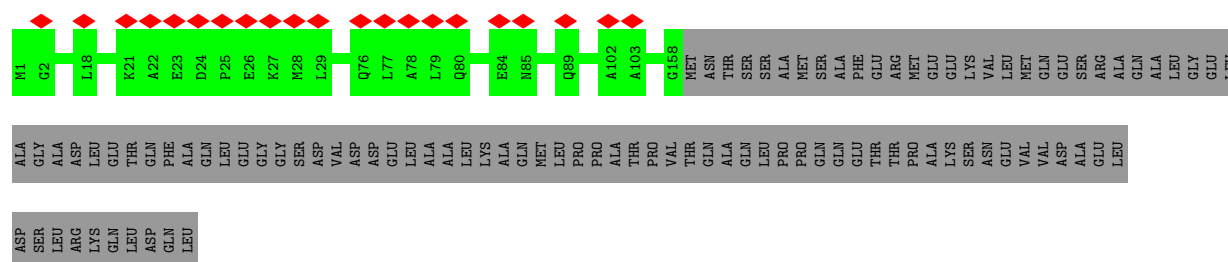
- Molecule 1: Vipp1



- Molecule 1: Vipp1



- Molecule 1: Vipp1



ASP
SER
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LYS
GLN
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GLN
LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3912	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	0.043	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0163	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	0/1085	0.92	1/1512 (0.1%)
1	AA	0.35	0/1085	0.92	1/1512 (0.1%)
1	AB	0.36	0/1085	0.94	1/1512 (0.1%)
1	B	0.34	0/1085	0.92	1/1512 (0.1%)
1	BA	0.36	0/1085	0.94	1/1512 (0.1%)
1	BB	0.35	0/1085	0.91	0/1512
1	C	0.36	0/1085	0.94	1/1512 (0.1%)
1	CA	0.35	0/1085	0.91	0/1512
1	CB	0.35	0/1080	0.95	0/1505
1	D	0.35	0/1085	0.91	0/1512
1	DA	0.35	0/1080	0.95	0/1505
1	DB	0.34	0/784	0.92	0/1093
1	E	0.35	0/1080	0.95	0/1505
1	EA	0.34	0/784	0.92	0/1093
1	F	0.34	0/784	0.92	0/1093
1	FA	0.34	0/1085	0.92	1/1512 (0.1%)
1	G	0.36	0/1085	0.94	1/1512 (0.1%)
1	GA	0.36	0/1085	0.94	1/1512 (0.1%)
1	H	0.35	0/1085	0.91	0/1512
1	HA	0.35	0/1085	0.91	0/1512
1	I	0.35	0/1080	0.95	0/1505
1	IA	0.36	0/1080	0.95	0/1505
1	J	0.34	0/784	0.92	0/1093
1	JA	0.34	0/784	0.92	0/1093
1	K	0.34	0/1085	0.92	1/1512 (0.1%)
1	KA	0.34	0/1085	0.92	1/1512 (0.1%)
1	L	0.36	0/1085	0.94	1/1512 (0.1%)
1	LA	0.36	0/1085	0.94	1/1512 (0.1%)
1	M	0.35	0/1085	0.91	0/1512
1	MA	0.35	0/1085	0.91	0/1512
1	N	0.35	0/1080	0.95	0/1505
1	NA	0.35	0/1080	0.95	0/1505
1	O	0.34	0/784	0.92	0/1093
1	OA	0.34	0/784	0.92	0/1093

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	P	0.34	0/1085	0.92	1/1512 (0.1%)
1	PA	0.34	0/1085	0.92	1/1512 (0.1%)
1	Q	0.36	0/1085	0.94	1/1512 (0.1%)
1	QA	0.36	0/1085	0.94	1/1512 (0.1%)
1	R	0.35	0/1085	0.91	0/1512
1	RA	0.35	0/1085	0.91	0/1512
1	S	0.35	0/1080	0.95	0/1505
1	SA	0.35	0/1080	0.95	0/1505
1	T	0.34	0/784	0.92	0/1093
1	TA	0.34	0/784	0.92	0/1093
1	UA	0.34	0/1085	0.92	1/1512 (0.1%)
1	V	0.35	0/1085	0.92	1/1512 (0.1%)
1	VA	0.36	0/1085	0.94	1/1512 (0.1%)
1	W	0.36	0/1085	0.94	1/1512 (0.1%)
1	WA	0.35	0/1085	0.91	0/1512
1	X	0.35	0/1085	0.91	0/1512
1	XA	0.35	0/1080	0.95	0/1505
1	Y	0.36	0/1080	0.95	0/1505
1	YA	0.34	0/784	0.92	0/1093
1	Z	0.34	0/784	0.92	0/1093
1	ZA	0.35	0/1085	0.92	1/1512 (0.1%)
All	All	0.35	0/56309	0.93	22/78474 (0.0%)

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AB	163	SER	N-CA-C	6.28	118.12	111.28
1	Q	163	SER	N-CA-C	6.27	118.11	111.28
1	BA	163	SER	N-CA-C	6.26	118.11	111.28
1	VA	163	SER	N-CA-C	6.26	118.10	111.28
1	QA	163	SER	N-CA-C	6.25	118.10	111.28

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	1086	0	531	5	0
1	AA	1086	0	531	5	0
1	AB	1086	0	531	8	0
1	B	1086	0	531	5	0
1	BA	1086	0	531	8	0
1	BB	1086	0	531	3	0
1	C	1086	0	531	8	0
1	CA	1086	0	531	3	0
1	CB	1081	0	530	0	0
1	D	1086	0	531	3	0
1	DA	1081	0	530	0	0
1	DB	785	0	376	0	0
1	E	1081	0	530	0	0
1	EA	785	0	376	0	0
1	F	785	0	376	0	0
1	FA	1086	0	531	5	0
1	G	1086	0	531	8	0
1	GA	1086	0	531	8	0
1	H	1086	0	531	3	0
1	HA	1086	0	531	3	0
1	I	1081	0	530	0	0
1	IA	1081	0	530	0	0
1	J	785	0	376	0	0
1	JA	785	0	376	0	0
1	K	1086	0	531	5	0
1	KA	1086	0	531	5	0
1	L	1086	0	531	8	0
1	LA	1086	0	531	8	0
1	M	1086	0	531	3	0
1	MA	1086	0	531	3	0
1	N	1081	0	530	0	0
1	NA	1081	0	530	0	0
1	O	785	0	376	0	0
1	OA	785	0	376	0	0
1	P	1086	0	531	5	0
1	PA	1086	0	531	5	0
1	Q	1086	0	531	8	0
1	QA	1086	0	531	8	0
1	R	1086	0	531	3	0
1	RA	1086	0	531	3	0
1	S	1081	0	530	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SA	1081	0	530	0	0
1	T	785	0	376	0	0
1	TA	785	0	376	0	0
1	UA	1086	0	531	5	0
1	V	1086	0	531	5	0
1	VA	1086	0	531	8	0
1	W	1086	0	531	8	0
1	WA	1086	0	531	3	0
1	X	1086	0	531	3	0
1	XA	1081	0	530	0	0
1	Y	1081	0	530	0	0
1	YA	785	0	376	0	0
1	Z	785	0	376	0	0
1	ZA	1086	0	531	5	0
All	All	56364	0	27489	88	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 88 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:GA:180:SER:CB	1:PA:52:ALA:HB2	1.21	1.67
1:B:52:ALA:HB2	1:VA:180:SER:CB	1.20	1.65
1:BA:180:SER:CB	1:KA:52:ALA:HB2	1.22	1.64
1:C:180:SER:CB	1:K:52:ALA:HB2	1.19	1.64
1:QA:180:SER:CB	1:ZA:52:ALA:HB2	1.21	1.64

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	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	AA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	AB	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	B	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	BA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	BB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	C	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	CA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CB	216/258 (84%)	216 (100%)	0	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	156/258 (60%)	156 (100%)	0	0	100	100
1	E	216/258 (84%)	216 (100%)	0	0	100	100
1	EA	156/258 (60%)	156 (100%)	0	0	100	100
1	F	156/258 (60%)	156 (100%)	0	0	100	100
1	FA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	G	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	GA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	H	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	HA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	I	216/258 (84%)	216 (100%)	0	0	100	100
1	IA	216/258 (84%)	216 (100%)	0	0	100	100
1	J	156/258 (60%)	156 (100%)	0	0	100	100
1	JA	156/258 (60%)	156 (100%)	0	0	100	100
1	K	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	KA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	L	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	LA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	M	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	MA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	N	216/258 (84%)	216 (100%)	0	0	100	100
1	NA	216/258 (84%)	216 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	156/258 (60%)	156 (100%)	0	0	100	100
1	OA	156/258 (60%)	156 (100%)	0	0	100	100
1	P	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	PA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	Q	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	QA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	R	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	RA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	S	216/258 (84%)	216 (100%)	0	0	100	100
1	SA	216/258 (84%)	216 (100%)	0	0	100	100
1	T	156/258 (60%)	156 (100%)	0	0	100	100
1	TA	156/258 (60%)	156 (100%)	0	0	100	100
1	UA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	V	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	VA	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	W	217/258 (84%)	215 (99%)	2 (1%)	0	100	100
1	WA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	X	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	XA	216/258 (84%)	216 (100%)	0	0	100	100
1	Y	216/258 (84%)	216 (100%)	0	0	100	100
1	YA	156/258 (60%)	156 (100%)	0	0	100	100
1	Z	156/258 (60%)	156 (100%)	0	0	100	100
1	ZA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
All	All	11253/14190 (79%)	11209 (100%)	44 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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.

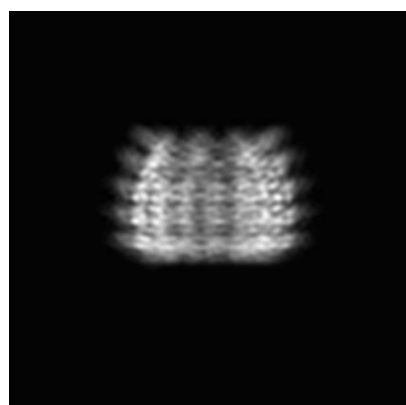
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11468. These allow visual inspection of the internal detail of the map and identification of artifacts.

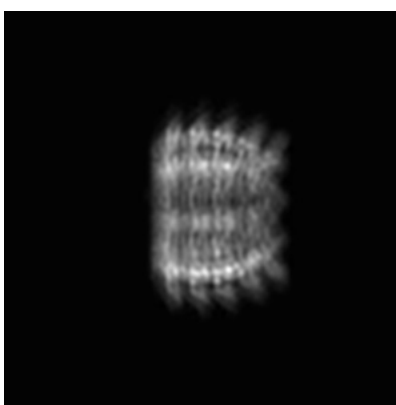
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

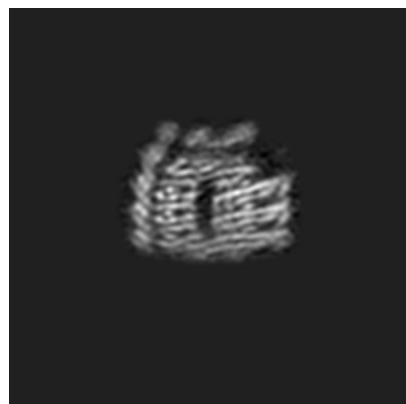


Z Index: 168

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: 116



Y Index: 126

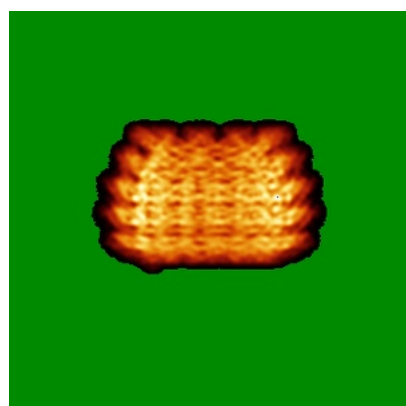


Z Index: 178

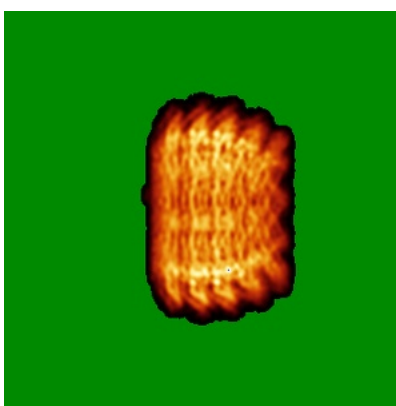
The images above show the largest variance slices of the map in three orthogonal directions.

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

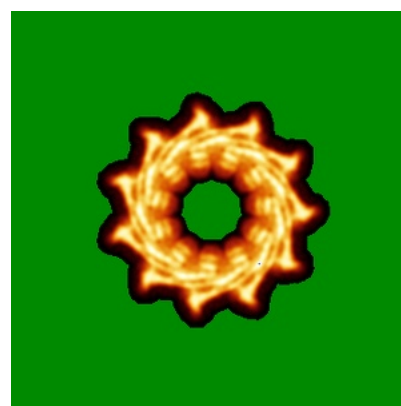
6.4.1 Primary map



X



Y

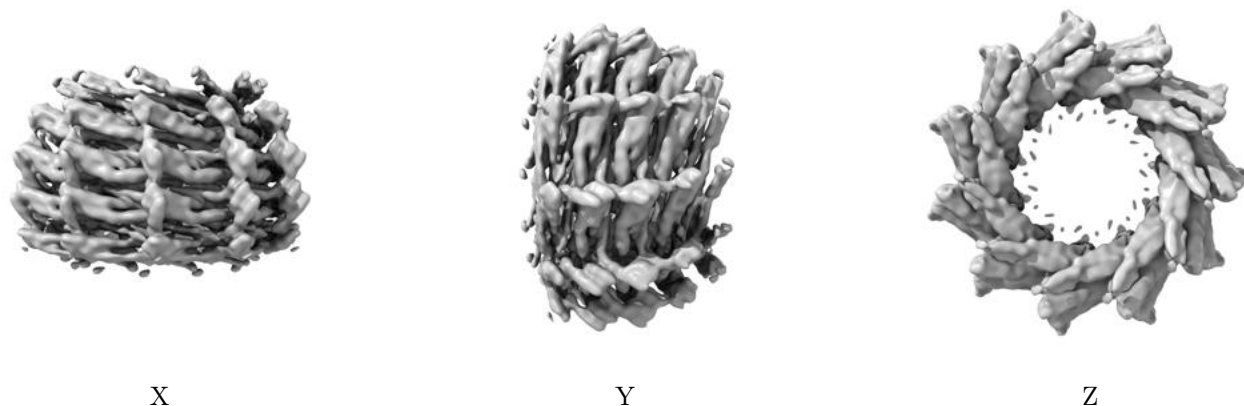


Z

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 0.0163. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

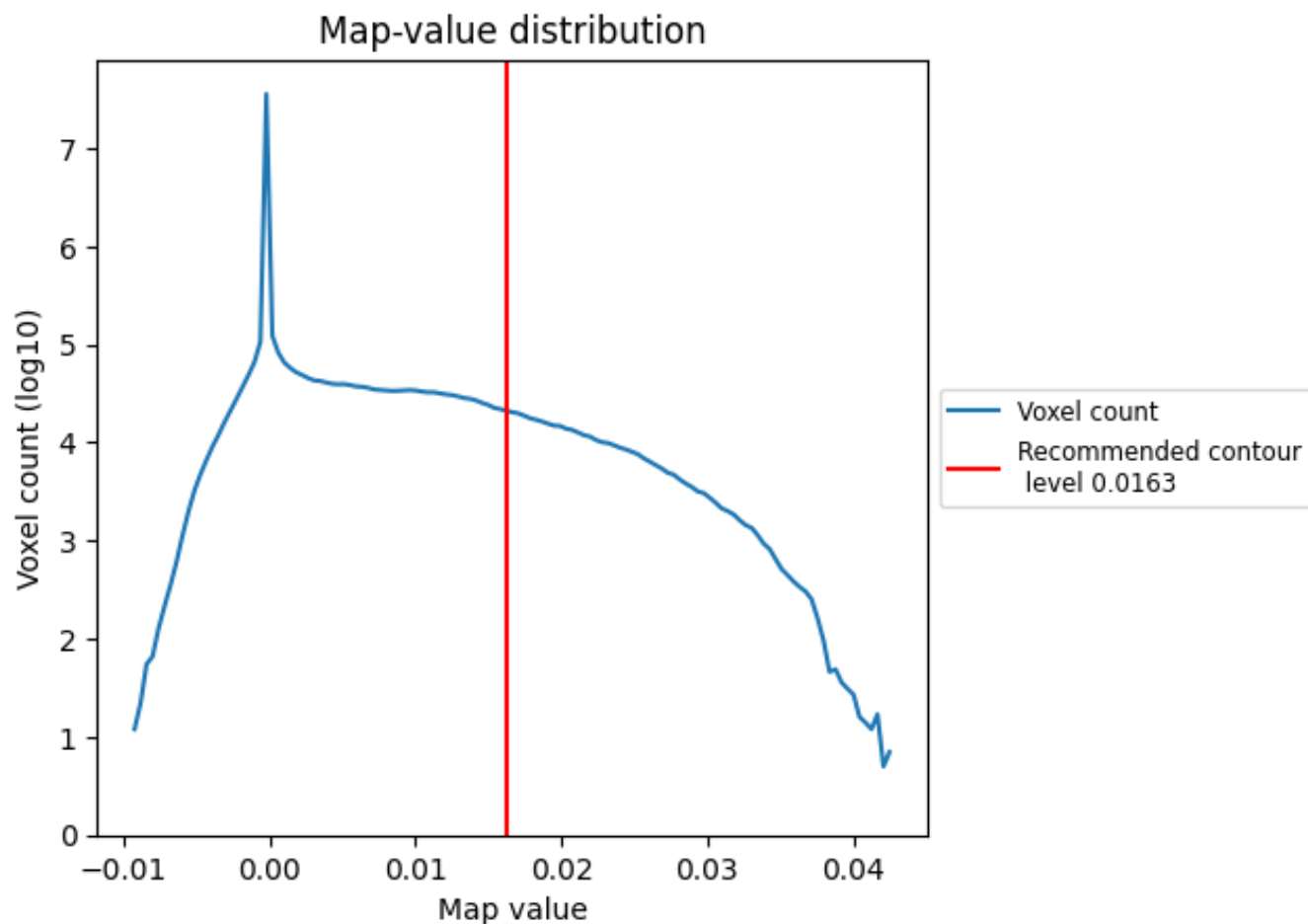
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

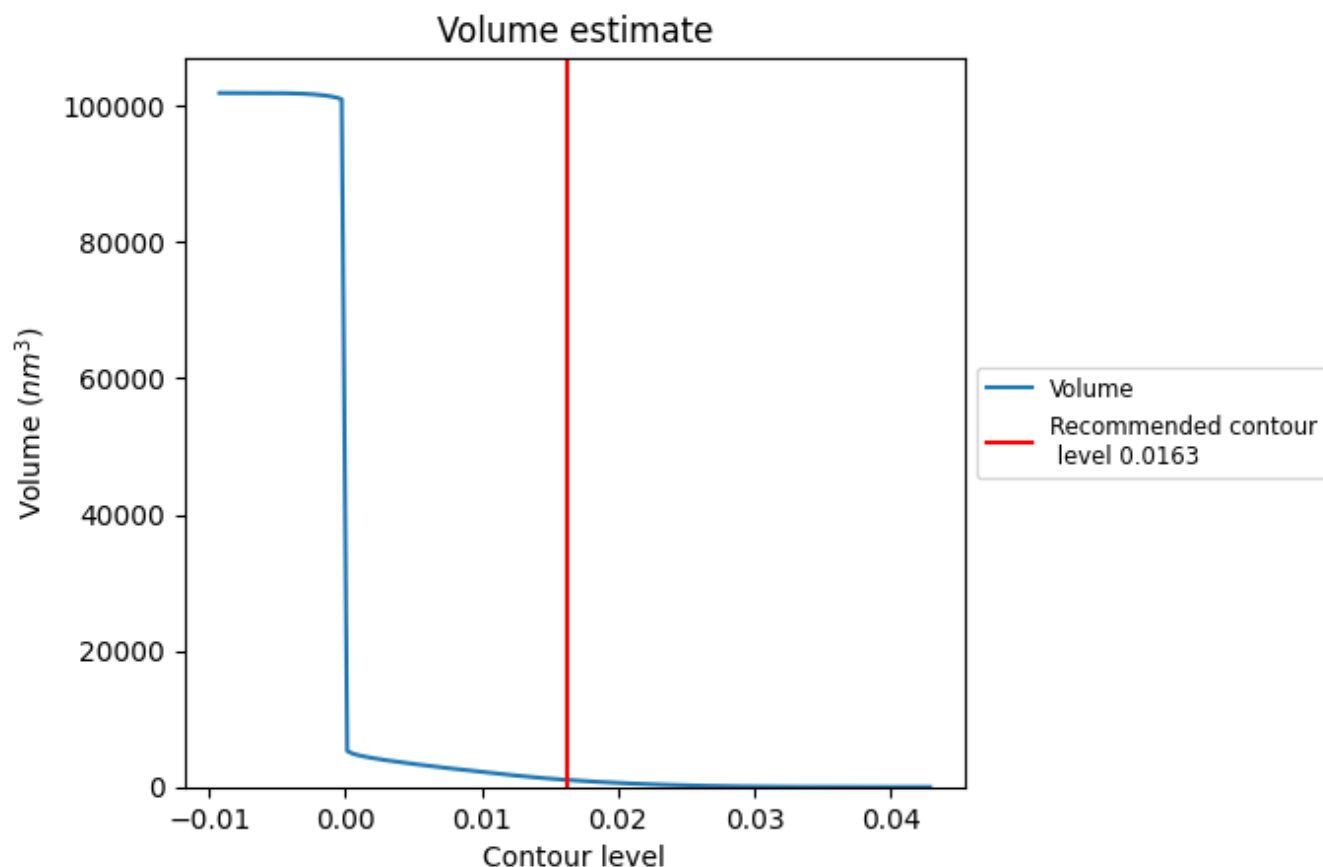
This section contains the results of statistical analysis of the map.

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.

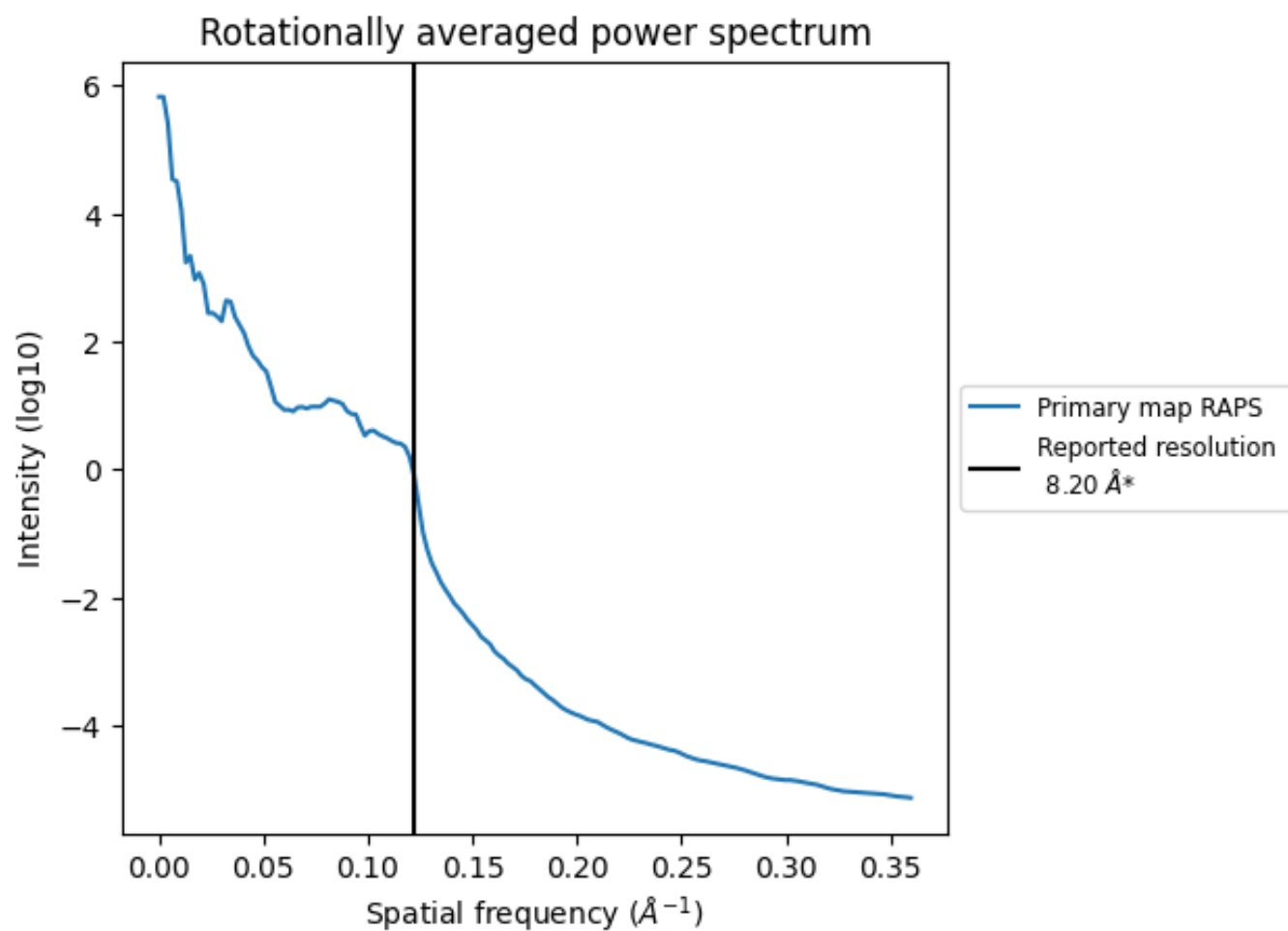
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1027 nm³; this corresponds to an approximate mass of 928 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 0.122 Å⁻¹

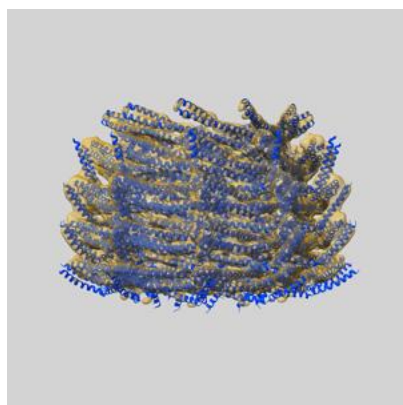
8 Fourier-Shell correlation

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

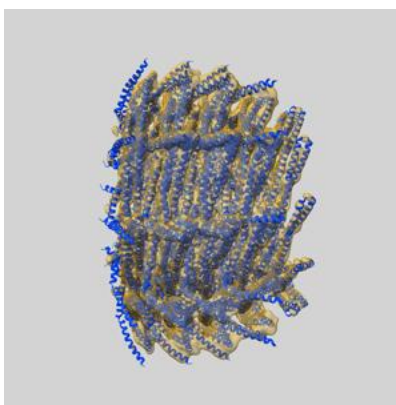
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11468 and PDB model 6ZVR. Per-residue inclusion information can be found in section [3](#) on page [8](#).

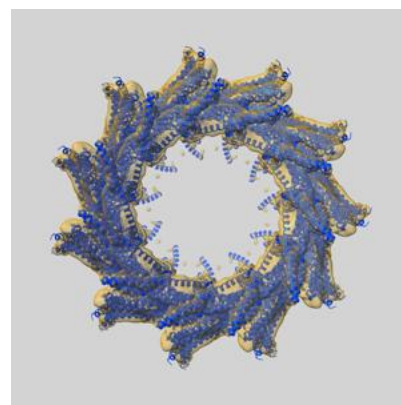
9.1 Map-model overlay [i](#)



X



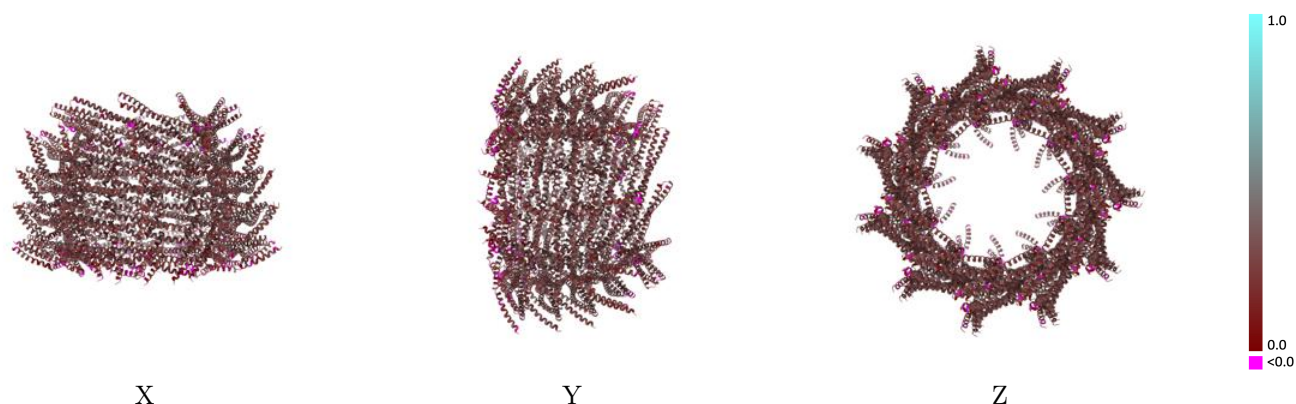
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0163 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](#)

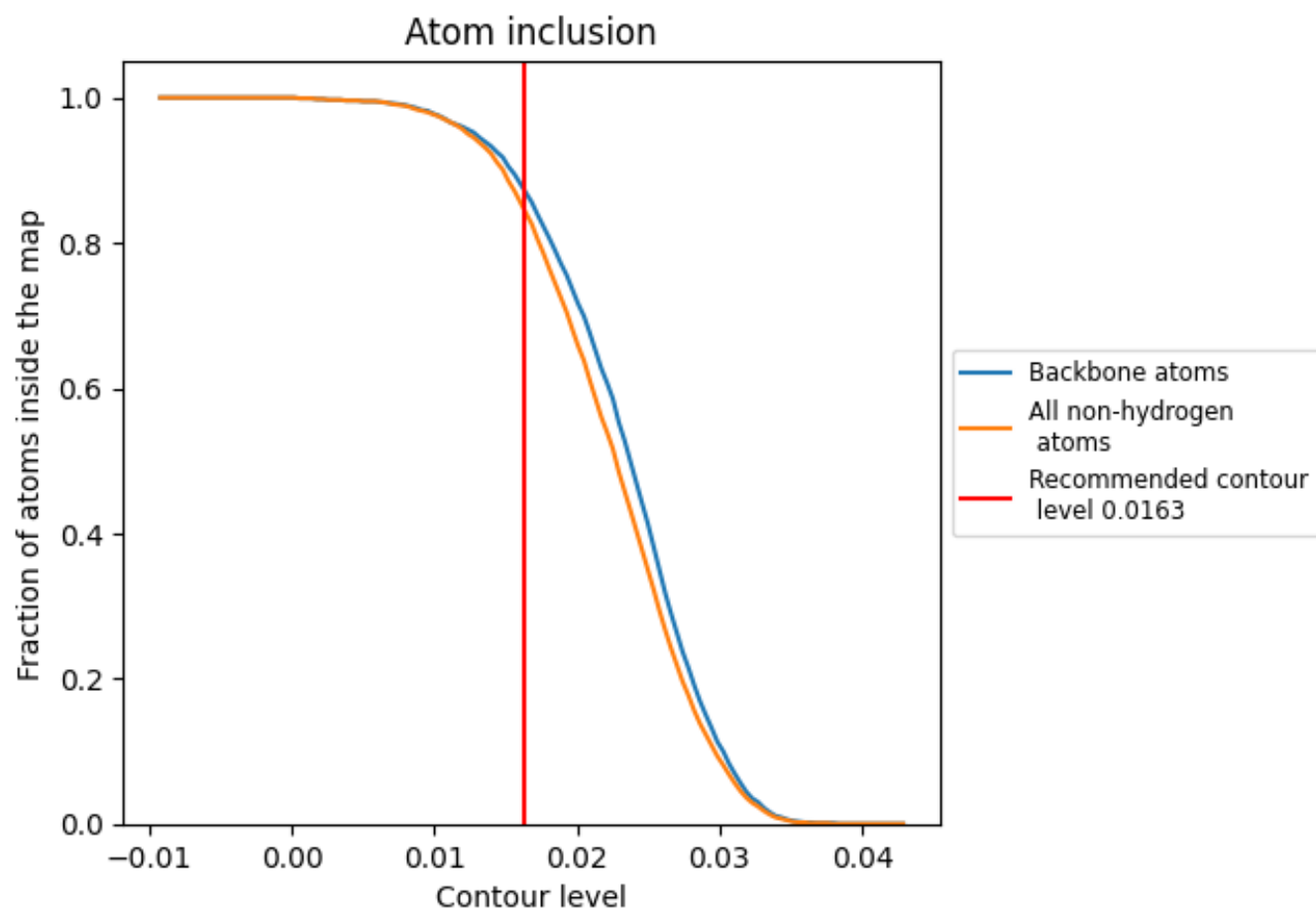


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.0163) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.2510
A	 0.6450	 0.2110
AA	 0.6450	 0.2110
AB	 0.8940	 0.2630
B	 0.6450	 0.2120
BA	 0.8940	 0.2620
BB	 0.9620	 0.2730
C	 0.8940	 0.2630
CA	 0.9630	 0.2700
CB	 0.9160	 0.2600
D	 0.9630	 0.2720
DA	 0.9180	 0.2600
DB	 0.7950	 0.2520
E	 0.9160	 0.2620
EA	 0.7940	 0.2490
F	 0.7940	 0.2550
FA	 0.6460	 0.2130
G	 0.8920	 0.2600
GA	 0.8950	 0.2640
H	 0.9610	 0.2720
HA	 0.9610	 0.2720
I	 0.9170	 0.2590
IA	 0.9150	 0.2600
J	 0.7900	 0.2500
JA	 0.7910	 0.2480
K	 0.6460	 0.2080
KA	 0.6450	 0.2120
L	 0.8930	 0.2590
LA	 0.8940	 0.2620
M	 0.9600	 0.2700
MA	 0.9600	 0.2700
N	 0.9180	 0.2590
NA	 0.9180	 0.2610
O	 0.7940	 0.2500
OA	 0.7950	 0.2510



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Chain	Atom inclusion	Q-score
P	 0.6460	 0.2120
PA	 0.6460	 0.2130
Q	 0.8930	 0.2610
QA	 0.8920	 0.2640
R	 0.9610	 0.2720
RA	 0.9610	 0.2730
S	 0.9140	 0.2600
SA	 0.9160	 0.2610
T	 0.7940	 0.2500
TA	 0.7920	 0.2510
UA	 0.6450	 0.2110
V	 0.6460	 0.2110
VA	 0.8930	 0.2640
W	 0.8950	 0.2630
WA	 0.9600	 0.2720
X	 0.9600	 0.2730
XA	 0.9160	 0.2610
Y	 0.9160	 0.2610
YA	 0.7920	 0.2540
Z	 0.7940	 0.2500
ZA	 0.6460	 0.2130