



Full wwPDB EM Validation Report ⓘ

Dec 18, 2022 – 04:51 am GMT

PDB ID : 6ZW6
EMDB ID : EMD-11482
Title : C16 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 : 7.40 Å(reported)

This is a Full wwPDB EM Validation 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:

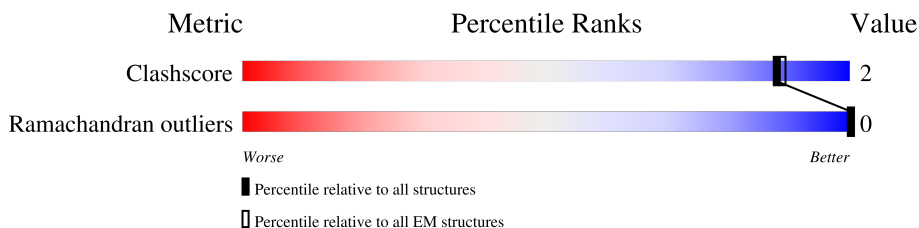
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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	
1	AA	258	
1	AB	258	
1	AC	258	
1	AD	258	
1	B	258	
1	BA	258	
1	BB	258	
1	BC	258	

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Mol	Chain	Length	Quality of chain
1	BD	258	
1	C	258	
1	CA	258	
1	CB	258	
1	CC	258	
1	CD	258	
1	D	258	
1	DA	258	
1	DB	258	
1	DC	258	
1	DD	258	
1	E	258	
1	EA	258	
1	EB	258	
1	EC	258	
1	ED	258	
1	F	258	
1	FA	258	
1	FB	258	
1	FC	258	
1	FD	258	
1	G	258	
1	GA	258	
1	GB	258	
1	GC	258	

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Mol	Chain	Length	Quality of chain
1	GD	258	84% 15%
1	H	258	22% 51% 48%
1	HA	258	84% 15%
1	HB	258	82% 15%
1	HC	258	21% 51% 48%
1	HD	258	10% 83% 16%
1	I	258	13% 83% 15%
1	IA	258	9% 83% 16%
1	IB	258	84% 15%
1	IC	258	14% 83% 15%
1	ID	258	16% 61% 39%
1	J	258	82% 15%
1	JA	258	16% 61% 39%
1	JB	258	84% 15%
1	JC	258	82% 15%
1	K	258	84% 15%
1	KA	258	22% 51% 48%
1	KB	258	9% 83% 16%
1	KC	258	84% 15%
1	L	258	84% 15%
1	LA	258	13% 83% 15%
1	LB	258	16% 61% 39%
1	LC	258	84% 15%
1	M	258	10% 83% 16%
1	MA	258	82% 15%














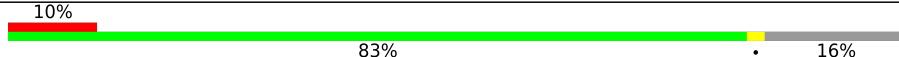
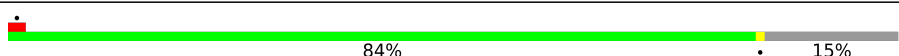

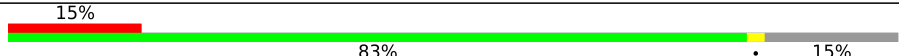
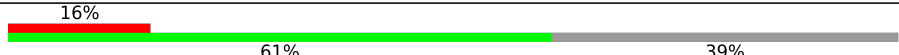
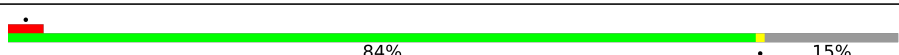
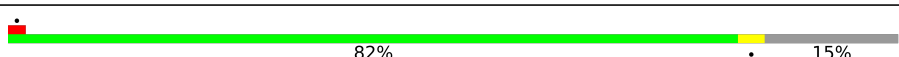
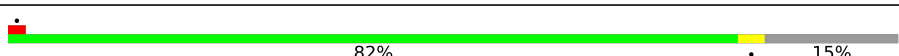
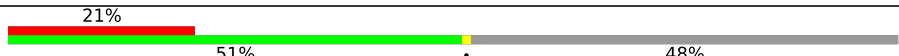


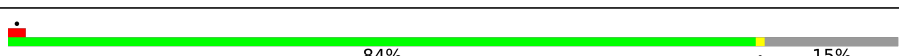
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Mol	Chain	Length	Quality of chain
1	MB	258	
1	MC	258	
1	N	258	
1	NA	258	
1	NB	258	
1	NC	258	
1	O	258	
1	OA	258	
1	OB	258	
1	OC	258	
1	P	258	
1	PA	258	
1	PB	258	
1	PC	258	
1	Q	258	
1	QA	258	
1	QB	258	
1	QC	258	
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1	RA	258	
1	RB	258	
1	RC	258	
1	S	258	
1	SA	258	
1	SB	258	

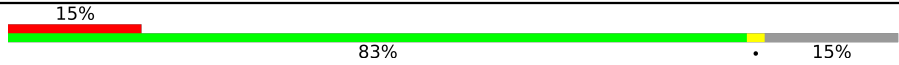

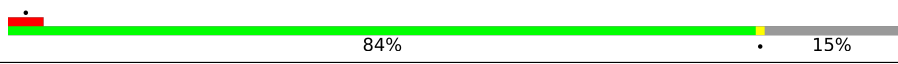
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Mol	Chain	Length	Quality of chain
1	SC	258	 84% 15%
1	T	258	 83% 16%
1	TA	258	 82% 15%
1	TB	258	 51% 48%
1	TC	258	 83% 16%
1	UA	258	 84% 15%
1	UB	258	 83% 15%
1	UC	258	 61% 39%
1	V	258	 61% 39%
1	VA	258	 84% 15%
1	VB	258	 82% 15%
1	VC	258	 51% 48%
1	W	258	 51% 48%
1	WA	258	 83% 16%
1	WB	258	 84% 15%
1	WC	258	 83% 15%
1	X	258	 83% 15%
1	XA	258	 61% 39%
1	XB	258	 84% 15%
1	XC	258	 82% 15%
1	Y	258	 82% 15%
1	YA	258	 51% 48%
1	YB	258	 83% 16%
1	YC	258	 84% 15%
1	Z	258	 84% 15%

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Mol	Chain	Length	Quality of chain
1	ZA	258	
1	ZB	258	
1	ZC	258	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 109936 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
			Total	C	N	O		
1	A	133	661	395	133	133	0	0
1	B	219	1086	648	219	219	0	0
1	C	219	1086	648	219	219	0	0
1	D	219	1086	648	219	219	0	0
1	E	219	1086	648	219	219	0	0
1	F	218	1081	645	218	218	0	0
1	G	158	785	469	158	158	0	0
1	H	133	661	395	133	133	0	0
1	I	219	1086	648	219	219	0	0
1	J	219	1086	648	219	219	0	0
1	K	219	1086	648	219	219	0	0
1	L	219	1086	648	219	219	0	0
1	M	218	1081	645	218	218	0	0
1	N	158	785	469	158	158	0	0
1	O	133	661	395	133	133	0	0
1	P	219	1086	648	219	219	0	0
1	Q	219	1086	648	219	219	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	219	Total 1086	C 648	N 219	O 219	0	0
1	S	219	Total 1086	C 648	N 219	O 219	0	0
1	T	218	Total 1081	C 645	N 218	O 218	0	0
1	V	158	Total 785	C 469	N 158	O 158	0	0
1	W	133	Total 661	C 395	N 133	O 133	0	0
1	X	219	Total 1086	C 648	N 219	O 219	0	0
1	Y	219	Total 1086	C 648	N 219	O 219	0	0
1	Z	219	Total 1086	C 648	N 219	O 219	0	0
1	AA	219	Total 1086	C 648	N 219	O 219	0	0
1	BA	218	Total 1081	C 645	N 218	O 218	0	0
1	CA	158	Total 785	C 469	N 158	O 158	0	0
1	DA	133	Total 661	C 395	N 133	O 133	0	0
1	EA	219	Total 1086	C 648	N 219	O 219	0	0
1	FA	219	Total 1086	C 648	N 219	O 219	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	218	Total 1081	C 645	N 218	O 218	0	0
1	JA	158	Total 785	C 469	N 158	O 158	0	0
1	KA	133	Total 661	C 395	N 133	O 133	0	0
1	LA	219	Total 1086	C 648	N 219	O 219	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
			Total	C	N	O		
1	NA	219	1086	648	219	219	0	0
1	OA	219	1086	648	219	219	0	0
1	PA	218	1081	645	218	218	0	0
1	QA	158	785	469	158	158	0	0
1	RA	133	661	395	133	133	0	0
1	SA	219	1086	648	219	219	0	0
1	TA	219	1086	648	219	219	0	0
1	UA	219	1086	648	219	219	0	0
1	VA	219	1086	648	219	219	0	0
1	WA	218	1081	645	218	218	0	0
1	XA	158	785	469	158	158	0	0
1	YA	133	661	395	133	133	0	0
1	ZA	219	1086	648	219	219	0	0
1	AB	219	1086	648	219	219	0	0
1	BB	219	1086	648	219	219	0	0
1	CB	219	1086	648	219	219	0	0
1	DB	218	1081	645	218	218	0	0
1	EB	158	785	469	158	158	0	0
1	FB	133	661	395	133	133	0	0
1	GB	219	1086	648	219	219	0	0
1	HB	219	1086	648	219	219	0	0

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

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	DC	219	1086	648	219	219	0	0
1	EC	219	1086	648	219	219	0	0
1	FC	218	1081	645	218	218	0	0
1	GC	158	785	469	158	158	0	0
1	HC	133	661	395	133	133	0	0
1	IC	219	1086	648	219	219	0	0
1	JC	219	1086	648	219	219	0	0
1	KC	219	1086	648	219	219	0	0
1	LC	219	1086	648	219	219	0	0
1	MC	218	1081	645	218	218	0	0
1	NC	158	785	469	158	158	0	0
1	OC	133	661	395	133	133	0	0
1	PC	219	1086	648	219	219	0	0
1	QC	219	1086	648	219	219	0	0
1	RC	219	1086	648	219	219	0	0
1	SC	219	1086	648	219	219	0	0
1	TC	218	1081	645	218	218	0	0
1	UC	158	785	469	158	158	0	0
1	VC	133	661	395	133	133	0	0
1	WC	219	1086	648	219	219	0	0
1	XC	219	1086	648	219	219	0	0

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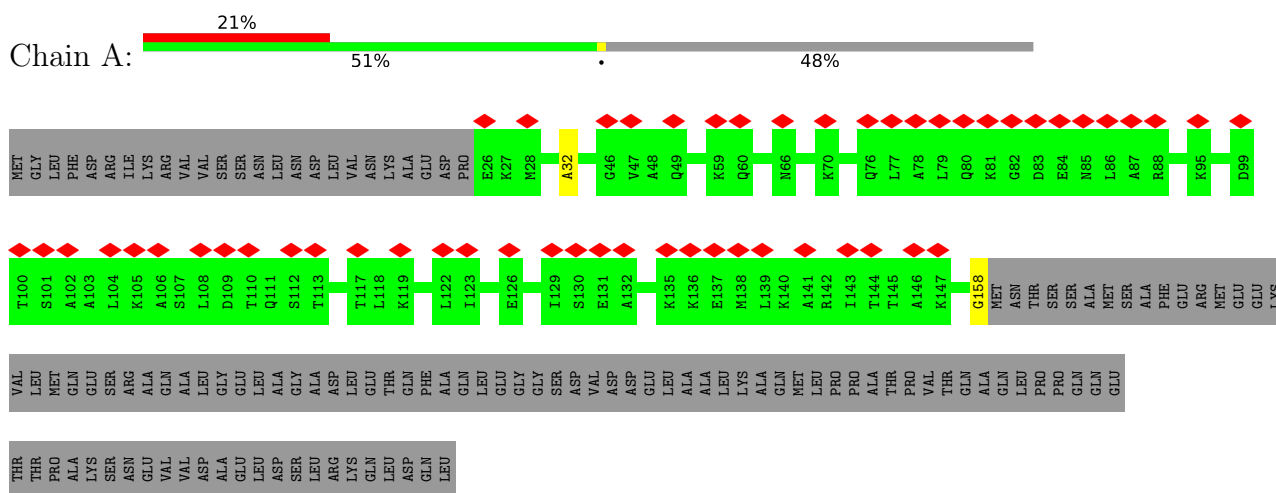
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	YC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	ZC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	AD	218	Total	C	N	O	0	0
			1081	645	218	218		
1	BD	158	Total	C	N	O	0	0
			785	469	158	158		
1	CD	133	Total	C	N	O	0	0
			661	395	133	133		
1	DD	219	Total	C	N	O	0	0
			1086	648	219	219		
1	ED	219	Total	C	N	O	0	0
			1086	648	219	219		
1	FD	219	Total	C	N	O	0	0
			1086	648	219	219		
1	GD	219	Total	C	N	O	0	0
			1086	648	219	219		
1	HD	218	Total	C	N	O	0	0
			1081	645	218	218		
1	ID	158	Total	C	N	O	0	0
			785	469	158	158		

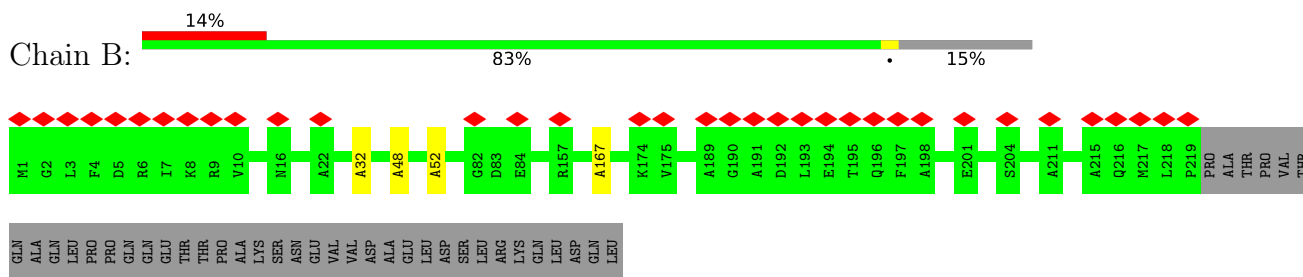
3 Residue-property plots [i](#)

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.

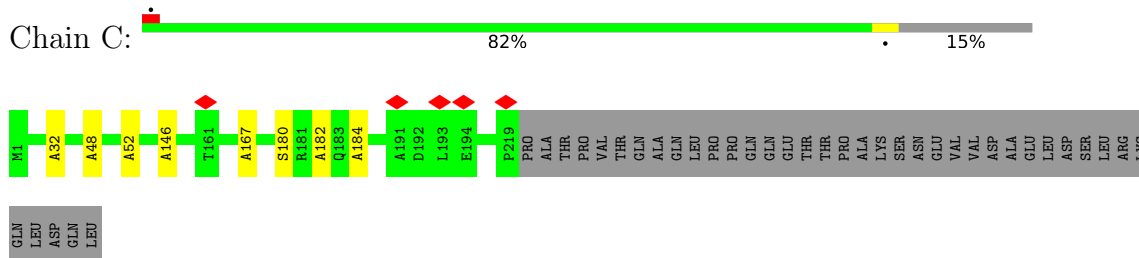
- Molecule 1: vipp1



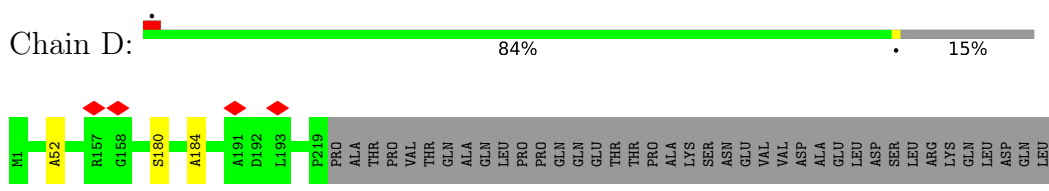
- Molecule 1: vipp1



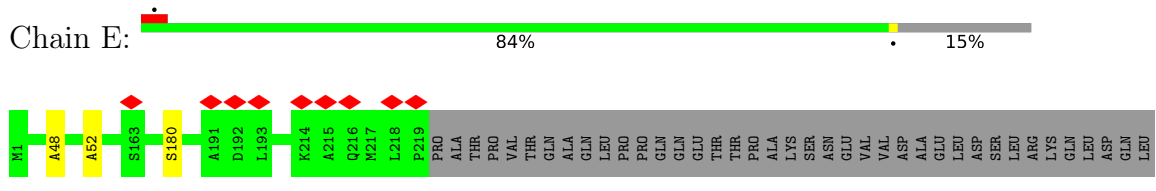
- Molecule 1: vipp1



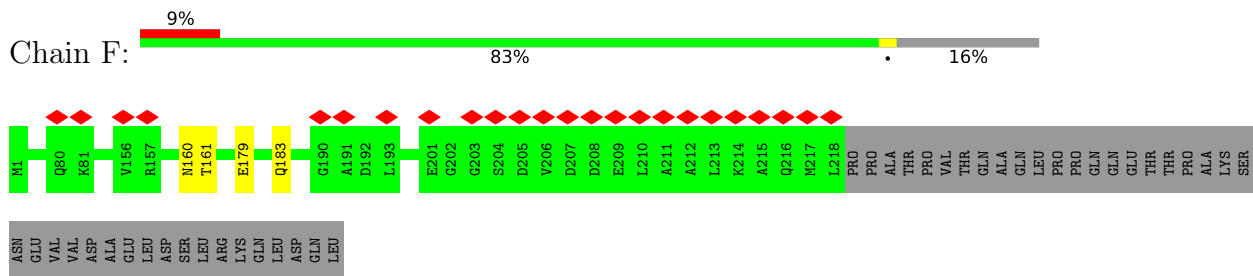
- Molecule 1: vipp1



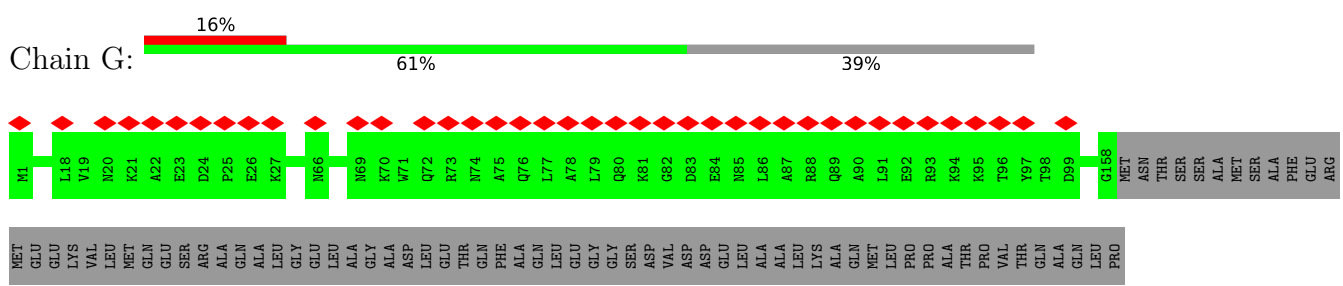
• Molecule 1: vipp1



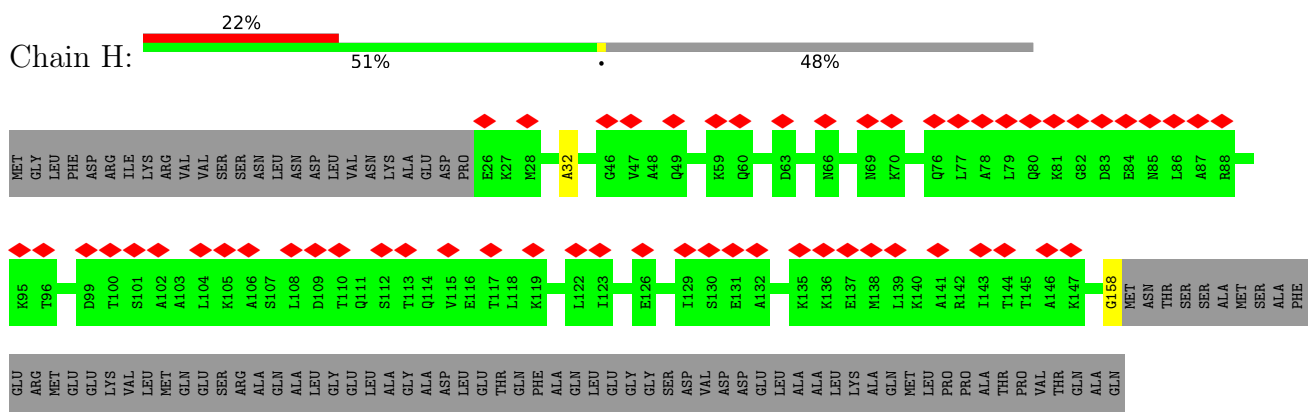
• Molecule 1: vipp1



• Molecule 1: vipp1

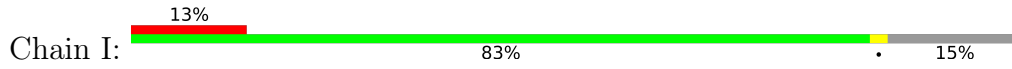


• Molecule 1: vipp1



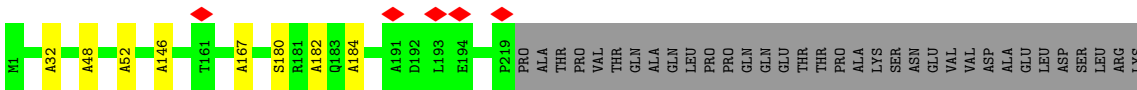
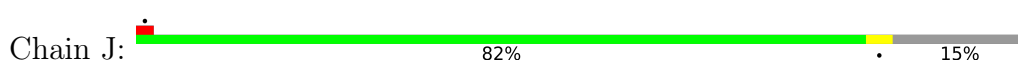
LEU PRO PRO GLN GLU THR THR PRO PRO LYS LYS SER ASN GLU VAL VAL ASP ALA GLU LEU ASP SER LEU SER LEU ARG LYS GLN LEU ASP ASP GLN LEU

• Molecule 1: vipp1



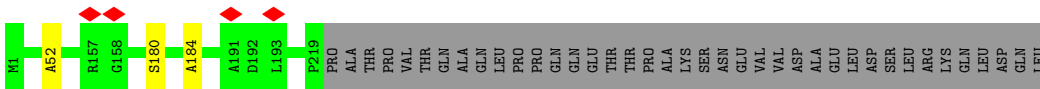
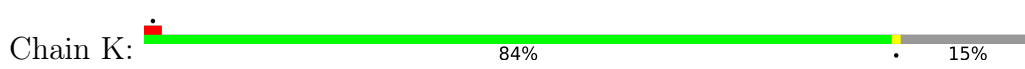
PRO PRO GLN GLU THR THR PRO PRO LYS LYS SER ASN GLU VAL VAL ASP ALA GLU LEU ASP SER LEU SER LEU ARG LYS GLN LEU ASP ASP GLN LEU

• Molecule 1: vipp1

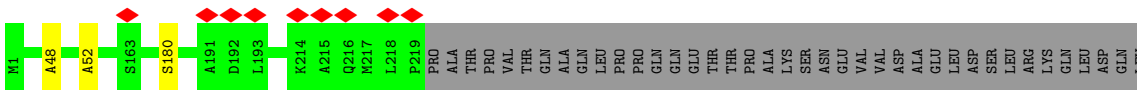
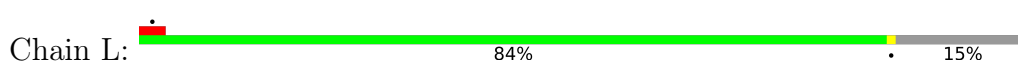


GLN LEU ASP GLN LEU

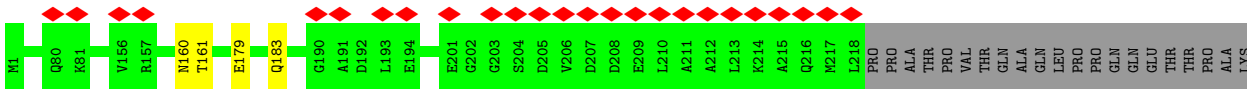
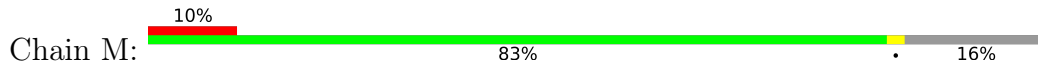
• Molecule 1: vipp1



• Molecule 1: vipp1

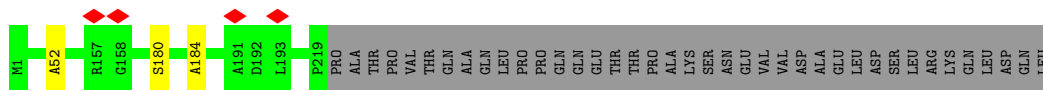


• Molecule 1: vipp1

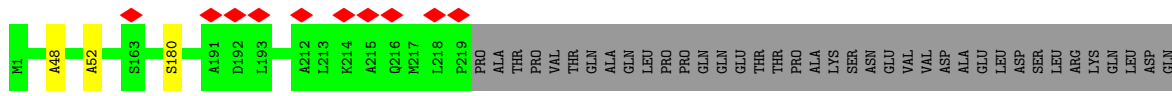
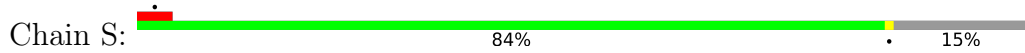


SER ASN GLU VAL VAL ASP ALA GLU LEU ASP SER ASP ARG LYS GLN LEU ASP GLN LEU

• Molecule 1: vipp1

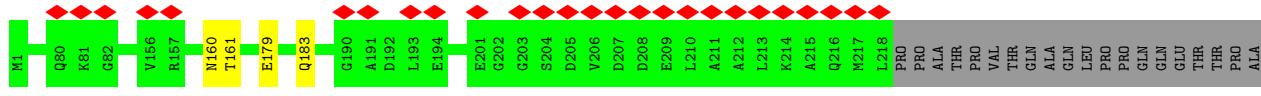
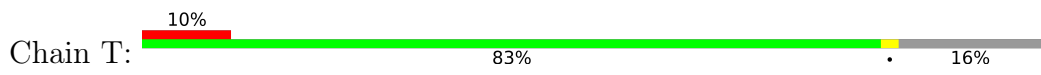


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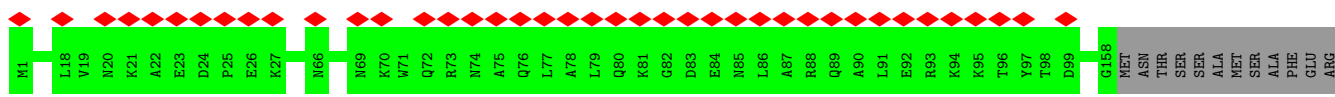
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• Molecule 1: vipp1



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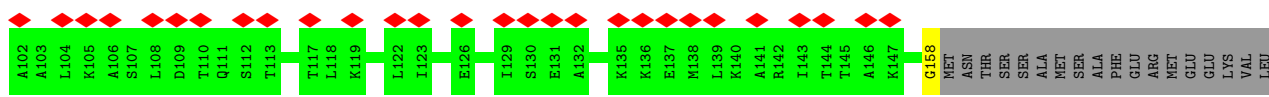
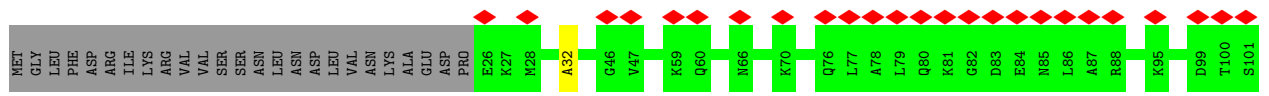
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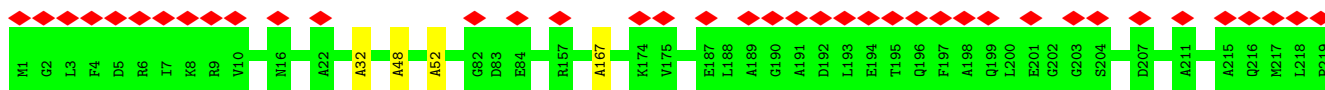
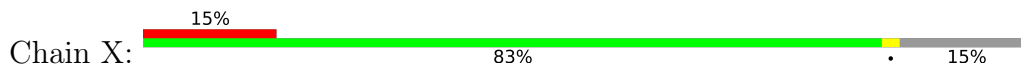
• Molecule 1: vipp1



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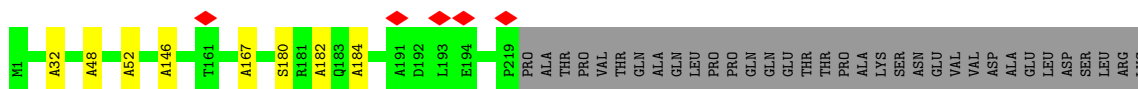
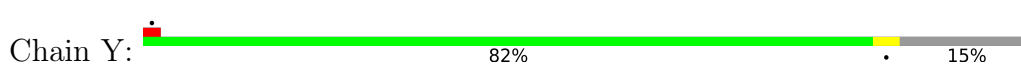
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• Molecule 1: vipp1



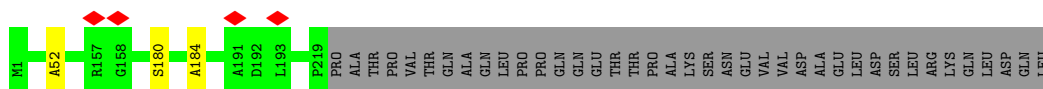
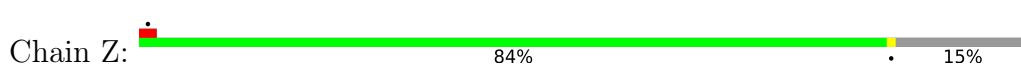
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• Molecule 1: vipp1

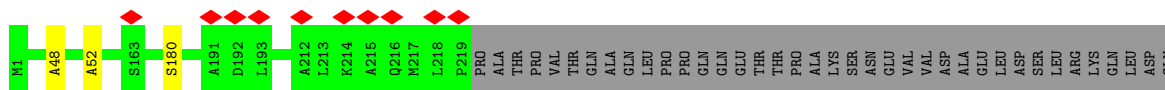
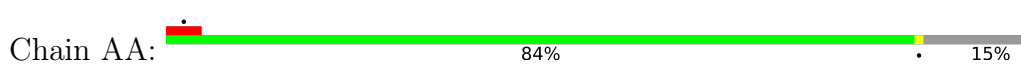


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• Molecule 1: vipp1

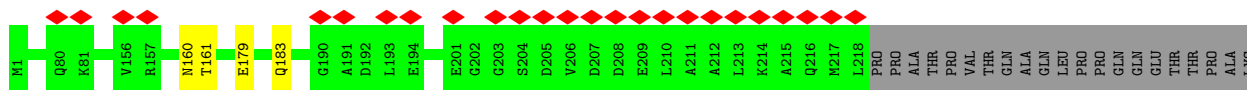
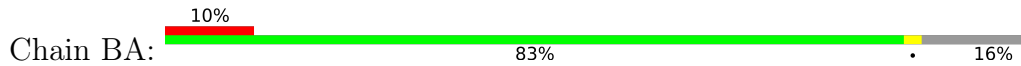


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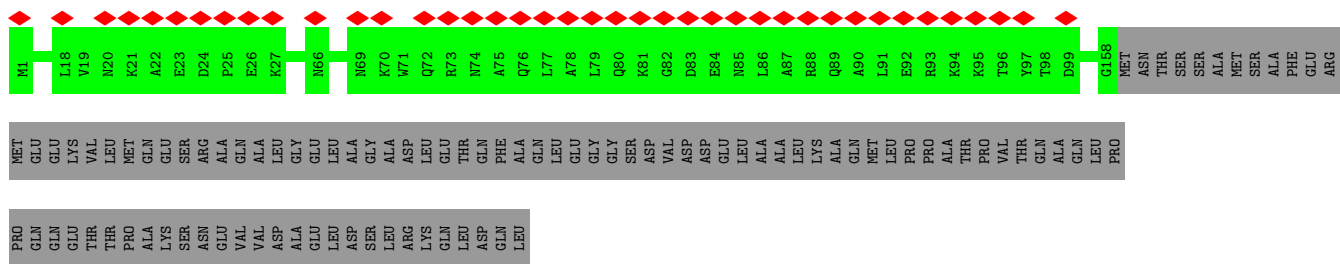
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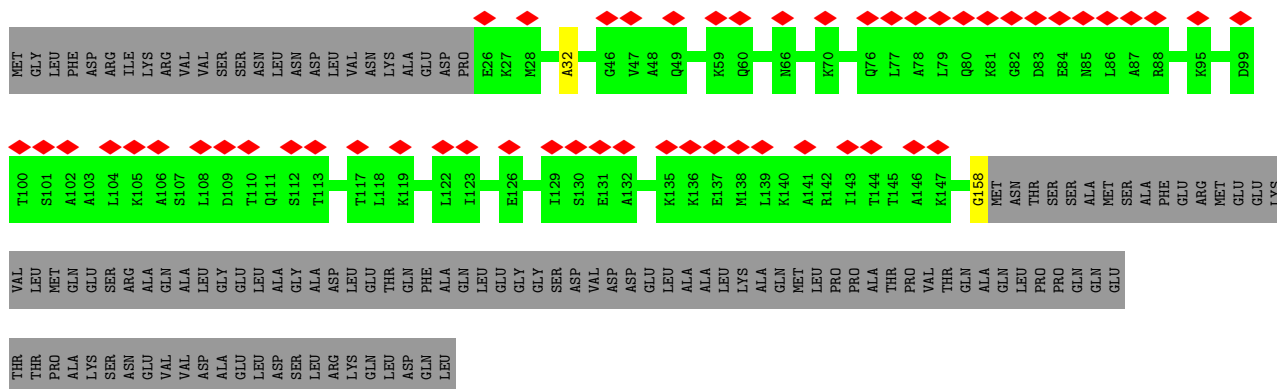


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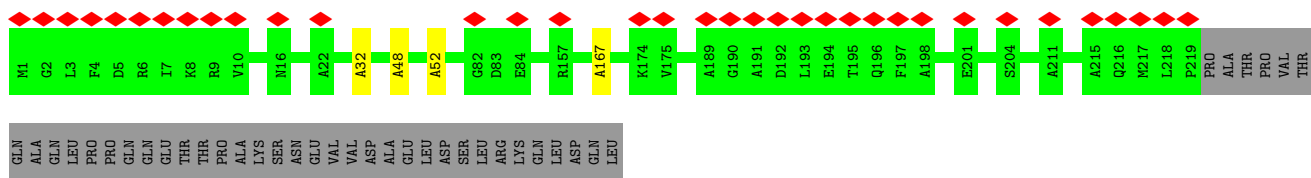
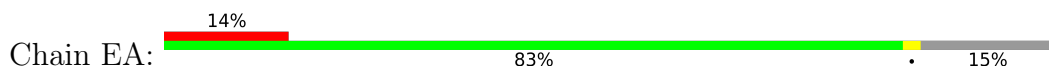
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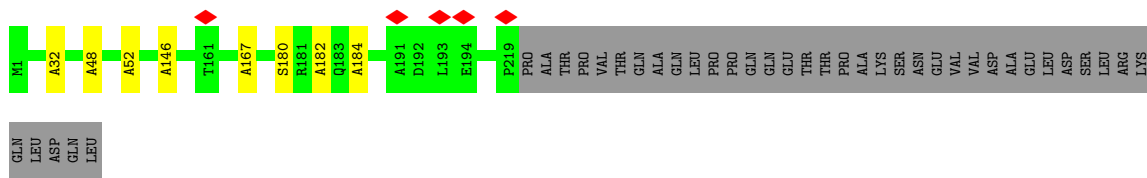
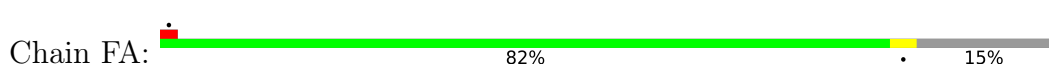
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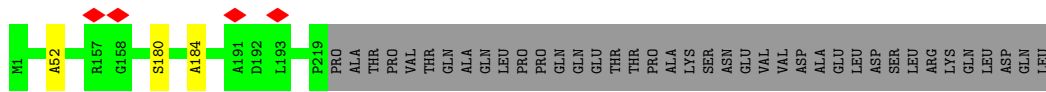
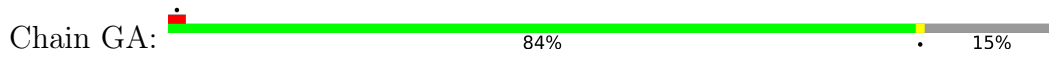
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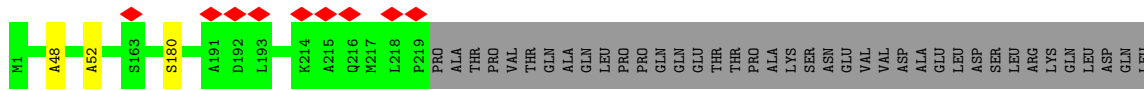
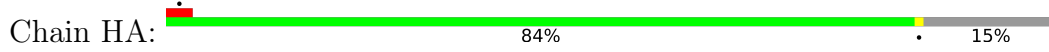
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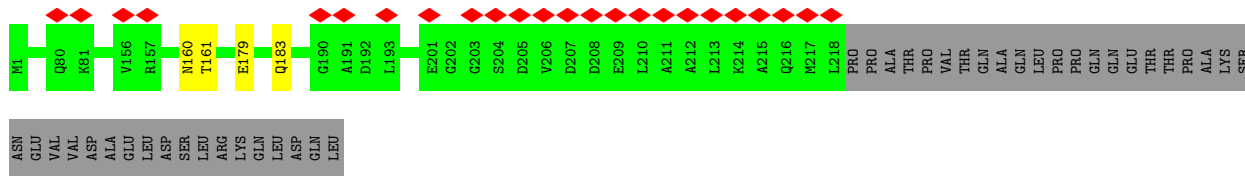
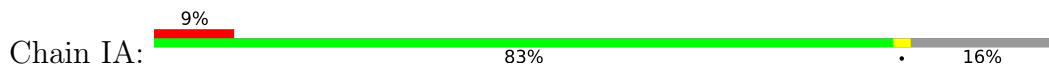
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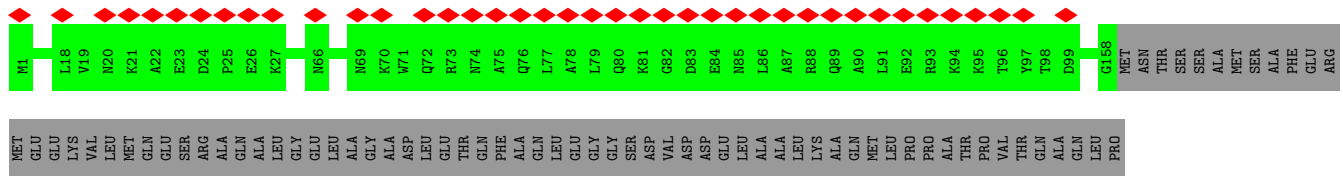
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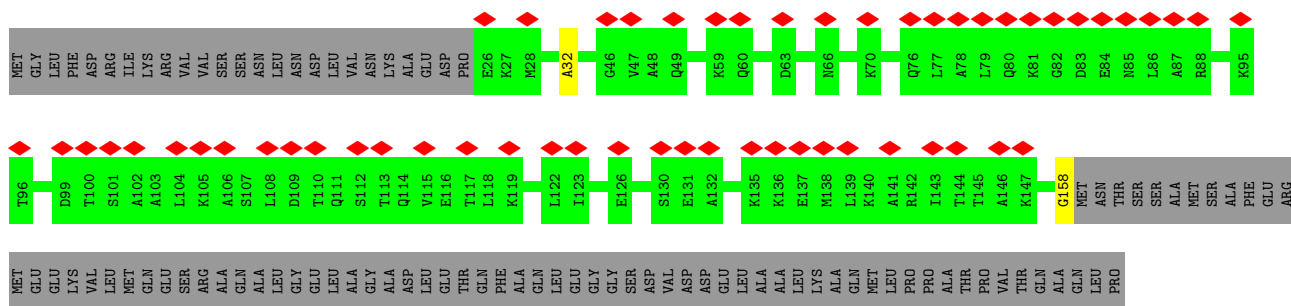
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• Molecule 1: vipp1

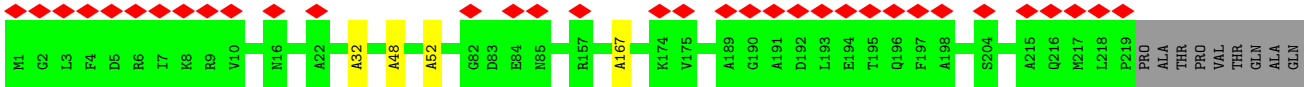
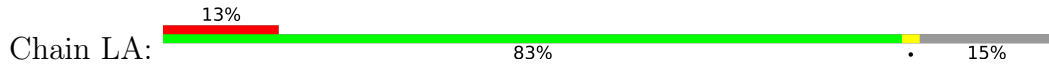


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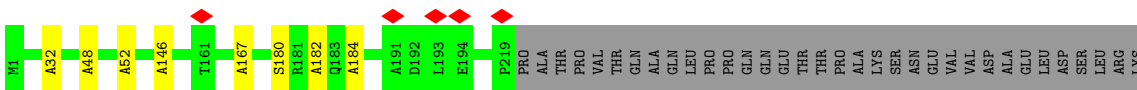
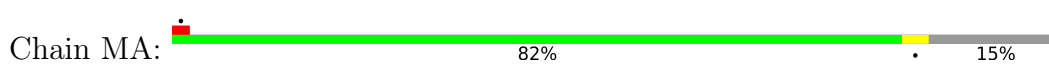
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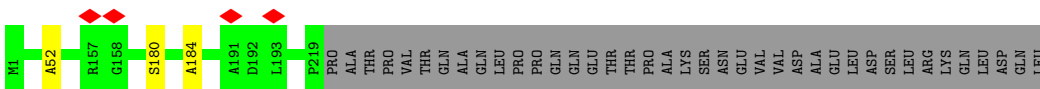
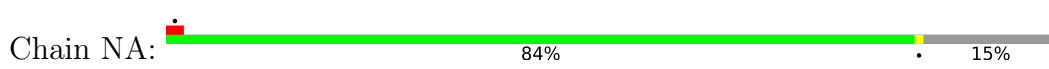
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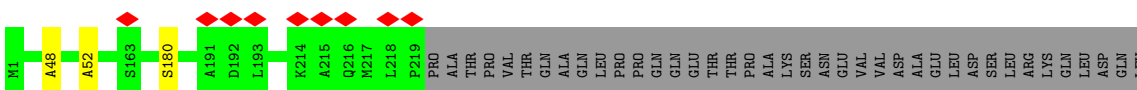
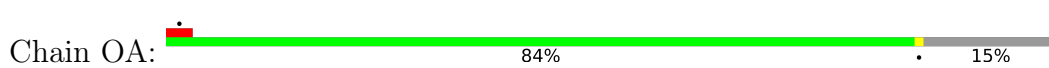


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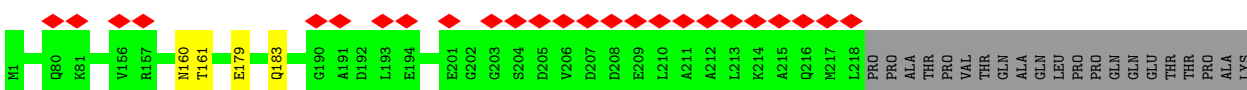
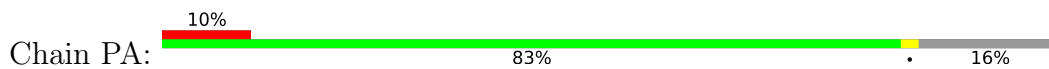
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• Molecule 1: vipp1

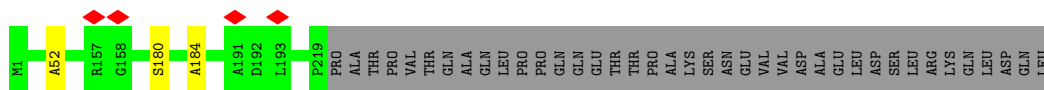
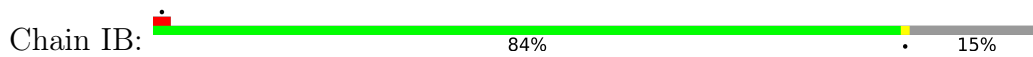


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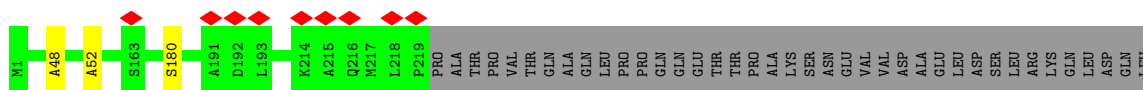
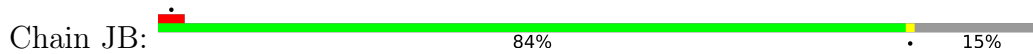


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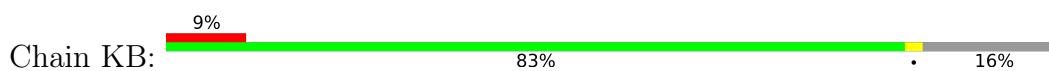
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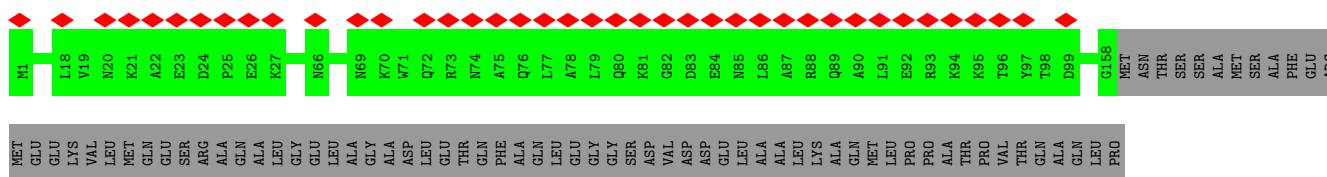
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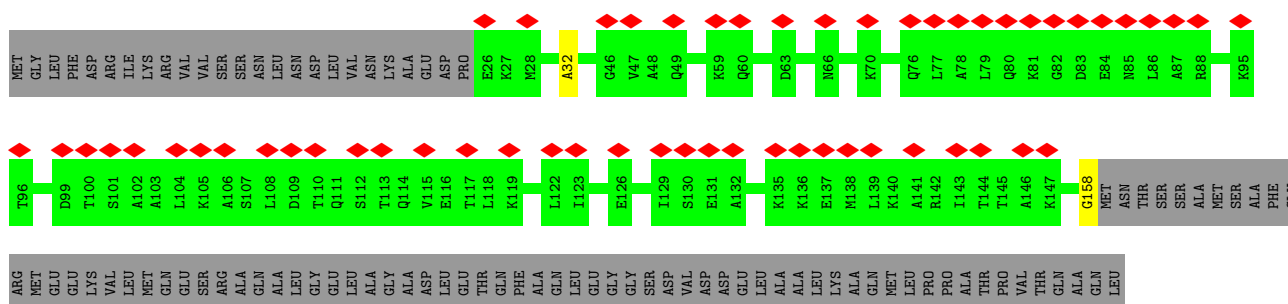
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• Molecule 1: vipp1

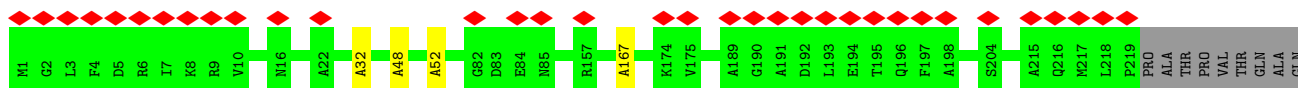
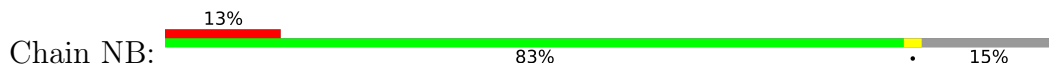


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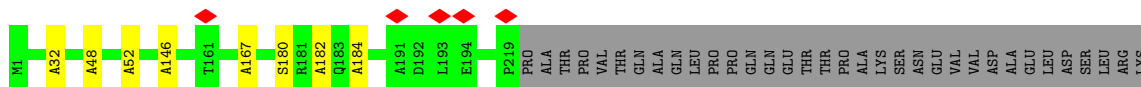
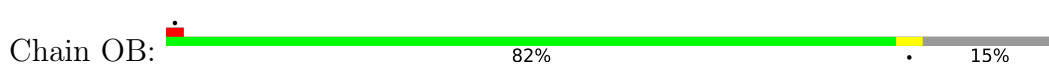
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• Molecule 1: vipp1



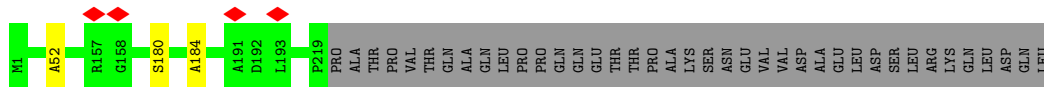
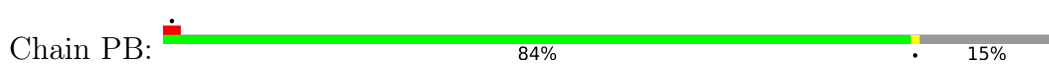
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• Molecule 1: vipp1

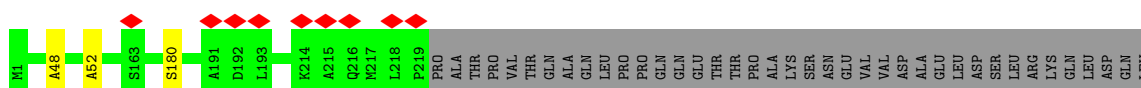
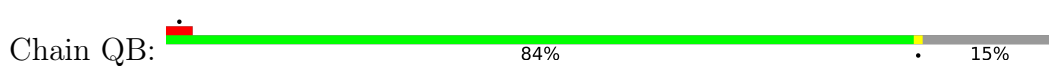


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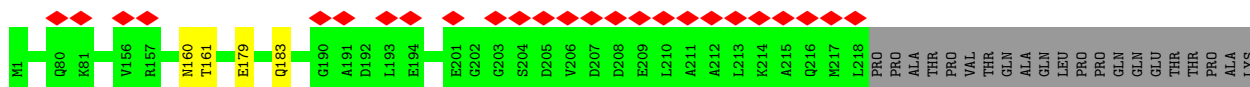
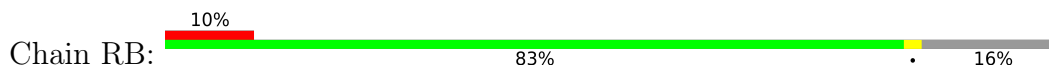
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• Molecule 1: vipp1

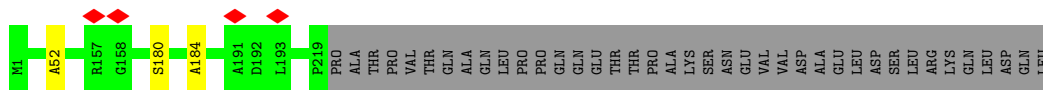


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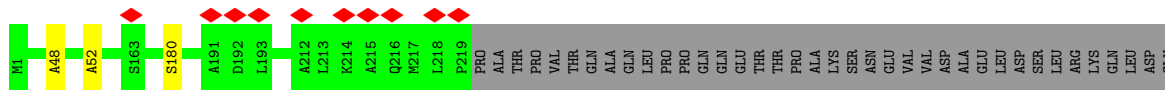
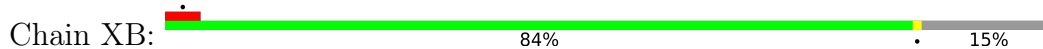


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• Molecule 1: vipp1

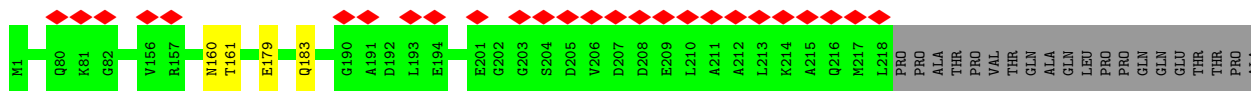
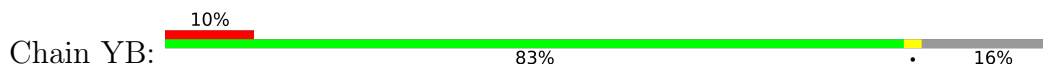


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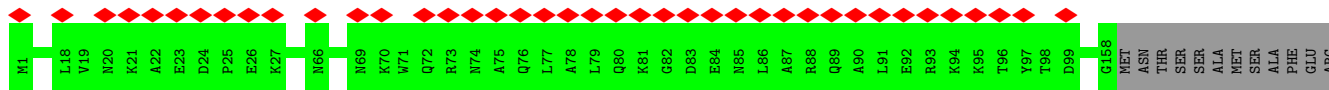
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• Molecule 1: vipp1



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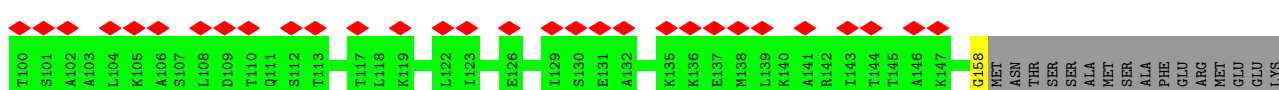
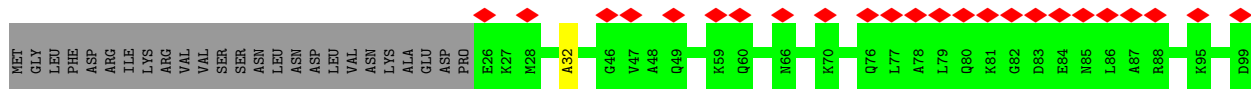
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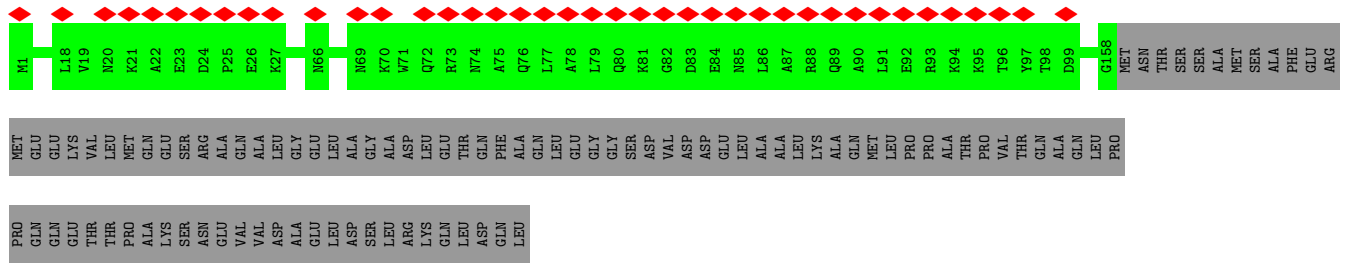
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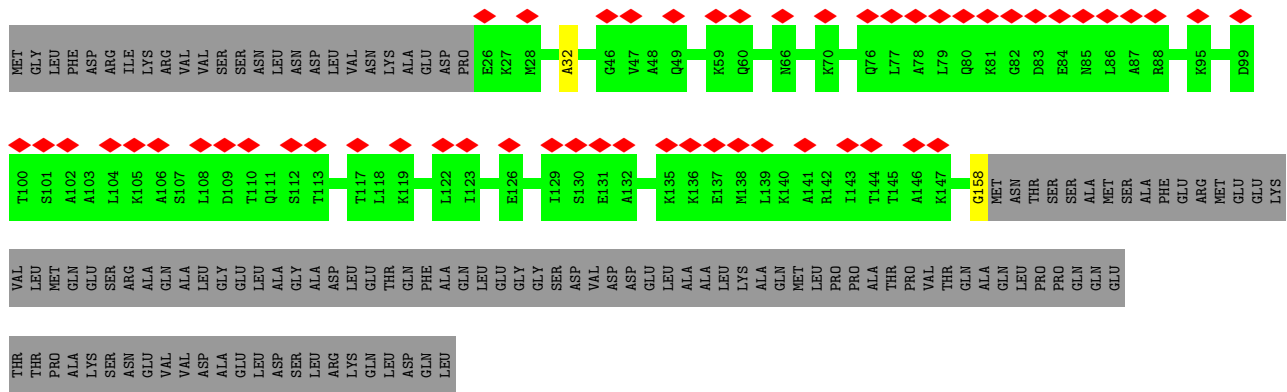


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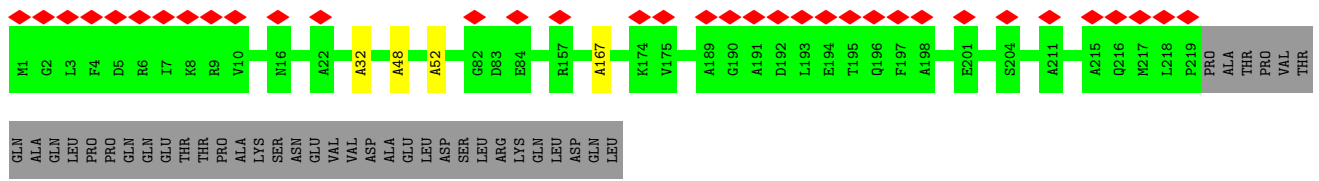
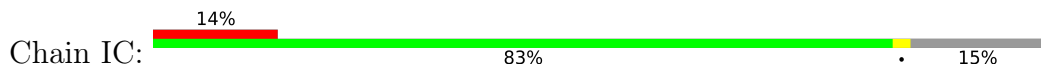
• Molecule 1: vipp1



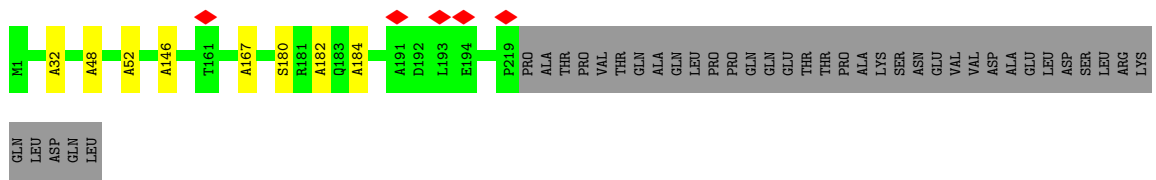
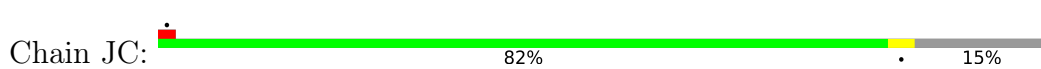
• Molecule 1: vipp1



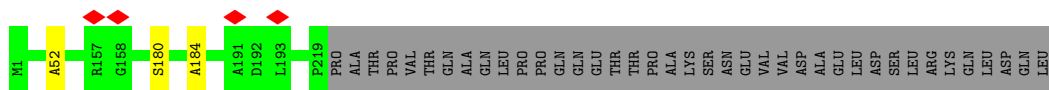
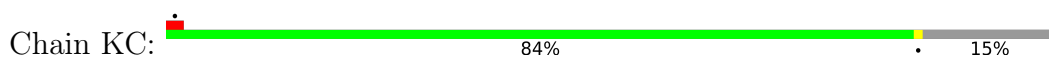
• Molecule 1: vipp1



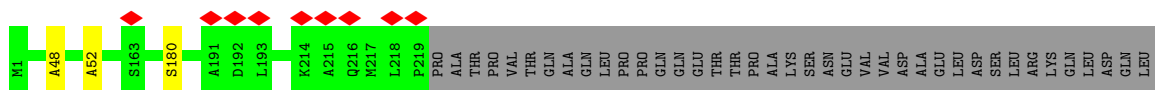
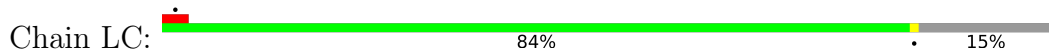
• Molecule 1: vipp1



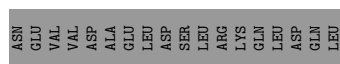
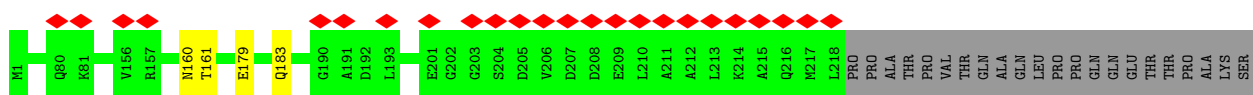
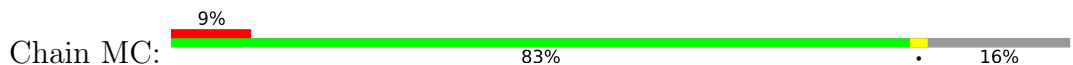
• Molecule 1: vipp1



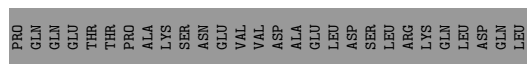
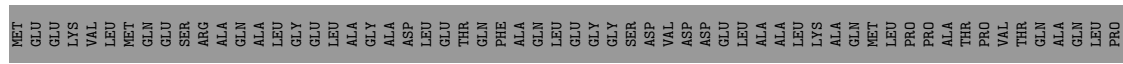
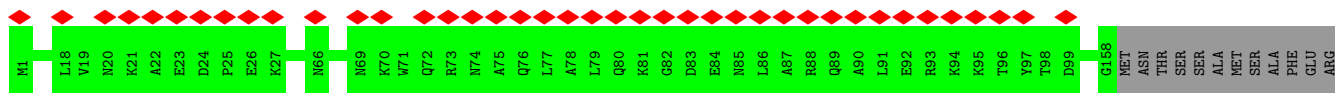
• Molecule 1: vipp1



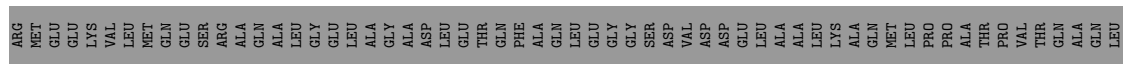
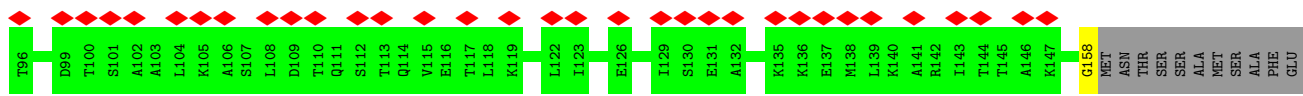
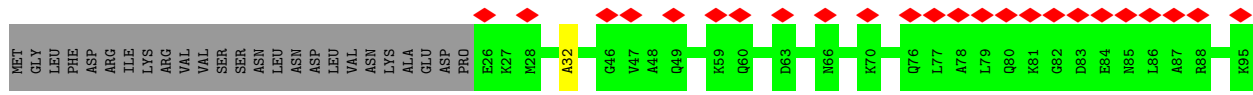
• Molecule 1: vipp1



• Molecule 1: vipp1

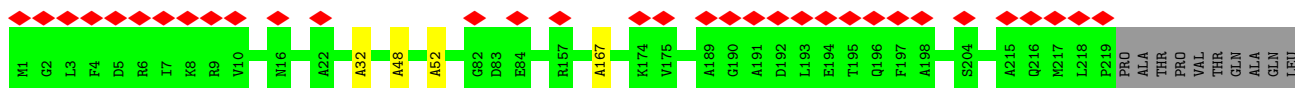
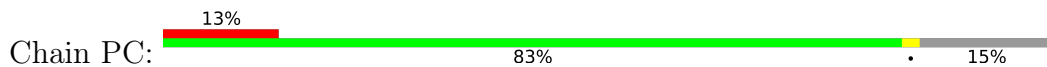


• Molecule 1: vipp1



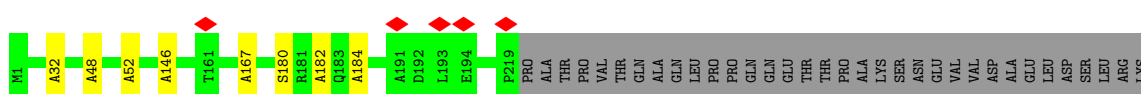
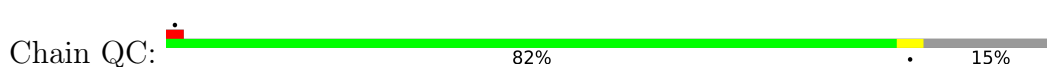
PRO PRO GLN GLN THR THR PRO PRO ALA LYS SER SER ASN GLU VAL VAL ASP ALA ALA GLU LEU LEU ASP ASP SER SER ARG LYS GLN LEU LEU ASP GLN LEU

• Molecule 1: vipp1



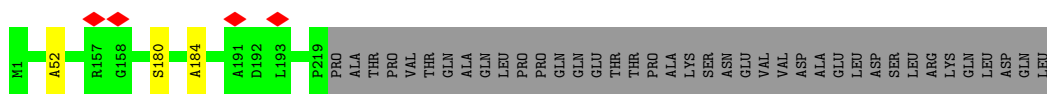
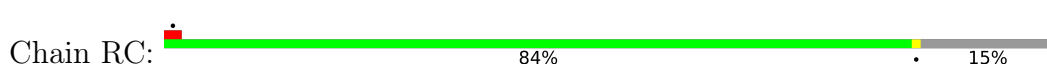
PRO PRO GLN GLN THR THR PRO PRO ALA LYS SER SER ASN GLU VAL VAL ASP ALA ALA GLU LEU LEU ASP ASP SER SER ARG LYS GLN LEU LEU ASP GLN LEU

• Molecule 1: vipp1

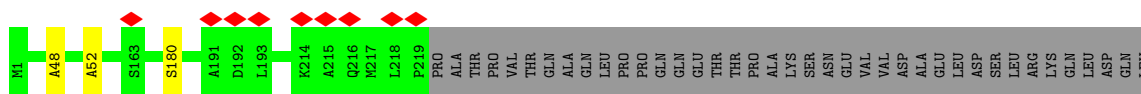
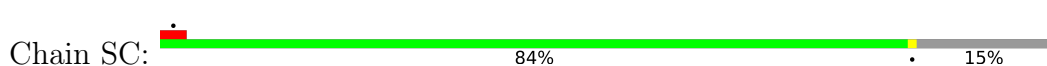


GLN LEU ASP GLN LEU

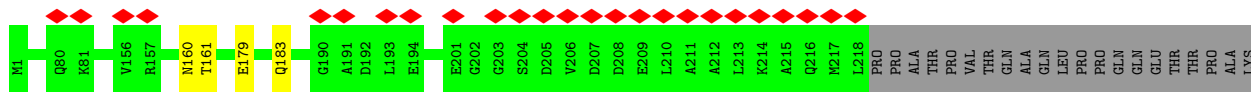
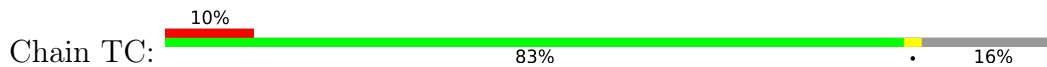
• Molecule 1: vipp1



• Molecule 1: vipp1



• Molecule 1: vipp1

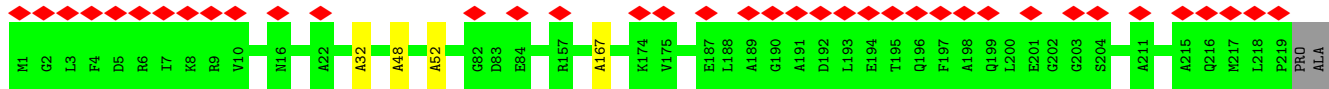
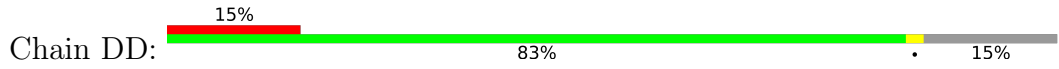


SER ASN GLU VAL VAL ASP ALA GLU LEU LEU ASP ASP SER SER LEU LEU ARG LYS GLN LEU LEU ASP ASP GLN LEU

• Molecule 1: vipp1

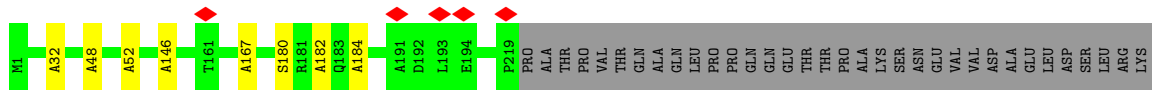
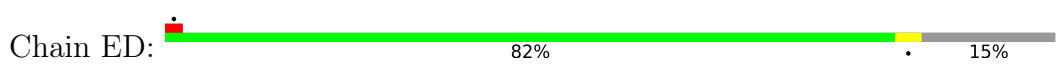
PRO
ALA
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VAL
ASP
ALA
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ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: vipp1



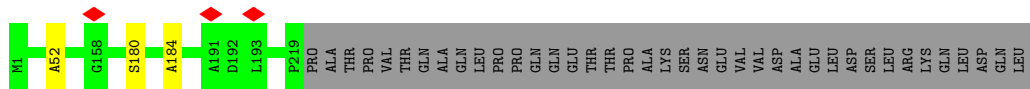
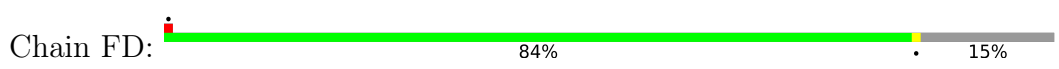
THR
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THR
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ALA
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PRO
GLN
GLN
THR
THR
PRO
ALA
LYS
SER
ASN
GLU
VAL
VAL
ASP
ALA
GLU
LEU
ASP
SER
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: vipp1

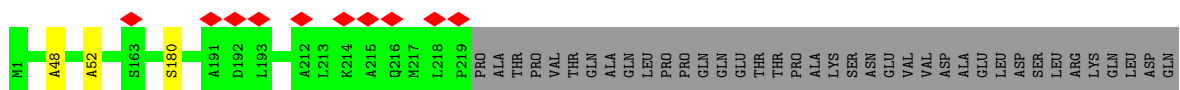
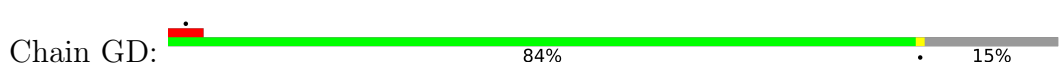


GLN
LEU
ASP
GLN
LEU

• Molecule 1: vipp1

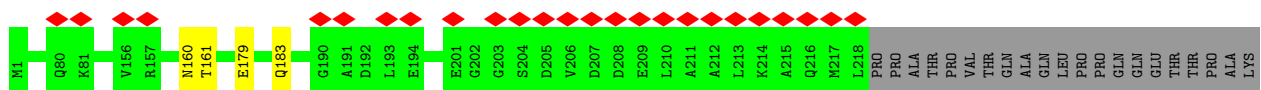
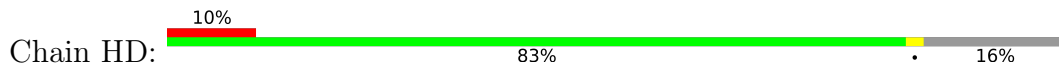


• Molecule 1: vipp1



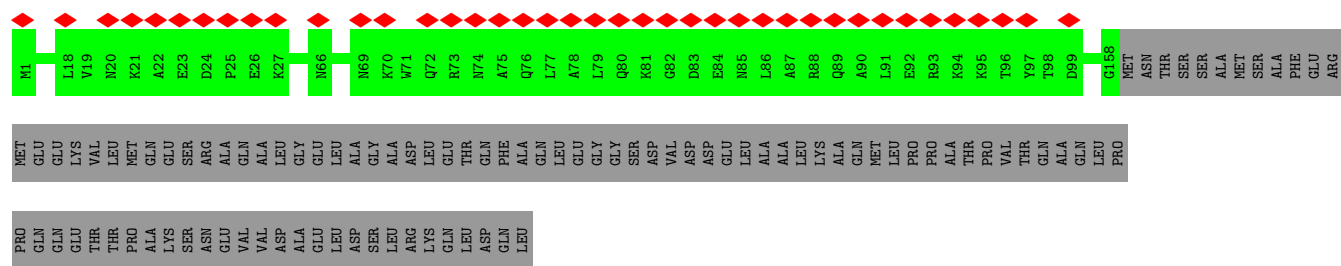
LEU

• Molecule 1: vipp1



SER
ASN
GLU
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ASP
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LEU
ASP
SER
SER
ARG
LYS
GLN
LEU
LEU
ASP
GLN
LEU

● Molecule 1: vipp1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7017	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	0.036	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (\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 (\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	0.18	0/660	0.37	0/920
1	AA	0.19	0/1085	0.40	0/1512
1	AB	0.19	0/1085	0.39	0/1512
1	AC	0.18	0/660	0.37	0/920
1	AD	0.21	0/1080	0.42	0/1505
1	B	0.19	0/1085	0.41	0/1512
1	BA	0.21	0/1080	0.42	0/1505
1	BB	0.19	0/1085	0.44	0/1512
1	BC	0.19	0/1085	0.41	0/1512
1	BD	0.18	0/784	0.37	0/1093
1	C	0.19	0/1085	0.39	0/1512
1	CA	0.18	0/784	0.37	0/1093
1	CB	0.19	0/1085	0.40	0/1512
1	CC	0.19	0/1085	0.39	0/1512
1	CD	0.18	0/660	0.37	0/920
1	D	0.19	0/1085	0.44	0/1512
1	DA	0.18	0/660	0.37	0/920
1	DB	0.21	0/1080	0.42	0/1505
1	DC	0.19	0/1085	0.44	0/1512
1	DD	0.19	0/1085	0.41	0/1512
1	E	0.19	0/1085	0.40	0/1512
1	EA	0.19	0/1085	0.41	0/1512
1	EB	0.18	0/784	0.37	0/1093
1	EC	0.19	0/1085	0.40	0/1512
1	ED	0.19	0/1085	0.39	0/1512
1	F	0.21	0/1080	0.42	0/1505
1	FA	0.19	0/1085	0.39	0/1512
1	FB	0.18	0/660	0.37	0/920
1	FC	0.21	0/1080	0.42	0/1505
1	FD	0.19	0/1085	0.44	0/1512
1	G	0.18	0/784	0.37	0/1093
1	GA	0.19	0/1085	0.44	0/1512
1	GB	0.19	0/1085	0.41	0/1512
1	GC	0.18	0/784	0.37	0/1093

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GD	0.19	0/1085	0.40	0/1512
1	H	0.19	0/660	0.37	0/920
1	HA	0.19	0/1085	0.40	0/1512
1	HB	0.19	0/1085	0.39	0/1512
1	HC	0.18	0/660	0.37	0/920
1	HD	0.21	0/1080	0.42	0/1505
1	I	0.19	0/1085	0.41	0/1512
1	IA	0.21	0/1080	0.42	0/1505
1	IB	0.19	0/1085	0.44	0/1512
1	IC	0.19	0/1085	0.41	0/1512
1	ID	0.18	0/784	0.37	0/1093
1	J	0.19	0/1085	0.39	0/1512
1	JA	0.18	0/784	0.37	0/1093
1	JB	0.19	0/1085	0.40	0/1512
1	JC	0.19	0/1085	0.39	0/1512
1	K	0.19	0/1085	0.44	0/1512
1	KA	0.19	0/660	0.37	0/920
1	KB	0.21	0/1080	0.42	0/1505
1	KC	0.19	0/1085	0.44	0/1512
1	L	0.19	0/1085	0.40	0/1512
1	LA	0.19	0/1085	0.41	0/1512
1	LB	0.18	0/784	0.37	0/1093
1	LC	0.19	0/1085	0.40	0/1512
1	M	0.21	0/1080	0.42	0/1505
1	MA	0.19	0/1085	0.39	0/1512
1	MB	0.18	0/660	0.37	0/920
1	MC	0.21	0/1080	0.42	0/1505
1	N	0.18	0/784	0.37	0/1093
1	NA	0.19	0/1085	0.44	0/1512
1	NB	0.19	0/1085	0.41	0/1512
1	NC	0.18	0/784	0.37	0/1093
1	O	0.18	0/660	0.37	0/920
1	OA	0.19	0/1085	0.40	0/1512
1	OB	0.19	0/1085	0.39	0/1512
1	OC	0.18	0/660	0.37	0/920
1	P	0.19	0/1085	0.41	0/1512
1	PA	0.21	0/1080	0.42	0/1505
1	PB	0.19	0/1085	0.44	0/1512
1	PC	0.19	0/1085	0.41	0/1512
1	Q	0.19	0/1085	0.39	0/1512
1	QA	0.18	0/784	0.37	0/1093
1	QB	0.19	0/1085	0.40	0/1512
1	QC	0.19	0/1085	0.39	0/1512

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	R	0.19	0/1085	0.44	0/1512
1	RA	0.18	0/660	0.37	0/920
1	RB	0.21	0/1080	0.42	0/1505
1	RC	0.19	0/1085	0.44	0/1512
1	S	0.19	0/1085	0.40	0/1512
1	SA	0.19	0/1085	0.41	0/1512
1	SB	0.18	0/784	0.37	0/1093
1	SC	0.19	0/1085	0.40	0/1512
1	T	0.21	0/1080	0.42	0/1505
1	TA	0.19	0/1085	0.39	0/1512
1	TB	0.18	0/660	0.37	0/920
1	TC	0.21	0/1080	0.42	0/1505
1	UA	0.19	0/1085	0.44	0/1512
1	UB	0.19	0/1085	0.41	0/1512
1	UC	0.18	0/784	0.37	0/1093
1	V	0.18	0/784	0.37	0/1093
1	VA	0.19	0/1085	0.40	0/1512
1	VB	0.19	0/1085	0.39	0/1512
1	VC	0.18	0/660	0.37	0/920
1	W	0.18	0/660	0.37	0/920
1	WA	0.21	0/1080	0.42	0/1505
1	WB	0.19	0/1085	0.44	0/1512
1	WC	0.19	0/1085	0.41	0/1512
1	X	0.19	0/1085	0.41	0/1512
1	XA	0.18	0/784	0.37	0/1093
1	XB	0.19	0/1085	0.40	0/1512
1	XC	0.19	0/1085	0.39	0/1512
1	Y	0.19	0/1085	0.39	0/1512
1	YA	0.18	0/660	0.37	0/920
1	YB	0.21	0/1080	0.42	0/1505
1	YC	0.19	0/1085	0.44	0/1512
1	Z	0.19	0/1085	0.44	0/1512
1	ZA	0.19	0/1085	0.41	0/1512
1	ZB	0.18	0/784	0.37	0/1093
1	ZC	0.19	0/1085	0.40	0/1512
All	All	0.19	0/109824	0.40	0/153056

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	661	0	320	6	0
1	AA	1086	0	531	6	0
1	AB	1086	0	531	10	0
1	AC	661	0	320	6	0
1	AD	1081	0	530	4	0
1	B	1086	0	531	6	0
1	BA	1081	0	530	5	0
1	BB	1086	0	531	5	0
1	BC	1086	0	531	6	0
1	BD	785	0	376	0	0
1	C	1086	0	531	10	0
1	CA	785	0	376	0	0
1	CB	1086	0	531	6	0
1	CC	1086	0	531	10	0
1	CD	661	0	320	6	0
1	D	1086	0	531	5	0
1	DA	661	0	320	6	0
1	DB	1081	0	530	4	0
1	DC	1086	0	531	5	0
1	DD	1086	0	531	6	0
1	E	1086	0	531	6	0
1	EA	1086	0	531	6	0
1	EB	785	0	376	0	0
1	EC	1086	0	531	6	0
1	ED	1086	0	531	10	0
1	F	1081	0	530	4	0
1	FA	1086	0	531	10	0
1	FB	661	0	320	6	0
1	FC	1081	0	530	4	0
1	FD	1086	0	531	5	0
1	G	785	0	376	0	0
1	GA	1086	0	531	5	0
1	GB	1086	0	531	6	0
1	GC	785	0	376	0	0
1	GD	1086	0	531	6	0
1	H	661	0	320	6	0
1	HA	1086	0	531	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HB	1086	0	531	10	0
1	HC	661	0	320	6	0
1	HD	1081	0	530	4	0
1	I	1086	0	531	6	0
1	IA	1081	0	530	4	0
1	IB	1086	0	531	5	0
1	IC	1086	0	531	6	0
1	ID	785	0	376	0	0
1	J	1086	0	531	10	0
1	JA	785	0	376	0	0
1	JB	1086	0	531	6	0
1	JC	1086	0	531	10	0
1	K	1086	0	531	5	0
1	KA	661	0	320	6	0
1	KB	1081	0	530	5	0
1	KC	1086	0	531	5	0
1	L	1086	0	531	6	0
1	LA	1086	0	531	6	0
1	LB	785	0	376	0	0
1	LC	1086	0	531	6	0
1	M	1081	0	530	4	0
1	MA	1086	0	531	10	0
1	MB	661	0	320	6	0
1	MC	1081	0	530	4	0
1	N	785	0	376	0	0
1	NA	1086	0	531	5	0
1	NB	1086	0	531	6	0
1	NC	785	0	376	0	0
1	O	661	0	320	6	0
1	OA	1086	0	531	7	0
1	OB	1086	0	531	10	0
1	OC	661	0	320	6	0
1	P	1086	0	531	6	0
1	PA	1081	0	530	4	0
1	PB	1086	0	531	5	0
1	PC	1086	0	531	6	0
1	Q	1086	0	531	10	0
1	QA	785	0	376	0	0
1	QB	1086	0	531	6	0
1	QC	1086	0	531	10	0
1	R	1086	0	531	5	0
1	RA	661	0	320	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RB	1081	0	530	4	0
1	RC	1086	0	531	5	0
1	S	1086	0	531	6	0
1	SA	1086	0	531	6	0
1	SB	785	0	376	0	0
1	SC	1086	0	531	6	0
1	T	1081	0	530	4	0
1	TA	1086	0	531	10	0
1	TB	661	0	320	6	0
1	TC	1081	0	530	4	0
1	UA	1086	0	531	5	0
1	UB	1086	0	531	6	0
1	UC	785	0	376	0	0
1	V	785	0	376	0	0
1	VA	1086	0	531	6	0
1	VB	1086	0	531	10	0
1	VC	661	0	320	6	0
1	W	661	0	320	6	0
1	WA	1081	0	530	4	0
1	WB	1086	0	531	5	0
1	WC	1086	0	531	6	0
1	X	1086	0	531	6	0
1	XA	785	0	376	0	0
1	XB	1086	0	531	7	0
1	XC	1086	0	531	10	0
1	Y	1086	0	531	10	0
1	YA	661	0	320	6	0
1	YB	1081	0	530	4	0
1	YC	1086	0	531	5	0
1	Z	1086	0	531	5	0
1	ZA	1086	0	531	6	0
1	ZB	785	0	376	0	0
1	ZC	1086	0	531	6	0
All	All	109936	0	53600	306	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 2.

All (306) 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:MA:184:ALA:CB	1:ZA:48:ALA:HB1	1.85	1.06
1:TA:184:ALA:CB	1:GB:48:ALA:HB1	1.85	1.06
1:JC:184:ALA:CB	1:WC:48:ALA:HB1	1.85	1.06
1:I:48:ALA:HB1	1:ED:184:ALA:CB	1.85	1.05
1:Q:184:ALA:CB	1:EA:48:ALA:HB1	1.85	1.05
1:CC:184:ALA:CB	1:PC:48:ALA:HB1	1.85	1.05
1:QC:184:ALA:CB	1:DD:48:ALA:HB1	1.85	1.05
1:B:48:ALA:HB1	1:XC:184:ALA:CB	1.85	1.05
1:AB:184:ALA:CB	1:NB:48:ALA:HB1	1.85	1.05
1:C:184:ALA:CB	1:P:48:ALA:HB1	1.85	1.05
1:J:184:ALA:CB	1:X:48:ALA:HB1	1.85	1.05
1:VB:184:ALA:CB	1:IC:48:ALA:HB1	1.85	1.05
1:Y:184:ALA:CB	1:LA:48:ALA:HB1	1.85	1.05
1:OB:184:ALA:CB	1:BC:48:ALA:HB1	1.85	1.05
1:FA:184:ALA:CB	1:SA:48:ALA:HB1	1.85	1.04
1:HB:184:ALA:CB	1:UB:48:ALA:HB1	1.85	1.04
1:Y:184:ALA:HB1	1:LA:48:ALA:HB1	1.00	1.00
1:FA:184:ALA:HB1	1:SA:48:ALA:HB1	1.00	1.00
1:FA:184:ALA:HB1	1:SA:48:ALA:CB	1.92	0.99
1:JC:184:ALA:HB1	1:WC:48:ALA:CB	1.92	0.99
1:MA:184:ALA:HB1	1:ZA:48:ALA:CB	1.92	0.99
1:CC:184:ALA:HB1	1:PC:48:ALA:CB	1.92	0.99
1:Y:184:ALA:HB1	1:LA:48:ALA:CB	1.92	0.99
1:QC:184:ALA:HB1	1:DD:48:ALA:CB	1.92	0.99
1:B:48:ALA:CB	1:XC:184:ALA:HB1	1.92	0.99
1:I:48:ALA:CB	1:ED:184:ALA:HB1	1.92	0.99
1:Q:184:ALA:HB1	1:EA:48:ALA:HB1	1.00	0.99
1:VB:184:ALA:HB1	1:IC:48:ALA:CB	1.92	0.99
1:OB:184:ALA:HB1	1:BC:48:ALA:CB	1.92	0.99
1:MA:184:ALA:HB1	1:ZA:48:ALA:HB1	1.00	0.98
1:VB:184:ALA:HB1	1:IC:48:ALA:HB1	1.00	0.98
1:I:48:ALA:HB1	1:ED:184:ALA:HB1	1.00	0.98
1:C:184:ALA:HB1	1:P:48:ALA:CB	1.92	0.98
1:C:184:ALA:HB1	1:P:48:ALA:HB1	1.00	0.98
1:OB:184:ALA:HB1	1:BC:48:ALA:HB1	1.00	0.98
1:QC:184:ALA:HB1	1:DD:48:ALA:HB1	1.01	0.98
1:J:184:ALA:HB1	1:X:48:ALA:CB	1.92	0.98
1:HB:184:ALA:HB1	1:UB:48:ALA:CB	1.92	0.98
1:Q:184:ALA:HB1	1:EA:48:ALA:CB	1.92	0.98
1:CC:184:ALA:HB1	1:PC:48:ALA:HB1	1.00	0.98
1:JC:184:ALA:HB1	1:WC:48:ALA:HB1	1.00	0.98
1:AB:184:ALA:HB1	1:NB:48:ALA:HB1	1.00	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HB:184:ALA:HB1	1:UB:48:ALA:HB1	1.00	0.97
1:TA:184:ALA:HB1	1:GB:48:ALA:CB	1.92	0.97
1:B:48:ALA:HB1	1:XC:184:ALA:HB1	1.00	0.97
1:AB:184:ALA:HB1	1:NB:48:ALA:CB	1.92	0.97
1:J:184:ALA:HB1	1:X:48:ALA:HB1	1.00	0.96
1:TA:184:ALA:HB1	1:GB:48:ALA:HB1	1.00	0.96
1:WA:179:GLU:CB	1:JB:52:ALA:HB1	2.01	0.91
1:DB:179:GLU:CB	1:QB:52:ALA:HB1	2.01	0.91
1:PA:179:GLU:CB	1:CB:52:ALA:HB1	2.01	0.91
1:KB:179:GLU:CB	1:XB:52:ALA:HB1	2.01	0.91
1:BA:179:GLU:CB	1:OA:52:ALA:HB1	2.00	0.91
1:IA:179:GLU:CB	1:VA:52:ALA:HB1	2.01	0.91
1:RB:179:GLU:CB	1:EC:52:ALA:HB1	2.01	0.91
1:YB:179:GLU:CB	1:LC:52:ALA:HB1	2.01	0.91
1:T:179:GLU:CB	1:HA:52:ALA:HB1	2.01	0.91
1:FC:179:GLU:CB	1:SC:52:ALA:HB1	2.01	0.91
1:MC:179:GLU:CB	1:ZC:52:ALA:HB1	2.01	0.91
1:F:179:GLU:CB	1:S:52:ALA:HB1	2.01	0.91
1:M:179:GLU:CB	1:AA:52:ALA:HB1	2.01	0.91
1:E:52:ALA:HB1	1:AD:179:GLU:CB	2.01	0.91
1:L:52:ALA:HB1	1:HD:179:GLU:CB	2.01	0.91
1:TC:179:GLU:CB	1:GD:52:ALA:HB1	2.01	0.91
1:WB:180:SER:CB	1:JC:52:ALA:HB1	2.05	0.87
1:IB:180:SER:CB	1:VB:52:ALA:HB1	2.05	0.86
1:NA:180:SER:CB	1:AB:52:ALA:HB1	2.05	0.86
1:UA:180:SER:CB	1:HB:52:ALA:HB1	2.05	0.86
1:RC:180:SER:CB	1:ED:52:ALA:HB1	2.05	0.86
1:KC:180:SER:CB	1:XC:52:ALA:HB1	2.05	0.86
1:BB:180:SER:CB	1:OB:52:ALA:HB1	2.05	0.86
1:PB:180:SER:CB	1:CC:52:ALA:HB1	2.05	0.86
1:Z:180:SER:CB	1:MA:52:ALA:HB1	2.05	0.86
1:D:180:SER:CB	1:Q:52:ALA:HB1	2.05	0.86
1:DC:180:SER:CB	1:QC:52:ALA:HB1	2.06	0.85
1:R:180:SER:CB	1:FA:52:ALA:HB1	2.05	0.85
1:LC:180:SER:CB	1:YC:52:ALA:CB	2.55	0.85
1:C:52:ALA:HB1	1:YC:180:SER:CB	2.05	0.85
1:J:52:ALA:HB1	1:FD:180:SER:CB	2.05	0.85
1:XB:180:SER:CB	1:KC:52:ALA:CB	2.54	0.85
1:EC:180:SER:CB	1:RC:52:ALA:CB	2.55	0.85
1:GA:180:SER:CB	1:TA:52:ALA:HB1	2.05	0.85
1:SC:180:SER:CB	1:FD:52:ALA:CB	2.54	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:180:SER:CB	1:NA:52:ALA:CB	2.54	0.85
1:L:180:SER:CB	1:Z:52:ALA:CB	2.55	0.85
1:S:180:SER:CB	1:GA:52:ALA:CB	2.55	0.85
1:HA:180:SER:CB	1:UA:52:ALA:CB	2.55	0.85
1:CB:180:SER:CB	1:PB:52:ALA:CB	2.54	0.85
1:VA:180:SER:CB	1:IB:52:ALA:CB	2.54	0.84
1:JB:180:SER:CB	1:WB:52:ALA:CB	2.55	0.84
1:E:180:SER:CB	1:R:52:ALA:CB	2.54	0.84
1:OA:180:SER:CB	1:BB:52:ALA:CB	2.55	0.84
1:K:180:SER:CB	1:Y:52:ALA:HB1	2.05	0.84
1:QB:180:SER:CB	1:DC:52:ALA:CB	2.55	0.84
1:D:52:ALA:CB	1:ZC:180:SER:CB	2.55	0.83
1:K:52:ALA:CB	1:GD:180:SER:CB	2.55	0.83
1:AA:180:SER:CB	1:NA:52:ALA:HB1	2.10	0.81
1:VA:180:SER:CB	1:IB:52:ALA:HB1	2.10	0.81
1:OA:180:SER:CB	1:BB:52:ALA:HB1	2.11	0.81
1:HA:180:SER:CB	1:UA:52:ALA:HB1	2.10	0.81
1:CB:180:SER:CB	1:PB:52:ALA:HB1	2.10	0.81
1:KC:184:ALA:HB1	1:XC:48:ALA:HB1	1.63	0.81
1:S:180:SER:CB	1:GA:52:ALA:HB1	2.11	0.81
1:JB:180:SER:CB	1:WB:52:ALA:HB1	2.11	0.81
1:J:48:ALA:HB1	1:FD:184:ALA:HB1	1.63	0.81
1:RC:184:ALA:HB1	1:ED:48:ALA:HB1	1.64	0.80
1:E:180:SER:CB	1:R:52:ALA:HB1	2.11	0.80
1:L:180:SER:CB	1:Z:52:ALA:HB1	2.10	0.80
1:DC:184:ALA:HB1	1:QC:48:ALA:HB1	1.64	0.80
1:C:48:ALA:HB1	1:YC:184:ALA:HB1	1.64	0.80
1:XB:180:SER:CB	1:KC:52:ALA:HB1	2.10	0.80
1:D:52:ALA:HB1	1:ZC:180:SER:CB	2.10	0.80
1:PB:184:ALA:HB1	1:CC:48:ALA:HB1	1.63	0.80
1:QB:180:SER:CB	1:DC:52:ALA:HB1	2.11	0.80
1:D:184:ALA:HB1	1:Q:48:ALA:HB1	1.63	0.80
1:SC:180:SER:CB	1:FD:52:ALA:HB1	2.10	0.80
1:T:183:GLN:CB	1:HA:48:ALA:HB1	2.12	0.80
1:WB:184:ALA:HB1	1:JC:48:ALA:HB1	1.64	0.80
1:EC:180:SER:CB	1:RC:52:ALA:HB1	2.11	0.80
1:K:52:ALA:HB1	1:GD:180:SER:CB	2.11	0.80
1:K:184:ALA:HB1	1:Y:48:ALA:HB1	1.64	0.80
1:M:183:GLN:CB	1:AA:48:ALA:HB1	2.12	0.80
1:BA:183:GLN:CB	1:OA:48:ALA:HB1	2.12	0.80
1:F:183:GLN:CB	1:S:48:ALA:HB1	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LC:180:SER:CB	1:YC:52:ALA:HB1	2.11	0.79
1:TC:183:GLN:CB	1:GD:48:ALA:HB1	2.12	0.79
1:L:48:ALA:HB1	1:HD:183:GLN:CB	2.12	0.79
1:IA:183:GLN:CB	1:VA:48:ALA:HB1	2.12	0.79
1:IB:184:ALA:HB1	1:VB:48:ALA:HB1	1.63	0.79
1:KB:183:GLN:CB	1:XB:48:ALA:HB1	2.12	0.79
1:RB:183:GLN:CB	1:EC:48:ALA:HB1	2.12	0.79
1:PA:183:GLN:CB	1:CB:48:ALA:HB1	2.12	0.79
1:MC:183:GLN:CB	1:ZC:48:ALA:HB1	2.12	0.79
1:R:184:ALA:HB1	1:FA:48:ALA:HB1	1.63	0.79
1:WA:183:GLN:CB	1:JB:48:ALA:HB1	2.12	0.79
1:YB:183:GLN:CB	1:LC:48:ALA:HB1	2.12	0.79
1:NA:184:ALA:HB1	1:AB:48:ALA:HB1	1.63	0.79
1:FC:183:GLN:CB	1:SC:48:ALA:HB1	2.12	0.79
1:E:48:ALA:HB1	1:AD:183:GLN:CB	2.12	0.78
1:DB:183:GLN:CB	1:QB:48:ALA:HB1	2.12	0.78
1:Z:184:ALA:HB1	1:MA:48:ALA:HB1	1.64	0.78
1:UA:184:ALA:HB1	1:HB:48:ALA:HB1	1.63	0.78
1:GA:184:ALA:HB1	1:TA:48:ALA:HB1	1.64	0.78
1:BB:184:ALA:HB1	1:OB:48:ALA:HB1	1.64	0.78
1:SC:180:SER:CB	1:FD:52:ALA:HB2	2.17	0.74
1:QB:180:SER:CB	1:DC:52:ALA:HB2	2.17	0.74
1:LC:180:SER:CB	1:YC:52:ALA:HB2	2.18	0.74
1:CB:180:SER:CB	1:PB:52:ALA:HB2	2.18	0.74
1:D:52:ALA:HB2	1:ZC:180:SER:CB	2.18	0.74
1:EC:180:SER:CB	1:RC:52:ALA:HB2	2.18	0.74
1:AA:180:SER:CB	1:NA:52:ALA:HB2	2.17	0.73
1:E:180:SER:CB	1:R:52:ALA:HB2	2.17	0.73
1:K:52:ALA:HB2	1:GD:180:SER:CB	2.18	0.73
1:JB:180:SER:CB	1:WB:52:ALA:HB2	2.18	0.73
1:HA:180:SER:CB	1:UA:52:ALA:HB2	2.18	0.73
1:VA:180:SER:CB	1:IB:52:ALA:HB2	2.17	0.73
1:XB:180:SER:CB	1:KC:52:ALA:HB2	2.17	0.73
1:L:180:SER:CB	1:Z:52:ALA:HB2	2.18	0.73
1:S:180:SER:CB	1:GA:52:ALA:HB2	2.18	0.73
1:OA:180:SER:CB	1:BB:52:ALA:HB2	2.18	0.73
1:WA:179:GLU:CB	1:JB:52:ALA:CB	2.69	0.70
1:MC:179:GLU:CB	1:ZC:52:ALA:CB	2.69	0.70
1:DB:179:GLU:CB	1:QB:52:ALA:CB	2.70	0.70
1:BA:179:GLU:CB	1:OA:52:ALA:CB	2.69	0.70
1:TC:179:GLU:CB	1:GD:52:ALA:CB	2.69	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KB:179:GLU:CB	1:XB:52:ALA:CB	2.70	0.70
1:RB:179:GLU:CB	1:EC:52:ALA:CB	2.69	0.70
1:PA:179:GLU:CB	1:CB:52:ALA:CB	2.70	0.70
1:F:179:GLU:CB	1:S:52:ALA:CB	2.69	0.70
1:T:179:GLU:CB	1:HA:52:ALA:CB	2.70	0.70
1:FC:179:GLU:CB	1:SC:52:ALA:CB	2.70	0.70
1:L:52:ALA:CB	1:HD:179:GLU:CB	2.70	0.69
1:IA:179:GLU:CB	1:VA:52:ALA:CB	2.70	0.69
1:YB:179:GLU:CB	1:LC:52:ALA:CB	2.69	0.69
1:M:179:GLU:CB	1:AA:52:ALA:CB	2.70	0.68
1:E:52:ALA:CB	1:AD:179:GLU:CB	2.70	0.68
1:X:167:ALA:HB2	1:EA:32:ALA:HB2	1.76	0.68
1:GB:167:ALA:HB2	1:NB:32:ALA:HB2	1.76	0.68
1:UB:167:ALA:HB2	1:BC:32:ALA:HB2	1.76	0.68
1:SA:167:ALA:HB2	1:ZA:32:ALA:HB2	1.76	0.68
1:I:167:ALA:HB2	1:P:32:ALA:HB2	1.76	0.67
1:EA:167:ALA:HB2	1:LA:32:ALA:HB2	1.76	0.67
1:WC:167:ALA:HB2	1:DD:32:ALA:HB2	1.76	0.67
1:B:167:ALA:HB2	1:I:32:ALA:HB2	1.76	0.67
1:BC:167:ALA:HB2	1:IC:32:ALA:HB2	1.76	0.67
1:LA:167:ALA:HB2	1:SA:32:ALA:HB2	1.76	0.67
1:PC:167:ALA:HB2	1:WC:32:ALA:HB2	1.76	0.67
1:ZA:167:ALA:HB2	1:GB:32:ALA:HB2	1.76	0.66
1:IC:167:ALA:HB2	1:PC:32:ALA:HB2	1.76	0.66
1:NB:167:ALA:HB2	1:UB:32:ALA:HB2	1.76	0.66
1:P:167:ALA:HB2	1:X:32:ALA:HB2	1.76	0.65
1:B:32:ALA:HB2	1:DD:167:ALA:HB2	1.76	0.65
1:Y:180:SER:CB	1:LA:52:ALA:HB1	2.31	0.61
1:C:180:SER:CB	1:P:52:ALA:HB1	2.31	0.61
1:I:52:ALA:HB1	1:ED:180:SER:CB	2.31	0.61
1:FA:180:SER:CB	1:SA:52:ALA:HB1	2.31	0.61
1:QC:180:SER:CB	1:DD:52:ALA:HB1	2.31	0.61
1:TA:180:SER:CB	1:GB:52:ALA:HB1	2.31	0.61
1:B:52:ALA:HB1	1:XC:180:SER:CB	2.31	0.61
1:J:180:SER:CB	1:X:52:ALA:HB1	2.31	0.61
1:Q:180:SER:CB	1:EA:52:ALA:HB1	2.31	0.61
1:AB:180:SER:CB	1:NB:52:ALA:HB1	2.31	0.61
1:MA:180:SER:CB	1:ZA:52:ALA:HB1	2.31	0.60
1:JC:180:SER:CB	1:WC:52:ALA:HB1	2.31	0.60
1:OB:180:SER:CB	1:BC:52:ALA:HB1	2.31	0.60
1:VB:180:SER:CB	1:IC:52:ALA:HB1	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:180:SER:CB	1:PC:52:ALA:HB1	2.31	0.60
1:HB:180:SER:CB	1:UB:52:ALA:HB1	2.31	0.60
1:RA:158:GLY:HA3	1:YA:32:ALA:HB1	1.88	0.56
1:FB:158:GLY:HA3	1:MB:32:ALA:HB1	1.88	0.56
1:TB:158:GLY:HA3	1:AC:32:ALA:HB1	1.88	0.56
1:A:32:ALA:HB1	1:CD:158:GLY:HA3	1.88	0.55
1:H:158:GLY:HA3	1:O:32:ALA:HB1	1.88	0.55
1:W:158:GLY:HA3	1:DA:32:ALA:HB1	1.89	0.55
1:DA:158:GLY:HA3	1:KA:32:ALA:HB1	1.88	0.55
1:OC:158:GLY:HA3	1:VC:32:ALA:HB1	1.89	0.55
1:VC:158:GLY:HA3	1:CD:32:ALA:HB1	1.89	0.55
1:O:158:GLY:HA3	1:W:32:ALA:HB1	1.89	0.55
1:HC:158:GLY:HA3	1:OC:32:ALA:HB1	1.89	0.55
1:KA:158:GLY:HA3	1:RA:32:ALA:HB1	1.89	0.55
1:YA:158:GLY:HA3	1:FB:32:ALA:HB1	1.89	0.55
1:A:158:GLY:HA3	1:H:32:ALA:HB1	1.89	0.54
1:AC:158:GLY:HA3	1:HC:32:ALA:HB1	1.89	0.54
1:MB:158:GLY:HA3	1:TB:32:ALA:HB1	1.90	0.54
1:DA:158:GLY:HA3	1:KA:32:ALA:CB	2.40	0.52
1:OC:158:GLY:HA3	1:VC:32:ALA:CB	2.39	0.52
1:RA:158:GLY:HA3	1:YA:32:ALA:CB	2.39	0.52
1:Q:167:ALA:HB1	1:Y:32:ALA:HB2	1.91	0.52
1:TB:158:GLY:HA3	1:AC:32:ALA:CB	2.40	0.52
1:A:32:ALA:CB	1:CD:158:GLY:HA3	2.40	0.52
1:FB:158:GLY:HA3	1:MB:32:ALA:CB	2.40	0.52
1:MA:167:ALA:HB1	1:TA:32:ALA:HB2	1.91	0.52
1:O:158:GLY:HA3	1:W:32:ALA:CB	2.40	0.52
1:Y:167:ALA:HB1	1:FA:32:ALA:HB2	1.92	0.52
1:TA:167:ALA:HB1	1:AB:32:ALA:HB2	1.92	0.52
1:CC:167:ALA:HB1	1:JC:32:ALA:HB2	1.91	0.52
1:HC:158:GLY:HA3	1:OC:32:ALA:CB	2.40	0.52
1:JC:167:ALA:HB1	1:QC:32:ALA:HB2	1.91	0.52
1:QC:167:ALA:HB1	1:XC:32:ALA:HB2	1.91	0.52
1:A:158:GLY:HA3	1:H:32:ALA:CB	2.40	0.51
1:AC:158:GLY:HA3	1:HC:32:ALA:CB	2.40	0.51
1:VC:158:GLY:HA3	1:CD:32:ALA:CB	2.41	0.51
1:J:167:ALA:HB1	1:Q:32:ALA:HB2	1.92	0.51
1:H:158:GLY:HA3	1:O:32:ALA:CB	2.40	0.51
1:FA:167:ALA:HB1	1:MA:32:ALA:HB2	1.91	0.51
1:OB:167:ALA:HB1	1:VB:32:ALA:HB2	1.91	0.51
1:MB:158:GLY:HA3	1:TB:32:ALA:CB	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:167:ALA:HB1	1:HB:32:ALA:HB2	1.91	0.51
1:C:32:ALA:HB2	1:ED:167:ALA:HB1	1.92	0.51
1:YA:158:GLY:HA3	1:FB:32:ALA:CB	2.41	0.51
1:HB:167:ALA:HB1	1:OB:32:ALA:HB2	1.92	0.51
1:XC:167:ALA:HB1	1:ED:32:ALA:HB2	1.92	0.51
1:C:167:ALA:HB1	1:J:32:ALA:HB2	1.91	0.51
1:KA:158:GLY:HA3	1:RA:32:ALA:CB	2.41	0.51
1:VB:167:ALA:HB1	1:CC:32:ALA:HB2	1.92	0.51
1:W:158:GLY:HA3	1:DA:32:ALA:CB	2.40	0.51
1:MA:182:ALA:HB2	1:TA:146:ALA:HB1	1.96	0.48
1:C:182:ALA:HB2	1:J:146:ALA:HB1	1.96	0.48
1:Q:182:ALA:HB2	1:Y:146:ALA:HB1	1.96	0.48
1:Y:182:ALA:HB2	1:FA:146:ALA:HB1	1.97	0.47
1:C:146:ALA:HB1	1:ED:182:ALA:HB2	1.97	0.47
1:JC:182:ALA:HB2	1:QC:146:ALA:HB1	1.96	0.47
1:AB:182:ALA:HB2	1:HB:146:ALA:HB1	1.96	0.47
1:XC:182:ALA:HB2	1:ED:146:ALA:HB1	1.96	0.46
1:QC:182:ALA:HB2	1:XC:146:ALA:HB1	1.97	0.46
1:OB:182:ALA:HB2	1:VB:146:ALA:HB1	1.96	0.46
1:J:182:ALA:HB2	1:Q:146:ALA:HB1	1.97	0.46
1:HB:182:ALA:HB2	1:OB:146:ALA:HB1	1.97	0.46
1:CC:182:ALA:HB2	1:JC:146:ALA:HB1	1.96	0.46
1:FA:182:ALA:HB2	1:MA:146:ALA:HB1	1.97	0.46
1:VB:182:ALA:HB2	1:CC:146:ALA:HB1	1.97	0.46
1:TA:182:ALA:HB2	1:AB:146:ALA:HB1	1.97	0.45
1:YB:160:ASN:O	1:YB:161:THR:C	2.57	0.43
1:KB:160:ASN:O	1:KB:161:THR:C	2.57	0.43
1:MC:160:ASN:O	1:MC:161:THR:C	2.57	0.43
1:HD:160:ASN:O	1:HD:161:THR:C	2.57	0.43
1:TC:160:ASN:O	1:TC:161:THR:C	2.57	0.42
1:FC:160:ASN:O	1:FC:161:THR:C	2.57	0.42
1:PA:160:ASN:O	1:PA:161:THR:C	2.57	0.42
1:T:160:ASN:O	1:T:161:THR:C	2.57	0.42
1:RA:158:GLY:CA	1:YA:32:ALA:HB2	2.50	0.42
1:OC:158:GLY:CA	1:VC:32:ALA:HB2	2.50	0.42
1:TB:158:GLY:CA	1:AC:32:ALA:HB2	2.50	0.42
1:RB:160:ASN:O	1:RB:161:THR:C	2.57	0.42
1:H:158:GLY:CA	1:O:32:ALA:HB2	2.50	0.41
1:O:158:GLY:CA	1:W:32:ALA:HB2	2.50	0.41
1:AC:158:GLY:CA	1:HC:32:ALA:HB2	2.50	0.41
1:FB:158:GLY:CA	1:MB:32:ALA:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:160:ASN:O	1:AD:161:THR:C	2.57	0.41
1:WA:160:ASN:O	1:WA:161:THR:C	2.57	0.41
1:F:160:ASN:O	1:F:161:THR:C	2.57	0.41
1:MB:158:GLY:CA	1:TB:32:ALA:HB2	2.50	0.41
1:HC:158:GLY:CA	1:OC:32:ALA:HB2	2.51	0.41
1:A:158:GLY:CA	1:H:32:ALA:HB2	2.51	0.41
1:BA:160:ASN:O	1:BA:161:THR:C	2.57	0.41
1:DA:158:GLY:CA	1:KA:32:ALA:HB2	2.50	0.41
1:KB:183:GLN:CB	1:XB:48:ALA:CB	2.94	0.41
1:BA:183:GLN:CB	1:OA:48:ALA:CB	2.94	0.41
1:W:158:GLY:CA	1:DA:32:ALA:HB2	2.51	0.41
1:IA:160:ASN:O	1:IA:161:THR:C	2.57	0.41
1:A:32:ALA:HB2	1:CD:158:GLY:CA	2.50	0.41
1:KA:158:GLY:CA	1:RA:32:ALA:HB2	2.51	0.41
1:YA:158:GLY:CA	1:FB:32:ALA:HB2	2.51	0.41
1:DB:160:ASN:O	1:DB:161:THR:C	2.57	0.41
1:VC:158:GLY:CA	1:CD:32:ALA:HB2	2.51	0.40
1:M:160:ASN:O	1:M:161:THR:C	2.57	0.40

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%)	216 (100%)	1 (0%)	0	100	100
1	AB	217/258 (84%)	217 (100%)	0	0	100	100
1	AC	131/258 (51%)	131 (100%)	0	0	100	100
1	AD	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	B	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	BB	217/258 (84%)	217 (100%)	0	0	100	100
1	BC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	BD	156/258 (60%)	156 (100%)	0	0	100	100
1	C	217/258 (84%)	217 (100%)	0	0	100	100
1	CA	156/258 (60%)	156 (100%)	0	0	100	100
1	CB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CC	217/258 (84%)	217 (100%)	0	0	100	100
1	CD	131/258 (51%)	131 (100%)	0	0	100	100
1	D	217/258 (84%)	217 (100%)	0	0	100	100
1	DA	131/258 (51%)	131 (100%)	0	0	100	100
1	DB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	DC	217/258 (84%)	217 (100%)	0	0	100	100
1	DD	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	E	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	EA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	EB	156/258 (60%)	156 (100%)	0	0	100	100
1	EC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ED	217/258 (84%)	217 (100%)	0	0	100	100
1	F	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	FA	217/258 (84%)	217 (100%)	0	0	100	100
1	FB	131/258 (51%)	131 (100%)	0	0	100	100
1	FC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	FD	217/258 (84%)	217 (100%)	0	0	100	100
1	G	156/258 (60%)	156 (100%)	0	0	100	100
1	GA	217/258 (84%)	217 (100%)	0	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	GD	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	H	131/258 (51%)	131 (100%)	0	0	100	100
1	HA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	HB	217/258 (84%)	217 (100%)	0	0	100	100
1	HC	131/258 (51%)	131 (100%)	0	0	100	100
1	HD	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	I	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	IA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	IB	217/258 (84%)	217 (100%)	0	0	100	100
1	IC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ID	156/258 (60%)	156 (100%)	0	0	100	100
1	J	217/258 (84%)	217 (100%)	0	0	100	100
1	JA	156/258 (60%)	156 (100%)	0	0	100	100
1	JB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	JC	217/258 (84%)	217 (100%)	0	0	100	100
1	K	217/258 (84%)	217 (100%)	0	0	100	100
1	KA	131/258 (51%)	131 (100%)	0	0	100	100
1	KB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	KC	217/258 (84%)	217 (100%)	0	0	100	100
1	L	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	LA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	LB	156/258 (60%)	156 (100%)	0	0	100	100
1	LC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	M	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	MA	217/258 (84%)	217 (100%)	0	0	100	100
1	MB	131/258 (51%)	131 (100%)	0	0	100	100
1	MC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	N	156/258 (60%)	156 (100%)	0	0	100	100
1	NA	217/258 (84%)	217 (100%)	0	0	100	100
1	NB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	NC	156/258 (60%)	156 (100%)	0	0	100	100
1	O	131/258 (51%)	131 (100%)	0	0	100	100
1	OA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	OB	217/258 (84%)	217 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	OC	131/258 (51%)	131 (100%)	0	0	100	100
1	P	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	PA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	PB	217/258 (84%)	217 (100%)	0	0	100	100
1	PC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	Q	217/258 (84%)	217 (100%)	0	0	100	100
1	QA	156/258 (60%)	156 (100%)	0	0	100	100
1	QB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	QC	217/258 (84%)	217 (100%)	0	0	100	100
1	R	217/258 (84%)	217 (100%)	0	0	100	100
1	RA	131/258 (51%)	131 (100%)	0	0	100	100
1	RB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	RC	217/258 (84%)	217 (100%)	0	0	100	100
1	S	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	SA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	SB	156/258 (60%)	156 (100%)	0	0	100	100
1	SC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	T	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	TA	217/258 (84%)	217 (100%)	0	0	100	100
1	TB	131/258 (51%)	131 (100%)	0	0	100	100
1	TC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	UA	217/258 (84%)	217 (100%)	0	0	100	100
1	UB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	UC	156/258 (60%)	156 (100%)	0	0	100	100
1	V	156/258 (60%)	156 (100%)	0	0	100	100
1	VA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	VB	217/258 (84%)	217 (100%)	0	0	100	100
1	VC	131/258 (51%)	131 (100%)	0	0	100	100
1	W	131/258 (51%)	131 (100%)	0	0	100	100
1	WA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	WB	217/258 (84%)	217 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	WC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	X	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	XA	156/258 (60%)	156 (100%)	0	0	100	100
1	XB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	XC	217/258 (84%)	217 (100%)	0	0	100	100
1	Y	217/258 (84%)	217 (100%)	0	0	100	100
1	YA	131/258 (51%)	131 (100%)	0	0	100	100
1	YB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	YC	217/258 (84%)	217 (100%)	0	0	100	100
1	Z	217/258 (84%)	217 (100%)	0	0	100	100
1	ZA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ZB	156/258 (60%)	156 (100%)	0	0	100	100
1	ZC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
All	All	21936/28896 (76%)	21872 (100%)	64 (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 monosaccharides 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.

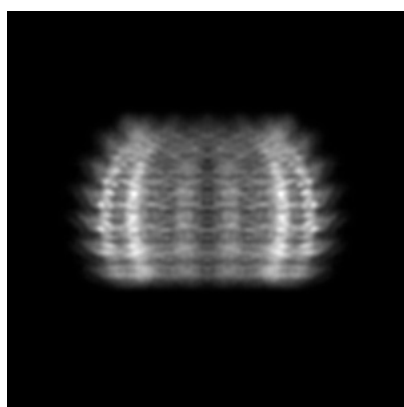
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11482. These allow visual inspection of the internal detail of the map and identification of artifacts.

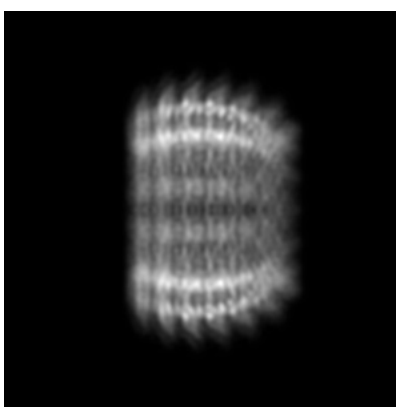
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

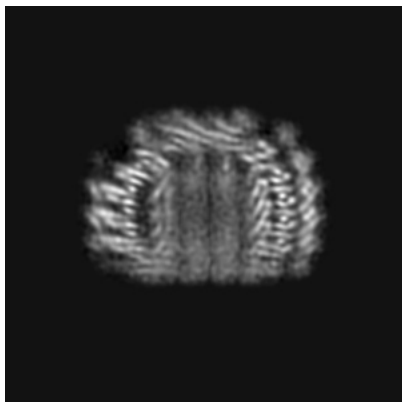


Z Index: 168

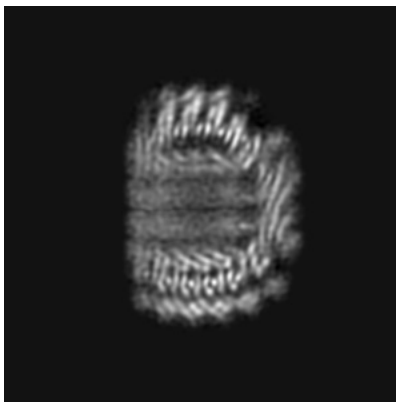
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 229



Y Index: 229



Z Index: 172

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

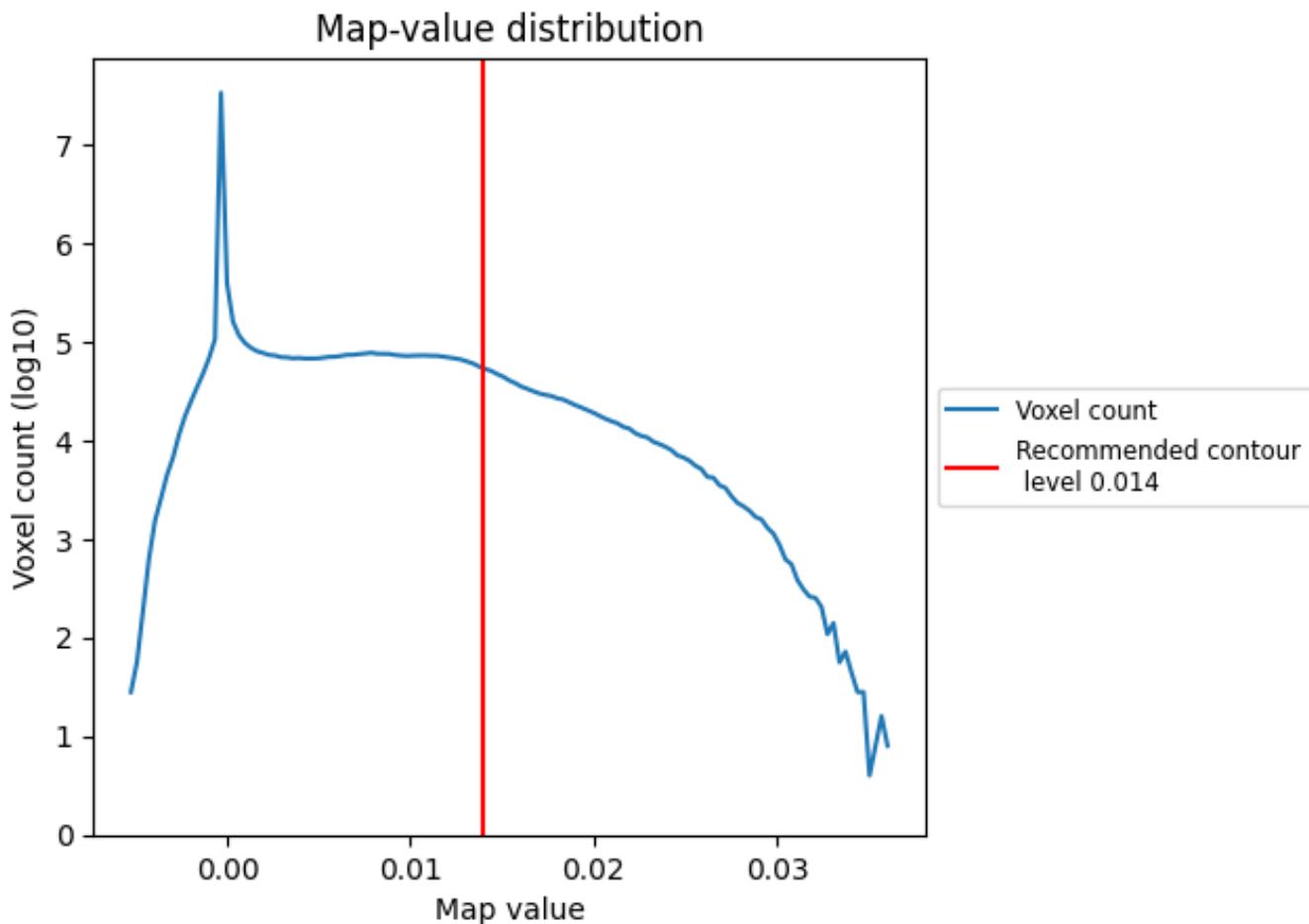
6.5 Mask visualisation

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

7 Map analysis [i](#)

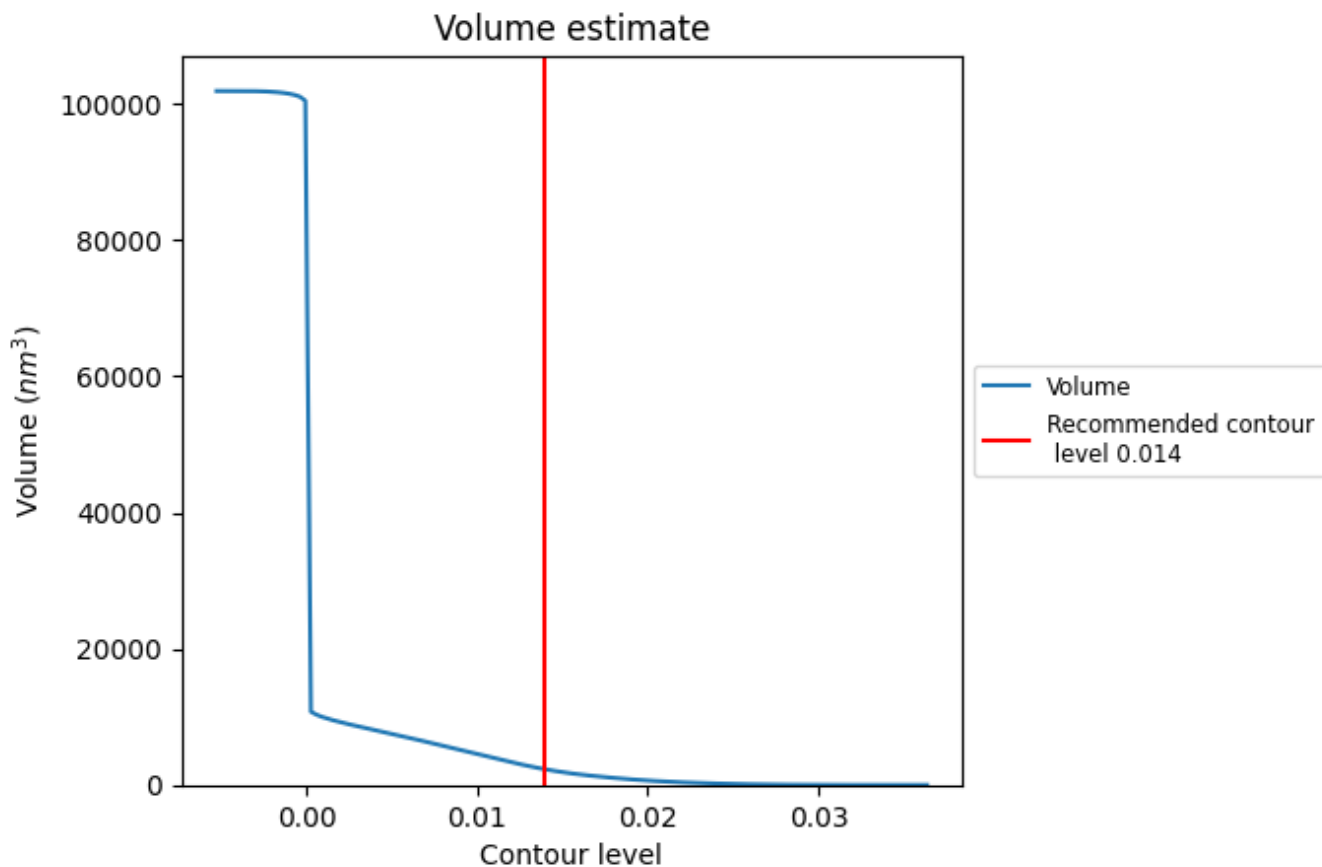
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

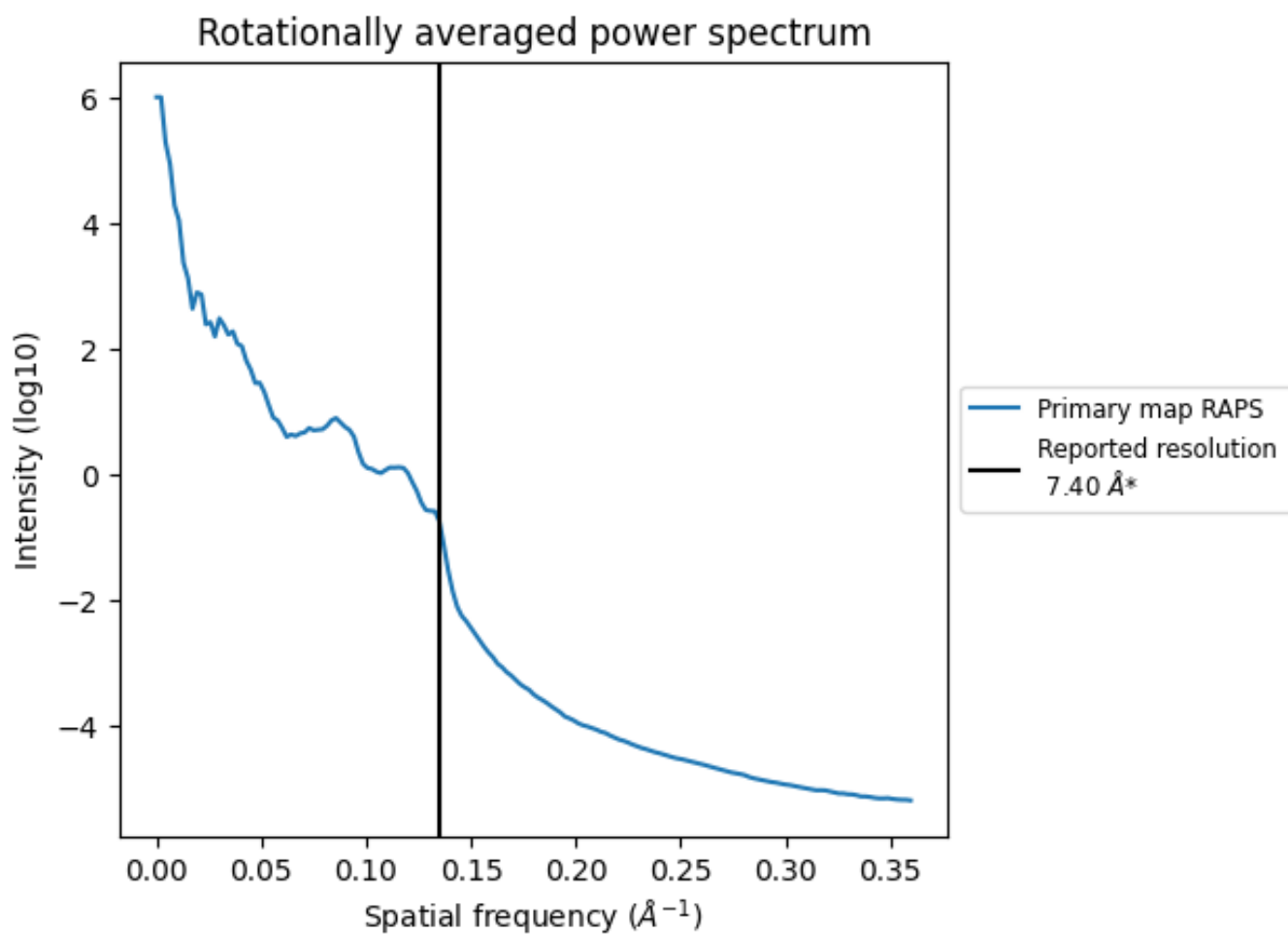
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2305 nm^3 ; this corresponds to an approximate mass of 2082 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.135\AA^{-1}

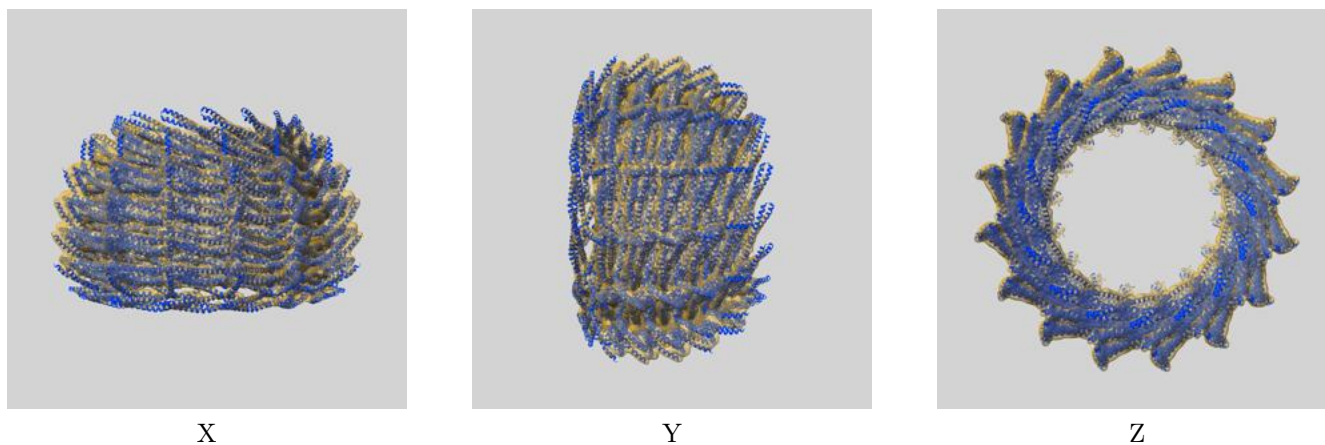
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

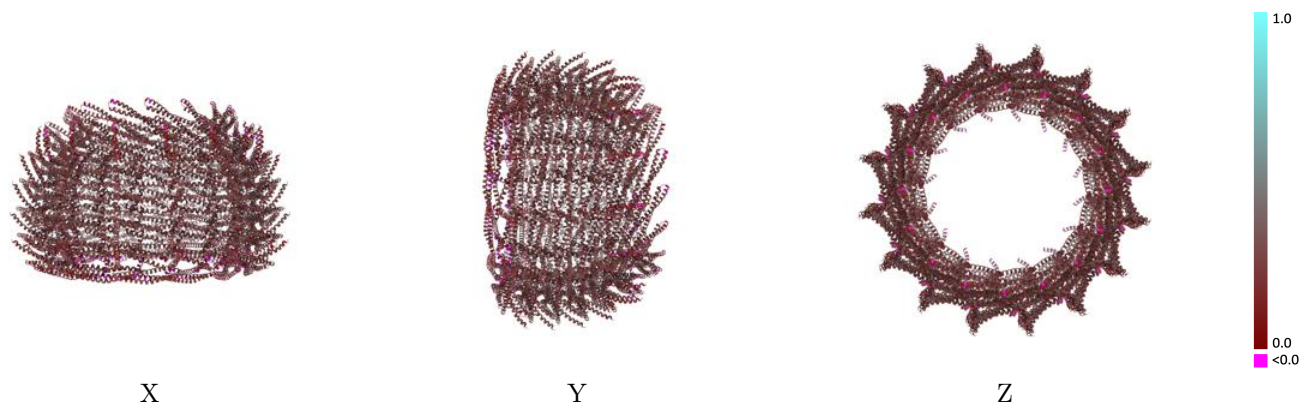
This section contains information regarding the fit between EMDB map EMD-11482 and PDB model 6ZW6. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



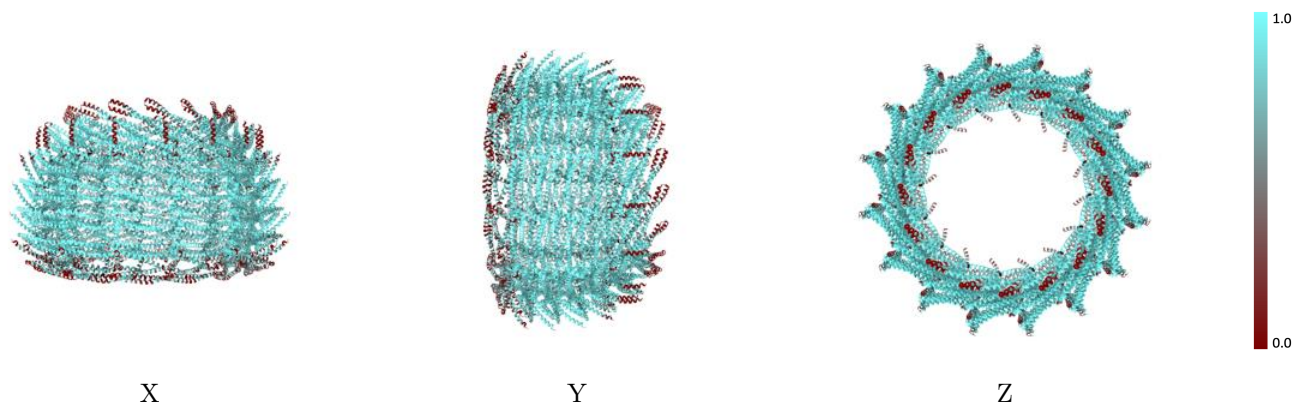
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



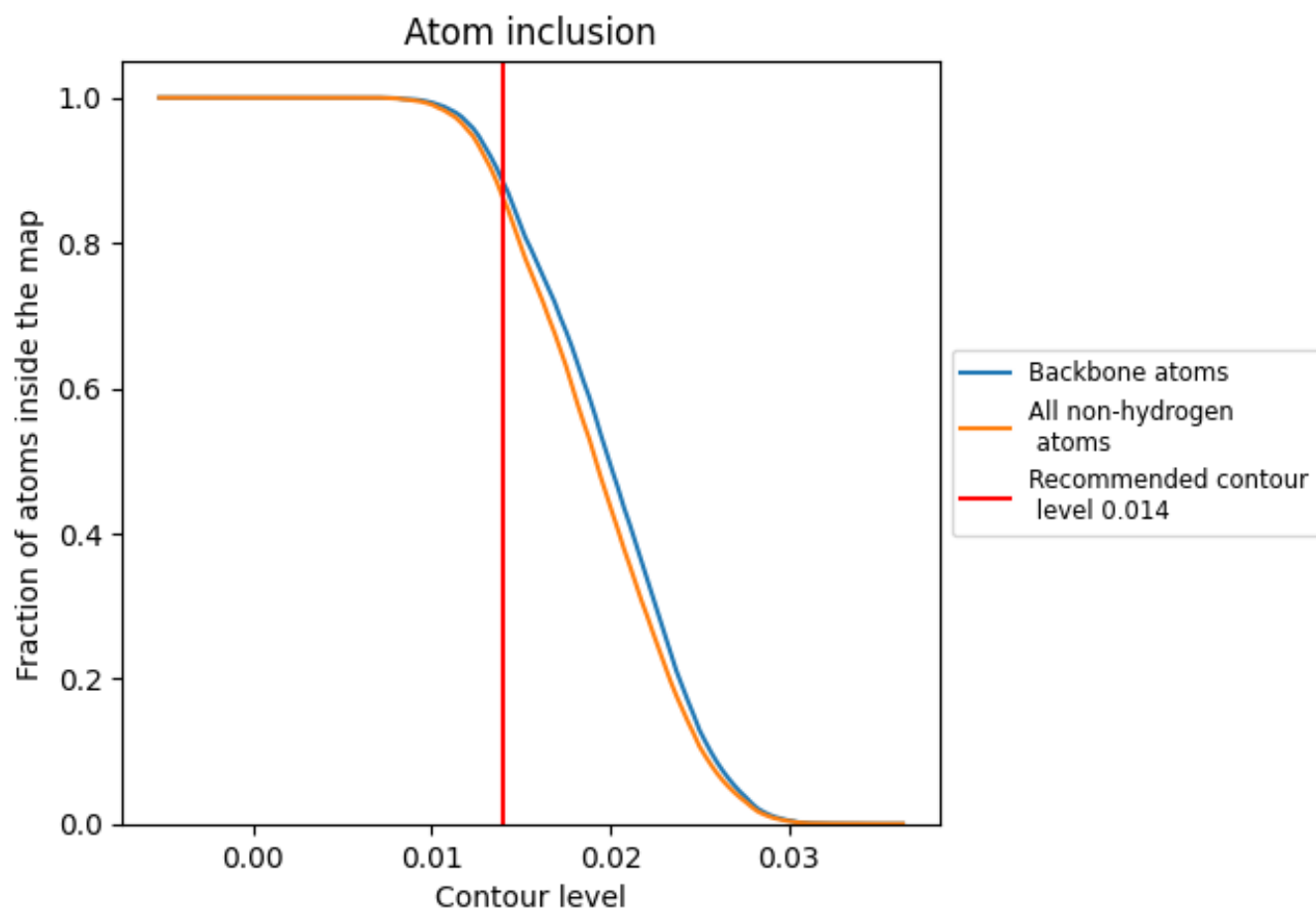
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8615	 0.2500
A	 0.5582	 0.2160
AA	 0.9438	 0.2630
AB	 0.9687	 0.2630
AC	 0.5613	 0.2170
AD	 0.8760	 0.2500
B	 0.8168	 0.2240
BA	 0.8788	 0.2530
BB	 0.9770	 0.2680
BC	 0.8085	 0.2220
BD	 0.7363	 0.2470
C	 0.9696	 0.2620
CA	 0.7350	 0.2550
CB	 0.9438	 0.2620
CC	 0.9696	 0.2630
CD	 0.5628	 0.2160
D	 0.9788	 0.2680
DA	 0.5582	 0.2150
DB	 0.8788	 0.2520
DC	 0.9770	 0.2680
DD	 0.8094	 0.2240
E	 0.9475	 0.2600
EA	 0.8168	 0.2220
EB	 0.7350	 0.2550
EC	 0.9438	 0.2600
ED	 0.9696	 0.2650
F	 0.8825	 0.2510
FA	 0.9696	 0.2630
FB	 0.5582	 0.2140
FC	 0.8788	 0.2480
FD	 0.9779	 0.2690
G	 0.7325	 0.2500
GA	 0.9788	 0.2690
GB	 0.8168	 0.2200
GC	 0.7338	 0.2500











































































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Chain	Atom inclusion	Q-score
GD	 0.9438	 0.2610
H	 0.5401	 0.2160
HA	 0.9475	 0.2620
HB	 0.9696	 0.2610
HC	 0.5582	 0.2160
HD	 0.8788	 0.2490
I	 0.8195	 0.2230
IA	 0.8825	 0.2500
IB	 0.9788	 0.2670
IC	 0.8168	 0.2220
ID	 0.7338	 0.2510
J	 0.9696	 0.2620
JA	 0.7325	 0.2530
JB	 0.9475	 0.2590
JC	 0.9696	 0.2650
K	 0.9788	 0.2700
KA	 0.5416	 0.2140
KB	 0.8825	 0.2500
KC	 0.9788	 0.2710
L	 0.9438	 0.2610
LA	 0.8186	 0.2230
LB	 0.7325	 0.2530
LC	 0.9475	 0.2640
M	 0.8834	 0.2500
MA	 0.9696	 0.2640
MB	 0.5401	 0.2160
MC	 0.8825	 0.2520
N	 0.7338	 0.2510
NA	 0.9788	 0.2710
NB	 0.8186	 0.2220
NC	 0.7325	 0.2510
O	 0.5537	 0.2170
OA	 0.9438	 0.2640
OB	 0.9696	 0.2620
OC	 0.5416	 0.2150
P	 0.8140	 0.2250
PA	 0.8834	 0.2550
PB	 0.9788	 0.2690
PC	 0.8195	 0.2220
Q	 0.9669	 0.2640
QA	 0.7350	 0.2550
QB	 0.9438	 0.2610

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Chain	Atom inclusion	Q-score
QC	 0.9696	 0.2610
R	 0.9779	 0.2710
RA	 0.5537	 0.2170
RB	 0.8834	 0.2510
RC	 0.9788	 0.2680
S	 0.9429	 0.2620
SA	 0.8140	 0.2230
SB	 0.7350	 0.2530
SC	 0.9438	 0.2590
T	 0.8760	 0.2520
TA	 0.9669	 0.2630
TB	 0.5552	 0.2170
TC	 0.8834	 0.2500
UA	 0.9779	 0.2700
UB	 0.8140	 0.2220
UC	 0.7350	 0.2500
V	 0.7363	 0.2500
VA	 0.9429	 0.2630
VB	 0.9669	 0.2630
VC	 0.5552	 0.2160
W	 0.5613	 0.2170
WA	 0.8760	 0.2530
WB	 0.9779	 0.2690
WC	 0.8140	 0.2220
X	 0.8094	 0.2250
XA	 0.7363	 0.2540
XB	 0.9429	 0.2610
XC	 0.9669	 0.2630
Y	 0.9696	 0.2640
YA	 0.5613	 0.2160
YB	 0.8760	 0.2510
YC	 0.9779	 0.2680
Z	 0.9770	 0.2690
ZA	 0.8085	 0.2220
ZB	 0.7363	 0.2520
ZC	 0.9429	 0.2610