



wwPDB EM Validation Summary Report ⓘ

May 5, 2026 – 11:21 pm BST

PDB ID : 9QW9 / pdb_00009qw9
EMDB ID : EMD-53415
Title : Human vault protein - primed conformation
Authors : Lapenta, F.; Marechal, N.; Durand, A.; Aupic, J.; Cassetta, A.
Deposited on : 2025-04-14
Resolution : 3.09 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

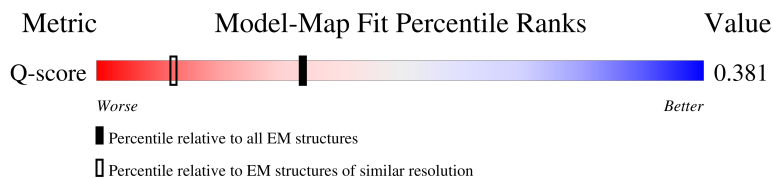
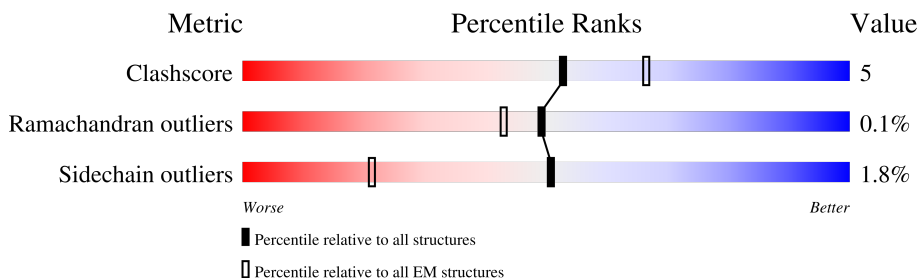
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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.









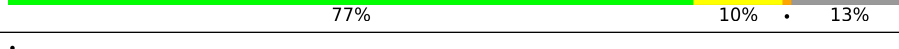
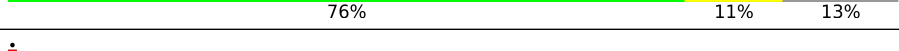
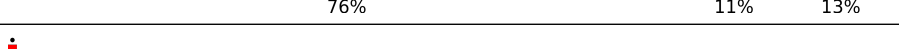
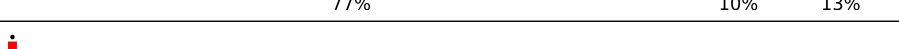
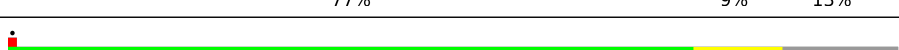

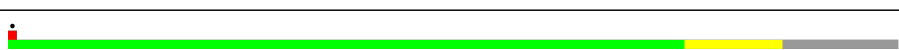

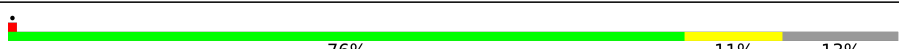





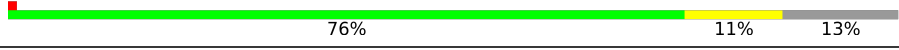
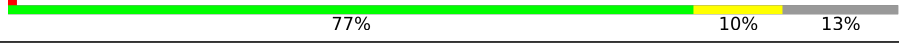



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14003 (2.59 - 3.59)

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	893	
1	AA	893	
1	AB	893	
1	AC	893	







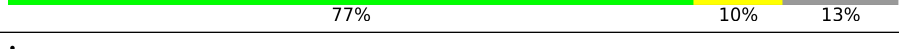
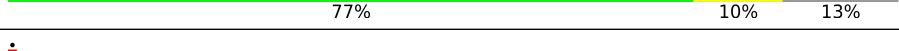
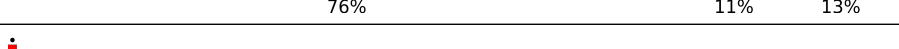
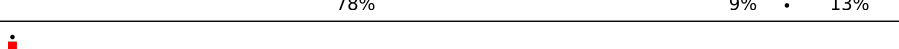
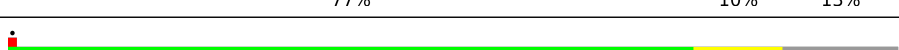

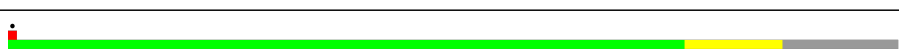

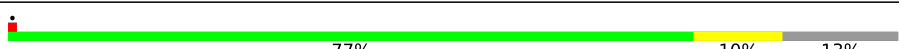





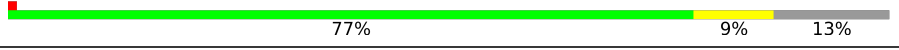
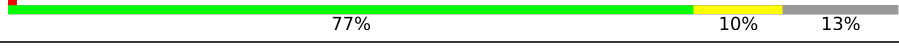



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Mol	Chain	Length	Quality of chain
1	B	893	
1	BA	893	
1	BB	893	
1	C	893	
1	CA	893	
1	CB	893	
1	D	893	
1	DA	893	
1	DB	893	
1	E	893	
1	EA	893	
1	EB	893	
1	F	893	
1	FA	893	
1	FB	893	
1	G	893	
1	GA	893	
1	GB	893	
1	H	893	
1	HA	893	
1	HB	893	
1	I	893	
1	IA	893	
1	IB	893	
1	J	893	



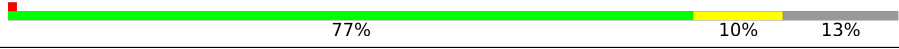




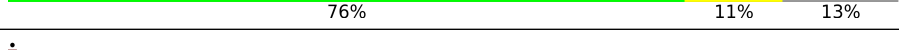
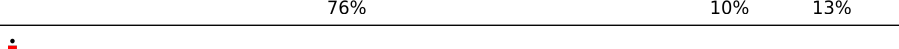
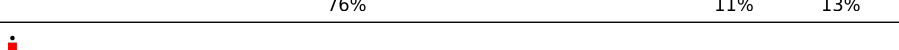

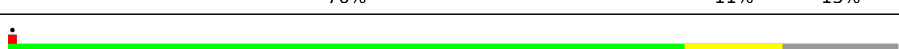


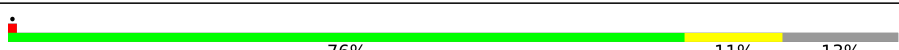





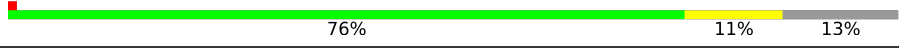



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Mol	Chain	Length	Quality of chain
1	JA	893	
1	JB	893	
1	K	893	
1	KA	893	
1	KB	893	
1	L	893	
1	LA	893	
1	LB	893	
1	M	893	
1	MA	893	
1	MB	893	
1	N	893	
1	NA	893	
1	NB	893	
1	O	893	
1	OA	893	
1	OB	893	
1	P	893	
1	PA	893	
1	PB	893	
1	Q	893	
1	QA	893	
1	QB	893	
1	R	893	
1	RA	893	

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Mol	Chain	Length	Quality of chain
1	RB	893	
1	S	893	
1	SA	893	
1	SB	893	
1	T	893	
1	TA	893	
1	TB	893	
1	UA	893	
1	UB	893	
1	V	893	
1	VA	893	
1	VB	893	
1	W	893	
1	WA	893	
1	WB	893	
1	X	893	
1	XA	893	
1	XB	893	
1	Y	893	
1	YA	893	
1	YB	893	
1	Z	893	
1	ZA	893	
1	ZB	893	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 966108 atoms, of which 483990 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 Major vault protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	AA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	AB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	AC	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	B	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	BA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	BB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	C	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	CA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	CB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	D	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	DA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	DB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	E	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	EA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	EB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	F	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	FA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	FB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	G	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	GA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	GB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	H	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	HA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	HB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	I	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	IA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	IB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	J	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	JA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	JB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	K	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	KA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	KB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	L	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	LA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	LB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	M	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	MA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	MB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	N	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	NA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	NB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	O	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	OA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	OB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	P	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	PA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	PB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	Q	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	QA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	QB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	R	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	RA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	RB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	S	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	SA	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	SB	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		
1	T	779	Total	C	H	N	O	S	0	0
			12386	3890	6205	1105	1176	10		

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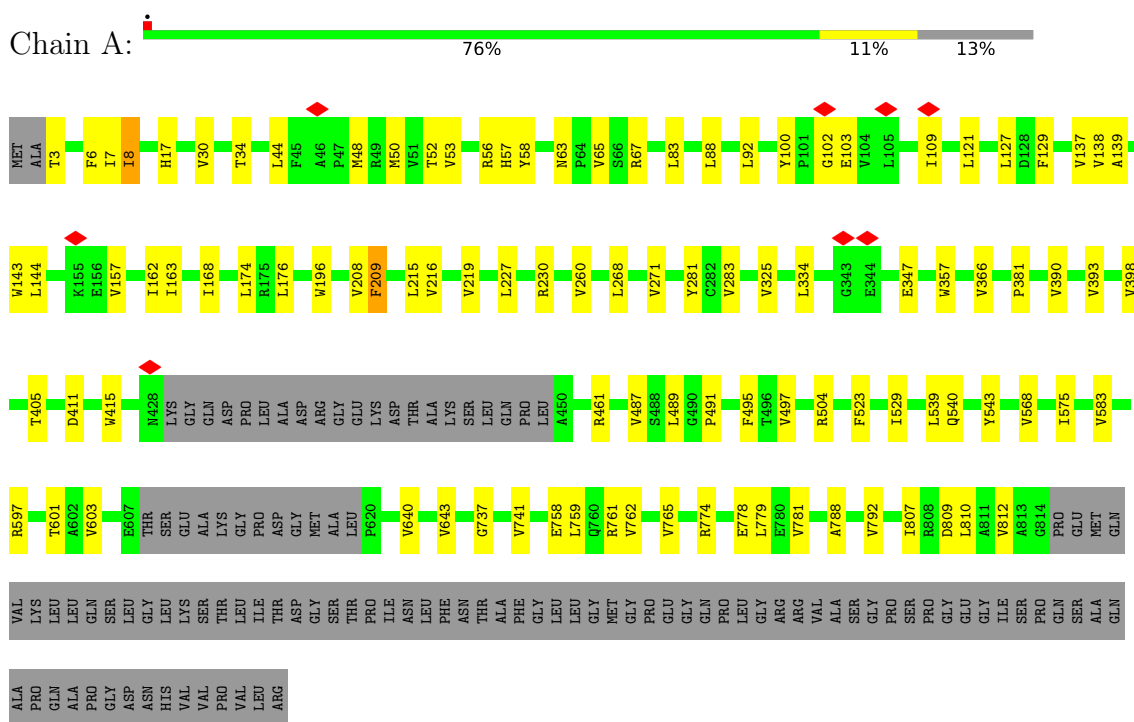
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Mol	Chain	Residues	Atoms						AltConf	Trace
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1	TB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	UA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	UB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	V	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	VA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	VB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	W	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	WA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	WB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	X	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	XA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	XB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	Y	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	YA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	YB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	Z	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	ZA	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0
1	ZB	779	Total 12386	C 3890	H 6205	N 1105	O 1176	S 10	0	0

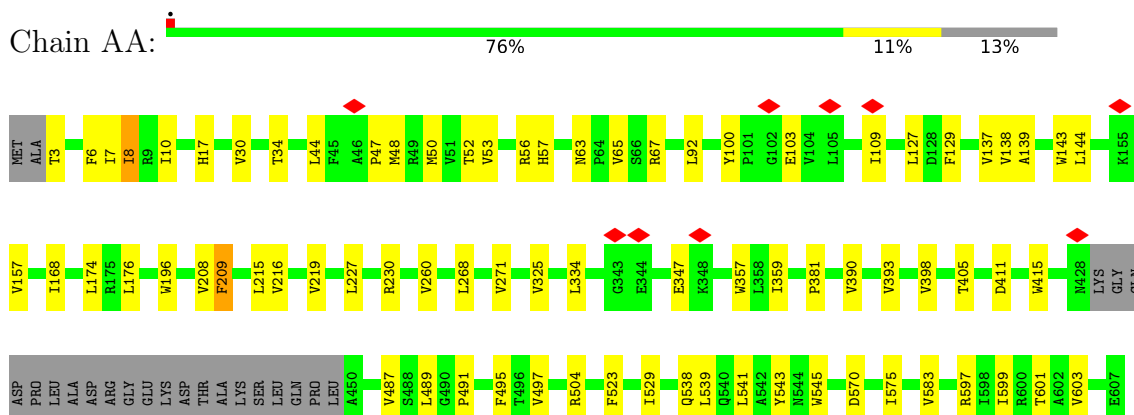
3 Residue-property plots

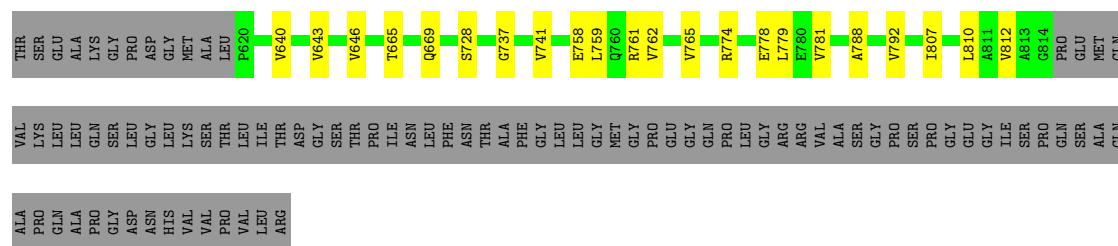
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Major vault protein



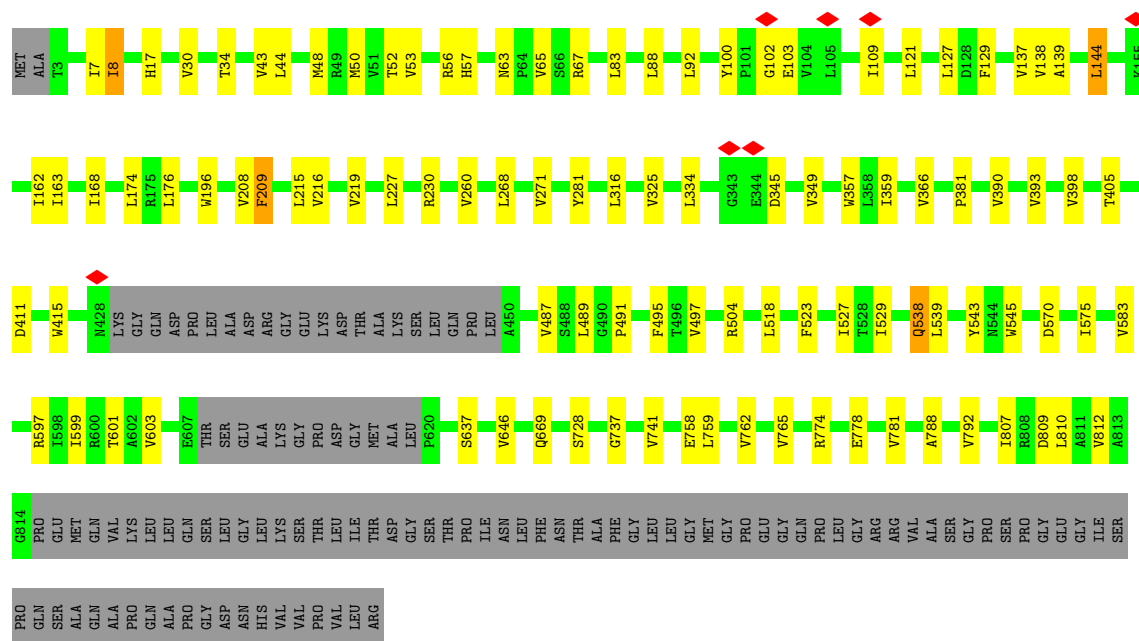
- Molecule 1: Major vault protein





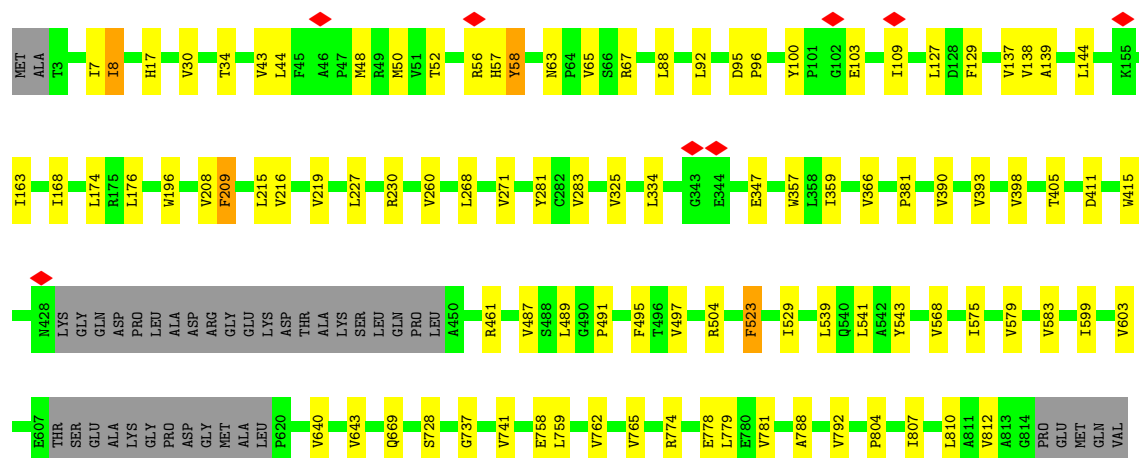
• Molecule 1: Major vault protein

Chain AB: 76% 11% 13%

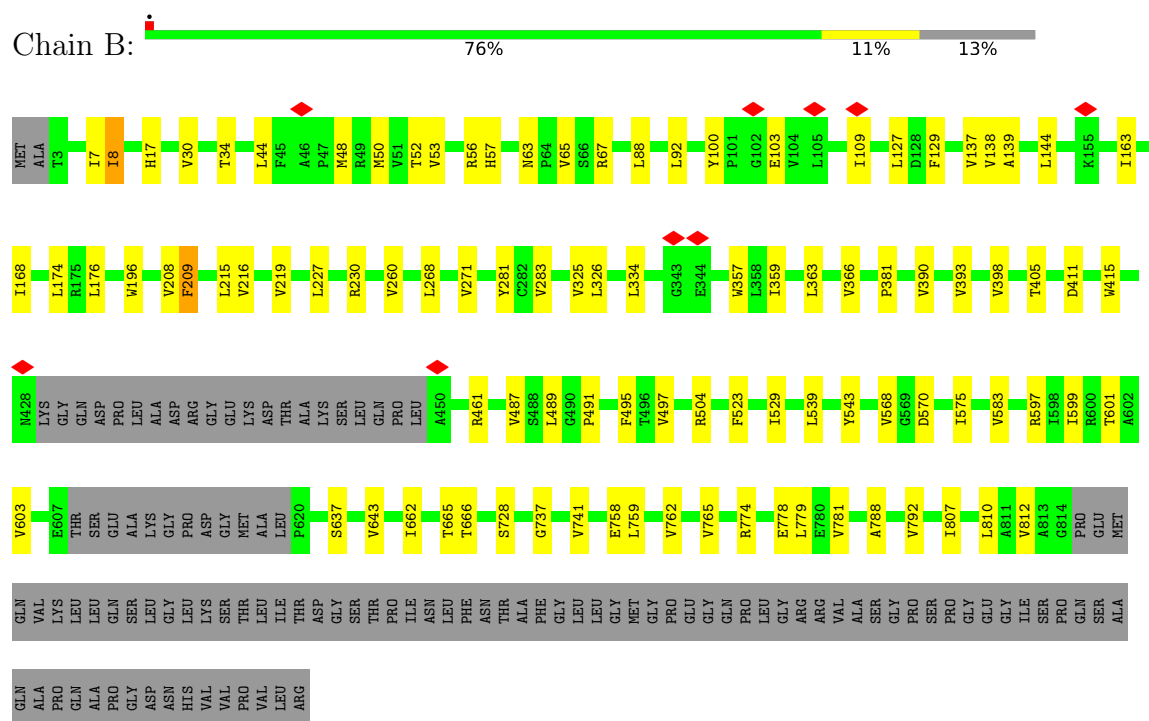


• Molecule 1: Major vault protein

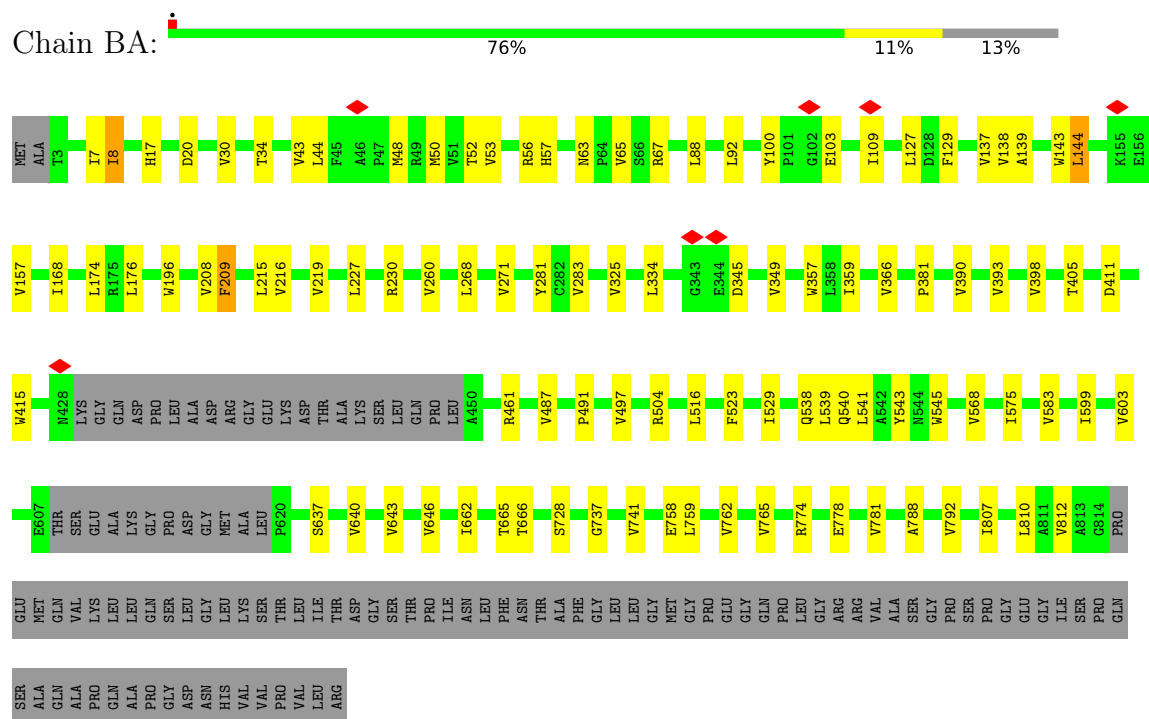
Chain AC: 76% 10% 13%



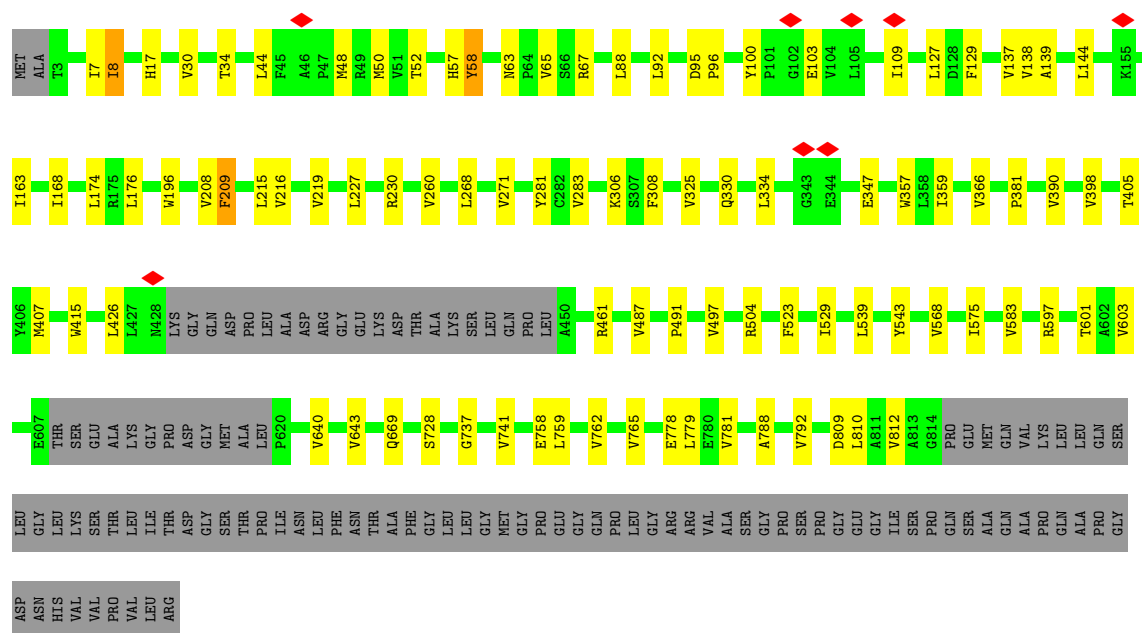
- Molecule 1: Major vault protein



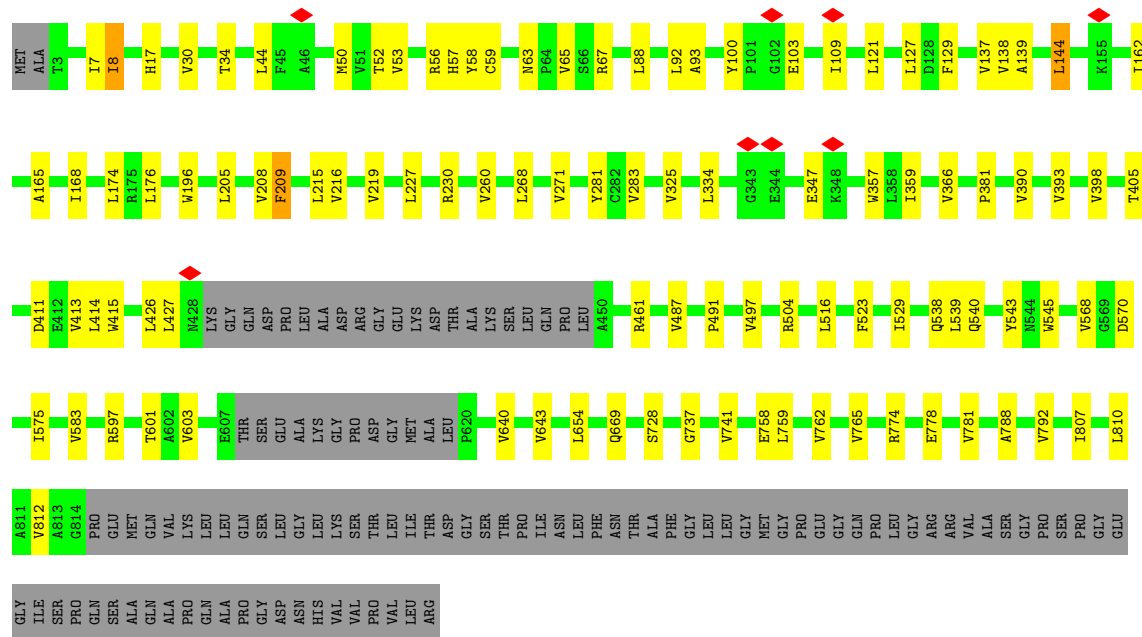
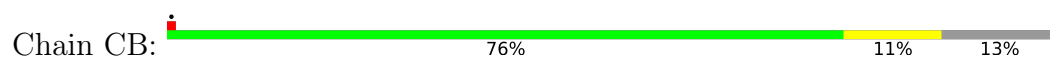
- Molecule 1: Major vault protein



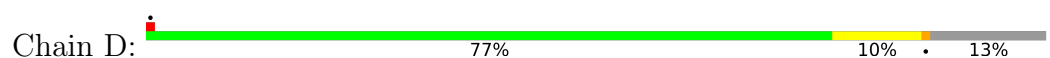


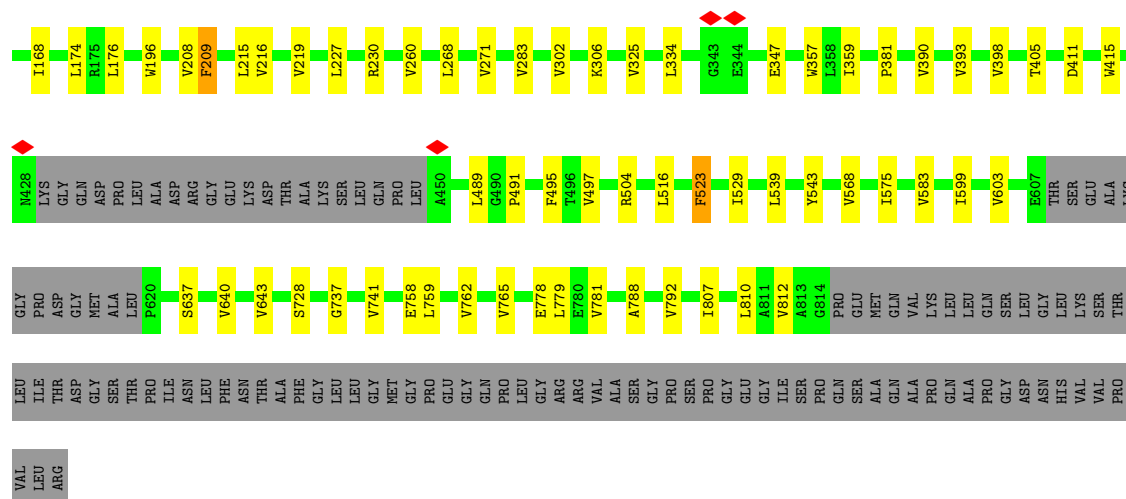


- Molecule 1: Major vault protein

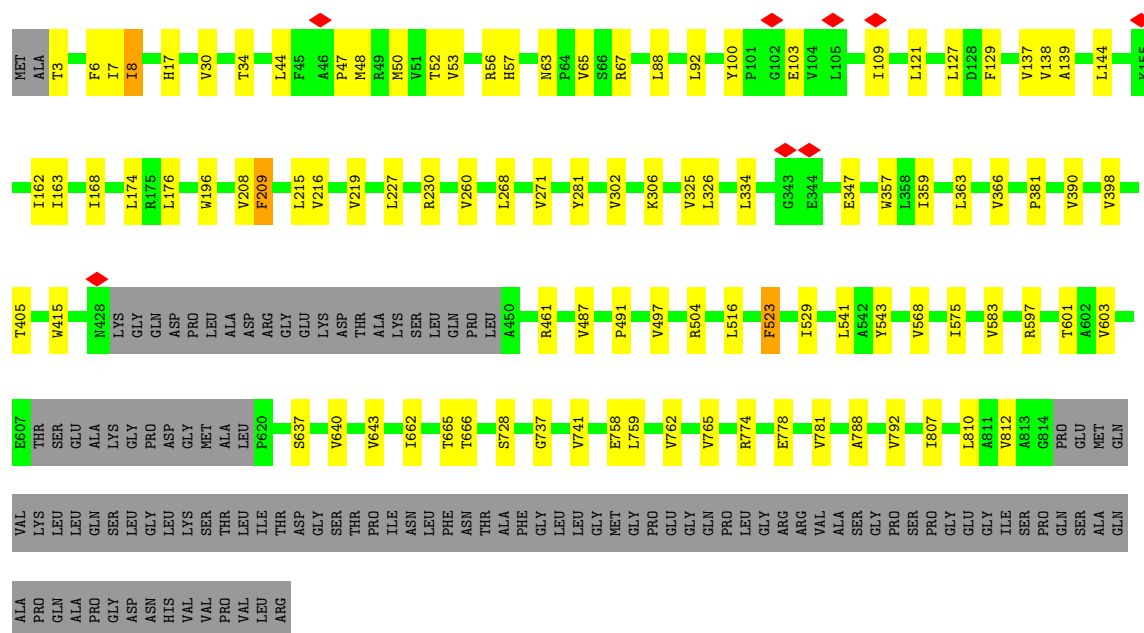
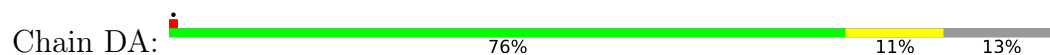


- Molecule 1: Major vault protein

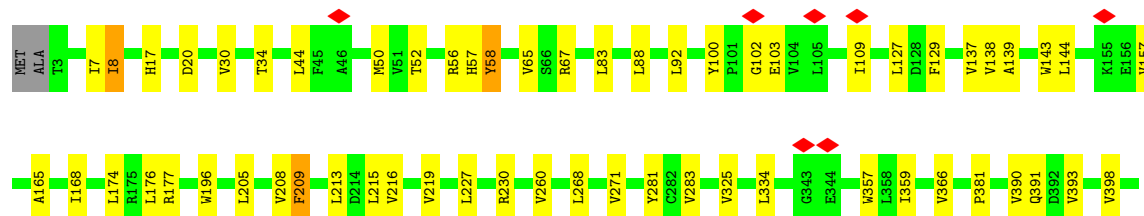
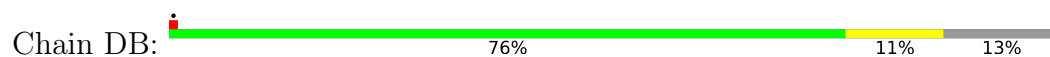




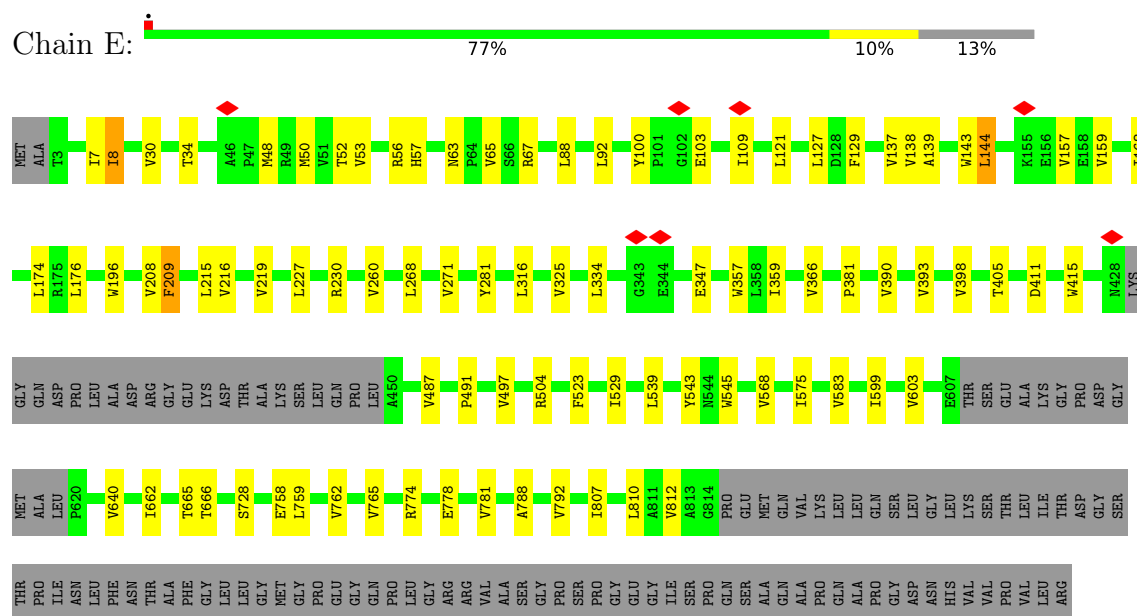
- Molecule 1: Major vault protein



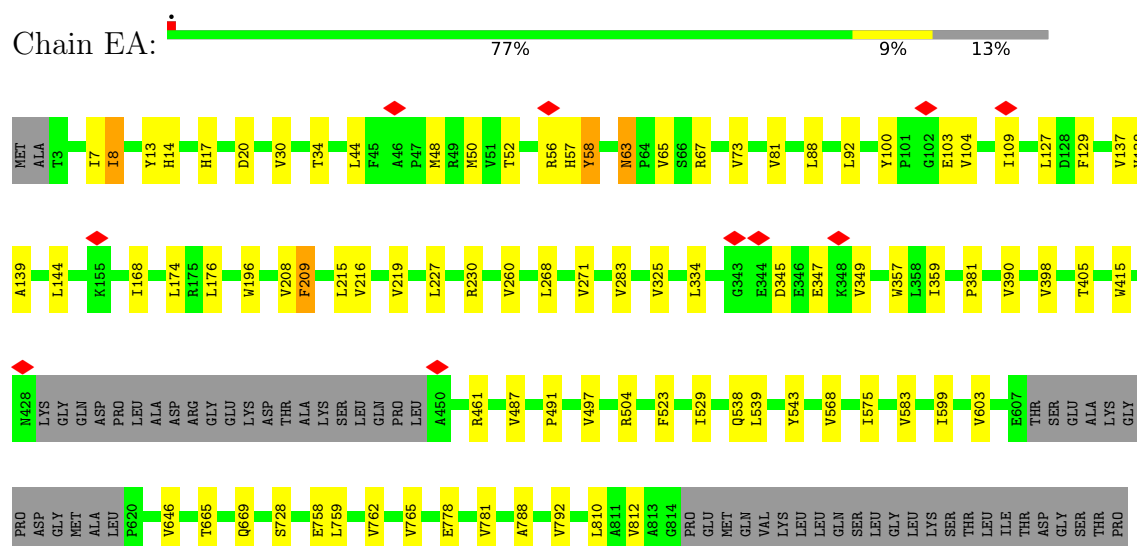
- Molecule 1: Major vault protein



- Molecule 1: Major vault protein



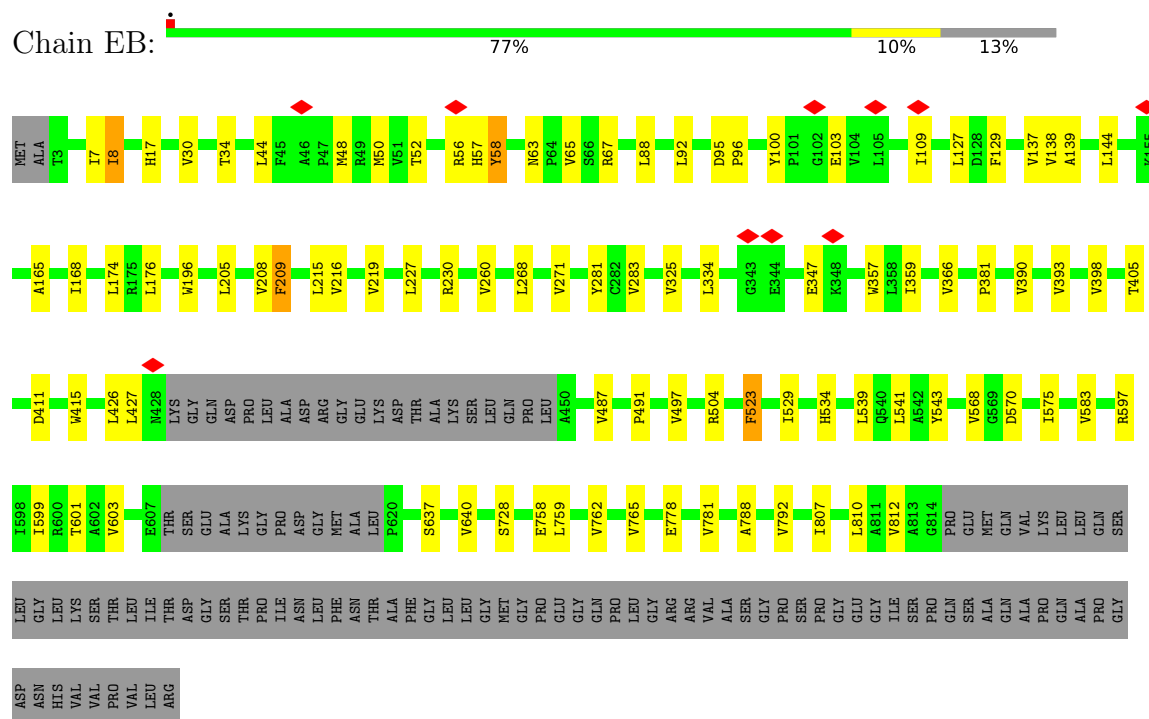
- Molecule 1: Major vault protein



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

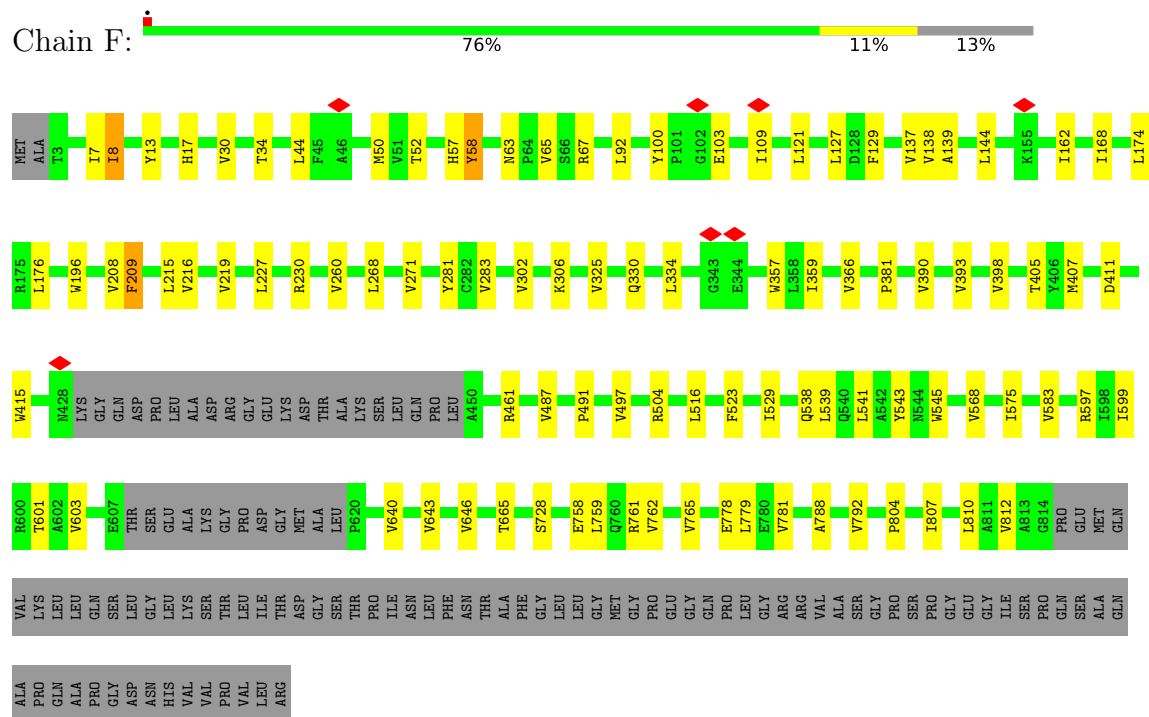
• Molecule 1: Major vault protein

Chain EB:

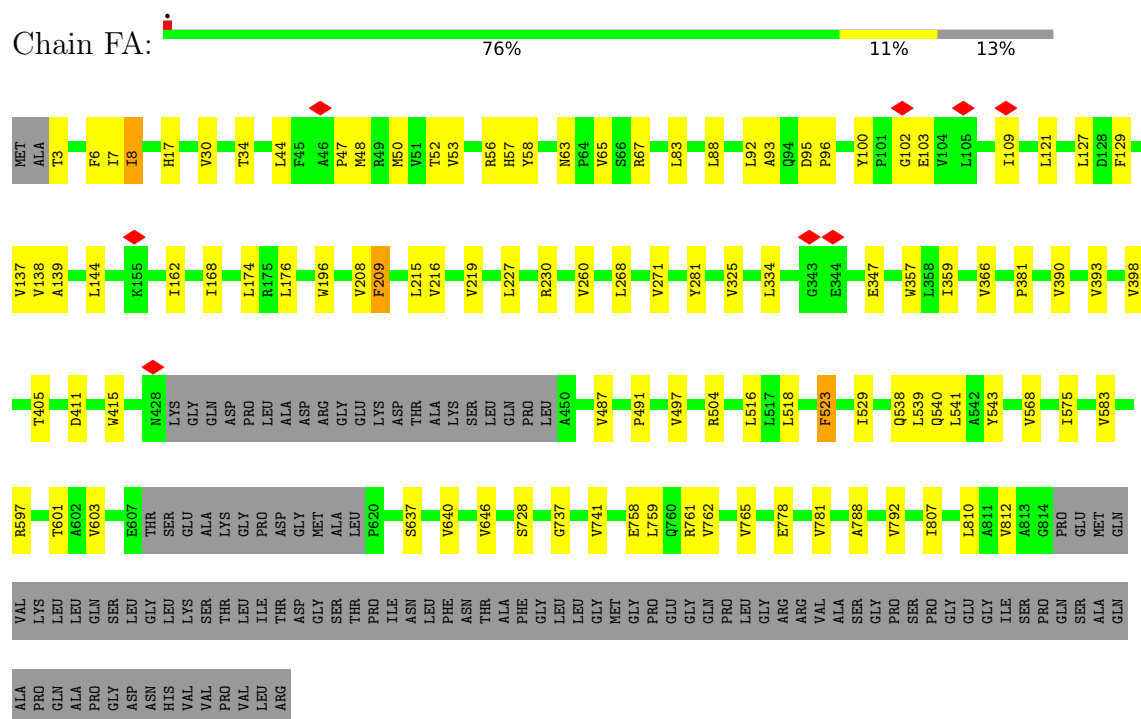


• Molecule 1: Major vault protein

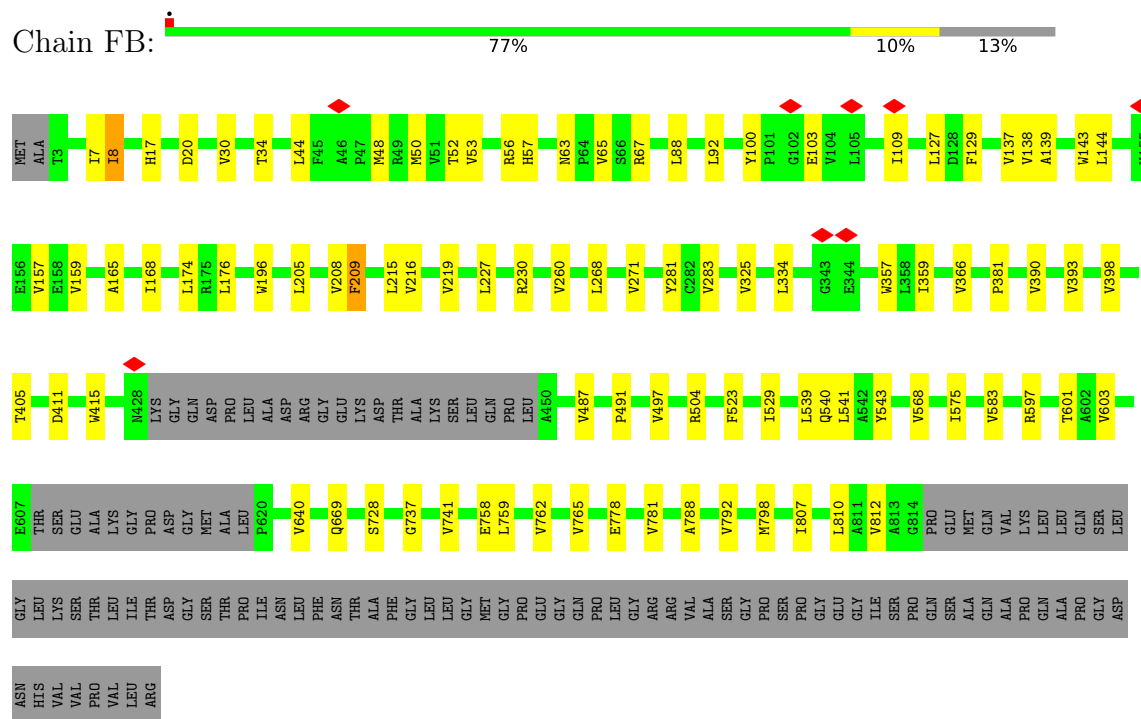
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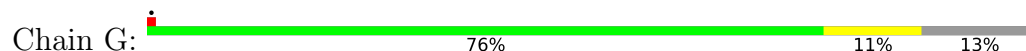
• Molecule 1: Major vault protein



- Molecule 1: Major vault protein

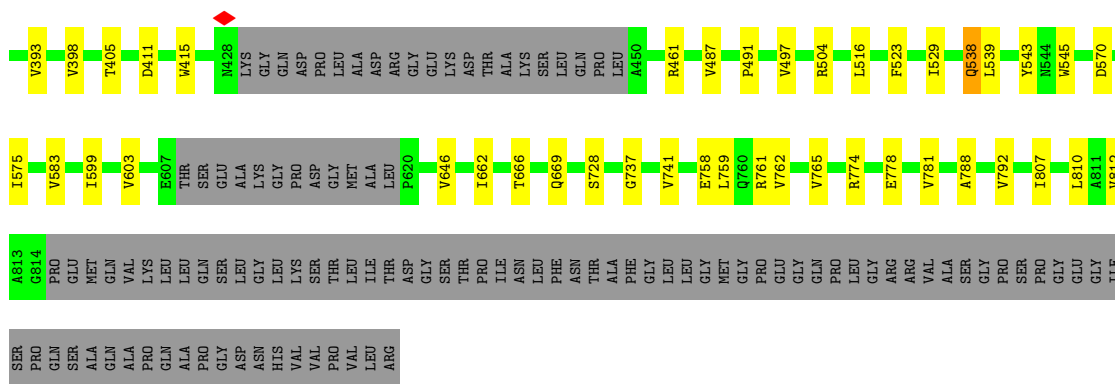


- Molecule 1: Major vault protein

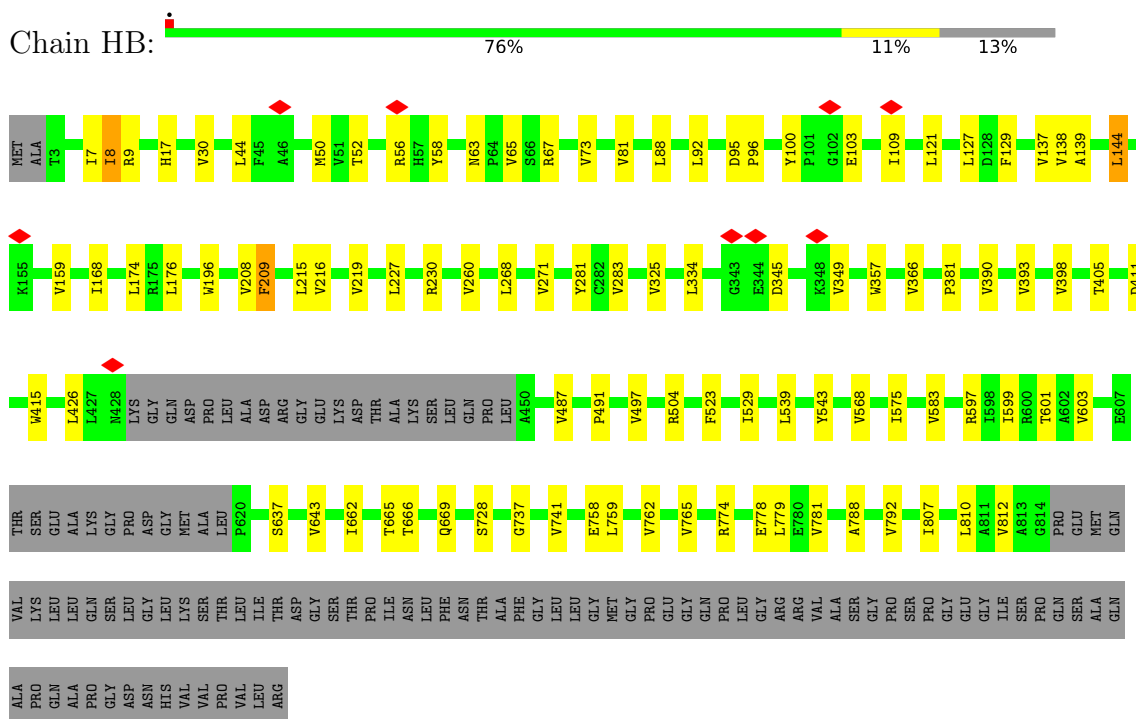




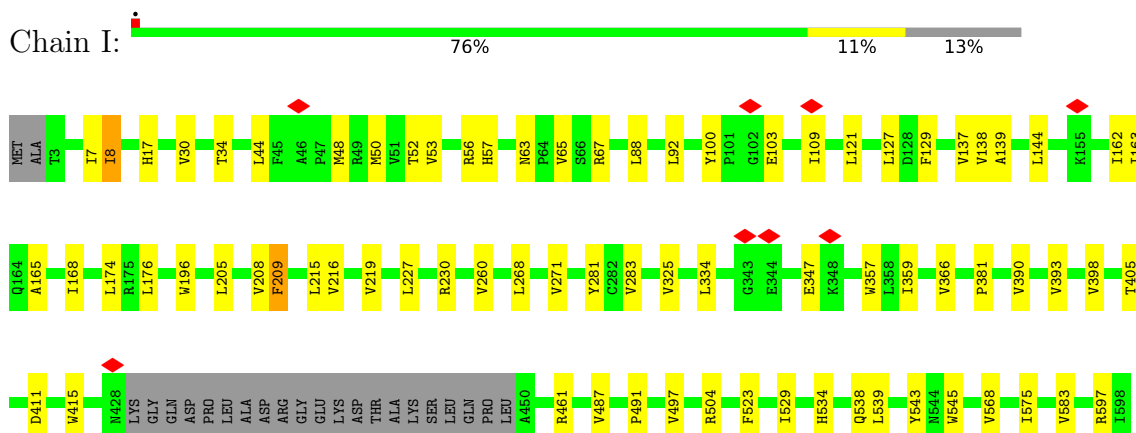


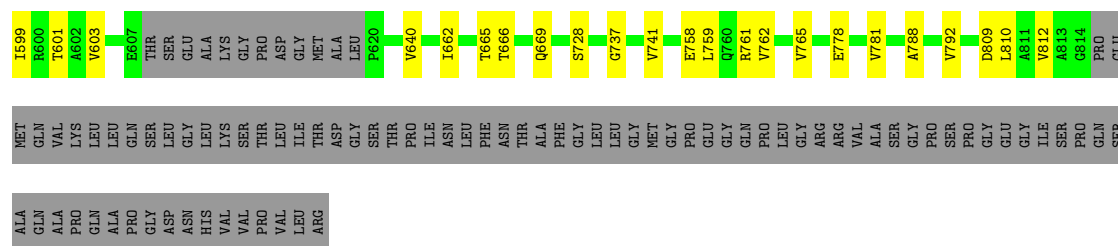


- Molecule 1: Major vault protein

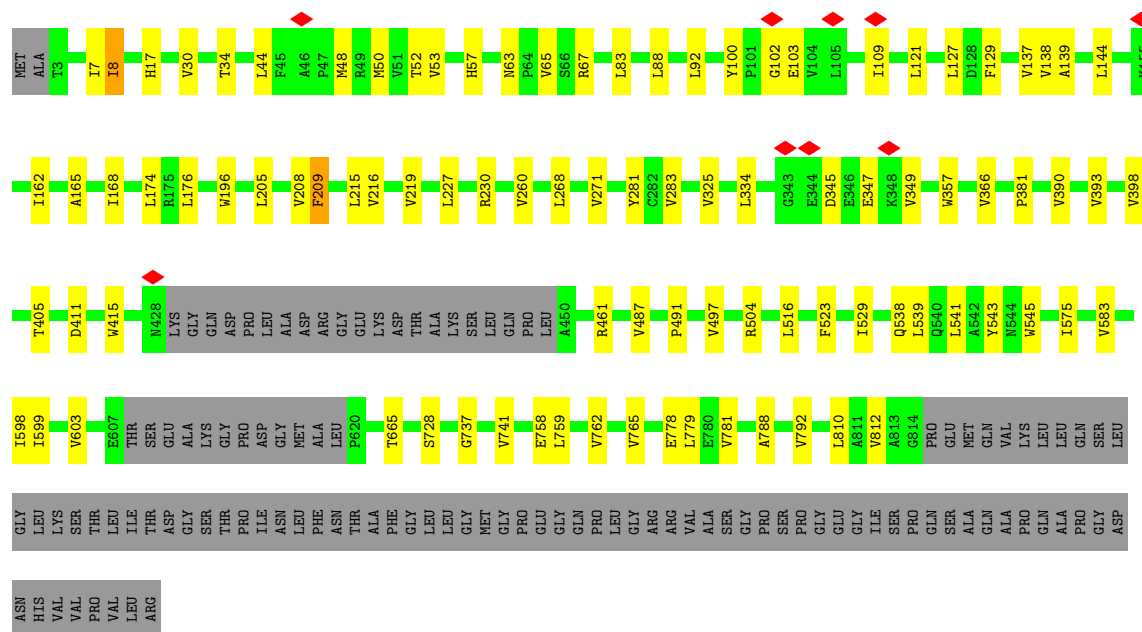
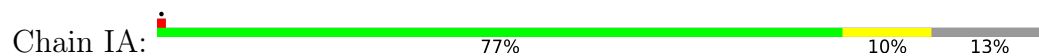


- Molecule 1: Major vault protein

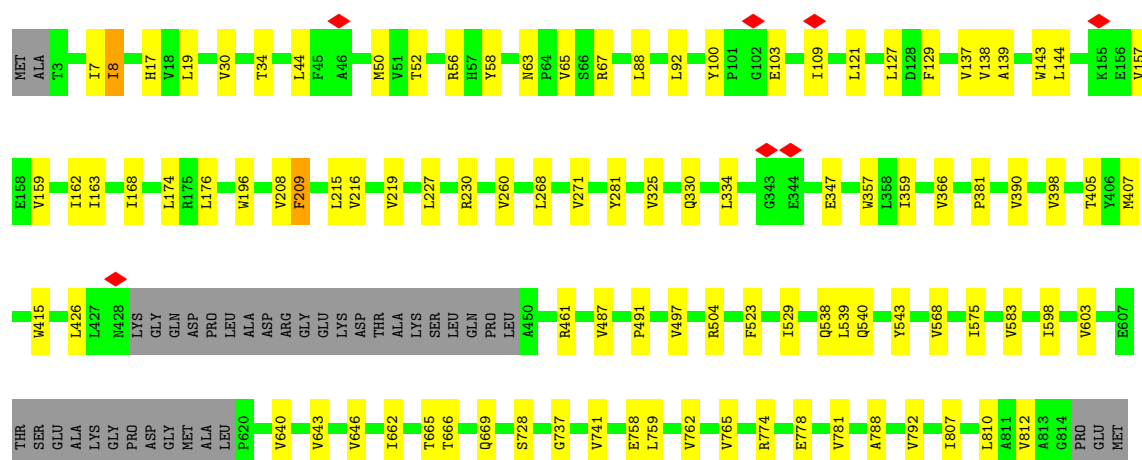
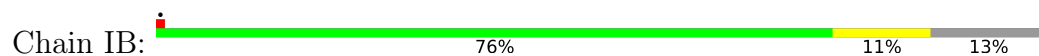


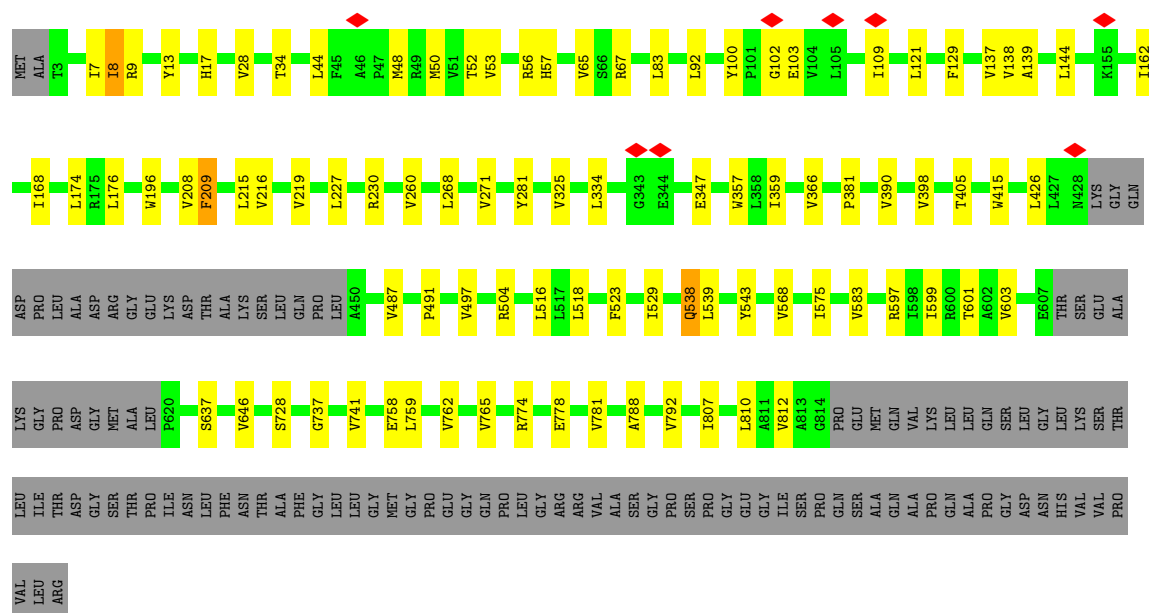


• Molecule 1: Major vault protein



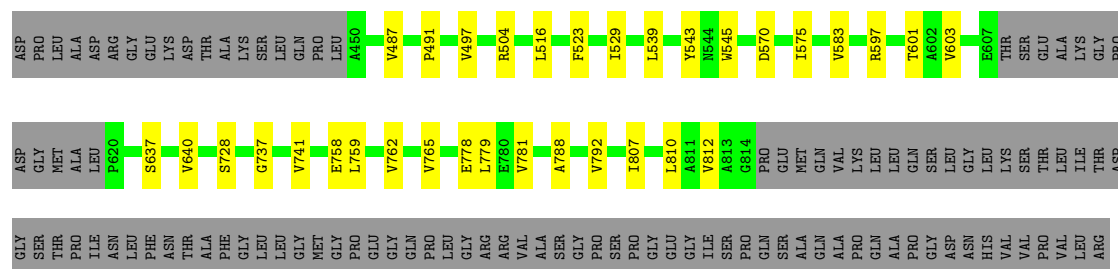
• Molecule 1: Major vault protein



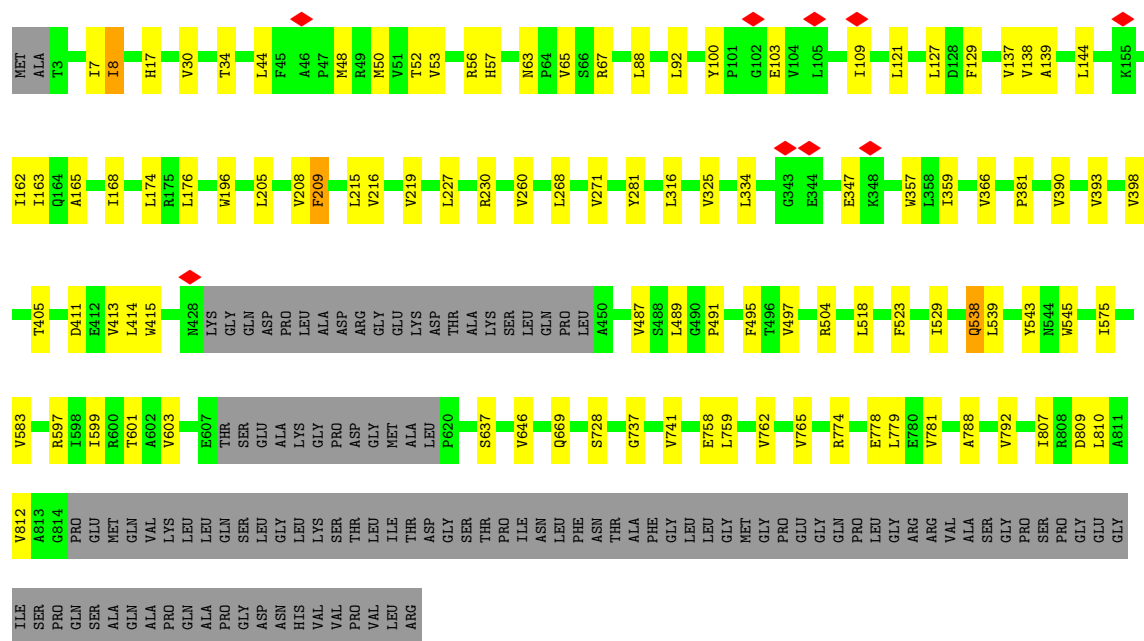
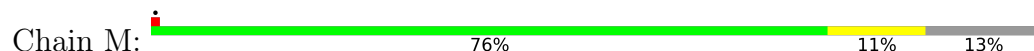




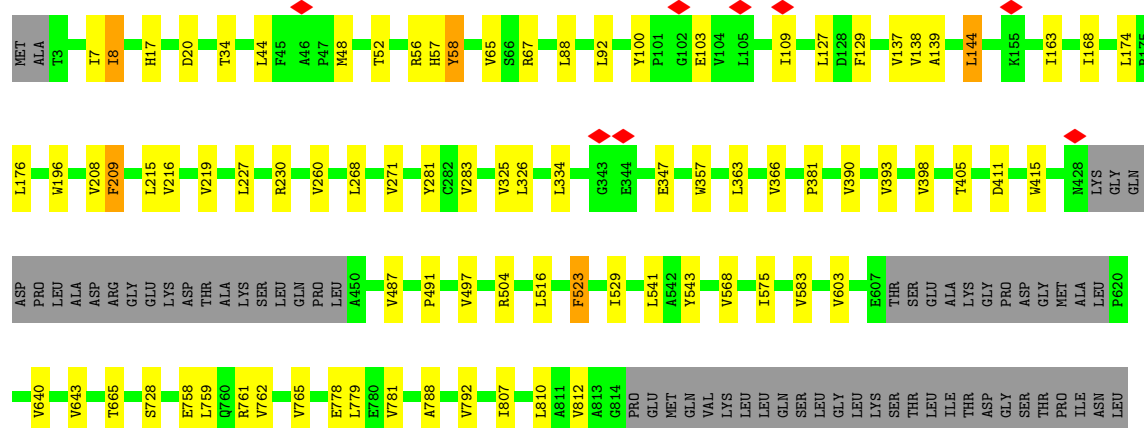
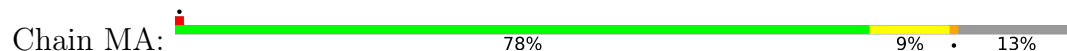




• Molecule 1: Major vault protein



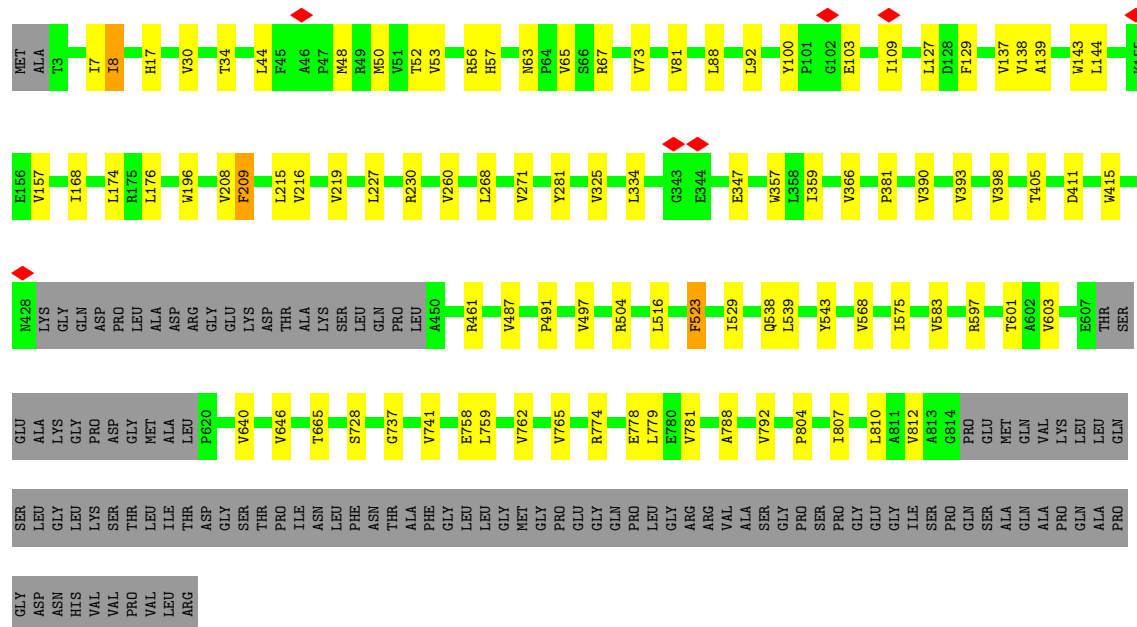
• Molecule 1: Major vault protein



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

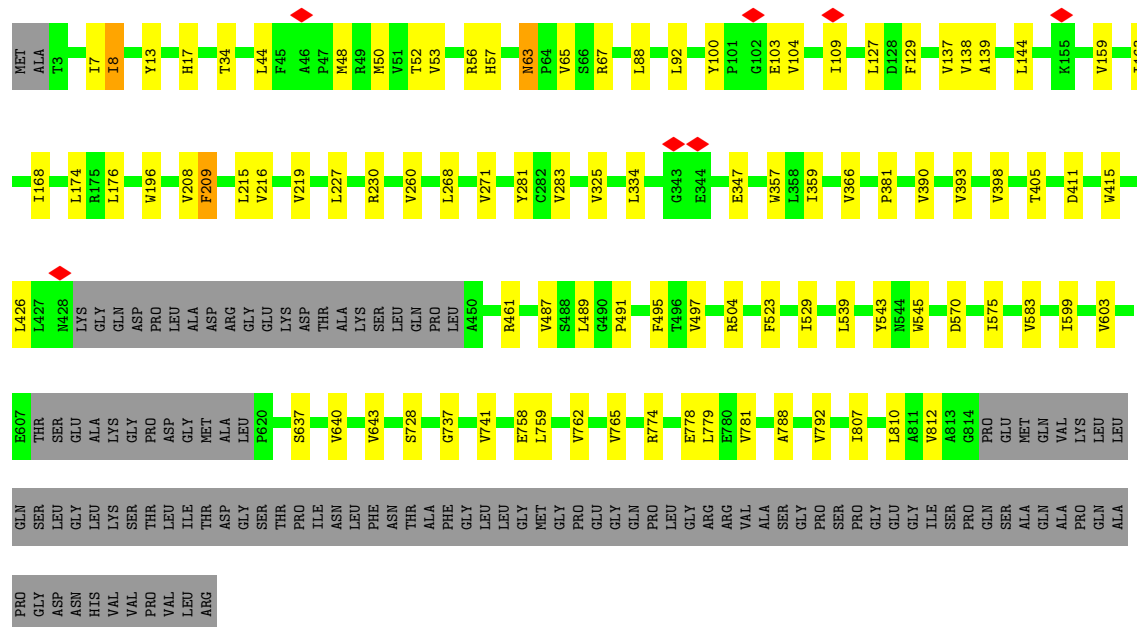
• Molecule 1: Major vault protein

Chain MB:

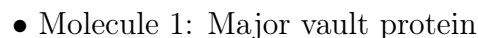
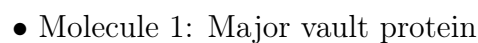


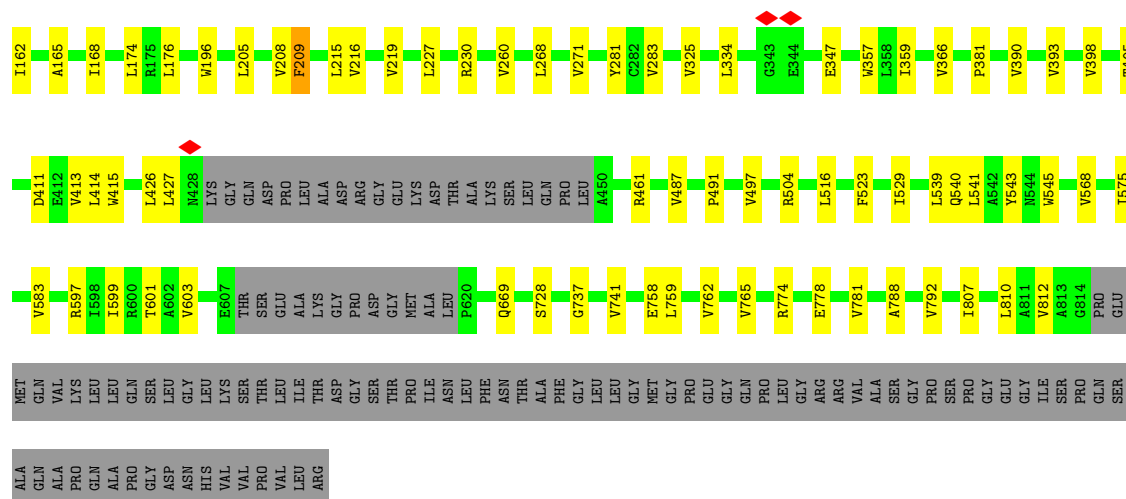
• Molecule 1: Major vault protein

Chain N:

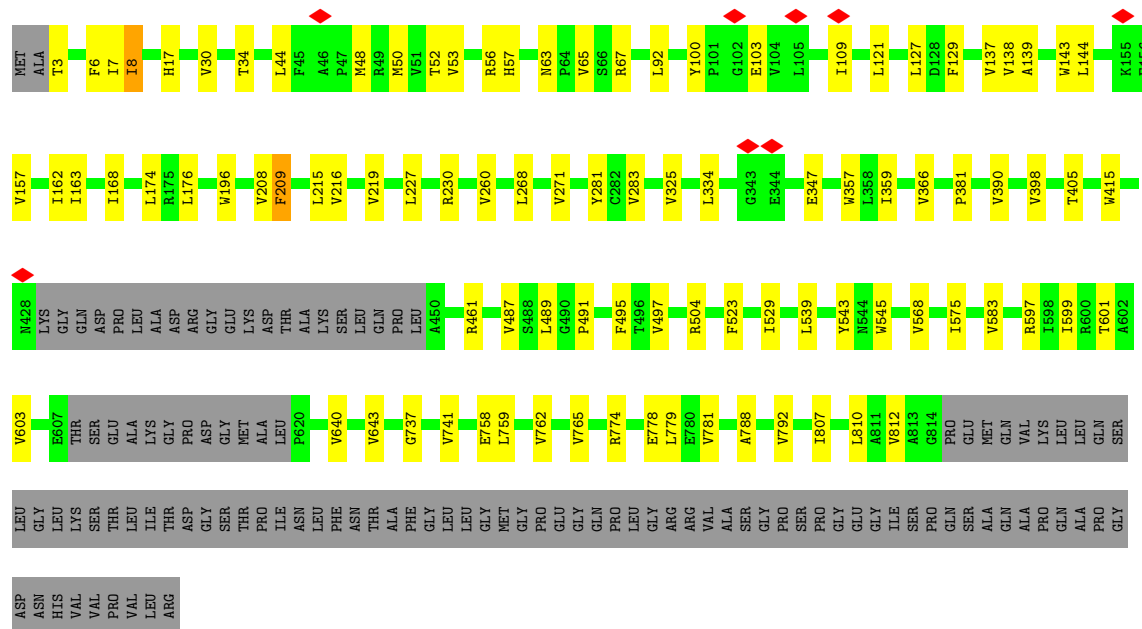
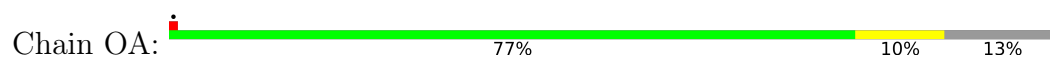


• Molecule 1: Major vault protein

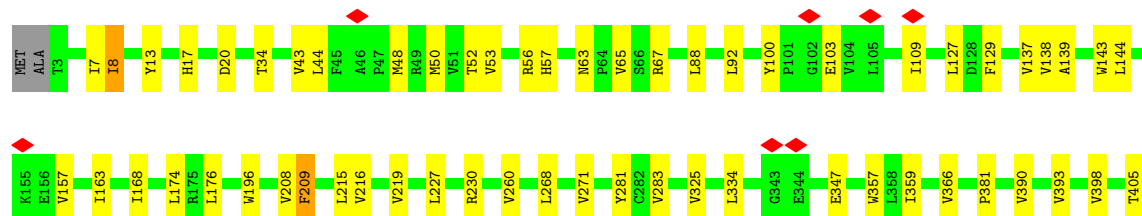
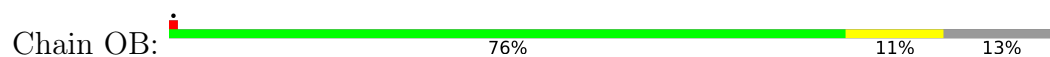


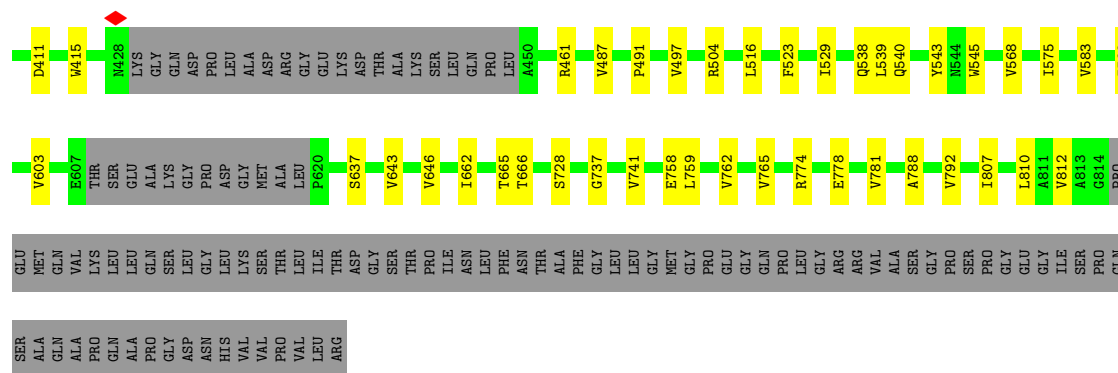


- Molecule 1: Major vault protein



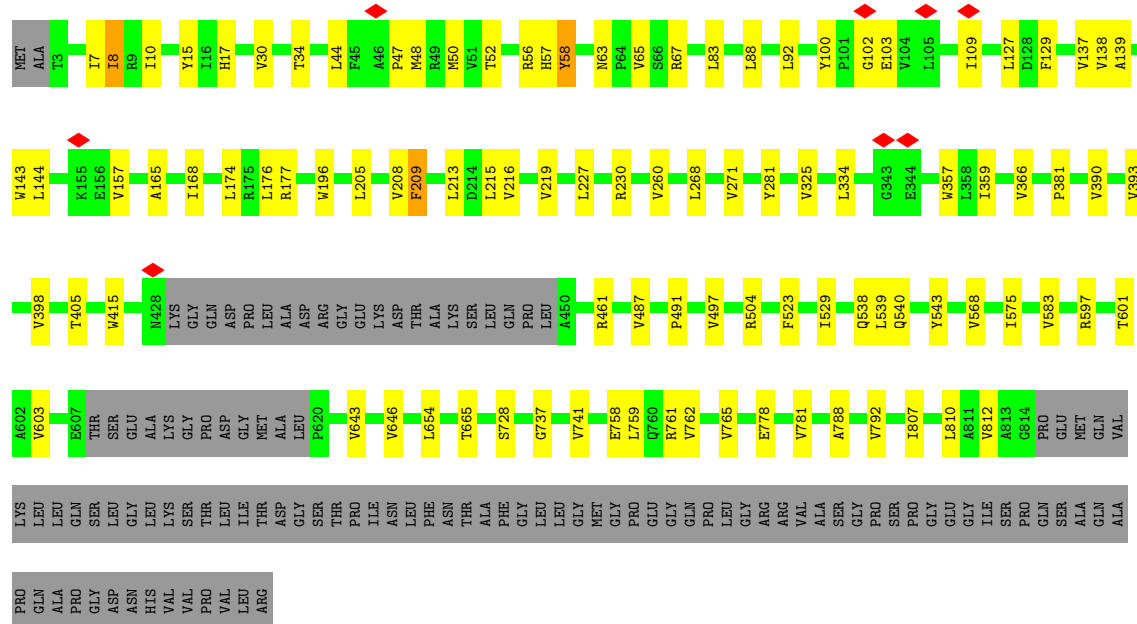
- Molecule 1: Major vault protein





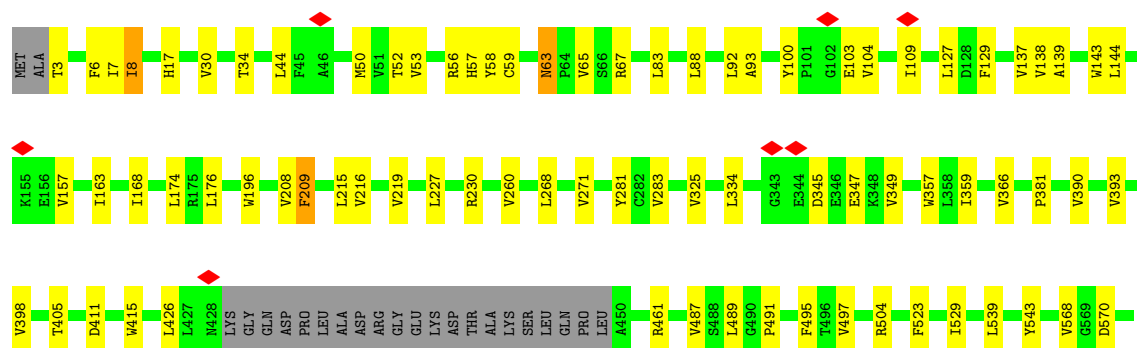
• Molecule 1: Major vault protein

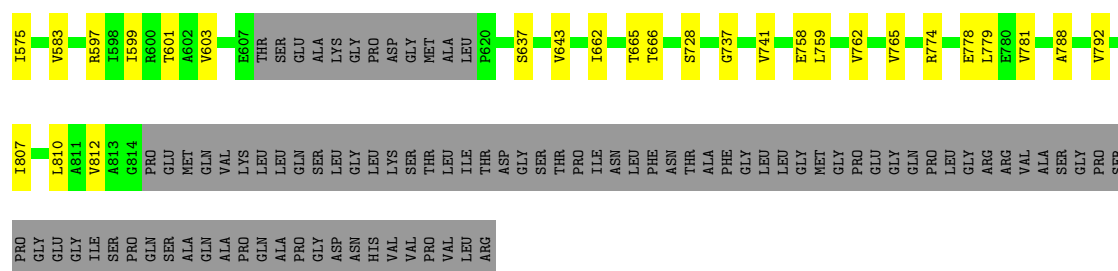
Chain P: 76% 11% 13%



• Molecule 1: Major vault protein

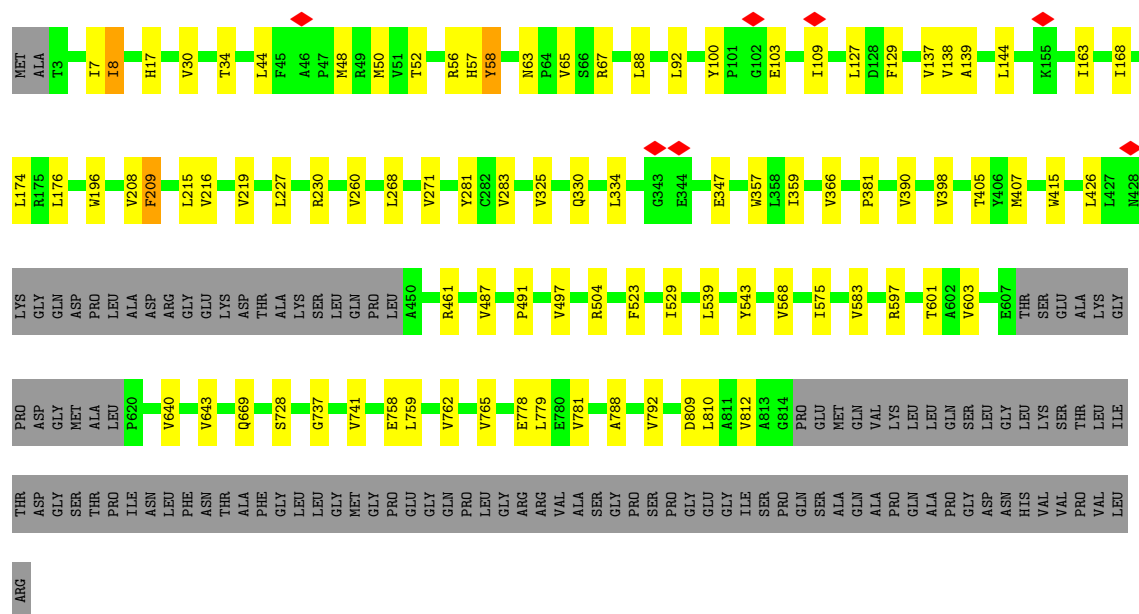
Chain PA: 75% 12% 13%





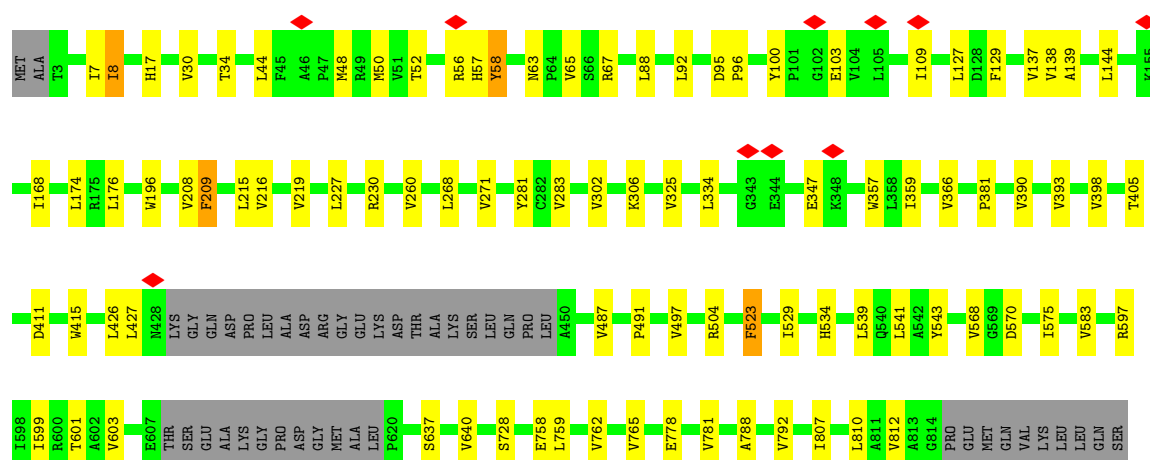
• Molecule 1: Major vault protein

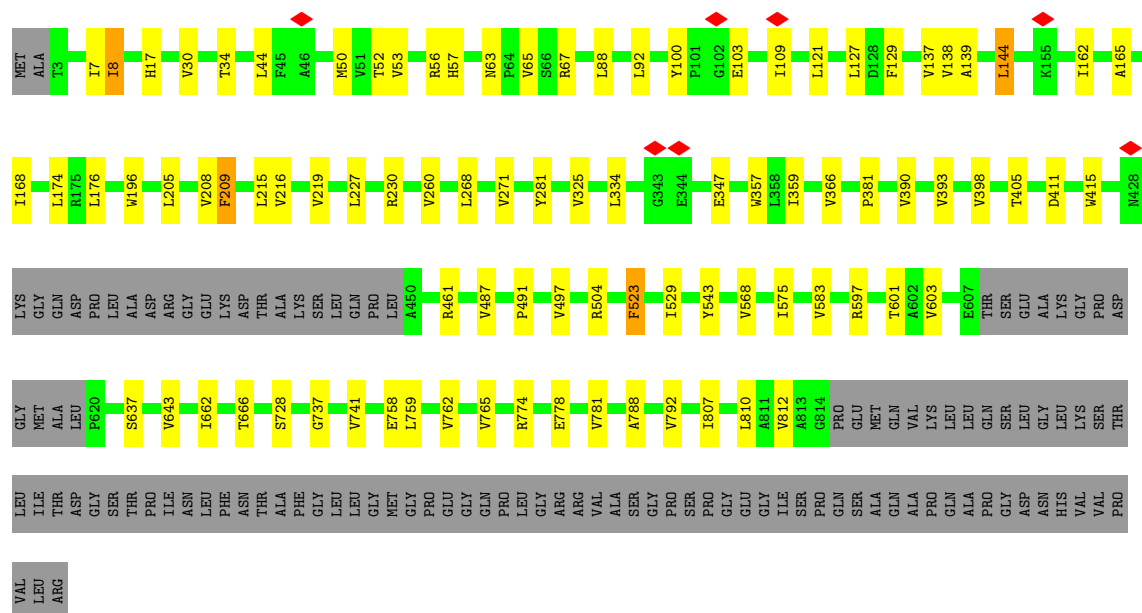
Chain PB: 77% 10% 13%



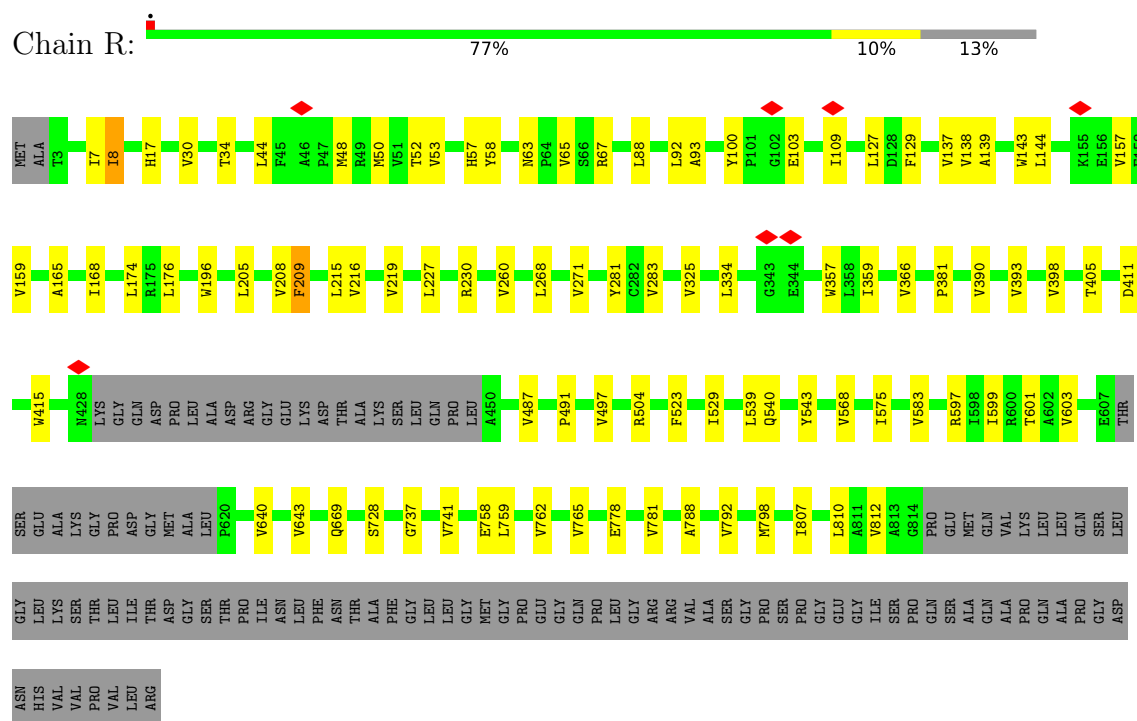
• Molecule 1: Major vault protein

Chain Q: 77% 10% 13%

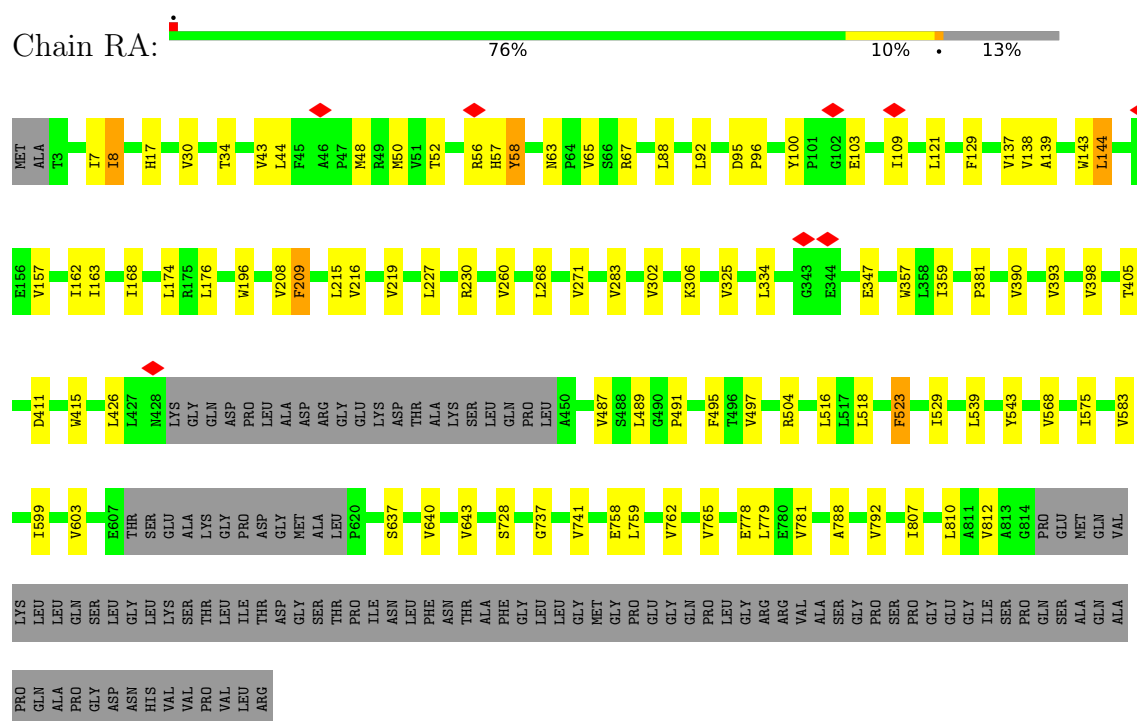




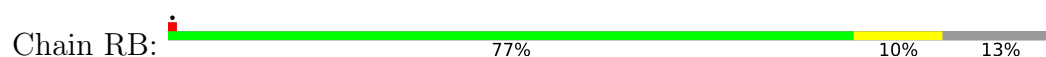
- Molecule 1: Major vault protein

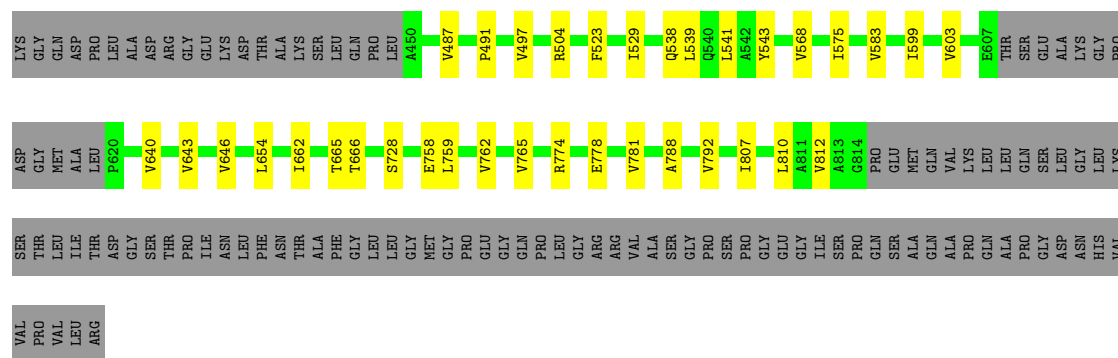


- Molecule 1: Major vault protein

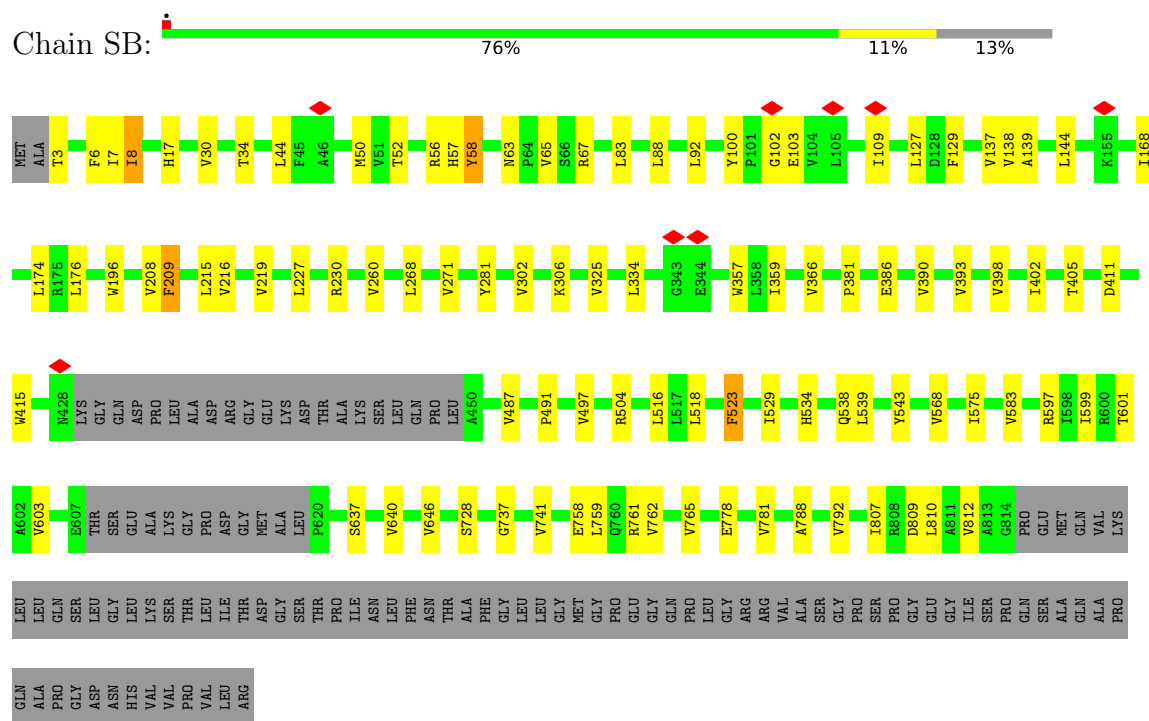


- Molecule 1: Major vault protein

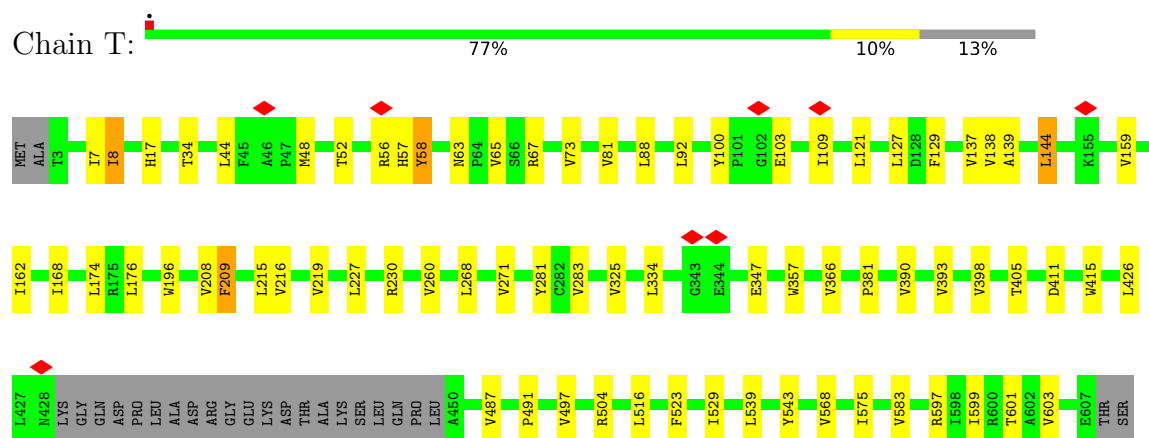




• Molecule 1: Major vault protein

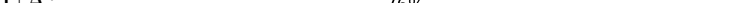


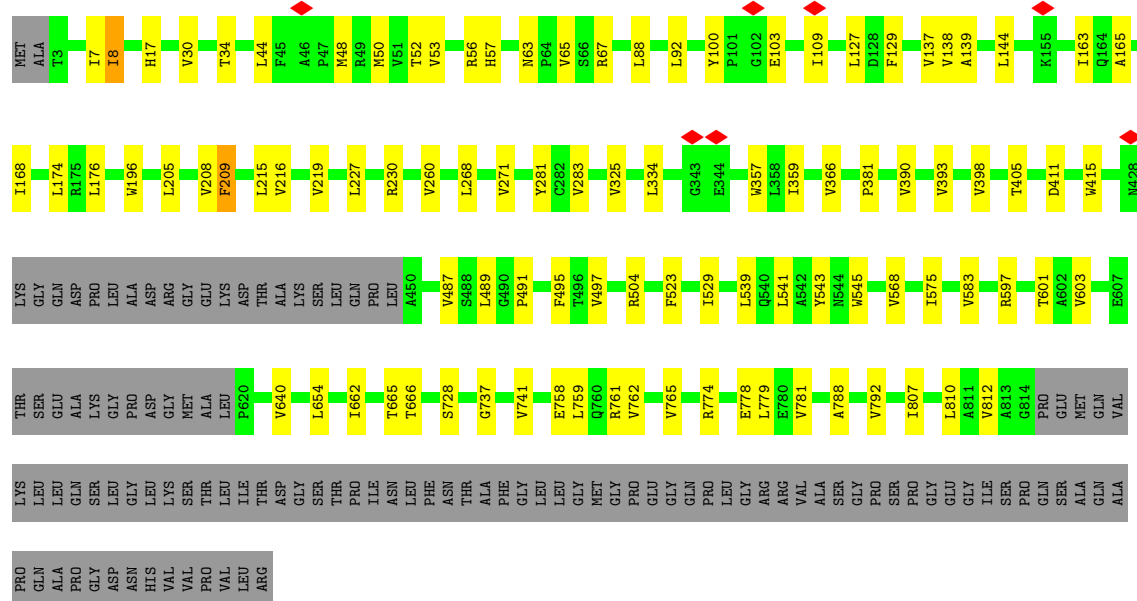
• Molecule 1: Major vault protein



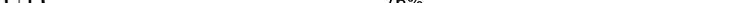
[illegible]

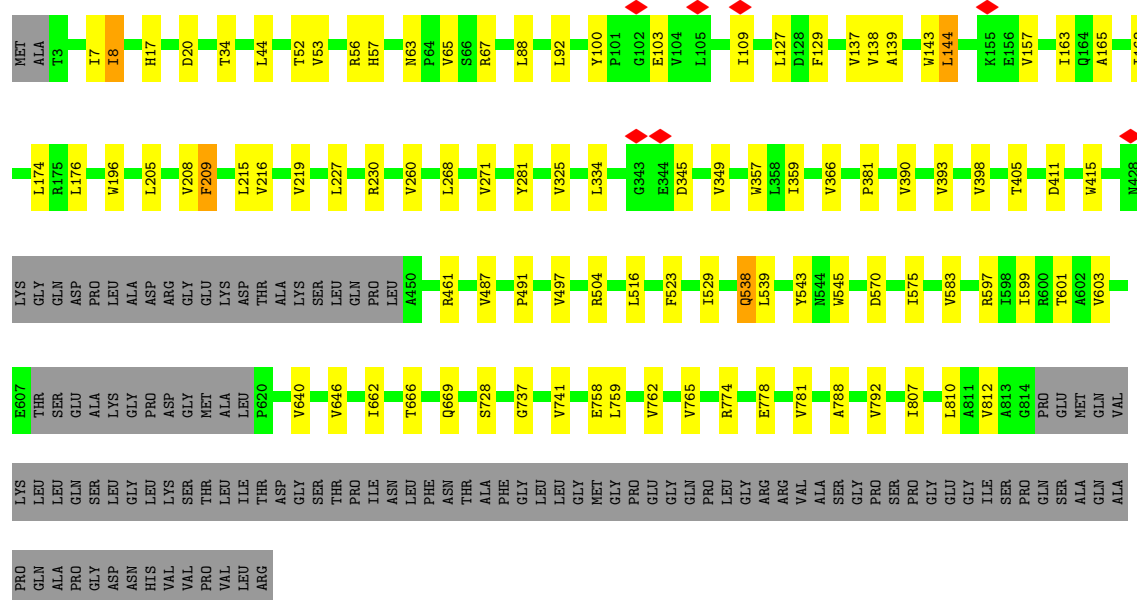
- Molecule 1: Major vault protein

Chain UA:  76% 11% 13%

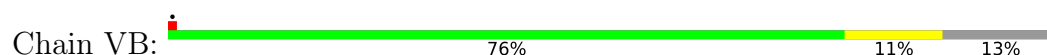
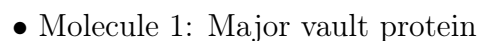


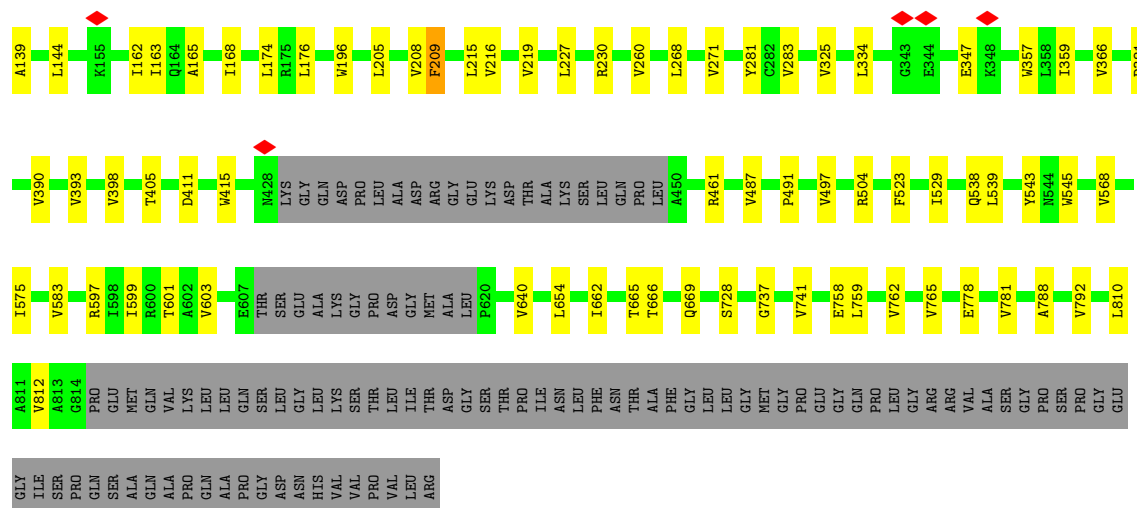
- Molecule 1: Major vault protein

Chain UB:  76% 10% 13%

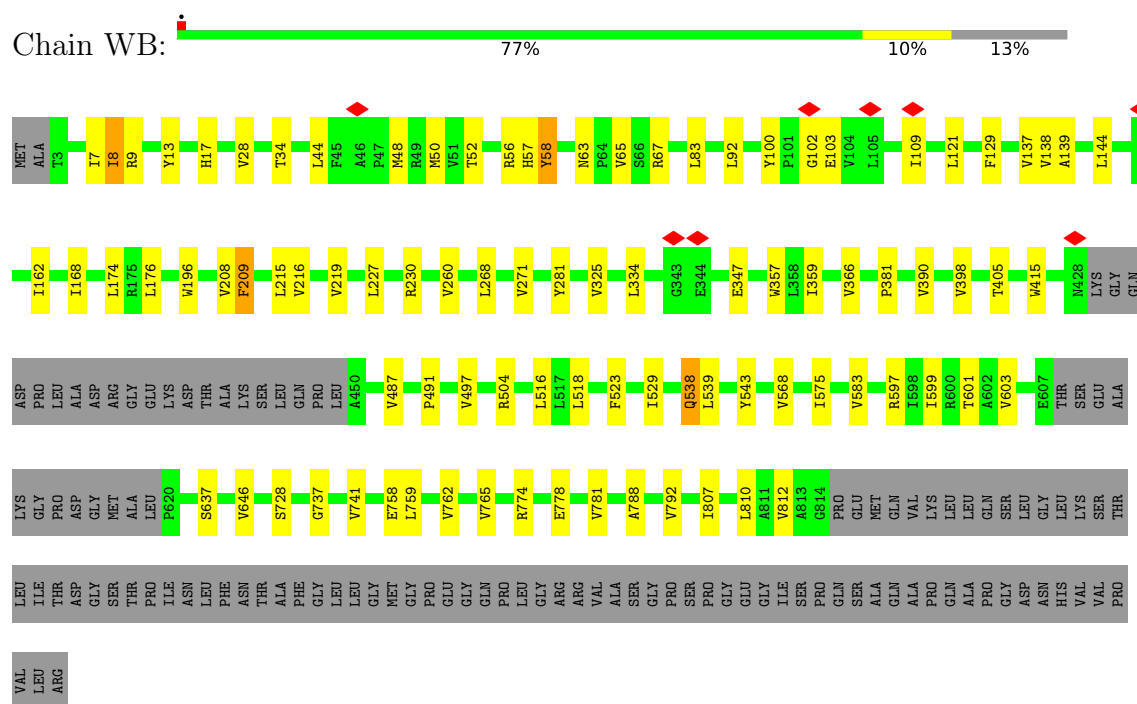


- Molecule 1: Major vault protein

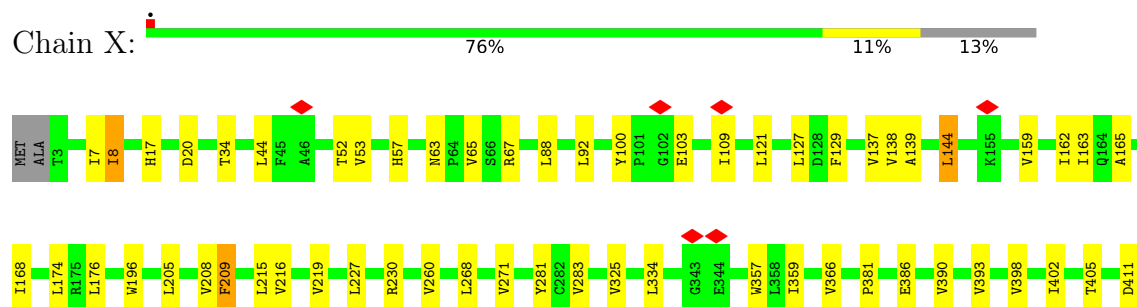


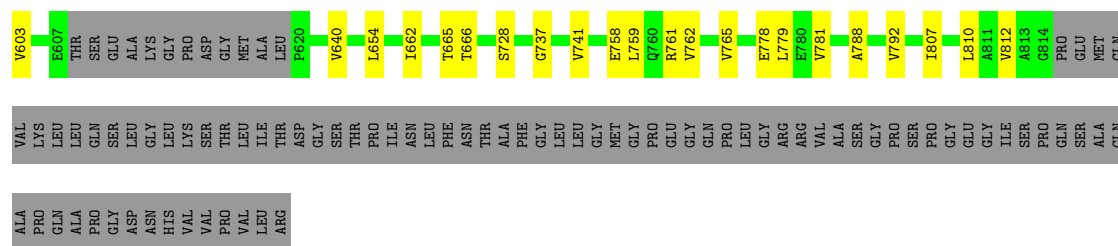


• Molecule 1: Major vault protein



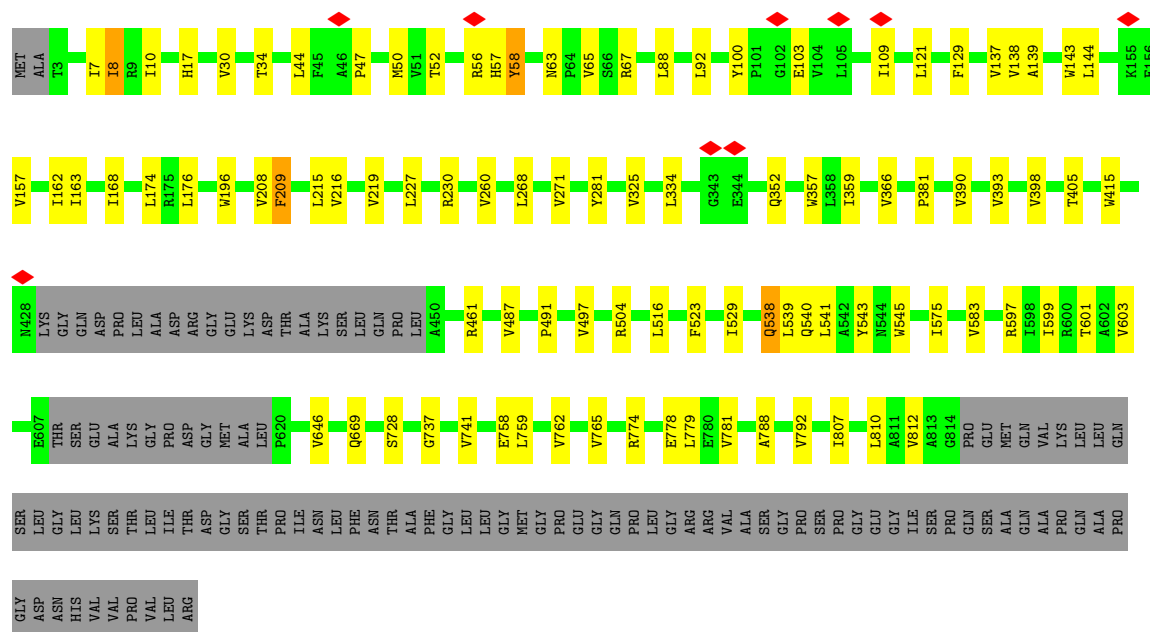
• Molecule 1: Major vault protein





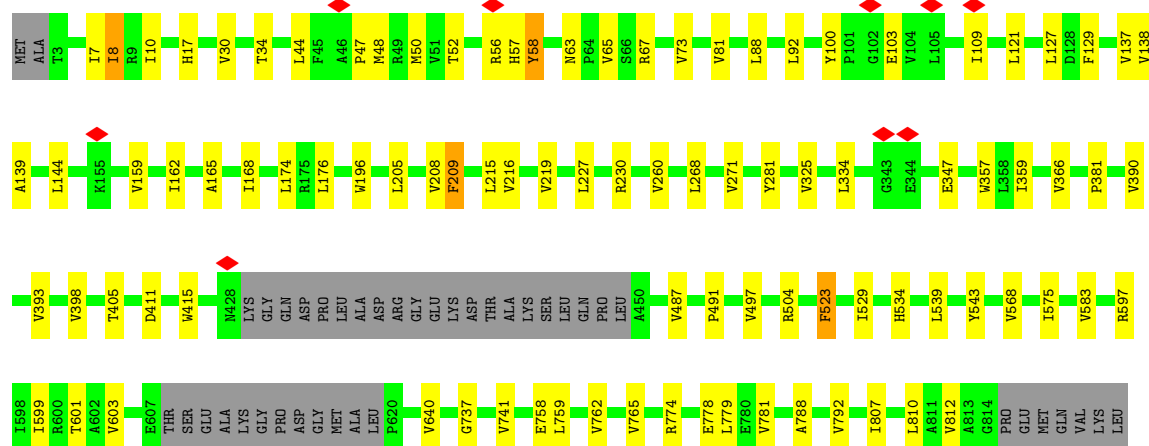
• Molecule 1: Major vault protein

Chain Y: 76% 10% 13%

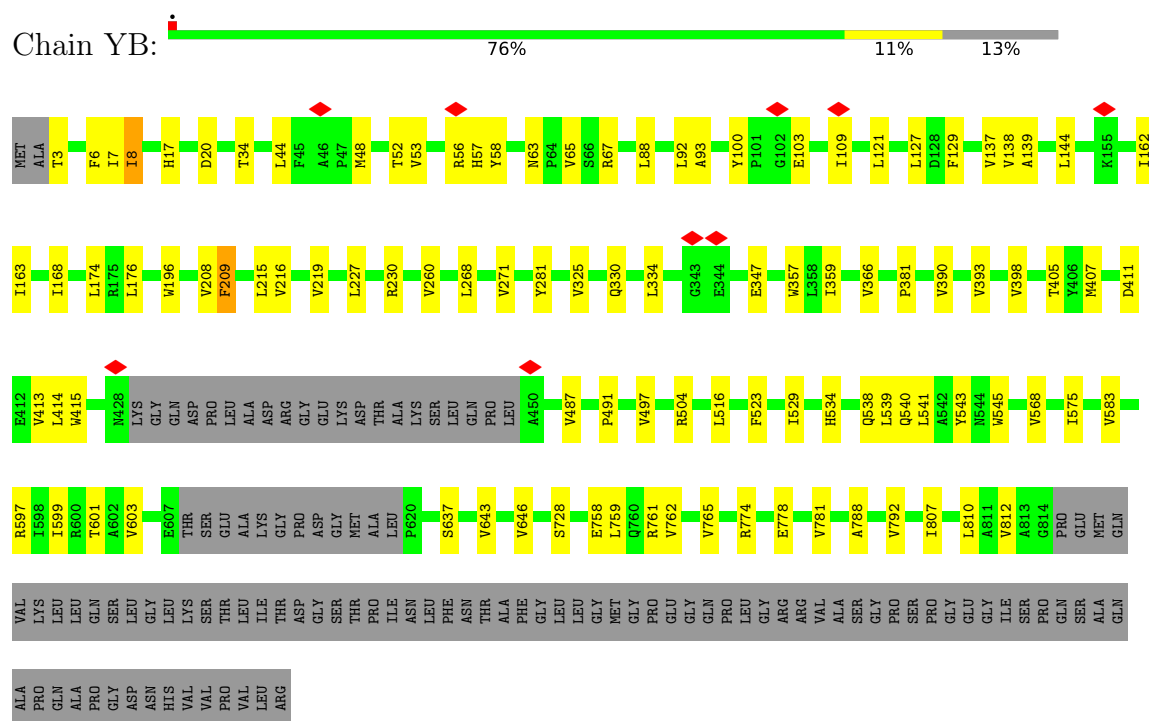


• Molecule 1: Major vault protein

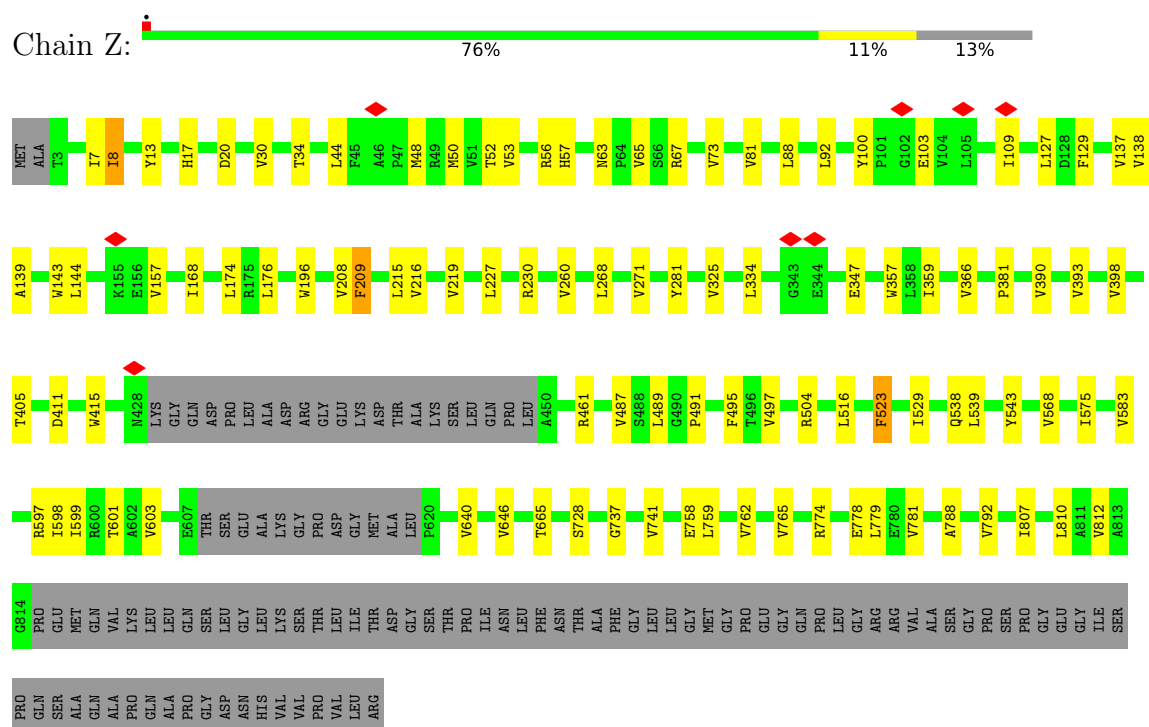
Chain YA: 77% 10% 13%



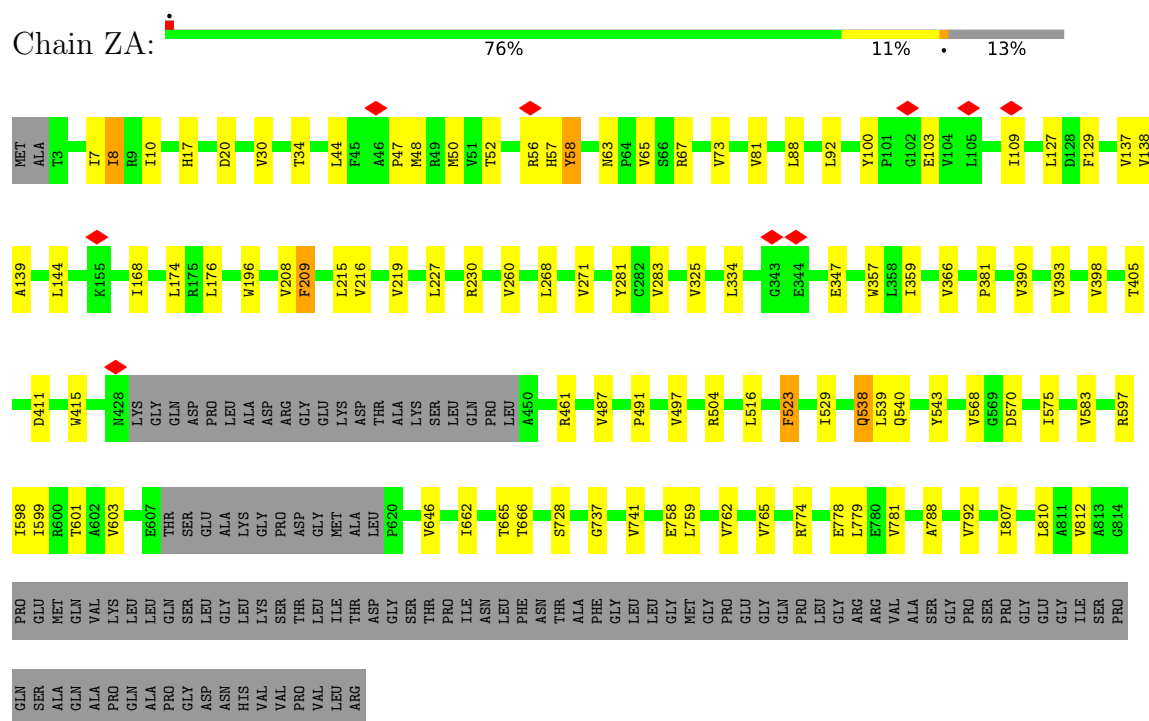
- Molecule 1: Major vault protein



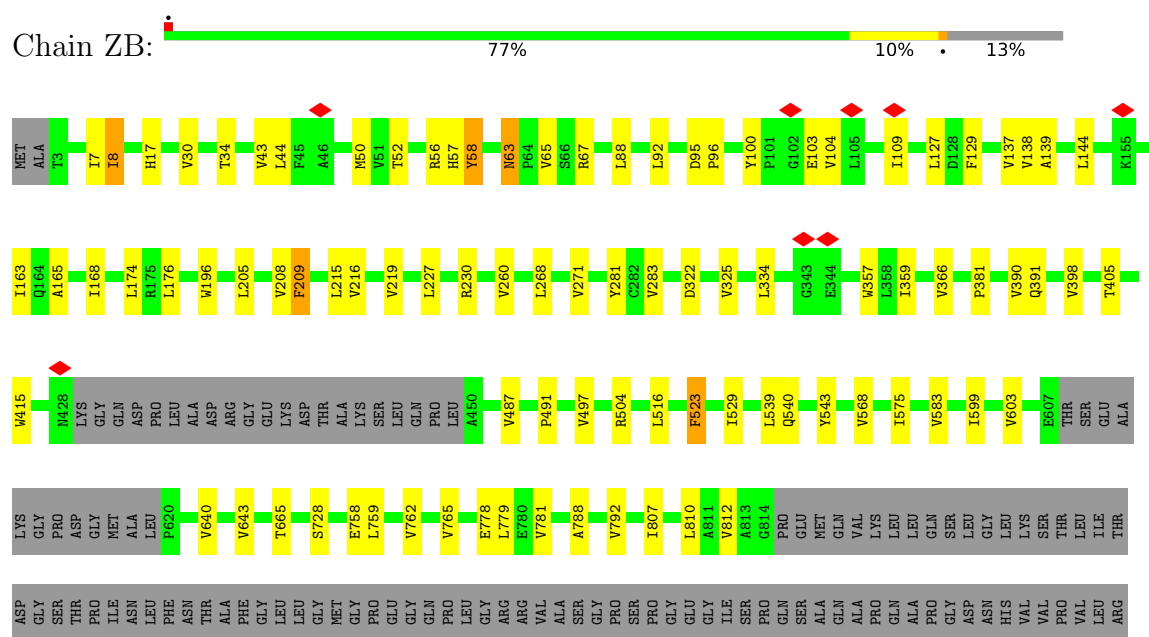
- Molecule 1: Major vault protein



- Molecule 1: Major vault protein



- Molecule 1: Major vault protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D39	Depositor
Number of particles used	11172	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.15	Depositor
Minimum defocus (nm)	551	Depositor
Maximum defocus (nm)	2330	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.881	Depositor
Minimum map value	-0.270	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.099	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	861.7984, 861.7984, 861.7984	wwPDB
Map dimensions	1024, 1024, 1024	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8416, 0.8416, 0.8416	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.17	0/6291	0.40	0/8533
1	AA	0.17	0/6291	0.40	0/8533
1	AB	0.17	0/6291	0.40	0/8533
1	AC	0.17	0/6291	0.40	0/8533
1	B	0.17	0/6291	0.40	0/8533
1	BA	0.17	0/6291	0.40	0/8533
1	BB	0.17	0/6291	0.40	0/8533
1	C	0.17	0/6291	0.39	0/8533
1	CA	0.17	0/6291	0.40	0/8533
1	CB	0.17	0/6291	0.40	0/8533
1	D	0.17	0/6291	0.40	0/8533
1	DA	0.17	0/6291	0.40	0/8533
1	DB	0.17	0/6291	0.40	0/8533
1	E	0.17	0/6291	0.40	0/8533
1	EA	0.17	0/6291	0.40	0/8533
1	EB	0.17	0/6291	0.39	0/8533
1	F	0.17	0/6291	0.40	0/8533
1	FA	0.17	0/6291	0.40	0/8533
1	FB	0.17	0/6291	0.40	0/8533
1	G	0.17	0/6291	0.40	0/8533
1	GA	0.17	0/6291	0.40	0/8533
1	GB	0.17	0/6291	0.40	0/8533
1	H	0.17	0/6291	0.39	0/8533
1	HA	0.17	0/6291	0.40	0/8533
1	HB	0.17	0/6291	0.40	0/8533
1	I	0.17	0/6291	0.39	0/8533
1	IA	0.17	0/6291	0.40	0/8533
1	IB	0.17	0/6291	0.40	0/8533
1	J	0.17	0/6291	0.40	0/8533
1	JA	0.17	0/6291	0.40	0/8533
1	JB	0.17	0/6291	0.40	0/8533
1	K	0.17	0/6291	0.40	0/8533
1	KA	0.17	0/6291	0.40	0/8533
1	KB	0.17	0/6291	0.40	0/8533

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.17	0/6291	0.40	0/8533
1	LA	0.17	0/6291	0.40	0/8533
1	LB	0.17	0/6291	0.40	0/8533
1	M	0.17	0/6291	0.40	0/8533
1	MA	0.17	0/6291	0.40	0/8533
1	MB	0.17	0/6291	0.40	0/8533
1	N	0.17	0/6291	0.40	0/8533
1	NA	0.17	0/6291	0.40	0/8533
1	NB	0.17	0/6291	0.39	0/8533
1	O	0.17	0/6291	0.40	0/8533
1	OA	0.17	0/6291	0.40	0/8533
1	OB	0.17	0/6291	0.40	0/8533
1	P	0.17	0/6291	0.40	0/8533
1	PA	0.17	0/6291	0.40	0/8533
1	PB	0.17	0/6291	0.40	0/8533
1	Q	0.17	0/6291	0.39	0/8533
1	QA	0.17	0/6291	0.40	0/8533
1	QB	0.17	0/6291	0.40	0/8533
1	R	0.17	0/6291	0.40	0/8533
1	RA	0.17	0/6291	0.40	0/8533
1	RB	0.17	0/6291	0.40	0/8533
1	S	0.17	0/6291	0.40	0/8533
1	SA	0.17	0/6291	0.40	0/8533
1	SB	0.17	0/6291	0.40	0/8533
1	T	0.17	0/6291	0.40	0/8533
1	TA	0.17	0/6291	0.40	0/8533
1	TB	0.17	0/6291	0.40	0/8533
1	UA	0.17	0/6291	0.40	0/8533
1	UB	0.17	0/6291	0.40	0/8533
1	V	0.17	0/6291	0.40	0/8533
1	VA	0.17	0/6291	0.40	0/8533
1	VB	0.17	0/6291	0.40	0/8533
1	W	0.17	0/6291	0.39	0/8533
1	WA	0.17	0/6291	0.40	0/8533
1	WB	0.17	0/6291	0.40	0/8533
1	X	0.17	0/6291	0.39	0/8533
1	XA	0.17	0/6291	0.39	0/8533
1	XB	0.17	0/6291	0.40	0/8533
1	Y	0.17	0/6291	0.40	0/8533
1	YA	0.17	0/6291	0.40	0/8533
1	YB	0.17	0/6291	0.40	0/8533
1	Z	0.17	0/6291	0.40	0/8533
1	ZA	0.17	0/6291	0.40	0/8533

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ZB	0.17	0/6291	0.40	0/8533
All	All	0.17	0/490698	0.40	0/665574

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	6181	6205	6203	75	0
1	AA	6181	6205	6203	66	0
1	AB	6181	6205	6203	75	0
1	AC	6181	6205	6203	74	0
1	B	6181	6205	6203	71	0
1	BA	6181	6205	6203	69	0
1	BB	6181	6205	6203	76	0
1	C	6181	6205	6203	65	0
1	CA	6181	6205	6203	66	0
1	CB	6181	6205	6203	76	0
1	D	6181	6205	6203	65	0
1	DA	6181	6205	6203	70	0
1	DB	6181	6205	6203	75	0
1	E	6181	6205	6203	65	0
1	EA	6181	6205	6203	62	0
1	EB	6181	6205	6203	71	0
1	F	6181	6205	6203	70	0
1	FA	6181	6205	6203	72	0
1	FB	6181	6205	6203	69	0
1	G	6181	6205	6203	66	0
1	GA	6181	6205	6203	68	0
1	GB	6181	6205	6203	67	0
1	H	6181	6205	6203	67	0
1	HA	6181	6205	6203	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HB	6181	6205	6203	70	0
1	I	6181	6205	6203	69	0
1	IA	6181	6205	6203	62	0
1	IB	6181	6205	6203	73	0
1	J	6181	6205	6203	73	0
1	JA	6181	6205	6203	66	0
1	JB	6181	6205	6203	68	0
1	K	6181	6205	6203	70	0
1	KA	6181	6205	6203	75	0
1	KB	6181	6205	6203	66	0
1	L	6181	6205	6203	69	0
1	LA	6181	6205	6203	73	0
1	LB	6181	6205	6203	62	0
1	M	6181	6205	6203	74	0
1	MA	6181	6205	6203	63	0
1	MB	6181	6205	6203	70	0
1	N	6181	6205	6203	70	0
1	NA	6181	6205	6203	72	0
1	NB	6181	6205	6203	68	0
1	O	6181	6205	6203	74	0
1	OA	6181	6205	6203	72	0
1	OB	6181	6205	6203	68	0
1	P	6181	6205	6203	74	0
1	PA	6181	6205	6203	75	0
1	PB	6181	6205	6203	67	0
1	Q	6181	6205	6203	69	0
1	QA	6181	6205	6203	64	0
1	QB	6181	6205	6203	64	0
1	R	6181	6205	6203	70	0
1	RA	6181	6205	6203	66	0
1	RB	6181	6205	6203	61	0
1	S	6181	6205	6203	66	0
1	SA	6181	6205	6203	69	0
1	SB	6181	6205	6203	67	0
1	T	6181	6205	6203	67	0
1	TA	6181	6205	6203	72	0
1	TB	6181	6205	6203	65	0
1	UA	6181	6205	6203	71	0
1	UB	6181	6205	6203	69	0
1	V	6181	6205	6203	69	0
1	VA	6181	6205	6203	69	0
1	VB	6181	6205	6203	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	6181	6205	6203	64	0
1	WA	6181	6205	6203	72	0
1	WB	6181	6205	6203	70	0
1	X	6181	6205	6203	70	0
1	XA	6181	6205	6203	73	0
1	XB	6181	6205	6203	76	0
1	Y	6181	6205	6203	67	0
1	YA	6181	6205	6203	75	0
1	YB	6181	6205	6203	77	0
1	Z	6181	6205	6203	70	0
1	ZA	6181	6205	6203	71	0
1	ZB	6181	6205	6203	67	0
All	All	482118	483990	483834	5156	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 5.

The worst 5 of 5156 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:O:168:ILE:HG22	1:O:215:LEU:HD21	1.64	0.80
1:MB:168:ILE:HG22	1:MB:215:LEU:HD21	1.64	0.79
1:Z:168:ILE:HG22	1:Z:215:LEU:HD21	1.64	0.79
1:T:168:ILE:HG22	1:T:215:LEU:HD21	1.64	0.79
1:VA:168:ILE:HG22	1:VA:215:LEU:HD21	1.63	0.79

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	773/893 (87%)	721 (93%)	51 (7%)	1 (0%)	48	78
1	AA	773/893 (87%)	715 (92%)	57 (7%)	1 (0%)	48	78
1	AB	773/893 (87%)	721 (93%)	52 (7%)	0	100	100
1	AC	773/893 (87%)	718 (93%)	54 (7%)	1 (0%)	48	78
1	B	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	BA	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	BB	773/893 (87%)	716 (93%)	57 (7%)	0	100	100
1	C	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	CA	773/893 (87%)	721 (93%)	51 (7%)	1 (0%)	48	78
1	CB	773/893 (87%)	718 (93%)	54 (7%)	1 (0%)	48	78
1	D	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	DA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	DB	773/893 (87%)	722 (93%)	51 (7%)	0	100	100
1	E	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	EA	773/893 (87%)	723 (94%)	49 (6%)	1 (0%)	48	78
1	EB	773/893 (87%)	716 (93%)	56 (7%)	1 (0%)	48	78
1	F	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	FA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	FB	773/893 (87%)	717 (93%)	56 (7%)	0	100	100
1	G	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	GA	773/893 (87%)	723 (94%)	49 (6%)	1 (0%)	48	78
1	GB	773/893 (87%)	719 (93%)	54 (7%)	0	100	100
1	H	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	HA	773/893 (87%)	722 (93%)	51 (7%)	0	100	100
1	HB	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	I	773/893 (87%)	718 (93%)	54 (7%)	1 (0%)	48	78
1	IA	773/893 (87%)	717 (93%)	55 (7%)	1 (0%)	48	78
1	IB	773/893 (87%)	716 (93%)	56 (7%)	1 (0%)	48	78
1	J	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	JA	773/893 (87%)	722 (93%)	50 (6%)	1 (0%)	48	78
1	JB	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	K	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	KA	773/893 (87%)	716 (93%)	56 (7%)	1 (0%)	48	78
1	KB	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	L	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	LA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	LB	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	M	773/893 (87%)	721 (93%)	51 (7%)	1 (0%)	48	78
1	MA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	MB	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	N	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	NA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	NB	773/893 (87%)	715 (92%)	57 (7%)	1 (0%)	48	78
1	O	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	OA	773/893 (87%)	718 (93%)	54 (7%)	1 (0%)	48	78
1	OB	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	P	773/893 (87%)	716 (93%)	57 (7%)	0	100	100
1	PA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	PB	773/893 (87%)	723 (94%)	49 (6%)	1 (0%)	48	78
1	Q	773/893 (87%)	717 (93%)	55 (7%)	1 (0%)	48	78
1	QA	773/893 (87%)	720 (93%)	53 (7%)	0	100	100
1	QB	773/893 (87%)	723 (94%)	49 (6%)	1 (0%)	48	78
1	R	773/893 (87%)	717 (93%)	56 (7%)	0	100	100
1	RA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	RB	773/893 (87%)	722 (93%)	50 (6%)	1 (0%)	48	78
1	S	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	SA	773/893 (87%)	717 (93%)	56 (7%)	0	100	100
1	SB	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	T	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	TA	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	TB	773/893 (87%)	725 (94%)	47 (6%)	1 (0%)	48	78
1	UA	773/893 (87%)	721 (93%)	52 (7%)	0	100	100
1	UB	773/893 (87%)	719 (93%)	54 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	V	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	VA	773/893 (87%)	722 (93%)	50 (6%)	1 (0%)	48	78
1	VB	773/893 (87%)	722 (93%)	50 (6%)	1 (0%)	48	78
1	W	773/893 (87%)	723 (94%)	50 (6%)	0	100	100
1	WA	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	WB	773/893 (87%)	720 (93%)	52 (7%)	1 (0%)	48	78
1	X	773/893 (87%)	722 (93%)	51 (7%)	0	100	100
1	XA	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
1	XB	773/893 (87%)	719 (93%)	54 (7%)	0	100	100
1	Y	773/893 (87%)	722 (93%)	51 (7%)	0	100	100
1	YA	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	YB	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	Z	773/893 (87%)	719 (93%)	53 (7%)	1 (0%)	48	78
1	ZA	773/893 (87%)	723 (94%)	49 (6%)	1 (0%)	48	78
1	ZB	773/893 (87%)	718 (93%)	55 (7%)	0	100	100
All	All	60294/69654 (87%)	56116 (93%)	4129 (7%)	49 (0%)	49	78

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	347	GLU
1	CB	347	GLU
1	E	347	GLU
1	LA	347	GLU
1	MA	347	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain 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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	666/755 (88%)	656 (98%)	10 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	AB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	AC	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	B	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	BA	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	BB	666/755 (88%)	657 (99%)	9 (1%)	59	76
1	C	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	CA	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	CB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	D	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	DA	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	DB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	E	666/755 (88%)	657 (99%)	9 (1%)	59	76
1	EA	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	EB	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	F	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	FA	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	FB	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	G	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	GA	666/755 (88%)	651 (98%)	15 (2%)	44	70
1	GB	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	H	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	HA	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	HB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	I	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	IA	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	IB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	J	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	JA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	JB	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	K	666/755 (88%)	657 (99%)	9 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	KA	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	KB	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	L	666/755 (88%)	650 (98%)	16 (2%)	43	69
1	LA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	LB	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	M	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	MA	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	MB	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	N	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	NA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	NB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	O	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	OA	666/755 (88%)	659 (99%)	7 (1%)	65	78
1	OB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	P	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	PA	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	PB	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	Q	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	QA	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	QB	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	R	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	RA	666/755 (88%)	650 (98%)	16 (2%)	43	69
1	RB	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	S	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	SA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	SB	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	T	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	TA	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	TB	666/755 (88%)	651 (98%)	15 (2%)	44	70
1	UA	666/755 (88%)	656 (98%)	10 (2%)	57	75
1	UB	666/755 (88%)	654 (98%)	12 (2%)	51	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	V	666/755 (88%)	652 (98%)	14 (2%)	47	71
1	VA	666/755 (88%)	659 (99%)	7 (1%)	65	78
1	VB	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	W	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	WA	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	WB	666/755 (88%)	655 (98%)	11 (2%)	53	74
1	X	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	XA	666/755 (88%)	654 (98%)	12 (2%)	51	73
1	XB	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	Y	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	YA	666/755 (88%)	657 (99%)	9 (1%)	59	76
1	YB	666/755 (88%)	657 (99%)	9 (1%)	59	76
1	Z	666/755 (88%)	653 (98%)	13 (2%)	48	72
1	ZA	666/755 (88%)	650 (98%)	16 (2%)	43	69
1	ZB	666/755 (88%)	652 (98%)	14 (2%)	47	71
All	All	51948/58890 (88%)	51012 (98%)	936 (2%)	51	73

5 of 936 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	MA	283	VAL
1	YB	34	THR
1	PB	88	LEU
1	YA	58	TYR
1	W	728	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 386 such sidechains are listed below:

Mol	Chain	Res	Type
1	OA	592	HIS
1	S	630	GLN
1	OB	630	GLN
1	QB	118	ASN
1	TA	85	HIS

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-53415. These allow visual inspection of the internal detail of the map and identification of artifacts.

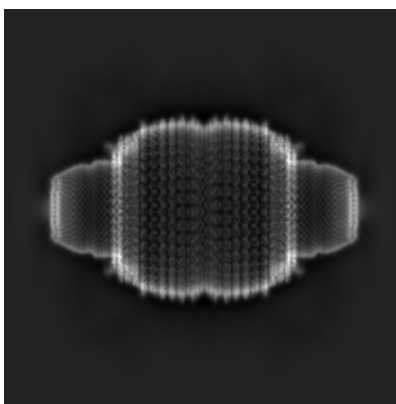
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

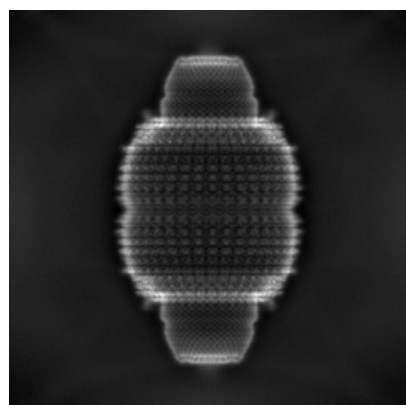


Y

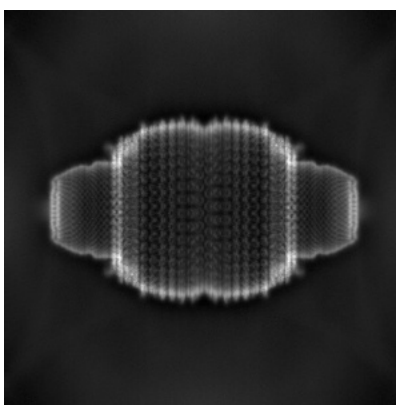


Z

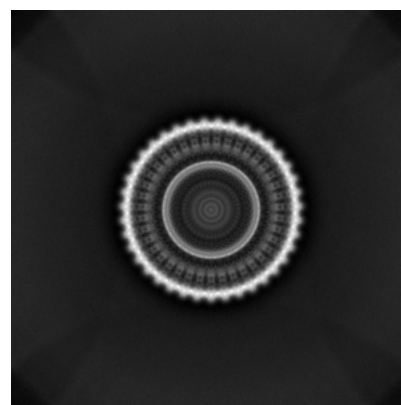
6.1.2 Raw map



X



Y

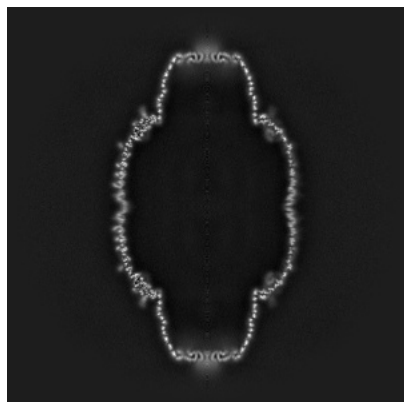


Z

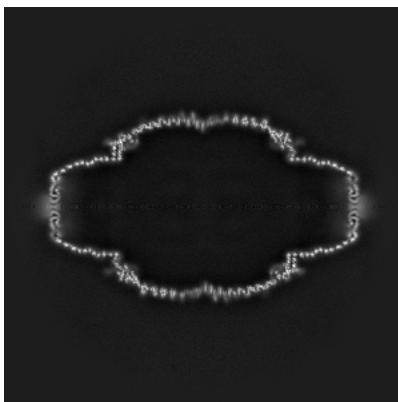
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

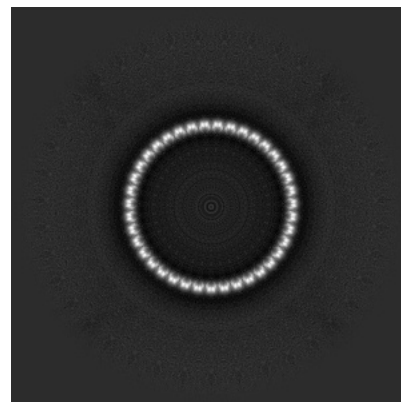
6.2.1 Primary map



X Index: 512

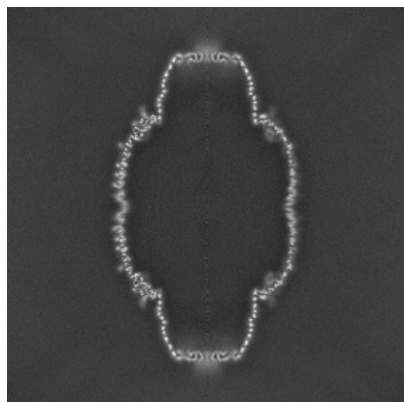


Y Index: 512

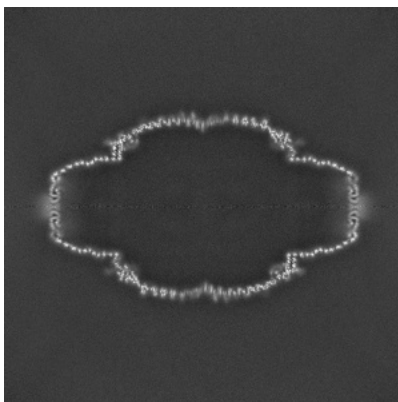


Z Index: 512

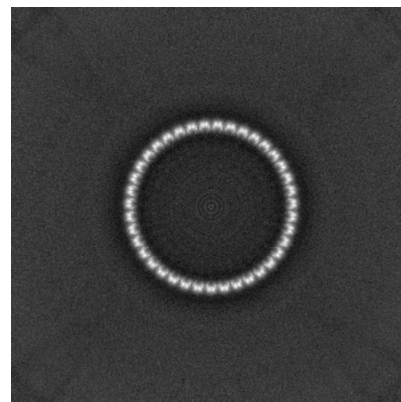
6.2.2 Raw map



X Index: 512



Y Index: 512

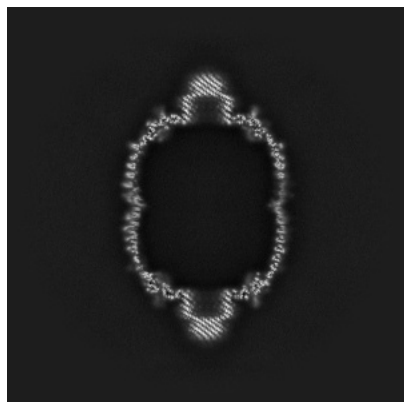


Z Index: 512

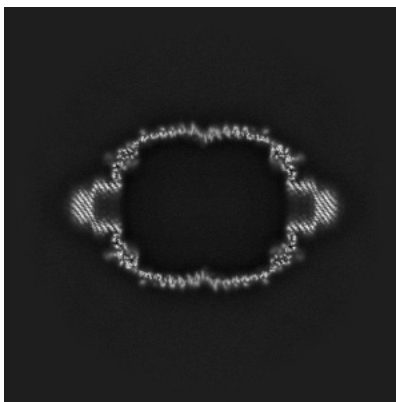
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

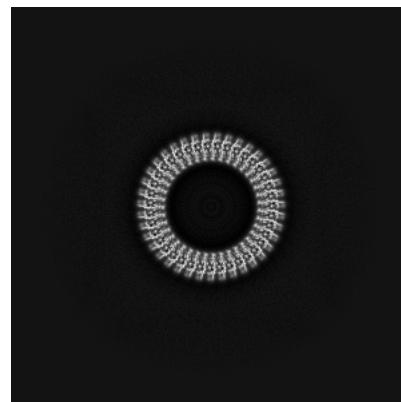
6.3.1 Primary map



X Index: 402

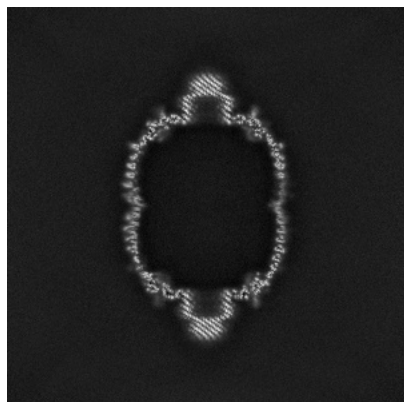


Y Index: 622

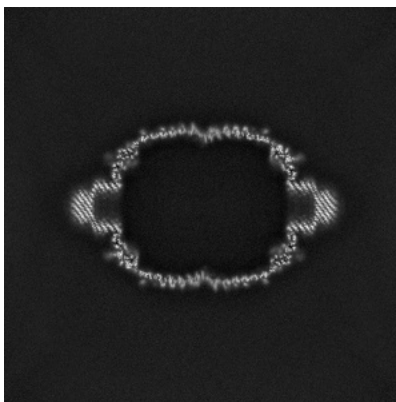


Z Index: 728

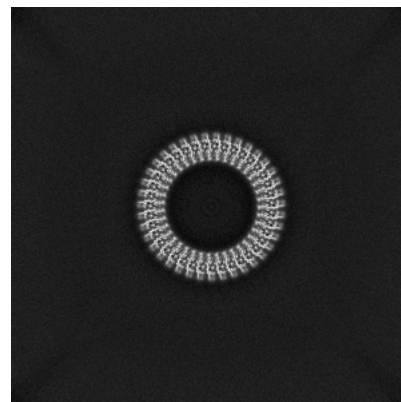
6.3.2 Raw map



X Index: 402



Y Index: 622

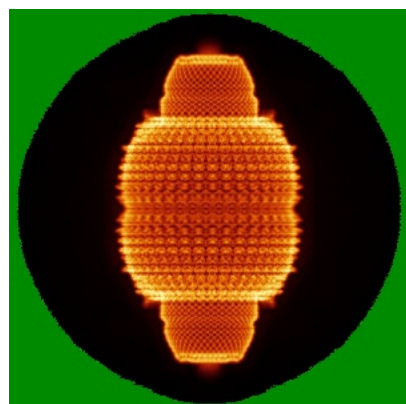


Z Index: 296

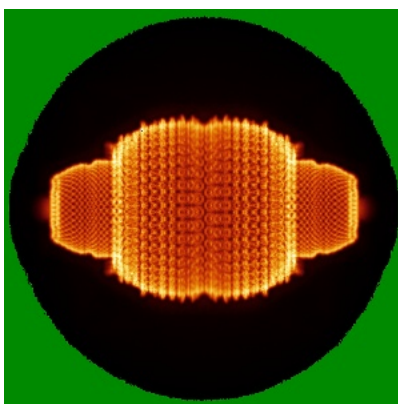
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

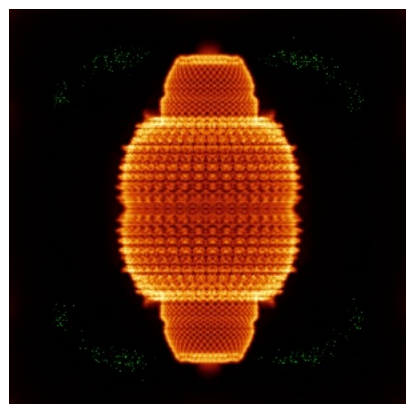


Y

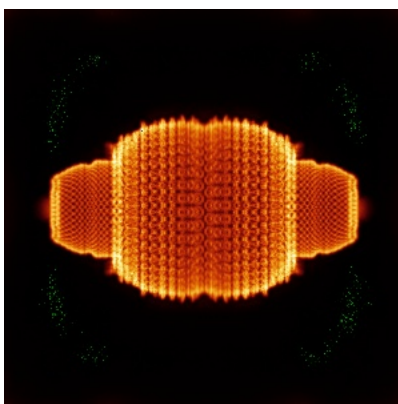


Z

6.4.2 Raw 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](#)

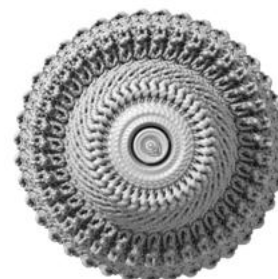
6.5.1 Primary map



X



Y



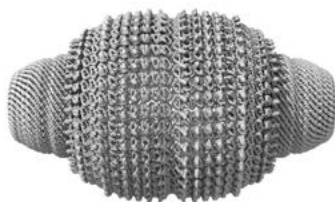
Z

The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

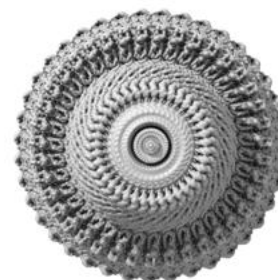
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

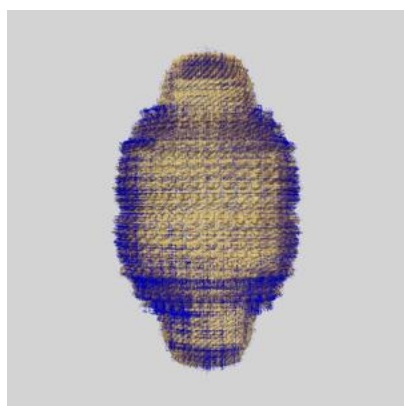
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

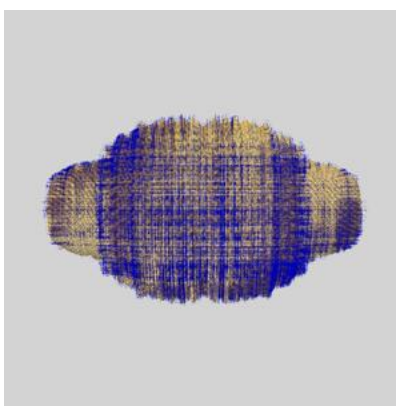
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

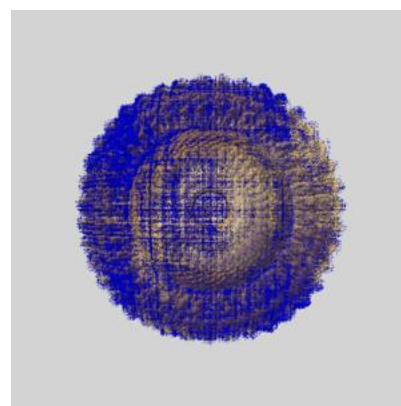
6.6.1 emd_53415_msk_1.map [i](#)



X



Y

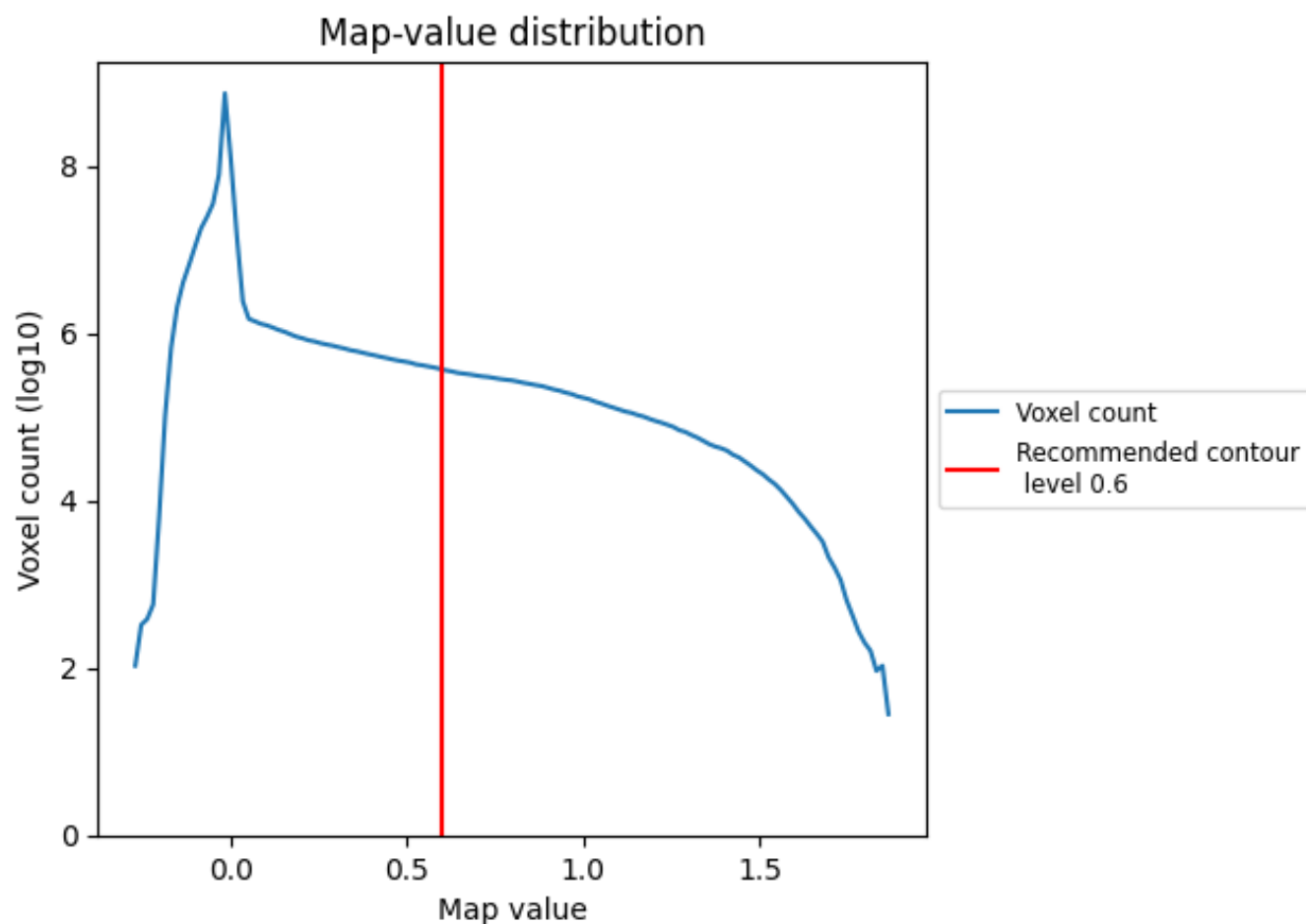


Z

7 Map analysis [i](#)

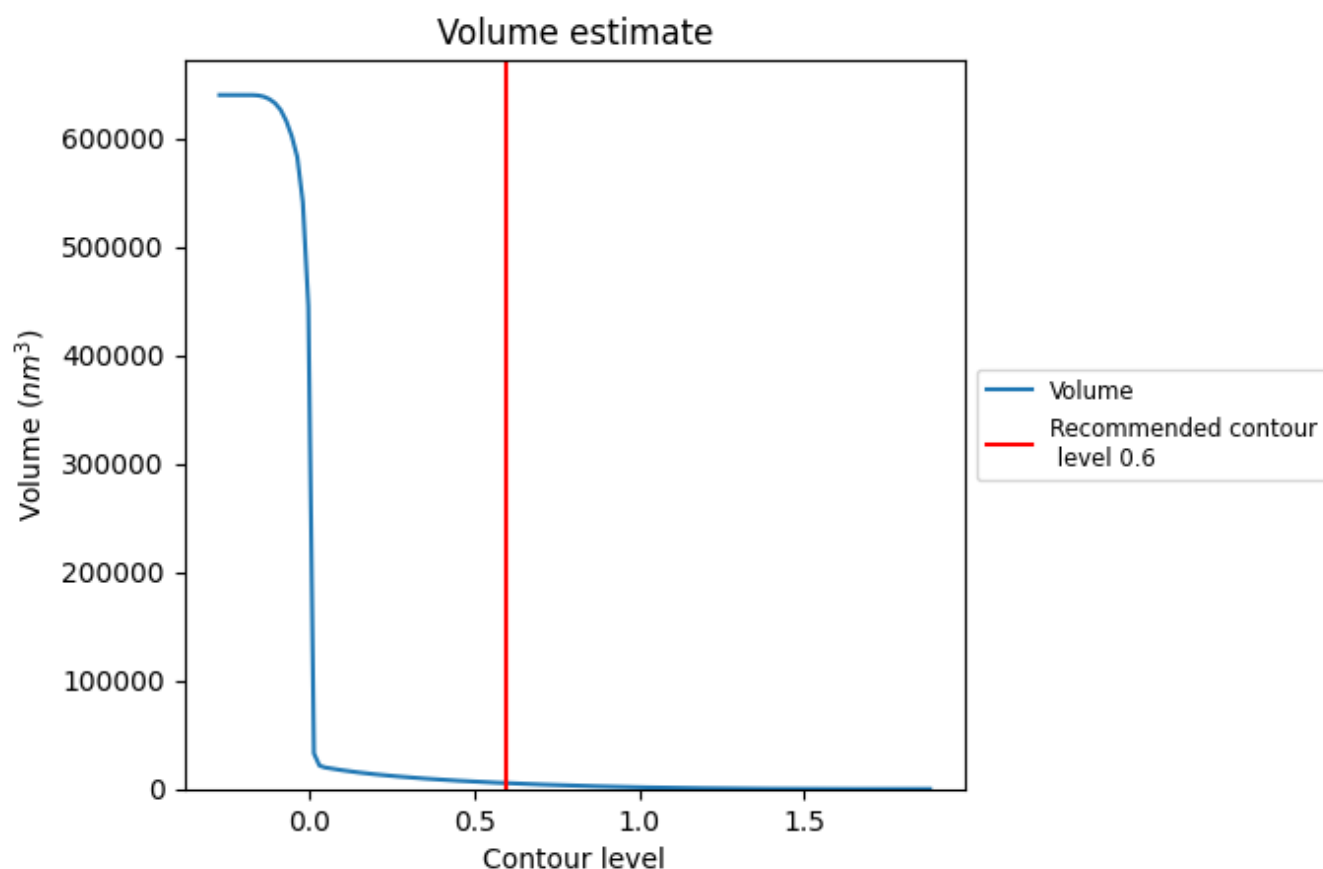
This section contains the results of statistical analysis of the map.

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.

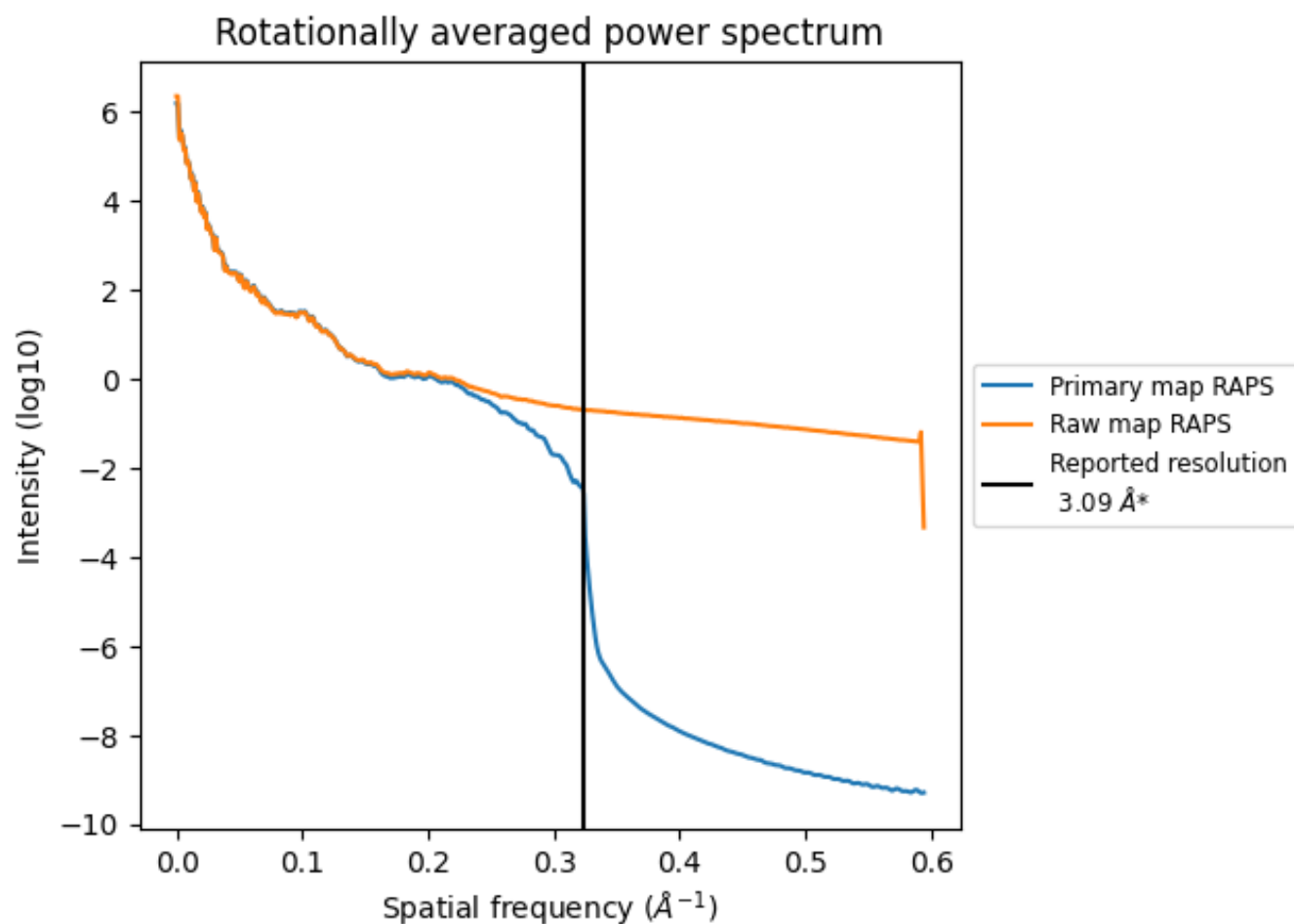
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5349 nm^3 ; this corresponds to an approximate mass of 4832 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 ⓘ

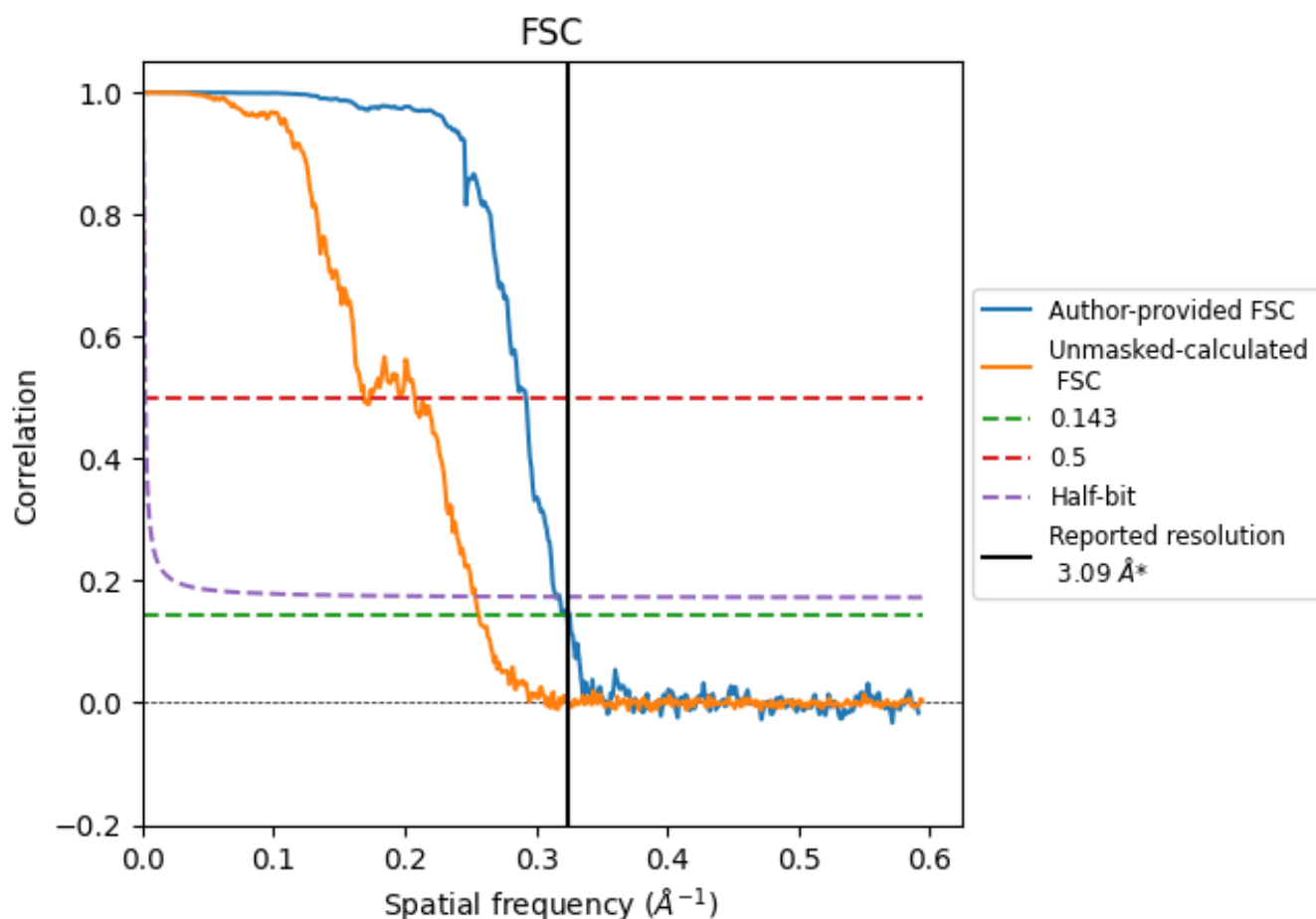


*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

8.2 Resolution estimates [i](#)

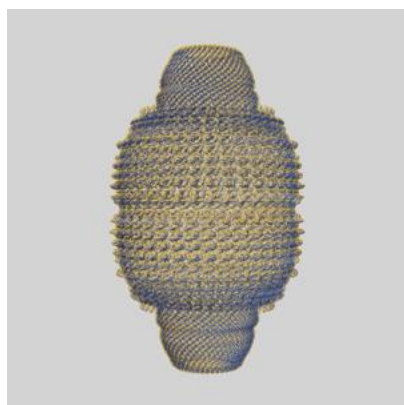
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	3.09	3.42	3.18
Unmasked-calculated*	3.90	5.91	3.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.90 differs from the reported value 3.09 by more than 10 %

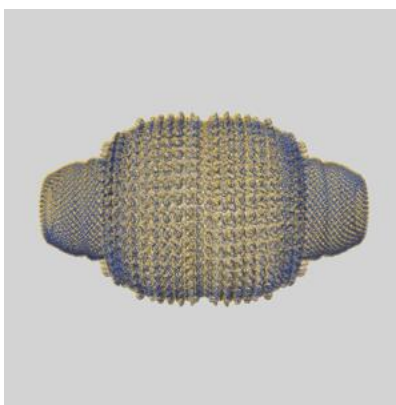
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53415 and PDB model 9QW9. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



X



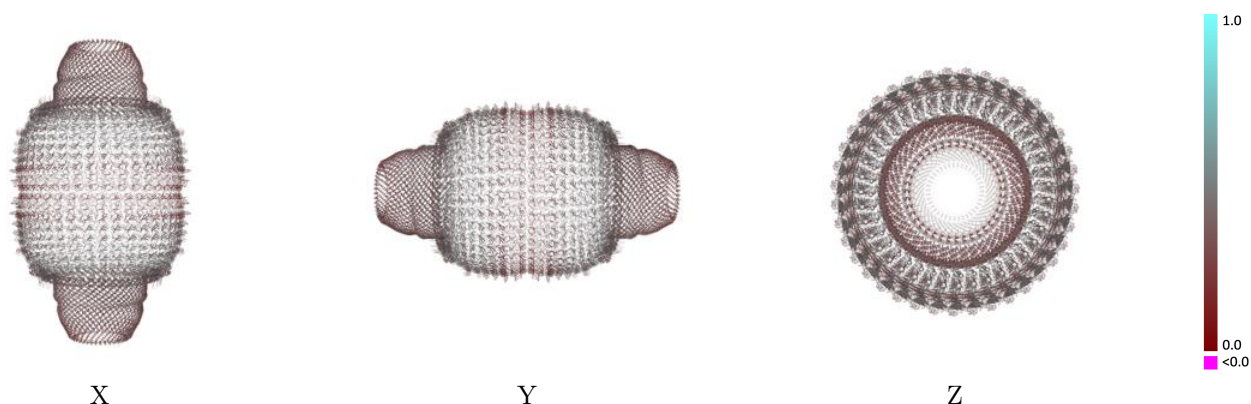
Y



Z

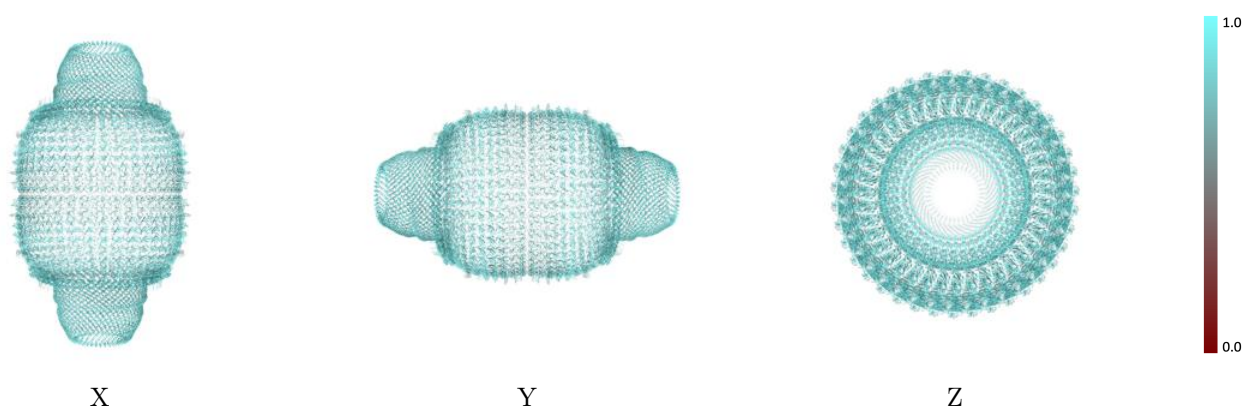
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



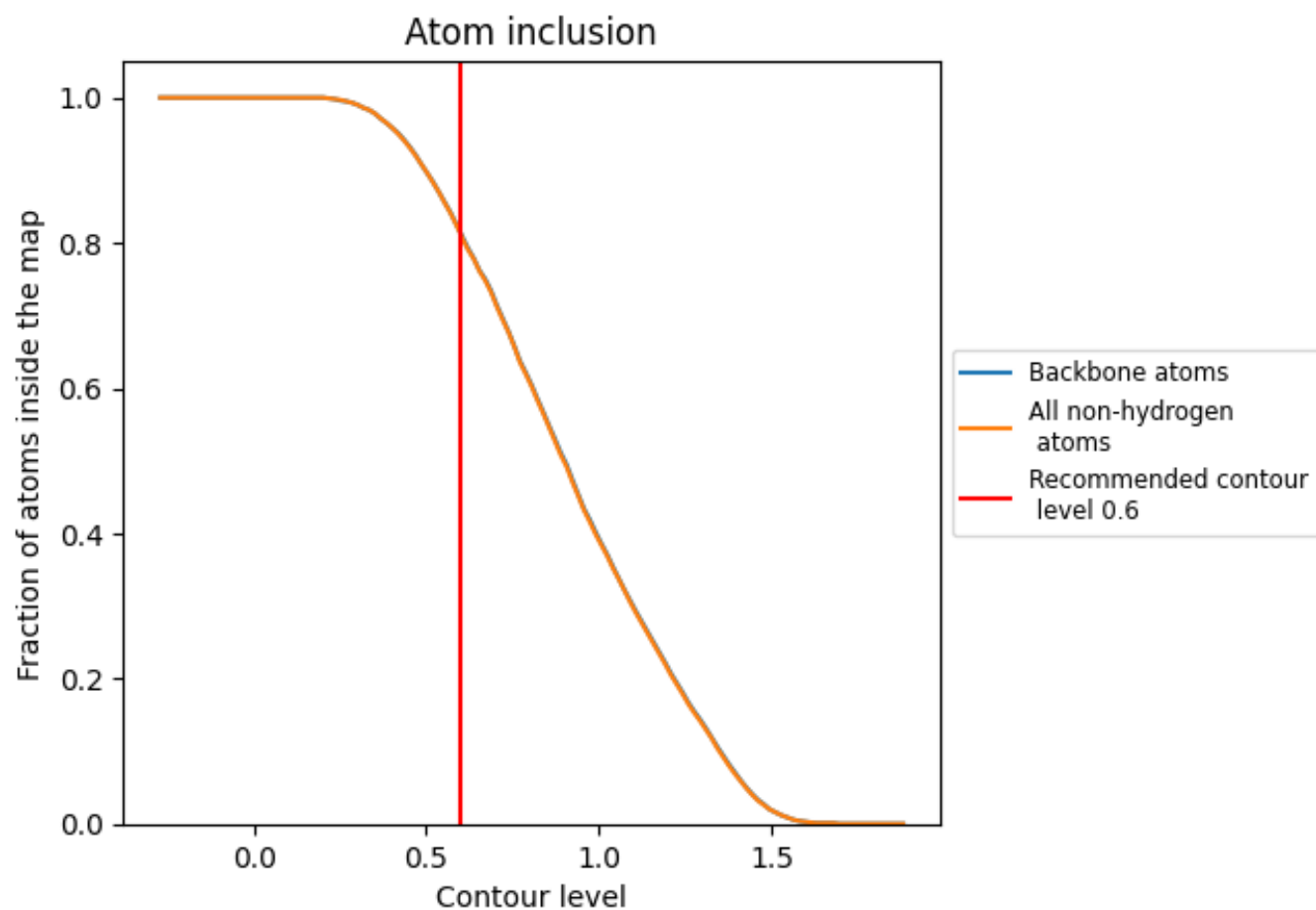
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8120	 0.3810
A	 0.8240	 0.3810
AA	 0.8250	 0.3800
AB	 0.8240	 0.3820
AC	 0.8220	 0.3810
B	 0.8250	 0.3810
BA	 0.8240	 0.3800
BB	 0.8260	 0.3820
C	 0.8240	 0.3810
CA	 0.8250	 0.3800
CB	 0.8250	 0.3810
D	 0.8230	 0.3810
DA	 0.8250	 0.3810
DB	 0.8260	 0.3800
E	 0.8250	 0.3810
EA	 0.8250	 0.3810
EB	 0.8240	 0.3800
F	 0.8250	 0.3820
FA	 0.8230	 0.3810
FB	 0.8260	 0.3800
G	 0.8240	 0.3820
GA	 0.8260	 0.3810
GB	 0.8240	 0.3810
H	 0.8240	 0.3820
HA	 0.8250	 0.3810
HB	 0.8250	 0.3810
I	 0.8250	 0.3810
IA	 0.8240	 0.3810
IB	 0.8260	 0.3810
J	 0.8250	 0.3800
JA	 0.8240	 0.3800
JB	 0.8240	 0.3800
K	 0.8250	 0.3800
KA	 0.8240	 0.3800
KB	 0.8250	 0.3800



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Chain	Atom inclusion	Q-score
L	 0.8240	 0.3800
LA	 0.8240	 0.3810
LB	 0.8250	 0.3800
M	 0.8250	 0.3800
MA	 0.8230	 0.3810
MB	 0.8260	 0.3800
N	 0.8250	 0.3800
NA	 0.8230	 0.3810
NB	 0.8250	 0.3800
O	 0.8250	 0.3800
OA	 0.8230	 0.3820
OB	 0.8250	 0.3810
P	 0.8250	 0.3800
PA	 0.8250	 0.3820
PB	 0.8250	 0.3810
Q	 0.8230	 0.3800
QA	 0.8260	 0.3820
QB	 0.8260	 0.3810
R	 0.8250	 0.3800
RA	 0.8230	 0.3820
RB	 0.8260	 0.3810
S	 0.8250	 0.3810
SA	 0.8240	 0.3820
SB	 0.8230	 0.3810
T	 0.8250	 0.3810
TA	 0.8260	 0.3820
TB	 0.8260	 0.3810
UA	 0.8250	 0.3820
UB	 0.8260	 0.3810
V	 0.8250	 0.3810
VA	 0.8240	 0.3810
VB	 0.8240	 0.3810
W	 0.8250	 0.3800
WA	 0.8250	 0.3810
WB	 0.8240	 0.3810
X	 0.8250	 0.3800
XA	 0.8250	 0.3810
XB	 0.8250	 0.3810
Y	 0.8250	 0.3790
YA	 0.8250	 0.3810
YB	 0.8250	 0.3820
Z	 0.8250	 0.3800

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Chain	Atom inclusion	Q-score
ZA	 0.8240	 0.3820
ZB	 0.8250	 0.3820