



wwPDB EM Validation Summary Report ⓘ

Jul 28, 2026 – 08:16 PM EDT

PDB ID : 9Z4W / pdb_00009z4w
EMDB ID : EMD-73814
Title : Cryo-EM structure of rabbit major vault protein complex
Authors : Li, H.; Clarke, O.B.
Deposited on : 2025-11-11
Resolution : 2.40 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:

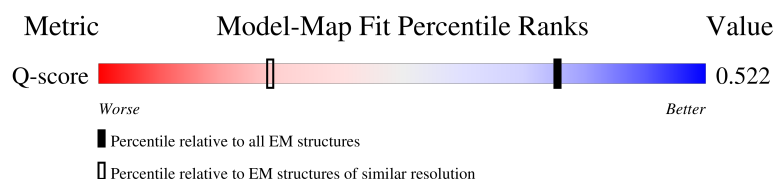
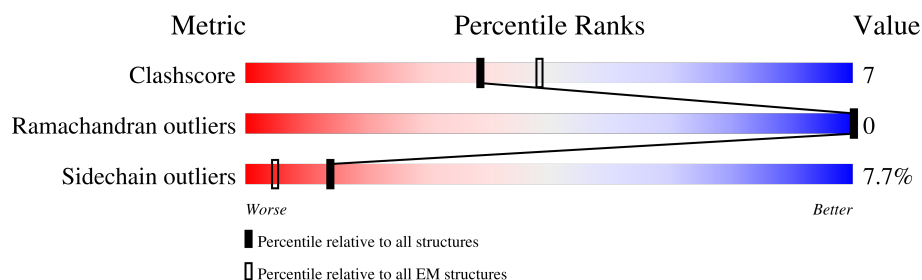
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.40 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.



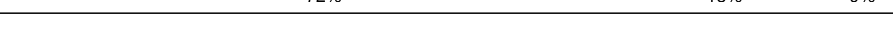
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	0	890	71% 17% • 11%
1	1	890	71% 18% • 9%
1	2	890	71% 17% • 11%
1	3	890	71% 17% • 10%

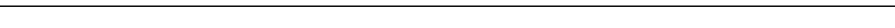
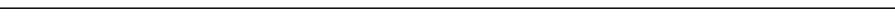
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Mol	Chain	Length	Quality of chain
1	4	890	 72% 17% 9%
1	5	890	 72% 16% 10%
1	6	890	 71% 17% 11%
1	7	890	 72% 18% 9%
1	8	890	 71% 17% 11%
1	9	890	 72% 17% 10%
1	A	890	 71% 17% 11%
1	AA	890	 72% 18% 9%
1	AB	890	 72% 16% 10%
1	AC	890	 71% 17% 11%
1	AD	890	 71% 19% 9%
1	AE	890	 71% 17% 11%
1	AF	890	 72% 17% 10%
1	AG	890	 72% 18% 9%
1	AH	890	 72% 16% 10%
1	AI	890	 71% 17% 11%
1	AJ	890	 71% 19% 9%
1	AK	890	 71% 16% 11%
1	AL	890	 71% 17% 10%
1	AM	890	 72% 18% 9%
1	AN	890	 72% 17% 10%
1	AO	890	 70% 17% 11%
1	AP	890	 71% 18% 9%
1	B	890	 72% 17% 10%
1	C	890	 72% 17% 9%

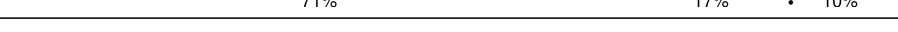
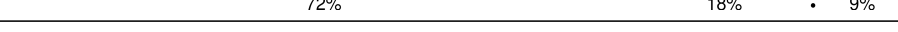
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Mol	Chain	Length	Quality of chain
1	D	890	 71% 17% 10%
1	E	890	 71% 17% 11%
1	F	890	 72% 18% 9%
1	G	890	 71% 17% 11%
1	H	890	 72% 17% 10%
1	I	890	 72% 17% 9%
1	J	890	 72% 17% 10%
1	K	890	 71% 17% 11%
1	L	890	 71% 18% 9%
1	M	890	 71% 17% 11%
1	N	890	 71% 17% 10%
1	O	890	 72% 17% 9%
1	P	890	 72% 17% 10%
1	Q	890	 71% 17% 11%
1	R	890	 71% 19% 9%
1	S	890	 71% 16% 11%
1	T	890	 71% 17% 10%
1	U	890	 72% 18% 9%
1	V	890	 72% 17% 10%
1	W	890	 71% 16% 11%
1	X	890	 71% 19% 9%
1	Y	890	 71% 17% 11%
1	Z	890	 71% 17% 10%
1	a	890	 72% 18% 9%
1	b	890	 72% 17% 10%

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Mol	Chain	Length	Quality of chain
1	c	890	 71% 16% • 11%
1	d	890	 72% 18% • 9%
1	e	890	 71% 17% • 11%
1	f	890	 72% 17% • 10%
1	g	890	 72% 18% • 9%
1	h	890	 71% 17% • 10%
1	i	890	 71% 17% • 11%
1	j	890	 71% 18% • 9%
1	k	890	 71% 17% • 11%
1	l	890	 71% 17% • 10%
1	m	890	 72% 18% • 9%
1	n	890	 72% 16% • 10%
1	o	890	 71% 16% • 11%
1	p	890	 72% 18% • 9%
1	q	890	 71% 17% • 11%
1	r	890	 71% 17% • 10%
1	s	890	 72% 18% • 9%
1	t	890	 72% 17% • 10%
1	u	890	 71% 17% • 11%
1	v	890	 71% 18% • 9%
1	w	890	 71% 17% • 11%
1	x	890	 71% 17% • 10%
1	y	890	 72% 18% • 9%
1	z	890	 72% 17% • 10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 491504 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 Major vault protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	B	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	C	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	D	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	E	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	F	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	G	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	H	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	I	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	J	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	K	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	L	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	M	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	N	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	O	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	P	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	Q	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	S	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	T	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	U	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	V	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	W	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	X	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	Y	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	Z	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	a	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	b	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	c	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	d	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	e	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	f	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	g	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	h	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	i	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	j	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	k	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	l	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	n	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	o	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	p	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	q	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	r	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	s	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	t	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	u	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	v	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	w	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	x	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	y	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	z	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	0	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	1	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	2	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	3	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	4	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	5	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	6	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		

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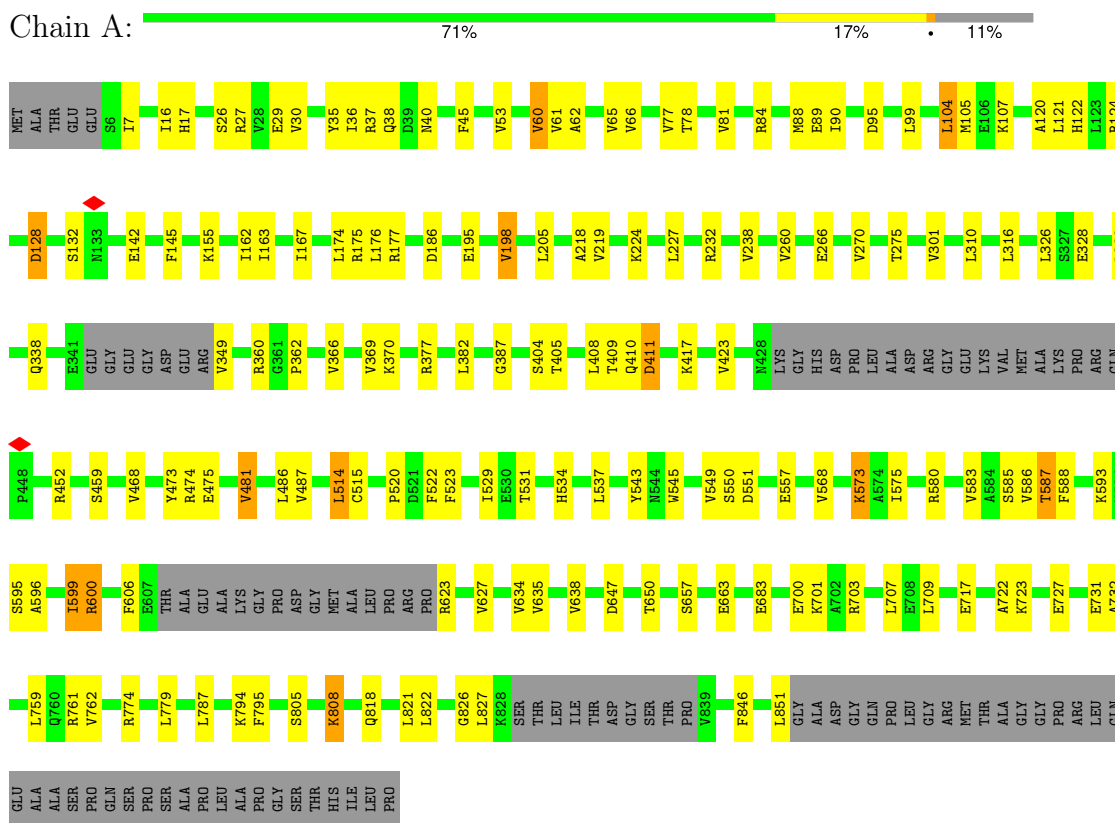
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	8	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	9	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AA	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	AB	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AC	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	AD	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	AE	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	AF	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AG	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	AH	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AI	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	AJ	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	AK	795	Total	C	N	O	S	0	0
			6247	3940	1117	1178	12		
1	AL	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AM	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		
1	AN	798	Total	C	N	O	S	0	0
			6275	3952	1121	1190	12		
1	AO	795	Total	C	N	O	S	0	0
			6253	3946	1117	1178	12		
1	AP	812	Total	C	N	O	S	0	0
			6379	4021	1137	1209	12		

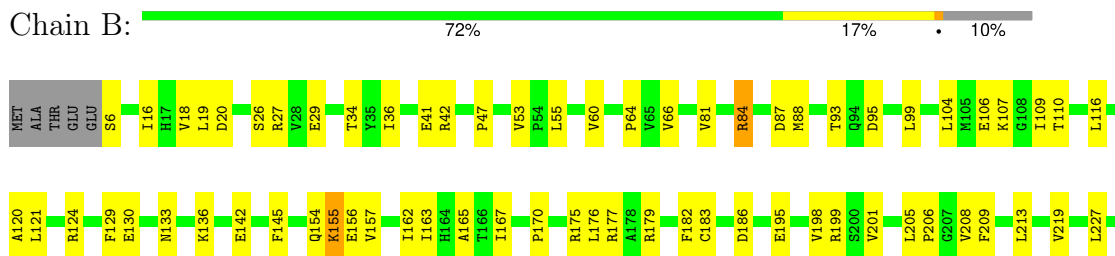
3 Residue-property plots

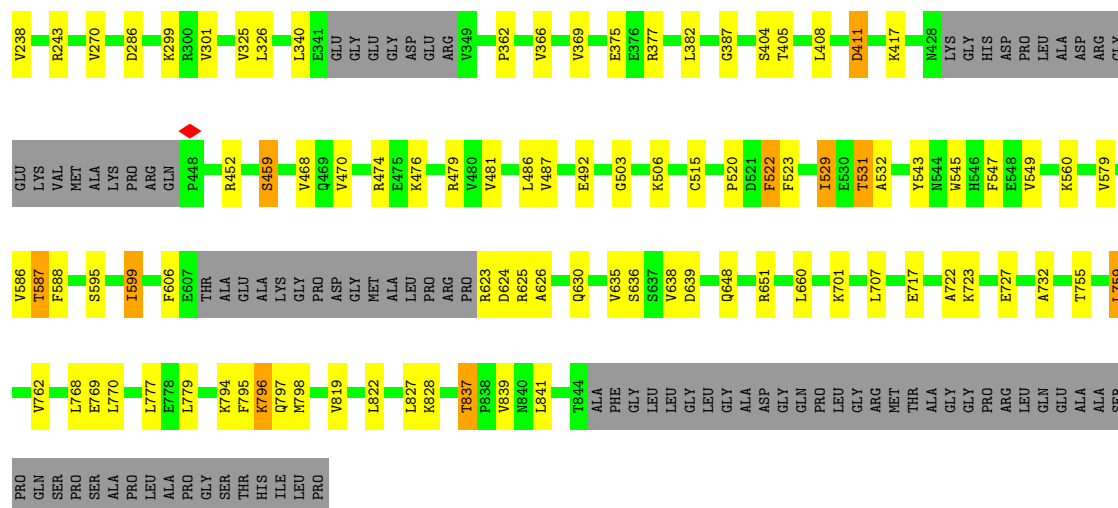
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



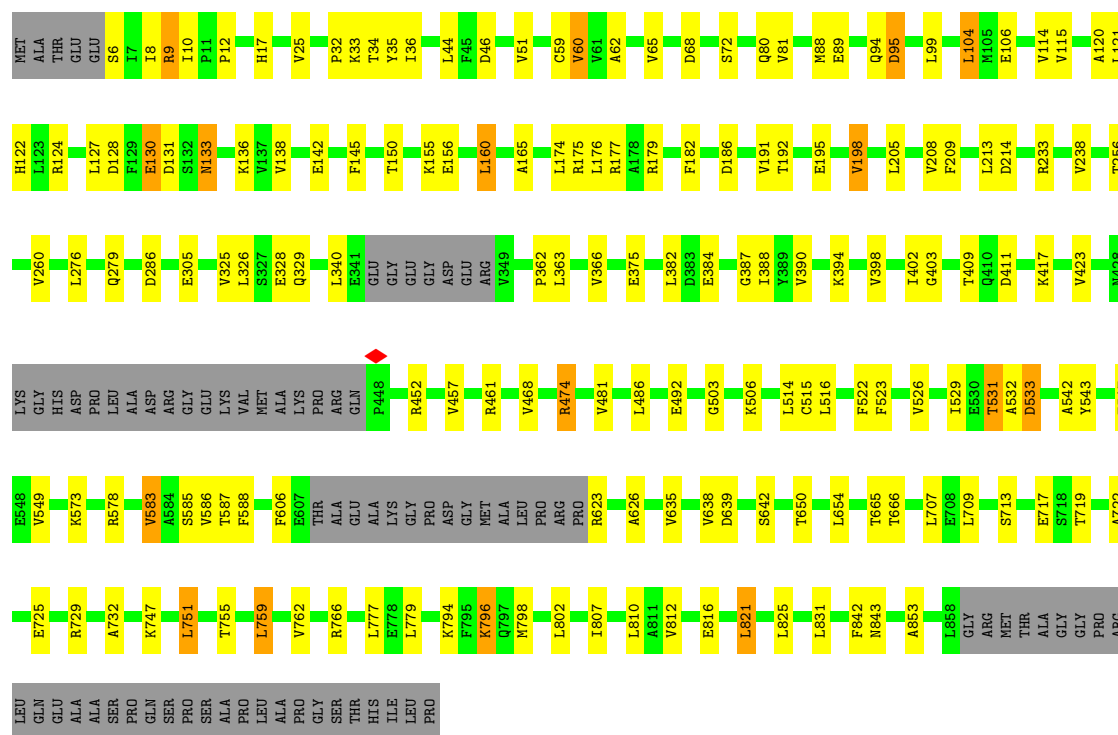
• Molecule 1: Major vault protein





• Molecule 1: Major vault protein

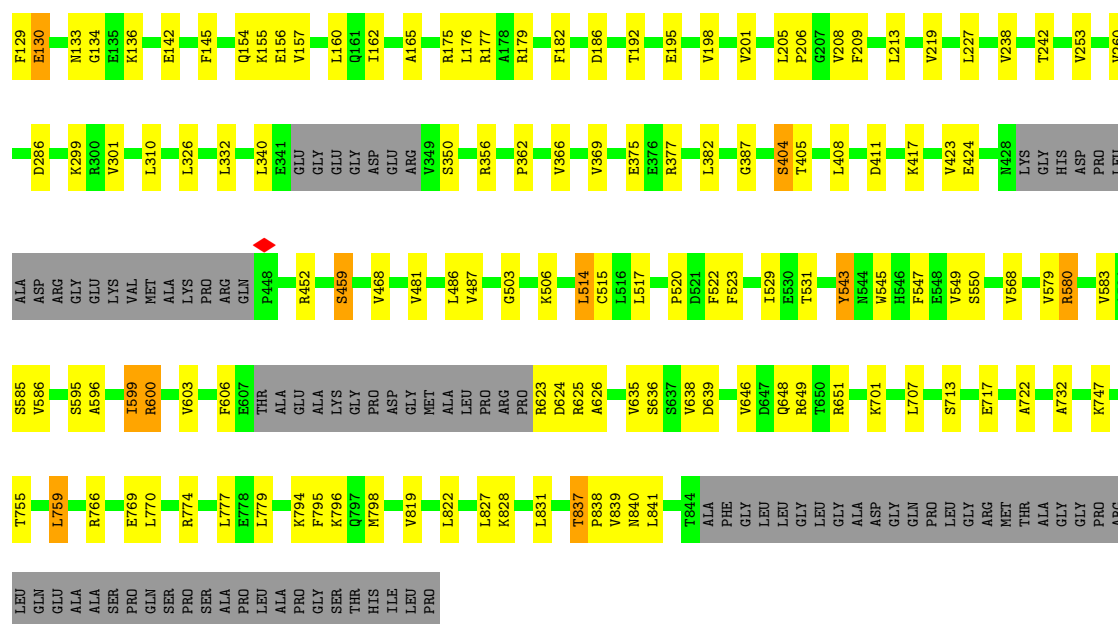
Chain C: 72% 17% 9%



• Molecule 1: Major vault protein

Chain D: 71% 17% 10%





- Molecule 1: Major vault protein



- Molecule 1: Major vault protein





WORLD WIDE
PDB
PROTEIN DATA BANK

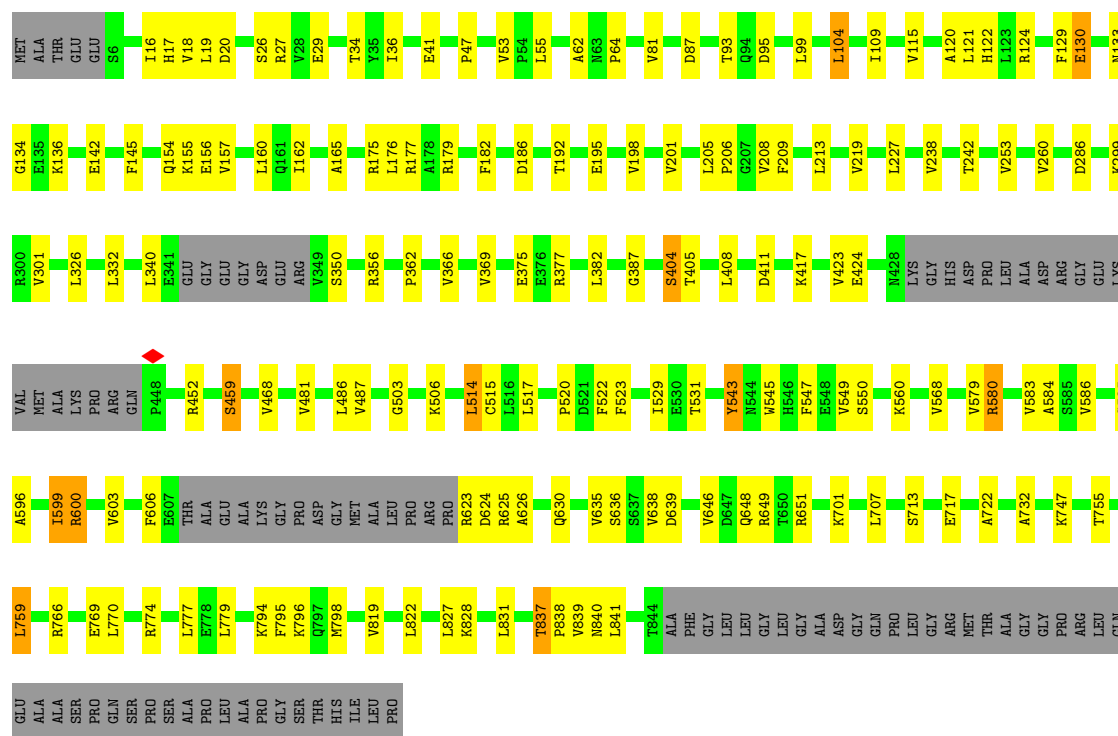
Response	Percentage
Yes	72%
No	17%
Don't know	10%



Category	Percentage
Very good	72%
Good	17%
Not good	9%
Very bad	2%

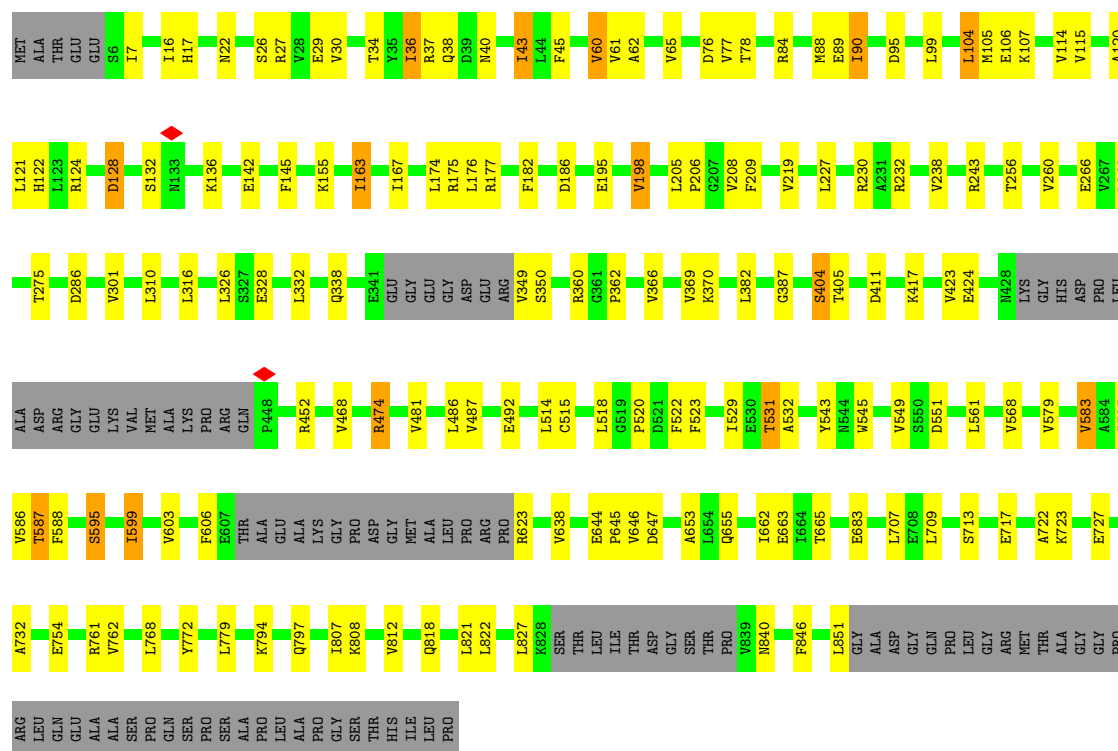


Chain J:  72% 17% 10%



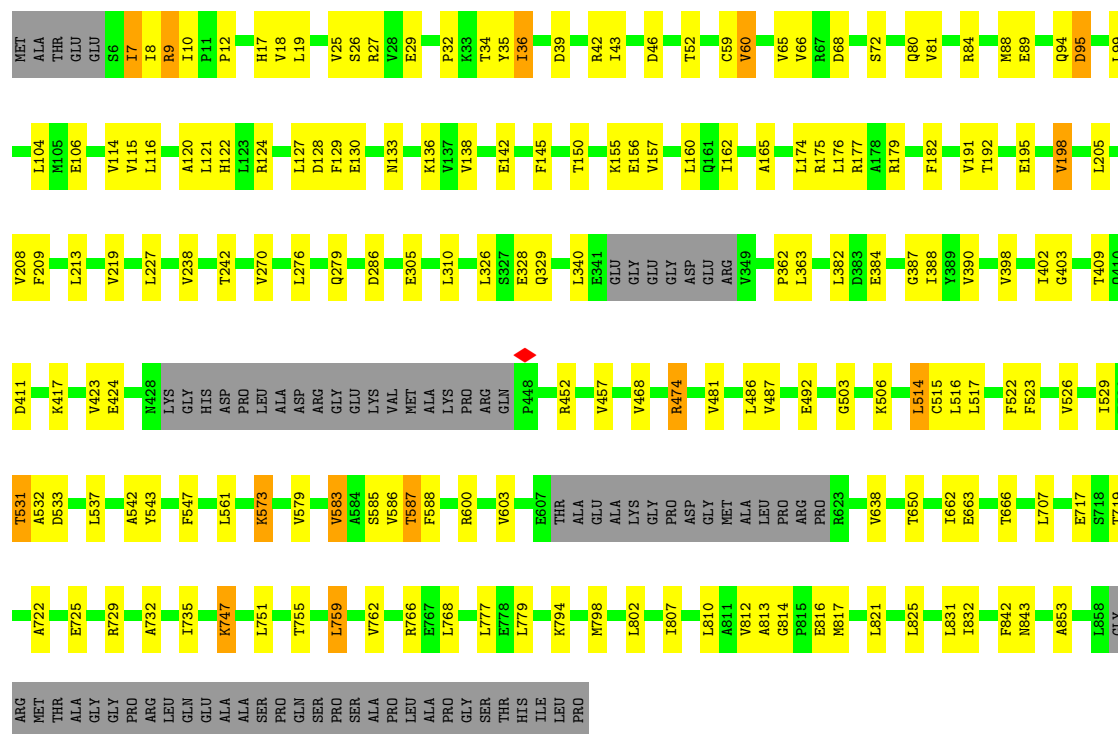
• Molecule 1: Major vault protein

Chain K:  71% 17% 11%



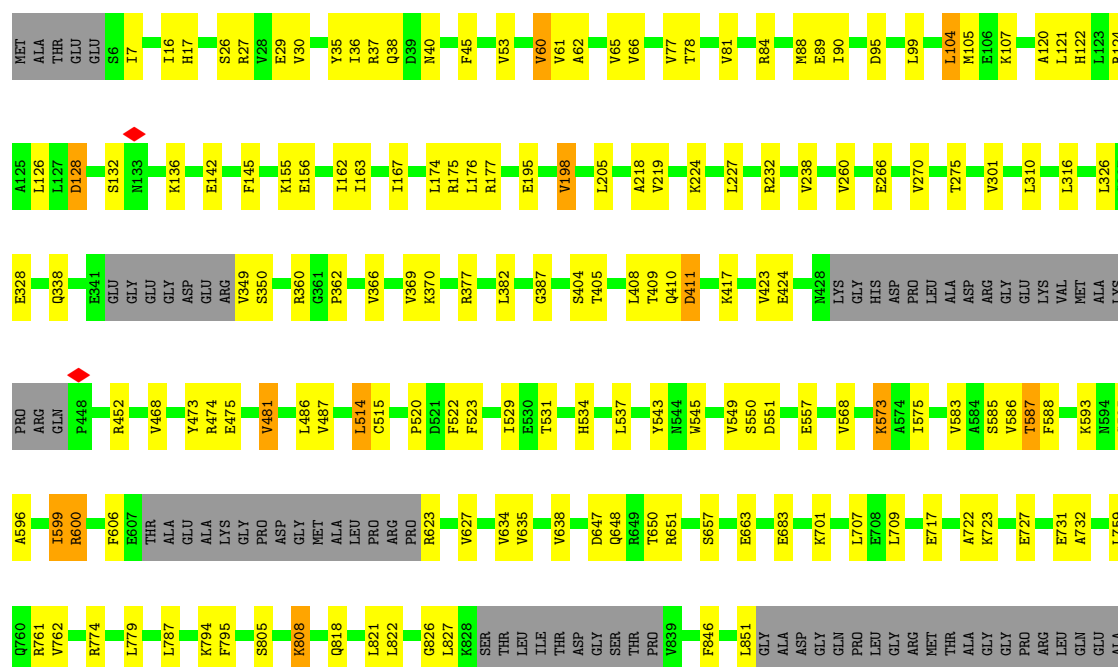
- Molecule 1: Major vault protein

Chain L:  71% 18% 9%



- Molecule 1: Major vault protein

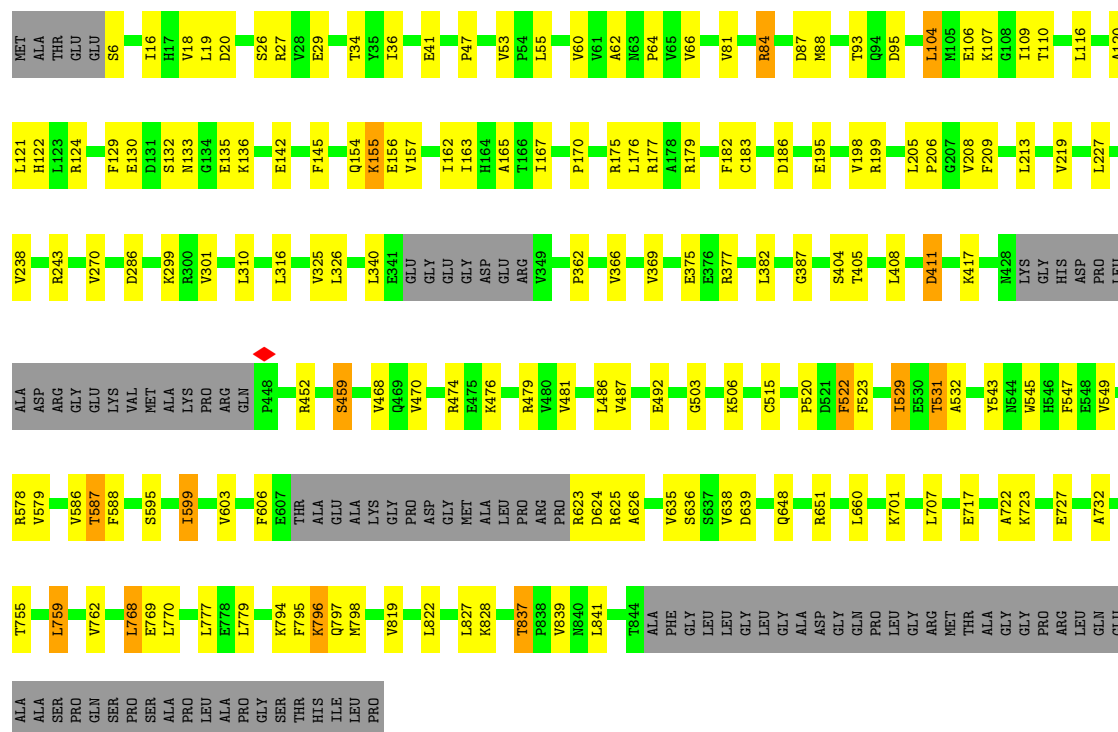
Chain M:  71% 17% 11%



ALA
SER
PRO
GLN
SER
PRO
SER
ALA
PRO
ALA
PRO
GLY
SER
THR
HIS
ILE
LEU
PRO

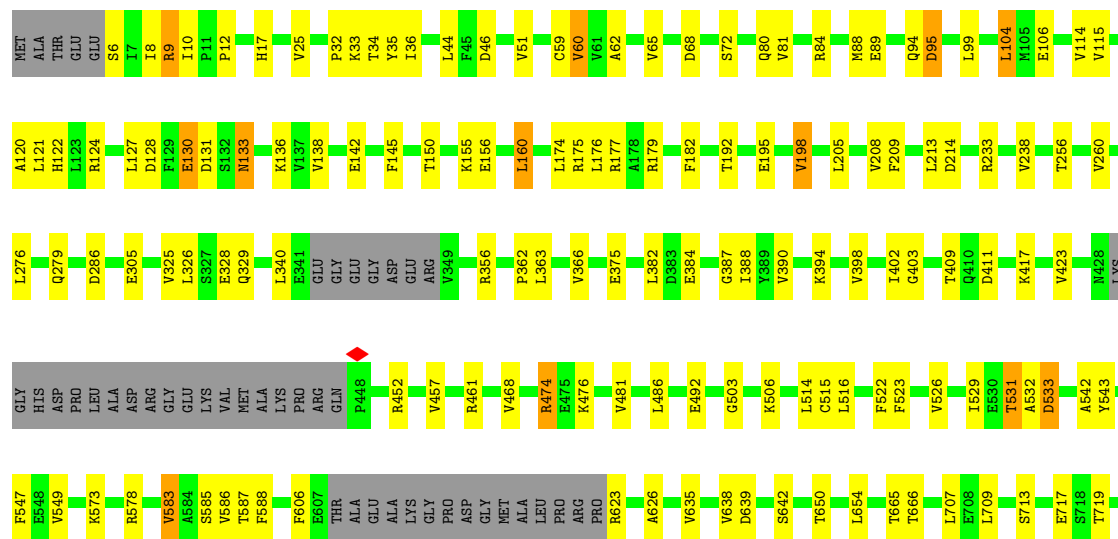
• Molecule 1: Major vault protein

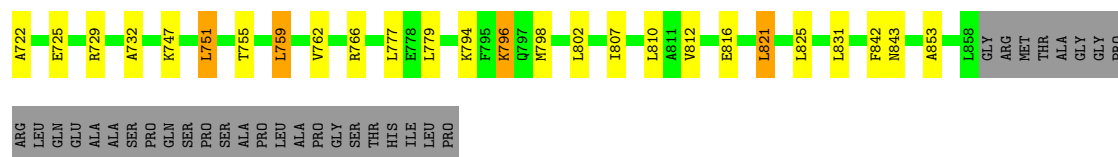
Chain N: 71% 17% 10%



• Molecule 1: Major vault protein

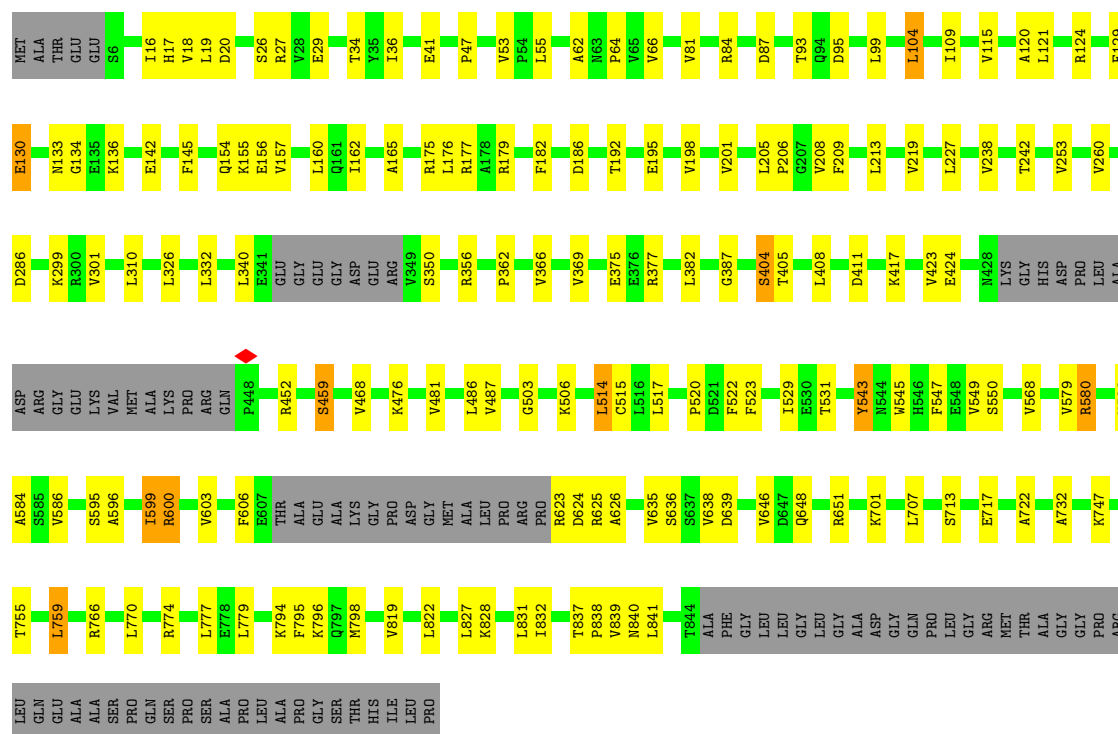
Chain O: 72% 17% 9%





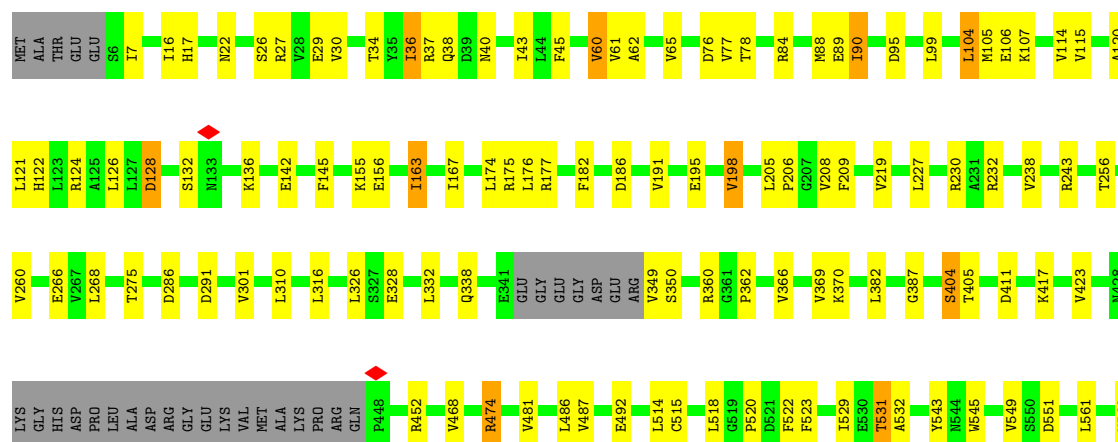
• Molecule 1: Major vault protein

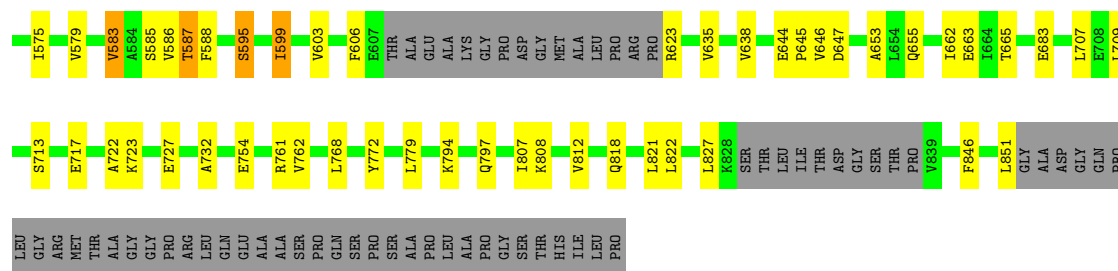
Chain P: 72% 17% 10%



• Molecule 1: Major vault protein

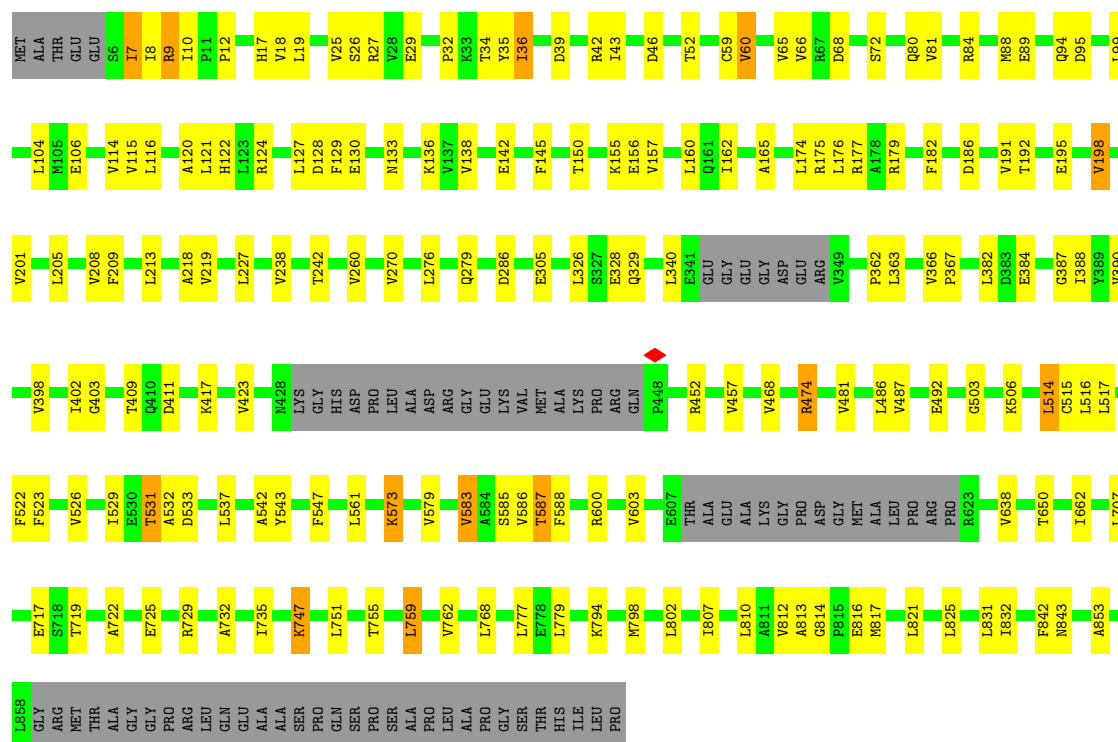
Chain Q: 71% 17% 11%





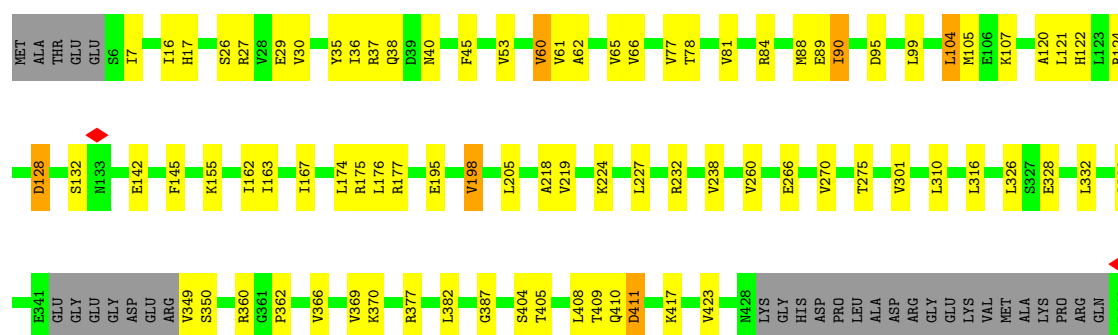
• Molecule 1: Major vault protein

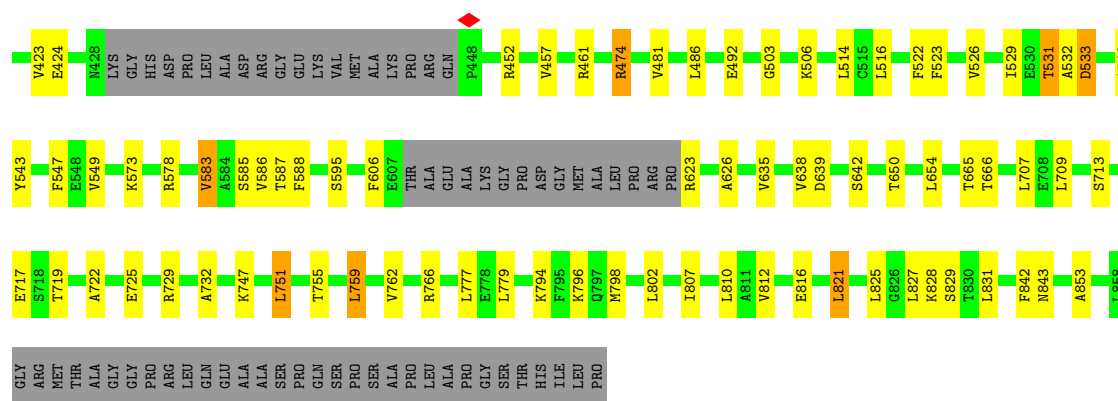
Chain R: 71% 19% 9%



• Molecule 1: Major vault protein

Chain S: 71% 16% 11%





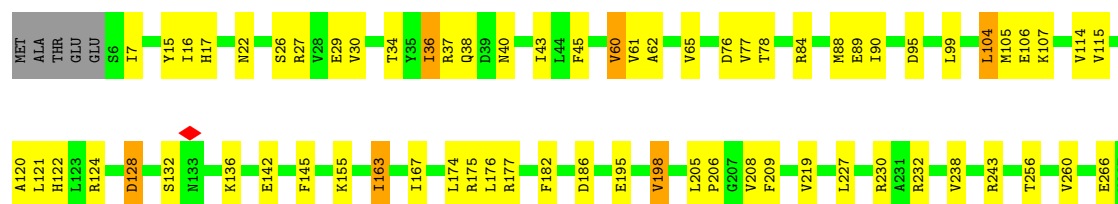
• Molecule 1: Major vault protein

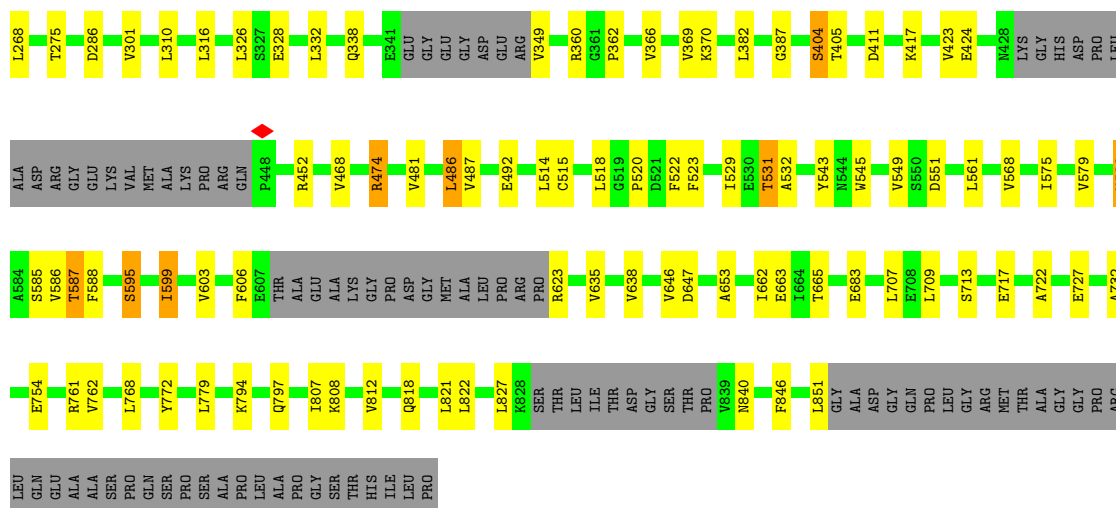
Chain V: 72% 17% 10%



• Molecule 1: Major vault protein

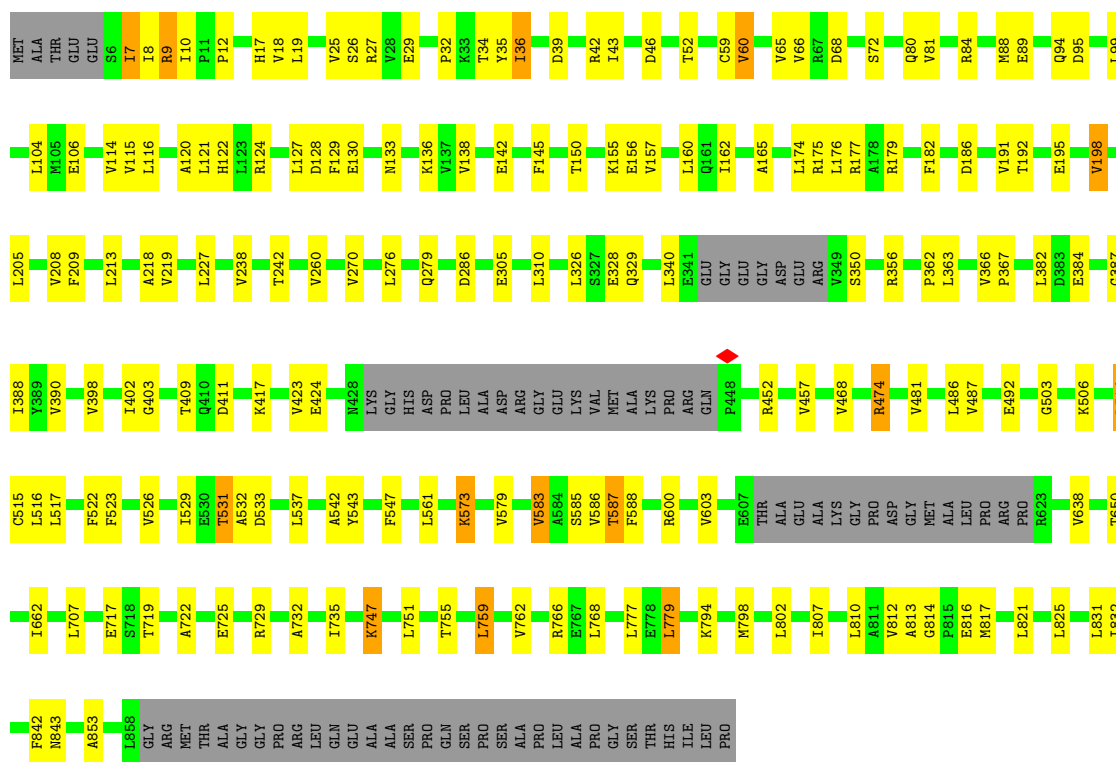
Chain W: 71% 16% 11%





• Molecule 1: Major vault protein

Chain X: 71% 19% 9%

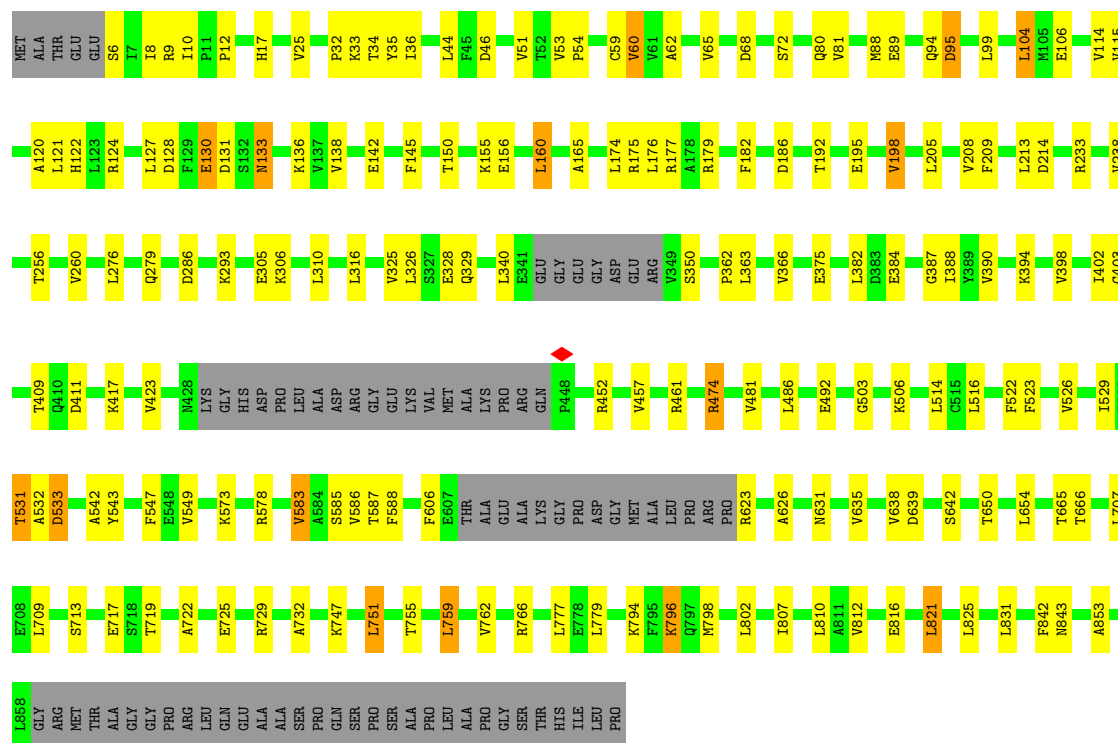


• Molecule 1: Major vault protein

Chain Y: 71% 17% 11%

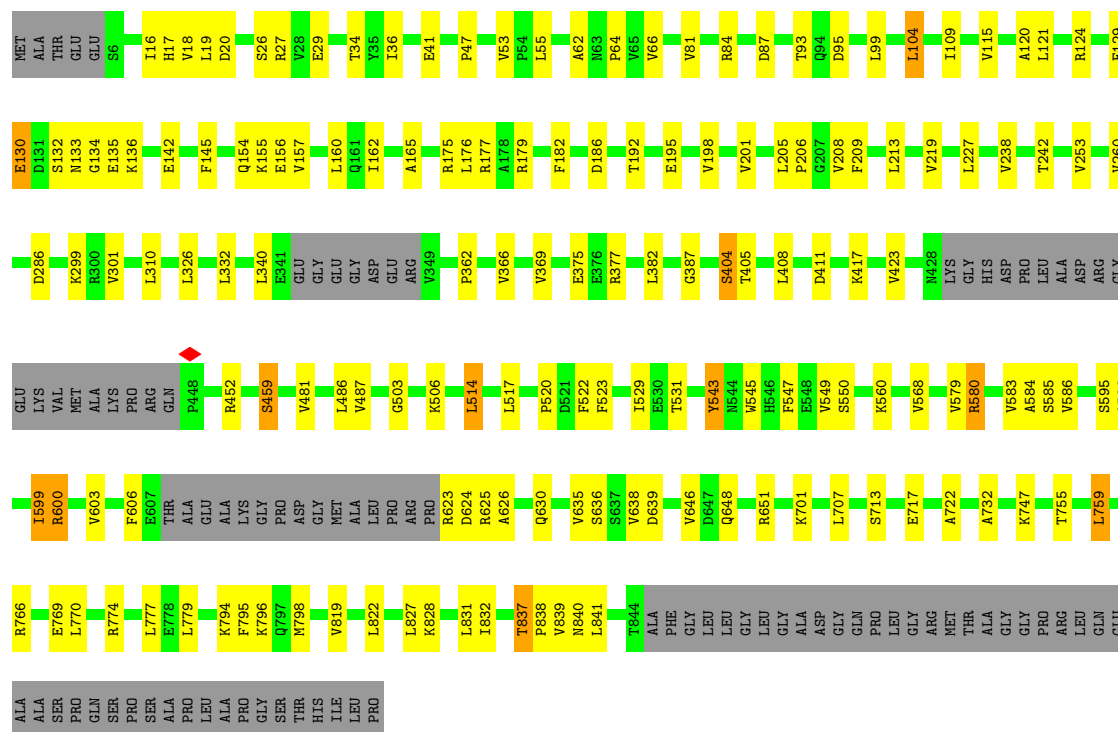






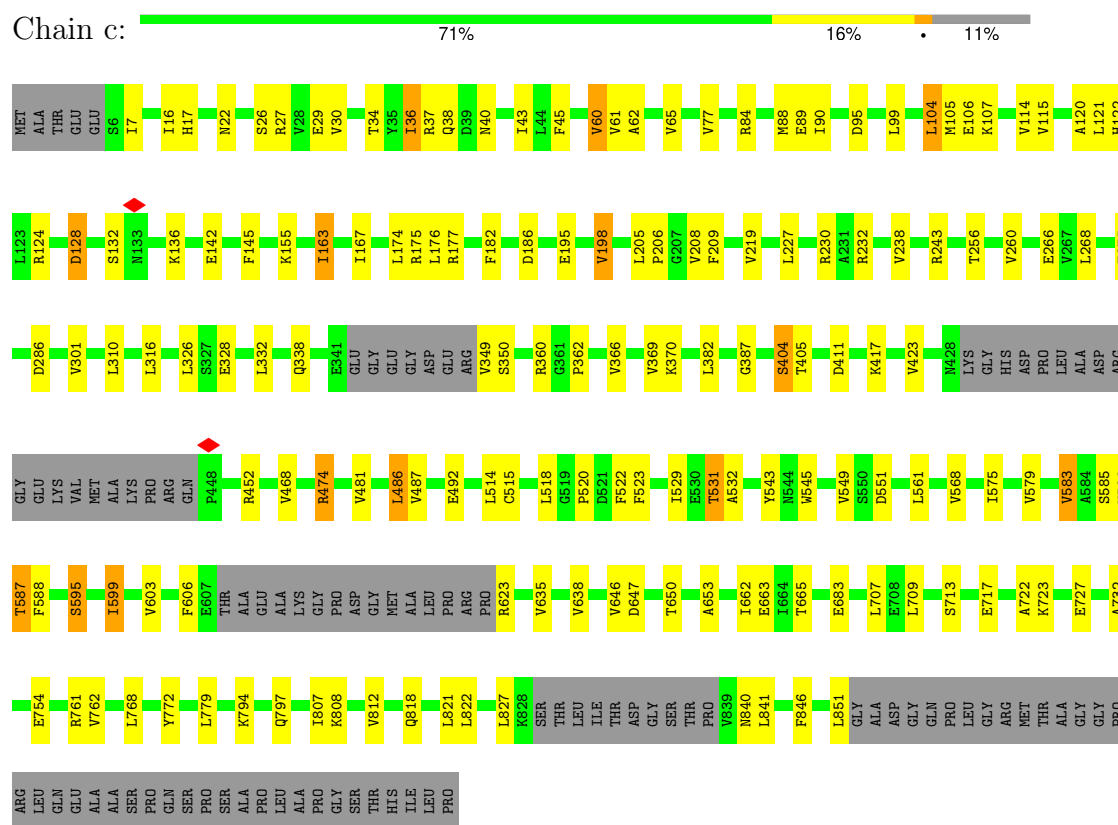
• Molecule 1: Major vault protein

Chain b: 72% 17% • 10%



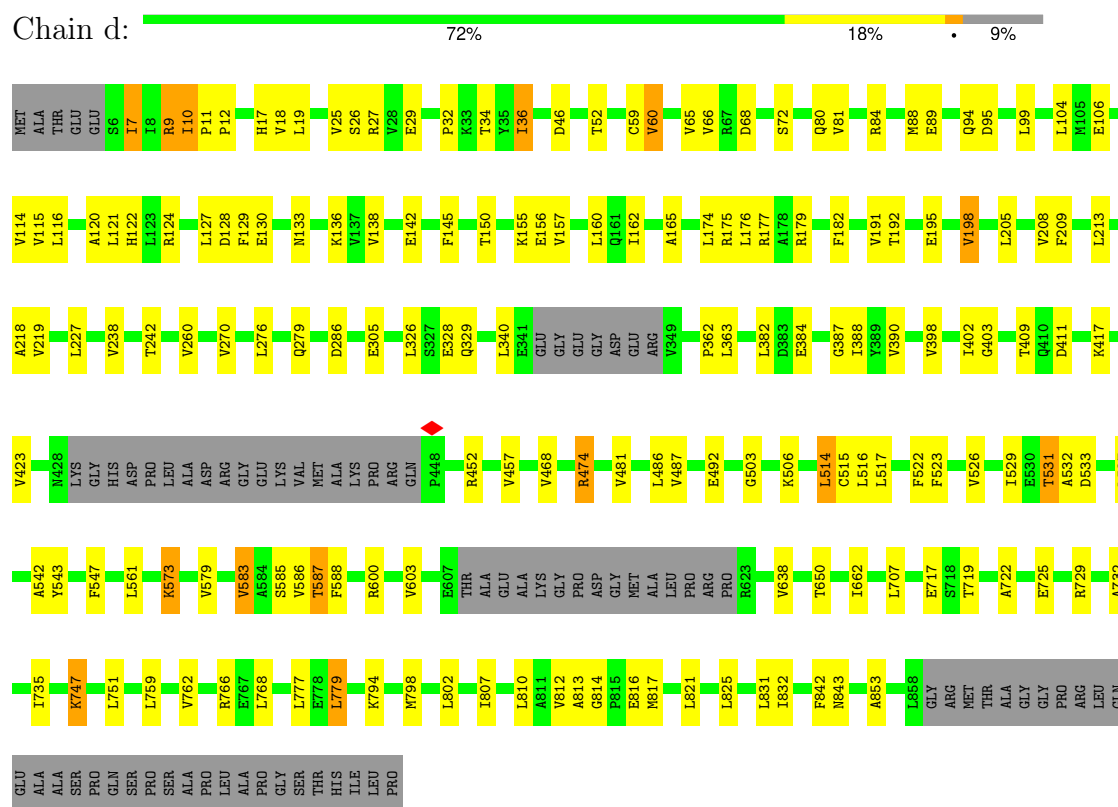
• Molecule 1: Major vault protein

Chain c:



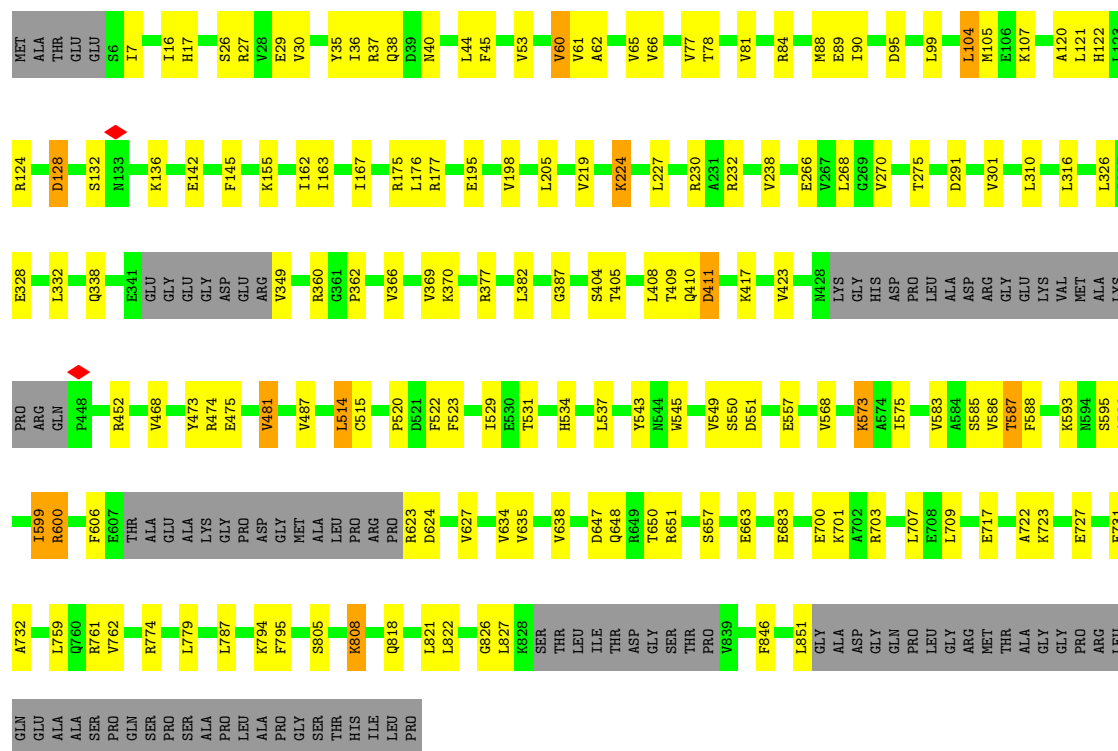
• Molecule 1: Major vault protein

Chain d:



- Molecule 1: Major vault protein

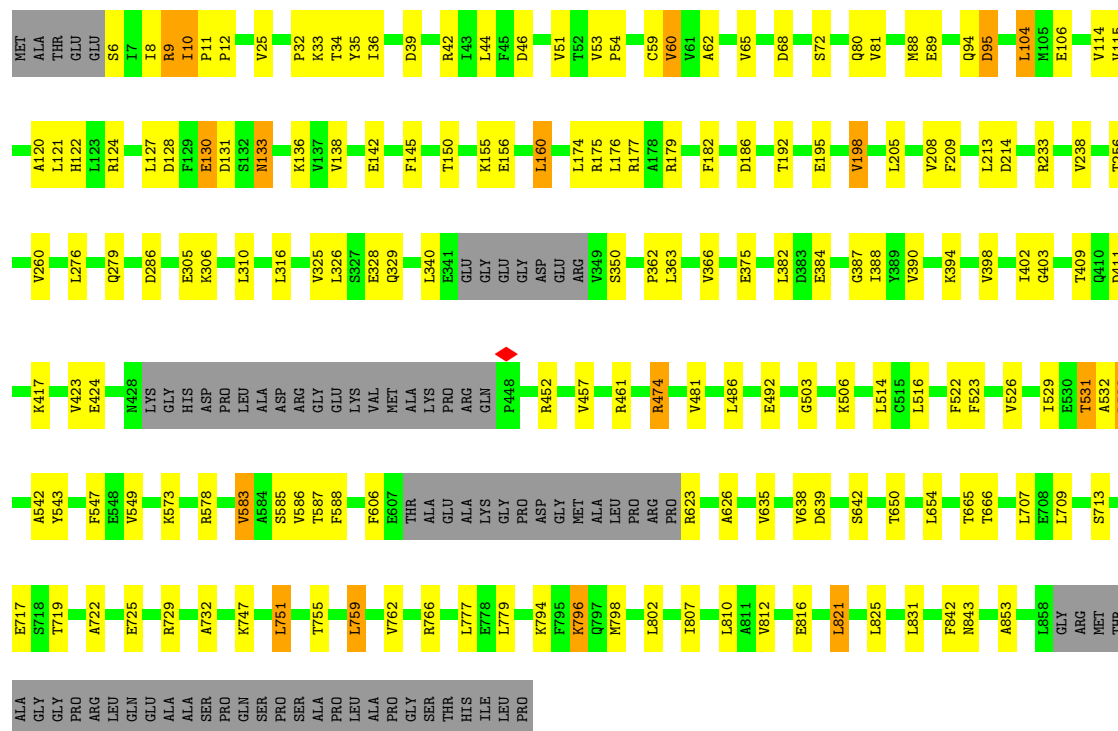
Chain e:  71% 17% 11%



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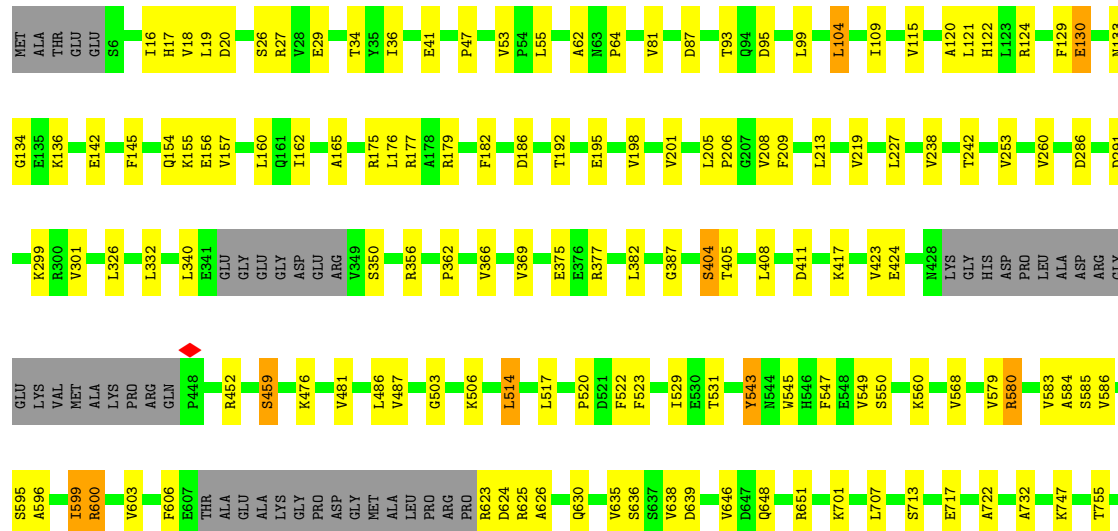
• Molecule 1: Major vault protein

Chain g:  72% 18% 9%



• Molecule 1: Major vault protein

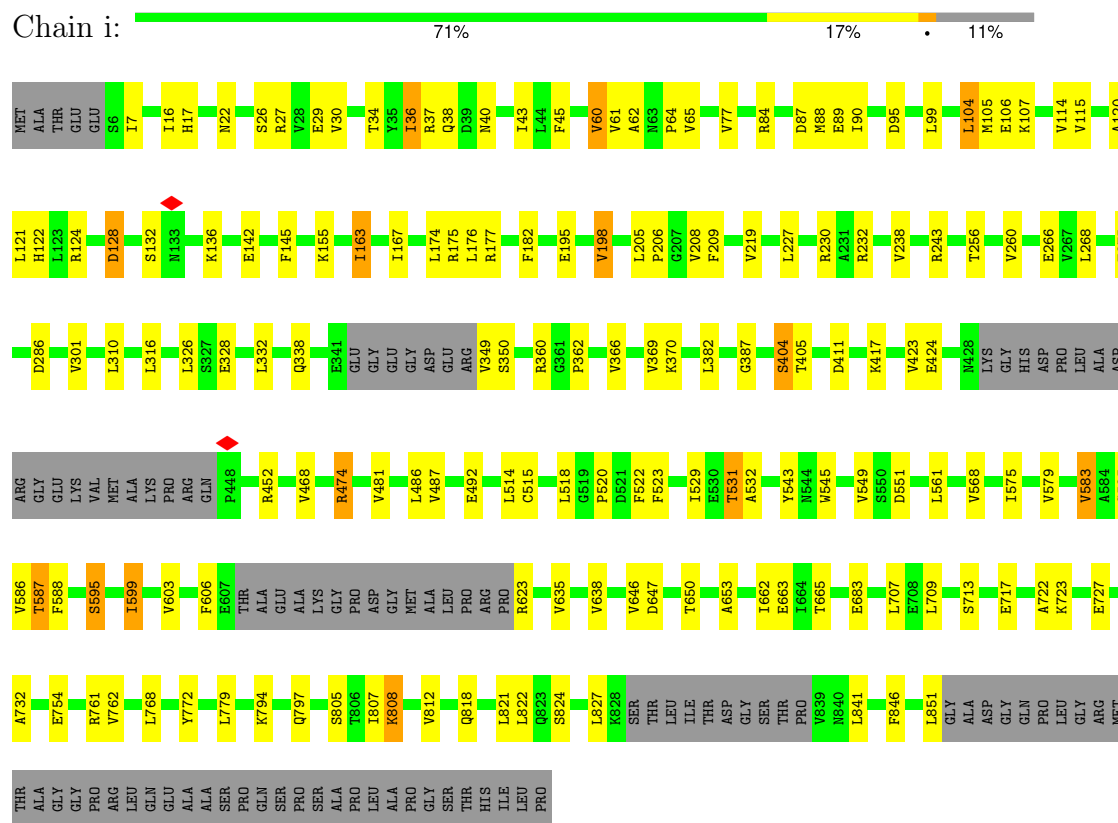
Chain h:  71% 17% 10%





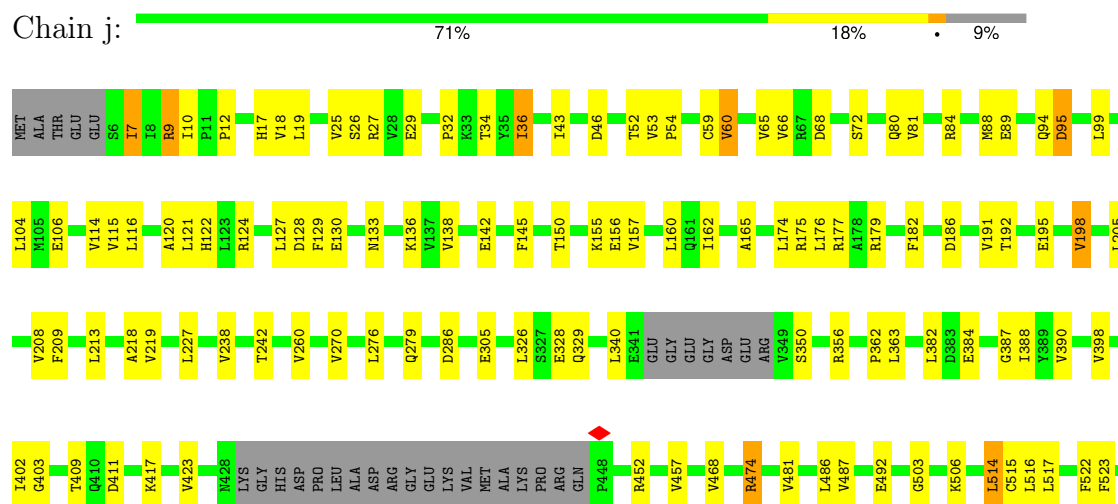
Molecule 1: Major vault protein

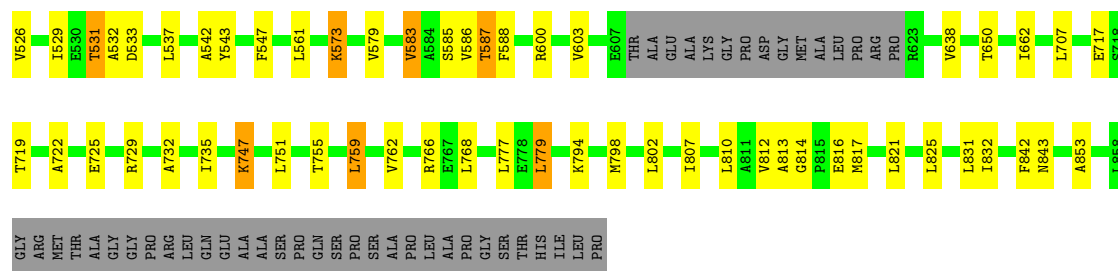
Chain i:



Molecule 1: Major vault protein

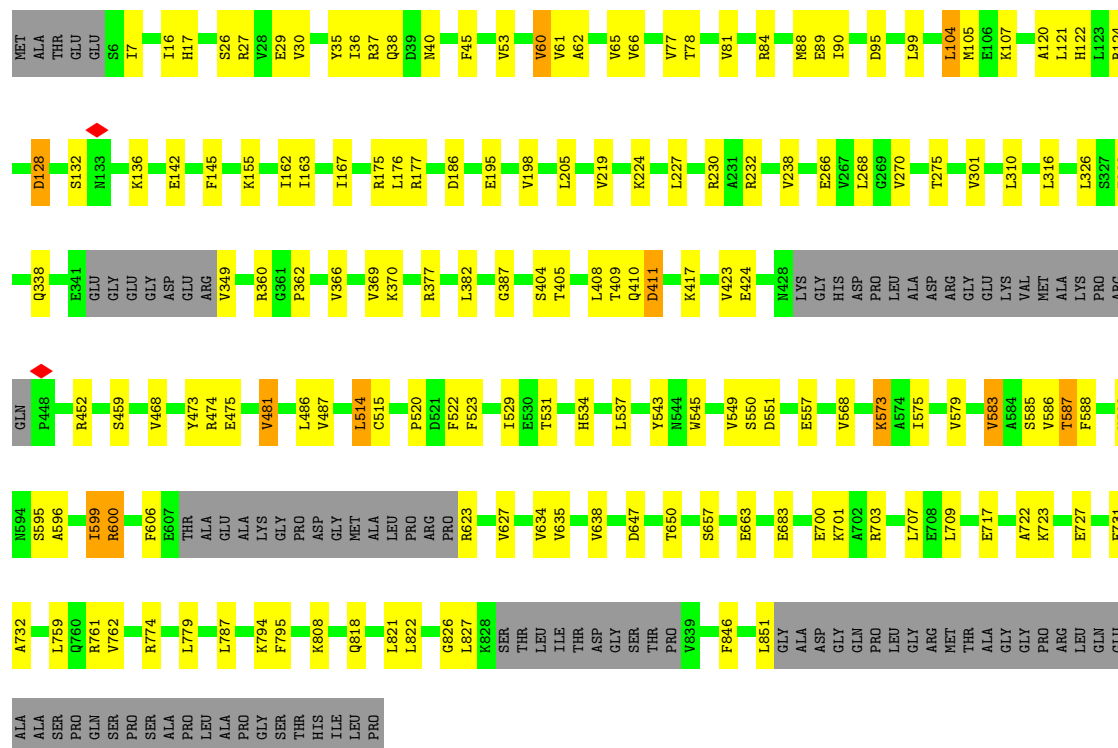
Chain j:





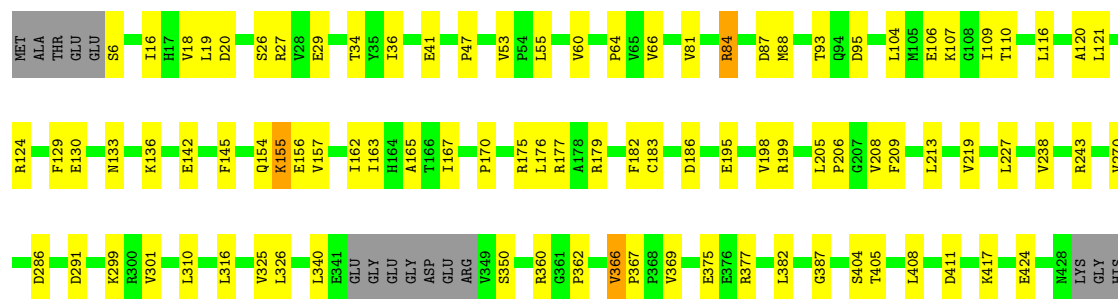
• Molecule 1: Major vault protein

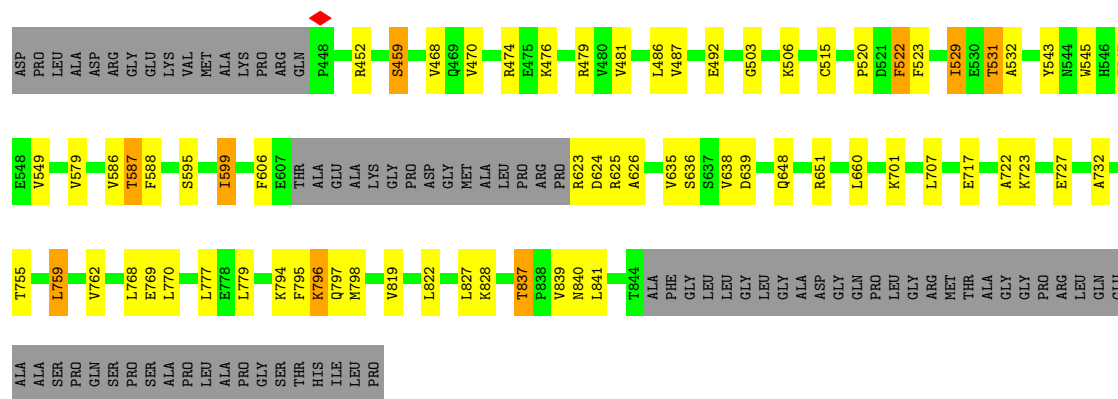
Chain k: 71% 17% 11%



• Molecule 1: Major vault protein

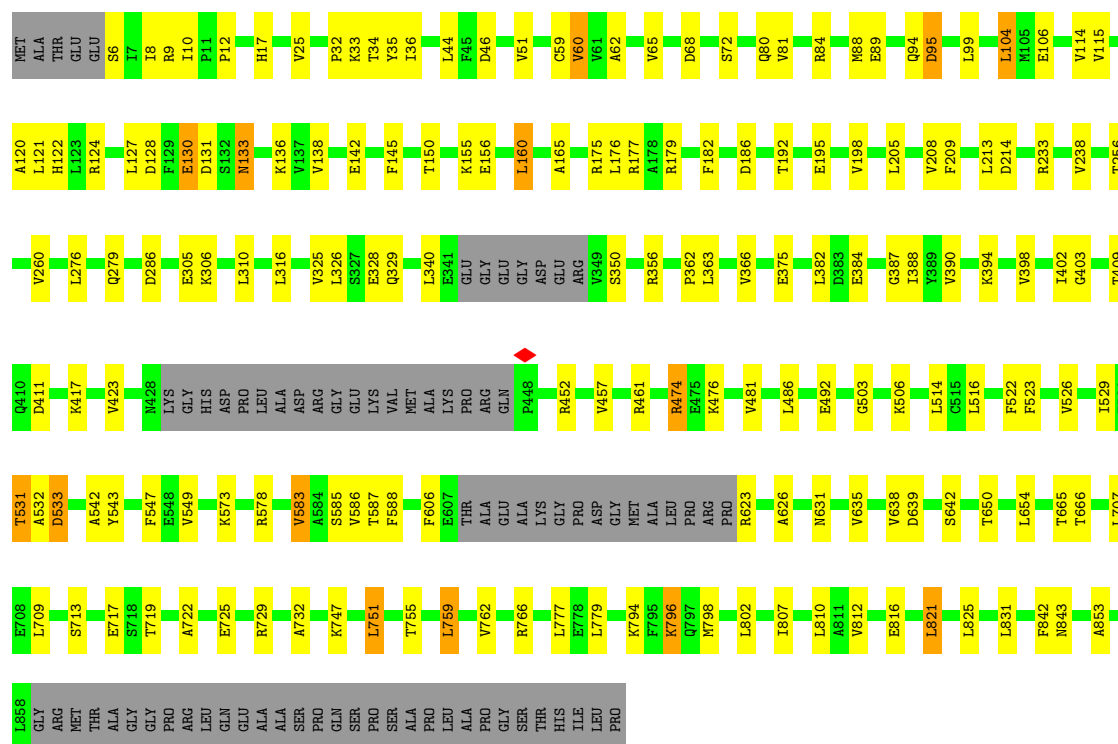
Chain l: 71% 17% 10%





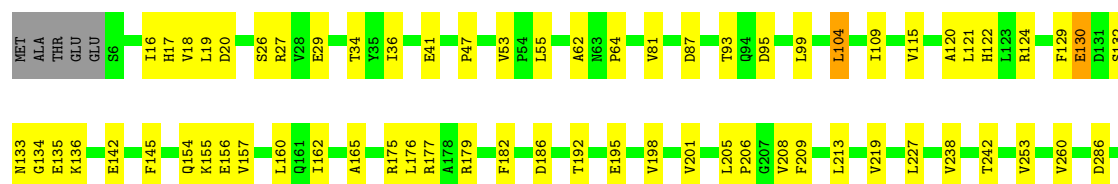
• Molecule 1: Major vault protein

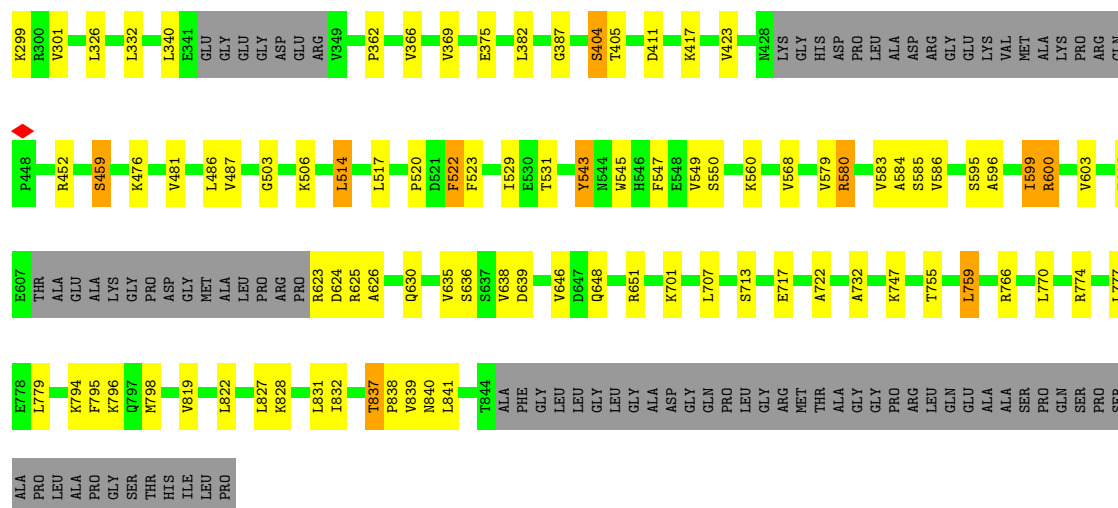
Chain m: 72% 18% 9%



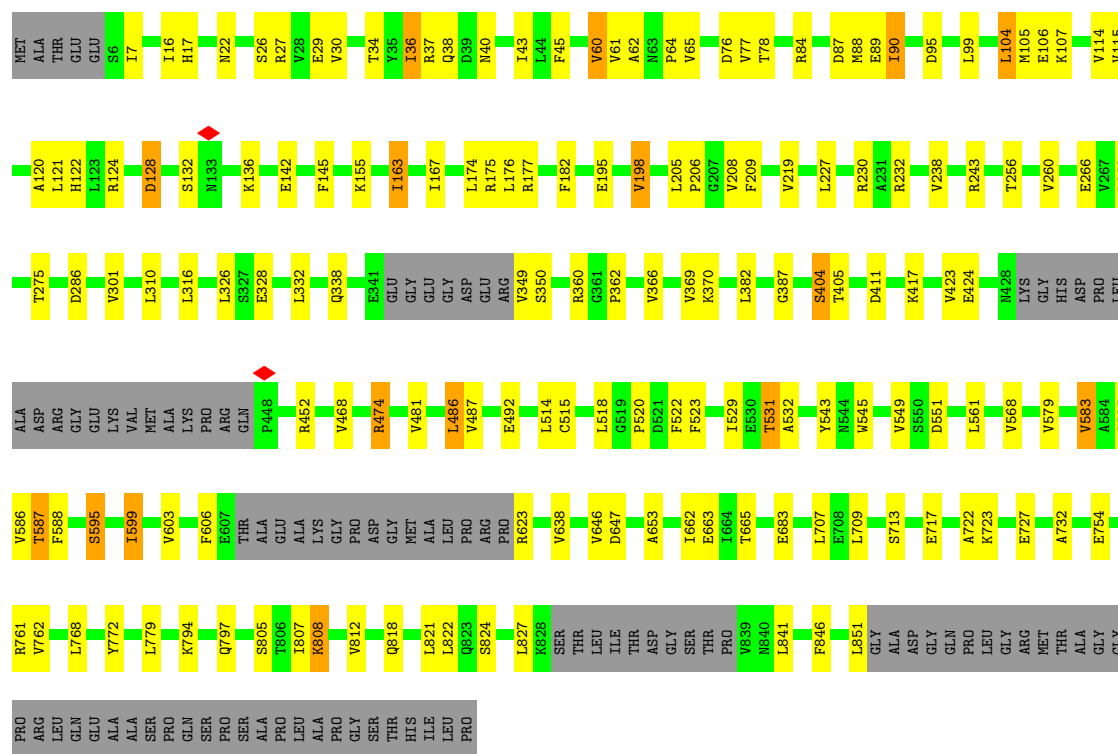
• Molecule 1: Major vault protein

Chain n: 72% 16% 10%



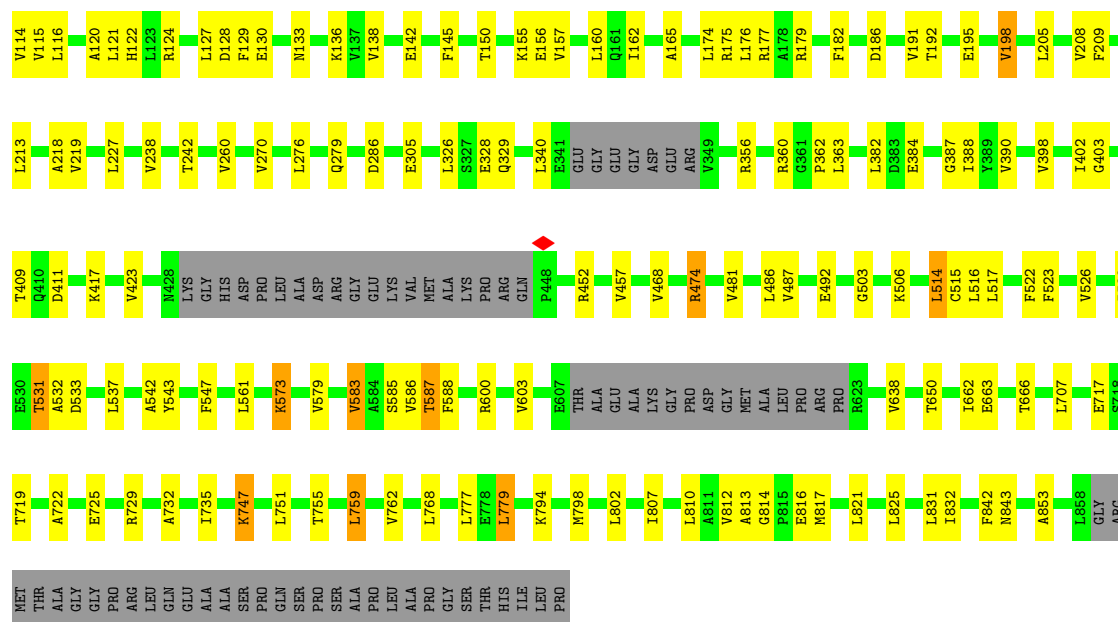


- Molecule 1: Major vault protein



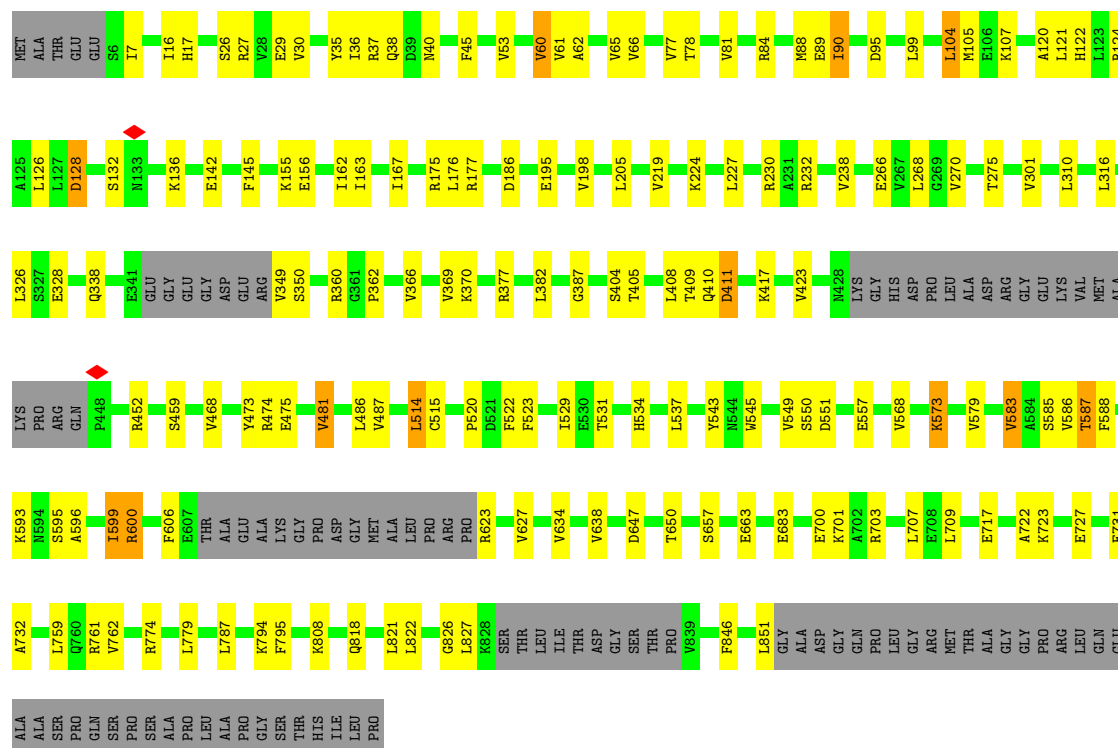
- Molecule 1: Major vault protein





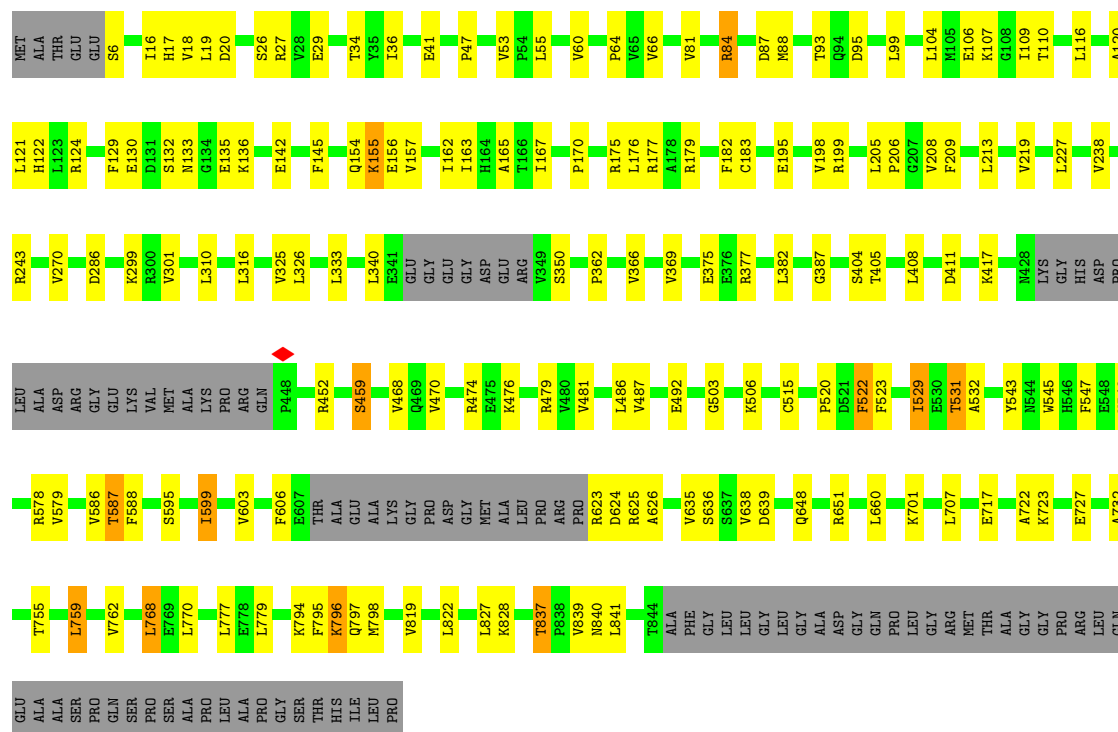
- Molecule 1: Major vault protein

Chain q: 71% 17% 11%



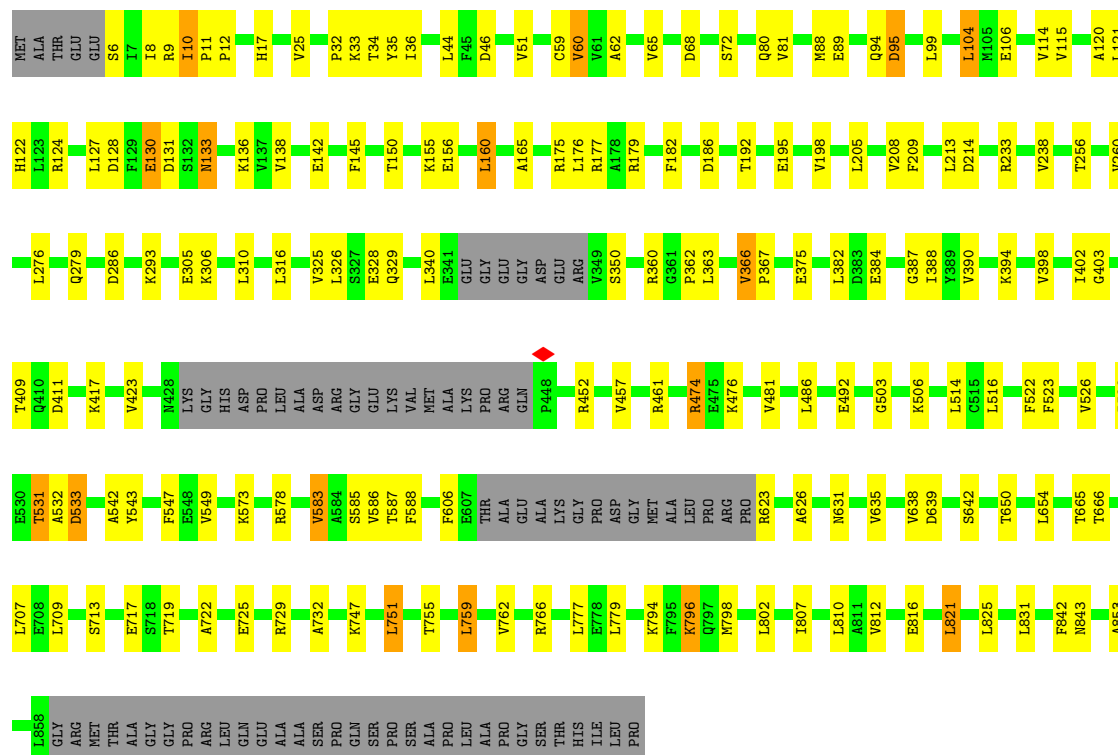
- Molecule 1: Major vault protein

Chain r: 71% 17% 10%



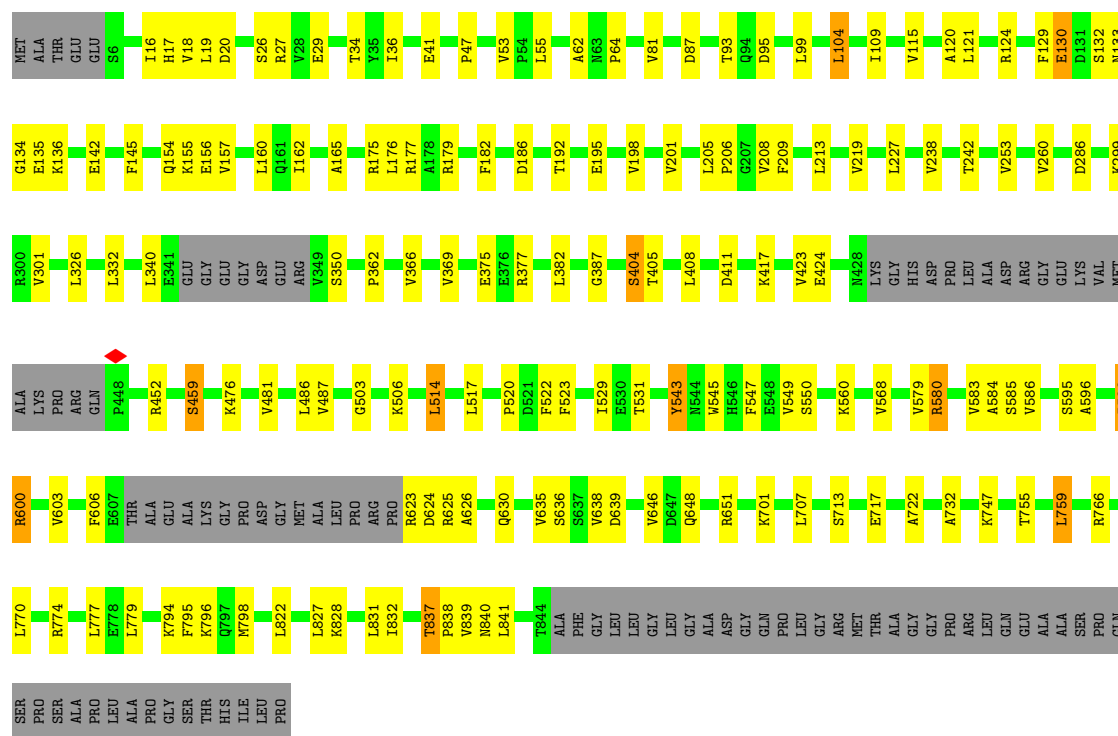
• Molecule 1: Major vault protein

Chain s: 72% 18% 9%



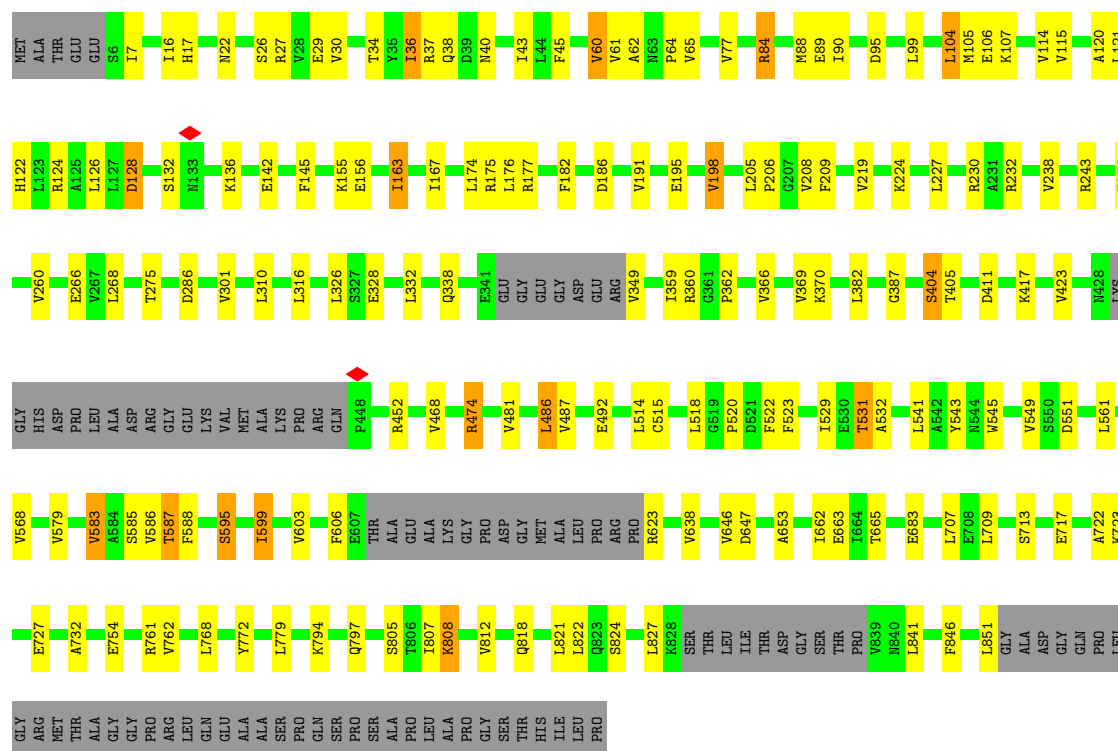
• Molecule 1: Major vault protein

Chain t:  72% 17% 10%



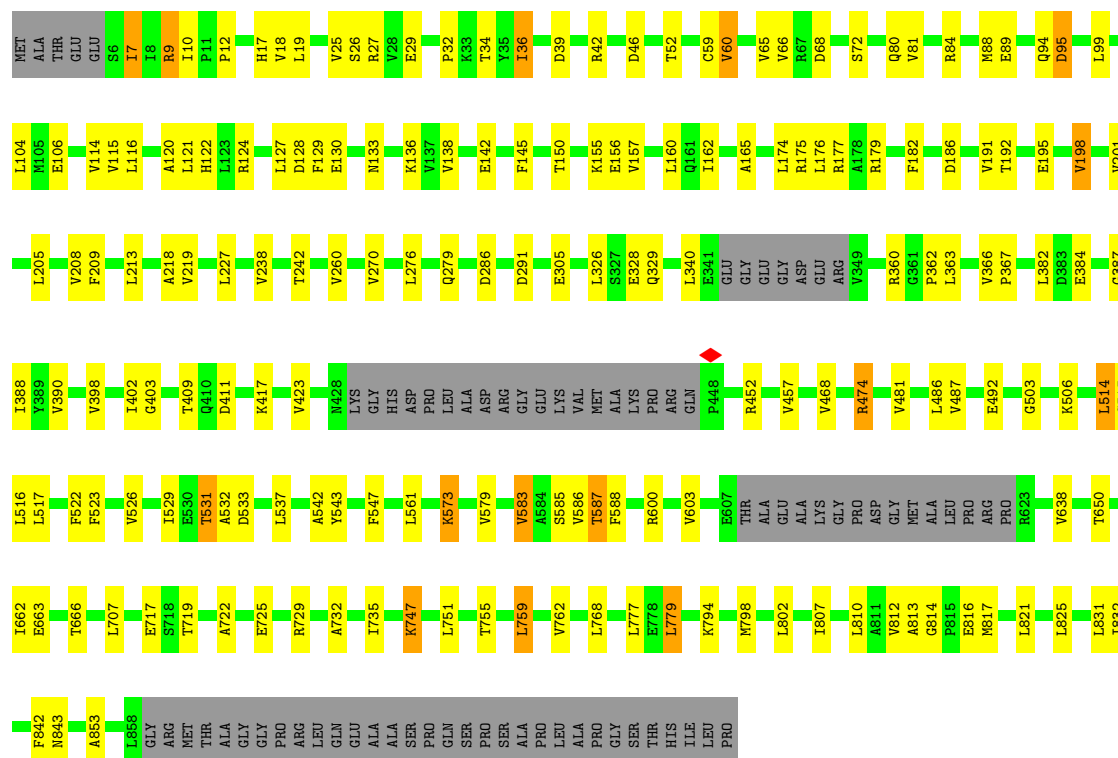
• Molecule 1: Major vault protein

Chain u:  71% 17% 11%



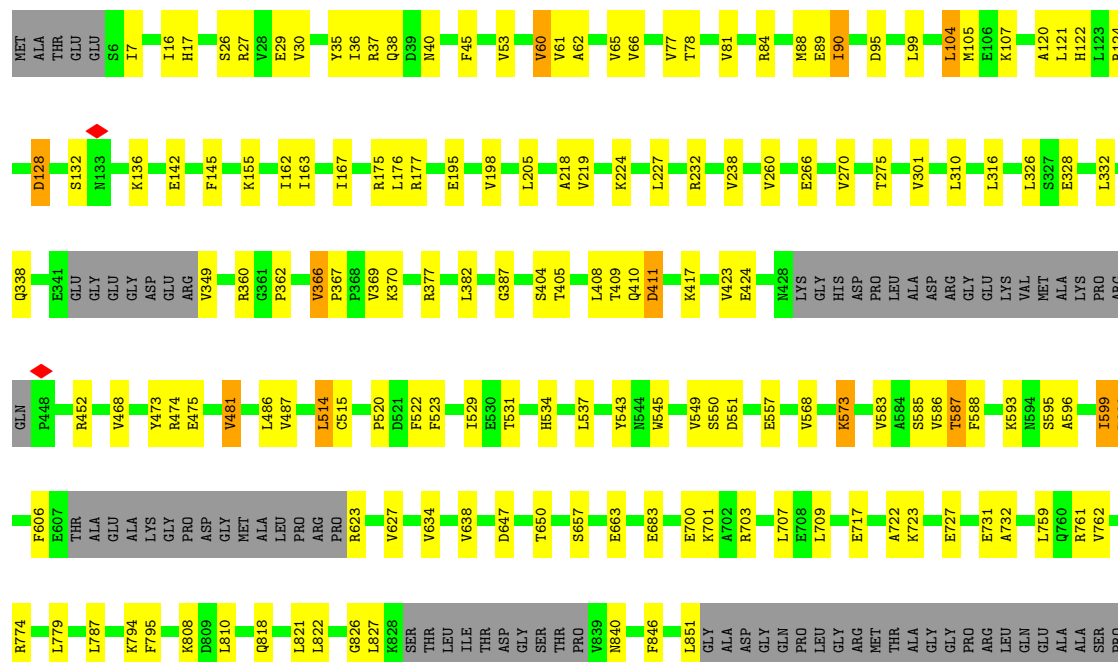
- Molecule 1: Major vault protein

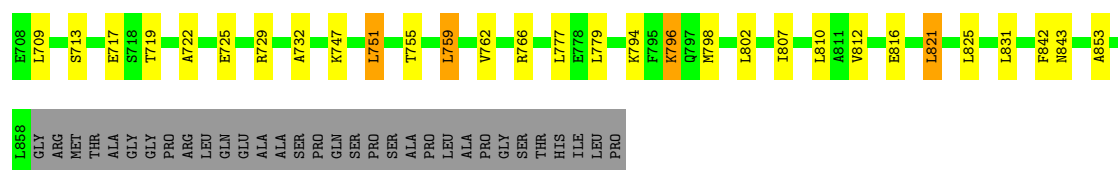
Chain v:  71% 18% 9%



- Molecule 1: Major vault protein

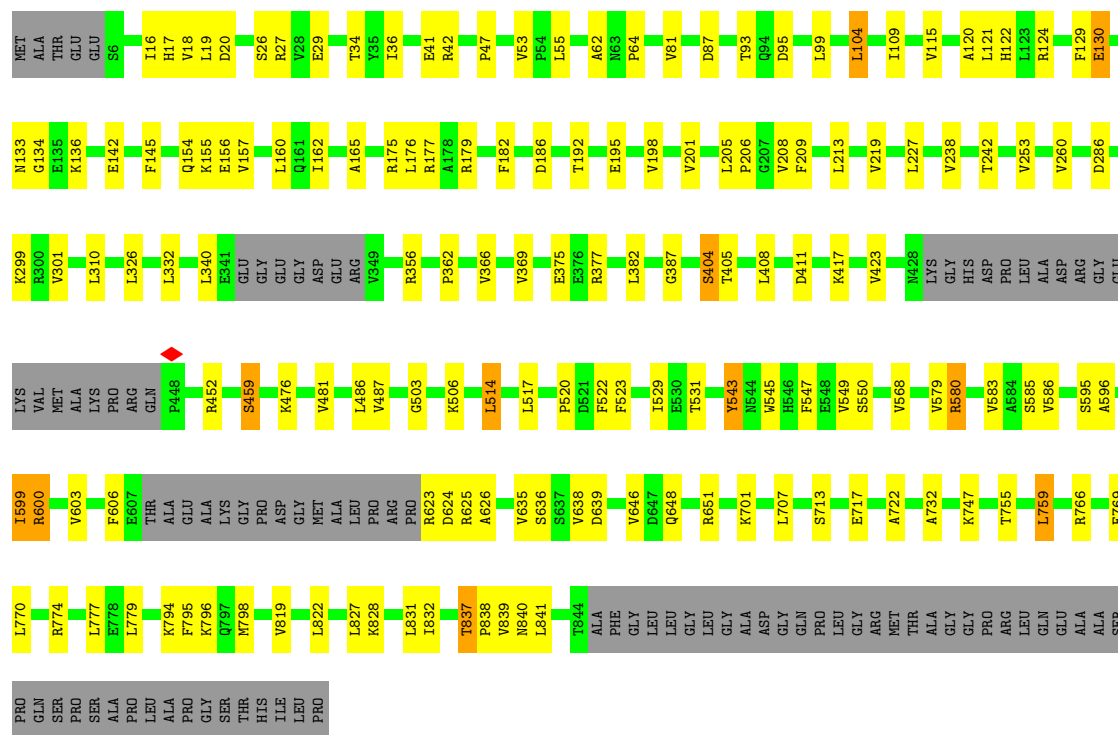
Chain w:  71% 17% 11%





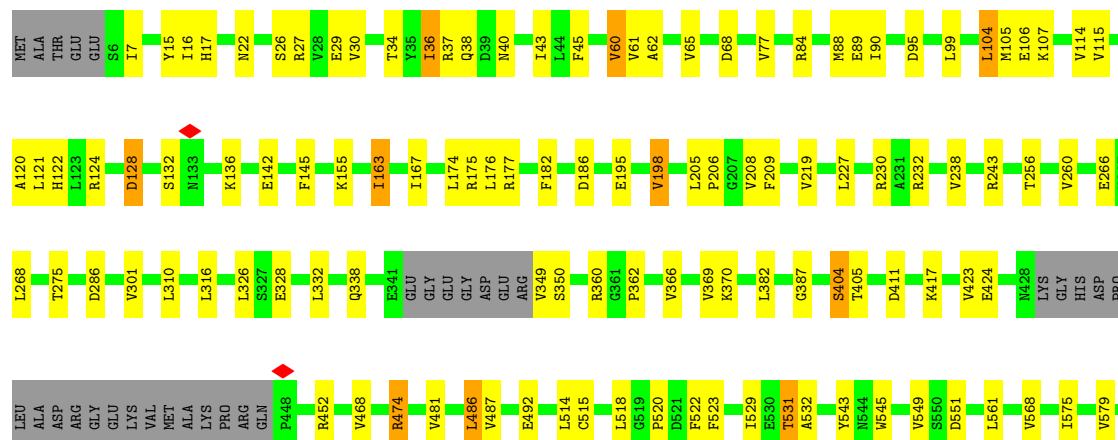
• Molecule 1: Major vault protein

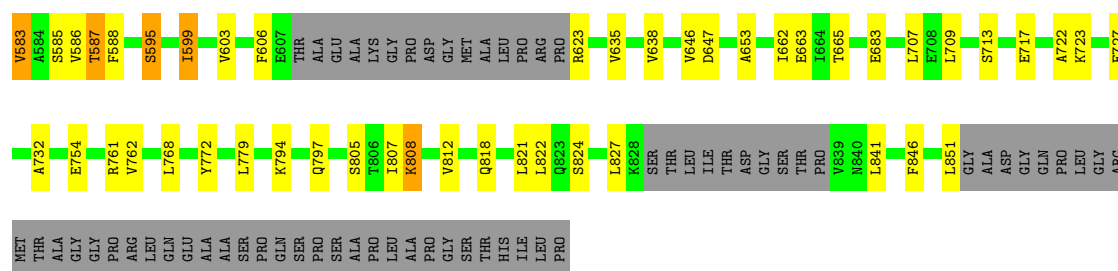
Chain z: 72% 17% 10%



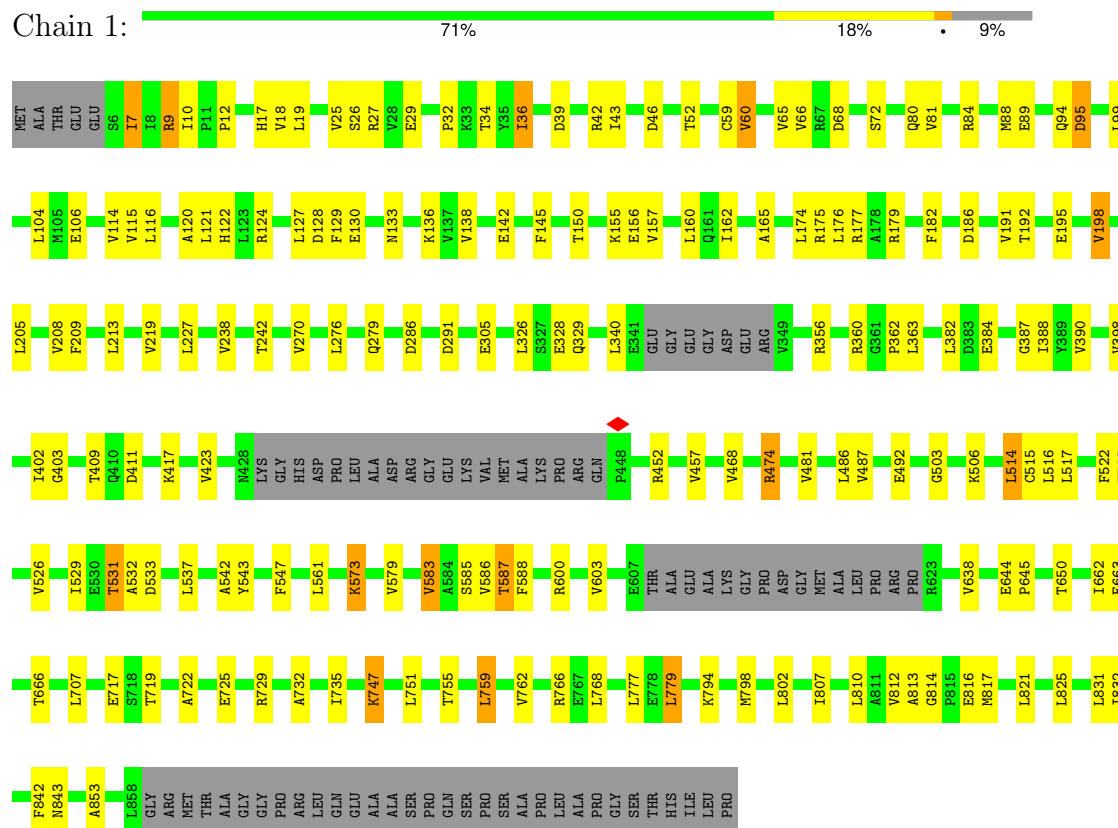
• Molecule 1: Major vault protein

Chain 0: 71% 17% 11%

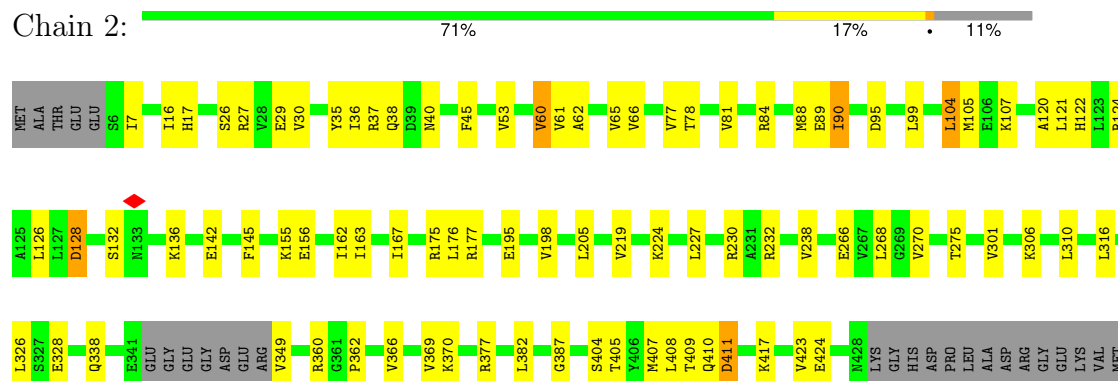


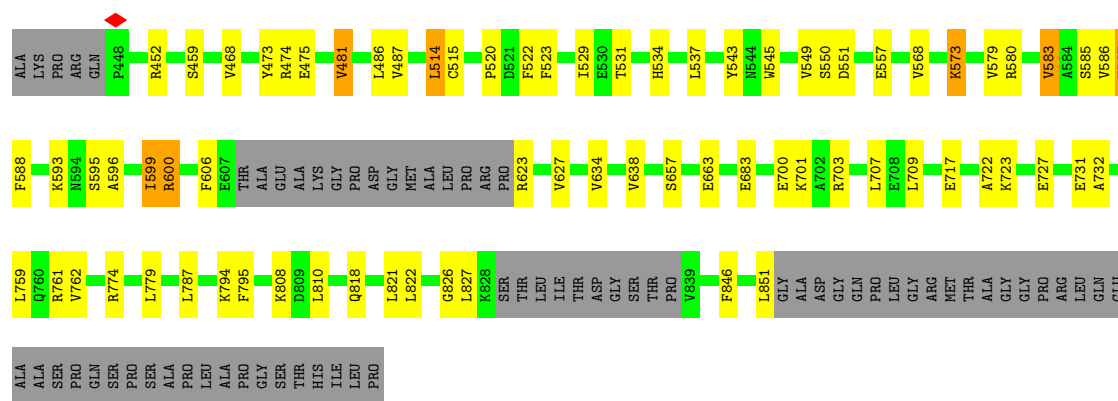


• Molecule 1: Major vault protein



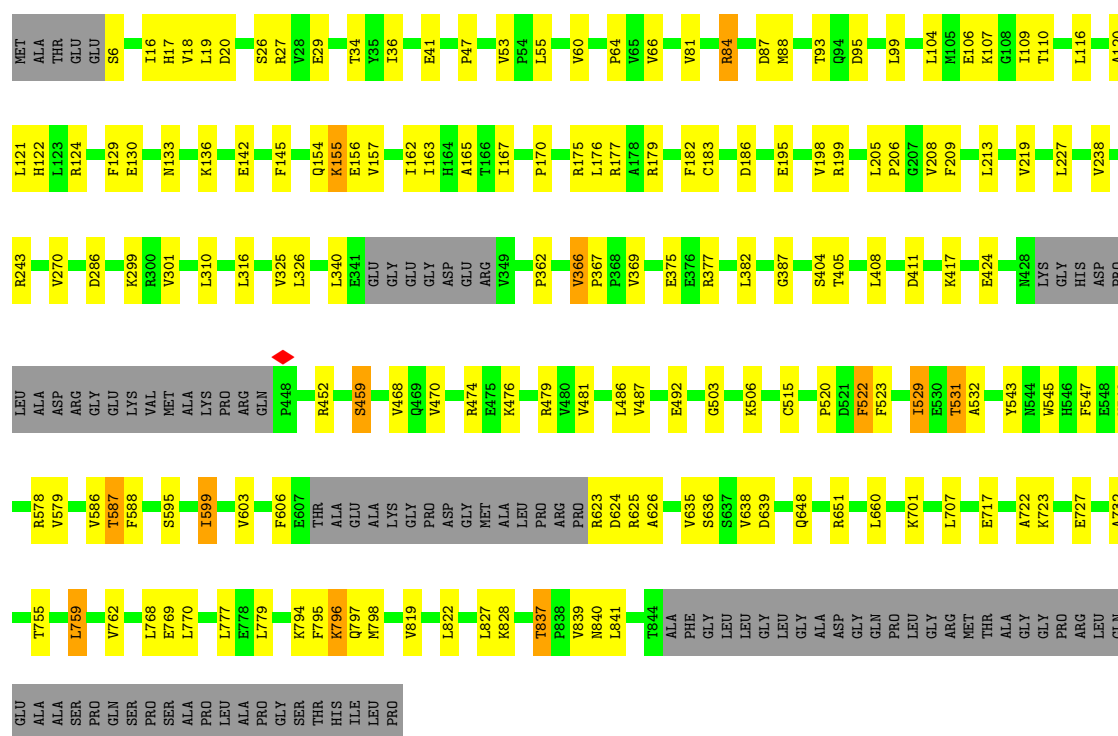
• Molecule 1: Major vault protein





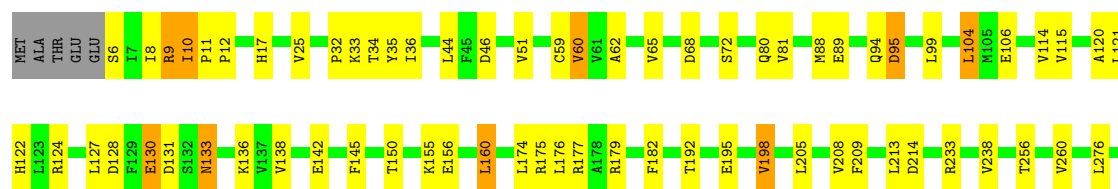
• Molecule 1: Major vault protein

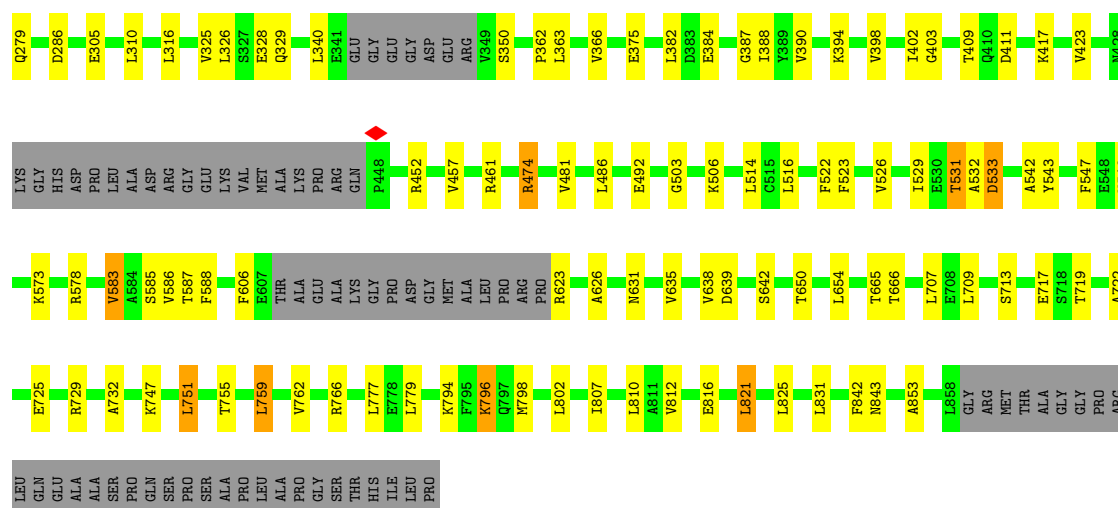
Chain 3: 71% 17% 10%



• Molecule 1: Major vault protein

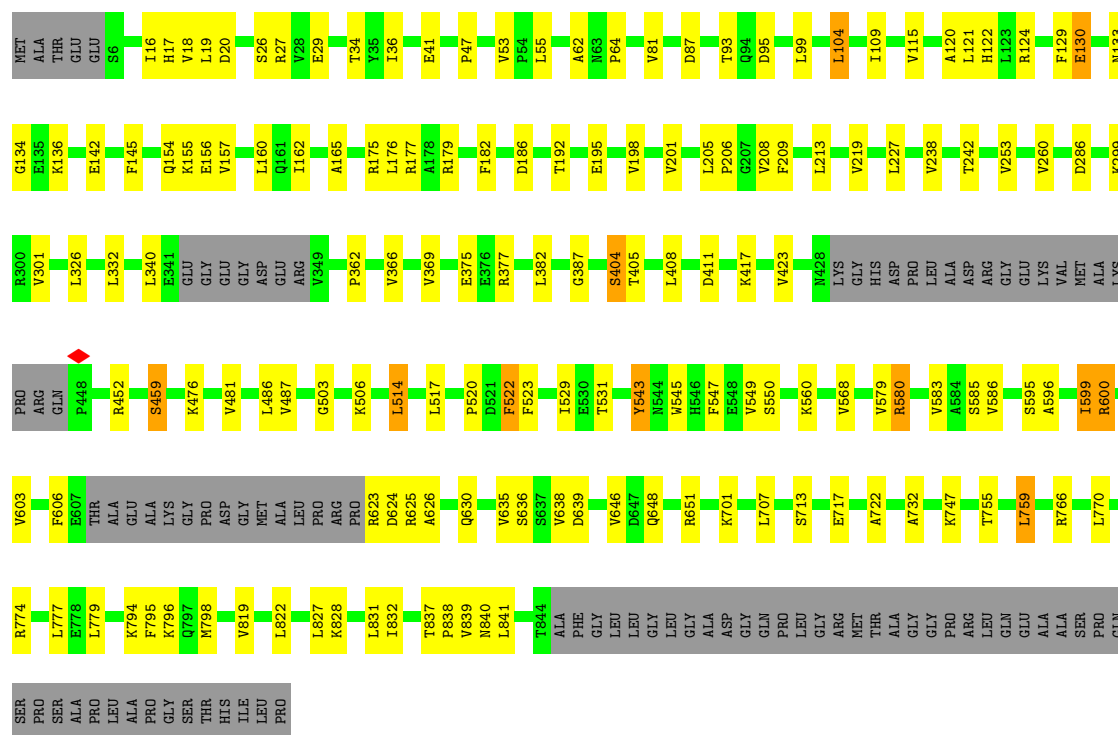
Chain 4: 72% 17% 9%





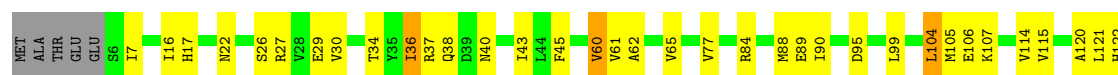
• Molecule 1: Major vault protein

Chain 5: 72% 16% 10%

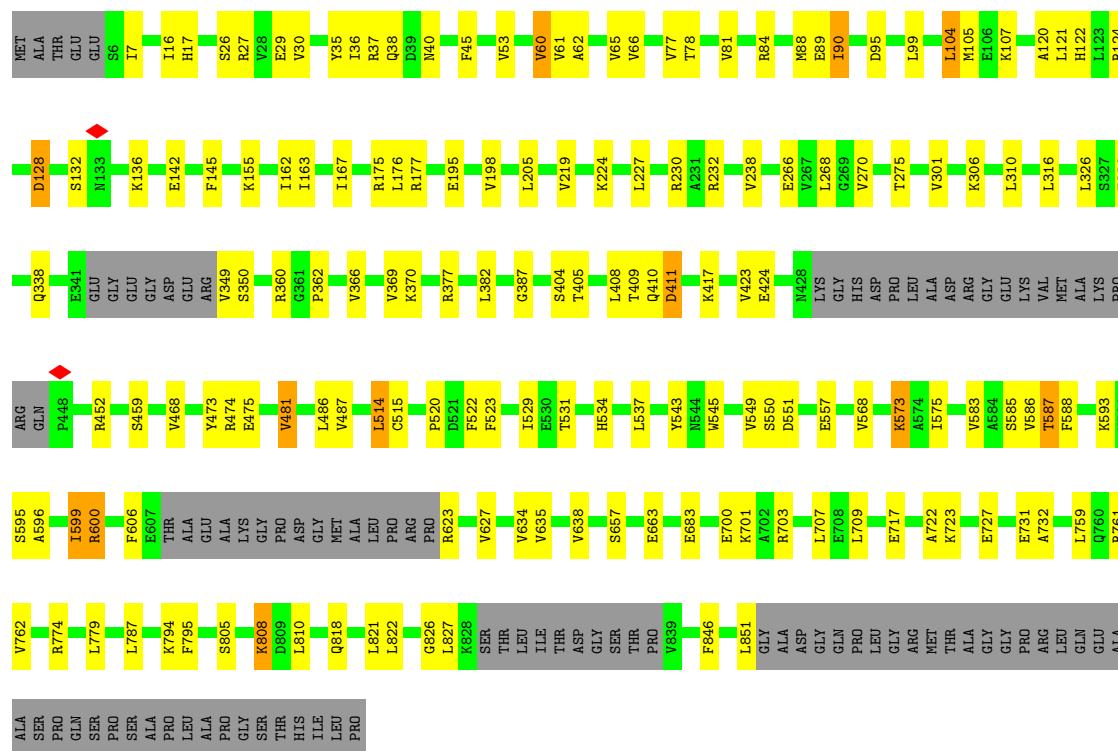


• Molecule 1: Major vault protein

Chain 6: 71% 17% 11%

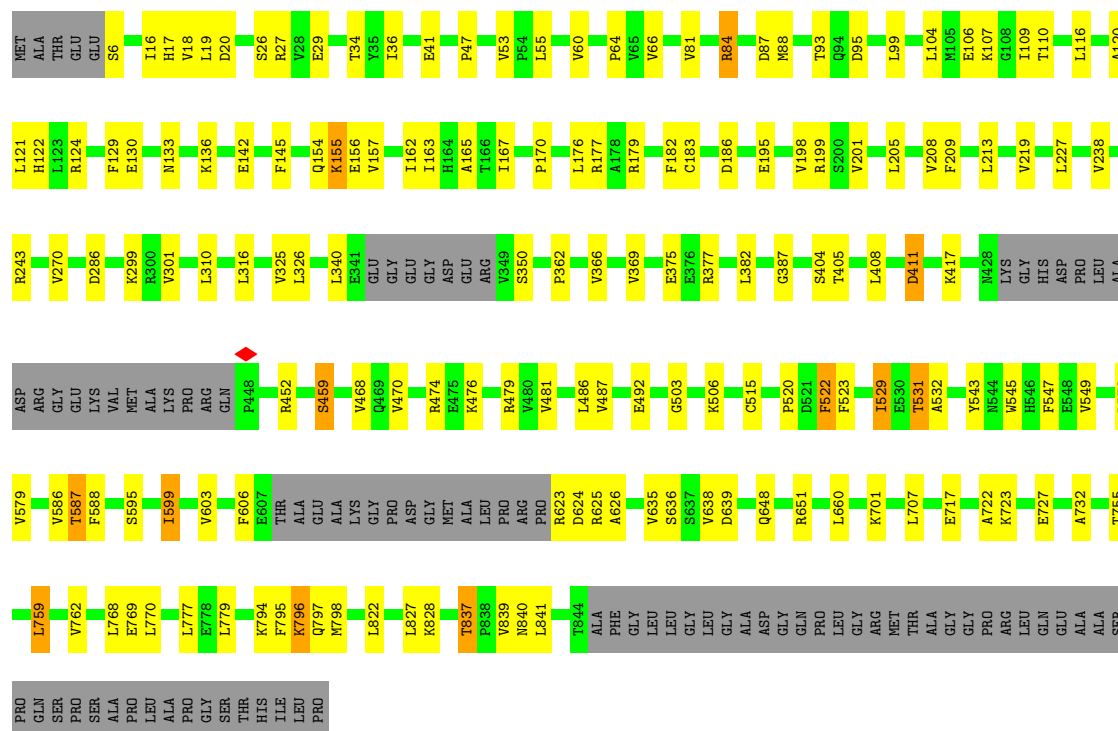






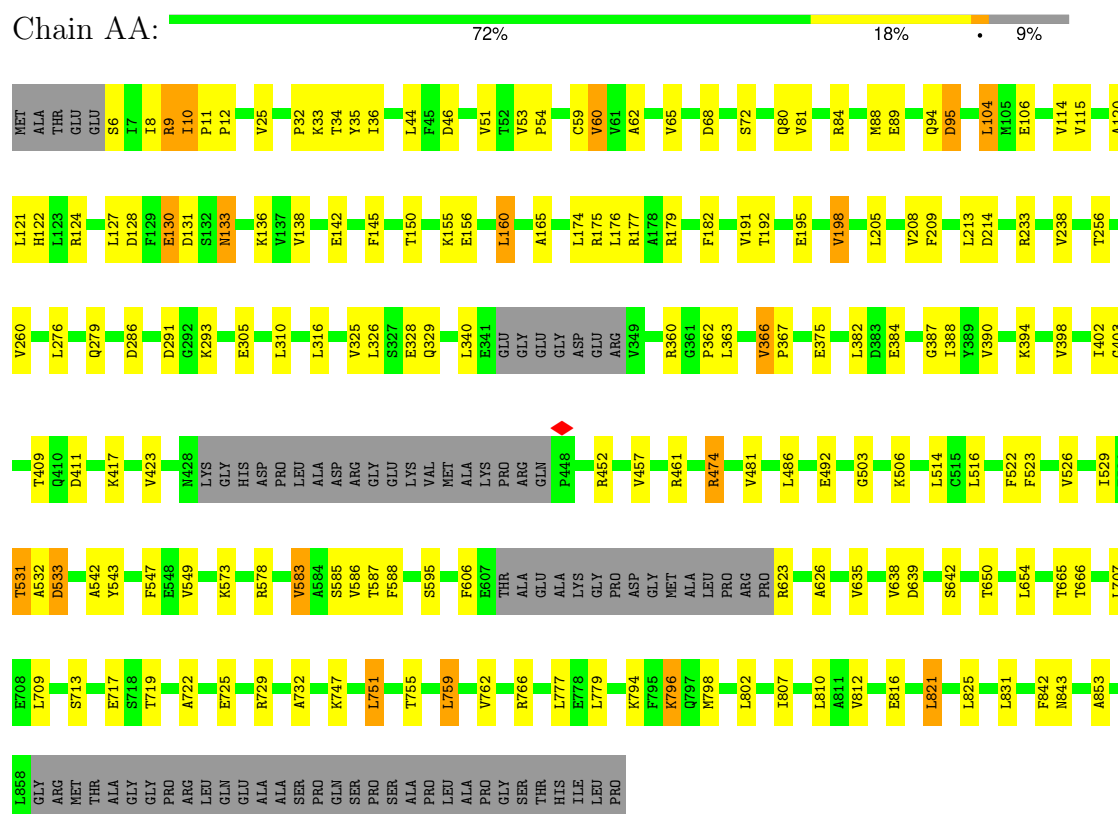
• Molecule 1: Major vault protein

Chain 9: 72% 17% 10%



• Molecule 1: Major vault protein

Chain AA:



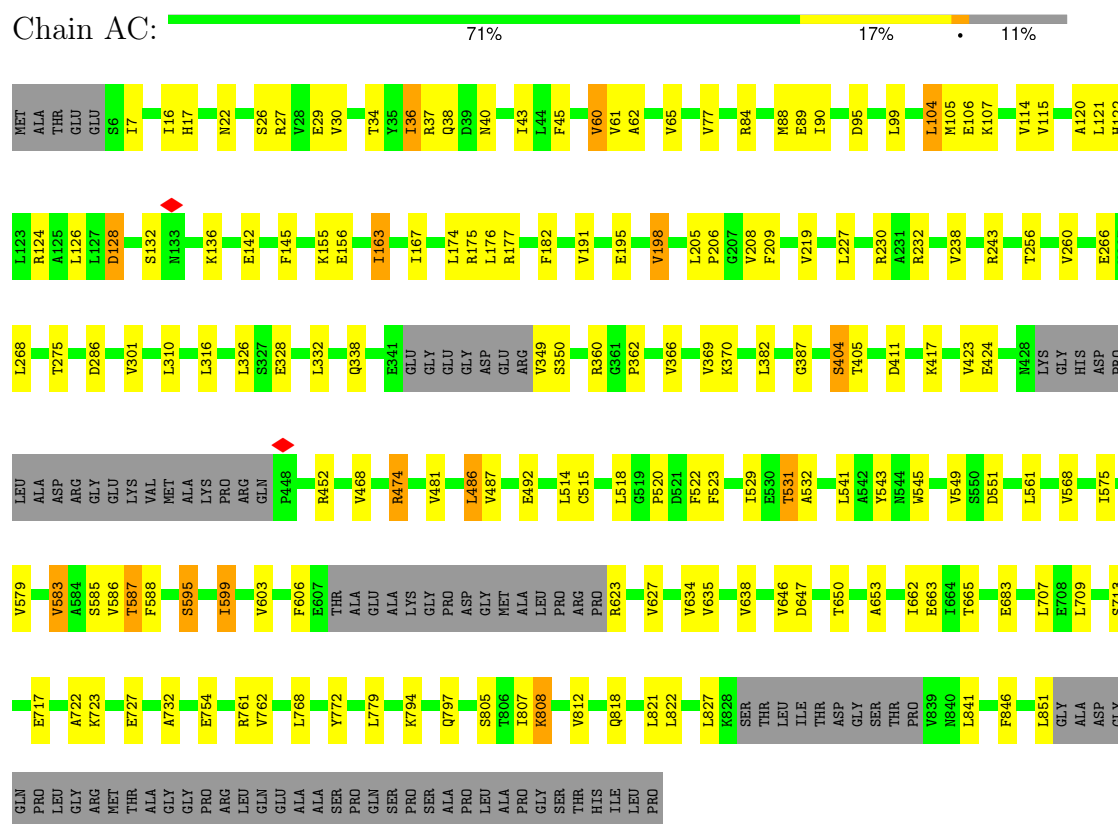
- Molecule 1: Major vault protein

Chain AB:



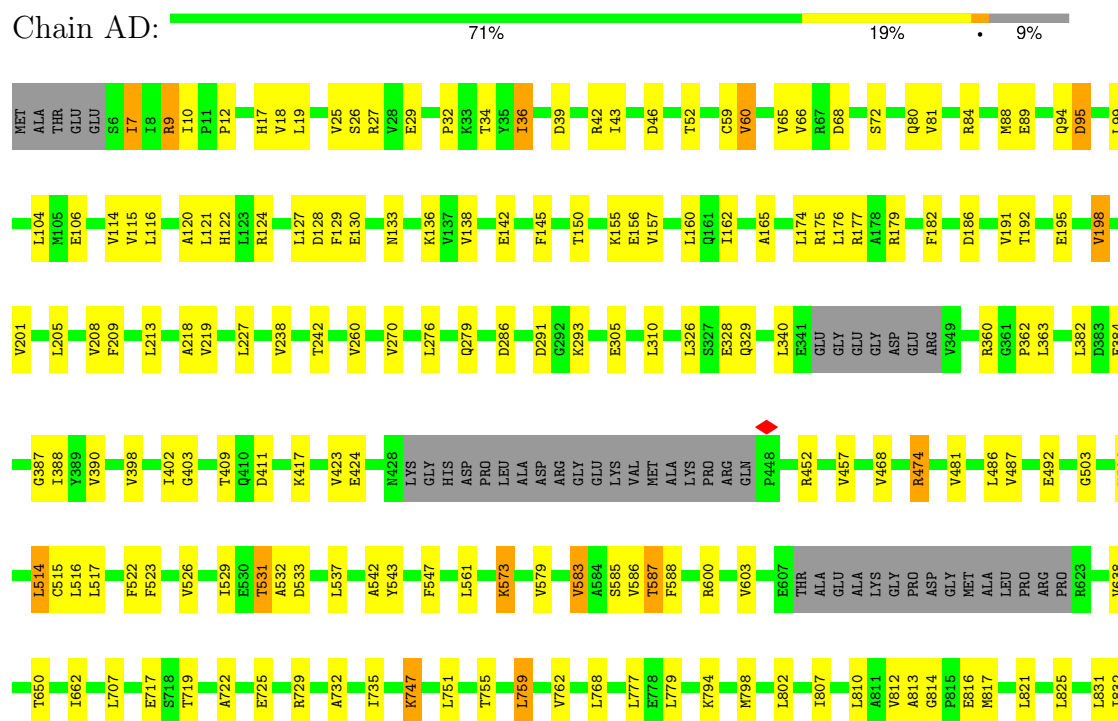
- Molecule 1: Major vault protein

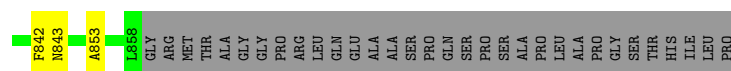
Chain AC:



- Molecule 1: Major vault protein

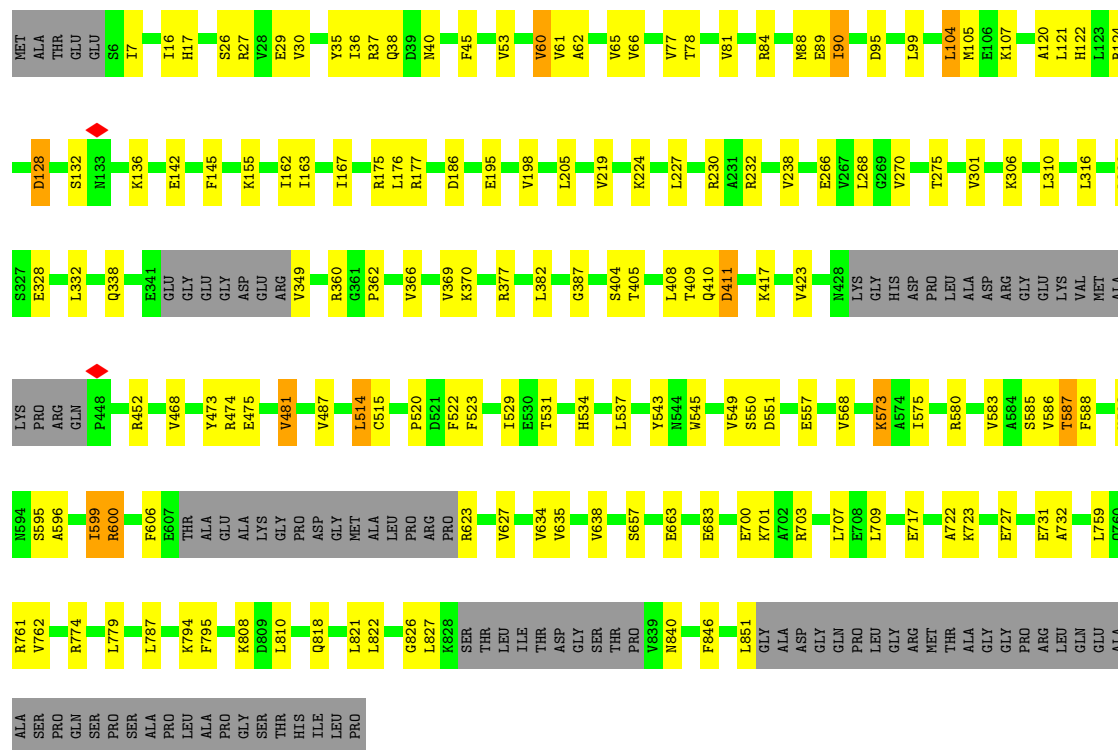
Chain AD:





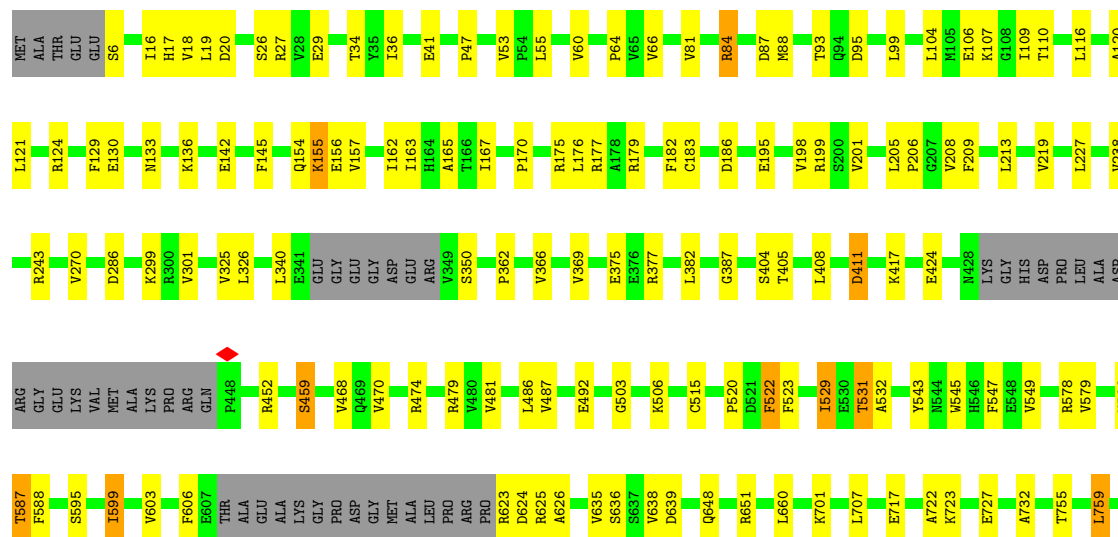
• Molecule 1: Major vault protein

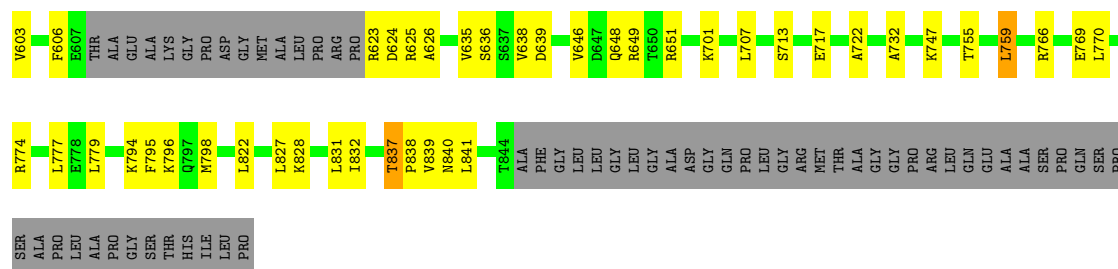
Chain AE: 71% 17% 11%



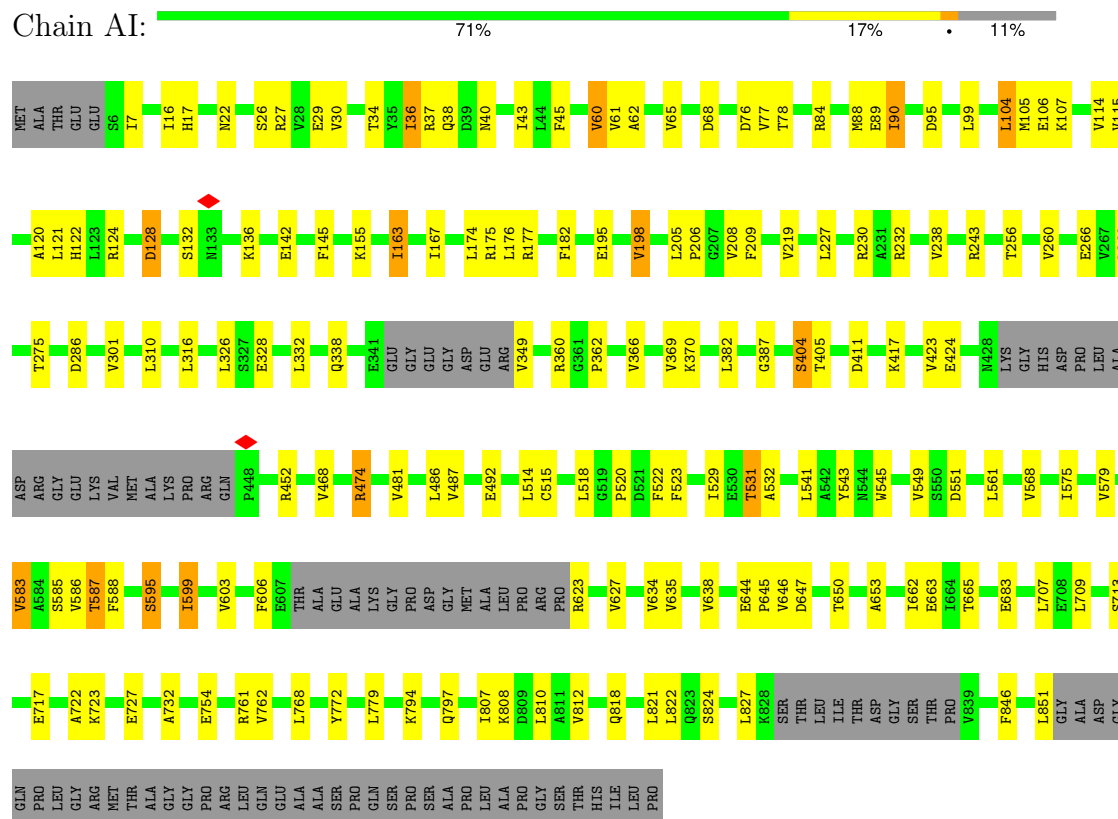
• Molecule 1: Major vault protein

Chain AF: 72% 17% 10%

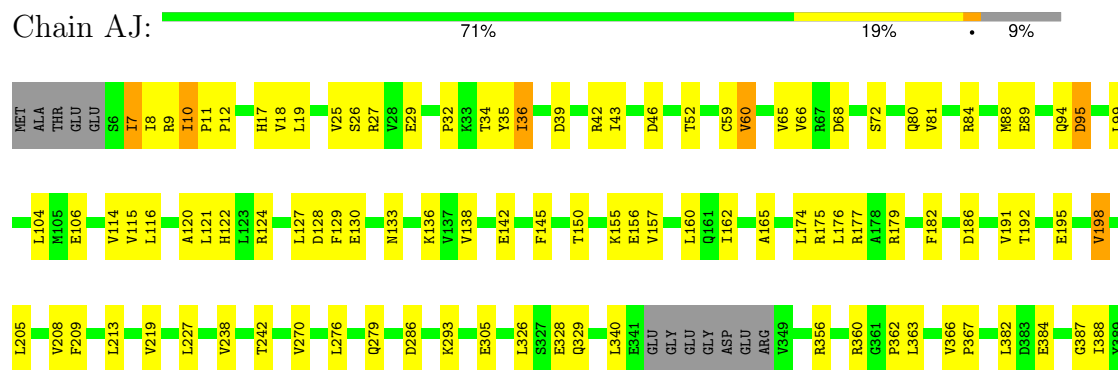


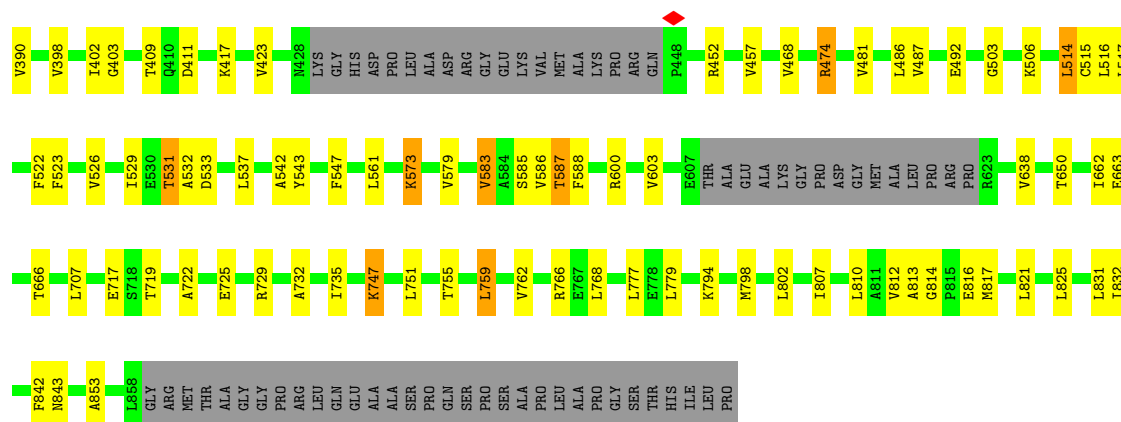


- Molecule 1: Major vault protein



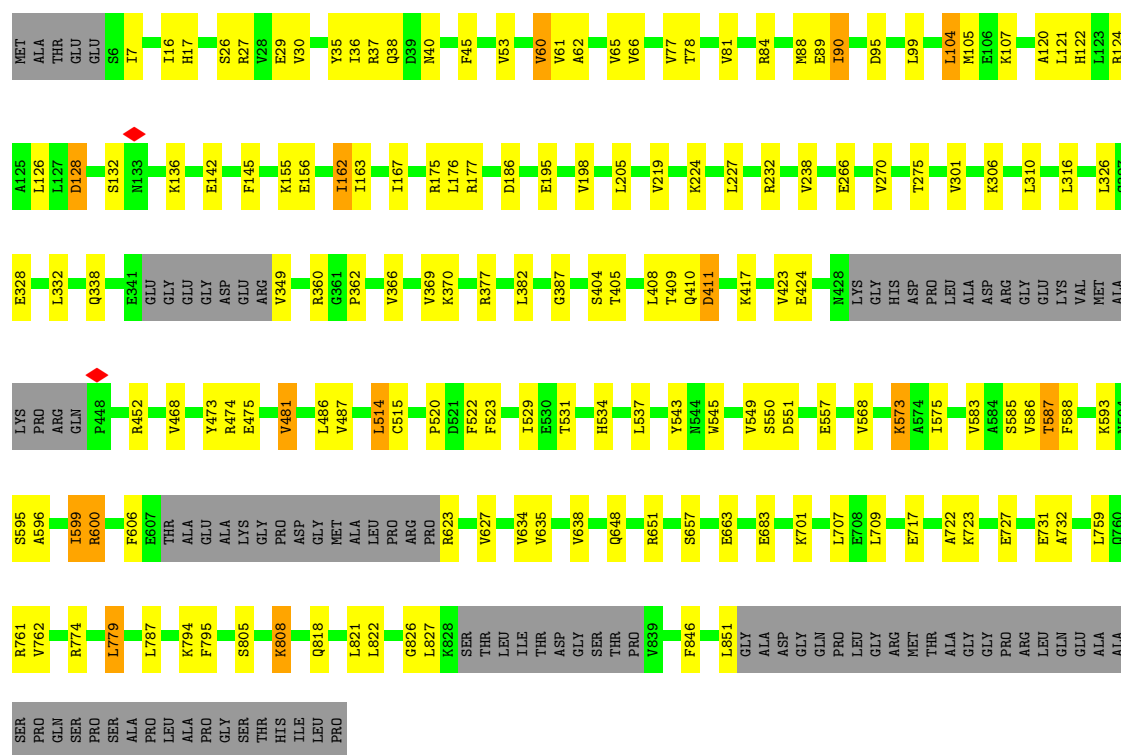
- Molecule 1: Major vault protein





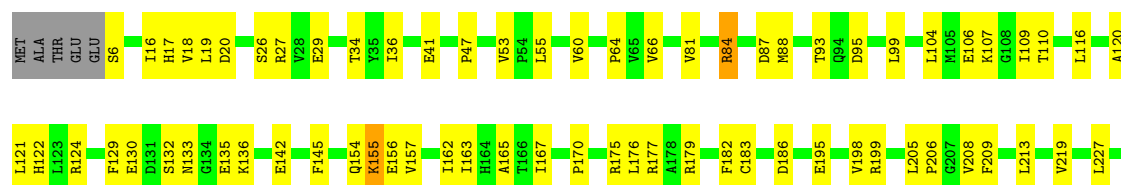
• Molecule 1: Major vault protein

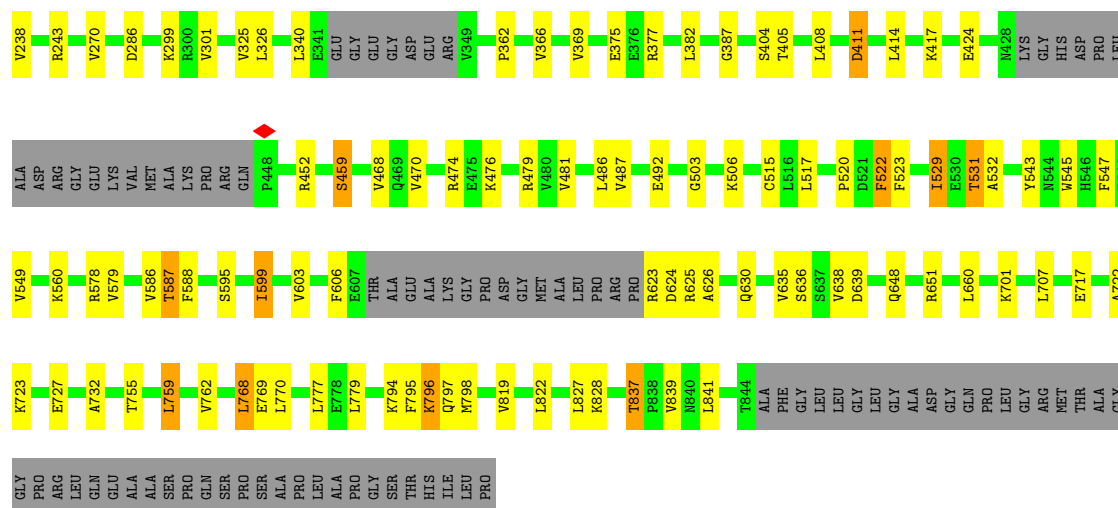
Chain AK: 71% 16% 11%



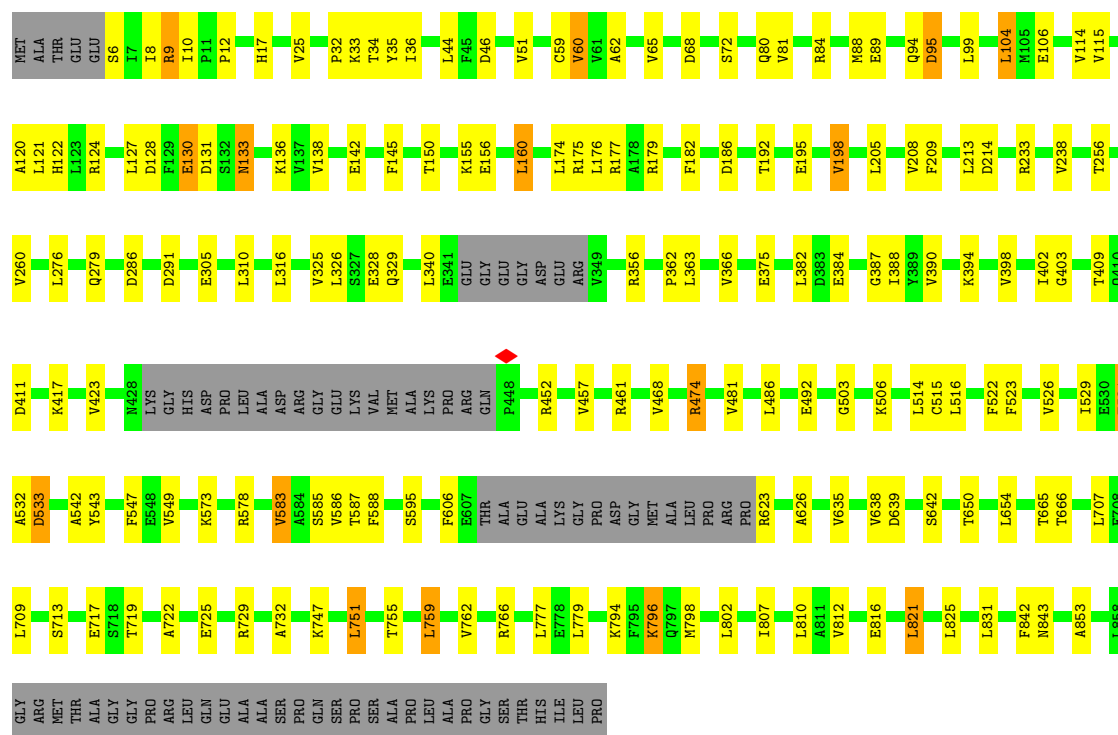
• Molecule 1: Major vault protein

Chain AL: 71% 17% 10%



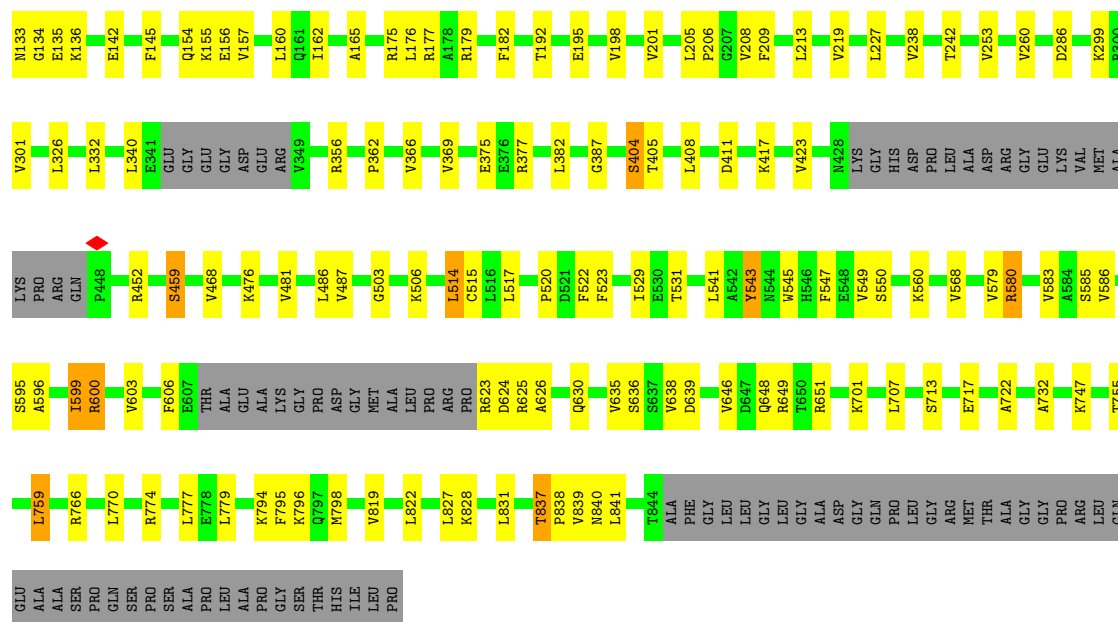


- Molecule 1: Major vault protein



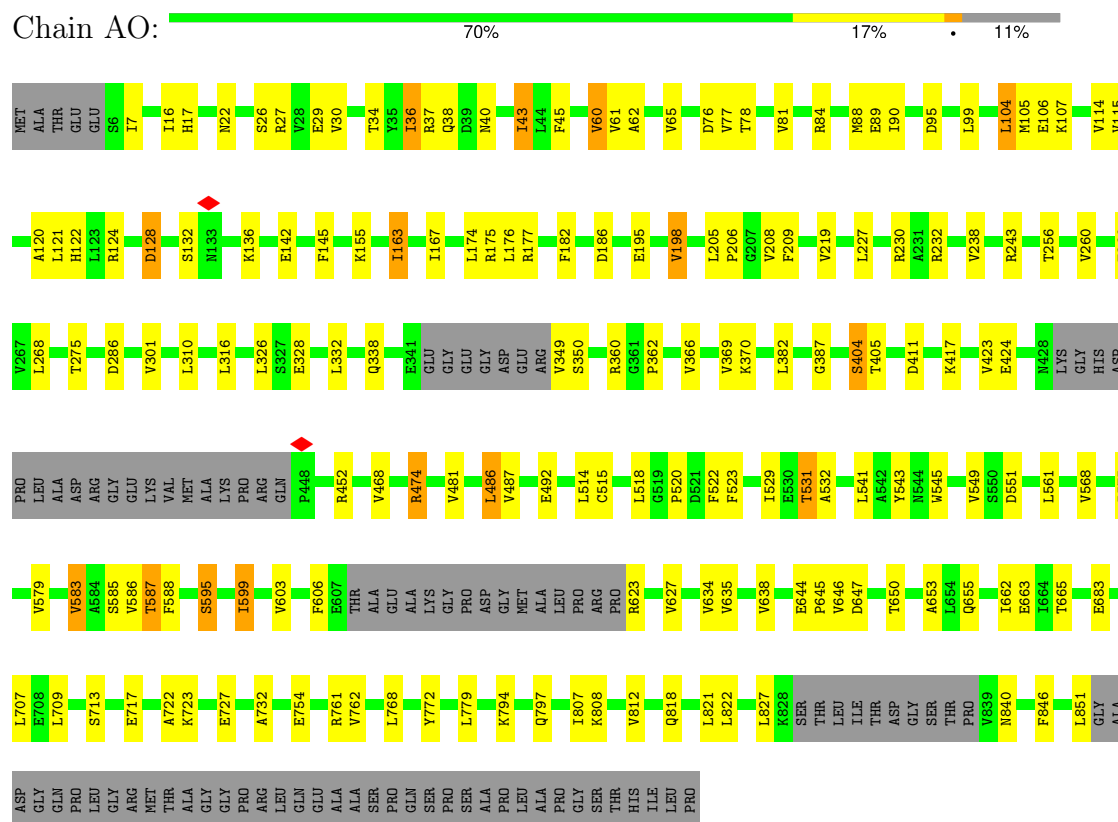
- Molecule 1: Major vault protein





• Molecule 1: Major vault protein

Chain AO:



• Molecule 1: Major vault protein

Chain AP:

THR	ALA	GLY	PRO	ARG	GLN	GLU	ALA	ALA	SER	PRO	GLN	SER	PRO	ALA	PRO	LEU	ALA	PRO	LEU	THR	HIS	ILE	LEU	PRO																			
A722	E725	E729	A732	I735	K747	L751	T755	L759	V762	L768	L777	E778	L779	K794	M798	L802	I807	L810	V811	A813	P815	E816	M817	L821	L825	L831	I832	F842	N843	A853	L858	GLY	ARG	MET									
T531	A532	D533	L537	A542	Y543	F547	L561	K573	V579	V583	A584	S585	V586	T587	F588	R600	V603	E607	THR	ALA	GLU	ALA	LYS	GLY	PRO	ASP	GLY	MET	ALA	LEU	PRO	ARG	PRO	R623	V638	T650	I662	E663	T666	L707	E717	S718	T719
D411	K417	E424	V423	A428	LYS	GLY	HIS	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	VAL	MET	ALA	LYS	PRO	ARG	GLN	P448	R452	V457	V468	R474	V481	L486	V487	E492	G503	K506	L514	C515	L516	L517	F522	F523	V526	I529	E530
V219	L227	R230	V238	T242	L268	G269	V270	L276	Q279	D286	K293	E305	L326	S327	E328	Q329	L340	E341	GLY	GLY	GLY	ASP	GLU	ARG	V349	S350	P362	L363	L382	D383	E384	G387	I388	Y389	V390	V398	I402	G403	T409	Q410			
V114	V115	L116	A120	L121	H122	L123	R124	L127	D128	F129	E130	N133	V138	E142	F145	T150	K155	E156	V157	L160	Q161	I162	A165	L174	R175	L176	R177	A178	R179	F182	D186	V191	T192	E195	V198	L205	V208	F209	L213				
MET	ALA	THR	GLU	S6	I7	I8	R9	I10	P11	P12	H17	V18	L19	V25	S26	R27	V28	E29	P32	K33	T34	I35	I36	D46	T52	C59	V60	V65	V66	R67	D68	S72	Q80	V81	R84	M88	E89	Q94	D95	L99	L104	M105	E106

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	159668	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 ($e^-/\text{\AA}^2$)	34.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.855	Depositor
Minimum map value	0.000	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.0753	Depositor
Map size (Å)	773.5, 773.5, 773.5	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.105, 1.105, 1.105	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	0	0.29	0/6360	0.56	0/8624
1	1	0.29	0/6489	0.54	0/8802
1	2	0.29	0/6353	0.54	0/8615
1	3	0.29	0/6382	0.55	0/8657
1	4	0.30	0/6489	0.55	0/8802
1	5	0.29	0/6382	0.54	0/8657
1	6	0.29	0/6360	0.55	0/8624
1	7	0.29	0/6489	0.54	0/8802
1	8	0.29	0/6353	0.54	0/8615
1	9	0.29	0/6382	0.55	0/8657
1	A	0.29	0/6353	0.54	0/8615
1	AA	0.29	0/6489	0.55	0/8802
1	AB	0.29	0/6382	0.54	0/8657
1	AC	0.29	0/6360	0.55	0/8624
1	AD	0.29	0/6489	0.54	0/8802
1	AE	0.29	0/6353	0.54	0/8615
1	AF	0.29	0/6382	0.55	0/8657
1	AG	0.29	0/6489	0.55	0/8802
1	AH	0.29	0/6382	0.54	0/8657
1	AI	0.29	0/6360	0.55	0/8624
1	AJ	0.29	0/6489	0.54	0/8802
1	AK	0.29	0/6353	0.54	0/8615
1	AL	0.29	0/6382	0.55	0/8657
1	AM	0.30	0/6489	0.55	0/8802
1	AN	0.29	0/6382	0.54	0/8657
1	AO	0.29	0/6360	0.55	0/8624
1	AP	0.29	0/6489	0.54	0/8802
1	B	0.29	0/6382	0.55	0/8657
1	C	0.29	0/6489	0.55	0/8802
1	D	0.29	0/6382	0.54	0/8657
1	E	0.29	0/6360	0.55	0/8624
1	F	0.29	0/6489	0.54	0/8802
1	G	0.29	0/6353	0.54	0/8615
1	H	0.29	0/6382	0.55	0/8657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	I	0.29	0/6489	0.55	0/8802
1	J	0.29	0/6382	0.54	0/8657
1	K	0.29	0/6360	0.55	0/8624
1	L	0.29	0/6489	0.54	0/8802
1	M	0.29	0/6353	0.54	0/8615
1	N	0.29	0/6382	0.55	0/8657
1	O	0.30	0/6489	0.54	0/8802
1	P	0.29	0/6382	0.54	0/8657
1	Q	0.29	0/6360	0.55	0/8624
1	R	0.29	0/6489	0.54	0/8802
1	S	0.30	0/6353	0.54	0/8615
1	T	0.29	0/6382	0.55	0/8657
1	U	0.29	0/6489	0.55	0/8802
1	V	0.29	0/6382	0.54	0/8657
1	W	0.29	0/6360	0.55	0/8624
1	X	0.29	0/6489	0.54	0/8802
1	Y	0.30	0/6353	0.54	0/8615
1	Z	0.29	0/6382	0.55	0/8657
1	a	0.29	0/6489	0.55	0/8802
1	b	0.29	0/6382	0.54	0/8657
1	c	0.29	0/6360	0.55	0/8624
1	d	0.29	0/6489	0.54	0/8802
1	e	0.29	0/6353	0.54	0/8615
1	f	0.29	0/6382	0.55	0/8657
1	g	0.29	0/6489	0.54	0/8802
1	h	0.29	0/6382	0.54	0/8657
1	i	0.29	0/6360	0.55	0/8624
1	j	0.29	0/6489	0.54	0/8802
1	k	0.30	0/6353	0.54	0/8615
1	l	0.29	0/6382	0.55	0/8657
1	m	0.29	0/6489	0.54	0/8802
1	n	0.29	0/6382	0.54	0/8657
1	o	0.29	0/6360	0.55	0/8624
1	p	0.29	0/6489	0.54	0/8802
1	q	0.29	0/6353	0.54	0/8615
1	r	0.29	0/6382	0.55	0/8657
1	s	0.29	0/6489	0.55	0/8802
1	t	0.29	0/6382	0.54	0/8657
1	u	0.29	0/6360	0.55	0/8624
1	v	0.29	0/6489	0.54	0/8802
1	w	0.29	0/6353	0.54	0/8615
1	x	0.29	0/6382	0.55	0/8657
1	y	0.29	0/6489	0.54	0/8802

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	z	0.29	0/6382	0.54	0/8657
All	All	0.29	0/499915	0.55	0/678041

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	0	6253	0	6316	107	0
1	1	6379	0	6449	104	0
1	2	6247	0	6309	111	0
1	3	6275	0	6339	122	0
1	4	6379	0	6449	95	0
1	5	6275	0	6339	111	0
1	6	6253	0	6316	106	0
1	7	6379	0	6449	99	0
1	8	6247	0	6309	110	0
1	9	6275	0	6339	121	0
1	A	6247	0	6309	108	0
1	AA	6379	0	6449	100	0
1	AB	6275	0	6339	111	0
1	AC	6253	0	6316	106	0
1	AD	6379	0	6449	102	0
1	AE	6247	0	6309	108	0
1	AF	6275	0	6339	119	0
1	AG	6379	0	6449	102	0
1	AH	6275	0	6339	111	0
1	AI	6253	0	6316	107	0
1	AJ	6379	0	6449	104	0
1	AK	6247	0	6309	112	0
1	AL	6275	0	6339	121	0
1	AM	6379	0	6449	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AN	6275	0	6339	113	0
1	AO	6253	0	6316	110	0
1	AP	6379	0	6449	101	0
1	B	6275	0	6339	118	0
1	C	6379	0	6449	92	0
1	D	6275	0	6339	114	0
1	E	6253	0	6316	105	0
1	F	6379	0	6449	97	0
1	G	6247	0	6309	104	0
1	H	6275	0	6339	116	0
1	I	6379	0	6449	96	0
1	J	6275	0	6339	114	0
1	K	6253	0	6316	105	0
1	L	6379	0	6449	100	0
1	M	6247	0	6309	107	0
1	N	6275	0	6339	121	0
1	O	6379	0	6449	95	0
1	P	6275	0	6339	113	0
1	Q	6253	0	6316	108	0
1	R	6379	0	6449	98	0
1	S	6247	0	6309	105	0
1	T	6275	0	6339	121	0
1	U	6379	0	6449	99	0
1	V	6275	0	6339	114	0
1	W	6253	0	6316	102	0
1	X	6379	0	6449	105	0
1	Y	6247	0	6309	109	0
1	Z	6275	0	6339	120	0
1	a	6379	0	6449	96	0
1	b	6275	0	6339	111	0
1	c	6253	0	6316	104	0
1	d	6379	0	6449	96	0
1	e	6247	0	6309	108	0
1	f	6275	0	6339	120	0
1	g	6379	0	6449	98	0
1	h	6275	0	6339	113	0
1	i	6253	0	6316	104	0
1	j	6379	0	6449	102	0
1	k	6247	0	6309	106	0
1	l	6275	0	6339	122	0
1	m	6379	0	6449	97	0
1	n	6275	0	6339	110	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	o	6253	0	6316	105	0
1	p	6379	0	6449	98	0
1	q	6247	0	6309	108	0
1	r	6275	0	6339	120	0
1	s	6379	0	6449	102	0
1	t	6275	0	6339	112	0
1	u	6253	0	6316	106	0
1	v	6379	0	6449	103	0
1	w	6247	0	6309	108	0
1	x	6275	0	6339	123	0
1	y	6379	0	6449	97	0
1	z	6275	0	6339	111	0
All	All	491504	0	496613	7201	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 7.

The worst 5 of 7201 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:B:129:PHE:CE2	1:B:156:GLU:HB2	1.85	1.12
1:H:129:PHE:CE2	1:H:156:GLU:HB2	1.84	1.12
1:N:129:PHE:CE2	1:N:156:GLU:HB2	1.84	1.12
1:T:129:PHE:CE2	1:T:156:GLU:HB2	1.85	1.12
1:Z:129:PHE:CE2	1:Z:156:GLU:HB2	1.84	1.12

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	0	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	1	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	2	785/890 (88%)	751 (96%)	34 (4%)	0	100	100
1	3	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	4	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	5	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	6	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	7	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	8	785/890 (88%)	749 (95%)	36 (5%)	0	100	100
1	9	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	A	785/890 (88%)	752 (96%)	33 (4%)	0	100	100
1	AA	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	AB	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	AC	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	AD	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	AE	785/890 (88%)	752 (96%)	33 (4%)	0	100	100
1	AF	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	AG	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	AH	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	AI	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	AJ	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	AK	785/890 (88%)	750 (96%)	35 (4%)	0	100	100
1	AL	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	AM	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	AN	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	AO	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	AP	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	B	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	C	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	D	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	E	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	F	804/890 (90%)	773 (96%)	31 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	785/890 (88%)	752 (96%)	33 (4%)	0	100	100
1	H	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	I	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	J	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	K	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	L	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	M	785/890 (88%)	751 (96%)	34 (4%)	0	100	100
1	N	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	O	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	P	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	Q	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	R	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	S	785/890 (88%)	750 (96%)	35 (4%)	0	100	100
1	T	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	U	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	V	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	W	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	X	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	Y	785/890 (88%)	751 (96%)	34 (4%)	0	100	100
1	Z	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	a	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	b	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	c	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	d	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	e	785/890 (88%)	752 (96%)	33 (4%)	0	100	100
1	f	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	g	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	h	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	i	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	j	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	k	785/890 (88%)	751 (96%)	34 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	l	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	m	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	n	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	o	785/890 (88%)	756 (96%)	29 (4%)	0	100	100
1	p	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	q	785/890 (88%)	752 (96%)	33 (4%)	0	100	100
1	r	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	s	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	t	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
1	u	785/890 (88%)	757 (96%)	28 (4%)	0	100	100
1	v	804/890 (90%)	773 (96%)	31 (4%)	0	100	100
1	w	785/890 (88%)	751 (96%)	34 (4%)	0	100	100
1	x	790/890 (89%)	753 (95%)	37 (5%)	0	100	100
1	y	804/890 (90%)	771 (96%)	33 (4%)	0	100	100
1	z	790/890 (89%)	750 (95%)	40 (5%)	0	100	100
All	All	61854/69420 (89%)	59210 (96%)	2644 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	0	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	1	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	2	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	3	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	4	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	5	680/748 (91%)	632 (93%)	48 (7%)	13	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	6	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	7	691/748 (92%)	634 (92%)	57 (8%)	10	18
1	8	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	9	680/748 (91%)	632 (93%)	48 (7%)	13	23
1	A	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	AA	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	AB	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	AC	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	AD	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	AE	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	AF	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	AG	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	AH	680/748 (91%)	632 (93%)	48 (7%)	13	23
1	AI	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	AJ	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	AK	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	AL	680/748 (91%)	630 (93%)	50 (7%)	13	22
1	AM	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	AN	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	AO	674/748 (90%)	620 (92%)	54 (8%)	11	19
1	AP	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	B	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	C	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	D	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	E	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	F	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	G	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	H	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	I	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	J	680/748 (91%)	632 (93%)	48 (7%)	13	23
1	K	674/748 (90%)	621 (92%)	53 (8%)	11	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	M	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	N	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	O	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	P	680/748 (91%)	633 (93%)	47 (7%)	14	24
1	Q	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	R	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	S	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	T	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	U	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	V	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	W	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	X	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	Y	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	Z	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	a	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	b	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	c	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	d	691/748 (92%)	634 (92%)	57 (8%)	10	18
1	e	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	f	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	g	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	h	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	i	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	j	691/748 (92%)	632 (92%)	59 (8%)	10	16
1	k	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	l	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	m	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	n	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	o	674/748 (90%)	621 (92%)	53 (8%)	11	19
1	p	691/748 (92%)	634 (92%)	57 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	q	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	r	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	s	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	t	680/748 (91%)	632 (93%)	48 (7%)	13	23
1	u	674/748 (90%)	620 (92%)	54 (8%)	11	19
1	v	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	w	673/748 (90%)	626 (93%)	47 (7%)	14	24
1	x	680/748 (91%)	631 (93%)	49 (7%)	13	23
1	y	691/748 (92%)	633 (92%)	58 (8%)	10	17
1	z	680/748 (91%)	631 (93%)	49 (7%)	13	23
All	All	53157/58344 (91%)	49076 (92%)	4081 (8%)	14	20

5 of 4081 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	j	286	ASP
1	AF	837	THR
1	s	6	SER
1	AF	154	GLN
1	AK	238	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1038 such sidechains are listed below:

Mol	Chain	Res	Type
1	AH	669	GLN
1	AJ	675	HIS
1	AH	378	GLN
1	d	594	ASN
1	c	749	GLN

5.3.3 RNA ⓘ

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.

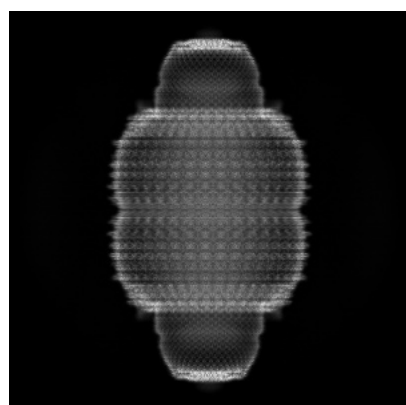
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73814. These allow visual inspection of the internal detail of the map and identification of artifacts.

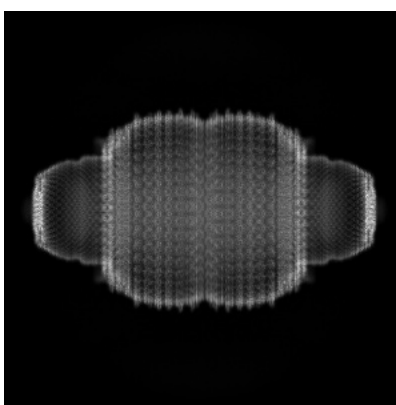
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

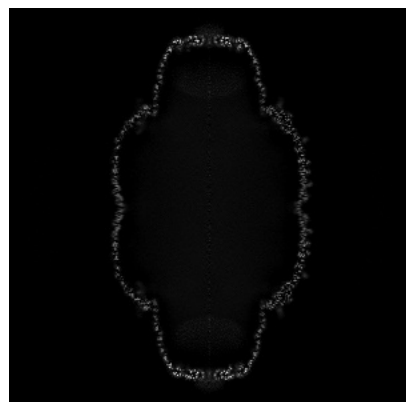


Z

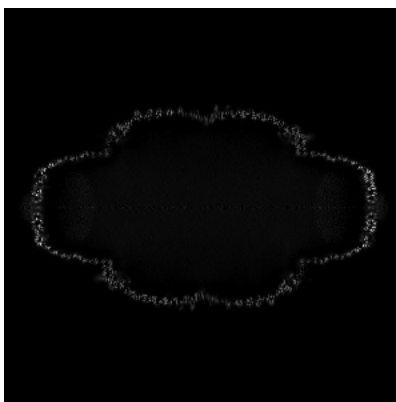
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

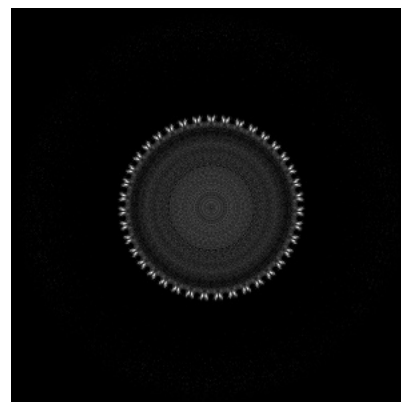
6.2.1 Primary map



X Index: 350



Y Index: 350



Z Index: 350

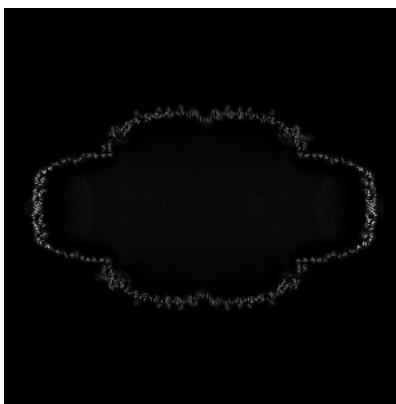
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

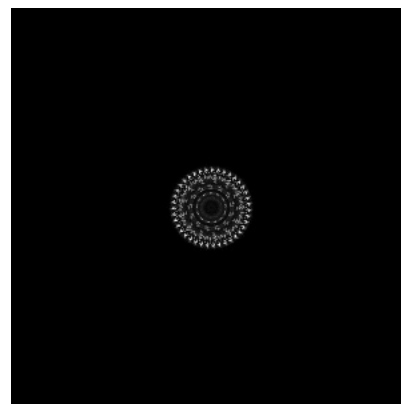
6.3.1 Primary map



X Index: 377



Y Index: 371

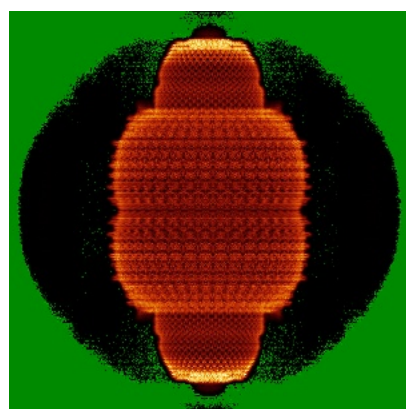


Z Index: 633

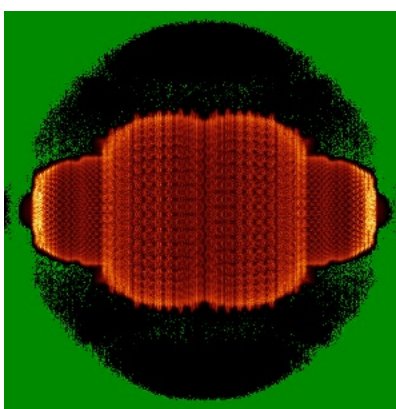
The images above show the largest variance slices of the map in three orthogonal directions.

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

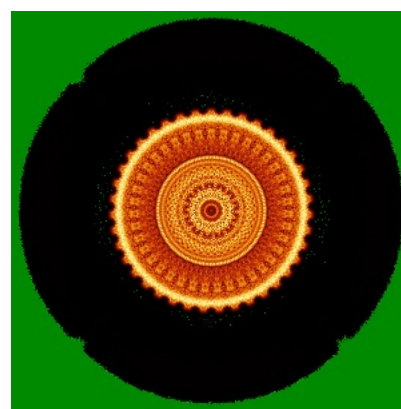
6.4.1 Primary map



X



Y



Z

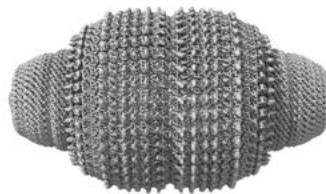
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

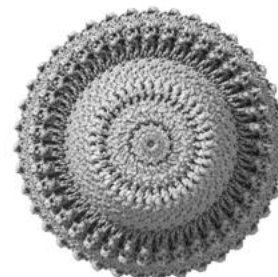
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0753. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

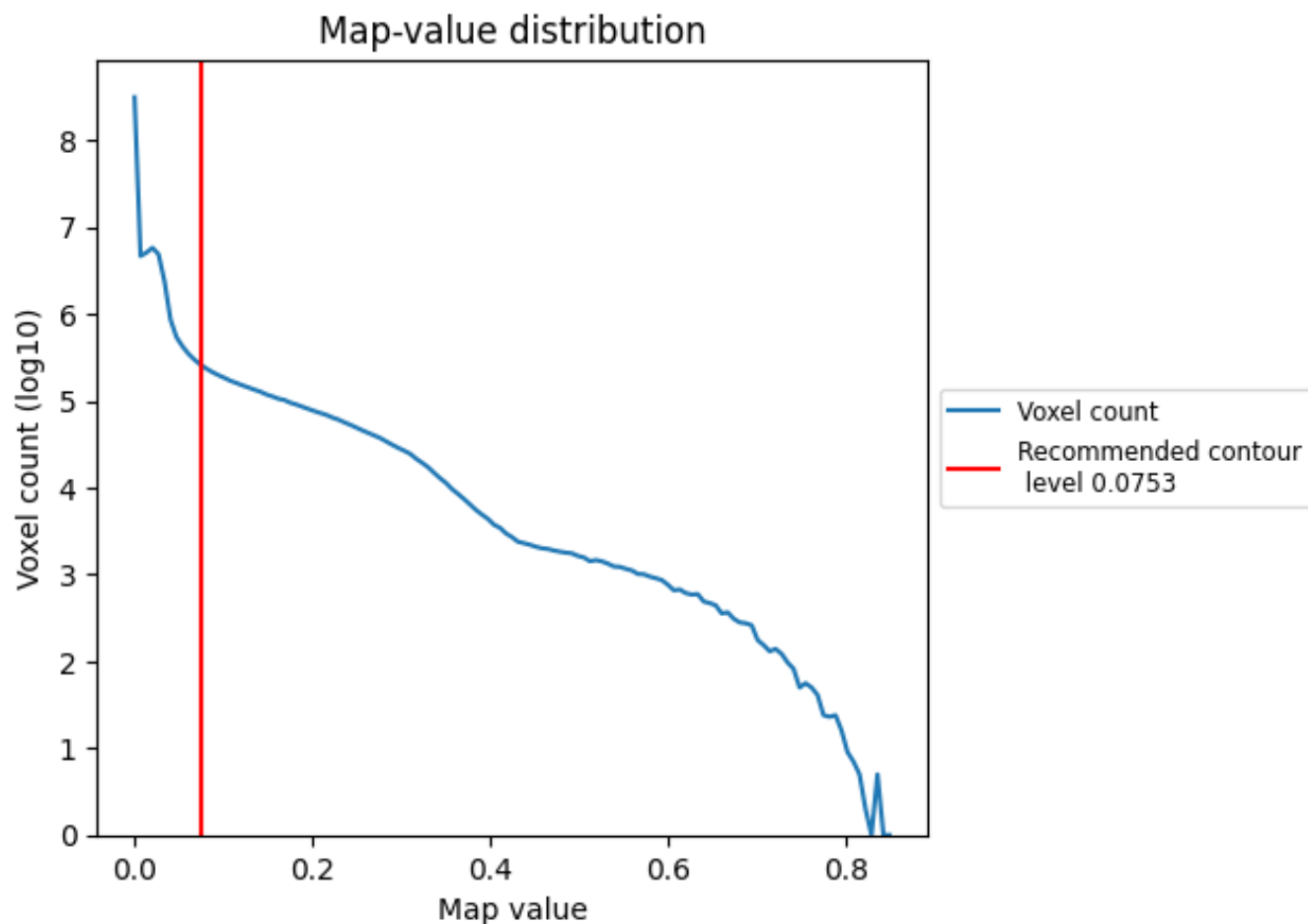
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

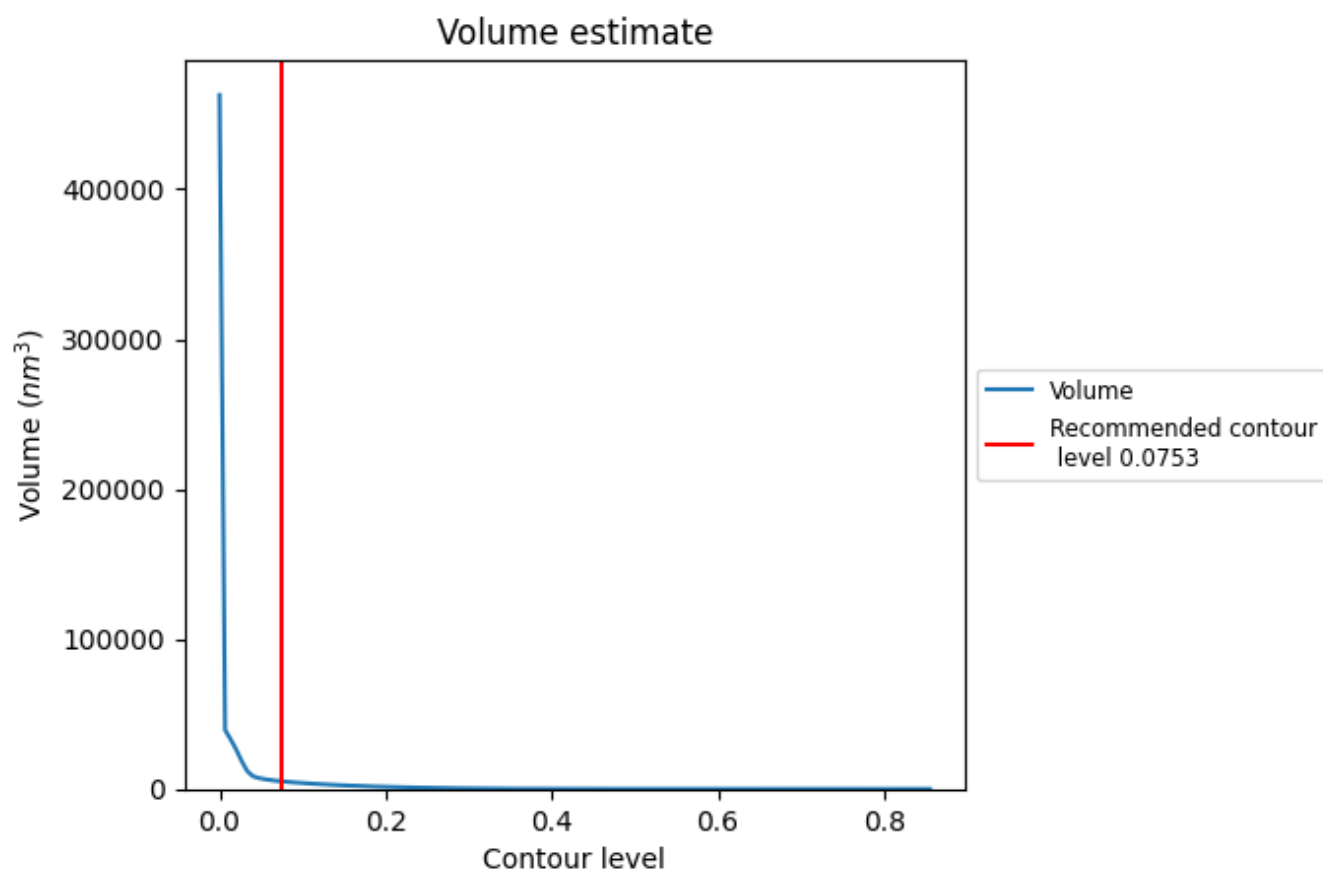
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

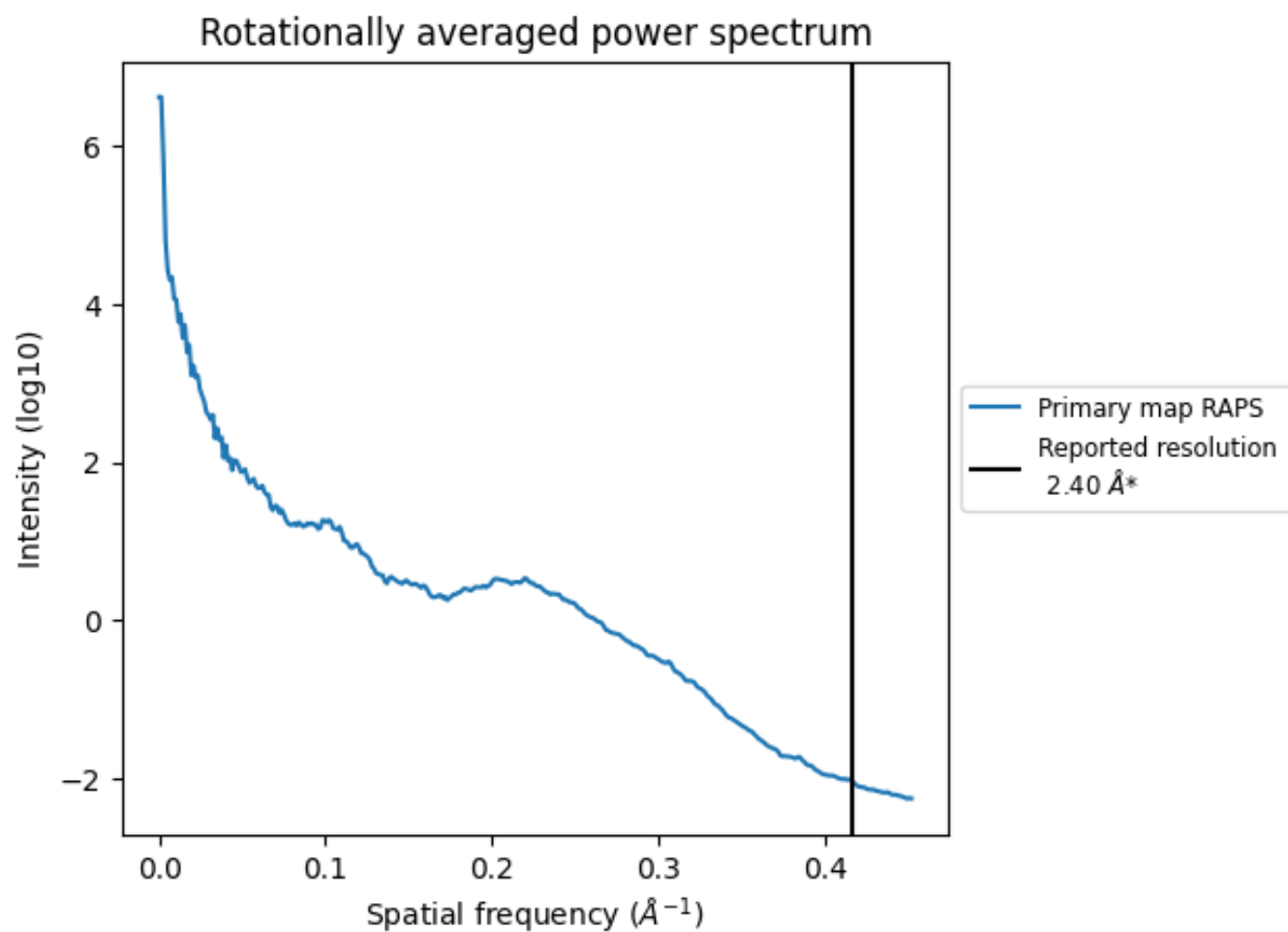
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5051 nm^3 ; this corresponds to an approximate mass of 4562 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 0.417 Å⁻¹

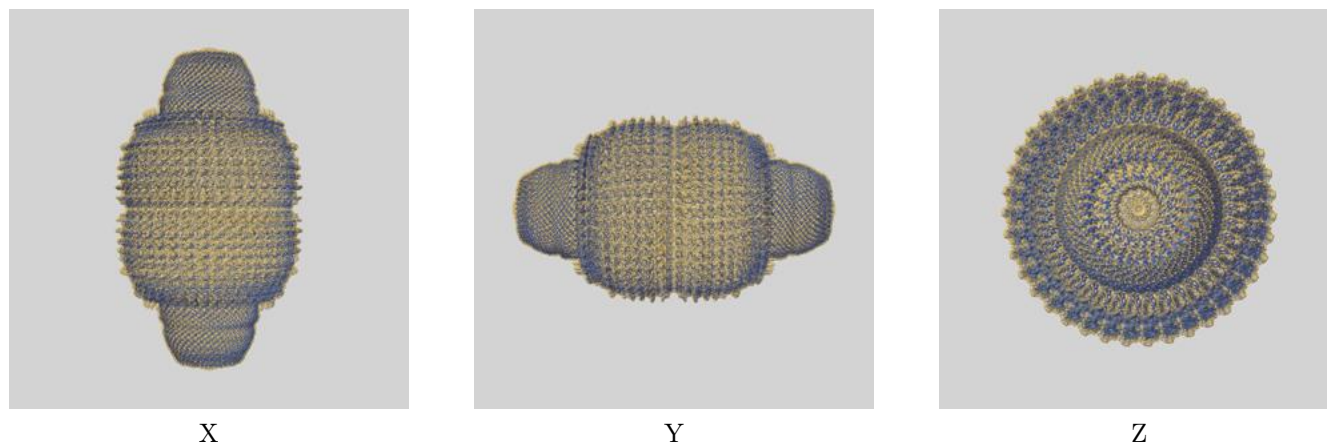
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73814 and PDB model 9Z4W. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



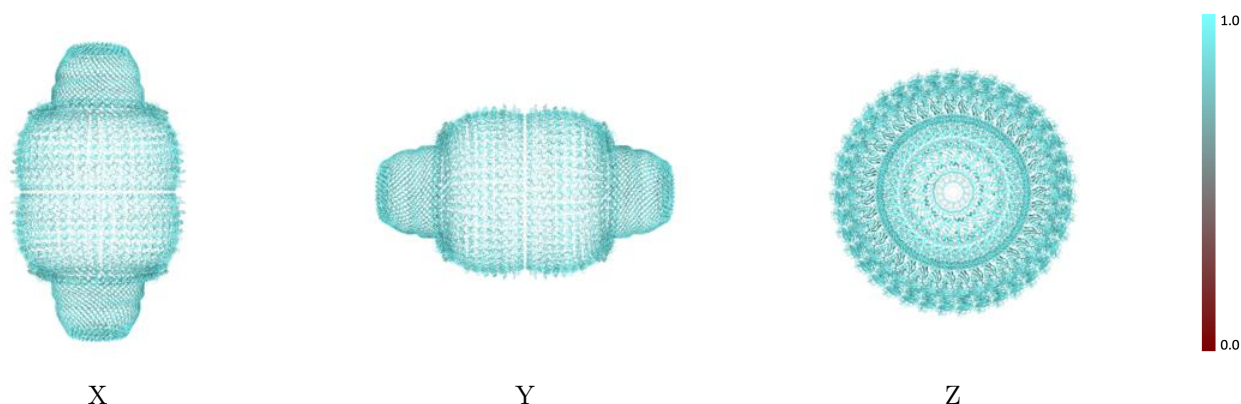
The images above show the 3D surface view of the map at the recommended contour level 0.0753 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



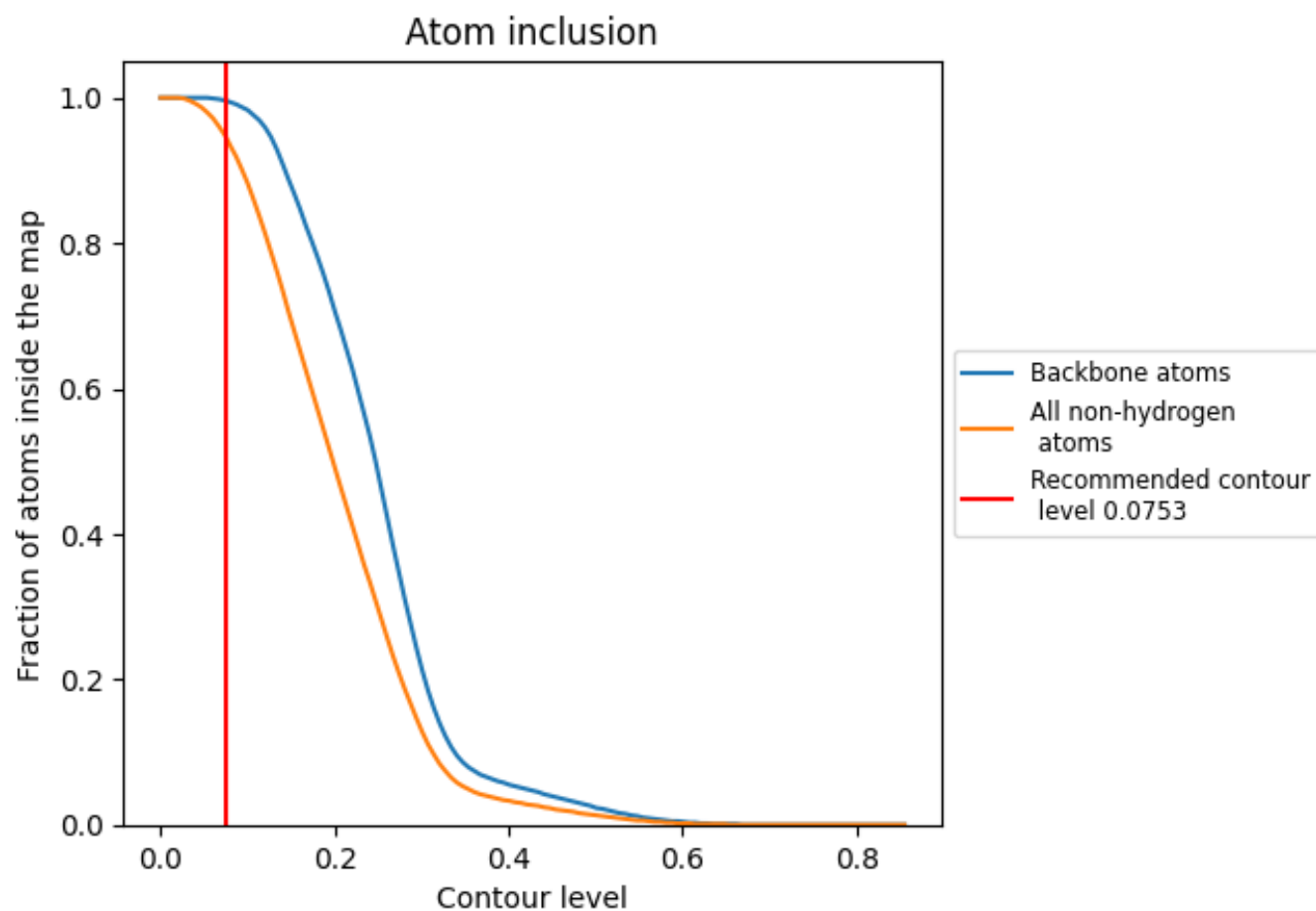
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0753).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 95% 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 (0.0753) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.5220
0	 0.9460	 0.5230
1	 0.9470	 0.5220
2	 0.9460	 0.5240
3	 0.9450	 0.5240
4	 0.9460	 0.5240
5	 0.9440	 0.5210
6	 0.9470	 0.5240
7	 0.9470	 0.5220
8	 0.9450	 0.5240
9	 0.9440	 0.5230
A	 0.9460	 0.5210
AA	 0.9470	 0.5240
AB	 0.9430	 0.5200
AC	 0.9460	 0.5240
AD	 0.9480	 0.5220
AE	 0.9450	 0.5230
AF	 0.9450	 0.5240
AG	 0.9470	 0.5240
AH	 0.9450	 0.5210
AI	 0.9470	 0.5230
AJ	 0.9470	 0.5220
AK	 0.9450	 0.5230
AL	 0.9450	 0.5230
AM	 0.9480	 0.5230
AN	 0.9450	 0.5200
AO	 0.9470	 0.5240
AP	 0.9460	 0.5220
B	 0.9440	 0.5220
C	 0.9480	 0.5230
D	 0.9440	 0.5210
E	 0.9460	 0.5230
F	 0.9460	 0.5230
G	 0.9450	 0.5210
H	 0.9440	 0.5210



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Chain	Atom inclusion	Q-score
I	 0.9480	 0.5230
J	 0.9440	 0.5200
K	 0.9460	 0.5240
L	 0.9470	 0.5230
M	 0.9450	 0.5210
N	 0.9440	 0.5210
O	 0.9470	 0.5230
P	 0.9450	 0.5210
Q	 0.9470	 0.5230
R	 0.9470	 0.5230
S	 0.9460	 0.5210
T	 0.9440	 0.5220
U	 0.9480	 0.5220
V	 0.9430	 0.5210
W	 0.9450	 0.5240
X	 0.9480	 0.5230
Y	 0.9440	 0.5210
Z	 0.9440	 0.5220
a	 0.9480	 0.5230
b	 0.9430	 0.5220
c	 0.9470	 0.5230
d	 0.9470	 0.5240
e	 0.9450	 0.5210
f	 0.9450	 0.5220
g	 0.9480	 0.5240
h	 0.9430	 0.5210
i	 0.9460	 0.5240
j	 0.9460	 0.5230
k	 0.9450	 0.5230
l	 0.9440	 0.5230
m	 0.9470	 0.5240
n	 0.9450	 0.5210
o	 0.9460	 0.5230
p	 0.9470	 0.5240
q	 0.9460	 0.5230
r	 0.9440	 0.5230
s	 0.9460	 0.5250
t	 0.9430	 0.5200
u	 0.9470	 0.5230
v	 0.9460	 0.5220
w	 0.9460	 0.5240
x	 0.9460	 0.5240

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Chain	Atom inclusion	Q-score
y	 0.9490	 0.5250
z	 0.9450	 0.5200