



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:31 AM UTC

PDB ID : 7PKZ / pdb_00007pkz
EMDB ID : EMD-13483
Title : Vault structure in committed conformation
Authors : Guerra, P.; Gonzalez-Alamos, M.; Llauro, A.; Casanas, A.; Querol-Audi, J.; de Pablo, P.; Verdaguer, N.
Deposited on : 2021-08-27
Resolution : 9.80 Å(reported)
Based on initial model : 4HL8

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:

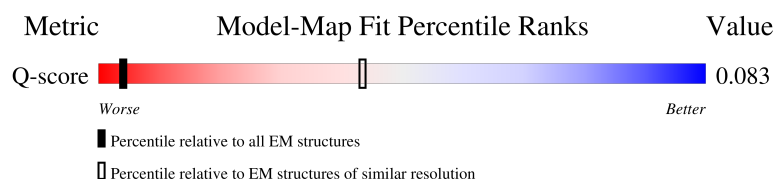
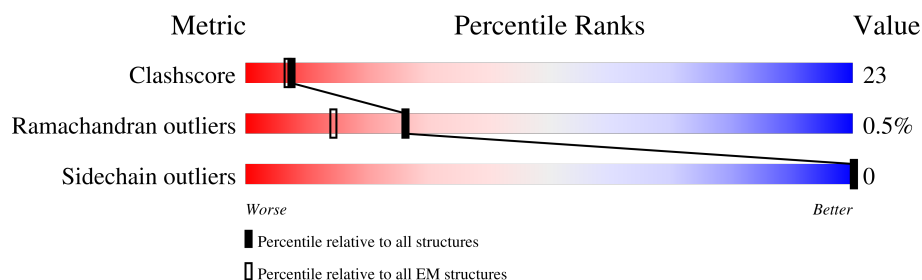
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.80 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	157 (9.30 - 10.30)

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	861	15% 50% 40% 9%
1	AA	861	6% 55% 35% 9%
1	AB	861	12% 55% 35% 9%
1	AC	861	34% 52% 38% 9%

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Mol	Chain	Length	Quality of chain
1	B	861	
1	BA	861	
1	BB	861	
1	C	861	
1	CA	861	
1	CB	861	
1	D	861	
1	DA	861	
1	DB	861	
1	E	861	
1	EA	861	
1	EB	861	
1	F	861	
1	FA	861	
1	FB	861	
1	G	861	
1	GA	861	
1	GB	861	
1	H	861	
1	HA	861	
1	HB	861	
1	I	861	
1	IA	861	
1	IB	861	
1	J	861	

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Mol	Chain	Length	Quality of chain
1	JA	861	
1	JB	861	
1	K	861	
1	KA	861	
1	KB	861	
1	L	861	
1	LA	861	
1	LB	861	
1	M	861	
1	MA	861	
1	MB	861	
1	N	861	
1	NA	861	
1	NB	861	
1	O	861	
1	OA	861	
1	OB	861	
1	P	861	
1	PA	861	
1	PB	861	
1	Q	861	
1	QA	861	
1	QB	861	
1	R	861	
1	RA	861	

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Mol	Chain	Length	Quality of chain
1	RB	861	
1	S	861	
1	SA	861	
1	SB	861	
1	T	861	
1	TA	861	
1	TB	861	
1	UA	861	
1	UB	861	
1	V	861	
1	VA	861	
1	VB	861	
1	W	861	
1	WA	861	
1	WB	861	
1	X	861	
1	XA	861	
1	XB	861	
1	Y	861	
1	YA	861	
1	YB	861	
1	Z	861	
1	ZA	861	
1	ZB	861	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 479700 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	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	B	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	C	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	D	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	E	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	F	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	G	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	H	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	I	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	J	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	K	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	L	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	M	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	N	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	O	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	P	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	Q	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	S	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	T	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	V	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	W	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	X	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	Y	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	Z	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	AA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	BA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	CA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	DA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	EA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	FA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	GA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	HA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	IA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	JA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	KA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	LA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	MA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	OA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	PA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	QA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	RA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	SA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	TA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	UA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	VA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	WA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	XA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	YA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	ZA	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	AB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	BB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	CB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	DB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	EB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	FB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	GB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0
1	HB	782	Total 6150	C 3869	N 1101	O 1165	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	JB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	KB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	LB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	MB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	NB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	OB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	PB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	QB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	RB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	SB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	TB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	UB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	VB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	WB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	XB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	YB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	ZB	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		
1	AC	782	Total	C	N	O	S	0	0
			6150	3869	1101	1165	15		

There are 624 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	ALA	THR	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
A	77	VAL	ILE	conflict	UNP Q62667
A	104	LEU	VAL	conflict	UNP Q62667
A	186	ASP	GLU	conflict	UNP Q62667
A	189	GLU	GLY	conflict	UNP Q62667
A	232	ARG	LEU	conflict	UNP Q62667
A	236	LYS	ARG	conflict	UNP Q62667
A	242	ALA	LEU	conflict	UNP Q62667
B	69	ALA	THR	conflict	UNP Q62667
B	77	VAL	ILE	conflict	UNP Q62667
B	104	LEU	VAL	conflict	UNP Q62667
B	186	ASP	GLU	conflict	UNP Q62667
B	189	GLU	GLY	conflict	UNP Q62667
B	232	ARG	LEU	conflict	UNP Q62667
B	236	LYS	ARG	conflict	UNP Q62667
B	242	ALA	LEU	conflict	UNP Q62667
C	69	ALA	THR	conflict	UNP Q62667
C	77	VAL	ILE	conflict	UNP Q62667
C	104	LEU	VAL	conflict	UNP Q62667
C	186	ASP	GLU	conflict	UNP Q62667
C	189	GLU	GLY	conflict	UNP Q62667
C	232	ARG	LEU	conflict	UNP Q62667
C	236	LYS	ARG	conflict	UNP Q62667
C	242	ALA	LEU	conflict	UNP Q62667
D	69	ALA	THR	conflict	UNP Q62667
D	77	VAL	ILE	conflict	UNP Q62667
D	104	LEU	VAL	conflict	UNP Q62667
D	186	ASP	GLU	conflict	UNP Q62667
D	189	GLU	GLY	conflict	UNP Q62667
D	232	ARG	LEU	conflict	UNP Q62667
D	236	LYS	ARG	conflict	UNP Q62667
D	242	ALA	LEU	conflict	UNP Q62667
E	69	ALA	THR	conflict	UNP Q62667
E	77	VAL	ILE	conflict	UNP Q62667
E	104	LEU	VAL	conflict	UNP Q62667
E	186	ASP	GLU	conflict	UNP Q62667
E	189	GLU	GLY	conflict	UNP Q62667
E	232	ARG	LEU	conflict	UNP Q62667
E	236	LYS	ARG	conflict	UNP Q62667
E	242	ALA	LEU	conflict	UNP Q62667
F	69	ALA	THR	conflict	UNP Q62667
F	77	VAL	ILE	conflict	UNP Q62667
F	104	LEU	VAL	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
F	186	ASP	GLU	conflict	UNP Q62667
F	189	GLU	GLY	conflict	UNP Q62667
F	232	ARG	LEU	conflict	UNP Q62667
F	236	LYS	ARG	conflict	UNP Q62667
F	242	ALA	LEU	conflict	UNP Q62667
G	69	ALA	THR	conflict	UNP Q62667
G	77	VAL	ILE	conflict	UNP Q62667
G	104	LEU	VAL	conflict	UNP Q62667
G	186	ASP	GLU	conflict	UNP Q62667
G	189	GLU	GLY	conflict	UNP Q62667
G	232	ARG	LEU	conflict	UNP Q62667
G	236	LYS	ARG	conflict	UNP Q62667
G	242	ALA	LEU	conflict	UNP Q62667
H	69	ALA	THR	conflict	UNP Q62667
H	77	VAL	ILE	conflict	UNP Q62667
H	104	LEU	VAL	conflict	UNP Q62667
H	186	ASP	GLU	conflict	UNP Q62667
H	189	GLU	GLY	conflict	UNP Q62667
H	232	ARG	LEU	conflict	UNP Q62667
H	236	LYS	ARG	conflict	UNP Q62667
H	242	ALA	LEU	conflict	UNP Q62667
I	69	ALA	THR	conflict	UNP Q62667
I	77	VAL	ILE	conflict	UNP Q62667
I	104	LEU	VAL	conflict	UNP Q62667
I	186	ASP	GLU	conflict	UNP Q62667
I	189	GLU	GLY	conflict	UNP Q62667
I	232	ARG	LEU	conflict	UNP Q62667
I	236	LYS	ARG	conflict	UNP Q62667
I	242	ALA	LEU	conflict	UNP Q62667
J	69	ALA	THR	conflict	UNP Q62667
J	77	VAL	ILE	conflict	UNP Q62667
J	104	LEU	VAL	conflict	UNP Q62667
J	186	ASP	GLU	conflict	UNP Q62667
J	189	GLU	GLY	conflict	UNP Q62667
J	232	ARG	LEU	conflict	UNP Q62667
J	236	LYS	ARG	conflict	UNP Q62667
J	242	ALA	LEU	conflict	UNP Q62667
K	69	ALA	THR	conflict	UNP Q62667
K	77	VAL	ILE	conflict	UNP Q62667
K	104	LEU	VAL	conflict	UNP Q62667
K	186	ASP	GLU	conflict	UNP Q62667
K	189	GLU	GLY	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
K	232	ARG	LEU	conflict	UNP Q62667
K	236	LYS	ARG	conflict	UNP Q62667
K	242	ALA	LEU	conflict	UNP Q62667
L	69	ALA	THR	conflict	UNP Q62667
L	77	VAL	ILE	conflict	UNP Q62667
L	104	LEU	VAL	conflict	UNP Q62667
L	186	ASP	GLU	conflict	UNP Q62667
L	189	GLU	GLY	conflict	UNP Q62667
L	232	ARG	LEU	conflict	UNP Q62667
L	236	LYS	ARG	conflict	UNP Q62667
L	242	ALA	LEU	conflict	UNP Q62667
M	69	ALA	THR	conflict	UNP Q62667
M	77	VAL	ILE	conflict	UNP Q62667
M	104	LEU	VAL	conflict	UNP Q62667
M	186	ASP	GLU	conflict	UNP Q62667
M	189	GLU	GLY	conflict	UNP Q62667
M	232	ARG	LEU	conflict	UNP Q62667
M	236	LYS	ARG	conflict	UNP Q62667
M	242	ALA	LEU	conflict	UNP Q62667
N	69	ALA	THR	conflict	UNP Q62667
N	77	VAL	ILE	conflict	UNP Q62667
N	104	LEU	VAL	conflict	UNP Q62667
N	186	ASP	GLU	conflict	UNP Q62667
N	189	GLU	GLY	conflict	UNP Q62667
N	232	ARG	LEU	conflict	UNP Q62667
N	236	LYS	ARG	conflict	UNP Q62667
N	242	ALA	LEU	conflict	UNP Q62667
O	69	ALA	THR	conflict	UNP Q62667
O	77	VAL	ILE	conflict	UNP Q62667
O	104	LEU	VAL	conflict	UNP Q62667
O	186	ASP	GLU	conflict	UNP Q62667
O	189	GLU	GLY	conflict	UNP Q62667
O	232	ARG	LEU	conflict	UNP Q62667
O	236	LYS	ARG	conflict	UNP Q62667
O	242	ALA	LEU	conflict	UNP Q62667
P	69	ALA	THR	conflict	UNP Q62667
P	77	VAL	ILE	conflict	UNP Q62667
P	104	LEU	VAL	conflict	UNP Q62667
P	186	ASP	GLU	conflict	UNP Q62667
P	189	GLU	GLY	conflict	UNP Q62667
P	232	ARG	LEU	conflict	UNP Q62667
P	236	LYS	ARG	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
P	242	ALA	LEU	conflict	UNP Q62667
Q	69	ALA	THR	conflict	UNP Q62667
Q	77	VAL	ILE	conflict	UNP Q62667
Q	104	LEU	VAL	conflict	UNP Q62667
Q	186	ASP	GLU	conflict	UNP Q62667
Q	189	GLU	GLY	conflict	UNP Q62667
Q	232	ARG	LEU	conflict	UNP Q62667
Q	236	LYS	ARG	conflict	UNP Q62667
Q	242	ALA	LEU	conflict	UNP Q62667
R	69	ALA	THR	conflict	UNP Q62667
R	77	VAL	ILE	conflict	UNP Q62667
R	104	LEU	VAL	conflict	UNP Q62667
R	186	ASP	GLU	conflict	UNP Q62667
R	189	GLU	GLY	conflict	UNP Q62667
R	232	ARG	LEU	conflict	UNP Q62667
R	236	LYS	ARG	conflict	UNP Q62667
R	242	ALA	LEU	conflict	UNP Q62667
S	69	ALA	THR	conflict	UNP Q62667
S	77	VAL	ILE	conflict	UNP Q62667
S	104	LEU	VAL	conflict	UNP Q62667
S	186	ASP	GLU	conflict	UNP Q62667
S	189	GLU	GLY	conflict	UNP Q62667
S	232	ARG	LEU	conflict	UNP Q62667
S	236	LYS	ARG	conflict	UNP Q62667
S	242	ALA	LEU	conflict	UNP Q62667
T	69	ALA	THR	conflict	UNP Q62667
T	77	VAL	ILE	conflict	UNP Q62667
T	104	LEU	VAL	conflict	UNP Q62667
T	186	ASP	GLU	conflict	UNP Q62667
T	189	GLU	GLY	conflict	UNP Q62667
T	232	ARG	LEU	conflict	UNP Q62667
T	236	LYS	ARG	conflict	UNP Q62667
T	242	ALA	LEU	conflict	UNP Q62667
V	69	ALA	THR	conflict	UNP Q62667
V	77	VAL	ILE	conflict	UNP Q62667
V	104	LEU	VAL	conflict	UNP Q62667
V	186	ASP	GLU	conflict	UNP Q62667
V	189	GLU	GLY	conflict	UNP Q62667
V	232	ARG	LEU	conflict	UNP Q62667
V	236	LYS	ARG	conflict	UNP Q62667
V	242	ALA	LEU	conflict	UNP Q62667
W	69	ALA	THR	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
W	77	VAL	ILE	conflict	UNP Q62667
W	104	LEU	VAL	conflict	UNP Q62667
W	186	ASP	GLU	conflict	UNP Q62667
W	189	GLU	GLY	conflict	UNP Q62667
W	232	ARG	LEU	conflict	UNP Q62667
W	236	LYS	ARG	conflict	UNP Q62667
W	242	ALA	LEU	conflict	UNP Q62667
X	69	ALA	THR	conflict	UNP Q62667
X	77	VAL	ILE	conflict	UNP Q62667
X	104	LEU	VAL	conflict	UNP Q62667
X	186	ASP	GLU	conflict	UNP Q62667
X	189	GLU	GLY	conflict	UNP Q62667
X	232	ARG	LEU	conflict	UNP Q62667
X	236	LYS	ARG	conflict	UNP Q62667
X	242	ALA	LEU	conflict	UNP Q62667
Y	69	ALA	THR	conflict	UNP Q62667
Y	77	VAL	ILE	conflict	UNP Q62667
Y	104	LEU	VAL	conflict	UNP Q62667
Y	186	ASP	GLU	conflict	UNP Q62667
Y	189	GLU	GLY	conflict	UNP Q62667
Y	232	ARG	LEU	conflict	UNP Q62667
Y	236	LYS	ARG	conflict	UNP Q62667
Y	242	ALA	LEU	conflict	UNP Q62667
Z	69	ALA	THR	conflict	UNP Q62667
Z	77	VAL	ILE	conflict	UNP Q62667
Z	104	LEU	VAL	conflict	UNP Q62667
Z	186	ASP	GLU	conflict	UNP Q62667
Z	189	GLU	GLY	conflict	UNP Q62667
Z	232	ARG	LEU	conflict	UNP Q62667
Z	236	LYS	ARG	conflict	UNP Q62667
Z	242	ALA	LEU	conflict	UNP Q62667
AA	69	ALA	THR	conflict	UNP Q62667
AA	77	VAL	ILE	conflict	UNP Q62667
AA	104	LEU	VAL	conflict	UNP Q62667
AA	186	ASP	GLU	conflict	UNP Q62667
AA	189	GLU	GLY	conflict	UNP Q62667
AA	232	ARG	LEU	conflict	UNP Q62667
AA	236	LYS	ARG	conflict	UNP Q62667
AA	242	ALA	LEU	conflict	UNP Q62667
BA	69	ALA	THR	conflict	UNP Q62667
BA	77	VAL	ILE	conflict	UNP Q62667
BA	104	LEU	VAL	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
BA	186	ASP	GLU	conflict	UNP Q62667
BA	189	GLU	GLY	conflict	UNP Q62667
BA	232	ARG	LEU	conflict	UNP Q62667
BA	236	LYS	ARG	conflict	UNP Q62667
BA	242	ALA	LEU	conflict	UNP Q62667
CA	69	ALA	THR	conflict	UNP Q62667
CA	77	VAL	ILE	conflict	UNP Q62667
CA	104	LEU	VAL	conflict	UNP Q62667
CA	186	ASP	GLU	conflict	UNP Q62667
CA	189	GLU	GLY	conflict	UNP Q62667
CA	232	ARG	LEU	conflict	UNP Q62667
CA	236	LYS	ARG	conflict	UNP Q62667
CA	242	ALA	LEU	conflict	UNP Q62667
DA	69	ALA	THR	conflict	UNP Q62667
DA	77	VAL	ILE	conflict	UNP Q62667
DA	104	LEU	VAL	conflict	UNP Q62667
DA	186	ASP	GLU	conflict	UNP Q62667
DA	189	GLU	GLY	conflict	UNP Q62667
DA	232	ARG	LEU	conflict	UNP Q62667
DA	236	LYS	ARG	conflict	UNP Q62667
DA	242	ALA	LEU	conflict	UNP Q62667
EA	69	ALA	THR	conflict	UNP Q62667
EA	77	VAL	ILE	conflict	UNP Q62667
EA	104	LEU	VAL	conflict	UNP Q62667
EA	186	ASP	GLU	conflict	UNP Q62667
EA	189	GLU	GLY	conflict	UNP Q62667
EA	232	ARG	LEU	conflict	UNP Q62667
EA	236	LYS	ARG	conflict	UNP Q62667
EA	242	ALA	LEU	conflict	UNP Q62667
FA	69	ALA	THR	conflict	UNP Q62667
FA	77	VAL	ILE	conflict	UNP Q62667
FA	104	LEU	VAL	conflict	UNP Q62667
FA	186	ASP	GLU	conflict	UNP Q62667
FA	189	GLU	GLY	conflict	UNP Q62667
FA	232	ARG	LEU	conflict	UNP Q62667
FA	236	LYS	ARG	conflict	UNP Q62667
FA	242	ALA	LEU	conflict	UNP Q62667
GA	69	ALA	THR	conflict	UNP Q62667
GA	77	VAL	ILE	conflict	UNP Q62667
GA	104	LEU	VAL	conflict	UNP Q62667
GA	186	ASP	GLU	conflict	UNP Q62667
GA	189	GLU	GLY	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
GA	232	ARG	LEU	conflict	UNP Q62667
GA	236	LYS	ARG	conflict	UNP Q62667
GA	242	ALA	LEU	conflict	UNP Q62667
HA	69	ALA	THR	conflict	UNP Q62667
HA	77	VAL	ILE	conflict	UNP Q62667
HA	104	LEU	VAL	conflict	UNP Q62667
HA	186	ASP	GLU	conflict	UNP Q62667
HA	189	GLU	GLY	conflict	UNP Q62667
HA	232	ARG	LEU	conflict	UNP Q62667
HA	236	LYS	ARG	conflict	UNP Q62667
HA	242	ALA	LEU	conflict	UNP Q62667
IA	69	ALA	THR	conflict	UNP Q62667
IA	77	VAL	ILE	conflict	UNP Q62667
IA	104	LEU	VAL	conflict	UNP Q62667
IA	186	ASP	GLU	conflict	UNP Q62667
IA	189	GLU	GLY	conflict	UNP Q62667
IA	232	ARG	LEU	conflict	UNP Q62667
IA	236	LYS	ARG	conflict	UNP Q62667
IA	242	ALA	LEU	conflict	UNP Q62667
JA	69	ALA	THR	conflict	UNP Q62667
JA	77	VAL	ILE	conflict	UNP Q62667
JA	104	LEU	VAL	conflict	UNP Q62667
JA	186	ASP	GLU	conflict	UNP Q62667
JA	189	GLU	GLY	conflict	UNP Q62667
JA	232	ARG	LEU	conflict	UNP Q62667
JA	236	LYS	ARG	conflict	UNP Q62667
JA	242	ALA	LEU	conflict	UNP Q62667
KA	69	ALA	THR	conflict	UNP Q62667
KA	77	VAL	ILE	conflict	UNP Q62667
KA	104	LEU	VAL	conflict	UNP Q62667
KA	186	ASP	GLU	conflict	UNP Q62667
KA	189	GLU	GLY	conflict	UNP Q62667
KA	232	ARG	LEU	conflict	UNP Q62667
KA	236	LYS	ARG	conflict	UNP Q62667
KA	242	ALA	LEU	conflict	UNP Q62667
LA	69	ALA	THR	conflict	UNP Q62667
LA	77	VAL	ILE	conflict	UNP Q62667
LA	104	LEU	VAL	conflict	UNP Q62667
LA	186	ASP	GLU	conflict	UNP Q62667
LA	189	GLU	GLY	conflict	UNP Q62667
LA	232	ARG	LEU	conflict	UNP Q62667
LA	236	LYS	ARG	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
LA	242	ALA	LEU	conflict	UNP Q62667
MA	69	ALA	THR	conflict	UNP Q62667
MA	77	VAL	ILE	conflict	UNP Q62667
MA	104	LEU	VAL	conflict	UNP Q62667
MA	186	ASP	GLU	conflict	UNP Q62667
MA	189	GLU	GLY	conflict	UNP Q62667
MA	232	ARG	LEU	conflict	UNP Q62667
MA	236	LYS	ARG	conflict	UNP Q62667
MA	242	ALA	LEU	conflict	UNP Q62667
NA	69	ALA	THR	conflict	UNP Q62667
NA	77	VAL	ILE	conflict	UNP Q62667
NA	104	LEU	VAL	conflict	UNP Q62667
NA	186	ASP	GLU	conflict	UNP Q62667
NA	189	GLU	GLY	conflict	UNP Q62667
NA	232	ARG	LEU	conflict	UNP Q62667
NA	236	LYS	ARG	conflict	UNP Q62667
NA	242	ALA	LEU	conflict	UNP Q62667
OA	69	ALA	THR	conflict	UNP Q62667
OA	77	VAL	ILE	conflict	UNP Q62667
OA	104	LEU	VAL	conflict	UNP Q62667
OA	186	ASP	GLU	conflict	UNP Q62667
OA	189	GLU	GLY	conflict	UNP Q62667
OA	232	ARG	LEU	conflict	UNP Q62667
OA	236	LYS	ARG	conflict	UNP Q62667
OA	242	ALA	LEU	conflict	UNP Q62667
PA	69	ALA	THR	conflict	UNP Q62667
PA	77	VAL	ILE	conflict	UNP Q62667
PA	104	LEU	VAL	conflict	UNP Q62667
PA	186	ASP	GLU	conflict	UNP Q62667
PA	189	GLU	GLY	conflict	UNP Q62667
PA	232	ARG	LEU	conflict	UNP Q62667
PA	236	LYS	ARG	conflict	UNP Q62667
PA	242	ALA	LEU	conflict	UNP Q62667
QA	69	ALA	THR	conflict	UNP Q62667
QA	77	VAL	ILE	conflict	UNP Q62667
QA	104	LEU	VAL	conflict	UNP Q62667
QA	186	ASP	GLU	conflict	UNP Q62667
QA	189	GLU	GLY	conflict	UNP Q62667
QA	232	ARG	LEU	conflict	UNP Q62667
QA	236	LYS	ARG	conflict	UNP Q62667
QA	242	ALA	LEU	conflict	UNP Q62667
RA	69	ALA	THR	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
RA	77	VAL	ILE	conflict	UNP Q62667
RA	104	LEU	VAL	conflict	UNP Q62667
RA	186	ASP	GLU	conflict	UNP Q62667
RA	189	GLU	GLY	conflict	UNP Q62667
RA	232	ARG	LEU	conflict	UNP Q62667
RA	236	LYS	ARG	conflict	UNP Q62667
RA	242	ALA	LEU	conflict	UNP Q62667
SA	69	ALA	THR	conflict	UNP Q62667
SA	77	VAL	ILE	conflict	UNP Q62667
SA	104	LEU	VAL	conflict	UNP Q62667
SA	186	ASP	GLU	conflict	UNP Q62667
SA	189	GLU	GLY	conflict	UNP Q62667
SA	232	ARG	LEU	conflict	UNP Q62667
SA	236	LYS	ARG	conflict	UNP Q62667
SA	242	ALA	LEU	conflict	UNP Q62667
TA	69	ALA	THR	conflict	UNP Q62667
TA	77	VAL	ILE	conflict	UNP Q62667
TA	104	LEU	VAL	conflict	UNP Q62667
TA	186	ASP	GLU	conflict	UNP Q62667
TA	189	GLU	GLY	conflict	UNP Q62667
TA	232	ARG	LEU	conflict	UNP Q62667
TA	236	LYS	ARG	conflict	UNP Q62667
TA	242	ALA	LEU	conflict	UNP Q62667
UA	69	ALA	THR	conflict	UNP Q62667
UA	77	VAL	ILE	conflict	UNP Q62667
UA	104	LEU	VAL	conflict	UNP Q62667
UA	186	ASP	GLU	conflict	UNP Q62667
UA	189	GLU	GLY	conflict	UNP Q62667
UA	232	ARG	LEU	conflict	UNP Q62667
UA	236	LYS	ARG	conflict	UNP Q62667
UA	242	ALA	LEU	conflict	UNP Q62667
VA	69	ALA	THR	conflict	UNP Q62667
VA	77	VAL	ILE	conflict	UNP Q62667
VA	104	LEU	VAL	conflict	UNP Q62667
VA	186	ASP	GLU	conflict	UNP Q62667
VA	189	GLU	GLY	conflict	UNP Q62667
VA	232	ARG	LEU	conflict	UNP Q62667
VA	236	LYS	ARG	conflict	UNP Q62667
VA	242	ALA	LEU	conflict	UNP Q62667
WA	69	ALA	THR	conflict	UNP Q62667
WA	77	VAL	ILE	conflict	UNP Q62667
WA	104	LEU	VAL	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
WA	186	ASP	GLU	conflict	UNP Q62667
WA	189	GLU	GLY	conflict	UNP Q62667
WA	232	ARG	LEU	conflict	UNP Q62667
WA	236	LYS	ARG	conflict	UNP Q62667
WA	242	ALA	LEU	conflict	UNP Q62667
XA	69	ALA	THR	conflict	UNP Q62667
XA	77	VAL	ILE	conflict	UNP Q62667
XA	104	LEU	VAL	conflict	UNP Q62667
XA	186	ASP	GLU	conflict	UNP Q62667
XA	189	GLU	GLY	conflict	UNP Q62667
XA	232	ARG	LEU	conflict	UNP Q62667
XA	236	LYS	ARG	conflict	UNP Q62667
XA	242	ALA	LEU	conflict	UNP Q62667
YA	69	ALA	THR	conflict	UNP Q62667
YA	77	VAL	ILE	conflict	UNP Q62667
YA	104	LEU	VAL	conflict	UNP Q62667
YA	186	ASP	GLU	conflict	UNP Q62667
YA	189	GLU	GLY	conflict	UNP Q62667
YA	232	ARG	LEU	conflict	UNP Q62667
YA	236	LYS	ARG	conflict	UNP Q62667
YA	242	ALA	LEU	conflict	UNP Q62667
ZA	69	ALA	THR	conflict	UNP Q62667
ZA	77	VAL	ILE	conflict	UNP Q62667
ZA	104	LEU	VAL	conflict	UNP Q62667
ZA	186	ASP	GLU	conflict	UNP Q62667
ZA	189	GLU	GLY	conflict	UNP Q62667
ZA	232	ARG	LEU	conflict	UNP Q62667
ZA	236	LYS	ARG	conflict	UNP Q62667
ZA	242	ALA	LEU	conflict	UNP Q62667
AB	69	ALA	THR	conflict	UNP Q62667
AB	77	VAL	ILE	conflict	UNP Q62667
AB	104	LEU	VAL	conflict	UNP Q62667
AB	186	ASP	GLU	conflict	UNP Q62667
AB	189	GLU	GLY	conflict	UNP Q62667
AB	232	ARG	LEU	conflict	UNP Q62667
AB	236	LYS	ARG	conflict	UNP Q62667
AB	242	ALA	LEU	conflict	UNP Q62667
BB	69	ALA	THR	conflict	UNP Q62667
BB	77	VAL	ILE	conflict	UNP Q62667
BB	104	LEU	VAL	conflict	UNP Q62667
BB	186	ASP	GLU	conflict	UNP Q62667
BB	189	GLU	GLY	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
BB	232	ARG	LEU	conflict	UNP Q62667
BB	236	LYS	ARG	conflict	UNP Q62667
BB	242	ALA	LEU	conflict	UNP Q62667
CB	69	ALA	THR	conflict	UNP Q62667
CB	77	VAL	ILE	conflict	UNP Q62667
CB	104	LEU	VAL	conflict	UNP Q62667
CB	186	ASP	GLU	conflict	UNP Q62667
CB	189	GLU	GLY	conflict	UNP Q62667
CB	232	ARG	LEU	conflict	UNP Q62667
CB	236	LYS	ARG	conflict	UNP Q62667
CB	242	ALA	LEU	conflict	UNP Q62667
DB	69	ALA	THR	conflict	UNP Q62667
DB	77	VAL	ILE	conflict	UNP Q62667
DB	104	LEU	VAL	conflict	UNP Q62667
DB	186	ASP	GLU	conflict	UNP Q62667
DB	189	GLU	GLY	conflict	UNP Q62667
DB	232	ARG	LEU	conflict	UNP Q62667
DB	236	LYS	ARG	conflict	UNP Q62667
DB	242	ALA	LEU	conflict	UNP Q62667
EB	69	ALA	THR	conflict	UNP Q62667
EB	77	VAL	ILE	conflict	UNP Q62667
EB	104	LEU	VAL	conflict	UNP Q62667
EB	186	ASP	GLU	conflict	UNP Q62667
EB	189	GLU	GLY	conflict	UNP Q62667
EB	232	ARG	LEU	conflict	UNP Q62667
EB	236	LYS	ARG	conflict	UNP Q62667
EB	242	ALA	LEU	conflict	UNP Q62667
FB	69	ALA	THR	conflict	UNP Q62667
FB	77	VAL	ILE	conflict	UNP Q62667
FB	104	LEU	VAL	conflict	UNP Q62667
FB	186	ASP	GLU	conflict	UNP Q62667
FB	189	GLU	GLY	conflict	UNP Q62667
FB	232	ARG	LEU	conflict	UNP Q62667
FB	236	LYS	ARG	conflict	UNP Q62667
FB	242	ALA	LEU	conflict	UNP Q62667
GB	69	ALA	THR	conflict	UNP Q62667
GB	77	VAL	ILE	conflict	UNP Q62667
GB	104	LEU	VAL	conflict	UNP Q62667
GB	186	ASP	GLU	conflict	UNP Q62667
GB	189	GLU	GLY	conflict	UNP Q62667
GB	232	ARG	LEU	conflict	UNP Q62667
GB	236	LYS	ARG	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
GB	242	ALA	LEU	conflict	UNP Q62667
HB	69	ALA	THR	conflict	UNP Q62667
HB	77	VAL	ILE	conflict	UNP Q62667
HB	104	LEU	VAL	conflict	UNP Q62667
HB	186	ASP	GLU	conflict	UNP Q62667
HB	189	GLU	GLY	conflict	UNP Q62667
HB	232	ARG	LEU	conflict	UNP Q62667
HB	236	LYS	ARG	conflict	UNP Q62667
HB	242	ALA	LEU	conflict	UNP Q62667
IB	69	ALA	THR	conflict	UNP Q62667
IB	77	VAL	ILE	conflict	UNP Q62667
IB	104	LEU	VAL	conflict	UNP Q62667
IB	186	ASP	GLU	conflict	UNP Q62667
IB	189	GLU	GLY	conflict	UNP Q62667
IB	232	ARG	LEU	conflict	UNP Q62667
IB	236	LYS	ARG	conflict	UNP Q62667
IB	242	ALA	LEU	conflict	UNP Q62667
JB	69	ALA	THR	conflict	UNP Q62667
JB	77	VAL	ILE	conflict	UNP Q62667
JB	104	LEU	VAL	conflict	UNP Q62667
JB	186	ASP	GLU	conflict	UNP Q62667
JB	189	GLU	GLY	conflict	UNP Q62667
JB	232	ARG	LEU	conflict	UNP Q62667
JB	236	LYS	ARG	conflict	UNP Q62667
JB	242	ALA	LEU	conflict	UNP Q62667
KB	69	ALA	THR	conflict	UNP Q62667
KB	77	VAL	ILE	conflict	UNP Q62667
KB	104	LEU	VAL	conflict	UNP Q62667
KB	186	ASP	GLU	conflict	UNP Q62667
KB	189	GLU	GLY	conflict	UNP Q62667
KB	232	ARG	LEU	conflict	UNP Q62667
KB	236	LYS	ARG	conflict	UNP Q62667
KB	242	ALA	LEU	conflict	UNP Q62667
LB	69	ALA	THR	conflict	UNP Q62667
LB	77	VAL	ILE	conflict	UNP Q62667
LB	104	LEU	VAL	conflict	UNP Q62667
LB	186	ASP	GLU	conflict	UNP Q62667
LB	189	GLU	GLY	conflict	UNP Q62667
LB	232	ARG	LEU	conflict	UNP Q62667
LB	236	LYS	ARG	conflict	UNP Q62667
LB	242	ALA	LEU	conflict	UNP Q62667
MB	69	ALA	THR	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
MB	77	VAL	ILE	conflict	UNP Q62667
MB	104	LEU	VAL	conflict	UNP Q62667
MB	186	ASP	GLU	conflict	UNP Q62667
MB	189	GLU	GLY	conflict	UNP Q62667
MB	232	ARG	LEU	conflict	UNP Q62667
MB	236	LYS	ARG	conflict	UNP Q62667
MB	242	ALA	LEU	conflict	UNP Q62667
NB	69	ALA	THR	conflict	UNP Q62667
NB	77	VAL	ILE	conflict	UNP Q62667
NB	104	LEU	VAL	conflict	UNP Q62667
NB	186	ASP	GLU	conflict	UNP Q62667
NB	189	GLU	GLY	conflict	UNP Q62667
NB	232	ARG	LEU	conflict	UNP Q62667
NB	236	LYS	ARG	conflict	UNP Q62667
NB	242	ALA	LEU	conflict	UNP Q62667
OB	69	ALA	THR	conflict	UNP Q62667
OB	77	VAL	ILE	conflict	UNP Q62667
OB	104	LEU	VAL	conflict	UNP Q62667
OB	186	ASP	GLU	conflict	UNP Q62667
OB	189	GLU	GLY	conflict	UNP Q62667
OB	232	ARG	LEU	conflict	UNP Q62667
OB	236	LYS	ARG	conflict	UNP Q62667
OB	242	ALA	LEU	conflict	UNP Q62667
PB	69	ALA	THR	conflict	UNP Q62667
PB	77	VAL	ILE	conflict	UNP Q62667
PB	104	LEU	VAL	conflict	UNP Q62667
PB	186	ASP	GLU	conflict	UNP Q62667
PB	189	GLU	GLY	conflict	UNP Q62667
PB	232	ARG	LEU	conflict	UNP Q62667
PB	236	LYS	ARG	conflict	UNP Q62667
PB	242	ALA	LEU	conflict	UNP Q62667
QB	69	ALA	THR	conflict	UNP Q62667
QB	77	VAL	ILE	conflict	UNP Q62667
QB	104	LEU	VAL	conflict	UNP Q62667
QB	186	ASP	GLU	conflict	UNP Q62667
QB	189	GLU	GLY	conflict	UNP Q62667
QB	232	ARG	LEU	conflict	UNP Q62667
QB	236	LYS	ARG	conflict	UNP Q62667
QB	242	ALA	LEU	conflict	UNP Q62667
RB	69	ALA	THR	conflict	UNP Q62667
RB	77	VAL	ILE	conflict	UNP Q62667
RB	104	LEU	VAL	conflict	UNP Q62667

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Chain	Residue	Modelled	Actual	Comment	Reference
RB	186	ASP	GLU	conflict	UNP Q62667
RB	189	GLU	GLY	conflict	UNP Q62667
RB	232	ARG	LEU	conflict	UNP Q62667
RB	236	LYS	ARG	conflict	UNP Q62667
RB	242	ALA	LEU	conflict	UNP Q62667
SB	69	ALA	THR	conflict	UNP Q62667
SB	77	VAL	ILE	conflict	UNP Q62667
SB	104	LEU	VAL	conflict	UNP Q62667
SB	186	ASP	GLU	conflict	UNP Q62667
SB	189	GLU	GLY	conflict	UNP Q62667
SB	232	ARG	LEU	conflict	UNP Q62667
SB	236	LYS	ARG	conflict	UNP Q62667
SB	242	ALA	LEU	conflict	UNP Q62667
TB	69	ALA	THR	conflict	UNP Q62667
TB	77	VAL	ILE	conflict	UNP Q62667
TB	104	LEU	VAL	conflict	UNP Q62667
TB	186	ASP	GLU	conflict	UNP Q62667
TB	189	GLU	GLY	conflict	UNP Q62667
TB	232	ARG	LEU	conflict	UNP Q62667
TB	236	LYS	ARG	conflict	UNP Q62667
TB	242	ALA	LEU	conflict	UNP Q62667
UB	69	ALA	THR	conflict	UNP Q62667
UB	77	VAL	ILE	conflict	UNP Q62667
UB	104	LEU	VAL	conflict	UNP Q62667
UB	186	ASP	GLU	conflict	UNP Q62667
UB	189	GLU	GLY	conflict	UNP Q62667
UB	232	ARG	LEU	conflict	UNP Q62667
UB	236	LYS	ARG	conflict	UNP Q62667
UB	242	ALA	LEU	conflict	UNP Q62667
VB	69	ALA	THR	conflict	UNP Q62667
VB	77	VAL	ILE	conflict	UNP Q62667
VB	104	LEU	VAL	conflict	UNP Q62667
VB	186	ASP	GLU	conflict	UNP Q62667
VB	189	GLU	GLY	conflict	UNP Q62667
VB	232	ARG	LEU	conflict	UNP Q62667
VB	236	LYS	ARG	conflict	UNP Q62667
VB	242	ALA	LEU	conflict	UNP Q62667
WB	69	ALA	THR	conflict	UNP Q62667
WB	77	VAL	ILE	conflict	UNP Q62667
WB	104	LEU	VAL	conflict	UNP Q62667
WB	186	ASP	GLU	conflict	UNP Q62667
WB	189	GLU	GLY	conflict	UNP Q62667

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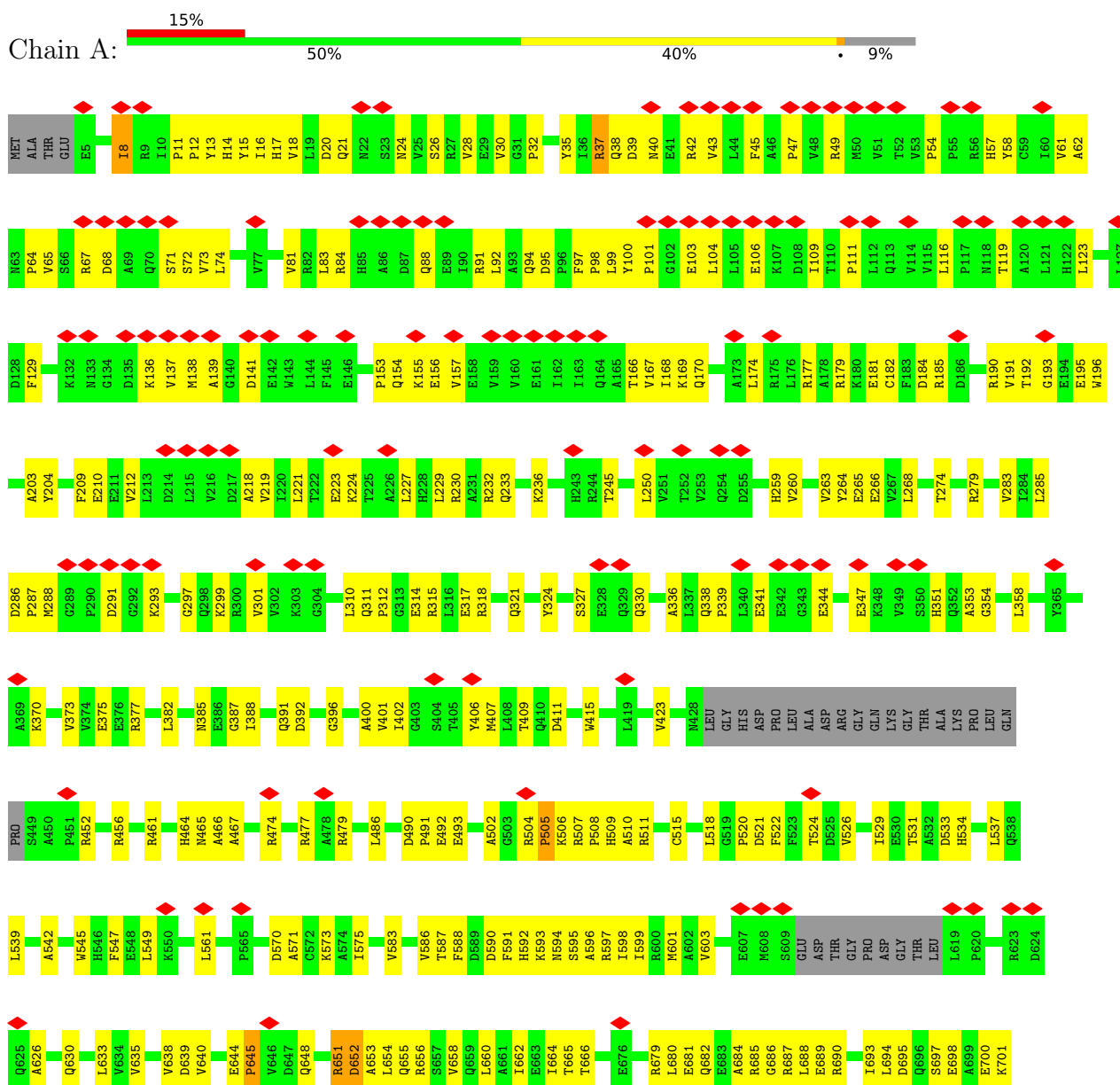
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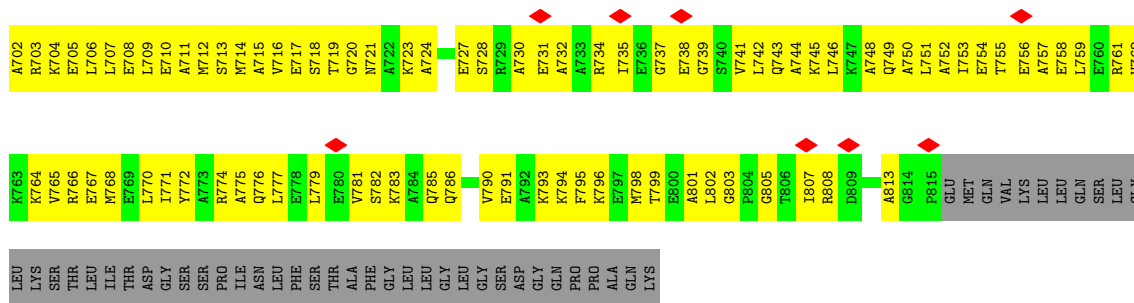
Chain	Residue	Modelled	Actual	Comment	Reference
WB	232	ARG	LEU	conflict	UNP Q62667
WB	236	LYS	ARG	conflict	UNP Q62667
WB	242	ALA	LEU	conflict	UNP Q62667
XB	69	ALA	THR	conflict	UNP Q62667
XB	77	VAL	ILE	conflict	UNP Q62667
XB	104	LEU	VAL	conflict	UNP Q62667
XB	186	ASP	GLU	conflict	UNP Q62667
XB	189	GLU	GLY	conflict	UNP Q62667
XB	232	ARG	LEU	conflict	UNP Q62667
XB	236	LYS	ARG	conflict	UNP Q62667
XB	242	ALA	LEU	conflict	UNP Q62667
YB	69	ALA	THR	conflict	UNP Q62667
YB	77	VAL	ILE	conflict	UNP Q62667
YB	104	LEU	VAL	conflict	UNP Q62667
YB	186	ASP	GLU	conflict	UNP Q62667
YB	189	GLU	GLY	conflict	UNP Q62667
YB	232	ARG	LEU	conflict	UNP Q62667
YB	236	LYS	ARG	conflict	UNP Q62667
YB	242	ALA	LEU	conflict	UNP Q62667
ZB	69	ALA	THR	conflict	UNP Q62667
ZB	77	VAL	ILE	conflict	UNP Q62667
ZB	104	LEU	VAL	conflict	UNP Q62667
ZB	186	ASP	GLU	conflict	UNP Q62667
ZB	189	GLU	GLY	conflict	UNP Q62667
ZB	232	ARG	LEU	conflict	UNP Q62667
ZB	236	LYS	ARG	conflict	UNP Q62667
ZB	242	ALA	LEU	conflict	UNP Q62667
AC	69	ALA	THR	conflict	UNP Q62667
AC	77	VAL	ILE	conflict	UNP Q62667
AC	104	LEU	VAL	conflict	UNP Q62667
AC	186	ASP	GLU	conflict	UNP Q62667
AC	189	GLU	GLY	conflict	UNP Q62667
AC	232	ARG	LEU	conflict	UNP Q62667
AC	236	LYS	ARG	conflict	UNP Q62667
AC	242	ALA	LEU	conflict	UNP Q62667

3 Residue-property plots

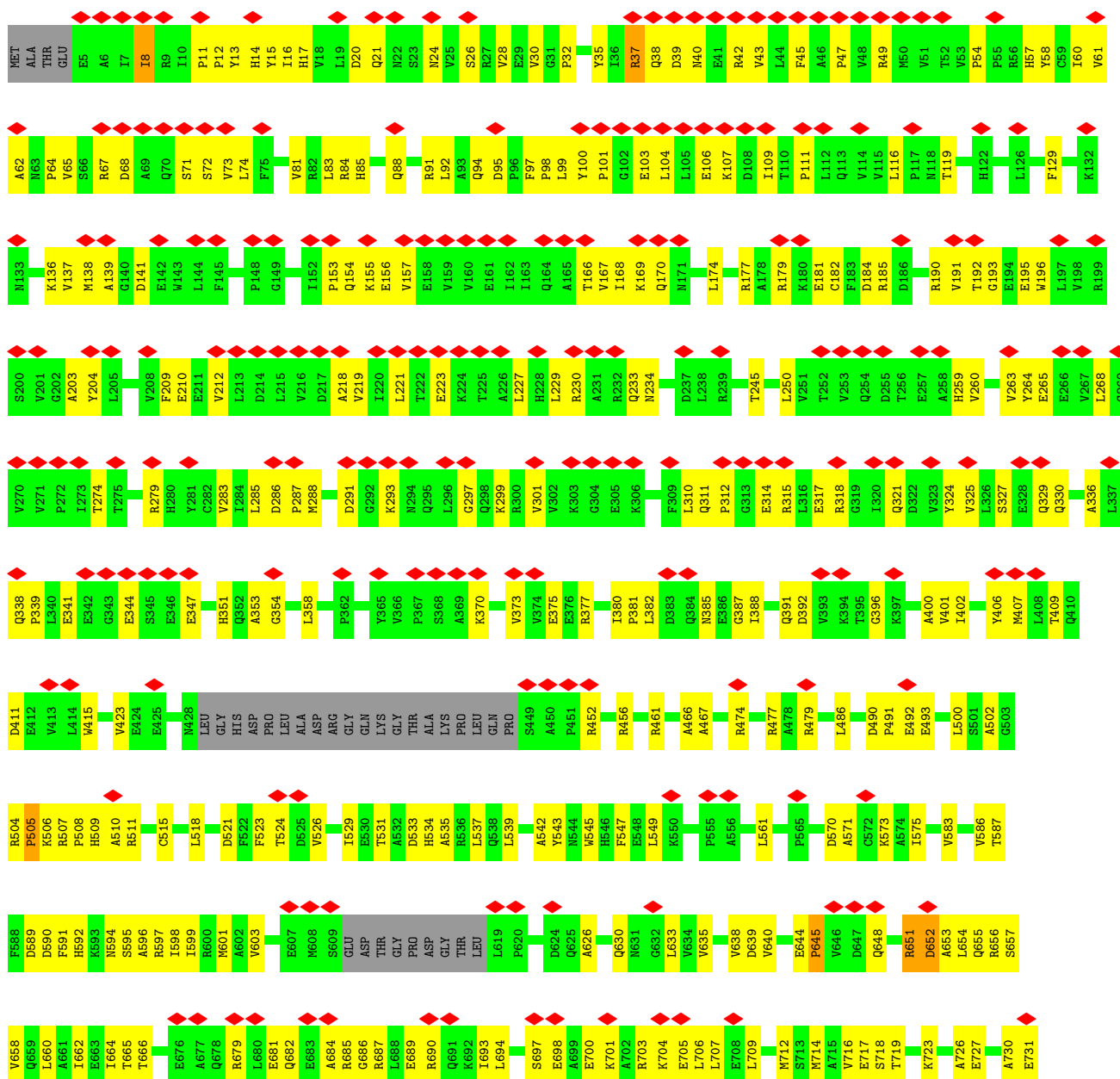
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

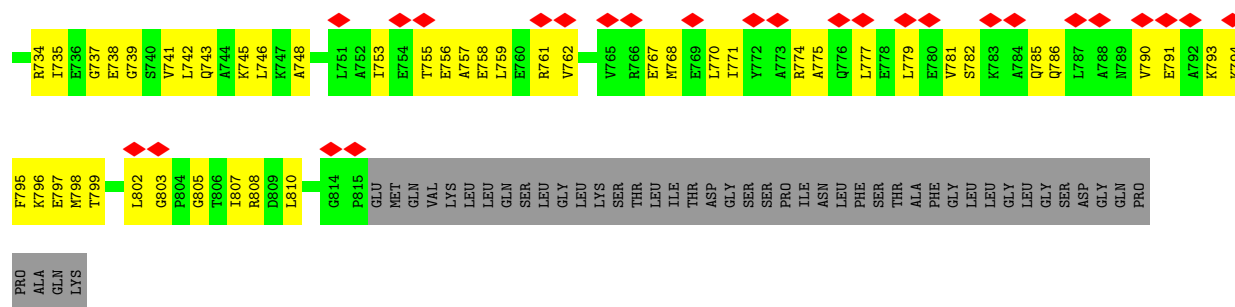
• Molecule 1: Major vault protein



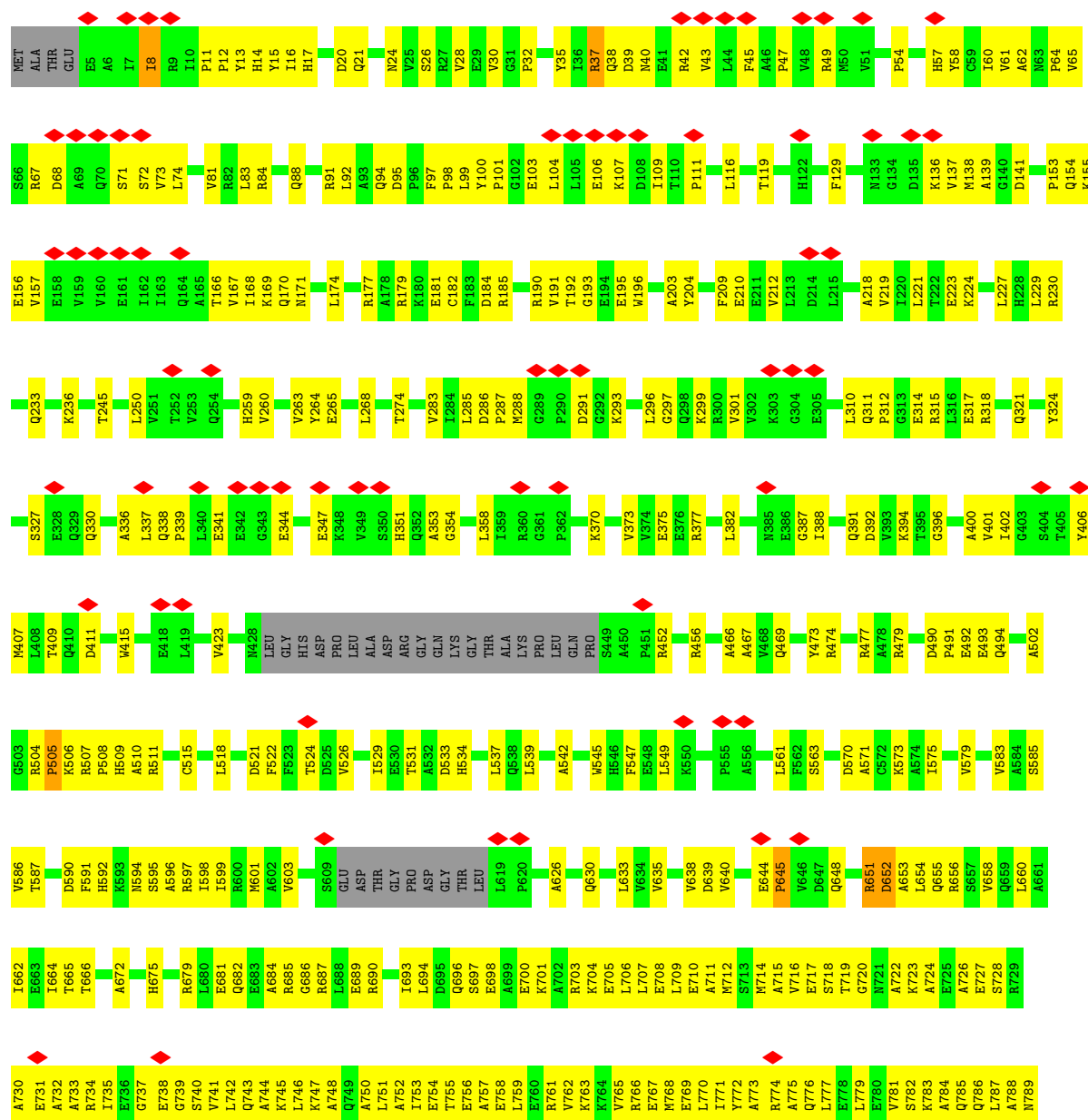


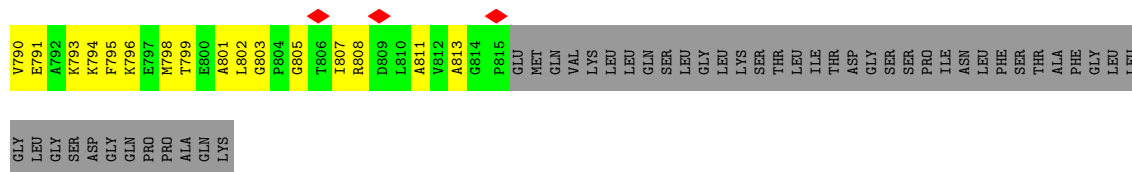
• Molecule 1: Major vault protein





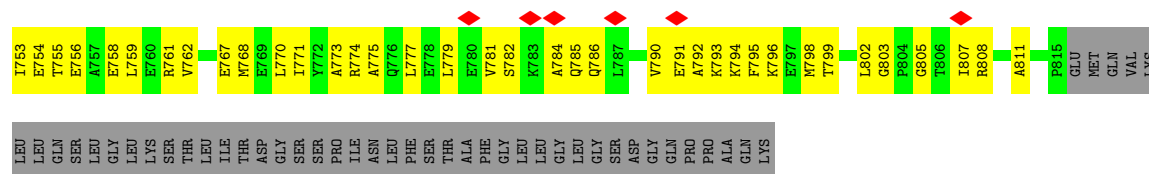
• Molecule 1: Major vault protein



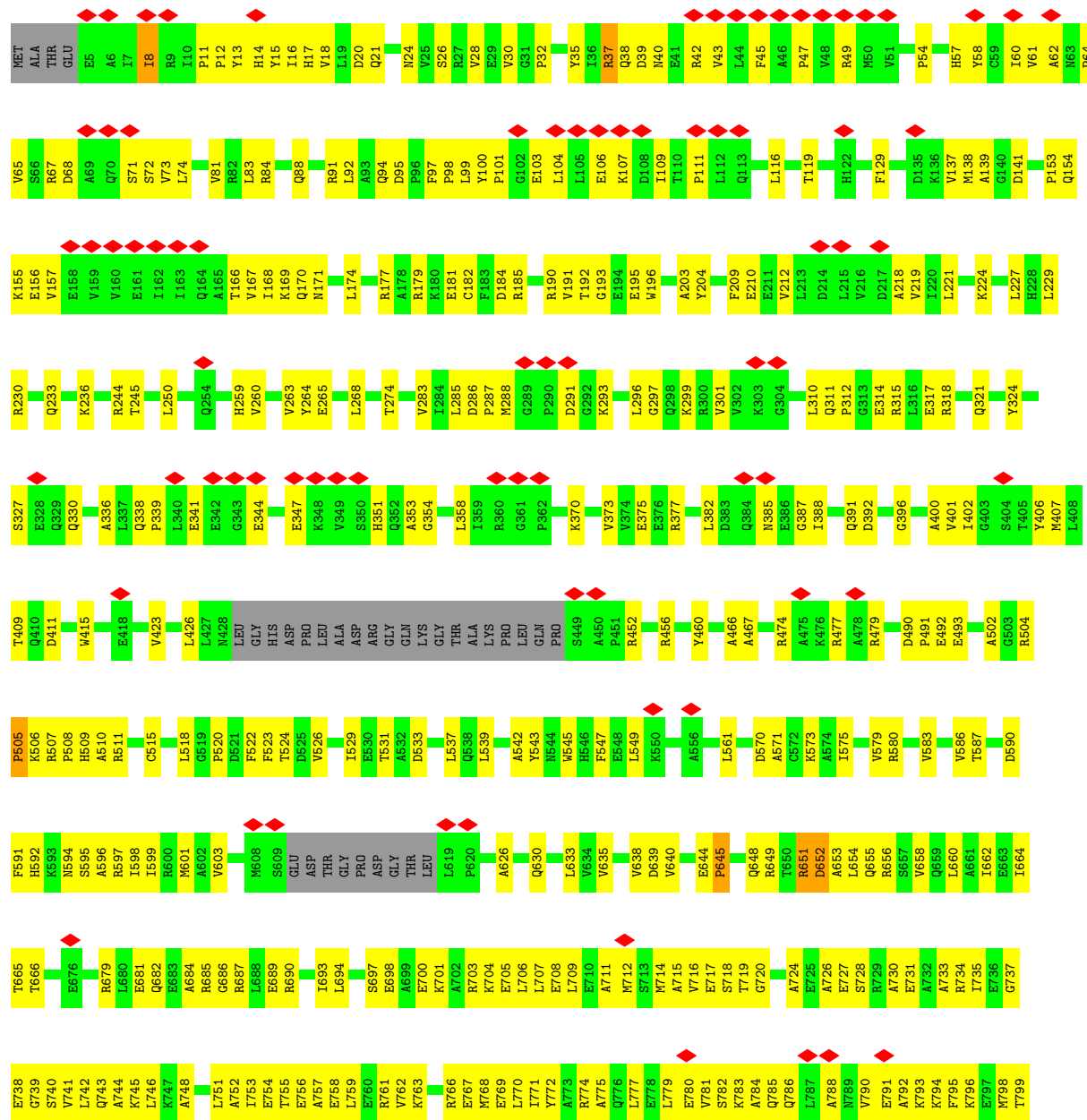


• Molecule 1: Major vault protein

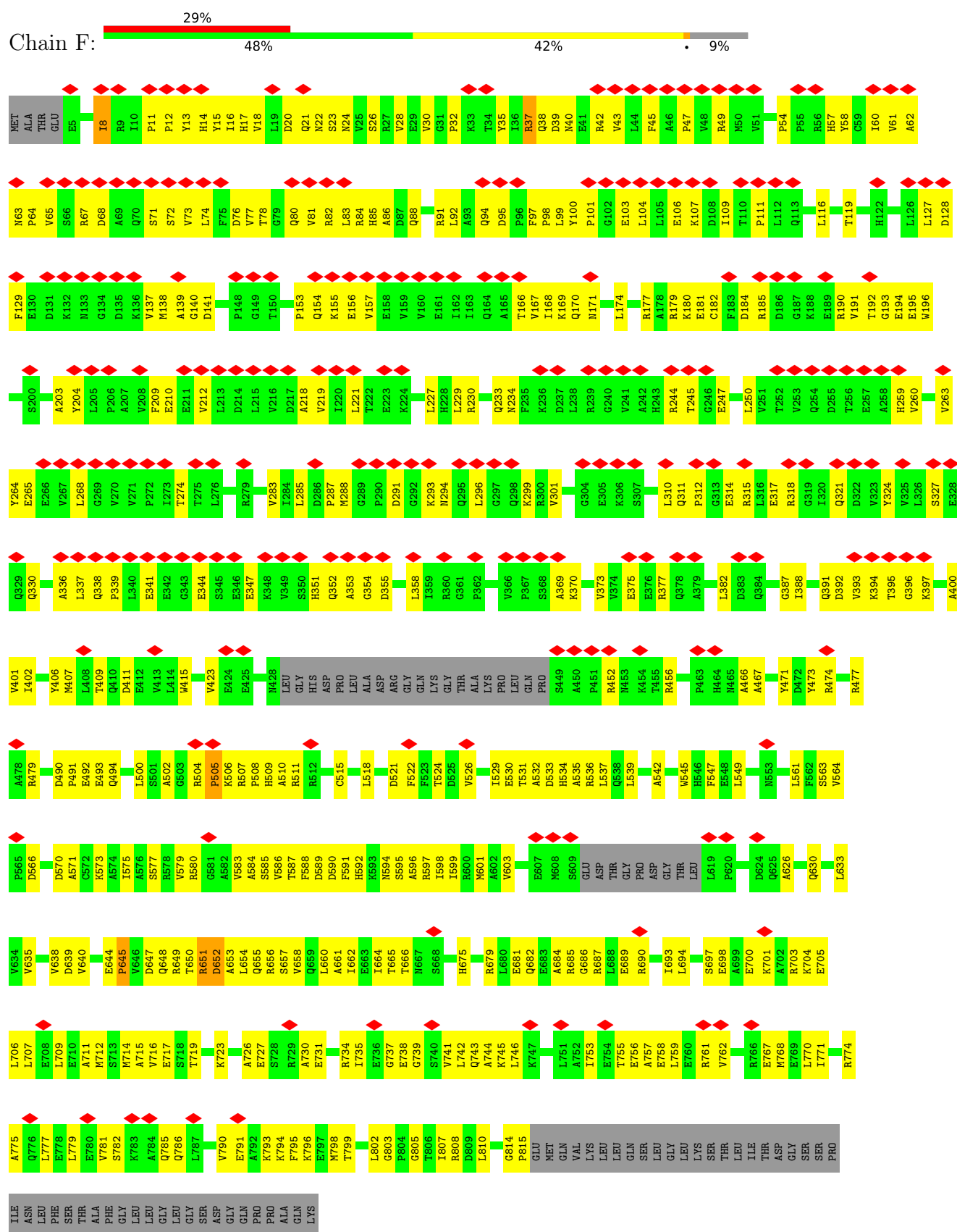




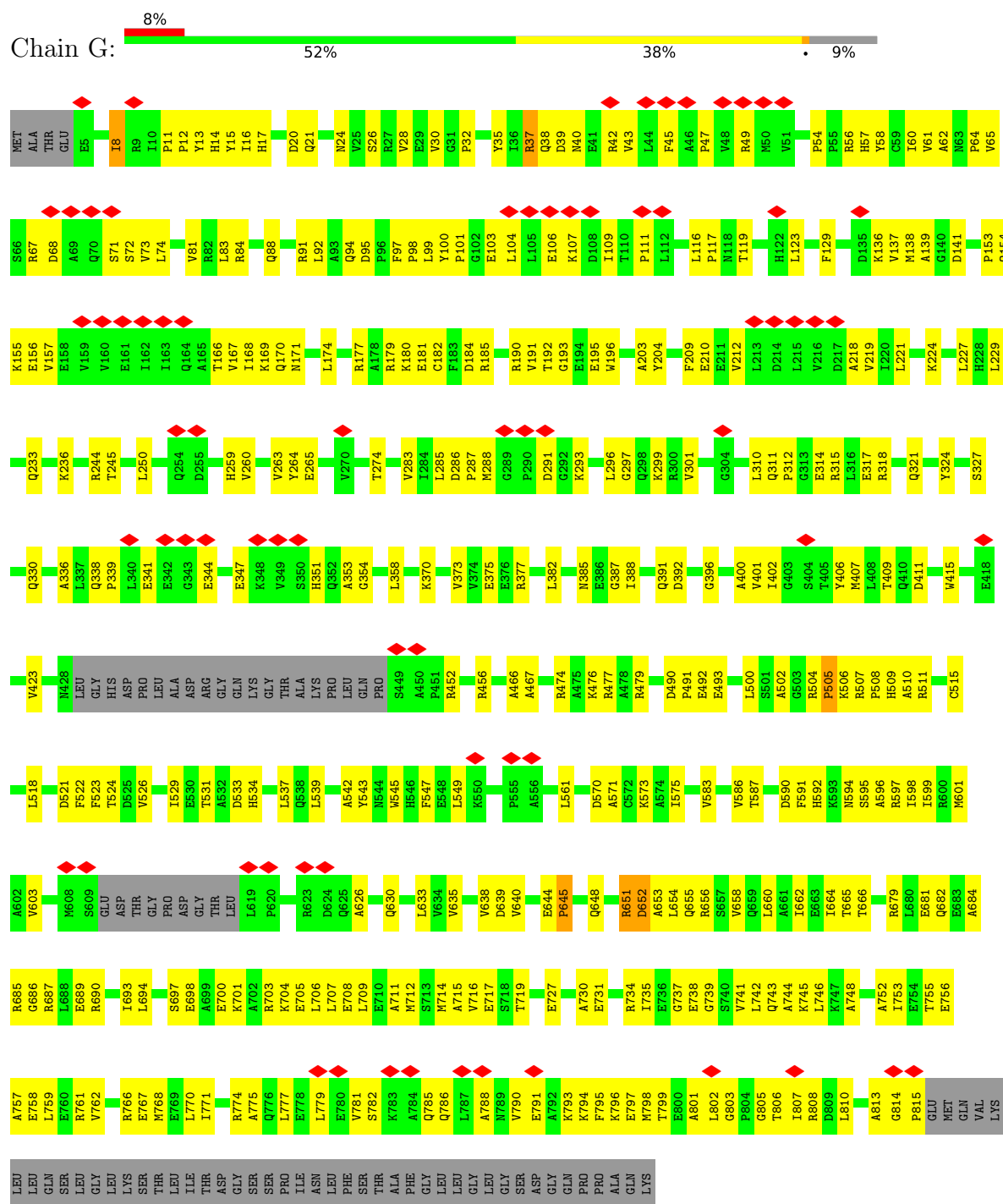
Molecule 1: Major vault protein



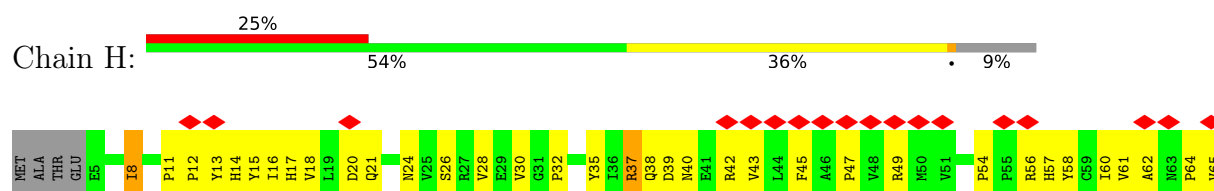
• Molecule 1: Major vault protein



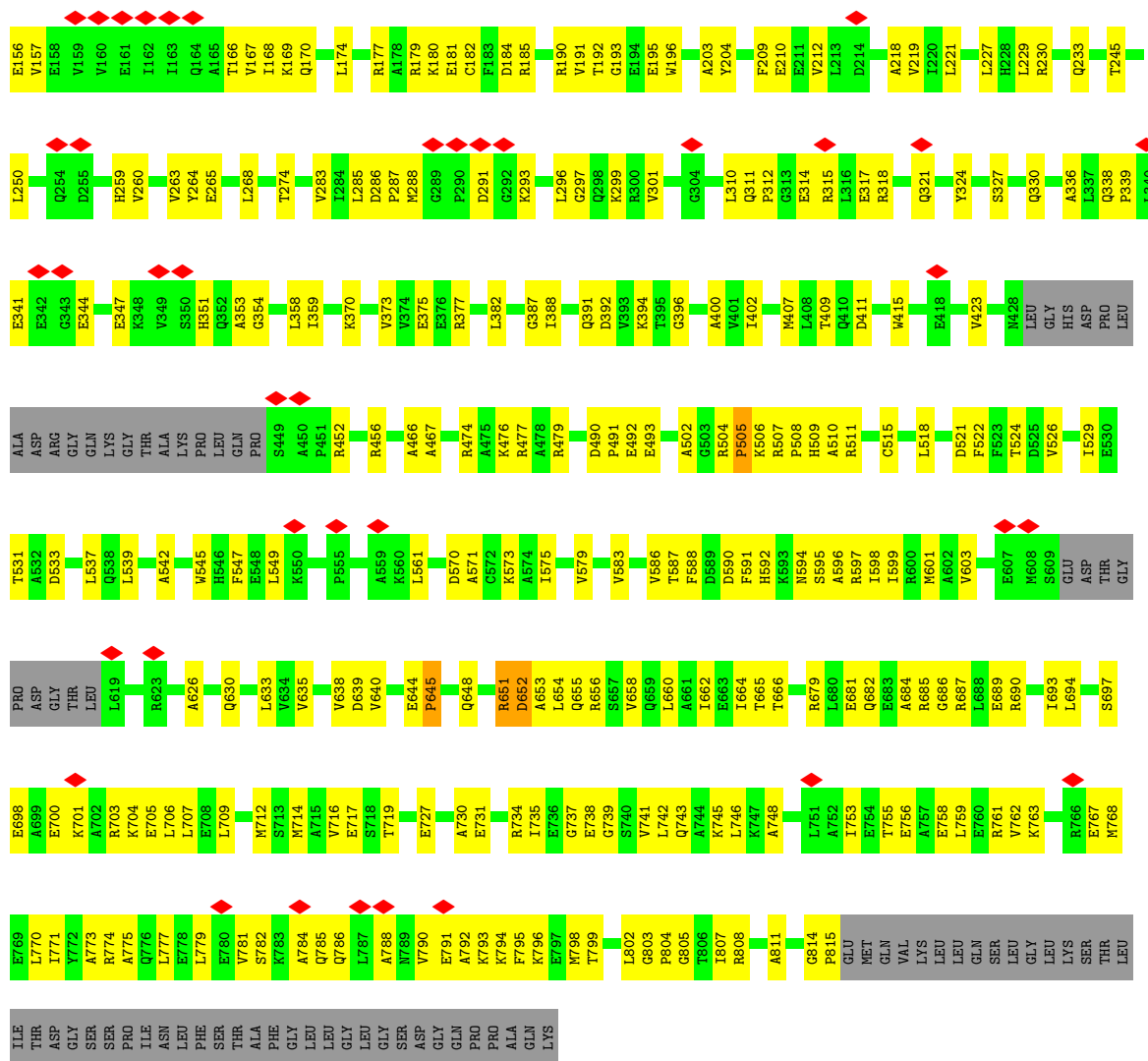
- Molecule 1: Major vault protein



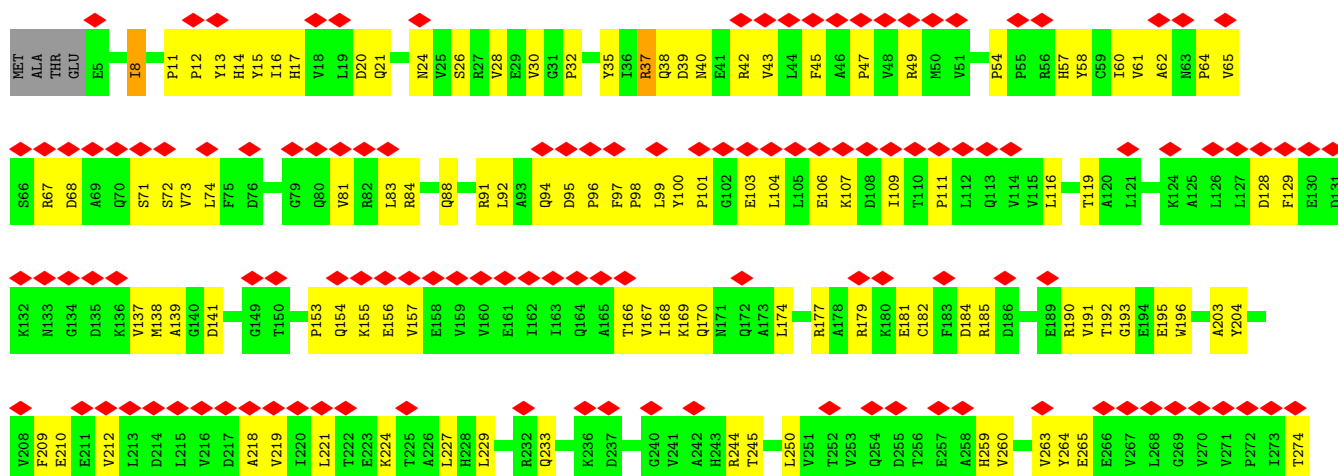
- Molecule 1: Major vault protein



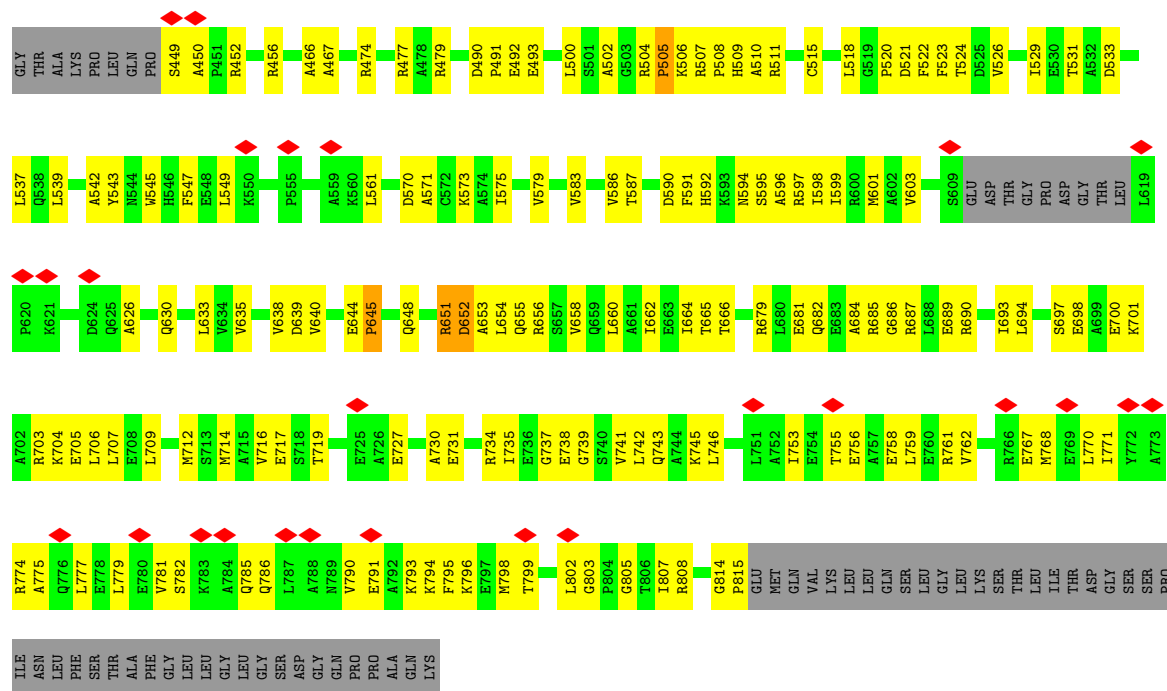




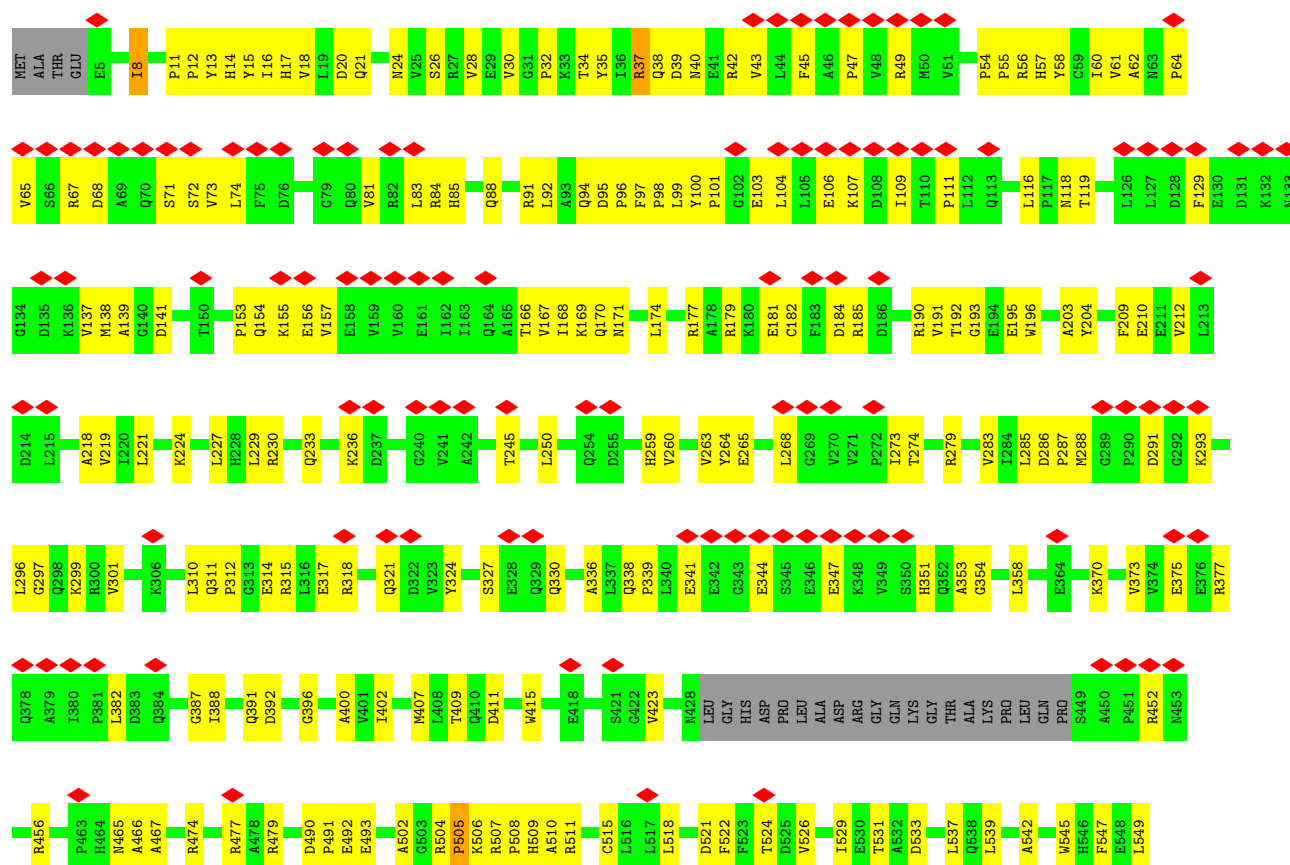
• Molecule 1: Major vault protein

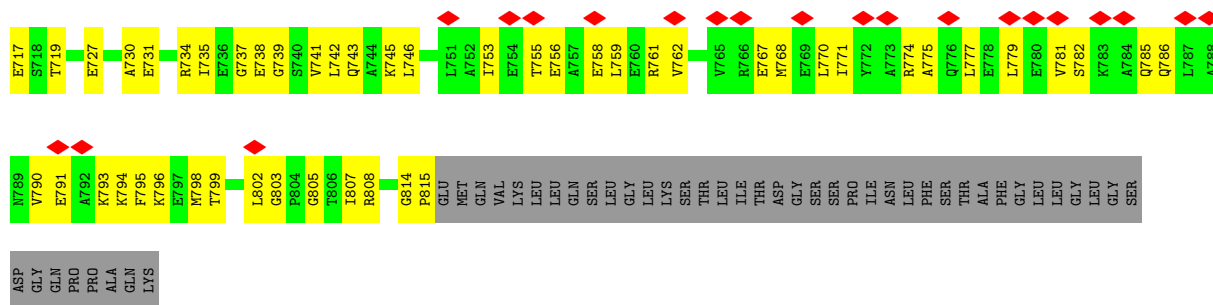




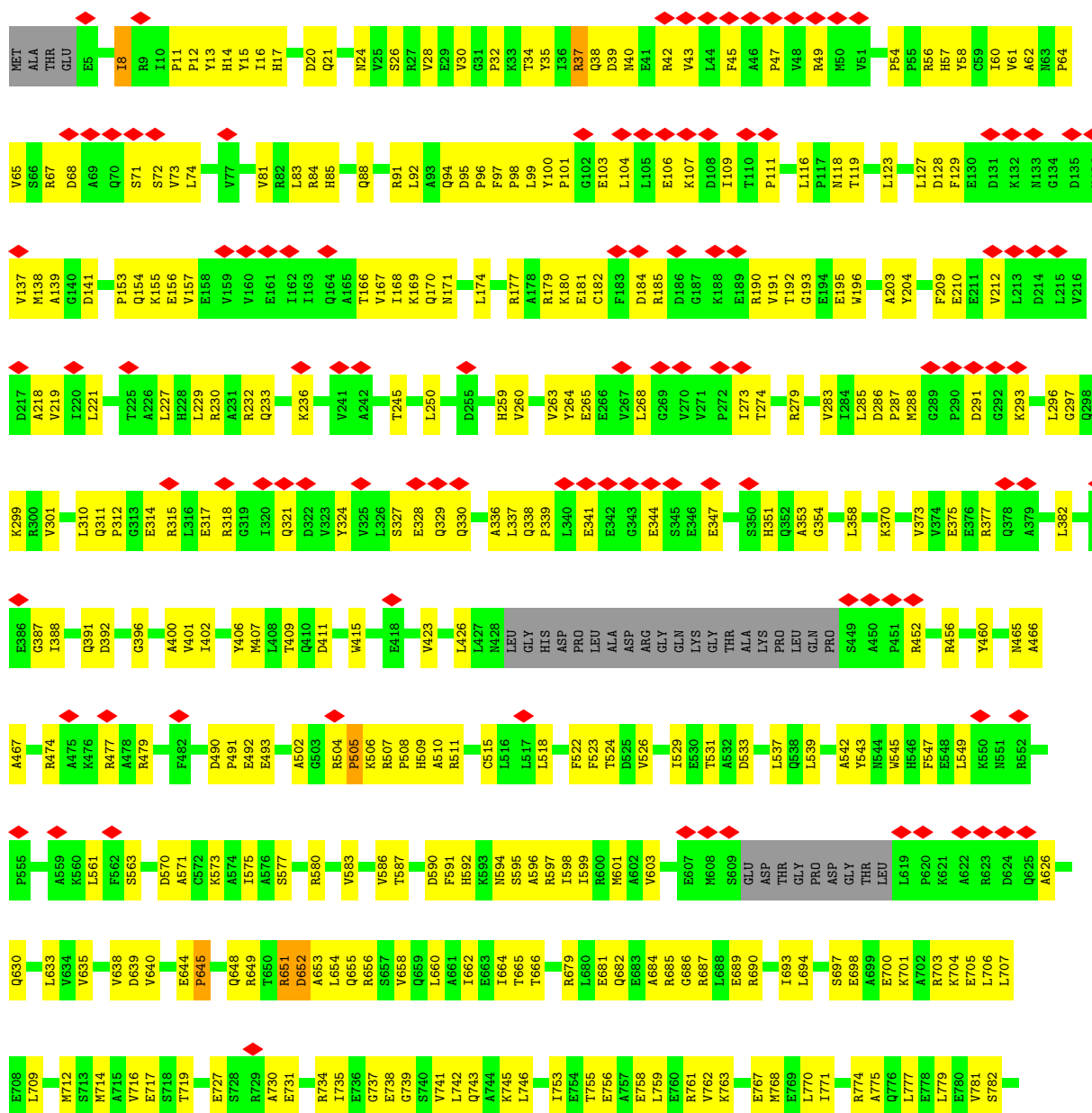


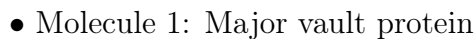
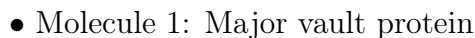
• Molecule 1: Major vault protein





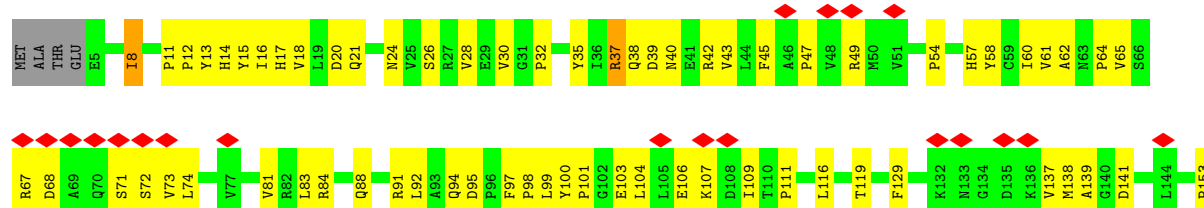
• Molecule 1: Major vault protein

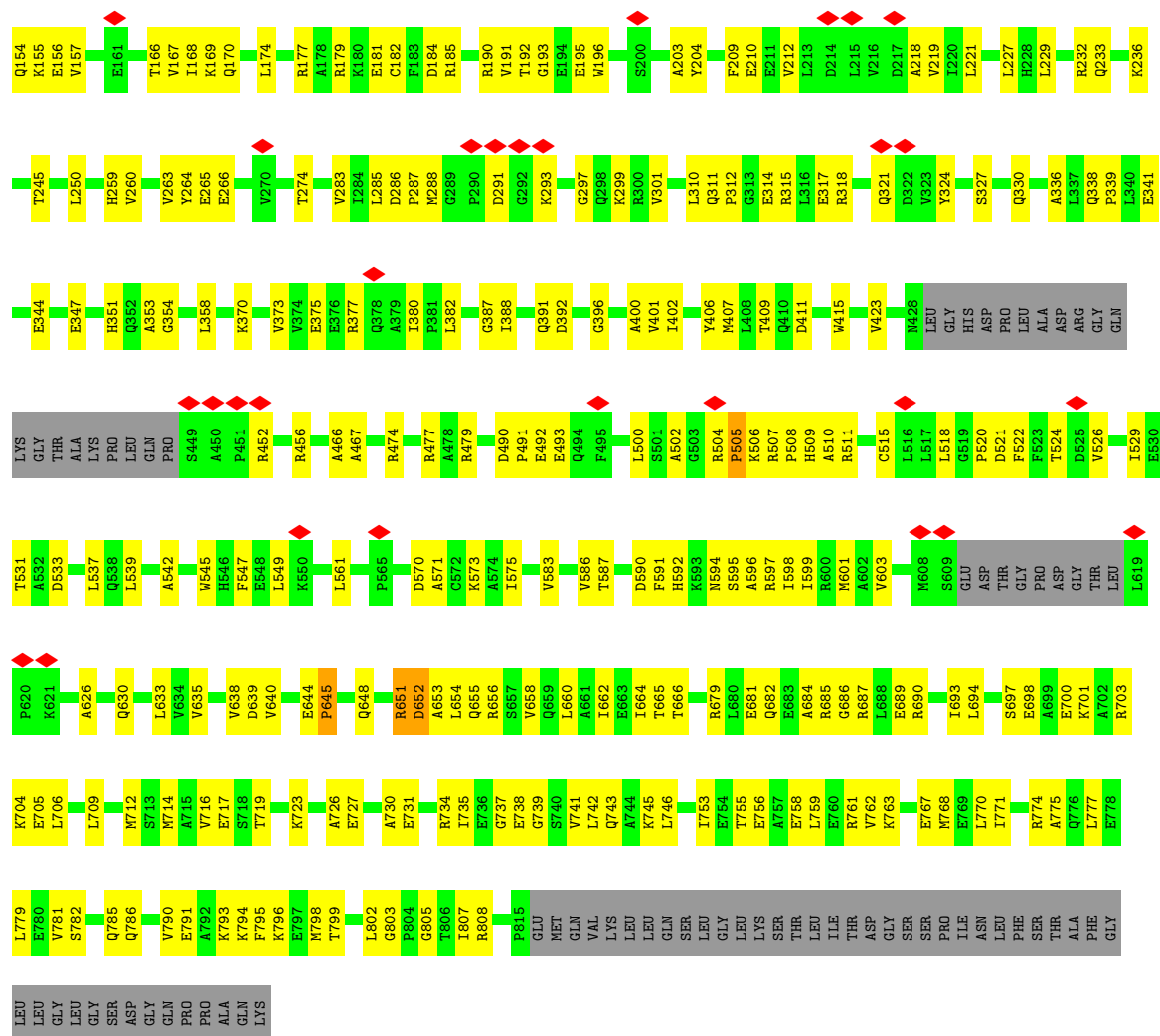




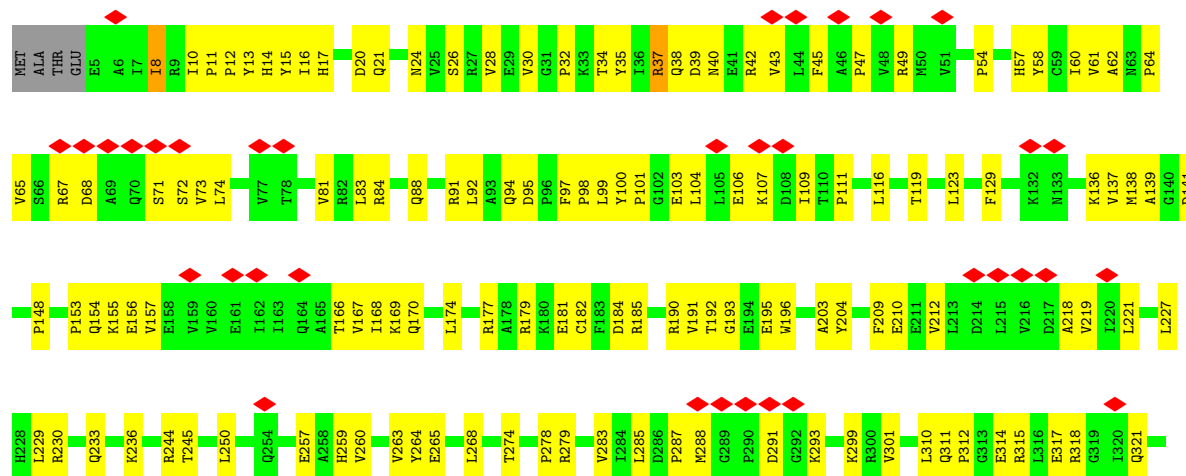


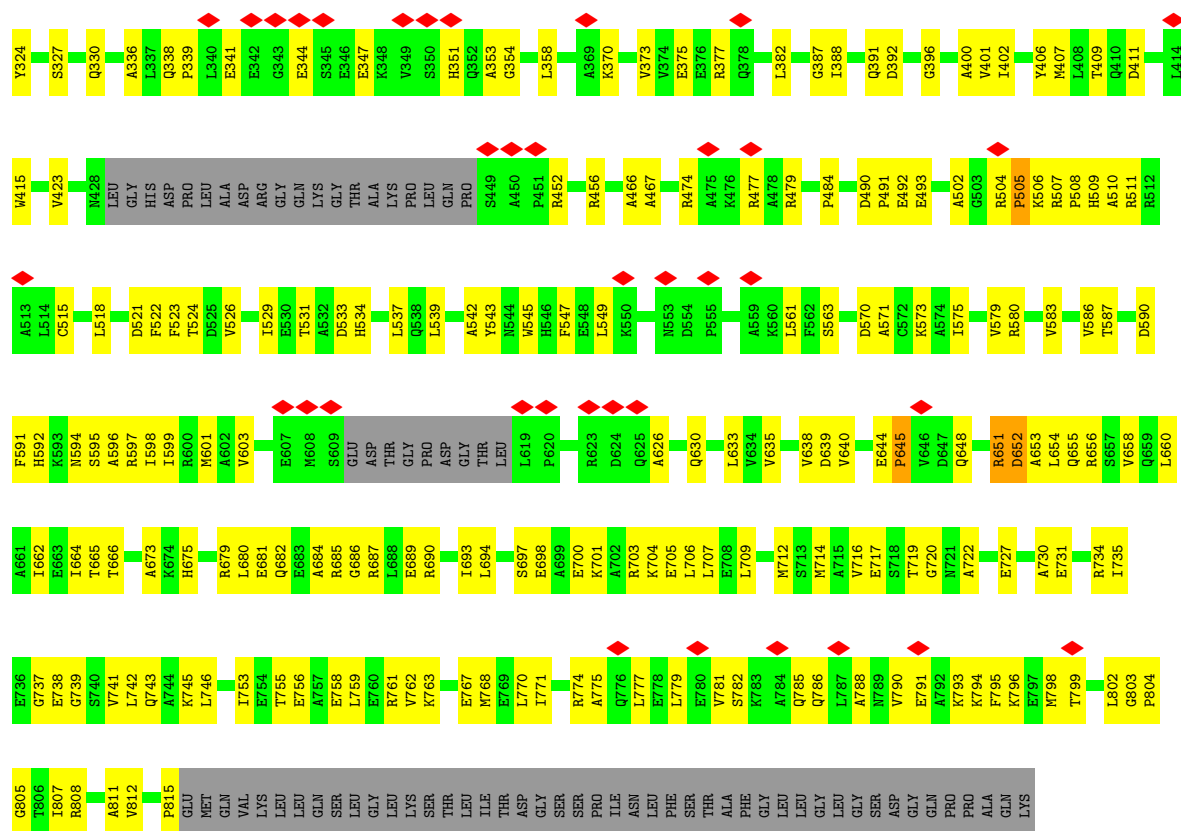
• Molecule 1: Major vault protein



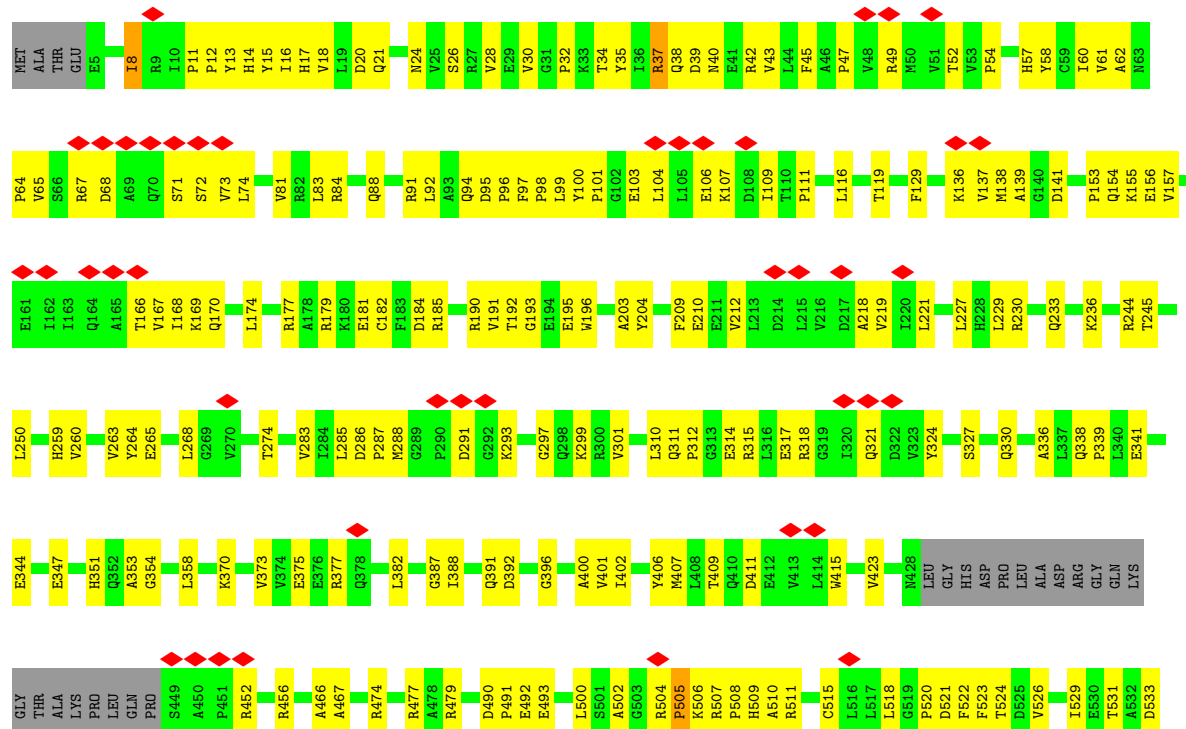


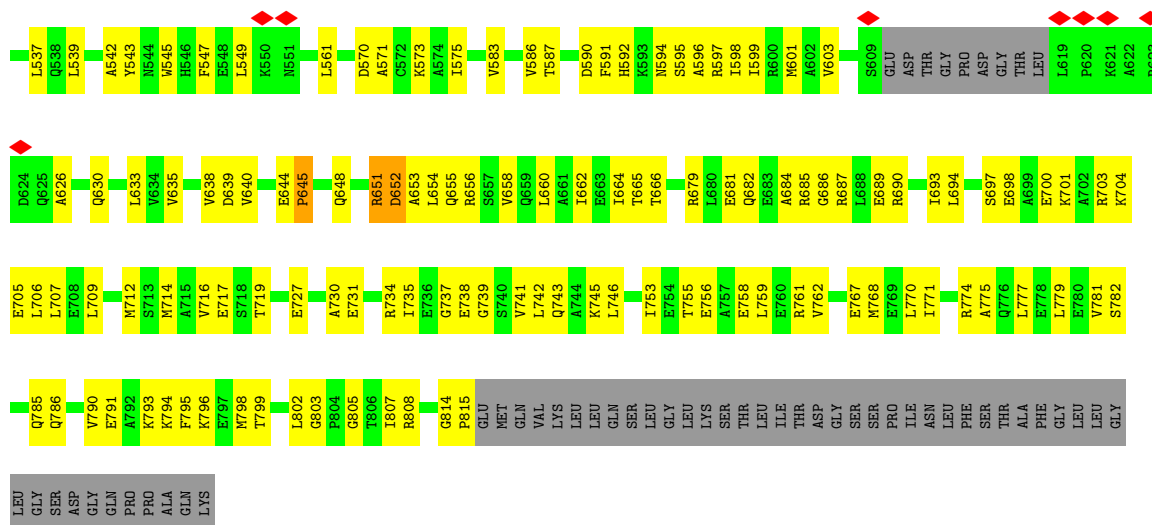
• Molecule 1: Major vault protein





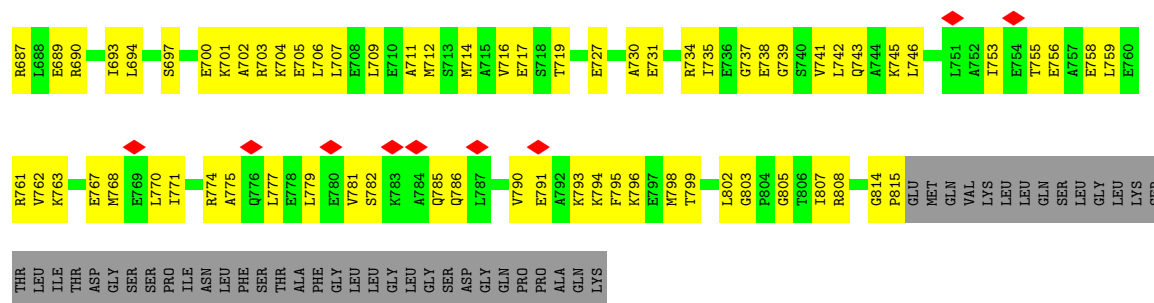
• Molecule 1: Major vault protein



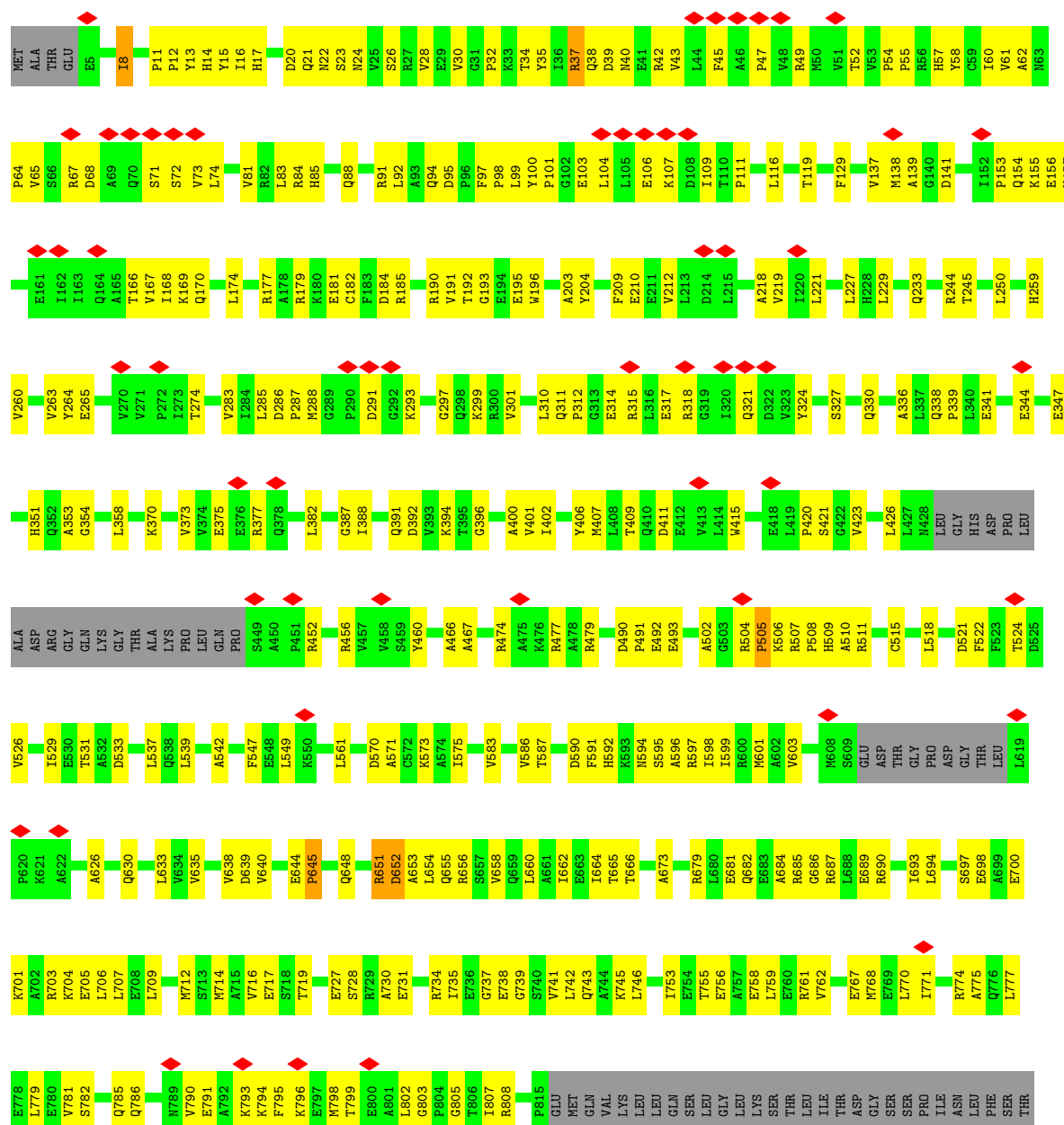


• Molecule 1: Major vault protein





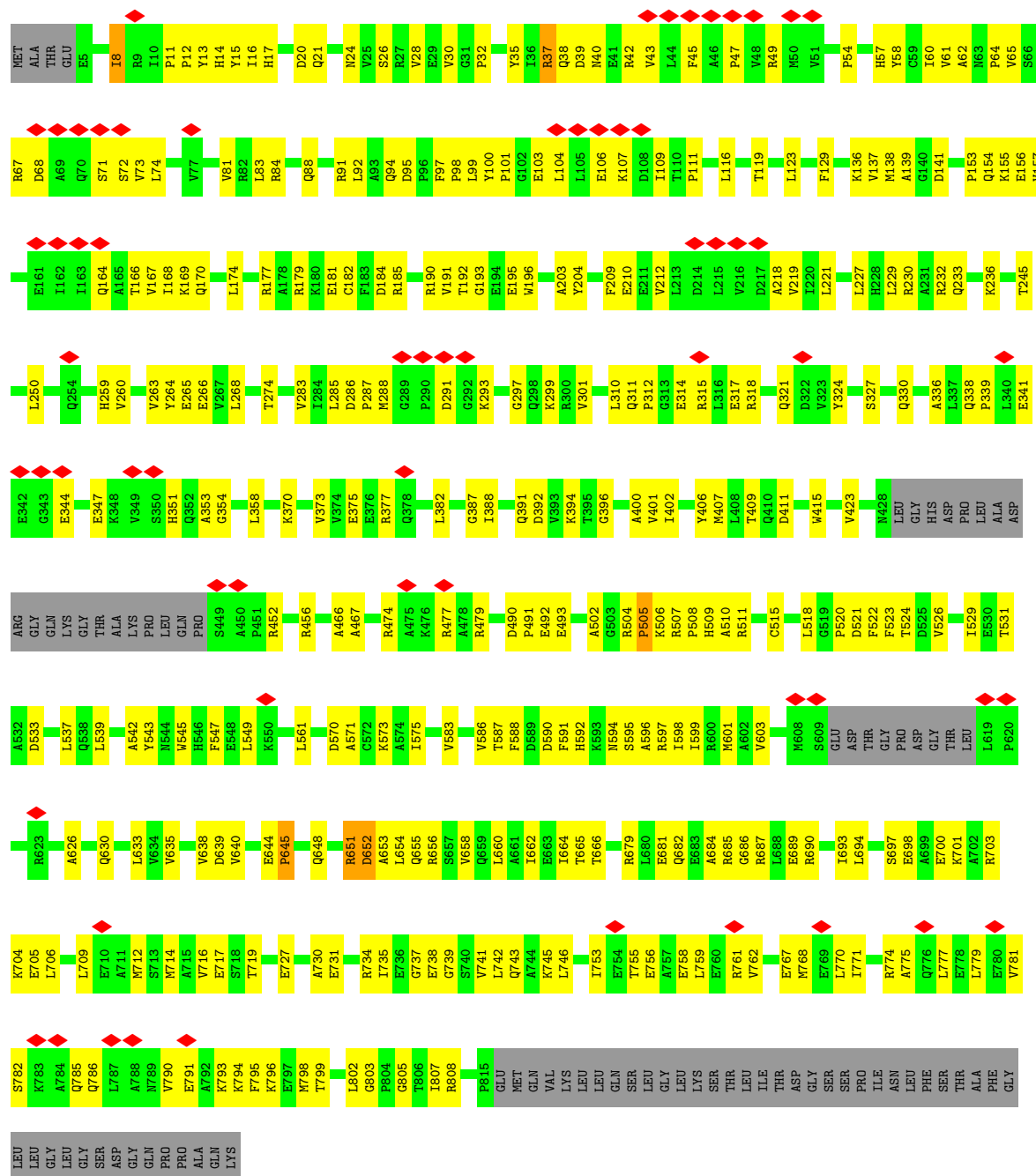
Molecule 1: Major vault protein



ALA
PHE
GLY
LEU
LEU
GLY
LEU
GLY
SER
ASP
GLY
GLN
PRO
PRO
ALA
GLN
LYS

• Molecule 1: Major vault protein

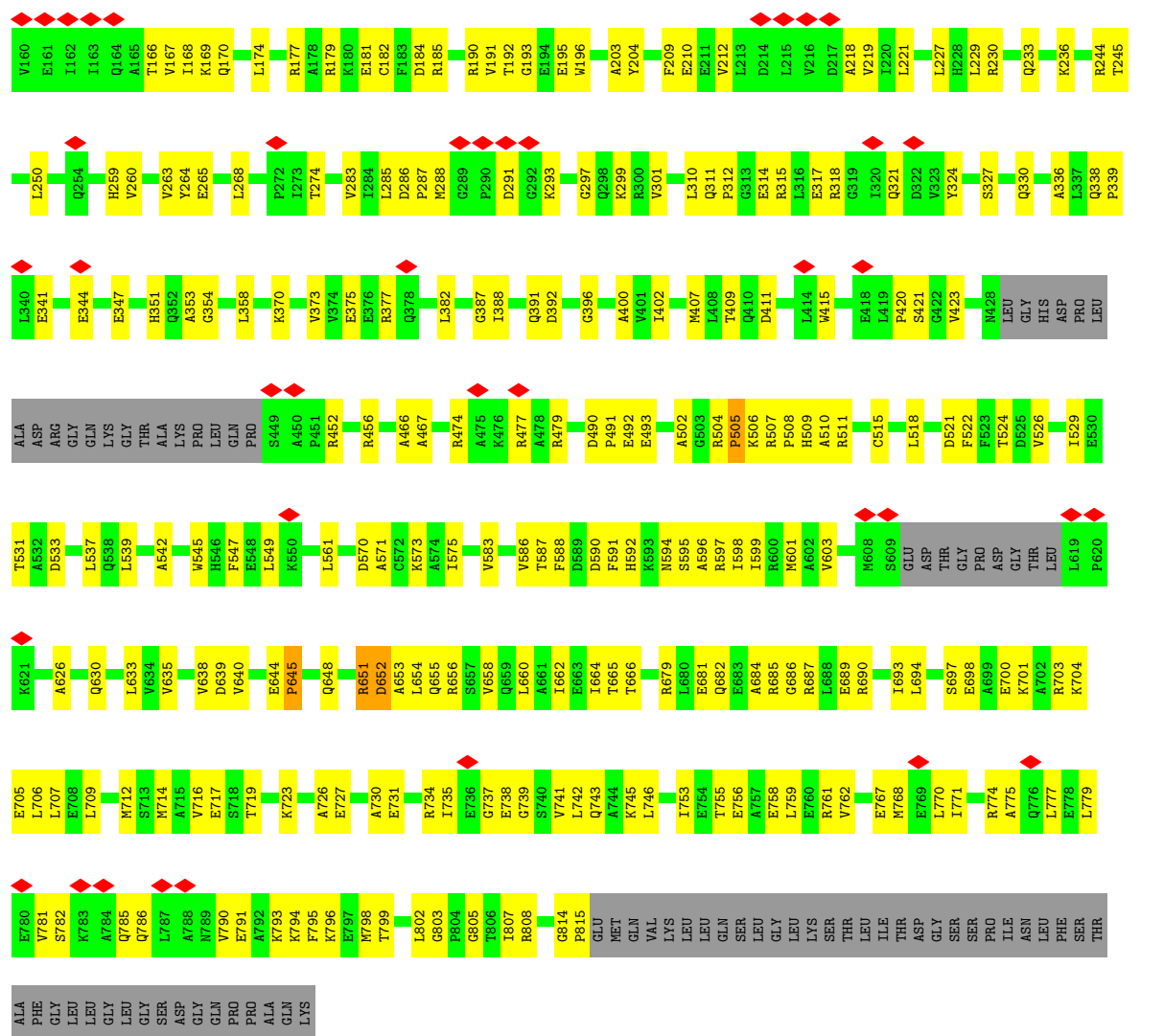
Chain W: 



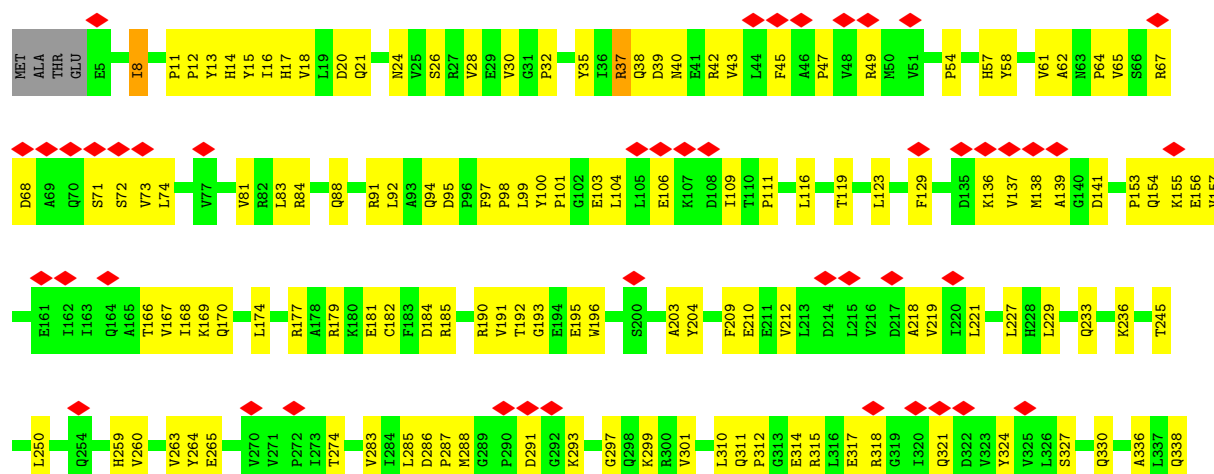
• Molecule 1: Major vault protein

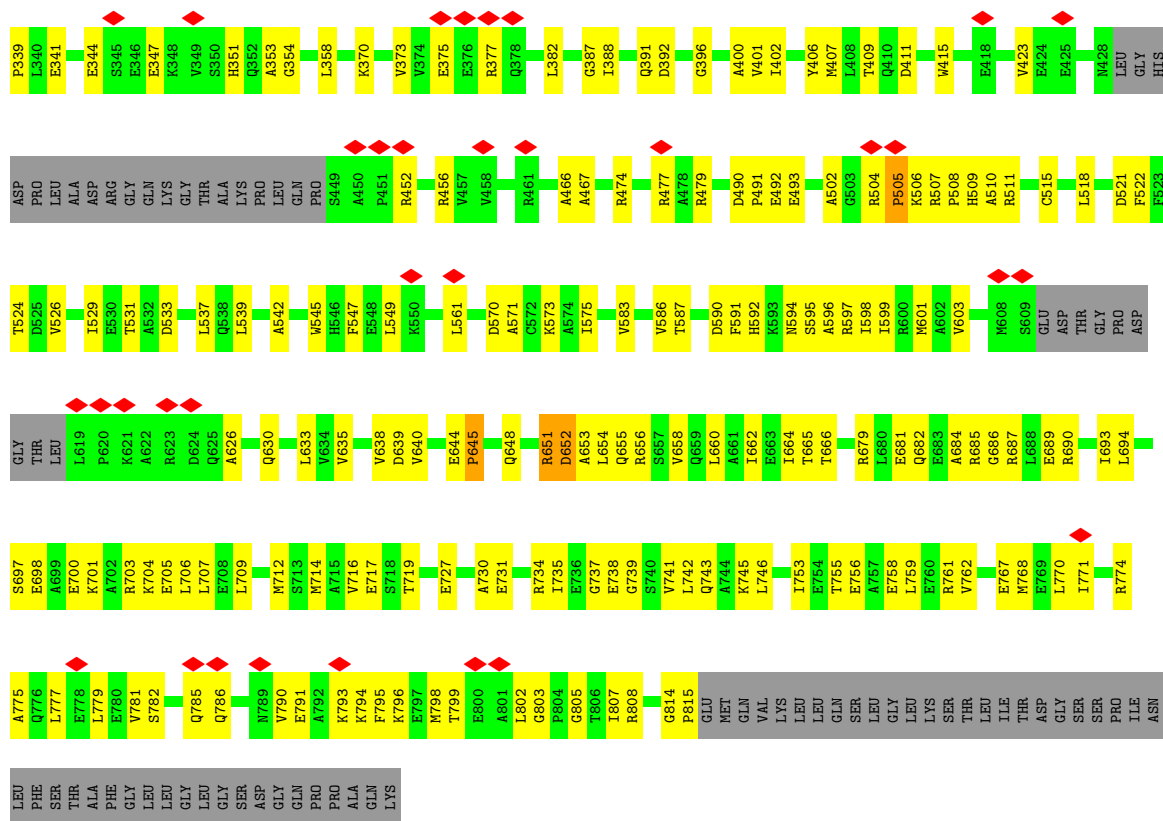
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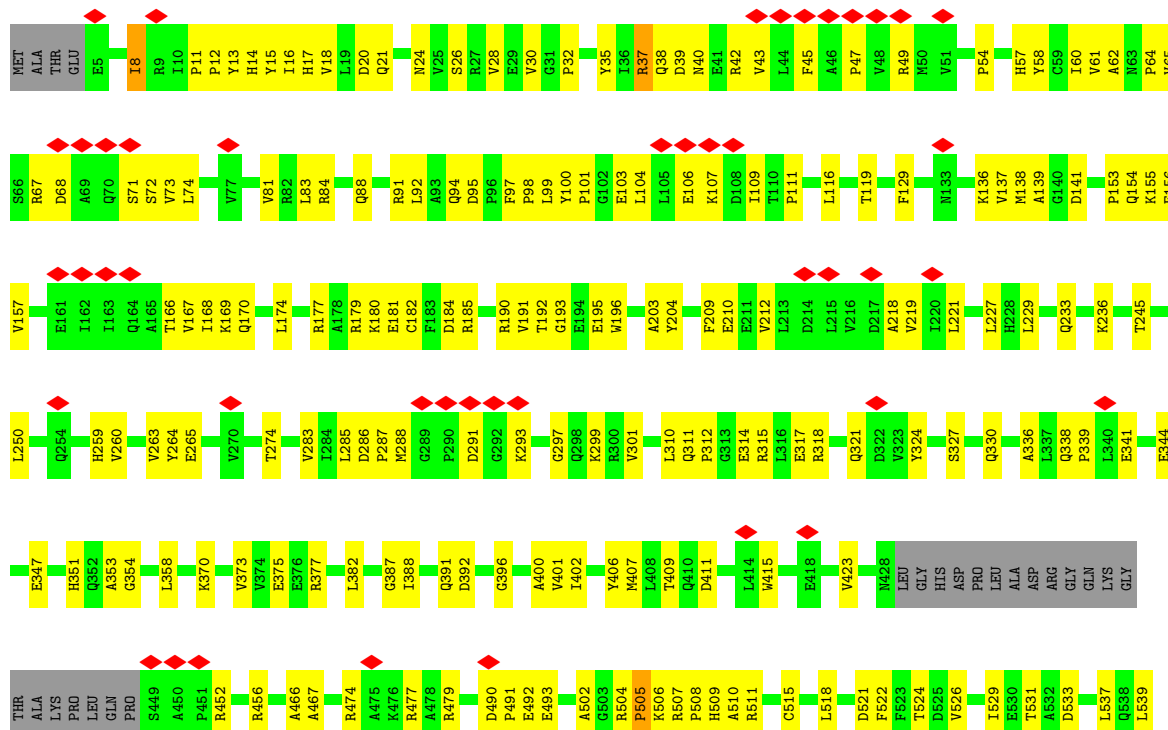


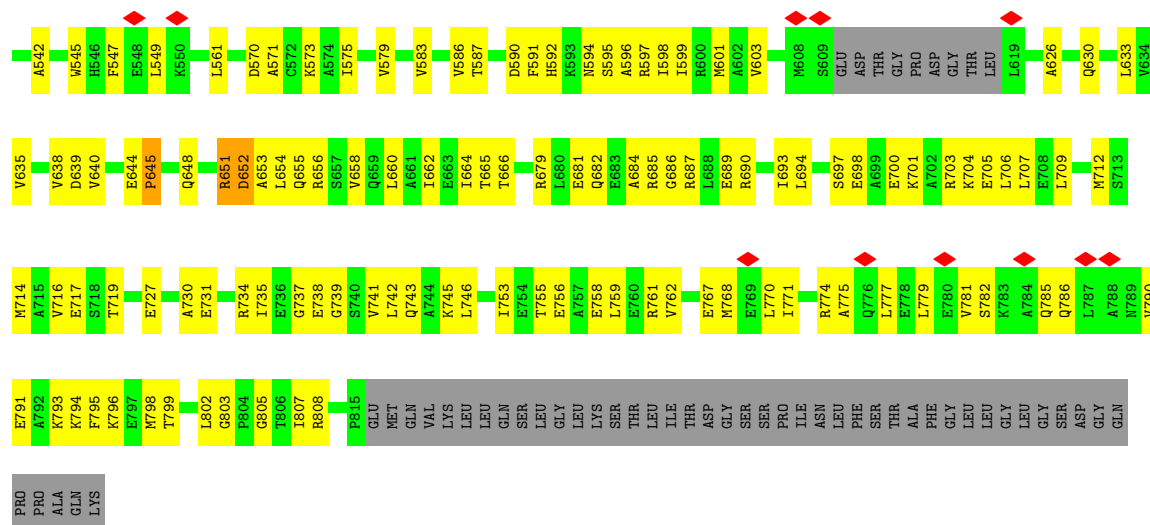
• Molecule 1: Major vault protein



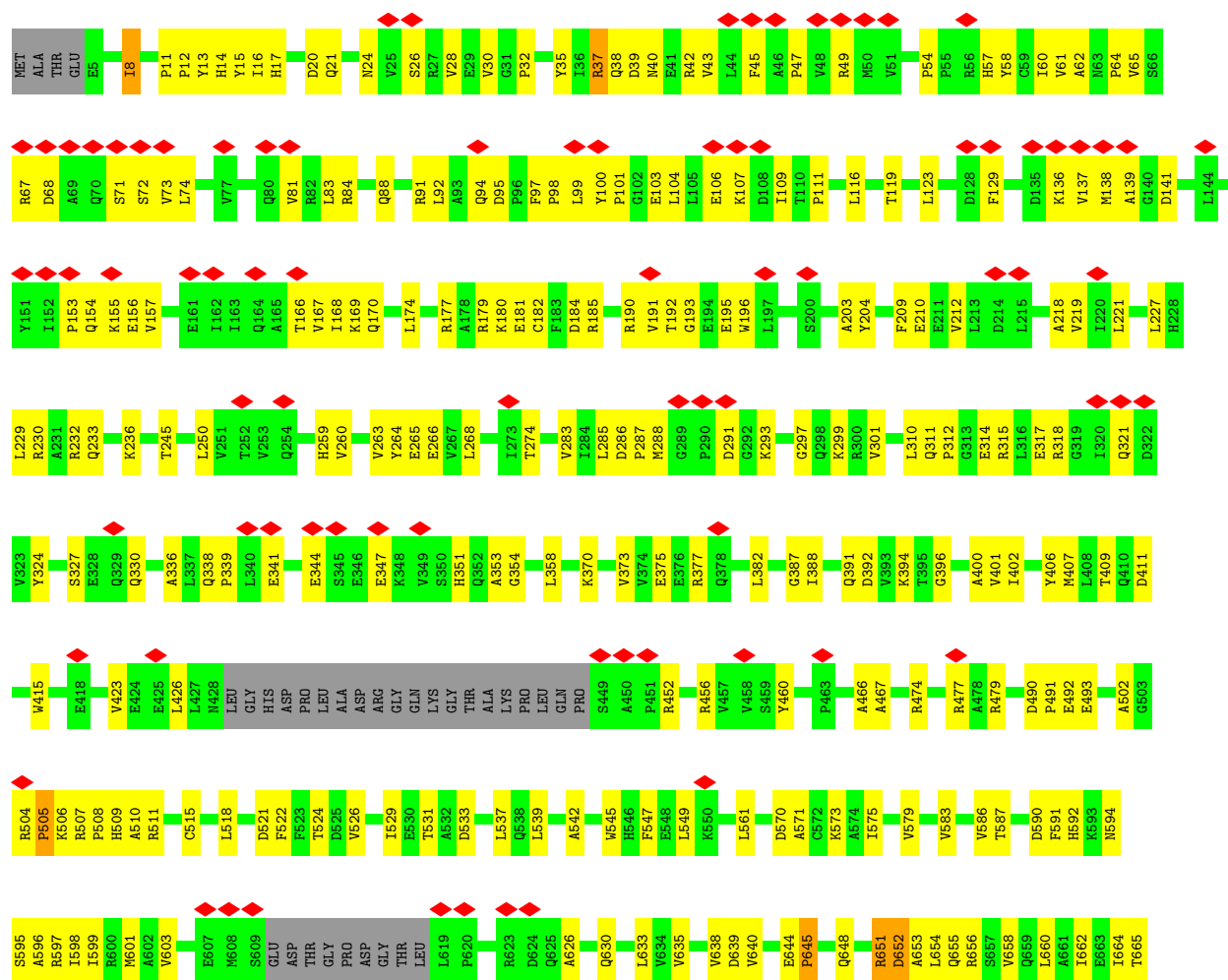


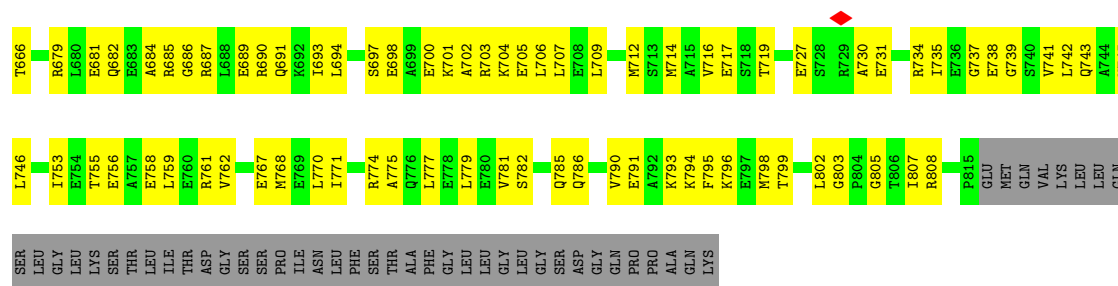
• Molecule 1: Major vault protein



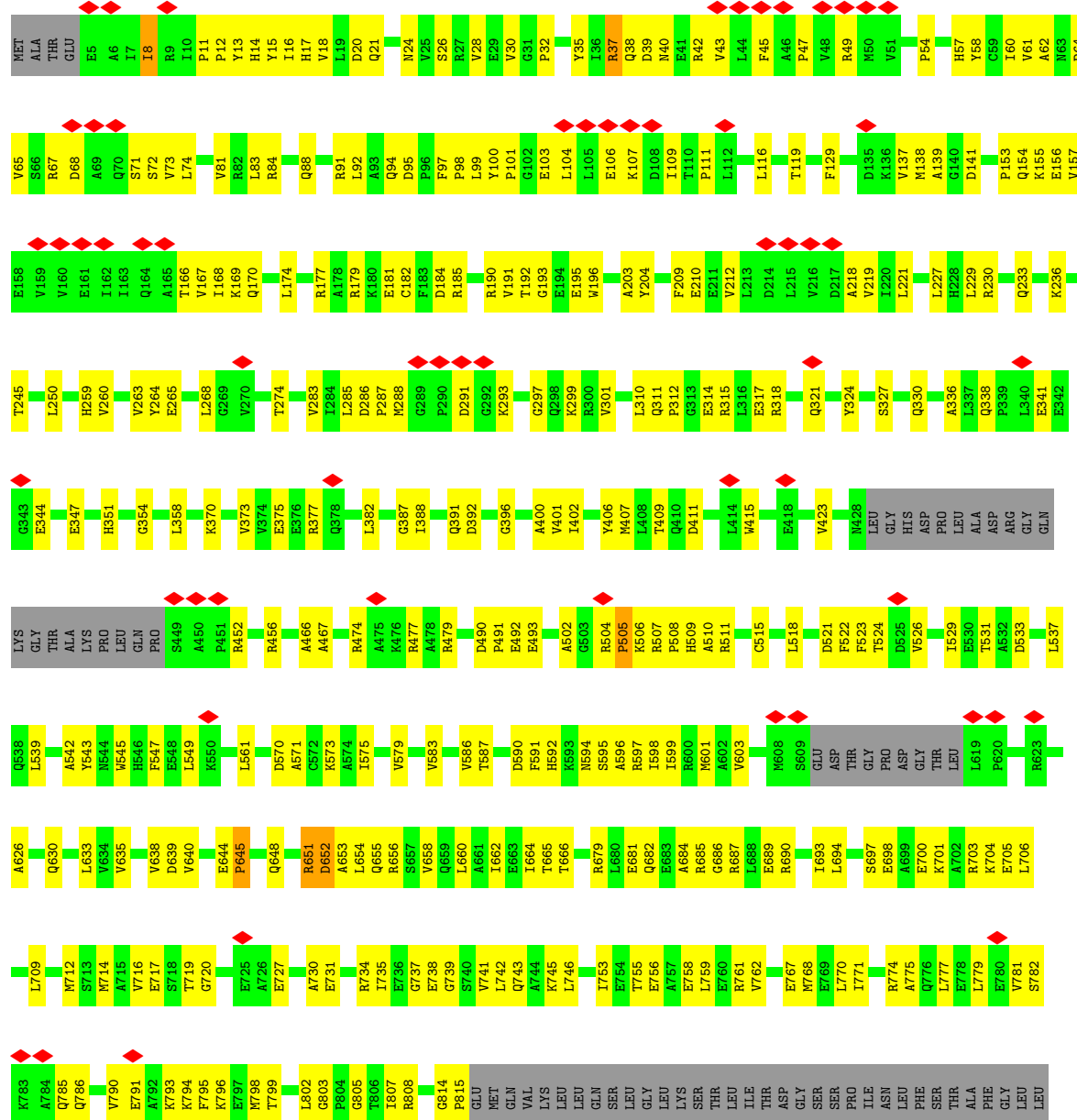


• Molecule 1: Major vault protein



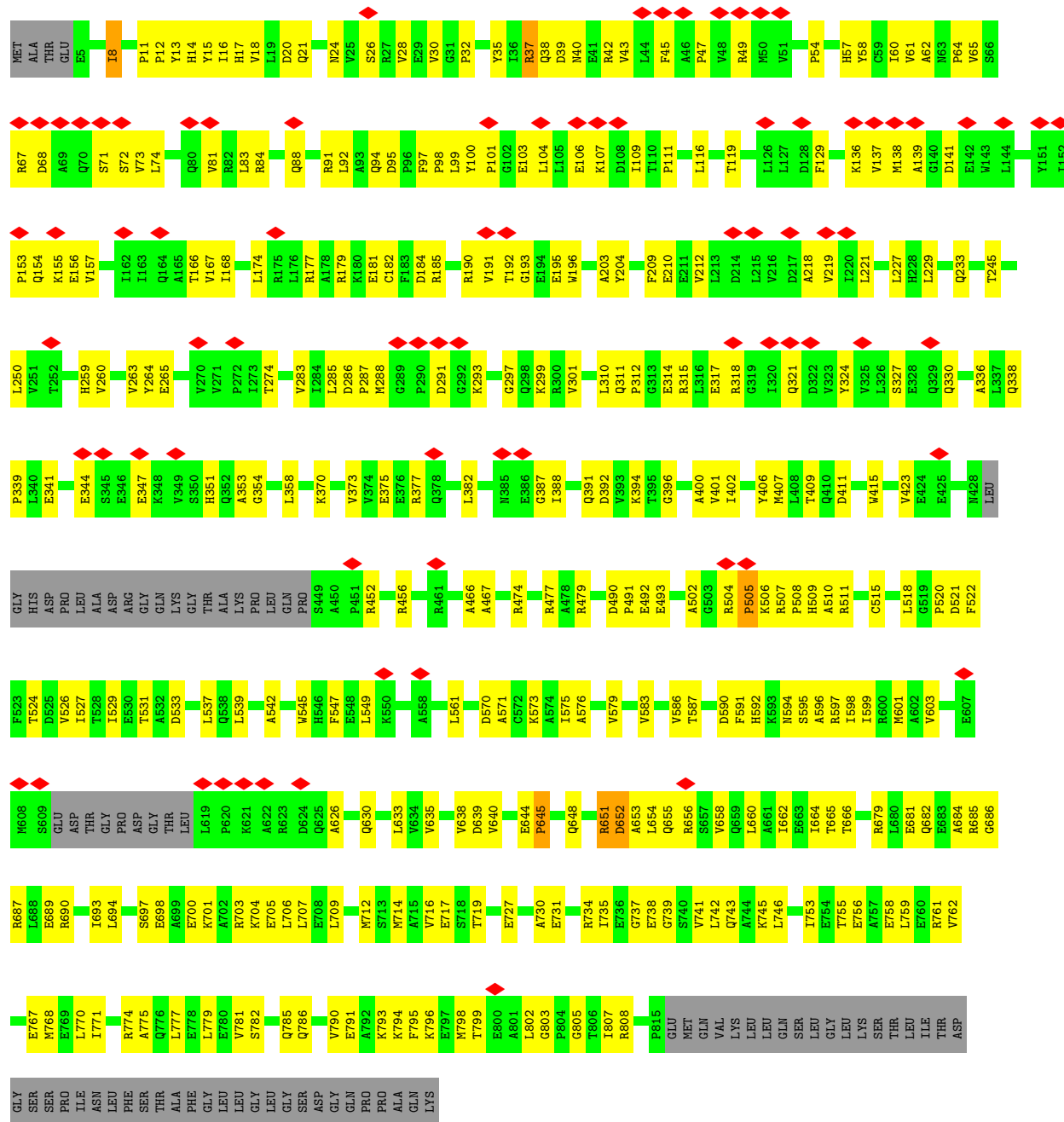


Molecule 1: Major vault protein



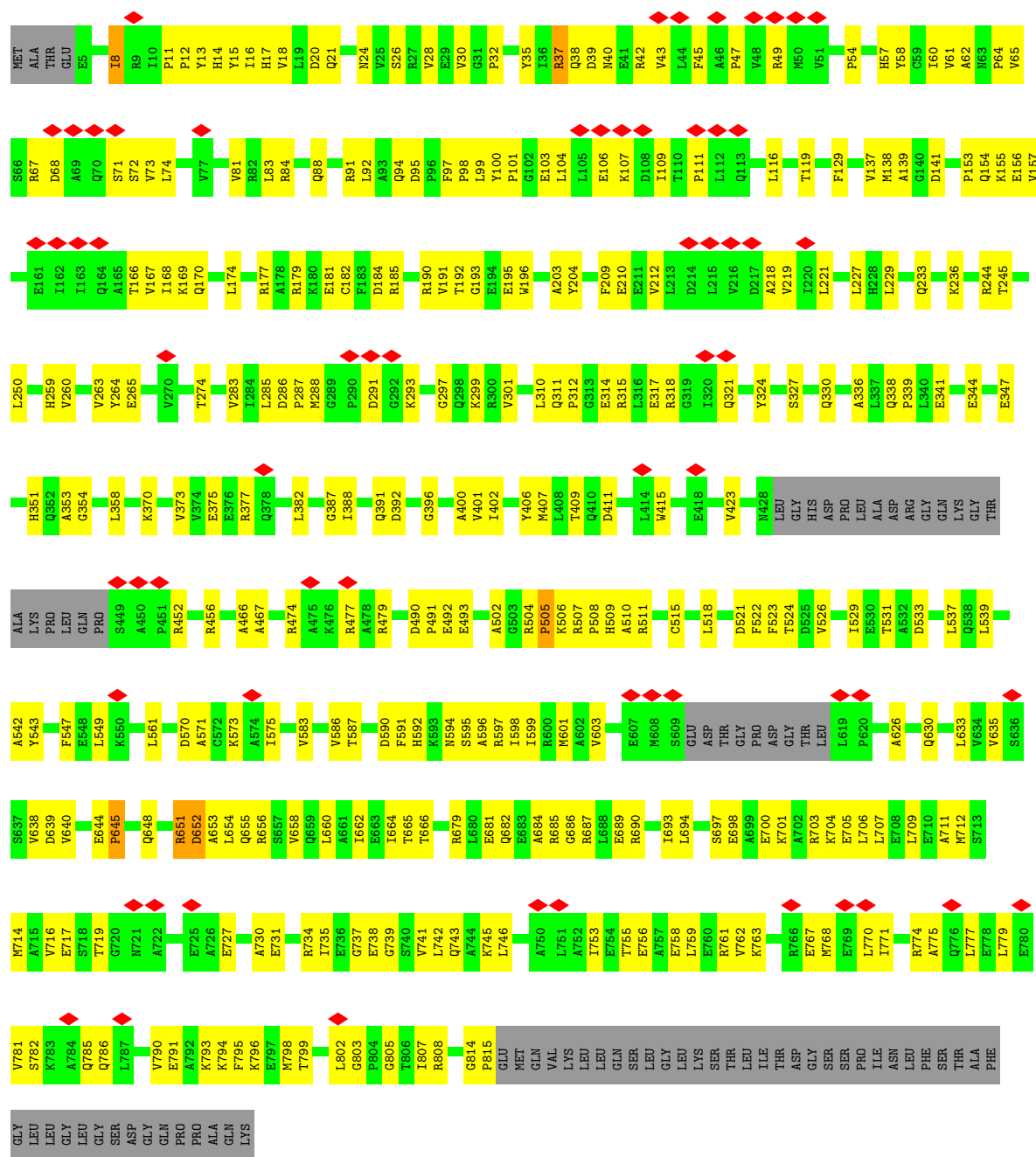
GLY
LEU
GLY
SER
GLU
ASP
GLY
GLN
PRO
PRO
ALA
ALA
GLN
LYS

• Molecule 1: Major vault protein

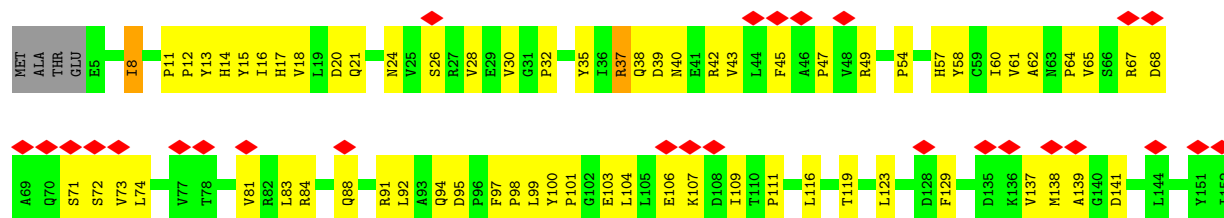


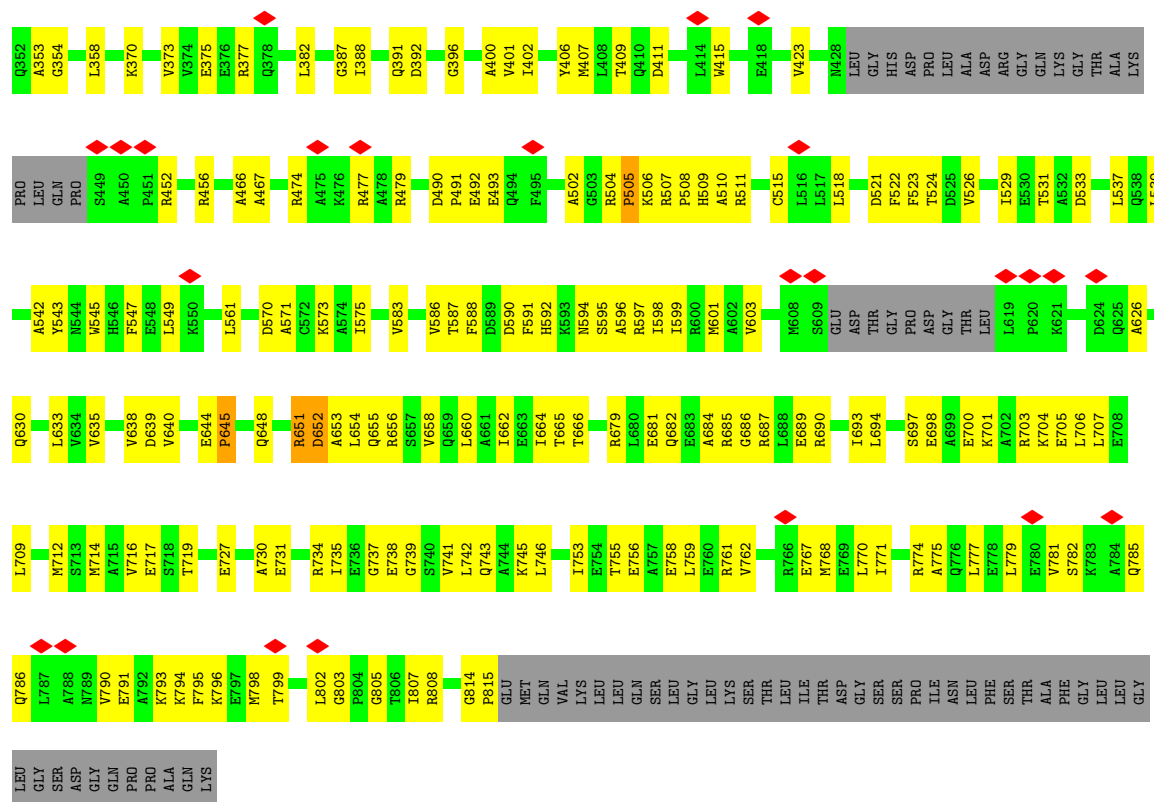
• Molecule 1: Major vault protein



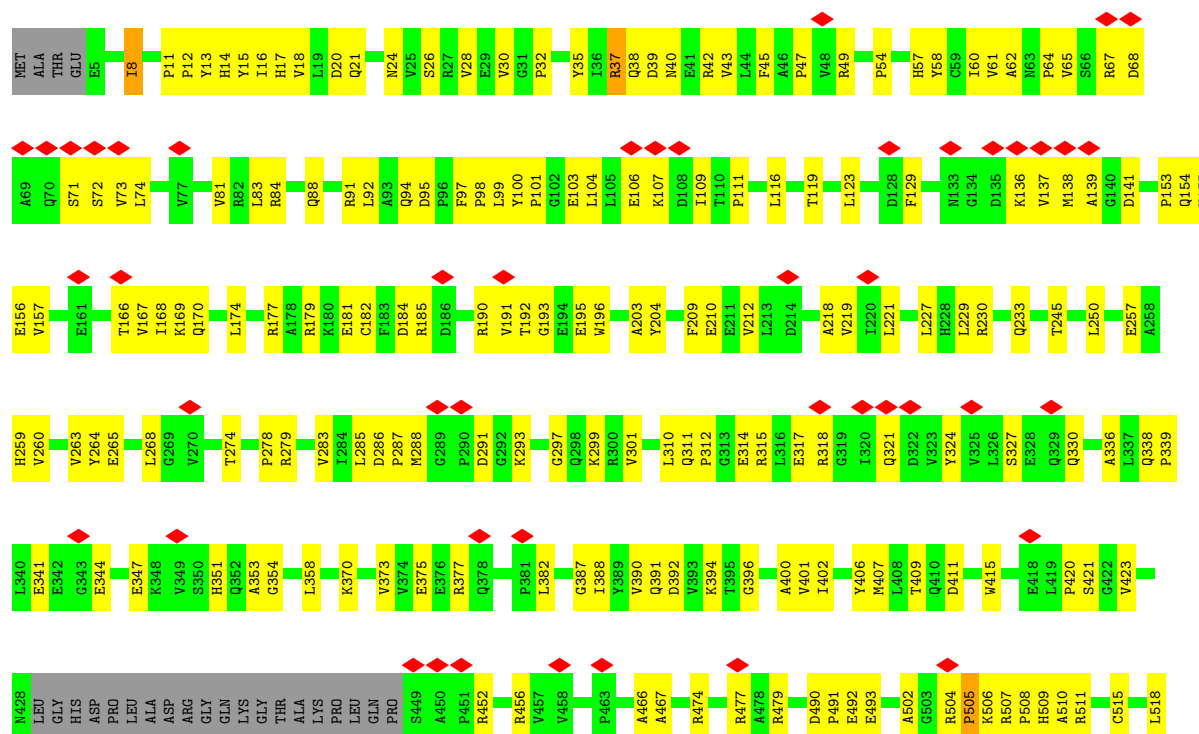


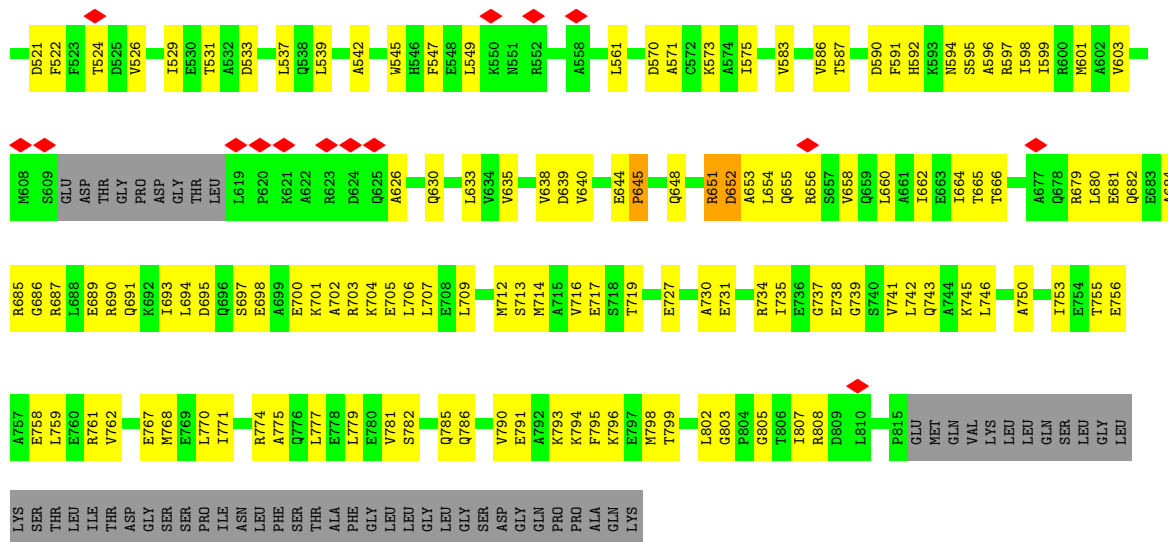
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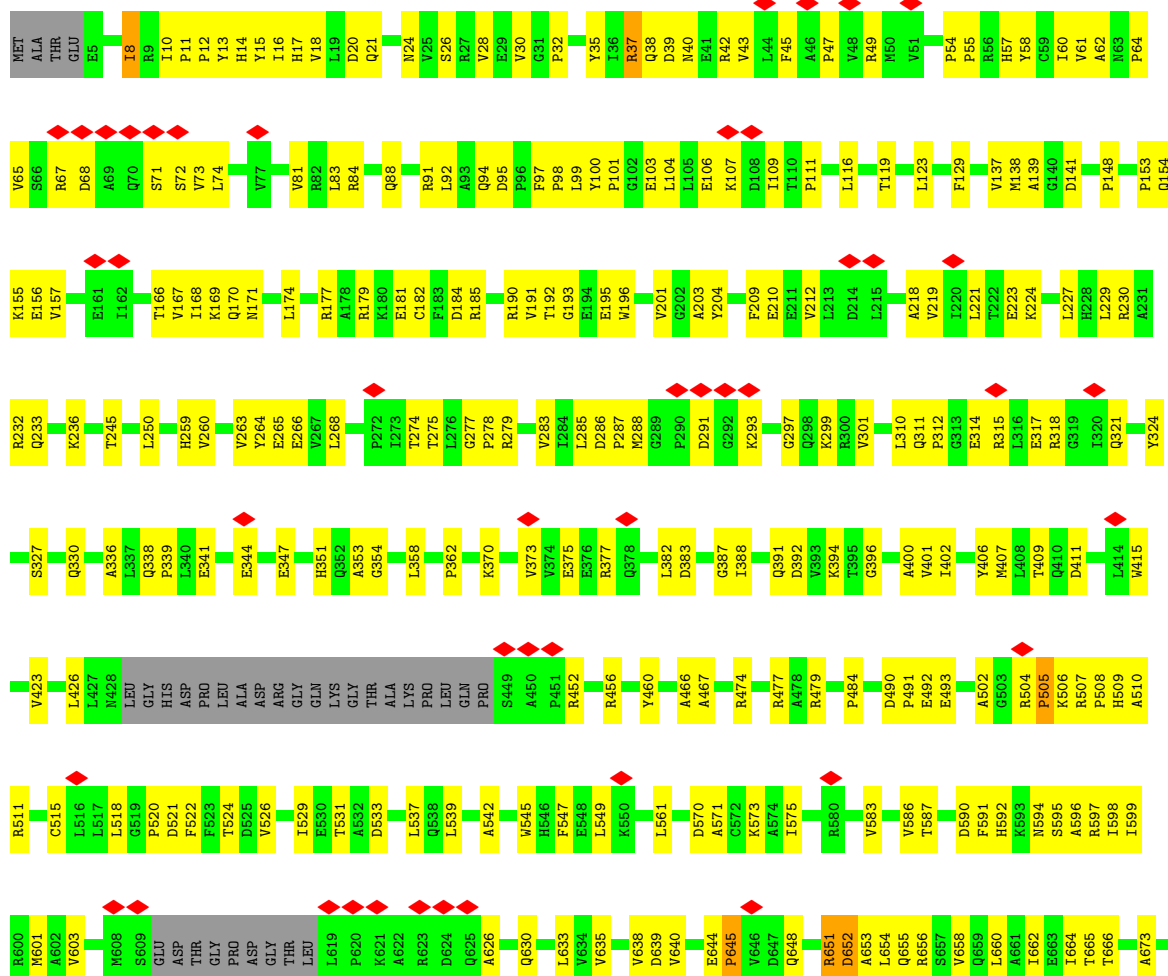


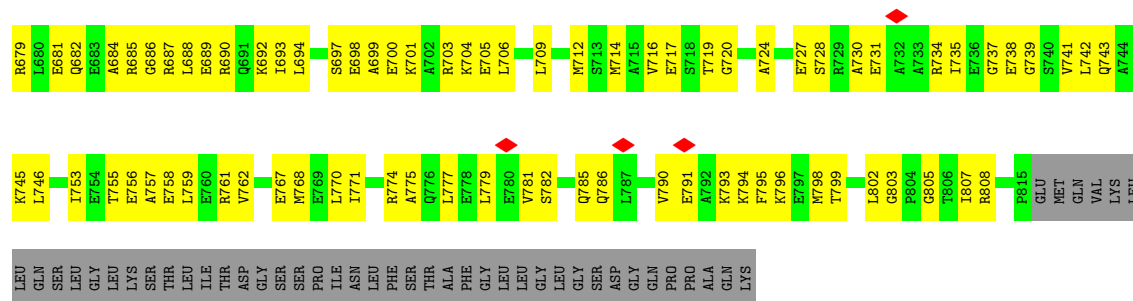
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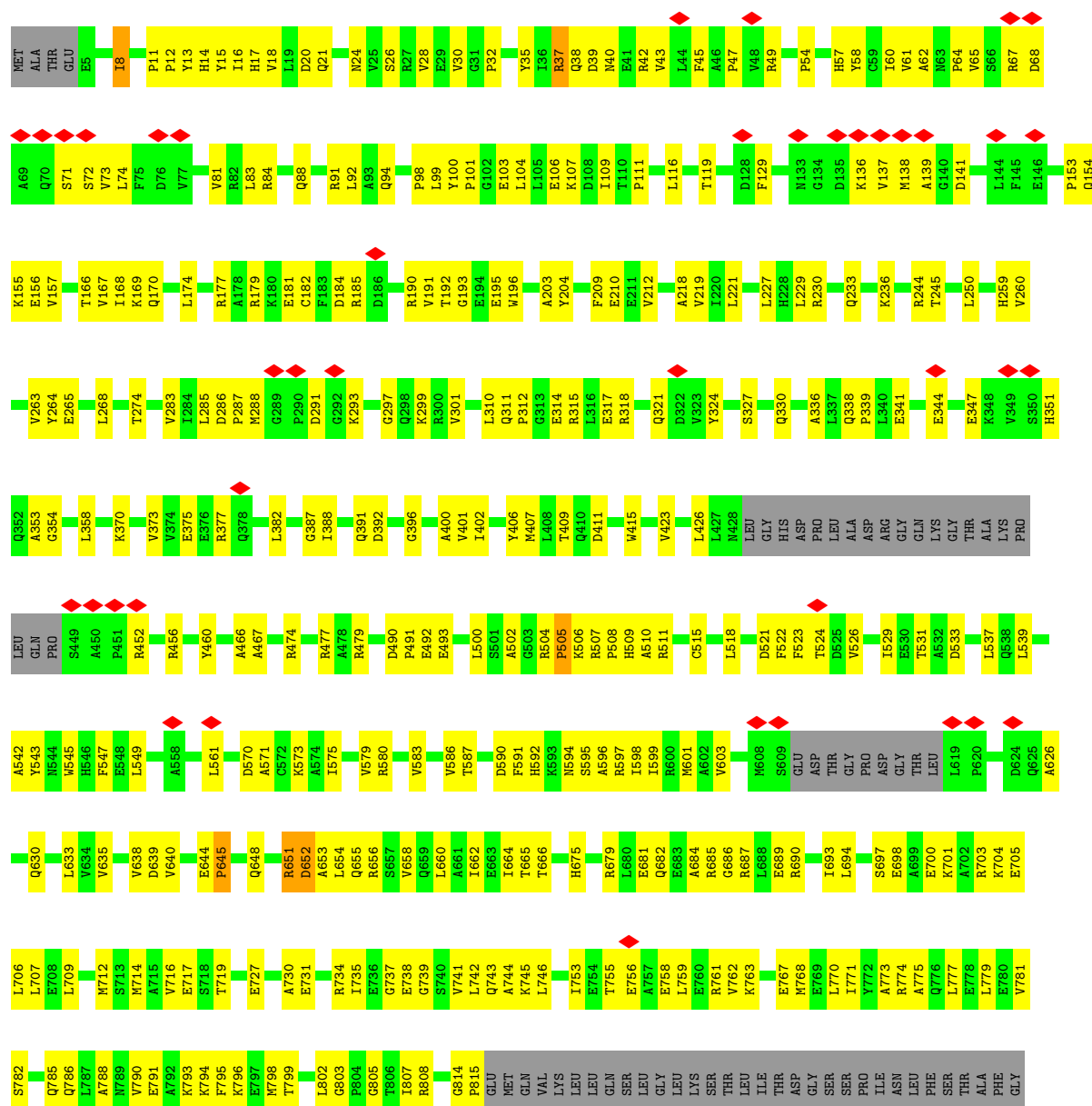


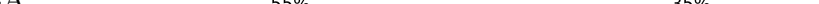
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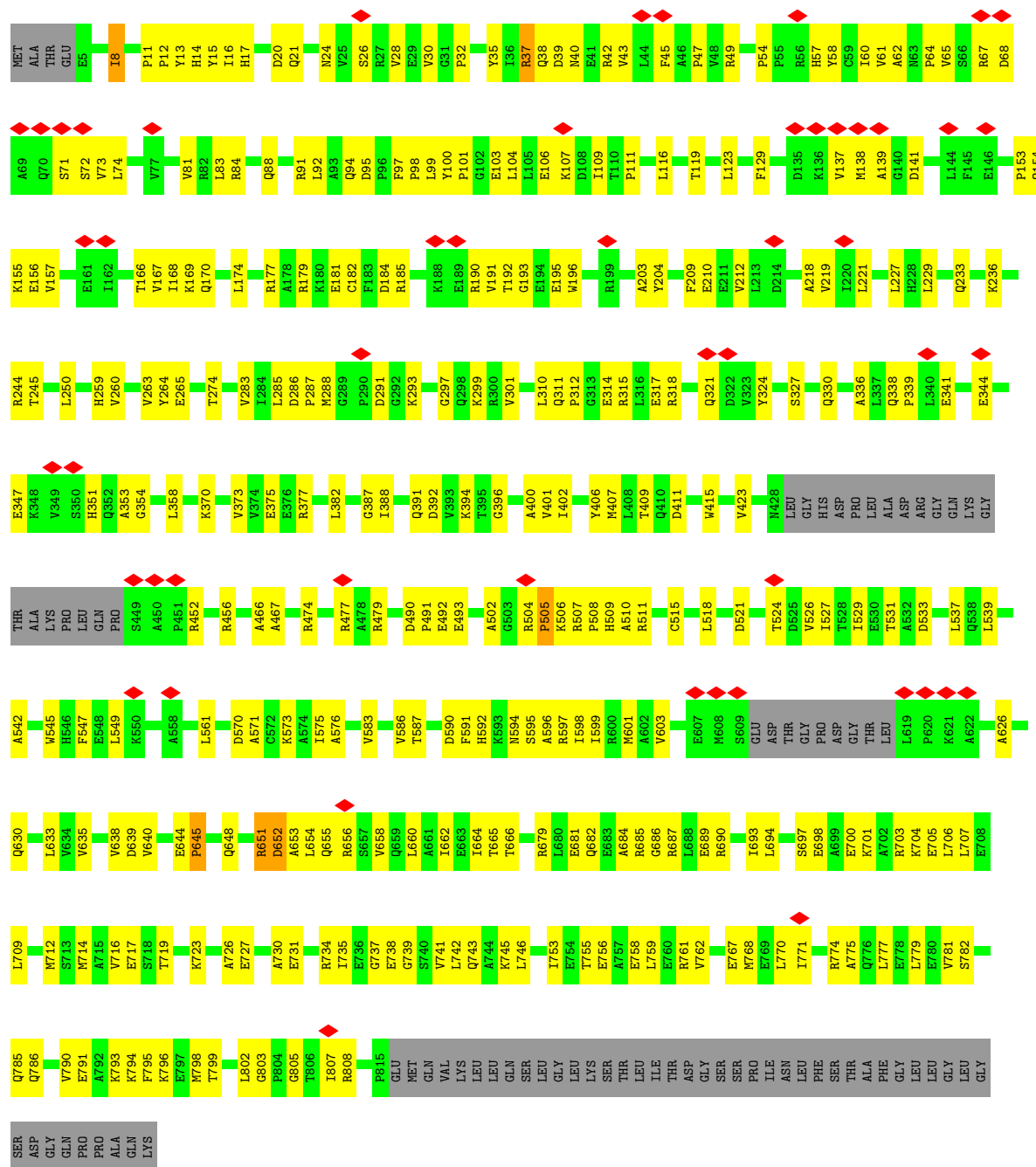




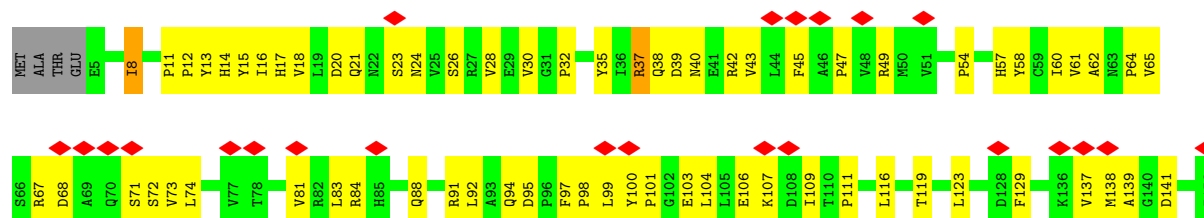
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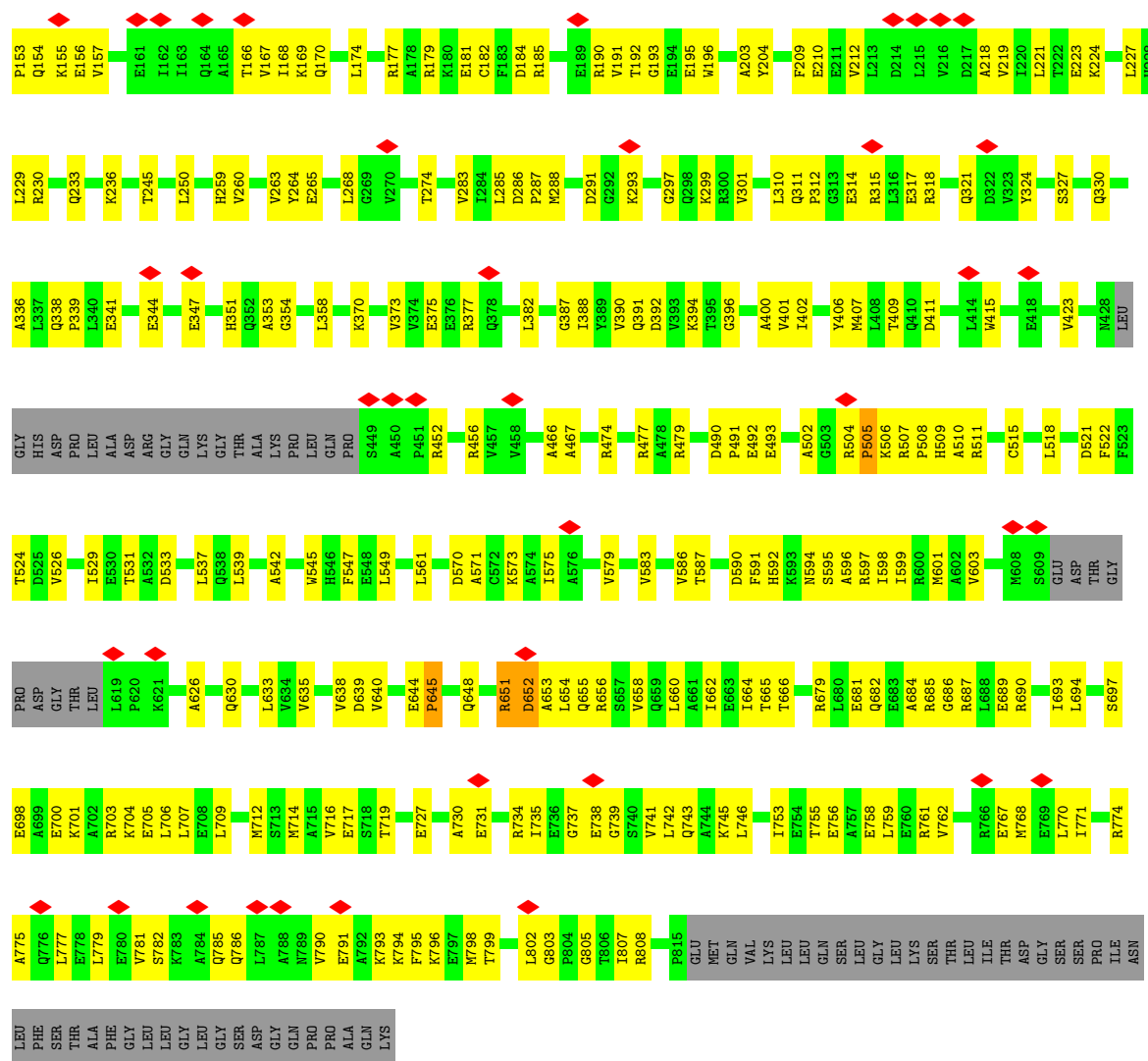


Chain LA: 

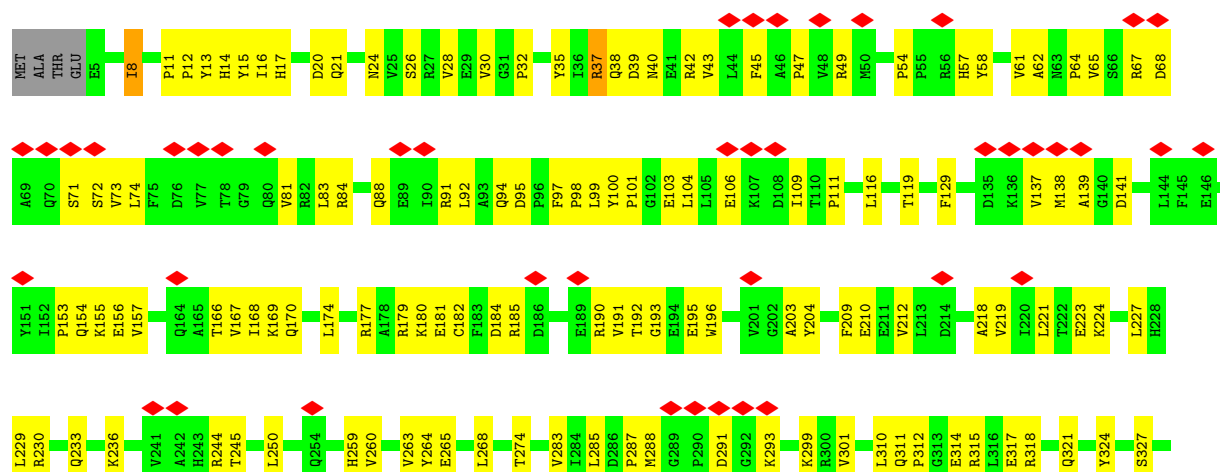


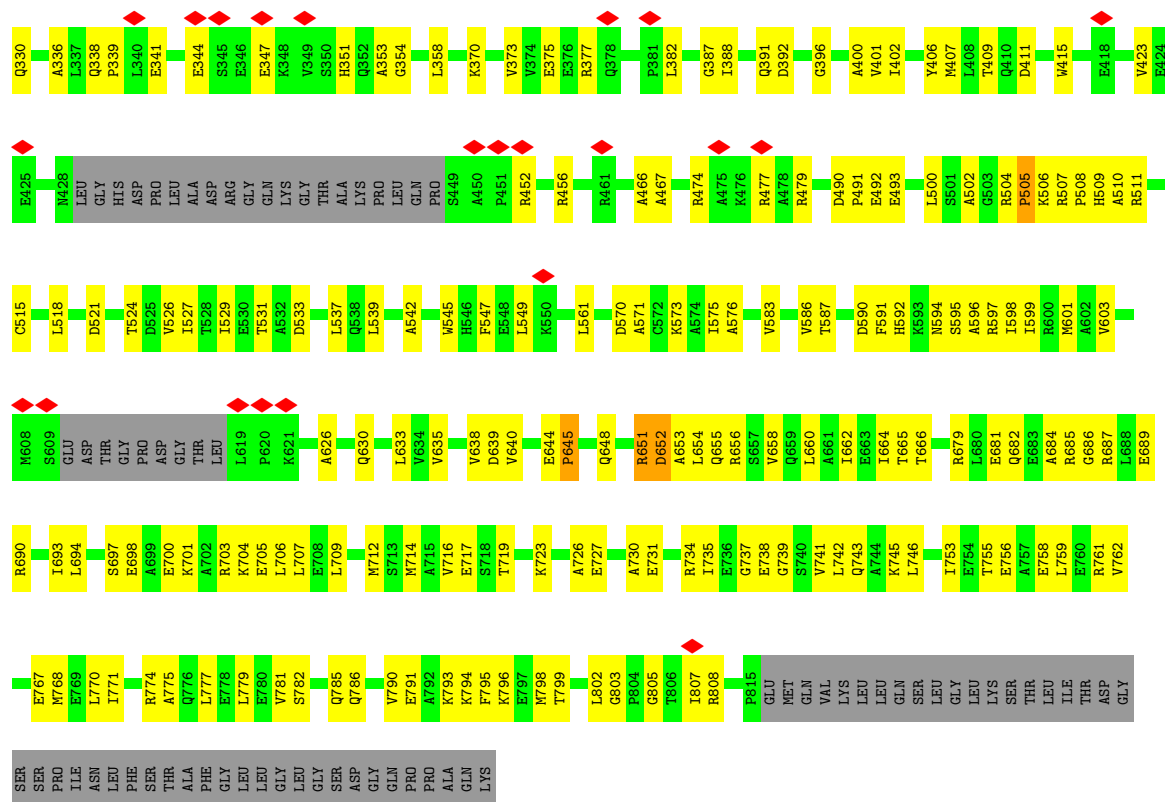
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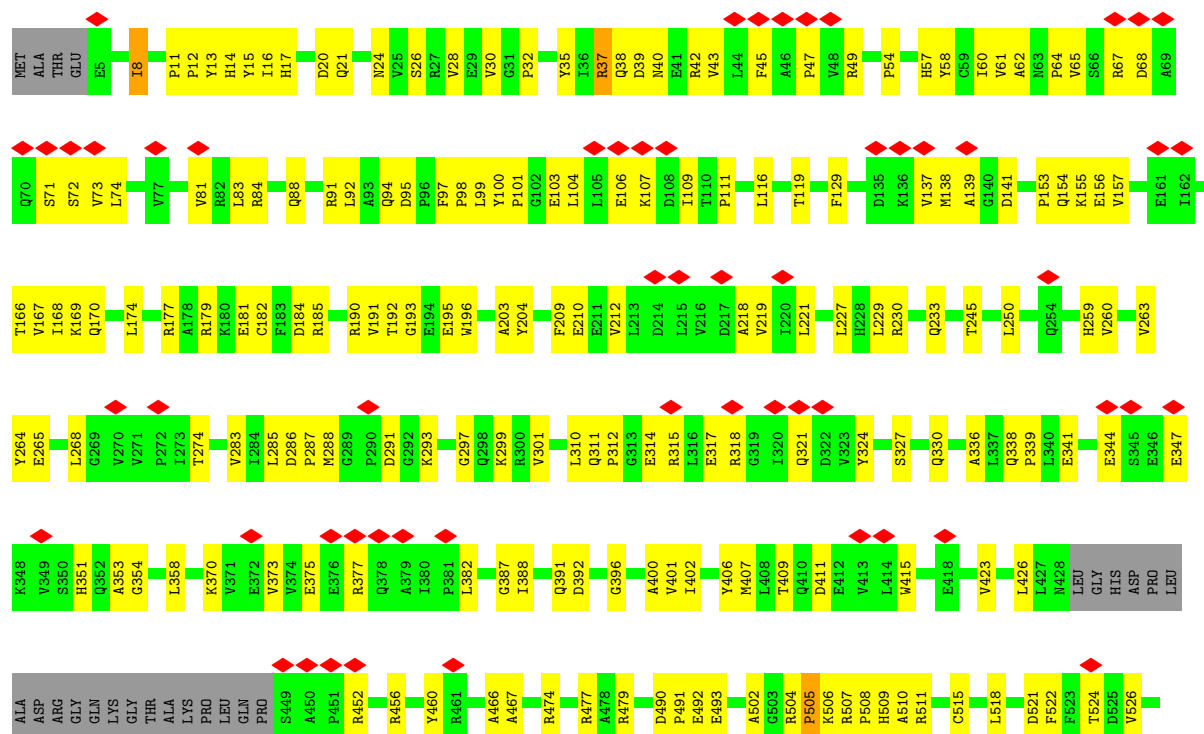


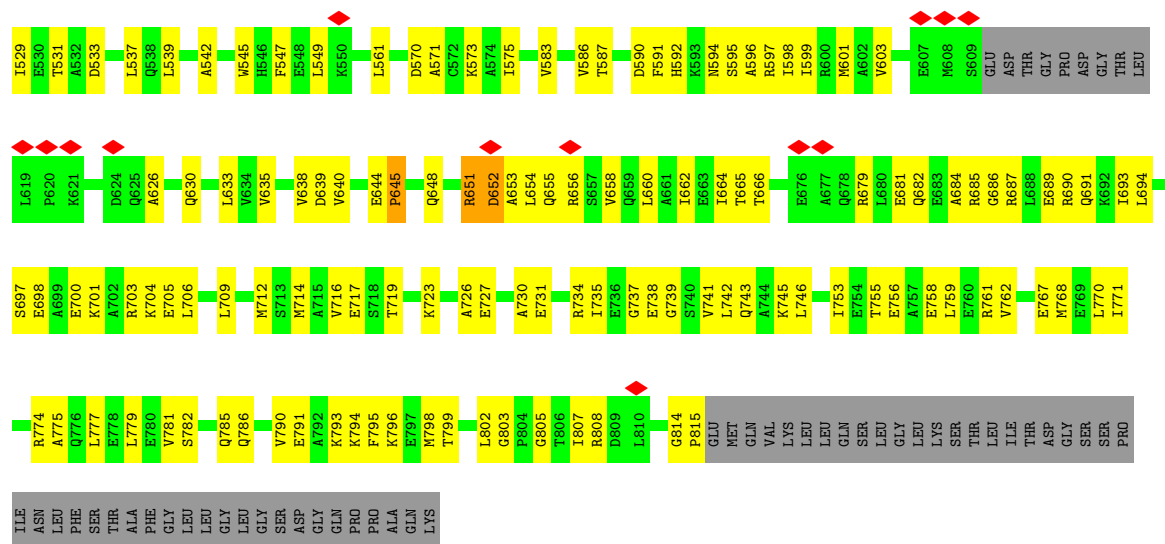
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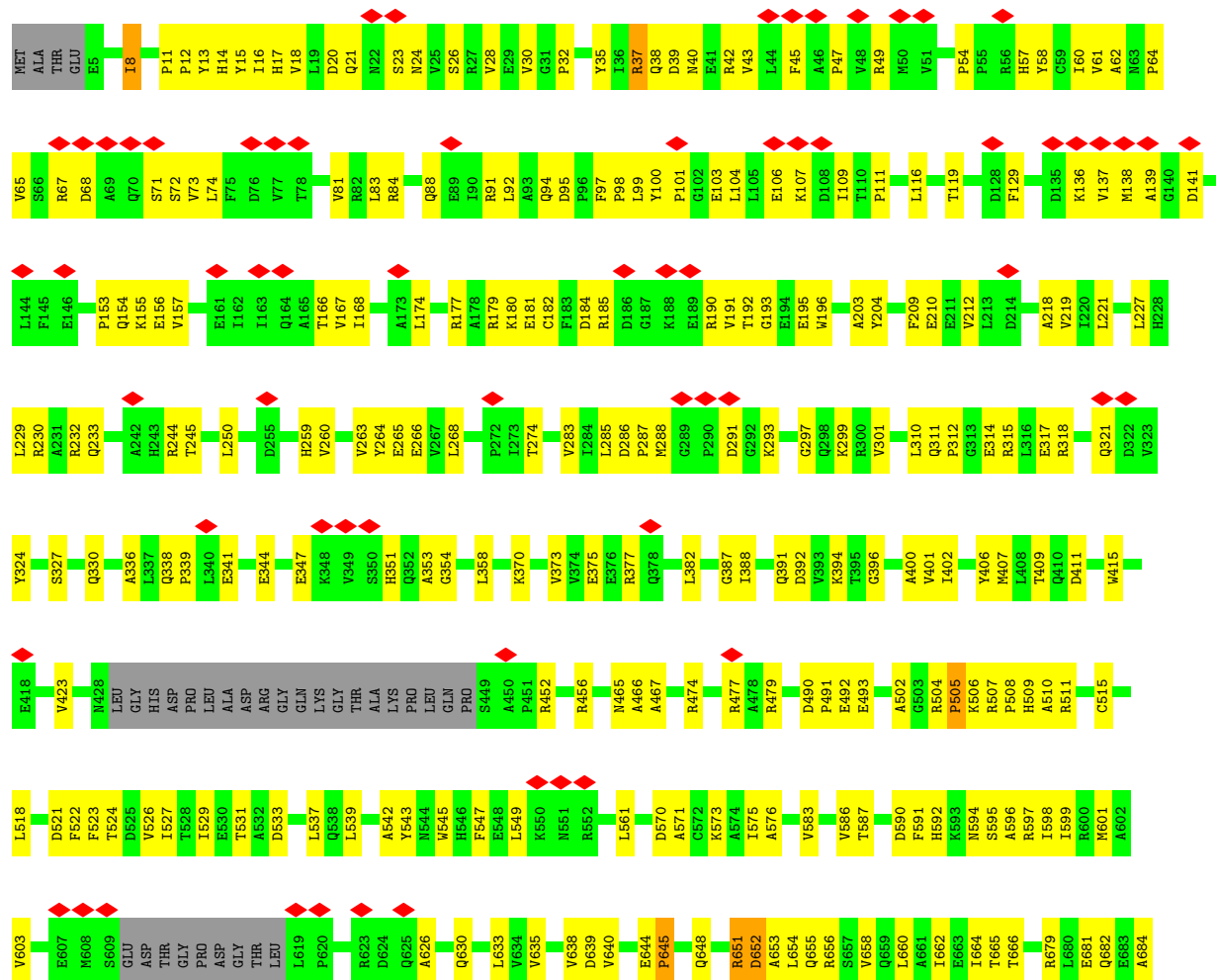


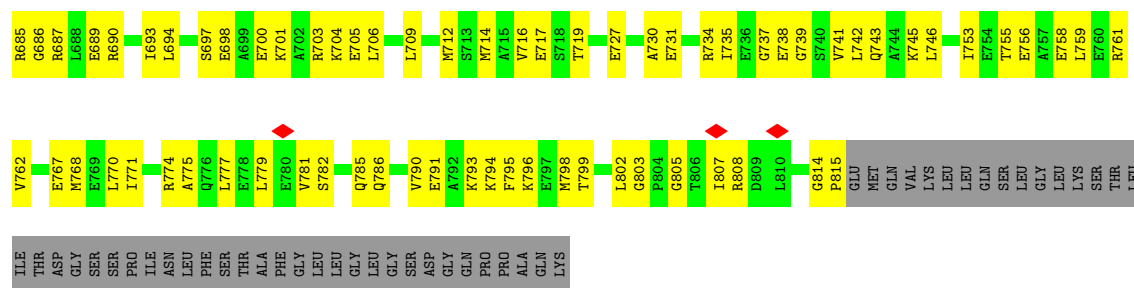
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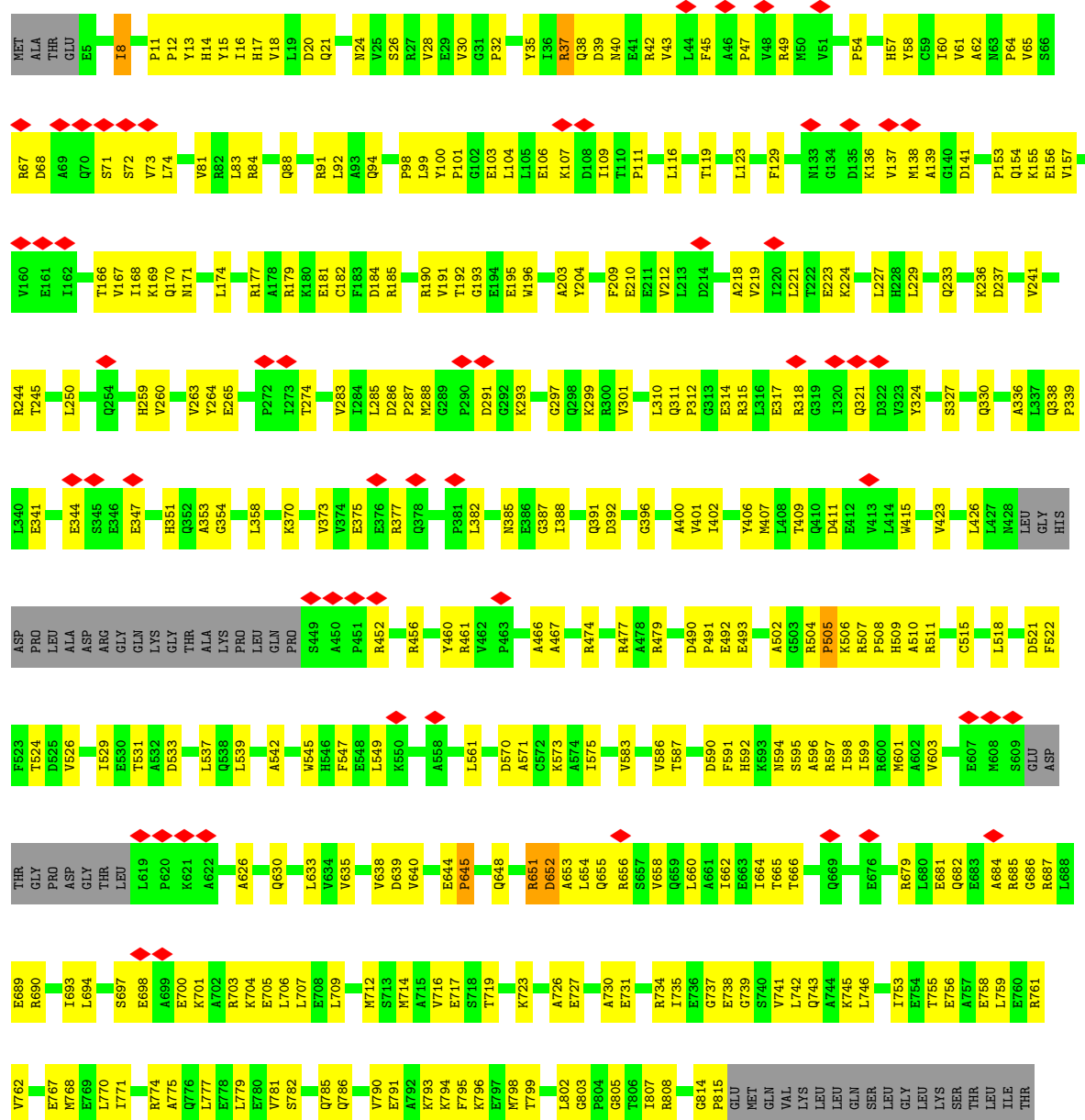


• Molecule 1: Major vault protein





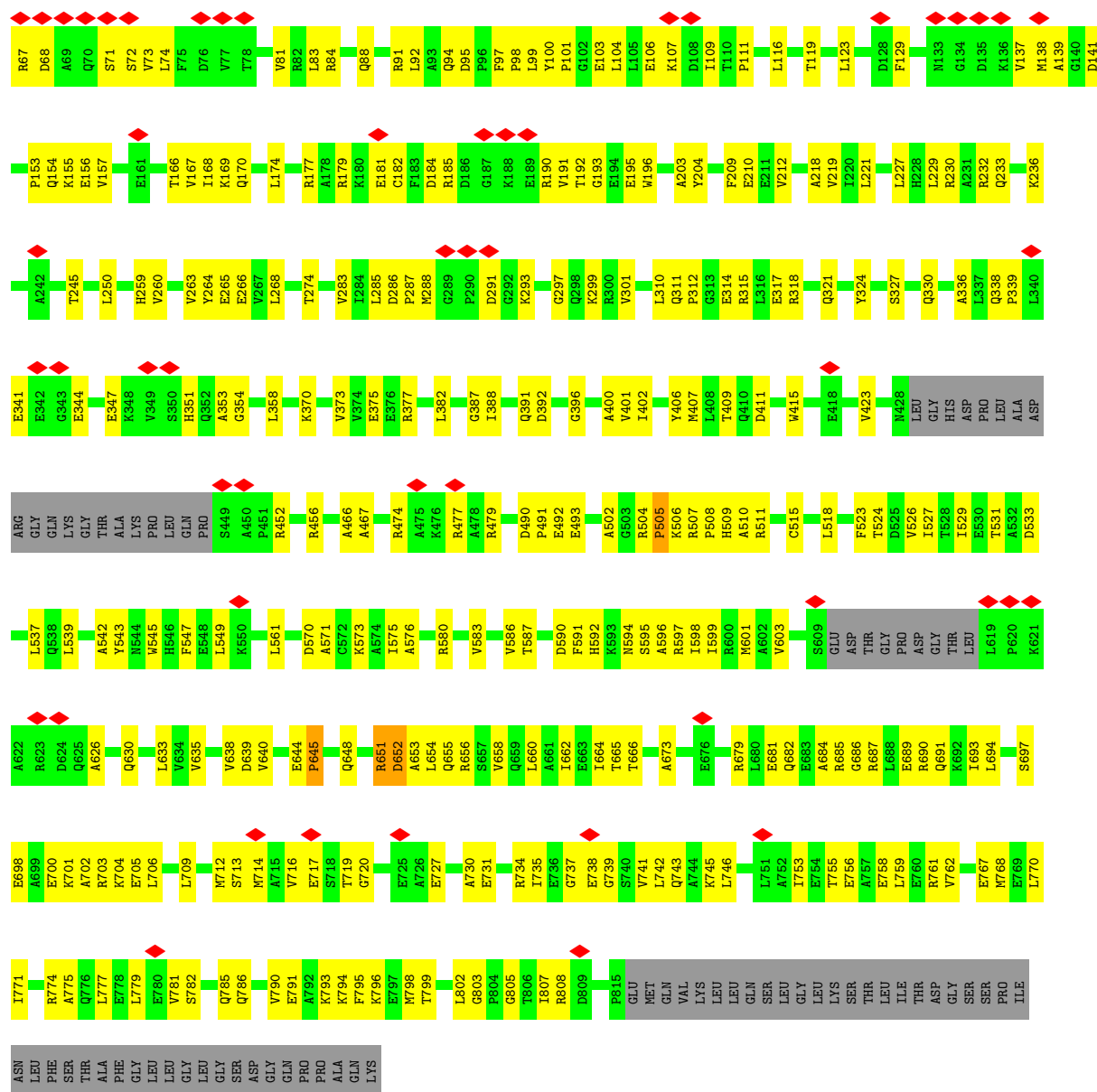
Molecule 1: Major vault protein



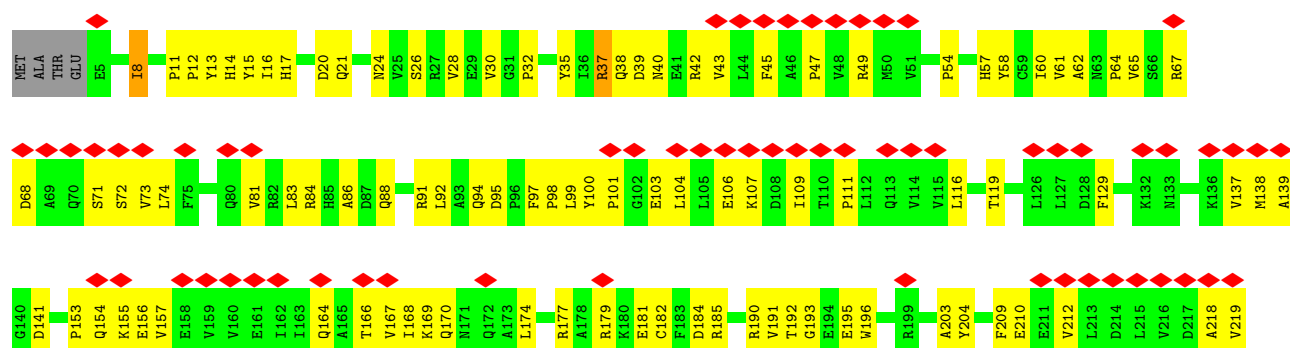
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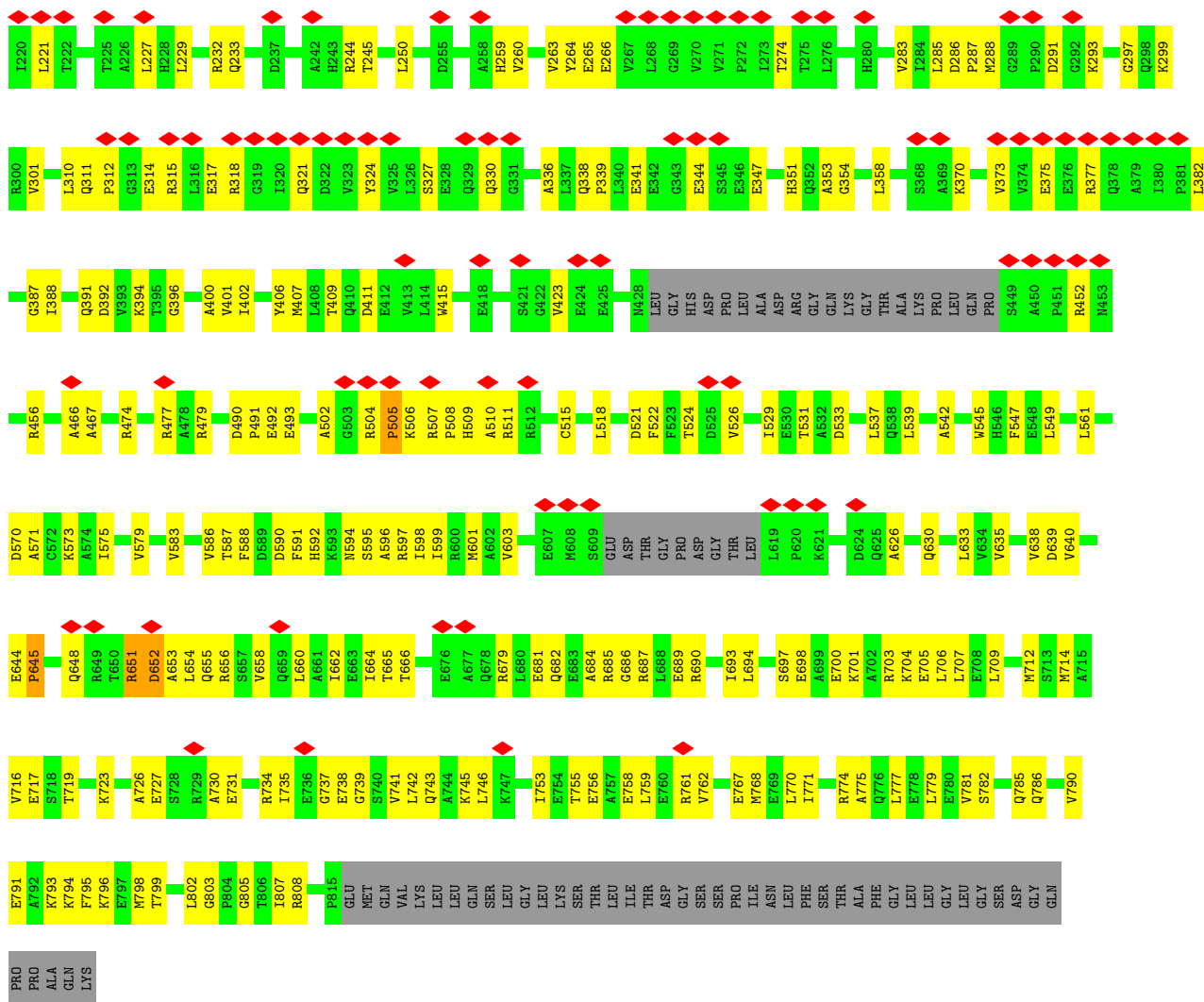




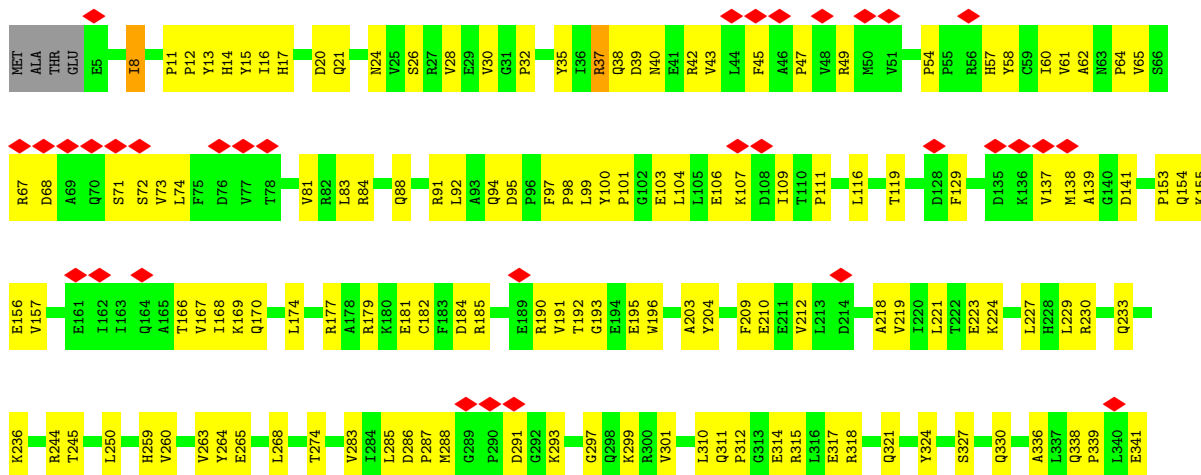


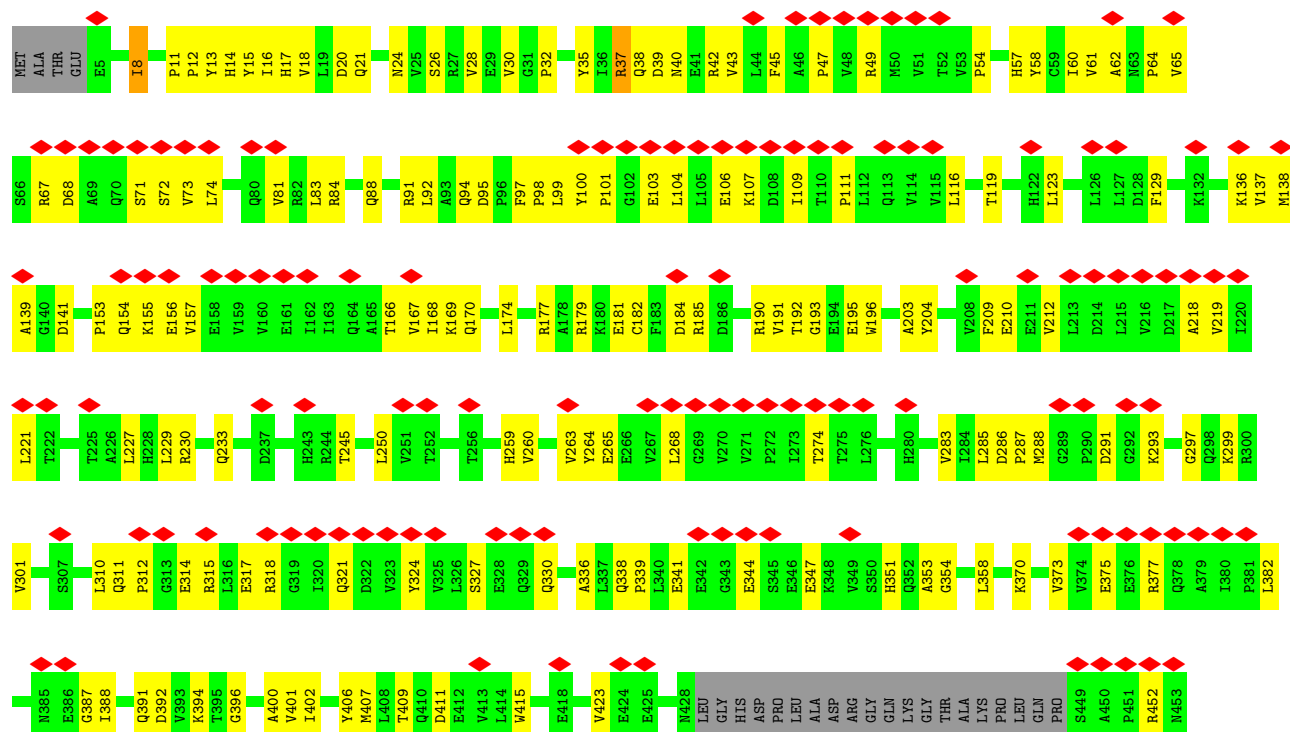
• Molecule 1: Major vault protein

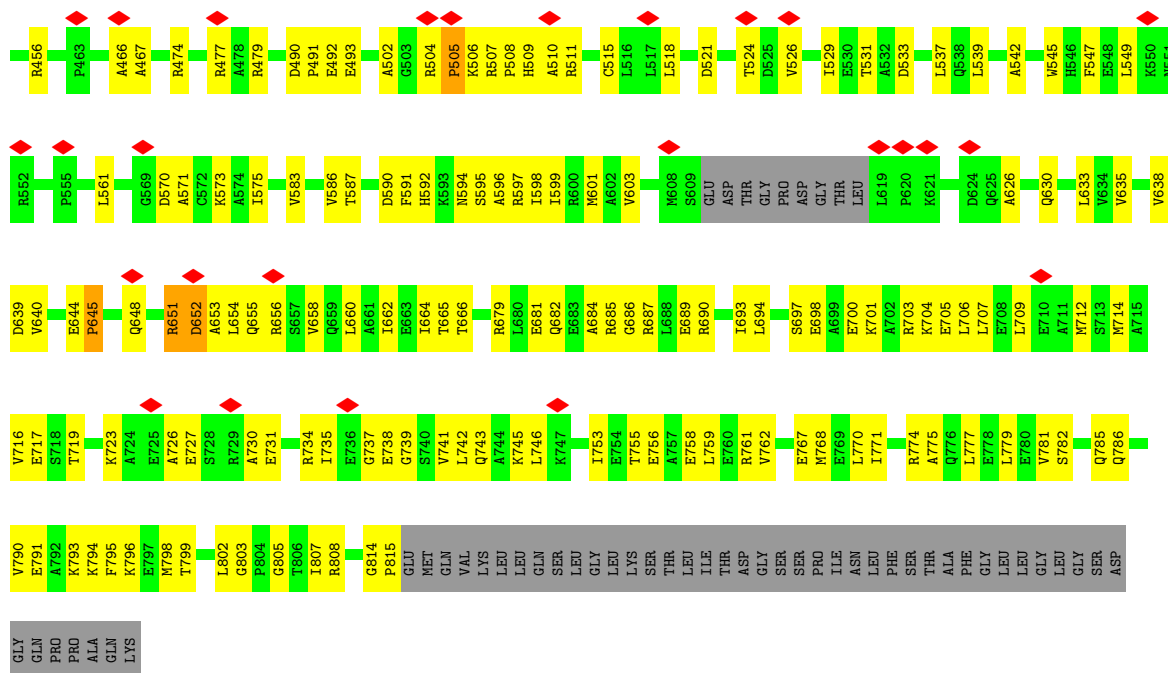




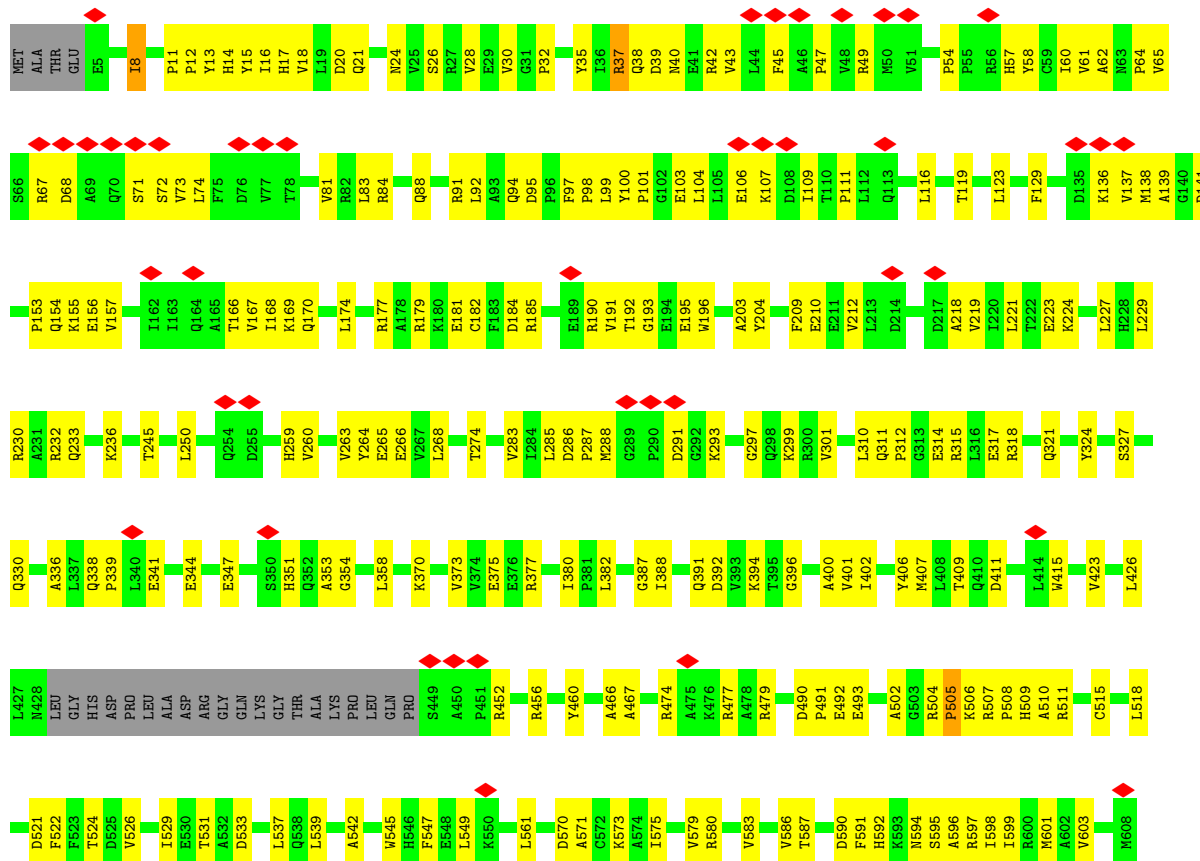
• Molecule 1: Major vault protein

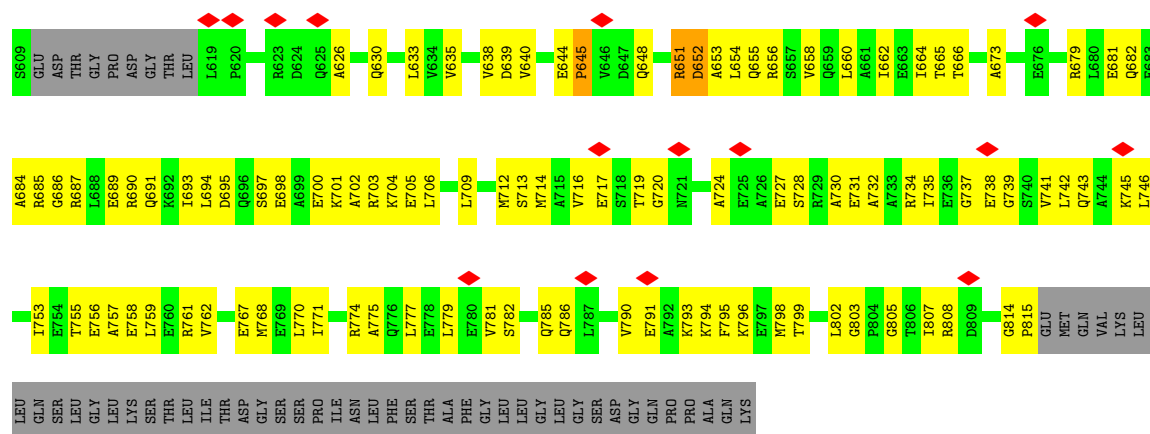




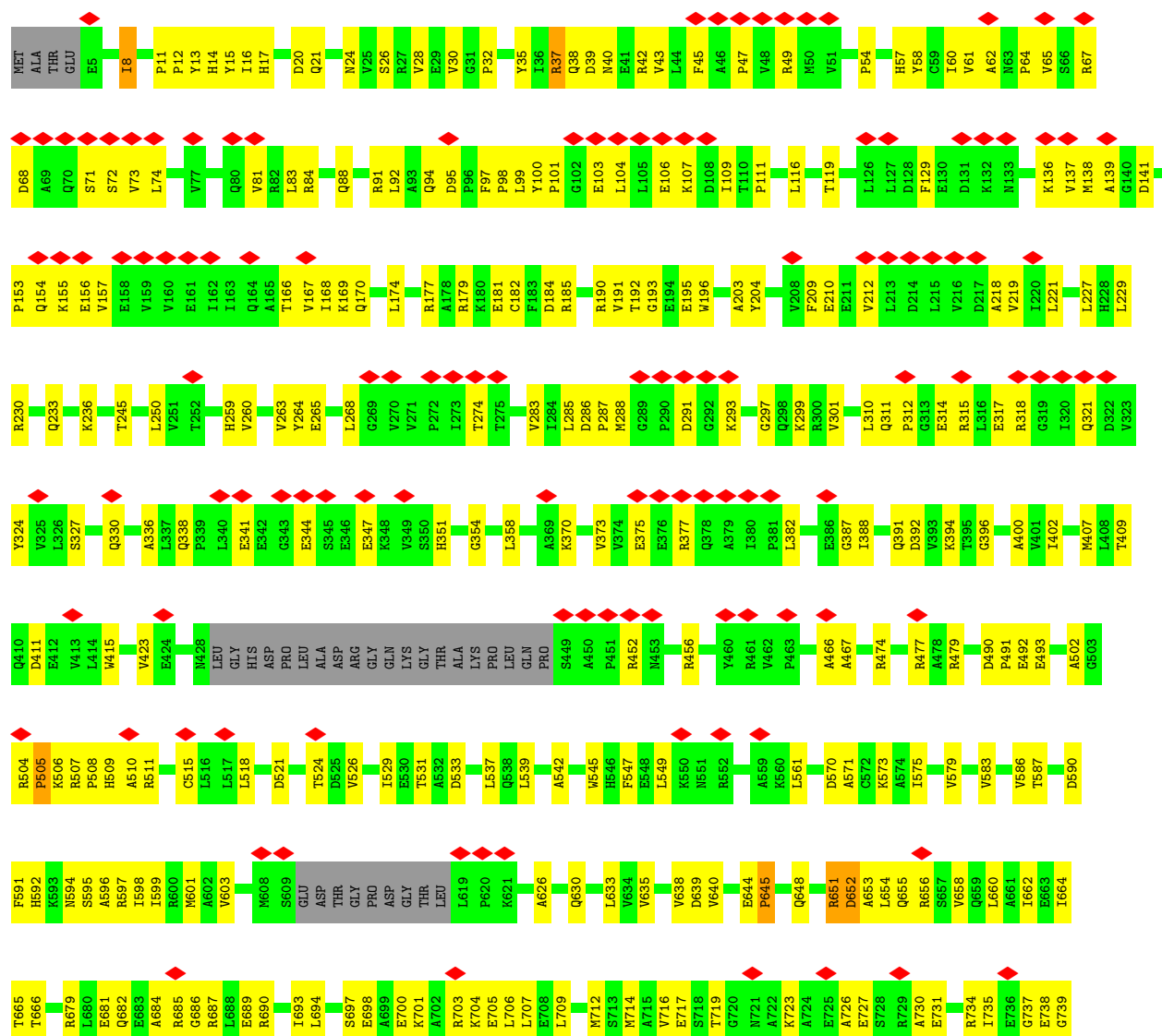


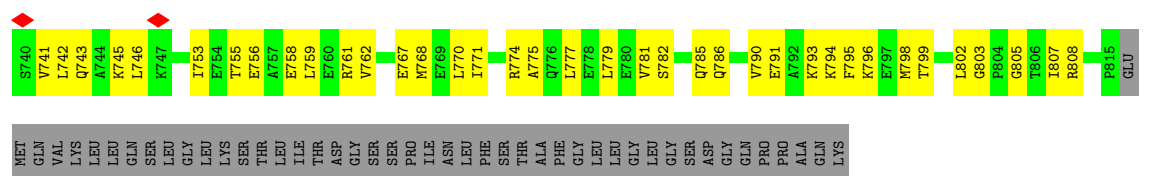
• Molecule 1: Major vault protein



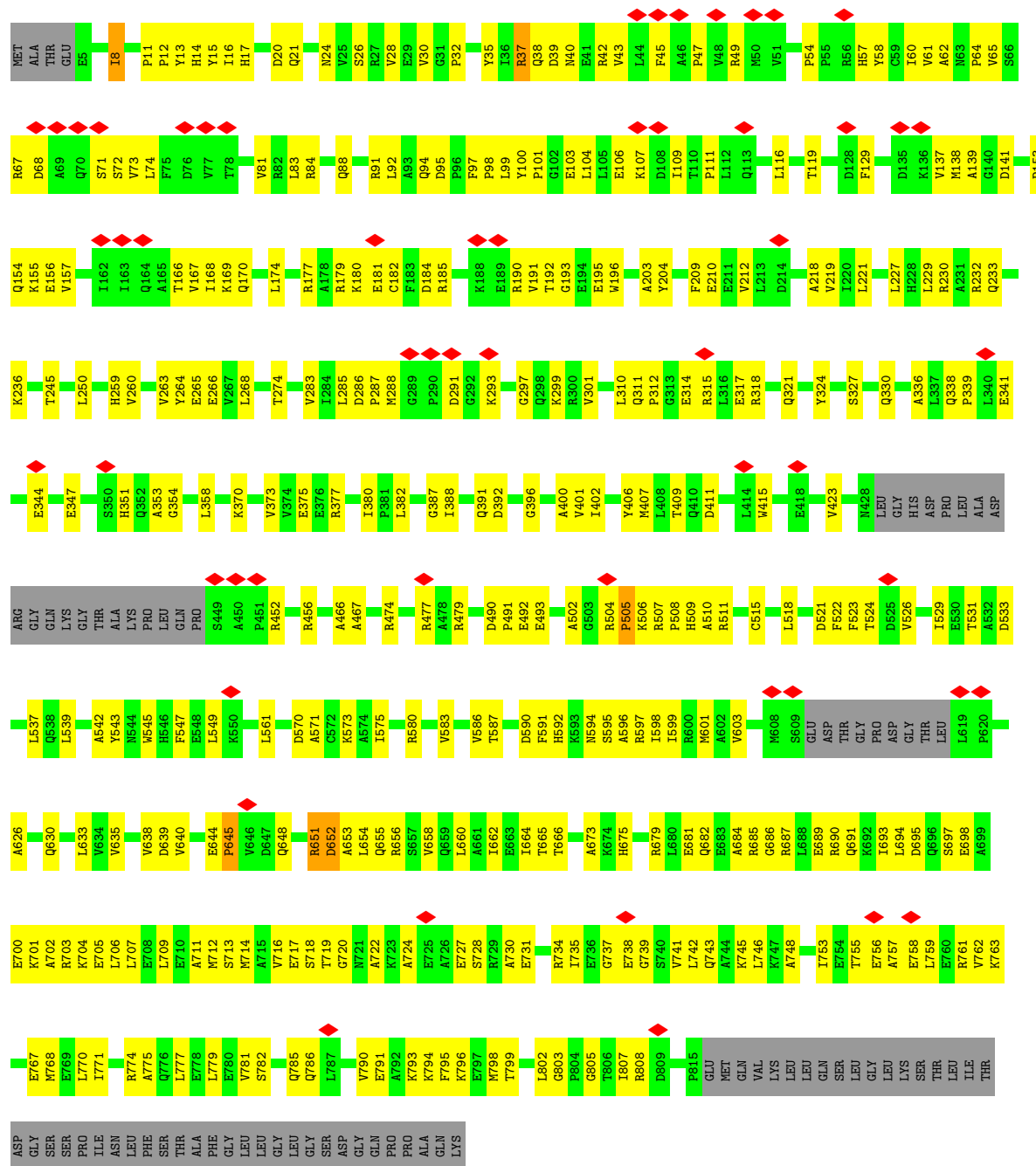


• Molecule 1: Major vault protein





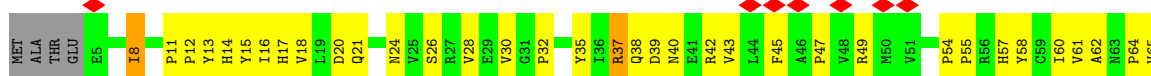
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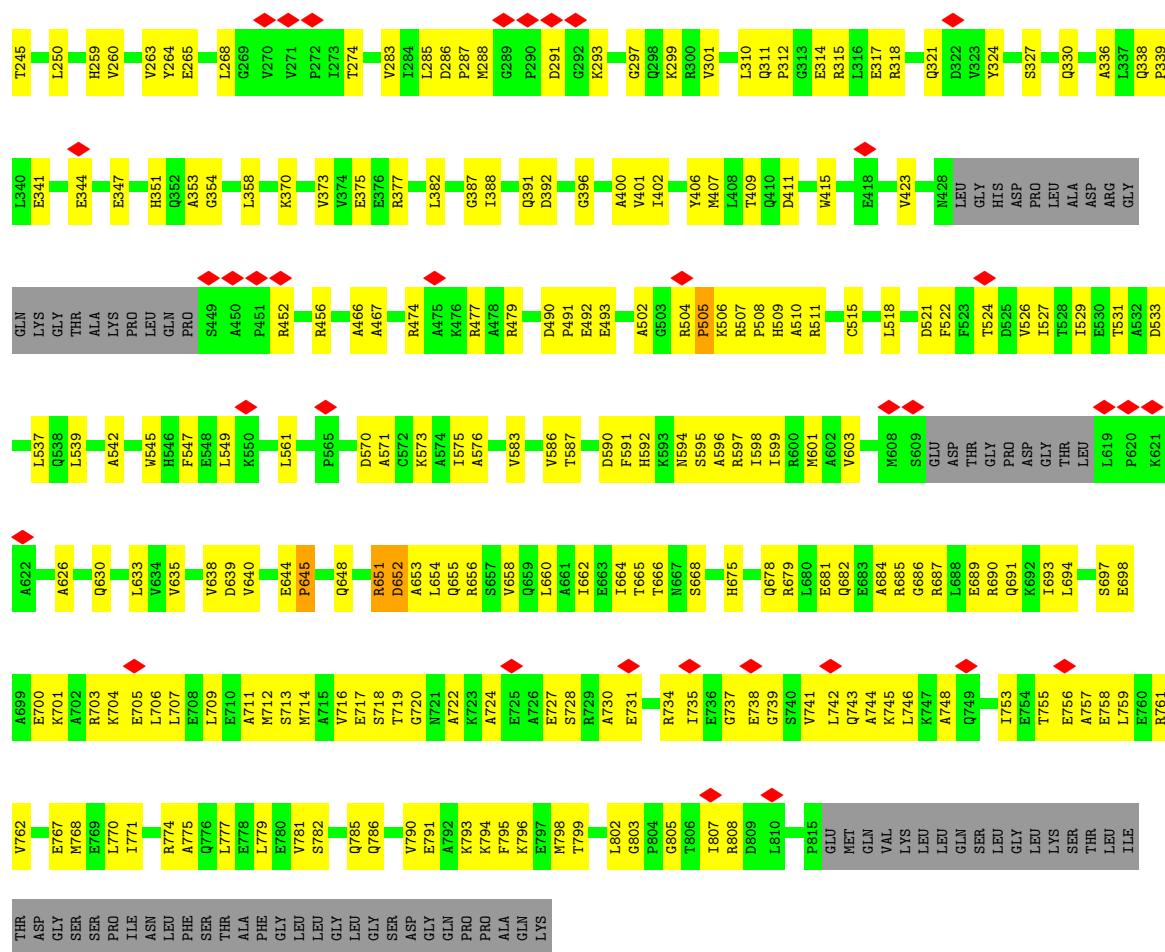


• Molecule 1: Major vault protein

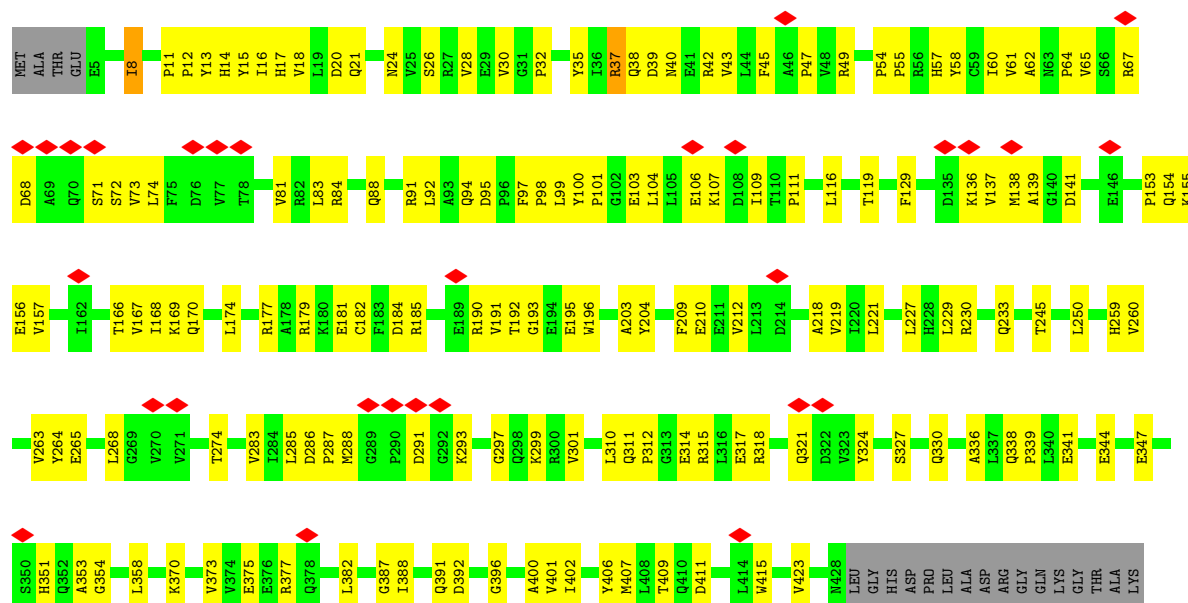


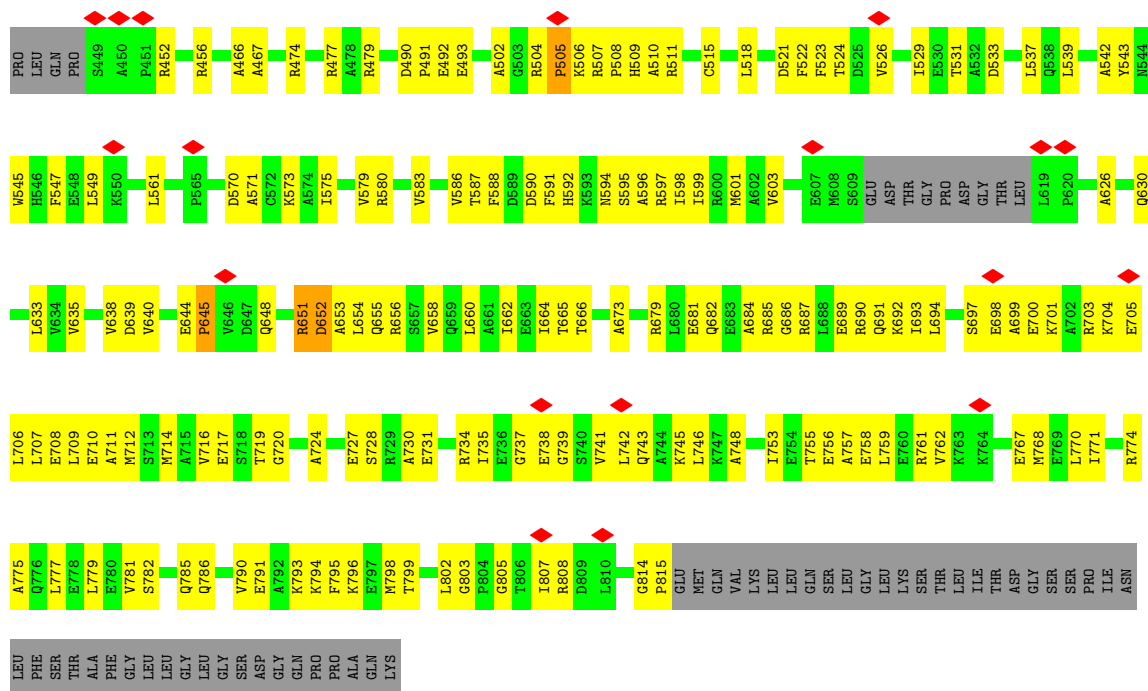
• Molecule 1: Major vault protein



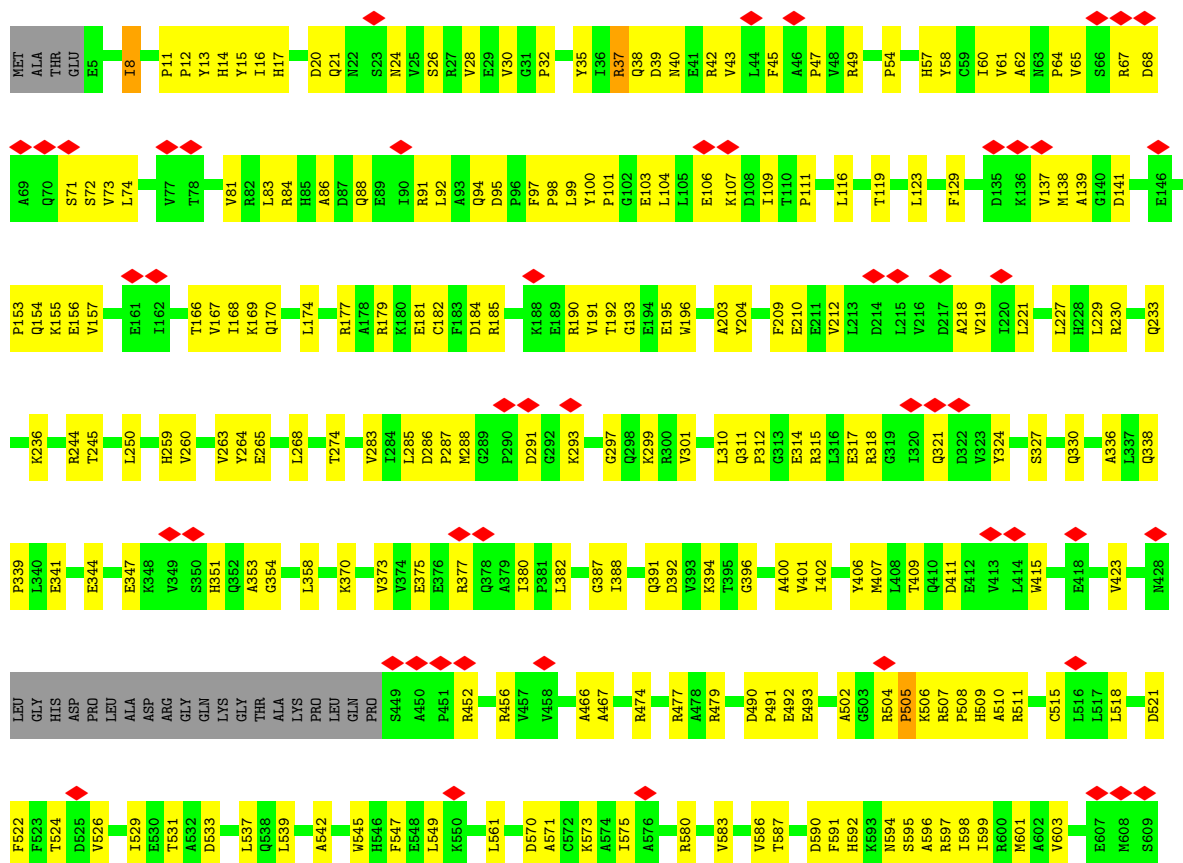


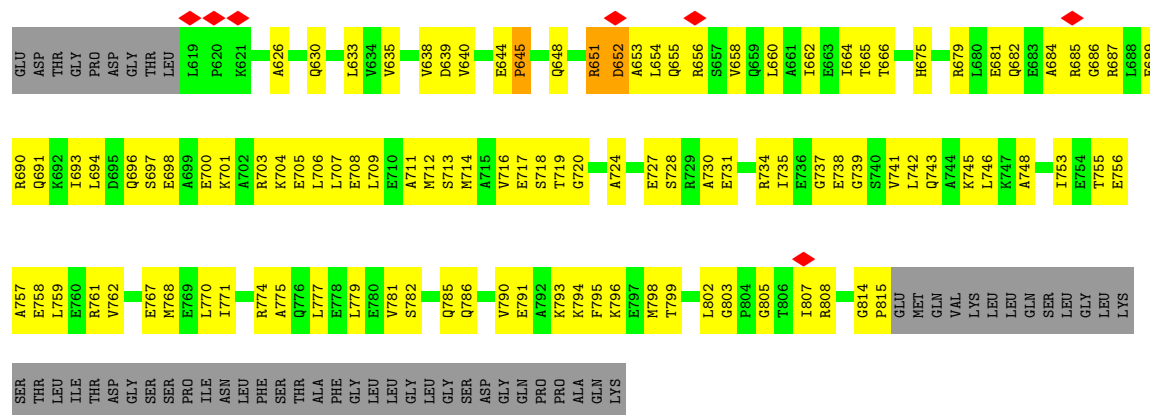
• Molecule 1: Major vault protein



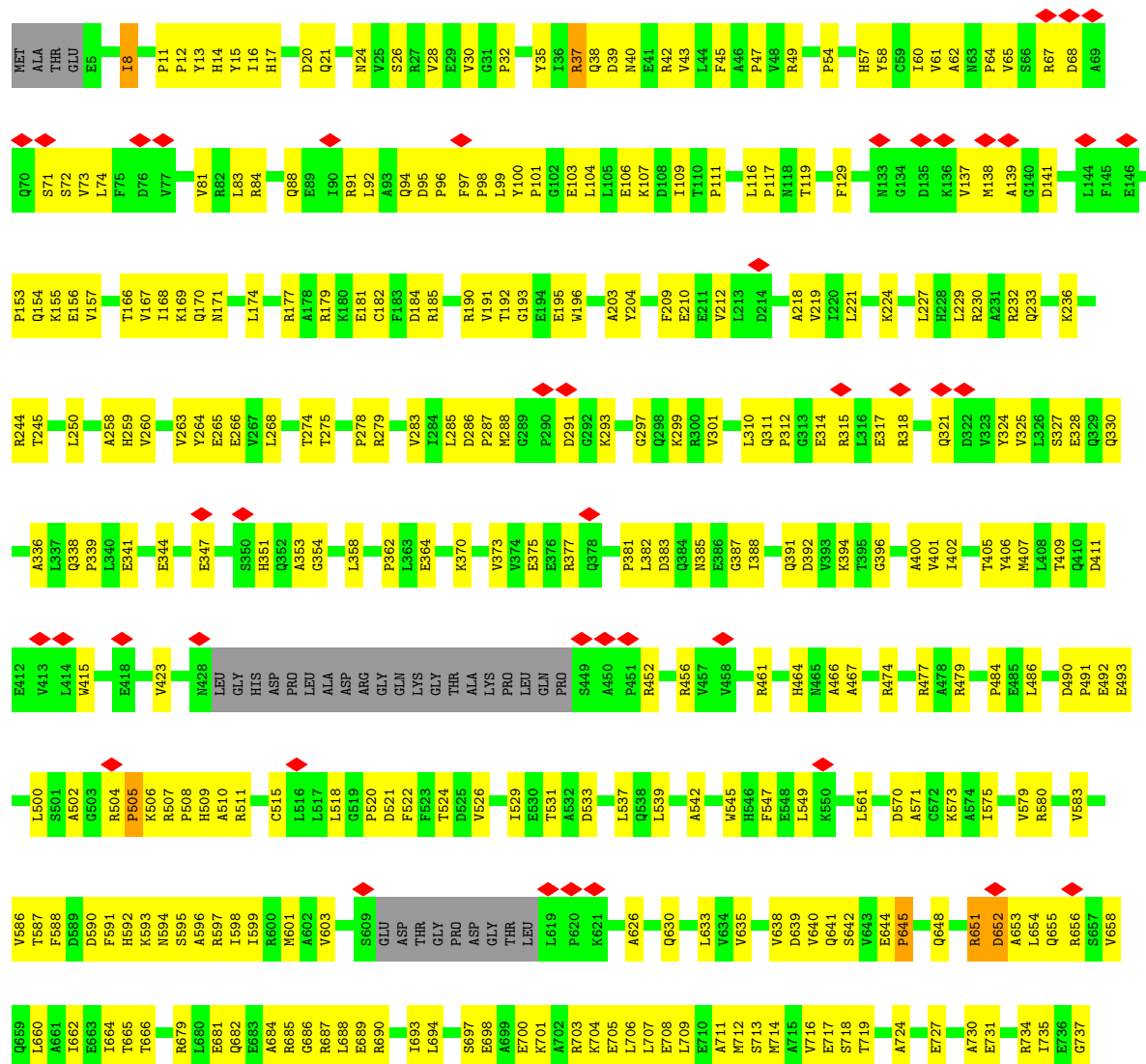


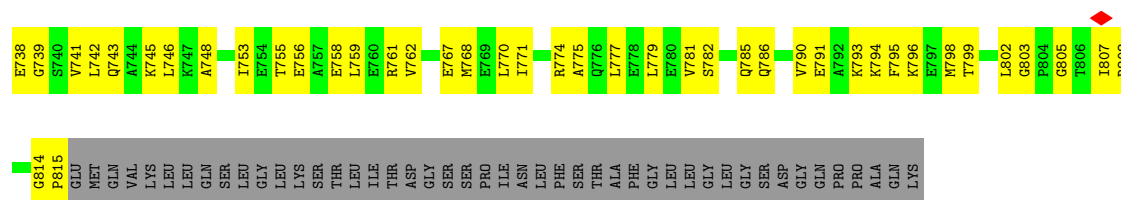
• Molecule 1: Major vault protein



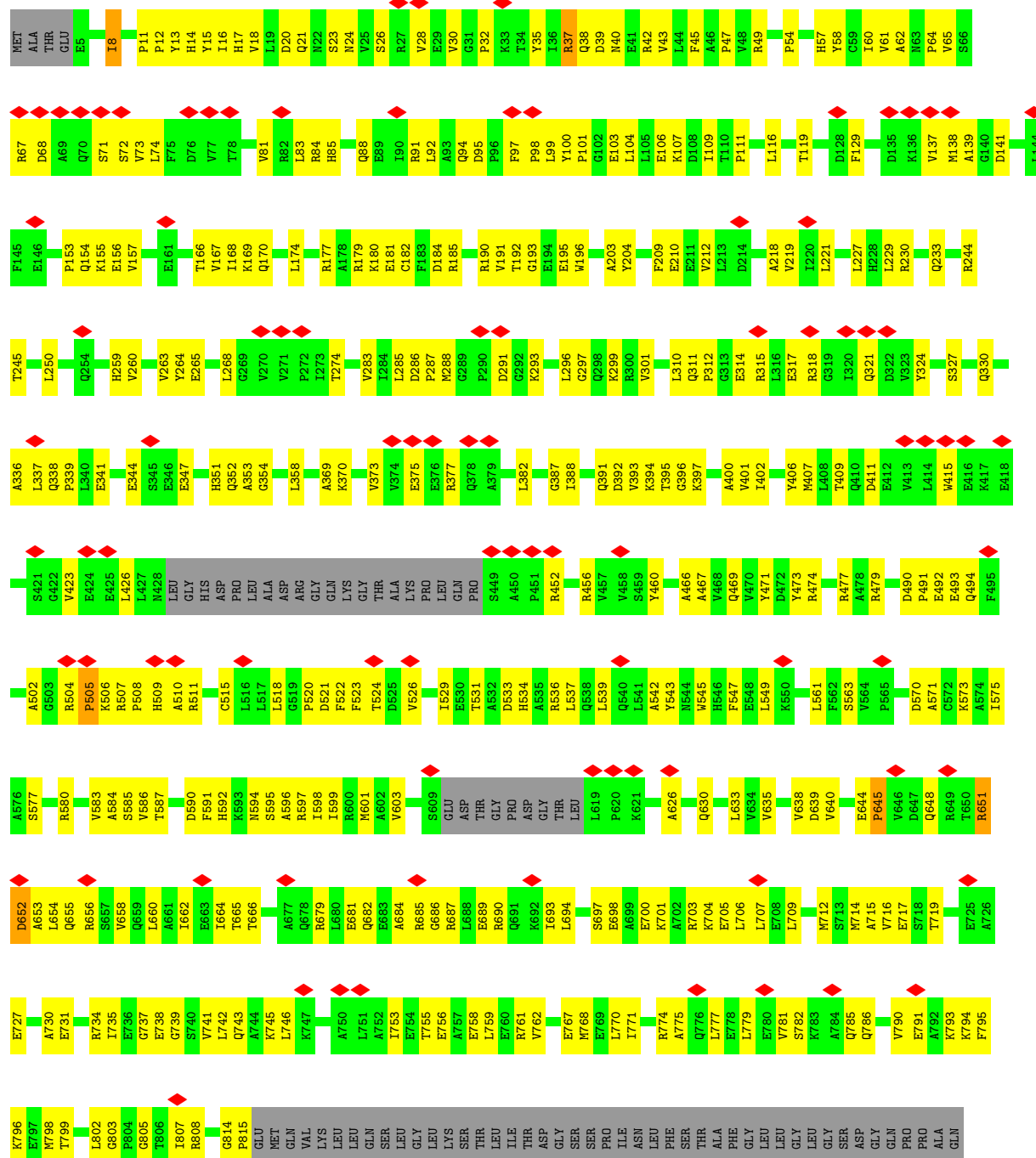


• Molecule 1: Major vault protein



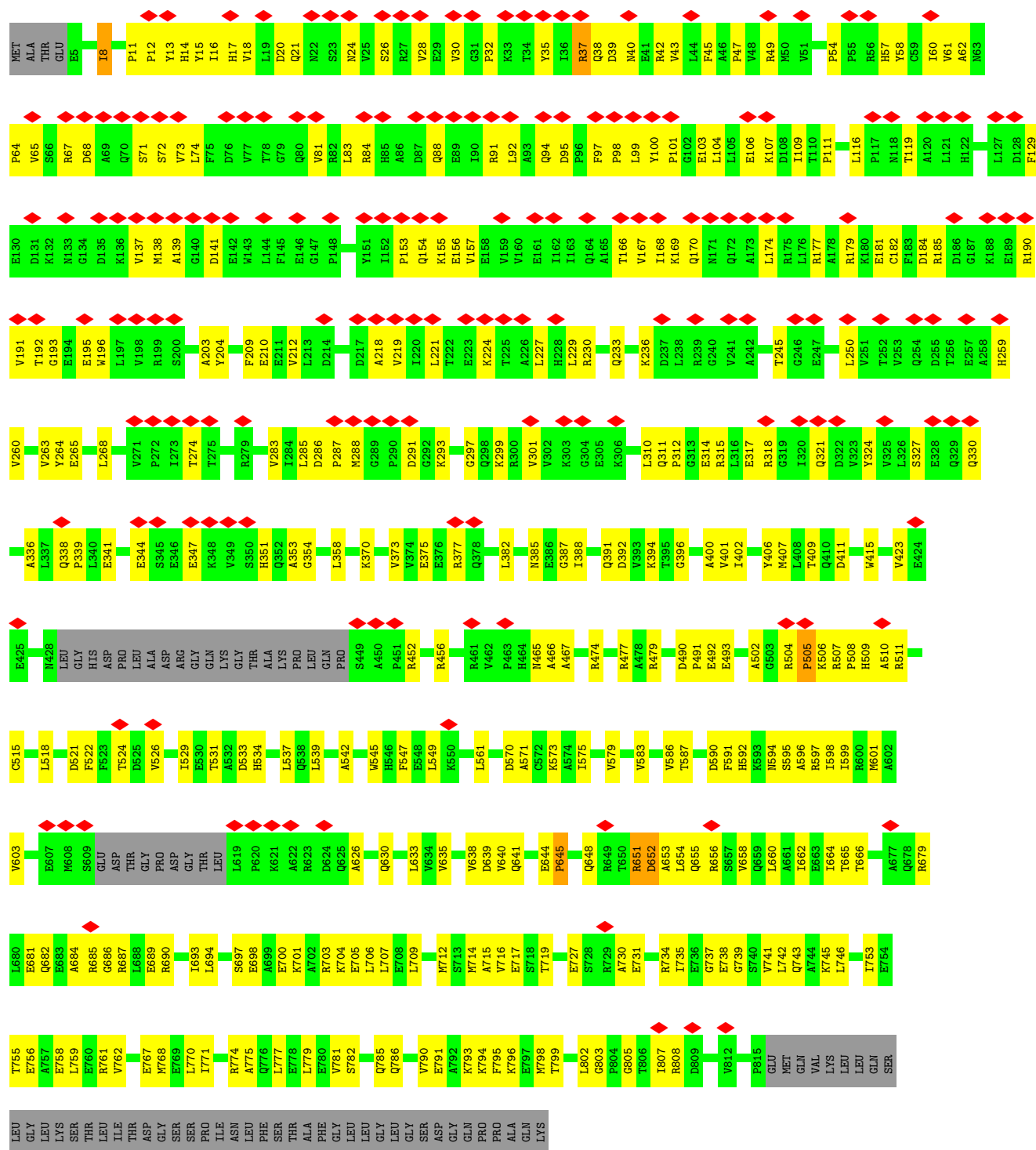


• Molecule 1: Major vault protein

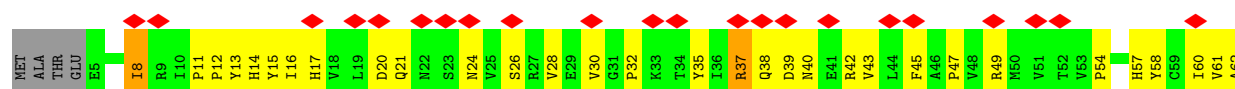


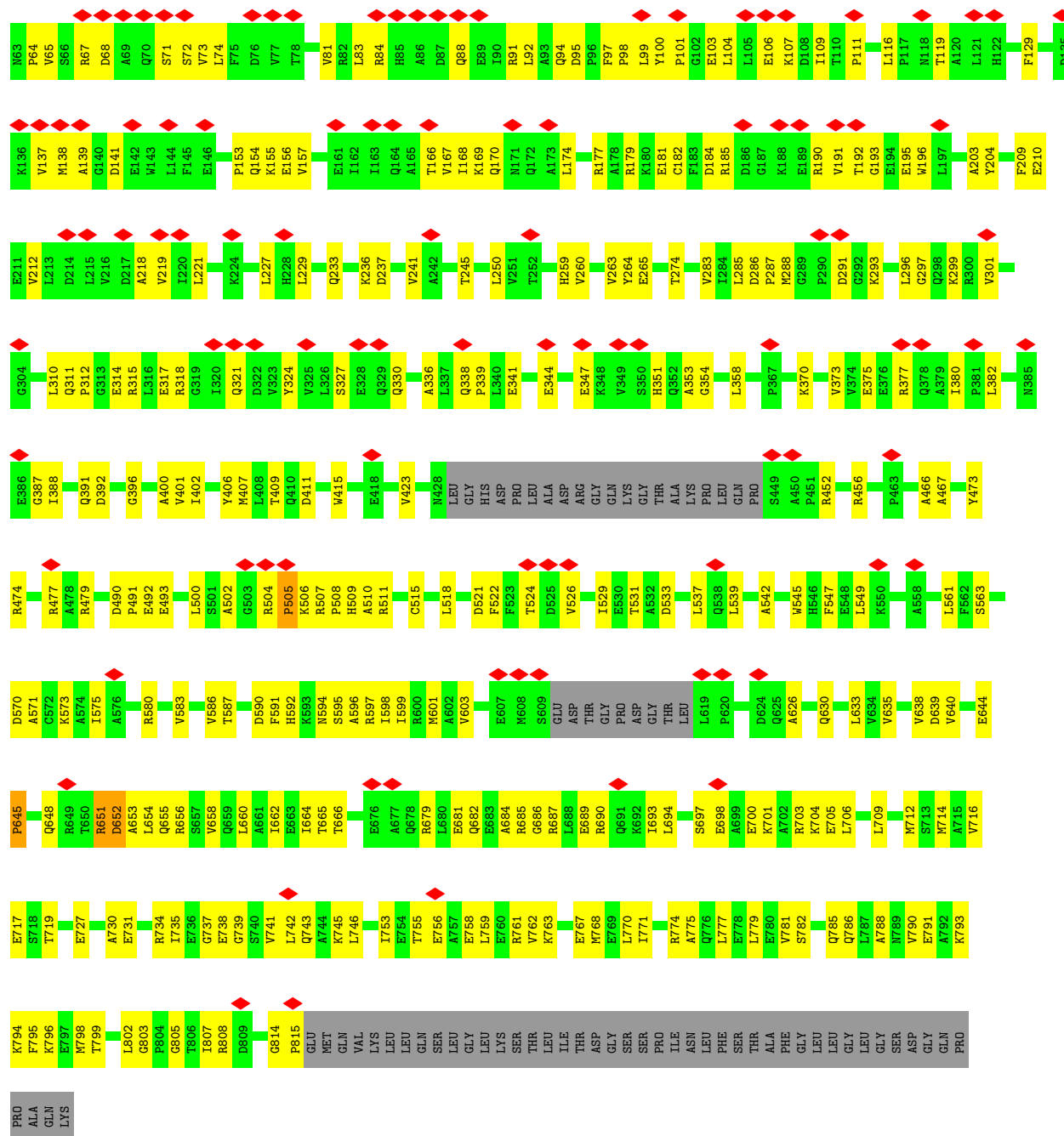
- Molecule 1: Major vault protein



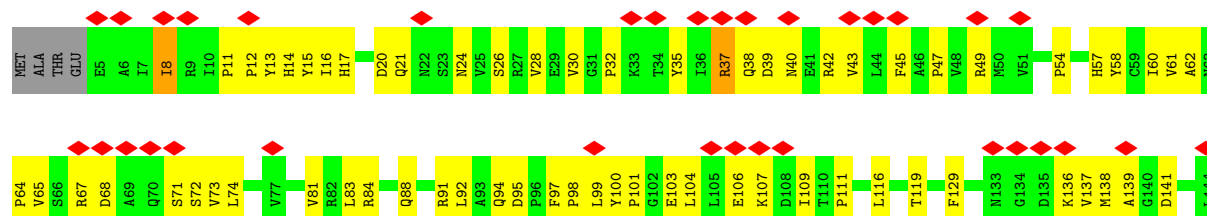


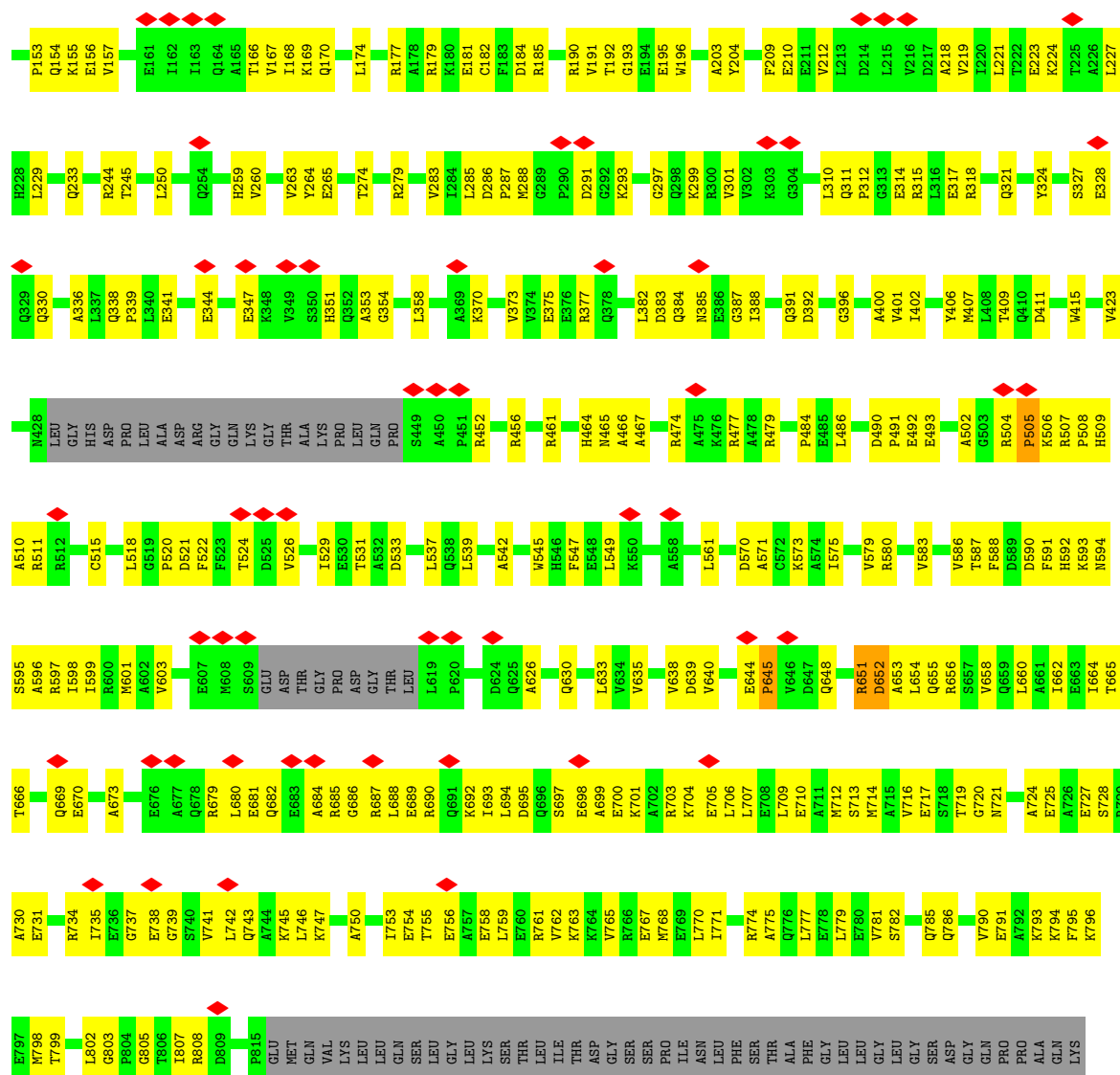
• Molecule 1: Major vault protein



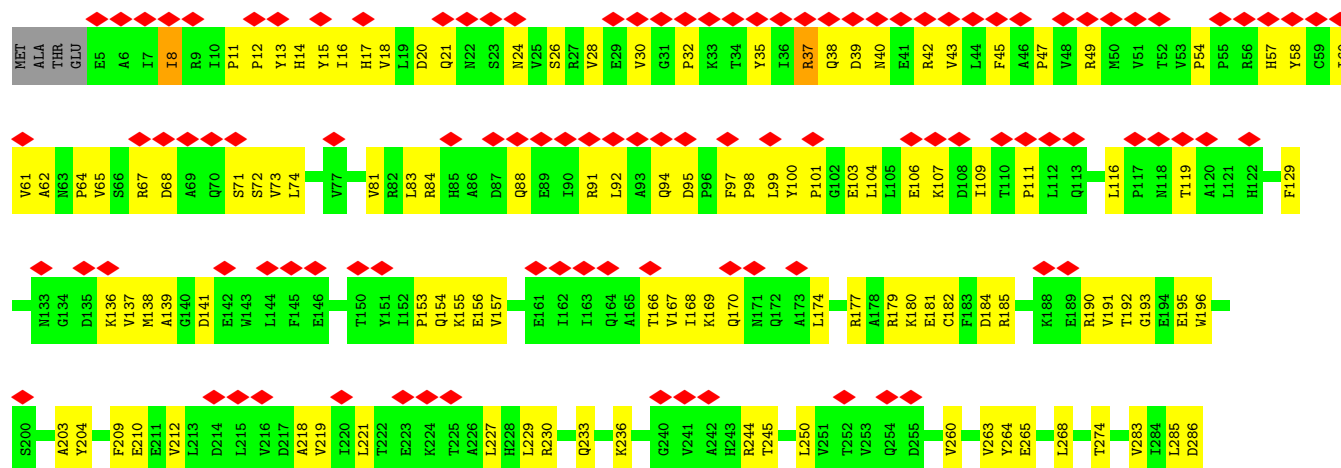


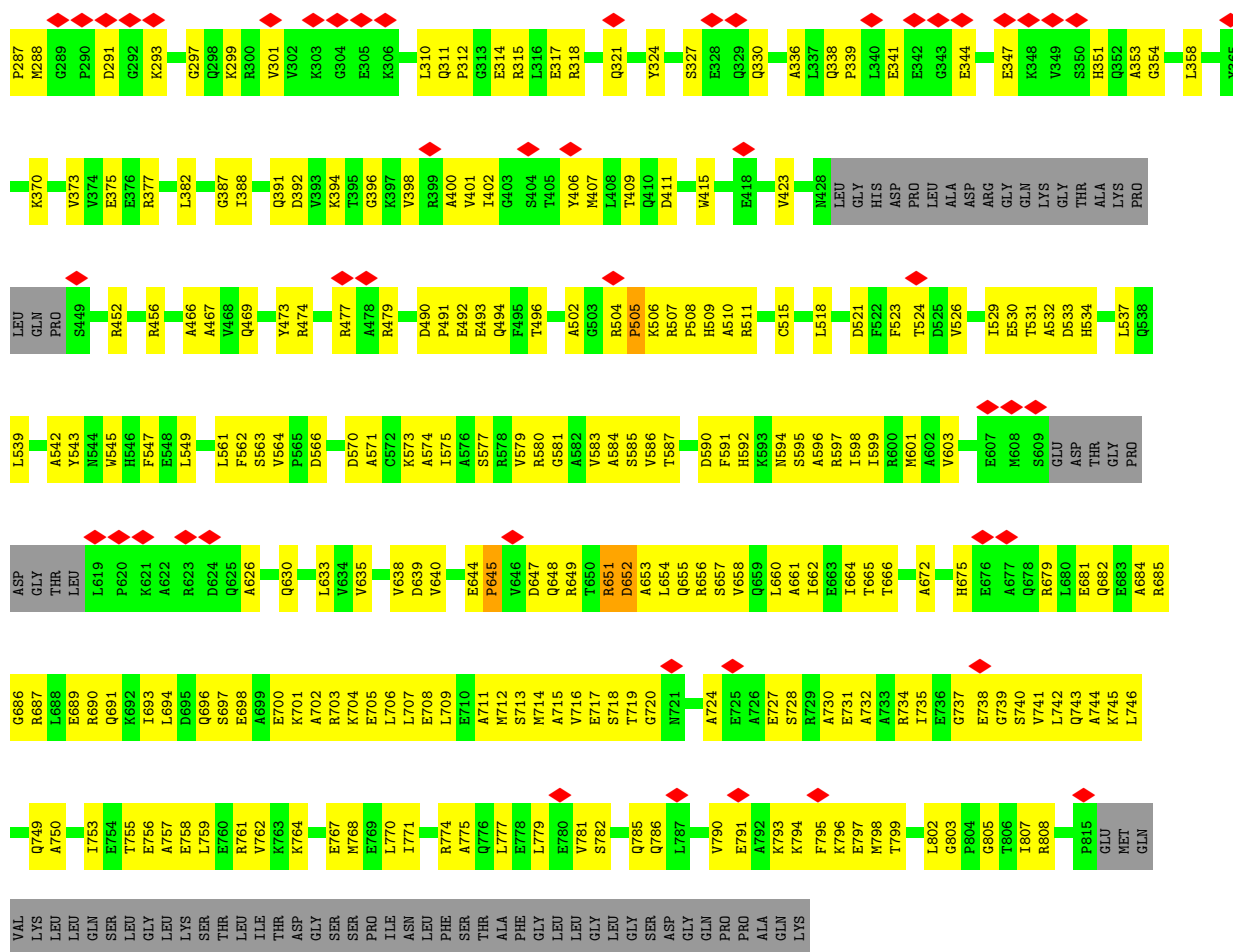
• Molecule 1: Major vault protein



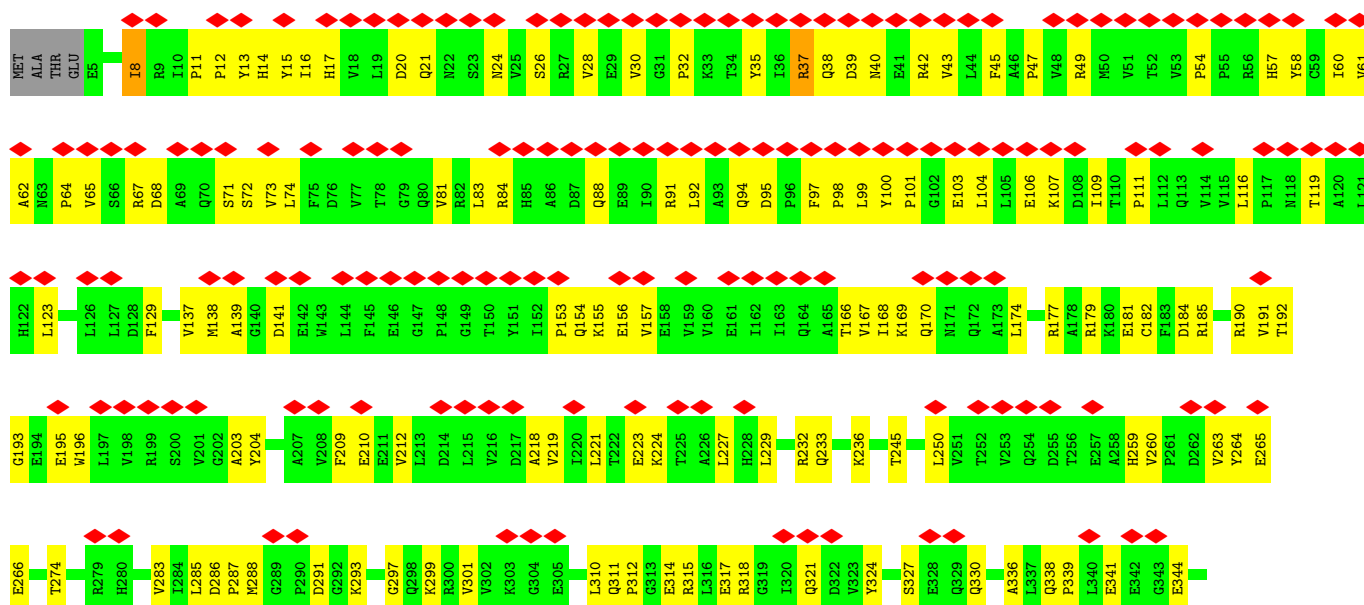


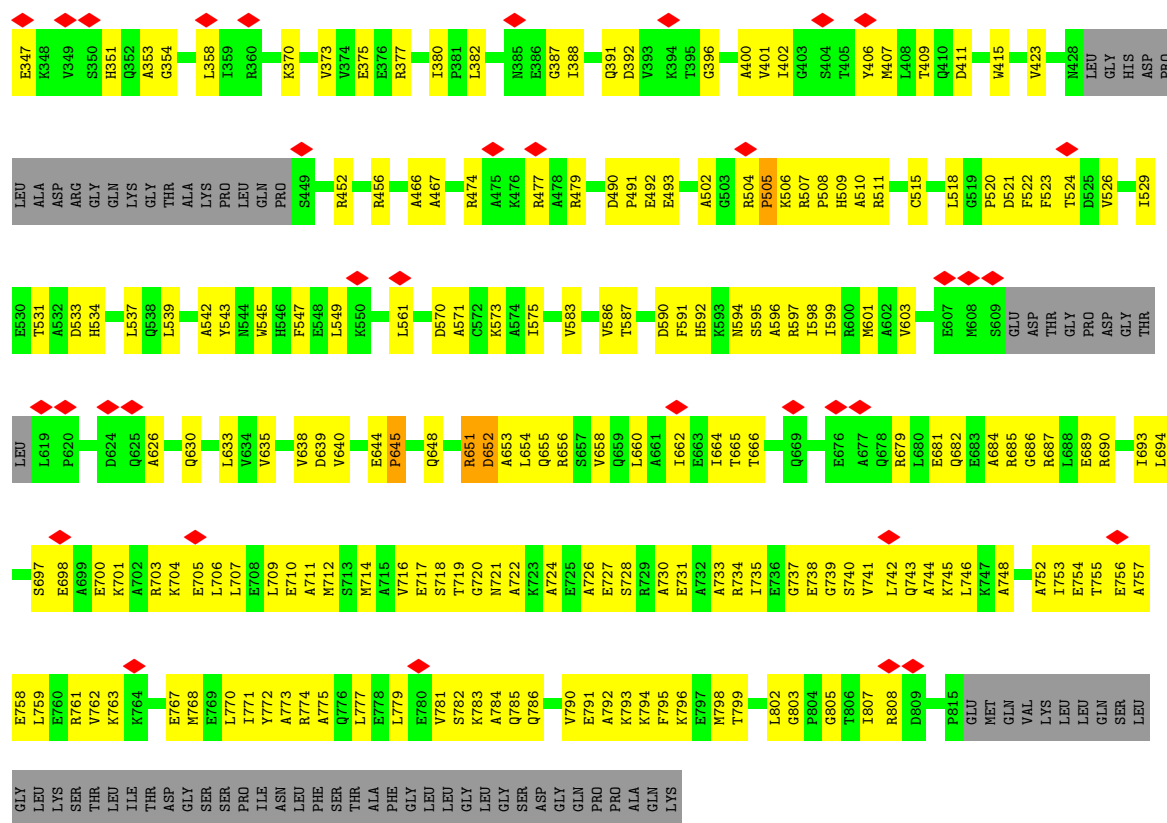
• Molecule 1: Major vault protein



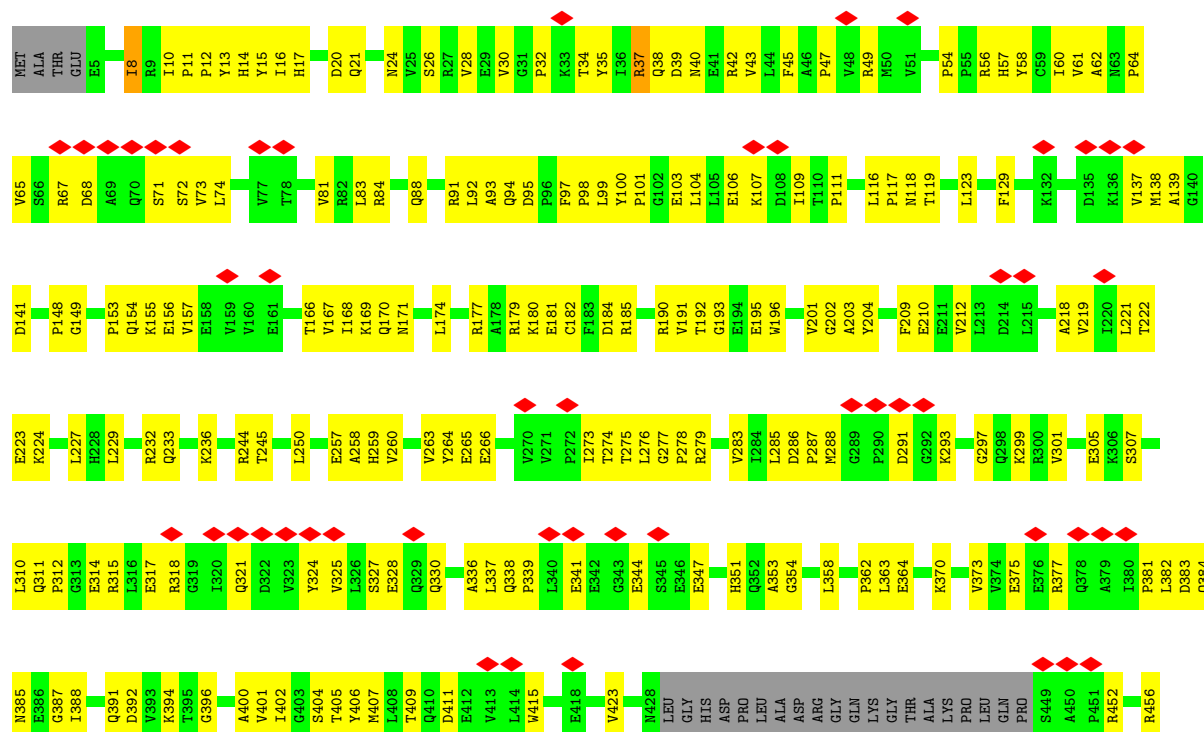


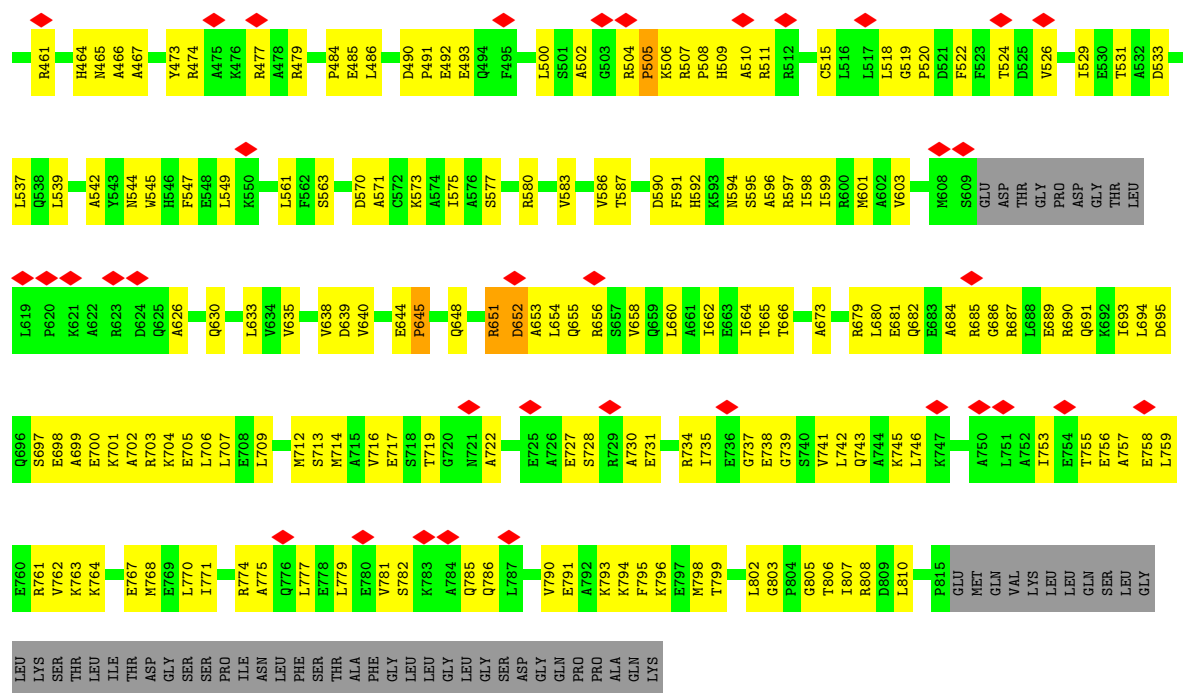
• Molecule 1: Major vault protein



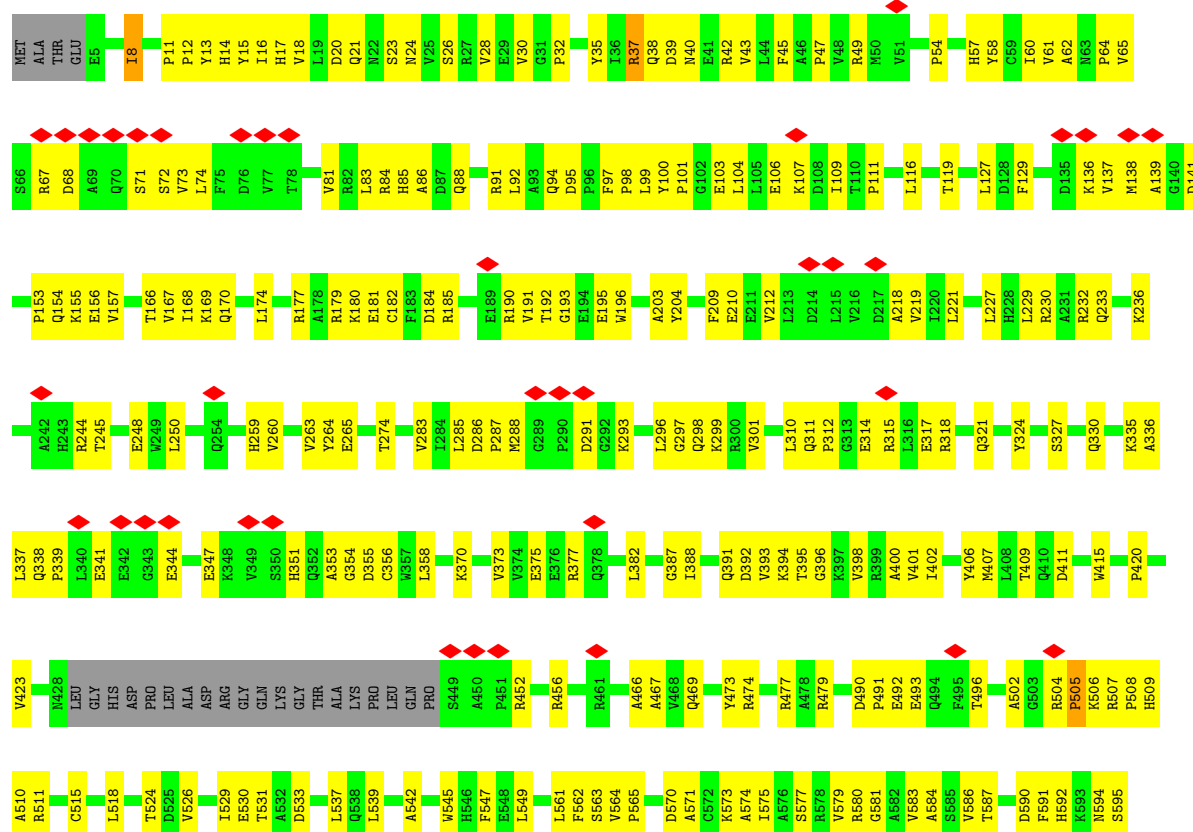


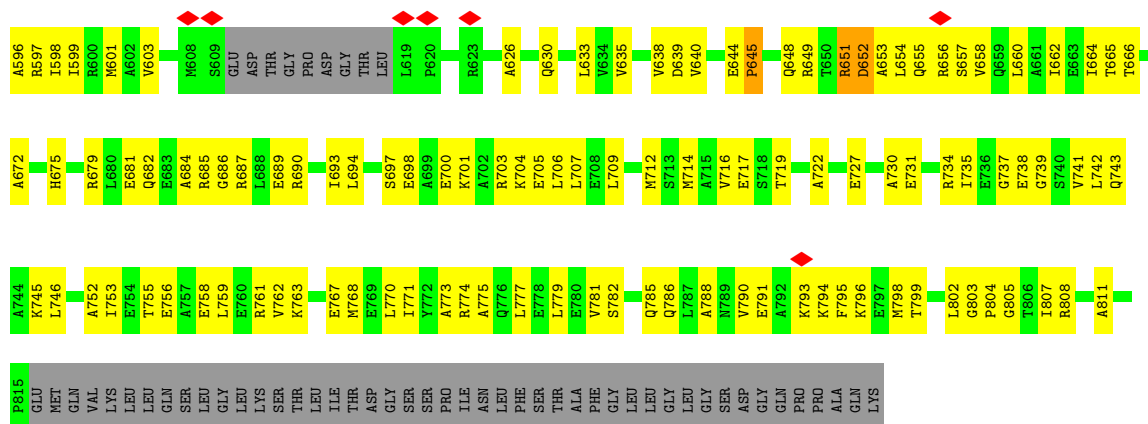
• Molecule 1: Major vault protein





• Molecule 1: Major vault protein

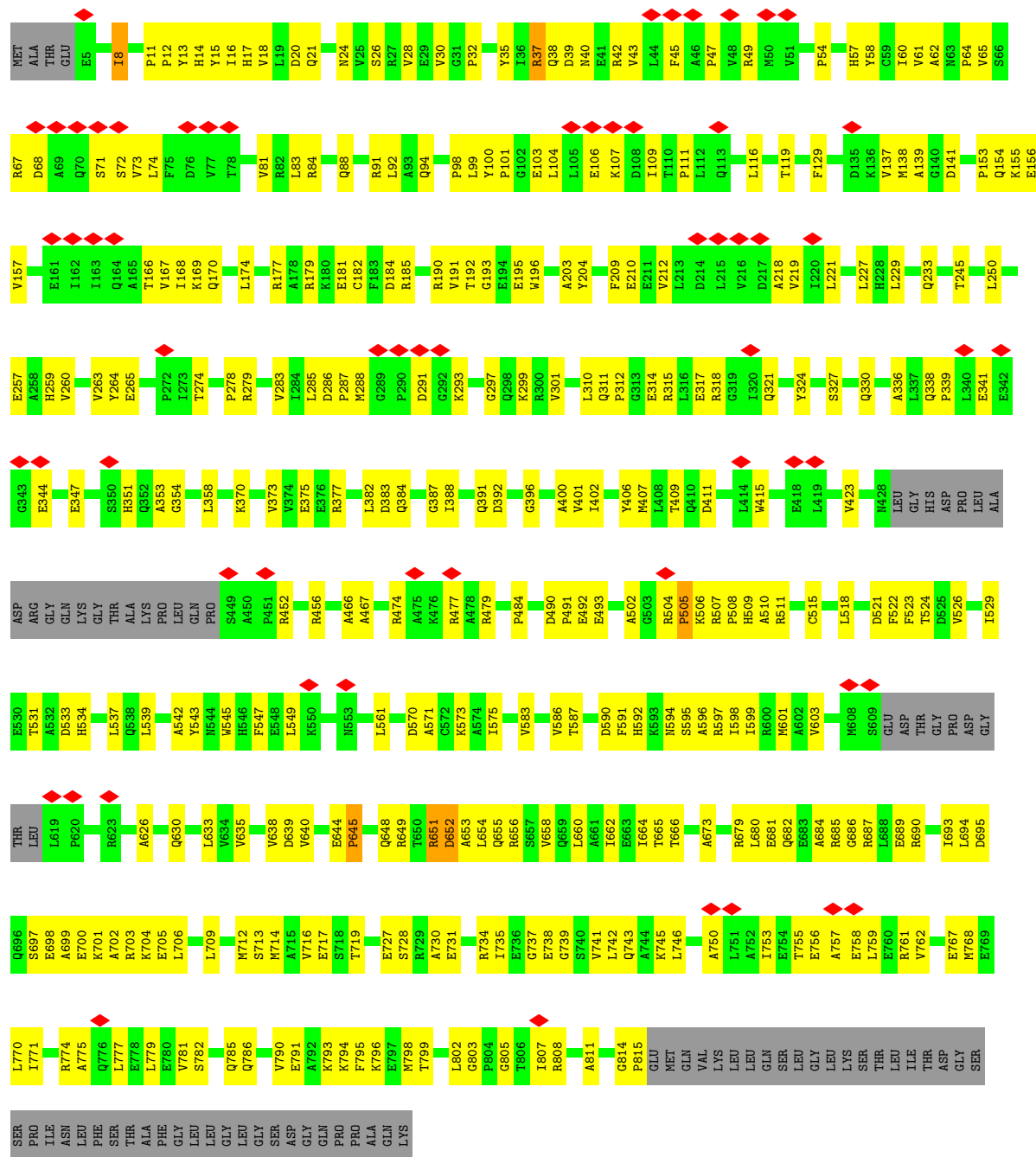




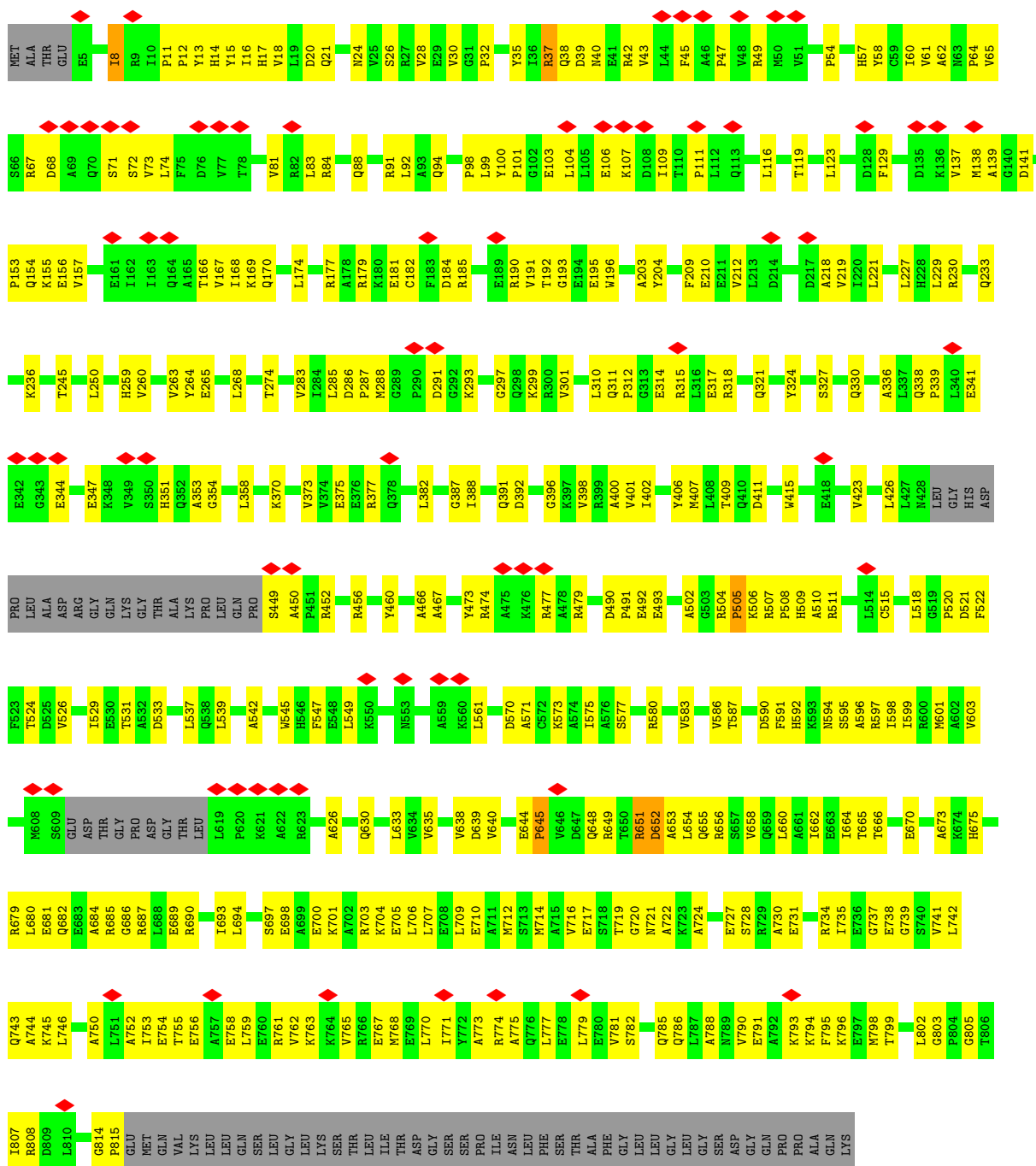
• Molecule 1: Major vault protein



- Molecule 1: Major vault protein

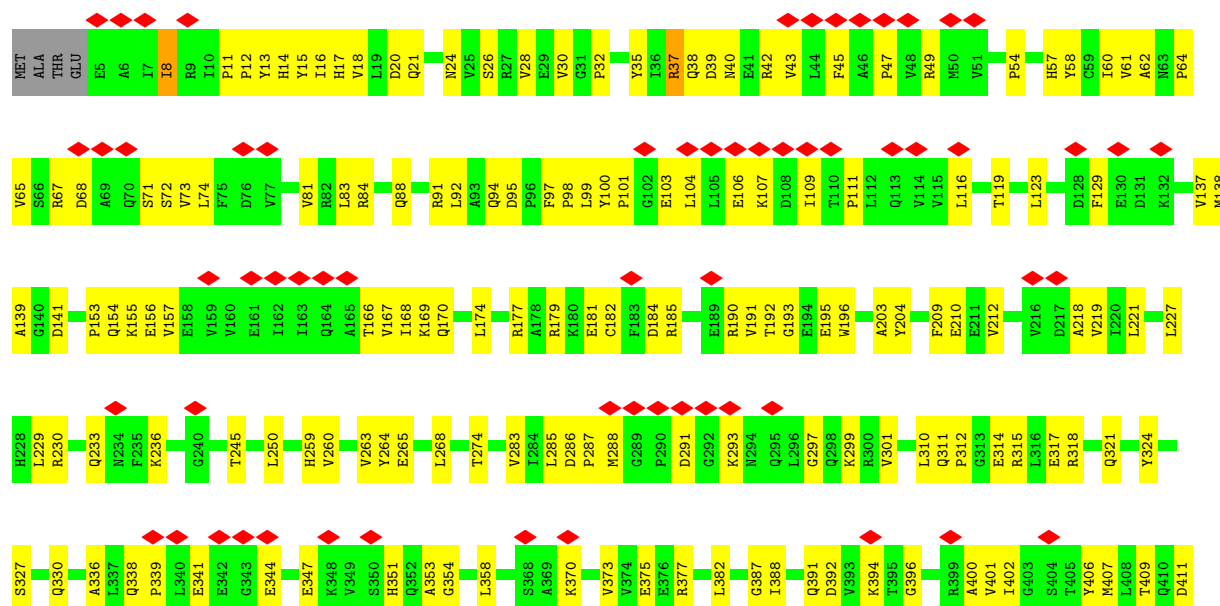


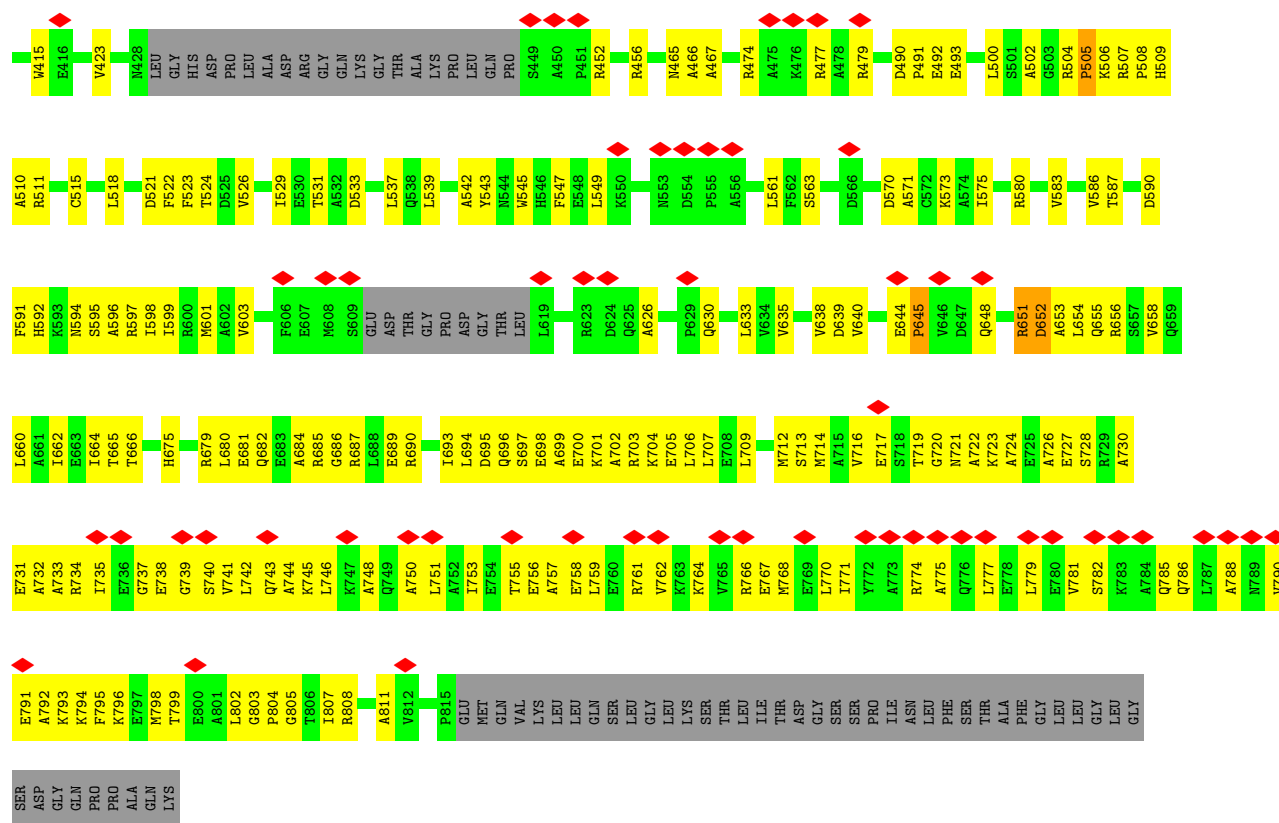
- Molecule 1: Major vault protein



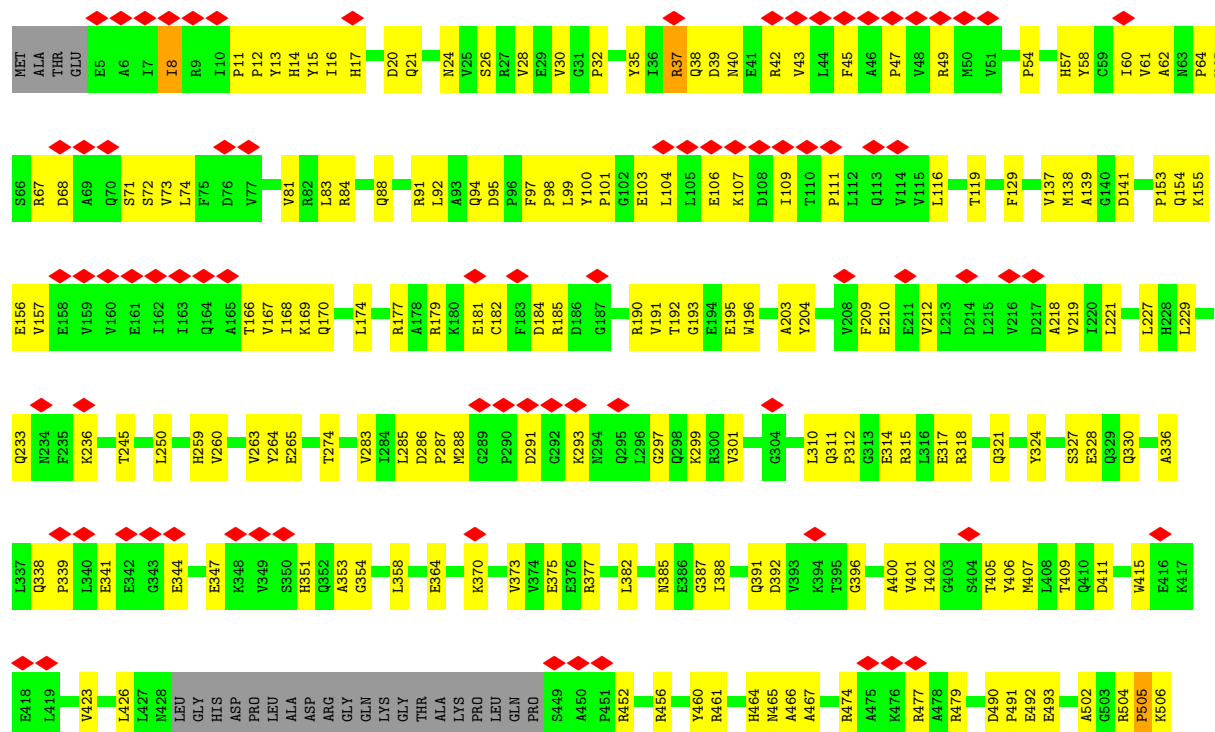
- Molecule 1: Major vault protein

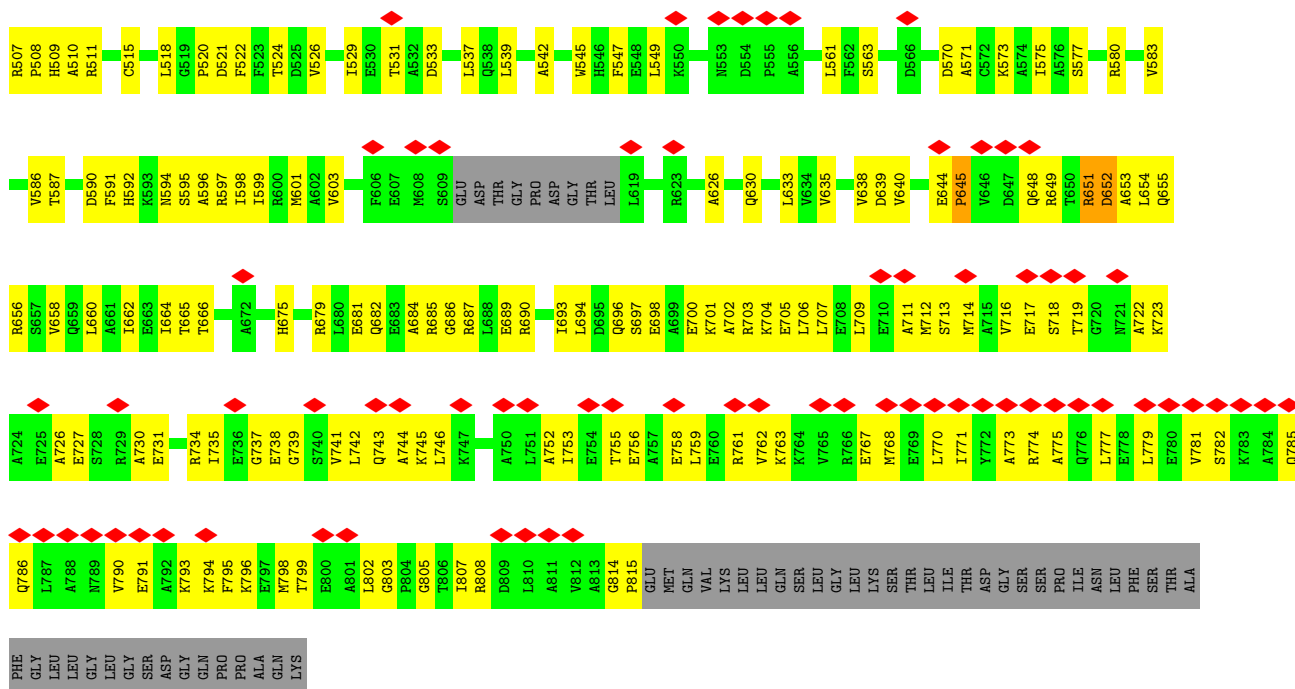




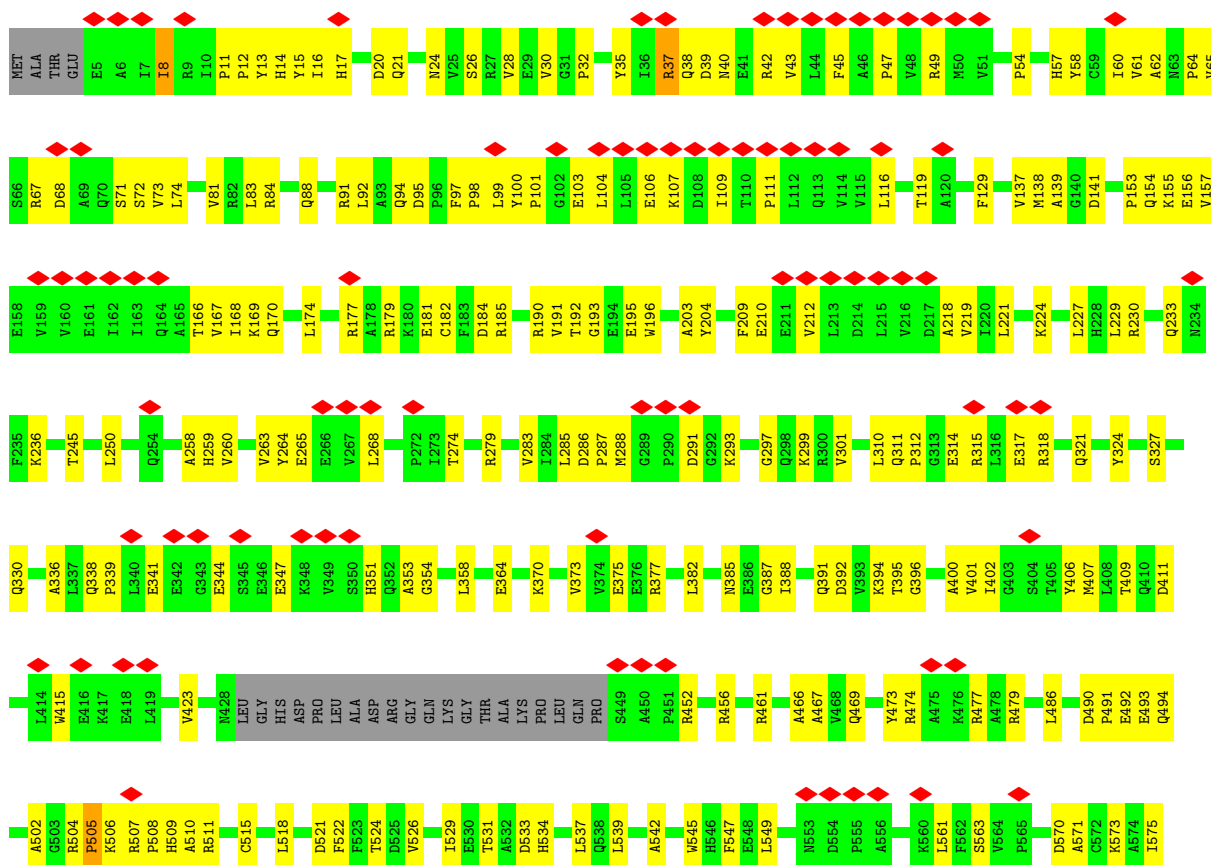


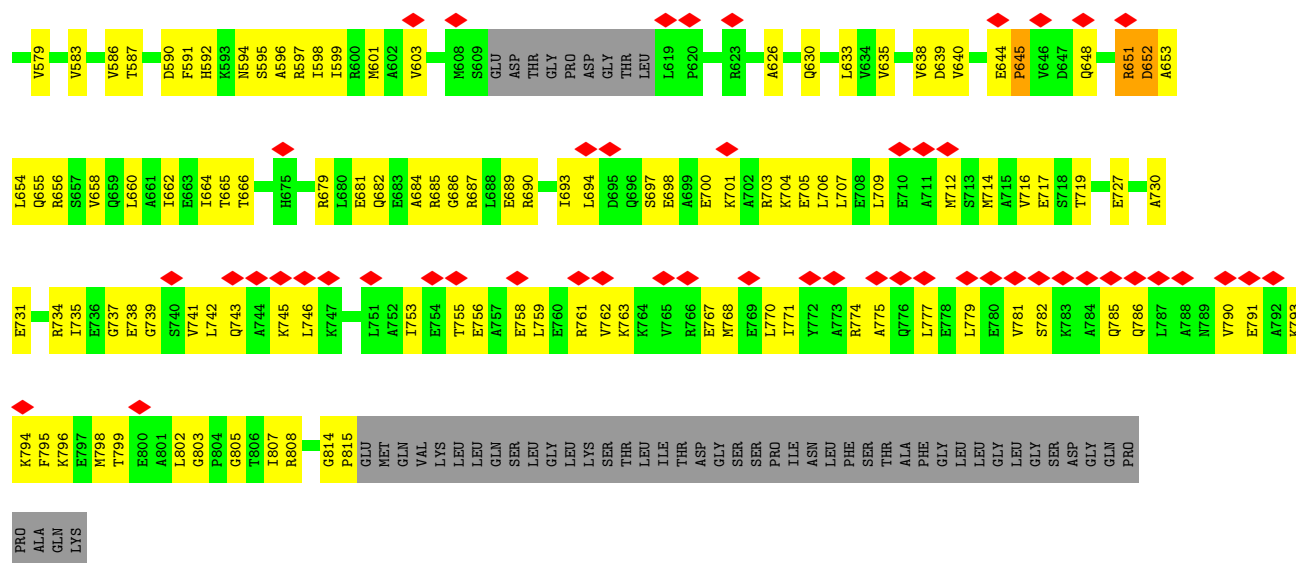
• Molecule 1: Major vault protein



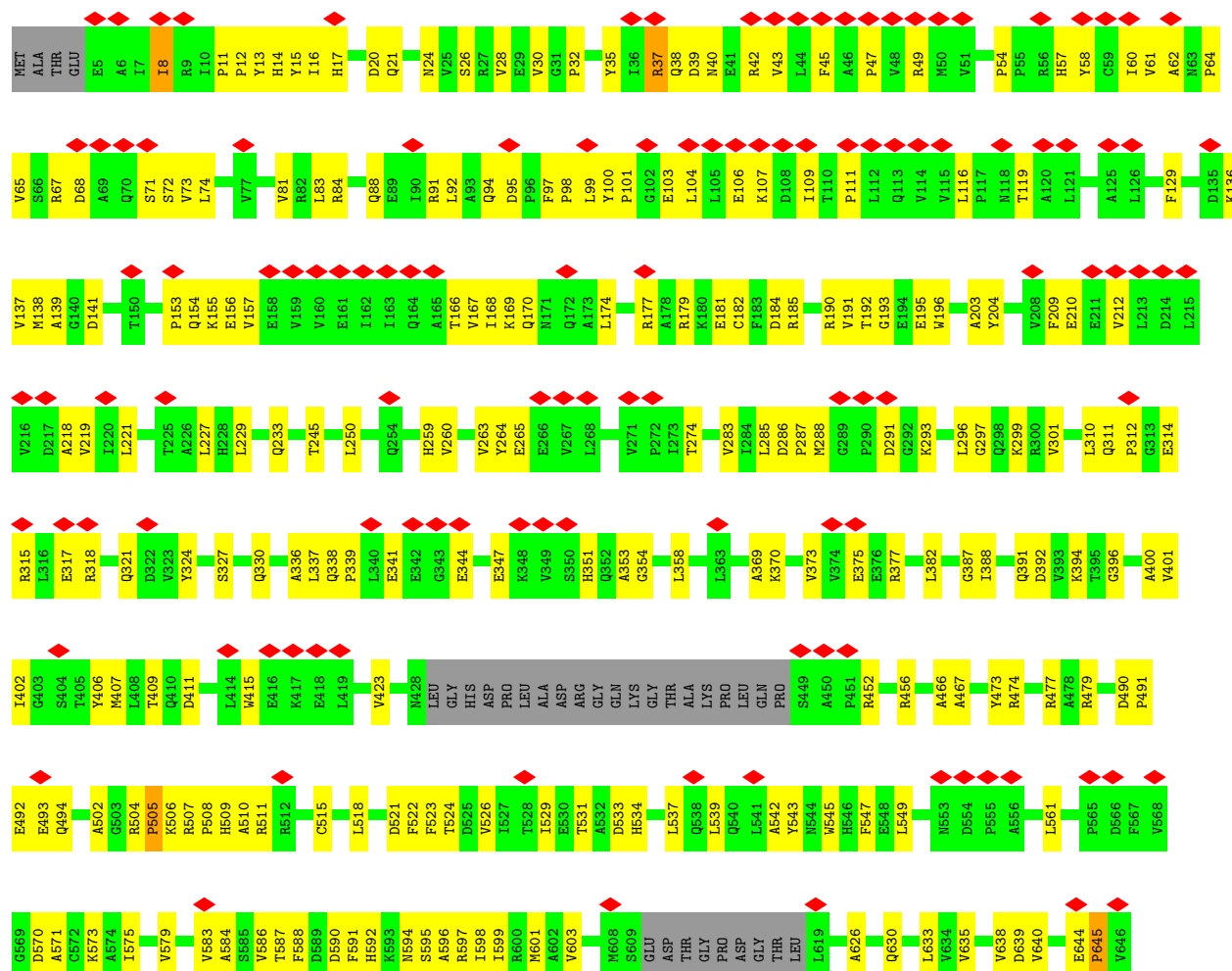


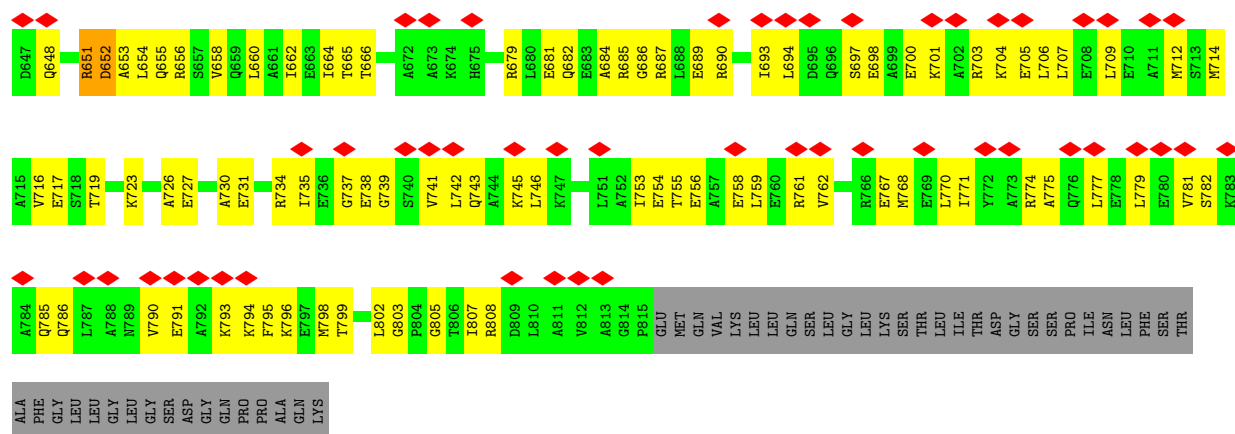
• Molecule 1: Major vault protein



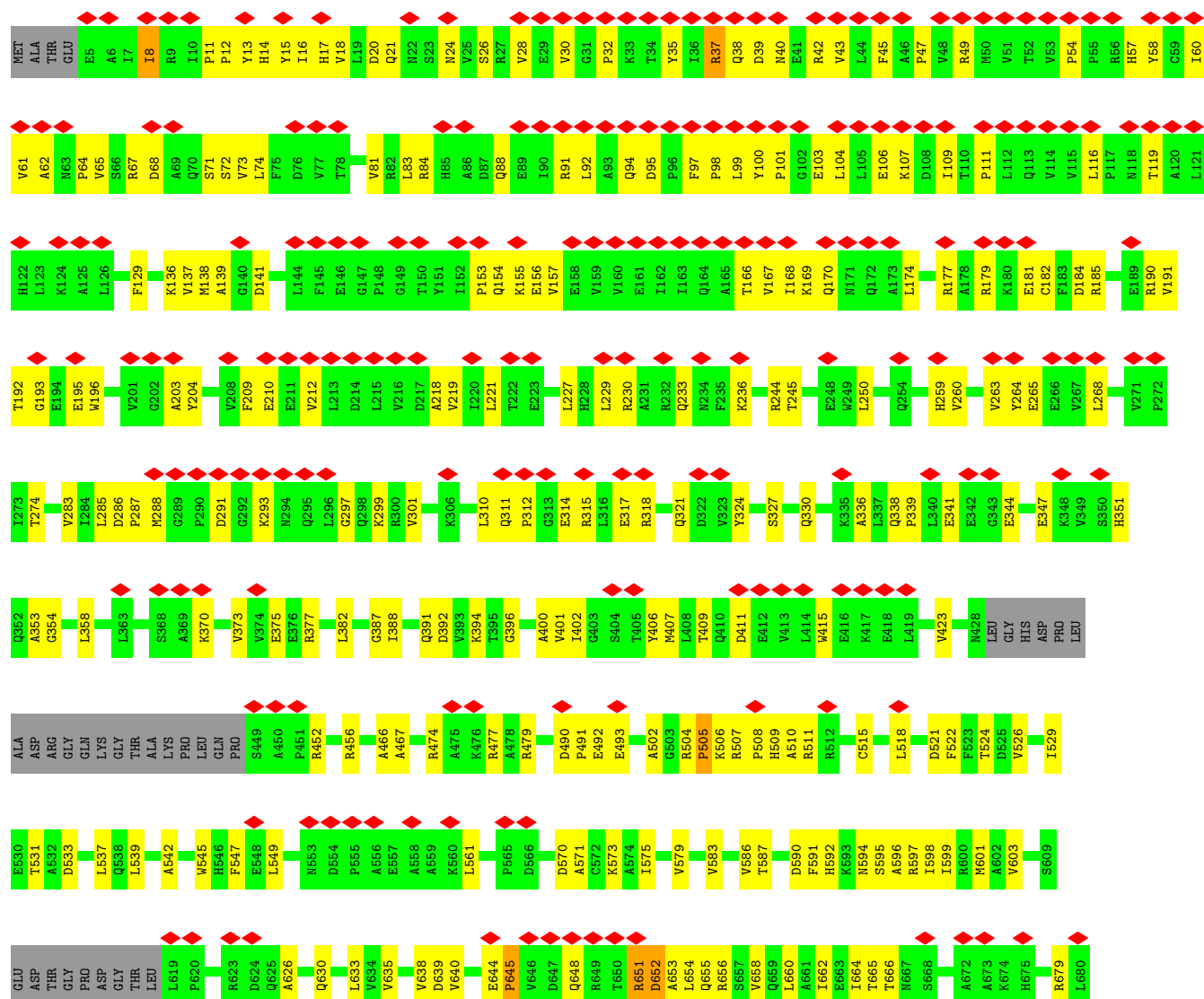


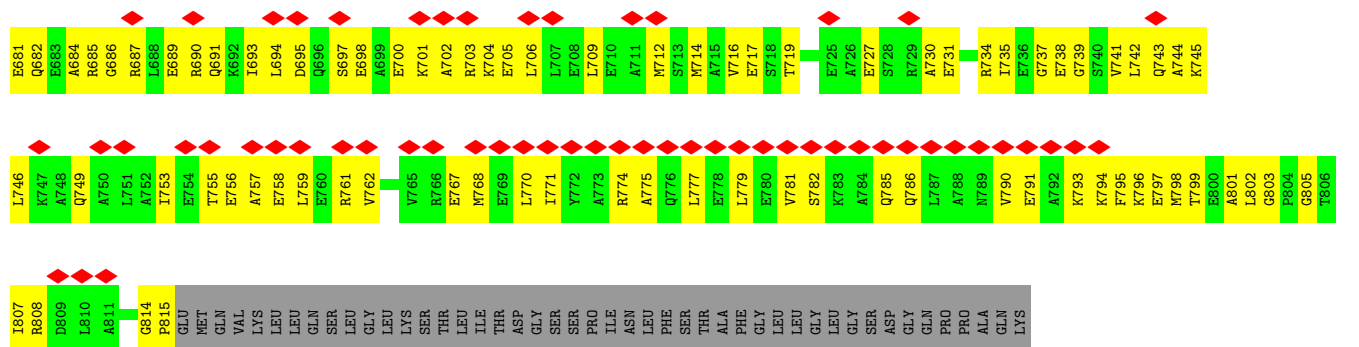
• Molecule 1: Major vault protein



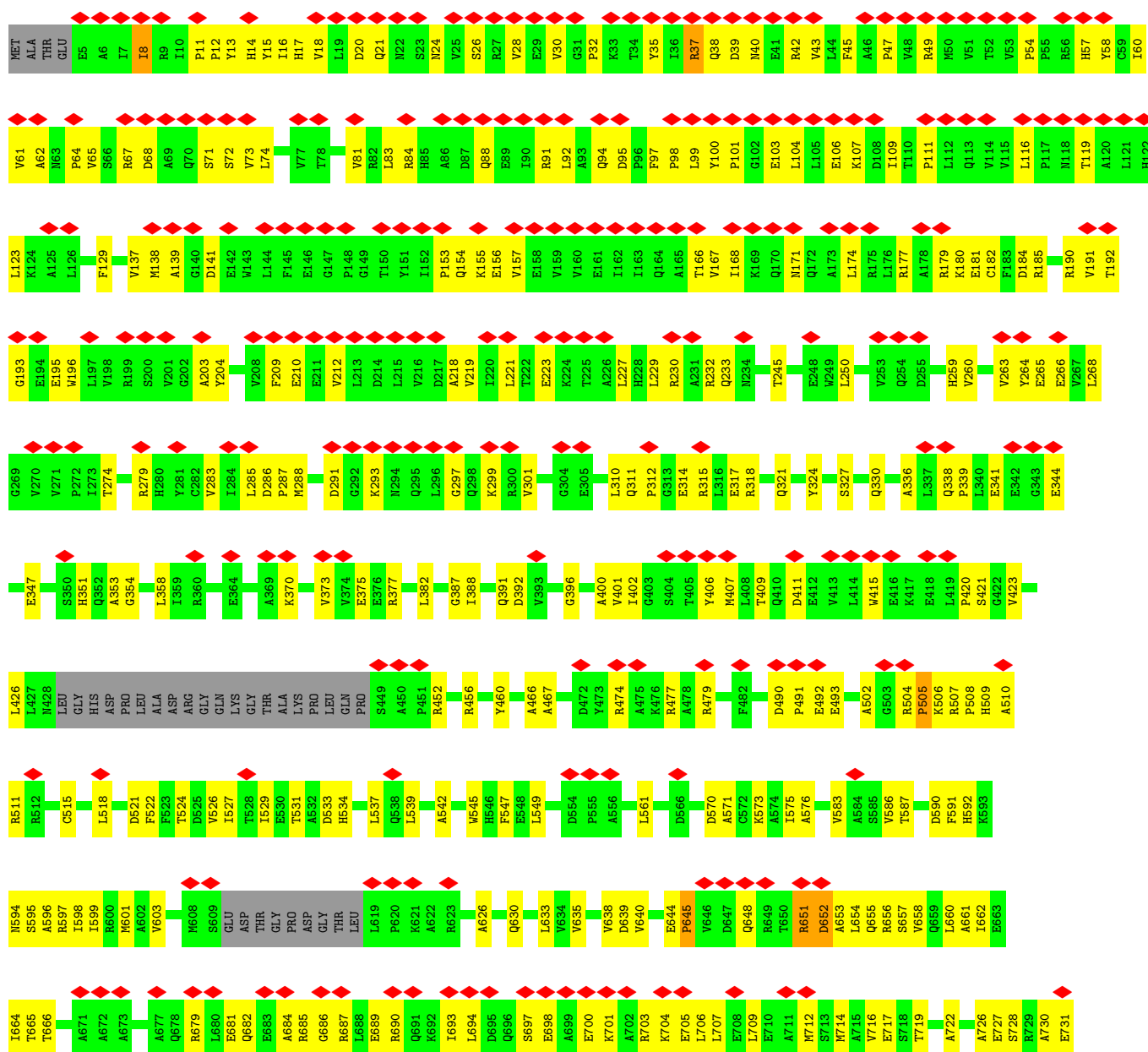


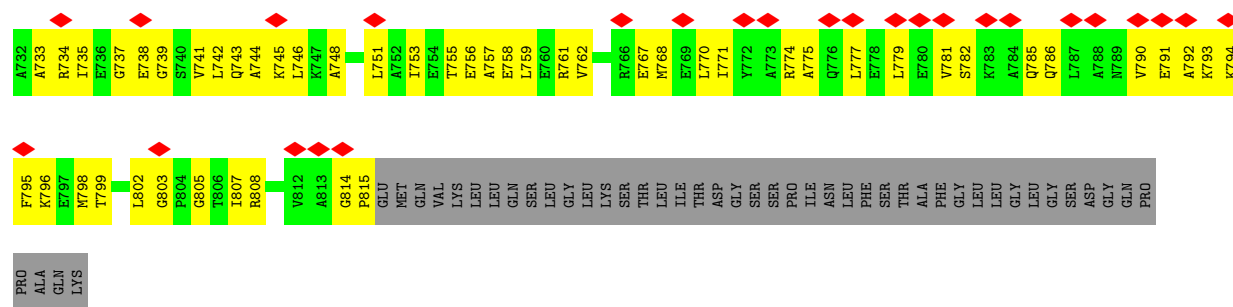
• Molecule 1: Major vault protein





• Molecule 1: Major vault protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20864	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.322	Depositor
Minimum map value	-0.098	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	735.0, 735.0, 735.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.675, 3.675, 3.675	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	0.21	0/6255	0.50	0/8474
1	AA	0.21	0/6255	0.50	0/8474
1	AB	0.21	0/6255	0.50	0/8474
1	AC	0.21	0/6255	0.50	0/8474
1	B	0.21	0/6255	0.50	0/8474
1	BA	0.21	0/6255	0.50	0/8474
1	BB	0.21	0/6255	0.50	0/8474
1	C	0.21	0/6255	0.50	0/8474
1	CA	0.21	0/6255	0.50	0/8474
1	CB	0.21	0/6255	0.50	0/8474
1	D	0.21	0/6255	0.50	0/8474
1	DA	0.21	0/6255	0.50	0/8474
1	DB	0.21	0/6255	0.50	0/8474
1	E	0.21	0/6255	0.50	0/8474
1	EA	0.21	0/6255	0.50	0/8474
1	EB	0.21	0/6255	0.50	0/8474
1	F	0.21	0/6255	0.50	0/8474
1	FA	0.21	0/6255	0.50	0/8474
1	FB	0.21	0/6255	0.50	0/8474
1	G	0.21	0/6255	0.50	0/8474
1	GA	0.21	0/6255	0.50	0/8474
1	GB	0.21	0/6255	0.50	0/8474
1	H	0.21	0/6255	0.50	0/8474
1	HA	0.21	0/6255	0.50	0/8474
1	HB	0.21	0/6255	0.50	0/8474
1	I	0.21	0/6255	0.50	0/8474
1	IA	0.21	0/6255	0.50	0/8474
1	IB	0.21	0/6255	0.50	0/8474
1	J	0.21	0/6255	0.50	0/8474
1	JA	0.21	0/6255	0.50	0/8474
1	JB	0.21	0/6255	0.50	0/8474
1	K	0.21	0/6255	0.50	0/8474
1	KA	0.21	0/6255	0.50	0/8474
1	KB	0.21	0/6255	0.50	0/8474

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.21	0/6255	0.50	0/8474
1	LA	0.21	0/6255	0.50	0/8474
1	LB	0.21	0/6255	0.50	0/8474
1	M	0.21	0/6255	0.50	0/8474
1	MA	0.21	0/6255	0.50	0/8474
1	MB	0.21	0/6255	0.50	0/8474
1	N	0.21	0/6255	0.50	0/8474
1	NA	0.21	0/6255	0.50	0/8474
1	NB	0.21	0/6255	0.50	0/8474
1	O	0.21	0/6255	0.50	0/8474
1	OA	0.21	0/6255	0.50	0/8474
1	OB	0.21	0/6255	0.50	0/8474
1	P	0.21	0/6255	0.50	0/8474
1	PA	0.21	0/6255	0.50	0/8474
1	PB	0.21	0/6255	0.50	0/8474
1	Q	0.21	0/6255	0.50	0/8474
1	QA	0.21	0/6255	0.50	0/8474
1	QB	0.21	0/6255	0.50	0/8474
1	R	0.21	0/6255	0.50	0/8474
1	RA	0.21	0/6255	0.50	0/8474
1	RB	0.21	0/6255	0.50	0/8474
1	S	0.21	0/6255	0.50	0/8474
1	SA	0.21	0/6255	0.50	0/8474
1	SB	0.21	0/6255	0.50	0/8474
1	T	0.21	0/6255	0.50	0/8474
1	TA	0.21	0/6255	0.50	0/8474
1	TB	0.21	0/6255	0.50	0/8474
1	UA	0.21	0/6255	0.50	0/8474
1	UB	0.21	0/6255	0.50	0/8474
1	V	0.21	0/6255	0.50	0/8474
1	VA	0.21	0/6255	0.50	0/8474
1	VB	0.21	0/6255	0.50	0/8474
1	W	0.21	0/6255	0.50	0/8474
1	WA	0.21	0/6255	0.50	0/8474
1	WB	0.21	0/6255	0.50	0/8474
1	X	0.21	0/6255	0.50	0/8474
1	XA	0.21	0/6255	0.50	0/8474
1	XB	0.21	0/6255	0.50	0/8474
1	Y	0.21	0/6255	0.50	0/8474
1	YA	0.21	0/6255	0.50	0/8474
1	YB	0.21	0/6255	0.50	0/8474
1	Z	0.21	0/6255	0.50	0/8474
1	ZA	0.21	0/6255	0.50	0/8474

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ZB	0.21	0/6255	0.50	0/8474
All	All	0.21	0/487890	0.50	0/660972

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	AA	0	3
1	AB	0	3
1	AC	0	3
1	B	0	3
1	BA	0	3
1	BB	0	3
1	C	0	3
1	CA	0	3
1	CB	0	3
1	D	0	3
1	DA	0	3
1	DB	0	3
1	E	0	3
1	EA	0	3
1	EB	0	3
1	F	0	3
1	FA	0	3
1	FB	0	3
1	G	0	3
1	GA	0	3
1	GB	0	3
1	H	0	3
1	HA	0	3
1	HB	0	3
1	I	0	3
1	IA	0	3
1	IB	0	3
1	J	0	3
1	JA	0	3
1	JB	0	3
1	K	0	3
1	KA	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	KB	0	3
1	L	0	3
1	LA	0	3
1	LB	0	3
1	M	0	3
1	MA	0	3
1	MB	0	3
1	N	0	3
1	NA	0	3
1	NB	0	3
1	O	0	3
1	OA	0	3
1	OB	0	3
1	P	0	3
1	PA	0	3
1	PB	0	3
1	Q	0	3
1	QA	0	3
1	QB	0	3
1	R	0	3
1	RA	0	3
1	RB	0	3
1	S	0	3
1	SA	0	3
1	SB	0	3
1	T	0	3
1	TA	0	3
1	TB	0	3
1	UA	0	3
1	UB	0	3
1	V	0	3
1	VA	0	3
1	VB	0	3
1	W	0	3
1	WA	0	3
1	WB	0	3
1	X	0	3
1	XA	0	3
1	XB	0	3
1	Y	0	3
1	YA	0	3
1	YB	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	3
1	ZA	0	3
1	ZB	0	3
All	All	0	234

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 234 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	37	ARG	Peptide
1	A	644	GLU	Peptide
1	A	8	ILE	Peptide
1	B	37	ARG	Peptide
1	B	8	ILE	Peptide

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	6150	0	6169	735	0
1	AA	6150	0	6170	232	0
1	AB	6150	0	6170	252	0
1	AC	6150	0	6169	430	0
1	B	6150	0	6170	393	0
1	BA	6150	0	6170	238	0
1	BB	6150	0	6170	324	0
1	C	6150	0	6168	888	0
1	CA	6150	0	6170	231	0
1	CB	6150	0	6170	307	0
1	D	6150	0	6169	924	0
1	DA	6150	0	6170	233	0
1	DB	6150	0	6170	321	0
1	E	6150	0	6170	498	0
1	EA	6150	0	6170	229	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EB	6150	0	6170	325	0
1	F	6150	0	6169	825	0
1	FA	6150	0	6170	233	0
1	FB	6150	0	6170	401	0
1	G	6150	0	6170	316	0
1	GA	6150	0	6170	234	0
1	GB	6150	0	6170	381	0
1	H	6150	0	6170	265	0
1	HA	6150	0	6170	264	0
1	HB	6150	0	6170	239	0
1	I	6150	0	6170	293	0
1	IA	6150	0	6170	363	0
1	IB	6150	0	6170	243	0
1	J	6150	0	6170	268	0
1	JA	6150	0	6170	261	0
1	JB	6150	0	6170	248	0
1	K	6150	0	6170	261	0
1	KA	6150	0	6170	364	0
1	KB	6150	0	6170	242	0
1	L	6150	0	6170	317	0
1	LA	6150	0	6170	233	0
1	LB	6150	0	6170	518	0
1	M	6150	0	6170	232	0
1	MA	6150	0	6170	243	0
1	MB	6150	0	6170	595	0
1	N	6150	0	6170	349	0
1	NA	6150	0	6170	234	0
1	NB	6150	0	6170	381	0
1	O	6150	0	6170	234	0
1	OA	6150	0	6170	236	0
1	OB	6150	0	6169	648	0
1	P	6150	0	6170	312	0
1	PA	6150	0	6170	244	0
1	PB	6150	0	6170	621	0
1	Q	6150	0	6170	237	0
1	QA	6150	0	6170	246	0
1	QB	6150	0	6170	246	0
1	R	6150	0	6170	322	0
1	RA	6150	0	6170	242	0
1	RB	6150	0	6170	293	0
1	S	6150	0	6170	243	0
1	SA	6150	0	6170	252	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SB	6150	0	6170	343	0
1	T	6150	0	6170	282	0
1	TA	6150	0	6170	249	0
1	TB	6150	0	6170	394	0
1	UA	6150	0	6170	236	0
1	UB	6150	0	6167	585	0
1	V	6150	0	6170	246	0
1	VA	6150	0	6170	244	0
1	VB	6150	0	6166	564	0
1	W	6150	0	6170	236	0
1	WA	6150	0	6170	229	0
1	WB	6150	0	6170	355	0
1	X	6150	0	6170	245	0
1	XA	6150	0	6170	267	0
1	XB	6150	0	6170	276	0
1	Y	6150	0	6170	230	0
1	YA	6150	0	6170	229	0
1	YB	6150	0	6170	252	0
1	Z	6150	0	6170	234	0
1	ZA	6150	0	6170	286	0
1	ZB	6150	0	6169	375	0
All	All	479700	0	481245	22069	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 23.

The worst 5 of 22069 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:UB:757:ALA:CB	1:VB:751:LEU:HB3	1.24	1.68
1:ZB:735:ILE:CB	1:AC:726:ALA:CB	1.77	1.62
1:C:779:LEU:CD1	1:E:770:LEU:HA	1.10	1.57
1:ZB:735:ILE:CG2	1:AC:726:ALA:HB1	1.33	1.57
1:A:768:MET:CE	1:C:763:LYS:HB2	1.08	1.54

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	AA	776/861 (90%)	671 (86%)	101 (13%)	4 (0%)	24	63
1	AB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	AC	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	B	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	BA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	BB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	C	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	CA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	CB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	D	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	DA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	DB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	E	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	EA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	EB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	F	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	FA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	FB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	G	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	GA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	GB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	H	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	HA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	HB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	IA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	IB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	J	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	JA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	JB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	K	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	KA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	KB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	L	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	LA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	LB	776/861 (90%)	672 (87%)	100 (13%)	4 (0%)	24	63
1	M	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	MA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	MB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	N	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	NA	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	NB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	O	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	OA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	OB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	P	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	PA	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	PB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	Q	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	QA	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	QB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	R	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	RA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	RB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	S	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	SB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	T	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	TA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	TB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	UA	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	UB	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	V	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	VA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	VB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	W	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	WA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	WB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	X	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	XA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	XB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
1	Y	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	YA	776/861 (90%)	673 (87%)	99 (13%)	4 (0%)	24	63
1	YB	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	Z	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	ZA	776/861 (90%)	674 (87%)	98 (13%)	4 (0%)	24	63
1	ZB	776/861 (90%)	675 (87%)	97 (12%)	4 (0%)	24	63
All	All	60528/67158 (90%)	52566 (87%)	7650 (13%)	312 (0%)	26	63

5 of 312 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	651	ARG
1	A	652	ASP
1	B	651	ARG
1	B	652	ASP
1	C	651	ARG

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	654/726 (90%)	654 (100%)	0	100	100
1	AA	654/726 (90%)	654 (100%)	0	100	100
1	AB	654/726 (90%)	654 (100%)	0	100	100
1	AC	654/726 (90%)	654 (100%)	0	100	100
1	B	654/726 (90%)	654 (100%)	0	100	100
1	BA	654/726 (90%)	654 (100%)	0	100	100
1	BB	654/726 (90%)	654 (100%)	0	100	100
1	C	654/726 (90%)	654 (100%)	0	100	100
1	CA	654/726 (90%)	654 (100%)	0	100	100
1	CB	654/726 (90%)	654 (100%)	0	100	100
1	D	654/726 (90%)	654 (100%)	0	100	100
1	DA	654/726 (90%)	654 (100%)	0	100	100
1	DB	654/726 (90%)	654 (100%)	0	100	100
1	E	654/726 (90%)	654 (100%)	0	100	100
1	EA	654/726 (90%)	654 (100%)	0	100	100
1	EB	654/726 (90%)	654 (100%)	0	100	100
1	F	654/726 (90%)	654 (100%)	0	100	100
1	FA	654/726 (90%)	654 (100%)	0	100	100
1	FB	654/726 (90%)	654 (100%)	0	100	100
1	G	654/726 (90%)	654 (100%)	0	100	100
1	GA	654/726 (90%)	654 (100%)	0	100	100
1	GB	654/726 (90%)	654 (100%)	0	100	100
1	H	654/726 (90%)	654 (100%)	0	100	100
1	HA	654/726 (90%)	654 (100%)	0	100	100
1	HB	654/726 (90%)	654 (100%)	0	100	100
1	I	654/726 (90%)	654 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IA	654/726 (90%)	654 (100%)	0	100	100
1	IB	654/726 (90%)	654 (100%)	0	100	100
1	J	654/726 (90%)	654 (100%)	0	100	100
1	JA	654/726 (90%)	654 (100%)	0	100	100
1	JB	654/726 (90%)	654 (100%)	0	100	100
1	K	654/726 (90%)	654 (100%)	0	100	100
1	KA	654/726 (90%)	654 (100%)	0	100	100
1	KB	654/726 (90%)	654 (100%)	0	100	100
1	L	654/726 (90%)	654 (100%)	0	100	100
1	LA	654/726 (90%)	654 (100%)	0	100	100
1	LB	654/726 (90%)	654 (100%)	0	100	100
1	M	654/726 (90%)	654 (100%)	0	100	100
1	MA	654/726 (90%)	654 (100%)	0	100	100
1	MB	654/726 (90%)	654 (100%)	0	100	100
1	N	654/726 (90%)	654 (100%)	0	100	100
1	NA	654/726 (90%)	654 (100%)	0	100	100
1	NB	654/726 (90%)	654 (100%)	0	100	100
1	O	654/726 (90%)	654 (100%)	0	100	100
1	OA	654/726 (90%)	654 (100%)	0	100	100
1	OB	654/726 (90%)	654 (100%)	0	100	100
1	P	654/726 (90%)	654 (100%)	0	100	100
1	PA	654/726 (90%)	654 (100%)	0	100	100
1	PB	654/726 (90%)	654 (100%)	0	100	100
1	Q	654/726 (90%)	654 (100%)	0	100	100
1	QA	654/726 (90%)	654 (100%)	0	100	100
1	QB	654/726 (90%)	654 (100%)	0	100	100
1	R	654/726 (90%)	654 (100%)	0	100	100
1	RA	654/726 (90%)	654 (100%)	0	100	100
1	RB	654/726 (90%)	654 (100%)	0	100	100
1	S	654/726 (90%)	654 (100%)	0	100	100
1	SA	654/726 (90%)	654 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	SB	654/726 (90%)	654 (100%)	0	100	100
1	T	654/726 (90%)	654 (100%)	0	100	100
1	TA	654/726 (90%)	654 (100%)	0	100	100
1	TB	654/726 (90%)	654 (100%)	0	100	100
1	UA	654/726 (90%)	654 (100%)	0	100	100
1	UB	654/726 (90%)	654 (100%)	0	100	100
1	V	654/726 (90%)	654 (100%)	0	100	100
1	VA	654/726 (90%)	654 (100%)	0	100	100
1	VB	654/726 (90%)	654 (100%)	0	100	100
1	W	654/726 (90%)	654 (100%)	0	100	100
1	WA	654/726 (90%)	654 (100%)	0	100	100
1	WB	654/726 (90%)	654 (100%)	0	100	100
1	X	654/726 (90%)	654 (100%)	0	100	100
1	XA	654/726 (90%)	654 (100%)	0	100	100
1	XB	654/726 (90%)	654 (100%)	0	100	100
1	Y	654/726 (90%)	654 (100%)	0	100	100
1	YA	654/726 (90%)	654 (100%)	0	100	100
1	YB	654/726 (90%)	654 (100%)	0	100	100
1	Z	654/726 (90%)	654 (100%)	0	100	100
1	ZA	654/726 (90%)	654 (100%)	0	100	100
1	ZB	654/726 (90%)	654 (100%)	0	100	100
All	All	51012/56628 (90%)	51012 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 407 such sidechains are listed below:

Mol	Chain	Res	Type
1	SA	243	HIS
1	FB	88	GLN
1	ZB	534	HIS
1	TA	469	GLN
1	YA	592	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.

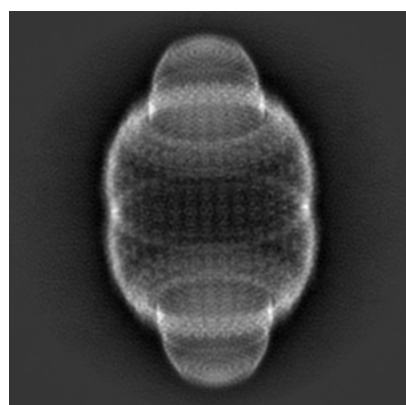
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13483. These allow visual inspection of the internal detail of the map and identification of artifacts.

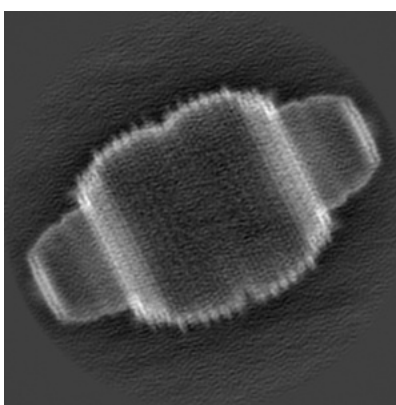
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

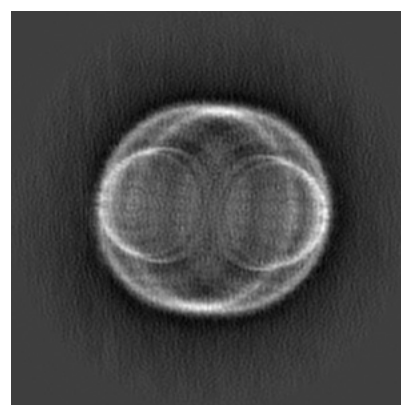
6.1.1 Primary map



X



Y

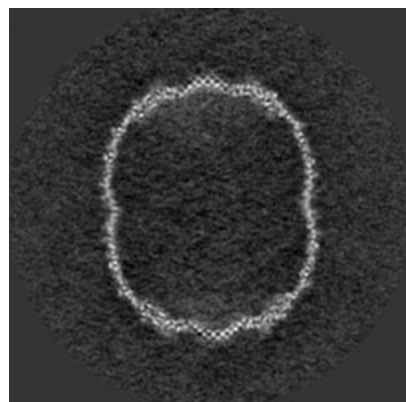


Z

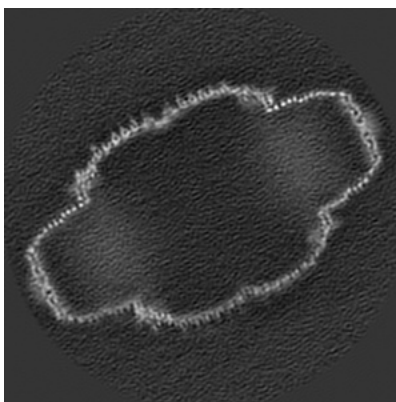
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

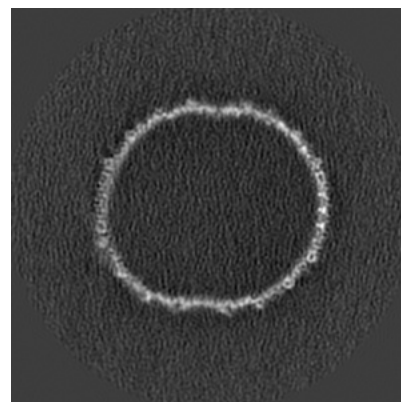
6.2.1 Primary map



X Index: 100



Y Index: 100

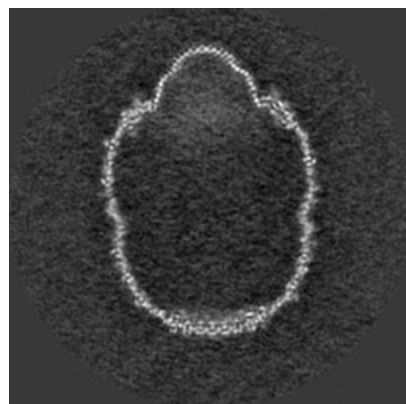


Z Index: 100

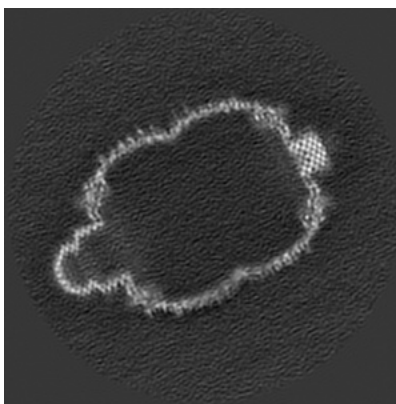
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

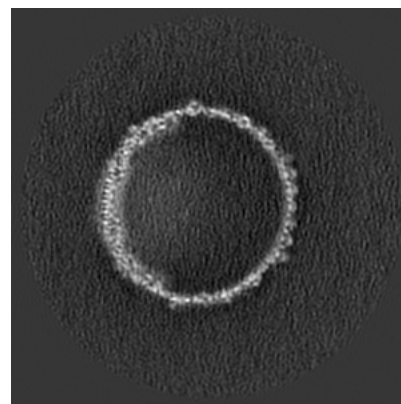
6.3.1 Primary map



X Index: 112



Y Index: 126

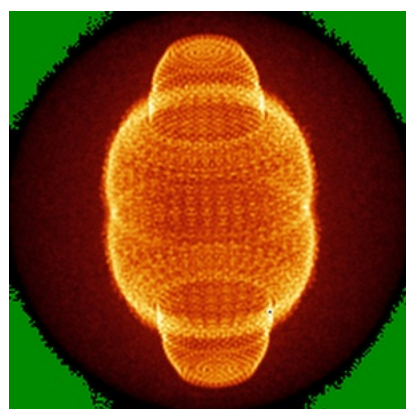


Z Index: 66

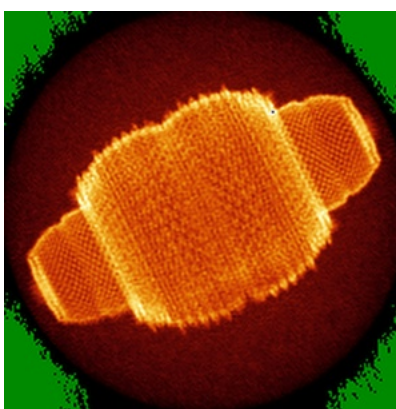
The images above show the largest variance slices of the map in three orthogonal directions.

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

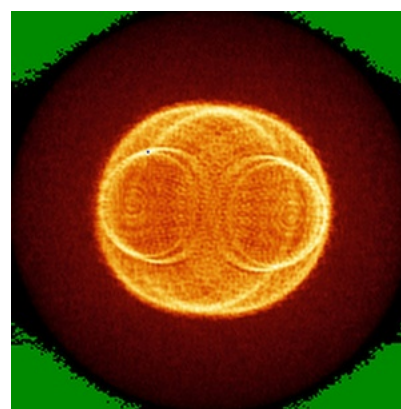
6.4.1 Primary map



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](#)

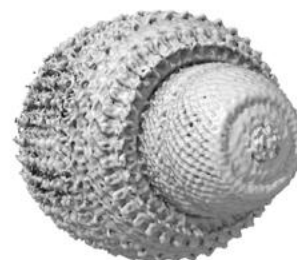
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

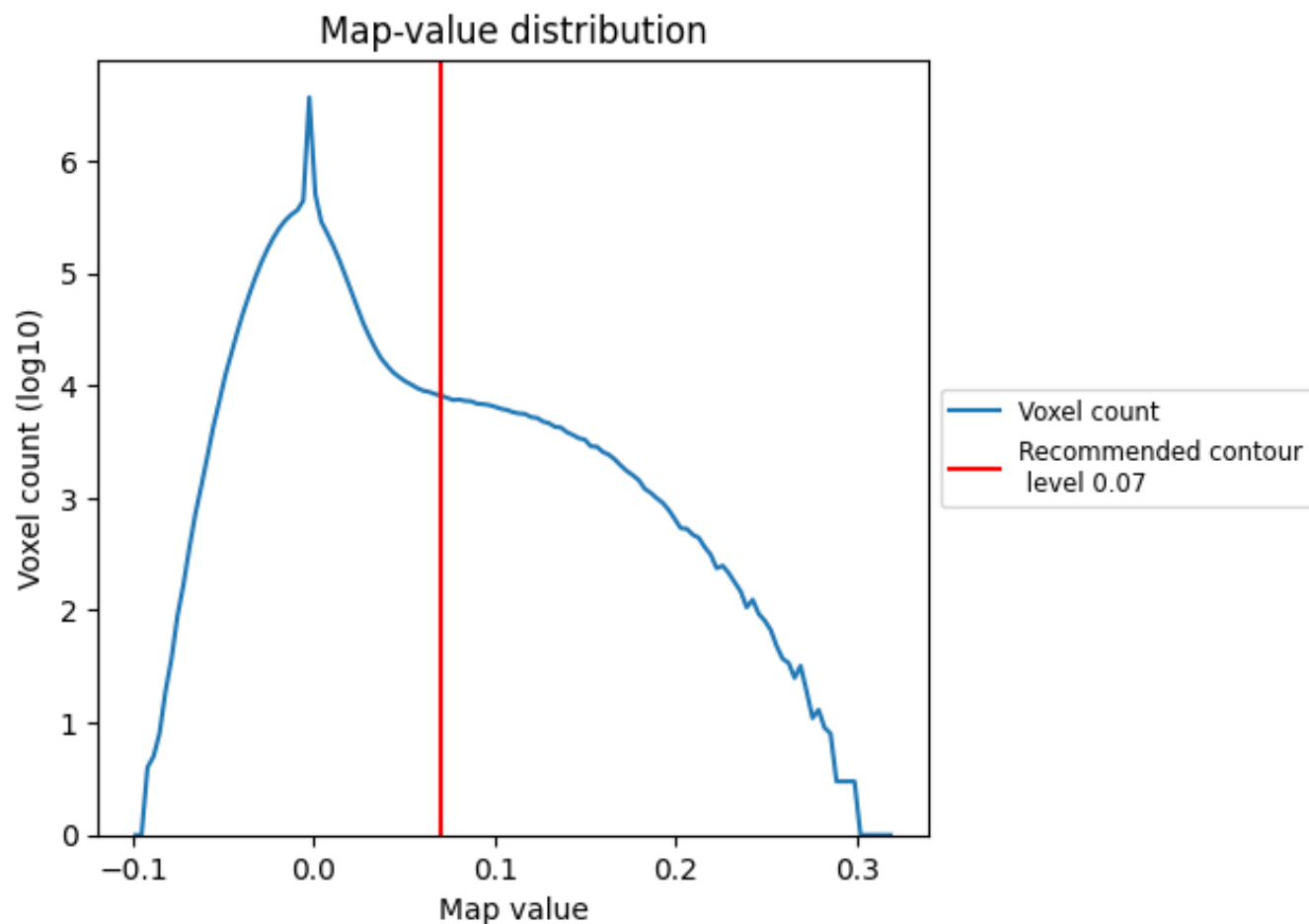
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

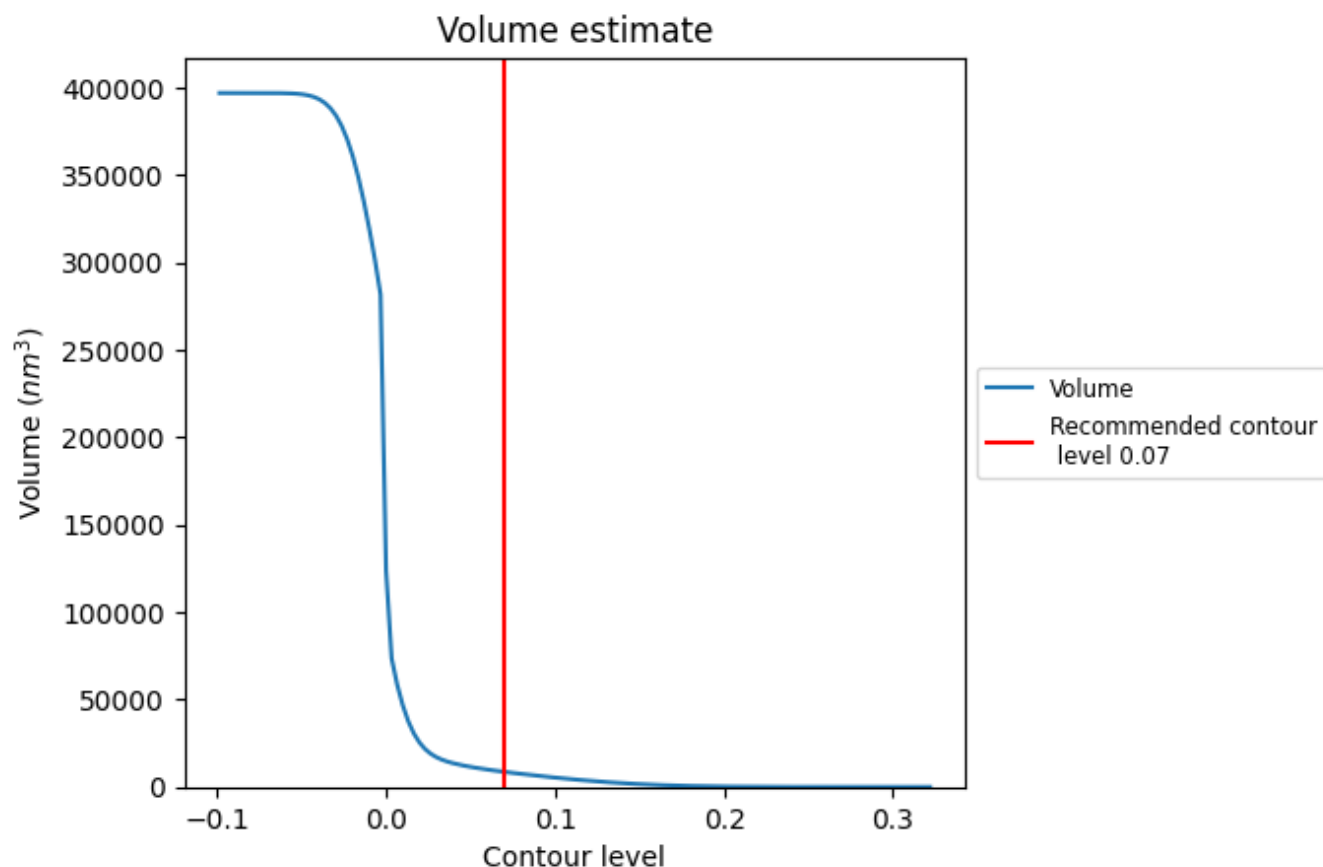
This section contains the results of statistical analysis of the map.

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.

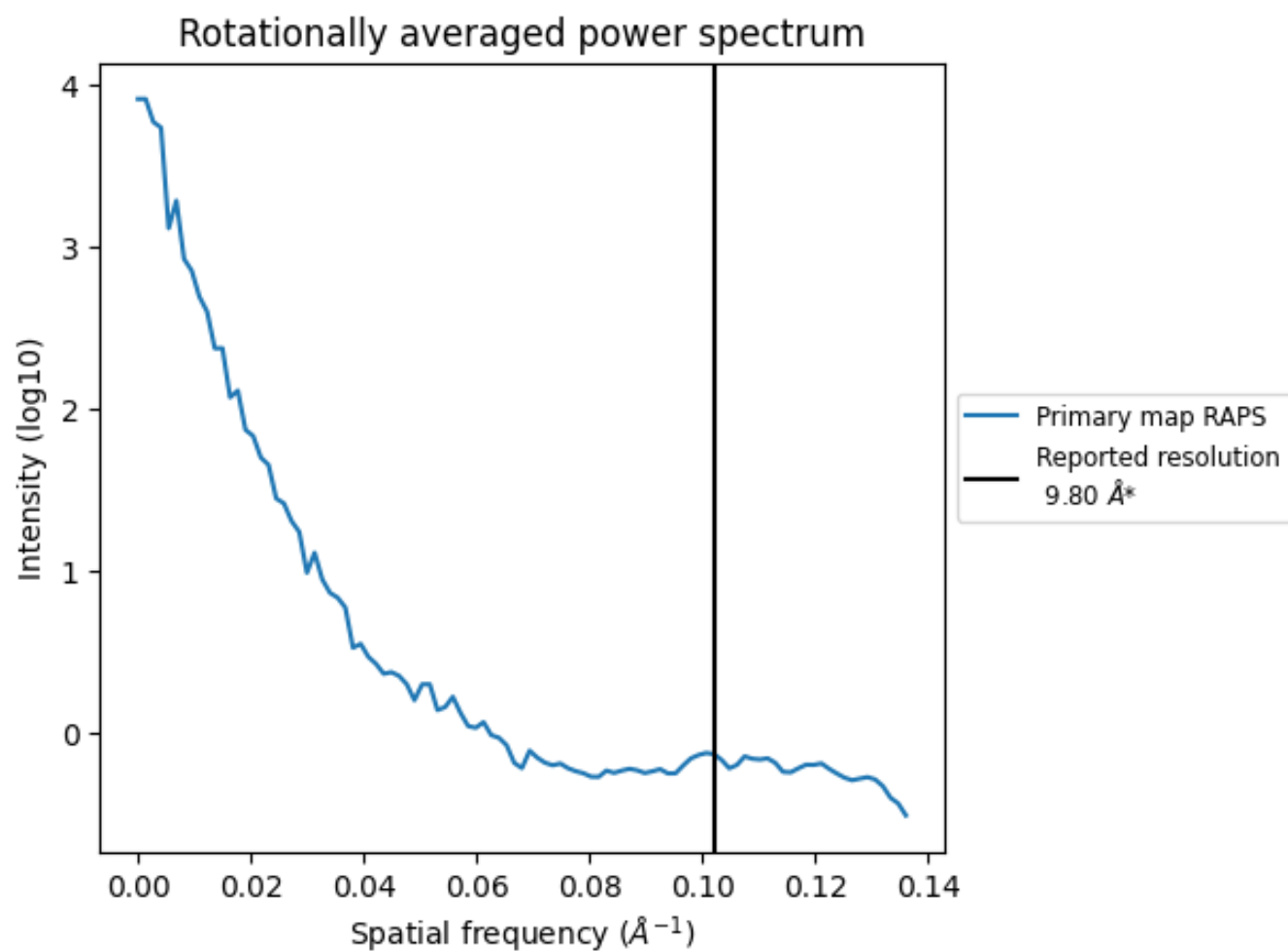
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 8639 nm^3 ; this corresponds to an approximate mass of 7804 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 0.102 Å⁻¹

8 Fourier-Shell correlation

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

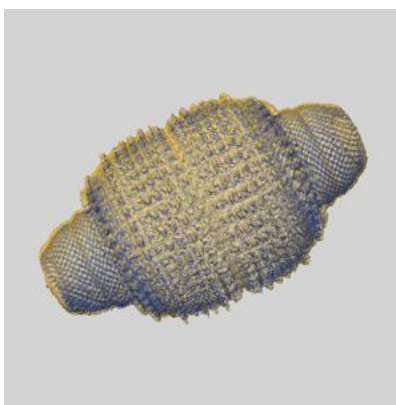
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13483 and PDB model 7PKZ. Per-residue inclusion information can be found in section [3](#) on page [25](#).

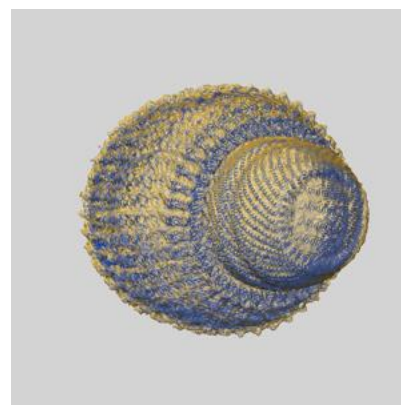
9.1 Map-model overlay [i](#)



X



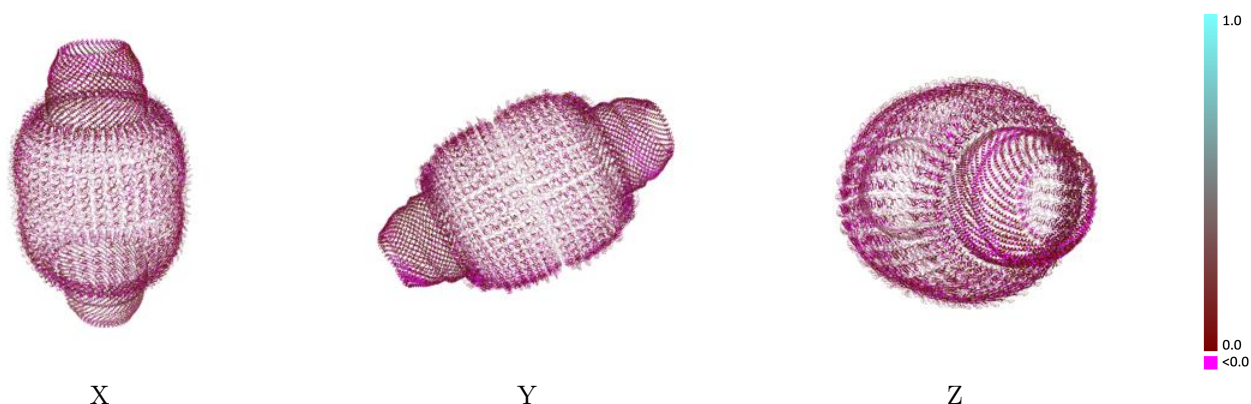
Y



Z

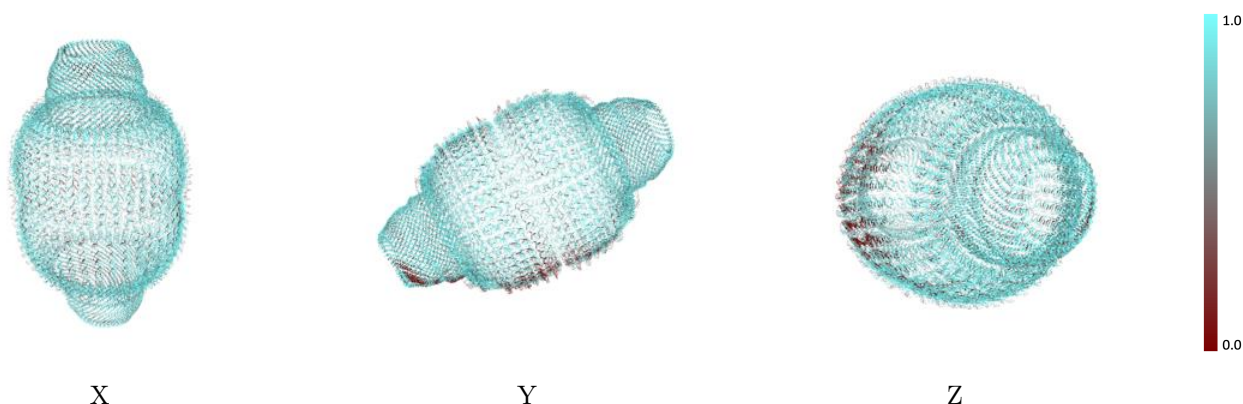
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



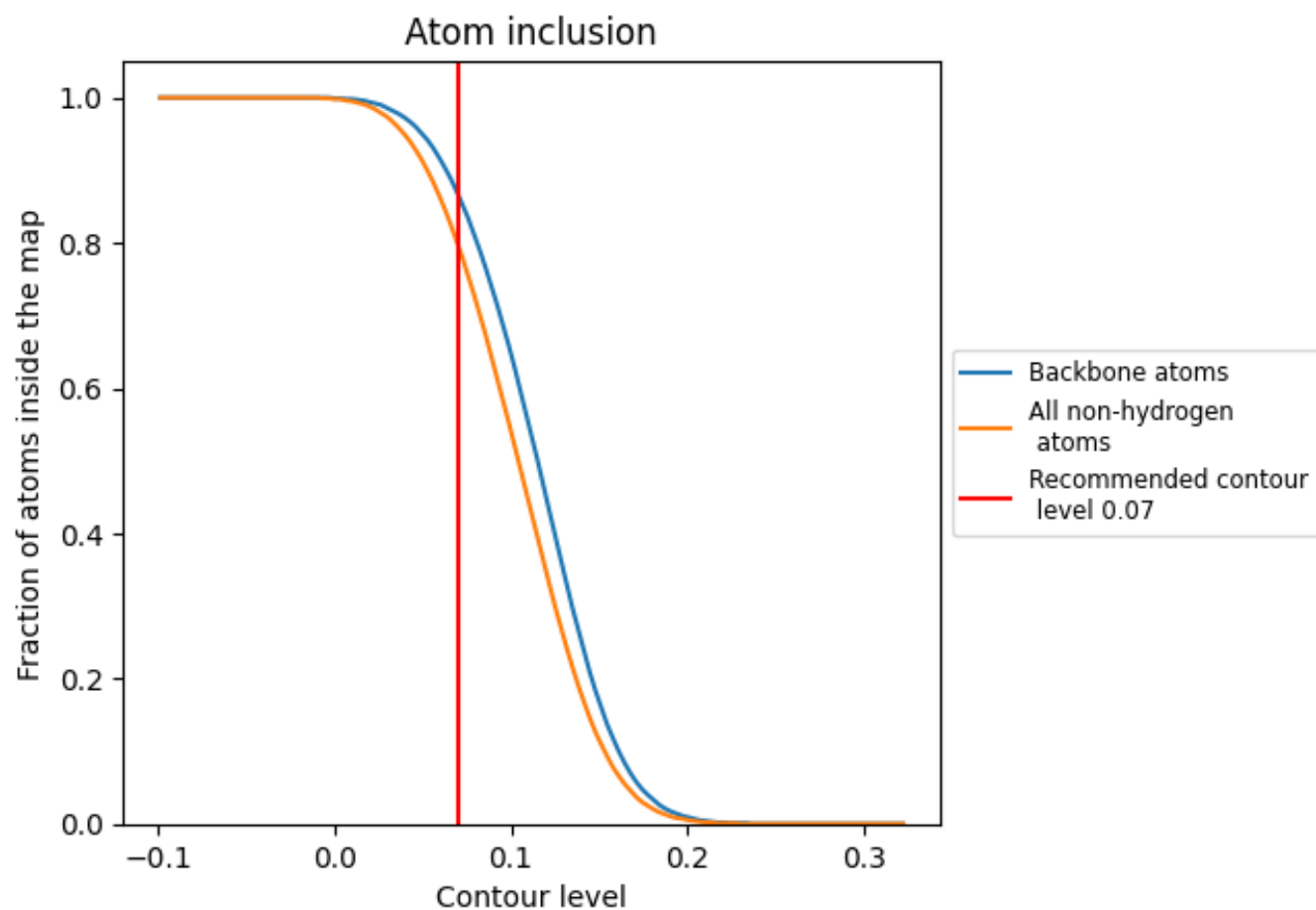
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 80% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.0830
A	 0.7460	 0.0900
AA	 0.8600	 0.1080
AB	 0.7930	 0.0780
AC	 0.5600	 0.0480
B	 0.6180	 0.0570
BA	 0.7990	 0.0950
BB	 0.8550	 0.0870
C	 0.8290	 0.0930
CA	 0.8500	 0.1030
CB	 0.8490	 0.0870
D	 0.5900	 0.0420
DA	 0.8030	 0.0950
DB	 0.8520	 0.0870
E	 0.8370	 0.0960
EA	 0.8570	 0.1020
EB	 0.8420	 0.0860
F	 0.6180	 0.0460
FA	 0.8230	 0.0940
FB	 0.8550	 0.0840
G	 0.8460	 0.0860
GA	 0.8600	 0.1020
GB	 0.8040	 0.0630
H	 0.6500	 0.0530
HA	 0.8350	 0.0930
HB	 0.7330	 0.0430
I	 0.8500	 0.0880
IA	 0.8660	 0.1040
IB	 0.6880	 0.0550
J	 0.6790	 0.0530
JA	 0.8510	 0.0970
JB	 0.6790	 0.0570
K	 0.8490	 0.0940
KA	 0.8420	 0.0950
KB	 0.7390	 0.0650



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Chain	Atom inclusion	Q-score
L	 0.7590	 0.0590
LA	 0.8400	 0.0970
LB	 0.7960	 0.0810
M	 0.8550	 0.0910
MA	 0.8450	 0.0970
MB	 0.7140	 0.0630
N	 0.7960	 0.0800
NA	 0.8240	 0.0920
NB	 0.6560	 0.0780
O	 0.8620	 0.1030
OA	 0.8280	 0.0890
OB	 0.8220	 0.0810
P	 0.8190	 0.0830
PA	 0.8340	 0.0810
PB	 0.8620	 0.1090
Q	 0.8620	 0.1120
QA	 0.8530	 0.1010
QB	 0.8660	 0.1050
R	 0.8400	 0.0930
RA	 0.8550	 0.0860
RB	 0.8490	 0.1000
S	 0.8610	 0.1080
SA	 0.7680	 0.0680
SB	 0.8370	 0.1000
T	 0.8590	 0.1070
TA	 0.8540	 0.0800
TB	 0.8290	 0.0940
UA	 0.7430	 0.0680
UB	 0.7340	 0.0530
V	 0.8480	 0.0980
VA	 0.8490	 0.0760
VB	 0.7820	 0.0700
W	 0.8610	 0.1060
WA	 0.7160	 0.0660
WB	 0.7610	 0.0570
X	 0.8390	 0.1030
XA	 0.8430	 0.0820
XB	 0.7660	 0.0570
Y	 0.8600	 0.1060
YA	 0.7640	 0.0740
YB	 0.7070	 0.0490
Z	 0.8160	 0.0940

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Chain	Atom inclusion	Q-score
ZA	 0.8510	 0.0860
ZB	 0.5850	 0.0380