



wwPDB EM Validation Summary Report ⓘ

May 5, 2026 – 09:17 pm BST

PDB ID : 9QWQ / pdb_00009qwq
EMDB ID : EMD-53423
Title : Human vault protein - committed conformation
Authors : Lapenta, F.; Marechal, N.; Durand, A.; Aupic, J.; Cassetta, A.
Deposited on : 2025-04-15
Resolution : 4.45 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

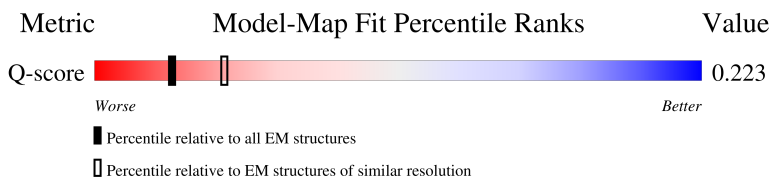
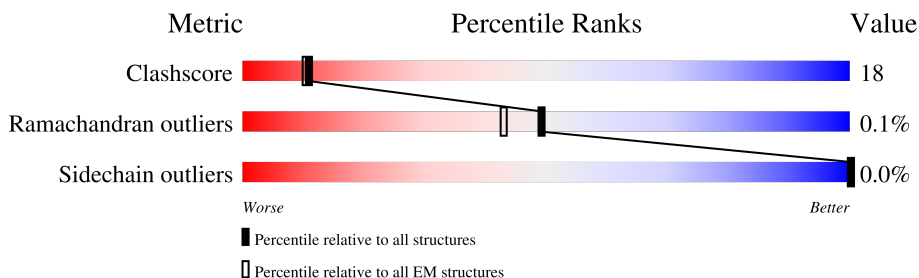
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.45 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.













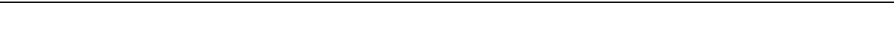

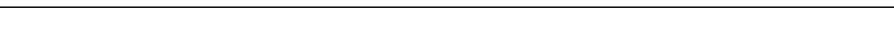
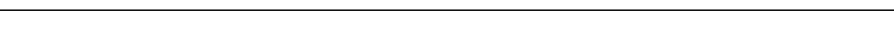











Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3027 (3.95 - 4.95)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	893	58% 30% 13%
1	AA	893	58% 29% 13%
1	AB	893	57% 30% 13%
1	AC	893	57% 30% 13%











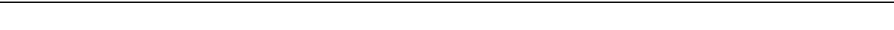

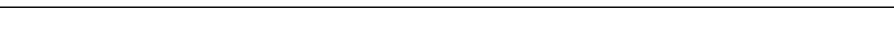
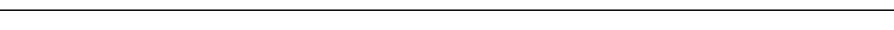











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Mol	Chain	Length	Quality of chain
1	B	893	
1	BA	893	
1	BB	893	
1	C	893	
1	CA	893	
1	CB	893	
1	D	893	
1	DA	893	
1	DB	893	
1	E	893	
1	EA	893	
1	EB	893	
1	F	893	
1	FA	893	
1	FB	893	
1	G	893	
1	GA	893	
1	GB	893	
1	H	893	
1	HA	893	
1	HB	893	
1	I	893	
1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



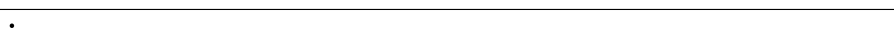
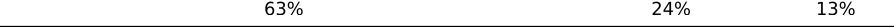


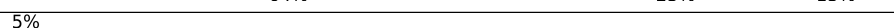



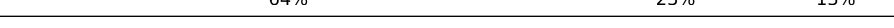



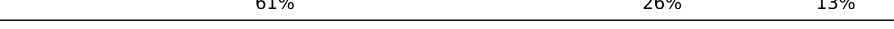


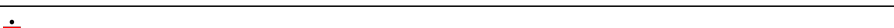






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Mol	Chain	Length	Quality of chain
1	JA	893	
1	JB	893	
1	K	893	
1	KA	893	
1	KB	893	
1	L	893	
1	LA	893	
1	LB	893	
1	M	893	
1	MA	893	
1	MB	893	
1	N	893	
1	NA	893	
1	NB	893	
1	O	893	
1	OA	893	
1	OB	893	
1	P	893	
1	PA	893	
1	PB	893	
1	Q	893	
1	QA	893	
1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

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

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 482118 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	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	AA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	AB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	AC	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	B	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	BA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	BB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	C	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	CA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	CB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	D	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	DA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	DB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	E	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	EA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	EB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	F	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	FB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	G	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	GA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	GB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	H	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	HA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	HB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	I	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	IA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	IB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	J	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	JA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	JB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	K	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	KA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	KB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	L	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	LA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	LB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	M	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	MA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	MB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	N	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	NA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	NB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	O	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	OA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	OB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	P	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	PA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	PB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	Q	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	QA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	QB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	R	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	RA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	RB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	S	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	SA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	SB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	T	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0

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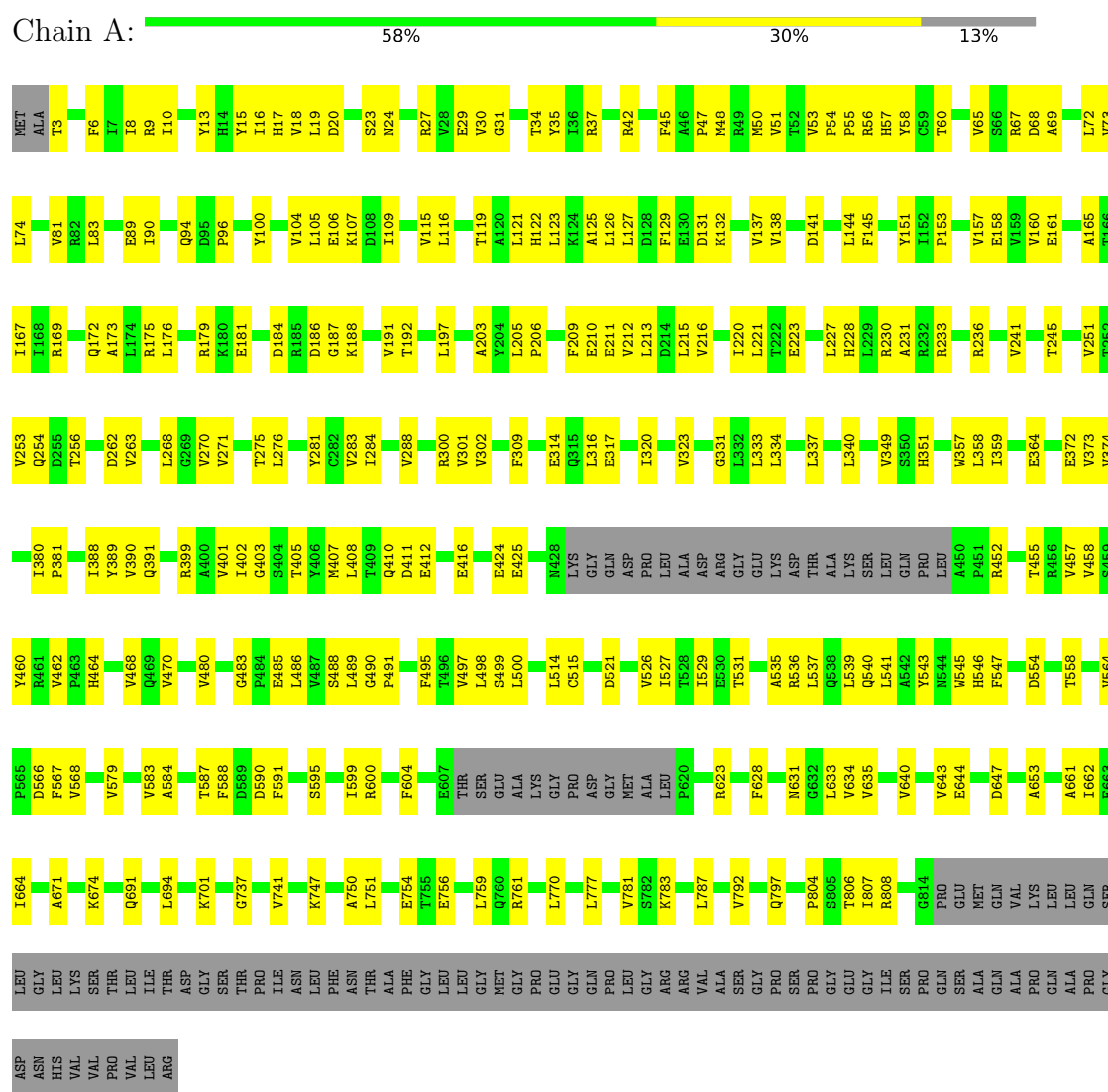
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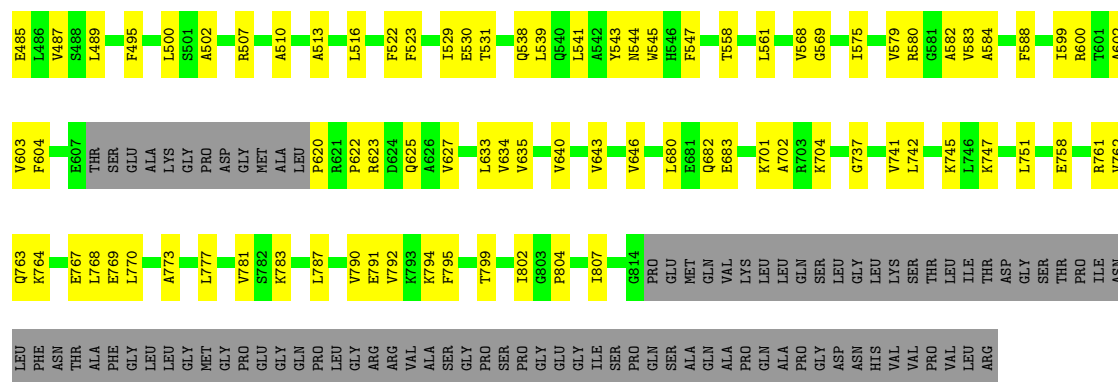
Mol	Chain	Residues	Atoms					AltConf	Trace
1	TA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	TB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	UA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	UB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	V	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	VA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	VB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	W	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	WA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	WB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	X	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	XA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	XB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	Y	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	YA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	YB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	Z	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	ZA	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0
1	ZB	779	Total 6181	C 3890	N 1105	O 1176	S 10	0	0

3 Residue-property plots

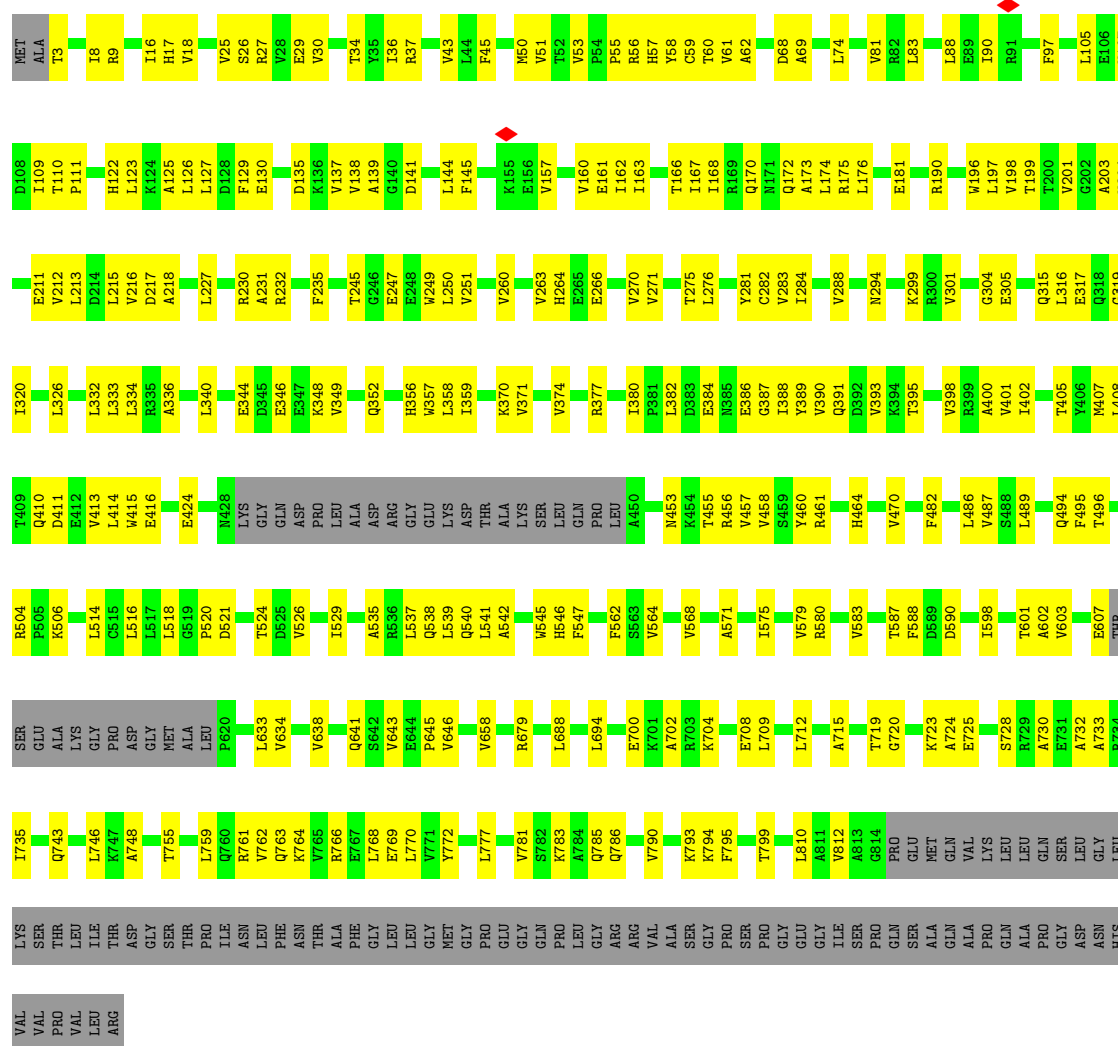
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Major vault protein





• Molecule 1: Major vault protein



• Molecule 1: Major vault protein



VAL	LEU	ARG	LEU	ILE	THR	ASP	GLY	SER	THR	PRO	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	MET	GLY	GLY	ARG	ARG	VAL	ALA	SER	GLY	PRO	SER	PRO	GLN	ALA	ALA	GLN	PRO	GLN	ALA	LEU	GLN	GLY	ASP	ASN	HIS	VAL	VAL	PRO					
V664	Q678	P685	I575	V579	R580	V741	K747	A750	L751	E754	T755	S595	E607	THR	SER	GLU	ALA	GLY	GLY	PRO	ASP	GLY	MET	ALA	LEU	P620	V627	L633	V634	V635	V638	D639	GLU	MET	R536	E644	P645	T650	A653	A661	L662	E663	L664	H675	THR									
F565	F567	V568	R479	V480	F482	E485	V487	S488	L489	Q494	F495	T496	V497	S499	L500	S501	A502	P505	K506	R507	A510	ALA	A513	D521	F522	V526	I529	E530	T531	H534	A535	R536	E544	P545	T546	V547	Y543	F547	E548	V549	R552													
G396	K397	V398	R399	T402	G403	S404	T405	M407	L408	T409	Q410	D411	E416	K417	L418	L419	E424	E425	L426	L427	M428	LYS	GLY	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	ASP	THR	ALA	LYS	SER	E375	LEU	GLN	PRO	LEU	A450	T455	R456	V457	Y460	R461	W462	P463	H464	A465	M466
L285	D286	P287	R300	V301	V302	F309	Q315	P309	Q315	L326	G331	L332	L333	L334	R335	A336	L337	Q338	P339	D345	V349	S350	H351	Q352	A353	L358	I359	R360	G361	P362	Y365	V366	V374	E375	E376	R377	I380	P381	L382	D383	E384	I388	Y389	V390	R461	W462	P463	H464	A465	K466	T467			
K188	T192	I199	V196	L197	E103	V104	L105	E106	K107	D108	I109	T110	P111	L112	V114	V115	L116	T119	H228	L229	R230	A231	R232	R233	N234	F235	R236	R239	G240	V241	T245	G246	E247	E248	W249	L250	D262	V263	H264	V267	L268	G269	V270	V271	P272	T273	T274	T275	C282	L284	G187			
MET	ALA	T3	E4	E5	I7	I8	R9	I10	Y13	H14	Y15	I16	H17	D20	V28	E29	G31	T34	R37	N40	P47	M50	V51	V53	H57	T58	C59	T60	V61	A62	V65	S66	R67	V73	V81	R82	L83	R84	L88	E89	I90	D95												

• Molecule 1: Major vault protein

Chain BA: 55% 32% 13%

D411	E412	V413	L414	W415	L419	M428	LYS	GLY	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	THR	ALA	LYS	SER	LEU	GLN	PRO	LEU	A450	R451	N453	K454	T455	R456	V457	V458	S459	Y460	R461	V462	P463	H464	N465	A466	A467	V468	Q469	V470	Y471	D472	G483	P484	E485	L486	V487	S488
Q329	Q330	G331	L332	L333	L334	R335	A336	P339	L340	E341	E342	G343	E344	E347	H351	Q352	A353	V357	L358	T359	R360	L363	E364	V365	V366	V374	E375	E376	R377	L382	E386	G387	L388	V389	Q391	V398	R399	A400	V401	L402	G403	S404	T405	Y406	M407	L408	T409	Q410						
V212	L213	D214	L215	V216	L221	L227	H228	L229	V251	G243	T256	D262	V263	H264	E265	L268	G269	V270	T273	T274	L275	L276	Y281	C282	V283	L284	L285	V288	N294	R300	V301	V302	S307	L310	E314	Q315	L316	E317	Q318	G319	L320	Q321	V325	L326										
L92	P96	F97	P101	V104	L105	K107	D108	I109	T110	P111	L112	V115	L116	A120	L121	L126	L127	E146	T150	V159	V160	E161	I162	I163	I168	R169	Q170	M171	Q172	R173	L174	R175	G187	K188	L197	V198	T199	T200	V201	Y204	L205	P206	A207	V208										
MET	ALA	T3	F6	I7	I8	R9	I10	Y13	H14	Y15	I16	H17	R27	V28	E29	V30	P32	I36	V43	L44	F45	A46	P47	M48	R49	M50	V53	H57	T60	N63	P64	V65	S66	R67	A69	L72	V73	L74	V81	R82	L83	A86	I90	R91										

L489	G490	P491	E492	E493	Q494	F495	T496	S501	R507	P508	L514	C515	L516	L517	L518	D521	F522	F523	T524	D525	V526	I527	T528	I529	E530	H534	Q538	L539	Q540	L541	A542	Y543	N544	W545	H546	F547	E548	V549	F567	K573	I575	A576	S577	R578	V579	R580	G581	A582	V583	A584
S585	V586	F587	F588	D589	A596	I599	R600	T601	F604	E607	THR	SER	GLU	ALA	LYS	GLY	PRO	ASP	GLY	MET	ALA	LEU	P620	R621	P622	R623	F628	L633	V634	V635	S636	S637	V638	D639	V640	Q641	S642	V643	E644	V645	V646	T650	L654	V658	I662	T666	R679			
L680	R687	R690	Q691	L694	E705	E708	A732	I735	V741	A744	K745	L746	K747	A750	L751	E754	E758	V762	Q763	R764	R765	R766	E767	L768	E769	L770	V771	Y772	V781	S782	Q786	L787	A788	E789	V790	E791	V792	I802	G803	I807	R808									
G814	PRO	GLU	MET	GLN	VAL	LYS	LEU	GLN	ALA	ASP	GLY	SER	THR	LEU	ILE	THR	ASP	GLY	PRO	THR	ALA	LEU	ASN	PHE	ASN	THR	ALA	PHE	GLY	LEU	GLY	LEU	ARG	ARG	VAL	ALA	SER	GLY	PRO	PRO	GLY	GLU	ILE	SER						
PRO	GLN	SER	ALA	GLN	ALA	PRO	GLN	ALA	ASP	ASN	HIS	VAL	VAL	PRO	PRO	VAL	ARG																																	

- Molecule 1: Major vault protein

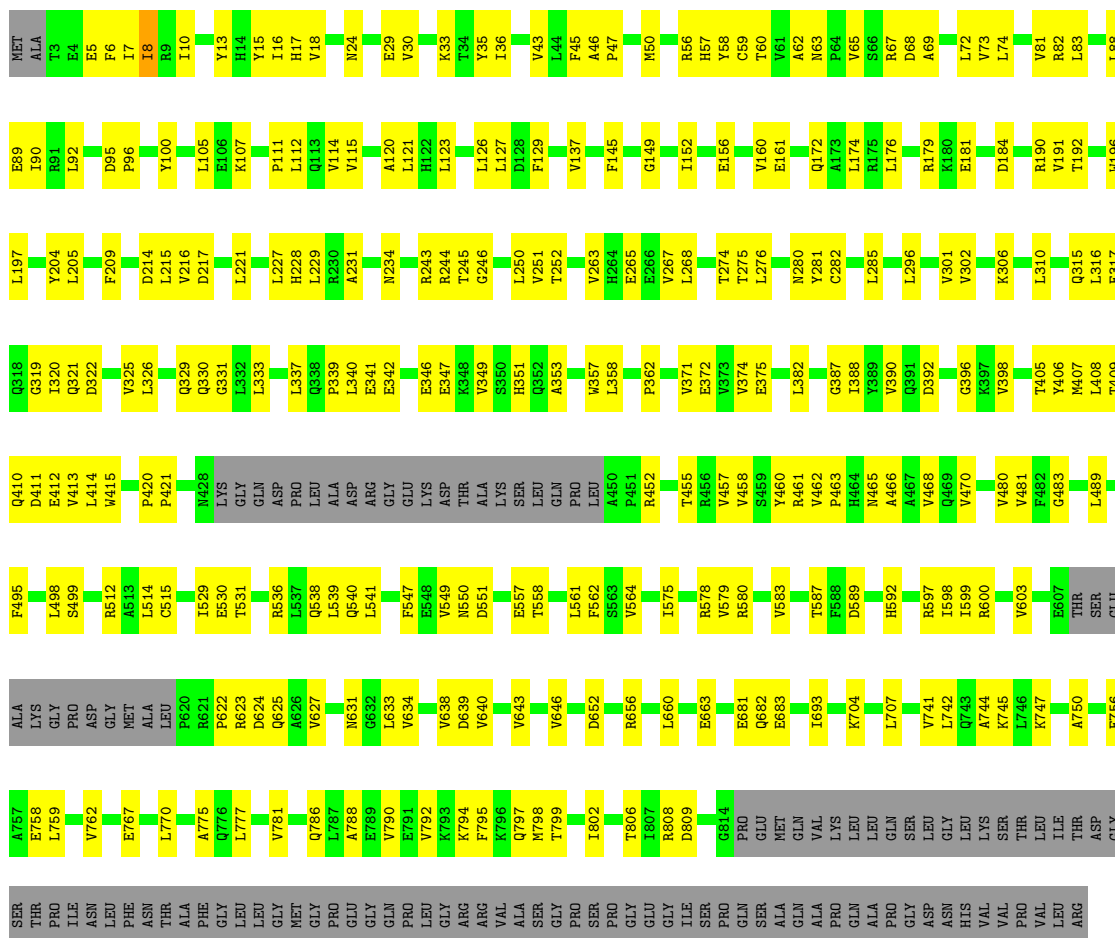
Chain BB:  58% 30% 13%

PRO	GLN	LEU	ALA	PRO	GLY	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	LEU	ARG	LYS	R679	W545	SER	G361	V267	Q170	L83	MET
																LEU	P362	LEU	P362	L84	ALA	T3		
PRO	GLN	LEU	ALA	PRO	GLY	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	LEU	ARG	GLN	I693	F547	GLN	L363	V270	Q172	H85	E4
																LEU	E364	LEU	E364	L90	E5			
ASP	ASN	LEU	GLY	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I8	R703	E557	LEU	Y365	L174	A173	R91	F6	
																LEU	P367	R175	L92	I7				
ASN	HIS	LEU	GLY	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I8	E717	V568	T455	S368	T274	R177	L92	I7	
																LEU	R456	T275	R177	I8				
VAL	VAL	PRO	PRO	VAL	VAL	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I8	T721	G569	V457	K370	L276	A178	F97	R9	
																LEU	V371	Y100	F97	R9				
PRO	VAL	LEU	LEU	VAL	VAL	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I16	R729	I575	R461	H279	C182	Y100	Y15		
																LEU	V371	Y100	Y15	I16				
LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I16	V741	V579	V462	Y281	D184	L105	H17		
																LEU	R580	E375	Y281	L105	H17			
ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I19	L742	R580	Q469	C282	R190	K107	L19		
																LEU	V283	R190	K107	L19				
SER	GLY	SER	THR	THR	THR	THR	THR	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I22	K745	V583	Y471	P381	V288	E195	T110		
																LEU	V583	Y471	P381	V288	E195	T110		
SER	GLY	SER	THR	THR	THR	THR	THR	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I22	L746	V586	E475	T388	N294	W196	P111		
																LEU	V586	E475	T388	N294	W196	P111		
ASN	GLY	ASN	PHE	PHE	PHE	PHE	PHE	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	T755	I755	K476	Y389	Q295	L197	L112		
																LEU	I755	K476	Y389	Q295	L197	L112		
ASN	GLY	ASN	PHE	PHE	PHE	PHE	PHE	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	E756	F591	R477	V390	L296	A203	V114		
																LEU	F591	R477	V390	L296	A203	V114		
ASN	GLY	ASN	PHE	PHE	PHE	PHE	PHE	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	L759	R597	V480	V393	V301	L205	V115		
																LEU	R597	V480	V393	V301	L205	V115		
ASN	GLY	ASN	PHE	PHE	PHE	PHE	PHE	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	Q760	I598	F495	T405	V302	P206	A120		
																LEU	I598	F495	T405	V302	P206	A120		
THR	GLY	THR	THR	THR	THR	THR	THR	PRO	PRO	VAL	LEU	LEU	LEU	ARG	I22	R761	I599	E485	G396	K303	A207	V30		
																LEU	I599	E485	G396	K303	A207	V30		
ALA	GLY	ALA	PHE	PHE	PHE	PHE	PHE	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	V765	T601	V487	V401	K306	E210	K124		
																LEU	T601	V487	V401	K306	E210	K124		
GLY	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	R766	E507	F495	T405	Q311	V212	Y36		
																LEU	E507	F495	T405	Q311	V212	Y36		
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLY	GLY	VAL	LEU	LEU	LEU	ARG	I22	E767	THR	L498	M407	L215	L127	P47		
																LEU	THR	L498	M407	L215	L127	P47		
GLY	MET	GLY	MET	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	L770	SER	L498	M407	L215	L127	P47		
																LEU	SER	L498	M407	L215	L127	P47		
GLY	MET	GLY	MET	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	Y771	GLU	L408	L408	V216	D128	V43		
																LEU	GLU	L408	L408	V216	D128	V43		
PRO	GLY	PRO	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	Y772	ALA	A502	T409	Q321	D217	E130		
																LEU	ALA	A502	T409	Q321	D217	E130		
PRO	GLY	PRO	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	A775	LYS	G503	Q410	Q322	R230	G140		
																LEU	LYS	G503	Q410	Q322	R230	G140		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	Q776	PRO	R504	D411	V323	R230	G140		
																LEU	PRO	R504	D411	V323	R230	G140		
GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	L777	ASP	A510	E412	V324	R233	G140		
																LEU	ASP	A510	E412	V324	R233	G140		
PRO	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	V781	GLY	A513	V413	V325	A226	M50		
																LEU	GLY	A513	V413	V325	A226	M50		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	S782	ALA	L514	E416	R335	H228	R56		
																LEU	ALA	L514	E416	R335	H228	R56		
ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	MET	GLY	LEU	LEU	LEU	ARG	I22	K783	LEU	C515	A336	L337	G140	Y58		
																LEU	LEU	C515	A336	L337	G140	Y58		
ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	MET	GLY	LEU	LEU	LEU	ARG	I22	A784	P620	L516	V423	R230	G140	C59		
																LEU	P620	L516	V423	R230	G140	C59		
VAL	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	MET	GLY	LEU	LEU	LEU	ARG	I22	Q785	R621	Q786	P622	Q338	R233	G140		
																LEU	R621	Q786	P622	Q338	R233	G140		
SER	SER	SER	SER	SER	SER	SER	SER	SER	MET	GLY	LEU	LEU	LEU	ARG	I22	L787	SER	D521	N428	F238	L144	T60		
																LEU	SER	D521	N428	F238	L144	T60		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	V634	GLY	E341	E342	V241	G147	A62		
																LEU	GLY	E341	E342	V241	G147	A62		
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	MET	GLY	LEU	LEU	LEU	ARG	I22	F795	VAL	V526	GLN	S242	T150	N63		
																LEU	VAL	V526	GLN	S242	T150	N63		
SER	SER	SER	SER	SER	SER	SER	SER	SER	MET	GLY	LEU	LEU	LEU	ARG	I22	T799	SER	I527	ASP	R243	G147	P64		
																LEU	SER	I527	ASP	R243	G147	P64		
PRO	GLY	PRO	GLY	PRO	GLY	PRO	GLY	PRO	MET	GLY	LEU	LEU	LEU	ARG	I22	R799	SER	I527	ASP	R243	G147	P64		
																LEU	SER	I527	ASP	R243	G147	P64		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	A801	E800	I529	LEU	R244	E156	R67		
																LEU	E800	I529	LEU	R244	E156	R67		
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	MET	GLY	LEU	LEU	LEU	ARG	I22	A801	E800	I529	LEU	R244	E156	R67		
																LEU	E800	I529	LEU	R244	E156	R67		
ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	MET	GLY	LEU	LEU	LEU	ARG	I22	T806	Q641	T531	ASP	G246	E159	A69		
																LEU	Q641	T531	ASP	G246	E159	A69		
SER	SER	SER	SER	SER	SER	SER	SER	SER	MET	GLY	LEU	LEU	LEU	ARG	I22	T806	Q641	T531	ASP	G246	E159	A69		
																LEU	Q641	T531	ASP	G246	E159	A69		
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
SER	SER	SER	SER	SER	SER	SER	SER	SER	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	MET	GLY	LEU	LEU	LEU	ARG	I22	G814	GLY	Q538	GLY	A353	V160	Q70		
																LEU	GLY	Q538	GLY	A353	V160	Q70		

- Molecule 1: Major vault protein

- Molecule 1: Major vault protein

Chain CB: 



- Molecule 1: Major vault protein

Chain D:  56% 31% 13%

MET	ALA	T3	E4	E5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15	F16	F17	F18	F19	F20	F21	F22	F23	F24	F25	F26	F27	F28	F29	F30	F31	F32	F33	F34	F35	F36	F37	F38	F39	F40	F41	F42	F43	F44	F45	F46	F47	F48	F49	F50	F51	F52	F53	F54	F55	F56	F57	F58	F59	F60	F61	F62	F63	F64	F65	F66	F67	F68	F69	F70	F71	F72	F73	F74	F75	F76	F77	F78	F79	F80	F81	F82	F83	F84	F85	F86	F87	F88	F89	F90	F91	F92	F93	F94	F95	F96	F97	F98	F99	F100	F101	F102	F103	F104	F105	F106	F107	F108	F109	F110	F111	F112	F113	F114	F115	F116	F117	F118	F119	F120	F121	F122	F123	F124	F125	F126	F127	F128	F129	F130	F131	F132	F133	F134	F135	F136	F137	F138	F139	F140	F141	F142	F143	F144	F145	F146	F147	F148	F149	F150	F151	F152	F153	F154	F155	F156	F157	F158	F159	F160	F161	F162	F163	F164	F165	F166	F167	F168	F169	F170	F171	F172	F173	F174	F175	F176	F177	F178	F179	F180	F181	F182	F183	F184	F185	F186	F187	F188	F189	F190	F191	F192	F193	F194	F195	F196	F197	F198	F199	F200	F201	F202	F203	F204	F205	F206	F207	F208	F209	F210	F211	F212	F213	F214	F215	F216	F217	F218	F219	F220	F221	F222	F223	F224	F225	F226	F227	F228	F229	F230	F231	F232	F233	F234	F235	F236	F237	F238	F239	F240	F241	F242	F243	F244	F245	F246	F247	F248	F249	F250	F251	F252	F253	F254	F255	F256	F257	F258	F259	F260	F261	F262	F263	F264	F265	F266	F267	F268	F269	F270	F271	F272	F273	F274	F275	F276	F277	F278	F279	F280	F281	F282	F283	F284	F285	F286	F287	F288	F289	F290	F291	F292	F293	F294	F295	F296	F297	F298	F299	F300	F301	F302	F303	F304	F305	F306	F307	F308	F309	F310	F311	F312	F313	F314	F315	F316	F317	F318	F319	F320	F321	F322	F323	F324	F325	F326	F327	F328	F329	F330	F331	F332	F333	F334	F335	F336	F337	F338	F339	F340	F341	F342	F343	F344	F345	F346	F347	F348	F349	F350	F351	F352	F353	F354	F355	F356	F357	F358	F359	F360	F361	F362	F363	F364	F365	F366	F367	F368	F369	F370	F371	F372	F373	F374	F375	F376	F377	F378	F379	F380	F381	F382	F383	F384	F385	F386	F387	F388	F389	F390	F391	F392	F393	F394	F395	F396	F397	F398	F399	F400	F401	F402	F403	F404	F405	F406	F407	F408	F409	F410	F411	F412	F413	F414	F415	F416	F417	F418	F419	F420	F421	F422	F423	F424	F425	F426	F427	F428	F429	F430	F431	F432	F433	F434	F435	F436	F437	F438	F439	F440	F441	F442	F443	F444	F445	F446	F447	F448	F449	F450	F451	F452	F453	F454	F455	F456	F457	F458	F459	F460	F461	F462	F463	F464	F465	F466	F467	F468	F469	F470	F471	F472	F473	F474	F475	F476	F477	F478	F479	F480	F481	F482	F483	F484	F485	F486	F487	F488	F489	F490	F491	F492	F493	F494	F495	F496	F497	F498	F499	F500	F501	F502	F503	F504	F505	F506	F507	F508	F509	F510	F511	F512	F513	F514	F515	F516	F517	F518	F519	F520	F521	F522	F523	F524	F525	F526	F527	F528	F529	F530	F531	F532	F533	F534	F535	F536	F537	F538	F539	F540	F541	F542	F543	F544	F545	F546	F547	F548	F549	F550	F551	F552	F553	F554	F555	F556	F557	F558	F559	F560	F561	F562	F563	F564	F565	F566	F567	F568	F569	F570	F571	F572	F573	F574	F575	F576	F577	F578	F579	F580	F581	F582	F583	F584	F585	F586	F587	F588	F589	F590	F591	F592	F593	F594	F595	F596	F597	F598	F599	F600	F601	F602	F603	F604	F605	F606	F607	F608	F609	F610	F611	F612	F613	F614	F615	F616	F617	F618	F619	F620	F621	F622	F623	F624	F625	F626	F627	F628	F629	F630	F631	F632	F633	F634	F635	F636	F637	F638	F639	F640	F641	F642	F643	F644	F645	F646	F647	F648	F649	F650	F651	F652	F653	F654	F655	F656	F657	F658	F659	F660	F661	F662	F663	F664	F665	F666	F667	F668	F669	F670	F671	F672	F673	F674	F675	F676	F677	F678	F679	F680	F681	F682	F683	F684	F685	F686	F687	F688	F689	F690	F691	F692	F693	F694	F695	F696	F697	F698	F699	F700	F701	F702	F703	F704	F705	F706	F707	F708	F709	F710	F711	F712	F713	F714	F715	F716	F717	F718	F719	F720	F721	F722	F723	F724	F725	F726	F727	F728	F729	F730	F731	F732	F733	F734	F735	F736	F737	F738	F739	F740	F741	F742	F743	F744	F745	F746	F747	F748	F749	F750	F751	F752	F753	F754	F755	F756	F757	F758	F759	F760	F761	F762	F763	F764	F765	F766	F767	F768	F769	F770	F771	F772	F773	F774	F775	F776	F777	F778	F779	F780	F781	F782	F783	F784	F785	F786	F787	F788	F789	F790	F791	F792	F793	F794	F795	F796	F797	F798	F799	F800	F801	F802	F803	F804	F805	F806	F807	F808	F809	F810	F811	F812	F813	F814	F815	F816	F817	F818	F819	F820	F821	F822	F823	F824	F825	F826	F827	F828	F829	F830	F831	F832	F833	F834	F835	F836	F837	F838	F839	F840	F841	F842	F843	F844	F845	F846	F847	F848	F849	F850	F851	F852	F853	F854	F855	F856	F857	F858	F859	F860	F861	F862	F863	F864	F865	F866	F867	F868	F869	F870	F871	F872	F873	F874	F875	F876	F877	F878	F879	F880	F881	F882	F883	F884	F885	F886	F887	F888	F889	F890	F891	F892	F893	F894	F895	F896	F897	F898	F899	F900	F901	F902	F903	F904	F905	F906	F907	F908	F909	F910	F911	F912	F913	F914	F915	F916	F917	F918	F919	F920	F921	F922	F923	F924	F925	F926	F927	F928	F929	F930	F931	F932	F933	F934	F935	F936	F937	F938	F939	F940	F941	F942	F943	F944	F945	F946	F947	F948	F949	F950	F951	F952	F953	F954	F955	F956	F957	F958	F959	F960	F961	F962	F963	F964	F965	F966	F967	F968	F969	F970	F971	F972	F973	F974	F975	F976	F977	F978	F979	F980	F981	F982	F983	F984	F985	F986	F987	F988	F989	F990	F991	F992	F993	F994	F995	F996	F997	F998	F999	F1000	F1001	F1002	F1003	F1004	F1005	F1006	F1007	F1008	F1009	F1010	F1011	F1012	F1013	F1014	F1015	F1016	F1017	F10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K348	V349	ASP	GLN	F523	GLY	R761	PHE
L350	L351	PRD	ASP	V526	MET	V762	ASN
H351	ALA	LEU	PRD	LEU	ALA		THR
Q352	ALA	ALA	ASP	LEU	PHE	V765	PHE
A353	ARG	ARG	GLY	I529	GLY	R766	LEU
			GLY	E530	LEU	E767	LEU
W357	GLU	GLY	GLY	H534	LEU	L768	LEU
L358	LYS	LYS	GLY	A535	MET	E769	GLY
I359	ASP	ASP	GLY	R536	GLY	L770	GLY
	THR	THR	THR	L537	PRO	V771	GLY
E364	ALA	ALA	ALA	Q538	GLY	Y772	GLY
	LYS	LYS	LYS	L539	GLY	A773	GLY
V371	SER	SER	SER	Q540	GLN		
E372	LEU	LEU	LEU	L541	PRO	L779	PRO
V373	GLN	GLN	GLN	A542	LEU	E780	LEU
V374	PRO	PRO	PRO	Y543	GLY	V781	GLY
E375	LEU	LEU	LEU	W544	ARG	S782	ARG
E376	LEU	LEU	LEU	W545	ARG	Q785	ARG
R377	P451	R452	P451	L561	VAL		VAL
	R456	V457	R456	S563	SER	A788	SER
I380	V457	V458	V457	V564	GLY	E789	GLY
P381	V458	S459	V458		PRO		PRO
L382	Y460	Y460	Y460		SER	V792	SER
G387	A467	A467	A467	L575	ILE		ILE
I388	V468	Q469	V468	V579	SER		SER
Y389	Q469	Y471	Q469	R580	PRO	G814	PRO
V390	Y471	Y471	Y471	V583	GLN	GLU	GLN
Q391	Y473	Y473	Y473	A584	ALA	GLN	ALA
	K476	R477	K476	F588	ALA	VAL	ALA
V401	T405	A478	T405	D589	PRO	LYS	PRO
I402	Y406	Y406	Y406	F591	GLN	LEU	GLN
G403	M407	L408	M407	S595	PRO	LEU	ALA
S404	L408	W409	L408	E705	ASP	SER	ASP
T405	Q410	S488	Q410	E708	ASN	GLY	ASN
M407	D411	L489	D411	G737	HIS	LEU	HIS
L408	V413	E493	V413	THR	VAL	LYS	VAL
Q403	L414	Q494	L414	THR	PRO	THR	PRO
G403	W415	L498	W415	ILE	VAL	LEU	VAL
S404	E416	S499	E416	THR	LEU	LEU	LEU
T405	K417	L500	T405	ASP	ARG	ARG	ARG
Y406	L419	R511	Y406	GLY	GLY	GLY	GLY
M407	V423	A513	M407	ALA	LYS	ALA	ALA
L408	R512	L516	L408	LYS	GLY	PRO	GLY
Q410	W428	L517	Q410	ASP	ASP	LEU	ASP

• Molecule 1: Major vault protein

Chain DB:  61% 26% 13%

SER	PRO	GLY	GLY	R808	V792	A626	L514	C515	V423	E424	E425	L518	V638	R639	V640	V643	V658	A661	I662	T665	T666	H675	L709	L712	E731	R734	A744	V745	L746	K747	A748	Q749	A750	L751	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	LEU	SER	VAL	VAL	HIS	ASN	ASP	GLY	SER	PRO	ALA	GLN	MET	GLU	PRO	GLN	SER	PRO	SER	ILE	THR	ASP	GLY	LEU	SER	THR	VAL	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN	SER	VAL	HIS	ASN	ASP	GLY	SER	PRO	GLN
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• Molecule 1: Major vault protein

Chain E: 

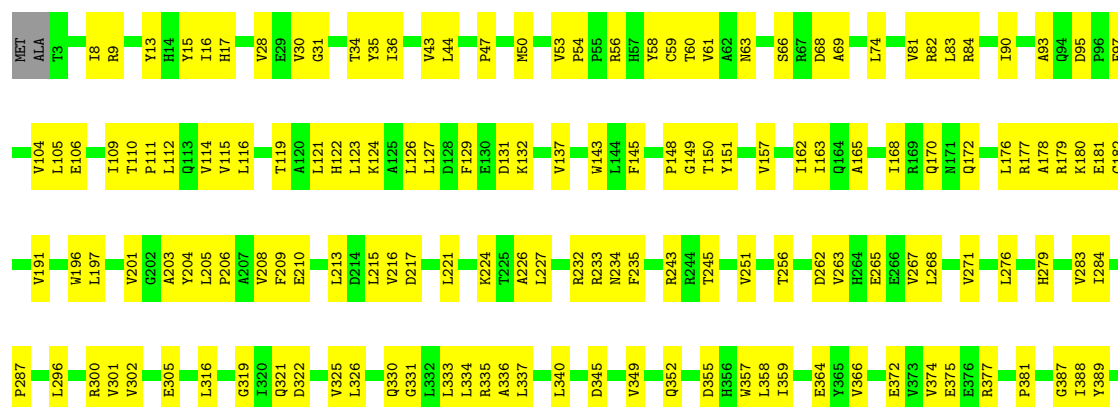
MET	ALA	T3	E4	E5	E6	F6	I7	I8	I9	I10	I11	I12	I13	I14	I15	I16	I17	I18	I19	I20	I21	I22	I23	I24	I25	I26	I27	I28	I29	I30	I31	I32	I33	I34	I35	I36	I37	I38	I39	I40	I41	I42	I43	I44	I45	I46	I47	I48	I49	I50	I51	I52	I53	I54	I55	I56	I57	I58	I59	I60	I61	I62	I63	I64	I65	I66	I67	I68	I69	I70	I71	I72	I73	I74	I75	I76	I77	I78	I79	I80	I81	I82	I83	I84	I85	I86	I87	I88	I89	I90	I91	I92	I93	I94	I95	I96	I97	I98	I99	I100	I101	I102	I103	I104	I105	I106	I107	I108	I109	I110	I111	I112	I113	I114	I115	I116	I117	I118	I119	I120	I121	I122	I123	I124	I125	I126	I127	I128	I129	I130	I131	I132	I133	I134	I135	I136	I137	I138	I139	I140	I141	I142	I143	I144	I145	I146	I147	I148	I149	I150	I151	I152	I153	I154	I155	I156	I157	I158	I159	I160	I161	I162	I163	I164	I165	I166	I167	I168	I169	I170	I171	I172	I173	I174	I175	I176	I177	I178	I179	I180	I181	I182	I183	I184	I185	I186	I187	I188	I189	I190	I191	I192	I193	I194	I195	I196	I197	I198	I199	I200	I201	I202	I203	I204	I205	I206	I207	I208	I209	I210	I211	I212	I213	I214	I215	I216	I217	I218	I219	I220	I221	I222	I223	I224	I225	I226	I227	I228	I229	I230	I231	I232	I233	I234	I235	I236	I237	I238	I239	I240	I241	I242	I243	I244	I245	I246	I247	I248	I249	I250	I251	I252	I253	I254	I255	I256	I257	I258	I259	I260	I261	I262	I263	I264	I265	I266	I267	I268	I269	I270	I271	I272	I273	I274	I275	I276	I277	I278	I279	I280	I281	I282	I283	I284	I285	I286	I287	I288	I289	I290	I291	I292	I293	I294	I295	I296	I297	I298	I299	I300	I301	I302	I303	I304	I305	I306	I307	I308	I309	I310	I311	I312	I313	I314	I315	I316	I317	I318	I319	I320	I321	I322	I323	I324	I325	I326	I327	I328	I329	I330	I331	I332	I333	I334	I335	I336	I337	I338	I339	I340	I341	I342	I343	I344	I345	I346	I347	I348	I349	I350	I351	I352	I353	I354	I355	I356	I357	I358	I359	I360	I361	I362	I363	I364	I365	I366	I367	I368	I369	I370	I371	I372	I373	I374	I375	I376	I377	I378	I379	I380	I381	I382	I383	I384	I385	I386	I387	I388	I389	I390	I391	I392	I393	I394	I395	I396	I397	I398	I399	I400	I401	I402	I403	I404	I405	I406	I407	I408	I409	I410	I411	I412	I413	I414	I415	I416	I417	I418	I419	I420	I421	I422	I423	I424	I425	I426	I427	I428	I429	I430	I431	I432	I433	I434	I435	I436	I437	I438	I439	I440	I441	I442	I443	I444	I445	I446	I447	I448	I449	I450	I451	I452	I453	I454	I455	I456	I457	I458	I459	I460	I461	I462	I463	I464	I465	I466	I467	I468	I469	I470	I471	I472	I473	I474	I475	I476	I477	I478	I479	I480	I481	I482	I483	I484	I485	I486	I487	I488	I489	I490	I491	I492	I493	I494	I495	I496	I497	I498	I499	I500	I501	I502	I503	I504	I505	I506	I507	I508	I509	I510	I511	I512	I513	I514	I515	I516	I517	I518	I519	I520	I521	I522	I523	I524	I525	I526	I527	I528	I529	I530	I531	I532	I533	I534	I535	I536	I537	I538	I539	I540	I541	I542	I543	I544	I545	I546	I547	I548	I549	I550	I551	I552	I553	I554	I555	I556	I557	I558	I559	I560	I561	I562	I563	I564	I565	I566	I567	I568	I569	I570	I571	I572	I573	I574	I575	I576	I577	I578	I579	I580	I581	I582	I583	I584	I585	I586	I587	I588	I589	I590	I591	I592	I593	I594	I595	I596	I597	I598	I599	I600	I601	I602	I603	I604	I605	I606	I607	I608	I609	I610	I611	I612	I613	I614	I615	I616	I617	I618	I619	I620	I621	I622	I623	I624	I625	I626	I627	I628	I629	I630	I631	I632	I633	I634	I635	I636	I637	I638	I639	I640	I641	I642	I643	I644	I645	I646	I647	I648	I649	I650	I651	I652	I653	I654	I655	I656	I657	I658	I659	I660	I661	I662	I663	I664	I665	I666	I667	I668	I669	I670	I671	I672	I673	I674	I675	I676	I677	I678	I679	I680	I681	I682	I683	I684	I685	I686	I687	I688	I689	I690	I691	I692	I693	I694	I695	I696	I697	I698	I699	I700	I701	I702	I703	I704	I705	I706	I707	I708	I709	I710	I711	I712	I713	I714	I715	I716	I717	I718	I719	I720	I721	I722	I723	I724	I725	I726	I727	I728	I729	I730	I731	I732	I733	I734	I735	I736	I737	I738	I739	I740	I741	I742	I743	I744	I745	I746	I747	I748	I749	I750	I751	I752	I753	I754	I755	I756	I757	I758	I759	I760	I761	I762	I763	I764	I765	I766	I767	I768	I769	I770	I771	I772	I773	I774	I775	I776	I777	I778	I779	I780	I781	I782	I783	I784	I785	I786	I787	I788	I789	I790	I791	I792	I793	I794	I795	I796	I797	I798	I799	I800	I801	I802	I803	I804	I805	I806	I807	I808	I809	I810	I811	I812	I813	I814	I815	I816	I817	I818	I819	I820	I821	I822	I823	I824	I825	I826	I827	I828	I829	I830	I831	I832	I833	I834	I835	I836	I837	I838	I839	I840	I841	I842	I843	I844	I845	I846	I847	I848	I849	I850	I851	I852	I853	I854	I855	I856	I857	I858	I859	I860	I861	I862	I863	I864	I865	I866	I867	I868	I869	I870	I871	I872	I873	I874	I875	I876	I877	I878	I879	I880	I881	I882	I883	I884	I885	I886	I887	I888	I889	I890	I891	I892	I893	I894	I895	I896	I897	I898	I899	I900	I901	I902	I903	I904	I905	I906	I907	I908	I909	I910	I911	I912	I913	I914	I915	I916	I917	I918	I919	I920	I921	I922	I923	I924	I925	I926	I927	I928	I929	I930	I931	I932	I933	I934	I935	I936	I937	I938	I939	I940	I941	I942	I943	I944	I945	I946	I947	I948	I949	I950	I951	I952	I953	I954	I955	I956	I957	I958	I959	I960	I961	I962	I963	I964	I965	I966	I967	I968	I969	I970	I971	I972	I973	I974	I975	I976	I977	I978	I979	I980	I981	I982	I983	I984	I985	I986	I987	I988	I989	I990	I991	I992	I993	I994	I995	I996	I997	I998	I999	I1000	I1001	I1002	I1003	I1004	I1005	I1006	I1007	I1008	I1009	I1010	I1011	I1012	I1013	I1014	I1015	I1016	I1017	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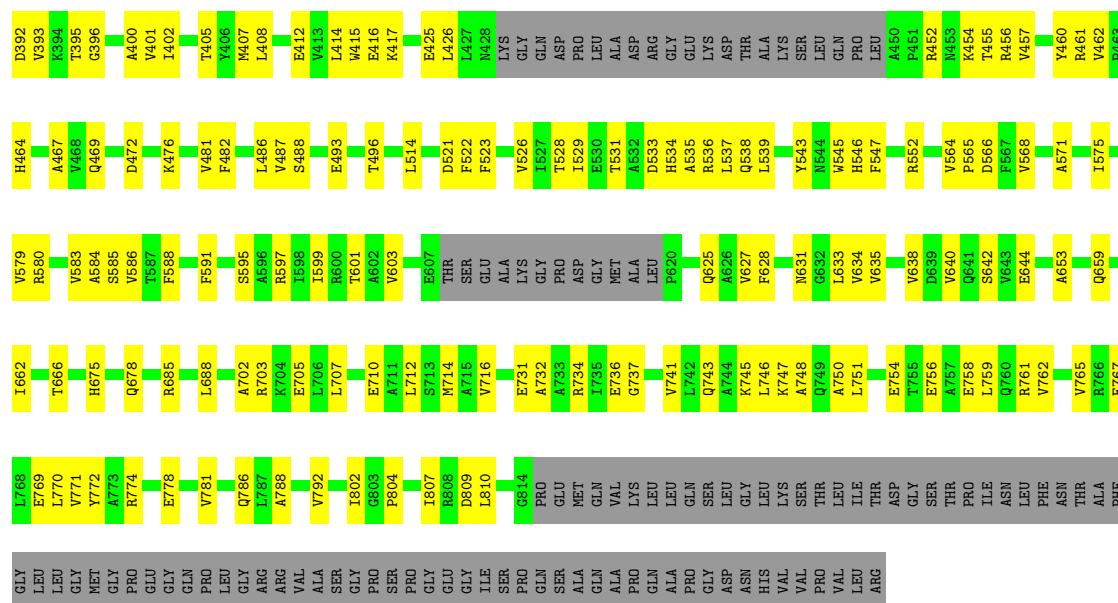


Response	Percentage
Doing a good job	58%
Not doing a good job	29%
Don't know	13%



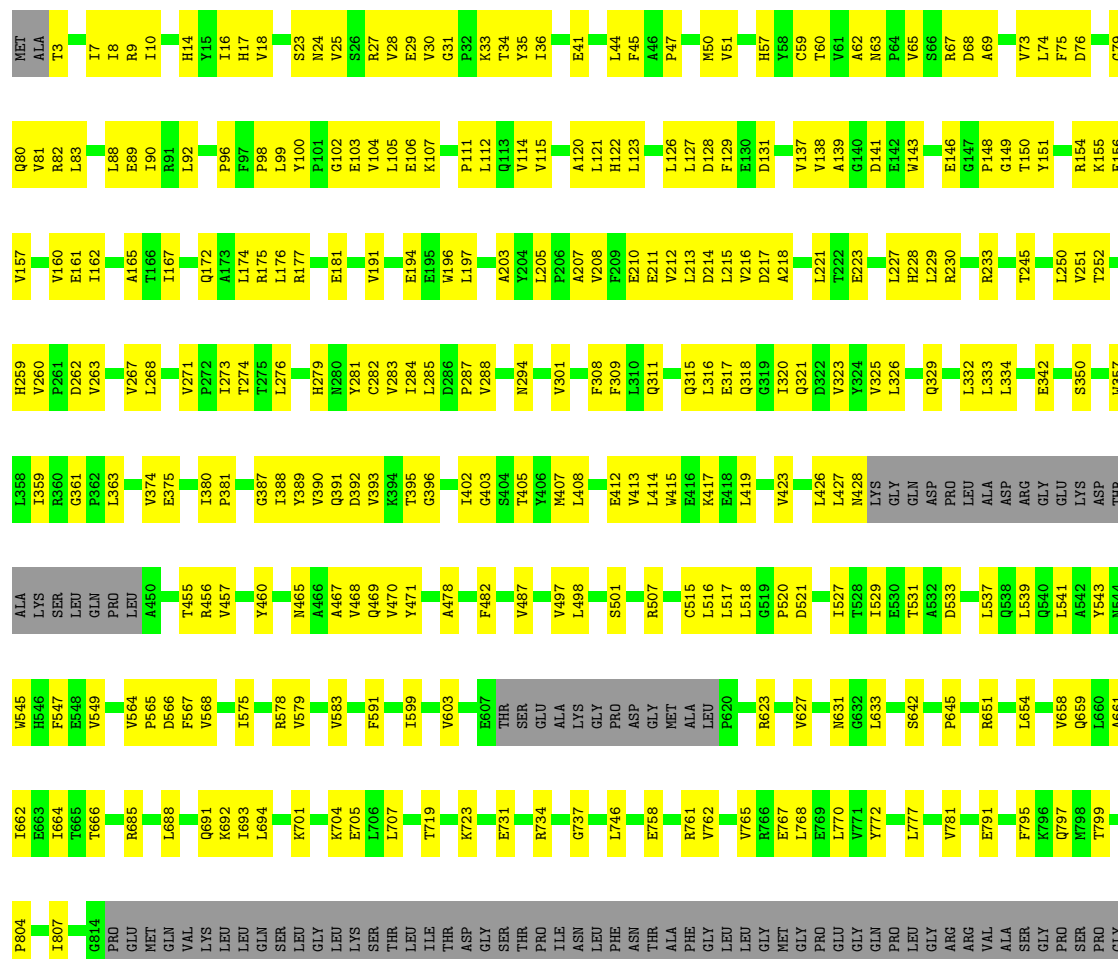
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PRO	GLY	G803	P804	I807	E676	H546	GLN	PRO	L363	H259	N171	A86	T3	
GLY	P804	E676	H546											GLN
GLY	P804			E676	H546	GLN	PRO	L363	H259	N171	A86	T3		
ILE	I807	E676	H546										GLN	PRO
SER				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
PRO	I807	E676	H546										GLN	PRO
PRO				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
GLN	I807	E676	H546										GLN	PRO
GLN				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
ALA	I807	E676	H546										GLN	PRO
ALA				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
GLN	I807	E676	H546										GLN	PRO
GLN				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL				I807	E676	H546	GLN	PRO	L363	H259	N171	A86		
VAL	I807	E676	H546										GLN	PRO
VAL														





• Molecule 1: Major vault protein

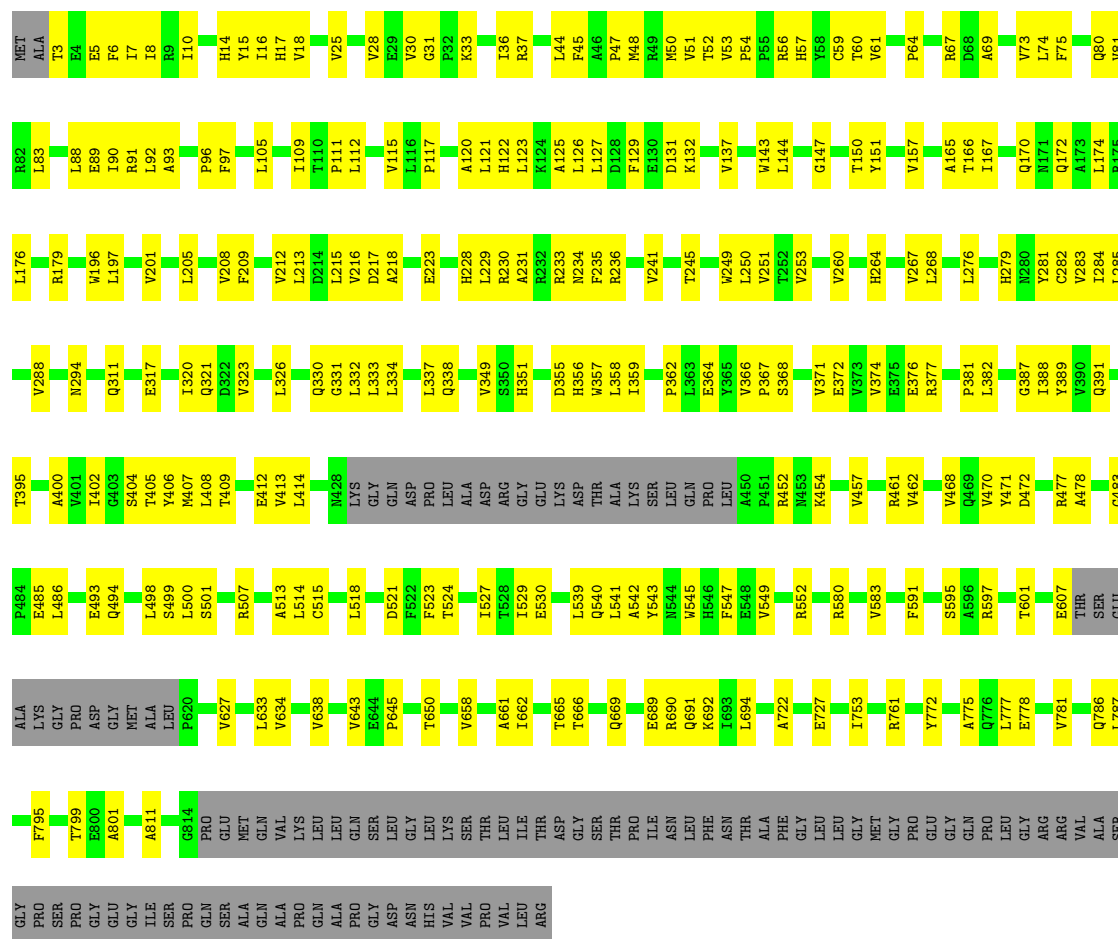
Chain FB: 55% 32% 13%



GLU
GLY
ILE
SER
PRO
GLN
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ALA
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ALA
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ALA
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ASP
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LEU
ARG

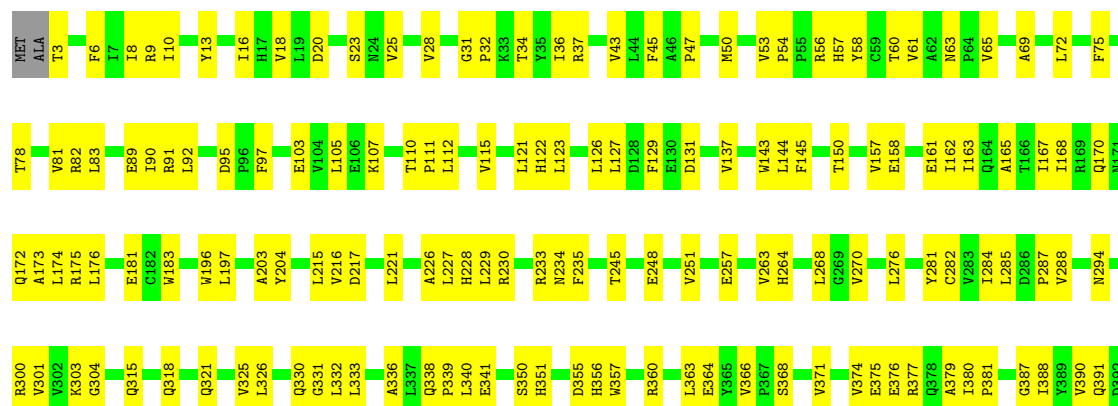
• Molecule 1: Major vault protein

Chain G:  59% 28% 13%



• Molecule 1: Major vault protein

Chain GA:  56% 31% 13%



V393	Q469	D566	R679	G814	SER
G396	V470	F567	L680	PRO	PRO
K397	V471	V568	R685	GLN	GLN
V398	A478	G569	E689	MET	ALA
R399	R479	D570	R690	GLN	ALA
A400	V480	A571	Q691	VAL	ALA
V401	V481	R580	L694	LYS	PRO
I402	P484	T587	E717	LEU	GLN
T405	L486	F588	E717	ALA	ALA
Y406	V487	D589	T721	SER	GLY
M407	S488	D590	T721	LEU	LEU
Q410	L489	F591	E731	GLY	ASN
D411	G490	H592	E731	HIS	HIS
L414	P491	K593	R734	VAL	VAL
W415	E492	N594	G737	PRO	PRO
E416	Q494	S595	A745	LEU	LEU
K417	F495	A596	L746	ILE	LEU
V423	T496	I598	L751	THR	ARG
E424	V497	I599	E754	THR	
E425	L498	R600	T755	PHE	
L436	S601	T601	E756	ASN	
L427	R507	F606	A757	THR	
N428	A513	E607	E759	ALA	
LYS	L516	THR	V762	GLY	
GLN	L517	GLU	E767	LEU	
ASP	L518	SER	L768	GLY	
PRO	L518	ALA	E769	GLY	
LEU	D521	GLY	L770	LEU	
ALA	F522	ASP	E780	LEU	
ARG	GLY	GLY	V781	GLN	
GLY	GLU	MET	S782	PRO	
GLU	T527	ALA	E783	LEU	
LYS	T528	LEU	Q786	GLY	
ASP	I529	P620	K794	VAL	
THR	E530	L633	I802	ALA	
ALA	T531	S642	G803	SER	
LYS	A535	V643	R804	GLY	
SER	R536	V646	S805	PRO	
LEU	L539	A653	T806	PRO	
GLN	Q540	L654	I807	GLY	
PRO	L541	L654	R808	GLY	
LEU	A542	I662	D809	ILE	
A450	Y543	E663			
T455	N544	E663			
R456	V545	T665			
V457	H546	T666			
Y460	F547	E548			
R461	E548	E670			
V462	V549				
	R552				

• Molecule 1: Major vault protein

Chain GB:  56% 31% 13%

MET	E89	E189	V301	I388	V462	V579	V658	GLU
ALA	I90	R190	V302	T389	P463	R580	Q659	MET
T3	R91	V191	K303	V390	P463	G581	A661	GLN
E4	T192	T192	G304	V393	V468	A582	A661	VAL
E5	P98	G193	E305	V393	Q469	V583	T662	LYS
F6	I99	E194	L310	G396	V480	V586	E663	LEU
I7	Y100	E195	Q311	K397	V481	T587	T664	LEU
I8	E103	W196	Q311	R398	E485	F588	T665	GLN
R9	V104	V198	E314	R399	E485	D589	T666	SER
Y13	E106	V201	L316	A400	E493	D590	A684	GLY
H14	K107	L205	G319	V401	T496	F591	R685	LEU
Y15	E108	P206	I320	I402	V497	R597	R687	LYS
I16	T110	V208	L332	T405	L498	I598	L688	SER
H17	T110	V212	L333	M407	Y406	R600	E731	THR
N22	V114	L213	L334	Q410	M407	T601	E732	ILE
V25	H122	D217	R335	D411	C515	G737	A733	THR
V28	A125	L126	A336	E412	L516	F606	R734	ASP
E29	V30	L127	L337	E413	L517	E607	I735	GLY
G31	G31	L127	L338	E414	L518	THR	E736	SER
T34	F129	D128	L340	E415	D521	SER	E737	THR
Y35	E130	F129	E341	E416	F522	GLU	G737	PRO
I36	D135	E130	E342		F523	ALA		ILE
N40	V137	D135	E343		V526	LYS	V741	ASN
F45	W143	D135	E344		I529	GLY	L742	LEU
A46	V137	D135	E345		E530	PRO	Q743	PHE
M50	V157	D135	F346		T531	ASP	I759	THR
V53	E158	D135	E347		A532	MET	L751	PHE
P54	V159	D135	A353		D533	ALA	T755	GLY
P55	E160	D135	H357		R536	LEU	P620	LEU
R56	E161	D135	L358		L537	ASP	P622	GLY
H57	I162	D135	L359		G538	PRO	R623	MET
Y58	I163	D135	L360		L539	LEU	L759	GLY
C59	T60	D135	R360		Q540	ALA	Q760	PRO
V61	R169	D135	L363		Y543	ASP	R761	GLU
A62	Q172	D135	V366		W544	GLY	Q625	GLN
V65	L174	D135	V373		W545	LEU	V627	PRO
S66	R175	D135	E374		H546	ASP	L633	PRO
R67	L176	D135	E375		F547	THR	V634	LEU
V73	R177	D135	E377		V549	ALA	V635	GLY
T78	R179	D135	Q378		T558	LYS	V638	ARG
V81	E181	D135	A379		F562	ASP	D639	VAL
R82	C182	D135	P381		S563	THR	V640	ALA
L83	W183	D135	L382		V564	LYS	Q641	SER
	P287	D135	D383		F567	LEU	S642	GLY
	V288	D135	E384		S563	GLN	E644	PRO
	G187	D135	E385		D570	PRO	R456	SER
	K188	D135	G387		I575	LEU	V457	GLN
		D135					Y460	
		D135					R461	

Q318	T409	V481	LYS	E756	LEU
Q321	Q410	F482	GLY	A757	GLY
D322	D411	G483	PRO	E758	MET
V323	V412	P484	ASP	L759	GLY
Y324	V413	E485	GLY	Q760	PRO
V325	L414	G490	MET	R761	GLU
	Y415		ALA	V762	GLY
	E416	E493	LEU	Y772	GLN
G331	G422	Q494	P620	L777	PRO
L332	V423	F495	R623		LEU
L333	E424		D624		GLY
L334	E425	L516	Q625		ARG
	L426	L517	A626		VAL
L340	L427	L518	V634		ALA
	N428		V635		SER
D345	LYS	D521	V638		GLY
	GLY	F522	D639		PRO
K348	GLN	F523			SER
V349	ASP				PRO
S350	PRO	I529	V643		GLY
H351	LEU	E530	E644		GLY
	ALA	T531	R27		GLY
W357	ASP		L654		ILE
L358	ARG	H534			SER
I359	GLY	A535	L660		PRO
	GLU	R536	A661		GLN
L363	LYS	Q538	T665		SER
E364	ASP				ALA
Y365	THR				GLN
V366	ALA	A542	Q669		ALA
P367	LYS	Y543	E676		PRO
S368	SER	W544			GLN
	LEU	H546	R679		ALA
V371	PRO		L680		PRO
	LEU	D566	E681		GLY
V374		A450	Q682		ASP
E375		P451	E683		LEU
E376		R452			ASN
I380			E710		VAL
P381	T455		E717		VAL
L382	R456				PRO
	V457		T721		LEU
I388	V458		A730		LEU
Y389	S459		E731		ARG
			S585		ASP
D392			V586		GLY
V393	P463		T587		SER
K394			F588		THR
T395	A466		D589		PRO
G396	A467		R734		ILE
			I599		ASN
I402	Q468		R600		LEU
G403	V470		E736		LEU
S404	Y471		G737		THR
T405					ASN
Y406	A478		V741		THR
M407	R479		K745		ALA
L408	V480		L746		GLY

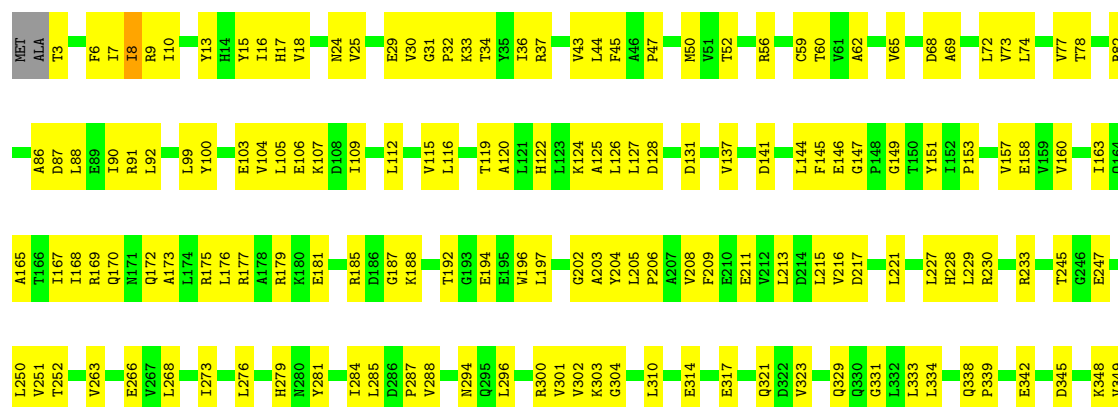
• Molecule 1: Major vault protein

Chain HB:  58% 30% 13%

MET	V81	P209	E317	B504	F606	W760	ILE
ALA	R82	V212	T320	P505	E607	R761	ASN
T3	L83					V762	LEU
							PHE
F6	R90	L215	V325	R512	LYS	W765	THR
I7	I91	V216	G331	L516	GLY	R766	ALA
I8	L92	D217	L332	L517	GLN	E767	ALA
R9	Y100		L333	L518	ASP	L768	PHE
I10		E223		F523	PRO	E769	GLY
					LEU	L770	LEU
Y13	E106	A226	P339	V526	GLY	R774	GLY
I16	I109	L227	L340	I527	MET		MET
H17	T110	H228	E346	T528	ALA		GLY
V18	P111		E347	E529	ARG		GLY
L19	P112	R233	K348	E530	GLY	W781	PRO
D20	Q113	F235	V349	T531	LYS	S782	GLU
	V114		S350		ASP		GLY
S23	V115	T245	H351	L537	THR	Q786	GLN
N24	L116		Q352	Q538	ALA	A788	PRO
V25	T119	V251	A353	L539	LYS	E789	LEU
S26	A120	T252	V371	Q540	SER	W790	GLY
R27	L126	E266	E372	L541	LEU	E791	ARG
V28	H122	Q254	V373	A542	GLN	W792	VAL
	L123		V374	Y543	PRO	T799	ALA
T34	A124	H264	E384	R544	LEU		SER
Y35	I36	E285		W545		P804	GLY
I36	L127	E267	V371	V549	A450		PRO
R37	L127	L268	E372		P451	I807	SER
	D128		V374		R452	R808	PRO
E41	F129					D809	GLY
R42	V137	L273	R377	R552	T455	L810	GLY
F45	W143	T274	I380	T558	R456	A811	GLY
A46	L144	L276	P381	F562	V457	W812	ILE
P47	F145	Q277	L382	C572	V458	A813	SER
					Y450	Q814	PRO
M50					R461		GLN
					V462		SER
					P463		ALA
							GLN
P54	V159	V283	G387	I575	V468	E670	ALA
P55	F160	T284	I388	R578	Q469	E671	VAL
R56	E161	L285	Y389	V579	V470	Q691	PRO
H57	I162	D286	Q391	R580	Y471		GLN
	A165	V287	D392	G581			LEU
		V288		A582	D472		PRO
T60		N294		V583			GLN
V65	Q172		T395	V584	V480		SER
S66	A173	V301	G396	A584	V481		GLY
R67	G187		K397	S585			ASN
D68	K188	G304	V401	V586	E485		VAL
A69		E305	I402	T587	L486		VAL
Q70	W196	F308	T405	F588			PRO
L72	L197	F309	Y406		L489		THR
V73	L310	Q311	M407		E598		LEU
L74	A203	Q312			I599		ILE
F75	Y204	P312	W415		T601		THR
	L205	Q315	E416		Q494		ASP
G79	V208				E495		GLY
Q80			L419		T496		SER
					V497		THR
							PRO

• Molecule 1: Major vault protein

PRO	LEU	A788	LEU	L633	IS29	GLU	H351	E257	I168	ALA	MET
GLY	GLY	V792	GLY	V634	A535	ASP	R356	E257	R169	T3	
ARG	ARG		ARG	V635	A535	THR	R357	V260	Q170	E4	
ARG	ARG	F795	ARG		Q638	ALA	L368		N171	E9	
VAL	VAL	K796	VAL	V638	L339	LYS	L359	H264	K172	E5	
ALA	ALA	Q797	ALA	D639	Q540	SER	R360		A173	F6	
SER	SER	M798	SER		L541	LEU			L174	I7	
GLY	GLY		GLY	S642	A542	GLN	L363	V267	R175	I8	
PRO	PRO	A801	PRO	V643	Y543	PRO	E364	G269	L176	R9	
SER	SER	I802	SER	N544	N544	LEU	V365	V270	P96	I10	
PRO	PRO		PRO	P644	W545	A450	V366	V271	F97	P11	
GLY	GLY	T806	GLY	P645	H546	A451		P272	R179	P12	
GLU	GLU	I807	GLU	V646	F547	R452	V371	T273	K180		
GLY	GLY	R808	GLY	I662	E548	N453	E372	T274	C182	H17	
ILE	ILE	D809	ILE	E663	V549	K454	V373	T275	L99		
SER	SER		SER	I664		T455	V374	L276	Y100		
PRO	PRO	S814	PRO		T558	R456			T192	S23	
PRO	GLN		PRO	R690		V457	R377		W196	S24	
SER	SER	GLU	SER	GLU	L561			Y281	L197	V25	
GLY	GLY		GLY	L707		R461	P381	C282	V201	S26	
GLN	GLN	ALA	GLN	GLN	F567	V462	L382	V283		R27	
ALA	ALA	VAL	ALA	A711	V568			L284	T109	V28	
LYS	LYS		LYS		G569	A466	G387	L285	L205	E29	
GLN	GLN		GLN	A715		A467	L388	G296	P206	G30	
LEU	LEU	ALA	LEU	V579	R580	V468	L389	P287	A207	V31	
ALA	ALA	PRO	ALA	LEU		Q469	V390	V288	V208	P32	
PRO	PRO	GLN	PRO	T721	SER	V470			F209	K33	
GLY	GLY		GLY						E210	G31	
ASP	ASP	LEU	ASP	E727	V583	Y471	V393	L296	E211	T34	
ASN	ASN	GLY	ASN	S728	A584		K394		V212	Y35	
VAL	VAL	LEU	VAL	R729		K476	T395	V301	L215	T36	
VAL	VAL	LYS	VAL	LYS	F591	R477	G396	K303	H122	R37	
VAL	VAL	SER	VAL	G737				G304	K124	N40	
LEU	LEU	THR	LEU	V741	S595	V480	V401		A125	E41	
ILE	ILE		ILE		A596	V481			L127		
THR	THR		THR	K747	R597	F482	T405	L310	D128	M50	
ASP	ASP	THR	ASP		I598		Y406		F129	V51	
GLY	GLY	ASP	GLY	L751	R600	L486	N407	E314	T52	V53	
SER	SER	THR	SER	T601	THR	V487	T409	L316	D131		
THR	THR		THR	T755		S488	Q410	E317	K132		
PRO	PRO	PRO	PRO		F806	L489			L227	R56	
ILE	ILE	ILE	ILE	E758	E507		E416	Q321	H228	H57	
ASN	ASN	THR	ASN	THR	THR	E492		D322	Y88		
LEU	LEU	LEU	LEU	Q760	SER	E493	P420	V323	W143	C59	
PHE	PHE	THR	PHE	R761	GLU	Q494	P421	R230	L144	T60	
ASN	ASN	ASN	ASN	V762	ALA	F495		A231	F145	V61	
THR	THR	THR	THR		LYS	T496	L426	R232	E146	A62	
ALA	ALA	ALA	ALA	E767	GLY	V497	L427	R233	G147	N63	
PHE	PHE	ALA	PHE		GLY	L498	N428	P234	P148	P64	
GLY	GLY	GLY	GLY								

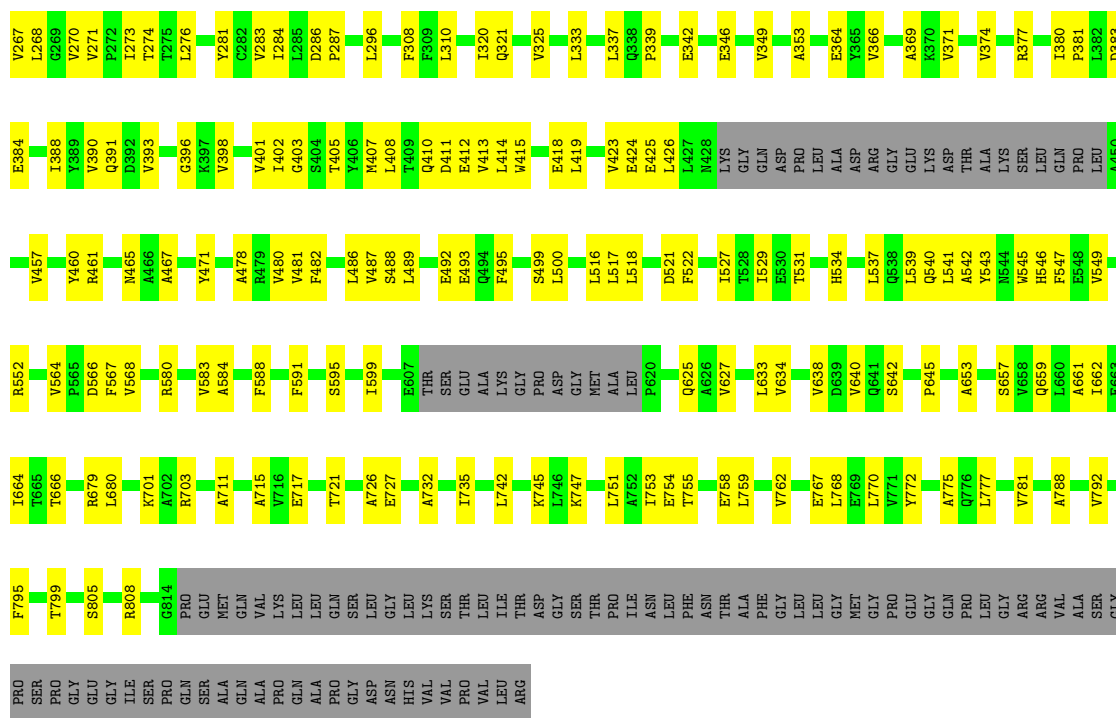


ALA	PRO	GLY	ASP	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	ARG		LEU	GLN	PRO	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
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• Molecule 1: Major vault protein

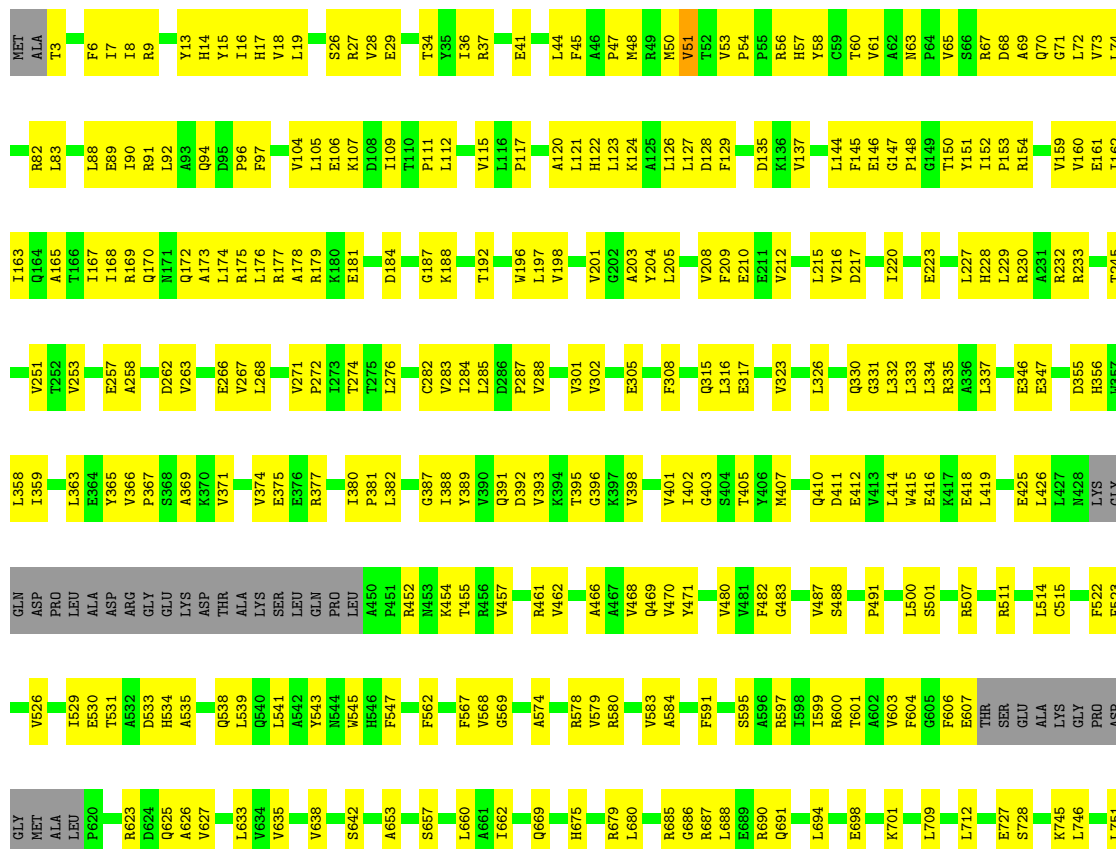
Chain IB:  55% 33% 13%

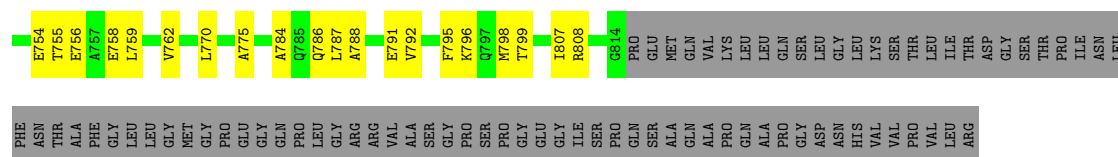
V790	T666	A584	V462	Y389	K293	L176	D87	MET	
E791	T666	F588	V462	V390	K293	L176	D87	ALA	
K793	R679	D589	V468	D392	N294	E189	L88	T3	
K794	E681	D590	Q469	V393	V301	L197	E89	E4	
T806	A684	S595	V480	G396	V302	V201	R91	F6	
									I7
I807	A596	V481	G303	K303	C304	P98	L8		
D809	L688	R597	F482	R399	E305	L205	Y100	E5	
V812	Q691	I598	P484	E485	S307	V208	P101	Y15	
									I16
A813	R600	T405	F308	E211	L105	E106	V18		
G814	A702	T601	S488	L408	Q311	L215	E106	V18	
PRO	L707	V603	F495	T409	P312	V216	T110	L19	
MET	E710	F604	S499	D410	T320	A218	P111	D20	
GLN	A711	E607	R504	D411	Q321	V219	L112	R27	
VAL	M714	THR	R512	V412	L332	L220	V115	V28	
LEU	E717	SER	GLU	L414	L333	L221	L116	E29	
GLN	L742	ALA	GLY	E415	L334	L227	T119	V30	
SER	Q743	LYS	C515	E416	R335	H228	A120	G31	
GLY	A744	PRO	L516	L419	L340	L229	H122	T34	
LEU	K745	ASP	L517	G422	E341	R233	H122	Y35	
LYS	L746	GLY	F522	M428	E342	T245	K124	R37	
SER	K747	MET	F523	LYS	E346	W249	A125	E41	
THR	A748	ALA	T524	GLY	E347	L250	L126	R62	
ILE	P820	LEU	I529	GLN	K348	L250	L127	V43	
LEU	R821	PRO	E530	ASP	V349	V253	D128	L44	
THR	E754	P822	T531	PRO	S350	E130	F129	F45	
ASP	T755	R623	A532	LEU	H351	E257	E130	A46	
GLY	E758	A626	D533	ALA	D355	E257	D131	P47	
SER	L759		ASP	ALA		K132			
THR	L759		ARG	ASP		V137			
PRO	Q760	THR	R536	GLY	H356	V260	V137	V51	
ILE	R761	L833	L537	GLY	W357	V260	L143	R56	
ASN	V762	V634	Q538	GLU	L358	V263	L144	H57	
LEU	E767	V635	L539	LYS	L359	V263	F145	Y58	
PHE		S836	Q540	ASP	L363	L268	E59	C59	
ASN		L768	L541	THR		E146	G147	T60	
THR	E769	V638	ALA	E364		G269	V61	V61	
ALA	L770	D639	Y543	LYS	V270	V271	A62	A62	
PHE	V771	V640	N544	SER	V366	V271	V160	A62	
GLY	Y772	Q641	V545	LEU	P367	P272	E161	N63	
LEU	A773	S642	H546	GLN	S368	T273	I162	P64	
LEU	R774	V643	E548	PRO	V371	T274	I163	V65	
GLY	A775	E644	E549	LEU	V371	T275	Q164	S66	
MET	E778	P845	V549	A450	V371	L276	A165	R67	
GLY		V646	V549	P451	G277	V277	D68	D68	
PRO		PRO	D554	R452	E375	T168	A69	A69	
GLU	V781	T650	D554	M453	Y281	R169	Q70	Q70	
GLY	S782	T558	T558	K454	C282	Q170	L72	G71	
GLN	PRO	S657	V579	T455	V283	M171	L72	L72	
PRO	Q785	V579	R580	R456	P381	I284	Q172	V81	
LEU	L660	V580	R580	V457	V457	A173	A173	R82	
GLY	A788	A661	V593	V458	G387	L174	L174	R82	
ARG	E789	I662	V593	V459	T388	P475	P475	L82	



• Molecule 1: Major vault protein

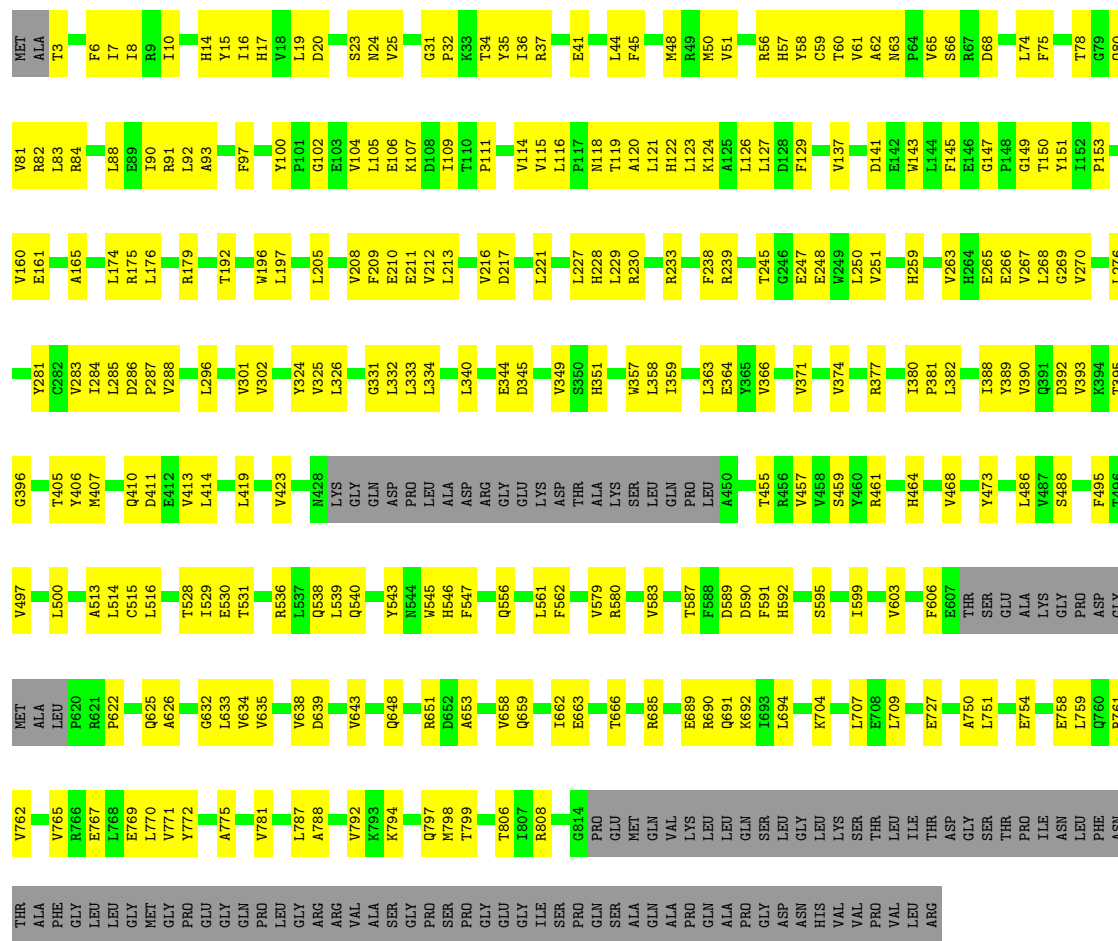
Chain JB: 52% 35% 13%





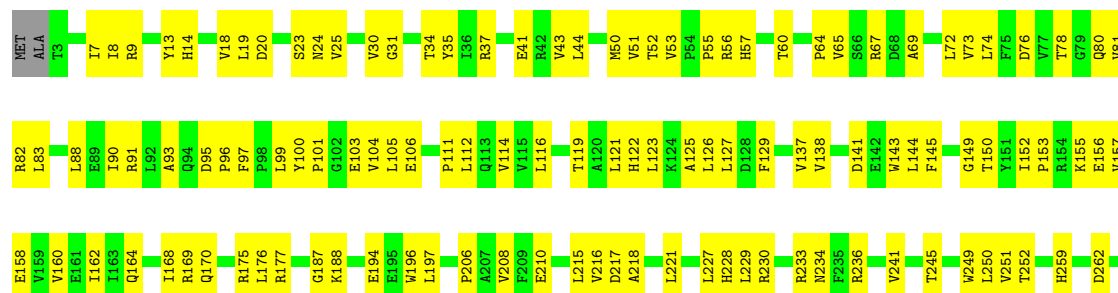
• Molecule 1: Major vault protein

Chain K: 57% 30% 13%

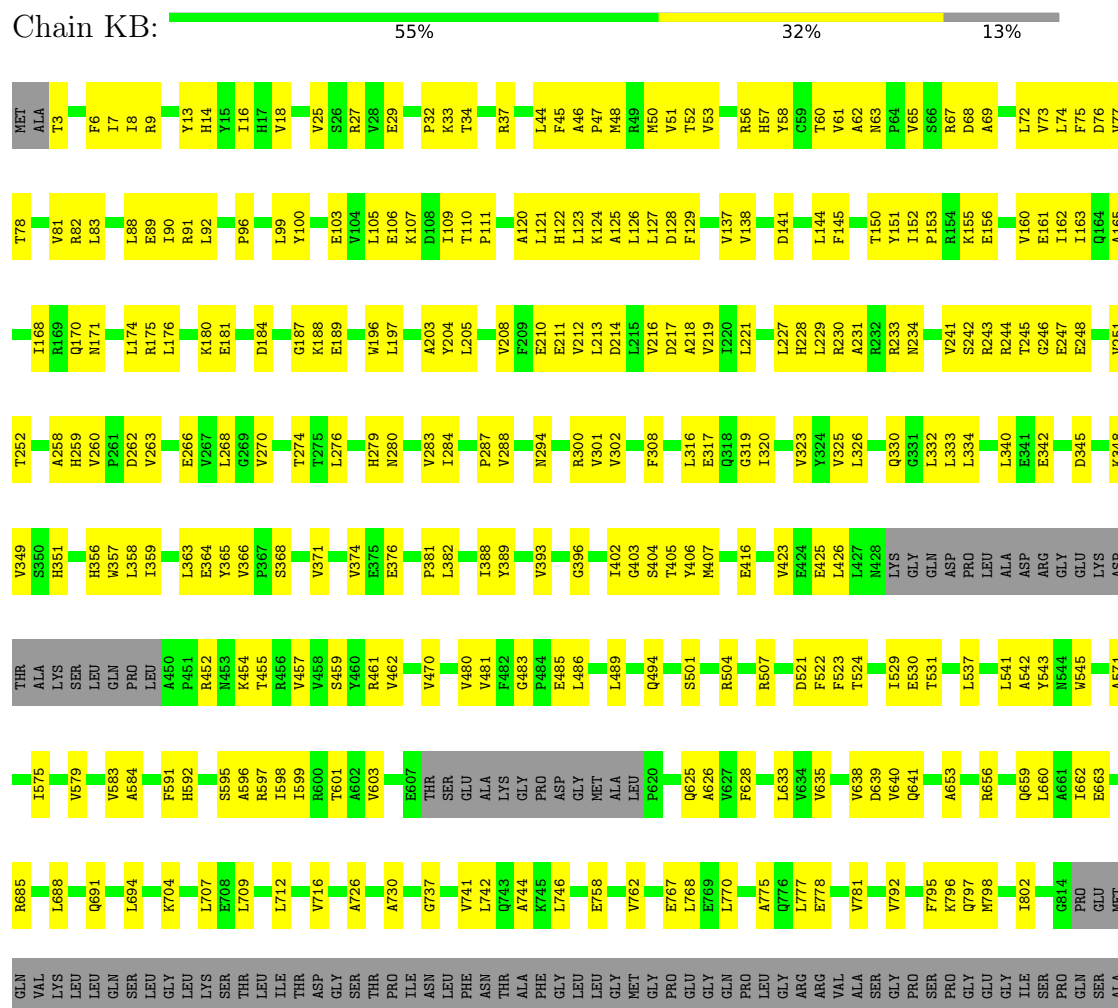


• Molecule 1: Major vault protein

Chain KA: 57% 30% 13%



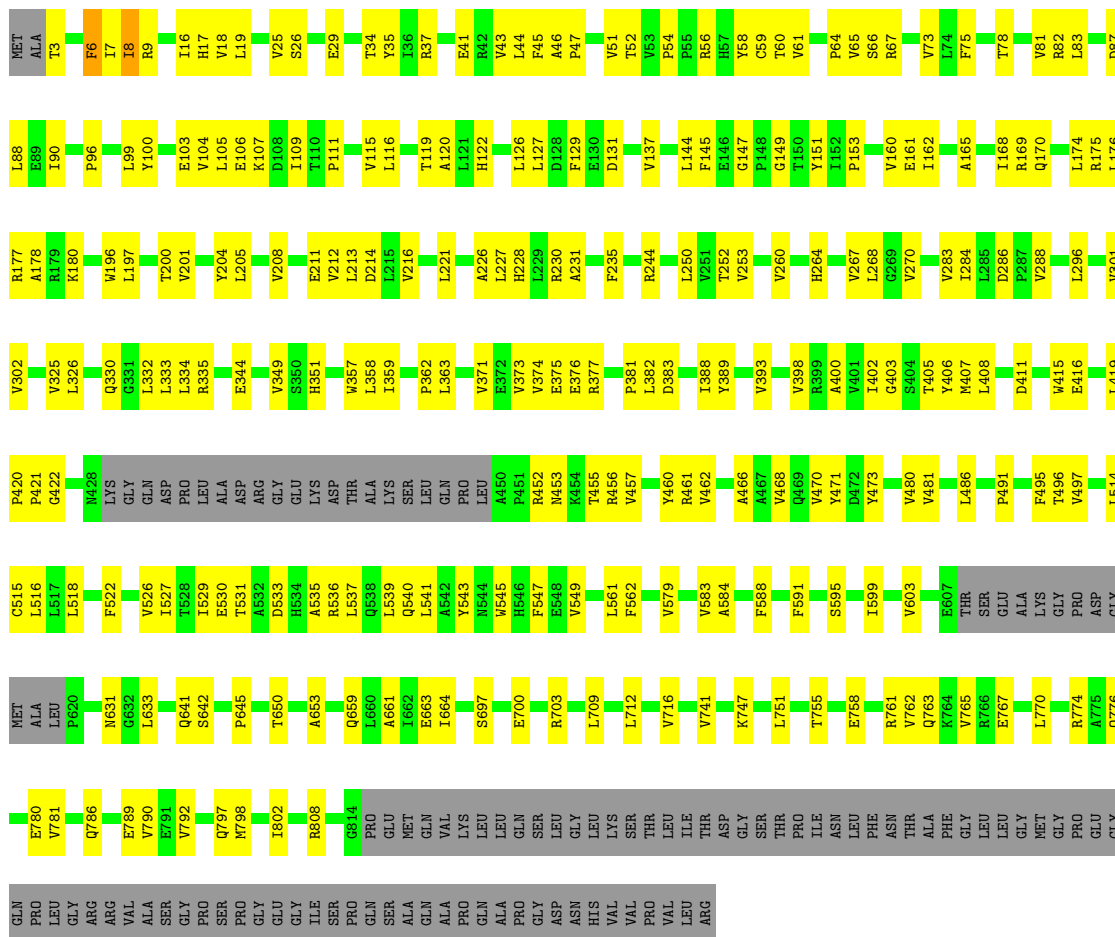
- Molecule 1: Major vault protein

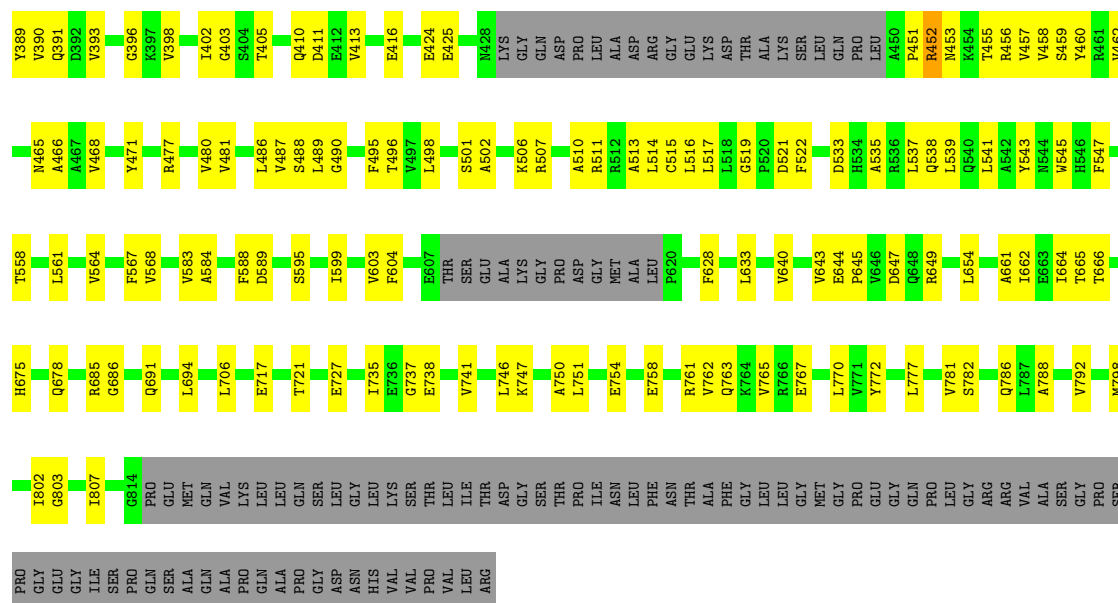


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• Molecule 1: Major vault protein

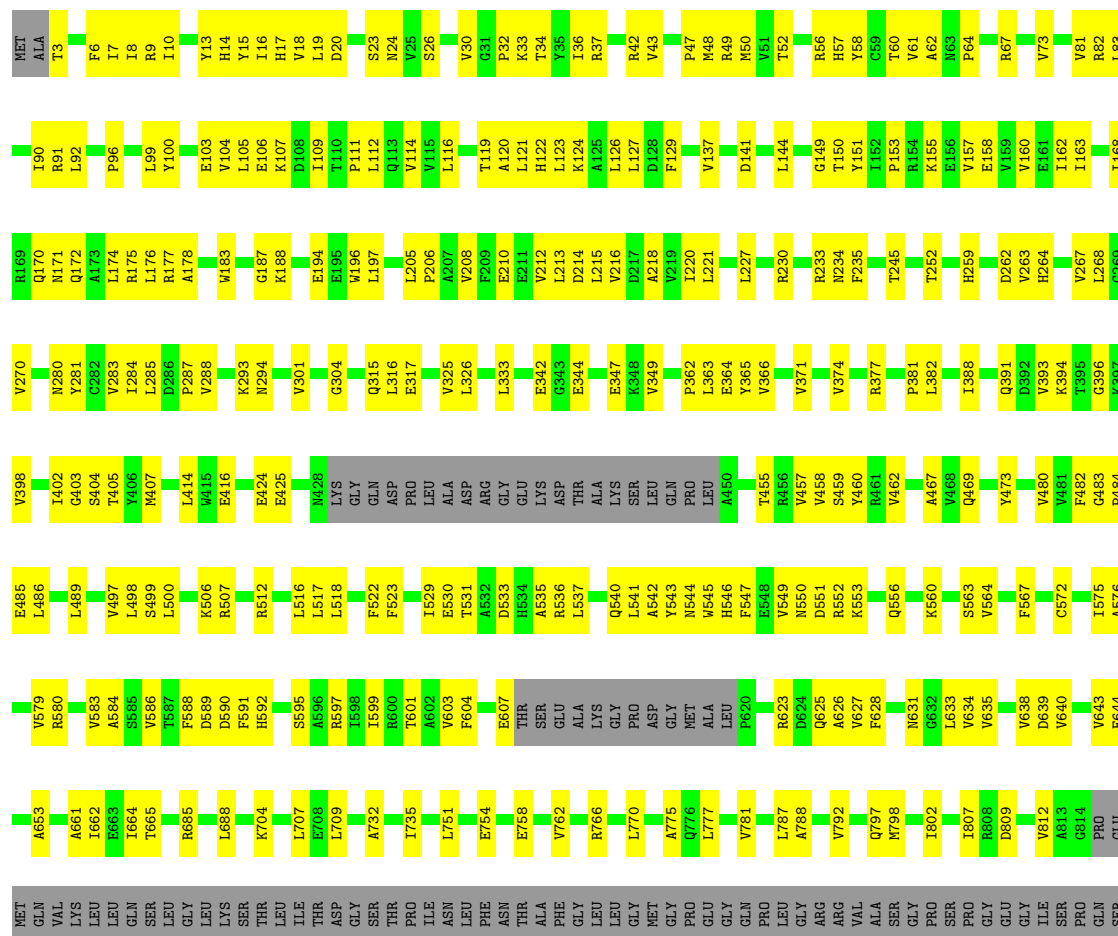
Chain L:  59% 28% 13%

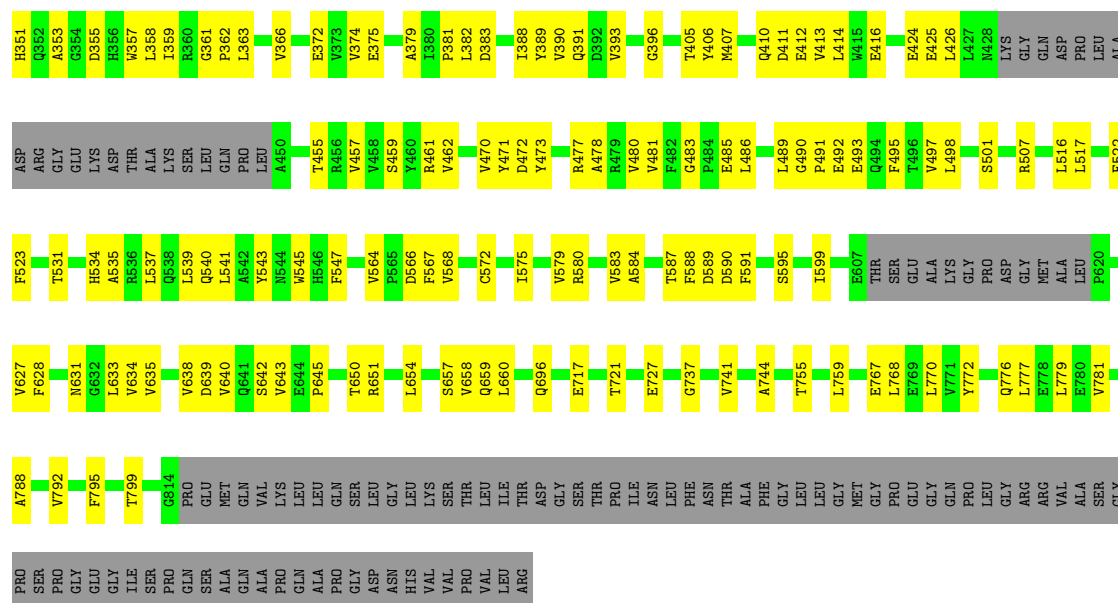




• Molecule 1: Major vault protein

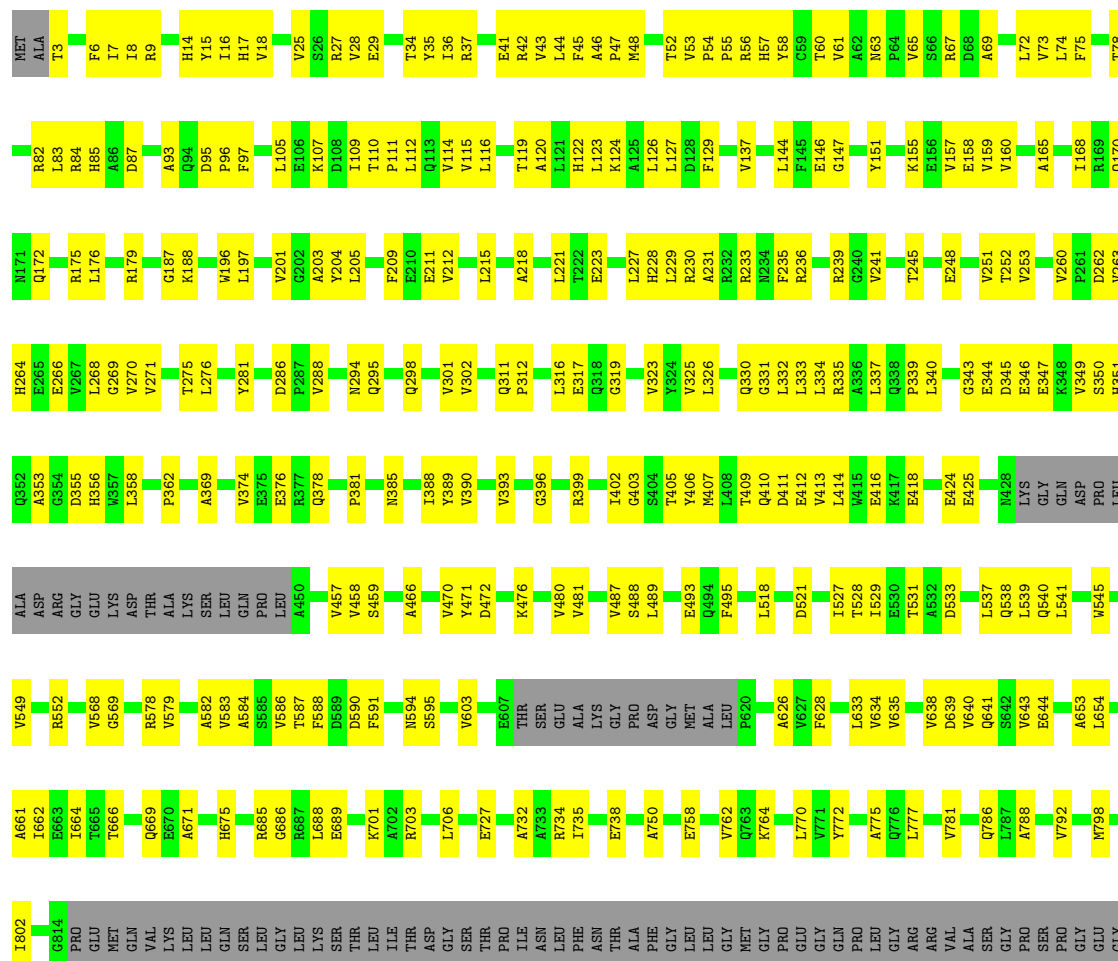
Chain LB: 55% 32% 13%





• Molecule 1: Major vault protein

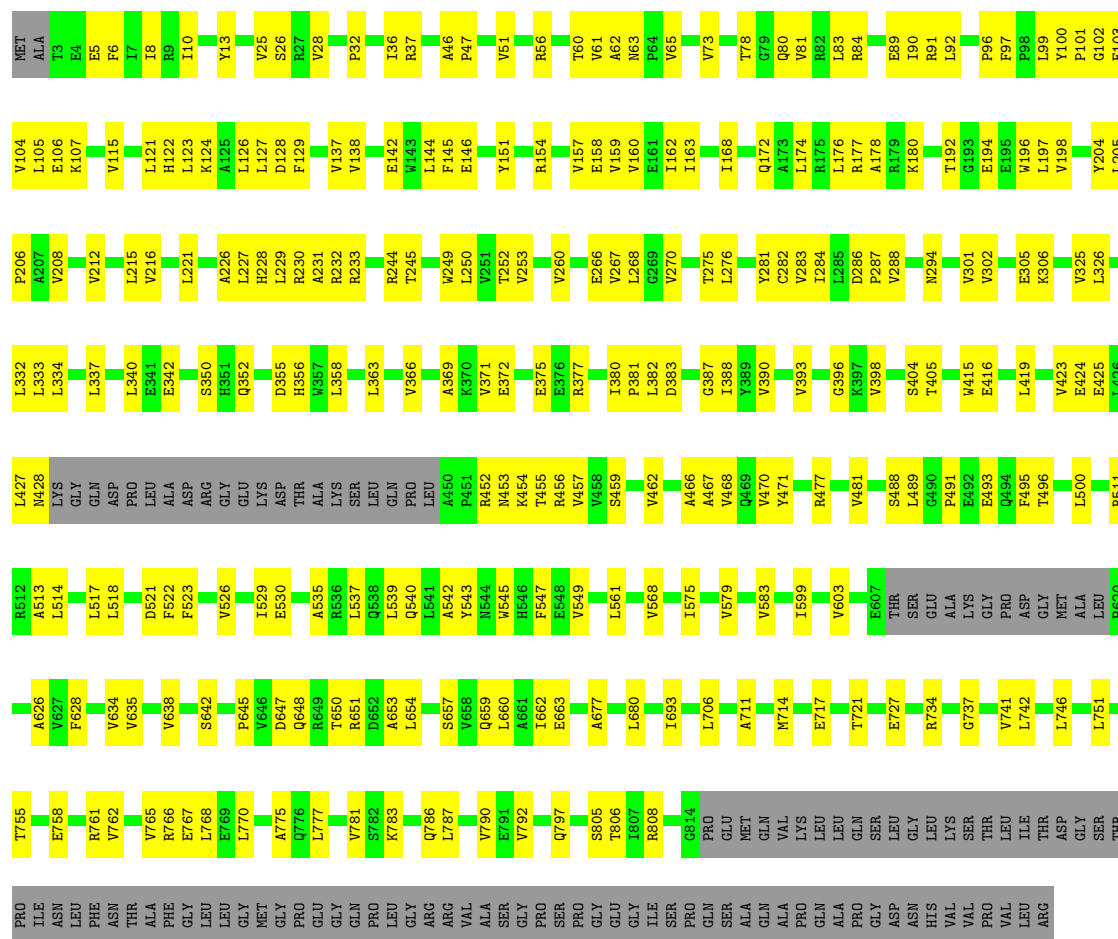
Chain MB: 55% 32% 13%



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• Molecule 1: Major vault protein

Chain N:  58% 29% 13%

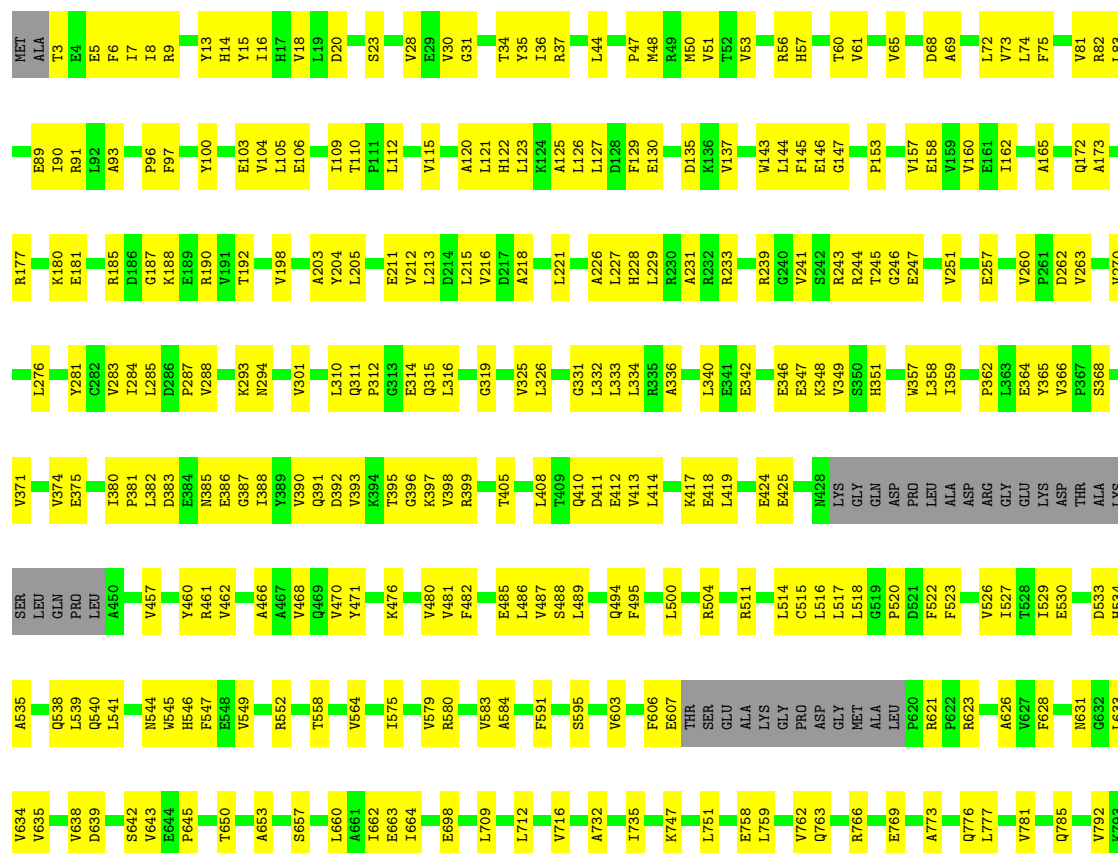
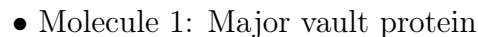


V371	LEU	GLN	PRO	LEU	A450	T455	R456	V457	Y460	R461	V462	Q469	V470	Y471	D472	Y473	A478	R479	V480	G483	L486	V487	S488	L489	Q494	F495	S501	R507	L514	L517	D521	F522	T524	D525	I529	E530	T531	H534	A535	GLY	R536	L537	Q538	L539	Q540	L541		
A542	Y543	N544	W545	V549	R552	R553	D554	T558	V564	F567	V568	C572	I575	V579	R580	V583	A584	F588	D589	D590	F591	H592	K593	S594	S595	I598	I599	V603	F606	E607	THR	SER	GLU	D525	ALA	LYS	GLY	PRO	LEU	ASP	ARG	GLY	LEU	ASP	THR	ALA	LYS	SER
S637	V638	D639	S642	V643	E644	P645	A661	I662	E663	I664	L709	E727	K747	L751	E756	E758	L759	Q760	R761	V762	V765	R766	E767	L768	E769	L770	V771	Y772	R774	K783	A788	V792	F795	K796	Q797	P798	T799	T806	G814	PRO	GLU	MET						
GLN	VAL	LYS	LEU	GLN	SER	LEU	GLY	ASP	HIS	VAL	VAL	PRO	LEU	ILE	THR	ASP	GLY	SER	THR	PRO	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	ARG	VAL	ALA	SER	GLY	PRO	SER	PRO	PRO	GLY	GLY	ILE	SER	PRO	GLN	SER	ALA
GLN	ALA	PRO	GLN	ALA	PRO	GLY	ASP	ASN	VAL	VAL	PRO	LEU	ARG																																			

• Molecule 1: Major vault protein

Chain NB:  55% 32% 13%

GLN	B670	L539	SER	I380	Y281	Q172	V77	MET
VAL	L693	Q540	LEU	P381	C282	R175	T78	ALA
LEU	Q696	A542	PRO	D383	V283	L176	G79	T3
LEU	K704	W545	LEU	E384	D286	W183	Q80	F6
SER	L707	H546	A450	N385	P287	W183	V81	I7
LEU	E727	F547	V457	G387	V288	G187	R82	I8
LEU	L751	V549	Y460	I388	K293	K188	L83	R9
LYS	E732	V568	R461	V389	L296	R94	H85	I10
SER	I735	G569	V462	Q391	L296	E189	P96	Y13
THR	E736	I575	P463	D382	V301	W196	I99	H14
LEU	G737	R578	A467	V393	V302	L197	Y100	Y15
THR	V741	V579	V468	K394	E305	A203	E103	I16
GLY	V741	B580	Q469	T395	E305	Y204	E104	V18
SER	K747	V583	Y471	K397	L316	P206	L105	V25
THR	L751	A584	D472	V398	G319	A207	E106	S26
PRO	E756	F588	R477	R399	V325	V208	K107	R27
ASN	A757	THR	A478	A400	L326	F209	D108	V28
LEU	L759	GLU	R479	I401	V212	T110	I109	E29
PHE	V762	ALA	V480	G403	L215	T110	V114	V30
LEU	E767	LYS	V481	S404	V216	W115	V115	G31
LEU	L768	GLY	F482	T405	D217	A120	I21	T34
MET	E769	PRO	SER	Y406	A218	L121	R37	I36
GLY	L770	GLY	E485	L408	R222	H122	V43	R37
PRO	W771	MET	G490	T409	E223	L126	L44	V43
GLU	Y772	LEU	P491	Q410	K224	L127	F45	L44
GLY	V781	P620	L498	D411	T225	A226	D128	L44
GLN	A788	R621	L498	E412	R225	E129	P47	F45
LEU	E789	P622	A502	V413	A226	F129	M48	A46
GLY	V790	L633	A510	L414	D345	E130	R49	A46
ARG	E791	V634	L516	W415	E346	D131	M50	M48
VAL	V792	V638	L518	Q422	E347	V137	T52	R49
SER	K794	D639	L518	V423	R348	W143	R56	M50
GLY	F795	S642	D521	E424	V349	L144	R56	T52
PRO	SER	V643	F523	E425	H351	T150	C59	T52
PRO	M798	V643	F523	L426	Q352	T60	C59	T52
PRO	A801	L654	F523	N428	L337	V61	T60	T52
GLY	I802	S657	I527	L427	L340	P153	V61	T52
ILE	L810	T662	T528	LYS	R360	A62	V61	T52
SER	G814	T665	I529	GLY	V260	N63	V61	T52
GLN	PRO	T666	T531	GLU	P261	P64	N63	T52
SER	GLU	THR	T531	GLU	D262	E158	P64	T52
ALA	MET	VAL	H534	GLY	V267	V160	E158	T52
				THR	L268	E161	V160	T52
				ASP	I167	D68	E161	T52
				LYS	I163	R67	E161	T52
				ASP	I167	I162	D68	T52
				THR	I163	A69	I162	T52
				ALA	I167	Q70	I162	T52
				LYS	I168	V73	I162	T52
				LYS	R169	L74	I162	T52
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				LYS	N171	D76	I162	T52



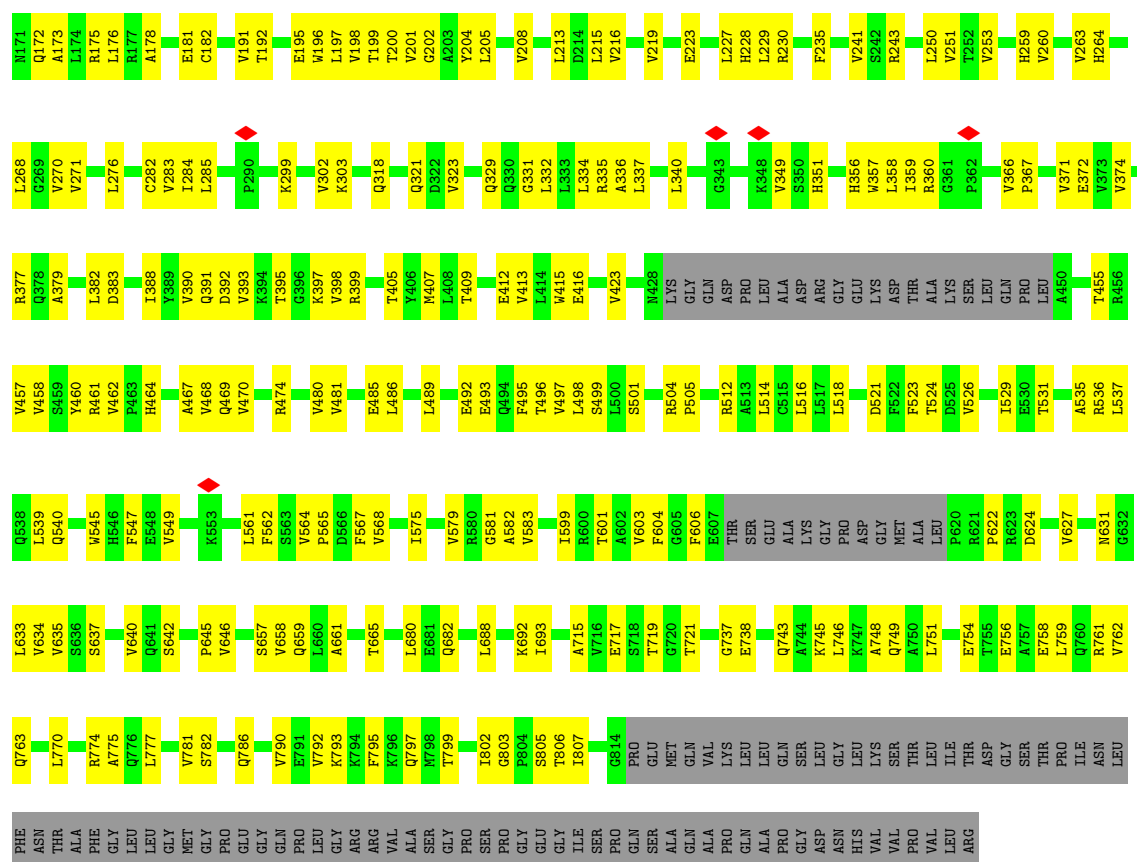
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Chain Q: 59% 28% 13%

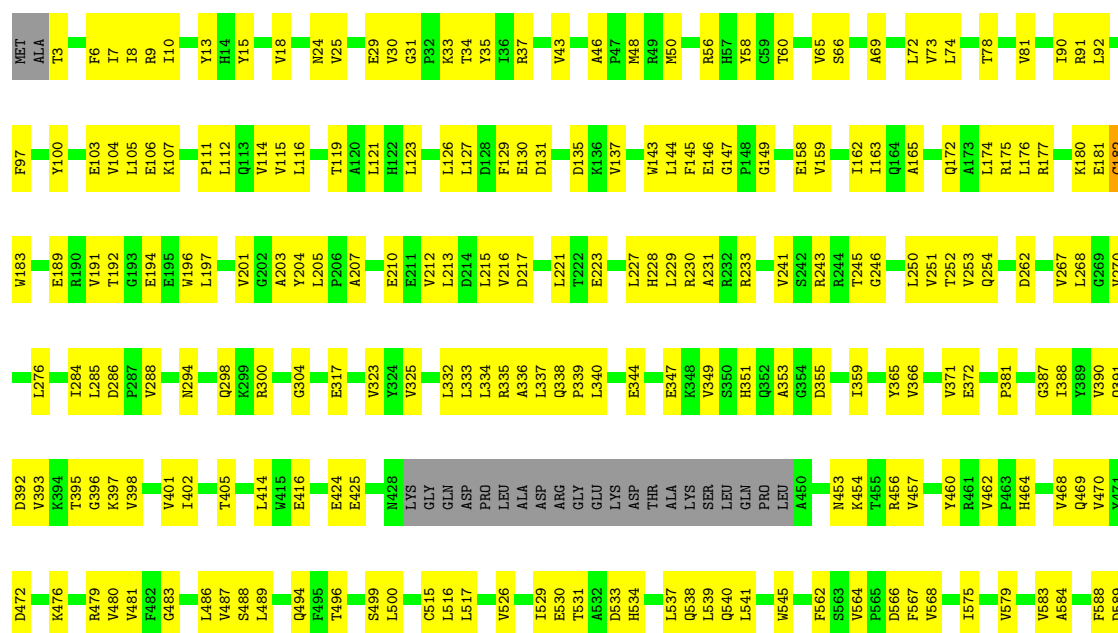
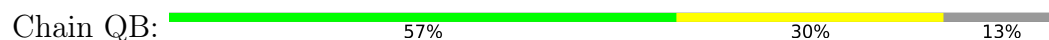
GLY	V771	THR	L489	L408	V301	R177	A93
	R774	SER	E493	T409	S307	C182	P96
	E780	ALA	F495	L414	L310	D184	L99
	K783	GLY	L514	L419	L316	T192	F101
	Q786	ASP	C515	P420	E317	G102	G102
	L787	GLY	L516	P421	W196	E103	E103
	A788	MET	L517	E424	Q321	V104	V104
	E789	ALA	L518		V201	L105	L105
	V790	LEU	D521	H428	Y324	G202	G202
	E791	P620	LYS	GLY	G331	Y204	I109
ARG	V792	A626	T529	GLN	L332	L205	L112
	F795	V634	E530	ASP	L334	V208	Q113
	T799	V636	L537	PRO	R335	F209	V115
	P804	S636	A542	LEU	E347	E210	
	L807	D639	W545	ASP	A353	V212	T119
	R808	P645	H546	GLY	G354	L213	A120
	V812	A661	F547	GLY	D355	D214	V30
	A813	E548	W549	LYS	L358	L215	H122
	G814	P664	D554	ASP	G361	L216	L123
	PRO	A677	T568	GLN	SER	R230	K124
ALA	LEU	L680	L561	LEU	T245	G134	
	GLN	L709	F567	PRO	E247	V137	
	LEU	A730	V568	A450	L260	W143	
	PRO	A733	R580	T455	V260	L144	
	GLY	SER	G581	R456	P261	G147	
	ASN	GLY	A582	V457	L382		
	LEU	Q743	W583	V458			
	VAL	LYS	A584	R461	E386	T150	
	VAL	SER	L746	V462	G387	L268	
	THR	THR	T587	A466	I388	K155	
VAL	LEU	L751	F588	A467	V270	E156	
	LEU	ILE	D589	V468	T274	V157	
	THR	T755	D590	Q469	T275	E158	
	ASP	F591	F591	V470	V393	V159	
	GLY	L759	R594	V471	A394	I162	
	SER	Q760	R761	Y471	T395	A165	
	THR	V762	S595	R477	K397	T284	
	ILE	Q763	I598		V398	I168	
	ASN	K764	I599	V480	R399	R169	
	LEU	V765	R600	V481	A400	D286	
PHE	R766	T601	F482	V482	Q172	A173	
	ASN	E767	A602	V603	V288	A173	
	THR	L768	V603	L486	T405	L174	
	ALA	E769	V607	C488	Y406	R177	
	THR	L770	V607	C488	Y406		
	THR	V771					
	T778						
	G779						
	Q80						
	V81						
L33	R82						
	L83						
	I90						
	R91						
	MET						
	ALA						
	T3						
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	I10						
	Y15						
H17							
V18							
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G31							
T34							
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V73							
V77							
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R91							

Chain QA: 54% 33% 13%

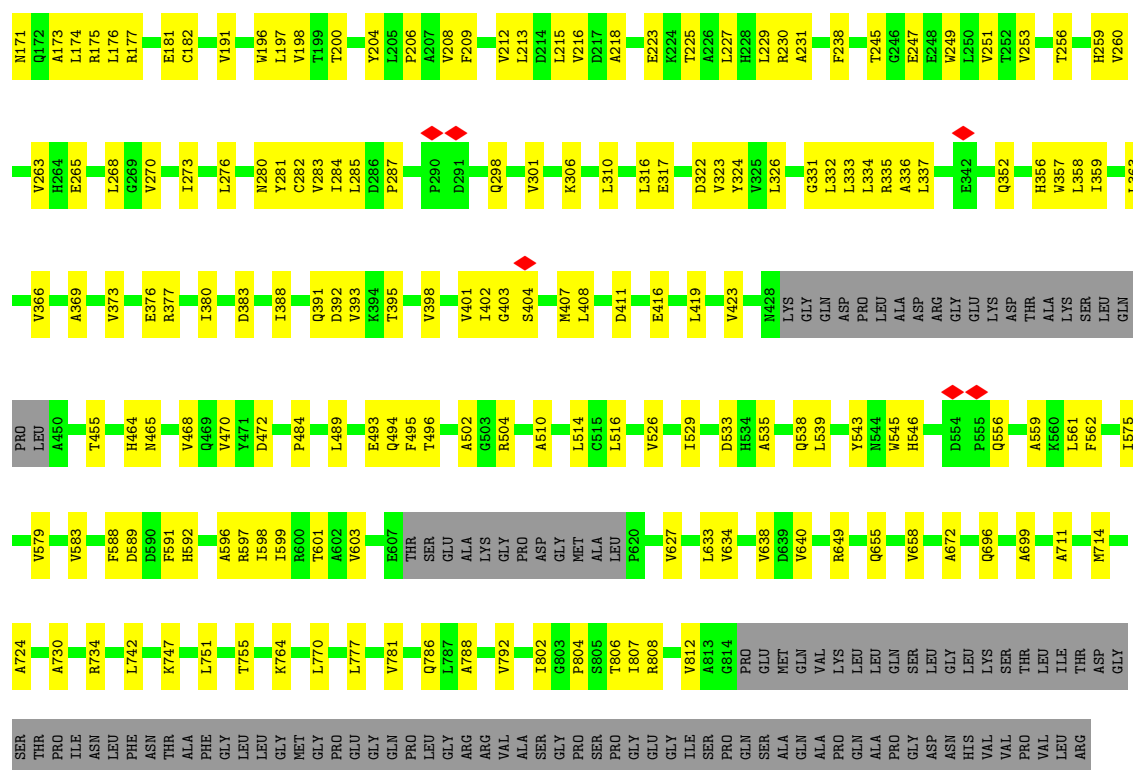
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ALA	ALA	T3		F6		R9	I10	Y15	H16	H17	V18	L19	D20		R27	V28	E29		P32	K33	T34	Y35	I36	R37	E41	R42	V43	L44	F45	A46	P47		T52	V53	P54	Y58	C59	T60	V61	A62	N63	P64	V65		D68	A69	V73	L74		V81	R82	L83		V88	L89



• Molecule 1: Major vault protein

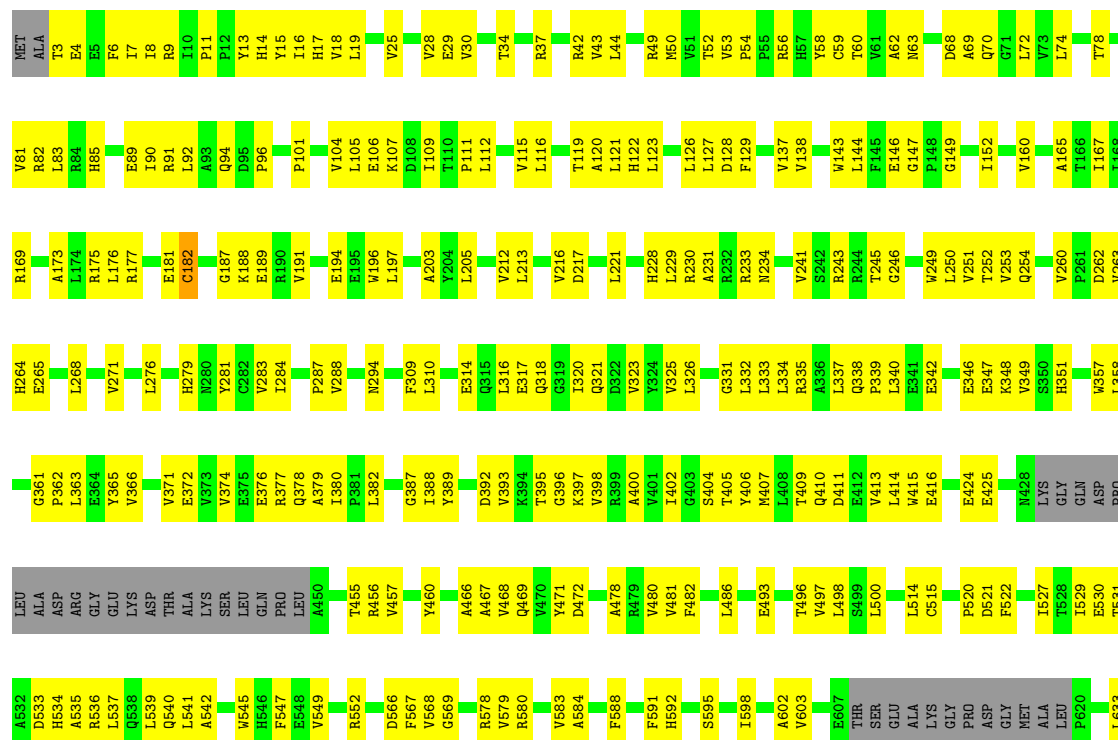


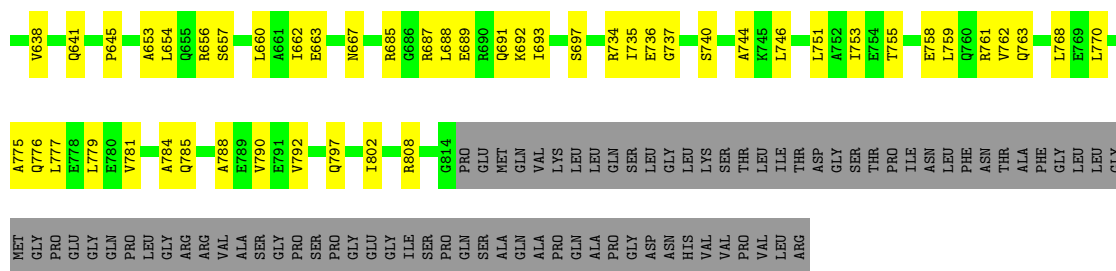




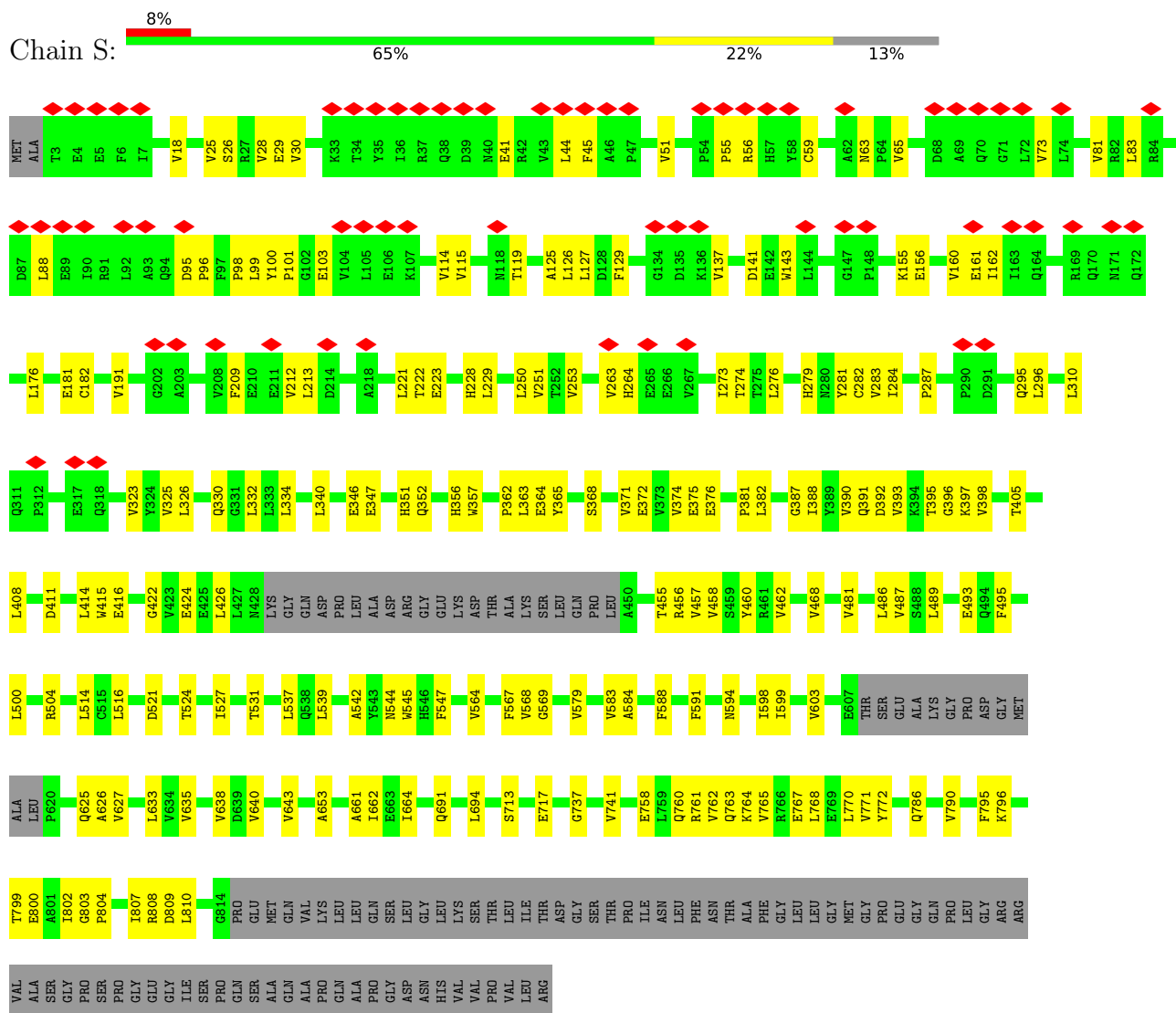
• Molecule 1: Major vault protein

Chain RB:

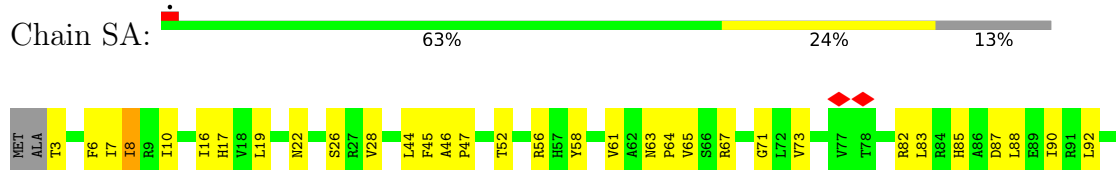


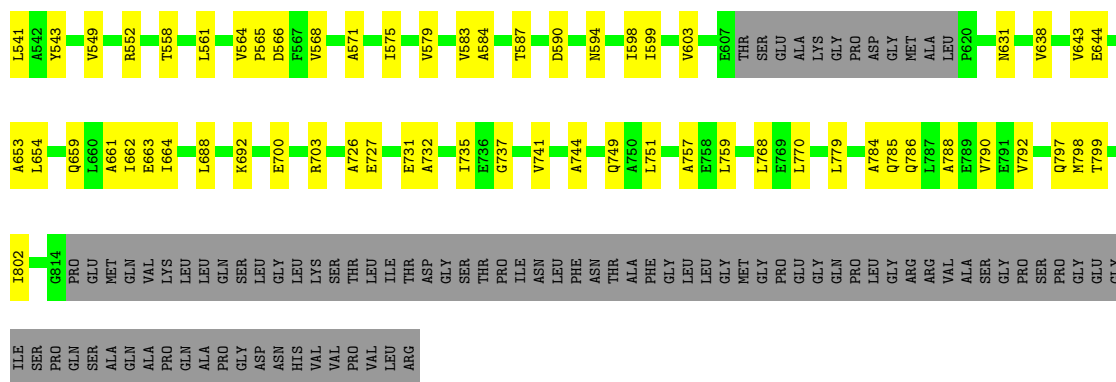


• Molecule 1: Major vault protein

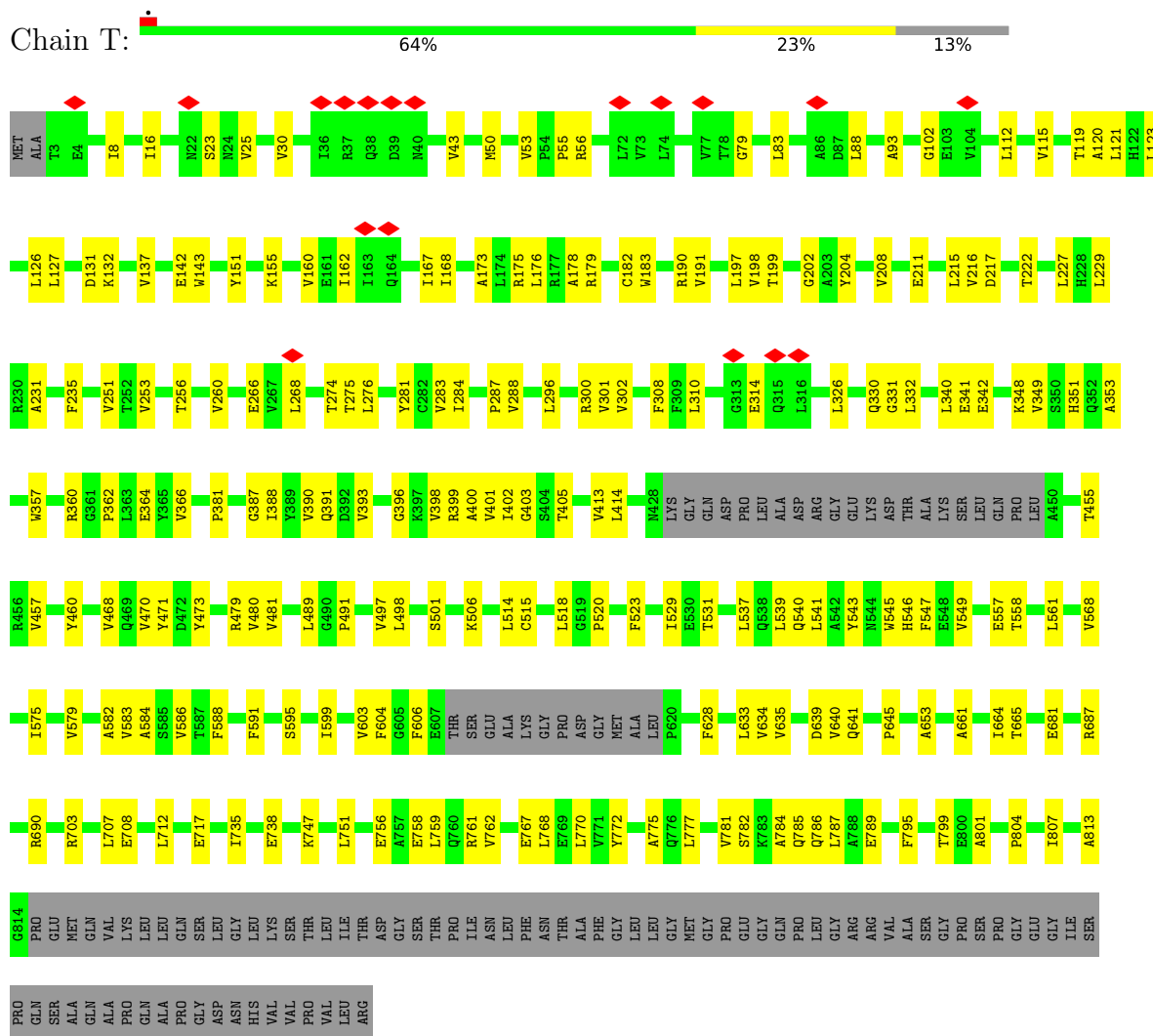


• Molecule 1: Major vault protein





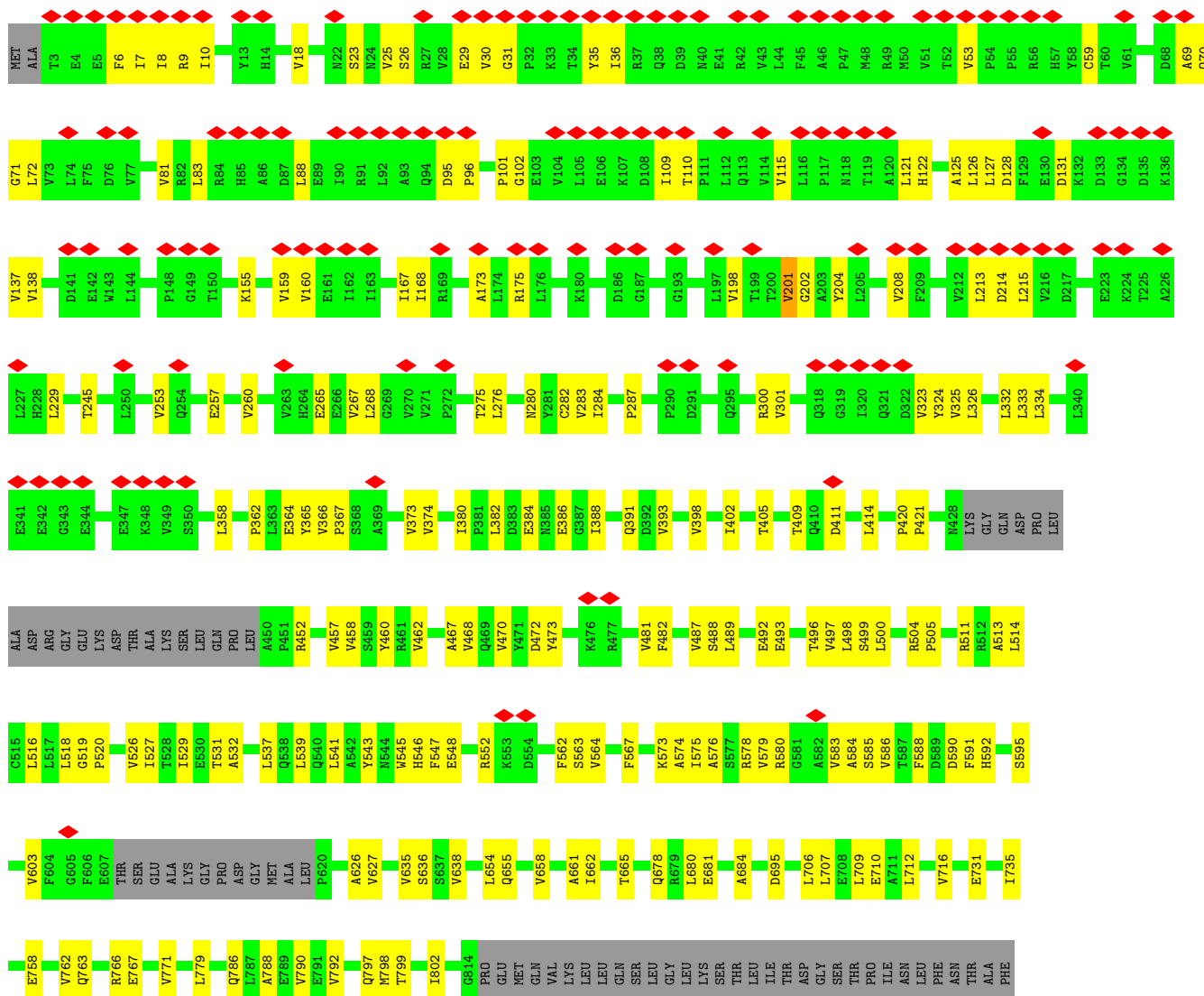
• Molecule 1: Major vault protein



• Molecule 1: Major vault protein



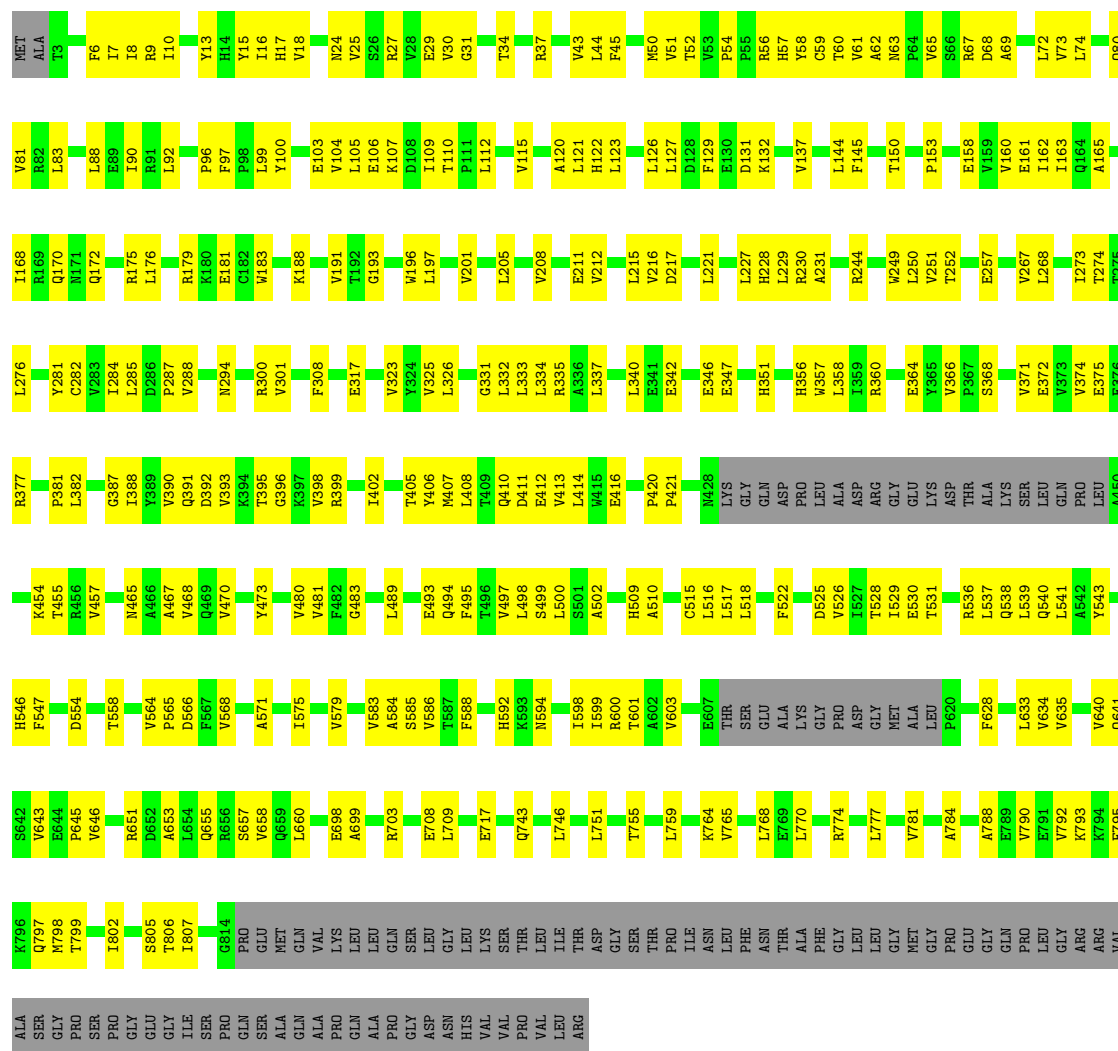
- Molecule 1: Major vault protein



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

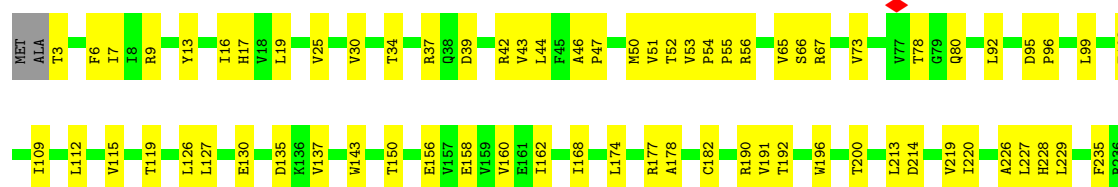
• Molecule 1: Major vault protein

Chain UB:  55% 32% 13%

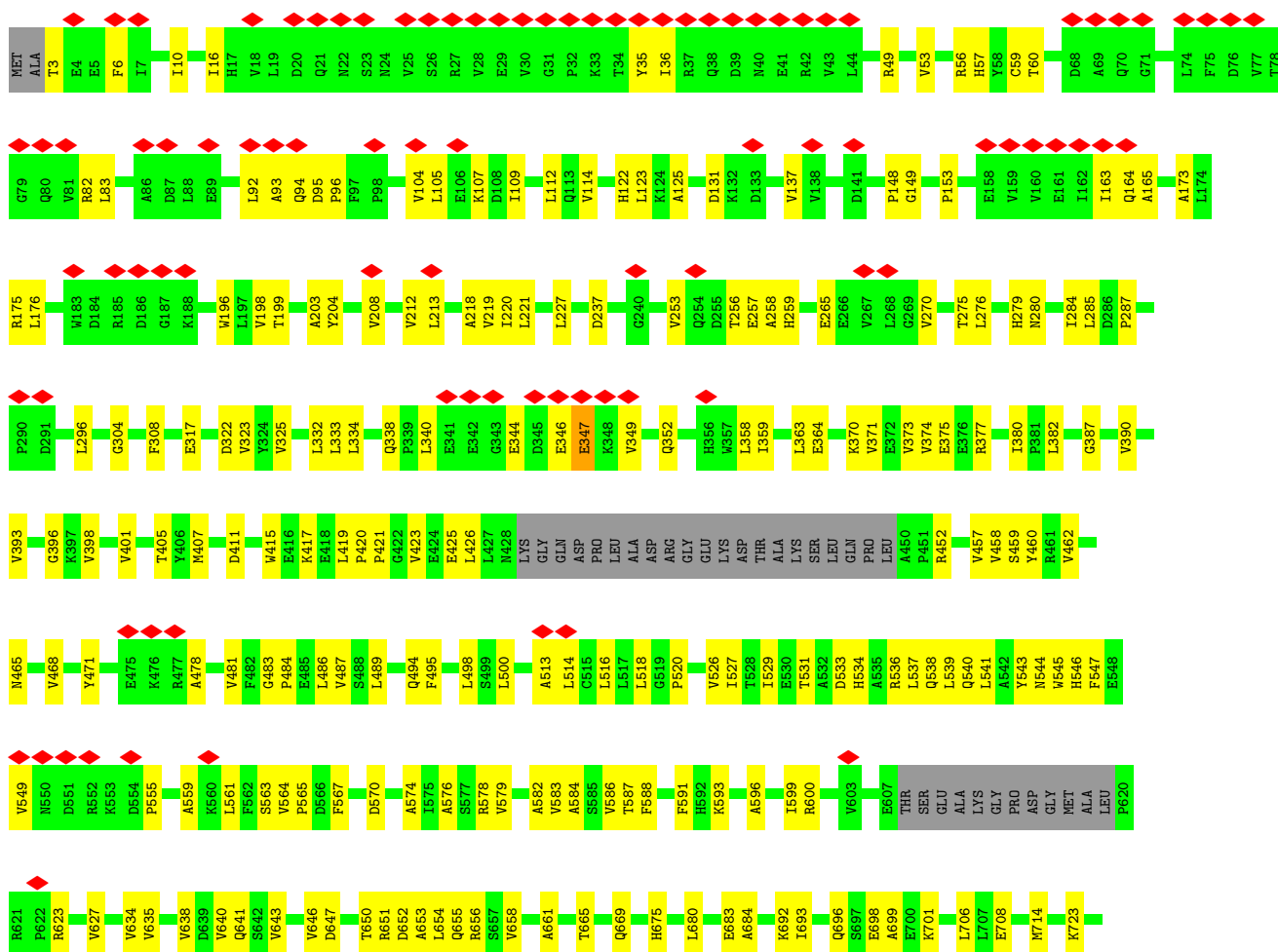


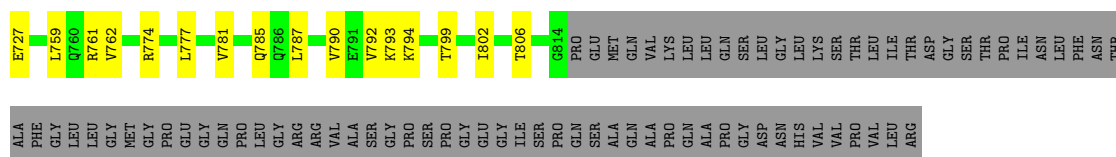
• Molecule 1: Major vault protein

Chain V:  64% 23% 13%



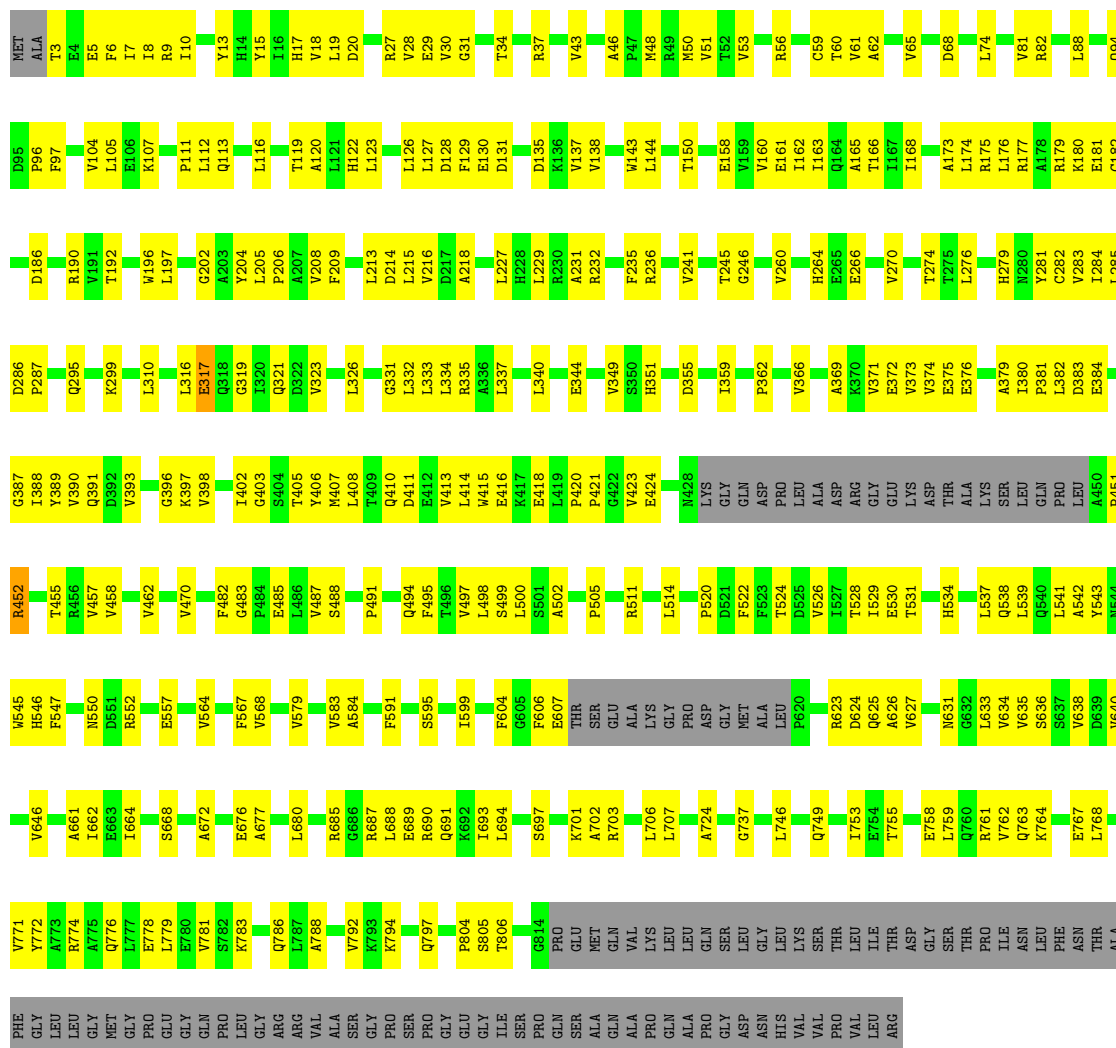
- Molecule 1: Major vault protein





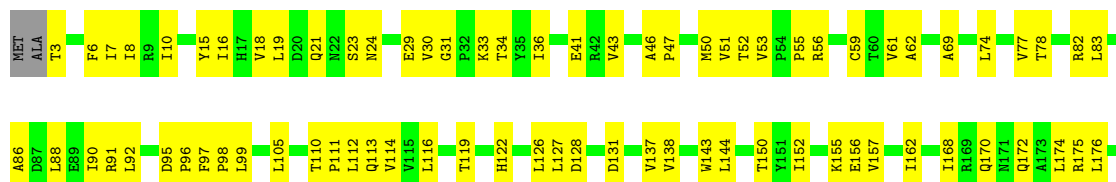
• Molecule 1: Major vault protein

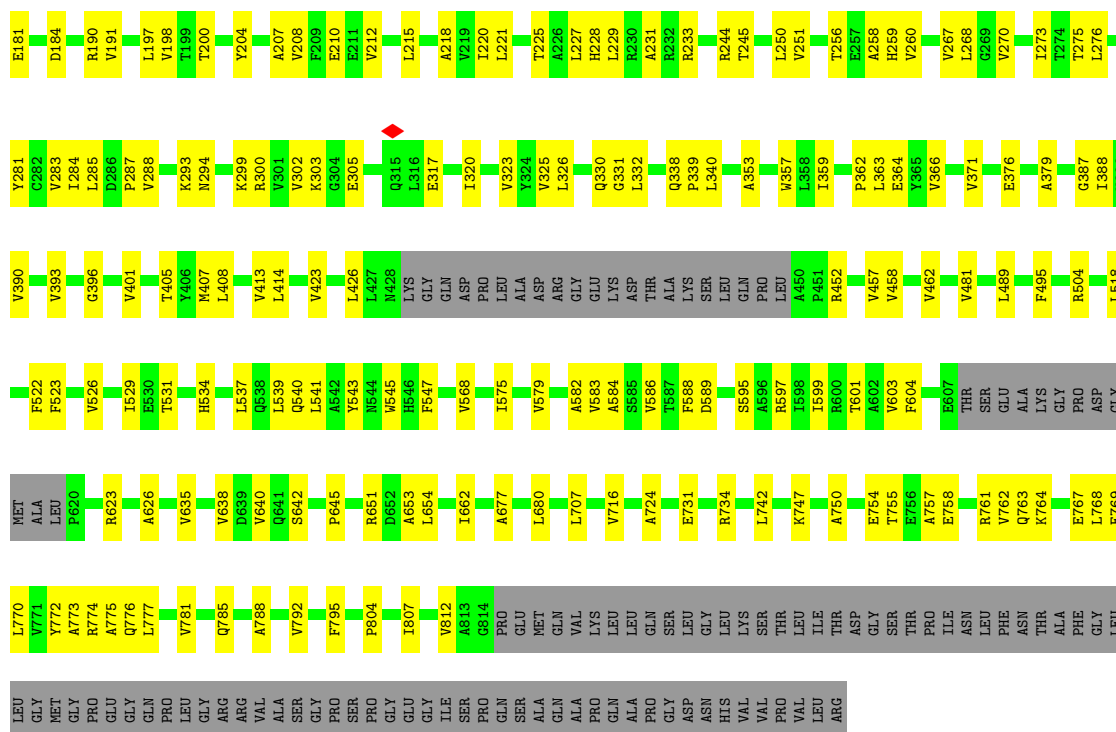
Chain VB: 53% 34% 13%



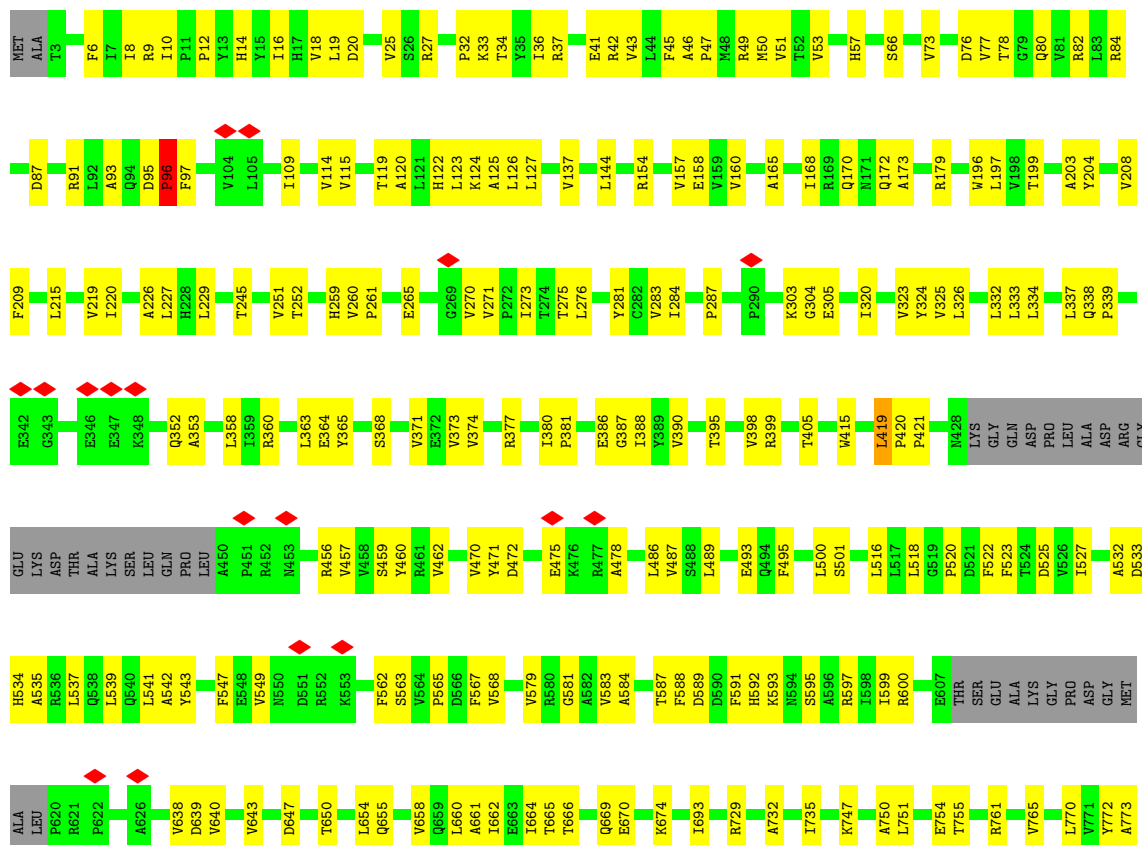
• Molecule 1: Major vault protein

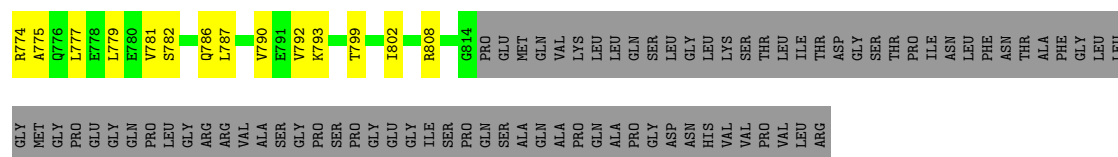
Chain W: 60% 27% 13%





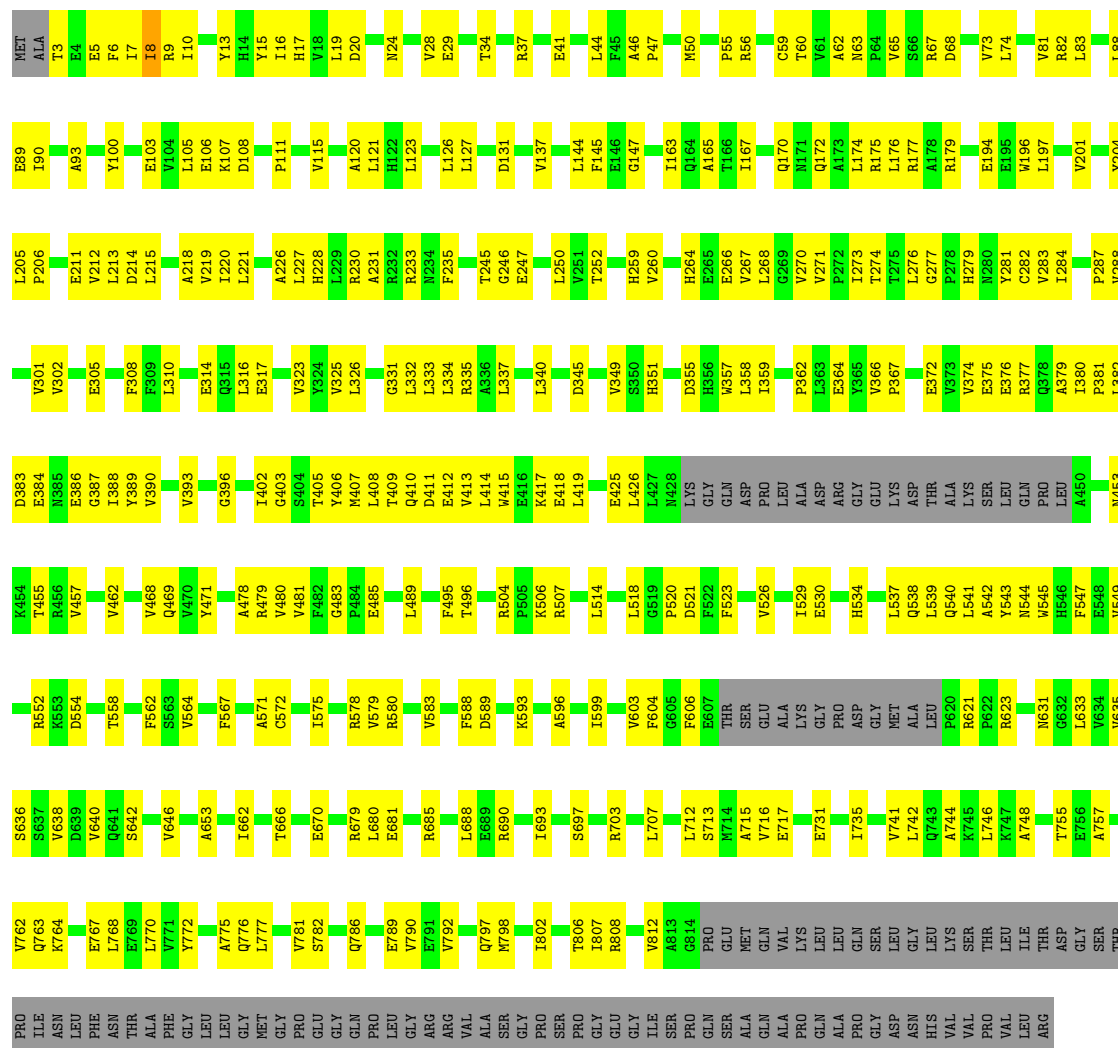
• Molecule 1: Major vault protein





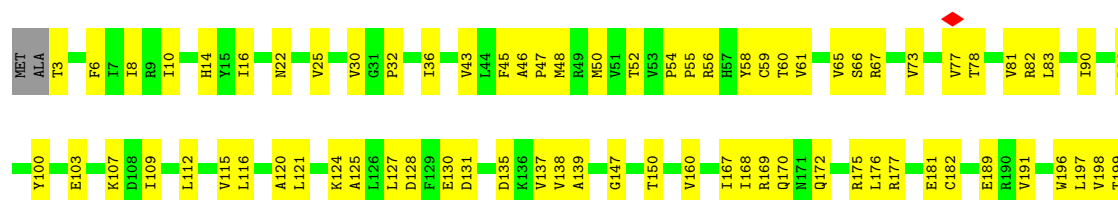
• Molecule 1: Major vault protein

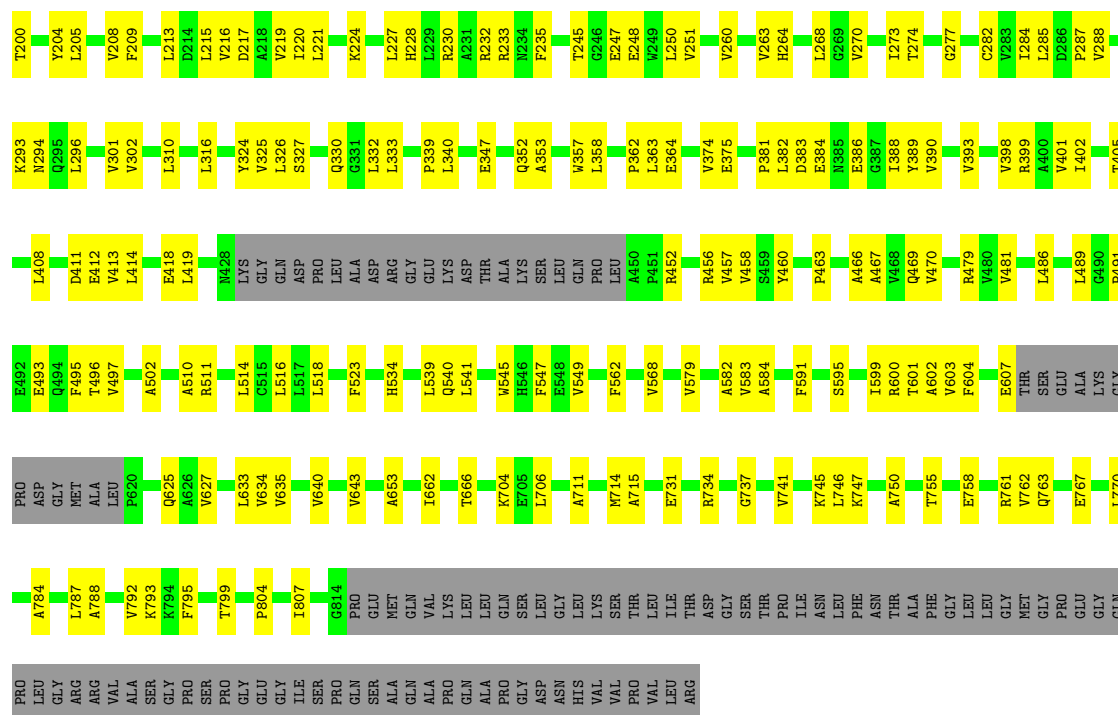
Chain WB: 53% 34% 13%



• Molecule 1: Major vault protein

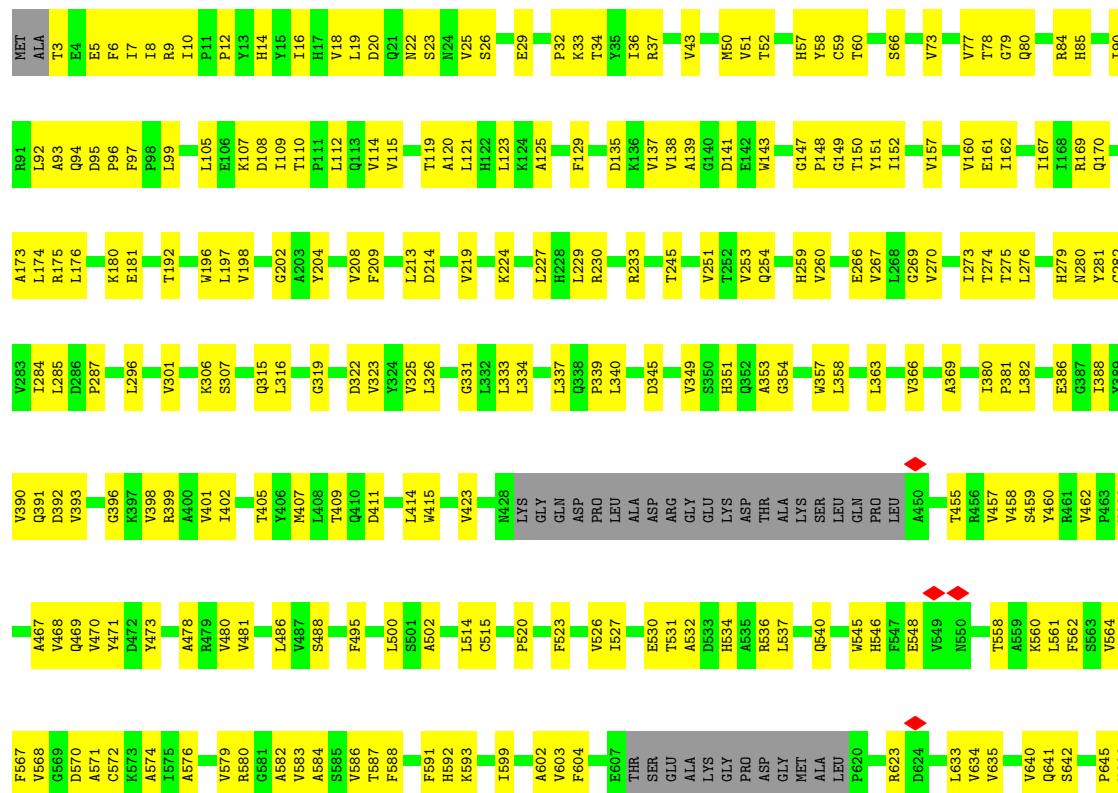
Chain X: 60% 27% 13%

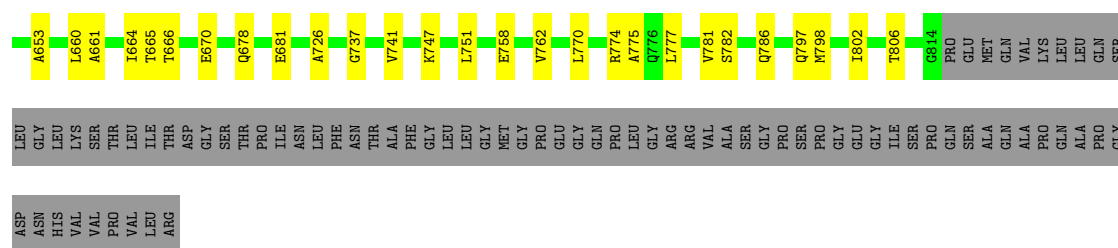




• Molecule 1: Major vault protein

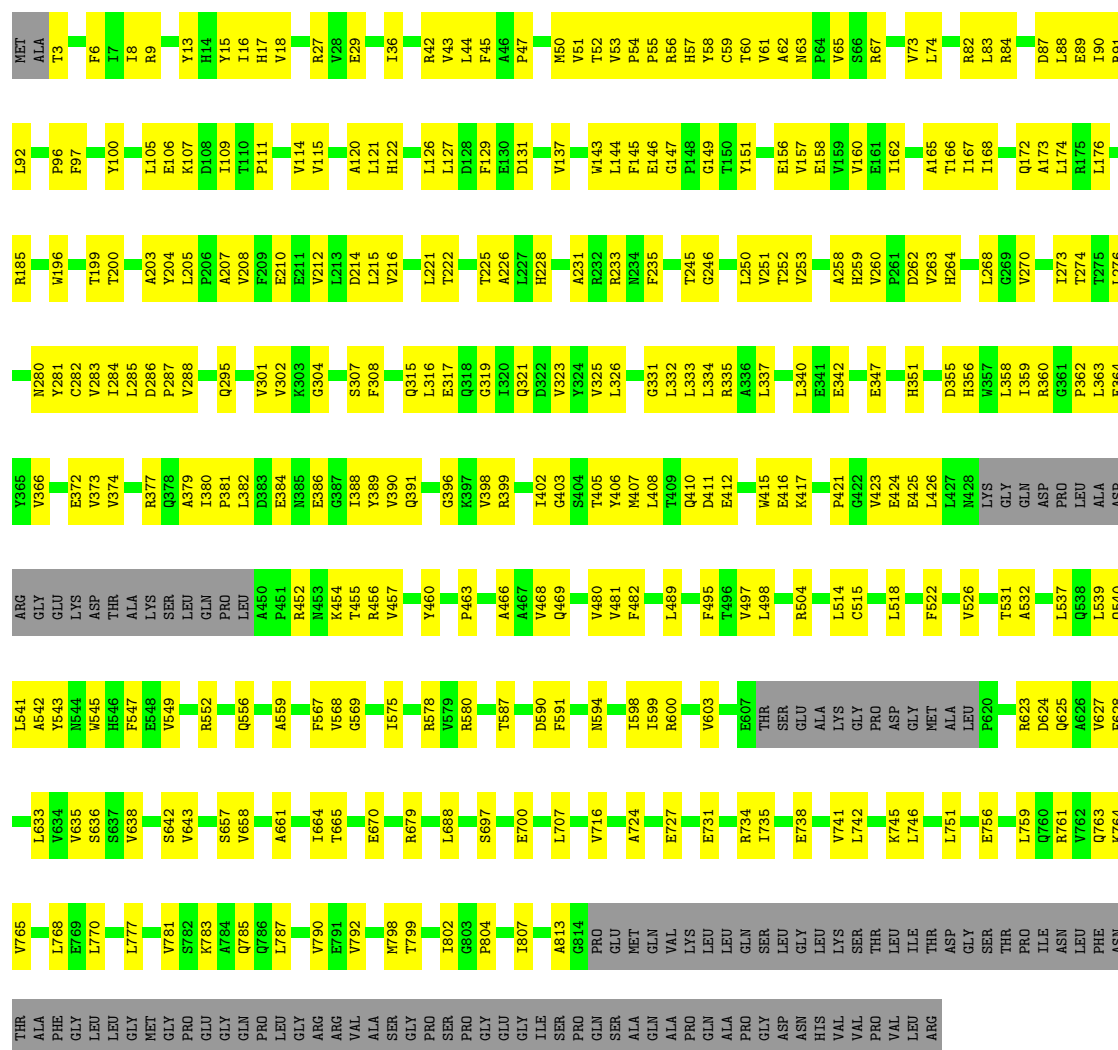
Chain XA: 57% 30% 13%





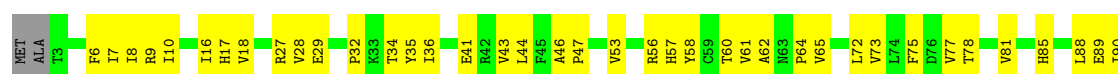
• Molecule 1: Major vault protein

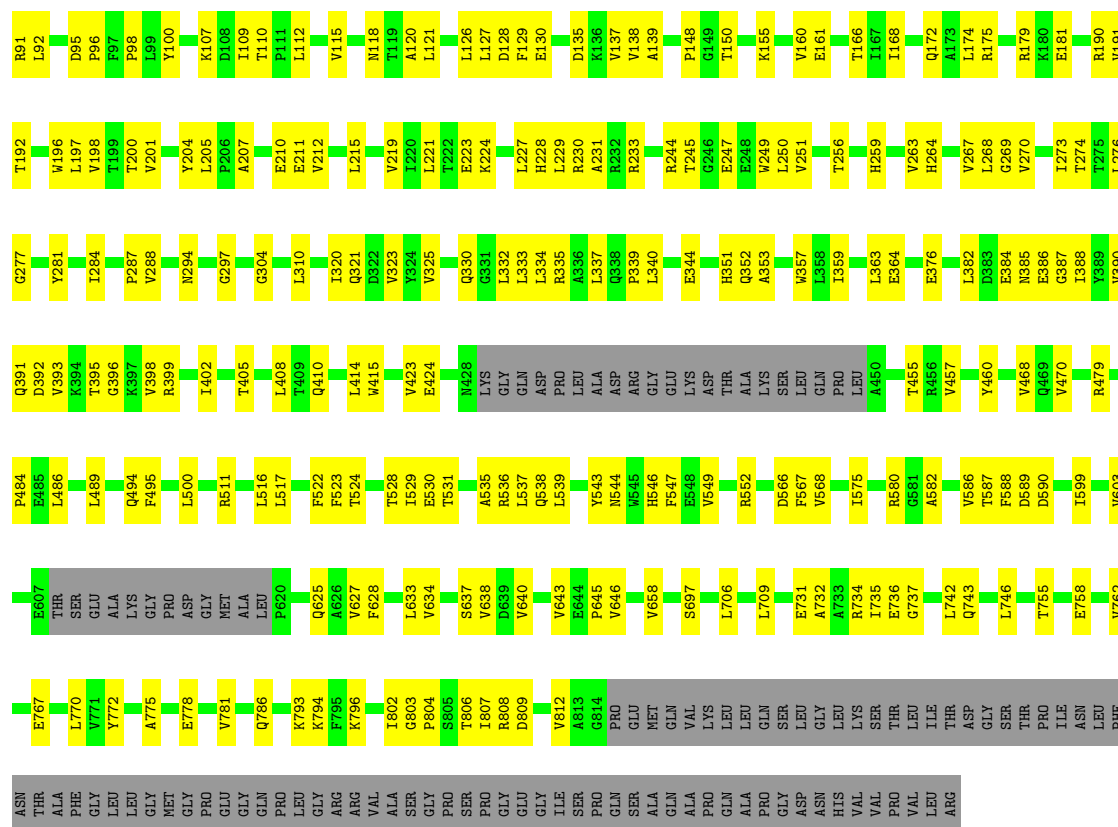
Chain XB: 53% 34% 13%



• Molecule 1: Major vault protein

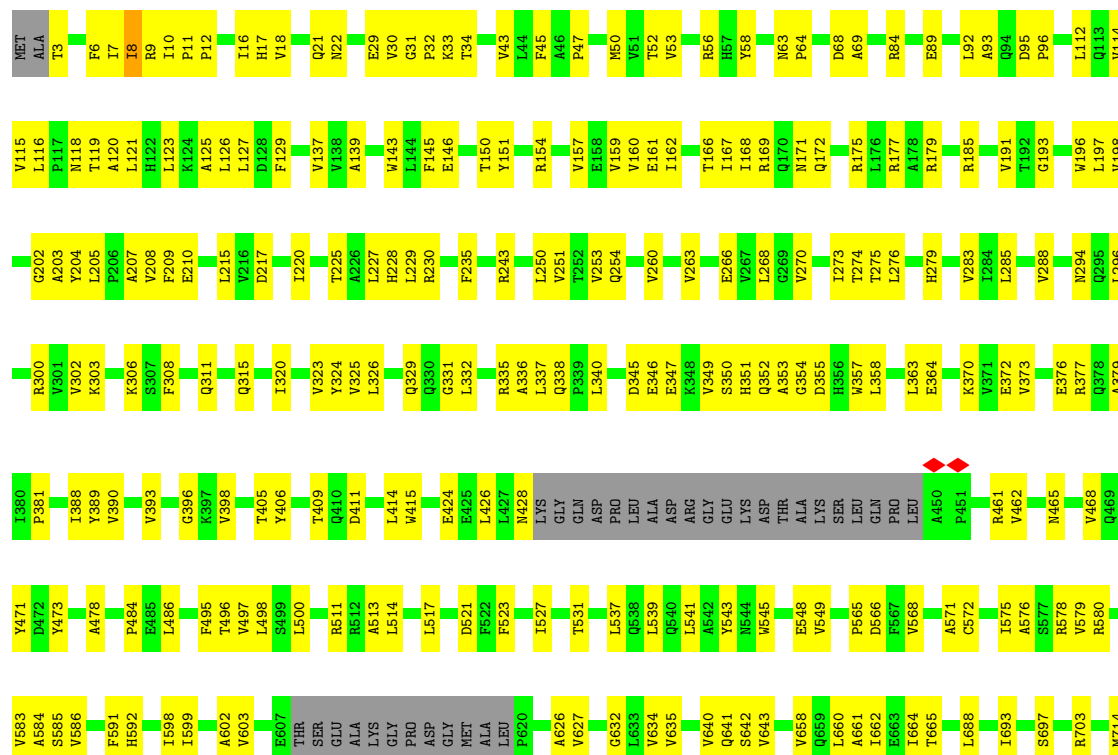
Chain Y: 58% 29% 13%

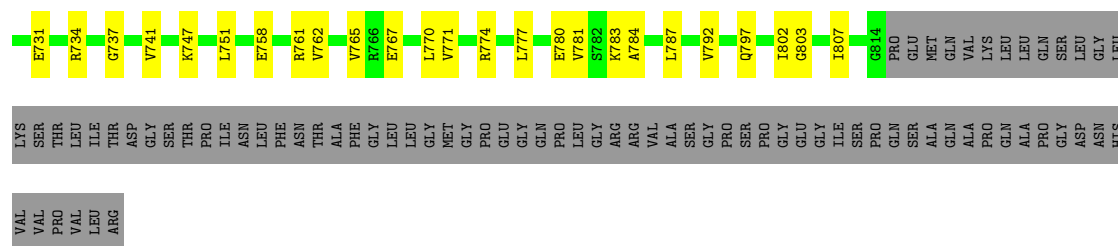




• Molecule 1: Major vault protein

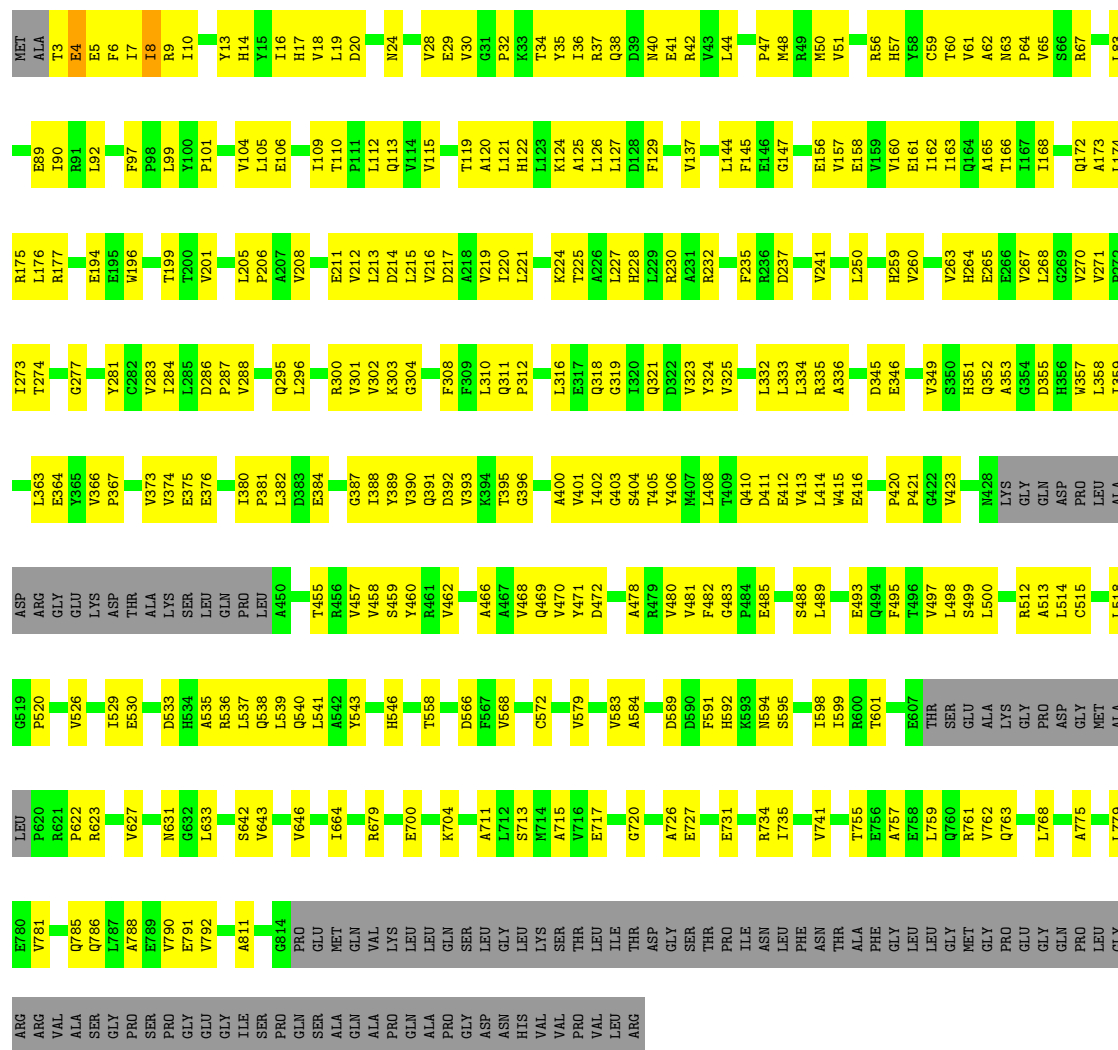
Chain YA:





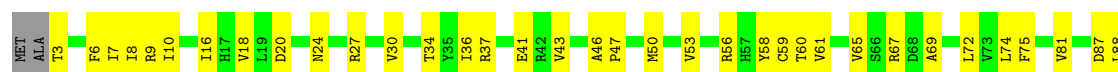
• Molecule 1: Major vault protein

Chain YB: 53% 34% 13%



• Molecule 1: Major vault protein

Chain Z: 57% 30% 13%



VAL	LYS	Q743	SER	L486	G396	F308	V201	E89
	SER	A744	GLU	V487	I402	F309	G202	I90
VAL	THR	Q749	ALA	S488	L405	L310	A203	R91
VAL	LEU	Q753	GLY	F495	T406	Q315	Y204	L92
ARG	THR	I753	PRO	L500	M407	L316	L205	A93
	ASP	E756	GLY	R507	L408	E317	P206	L105
	GLY	A757	ASP	L507	T409	D322	F209	
	SER	E758	MET	Q409	Q410	V323	E210	I109
	THR	L759	ALA	D411	D411	Y324	E211	P111
	PRO	Q760	LEU	A510	L414	V325	V212	L112
	ILE	R761	R621	R511	L414	L326	L213	Q113
	ASN	V762	P622	R512	W415	G331	D214	V115
	LEU	V765	R623	A513	E416	L332	I220	L116
	PHE	E766	R623	L514	K417	L333	I220	
	ASN	R766	V627	C515	K417	L334	I221	
	THR	V765	V627	L516	P421	R335	L221	A120
	ALA	E767	V634	D521	E424	A336	L227	L121
	PHE	L770	V635	F522	E424	R337	H228	H122
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	PRO	R781	Q641	E530	GLN	E342		
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	GLY	K783	V643	A532	PRO	D345	V251	V138
	GLN	A784	V643	D533	LEU	D345		A139
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	VAL	M798	VAL	Q540	GLU	D355	E266	V157
	ALA		ALA	L541	LYS	H356	V267	E158
	SER	I802	SER	A542	ASP	W357	L268	V159
	GLY	G803	PRO	V543	THR	L388	G269	V160
	PRO	P804	SER	H544	ALA	I359	V270	E161
	SER	S805	PRO	W545	LYS	R360	I162	
	GLY	T806	PRO	F567	SER	L363	I273	A165
	GLU	I807	GLY	R580	LEU	E364	T274	T166
	GLY	R808	GLY	V583	GLN	E372	T275	
	ILE	A813	ILE	A584	PRO	L276	L276	Q170
	PRO	G814	PRO	F588	LEU	H279		
	GLN	PRO	GLN	F591	A450	V373	N280	L174
	SER	GLU	GLU	F591	T455	V374	Y281	L175
	ALA	MET	ALA	F591	R456	E375		R175
	GLN	GLN	ALA	F591	V457	E376		L176
	ALA	VAL	ALA	S595	V458	R377	I284	
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	ALA	LEU	ALA	S595	Y460	L382		
	PRO	GLN	GLN	S595	Y460	L382		
	GLN	GLN	GLN	S595	Y460	L382		
	PRO	GLN	GLN	S595	Y460	L382		
	GLY	GLY	GLY	S595	Y460	L382		
	ASP	LEU	GLY	S595	Y460	L382		
	ASN	GLY	GLY	S595	Y460	L382		
	HIS	LEU	LEU	S595	Y460	L382		
				S595	Y460	L382		
				S595	Y460	L382		
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				S595	Y460	L382		
				S595	Y460	L382		</

• Molecule 1: Major vault protein

Chain ZA:

MET	ALA	T3	F6	I7	I8	R9	I10	P11	P12	Y13	I16	H17	V18	L19	N22	V25	S26	R27	G31	P32	K33	T34	Y35	I36	F45	M48	R49	N50	R56	H57	Y58	V61	A62	N63	P64	V65	S66	V73	T78	L83	R84	H85	L88	G102					
P111	L112	V115	L121	L127	D128	D131	V137	V138	A139	F145	E146	G147	T150	E156	V160	E161	I162	T168	R169	Q170	N171	Q172	A173	L176	R177	A178	R179	K180	E181	C182	R190	V191	T192	G193	V196	L197	V198	A203	Y204	V302	K303	E210	E211	V212	L213				
D214	L215	D217	A218	V219	I220	L221	K224	T225	A226	L227	H228	L229	R230	R231	R232	R233	N234	F235	R243	R244	T245	L250	V251	T252	T256	H259	V260	V267	V271	P272	I273	L276	H279	N280	Y281	C282	V283	L296	G297	R300	V301	R302	V303	V304	F209	E210	E211	V212	P312
L316	Q321	V325	L326	S327	Q329	Q330	G331	L332	R335	A336	L337	Q338	E342	D345	V349	Q352	A353	H356	R360	G361	P362	L363	E364	Y365	V366	K370	E376	A379	I380	P381	L382	N385	E386	G387	V390	Q391	D392	V393	K394	T395	G396	R399							
A400	V401	I402	G403	S404	T405	Y406	M407	L408	T409	Q410	D411	E412	V413	L414	L419	P420	P421	N428	LYS	GLY	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	SER	LEU	GLN	PRO	A450	P451	R452	Y460	R461	V468	Q469	Y470	Y471	D472	Y473	K476	R479	V480	
V481	L486	L489	F495	S501	A502	R507	P508	H509	A510	C515	D521	F522	F523	V526	I527	T528	I529	E530	T531	A532	D533	L537	Q538	L539	Q540	L541	A542	Y543	N544	W545	H546	F547	P555	D566	F567	V568	I575	V579	R580	V583	A584	T587	F588	D589	D590				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23998	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.15	Depositor
Minimum defocus (nm)	551	Depositor
Maximum defocus (nm)	2330	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.709	Depositor
Minimum map value	-0.418	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	861.7984, 861.7984, 861.7984	wwPDB
Map dimensions	1024, 1024, 1024	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8416, 0.8416, 0.8416	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.24	0/6291	0.45	0/8533
1	AA	0.19	0/6291	0.44	0/8533
1	AB	0.17	0/6291	0.45	0/8533
1	AC	0.17	0/6291	0.45	0/8533
1	B	0.23	0/6291	0.45	0/8533
1	BA	0.20	0/6291	0.45	0/8533
1	BB	0.17	0/6291	0.43	0/8533
1	C	0.24	0/6291	0.46	0/8533
1	CA	0.20	0/6291	0.46	0/8533
1	CB	0.18	0/6291	0.43	0/8533
1	D	0.24	0/6291	0.45	0/8533
1	DA	0.21	0/6291	0.46	0/8533
1	DB	0.19	0/6291	0.44	0/8533
1	E	0.24	0/6291	0.46	0/8533
1	EA	0.22	0/6291	0.45	0/8533
1	EB	0.20	0/6291	0.45	0/8533
1	F	0.23	0/6291	0.46	0/8533
1	FA	0.23	0/6291	0.45	0/8533
1	FB	0.20	0/6291	0.44	0/8533
1	G	0.22	0/6291	0.45	0/8533
1	GA	0.22	0/6291	0.45	0/8533
1	GB	0.21	0/6291	0.45	0/8533
1	H	0.24	0/6291	0.46	1/8533 (0.0%)
1	HA	0.23	0/6291	0.45	0/8533
1	HB	0.21	0/6291	0.44	0/8533
1	I	0.23	0/6291	0.48	2/8533 (0.0%)
1	IA	0.23	0/6291	0.45	0/8533
1	IB	0.22	0/6291	0.46	0/8533
1	J	0.21	0/6291	0.45	0/8533
1	JA	0.23	0/6291	0.45	0/8533
1	JB	0.22	0/6291	0.46	0/8533
1	K	0.20	0/6291	0.44	0/8533
1	KA	0.23	0/6291	0.45	0/8533
1	KB	0.22	0/6291	0.45	0/8533

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.20	0/6291	0.44	0/8533
1	LA	0.23	0/6291	0.45	0/8533
1	LB	0.23	0/6291	0.46	0/8533
1	M	0.19	0/6291	0.44	0/8533
1	MA	0.24	0/6291	0.46	0/8533
1	MB	0.22	0/6291	0.45	0/8533
1	N	0.19	0/6291	0.44	0/8533
1	NA	0.24	0/6291	0.45	0/8533
1	NB	0.23	0/6291	0.45	0/8533
1	O	0.18	0/6291	0.44	0/8533
1	OA	0.16	0/6291	0.44	0/8533
1	OB	0.22	0/6291	0.44	0/8533
1	P	0.18	0/6291	0.43	0/8533
1	PA	0.16	0/6291	0.44	0/8533
1	PB	0.22	0/6291	0.45	0/8533
1	Q	0.19	0/6291	0.45	0/8533
1	QA	0.16	0/6291	0.45	0/8533
1	QB	0.22	0/6291	0.45	0/8533
1	R	0.16	0/6291	0.43	0/8533
1	RA	0.15	0/6291	0.43	0/8533
1	RB	0.21	0/6291	0.44	0/8533
1	S	0.16	0/6291	0.41	0/8533
1	SA	0.17	0/6291	0.43	0/8533
1	SB	0.22	0/6291	0.45	0/8533
1	T	0.16	0/6291	0.42	0/8533
1	TA	0.14	0/6291	0.41	0/8533
1	TB	0.21	0/6291	0.45	0/8533
1	UA	0.14	0/6291	0.41	0/8533
1	UB	0.21	0/6291	0.45	0/8533
1	V	0.17	0/6291	0.43	0/8533
1	VA	0.14	0/6291	0.43	0/8533
1	VB	0.21	0/6291	0.45	0/8533
1	W	0.17	0/6291	0.44	0/8533
1	WA	0.17	0/6291	0.46	0/8533
1	WB	0.20	0/6291	0.45	0/8533
1	X	0.17	0/6291	0.43	0/8533
1	XA	0.16	0/6291	0.44	0/8533
1	XB	0.19	0/6291	0.46	0/8533
1	Y	0.18	0/6291	0.43	0/8533
1	YA	0.16	0/6291	0.45	0/8533
1	YB	0.18	0/6291	0.45	0/8533
1	Z	0.19	0/6291	0.44	0/8533
1	ZA	0.16	0/6291	0.44	0/8533

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ZB	0.17	0/6291	0.44	0/8533
All	All	0.20	0/490698	0.45	3/665574 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	84	ARG	N-CA-C	-6.73	102.17	110.65
1	H	411	ASP	CA-CB-CG	5.23	117.83	112.60
1	I	83	LEU	N-CA-CB	-5.22	102.05	110.81

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6181	0	6203	231	0
1	AA	6181	0	6203	249	0
1	AB	6181	0	6203	261	0
1	AC	6181	0	6203	261	0
1	B	6181	0	6203	236	0
1	BA	6181	0	6203	270	0
1	BB	6181	0	6203	230	0
1	C	6181	0	6203	247	0
1	CA	6181	0	6203	258	0
1	CB	6181	0	6203	237	0
1	D	6181	0	6203	266	0
1	DA	6181	0	6203	299	0
1	DB	6181	0	6203	203	0
1	E	6181	0	6203	250	0
1	EA	6181	0	6203	241	0
1	EB	6181	0	6203	217	0
1	F	6181	0	6203	238	0
1	FA	6181	0	6203	248	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	FB	6181	0	6203	234	0
1	G	6181	0	6203	236	0
1	GA	6181	0	6203	229	0
1	GB	6181	0	6203	250	0
1	H	6181	0	6203	266	0
1	HA	6181	0	6203	229	0
1	HB	6181	0	6203	220	0
1	I	6181	0	6203	279	0
1	IA	6181	0	6203	242	0
1	IB	6181	0	6203	264	0
1	J	6181	0	6203	259	0
1	JA	6181	0	6203	229	0
1	JB	6181	0	6203	291	0
1	K	6181	0	6203	269	0
1	KA	6181	0	6203	224	0
1	KB	6181	0	6203	262	0
1	L	6181	0	6203	210	0
1	LA	6181	0	6203	253	0
1	LB	6181	0	6203	248	0
1	M	6181	0	6203	222	0
1	MA	6181	0	6203	262	0
1	MB	6181	0	6203	255	0
1	N	6181	0	6203	232	0
1	NA	6181	0	6203	255	0
1	NB	6181	0	6203	259	0
1	O	6181	0	6203	259	0
1	OA	6181	0	6203	317	0
1	OB	6181	0	6203	259	0
1	P	6181	0	6203	236	0
1	PA	6181	0	6203	288	0
1	PB	6181	0	6203	259	0
1	Q	6181	0	6203	228	0
1	QA	6181	0	6203	289	0
1	QB	6181	0	6203	232	0
1	R	6181	0	6203	180	0
1	RA	6181	0	6203	241	0
1	RB	6181	0	6203	262	0
1	S	6181	0	6203	174	0
1	SA	6181	0	6203	182	0
1	SB	6181	0	6203	241	0
1	T	6181	0	6203	176	0
1	TA	6181	0	6203	212	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	TB	6181	0	6203	264	0
1	UA	6181	0	6203	191	0
1	UB	6181	0	6203	276	0
1	V	6181	0	6203	201	0
1	VA	6181	0	6203	220	0
1	VB	6181	0	6203	277	0
1	W	6181	0	6203	256	0
1	WA	6181	0	6203	244	0
1	WB	6181	0	6203	298	0
1	X	6181	0	6203	229	0
1	XA	6181	0	6203	267	0
1	XB	6181	0	6203	303	0
1	Y	6181	0	6203	235	0
1	YA	6181	0	6203	253	0
1	YB	6181	0	6203	326	0
1	Z	6181	0	6203	244	0
1	ZA	6181	0	6203	244	0
1	ZB	6181	0	6203	267	0
All	All	482118	0	483834	17748	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 18.

The worst 5 of 17748 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:QB:18:VAL:HG12	1:QB:43:VAL:HG12	1.29	1.14
1:C:81:VAL:HG13	1:C:83:LEU:HD11	1.33	1.07
1:P:215:LEU:O	1:P:215:LEU:HD12	1.54	1.07
1:UA:470:VAL:HG13	1:UA:481:VAL:HG21	1.35	1.01
1:D:529:ILE:HD12	1:D:583:VAL:HG21	1.39	1.00

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	773/893 (87%)	646 (84%)	126 (16%)	1 (0%)	48	83
1	AA	773/893 (87%)	637 (82%)	135 (18%)	1 (0%)	48	83
1	AB	773/893 (87%)	650 (84%)	123 (16%)	0	100	100
1	AC	773/893 (87%)	647 (84%)	126 (16%)	0	100	100
1	B	773/893 (87%)	659 (85%)	114 (15%)	0	100	100
1	BA	773/893 (87%)	638 (82%)	134 (17%)	1 (0%)	48	83
1	BB	773/893 (87%)	672 (87%)	101 (13%)	0	100	100
1	C	773/893 (87%)	644 (83%)	128 (17%)	1 (0%)	48	83
1	CA	773/893 (87%)	631 (82%)	142 (18%)	0	100	100
1	CB	773/893 (87%)	640 (83%)	132 (17%)	1 (0%)	48	83
1	D	773/893 (87%)	664 (86%)	108 (14%)	1 (0%)	48	83
1	DA	773/893 (87%)	634 (82%)	139 (18%)	0	100	100
1	DB	773/893 (87%)	654 (85%)	119 (15%)	0	100	100
1	E	773/893 (87%)	650 (84%)	123 (16%)	0	100	100
1	EA	773/893 (87%)	642 (83%)	130 (17%)	1 (0%)	48	83
1	EB	773/893 (87%)	649 (84%)	124 (16%)	0	100	100
1	F	773/893 (87%)	659 (85%)	113 (15%)	1 (0%)	48	83
1	FA	773/893 (87%)	629 (81%)	144 (19%)	0	100	100
1	FB	773/893 (87%)	648 (84%)	125 (16%)	0	100	100
1	G	773/893 (87%)	640 (83%)	133 (17%)	0	100	100
1	GA	773/893 (87%)	646 (84%)	127 (16%)	0	100	100
1	GB	773/893 (87%)	640 (83%)	132 (17%)	1 (0%)	48	83
1	H	773/893 (87%)	655 (85%)	118 (15%)	0	100	100
1	HA	773/893 (87%)	642 (83%)	129 (17%)	2 (0%)	36	71
1	HB	773/893 (87%)	655 (85%)	118 (15%)	0	100	100
1	I	773/893 (87%)	657 (85%)	115 (15%)	1 (0%)	48	83
1	IA	773/893 (87%)	648 (84%)	124 (16%)	1 (0%)	48	83
1	IB	773/893 (87%)	649 (84%)	122 (16%)	2 (0%)	36	71
1	J	773/893 (87%)	649 (84%)	124 (16%)	0	100	100
1	JA	773/893 (87%)	641 (83%)	132 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	JB	773/893 (87%)	647 (84%)	125 (16%)	1 (0%)	48	83
1	K	773/893 (87%)	651 (84%)	122 (16%)	0	100	100
1	KA	773/893 (87%)	643 (83%)	130 (17%)	0	100	100
1	KB	773/893 (87%)	666 (86%)	107 (14%)	0	100	100
1	L	773/893 (87%)	652 (84%)	119 (15%)	2 (0%)	36	71
1	LA	773/893 (87%)	655 (85%)	117 (15%)	1 (0%)	48	83
1	LB	773/893 (87%)	658 (85%)	115 (15%)	0	100	100
1	M	773/893 (87%)	655 (85%)	118 (15%)	0	100	100
1	MA	773/893 (87%)	638 (82%)	135 (18%)	0	100	100
1	MB	773/893 (87%)	656 (85%)	117 (15%)	0	100	100
1	N	773/893 (87%)	657 (85%)	116 (15%)	0	100	100
1	NA	773/893 (87%)	646 (84%)	127 (16%)	0	100	100
1	NB	773/893 (87%)	653 (84%)	119 (15%)	1 (0%)	48	83
1	O	773/893 (87%)	652 (84%)	121 (16%)	0	100	100
1	OA	773/893 (87%)	661 (86%)	112 (14%)	0	100	100
1	OB	773/893 (87%)	655 (85%)	118 (15%)	0	100	100
1	P	773/893 (87%)	668 (86%)	105 (14%)	0	100	100
1	PA	773/893 (87%)	646 (84%)	127 (16%)	0	100	100
1	PB	773/893 (87%)	654 (85%)	119 (15%)	0	100	100
1	Q	773/893 (87%)	654 (85%)	118 (15%)	1 (0%)	48	83
1	QA	773/893 (87%)	640 (83%)	133 (17%)	0	100	100
1	QB	773/893 (87%)	664 (86%)	107 (14%)	2 (0%)	36	71
1	R	773/893 (87%)	654 (85%)	118 (15%)	1 (0%)	48	83
1	RA	773/893 (87%)	655 (85%)	118 (15%)	0	100	100
1	RB	773/893 (87%)	671 (87%)	100 (13%)	2 (0%)	36	71
1	S	773/893 (87%)	677 (88%)	96 (12%)	0	100	100
1	SA	773/893 (87%)	681 (88%)	90 (12%)	2 (0%)	36	71
1	SB	773/893 (87%)	643 (83%)	128 (17%)	2 (0%)	36	71
1	T	773/893 (87%)	665 (86%)	107 (14%)	1 (0%)	48	83
1	TA	773/893 (87%)	679 (88%)	93 (12%)	1 (0%)	48	83
1	TB	773/893 (87%)	654 (85%)	119 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	UA	773/893 (87%)	662 (86%)	108 (14%)	3 (0%)	30	67
1	UB	773/893 (87%)	665 (86%)	108 (14%)	0	100	100
1	V	773/893 (87%)	665 (86%)	108 (14%)	0	100	100
1	VA	773/893 (87%)	652 (84%)	120 (16%)	1 (0%)	48	83
1	VB	773/893 (87%)	654 (85%)	117 (15%)	2 (0%)	36	71
1	W	773/893 (87%)	647 (84%)	126 (16%)	0	100	100
1	WA	773/893 (87%)	662 (86%)	109 (14%)	2 (0%)	36	71
1	WB	773/893 (87%)	666 (86%)	106 (14%)	1 (0%)	48	83
1	X	773/893 (87%)	656 (85%)	116 (15%)	1 (0%)	48	83
1	XA	773/893 (87%)	669 (86%)	104 (14%)	0	100	100
1	XB	773/893 (87%)	643 (83%)	130 (17%)	0	100	100
1	Y	773/893 (87%)	650 (84%)	123 (16%)	0	100	100
1	YA	773/893 (87%)	654 (85%)	118 (15%)	1 (0%)	48	83
1	YB	773/893 (87%)	666 (86%)	104 (14%)	3 (0%)	30	67
1	Z	773/893 (87%)	645 (83%)	128 (17%)	0	100	100
1	ZA	773/893 (87%)	668 (86%)	105 (14%)	0	100	100
1	ZB	773/893 (87%)	660 (85%)	113 (15%)	0	100	100
All	All	60294/69654 (87%)	50949 (84%)	9299 (15%)	46 (0%)	49	83

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	6	PHE
1	CB	8	ILE
1	EA	452	ARG
1	GB	161	GLU
1	HA	452	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	666/755 (88%)	666 (100%)	0	100	100
1	AA	666/755 (88%)	666 (100%)	0	100	100
1	AB	666/755 (88%)	666 (100%)	0	100	100
1	AC	666/755 (88%)	666 (100%)	0	100	100
1	B	666/755 (88%)	666 (100%)	0	100	100
1	BA	666/755 (88%)	666 (100%)	0	100	100
1	BB	666/755 (88%)	666 (100%)	0	100	100
1	C	666/755 (88%)	666 (100%)	0	100	100
1	CA	666/755 (88%)	666 (100%)	0	100	100
1	CB	666/755 (88%)	666 (100%)	0	100	100
1	D	666/755 (88%)	666 (100%)	0	100	100
1	DA	666/755 (88%)	666 (100%)	0	100	100
1	DB	666/755 (88%)	666 (100%)	0	100	100
1	E	666/755 (88%)	666 (100%)	0	100	100
1	EA	666/755 (88%)	666 (100%)	0	100	100
1	EB	666/755 (88%)	666 (100%)	0	100	100
1	F	666/755 (88%)	666 (100%)	0	100	100
1	FA	666/755 (88%)	666 (100%)	0	100	100
1	FB	666/755 (88%)	666 (100%)	0	100	100
1	G	666/755 (88%)	666 (100%)	0	100	100
1	GA	666/755 (88%)	666 (100%)	0	100	100
1	GB	666/755 (88%)	666 (100%)	0	100	100
1	H	666/755 (88%)	665 (100%)	1 (0%)	87	85
1	HA	666/755 (88%)	666 (100%)	0	100	100
1	HB	666/755 (88%)	666 (100%)	0	100	100
1	I	666/755 (88%)	665 (100%)	1 (0%)	87	85
1	IA	666/755 (88%)	666 (100%)	0	100	100
1	IB	666/755 (88%)	666 (100%)	0	100	100
1	J	666/755 (88%)	666 (100%)	0	100	100
1	JA	666/755 (88%)	666 (100%)	0	100	100
1	JB	666/755 (88%)	666 (100%)	0	100	100
1	K	666/755 (88%)	666 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	KA	666/755 (88%)	666 (100%)	0	100	100
1	KB	666/755 (88%)	666 (100%)	0	100	100
1	L	666/755 (88%)	666 (100%)	0	100	100
1	LA	666/755 (88%)	666 (100%)	0	100	100
1	LB	666/755 (88%)	666 (100%)	0	100	100
1	M	666/755 (88%)	666 (100%)	0	100	100
1	MA	666/755 (88%)	666 (100%)	0	100	100
1	MB	666/755 (88%)	666 (100%)	0	100	100
1	N	666/755 (88%)	666 (100%)	0	100	100
1	NA	666/755 (88%)	666 (100%)	0	100	100
1	NB	666/755 (88%)	666 (100%)	0	100	100
1	O	666/755 (88%)	666 (100%)	0	100	100
1	OA	666/755 (88%)	666 (100%)	0	100	100
1	OB	666/755 (88%)	666 (100%)	0	100	100
1	P	666/755 (88%)	666 (100%)	0	100	100
1	PA	666/755 (88%)	666 (100%)	0	100	100
1	PB	666/755 (88%)	666 (100%)	0	100	100
1	Q	666/755 (88%)	665 (100%)	1 (0%)	87	85
1	QA	666/755 (88%)	666 (100%)	0	100	100
1	QB	666/755 (88%)	666 (100%)	0	100	100
1	R	666/755 (88%)	666 (100%)	0	100	100
1	RA	666/755 (88%)	666 (100%)	0	100	100
1	RB	666/755 (88%)	666 (100%)	0	100	100
1	S	666/755 (88%)	666 (100%)	0	100	100
1	SA	666/755 (88%)	666 (100%)	0	100	100
1	SB	666/755 (88%)	666 (100%)	0	100	100
1	T	666/755 (88%)	666 (100%)	0	100	100
1	TA	666/755 (88%)	666 (100%)	0	100	100
1	TB	666/755 (88%)	666 (100%)	0	100	100
1	UA	666/755 (88%)	666 (100%)	0	100	100
1	UB	666/755 (88%)	666 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	V	666/755 (88%)	666 (100%)	0	100	100
1	VA	666/755 (88%)	666 (100%)	0	100	100
1	VB	666/755 (88%)	666 (100%)	0	100	100
1	W	666/755 (88%)	666 (100%)	0	100	100
1	WA	666/755 (88%)	665 (100%)	1 (0%)	87	85
1	WB	666/755 (88%)	666 (100%)	0	100	100
1	X	666/755 (88%)	666 (100%)	0	100	100
1	XA	666/755 (88%)	666 (100%)	0	100	100
1	XB	666/755 (88%)	666 (100%)	0	100	100
1	Y	666/755 (88%)	666 (100%)	0	100	100
1	YA	666/755 (88%)	666 (100%)	0	100	100
1	YB	666/755 (88%)	666 (100%)	0	100	100
1	Z	666/755 (88%)	666 (100%)	0	100	100
1	ZA	666/755 (88%)	666 (100%)	0	100	100
1	ZB	666/755 (88%)	666 (100%)	0	100	100
All	All	51948/58890 (88%)	51944 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	412	GLU
1	I	83	LEU
1	Q	457	VAL
1	WA	96	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 422 such sidechains are listed below:

Mol	Chain	Res	Type
1	NA	550	ASN
1	R	63	ASN
1	YB	17	HIS
1	O	295	GLN
1	P	294	ASN

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.

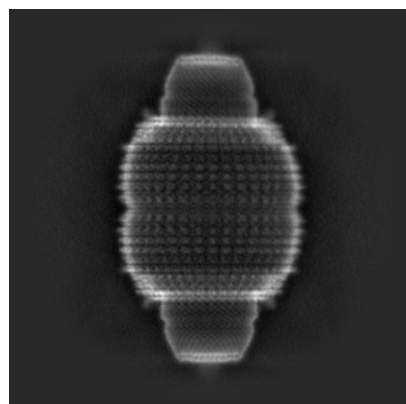
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53423. These allow visual inspection of the internal detail of the map and identification of artifacts.

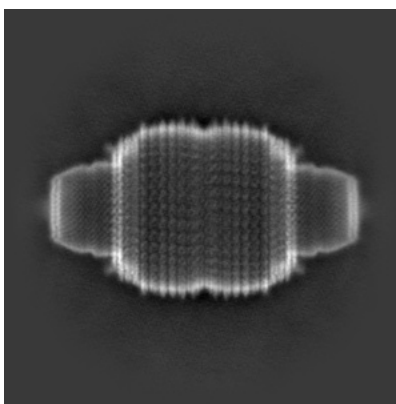
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

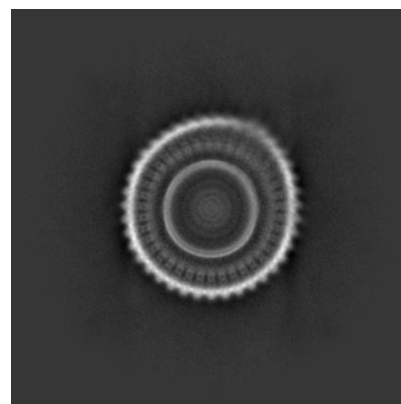
6.1.1 Primary map



X

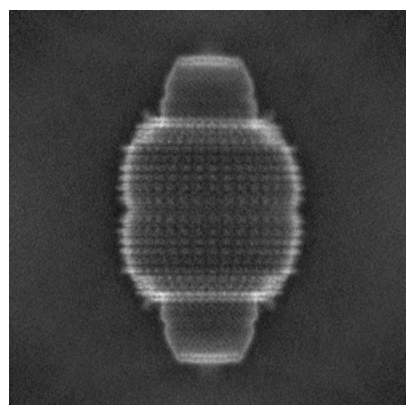


Y

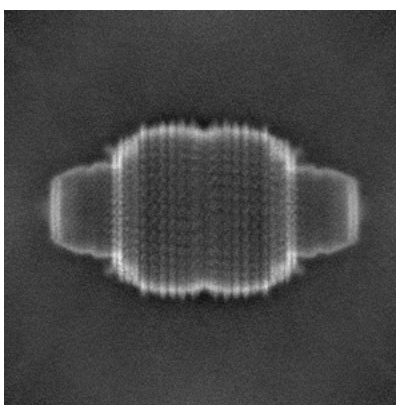


Z

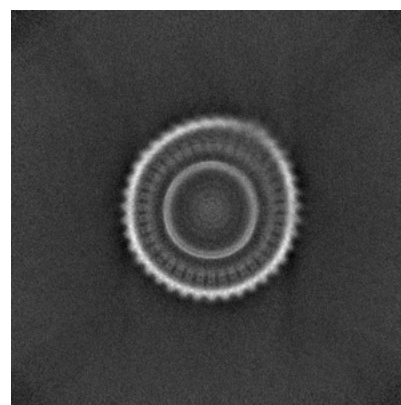
6.1.2 Raw map



X



Y

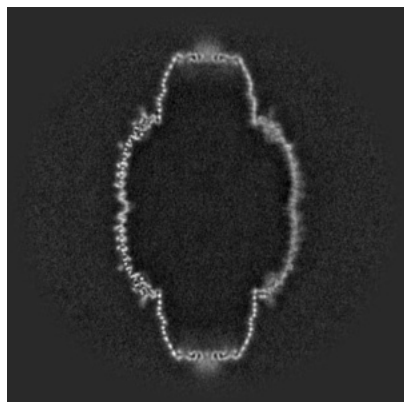


Z

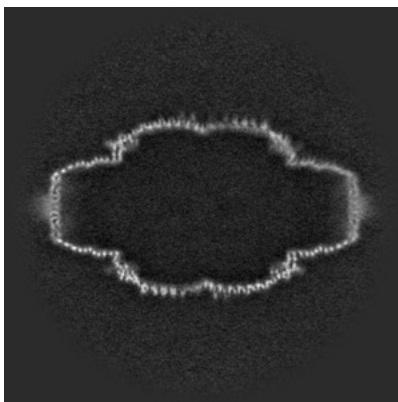
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

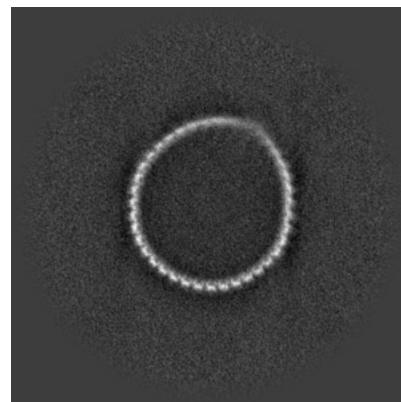
6.2.1 Primary map



X Index: 512

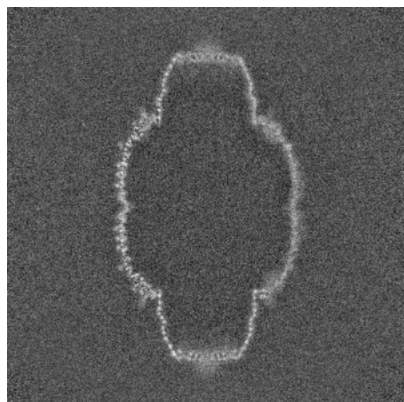


Y Index: 512

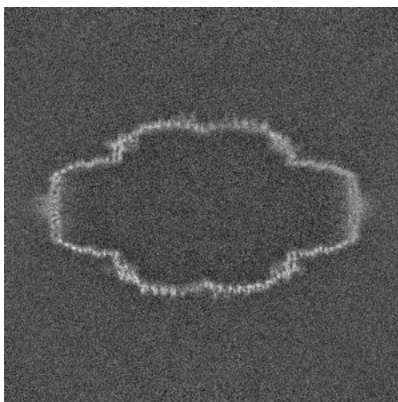


Z Index: 512

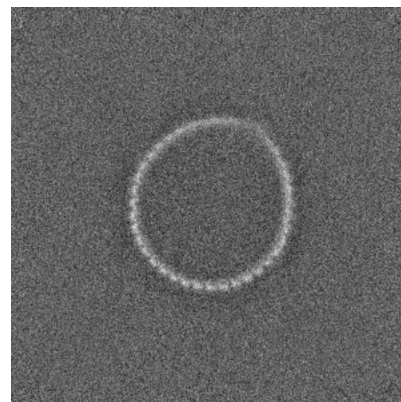
6.2.2 Raw map



X Index: 512



Y Index: 512

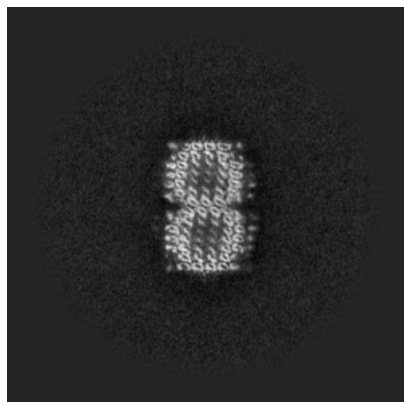


Z Index: 512

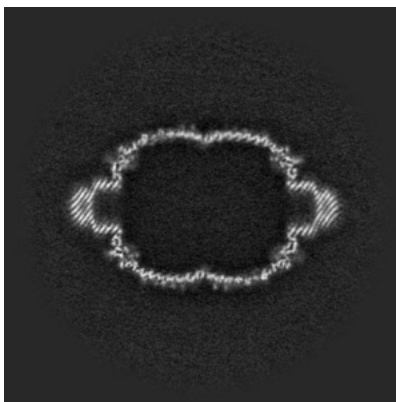
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

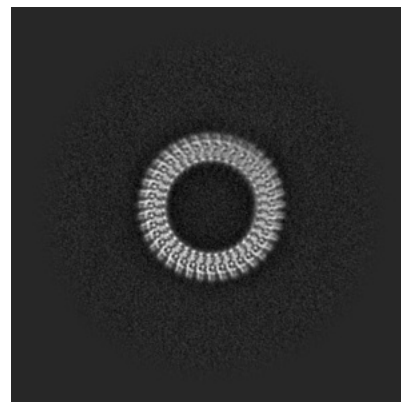
6.3.1 Primary map



X Index: 310

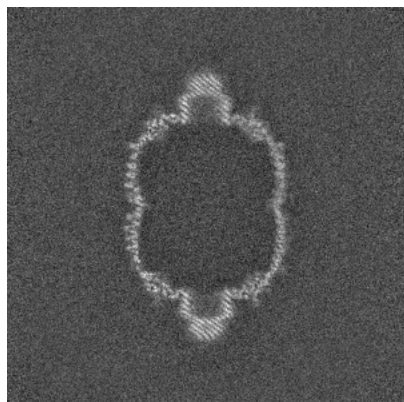


Y Index: 404

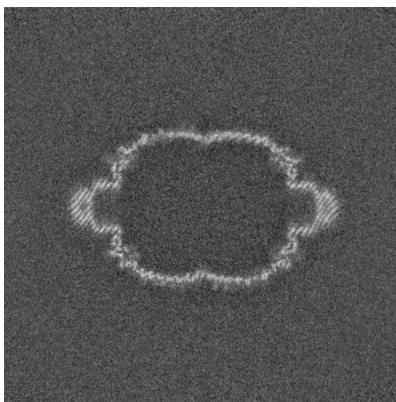


Z Index: 296

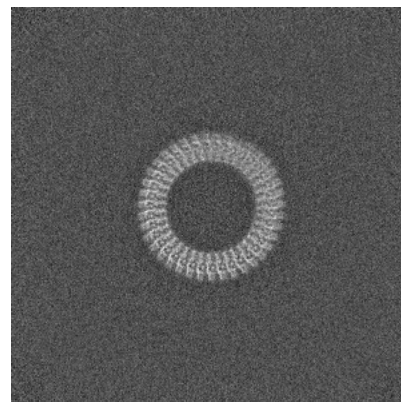
6.3.2 Raw map



X Index: 404



Y Index: 404

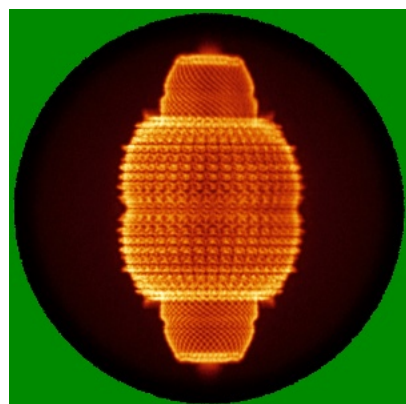


Z Index: 297

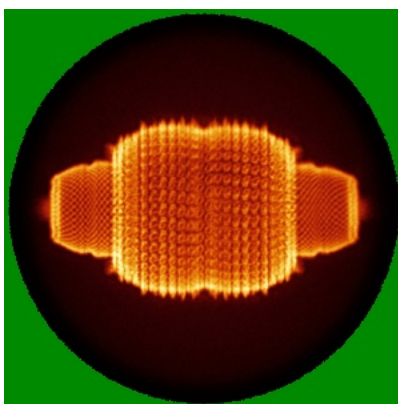
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

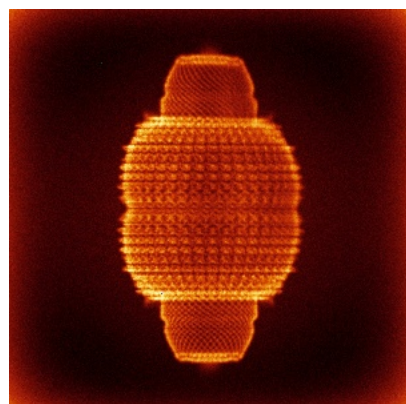


Y

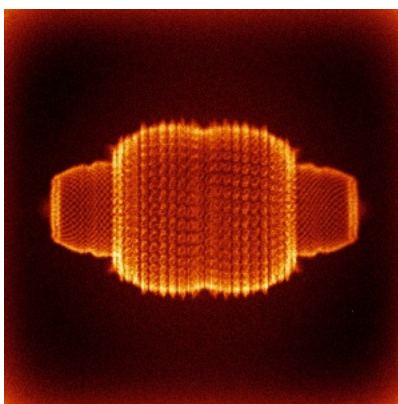


Z

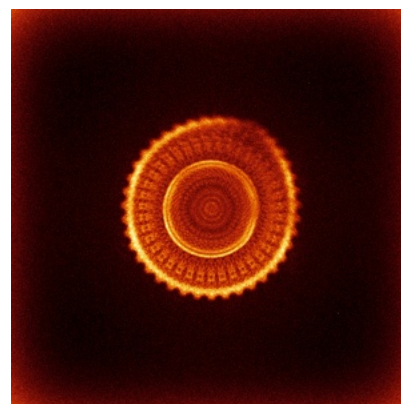
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

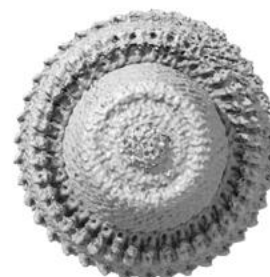
6.5.1 Primary map



X



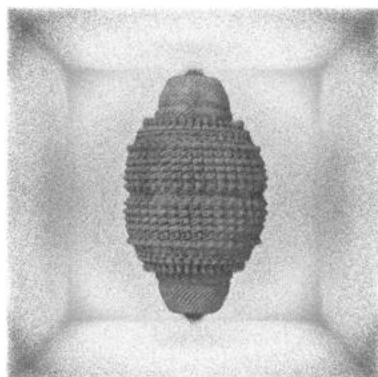
Y



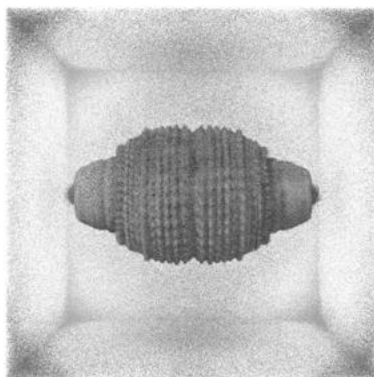
Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

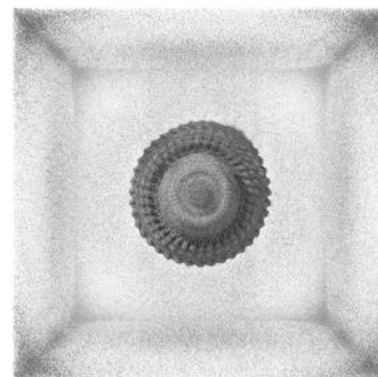
6.5.2 Raw map



X



Y



Z

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

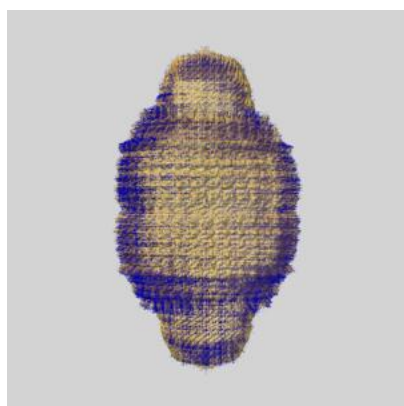
6.6 Mask visualisation [i](#)

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

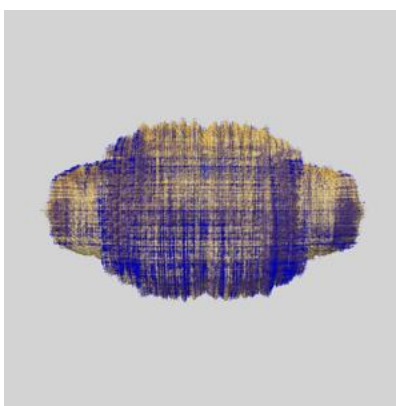
A mask typically either:

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

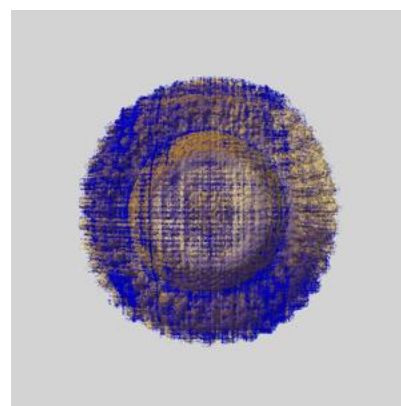
6.6.1 emd_53423_msk_1.map [i](#)



X



Y

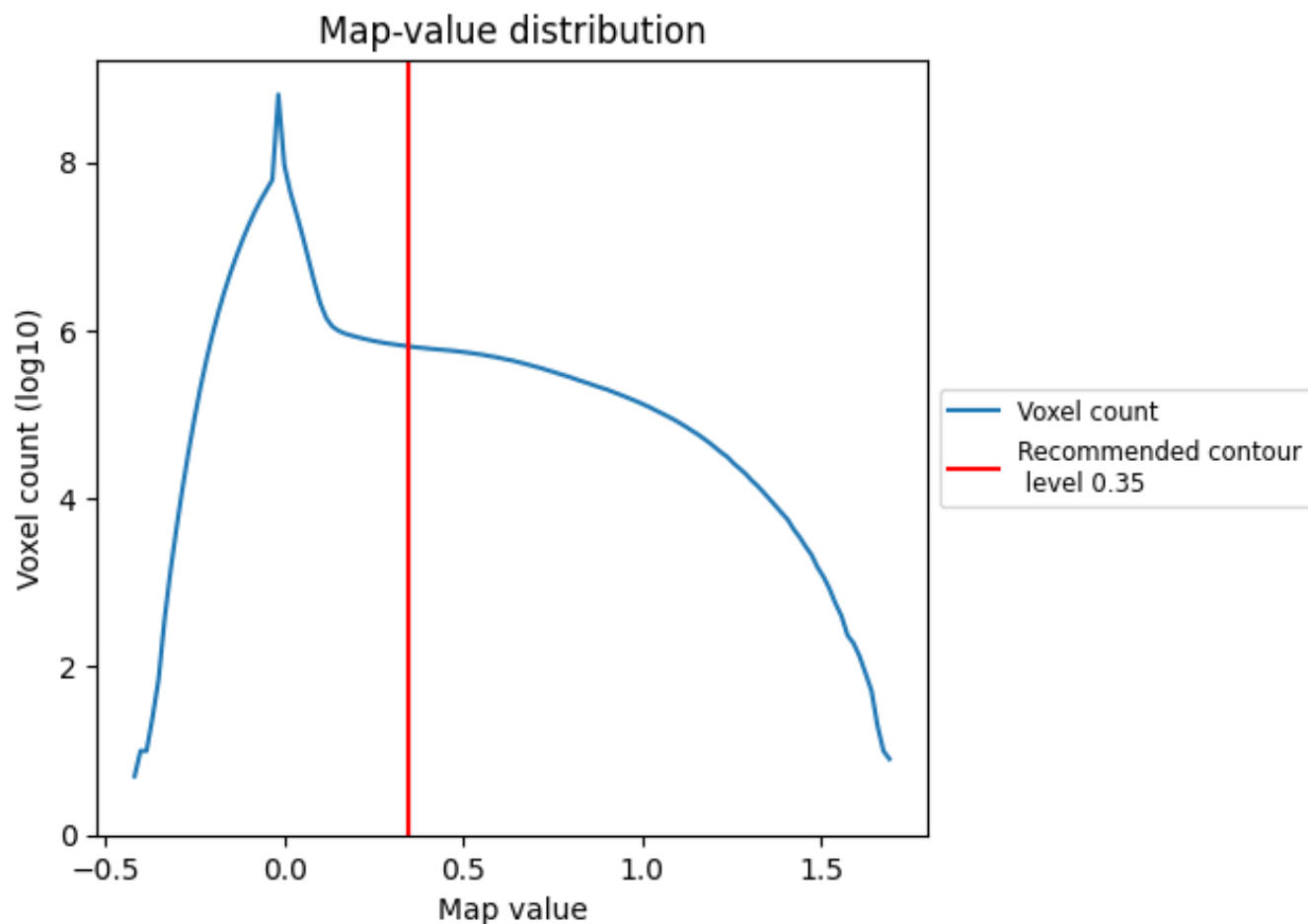


Z

7 Map analysis [i](#)

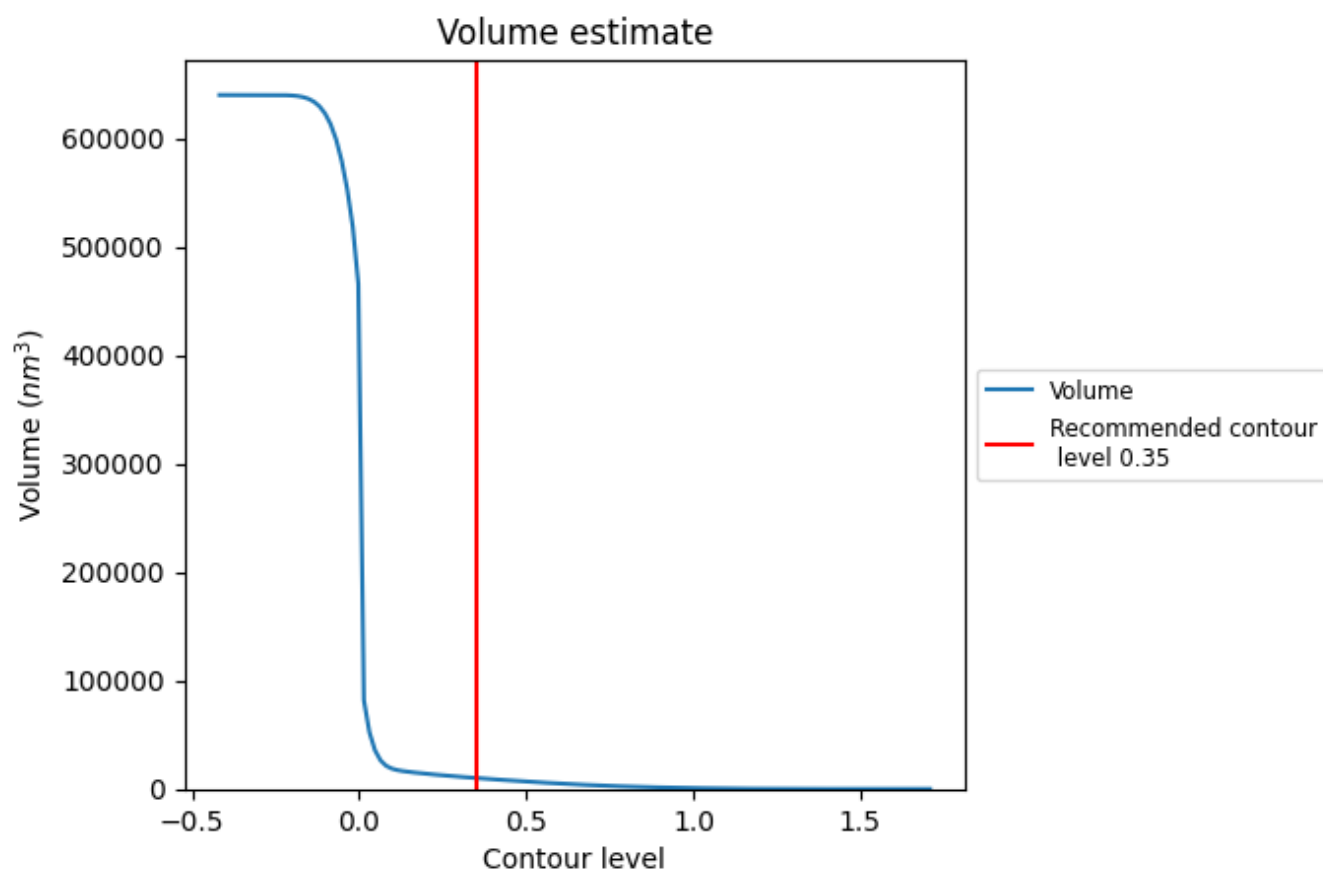
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

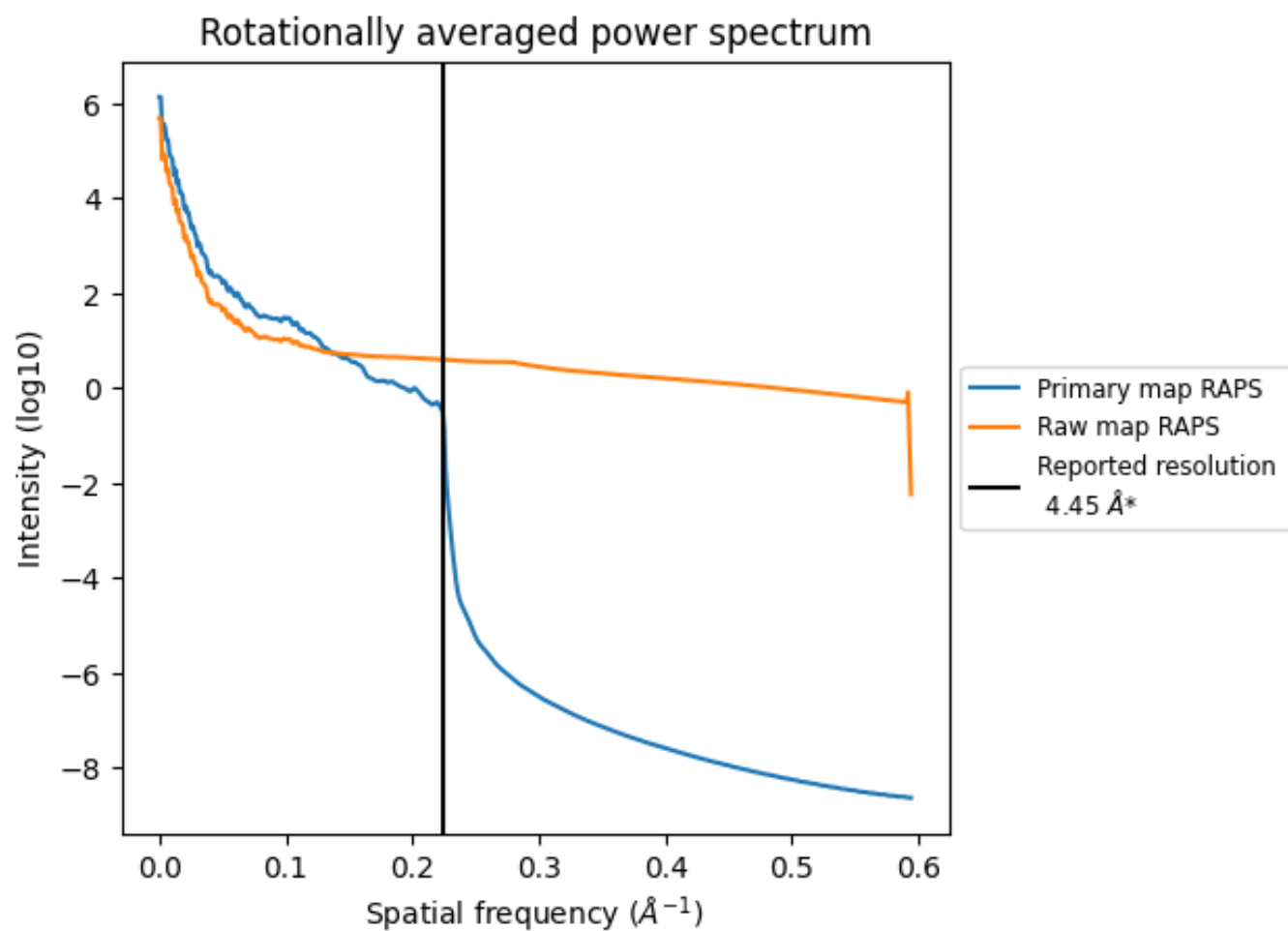
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10088 nm^3 ; this corresponds to an approximate mass of 9113 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 ⓘ

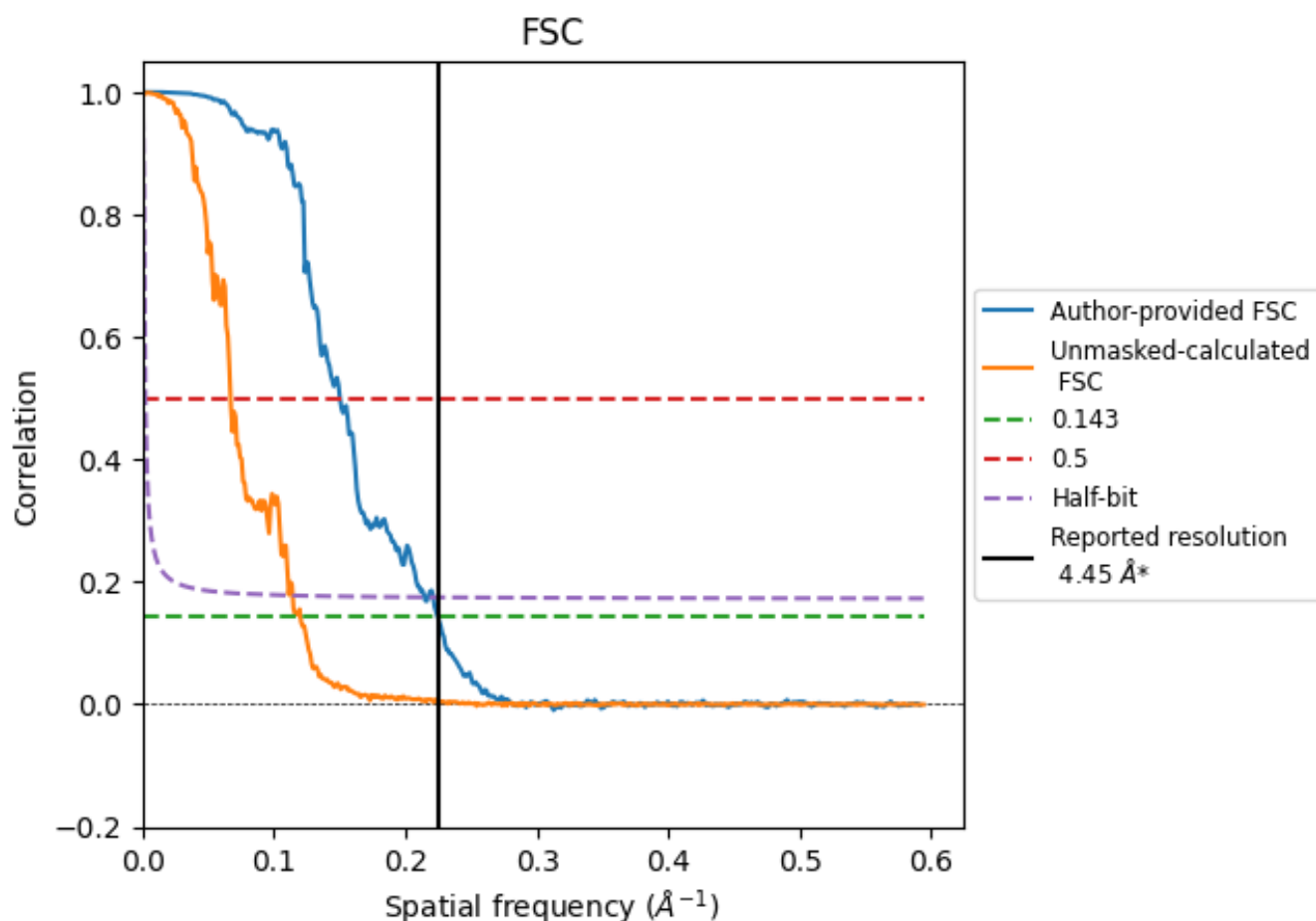


*Reported resolution corresponds to spatial frequency of 0.225 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.225 Å⁻¹

8.2 Resolution estimates [i](#)

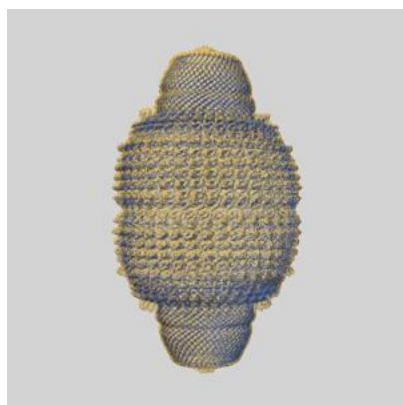
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.45	-	-
Author-provided FSC curve	4.45	6.66	4.66
Unmasked-calculated*	8.32	14.90	8.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.32 differs from the reported value 4.45 by more than 10 %

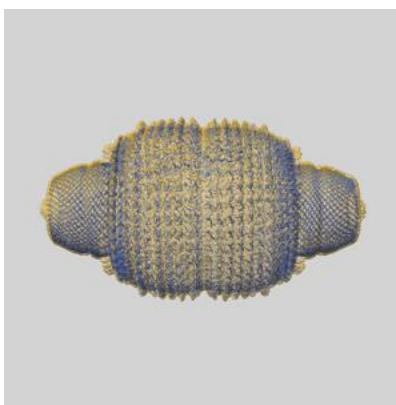
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53423 and PDB model 9QWQ. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

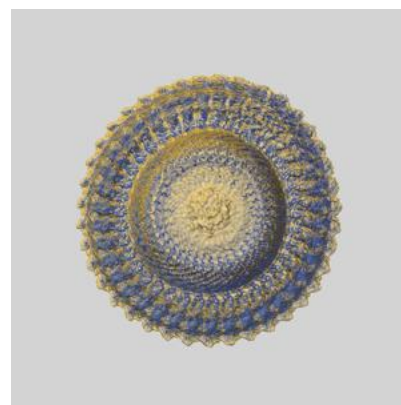
9.1 Map-model overlay [i](#)



X



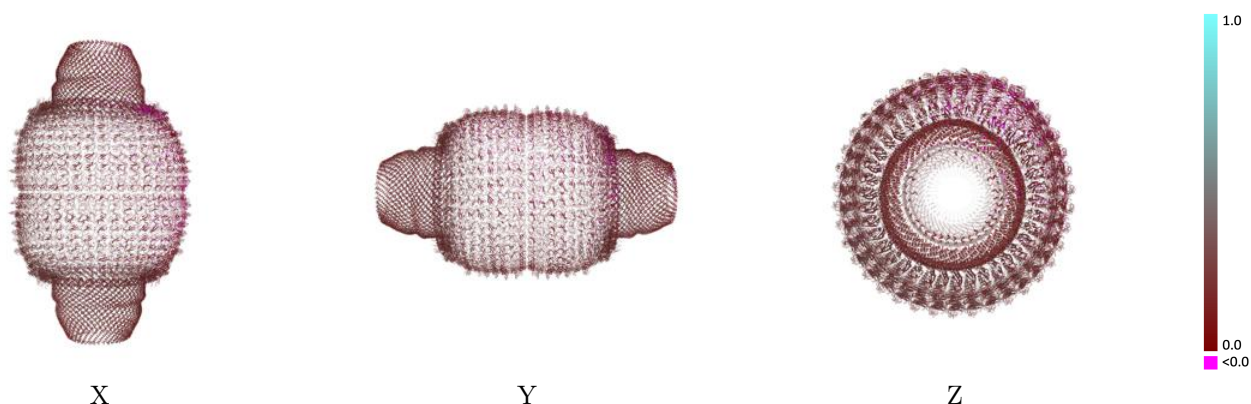
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.35 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](#)



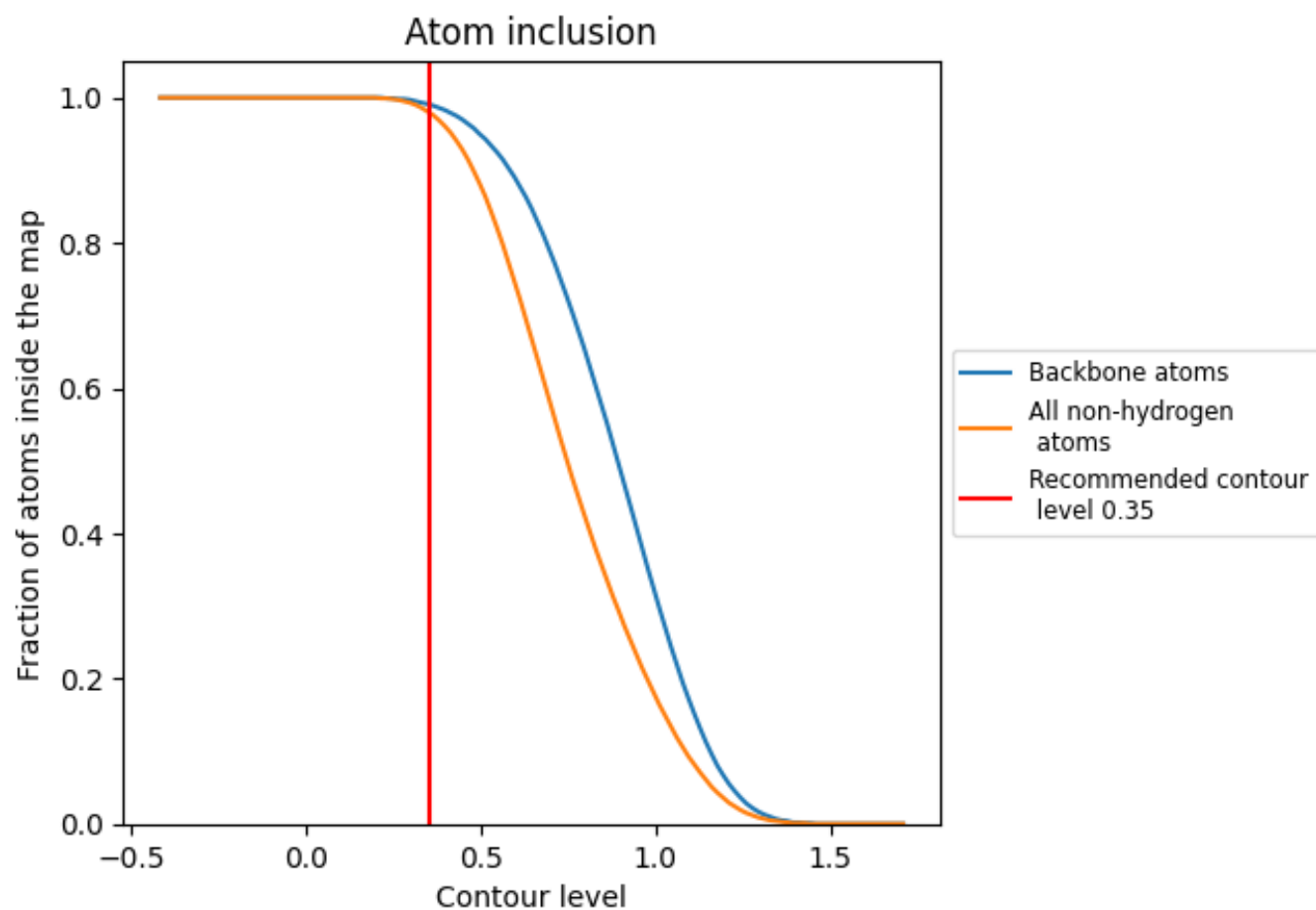
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9800	 0.2230
A	 0.9920	 0.2640
AA	 0.9800	 0.2250
AB	 0.9940	 0.1880
AC	 0.9780	 0.1870
B	 0.9930	 0.2640
BA	 0.9760	 0.2270
BB	 0.9940	 0.2040
C	 0.9920	 0.2630
CA	 0.9820	 0.2260
CB	 0.9950	 0.2160
D	 0.9940	 0.2620
DA	 0.9910	 0.2320
DB	 0.9940	 0.2230
E	 0.9950	 0.2540
EA	 0.9940	 0.2430
EB	 0.9960	 0.2340
F	 0.9890	 0.2530
FA	 0.9940	 0.2480
FB	 0.9940	 0.2360
G	 0.9910	 0.2520
GA	 0.9910	 0.2540
GB	 0.9920	 0.2410
H	 0.9910	 0.2430
HA	 0.9920	 0.2590
HB	 0.9890	 0.2440
I	 0.9930	 0.2380
IA	 0.9920	 0.2610
IB	 0.9920	 0.2460
J	 0.9950	 0.2370
JA	 0.9880	 0.2620
JB	 0.9930	 0.2500
K	 0.9920	 0.2360
KA	 0.9910	 0.2660
KB	 0.9940	 0.2560







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Chain	Atom inclusion	Q-score
L	 0.9910	 0.2340
LA	 0.9890	 0.2630
LB	 0.9930	 0.2550
M	 0.9920	 0.2250
MA	 0.9910	 0.2640
MB	 0.9910	 0.2580
N	 0.9930	 0.2230
NA	 0.9900	 0.2650
NB	 0.9910	 0.2580
O	 0.9920	 0.2170
OA	 0.9830	 0.1810
OB	 0.9910	 0.2580
P	 0.9910	 0.2040
PA	 0.9860	 0.1750
PB	 0.9890	 0.2560
Q	 0.9880	 0.2020
QA	 0.9780	 0.1640
QB	 0.9870	 0.2560
R	 0.9610	 0.1900
RA	 0.9710	 0.1640
RB	 0.9890	 0.2510
S	 0.8700	 0.1770
SA	 0.9420	 0.1590
SB	 0.9890	 0.2500
T	 0.9570	 0.1780
TA	 0.8820	 0.1460
TB	 0.9930	 0.2500
UA	 0.7690	 0.1330
UB	 0.9910	 0.2430
V	 0.9820	 0.1810
VA	 0.8320	 0.1360
VB	 0.9900	 0.2370
W	 0.9910	 0.1900
WA	 0.9540	 0.1530
WB	 0.9940	 0.2270
X	 0.9940	 0.2080
XA	 0.9770	 0.1600
XB	 0.9940	 0.2160
Y	 0.9930	 0.2190
YA	 0.9860	 0.1680
YB	 0.9960	 0.2000
Z	 0.9890	 0.2210

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Chain	Atom inclusion	Q-score
ZA	 0.9930	 0.1880
ZB	 0.9880	 0.1970