



wwPDB EM Validation Summary Report ⓘ

Apr 30, 2026 – 10:12 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

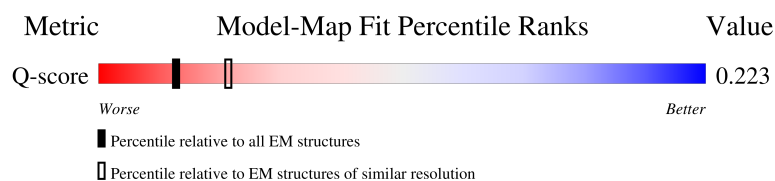
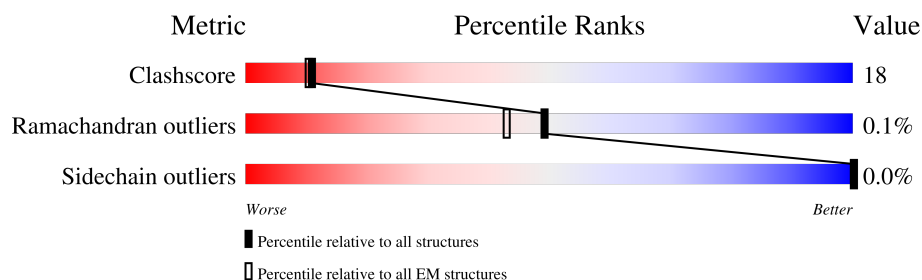
1 Overall quality at a glance

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	



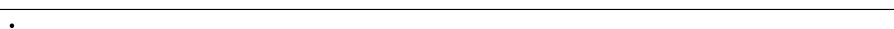
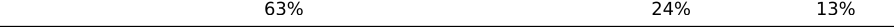


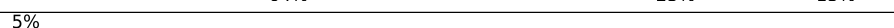



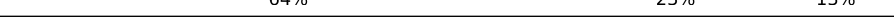



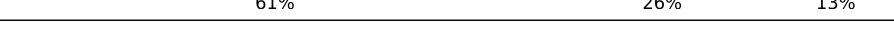


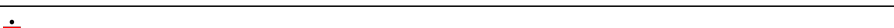






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Mol	Chain	Length	Quality of chain
1	JA	893	
1	JB	893	
1	K	893	
1	KA	893	
1	KB	893	
1	L	893	
1	LA	893	
1	LB	893	
1	M	893	
1	MA	893	
1	MB	893	
1	N	893	
1	NA	893	
1	NB	893	
1	O	893	
1	OA	893	
1	OB	893	
1	P	893	
1	PA	893	
1	PB	893	
1	Q	893	
1	QA	893	
1	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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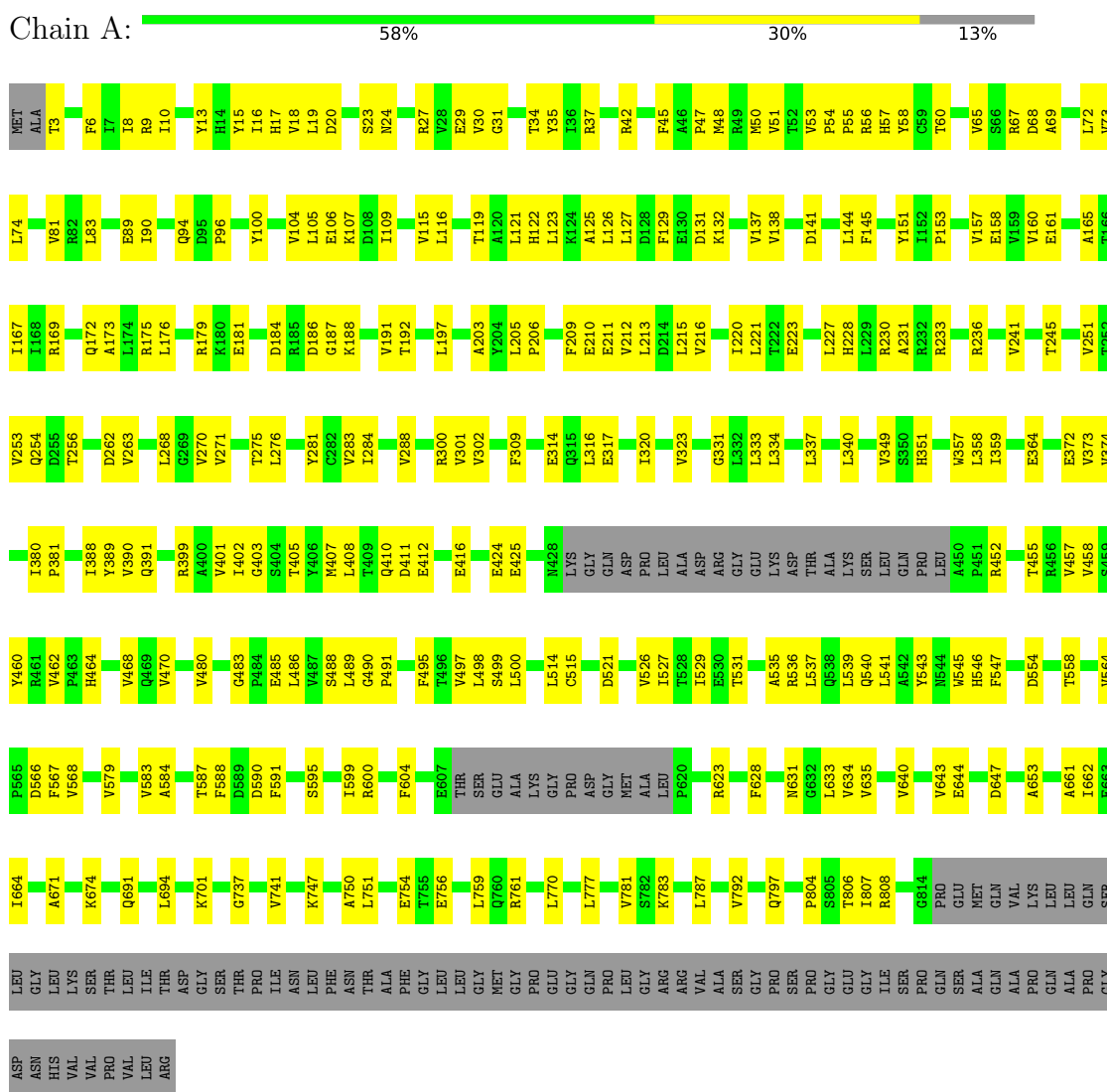
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	TA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	TB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	UA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	UB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	V	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	VA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	VB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	W	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	WA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	WB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	X	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	XA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	XB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	Y	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	YA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	YB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	Z	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	ZA	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		
1	ZB	779	Total	C	N	O	S	0	0
			6181	3890	1105	1176	10		

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



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	H545	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	P645	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	Y771	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

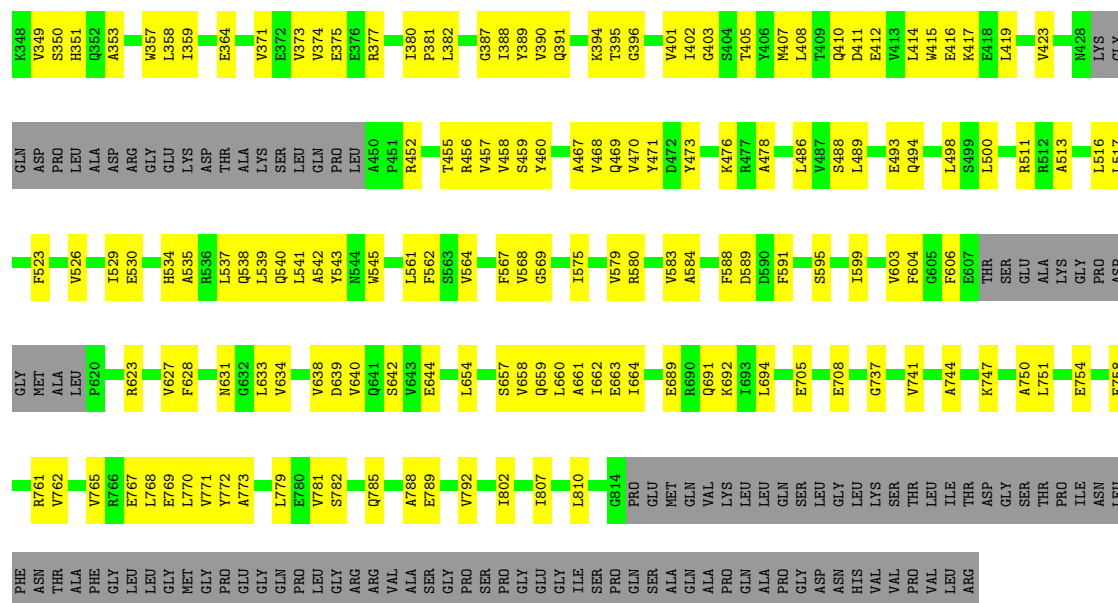
Chain BB:  58% 30% 13%

PRO	GLN	LEU	ALA	PRO	GLY	ASN	HIS	VAL	VAL	PRO	PRO	VAL	LEU	LEU	ARG	LYS	LEU	L680	R679	W545	SER	MET	G361	V267	Q170	L83	MET	ALA	T3																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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- Molecule 1: Major vault protein

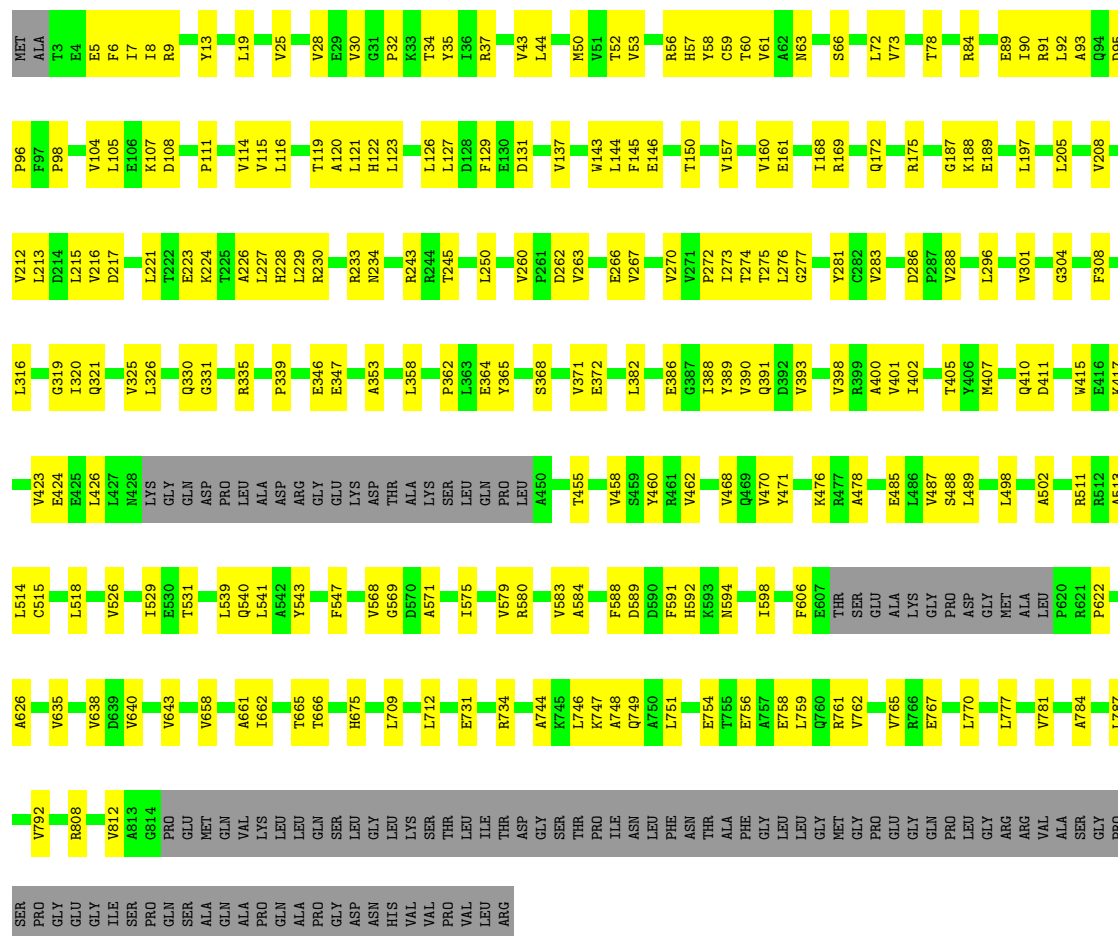
Chain D:  56% 31% 13%

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	F1018	F1019	F1020	F1021	F1022	F1023	F1024	F1025	F1026	F1027	F1028	F1029	F1030	F1031	F1032	F1033	F1034	F1035	F1036	F1037	F1038	F1039	F1040	F1041	F1042	F1043	F1044	F1045	F1046	F1047	F1048	F1049	F1050	F1051	F1052	F1053	F1054	F1055	F1056	F1057	F1058	F1059	F1060	F1061	F1062	F1063	F1064	F1065	F1066	F1067	F1068	F1069	F1070	F1071	F1072	F1073	F1074	F1075	F1076	F1077	F1078	F1079	F1080	F1081	F1082	F1083	F1084	F1085	F1086	F1087	F1088	F1089	F1090	F1091	F1092	F1093	F1094	F1095	F1096	F1097	F1098	F1099	F1100	F1101	F1102	F1103	F1104	F1105	F1106	F1107	F1108	F1109	F1110	F1111	F1112	F1113	F1114	F1115	F1116	F1117	F1118	F1119	F1120	F1121	F1122	F1123	F1124	F1125	F1126	F1127	F1128	F1129	F1130	F1131	F1132	F1133	F1134	F1135	F1136	F1137	F1138	F1139	F1140	F1141	F1142	F1143	F1144	F1145	F1146	F1147	F1148	F1149	F1150	F1151	F1152	F1153	F1154	F1155	F1156	F1157	F1158	F1159	F1160	F1161	F1162	F1163	F1164	F1165	F1166	F1167	F1168	F1169	F1170	F1171	F1172	F1173	F1174	F1175	F1176	F1177	F1178	F1179	F1180	F1181	F1182	F1183	F1184	F1185	F1186	F1187	F1188	F1189	F1190	F1191	F1192	F1193	F1194	F1195	F1196	F1197	F1198	F1199	F1200	F1201	F1202	F1203	F1204	F1205	F1206	F1207	F1208	F1209	F1210	F1211	F1212	F1213	F1214	F1215	F1216	F1217	F1218	F1219	F1220	F1221	F1222	F1223	F1224	F1225	F1226	F1227	F1228	F1229	F1230	F1231	F1232	F1233	F1234	F1235	F1236	F1237	F1238	F1239	F1240	F1241	F1242	F1243	F1244	F1245	F1246	F1247	F1248	F1249	F1250	F1251	F1252	F1253	F1254	F1255	F1256	F1257	F1258	F1259	F1260	F1261	F1262	F1263	F1264	F1265	F1266	F1267	F1268	F1269	F1270	F1271	F1272	F1273	F1274	F1275	F1276	F1277	F1278	F1279	F1280	F1281	F1282	F1283	F1284	F1285	F1286	F1287	F1288	F1289	F1290	F1291	F1292	F1293	F1294	F1295	F1296	F1297	F1298	F1299	F1300	F1301	F1302	F1303	F1304	F1305	F1306	F1307	F1308	F1309	F1310	F1311	F1312	F1313	F1314	F1315	F1316	F1317	F1318	F1319	F1320	F1321	F1322	F1323	F1324	F1325	F1326	F1327	F1328	F1329	F1330	F1331	F1332	F1333	F1334	F1335	F1336	F1337	F1338	F1339	F1340	F1341	F1342	F1343	F1344	F1345	F1346	F1347	F1348	F1349	F1350	F1351	F1352	F1353	F1354	F1355	F1356	F1357	F1358	F1359	F1360	F1361	F1362	F1363	F1364	F1365	F1366	F1367	F1368	F1369	F1370	F1371	F1372	F1373	F1374	F1375	F1376	F1377	F1378	F1379	F1380	F1381	F1382	F1383	F1384	F1385	F1386	F1387	F1388	F1389	F1390	F1391	F1392	F1393	F1394	F1395	F1396	F1397	F1398	F1399	F1400	F1401	F1402	F1403	F1404	F1405	F1406	F1407	F1408	F1409	F1410	F1411	F1412	F1413	F1414	F1415	F1416	F1417	F1418	F1419	F1420	F1421	F1422	F1423	F1424	F1425	F1426	F1427	F1428	F1429	F1430	F1431	F1432	F1433	F1434	F1435	F1436	F1437	F1438	F1439	F1440	F1441	F1442	F1443	F1444	F1445	F1446	F1447	F1448	F1449	F1450	F1451	F1452	F1453	F1454	F1455	F1456	F1457	F1458	F1459	F1460	F1461	F1462	F1463	F1464	F1465	F1466	F1467	F1468	F1469	F1470	F1471	F1472
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• Molecule 1: Major vault protein

Chain DB: 61% 26% 13%



• Molecule 1: Major vault protein

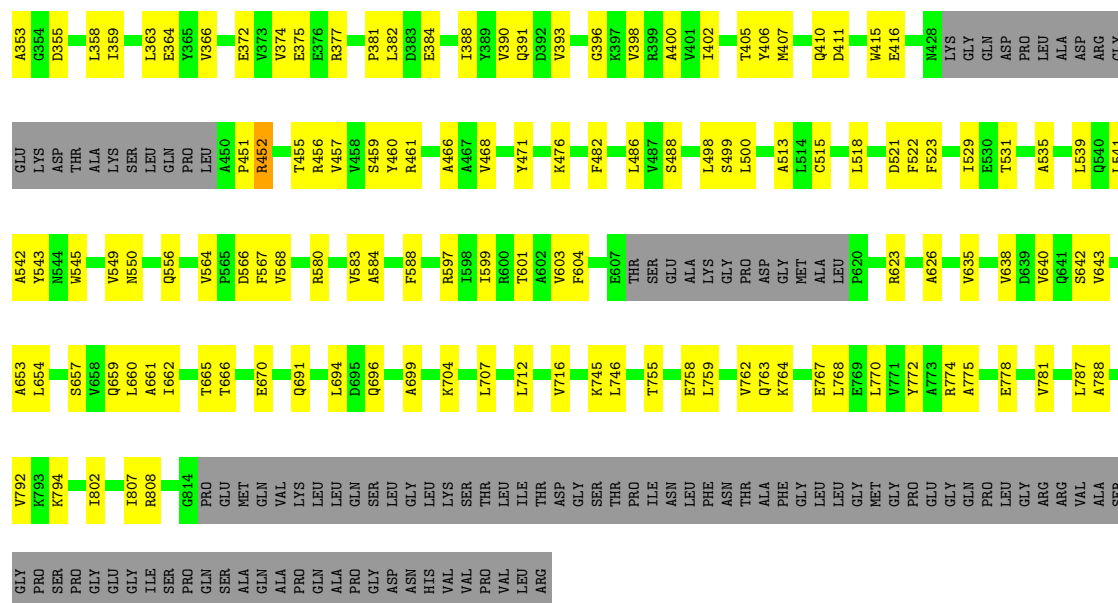
Chain E:  56% 31% 13%

ILE	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	MET	PRO	GLY	GLY	PRO	GLY	ARG	VAL	ALA	SER	GLY	GLY	ILE	SER	PRO	GLN	ALA	ALA	ALA	GLY	ASP	ASN	HIS	VAL	VAL	PRO	VAL			
A661	I662	T666	E727	S728	A732	I735	A750	V762	Q763	L768	E769	Y772	A775	Q776	L777	E778	L779	E780	V781	S782	Q786	L787	A788	E789	V792	Q797	M798	L799	G814	PRO	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL						
I575	V583	A584	F588	F591	H592	S595	I599	V603	F604	E607	THR	SER	GLY	ALA	LYS	GLY	PRO	ASP	GLY	MET	GLY	ALA	R623	A626	V627	V628	L633	V634	V635	V638	D639	V640	V643	E644	P645	V646	R651	L654	Q655	R656	S657	V658	Q659	A571	C572	K573	A574	
LEU	GLN	PRO	LEU	A450	K454	T455	R456	V457	V462	P463	A466	A467	V468	Y471	R477	E485	L408	T409	Q410	D411	V497	L498	C515	V526	L529	E530	R536	Q538	L539	Y543	H546	F547	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLY	LYS	ASP	THR	ALA	LYS	SER	
E372	V373	V374	I380	P381	I388	Y389	V390	Q391	D392	V393	G396	K397	V398	V401	T405	Y406	W407	L408	T409	Q410	D411	V497	L498	C515	V526	L529	E530	R536	Q538	L539	Y543	H546	F547	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLY	LYS	ASP	THR	ALA	LYS	SER
L276	H279	E280	Y281	C282	V283	L284	L285	P287	V302	E305	L310	Q315	L316	E317	Q318	G319	V320	V323	V324	V325	L326	Q330	Q331	L332	L333	L334	R335	A336	L337	E342	D345	E346	F347	R348	V349	S350	H351	Q352	A353	H356	E357	W358	L358	I359	P362	L363	E364	
Q172	A173	L174	R175	L176	R177	A178	R179	W196	L197	V198	T199	T200	L205	P206	V208	F209	E210	E211	V212	L213	D214	L215	V216	L220	L221	T222	E223	L227	H228	L229	R230	R236	V241	L250	V260	P261	D262	V263	H264	E265	E266	V267	V270	V271	P272	L273	T274	T275
L83	D87	L88	R89	E89	L176	R177	R91	L92	L99	E103	V104	K107	D108	I109	T110	P111	L112	Q113	V114	V115	T119	A120	L121	H122	L123	L126	L127	D131	V137	L144	F145	E146	G147	P148	T149	Y151	P153	E158	V159	V160	E161	I162	I163	Q164	A165	T166	I167	I168
MET	ALA	T3	E4	E5	E6	F6	I7	I8	R9	I10	Y13	H14	I15	I16	V18	L19	D20	S23	S26	G31	T34	Y35	I36	V43	A46	P47	M48	R49	M50	V53	P54	P55	R56	H57	Y58	C59	T60	N63	P64	V65	S66	R67	V73	V77	T78	V81	R82	

• Molecule 1: Major vault protein

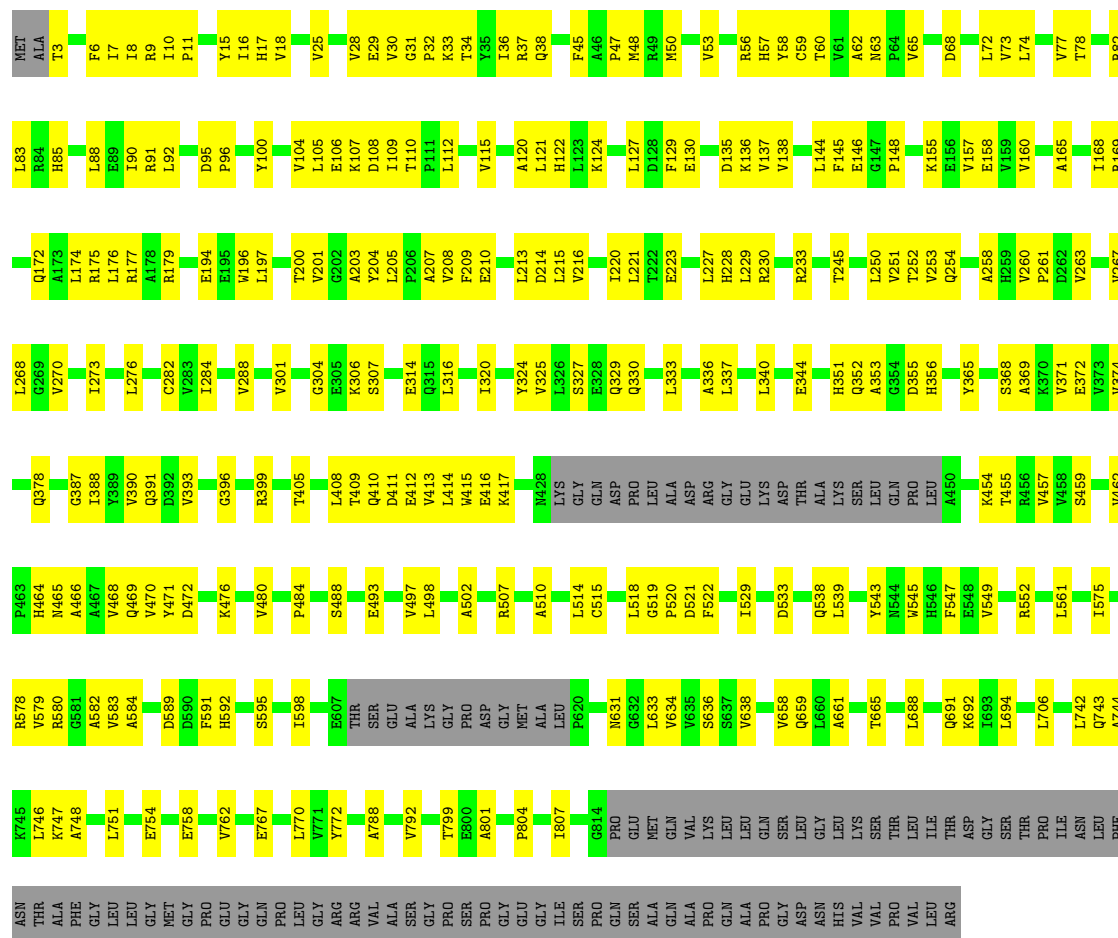
Chain EA:  55% 32% 13%

MET	ALA	T3	E4	E5	F6	I7	I8	I9	Y13	H14	Y15	I16	H17	V18	I19	D20	S23	N24	V25	V28	E29	T34	Y35	I36	E41	R42	V43	L44	F45	A46	P47	M48	R49	M50	V51	P55	R56	H57	C59	T60	V61	A62	V65	A69	V73	L74	F75	D76	V77
	Q80	R81	R82	L83	R84	D87	L88	E89	I90	A93	P96	F97	P98	L99	Y100	P101	L105	P111	L112	Q113	V114	V115	L116	T119	A120	L121	H122	L123	K124	A125	L126	L127	D128	F129	V137	V138	D141	E142	W143	G147	P148	T149	T150	Y151	K155	E156	V157	V160	
	E161	I162	I163	T166	I167	I168	Q172	A173	L174	R175	L176	C182	G193	W196	L197	T199	T200	V201	G202	A203	Y204	L205	P206	A207	V208	F209	E210	E211	D214	L215	V216	D217	L220	L221	K224	L227	H228	L229	R233	V241	S242	R243	R244	T245	L250	V251	T252		
	V253	E257	V260	P261	D262	V263	V267	L268	G269	V270	T273	T274	T275	H279	R280	Y281	C282	V283	L284	V288	K289	R300	V301	V302	K303	G304	S307	F308	F309	L310	Q311	E314	Q321	D322	V323	Y324	V325	G331	L332	L333	L334	L337	Q338	P339	L340	E341	Q352		
	Q353	E357	V360	P361	D362	V363	V367	L368	G369	V370	T373	T374	T375	H379	R380	Y381	C382	V383	L384	V388	K389	R400	V401	V402	K403	G404	S407	F408	F409	L410	Q411	E414	Q421	D422	V423	Y424	V425	G431	L432	L433	L434	L437	Q438	P439	L440	E441	Q452		



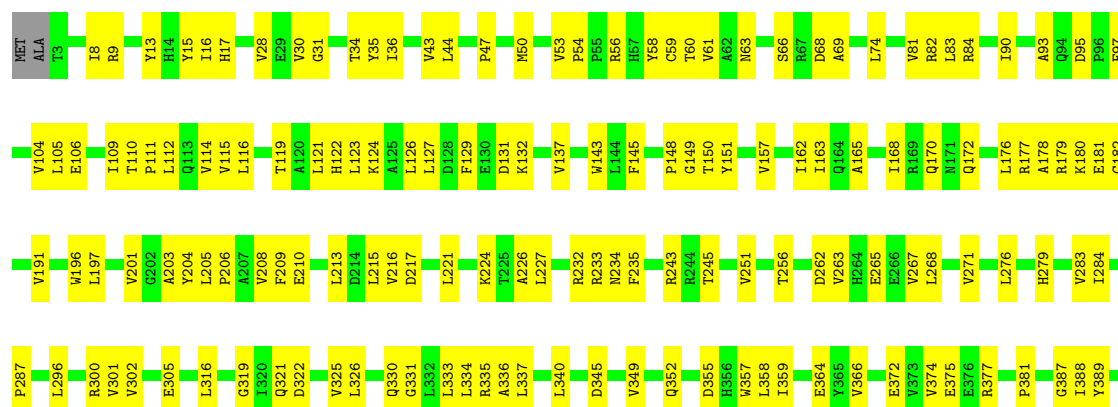
• Molecule 1: Major vault protein

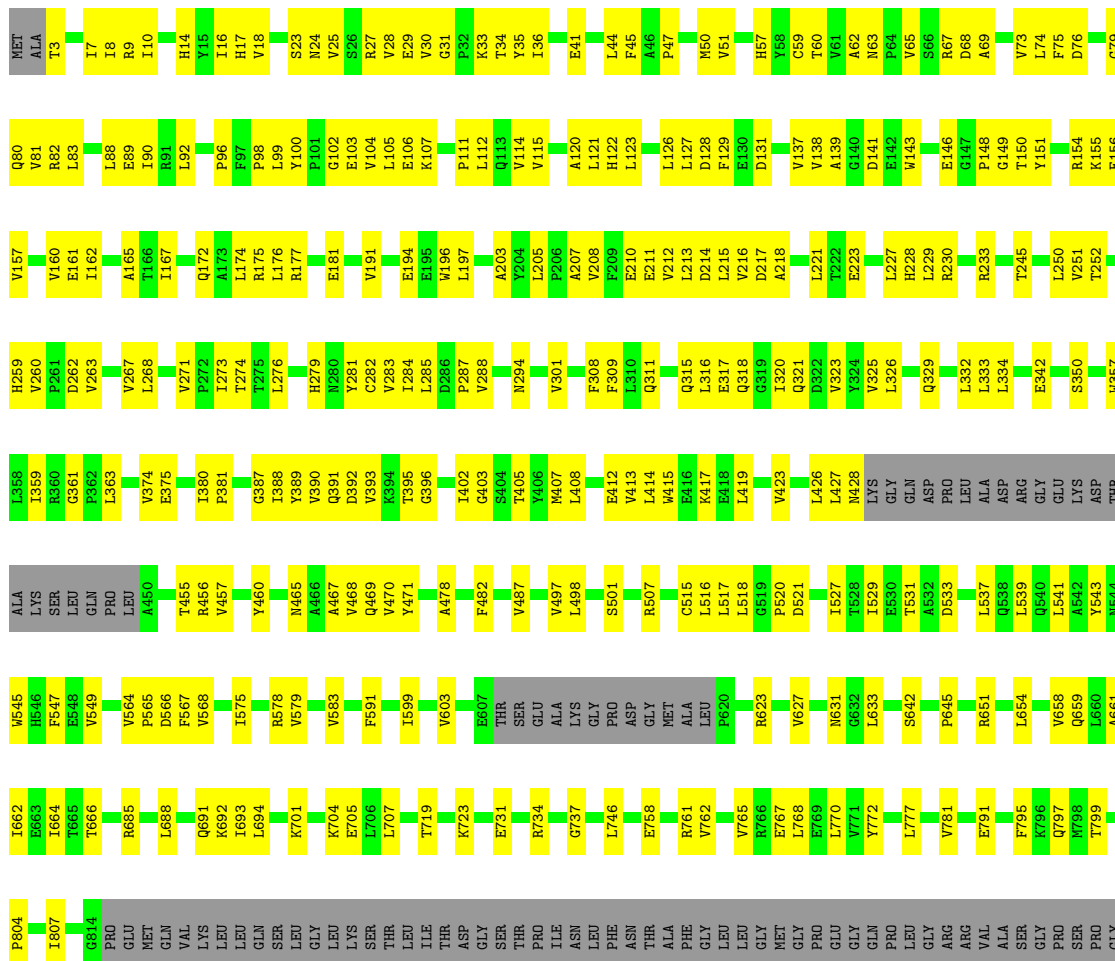
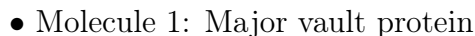
Chain EB: 58% 29% 13%



• Molecule 1: Major vault protein

SER	PRO	GLY	GLY	GLY	ILE	SER	PRO	PRO	GLU	MET	P802	E676	H546	GLN	P862	A258	Q170	A86	MET
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E364	F547	F547	LEU	E364	H259	N171	D87	T3
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E365	R552	R552	A450	E365	V263	A173	L38	F6
ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	E366	R687	Q856	R456	E374	V267	A178	L92	R17
SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	E375	R690	E557	V457	E375	L268	R179	L92	R18
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	E376	Q691	T558	GLY	E376	L268	R180	L92	R19
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	E377	L694	L561	R461	E377	L268	E181	L92	R20
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	E378	L694	D566	V462	E378	L268	E182	L92	R21
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	E379	L694	D566	V462	E379	L268	E182	L92	R22
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	E380	L694	D566	V462	E380	L268	E182	L92	R23
GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	E381	L694	D566	V462	E381	L268	E182	L92	R24
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E382	L694	D566	V462	E382	L268	E182	L92	R25
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	E383	L694	D566	V462	E383	L268	E182	L92	R26
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	E384	L694	D566	V462	E384	L268	E182	L92	R27
HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	E385	L694	D566	V462	E385	L268	E182	L92	R28
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	E386	L694	D566	V462	E386	L268	E182	L92	R29
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	E387	L694	D566	V462	E387	L268	E182	L92	R30
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	E388	L694	D566	V462	E388	L268	E182	L92	R31
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	E389	L694	D566	V462	E389	L268	E182	L92	R32
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	E390	L694	D566	V462	E390	L268	E182	L92	R33
ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	E391	L694	D566	V462	E391	L268	E182	L92	R34
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	E392	L694	D566	V462	E392	L268	E182	L92	R35
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	E393	L694	D566	V462	E393	L268	E182	L92	R36
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E394	L694	D566	V462	E394	L268	E182	L92	R37
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	E395	L694	D566	V462	E395	L268	E182	L92	R38
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E396	L694	D566	V462	E396	L268	E182	L92	R39
SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	E397	L694	D566	V462	E397	L268	E182	L92	R40
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	E398	L694	D566	V462	E398	L268	E182	L92	R41





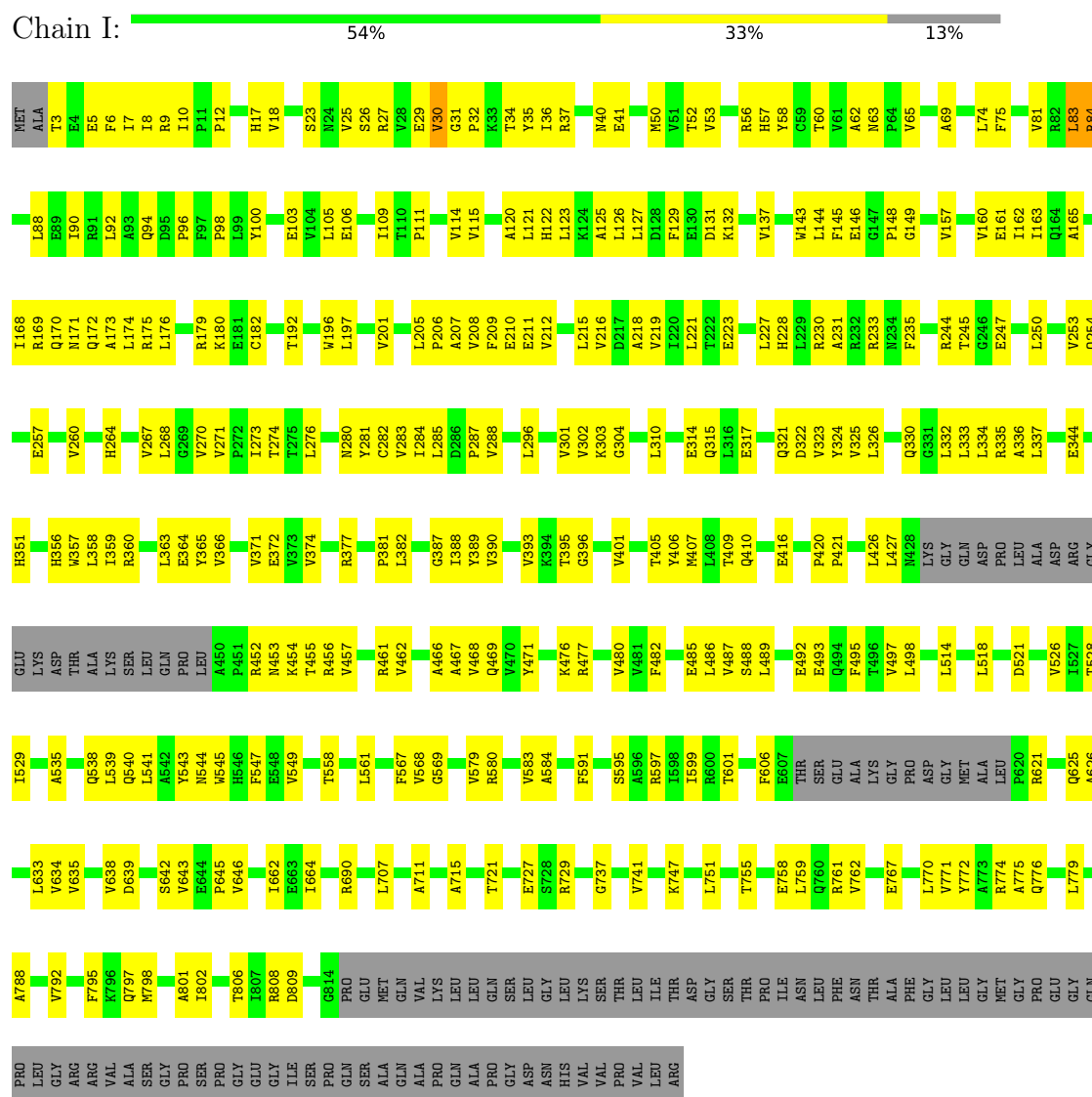
V393	Q469	D566	R679	G814	SER
G396	V470	F567	L680	PRO	PRO
K397	V471	V568	R685	GLN	GLN
V398	A478	G569	E689	MET	ALA
R399	R479	D570	R690	GLN	GLN
A400	V480	A571	Q691	VAL	ALA
V401	V481	R580	L694	LYS	PRO
I402	P484	T587	E717	LEU	GLN
T405	L486	F588	E731	ALA	ALA
Y406	V487	D589	T721	SER	GLY
M407	S488	F591	E734	LEU	ASN
Q410	L489	H592	G737	GLY	HIS
D411	G490	K593	V741	LYS	VAL
L414	P491	N594	A744	THR	PRO
W415	E492	S595	K745	LEU	VAL
E416	Q494	A596	L746	ILE	LEU
K417	F495	A597	T751	THR	ARG
V423	V496	I598	L754	PHE	
E424	V497	I599	E755	ASN	
E425	L498	T600	E756	THR	
L426	S601	F606	A757	ALA	
L427	R507	E607	L759	PHE	
L428	A513	THR	V762	GLY	
LYS	L516	GLU	E767	LEU	
GLN	L517	SER	L768	GLY	
ASP	L518	ALA	E769	GLY	
PRO	L518	LYS	L770	GLY	
LEU	D521	ASP	E780	GLN	
ALA	F522	GLY	V781	PRO	
ARG	T527	MET	S782	LEU	
GLY	T528	ALA	K783	GLY	
GLU	I529	LEU	Q786	ARG	
ASP	E530	P620	K794	VAL	
THR	T531	L633	I802	ALA	
ALA	A535	S642	G803	SER	
LYS	R536	V643	R804	GLY	
SER	L539	V646	S805	PRO	
LEU	Q540	A653	T806	PRO	
PRO	L541	L654	I807	GLY	
LEU	A542	I662	R808	GLY	
A450	Y543	E663	D809	ILE	
T455	N544	E663			
R456	V545	I664			
V457	H546	T665			
Y460	F547	T666			
R461	E548	E670			
V462	V549				
	R552				

• Molecule 1: Major vault protein

Chain GB:  56% 31% 13%

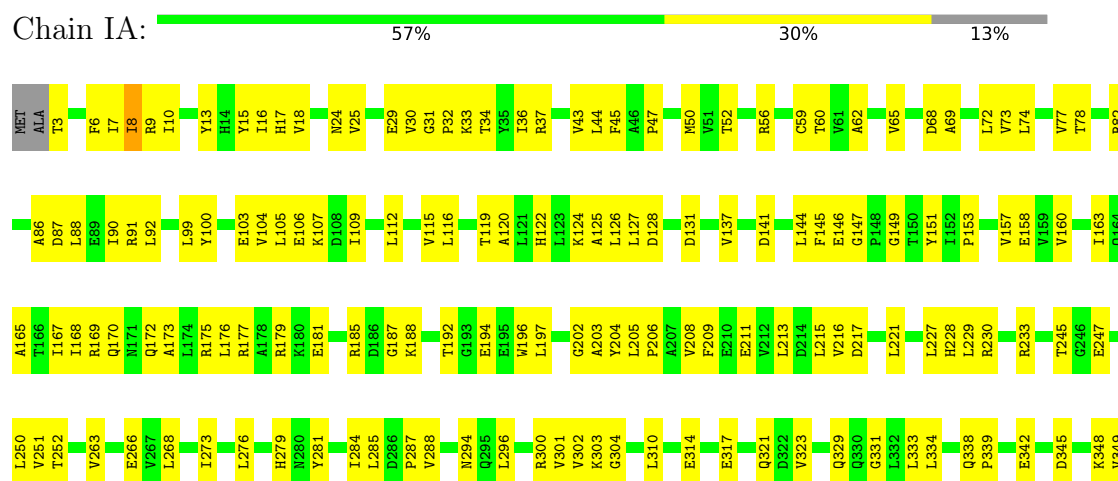
MET	E89	E189	V301	I388	V462	V579	V658	GLU
ALA	I90	R190	V302	T389	P463	R580	Q659	MET
T3	R91	V191	K303	V390	P463	G581	A661	GLN
E4	T192	T192	G304	G304	V468	A582	A661	VAL
E5	P98	G193	E305	V393	Q469	V583	T662	LYS
F6	I99	E194	L310	G396	V480	V586	E663	LEU
I7	Y100	E195	Q311	K397	V481	T587	T664	LEU
I8	E103	W196	E314	R398	E485	F588	T665	GLN
R9	V104	V198	E315	R399	V485	D589	T666	GLN
Y13	L105	V201	L316	A400	E493	D590	A684	GLY
H14	K107	L205	G319	V401	T496	F591	R685	LEU
Y15	E106	P206	I320	I402	V497	R597	R687	LYS
I16	K107	V208	G331	T405	L498	I598	L688	SER
H17	E108	V114	L332	M407		T600	E731	THR
N22	T110	H122	L333	Q410	C515	G601	A732	ILE
V25	H122	A125	L334	D411	L516	F606	A733	ASP
V28	A126	D217	R335	E412	L517	E607	R734	GLY
E29	V30	L126	A336	V413	L518	THR	I735	SER
V30	G31	L127	L337	L414	D521	GLU	E736	THR
T34	F129	E128	Q338	W415	F522	ALA	G737	PRO
Y35	E130	D128	L340	E416	F523	LYS	V741	ILE
I36	D135	D135	E341		V526	LEU	L742	LEU
N40	V137	D135	E342		I529	GLY	Q743	PHE
F45	W143	D135	E343		E424	ASP	E744	ASN
A46	V157	E156	D345		E425	GLY	K747	ALA
M50	E157	E156	F346		LYS	MET	L751	PHE
V53	E158	V159	E347		E428	ALA	T755	GLY
P54	E159	E160	A353		GLY	LEU	E756	LEU
P55	E160	E161	H356		GLN	P620	R756	GLY
R56	E161	I162	V357		ASP	P622	E757	MET
H57	I163	I163	L358		LEU	R623	L759	GLY
Y58	I163	I163	L359		ALA	D694	Q760	PRO
C59	T60	R169	R360		ASP	Q625	R761	GLU
V61	A62	Q172	L363		GLY	V627	V762	GLY
A62	V65	L174	V366		LYS	L633	V765	GLN
V65	S66	R175	V373		ASP	V634	R766	PRO
R67	R176	L176	E374		THR	V635	E767	GLY
V73	A177	R177	E375		ALA	V638	E769	ARG
T78	K180	R179	E376		LYS	D639	L768	ARG
V81	E181	L182	E377		LEU	V640	L770	VAL
R82	C182	W183	Q378		GLN	Q641	L777	ALA
L83	W183	G187	Q378		PRO	S642	V781	SER
L88	K188	K188	A379		LEU	E644	V781	PRO
			P381		A450	V564	L787	SER
			L382		T455	F567	V792	GLY
			E384		R456	D570	W798	GLY
			E385		V457	I575	G814	ILE
			G387		Y460		R566	SER
					R461		S657	PRO
								GLN

Chain I:



- Molecule 1: Major vault protein

Chain IA:



ALA	PRO	GLY	ASP	ASN	HIS	VAL	VAL	PRO	VAL	LEU	ARG	LEU	GLN	PRO	LEU	A450	V457	V462	V468	V480	V481	F482	G483	P484	E485	L486	V487	L489	G490	E493	Q494	F495	S501	R507	L514	C515	L516	D521	F522	F523	T524	D525	V526	I527	T528	I529	E530	T531	H534	L537	Q538	L539	Q540	L541	A542	Y543	W544	H545	H546
												F547	E548	V549	R552	V564	F567	V568	A582	V583	A584	S585	V586	T587	F588	T601	F604	E607	THR	SER	GLU	ALA	LYS	PRO	ASP	GLY	C515	L516	D521	F522	F523	T524	D525	V526	I527	T528	I529	E530	T531	H534	L537	Q538	L539	Q540	L541	A542	Y543	W544	H545
I662	E663	T664	T665	T666	Q669	H675	Q678	L688	Q691	S695	T699	L709	L742	K745	L746	L751	E754	T755	L759	R766	E767	L768	E769	L770	A773	R774	A775	E780	K783	A788	V792	I802	I807	G814	PRO	GLU	MET	GLN	VAL	LYS	LEU																		
LEU	GLN	SER	GLY	LEU	GLY	LEU	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	ALA	PHE	GLY	LEU	GLY	MET	PRO	GLU	GLN	PRO	LEU	GLY	ARG	VAL	ALA	SER	PRO	GLY	ILE	PRO	PRO	SER	GLN	SER	ALA	GLN	ALA	PRO	GLN	LEU														
S350	H351	L358	T359	R360	K370	V374	E375	R376	R377	Q378	A379	P381	I388	R389	V390	V393	G396	R399	T405	Y406	M407	Q410	D411	E418	L419	E424	E425	L426	L427	M428	LYS	GLY	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	Q540	L541	ASP	THR	ALA	LYS	W545	H546										

• Molecule 1: Major vault protein

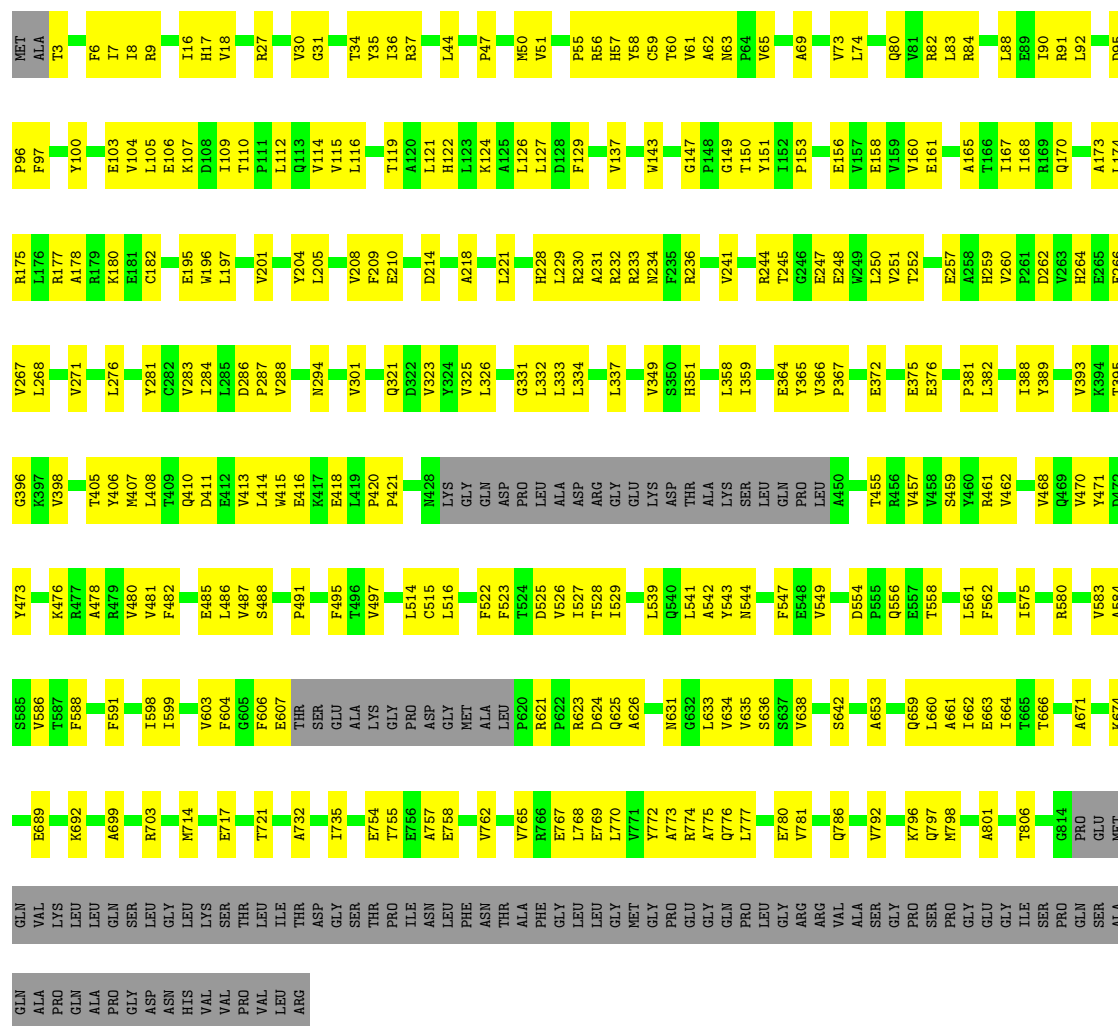
Chain IB:  55% 33% 13%

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	L680	D590	Q469	V393	V301	L197	E89	E4
T806	E681	F591	V480	G396	V302	V201	R91	F6
	A684	K303			P98		I7	
	L688	C304			L18		R9	
	Q691	E305			Y100			
V812	Q691	I598	P484	A400	K306	V208	P101	Y15
A813	A702	R600	E485	T405	F308	E211	L105	I16
G814	L707	A602	S488	L408	L310	L215	E106	H17
PRO	L707	V603	F495	T409	Q311	V216	L19	V18
GLU	E710	F604	S499	D411	P312	D217	T110	D20
MET	A711	E607	R504	E412	T320	A218	P111	
GLN	M714	THR	R512	V413	Q321	V219	L112	
VAL	E717	GLU	C515	L414	L332	L220	V115	R27
LEU	L742	ALA	L516	W415	L333	L221	L116	V28
LEU	Q743	GLY	L517	E416	L334	L227	T119	E29
GLN	A744	ASP	ASP	L419	R335	H228	A120	G31
SER	K745	GLY	F522	G422	L340	L229	H122	
LEU	L746	MET	F523	F428	E341	R233	L123	
THR	K747	ALA	T524	LYS	E342	T245	K124	E41
ILE	A748	LEU	ALA	GLY	E346	W249	L126	R42
LEU	P820	ILE	I529	GLN	E347	L250	L127	V43
THR	E754	R821	E530	ASP	K348	L250	D128	L44
ASP	T755	P822	T531	PRO	V349	V253	F129	F45
GLY	R623	R623	A532	LEU	S350	V253	E130	A46
SER	E758		D533	ALA	H351	E257	D131	P47
THR	L759	A626	R536	ASP	D355	A258	K132	M50
PRO	Q760	Q760	L537	ARG	H356	V259	V137	V51
ILE	R761	L833	V637	GLY	W357	V260	L143	R56
ASN	V762	V634	Q538	GLU	L358	V263	L144	H57
LEU		V635	L539	LYS	L359		F145	Y58
PHE	E767	S836	Q540	ASP			E146	C59
ASN	L768	S937	L541	THR	L363	L268	G147	V61
THR	E769	V638	A542	ALA	E364	G269	T60	T60
ALA	L770	D639	Y543	LYS	V365	V270	V61	
PHE	V771	V640	N544	SER	V366	V271	V160	A62
GLY	Y772	Q641	V545	LEU	P367	P272	E161	N63
LEU	A773	S842	H546	GLN	S368	I273	I162	P64
LEU	R774	V643	E548	LEU	V371	T274	I163	V65
GLY	A775	P845	V549	LEU		T275	Q164	S66
MET						L276	A165	R67
GLY	E778	V646				G277	D68	
PRO			D554	P451	V374		I168	A69
GLU	V781	T650		R452	E375		R169	Q70
GLY	S782		T558	M453	A379	Y281	L170	G71
GLN		S857		K454	L380	C282	M171	L72
PRO	Q785		V579	T455	P381	I284	Q172	
LEU		L660	R580	R456	V457	A173	A173	V81
GLY	A788	A661	V532	V458	G387	P287	L174	R82
ARG	E789	I662	V532	S459	L388	V288	P475	L83

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

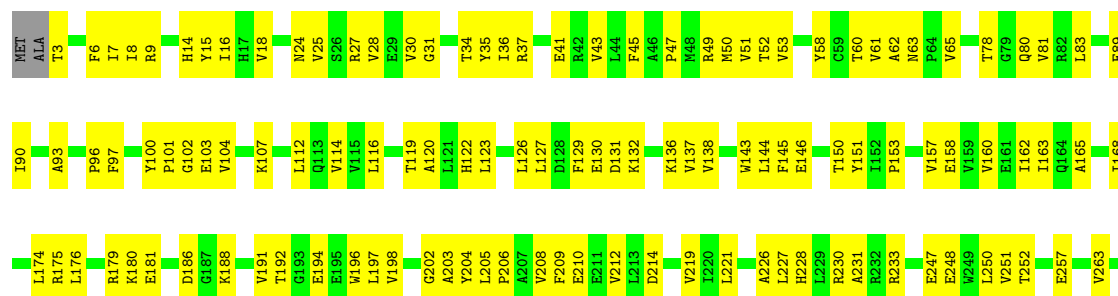
• Molecule 1: Major vault protein

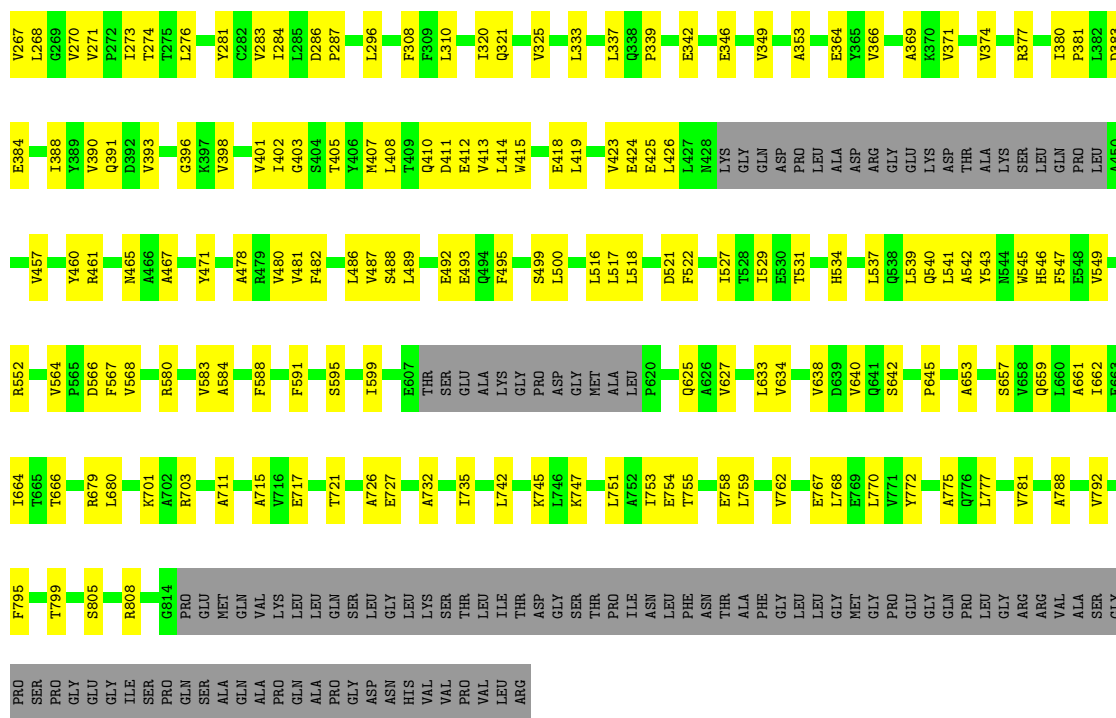
Chain J:  56% 32% 13%



• Molecule 1: Major vault protein

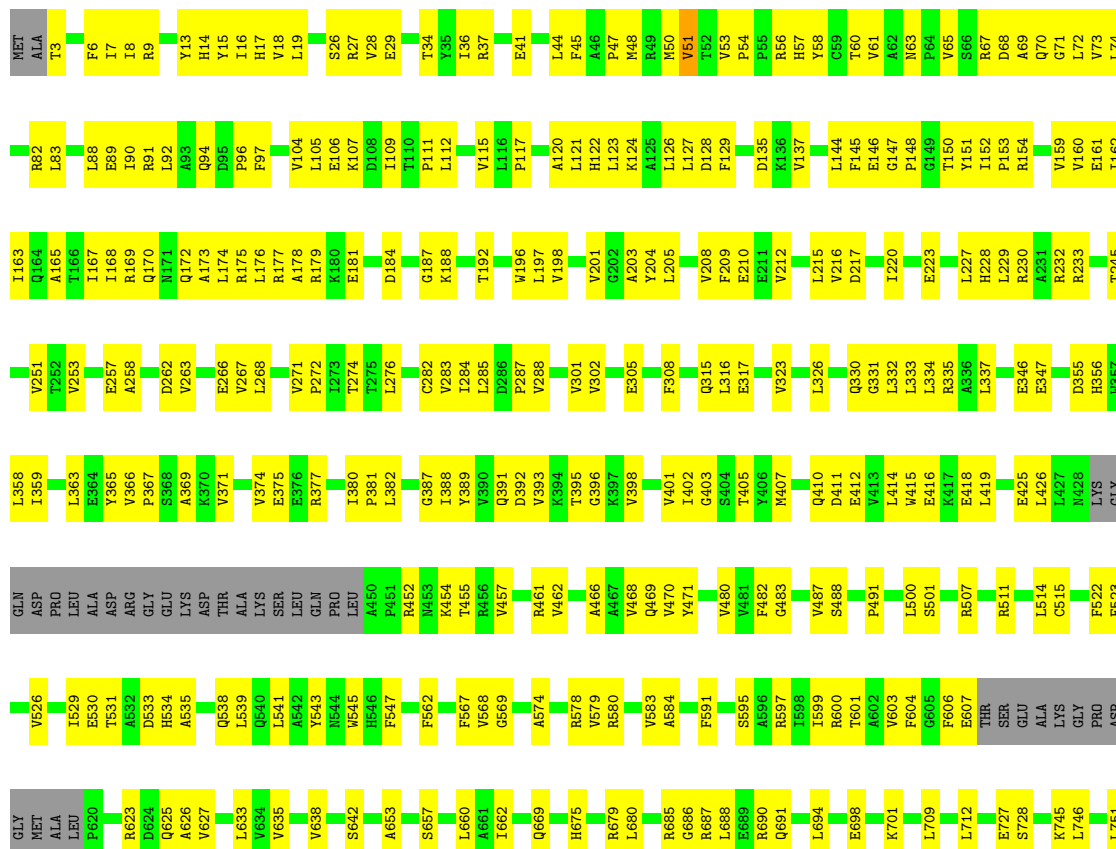
Chain JA:  56% 31% 13%

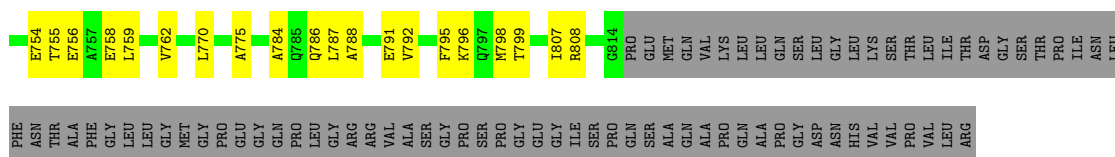




• Molecule 1: Major vault protein

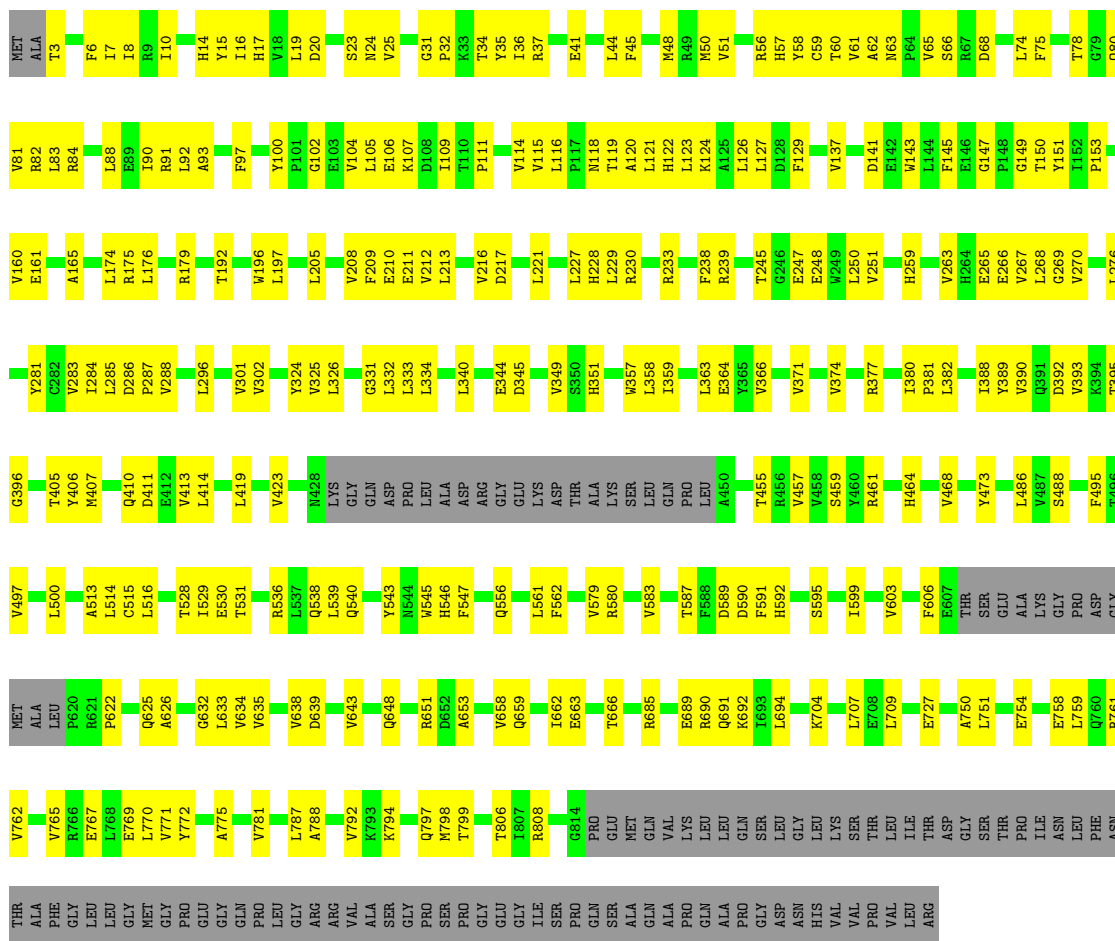
Chain JB: 52% 35% 13%





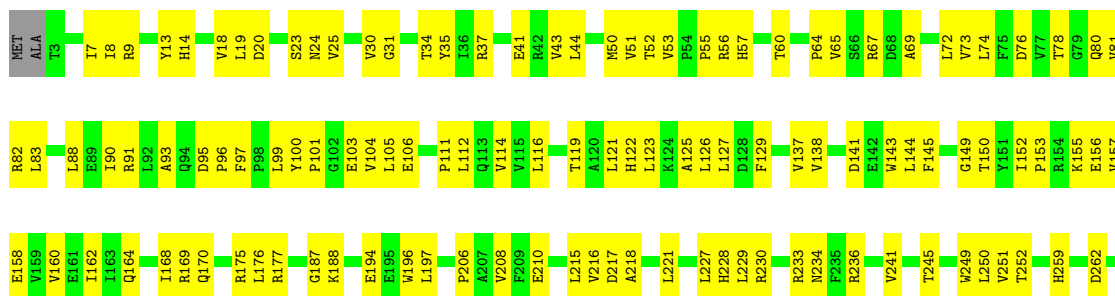
• Molecule 1: Major vault protein

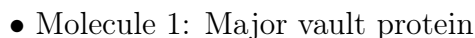
Chain K: 57% 30% 13%

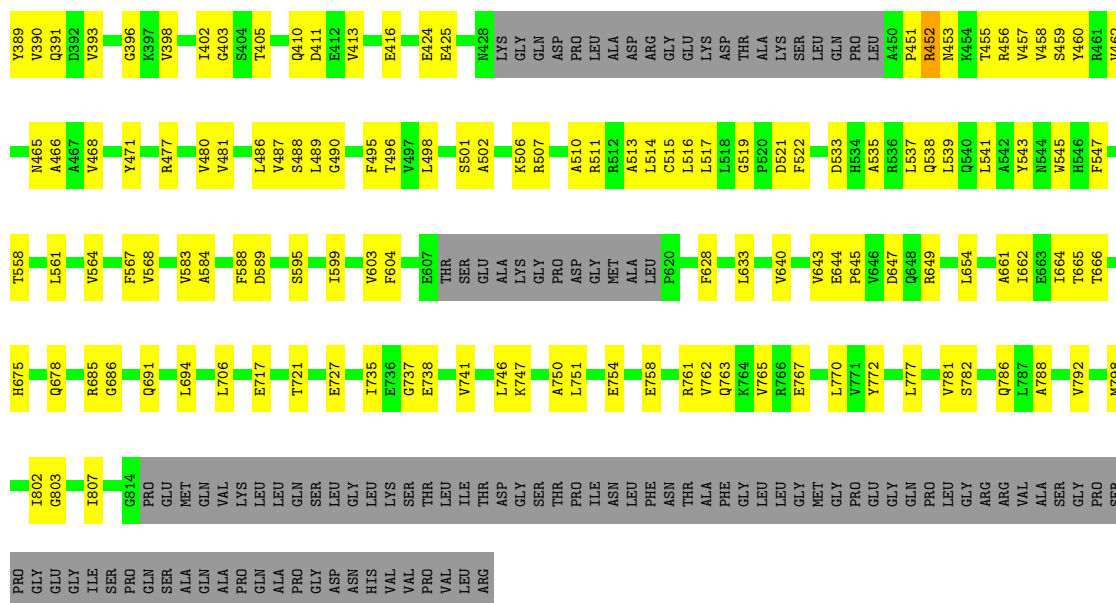


• Molecule 1: Major vault protein

Chain KA: 57% 30% 13%

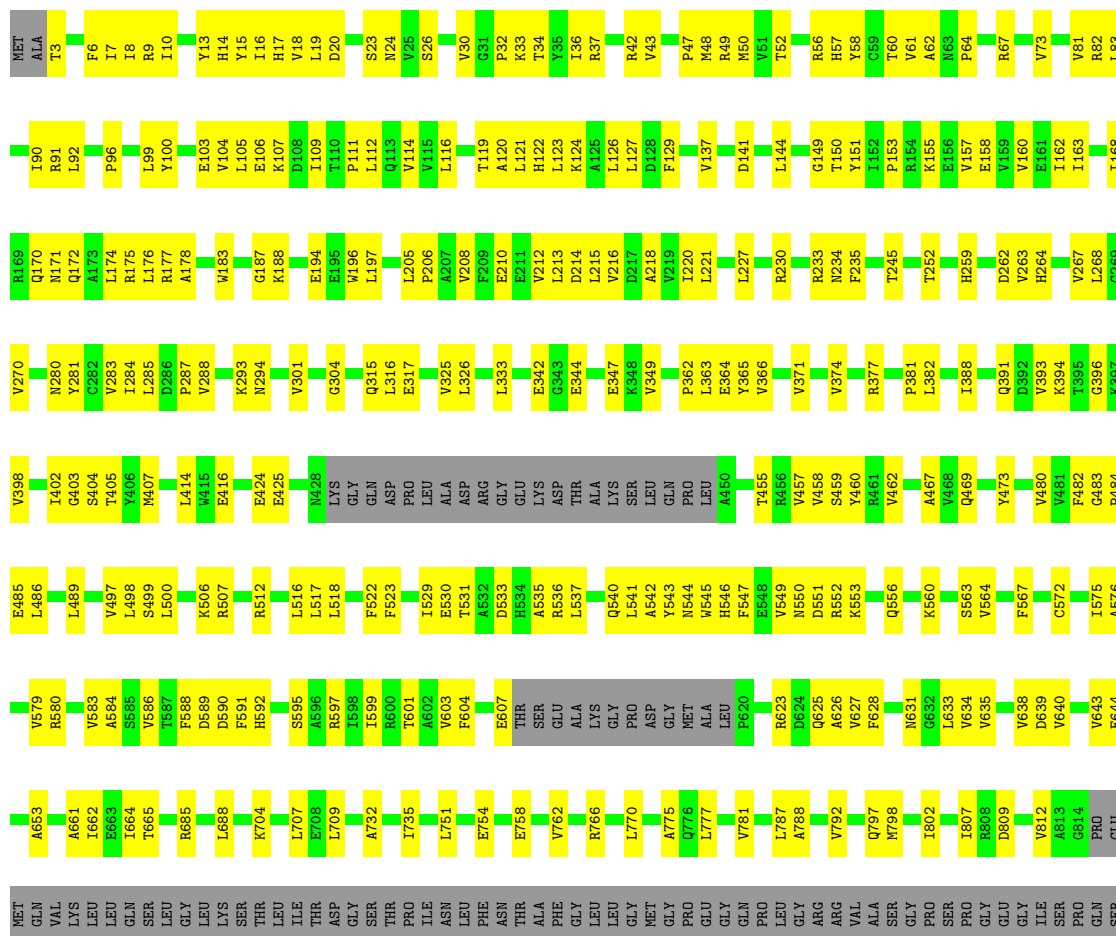






• Molecule 1: Major vault protein

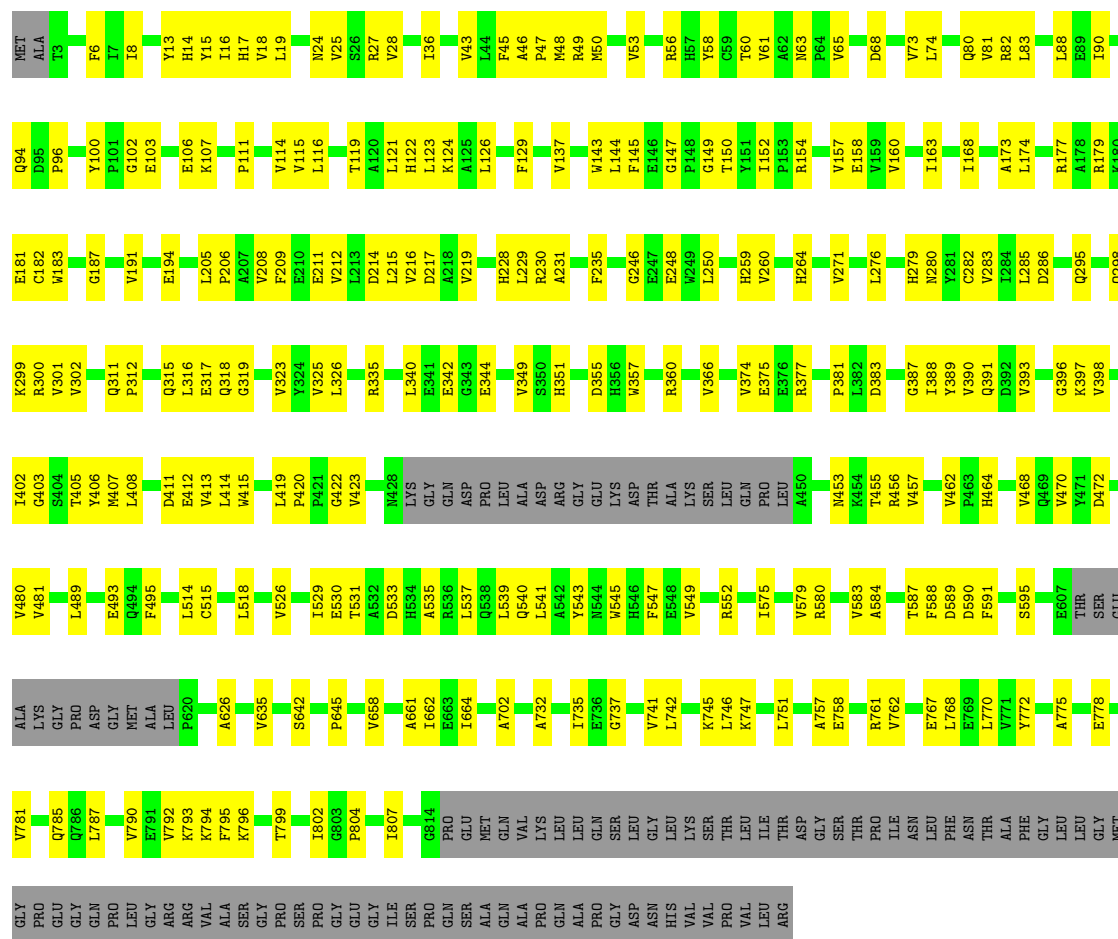
Chain LB: 55% 32% 13%



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• Molecule 1: Major vault protein

Chain M: 59% 28% 13%



PRO	SER	PRO	GLY	GLY	GLY	ILE	SER	PRO	GLN	GLN	ALA	ALA	GLN	ALA	VAL	PRO	PRO	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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• Molecule 1: Major vault protein

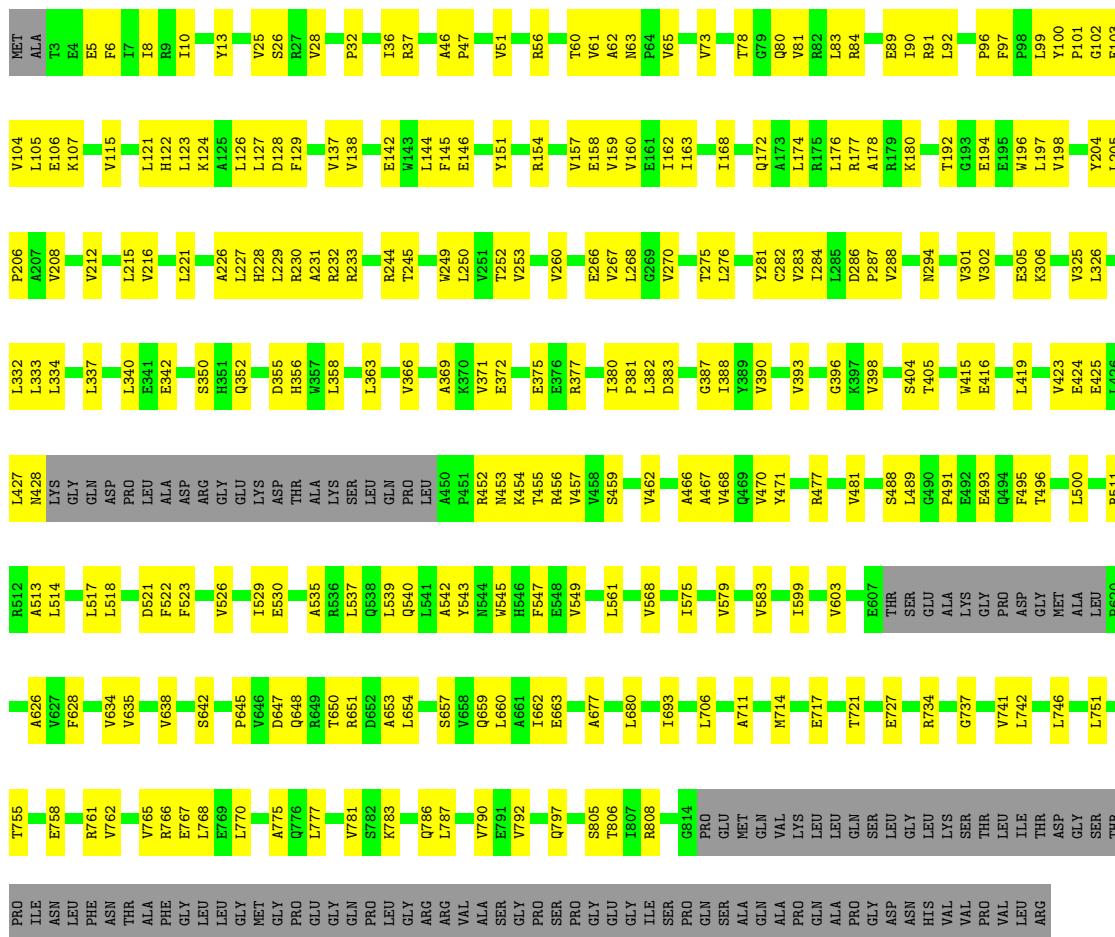
Chain MB:  55% 32% 13%

MET	ALA	T3	F6	I7	I8	R9	H14	Y15	I16	H17	V18	V25	S26	R27	V28	E29	T34	Y35	I36	R37	E41	R42	V43	L44	F45	A46	P47	M48	T52	V53	P54	P55	R56	H57	Y58	C59	T60	V61	A62	N63	V64	V65	S66	R67	D68	A69	L72	V73	L74	F75	T78																																																		
																																																				R82	R83	R84	H85	A86	D87	A93	Q94	D95	P96	F97	L105	E106	K107	D108	I109	T110	P111	Q112	I113	V114	V115	L116	T119	A120	L121	H122	L123	K124	A125	L126	L127	D128	F129	V137	L144	F145	E146	G147	Y151	K155	E156	V157	E158	V159	V160	A165	I168	R169	Q170
																																																				H171	Q172	R175	L176	R179	G187	K188	W196	L197	V201	G202	A203	Y204	L205	P209	E210	E211	V212	L215	A218	L221	T222	E223	L227	H228	L229	R230	A231	R232	R233	N234	F235	R236	R239	G240	V241	T245	E248	V251	T252	V253	V260	D261	L262	V263					
																																																				H264	E265	E266	V267	L268	G269	V270	V271	T275	L276	Y281	D286	P287	V288	N294	Q295	Q298	V301	V302	Q311	P312	L316	E317	Q318	G319	V323	Y324	V325	L326	Q330	G331	L332	L333	L334	R335	A336	Q338	P339	L340	G343	E344	D345	E346	E347	K348	V349	H351			
																																																				Q352	A353	G354	D355	H356	K357	L358	P362	A369	V374	E375	E376	Q377	Q378	P381	N385	I388	Y389	V390	V393	G396	R399	I402	G403	S404	T405	Y406	M407	L408	T409	Q410	D411	E412	V413	L414	W415	E416	K417	E418	E424	E425	N428	LYS	GLN	ASP	PRO	LEU			
																																																				ALA	ASP	ARG	GLY	GLY	LYS	ASP	THR	ALA	LYS	SER	LEU	GLN	PRO	A450	V457	V458	S459	A466	V470	Y471	D472	K476	V480	V481	V487	S488	L489	E493	Q494	F495	L518	D521	I527	T528	V529	V530	T531	A532	D533	L537	Q538	L539	Q540	L541	W545				
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• Molecule 1: Major vault protein

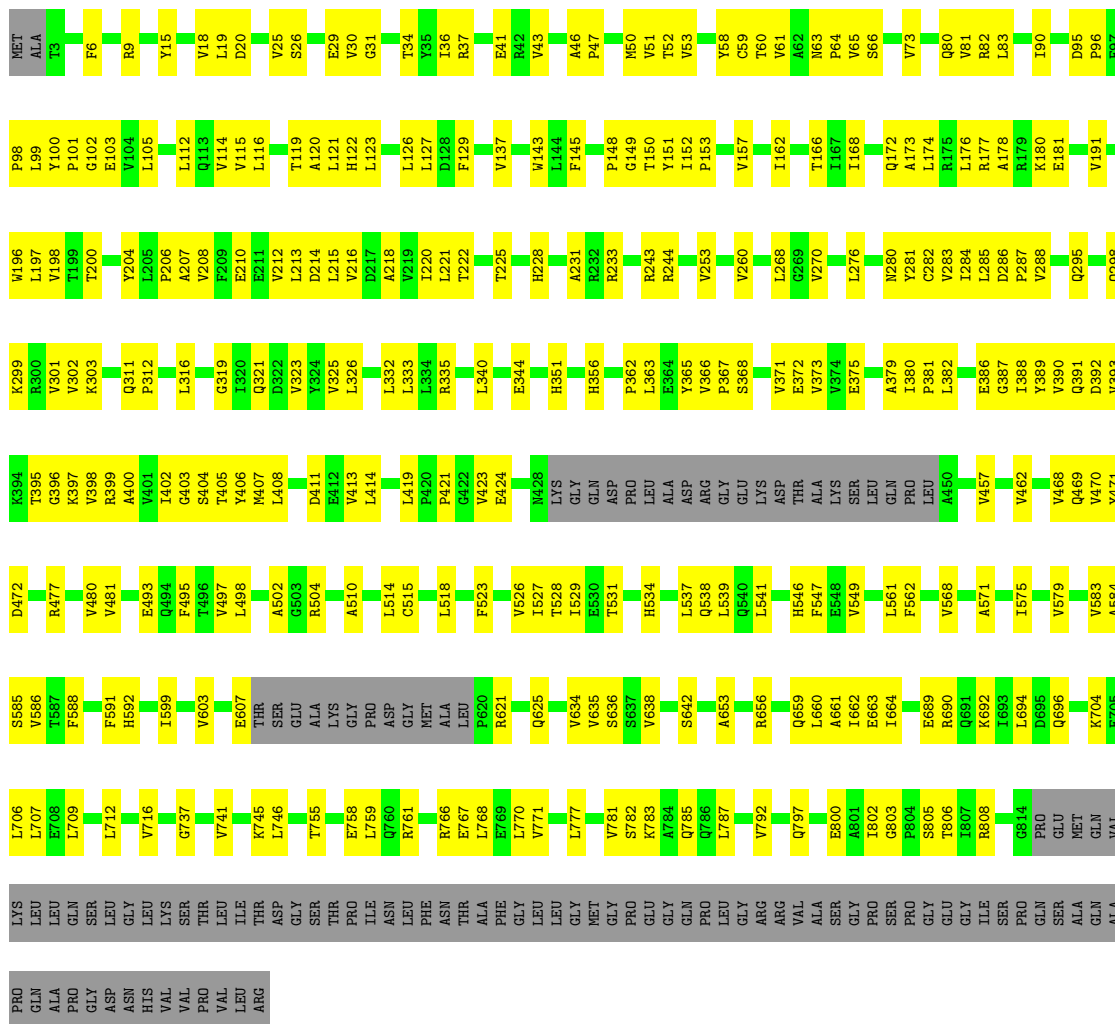
Chain N:  58% 29% 13%



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VAL
LEU
ARG

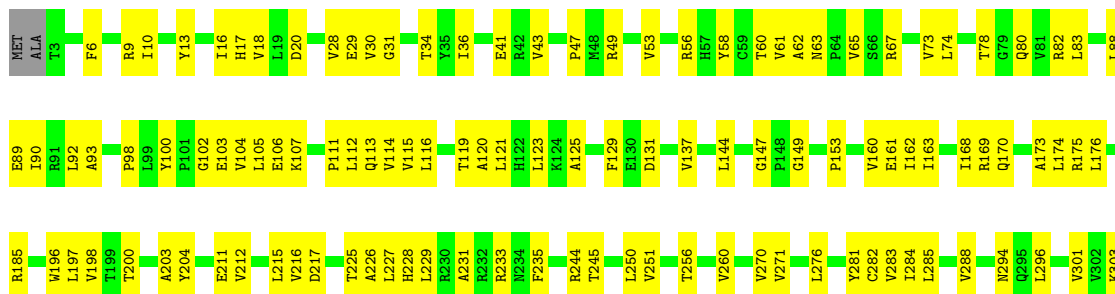
• Molecule 1: Major vault protein

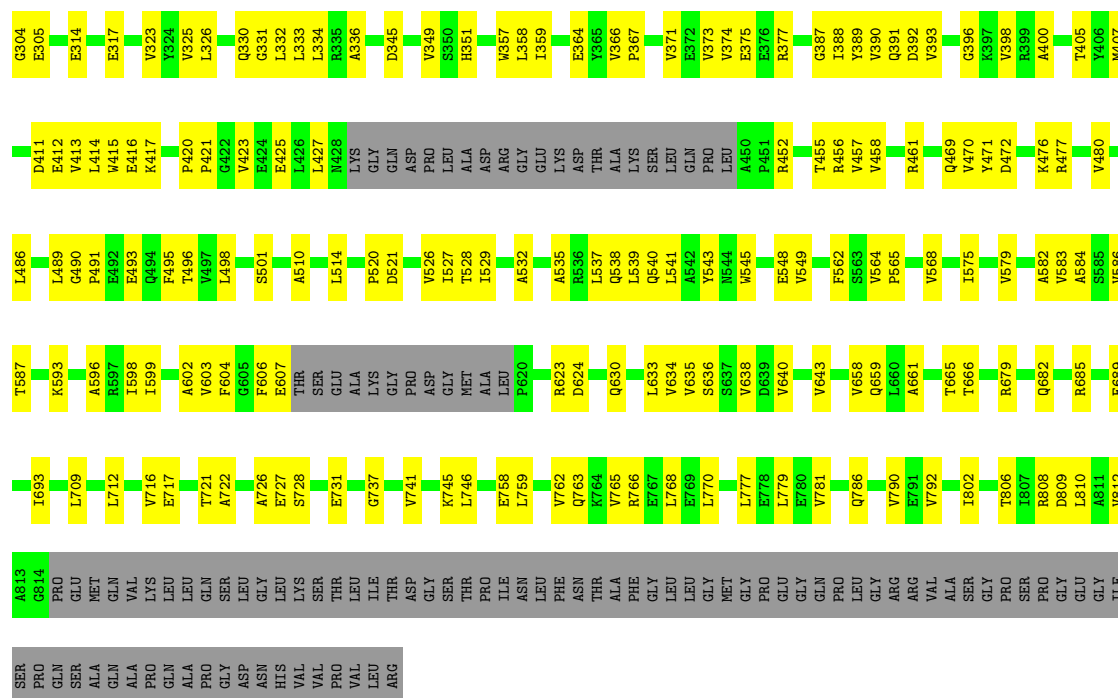
Chain O: 56% 32% 13%



• Molecule 1: Major vault protein

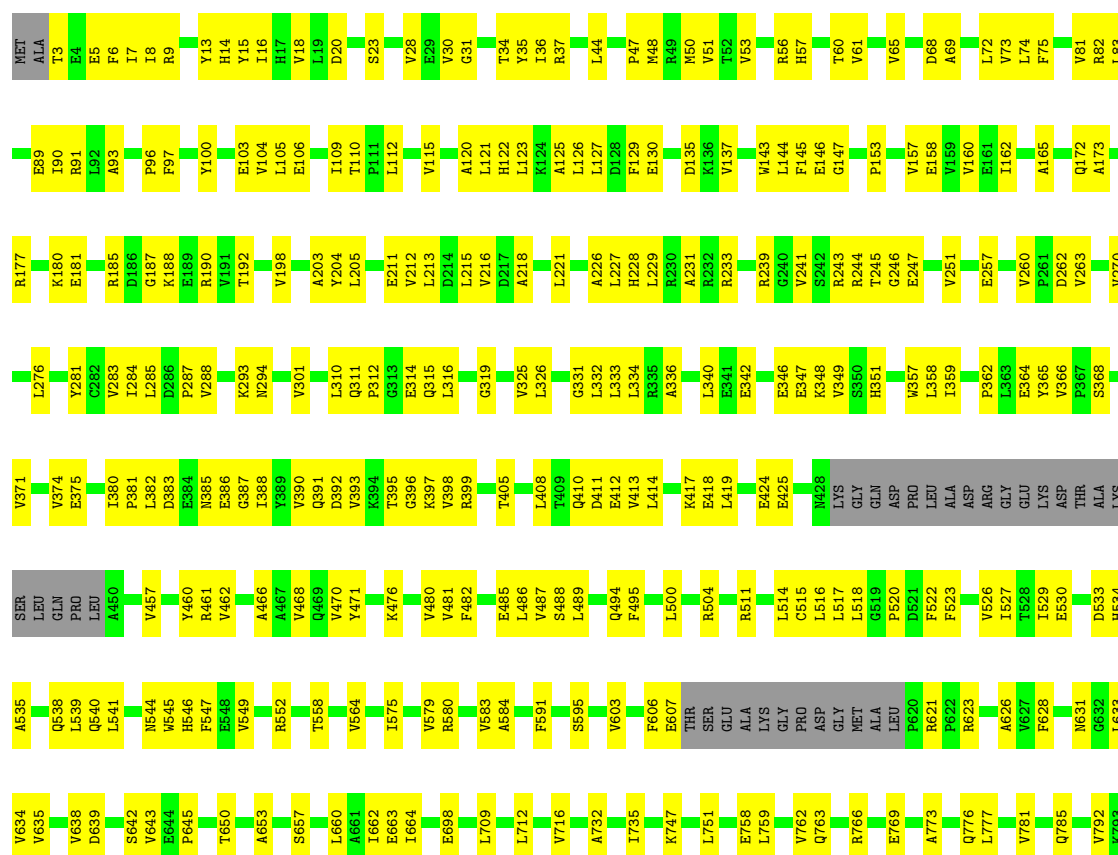
Chain OA: 56% 31% 13%





• Molecule 1: Major vault protein

Chain OB:



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

• Molecule 1: Major vault protein

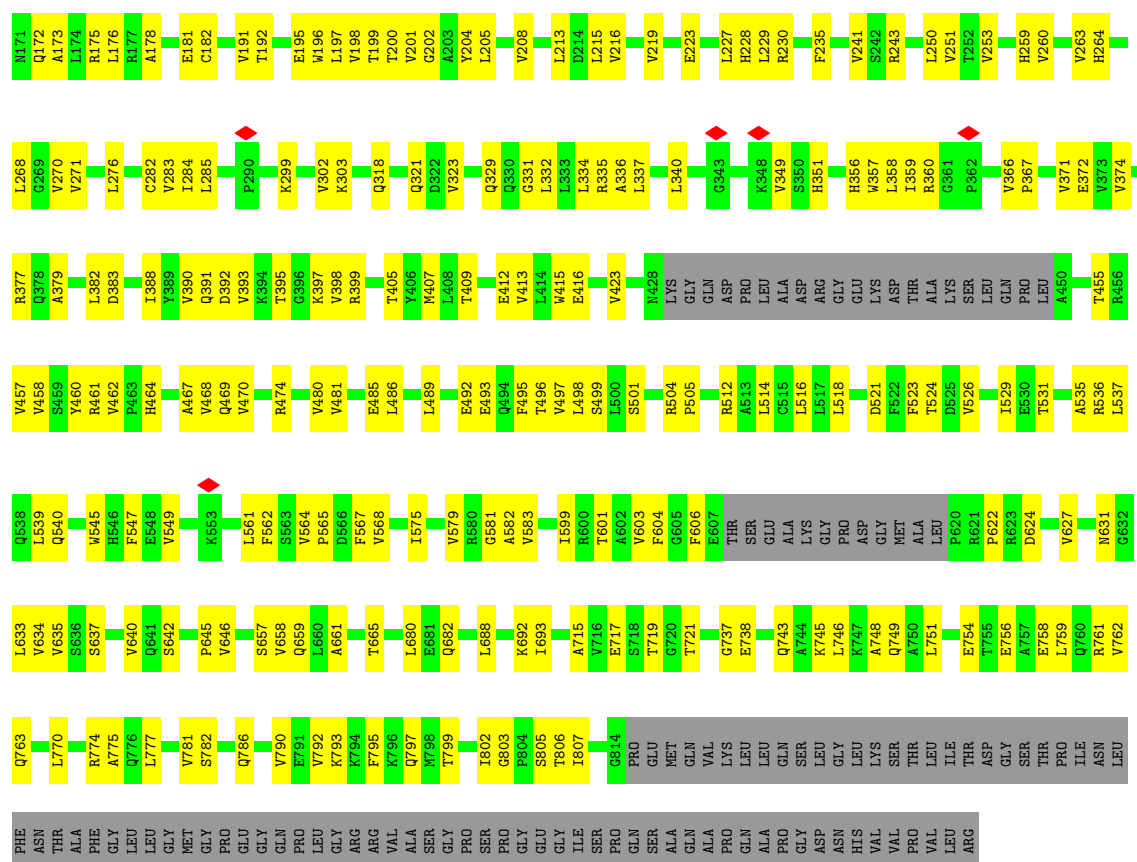
Chain Q:  59% 28% 13%

GLY	LEU	LEU	GLY	GLY	PRO	GLU	GLY	GLN	PRO	LEU	GLY	ARG	ARG	VAL	ALA	SER	GLY	PRO	SER	PRO	GLY	GLU	GLY	ILE	SER	PRO	GLN	SER	ALA	GLN	ALA	VAL	GLN	ALA	ALA	PRO	GLY	GLY	LEU	VAL	VAL	ARG				
V771	R774	E780	K783	Q786	L787	A788	E789	W790	E791	V792	F795	T799	P804	A813	G814	PRO	GLU	MET	GLN	VAL	LYS	LEU	LEU	GLN	GLN	VAL	LEU	GLN	GLN	GLN	LEU	GLN	GLN	GLN	GLN	GLY	GLY	GLY	GLY	GLY	ARG					
L489	E493	F495	L514	C515	L516	L517	L518	D521	L529	E530	T531	L537	A542	W545	H546	F547	E548	V549	D554	T558	L561	F567	V568	R580	G581	A582	V583	A584	T587	F588	D589	D590	F591	N594	S595	I598	I599	R600	V601	A602	V603	E607	F608			
L408	T409	Q410	L414	L419	P420	P421	E424	W428	LYS	GLY	GLN	ASP	PRO	LEU	ALA	ASP	ARG	GLY	GLU	LYS	ASP	THR	ALA	ALA	T455	R456	W457	V458	R461	V462	A466	A467	V468	Q469	V470	Y471	R477	V480	W481	F482	L486	V487	S488			
V301	S307	L310	L316	E317	Q321	Y324	G331	L332	L333	L334	R335	E347	A353	G354	D355	L358	I359	R360	G361	L362	L363	E364	E376	R377	Q378	A379	I380	P381	L382	E386	G387	I388	Y389	V390	V393	K394	T395	G396	K397	V398	R399	A400	V401	T405	Y406	M407
R177	C182	W183	L199	T192	W196	V201	G202	A203	Y204	L205	V208	F209	E210	E211	V212	L213	D214	L215	V216	L227	H228	L229	R230	T245	G246	E247	L250	V260	P261	V267	G269	V270	T274	T275	N280	Y281	C282	V283	I284	L285	D286	P287	V288	N294		
A93	P96	L99	Y100	P101	G102	E103	V104	L105	I109	L112	Q113	V114	V115	T119	A120	H121	H122	L123	K124	A125	L126	L127	F129	G134	V137	W143	L144	G147	T150	K155	E156	V157	E158	V159	I162	A165	I168	R169	Q172	A173	L174	R175				
MET	ALA	T3	I7	I10	Y15	I16	H17	V18	L19	N24	V25	S26	R27	V28	E29	V30	G31	T34	E41	L44	F45	V51	T52	V53	P54	V61	A62	N63	P64	S66	R67	D68	A69	Q70	G71	L72	V73	V77	T78	Q79	Q80	V81	R82	L83	I90	R91

• Molecule 1: Major vault protein

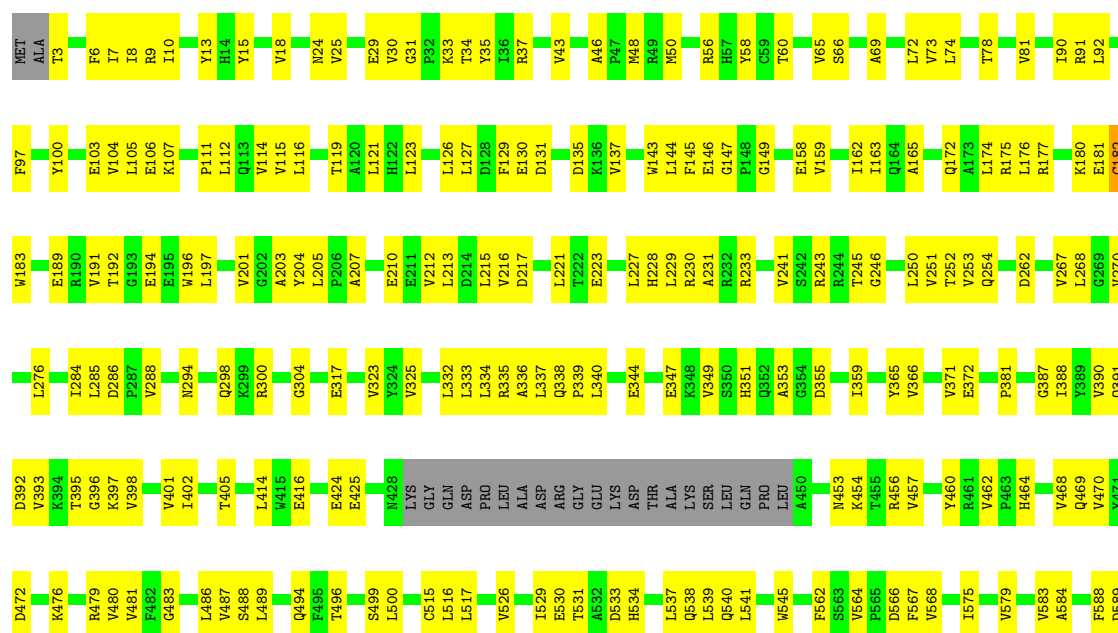
Chain QA:  54% 33% 13%

MET	ALA	T3	F6	R9	I10	Y15	I16	L787	A788	E789	W790	E791	V792	F795	T799	P804	A813	G814	PRO	GLN	MET	GLN	ALA	VAL	LYS	LEU	LEU	GLN	ALA	VAL	LEU	GLY	LEU	THR	LEU	ILE	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE
I90	R91	L92	A93	P96	F97	P98	L99	Y100	P101	G102	E103	V104	E106	K107	D108	I103	V114	V115	T119	A120	H121	H122	L123	K124	A125	L126	L127	G134	V137	W143	L144	F145	E146	G147	P148	G149	T150	Y151	I152	E158	V159	V160	E161	I162	I163	R166	T167	I168	R169	Q170



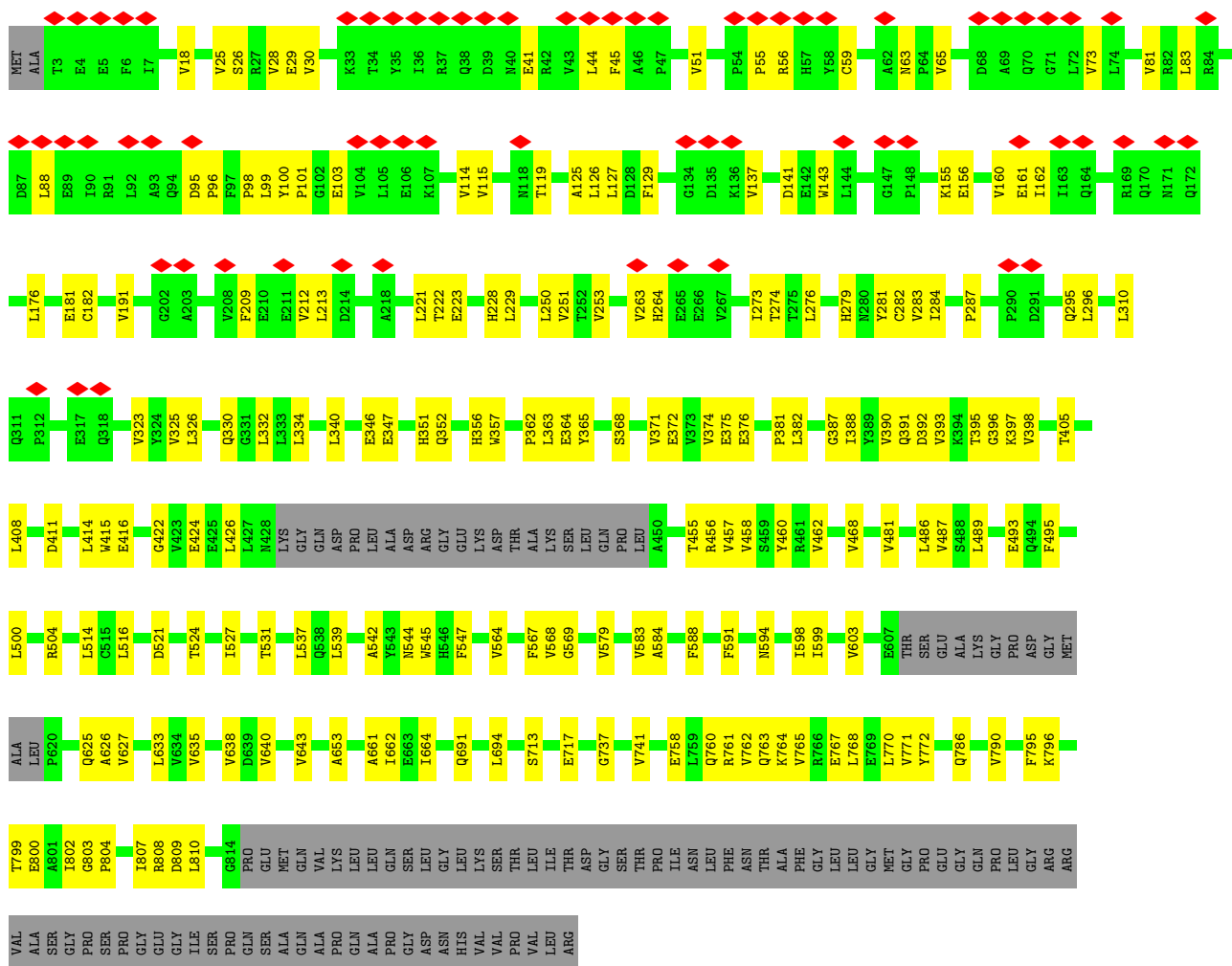
• Molecule 1: Major vault protein

Chain QB: 57% 30% 13%



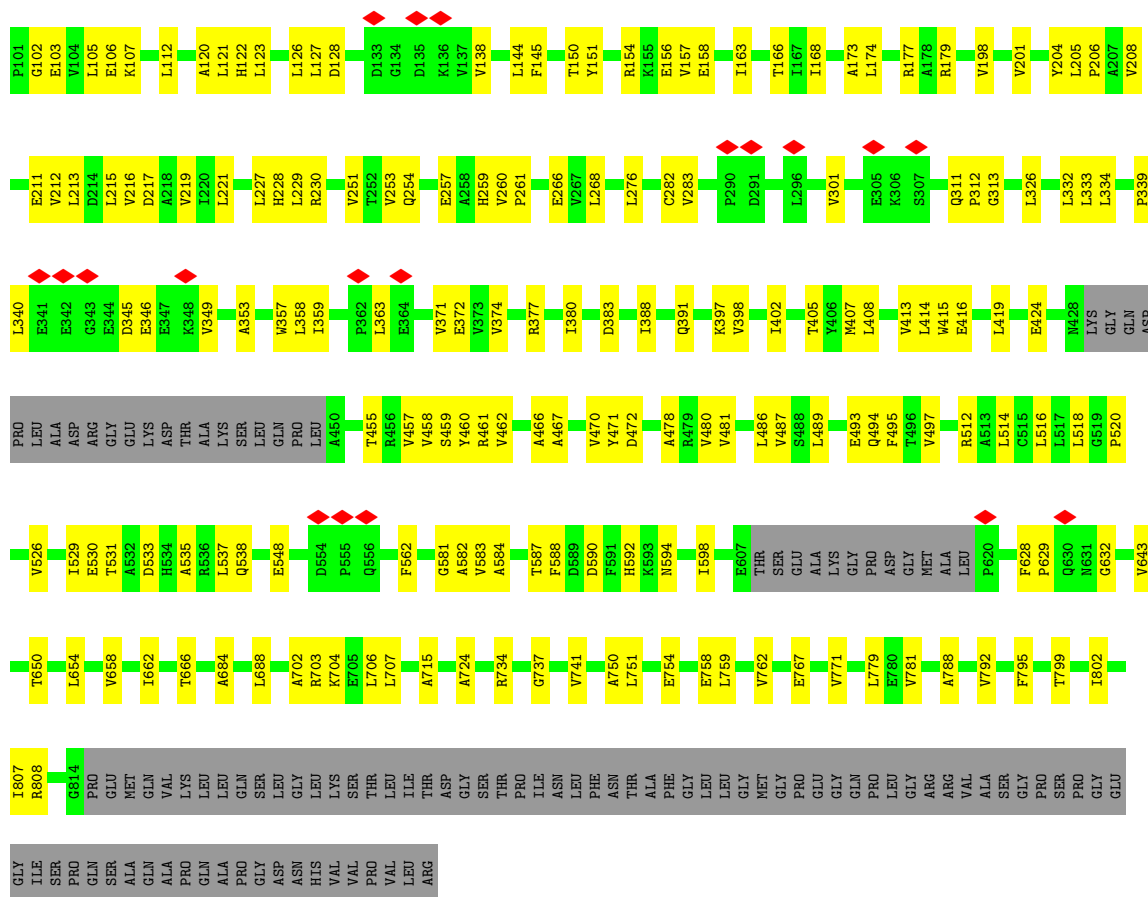


- Molecule 1: Major vault protein



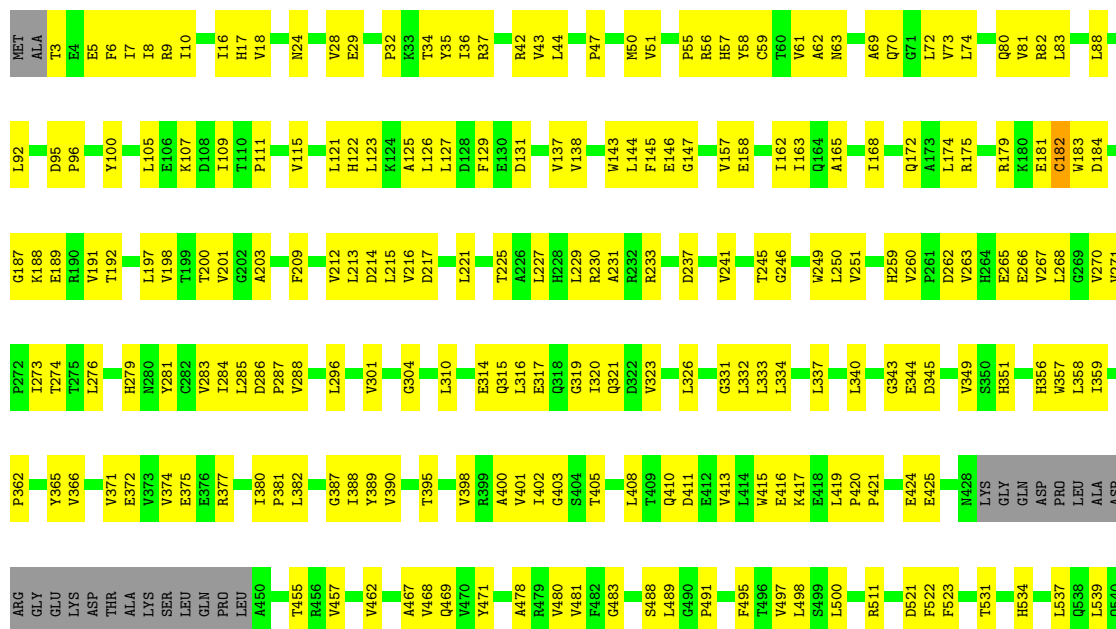
- Molecule 1: Major vault protein

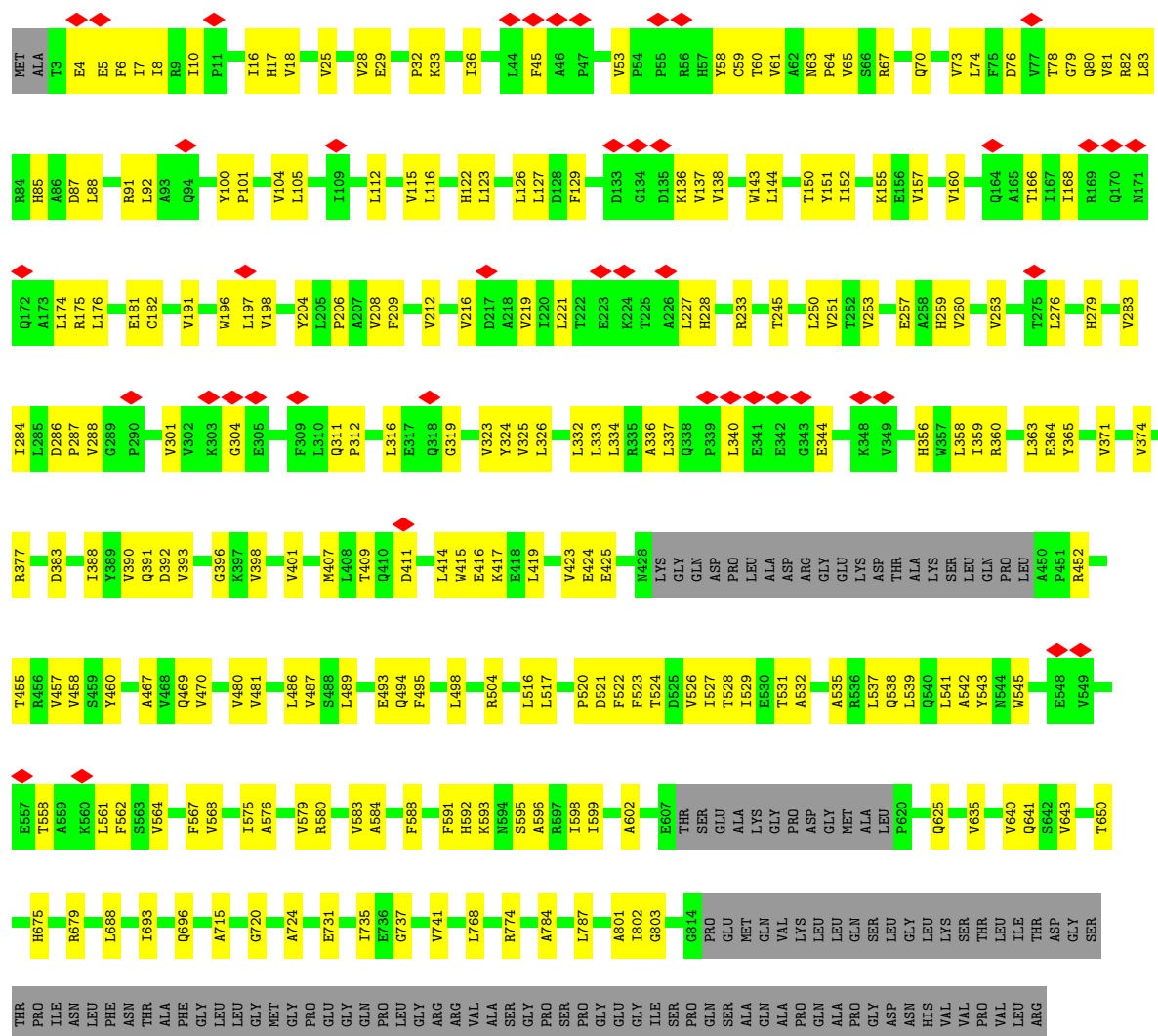




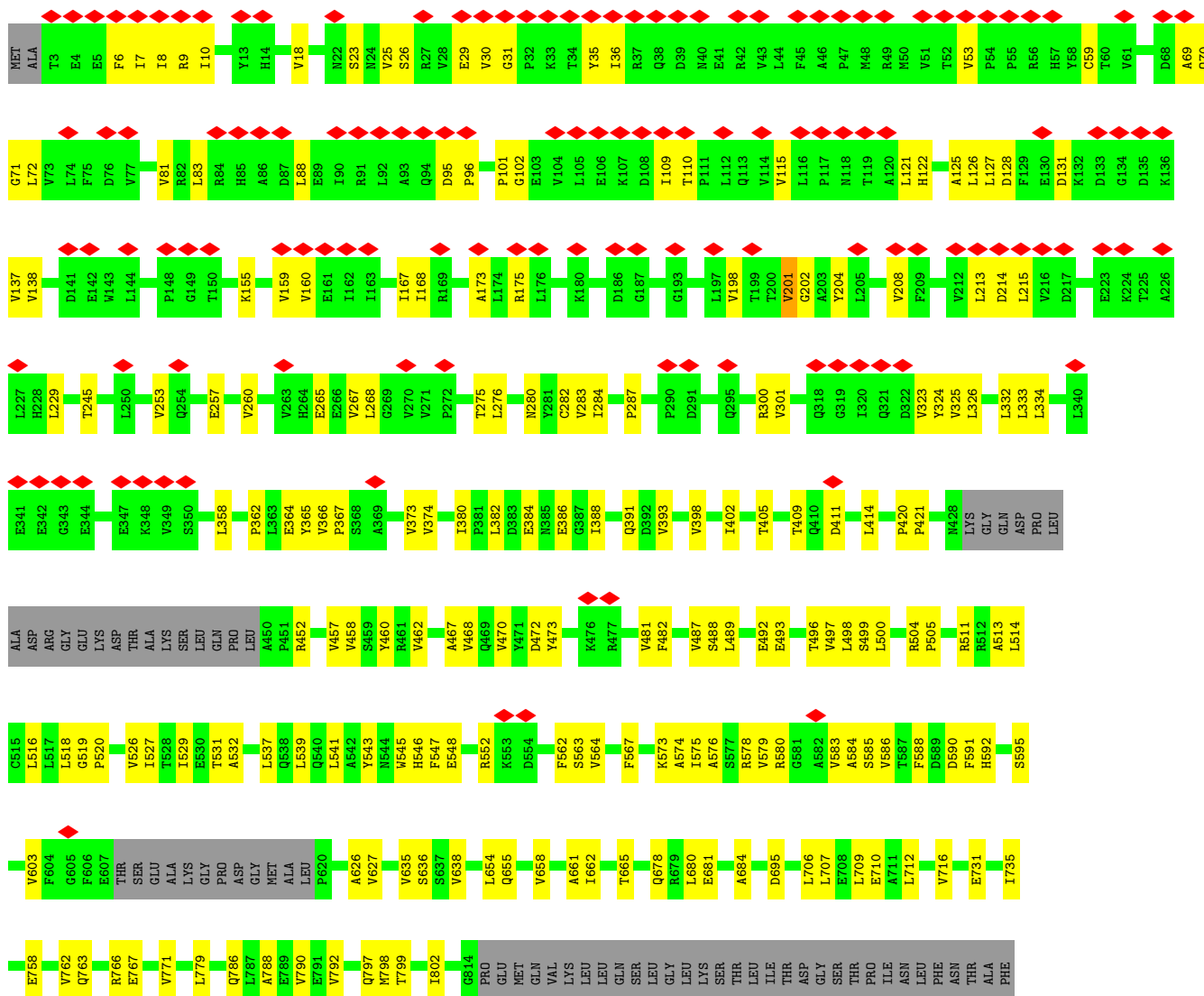
• Molecule 1: Major vault protein

Chain SB:





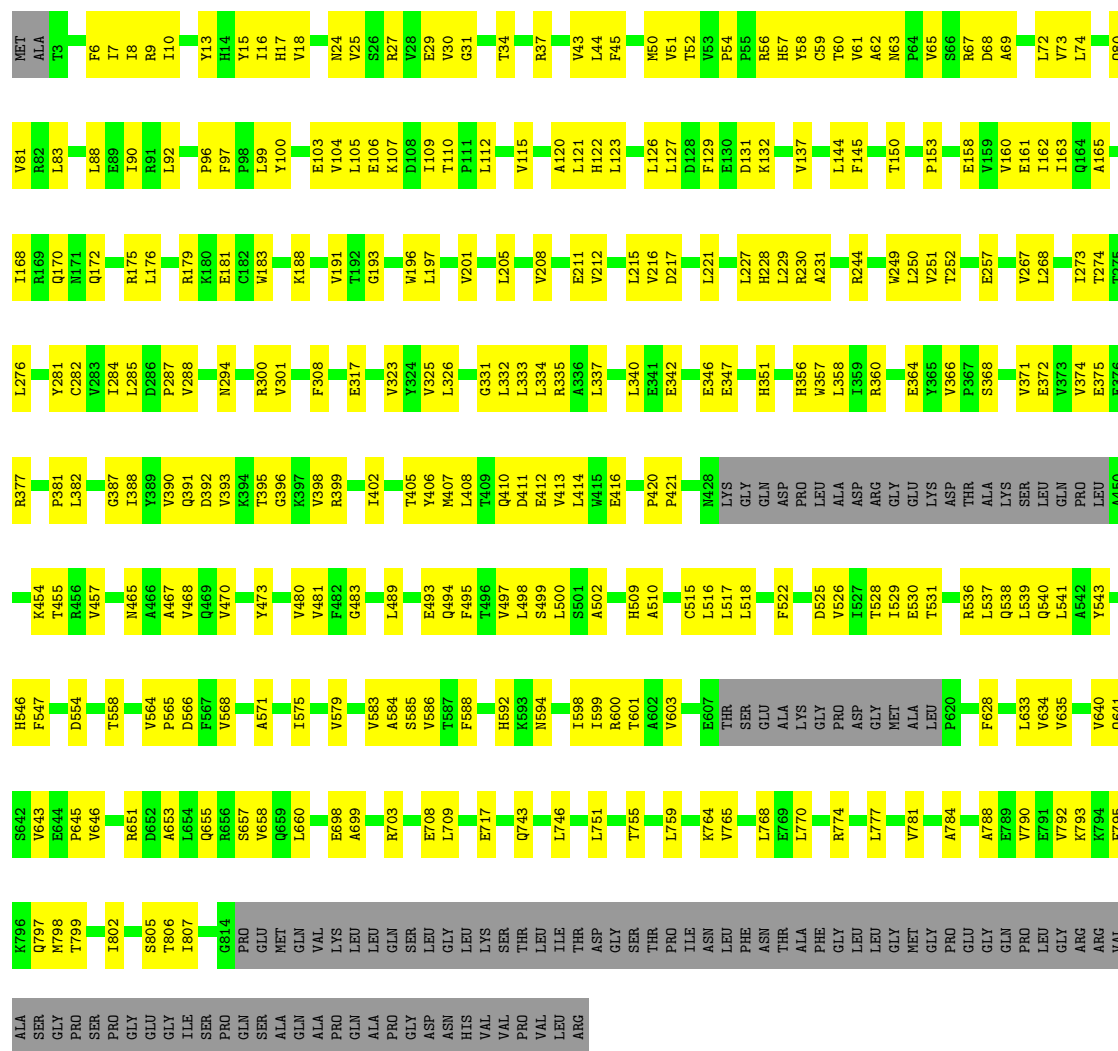
- Molecule 1: Major vault protein



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 GLN PRO PRO GLY ASP ASN HIS VAL VAL PRO VAL LEU ARG

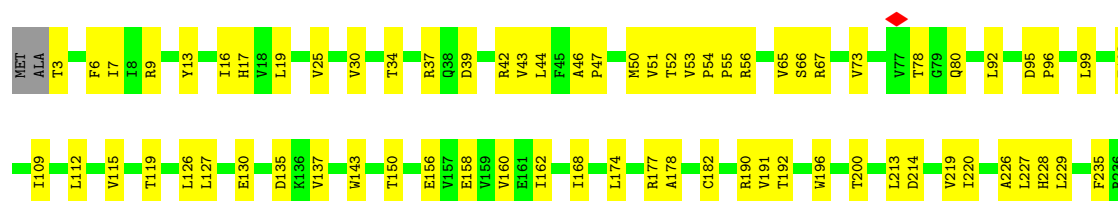
• Molecule 1: Major vault protein

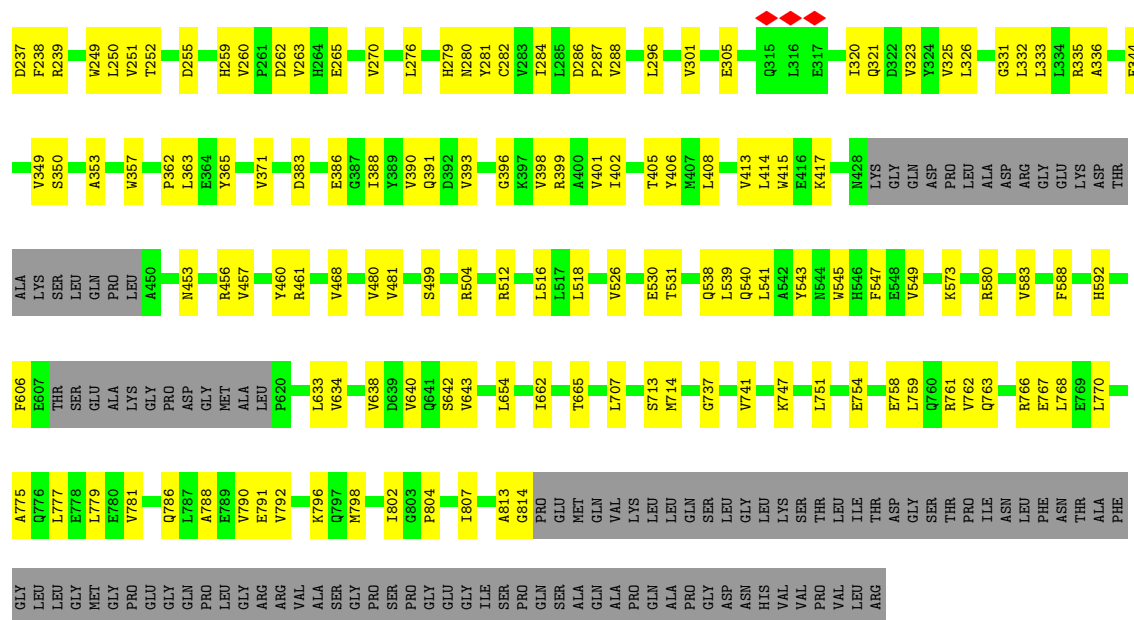
Chain UB:  55% 32% 13%



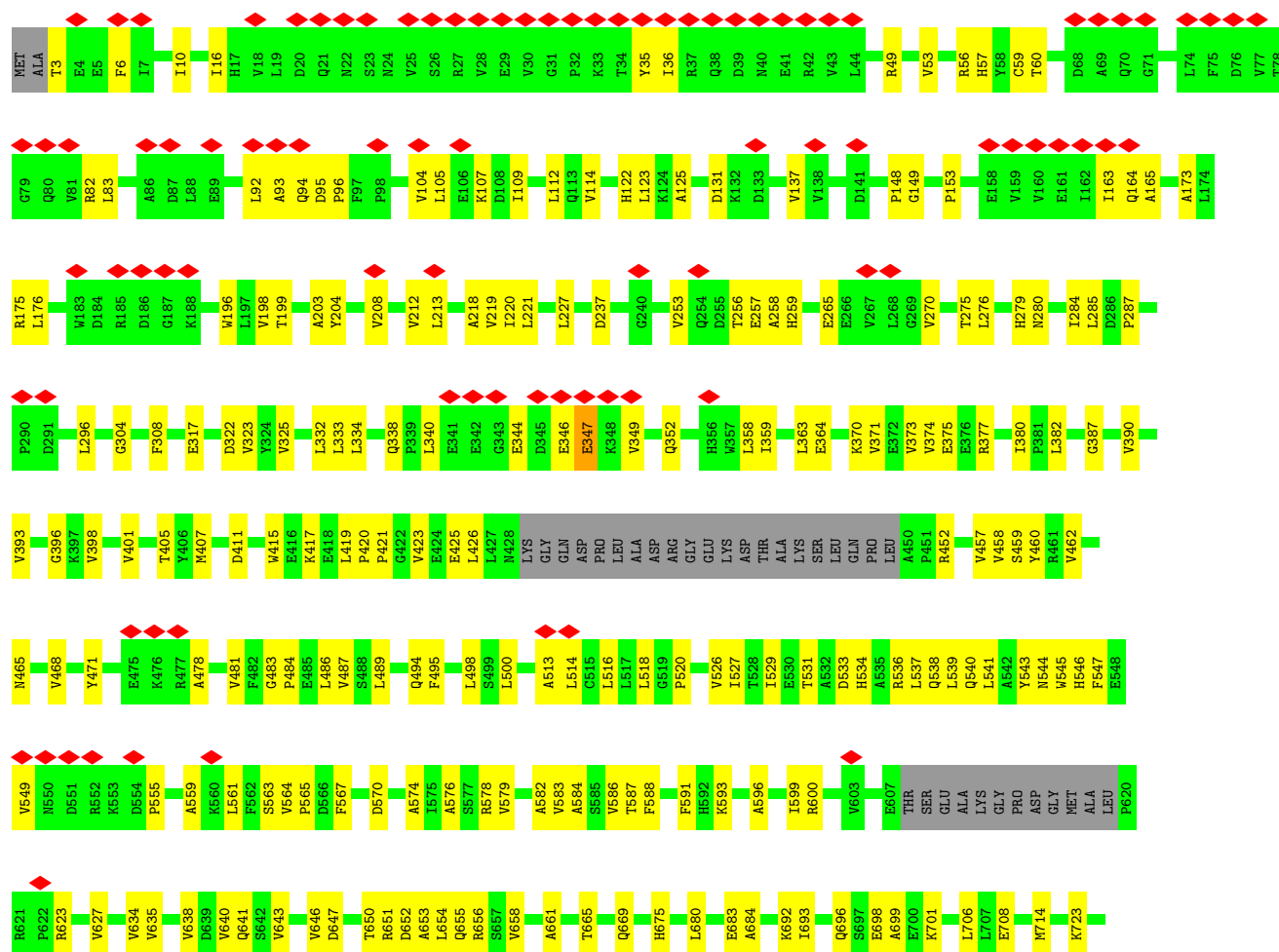
• Molecule 1: Major vault protein

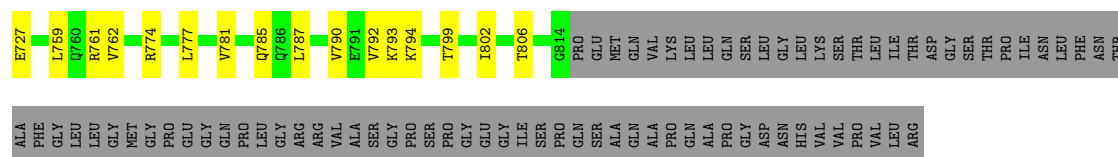
Chain V:  64% 23% 13%





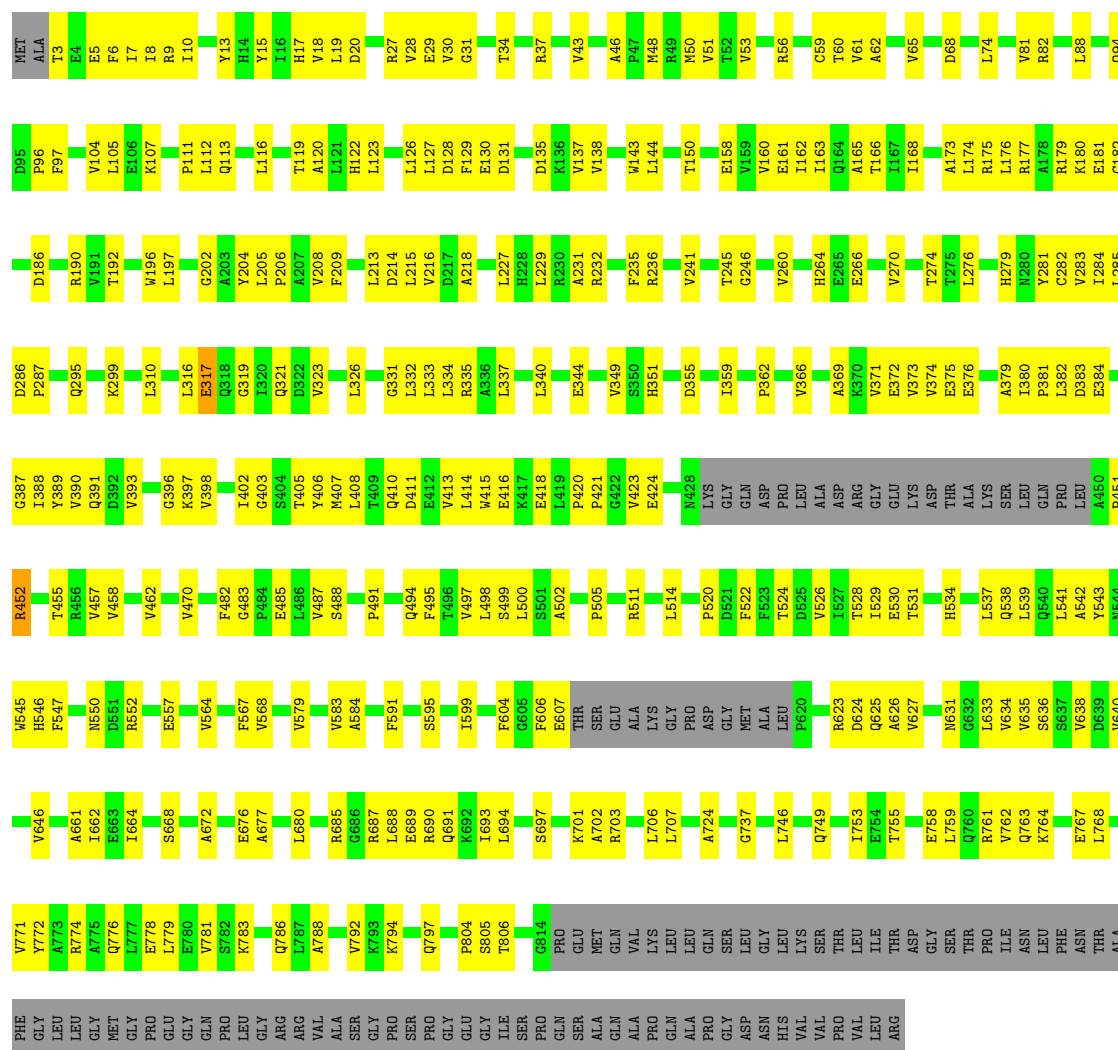
• Molecule 1: Major vault protein





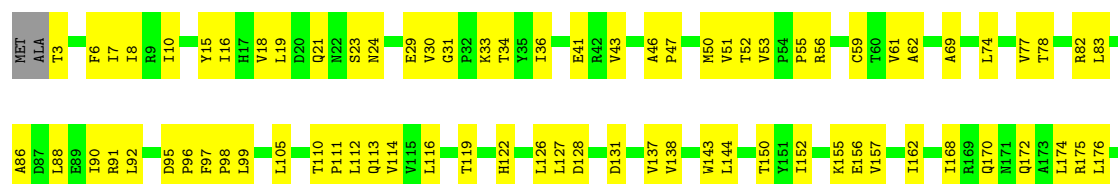
• Molecule 1: Major vault protein

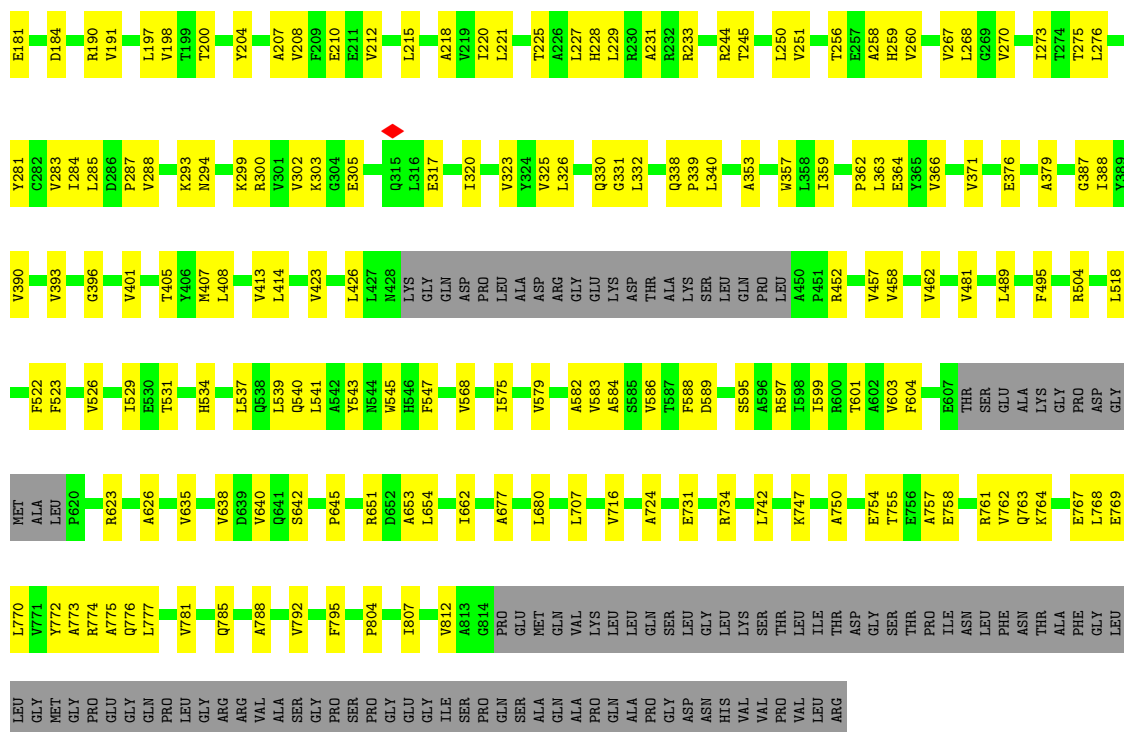
Chain VB: 53% 34% 13%



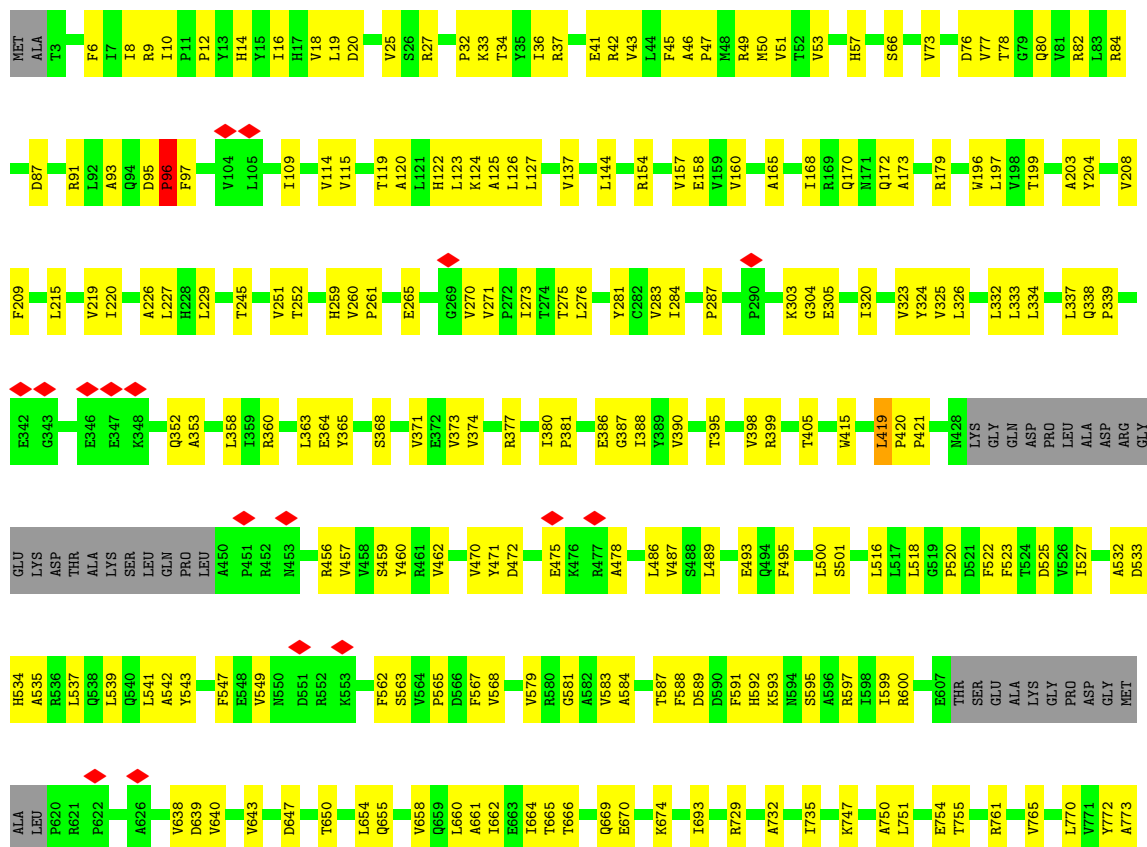
• Molecule 1: Major vault protein

Chain W: 60% 27% 13%





• Molecule 1: Major vault protein



R774	A775	Q776	L777	E778	L779	E780	V781	S782	Q786	L787	V790	E791	V792	K793	T799	I802	R808	G814	PRO	GLU	MET	GLN	ALA	VAL	LYS	LEU	LEU	GLN	PRO	GLY	ASP	GLY	LEU	LEU	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU
GLY	MET	GLY	PRO	GLY	GLY	GLN	PRO	LEU	GLY	ARG	ARG	VAL	ALA	SER	GLY	PRO	SER	SER	PRO	GLY	GLY	ILE	SER	PRO	GLN	ALA	ALA	GLN	PRO	GLY	ASP	GLY	LEU	LEU	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU

• Molecule 1: Major vault protein

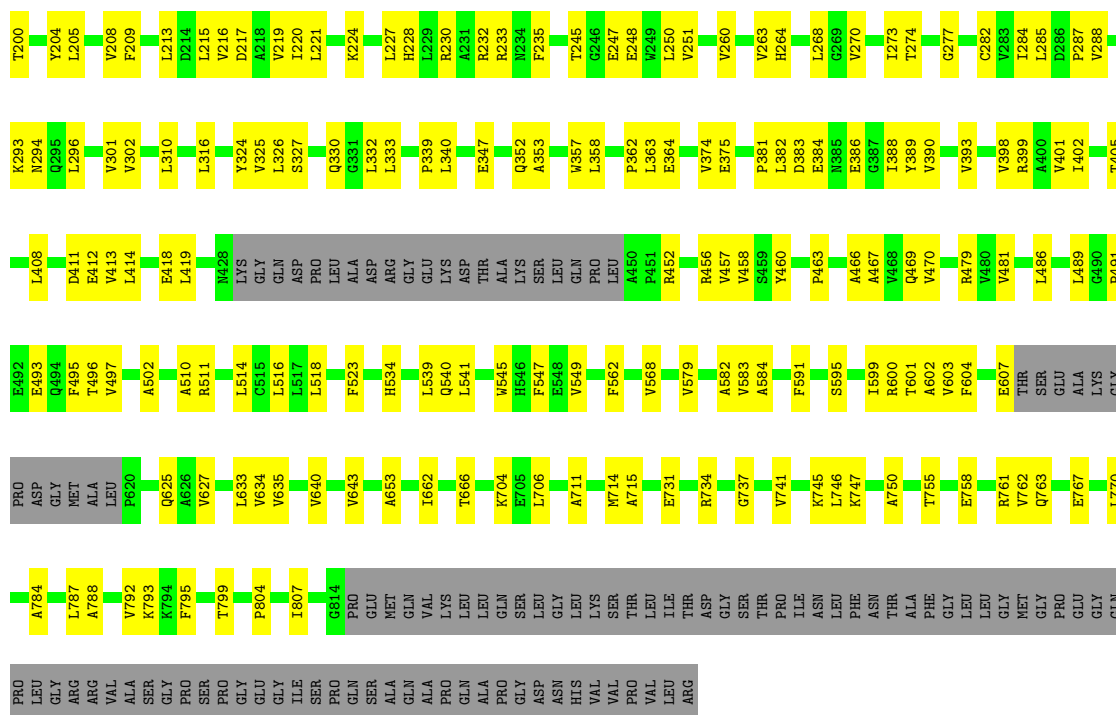
Chain WB:  53% 34% 13%

PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	MET	GLY	PRO	GLU	GLY	GLN	PRO	LEU	LEU	GLY	ARG	ARG	VAL	ALA	SER	GLY	PRO	GLY	PRO	SER	PRO	GLY	GLU	GLY	ILE	SER	PRO	GLN	SER	GLU	GLN	GLN	ALA	ALA	PRO	LYS	LEU	LEU	ALA	LEU	PRO	ALA	GLY	ASP	ASN	HIS	VAL	VAL	PRO	VAL	VAL	LEU	ILE	THR	ASP	GLY	ARG																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
W762	S636	Q763	S637	K764	E767	L768	E769	L770	V771	Y772	A653	I662	T666	V781	S782	Q786	E789	V790	E791	V792	Q797	M798	I802	T806	I807	R808	V812	A813	G814	PRO	GLU	MET	GLN	GLN	VAL	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	VAL	PRO	LYS	LEU	LEU	ALA	

• Molecule 1: Major vault protein

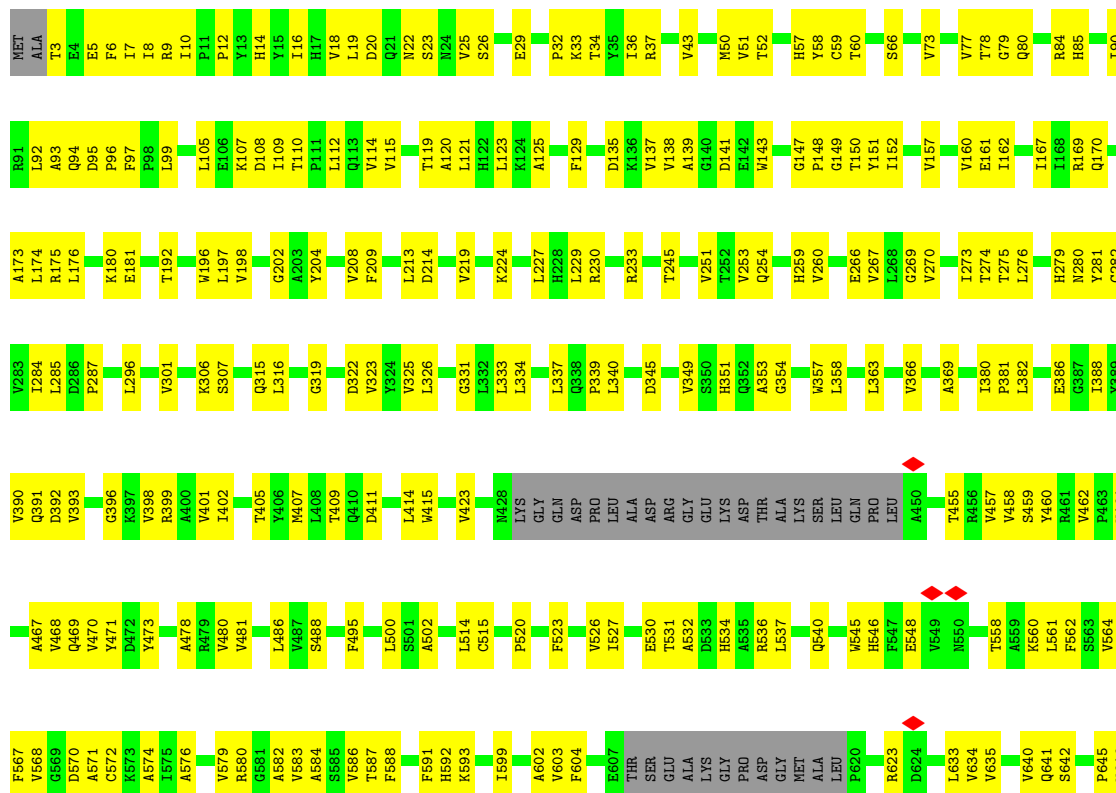
Chain X:  60% 27% 13%

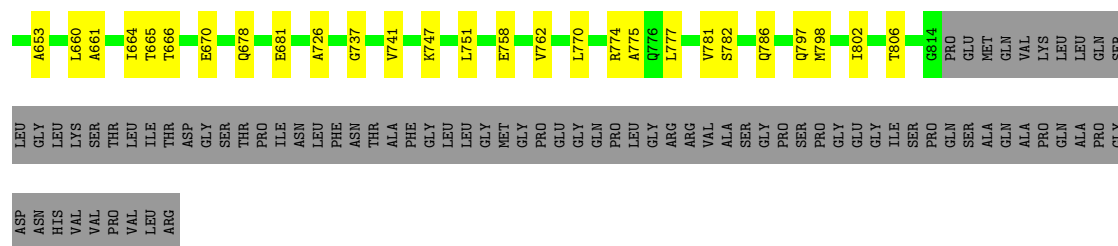
MET	ALA	T3	F6	I7	I8	R9	I10	H14	Y15	I16	N22	V25	V30	G31	P32	I36	V43	L44	F45	A46	P47	M48	R49	M50	V51	T52	P54	P55	R56	H57	Y58	C59	T60	V61	V65	S66	R67	V73	V77	T78	V81	R82	L83	I90	P96
Y100	E103	K107	D108	I109	L112	V115	L116	A120	L121	K124	A125	L126	L127	D128	F129	E130	D131	D135	K136	V137	V138	A139	G147	T150	V160	I167	I168	R169	Q170	N171	Q172	R175	L176	R177	E181	C182	E189	R190	V191	W196	L197	V198	T199		



• Molecule 1: Major vault protein

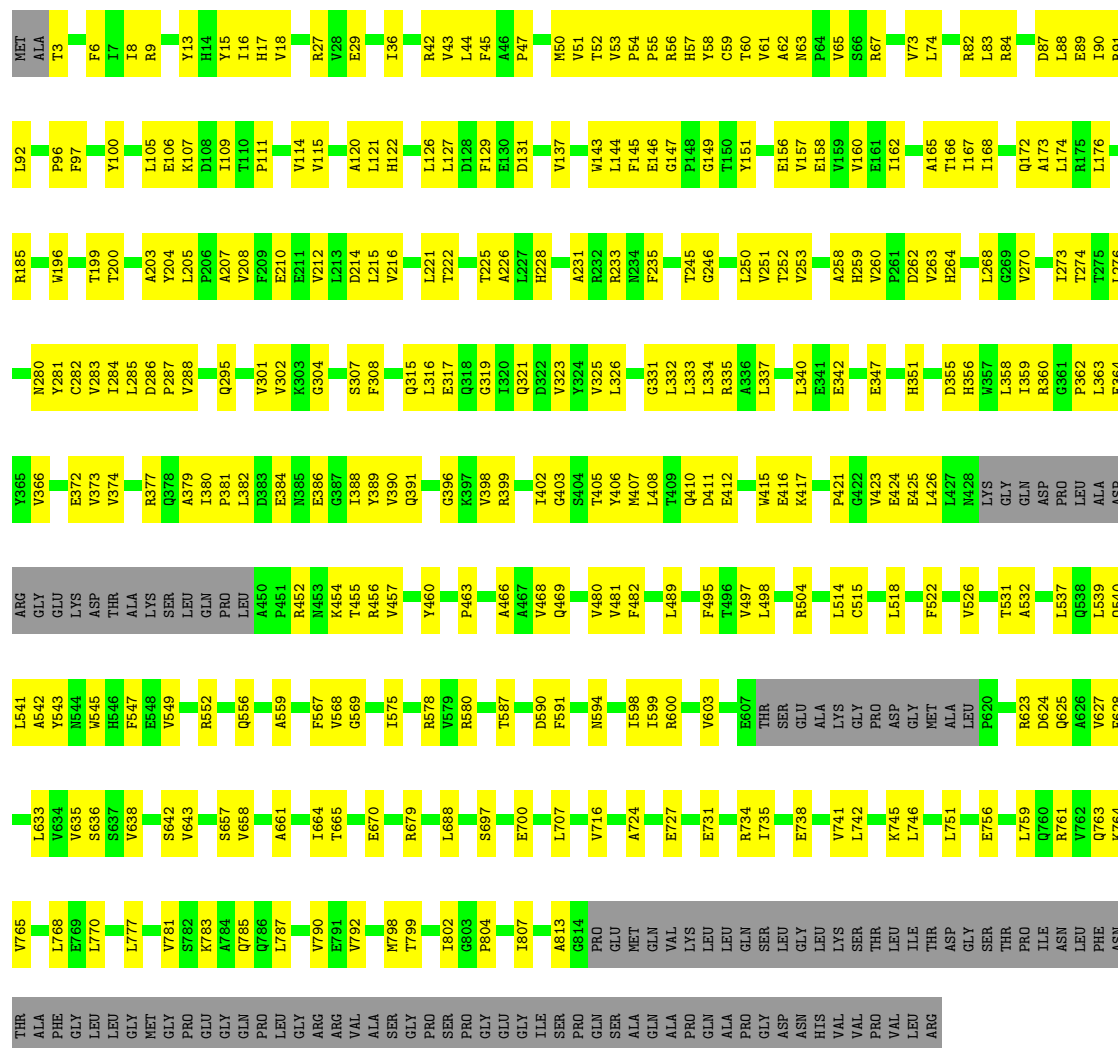
Chain XA: 57% 30% 13%





• Molecule 1: Major vault protein

Chain XB: 53% 34% 13%

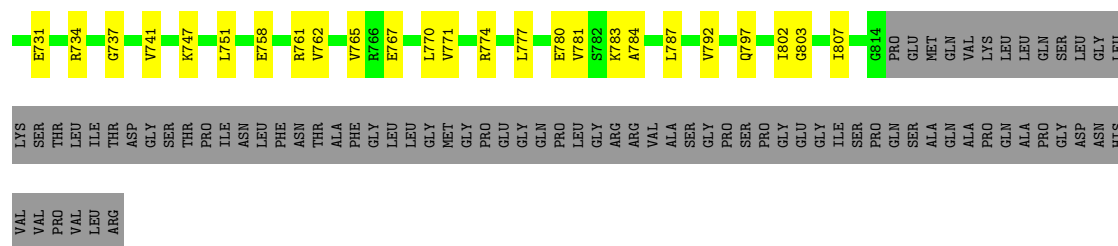


ASN	THR	E767	ALA	THR	E607	P484	Q391	G277	T192	R91
ALA	ALA	L770	ALA	THR	E607	E485	D392	Y281	W196	L92
PHE	GLY	L771	GLY	SER	GLU	L486	V393	Y281	L197	D95
LEU	LEU	Y772	ALA	GLU	ALA	L489	T395	I284	V198	P96
LEU	GLY	A775	LYS	LYS	LYS	Q494	K397	P287	T199	F97
MET	MET	E778	PRO	PRO	GLY	F495	V398	V288	V201	P98
GLY	GLY	E778	ASP	ASP	ASP	L500	R399	N294	Y204	Y100
PRO	PRO	V781	GLY	GLY	GLY	R511	I402	N294	L205	K107
GLY	GLY	Q786	MET	MET	MET	L516	T405	G297	P206	D108
GLN	GLN	P620	LEU	LEU	LEU	L517	L408	G304	A207	T110
PRO	PRO	K793	P620	P620	P620	F522	T409	L310	E210	P111
LEU	LEU	K794	Q625	Q625	Q625	F523	Q410	I320	E211	L112
GLY	GLY	F795	A626	A626	A626	T524	Q410	Q321	V212	
ARG	ARG	K796	F627	F627	F627	T524	L414	B322	L215	V115
VAL	VAL	P628	F628	F628	F628	T524	W415	Q322	L215	
ALA	ALA	I802	L633	L633	L633	T528	V423	V323	V219	N118
SER	SER	G803	V634	V634	V634	I529	E424	V324	L220	T119
GLY	GLY	P804	V634	V634	V634	E530	E424	V325	L221	A120
PRO	PRO	S805	S637	S637	S637	T531	K428	Q330	T222	L121
SER	SER	T806	V638	V638	V638	A535	LYS	G331	E223	L126
PRO	PRO	R807	P639	P639	P639	R536	GLY	L332	K224	L127
GLY	GLY	D809	V640	V640	V640	L537	GLN	L333	L227	D128
GLY	GLY		V643	V643	V643	Q538	ASP	L334	L228	F129
ILE	ILE	V812	V643	V643	V643	L539	PRO	R335	L229	E130
ALA	ALA	A813	E644	E644	E644	Y543	LEU	A336	R230	D135
PRO	PRO	G814	P645	P645	P645	N544	ALA	L337	A231	K136
GLN	GLN	PRO	V646	V646	V646	W545	ASP	Q338	R232	V137
SER	SER	GLU	V658	V658	V658	H546	ARG	P339	R233	V138
ALA	ALA	MET	V658	V658	V658	F547	GLY	L340		A139
GLN	GLN	GLN				F547	GLU		R244	
ALA	ALA	VAL	S697	S697	S697	E548	LYS	E344	T245	P148
PRO	PRO	LYS	L706	L706	L706	V549	ASP		G246	G149
GLN	GLN	LEU					THR	H351	E247	T150
ALA	ALA	LEU				R552	ALA	Q352	E248	
PRO	PRO	GLN	L709	L709	L709		LYS	A353	W249	K155
GLY	GLY	SER				D566	SER		L250	
LEU	LEU	LEU	E731	E731	E731	F567	LEU	W357	V251	V160
ASN	ASN	GLY	A732	A732	A732	V568	GLN	L358	E161	
HIS	HIS	LEU	R733	R733	R733		PRO	P359	T256	
VAL	VAL	LYS	R734	R734	R734	I575	LEU			
SER	SER	SER	I735	I735	I735				H259	T166
VAL	VAL	THR	E736	E736	E736	R580			I167	I168
PRO	PRO	THR	G737	G737	G737	G581	T455	E364	I168	
VAL	VAL	ILE				A582	R456		V263	
ARG	ARG	THR	L742	L742	L742	V587	V457	E376	H264	Q172
		ASP	Q743	Q743	Q743	T587	Y460		V267	A173
		GLY				F588			L268	L174
		SER	L746	L746	L746				G269	R175
		THR				D589	V468		V270	K179
		PRO	T755	T755	T755	D590	Q469		I273	K180
		ILE					V470		T274	E181
		ASN	E758	E758	E758	I599			T274	
		LEU				V603	R479		T276	R190
		PHE	V762	V762	V762				T276	V191

- Molecule 1: Major vault protein

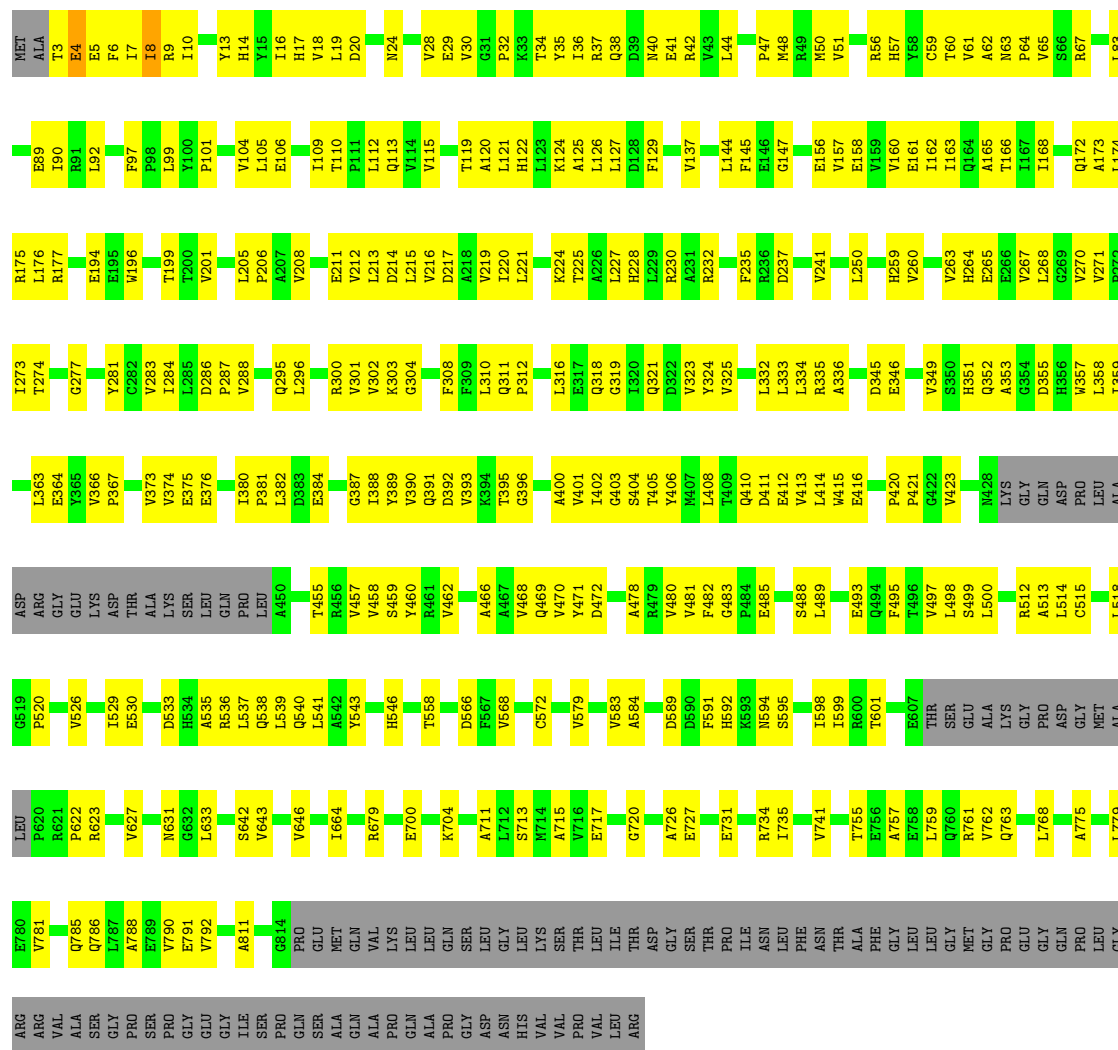
Chain YA:  57% 30% 13%

V583	A584	S585	V586	F591	H592	I598	I599	A602	V603	E607	THR	SER	GLU	ALA	LYS	GLY	PRO	ASP	GLY	MET	ALA	LEU	P620	A626	V627	G632	L633	V634	V635	V640	Q641	S642	V643	V658	Q659	L660	A661	I662	E663	I664	T665	L688	I693	S697	R703	M714		
Y471	D472	Y473	A478	P484	E485	L486	F495	T496	V497	L498	S499	L500	R511	R512	A513	L514	GLY	ASP	GLY	D521	F522	F523	I527	T531	L537	Q538	L539	Q540	L541	A542	Y543	W544	W545	E548	V549	P565	D566	F567	V568	A571	C572	I575	A576	S577	R578	V579	R580	
I380	P381	I388	Y389	V390	V393	G396	K397	V398	T405	Y406	T409	Q410	D411	L414	W415	E424	F425	L427	N428	LYS	GLY	GLN	ASP	PRO	ALA	ASP	ARG	V349	S350	H351	Q352	A353	G354	D355	R356	W357	L358	L363	E364	K370	V371	E372	V373	E376	R377	Q378	A379	
G202	A203	Y204	L205	P206	A207	V208	F209	E210	L215	V216	D217	T220	T225	A226	L227	H228	L229	R230	F235	R243	L250	V251	V252	V253	Q254	V260	V263	E266	V267	L268	G269	V270	I273	T274	T275	L276	H279	V283	T284	L285	V288	N294	Q295	L296				
R300	V301	V302	K303	K306	S307	P308	Q311	Q315	I320	V323	Y324	V325	L326	Q329	Q330	G331	L332	R335	A336	L337	Q338	P339	L340	D345	E346	E347	K348	V349	S350	H351	Q352	A353	G354	D355	R356	W357	L358	L363	E364	K370	V371	E372	V373	E376	R377	Q378	A379	
V115	L116	P117	N118	T119	A120	L121	R122	K124	A125	L126	L127	D128	F129	V137	V138	A139	W143	L144	F145	E146	T150	Y151	R154	V157	E158	V159	V160	E161	I162	T166	I167	L168	R169	Q170	N171	Q172	R175	L176	R177	A178	R179	R185	V191	T192	G193	W196	L197	V198
MET	ALA	T3	F6	I7	I8	R9	I10	P11	P12	I16	H17	V18	Q21	N22	E29	V30	G31	P32	K33	T34	V43	L44	F45	A46	P47	M50	V51	V52	V53	B56	R57	Y58	N63	P64	D68	A69	R84	E89	L92	A93	Q94	D95	P96	L112	Q113	V114		



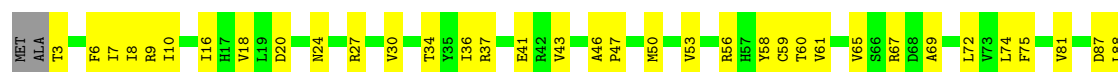
• Molecule 1: Major vault protein

Chain YB: 53% 34% 13%



• Molecule 1: Major vault protein

Chain Z: 57% 30% 13%



VAL	VAL	VAL	VAL	VAL	ARG	LYS	Q743	SER	L486	G396	F308	E89
	SER	GLU	ALA	LYS	V487		F309	I90				
THR	THR	LEU	GLY	LYS	S488	L310	R91					
LEU	LEU	LEU	GLY	GLY	F495	Q315	L92					
ARG	THR	THR	ASP	PRO	L500	L316	A93					
	ASP	E756	GLY	GLY	R507	E317	L105					
	SER	A757	MET	ALA	T409	D322	I109					
	THR	E758	LEU	LEU	Q410	V323	T110					
	PRO	L759	ALA	ALA	Y324	E211	P111					
	ILE	Q760	P620	P620	V325	V212	L112					
	ASN	V761	R621	R621	L326	L213	Q113					
	LEU	V762	P622	A513	G331	D214	V114					
	PHE	R623	R623	L514	L332	I220	V115					
	ASN	V765	ASN	C515	L333	L221	L116					
	THR	R766	V627	L516	L334	L221	L116					
	ALA	E767	V634	D521	R335	L227	A120					
	PHE	L770	V635	F522	A336	H228	H122					
	GLY	L770	S636	F523	L337	L229	L123					
	LEU	L777	S637	T524	Q338	R230	L126					
	GLY	E778	V638	T528	P339	A231	L127					
	MET	L779	D639	F529	L340	R244	D128					
	GLY	E780	V640	I529	E341	L250	V137					
	PRO	V781	Q641	E530	E342	V251	V138					
	GLU	S782	S642	T531	D345	T256	A139					
	GLY	K783	V643	A532	H351	P261	W143					
	GLN	A784	V646	D533	Q352	L144	L144					
	PRO	Q785	V646	H534	G354	E266	V157					
	LEU			A535	GLY	V267	E158					
	GLY	V792	L654	L539	GLY	L268	V159					
	ARG	K793	ARG	V658	LYS	G269	V160					
	ARG	R794	VAL		ASP	V270	I162					
	ALA	M798	ALA		THR	I273	A165					
	SER	I802	SER		ALA	T274	T166					
	GLY	G803	PRO	L688	THR	L276	Q170					
	PRO	G803	SER	P692	ALA	H279	L174					
	SER	P804	SER	K692	LYS	N280	R175					
	PRO	S805	PRO	Q805	SER	Y281	L176					
	GLY	T806	GLY	Q696	LEU	I284	R179					
	GLU	R807	GLY	R580	GLN	D286	K180					
	GLY	R808	GLY	K701	LEU	P287	E181					
	ILE		ILE		A450	L296	G187					
	SER	A813	GLN	L712	T455	L388	K188					
	PRO	G814	GLN	V716	R456	V389	K188					
	GLN		SER	GLU	V457	V390	V191					
	SER	GLU	ALA		V458	Q391	V191					
	ALA	MET	GLN	A726	S459	D392	W196					
	GLN	GLN	ALA	E727	Y460	G304	L197					
	ALA	VAL	ALA	S728								
	PRO	LYS	PRO	LYS								
	GLN	LEU	GLN	LEU	V468							
	ALA	LEU	ALA	LEU	Q469							
	PRO	GLN	PRO	GLN	V470							
	GLY	LEU	GLY	E736	Y471							
	ASP	SER	LEU	E736	F605							
	ASN	ASN	GLY	V741	E607							
	HIS	HIS	LEU	L742	THR							

● Molecule 1: Major vault protein

Chain ZA:

MET	ALA	T3	F6	I7	I8	R9	I10	P11	Y13	I16	H17	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	G146	G147	T150	E156	V160	E161	I162	V168	R169	G170	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	D392	V393	K394	T395	G396	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			

PRO	VAL	LEU	ARG	THR	LEU	ILE	THR	ASP	GLY	SER	THR	PRO	ILE	ASN	LEU	PHE	ASN	THR	ALA	PHE	GLY	LEU	LEU	GLY	MET	GLY	PRO	GLU	GLN	PRO	LEU	GLY	ARG	ARG	VAL	VAL	ALA	GLY	GLY	ILE	PRO	GLN	SER	ALA	GLN	ALA	PRO	GLN	ALA	LEU	GLN	PRO	GLY	ASP	ASN	HIS	VAL	VAL	SER							
				K723			A732		I735	E736	G737		V741		L751		E754		Q763	K764		L768		Y772		A775	Q776	L777		V781		A784		L787		E791	V792	K793	K794		T799		I802	G803	P804		I807			G814	PRO	GLU	MET	GLN	VAL	LYS	LEU	ALA	LEU	GLN	ASP	GLY	LEU	HIS	VAL	SER
				F591			I598	I599		A602	V603		E607	THR	SER	GLU	ALA	LYS	GLY	PRO	ASP	GLY	MET	ALA	LEU	P620		V627		Q630	N631	L632	L633	V634	V635		V638	D639	V640		V643	E644	V645	V646		R651		L654		A661		H675		L688	E689	R690		I693		E700		R703		A722		

● Molecule 1: Major vault protein

Chain ZB: 56% 31% 13%

SER	GLU	E708	S595	R477	T405	V325	G331	N234	L121	T225	D108	MET	ALA	T3
ALA	MET	A711	S595	R477	T405	V325	G331	N234	L121	T225	D108	MET	ALA	T3
GLN	GLN	L712	F606	A478	M407	L408	G319	T110	P111	L112	E4	GLN	GLN	E4
PRO	LYS	V716	E607	R479	T409	L408	Q321	L227	H228	L229	P111	PRO	PRO	E5
GLN	LEU	THR	THR	V480	Q410	D411	V323	R230	A231	Q113	F6	GLN	GLN	F6
ALA	LEU	A724	SER	F482	E481	D411	V323	R230	A231	Q113	F6	ALA	ALA	I7
PRO	GLN	E725	GLU	G483	E412	V324	Y324	R232	R233	V115	I8	PRO	PRO	I8
GLY	SER	A726	ALA		V413	R233	V325	R233	R233	V115	I8	GLY	GLY	R9
ASP	LEU		LYS	V487	L414	R234	V325	R234	L121			ASP	ASP	
ASN	GLY	A730	GLY	S488	W415	F235	G331	F235	H122	Y13		ASN	ASN	Y13
HIS	LEU		PRO	L489	E416		L332					HIS	HIS	
VAL	SER	I735	ASP	LYS	V241	S242	L333	V241	A125	I16		VAL	VAL	I16
VAL	THR		GLY	LYS	R243	R243	L334	L126	L126	H17		VAL	VAL	H17
PRO	THR		MET	Q494	R335	R335	R335	L127	L127			PRO	PRO	
VAL	LEU	E738	ALA	F495	L340	R244	L340	D128	D128	N24		VAL	VAL	N24
LEU	ILE		LEU	T496	L427	T245		R244	F129	V28		LEU	LEU	V28
THR	THR	L742	P620	V497	N428	V251	D345	E29	V30			THR	THR	E29
ASP	ASP			L498	LYS	E346	E346	V137	V30			ASP	ASP	V30
GLY	GLY	L751	Q625	S499	GLN	T253	V349	V137				GLY	GLY	
SER	SER		A626	L500	ASP	V253	S350	L144	T34			SER	SER	T34
THR	THR	E754	V627	R504	PRO	V256	S350	T150	F45			THR	THR	
PRO	PRO				LEU	T256		T150				PRO	PRO	
ILE	ILE	L759	V634	L514	ALA	I152	A353	I152				ILE	ILE	
ASN	ASN	Q760	V635	C515	ASP	V263	ASP	V263	M50			ASN	ASN	M50
LEU	LEU	R761	S636	L516	ARG	H264	ARG	V51	V51			LEU	LEU	V51
PHE	PHE	V762	S637	L517	GLY	L358	GLY	V57	V53			PHE	PHE	
ASN	ASN	Q763	V638	L518	GLU	L358	GLU	V160				ASN	ASN	
THR	THR	K764	D639	L518	LYS	E364	LYS	E161	H57			THR	THR	H57
ALA	ALA	V765	G519	ASP	ASP	V365	ASP	I162	V58			ALA	ALA	V58
PHE	PHE	R766	Q641	P520	THR	V366	THR	I163	C59			PHE	PHE	
GLY	GLY	E767	S642		ALA	P367		I163				GLY	GLY	
LEU	LEU	L768	V643	V526	LYS		ALA	V271	T60			LEU	LEU	
LEU	LEU	E769	E644	I527	LYS	P272	LYS	P272				LEU	LEU	
GLY	GLY	L770	V645	T528	SER	I167	SER	I167				GLY	GLY	
MET	MET	V771	V646	I529	LEU	T274	LEU	T274	P64			MET	MET	
GLY	GLY	Y772	D647		GLN	T275	GLN	R169				GLY	GLY	
PRO	PRO	A773		L537	PRO	L276	PRO					PRO	PRO	
GLU	GLU	R774	T650	Q538	LEU	Q172	LEU	Q172	A69			GLU	GLU	
GLY	GLY	A775		L539	A450	A173	A450	A173				GLY	GLY	
GLN	GLN	Q776	V658	Q540	P451	L74	A379	L74	L72			GLN	GLN	L72
PRO	PRO	L777		L541	R452	R175	I380	R175	V73			PRO	PRO	V73
LEU	LEU	E778	A677	A542	N453	L284	P381	L284	L74			LEU	LEU	L74
GLY	GLY	L779			K454	R185		R185				GLY	GLY	
ARG	ARG		L680	W545	T455	L285	G387	L285	V81			ARG	ARG	V81
ARG	ARG	Q785		H546	R456	D286	I388	D286	L83			ARG	ARG	L83
VAL	VAL	Q786	L688		V457	V288		V288				VAL	VAL	
ALA	ALA	L787	E689	T558	V458	E89	Q391	E89	I90			ALA	ALA	I90
SER	SER	A788	R690			V198	D392	V198	R91			SER	SER	
GLY	GLY	E789		F562	V393	Y204	K300	Y204	L92			GLY	GLY	L92
PRO	PRO	V790	L694	P565	H465		V301					PRO	PRO	
SER	SER	E791	D695		P463	S395	K394	S395	P96			SER	SER	P96
PRO	PRO	V792	Q696	I575	A466	G396	G396	G396	P97			PRO	PRO	P97
GLY	GLY				A467	F308	V398	F308	P98			GLY	GLY	
GLY	GLY	R808	A699	V579	V468	R399	R399	L310	L99			GLY	GLY	L99
ILE	ILE	V812	A702		Q469	A400	A400	L221	Y100			ILE	ILE	
SER	SER	A813		V583	V470	V401	V401	T222	Y100			SER	SER	
PRO	PRO	G814	L706		Y471	L402	L402	E223				PRO	PRO	
GLN	GLN		L707	F591	D472			K224	L105			GLN	GLN	

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 [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.24	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.

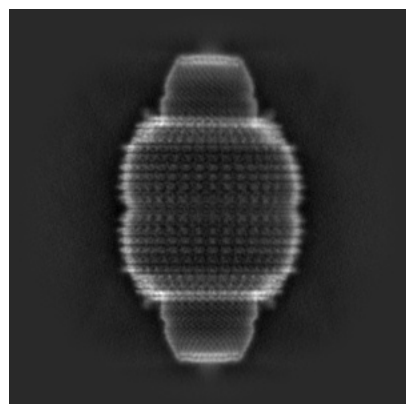
6 Map visualisation [i](#)

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.

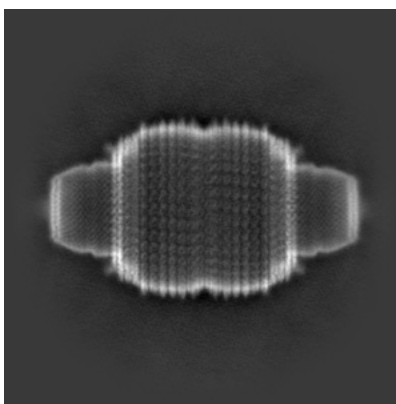
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

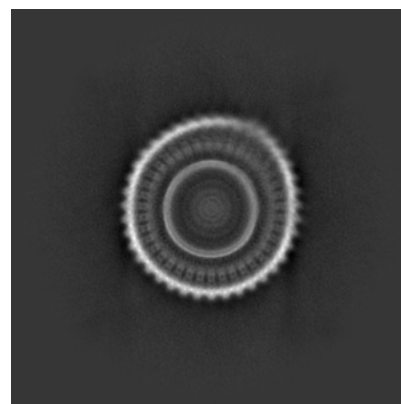
6.1.1 Primary map



X

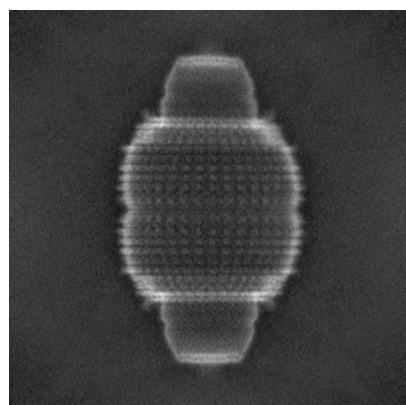


Y

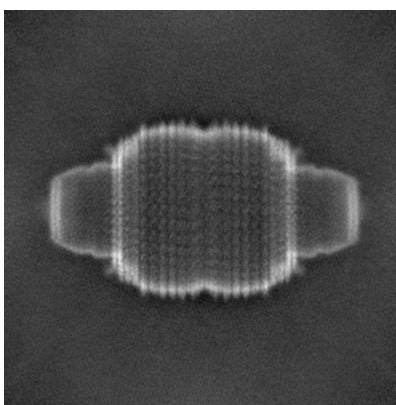


Z

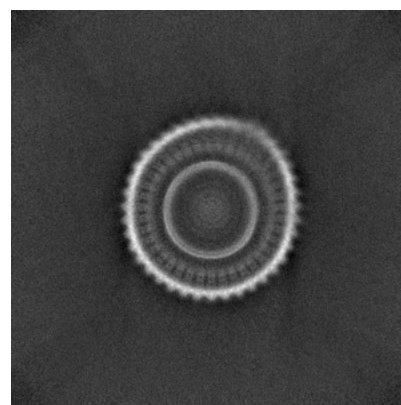
6.1.2 Raw map



X



Y

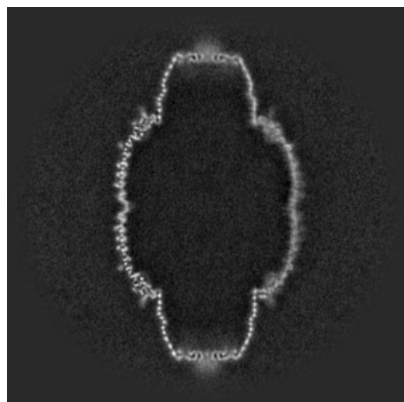


Z

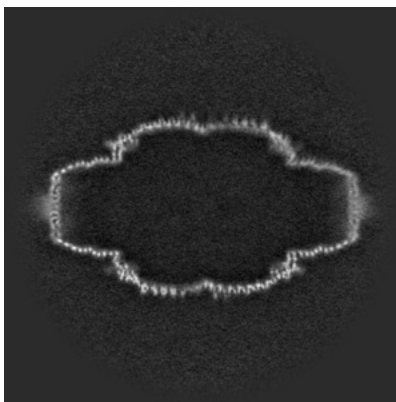
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

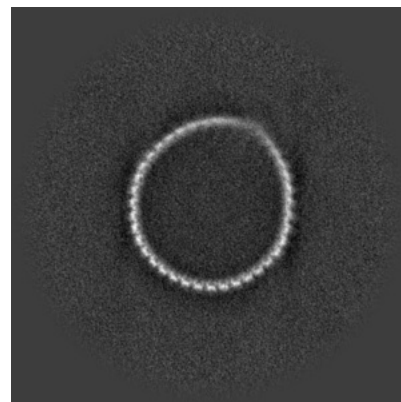
6.2.1 Primary map



X Index: 512

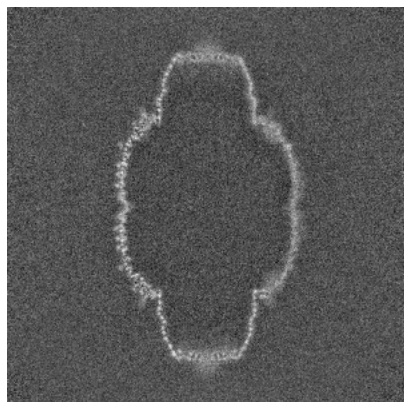


Y Index: 512

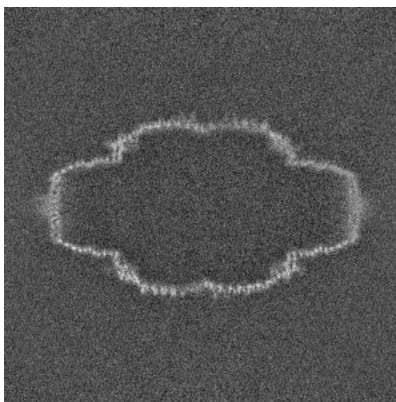


Z Index: 512

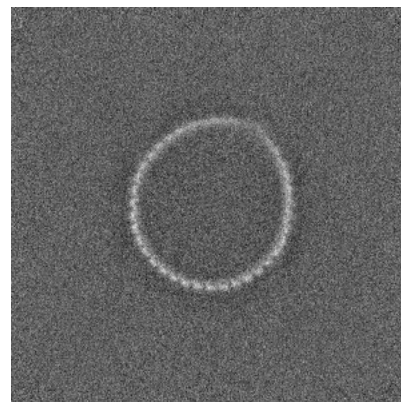
6.2.2 Raw map



X Index: 512



Y Index: 512

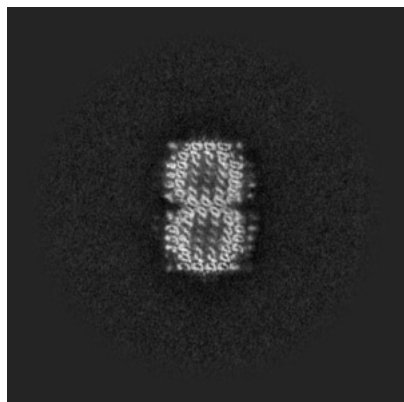


Z Index: 512

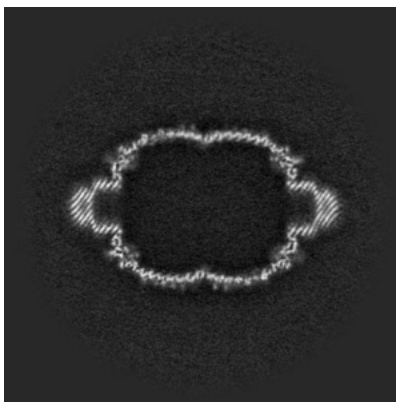
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

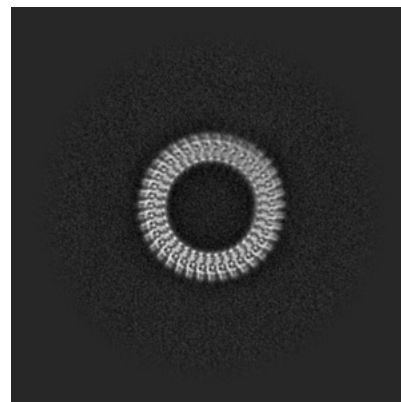
6.3.1 Primary map



X Index: 310

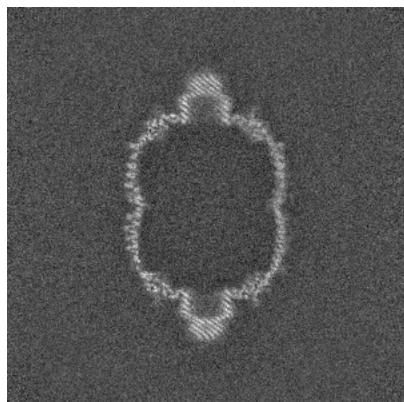


Y Index: 404

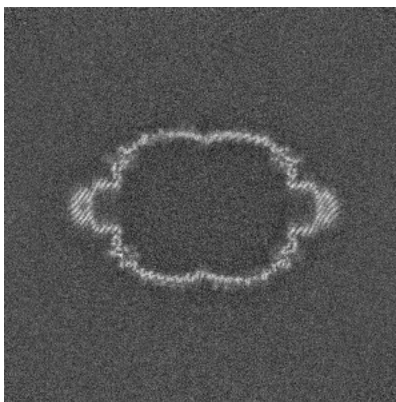


Z Index: 296

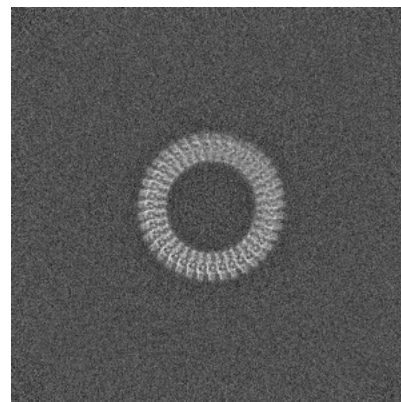
6.3.2 Raw map



X Index: 404



Y Index: 404

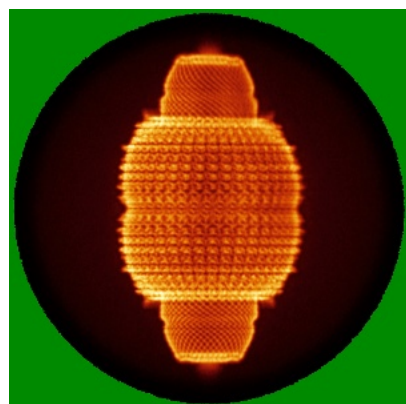


Z Index: 297

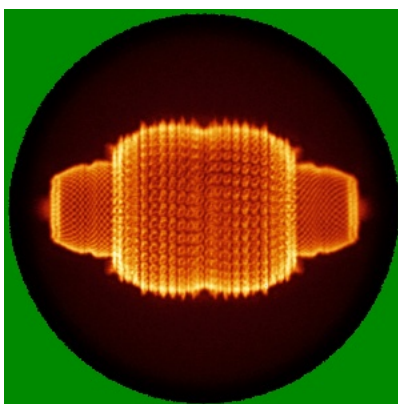
The images above show the largest variance slices of the map in three orthogonal directions.

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

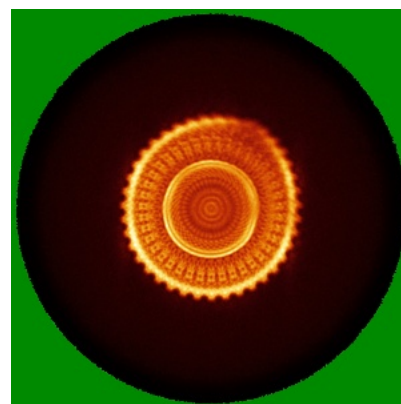
6.4.1 Primary map



X

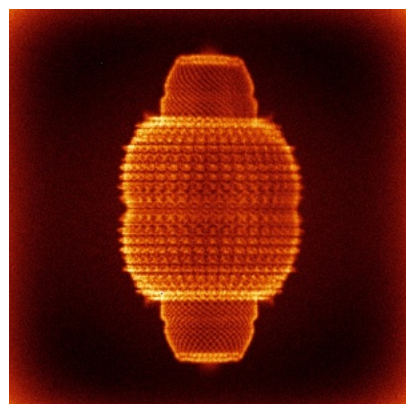


Y

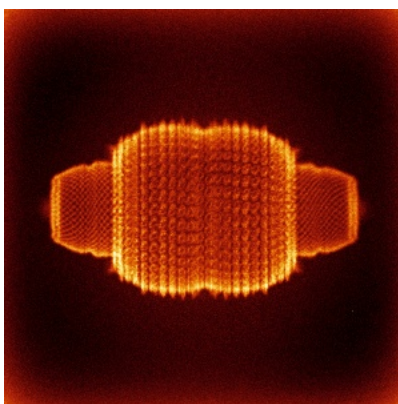


Z

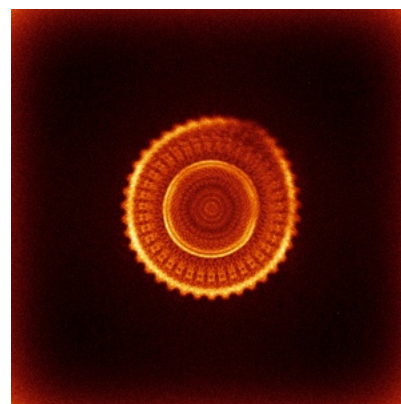
6.4.2 Raw map



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](#)

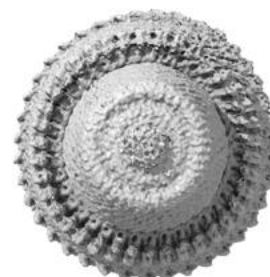
6.5.1 Primary map



X



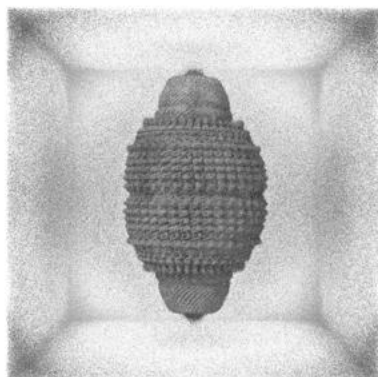
Y



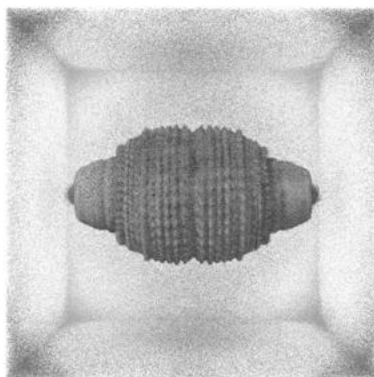
Z

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.

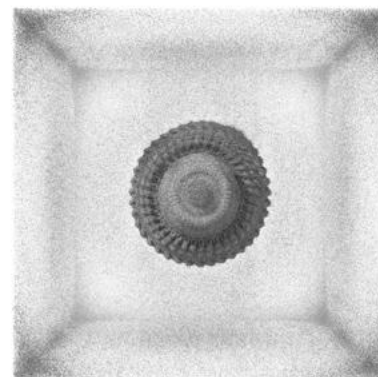
6.5.2 Raw map



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.

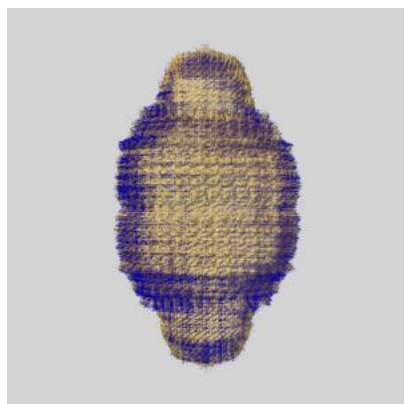
6.6 Mask visualisation [i](#)

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

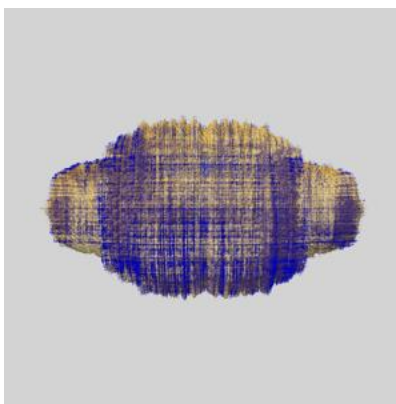
A mask typically either:

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

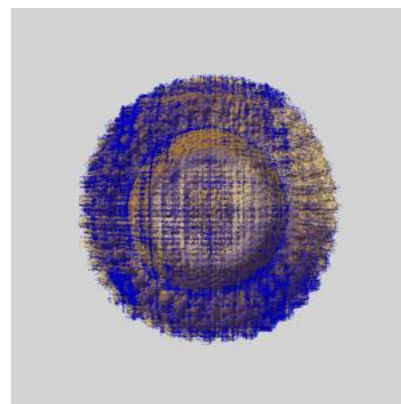
6.6.1 emd_53423_msk_1.map [i](#)



X



Y

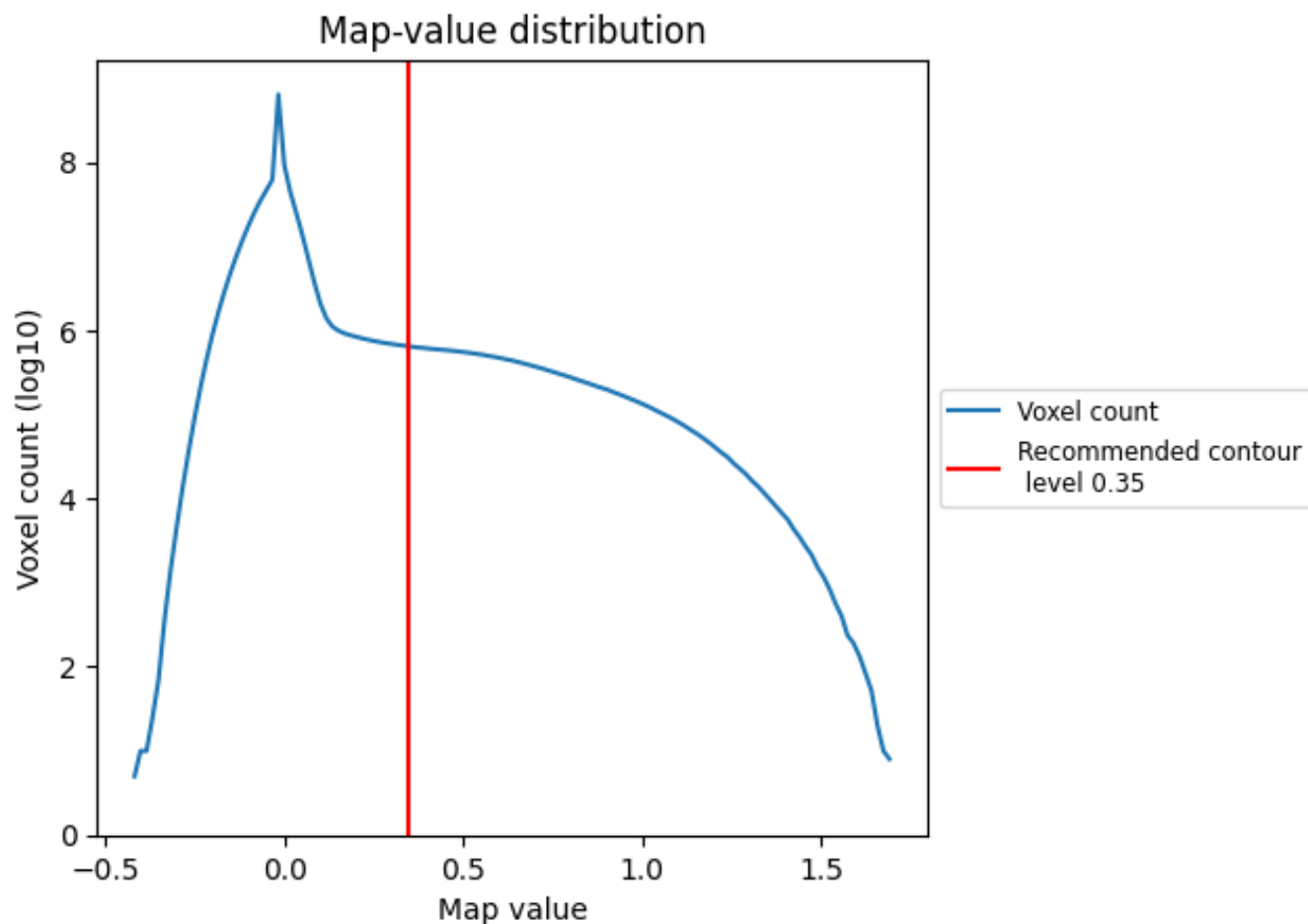


Z

7 Map analysis [i](#)

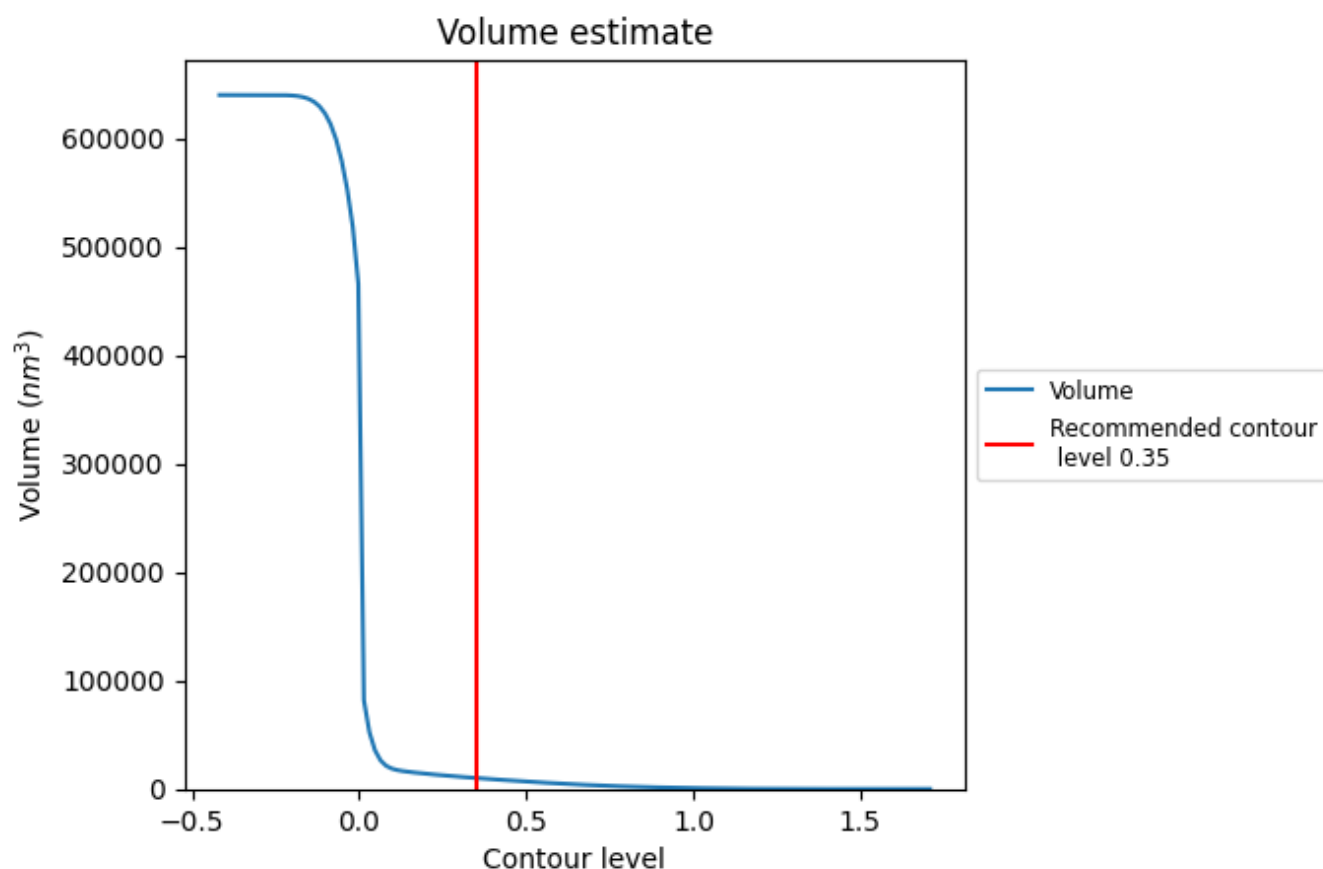
This section contains the results of statistical analysis of the map.

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.

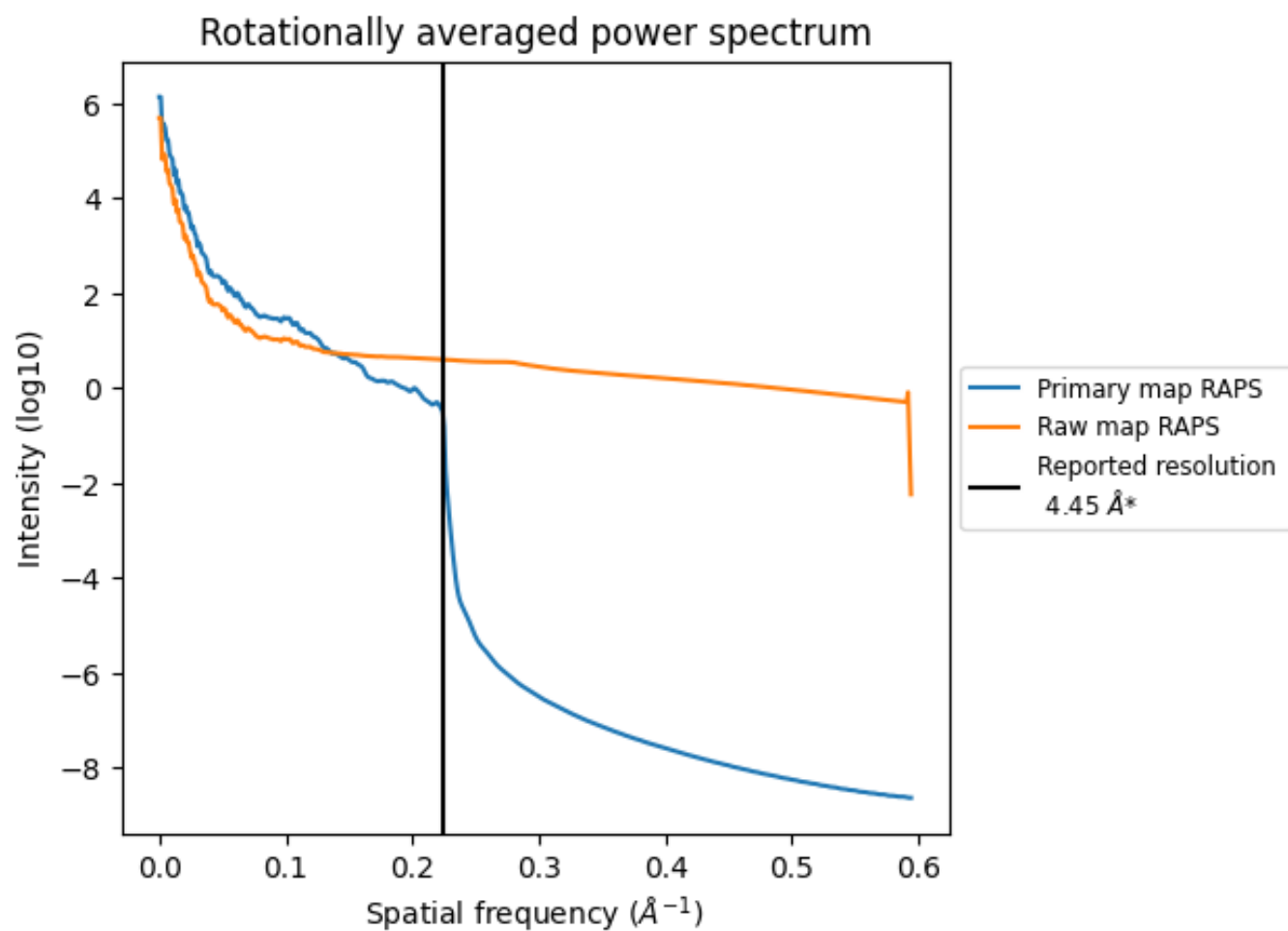
7.2 Volume estimate [i](#)



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 ⓘ

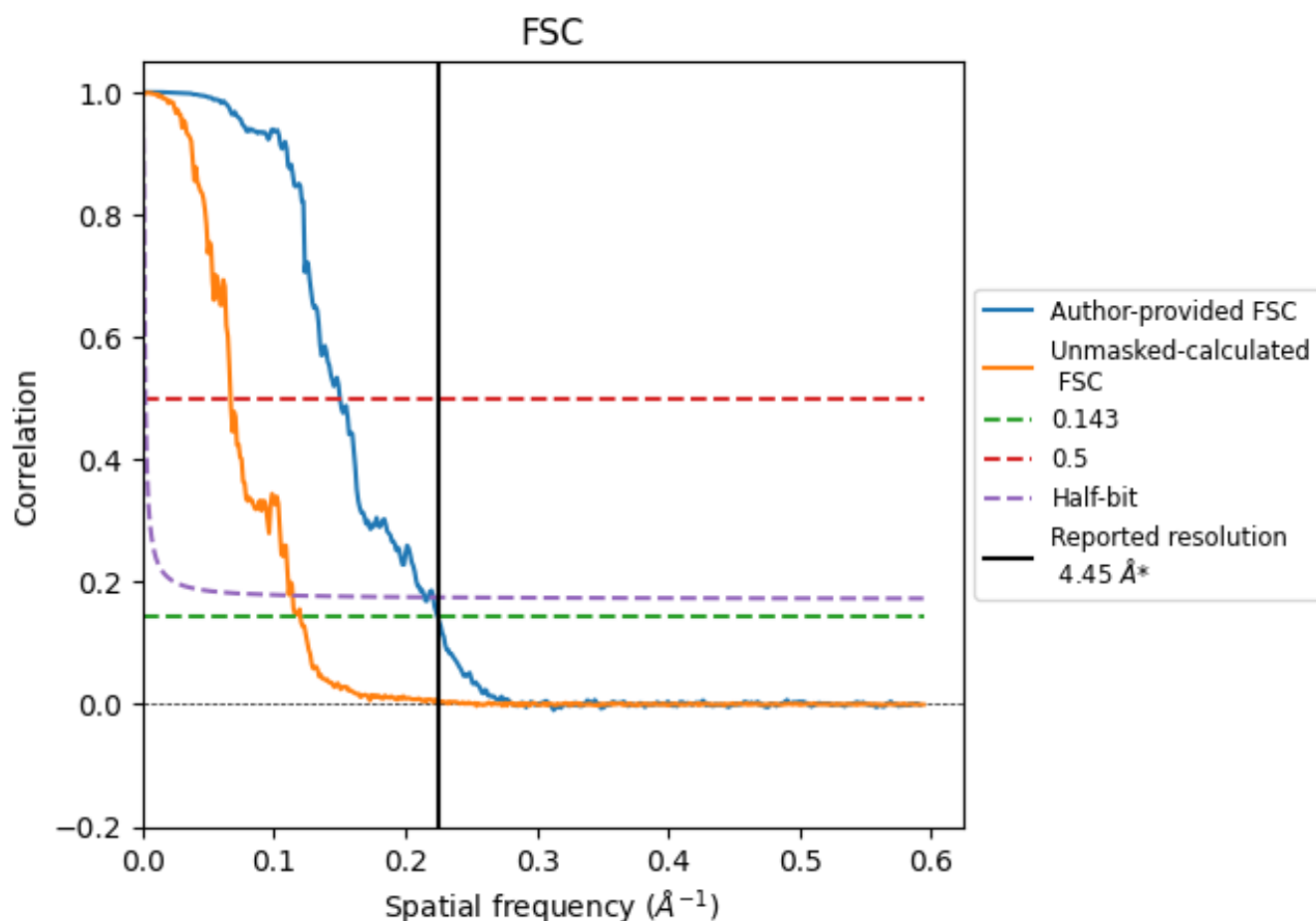


*Reported resolution corresponds to spatial frequency of 0.225 \AA^{-1}

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](#)

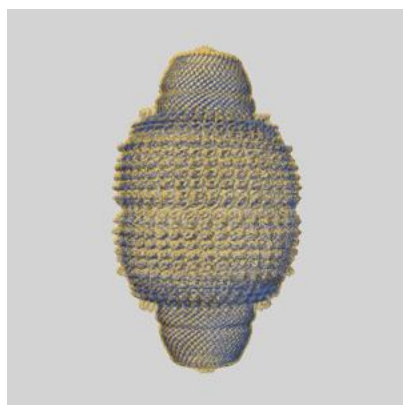
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.45	-	-
Author-provided FSC curve	4.45	6.66	4.66
Unmasked-calculated*	8.32	14.90	8.76

*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 %

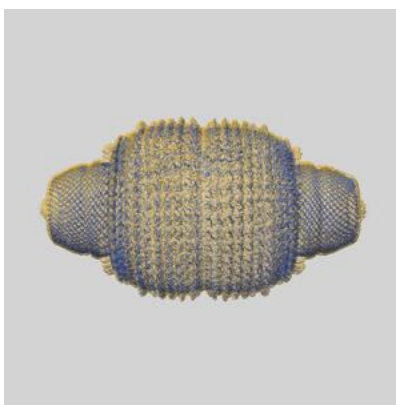
9 Map-model fit [i](#)

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](#)



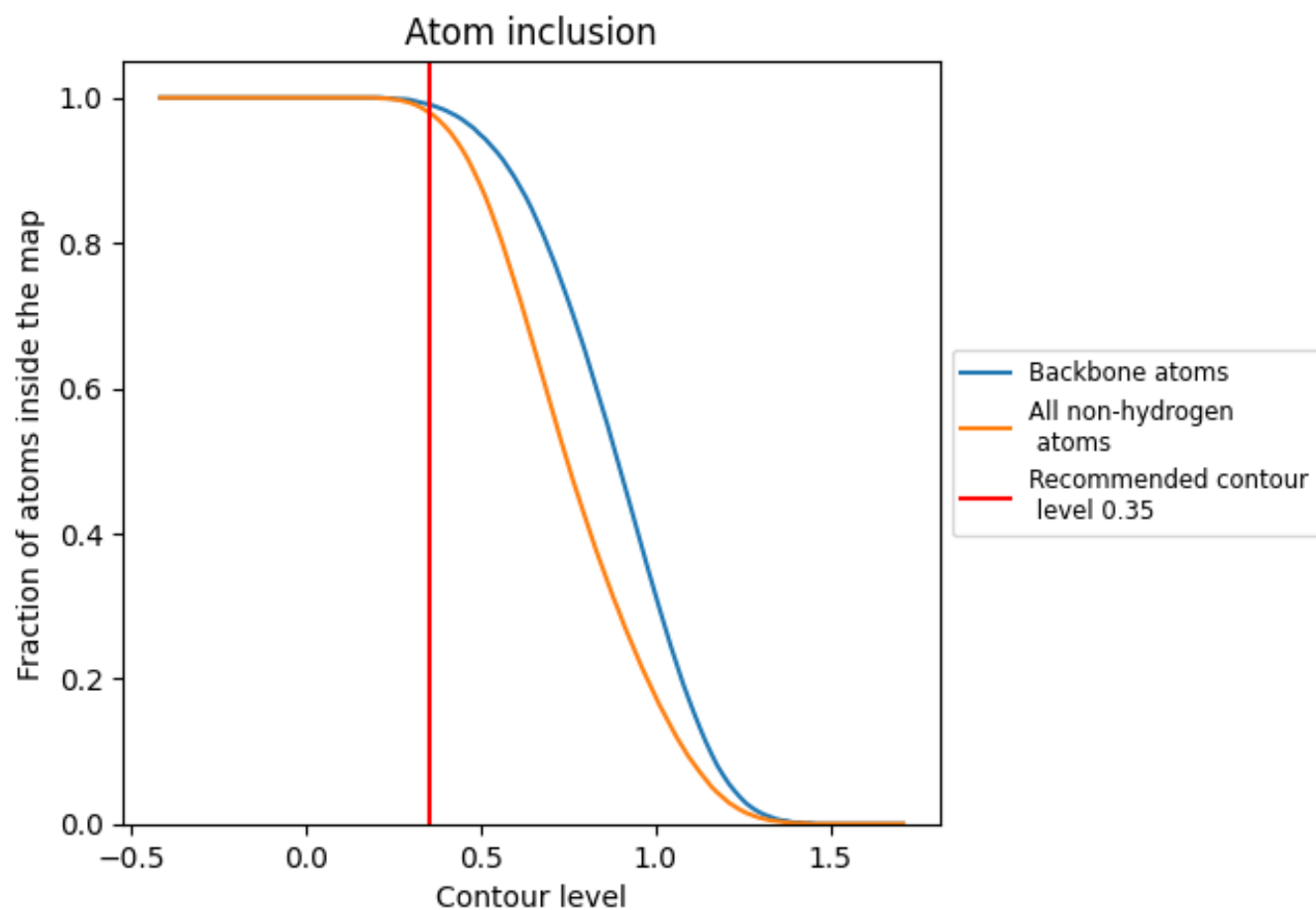
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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