



## wwPDB EM Validation Summary Report ⓘ

May 19, 2025 – 09:52 PM EDT

PDB ID : 6BX0 / pdb\_00006bx0  
EMDB ID : EMD-7301  
Title : Atomic resolution structure of human bufavirus 2  
Authors : Mietzsch, M.; Agbandje-McKenna, M.  
Deposited on : 2017-12-15  
Resolution : 3.79 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

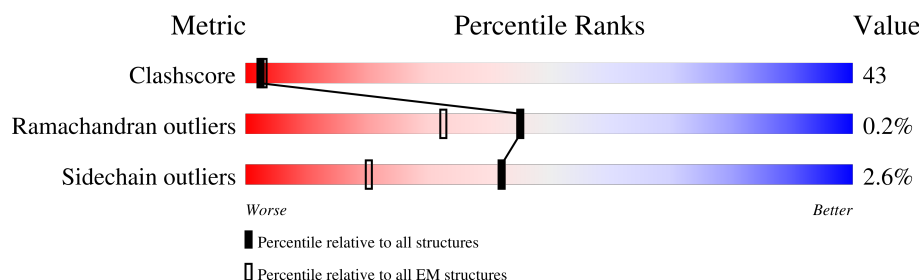
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.79 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.



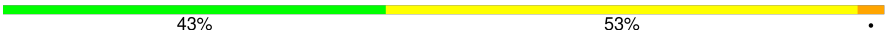


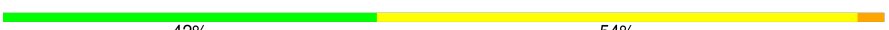
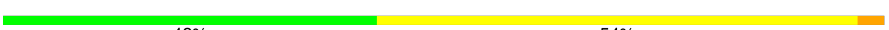
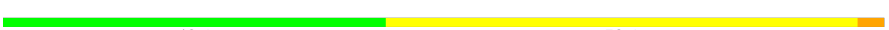




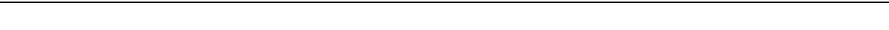

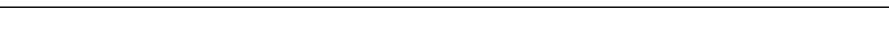
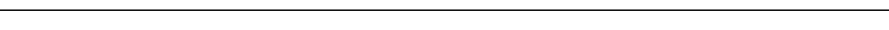










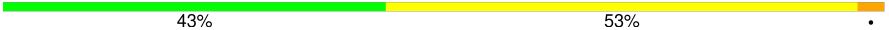
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	537	
1	1	537	
1	2	537	
1	3	537	
1	4	537	
1	5	537	
1	6	537	
1	7	537	




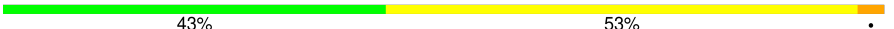
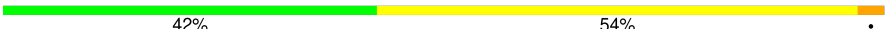
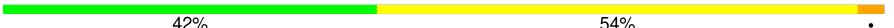
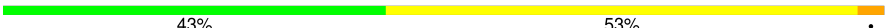


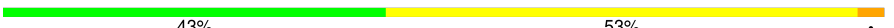
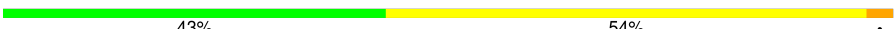
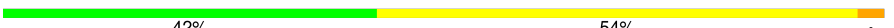




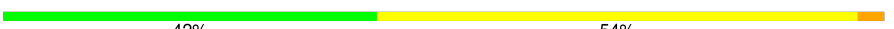
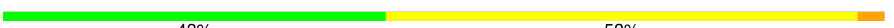

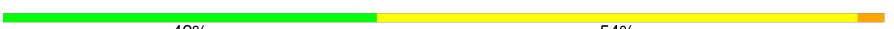
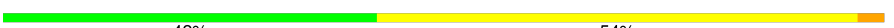

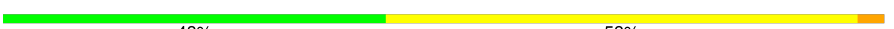


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Mol	Chain	Length	Quality of chain	
1	A	537		.
1	B	537		.
1	C	537		.
1	D	537		.
1	E	537		.
1	F	537		.
1	G	537		.
1	H	537		.
1	I	537		.
1	J	537		.
1	K	537		.
1	L	537		.
1	M	537		.
1	N	537		.
1	O	537		.
1	P	537		.
1	Q	537		.
1	R	537		.
1	S	537		.
1	T	537		.
1	U	537		.
1	V	537		.
1	W	537		.
1	X	537		.
1	Y	537		.

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Mol	Chain	Length	Quality of chain	
1	Z	537		.
1	a	537		.
1	b	537		.
1	c	537		.
1	d	537		.
1	e	537		.
1	f	537		.
1	g	537		.
1	h	537		.
1	i	537		.
1	j	537		.
1	k	537		.
1	l	537		.
1	m	537		.
1	n	537		.
1	o	537		.
1	p	537		.
1	q	537		.
1	r	537		.
1	s	537		.
1	t	537		.
1	u	537		.
1	v	537		.
1	w	537		.
1	x	537		.

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Mol	Chain	Length	Quality of chain	
1	y	537	<div><div></div></div>	•
1	z	537	<div><div></div></div>	•

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 259560 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 VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	B	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	C	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	D	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	E	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	F	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	G	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	H	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	I	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	J	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	K	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	L	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	M	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	N	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	O	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	P	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		
1	Q	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	S	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	T	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	U	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	V	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	W	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	X	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	Y	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	Z	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	0	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	1	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	2	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	3	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	4	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	5	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	a	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	b	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	c	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	d	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	e	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	f	535	Total 4326	C 2727	N 763	O 817	S 19	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	h	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	i	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	j	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	k	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	l	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	m	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	n	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	o	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	p	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	q	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	r	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	s	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	t	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	u	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	v	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	w	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	x	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	y	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	z	535	Total 4326	C 2727	N 763	O 817	S 19	0	0
1	6	535	Total 4326	C 2727	N 763	O 817	S 19	0	0

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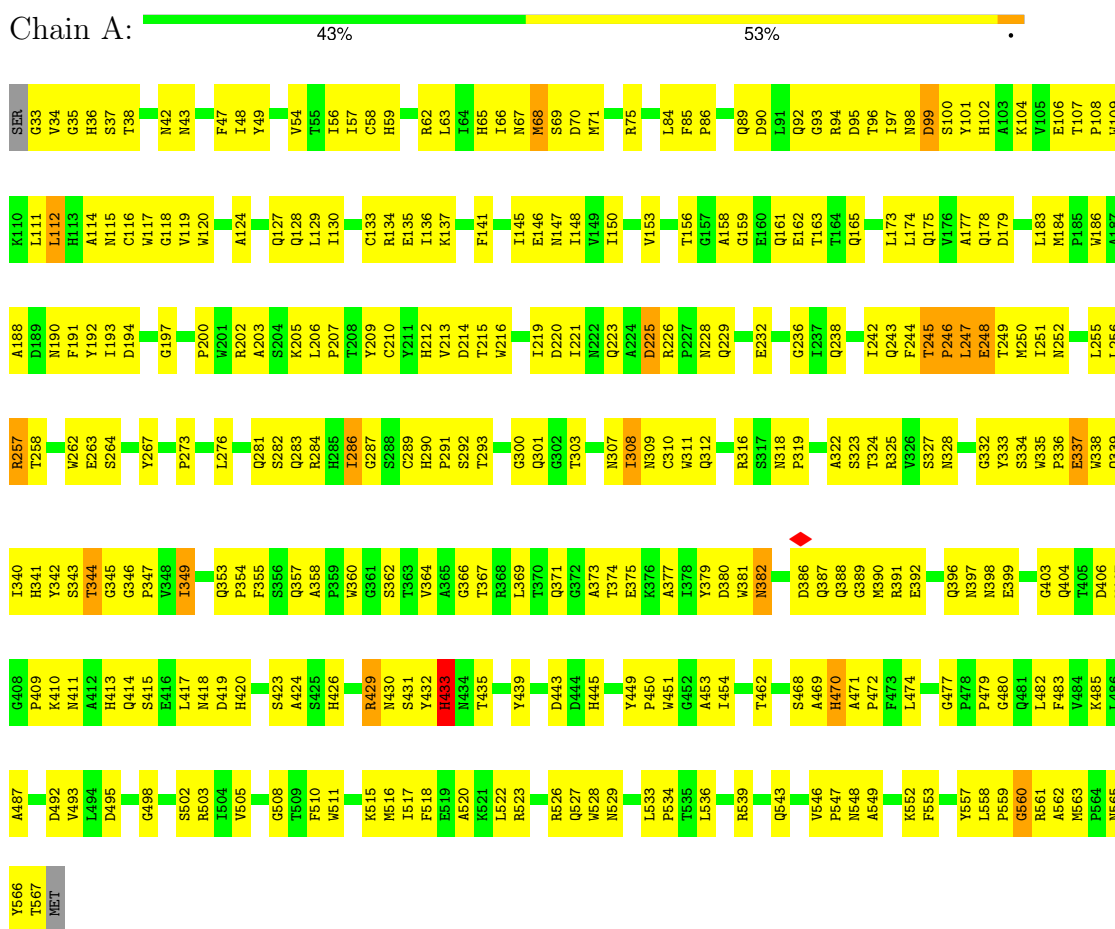
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7	535	Total	C	N	O	S	0	0
			4326	2727	763	817	19		

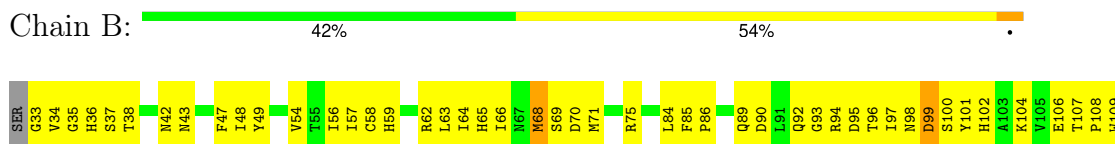
### 3 Residue-property plots

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: VP2



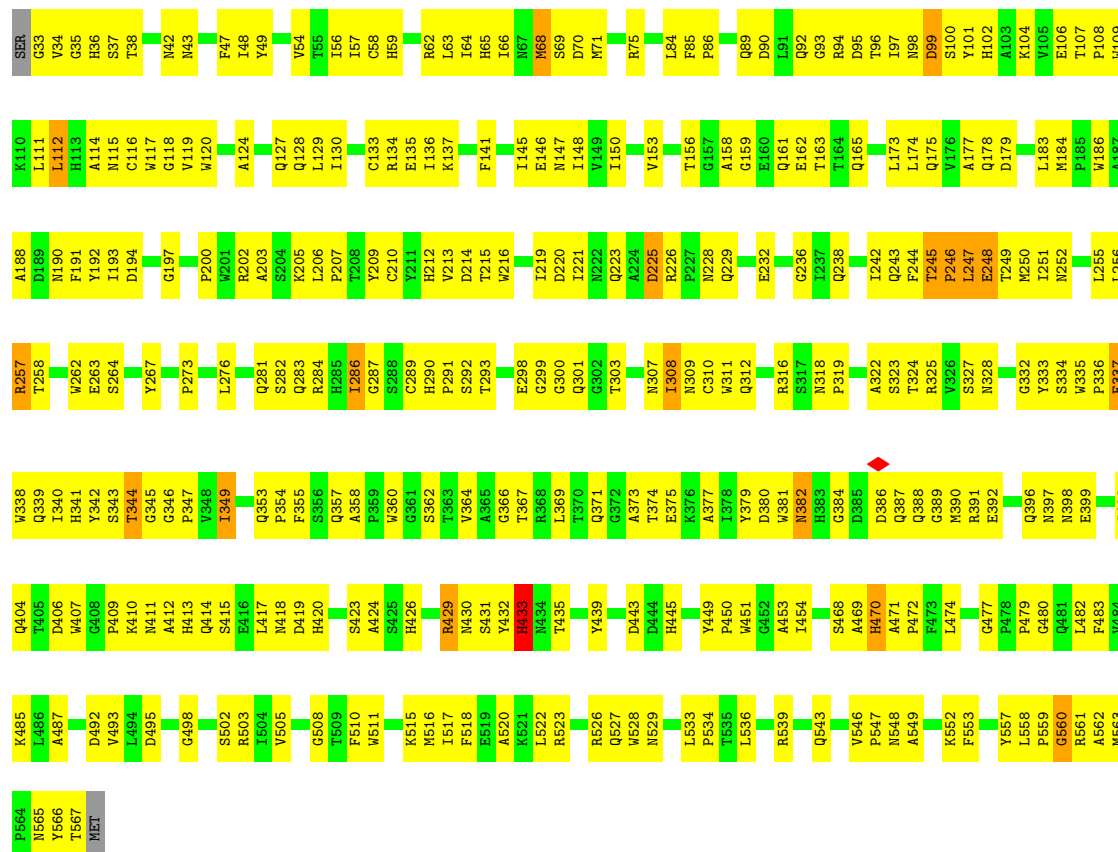
#### • Molecule 1: VP2





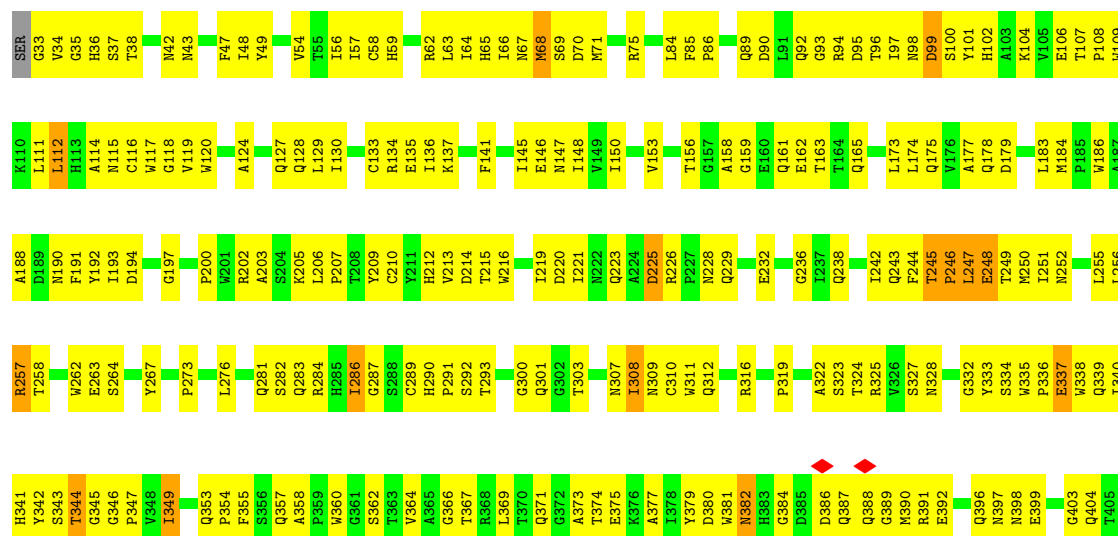
- Molecule 1: VP2

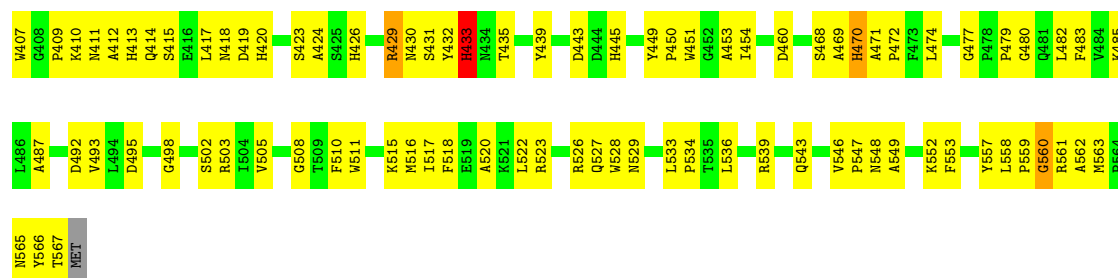
Chain D: 



- Molecule 1: VP2

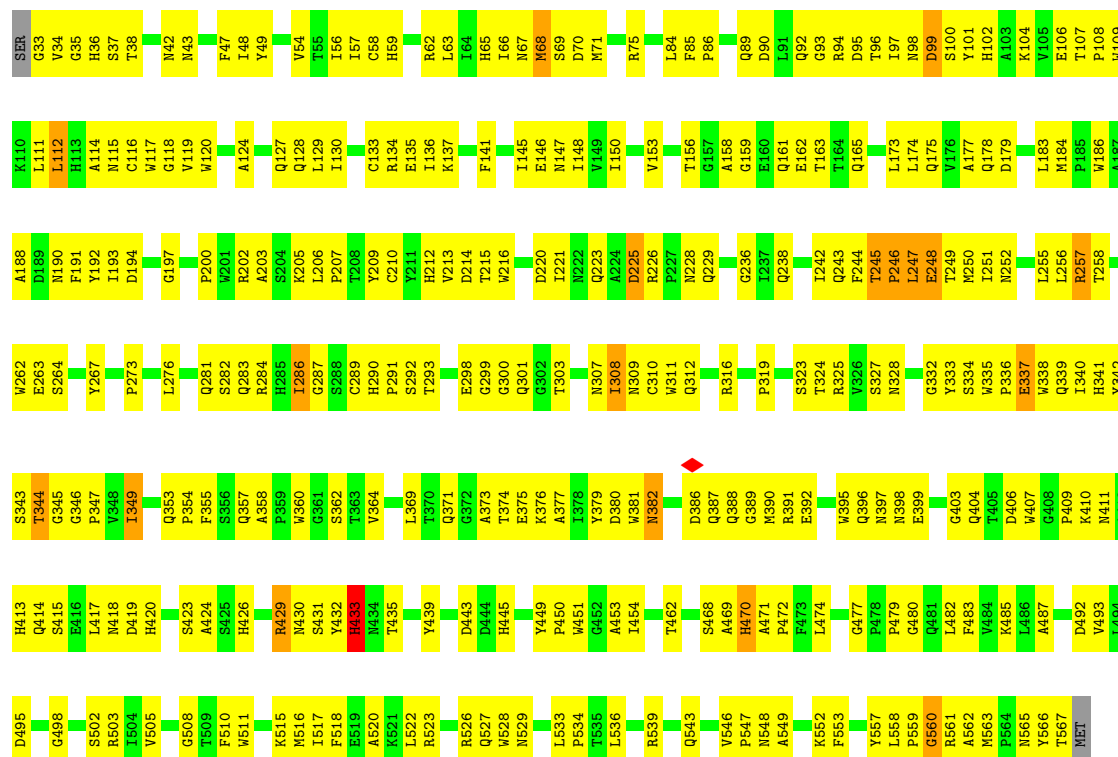
Chain E: 





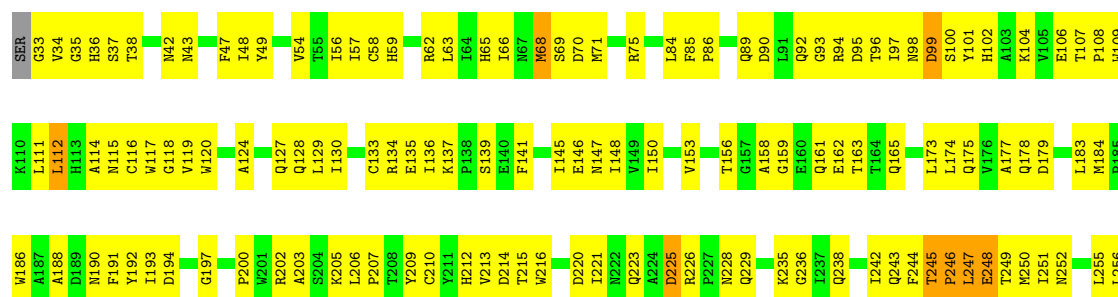
• Molecule 1: VP2

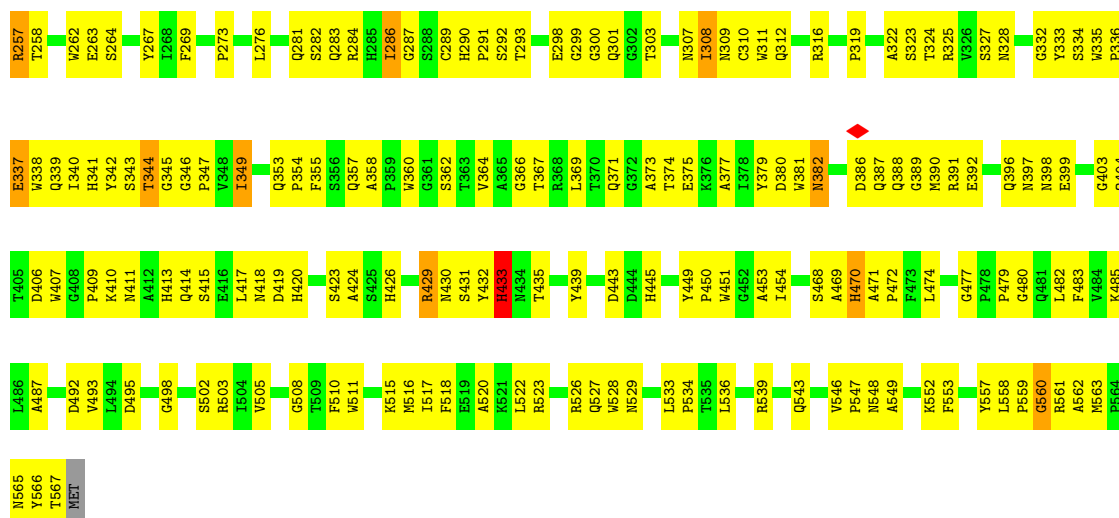
Chain F: 43% 53%



• Molecule 1: VP2

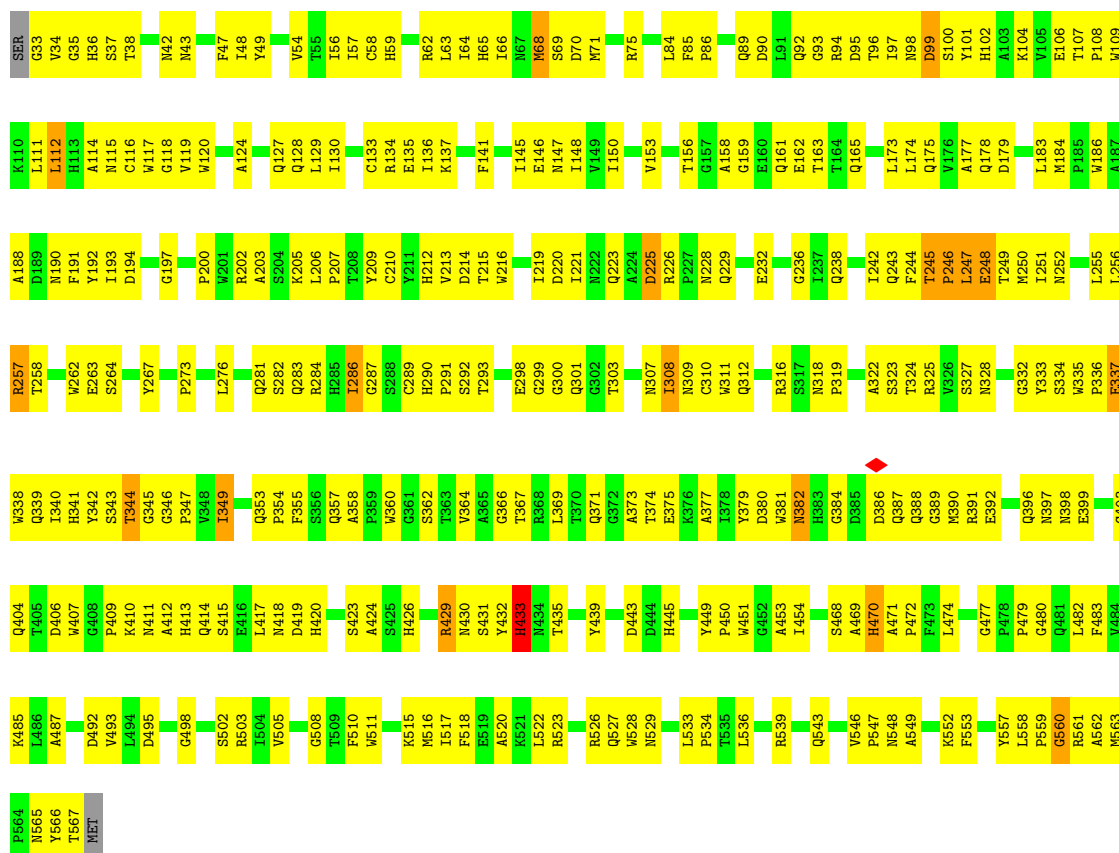
Chain G: 43% 53%





### • Molecule 1: VP2

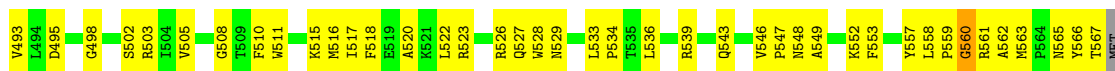
Chain H: 42% 54%



### • Molecule 1: VP2

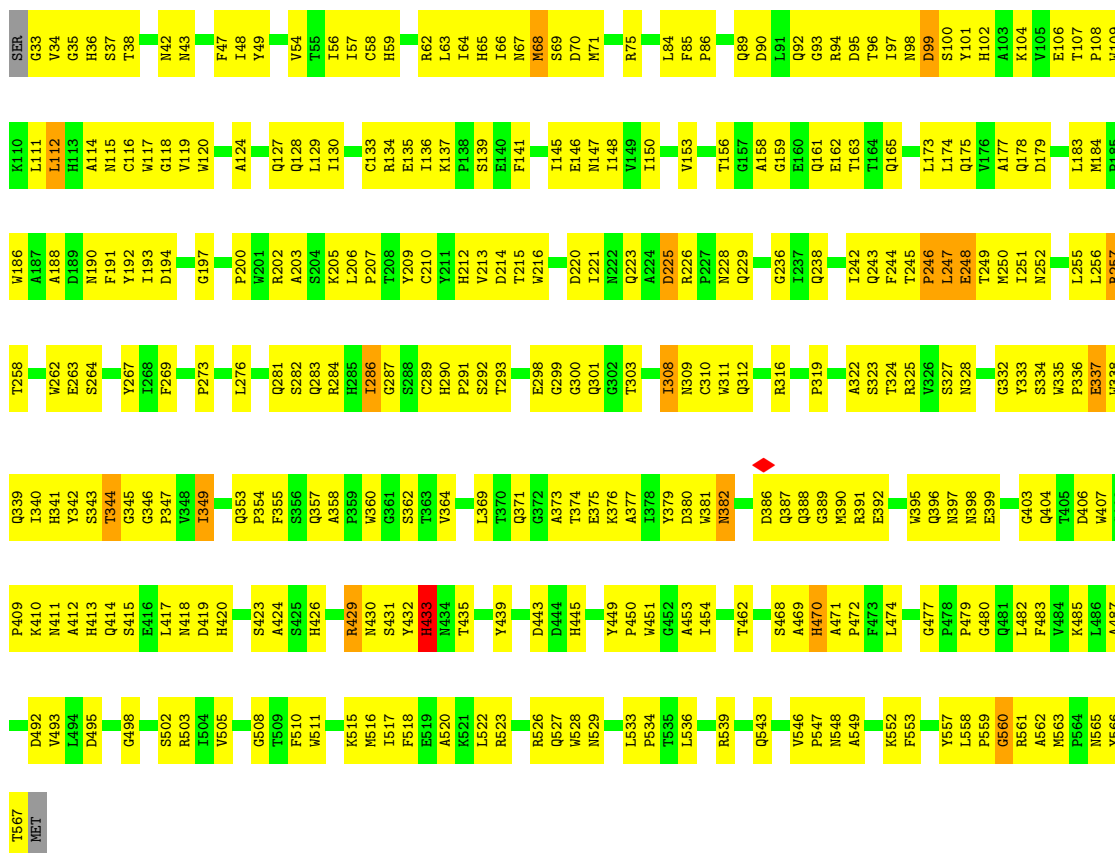
Chain I: 42% 54%





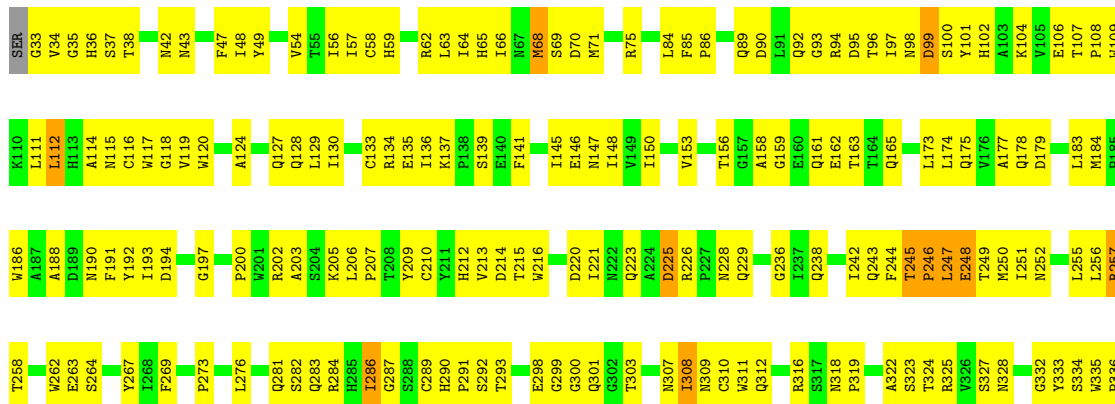
• Molecule 1: VP2

Chain K: 42% 54%

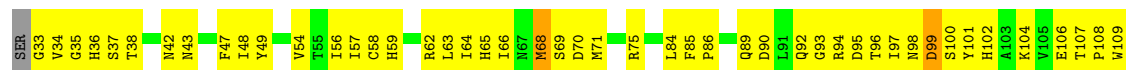


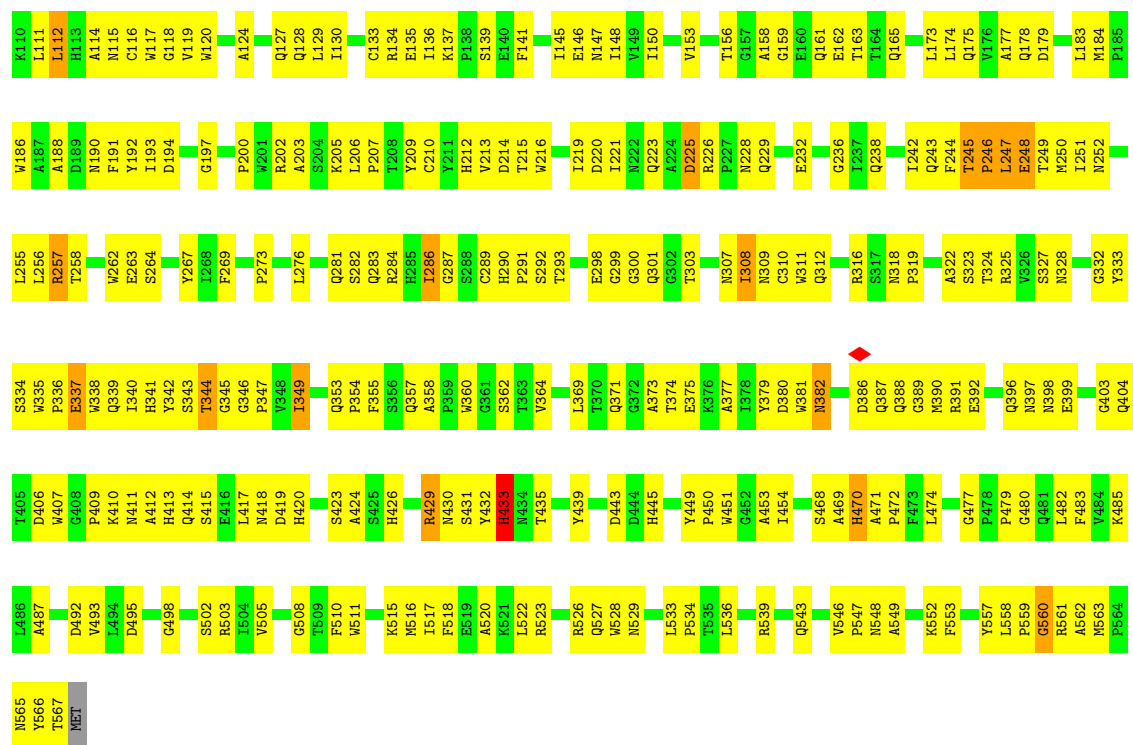
• Molecule 1: VP2

Chain L: 42% 54%

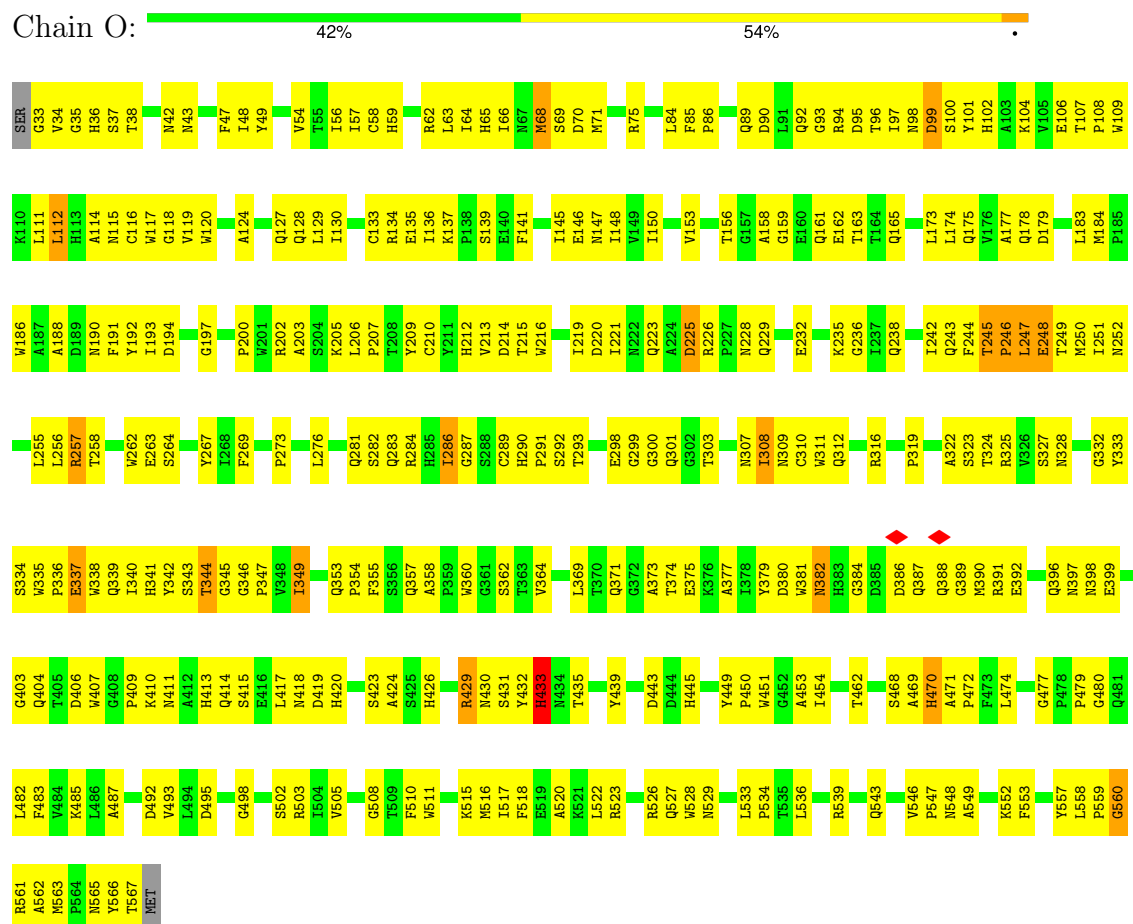




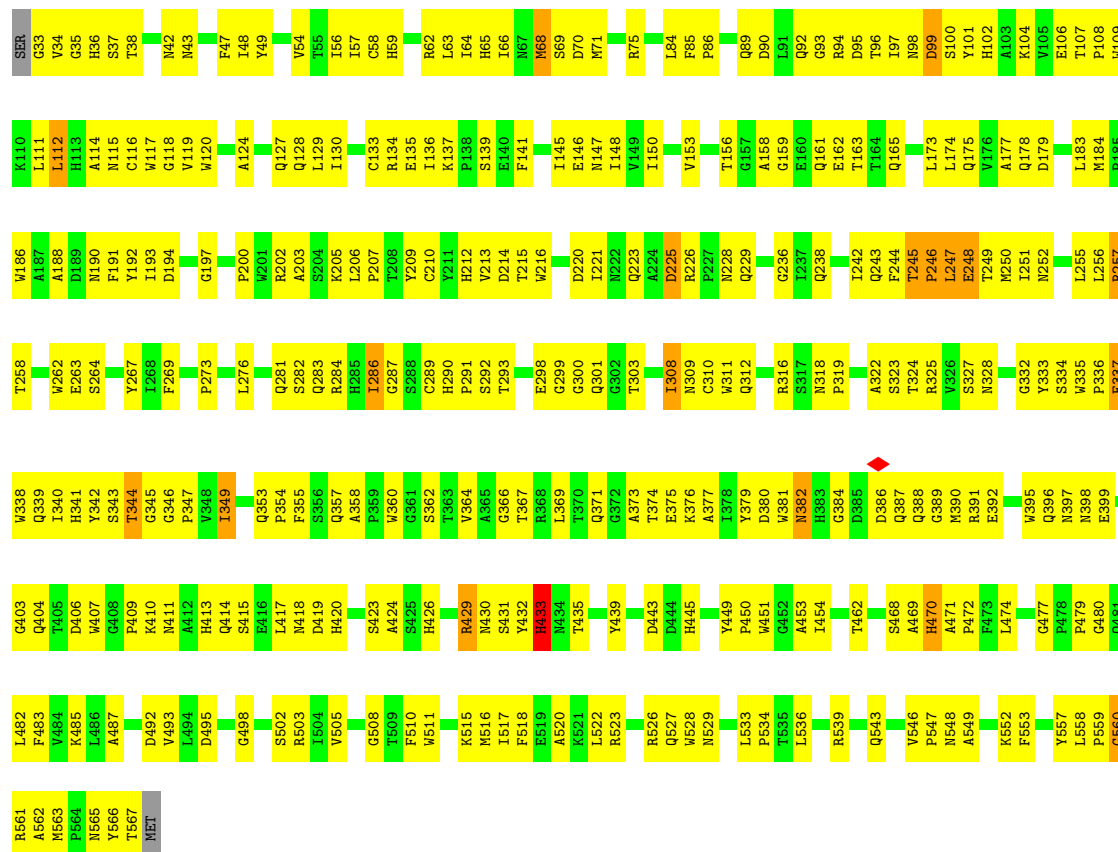




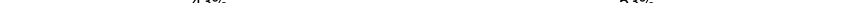
- Molecule 1: VP2

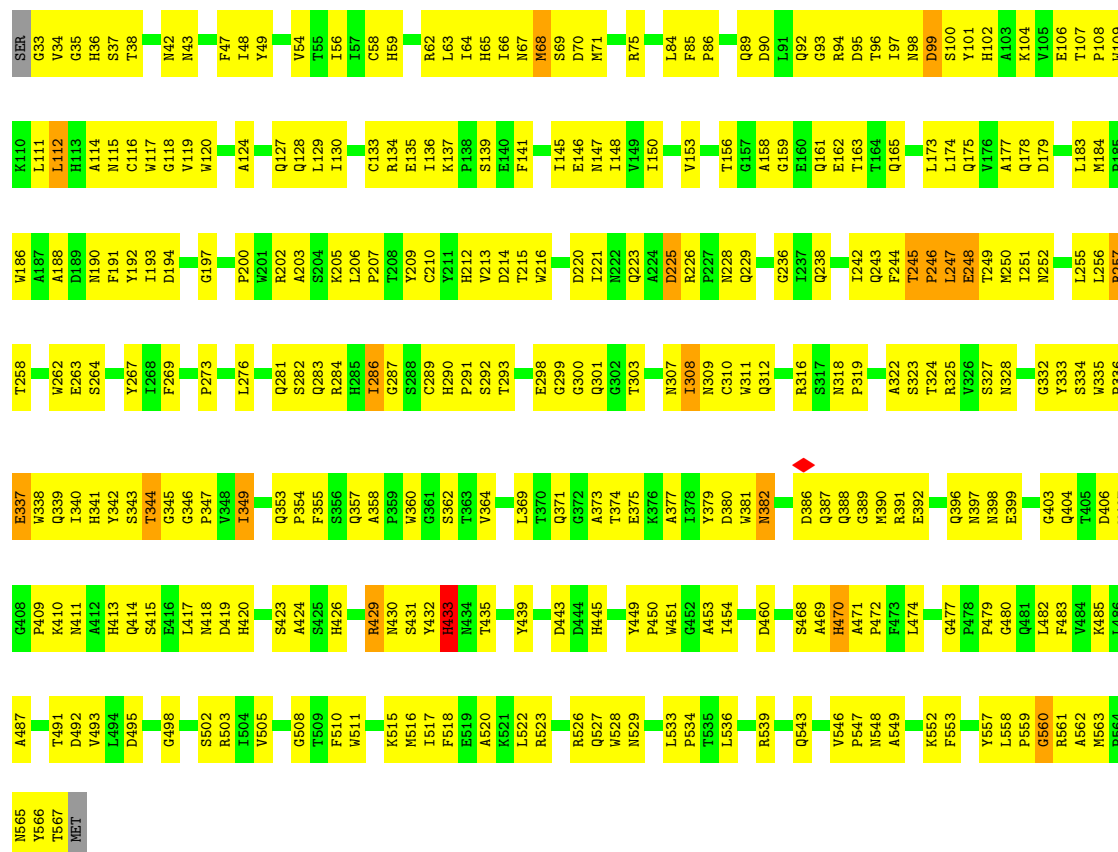


## ● Molecule 1: VP2

Chain P: 

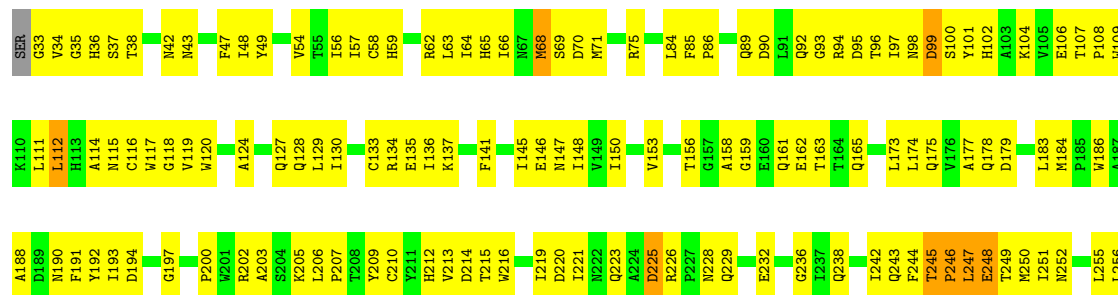
- Molecule 1: VP2

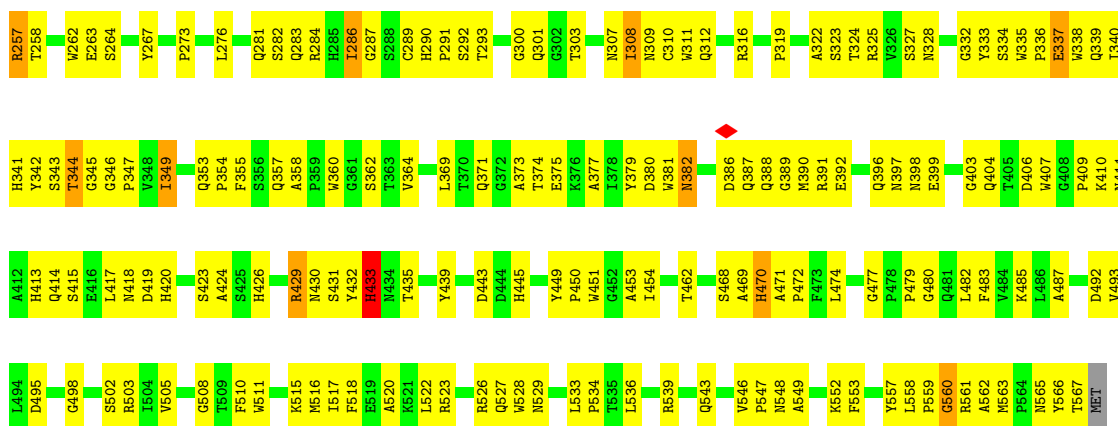
Chain R:  43% 53% .



- Molecule 1: VP2

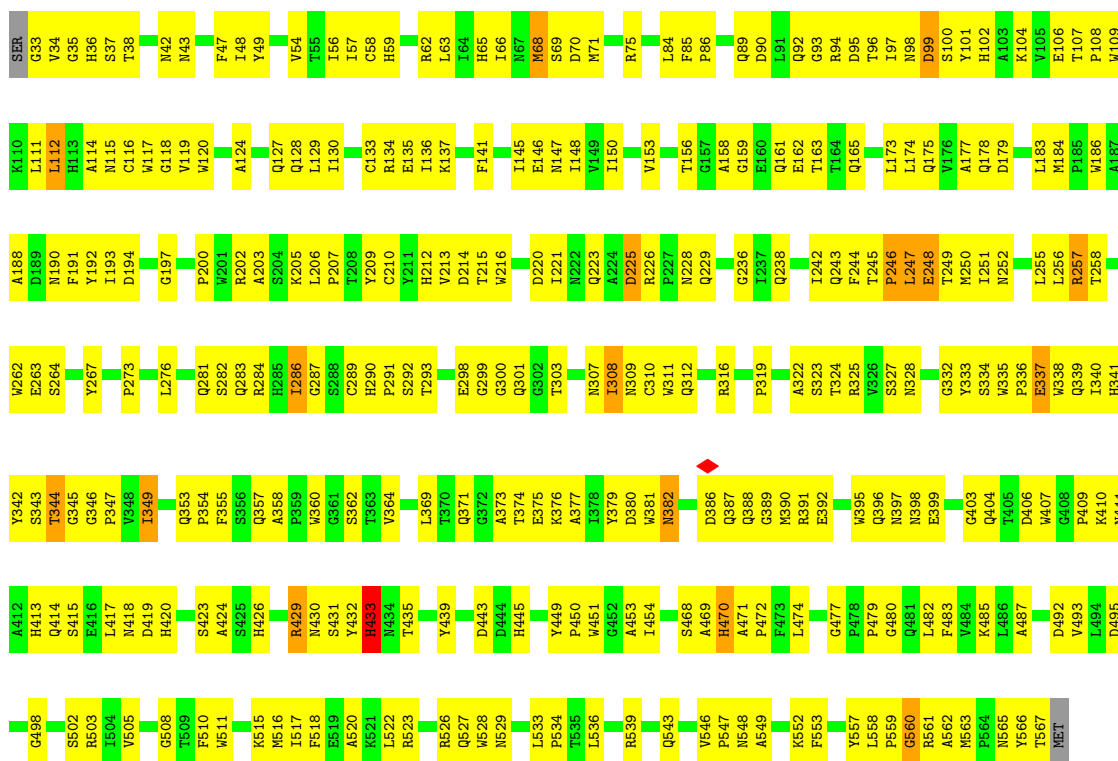
Chain S:  43% 53% .





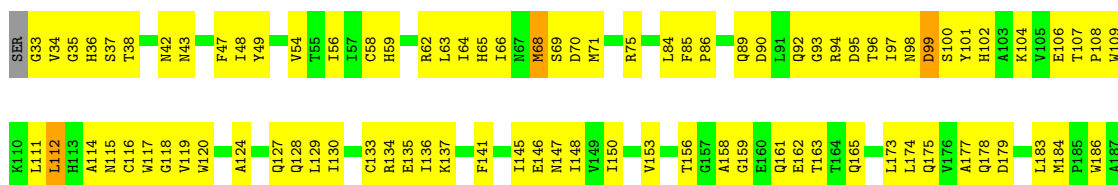
### • Molecule 1: VP2

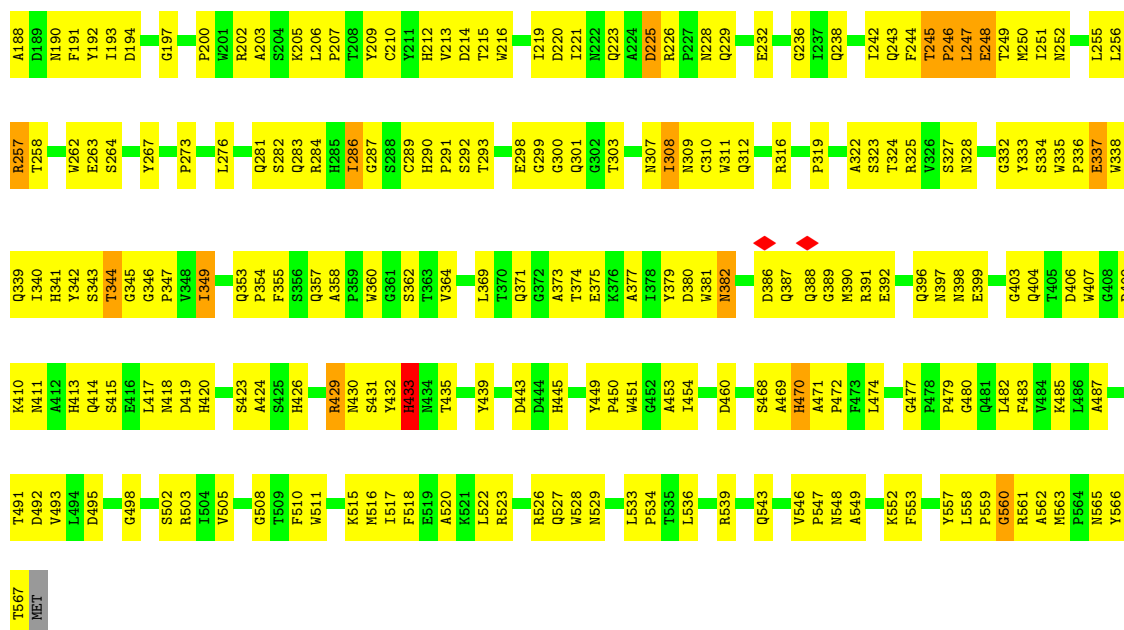
Chain T: 43% 53%



### • Molecule 1: VP2

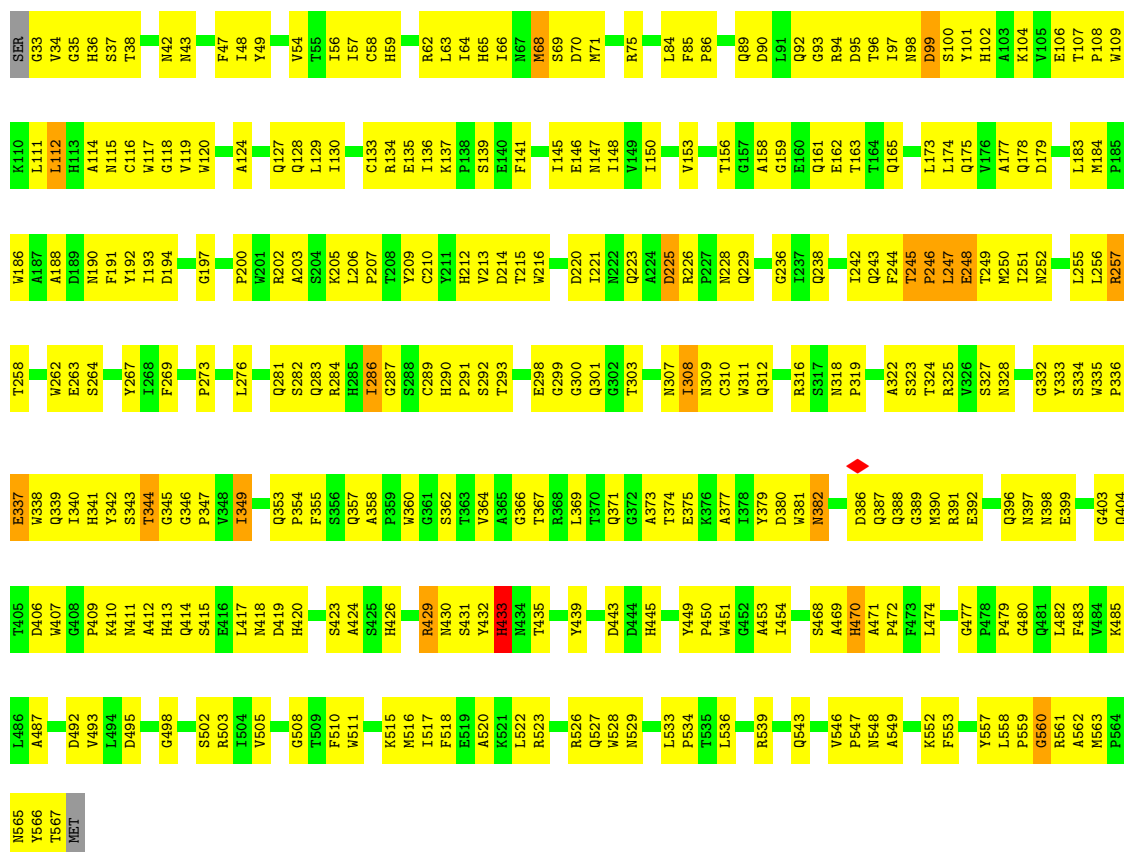
Chain U: 43% 53%





• Molecule 1: VP2

Chain V: 42% 54%



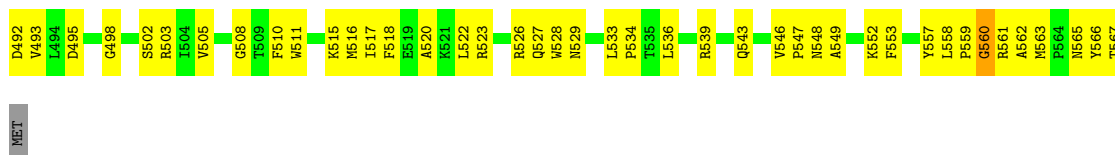
• Molecule 1: VP2

Government	Percentage
Current government	43%
Previous government	53%

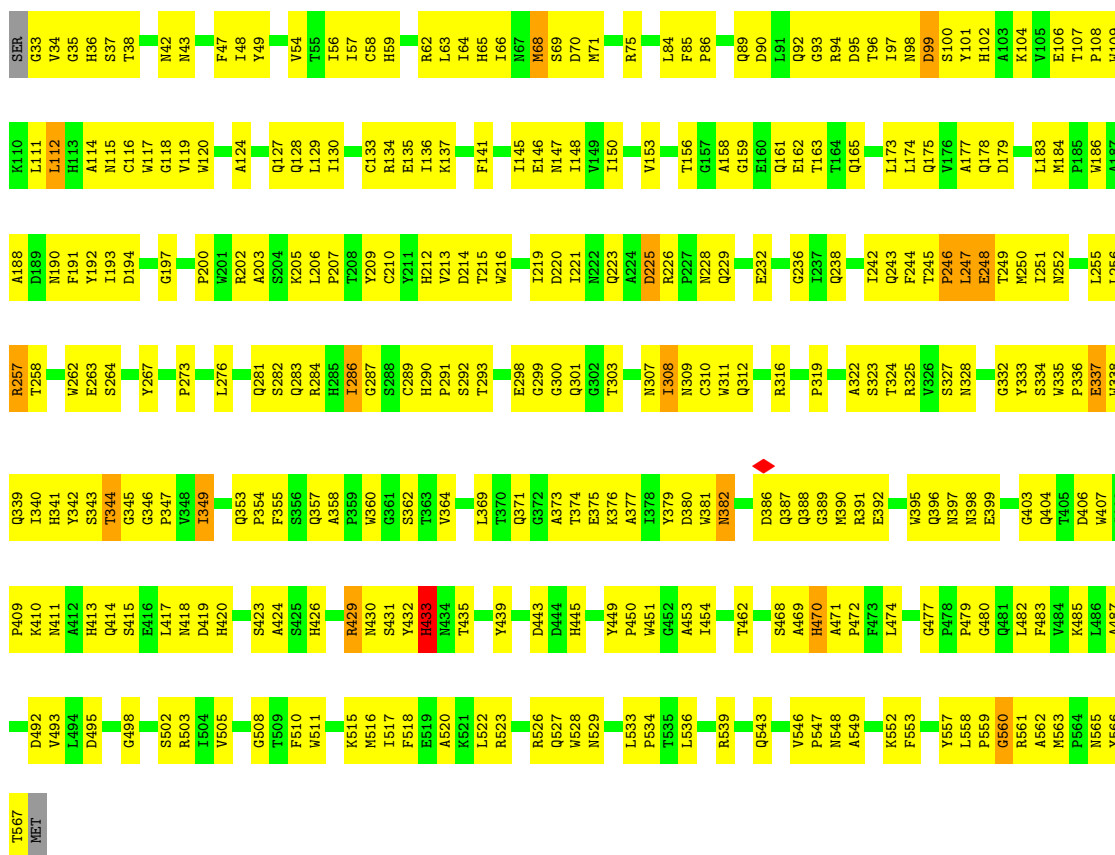


Government	Percentage
Current government	43%
Previous government	53%

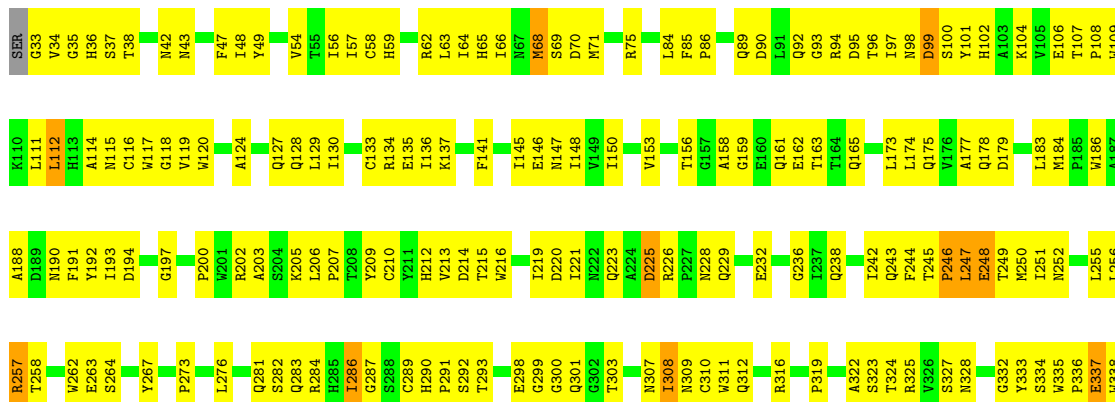




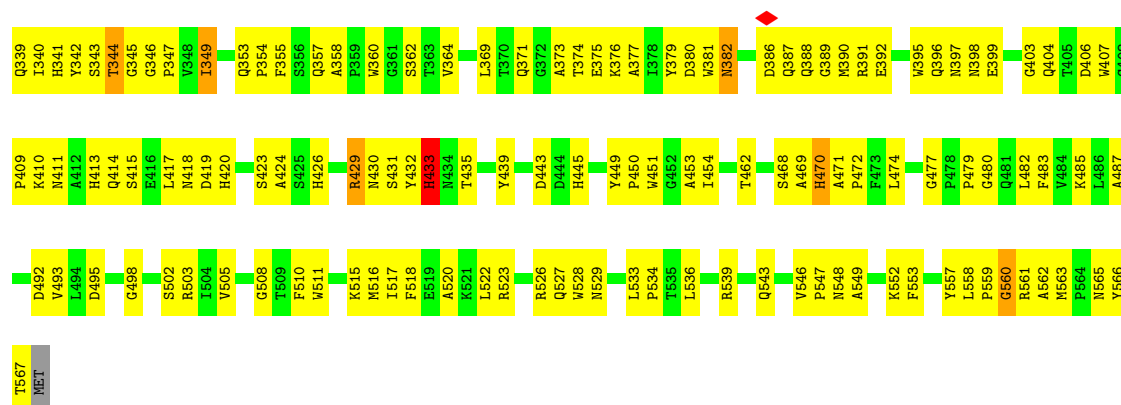
• Molecule 1: VP2



• Molecule 1: VP2

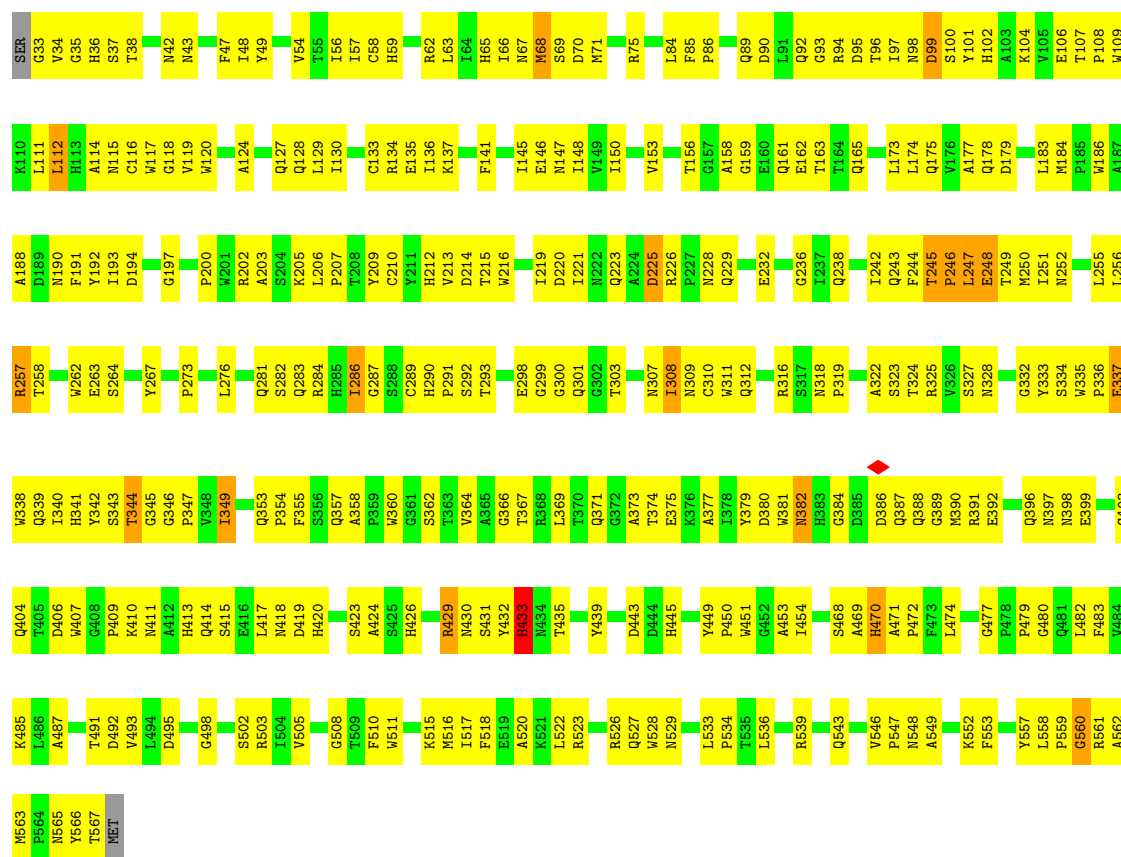






• Molecule 1: VP2

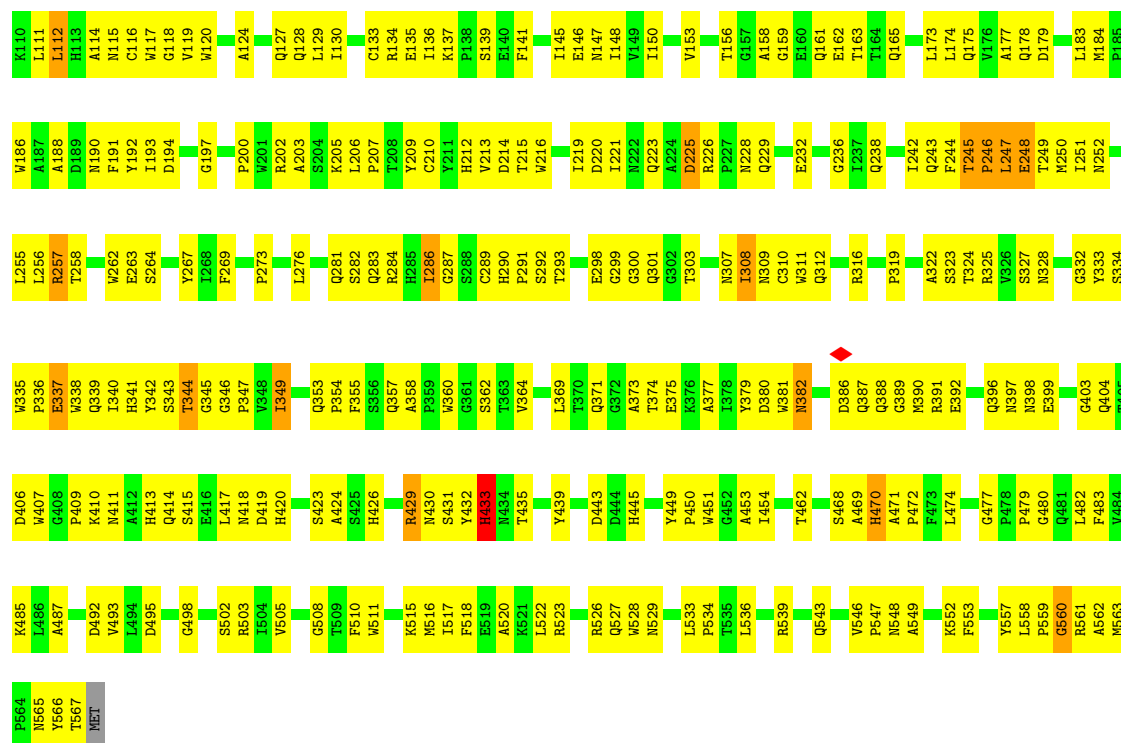
Chain 0: 42% 54%



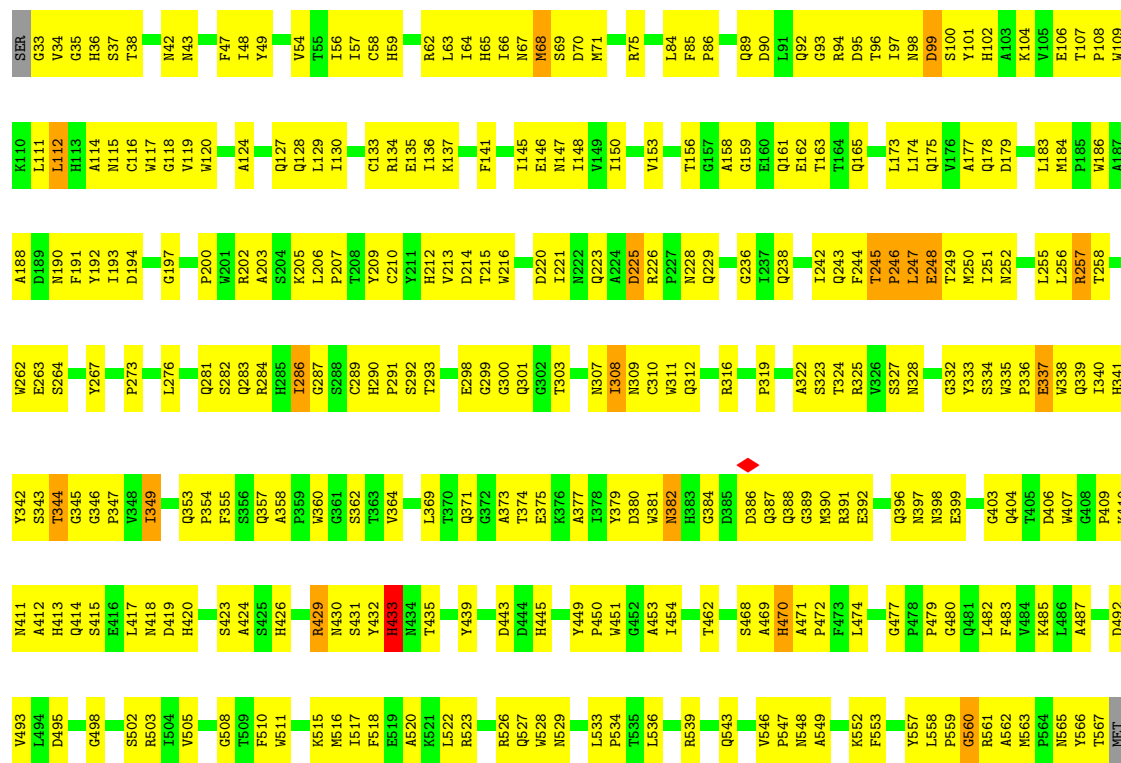
• Molecule 1: VP2

Chain 1: 43% 53%



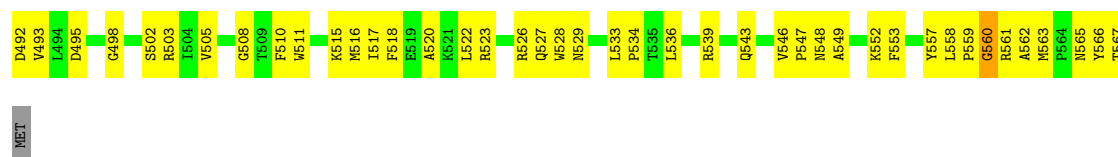


• Molecule 1: VP2



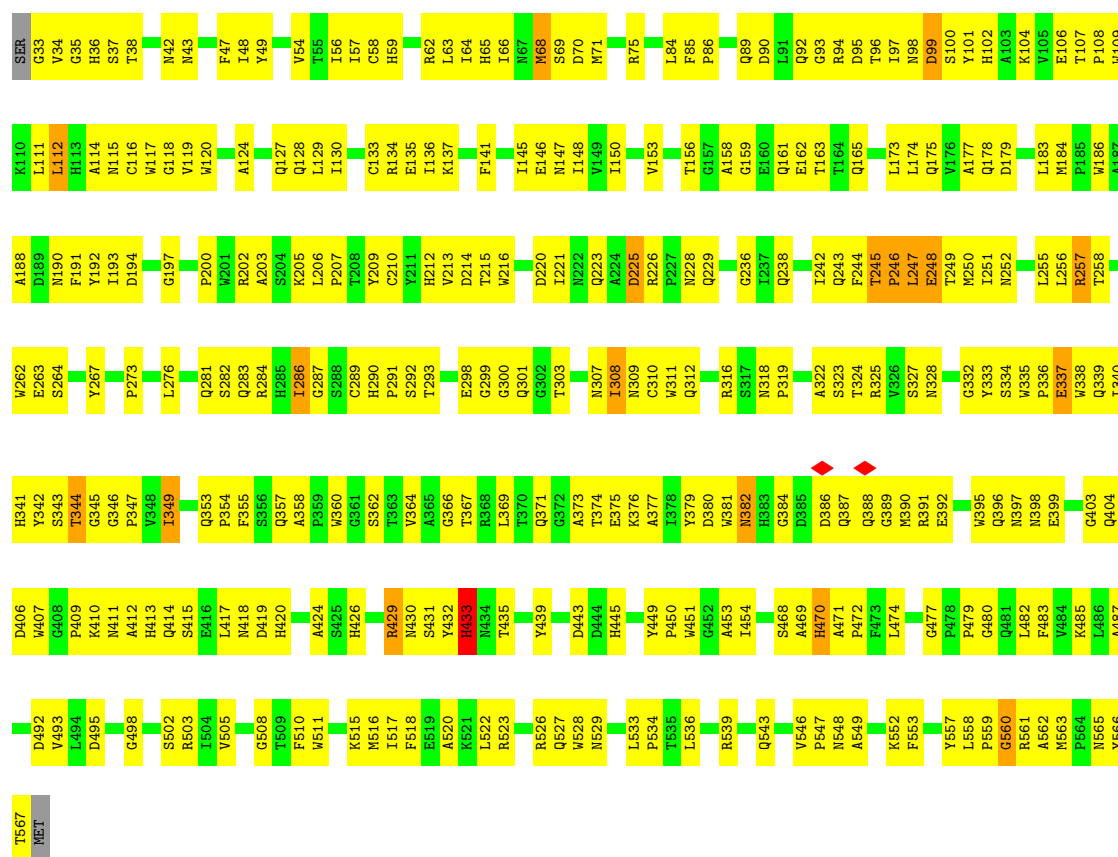
• Molecule 1: VP2





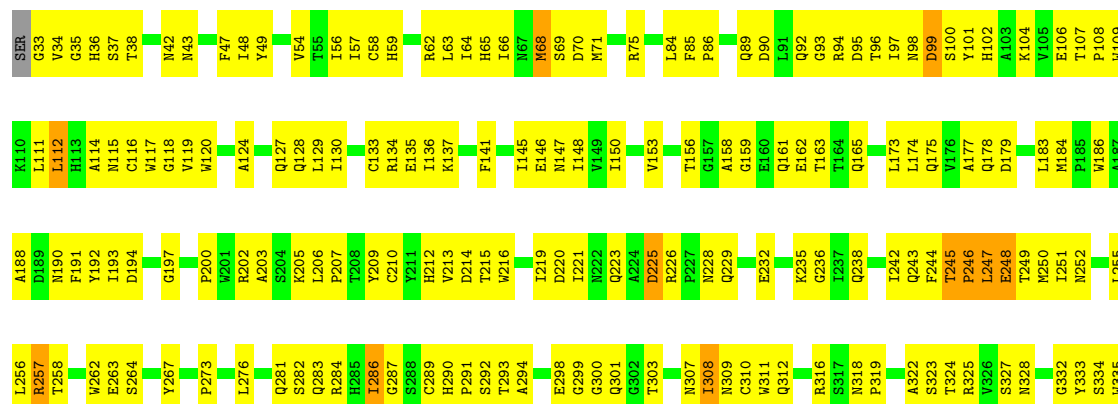
• Molecule 1: VP2

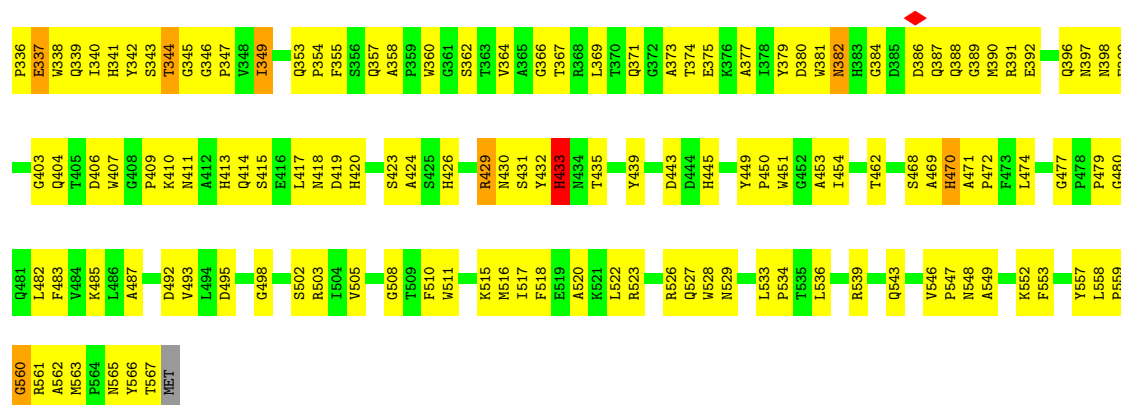
Chain 5: 42% 54%



• Molecule 1: VP2

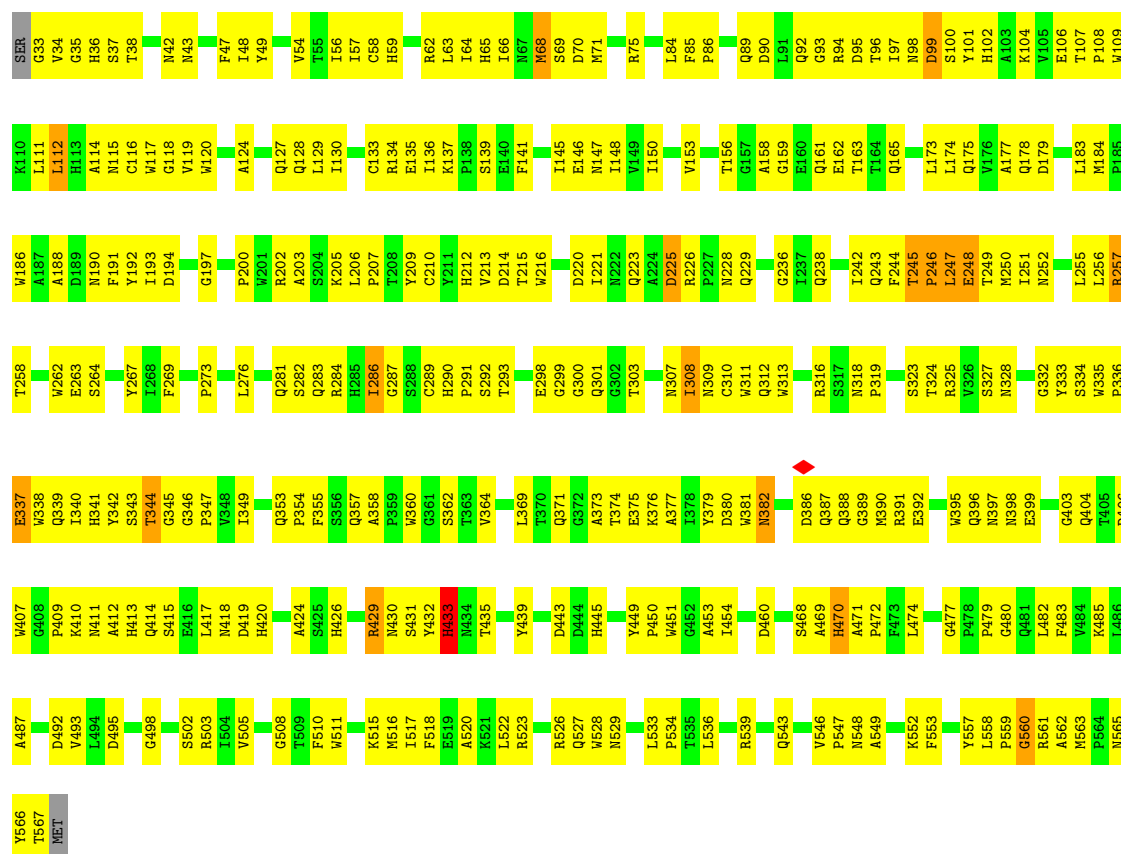
Chain a: 42% 54%





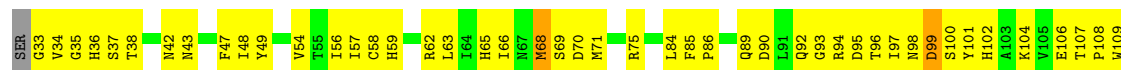
• Molecule 1: VP2

Chain b: 42% 54%



• Molecule 1: VP2

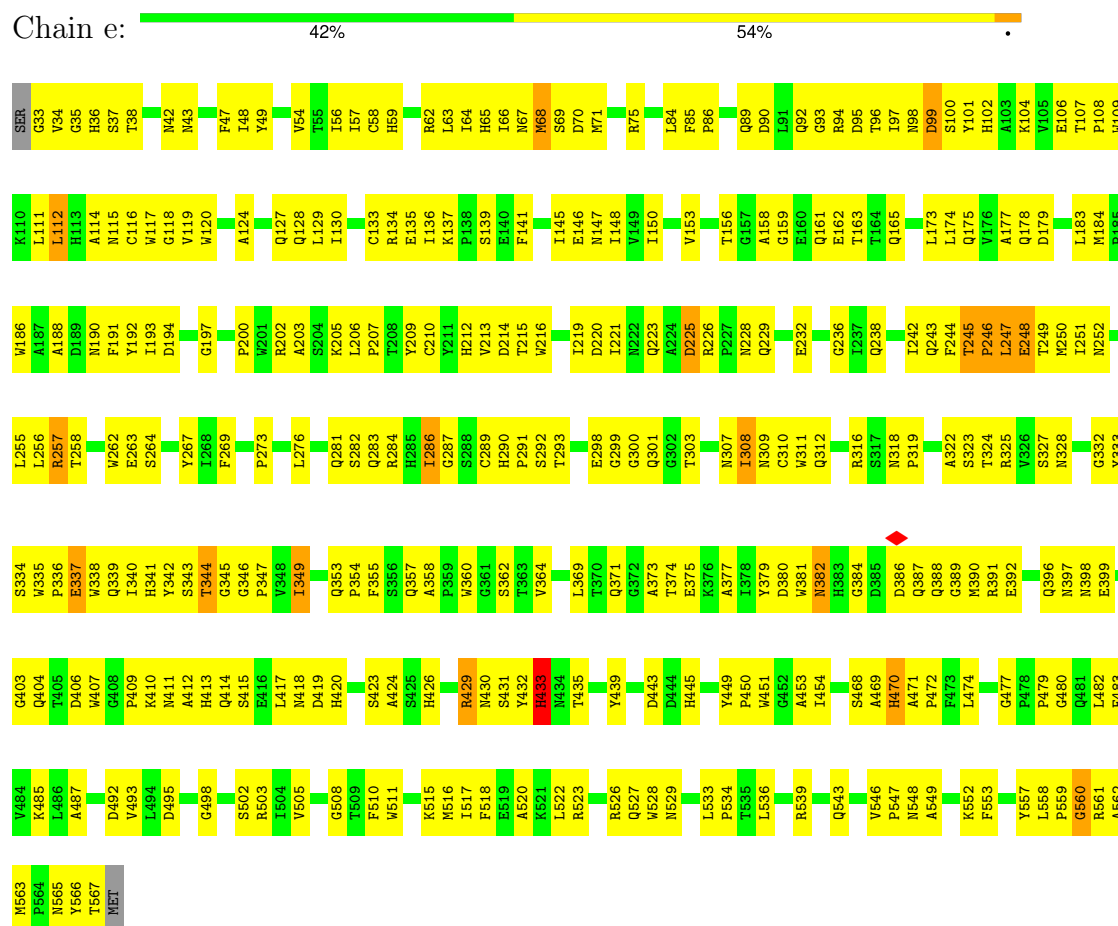
Chain c: 43% 53%



L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160	L1161	L1162	L1163	L1164	L1165	L1166	L1167	L1168	L1169	L1170	L1171	L1172	L1173	L1174	L1175	L1176	L1177	L1178	L1179	L1180	L1181	L1182	L1183	L1184	L1185	L1186	L1187	L1188	L1189	L1190	L1191	L1192	L1193	L1194	L1195	L1196	L1197	L1198	L1199	L1200	L1201	L1202	L1203	L1204	L1205	L1206	L1207	L1208	L1209	L1210	L1211	L1212	L1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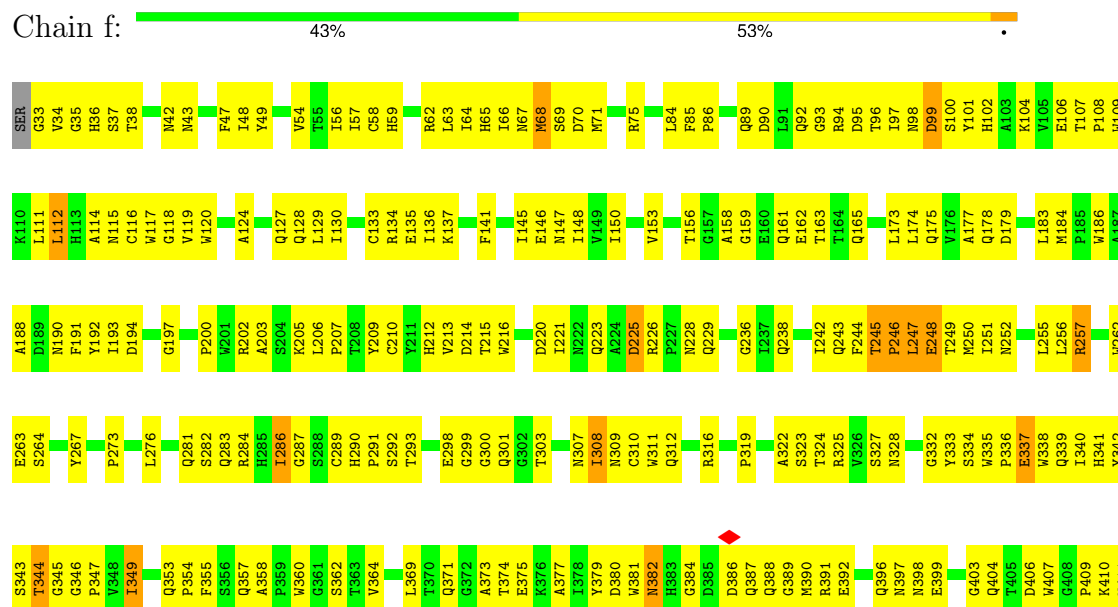
• Molecule 1: VP2

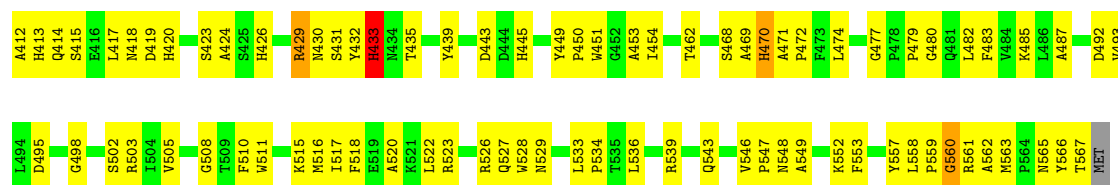
Chain e:



• Molecule 1: VP2

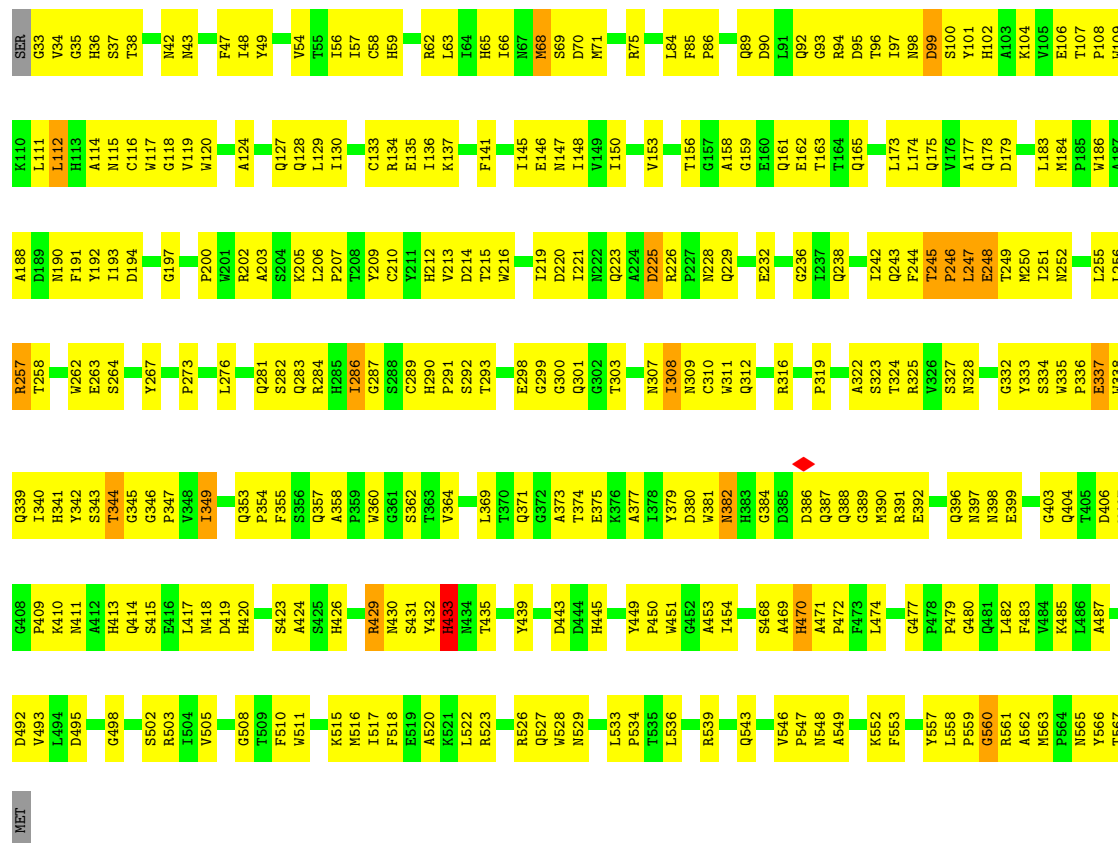
Chain f:





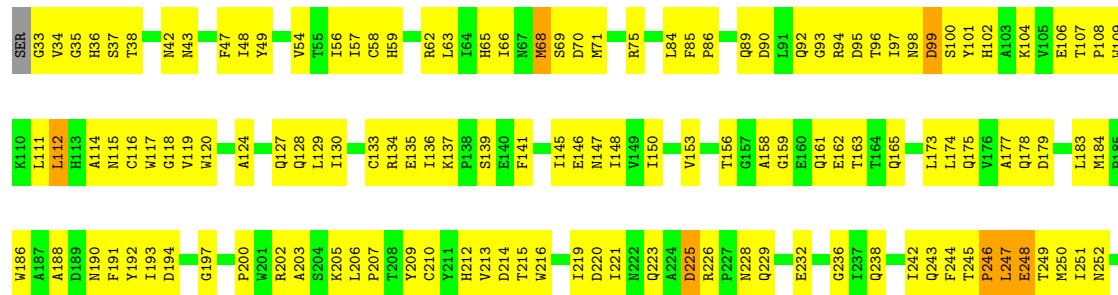
• Molecule 1: VP2

Chain g: 43% 53%



• Molecule 1: VP2

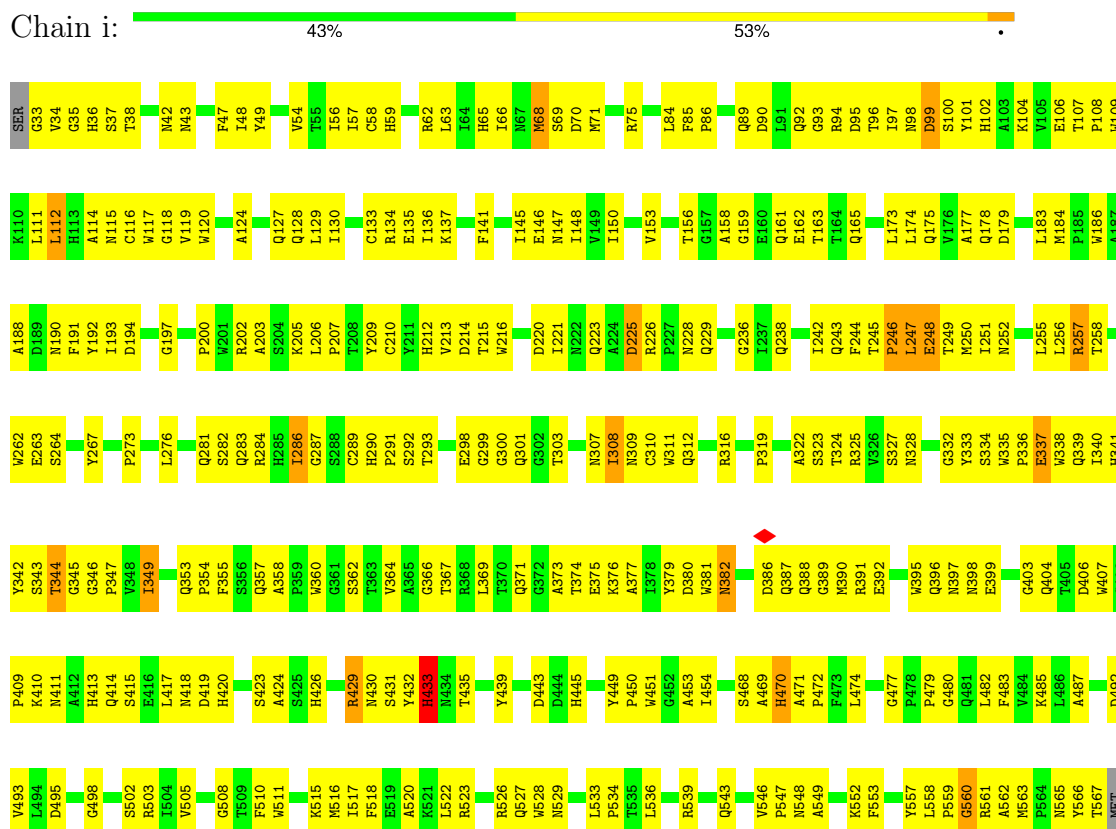
Chain h: 42% 54%



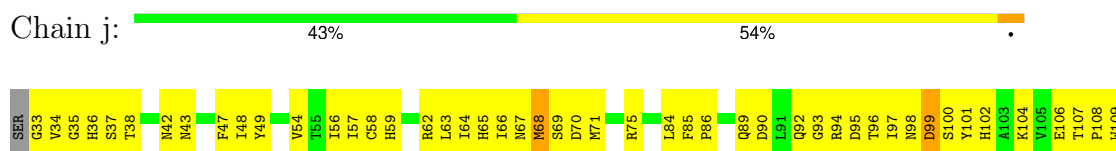




• Molecule 1: VP2



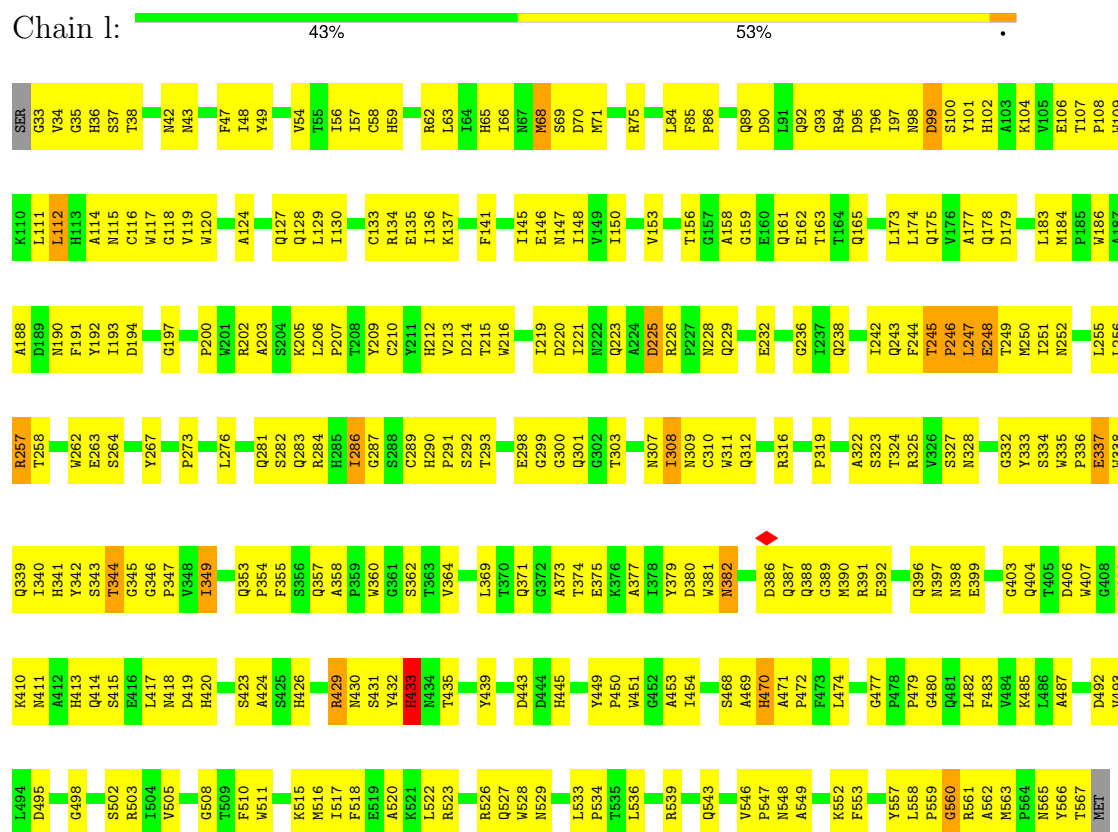
• Molecule 1: VP2





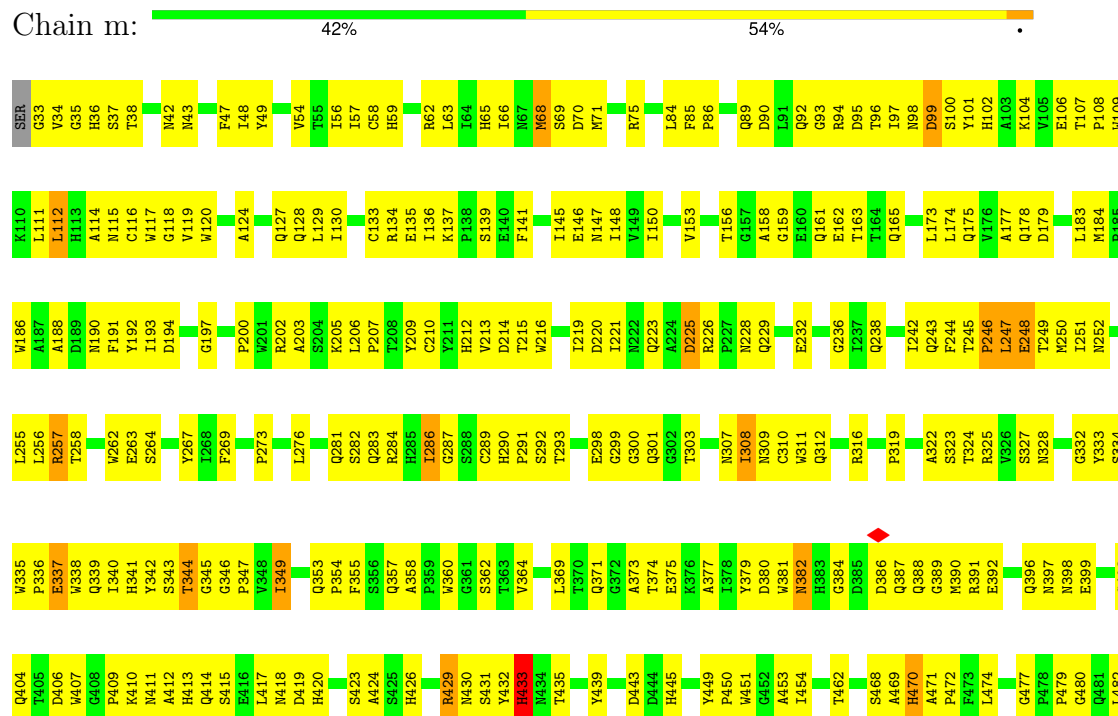
## ● Molecule 1: VP2

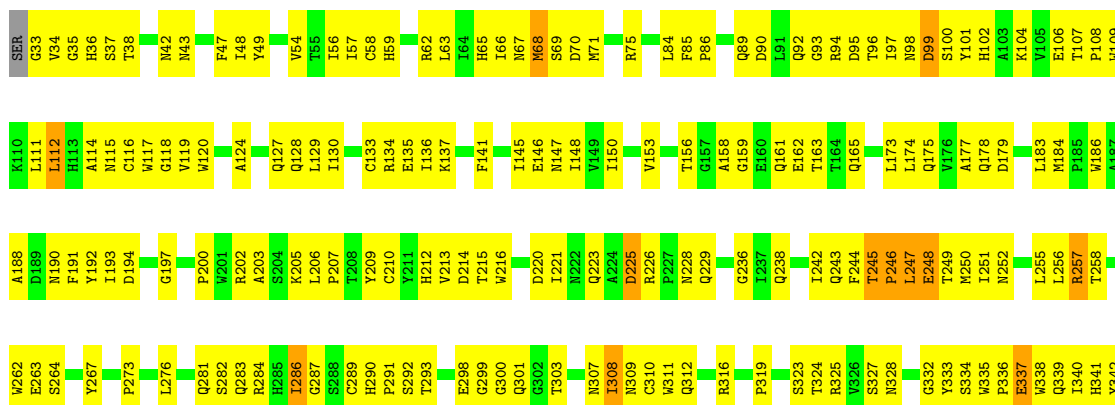
Chain l:

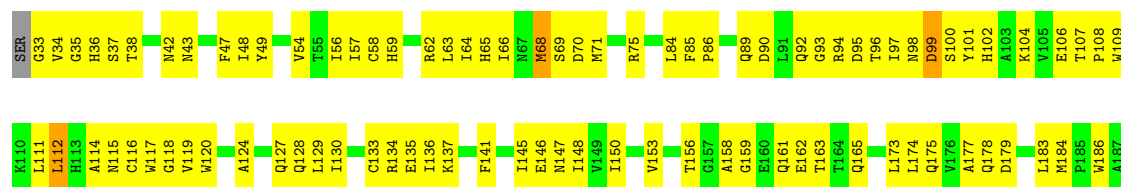


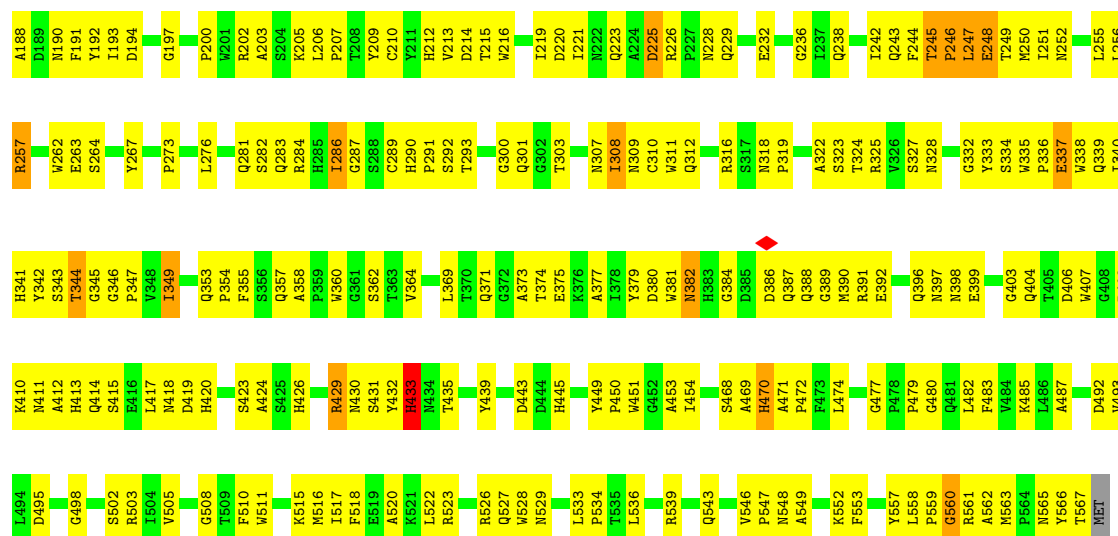
## ● Molecule 1: VP2

Chain m:



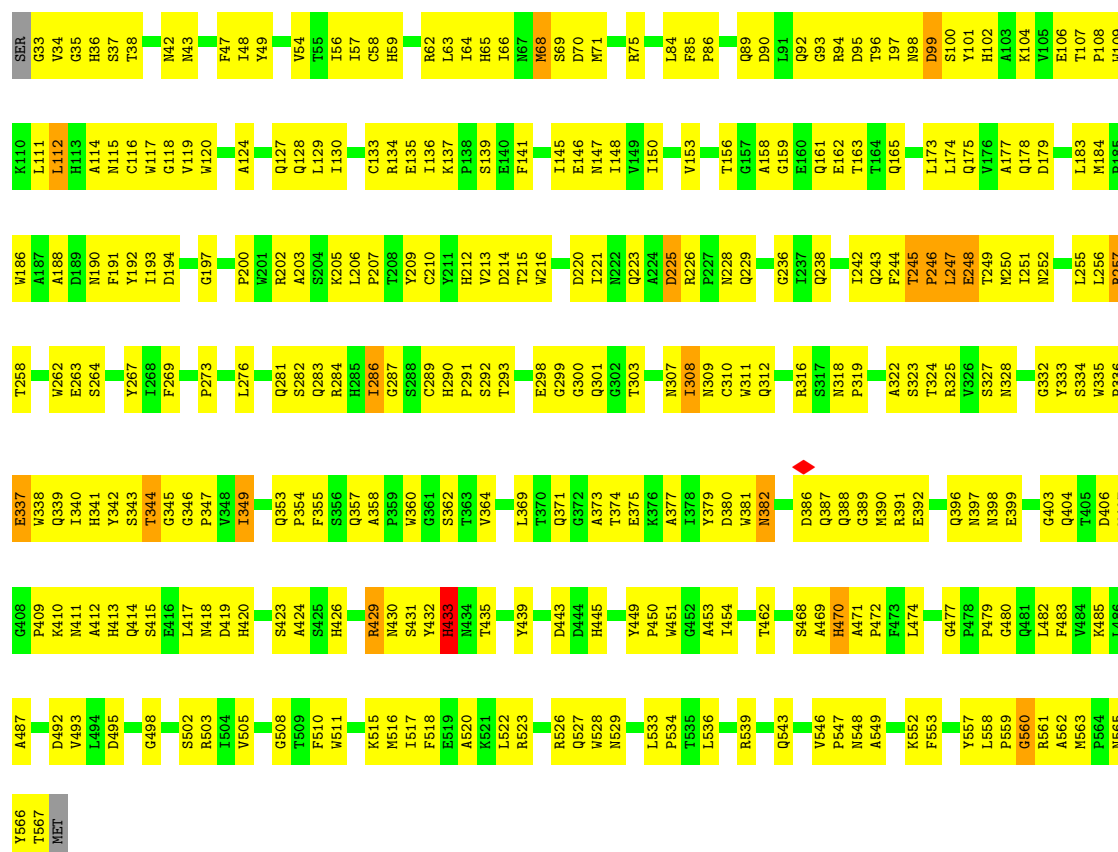






• Molecule 1: VP2

Chain r: 43% 53%



• Molecule 1: VP2

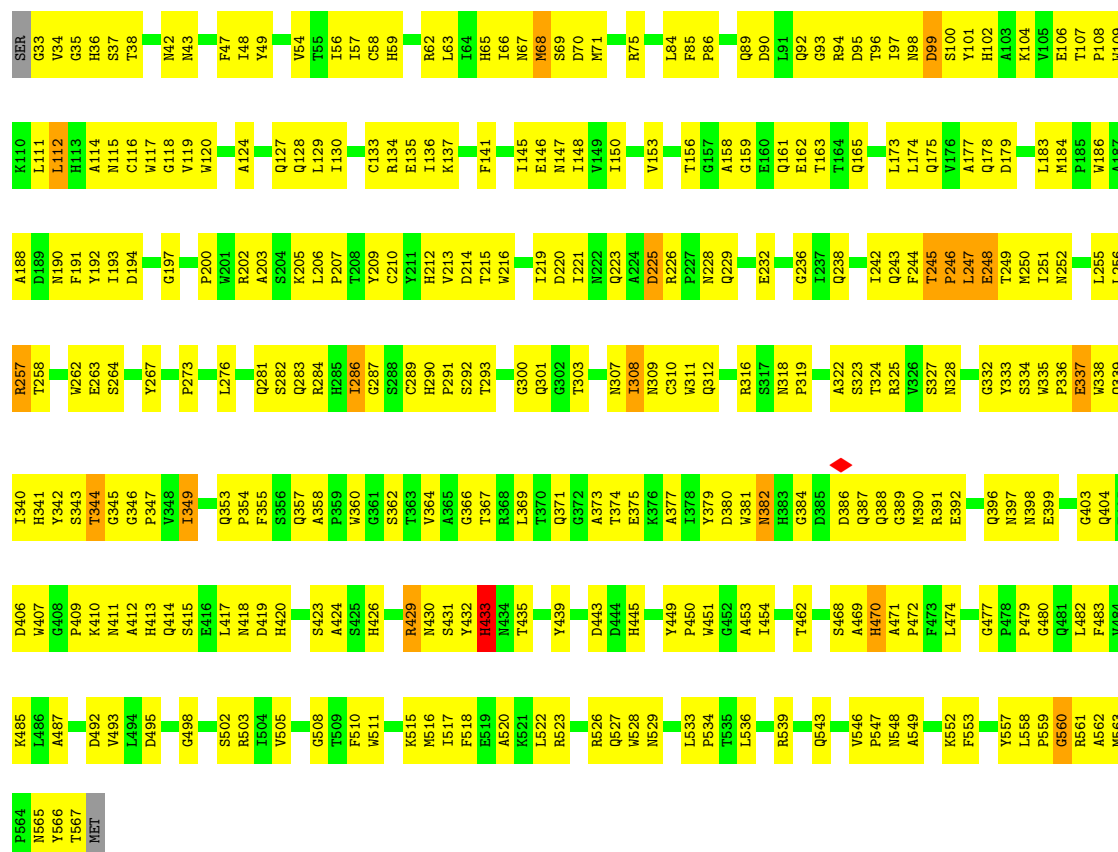
Chain s: 42% 54%





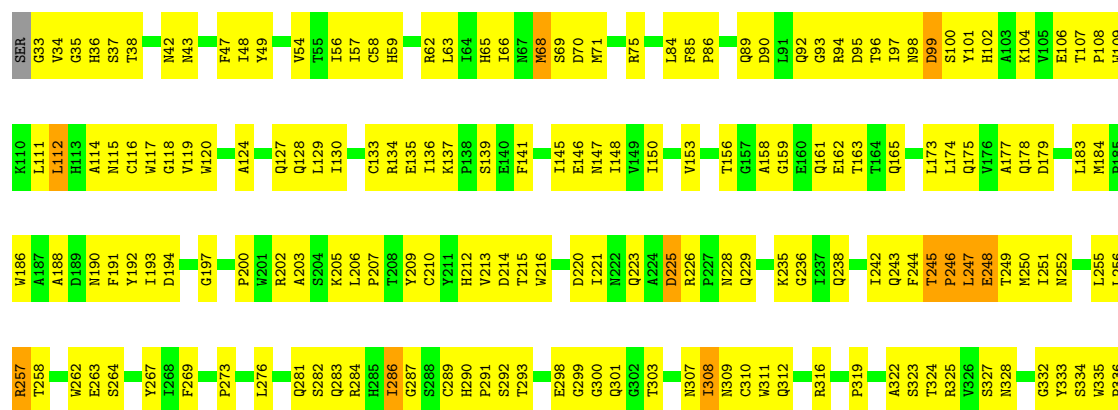
• Molecule 1: VP2

Chain u: 42% 54%



• Molecule 1: VP2

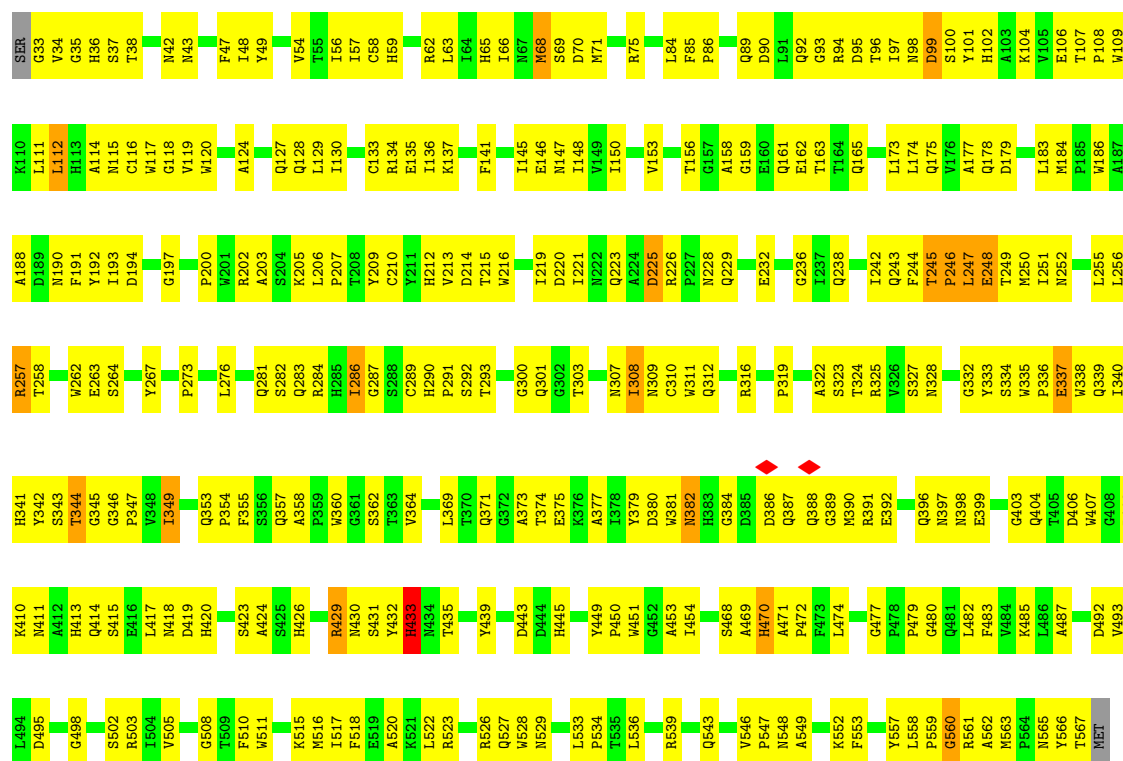
Chain v: 43% 53%





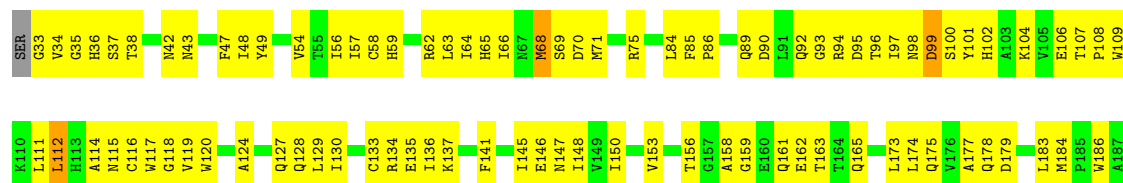
- Molecule 1: VP2

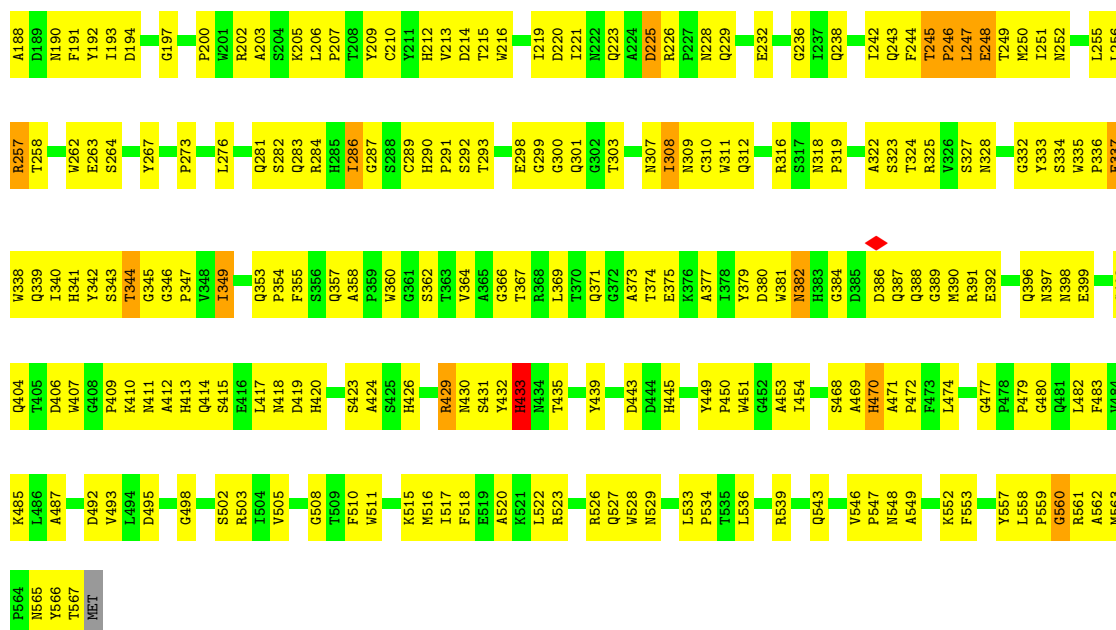
Chain w:  44% 53% .



- Molecule 1: VP2

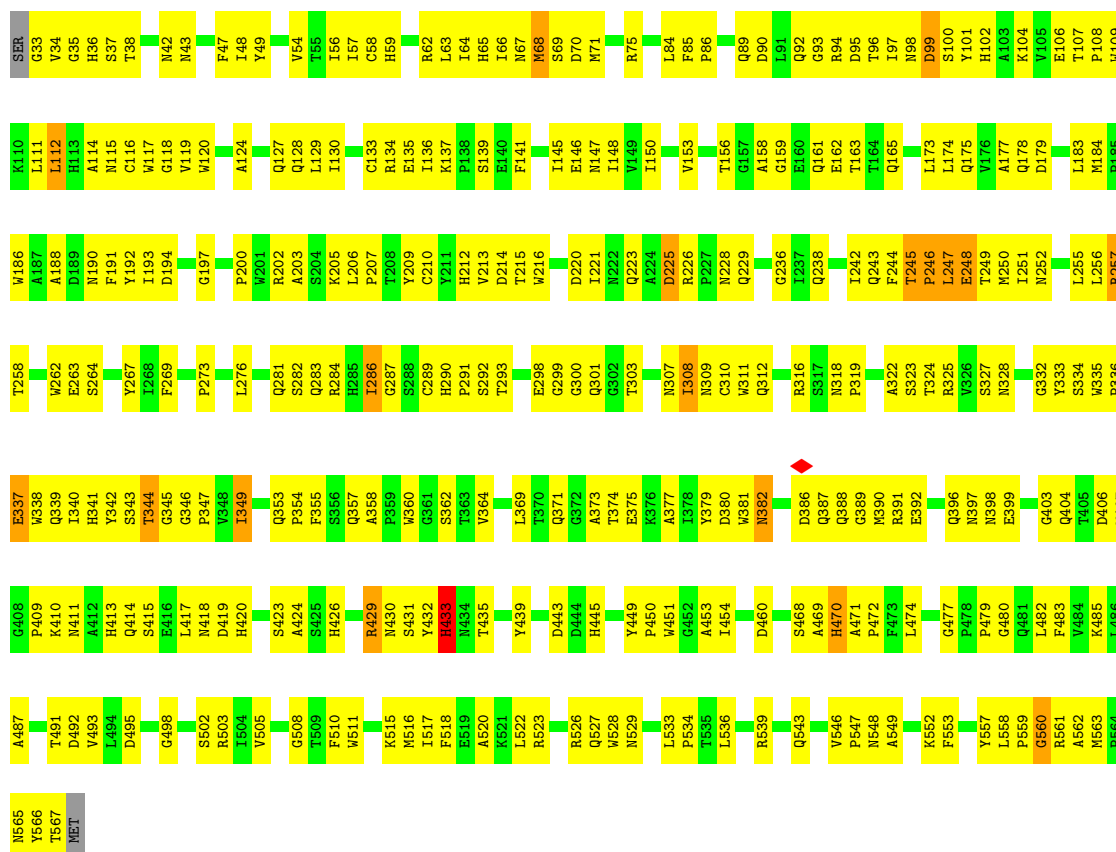
Chain x:  42% 54% .





- Molecule 1: VP2

Chain y: 42% 54%



- Molecule 1: VP2

Chain z:  44% 53%

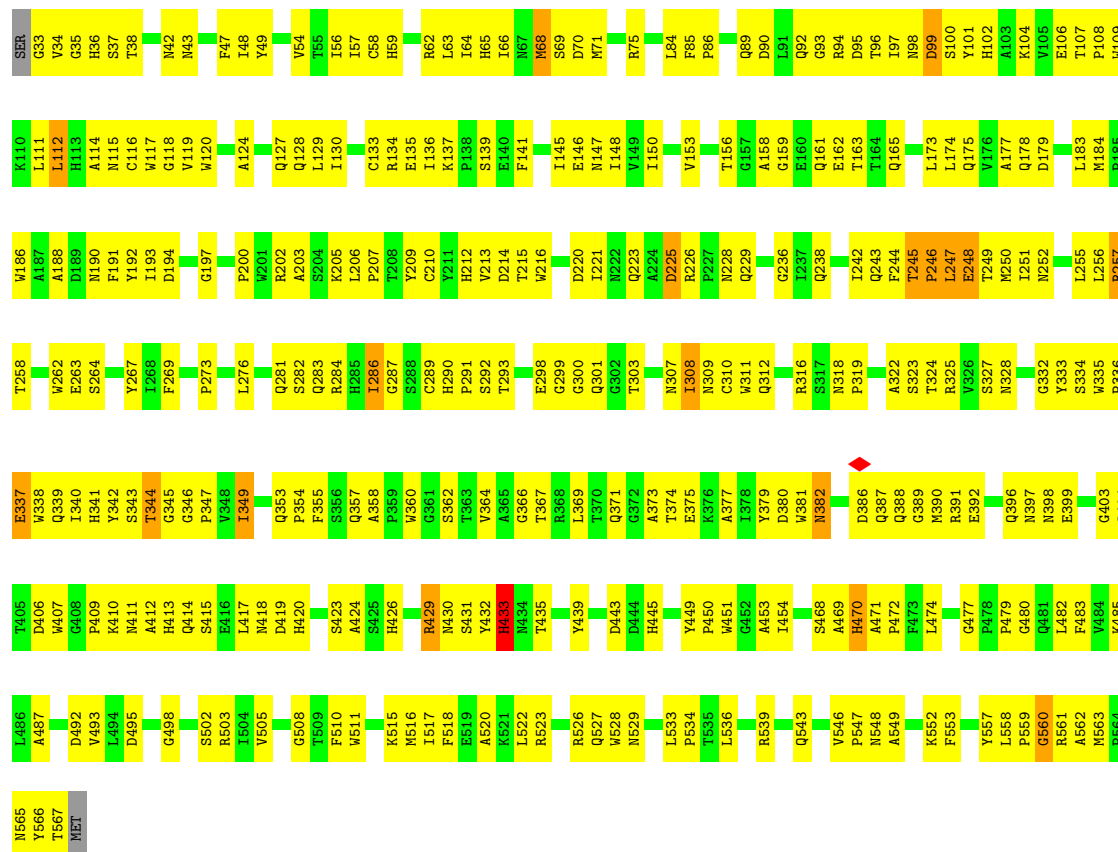
L494	D495	G498	S502	R503	T504	V505	G508	T509	F510	S511	K515	M516	L517	F518	S519	A520	K521	L522	R523	R526	Q527	W528	N529	L533	P534	T535	L536	R539	Q543	V546	P547	N548	A549	K552	F553	Y557	L558	P559	G560	R561	A562	M563	P564	N565	Y566	T567	MET							
H341	Y342	S343	T344	G345	G346	P347	V348	I349	Q353	P354	F355	S356	Q357	A358	P359	W360	G361	S362	T363	V364	L369	T370	Q371	G372	A373	T374	E375	K376	A377	G378	Y379	D380	W381	N382	D386	Q387	Q388	G389	K390	R391	E392	Q396	N397	N398	E399	G403	Q404	T405	D406	W407	G408	P409	K410	N411
R257	T258	W262	F263	S264	Y267	P273	L276	Q281	S282	Q283	L284	H285	I286	G287	S288	C289	H290	P291	S292	T293	G300	Q301	S302	T303	N307	T308	R309	C310	W311	Q312	R316	P319	A322	S323	T324	R325	Q326	S327	N328	G332	Y333	S334	W335	P336	E337	W338	Q339	I340						
A188	D189	N190	F191	Y192	L193	D194	G197	P200	W201	R202	A203	S204	K205	L206	P207	T208	Y209	C210	H211	H212	V213	D214	T215	W216	G219	D220	I221	W222	Q223	A224	D225	R226	P227	N228	Q229	E232	G236	L237	Q238	L242	Q243	F244	T245	P246	L247	Q248	T249	M250	N252	L255	T256			
K110	L111	L112	H113	A114	N115	C116	W117	G118	W119	W120	A124	Q127	Q128	L129	I130	C133	R134	E135	I136	K137	F141	I145	E146	N147	I148	V149	I150	V153	T156	G157	A158	G159	E160	Q161	E162	T163	T164	Q165	L173	L174	Q175	V176	A177	Q178	D179	L183	M184	P185	W186	A187				
SER	G33	V34	G35	H36	S37	T38	N42	N43	F47	I48	Y49	V54	T55	I56	I57	C58	H59	R62	L63	L64	H65	I66	N67	M68	S69	D70	M71	R75	L84	F85	P86	Q89	D90	L91	Q92	G93	R94	D95	T96	I97	N98	D99	S100	Y101	H102	A103	K104	V105	E106	T107	P108	W109		

• Molecule 1: VP2

Chain 6:  43% 53%

V493	N411	T340	R257	A188	K110	SER
L494	A412	H341		D189	L111	
D495	H413	Y342	W262	N190	L112	G33
	Q414	S343	E263	F191	H113	V34
G498	S415	T344	S264	I192	A114	G35
	E416	G345		I193	N115	H36
S502	L417	G346	Y267	D194	C116	S37
R503	N418	P347			W117	T38
T504	D419	V348	P273	G197	G118	
V505	H420	I349			V119	N42
					W120	N43
G508	S423	Q353	L276	P200		F47
T509	A424	P354		W201		I48
F510	S425	P354	Q281	R202	A124	
W511	H426	S356	Q283	A203		Y49
			Q284	S204	Q127	
K515	R429	Q357	H285	K205	Q128	V54
M516	N430	P359	I286	L206	L129	T55
L517	L431	W360	G287	P207	I130	I56
F518	Y432	G361	S288	T208		I57
E519	H433	S362	C289	C210	C133	C58
A520	N434	T363	H290	V211	E135	H59
K521	T435	V364	P291	H212	E136	
L522			S292	V213	K137	R62
R523	Y439	L369	T293	D214		L63
		T370		T215	F141	L64
R526	D443	Q371	E298	W216		H65
Q527	D444	G372	Q299			I66
W528	H445	A373	G300	T219	I145	N67
N529		T374	Q301	D220	E146	M68
	Y449	E375	G302	I221	N147	S69
L533	P450	K376	T303	W222	I148	D70
P534	W451	A377		Q223	V149	M71
T535	G452	Q378	N307	A224	I150	
L536	A453	Y379	I308	D225	V153	R75
	I454	D380	N309	R226		
R539		W381	C310	F227	T156	L84
	D460	N382	W311	N228	G157	F85
			Q312	Q229	A158	P86
Q543					G159	
V546	S468	D386		E232	F160	Q89
P547	H470	Q387			Q161	D90
N548	A471	Q388	P319	Q236	E162	L91
A549	P472	G389		I237	T163	Q92
	F473	N390	A322	Q238	T164	G93
K552	L474	R391	S323		Q165	R94
F553		E392	T324	L242		D95
			R325	Q243		T96
Y557	P478	Q396	V326	Q244	L173	I97
L558	P479	N397		F244	L174	N98
P559	Q480	N398	S327	T245	Q175	D99
G560	Q481	E399	N328	P246	V176	S100
				L247	A177	Y101
R561	L482	G403	G332	E248	Q178	H102
A562	F483	Q404	Y333	T249	D179	A103
M563	V484	T405	S334	K250		K104
P564	K485	D406	W335	I251	L183	V105
N565	L486	W407	P336	N252	M184	E106
Y566	A487	D408	E337		P185	T107
T567		P409	W338	L255	W186	P108
			Q230	T256	A187	W109

Chain 7:  42% 54% .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	57	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	17.508	Depositor
Minimum map value	-11.269	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	437.98, 437.98, 437.98	wwPDB
Map dimensions	359, 359, 359	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.22, 1.22, 1.22	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0	0.49	0/4472	0.79	14/6114 (0.2%)
1	1	0.49	0/4472	0.79	14/6114 (0.2%)
1	2	0.49	0/4472	0.79	14/6114 (0.2%)
1	3	0.49	0/4472	0.79	14/6114 (0.2%)
1	4	0.49	0/4472	0.79	14/6114 (0.2%)
1	5	0.49	0/4472	0.79	14/6114 (0.2%)
1	6	0.49	0/4472	0.79	14/6114 (0.2%)
1	7	0.49	0/4472	0.79	14/6114 (0.2%)
1	A	0.49	0/4472	0.79	14/6114 (0.2%)
1	B	0.49	0/4472	0.79	14/6114 (0.2%)
1	C	0.49	0/4472	0.79	14/6114 (0.2%)
1	D	0.49	0/4472	0.79	14/6114 (0.2%)
1	E	0.49	0/4472	0.79	14/6114 (0.2%)
1	F	0.49	0/4472	0.79	14/6114 (0.2%)
1	G	0.49	0/4472	0.79	14/6114 (0.2%)
1	H	0.49	0/4472	0.79	14/6114 (0.2%)
1	I	0.49	0/4472	0.79	14/6114 (0.2%)
1	J	0.49	0/4472	0.79	14/6114 (0.2%)
1	K	0.49	0/4472	0.79	14/6114 (0.2%)
1	L	0.49	0/4472	0.79	14/6114 (0.2%)
1	M	0.49	0/4472	0.79	14/6114 (0.2%)
1	N	0.49	0/4472	0.79	14/6114 (0.2%)
1	O	0.49	0/4472	0.79	14/6114 (0.2%)
1	P	0.49	0/4472	0.79	14/6114 (0.2%)
1	Q	0.49	0/4472	0.79	14/6114 (0.2%)
1	R	0.49	0/4472	0.79	14/6114 (0.2%)
1	S	0.49	0/4472	0.79	14/6114 (0.2%)
1	T	0.49	0/4472	0.79	14/6114 (0.2%)
1	U	0.49	0/4472	0.79	14/6114 (0.2%)
1	V	0.49	0/4472	0.79	14/6114 (0.2%)
1	W	0.49	0/4472	0.79	14/6114 (0.2%)
1	X	0.49	0/4472	0.79	14/6114 (0.2%)
1	Y	0.49	0/4472	0.79	14/6114 (0.2%)
1	Z	0.49	0/4472	0.79	14/6114 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	a	0.49	0/4472	0.79	14/6114 (0.2%)
1	b	0.49	0/4472	0.79	14/6114 (0.2%)
1	c	0.49	0/4472	0.79	14/6114 (0.2%)
1	d	0.49	0/4472	0.79	14/6114 (0.2%)
1	e	0.49	0/4472	0.79	14/6114 (0.2%)
1	f	0.49	0/4472	0.79	14/6114 (0.2%)
1	g	0.49	0/4472	0.79	14/6114 (0.2%)
1	h	0.49	0/4472	0.79	14/6114 (0.2%)
1	i	0.49	0/4472	0.79	14/6114 (0.2%)
1	j	0.49	0/4472	0.79	14/6114 (0.2%)
1	k	0.49	0/4472	0.79	14/6114 (0.2%)
1	l	0.49	0/4472	0.79	14/6114 (0.2%)
1	m	0.49	0/4472	0.79	14/6114 (0.2%)
1	n	0.49	0/4472	0.79	14/6114 (0.2%)
1	o	0.49	0/4472	0.79	14/6114 (0.2%)
1	p	0.49	0/4472	0.79	14/6114 (0.2%)
1	q	0.49	0/4472	0.79	14/6114 (0.2%)
1	r	0.49	0/4472	0.79	14/6114 (0.2%)
1	s	0.49	0/4472	0.79	14/6114 (0.2%)
1	t	0.49	0/4472	0.79	14/6114 (0.2%)
1	u	0.49	0/4472	0.79	14/6114 (0.2%)
1	v	0.49	0/4472	0.79	14/6114 (0.2%)
1	w	0.49	0/4472	0.79	14/6114 (0.2%)
1	x	0.49	0/4472	0.79	14/6114 (0.2%)
1	y	0.49	0/4472	0.79	14/6114 (0.2%)
1	z	0.49	0/4472	0.79	14/6114 (0.2%)
All	All	0.49	0/268320	0.79	840/366840 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	2
1	1	0	2
1	2	0	2
1	3	0	2
1	4	0	2
1	5	0	2
1	6	0	2
1	7	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	2
1	I	0	2
1	J	0	2
1	K	0	2
1	L	0	2
1	M	0	2
1	N	0	2
1	O	0	2
1	P	0	2
1	Q	0	2
1	R	0	2
1	S	0	2
1	T	0	2
1	U	0	2
1	V	0	2
1	W	0	2
1	X	0	2
1	Y	0	2
1	Z	0	2
1	a	0	2
1	b	0	2
1	c	0	2
1	d	0	2
1	e	0	2
1	f	0	2
1	g	0	2
1	h	0	2
1	i	0	2
1	j	0	2
1	k	0	2
1	l	0	2
1	m	0	2
1	n	0	2
1	o	0	2
1	p	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	q	0	2
1	r	0	2
1	s	0	2
1	t	0	2
1	u	0	2
1	v	0	2
1	w	0	2
1	x	0	2
1	y	0	2
1	z	0	2
All	All	0	120

There are no bond length outliers.

The worst 5 of 840 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	r	245	THR	CA-C-N	10.94	131.38	119.90
1	r	245	THR	C-N-CA	10.94	131.38	119.90
1	7	245	THR	CA-C-N	10.94	131.38	119.90
1	7	245	THR	C-N-CA	10.94	131.38	119.90
1	E	245	THR	CA-C-N	10.93	131.37	119.90

There are no chirality outliers.

5 of 120 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	382	ASN	Peptide
1	A	68	MET	Peptide
1	B	382	ASN	Peptide
1	B	68	MET	Peptide
1	C	68	MET	Peptide

## 5.2 Too-close contacts [i](#)

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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	4326	0	4014	467	0
1	1	4326	0	4013	456	0
1	2	4326	0	4014	462	0
1	3	4326	0	4014	470	0
1	4	4326	0	4013	463	0
1	5	4326	0	4013	463	0
1	6	4326	0	4014	456	0
1	7	4326	0	4013	465	0
1	A	4326	0	4014	462	0
1	B	4326	0	4013	466	0
1	C	4326	0	4014	465	0
1	D	4326	0	4013	459	0
1	E	4326	0	4014	461	0
1	F	4326	0	4013	454	0
1	G	4326	0	4014	458	0
1	H	4326	0	4013	470	0
1	I	4326	0	4014	463	0
1	J	4326	0	4013	461	0
1	K	4326	0	4013	464	0
1	L	4326	0	4014	467	0
1	M	4326	0	4014	466	0
1	N	4326	0	4014	464	0
1	O	4326	0	4014	466	0
1	P	4326	0	4013	463	0
1	Q	4326	0	4014	464	0
1	R	4326	0	4014	461	0
1	S	4326	0	4013	454	0
1	T	4326	0	4014	462	0
1	U	4326	0	4014	461	0
1	V	4326	0	4014	469	0
1	W	4326	0	4014	468	0
1	X	4326	0	4013	463	0
1	Y	4326	0	4014	464	0
1	Z	4326	0	4014	464	0
1	a	4326	0	4013	463	0
1	b	4326	0	4014	470	0
1	c	4326	0	4013	456	0
1	d	4326	0	4013	465	0
1	e	4326	0	4014	469	0
1	f	4326	0	4014	459	0
1	g	4326	0	4014	462	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	h	4326	0	4014	466	0
1	i	4326	0	4014	461	0
1	j	4326	0	4014	466	0
1	k	4326	0	4014	465	0
1	l	4326	0	4014	461	0
1	m	4326	0	4014	465	0
1	n	4326	0	4014	465	0
1	o	4326	0	4013	456	0
1	p	4326	0	4014	462	0
1	q	4326	0	4014	459	0
1	r	4326	0	4014	463	0
1	s	4326	0	4013	465	0
1	t	4326	0	4014	464	0
1	u	4326	0	4014	461	0
1	v	4326	0	4014	458	0
1	w	4326	0	4014	463	0
1	x	4326	0	4013	467	0
1	y	4326	0	4014	460	0
1	z	4326	0	4013	450	0
All	All	259560	0	240820	21372	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 43.

The worst 5 of 21372 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:X:34:VAL:N	1:5:36:HIS:CE1	1.71	1.58
1:a:34:VAL:N	1:e:36:HIS:CE1	1.71	1.58
1:J:36:HIS:CE1	1:0:34:VAL:N	1.72	1.58
1:p:34:VAL:H	1:u:36:HIS:CE1	1.22	1.58
1:h:34:VAL:H	1:l:36:HIS:CE1	1.22	1.58

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	0	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	1	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	2	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	3	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	4	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	5	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	6	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	7	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	A	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	B	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	C	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	D	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	E	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	F	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	G	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	H	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	I	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	J	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	K	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	L	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	M	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	N	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	O	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	P	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	Q	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	S	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	T	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	U	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	V	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	W	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	X	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	Y	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	Z	533/537 (99%)	507 (95%)	25 (5%)	1 (0%)	44	74
1	a	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	b	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	c	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	d	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	e	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	f	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	g	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	h	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	i	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	j	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	k	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	l	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	m	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	n	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	o	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	p	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	q	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	r	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	s	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	t	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	u	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	v	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	x	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	y	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
1	z	533/537 (99%)	508 (95%)	24 (4%)	1 (0%)	44	74
All	All	31980/32220 (99%)	30479 (95%)	1441 (4%)	60 (0%)	45	74

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	193	ILE
1	H	193	ILE
1	S	193	ILE
1	V	193	ILE
1	1	193	ILE

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	1	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	2	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	3	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	4	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	5	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	6	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	7	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	A	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	B	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	C	464/466 (100%)	452 (97%)	12 (3%)	41	61
1	D	464/466 (100%)	452 (97%)	12 (3%)	41	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	E	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	F	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	G	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	H	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	I	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	J	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	K	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	L	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	M	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	N	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	O	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	P	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	Q	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	R	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	S	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	T	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	U	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	V	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	W	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	X	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	Y	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	Z	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	a	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	b	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	c	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	d	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	e	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	f	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	g	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	h	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	i	464/466 (100%)	452 (97%)	12 (3%)	41	61	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	j	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	k	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	l	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	m	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	n	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	o	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	p	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	q	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	r	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	s	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	t	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	u	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	v	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	w	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	x	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	y	464/466 (100%)	452 (97%)	12 (3%)	41	61	
1	z	464/466 (100%)	452 (97%)	12 (3%)	41	61	
All	All	27840/27960 (100%)	27120 (97%)	720 (3%)	42	61	

5 of 720 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	g	430	ASN
1	p	470	HIS
1	h	433	HIS
1	g	349	ILE
1	l	257	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1178 such sidechains are listed below:

Mol	Chain	Res	Type
1	p	113	HIS
1	6	212	HIS
1	q	290	HIS
1	p	98	ASN

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Mol	Chain	Res	Type
1	v	113	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

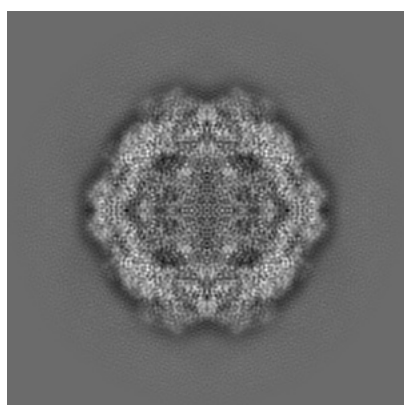
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7301. These allow visual inspection of the internal detail of the map and identification of artifacts.

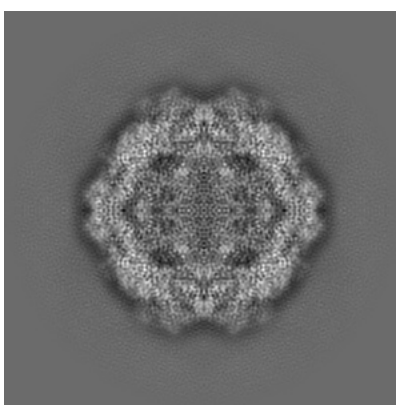
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

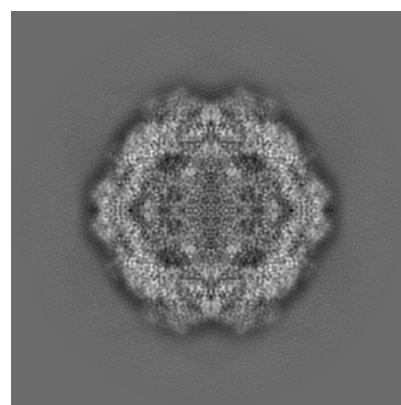
#### 6.1.1 Primary map



X



Y

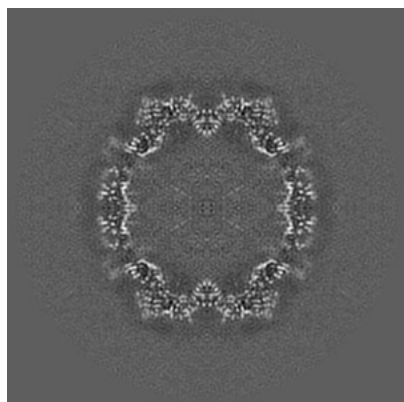


Z

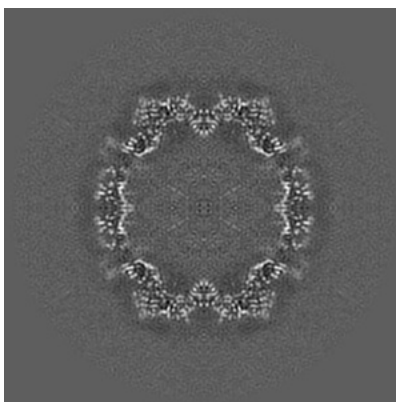
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

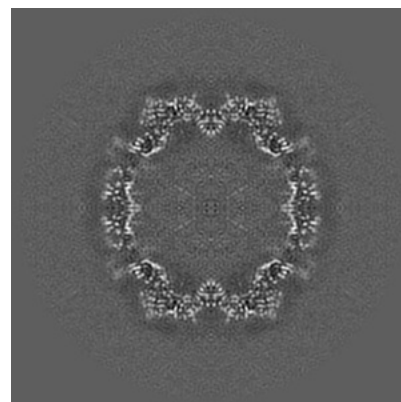
#### 6.2.1 Primary map



X Index: 179



Y Index: 179

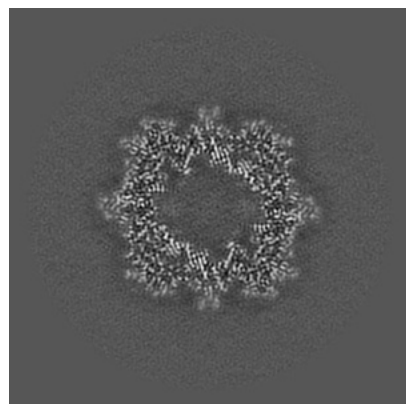


Z Index: 179

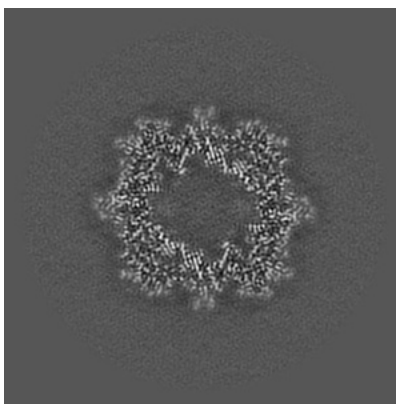
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

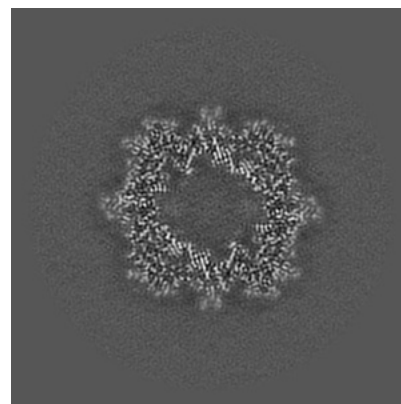
### 6.3.1 Primary map



X Index: 123



Y Index: 123

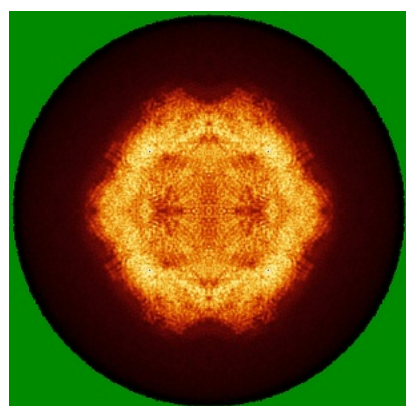


Z Index: 123

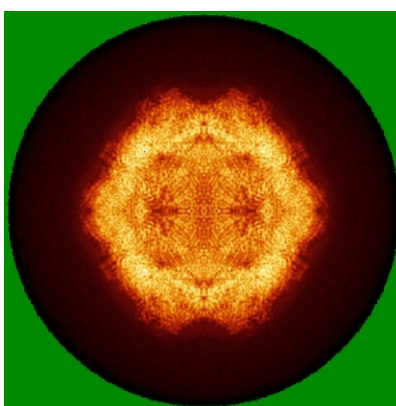
The images above show the largest variance slices of the map in three orthogonal directions.

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

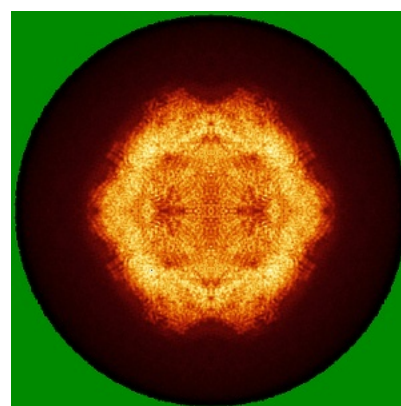
### 6.4.1 Primary map



X



Y

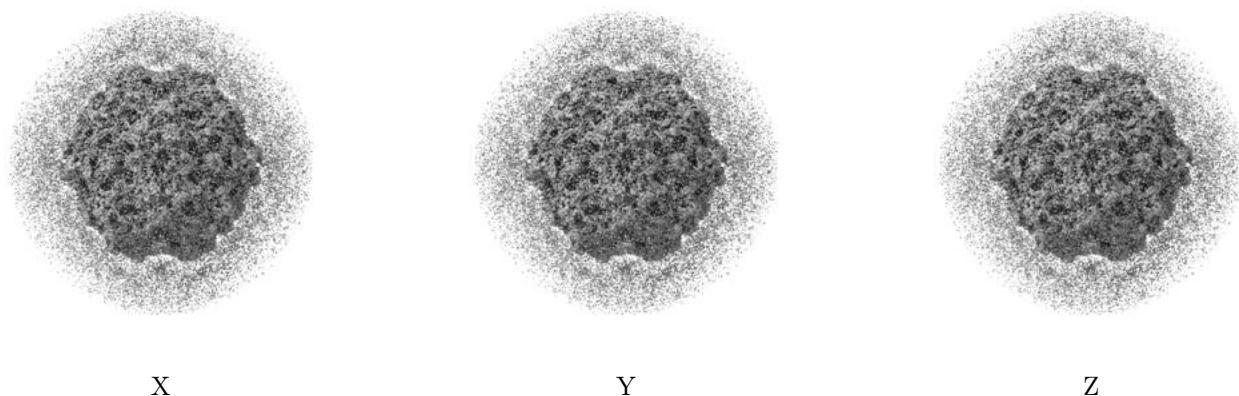


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

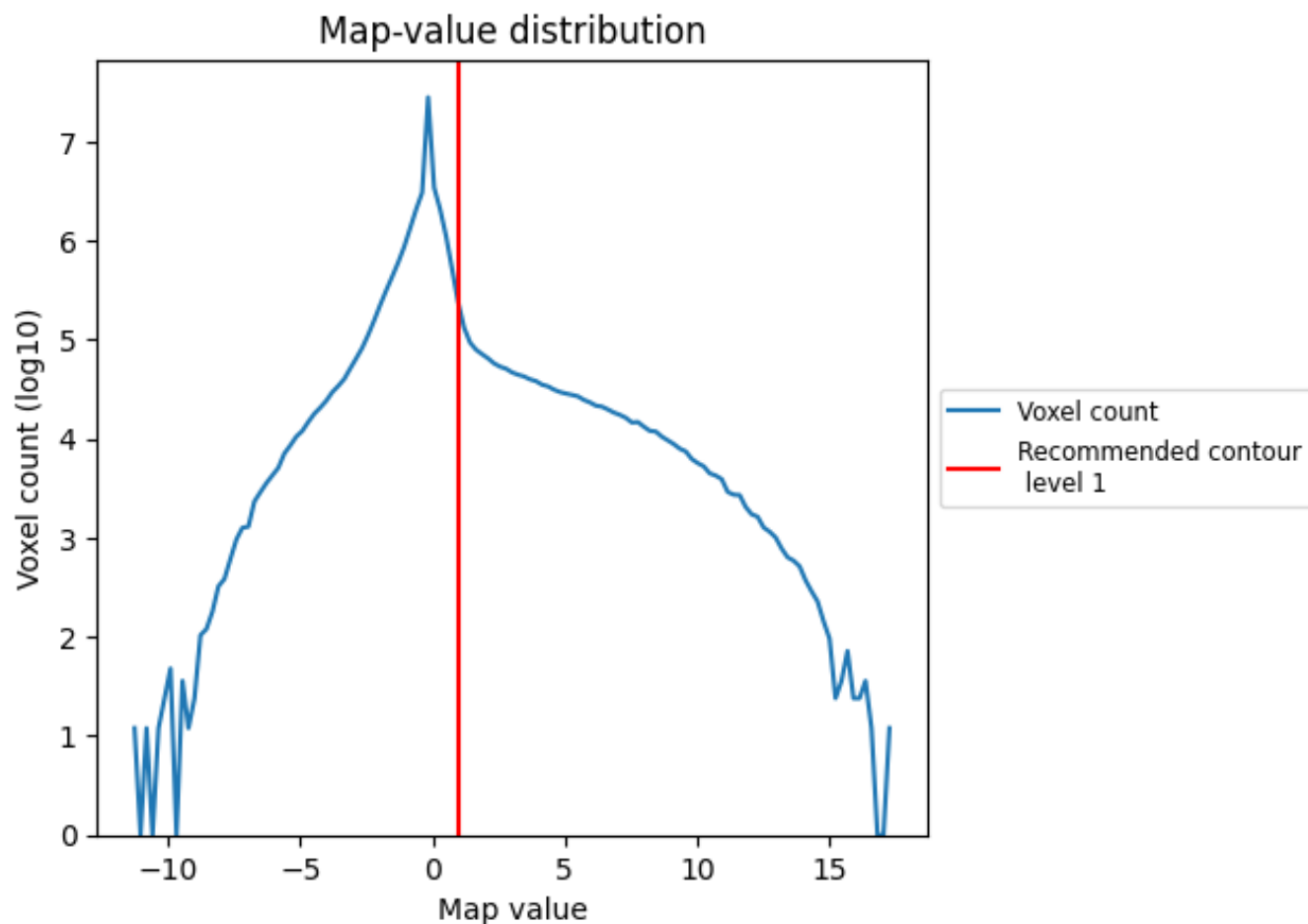
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

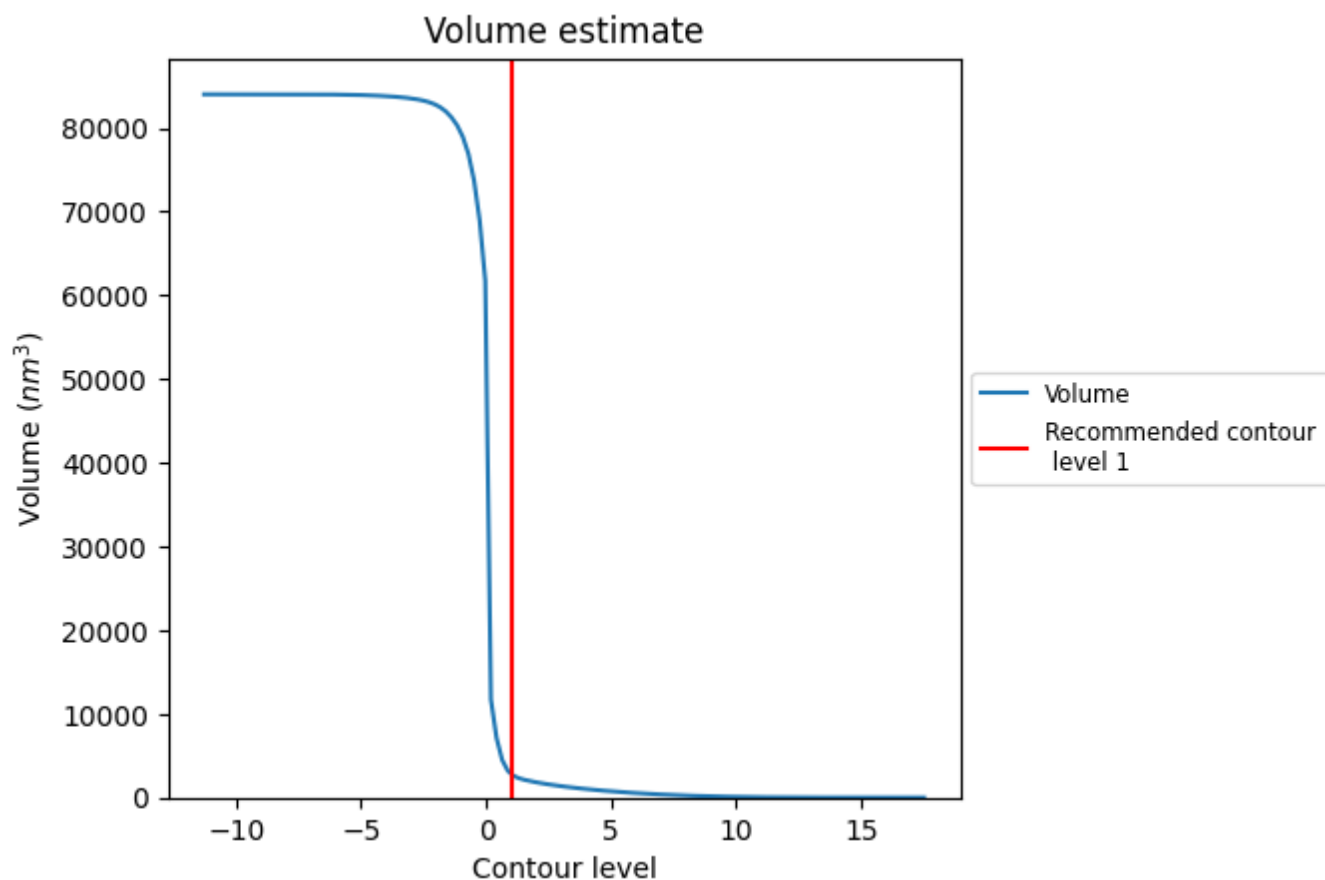
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

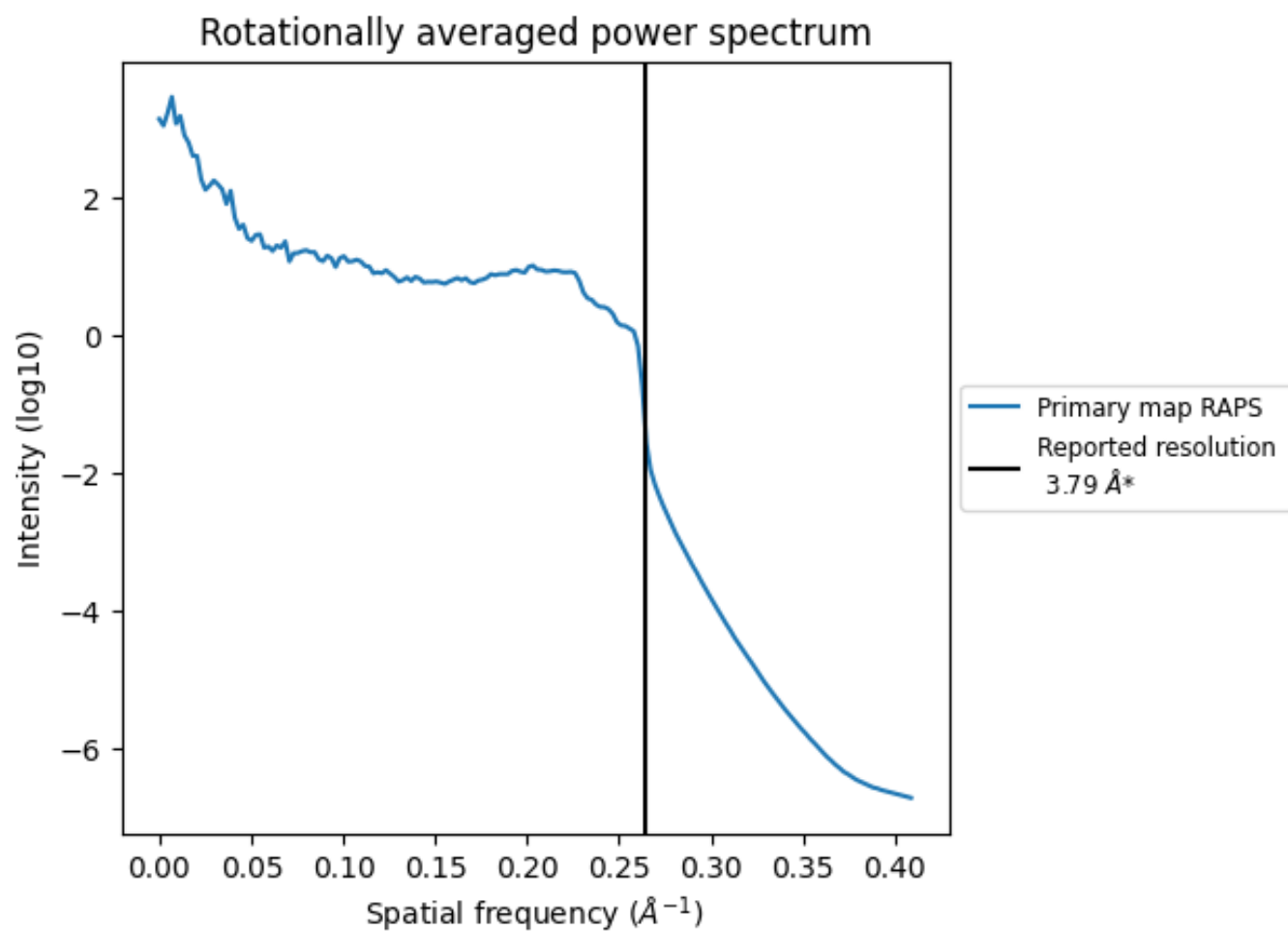
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2859 nm<sup>3</sup>; this corresponds to an approximate mass of 2582 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 0.264 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

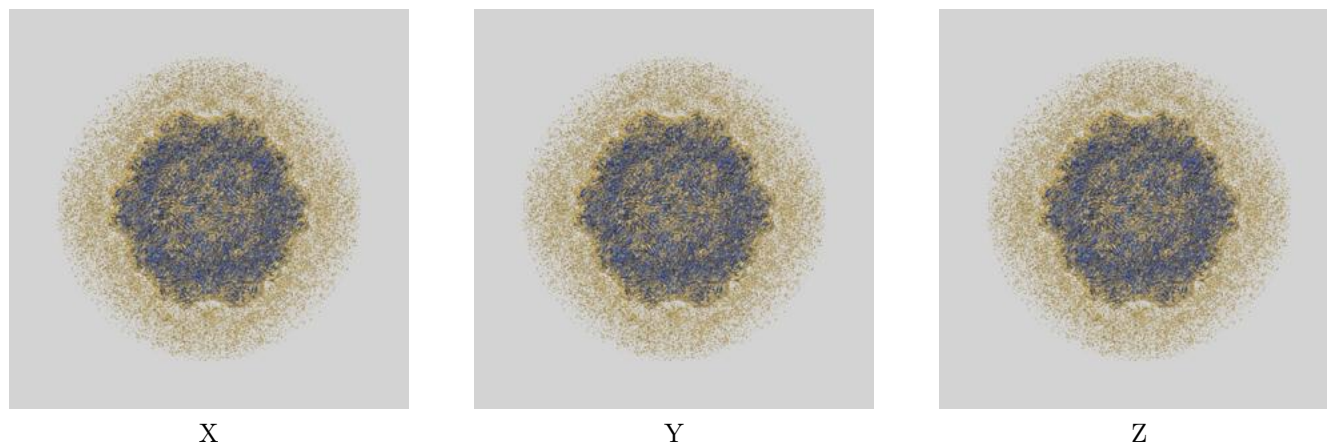
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

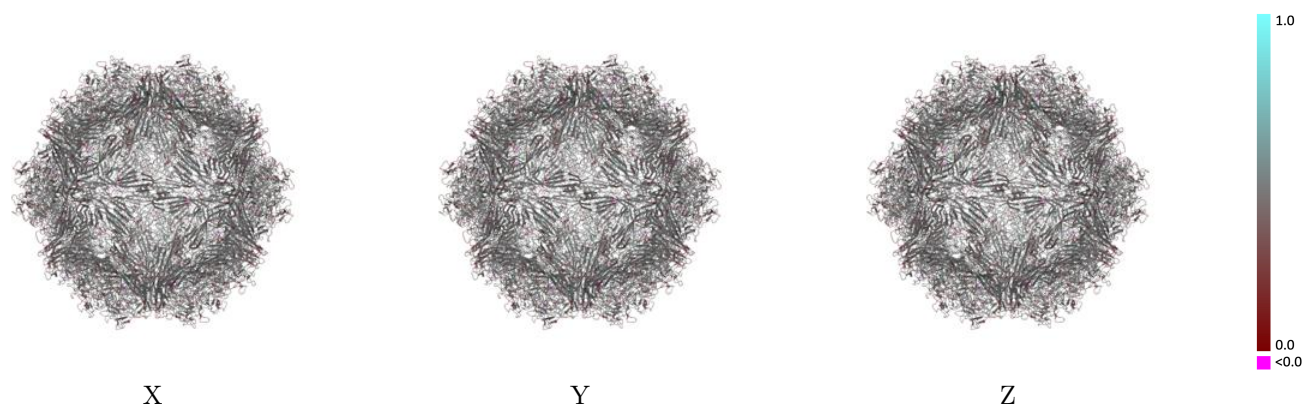
This section contains information regarding the fit between EMDB map EMD-7301 and PDB model 6BX0. Per-residue inclusion information can be found in section [3](#) on page [10](#).

### 9.1 Map-model overlay [i](#)



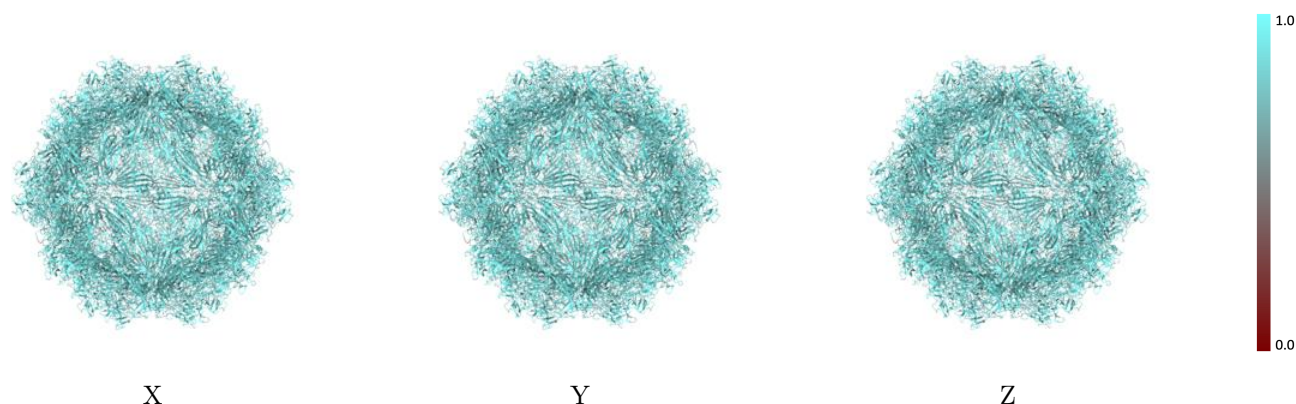
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



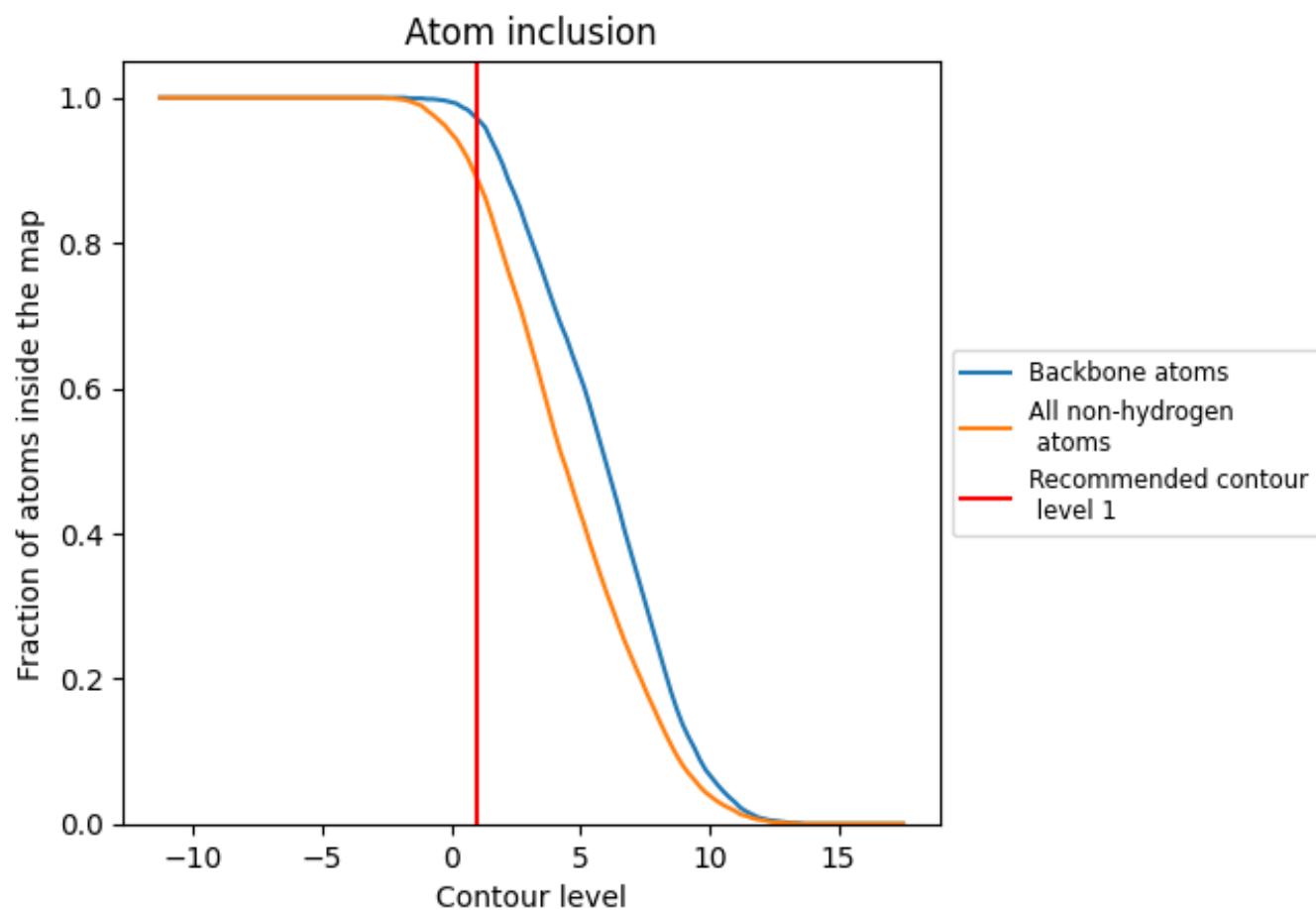
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 89% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.4470
0	 0.8880	 0.4450
1	 0.8890	 0.4460
2	 0.8890	 0.4470
3	 0.8890	 0.4480
4	 0.8880	 0.4450
5	 0.8890	 0.4450
6	 0.8880	 0.4450
7	 0.8880	 0.4460
A	 0.8900	 0.4470
B	 0.8890	 0.4470
C	 0.8880	 0.4480
D	 0.8880	 0.4450
E	 0.8880	 0.4440
F	 0.8890	 0.4460
G	 0.8890	 0.4470
H	 0.8890	 0.4470
I	 0.8890	 0.4460
J	 0.8880	 0.4460
K	 0.8880	 0.4460
L	 0.8890	 0.4470
M	 0.8880	 0.4460
N	 0.8880	 0.4450
O	 0.8880	 0.4450
P	 0.8880	 0.4470
Q	 0.8890	 0.4470
R	 0.8890	 0.4470
S	 0.8890	 0.4470
T	 0.8890	 0.4480
U	 0.8880	 0.4450
V	 0.8880	 0.4450
W	 0.8880	 0.4450
X	 0.8880	 0.4460
Y	 0.8890	 0.4480
Z	 0.8890	 0.4480



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Chain	Atom inclusion	Q-score
a	 0.8890	 0.4460
b	 0.8870	 0.4480
c	 0.8890	 0.4460
d	 0.8880	 0.4460
e	 0.8880	 0.4470
f	 0.8890	 0.4460
g	 0.8890	 0.4470
h	 0.8890	 0.4480
i	 0.8890	 0.4480
j	 0.8890	 0.4470
k	 0.8880	 0.4440
l	 0.8890	 0.4470
m	 0.8890	 0.4470
n	 0.8890	 0.4460
o	 0.8890	 0.4470
p	 0.8880	 0.4460
q	 0.8880	 0.4450
r	 0.8880	 0.4460
s	 0.8880	 0.4450
t	 0.8890	 0.4470
u	 0.8890	 0.4470
v	 0.8890	 0.4480
w	 0.8880	 0.4460
x	 0.8890	 0.4470
y	 0.8890	 0.4480
z	 0.8890	 0.4470