



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:54 AM UTC

PDB ID : 7QOI / pdb_00007qoi
EMDB ID : EMD-14091
Title : Unique vertex of the phicrAss001 virion
Authors : Bayfield, O.W.; Shkoporov, A.N.; Yutin, N.; Khokhlova, E.V.; Smith, J.L.R.;
Hawkins, D.E.D.P.; Koonin, E.V.; Hill, C.; Antson, A.A.
Deposited on : 2021-12-24
Resolution : 3.62 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:

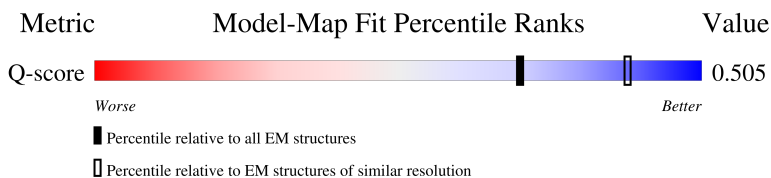
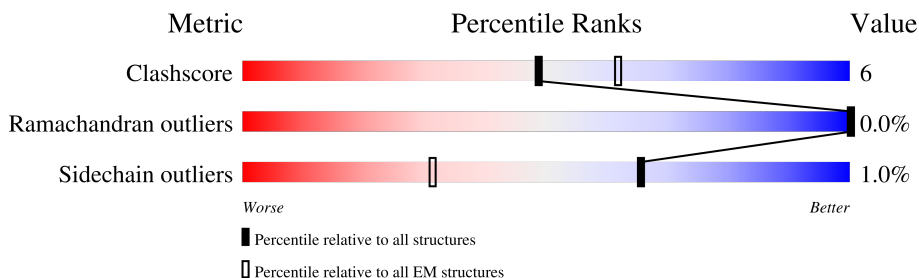
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.62 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	11773 (3.12 - 4.12)

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	AA	504	
1	AB	504	
1	AC	504	
1	AD	504	

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Mol	Chain	Length	Quality of chain
1	AE	504	
1	AF	504	
1	BA	504	
1	BB	504	
1	BC	504	
1	BD	504	
1	BE	504	
1	BF	504	
1	CA	504	
1	CB	504	
1	CC	504	
1	CD	504	
1	CE	504	
1	CF	504	
1	DA	504	
1	DB	504	
1	DC	504	
1	DD	504	
1	DE	504	
1	DF	504	
1	EA	504	
1	EB	504	
1	EC	504	
1	ED	504	
1	EE	504	

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Mol	Chain	Length	Quality of chain
1	EF	504	
2	Aa	333	
2	Ab	333	
2	Ad	333	
2	Ae	333	
2	Af	333	
2	Ba	333	
2	Bb	333	
2	Bd	333	
2	Be	333	
2	Bf	333	
2	Ca	333	
2	Cb	333	
2	Cd	333	
2	Ce	333	
2	Cf	333	
2	Da	333	
2	Db	333	
2	Dd	333	
2	De	333	
2	Df	333	
2	Ea	333	
2	Eb	333	
2	Ed	333	
2	Ee	333	

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Mol	Chain	Length	Quality of chain
2	Ef	333	
3	Ag	104	
3	Ah	104	
3	Bg	104	
3	Bh	104	
3	Cg	104	
3	Ch	104	
3	Dg	104	
3	Dh	104	
3	Eg	104	
3	Eh	104	
4	Ai	97	
4	Aj	97	
4	Ak	97	
4	Bi	97	
4	Bj	97	
4	Bk	97	
4	Ci	97	
4	Cj	97	
4	Ck	97	
4	Di	97	
4	Dj	97	
4	Dk	97	
4	Ei	97	
4	Ej	97	

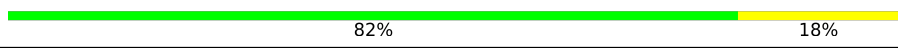
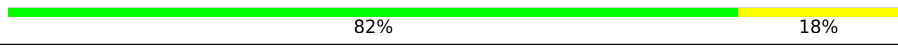
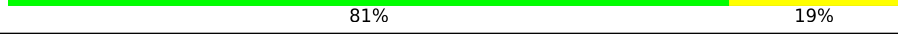
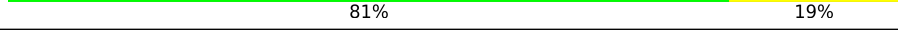
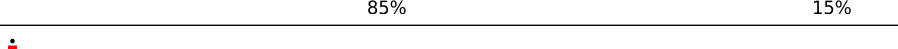
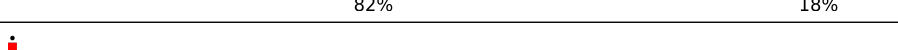
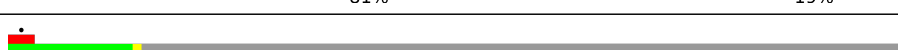
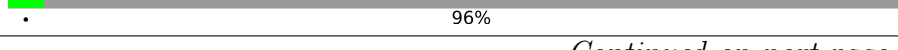
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Mol	Chain	Length	Quality of chain
4	Ek	97	
5	FA	806	
5	FB	806	
5	FC	806	
5	FD	806	
5	FE	806	
5	FF	806	
5	FG	806	
5	FH	806	
5	FI	806	
5	FJ	806	
5	FK	806	
5	FL	806	
6	FM	236	
6	FN	236	
6	FO	236	
6	FP	236	
6	FQ	236	
6	FR	236	
6	FS	236	
6	FT	236	
6	FU	236	
6	FV	236	
6	FW	236	
6	FX	236	

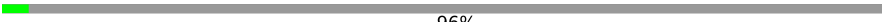
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Mol	Chain	Length	Quality of chain
7	FY	225	
7	FZ	225	
7	GA	225	
7	GB	225	
7	GC	225	
7	GD	225	
7	GE	225	
7	GF	225	
7	GG	225	
7	GH	225	
7	GI	225	
7	GJ	225	
8	GK	842	
8	GL	842	
8	GM	842	
8	GN	842	
8	GO	842	
8	GP	842	
8	GQ	842	
8	GR	842	
8	GS	842	
8	GT	842	
8	GU	842	
8	GV	842	
8	IK	842	

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Mol	Chain	Length	Quality of chain
8	IL	842	 96%
8	IM	842	 96%
8	IN	842	 96%
8	IO	842	 96%
8	IP	842	 96%
8	IQ	842	 96%
8	IR	842	 96%
8	IS	842	 96%
8	IT	842	 96%
8	IU	842	 96%
8	IV	842	 96%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 310209 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 capsid protein gp32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	484	Total	C	N	O	S	0	0
			3861	2451	668	723	19		
1	AB	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	AC	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	AD	456	Total	C	N	O	S	0	0
			3649	2329	631	671	18		
1	AE	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	AF	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	BA	485	Total	C	N	O	S	0	0
			3868	2455	669	725	19		
1	BB	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	BC	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	BD	456	Total	C	N	O	S	0	0
			3649	2329	631	671	18		
1	BE	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	BF	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	CA	483	Total	C	N	O	S	0	0
			3855	2448	667	721	19		
1	CB	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	CC	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	CD	451	Total	C	N	O	S	0	0
			3612	2307	623	664	18		
1	CE	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CF	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	DA	485	Total	C	N	O	S	0	0
			3868	2455	669	725	19		
1	DB	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	DC	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	DD	456	Total	C	N	O	S	0	0
			3649	2329	631	671	18		
1	DE	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	DF	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	EA	485	Total	C	N	O	S	0	0
			3868	2455	669	725	19		
1	EB	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	EC	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	ED	456	Total	C	N	O	S	0	0
			3649	2329	631	671	18		
1	EE	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		
1	EF	503	Total	C	N	O	S	0	0
			4012	2552	695	745	20		

- Molecule 2 is a protein called Auxiliary capsid protein gp36.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Aa	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ab	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ad	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ae	267	Total	C	N	O	S	0	0
			2077	1335	332	401	9		
2	Af	185	Total	C	N	O	S	0	0
			1434	919	226	283	6		
2	Ba	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Bb	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Bd	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Be	266	Total	C	N	O	S	0	0
			2070	1330	331	400	9		
2	Bf	185	Total	C	N	O	S	0	0
			1434	919	226	283	6		
2	Ca	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Cb	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Cd	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ce	267	Total	C	N	O	S	0	0
			2077	1335	332	401	9		
2	Cf	185	Total	C	N	O	S	0	0
			1434	919	226	283	6		
2	Da	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Db	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Dd	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	De	267	Total	C	N	O	S	0	0
			2077	1335	332	401	9		
2	Df	185	Total	C	N	O	S	0	0
			1434	919	226	283	6		
2	Ea	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Eb	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ed	333	Total	C	N	O	S	0	0
			2542	1624	410	498	10		
2	Ee	267	Total	C	N	O	S	0	0
			2077	1335	332	401	9		
2	Ef	185	Total	C	N	O	S	0	0
			1434	919	226	283	6		

- Molecule 3 is a protein called Portal vertex capsid protein gp57.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ag	82	Total	C	N	O	S	0	0
			619	392	100	118	9		
3	Ah	73	Total	C	N	O	S	0	0
			563	359	91	105	8		
3	Bg	82	Total	C	N	O	S	0	0
			619	392	100	118	9		
3	Bh	73	Total	C	N	O	S	0	0
			563	359	91	105	8		
3	Cg	82	Total	C	N	O	S	0	0
			619	392	100	118	9		
3	Ch	73	Total	C	N	O	S	0	0
			563	359	91	105	8		
3	Dg	82	Total	C	N	O	S	0	0
			619	392	100	118	9		
3	Dh	73	Total	C	N	O	S	0	0
			563	359	91	105	8		
3	Eg	82	Total	C	N	O	S	0	0
			619	392	100	118	9		
3	Eh	73	Total	C	N	O	S	0	0
			563	359	91	105	8		

- Molecule 4 is a protein called Head fiber trimer protein gp21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ai	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Aj	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ak	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Bi	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Bj	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Bk	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ci	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Cj	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ck	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Di	38	Total	C	N	O	S	0	0
			310	201	51	56	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Dj	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Dk	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ei	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ej	38	Total	C	N	O	S	0	0
			310	201	51	56	2		
4	Ek	38	Total	C	N	O	S	0	0
			310	201	51	56	2		

- Molecule 5 is a protein called Portal protein gp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	FA	688	Total	C	N	O	S	0	0
			5617	3558	957	1077	25		
5	FB	678	Total	C	N	O	S	0	0
			5545	3519	941	1062	23		
5	FC	684	Total	C	N	O	S	0	0
			5597	3550	951	1072	24		
5	FD	705	Total	C	N	O	S	0	0
			5759	3657	976	1102	24		
5	FE	660	Total	C	N	O	S	0	0
			5400	3426	920	1031	23		
5	FF	684	Total	C	N	O	S	0	0
			5593	3543	952	1074	24		
5	FG	680	Total	C	N	O	S	0	0
			5569	3531	948	1066	24		
5	FH	689	Total	C	N	O	S	0	0
			5618	3558	958	1078	24		
5	FI	694	Total	C	N	O	S	0	0
			5671	3601	961	1085	24		
5	FJ	698	Total	C	N	O	S	0	0
			5699	3613	967	1094	25		
5	FK	669	Total	C	N	O	S	0	0
			5478	3483	929	1043	23		
5	FL	681	Total	C	N	O	S	0	0
			5563	3529	945	1066	23		

- Molecule 6 is a protein called Ring protein 1 gp43.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FM	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FN	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FO	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FP	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FQ	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FR	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FS	229	Total	C	N	O	S	0	0
			1868	1204	314	341	9		
6	FT	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FU	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FV	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FW	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		
6	FX	226	Total	C	N	O	S	0	0
			1841	1188	308	336	9		

- Molecule 7 is a protein called Ring protein 2 gp40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	FY	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	FZ	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GA	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GB	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GC	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GD	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GE	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GF	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	GG	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GH	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GI	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		
7	GJ	225	Total	C	N	O	S	0	0
			1841	1180	292	357	12		

- Molecule 8 is a protein called Cargo protein 1 gp45.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GK	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GL	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GM	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GN	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GO	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GP	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GQ	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GR	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GS	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GT	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GU	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	GV	126	Total	C	N	O	S	0	0
			987	605	179	201	2		
8	IK	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IL	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IM	32	Total	C	N	O	S	0	0
			251	157	44	49	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	IN	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IO	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IP	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IQ	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IR	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IS	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IT	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IU	32	Total	C	N	O	S	0	0
			251	157	44	49	1		
8	IV	32	Total	C	N	O	S	0	0
			251	157	44	49	1		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	AB	1	Total	Mg	0
			1	1	
9	AC	1	Total	Mg	0
			1	1	
9	AD	1	Total	Mg	0
			1	1	
9	AE	1	Total	Mg	0
			1	1	
9	BB	1	Total	Mg	0
			1	1	
9	BD	1	Total	Mg	0
			1	1	
9	CB	1	Total	Mg	0
			1	1	
9	CD	1	Total	Mg	0
			1	1	
9	CE	1	Total	Mg	0
			1	1	
9	CF	1	Total	Mg	0
			1	1	

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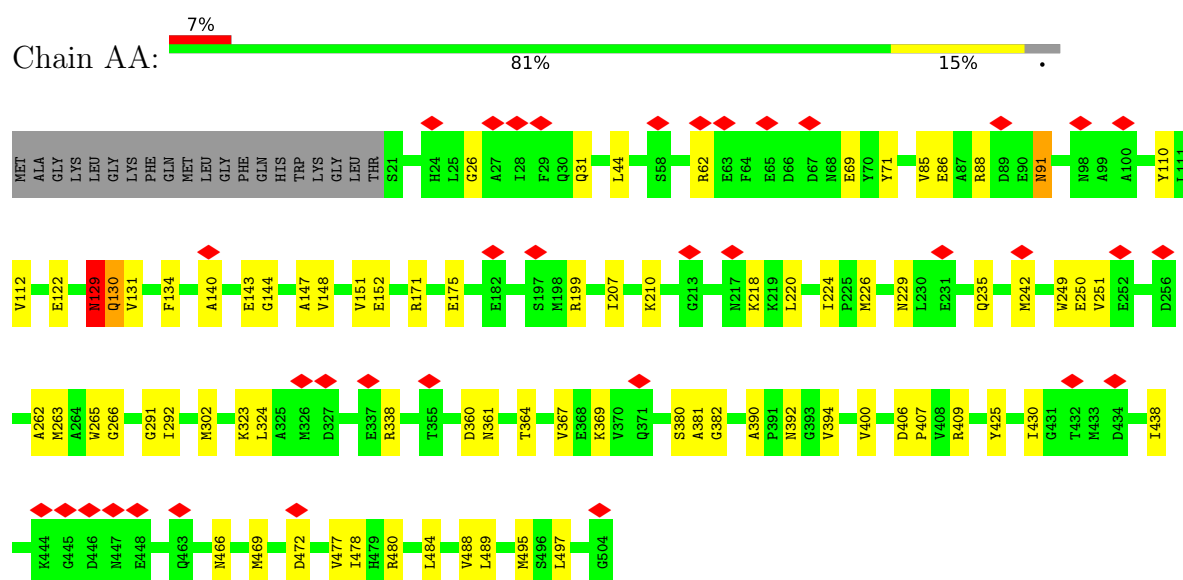
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Mol	Chain	Residues	Atoms		AltConf
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9	DE	1	Total 1	Mg 1	0
9	DF	1	Total 1	Mg 1	0
9	EB	1	Total 1	Mg 1	0
9	ED	1	Total 1	Mg 1	0
9	FA	1	Total 1	Mg 1	0
9	FB	1	Total 1	Mg 1	0
9	FC	1	Total 1	Mg 1	0
9	FD	1	Total 1	Mg 1	0
9	FE	1	Total 1	Mg 1	0
9	FF	1	Total 1	Mg 1	0
9	FG	1	Total 1	Mg 1	0
9	FH	1	Total 1	Mg 1	0
9	FI	1	Total 1	Mg 1	0
9	FJ	1	Total 1	Mg 1	0
9	FK	1	Total 1	Mg 1	0
9	FL	1	Total 1	Mg 1	0

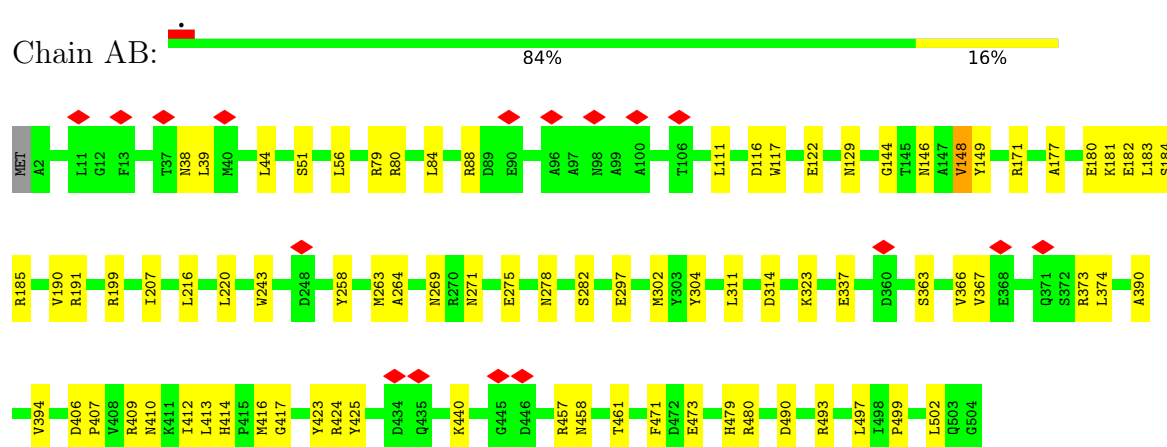
3 Residue-property plots

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

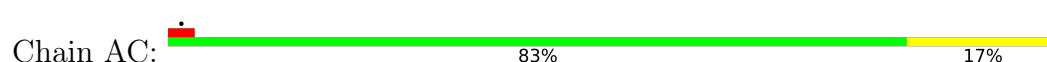
- Molecule 1: Major capsid protein gp32

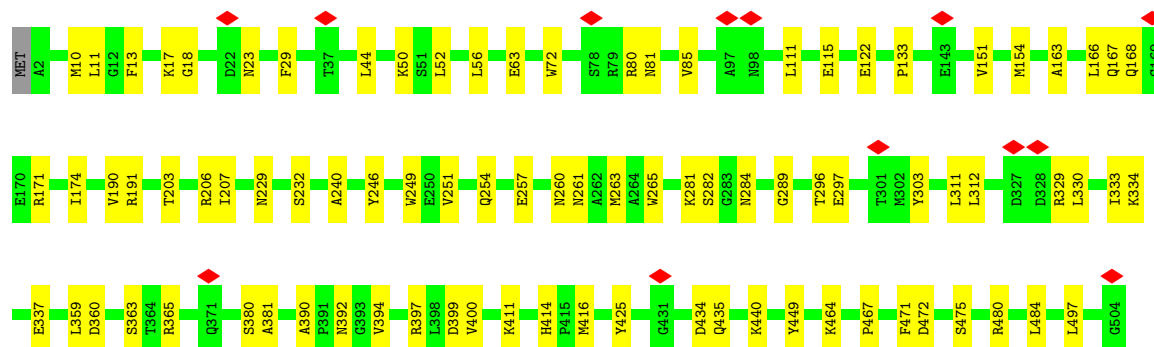


- Molecule 1: Major capsid protein gp32



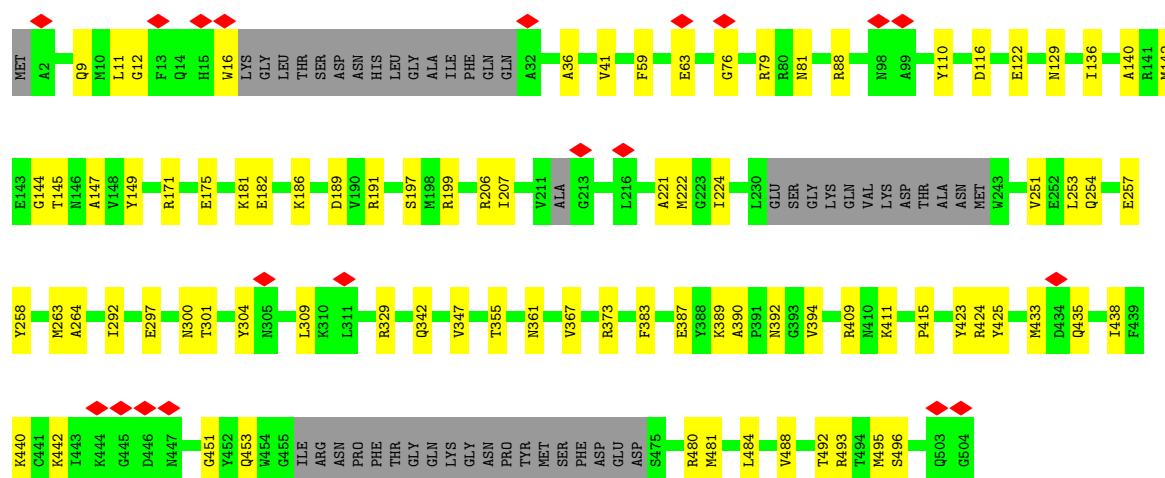
- Molecule 1: Major capsid protein gp32





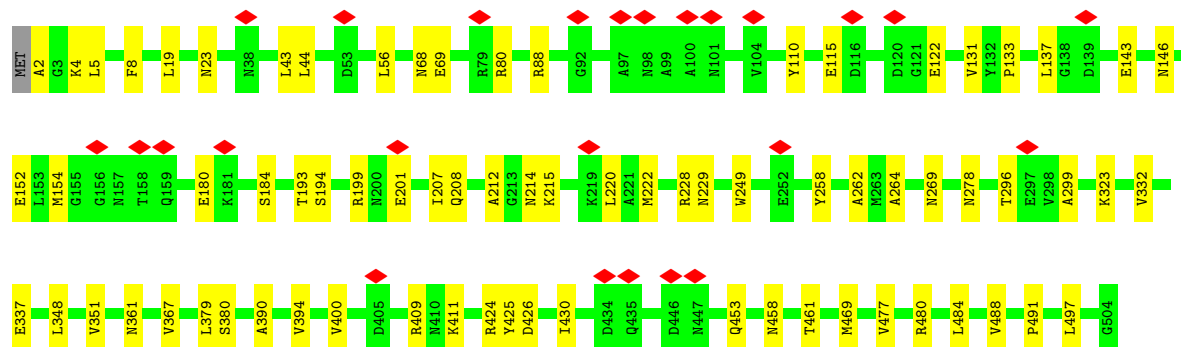
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Chain AD: 74% 17% 10%



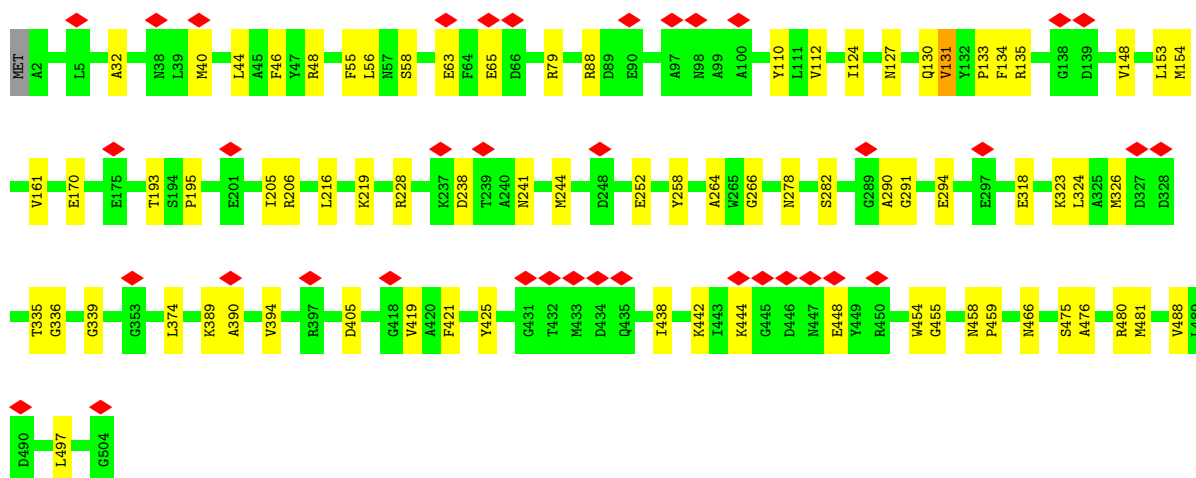
- Molecule 1: Major capsid protein gp32

Chain AE: 5% 85% 15%

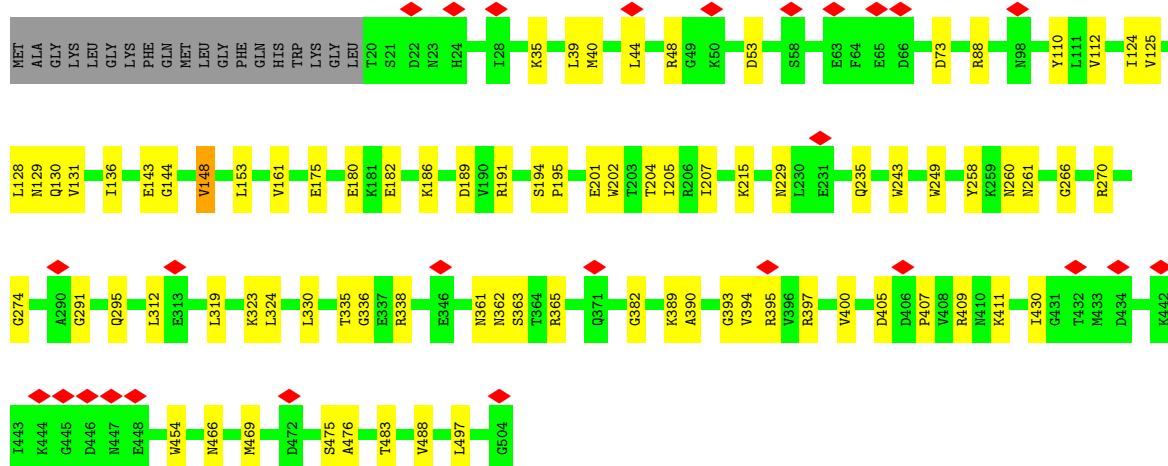
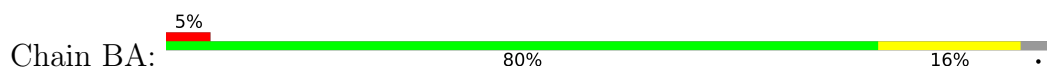


- Molecule 1: Major capsid protein gp32

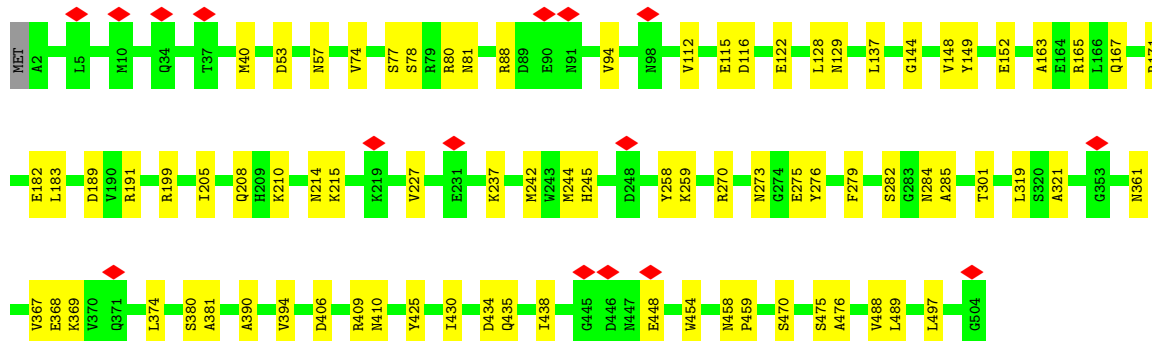
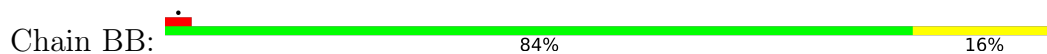
Chain AF: 8% 85% 15%



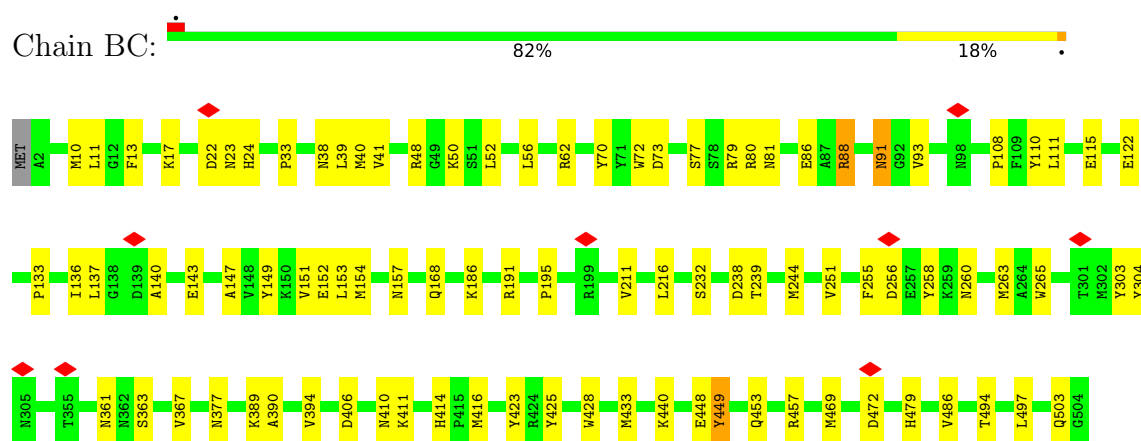
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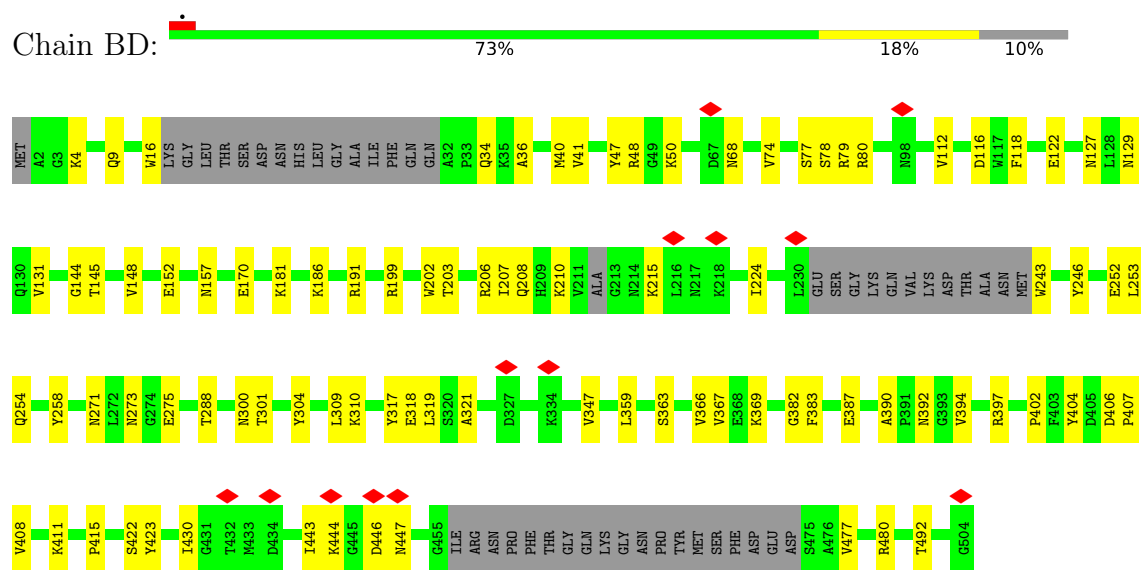
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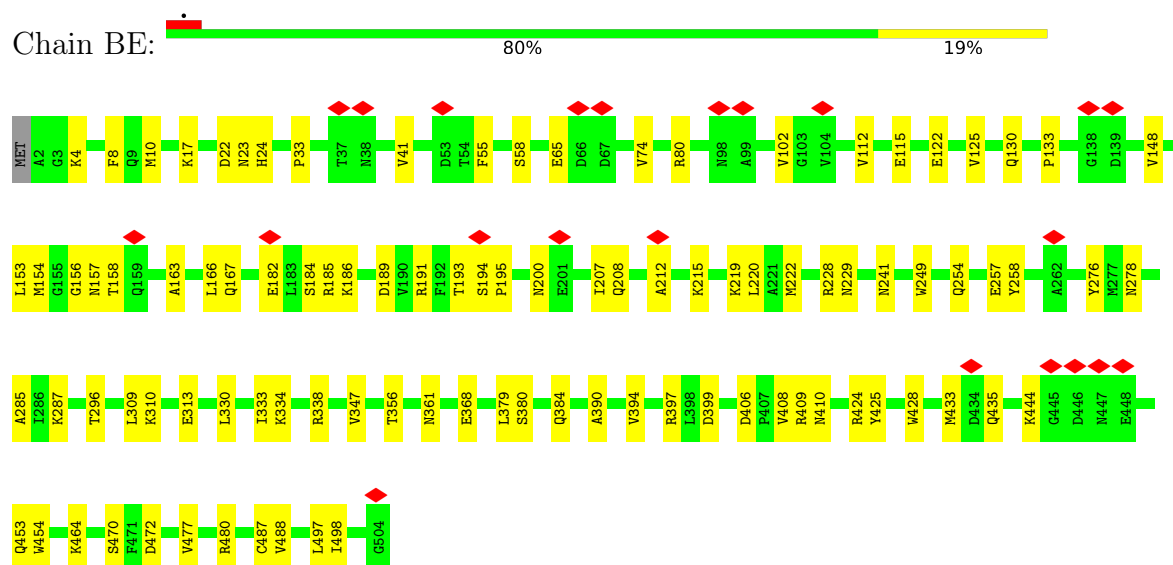
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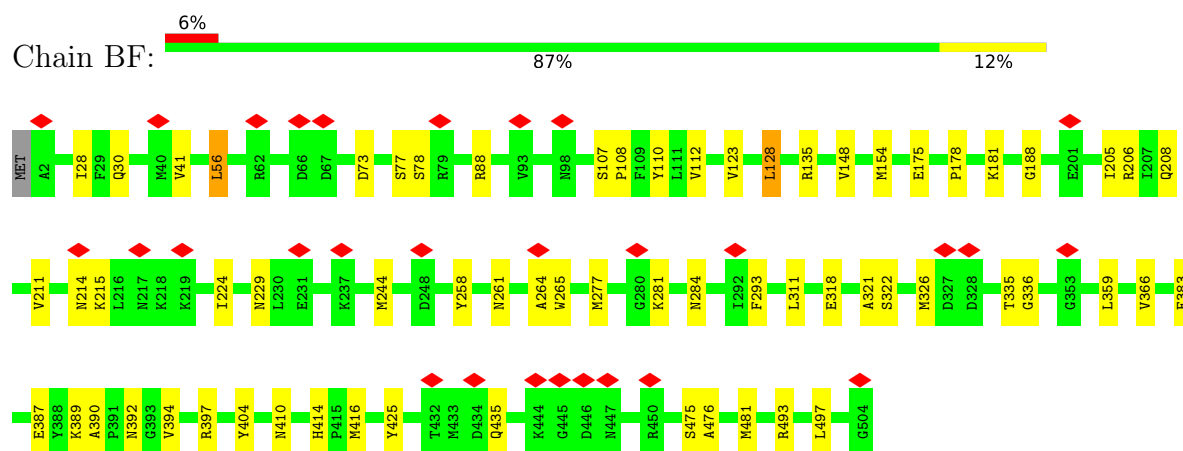
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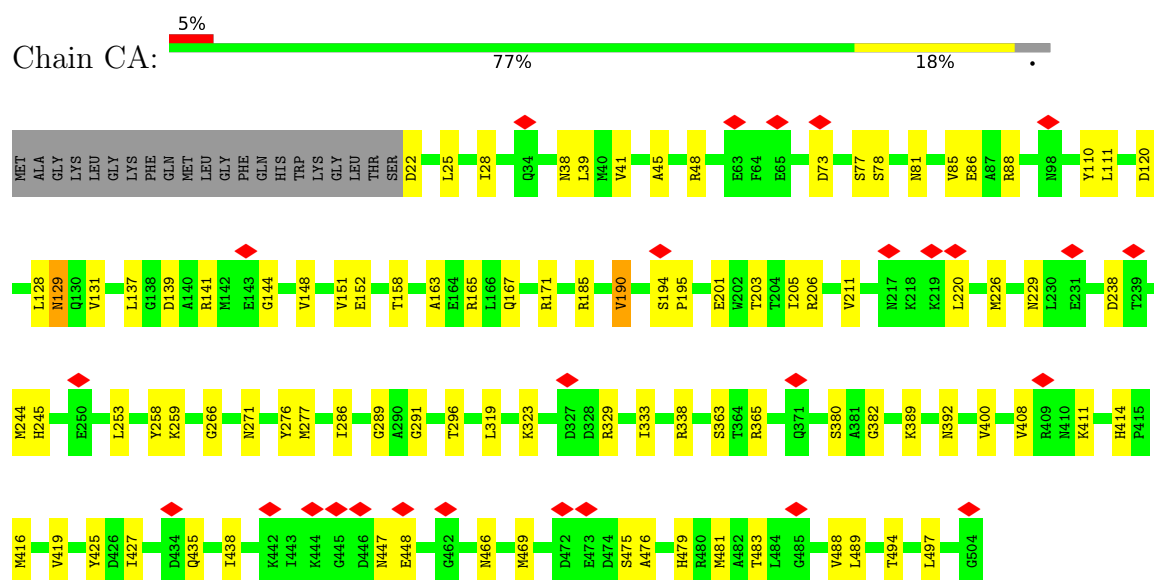
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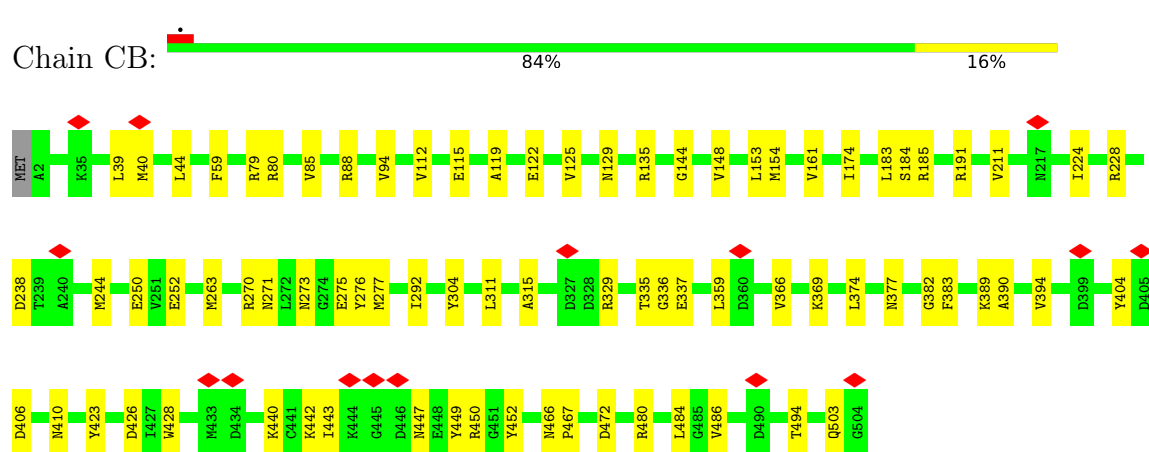
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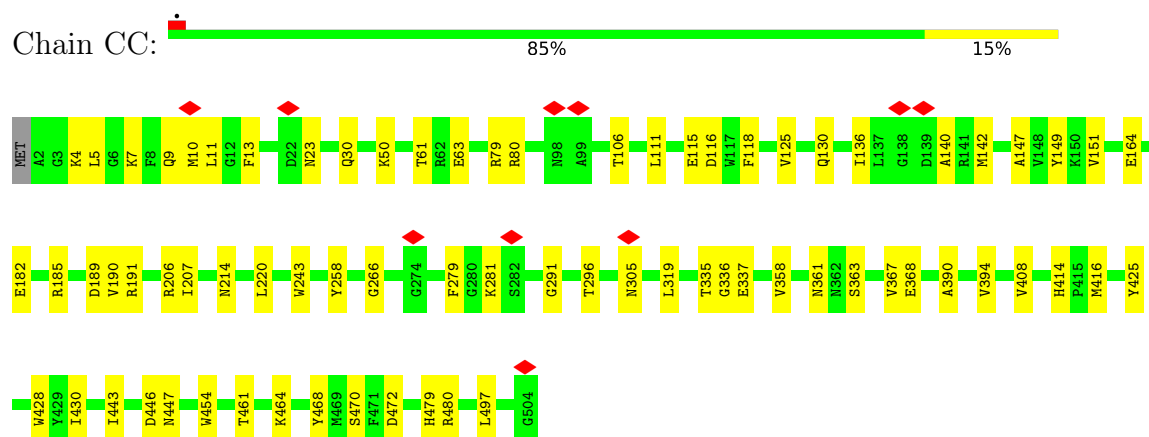
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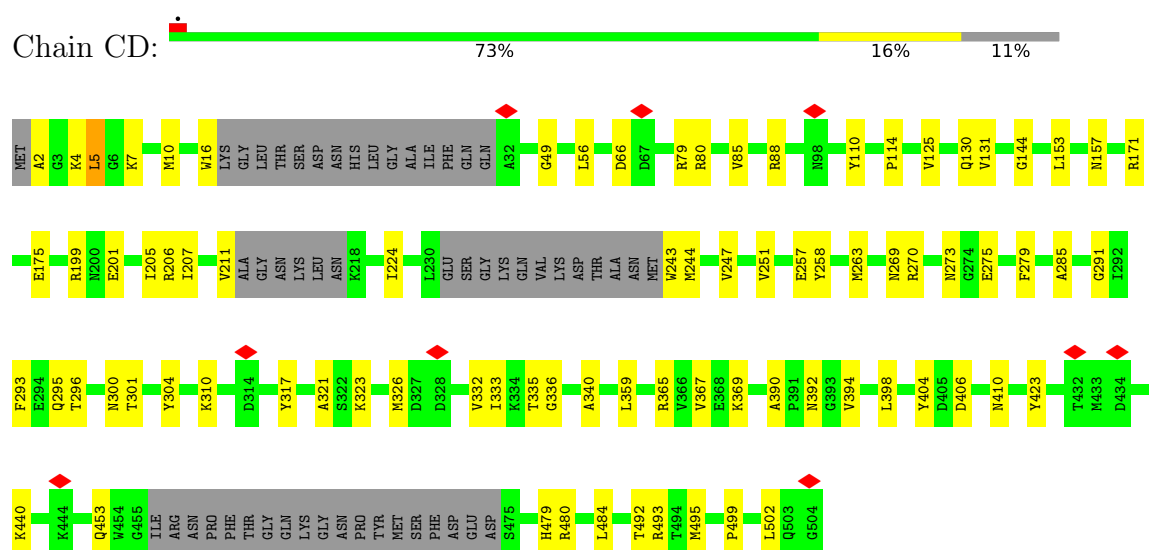
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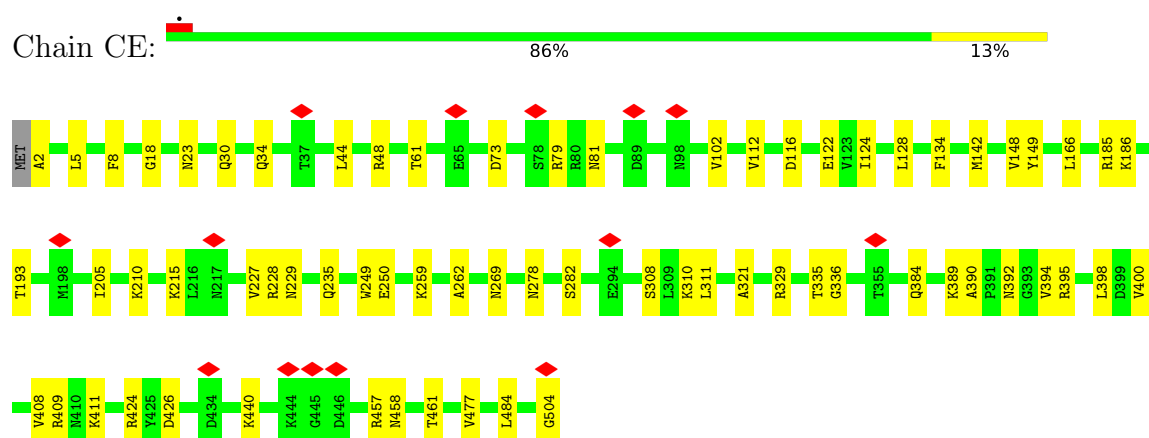
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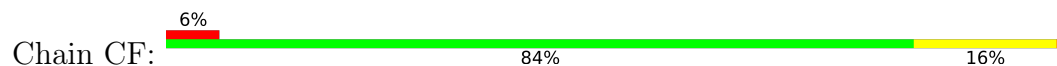
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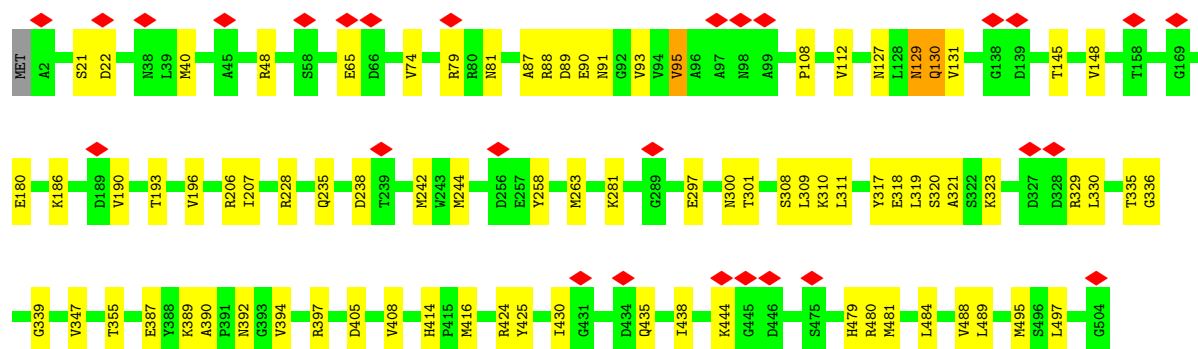


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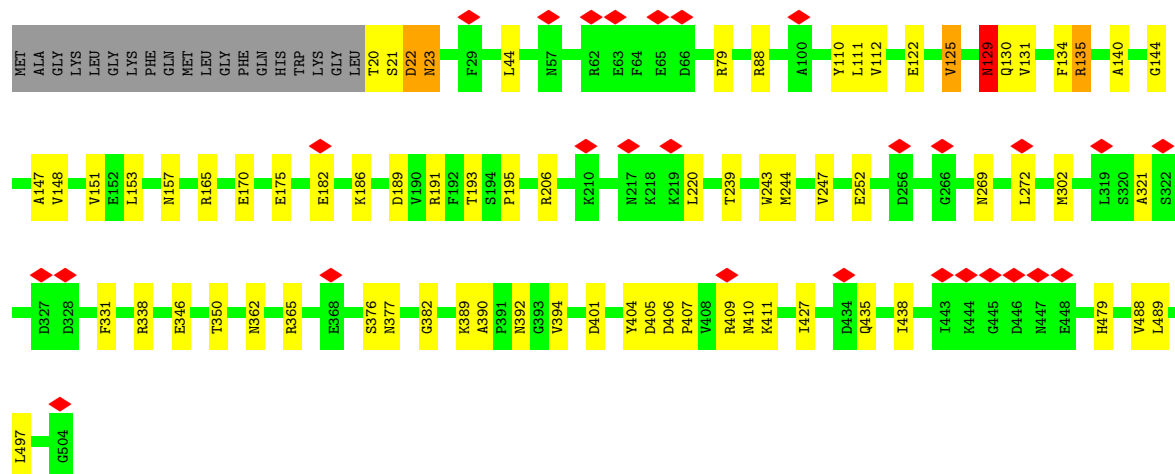
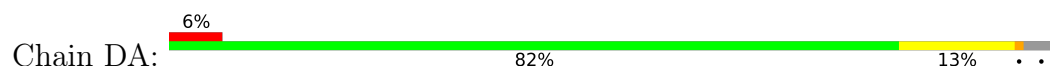


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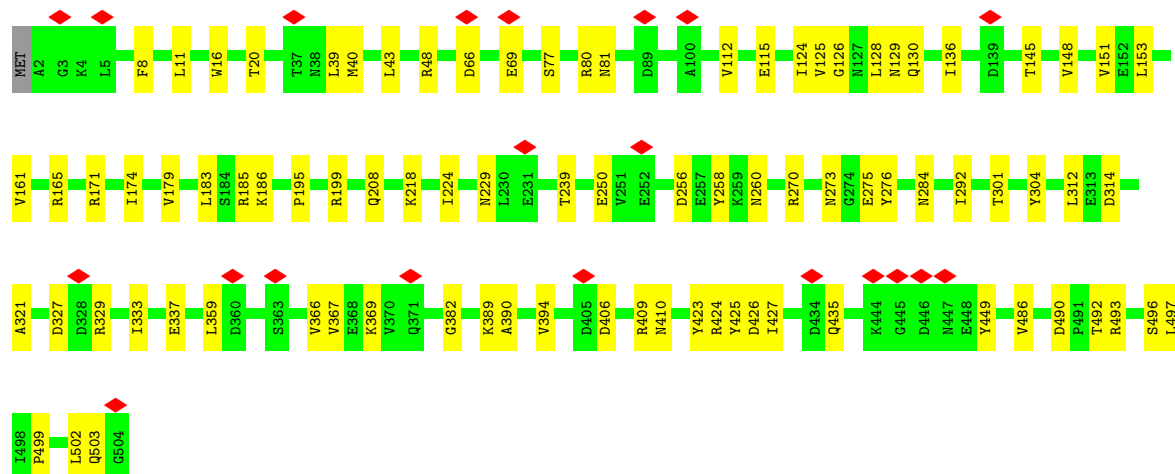
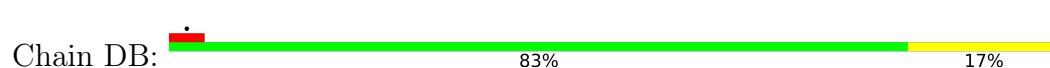




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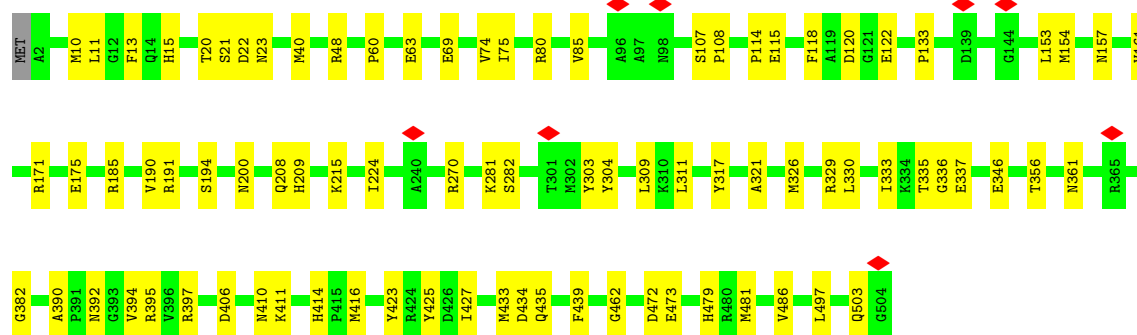


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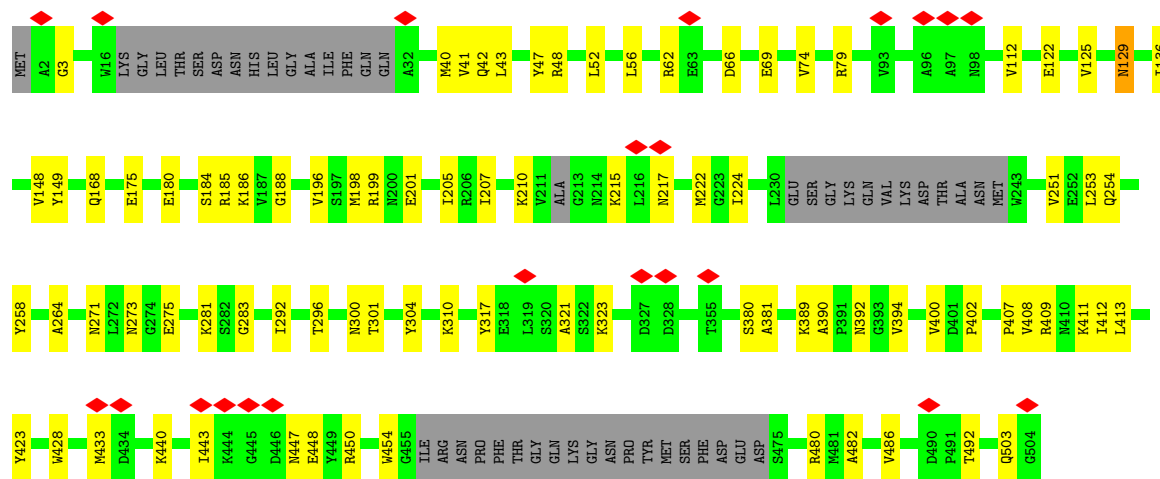
• Molecule 1: Major capsid protein gp32

Chain DC:  83% 17%



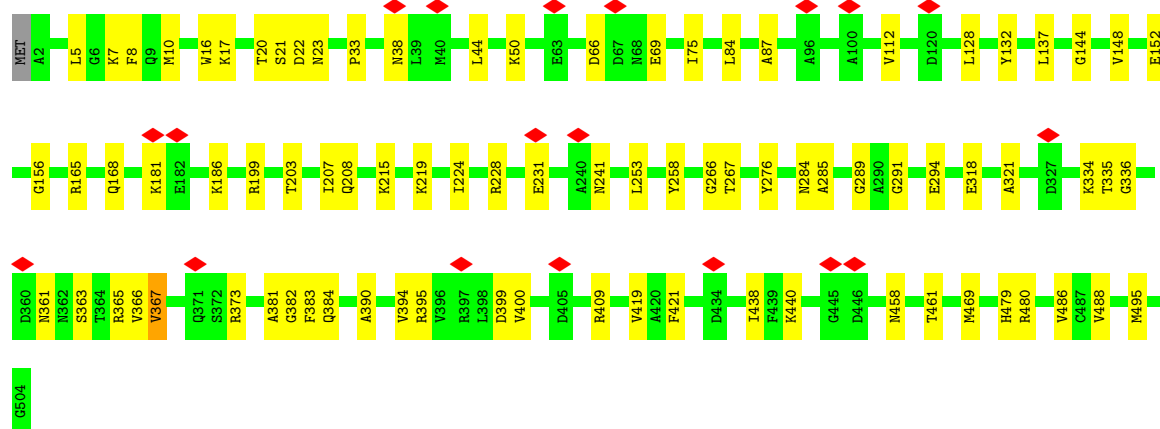
• Molecule 1: Major capsid protein gp32

Chain DD:  73% 17% 10%

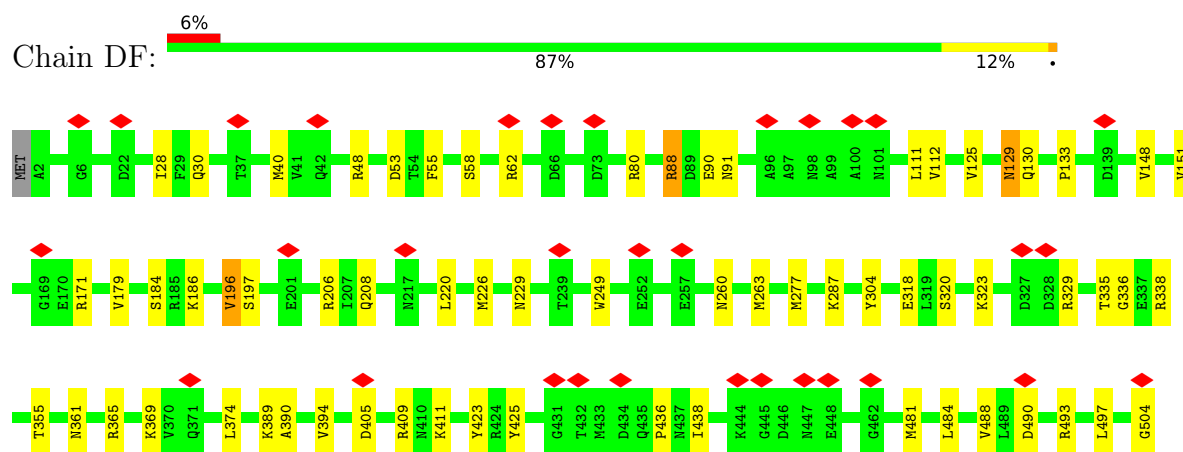


• Molecule 1: Major capsid protein gp32

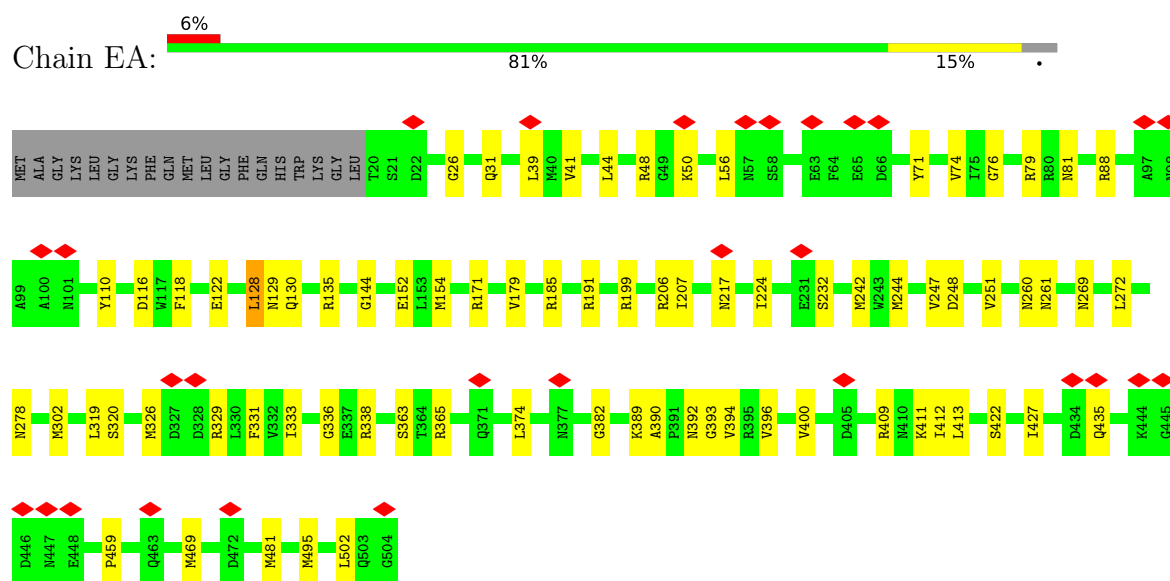
Chain DE:  83% 16%



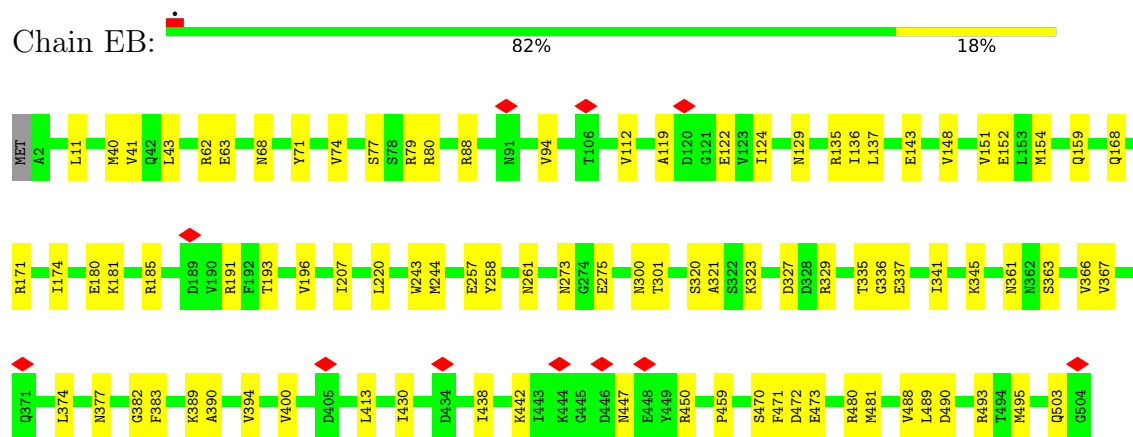
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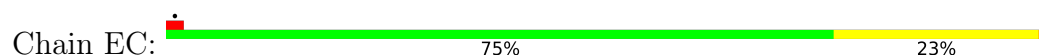
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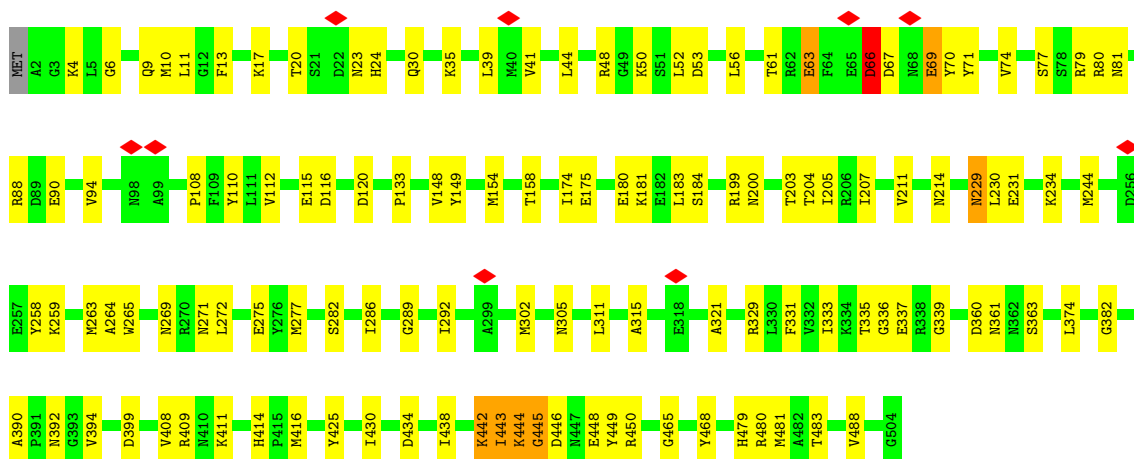


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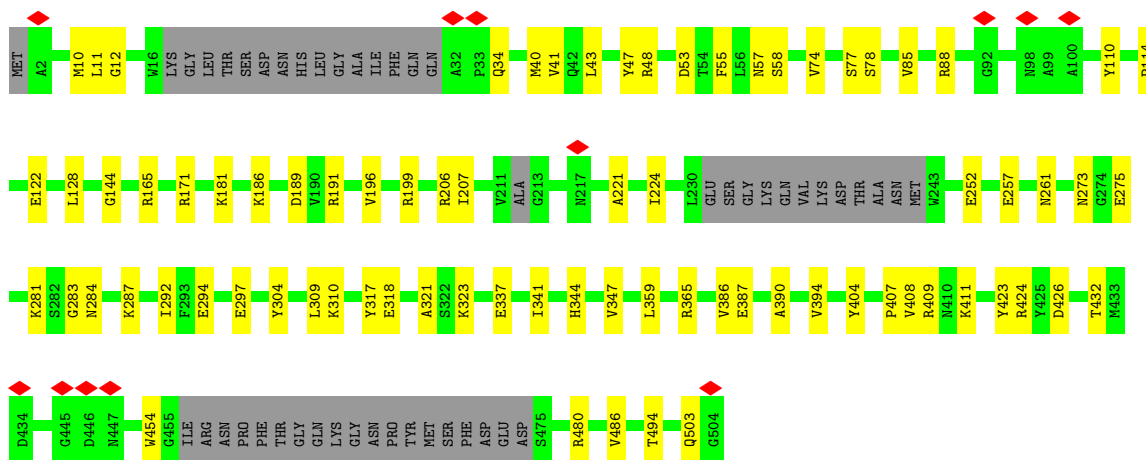
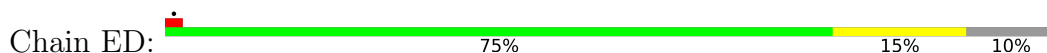


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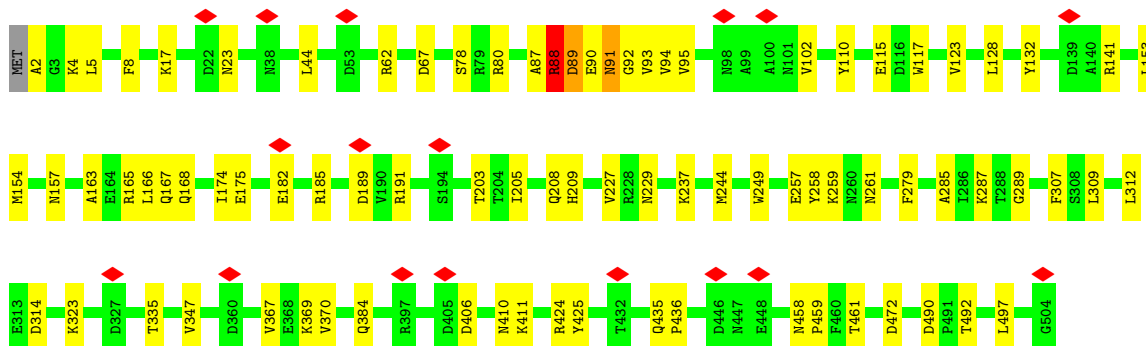
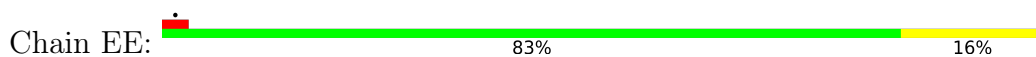




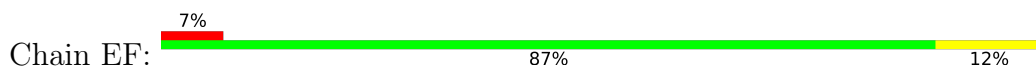
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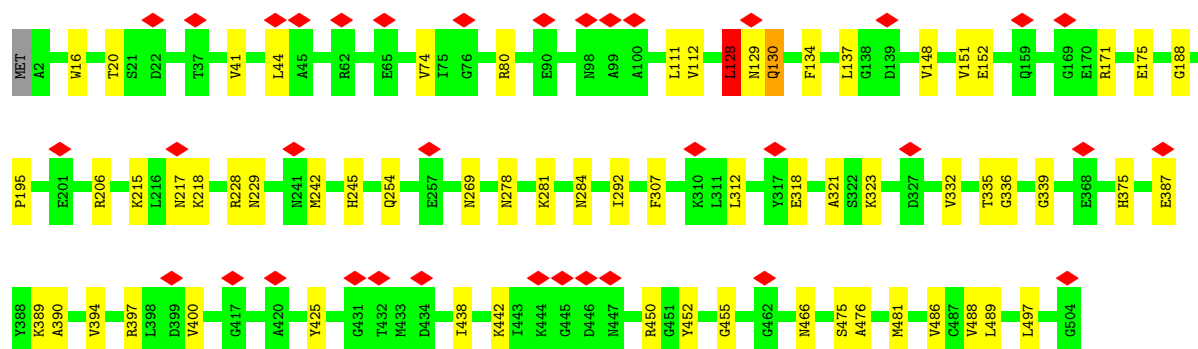


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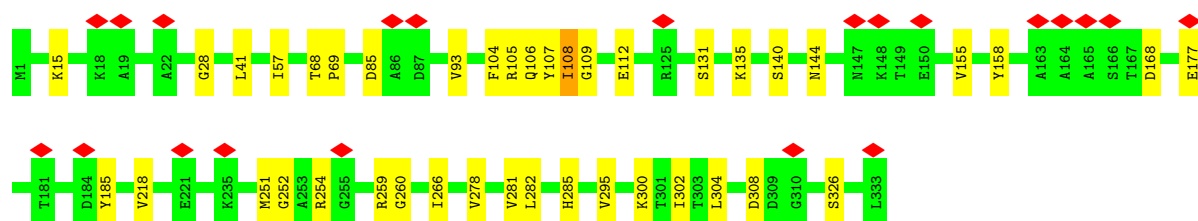


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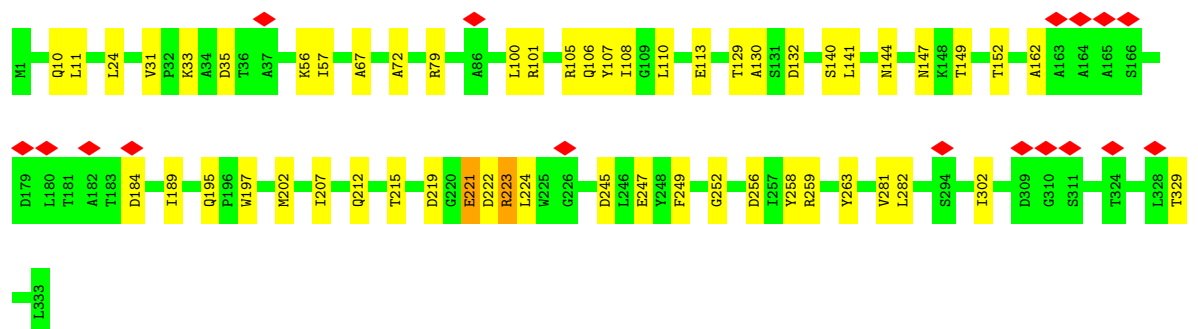
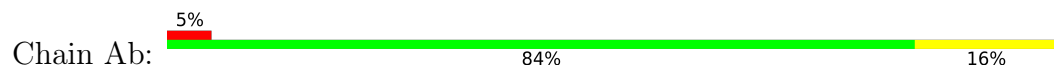




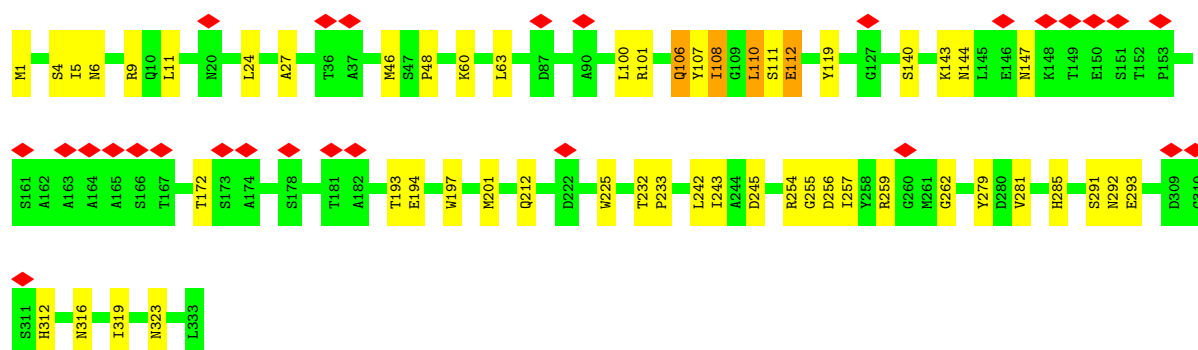
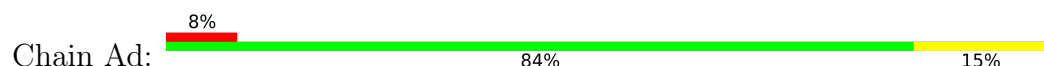
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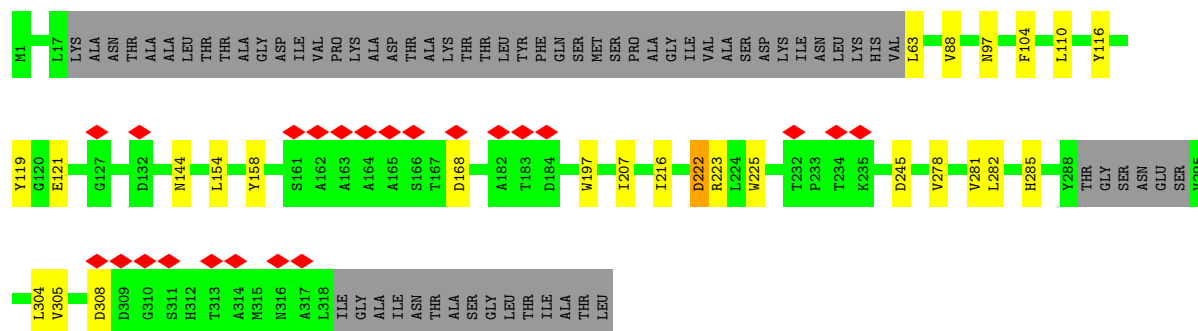
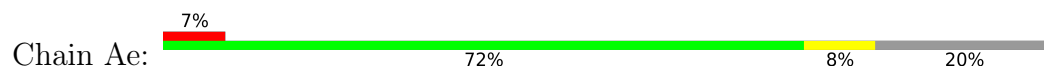
• Molecule 2: Auxiliary capsid protein gp36



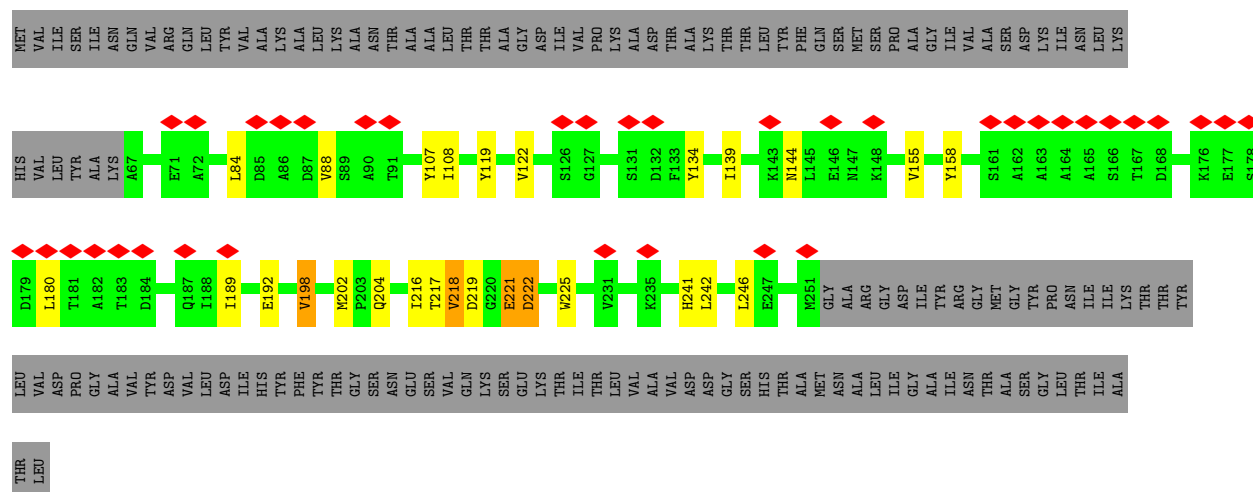
• Molecule 2: Auxiliary capsid protein gp36



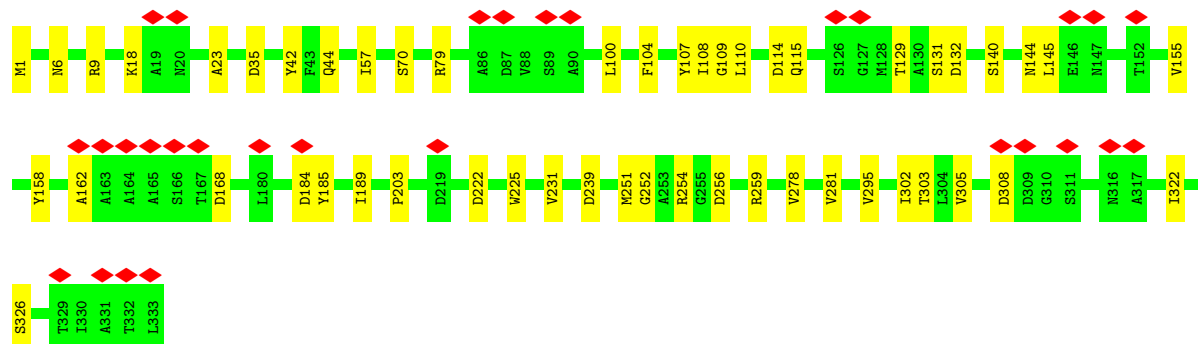
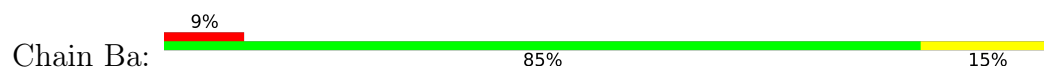
- Molecule 2: Auxiliary capsid protein gp36



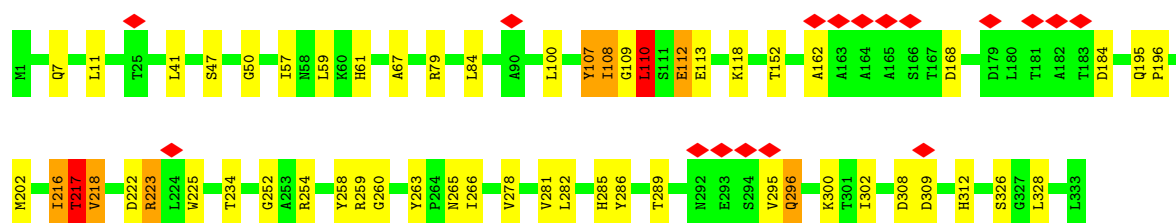
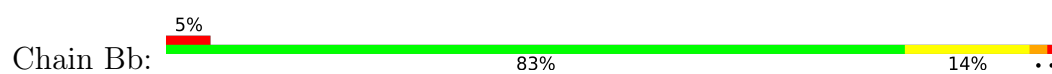
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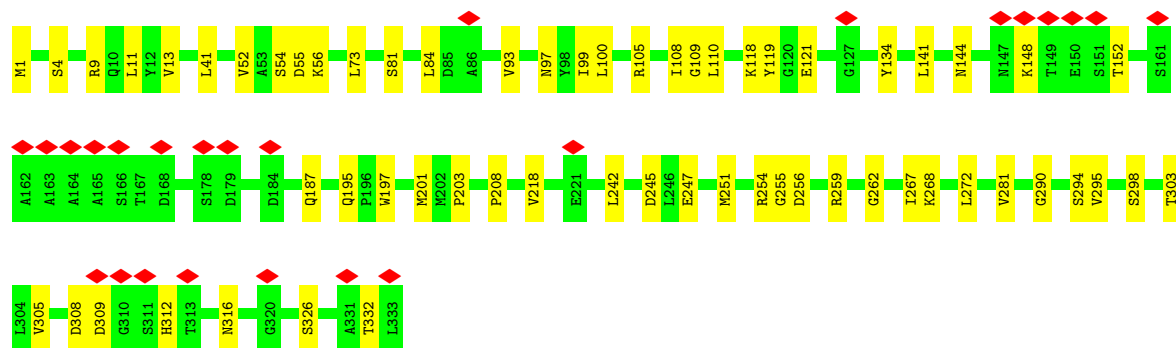
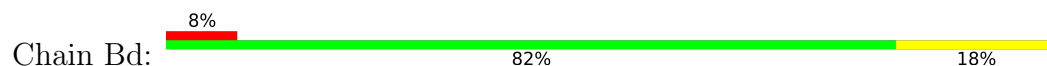
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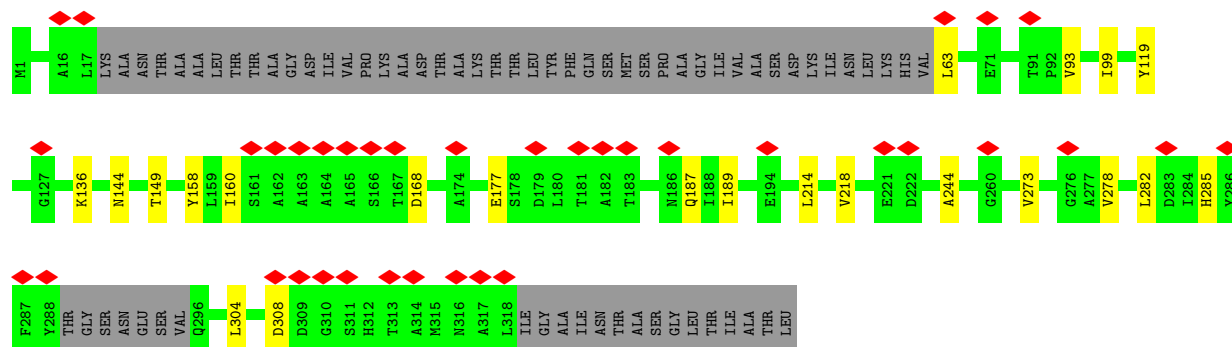
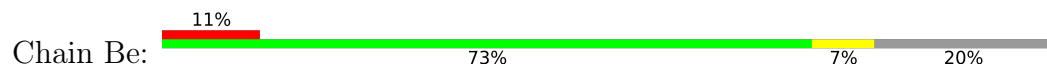
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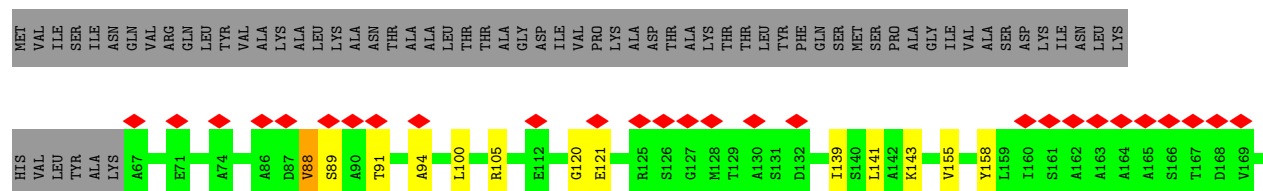
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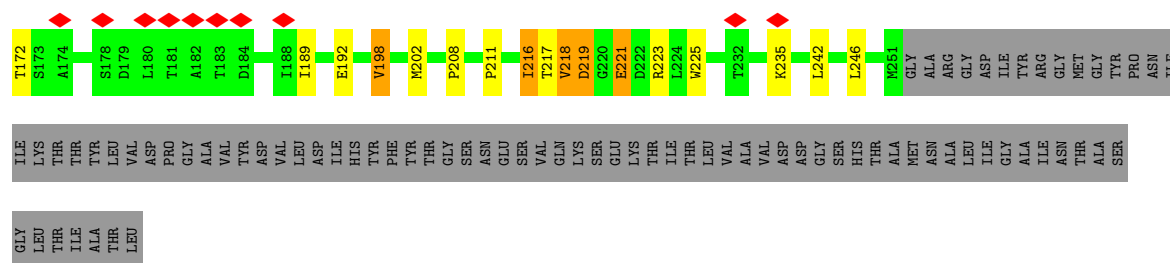


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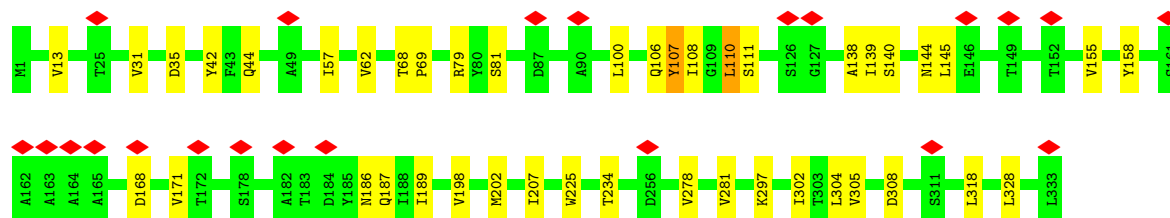
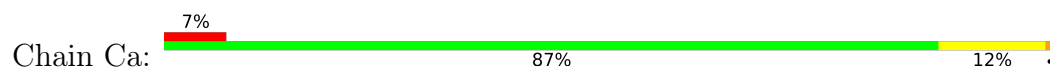


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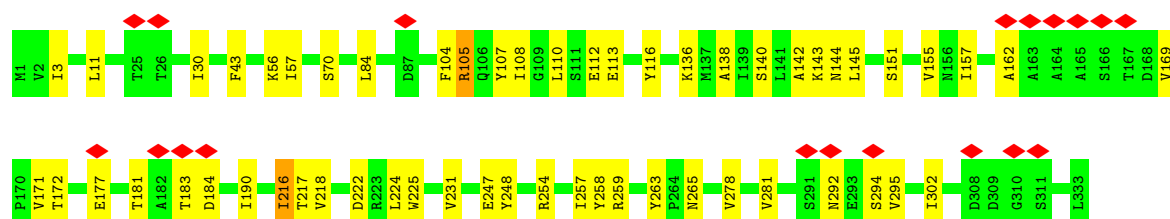
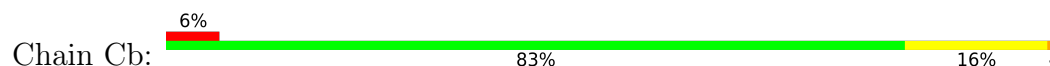




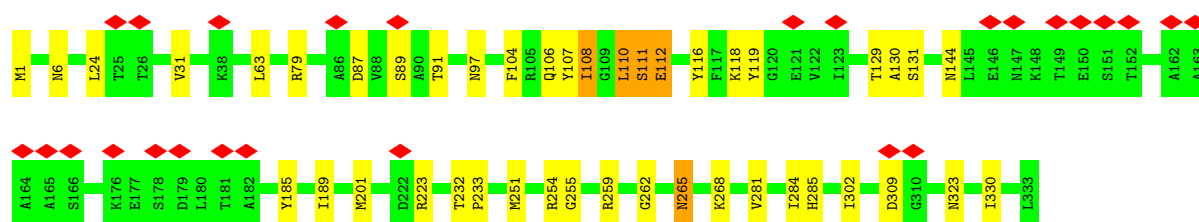
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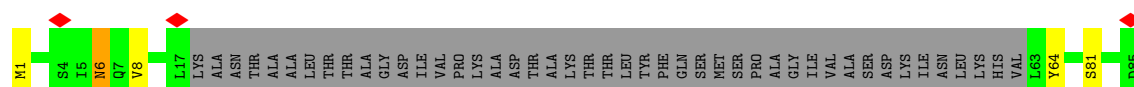
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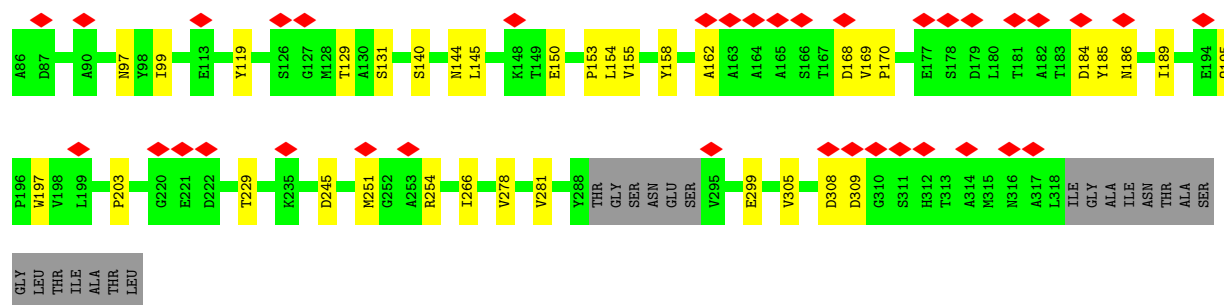


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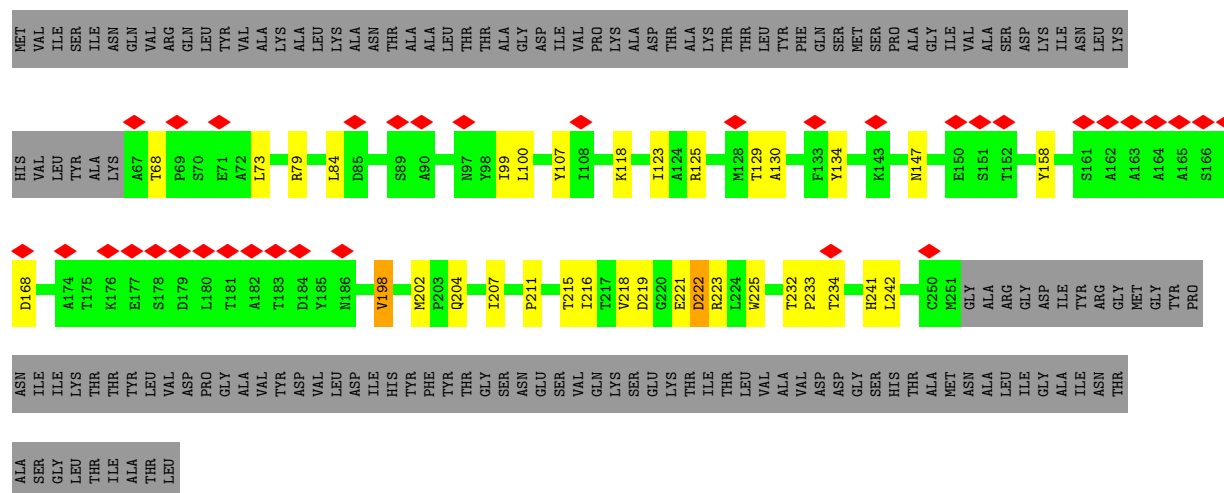


• Molecule 2: Auxiliary capsid protein gp36

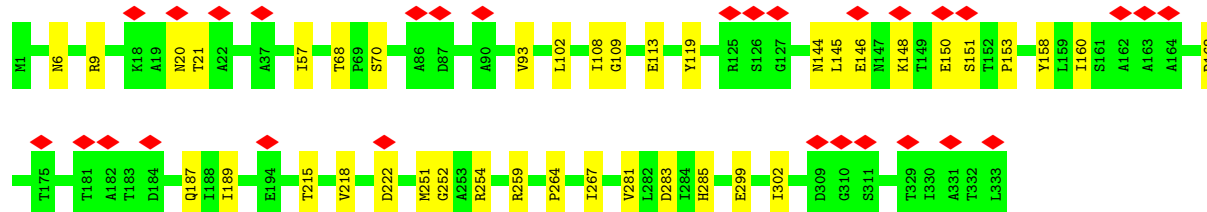




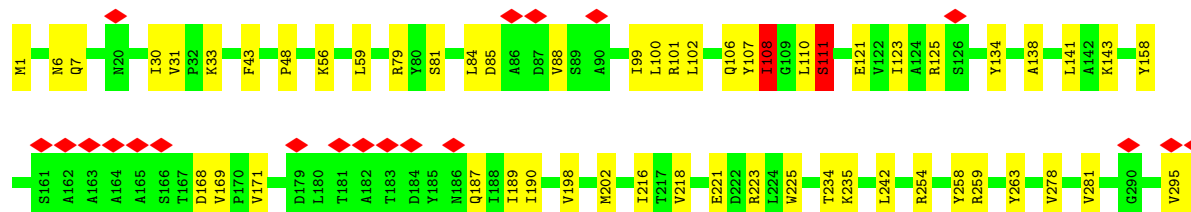
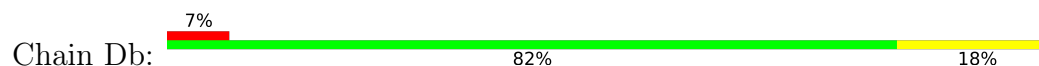
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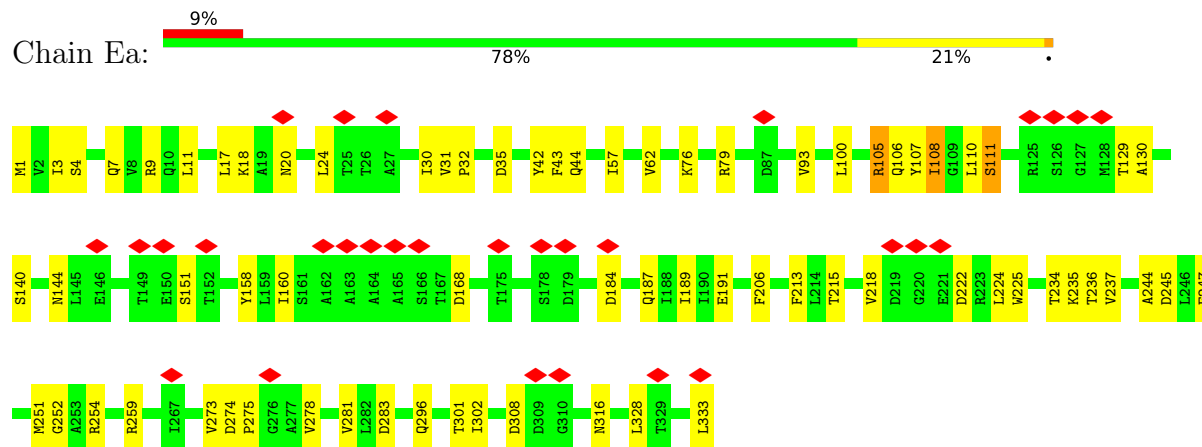
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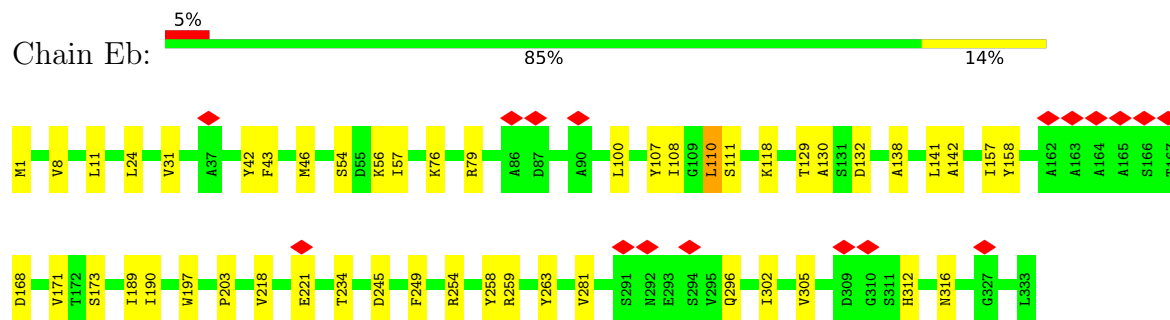
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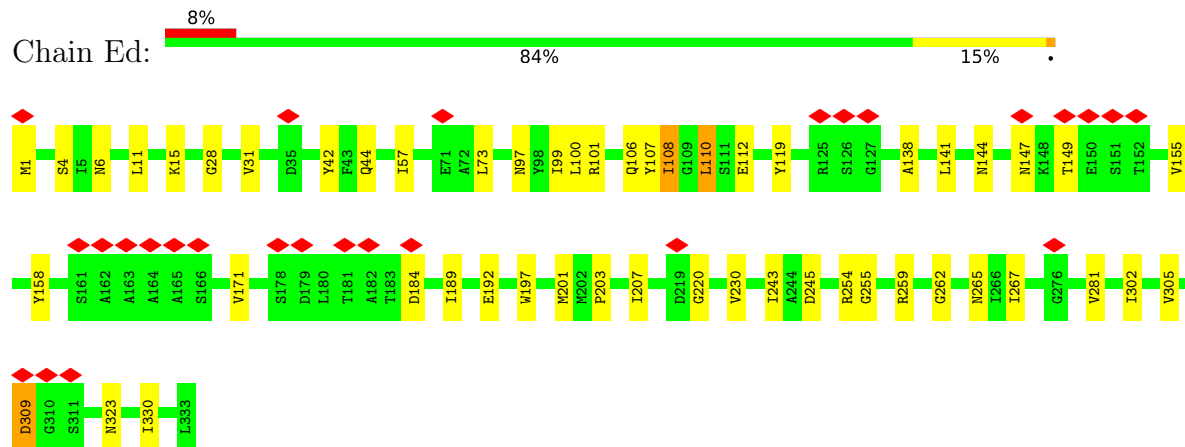
- Molecule 2: Auxiliary capsid protein gp36



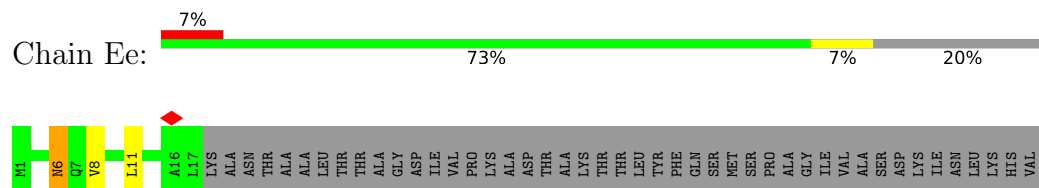
- Molecule 2: Auxiliary capsid protein gp36

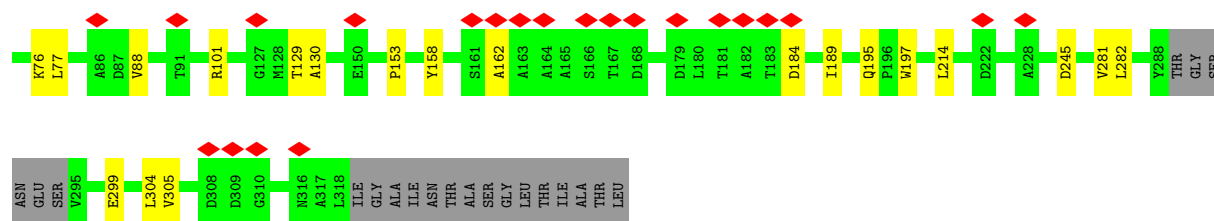


- Molecule 2: Auxiliary capsid protein gp36

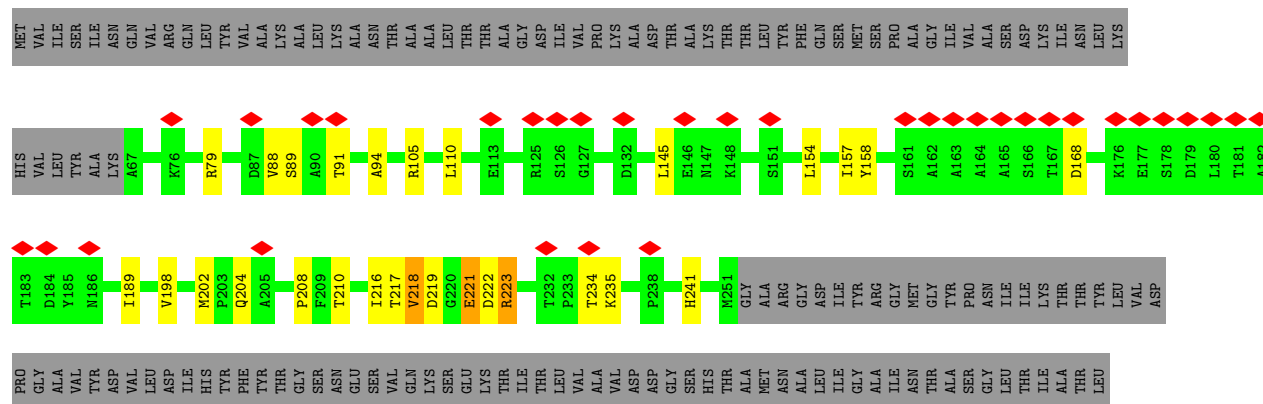


- Molecule 2: Auxiliary capsid protein gp36

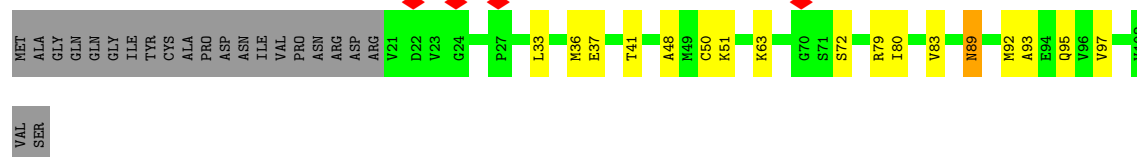




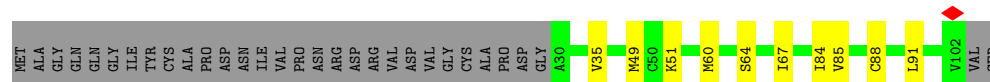
• Molecule 2: Auxiliary capsid protein gp36



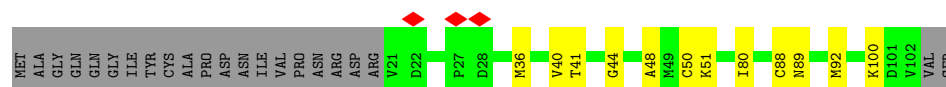
• Molecule 3: Portal vertex capsid protein gp57



• Molecule 3: Portal vertex capsid protein gp57

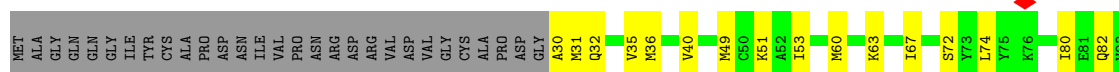


• Molecule 3: Portal vertex capsid protein gp57



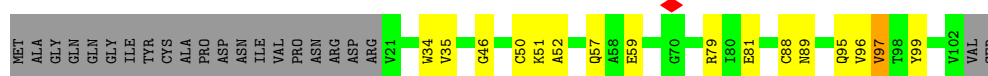
• Molecule 3: Portal vertex capsid protein gp57

Chain Bh: 



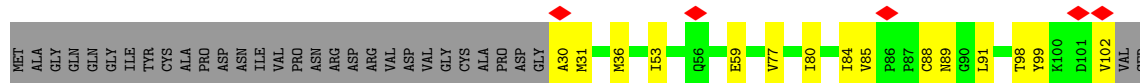
- Molecule 3: Portal vertex capsid protein gp57

Chain Cg: 



- Molecule 3: Portal vertex capsid protein gp57

Chain Ch: 



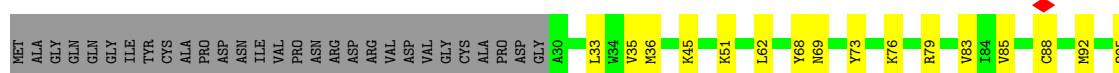
- Molecule 3: Portal vertex capsid protein gp57

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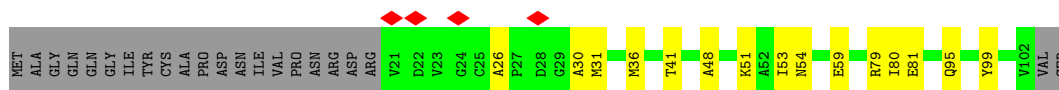
- Molecule 3: Portal vertex capsid protein gp57

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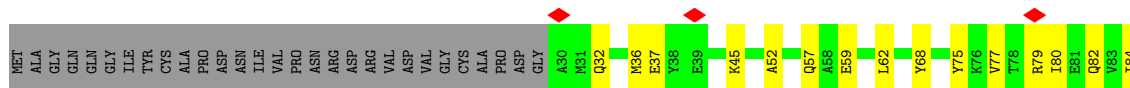


- Molecule 3: Portal vertex capsid protein gp57

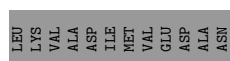
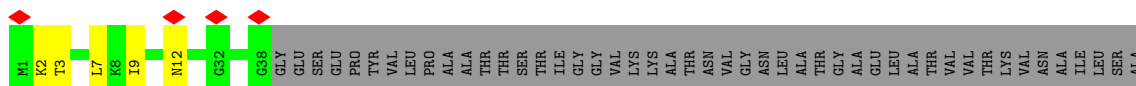
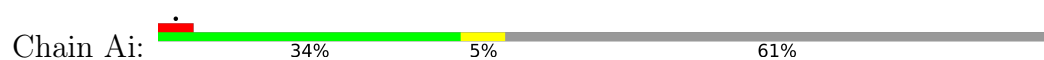
Chain Eg: 



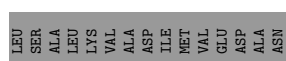
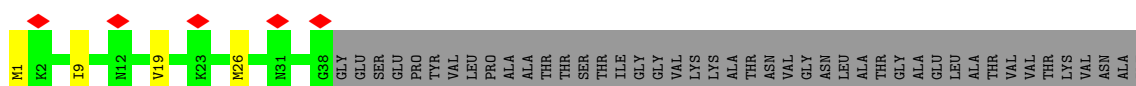
- Molecule 3: Portal vertex capsid protein gp57



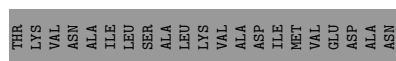
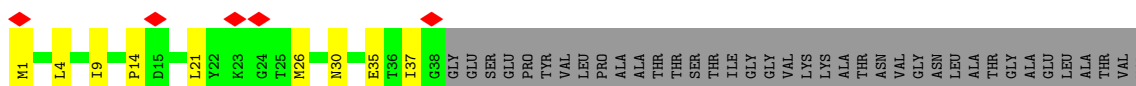
- Molecule 4: Head fiber trimer protein gp21



- Molecule 4: Head fiber trimer protein gp21

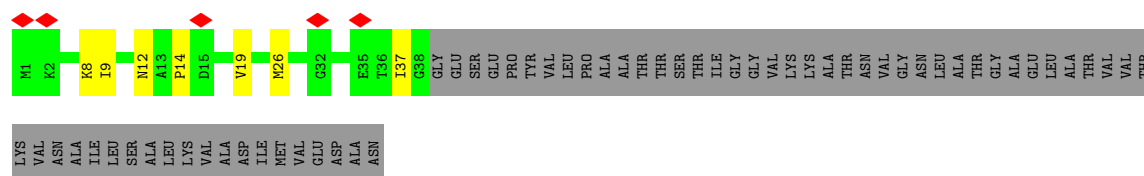


- Molecule 4: Head fiber trimer protein gp21

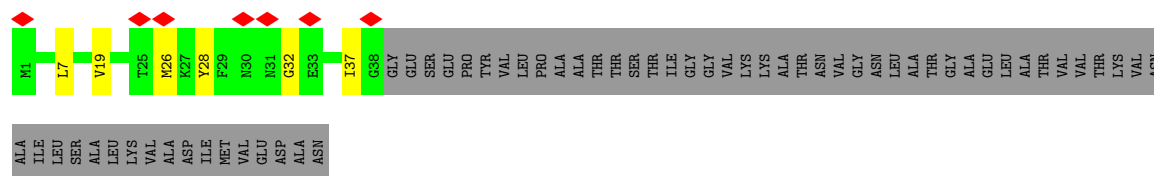


- Molecule 4: Head fiber trimer protein gp21

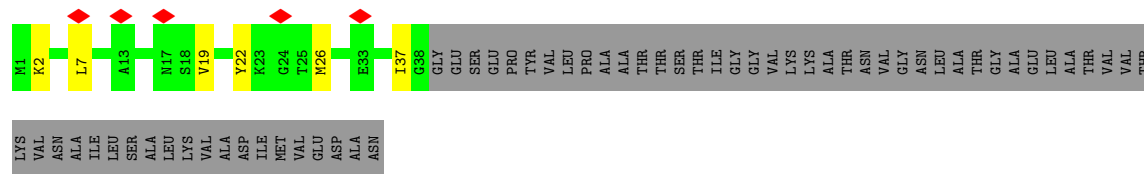




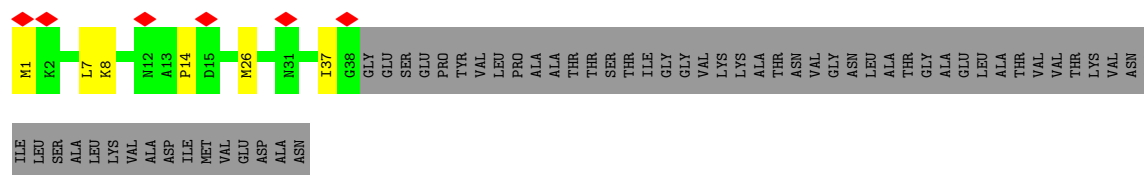
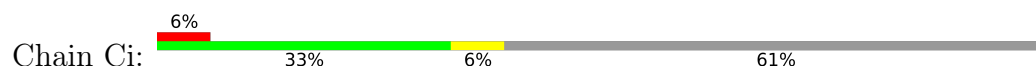
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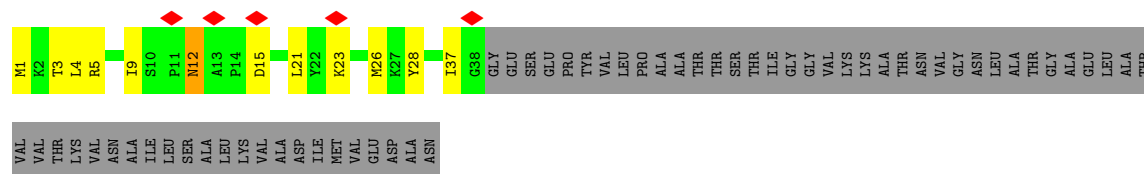
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• Molecule 4: Head fiber trimer protein gp21

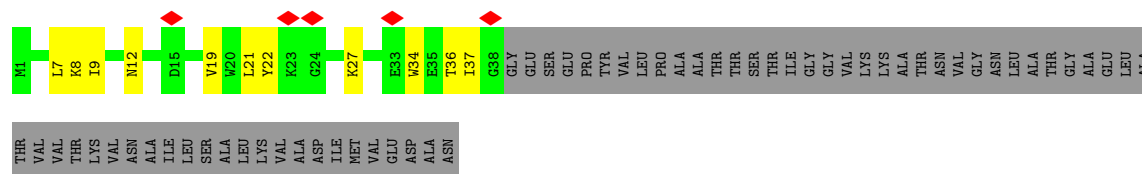


• Molecule 4: Head fiber trimer protein gp21

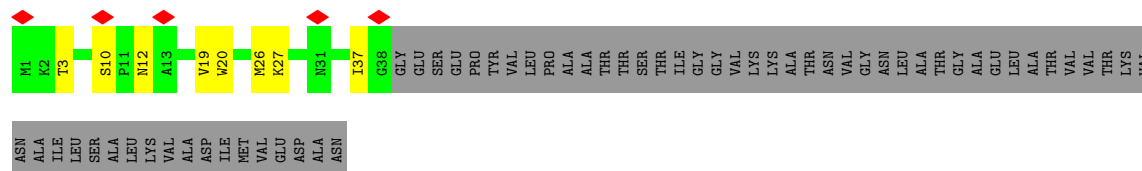


• Molecule 4: Head fiber trimer protein gp21

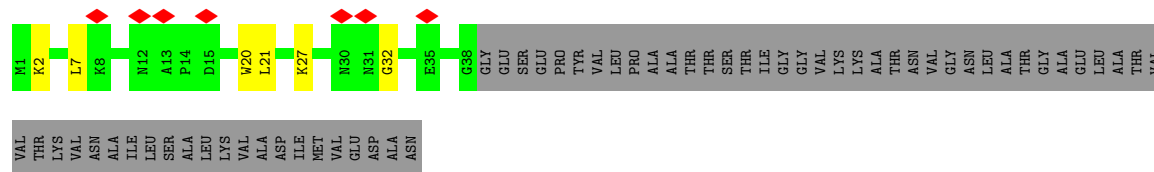
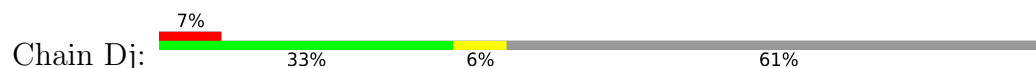




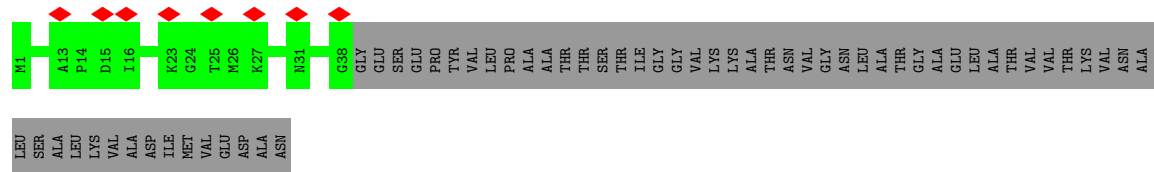
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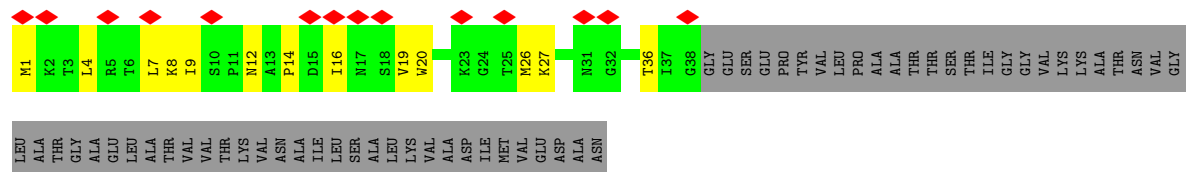
• Molecule 4: Head fiber trimer protein gp21



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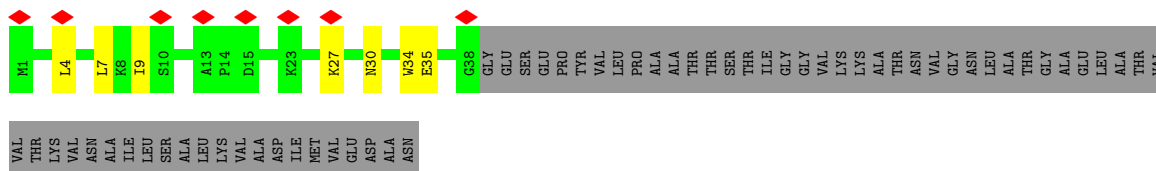
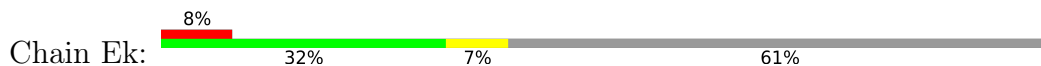
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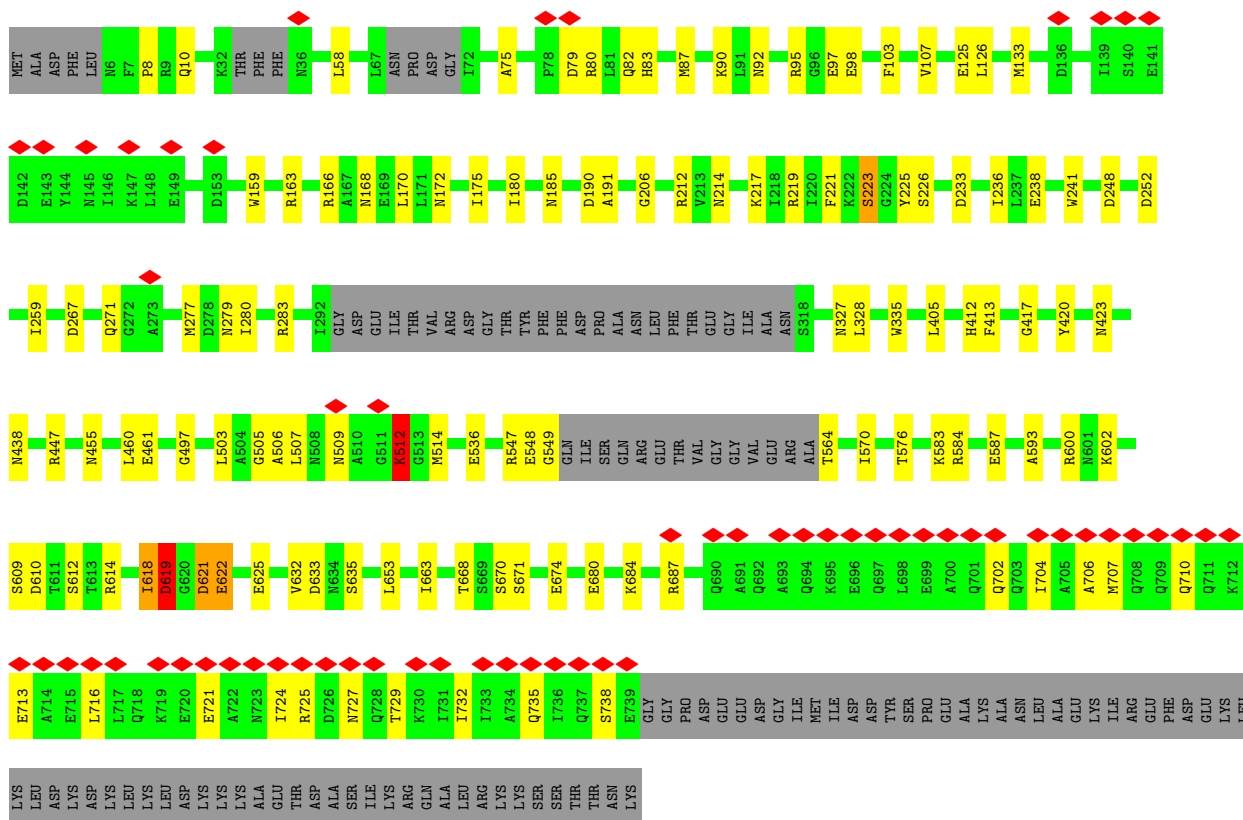
• Molecule 4: Head fiber trimer protein gp21



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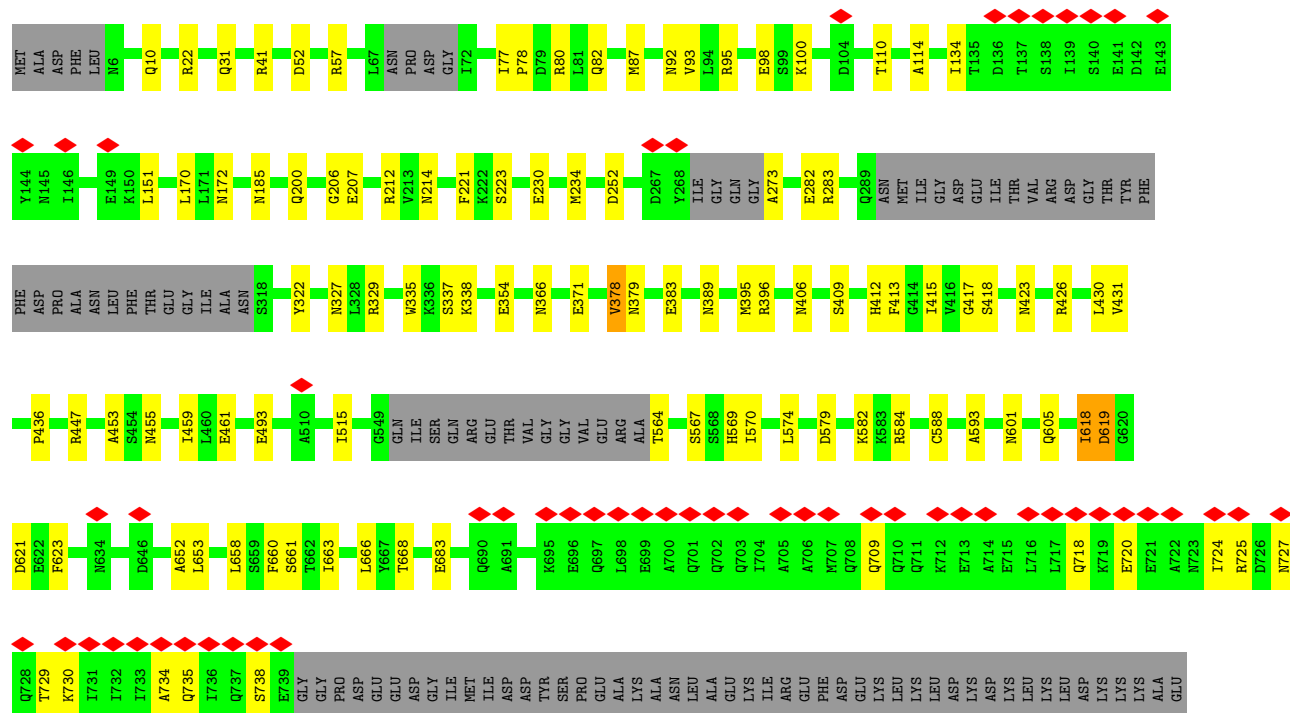
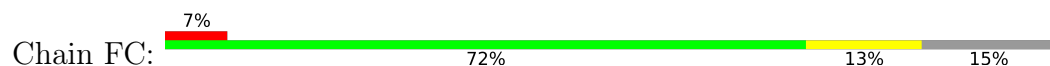
- Molecule 5: Portal protein gp20



- Molecule 5: Portal protein gp20



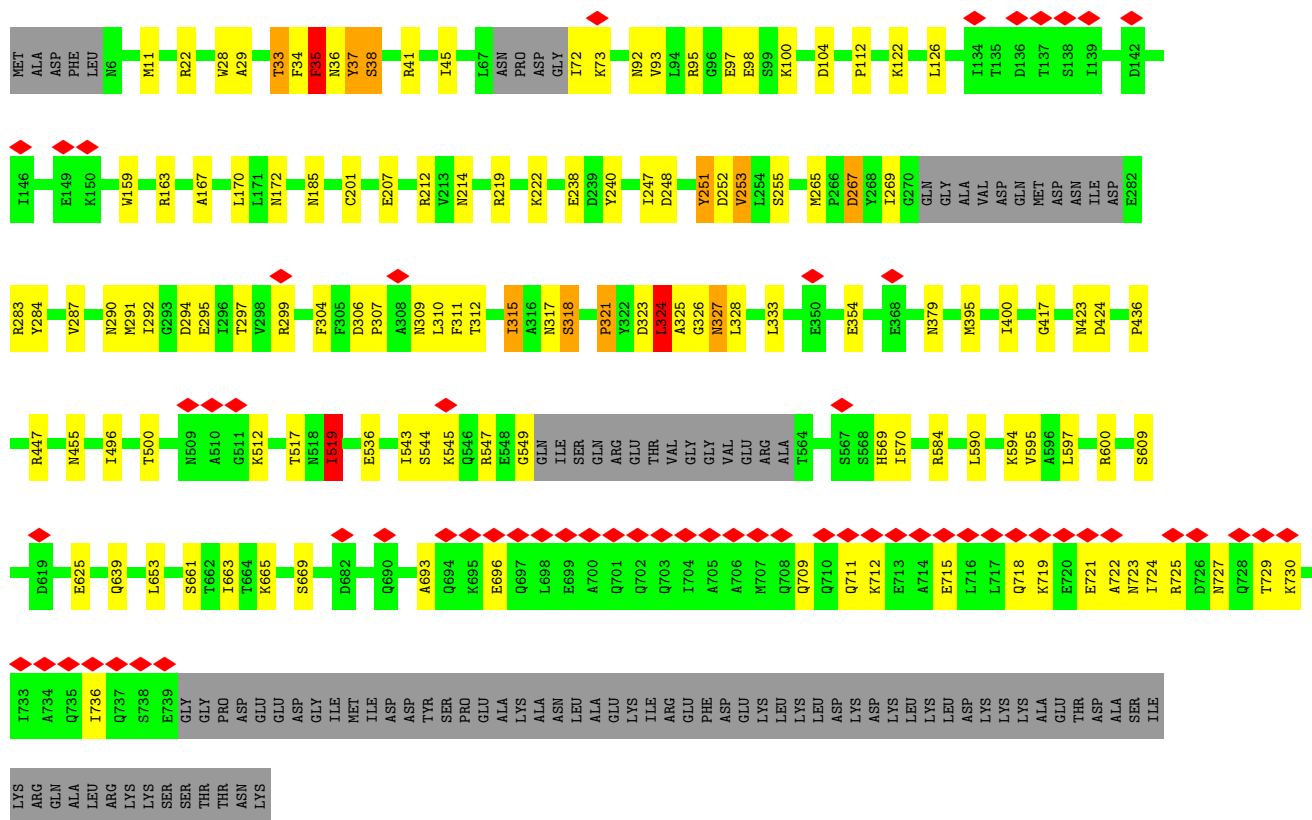
- Molecule 5: Portal protein gp20



THR
ASP
ALA
PHE
SER
ILE
LYS
ARG
GLN
GLN
ALA
LEU
ARG
LYS
LYS
SER
SER
THR
THR
ASN
LYS

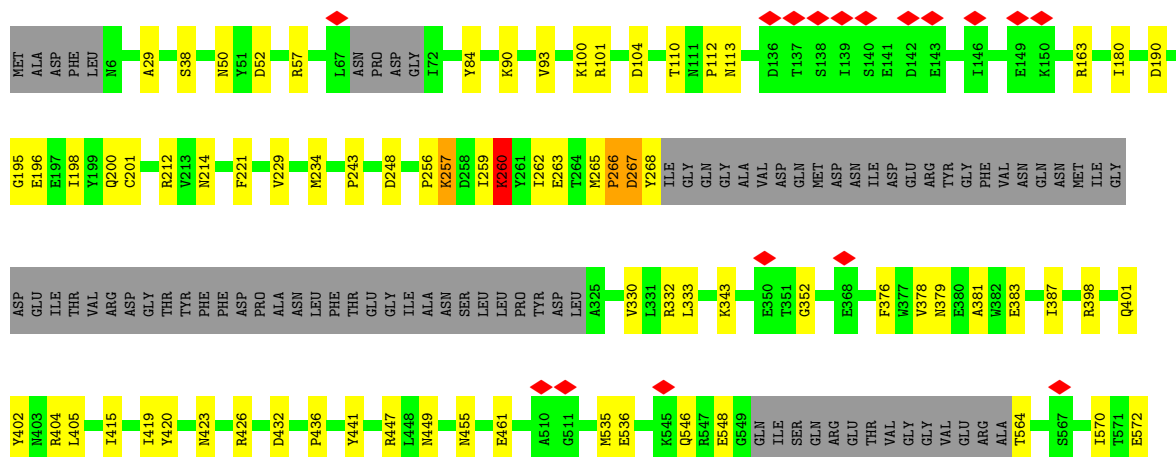
• Molecule 5: Portal protein gp20

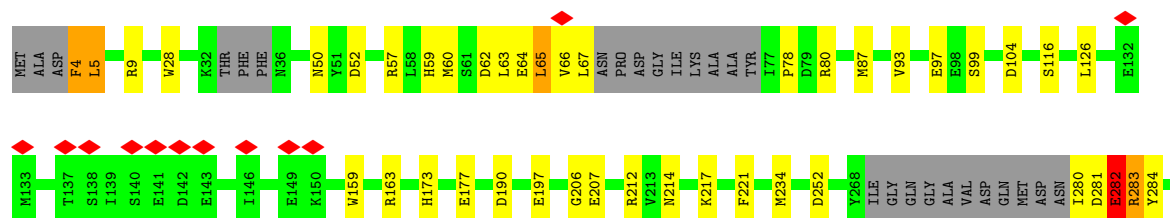
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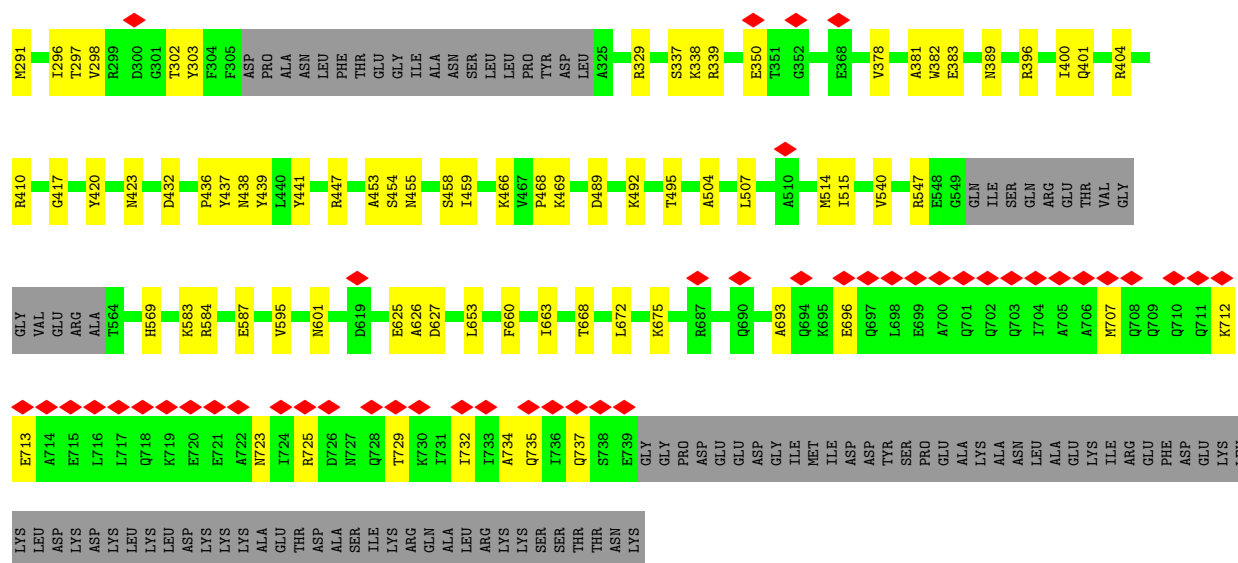


• Molecule 5: Portal protein gp20

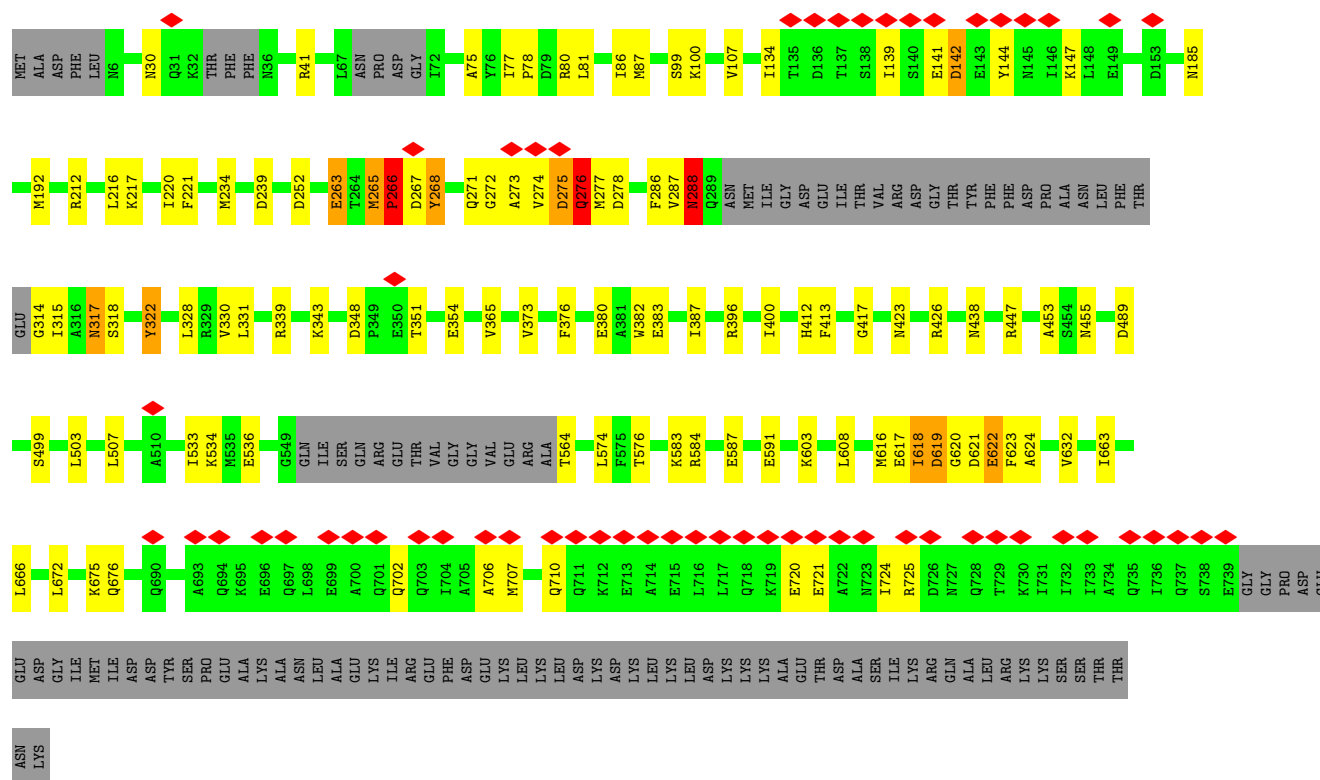
Chain FE: 



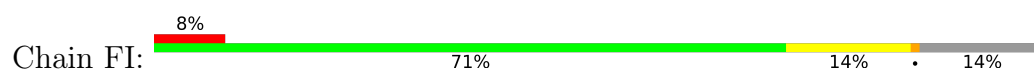




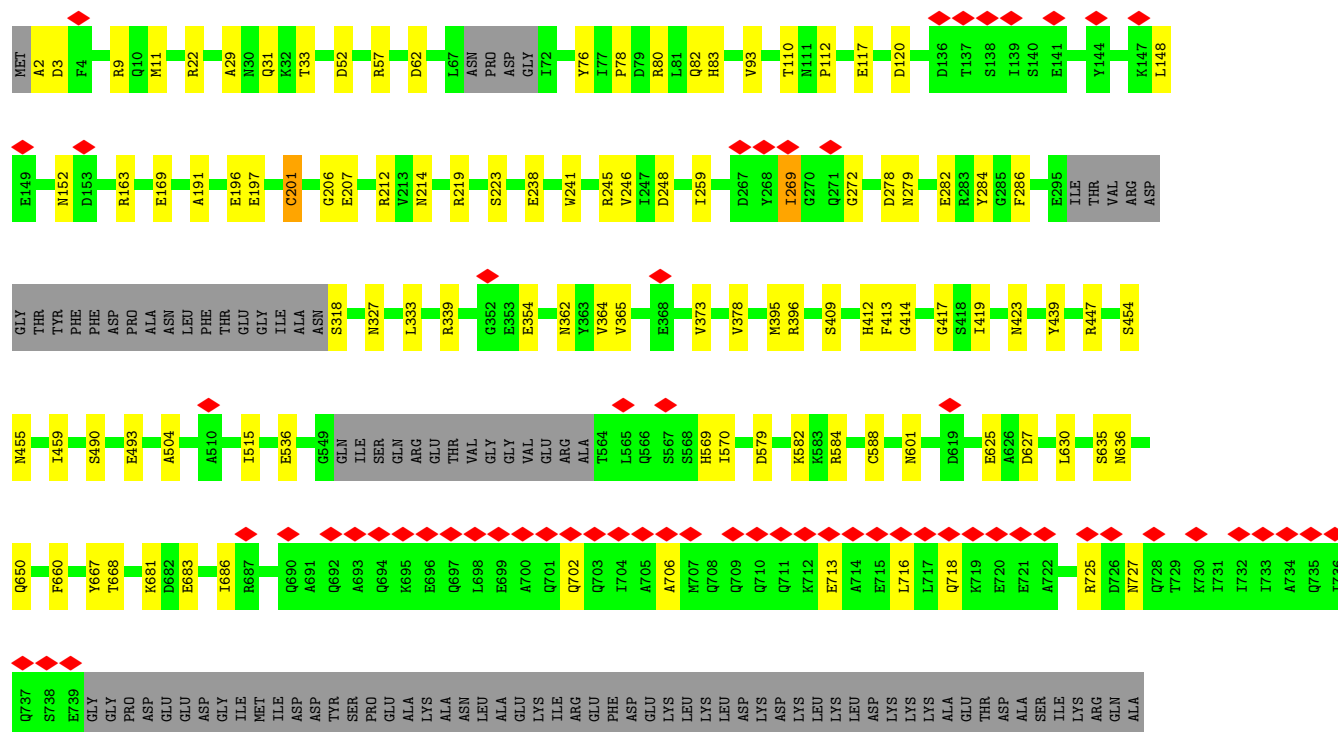
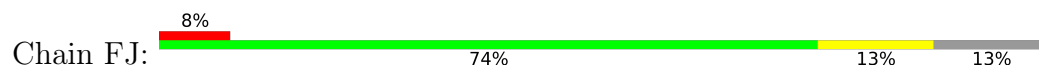
• Molecule 5: Portal protein gp20



• Molecule 5: Portal protein gp20



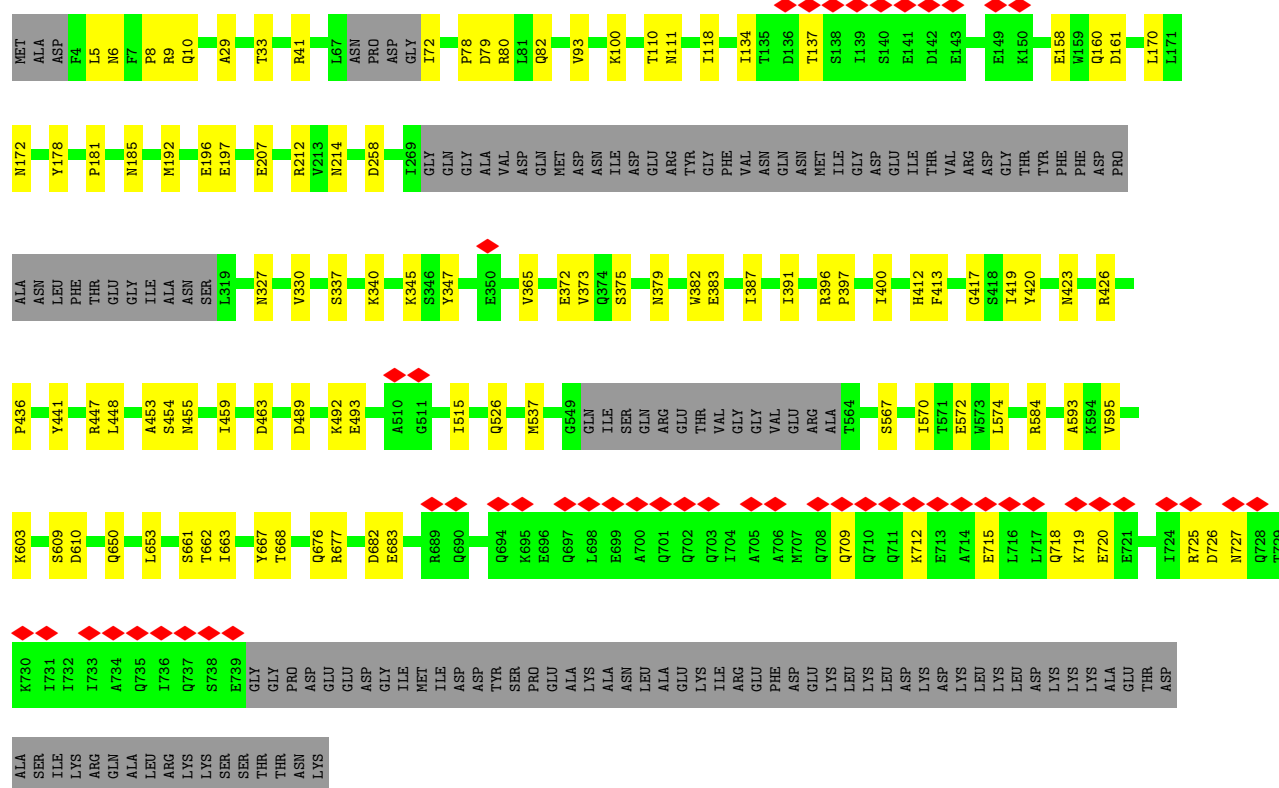
- Molecule 5: Portal protein gp20



LEU
ARG
LYS
LYS
SER
SER
THR
THR
ASN
LYS

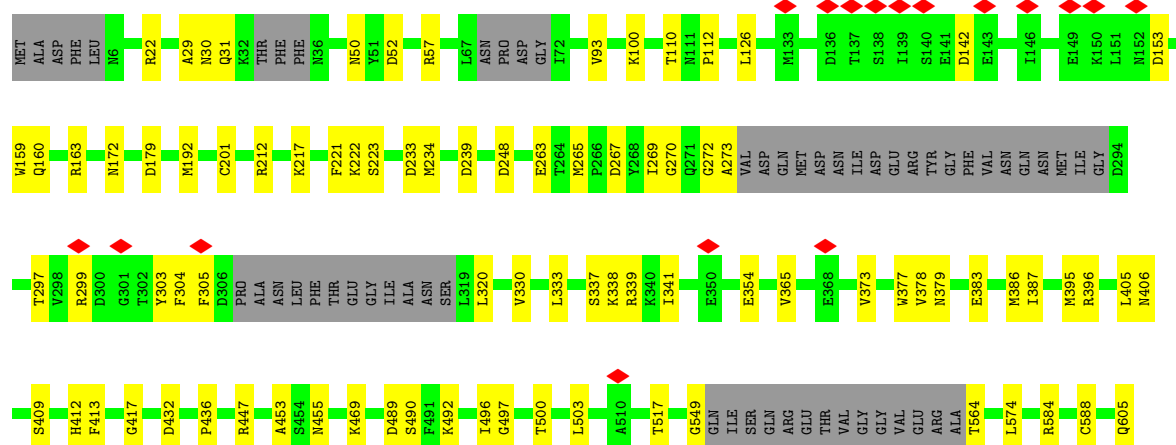
• Molecule 5: Portal protein gp20

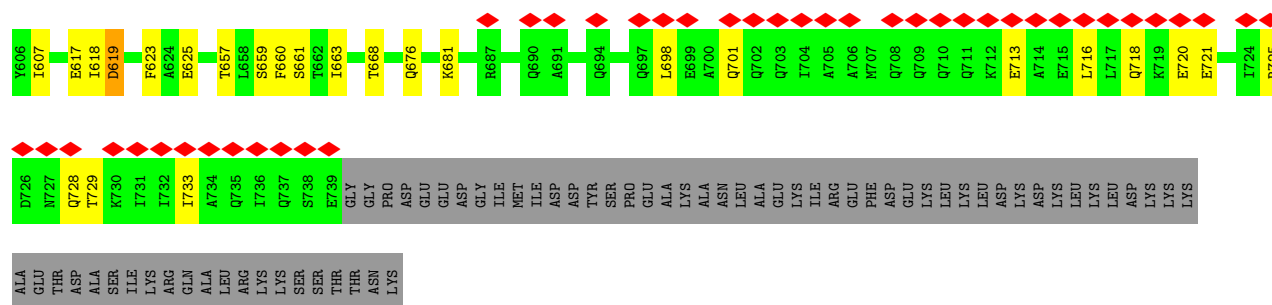
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• Molecule 5: Portal protein gp20

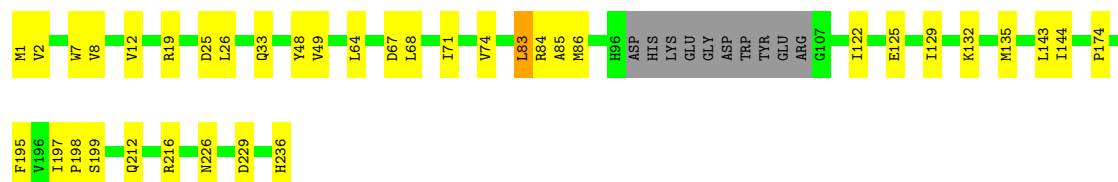
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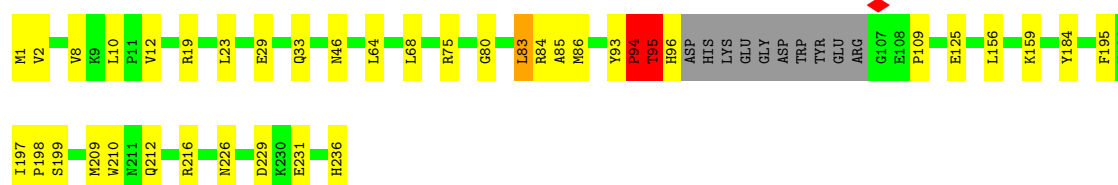
- Molecule 6: Ring protein 1 gp43

Chain FM: 80% 15% .



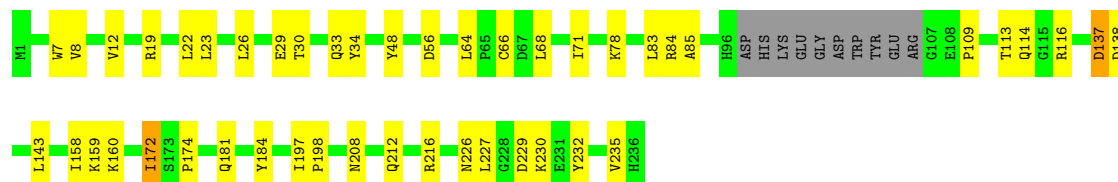
- Molecule 6: Ring protein 1 gp43

Chain FN: 79% 15% . .



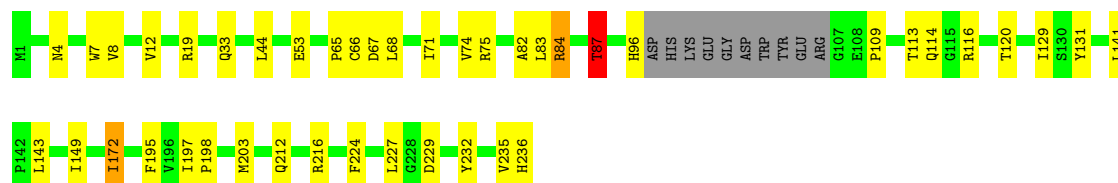
- Molecule 6: Ring protein 1 gp43

Chain FO: 76% 19% . .



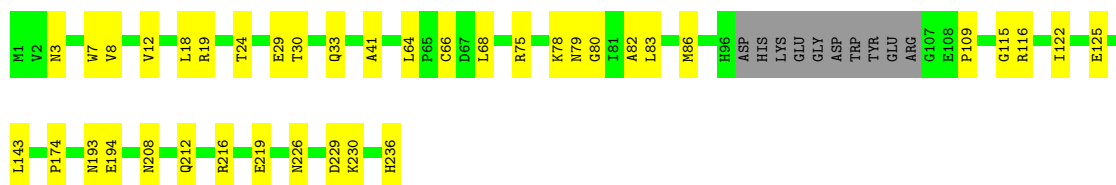
- Molecule 6: Ring protein 1 gp43

Chain FP: 78% 17% . .



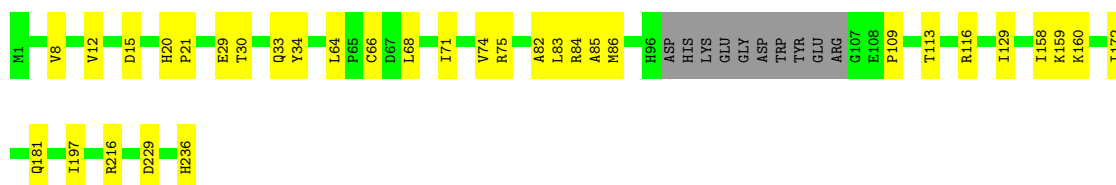
- Molecule 6: Ring protein 1 gp43

Chain FQ:  80% 16% .



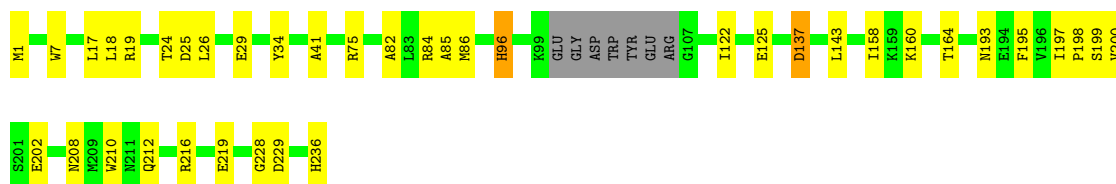
- Molecule 6: Ring protein 1 gp43

Chain FR:  82% 14% .



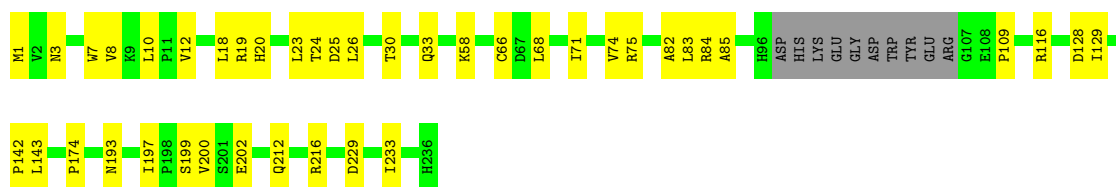
- Molecule 6: Ring protein 1 gp43

Chain FS:  81% 16% ..



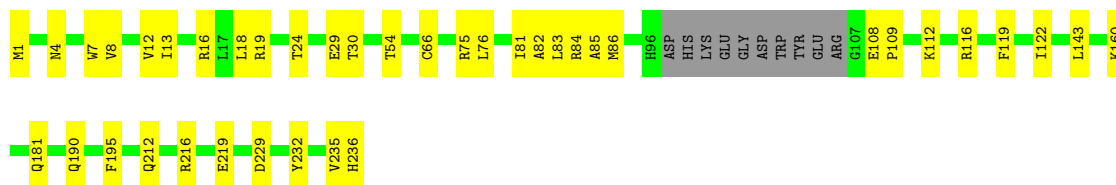
- Molecule 6: Ring protein 1 gp43

Chain FT:  78% 17% .

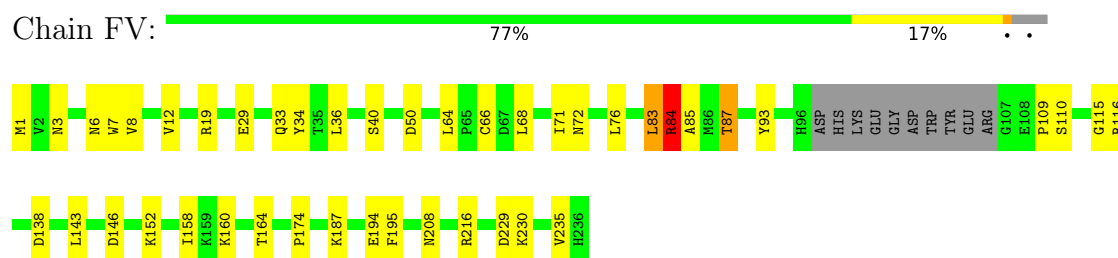


- Molecule 6: Ring protein 1 gp43

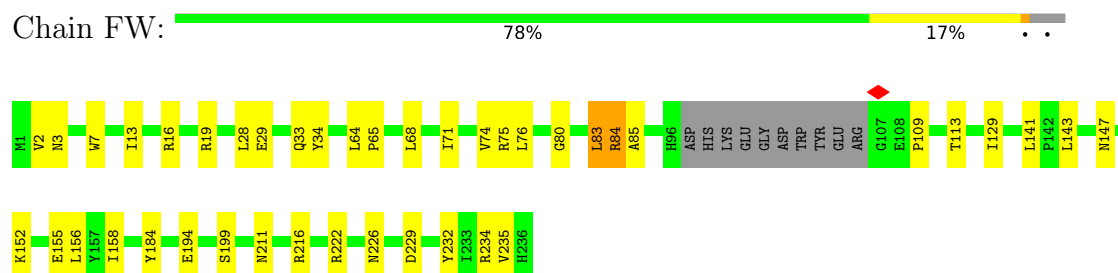
Chain FU:  79% 17% .



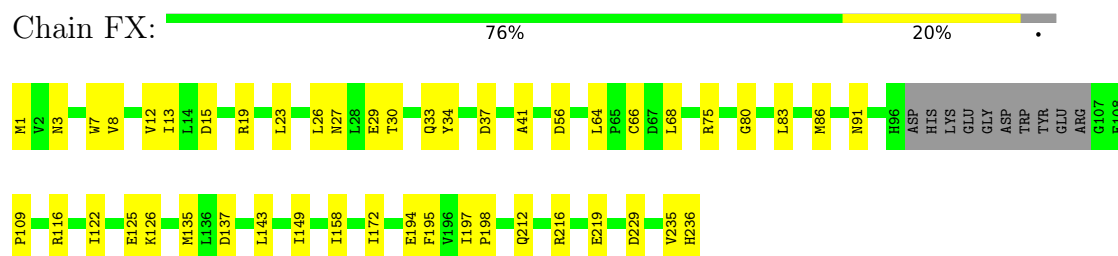
- Molecule 6: Ring protein 1 gp43



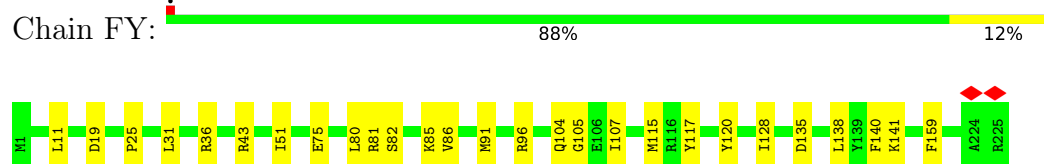
- Molecule 6: Ring protein 1 gp43



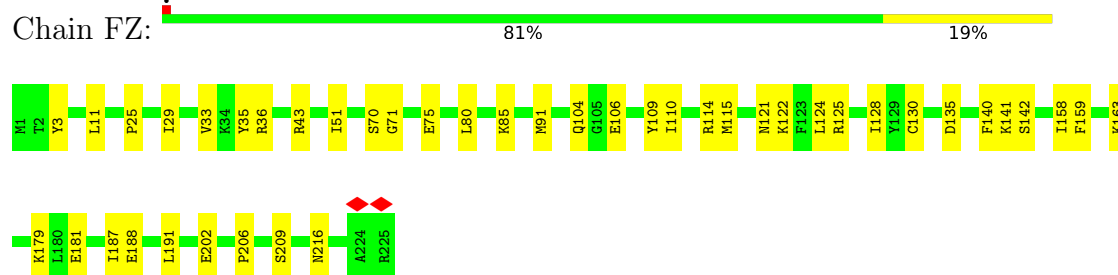
- Molecule 6: Ring protein 1 gp43



- Molecule 7: Ring protein 2 gp40

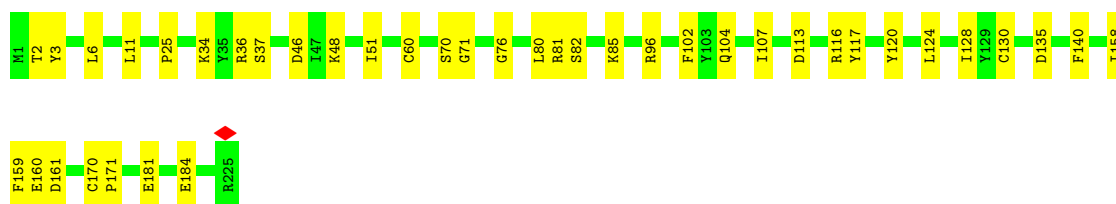


- Molecule 7: Ring protein 2 gp40



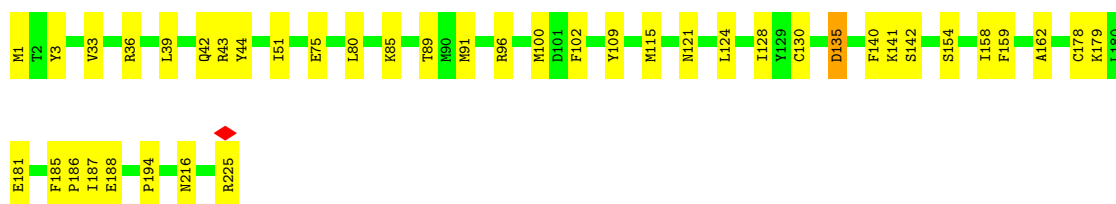
- Molecule 7: Ring protein 2 gp40

Chain GA:  82% 18%



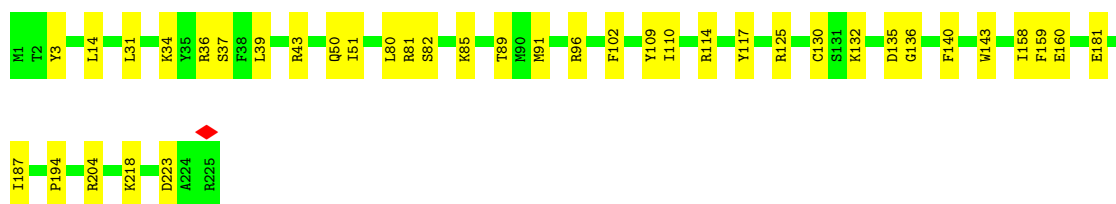
- Molecule 7: Ring protein 2 gp40

Chain GB:  82% 18%



- Molecule 7: Ring protein 2 gp40

Chain GC:  83% 17%



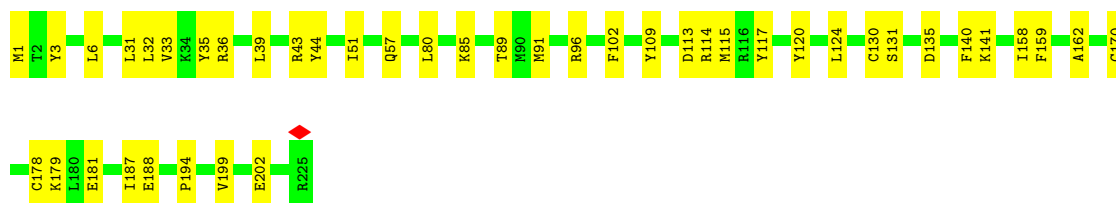
- Molecule 7: Ring protein 2 gp40

Chain GD:  87% 13%

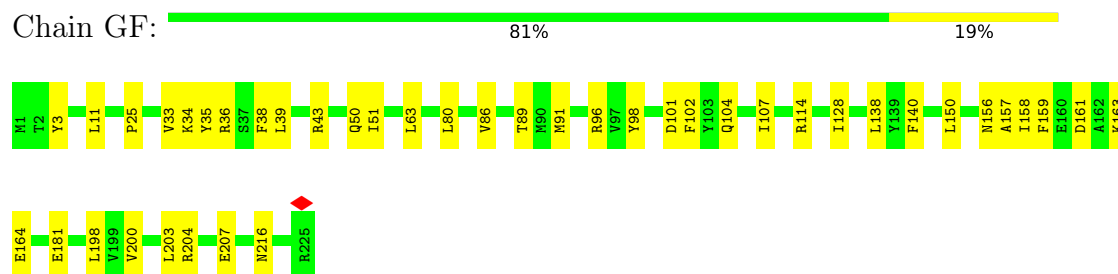


- Molecule 7: Ring protein 2 gp40

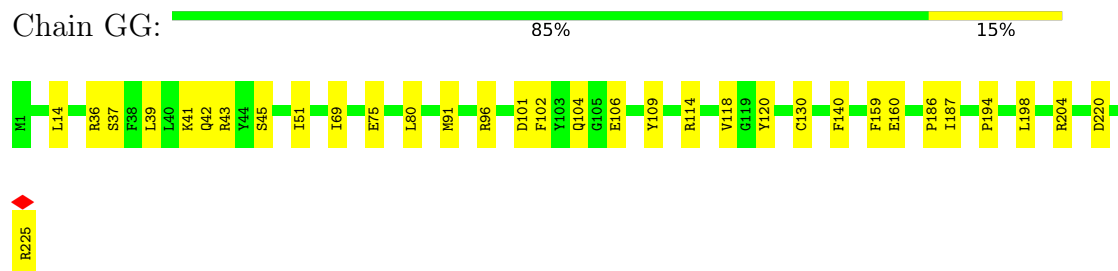
Chain GE:  81% 19%



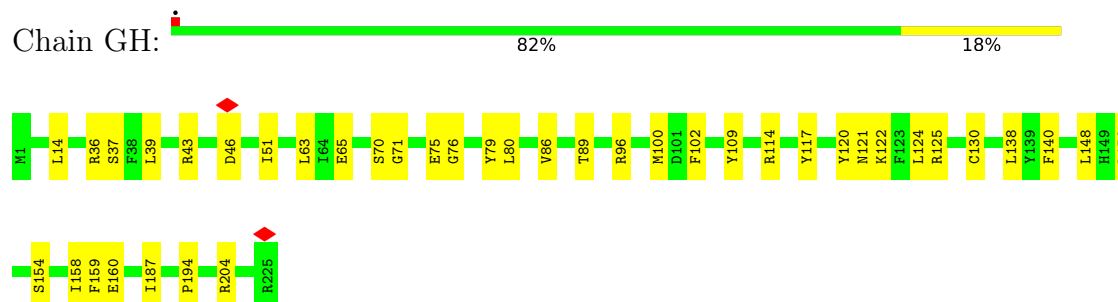
- Molecule 7: Ring protein 2 gp40



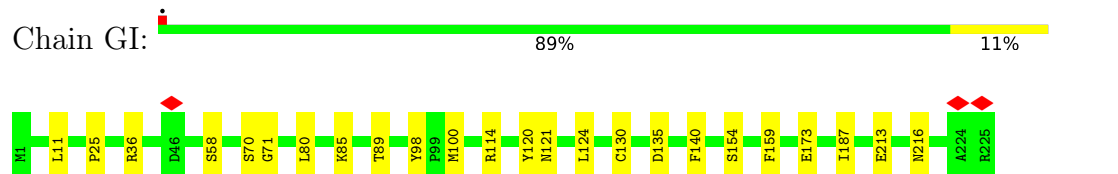
- Molecule 7: Ring protein 2 gp40



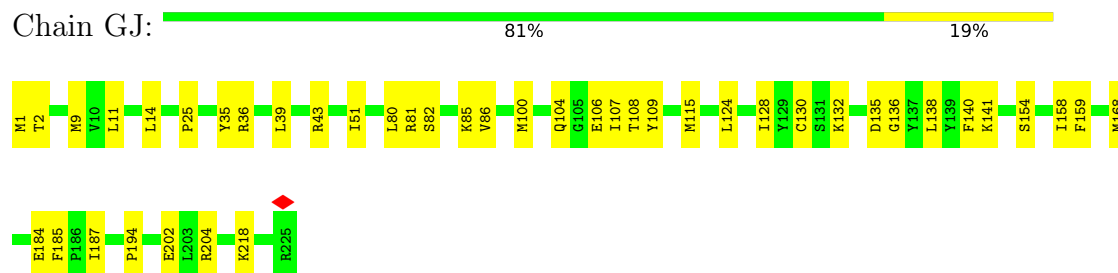
- Molecule 7: Ring protein 2 gp40



- Molecule 7: Ring protein 2 gp40



- Molecule 7: Ring protein 2 gp40

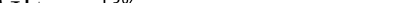


- Molecule 8: Cargo protein 1 gp45

Chain GK: 14% 85%

[illegible]

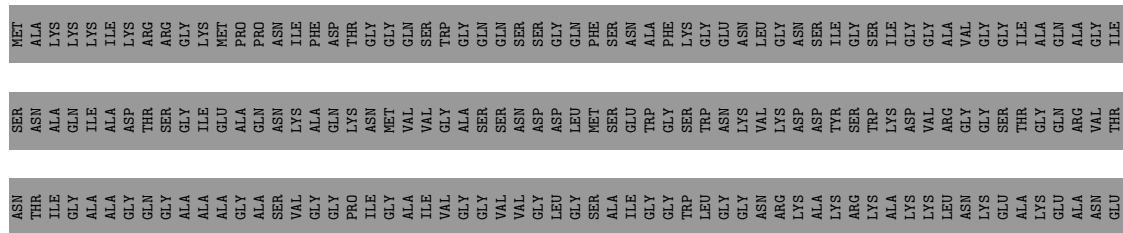
- Molecule 8: Cargo protein 1 gp45

Chain GL:  13% 85%

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



Chain GO: 13% . 85%





[illegible]

- Molecule 8: Cargo protein 1 gp45

Chain IK: 96%

[illegible]

- Molecule 8: Cargo protein 1 gp45

96%

- Molecule 8: Cargo protein 1 gp45

96%

[illegible]

- Molecule 8: Cargo protein 1 gp45

[illegible]

ASP	THR	LEU	ALA	LYS	SER	GLY	VAL	LEU	LYS	MET	ASN	THR	THR	LYS	GLY	GLU	TYR	THR	GLY	GLY	THR	THR	LYS	LYS	LYS	GLY	GLY	VAL	ARG	THR	THR	LYS	LYS	LYS	GLY	LEU	THR	TYR	GLY
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- Molecule 8: Cargo protein 1 gp45

Chain IP: ■ 96%

SER	ASN	ALA	ALA	GLN	ILE	ASP	THR	SER	SER	GLY	ILE	ALA	ALA	GLN	ASN	LYS	ALA	ALA	GLN	LYS	ASN	VAL	VAL	GLY	ALA	SER	SER	SER	ASN	ASN	ASP	ASP	LEU	SER	GLU	GLU	TRP	TRP	GLY	SER	SER	TRP	TRP	ASN	ASN	LYS	VAL	VAL	LYS	ASP	ASP	TYR	ASP	VAL	VAL	ARG	ARG	GLY	GLY	SER	THR	GLY	GLN	ARG	VAL	THR
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ASN	THR	ILE	GLY	ALA	ALA	GLY	GLN	GLY	ALA	ALA	ALA	ALA	ALA	GLY	GLY	GLY	PRO	ILE	GLY	ALA	ALA	ILE	ILE	VAL	VAL	GLY	GLY	GLY	LEU	GLY	SER	SER	GLY	ARG	LYS	ALA	ALA	LYS	ARG	LYS	ALA	LYS	LYS	ASN	ASN	GLU	ALA	LYS	GLU	ALA	ALA	ASN	TRP
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ARG	ALA	LEU	THR	SER	PHE	GLU	THR	ARG	ALA	ASP	ASN	ASN	ASP	PHE	ASN	ASN	LEU	MET	ALA	ALA	ASN	ASN	PHE	SER	ALA	ALA	TYR	GLY	GLY	PRO	PRO	GLU	F214	Y221	N225	R226	N229	L244	P245	ASN	SER	PHE	THR	GLN	ALA	ALA	LEU	PRO	GLU	GLU	MET	ASN	THR	TYR	ASN	ASN	PHE
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GLU GLY GLY GLY LEU SER ARG GLU GLU LYS ASN TYR GLY SER LYS LYS LYS PRO PRO TYR PRO SER SER VAL VAL ASP GLY PHE ALA ALA GLY PRO PRO HIS ARG SER TYR PRO PRO PRO THR THR LYS LYS ALA ALA ASP ASP ARG ASP ARG ASP THR THR LYS LEU LEU LEU ALA ALA ALA ARG ASP ALA ALA ARG ARG ARG ARG LYS LYS

LEU
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ASN	LYS	GLY	LYS	PHE	THR	ALA	TYR	GLY	GLY	LYS	VAL	THR	GLU	ALA	CYS	ILE	ARG	LYS	GLY	LYS	ASN	SER	SER	PRO	THR	THR	THR	ARG	LYS	ARG	ALA	ALA	ALA	ARG	ARG	THR	PHE	ALA	PHE	GLN	ASN	ASN	ALA	ALA	ASN	THR	TRP	TRP	ASN	ASN	LEU	ASN	THR	THR	GLN	GLY	GLY	ASP	PHE	THR	ASN	ASN	GLY	VAL
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THR	PHE	ILE	ILE	ASN	GLU	GLY	GLY	SER	HIS	GLU	GLU	GLN	ASN	PRO	TYR	GLN	GLY	ILE	ILE	GLN	ILE	GLY	VAL	ASP	PRO	GLU	GLY	ALA	PRO	ASN	VAL	VAL	GLU	GLN	GLY	GLY	VAL	VAL	VAL	TYR	ASP	ASP	PHE	SER	ASP	ASP	ARG	MET	LEU	GLU	ILE	PRO	GLU	TYR	LYS	LEU	ARG	GLY
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LYS
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[illegible]

ASP LEU PHE SER PRO ASP TYR TYR ASP ASP ALA ASP LEU ILE SER VAL LYS ASP LEU GLY VAL LYS ASP LEU ILE VAL GLY TYR TYR PRO PRO LEU LEU LEU LEU ASP ASN TYR TYR ARG ARG ASP ASP PHE TYR ILE LYS MET ASN ASN LYS LYS THR ARG ARG TYR TYR LEU LEU MET ASN

[illegible][illegible]

EU	SP	HR	EU	LA	YS	ER	LY	AL	AL	EU	YS	ET	SN	HR	YS	LY	LU	YR	HR	LY	LY	HR	YS	YS	LA	YS	LY	LY	YS	AL	RG	HR	YS	YS	YS	LY	LY	EU	HR	YR	LY
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- Molecule 8: Cargo protein 1 gp45

Chain IQ: 96%

[illegible]

- Molecule 8: Cargo protein 1 gp45

Chain IS: 96%

Tyr	Phe	Lys	Val	Tyr	Arg	Asn	Ser	Met
Lys	Thr	Ile	Arg	Asn	Ala	Thr	Asn	Met
Leu	Asn	Lys	Arg	Ala	Leu	Ile	Ala	Lys
Arg	Gly	Val	Lys	Phe	Thr	Gly	Gln	Lys
Gly	Val	Lys	Leu	Ala	Ser	Ala	Ile	Lys
Lys	Thr	Asn	Leu	Glu	Phe	Ala	Ala	Ile
Thr	Phe	Lys	Ala	Gly	Glu	Gly	Asp	Lys
Phe	Ile	Gly	Lys	Gly	Thr	Thr	Thr	Arg
Leu	Asn	Lys	Tyr	Leu	Arg	Gly	Ser	Arg
Lys	Glu	Phe	Pro	Gly	Ala	Ala	Gly	Lys
Ala	Gly	Thr	Leu	Ser	Asp	Ala	Ile	Lys
Ala	Gly	Ala	Leu	Arg	Asn	Ala	Glu	Met
Lys	Ser	Tyr	Lys	Glu	Ile	Gly	Ala	Pro
Ser	His	Lys	Ala	Lys	Asp	Ala	Gln	Pro
Ala	Glu	Gly	Phe	Asn	Thr	Ser	Asn	Asn
Gln	Glu	Lys	Gly	Tyr	Gln	Val	Lys	Ile
Arg	Asn	Lys	Gly	Gly	Asn	Gly	Ala	Phe
Glu	Pro	Val	Ser	Ser	Asp	Gly	Gln	Asp
Ser	Tyr	Thr	Leu	Lys	Phe	Pro	Lys	Thr
Glu	Gln	Glu	Phe	Lys	Asn	Ile	Asn	Gly
Glu	Gly	Ala	Asp	Lys	Met	Gly	Met	Gly
Arg	Ile	Cys	Ser	Pro	Leu	Ala	Val	Gln
Pro	Gln	Ile	Val	Tyr	Ala	Ile	Val	Ser
Asn	Tle	Arg	Val	Pro	Asn	Val	Gly	Trp
Asp	Gly	Lys	Gly	Ser	Phe	Gly	Ala	Gly
Pro	Val	Gly	Asn	Pro	Ser	Gly	Ser	Gln
Pro	Asp	Lys	Asn	Val	Ser	Val	Ser	Asn
Leu	Asp	Lys	Phe	Ser	Tyr	Val	Asn	Ser
Ser	Pro	Asn	Asn	Gly	Gly	Gly	Asp	Ser
Thr	Glu	Ser	Gln	Asp	Gly	Leu	Asp	Gly
Lys	Gly	Ser	Gln	Asn	Pro	Gly	Leu	Gln
Gly	Ala	Asn	Ser	Phe	Leu	Ser	Met	Phe
Leu	Pro	Pro	Phe	Ala	Leu	Ser	Ser	Ser
Gln	Asn	Thr	Thr	Gly	Glu	Ile	Glu	Asn
Ala	Leu	Thr	Gln	Pro	F214	Ile	Trp	Ala
Ala	Val	Arg	Gly	His	Y221	Gly	Gly	Phe
Met	Glu	Lys	Ile	Arg	E222	Trp	Gly	Lys
Glu	Gln	Arg	Gln	Ser		Trp	Ser	Leu
Arg	Gly	Ala	Gly	Thr	N225	Gly	Asn	Glu
Ile	Glu	Thr	Met	Pro	R226	Asn	Lys	Asn
Ala	Val	Phe	Phe	Ile		Gly	Val	Leu
Val	Ala	Ala	Gln	Pro	N229	Asn	Val	Lys
Thr	Val	Ala	Gln	Thr		Arg	Lys	Gly
Ala	Tyr	Gln	Gln	Pro		Arg	Asp	Asn
Gln	Asp	Asn	Glu	Lys	Q239	Lys	Asp	Ser
Leu	Asp	Ala	Pro	Ala		Ala	Asn	Ala
Glu	Tyr	Arg	Glu	Asp		Glu	Tyr	Ile
Ala	Val	Asn	Gln	Ala	T242	Arg	Ser	Gly
Arg	Phe	Trp	Thr	Arg	S243	Lys	Trp	Ser
Gln	Ser	Asn	Val	Asp	L244	Ala	Lys	Ile
Arg	Asp	Ala	Gln	Ala	P245	Lys	Asp	Gly
Lys	Met	Phe	Ala	Leu	Asn	Val	Val	Val
Glu	Arg	Gly	Ala	Ser	Ser	Leu	Arg	Ala
His	Tle	Trp	Ile	Leu	Phe	Gly	Val	Gly
Arg	Pro	Leu	Ala	Gly	Gln	Ser	Gly	Gly
Glu	Asp	Asn	Lys	Leu	Ala	Thr	Thr	Ile
Gly	Thr	Thr	Asp	His	Pro	Lys	Gly	Ala
Asn	Ile	Gly	Asp	Gly	Glu	Ala	Gln	Arg
Glu	Arg	Gly	Gly	Asn	Met	Ala	Arg	Ala
Pro	Glu	Asp	Thr	Lys	Gly	Asn	Val	Gly
Tyr	Cys	Ser	Tle	Ser	Thr	Cys	Thr	Ile

[illegible]

- Molecule 8: Cargo protein 1 gp45

Chain IT: 96%

[illegible]

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	122709	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 ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.628	Depositor
Minimum map value	-0.478	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	398.71204, 398.71204, 398.71204	wwPDB
Map dimensions	286, 286, 286	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.394098, 1.394098, 1.394098	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	AA	0.22	0/3950	0.50	3/5346 (0.1%)
1	AB	0.22	0/4106	0.46	0/5553
1	AC	0.25	0/4106	0.47	0/5553
1	AD	0.24	0/3732	0.48	0/5044
1	AE	0.22	0/4106	0.45	2/5553 (0.0%)
1	AF	0.26	0/4106	0.49	0/5553
1	BA	0.25	0/3957	0.50	2/5356 (0.0%)
1	BB	0.22	0/4106	0.44	0/5553
1	BC	0.27	0/4106	0.54	1/5553 (0.0%)
1	BD	0.24	0/3732	0.48	0/5044
1	BE	0.21	0/4106	0.44	0/5553
1	BF	0.21	0/4106	0.46	0/5553
1	CA	0.22	0/3944	0.47	1/5338 (0.0%)
1	CB	0.23	0/4106	0.46	0/5553
1	CC	0.26	0/4106	0.50	0/5553
1	CD	0.25	0/3695	0.49	1/4995 (0.0%)
1	CE	0.21	0/4106	0.42	0/5553
1	CF	0.27	0/4106	0.55	2/5553 (0.0%)
1	DA	0.27	0/3957	0.52	4/5356 (0.1%)
1	DB	0.22	0/4106	0.45	0/5553
1	DC	0.25	0/4106	0.46	0/5553
1	DD	0.24	0/3732	0.48	4/5044 (0.1%)
1	DE	0.21	0/4106	0.43	0/5553
1	DF	0.23	0/4106	0.48	0/5553
1	EA	0.23	0/3957	0.47	2/5356 (0.0%)
1	EB	0.22	0/4106	0.43	0/5553
1	EC	0.33	0/4106	0.72	9/5553 (0.2%)
1	ED	0.24	0/3732	0.46	0/5044
1	EE	0.25	0/4106	0.50	1/5553 (0.0%)
1	EF	0.23	0/4106	0.48	2/5553 (0.0%)
2	Aa	0.24	0/2591	0.50	0/3533
2	Ab	0.29	0/2591	0.58	3/3533 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Ad	0.27	0/2591	0.53	3/3533 (0.1%)
2	Ae	0.19	0/2119	0.46	0/2887
2	Af	0.24	0/1465	0.53	0/2001
2	Ba	0.24	0/2591	0.55	3/3533 (0.1%)
2	Bb	0.35	0/2591	0.64	5/3533 (0.1%)
2	Bd	0.27	0/2591	0.51	1/3533 (0.0%)
2	Be	0.20	0/2112	0.46	0/2877
2	Bf	0.25	0/1465	0.56	1/2001 (0.0%)
2	Ca	0.24	0/2591	0.55	3/3533 (0.1%)
2	Cb	0.31	0/2591	0.60	3/3533 (0.1%)
2	Cd	0.26	0/2591	0.50	1/3533 (0.0%)
2	Ce	0.18	0/2119	0.45	2/2887 (0.1%)
2	Cf	0.28	0/1465	0.61	1/2001 (0.0%)
2	Da	0.23	0/2591	0.52	3/3533 (0.1%)
2	Db	0.32	1/2591 (0.0%)	0.56	1/3533 (0.0%)
2	Dd	0.26	0/2591	0.57	5/3533 (0.1%)
2	De	0.19	0/2119	0.45	0/2887
2	Df	0.26	0/1465	0.52	0/2001
2	Ea	0.25	0/2591	0.51	0/3533
2	Eb	0.29	0/2591	0.59	2/3533 (0.1%)
2	Ed	0.26	0/2591	0.52	1/3533 (0.0%)
2	Ee	0.19	0/2119	0.43	2/2887 (0.1%)
2	Ef	0.27	0/1465	0.60	3/2001 (0.1%)
3	Ag	0.26	0/629	0.45	0/852
3	Ah	0.27	0/572	0.55	0/773
3	Bg	0.24	0/629	0.45	0/852
3	Bh	0.27	0/572	0.56	0/773
3	Cg	0.24	0/629	0.43	0/852
3	Ch	0.27	0/572	0.59	1/773 (0.1%)
3	Dg	0.24	0/629	0.43	0/852
3	Dh	0.28	0/572	0.58	0/773
3	Eg	0.25	0/629	0.43	0/852
3	Eh	0.29	0/572	0.59	0/773
4	Ai	0.20	0/318	0.43	0/430
4	Aj	0.19	0/318	0.44	0/430
4	Ak	0.19	0/318	0.45	0/430
4	Bi	0.18	0/318	0.39	0/430
4	Bj	0.17	0/318	0.42	0/430
4	Bk	0.18	0/318	0.45	0/430
4	Ci	0.20	0/318	0.50	0/430
4	Cj	0.18	0/318	0.49	0/430
4	Ck	0.24	0/318	0.60	0/430
4	Di	0.22	0/318	0.51	0/430

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	Dj	0.16	0/318	0.43	0/430
4	Dk	0.18	0/318	0.51	0/430
4	Ei	0.19	0/318	0.39	0/430
4	Ej	0.19	0/318	0.44	0/430
4	Ek	0.23	0/318	0.49	0/430
5	FA	0.38	0/5718	0.64	8/7713 (0.1%)
5	FB	0.33	0/5646	0.54	3/7616 (0.0%)
5	FC	0.36	0/5700	0.57	3/7690 (0.0%)
5	FD	0.42	2/5868 (0.0%)	0.71	19/7920 (0.2%)
5	FE	0.38	2/5500 (0.0%)	0.63	10/7419 (0.1%)
5	FF	0.34	0/5697	0.56	1/7687 (0.0%)
5	FG	0.35	0/5670	0.59	4/7645 (0.1%)
5	FH	0.41	0/5719	0.71	9/7715 (0.1%)
5	FI	0.44	5/5776 (0.1%)	0.71	16/7793 (0.2%)
5	FJ	0.33	0/5804	0.54	1/7831 (0.0%)
5	FK	0.33	0/5581	0.52	0/7531
5	FL	0.38	0/5664	0.61	7/7640 (0.1%)
6	FM	0.45	1/1881 (0.1%)	0.61	1/2548 (0.0%)
6	FN	0.41	1/1881 (0.1%)	0.69	4/2548 (0.2%)
6	FO	0.38	0/1881	0.55	0/2548
6	FP	0.47	1/1881 (0.1%)	0.65	2/2548 (0.1%)
6	FQ	0.37	0/1881	0.57	0/2548
6	FR	0.38	0/1881	0.53	0/2548
6	FS	0.37	0/1909	0.56	0/2585
6	FT	0.37	0/1881	0.58	0/2548
6	FU	0.38	0/1881	0.55	0/2548
6	FV	0.49	1/1881 (0.1%)	0.66	4/2548 (0.2%)
6	FW	0.46	1/1881 (0.1%)	0.62	1/2548 (0.0%)
6	FX	0.37	0/1881	0.53	1/2548 (0.0%)
7	FY	0.36	0/1886	0.52	0/2552
7	FZ	0.36	0/1886	0.52	0/2552
7	GA	0.35	0/1886	0.49	0/2552
7	GB	0.35	0/1886	0.50	0/2552
7	GC	0.35	0/1886	0.49	0/2552
7	GD	0.36	0/1886	0.49	0/2552
7	GE	0.36	0/1886	0.51	0/2552
7	GF	0.36	0/1886	0.52	0/2552
7	GG	0.38	0/1886	0.51	0/2552
7	GH	0.36	0/1886	0.51	0/2552
7	GI	0.37	0/1886	0.48	0/2552
7	GJ	0.36	0/1886	0.51	0/2552
8	GK	0.30	0/1003	0.63	0/1347
8	GL	0.25	0/1003	0.58	0/1347

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	GM	0.26	0/1003	0.60	0/1347
8	GN	0.25	0/1003	0.58	0/1347
8	GO	0.29	0/1003	0.62	0/1347
8	GP	0.34	0/1003	0.66	1/1347 (0.1%)
8	GQ	0.33	0/1003	0.68	1/1347 (0.1%)
8	GR	0.25	0/1003	0.58	0/1347
8	GS	0.26	0/1003	0.58	0/1347
8	GT	0.25	0/1003	0.56	0/1347
8	GU	0.25	0/1003	0.56	0/1347
8	GV	0.33	0/1003	0.71	2/1347 (0.1%)
8	IK	0.27	0/255	0.56	0/342
8	IL	0.26	0/255	0.47	0/342
8	IM	0.25	0/255	0.51	0/342
8	IN	0.25	0/255	0.47	0/342
8	IO	0.25	0/255	0.51	0/342
8	IP	0.23	0/255	0.53	0/342
8	IQ	0.27	0/255	0.61	1/342 (0.3%)
8	IR	0.22	0/255	0.48	0/342
8	IS	0.55	0/255	0.97	3/342 (0.9%)
8	IT	0.23	0/255	0.50	0/342
8	IU	0.23	0/255	0.48	0/342
8	IV	0.23	0/255	0.48	0/342
All	All	0.30	15/316732 (0.0%)	0.54	180/428688 (0.0%)

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	BF	0	1
2	Ab	0	1
2	Ad	0	2
2	Bb	0	2
2	Bd	0	1
2	Cb	0	1
2	Cd	0	2
2	Db	0	1
2	Dd	0	1
2	Eb	0	1
2	Ed	0	2
3	Ah	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	Eh	0	1
6	FS	0	1
All	All	0	18

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	FE	256	PRO	C-O	-7.76	1.14	1.24
5	FI	626	ALA	C-O	-6.36	1.16	1.24
5	FD	321	PRO	C-O	-6.32	1.16	1.23
5	FE	260	LYS	C-O	-6.30	1.16	1.24
5	FI	323	ASP	C-O	-6.07	1.17	1.23

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EC	66	ASP	CB-CA-C	-25.40	87.17	116.63
6	FN	95	THR	CB-CA-C	-18.15	80.82	111.31
5	FE	266	PRO	N-CA-C	17.28	138.19	113.47
5	FD	34	PHE	N-CA-C	-13.05	91.98	112.99
5	FG	284	TYR	N-CA-C	-12.74	97.44	113.23

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Ab	263	TYR	Peptide
2	Ad	262	GLY	Peptide
2	Ad	6	ASN	Peptide
3	Ah	85	VAL	Peptide
1	BF	128	LEU	Peptide

5.2 Too-close contacts ⓘ

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	AA	3861	0	3765	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AB	4012	0	3920	61	0
1	AC	4012	0	3921	67	0
1	AD	3649	0	3574	66	0
1	AE	4012	0	3920	54	0
1	AF	4012	0	3921	51	0
1	BA	3868	0	3772	55	0
1	BB	4012	0	3921	59	0
1	BC	4012	0	3921	73	0
1	BD	3649	0	3574	73	0
1	BE	4012	0	3921	67	0
1	BF	4012	0	3921	47	0
1	CA	3855	0	3760	64	0
1	CB	4012	0	3921	61	0
1	CC	4012	0	3921	62	0
1	CD	3612	0	3535	59	0
1	CE	4012	0	3920	53	0
1	CF	4012	0	3920	59	0
1	DA	3868	0	3772	52	0
1	DB	4012	0	3921	70	0
1	DC	4012	0	3921	70	0
1	DD	3649	0	3574	71	0
1	DE	4012	0	3920	65	0
1	DF	4012	0	3921	46	0
1	EA	3868	0	3772	58	0
1	EB	4012	0	3921	70	0
1	EC	4012	0	3921	96	0
1	ED	3649	0	3574	60	0
1	EE	4012	0	3921	60	0
1	EF	4012	0	3921	48	0
2	Aa	2542	0	2558	26	0
2	Ab	2542	0	2558	37	0
2	Ad	2542	0	2558	34	0
2	Ae	2077	0	2075	14	0
2	Af	1434	0	1419	14	0
2	Ba	2542	0	2558	29	0
2	Bb	2542	0	2558	41	0
2	Bd	2542	0	2558	42	0
2	Be	2070	0	2066	13	0
2	Bf	1434	0	1419	17	0
2	Ca	2542	0	2558	24	0
2	Cb	2542	0	2558	35	0
2	Cd	2542	0	2558	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Ce	2077	0	2075	22	0
2	Cf	1434	0	1419	20	0
2	Da	2542	0	2558	23	0
2	Db	2542	0	2558	44	0
2	Dd	2542	0	2558	37	0
2	De	2077	0	2075	24	0
2	Df	1434	0	1419	10	0
2	Ea	2542	0	2558	44	0
2	Eb	2542	0	2558	36	0
2	Ed	2542	0	2558	38	0
2	Ee	2077	0	2075	14	0
2	Ef	1434	0	1419	19	0
3	Ag	619	0	619	14	0
3	Ah	563	0	570	7	0
3	Bg	619	0	619	12	0
3	Bh	563	0	570	15	0
3	Cg	619	0	619	14	0
3	Ch	563	0	570	10	0
3	Dg	619	0	619	15	0
3	Dh	563	0	570	11	0
3	Eg	619	0	619	13	0
3	Eh	563	0	570	11	0
4	Ai	310	0	313	5	0
4	Aj	310	0	313	3	0
4	Ak	310	0	313	9	0
4	Bi	310	0	313	6	0
4	Bj	310	0	313	6	0
4	Bk	310	0	313	5	0
4	Ci	310	0	313	7	0
4	Cj	310	0	313	11	0
4	Ck	310	0	313	11	0
4	Di	310	0	313	5	0
4	Dj	310	0	313	5	0
4	Dk	310	0	313	0	0
4	Ei	310	0	313	10	0
4	Ej	310	0	313	9	0
4	Ek	310	0	313	7	0
5	FA	5617	0	5565	83	0
5	FB	5545	0	5492	79	0
5	FC	5597	0	5537	84	0
5	FD	5759	0	5692	106	0
5	FE	5400	0	5357	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	FF	5593	0	5522	74	0
5	FG	5569	0	5507	89	0
5	FH	5618	0	5564	78	0
5	FI	5671	0	5610	80	0
5	FJ	5699	0	5631	78	0
5	FK	5478	0	5443	79	0
5	FL	5563	0	5508	73	0
6	FM	1841	0	1864	24	0
6	FN	1841	0	1864	25	0
6	FO	1841	0	1864	34	0
6	FP	1841	0	1864	34	0
6	FQ	1841	0	1864	29	0
6	FR	1841	0	1864	23	0
6	FS	1868	0	1888	30	0
6	FT	1841	0	1864	28	0
6	FU	1841	0	1864	30	0
6	FV	1841	0	1864	33	0
6	FW	1841	0	1864	36	0
6	FX	1841	0	1864	33	0
7	FY	1841	0	1801	16	0
7	FZ	1841	0	1801	28	0
7	GA	1841	0	1801	23	0
7	GB	1841	0	1801	25	0
7	GC	1841	0	1801	22	0
7	GD	1841	0	1801	21	0
7	GE	1841	0	1801	27	0
7	GF	1841	0	1801	25	0
7	GG	1841	0	1801	26	0
7	GH	1841	0	1801	26	0
7	GI	1841	0	1801	16	0
7	GJ	1841	0	1801	27	0
8	GK	987	0	930	7	0
8	GL	987	0	930	10	0
8	GM	987	0	930	13	0
8	GN	987	0	930	6	0
8	GO	987	0	930	11	0
8	GP	987	0	930	8	0
8	GQ	987	0	930	8	0
8	GR	987	0	930	10	0
8	GS	987	0	930	12	0
8	GT	987	0	930	12	0
8	GU	987	0	930	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	GV	987	0	930	20	0
8	IK	251	0	239	2	0
8	IL	251	0	239	3	0
8	IM	251	0	239	5	0
8	IN	251	0	239	6	0
8	IO	251	0	239	2	0
8	IP	251	0	239	4	0
8	IQ	251	0	239	4	0
8	IR	251	0	239	4	0
8	IS	251	0	239	13	0
8	IT	251	0	239	6	0
8	IU	251	0	239	4	0
8	IV	251	0	239	6	0
9	AB	1	0	0	0	0
9	AC	1	0	0	0	0
9	AD	1	0	0	0	0
9	AE	1	0	0	0	0
9	BB	1	0	0	0	0
9	BD	1	0	0	0	0
9	CB	1	0	0	0	0
9	CD	1	0	0	0	0
9	CE	1	0	0	0	0
9	CF	1	0	0	0	0
9	DB	1	0	0	0	0
9	DE	1	0	0	0	0
9	DF	1	0	0	0	0
9	EB	1	0	0	0	0
9	ED	1	0	0	1	0
9	FA	1	0	0	0	0
9	FB	1	0	0	0	0
9	FC	1	0	0	0	0
9	FD	1	0	0	0	0
9	FE	1	0	0	0	0
9	FF	1	0	0	0	0
9	FG	1	0	0	0	0
9	FH	1	0	0	0	0
9	FI	1	0	0	0	0
9	FJ	1	0	0	0	0
9	FK	1	0	0	0	0
9	FL	1	0	0	0	0
All	All	310209	0	306018	3568	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 6.

The worst 5 of 3568 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)
5:FG:280:ILE:HG21	5:FG:302:THR:CG2	1.59	1.30
5:FD:269:ILE:CG1	5:FD:325:ALA:H	1.49	1.23
5:FD:269:ILE:HG12	5:FD:325:ALA:CA	1.70	1.22
5:FD:269:ILE:HG12	5:FD:325:ALA:N	1.56	1.18
5:FG:280:ILE:CG2	5:FG:302:THR:HG21	1.73	1.17

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	482/504 (96%)	466 (97%)	16 (3%)	0	100	100
1	AB	501/504 (99%)	479 (96%)	22 (4%)	0	100	100
1	AC	501/504 (99%)	484 (97%)	17 (3%)	0	100	100
1	AD	446/504 (88%)	426 (96%)	20 (4%)	0	100	100
1	AE	501/504 (99%)	488 (97%)	13 (3%)	0	100	100
1	AF	501/504 (99%)	485 (97%)	16 (3%)	0	100	100
1	BA	483/504 (96%)	472 (98%)	11 (2%)	0	100	100
1	BB	501/504 (99%)	478 (95%)	23 (5%)	0	100	100
1	BC	501/504 (99%)	482 (96%)	19 (4%)	0	100	100
1	BD	446/504 (88%)	427 (96%)	19 (4%)	0	100	100
1	BE	501/504 (99%)	488 (97%)	13 (3%)	0	100	100
1	BF	501/504 (99%)	481 (96%)	20 (4%)	0	100	100
1	CA	199/504 (40%)	197 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CB	75/504 (15%)	70 (93%)	5 (7%)	0	100	100
1	CC	478/504 (95%)	457 (96%)	21 (4%)	0	100	100
1	CD	309/504 (61%)	295 (96%)	14 (4%)	0	100	100
1	CE	143/504 (28%)	137 (96%)	6 (4%)	0	100	100
1	CF	26/504 (5%)	24 (92%)	2 (8%)	0	100	100
1	DA	148/504 (29%)	147 (99%)	1 (1%)	0	100	100
1	DB	294/504 (58%)	282 (96%)	12 (4%)	0	100	100
1	DC	226/504 (45%)	220 (97%)	6 (3%)	0	100	100
1	DD	331/504 (66%)	319 (96%)	12 (4%)	0	100	100
1	DE	472/504 (94%)	453 (96%)	19 (4%)	0	100	100
1	DF	487/504 (97%)	471 (97%)	16 (3%)	0	100	100
1	EA	283/504 (56%)	274 (97%)	9 (3%)	0	100	100
1	EB	344/504 (68%)	336 (98%)	8 (2%)	0	100	100
1	EC	501/504 (99%)	474 (95%)	27 (5%)	0	100	100
1	ED	446/504 (88%)	427 (96%)	19 (4%)	0	100	100
1	EE	501/504 (99%)	486 (97%)	15 (3%)	0	100	100
1	EF	353/504 (70%)	337 (96%)	16 (4%)	0	100	100
2	Aa	331/333 (99%)	315 (95%)	16 (5%)	0	100	100
2	Ab	331/333 (99%)	308 (93%)	23 (7%)	0	100	100
2	Ad	331/333 (99%)	313 (95%)	18 (5%)	0	100	100
2	Ae	261/333 (78%)	248 (95%)	13 (5%)	0	100	100
2	Af	183/333 (55%)	175 (96%)	8 (4%)	0	100	100
2	Ba	331/333 (99%)	310 (94%)	21 (6%)	0	100	100
2	Bb	331/333 (99%)	313 (95%)	17 (5%)	1 (0%)	36	64
2	Bd	317/333 (95%)	295 (93%)	22 (7%)	0	100	100
2	Be	59/333 (18%)	56 (95%)	3 (5%)	0	100	100
2	Bf	24/333 (7%)	24 (100%)	0	0	100	100
2	Cb	174/333 (52%)	163 (94%)	11 (6%)	0	100	100
2	Cd	216/333 (65%)	205 (95%)	11 (5%)	0	100	100
2	Da	150/333 (45%)	142 (95%)	8 (5%)	0	100	100
2	Db	133/333 (40%)	126 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Dd	95/333 (28%)	90 (95%)	5 (5%)	0	100	100
2	De	125/333 (38%)	120 (96%)	5 (4%)	0	100	100
2	Df	99/333 (30%)	94 (95%)	5 (5%)	0	100	100
2	Ea	191/333 (57%)	179 (94%)	12 (6%)	0	100	100
2	Eb	331/333 (99%)	308 (93%)	23 (7%)	0	100	100
2	Ed	331/333 (99%)	315 (95%)	16 (5%)	0	100	100
2	Ee	261/333 (78%)	247 (95%)	14 (5%)	0	100	100
2	Ef	183/333 (55%)	171 (93%)	12 (7%)	0	100	100
3	Ag	80/104 (77%)	76 (95%)	4 (5%)	0	100	100
3	Ah	71/104 (68%)	64 (90%)	7 (10%)	0	100	100
3	Bg	17/104 (16%)	15 (88%)	2 (12%)	0	100	100
3	Dg	79/104 (76%)	75 (95%)	4 (5%)	0	100	100
3	Dh	48/104 (46%)	46 (96%)	2 (4%)	0	100	100
3	Eg	80/104 (77%)	77 (96%)	3 (4%)	0	100	100
3	Eh	71/104 (68%)	66 (93%)	5 (7%)	0	100	100
4	Ai	36/97 (37%)	35 (97%)	1 (3%)	0	100	100
4	Aj	36/97 (37%)	34 (94%)	2 (6%)	0	100	100
4	Ak	36/97 (37%)	32 (89%)	3 (8%)	1 (3%)	4	23
4	Bk	10/97 (10%)	9 (90%)	1 (10%)	0	100	100
4	Cj	4/97 (4%)	4 (100%)	0	0	100	100
4	Di	25/97 (26%)	24 (96%)	1 (4%)	0	100	100
4	Dj	36/97 (37%)	35 (97%)	1 (3%)	0	100	100
4	Dk	36/97 (37%)	33 (92%)	3 (8%)	0	100	100
4	Ei	36/97 (37%)	34 (94%)	2 (6%)	0	100	100
4	Ej	36/97 (37%)	35 (97%)	1 (3%)	0	100	100
4	Ek	36/97 (37%)	33 (92%)	3 (8%)	0	100	100
5	FA	678/806 (84%)	657 (97%)	21 (3%)	0	100	100
5	FB	666/806 (83%)	647 (97%)	19 (3%)	0	100	100
5	FC	674/806 (84%)	658 (98%)	16 (2%)	0	100	100
5	FD	697/806 (86%)	662 (95%)	34 (5%)	1 (0%)	48	78
5	FE	652/806 (81%)	634 (97%)	18 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	FF	676/806 (84%)	658 (97%)	18 (3%)	0	100	100
5	FG	668/806 (83%)	643 (96%)	25 (4%)	0	100	100
5	FH	679/806 (84%)	656 (97%)	21 (3%)	2 (0%)	36	64
5	FI	684/806 (85%)	669 (98%)	15 (2%)	0	100	100
5	FJ	690/806 (86%)	672 (97%)	18 (3%)	0	100	100
5	FK	661/806 (82%)	636 (96%)	25 (4%)	0	100	100
5	FL	669/806 (83%)	645 (96%)	24 (4%)	0	100	100
6	FM	222/236 (94%)	215 (97%)	7 (3%)	0	100	100
6	FN	222/236 (94%)	208 (94%)	14 (6%)	0	100	100
6	FO	222/236 (94%)	211 (95%)	11 (5%)	0	100	100
6	FP	222/236 (94%)	212 (96%)	10 (4%)	0	100	100
6	FQ	222/236 (94%)	208 (94%)	14 (6%)	0	100	100
6	FR	222/236 (94%)	209 (94%)	13 (6%)	0	100	100
6	FS	225/236 (95%)	214 (95%)	11 (5%)	0	100	100
6	FT	222/236 (94%)	211 (95%)	11 (5%)	0	100	100
6	FU	222/236 (94%)	210 (95%)	12 (5%)	0	100	100
6	FV	222/236 (94%)	213 (96%)	9 (4%)	0	100	100
6	FW	222/236 (94%)	210 (95%)	12 (5%)	0	100	100
6	FX	222/236 (94%)	214 (96%)	8 (4%)	0	100	100
7	FY	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
7	FZ	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
7	GA	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
7	GB	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
7	GC	223/225 (99%)	217 (97%)	6 (3%)	0	100	100
7	GD	223/225 (99%)	219 (98%)	4 (2%)	0	100	100
7	GE	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
7	GF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
7	GG	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
7	GH	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
7	GI	223/225 (99%)	217 (97%)	6 (3%)	0	100	100
7	GJ	223/225 (99%)	210 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	GK	122/842 (14%)	117 (96%)	5 (4%)	0	100	100
8	GL	122/842 (14%)	116 (95%)	6 (5%)	0	100	100
8	GM	122/842 (14%)	116 (95%)	6 (5%)	0	100	100
8	GN	122/842 (14%)	112 (92%)	10 (8%)	0	100	100
8	GO	122/842 (14%)	116 (95%)	6 (5%)	0	100	100
8	GP	122/842 (14%)	120 (98%)	1 (1%)	1 (1%)	16	46
8	GQ	122/842 (14%)	116 (95%)	6 (5%)	0	100	100
8	GR	122/842 (14%)	112 (92%)	10 (8%)	0	100	100
8	GS	122/842 (14%)	117 (96%)	5 (4%)	0	100	100
8	GT	122/842 (14%)	116 (95%)	6 (5%)	0	100	100
8	GU	122/842 (14%)	114 (93%)	8 (7%)	0	100	100
8	GV	122/842 (14%)	115 (94%)	7 (6%)	0	100	100
8	IK	30/842 (4%)	25 (83%)	5 (17%)	0	100	100
8	IL	30/842 (4%)	29 (97%)	1 (3%)	0	100	100
8	IM	30/842 (4%)	25 (83%)	5 (17%)	0	100	100
8	IN	30/842 (4%)	27 (90%)	3 (10%)	0	100	100
8	IO	30/842 (4%)	26 (87%)	4 (13%)	0	100	100
8	IP	30/842 (4%)	28 (93%)	2 (7%)	0	100	100
8	IQ	30/842 (4%)	26 (87%)	4 (13%)	0	100	100
8	IR	30/842 (4%)	27 (90%)	3 (10%)	0	100	100
8	IS	30/842 (4%)	29 (97%)	1 (3%)	0	100	100
8	IT	30/842 (4%)	28 (93%)	2 (7%)	0	100	100
8	IU	30/842 (4%)	27 (90%)	3 (10%)	0	100	100
8	IV	30/842 (4%)	27 (90%)	3 (10%)	0	100	100
All	All	32303/59653 (54%)	30962 (96%)	1335 (4%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	FH	266	PRO
5	FH	276	GLN
5	FD	267	ASP
2	Bb	107	TYR
8	GP	426	PHE

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	AA	412/427 (96%)	409 (99%)	3 (1%)	76	76
1	AB	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	AC	426/427 (100%)	426 (100%)	0	100	100
1	AD	387/427 (91%)	387 (100%)	0	100	100
1	AE	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	AF	426/427 (100%)	424 (100%)	2 (0%)	81	78
1	BA	413/427 (97%)	410 (99%)	3 (1%)	76	76
1	BB	426/427 (100%)	426 (100%)	0	100	100
1	BC	426/427 (100%)	423 (99%)	3 (1%)	76	76
1	BD	387/427 (91%)	387 (100%)	0	100	100
1	BE	426/427 (100%)	423 (99%)	3 (1%)	76	76
1	BF	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	CA	411/427 (96%)	407 (99%)	4 (1%)	68	72
1	CB	426/427 (100%)	426 (100%)	0	100	100
1	CC	426/427 (100%)	426 (100%)	0	100	100
1	CD	383/427 (90%)	379 (99%)	4 (1%)	68	72
1	CE	426/427 (100%)	426 (100%)	0	100	100
1	CF	426/427 (100%)	418 (98%)	8 (2%)	50	64
1	DA	413/427 (97%)	404 (98%)	9 (2%)	45	62
1	DB	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	DC	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	DD	387/427 (91%)	386 (100%)	1 (0%)	86	81
1	DE	426/427 (100%)	425 (100%)	1 (0%)	87	84
1	DF	426/427 (100%)	420 (99%)	6 (1%)	59	68
1	EA	413/427 (97%)	409 (99%)	4 (1%)	68	72
1	EB	426/427 (100%)	424 (100%)	2 (0%)	81	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EC	426/427 (100%)	418 (98%)	8 (2%)	50	64
1	ED	387/427 (91%)	385 (100%)	2 (0%)	81	78
1	EE	426/427 (100%)	421 (99%)	5 (1%)	63	70
1	EF	426/427 (100%)	422 (99%)	4 (1%)	70	73
2	Aa	275/275 (100%)	273 (99%)	2 (1%)	76	76
2	Ab	275/275 (100%)	270 (98%)	5 (2%)	51	65
2	Ad	275/275 (100%)	270 (98%)	5 (2%)	51	65
2	Ae	225/275 (82%)	224 (100%)	1 (0%)	84	79
2	Af	157/275 (57%)	151 (96%)	6 (4%)	29	51
2	Ba	275/275 (100%)	272 (99%)	3 (1%)	65	71
2	Bb	275/275 (100%)	268 (98%)	7 (2%)	42	59
2	Bd	275/275 (100%)	275 (100%)	0	100	100
2	Be	224/275 (82%)	223 (100%)	1 (0%)	84	79
2	Bf	157/275 (57%)	149 (95%)	8 (5%)	21	46
2	Ca	275/275 (100%)	273 (99%)	2 (1%)	76	76
2	Cb	275/275 (100%)	266 (97%)	9 (3%)	33	54
2	Cd	275/275 (100%)	270 (98%)	5 (2%)	51	65
2	Ce	225/275 (82%)	221 (98%)	4 (2%)	51	65
2	Cf	157/275 (57%)	150 (96%)	7 (4%)	24	48
2	Da	275/275 (100%)	275 (100%)	0	100	100
2	Db	275/275 (100%)	270 (98%)	5 (2%)	51	65
2	Dd	275/275 (100%)	271 (98%)	4 (2%)	57	66
2	De	225/275 (82%)	225 (100%)	0	100	100
2	Df	157/275 (57%)	155 (99%)	2 (1%)	61	69
2	Ea	275/275 (100%)	271 (98%)	4 (2%)	57	66
2	Eb	275/275 (100%)	273 (99%)	2 (1%)	76	76
2	Ed	275/275 (100%)	271 (98%)	4 (2%)	57	66
2	Ee	225/275 (82%)	222 (99%)	3 (1%)	61	69
2	Ef	157/275 (57%)	153 (98%)	4 (2%)	42	59
3	Ag	68/86 (79%)	66 (97%)	2 (3%)	37	56
3	Ah	62/86 (72%)	62 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Bg	68/86 (79%)	68 (100%)	0	100	100
3	Bh	62/86 (72%)	62 (100%)	0	100	100
3	Cg	68/86 (79%)	67 (98%)	1 (2%)	57	66
3	Ch	62/86 (72%)	62 (100%)	0	100	100
3	Dg	68/86 (79%)	68 (100%)	0	100	100
3	Dh	62/86 (72%)	62 (100%)	0	100	100
3	Eg	68/86 (79%)	68 (100%)	0	100	100
3	Eh	62/86 (72%)	62 (100%)	0	100	100
4	Ai	34/78 (44%)	34 (100%)	0	100	100
4	Aj	34/78 (44%)	34 (100%)	0	100	100
4	Ak	34/78 (44%)	34 (100%)	0	100	100
4	Bi	34/78 (44%)	34 (100%)	0	100	100
4	Bj	34/78 (44%)	34 (100%)	0	100	100
4	Bk	34/78 (44%)	34 (100%)	0	100	100
4	Ci	34/78 (44%)	34 (100%)	0	100	100
4	Cj	34/78 (44%)	33 (97%)	1 (3%)	37	56
4	Ck	34/78 (44%)	34 (100%)	0	100	100
4	Di	34/78 (44%)	33 (97%)	1 (3%)	37	56
4	Dj	34/78 (44%)	34 (100%)	0	100	100
4	Dk	34/78 (44%)	34 (100%)	0	100	100
4	Ei	34/78 (44%)	34 (100%)	0	100	100
4	Ej	34/78 (44%)	34 (100%)	0	100	100
4	Ek	34/78 (44%)	34 (100%)	0	100	100
5	FA	615/714 (86%)	608 (99%)	7 (1%)	65	71
5	FB	607/714 (85%)	599 (99%)	8 (1%)	61	69
5	FC	613/714 (86%)	608 (99%)	5 (1%)	73	74
5	FD	629/714 (88%)	619 (98%)	10 (2%)	55	66
5	FE	591/714 (83%)	585 (99%)	6 (1%)	68	72
5	FF	612/714 (86%)	604 (99%)	8 (1%)	61	69
5	FG	610/714 (85%)	599 (98%)	11 (2%)	51	65
5	FH	614/714 (86%)	593 (97%)	21 (3%)	32	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	FI	620/714 (87%)	606 (98%)	14 (2%)	44	61
5	FJ	623/714 (87%)	619 (99%)	4 (1%)	78	77
5	FK	600/714 (84%)	598 (100%)	2 (0%)	86	81
5	FL	608/714 (85%)	598 (98%)	10 (2%)	55	66
6	FM	206/215 (96%)	203 (98%)	3 (2%)	57	66
6	FN	206/215 (96%)	200 (97%)	6 (3%)	37	56
6	FO	206/215 (96%)	203 (98%)	3 (2%)	57	66
6	FP	206/215 (96%)	202 (98%)	4 (2%)	50	64
6	FQ	206/215 (96%)	206 (100%)	0	100	100
6	FR	206/215 (96%)	205 (100%)	1 (0%)	81	78
6	FS	209/215 (97%)	208 (100%)	1 (0%)	81	78
6	FT	206/215 (96%)	205 (100%)	1 (0%)	81	78
6	FU	206/215 (96%)	206 (100%)	0	100	100
6	FV	206/215 (96%)	204 (99%)	2 (1%)	68	72
6	FW	206/215 (96%)	204 (99%)	2 (1%)	68	72
6	FX	206/215 (96%)	203 (98%)	3 (2%)	57	66
7	FY	208/208 (100%)	206 (99%)	2 (1%)	68	72
7	FZ	208/208 (100%)	208 (100%)	0	100	100
7	GA	208/208 (100%)	206 (99%)	2 (1%)	68	72
7	GB	208/208 (100%)	207 (100%)	1 (0%)	81	78
7	GC	208/208 (100%)	207 (100%)	1 (0%)	81	78
7	GD	208/208 (100%)	208 (100%)	0	100	100
7	GE	208/208 (100%)	207 (100%)	1 (0%)	81	78
7	GF	208/208 (100%)	208 (100%)	0	100	100
7	GG	208/208 (100%)	206 (99%)	2 (1%)	68	72
7	GH	208/208 (100%)	208 (100%)	0	100	100
7	GI	208/208 (100%)	207 (100%)	1 (0%)	81	78
7	GJ	208/208 (100%)	208 (100%)	0	100	100
8	GK	100/644 (16%)	100 (100%)	0	100	100
8	GL	100/644 (16%)	100 (100%)	0	100	100
8	GM	100/644 (16%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	GN	100/644 (16%)	99 (99%)	1 (1%)	68	72
8	GO	100/644 (16%)	97 (97%)	3 (3%)	36	56
8	GP	100/644 (16%)	98 (98%)	2 (2%)	48	63
8	GQ	100/644 (16%)	99 (99%)	1 (1%)	68	72
8	GR	100/644 (16%)	100 (100%)	0	100	100
8	GS	100/644 (16%)	99 (99%)	1 (1%)	68	72
8	GT	100/644 (16%)	100 (100%)	0	100	100
8	GU	100/644 (16%)	98 (98%)	2 (2%)	48	63
8	GV	100/644 (16%)	97 (97%)	3 (3%)	36	56
8	IK	26/644 (4%)	26 (100%)	0	100	100
8	IL	26/644 (4%)	26 (100%)	0	100	100
8	IM	26/644 (4%)	26 (100%)	0	100	100
8	IN	26/644 (4%)	26 (100%)	0	100	100
8	IO	26/644 (4%)	25 (96%)	1 (4%)	29	51
8	IP	26/644 (4%)	26 (100%)	0	100	100
8	IQ	26/644 (4%)	26 (100%)	0	100	100
8	IR	26/644 (4%)	26 (100%)	0	100	100
8	IS	26/644 (4%)	24 (92%)	2 (8%)	12	36
8	IT	26/644 (4%)	26 (100%)	0	100	100
8	IU	26/644 (4%)	26 (100%)	0	100	100
8	IV	26/644 (4%)	26 (100%)	0	100	100
All	All	33532/50815 (66%)	33199 (99%)	333 (1%)	65	72

5 of 333 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	FH	142	ASP
6	FN	94	PRO
5	FH	274	VAL
5	FI	393	VAL
6	FV	84	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 699 such sidechains are listed below:

Mol	Chain	Res	Type
5	FC	711	GLN
5	FL	401	GLN
5	FD	727	ASN
5	FC	709	GLN
5	FH	30	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](#)

Of 27 ligands modelled in this entry, 27 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

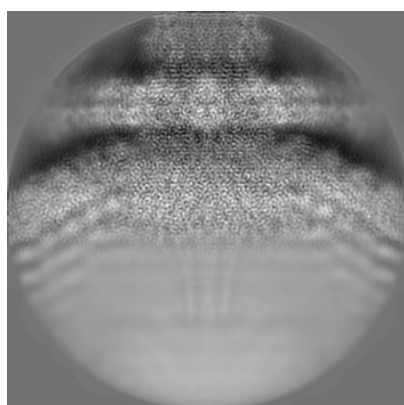
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14091. These allow visual inspection of the internal detail of the map and identification of artifacts.

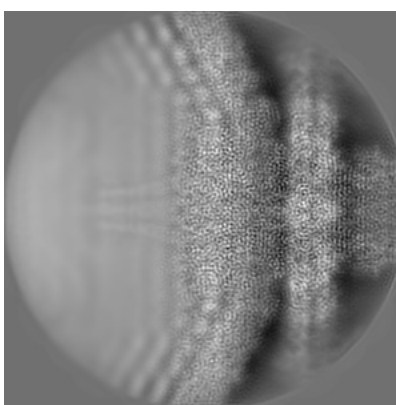
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

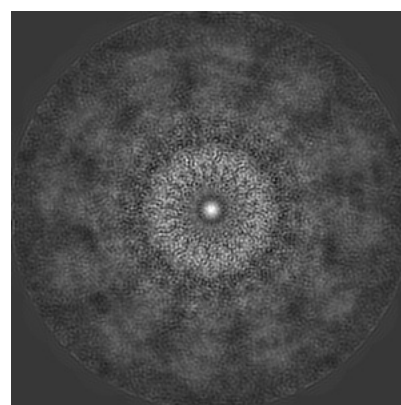
6.1.1 Primary map



X



Y

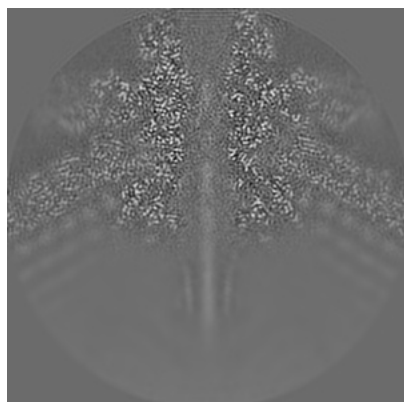


Z

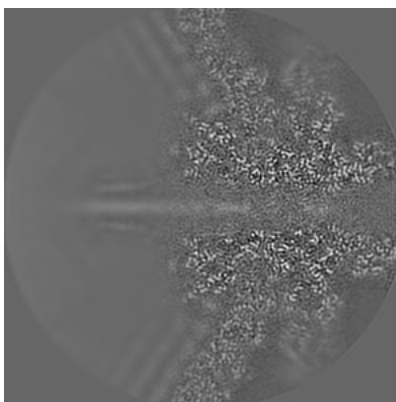
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

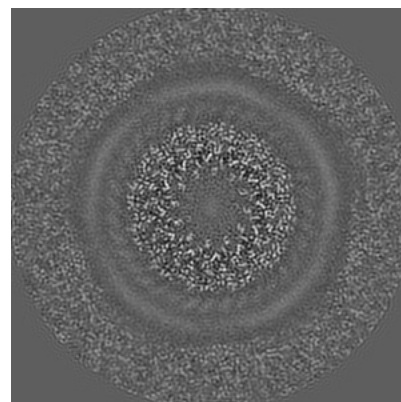
6.2.1 Primary map



X Index: 143



Y Index: 143

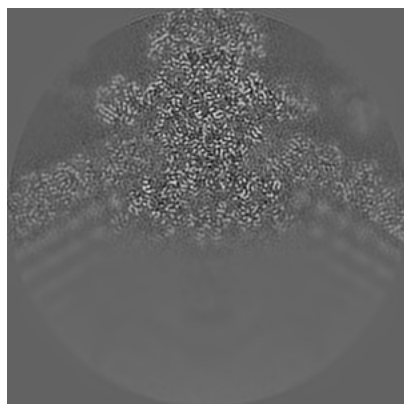


Z Index: 143

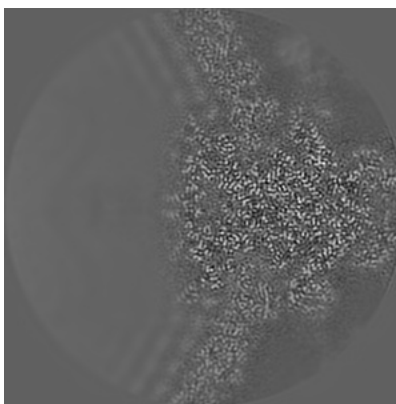
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

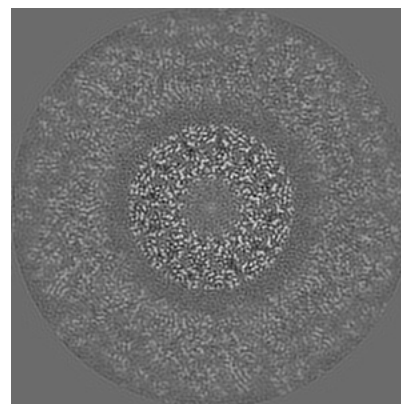
6.3.1 Primary map



X Index: 166



Y Index: 121

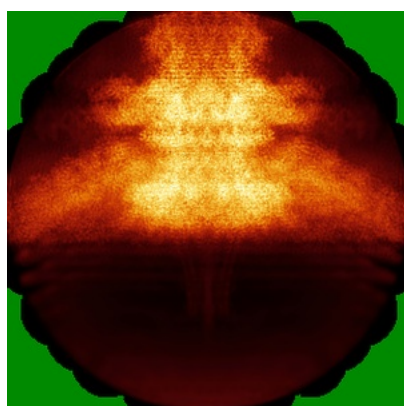


Z Index: 158

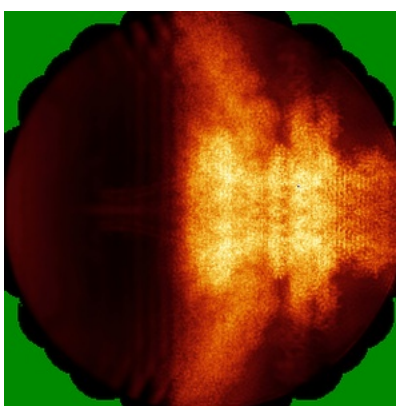
The images above show the largest variance slices of the map in three orthogonal directions.

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

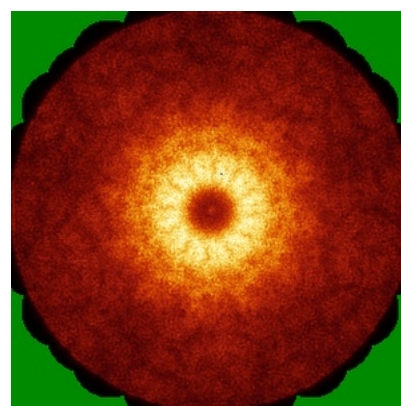
6.4.1 Primary map



X



Y

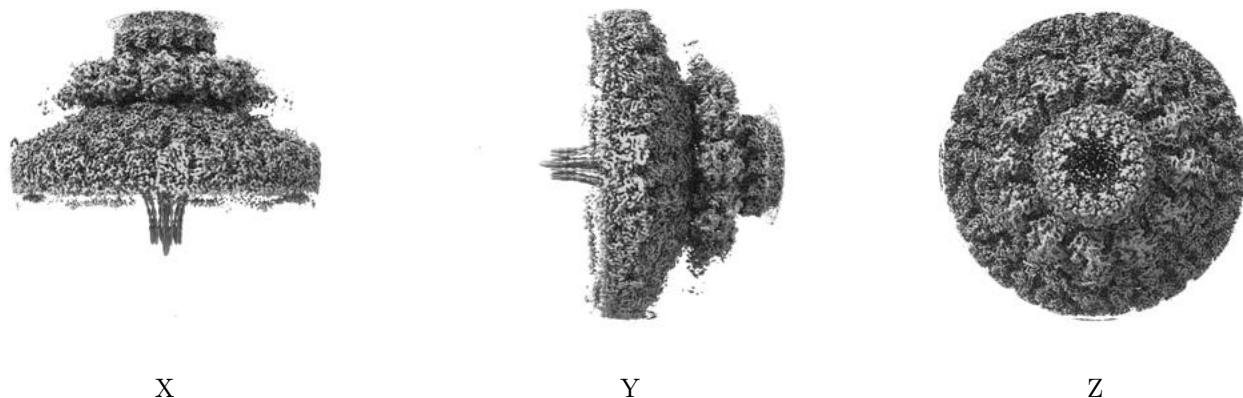


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

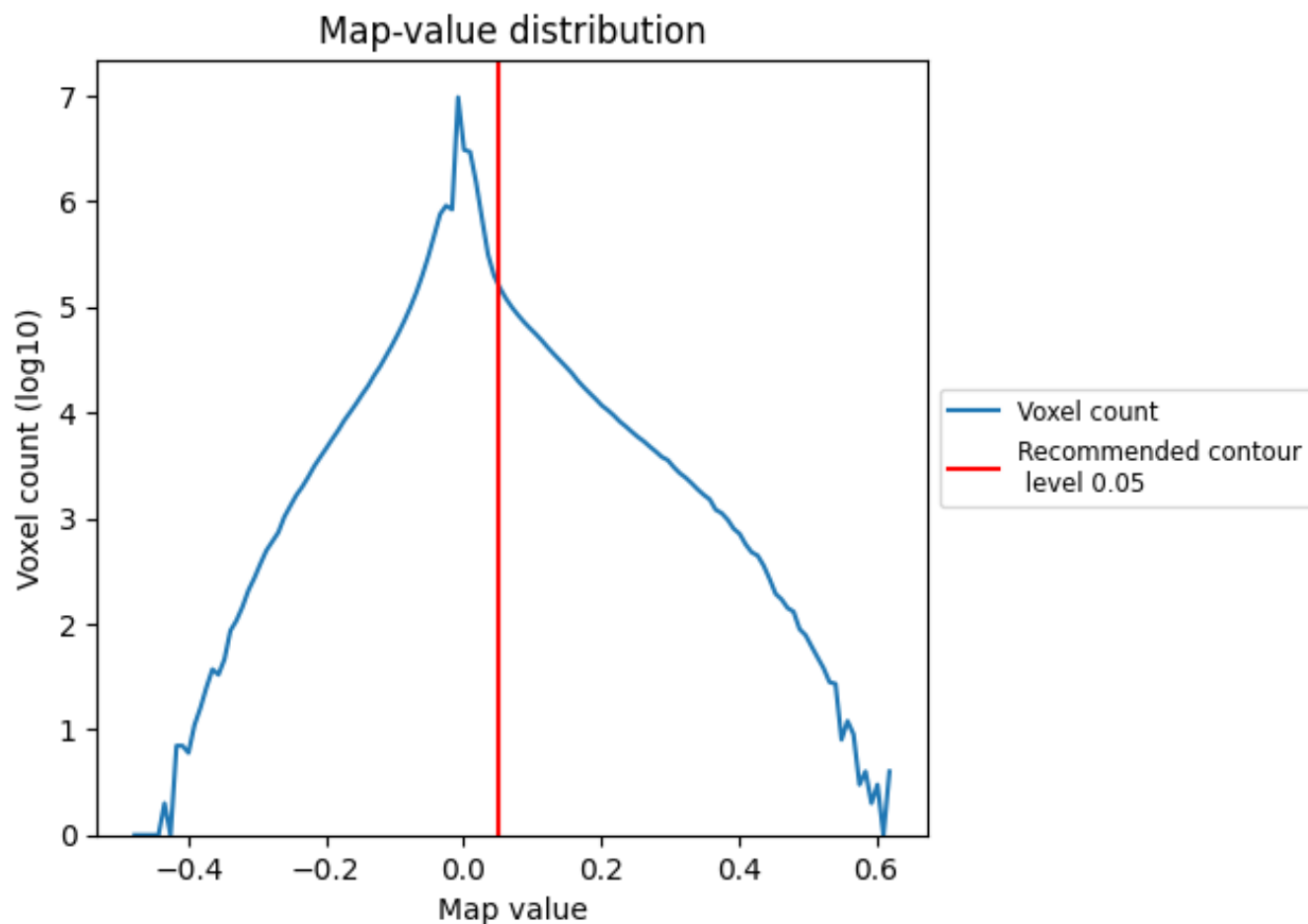
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

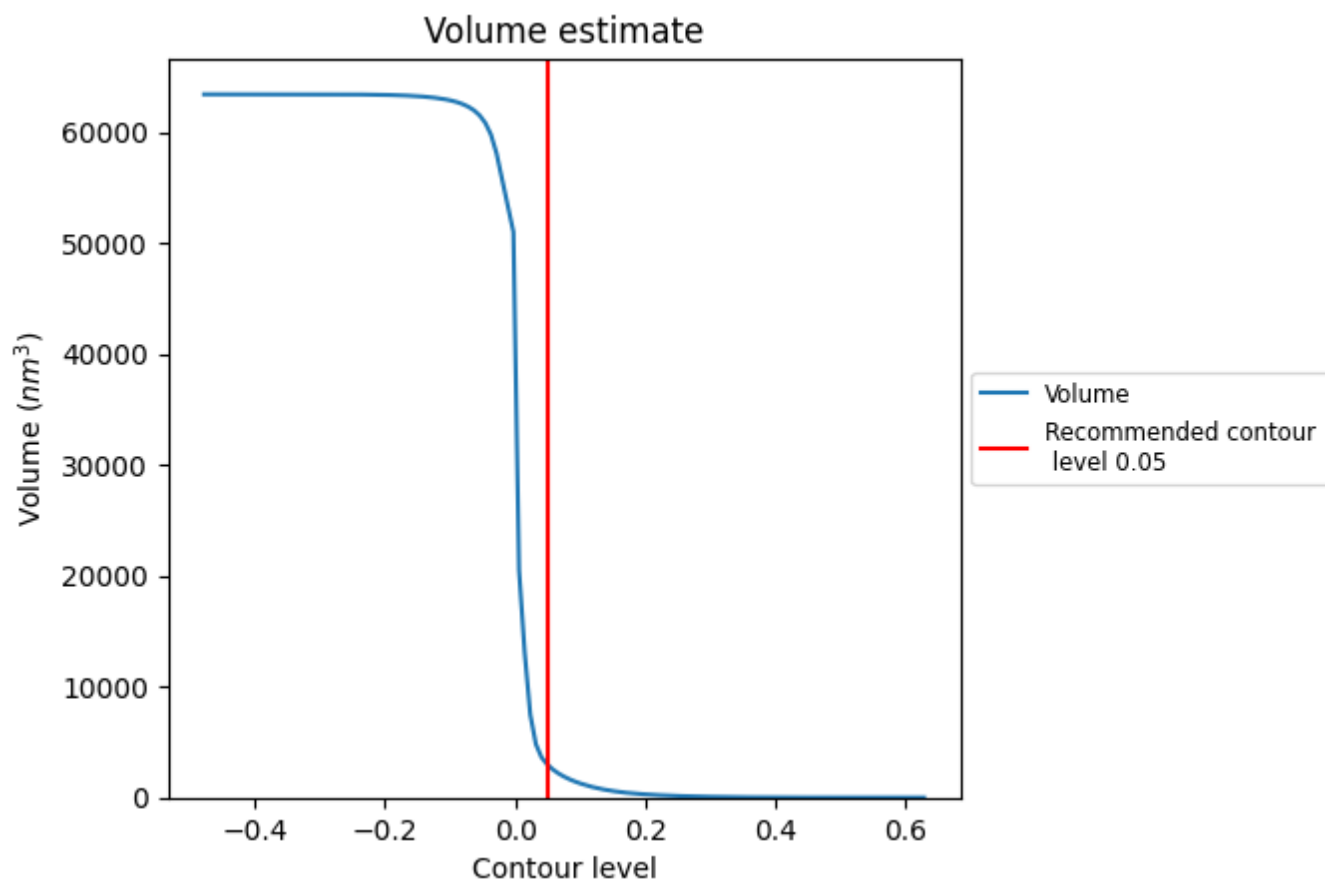
This section contains the results of statistical analysis of the map.

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.

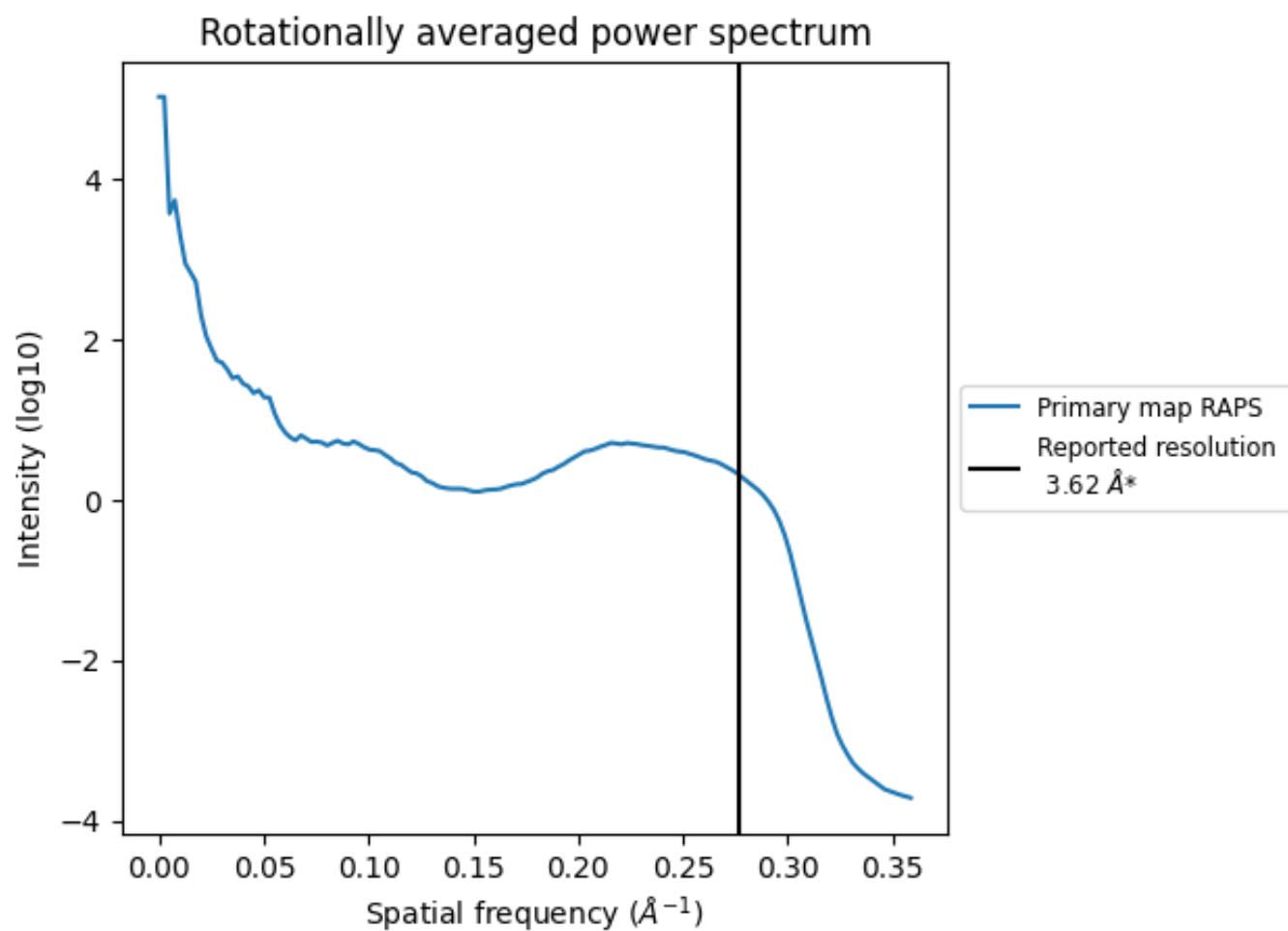
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2949 nm^3 ; this corresponds to an approximate mass of 2664 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 ⓘ

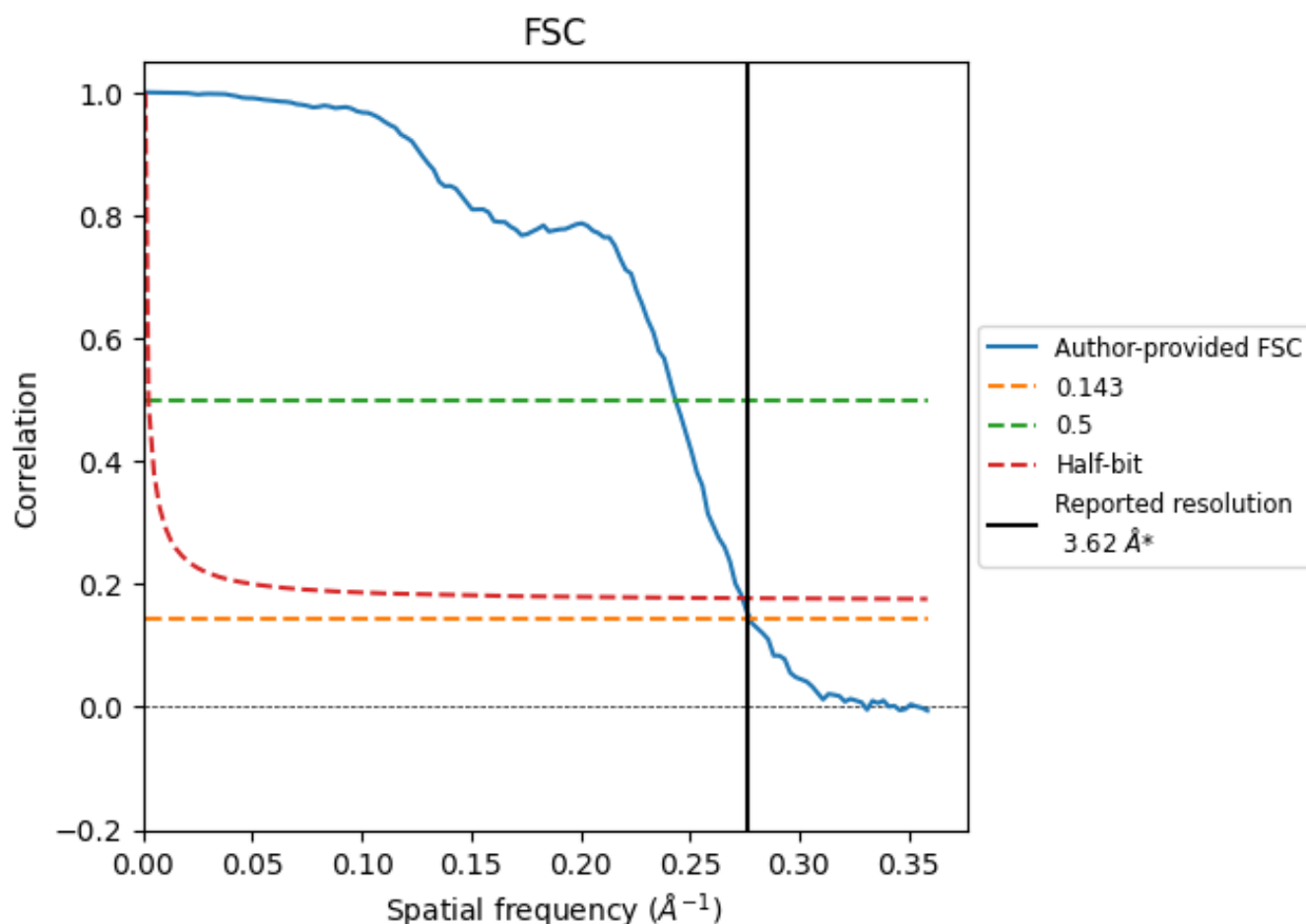


*Reported resolution corresponds to spatial frequency of 0.276 Å⁻¹

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 0.276 Å⁻¹

8.2 Resolution estimates [i](#)

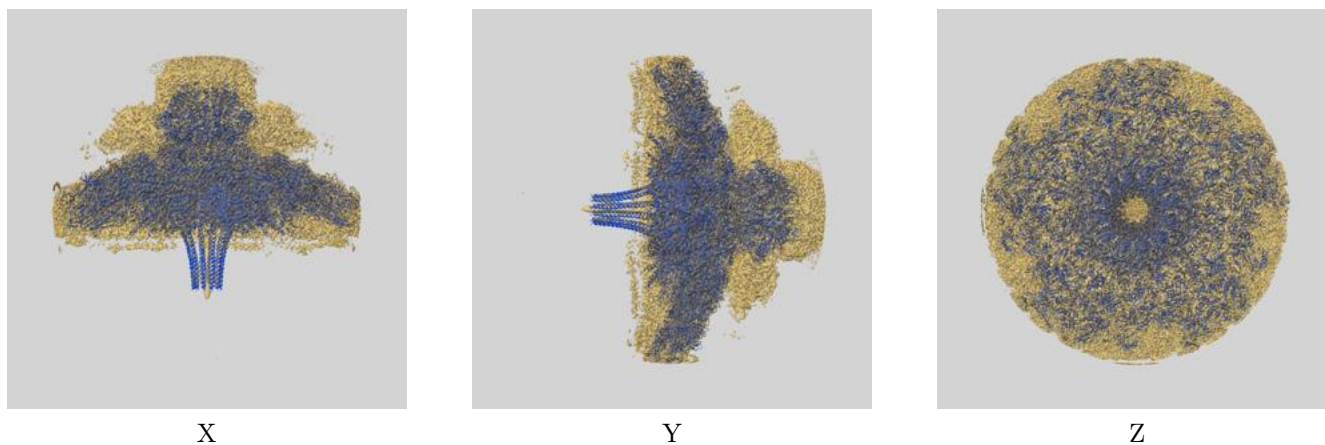
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.62	-	-
Author-provided FSC curve	3.60	4.11	3.65
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

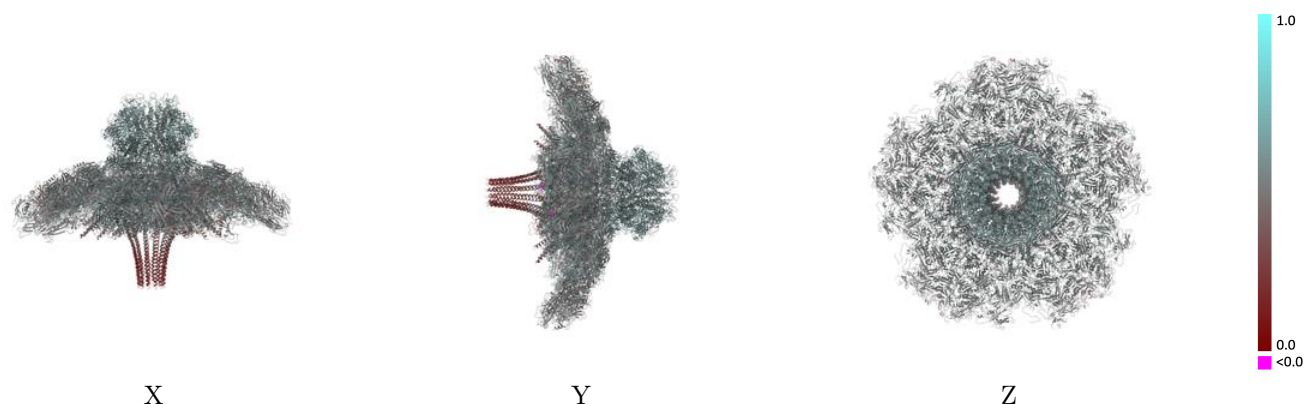
This section contains information regarding the fit between EMDB map EMD-14091 and PDB model 7QOI. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



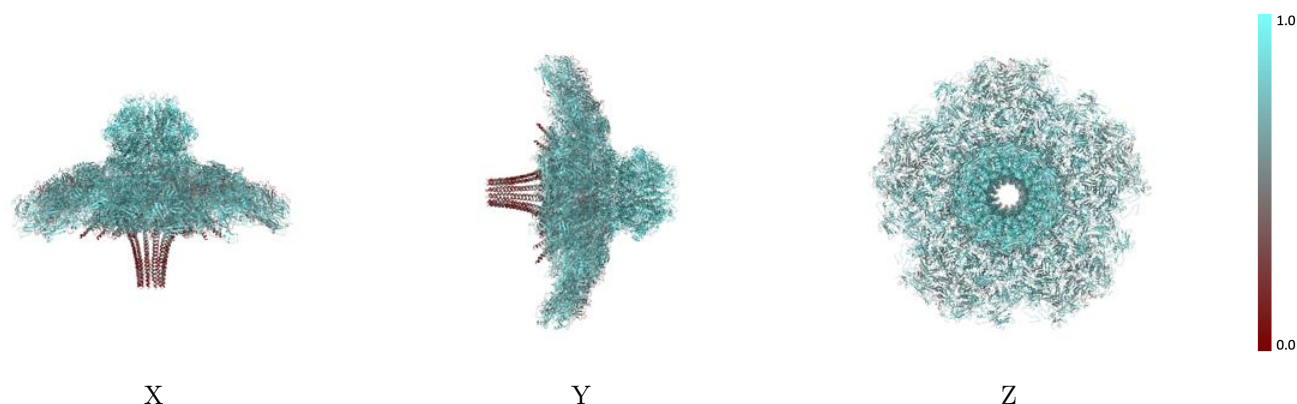
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



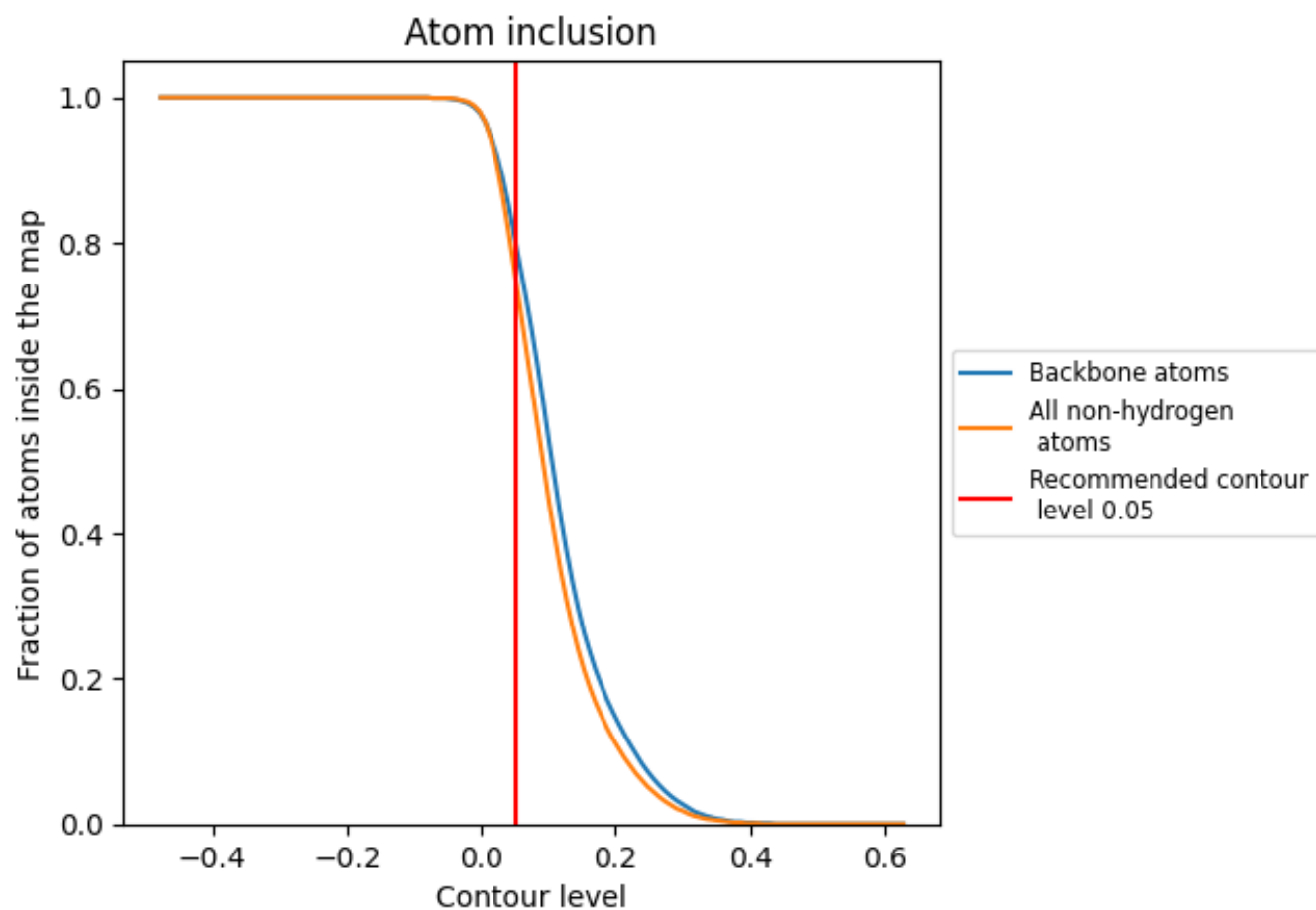
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 76% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.5050
AA	 0.7010	 0.4810
AB	 0.7480	 0.5010
AC	 0.7830	 0.5100
AD	 0.7680	 0.4980
AE	 0.7460	 0.4960
AF	 0.6950	 0.4760
Aa	 0.7240	 0.4850
Ab	 0.7370	 0.4910
Ad	 0.7280	 0.4950
Ae	 0.6870	 0.4820
Af	 0.5810	 0.4460
Ag	 0.7510	 0.4960
Ah	 0.7410	 0.4970
Ai	 0.6480	 0.4900
Aj	 0.6220	 0.4830
Ak	 0.6120	 0.4880
BA	 0.7130	 0.4870
BB	 0.7580	 0.5050
BC	 0.7880	 0.5130
BD	 0.7660	 0.5010
BE	 0.7430	 0.4960
BF	 0.7000	 0.4820
Ba	 0.7040	 0.4860
Bb	 0.7530	 0.5030
Bd	 0.7310	 0.4950
Be	 0.6590	 0.4590
Bf	 0.6070	 0.4570
Bg	 0.7760	 0.5030
Bh	 0.7330	 0.4980
Bi	 0.6580	 0.4920
Bj	 0.5620	 0.4810
Bk	 0.6150	 0.4780
CA	 0.7180	 0.4900
CB	 0.7610	 0.5010



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Chain	Atom inclusion	Q-score
CC	 0.7860	 0.5080
CD	 0.7660	 0.5030
CE	 0.7450	 0.5020
CF	 0.7030	 0.4830
Ca	 0.7100	 0.4860
Cb	 0.7470	 0.5020
Cd	 0.7260	 0.4910
Ce	 0.6490	 0.4730
Cf	 0.6140	 0.4430
Cg	 0.7610	 0.5020
Ch	 0.7460	 0.5030
Ci	 0.5790	 0.4840
Cj	 0.6220	 0.4810
Ck	 0.5950	 0.4710
DA	 0.7080	 0.4910
DB	 0.7510	 0.5010
DC	 0.7880	 0.5100
DD	 0.7520	 0.4960
DE	 0.7480	 0.4990
DF	 0.7140	 0.4890
Da	 0.6930	 0.4840
Db	 0.7350	 0.5020
Dd	 0.7200	 0.4880
De	 0.6810	 0.4800
Df	 0.6250	 0.4580
Dg	 0.7500	 0.4920
Dh	 0.7480	 0.4860
Di	 0.6120	 0.4720
Dj	 0.5790	 0.4800
Dk	 0.5790	 0.4860
EA	 0.7230	 0.4910
EB	 0.7710	 0.5040
EC	 0.7870	 0.5080
ED	 0.7830	 0.5040
EE	 0.7510	 0.5010
EF	 0.7000	 0.4780
Ea	 0.6960	 0.4830
Eb	 0.7530	 0.5040
Ed	 0.7370	 0.4940
Ee	 0.6820	 0.4790
Ef	 0.6090	 0.4530
Eg	 0.7640	 0.4950

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Chain	Atom inclusion	Q-score
Eh	 0.7550	 0.4960
Ei	 0.5130	 0.4500
Ej	 0.4700	 0.4560
Ek	 0.5660	 0.4720
FA	 0.7890	 0.5170
FB	 0.7830	 0.5150
FC	 0.7830	 0.5170
FD	 0.7810	 0.5120
FE	 0.7820	 0.5120
FF	 0.7890	 0.5180
FG	 0.7840	 0.5140
FH	 0.7880	 0.5180
FI	 0.7870	 0.5180
FJ	 0.7820	 0.5160
FK	 0.7980	 0.5180
FL	 0.7850	 0.5110
FM	 0.9040	 0.5640
FN	 0.8910	 0.5560
FO	 0.8790	 0.5540
FP	 0.8830	 0.5570
FQ	 0.8920	 0.5610
FR	 0.8910	 0.5620
FS	 0.8970	 0.5610
FT	 0.8920	 0.5630
FU	 0.8810	 0.5560
FV	 0.8870	 0.5590
FW	 0.8990	 0.5630
FX	 0.8950	 0.5580
FY	 0.8710	 0.5470
FZ	 0.8860	 0.5540
GA	 0.8860	 0.5510
GB	 0.8830	 0.5500
GC	 0.8880	 0.5550
GD	 0.8770	 0.5510
GE	 0.8830	 0.5510
GF	 0.8850	 0.5520
GG	 0.8820	 0.5510
GH	 0.8840	 0.5500
GI	 0.8810	 0.5510
GJ	 0.8770	 0.5460
GK	 0.6080	 0.4640
GL	 0.6380	 0.4750

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Chain	Atom inclusion	Q-score
GM	 0.6270	 0.4660
GN	 0.6050	 0.4620
GO	 0.5980	 0.4550
GP	 0.5950	 0.4650
GQ	 0.6120	 0.4620
GR	 0.5980	 0.4720
GS	 0.6160	 0.4700
GT	 0.5950	 0.4580
GU	 0.5770	 0.4550
GV	 0.6220	 0.4760
IK	 0.7310	 0.5020
IL	 0.7220	 0.5000
IM	 0.7390	 0.4880
IN	 0.7220	 0.5140
IO	 0.7140	 0.5060
IP	 0.7350	 0.5050
IQ	 0.7220	 0.5080
IR	 0.7960	 0.5280
IS	 0.8330	 0.5290
IT	 0.7430	 0.5040
IU	 0.7550	 0.4960
IV	 0.7630	 0.5020