



wwPDB EM Validation Summary Report ⓘ

Oct 15, 2026 – 11:13 pm BST

PDB ID : 29KH / pdb_000029kh
EMDB ID : EMD-57237
Title : Outer capsid of the ranavirus Frog Virus 3
Authors : Sandoval-Valencia, J.D.; Shah, P.N.M.; Stuart, D.; Fry, E.
Deposited on : 2026-03-17
Resolution : 3.00 Å(reported)
Based on initial model : .

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:

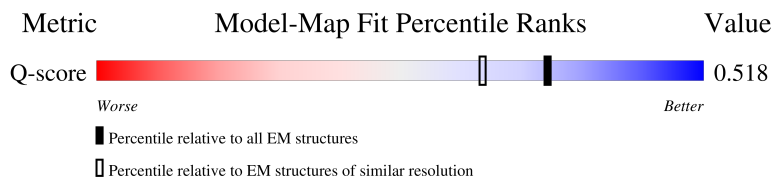
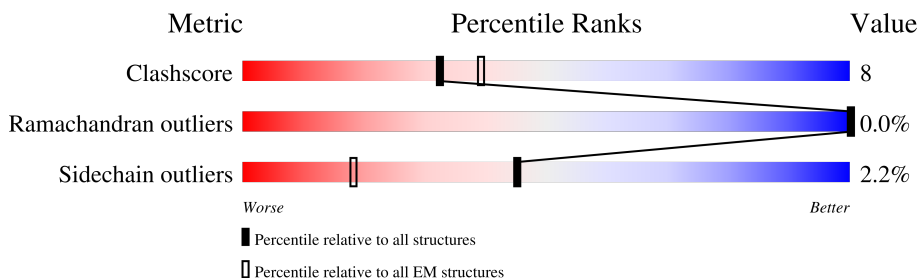
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 3.00 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.



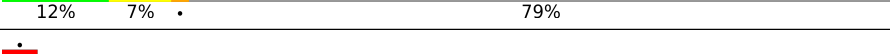
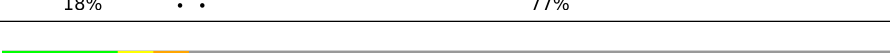
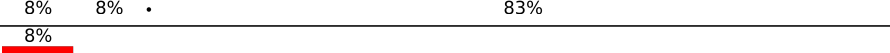
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	A1	106	
1	A2	106	
1	B1	106	
1	B2	106	

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Mol	Chain	Length	Quality of chain
1	C1	106	 17% 79%
1	C2	106	 9% 82%
1	D1	106	 13% 79%
1	D2	106	 16% 76%
1	E1	106	 12% 79%
1	E2	106	 18% 77%
1	F1	106	 13% 79%
1	F2	106	 15% 80%
1	G1	106	 11% 79%
1	G2	106	 7% 80%
1	H1	106	 9% 79%
1	I1	106	 12% 79%
1	I2	106	 7% 79%
1	J1	106	 8% 79%
1	J2	106	 8% 83%
1	J3	106	 14% 84%
1	K1	106	 11% 79%
1	K2	106	 9% 83%
1	K3	106	 12% 84%
1	L1	106	 14% 79%
1	L2	106	 11% 83%
1	L3	106	 13% 84%
1	M1	106	 18% 79%
1	M2	106	 8% 83%
1	M3	106	 8% 84%

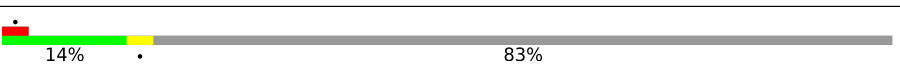
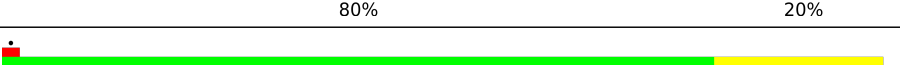
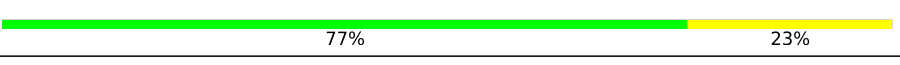
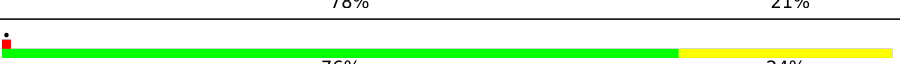
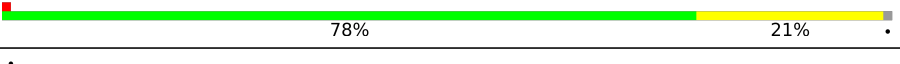
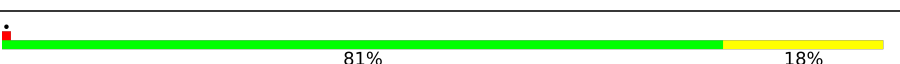
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Mol	Chain	Length	Quality of chain
1	N1	106	
1	N2	106	
1	O1	106	
1	O2	106	
1	P1	106	
1	P2	106	
1	Q1	106	
1	Q2	106	
1	R1	106	
1	R2	106	
1	S1	106	
1	S2	106	
1	T1	106	
1	T2	106	
1	T3	106	
1	U1	106	
1	U2	106	
1	U3	106	
1	V1	106	
1	V2	106	
1	V3	106	
1	a3	106	
1	b1	106	
1	b2	106	
1	c2	106	

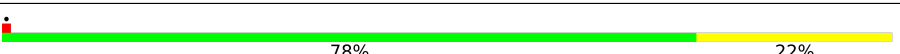
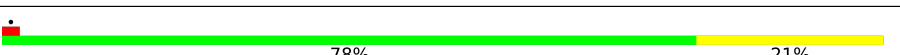
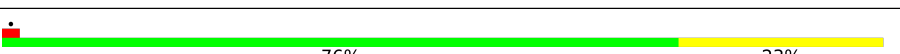
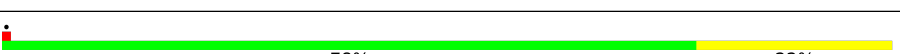
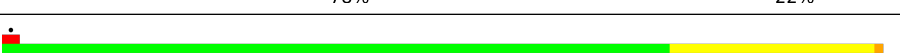
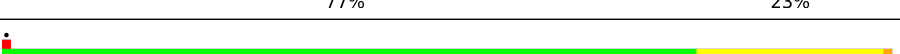
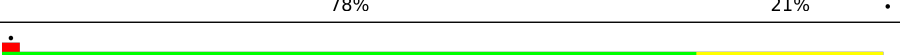
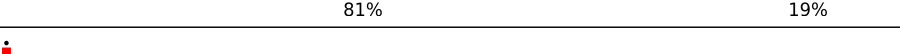
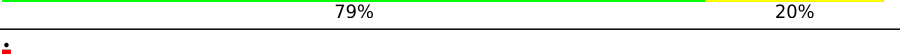
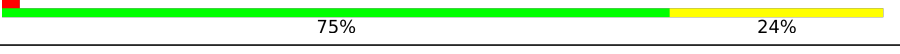
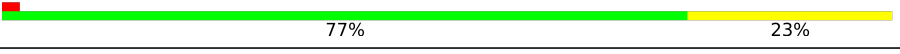
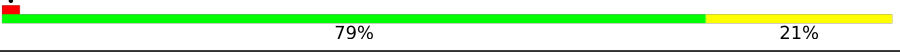
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Mol	Chain	Length	Quality of chain
1	c3	106	
1	d1	106	
1	d2	106	
1	e1	106	
1	f1	106	
1	f3	106	
2	Aa	463	
2	Ab	463	
2	Ac	463	
2	Ba	463	
2	Bb	463	
2	Bc	463	
2	Ca	463	
2	Cb	463	
2	Cc	463	
2	Da	463	
2	Db	463	
2	Dc	463	
2	Ea	463	
2	Eb	463	
2	Ec	463	
2	Fa	463	
2	Fb	463	
2	Fc	463	
2	Ga	463	

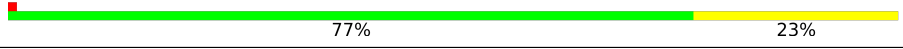
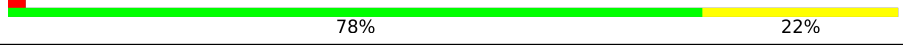
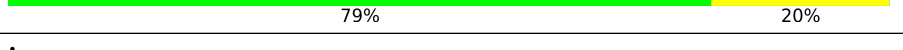
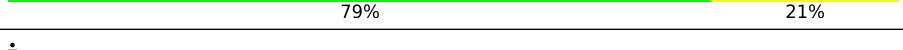
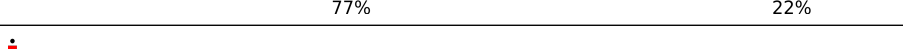
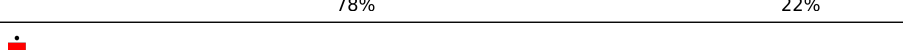
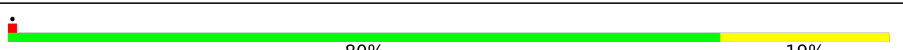
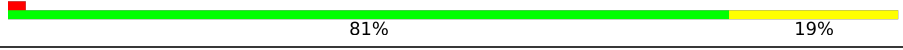
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Mol	Chain	Length	Quality of chain
2	Gb	463	 80% 19%
2	Gc	463	 78% 19%
2	Ha	463	 78% 22%
2	Hb	463	 78% 22%
2	Hc	463	 78% 21%
2	Ia	463	 76% 23%
2	Ib	463	 78% 22%
2	Ic	463	 75% 23%
2	Ja	463	 77% 23%
2	Jb	463	 78% 21%
2	Jc	463	 78% 21%
2	Ka	463	 81% 19%
2	Kb	463	 79% 20%
2	Kc	463	 76% 23%
2	La	463	 80% 19%
2	Lb	463	 78% 21%
2	Lc	463	 76% 24%
2	Ma	463	 79% 21%
2	Mb	463	 75% 24%
2	Mc	463	 77% 23%
2	Na	463	 79% 21%
2	Nb	463	 77% 22%
2	Nc	463	 75% 25%
2	Oa	463	 81% 19%
2	Ob	463	 79% 21%

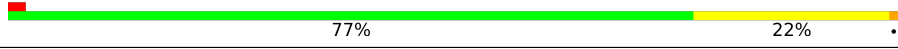
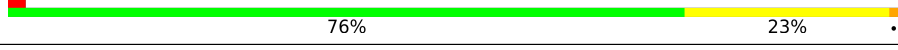
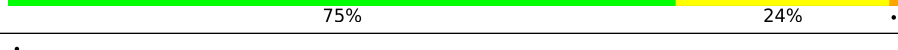
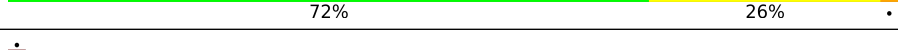
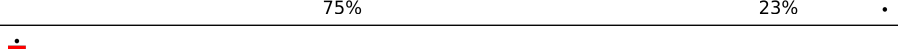
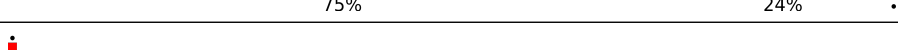
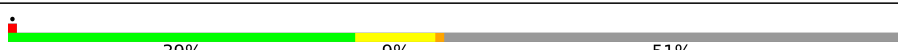
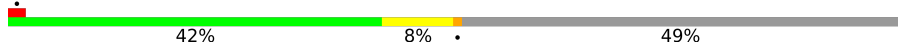
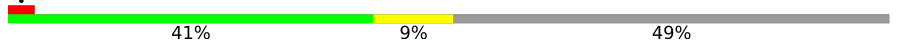
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Mol	Chain	Length	Quality of chain
2	Oc	463	
2	Pa	463	
2	Pb	463	
2	Pc	463	
2	Qa	463	
2	Qb	463	
2	Qc	463	
2	Ra	463	
2	Rb	463	
2	Rc	463	
2	Sa	463	
2	Sb	463	
2	Sc	463	
2	Ta	463	
2	Tb	463	
2	Tc	463	
2	Ua	463	
2	Ub	463	
2	Uc	463	
2	Va	463	
2	Vb	463	
2	Vc	463	
2	aa	463	
2	ab	463	
2	ac	463	

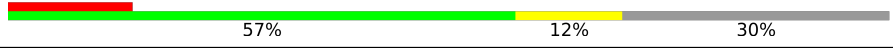
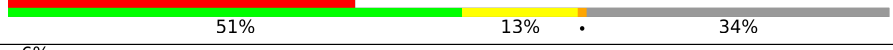
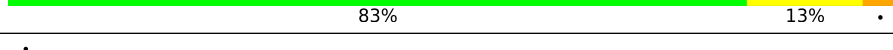
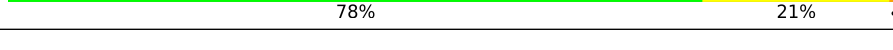
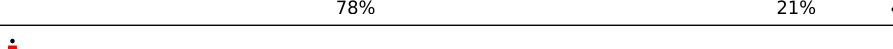
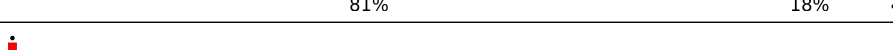
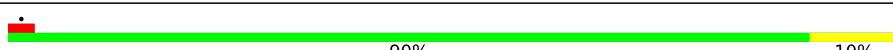
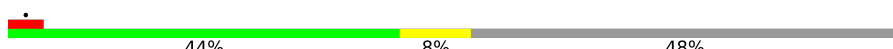
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Mol	Chain	Length	Quality of chain
2	ba	463	
2	bb	463	
2	bc	463	
2	ca	463	
2	cb	463	
2	cc	463	
2	da	463	
2	db	463	
2	dc	463	
2	ea	463	
2	eb	463	
2	ec	463	
2	fa	463	
2	fb	463	
2	fc	463	
3	Za	148	
3	Zb	148	
3	Zc	148	
3	Zd	148	
3	Ze	148	
3	Zf	148	
3	Zg	148	
3	Zh	148	
3	Zi	148	
3	Zj	148	

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Mol	Chain	Length	Quality of chain
3	Zk	148	
3	Zl	148	
4	m1	521	
4	m2	521	
5	n1	314	
5	n2	314	
6	pp	139	
7	rI	73	
7	rJ	73	
7	rK	73	
7	rL	73	
7	rM	73	
7	rO	73	
7	rP	73	
7	rQ	73	
7	rR	73	
8	sa	137	
9	sb	124	
10	tm	362	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 330022 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 Vp34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	A2	33	Total	C	N	O	S	0	0
			249	155	50	43	1		
1	B1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	B2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	C1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	C2	19	Total	C	N	O	S	0	0
			160	101	34	24	1		
1	D1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	D2	25	Total	C	N	O	S	0	0
			192	121	40	30	1		
1	E1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	E2	24	Total	C	N	O	S	0	0
			187	118	39	29	1		
1	F1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	F2	21	Total	C	N	O	S	0	0
			169	106	36	26	1		
1	G1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	G2	21	Total	C	N	O	S	0	0
			169	106	36	26	1		
1	H1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	I1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	I2	22	Total	C	N	O	S	0	0
			175	109	37	28	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	J1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	J2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	J3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	K1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	K2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	K3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	L1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	L2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	L3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	M1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	M2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	M3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	N1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	N2	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	O1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	O2	19	Total	C	N	O	S	0	0
			160	101	34	24	1		
1	P1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	P2	21	Total	C	N	O	S	0	0
			169	106	36	26	1		
1	Q1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	Q2	21	Total	C	N	O	S	0	0
			169	106	36	26	1		
1	R1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R2	21	Total	C	N	O	S	0	0
			169	106	36	26	1		
1	S1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	S2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	T1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	T2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	T3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	U1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	U2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	U3	17	Total	C	N	O	S	0	0
			142	89	30	22	1		
1	V1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	V2	18	Total	C	N	O	S	0	0
			150	95	31	23	1		
1	V3	18	Total	C	N	O	S	0	0
			147	92	31	23	1		
1	a3	23	Total	C	N	O	S	0	0
			183	115	38	29	1		
1	b1	23	Total	C	N	O	S	0	0
			183	115	38	29	1		
1	b2	23	Total	C	N	O	S	0	0
			183	115	38	29	1		
1	c2	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	c3	20	Total	C	N	O	S	0	0
			164	103	35	25	1		
1	d1	22	Total	C	N	O	S	0	0
			175	109	37	28	1		
1	d2	27	Total	C	N	O	S	0	0
			214	134	44	35	1		
1	e1	23	Total	C	N	O	S	0	0
			183	114	38	29	2		
1	f1	18	Total	C	N	O	S	0	0
			152	95	33	23	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	f3	22	Total	C	N	O	S	0	0
			175	109	37	28	1		

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Aa	461	Total	C	N	O	S	0	0
			3499	2222	587	674	16		
2	Ab	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Ac	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Ba	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Bb	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Bc	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Ca	461	Total	C	N	O	S	0	0
			3499	2222	587	674	16		
2	Cb	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Cc	461	Total	C	N	O	S	0	0
			3499	2222	587	674	16		
2	Da	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Db	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Dc	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Ea	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Eb	460	Total	C	N	O	S	0	0
			3493	2219	586	672	16		
2	Ec	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Fa	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Fb	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	Fc	461	Total	C	N	O	S	0	0
			3499	2222	587	674	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ga	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Gb	460	Total 3493	C 2219	N 586	O 672	S 16	0	0
2	Gc	455	Total 3465	C 2203	N 581	O 665	S 16	0	0
2	Ha	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Hb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Hc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ia	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ib	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Ic	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ja	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Jb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Jc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ka	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Kb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Kc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	La	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Lb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Lc	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Ma	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Mb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Mc	461	Total 3499	C 2222	N 587	O 674	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Na	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Nb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Nc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Oa	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ob	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Oc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Pa	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Pb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Pc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Qa	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Qb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Qc	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Ra	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Rb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Rc	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Sa	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Sb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Sc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ta	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Tb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	Tc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ua	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Ub	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Uc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Va	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Vb	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	Vc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	aa	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	ab	460	Total 3493	C 2219	N 586	O 672	S 16	0	0
2	ac	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	ba	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	bb	461	Total 3498	C 2222	N 587	O 673	S 16	0	0
2	bc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	ca	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	cb	460	Total 3493	C 2219	N 586	O 672	S 16	0	0
2	cc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	da	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	db	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	dc	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	ea	462	Total 3505	C 2225	N 588	O 676	S 16	0	0
2	eb	461	Total 3499	C 2222	N 587	O 674	S 16	0	0
2	ec	461	Total 3499	C 2222	N 587	O 674	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	fa	461	Total	C	N	O	S	0	0
			3499	2222	587	674	16		
2	fb	462	Total	C	N	O	S	0	0
			3505	2225	588	676	16		
2	fc	459	Total	C	N	O	S	0	0
			3486	2214	585	671	16		

- Molecule 3 is a protein called Vp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Za	72	Total	C	N	O	S	0	0
			538	334	101	100	3		
3	Zb	61	Total	C	N	O	S	0	0
			465	290	87	85	3		
3	Zc	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zd	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Ze	75	Total	C	N	O	S	0	0
			569	357	104	105	3		
3	Zf	75	Total	C	N	O	S	0	0
			569	357	104	105	3		
3	Zg	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zh	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zi	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zj	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zk	97	Total	C	N	O	S	0	0
			723	448	134	137	4		
3	Zl	97	Total	C	N	O	S	0	0
			723	448	134	137	4		

- Molecule 4 is a protein called Putative myristoylated protein 053R.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	m1	365	Total	C	N	O	S	0	0
			2729	1723	466	526	14		
4	m2	343	Total	C	N	O	S	0	0
			2558	1618	439	489	12		

- Molecule 5 is a protein called Putative myristylated membrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	n1	150	Total	C	N	O	S	0	0
			1139	699	204	226	10		
5	n2	153	Total	C	N	O	S	0	0
			1156	711	207	228	10		

- Molecule 6 is a protein called Vp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	pp	138	Total	C	N	O	S	0	0
			1062	686	175	193	8		

- Molecule 7 is a protein called Vp76.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	rI	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rJ	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rK	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rL	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rM	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rO	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rP	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rQ	73	Total	C	N	O	S	0	0
			560	347	110	100	3		
7	rR	73	Total	C	N	O	S	0	0
			560	347	110	100	3		

- Molecule 8 is a protein called Vp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sa	71	Total	C	N	O	S	0	0
			547	347	97	101	2		

- Molecule 9 is a protein called Vp70.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	sb	122	Total 921	C 570	N 178	O 169	S 4	0	0

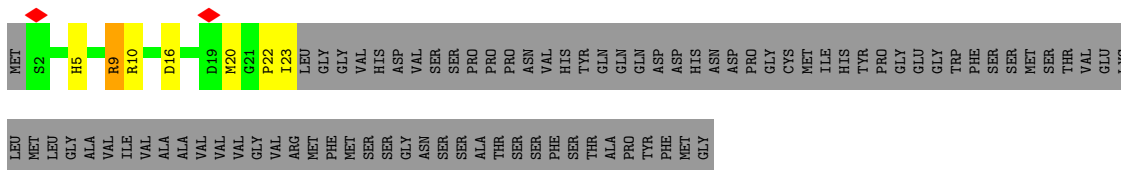
- Molecule 10 is a protein called Vp74.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	tm	360	Total 2687	C 1641	N 540	O 495	S 11	2	0

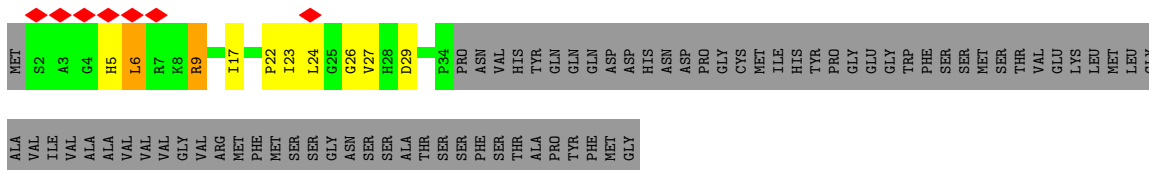
3 Residue-property plots [i](#)

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.

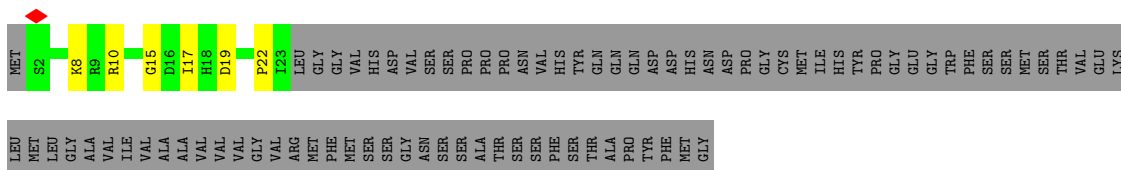
- Molecule 1: Vp34



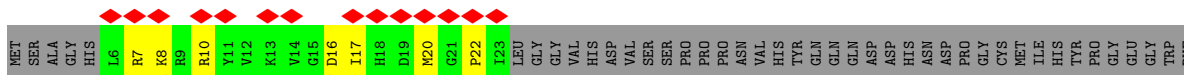
- Molecule 1: Vp34



- Molecule 1: Vp34



- Molecule 1: Vp34



[illegible]

MET SER A3 G4 H5 L6 R7 K8 R9 R10 K13 H18 D19 M20 I23 LEU GLY VAL HIS ASP VAL SER SER PRO PRO PRO ASN VAL HIS TYR GLN GLN GLN ASP ASP ASN HIS ASP ASP PRO PRO GLY CYS MET ILE HIS TYR PRO PRO GLY GLY TRP PHE SER SER MET SER

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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34



MET	SER	ALA	GLY	HIS	LEU	R7	R8	R9	R10	Y11	Y12	V13	V14	V15	G16	D17	I18	H19	D20	G21	P22	I23	LEU	GLY	GLY	VAL	HIS	SER	ASP	THR	SER	SER	PRO	PRO	PRO	ASN	VAL	ALA	PRO	HIS	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	PRO	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE
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SER	MET	SER	THR	GLY	VAL	GLU	LYS	LEU	MET	GLY	ALA	VAL	ILE	VAL	ALA	ALA	VAL	VAL	VAL	VAL	GLY	VAL	ARG	ARG	MET	PHE	MET	SER	SER	GLY	GLY	ASN	SER	SER	ALA	THR	SER	SER	PHE	SER	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	S2	A3	G4	H5	R6	R7	R8	R9	R10	Y11	Y12	V13	V14	V15	G16	D17	H18	D19	M20	G21	P22	I23	LEU	GLY	GLY	VAL	HIS	SER	ASP	THR	SER	PRO	PRO	ASN	VAL	ALA	PRO	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE	SER
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SER	MET	SER	THR	GLY	VAL	GLU	LYS	LEU	MET	GLY	ALA	VAL	ILE	VAL	ALA	ALA	VAL	VAL	VAL	VAL	GLY	VAL	ARG	ARG	MET	PHE	MET	SER	SER	GLY	GLY	ASN	SER	SER	ALA	THR	SER	SER	PHE	SER	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	SER	ALA	GLY	HIS	L6	R7	R8	Y11	Y12	V13	V14	I17	P22	I23	LEU	GLY	GLY	VAL	HIS	ASP	THR	SER	PRO	PRO	PRO	ASN	VAL	HIS	SER	ASP	THR	SER	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	GLY	TRP	PHE	SER	MET	SER	THR
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VAL	GLU	LYS	LEU	MET	GLY	ALA	VAL	ILE	VAL	VAL	ALA	VAL	VAL	VAL	GLY	VAL	ARG	MET	PHE	MET	SER	ASN	SER	SER	ALA	THR	SER	SER	PHE	SER	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	SER	ALA	GLY	HIS	LEU	R7	R8	R9	R10	Y11	Y12	V13	V14	V15	G16	D17	I18	H19	D20	G21	P22	I23	LEU	GLY	GLY	VAL	HIS	ASP	THR	SER	SER	PRO	PRO	PRO	ASN	VAL	HIS	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE
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SER	SER	MET	THR	GLY	VAL	GLU	LYS	LEU	MET	GLY	ALA	VAL	ILE	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	GLY	VAL	ARG	ARG	MET	PHE	MET	SER	SER	GLY	GLY	ASN	SER	SER	ALA	THR	SER	SER	PHE	SER	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	S2	A3	G4	H5	L6	R7	R10	Y11	Y12	V13	V14	V15	G16	D17	I18	H19	D20	G21	P22	I23	LEU	GLY	GLY	VAL	HIS	ASP	THR	SER	SER	PRO	PRO	PRO	ASN	VAL	HIS	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE	SER
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[illegible]

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

• Molecule 1: Vp34

Chain P2: 

MET SER A3 G4 H5 L6 R7 K8 R9 R10 K13 V14 G15 D16 I17 H18 P22 I23 LEU GLY GLY MET MET SER SER VAL HIS ASP VAL SER SER ALA PRO PRO PRO PHE THR HIS ALA GLN GLN GLN ASP ASP HIS HIS ASP PRO GLY CYS MET ILE HIS TYR PRO GLY GLY TRP PHE SER MET

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

• Molecule 1: Vp34

Chain Q1: 

MET S2 A3 G4 H5 L6 R7 K8 R9 R10 Y11 V14 D19 D20 G21 P22 I23 LEU GLY GLY VAL HIS ASP VAL SER SER PRO PRO PRO ASN VAL HIS TYR GLN GLN GLN ASP ASP HIS HIS ASP PRO GLY CYS MET ILE HIS TYR PRO GLY GLY TRP PHE SER MET SER

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

• Molecule 1: Vp34

Chain Q2: 

MET SER A3 G4 H5 L6 R7 K8 R9 R10 K13 V14 H18 P22 I23 LEU GLY GLY VAL HIS ASP VAL SER SER PRO PRO PRO ASN VAL HIS TYR GLN GLN GLN ASP ASP HIS HIS ASP PRO GLY CYS MET ILE HIS TYR PRO GLY GLY TRP PHE SER MET THR

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

• Molecule 1: Vp34

Chain R1: 

MET S2 A3 L6 R7 K8 R9 R10 K13 V14 H18 D19 D20 G21 P22 I23 LEU GLY GLY VAL HIS ASP VAL SER SER PRO PRO PRO ASN VAL HIS TYR GLN GLN GLN ASP ASP HIS HIS ASP PRO GLY CYS MET ILE HIS TYR PRO GLY GLU GLY TRP PHE SER MET SER

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

• Molecule 1: Vp34

Chain R2: 

MET SER A3 G4 H5 L6 R7 K8 R9 R10 Y11 V14 G15 D16 I17 H18 D19 I23 LEU GLY GLY VAL HIS ASP VAL SER SER PRO PRO PRO ASN VAL HIS TYR GLN GLN GLN ASP ASP HIS HIS ASP PRO GLY CYS MET ILE HIS TYR PRO GLY GLU GLY TRP PHE SER SER MET

MET	SER	THR	VAL	GLU	LYS	LEU	MET	LEU	GLY	ALA	VAL	ILE	VAL	ALA	VAL	VAL	VAL	GLY	VAL	ARG	MET	PHE	MET	SER	SER	GLY	GLY	ASN	SER	SER	SER	ALA	THR	SER	SER	PHE	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	SER	ALA	GLY	HIS	LEU	R7	K8	R9	R10	Y11	Y12	K13	V14	I17	H18	D19	M20	G21	P22	I23	L24	GLY	GLY	VAL	ASN	HIS	ASP	SER	VAL	SER	THR	SER	PRO	PRO	ASN	VAL	HIS	PRO	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASP	ASN	GLY	CYS	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE	SER
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• Molecule 1: Vp34



MET	S2	R10	Y11	V12	K13	V14	H18	D19	M20	G21	P22	I23	L24	GLY	GLY	VAL	HIS	ASP	VAL	ASN	PRO	PRO	SER	SER	ALA	THR	THR	THR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	PRO	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLY	TRP	PHE	MET	SER	THR	VAL	GLU	GLY	TRP	PHE	SER	LYS
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• Molecule 1: Vp34



MET	S2	A3	G4	H5	L6	R7	K8	R9	R10	Y11	Y12	K13	V14	I17	H18	D19	M20	I23	L24	GLY	GLY	VAL	HIS	ASP	VAL	SER	THR	SER	PRO	PRO	PRO	ASN	VAL	HIS	PRO	TYR	GLN	GLN	ASP	ASP	HIS	ASN	ASP	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLU	GLY	TRP	PHE	SER
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MET	SER	THR	VAL	GLU	LYS	LEU	MET	LEU	GLY	ALA	VAL	ILE	VAL	ALA	VAL	VAL	VAL	GLY	VAL	ARG	MET	PHE	MET	SER	SER	GLY	GLY	ASN	SER	SER	ALA	THR	SER	SER	PHE	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	S2	A3	G4	H5	L6	R7	K8	R9	R10	Y11	Y12	K13	V14	I17	H18	D19	M20	G21	P22	I23	L24	GLY	GLY	VAL	HIS	ASP	VAL	SER	THR	SER	PRO	PRO	PRO	ASN	VAL	HIS	PRO	TYR	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLU	GLY	TRP	PHE	SER
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SER	MET	THR	VAL	GLU	LYS	LEU	MET	LEU	GLY	ALA	VAL	ILE	VAL	ALA	ALA	VAL	VAL	VAL	GLY	VAL	ARG	MET	PHE	MET	SER	SER	GLY	ASN	SER	SER	ALA	THR	SER	THR	SER	PHE	THR	ALA	PRO	TYR	PHE	MET	GLY
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• Molecule 1: Vp34



MET	S2	A3	G4	H5	R10	Y11	V12	K13	V14	G15	D16	I17	H18	D19	I23	LEU	GLY	GLY	VAL	HIS	ASP	VAL	SER	SER	PRO	PRO	ASN	VAL	HIS	THR	SER	GLN	GLN	GLN	ASP	ASP	HIS	ASN	ASP	PRO	GLY	CYS	MET	ILE	HIS	TYR	PRO	GLY	GLU	TRP	PHE	SER	SER	MET	THR
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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34



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• Molecule 1: Vp34

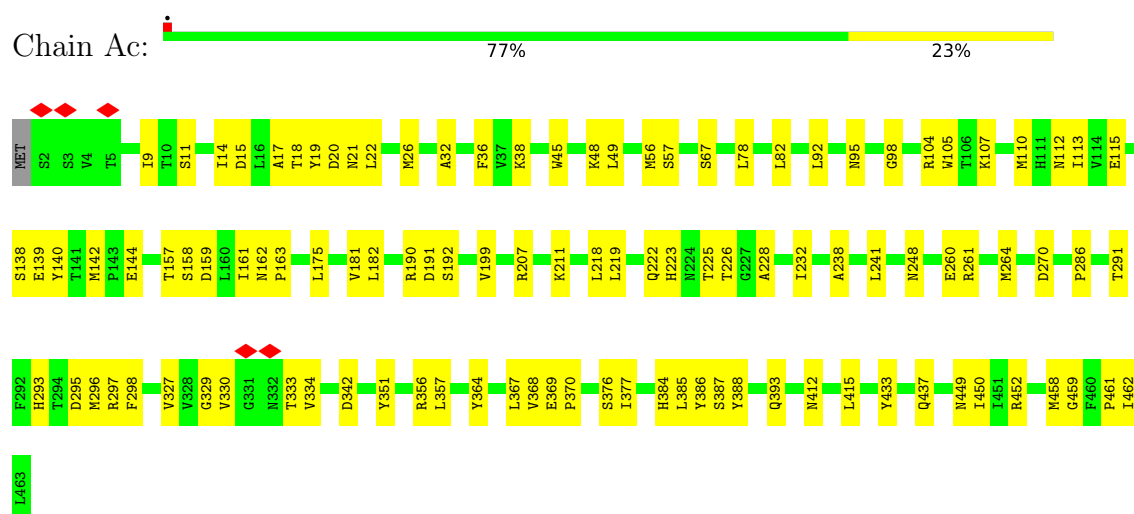


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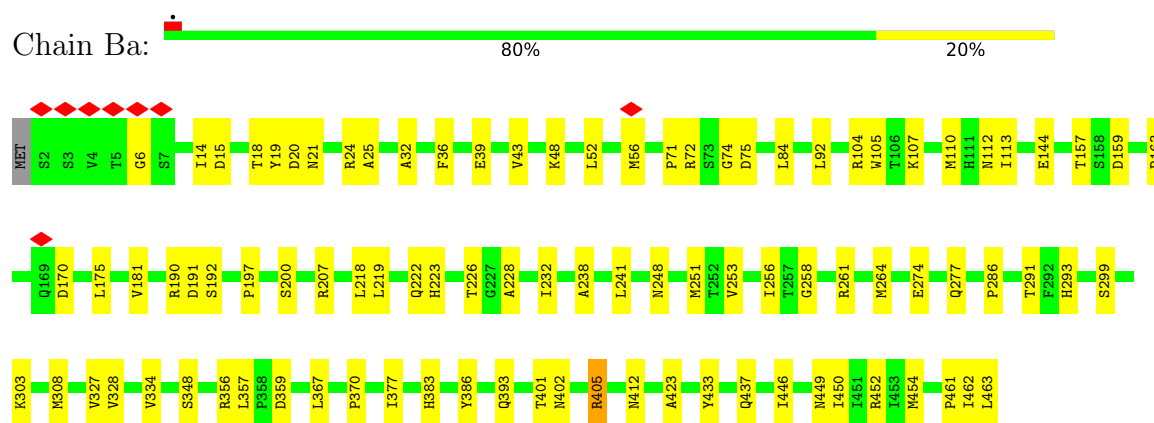
• Molecule 1: Vp34



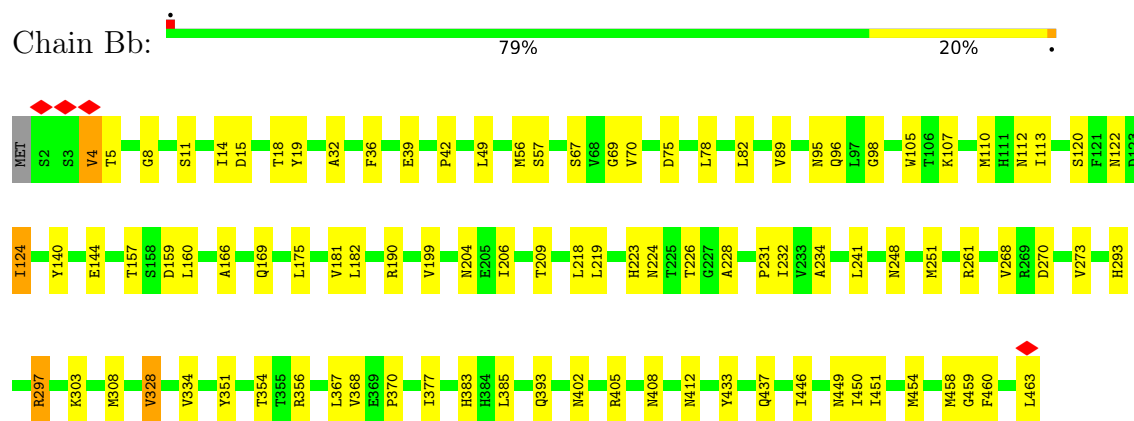
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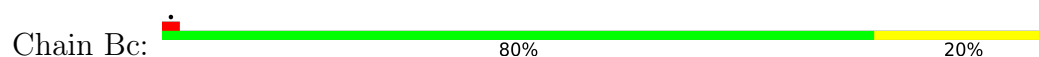
- Molecule 2: Major capsid protein

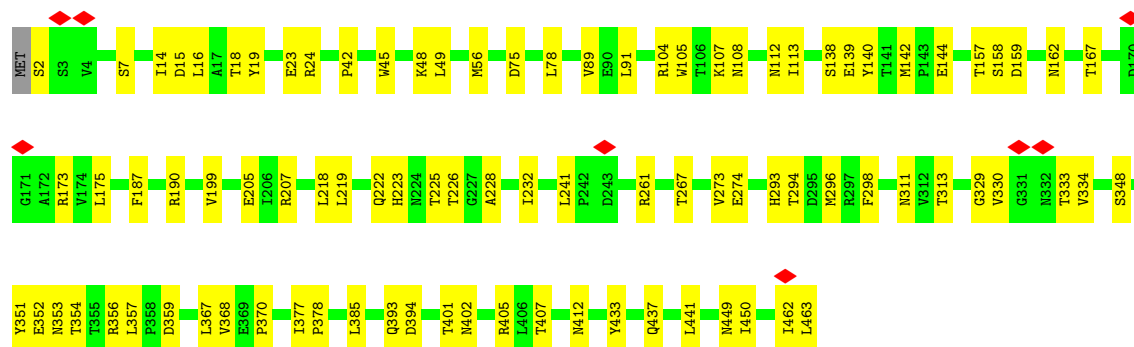


- Molecule 2: Major capsid protein

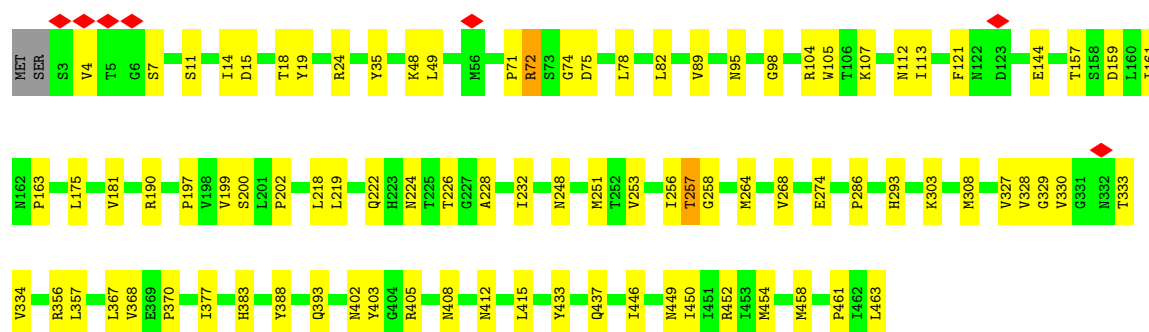
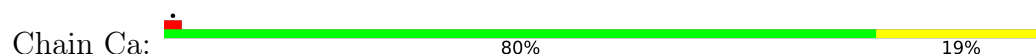


- Molecule 2: Major capsid protein

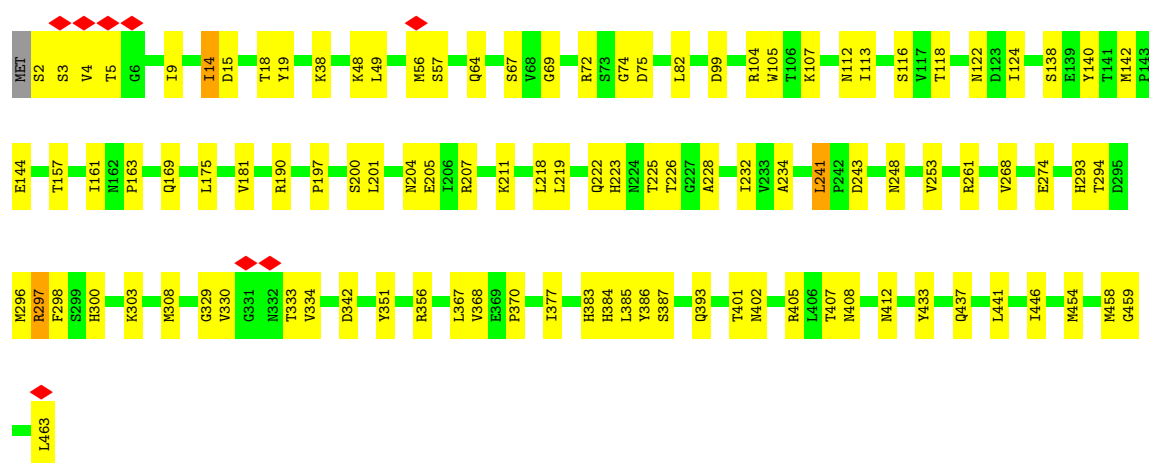
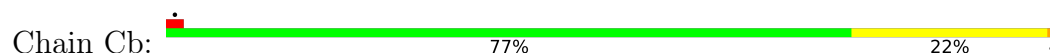




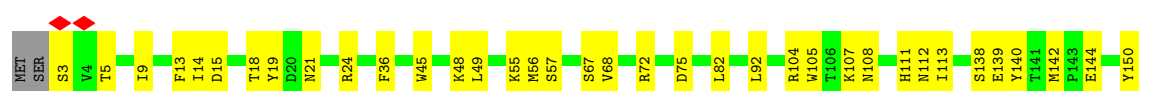
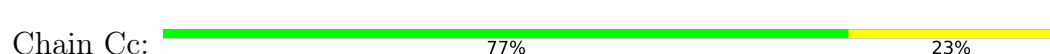
• Molecule 2: Major capsid protein

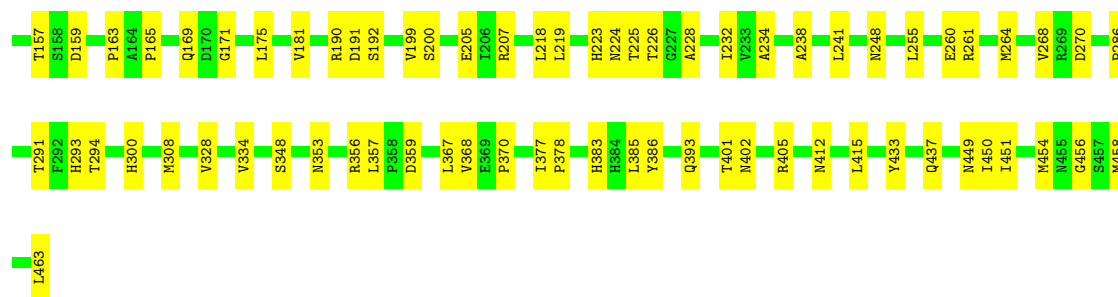


• Molecule 2: Major capsid protein



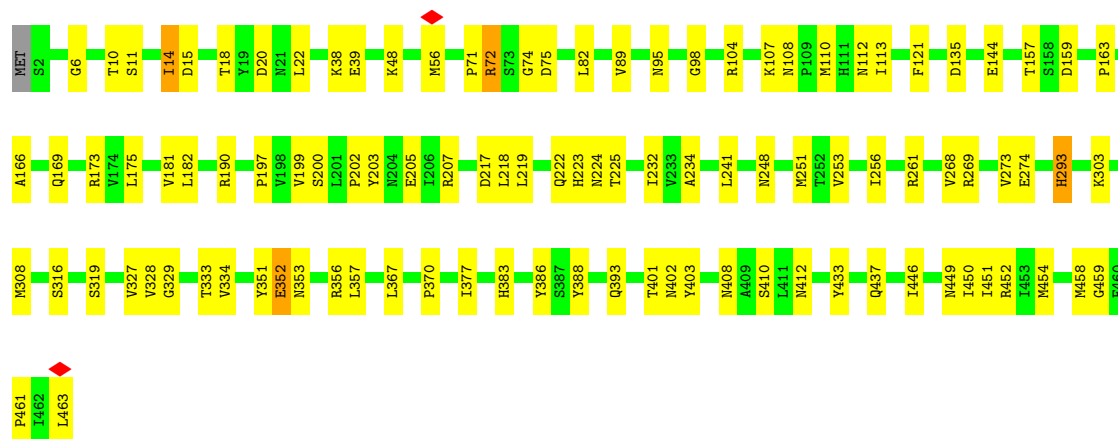
• Molecule 2: Major capsid protein





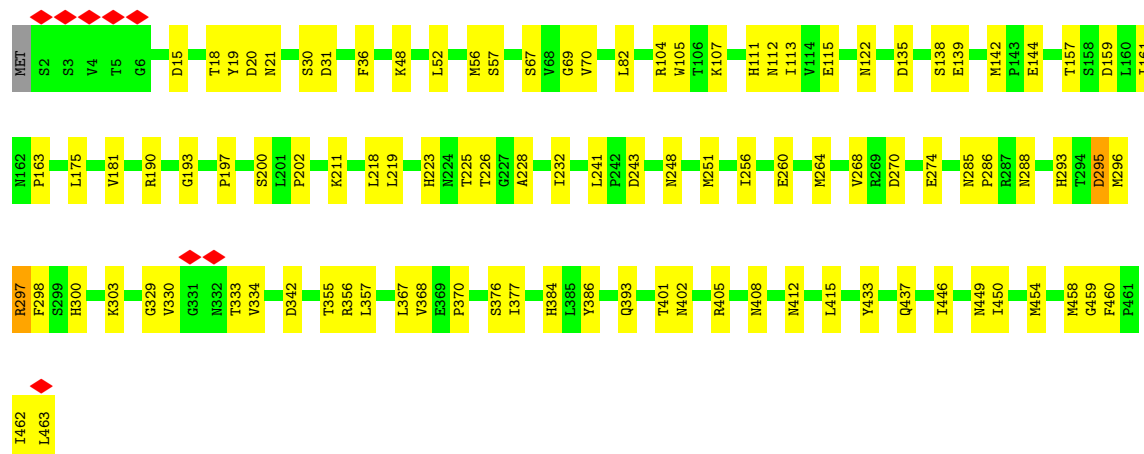
• Molecule 2: Major capsid protein

Chain Da: 77% 22%



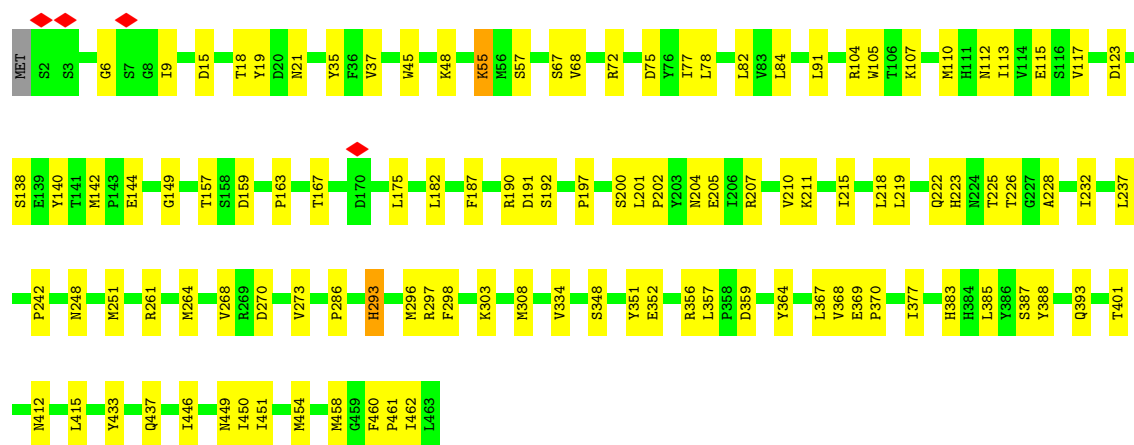
• Molecule 2: Major capsid protein

Chain Db: 78% 21%

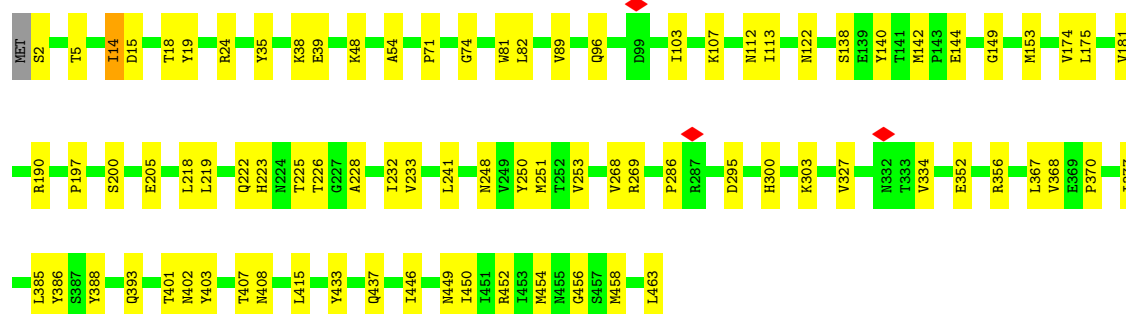
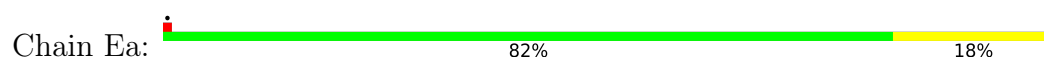


• Molecule 2: Major capsid protein

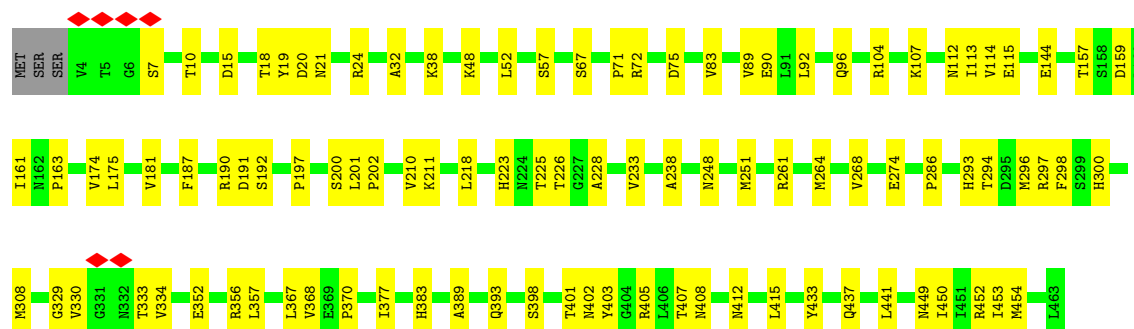
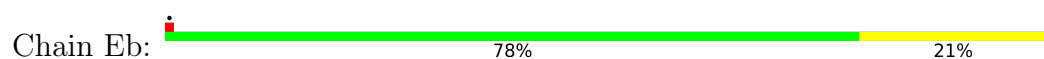
Chain Dc: 76% 24%



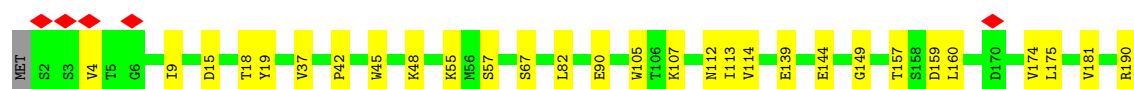
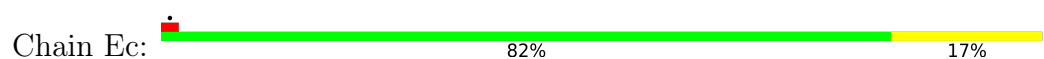
• Molecule 2: Major capsid protein

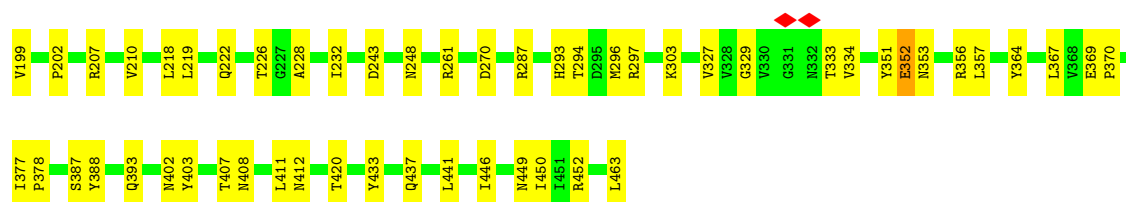


• Molecule 2: Major capsid protein

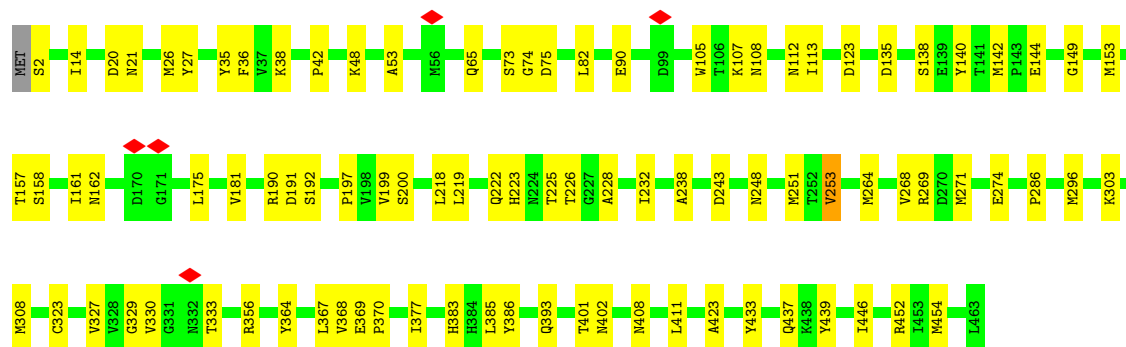
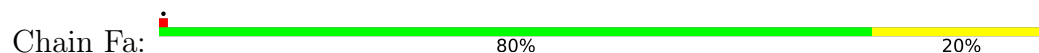


• Molecule 2: Major capsid protein

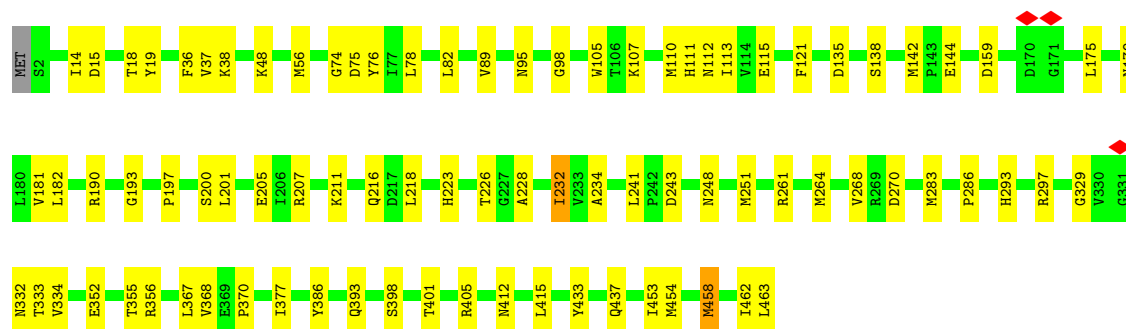
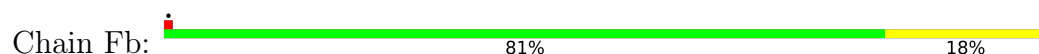




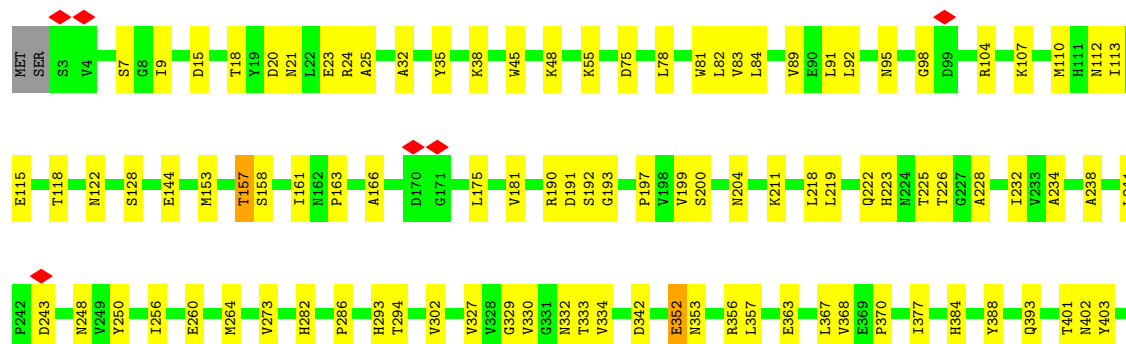
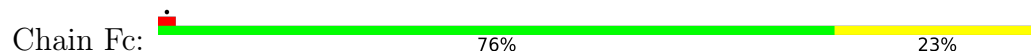
• Molecule 2: Major capsid protein



• Molecule 2: Major capsid protein

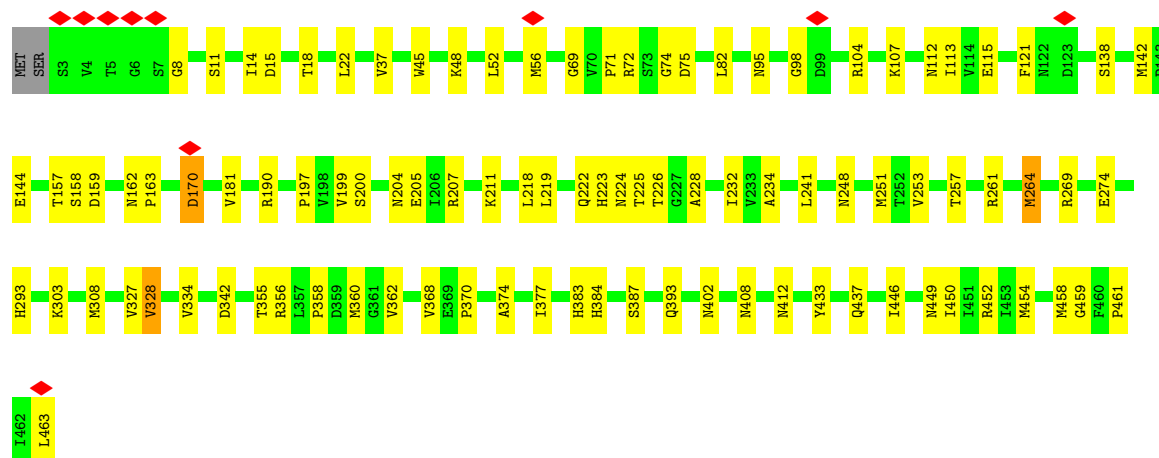
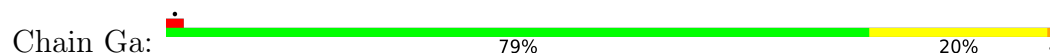


• Molecule 2: Major capsid protein

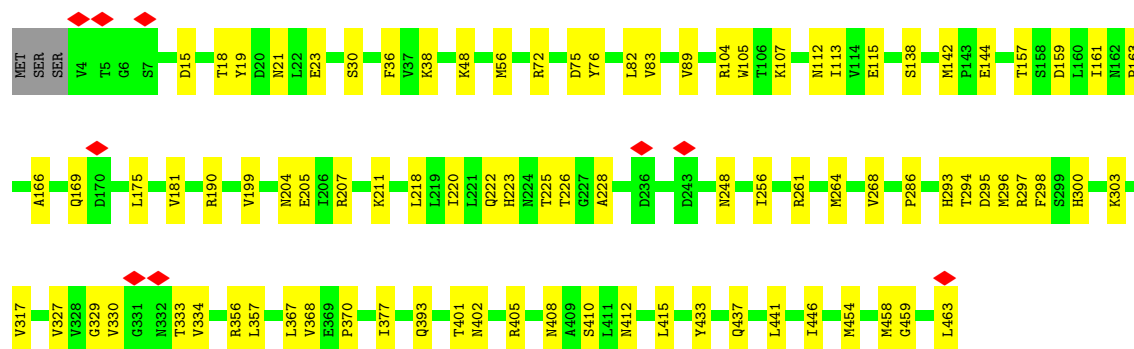
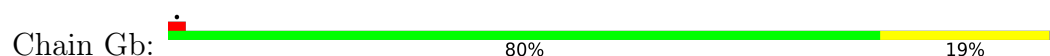




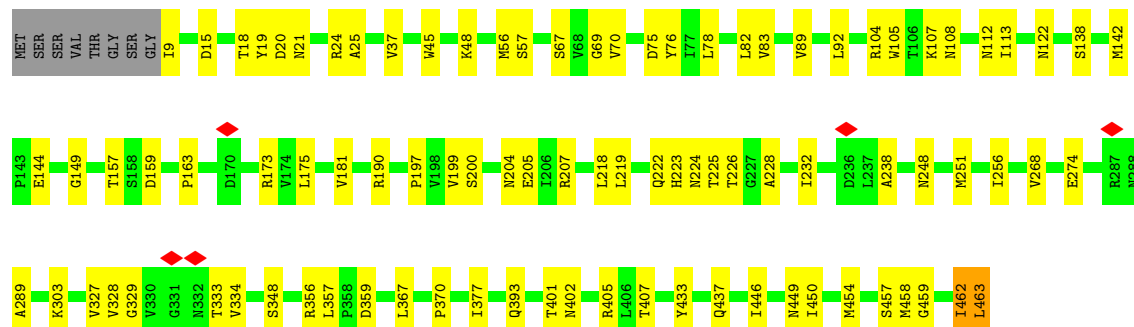
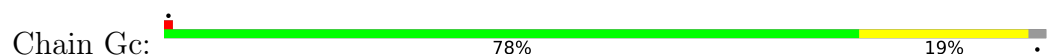
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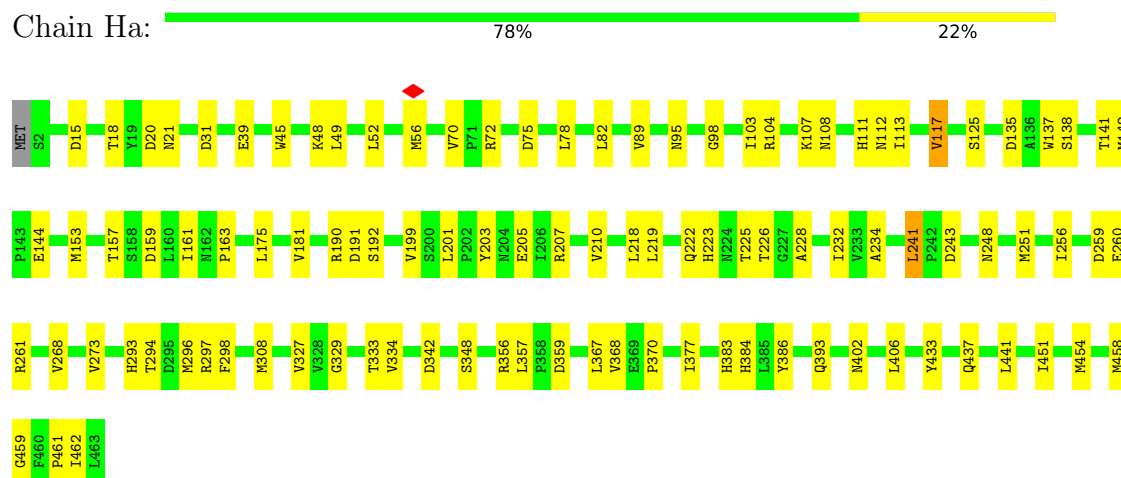
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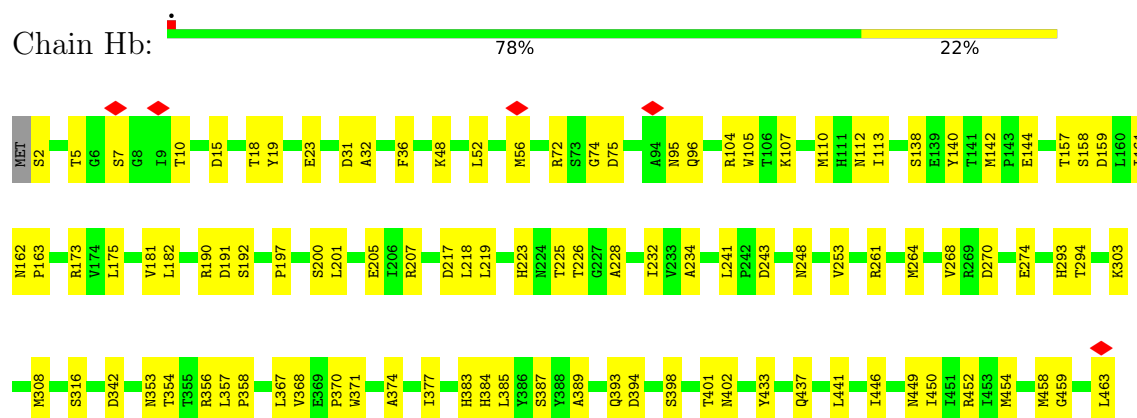
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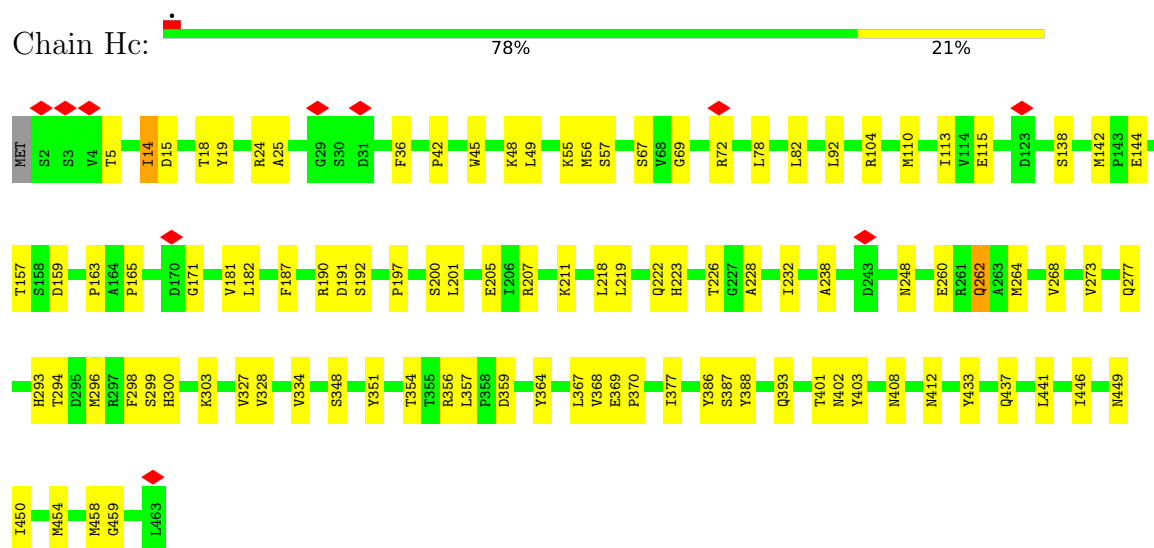
- Molecule 2: Major capsid protein



- Molecule 2: Major capsid protein

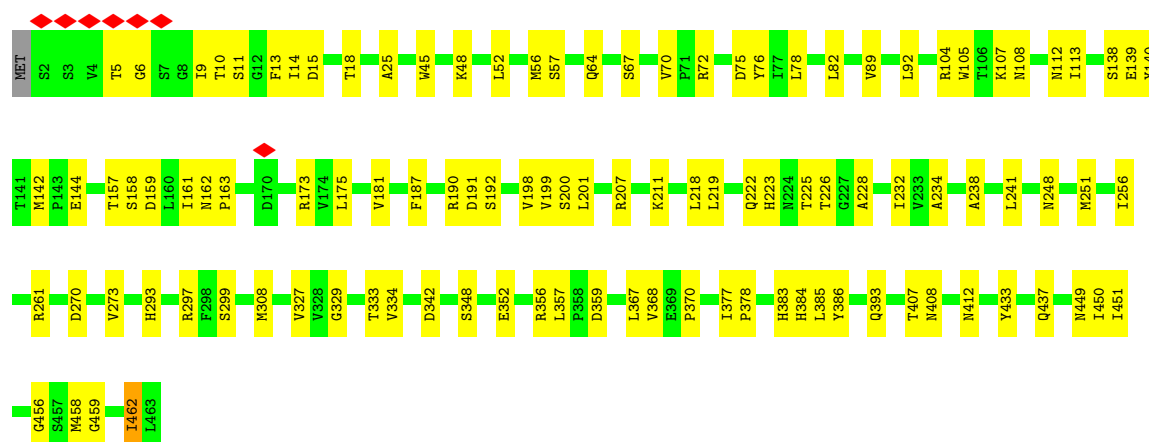


- Molecule 2: Major capsid protein



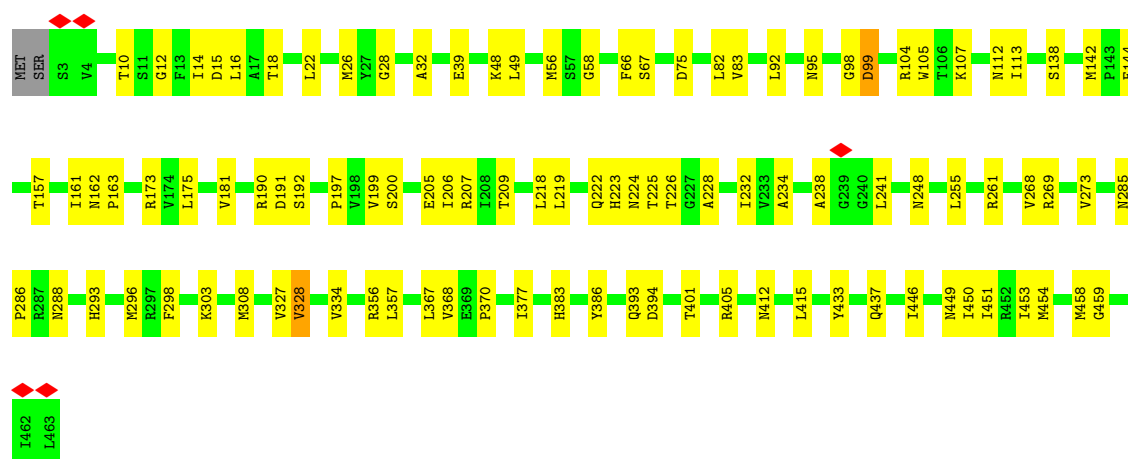
- Molecule 2: Major capsid protein

Chain Ia:  76% 23%



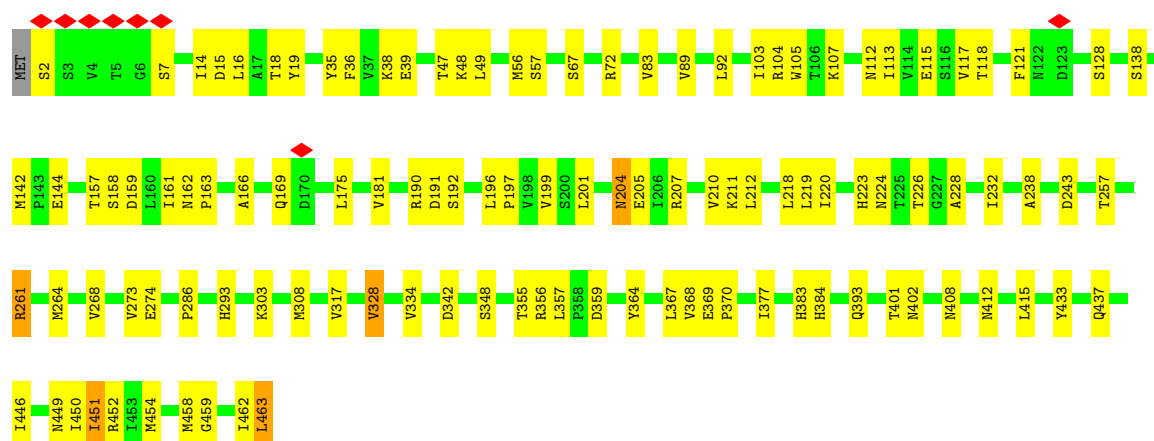
• Molecule 2: Major capsid protein

Chain Ib:  78% 22%

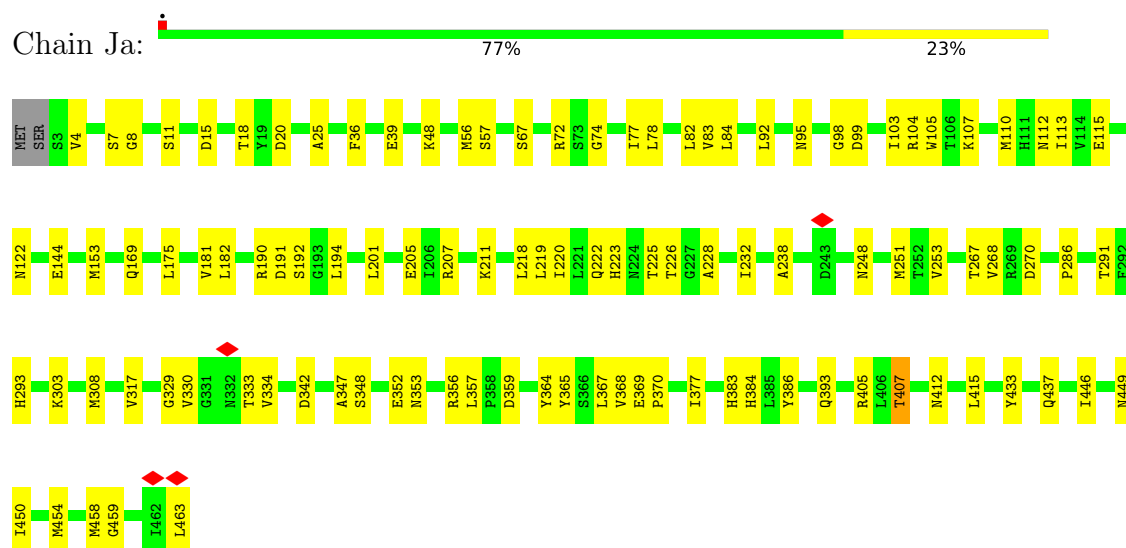


• Molecule 2: Major capsid protein

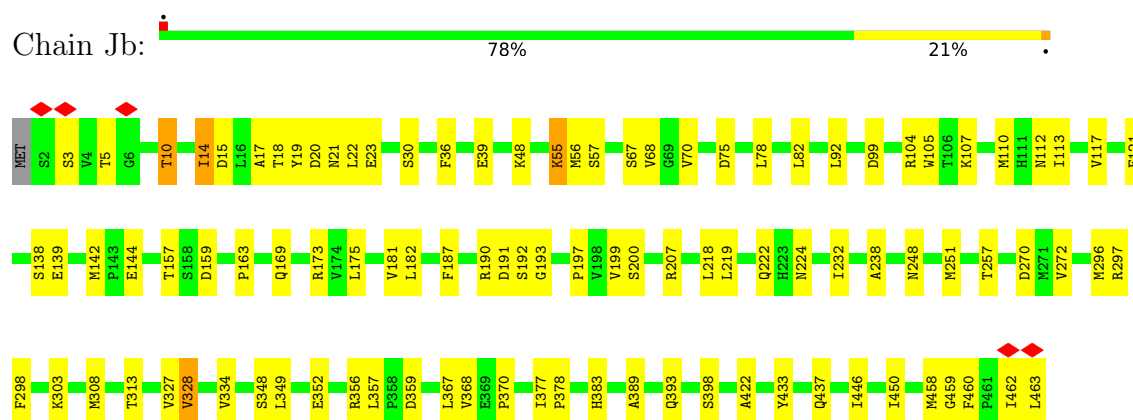
Chain Ic:  75% 23%



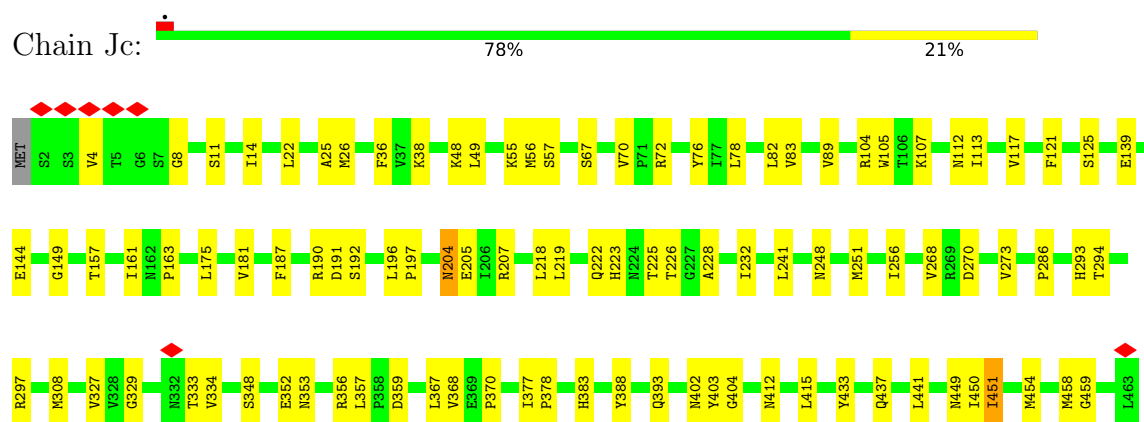
- Molecule 2: Major capsid protein



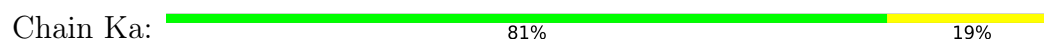
- Molecule 2: Major capsid protein

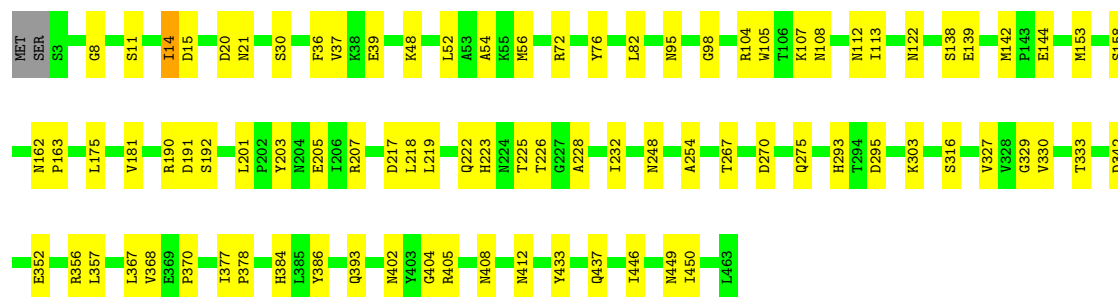


- Molecule 2: Major capsid protein

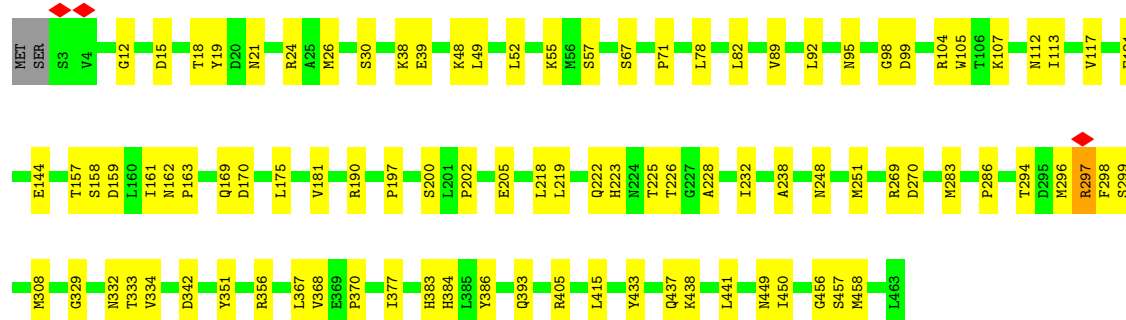
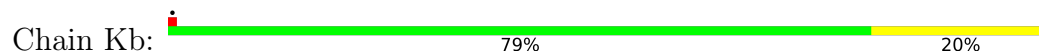


- Molecule 2: Major capsid protein

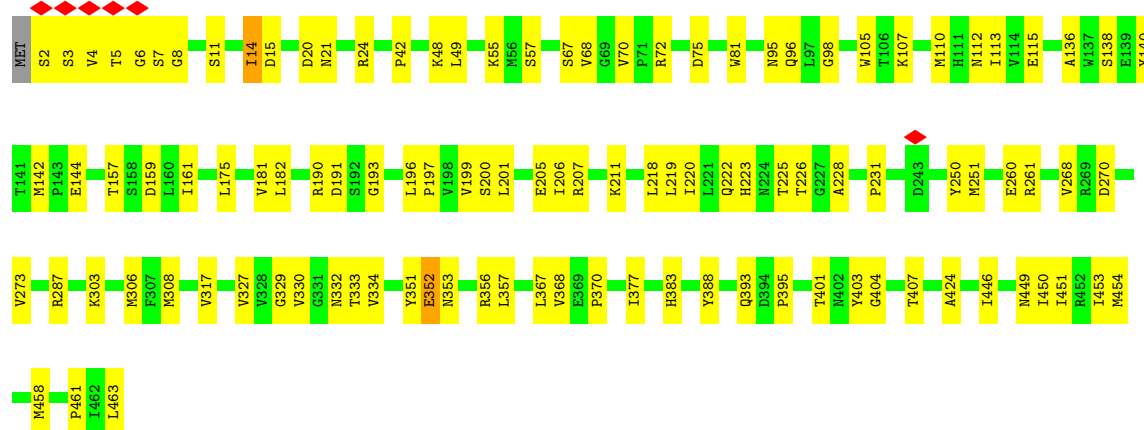
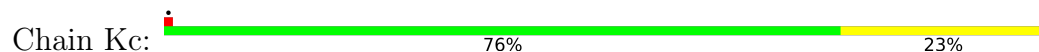




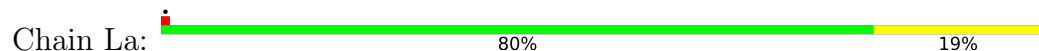
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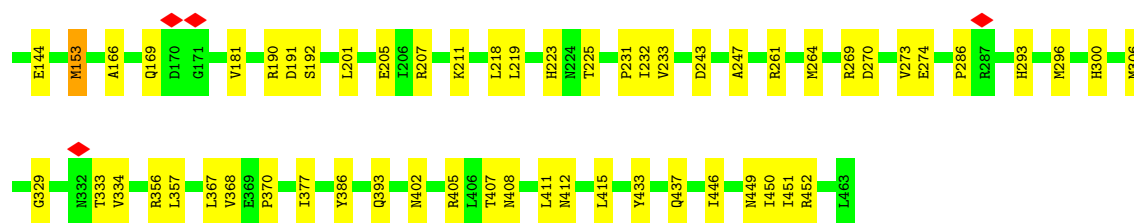


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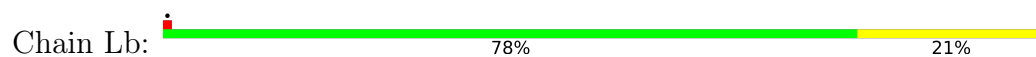


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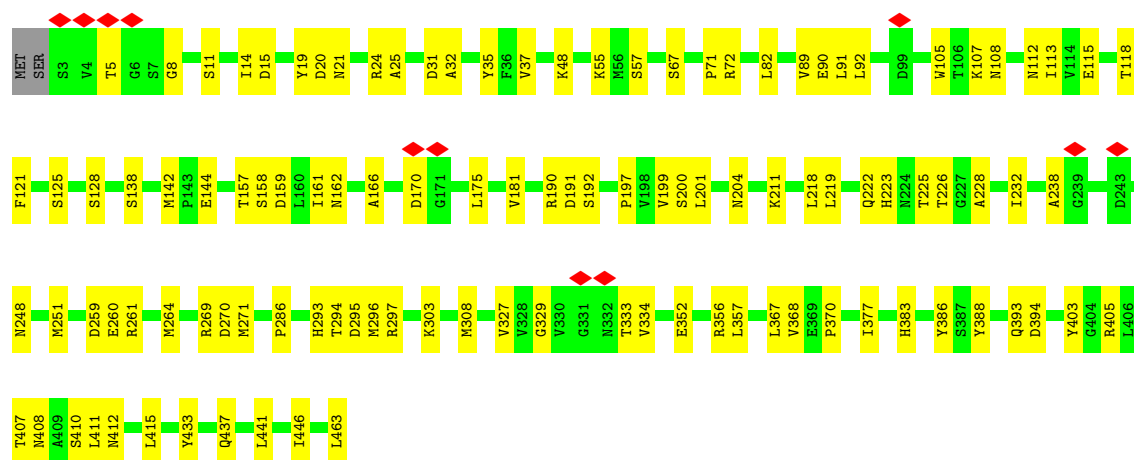
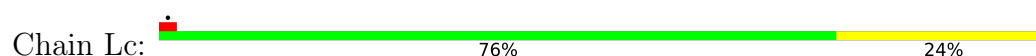




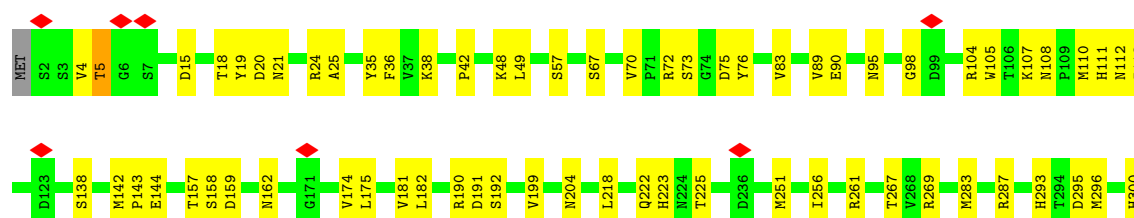
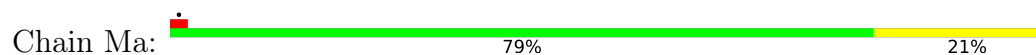
• Molecule 2: Major capsid protein



• Molecule 2: Major capsid protein

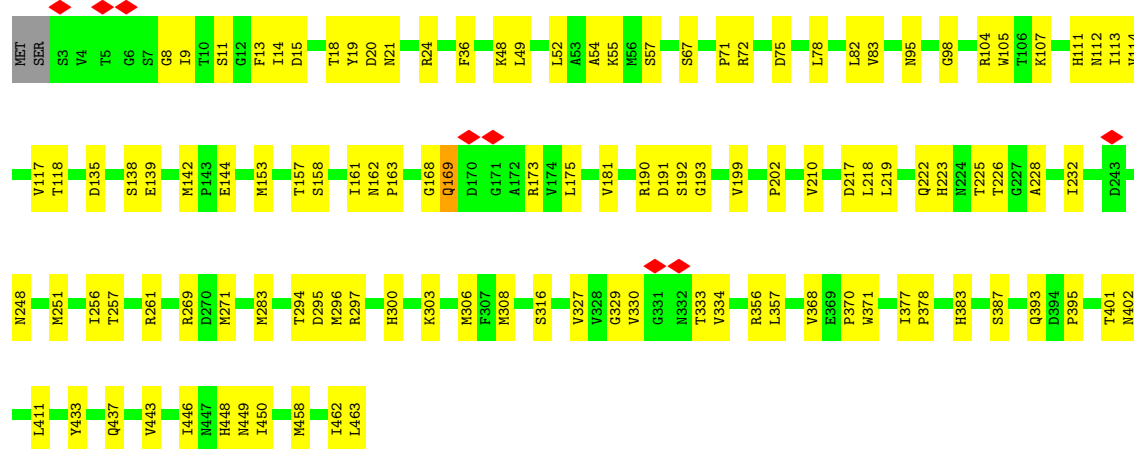
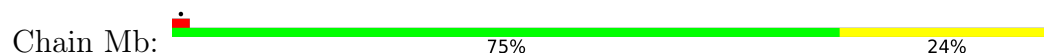


• Molecule 2: Major capsid protein

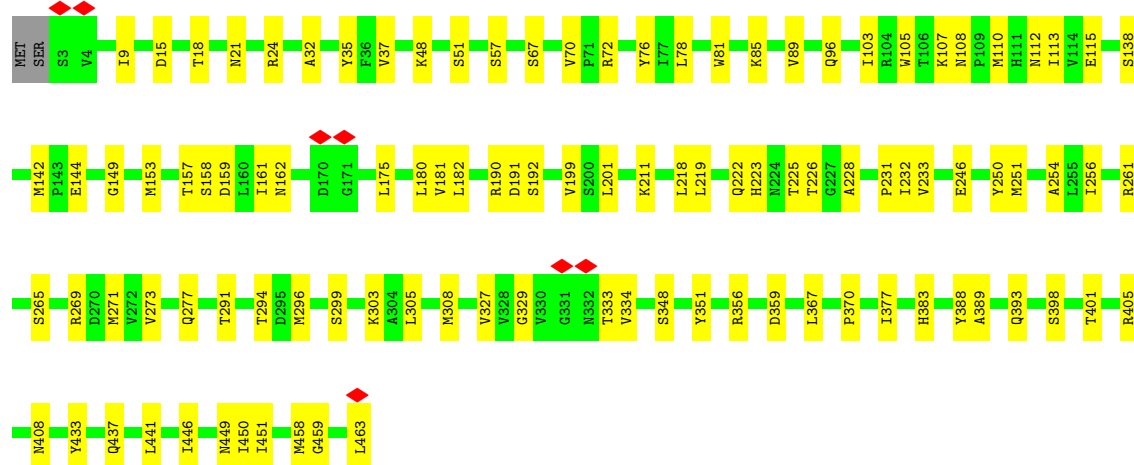
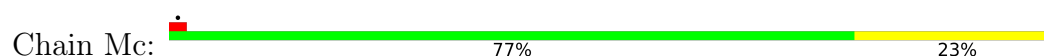




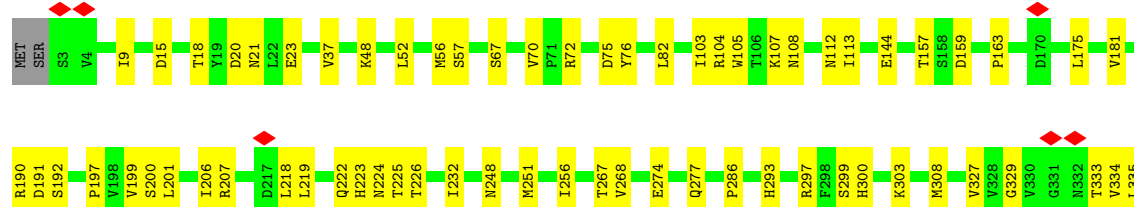
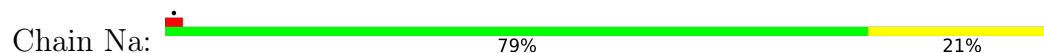
• Molecule 2: Major capsid protein



• Molecule 2: Major capsid protein

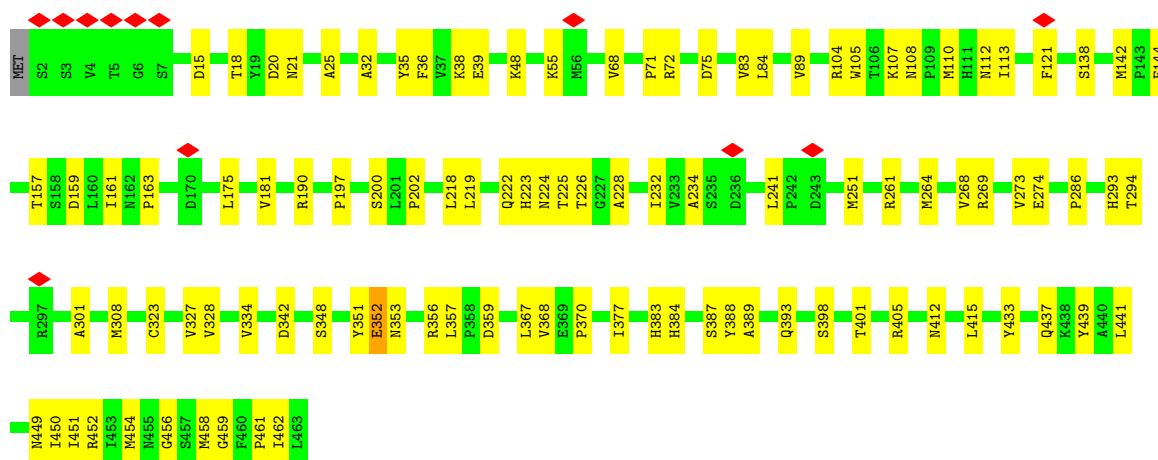
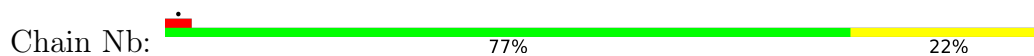


• Molecule 2: Major capsid protein

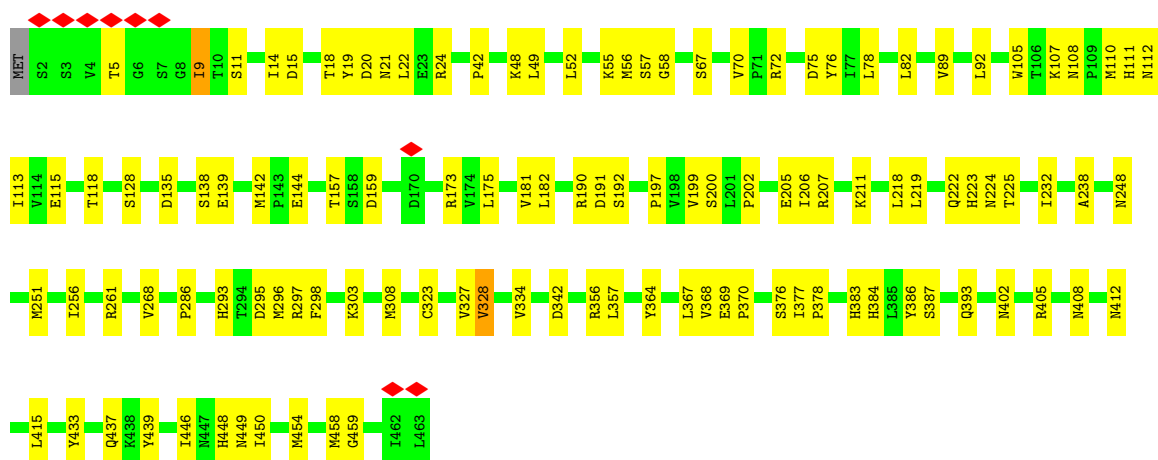
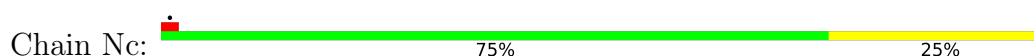




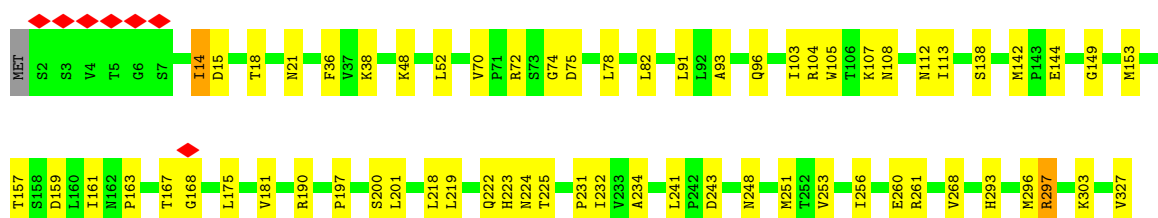
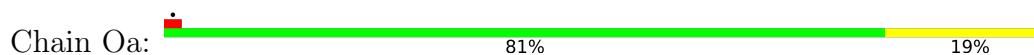
• Molecule 2: Major capsid protein



• Molecule 2: Major capsid protein

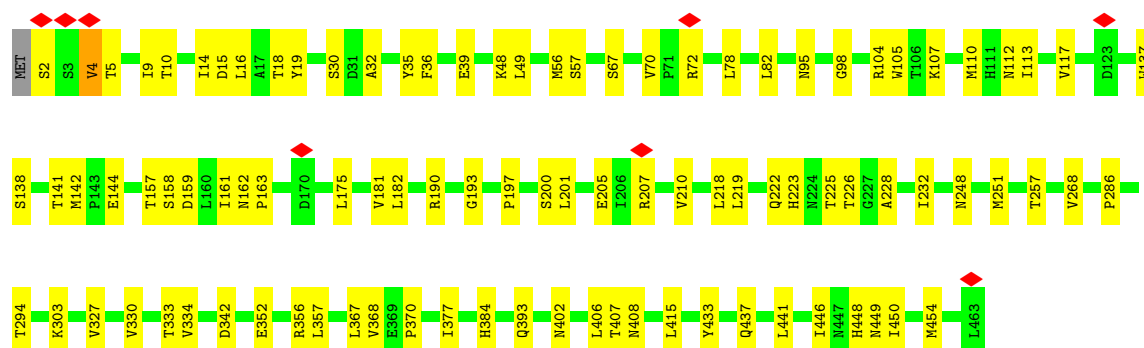
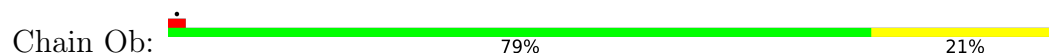


• Molecule 2: Major capsid protein

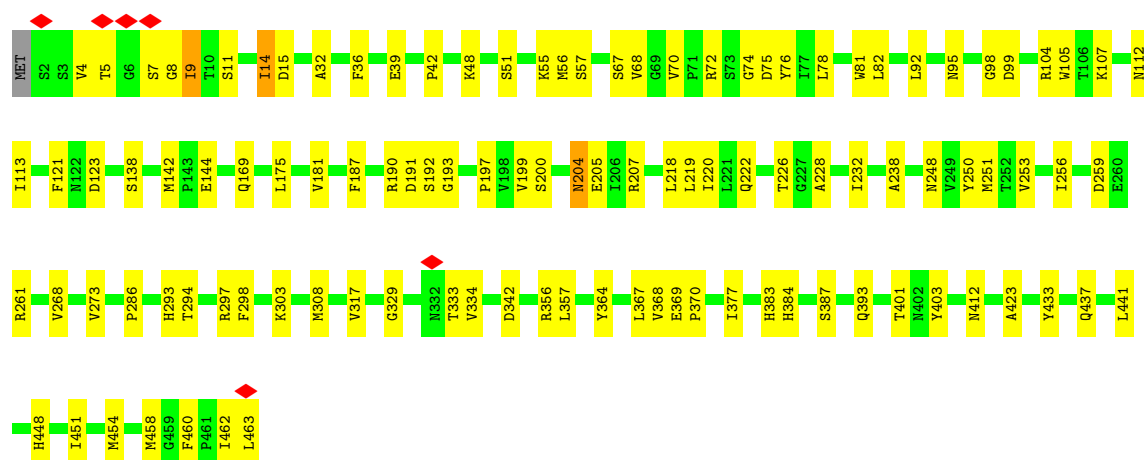
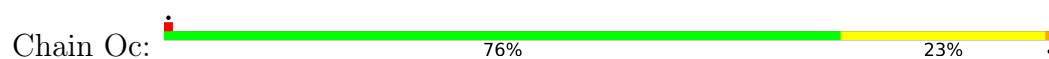




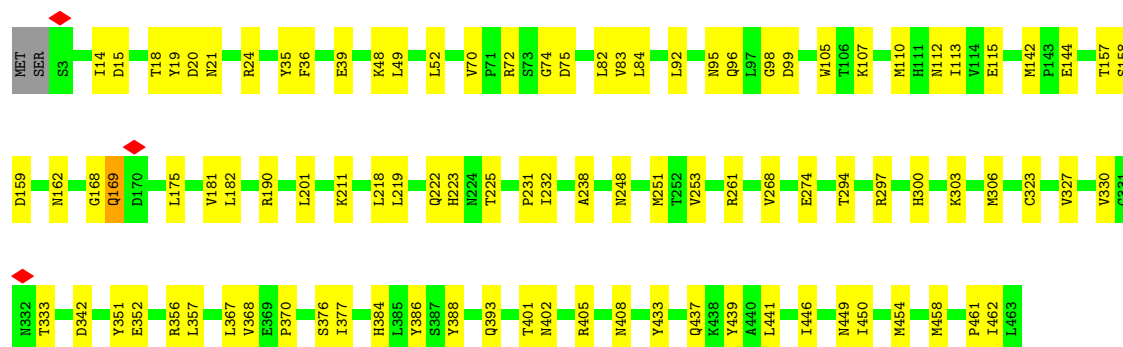
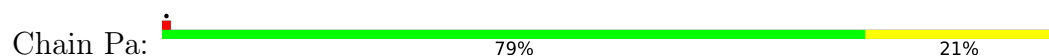
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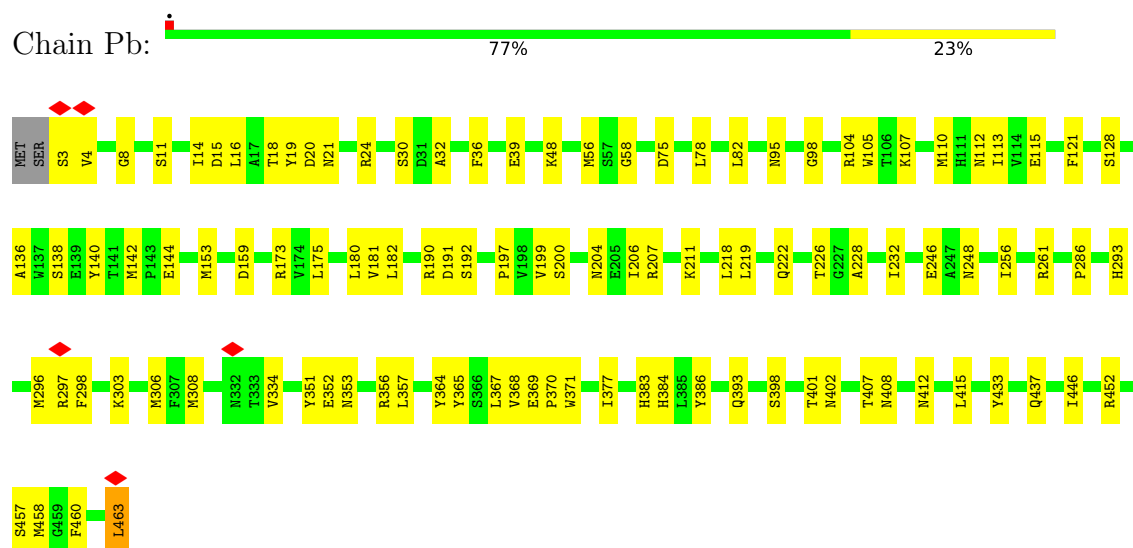
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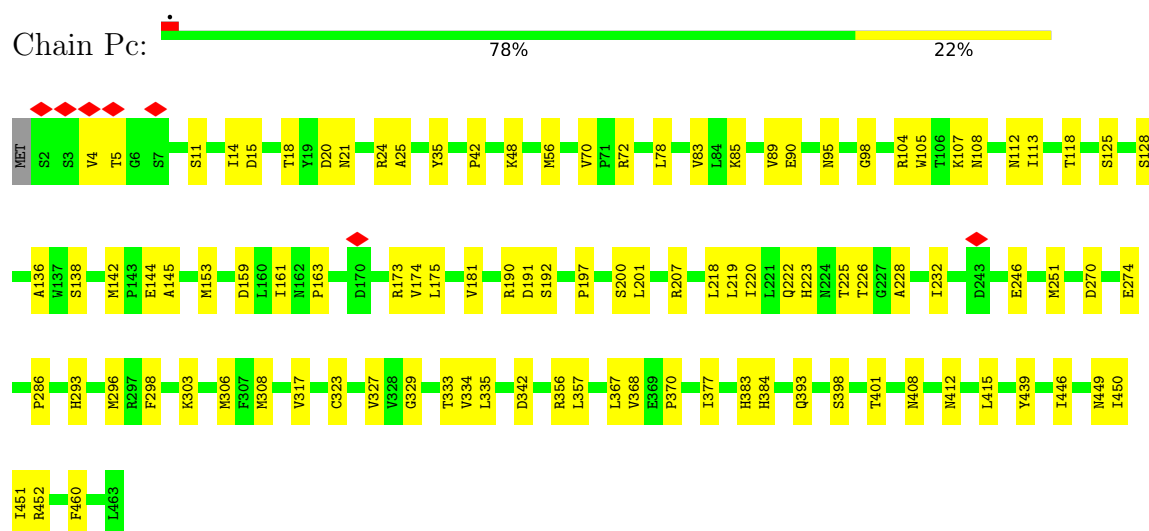
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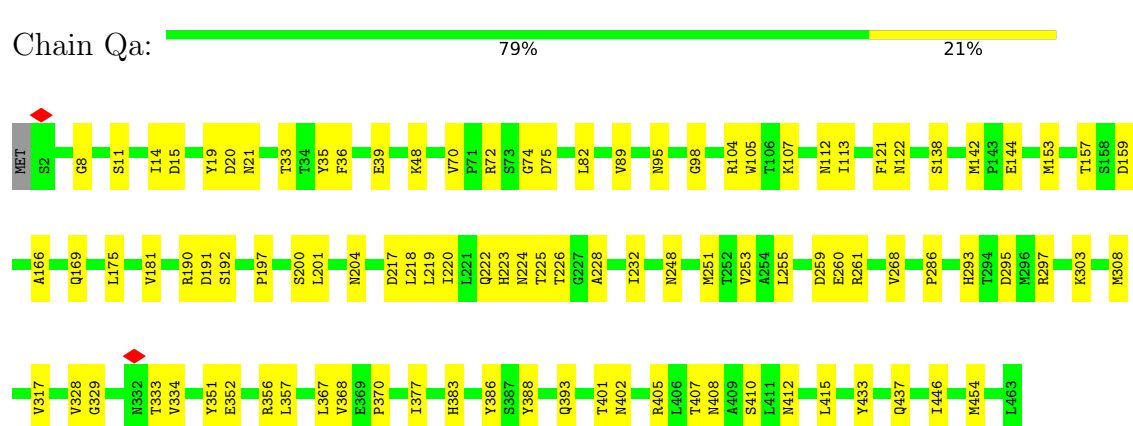
- Molecule 2: Major capsid protein



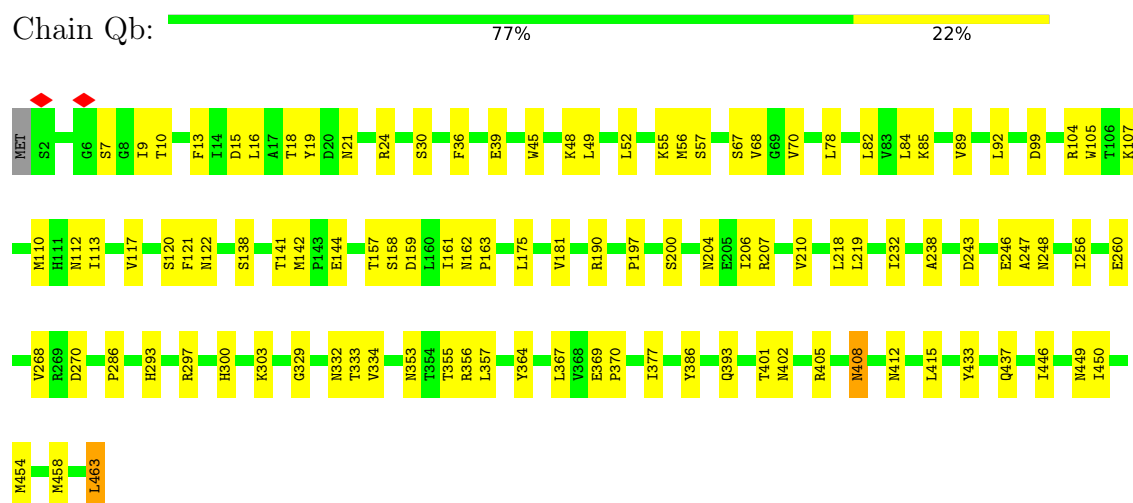
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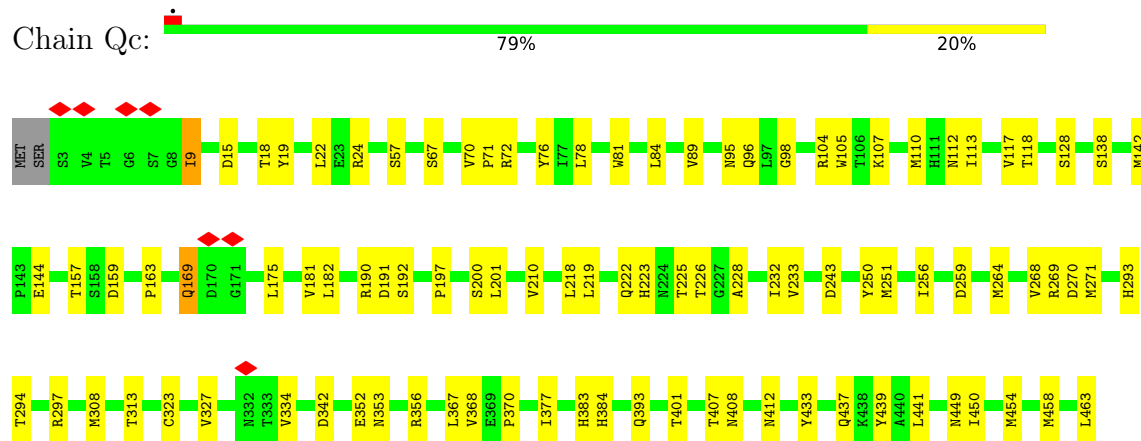
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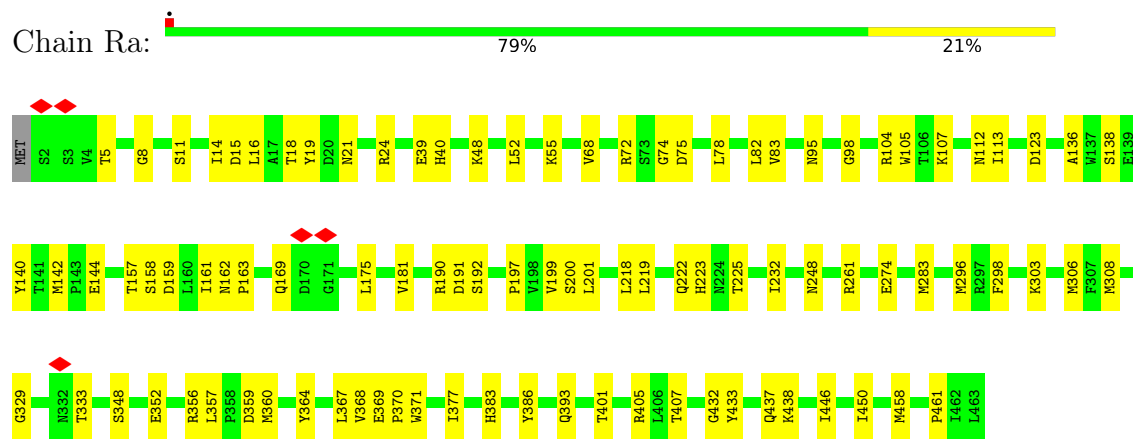
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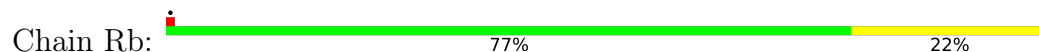
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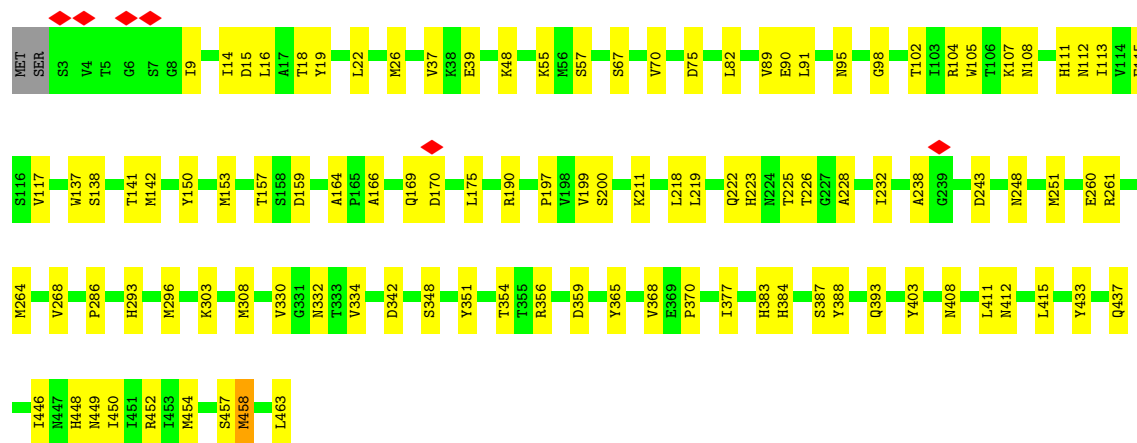


- Molecule 2: Major capsid protein

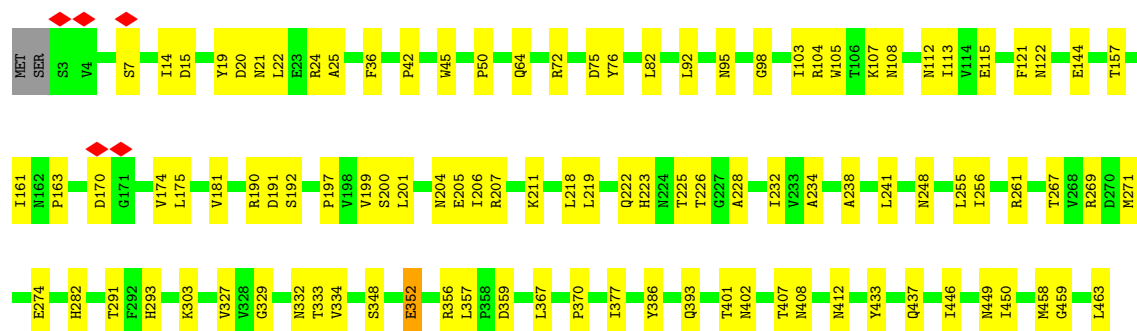
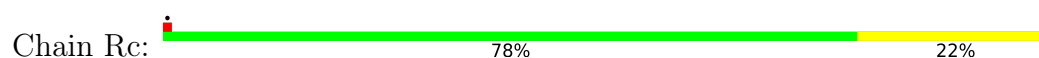


- Molecule 2: Major capsid protein

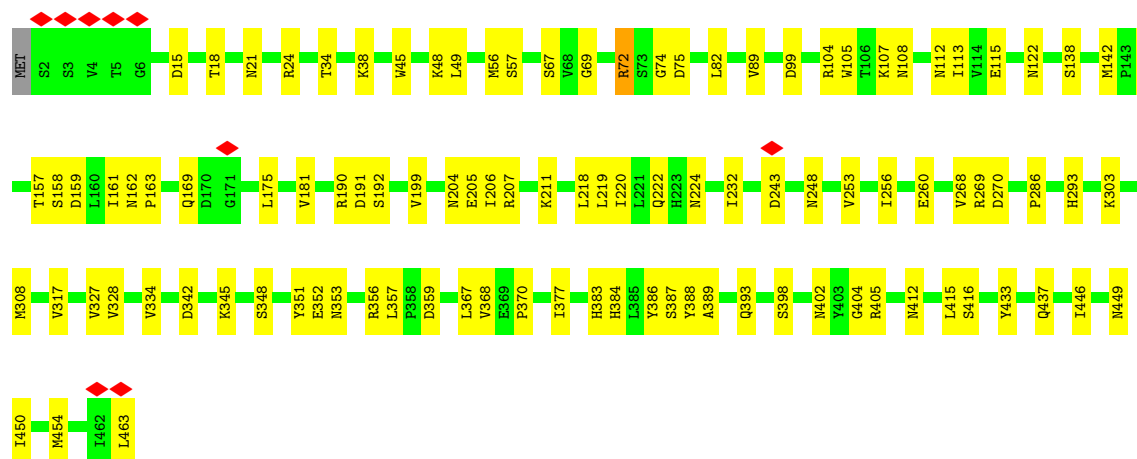
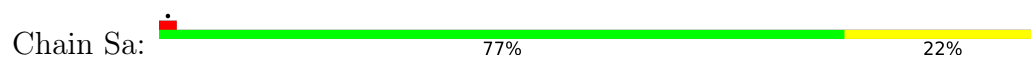




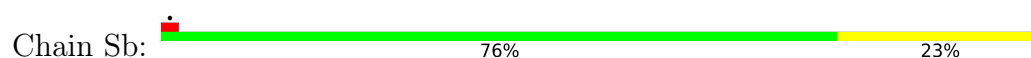
• Molecule 2: Major capsid protein

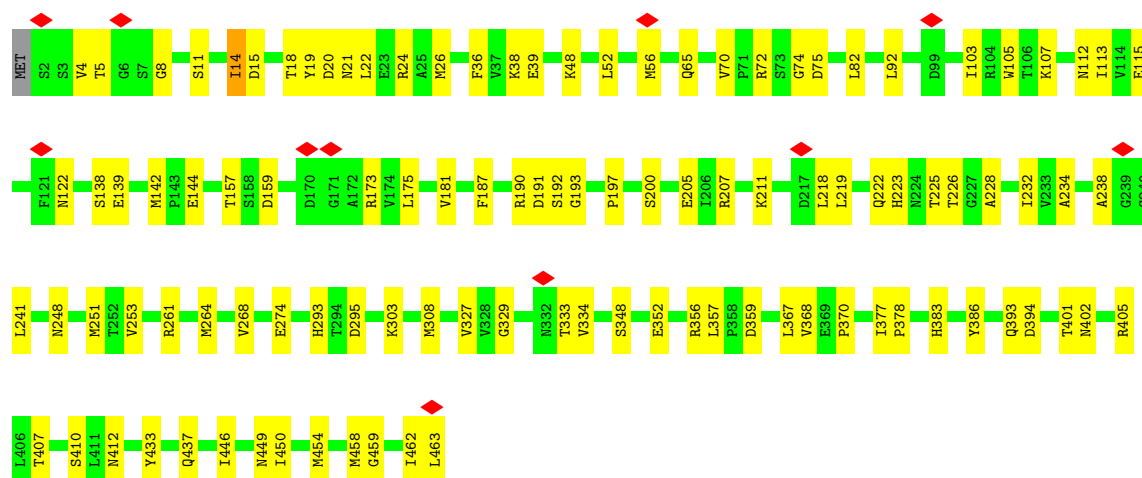


• Molecule 2: Major capsid protein

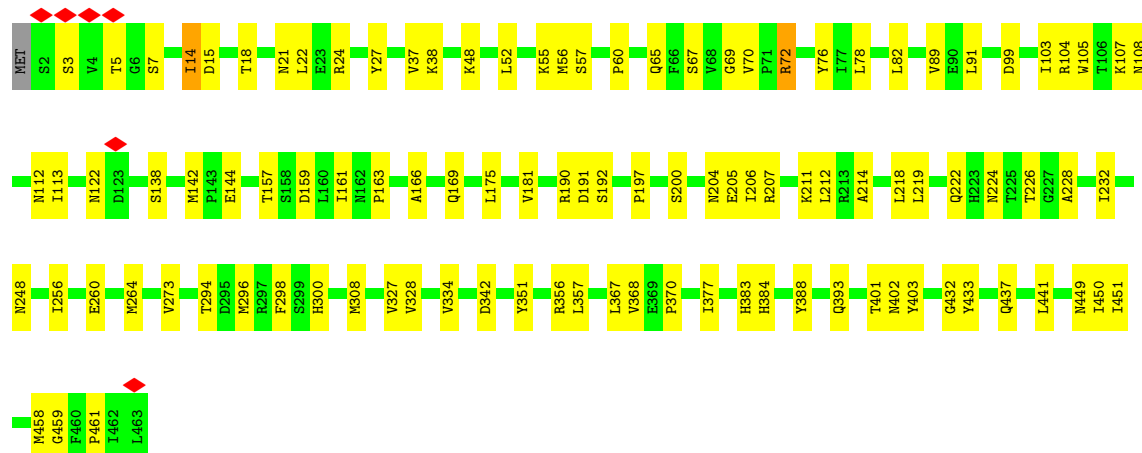
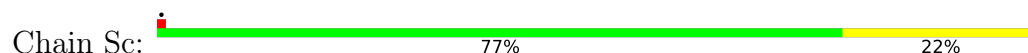


• Molecule 2: Major capsid protein

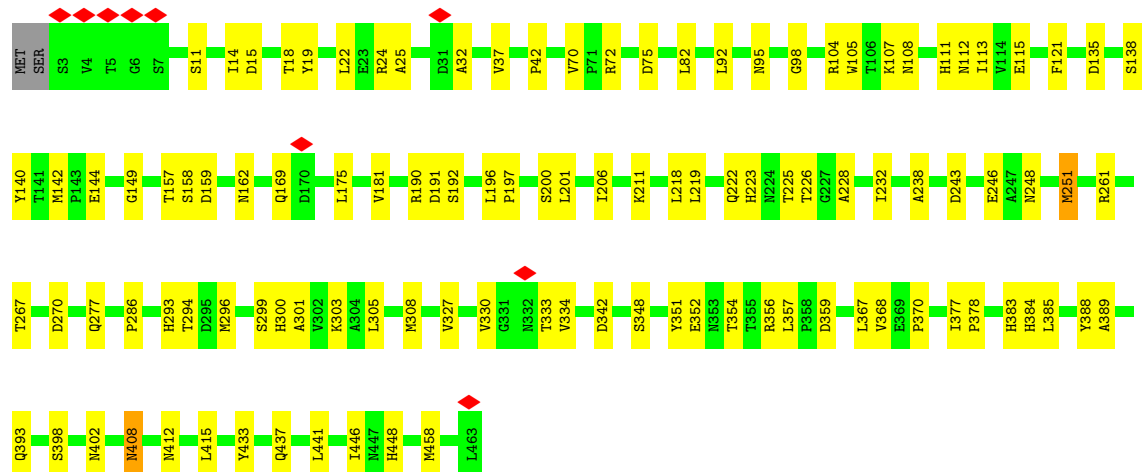
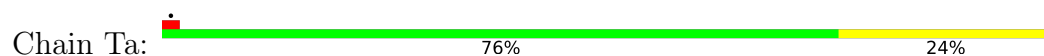




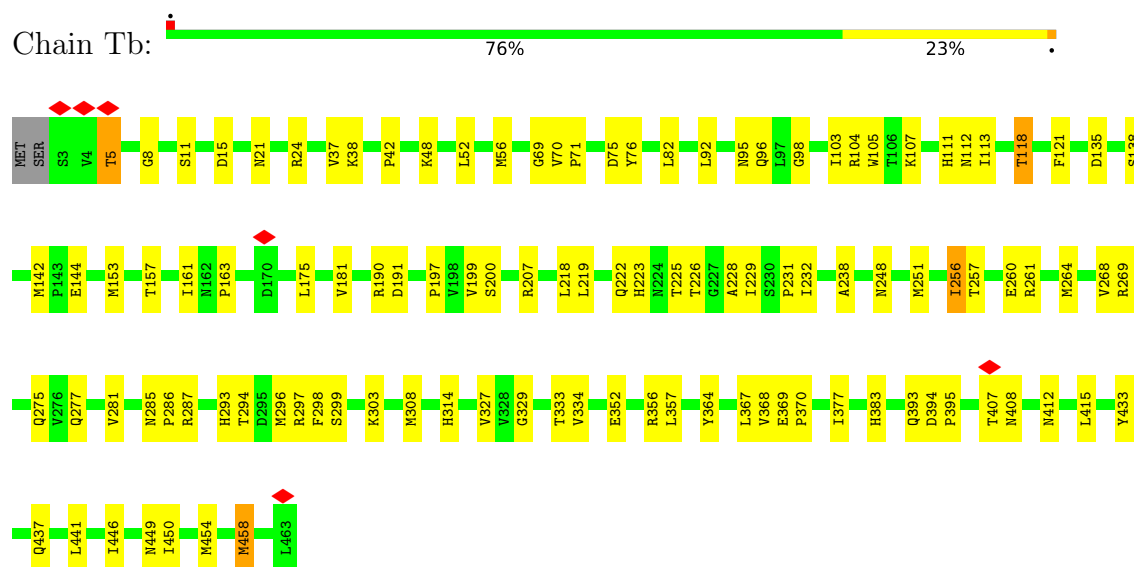
• Molecule 2: Major capsid protein



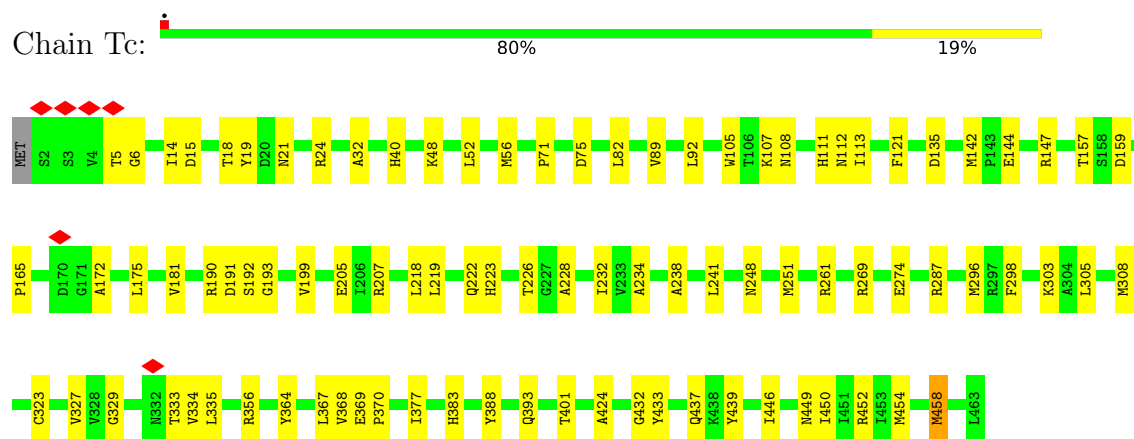
• Molecule 2: Major capsid protein



- Molecule 2: Major capsid protein



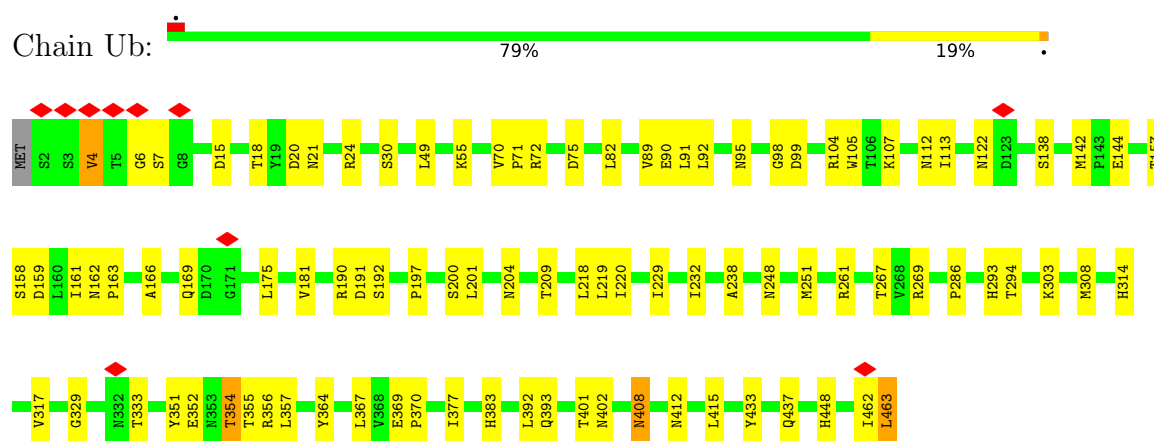
- Molecule 2: Major capsid protein



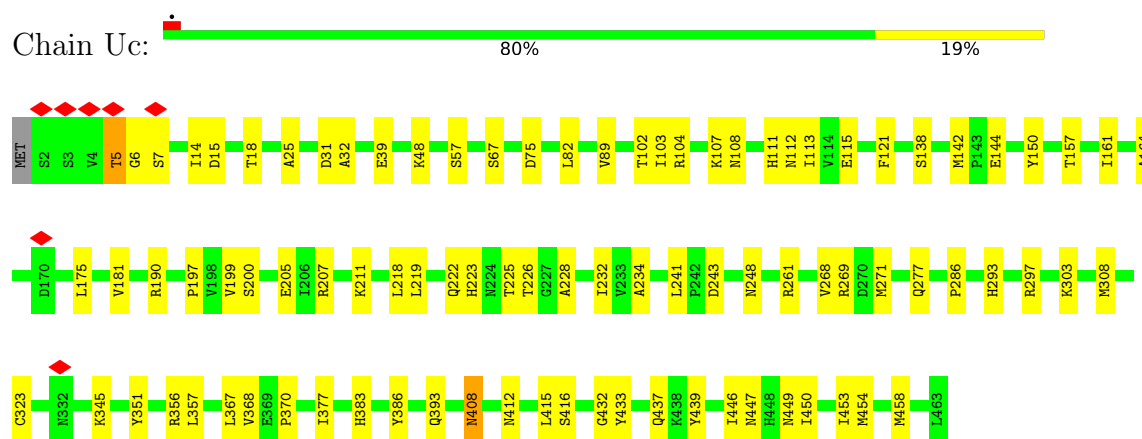
- Molecule 2: Major capsid protein



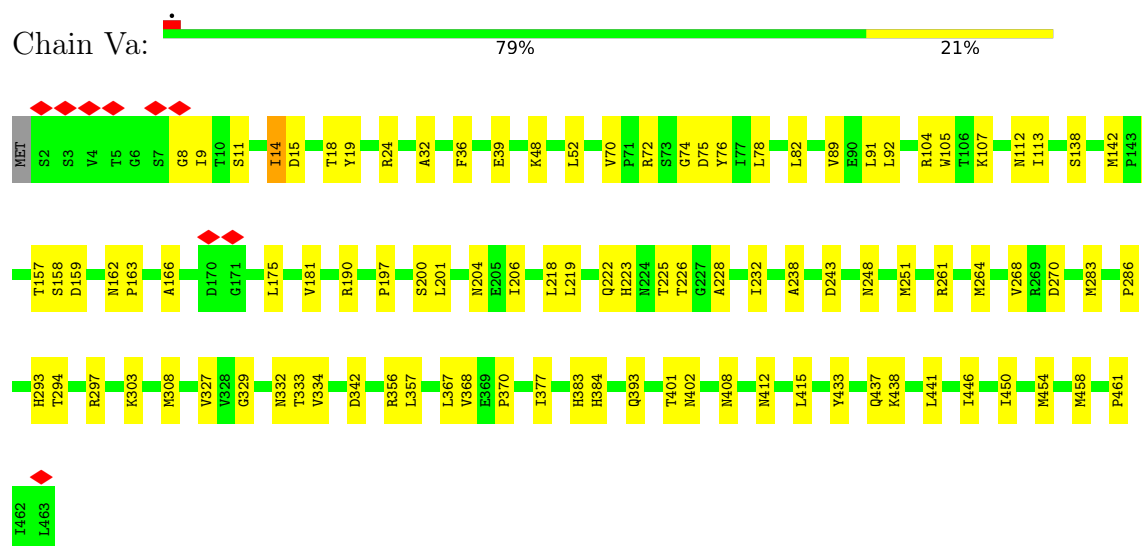
- Molecule 2: Major capsid protein



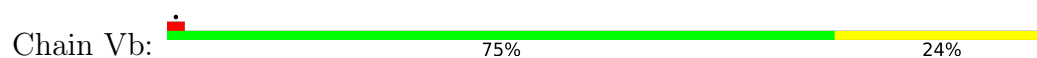
• Molecule 2: Major capsid protein

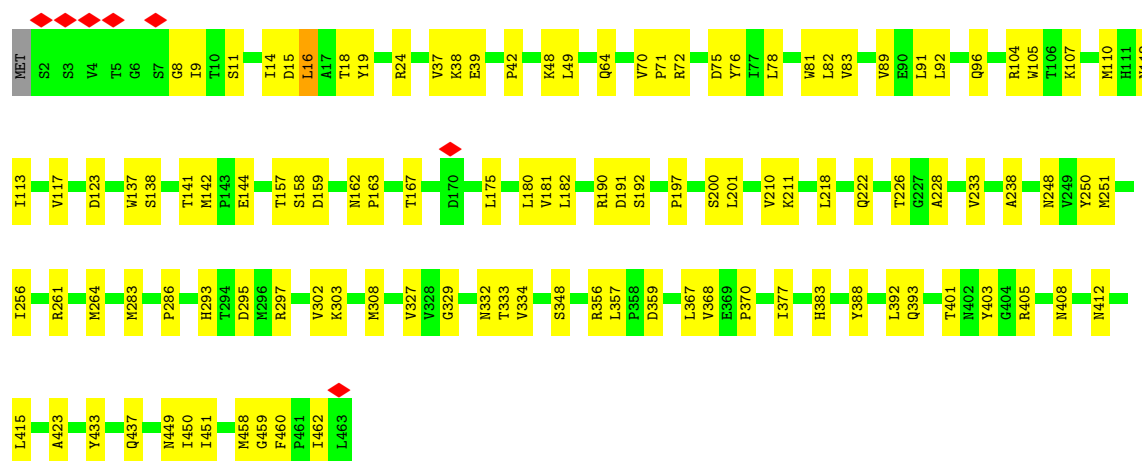


• Molecule 2: Major capsid protein

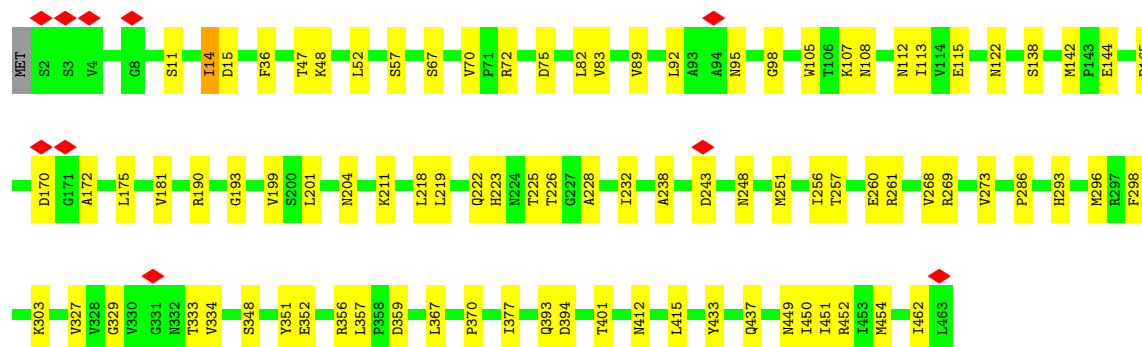
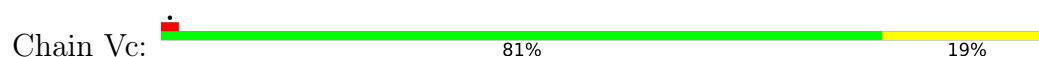


• Molecule 2: Major capsid protein

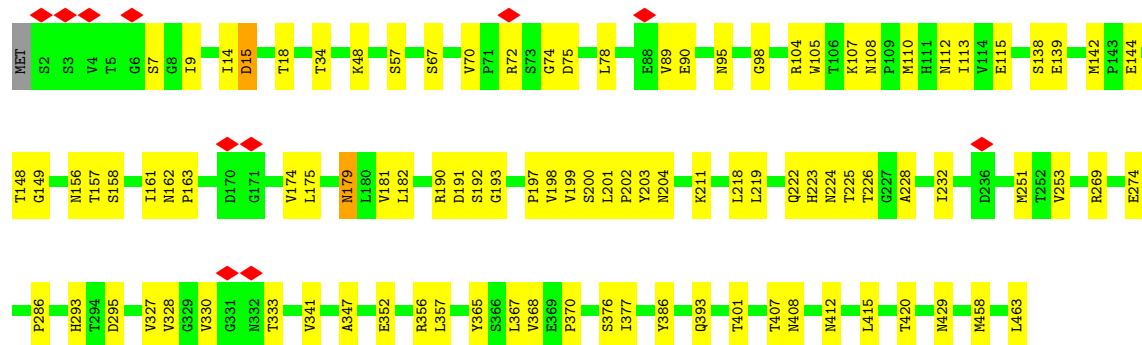
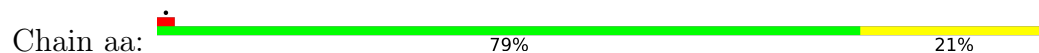




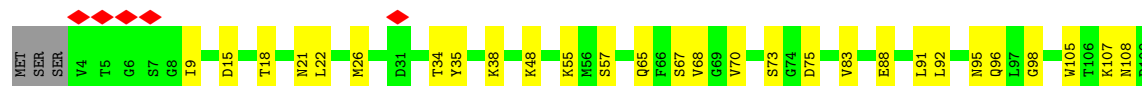
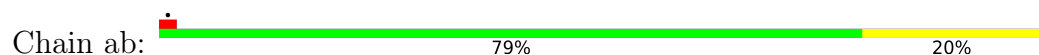
• Molecule 2: Major capsid protein

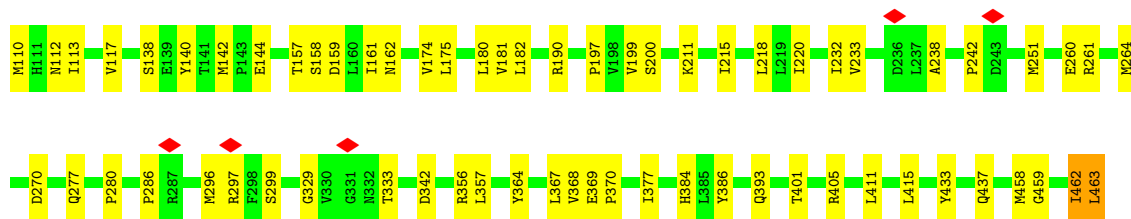


• Molecule 2: Major capsid protein

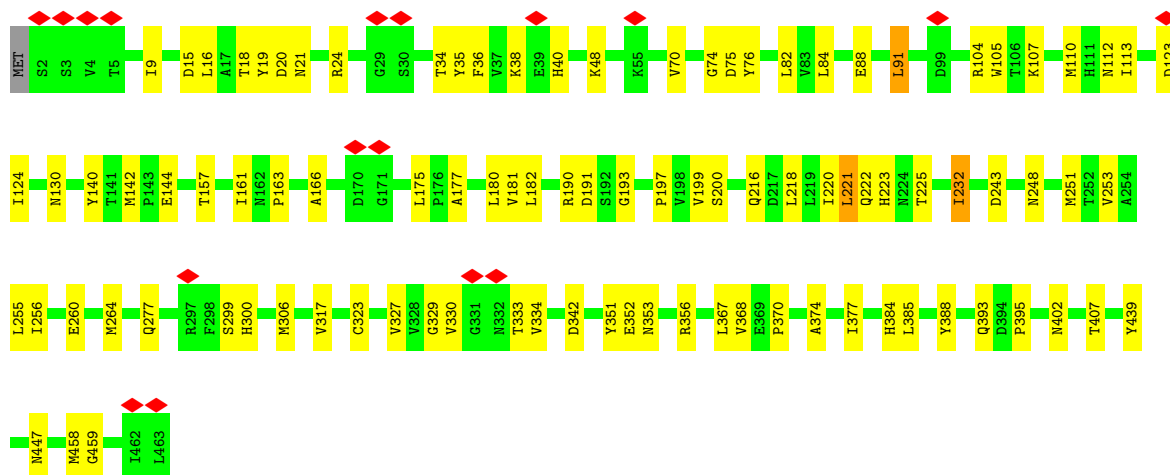
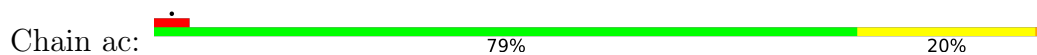


• Molecule 2: Major capsid protein

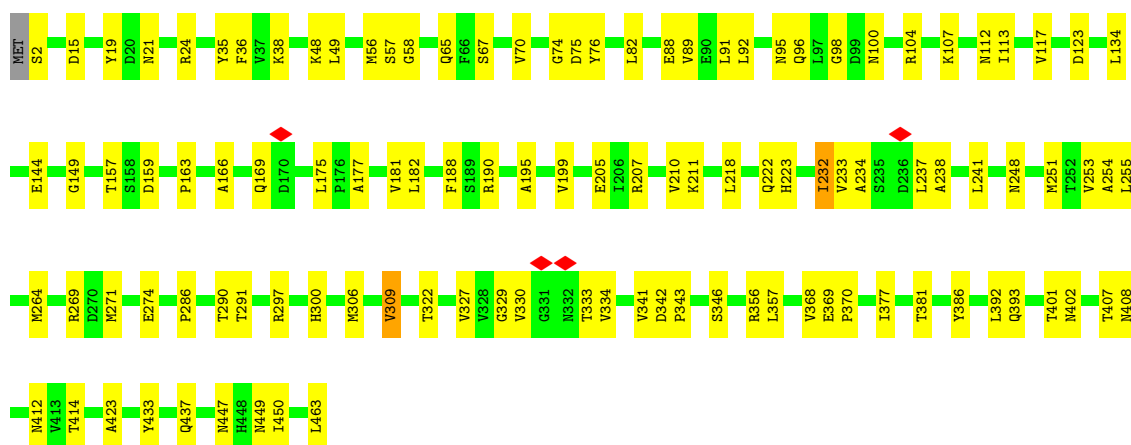
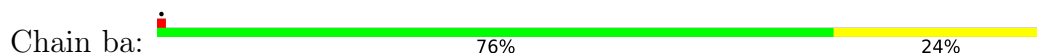




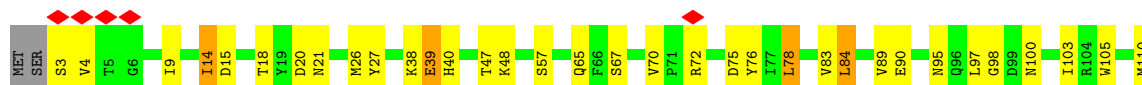
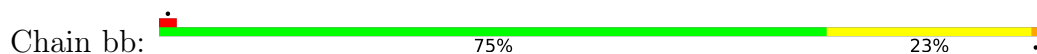
• Molecule 2: Major capsid protein



• Molecule 2: Major capsid protein

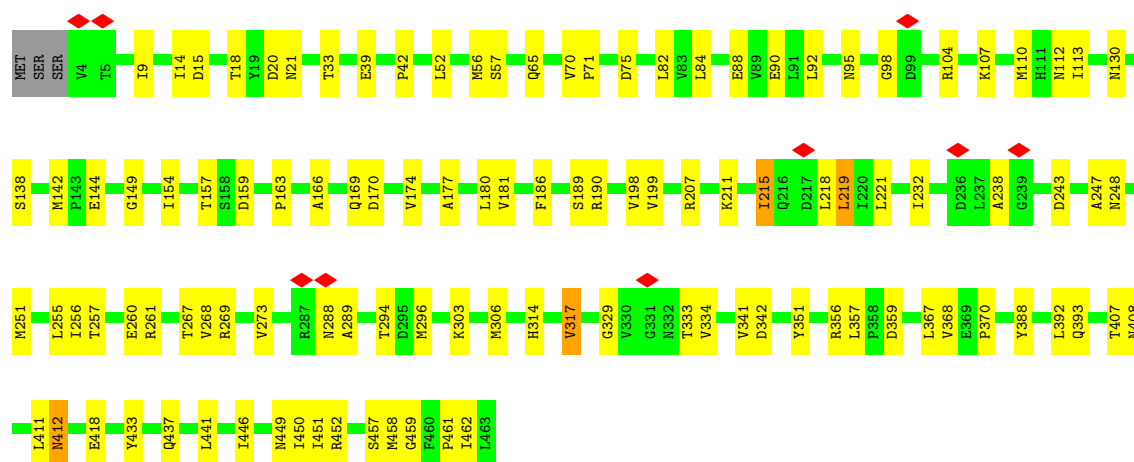


• Molecule 2: Major capsid protein



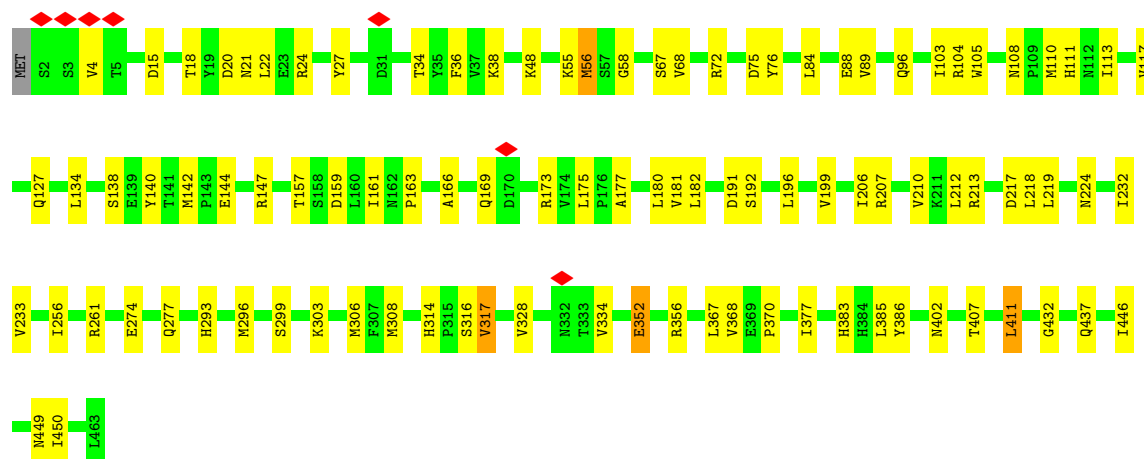


Chain cb:  75% 23% ..



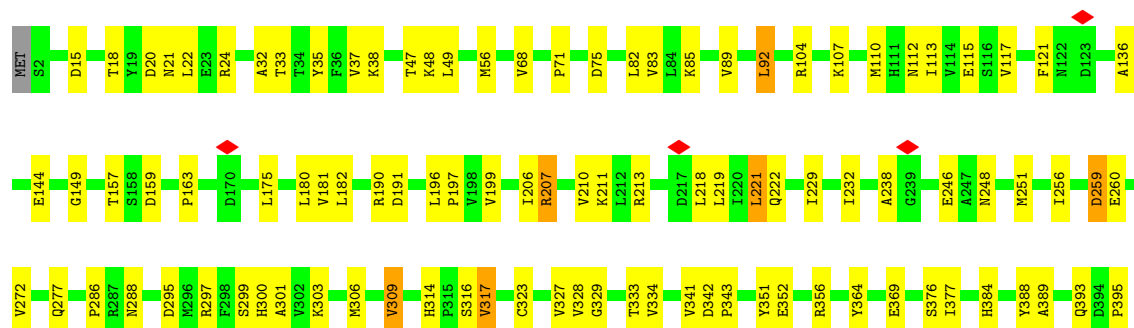
• Molecule 2: Major capsid protein

Chain cc:  79% 20% .



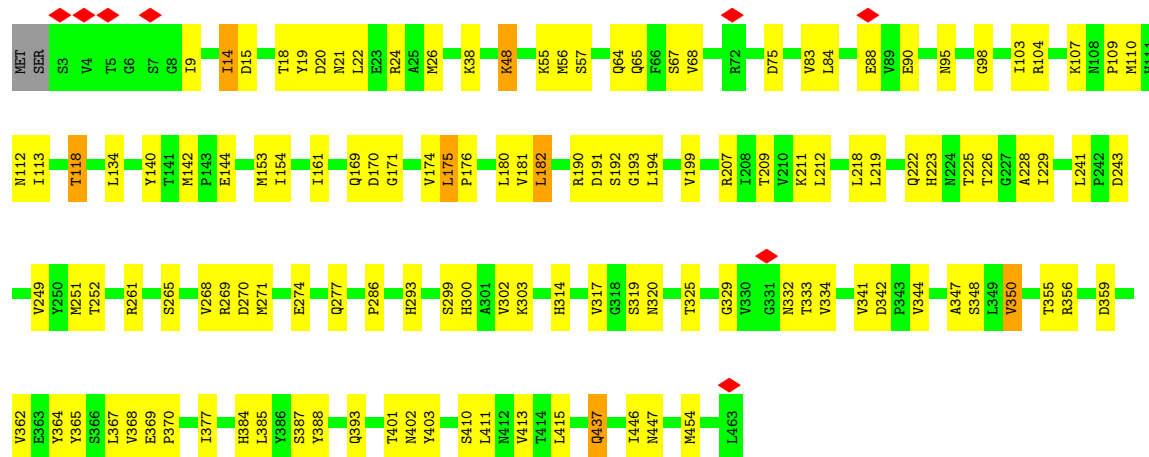
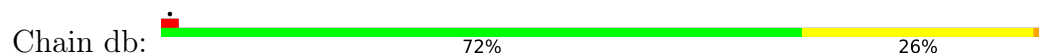
• Molecule 2: Major capsid protein

Chain da:  75% 24% .

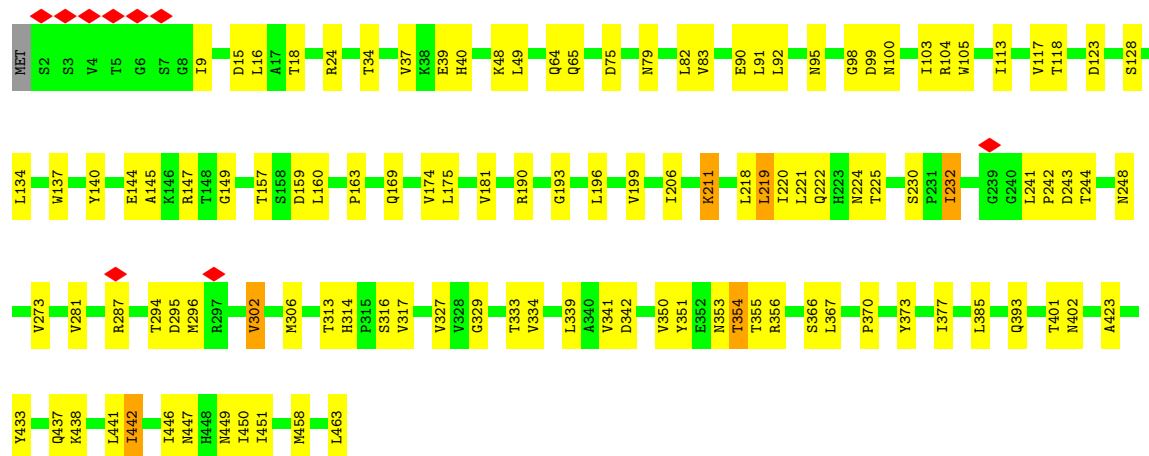
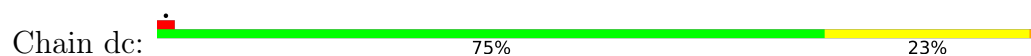




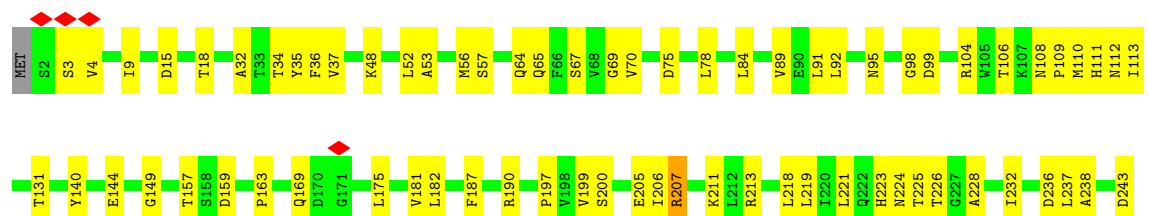
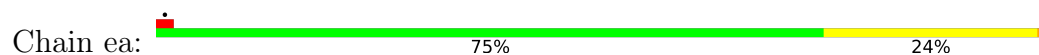
• Molecule 2: Major capsid protein

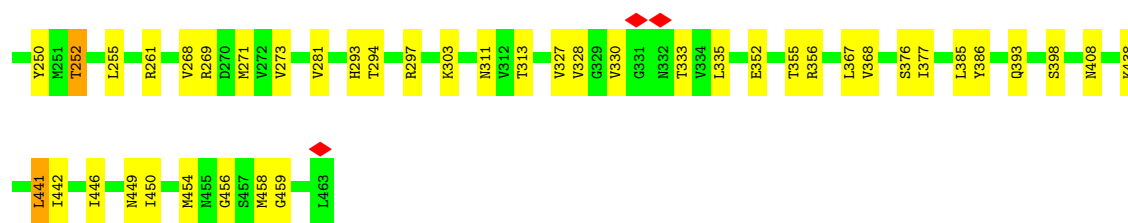


• Molecule 2: Major capsid protein

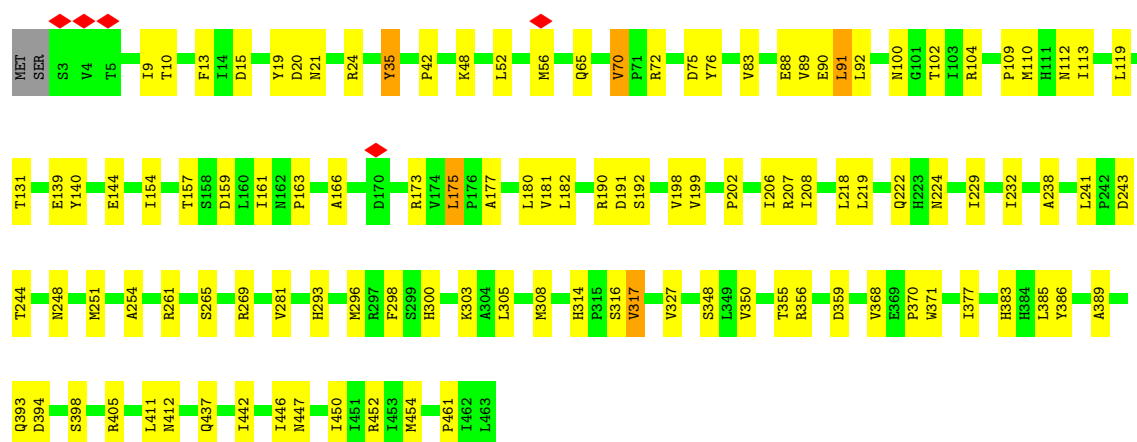
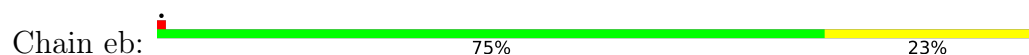


• Molecule 2: Major capsid protein

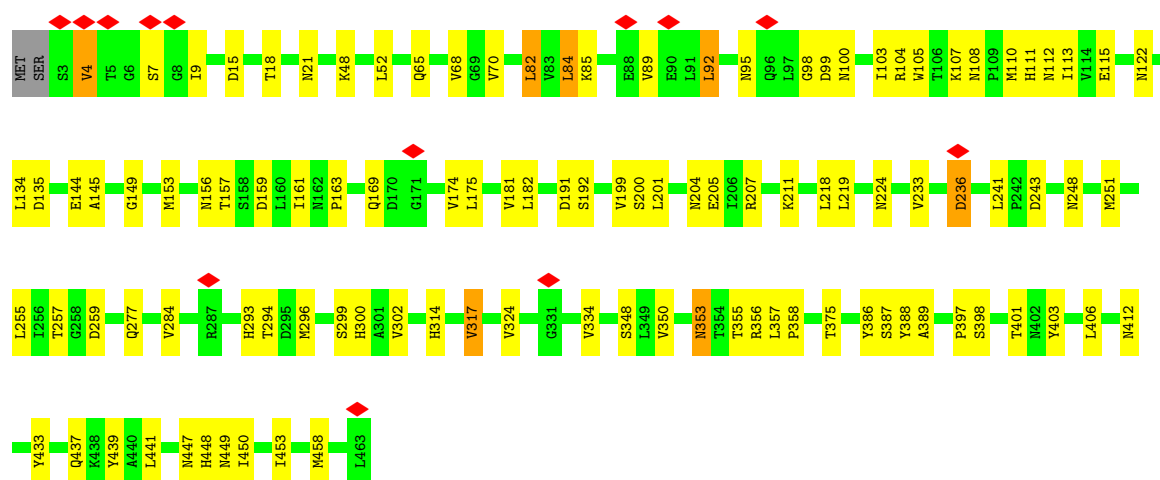
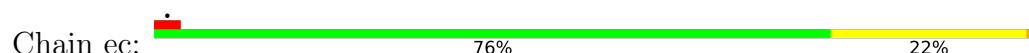




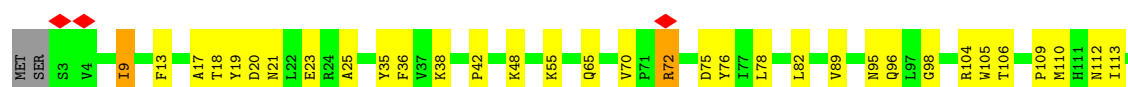
• Molecule 2: Major capsid protein

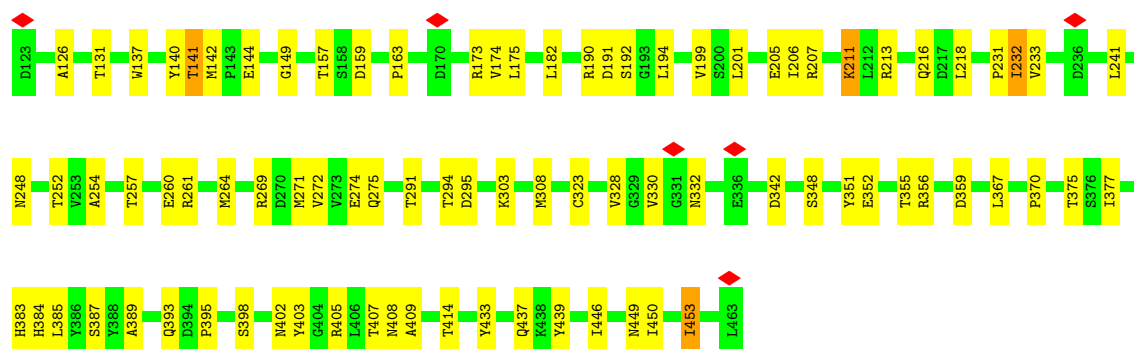


• Molecule 2: Major capsid protein

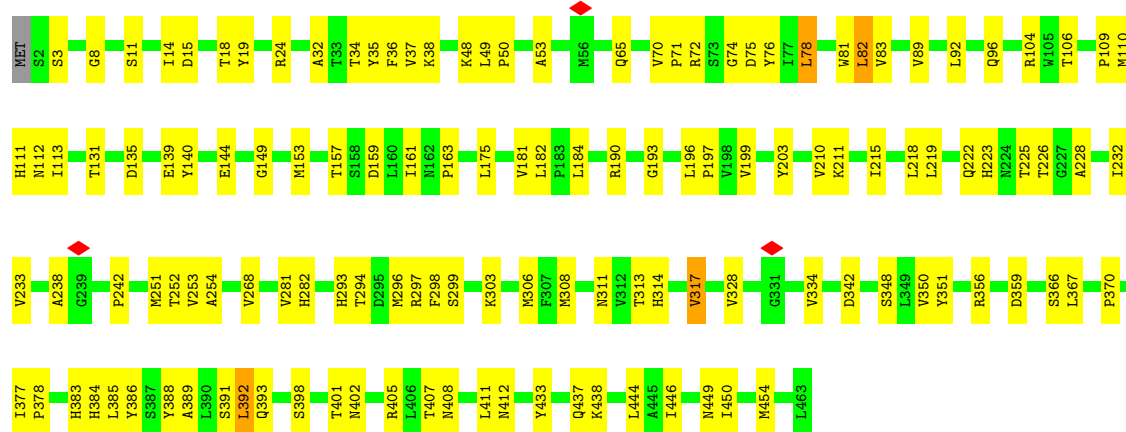


• Molecule 2: Major capsid protein

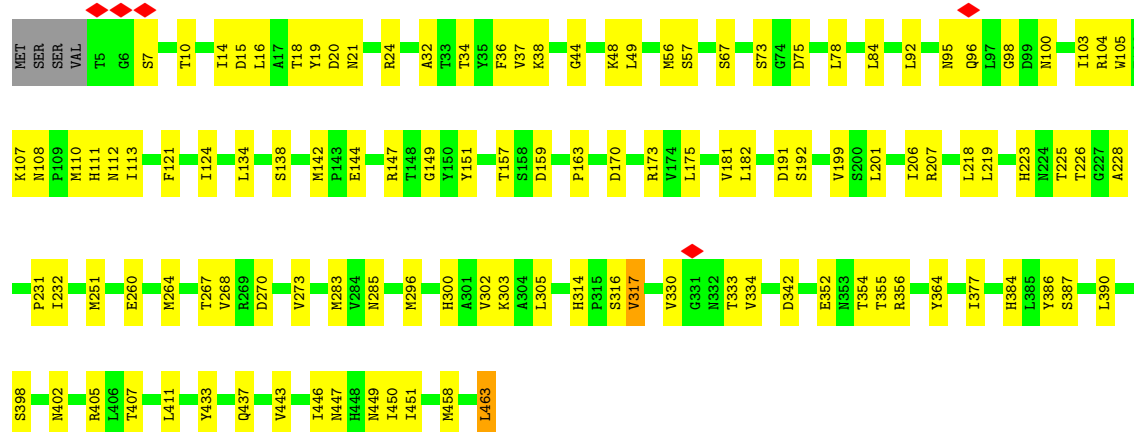




• Molecule 2: Major capsid protein

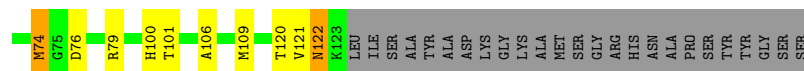
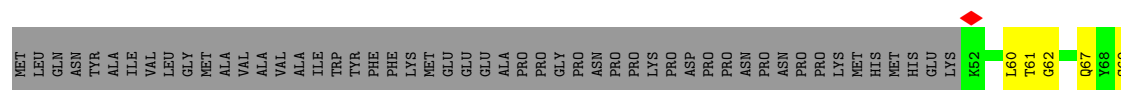


• Molecule 2: Major capsid protein

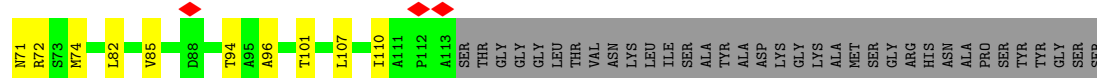
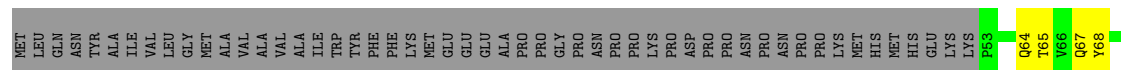
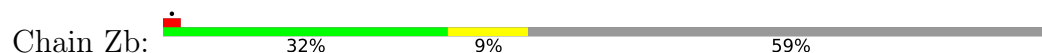


• Molecule 3: Vp20

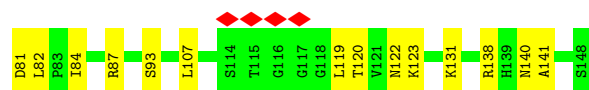
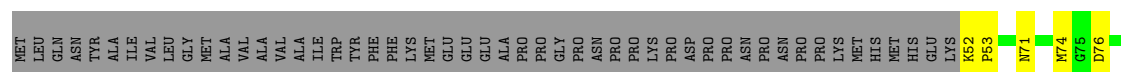




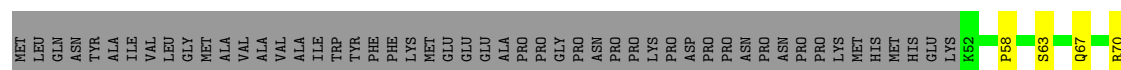
• Molecule 3: Vp20



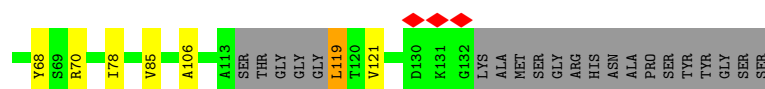
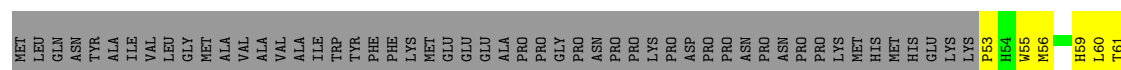
• Molecule 3: Vp20



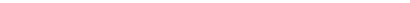
• Molecule 3: Vp20

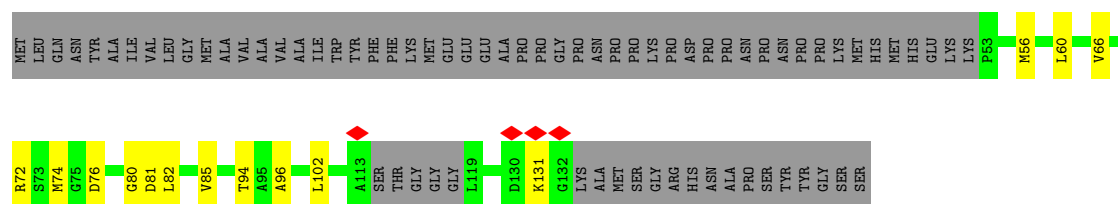


• Molecule 3: Vp20

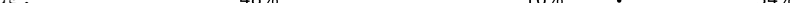


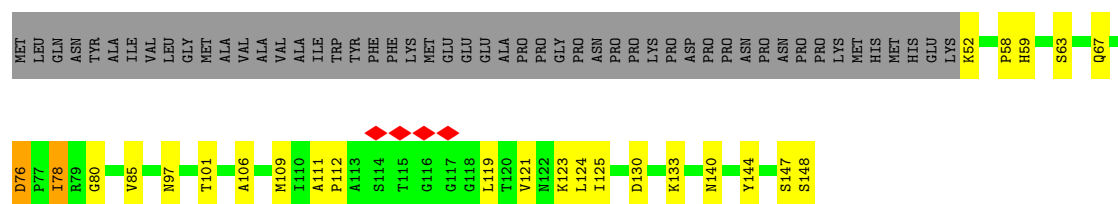
• Molecule 3: Vp20

Chain Zf: 

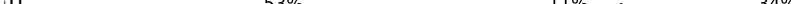


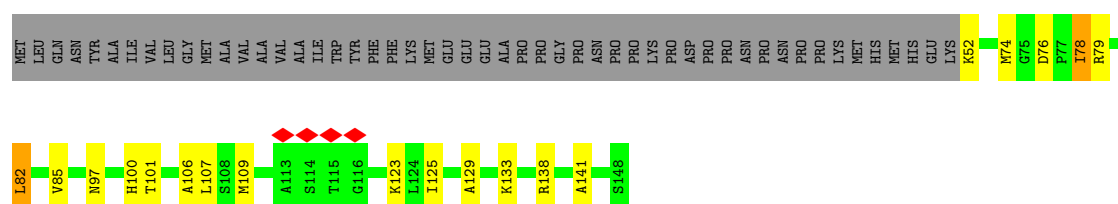
- Molecule 3: Vp20

Chain Zg: 

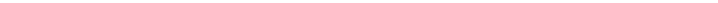


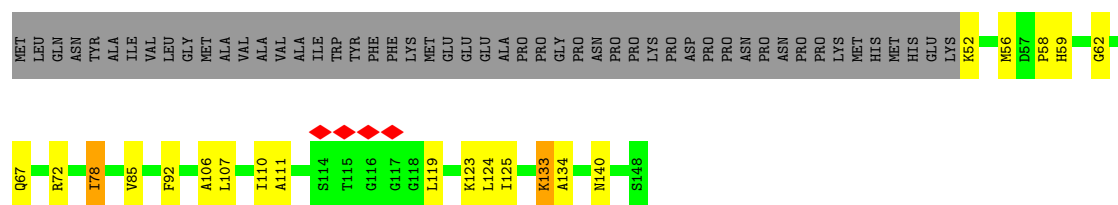
- Molecule 3: Vp20

Chain Zh: 

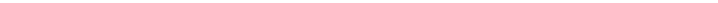


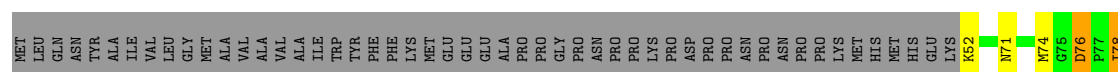
- Molecule 3: Vp20

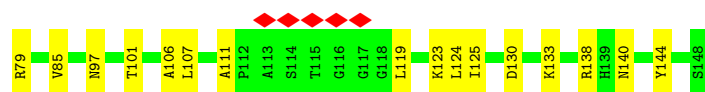
Chain Zi:  51% 13% 34%



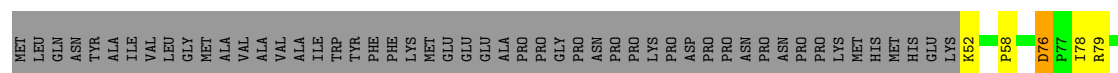
- Molecule 3: Vp20

Chain Zi:  51% 13% 34%

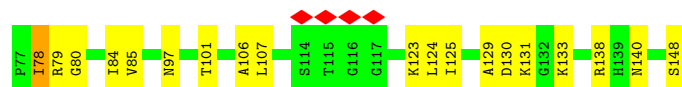
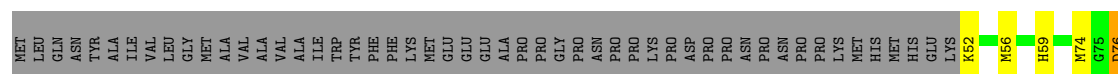




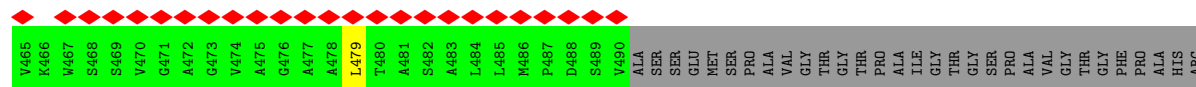
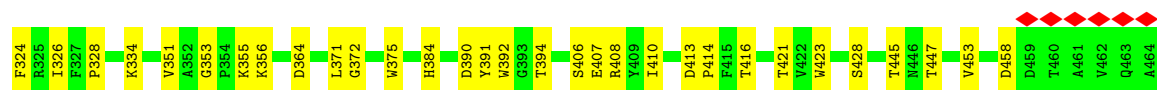
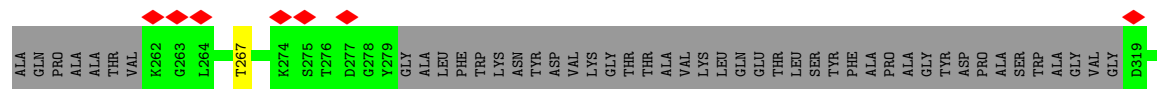
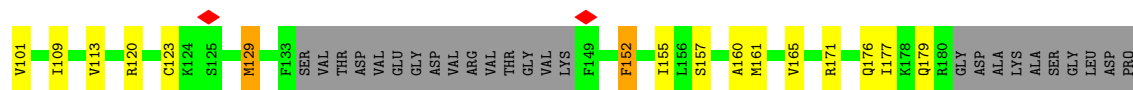
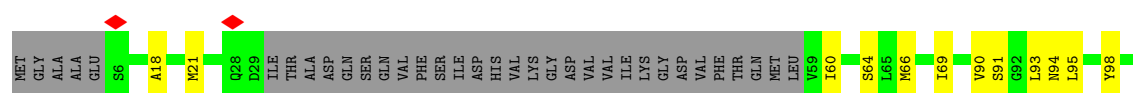
• Molecule 3: Vp20



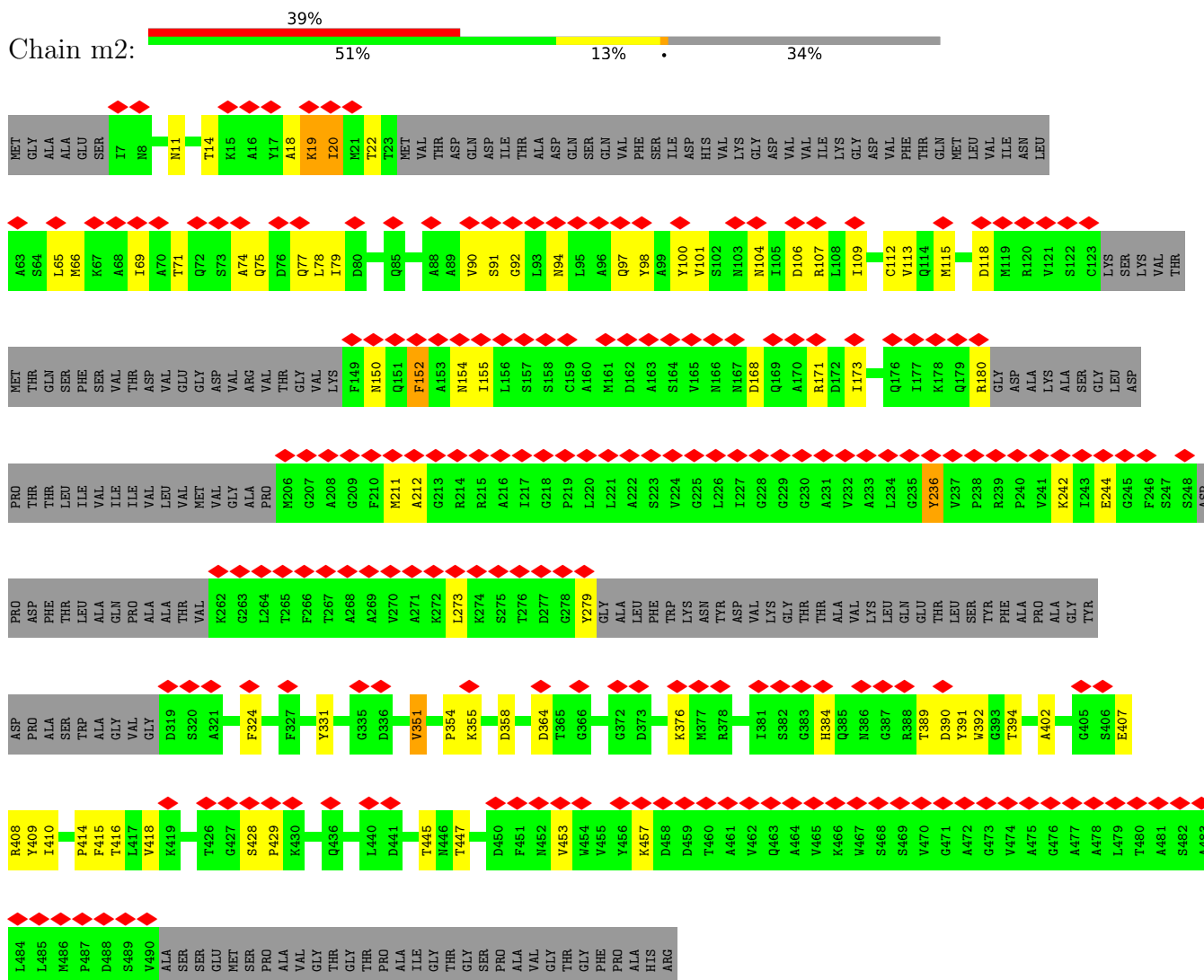
• Molecule 3: Vp20



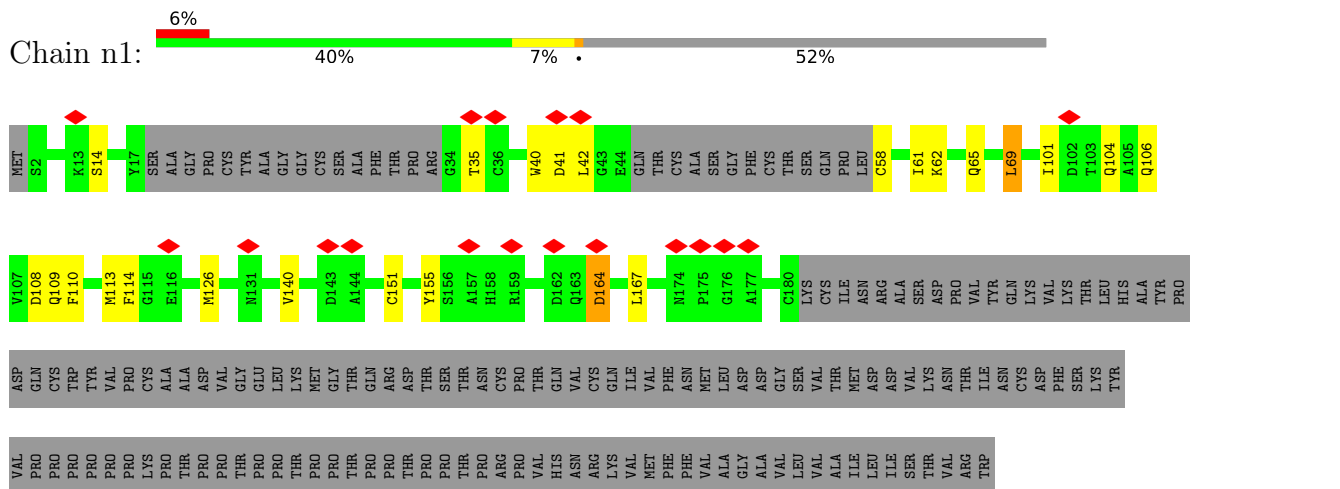
• Molecule 4: Putative myristoylated protein 053R



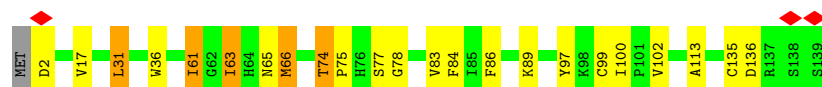
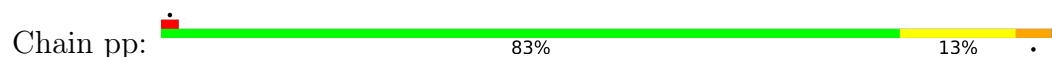
Chain m2:



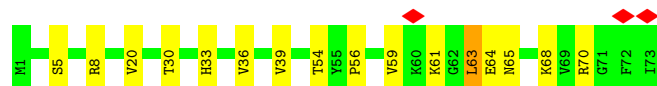
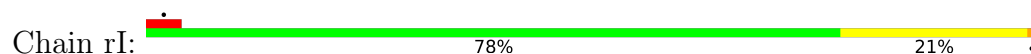
Chain n1:



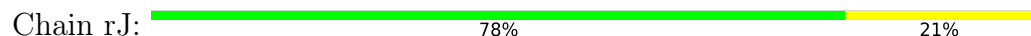
- Molecule 6: Vp31



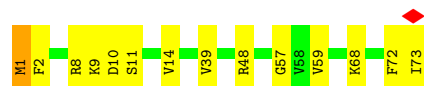
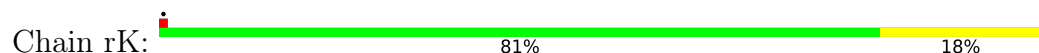
- Molecule 7: Vp76



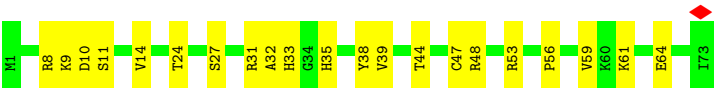
- Molecule 7: Vp76



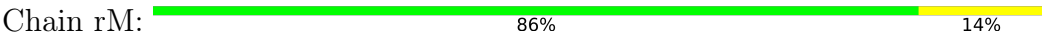
- Molecule 7: Vp76



- Molecule 7: Vp76



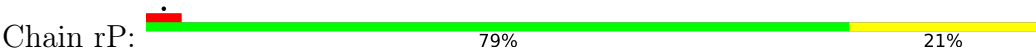
• Molecule 7: Vp76



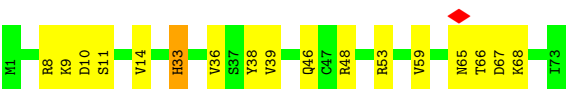
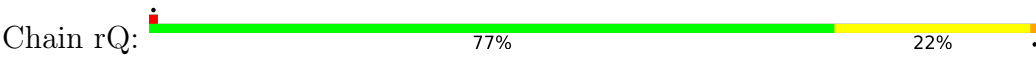
• Molecule 7: Vp76



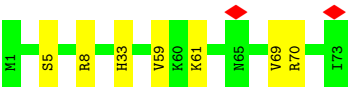
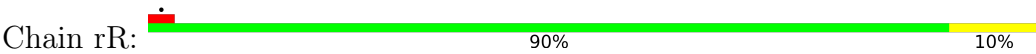
• Molecule 7: Vp76



• Molecule 7: Vp76



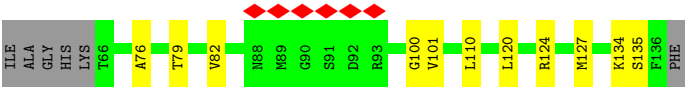
• Molecule 7: Vp76



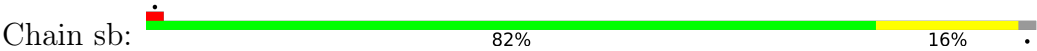
• Molecule 8: Vp10



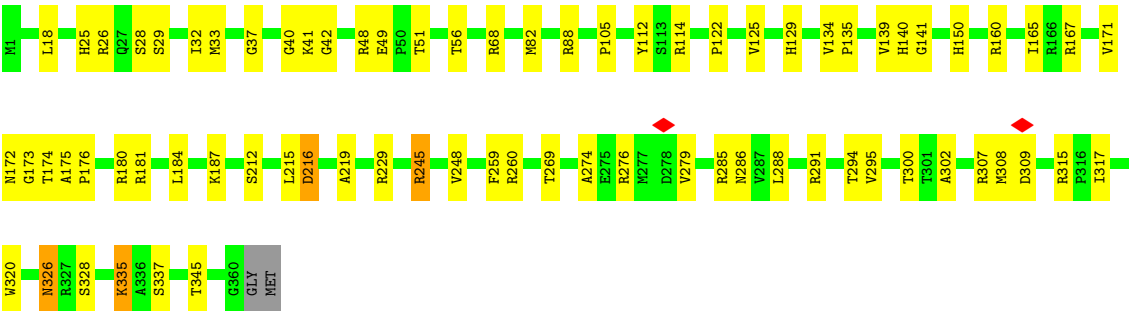
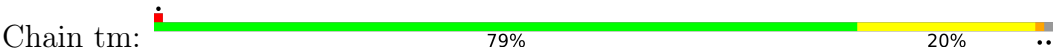
MET	LYS	MET	ASP	THR	ASP	CYS	ARG	HIS	TRP	ILE	VAL	LEU	ALA	SER	VAL	PRO	VAL	LEU	THR	LEU	ALA	PHE	LYS	GLY	GLY	GLY	ALA	LEU	ALA	LEU	ALA	GLY	LEU	LEU	VAL	MET	ALA	ALA	VAL	ALA	ALA	MET	TYR	ARG	ASP	THR	GLU	LYS	LYS	TYR	SER	ALA	ALA	ARG	ALA	PRO	SER	PRO
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• Molecule 9: Vp70



• Molecule 10: Vp74



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	2525	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0019	Depositor
Map size (Å)	1059.1, 1059.1, 1059.1	wwPDB
Map dimensions	1400, 1400, 1400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7565, 0.7565, 0.7565	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A1	0.15	0/178	0.37	0/236
1	A2	0.14	0/255	0.40	0/343
1	B1	0.14	0/178	0.37	0/236
1	B2	0.11	0/152	0.33	0/201
1	C1	0.15	0/178	0.37	0/236
1	C2	0.15	0/163	0.38	0/216
1	D1	0.17	0/178	0.33	0/236
1	D2	0.14	0/195	0.30	0/259
1	E1	0.14	0/178	0.29	0/236
1	E2	0.12	0/190	0.32	0/252
1	F1	0.13	0/178	0.50	1/236 (0.4%)
1	F2	0.15	0/172	0.30	0/228
1	G1	0.12	0/178	0.30	0/236
1	G2	0.13	0/172	0.22	0/228
1	H1	0.13	0/178	0.29	0/236
1	I1	0.14	0/178	0.33	0/236
1	I2	0.15	0/178	0.35	0/236
1	J1	0.14	0/178	0.37	0/236
1	J2	0.17	0/152	0.39	0/201
1	J3	0.13	0/144	0.39	0/190
1	K1	0.13	0/178	0.35	0/236
1	K2	0.15	0/152	0.37	0/201
1	K3	0.10	0/144	0.32	0/190
1	L1	0.11	0/178	0.34	0/236
1	L2	0.15	0/152	0.42	0/201
1	L3	0.11	0/144	0.34	0/190
1	M1	0.09	0/178	0.27	0/236
1	M2	0.13	0/152	0.59	1/201 (0.5%)
1	M3	0.12	0/144	0.36	0/190
1	N1	0.12	0/178	0.31	0/236
1	N2	0.12	0/144	0.33	0/190
1	O1	0.13	0/178	0.33	0/236
1	O2	0.10	0/163	0.27	0/216
1	P1	0.10	0/178	0.26	0/236

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	P2	0.16	0/172	0.48	0/228
1	Q1	0.11	0/178	0.35	0/236
1	Q2	0.14	0/172	0.42	0/228
1	R1	0.10	0/178	0.27	0/236
1	R2	0.15	0/172	0.37	0/228
1	S1	0.13	0/178	0.29	0/236
1	S2	0.12	0/152	0.33	0/201
1	T1	0.10	0/178	0.33	0/236
1	T2	0.10	0/152	0.29	0/201
1	T3	0.10	0/144	0.35	0/190
1	U1	0.13	0/178	0.40	0/236
1	U2	0.13	0/152	0.32	0/201
1	U3	0.12	0/144	0.36	0/190
1	V1	0.12	0/178	0.36	0/236
1	V2	0.10	0/152	0.29	0/201
1	V3	0.12	0/149	0.44	0/197
1	a3	0.15	0/186	0.26	0/247
1	b1	0.14	0/186	0.25	0/247
1	b2	0.13	0/186	0.34	0/247
1	c2	0.15	0/178	0.30	0/236
1	c3	0.11	0/167	0.25	0/221
1	d1	0.13	0/178	0.26	0/236
1	d2	0.16	0/218	0.34	0/291
1	e1	0.15	0/186	0.34	0/246
1	f1	0.12	0/155	0.23	0/205
1	f3	0.13	0/178	0.33	0/236
2	Aa	0.20	0/3583	0.28	0/4902
2	Ab	0.19	0/3589	0.28	0/4910
2	Ac	0.20	0/3589	0.28	0/4910
2	Ba	0.22	0/3589	0.29	0/4910
2	Bb	0.20	0/3589	0.29	0/4910
2	Bc	0.19	0/3589	0.29	0/4910
2	Ca	0.21	0/3583	0.29	0/4902
2	Cb	0.20	0/3589	0.29	0/4910
2	Cc	0.21	0/3583	0.29	0/4902
2	Da	0.20	0/3589	0.29	0/4910
2	Db	0.21	0/3589	0.29	0/4910
2	Dc	0.20	0/3589	0.29	0/4910
2	Ea	0.20	0/3589	0.30	0/4910
2	Eb	0.20	0/3577	0.29	0/4894
2	Ec	0.20	0/3589	0.29	0/4910
2	Fa	0.20	0/3589	0.30	0/4910
2	Fb	0.20	0/3589	0.29	0/4910

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Fc	0.19	0/3583	0.28	0/4902
2	Ga	0.19	0/3583	0.28	0/4902
2	Gb	0.19	0/3577	0.28	0/4894
2	Gc	0.19	0/3549	0.28	0/4856
2	Ha	0.19	0/3589	0.28	0/4910
2	Hb	0.20	0/3589	0.29	0/4910
2	Hc	0.19	0/3589	0.28	0/4910
2	Ia	0.20	0/3589	0.29	0/4910
2	Ib	0.19	0/3583	0.28	0/4902
2	Ic	0.21	0/3589	0.29	0/4910
2	Ja	0.22	0/3583	0.30	0/4902
2	Jb	0.22	0/3589	0.29	0/4910
2	Jc	0.22	0/3589	0.30	0/4910
2	Ka	0.20	0/3583	0.29	0/4902
2	Kb	0.21	0/3583	0.30	0/4902
2	Kc	0.21	0/3589	0.30	0/4910
2	La	0.19	0/3589	0.29	0/4910
2	Lb	0.20	0/3589	0.29	0/4910
2	Lc	0.19	0/3583	0.30	0/4902
2	Ma	0.19	0/3589	0.28	0/4910
2	Mb	0.19	0/3583	0.29	0/4902
2	Mc	0.19	0/3583	0.29	0/4902
2	Na	0.18	0/3583	0.27	0/4902
2	Nb	0.19	0/3589	0.28	0/4910
2	Nc	0.19	0/3589	0.29	0/4910
2	Oa	0.21	0/3589	0.30	0/4910
2	Ob	0.19	0/3589	0.29	0/4910
2	Oc	0.20	0/3589	0.28	0/4910
2	Pa	0.21	0/3583	0.28	0/4902
2	Pb	0.21	0/3583	0.29	0/4902
2	Pc	0.20	0/3589	0.29	0/4910
2	Qa	0.20	0/3589	0.30	0/4910
2	Qb	0.20	0/3589	0.29	0/4910
2	Qc	0.20	0/3583	0.29	0/4902
2	Ra	0.20	0/3589	0.29	0/4910
2	Rb	0.20	0/3583	0.30	0/4902
2	Rc	0.20	0/3583	0.30	0/4902
2	Sa	0.18	0/3589	0.28	0/4910
2	Sb	0.19	0/3589	0.30	0/4910
2	Sc	0.18	0/3589	0.28	0/4910
2	Ta	0.19	0/3583	0.30	0/4902
2	Tb	0.19	0/3583	0.29	0/4902
2	Tc	0.19	0/3589	0.29	0/4910

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Ua	0.20	0/3589	0.28	0/4910
2	Ub	0.20	0/3589	0.29	0/4910
2	Uc	0.20	0/3589	0.29	0/4910
2	Va	0.19	0/3589	0.29	0/4910
2	Vb	0.19	0/3589	0.29	0/4910
2	Vc	0.18	0/3589	0.29	0/4910
2	aa	0.21	0/3589	0.29	0/4910
2	ab	0.22	0/3577	0.30	0/4894
2	ac	0.21	0/3589	0.29	0/4910
2	ba	0.21	0/3589	0.28	0/4910
2	bb	0.21	0/3582	0.32	0/4902
2	bc	0.21	0/3589	0.30	0/4910
2	ca	0.22	0/3589	0.29	0/4910
2	cb	0.21	0/3577	0.29	0/4894
2	cc	0.21	0/3589	0.29	0/4910
2	da	0.20	0/3589	0.29	0/4910
2	db	0.21	0/3583	0.31	0/4902
2	dc	0.21	0/3589	0.31	0/4910
2	ea	0.21	0/3589	0.29	0/4910
2	eb	0.21	0/3583	0.29	0/4902
2	ec	0.20	0/3583	0.30	0/4902
2	fa	0.18	0/3583	0.29	0/4902
2	fb	0.19	0/3589	0.29	0/4910
2	fc	0.19	0/3570	0.29	0/4884
3	Za	0.17	0/554	0.30	0/756
3	Zb	0.18	0/481	0.27	0/658
3	Zc	0.15	0/744	0.25	0/1010
3	Zd	0.16	0/744	0.27	0/1010
3	Ze	0.15	0/585	0.25	0/797
3	Zf	0.16	0/585	0.27	0/797
3	Zg	0.17	0/744	0.27	0/1010
3	Zh	0.18	0/744	0.27	0/1010
3	Zi	0.16	0/744	0.27	0/1010
3	Zj	0.16	0/744	0.26	0/1010
3	Zk	0.17	0/744	0.27	0/1010
3	Zl	0.16	0/744	0.26	0/1010
4	m1	0.14	0/2780	0.27	0/3776
4	m2	0.11	0/2608	0.24	0/3544
5	n1	0.12	0/1160	0.26	0/1564
5	n2	0.12	0/1178	0.29	0/1590
6	pp	0.21	0/1093	0.30	0/1487
7	rI	0.18	0/573	0.29	0/774
7	rJ	0.19	0/573	0.28	0/774

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	rK	0.16	0/573	0.21	0/774
7	rL	0.18	0/573	0.27	0/774
7	rM	0.15	0/573	0.27	0/774
7	rO	0.28	1/573 (0.2%)	0.25	0/774
7	rP	0.16	0/573	0.23	0/774
7	rQ	0.17	0/573	0.23	0/774
7	rR	0.13	0/573	0.24	0/774
8	sa	0.18	0/563	0.29	0/763
9	sb	0.17	0/946	0.30	0/1284
10	tm	0.22	0/2761	0.30	0/3755
All	All	0.20	1/337884 (0.0%)	0.29	2/461515 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	rO	70	ARG	C-N	-5.70	1.30	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M2	17	ILE	N-CA-C	-6.59	106.37	112.96
1	F1	17	ILE	N-CA-C	-5.42	107.53	112.96

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	175	0	181	4	0
1	A2	249	0	251	8	0
1	B1	175	0	181	6	0
1	B2	150	0	161	5	0
1	C1	175	0	181	2	0
1	C2	160	0	168	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D1	175	0	181	4	0
1	D2	192	0	202	5	0
1	E1	175	0	181	8	0
1	E2	187	0	197	4	0
1	F1	175	0	181	8	0
1	F2	169	0	176	5	0
1	G1	175	0	181	6	0
1	G2	169	0	176	4	0
1	H1	175	0	181	4	0
1	I1	175	0	181	5	0
1	I2	175	0	181	5	0
1	J1	175	0	181	11	0
1	J2	150	0	161	8	0
1	J3	142	0	150	6	0
1	K1	175	0	181	4	0
1	K2	150	0	161	5	0
1	K3	142	0	150	5	0
1	L1	175	0	181	6	0
1	L2	150	0	161	7	0
1	L3	142	0	150	6	0
1	M1	175	0	181	4	0
1	M2	150	0	161	6	0
1	M3	142	0	150	3	0
1	N1	175	0	181	3	0
1	N2	142	0	150	5	0
1	O1	175	0	181	8	0
1	O2	160	0	168	4	0
1	P1	175	0	181	4	0
1	P2	169	0	176	6	0
1	Q1	175	0	181	7	0
1	Q2	169	0	176	7	0
1	R1	175	0	181	4	0
1	R2	169	0	176	8	0
1	S1	175	0	181	5	0
1	S2	150	0	161	3	0
1	T1	175	0	181	2	0
1	T2	150	0	161	1	0
1	T3	142	0	150	3	0
1	U1	175	0	181	5	0
1	U2	150	0	161	3	0
1	U3	142	0	150	3	0
1	V1	175	0	181	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V2	150	0	161	6	0
1	V3	147	0	152	4	0
1	a3	183	0	192	6	0
1	b1	183	0	192	5	0
1	b2	183	0	192	9	0
1	c2	175	0	181	7	0
1	c3	164	0	171	6	0
1	d1	175	0	181	3	0
1	d2	214	0	219	11	0
1	e1	183	0	193	3	0
1	f1	152	0	157	0	0
1	f3	175	0	181	4	0
2	Aa	3499	0	3443	73	0
2	Ab	3505	0	3448	88	0
2	Ac	3505	0	3448	70	0
2	Ba	3505	0	3448	64	0
2	Bb	3505	0	3448	71	0
2	Bc	3505	0	3448	63	0
2	Ca	3499	0	3443	64	0
2	Cb	3505	0	3448	74	0
2	Cc	3499	0	3443	68	0
2	Da	3505	0	3448	78	0
2	Db	3505	0	3448	71	0
2	Dc	3505	0	3448	75	0
2	Ea	3505	0	3448	57	0
2	Eb	3493	0	3438	73	0
2	Ec	3505	0	3448	57	0
2	Fa	3505	0	3448	60	0
2	Fb	3505	0	3448	61	0
2	Fc	3499	0	3443	72	0
2	Ga	3499	0	3443	61	0
2	Gb	3493	0	3438	62	0
2	Gc	3465	0	3411	64	0
2	Ha	3505	0	3448	72	0
2	Hb	3505	0	3448	72	0
2	Hc	3505	0	3448	66	0
2	Ia	3505	0	3448	74	0
2	Ib	3499	0	3443	65	0
2	Ic	3505	0	3448	76	0
2	Ja	3499	0	3443	77	0
2	Jb	3505	0	3448	72	0
2	Jc	3505	0	3448	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Ka	3499	0	3443	65	0
2	Kb	3499	0	3443	70	0
2	Kc	3505	0	3448	75	0
2	La	3505	0	3448	64	0
2	Lb	3505	0	3448	62	0
2	Lc	3499	0	3443	78	0
2	Ma	3505	0	3448	76	0
2	Mb	3499	0	3443	73	0
2	Mc	3499	0	3443	67	0
2	Na	3499	0	3443	68	0
2	Nb	3505	0	3448	70	0
2	Nc	3505	0	3448	75	0
2	Oa	3505	0	3448	66	0
2	Ob	3505	0	3448	72	0
2	Oc	3505	0	3448	76	0
2	Pa	3499	0	3443	71	0
2	Pb	3499	0	3443	80	0
2	Pc	3505	0	3448	73	0
2	Qa	3505	0	3448	66	0
2	Qb	3505	0	3448	75	0
2	Qc	3499	0	3443	65	0
2	Ra	3505	0	3448	62	0
2	Rb	3499	0	3443	69	0
2	Rc	3499	0	3443	71	0
2	Sa	3505	0	3448	72	0
2	Sb	3505	0	3448	74	0
2	Sc	3505	0	3448	74	0
2	Ta	3499	0	3443	69	0
2	Tb	3499	0	3443	72	0
2	Tc	3505	0	3448	60	0
2	Ua	3505	0	3448	65	0
2	Ub	3505	0	3448	61	0
2	Uc	3505	0	3448	63	0
2	Va	3505	0	3448	65	0
2	Vb	3505	0	3448	74	0
2	Vc	3505	0	3448	56	0
2	aa	3505	0	3448	68	0
2	ab	3493	0	3438	62	0
2	ac	3505	0	3448	65	0
2	ba	3505	0	3448	73	0
2	bb	3498	0	3443	83	0
2	bc	3505	0	3448	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	ca	3505	0	3448	71	0
2	cb	3493	0	3438	72	0
2	cc	3505	0	3448	68	0
2	da	3505	0	3448	76	0
2	db	3499	0	3443	82	0
2	dc	3505	0	3448	70	0
2	ea	3505	0	3448	74	0
2	eb	3499	0	3443	70	0
2	ec	3499	0	3443	72	0
2	fa	3499	0	3443	82	0
2	fb	3505	0	3448	95	0
2	fc	3486	0	3429	74	0
3	Za	538	0	519	10	0
3	Zb	465	0	440	6	0
3	Zc	723	0	694	14	0
3	Zd	723	0	694	14	0
3	Ze	569	0	551	10	0
3	Zf	569	0	551	8	0
3	Zg	723	0	694	17	0
3	Zh	723	0	694	15	0
3	Zi	723	0	694	14	0
3	Zj	723	0	694	12	0
3	Zk	723	0	694	10	0
3	Zl	723	0	694	18	0
4	m1	2729	0	2707	39	0
4	m2	2558	0	2535	39	0
5	n1	1139	0	1074	14	0
5	n2	1156	0	1098	20	0
6	pp	1062	0	1051	14	0
7	rI	560	0	561	17	0
7	rJ	560	0	561	10	0
7	rK	560	0	561	12	0
7	rL	560	0	561	17	0
7	rM	560	0	561	6	0
7	rO	560	0	561	16	0
7	rP	560	0	561	13	0
7	rQ	560	0	561	16	0
7	rR	560	0	561	6	0
8	sa	547	0	521	10	0
9	sb	921	0	903	15	0
10	tm	2687	0	2608	66	0
All	All	330022	0	325109	5553	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 8.

The worst 5 of 5553 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)
2:Cb:2:SER:N	2:Cb:5:THR:HG1	1.56	1.02
2:Ja:352:GLU:HB3	2:Kb:297:ARG:HE	1.38	0.86
5:n2:159:ARG:HA	5:n2:163:GLN:HG2	1.59	0.85
1:d2:13:LYS:HE2	1:d2:16:ASP:HB3	1.62	0.82
2:Cb:72:ARG:NH2	2:Cb:201:LEU:O	2.14	0.81

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	A1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	A2	31/106 (29%)	25 (81%)	6 (19%)	0	100	100
1	B1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	B2	16/106 (15%)	12 (75%)	4 (25%)	0	100	100
1	C1	20/106 (19%)	18 (90%)	2 (10%)	0	100	100
1	C2	17/106 (16%)	15 (88%)	2 (12%)	0	100	100
1	D1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	D2	23/106 (22%)	19 (83%)	4 (17%)	0	100	100
1	E1	20/106 (19%)	18 (90%)	2 (10%)	0	100	100
1	E2	22/106 (21%)	18 (82%)	4 (18%)	0	100	100
1	F1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	F2	19/106 (18%)	15 (79%)	4 (21%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	G2	19/106 (18%)	16 (84%)	3 (16%)	0	100	100
1	H1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	I1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	I2	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	J1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	J2	16/106 (15%)	12 (75%)	4 (25%)	0	100	100
1	J3	15/106 (14%)	12 (80%)	3 (20%)	0	100	100
1	K1	20/106 (19%)	15 (75%)	5 (25%)	0	100	100
1	K2	16/106 (15%)	12 (75%)	4 (25%)	0	100	100
1	K3	15/106 (14%)	12 (80%)	3 (20%)	0	100	100
1	L1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	L2	16/106 (15%)	13 (81%)	3 (19%)	0	100	100
1	L3	15/106 (14%)	11 (73%)	4 (27%)	0	100	100
1	M1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	M2	16/106 (15%)	13 (81%)	3 (19%)	0	100	100
1	M3	15/106 (14%)	10 (67%)	5 (33%)	0	100	100
1	N1	20/106 (19%)	18 (90%)	2 (10%)	0	100	100
1	N2	15/106 (14%)	14 (93%)	1 (7%)	0	100	100
1	O1	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	O2	17/106 (16%)	14 (82%)	3 (18%)	0	100	100
1	P1	20/106 (19%)	18 (90%)	2 (10%)	0	100	100
1	P2	19/106 (18%)	16 (84%)	3 (16%)	0	100	100
1	Q1	20/106 (19%)	18 (90%)	2 (10%)	0	100	100
1	Q2	19/106 (18%)	15 (79%)	4 (21%)	0	100	100
1	R1	20/106 (19%)	20 (100%)	0	0	100	100
1	R2	19/106 (18%)	14 (74%)	5 (26%)	0	100	100
1	S1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	S2	16/106 (15%)	13 (81%)	3 (19%)	0	100	100
1	T1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	T2	16/106 (15%)	14 (88%)	2 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T3	15/106 (14%)	11 (73%)	4 (27%)	0	100	100
1	U1	20/106 (19%)	15 (75%)	5 (25%)	0	100	100
1	U2	16/106 (15%)	12 (75%)	4 (25%)	0	100	100
1	U3	15/106 (14%)	9 (60%)	6 (40%)	0	100	100
1	V1	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
1	V2	16/106 (15%)	13 (81%)	3 (19%)	0	100	100
1	V3	16/106 (15%)	14 (88%)	2 (12%)	0	100	100
1	a3	21/106 (20%)	20 (95%)	1 (5%)	0	100	100
1	b1	21/106 (20%)	18 (86%)	3 (14%)	0	100	100
1	b2	21/106 (20%)	18 (86%)	3 (14%)	0	100	100
1	c2	20/106 (19%)	19 (95%)	1 (5%)	0	100	100
1	c3	18/106 (17%)	17 (94%)	1 (6%)	0	100	100
1	d1	20/106 (19%)	16 (80%)	4 (20%)	0	100	100
1	d2	25/106 (24%)	24 (96%)	1 (4%)	0	100	100
1	e1	21/106 (20%)	18 (86%)	3 (14%)	0	100	100
1	f1	16/106 (15%)	15 (94%)	1 (6%)	0	100	100
1	f3	20/106 (19%)	17 (85%)	3 (15%)	0	100	100
2	Aa	459/463 (99%)	444 (97%)	15 (3%)	0	100	100
2	Ab	460/463 (99%)	439 (95%)	21 (5%)	0	100	100
2	Ac	460/463 (99%)	448 (97%)	12 (3%)	0	100	100
2	Ba	460/463 (99%)	444 (96%)	16 (4%)	0	100	100
2	Bb	460/463 (99%)	439 (95%)	21 (5%)	0	100	100
2	Bc	460/463 (99%)	438 (95%)	22 (5%)	0	100	100
2	Ca	459/463 (99%)	442 (96%)	17 (4%)	0	100	100
2	Cb	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Cc	459/463 (99%)	442 (96%)	17 (4%)	0	100	100
2	Da	460/463 (99%)	438 (95%)	21 (5%)	1 (0%)	43	76
2	Db	460/463 (99%)	446 (97%)	14 (3%)	0	100	100
2	Dc	460/463 (99%)	442 (96%)	17 (4%)	1 (0%)	43	76
2	Ea	460/463 (99%)	445 (97%)	15 (3%)	0	100	100
2	Eb	458/463 (99%)	439 (96%)	18 (4%)	1 (0%)	43	76

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ec	460/463 (99%)	442 (96%)	17 (4%)	1 (0%)	43	76
2	Fa	460/463 (99%)	444 (96%)	16 (4%)	0	100	100
2	Fb	460/463 (99%)	441 (96%)	18 (4%)	1 (0%)	43	76
2	Fc	459/463 (99%)	444 (97%)	14 (3%)	1 (0%)	43	76
2	Ga	459/463 (99%)	445 (97%)	14 (3%)	0	100	100
2	Gb	458/463 (99%)	444 (97%)	14 (3%)	0	100	100
2	Gc	453/463 (98%)	442 (98%)	11 (2%)	0	100	100
2	Ha	460/463 (99%)	447 (97%)	13 (3%)	0	100	100
2	Hb	460/463 (99%)	442 (96%)	18 (4%)	0	100	100
2	Hc	460/463 (99%)	444 (96%)	16 (4%)	0	100	100
2	Ia	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Ib	459/463 (99%)	441 (96%)	18 (4%)	0	100	100
2	Ic	460/463 (99%)	440 (96%)	20 (4%)	0	100	100
2	Ja	459/463 (99%)	446 (97%)	13 (3%)	0	100	100
2	Jb	460/463 (99%)	442 (96%)	17 (4%)	1 (0%)	43	76
2	Jc	460/463 (99%)	441 (96%)	19 (4%)	0	100	100
2	Ka	459/463 (99%)	443 (96%)	16 (4%)	0	100	100
2	Kb	459/463 (99%)	444 (97%)	15 (3%)	0	100	100
2	Kc	460/463 (99%)	446 (97%)	13 (3%)	1 (0%)	43	76
2	La	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Lb	460/463 (99%)	437 (95%)	23 (5%)	0	100	100
2	Lc	459/463 (99%)	438 (95%)	21 (5%)	0	100	100
2	Ma	460/463 (99%)	436 (95%)	24 (5%)	0	100	100
2	Mb	459/463 (99%)	444 (97%)	15 (3%)	0	100	100
2	Mc	459/463 (99%)	443 (96%)	16 (4%)	0	100	100
2	Na	459/463 (99%)	439 (96%)	19 (4%)	1 (0%)	43	76
2	Nb	460/463 (99%)	445 (97%)	14 (3%)	1 (0%)	43	76
2	Nc	460/463 (99%)	442 (96%)	18 (4%)	0	100	100
2	Oa	460/463 (99%)	449 (98%)	11 (2%)	0	100	100
2	Ob	460/463 (99%)	442 (96%)	18 (4%)	0	100	100
2	Oc	460/463 (99%)	442 (96%)	18 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Pa	459/463 (99%)	442 (96%)	17 (4%)	0	100	100
2	Pb	459/463 (99%)	441 (96%)	17 (4%)	1 (0%)	43	76
2	Pc	460/463 (99%)	440 (96%)	20 (4%)	0	100	100
2	Qa	460/463 (99%)	441 (96%)	19 (4%)	0	100	100
2	Qb	460/463 (99%)	442 (96%)	18 (4%)	0	100	100
2	Qc	459/463 (99%)	440 (96%)	19 (4%)	0	100	100
2	Ra	460/463 (99%)	446 (97%)	14 (3%)	0	100	100
2	Rb	459/463 (99%)	439 (96%)	20 (4%)	0	100	100
2	Rc	459/463 (99%)	437 (95%)	21 (5%)	1 (0%)	43	76
2	Sa	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Sb	460/463 (99%)	447 (97%)	13 (3%)	0	100	100
2	Sc	460/463 (99%)	445 (97%)	15 (3%)	0	100	100
2	Ta	459/463 (99%)	439 (96%)	19 (4%)	1 (0%)	43	76
2	Tb	459/463 (99%)	444 (97%)	15 (3%)	0	100	100
2	Tc	460/463 (99%)	440 (96%)	20 (4%)	0	100	100
2	Ua	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Ub	460/463 (99%)	442 (96%)	17 (4%)	1 (0%)	43	76
2	Uc	460/463 (99%)	437 (95%)	23 (5%)	0	100	100
2	Va	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	Vb	460/463 (99%)	440 (96%)	20 (4%)	0	100	100
2	Vc	460/463 (99%)	440 (96%)	19 (4%)	1 (0%)	43	76
2	aa	460/463 (99%)	443 (96%)	17 (4%)	0	100	100
2	ab	458/463 (99%)	441 (96%)	17 (4%)	0	100	100
2	ac	460/463 (99%)	445 (97%)	15 (3%)	0	100	100
2	ba	460/463 (99%)	444 (96%)	16 (4%)	0	100	100
2	bb	459/463 (99%)	443 (96%)	16 (4%)	0	100	100
2	bc	460/463 (99%)	444 (96%)	16 (4%)	0	100	100
2	ca	460/463 (99%)	445 (97%)	15 (3%)	0	100	100
2	cb	458/463 (99%)	444 (97%)	14 (3%)	0	100	100
2	cc	460/463 (99%)	442 (96%)	17 (4%)	1 (0%)	43	76
2	da	460/463 (99%)	447 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	db	459/463 (99%)	438 (95%)	21 (5%)	0	100	100
2	dc	460/463 (99%)	441 (96%)	19 (4%)	0	100	100
2	ea	460/463 (99%)	441 (96%)	19 (4%)	0	100	100
2	eb	459/463 (99%)	450 (98%)	9 (2%)	0	100	100
2	ec	459/463 (99%)	441 (96%)	18 (4%)	0	100	100
2	fa	459/463 (99%)	445 (97%)	14 (3%)	0	100	100
2	fb	460/463 (99%)	442 (96%)	18 (4%)	0	100	100
2	fc	457/463 (99%)	440 (96%)	17 (4%)	0	100	100
3	Za	70/148 (47%)	66 (94%)	4 (6%)	0	100	100
3	Zb	59/148 (40%)	56 (95%)	3 (5%)	0	100	100
3	Zc	95/148 (64%)	93 (98%)	2 (2%)	0	100	100
3	Zd	95/148 (64%)	90 (95%)	5 (5%)	0	100	100
3	Ze	71/148 (48%)	70 (99%)	1 (1%)	0	100	100
3	Zf	71/148 (48%)	66 (93%)	5 (7%)	0	100	100
3	Zg	95/148 (64%)	90 (95%)	5 (5%)	0	100	100
3	Zh	95/148 (64%)	88 (93%)	7 (7%)	0	100	100
3	Zi	95/148 (64%)	89 (94%)	6 (6%)	0	100	100
3	Zj	95/148 (64%)	92 (97%)	3 (3%)	0	100	100
3	Zk	95/148 (64%)	91 (96%)	4 (4%)	0	100	100
3	Zl	95/148 (64%)	94 (99%)	1 (1%)	0	100	100
4	m1	353/521 (68%)	343 (97%)	10 (3%)	0	100	100
4	m2	331/521 (64%)	324 (98%)	7 (2%)	0	100	100
5	n1	144/314 (46%)	141 (98%)	3 (2%)	0	100	100
5	n2	147/314 (47%)	140 (95%)	7 (5%)	0	100	100
6	pp	136/139 (98%)	133 (98%)	3 (2%)	0	100	100
7	rI	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
7	rJ	71/73 (97%)	71 (100%)	0	0	100	100
7	rK	71/73 (97%)	71 (100%)	0	0	100	100
7	rL	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
7	rM	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
7	rO	71/73 (97%)	70 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	rP	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
7	rQ	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
7	rR	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
8	sa	69/137 (50%)	60 (87%)	9 (13%)	0	100	100
9	sb	120/124 (97%)	118 (98%)	2 (2%)	0	100	100
10	tm	360/362 (99%)	341 (95%)	19 (5%)	0	100	100
All	All	43060/50117 (86%)	41336 (96%)	1708 (4%)	16 (0%)	100	100

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Da	352	GLU
2	Rc	352	GLU
2	Dc	352	GLU
2	Eb	352	GLU
2	Ec	352	GLU

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	A1	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	A2	27/88 (31%)	22 (82%)	5 (18%)	1	9
1	B1	18/88 (20%)	18 (100%)	0	100	100
1	B2	16/88 (18%)	14 (88%)	2 (12%)	4	20
1	C1	18/88 (20%)	15 (83%)	3 (17%)	2	12
1	C2	17/88 (19%)	14 (82%)	3 (18%)	2	10
1	D1	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	D2	19/88 (22%)	17 (90%)	2 (10%)	6	27
1	E1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	E2	19/88 (22%)	18 (95%)	1 (5%)	20	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F1	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	F2	17/88 (19%)	16 (94%)	1 (6%)	18	50
1	G1	18/88 (20%)	15 (83%)	3 (17%)	2	12
1	G2	17/88 (19%)	16 (94%)	1 (6%)	18	50
1	H1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	I1	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	I2	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	J1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	J2	16/88 (18%)	14 (88%)	2 (12%)	4	20
1	J3	15/88 (17%)	13 (87%)	2 (13%)	4	18
1	K1	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	K2	16/88 (18%)	14 (88%)	2 (12%)	4	20
1	K3	15/88 (17%)	15 (100%)	0	100	100
1	L1	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	L2	16/88 (18%)	15 (94%)	1 (6%)	16	48
1	L3	15/88 (17%)	15 (100%)	0	100	100
1	M1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	M2	16/88 (18%)	15 (94%)	1 (6%)	16	48
1	M3	15/88 (17%)	15 (100%)	0	100	100
1	N1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	N2	15/88 (17%)	14 (93%)	1 (7%)	15	46
1	O1	18/88 (20%)	14 (78%)	4 (22%)	1	5
1	O2	17/88 (19%)	15 (88%)	2 (12%)	5	22
1	P1	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	P2	17/88 (19%)	15 (88%)	2 (12%)	5	22
1	Q1	18/88 (20%)	18 (100%)	0	100	100
1	Q2	17/88 (19%)	16 (94%)	1 (6%)	18	50
1	R1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	R2	17/88 (19%)	16 (94%)	1 (6%)	18	50
1	S1	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	S2	16/88 (18%)	13 (81%)	3 (19%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	T2	16/88 (18%)	16 (100%)	0	100	100
1	T3	15/88 (17%)	15 (100%)	0	100	100
1	U1	18/88 (20%)	15 (83%)	3 (17%)	2	12
1	U2	16/88 (18%)	15 (94%)	1 (6%)	16	48
1	U3	15/88 (17%)	14 (93%)	1 (7%)	15	46
1	V1	18/88 (20%)	16 (89%)	2 (11%)	6	25
1	V2	16/88 (18%)	16 (100%)	0	100	100
1	V3	15/88 (17%)	14 (93%)	1 (7%)	15	46
1	a3	19/88 (22%)	19 (100%)	0	100	100
1	b1	19/88 (22%)	18 (95%)	1 (5%)	20	54
1	b2	19/88 (22%)	17 (90%)	2 (10%)	6	27
1	c2	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	c3	17/88 (19%)	17 (100%)	0	100	100
1	d1	18/88 (20%)	17 (94%)	1 (6%)	19	52
1	d2	23/88 (26%)	21 (91%)	2 (9%)	9	35
1	e1	19/88 (22%)	17 (90%)	2 (10%)	6	27
1	f1	16/88 (18%)	13 (81%)	3 (19%)	1	9
1	f3	18/88 (20%)	17 (94%)	1 (6%)	19	52
2	Aa	382/384 (100%)	372 (97%)	10 (3%)	40	72
2	Ab	383/384 (100%)	376 (98%)	7 (2%)	51	77
2	Ac	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Ba	383/384 (100%)	375 (98%)	8 (2%)	47	75
2	Bb	383/384 (100%)	376 (98%)	7 (2%)	51	77
2	Bc	383/384 (100%)	378 (99%)	5 (1%)	61	81
2	Ca	382/384 (100%)	377 (99%)	5 (1%)	61	81
2	Cb	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Cc	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Da	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Db	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Dc	383/384 (100%)	377 (98%)	6 (2%)	55	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ea	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Eb	381/384 (99%)	380 (100%)	1 (0%)	86	91
2	Ec	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Fa	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Fb	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Fc	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Ga	382/384 (100%)	374 (98%)	8 (2%)	47	75
2	Gb	381/384 (99%)	380 (100%)	1 (0%)	86	91
2	Gc	378/384 (98%)	373 (99%)	5 (1%)	61	81
2	Ha	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Hb	383/384 (100%)	381 (100%)	2 (0%)	81	89
2	Hc	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Ia	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Ib	382/384 (100%)	376 (98%)	6 (2%)	55	79
2	Ic	383/384 (100%)	375 (98%)	8 (2%)	47	75
2	Ja	382/384 (100%)	379 (99%)	3 (1%)	73	86
2	Jb	383/384 (100%)	375 (98%)	8 (2%)	47	75
2	Jc	383/384 (100%)	374 (98%)	9 (2%)	44	74
2	Ka	382/384 (100%)	381 (100%)	1 (0%)	86	91
2	Kb	382/384 (100%)	377 (99%)	5 (1%)	61	81
2	Kc	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	La	383/384 (100%)	378 (99%)	5 (1%)	61	81
2	Lb	383/384 (100%)	373 (97%)	10 (3%)	40	72
2	Lc	382/384 (100%)	380 (100%)	2 (0%)	81	89
2	Ma	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Mb	382/384 (100%)	372 (97%)	10 (3%)	40	72
2	Mc	382/384 (100%)	379 (99%)	3 (1%)	73	86
2	Na	382/384 (100%)	379 (99%)	3 (1%)	73	86
2	Nb	383/384 (100%)	381 (100%)	2 (0%)	81	89
2	Nc	383/384 (100%)	376 (98%)	7 (2%)	51	77
2	Oa	383/384 (100%)	380 (99%)	3 (1%)	73	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ob	383/384 (100%)	378 (99%)	5 (1%)	61	81
2	Oc	383/384 (100%)	376 (98%)	7 (2%)	51	77
2	Pa	382/384 (100%)	378 (99%)	4 (1%)	68	84
2	Pb	382/384 (100%)	378 (99%)	4 (1%)	68	84
2	Pc	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Qa	383/384 (100%)	381 (100%)	2 (0%)	81	89
2	Qb	383/384 (100%)	378 (99%)	5 (1%)	61	81
2	Qc	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Ra	383/384 (100%)	378 (99%)	5 (1%)	61	81
2	Rb	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Rc	382/384 (100%)	377 (99%)	5 (1%)	61	81
2	Sa	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Sb	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Sc	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	Ta	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Tb	382/384 (100%)	375 (98%)	7 (2%)	51	77
2	Tc	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Ua	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Ub	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Uc	383/384 (100%)	380 (99%)	3 (1%)	73	86
2	Va	383/384 (100%)	381 (100%)	2 (0%)	81	89
2	Vb	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	Vc	383/384 (100%)	379 (99%)	4 (1%)	68	84
2	aa	383/384 (100%)	377 (98%)	6 (2%)	55	79
2	ab	381/384 (99%)	371 (97%)	10 (3%)	40	72
2	ac	383/384 (100%)	376 (98%)	7 (2%)	51	77
2	ba	383/384 (100%)	373 (97%)	10 (3%)	40	72
2	bb	382/384 (100%)	372 (97%)	10 (3%)	40	72
2	bc	383/384 (100%)	371 (97%)	12 (3%)	35	68
2	ca	383/384 (100%)	372 (97%)	11 (3%)	37	70
2	cb	381/384 (99%)	369 (97%)	12 (3%)	35	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	cc	383/384 (100%)	375 (98%)	8 (2%)	47	75
2	da	383/384 (100%)	372 (97%)	11 (3%)	37	70
2	db	382/384 (100%)	358 (94%)	24 (6%)	16	48
2	dc	383/384 (100%)	365 (95%)	18 (5%)	23	58
2	ea	383/384 (100%)	372 (97%)	11 (3%)	37	70
2	eb	382/384 (100%)	372 (97%)	10 (3%)	40	72
2	ec	382/384 (100%)	368 (96%)	14 (4%)	30	64
2	fa	382/384 (100%)	367 (96%)	15 (4%)	28	62
2	fb	383/384 (100%)	367 (96%)	16 (4%)	26	61
2	fc	380/384 (99%)	364 (96%)	16 (4%)	26	61
3	Za	57/119 (48%)	53 (93%)	4 (7%)	14	44
3	Zb	49/119 (41%)	42 (86%)	7 (14%)	3	16
3	Zc	75/119 (63%)	73 (97%)	2 (3%)	39	71
3	Zd	75/119 (63%)	69 (92%)	6 (8%)	11	38
3	Ze	60/119 (50%)	54 (90%)	6 (10%)	7	29
3	Zf	60/119 (50%)	56 (93%)	4 (7%)	15	46
3	Zg	75/119 (63%)	69 (92%)	6 (8%)	11	38
3	Zh	75/119 (63%)	70 (93%)	5 (7%)	15	46
3	Zi	75/119 (63%)	70 (93%)	5 (7%)	15	46
3	Zj	75/119 (63%)	70 (93%)	5 (7%)	15	46
3	Zk	75/119 (63%)	68 (91%)	7 (9%)	8	32
3	Zl	75/119 (63%)	70 (93%)	5 (7%)	15	46
4	m1	288/405 (71%)	280 (97%)	8 (3%)	38	70
4	m2	266/405 (66%)	253 (95%)	13 (5%)	22	56
5	n1	120/265 (45%)	116 (97%)	4 (3%)	33	67
5	n2	122/265 (46%)	119 (98%)	3 (2%)	42	72
6	pp	120/121 (99%)	112 (93%)	8 (7%)	15	46
7	rI	60/60 (100%)	55 (92%)	5 (8%)	10	37
7	rJ	60/60 (100%)	54 (90%)	6 (10%)	7	29
7	rK	60/60 (100%)	57 (95%)	3 (5%)	22	56
7	rL	60/60 (100%)	57 (95%)	3 (5%)	22	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	rM	60/60 (100%)	56 (93%)	4 (7%)	15	46
7	rO	60/60 (100%)	52 (87%)	8 (13%)	4	18
7	rP	60/60 (100%)	60 (100%)	0	100	100
7	rQ	60/60 (100%)	56 (93%)	4 (7%)	15	46
7	rR	60/60 (100%)	58 (97%)	2 (3%)	33	67
8	sa	56/106 (53%)	55 (98%)	1 (2%)	51	77
9	sb	96/98 (98%)	96 (100%)	0	100	100
10	tm	277/276 (100%)	262 (95%)	15 (5%)	20	53
All	All	35890/41445 (87%)	35083 (98%)	807 (2%)	45	74

5 of 807 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Zh	133	LYS
2	cc	317	VAL
10	tm	184	LEU
3	Zk	78	ILE
3	Zh	85	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 253 such sidechains are listed below:

Mol	Chain	Res	Type
2	Qc	65	GLN
2	fa	314	HIS
2	Uc	393	GLN
2	ec	383	HIS
7	rK	33	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

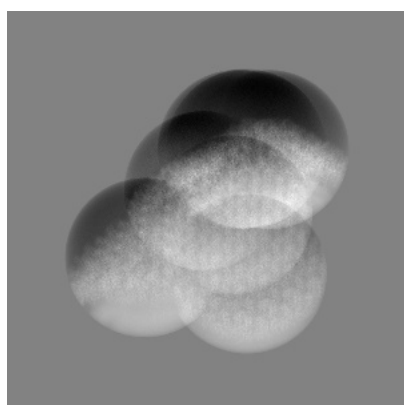
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-57237. 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](#)

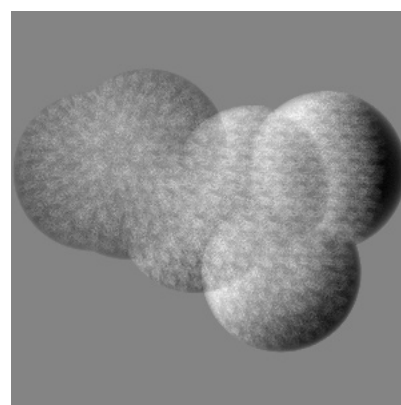
6.1.1 Primary map



X



Y

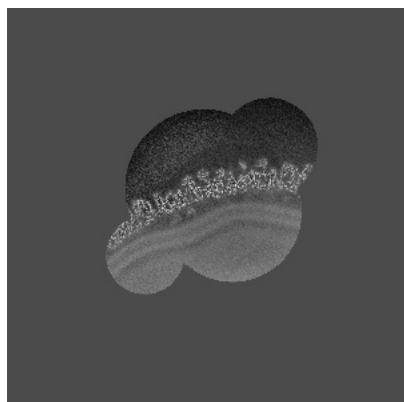


Z

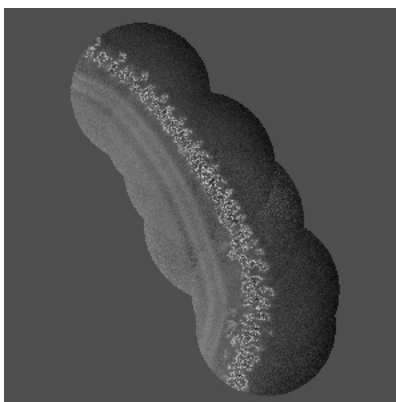
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

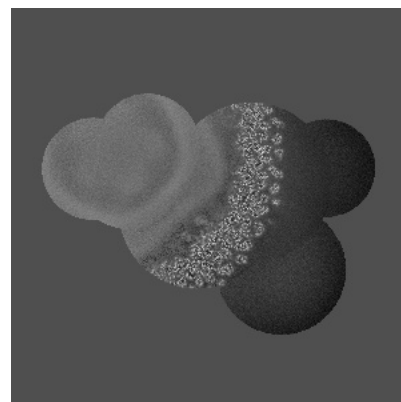
6.2.1 Primary map



X Index: 700



Y Index: 700

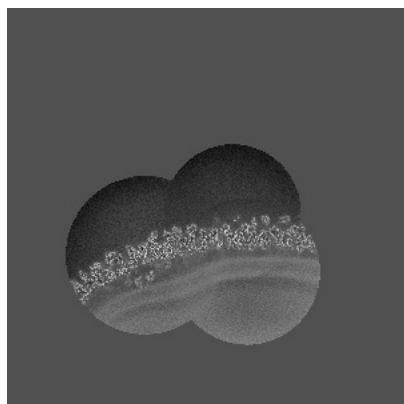


Z Index: 700

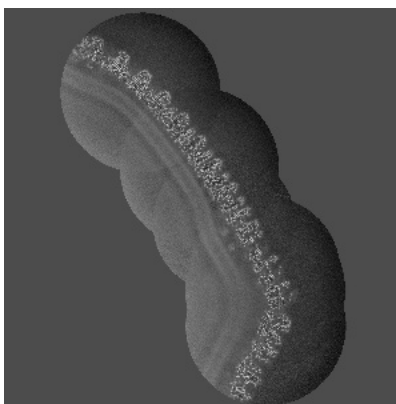
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

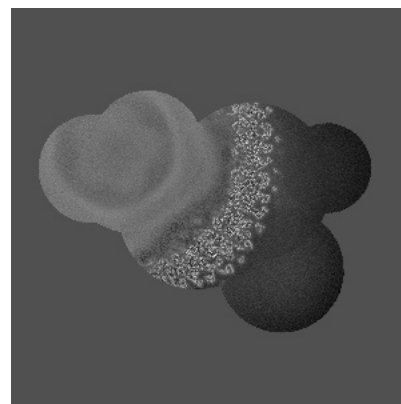
6.3.1 Primary map



X Index: 989



Y Index: 819

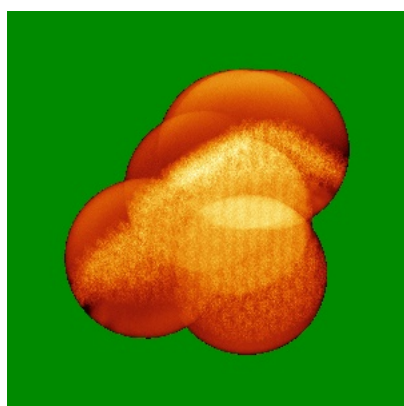


Z Index: 710

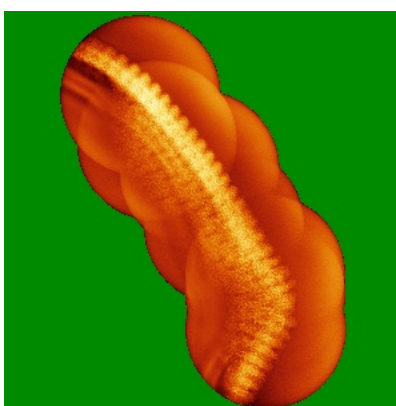
The images above show the largest variance slices of the map in three orthogonal directions.

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

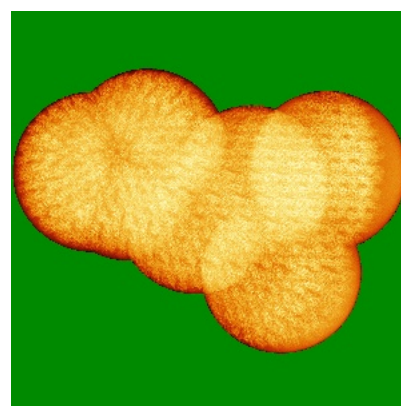
6.4.1 Primary map



X



Y

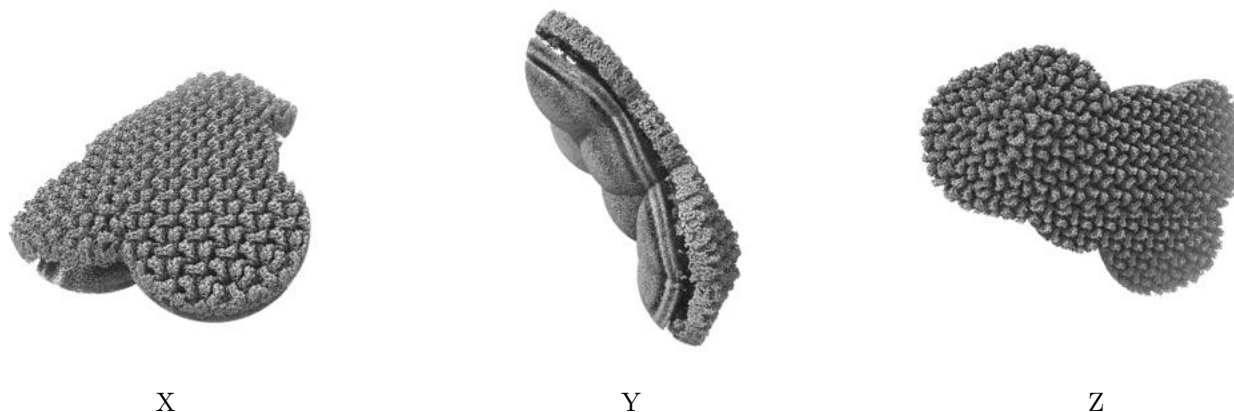


Z

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 0.0019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

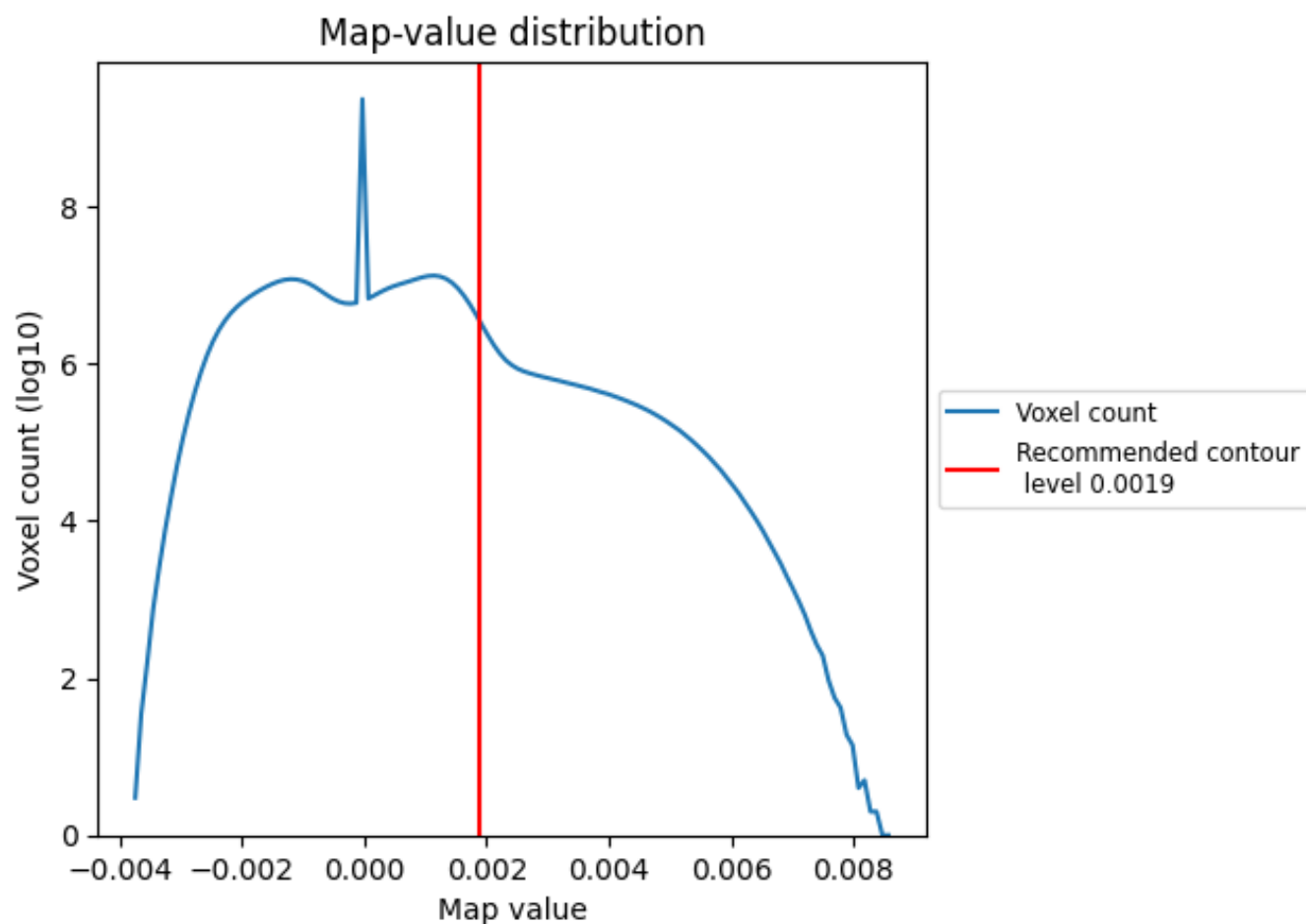
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

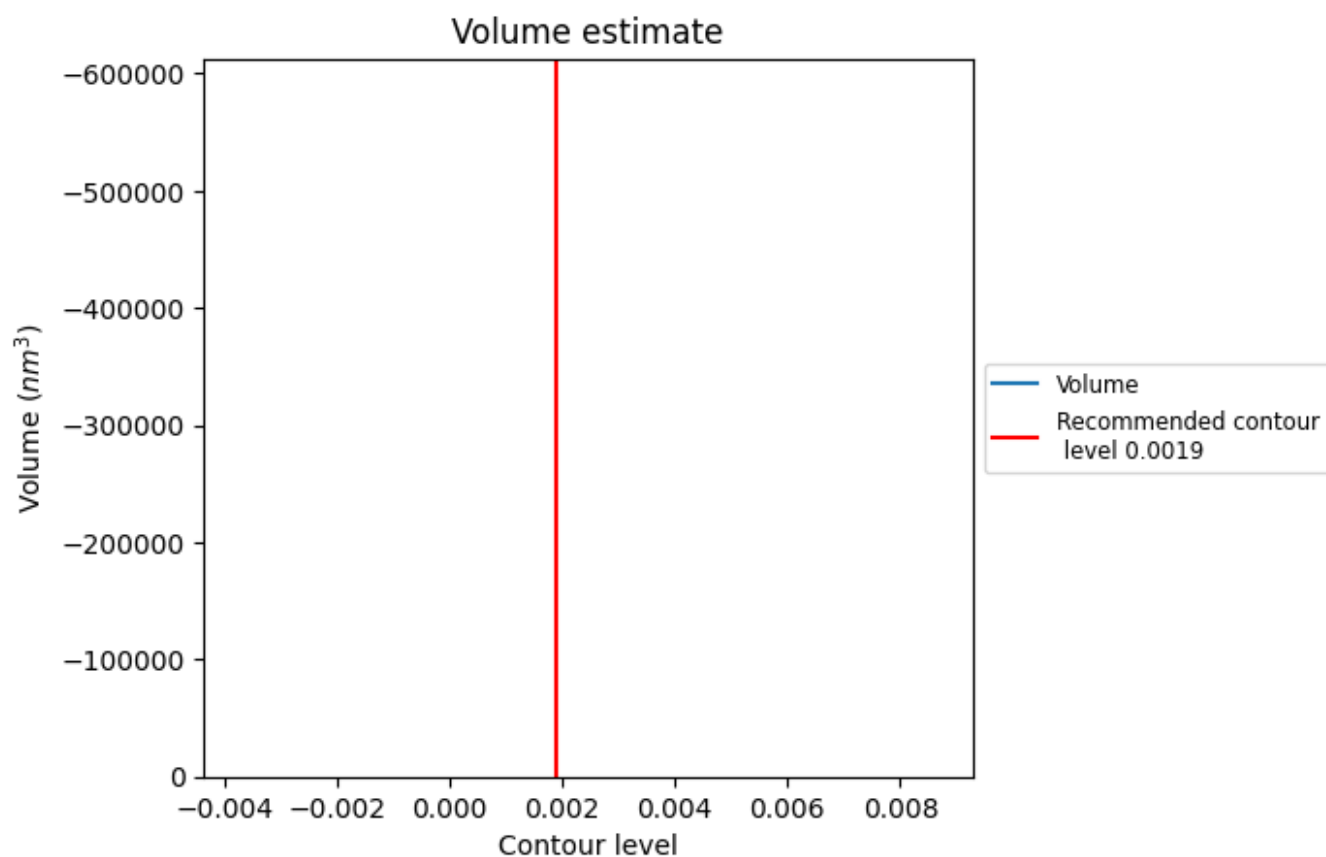
This section contains the results of statistical analysis of the map.

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.

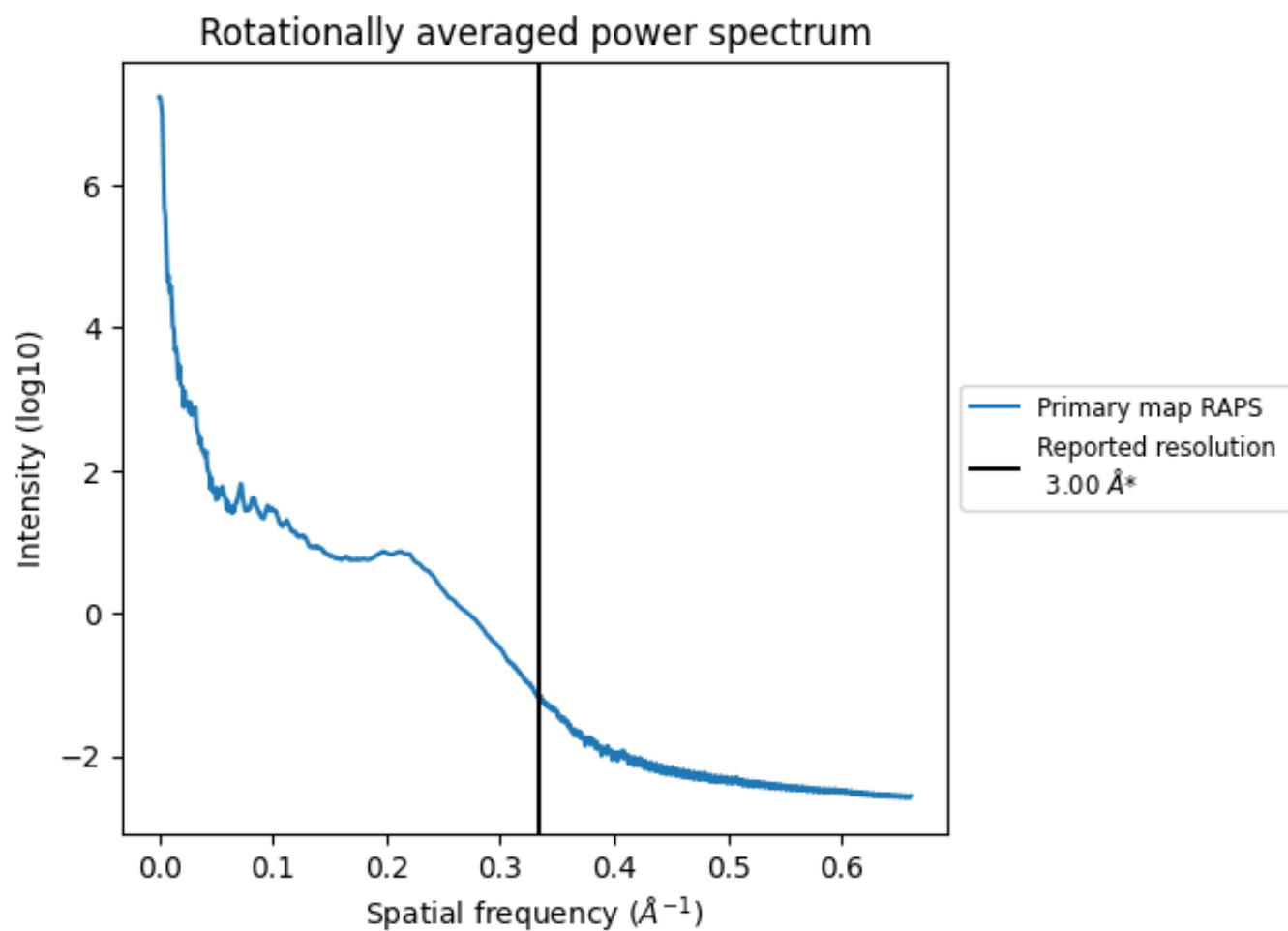
7.2 Volume estimate [i](#)



The volume at the recommended contour level is -1848564 nm³; this corresponds to an approximate mass of -1669856 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 0.333 Å⁻¹

8 Fourier-Shell correlation

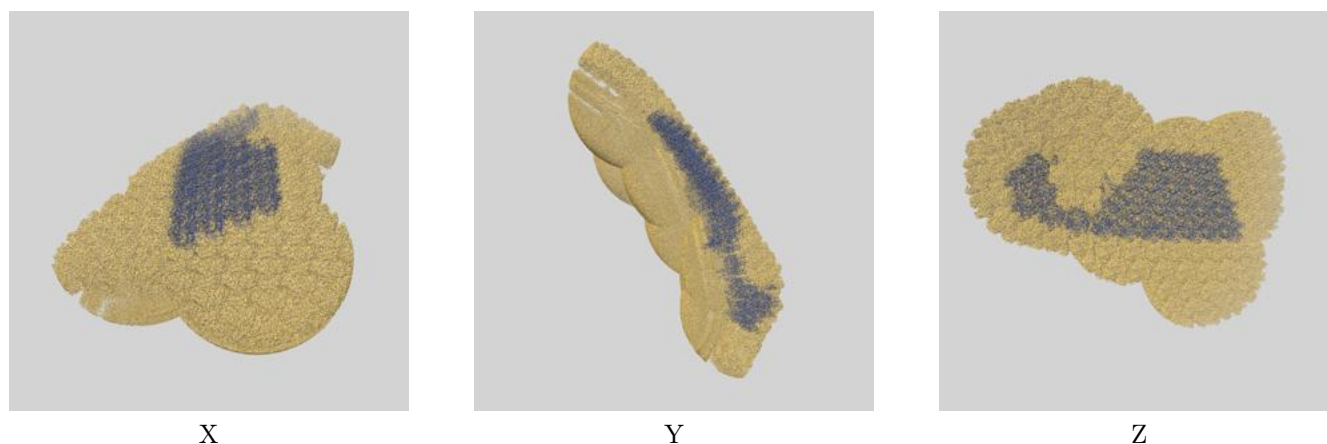
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

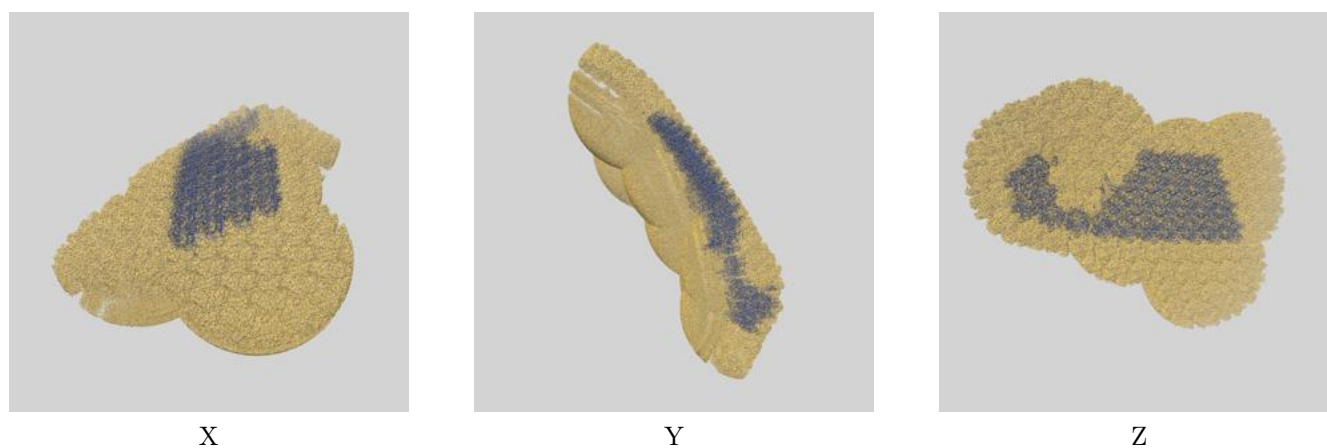
This section contains information regarding the fit between EMDB map EMD-57237 and PDB model 29KH. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

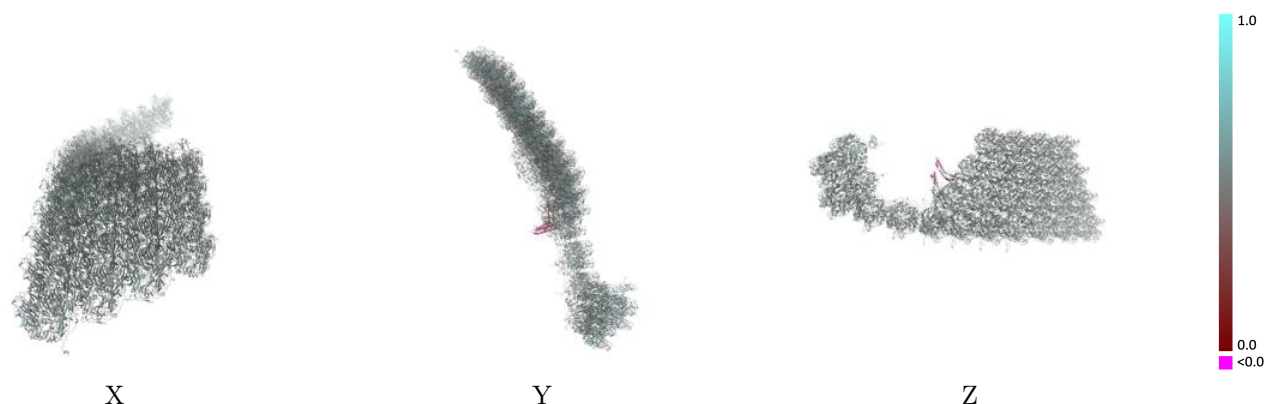


9.1.2 Map-model assembly overlay [i](#)



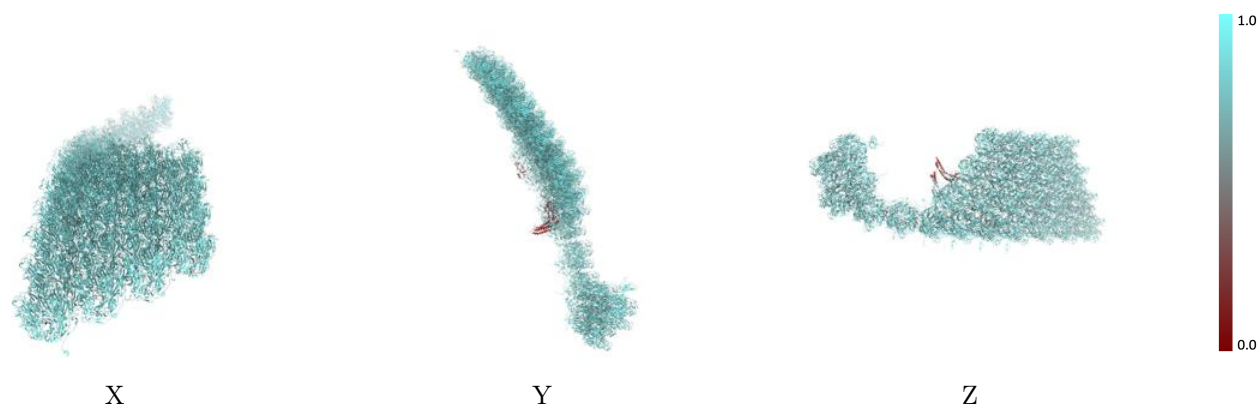
The images above show the 3D surface view of the map at the recommended contour level 0.0019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



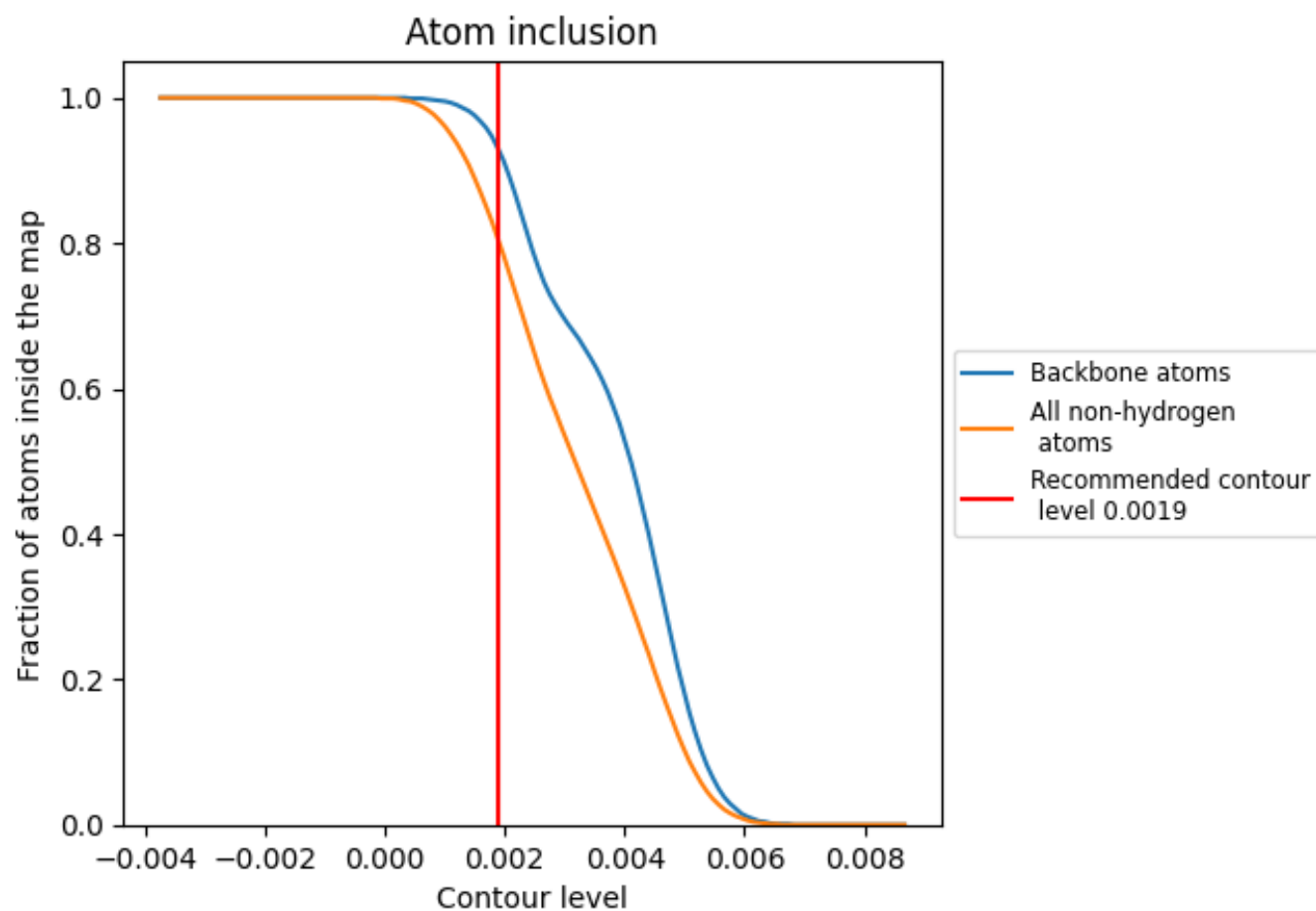
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.5180
A1	 0.6250	 0.4150
A2	 0.6240	 0.3870
Aa	 0.8420	 0.5270
Ab	 0.8140	 0.5170
Ac	 0.8240	 0.5260
B1	 0.7380	 0.4500
B2	 0.2800	 0.3700
Ba	 0.8550	 0.5380
Bb	 0.8470	 0.5310
Bc	 0.8180	 0.5260
C1	 0.6490	 0.4270
C2	 0.6400	 0.4190
Ca	 0.8310	 0.5350
Cb	 0.8250	 0.5300
Cc	 0.8480	 0.5350
D1	 0.6910	 0.4490
D2	 0.6490	 0.4100
Da	 0.8390	 0.5280
Db	 0.8430	 0.5340
Dc	 0.8340	 0.5270
E1	 0.7440	 0.4260
E2	 0.6280	 0.4280
Ea	 0.8290	 0.5320
Eb	 0.8290	 0.5280
Ec	 0.8260	 0.5260
F1	 0.7440	 0.4420
F2	 0.6050	 0.4250
Fa	 0.8160	 0.5250
Fb	 0.8260	 0.5270
Fc	 0.8040	 0.5200
G1	 0.7260	 0.4180
G2	 0.5370	 0.4040
Ga	 0.7930	 0.5140
Gb	 0.7900	 0.5120



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Chain	Atom inclusion	Q-score
Gc	 0.8050	 0.5150
H1	 0.5000	 0.4210
Ha	 0.8380	 0.5280
Hb	 0.8180	 0.5240
Hc	 0.8150	 0.5190
I1	 0.6610	 0.4430
I2	 0.5770	 0.3890
Ia	 0.8220	 0.5250
Ib	 0.8130	 0.5210
Ic	 0.8340	 0.5290
J1	 0.5000	 0.4160
J2	 0.6990	 0.4330
J3	 0.1410	 0.3880
Ja	 0.8570	 0.5360
Jb	 0.8440	 0.5350
Jc	 0.8560	 0.5350
K1	 0.4230	 0.4030
K2	 0.6920	 0.4110
K3	 0.2960	 0.3530
Ka	 0.8310	 0.5310
Kb	 0.8530	 0.5330
Kc	 0.8470	 0.5310
L1	 0.3750	 0.3820
L2	 0.7200	 0.3950
L3	 0.2370	 0.3140
La	 0.8130	 0.5220
Lb	 0.8310	 0.5240
Lc	 0.8200	 0.5200
M1	 0.2020	 0.3650
M2	 0.6710	 0.3970
M3	 0.4810	 0.3360
Ma	 0.8040	 0.5150
Mb	 0.8160	 0.5170
Mc	 0.8160	 0.5170
N1	 0.6130	 0.4380
N2	 0.5180	 0.3960
Na	 0.8000	 0.5160
Nb	 0.8030	 0.5210
Nc	 0.8020	 0.5160
O1	 0.5710	 0.4370
O2	 0.3400	 0.3730
Oa	 0.8390	 0.5280

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Chain	Atom inclusion	Q-score
Ob	 0.8110	 0.5120
Oc	 0.8190	 0.5180
P1	 0.4820	 0.4170
P2	 0.5430	 0.4200
Pa	 0.8520	 0.5340
Pb	 0.8460	 0.5290
Pc	 0.8410	 0.5250
Q1	 0.5830	 0.4130
Q2	 0.5680	 0.3910
Qa	 0.8420	 0.5290
Qb	 0.8430	 0.5270
Qc	 0.8400	 0.5260
R1	 0.5300	 0.4010
R2	 0.5120	 0.4160
Ra	 0.8430	 0.5270
Rb	 0.8330	 0.5230
Rc	 0.8340	 0.5240
S1	 0.6130	 0.3850
S2	 0.5240	 0.3590
Sa	 0.8030	 0.5100
Sb	 0.8020	 0.5090
Sc	 0.7910	 0.5050
T1	 0.3040	 0.3790
T2	 0.4620	 0.4190
T3	 0.1260	 0.3200
Ta	 0.8200	 0.5150
Tb	 0.8060	 0.5110
Tc	 0.8140	 0.5120
U1	 0.1730	 0.3810
U2	 0.5590	 0.4290
U3	 0.2810	 0.3490
Ua	 0.8430	 0.5290
Ub	 0.8240	 0.5210
Uc	 0.8310	 0.5220
V1	 0.2560	 0.3750
V2	 0.4960	 0.4100
V3	 0.4070	 0.3510
Va	 0.8340	 0.5180
Vb	 0.8180	 0.5140
Vc	 0.8090	 0.5080
Za	 0.8500	 0.5110
Zb	 0.8370	 0.4970

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Chain	Atom inclusion	Q-score
Zc	 0.8100	 0.4870
Zd	 0.8180	 0.4900
Ze	 0.8010	 0.4880
Zf	 0.8210	 0.4940
Zg	 0.8330	 0.5220
Zh	 0.8250	 0.5150
Zi	 0.8350	 0.5090
Zj	 0.8300	 0.5080
Zk	 0.8330	 0.5100
Zl	 0.8370	 0.5110
a3	 0.6250	 0.4660
aa	 0.7690	 0.5410
ab	 0.7870	 0.5410
ac	 0.7680	 0.5380
b1	 0.3920	 0.4000
b2	 0.3240	 0.3970
ba	 0.7860	 0.5340
bb	 0.7880	 0.5270
bc	 0.7930	 0.5320
c2	 0.6730	 0.4540
c3	 0.5600	 0.4470
ca	 0.7940	 0.5390
cb	 0.7820	 0.5350
cc	 0.7970	 0.5380
d1	 0.6310	 0.4580
d2	 0.6760	 0.4260
da	 0.7990	 0.5300
db	 0.8080	 0.5300
dc	 0.7950	 0.5250
e1	 0.6140	 0.4510
ea	 0.8050	 0.5330
eb	 0.8220	 0.5360
ec	 0.7930	 0.5300
f1	 0.6210	 0.4280
f3	 0.6430	 0.4520
fa	 0.7820	 0.5140
fb	 0.8200	 0.5210
fc	 0.8050	 0.5240
m1	 0.6550	 0.4110
m2	 0.3390	 0.3750
n1	 0.6390	 0.4430
n2	 0.2950	 0.4360

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Chain	Atom inclusion	Q-score
pp	 0.7700	 0.5470
rI	 0.8160	 0.5130
rJ	 0.8360	 0.5290
rK	 0.8580	 0.5320
rL	 0.8490	 0.5250
rM	 0.8180	 0.5090
rO	 0.6910	 0.4950
rP	 0.7960	 0.5250
rQ	 0.8380	 0.5220
rR	 0.7530	 0.5190
sa	 0.7780	 0.5150
sb	 0.8590	 0.5220
tm	 0.8410	 0.5260