



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:51 AM UTC

PDB ID : 6NCL / pdb_00006ncl
EMDB ID : EMD-0436
Title : Near-atomic structure of icosahedrally averaged PBCV-1 capsid
Authors : Fang, Q.; Rossmann, M.G.
Deposited on : 2018-12-11
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

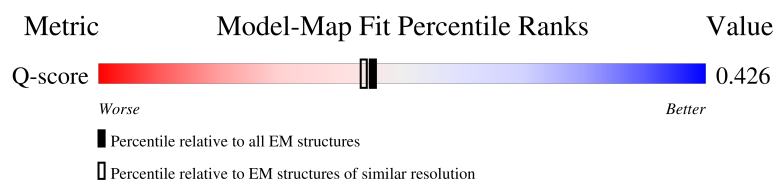
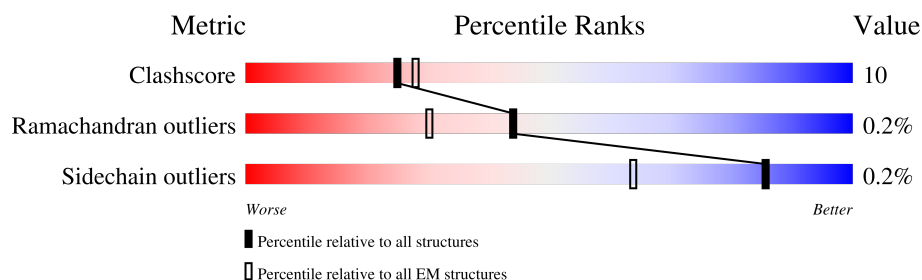
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



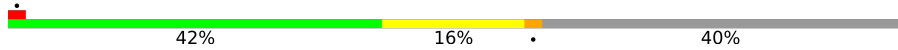
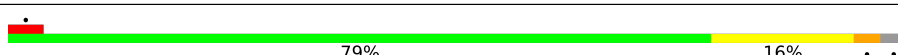
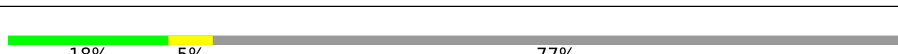
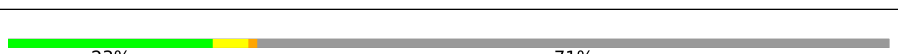
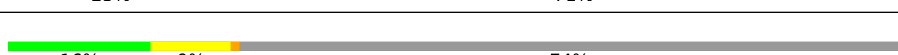
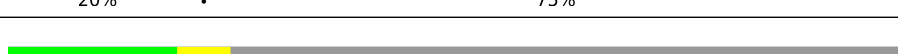
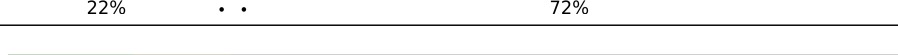
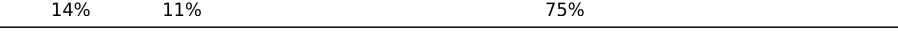
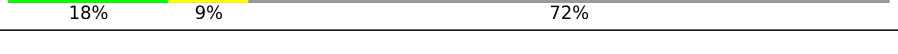
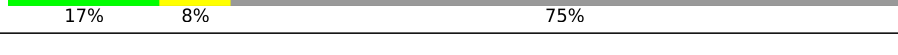
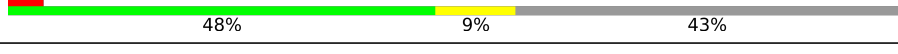
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	a0	352	
2	a1	210	
3	a2	289	
3	a3	289	

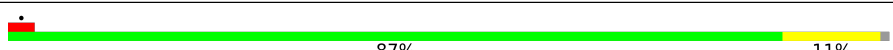
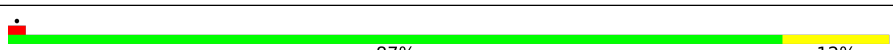
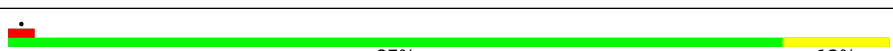
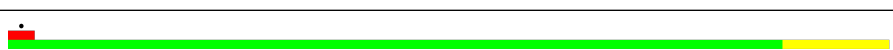
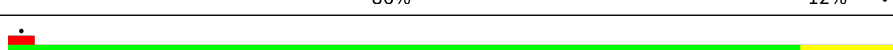
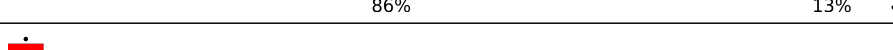
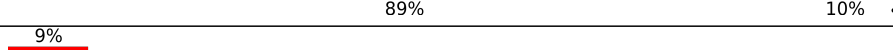
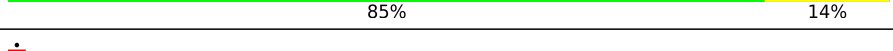
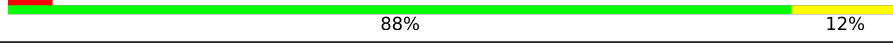
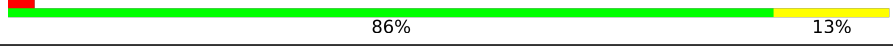
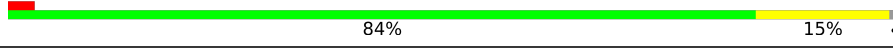
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Mol	Chain	Length	Quality of chain
4	a4	256	
5	a5	216	
6	a6	170	
7	a7	151	
8	a8	146	
9	a9	207	
9	b0	207	
9	b1	207	
9	b2	207	
9	b3	207	
9	b4	207	
9	b5	207	
9	b7	207	
9	b8	207	
9	c0	207	
9	c1	207	
9	l5	207	
10	b6	576	
11	c2	181	
11	c3	181	
11	c4	181	
11	c5	181	
12	c6	171	
12	c7	171	
12	c8	171	

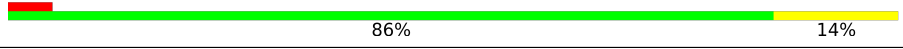
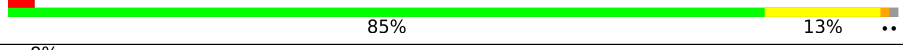
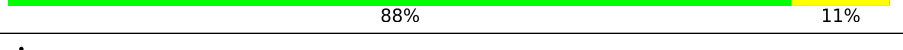
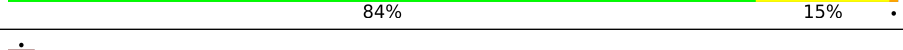
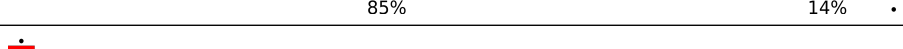
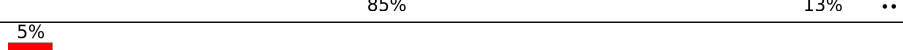
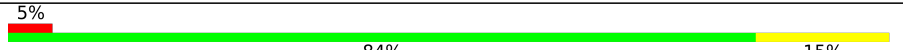
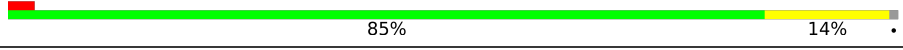
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Mol	Chain	Length	Quality of chain
13	c9	173	
14	d0	437	
14	d1	437	
14	d2	437	
14	d3	437	
14	d4	437	
14	d5	437	
14	d6	437	
14	d7	437	
14	d8	437	
14	d9	437	
14	e0	437	
14	e1	437	
14	e2	437	
14	e3	437	
14	e4	437	
14	e5	437	
14	e6	437	
14	e7	437	
14	e8	437	
14	e9	437	
14	f0	437	
14	f1	437	
14	f2	437	
14	f3	437	

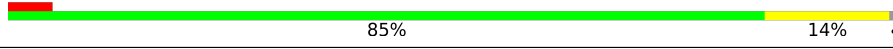
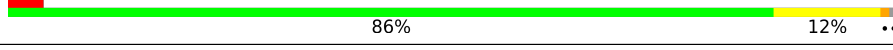
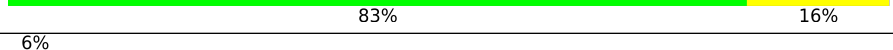
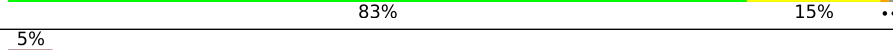
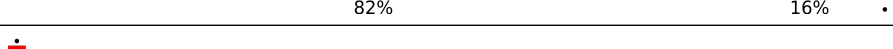
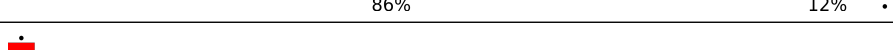
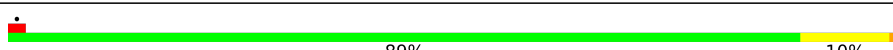
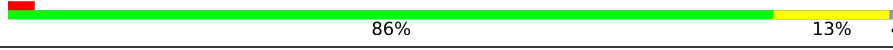
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Mol	Chain	Length	Quality of chain
14	f4	437	
14	f5	437	
14	f6	437	
14	f7	437	
14	f8	437	
14	f9	437	
14	g0	437	
14	g1	437	
14	g2	437	
14	g3	437	
14	g4	437	
14	g5	437	
14	g6	437	
14	g7	437	
14	g8	437	
14	g9	437	
14	h0	437	
14	h1	437	
14	h2	437	
14	h3	437	
14	h4	437	
14	h5	437	
14	h6	437	
14	h7	437	
14	h8	437	

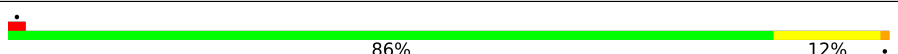
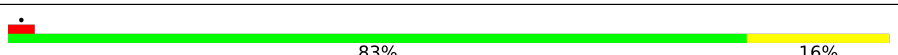
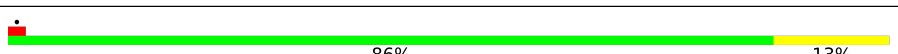
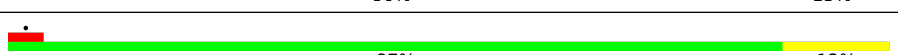
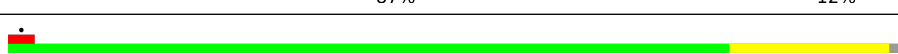
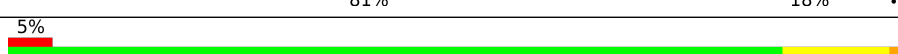
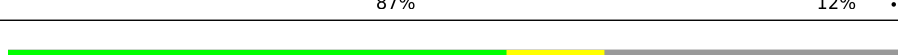
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Mol	Chain	Length	Quality of chain
14	h9	437	
14	i0	437	
14	i1	437	
14	i2	437	
14	i3	437	
14	i4	437	
14	i5	437	
14	i6	437	
14	i7	437	
14	i8	437	
14	i9	437	
14	j0	437	
14	j1	437	
14	j2	437	
14	j3	437	
14	j4	437	
14	j5	437	
14	j6	437	
14	j7	437	
14	j8	437	
14	j9	437	
14	k0	437	
14	k1	437	
14	k2	437	
14	k3	437	

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Mol	Chain	Length	Quality of chain
14	k4	437	
14	k5	437	
14	k6	437	
14	k7	437	
14	k8	437	
14	k9	437	
14	l0	437	
14	l1	437	
14	l2	437	
14	l3	437	
15	l4	98	

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 305842 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 P14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a0	97	Total	C	N	O	S	0	0
			733	463	122	145	3		

- Molecule 2 is a protein called P9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a1	107	Total	C	N	O	S	0	0
			718	445	122	146	5		

- Molecule 3 is a protein called P10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a2	94	Total	C	N	O	S	0	0
			650	411	110	125	4		
3	a3	74	Total	C	N	O	S	0	0
			485	308	86	88	3		

- Molecule 4 is a protein called P7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a4	153	Total	C	N	O	S	0	0
			1088	689	192	197	10		

- Molecule 5 is a protein called P6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	a5	189	Total	C	N	O	S	0	0
			1326	878	210	236	2		

- Molecule 6 is a protein called P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a6	167	Total	C	N	O	S	0	0
			1192	756	203	229	4		

- Molecule 7 is a protein called P12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a7	78	Total	C	N	O	S	0	0
			543	357	88	95	3		

- Molecule 8 is a protein called P5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a8	142	Total	C	N	O	S	0	0
			988	638	168	180	2		

- Molecule 9 is a protein called P11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a9	47	Total	C	N	O	S	0	0
			311	200	53	57	1		
9	b0	59	Total	C	N	O	S	0	0
			398	248	70	79	1		
9	b1	54	Total	C	N	O		0	0
			368	238	64	66			
9	b2	51	Total	C	N	O	S	0	0
			350	227	59	63	1		
9	b3	51	Total	C	N	O	S	0	0
			335	216	56	62	1		
9	b4	52	Total	C	N	O	S	0	0
			350	228	61	60	1		
9	b5	57	Total	C	N	O	S	0	0
			367	237	64	64	2		
9	b7	52	Total	C	N	O	S	0	0
			375	244	63	67	1		
9	b8	57	Total	C	N	O		0	0
			379	244	66	69			
9	c0	51	Total	C	N	O	S	0	0
			338	214	59	64	1		
9	c1	51	Total	C	N	O	S	0	0
			335	213	59	61	2		
9	l5	58	Total	C	N	O		0	0
			392	253	67	72			

- Molecule 10 is a protein called P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b6	475	Total	C	N	O	S	0	0
			3210	2016	587	603	4		

- Molecule 11 is a protein called P4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c2	103	Total	C	N	O	S	0	0
			603	369	110	123	1		
11	c3	60	Total	C	N	O		0	0
			389	242	69	78			
11	c4	58	Total	C	N	O		0	0
			369	230	65	74			
11	c5	58	Total	C	N	O		0	0
			396	252	72	72			

- Molecule 12 is a protein called P3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c6	141	Total	C	N	O	S	0	0
			951	602	170	177	2		
12	c7	147	Total	C	N	O	S	0	0
			1004	648	172	180	4		
12	c8	116	Total	C	N	O	S	0	0
			813	519	141	149	4		

- Molecule 13 is a protein called P8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c9	166	Total	C	N	O	S	0	0
			1191	776	198	214	3		

- Molecule 14 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d0	432	Total	C	N	O	S	0	0
			3369	2142	570	649	8		
14	d1	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	d2	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	d3	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	d4	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	d5	435	Total	C	N	O	S	0	0
			3383	2150	574	651	8		
14	d6	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	d7	435	Total	C	N	O	S	0	0
			3381	2149	571	653	8		
14	d8	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	d9	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	e0	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	e1	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	e2	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	e3	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	e4	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	e5	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	e6	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	e7	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	e8	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	e9	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	f0	434	Total	C	N	O	S	0	0
			3375	2143	573	651	8		
14	f1	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	f2	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	f3	435	Total	C	N	O	S	0	0
			3383	2147	575	653	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	f4	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	f5	434	Total	C	N	O	S	0	0
			3376	2146	570	652	8		
14	f6	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	f7	434	Total	C	N	O	S	0	0
			3372	2142	572	650	8		
14	f8	433	Total	C	N	O	S	0	0
			3378	2147	572	651	8		
14	f9	434	Total	C	N	O	S	0	0
			3379	2145	574	652	8		
14	g0	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	g1	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	g2	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	g3	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	g4	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	g5	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	g6	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	g7	434	Total	C	N	O	S	0	0
			3376	2146	570	652	8		
14	g8	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	g9	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	h0	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	h1	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	h2	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	h3	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	h4	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	h5	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	h6	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	h7	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	h8	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	h9	435	Total	C	N	O	S	0	0
			3381	2149	571	653	8		
14	i0	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	i1	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	i2	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	i3	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	i4	435	Total	C	N	O	S	0	0
			3384	2150	572	654	8		
14	i5	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	i6	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	i7	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	i8	436	Total	C	N	O	S	0	0
			3388	2150	576	654	8		
14	i9	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	j0	436	Total	C	N	O	S	0	0
			3392	2155	576	653	8		
14	j1	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	j2	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	j3	435	Total	C	N	O	S	0	0
			3387	2152	575	652	8		
14	j4	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	j5	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		

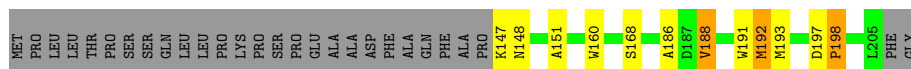
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Mol	Chain	Residues	Atoms					AltConf	Trace
14	j6	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	j7	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	j8	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
14	j9	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	k0	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	k1	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	k2	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
14	k3	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	k4	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	k5	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
14	k6	435	Total	C	N	O	S	0	0
			3391	2153	575	655	8		
14	k7	435	Total	C	N	O	S	0	0
			3387	2151	574	654	8		
14	k8	435	Total	C	N	O	S	0	0
			3391	2153	575	655	8		
14	k9	435	Total	C	N	O	S	0	0
			3381	2149	571	653	8		
14	l0	435	Total	C	N	O	S	0	0
			3391	2153	575	655	8		
14	l1	435	Total	C	N	O	S	0	0
			3391	2153	575	655	8		
14	l2	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
14	l3	436	Total	C	N	O	S	0	0
			3396	2156	576	656	8		

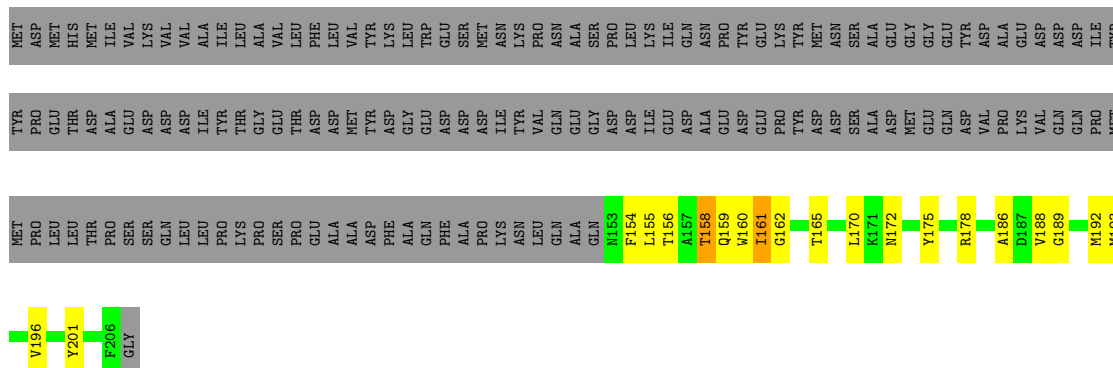
- Molecule 15 is a protein called P13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l4	66	Total	C	N	O	S	0	0
			487	313	82	90	2		



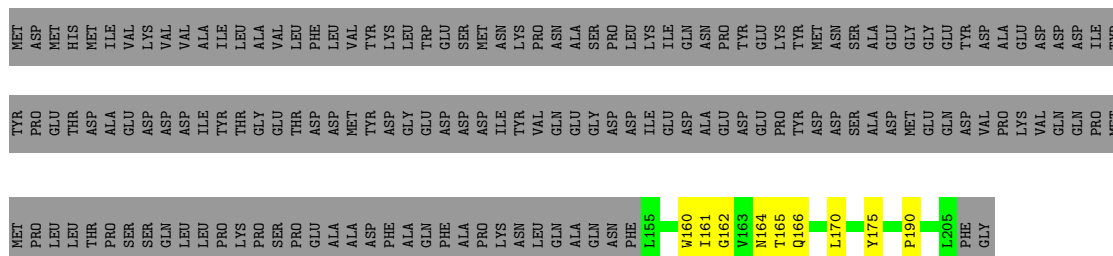
- Molecule 9: P11

Chain b1: 16% 9% . 74%



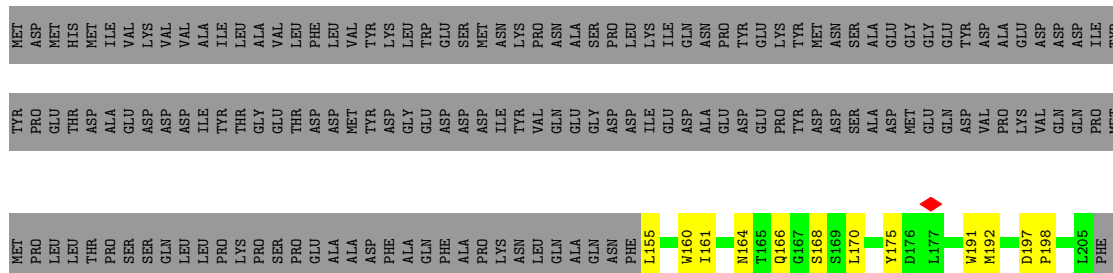
- Molecule 9: P11

Chain b2: 20% . 75%



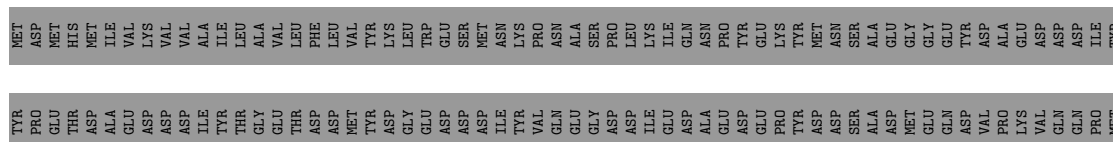
- Molecule 9: P11

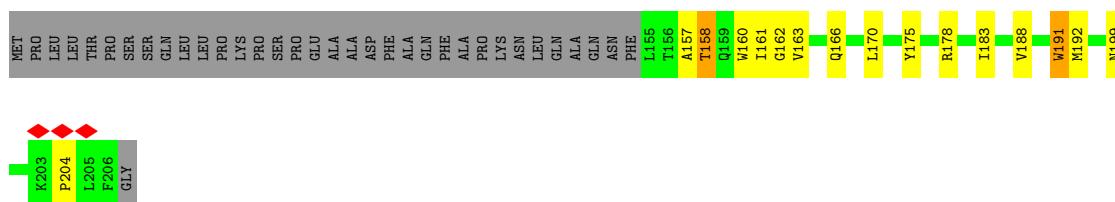
Chain b3: 19% 6% 75%



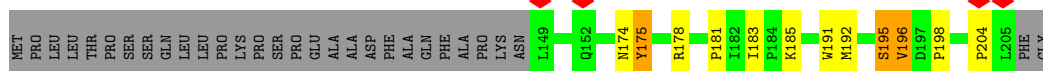
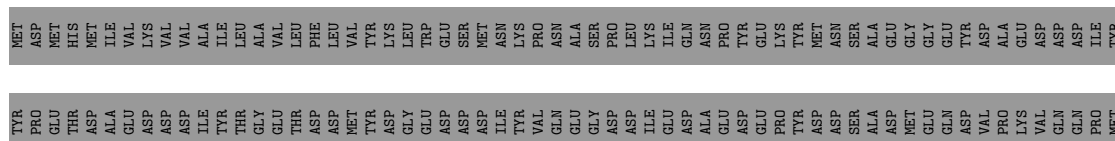
- Molecule 9: P11

Chain b4: 17% 7% . 75%

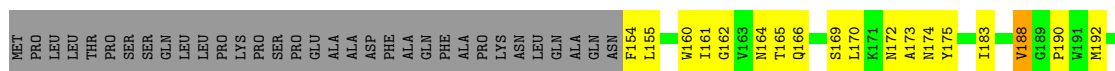
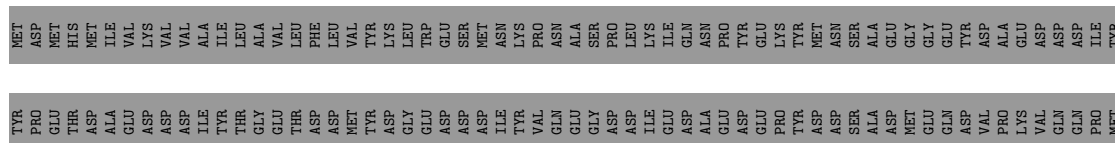




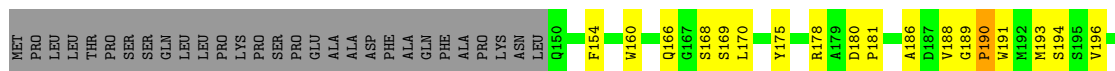
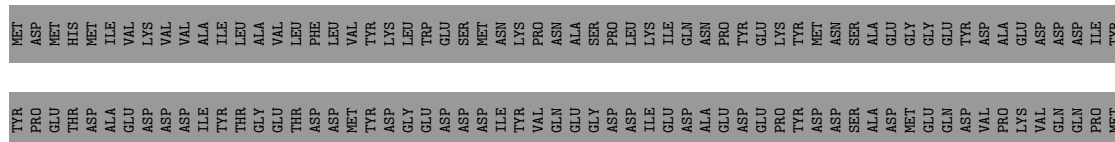
• Molecule 9: P11



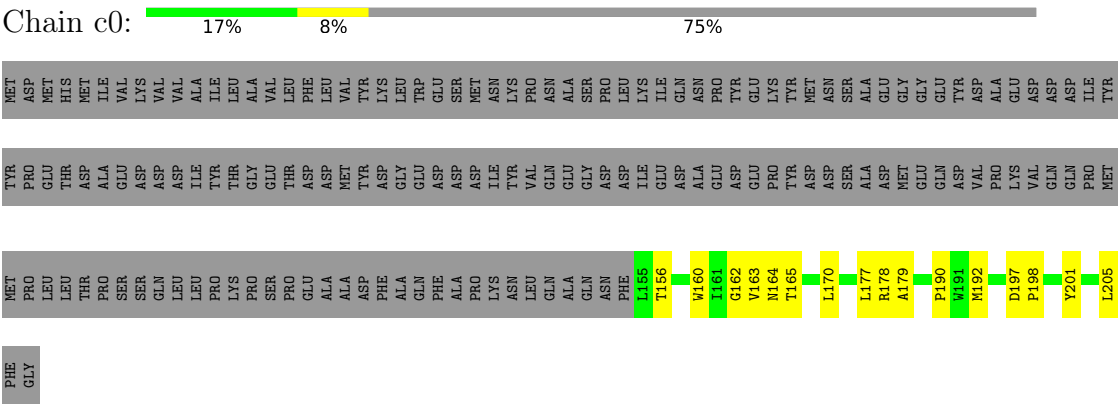
• Molecule 9: P11



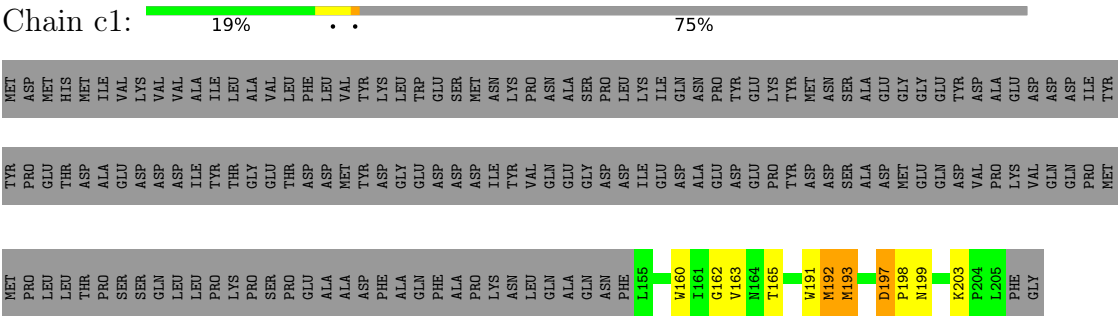
• Molecule 9: P11



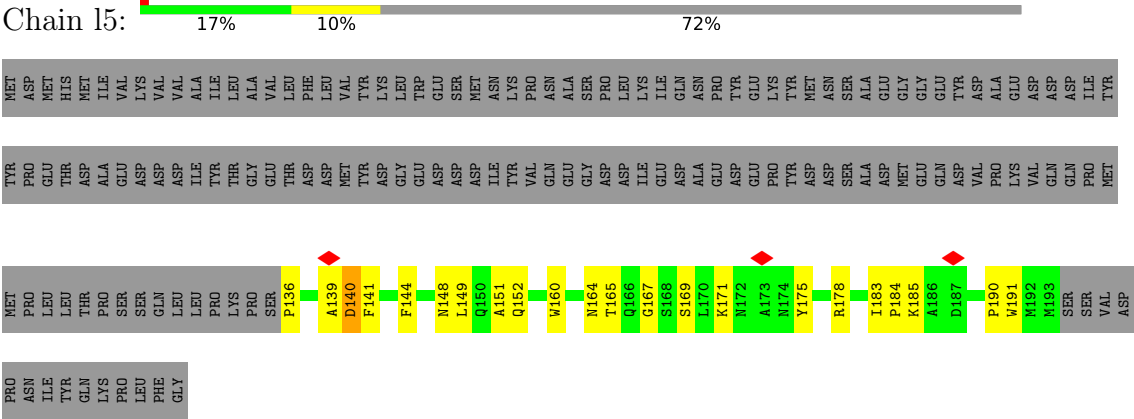
• Molecule 9: P11



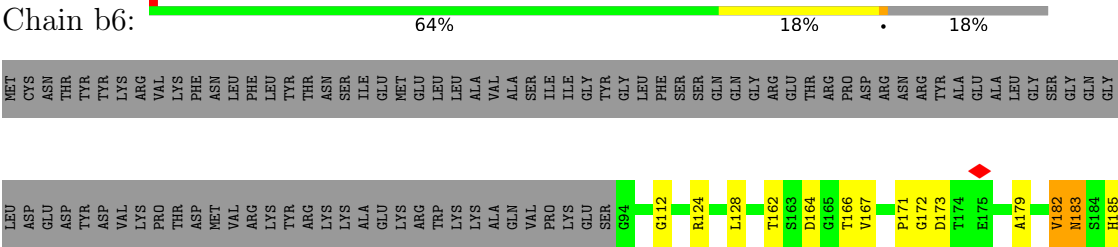
• Molecule 9: P11

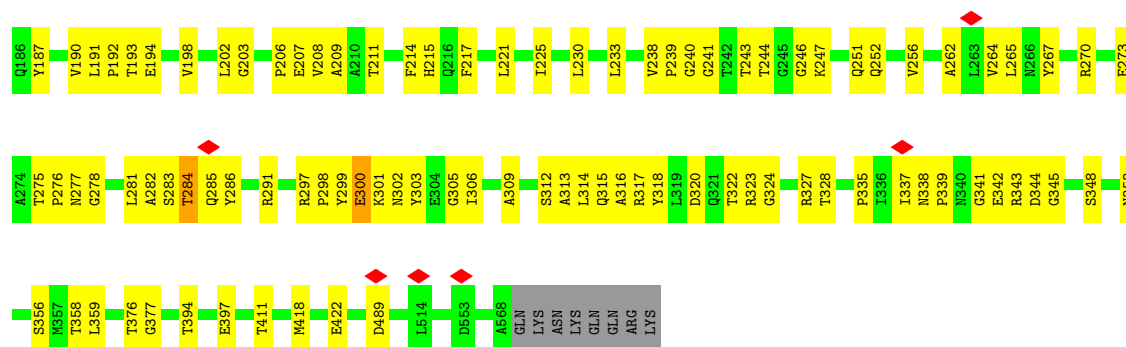


• Molecule 9: P11

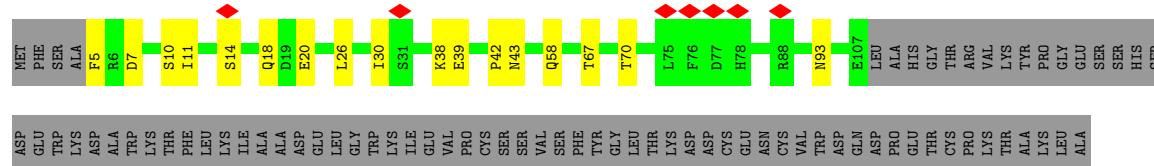


• Molecule 10: P2

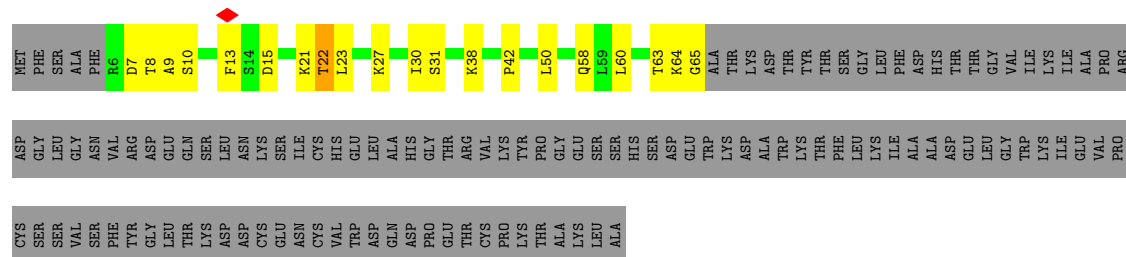




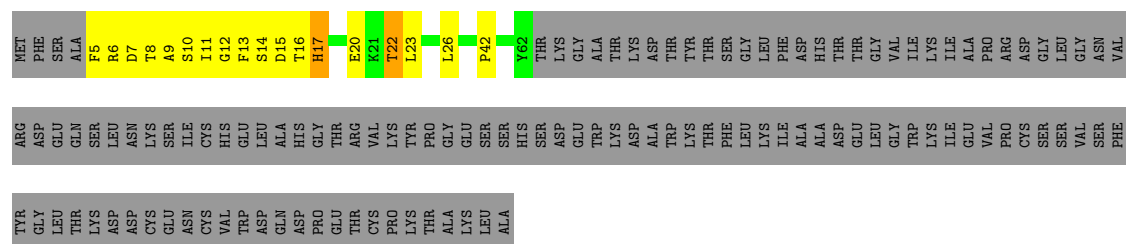
• Molecule 11: P4



• Molecule 11: P4

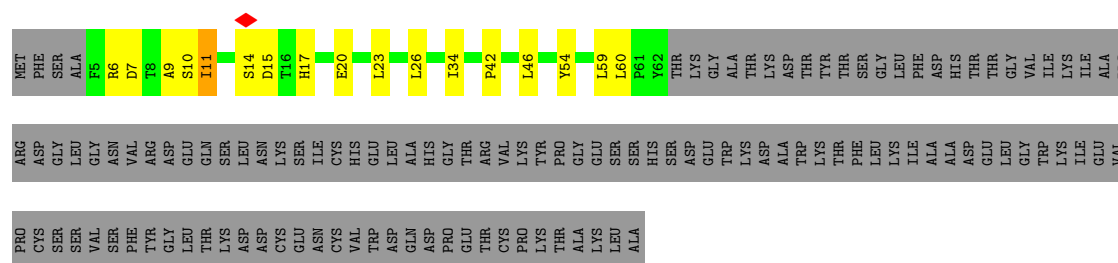


• Molecule 11: P4



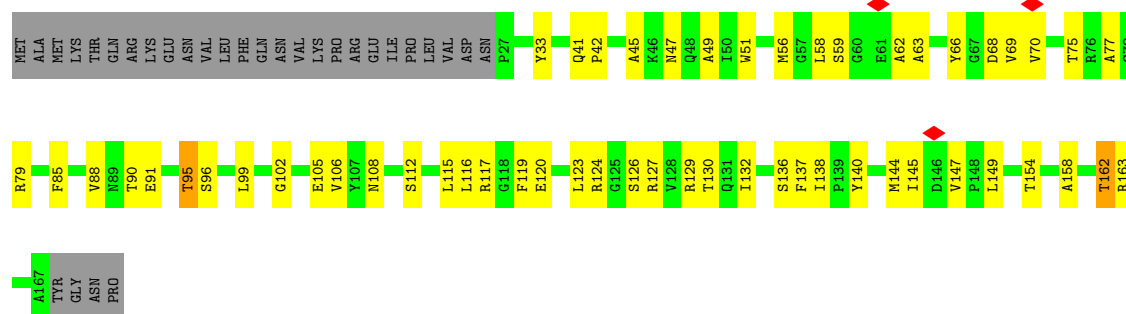
• Molecule 11: P4





• Molecule 12: P3

Chain c6: 50% 31% 18%



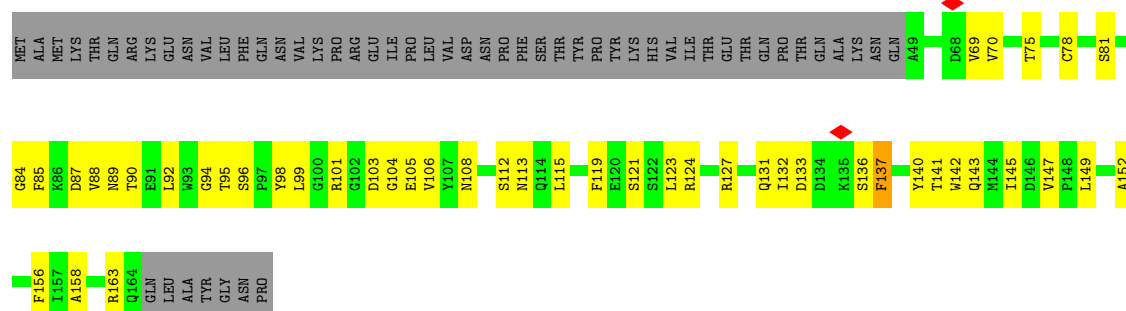
• Molecule 12: P3

Chain c7: 48% 32% 5% 14%



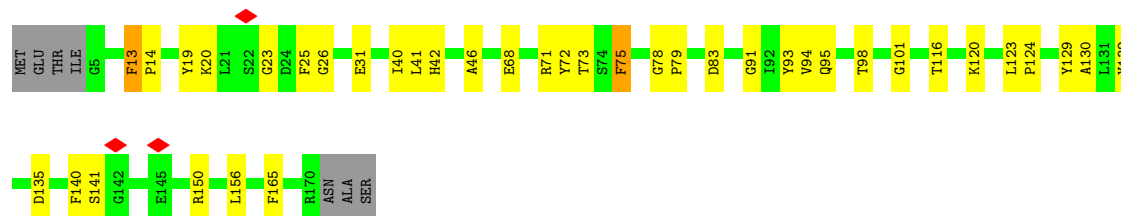
• Molecule 12: P3

Chain c8: 40% 27% 32%



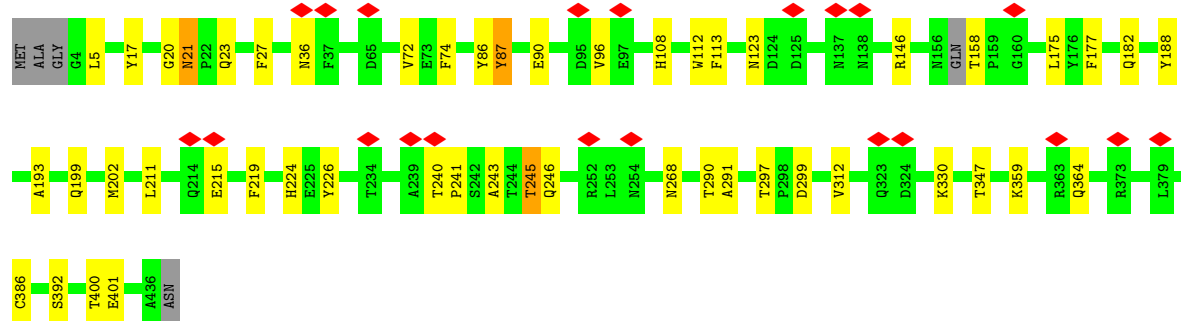
- Molecule 13: P8

Chain c9:  73% 21%



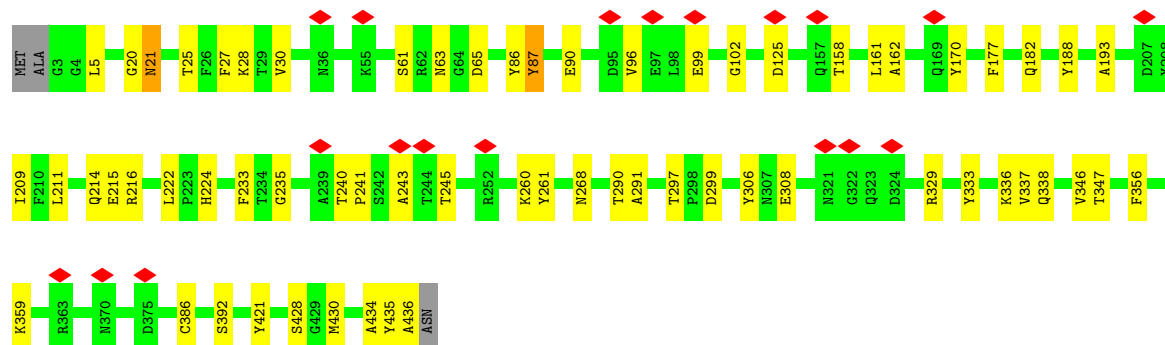
- Molecule 14: Major capsid protein

Chain d0:  5% 87% 11%



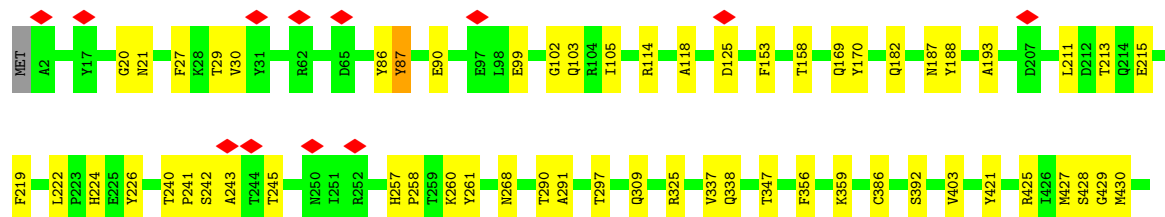
- Molecule 14: Major capsid protein

Chain d1:  85% 14%



- Molecule 14: Major capsid protein

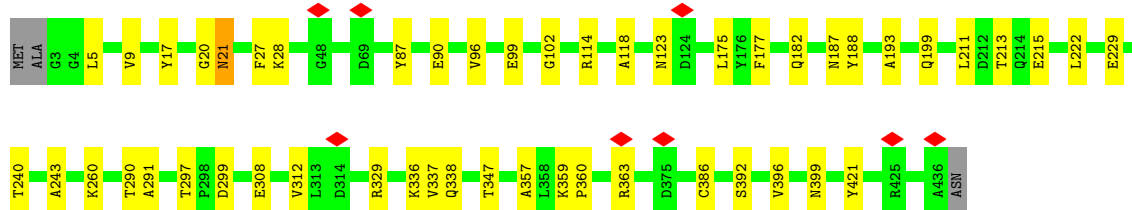
Chain d2:  86% 14%





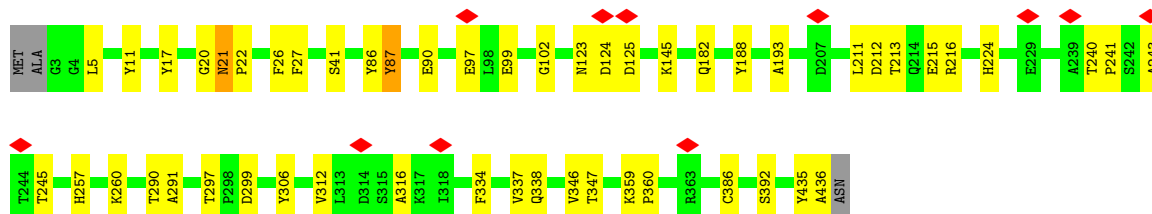
- Molecule 14: Major capsid protein

Chain d3: 88% 11%



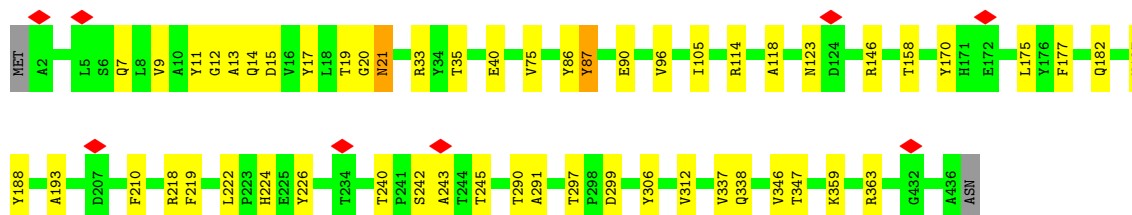
- Molecule 14: Major capsid protein

Chain d4: 87% 11%



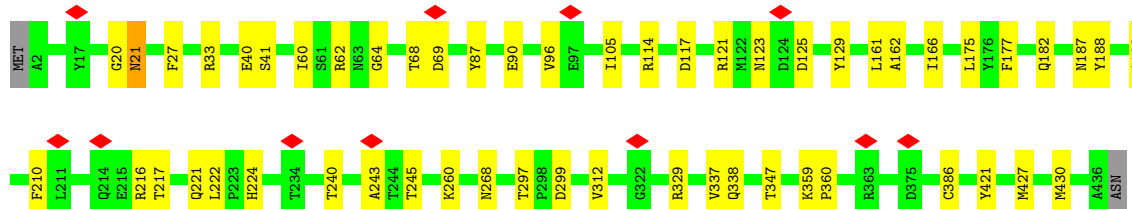
- Molecule 14: Major capsid protein

Chain d5: 87% 12%

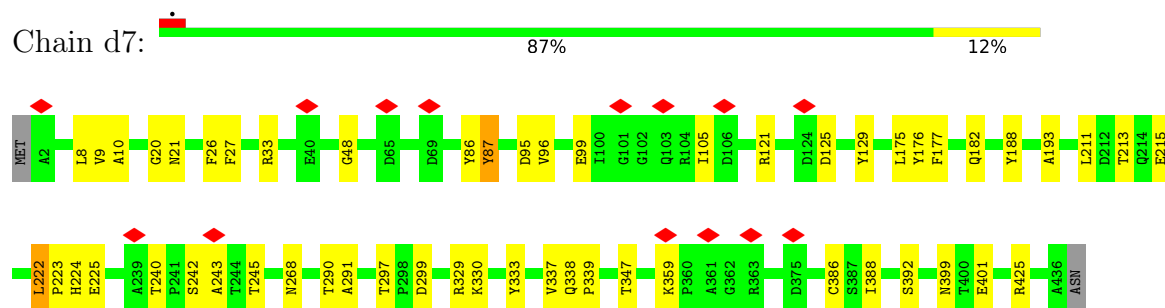


- Molecule 14: Major capsid protein

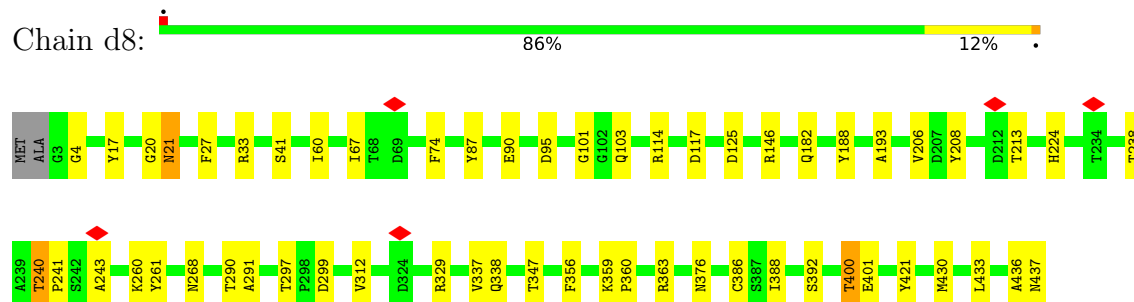
Chain d6: 87% 12%



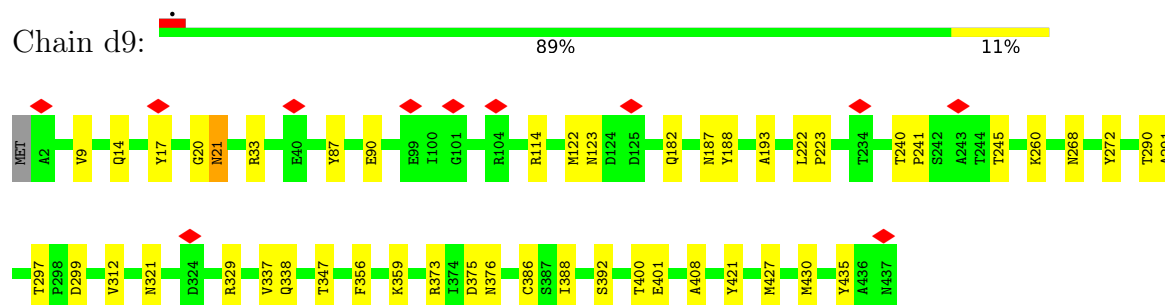
- Molecule 14: Major capsid protein



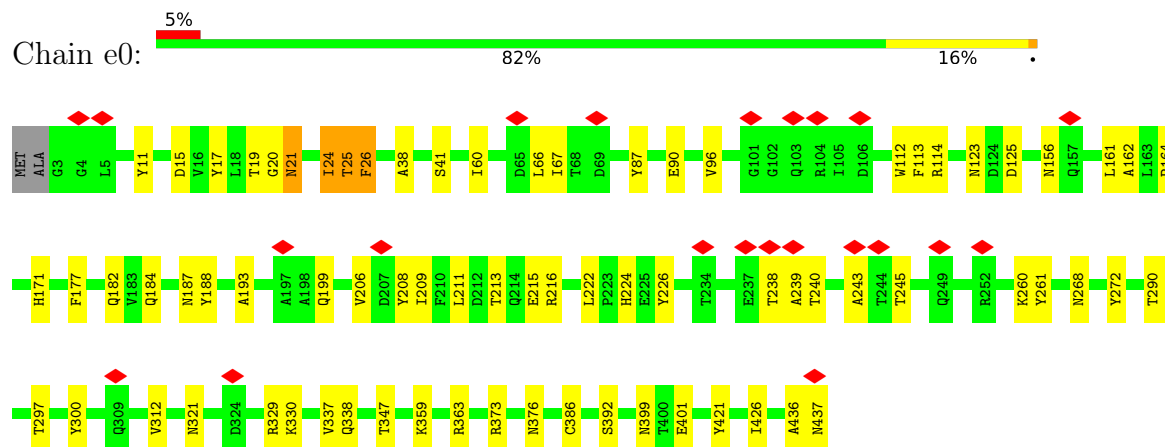
- Molecule 14: Major capsid protein



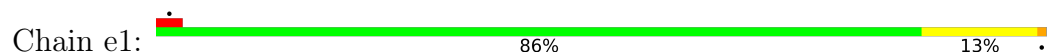
- Molecule 14: Major capsid protein

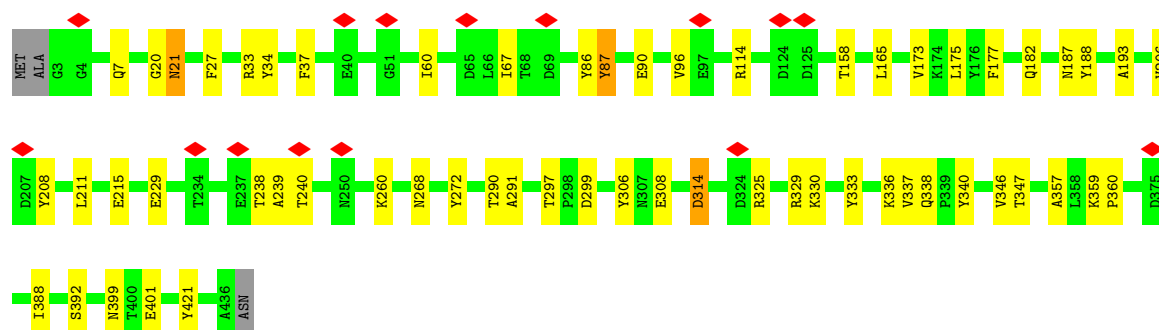


- Molecule 14: Major capsid protein

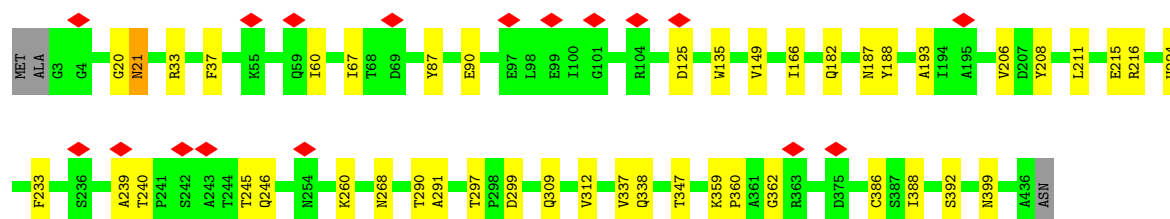
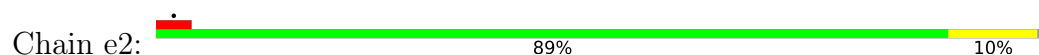


- Molecule 14: Major capsid protein

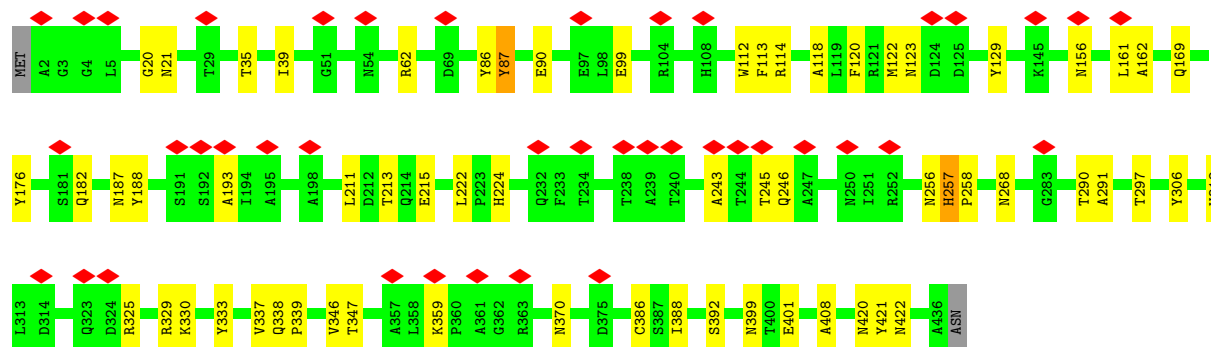
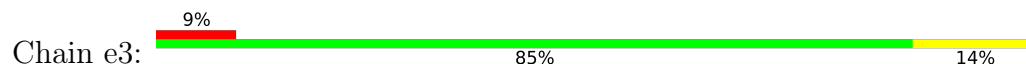




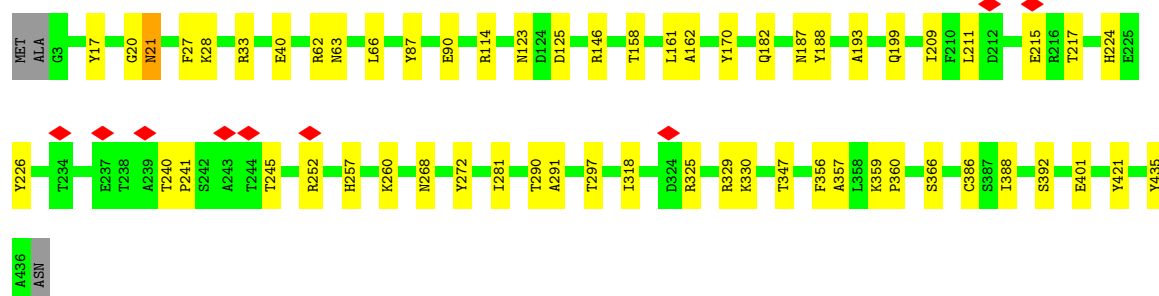
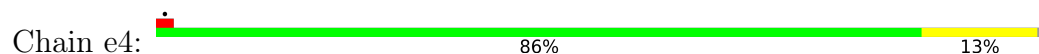
• Molecule 14: Major capsid protein



• Molecule 14: Major capsid protein

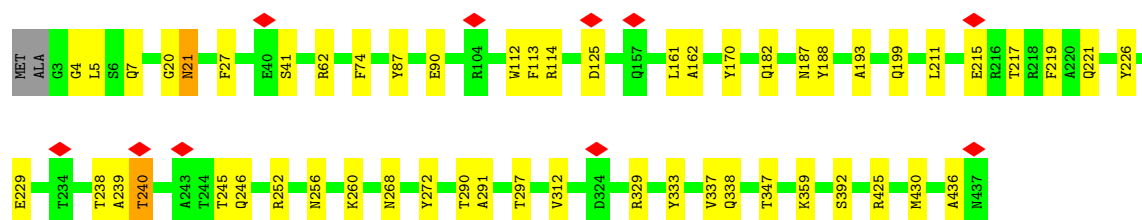


• Molecule 14: Major capsid protein



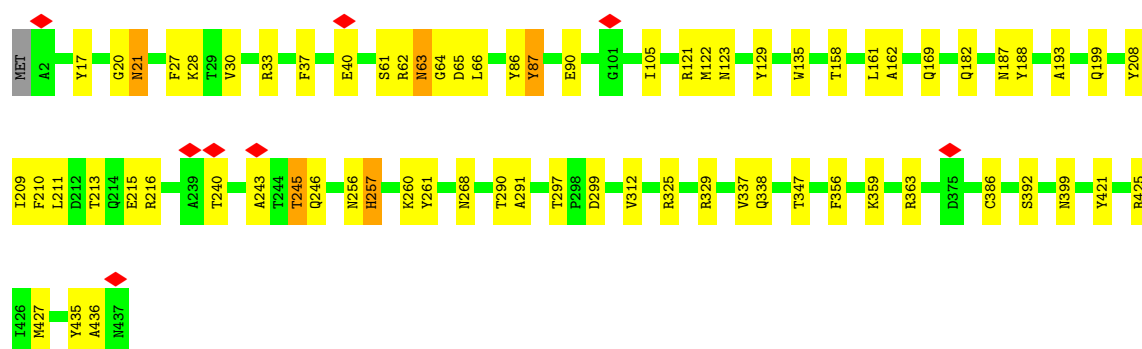
- Molecule 14: Major capsid protein

Chain e5:  87% 12%



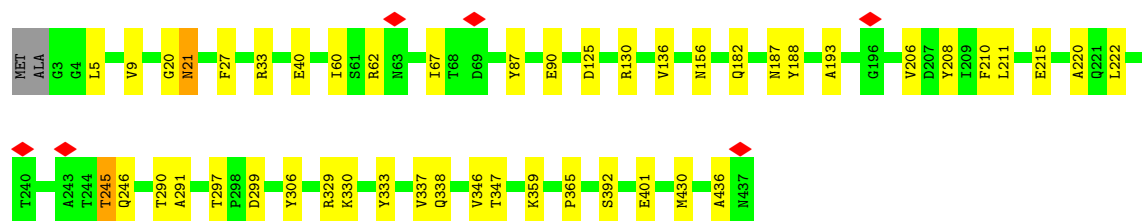
- Molecule 14: Major capsid protein

Chain e6:  84% 15%

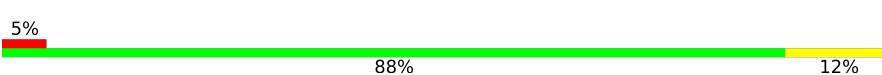


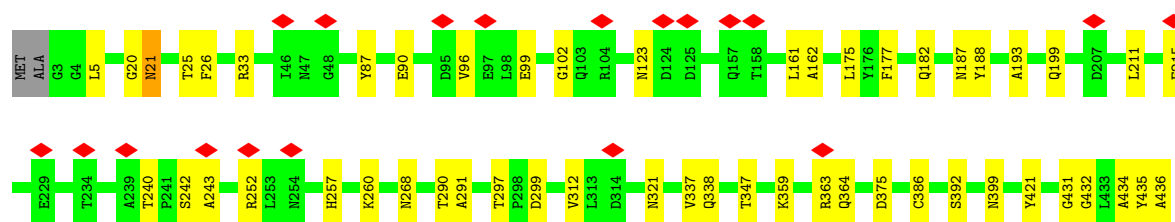
- Molecule 14: Major capsid protein

Chain e7:  89% 10%



- Molecule 14: Major capsid protein

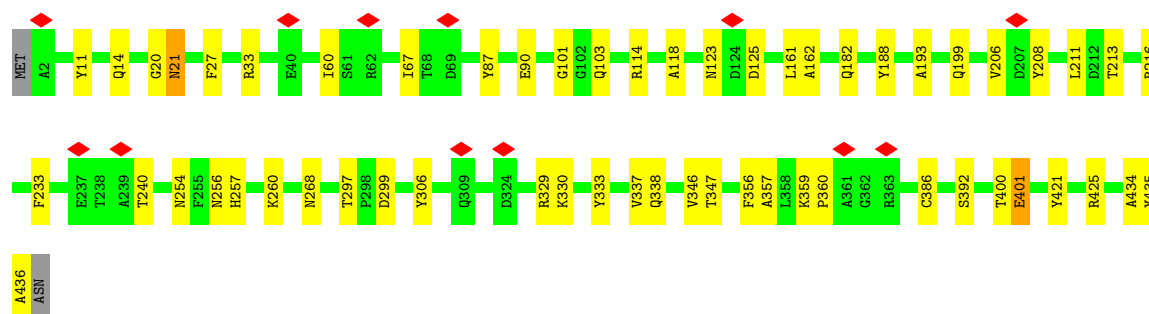
Chain e8:  5% 88% 12%





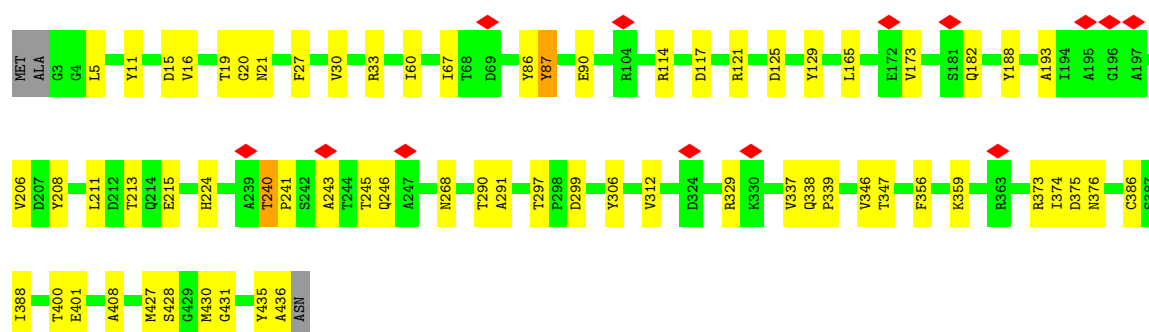
- Molecule 14: Major capsid protein

Chain e9: 86% 13%



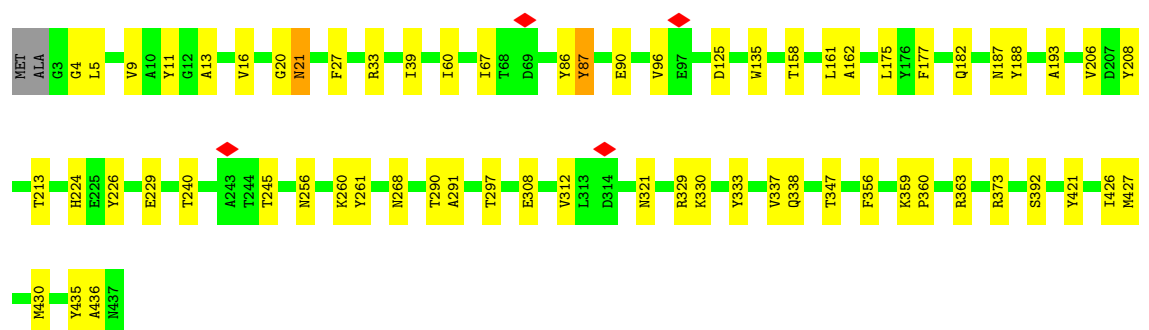
- Molecule 14: Major capsid protein

Chain f0: 84% 15%



- Molecule 14: Major capsid protein

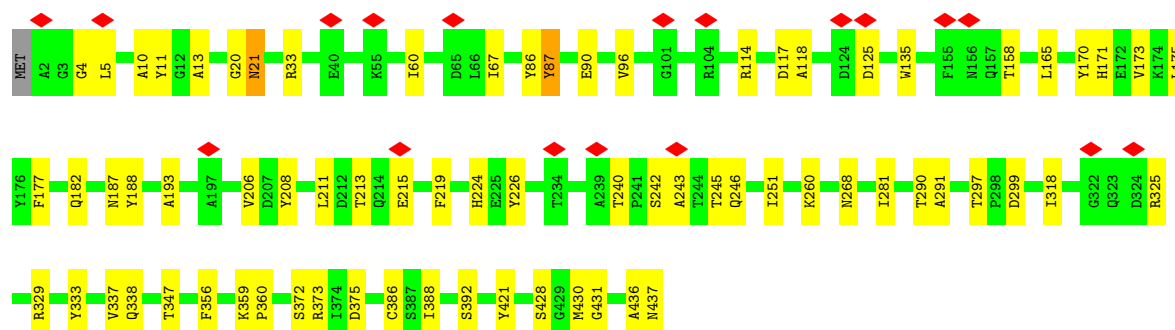
Chain f1: 85% 14%



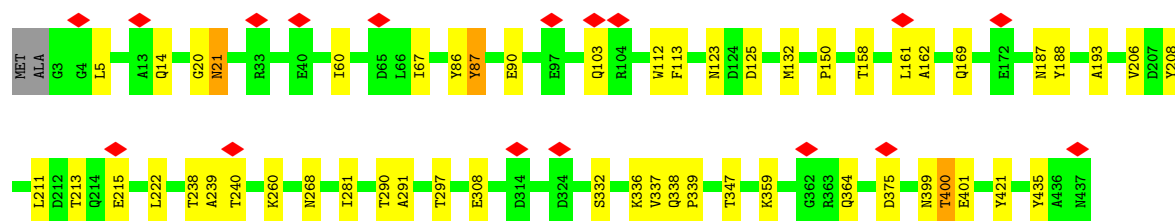
- Molecule 14: Major capsid protein

Chain f2: 83% 16%

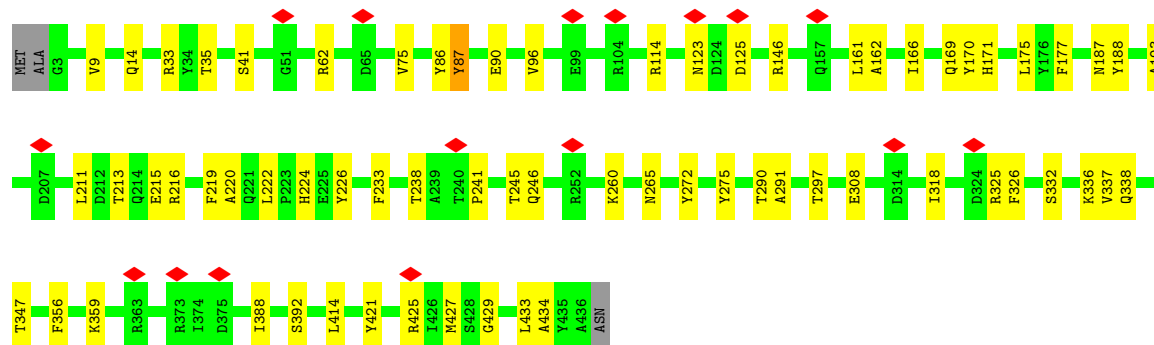
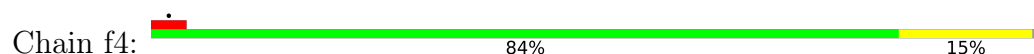




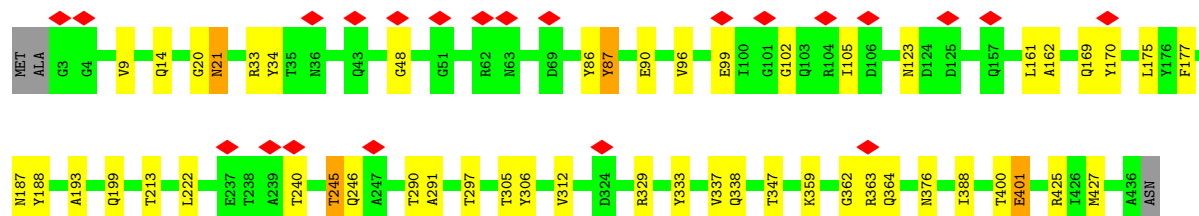
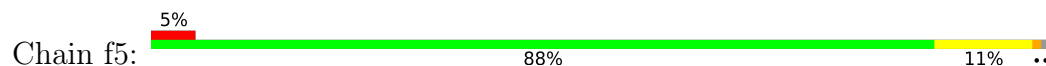
- Molecule 14: Major capsid protein



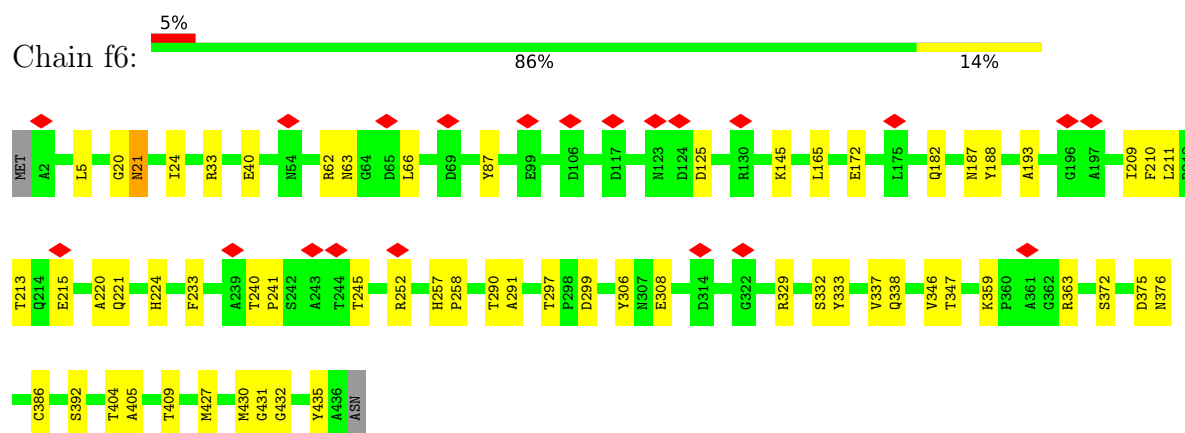
- Molecule 14: Major capsid protein



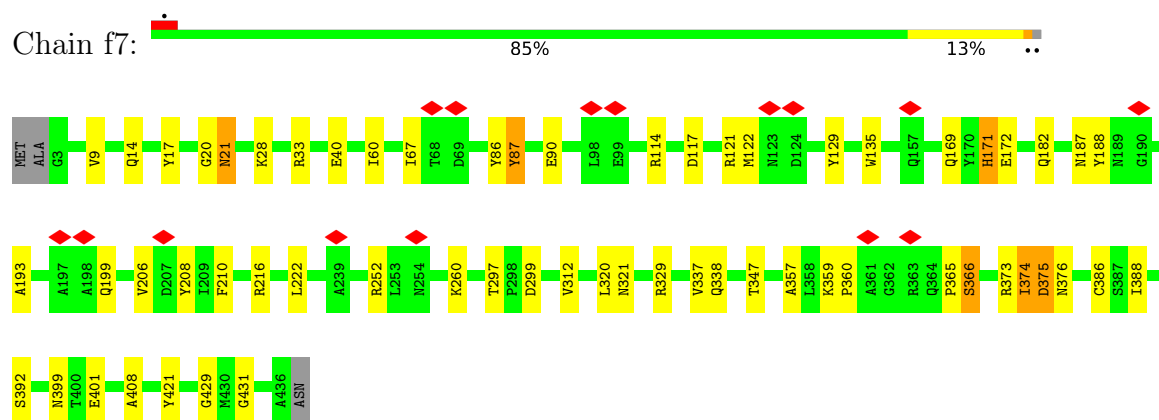
- Molecule 14: Major capsid protein



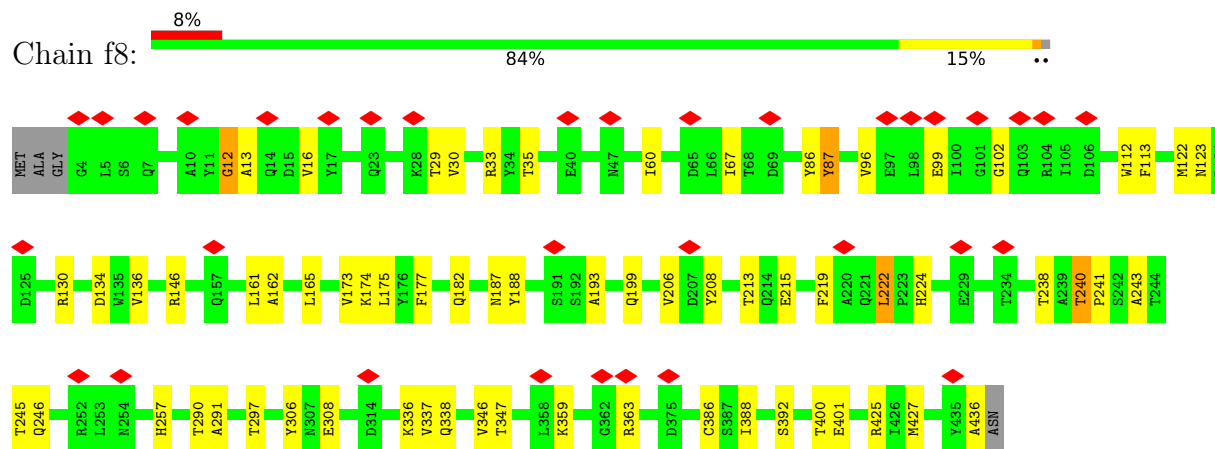
- Molecule 14: Major capsid protein



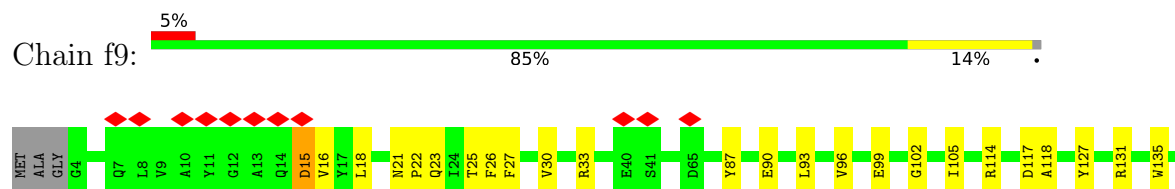
• Molecule 14: Major capsid protein

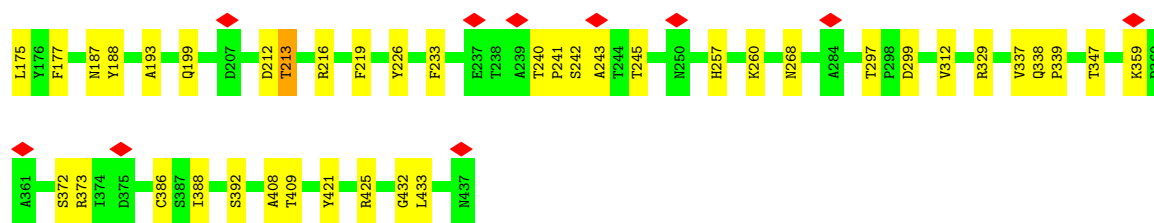


• Molecule 14: Major capsid protein

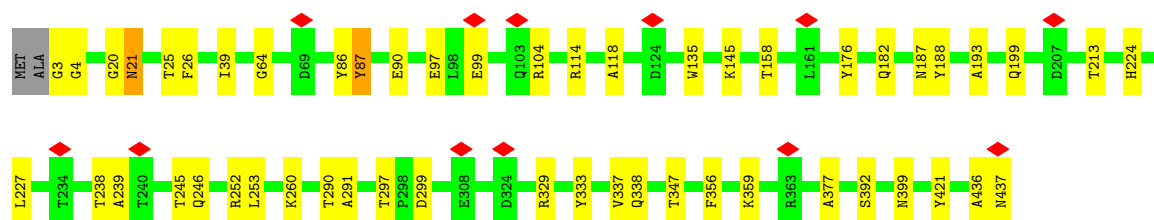


• Molecule 14: Major capsid protein

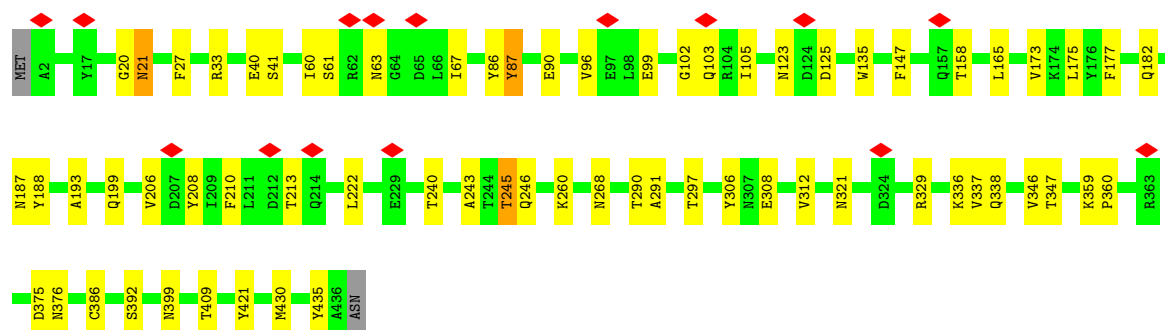
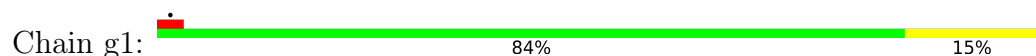




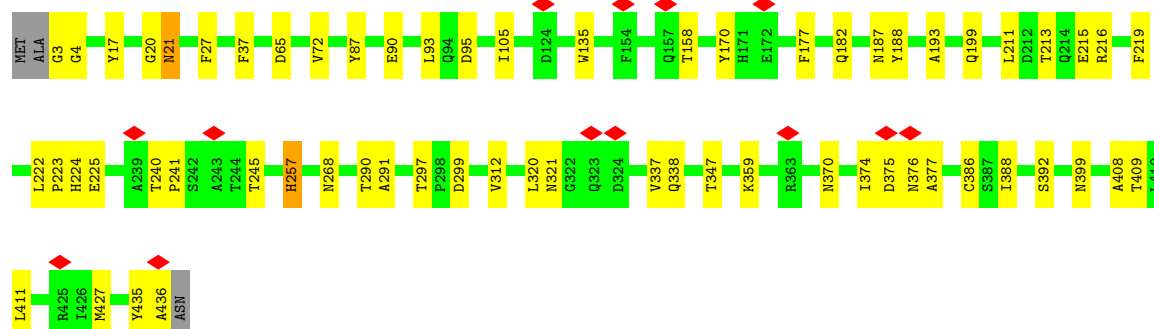
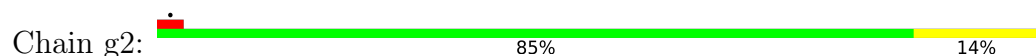
- Molecule 14: Major capsid protein



- Molecule 14: Major capsid protein

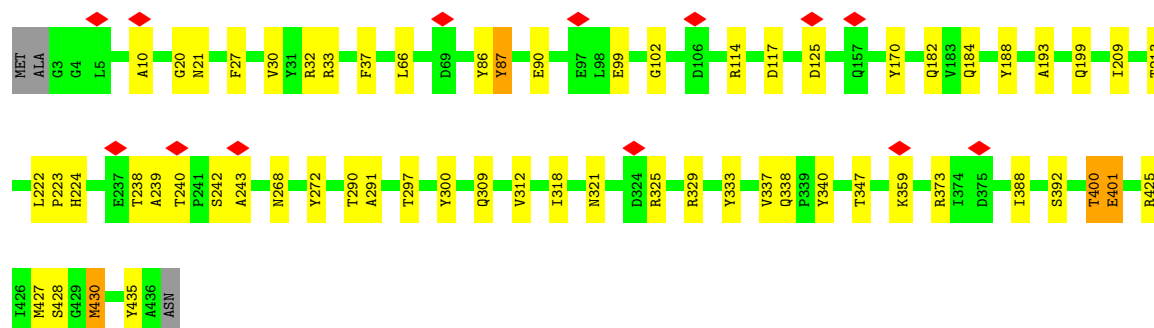


- Molecule 14: Major capsid protein



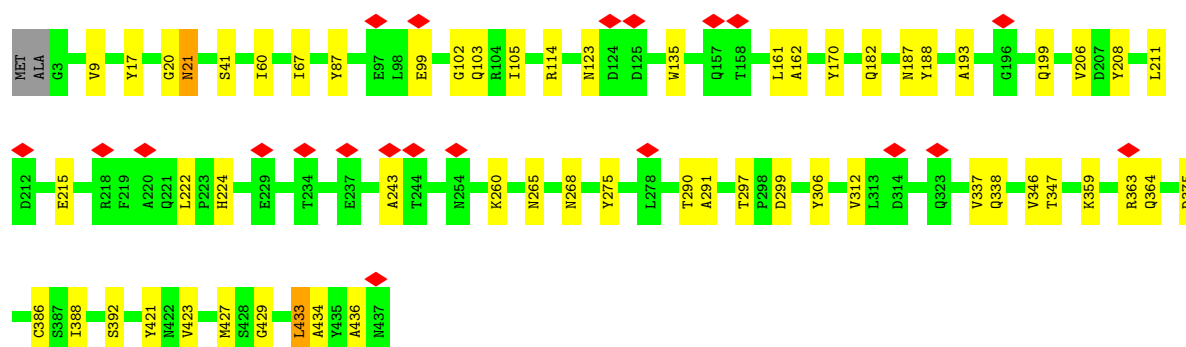
- Molecule 14: Major capsid protein

Chain g3:  85% 13% ..



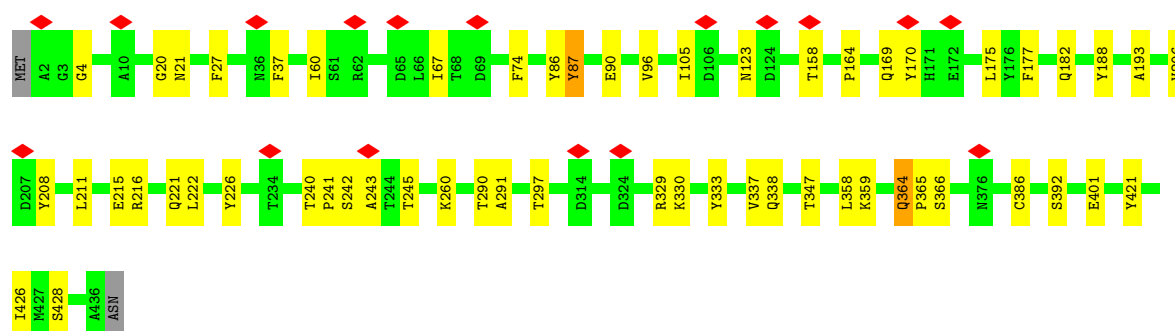
• Molecule 14: Major capsid protein

Chain g4:  5% 86% 13%



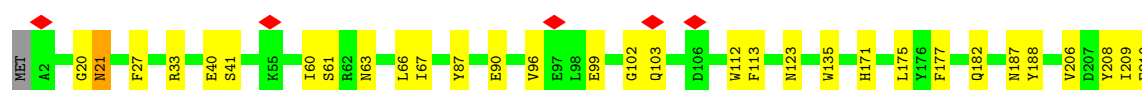
• Molecule 14: Major capsid protein

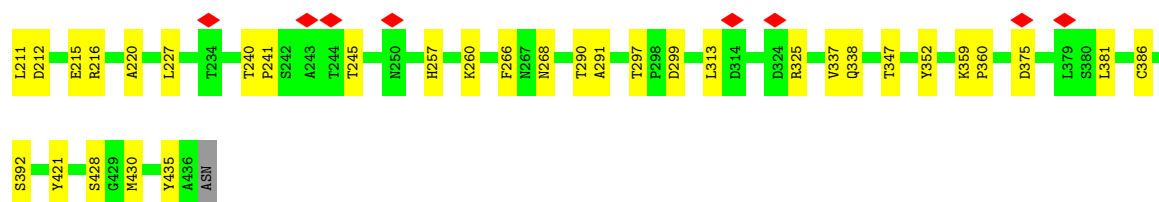
Chain g5:  86% 13%



• Molecule 14: Major capsid protein

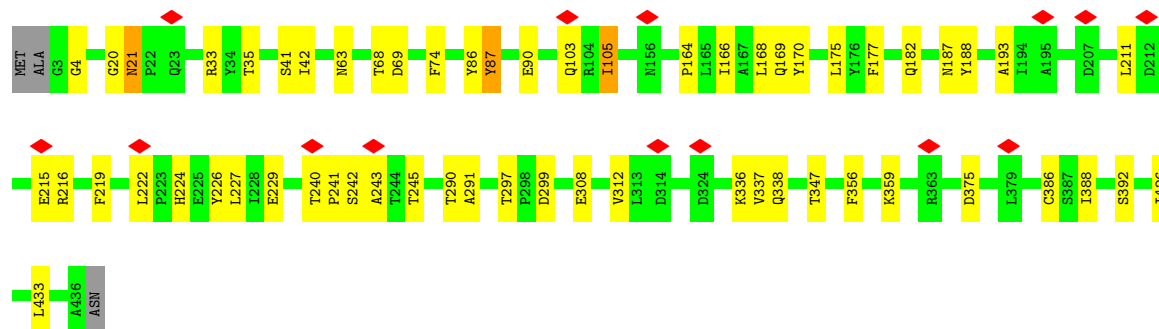
Chain g6:  85% 14%





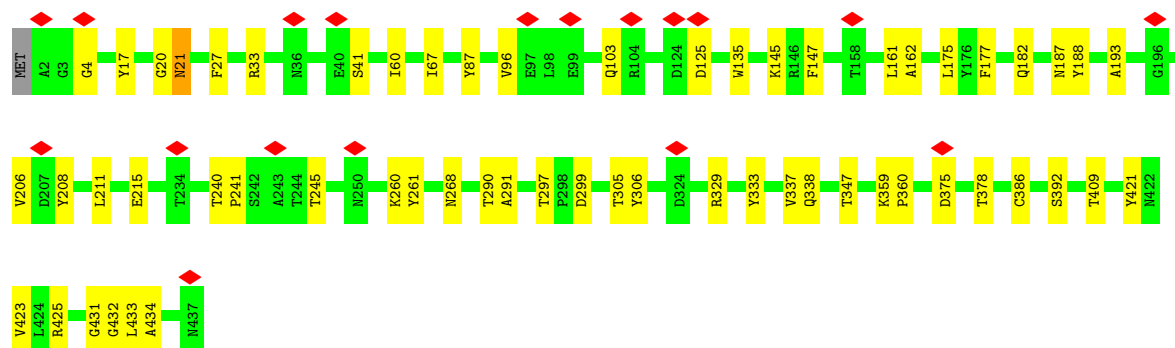
- Molecule 14: Major capsid protein

Chain g7: 86% 13% ..



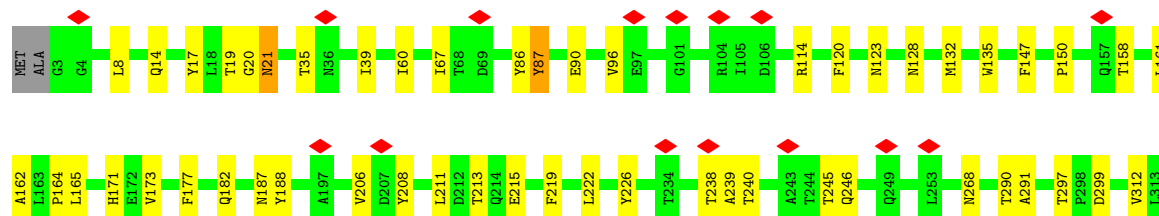
- Molecule 14: Major capsid protein

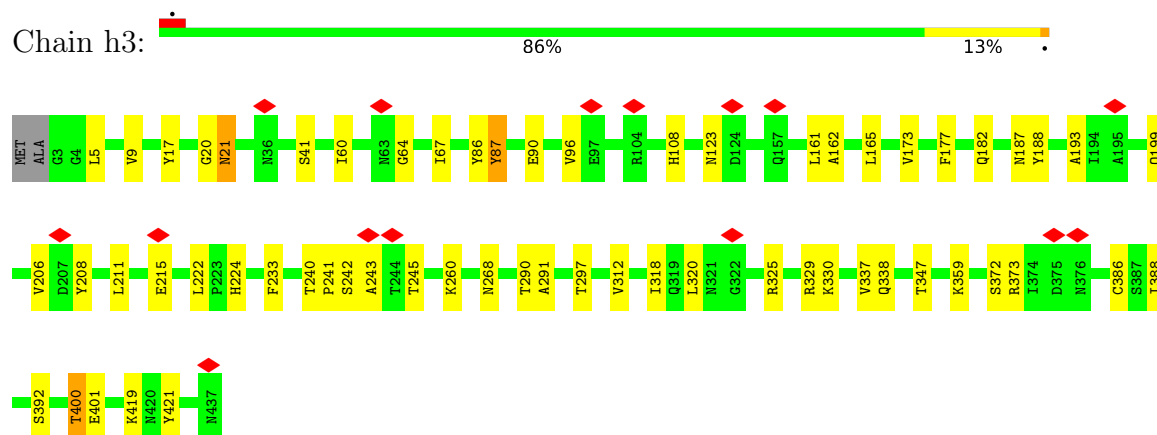
Chain g8: 86% 13%



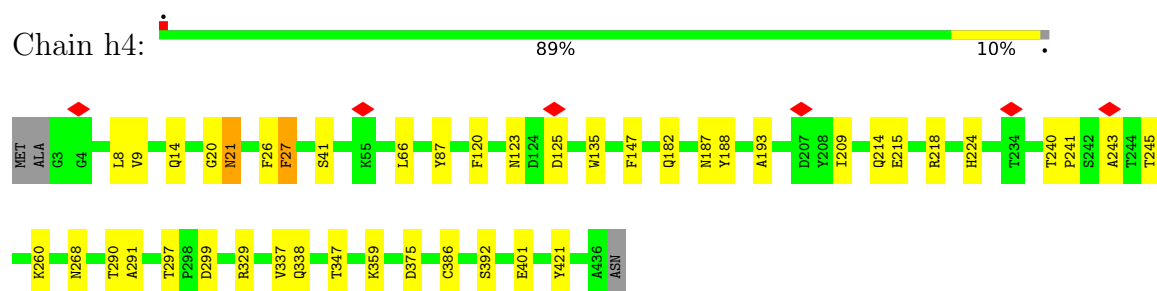
- Molecule 14: Major capsid protein

Chain g9: 5% 84% 15%

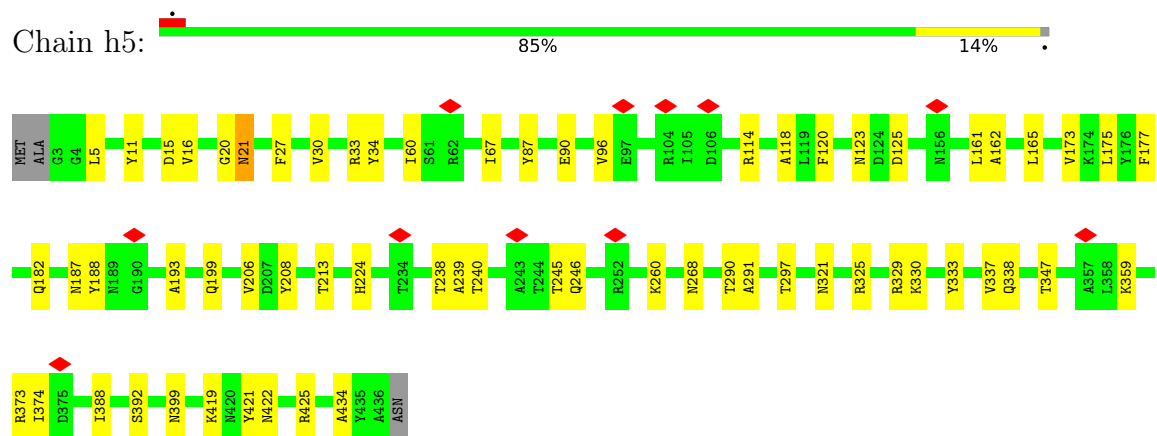




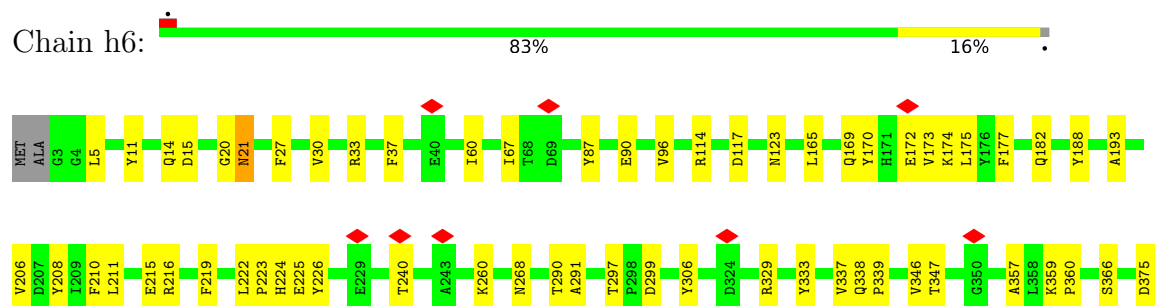
- Molecule 14: Major capsid protein

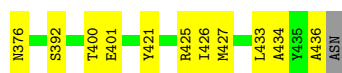


- Molecule 14: Major capsid protein



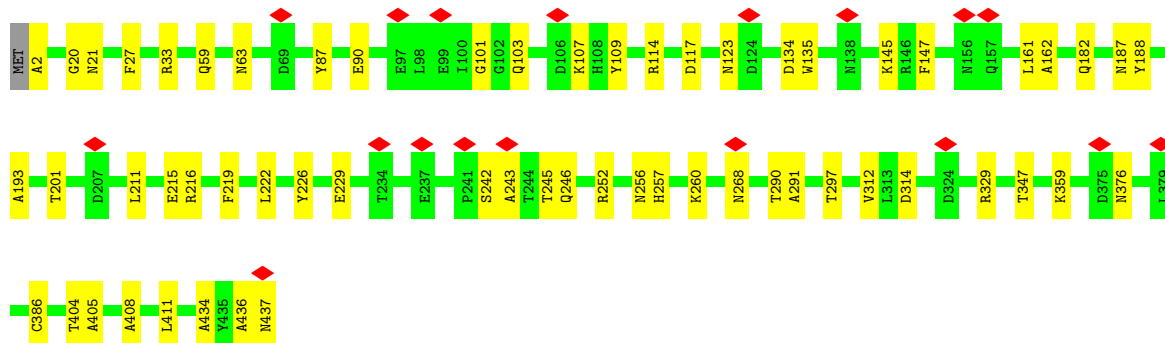
- Molecule 14: Major capsid protein





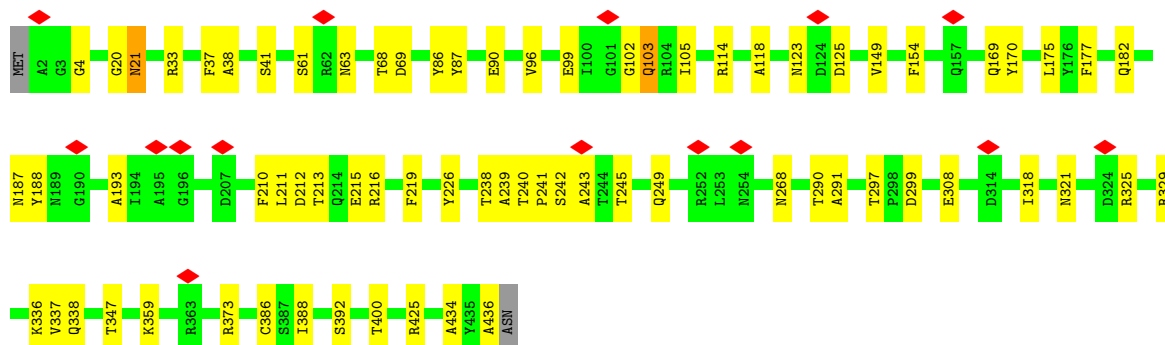
- Molecule 14: Major capsid protein

Chain h7: 86% 14%



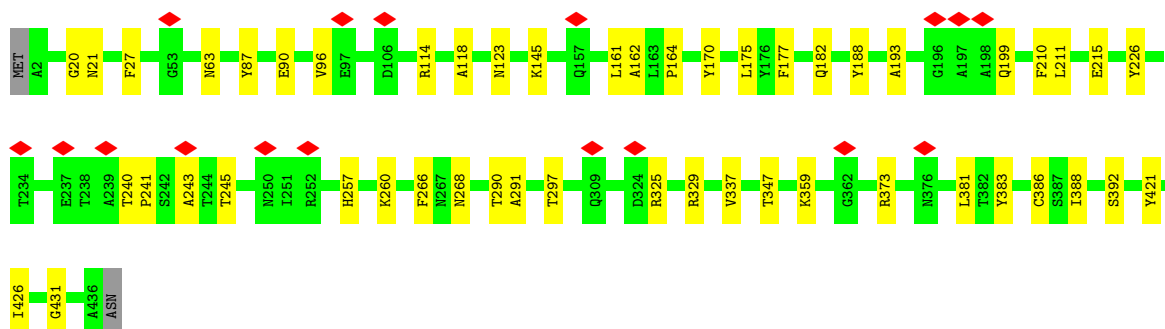
- Molecule 14: Major capsid protein

Chain h8: 83% 16%



- Molecule 14: Major capsid protein

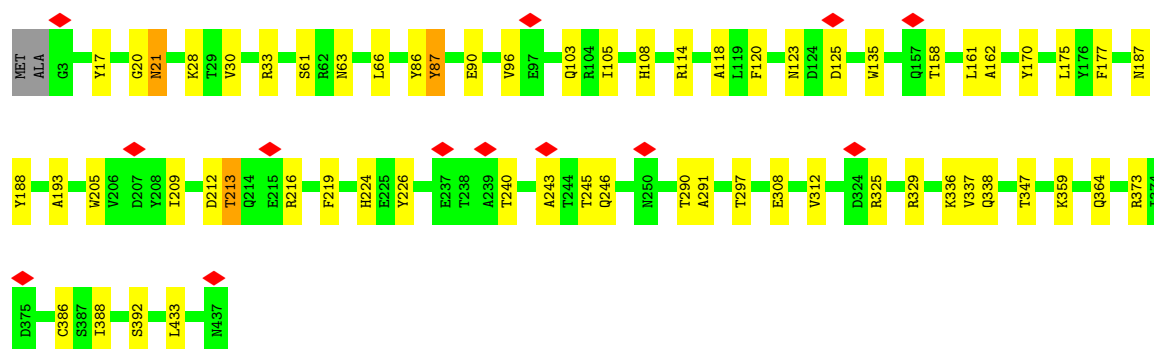
Chain h9: 88% 11%



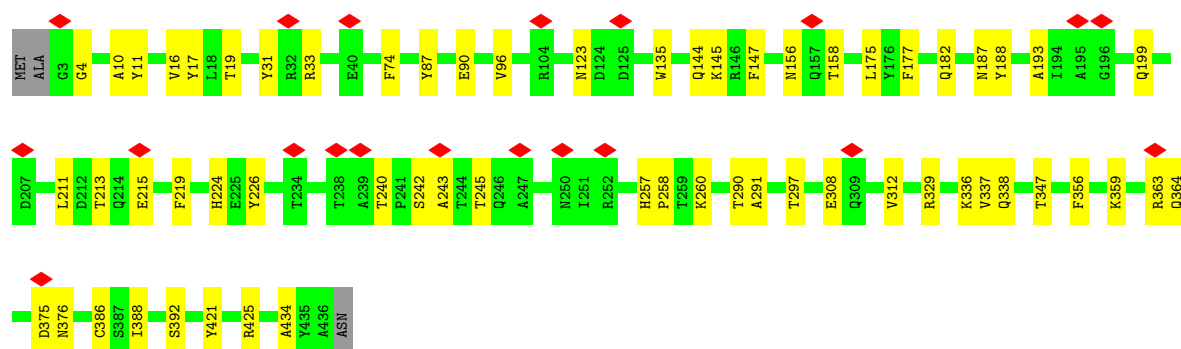
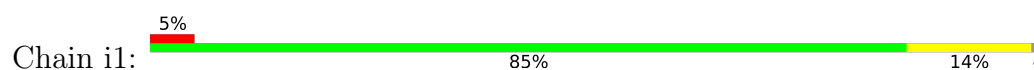
- Molecule 14: Major capsid protein

Chain i0: 86% 13%

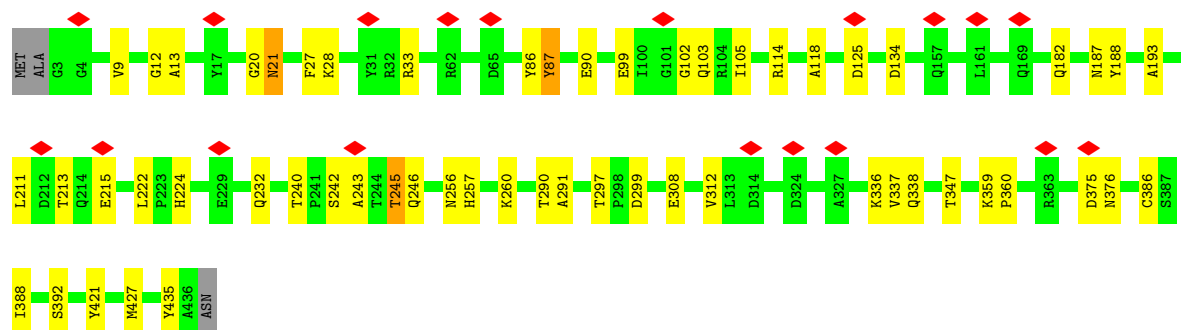
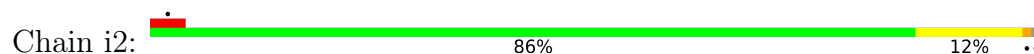




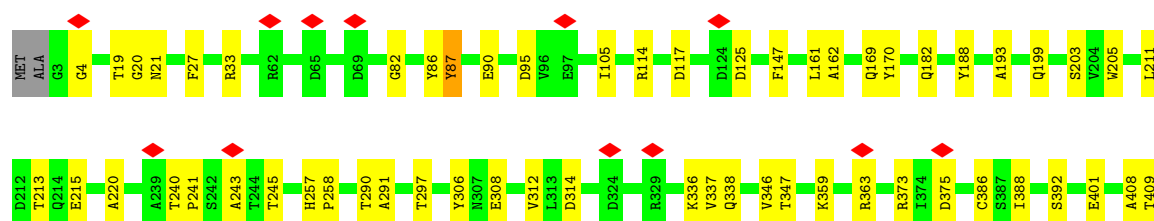
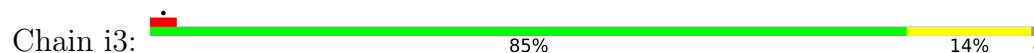
• Molecule 14: Major capsid protein



• Molecule 14: Major capsid protein

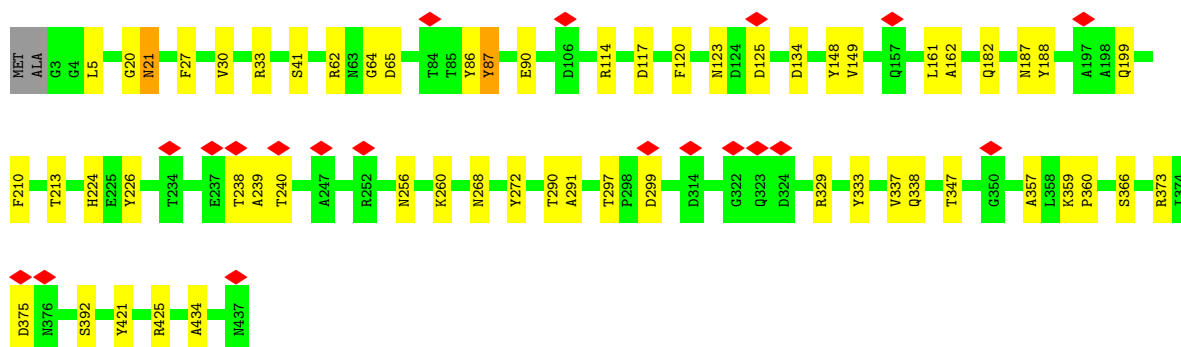
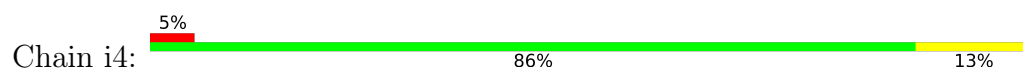


• Molecule 14: Major capsid protein

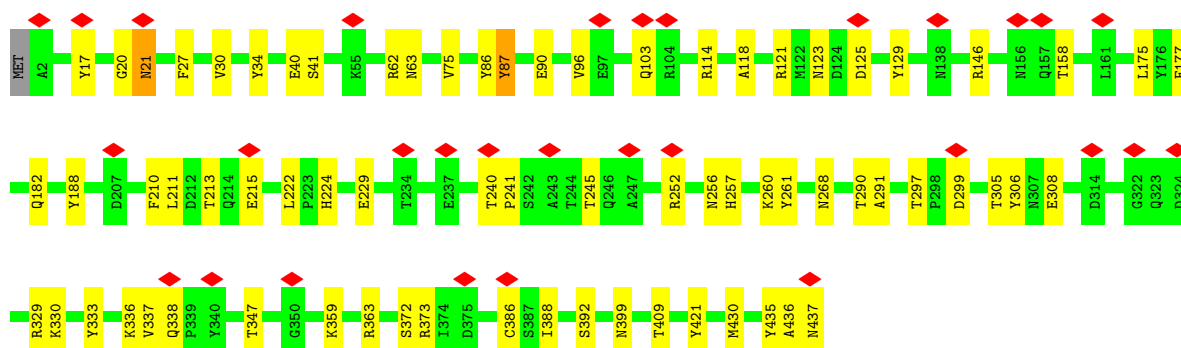
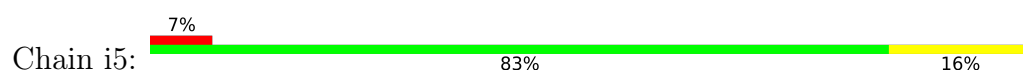




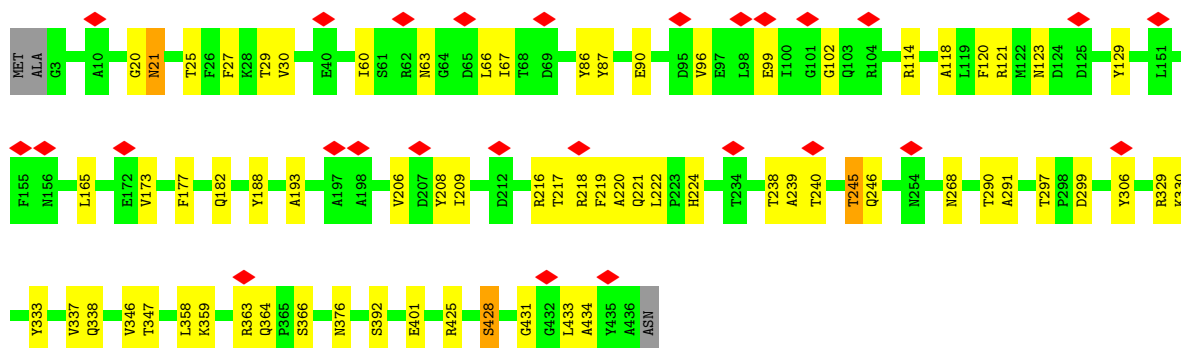
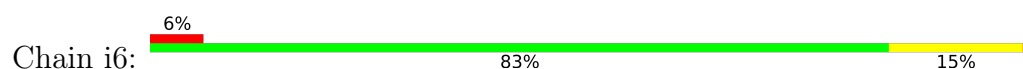
- Molecule 14: Major capsid protein



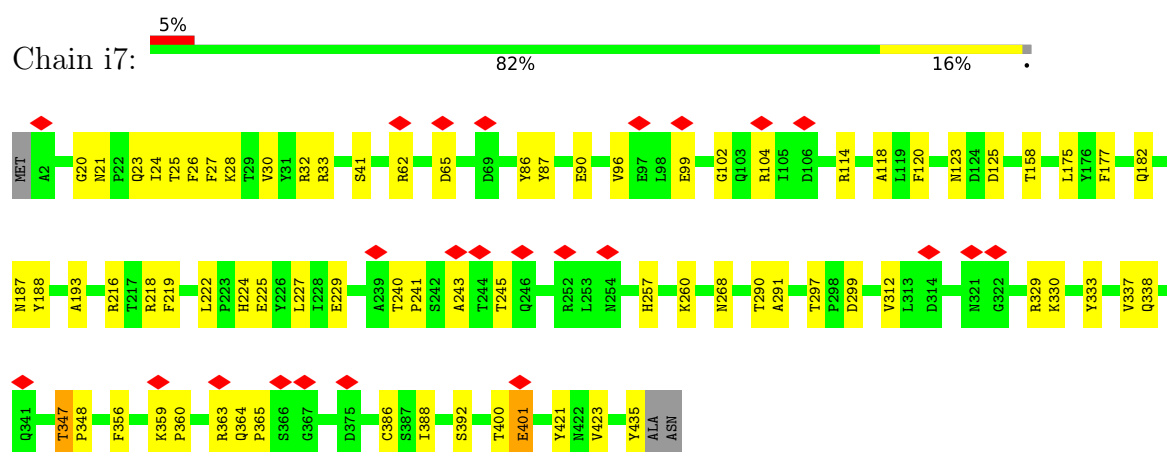
- Molecule 14: Major capsid protein



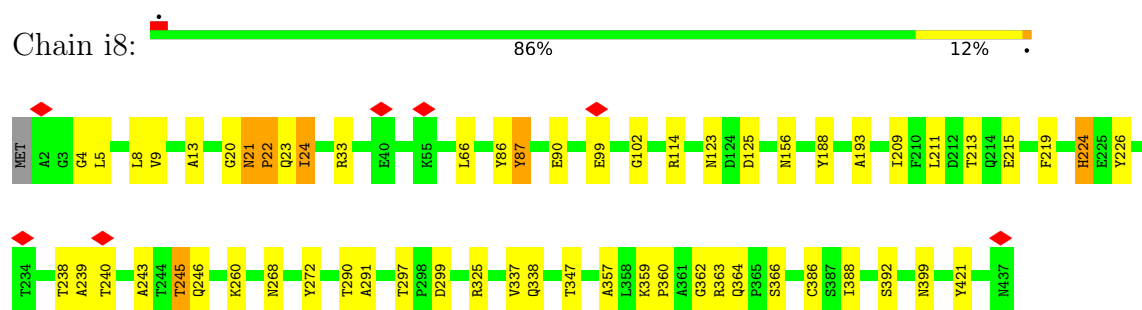
- Molecule 14: Major capsid protein



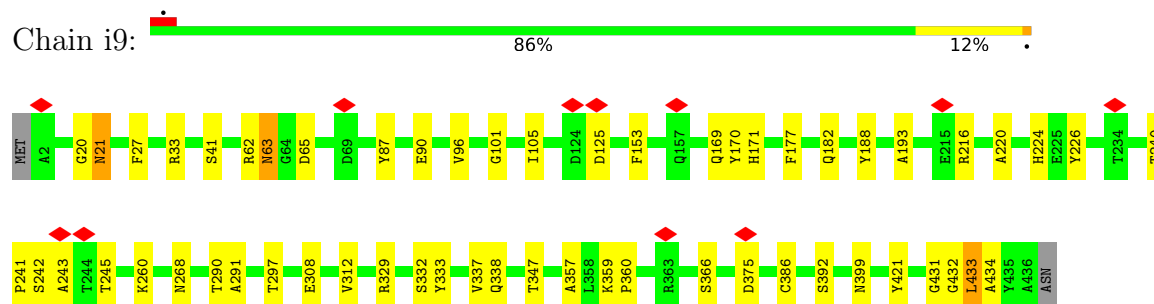
- Molecule 14: Major capsid protein



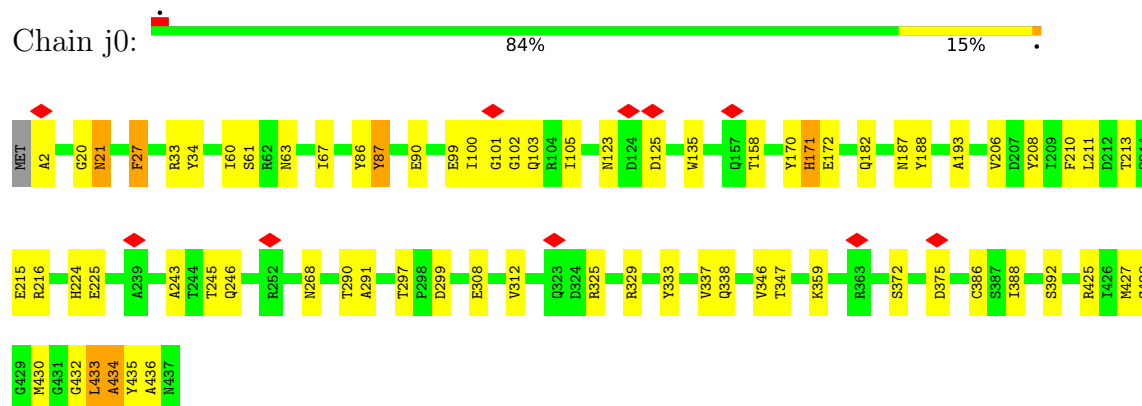
- Molecule 14: Major capsid protein



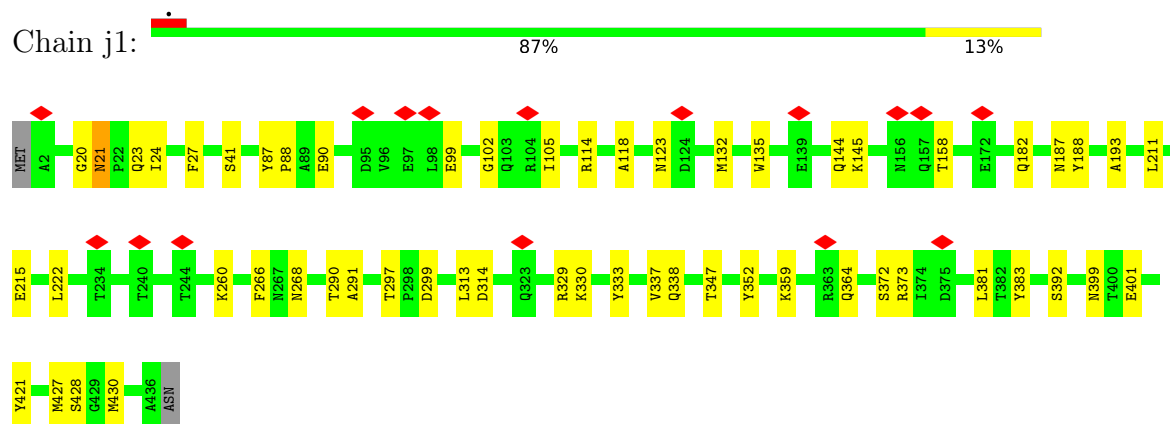
- Molecule 14: Major capsid protein



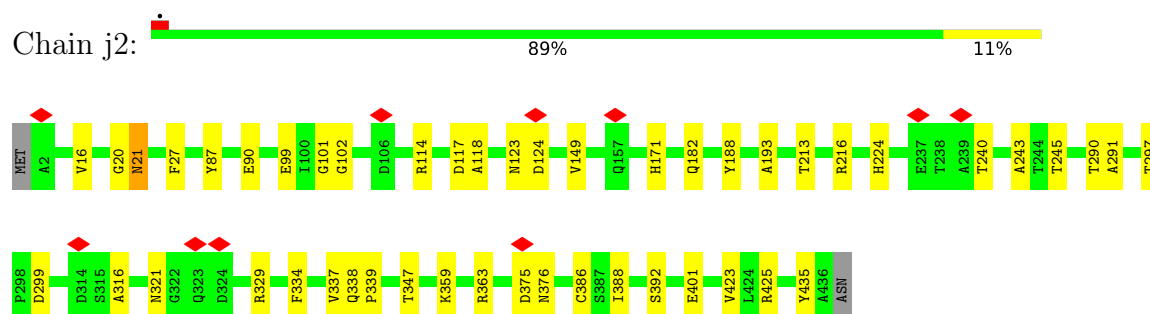
- Molecule 14: Major capsid protein



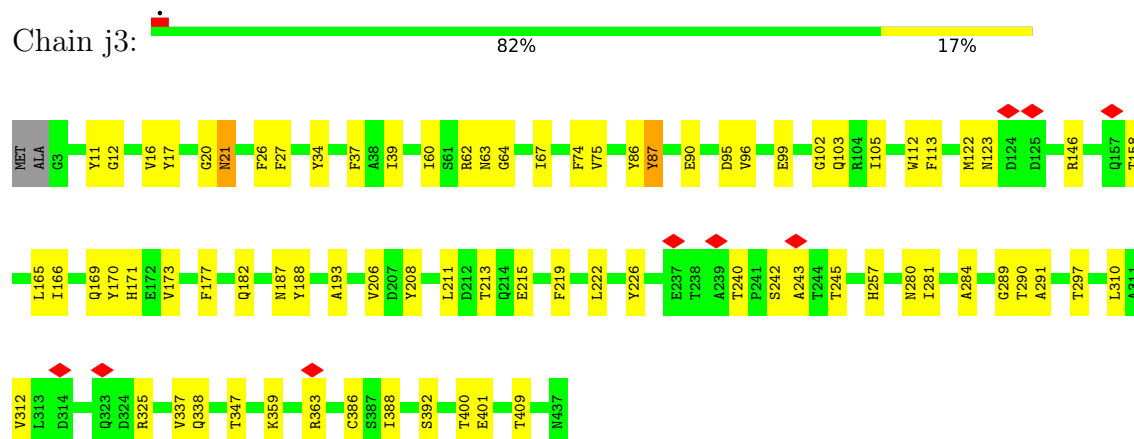
- Molecule 14: Major capsid protein



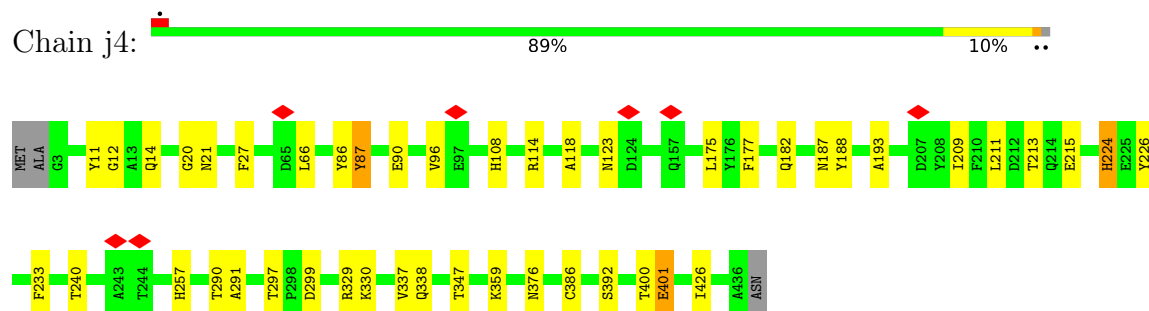
- Molecule 14: Major capsid protein



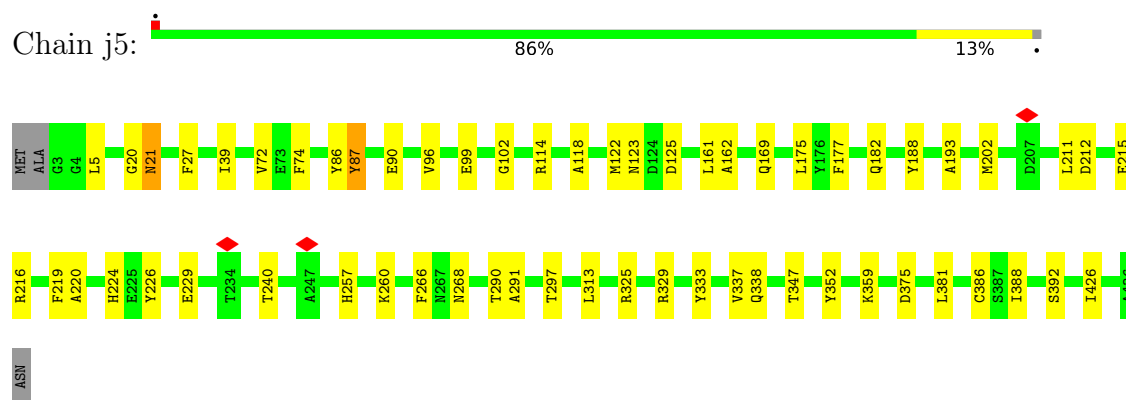
- Molecule 14: Major capsid protein



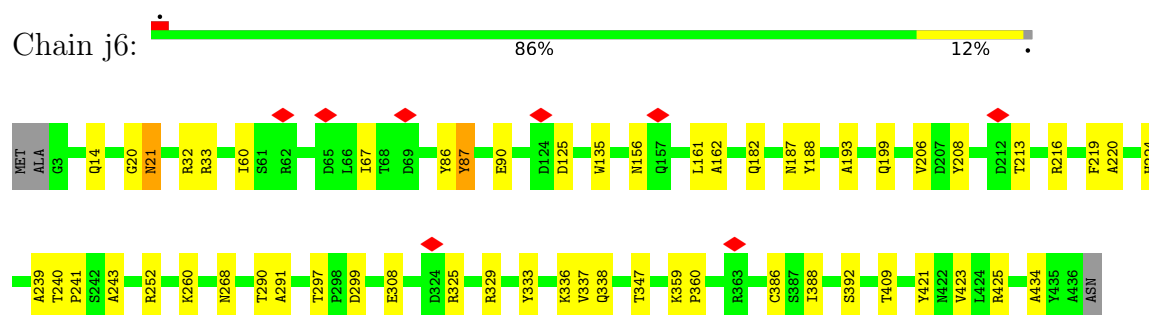
- Molecule 14: Major capsid protein



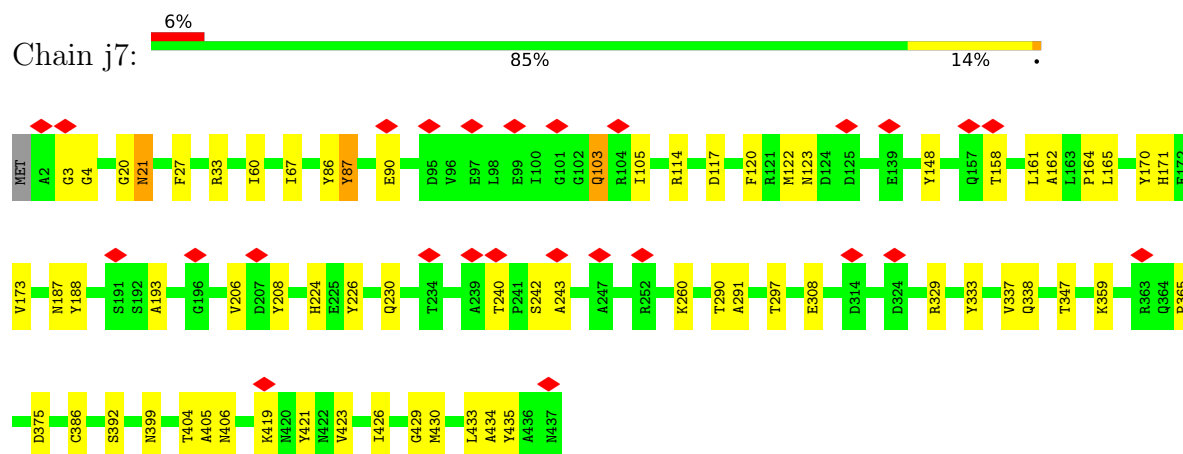
- Molecule 14: Major capsid protein



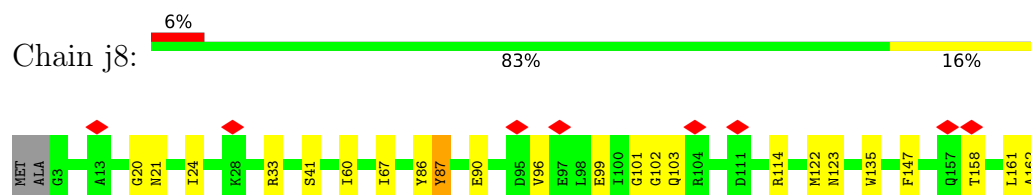
- Molecule 14: Major capsid protein

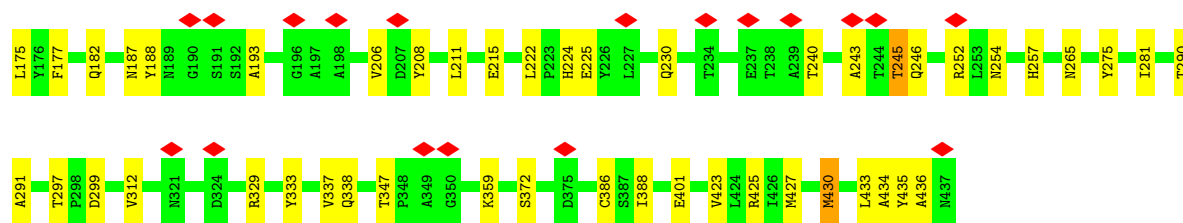


- Molecule 14: Major capsid protein

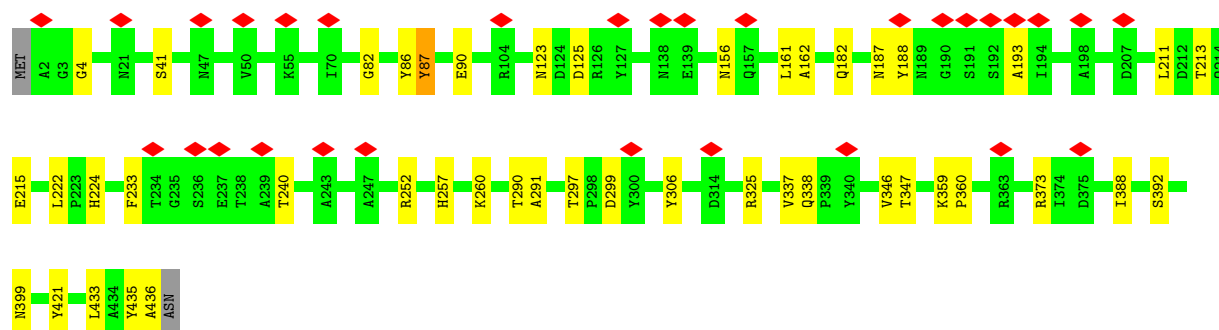
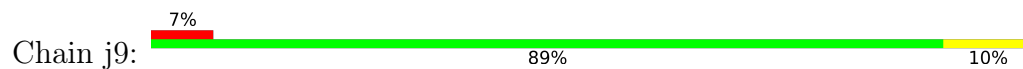


- Molecule 14: Major capsid protein

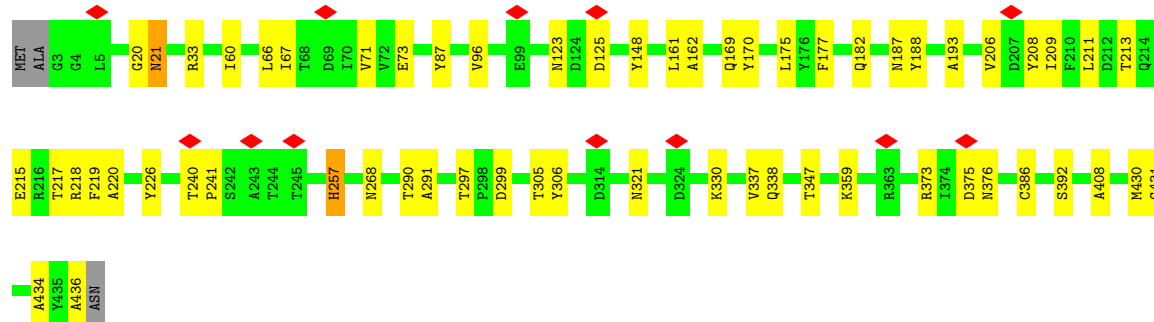
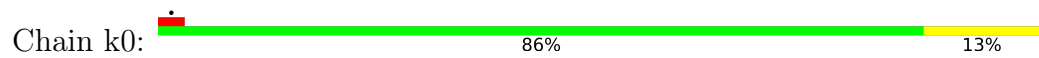




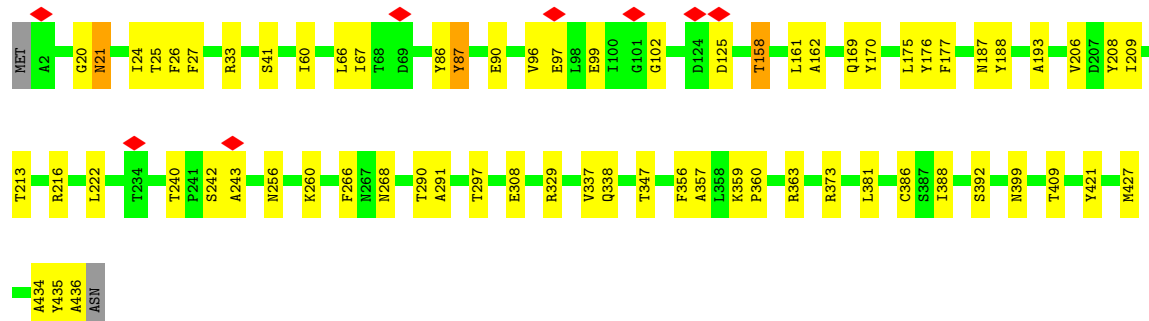
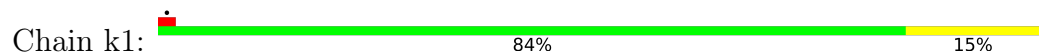
• Molecule 14: Major capsid protein



• Molecule 14: Major capsid protein

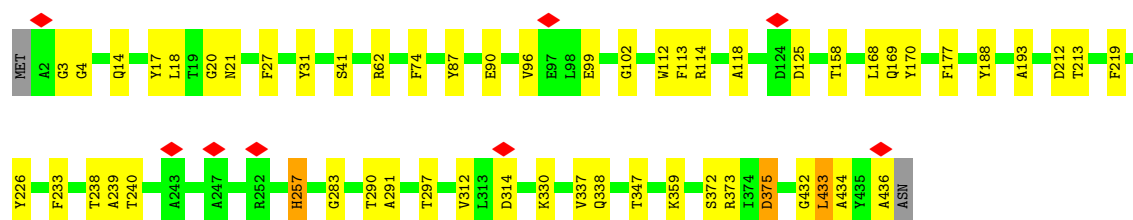


• Molecule 14: Major capsid protein



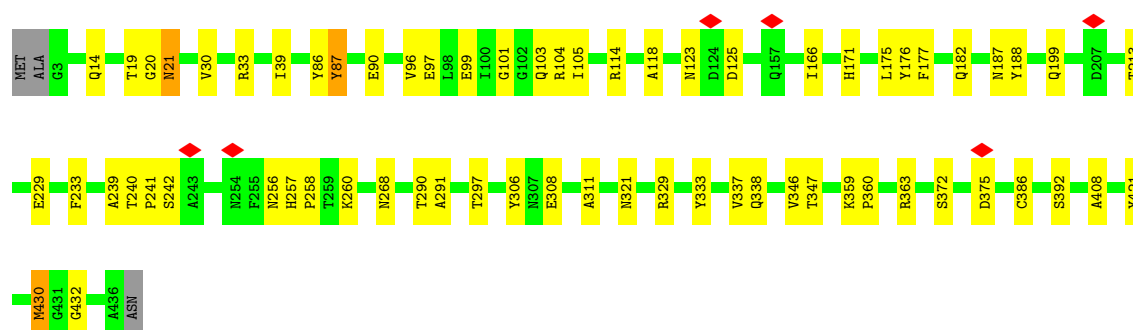
- Molecule 14: Major capsid protein

Chain k2:  87% 12% .



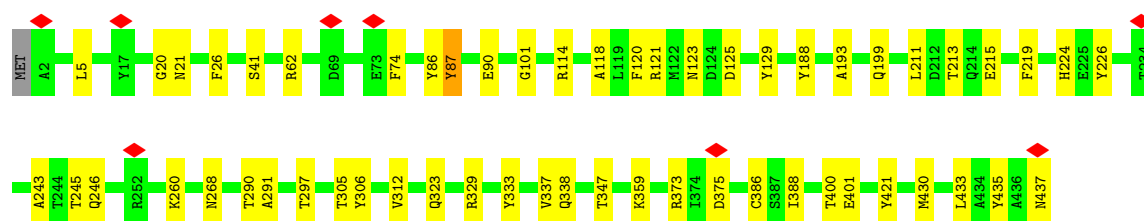
- Molecule 14: Major capsid protein

Chain k3:  84% 14% ..



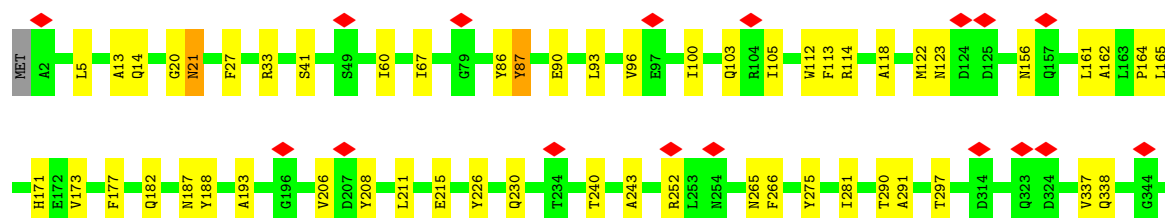
- Molecule 14: Major capsid protein

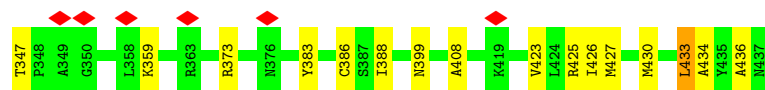
Chain k4:  87% 13%



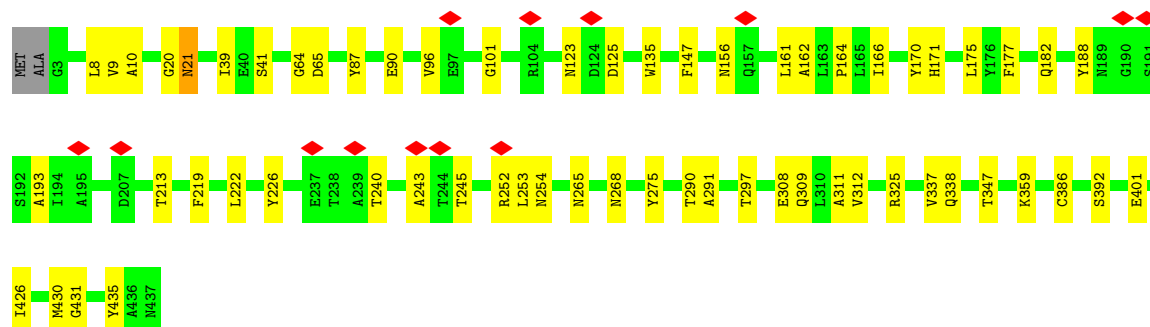
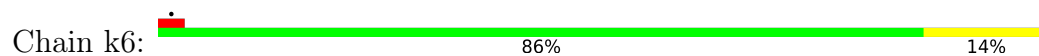
- Molecule 14: Major capsid protein

Chain k5:  5% 84% 15% .

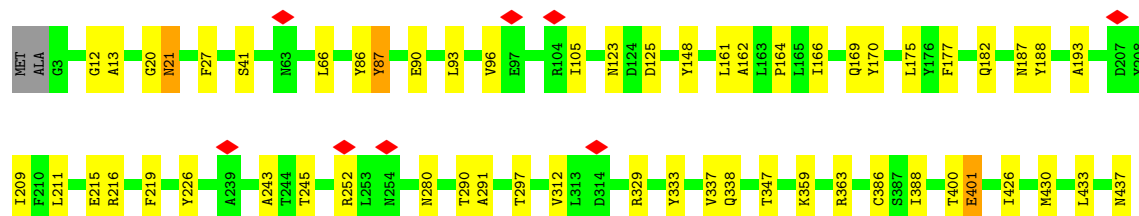
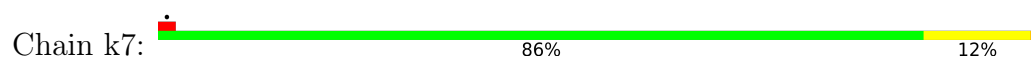




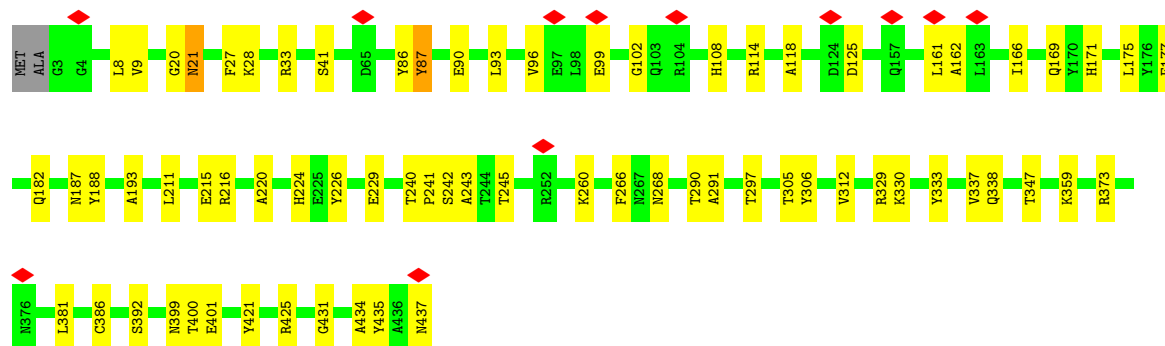
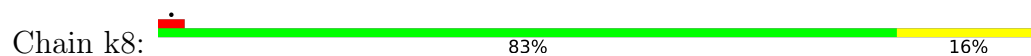
- Molecule 14: Major capsid protein



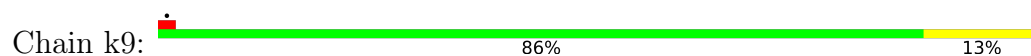
- Molecule 14: Major capsid protein

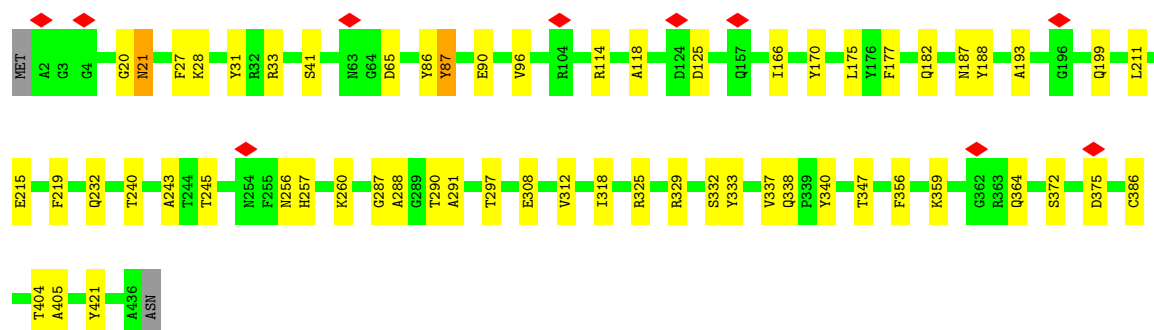


- Molecule 14: Major capsid protein

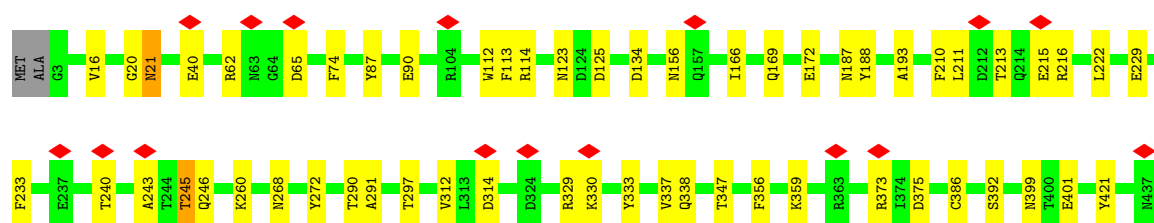
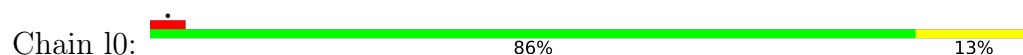


- Molecule 14: Major capsid protein

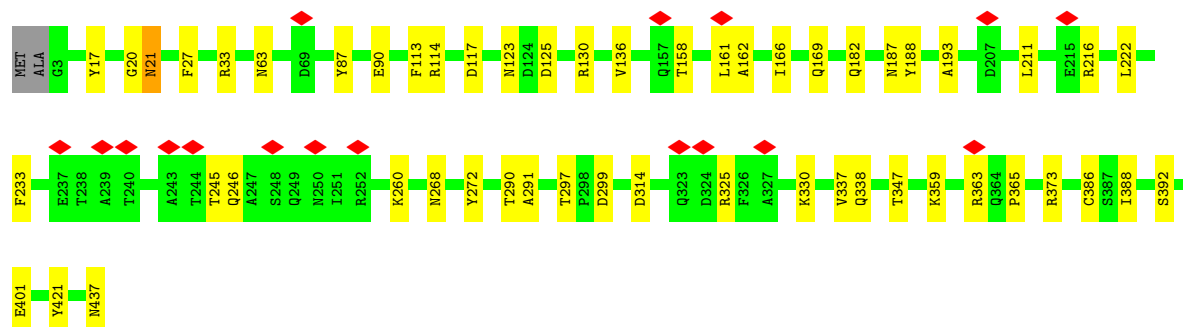




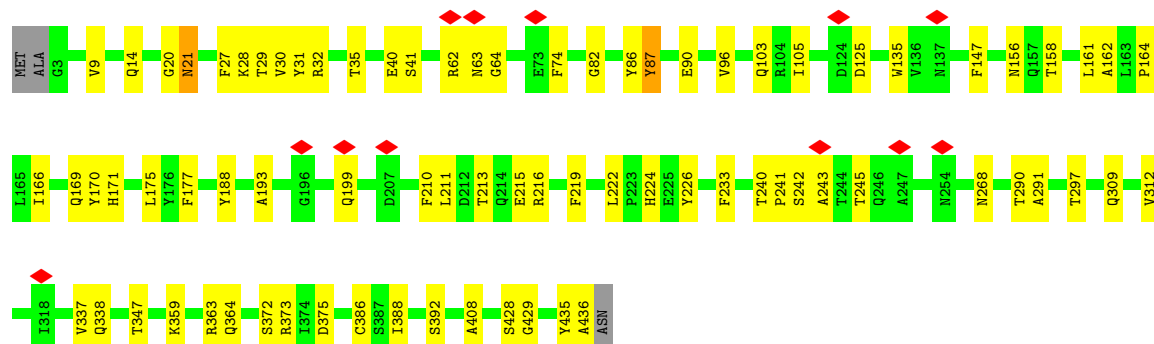
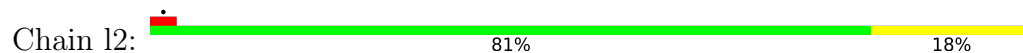
- Molecule 14: Major capsid protein



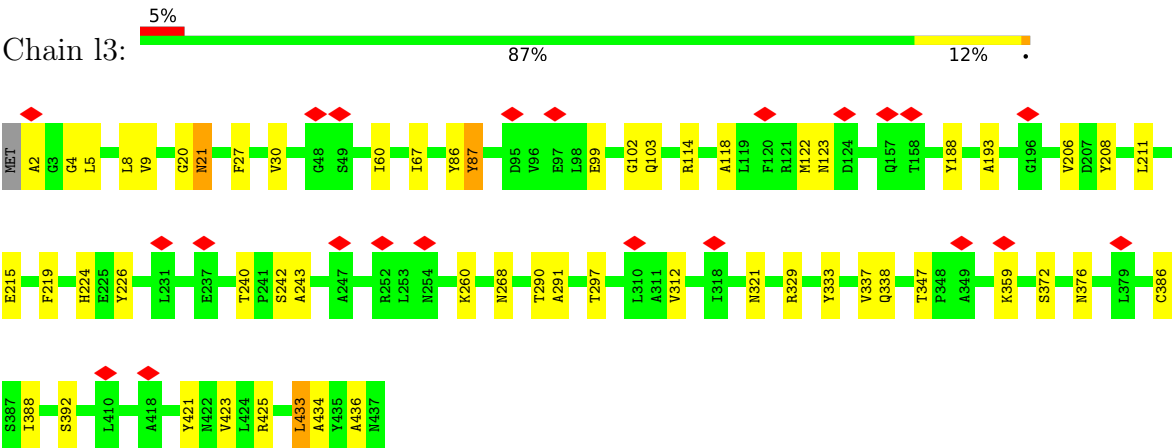
- Molecule 14: Major capsid protein



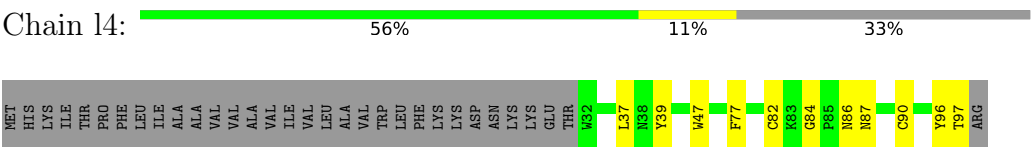
- Molecule 14: Major capsid protein



● Molecule 14: Major capsid protein



● Molecule 15: P13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	13000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	69.604	Depositor
Minimum map value	-56.026	Depositor
Average map value	0.028	Depositor
Map value standard deviation	2.763	Depositor
Recommended contour level	7	Depositor
Map size (Å)	1944.0, 1944.0, 1944.0	wwPDB
Map dimensions	1200, 1200, 1200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.62, 1.62, 1.62	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	a0	0.85	0/741	1.06	0/1006
2	a1	0.62	2/734 (0.3%)	1.29	6/1011 (0.6%)
3	a2	0.59	1/667 (0.1%)	1.08	3/920 (0.3%)
3	a3	0.28	0/497	0.64	0/688
4	a4	0.96	0/1124	1.45	14/1543 (0.9%)
5	a5	0.36	0/1365	0.81	0/1883
6	a6	0.96	1/1220 (0.1%)	1.40	21/1677 (1.3%)
7	a7	0.89	0/559	1.57	15/771 (1.9%)
8	a8	0.97	0/1014	1.47	8/1402 (0.6%)
9	a9	0.59	0/320	1.00	0/446
9	b0	0.46	0/408	0.96	1/567 (0.2%)
9	b1	0.55	0/379	0.92	0/526
9	b2	0.54	0/360	0.94	1/500 (0.2%)
9	b3	0.46	0/345	0.90	0/481
9	b4	0.54	0/360	0.90	0/500
9	b5	0.70	0/377	1.14	0/523
9	b7	0.47	0/386	0.89	1/533 (0.2%)
9	b8	0.45	0/391	0.83	0/543
9	c0	0.65	0/346	0.98	0/480
9	c1	0.51	0/344	1.05	0/476
9	l5	0.49	0/404	0.88	0/559
10	b6	0.36	0/3289	0.76	0/4533
11	c2	0.48	0/608	0.98	0/838
11	c3	0.43	0/393	1.02	2/538 (0.4%)
11	c4	0.55	0/374	1.04	0/515
11	c5	0.43	0/403	1.15	1/550 (0.2%)
12	c6	0.39	0/972	0.82	1/1332 (0.1%)
12	c7	0.63	0/1030	1.20	6/1417 (0.4%)
12	c8	0.32	0/830	0.77	4/1133 (0.4%)
13	c9	0.98	0/1218	1.33	17/1663 (1.0%)
14	d0	0.99	1/3446 (0.0%)	1.24	26/4697 (0.6%)
14	d1	1.00	1/3460 (0.0%)	1.25	28/4717 (0.6%)
14	d2	1.01	1/3465 (0.0%)	1.25	28/4724 (0.6%)
14	d3	1.01	0/3460	1.26	25/4717 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
14	d4	1.06	1/3460 (0.0%)	1.27	24/4717 (0.5%)
14	d5	1.05	1/3461 (0.0%)	1.24	22/4719 (0.5%)
14	d6	1.02	1/3465 (0.0%)	1.25	23/4724 (0.5%)
14	d7	0.99	0/3459	1.25	27/4717 (0.6%)
14	d8	1.04	1/3468 (0.0%)	1.26	26/4728 (0.5%)
14	d9	1.03	0/3473	1.25	24/4735 (0.5%)
14	e0	1.03	0/3468	1.28	31/4728 (0.7%)
14	e1	1.02	0/3460	1.26	23/4717 (0.5%)
14	e2	1.03	2/3460 (0.1%)	1.29	27/4717 (0.6%)
14	e3	1.00	1/3465 (0.0%)	1.28	22/4724 (0.5%)
14	e4	1.03	0/3460	1.27	28/4717 (0.6%)
14	e5	1.03	0/3468	1.26	21/4728 (0.4%)
14	e6	1.02	1/3473 (0.0%)	1.29	32/4735 (0.7%)
14	e7	1.01	0/3468	1.27	21/4728 (0.4%)
14	e8	1.04	0/3468	1.27	28/4728 (0.6%)
14	e9	1.05	0/3465	1.25	26/4724 (0.6%)
14	f0	1.00	1/3452 (0.0%)	1.26	22/4706 (0.5%)
14	f1	1.04	2/3465 (0.1%)	1.26	25/4724 (0.5%)
14	f2	1.02	3/3473 (0.1%)	1.25	24/4735 (0.5%)
14	f3	1.05	0/3460	1.23	24/4717 (0.5%)
14	f4	1.01	0/3460	1.23	20/4717 (0.4%)
14	f5	1.00	0/3454	1.24	28/4710 (0.6%)
14	f6	1.02	1/3465 (0.0%)	1.25	19/4724 (0.4%)
14	f7	1.04	2/3449 (0.1%)	1.27	24/4702 (0.5%)
14	f8	0.99	0/3456	1.28	27/4712 (0.6%)
14	f9	1.03	1/3456 (0.0%)	1.28	32/4712 (0.7%)
14	g0	1.05	2/3465 (0.1%)	1.26	24/4724 (0.5%)
14	g1	1.01	0/3465	1.26	31/4724 (0.7%)
14	g2	1.05	1/3460 (0.0%)	1.27	32/4717 (0.7%)
14	g3	1.04	1/3460 (0.0%)	1.26	26/4717 (0.6%)
14	g4	1.02	2/3468 (0.1%)	1.25	24/4728 (0.5%)
14	g5	1.02	0/3465	1.27	24/4724 (0.5%)
14	g6	0.99	1/3465 (0.0%)	1.25	24/4724 (0.5%)
14	g7	1.02	1/3454 (0.0%)	1.27	25/4710 (0.5%)
14	g8	0.99	0/3473	1.24	21/4735 (0.4%)
14	g9	1.05	0/3468	1.26	22/4728 (0.5%)
14	h0	1.00	0/3465	1.24	19/4724 (0.4%)
14	h1	1.01	1/3465 (0.0%)	1.25	25/4724 (0.5%)
14	h2	1.01	0/3460	1.26	27/4717 (0.6%)
14	h3	1.02	1/3468 (0.0%)	1.26	29/4728 (0.6%)
14	h4	1.02	1/3460 (0.0%)	1.26	24/4717 (0.5%)
14	h5	0.99	1/3460 (0.0%)	1.26	28/4717 (0.6%)
14	h6	1.04	0/3460	1.24	23/4717 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
14	h7	1.01	0/3473	1.25	20/4735 (0.4%)
14	h8	1.00	0/3465	1.28	29/4724 (0.6%)
14	h9	1.00	0/3459	1.27	23/4717 (0.5%)
14	i0	1.03	3/3468 (0.1%)	1.27	26/4728 (0.5%)
14	i1	1.03	1/3460 (0.0%)	1.26	25/4717 (0.5%)
14	i2	1.05	1/3460 (0.0%)	1.25	26/4717 (0.6%)
14	i3	1.03	0/3460	1.28	26/4717 (0.6%)
14	i4	1.01	1/3462 (0.0%)	1.26	28/4721 (0.6%)
14	i5	1.04	1/3473 (0.0%)	1.27	32/4735 (0.7%)
14	i6	0.99	0/3460	1.26	25/4717 (0.5%)
14	i7	1.01	1/3460 (0.0%)	1.26	31/4717 (0.7%)
14	i8	1.01	1/3465 (0.0%)	1.26	26/4724 (0.6%)
14	i9	1.00	1/3465 (0.0%)	1.26	27/4724 (0.6%)
14	j0	1.03	2/3470 (0.1%)	1.27	28/4731 (0.6%)
14	j1	1.00	0/3465	1.24	25/4724 (0.5%)
14	j2	1.04	1/3465 (0.0%)	1.25	24/4724 (0.5%)
14	j3	1.03	0/3465	1.30	35/4724 (0.7%)
14	j4	1.02	2/3460 (0.1%)	1.26	21/4717 (0.4%)
14	j5	1.03	1/3460 (0.0%)	1.25	25/4717 (0.5%)
14	j6	1.04	1/3460 (0.0%)	1.26	22/4717 (0.5%)
14	j7	1.04	0/3473	1.24	24/4735 (0.5%)
14	j8	1.00	1/3468 (0.0%)	1.27	25/4728 (0.5%)
14	j9	1.02	2/3465 (0.1%)	1.26	26/4724 (0.6%)
14	k0	1.01	0/3460	1.27	23/4717 (0.5%)
14	k1	1.03	0/3465	1.27	28/4724 (0.6%)
14	k2	1.01	0/3465	1.27	28/4724 (0.6%)
14	k3	1.05	0/3460	1.28	33/4717 (0.7%)
14	k4	1.05	1/3473 (0.0%)	1.26	22/4735 (0.5%)
14	k5	1.03	0/3473	1.26	20/4735 (0.4%)
14	k6	1.01	0/3469	1.26	26/4728 (0.5%)
14	k7	1.02	0/3465	1.27	24/4723 (0.5%)
14	k8	1.03	1/3469 (0.0%)	1.25	24/4728 (0.5%)
14	k9	1.04	0/3459	1.25	24/4717 (0.5%)
14	l0	1.02	0/3469	1.24	29/4728 (0.6%)
14	l1	1.05	0/3469	1.26	26/4728 (0.5%)
14	l2	1.02	1/3460 (0.0%)	1.28	36/4717 (0.8%)
14	l3	1.04	1/3474 (0.0%)	1.26	26/4735 (0.5%)
15	l4	0.90	0/501	1.19	3/684 (0.4%)
All	All	1.00	61/312913 (0.0%)	1.25	2257/426903 (0.5%)

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	a1	197	ASP	C-N	7.06	1.50	1.33
14	e3	224	HIS	CB-CG	-6.49	1.41	1.50
2	a1	202	THR	C-N	6.47	1.49	1.33
14	d4	224	HIS	CB-CG	-6.43	1.41	1.50
14	h3	224	HIS	CB-CG	-6.31	1.41	1.50

The worst 5 of 2257 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	a1	202	THR	CA-C-N	11.36	134.04	119.84
2	a1	202	THR	C-N-CA	11.36	134.04	119.84
8	a8	35	GLU	CA-C-N	10.30	132.71	119.84
8	a8	35	GLU	C-N-CA	10.30	132.71	119.84
2	a1	197	ASP	CA-C-N	9.85	134.85	120.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a0	733	0	706	9	0
2	a1	718	0	588	110	0
3	a2	650	0	564	103	0
3	a3	485	0	425	84	0
4	a4	1088	0	874	46	0
5	a5	1326	0	1193	115	0
6	a6	1192	0	1133	10	0
7	a7	543	0	455	10	0
8	a8	988	0	900	35	0
9	a9	311	0	257	38	0
9	b0	398	0	325	23	0
9	b1	368	0	314	54	0
9	b2	350	0	314	26	0
9	b3	335	0	275	52	0
9	b4	350	0	299	52	0
9	b5	367	0	296	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	b7	375	0	345	47	0
9	b8	379	0	301	34	0
9	c0	338	0	292	31	0
9	c1	335	0	285	30	0
9	l5	392	0	325	76	0
10	b6	3210	0	2777	308	0
11	c2	603	0	404	42	0
11	c3	389	0	308	47	0
11	c4	369	0	262	35	0
11	c5	396	0	327	35	0
12	c6	951	0	834	165	0
12	c7	1004	0	875	163	0
12	c8	813	0	754	133	0
13	c9	1191	0	1134	73	0
14	d0	3369	0	3266	75	0
14	d1	3382	0	3278	96	0
14	d2	3387	0	3283	78	0
14	d3	3382	0	3278	47	0
14	d4	3382	0	3278	48	0
14	d5	3383	0	3279	50	0
14	d6	3387	0	3283	78	0
14	d7	3381	0	3272	59	0
14	d8	3390	0	3284	82	0
14	d9	3395	0	3289	84	0
14	e0	3390	0	3284	93	0
14	e1	3382	0	3278	76	0
14	e2	3382	0	3278	47	0
14	e3	3387	0	3283	61	0
14	e4	3382	0	3278	97	0
14	e5	3390	0	3284	69	0
14	e6	3395	0	3289	81	0
14	e7	3390	0	3284	61	0
14	e8	3390	0	3284	58	0
14	e9	3387	0	3283	62	0
14	f0	3375	0	3271	97	0
14	f1	3387	0	3280	96	0
14	f2	3395	0	3289	101	0
14	f3	3383	0	3277	68	0
14	f4	3382	0	3278	100	0
14	f5	3376	0	3267	69	0
14	f6	3387	0	3283	90	0
14	f7	3372	0	3267	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	f8	3378	0	3275	97	0
14	f9	3379	0	3274	117	0
14	g0	3387	0	3280	35	0
14	g1	3387	0	3283	67	0
14	g2	3382	0	3278	58	0
14	g3	3382	0	3278	126	0
14	g4	3390	0	3284	69	0
14	g5	3387	0	3283	66	0
14	g6	3387	0	3283	90	0
14	g7	3376	0	3267	66	0
14	g8	3395	0	3289	81	0
14	g9	3390	0	3284	91	0
14	h0	3387	0	3283	63	0
14	h1	3387	0	3283	59	0
14	h2	3382	0	3278	74	0
14	h3	3390	0	3284	61	0
14	h4	3382	0	3278	63	0
14	h5	3382	0	3278	73	0
14	h6	3382	0	3278	111	0
14	h7	3395	0	3289	80	0
14	h8	3387	0	3283	73	0
14	h9	3381	0	3272	61	0
14	i0	3390	0	3284	60	0
14	i1	3382	0	3278	76	0
14	i2	3382	0	3278	65	0
14	i3	3382	0	3278	87	0
14	i4	3384	0	3273	71	0
14	i5	3395	0	3289	100	0
14	i6	3382	0	3278	117	0
14	i7	3382	0	3278	102	0
14	i8	3388	0	3282	74	0
14	i9	3387	0	3283	66	0
14	j0	3392	0	3287	119	0
14	j1	3387	0	3283	85	0
14	j2	3387	0	3283	49	0
14	j3	3387	0	3282	105	0
14	j4	3382	0	3278	69	0
14	j5	3382	0	3278	67	0
14	j6	3382	0	3278	67	0
14	j7	3395	0	3289	95	0
14	j8	3390	0	3284	85	0
14	j9	3387	0	3283	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	k0	3382	0	3278	93	0
14	k1	3387	0	3283	101	0
14	k2	3387	0	3283	75	0
14	k3	3382	0	3278	76	0
14	k4	3395	0	3289	62	0
14	k5	3395	0	3289	105	0
14	k6	3391	0	3284	79	0
14	k7	3387	0	3278	78	0
14	k8	3391	0	3284	82	0
14	k9	3381	0	3272	89	0
14	l0	3391	0	3284	60	0
14	l1	3391	0	3284	53	0
14	l2	3382	0	3278	100	0
14	l3	3396	0	3289	71	0
15	l4	487	0	428	13	0
All	All	305842	0	294139	6281	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 10.

The worst 5 of 6281 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)
14:e5:27:PHE:CZ	14:k1:209:ILE:HG21	1.36	1.60
14:e9:260:LYS:HE2	14:e9:360:PRO:CA	1.34	1.54
9:b5:198:PRO:HG3	14:g7:170:TYR:CE2	1.45	1.48
14:e5:27:PHE:CE2	14:k1:209:ILE:HG21	1.49	1.48
14:e9:260:LYS:CE	14:e9:360:PRO:HA	1.42	1.46

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	a0	95/352 (27%)	93 (98%)	2 (2%)	0	100	100
2	a1	105/210 (50%)	85 (81%)	17 (16%)	3 (3%)	3	26
3	a2	92/289 (32%)	76 (83%)	14 (15%)	2 (2%)	5	30
3	a3	72/289 (25%)	60 (83%)	12 (17%)	0	100	100
4	a4	149/256 (58%)	130 (87%)	14 (9%)	5 (3%)	3	23
5	a5	187/216 (87%)	162 (87%)	24 (13%)	1 (0%)	24	57
6	a6	165/170 (97%)	155 (94%)	9 (6%)	1 (1%)	21	54
7	a7	76/151 (50%)	65 (86%)	7 (9%)	4 (5%)	1	14
8	a8	140/146 (96%)	126 (90%)	12 (9%)	2 (1%)	9	38
9	a9	45/207 (22%)	34 (76%)	11 (24%)	0	100	100
9	b0	57/207 (28%)	45 (79%)	10 (18%)	2 (4%)	3	23
9	b1	52/207 (25%)	43 (83%)	8 (15%)	1 (2%)	6	33
9	b2	49/207 (24%)	39 (80%)	10 (20%)	0	100	100
9	b3	49/207 (24%)	38 (78%)	9 (18%)	2 (4%)	2	19
9	b4	50/207 (24%)	40 (80%)	9 (18%)	1 (2%)	6	32
9	b5	55/207 (27%)	36 (66%)	16 (29%)	3 (6%)	1	13
9	b7	50/207 (24%)	45 (90%)	5 (10%)	0	100	100
9	b8	55/207 (27%)	47 (86%)	8 (14%)	0	100	100
9	c0	49/207 (24%)	41 (84%)	6 (12%)	2 (4%)	2	19
9	c1	49/207 (24%)	38 (78%)	7 (14%)	4 (8%)	0	8
9	l5	56/207 (27%)	42 (75%)	13 (23%)	1 (2%)	6	34
10	b6	473/576 (82%)	392 (83%)	77 (16%)	4 (1%)	16	49
11	c2	101/181 (56%)	76 (75%)	25 (25%)	0	100	100
11	c3	58/181 (32%)	40 (69%)	17 (29%)	1 (2%)	7	35
11	c4	56/181 (31%)	46 (82%)	8 (14%)	2 (4%)	2	22
11	c5	56/181 (31%)	42 (75%)	13 (23%)	1 (2%)	6	34
12	c6	139/171 (81%)	114 (82%)	24 (17%)	1 (1%)	18	51
12	c7	145/171 (85%)	111 (77%)	27 (19%)	7 (5%)	2	16
12	c8	114/171 (67%)	100 (88%)	14 (12%)	0	100	100
13	c9	164/173 (95%)	160 (98%)	2 (1%)	2 (1%)	10	41
14	d0	428/437 (98%)	419 (98%)	9 (2%)	0	100	100
14	d1	432/437 (99%)	422 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	d2	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	d3	432/437 (99%)	424 (98%)	7 (2%)	1 (0%)	43	74
14	d4	432/437 (99%)	422 (98%)	10 (2%)	0	100	100
14	d5	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	d6	433/437 (99%)	427 (99%)	6 (1%)	0	100	100
14	d7	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	d8	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	d9	434/437 (99%)	422 (97%)	12 (3%)	0	100	100
14	e0	433/437 (99%)	424 (98%)	8 (2%)	1 (0%)	43	74
14	e1	432/437 (99%)	424 (98%)	8 (2%)	0	100	100
14	e2	432/437 (99%)	419 (97%)	13 (3%)	0	100	100
14	e3	433/437 (99%)	426 (98%)	6 (1%)	1 (0%)	43	74
14	e4	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	e5	433/437 (99%)	428 (99%)	5 (1%)	0	100	100
14	e6	434/437 (99%)	424 (98%)	10 (2%)	0	100	100
14	e7	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	e8	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	e9	433/437 (99%)	423 (98%)	9 (2%)	1 (0%)	43	74
14	f0	432/437 (99%)	424 (98%)	8 (2%)	0	100	100
14	f1	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	f2	434/437 (99%)	426 (98%)	7 (2%)	1 (0%)	43	74
14	f3	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	f4	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	f5	432/437 (99%)	423 (98%)	9 (2%)	0	100	100
14	f6	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	f7	432/437 (99%)	420 (97%)	12 (3%)	0	100	100
14	f8	431/437 (99%)	421 (98%)	10 (2%)	0	100	100
14	f9	432/437 (99%)	419 (97%)	13 (3%)	0	100	100
14	g0	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	g1	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	g2	432/437 (99%)	423 (98%)	8 (2%)	1 (0%)	43	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	g3	432/437 (99%)	421 (98%)	11 (2%)	0	100	100
14	g4	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	g5	433/437 (99%)	426 (98%)	6 (1%)	1 (0%)	43	74
14	g6	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	g7	432/437 (99%)	422 (98%)	10 (2%)	0	100	100
14	g8	434/437 (99%)	427 (98%)	7 (2%)	0	100	100
14	g9	433/437 (99%)	427 (99%)	6 (1%)	0	100	100
14	h0	433/437 (99%)	429 (99%)	4 (1%)	0	100	100
14	h1	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	h2	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	h3	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	h4	432/437 (99%)	424 (98%)	8 (2%)	0	100	100
14	h5	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	h6	432/437 (99%)	424 (98%)	8 (2%)	0	100	100
14	h7	434/437 (99%)	427 (98%)	7 (2%)	0	100	100
14	h8	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	h9	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	i0	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	i1	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	i2	432/437 (99%)	424 (98%)	8 (2%)	0	100	100
14	i3	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	i4	433/437 (99%)	427 (99%)	6 (1%)	0	100	100
14	i5	434/437 (99%)	428 (99%)	6 (1%)	0	100	100
14	i6	432/437 (99%)	423 (98%)	9 (2%)	0	100	100
14	i7	432/437 (99%)	425 (98%)	7 (2%)	0	100	100
14	i8	434/437 (99%)	421 (97%)	11 (2%)	2 (0%)	24	57
14	i9	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	j0	434/437 (99%)	426 (98%)	7 (2%)	1 (0%)	43	74
14	j1	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	j2	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	j3	433/437 (99%)	421 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	j4	432/437 (99%)	422 (98%)	10 (2%)	0	100	100
14	j5	432/437 (99%)	423 (98%)	9 (2%)	0	100	100
14	j6	432/437 (99%)	423 (98%)	9 (2%)	0	100	100
14	j7	434/437 (99%)	423 (98%)	11 (2%)	0	100	100
14	j8	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	j9	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	k0	432/437 (99%)	426 (99%)	5 (1%)	1 (0%)	43	74
14	k1	433/437 (99%)	427 (99%)	6 (1%)	0	100	100
14	k2	433/437 (99%)	424 (98%)	8 (2%)	1 (0%)	43	74
14	k3	432/437 (99%)	422 (98%)	10 (2%)	0	100	100
14	k4	434/437 (99%)	426 (98%)	8 (2%)	0	100	100
14	k5	434/437 (99%)	425 (98%)	9 (2%)	0	100	100
14	k6	433/437 (99%)	426 (98%)	7 (2%)	0	100	100
14	k7	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	k8	433/437 (99%)	425 (98%)	8 (2%)	0	100	100
14	k9	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	l0	433/437 (99%)	424 (98%)	9 (2%)	0	100	100
14	l1	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
14	l2	432/437 (99%)	423 (98%)	9 (2%)	0	100	100
14	l3	434/437 (99%)	426 (98%)	8 (2%)	0	100	100
15	l4	64/98 (65%)	63 (98%)	1 (2%)	0	100	100
All	All	39415/43355 (91%)	38213 (97%)	1138 (3%)	64 (0%)	44	74

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a1	203	PRO
3	a2	283	ASN
4	a4	199	TRP
9	b0	198	PRO
9	b1	192	MET

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	a0	78/309 (25%)	77 (99%)	1 (1%)	61	72
2	a1	64/179 (36%)	61 (95%)	3 (5%)	23	49
3	a2	60/249 (24%)	56 (93%)	4 (7%)	15	41
3	a3	42/249 (17%)	42 (100%)	0	100	100
4	a4	92/222 (41%)	88 (96%)	4 (4%)	26	51
5	a5	119/188 (63%)	116 (98%)	3 (2%)	42	63
6	a6	124/145 (86%)	124 (100%)	0	100	100
7	a7	45/139 (32%)	42 (93%)	3 (7%)	15	41
8	a8	87/125 (70%)	86 (99%)	1 (1%)	65	74
9	a9	25/181 (14%)	25 (100%)	0	100	100
9	b0	34/181 (19%)	31 (91%)	3 (9%)	9	32
9	b1	30/181 (17%)	27 (90%)	3 (10%)	7	28
9	b2	31/181 (17%)	31 (100%)	0	100	100
9	b3	26/181 (14%)	26 (100%)	0	100	100
9	b4	26/181 (14%)	22 (85%)	4 (15%)	2	16
9	b5	25/181 (14%)	23 (92%)	2 (8%)	11	35
9	b7	35/181 (19%)	34 (97%)	1 (3%)	37	60
9	b8	28/181 (16%)	27 (96%)	1 (4%)	31	57
9	c0	29/181 (16%)	29 (100%)	0	100	100
9	c1	27/181 (15%)	27 (100%)	0	100	100
9	l5	29/181 (16%)	29 (100%)	0	100	100
10	b6	264/479 (55%)	255 (97%)	9 (3%)	32	57
11	c2	32/161 (20%)	31 (97%)	1 (3%)	35	59
11	c3	29/161 (18%)	29 (100%)	0	100	100
11	c4	24/161 (15%)	22 (92%)	2 (8%)	10	34
11	c5	31/161 (19%)	30 (97%)	1 (3%)	34	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	c6	78/144 (54%)	77 (99%)	1 (1%)	61	72
12	c7	81/144 (56%)	73 (90%)	8 (10%)	7	29
12	c8	73/144 (51%)	73 (100%)	0	100	100
13	c9	114/148 (77%)	114 (100%)	0	100	100
14	d0	355/358 (99%)	355 (100%)	0	100	100
14	d1	356/358 (99%)	356 (100%)	0	100	100
14	d2	356/358 (99%)	356 (100%)	0	100	100
14	d3	356/358 (99%)	356 (100%)	0	100	100
14	d4	356/358 (99%)	356 (100%)	0	100	100
14	d5	355/358 (99%)	355 (100%)	0	100	100
14	d6	356/358 (99%)	356 (100%)	0	100	100
14	d7	355/358 (99%)	355 (100%)	0	100	100
14	d8	357/358 (100%)	357 (100%)	0	100	100
14	d9	357/358 (100%)	357 (100%)	0	100	100
14	e0	357/358 (100%)	357 (100%)	0	100	100
14	e1	356/358 (99%)	356 (100%)	0	100	100
14	e2	356/358 (99%)	356 (100%)	0	100	100
14	e3	356/358 (99%)	356 (100%)	0	100	100
14	e4	356/358 (99%)	356 (100%)	0	100	100
14	e5	357/358 (100%)	357 (100%)	0	100	100
14	e6	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	e7	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	e8	357/358 (100%)	357 (100%)	0	100	100
14	e9	356/358 (99%)	356 (100%)	0	100	100
14	f0	355/358 (99%)	355 (100%)	0	100	100
14	f1	356/358 (99%)	356 (100%)	0	100	100
14	f2	357/358 (100%)	357 (100%)	0	100	100
14	f3	356/358 (99%)	356 (100%)	0	100	100
14	f4	356/358 (99%)	356 (100%)	0	100	100
14	f5	355/358 (99%)	355 (100%)	0	100	100
14	f6	356/358 (99%)	356 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	f7	354/358 (99%)	353 (100%)	1 (0%)	86	83
14	f8	356/358 (99%)	356 (100%)	0	100	100
14	f9	356/358 (99%)	356 (100%)	0	100	100
14	g0	356/358 (99%)	356 (100%)	0	100	100
14	g1	356/358 (99%)	356 (100%)	0	100	100
14	g2	356/358 (99%)	356 (100%)	0	100	100
14	g3	356/358 (99%)	356 (100%)	0	100	100
14	g4	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	g5	356/358 (99%)	356 (100%)	0	100	100
14	g6	356/358 (99%)	356 (100%)	0	100	100
14	g7	355/358 (99%)	355 (100%)	0	100	100
14	g8	357/358 (100%)	357 (100%)	0	100	100
14	g9	357/358 (100%)	357 (100%)	0	100	100
14	h0	356/358 (99%)	356 (100%)	0	100	100
14	h1	356/358 (99%)	356 (100%)	0	100	100
14	h2	356/358 (99%)	356 (100%)	0	100	100
14	h3	357/358 (100%)	357 (100%)	0	100	100
14	h4	356/358 (99%)	356 (100%)	0	100	100
14	h5	356/358 (99%)	356 (100%)	0	100	100
14	h6	356/358 (99%)	356 (100%)	0	100	100
14	h7	357/358 (100%)	357 (100%)	0	100	100
14	h8	356/358 (99%)	356 (100%)	0	100	100
14	h9	355/358 (99%)	355 (100%)	0	100	100
14	i0	357/358 (100%)	357 (100%)	0	100	100
14	i1	356/358 (99%)	356 (100%)	0	100	100
14	i2	356/358 (99%)	356 (100%)	0	100	100
14	i3	356/358 (99%)	356 (100%)	0	100	100
14	i4	356/358 (99%)	356 (100%)	0	100	100
14	i5	357/358 (100%)	357 (100%)	0	100	100
14	i6	356/358 (99%)	355 (100%)	1 (0%)	86	83
14	i7	356/358 (99%)	356 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	i8	356/358 (99%)	356 (100%)	0	100	100
14	i9	356/358 (99%)	356 (100%)	0	100	100
14	j0	356/358 (99%)	354 (99%)	2 (1%)	78	79
14	j1	356/358 (99%)	356 (100%)	0	100	100
14	j2	356/358 (99%)	356 (100%)	0	100	100
14	j3	356/358 (99%)	356 (100%)	0	100	100
14	j4	356/358 (99%)	356 (100%)	0	100	100
14	j5	356/358 (99%)	356 (100%)	0	100	100
14	j6	356/358 (99%)	356 (100%)	0	100	100
14	j7	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	j8	357/358 (100%)	355 (99%)	2 (1%)	78	79
14	j9	356/358 (99%)	356 (100%)	0	100	100
14	k0	356/358 (99%)	356 (100%)	0	100	100
14	k1	356/358 (99%)	356 (100%)	0	100	100
14	k2	356/358 (99%)	356 (100%)	0	100	100
14	k3	356/358 (99%)	356 (100%)	0	100	100
14	k4	357/358 (100%)	357 (100%)	0	100	100
14	k5	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	k6	357/358 (100%)	357 (100%)	0	100	100
14	k7	356/358 (99%)	355 (100%)	1 (0%)	86	83
14	k8	357/358 (100%)	356 (100%)	1 (0%)	86	83
14	k9	355/358 (99%)	355 (100%)	0	100	100
14	l0	357/358 (100%)	357 (100%)	0	100	100
14	l1	357/358 (100%)	357 (100%)	0	100	100
14	l2	356/358 (99%)	356 (100%)	0	100	100
14	l3	357/358 (100%)	357 (100%)	0	100	100
15	l4	42/79 (53%)	42 (100%)	0	100	100
All	All	31742/35831 (89%)	31674 (100%)	68 (0%)	85	85

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	f7	374	ILE

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Mol	Chain	Res	Type
14	i6	358	LEU
14	k5	433	LEU
9	b1	165	THR
9	b1	161	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 184 such sidechains are listed below:

Mol	Chain	Res	Type
14	h7	256	ASN
14	j2	341	GLN
14	h8	267	ASN
14	i5	250	ASN
14	j7	267	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

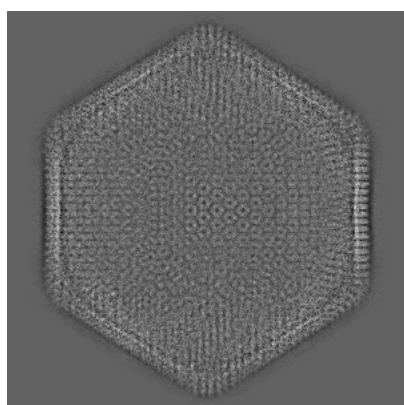
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0436. These allow visual inspection of the internal detail of the map and identification of artifacts.

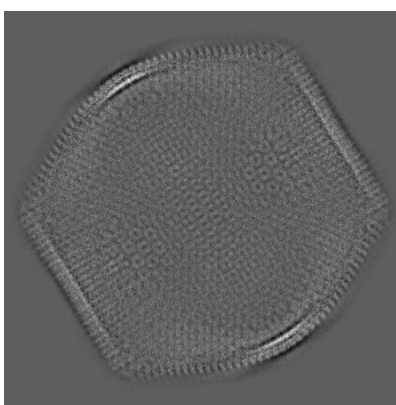
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

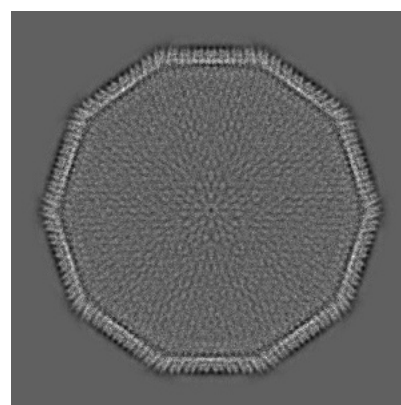
6.1.1 Primary map



X



Y

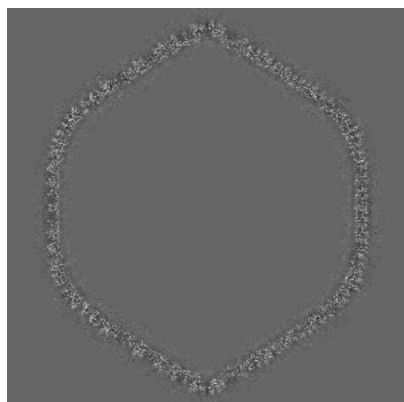


Z

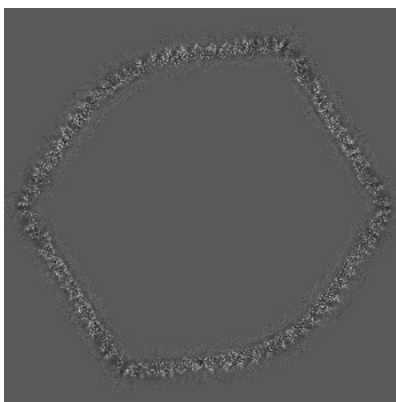
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

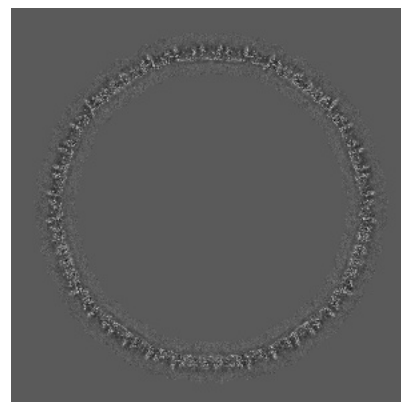
6.2.1 Primary map



X Index: 600



Y Index: 600

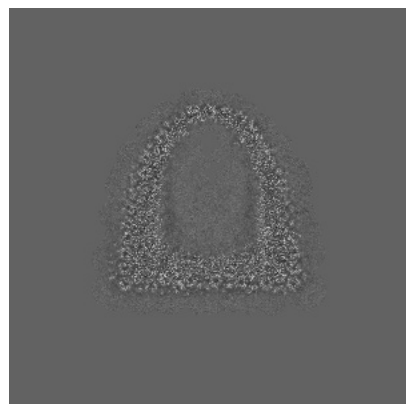


Z Index: 600

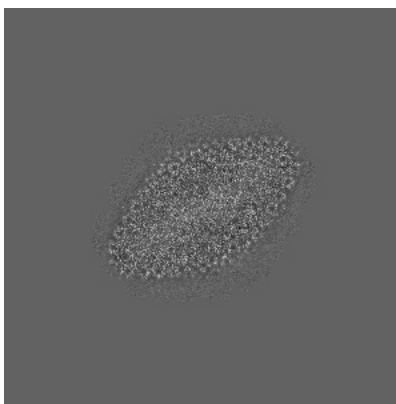
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

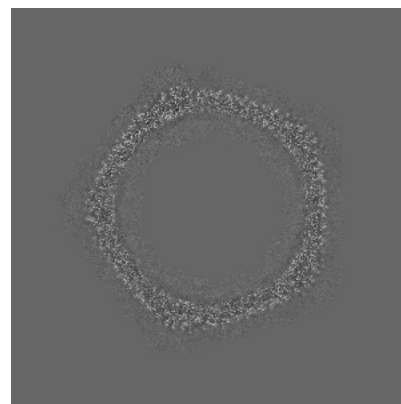
6.3.1 Primary map



X Index: 1020



Y Index: 1050

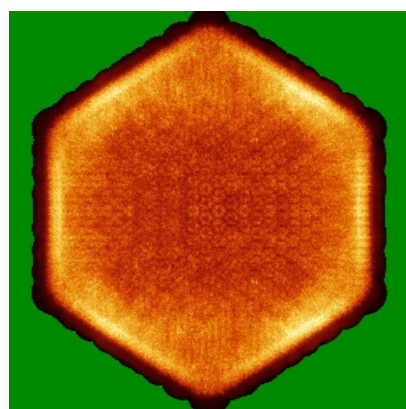


Z Index: 258

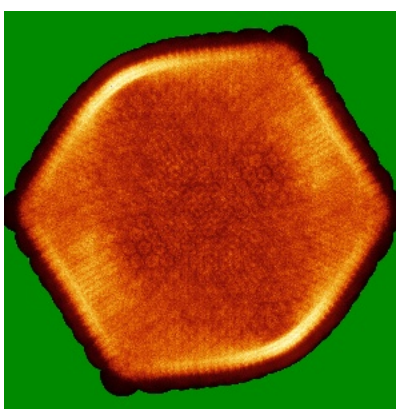
The images above show the largest variance slices of the map in three orthogonal directions.

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

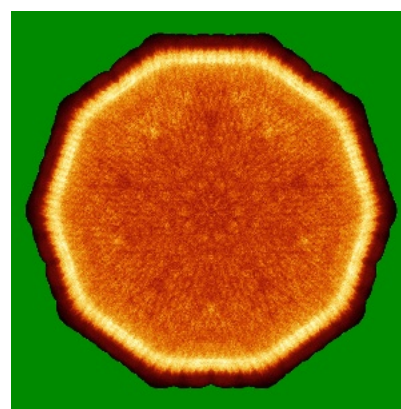
6.4.1 Primary map



X



Y

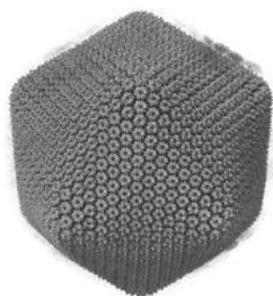


Z

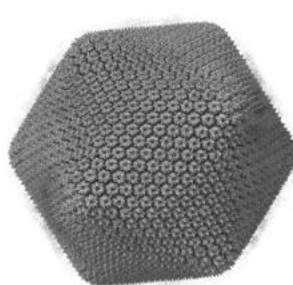
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

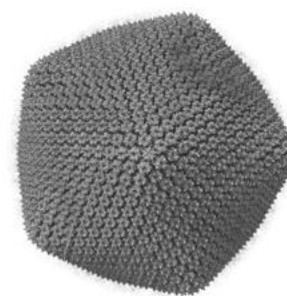
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

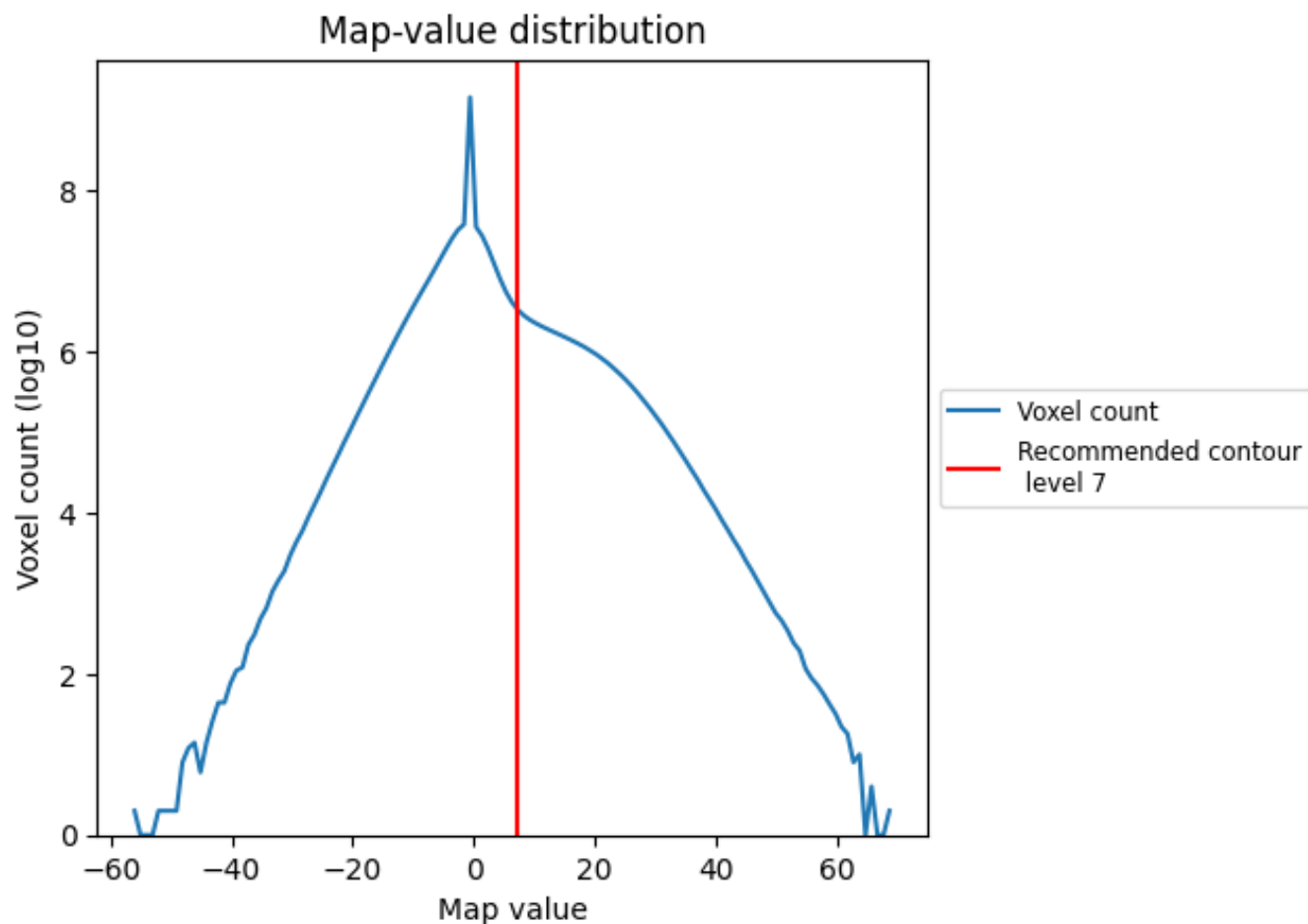
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

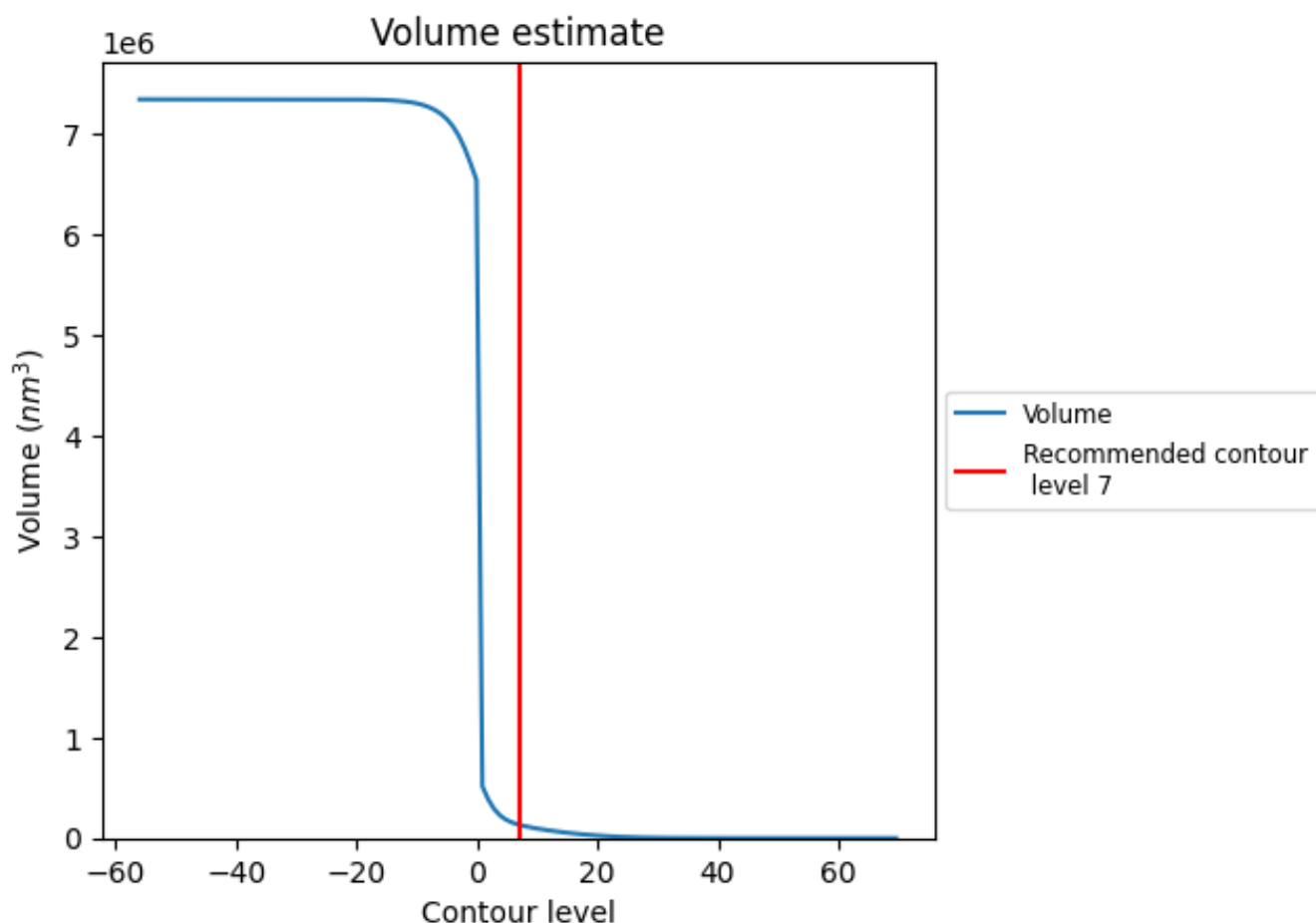
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

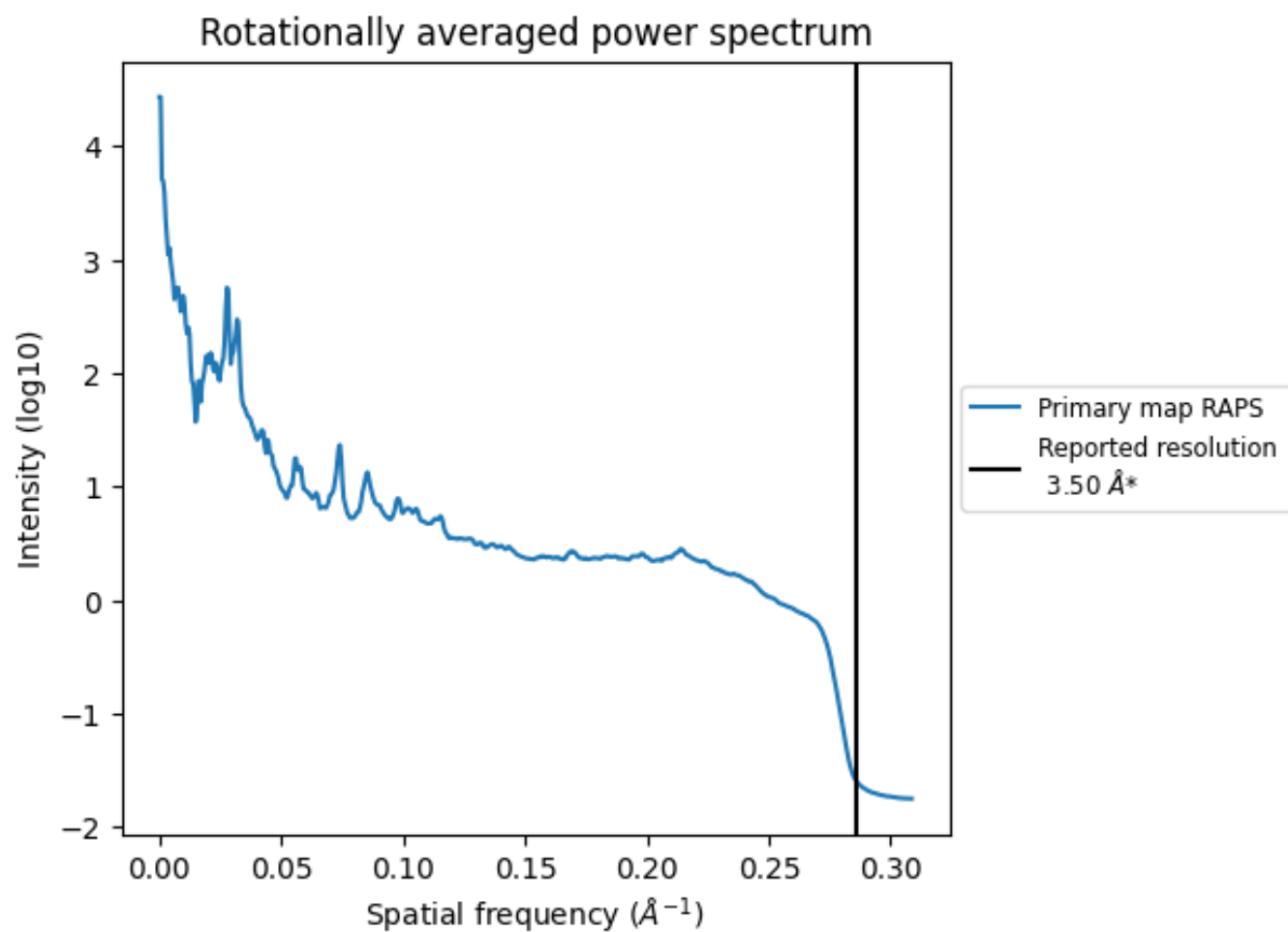
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 132822 nm³; this corresponds to an approximate mass of 119981 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 0.286 Å⁻¹

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

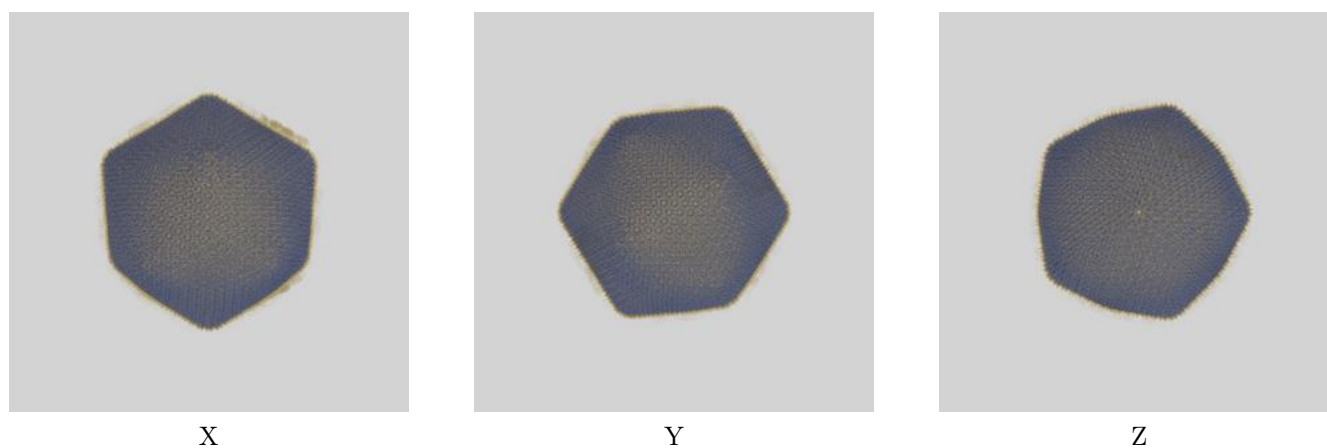
This section contains information regarding the fit between EMDB map EMD-0436 and PDB model 6NCL. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

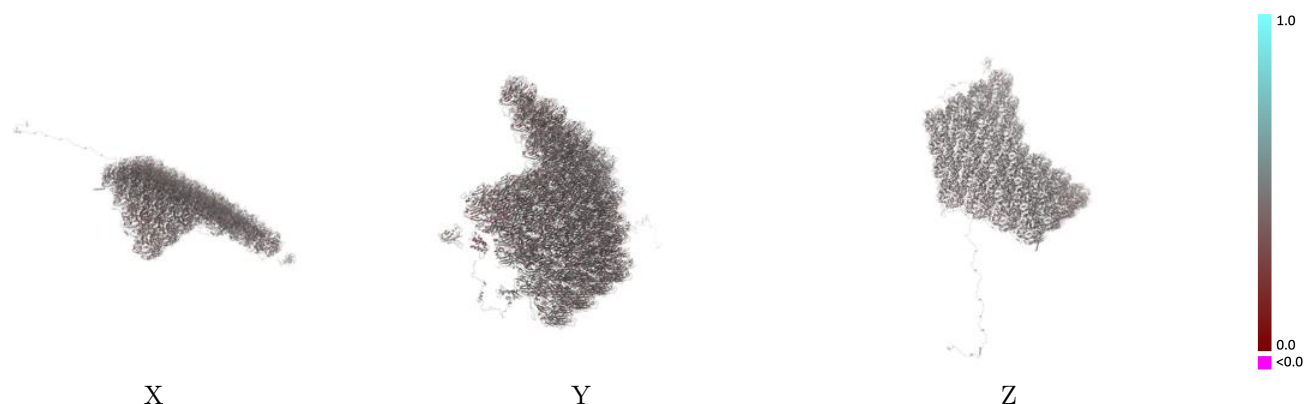


9.1.2 Map-model assembly overlay [i](#)



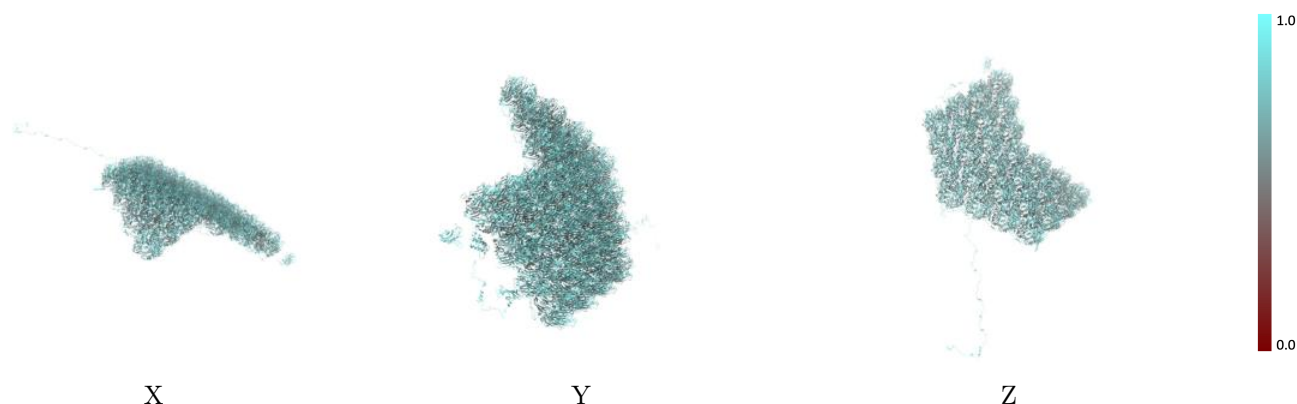
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



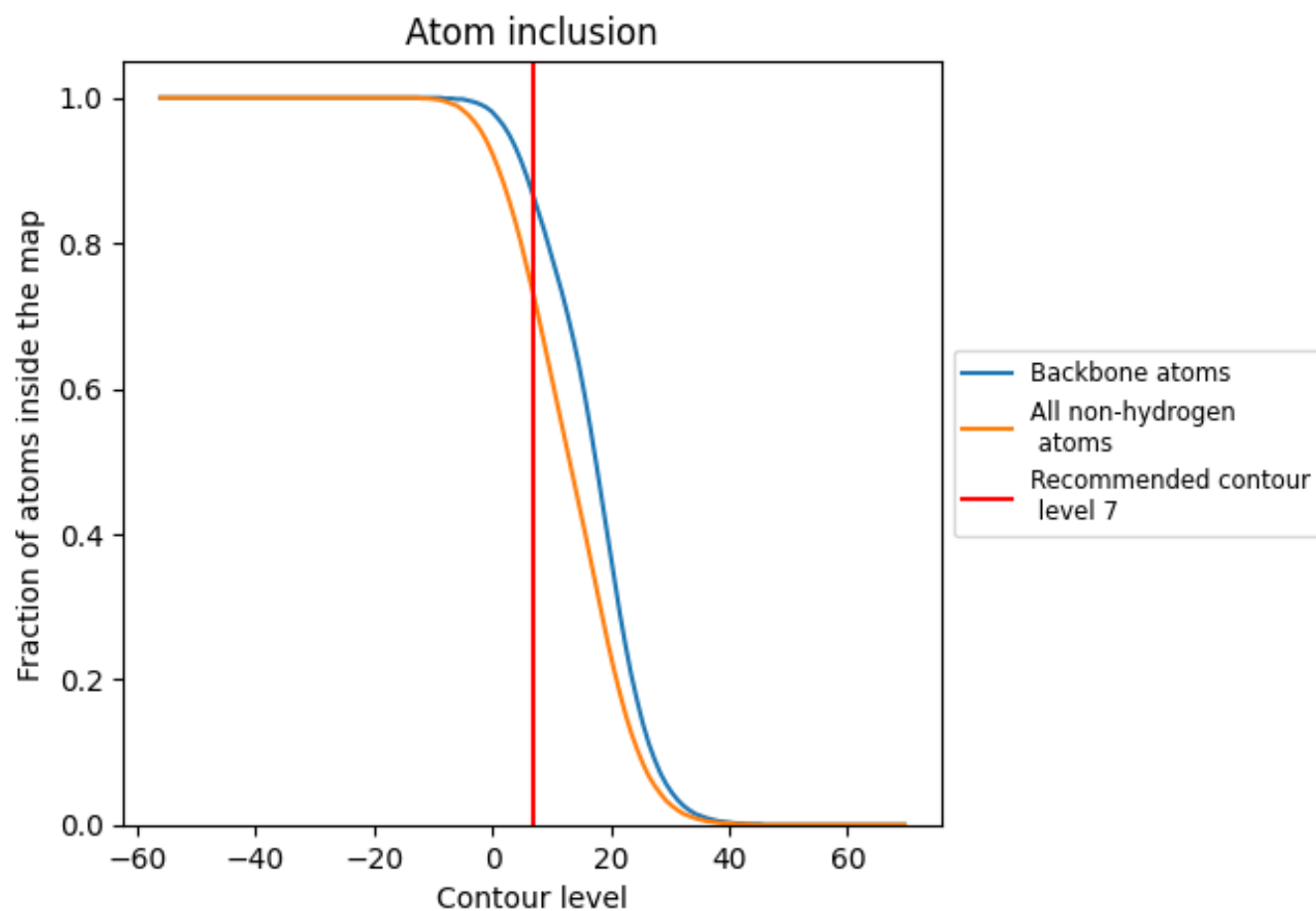
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 73% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7270	 0.4260
a0	 0.6990	 0.3870
a1	 0.7430	 0.4520
a2	 0.7520	 0.4690
a3	 0.7740	 0.4660
a4	 0.7370	 0.4130
a5	 0.7560	 0.4520
a6	 0.7510	 0.4230
a7	 0.8390	 0.4030
a8	 0.7430	 0.4120
a9	 0.8210	 0.4770
b0	 0.8250	 0.4480
b1	 0.8670	 0.4970
b2	 0.8080	 0.4730
b3	 0.8160	 0.4540
b4	 0.7330	 0.4840
b5	 0.7100	 0.4780
b6	 0.7920	 0.4610
b7	 0.8240	 0.4850
b8	 0.8530	 0.4860
c0	 0.8080	 0.4950
c1	 0.8390	 0.4690
c2	 0.8360	 0.4500
c3	 0.8330	 0.4630
c4	 0.8590	 0.4730
c5	 0.8900	 0.4560
c6	 0.8330	 0.4740
c7	 0.8100	 0.4860
c8	 0.7480	 0.4550
c9	 0.8100	 0.4130
d0	 0.6890	 0.4130
d1	 0.6790	 0.4230
d2	 0.7230	 0.4280
d3	 0.7370	 0.4290
d4	 0.7220	 0.4340



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Chain	Atom inclusion	Q-score
d5	 0.7240	 0.4390
d6	 0.7220	 0.4290
d7	 0.7260	 0.4240
d8	 0.7650	 0.4330
d9	 0.7320	 0.4300
e0	 0.7020	 0.4270
e1	 0.7160	 0.4160
e2	 0.7200	 0.4010
e3	 0.6440	 0.3880
e4	 0.7290	 0.4290
e5	 0.7570	 0.4330
e6	 0.7520	 0.4280
e7	 0.7420	 0.4230
e8	 0.7000	 0.4200
e9	 0.7400	 0.4240
f0	 0.7190	 0.4230
f1	 0.7810	 0.4330
f2	 0.7220	 0.4340
f3	 0.7060	 0.4300
f4	 0.7100	 0.4270
f5	 0.6930	 0.4190
f6	 0.6930	 0.4060
f7	 0.7150	 0.4110
f8	 0.6520	 0.4110
f9	 0.7140	 0.4270
g0	 0.7320	 0.4350
g1	 0.7290	 0.4300
g2	 0.7260	 0.4330
g3	 0.7270	 0.4380
g4	 0.7200	 0.4300
g5	 0.7380	 0.4290
g6	 0.7300	 0.4290
g7	 0.7310	 0.4290
g8	 0.7240	 0.4250
g9	 0.6880	 0.4060
h0	 0.7060	 0.4050
h1	 0.6590	 0.3970
h2	 0.7600	 0.4350
h3	 0.7410	 0.4310
h4	 0.7490	 0.4300
h5	 0.7430	 0.4310
h6	 0.7420	 0.4300

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Chain	Atom inclusion	Q-score
h7	 0.7150	 0.4220
h8	 0.7340	 0.4190
h9	 0.7170	 0.4160
i0	 0.7400	 0.4290
i1	 0.6980	 0.4220
i2	 0.7170	 0.4390
i3	 0.7280	 0.4270
i4	 0.7010	 0.4130
i5	 0.6870	 0.4080
i6	 0.6660	 0.4130
i7	 0.7020	 0.4300
i8	 0.7510	 0.4310
i9	 0.7290	 0.4260
j0	 0.7350	 0.4310
j1	 0.7120	 0.4310
j2	 0.7530	 0.4340
j3	 0.7640	 0.4290
j4	 0.7510	 0.4290
j5	 0.7620	 0.4310
j6	 0.7470	 0.4340
j7	 0.6920	 0.4140
j8	 0.7140	 0.4080
j9	 0.6600	 0.3920
k0	 0.7470	 0.4270
k1	 0.7450	 0.4240
k2	 0.7370	 0.4250
k3	 0.7570	 0.4220
k4	 0.7570	 0.4340
k5	 0.7000	 0.4220
k6	 0.7400	 0.4210
k7	 0.7540	 0.4230
k8	 0.7370	 0.4300
k9	 0.7300	 0.4270
l0	 0.7110	 0.4320
l1	 0.7230	 0.4260
l2	 0.7320	 0.4150
l3	 0.6990	 0.4080
l4	 0.7500	 0.4140
l5	 0.8090	 0.4810