



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:31 AM UTC

PDB ID : 8H2I / pdb_00008h2i
EMDB ID : EMD-34438
Title : Near-atomic structure of five-fold averaged PBCV-1 capsid
Authors : Shao, Q.; Agarkova, I.V.; Noel, E.A.; Dunigan, D.D.; Liu, Y.; Wang, A.; Guo, M.; Xie, L.; Zhao, X.; Rossmann, M.G.; Van Etten, J.L.; Klose, T.; Fang, Q.
Deposited on : 2022-10-06
Resolution : 3.80 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:

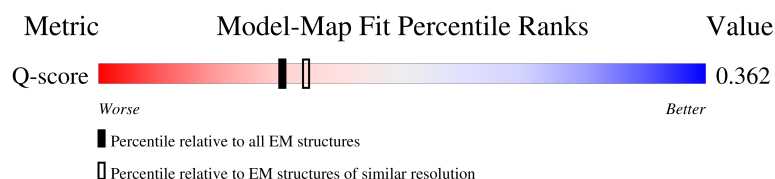
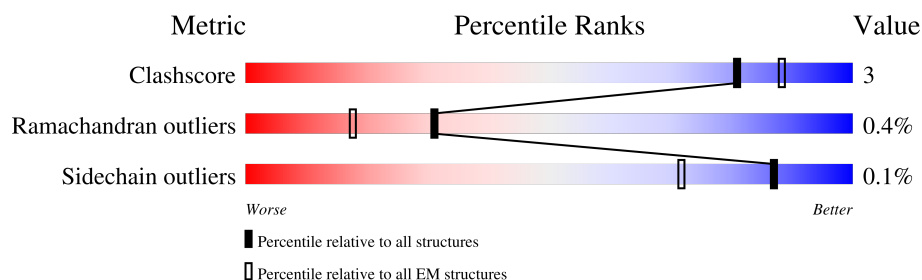
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	aA	437	85% 94% 5%
1	aB	437	81% 95% 5%
1	aC	437	78% 95% .
1	aD	437	78% 91% 8% .

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Mol	Chain	Length	Quality of chain
1	aE	437	52% 95% 5%
1	aF	437	44% 95% ..
1	aG	437	59% 96% .
1	aH	437	38% 95% ..
1	aI	437	40% 93% 6%
1	aJ	437	46% 94% 5%
1	aK	437	54% 94% 5%
1	aL	437	60% 95% .
1	aM	437	62% 95% 5%
1	aN	437	58% 96% .
1	aO	437	63% 97% .
1	aP	437	57% 97% .
1	aQ	437	68% 94% 5% .
1	aR	437	71% 95% 5%
1	aS	437	65% 96% .
1	aT	437	62% 96% .
1	aU	437	56% 96% .
1	aV	437	57% 97% .
1	aW	437	70% 95% 5%
1	aX	437	70% 97% .
1	aY	437	72% 96% .
1	aZ	437	66% 97% .
1	aa	437	45% 86% 12% .
1	ab	437	45% 89% 9% .
1	ac	437	42% 87% 12%

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Mol	Chain	Length	Quality of chain
1	ad	437	43% 95% .
1	ae	437	42% 97% .
1	af	437	47% 95% 5%
1	ag	437	45% 96% .
1	ah	437	37% 96% .
1	ai	437	44% 96% .
1	aj	437	75% 95% 5%
1	ak	437	62% 94% 5%
1	al	437	78% 94% 5%
1	am	437	41% 93% 6%
1	an	437	41% 96% .
1	ao	437	41% 96% .
1	ap	437	38% 95% .
1	aq	437	33% 95% 5%
1	ar	437	31% 95% ..
1	as	437	44% 95% .
1	at	437	58% 97% .
1	au	437	51% 94% 5%.
1	av	437	69% 98% .
1	aw	437	75% 96% .
1	ax	437	65% 96% ..
1	ay	437	88% 96% .
1	az	437	89% 97% ..
1	ba	437	57% 98% .
1	bb	437	67% 95% .

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Mol	Chain	Length	Quality of chain
1	bc	437	58% 96% .
1	bd	437	62% 95% 5%
1	be	437	61% 96% .
1	bf	437	55% 95% 5%
1	bg	437	58% 96% .
1	bh	437	55% 95% 5%
1	bi	437	62% 96% .
1	bj	437	68% 96% .
1	bk	437	61% 97% .
1	bl	437	67% 95% 5%
1	bm	437	66% 94% 6%
1	bn	437	70% 95% ..
1	bo	437	68% 94% 5%
1	bp	437	60% 94% 5%
1	bq	437	68% 97% .
1	br	437	48% 96% .
1	bs	437	58% 96% .
1	bt	437	56% 96% .
2	bA	520	58% 91% 8% .
2	bB	520	79% 94% 5% .
2	bu	520	31% 89% 10% ..
2	bv	520	36% 88% 11% ..
2	bw	520	34% 89% 10% ..
2	bx	520	42% 86% 12% ..
2	by	520	49% 88% 11% ..

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Mol	Chain	Length	Quality of chain
2	bz	520	48% 87% 10%
3	bC	486	61% 90% 9%
4	bD	403	84% 92% 8%
4	bF	403	77% 93% 6%
4	cX	403	68% 93% 6%
4	cZ	403	69% 93% 6%
4	dd	403	85% 92% 6%
4	df	403	85% 92% 6%
4	dj	403	75% 93% 6%
4	dk	403	76% 91% 8%
4	dl	403	70% 92% 7%
4	dp	403	73% 93% 6%
4	dr	403	71% 92% 6%
5	bE	401	74% 92% 7%
5	cY	401	83% 92% 6%
5	de	401	86% 89% 9%
5	dq	401	77% 91% 7%
6	bG	530	54% 92% 5%
7	bH	576	48% 63% 10% 26%
8	bI	171	63% 73% 8% 18%
8	bJ	171	63% 75% 10% 14%
8	bK	171	51% 54% 13% 32%
9	bL	181	29% 27% 8% 65%
9	bM	181	31% 28% 6% 65%
9	bN	181	29% 29% • • 66%

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Mol	Chain	Length	Quality of chain
9	bO	181	
10	bP	146	
11	bQ	216	
12	bR	173	
13	bS	210	
14	bT	207	
14	bU	207	
14	bV	207	
14	bW	207	
14	bX	207	
14	bY	207	
14	bZ	207	
14	ca	207	
14	cb	207	
14	cc	207	
14	cd	207	
14	ce	207	
15	cf	151	
16	cg	98	
17	ch	155	
18	ci	93	
19	cj	80	
19	ck	80	
19	cl	80	
19	cm	80	

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Mol	Chain	Length	Quality of chain
20	cn	148	
20	co	148	
21	cA	378	
21	cB	378	
21	cC	378	
21	cD	378	
21	cE	378	
21	cF	378	
21	cG	378	
21	cH	378	
21	cI	378	
21	cJ	378	
21	cK	378	
21	cL	378	
21	cM	378	
21	cN	378	
21	cp	378	
21	cq	378	
21	cr	378	
21	cs	378	
21	ct	378	
21	cu	378	
21	cv	378	
21	cw	378	
21	cx	378	

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Mol	Chain	Length	Quality of chain
21	cy	378	
21	cz	378	
22	cO	1335	
22	cQ	1335	
22	da	1335	
22	dc	1335	
22	dg	1335	
22	di	1335	
22	ds	1335	
22	du	1335	
23	cP	1369	
23	db	1369	
23	dh	1369	
23	dt	1369	
24	cR	400	
24	cS	400	
24	cT	400	
25	cU	1343	
25	cV	1343	
25	cW	1343	
26	dm	1359	
26	dn	1359	
26	do	1359	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 427569 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major capsid protein (MCP).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	aa	432	Total	C	N	O	S	0	0
			3374	2145	571	650	8		
1	ab	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ac	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ad	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ae	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	af	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ag	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ah	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ai	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aj	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ak	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	al	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
1	am	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	an	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		
1	ao	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	ap	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aq	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ar	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	as	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	at	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	au	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	av	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aw	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ax	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	ay	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	az	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	aA	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aB	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aC	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aD	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	aE	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aF	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	aG	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aH	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	aI	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aJ	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aK	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aL	435	Total	C	N	O	S	0	0
			3387	2152	574	653	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	aM	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aN	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aO	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aP	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aQ	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	aR	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aS	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aT	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aU	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aV	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aW	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aX	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		
1	aY	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	aZ	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	ba	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bb	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bc	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bd	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	be	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bf	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bg	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	bh	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bi	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bj	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bk	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bl	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bm	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bn	434	Total	C	N	O	S	0	0
			3382	2149	573	652	8		
1	bo	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bp	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bq	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	br	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bs	436	Total	C	N	O	S	0	0
			3395	2156	576	655	8		
1	bt	435	Total	C	N	O	S	0	0
			3390	2153	575	654	8		

- Molecule 2 is a protein called MCPv1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	bu	517	Total	C	N	O	S	0	0
			4090	2621	680	778	11		
2	bv	517	Total	C	N	O	S	0	0
			4090	2621	680	778	11		
2	bw	517	Total	C	N	O	S	0	0
			4090	2621	680	778	11		
2	bx	514	Total	C	N	O	S	0	0
			4074	2611	677	775	11		
2	by	517	Total	C	N	O	S	0	0
			4090	2621	680	778	11		
2	bz	508	Total	C	N	O	S	0	0
			4030	2583	670	766	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	bA	516	Total	C	N	O	S	0	0
			4079	2612	679	777	11		
2	bB	517	Total	C	N	O	S	0	0
			4090	2621	680	778	11		

- Molecule 3 is a protein called MCPv2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	bC	485	Total	C	N	O	S	0	0
			3921	2518	645	742	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
bC	343	SER	GLY	variant	UNP M1I493

- Molecule 4 is a protein called MCPv3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	bD	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	bF	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	cX	401	Total	C	N	O	S	0	0
			3165	2029	521	605	10		
4	cZ	401	Total	C	N	O	S	0	0
			3165	2029	521	605	10		
4	dd	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	df	401	Total	C	N	O	S	0	0
			3165	2029	521	605	10		
4	dj	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	dk	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	dl	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	dp	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		
4	dr	401	Total	C	N	O	S	0	0
			3169	2031	521	607	10		

- Molecule 5 is a protein called MCPv4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	bE	397	Total	C	N	O	S	0	0
			3146	2021	513	601	11		
5	cY	397	Total	C	N	O	S	0	0
			3146	2021	513	601	11		
5	de	397	Total	C	N	O	S	0	0
			3146	2021	513	601	11		
5	dq	397	Total	C	N	O	S	0	0
			3146	2021	513	601	11		

- Molecule 6 is a protein called P1v1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	bG	504	Total	C	N	O	S	0	0
			3864	2454	633	771	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
bG	113	ASN	SER	variant	UNP M1I677
bG	348	ILE	VAL	variant	UNP M1I677
bG	364	SER	THR	variant	UNP M1I677

- Molecule 7 is a protein called P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	bH	424	Total	C	N	O	S	0	0
			3258	2015	591	642	10		

- Molecule 8 is a protein called P3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	bI	141	Total	C	N	O	S	0	0
			1096	691	191	209	5		
8	bJ	147	Total	C	N	O	S	0	0
			1146	724	198	219	5		
8	bK	116	Total	C	N	O	S	0	0
			892	560	157	170	5		

- Molecule 9 is a protein called P4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	bL	63	Total	C	N	O	S	0	0
			526	340	88	97	1		
9	bM	63	Total	C	N	O	S	0	0
			526	340	88	97	1		
9	bN	62	Total	C	N	O	S	0	0
			519	336	87	95	1		
9	bO	62	Total	C	N	O	S	0	0
			519	336	87	95	1		

- Molecule 10 is a protein called P5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	bP	142	Total	C	N	O	S	0	0
			1126	724	192	208	2		

- Molecule 11 is a protein called P6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	bQ	162	Total	C	N	O	S	0	0
			1275	830	202	242	1		

- Molecule 12 is a protein called P8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	bR	159	Total	C	N	O	S	0	0
			1244	798	207	235	4		

- Molecule 13 is a protein called P9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	bS	191	Total	C	N	O	S	0	0
			1504	953	258	285	8		

- Molecule 14 is a protein called P11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	bT	48	Total	C	N	O	S	0	0
			373	237	65	69	2		
14	bU	54	Total	C	N	O	S	0	0
			424	273	70	79	2		
14	bV	53	Total	C	N	O	S	0	0
			416	269	68	77	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	bW	52	Total	C	N	O	S	0	0
			405	260	67	76	2		
14	bX	41	Total	C	N	O	S	0	0
			312	195	53	62	2		
14	bY	74	Total	C	N	O	S	0	0
			576	370	96	108	2		
14	bZ	52	Total	C	N	O	S	0	0
			405	260	67	76	2		
14	ca	52	Total	C	N	O	S	0	0
			405	260	67	76	2		
14	cb	52	Total	C	N	O	S	0	0
			405	260	67	76	2		
14	cc	84	Total	C	N	O	S	0	0
			646	415	107	122	2		
14	cd	75	Total	C	N	O	S	0	0
			583	375	97	109	2		
14	ce	72	Total	C	N	O	S	0	0
			560	359	93	106	2		

- Molecule 15 is a protein called P12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	cf	78	Total	C	N	O	S	0	0
			631	408	103	116	4		

- Molecule 16 is a protein called P13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	cg	66	Total	C	N	O	S	0	0
			521	333	89	96	3		

- Molecule 17 is a protein called P15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	ch	152	Total	C	N	O	S	0	0
			1288	838	212	233	5		

- Molecule 18 is a protein called P16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	ci	80	Total	C	N	O	S	0	0
			553	358	95	94	6		

- Molecule 19 is a protein called P17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	cj	59	Total	C	N	O	S	0	0
			463	295	76	90	2		
19	ck	57	Total	C	N	O	S	0	0
			455	293	76	84	2		
19	cl	55	Total	C	N	O	S	0	0
			431	275	71	82	3		
19	cm	63	Total	C	N	O	S	0	0
			503	320	86	95	2		

- Molecule 20 is a protein called P18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	cn	98	Total	C	N	O	S	0	0
			769	488	134	146	1		
20	co	95	Total	C	N	O	S	0	0
			733	470	123	139	1		

- Molecule 21 is a protein called P19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	cp	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cq	282	Total	C	N	O	S	0	0
			2212	1420	371	413	8		
21	cr	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cs	275	Total	C	N	O	S	0	0
			2159	1387	363	402	7		
21	ct	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cu	280	Total	C	N	O	S	0	0
			2199	1413	369	410	7		
21	cv	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cw	280	Total	C	N	O	S	0	0
			2199	1413	369	410	7		
21	cx	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cy	280	Total	C	N	O	S	0	0
			2199	1413	369	410	7		
21	cz	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
21	cA	279	Total	C	N	O	S	0	0
			2191	1409	367	408	7		
21	cB	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cC	279	Total	C	N	O	S	0	0
			2191	1409	367	408	7		
21	cD	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cE	280	Total	C	N	O	S	0	0
			2199	1413	369	410	7		
21	cF	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cG	282	Total	C	N	O	S	0	0
			2212	1420	371	413	8		
21	cH	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cI	279	Total	C	N	O	S	0	0
			2191	1409	367	408	7		
21	cJ	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cK	279	Total	C	N	O	S	0	0
			2191	1409	367	408	7		
21	cL	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		
21	cM	277	Total	C	N	O	S	0	0
			2173	1396	365	405	7		
21	cN	292	Total	C	N	O	S	0	0
			2299	1479	385	426	9		

- Molecule 22 is a protein called P20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	cO	30	Total	C	N	O	S	0	0
			218	142	35	39	2		
22	cQ	31	Total	C	N	O	S	0	0
			233	149	38	44	2		
22	da	32	Total	C	N	O	S	0	0
			228	144	37	45	2		
22	dc	28	Total	C	N	O	S	0	0
			209	134	34	39	2		
22	dg	32	Total	C	N	O	S	0	0
			241	153	40	46	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	di	29	Total	C	N	O	S	0	0
			211	137	32	40	2		
22	ds	32	Total	C	N	O	S	0	0
			238	152	40	44	2		
22	du	30	Total	C	N	O	S	0	0
			224	144	36	42	2		

- Molecule 23 is a protein called P21.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	cP	35	Total	C	N	O	0	0
			239	152	42	45		
23	db	30	Total	C	N	O	0	0
			200	127	36	37		
23	dh	35	Total	C	N	O	0	0
			249	157	45	47		
23	dt	35	Total	C	N	O	0	0
			236	147	44	45		

- Molecule 24 is a protein called MCPv5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	cR	399	Total	C	N	O	S	0	0
			3203	2060	518	611	14		
24	cS	399	Total	C	N	O	S	0	0
			3203	2060	518	611	14		
24	cT	399	Total	C	N	O	S	0	0
			3203	2060	518	611	14		

- Molecule 25 is a protein called P22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	cU	43	Total	C	N	O	0	0
			311	203	51	57		
25	cV	43	Total	C	N	O	0	0
			305	201	50	54		
25	cW	43	Total	C	N	O	0	0
			308	202	51	55		

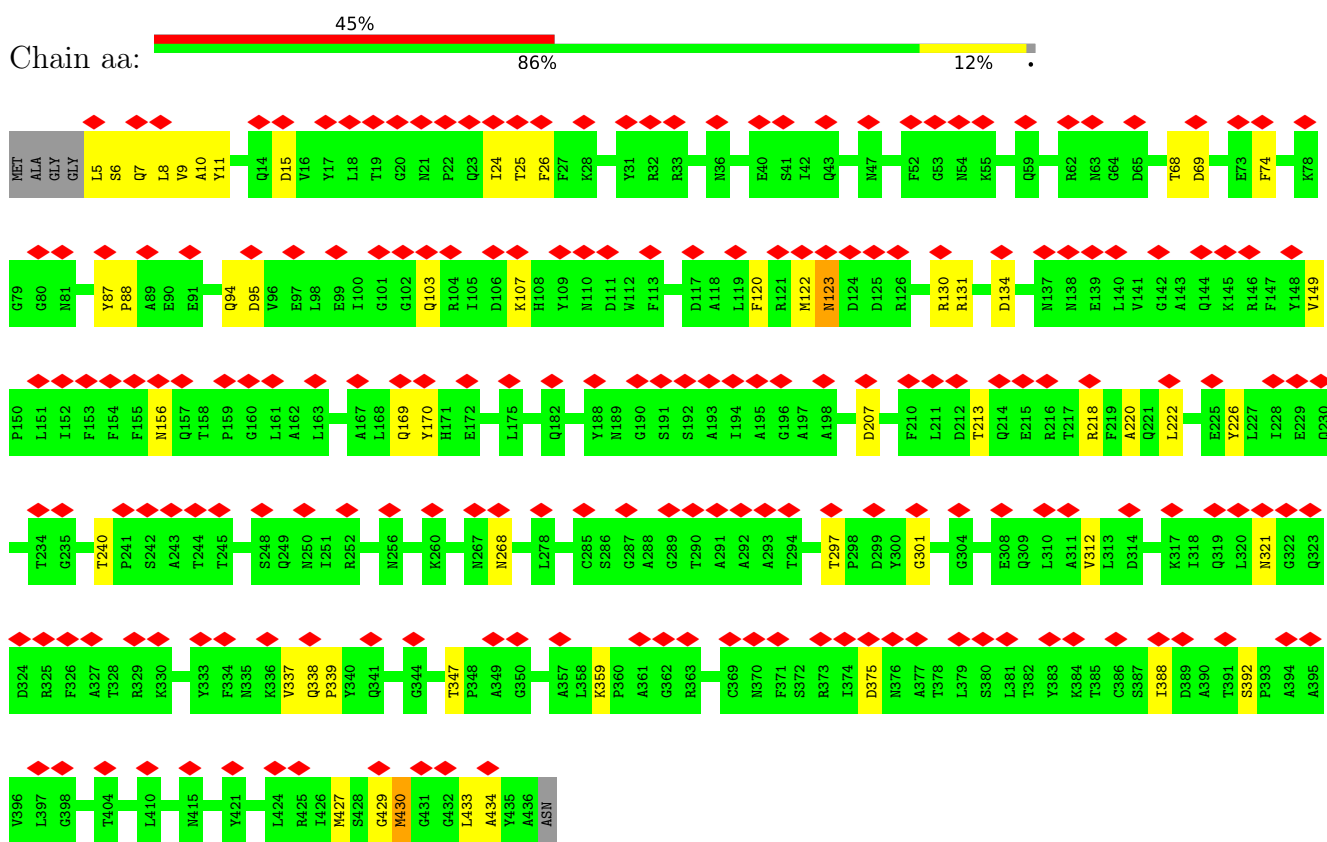
- Molecule 26 is a protein called P23.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	dm	25	Total 174	C 111	N 28	O 35	0	0
26	dn	25	Total 181	C 116	N 29	O 36	0	0
26	do	25	Total 182	C 121	N 28	O 33	0	0

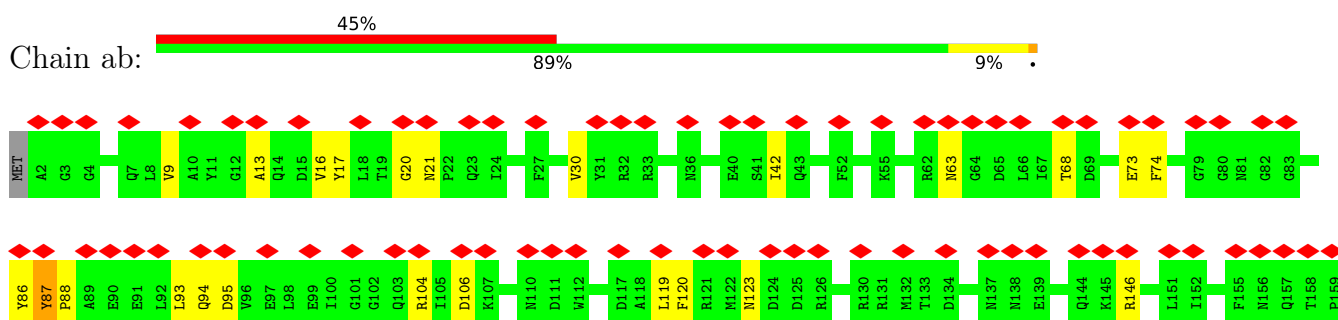
3 Residue-property plots

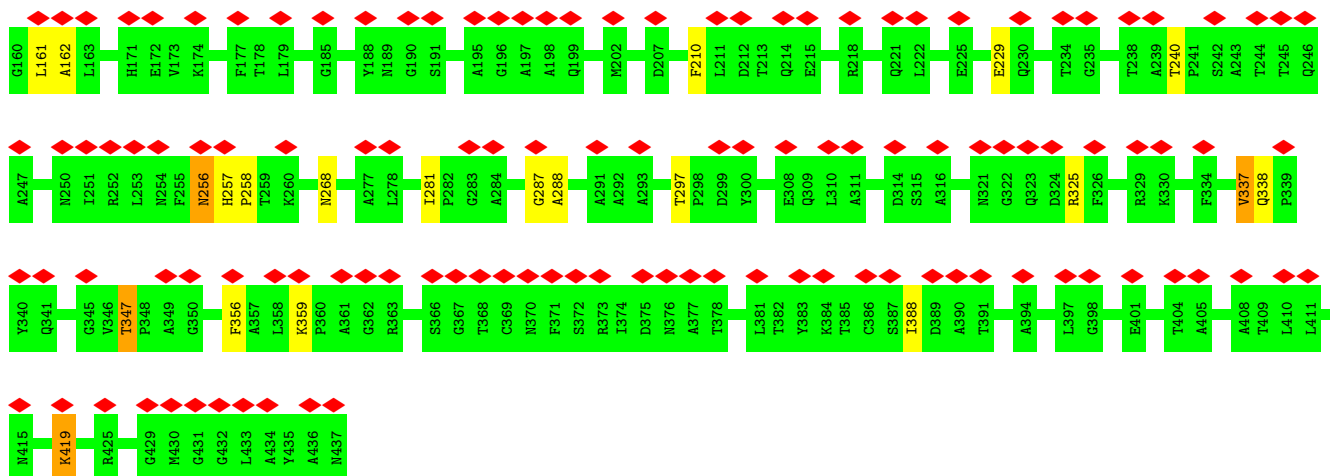
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Major capsid protein (MCP)

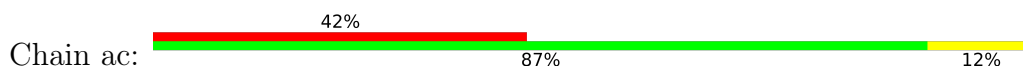


• Molecule 1: Major capsid protein (MCP)

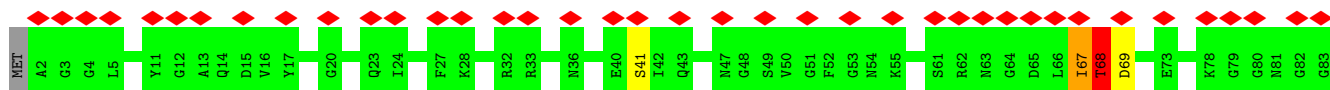
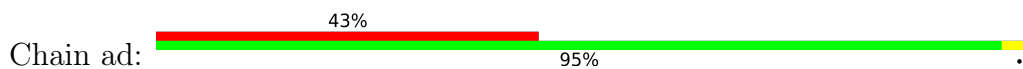


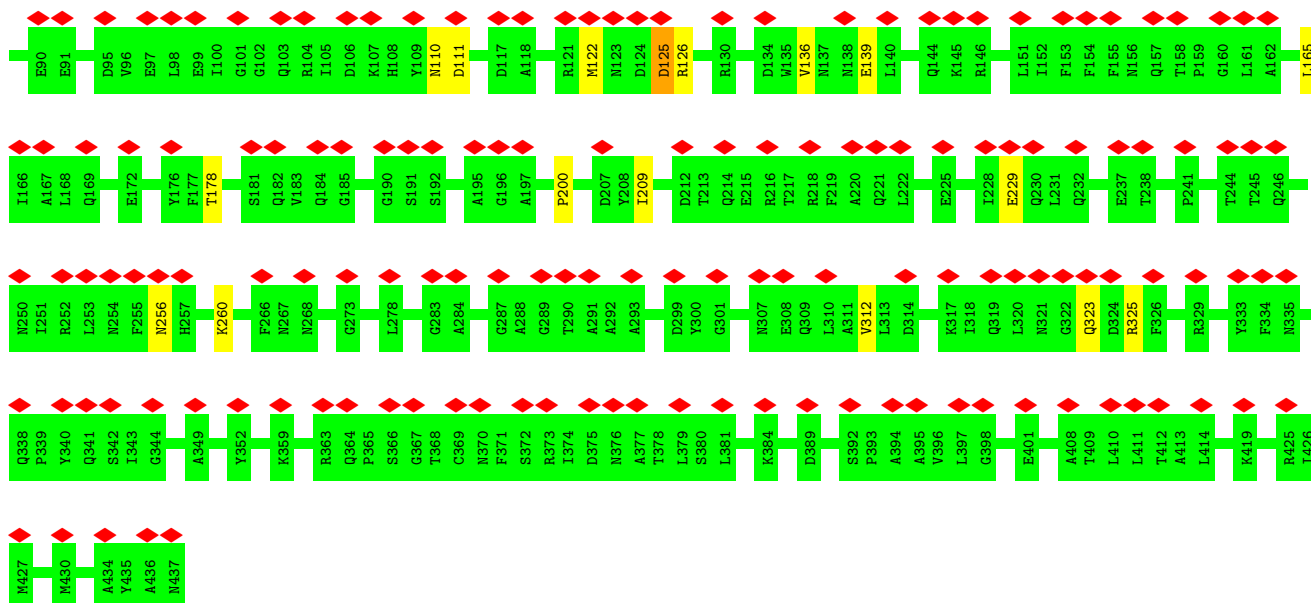


• Molecule 1: Major capsid protein (MCP)

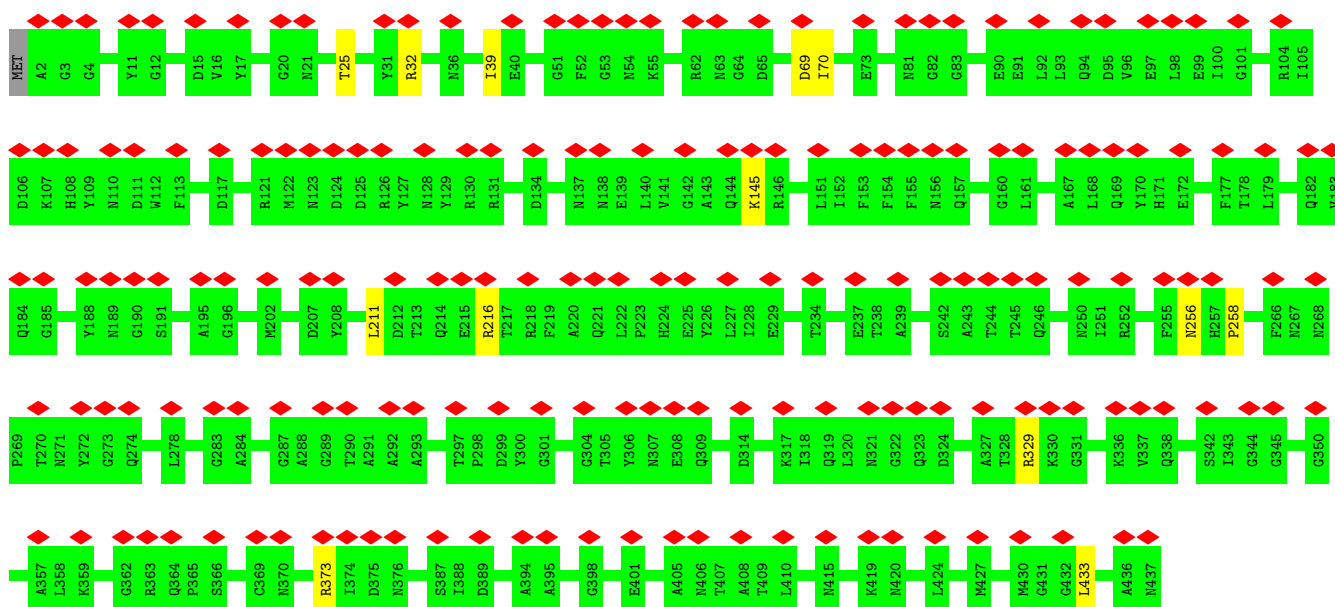


• Molecule 1: Major capsid protein (MCP)

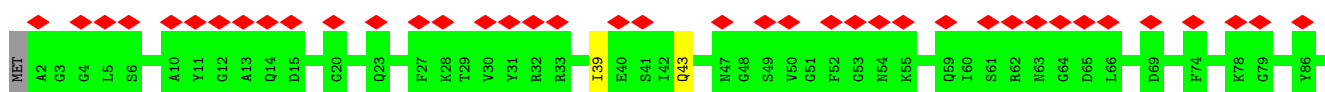


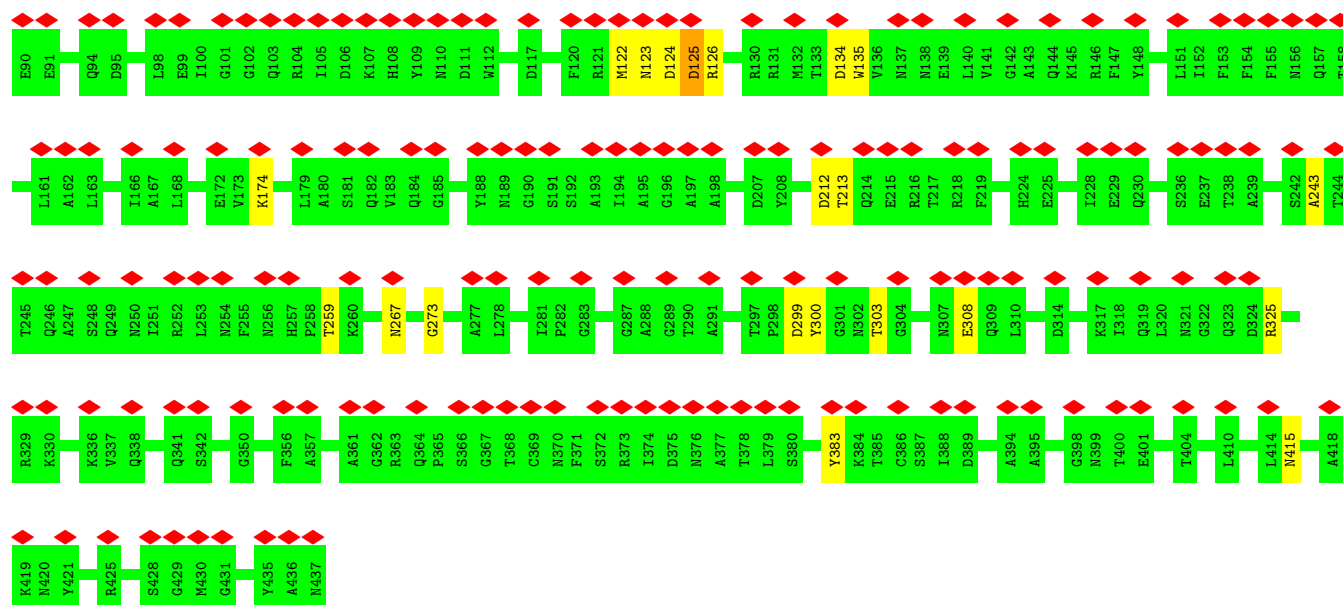


• Molecule 1: Major capsid protein (MCP)

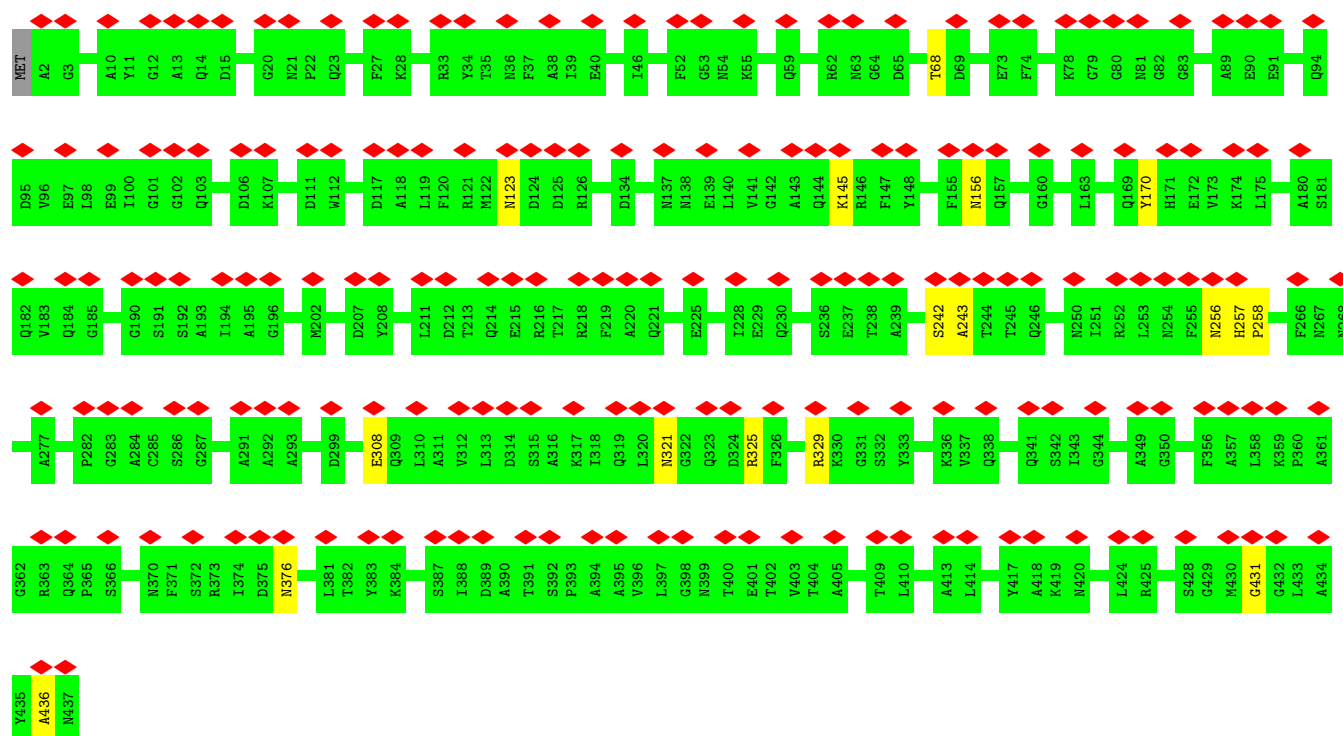


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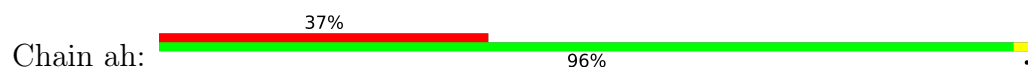


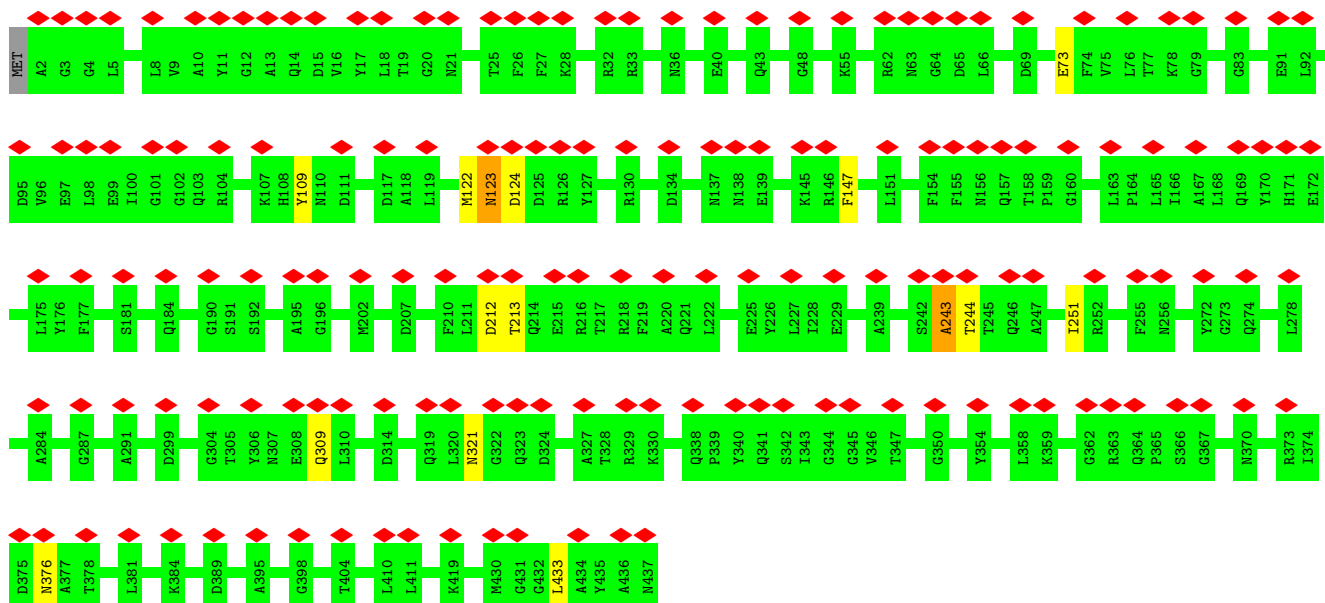


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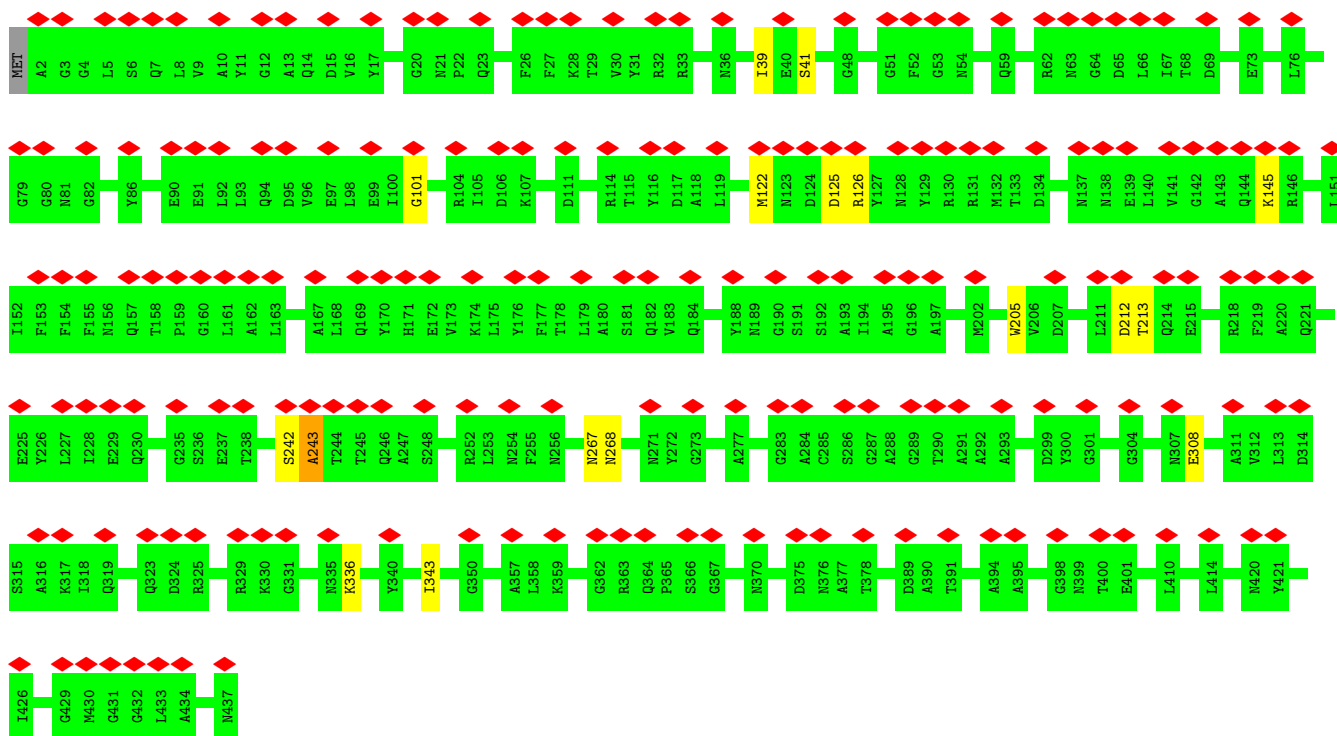
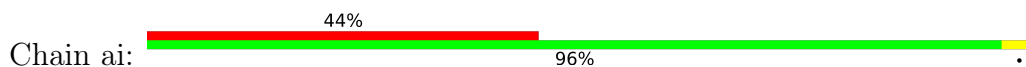


• Molecule 1: Major capsid protein (MCP)

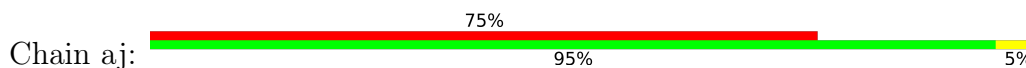


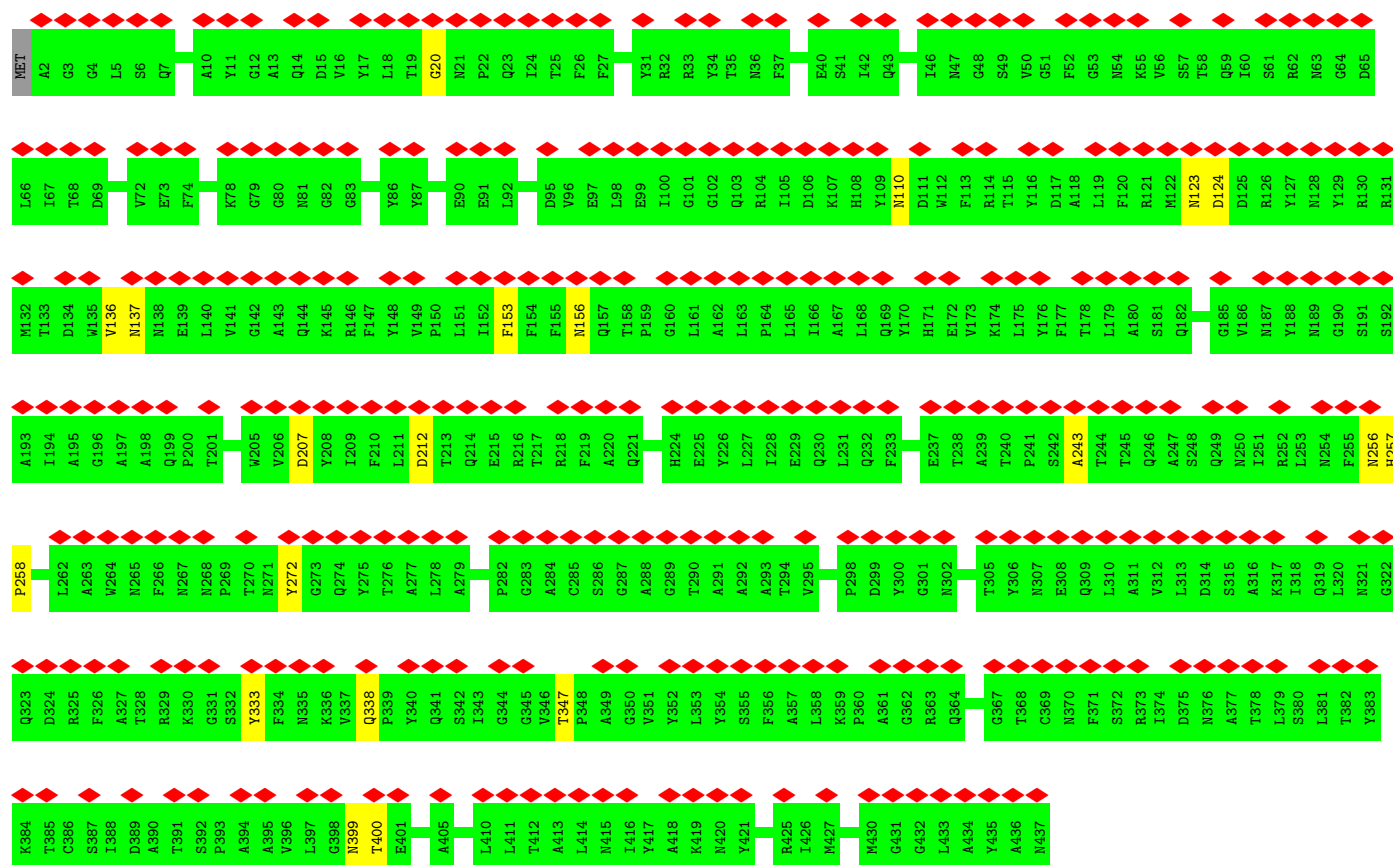


• Molecule 1: Major capsid protein (MCP)

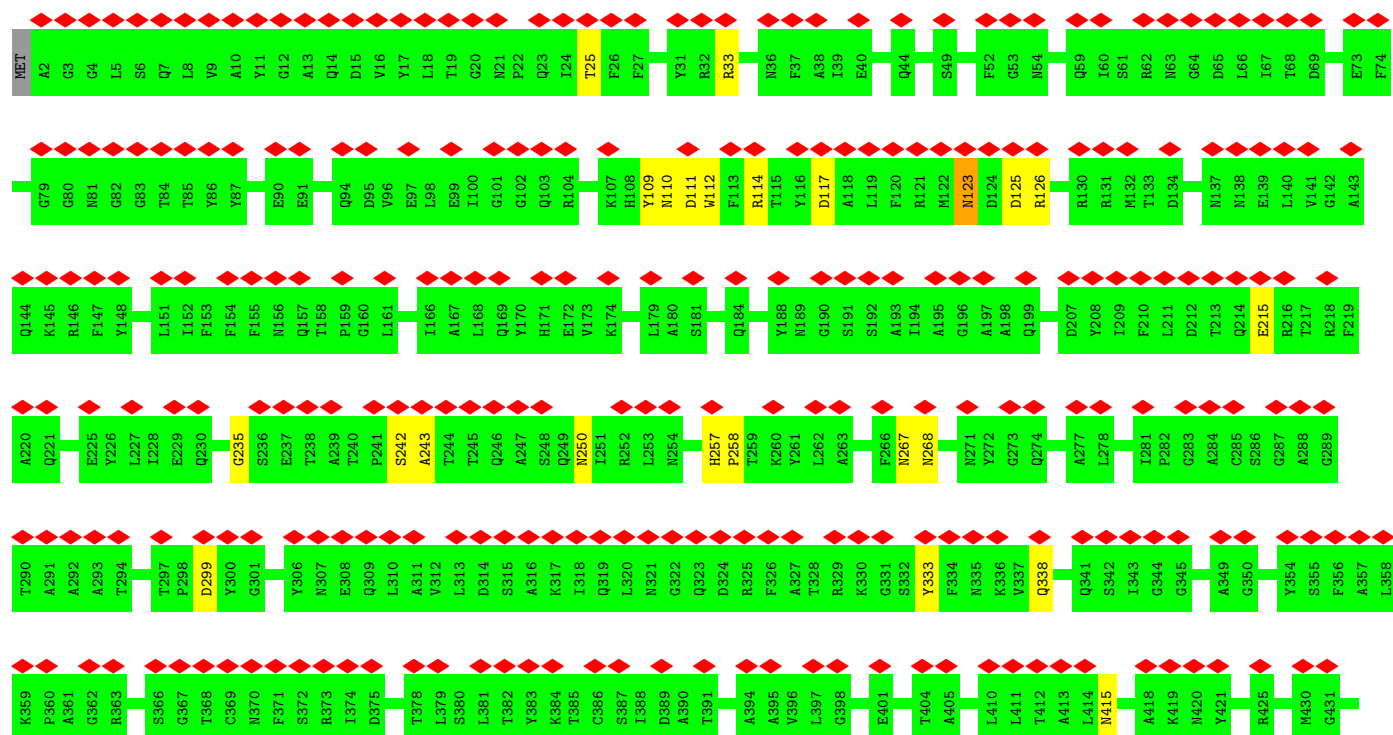


• Molecule 1: Major capsid protein (MCP)



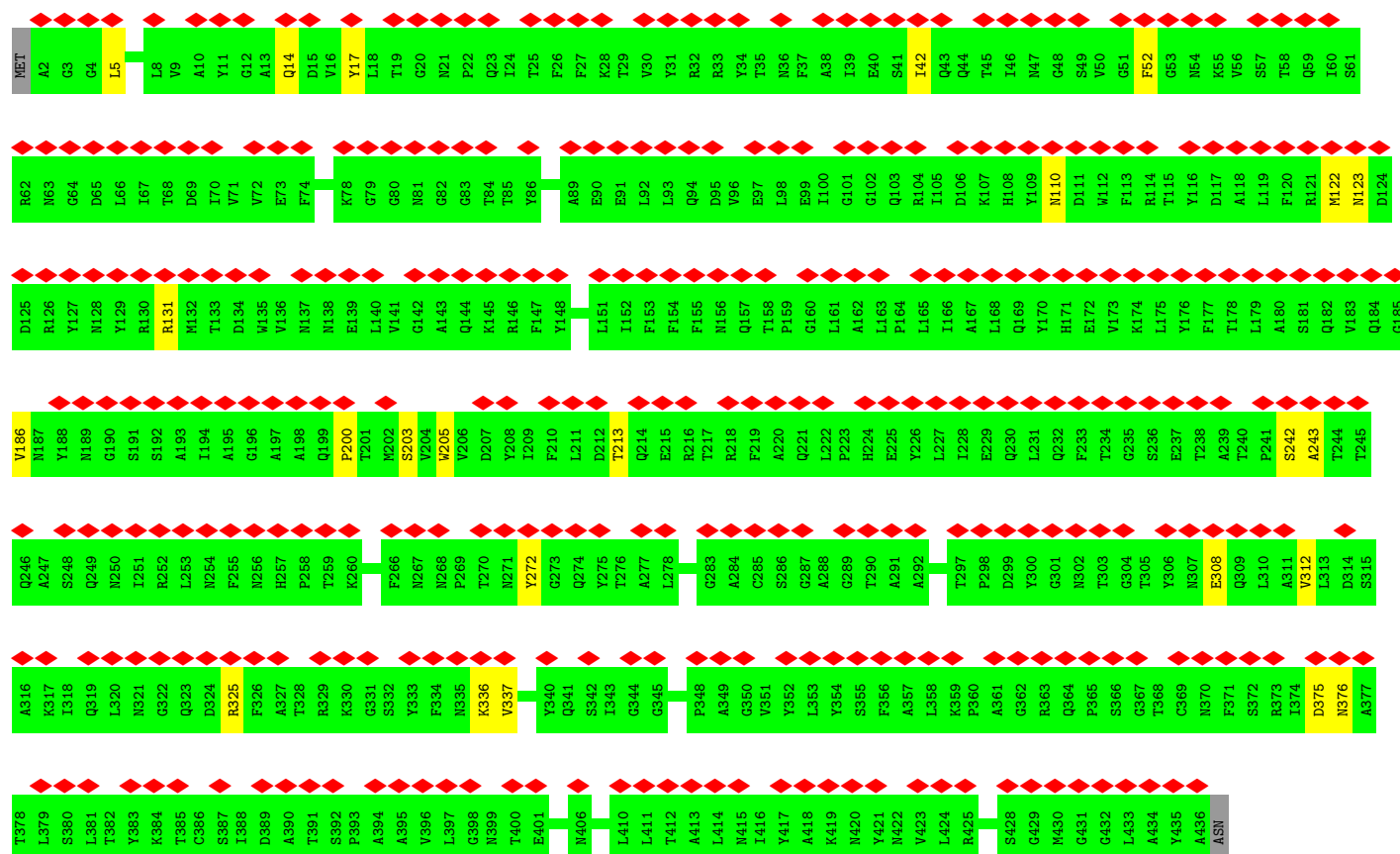
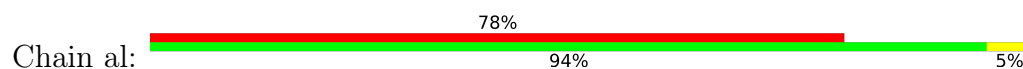


• Molecule 1: Major capsid protein (MCP)

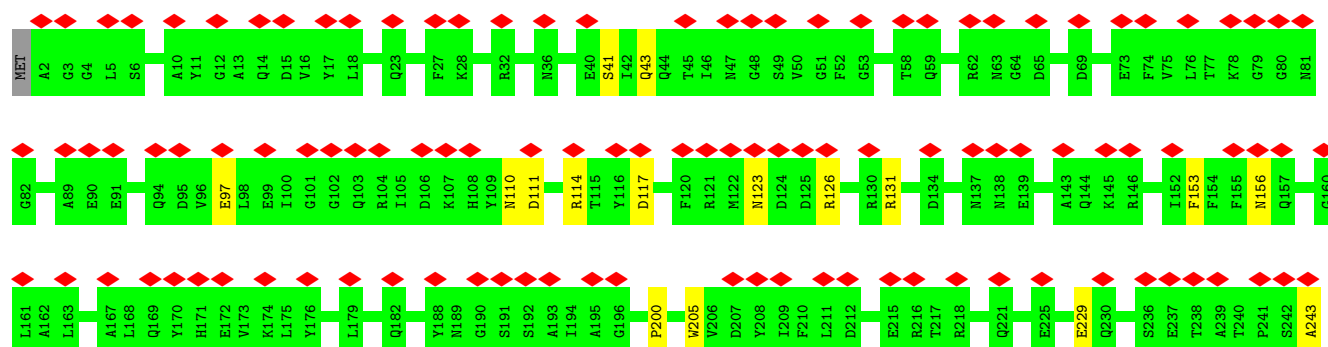
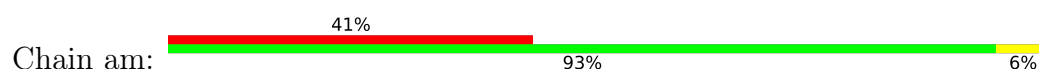


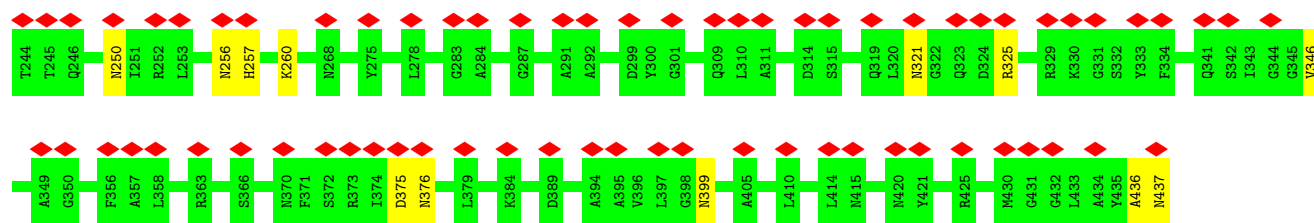


• Molecule 1: Major capsid protein (MCP)

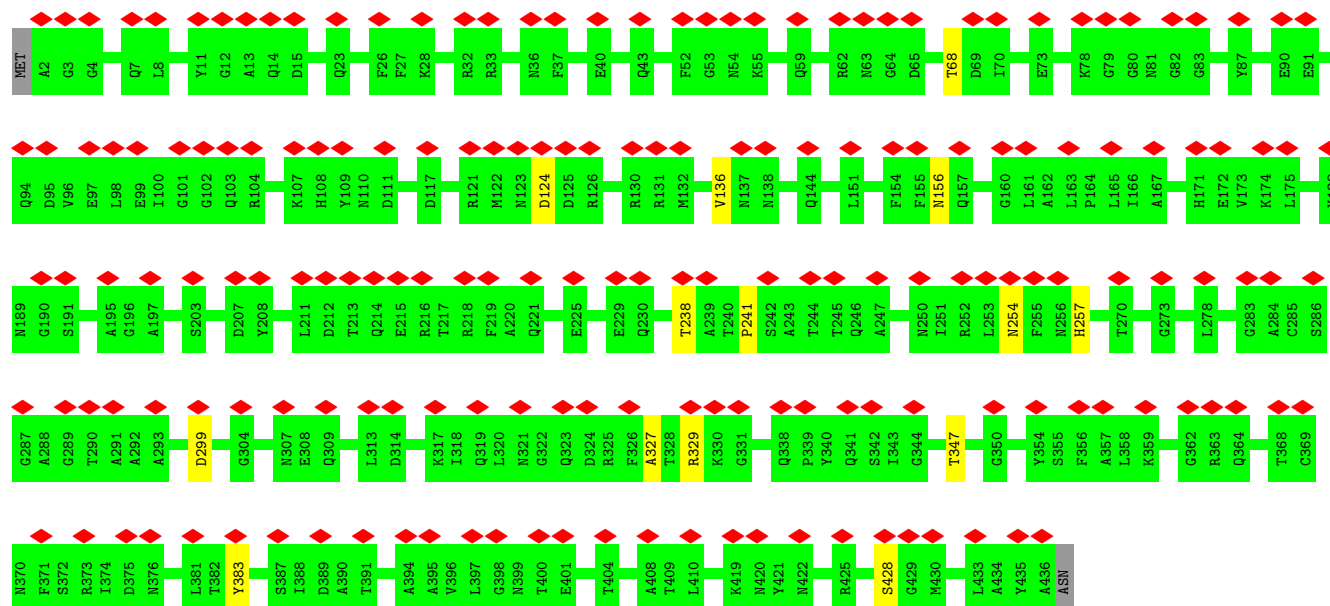
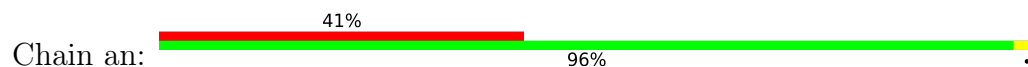


• Molecule 1: Major capsid protein (MCP)

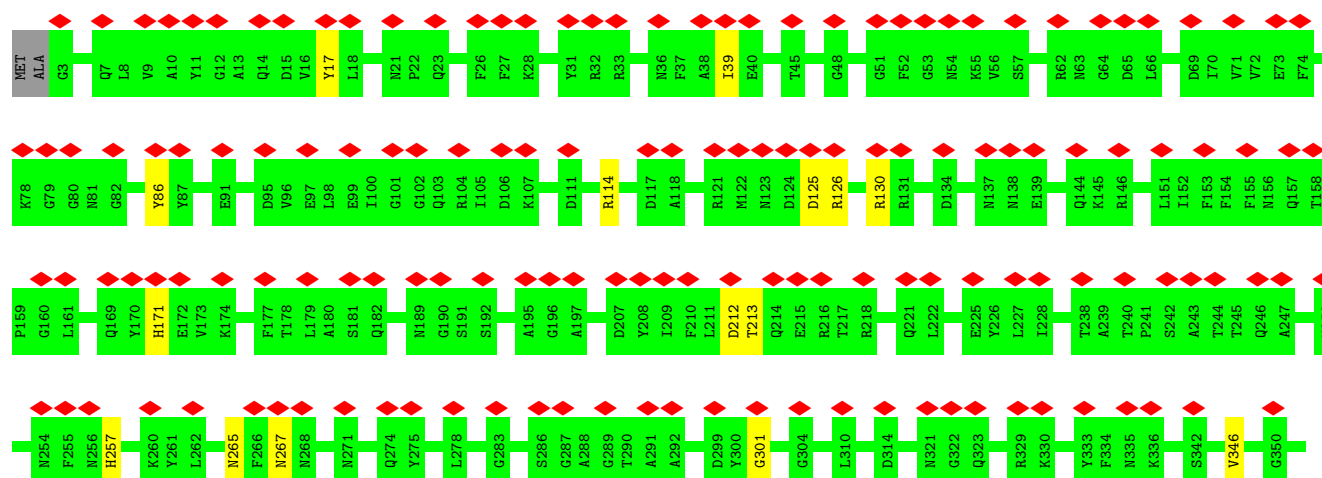
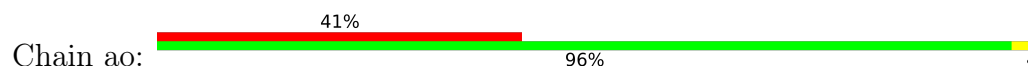


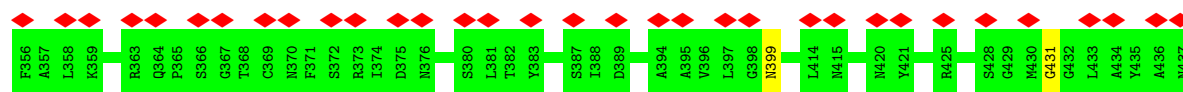


• Molecule 1: Major capsid protein (MCP)

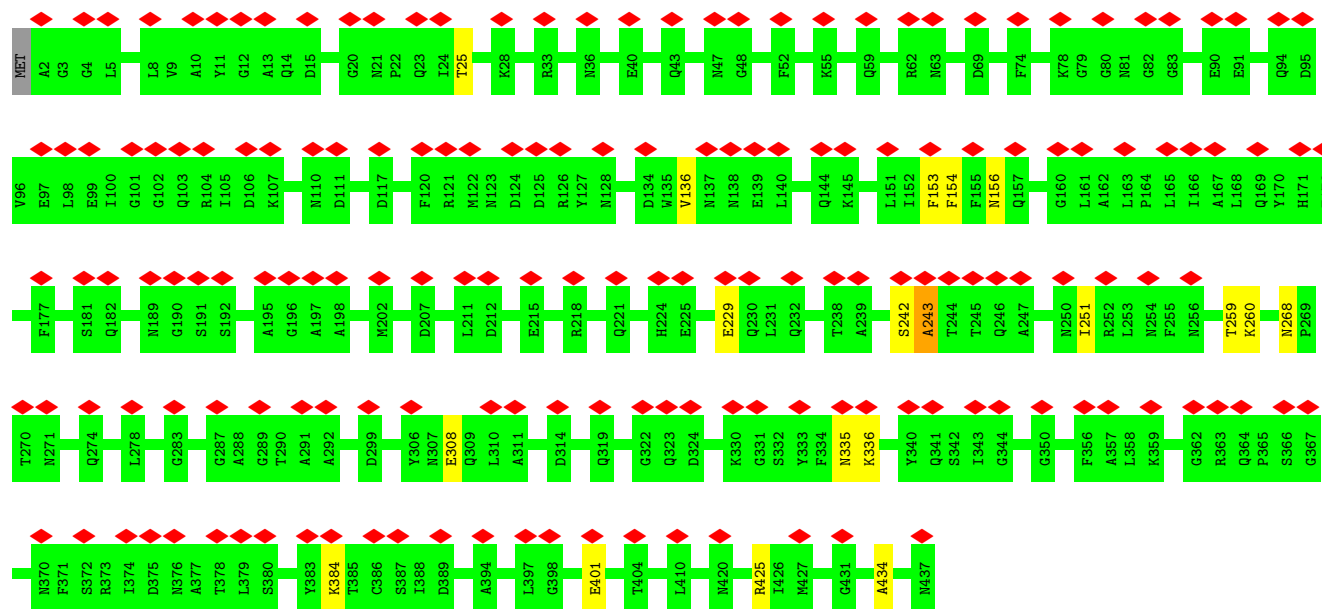
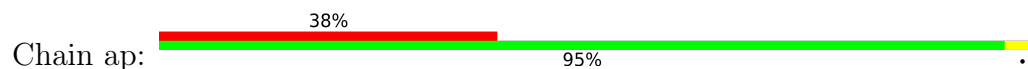


• Molecule 1: Major capsid protein (MCP)

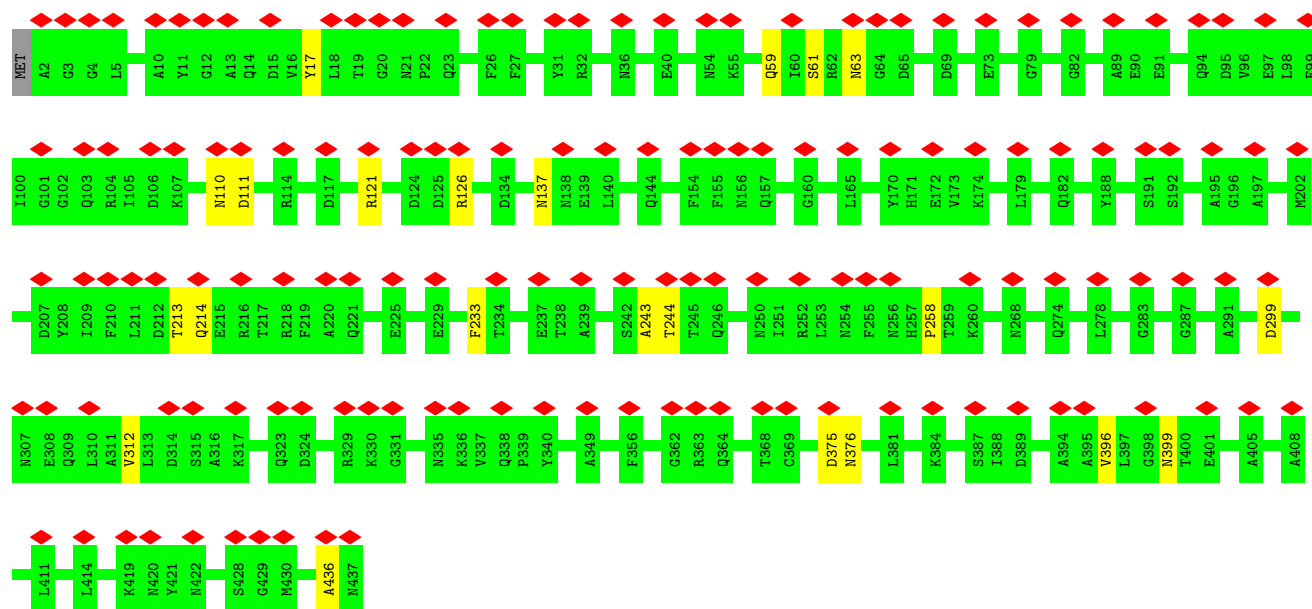




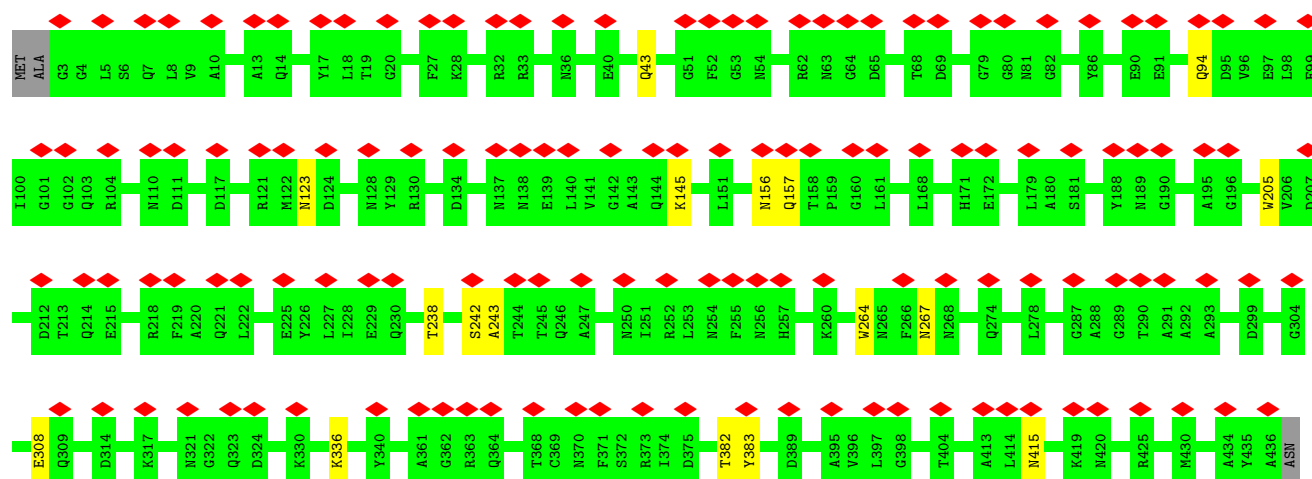
• Molecule 1: Major capsid protein (MCP)



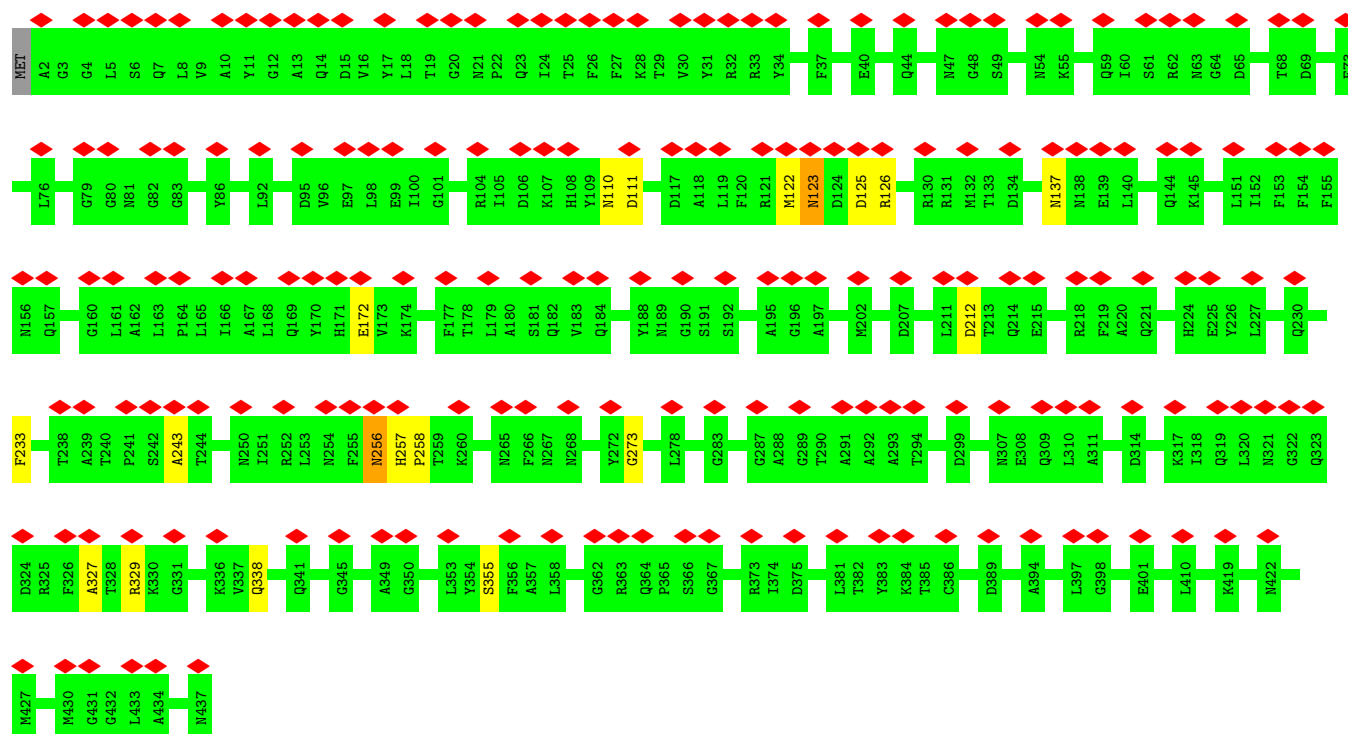
• Molecule 1: Major capsid protein (MCP)



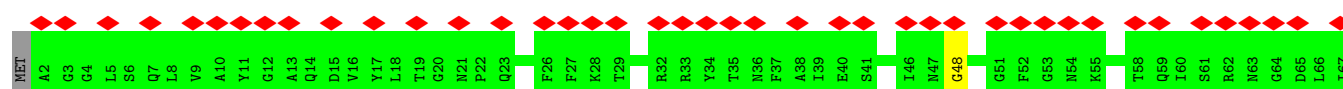
• Molecule 1: Major capsid protein (MCP)

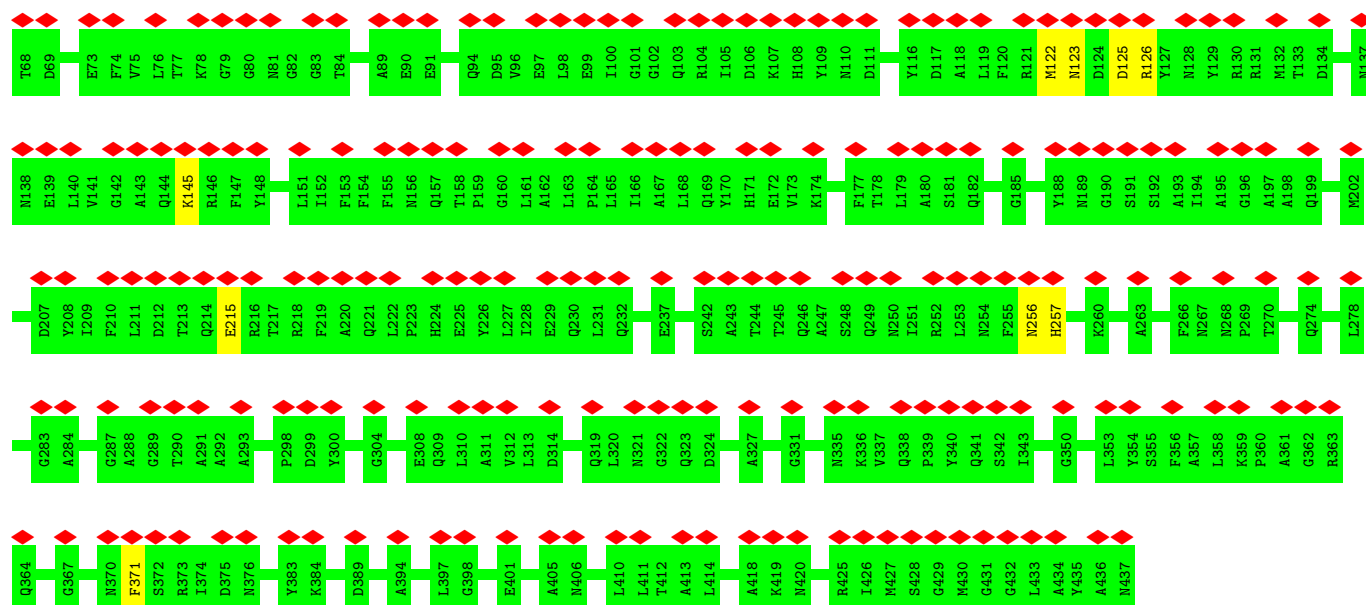


• Molecule 1: Major capsid protein (MCP)

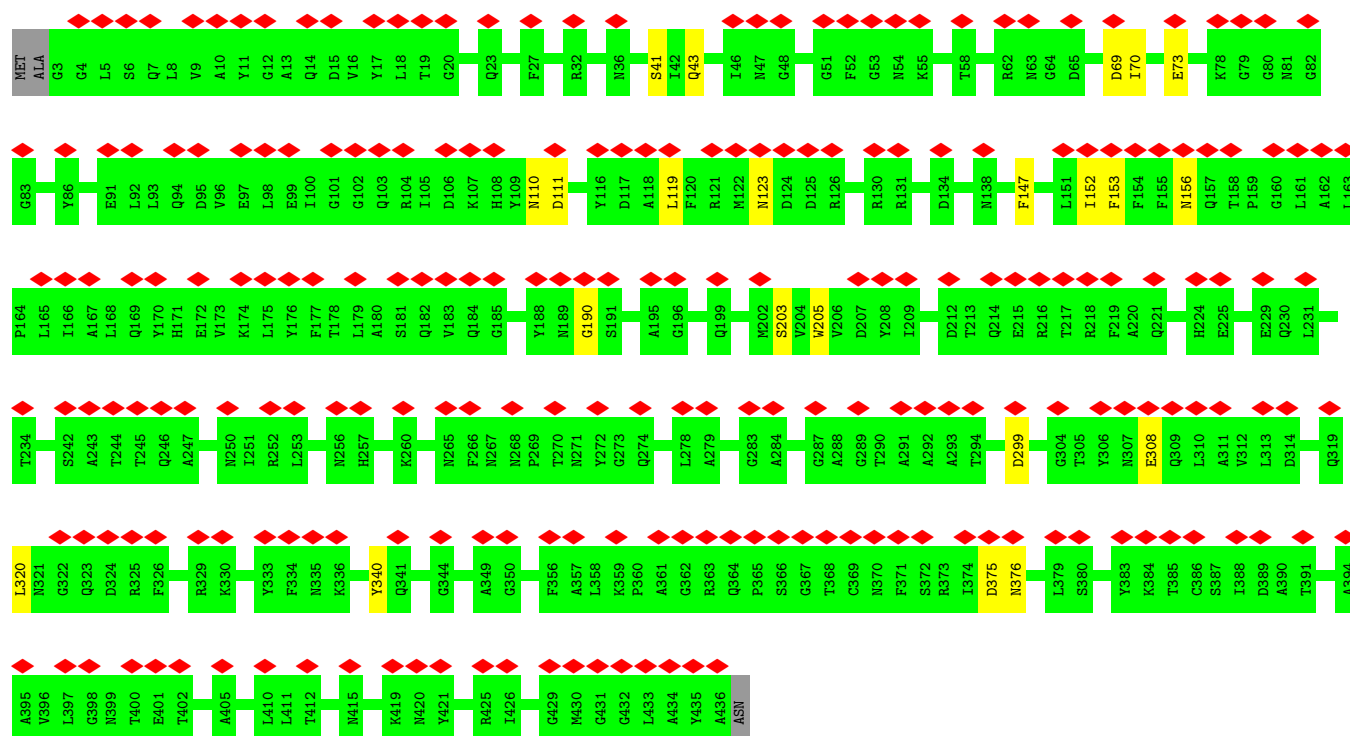


• Molecule 1: Major capsid protein (MCP)



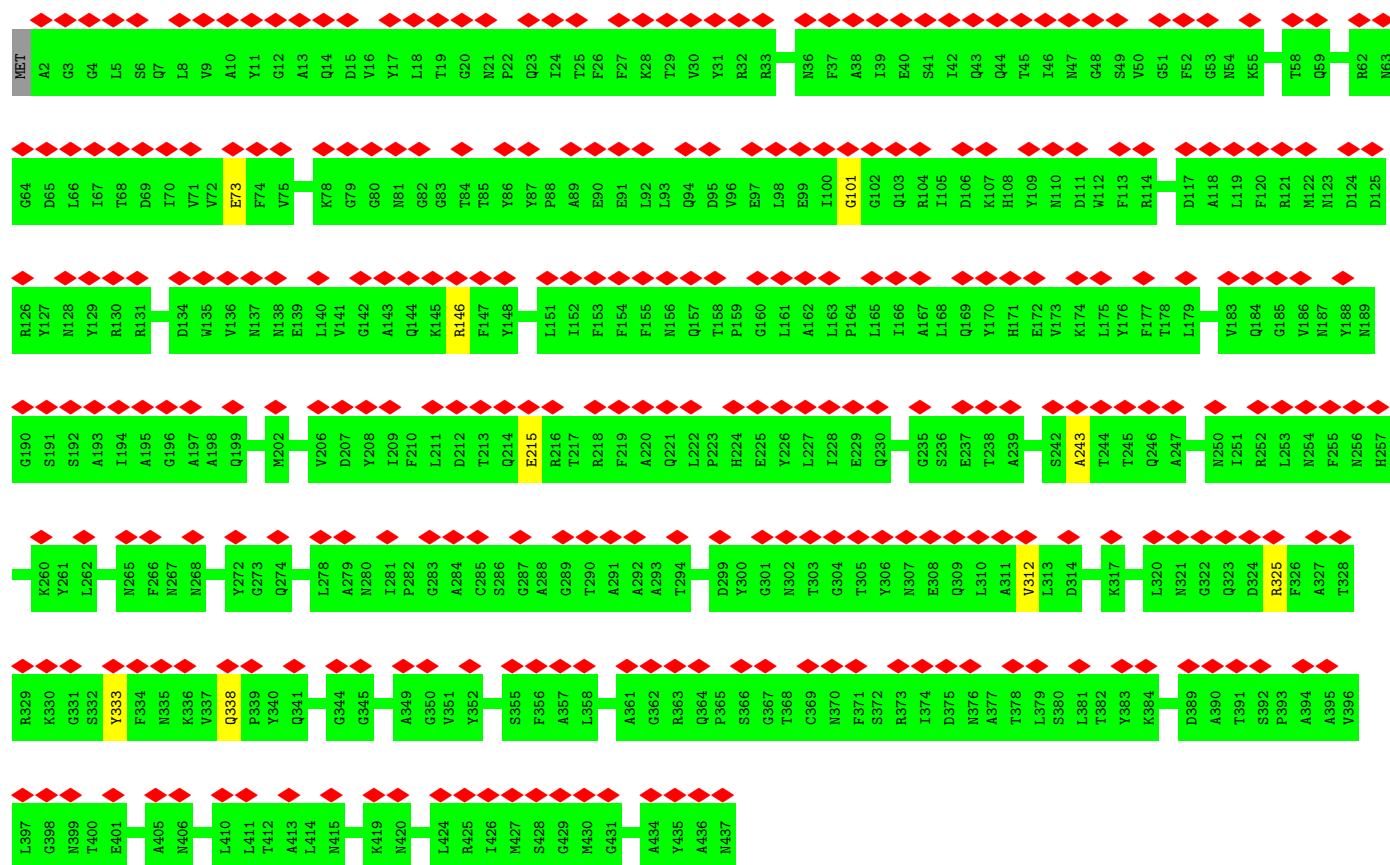


• Molecule 1: Major capsid protein (MCP)

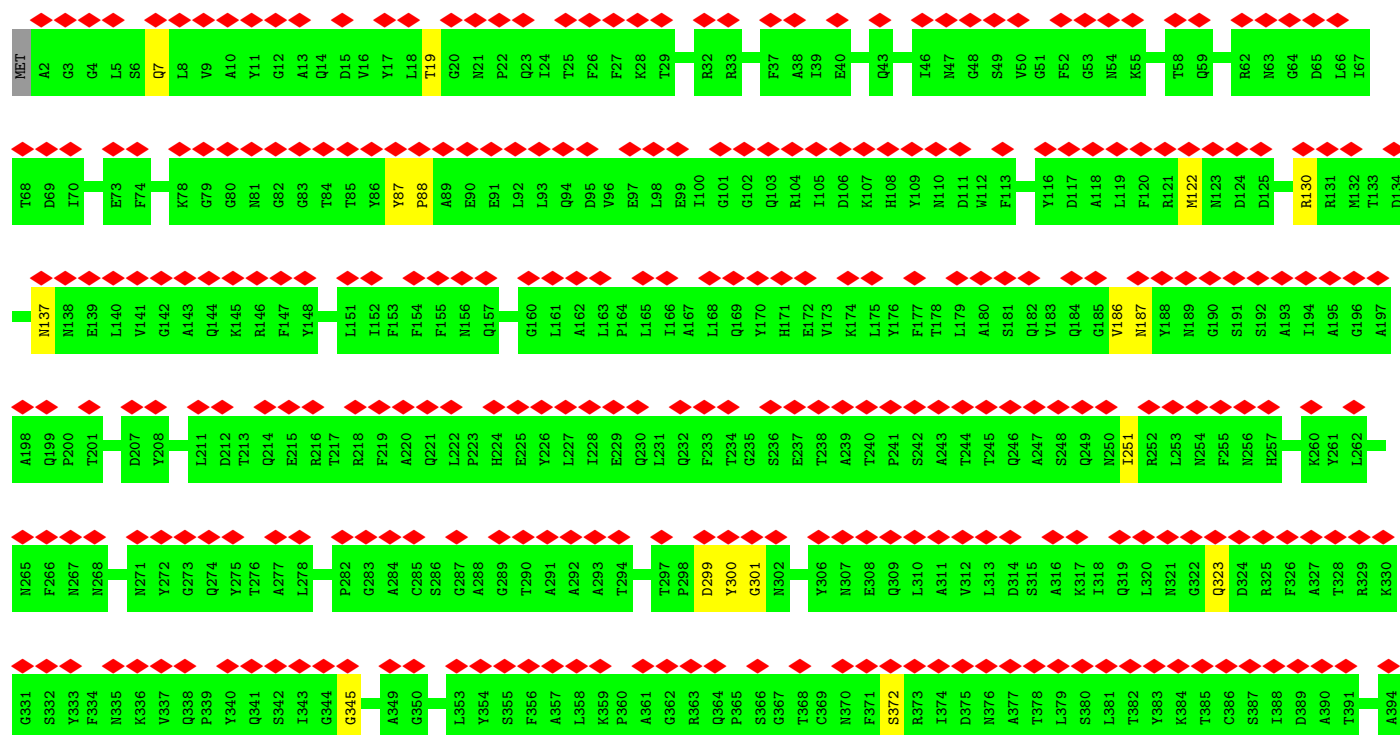
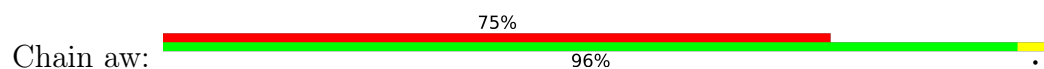


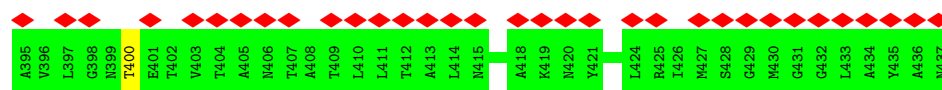
• Molecule 1: Major capsid protein (MCP)





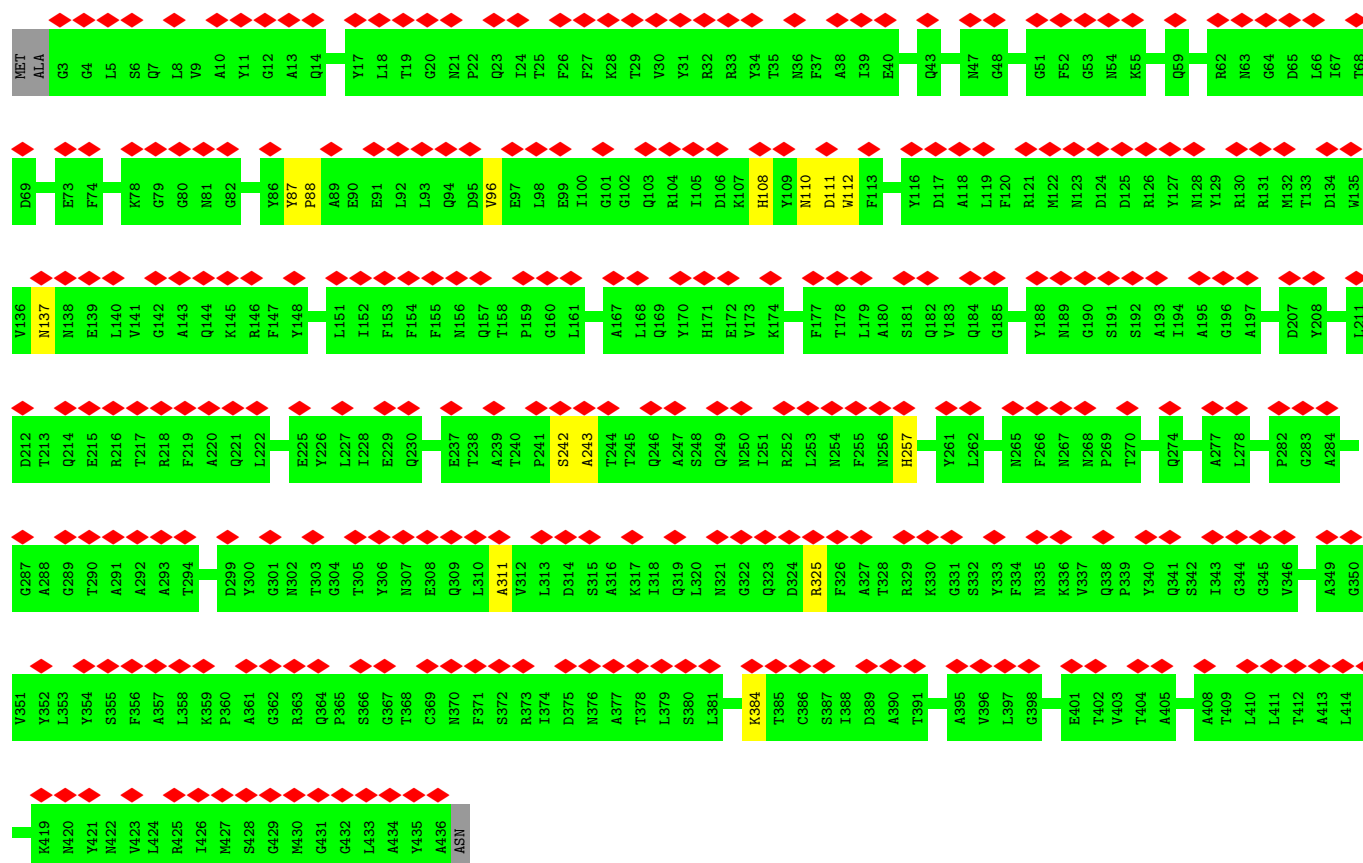
• Molecule 1: Major capsid protein (MCP)





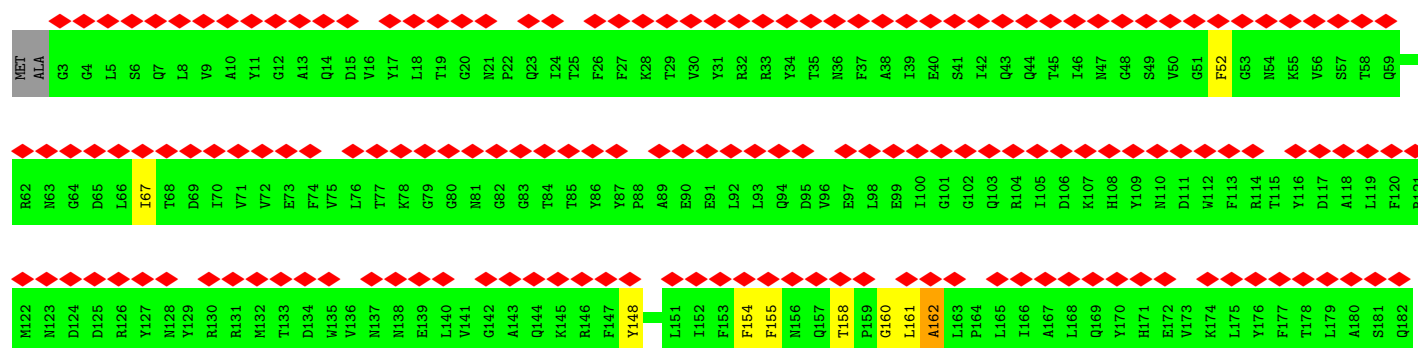
• Molecule 1: Major capsid protein (MCP)

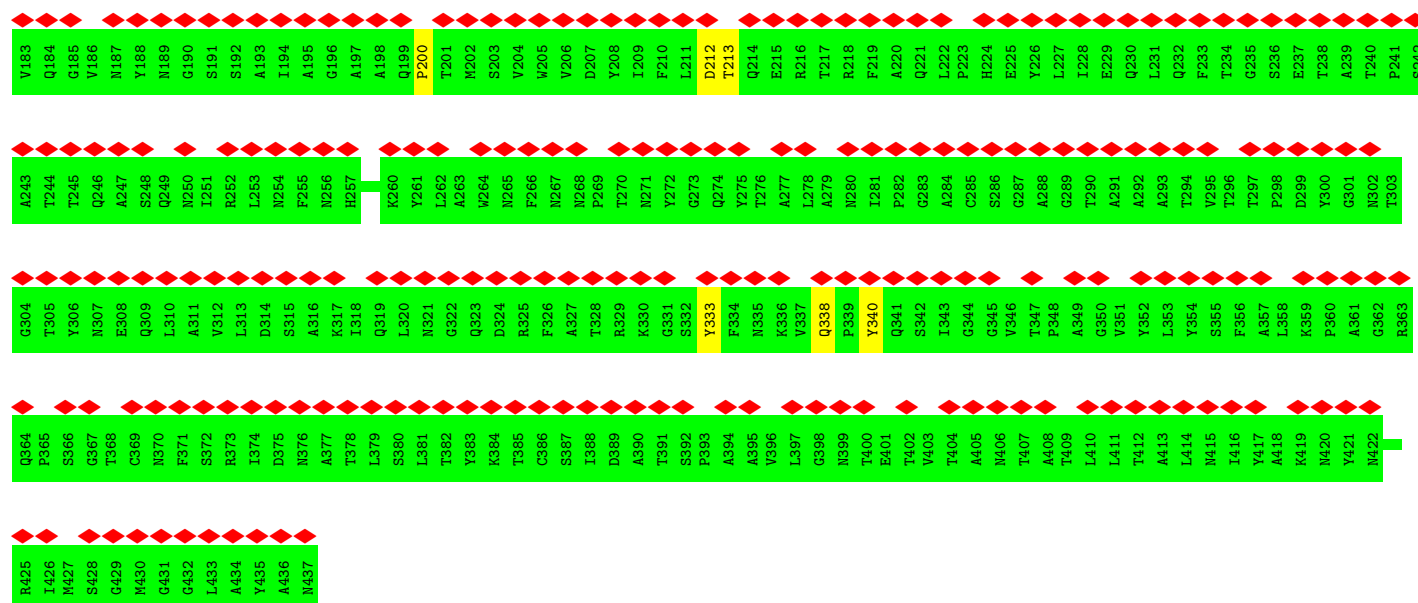
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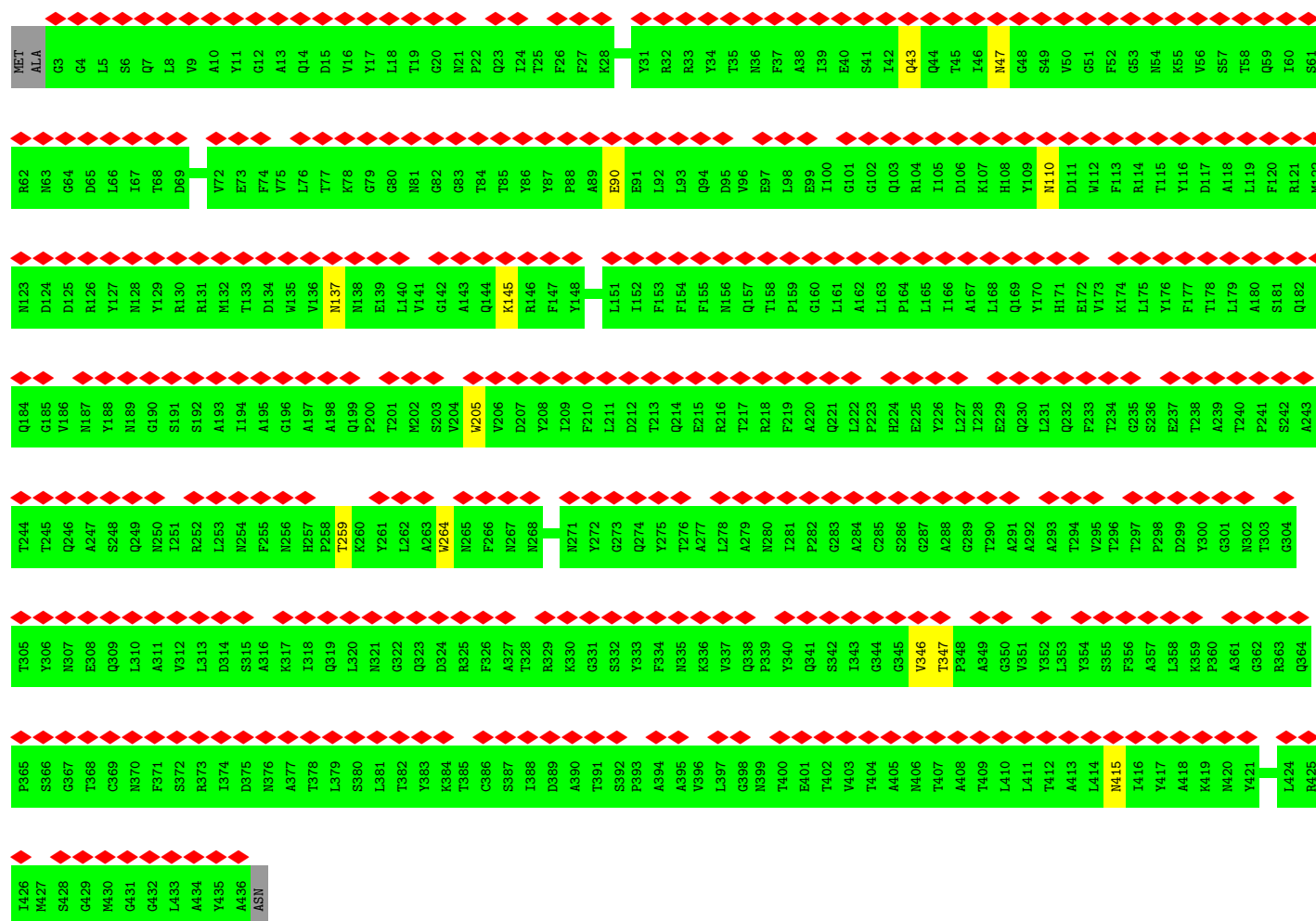
• Molecule 1: Major capsid protein (MCP)

Chain ay: 88% 96%



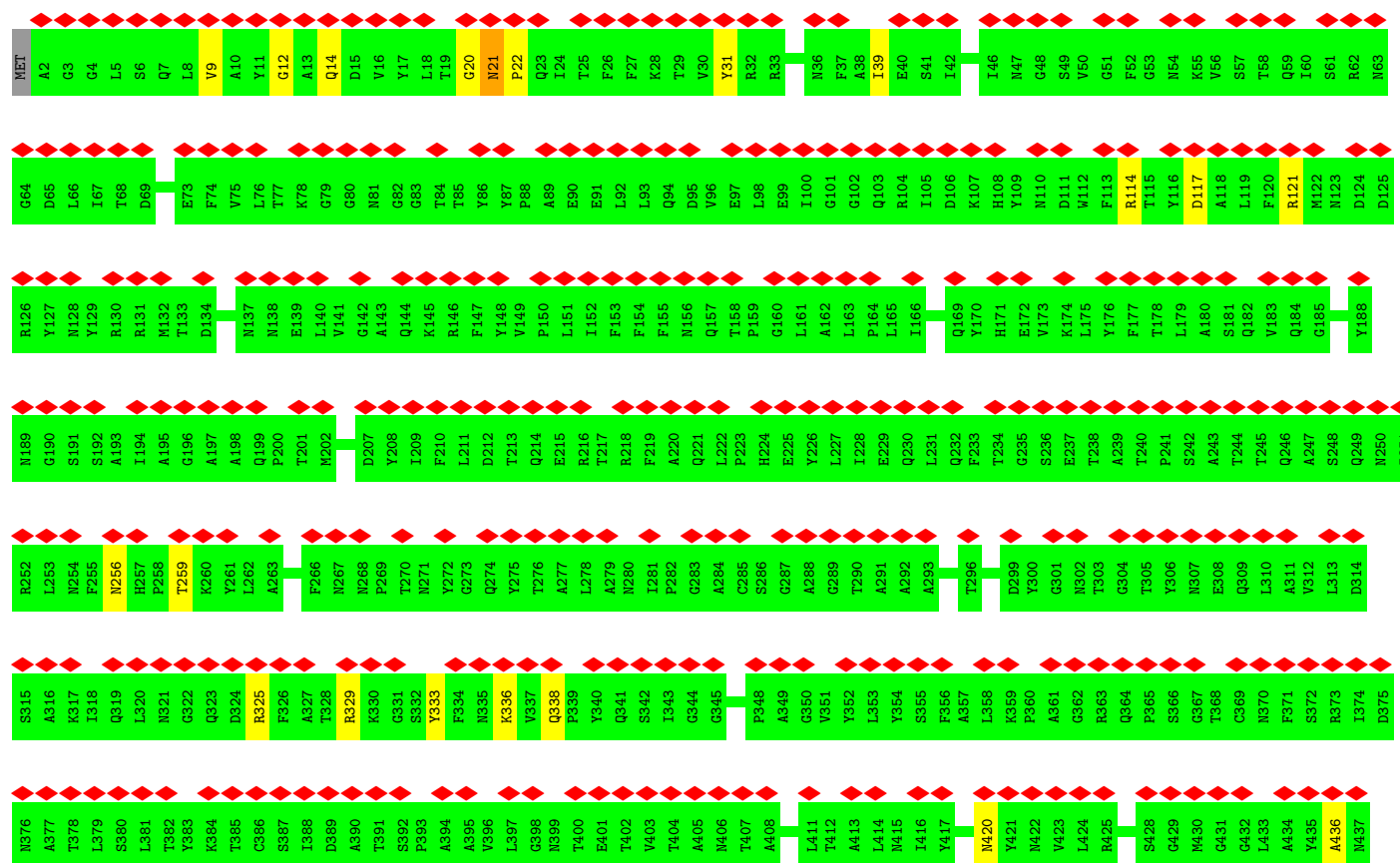
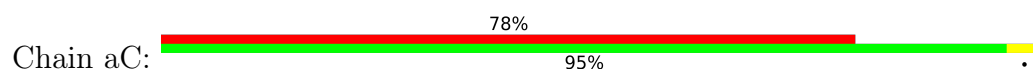


• Molecule 1: Major capsid protein (MCP)

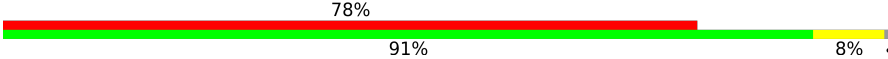


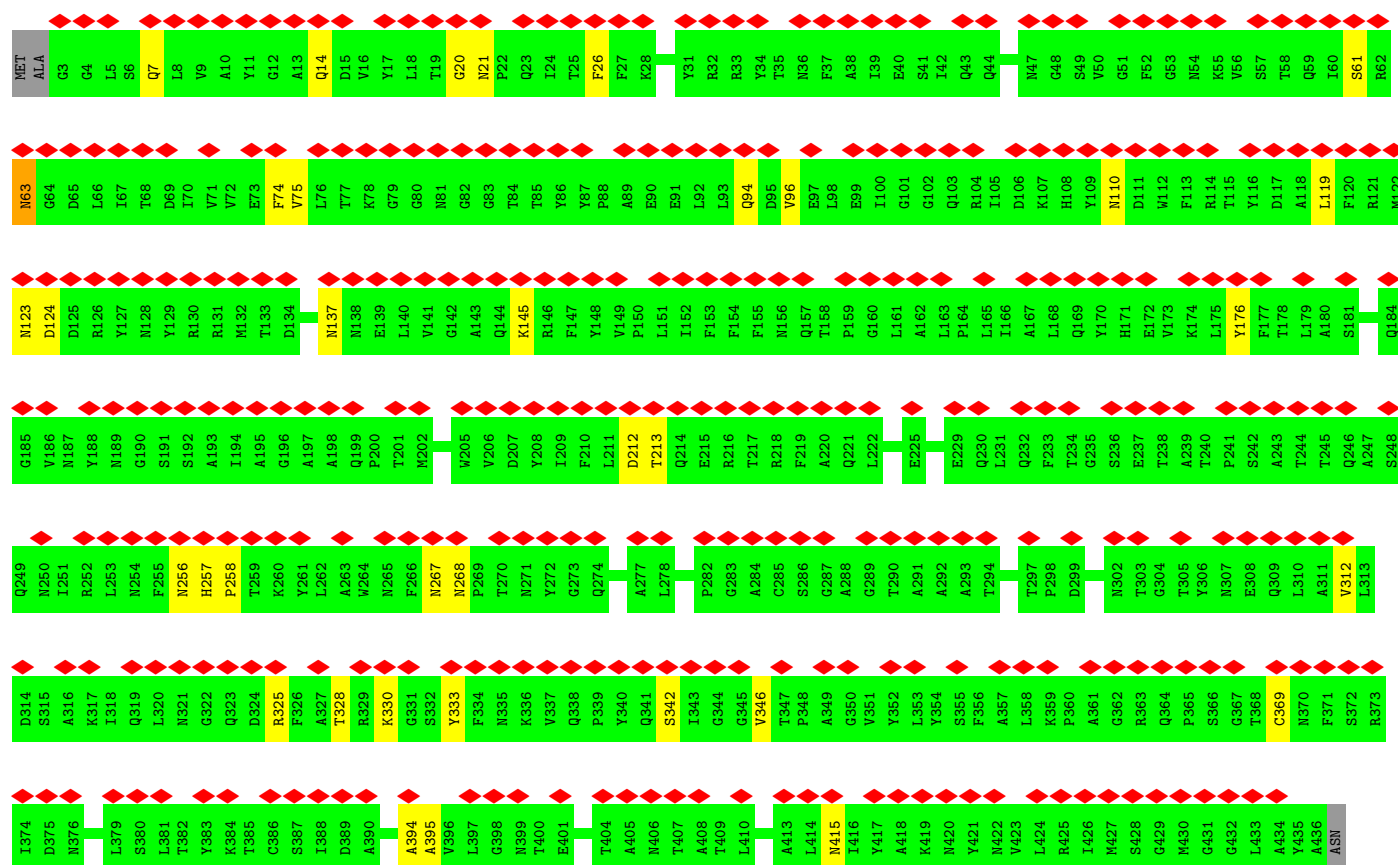


• Molecule 1: Major capsid protein (MCP)

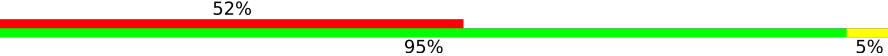


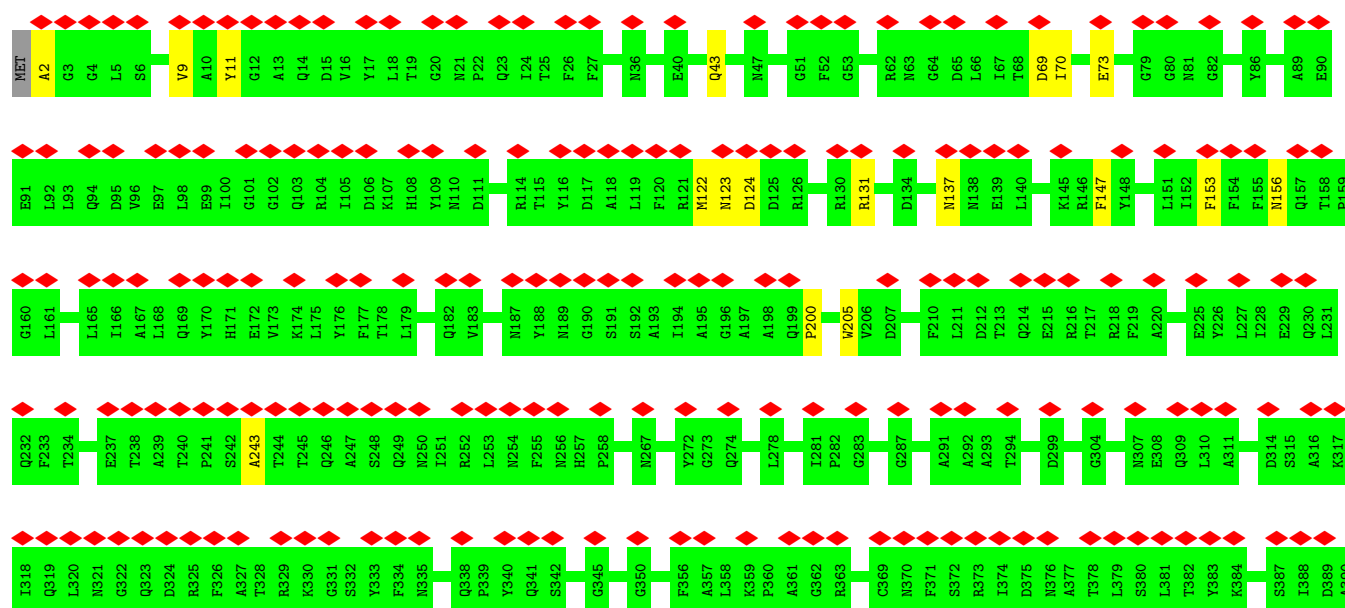
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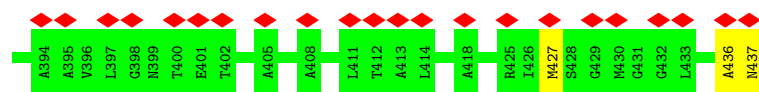
Chain aD: 



• Molecule 1: Major capsid protein (MCP)

Chain aE: 





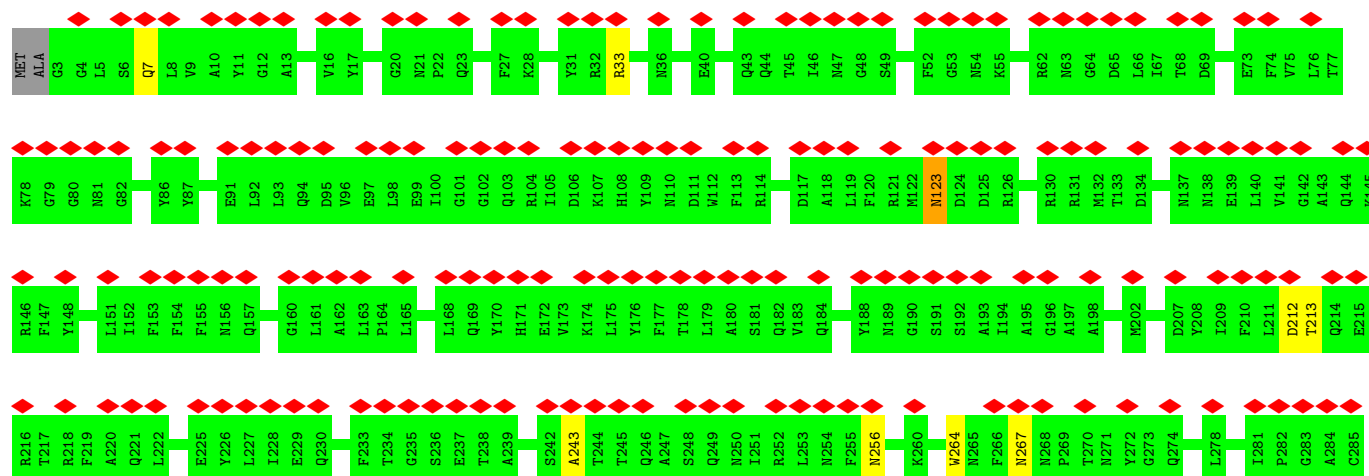
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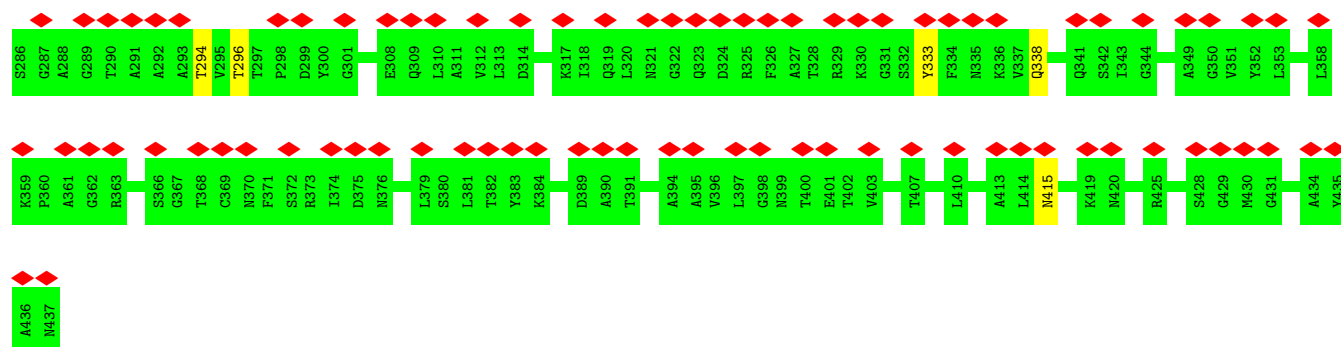
Chain aF: 44% 95%



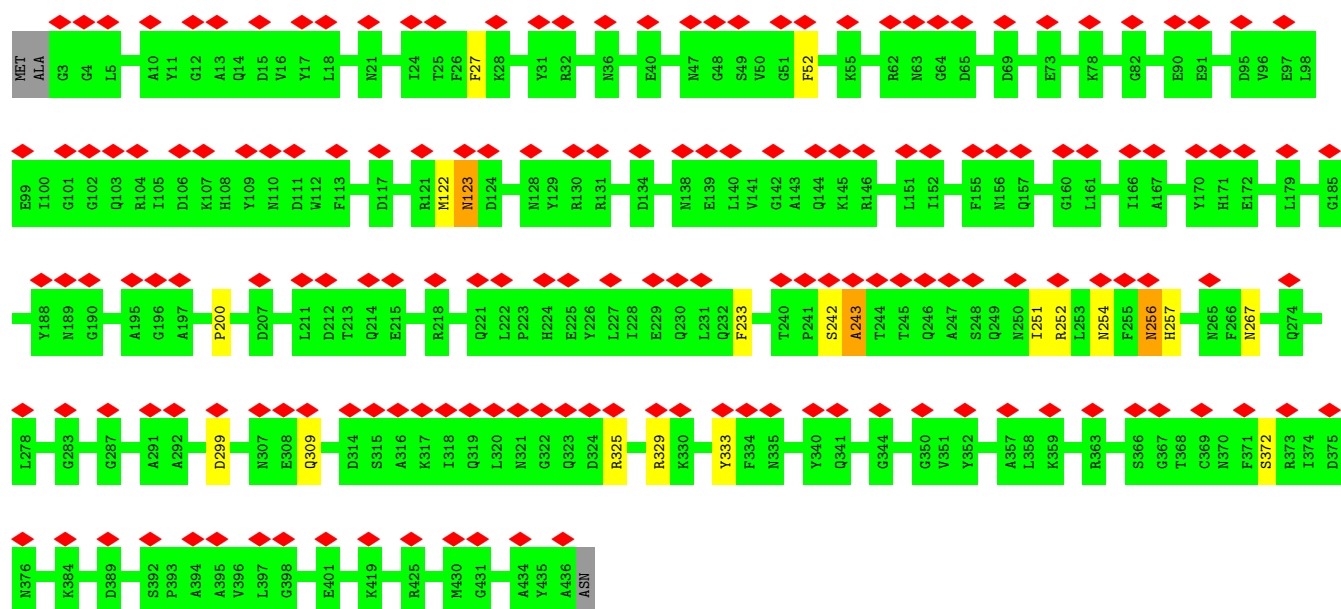
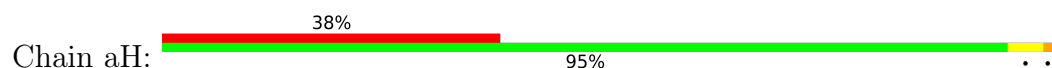
• Molecule 1: Major capsid protein (MCP)

Chain aG: 59% 96%

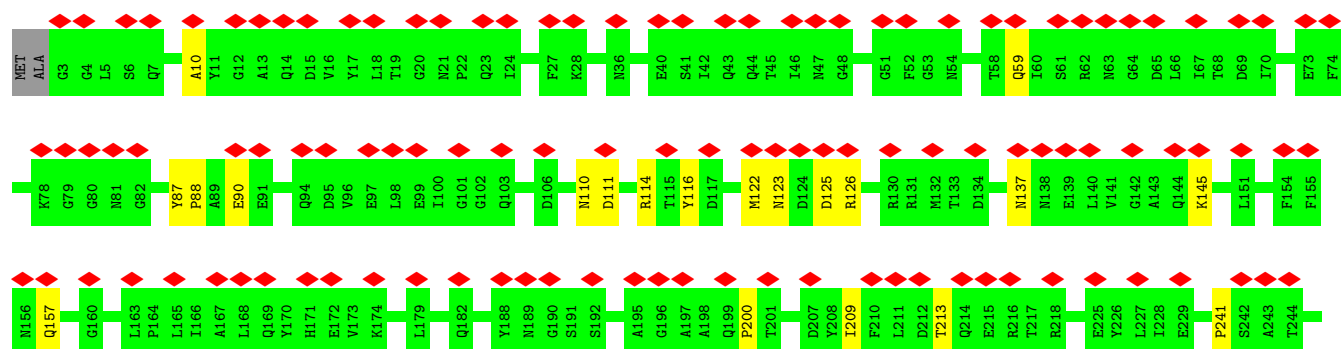


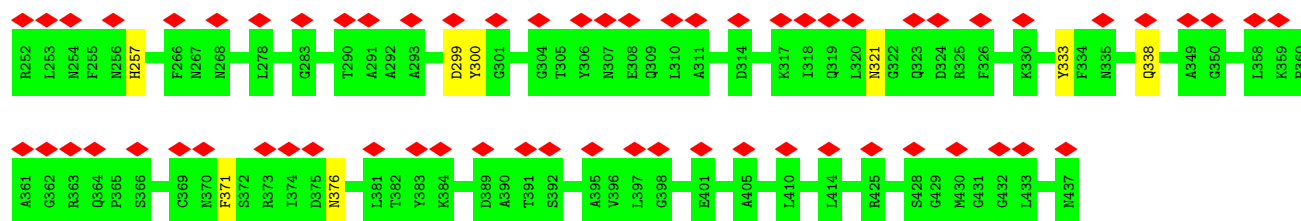


• Molecule 1: Major capsid protein (MCP)

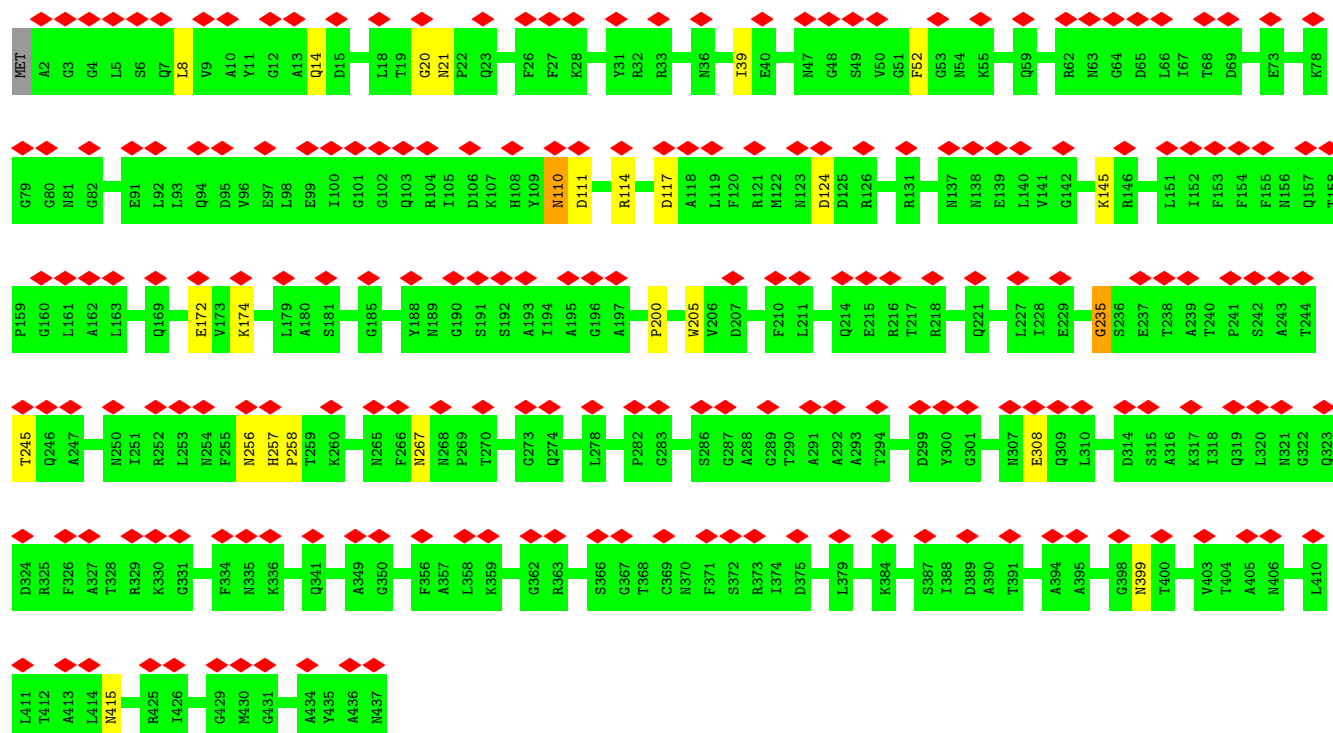


• Molecule 1: Major capsid protein (MCP)

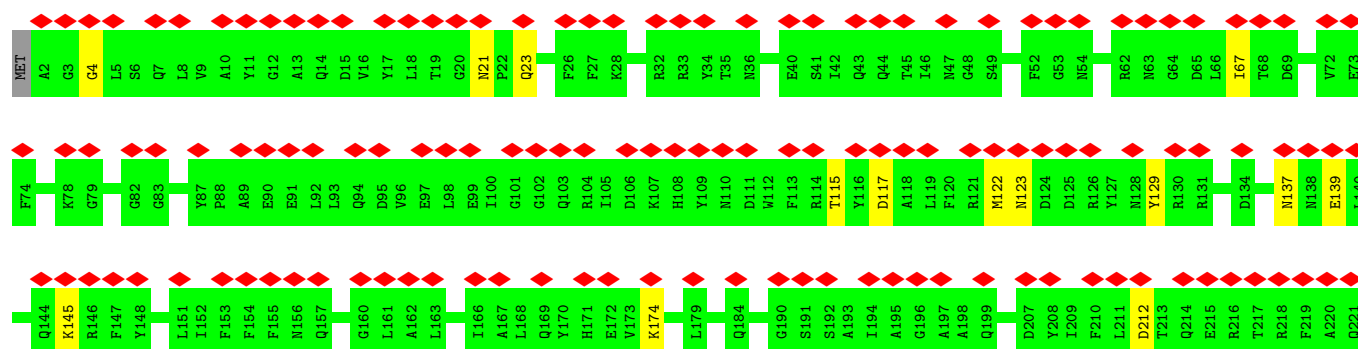


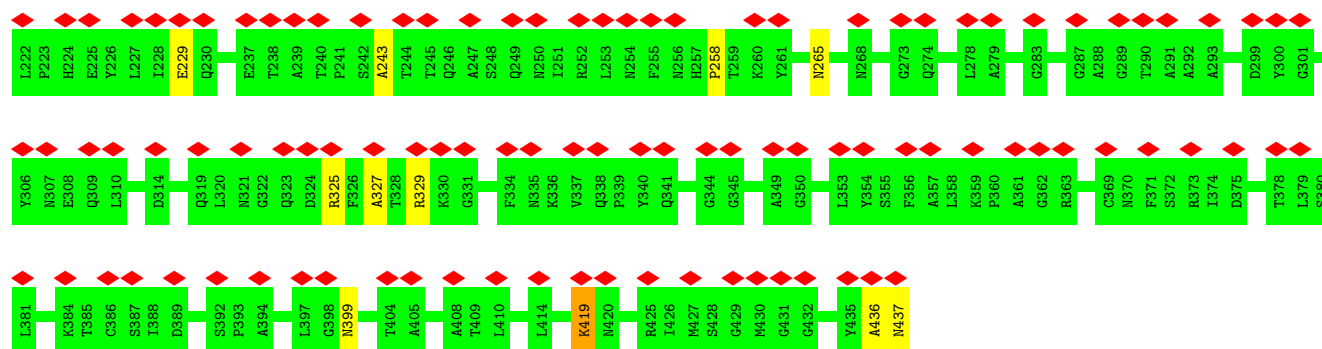


• Molecule 1: Major capsid protein (MCP)

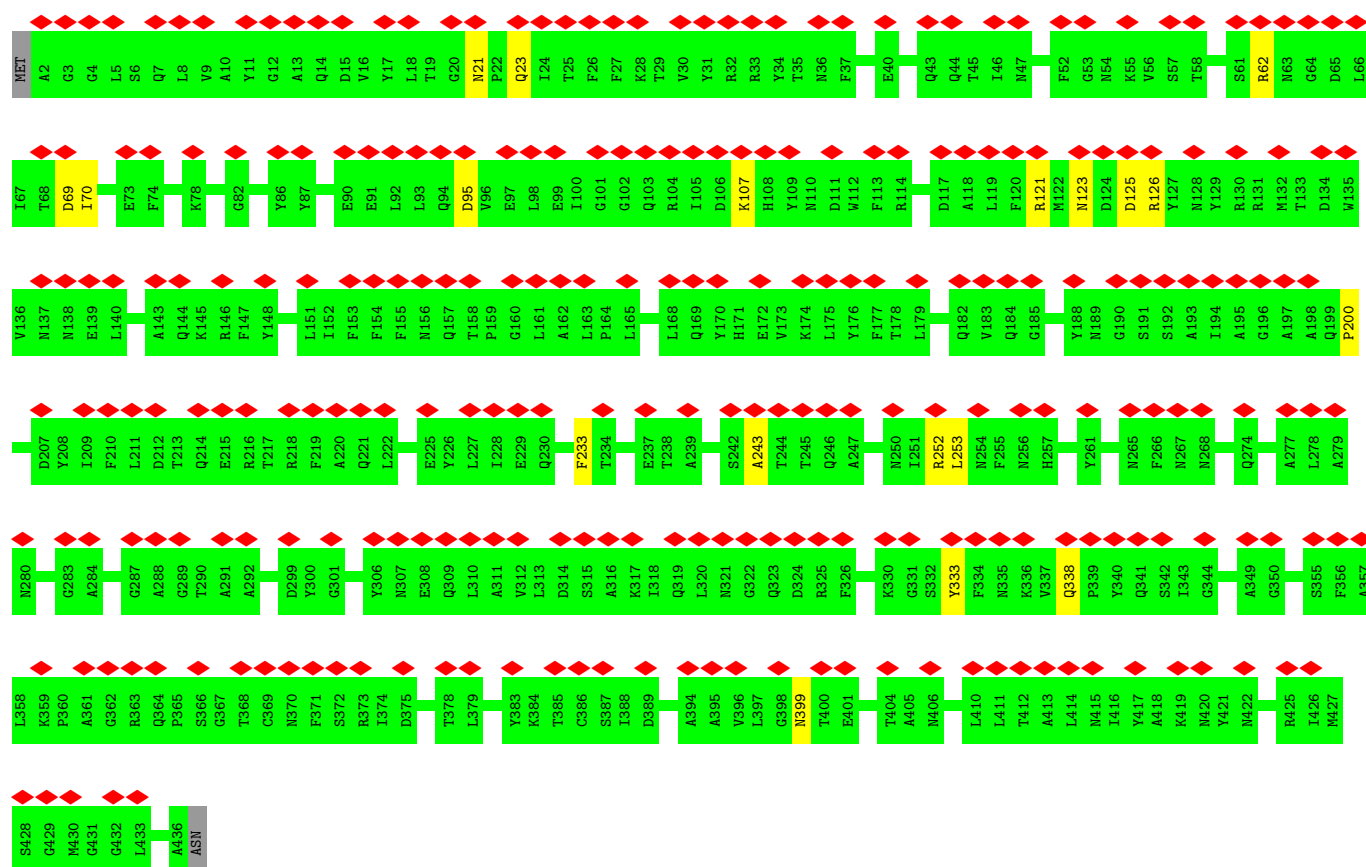


• Molecule 1: Major capsid protein (MCP)

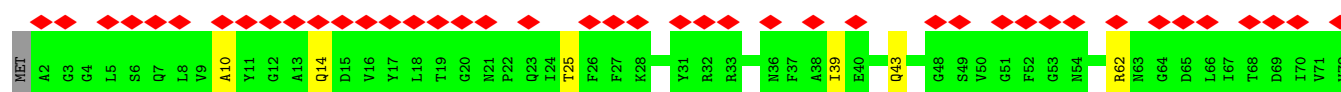


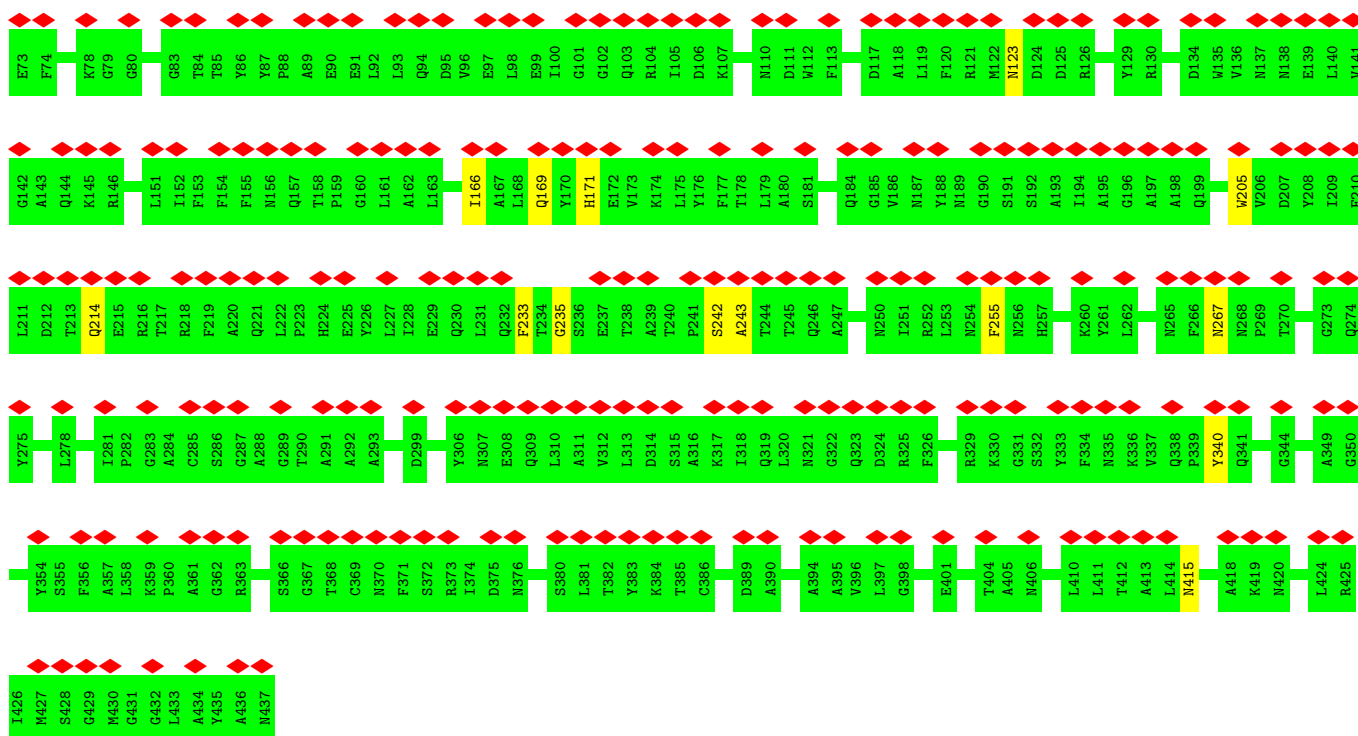


• Molecule 1: Major capsid protein (MCP)

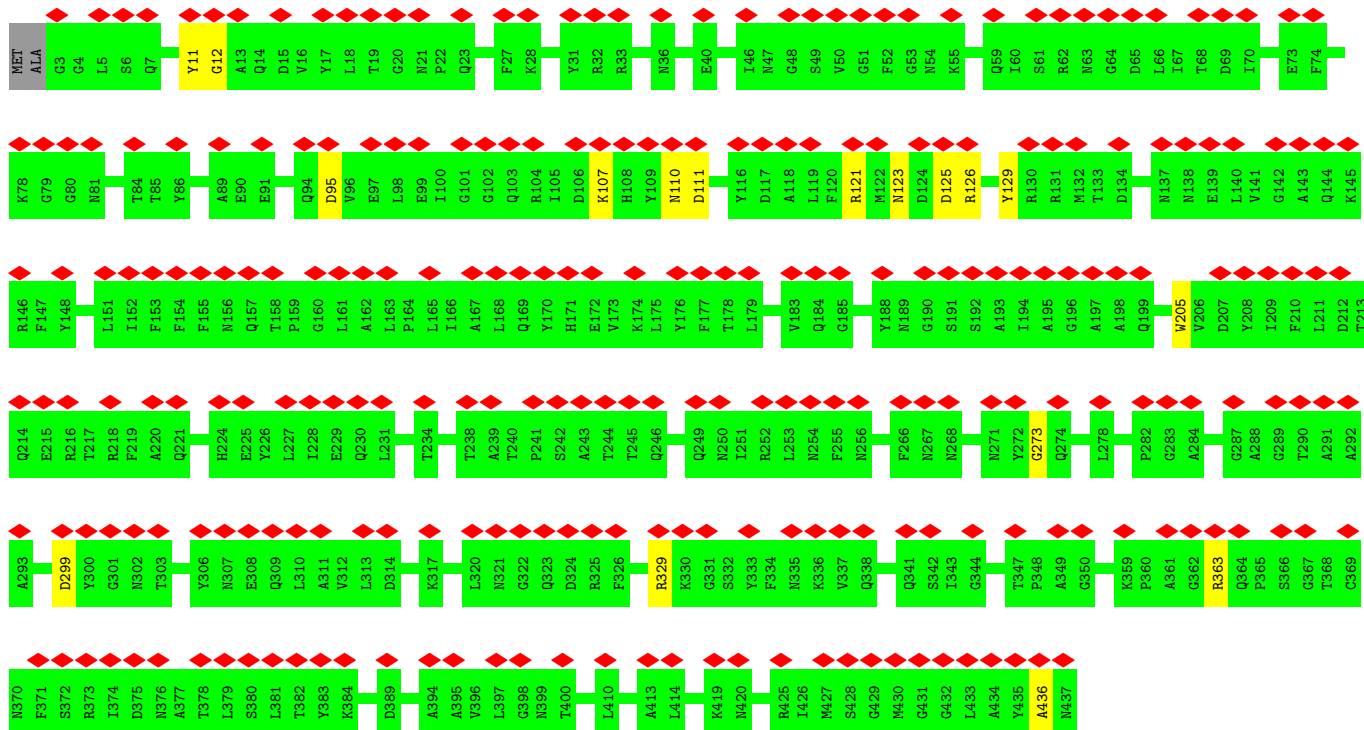


• Molecule 1: Major capsid protein (MCP)

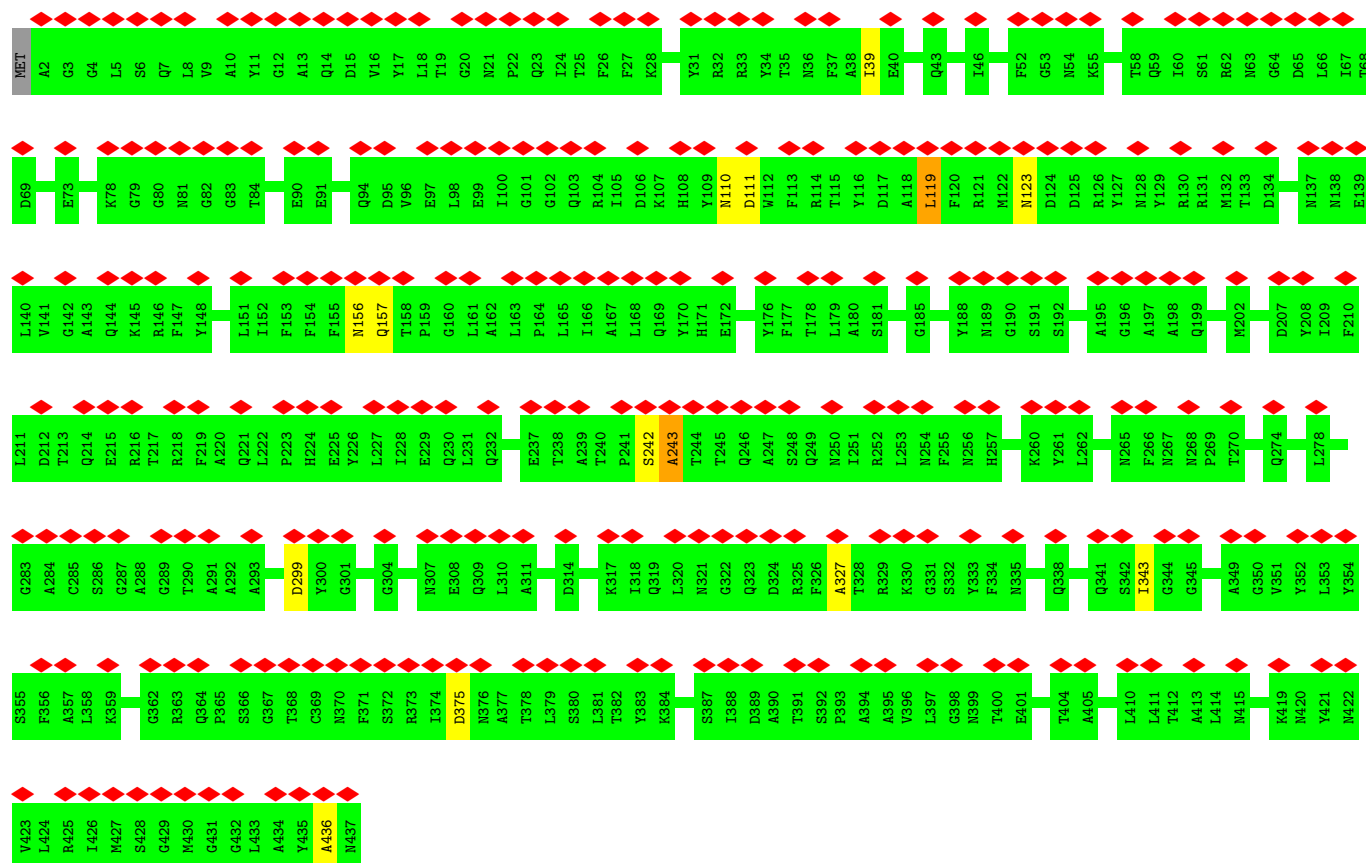




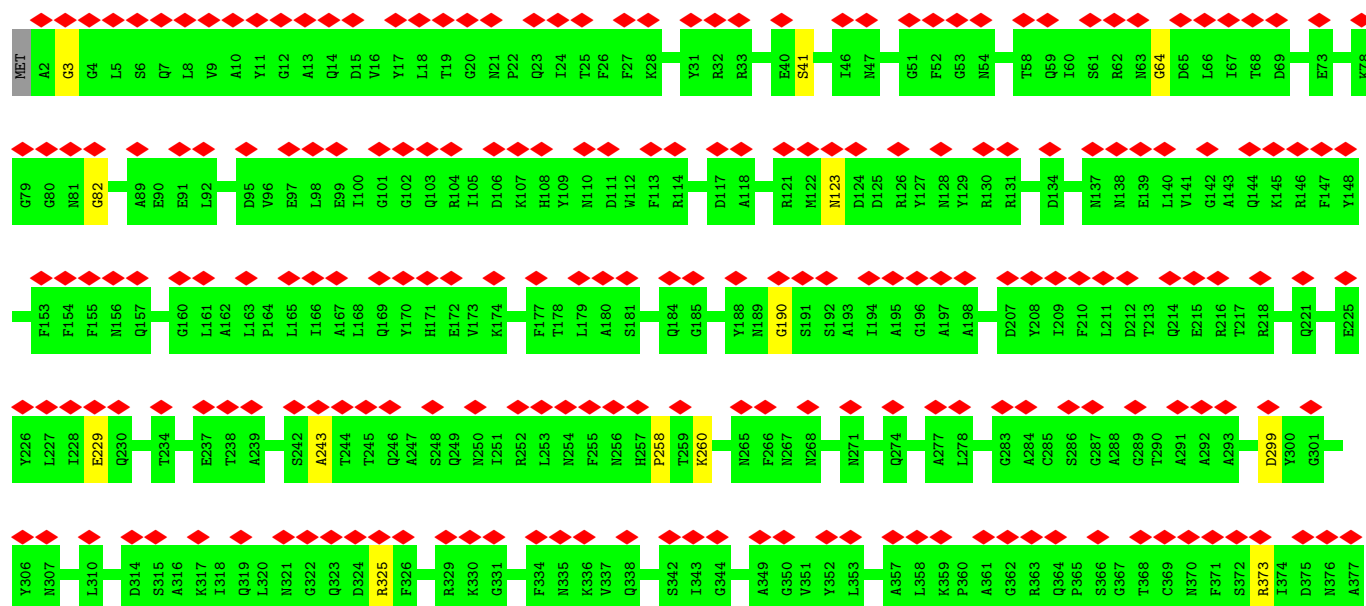
• Molecule 1: Major capsid protein (MCP)

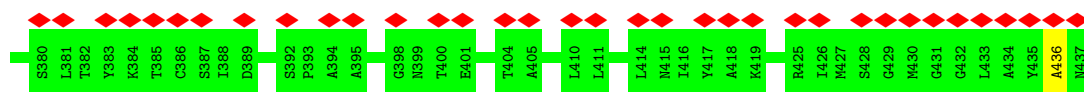


• Molecule 1: Major capsid protein (MCP)

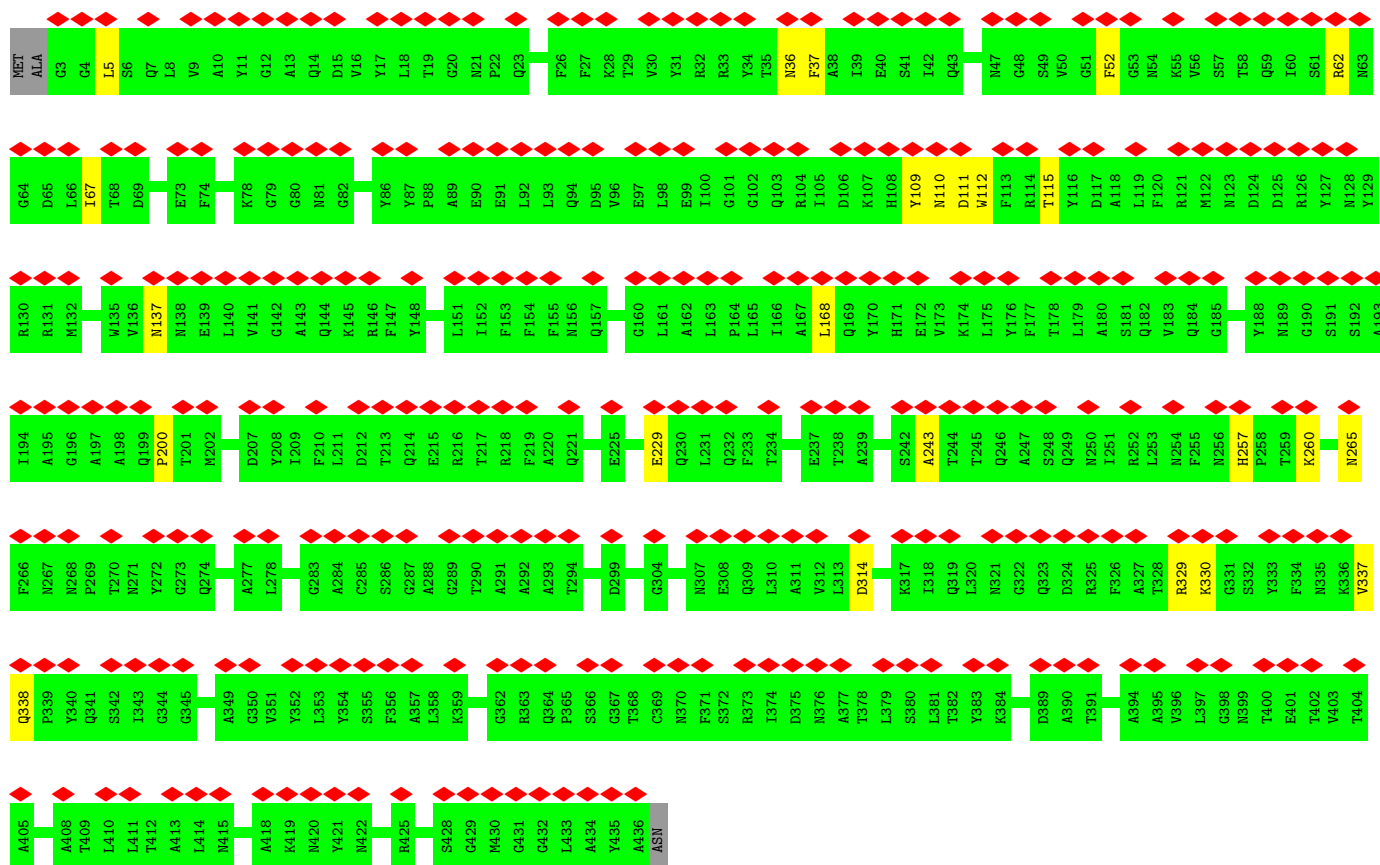


• Molecule 1: Major capsid protein (MCP)

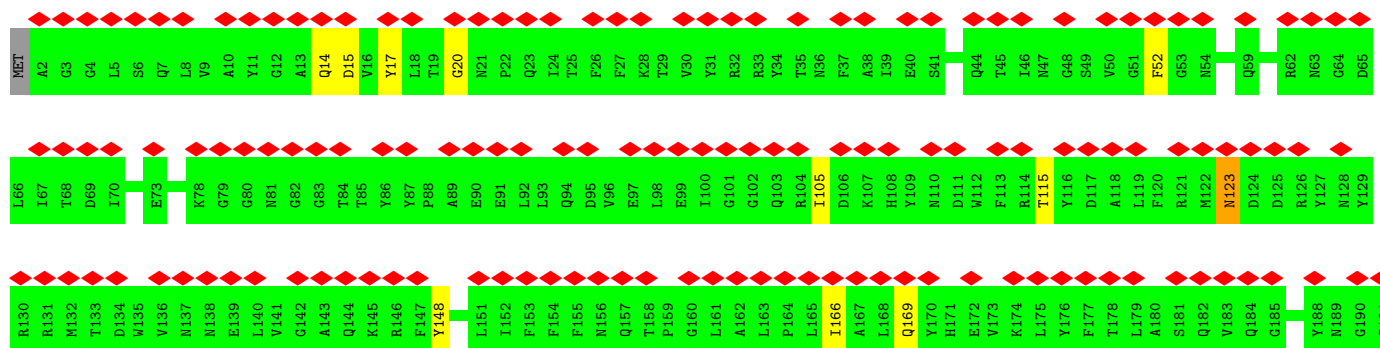
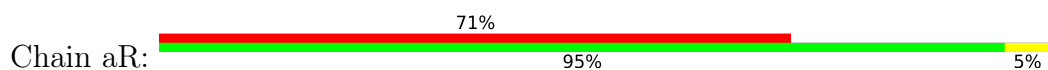


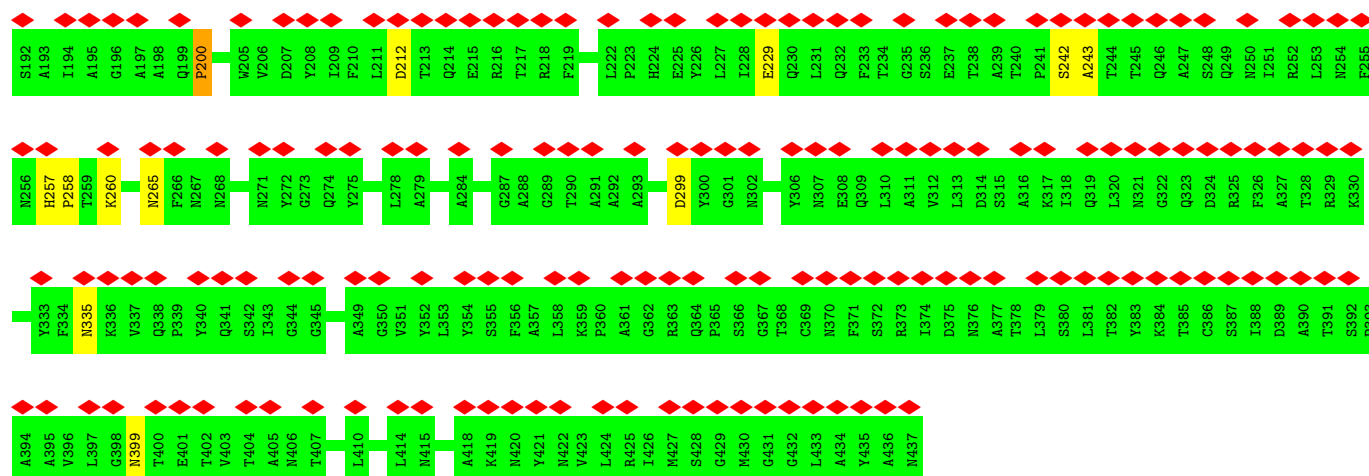


• Molecule 1: Major capsid protein (MCP)

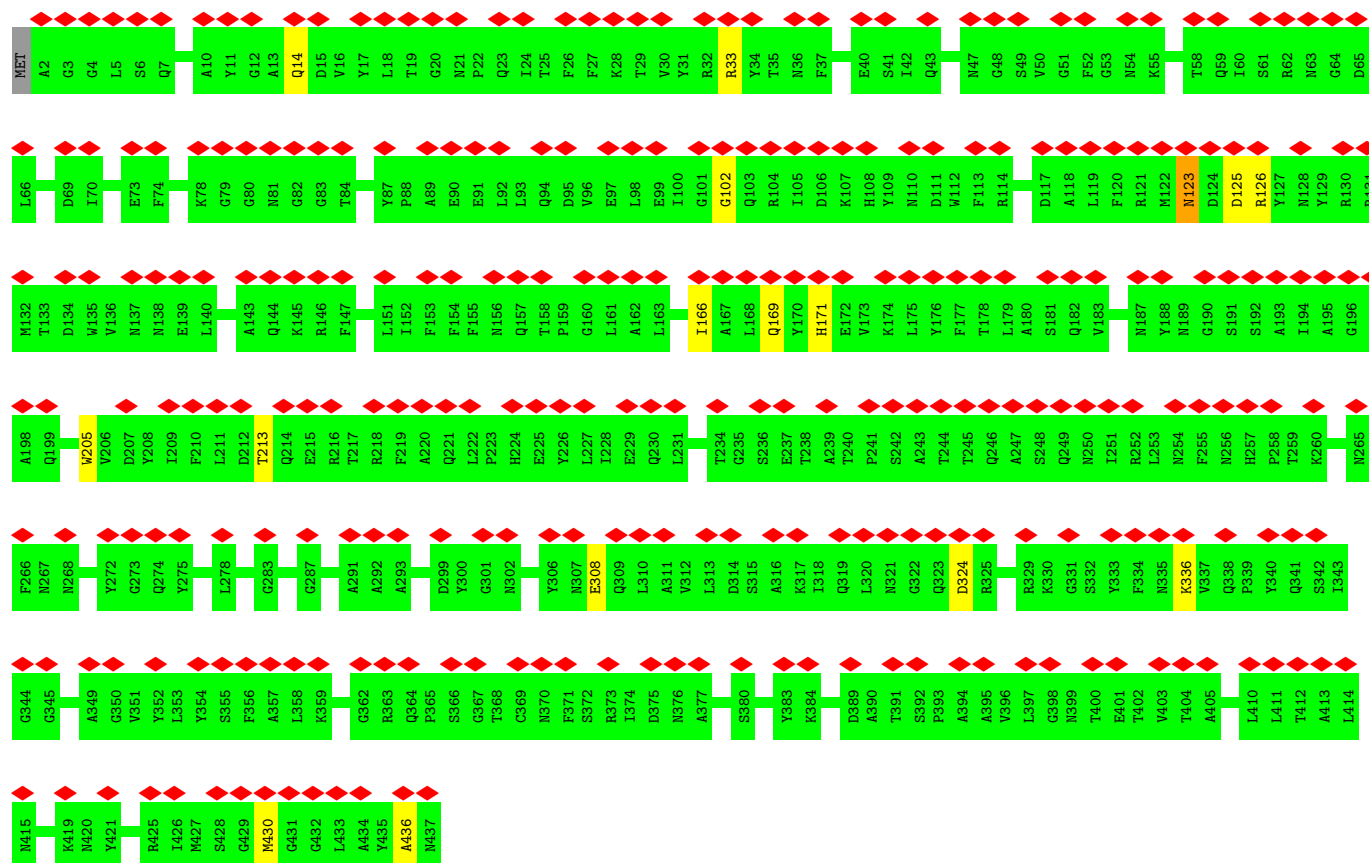


• Molecule 1: Major capsid protein (MCP)



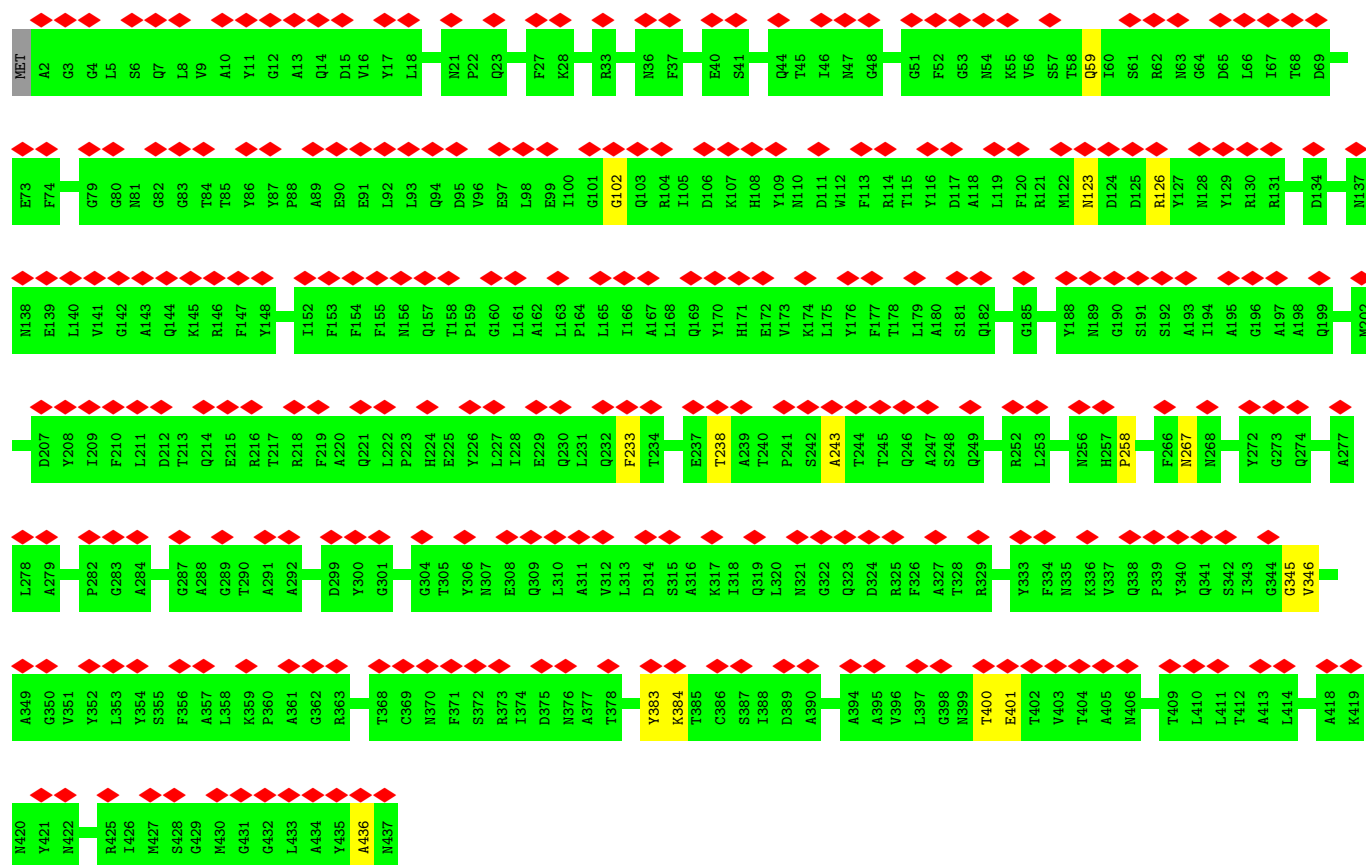


• Molecule 1: Major capsid protein (MCP)

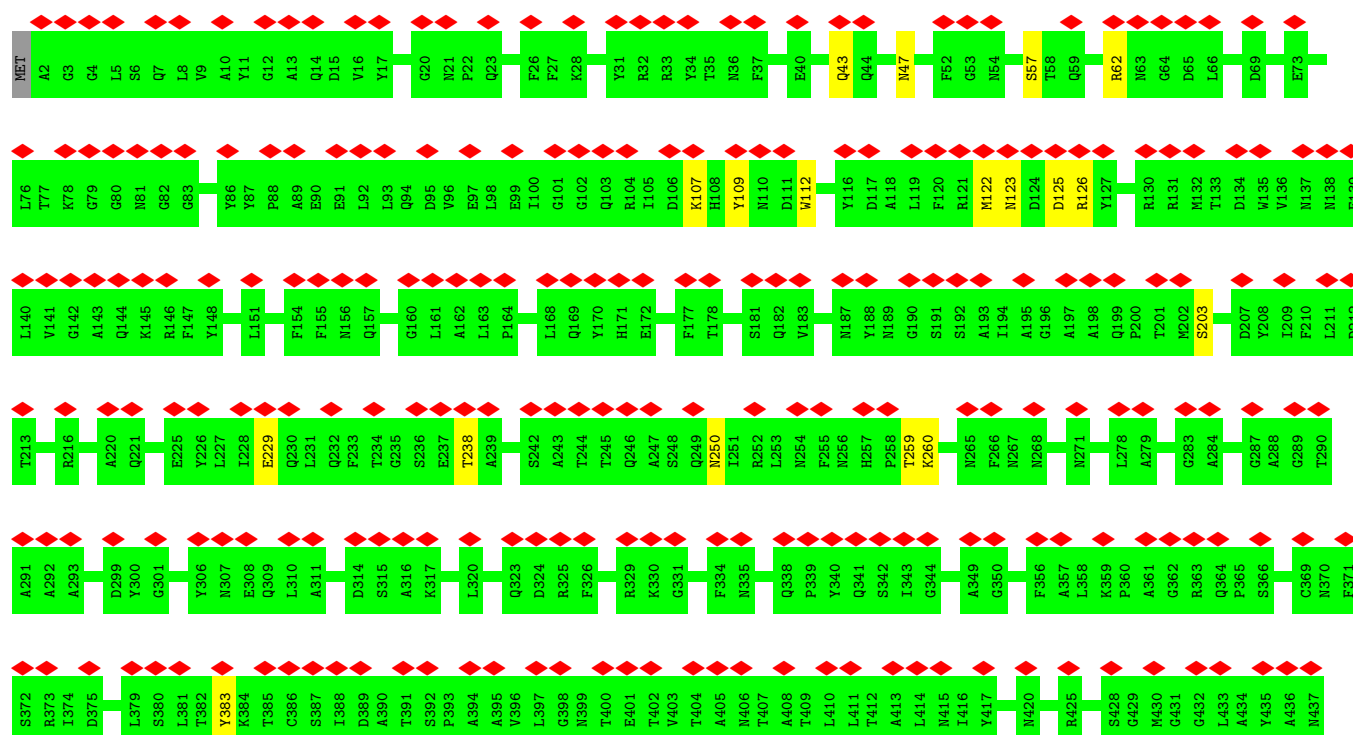


• Molecule 1: Major capsid protein (MCP)

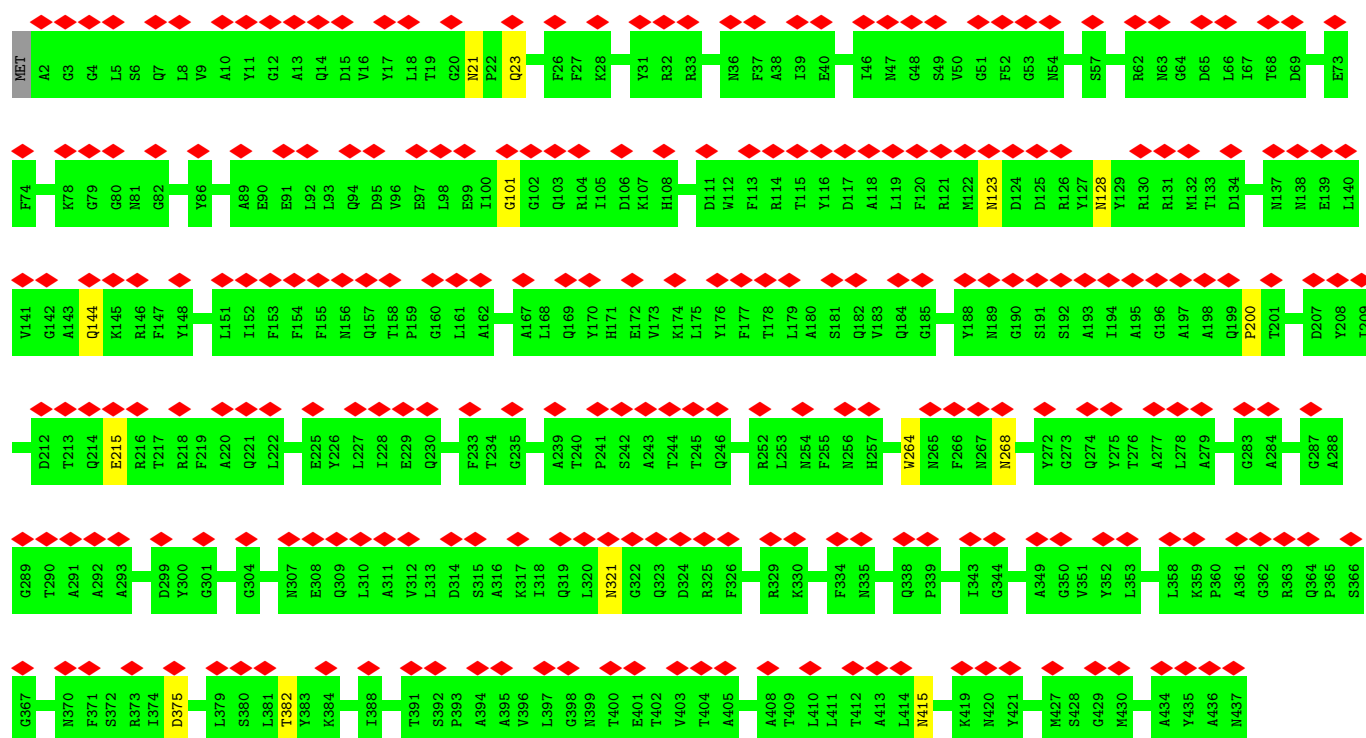




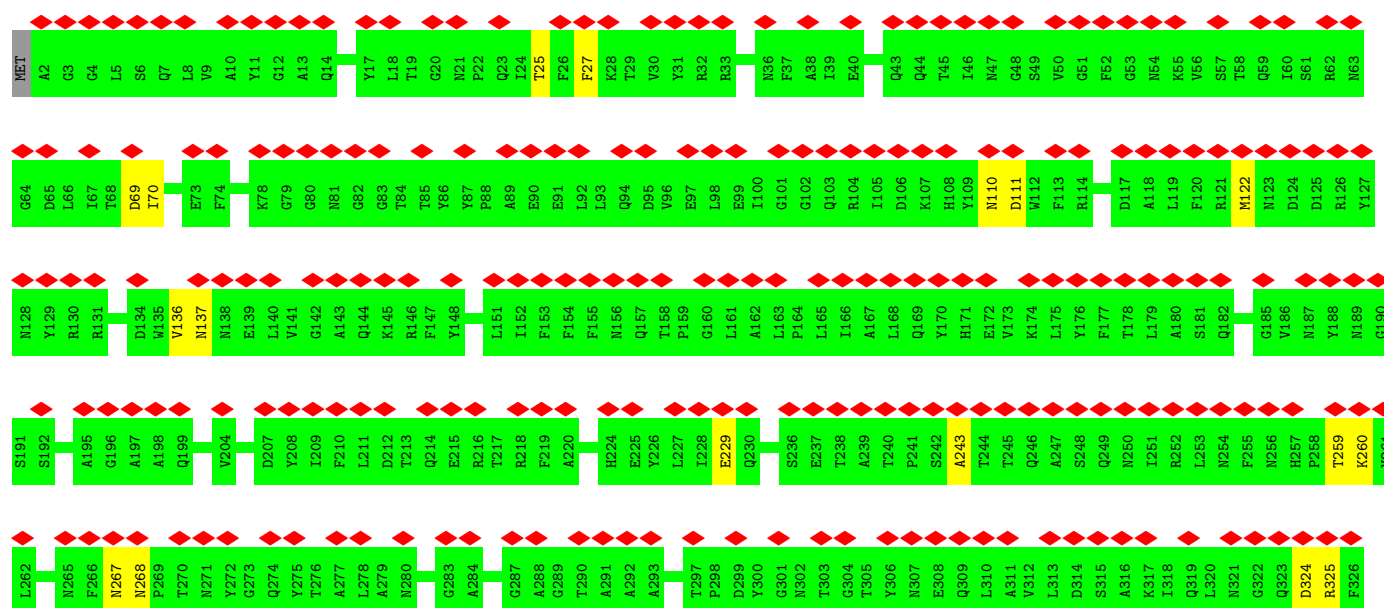
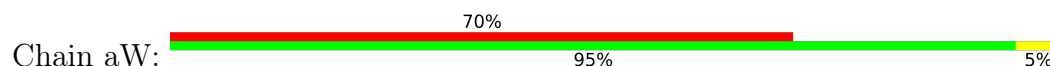
• Molecule 1: Major capsid protein (MCP)

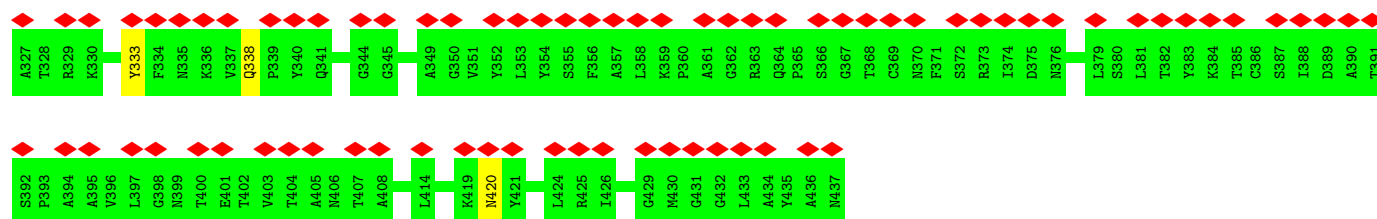


- Molecule 1: Major capsid protein (MCP)

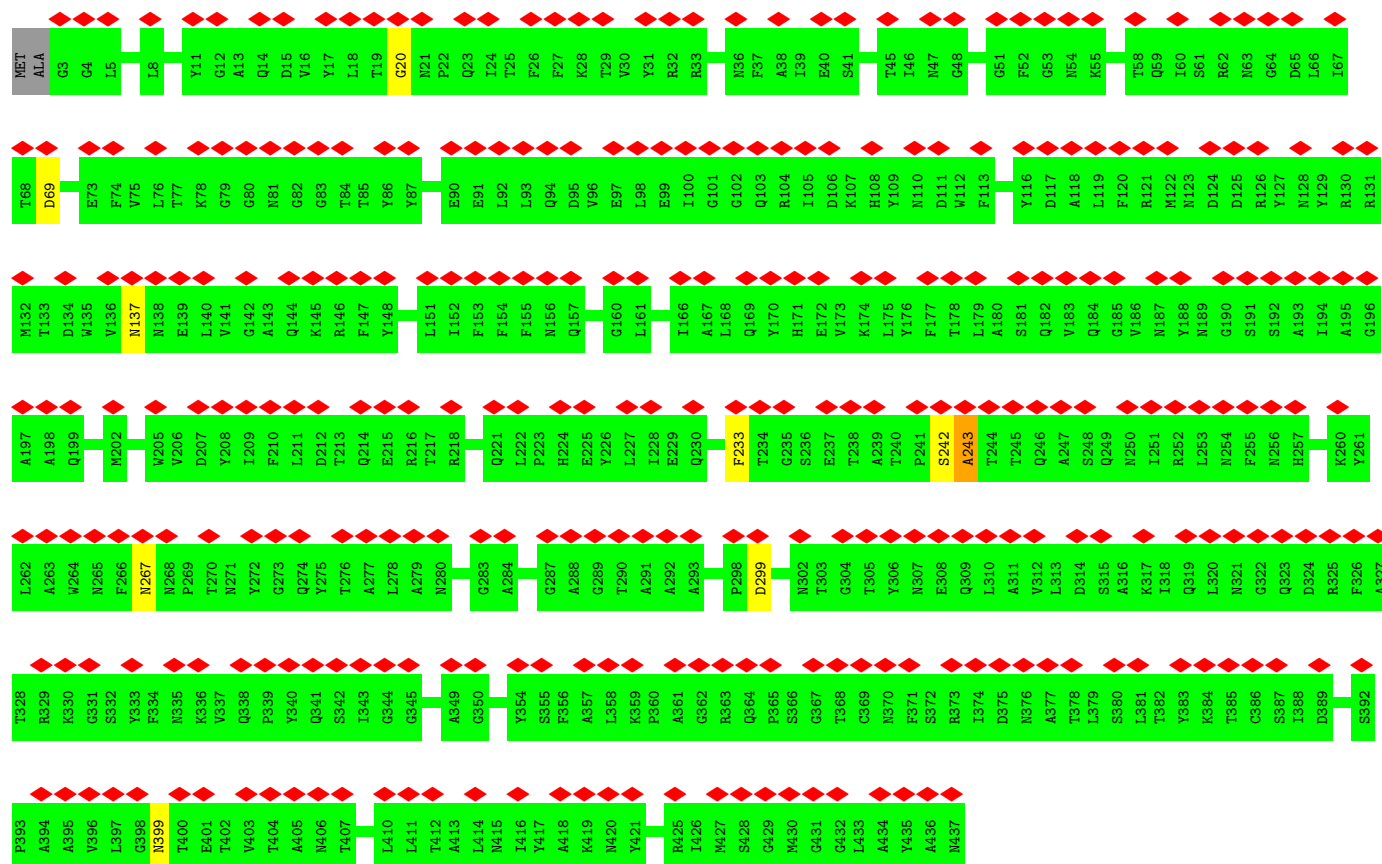
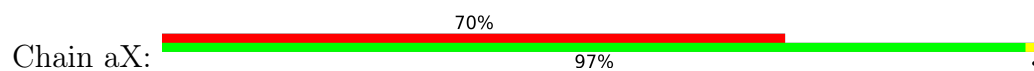


- Molecule 1: Major capsid protein (MCP)

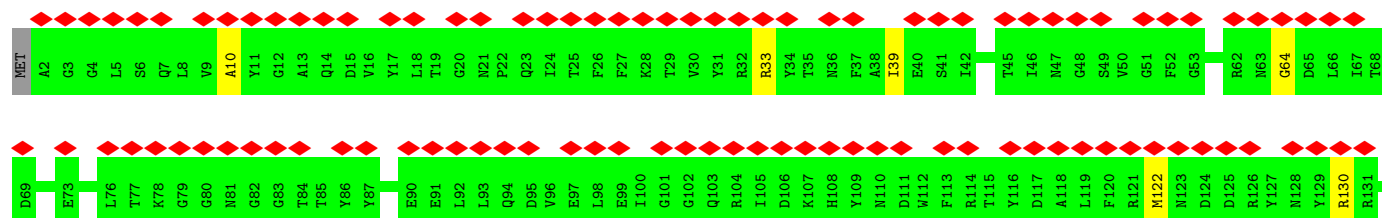
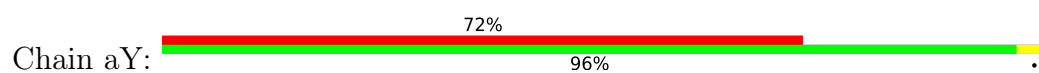


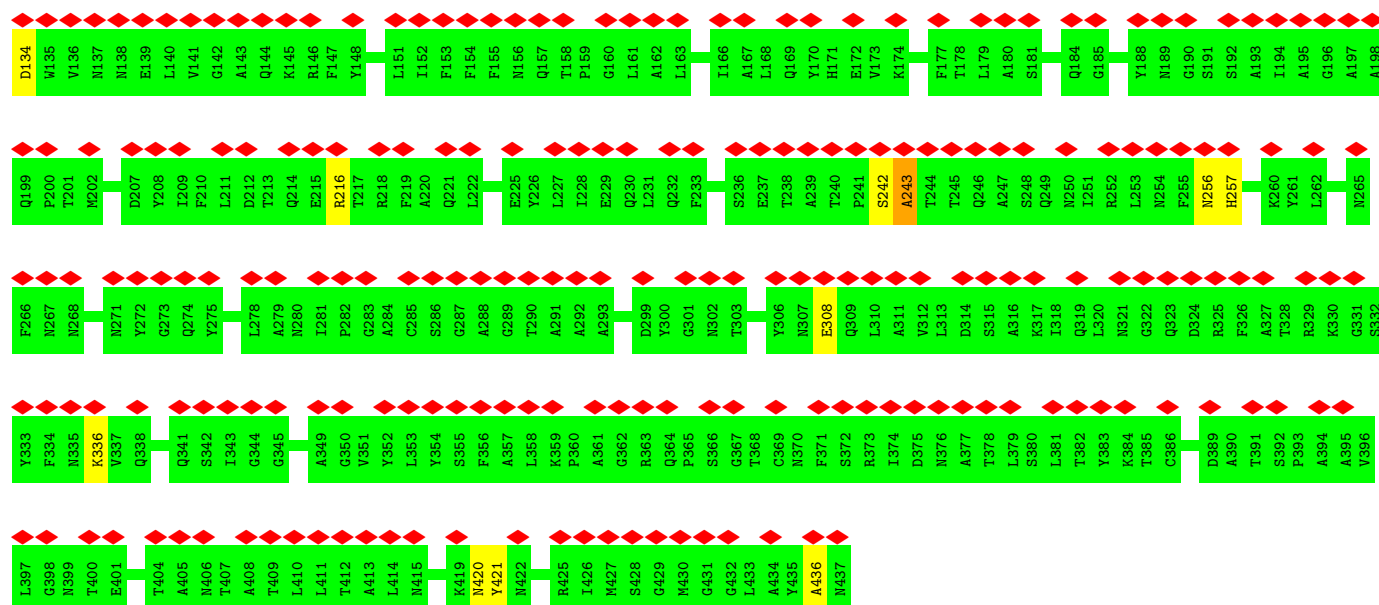


• Molecule 1: Major capsid protein (MCP)



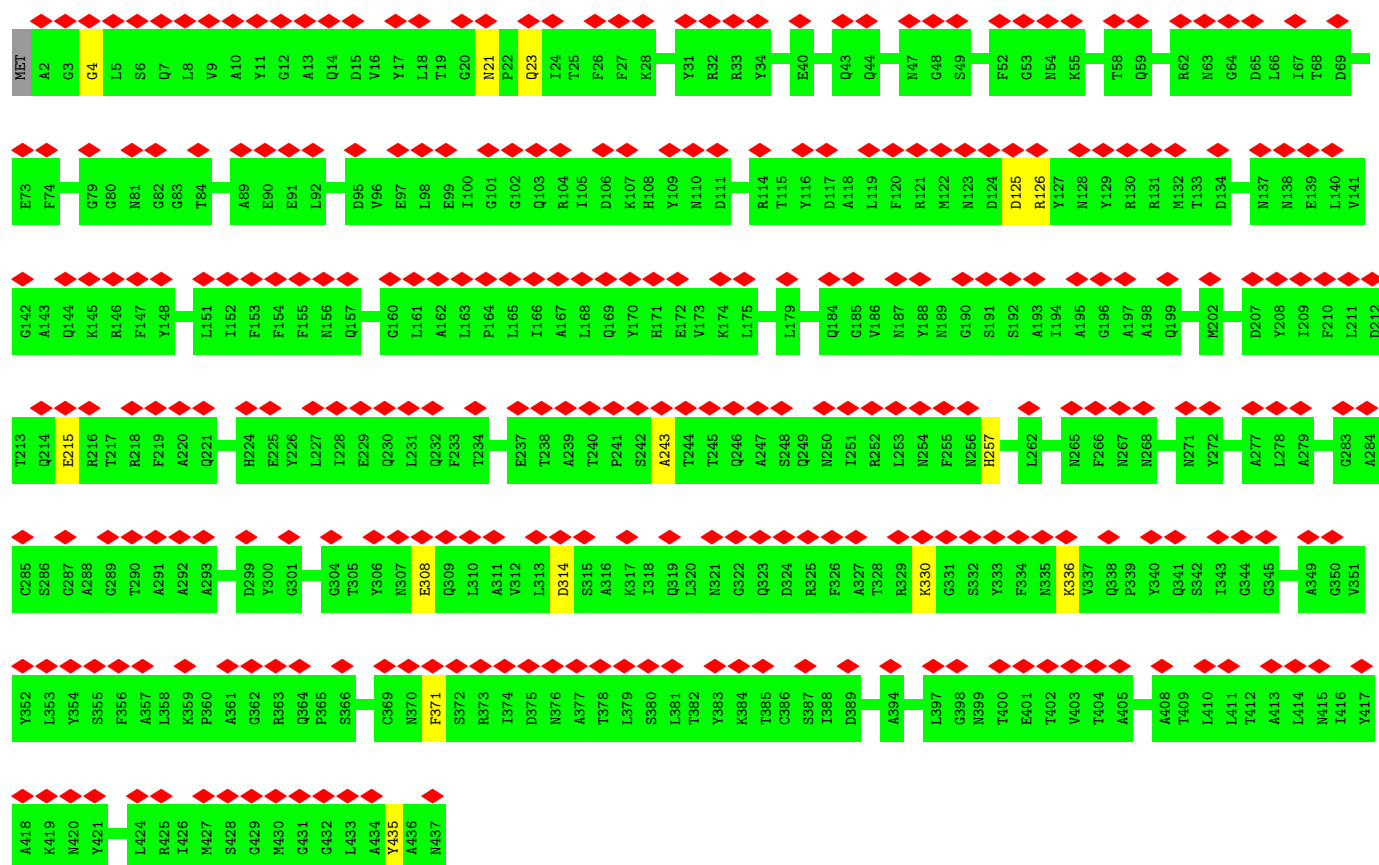
• Molecule 1: Major capsid protein (MCP)



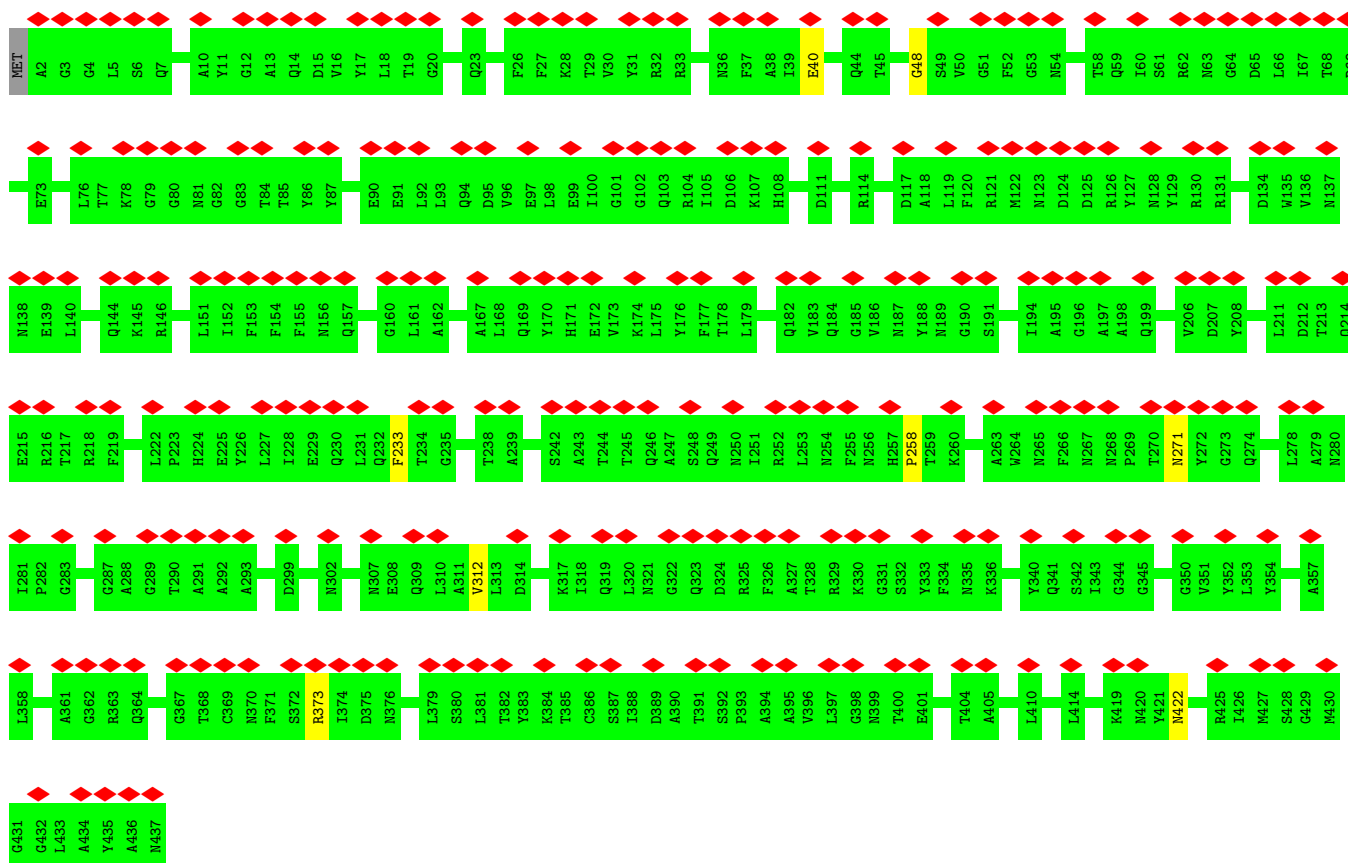


• Molecule 1: Major capsid protein (MCP)

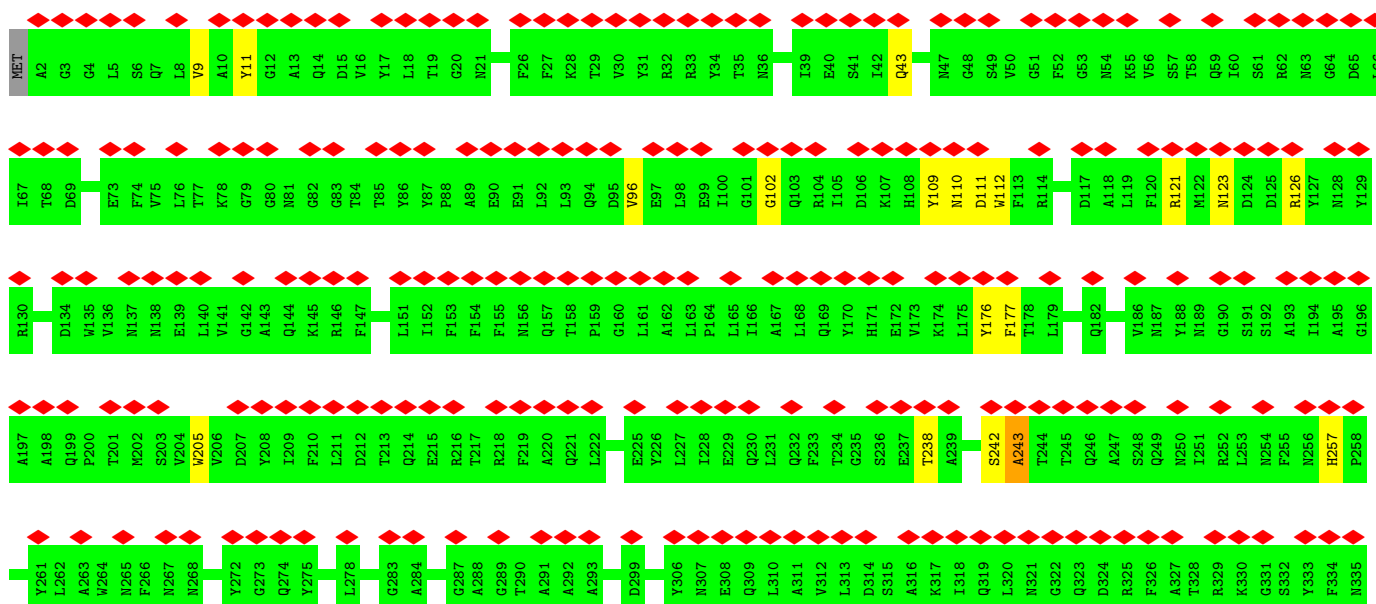
Chain aZ: .



• Molecule 1: Major capsid protein (MCP)

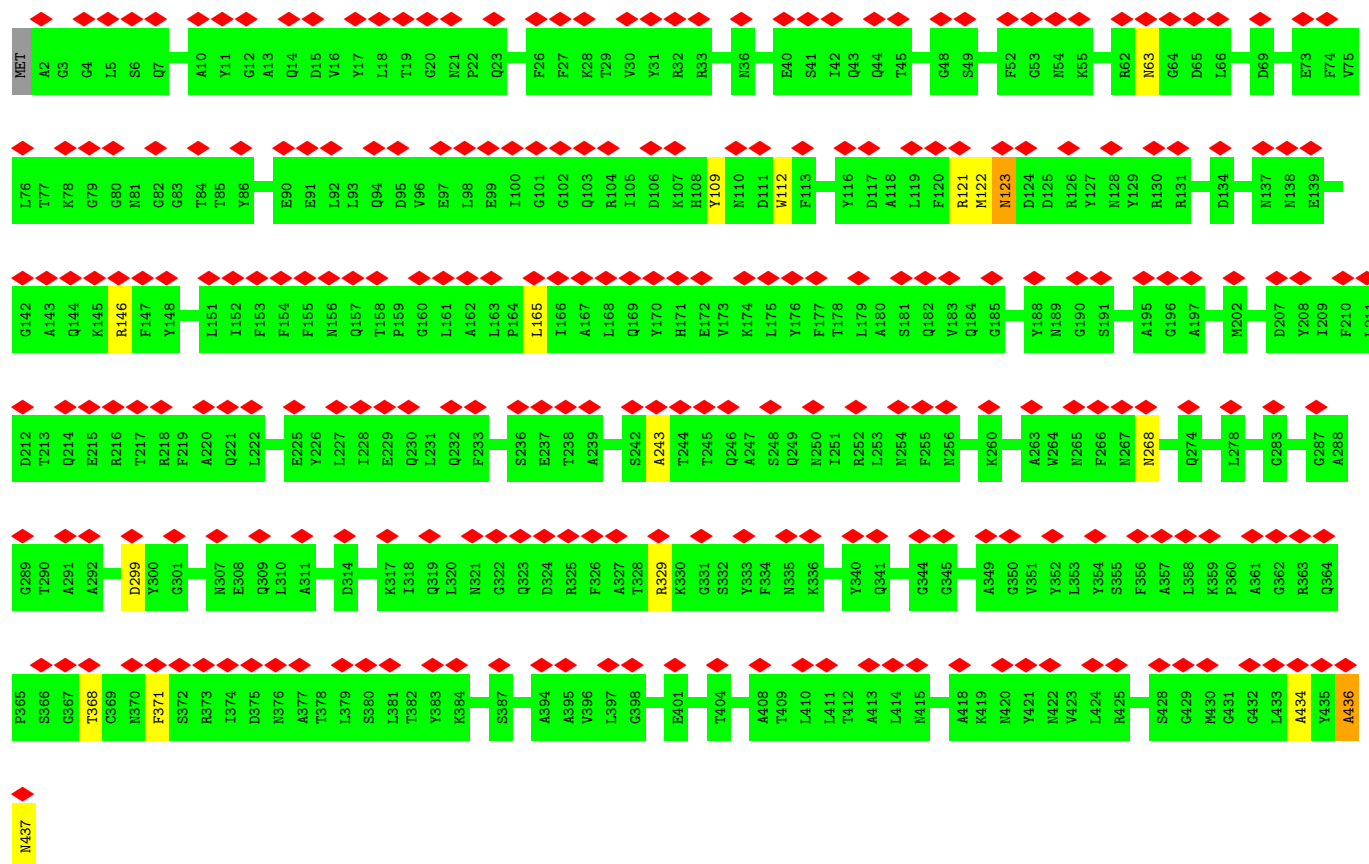


• Molecule 1: Major capsid protein (MCP)

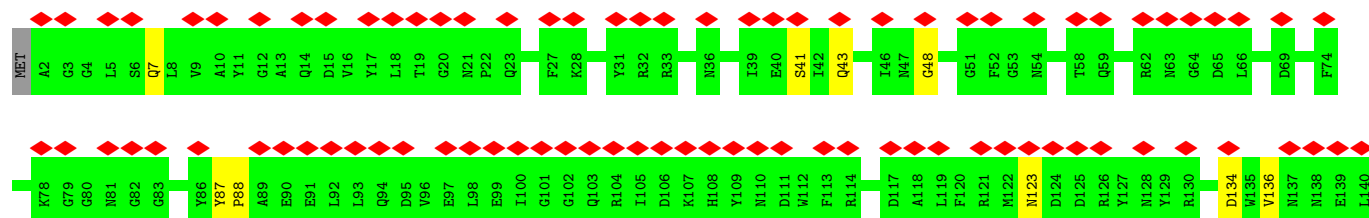


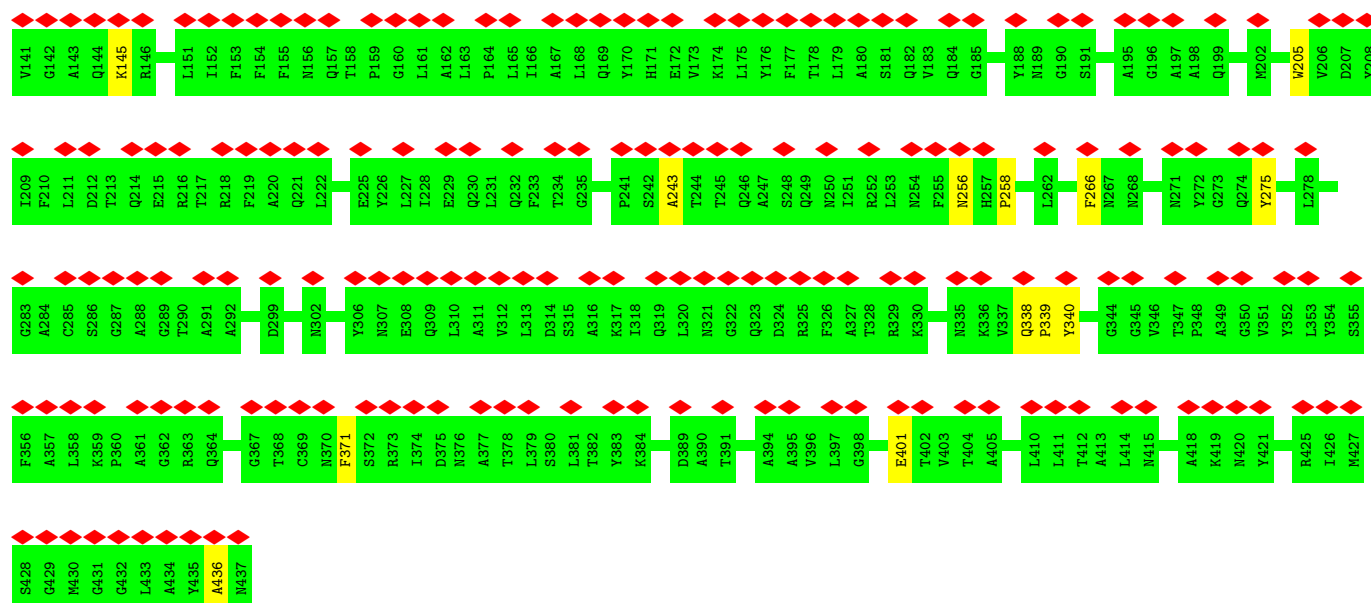


• Molecule 1: Major capsid protein (MCP)

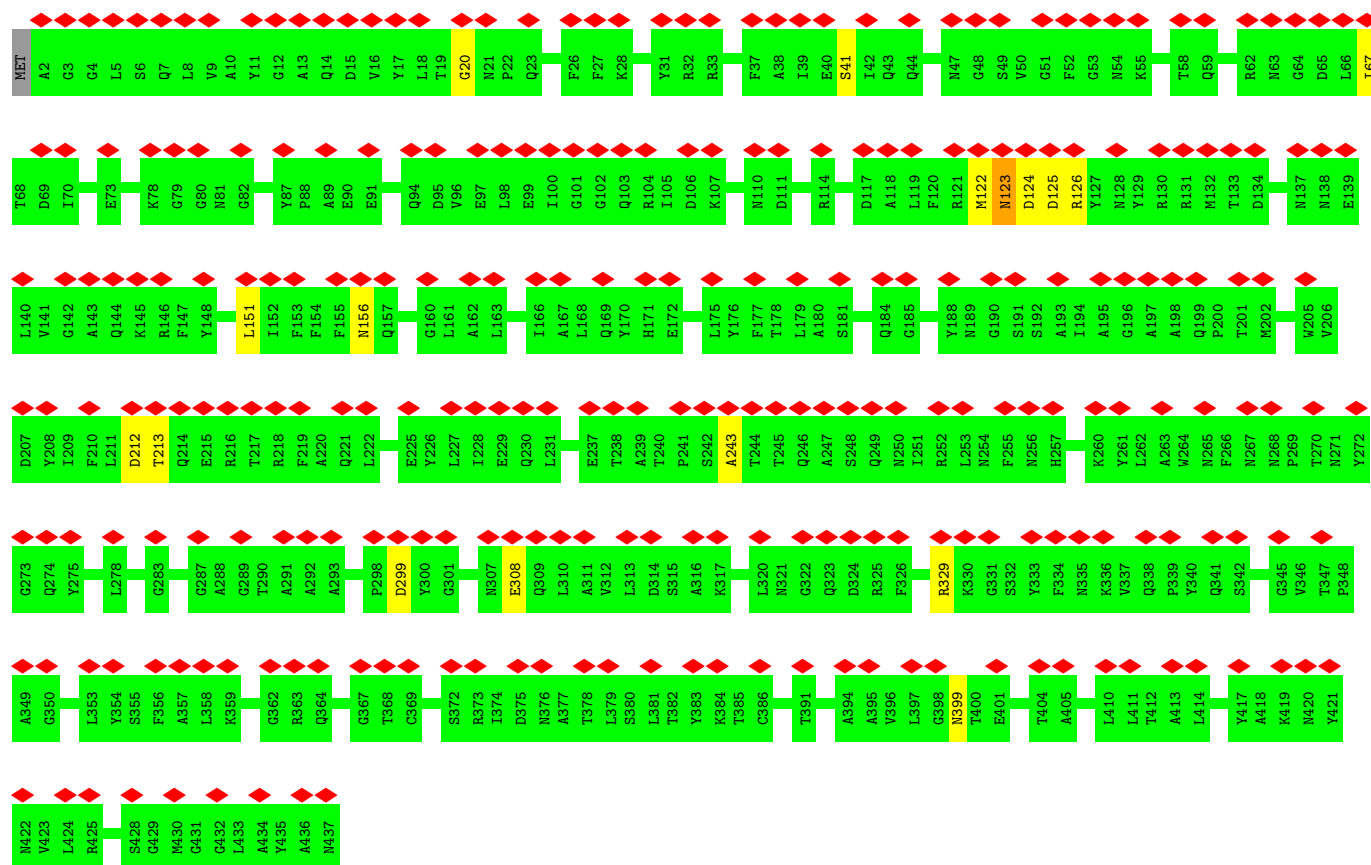


• Molecule 1: Major capsid protein (MCP)

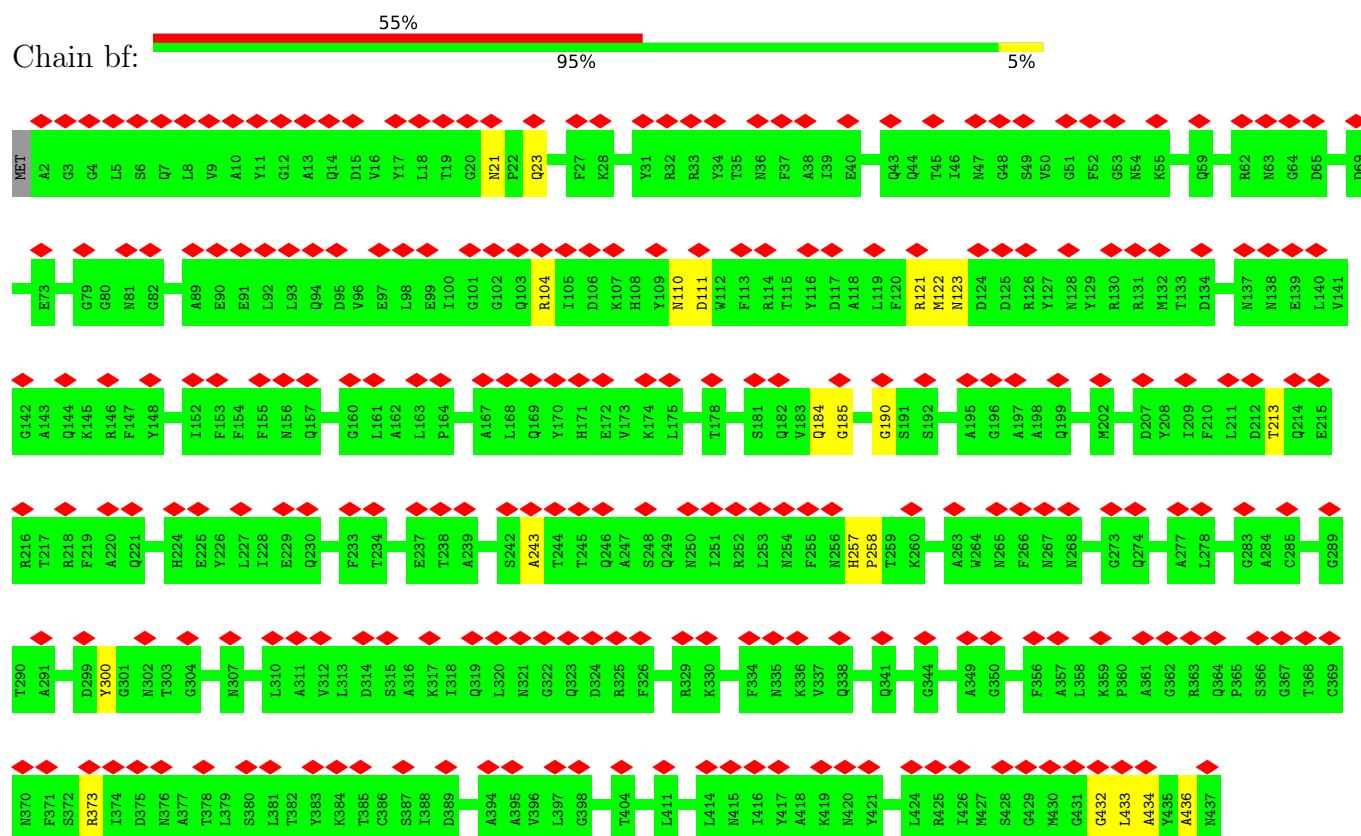




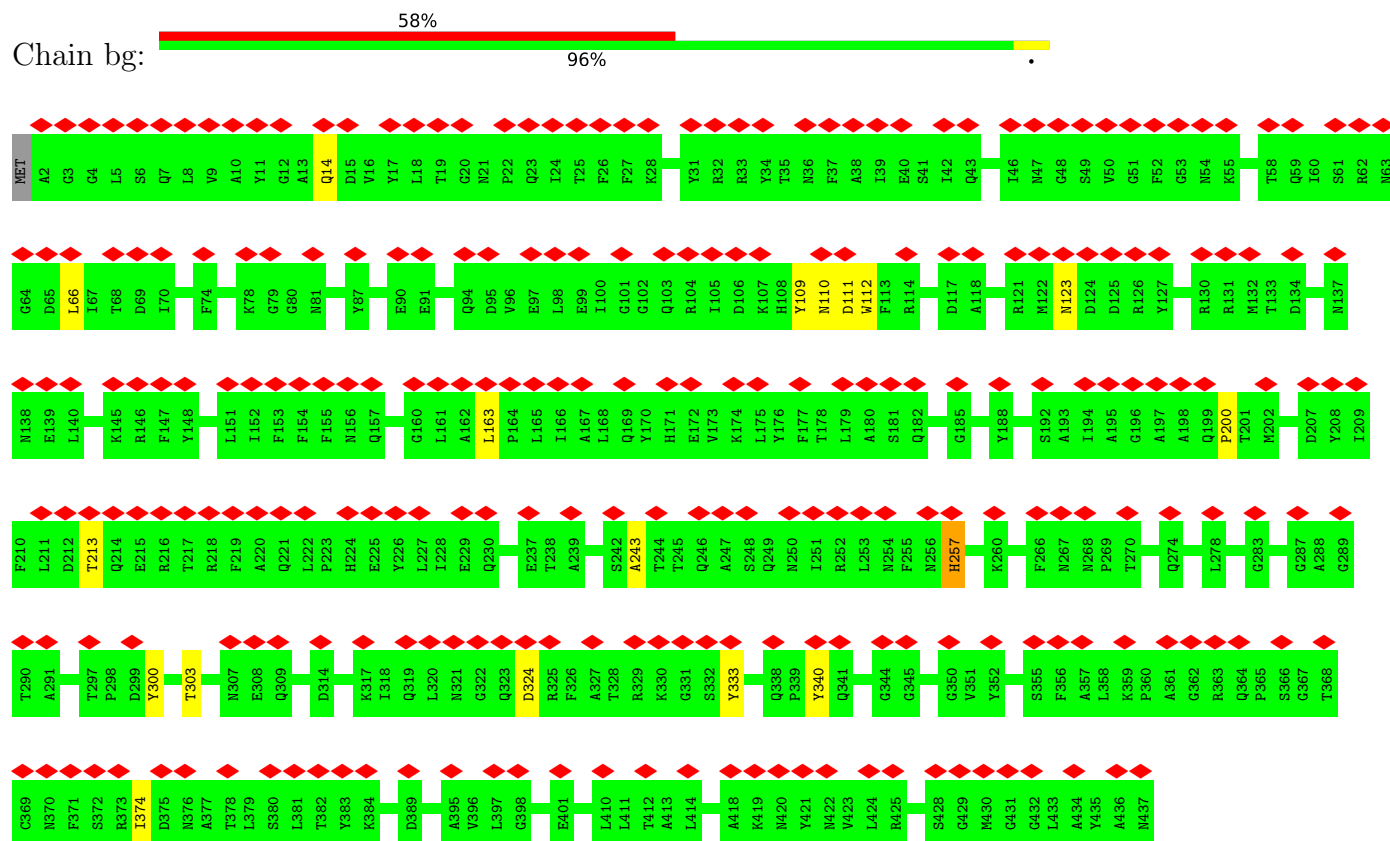
• Molecule 1: Major capsid protein (MCP)



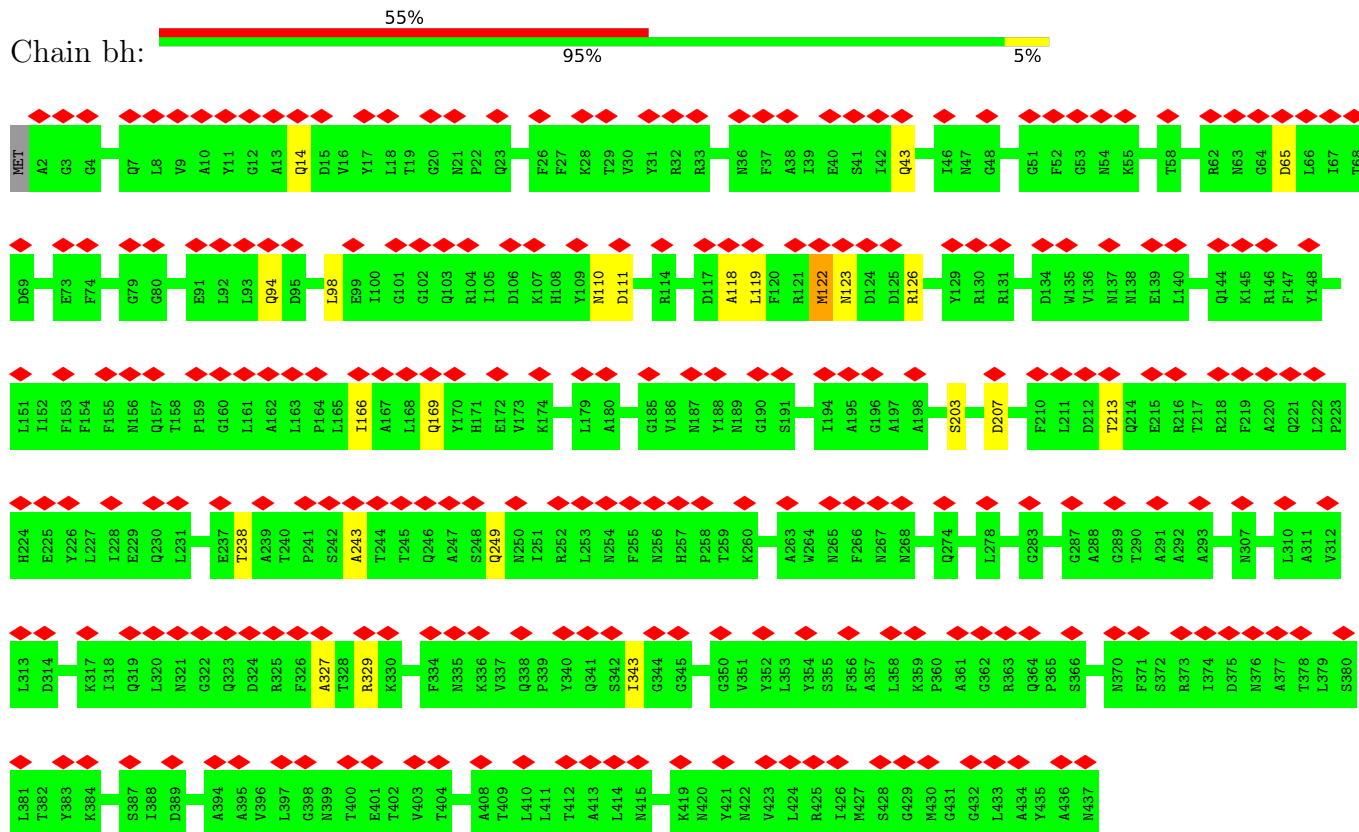
• Molecule 1: Major capsid protein (MCP)



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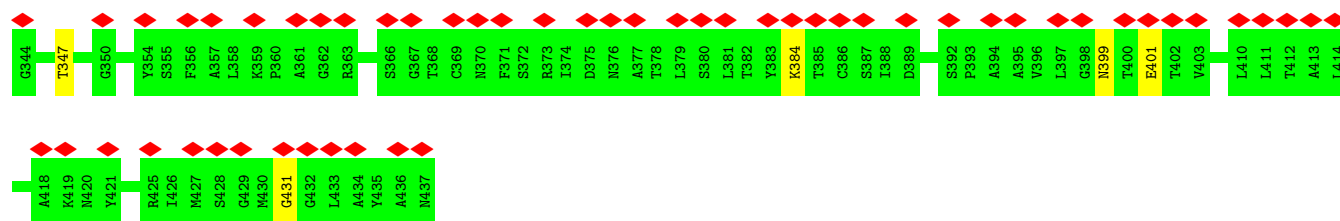


- Molecule 1: Major capsid protein (MCP)

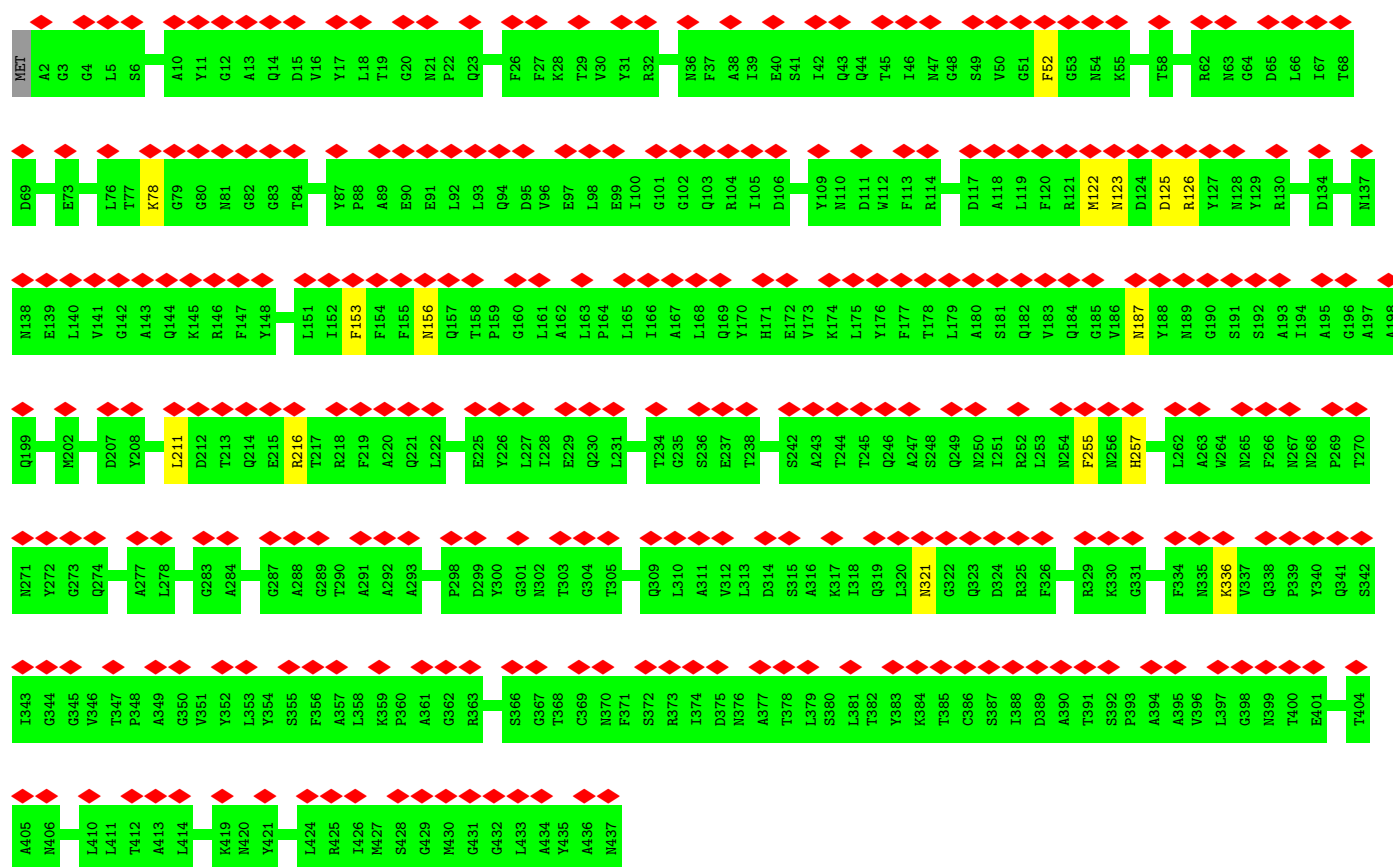


- Molecule 1: Major capsid protein (MCP)

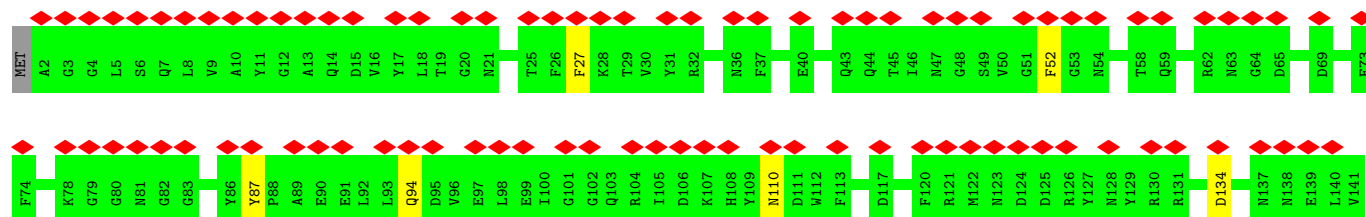


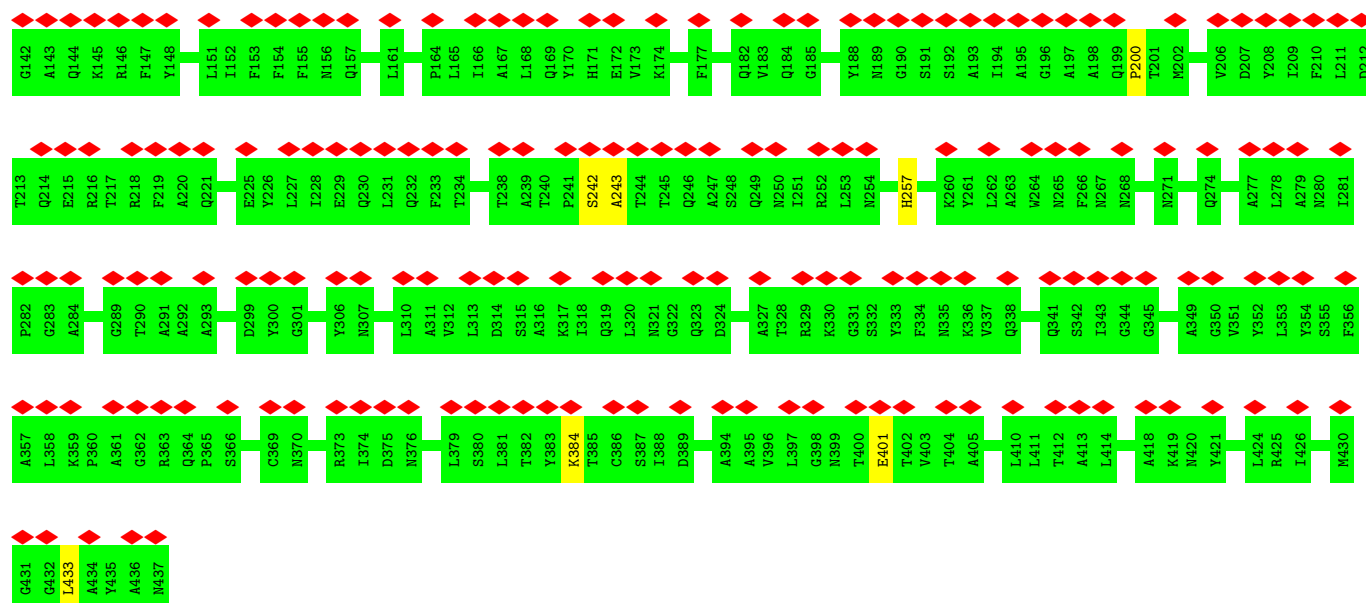


• Molecule 1: Major capsid protein (MCP)

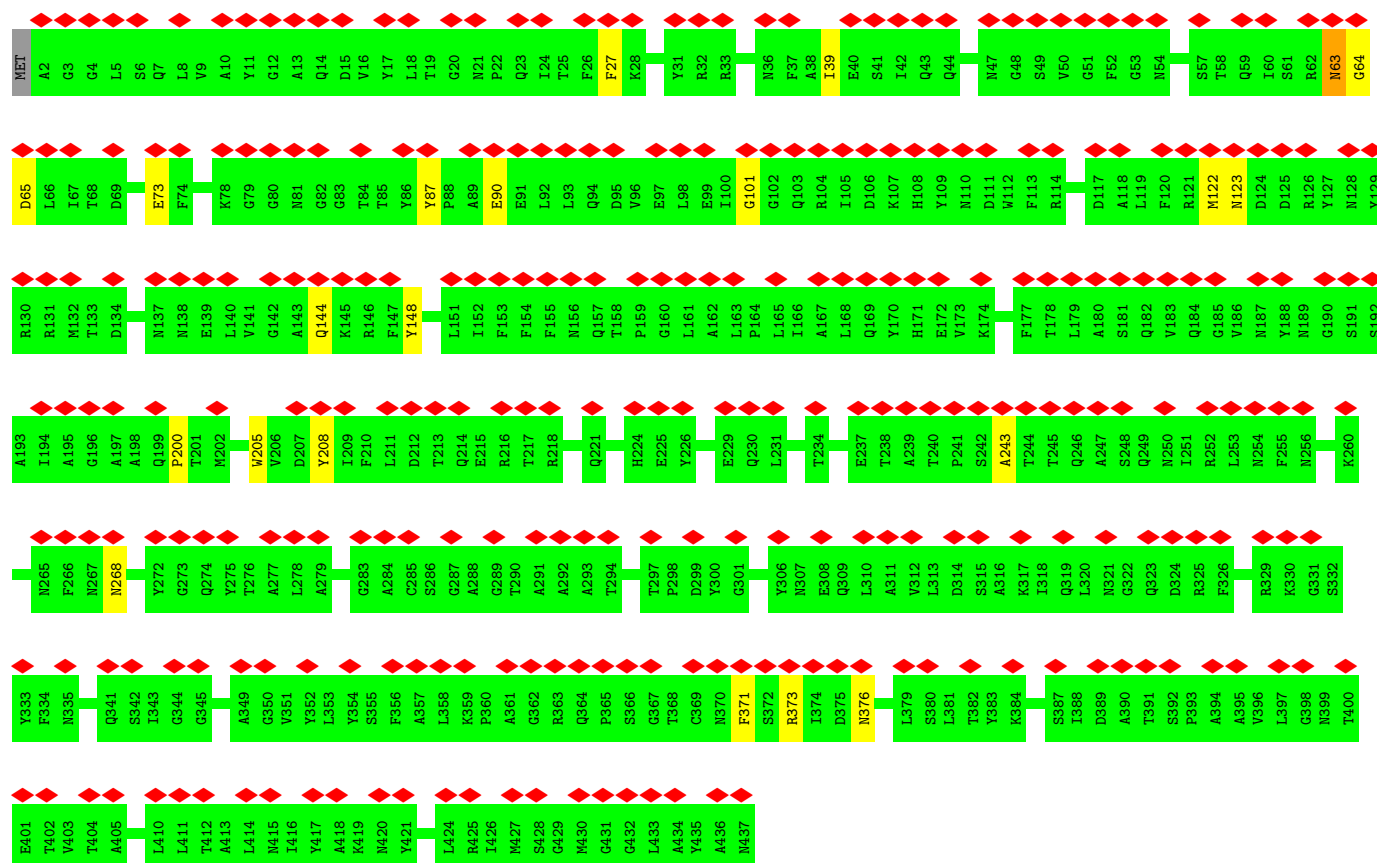


• Molecule 1: Major capsid protein (MCP)

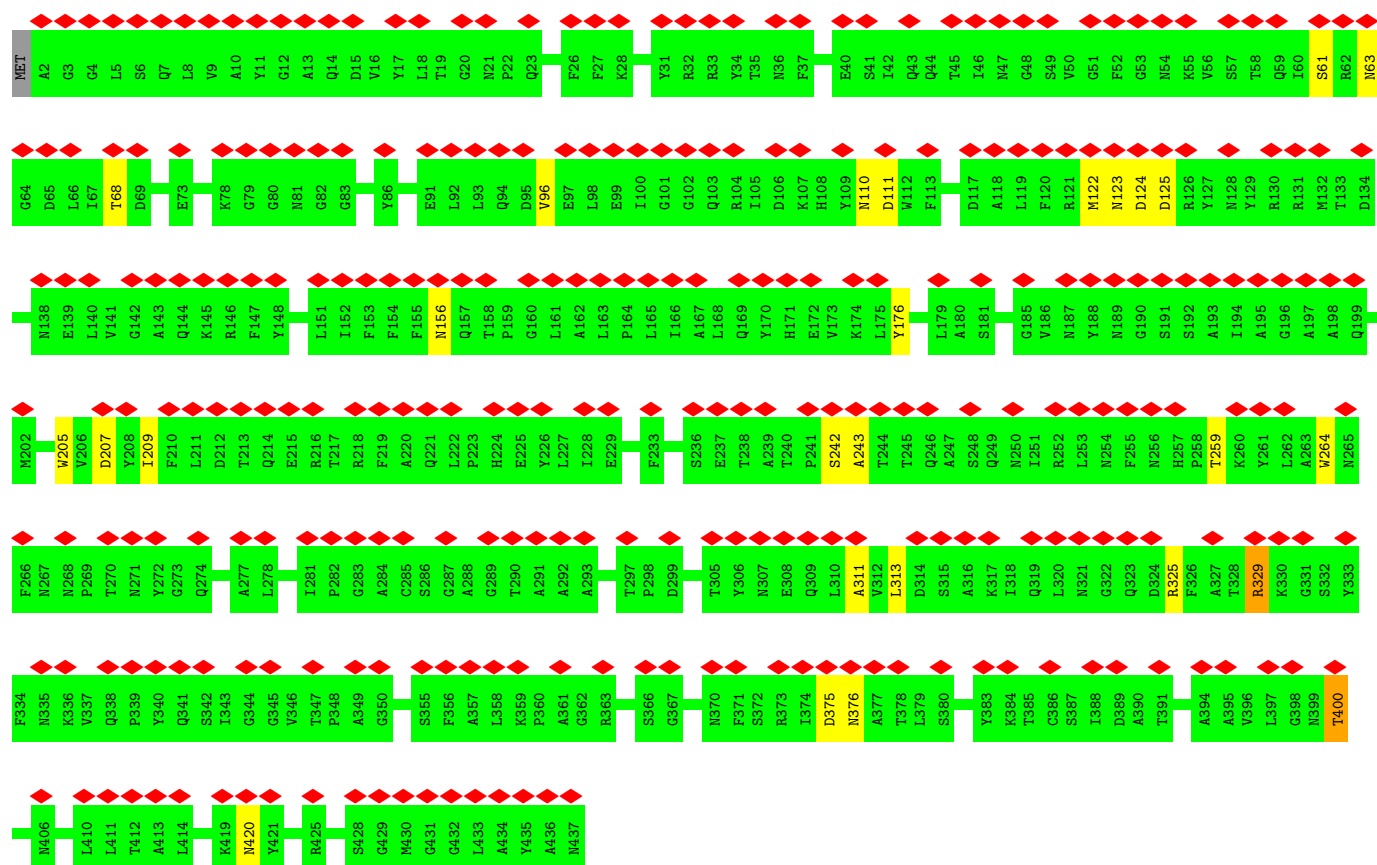




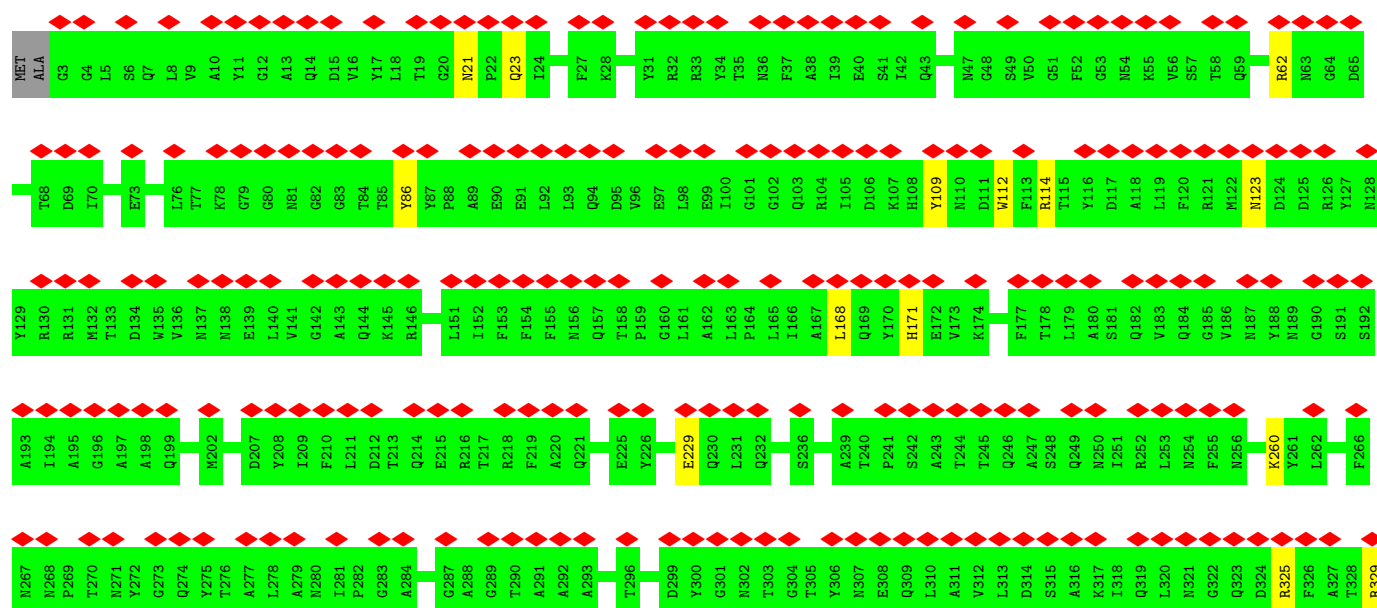
• Molecule 1: Major capsid protein (MCP)

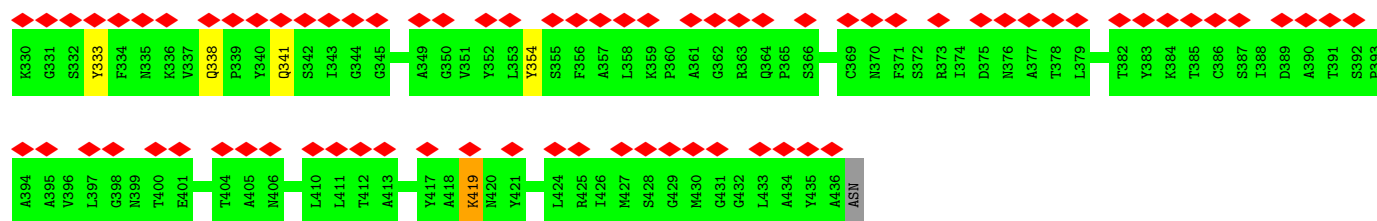


• Molecule 1: Major capsid protein (MCP)

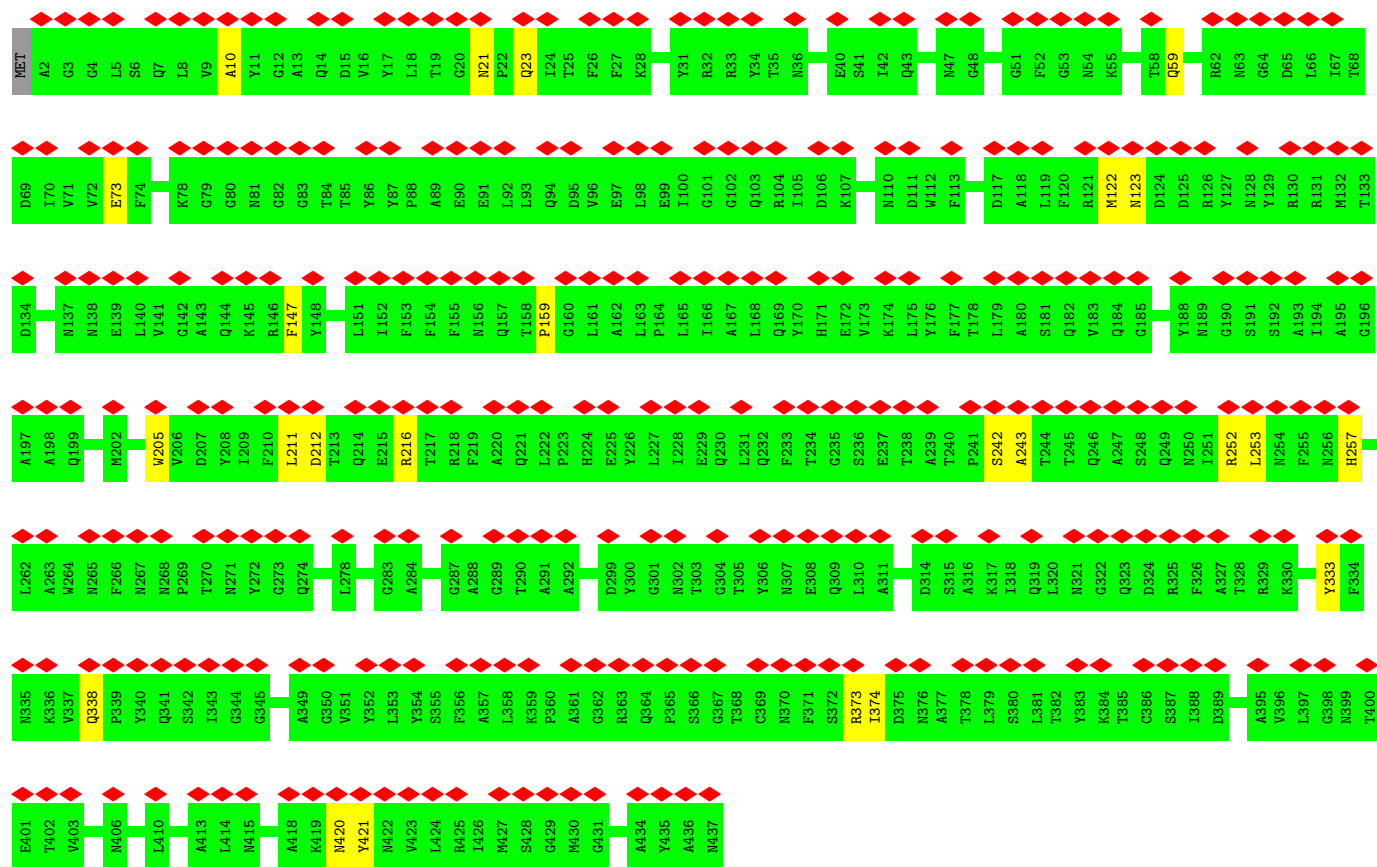


• Molecule 1: Major capsid protein (MCP)

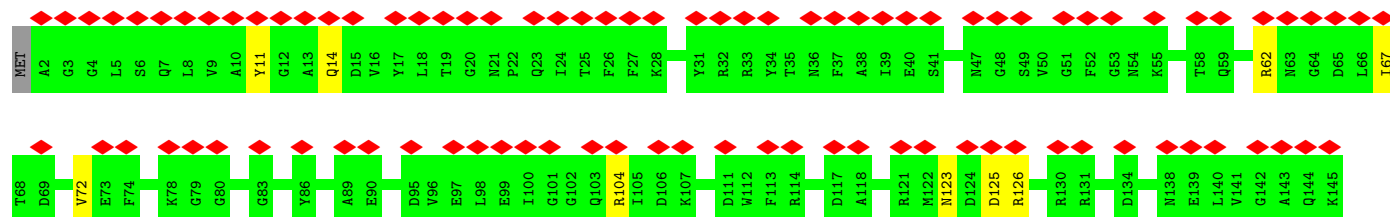


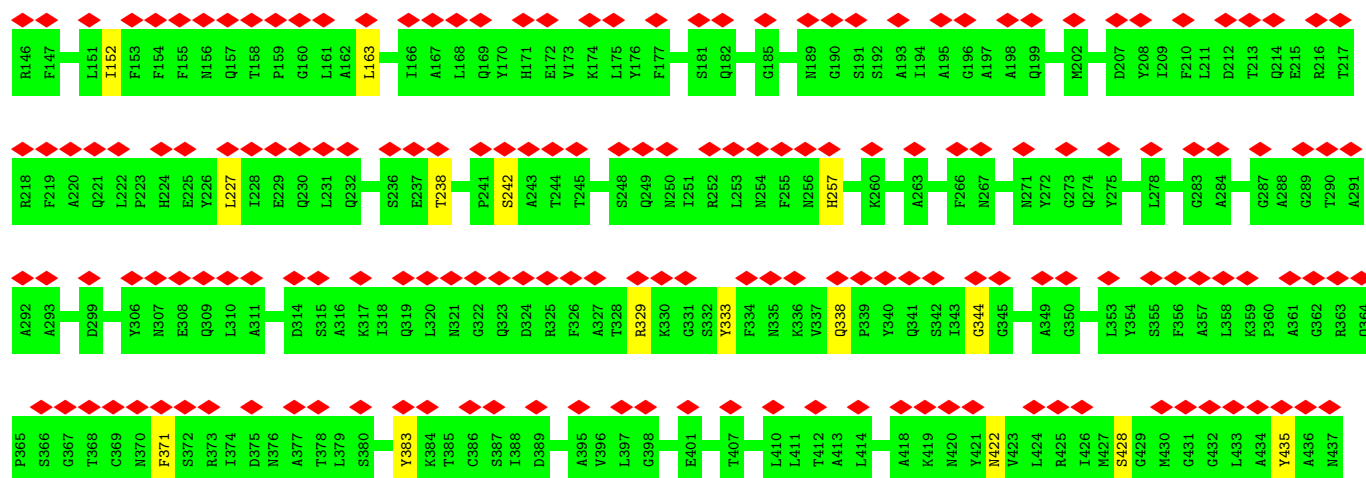


• Molecule 1: Major capsid protein (MCP)

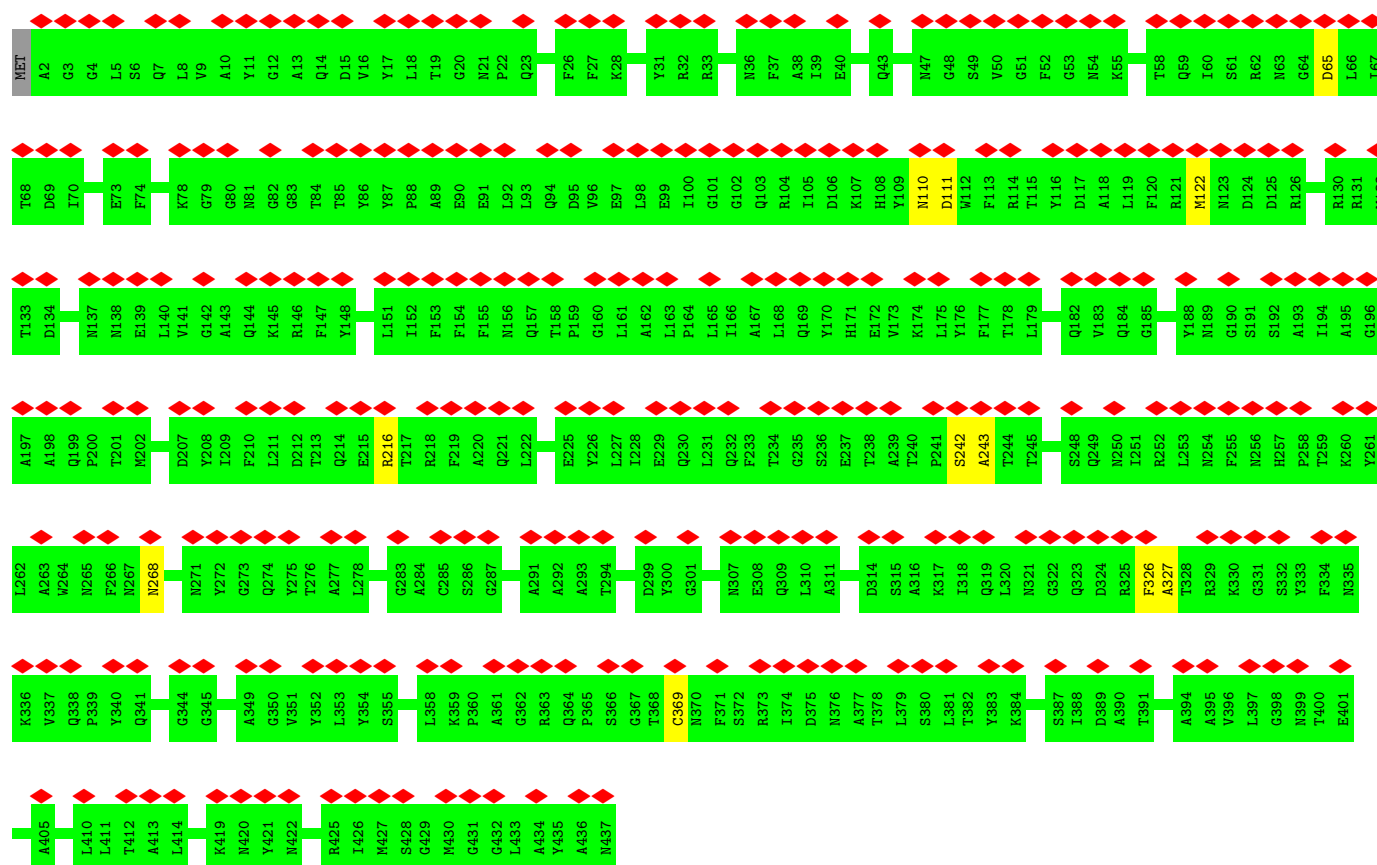


• Molecule 1: Major capsid protein (MCP)





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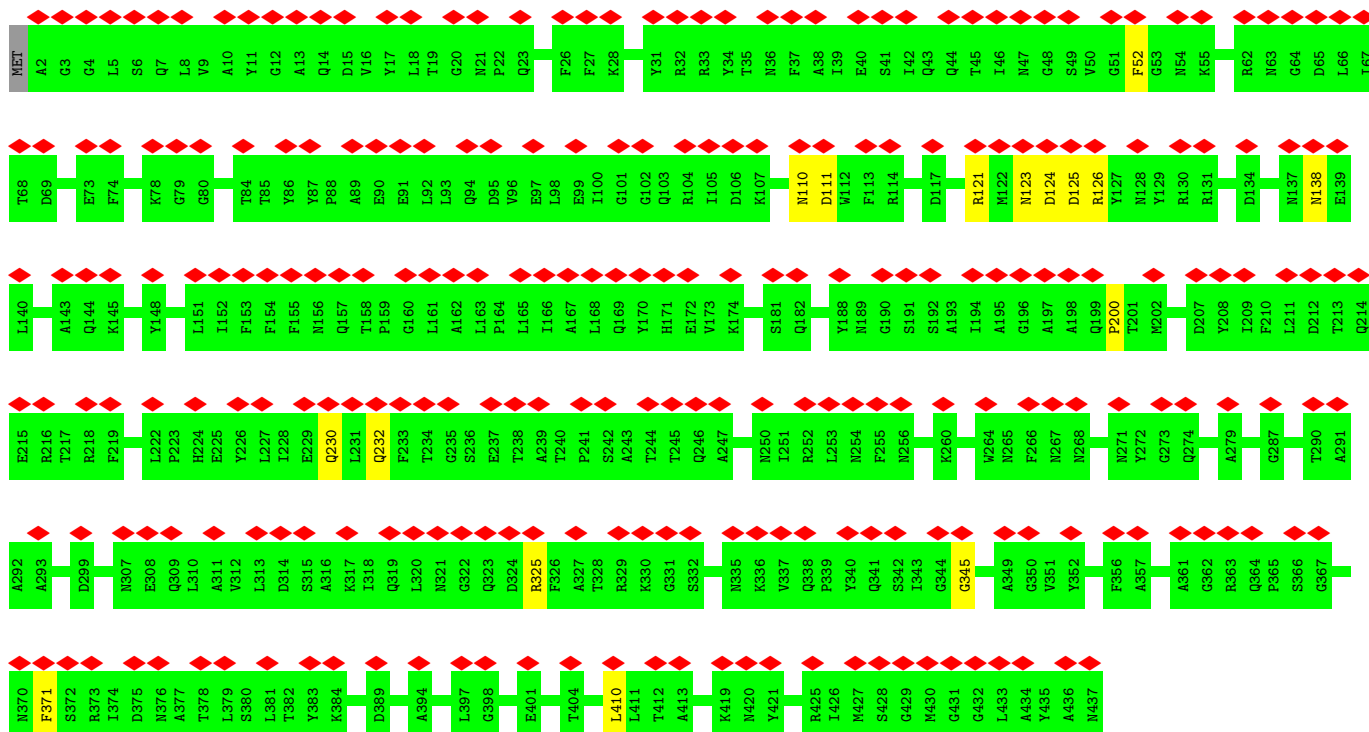


• Molecule 1: Major capsid protein (MCP)





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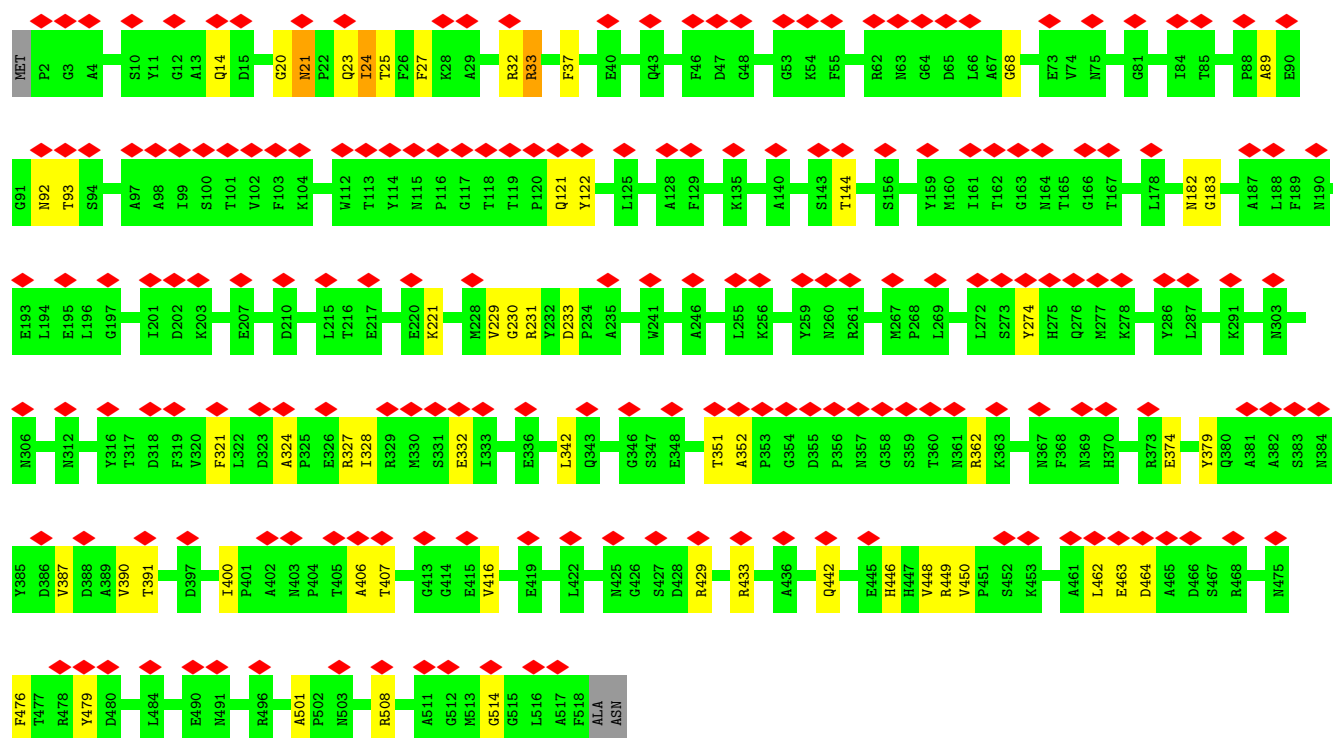


• Molecule 2: MCPv1



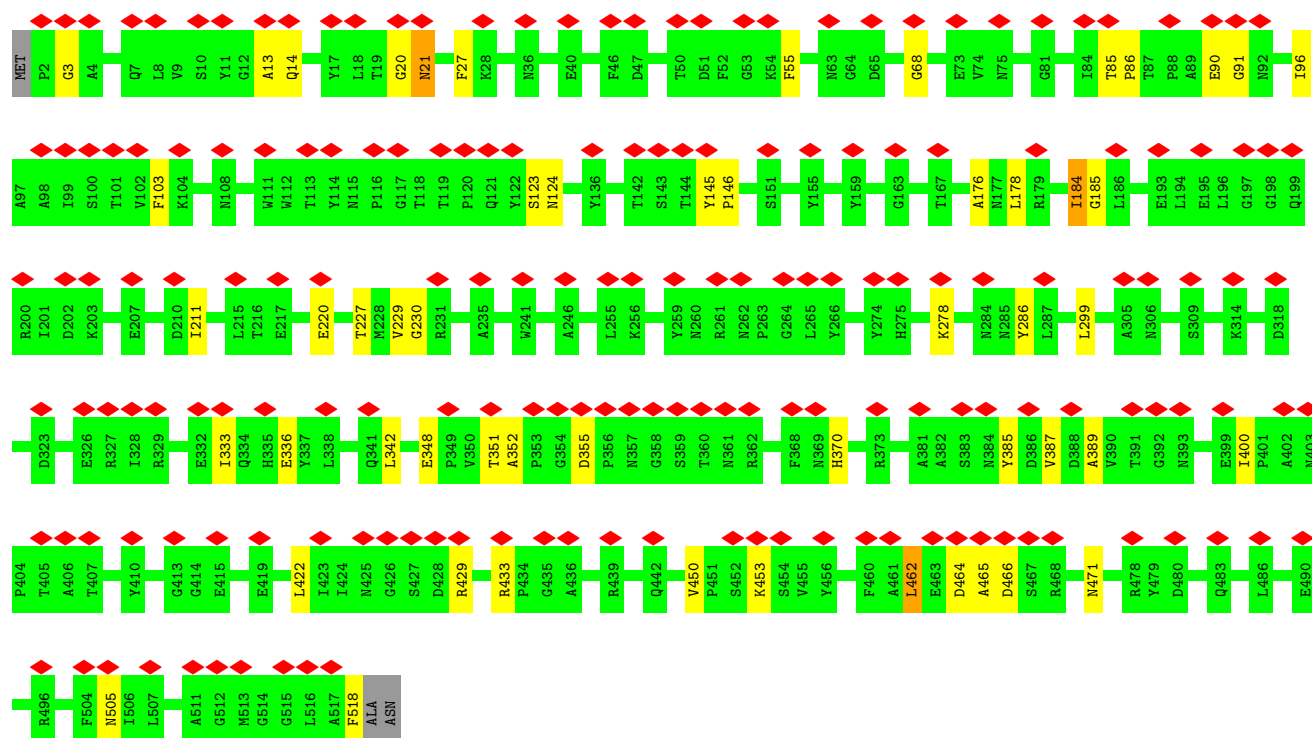
• Molecule 2: MCPv1

Chain bv: 



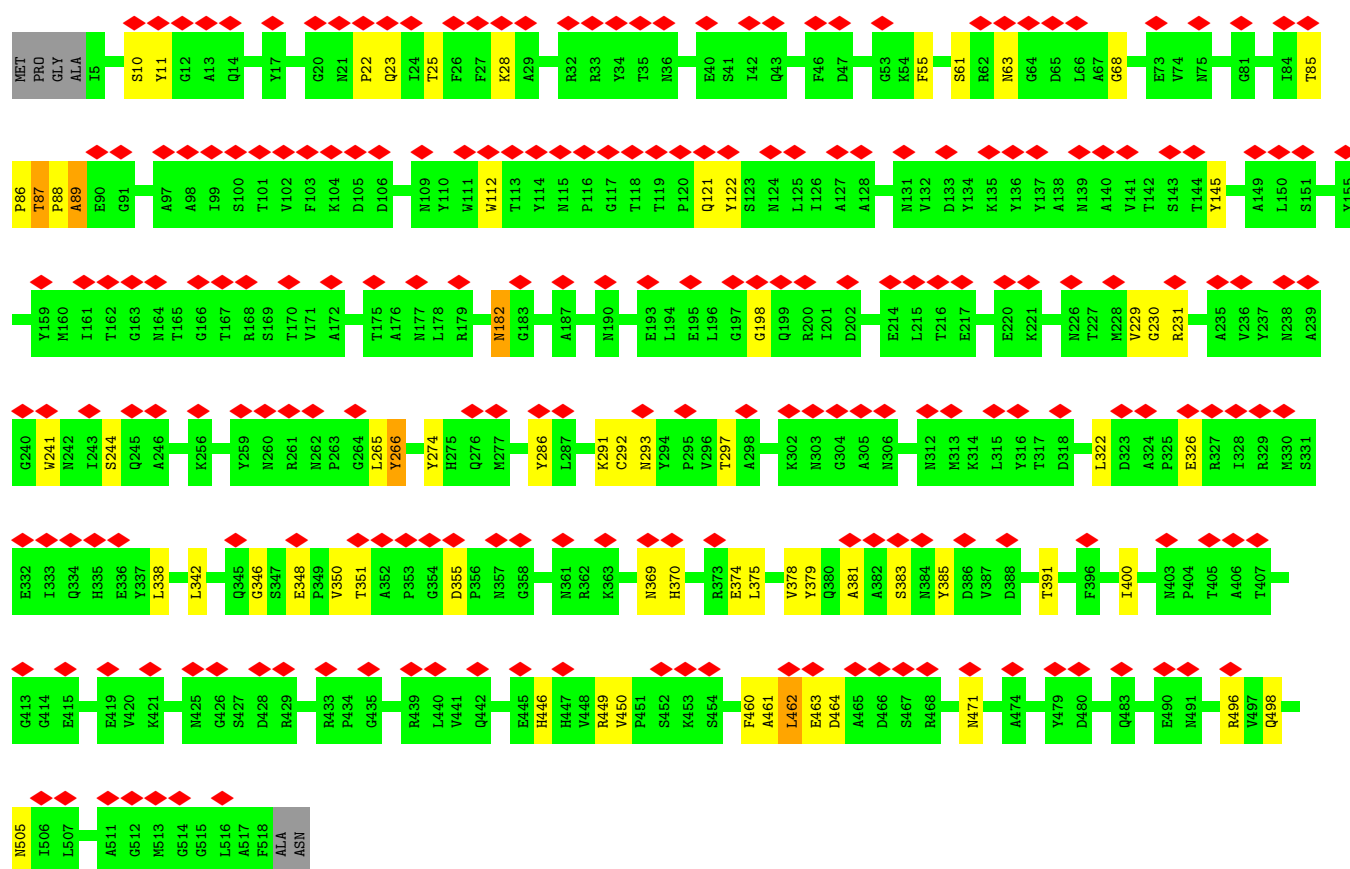
• Molecule 2: MCPv1

Chain bw: 



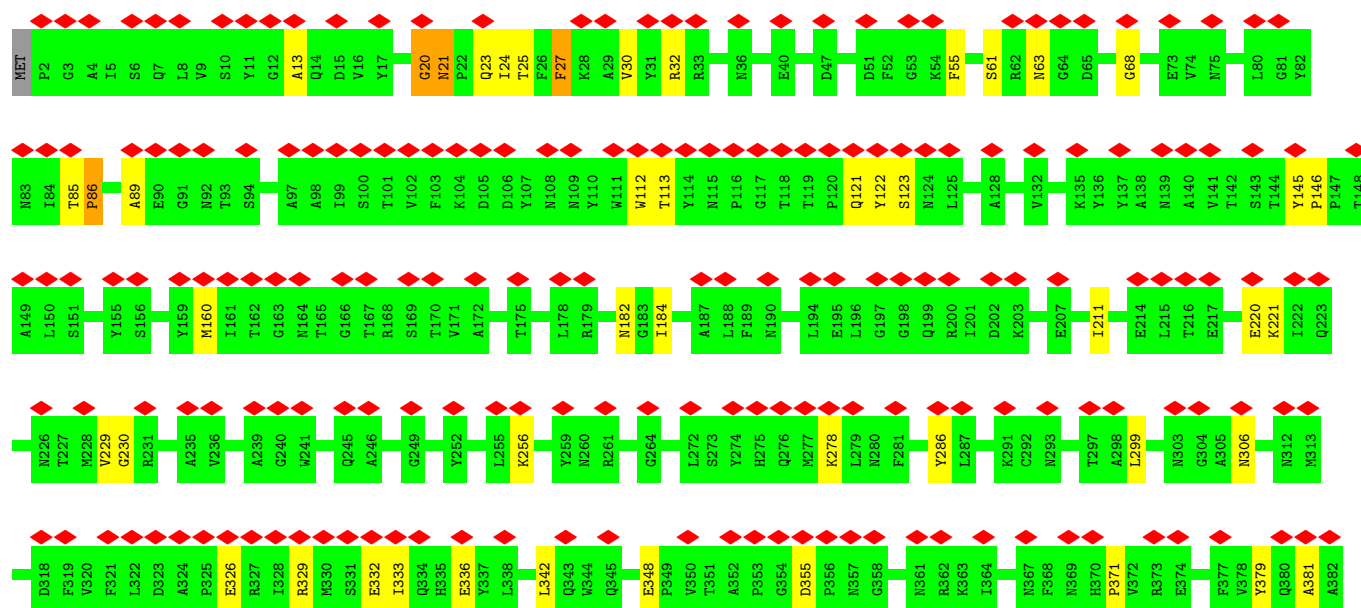
• Molecule 2: MCPv1

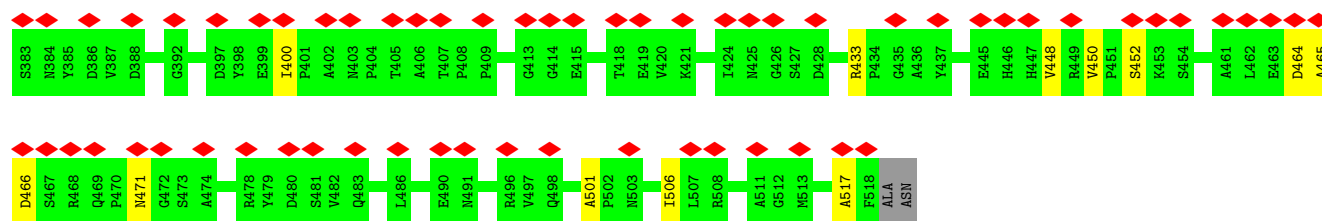
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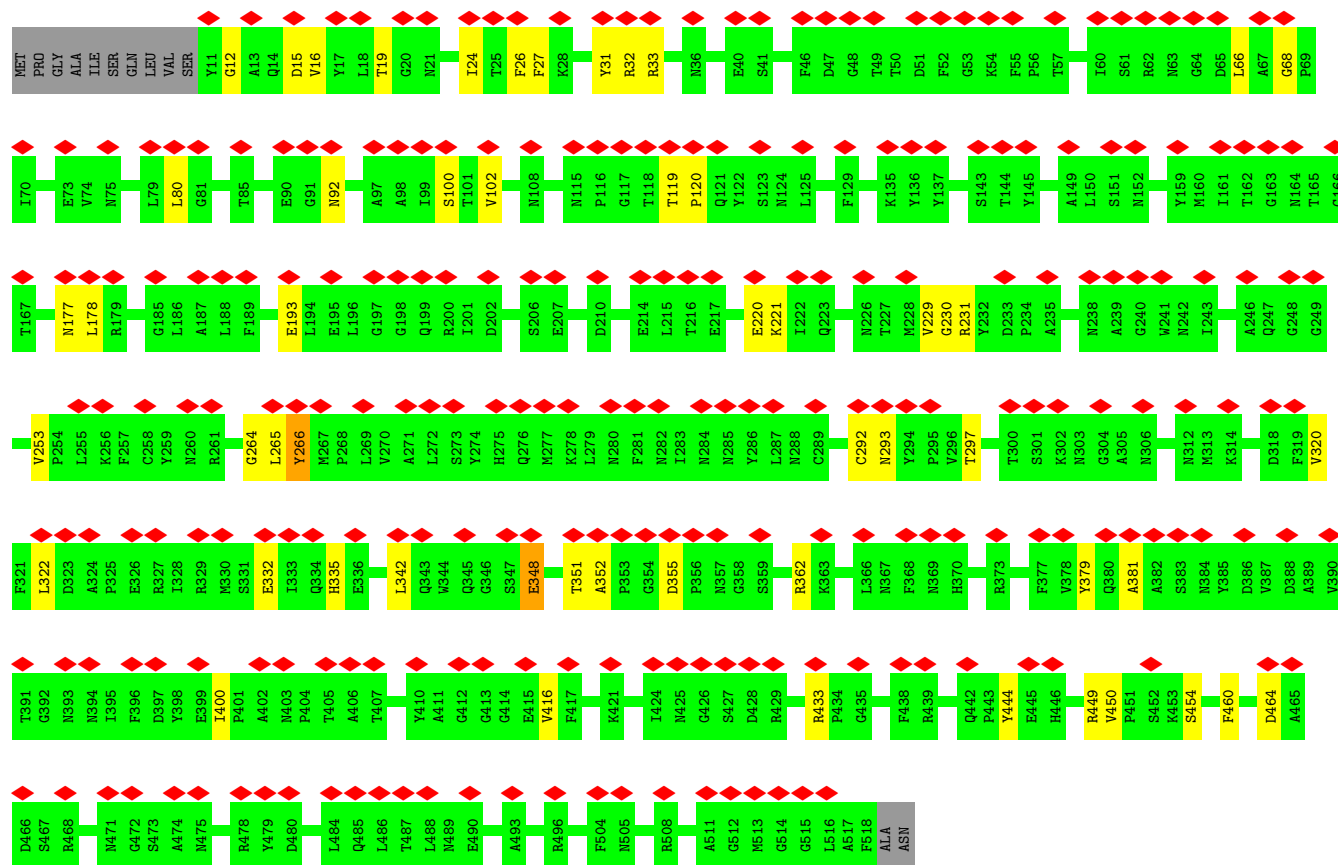
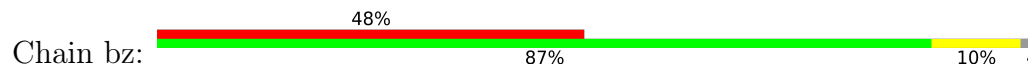
• Molecule 2: MCPv1

Chain by: 

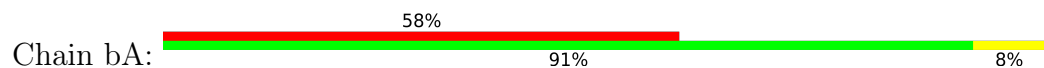


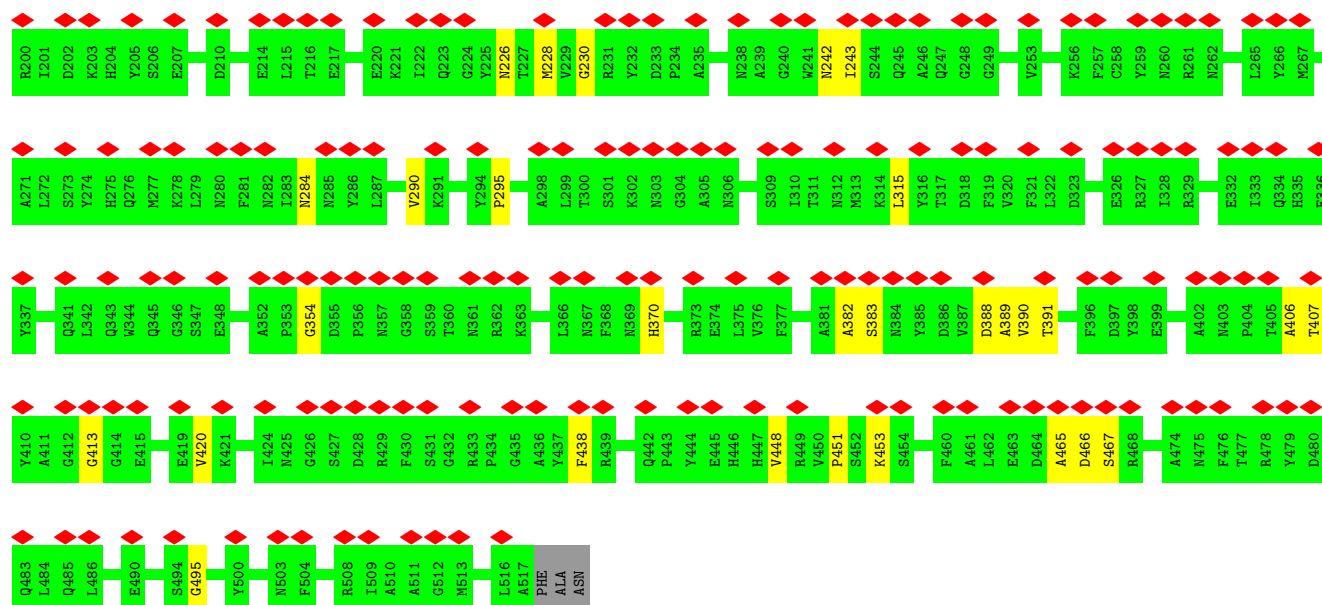


• Molecule 2: MCPv1

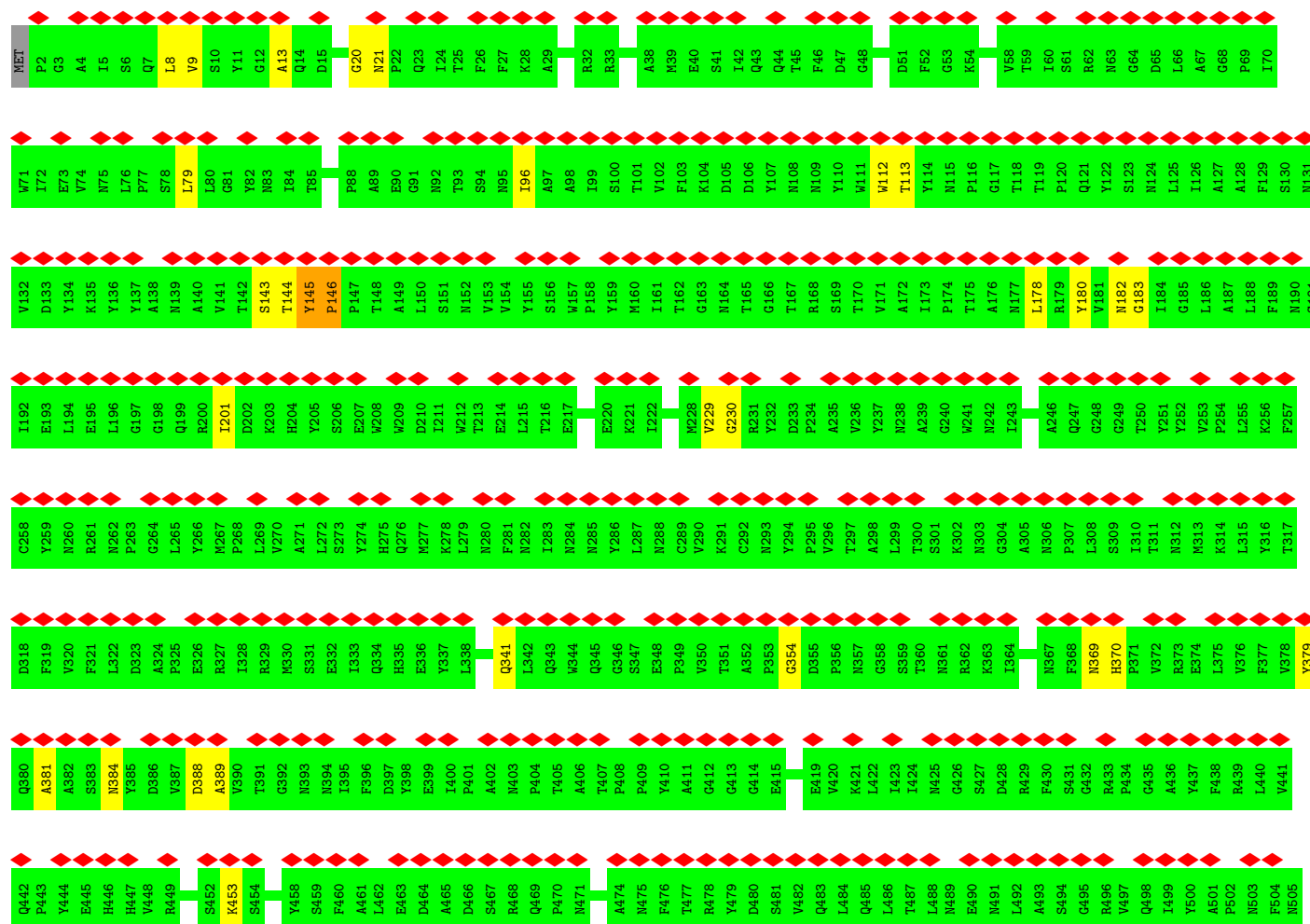
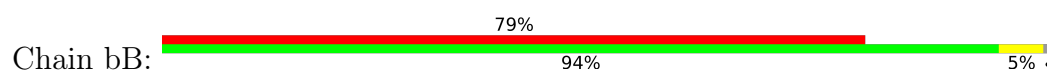


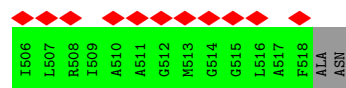
• Molecule 2: MCPv1



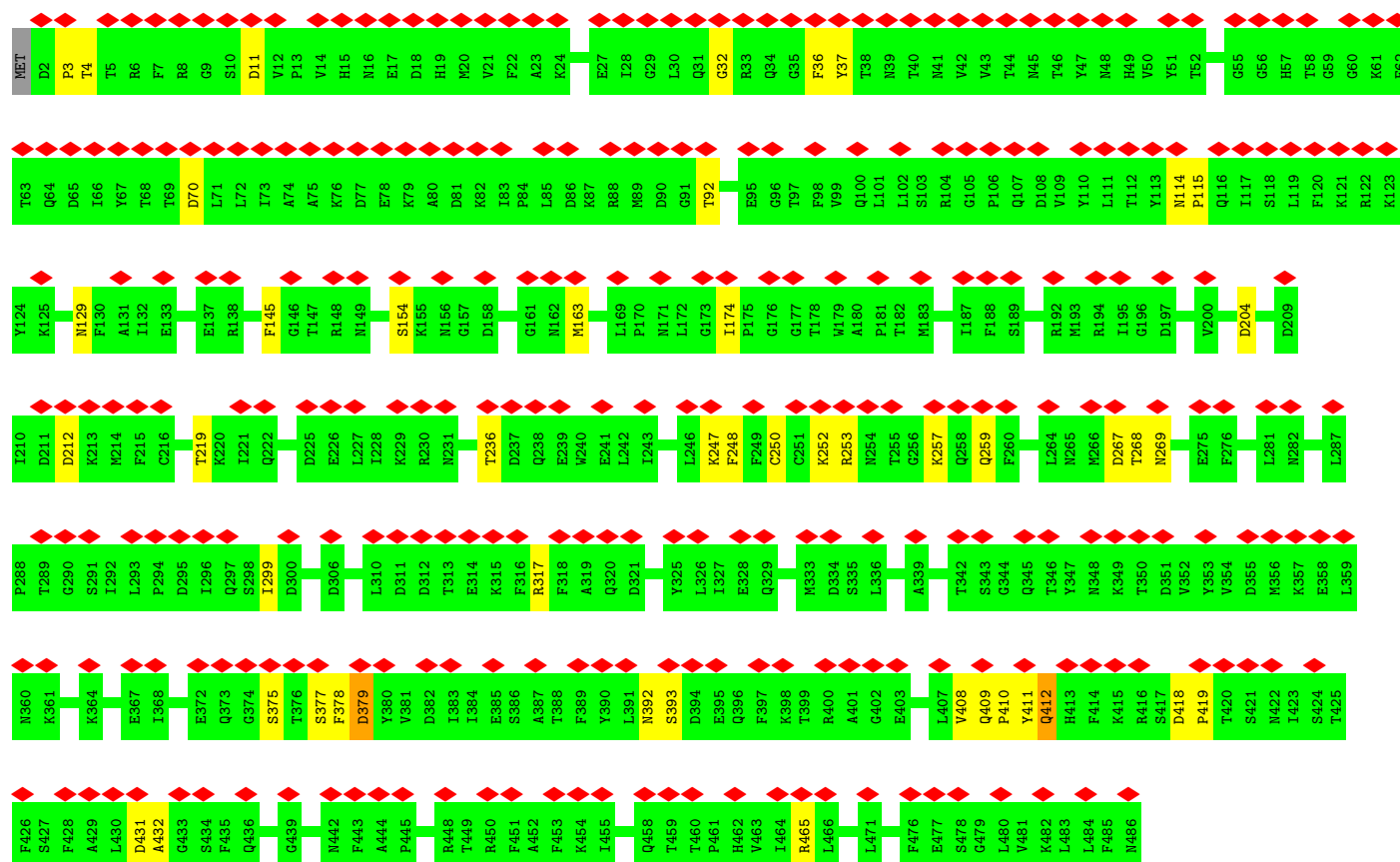
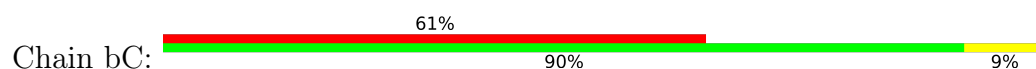


• Molecule 2: MCPv1

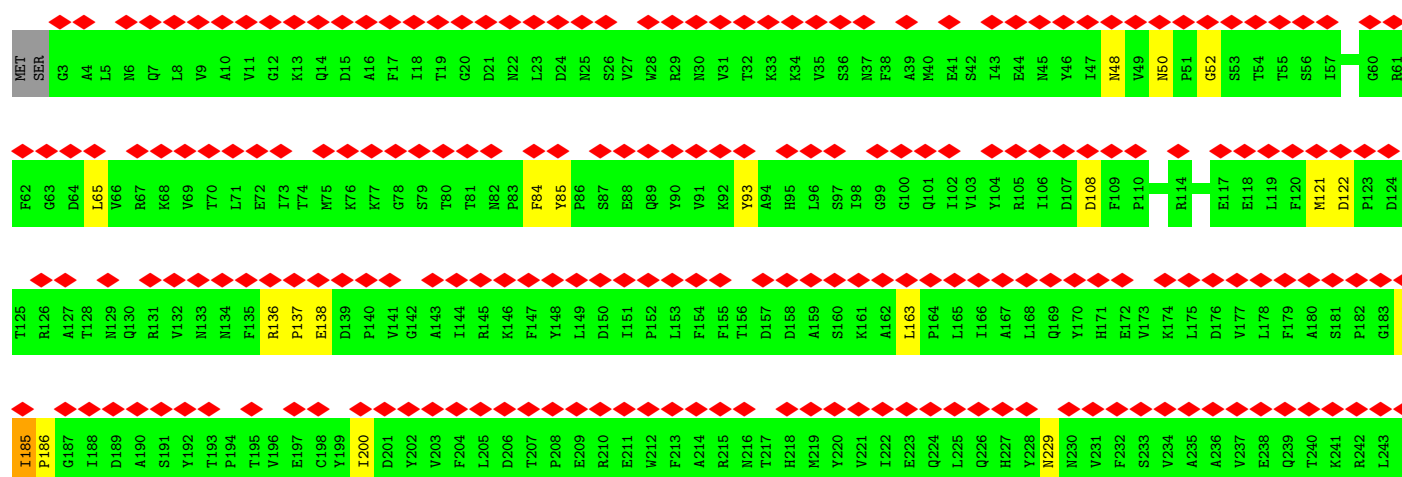
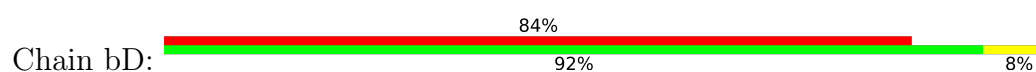


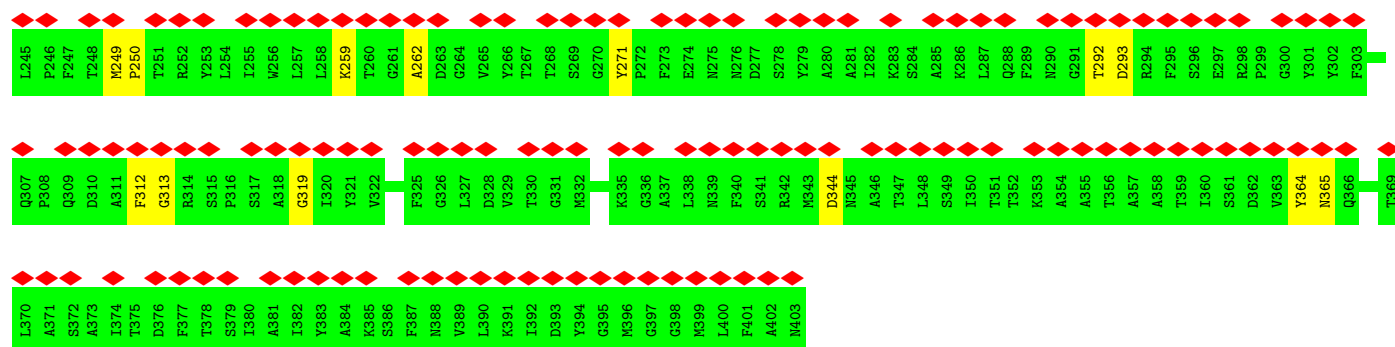


• Molecule 3: MCPv2

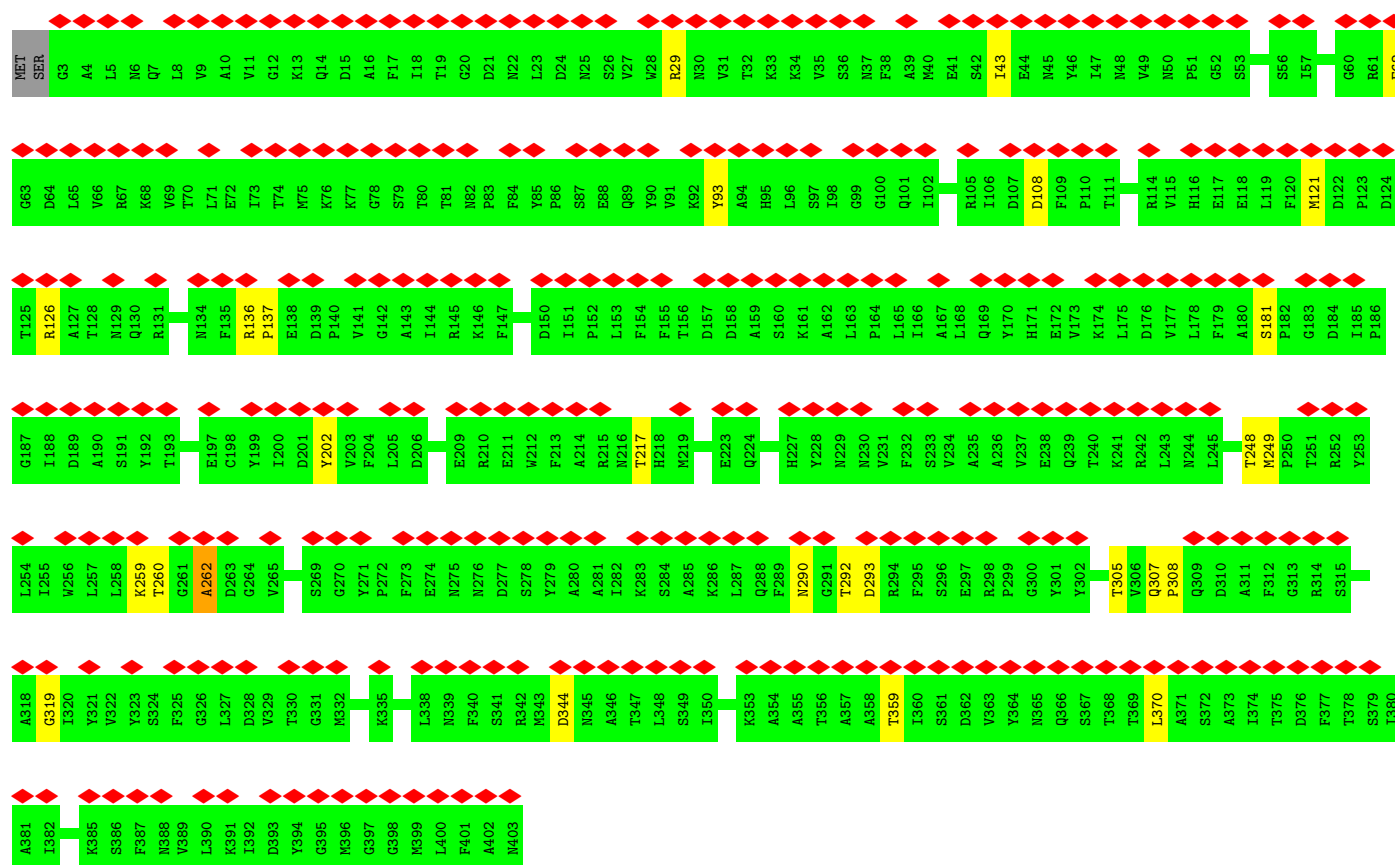
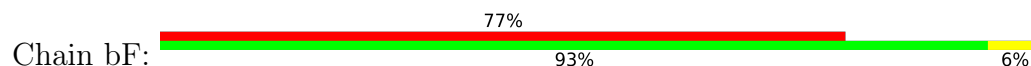


• Molecule 4: MCPv3

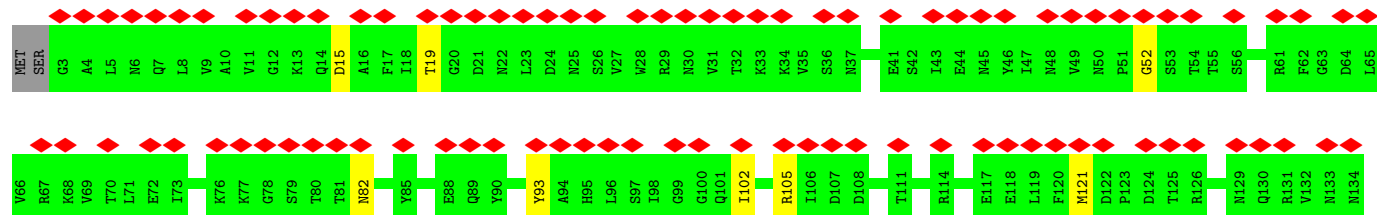


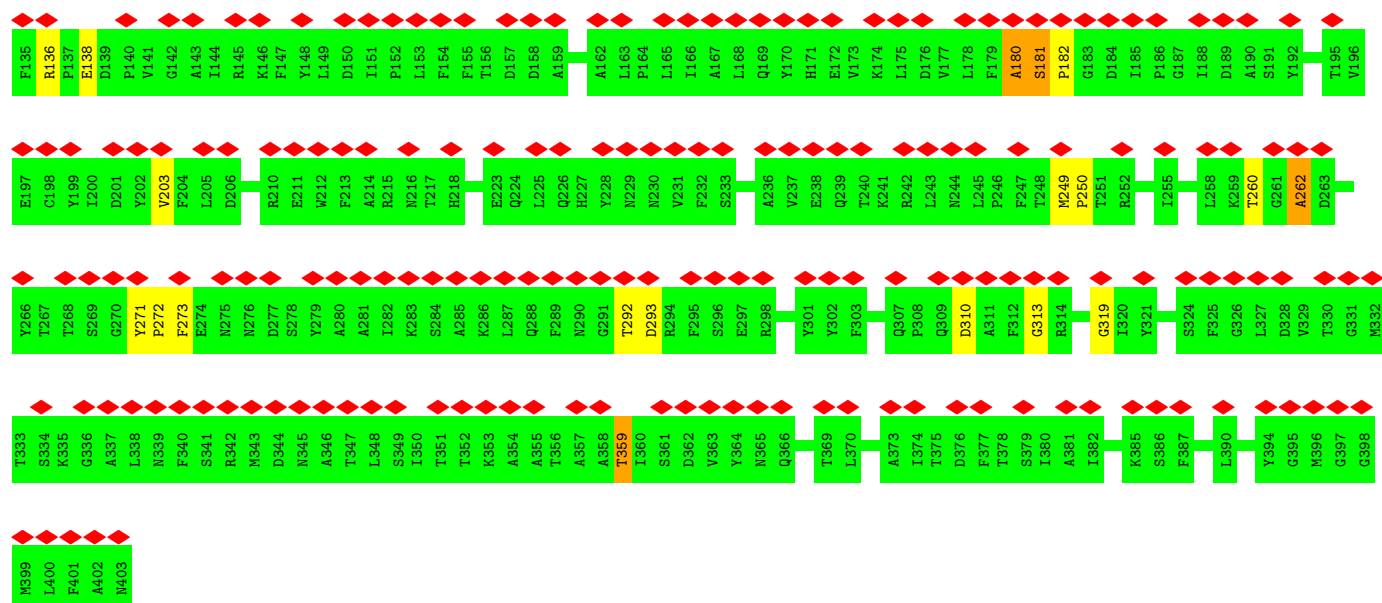


• Molecule 4: MCPv3

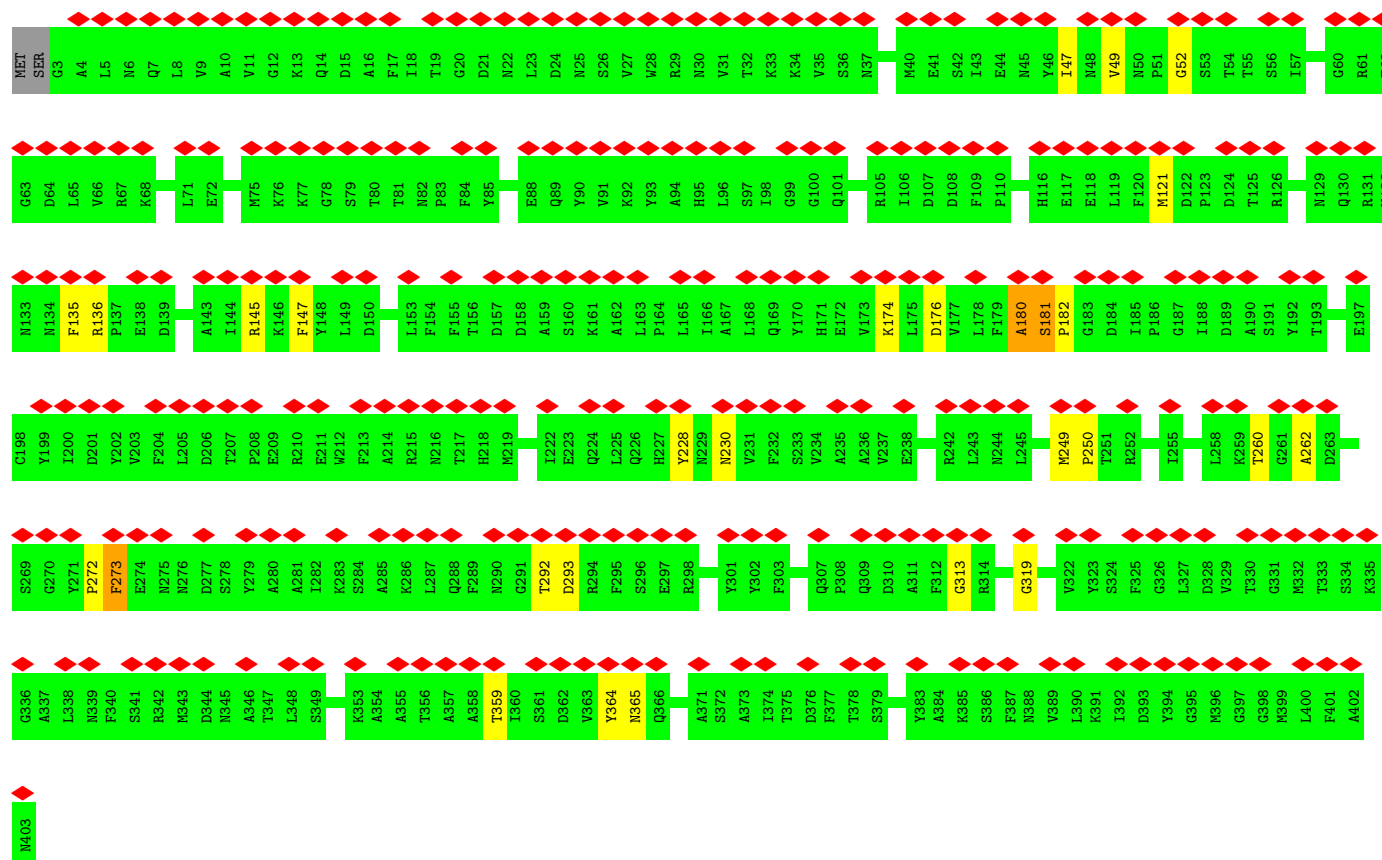


• Molecule 4: MCPv3

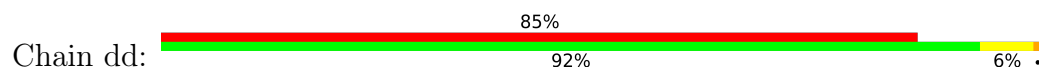


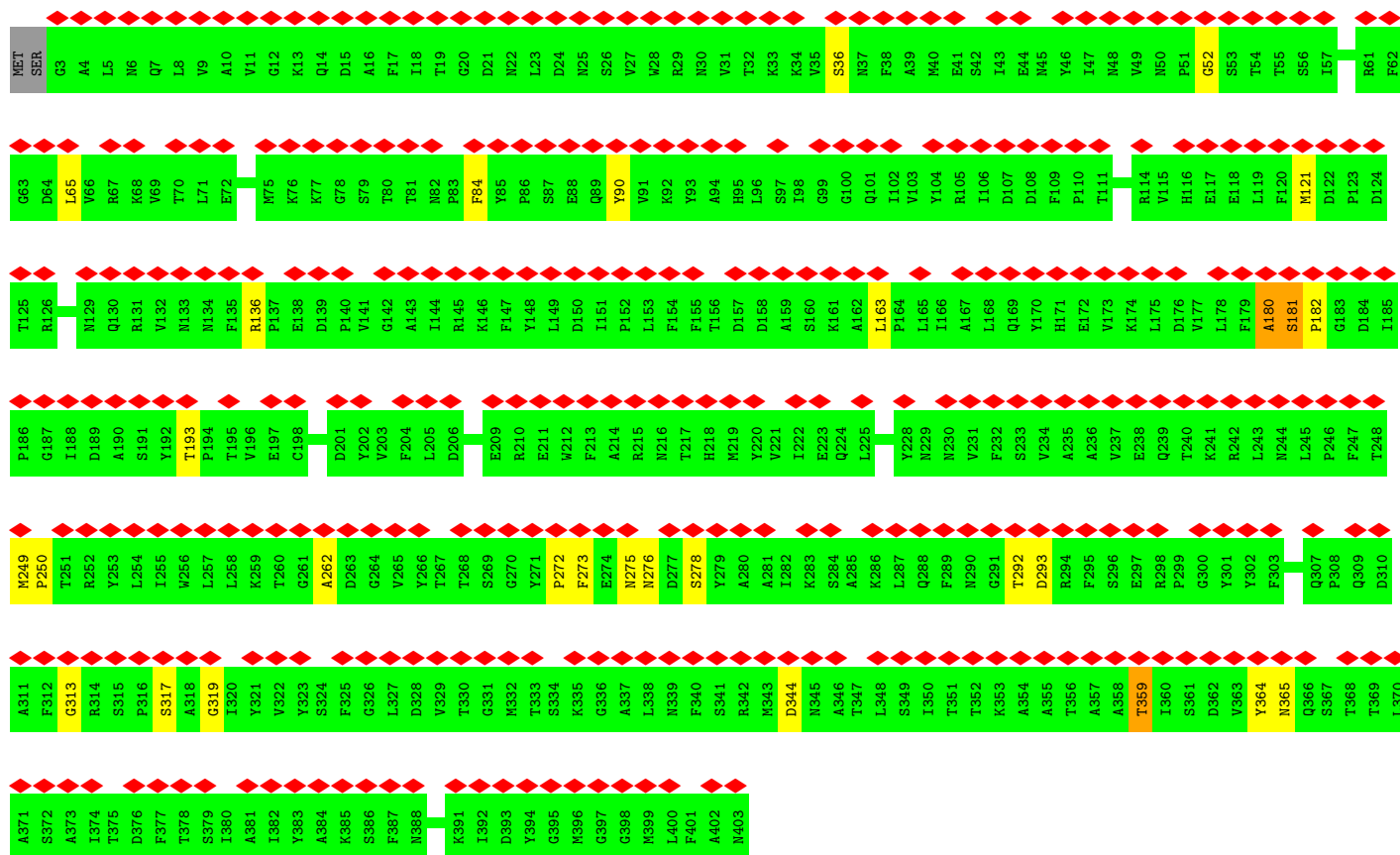


• Molecule 4: MCPv3



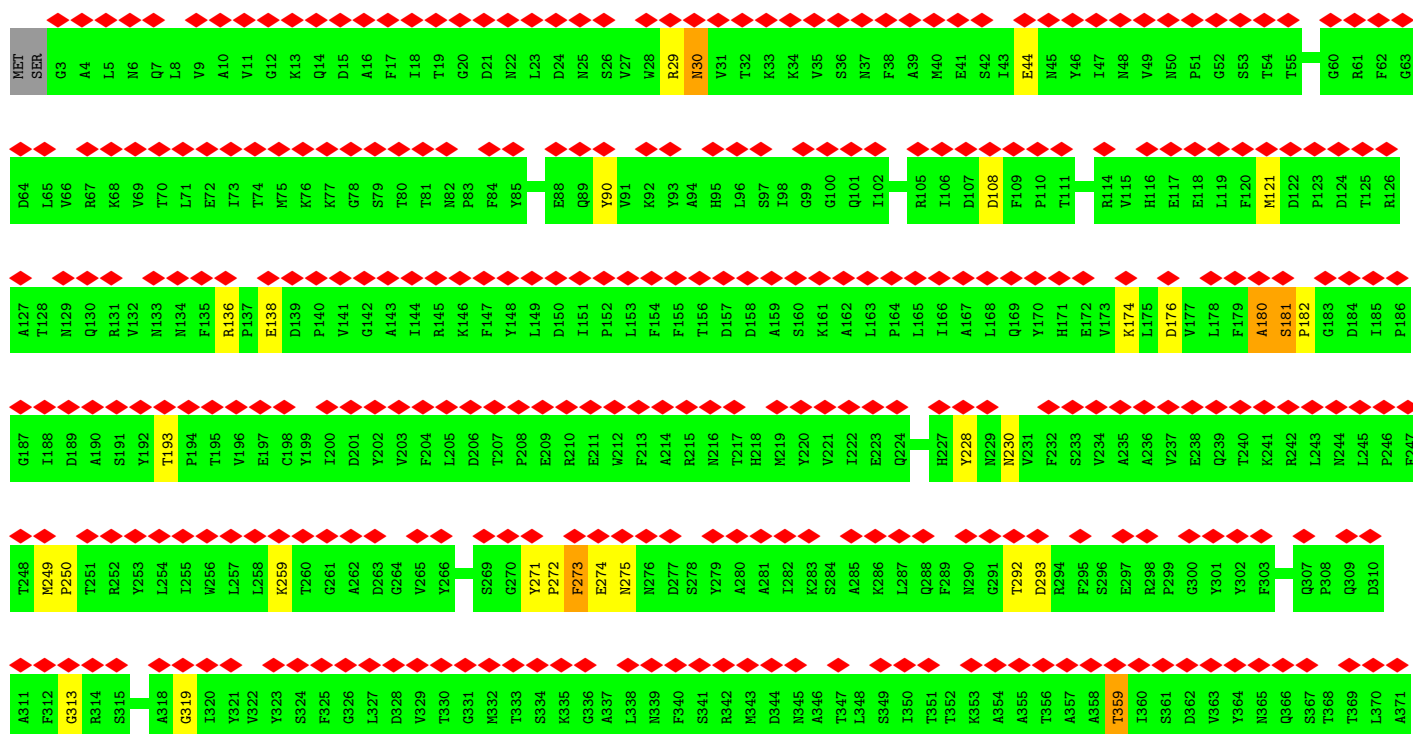
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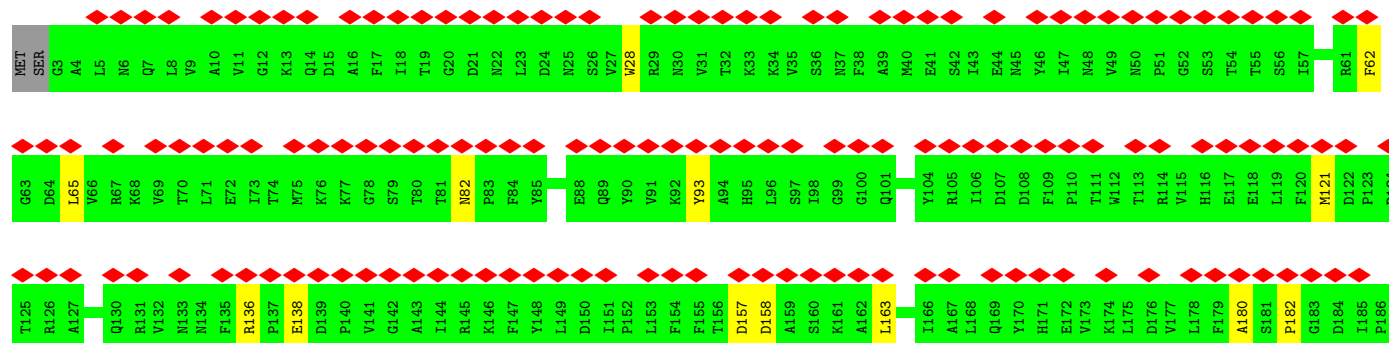
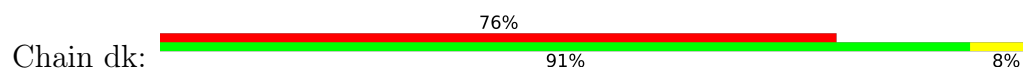
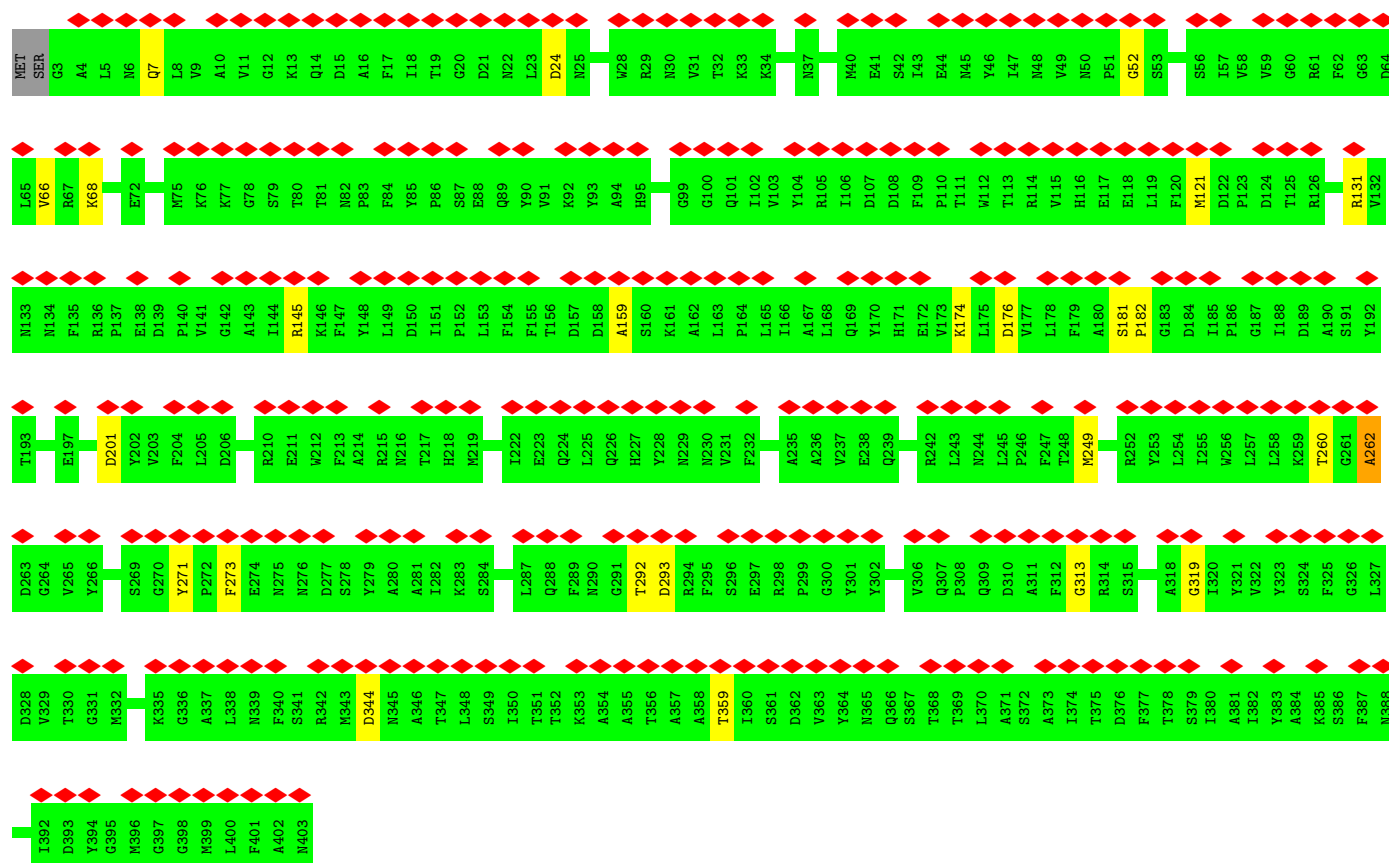
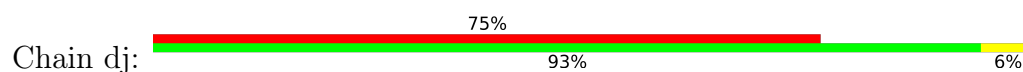


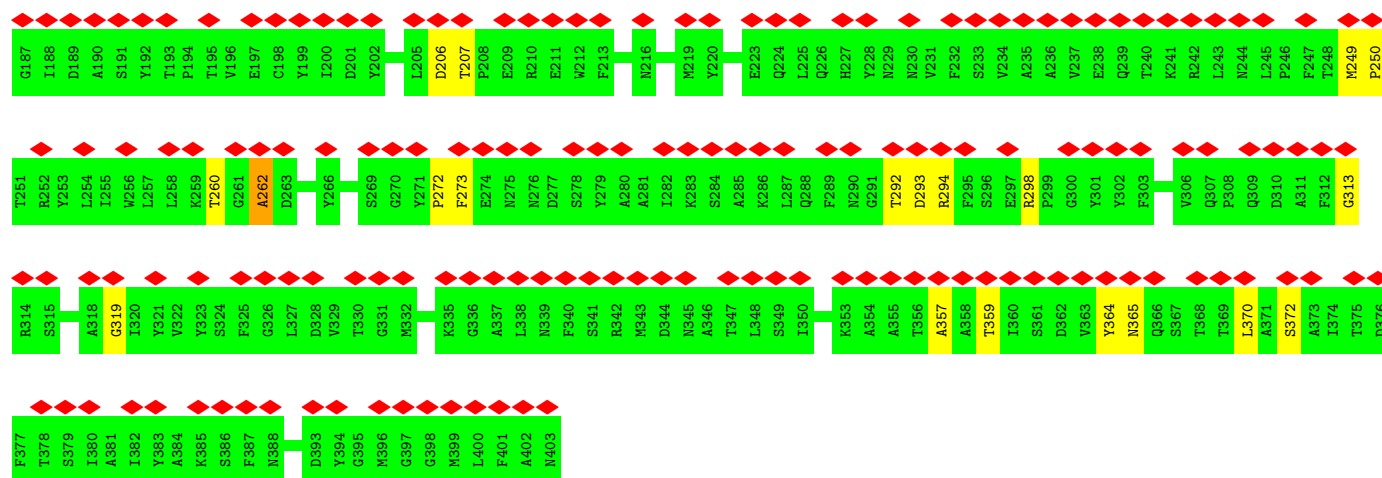


• Molecule 4: MCPv3

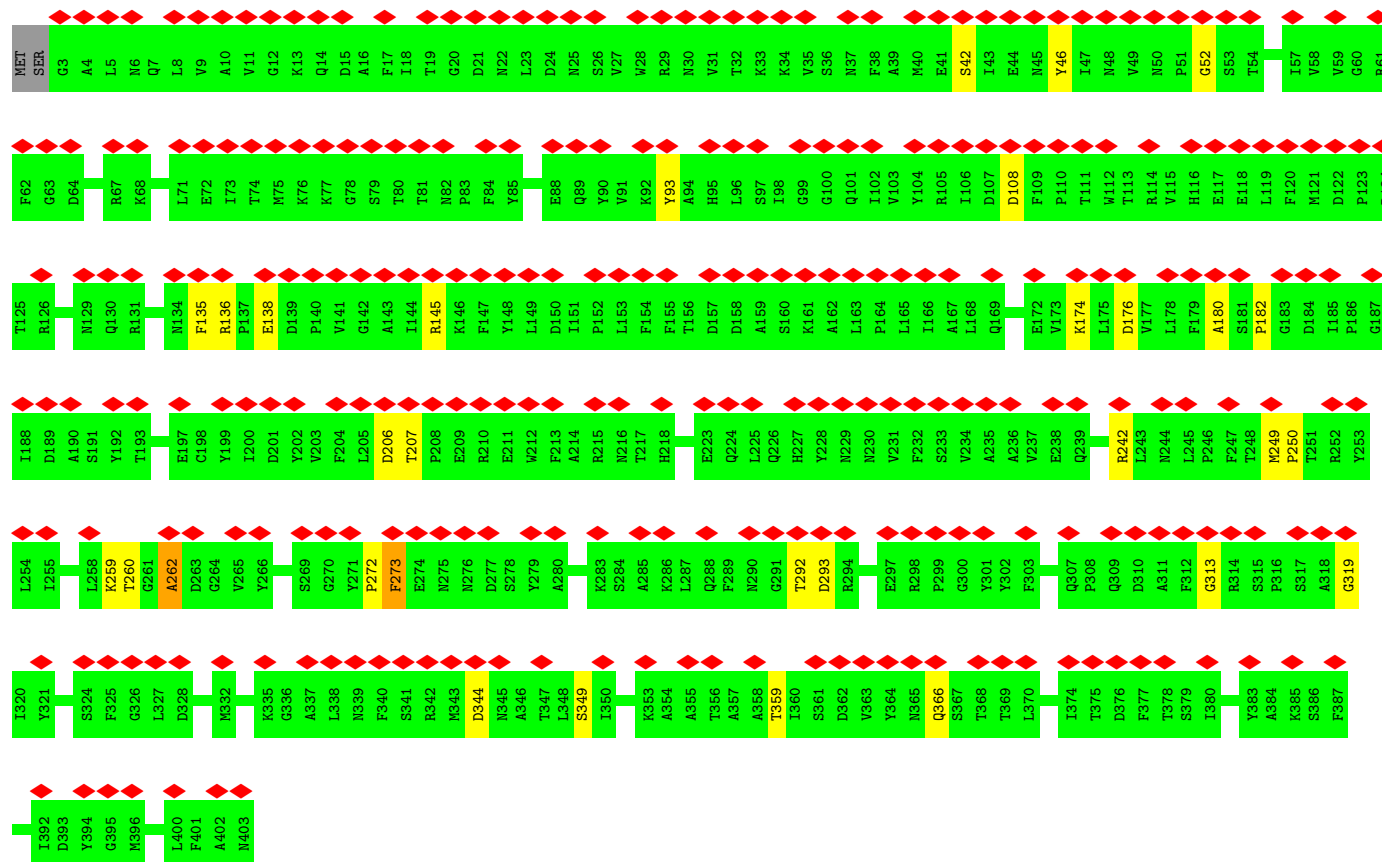
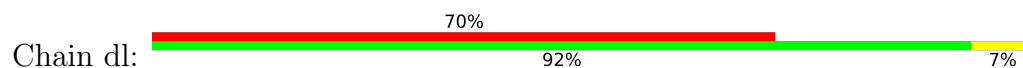
Chain df:



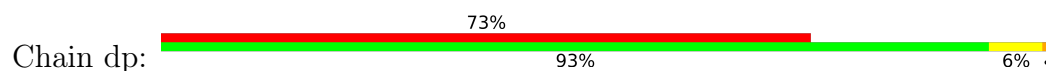


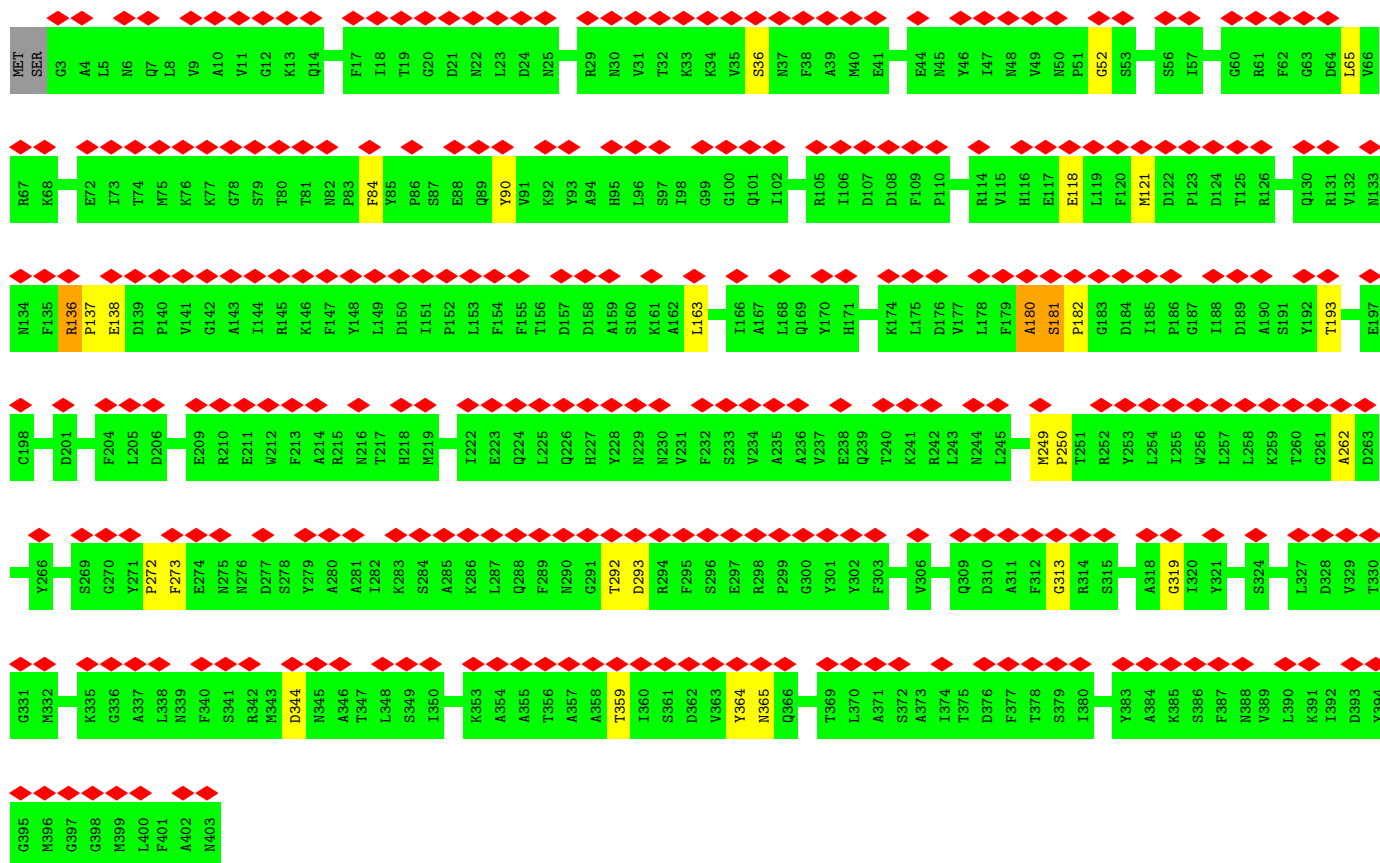


• Molecule 4: MCPv3

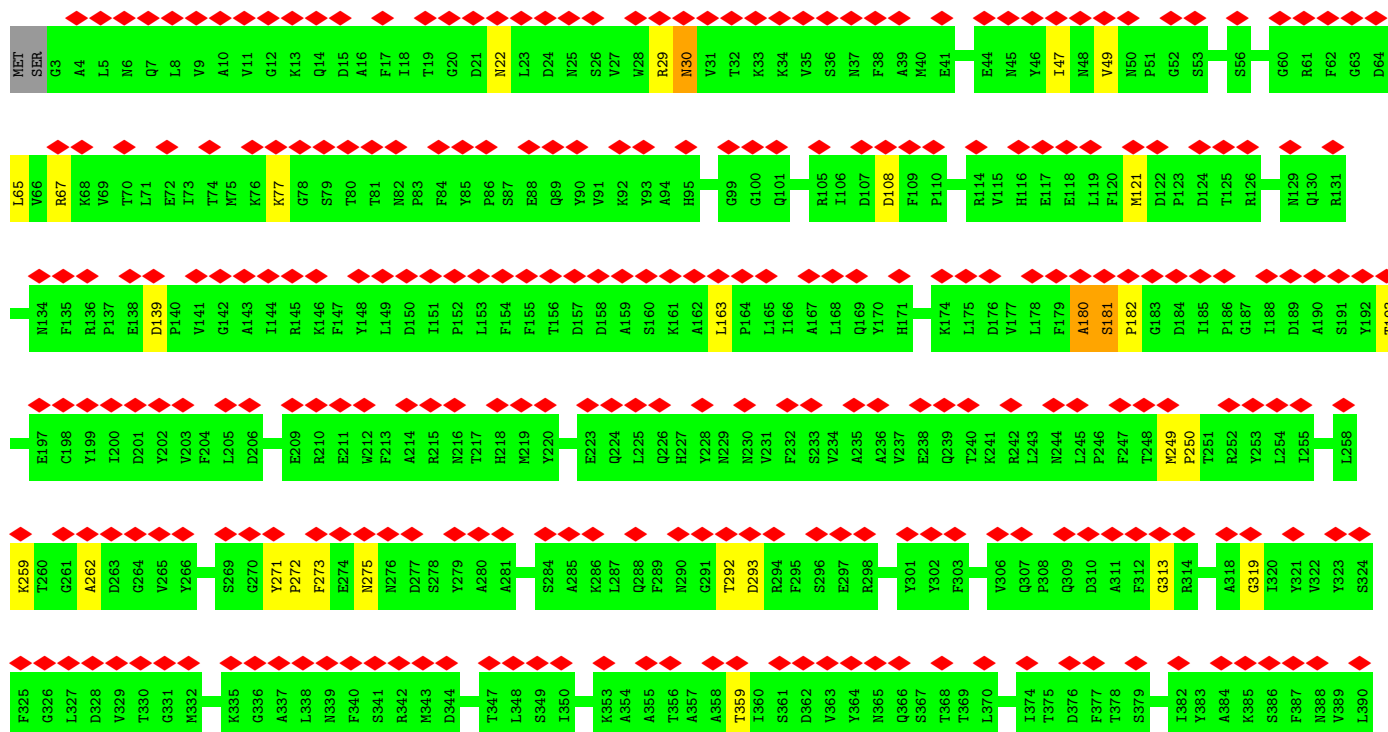
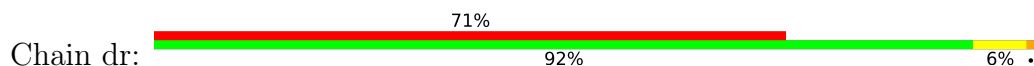


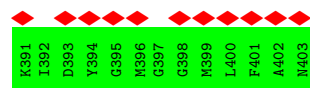
• Molecule 4: MCPv3



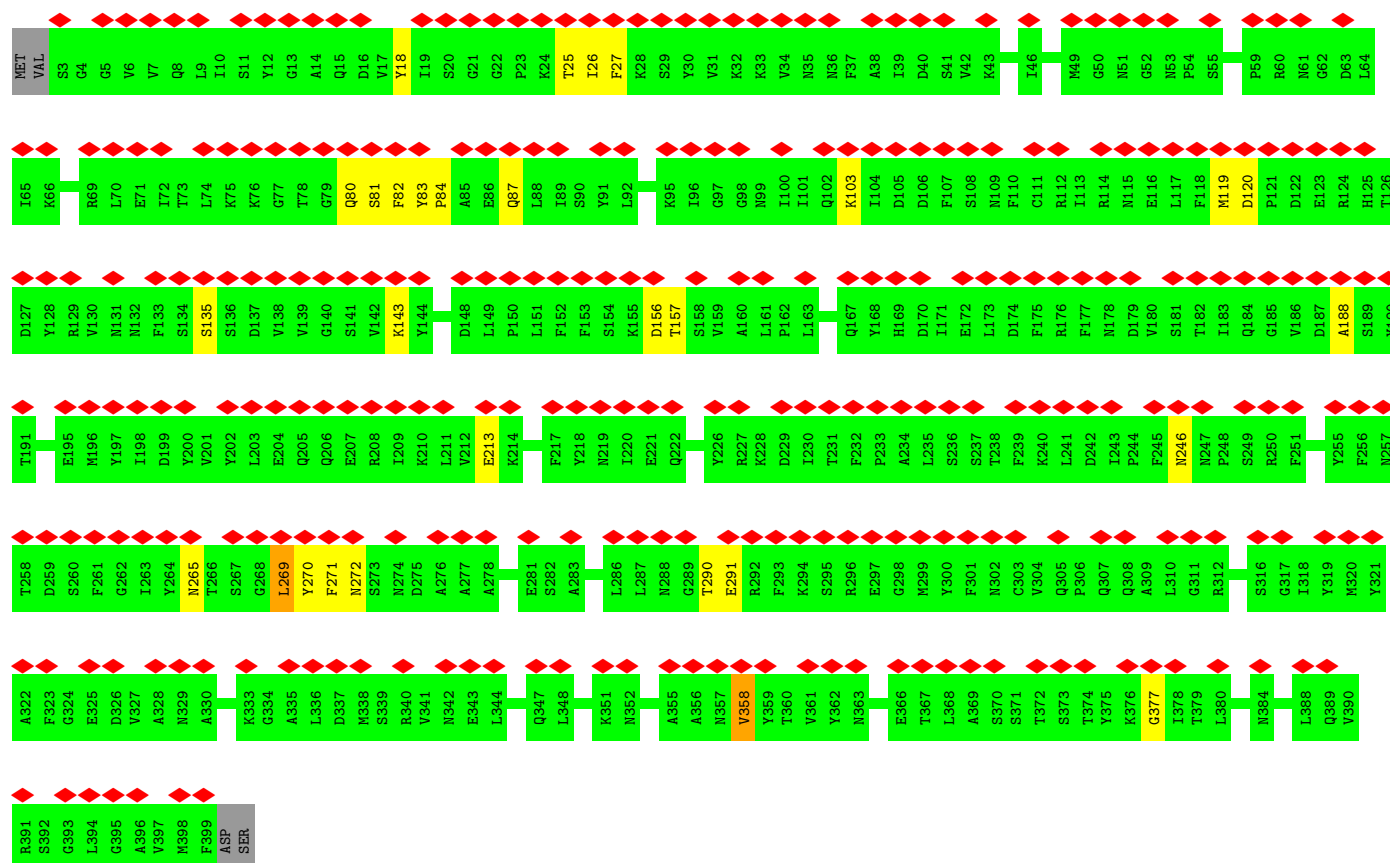
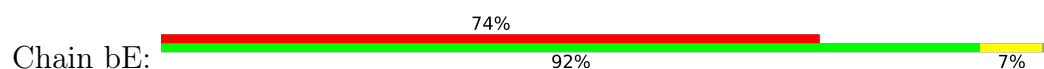


• Molecule 4: MCPv3

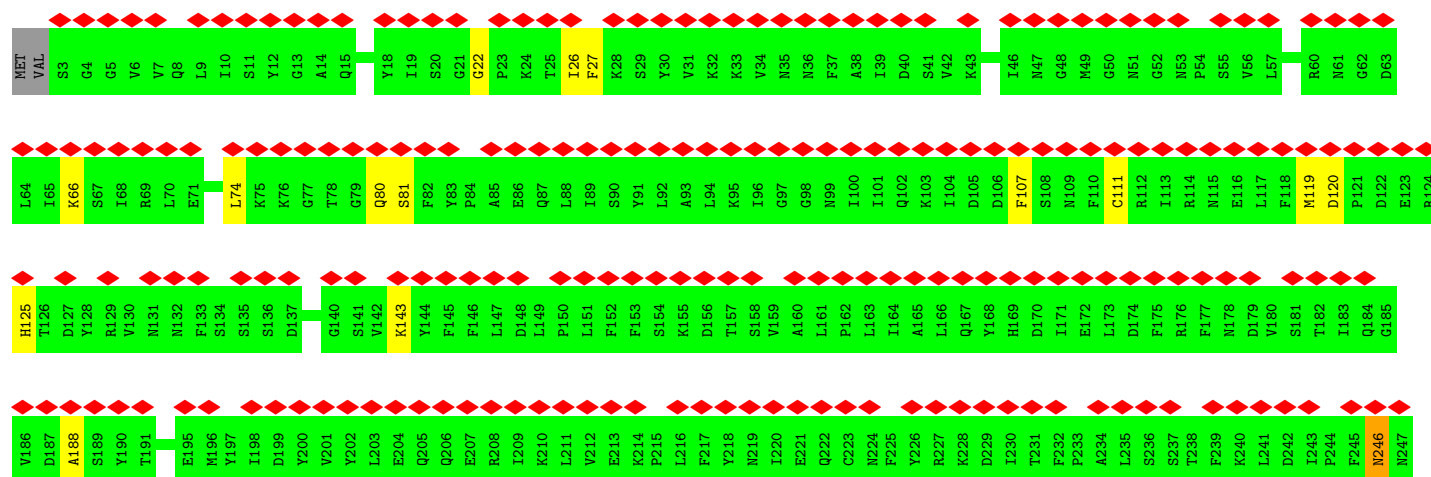
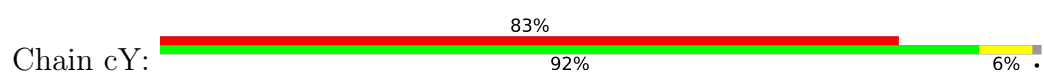


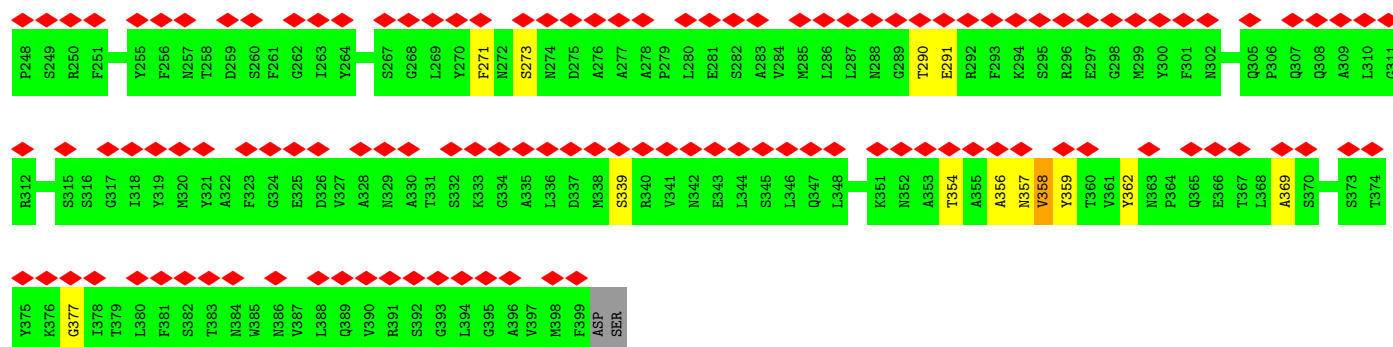


• Molecule 5: MCPv4

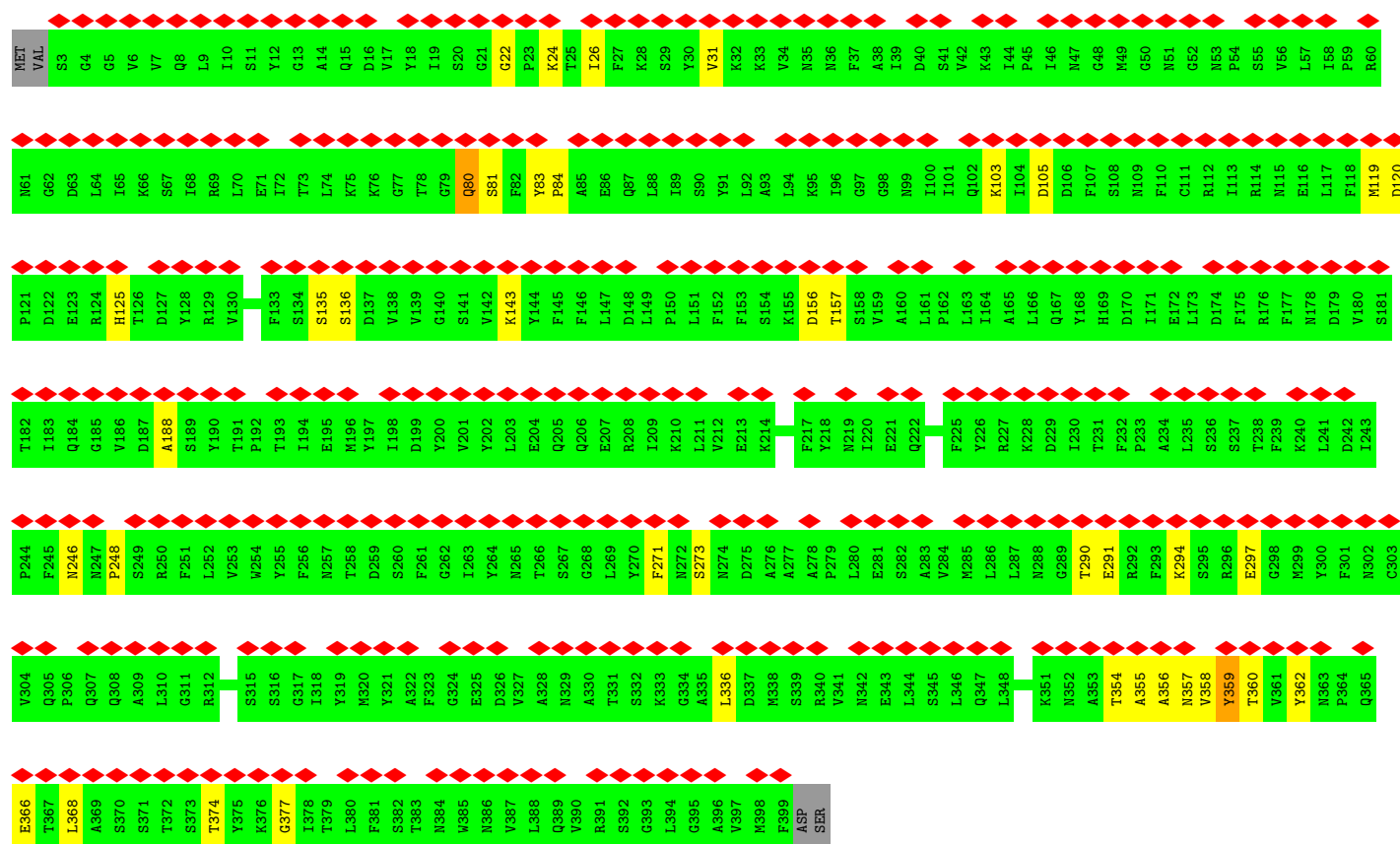
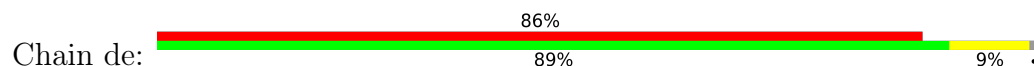


• Molecule 5: MCPv4

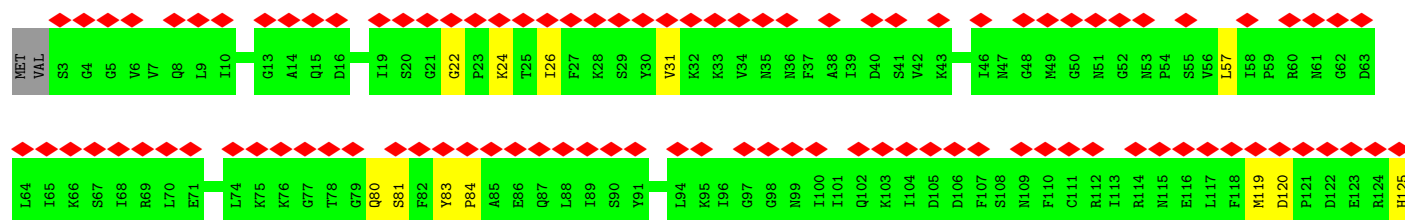
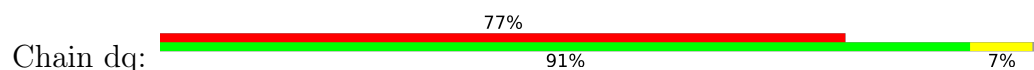


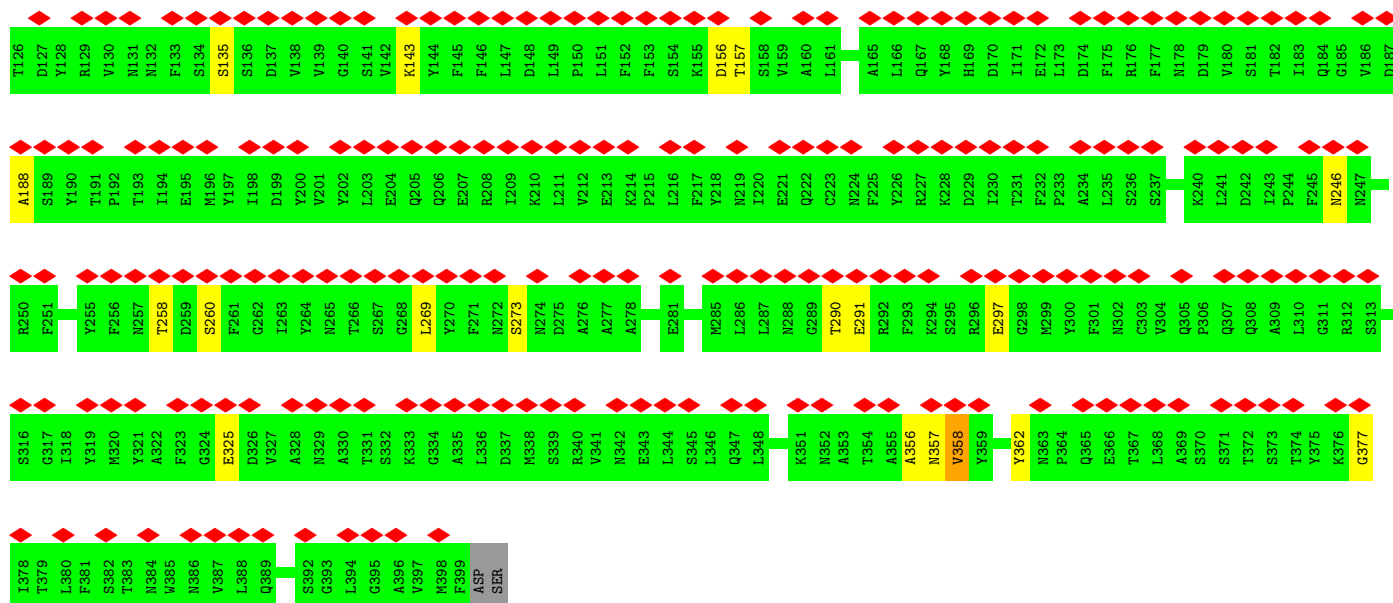


• Molecule 5: MCPv4

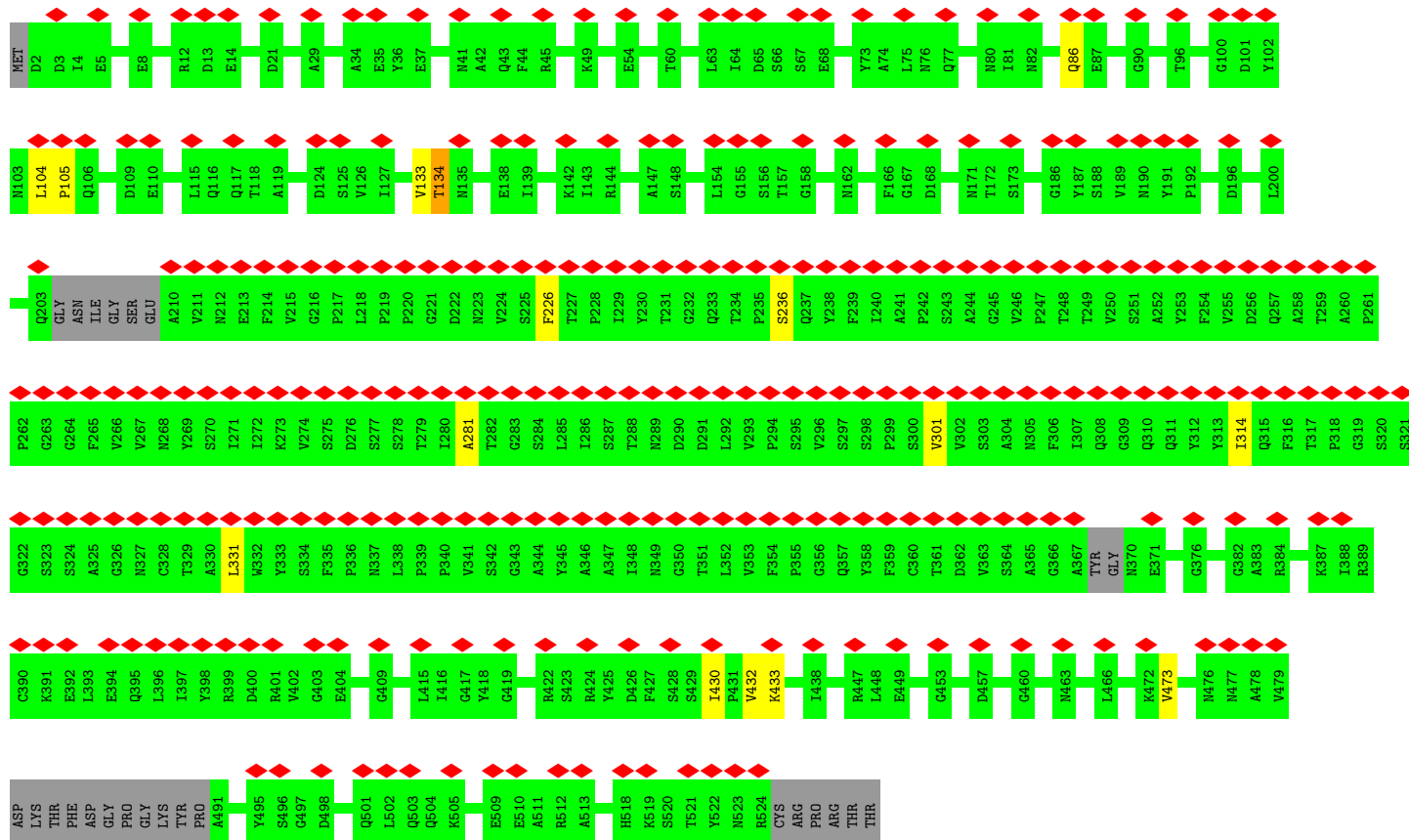


• Molecule 5: MCPv4



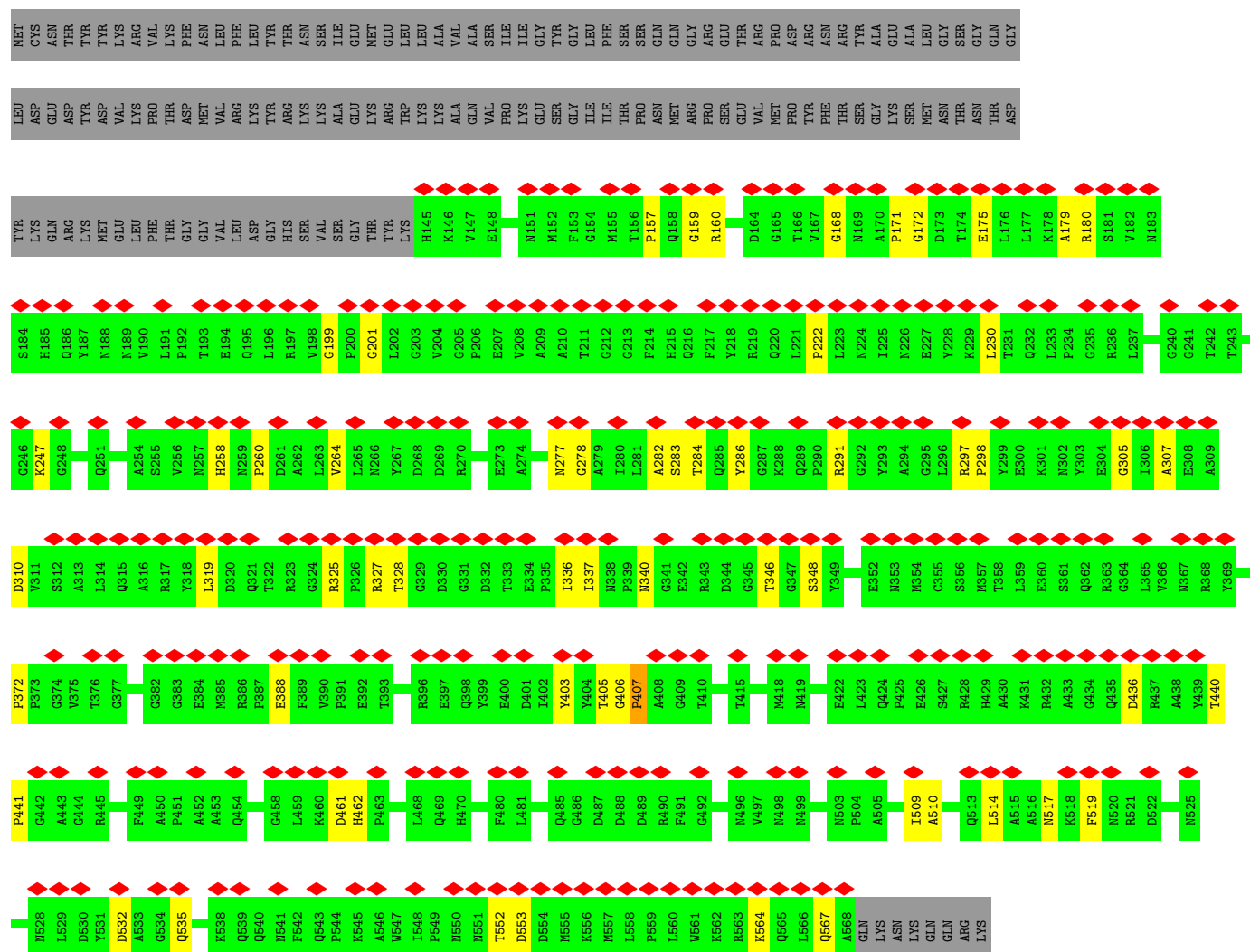


• Molecule 6: P1v1

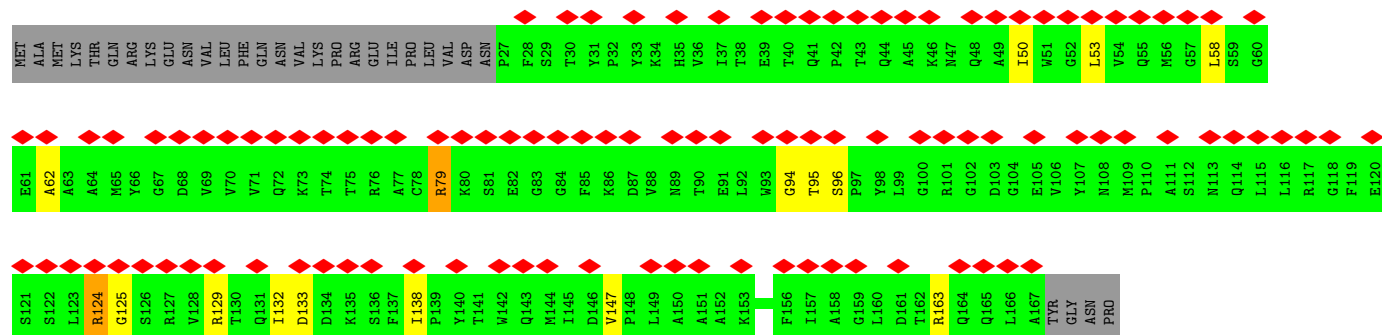
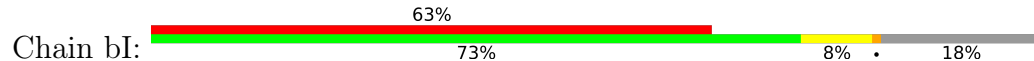


• Molecule 7: P2

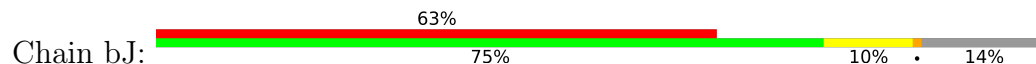




• Molecule 8: P3



• Molecule 8: P3



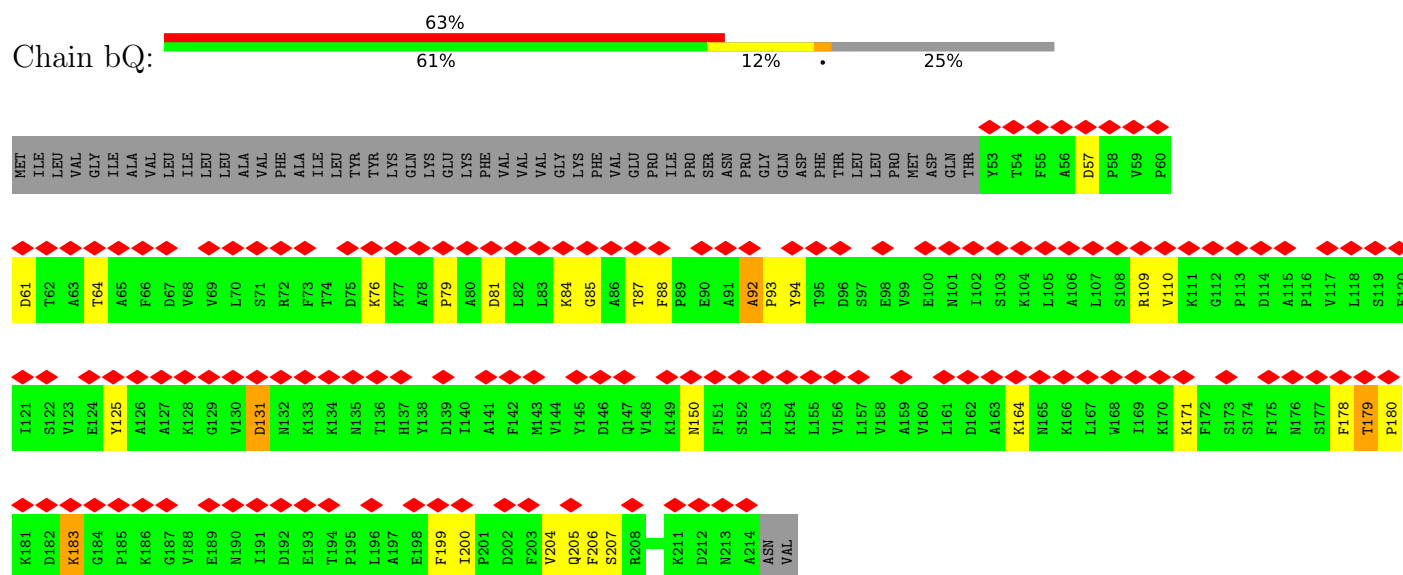
- Molecule 9: P4

- Molecule 9: P4

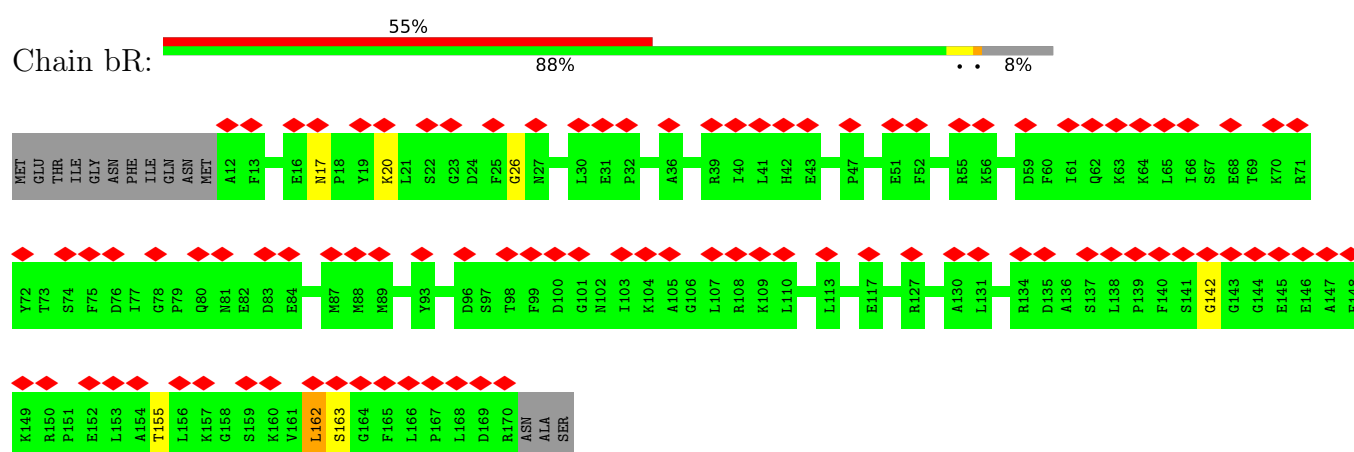
- Molecule 10: P5



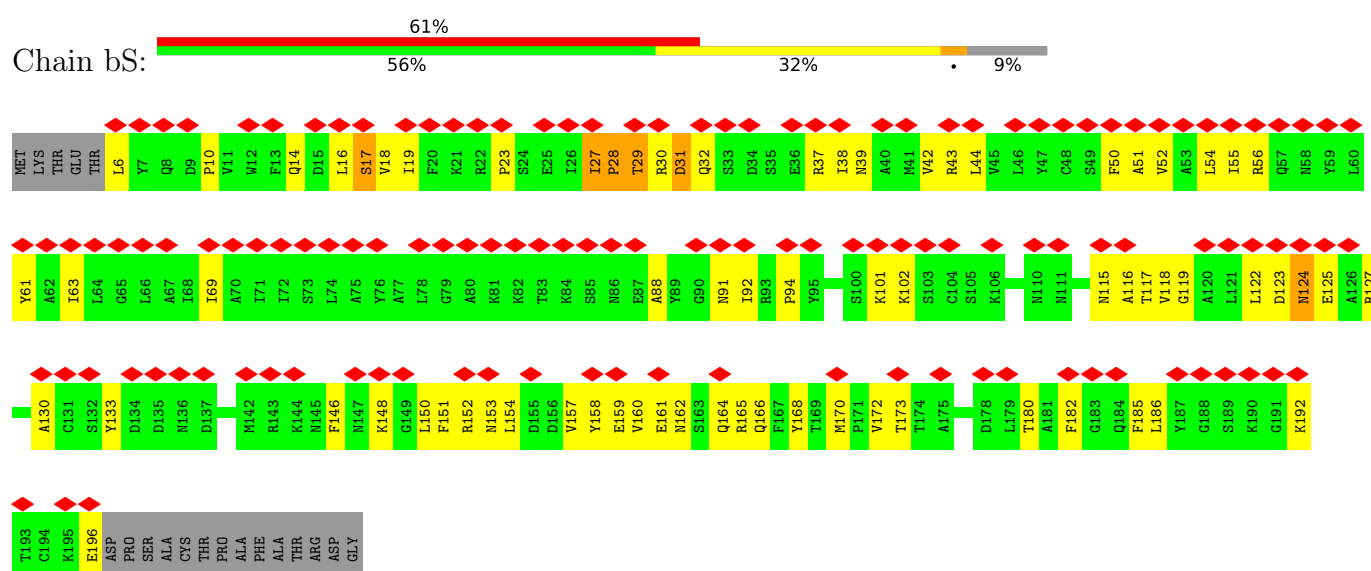
- Molecule 11: P6



- Molecule 12: P8



- Molecule 13: P9



- Molecule 14: P11

- Molecule 14: P11

- Molecule 14: P11

- Molecule 14: P11



P181	P182	P183	P184	P185	P186	P187	P188	P189	P190	P191	P192	P193	P194	P195	P196	P197	P198	P199	T200	Z201	Z202	Z203	P204	L205	PHE	GLY
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----

Chain ca:

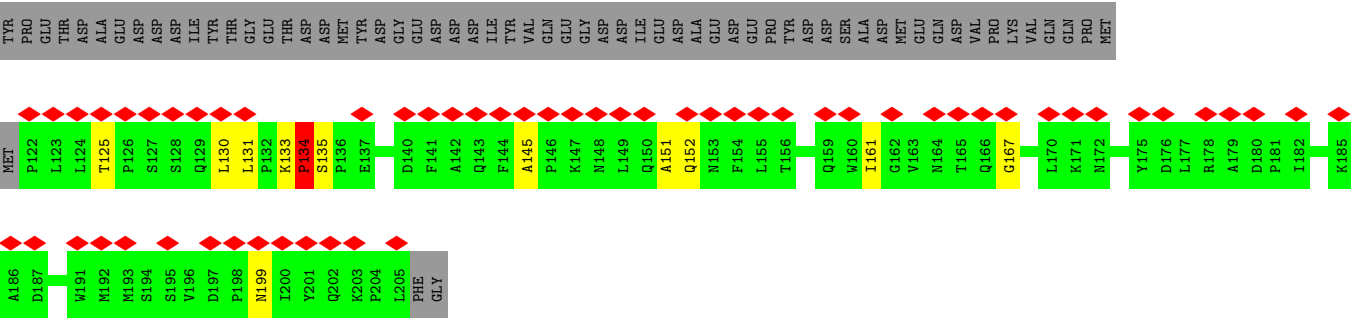
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Chain cb:

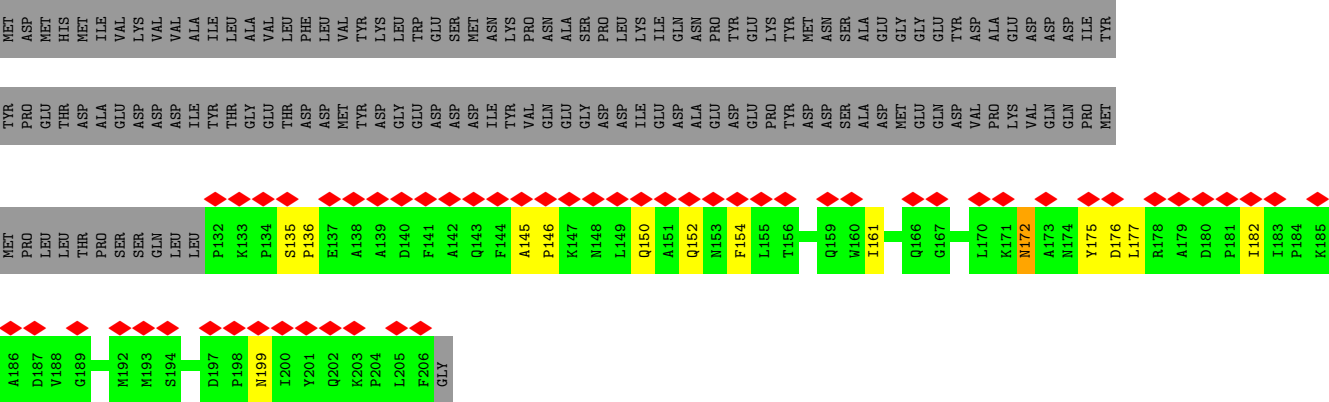
I183	P184	K185	A186	D187	V188	G189	P190	W191	M192	M193	S194	S195	V196	D197	P198	N199	I200	Y201	Q202	K203	P204	L205	F206	GLY
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Chain cc:

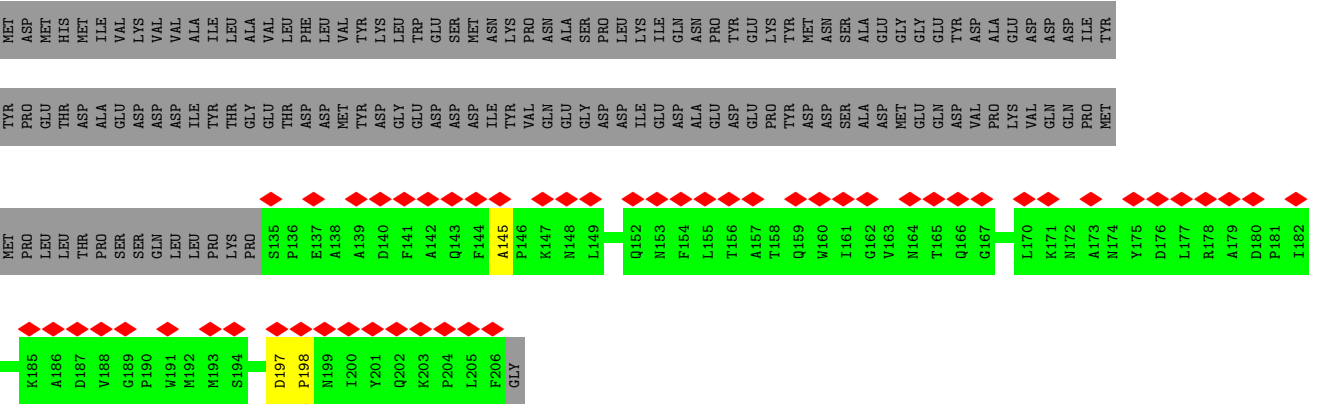
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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



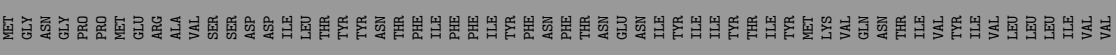
• Molecule 14: P11

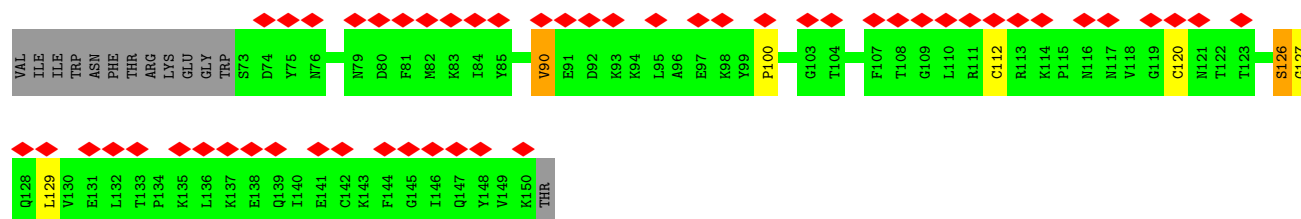


• Molecule 14: P11

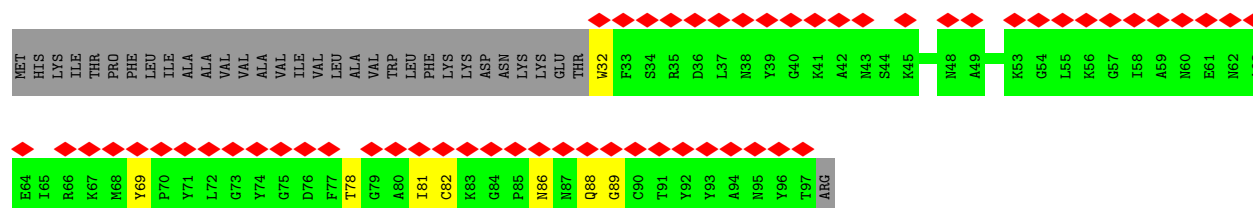


• Molecule 15: P12

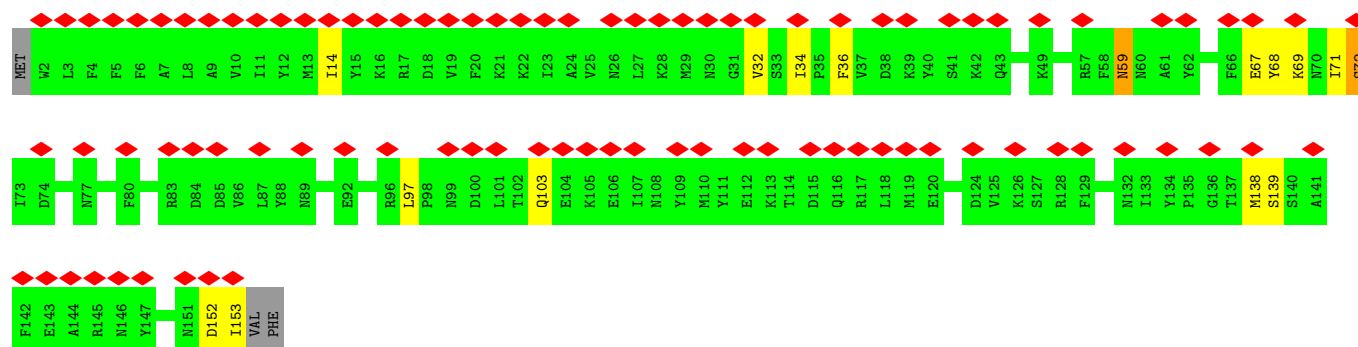
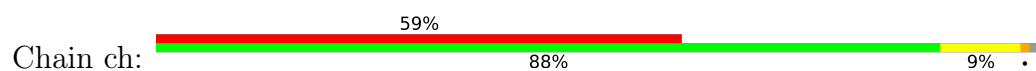




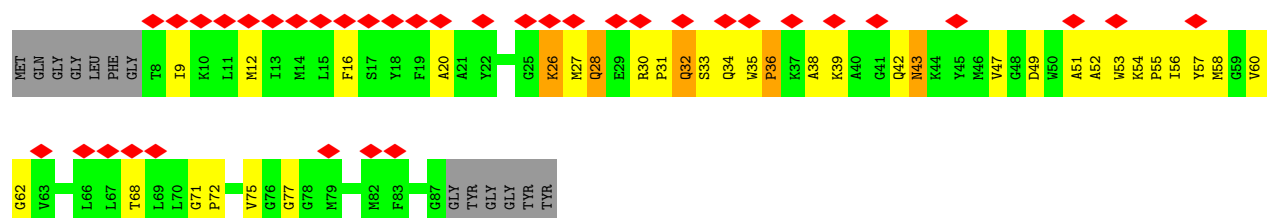
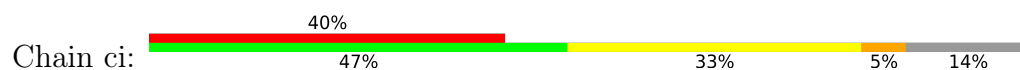
• Molecule 16: P13



• Molecule 17: P15

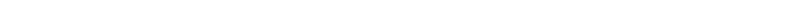


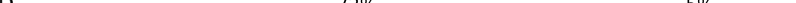
• Molecule 18: P16

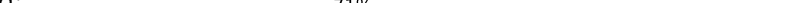


• Molecule 19: P17

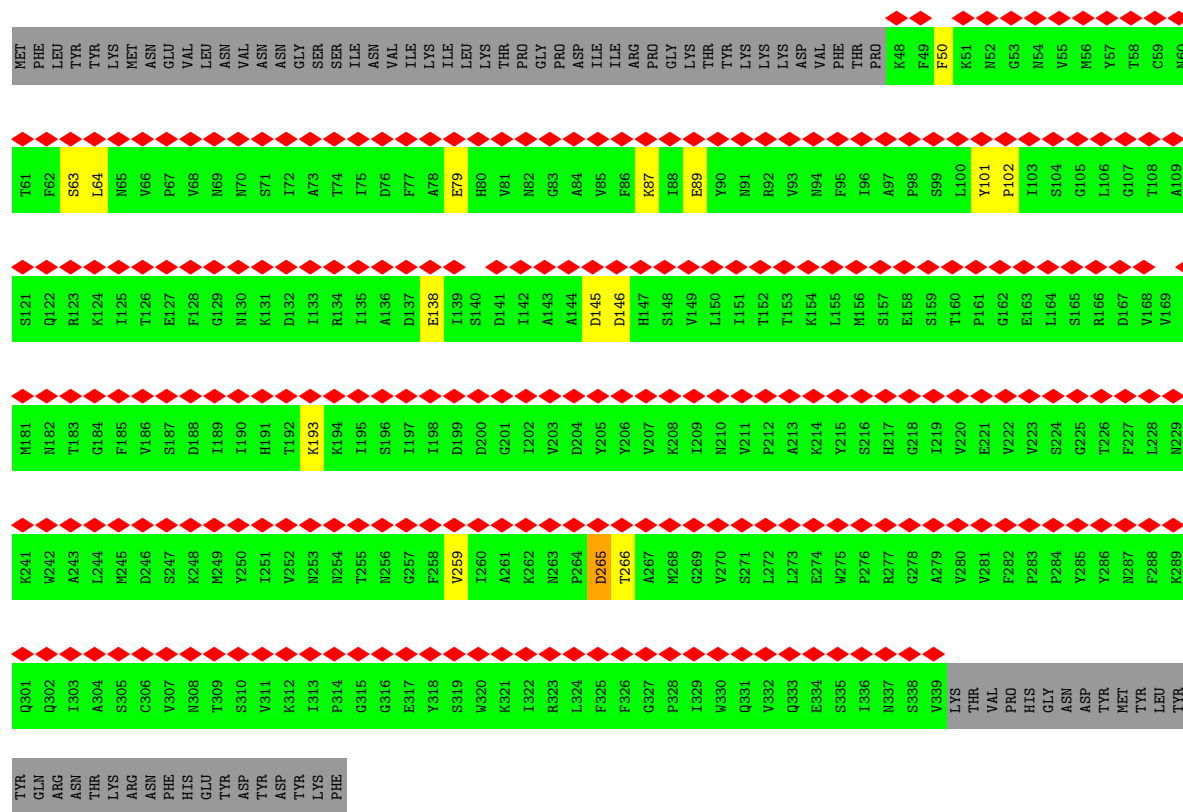
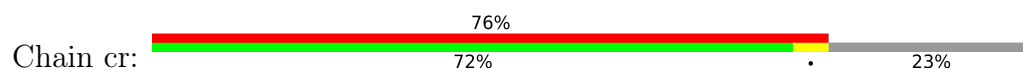


Chain co: 

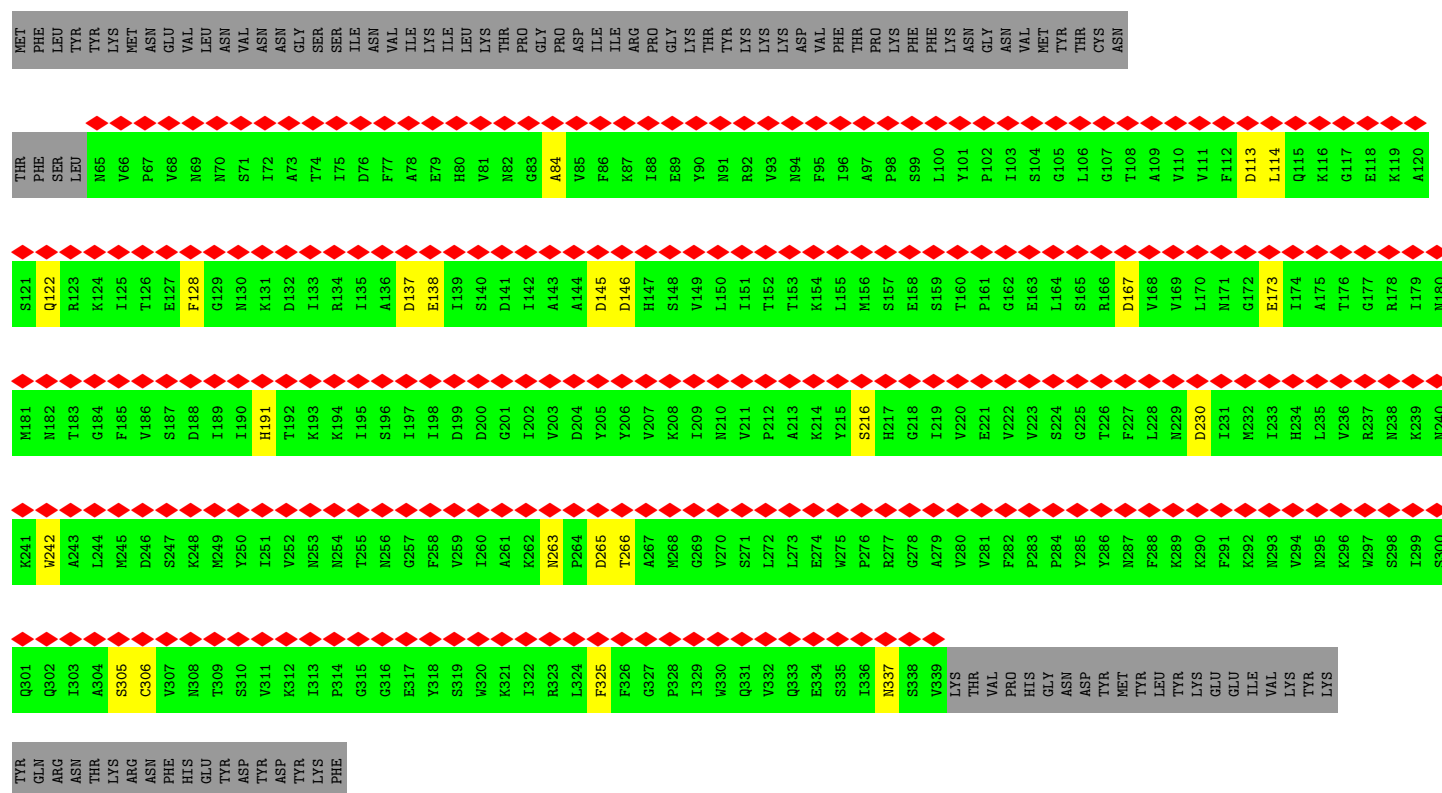
Chain cp: 

Chain eq: 

- Molecule 21: P19

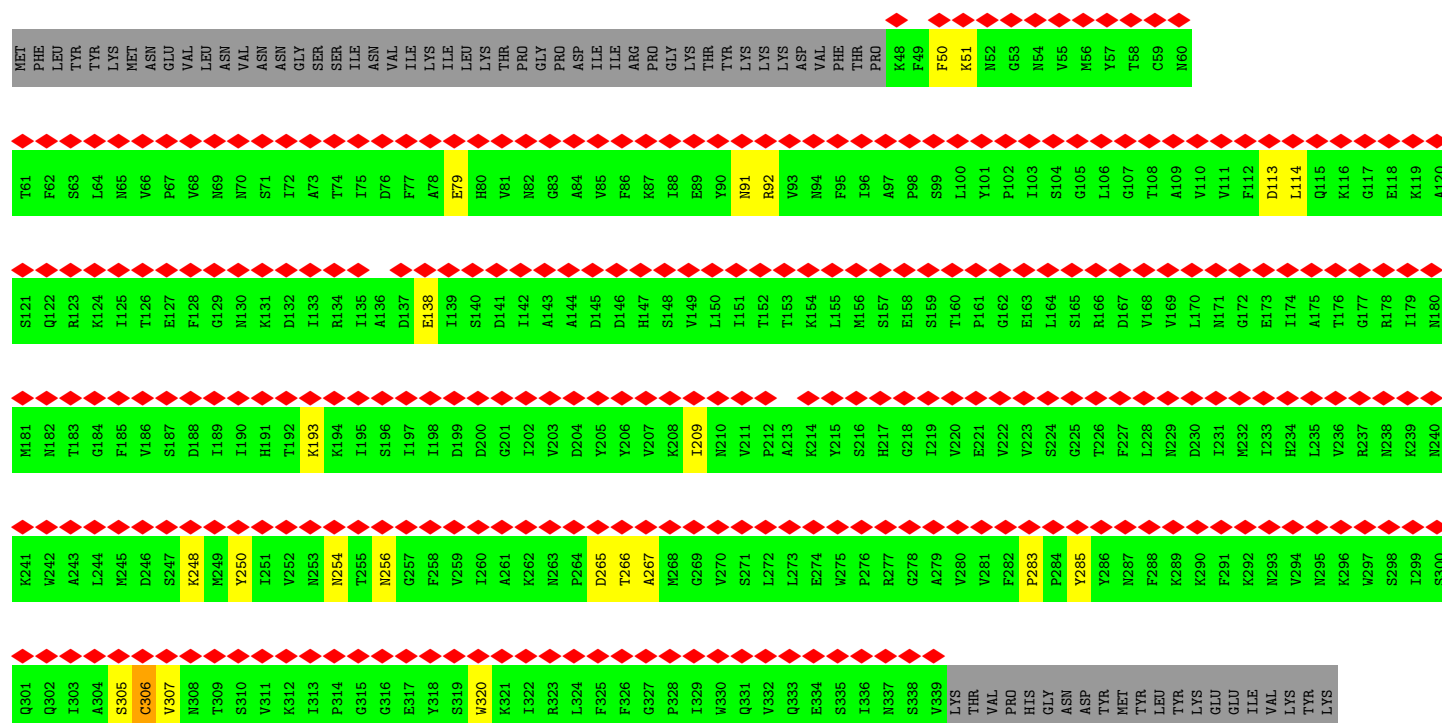


- Molecule 21: P19



Chain ct:

Category	Chain ct
Red	76%
Green	71%
Yellow	6%
Grey	23%



TYR
GLN
ARG
ASN
THR
LYS
LYS
ARG
ASN
PHE
HIS
GLU
TYR
ASP
TYR
PHE

● Molecule 21: P19

Chain cu: 

MET PHE LEU TYR TYR LYS MET ASN GLU VAL LEU ASN VAL ASN GLY SER SER ILE ASN VAL ILE LYS LYS LEU LYS THR THR PRO PRO GLY ASP ASP ILE ILE ARG PRO GLY LYS THR TYR LYS LYS ASP VAL PHE THR PRO LYS PHE PHE LYS ASN ASN VAL MET THR CYS N60

T61 F62 S63 L64 N65 V66 P67 V68 N69 N70 S71 I72 A73 T74 I75 D76 F77 A78 E79 H80 N82 G83 A84 V85 V86 F86 K87 I88 E89 Y90 N91 R92 L93 V93 N94 F95 I96 I97 A97 S98 S99 L100 Y101 P102 I103 I104 S104 G105 L106 G107 T108 A109 V110 V111 F112 D113 L114 Q115 K116 G117 E118 K119 A120

S121 Q122 K124 T125 T126 E127 F128 G129 N130 K131 D132 I133 R134 I135 A136 D137 E138 I139 S140 D141 I142 A143 A144 D145 D146 H147 S148 V149 L150 I151 T152 T153 K154 L155 M156 S157 E158 S159 T160 P161 G162 E163 L164 S165 R166 D167 V168 L169 N170 N171 G172 E173 I174 A175 T176 G177 I179 N180

M181 N182 T183 G184 F185 V186 S187 D188 N189 I190 H191 T192 K193 K194 I195 S196 I197 N198 D199 D200 G201 T202 V203 D204 Y205 Y206 V207 K208 I209 N210 V211 P212 A213 K214 Y215 S216 H217 G218 I219 V220 E221 V222 V223 S224 G225 T226 F227 L228 N229 D230 I231 M232 K233 H234 L235 V236 N237 N238 K239 N240

K241 W242 A243 L244 M245 S247 K248 W249 Y250 I251 V252 N253 N254 T255 N256 G257 F258 V259 T260 A261 K262 N263 P264 D265 T266 A267 M268 G269 V270 S271 L272 L273 E274 W275 P276 R277 G278 A279 V280 V281 F282 P283 P284 V285 Y286 N287 F288 K289 F291 K292 N293 V294 N295 K296 W297 S298 I299 S300

Q301 Q302 T303 A304 S305 C306 V307 N308 T309 S310 V311 K312 L313 P314 G315 G316 E317 Y318 S319 W320 K321 T322 R323 L324 F325 F326 G327 P328 I329 W330 Q331 V332 Q333 E334 S335 I336 N337 S338 V339 LYS THR VAL PRO HIS GLY ASN ASP TYR MET LEU TYR LYS GLU ILE VAL LYS LYS

TYR
GLN
ARG
ASN
THR
LYS
LYS
ARG
ASN
PHE
HIS
GLU
TYR
ASP
TYR
PHE

● Molecule 21: P19

Chain cv: 

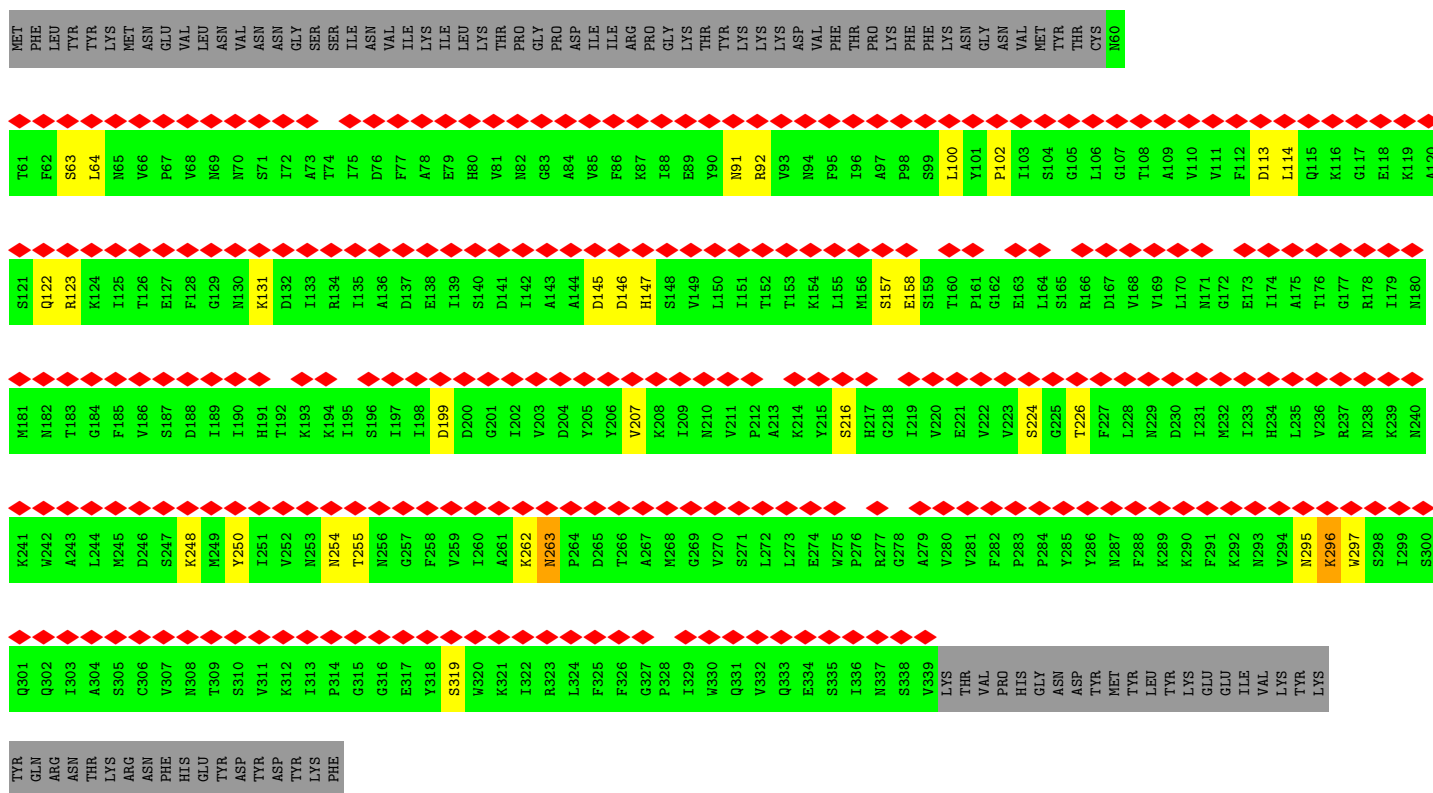
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T61 F62 S63 L64 N65 V66 P67 V68 N69 N70 S71 I72 A73 D76 F77 A78 E79 H80 N82 G83 A84 V85 V86 F86 K87 I88 E89 Y90 N91 R92 V93 L94 L95 P95 I96 I97 A97 S98 S99 L100 Y101 P102 I103 I104 S104 G105 L106 G107 T108 A109 V110 V111 F112 D113 L114 Q115 K116 G117 E118 S121 Q122

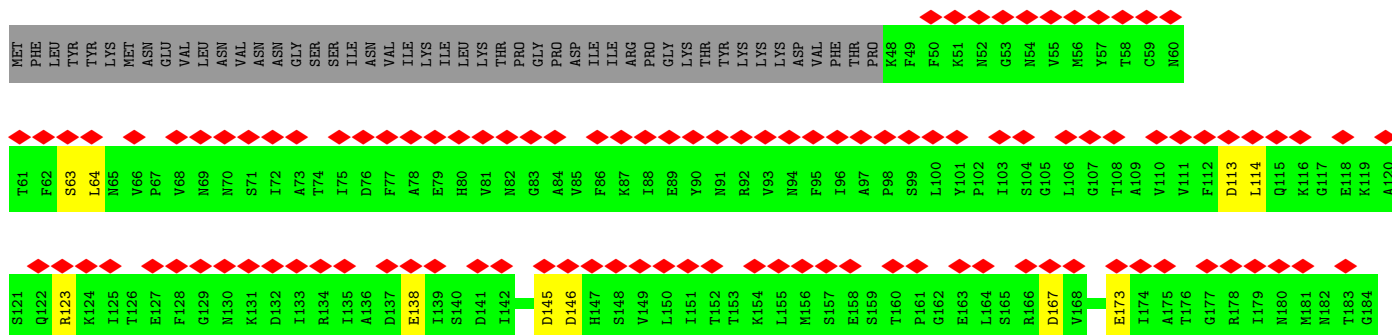
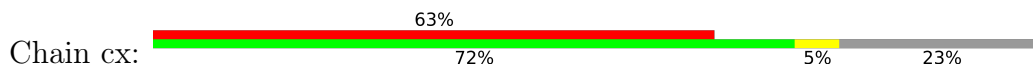
R123 K124 I125 T126 T127 F128 G129 N130 K131 D132 I133 R134 I135 A136 D137 E138 I139 S140 D141 I142 A143 A144 D145 D146 H147 S148 V149 L150 I151 T152 T153 K154 L155 M156 S157 E158 S159 T160 P161 G162 E163 L164 R166 D167 V168 L169 N170 N171 G172 E173 I174 A175 T176 G177 I179 N180 M181 N182

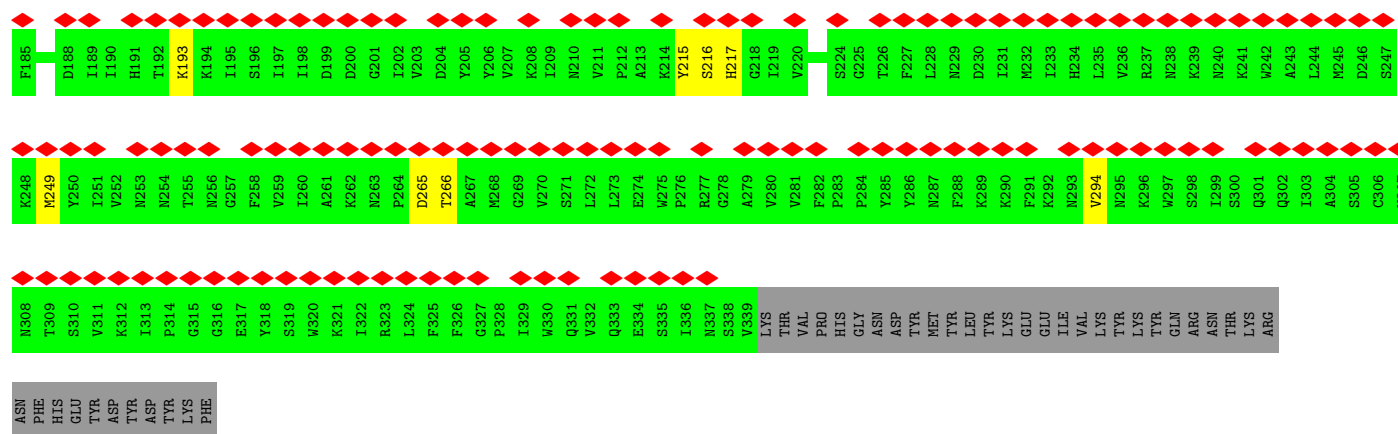
T183 G184 F185 V186 S187 D188 I189 N190 H191 T192 K193 K194 I195 S196 I197 N198 D199 D200 G201 I202 V203 D204 Y205 Y206 V207 K208 I209 N210 V211 P212 A213 K214 L215 M216 S217 E218 S219 T220 E221 V222 S224 G225 T226 F227 L228 N229 D230 I231 M232 K233 H234 L235 V236 N237 N238 K239 N240 K241 W242

- Molecule 21: P19

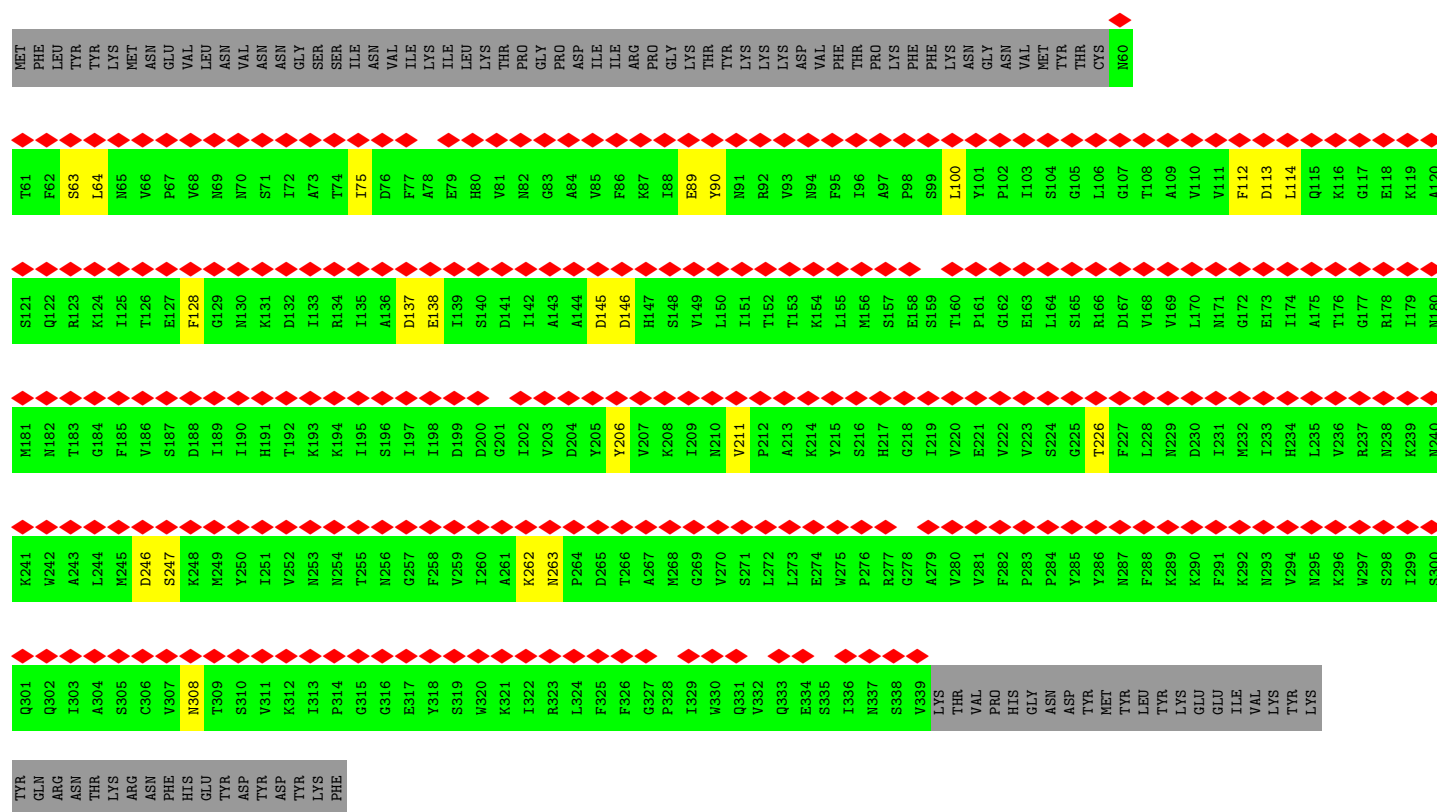
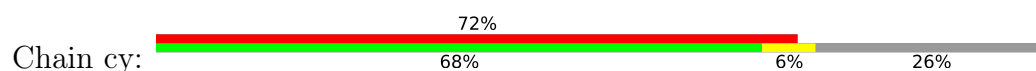


- Molecule 21: P19

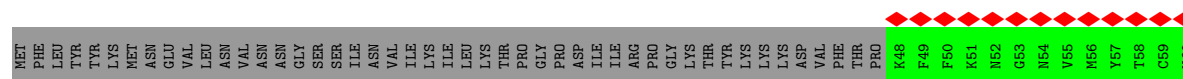
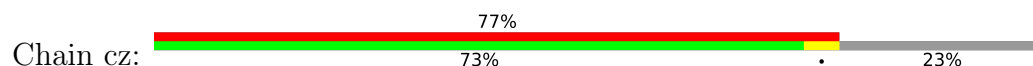




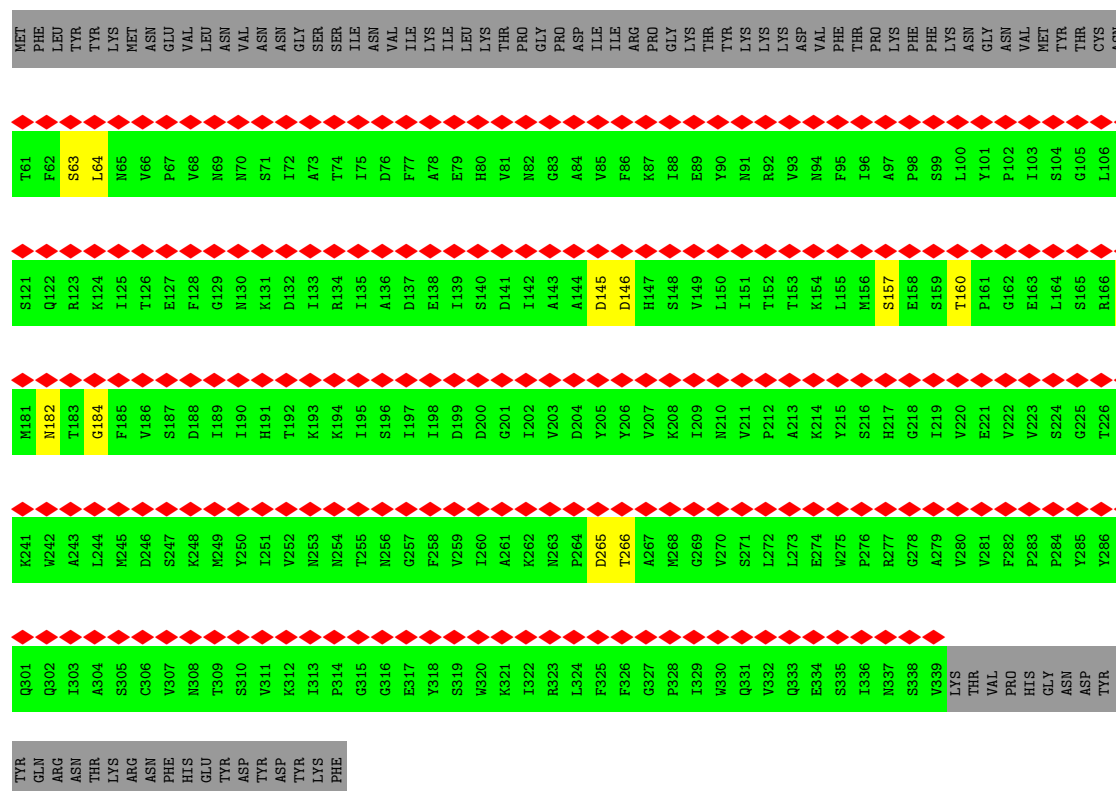
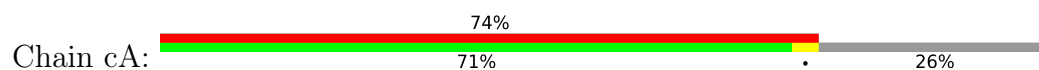
• Molecule 21: P19



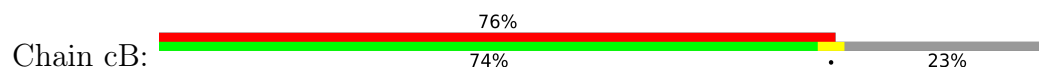
• Molecule 21: P19

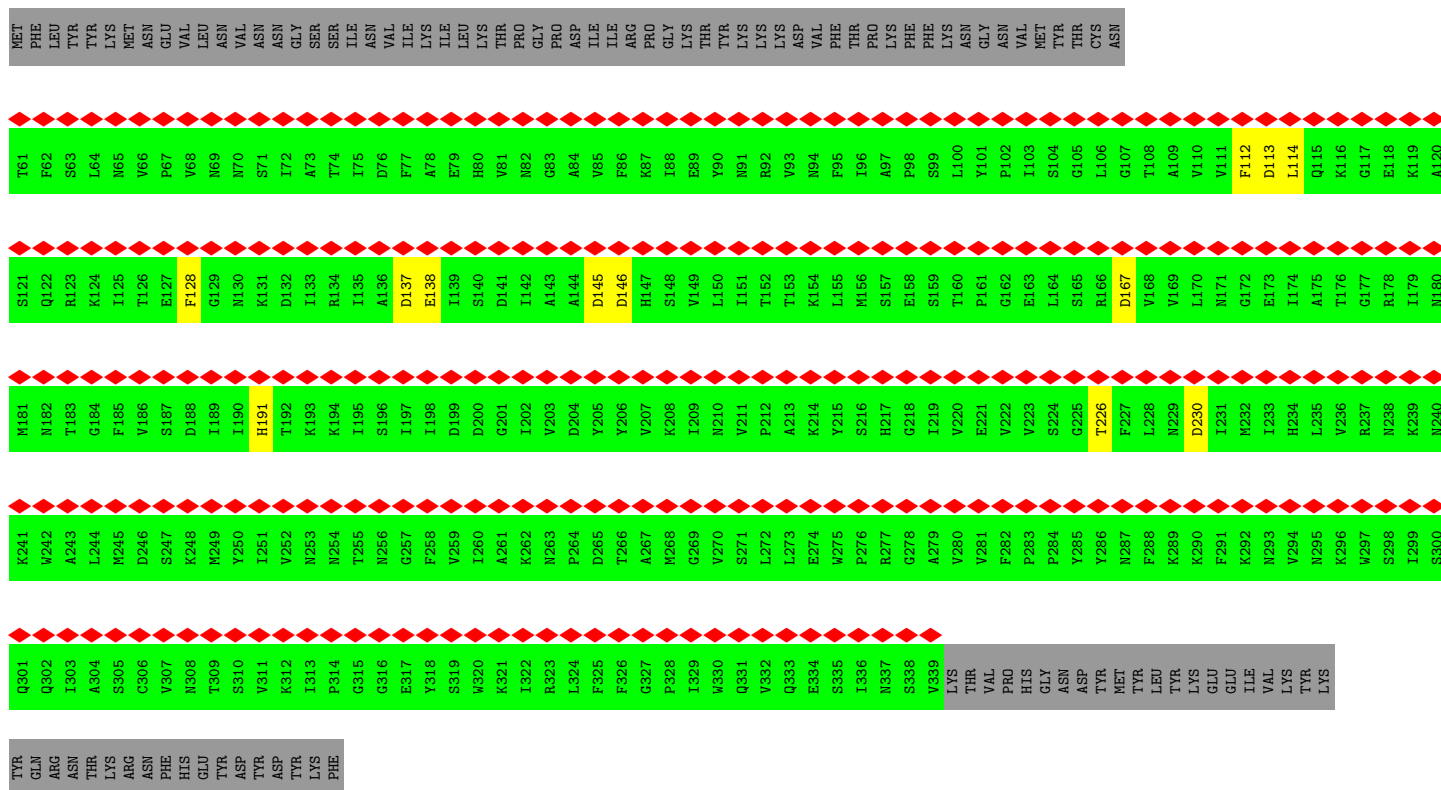


- Molecule 21: P19



- Molecule 21: P19

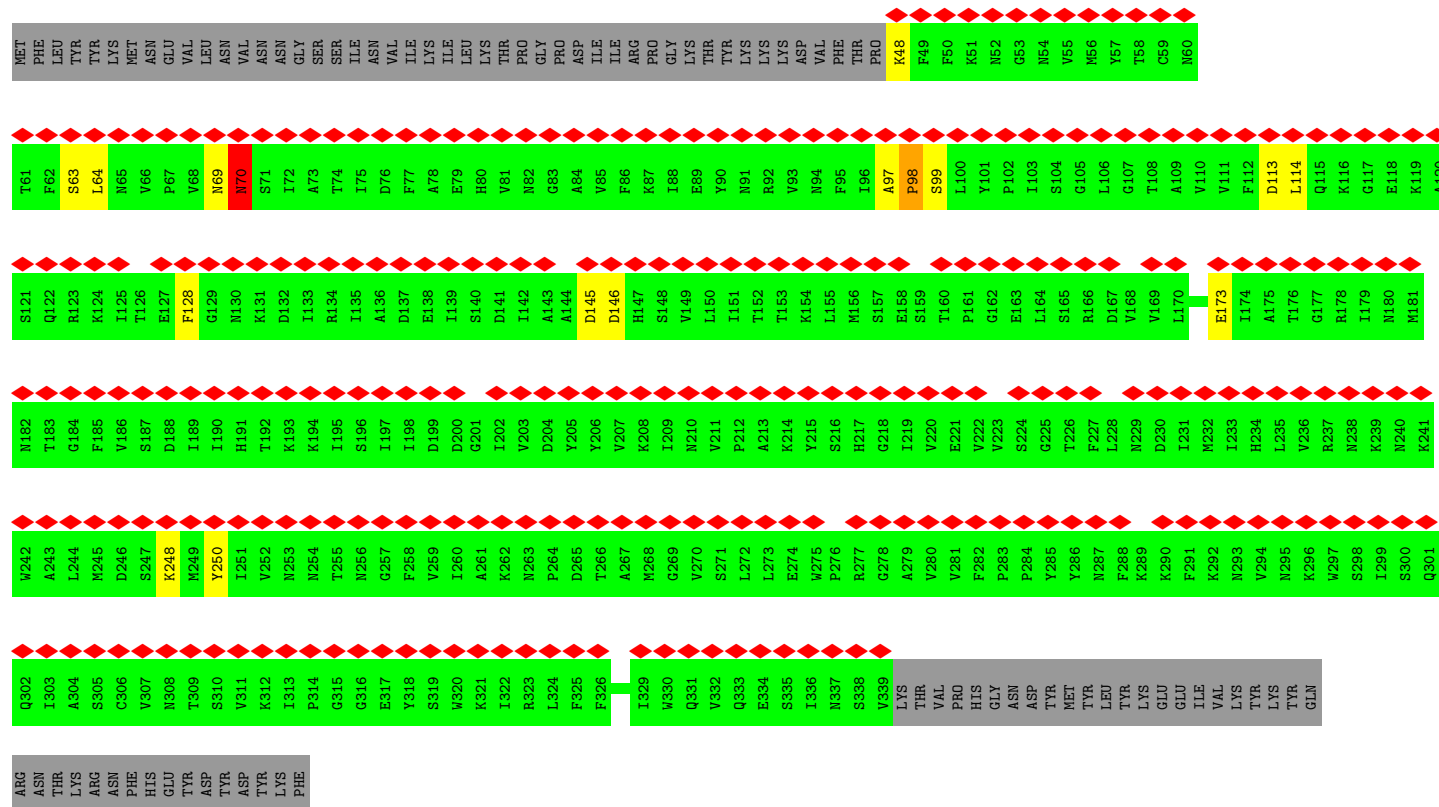
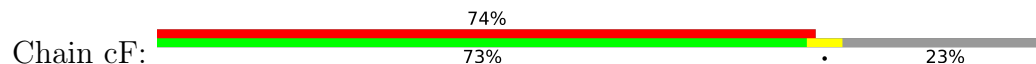




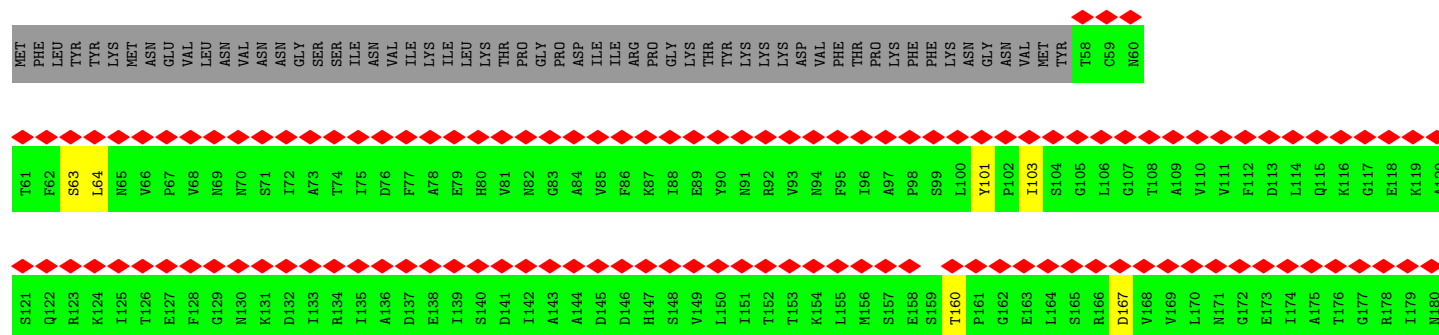
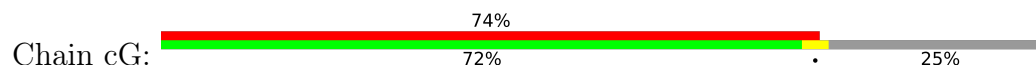
Chain cD:

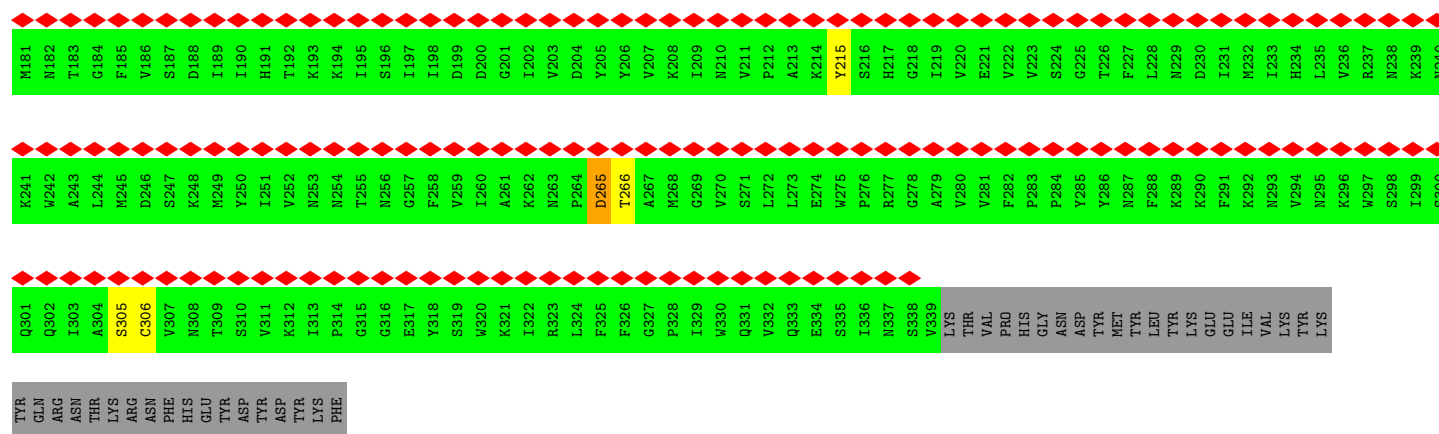


• Molecule 21: P19

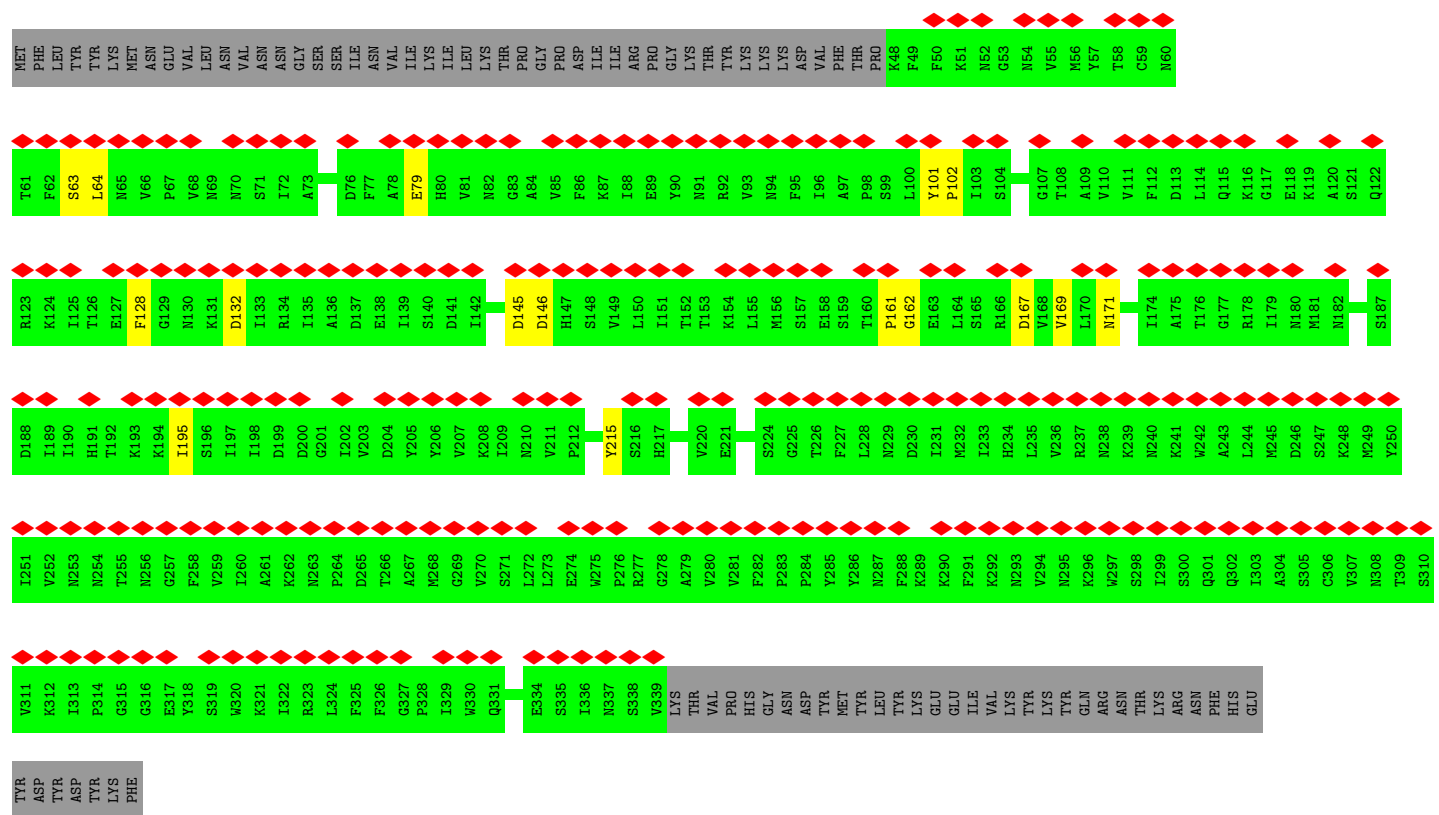
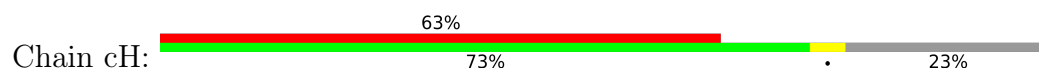


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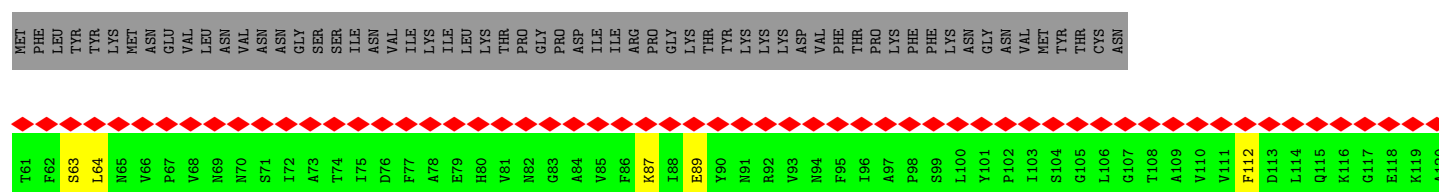
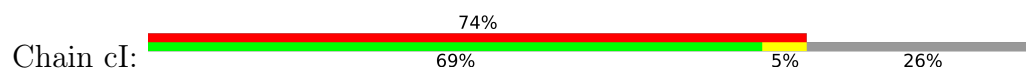




• Molecule 21: P19



• Molecule 21: P19



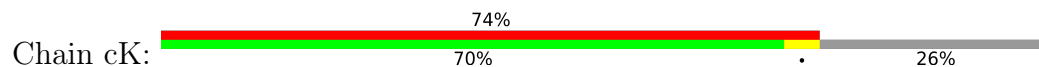
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Q122	N182	W242	Q302	GLN
R123	T183	W243	I303	ARG
K124	G184	L244	A304	THR
I125	F185	M245	S305	LYS
T126	V186	D246	C306	ARG
E127	S187	S247	V307	PHE
F128	D188	K248	N308	HIS
G129	I189	M249	T309	GLU
M130	I190	Y250	S310	ASP
K131	H191	I251	V311	TYR
D132	T192	V252	K312	ASP
R133	K193	N253	I313	LYS
K134	K194	N254	P314	PHE
I135	I195	T255	G315	
A136	S196	N256	G316	
D137	I197	F257	E317	
E138	I198	F258	Y318	
I139	D199	V259	S319	
S140	D200	I260	W320	
D141	G201	A261	K321	
I142	I202	K262	I322	
A143	V203	N263	R323	
A144	D204	P264	L324	
D145	Y205	D265	F325	
D146	Y206	T266	F326	
H147	V207	A267	G327	
S148	K208	M268	P328	
V149	I209	G269	I329	
L150	N210	V270	W330	
I151	V211	S271	Q331	
T152	P212	L272	V332	
T153	A213	L273	Q333	
K154	K214	E274	E334	
L155	Y215	W275	S335	
M156	S216	P276	I336	
S157	H217	R277	N337	
E158	G218	G278	S338	
S159	I219	A279	V339	
T160	V220	V280	LYS	
P161	E221	V281	THR	
G162	V222	F282	VAL	
E163	V223	P283	PRO	
L164	S224	P284	HIS	
S165	G225	Y285	GLY	
R166	T226	Y286	ASN	
D167	F227	N287	ASP	
V168	L228	F288	TYR	
V169	N229	K289	LEU	
L170	D230	K290	LYS	
M171	I231	F291	GLU	
G172	M232	K292	ILE	
E173	I233	N293	VAL	
I174	H234	V294	LYS	
A175	L235	N295	THR	
T176	V236	K296	LYS	
G177	R237	W297		
R178	N238	S298		
I179	K239	I299		
N180	N240	S300		

• Molecule 21: P19

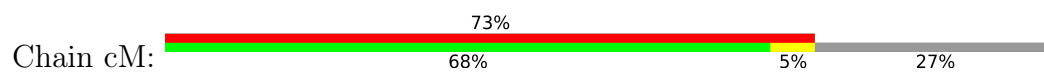


MET	T61	S121	M182	A243	I303	ARG
PHE	F62	Q122	T183	L244	A304	ASN
LEU	S63	R123	G184	M245	S305	THR
TYR	L64	K124	F185	D246	C306	LYS
LYS	N65	T125	V186	S247	V307	ARG
VAL	P67	E127	D188	K248	N308	PHE
ASN	V68	F128	I189	M249	T309	HIS
GLU	N69	G129	K193	Y250	S310	GLU
ASP	M70	M130	K194	I251	V311	TYR
ASP	S71	D132	I195	V252	K312	ASP
GLY	A73	I313	S196	N253	I313	LYS
SER	T74	R134	I197	N254	P314	LYS
ILE	I75	I135	I198	T255	G315	PHE
ASN	D76	A136	F258	G257	E317	
VAL	F77	D137	V259	F258	Y318	
ILE	A78	E138	I260	I261	S319	
LYS	E79	I139	I202	K262	W320	
LEU	H80	S140	D204	N263	K321	
LYS	N82	D141	Y205	P264	I322	
THR	C83	I142	Y206	D265	R323	
ARG	A84	D145	V207	T266	L324	
GLY	F85	D146	K208	A267	F325	
PRO	K87	H147	I209	M268	F326	
LYS	E88	S148	N210	G269	G327	
THR	I89	V149	V211	V270	P328	
LYS	Y90	L150	P212	S271	W330	
LYS	N91	I151	A213	L272	Q331	
LYS	A92	T152	K214	L273	V332	
LYS	Y93	T153	Y215	E274	I333	
ASP	N94	K154	S216	W275	S335	
VAL	F95	L155	H217	P276	L336	
PHE	I96	M156	G218	R277	N337	
THR	P97	S157	I219	G278	S338	
PRO	A97	E158	V220	A279	V339	
K48	P98	S159	E221	V280	LYS	
F49	S99	T160	V222	V281	THR	
F50	L100	P161	V223	F282	VAL	
A51	Y101	G162	S224	P283	PRO	
N52	P102	E163	G225	P284	HIS	
G53	I103	L164	T226	Y285	GLY	
N54	S104	S165	F227	Y286	ASN	
V55	G105	R166	D228	M287	TYR	
M56	L106	D167	N229	F288	MET	
V57	G107	V168	D230	K289	TYR	
T58	T108	V169	I231	F291	LEU	
C59	A109	M171	M232	K292	LYS	
N60	V110	G172	I233	H234	GLU	
	V111	E173	H235	V294	ILE	
	F112	I174	L236	N295	VAL	
	D113	A175	V236	K296	LYS	
	Q115	T176	R237	W297	TYR	
	K116	G177	N238	S298	LYS	
	E117	R178	K239	I299	GLN	
	E118	I179	N240	S300		
	K119	M180	Q301	Q302		
	A120	M181				

• Molecule 21: P19

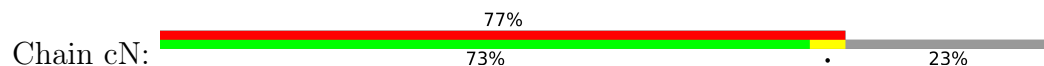


MET	ARG
PHE	ASN
LEU	THR
TYR	LYS
LYS	ARG
LYS	ASN
ASN	PHE
ASN	HIS
GLU	GLU
GLU	TYR
VAL	ASP
LEU	TYR
LEU	ASP
ASN	LYS
ASN	PHE



TYR	GLN	ARG	ASN	THR	LYS	ARG	ASN	PHE	HIS	GLU	TYR	ASP	TYR	ASP	LYS	TYR	PHE																																										
Q301	Q302	I303	A304	S305	C306	V307	N308	T309	S310	V311	K312	I313	P314	G315	G316	E317	Y318	S319	W320	K321	I322	K323	L324	F325	F326	G327	P328	I329	W330	Q331	V332	Q333	E334	S335	I336	N337	S338	V339																					
LYS	THR	VAL	PRO	HIS	GLY	ASN	ASP	TYR	MET	TYR	LEU	LYS	GLU	ILE	VAL	LYS	TYR	LYS	GLU	GLY	ASN	CYS	ASN																																				
S121	Q122	R123	K124	I125	T126	E127	F128	G129	N130	K131	D132	I133	R134	I135	A136	D137	E138	I139	S140	D141	I142	A143	A144	D145	D146	H147	S148	V149	L150	I151	T152	T153	K154	L155	M156	S157	E158	S159	T160	P161	G162	E163	L164	S165	R166	D167	V168	V169	L170	N171	G172	D173	E174	A175	T176	G177	R178	I179	N180
M181	N182	T183	G184	F185	V186	S187	D188	I189	I190	H191	T192	K193	K194	I195	S196	I197	I198	D199	D200	G201	T202	V203	D204	Y205	Y206	V207	K208	I209	N210	V211	P212	A213	K214	Y215	S216	H217	G218	I219	V220	E221	V222	V223	S224	G225	T226	F227	L228	N229	D230	I231	M232	I233	H234	L235	V236	R237	N238	K239	N240
K241	W242	A243	L244	M245	D246	S247	K248	M249	Y250	I251	V252	M253	N254	T255	N256	G257	F258	V259	L260	A261	K262	M263	P264	D265	T266	A267	M268	G269	V270	S271	L272	L273	E274	W275	P276	R277	G278	A279	V280	V281	F282	P283	P284	Y285	Y286	N287	F288	K289	L290	F291	K292	N293	V294	N295	W297	S298	I299	S300	
THR	PHE	LEU	TYR	LYS	MET	ASN	VAL	LEU	ASN	VAL	ASN	ASN	GLY	SER	ILE	ASN	VAL	ILE	LYS	ILE	LEU	LYS	THR	PRO	GLY	PRO	ARG	ARG	ILE	ILE	ASP	PRO	GLY	LYS	THR	TYR	LYS	LYS	ASP	VAL	PHE	THR	PRO	LYS	PHE	PHE	LYS	ASN	GLY	ASN	VAL	MET	TYR	THR	CYS	ASN			

• Molecule 21: P19



Q301	Q302	I303	A304	S305	C306	V307	N308	T309	S310	V311	K312	I313	P314	G315	G316	E317	Y318	S319	W320	K321	I322	K323	L324	F325	F326	G327	P328	I329	W330	Q331	V332	Q333	E334	S335	I336	N337	S338	V339	LYS	THR	VAL	PRO	HIS	GLY	ASN	ASP	TYR	MET	TYR	LEU	LYS	GLU	ILE	VAL	LYS	TYR	LYS		
K241	W242	A243	L244	M245	D246	S247	K248	M249	Y250	I251	V252	M253	N254	T255	N256	G257	F258	V259	L260	A261	K262	M263	P264	D265	T266	A267	M268	G269	V270	S271	L272	L273	E274	W275	P276	R277	G278	A279	V280	V281	F282	P283	P284	Y285	Y286	N287	F288	K289	L290	F291	K292	N293	V294	N295	K296	W297	S298	I299	S300
M181	N182	T183	G184	F185	V186	S187	D188	I189	I190	H191	T192	K193	K194	I195	S196	I197	I198	D199	D200	G201	T202	V203	D204	Y205	Y206	V207	K208	I209	N210	V211	P212	A213	K214	Y215	S216	H217	G218	I219	V220	E221	V222	V223	S224	G225	T226	F227	L228	N229	D230	I231	M232	I233	H234	L235	V236	R237	N238	K239	N240
S121	Q122	R123	K124	I125	T126	E127	F128	G129	N130	K131	D132	I133	R134	I135	A136	D137	E138	I139	S140	D141	I142	A143	A144	D145	D146	H147	S148	V149	L150	I151	T152	T153	K154	L155	M156	S157	E158	S159	T160	P161	G162	E163	L164	S165	R166	D167	V168	V169	L170	N171	G172	D173	E174	A175	T176	G177	R178	I179	N180
T61	F62	S63	L64	N65	V66	P67	V68	N69	N70	S71	I72	A73	T74	I75	D76	F77	A78	E79	H80	V81	N82	G83	A84	V85	F86	K87	I88	E89	Y90	N91	R92	V93	N94	F95	I96	A97	P98	S99	L100	Y101	P102	I103	S104	G105	L106	G107	T108	A109	V110	V111	F112	D113	L114	Q115	K116	G117	E118	K119	A120
MET	PHE	LEU	TYR	LYS	MET	ASN	GLU	LEU	ASN	VAL	ASN	GLY	SER	SER	ILE	ASN	VAL	ILE	LYS	THR	PRO	GLY	PRO	ASP	ILE	ILE	ARG	PRO	GLY	LYS	THR	TYR	LYS	LYS	ASP	VAL	PHE	THR	PRO	K48	F49	F50	K51	N52	G53	N54	V55	M56	Y57	T58	C59	N60							

TYR	GLN	ARG	ASN	THR	LYS	ARG	ASN	PHE	GLU	HIS	ASP	TYR	ASP	TYR	LYS	PHE
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● Molecule 22: P20



MET	ASN	GLN	TYR	ASN	LYS	ARG	ASN	PHE	GLU	HIS	ASP	TYR	ASP	TYR	LYS	PHE
F7	L8	N9	D10	P11	I12	M13	I14	R15	T16	M17	I18	V19	Y20	G21	L23	S24
A25	Y27	F28	T29	G30	N31	G32	A33	A34	L35	T36	GLN	PRO	ILE	ILE	ALA	ASN
ASN	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

ASN	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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LEU	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ILE	ASN	LEU	PHE	GLY	ASN	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ALA	THR	PHE	ASP	THR	ALA	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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VAL	GLN	SER	MET	ASN	ILE	GLY	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ASP	ALA	TYR	GLY	ASN	THR	GLN	PHE	THR	GLU	SER	THR	THR	THR	THR	THR	THR
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ASN	VAL	ILE	TYR	SER	ASN	VAL	PHE	THR	GLY	SER	THR	THR	THR	THR	THR	THR
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SER	ASN	LEU	ASN	ALA	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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SER	ILE	VAL	THR	LEU	ASN	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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SER	ALA	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ILE	VAL	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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GLU	ASN	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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SER	LEU	GLY	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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LEU	THR	THR	GLU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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LEU	THR	VAL	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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LEU	THR	ALA	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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ARG	ALA	PHE	VAL	GLY	ASN	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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- Molecule 22: P20

[illegible]





SER THR SER PHE PHE GLY LEU MET VAL THR ALA VAL GLN THR VAL

Chain di: 98%

LEU	THR	VAL	SER	ASN	VAL	I LE	ASN	VAL	GLN	ASN	LEU	THR	ALA	ASN	VAL	GLY	ASN	I LE	TRP	GLN	ALA	VAL	SER	ASN	I LE	GLN	SER	MET	THR	THR	ALA	ASN	PHE	THR	ASN	THR	THR	THR	I LE	I LE	ASN	SER	PHE	THR	THR	TVR	SER	ASN	ARG	LEU	I LE	ALA	THR	THR	ASN	THR
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ASN	PHE	SER	ILE	ASN	CYS	LEU	ILE	ILE	ASN	ALA	THR	THR	THR	GLY	LEU	GLU	VAL	ILE	ILE	TYR	ASN	PRO	PHE	GLY	ILE	ALA	ALA	SER	SER	LEU	SER	SER	SER	THR	THR	PRO	GLU	LEU	LEU	TYR	PHE	THR	ILE	THR	THR	SER	ILE	ALA	THR	SER	THR	GLN
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- Molecule 23: P21

[illegible]

SER	GLY	PRO	THR	THR	THR	GLN	SER	ILE	ASN
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

ASN	PHE	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

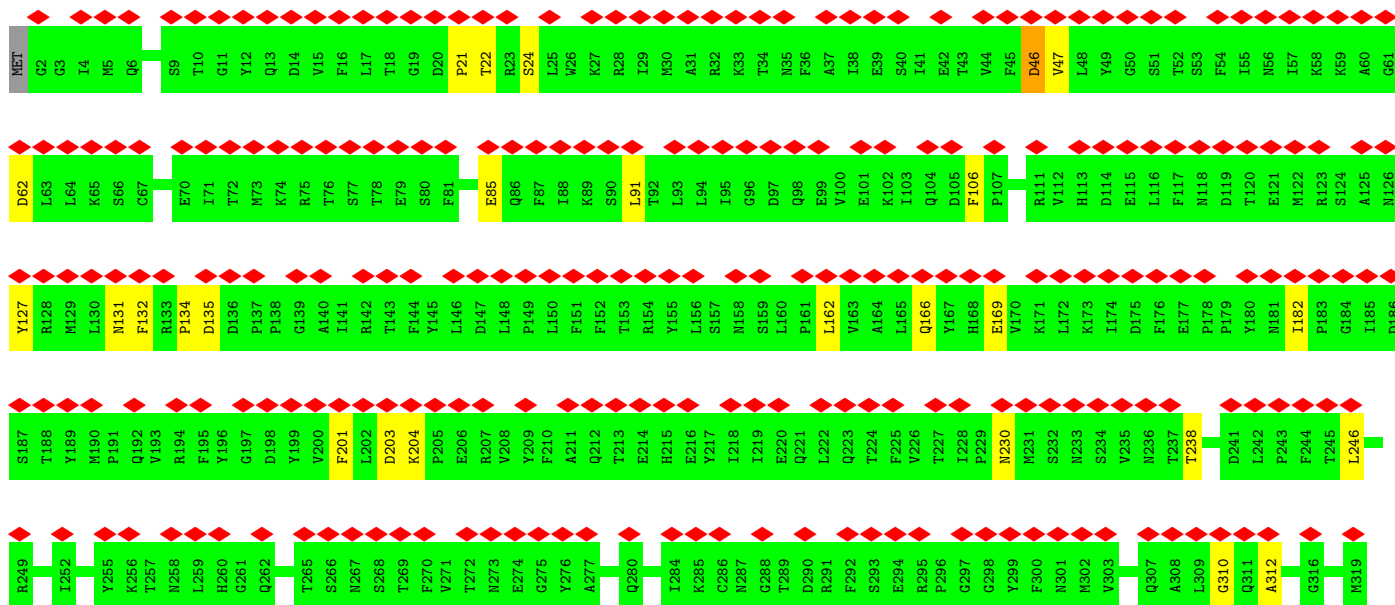
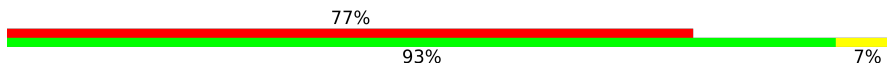
● Molecule 23: P21

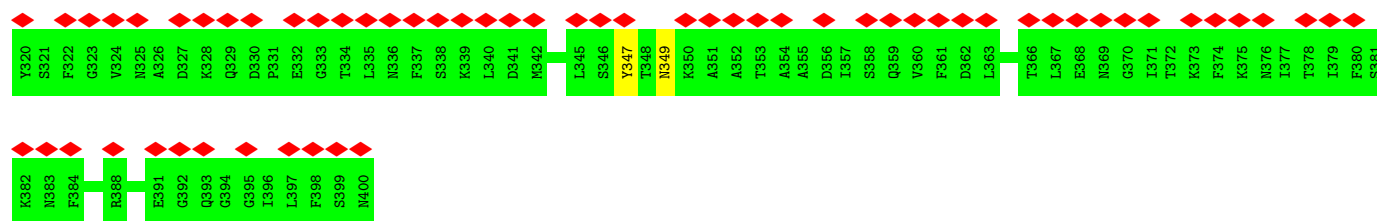


MET	SER	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

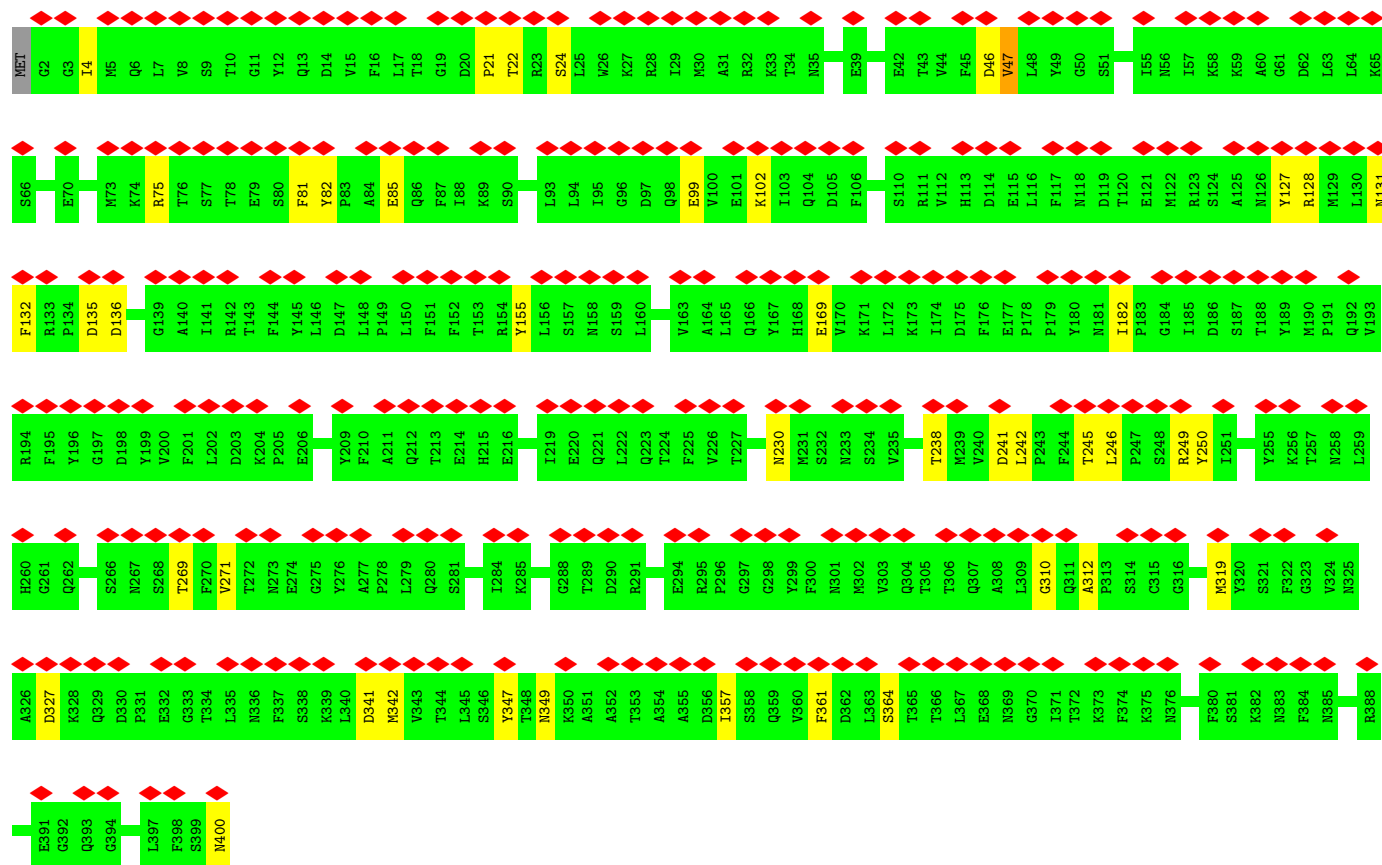
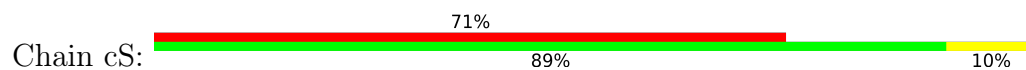
- Molecule 24: MCPv5

Chain cR:

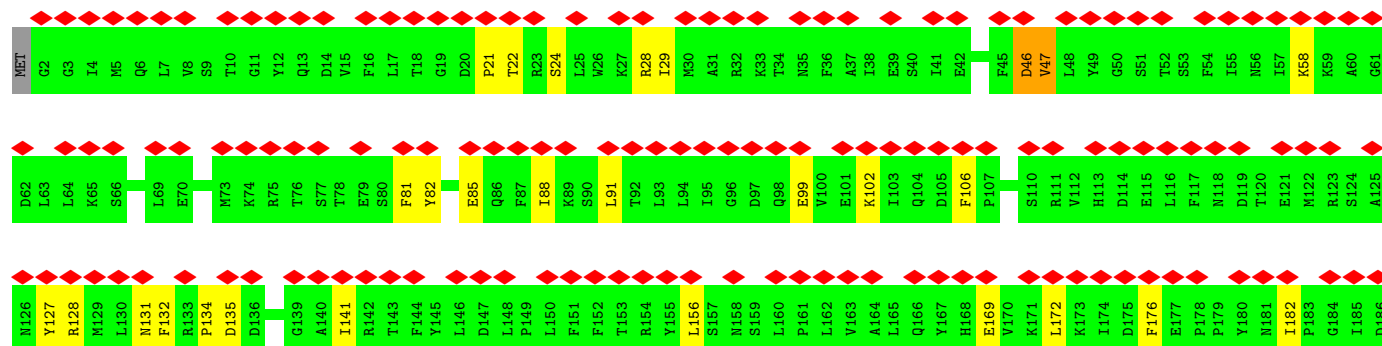
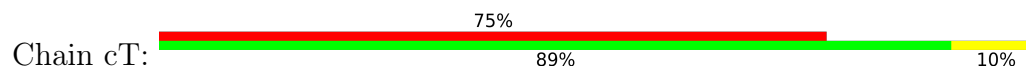


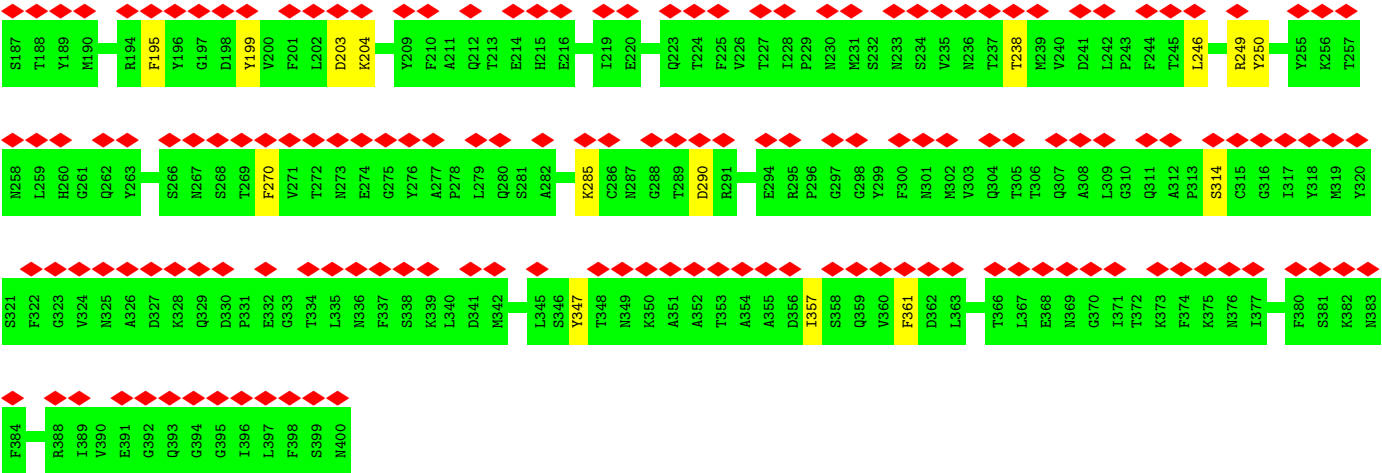


• Molecule 24: MCPv5

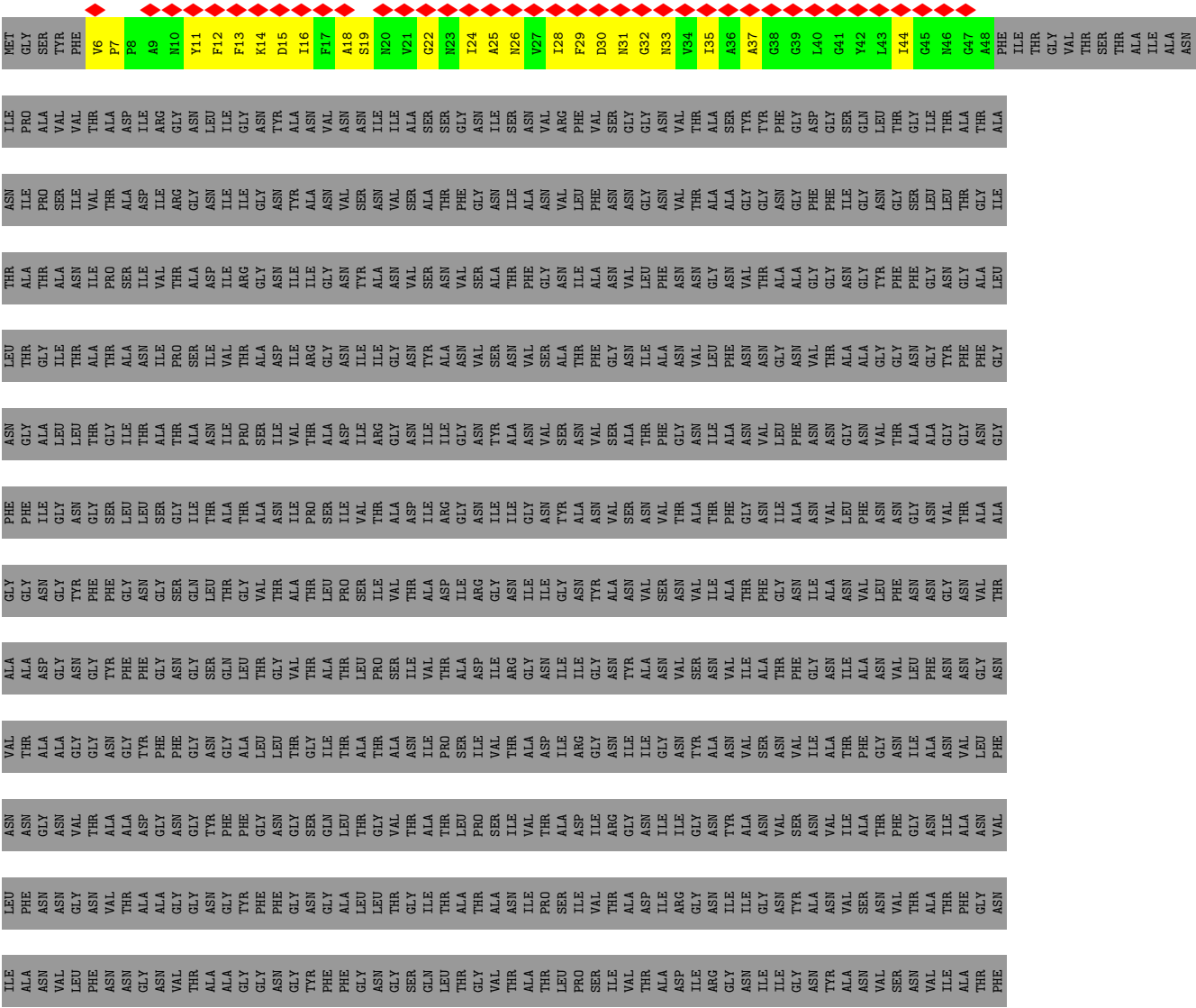


• Molecule 24: MCPv5





● Molecule 25: P22



- Molecule 25: P22

[illegible]



- Molecule 26: P23

98%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56500	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)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.269	Depositor
Minimum map value	-1.541	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.55	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	aA	0.51	0/3468	0.88	8/4728 (0.2%)
1	aB	0.56	3/3468 (0.1%)	0.97	15/4728 (0.3%)
1	aC	0.58	0/3473	0.95	13/4735 (0.3%)
1	aD	0.60	1/3460 (0.0%)	1.06	21/4717 (0.4%)
1	aE	0.53	0/3473	0.90	10/4735 (0.2%)
1	aF	0.54	1/3460 (0.0%)	0.88	7/4717 (0.1%)
1	aG	0.52	0/3468	0.86	3/4728 (0.1%)
1	aH	0.51	0/3460	0.91	13/4717 (0.3%)
1	aI	0.53	1/3468 (0.0%)	0.91	16/4728 (0.3%)
1	aJ	0.56	0/3473	0.92	8/4735 (0.2%)
1	aK	0.51	0/3473	0.96	13/4735 (0.3%)
1	aL	0.53	0/3465	0.91	7/4724 (0.1%)
1	aM	0.52	0/3473	0.91	7/4735 (0.1%)
1	aN	0.54	0/3468	0.91	7/4728 (0.1%)
1	aO	0.53	0/3473	0.89	12/4735 (0.3%)
1	aP	0.51	0/3473	0.89	10/4735 (0.2%)
1	aQ	0.55	0/3460	0.91	5/4717 (0.1%)
1	aR	0.54	0/3473	0.94	13/4735 (0.3%)
1	aS	0.53	0/3473	0.89	5/4735 (0.1%)
1	aT	0.53	0/3473	0.87	10/4735 (0.2%)
1	aU	0.53	0/3473	0.89	3/4735 (0.1%)
1	aV	0.52	0/3473	0.85	5/4735 (0.1%)
1	aW	0.51	0/3473	0.94	10/4735 (0.2%)
1	aX	0.53	0/3468	0.92	11/4728 (0.2%)
1	aY	0.53	0/3473	0.90	9/4735 (0.2%)
1	aZ	0.54	0/3473	0.90	2/4735 (0.0%)
1	aa	0.91	0/3452	1.24	31/4707 (0.7%)
1	ab	0.91	0/3473	1.26	27/4735 (0.6%)
1	ac	0.90	0/3473	1.24	29/4735 (0.6%)
1	ad	0.54	0/3473	0.91	9/4735 (0.2%)
1	ae	0.51	0/3473	0.86	5/4735 (0.1%)
1	af	0.52	0/3473	0.91	12/4735 (0.3%)
1	ag	0.53	2/3473 (0.1%)	0.87	6/4735 (0.1%)
1	ah	0.51	0/3473	0.89	5/4735 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ai	0.52	0/3473	0.89	12/4735 (0.3%)
1	aj	0.53	0/3473	0.90	13/4735 (0.3%)
1	ak	0.51	0/3473	0.85	7/4735 (0.1%)
1	al	0.51	0/3465	0.91	11/4724 (0.2%)
1	am	0.53	1/3473 (0.0%)	0.93	10/4735 (0.2%)
1	an	0.53	0/3465	0.86	8/4724 (0.2%)
1	ao	0.52	0/3468	0.89	4/4728 (0.1%)
1	ap	0.52	0/3473	0.93	11/4735 (0.2%)
1	aq	0.52	0/3473	0.90	10/4735 (0.2%)
1	ar	0.53	0/3460	0.91	6/4717 (0.1%)
1	as	0.52	0/3473	0.90	11/4735 (0.2%)
1	at	0.52	1/3473 (0.0%)	0.83	5/4735 (0.1%)
1	au	0.51	0/3460	0.89	10/4717 (0.2%)
1	av	0.52	0/3473	0.89	3/4735 (0.1%)
1	aw	0.52	0/3473	0.94	11/4735 (0.2%)
1	ax	0.53	0/3460	0.84	6/4717 (0.1%)
1	ay	0.53	1/3468 (0.0%)	0.83	5/4728 (0.1%)
1	az	0.53	0/3460	0.85	4/4717 (0.1%)
1	ba	0.55	0/3473	0.92	6/4735 (0.1%)
1	bb	0.52	0/3473	0.85	4/4735 (0.1%)
1	bc	0.53	0/3473	0.93	10/4735 (0.2%)
1	bd	0.52	0/3473	0.91	5/4735 (0.1%)
1	be	0.52	0/3473	0.91	14/4735 (0.3%)
1	bf	0.51	0/3473	0.95	17/4735 (0.4%)
1	bg	0.53	1/3473 (0.0%)	0.89	6/4735 (0.1%)
1	bh	0.53	0/3473	0.85	7/4735 (0.1%)
1	bi	0.51	0/3473	0.89	14/4735 (0.3%)
1	bj	0.53	1/3473 (0.0%)	0.86	3/4735 (0.1%)
1	bk	0.51	0/3473	0.84	2/4735 (0.0%)
1	bl	0.51	0/3473	0.87	11/4735 (0.2%)
1	bm	0.53	0/3473	0.93	8/4735 (0.2%)
1	bn	0.50	0/3460	0.86	0/4717
1	bo	0.52	0/3473	0.87	6/4735 (0.1%)
1	bp	0.55	0/3473	0.97	12/4735 (0.3%)
1	bq	0.54	0/3473	0.91	5/4735 (0.1%)
1	br	0.53	0/3473	0.90	4/4735 (0.1%)
1	bs	0.53	0/3473	0.89	3/4735 (0.1%)
1	bt	0.52	0/3468	0.90	15/4728 (0.3%)
2	bA	0.56	1/4196 (0.0%)	0.94	20/5743 (0.3%)
2	bB	0.55	1/4208 (0.0%)	0.72	11/5759 (0.2%)
2	bu	0.87	0/4208	1.18	31/5759 (0.5%)
2	bv	0.86	0/4208	1.16	28/5759 (0.5%)
2	bw	0.85	1/4208 (0.0%)	1.16	28/5759 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	bx	0.86	1/4191 (0.0%)	1.19	32/5736 (0.6%)
2	by	0.85	0/4208	1.16	32/5759 (0.6%)
2	bz	0.86	1/4147 (0.0%)	1.19	26/5676 (0.5%)
3	bC	0.52	0/4020	0.66	2/5461 (0.0%)
4	bD	0.57	1/3248 (0.0%)	0.92	16/4423 (0.4%)
4	bF	0.56	1/3248 (0.0%)	0.92	15/4423 (0.3%)
4	cX	0.55	0/3244	0.96	15/4418 (0.3%)
4	cZ	0.55	0/3244	0.95	14/4418 (0.3%)
4	dd	0.55	0/3248	0.96	18/4423 (0.4%)
4	df	0.56	0/3244	0.95	13/4418 (0.3%)
4	dj	0.55	0/3248	0.94	14/4423 (0.3%)
4	dk	0.55	0/3248	0.94	14/4423 (0.3%)
4	dl	0.55	0/3248	0.94	14/4423 (0.3%)
4	dp	0.55	0/3248	0.96	16/4423 (0.4%)
4	dr	0.55	0/3248	0.95	14/4423 (0.3%)
5	bE	0.56	0/3218	0.96	14/4365 (0.3%)
5	cY	0.56	0/3218	0.98	17/4365 (0.4%)
5	de	0.56	0/3218	0.97	17/4365 (0.4%)
5	dq	0.56	0/3218	1.00	19/4365 (0.4%)
6	bG	0.54	0/3957	0.62	3/5413 (0.1%)
7	bH	0.63	2/3333 (0.1%)	1.13	35/4542 (0.8%)
8	bI	0.70	1/1120 (0.1%)	1.29	10/1517 (0.7%)
8	bJ	0.70	0/1172	1.32	20/1590 (1.3%)
8	bK	0.68	0/909	1.32	18/1228 (1.5%)
9	bL	0.62	0/537	1.24	8/720 (1.1%)
9	bM	0.67	0/537	1.13	7/720 (1.0%)
9	bN	0.67	0/530	1.27	6/710 (0.8%)
9	bO	0.60	0/530	1.08	1/710 (0.1%)
10	bP	0.77	0/1155	1.11	6/1573 (0.4%)
11	bQ	0.79	0/1307	1.41	26/1775 (1.5%)
12	bR	0.62	0/1270	1.05	8/1716 (0.5%)
13	bS	0.18	0/1534	0.53	4/2075 (0.2%)
14	bT	0.64	0/382	1.50	9/520 (1.7%)
14	bU	0.77	0/436	1.25	5/596 (0.8%)
14	bV	0.57	0/428	1.06	2/585 (0.3%)
14	bW	0.59	0/416	1.16	5/569 (0.9%)
14	bX	0.65	0/319	1.17	2/435 (0.5%)
14	bY	0.71	0/593	1.41	9/810 (1.1%)
14	bZ	0.65	0/416	1.12	2/569 (0.4%)
14	ca	0.60	0/416	1.07	0/569
14	cb	0.75	1/416 (0.2%)	1.39	6/569 (1.1%)
14	cc	0.67	1/665 (0.2%)	1.16	8/911 (0.9%)
14	cd	0.75	0/601	1.41	14/821 (1.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
14	ce	0.66	0/576	1.13	2/787 (0.3%)
15	cf	0.68	0/647	1.08	6/873 (0.7%)
16	cg	0.72	0/535	1.06	2/723 (0.3%)
17	ch	0.83	0/1319	1.10	7/1781 (0.4%)
18	ci	0.63	0/565	1.19	8/760 (1.1%)
19	cj	0.19	0/471	0.38	0/643
19	ck	0.12	0/464	0.27	0/629
19	cl	0.16	0/438	0.38	0/595
19	cm	0.14	0/513	0.37	0/697
20	cn	0.16	0/778	0.49	0/1051
20	co	0.18	0/744	0.46	0/1010
21	cA	0.48	0/2239	0.56	0/3040
21	cB	0.54	0/2350	0.70	0/3188
21	cC	0.50	0/2239	0.58	0/3040
21	cD	0.51	0/2350	0.64	0/3188
21	cE	0.51	0/2247	0.66	1/3051 (0.0%)
21	cF	0.55	0/2350	0.70	1/3188 (0.0%)
21	cG	0.51	0/2260	0.64	0/3069
21	cH	0.58	0/2350	0.73	2/3188 (0.1%)
21	cI	0.50	0/2239	0.63	0/3040
21	cJ	0.56	1/2350 (0.0%)	0.70	0/3188
21	cK	0.50	0/2239	0.60	0/3040
21	cL	0.53	0/2350	0.72	3/3188 (0.1%)
21	cM	0.48	0/2220	0.60	0/3014
21	cN	0.50	0/2350	0.62	0/3188
21	cp	0.52	0/2350	0.63	0/3188
21	cq	0.50	0/2260	0.61	0/3069
21	cr	0.53	0/2350	0.67	2/3188 (0.1%)
21	cs	0.50	0/2206	0.59	0/2995
21	ct	0.53	0/2350	0.69	0/3188
21	cu	0.49	0/2247	0.62	0/3051
21	cv	0.56	0/2350	0.70	0/3188
21	cw	0.57	1/2247 (0.0%)	0.73	0/3051
21	cx	0.58	0/2350	0.72	3/3188 (0.1%)
21	cy	0.52	0/2247	0.65	2/3051 (0.1%)
21	cz	0.51	0/2350	0.63	0/3188
22	cO	0.39	0/222	0.72	0/302
22	cQ	0.39	0/237	0.59	0/322
22	da	0.38	0/231	0.58	0/316
22	dc	0.39	0/213	0.62	0/289
22	dg	0.32	0/245	0.55	0/334
22	di	0.31	0/215	0.59	0/293
22	ds	0.29	0/242	0.50	0/330

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
22	du	0.27	0/228	0.60	0/310
23	cP	0.36	0/244	0.66	0/333
23	db	0.38	0/203	0.68	0/277
23	dh	0.32	0/254	0.69	0/345
23	dt	0.23	0/239	0.65	0/324
24	cR	0.56	0/3281	0.98	4/4457 (0.1%)
24	cS	0.56	0/3281	0.97	4/4457 (0.1%)
24	cT	0.56	0/3281	0.98	4/4457 (0.1%)
25	cU	0.30	0/318	0.62	0/433
25	cV	0.30	0/312	0.66	0/425
25	cW	0.31	0/315	0.59	0/429
26	dm	0.37	0/176	0.82	0/243
26	dn	0.36	0/183	0.76	0/252
26	do	0.47	0/185	1.19	1/255 (0.4%)
All	All	0.57	27/437605 (0.0%)	0.91	1372/596073 (0.2%)

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	bH	372	PRO	C-O	-9.01	1.17	1.25
4	bD	50	ASN	C-N	7.35	1.40	1.33
1	at	257	HIS	C-N	7.02	1.41	1.33
4	bF	181	SER	C-N	6.96	1.40	1.34
1	aB	257	HIS	C-N	6.63	1.41	1.33

The worst 5 of 1372 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	do	17	GLN	N-CA-C	12.75	125.18	111.03
8	bI	125	GLY	N-CA-C	-11.33	101.46	113.58
8	bJ	69	VAL	N-CA-C	10.96	120.78	111.90
14	bT	179	ALA	N-CA-C	10.88	124.22	111.71
9	bL	55	SER	N-CA-C	10.10	122.83	110.41

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	aA	3390	0	3284	13	0
1	aB	3390	0	3284	9	0
1	aC	3395	0	3289	8	0
1	aD	3382	0	3278	13	0
1	aE	3395	0	3289	9	0
1	aF	3382	0	3278	11	0
1	aG	3390	0	3284	8	0
1	aH	3382	0	3278	11	0
1	aI	3390	0	3284	10	0
1	aJ	3395	0	3289	13	0
1	aK	3395	0	3289	9	0
1	aL	3387	0	3283	8	0
1	aM	3395	0	3289	9	0
1	aN	3390	0	3284	7	0
1	aO	3395	0	3289	5	0
1	aP	3395	0	3289	4	0
1	aQ	3382	0	3278	12	0
1	aR	3395	0	3289	8	0
1	aS	3395	0	3289	9	0
1	aT	3395	0	3289	5	0
1	aU	3395	0	3289	9	0
1	aV	3395	0	3289	6	0
1	aW	3395	0	3289	8	0
1	aX	3390	0	3284	3	0
1	aY	3395	0	3289	8	0
1	aZ	3395	0	3289	8	0
1	aa	3374	0	3272	99	0
1	ab	3395	0	3289	32	0
1	ac	3395	0	3289	58	0
1	ad	3395	0	3289	10	0
1	ae	3395	0	3289	6	0
1	af	3395	0	3289	10	0
1	ag	3395	0	3289	9	0
1	ah	3395	0	3289	9	0
1	ai	3395	0	3289	7	0
1	aj	3395	0	3289	8	0
1	ak	3395	0	3289	12	0
1	al	3387	0	3283	8	0
1	am	3395	0	3289	16	0
1	an	3387	0	3283	7	0
1	ao	3390	0	3284	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	ap	3395	0	3289	8	0
1	aq	3395	0	3289	9	0
1	ar	3382	0	3278	7	0
1	as	3395	0	3289	9	0
1	at	3395	0	3289	4	0
1	au	3382	0	3278	11	0
1	av	3395	0	3289	4	0
1	aw	3395	0	3289	6	0
1	ax	3382	0	3278	6	0
1	ay	3390	0	3284	9	0
1	az	3382	0	3278	6	0
1	ba	3395	0	3289	3	0
1	bb	3395	0	3289	22	0
1	bc	3395	0	3289	9	0
1	bd	3395	0	3289	13	0
1	be	3395	0	3289	7	0
1	bf	3395	0	3289	7	0
1	bg	3395	0	3289	10	0
1	bh	3395	0	3289	13	0
1	bi	3395	0	3289	3	0
1	bj	3395	0	3289	6	0
1	bk	3395	0	3289	6	0
1	bl	3395	0	3289	22	0
1	bm	3395	0	3289	16	0
1	bn	3382	0	3278	11	0
1	bo	3395	0	3289	11	0
1	bp	3395	0	3289	9	0
1	bq	3395	0	3289	4	0
1	br	3395	0	3289	8	0
1	bs	3395	0	3289	8	0
1	bt	3390	0	3284	3	0
2	bA	4079	0	3911	13	0
2	bB	4090	0	3920	18	0
2	bu	4090	0	3920	47	0
2	bv	4090	0	3920	38	0
2	bw	4090	0	3920	22	0
2	bx	4074	0	3904	37	0
2	by	4090	0	3920	82	0
2	bz	4030	0	3855	48	0
3	bC	3921	0	3830	30	0
4	bD	3169	0	3084	19	0
4	bF	3169	0	3084	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	cX	3165	0	3080	18	0
4	cZ	3165	0	3080	10	0
4	dd	3169	0	3084	24	0
4	df	3165	0	3080	32	0
4	dj	3169	0	3084	9	0
4	dk	3169	0	3084	14	0
4	dl	3169	0	3084	13	0
4	dp	3169	0	3084	54	0
4	dr	3169	0	3084	13	0
5	bE	3146	0	3091	28	0
5	cY	3146	0	3091	12	0
5	de	3146	0	3091	50	0
5	dq	3146	0	3091	34	0
6	bG	3864	0	3724	7	0
7	bH	3258	0	3136	31	0
8	bI	1096	0	1079	15	0
8	bJ	1146	0	1125	5	0
8	bK	892	0	879	8	0
9	bL	526	0	535	7	0
9	bM	526	0	535	5	0
9	bN	519	0	528	4	0
9	bO	519	0	528	1	0
10	bP	1126	0	1142	7	0
11	bQ	1275	0	1274	13	0
12	bR	1244	0	1254	1	0
13	bS	1504	0	1497	163	0
14	bT	373	0	370	1	0
14	bU	424	0	415	2	0
14	bV	416	0	409	3	0
14	bW	405	0	400	3	0
14	bX	312	0	301	4	0
14	bY	576	0	561	6	0
14	bZ	405	0	400	5	0
14	ca	405	0	400	2	0
14	cb	405	0	400	1	0
14	cc	646	0	643	4	0
14	cd	583	0	569	2	0
14	ce	560	0	541	0	0
15	cf	631	0	625	1	0
16	cg	521	0	494	2	0
17	ch	1288	0	1280	11	0
18	ci	553	0	539	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	cj	463	0	449	49	0
19	ck	455	0	448	32	0
19	cl	431	0	422	33	0
19	cm	503	0	486	51	0
20	cn	769	0	785	40	0
20	co	733	0	728	91	0
21	cA	2191	0	2203	6	0
21	cB	2299	0	2307	8	0
21	cC	2191	0	2203	6	0
21	cD	2299	0	2307	8	0
21	cE	2199	0	2209	11	0
21	cF	2299	0	2307	10	0
21	cG	2212	0	2221	7	0
21	cH	2299	0	2307	9	0
21	cI	2191	0	2203	9	0
21	cJ	2299	0	2307	13	0
21	cK	2191	0	2203	8	0
21	cL	2299	0	2307	10	0
21	cM	2173	0	2187	11	0
21	cN	2299	0	2307	7	0
21	cp	2299	0	2307	11	0
21	cq	2212	0	2221	5	0
21	cr	2299	0	2307	9	0
21	cs	2159	0	2171	13	0
21	ct	2299	0	2307	14	0
21	cu	2199	0	2209	4	0
21	cv	2299	0	2307	13	0
21	cw	2199	0	2209	16	0
21	cx	2299	0	2307	10	0
21	cy	2199	0	2209	11	0
21	cz	2299	0	2307	8	0
22	cO	218	0	220	28	0
22	cQ	233	0	234	35	0
22	da	228	0	221	22	0
22	dc	209	0	208	36	0
22	dg	241	0	239	39	0
22	di	211	0	208	36	0
22	ds	238	0	237	39	0
22	du	224	0	226	41	0
23	cP	239	0	226	32	0
23	db	200	0	188	45	0
23	dh	249	0	241	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	dt	236	0	229	27	0
24	cR	3203	0	3142	27	0
24	cS	3203	0	3142	24	0
24	cT	3203	0	3142	34	0
25	cU	311	0	299	37	0
25	cV	305	0	293	32	0
25	cW	308	0	297	28	0
26	dm	174	0	154	37	0
26	dn	181	0	169	36	0
26	do	182	0	175	37	0
All	All	427569	0	416835	2222	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 3.

The worst 5 of 2222 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)
4:dp:138:GLU:CD	23:dt:17:ILE:HD11	1.38	1.46
5:dq:269:LEU:HD22	22:du:15:ARG:CD	1.46	1.44
4:dd:272:PRO:CD	22:dg:14:ILE:HD13	1.47	1.42
5:dq:269:LEU:HD22	22:du:15:ARG:CG	1.48	1.39
4:dp:84:PHE:HZ	4:dp:273:PHE:CZ	1.43	1.34

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aA	433/437 (99%)	421 (97%)	12 (3%)	0	100	100
1	aB	433/437 (99%)	424 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aC	434/437 (99%)	423 (98%)	11 (2%)	0	100	100
1	aD	432/437 (99%)	421 (98%)	11 (2%)	0	100	100
1	aE	434/437 (99%)	419 (96%)	15 (4%)	0	100	100
1	aF	432/437 (99%)	421 (98%)	11 (2%)	0	100	100
1	aG	433/437 (99%)	420 (97%)	13 (3%)	0	100	100
1	aH	432/437 (99%)	422 (98%)	9 (2%)	1 (0%)	43	73
1	aI	433/437 (99%)	422 (98%)	10 (2%)	1 (0%)	43	73
1	aJ	434/437 (99%)	421 (97%)	13 (3%)	0	100	100
1	aK	434/437 (99%)	420 (97%)	12 (3%)	2 (0%)	24	57
1	aL	433/437 (99%)	419 (97%)	13 (3%)	1 (0%)	43	73
1	aM	434/437 (99%)	418 (96%)	16 (4%)	0	100	100
1	aN	433/437 (99%)	419 (97%)	13 (3%)	1 (0%)	43	73
1	aO	434/437 (99%)	419 (96%)	14 (3%)	1 (0%)	43	73
1	aP	434/437 (99%)	422 (97%)	11 (2%)	1 (0%)	43	73
1	aQ	432/437 (99%)	420 (97%)	11 (2%)	1 (0%)	43	73
1	aR	434/437 (99%)	416 (96%)	14 (3%)	4 (1%)	14	45
1	aS	434/437 (99%)	418 (96%)	15 (4%)	1 (0%)	43	73
1	aT	434/437 (99%)	417 (96%)	15 (4%)	2 (0%)	24	57
1	aU	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	aV	434/437 (99%)	420 (97%)	13 (3%)	1 (0%)	43	73
1	aW	434/437 (99%)	420 (97%)	14 (3%)	0	100	100
1	aX	433/437 (99%)	420 (97%)	13 (3%)	0	100	100
1	aY	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	aZ	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	aa	430/437 (98%)	420 (98%)	10 (2%)	0	100	100
1	ab	434/437 (99%)	430 (99%)	4 (1%)	0	100	100
1	ac	434/437 (99%)	425 (98%)	9 (2%)	0	100	100
1	ad	434/437 (99%)	419 (96%)	13 (3%)	2 (0%)	24	57
1	ae	434/437 (99%)	419 (96%)	15 (4%)	0	100	100
1	af	434/437 (99%)	422 (97%)	12 (3%)	0	100	100
1	ag	434/437 (99%)	415 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ah	434/437 (99%)	417 (96%)	16 (4%)	1 (0%)	43	73
1	ai	434/437 (99%)	418 (96%)	16 (4%)	0	100	100
1	aj	434/437 (99%)	423 (98%)	11 (2%)	0	100	100
1	ak	434/437 (99%)	422 (97%)	10 (2%)	2 (0%)	24	57
1	al	433/437 (99%)	425 (98%)	7 (2%)	1 (0%)	43	73
1	am	434/437 (99%)	423 (98%)	11 (2%)	0	100	100
1	an	433/437 (99%)	423 (98%)	10 (2%)	0	100	100
1	ao	433/437 (99%)	419 (97%)	14 (3%)	0	100	100
1	ap	434/437 (99%)	417 (96%)	17 (4%)	0	100	100
1	aq	434/437 (99%)	425 (98%)	8 (2%)	1 (0%)	43	73
1	ar	432/437 (99%)	420 (97%)	12 (3%)	0	100	100
1	as	434/437 (99%)	418 (96%)	14 (3%)	2 (0%)	24	57
1	at	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	au	432/437 (99%)	421 (98%)	11 (2%)	0	100	100
1	av	434/437 (99%)	425 (98%)	9 (2%)	0	100	100
1	aw	434/437 (99%)	418 (96%)	15 (4%)	1 (0%)	43	73
1	ax	432/437 (99%)	417 (96%)	14 (3%)	1 (0%)	43	73
1	ay	433/437 (99%)	419 (97%)	14 (3%)	0	100	100
1	az	432/437 (99%)	420 (97%)	12 (3%)	0	100	100
1	ba	434/437 (99%)	416 (96%)	17 (4%)	1 (0%)	43	73
1	bb	434/437 (99%)	420 (97%)	12 (3%)	2 (0%)	24	57
1	bc	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	bd	434/437 (99%)	423 (98%)	9 (2%)	2 (0%)	24	57
1	be	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	bf	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	bg	434/437 (99%)	421 (97%)	12 (3%)	1 (0%)	43	73
1	bh	434/437 (99%)	422 (97%)	11 (2%)	1 (0%)	43	73
1	bi	434/437 (99%)	419 (96%)	14 (3%)	1 (0%)	43	73
1	bj	434/437 (99%)	420 (97%)	13 (3%)	1 (0%)	43	73
1	bk	434/437 (99%)	419 (96%)	14 (3%)	1 (0%)	43	73
1	bl	434/437 (99%)	418 (96%)	15 (4%)	1 (0%)	43	73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	bm	434/437 (99%)	420 (97%)	13 (3%)	1 (0%)	43	73
1	bn	432/437 (99%)	416 (96%)	15 (4%)	1 (0%)	43	73
1	bo	434/437 (99%)	419 (96%)	13 (3%)	2 (0%)	24	57
1	bp	434/437 (99%)	422 (97%)	11 (2%)	1 (0%)	43	73
1	bq	434/437 (99%)	420 (97%)	14 (3%)	0	100	100
1	br	434/437 (99%)	420 (97%)	13 (3%)	1 (0%)	43	73
1	bs	434/437 (99%)	421 (97%)	13 (3%)	0	100	100
1	bt	433/437 (99%)	423 (98%)	9 (2%)	1 (0%)	43	73
2	bA	514/520 (99%)	486 (95%)	26 (5%)	2 (0%)	30	62
2	bB	515/520 (99%)	480 (93%)	34 (7%)	1 (0%)	43	73
2	bu	515/520 (99%)	489 (95%)	25 (5%)	1 (0%)	43	73
2	bv	515/520 (99%)	485 (94%)	29 (6%)	1 (0%)	43	73
2	bw	515/520 (99%)	490 (95%)	25 (5%)	0	100	100
2	bx	512/520 (98%)	483 (94%)	27 (5%)	2 (0%)	30	62
2	by	515/520 (99%)	482 (94%)	32 (6%)	1 (0%)	43	73
2	bz	506/520 (97%)	473 (94%)	32 (6%)	1 (0%)	43	73
3	bC	483/486 (99%)	459 (95%)	22 (5%)	2 (0%)	30	62
4	bD	399/403 (99%)	383 (96%)	14 (4%)	2 (0%)	24	57
4	bF	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	cX	399/403 (99%)	380 (95%)	14 (4%)	5 (1%)	9	38
4	cZ	399/403 (99%)	380 (95%)	14 (4%)	5 (1%)	9	38
4	dd	399/403 (99%)	379 (95%)	15 (4%)	5 (1%)	9	38
4	df	399/403 (99%)	377 (94%)	14 (4%)	8 (2%)	6	32
4	dj	399/403 (99%)	376 (94%)	20 (5%)	3 (1%)	16	48
4	dk	399/403 (99%)	374 (94%)	22 (6%)	3 (1%)	16	48
4	dl	399/403 (99%)	374 (94%)	20 (5%)	5 (1%)	9	38
4	dp	399/403 (99%)	381 (96%)	14 (4%)	4 (1%)	12	43
4	dr	399/403 (99%)	378 (95%)	14 (4%)	7 (2%)	6	33
5	bE	395/401 (98%)	382 (97%)	12 (3%)	1 (0%)	36	67
5	cY	395/401 (98%)	382 (97%)	12 (3%)	1 (0%)	36	67
5	de	395/401 (98%)	385 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	dq	395/401 (98%)	384 (97%)	10 (2%)	1 (0%)	36	67
6	bG	496/530 (94%)	478 (96%)	17 (3%)	1 (0%)	43	73
7	bH	422/576 (73%)	388 (92%)	32 (8%)	2 (0%)	24	57
8	bI	139/171 (81%)	131 (94%)	7 (5%)	1 (1%)	18	51
8	bJ	145/171 (85%)	135 (93%)	9 (6%)	1 (1%)	18	51
8	bK	114/171 (67%)	111 (97%)	3 (3%)	0	100	100
9	bL	61/181 (34%)	59 (97%)	1 (2%)	1 (2%)	7	35
9	bM	61/181 (34%)	55 (90%)	5 (8%)	1 (2%)	7	35
9	bN	60/181 (33%)	56 (93%)	3 (5%)	1 (2%)	7	34
9	bO	60/181 (33%)	54 (90%)	5 (8%)	1 (2%)	7	34
10	bP	140/146 (96%)	133 (95%)	7 (5%)	0	100	100
11	bQ	160/216 (74%)	149 (93%)	8 (5%)	3 (2%)	6	32
12	bR	157/173 (91%)	153 (98%)	4 (2%)	0	100	100
13	bS	189/210 (90%)	172 (91%)	15 (8%)	2 (1%)	11	41
14	bT	46/207 (22%)	40 (87%)	3 (6%)	3 (6%)	1	14
14	bU	52/207 (25%)	48 (92%)	3 (6%)	1 (2%)	6	32
14	bV	51/207 (25%)	42 (82%)	8 (16%)	1 (2%)	6	32
14	bW	50/207 (24%)	45 (90%)	4 (8%)	1 (2%)	6	32
14	bX	39/207 (19%)	34 (87%)	4 (10%)	1 (3%)	4	27
14	bY	72/207 (35%)	58 (81%)	10 (14%)	4 (6%)	1	15
14	bZ	50/207 (24%)	46 (92%)	4 (8%)	0	100	100
14	ca	50/207 (24%)	47 (94%)	2 (4%)	1 (2%)	6	32
14	cb	50/207 (24%)	45 (90%)	4 (8%)	1 (2%)	6	32
14	cc	82/207 (40%)	73 (89%)	8 (10%)	1 (1%)	10	40
14	cd	73/207 (35%)	66 (90%)	7 (10%)	0	100	100
14	ce	70/207 (34%)	63 (90%)	6 (9%)	1 (1%)	9	37
15	cf	76/151 (50%)	67 (88%)	7 (9%)	2 (3%)	4	27
16	cg	64/98 (65%)	58 (91%)	3 (5%)	3 (5%)	2	18
17	ch	150/155 (97%)	143 (95%)	5 (3%)	2 (1%)	9	38
18	ci	78/93 (84%)	72 (92%)	5 (6%)	1 (1%)	9	38
19	cj	57/80 (71%)	51 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	ck	55/80 (69%)	52 (94%)	3 (6%)	0	100	100
19	cl	53/80 (66%)	51 (96%)	2 (4%)	0	100	100
19	cm	61/80 (76%)	58 (95%)	3 (5%)	0	100	100
20	cn	96/148 (65%)	93 (97%)	3 (3%)	0	100	100
20	co	93/148 (63%)	87 (94%)	6 (6%)	0	100	100
21	cA	277/378 (73%)	254 (92%)	23 (8%)	0	100	100
21	cB	290/378 (77%)	267 (92%)	23 (8%)	0	100	100
21	cC	277/378 (73%)	250 (90%)	26 (9%)	1 (0%)	30	62
21	cD	290/378 (77%)	267 (92%)	20 (7%)	3 (1%)	12	43
21	cE	278/378 (74%)	255 (92%)	21 (8%)	2 (1%)	18	51
21	cF	290/378 (77%)	257 (89%)	30 (10%)	3 (1%)	12	43
21	cG	280/378 (74%)	253 (90%)	26 (9%)	1 (0%)	30	62
21	cH	290/378 (77%)	261 (90%)	28 (10%)	1 (0%)	36	67
21	cI	277/378 (73%)	256 (92%)	21 (8%)	0	100	100
21	cJ	290/378 (77%)	263 (91%)	24 (8%)	3 (1%)	12	43
21	cK	277/378 (73%)	258 (93%)	18 (6%)	1 (0%)	30	62
21	cL	290/378 (77%)	265 (91%)	24 (8%)	1 (0%)	36	67
21	cM	275/378 (73%)	252 (92%)	22 (8%)	1 (0%)	30	62
21	cN	290/378 (77%)	267 (92%)	21 (7%)	2 (1%)	18	51
21	cp	290/378 (77%)	263 (91%)	24 (8%)	3 (1%)	12	43
21	cq	280/378 (74%)	257 (92%)	21 (8%)	2 (1%)	18	51
21	cr	290/378 (77%)	264 (91%)	25 (9%)	1 (0%)	36	67
21	cs	273/378 (72%)	248 (91%)	23 (8%)	2 (1%)	18	51
21	ct	290/378 (77%)	258 (89%)	30 (10%)	2 (1%)	18	51
21	cu	278/378 (74%)	260 (94%)	18 (6%)	0	100	100
21	cv	290/378 (77%)	254 (88%)	34 (12%)	2 (1%)	18	51
21	cw	278/378 (74%)	252 (91%)	22 (8%)	4 (1%)	9	37
21	cx	290/378 (77%)	260 (90%)	30 (10%)	0	100	100
21	cy	278/378 (74%)	248 (89%)	29 (10%)	1 (0%)	30	62
21	cz	290/378 (77%)	267 (92%)	21 (7%)	2 (1%)	18	51
22	cO	28/1335 (2%)	21 (75%)	7 (25%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	cQ	29/1335 (2%)	22 (76%)	7 (24%)	0	100	100
22	da	30/1335 (2%)	24 (80%)	6 (20%)	0	100	100
22	dc	26/1335 (2%)	21 (81%)	5 (19%)	0	100	100
22	dg	30/1335 (2%)	27 (90%)	3 (10%)	0	100	100
22	di	27/1335 (2%)	21 (78%)	6 (22%)	0	100	100
22	ds	30/1335 (2%)	30 (100%)	0	0	100	100
22	du	28/1335 (2%)	24 (86%)	4 (14%)	0	100	100
23	cP	33/1369 (2%)	22 (67%)	11 (33%)	0	100	100
23	db	28/1369 (2%)	20 (71%)	6 (21%)	2 (7%)	1	12
23	dh	33/1369 (2%)	26 (79%)	7 (21%)	0	100	100
23	dt	33/1369 (2%)	25 (76%)	8 (24%)	0	100	100
24	cR	397/400 (99%)	358 (90%)	34 (9%)	5 (1%)	9	38
24	cS	397/400 (99%)	359 (90%)	34 (9%)	4 (1%)	12	43
24	cT	397/400 (99%)	358 (90%)	35 (9%)	4 (1%)	12	43
25	cU	41/1343 (3%)	36 (88%)	5 (12%)	0	100	100
25	cV	41/1343 (3%)	35 (85%)	5 (12%)	1 (2%)	4	29
25	cW	41/1343 (3%)	36 (88%)	5 (12%)	0	100	100
26	dm	23/1359 (2%)	19 (83%)	4 (17%)	0	100	100
26	dn	23/1359 (2%)	18 (78%)	5 (22%)	0	100	100
26	do	23/1359 (2%)	21 (91%)	2 (9%)	0	100	100
All	All	54281/83744 (65%)	51687 (95%)	2389 (4%)	205 (0%)	31	62

5 of 205 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	ah	123	ASN
1	aU	123	ASN
1	bm	123	ASN
1	bo	123	ASN
1	br	123	ASN

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	aA	357/358 (100%)	357 (100%)	0	100	100
1	aB	357/358 (100%)	357 (100%)	0	100	100
1	aC	357/358 (100%)	357 (100%)	0	100	100
1	aD	356/358 (99%)	355 (100%)	1 (0%)	86	84
1	aE	357/358 (100%)	357 (100%)	0	100	100
1	aF	356/358 (99%)	356 (100%)	0	100	100
1	aG	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	aH	356/358 (99%)	356 (100%)	0	100	100
1	aI	357/358 (100%)	357 (100%)	0	100	100
1	aJ	357/358 (100%)	357 (100%)	0	100	100
1	aK	357/358 (100%)	355 (99%)	2 (1%)	78	79
1	aL	356/358 (99%)	356 (100%)	0	100	100
1	aM	357/358 (100%)	357 (100%)	0	100	100
1	aN	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	aO	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	aP	357/358 (100%)	357 (100%)	0	100	100
1	aQ	356/358 (99%)	356 (100%)	0	100	100
1	aR	357/358 (100%)	357 (100%)	0	100	100
1	aS	357/358 (100%)	357 (100%)	0	100	100
1	aT	357/358 (100%)	357 (100%)	0	100	100
1	aU	357/358 (100%)	357 (100%)	0	100	100
1	aV	357/358 (100%)	357 (100%)	0	100	100
1	aW	357/358 (100%)	357 (100%)	0	100	100
1	aX	357/358 (100%)	357 (100%)	0	100	100
1	aY	357/358 (100%)	357 (100%)	0	100	100
1	aZ	357/358 (100%)	357 (100%)	0	100	100
1	aa	356/358 (99%)	356 (100%)	0	100	100
1	ab	357/358 (100%)	354 (99%)	3 (1%)	73	76
1	ac	357/358 (100%)	357 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	ad	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	ae	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	af	357/358 (100%)	357 (100%)	0	100	100
1	ag	357/358 (100%)	357 (100%)	0	100	100
1	ah	357/358 (100%)	357 (100%)	0	100	100
1	ai	357/358 (100%)	357 (100%)	0	100	100
1	aj	357/358 (100%)	357 (100%)	0	100	100
1	ak	357/358 (100%)	357 (100%)	0	100	100
1	al	356/358 (99%)	356 (100%)	0	100	100
1	am	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	an	356/358 (99%)	356 (100%)	0	100	100
1	ao	357/358 (100%)	357 (100%)	0	100	100
1	ap	357/358 (100%)	357 (100%)	0	100	100
1	aq	357/358 (100%)	357 (100%)	0	100	100
1	ar	356/358 (99%)	356 (100%)	0	100	100
1	as	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	at	357/358 (100%)	357 (100%)	0	100	100
1	au	356/358 (99%)	356 (100%)	0	100	100
1	av	357/358 (100%)	357 (100%)	0	100	100
1	aw	357/358 (100%)	357 (100%)	0	100	100
1	ax	356/358 (99%)	356 (100%)	0	100	100
1	ay	357/358 (100%)	357 (100%)	0	100	100
1	az	356/358 (99%)	356 (100%)	0	100	100
1	ba	357/358 (100%)	357 (100%)	0	100	100
1	bb	357/358 (100%)	357 (100%)	0	100	100
1	bc	357/358 (100%)	357 (100%)	0	100	100
1	bd	357/358 (100%)	357 (100%)	0	100	100
1	be	357/358 (100%)	357 (100%)	0	100	100
1	bf	357/358 (100%)	357 (100%)	0	100	100
1	bg	357/358 (100%)	357 (100%)	0	100	100
1	bh	357/358 (100%)	356 (100%)	1 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	bi	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	bj	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	bk	357/358 (100%)	357 (100%)	0	100	100
1	bl	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	bm	357/358 (100%)	357 (100%)	0	100	100
1	bn	356/358 (99%)	355 (100%)	1 (0%)	86	84
1	bo	357/358 (100%)	357 (100%)	0	100	100
1	bp	357/358 (100%)	357 (100%)	0	100	100
1	bq	357/358 (100%)	357 (100%)	0	100	100
1	br	357/358 (100%)	356 (100%)	1 (0%)	86	84
1	bs	357/358 (100%)	357 (100%)	0	100	100
1	bt	357/358 (100%)	357 (100%)	0	100	100
2	bA	438/441 (99%)	437 (100%)	1 (0%)	87	87
2	bB	439/441 (100%)	439 (100%)	0	100	100
2	bu	439/441 (100%)	434 (99%)	5 (1%)	65	73
2	bv	439/441 (100%)	434 (99%)	5 (1%)	65	73
2	bw	439/441 (100%)	439 (100%)	0	100	100
2	bx	438/441 (99%)	435 (99%)	3 (1%)	76	77
2	by	439/441 (100%)	439 (100%)	0	100	100
2	bz	432/441 (98%)	430 (100%)	2 (0%)	81	81
3	bC	439/440 (100%)	439 (100%)	0	100	100
4	bD	344/346 (99%)	343 (100%)	1 (0%)	86	84
4	bF	344/346 (99%)	343 (100%)	1 (0%)	86	84
4	cX	343/346 (99%)	343 (100%)	0	100	100
4	cZ	343/346 (99%)	343 (100%)	0	100	100
4	dd	344/346 (99%)	344 (100%)	0	100	100
4	df	343/346 (99%)	343 (100%)	0	100	100
4	dj	344/346 (99%)	343 (100%)	1 (0%)	86	84
4	dk	344/346 (99%)	342 (99%)	2 (1%)	78	79
4	dl	344/346 (99%)	344 (100%)	0	100	100
4	dp	344/346 (99%)	344 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	dr	344/346 (99%)	344 (100%)	0	100	100
5	bE	349/353 (99%)	348 (100%)	1 (0%)	86	84
5	cY	349/353 (99%)	347 (99%)	2 (1%)	78	79
5	de	349/353 (99%)	347 (99%)	2 (1%)	78	79
5	dq	349/353 (99%)	348 (100%)	1 (0%)	86	84
6	bG	424/446 (95%)	424 (100%)	0	100	100
7	bH	345/479 (72%)	344 (100%)	1 (0%)	86	84
8	bI	116/144 (81%)	116 (100%)	0	100	100
8	bJ	122/144 (85%)	122 (100%)	0	100	100
8	bK	93/144 (65%)	93 (100%)	0	100	100
9	bL	59/161 (37%)	59 (100%)	0	100	100
9	bM	59/161 (37%)	58 (98%)	1 (2%)	53	67
9	bN	58/161 (36%)	57 (98%)	1 (2%)	53	67
9	bO	58/161 (36%)	58 (100%)	0	100	100
10	bP	121/125 (97%)	121 (100%)	0	100	100
11	bQ	140/188 (74%)	139 (99%)	1 (1%)	76	77
12	bR	136/148 (92%)	136 (100%)	0	100	100
13	bS	164/179 (92%)	164 (100%)	0	100	100
14	bT	40/181 (22%)	40 (100%)	0	100	100
14	bU	47/181 (26%)	47 (100%)	0	100	100
14	bV	46/181 (25%)	46 (100%)	0	100	100
14	bW	45/181 (25%)	45 (100%)	0	100	100
14	bX	35/181 (19%)	35 (100%)	0	100	100
14	bY	62/181 (34%)	62 (100%)	0	100	100
14	bZ	45/181 (25%)	45 (100%)	0	100	100
14	ca	45/181 (25%)	45 (100%)	0	100	100
14	cb	45/181 (25%)	45 (100%)	0	100	100
14	cc	72/181 (40%)	71 (99%)	1 (1%)	59	70
14	cd	63/181 (35%)	62 (98%)	1 (2%)	55	68
14	ce	60/181 (33%)	60 (100%)	0	100	100
15	cf	70/139 (50%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	cg	51/79 (65%)	51 (100%)	0	100	100
17	ch	142/145 (98%)	142 (100%)	0	100	100
18	ci	47/63 (75%)	46 (98%)	1 (2%)	47	64
19	cj	51/70 (73%)	51 (100%)	0	100	100
19	ck	49/70 (70%)	49 (100%)	0	100	100
19	cl	47/70 (67%)	47 (100%)	0	100	100
19	cm	54/70 (77%)	54 (100%)	0	100	100
20	cn	84/130 (65%)	84 (100%)	0	100	100
20	co	78/130 (60%)	78 (100%)	0	100	100
21	cA	245/339 (72%)	245 (100%)	0	100	100
21	cB	257/339 (76%)	257 (100%)	0	100	100
21	cC	245/339 (72%)	245 (100%)	0	100	100
21	cD	257/339 (76%)	257 (100%)	0	100	100
21	cE	246/339 (73%)	246 (100%)	0	100	100
21	cF	257/339 (76%)	256 (100%)	1 (0%)	84	83
21	cG	248/339 (73%)	248 (100%)	0	100	100
21	cH	257/339 (76%)	257 (100%)	0	100	100
21	cI	245/339 (72%)	245 (100%)	0	100	100
21	cJ	257/339 (76%)	257 (100%)	0	100	100
21	cK	245/339 (72%)	245 (100%)	0	100	100
21	cL	257/339 (76%)	257 (100%)	0	100	100
21	cM	243/339 (72%)	243 (100%)	0	100	100
21	cN	257/339 (76%)	257 (100%)	0	100	100
21	cp	257/339 (76%)	257 (100%)	0	100	100
21	cq	248/339 (73%)	247 (100%)	1 (0%)	84	83
21	cr	257/339 (76%)	257 (100%)	0	100	100
21	cs	241/339 (71%)	241 (100%)	0	100	100
21	ct	257/339 (76%)	257 (100%)	0	100	100
21	cu	246/339 (73%)	246 (100%)	0	100	100
21	cv	257/339 (76%)	257 (100%)	0	100	100
21	cw	246/339 (73%)	246 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	cx	257/339 (76%)	257 (100%)	0	100	100
21	cy	246/339 (73%)	245 (100%)	1 (0%)	84	83
21	cz	257/339 (76%)	257 (100%)	0	100	100
22	cO	22/1123 (2%)	22 (100%)	0	100	100
22	cQ	25/1123 (2%)	24 (96%)	1 (4%)	28	52
22	da	24/1123 (2%)	24 (100%)	0	100	100
22	dc	22/1123 (2%)	22 (100%)	0	100	100
22	dg	26/1123 (2%)	26 (100%)	0	100	100
22	di	22/1123 (2%)	22 (100%)	0	100	100
22	ds	25/1123 (2%)	25 (100%)	0	100	100
22	du	24/1123 (2%)	24 (100%)	0	100	100
23	cP	24/1147 (2%)	24 (100%)	0	100	100
23	db	19/1147 (2%)	18 (95%)	1 (5%)	20	45
23	dh	26/1147 (2%)	25 (96%)	1 (4%)	29	53
23	dt	24/1147 (2%)	24 (100%)	0	100	100
24	cR	359/360 (100%)	359 (100%)	0	100	100
24	cS	359/360 (100%)	359 (100%)	0	100	100
24	cT	359/360 (100%)	359 (100%)	0	100	100
25	cU	30/1015 (3%)	30 (100%)	0	100	100
25	cV	28/1015 (3%)	28 (100%)	0	100	100
25	cW	29/1015 (3%)	29 (100%)	0	100	100
26	dm	17/1144 (2%)	16 (94%)	1 (6%)	18	43
26	dn	19/1144 (2%)	18 (95%)	1 (5%)	20	45
26	do	19/1144 (2%)	17 (90%)	2 (10%)	6	26
All	All	45770/70345 (65%)	45707 (100%)	63 (0%)	87	89

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	bv	442	GLN
4	dj	66	VAL
4	bD	200	ILE
23	dh	14	ARG
26	dn	20	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 359 such sidechains are listed below:

Mol	Chain	Res	Type
2	bB	483	GLN
21	cA	229	ASN
6	bG	77	GLN
21	cp	333	GLN
21	cF	171	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.

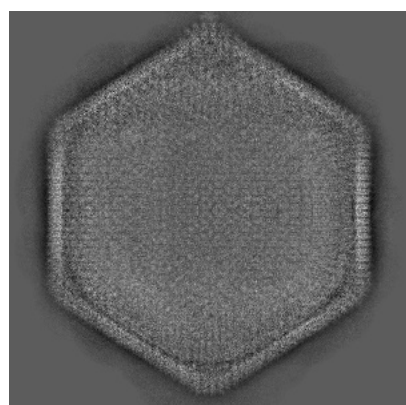
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34438. These allow visual inspection of the internal detail of the map and identification of artifacts.

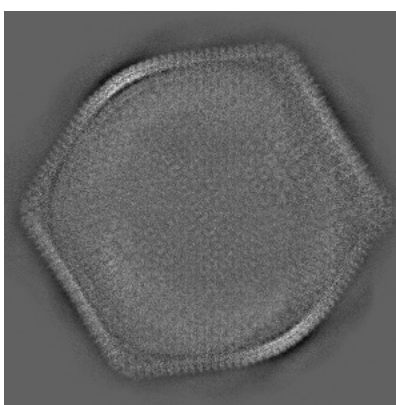
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

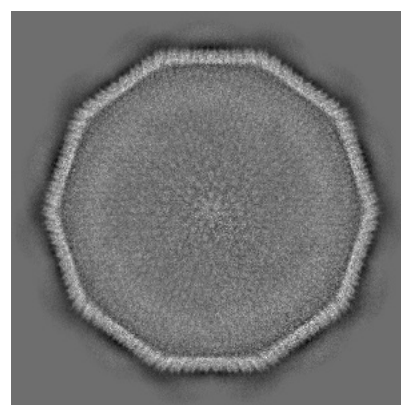
6.1.1 Primary map



X



Y

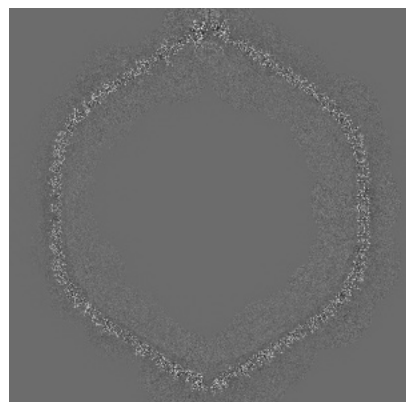


Z

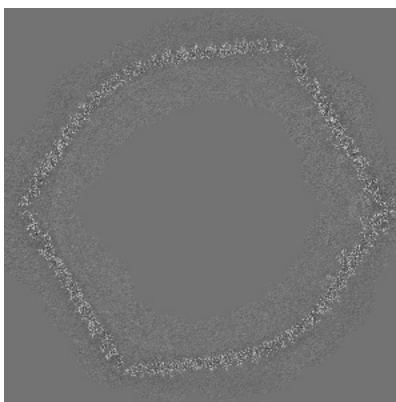
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

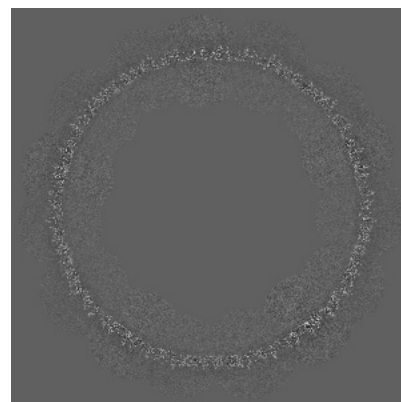
6.2.1 Primary map



X Index: 600



Y Index: 600

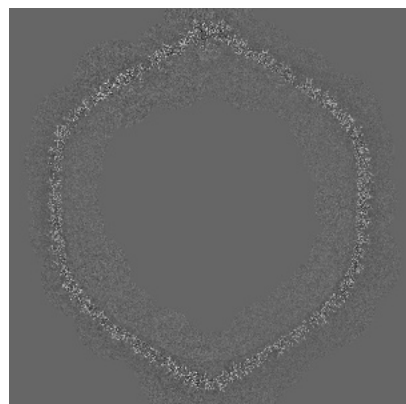


Z Index: 600

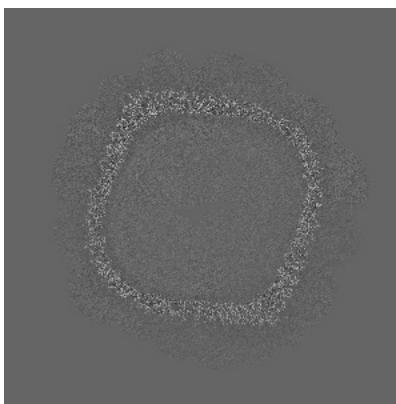
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

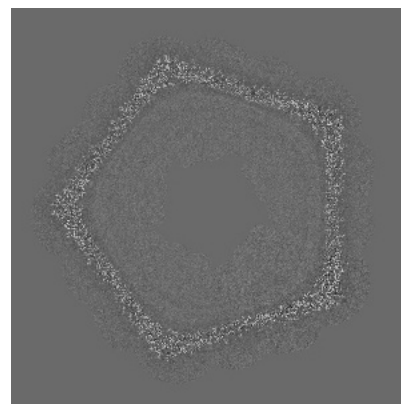
6.3.1 Primary map



X Index: 628



Y Index: 257

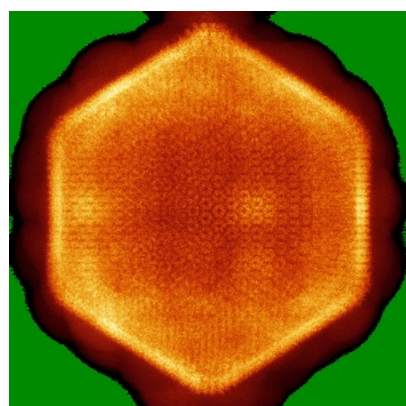


Z Index: 320

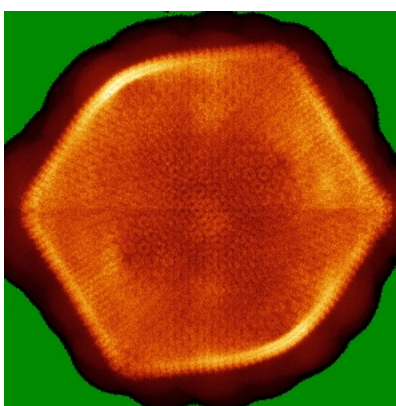
The images above show the largest variance slices of the map in three orthogonal directions.

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

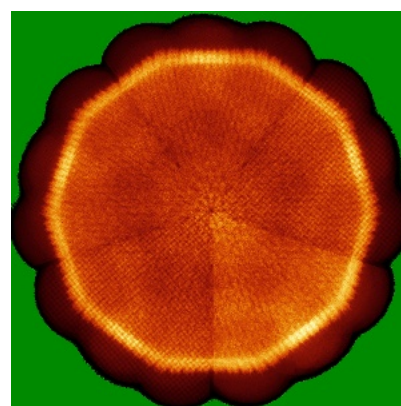
6.4.1 Primary map



X



Y

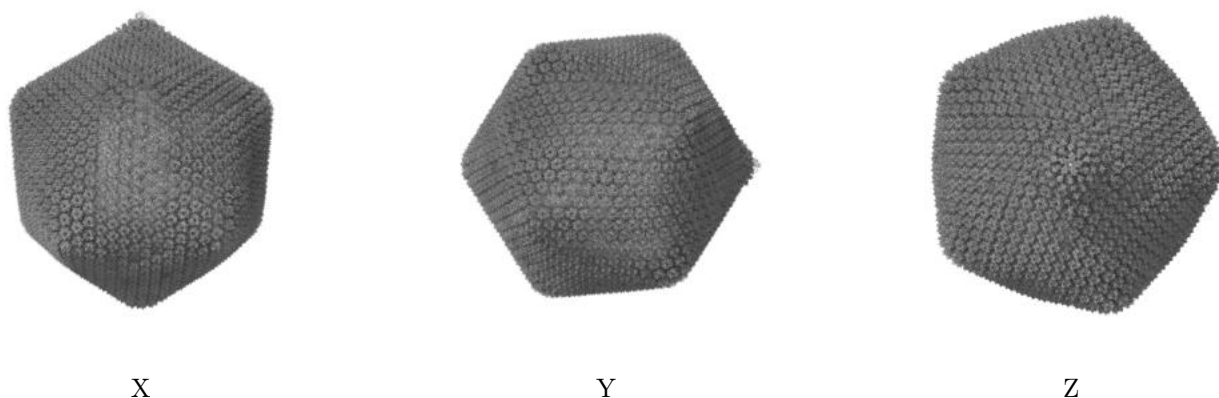


Z

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

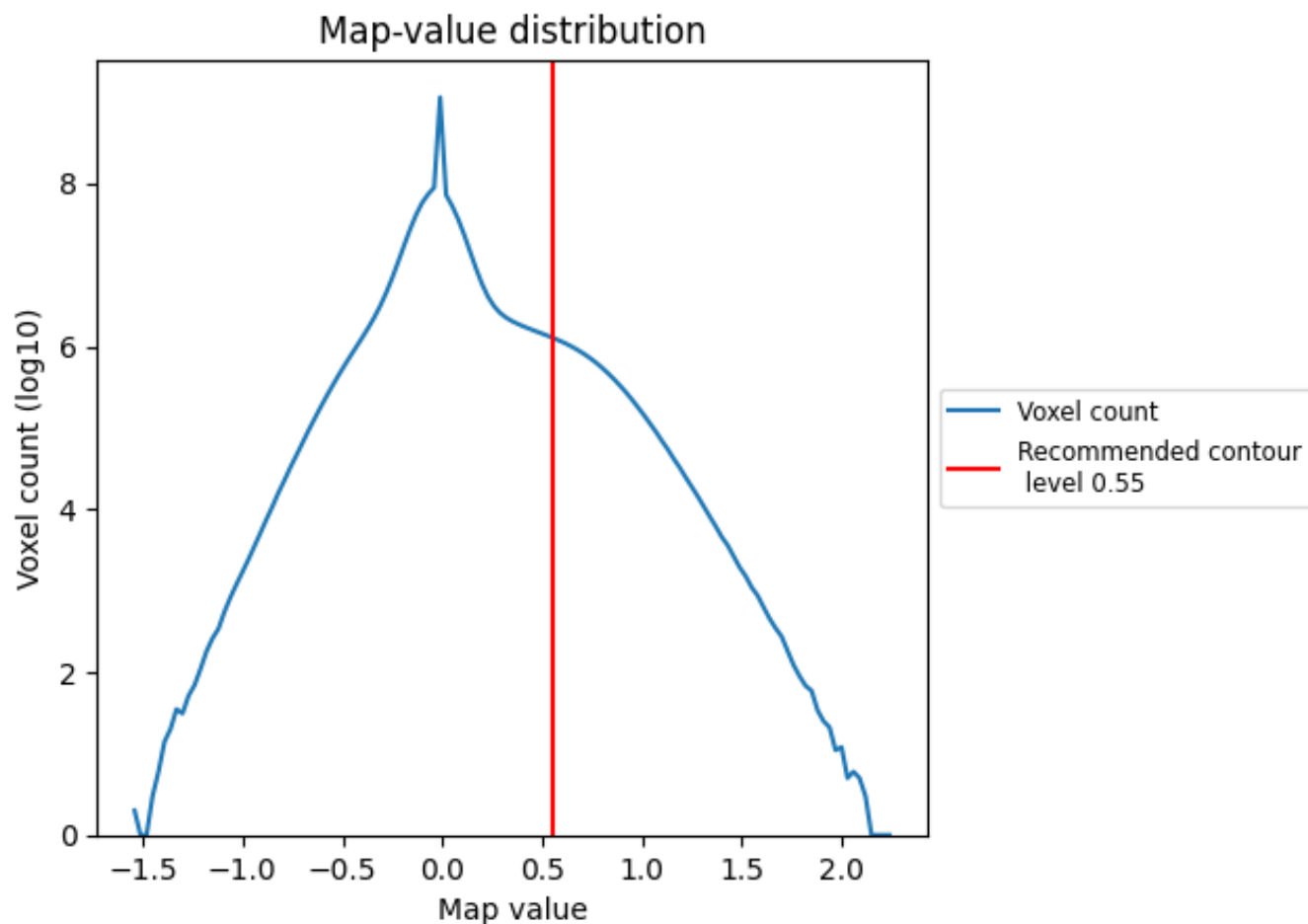
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

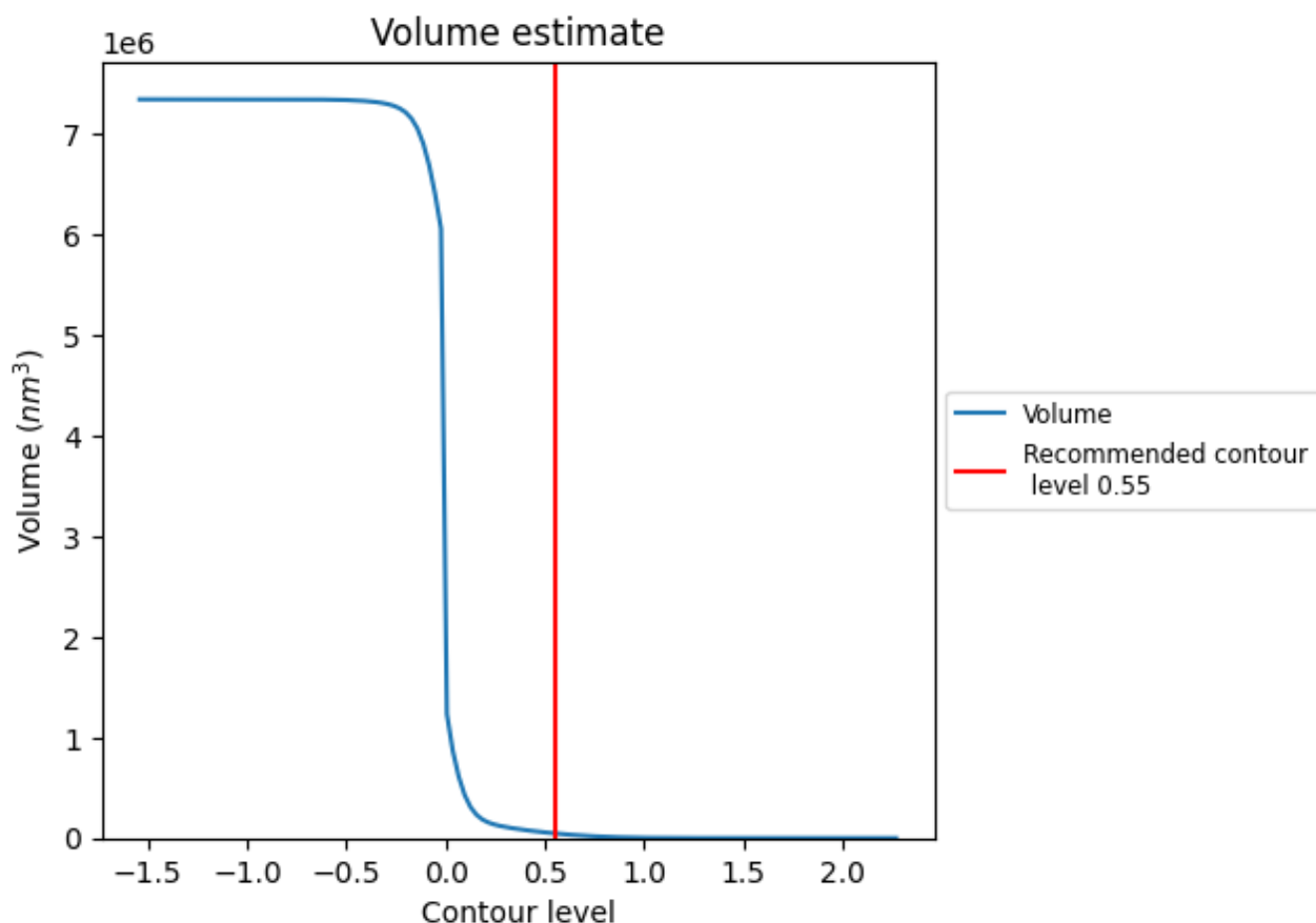
This section contains the results of statistical analysis of the map.

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.

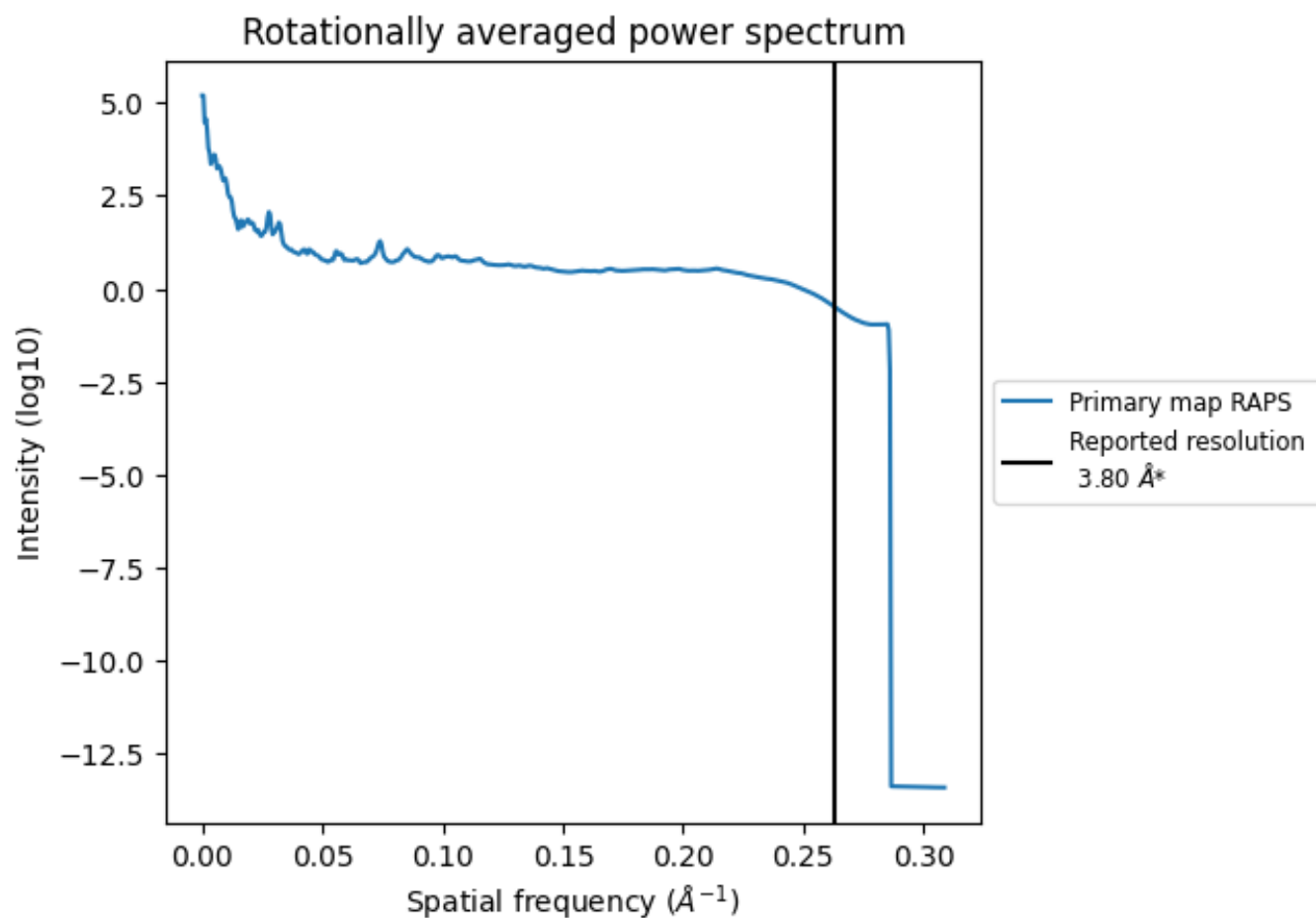
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46843 nm³; this corresponds to an approximate mass of 42315 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 0.263 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 EMD map EMD-34438 and PDB model 8H2I. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)

This section was not generated.

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



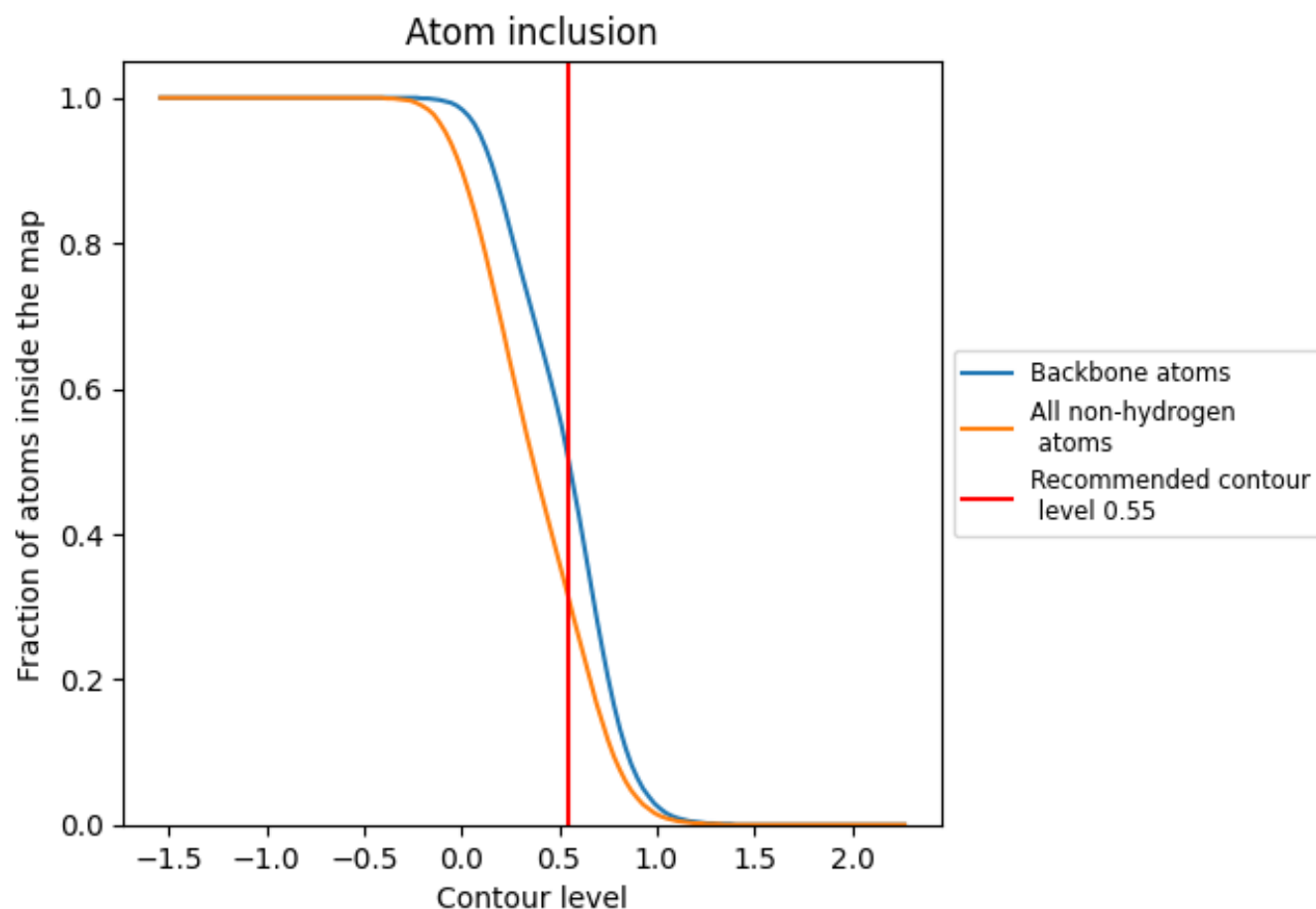
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 31% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3110	 0.3620
aA	 0.2580	 0.3860
aB	 0.2670	 0.3810
aC	 0.2860	 0.3790
aD	 0.2940	 0.3800
aE	 0.3830	 0.4000
aF	 0.4160	 0.3950
aG	 0.3710	 0.3900
aH	 0.4420	 0.4010
aI	 0.4390	 0.4000
aJ	 0.4140	 0.3930
aK	 0.3900	 0.3960
aL	 0.3660	 0.3930
aM	 0.3610	 0.3940
aN	 0.3690	 0.3970
aO	 0.3660	 0.3900
aP	 0.3750	 0.3960
aQ	 0.3370	 0.3910
aR	 0.3310	 0.3900
aS	 0.3510	 0.3970
aT	 0.3660	 0.3910
aU	 0.3800	 0.3960
aV	 0.3800	 0.3970
aW	 0.3310	 0.3900
aX	 0.3340	 0.3900
aY	 0.3320	 0.3900
aZ	 0.3520	 0.3910
aa	 0.4210	 0.3970
ab	 0.4250	 0.3940
ac	 0.4330	 0.4050
ad	 0.4340	 0.3980
ae	 0.4250	 0.4010
af	 0.4220	 0.4010
ag	 0.4150	 0.3910
ah	 0.4500	 0.4050



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Chain	Atom inclusion	Q-score
ai	0.4230	0.3990
aj	0.3020	0.3830
ak	0.3610	0.3940
al	0.2940	0.3800
am	0.4340	0.3980
an	0.4370	0.3950
ao	0.4260	0.3960
ap	0.4430	0.3980
aq	0.4620	0.3980
ar	0.4610	0.4010
as	0.4250	0.3900
at	0.3850	0.3990
au	0.3930	0.4020
av	0.3320	0.3890
aw	0.3030	0.3940
ax	0.3480	0.3980
ay	0.2330	0.3780
az	0.2220	0.3830
bA	0.3620	0.3680
bB	0.2710	0.3590
bC	0.3450	0.3730
bD	0.2300	0.3510
bE	0.2900	0.3580
bF	0.2640	0.3460
bG	0.3260	0.3190
bH	0.3210	0.3860
bI	0.3010	0.3470
bJ	0.3120	0.3430
bK	0.3060	0.3660
bL	0.2550	0.2560
bM	0.2370	0.2780
bN	0.2580	0.2770
bO	0.2130	0.2690
bP	0.2440	0.3230
bQ	0.2140	0.3340
bR	0.3370	0.3500
bS	0.3120	0.3890
bT	0.3150	0.3600
bU	0.4400	0.3720
bV	0.3780	0.3510
bW	0.3780	0.3380
bX	0.3420	0.3510

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Chain	Atom inclusion	Q-score
bY	 0.2230	 0.3100
bZ	 0.1960	 0.3360
ba	 0.3790	 0.3920
bb	 0.3440	 0.3980
bc	 0.3710	 0.3880
bd	 0.3590	 0.3920
be	 0.3650	 0.3910
bf	 0.3860	 0.3930
bg	 0.3700	 0.3880
bh	 0.3880	 0.3900
bi	 0.3690	 0.3950
bj	 0.3390	 0.3920
bk	 0.3720	 0.3900
bl	 0.3490	 0.3960
bm	 0.3400	 0.3930
bn	 0.3350	 0.4010
bo	 0.3390	 0.3910
bp	 0.3670	 0.3890
bq	 0.3350	 0.3870
br	 0.3990	 0.3920
bs	 0.3730	 0.3880
bt	 0.3840	 0.3930
bu	 0.4830	 0.3820
bv	 0.4510	 0.3760
bw	 0.4610	 0.3780
bx	 0.4270	 0.3790
by	 0.4070	 0.3760
bz	 0.4050	 0.3700
cA	 0.0000	 0.1280
cB	 0.0590	 0.2680
cC	 0.0010	 0.2080
cD	 0.0220	 0.2300
cE	 0.0380	 0.2070
cF	 0.1190	 0.2600
cG	 0.0270	 0.1770
cH	 0.2280	 0.2810
cI	 0.0090	 0.2100
cJ	 0.1480	 0.2890
cK	 0.0010	 0.1880
cL	 0.0800	 0.2810
cM	 0.0000	 0.1290
cN	 0.0110	 0.2370

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Chain	Atom inclusion	Q-score
cO	 0.0000	 0.4580
cP	 0.0080	 0.4540
cQ	 0.0130	 0.4490
cR	 0.2880	 0.3690
cS	 0.3090	 0.3610
cT	 0.2750	 0.3470
cU	 0.1420	 0.4210
cV	 0.1580	 0.4140
cW	 0.1700	 0.4200
cX	 0.3110	 0.3360
cY	 0.2550	 0.3320
cZ	 0.3020	 0.3400
ca	 0.2260	 0.3680
cb	 0.2460	 0.3550
cc	 0.2610	 0.3240
cd	 0.2650	 0.3370
ce	 0.3120	 0.3590
cf	 0.3640	 0.3430
cg	 0.1610	 0.3070
ch	 0.3600	 0.3560
ci	 0.4020	 0.3530
cj	 0.2720	 0.3750
ck	 0.2080	 0.3810
cl	 0.2500	 0.3610
cm	 0.2690	 0.3710
cn	 0.2410	 0.3910
co	 0.2670	 0.3680
cp	 0.0240	 0.2540
cq	 0.0000	 0.1670
cr	 0.0610	 0.2610
cs	 0.0020	 0.1780
ct	 0.0520	 0.2710
cu	 0.0010	 0.1850
cv	 0.1610	 0.2950
cw	 0.1090	 0.2620
cx	 0.2120	 0.2930
cy	 0.0350	 0.2420
cz	 0.0110	 0.2100
da	 0.0880	 0.4680
db	 0.1110	 0.4280
dc	 0.1120	 0.4710
dd	 0.2410	 0.3720

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Chain	Atom inclusion	Q-score
de	 0.2250	 0.3630
df	 0.2390	 0.3680
dg	 0.0080	 0.4510
dh	 0.0080	 0.4250
di	 0.0000	 0.4400
dj	 0.2870	 0.3620
dk	 0.2660	 0.3550
dl	 0.2990	 0.3340
dm	 0.0000	 0.3540
dn	 0.0110	 0.3860
do	 0.0000	 0.3280
dp	 0.3010	 0.3750
dq	 0.2960	 0.3750
dr	 0.3090	 0.3720
ds	 0.0300	 0.4410
dt	 0.0170	 0.4570
du	 0.0040	 0.4400