



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:59 PM UTC

PDB ID : 9F4A / pdb_00009f4a
EMDB ID : EMD-50186
Title : Interface between baseplate cup and extended tail tube/sheath of Klebsiella phage KP1 variant vB_Kpn_Lilla1
Authors : Orlova, E.V.; Isupov, M.N.
Deposited on : 2024-04-26
Resolution : 3.95 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:

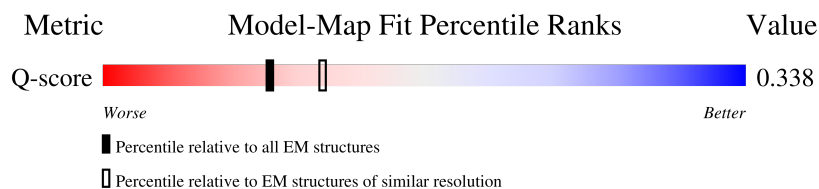
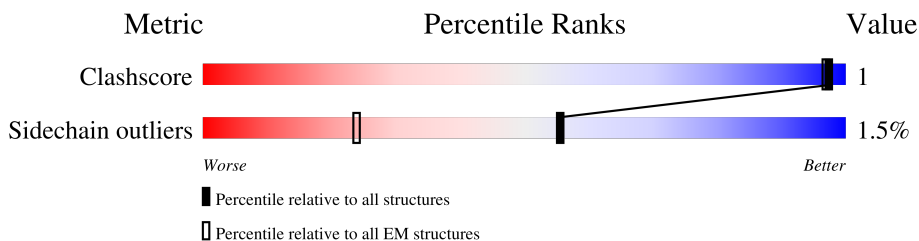
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.95 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7707 (3.45 - 4.45)

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	LS	1281	
1	LT	1281	
1	LU	1281	
1	LV	1281	
1	LW	1281	

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Mol	Chain	Length	Quality of chain
1	LX	1281	48% 46% 52%
1	LY	1281	48% 46% 52%
1	LZ	1281	48% 47% 52%
1	La	1281	48% 46% 52%
1	Lb	1281	48% 46% 52%
1	Lc	1281	48% 46% 52%
1	Ld	1281	48% 47% 52%
1	Le	1281	48% 46% 52%
1	Lf	1281	48% 46% 52%
1	Lg	1281	48% 46% 52%
1	Lh	1281	48% 46% 52%
1	Li	1281	48% 46% 52%
1	Lj	1281	48% 46% 52%
2	BK	350	47% 95%
2	BL	350	28% 76% 21%
2	BM	350	46% 94% 5%
2	BN	350	27% 75% 21%
2	BO	350	45% 95%
2	BP	350	27% 74% 5% 21%
3	BQ	308	19% 90% 5%
3	BR	308	18% 90% 5%
3	BS	308	19% 91% 5%
3	BT	308	19% 90% 5%
3	BU	308	19% 90% 5%
3	BV	308	18% 91% 5%

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Mol	Chain	Length	Quality of chain
4	AM	655	12% 97%
4	AN	655	11% 97%
4	AO	655	12% 96%
4	AP	655	11% 97%
4	AQ	655	10% 97%
4	AR	655	11% 97%
4	AS	655	15% 97%
4	AT	655	13% 96%
4	AU	655	15% 96%
4	AV	655	14% 95%
4	AW	655	15% 97%
4	AX	655	14% 95%
5	A0	1032	47% 96%
5	A1	1032	45% 96%
5	A2	1032	46% 96%
5	A3	1032	46% 96%
5	AY	1032	45% 96%
5	AZ	1032	46% 96%
6	A4	341	40% 94%
6	A5	341	40% 94%
6	A6	341	40% 94%
6	A7	341	39% 94%
6	A8	341	39% 94%
6	A9	341	40% 95%
6	Aa	341	55% 92%

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Mol	Chain	Length	Quality of chain
6	Ab	341	52% 93%
6	Ac	341	54% 92%
6	Ad	341	54% 92%
6	Ae	341	55% 93%
6	Af	341	52% 93%
7	LA	303	93% 96%
7	LB	303	95% 97%
7	LC	303	96% 98%
7	LD	303	93% 97%
7	LE	303	97% 97%
7	LF	303	97% 97%
7	LG	303	93% 96%
7	LH	303	97% 97%
7	LI	303	96% 98%
7	LJ	303	93% 97%
7	LK	303	96% 98%
7	LL	303	96% 97%
7	LM	303	93% 97%
7	LN	303	97% 96%
7	LO	303	97% 97%
7	LP	303	94% 97%
7	LQ	303	96% 97%
7	LR	303	97% 97%
8	FA	607	9% 10% 89%
8	FB	607	9% 10% 89%

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Mol	Chain	Length	Quality of chain
8	FC	607	8% 10% . 89%
8	FJ	607	9% 10% . 89%
8	FK	607	9% 10% . 89%
8	FL	607	9% 10% . 89%
8	FS	607	9% 10% . 89%
8	FT	607	10% 10% . 89%
8	FU	607	9% 10% . 89%
8	Fb	607	9% 10% . 89%
8	Fc	607	9% 10% . 89%
8	Fd	607	8% 10% . 89%
8	Fk	607	9% 10% . 89%
8	Fl	607	10% 10% . 89%
8	Fm	607	9% 10% . 89%
8	Ft	607	9% 10% . 89%
8	Fu	607	10% 10% . 89%
8	Fv	607	9% 10% . 89%
9	SA	656	16% 95% . .
9	SB	656	17% 95% . .
9	SC	656	16% 96% . .
9	SD	656	17% 96% . .
9	SE	656	16% 96% . .
9	SF	656	17% 96% . .
9	SG	656	11% 95% .
9	SH	656	11% 96% .
9	SI	656	11% 95% .

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Mol	Chain	Length	Quality of chain
9	SJ	656	11% 96%
9	SK	656	11% 96%
9	SL	656	11% 95%
9	SM	656	11% 96%
9	SN	656	12% 97%
9	SO	656	13% 96%
9	SP	656	12% 96%
9	SQ	656	12% 98%
9	SR	656	12% 96%
9	SS	656	13% 97%
9	ST	656	14% 97%
9	SU	656	13% 98%
9	SV	656	13% 97%
9	SW	656	14% 97%
9	SX	656	13% 98%
9	SY	656	16% 98%
9	SZ	656	17% 98%
9	Sa	656	16% 98%
9	Sb	656	16% 98%
9	Sc	656	17% 98%
9	Sd	656	16% 99%
9	Se	656	20% 97%
9	Sf	656	19% 97%
9	Sg	656	19% 97%
9	Sh	656	20% 97%

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Mol	Chain	Length	Quality of chain	
9	Si	656	19%	97%
9	Sj	656	19%	97%
9	Sk	656	55%	98%
9	Sl	656	55%	98%
9	Sm	656	56%	98%
9	Sn	656	55%	98%
9	So	656	56%	97%
9	Sp	656	55%	98%
10	TM	163	10%	92%
10	TN	163	9%	93%
10	TO	163	10%	92%
10	TP	163	10%	92%
10	TQ	163	9%	92%
10	TR	163	10%	93%
10	TS	163	7%	97%
10	TT	163	7%	95%
10	TU	163	7%	93%
10	TV	163	7%	95%
10	TW	163	7%	93%
10	TX	163	8%	94%
10	TY	163	7%	94%
10	TZ	163	7%	96%
10	Ta	163	6%	96%
10	Tb	163	6%	96%
10	Tc	163	6%	95%

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Mol	Chain	Length	Quality of chain
10	Td	163	6% 95% ..
10	Te	163	12% 95% ..
10	Tf	163	12% 94% 5% .
10	Tg	163	12% 94% 5% .
10	Th	163	11% 96% ..
10	Ti	163	12% 92% 7% .
10	Tj	163	12% 93% 7% .
10	Tk	163	12% 95% ..
10	Tl	163	14% 93% 7% .
10	Tm	163	12% 95% ..
10	Tn	163	12% 94% 5% .
10	To	163	13% 93% 7% .
10	Tp	163	13% 95% ..
10	Tq	163	85% 98% ..
10	Tr	163	84% 98% ..
10	Ts	163	85% 98% ..
10	Tt	163	85% 98% ..
10	Tu	163	85% 97% ..
10	Tv	163	85% 98% ..
11	AA	136	27% 91% 5% ..
11	AB	136	27% 94% ..
11	AC	136	26% 90% 5% ..
11	AD	136	28% 93% ..
11	AE	136	28% 93% ..
11	AF	136	27% 91% 6% .

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Mol	Chain	Length	Quality of chain
12	BE	380	
12	BF	380	
12	BG	380	
13	AG	212	
13	AH	212	
13	AI	212	
13	AJ	212	
13	AK	212	
13	AL	212	
14	BB	576	
14	BC	576	
14	BD	576	

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 605128 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 Long tail fiber proximal subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Le	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lf	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lg	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lh	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Li	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lj	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LS	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LT	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LU	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LV	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LW	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LX	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LY	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	LZ	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	La	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lb	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		
1	Lc	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Ld	617	4752	2963	834	947	8	0	0

There are 306 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Le	217	SER	ALA	conflict	UNP A0A5B9NKG2
Le	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Le	328	THR	ALA	conflict	UNP A0A5B9NKG2
Le	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Le	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Le	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Le	422	THR	SER	conflict	UNP A0A5B9NKG2
Le	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Le	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Le	535	SER	THR	conflict	UNP A0A5B9NKG2
Le	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Le	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Le	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Le	964	SER	THR	conflict	UNP A0A5B9NKG2
Le	973	PRO	THR	conflict	UNP A0A5B9NKG2
Le	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Le	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lf	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lf	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Lf	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lf	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lf	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lf	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lf	422	THR	SER	conflict	UNP A0A5B9NKG2
Lf	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lf	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lf	535	SER	THR	conflict	UNP A0A5B9NKG2
Lf	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lf	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lf	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lf	964	SER	THR	conflict	UNP A0A5B9NKG2
Lf	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lf	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Lf	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lg	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lg	278	ILE	VAL	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
Lg	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lg	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lg	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lg	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lg	422	THR	SER	conflict	UNP A0A5B9NKG2
Lg	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lg	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lg	535	SER	THR	conflict	UNP A0A5B9NKG2
Lg	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lg	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lg	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lg	964	SER	THR	conflict	UNP A0A5B9NKG2
Lg	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lg	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Lg	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lh	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lh	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Lh	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lh	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lh	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lh	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lh	422	THR	SER	conflict	UNP A0A5B9NKG2
Lh	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lh	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lh	535	SER	THR	conflict	UNP A0A5B9NKG2
Lh	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lh	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lh	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lh	964	SER	THR	conflict	UNP A0A5B9NKG2
Lh	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lh	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Lh	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Li	217	SER	ALA	conflict	UNP A0A5B9NKG2
Li	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Li	328	THR	ALA	conflict	UNP A0A5B9NKG2
Li	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Li	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Li	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Li	422	THR	SER	conflict	UNP A0A5B9NKG2
Li	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Li	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Li	535	SER	THR	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
Li	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Li	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Li	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Li	964	SER	THR	conflict	UNP A0A5B9NKG2
Li	973	PRO	THR	conflict	UNP A0A5B9NKG2
Li	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Li	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lj	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lj	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Lj	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lj	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lj	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lj	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lj	422	THR	SER	conflict	UNP A0A5B9NKG2
Lj	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lj	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lj	535	SER	THR	conflict	UNP A0A5B9NKG2
Lj	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lj	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lj	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lj	964	SER	THR	conflict	UNP A0A5B9NKG2
Lj	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lj	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Lj	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LS	217	SER	ALA	conflict	UNP A0A5B9NKG2
LS	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LS	328	THR	ALA	conflict	UNP A0A5B9NKG2
LS	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LS	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LS	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LS	422	THR	SER	conflict	UNP A0A5B9NKG2
LS	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LS	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LS	535	SER	THR	conflict	UNP A0A5B9NKG2
LS	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LS	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LS	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LS	964	SER	THR	conflict	UNP A0A5B9NKG2
LS	973	PRO	THR	conflict	UNP A0A5B9NKG2
LS	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LS	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LT	217	SER	ALA	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
LT	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LT	328	THR	ALA	conflict	UNP A0A5B9NKG2
LT	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LT	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LT	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LT	422	THR	SER	conflict	UNP A0A5B9NKG2
LT	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LT	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LT	535	SER	THR	conflict	UNP A0A5B9NKG2
LT	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LT	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LT	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LT	964	SER	THR	conflict	UNP A0A5B9NKG2
LT	973	PRO	THR	conflict	UNP A0A5B9NKG2
LT	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LT	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LU	217	SER	ALA	conflict	UNP A0A5B9NKG2
LU	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LU	328	THR	ALA	conflict	UNP A0A5B9NKG2
LU	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LU	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LU	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LU	422	THR	SER	conflict	UNP A0A5B9NKG2
LU	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LU	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LU	535	SER	THR	conflict	UNP A0A5B9NKG2
LU	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LU	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LU	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LU	964	SER	THR	conflict	UNP A0A5B9NKG2
LU	973	PRO	THR	conflict	UNP A0A5B9NKG2
LU	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LU	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LV	217	SER	ALA	conflict	UNP A0A5B9NKG2
LV	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LV	328	THR	ALA	conflict	UNP A0A5B9NKG2
LV	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LV	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LV	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LV	422	THR	SER	conflict	UNP A0A5B9NKG2
LV	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LV	467	ALA	PRO	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
LV	535	SER	THR	conflict	UNP A0A5B9NKG2
LV	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LV	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LV	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LV	964	SER	THR	conflict	UNP A0A5B9NKG2
LV	973	PRO	THR	conflict	UNP A0A5B9NKG2
LV	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LV	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LW	217	SER	ALA	conflict	UNP A0A5B9NKG2
LW	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LW	328	THR	ALA	conflict	UNP A0A5B9NKG2
LW	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LW	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LW	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LW	422	THR	SER	conflict	UNP A0A5B9NKG2
LW	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LW	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LW	535	SER	THR	conflict	UNP A0A5B9NKG2
LW	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LW	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LW	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LW	964	SER	THR	conflict	UNP A0A5B9NKG2
LW	973	PRO	THR	conflict	UNP A0A5B9NKG2
LW	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LW	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LX	217	SER	ALA	conflict	UNP A0A5B9NKG2
LX	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LX	328	THR	ALA	conflict	UNP A0A5B9NKG2
LX	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LX	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LX	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LX	422	THR	SER	conflict	UNP A0A5B9NKG2
LX	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LX	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LX	535	SER	THR	conflict	UNP A0A5B9NKG2
LX	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LX	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LX	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LX	964	SER	THR	conflict	UNP A0A5B9NKG2
LX	973	PRO	THR	conflict	UNP A0A5B9NKG2
LX	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LX	1180	ILE	VAL	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
LY	217	SER	ALA	conflict	UNP A0A5B9NKG2
LY	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LY	328	THR	ALA	conflict	UNP A0A5B9NKG2
LY	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LY	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LY	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LY	422	THR	SER	conflict	UNP A0A5B9NKG2
LY	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LY	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LY	535	SER	THR	conflict	UNP A0A5B9NKG2
LY	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LY	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LY	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LY	964	SER	THR	conflict	UNP A0A5B9NKG2
LY	973	PRO	THR	conflict	UNP A0A5B9NKG2
LY	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LY	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
LZ	217	SER	ALA	conflict	UNP A0A5B9NKG2
LZ	278	ILE	VAL	conflict	UNP A0A5B9NKG2
LZ	328	THR	ALA	conflict	UNP A0A5B9NKG2
LZ	369	GLY	ASP	conflict	UNP A0A5B9NKG2
LZ	413	GLU	GLY	conflict	UNP A0A5B9NKG2
LZ	419	GLU	ASP	conflict	UNP A0A5B9NKG2
LZ	422	THR	SER	conflict	UNP A0A5B9NKG2
LZ	429	ILE	VAL	conflict	UNP A0A5B9NKG2
LZ	467	ALA	PRO	conflict	UNP A0A5B9NKG2
LZ	535	SER	THR	conflict	UNP A0A5B9NKG2
LZ	567	VAL	ILE	conflict	UNP A0A5B9NKG2
LZ	580	ASN	ALA	conflict	UNP A0A5B9NKG2
LZ	727	GLY	ASP	conflict	UNP A0A5B9NKG2
LZ	964	SER	THR	conflict	UNP A0A5B9NKG2
LZ	973	PRO	THR	conflict	UNP A0A5B9NKG2
LZ	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
LZ	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
La	217	SER	ALA	conflict	UNP A0A5B9NKG2
La	278	ILE	VAL	conflict	UNP A0A5B9NKG2
La	328	THR	ALA	conflict	UNP A0A5B9NKG2
La	369	GLY	ASP	conflict	UNP A0A5B9NKG2
La	413	GLU	GLY	conflict	UNP A0A5B9NKG2
La	419	GLU	ASP	conflict	UNP A0A5B9NKG2
La	422	THR	SER	conflict	UNP A0A5B9NKG2
La	429	ILE	VAL	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
La	467	ALA	PRO	conflict	UNP A0A5B9NKG2
La	535	SER	THR	conflict	UNP A0A5B9NKG2
La	567	VAL	ILE	conflict	UNP A0A5B9NKG2
La	580	ASN	ALA	conflict	UNP A0A5B9NKG2
La	727	GLY	ASP	conflict	UNP A0A5B9NKG2
La	964	SER	THR	conflict	UNP A0A5B9NKG2
La	973	PRO	THR	conflict	UNP A0A5B9NKG2
La	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
La	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lb	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lb	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Lb	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lb	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lb	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lb	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lb	422	THR	SER	conflict	UNP A0A5B9NKG2
Lb	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lb	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lb	535	SER	THR	conflict	UNP A0A5B9NKG2
Lb	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lb	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lb	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lb	964	SER	THR	conflict	UNP A0A5B9NKG2
Lb	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lb	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Lb	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Lc	217	SER	ALA	conflict	UNP A0A5B9NKG2
Lc	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Lc	328	THR	ALA	conflict	UNP A0A5B9NKG2
Lc	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Lc	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Lc	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Lc	422	THR	SER	conflict	UNP A0A5B9NKG2
Lc	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Lc	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Lc	535	SER	THR	conflict	UNP A0A5B9NKG2
Lc	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Lc	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Lc	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Lc	964	SER	THR	conflict	UNP A0A5B9NKG2
Lc	973	PRO	THR	conflict	UNP A0A5B9NKG2
Lc	1141	LYS	GLN	conflict	UNP A0A5B9NKG2

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Chain	Residue	Modelled	Actual	Comment	Reference
Lc	1180	ILE	VAL	conflict	UNP A0A5B9NKG2
Ld	217	SER	ALA	conflict	UNP A0A5B9NKG2
Ld	278	ILE	VAL	conflict	UNP A0A5B9NKG2
Ld	328	THR	ALA	conflict	UNP A0A5B9NKG2
Ld	369	GLY	ASP	conflict	UNP A0A5B9NKG2
Ld	413	GLU	GLY	conflict	UNP A0A5B9NKG2
Ld	419	GLU	ASP	conflict	UNP A0A5B9NKG2
Ld	422	THR	SER	conflict	UNP A0A5B9NKG2
Ld	429	ILE	VAL	conflict	UNP A0A5B9NKG2
Ld	467	ALA	PRO	conflict	UNP A0A5B9NKG2
Ld	535	SER	THR	conflict	UNP A0A5B9NKG2
Ld	567	VAL	ILE	conflict	UNP A0A5B9NKG2
Ld	580	ASN	ALA	conflict	UNP A0A5B9NKG2
Ld	727	GLY	ASP	conflict	UNP A0A5B9NKG2
Ld	964	SER	THR	conflict	UNP A0A5B9NKG2
Ld	973	PRO	THR	conflict	UNP A0A5B9NKG2
Ld	1141	LYS	GLN	conflict	UNP A0A5B9NKG2
Ld	1180	ILE	VAL	conflict	UNP A0A5B9NKG2

- Molecule 2 is a protein called Baseplate tail tube cap.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BM	347	Total	C	N	O	S	0	0
			2664	1664	459	533	8		
2	BK	347	Total	C	N	O	S	0	0
			2664	1664	459	533	8		
2	BO	347	Total	C	N	O	S	0	0
			2664	1664	459	533	8		
2	BP	277	Total	C	N	O	S	0	0
			2180	1373	377	424	6		
2	BL	277	Total	C	N	O	S	0	0
			2180	1373	377	424	6		
2	BN	277	Total	C	N	O	S	0	0
			2180	1373	377	424	6		

- Molecule 3 is a protein called Baseplate subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BQ	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		
3	BV	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	BS	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		
3	BR	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		
3	BT	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		
3	BU	295	Total	C	N	O	S	0	0
			2263	1426	385	436	16		

- Molecule 4 is a protein called Baseplate wedge protein gp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AX	646	Total	C	N	O	S	0	0
			5125	3252	853	1009	11		
4	AW	648	Total	C	N	O	S	0	0
			5145	3265	856	1013	11		
4	AT	646	Total	C	N	O	S	0	0
			5125	3252	853	1009	11		
4	AS	648	Total	C	N	O	S	0	0
			5145	3265	856	1013	11		
4	AV	646	Total	C	N	O	S	0	0
			5125	3252	853	1009	11		
4	AU	648	Total	C	N	O	S	0	0
			5145	3265	856	1013	11		
4	AR	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		
4	AQ	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		
4	AN	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		
4	AM	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		
4	AP	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		
4	AO	654	Total	C	N	O	S	0	0
			5191	3296	863	1021	11		

- Molecule 5 is a protein called Baseplate wedge protein gp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AY	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AZ	1031	8438	5377	1416	1617	28	0	0
5	A0	1031	8438	5377	1416	1617	28	0	0
5	A1	1031	8438	5377	1416	1617	28	0	0
5	A2	1031	8438	5377	1416	1617	28	0	0
5	A3	1031	8438	5377	1416	1617	28	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AY	530	ALA	SER	conflict	UNP A0A2K9V5T9
AY	532	HIS	ASN	conflict	UNP A0A2K9V5T9
AY	536	ILE	VAL	conflict	UNP A0A2K9V5T9
AZ	530	ALA	SER	conflict	UNP A0A2K9V5T9
AZ	532	HIS	ASN	conflict	UNP A0A2K9V5T9
AZ	536	ILE	VAL	conflict	UNP A0A2K9V5T9
A0	530	ALA	SER	conflict	UNP A0A2K9V5T9
A0	532	HIS	ASN	conflict	UNP A0A2K9V5T9
A0	536	ILE	VAL	conflict	UNP A0A2K9V5T9
A1	530	ALA	SER	conflict	UNP A0A2K9V5T9
A1	532	HIS	ASN	conflict	UNP A0A2K9V5T9
A1	536	ILE	VAL	conflict	UNP A0A2K9V5T9
A2	530	ALA	SER	conflict	UNP A0A2K9V5T9
A2	532	HIS	ASN	conflict	UNP A0A2K9V5T9
A2	536	ILE	VAL	conflict	UNP A0A2K9V5T9
A3	530	ALA	SER	conflict	UNP A0A2K9V5T9
A3	532	HIS	ASN	conflict	UNP A0A2K9V5T9
A3	536	ILE	VAL	conflict	UNP A0A2K9V5T9

- Molecule 6 is a protein called Baseplate wedge subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A4	334	2669	1693	446	513	17	0	0
6	A9	334	2669	1693	446	513	17	0	0
6	A6	334	2669	1693	446	513	17	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	A5	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		
6	A8	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		
6	A7	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		
6	Ad	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		
6	Ac	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		
6	Af	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		
6	Ae	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		
6	Ab	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		
6	Aa	329	Total	C	N	O	S	0	0
			2633	1674	438	504	17		

- Molecule 7 is a protein called Baseplate wedge tail fiber connector.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LN	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LO	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LM	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LQ	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LR	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LP	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LB	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LC	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LA	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LE	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	LF	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LD	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LH	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LI	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LG	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LK	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LL	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		
7	LJ	303	Total	C	N	O	S	0	0
			2270	1412	386	461	11		

- Molecule 8 is a protein called Baseplate wedge protein gp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	FA	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FB	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FC	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FJ	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FK	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FL	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FS	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FT	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	FU	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	Fb	66	Total	C	N	O	S	0	0
			499	311	85	101	2		
8	Fc	66	Total	C	N	O	S	0	0
			499	311	85	101	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	Fd	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Fk	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Fl	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Fm	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Ft	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Fu	66	Total 499	C 311	N 85	O 101	S 2	0	0
8	Fv	66	Total 499	C 311	N 85	O 101	S 2	0	0

- Molecule 9 is a protein called Tail sheath protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SA	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SB	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SC	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SD	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SE	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SF	649	Total 4993	C 3142	N 850	O 985	S 16	0	0
9	SK	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SG	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SL	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SH	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SI	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SJ	655	Total 5037	C 3170	N 856	O 995	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	SQ	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SP	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SM	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SN	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SO	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SR	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SW	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SS	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	ST	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SU	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SV	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SX	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SY	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	SZ	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sa	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sb	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sc	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sd	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Se	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sf	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sg	655	Total 5037	C 3170	N 856	O 995	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Sh	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Si	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sj	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sk	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sl	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sm	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sn	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	So	655	Total 5037	C 3170	N 856	O 995	S 16	0	0
9	Sp	655	Total 5037	C 3170	N 856	O 995	S 16	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SA	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SB	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SC	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SD	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SE	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SF	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SK	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SG	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SL	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SH	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SI	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SJ	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SQ	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SP	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SM	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SN	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SO	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SR	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SW	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SS	482	ILE	VAL	conflict	UNP A0A2K9V5S7
ST	482	ILE	VAL	conflict	UNP A0A2K9V5S7

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Chain	Residue	Modelled	Actual	Comment	Reference
SU	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SV	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SX	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SY	482	ILE	VAL	conflict	UNP A0A2K9V5S7
SZ	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sa	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sb	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sc	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sd	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Se	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sf	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sg	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sh	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Si	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sj	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sk	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sl	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sm	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sn	482	ILE	VAL	conflict	UNP A0A2K9V5S7
So	482	ILE	VAL	conflict	UNP A0A2K9V5S7
Sp	482	ILE	VAL	conflict	UNP A0A2K9V5S7

- Molecule 10 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	TM	162	1305	825	222	253	5	0	0
10	TN	162	1305	825	222	253	5	0	0
10	TO	162	1305	825	222	253	5	0	0
10	TP	162	1305	825	222	253	5	0	0
10	TQ	162	1305	825	222	253	5	0	0
10	TR	162	1305	825	222	253	5	0	0
10	TW	162	1305	825	222	253	5	0	0
10	TS	162	1305	825	222	253	5	0	0
10	TT	162	1305	825	222	253	5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	TU	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	TV	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	TX	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	TY	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	TZ	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Ta	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tb	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tc	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Td	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Te	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tf	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tg	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Th	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Ti	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tj	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tk	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tl	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tm	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tn	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	To	162	Total 1305	C 825	N 222	O 253	S 5	0	0
10	Tp	162	Total 1305	C 825	N 222	O 253	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	Tq	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	Tr	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	Ts	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	Tt	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	Tu	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	Tv	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		

- Molecule 11 is a protein called IraD/Gp25-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		
11	AB	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		
11	AD	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		
11	AC	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		
11	AE	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		
11	AF	132	Total	C	N	O	S	0	0
			1044	648	183	209	4		

- Molecule 12 is a protein called Putative baseplate hub subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BE	379	Total	C	N	O	S	0	0
			3055	1945	511	583	16		
12	BF	379	Total	C	N	O	S	0	0
			3055	1945	511	583	16		
12	BG	379	Total	C	N	O	S	0	0
			3055	1945	511	583	16		

- Molecule 13 is a protein called Baseplate wedge subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		
13	AI	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		
13	AG	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		
13	AK	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		
13	AH	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		
13	AJ	212	Total	C	N	O	S	0	0
			1747	1123	279	340	5		

- Molecule 14 is a protein called Baseplate central spike protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BB	564	Total	C	N	O	S	0	0
			4354	2709	753	871	21		
14	BC	564	Total	C	N	O	S	0	0
			4354	2709	753	871	21		
14	BD	564	Total	C	N	O	S	0	0
			4354	2709	753	871	21		

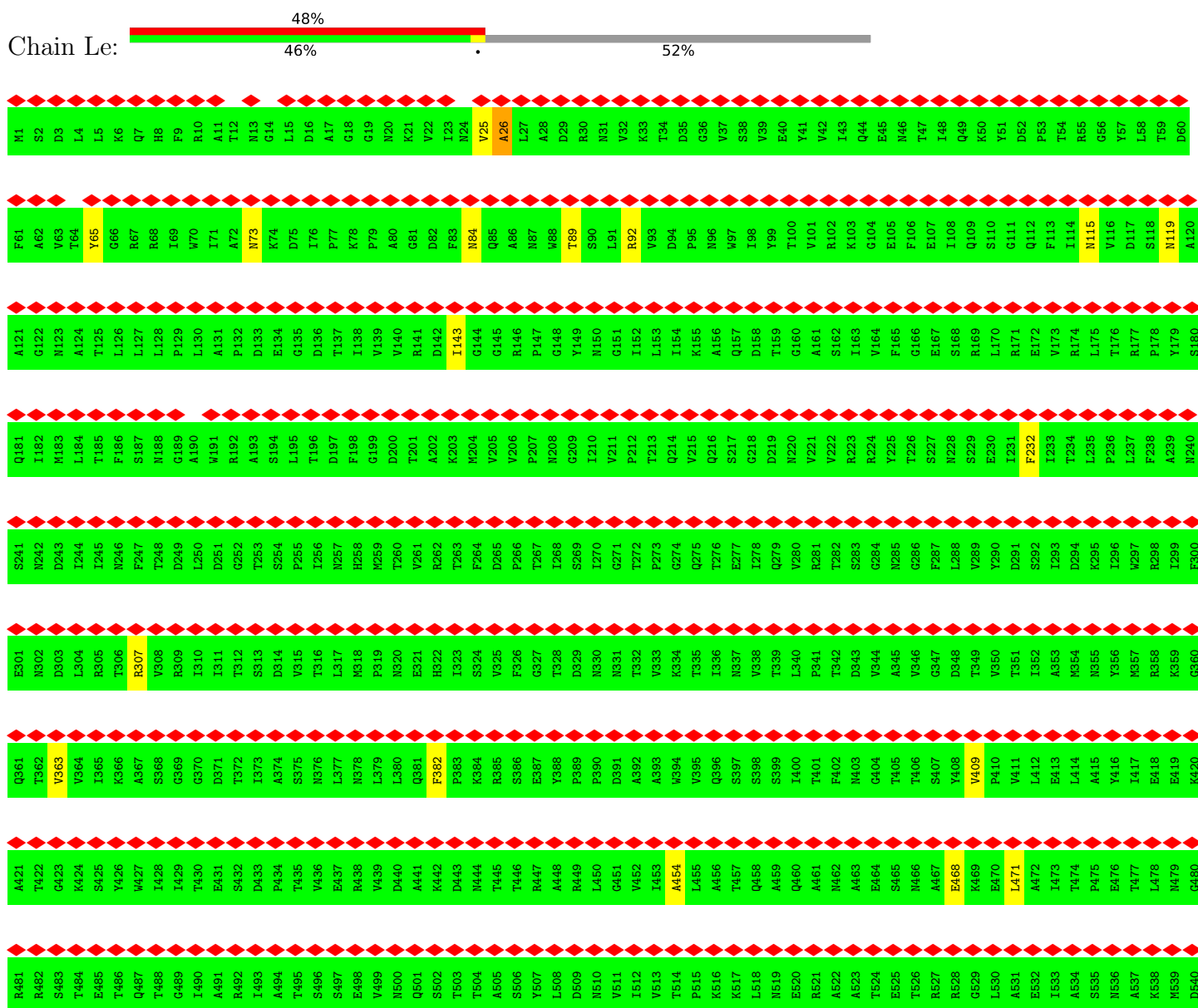
- Molecule 15 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		AltConf
15	BB	1	Total	Cl	0
			1	1	

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: Long tail fiber proximal subunit



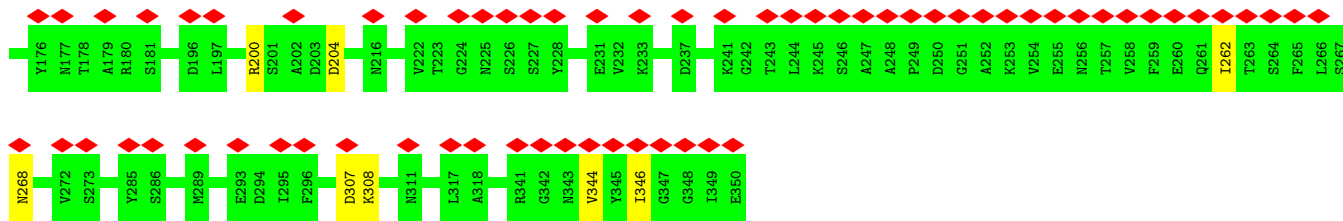
GLY
PRO
VAL
LYS
ILE
TRP
PRO
ASP
ARG
PRO
ASN
GLN
THR
LEU
LYS
PHE
GLU
TRP
VAL
GLY
ASP

● Molecule 1: Long tail fiber proximal subunit

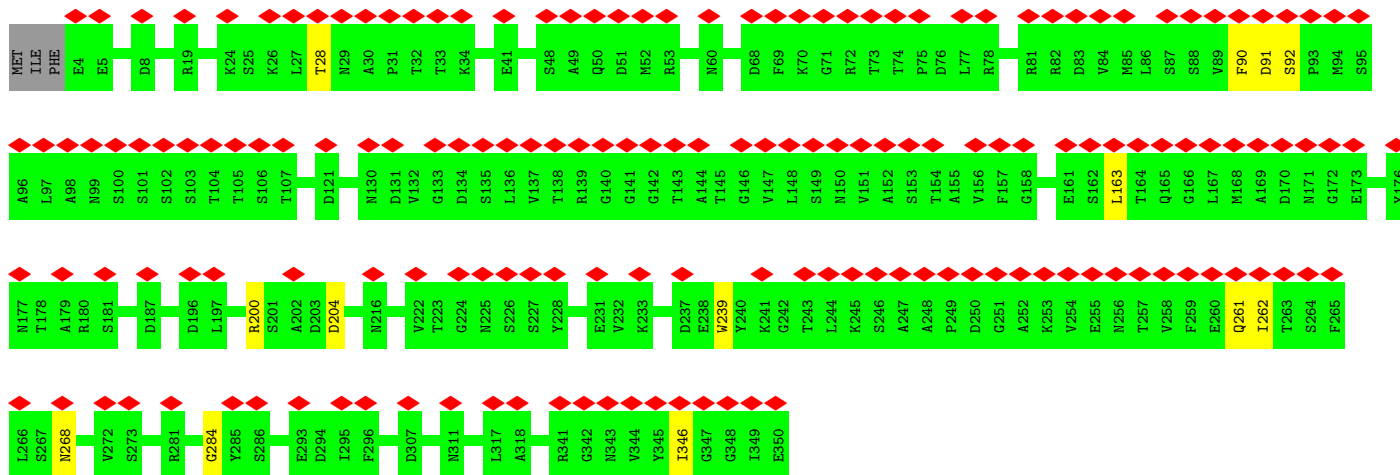


M1	S2	D3	L4	L5	K6	H7	H8	F9	R10	A11	T12	M13	G14	L15	D16	A17	G18	G19	N20	K21	V22	I23	N24	V25	A26	L27	A28	D29	R30	N31	V32	K33	T34	D35	G36	V37	S38	V39	E40	Y41	V42	R102	I43	O44	E45	N46	T47	I48	Q49	K50	S110	G111	O112	F53	T54	R55	G56	H57	L58	T59	D60
F61	A62	W63	T64	Y65	G66	H68	I69	W70	I71	A72	M73	K74	D75	I76	F77	K78	F79	A80	G81	D82	F83	N84	Q85	A86	H87	W88	T89	S90	L91	R92	W93	D94	P95	N96	H97	I98	Y99	T100	V101	R102	K103	G104	F105	E107	I108	Q109	S110	G111	O112	F113	T114	M115	V116	D117	L118	M119	A120				
A121	G122	M123	A124	T125	L126	L127	L128	P129	L130	A131	P132	D133	E134	G135	D136	I137	I138	V139	F139	V140	R141	D142	I143	G144	G145	R146	P147	G148	Y149	M150	G151	I152	T153	L154	K155	A156	Q157	T159	G160	A161	S162	I163	V164	F165	E167	S168	R169	L170	G171	E172	V173	R174	L175	T176	R177	P178	Y179	S180			
Q181	I182	M183	L184	T185	F186	S187	M188	G189	A190	W191	R192	A193	S194	L195	T196	D197	F198	G199	D200	T201	A202	K203	M204	V205	V206	P207	M208	G209	I210	V211	P212	T213	O214	V215	Q216	S217	G218	D219	M220	V221	V222	R223	R224	Y225	S226	S227	M228	S229	E230	I231	F232	T233	T234	L235	P236	L237	F238	A239	M240		
S241	N242	D243	I244	I245	N246	F247	T248	R249	L250	D251	G252	T253	S254	P255	I256	H258	M259	T260	V261	R262	K263	F264	D265	V266	T267	L268	S269	I270	G271	T272	T273	G274	Q275	T276	E277	I278	Q279	V280	R281	V282	S283	G284	N285	G286	F287	L288	V289	Y290	D291	S292	I293	D294	K295	I296	W297	R298	I299	F300			
E301	N302	D303	L304	R305	T306	R307	V308	R309	I310	I311	T312	S313	D314	V315	T316	L317	M318	P319	N320	E321	H322	I323	S324	V325	F326	G327	T328	D329	N330	N331	T332	V333	K334	V335	I336	N337	V338	T339	L340	P341	T342	D343	V344	A345	G347	D348	T349	V350	T351	I352	A353	M354	N355	Y356	M357	R358	K359	G360			
Q361	T362	V363	V364	I365	K366	A367	S368	G369	G370	D371	T372	I373	A374	S375	N376	L377	N378	L379	L380	Q381	F382	P383	K384	R385	S386	E387	Y388	P389	P390	D391	A392	A393	V394	V395	Q396	S397	S398	S399	I400	T401	F402	M403	G404	T405	T406	S407	Y408	V409	P410	V411	L412	E413	L414	A415	Y416	I417	E418	E419	K420		
A421	T422	G423	K424	Y425	Y426	W427	I428	I429	T430	E431	S432	D433	P434	T435	V436	E437	R438	V439	D440	A441	K442	D443	N444	T445	T446	R447	A448	R449	L450	G451	V452	I453	A454	L455	A456	T457	A458	A459	Q460	A461	M462	A463	E464	S465	M466	A467	E468	K469	E470	L471	A472	I473	T474	P475	E476	T477	L478	N479	G480		
R481	R482	S483	T484	E485	T486	Q487	T488	G489	I490	A491	R492	I493	A494	T495	S496	A497	E498	V499	N500	Q501	S502	T503	T504	A505	S506	Y507	L508	D509	N510	V511	I512	V513	L514	P515	K516	K517	L518	N519	E520	R521	A522	A523	T524	E525	T526	R527	R528	G529	L530	A531	E532	I533	A534	S535	N536	A537	L538	M539	D540		
A541	G542	T543	D544	D545	F546	T547	I548	V549	T550	P551	K552	K553	L554	L555	Y556	R557	T558	T559	S560	D561	S562	R563	L564	G565	V566	V567	Q568	L569	V570	K571	T572	G573	L574	G575	A576	P576	N577	T578	S579	N580	D581	R582	S583	S584	A585	A586	G586	T587	G588	I589	F590	D591	H592	S593	D594	Y595	K596	N597	A598	V599	T600
P601	K602	T603	L604	R605	E606	Y607	K608	A609	T610	V611	K652	Q613	S614	G615	I616	V617	TRP	LEU	ALA	THR	ASP	GLU	ARG	ASN	ILE	GLN	GLY	ALA	PRO	ALA	THR	GLN	VAL	PHE	ALA	GLY	ALA	LEU	HIS	LYS	LYS	VAL	VAL	ALA	THR	ASP	PRO	ALA	LYS	LYS	LEU	LEU	PHE	VAL							
THR	GLN	GLU	VAL	ASN	ALA	GLY	VAL	ASN	LYS	ALA	VAL	PRO	LYS	THR	LEU	ASN	ASP	ARG	ALA	THR	ASN	ARG	THR	ILE	GLN	GLY	ALA	PRO	ALA	THR	GLN	VAL	PHE	ALA	GLY	ALA	LEU	HIS	LYS	LYS	VAL	VAL	ALA	THR	ASP	PRO	ALA	LYS	LYS	LEU	LEU	PHE	VAL								
ASP	LYS	PHE	ALA	ASN	VAL	THR	ASN	ALA	LYS	SER	VAL	GLY	THR	LEU	THR	ASN	ASP	ARG	ALA	THR	ASN	ARG	THR	ILE	GLN	GLY	ALA	PRO	ALA	THR	GLN	VAL	PHE	ALA	GLY	ALA	LEU	HIS	LYS	LYS	VAL	VAL	ALA	THR	ASP	PRO	ALA	LYS	LYS	LEU	LEU	PHE	VAL								

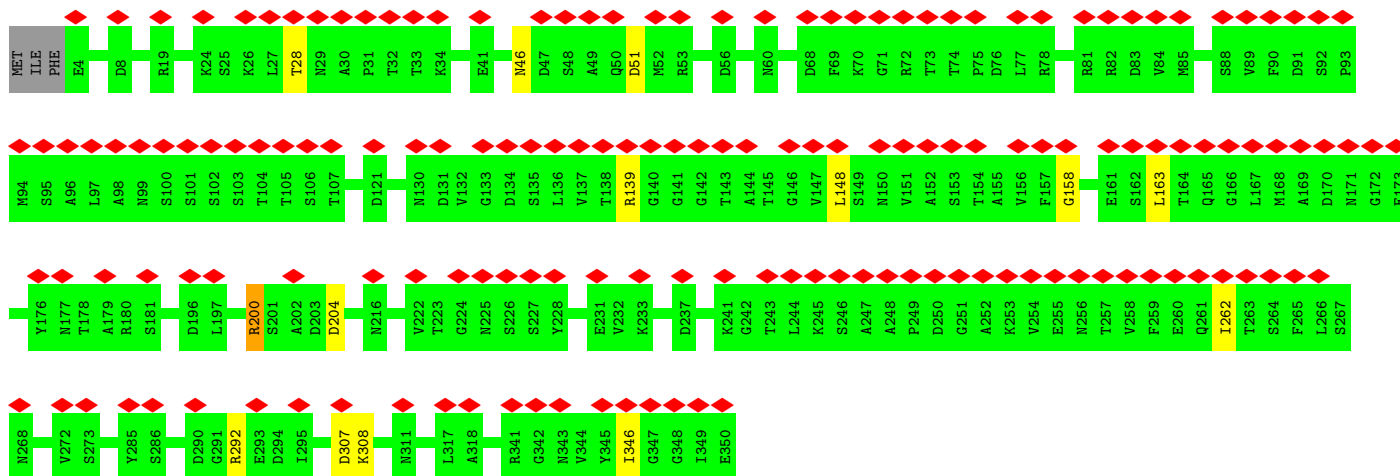
ARG	THR	VAL	THR	ASP	THR	P601	A541	R481	A421	Q361	E501	S241	Q181	A121	F61
ASP	GLN	ARG	GLN	LYS	THR	K602	G542	R482	T422	T362	N302	N242	I182	G122	A62
LYS	THR	LEU	VAL	PHE	GLU	T603	T543	S483	G423	V363	D303	D243	M183	N123	V63
THR	VAL	LEU	VAL	ASN	VAL	L604	D544	T484	K424	V364	L304	I244	L184	A124	T64
ASN	THR	HIS	THR	THR	ASN	R605	D545	E485	S425	I365	T306	I245	F185	T125	Y65
ALA	GLY	ALA	ALA	ARG	ALA	F606	F546	T486	Y426	K366	R307	N246	F186	L126	G66
GLY	GLY	GLY	GLY	GLY	GLY	Y607	T547	Q487	W427	A367	V308	T248	F187	L127	R67
THR	VAL	THR	VAL	ILE	VAL	K608	I548	T488	L428	S368	R309	T249	M188	L128	R68
VAL	THR	THR	THR	GLN	THR	A609	V549	G489	L429	G369	R309	D249	G189	P129	I69
ASN	ASN	GLY	ASN	ASN	ASN	T610	T550	L490	T430	G370	I310	L250	A190	L130	W70
ALA	ALA	ALA	ALA	SER	ALA	V611	P851	A491	E431	D371	I311	D251	W191	A131	I71
THR	VAL	THR	VAL	SER	VAL	N612	K552	R492	S432	T372	T312	G252	R192	P132	A72
GLY	GLY	GLY	GLY	GLY	GLY	R613	K553	I493	D433	I373	S133	T253	A193	D133	N73
ALA	THR	ALA	THR	THR	LYS	R614	L554	A494	P434	A374	D314	S254	K74	E134	K74
ALA	THR	GLN	THR	ILE	THR	R615	L855	T495	T435	S375	V315	P255	D76	G135	D76
LEU	THR	TYR	THR	THR	LEU	I616	Y556	S496	W436	N376	T316	I256	I76	D136	I76
PRO	ASN	ALA	ALA	GLY	ASN	W617	R557	S497	E437	L377	L317	N257	P77	T137	P77
ASP	THR	THR	THR	THR	THR	T617	T558	E498	R438	N378	M318	H258	K78	I138	K78
LEU	LEU	LEU	LEU	THR	THR	A608	T559	E499	A439	L379	P319	M259	P79	V139	P79
ALA	ALA	ALA	ALA	THR	ALA	A609	S560	N500	V439	L380	N320	T260	A80	V140	A80
ALA	THR	THR	THR	THR	THR	D561	D561	Q501	D440	L380	E321	T261	G81	R141	G81
ASP	ASP	ASP	ASP	ASP	ASP	S562	S562	S502	A441	Q382	H322	R262	D82	D142	D82
GLY	GLY	GLY	GLY	GLY	GLY	R663	R663	T503	K442	F382	I323	T263	F83	I143	F83
THR	THR	THR	THR	THR	THR	L564	L564	T504	D443	P383	S324	F264	N84	G144	N84
ASN	ASN	ASN	ASN	ASN	ASN	G565	G565	A505	N444	K384	S224	D265	Q86	G145	Q86
GLN	GLN	GLN	GLN	GLN	GLN	G566	G566	S506	T446	R386	F326	P266	A86	G146	A86
ALA	ALA	ALA	ALA	ALA	ALA	V567	V567	T507	R447	E387	G327	T267	N87	P147	N87
ALA	ALA	ALA	ALA	ALA	ALA	Q568	Q568	L508	A448	P388	T328	I268	W88	G148	W88
PRO	PRO	PRO	PRO	PRO	PRO	L569	L569	D509	R449	P389	D329	S269	T89	Y149	T89
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GLY	GLY	GLY	GLY	GLY	GLY	A571	A571	V511	G451	D391	N331	G271	L91	G151	L91
THR	THR	THR	THR	THR	THR	T572	T572	L512	V452	A392	T332	T272	R92	I152	R92
LYS	LYS	LYS	LYS	LYS	LYS	G573	G573	V513	I453	A393	V333	P273	V93	L153	V93
THR	THR	THR	THR	THR	THR	A574	A574	T514	A454	G394	K334	G274	D94	I154	D94
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ALA	ALA	ALA	ALA	ALA	ALA	N577	N577	K517	T457	S397	T336	E277	W97	Q157	W97
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SER	SER	SER	SER	SER	SER	V579	V579	N519	A459	S399	T339	Q279	Y99	T159	Y99
VAL	VAL	VAL	VAL	VAL	VAL	N580	N580	E520	Q460	I400	L340	V280	T100	G160	T100
THR	THR	THR	THR	THR	THR	D581	D581	R521	A461	T401	F341	R281	V101	A161	V101
VAL	VAL	VAL	VAL	VAL	VAL	R582	R582	A522	N462	F402	T342	T282	R102	S162	R102
THR	THR	THR	THR	THR	THR	S583	S583	A523	M403	D343	D343	S283	K103	I163	K103
ASP	ASP	ASP	ASP	ASP	ASP	R584	R584	T524	G404	G404	V344	G284	G104	V164	G104
VAL	VAL	VAL	VAL	VAL	VAL	A585	A585	E525	S465	T406	A346	N285	E105	F165	E105
ARG	ARG	ARG	ARG	ARG	ARG	G586	G586	T526	N466	T406	V346	G286	F106	G166	F106
ILE	ILE	ILE	ILE	ILE	ILE	T587	T587	R527	A467	S407	G347	F287	E107	E167	E107
LEU	LEU	LEU	LEU	LEU	LEU	G588	G588	R528	E468	Y408	D348	L288	I108	S168	I108
LEU	LEU	LEU	LEU	LEU	LEU	F589	F589	G529	K469	V409	T349	S229	Q109	R169	Q109
ALA	ALA	ALA	ALA	ALA	ALA	D591	D591	L530	E470	P410	V350	E230	S110	L170	S110
ASN	ASN	ASN	ASN	ASN	ASN	H592	H592	A531	L471	V411	T351	E231	G111	R171	G111
THR	THR	THR	THR	THR	THR	S593	S593	E532	A472	L412	I352	S292	Q112	E172	Q112
GLN	GLN	GLN	GLN	GLN	GLN	D594	D594	I633	I473	E413	A353	I293	F113	V173	F113
GLY	GLY	GLY	GLY	GLY	GLY	R595	R595	A534	T474	L414	M354	D294	I114	R174	I114
ARG	ARG	ARG	ARG	ARG	ARG	Y596	Y596	S535	P475	A415	N355	K295	N115	L175	N115
GLN	GLN	GLN	GLN	GLN	GLN	K597	K597	N536	E476	Y416	Y356	I296	V116	T176	V116
THR	THR	THR	THR	THR	THR	N597	N597	A537	T477	I417	M357	W297	D117	R177	D117
ASP	ASP	ASP	ASP	ASP	ASP	V599	V599	K538	L478	E418	R358	F238	S118	P178	S118
SER	SER	SER	SER	SER	SER	T600	T600	N539	N479	E419	K359	I299	N119	Y179	N119
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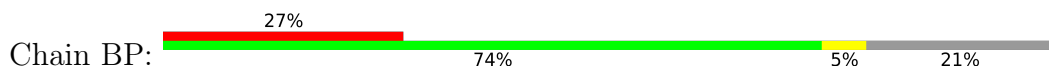
• Molecule 2: Baseplate tail tube cap

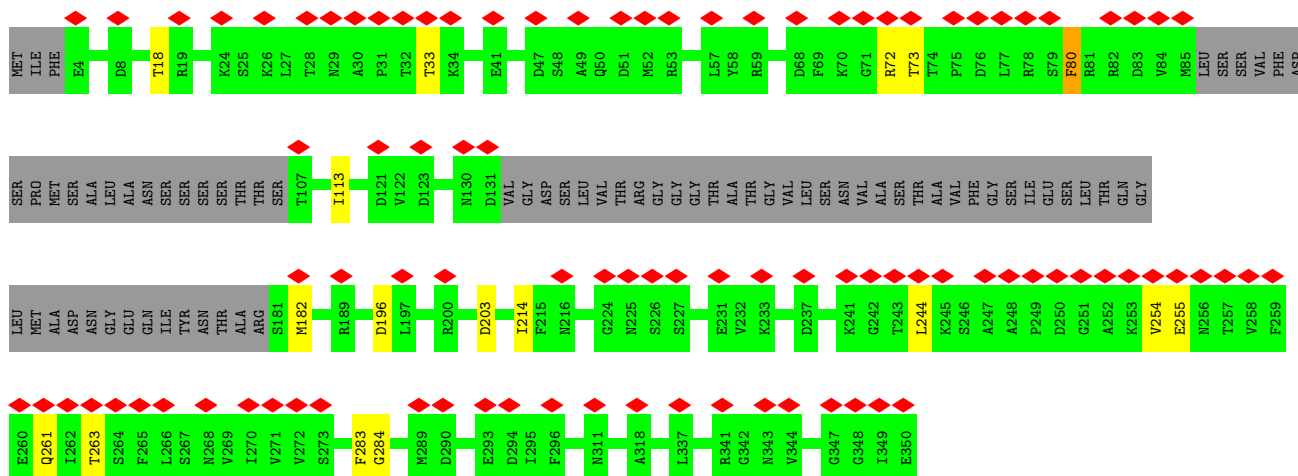


• Molecule 2: Baseplate tail tube cap

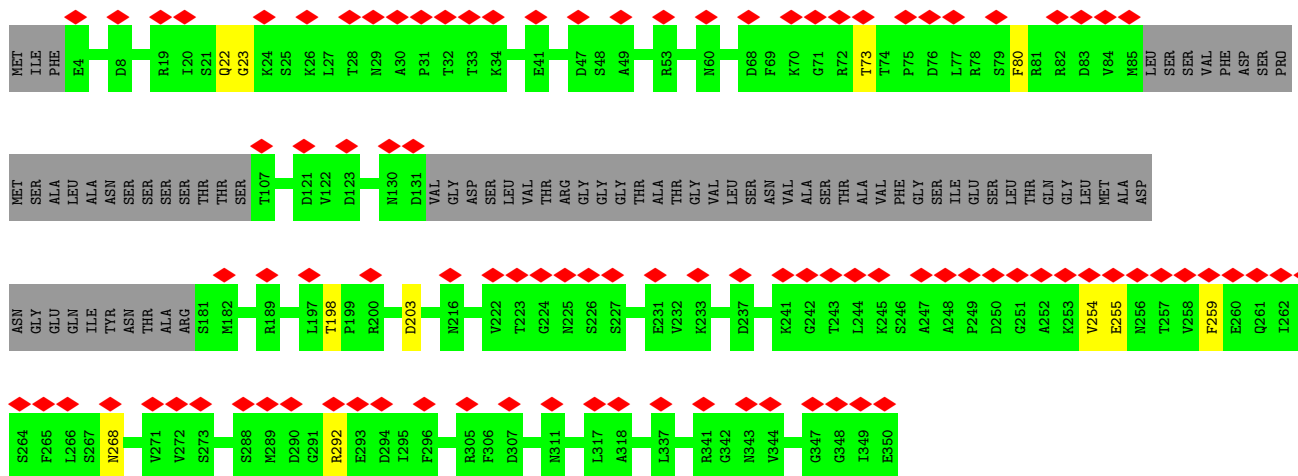
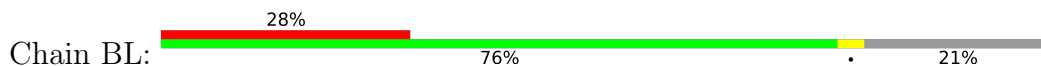


• Molecule 2: Baseplate tail tube cap

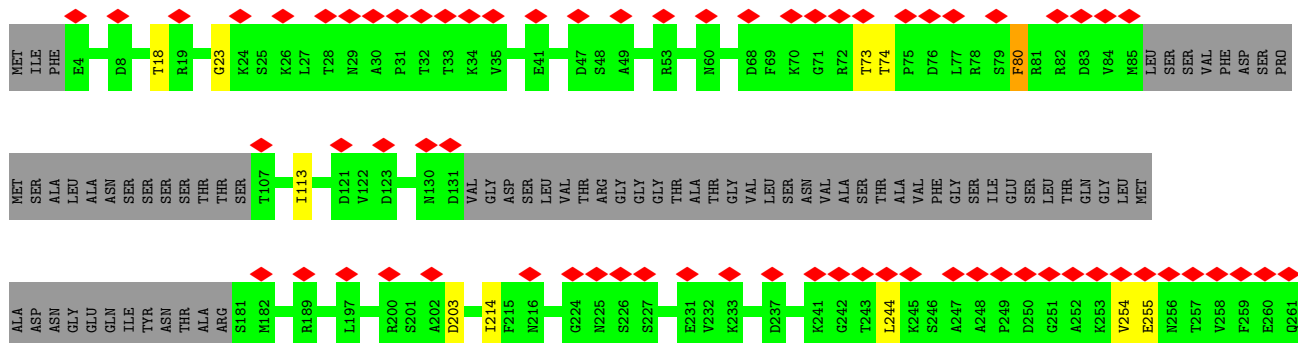
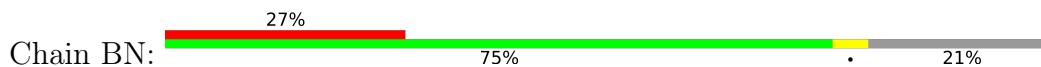


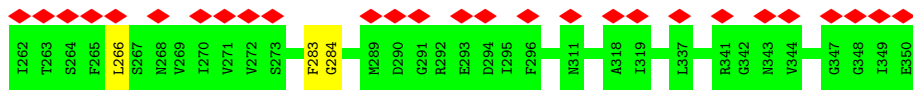


• Molecule 2: Baseplate tail tube cap

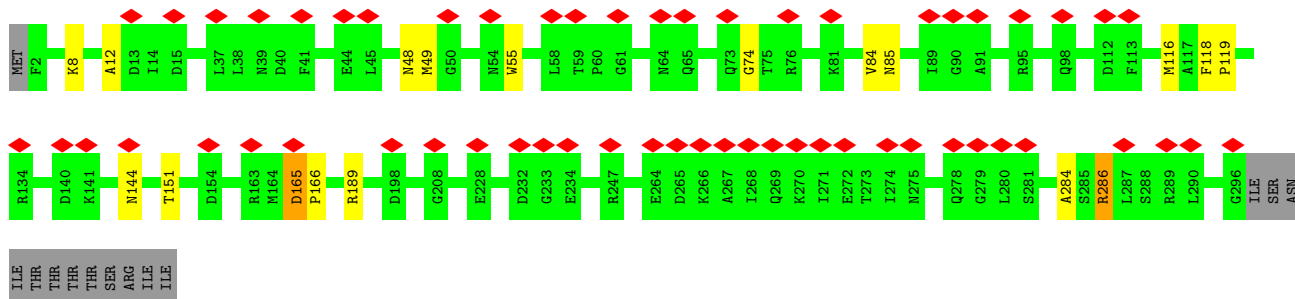
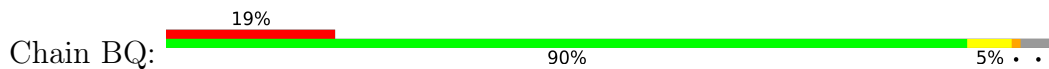


• Molecule 2: Baseplate tail tube cap

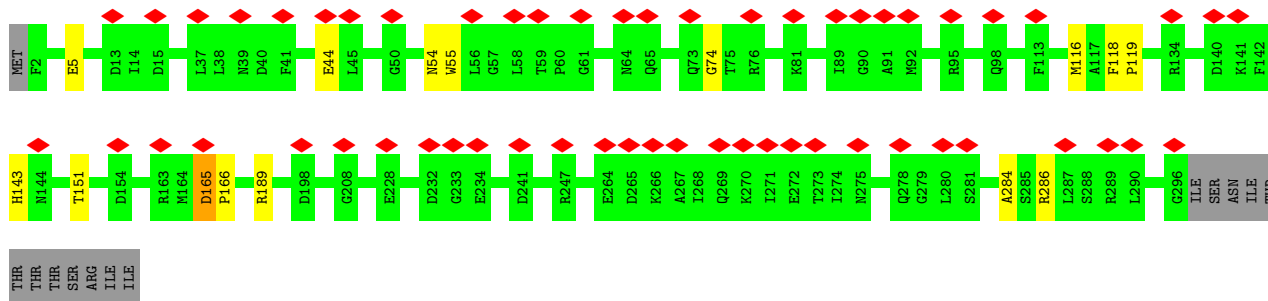
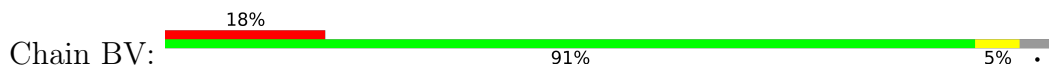




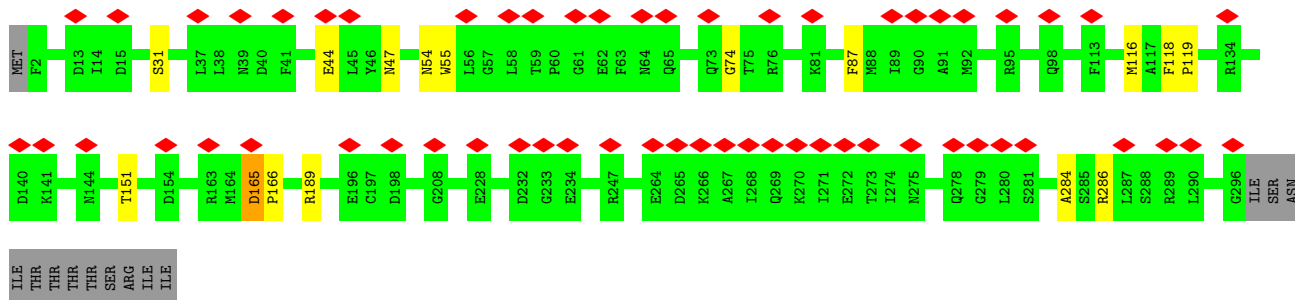
• Molecule 3: Baseplate subunit



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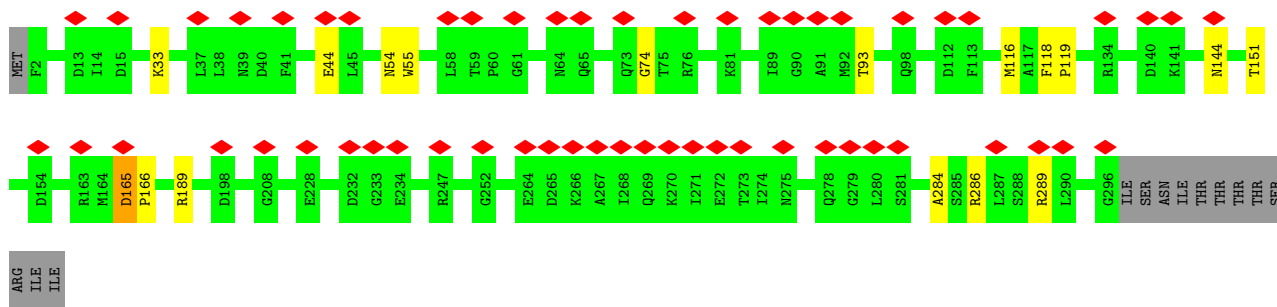


• Molecule 3: Baseplate subunit

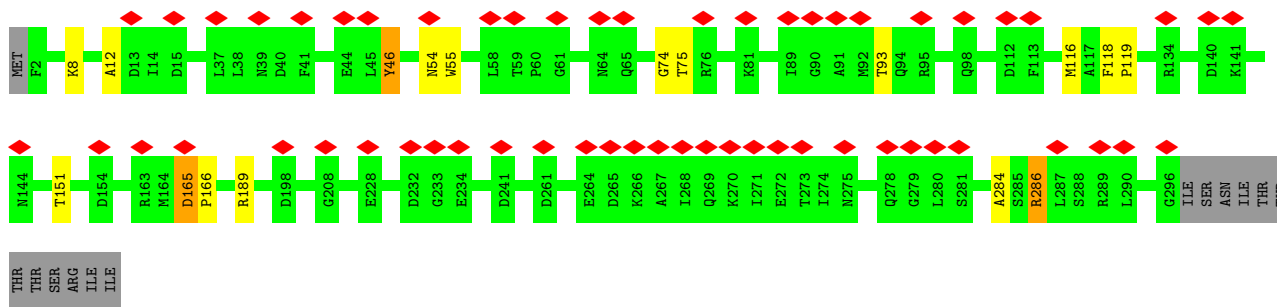
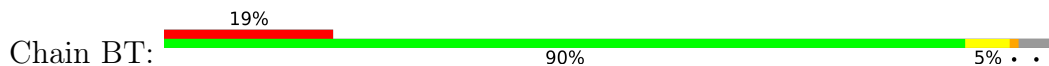


• Molecule 3: Baseplate subunit

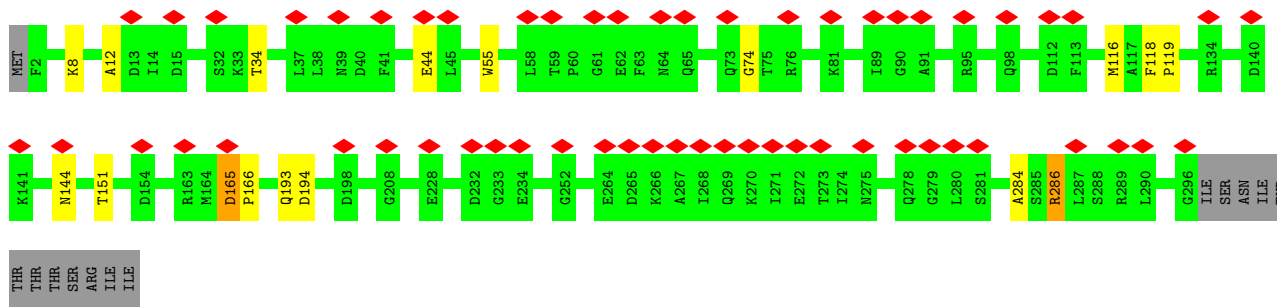
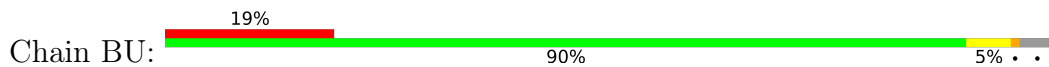




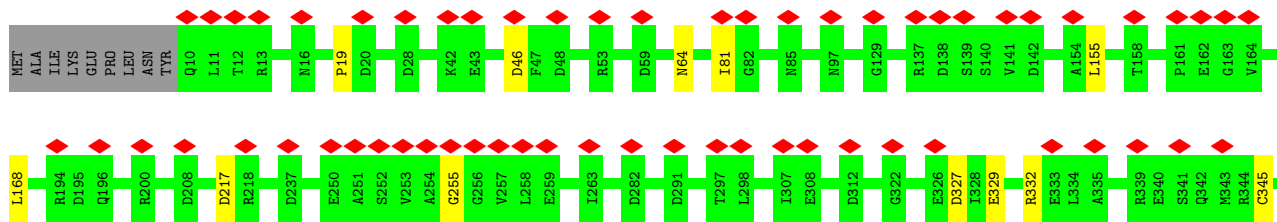
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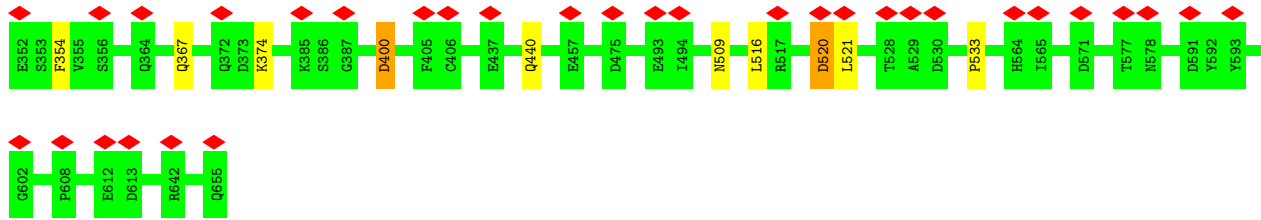


• Molecule 3: Baseplate subunit

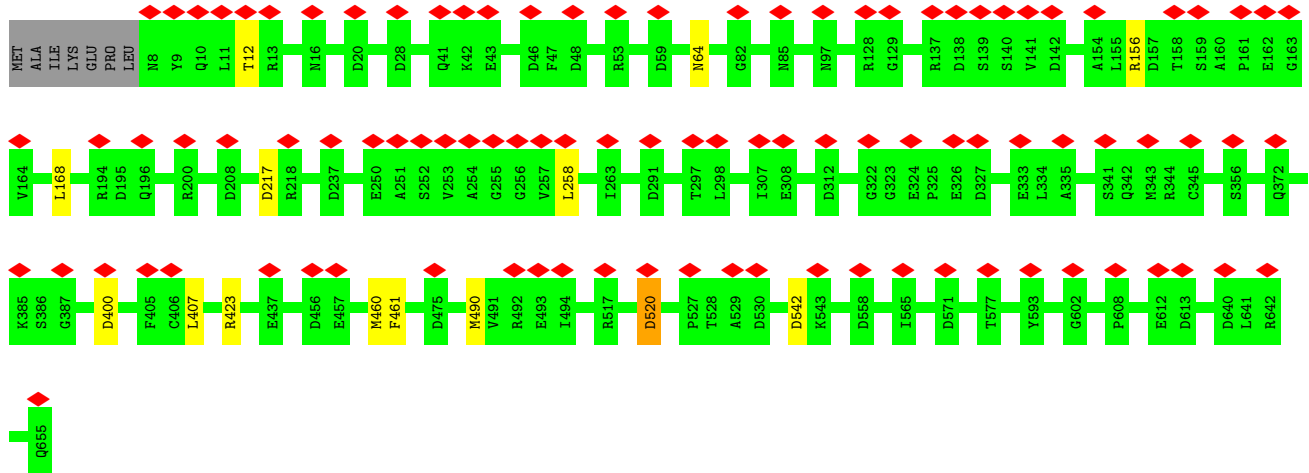


• Molecule 4: Baseplate wedge protein gp6

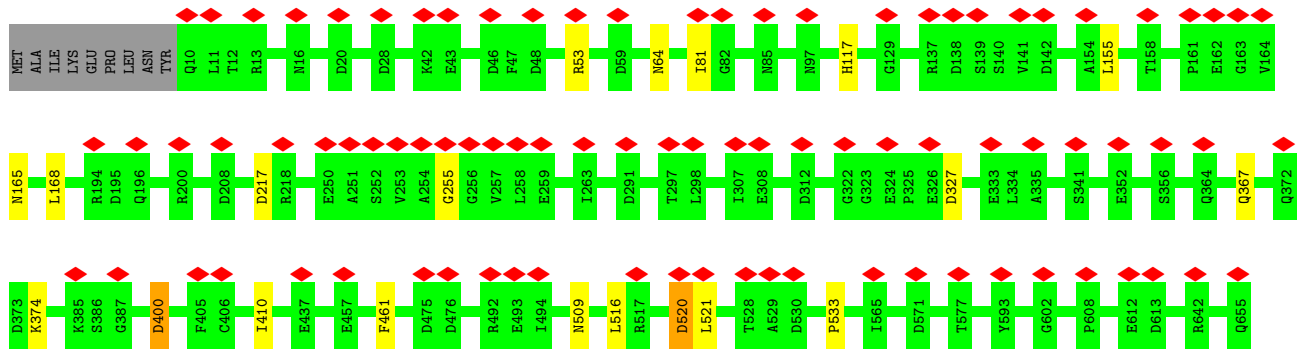




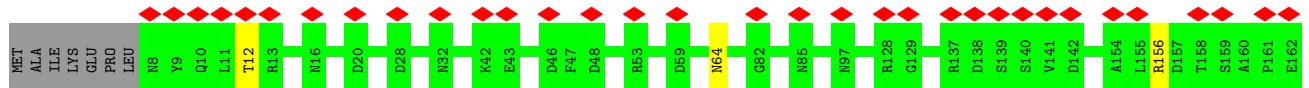
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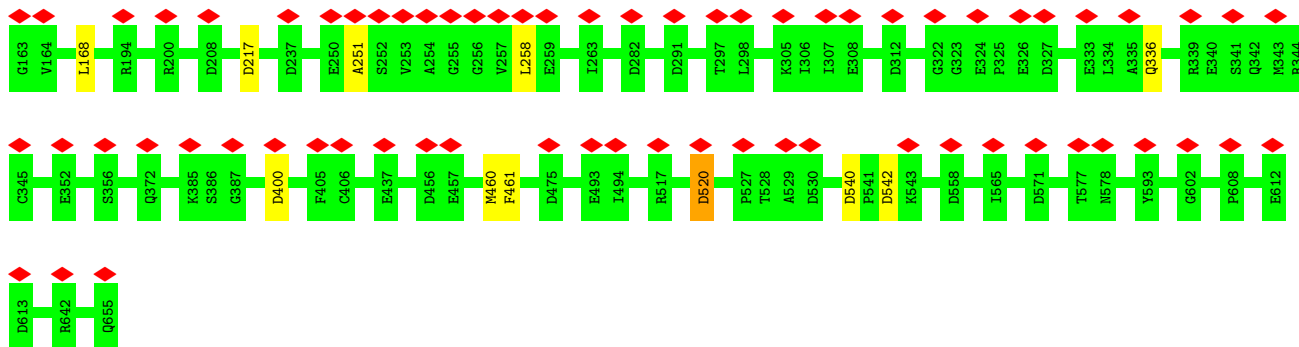


• Molecule 4: Baseplate wedge protein gp6

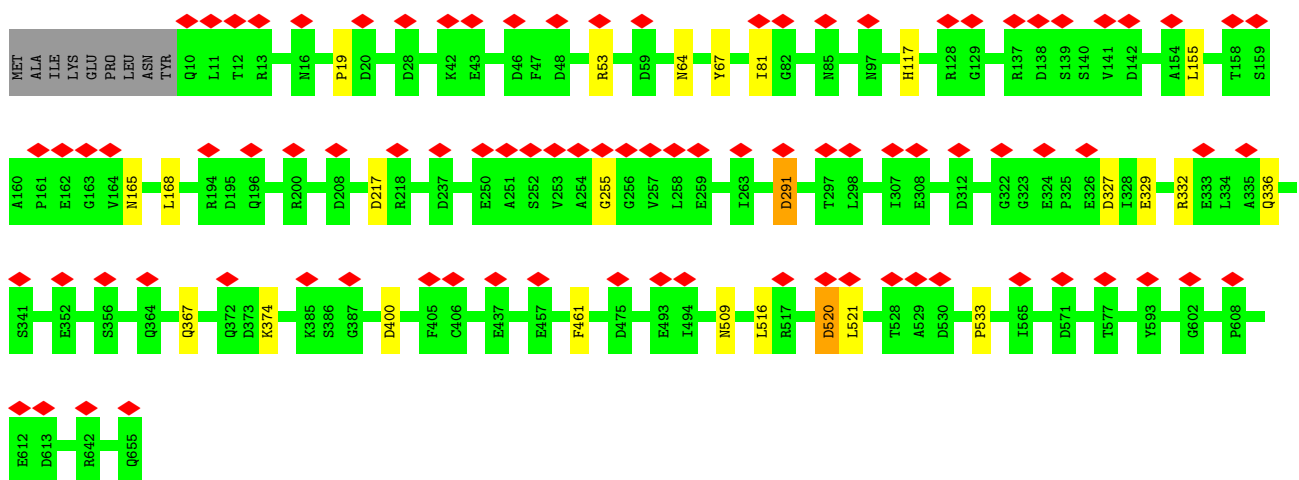


• Molecule 4: Baseplate wedge protein gp6

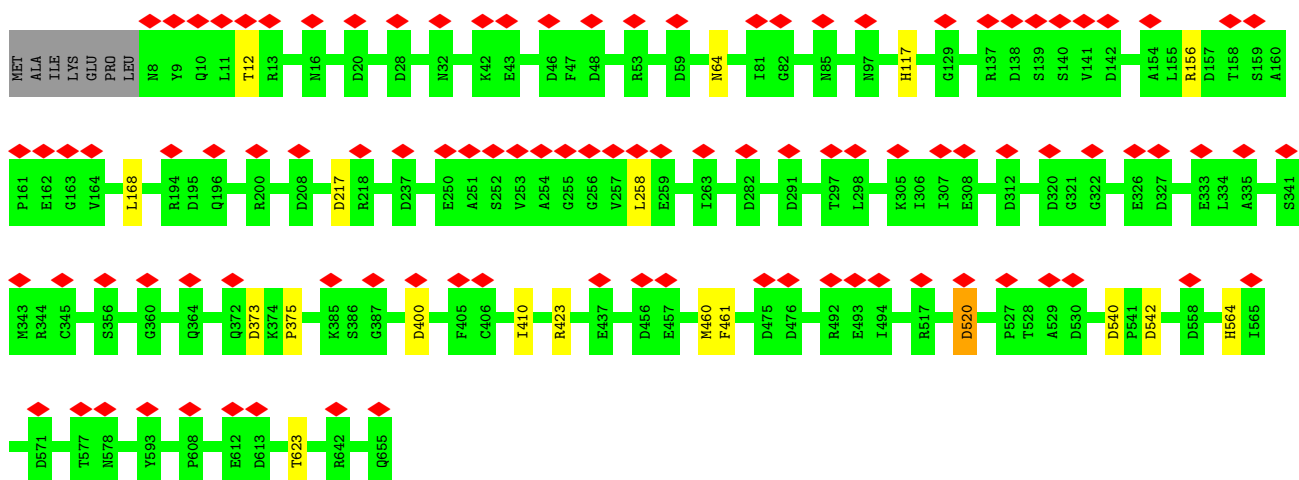




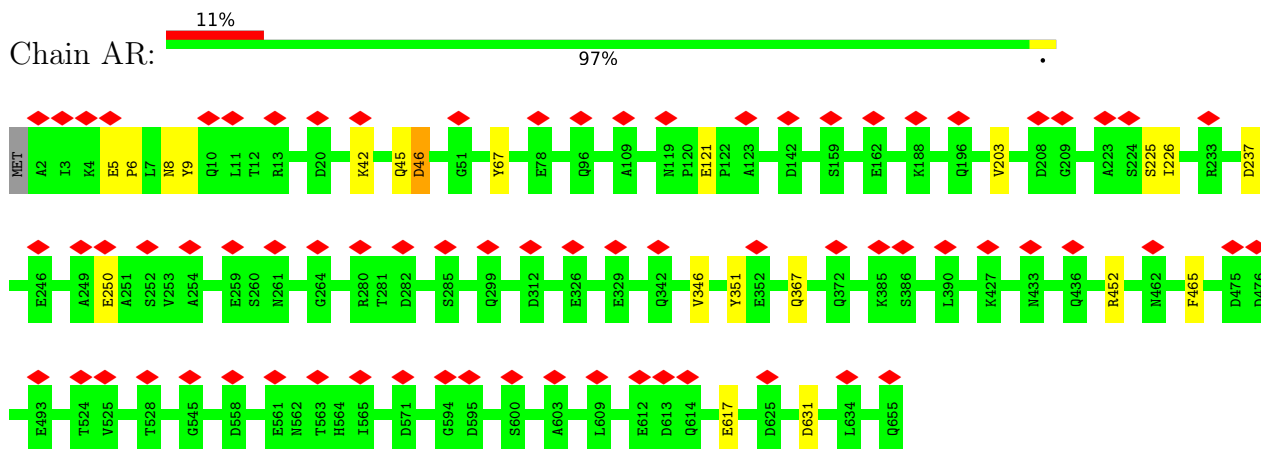
• Molecule 4: Baseplate wedge protein gp6



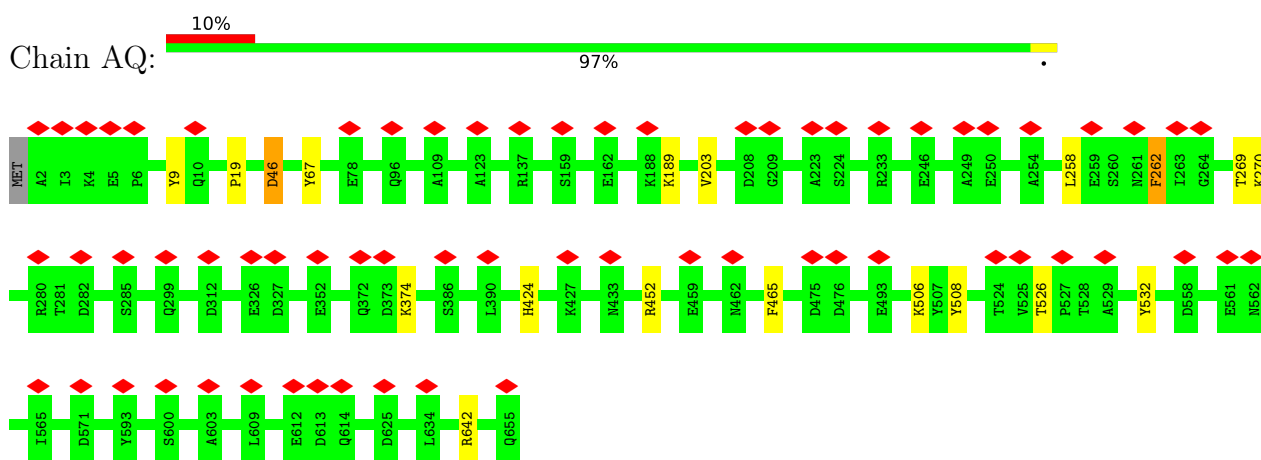
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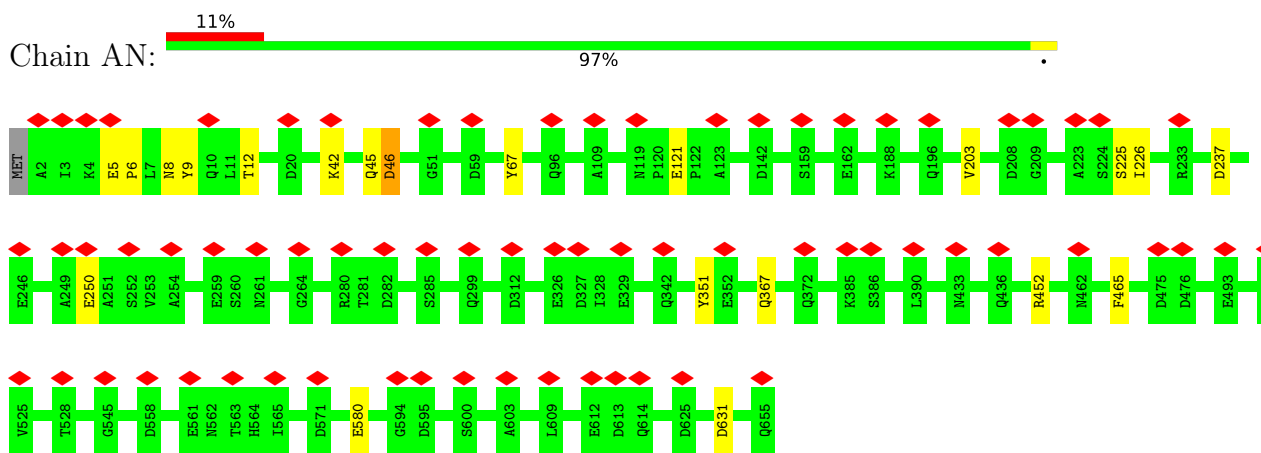
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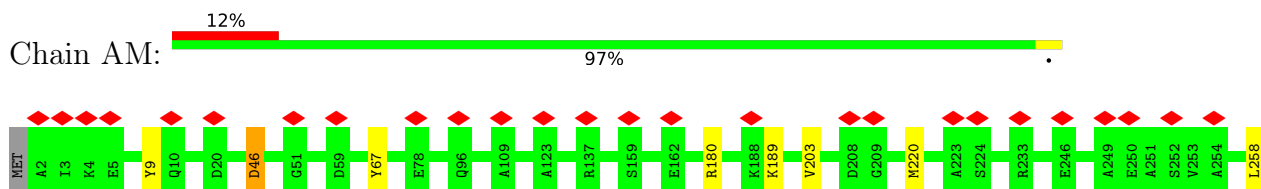
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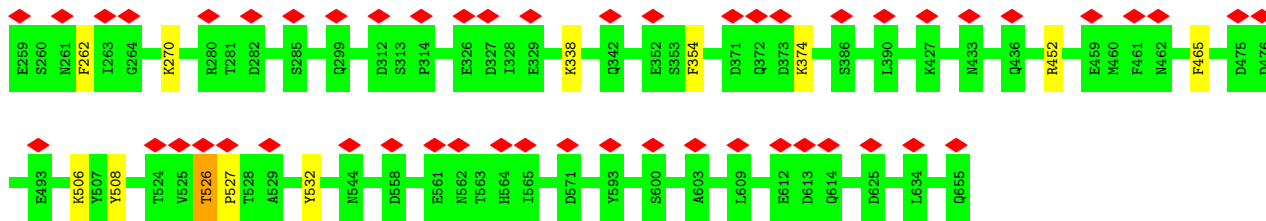


• Molecule 4: Baseplate wedge protein gp6

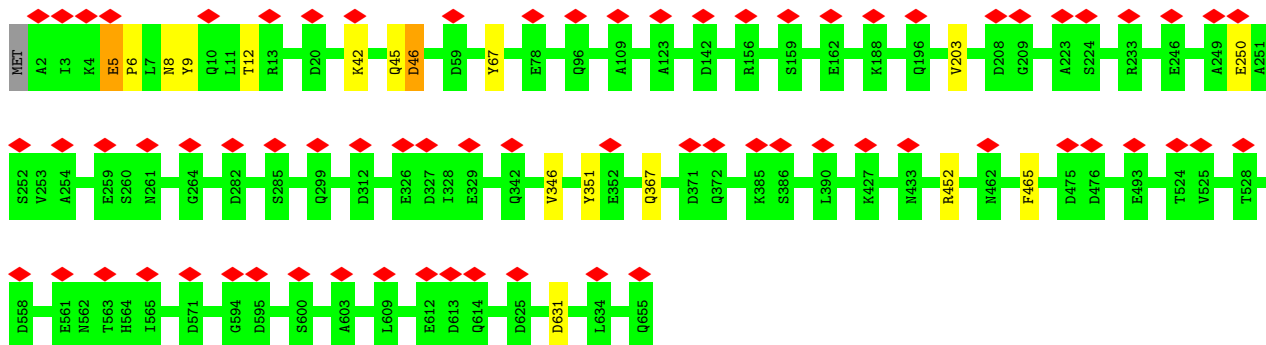


• Molecule 4: Baseplate wedge protein gp6

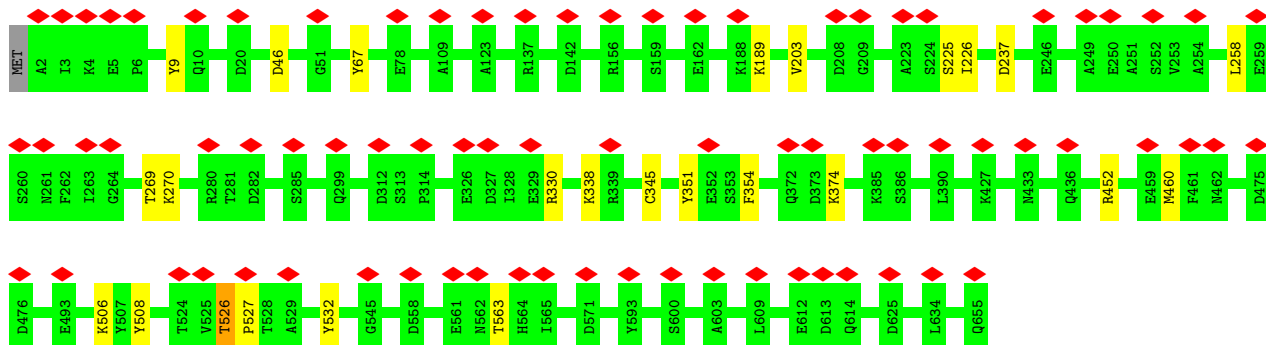




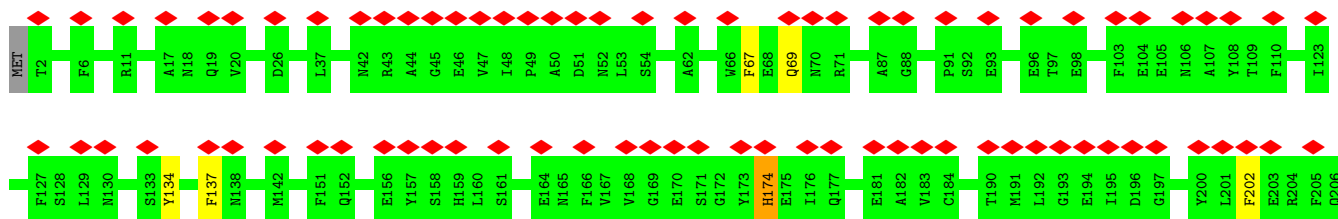
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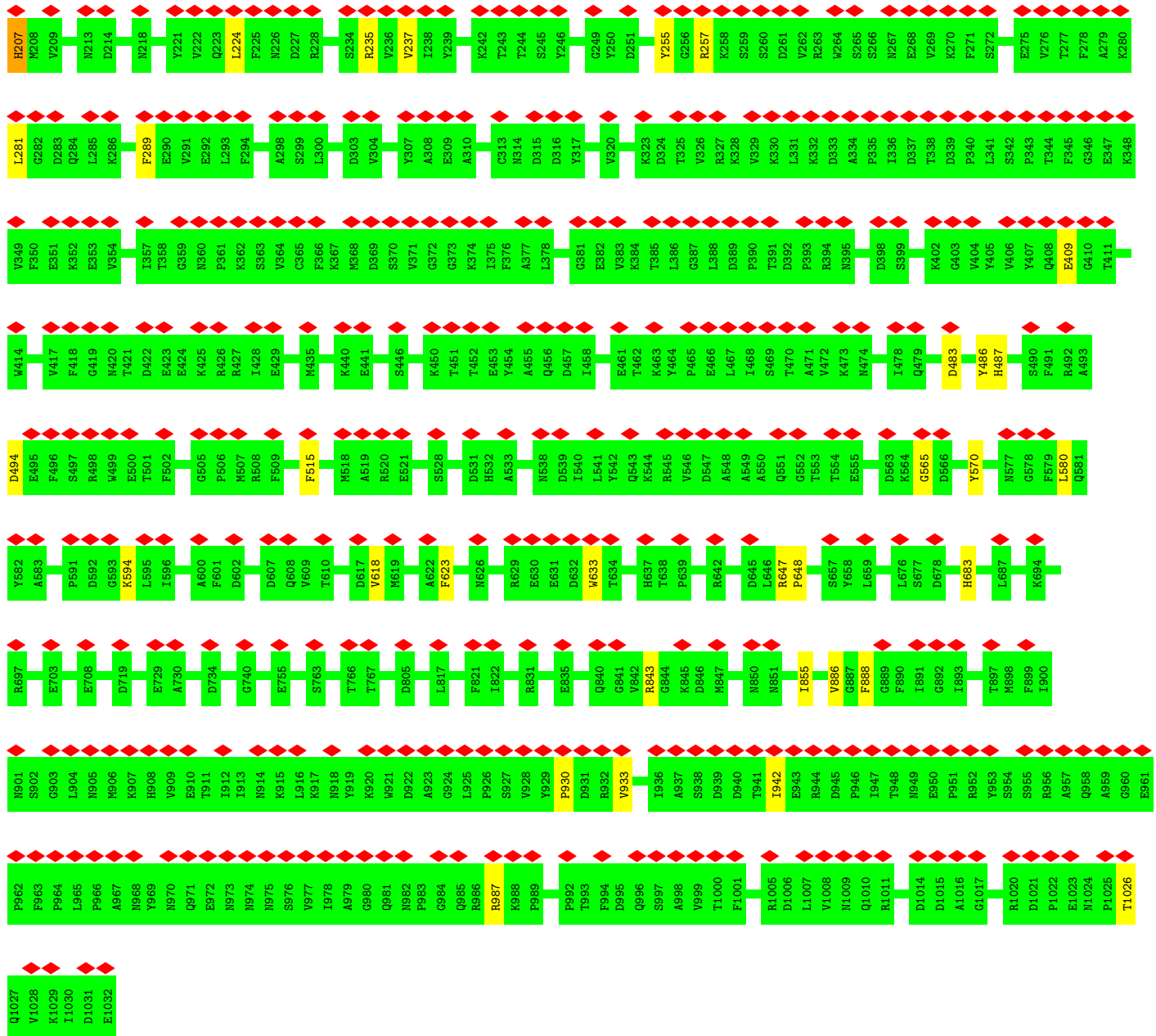


• Molecule 4: Baseplate wedge protein gp6

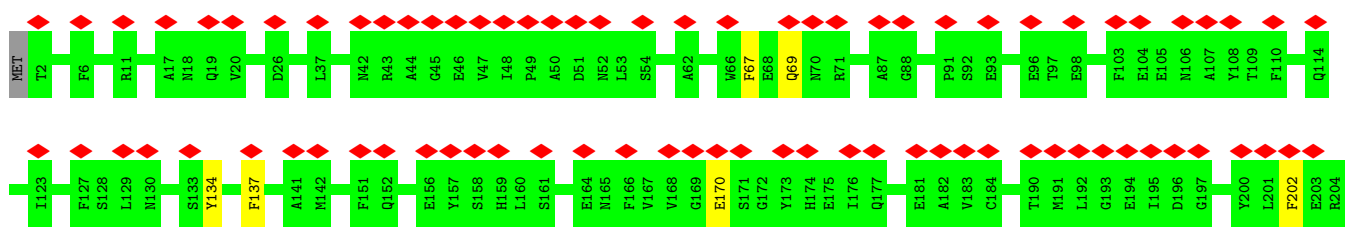


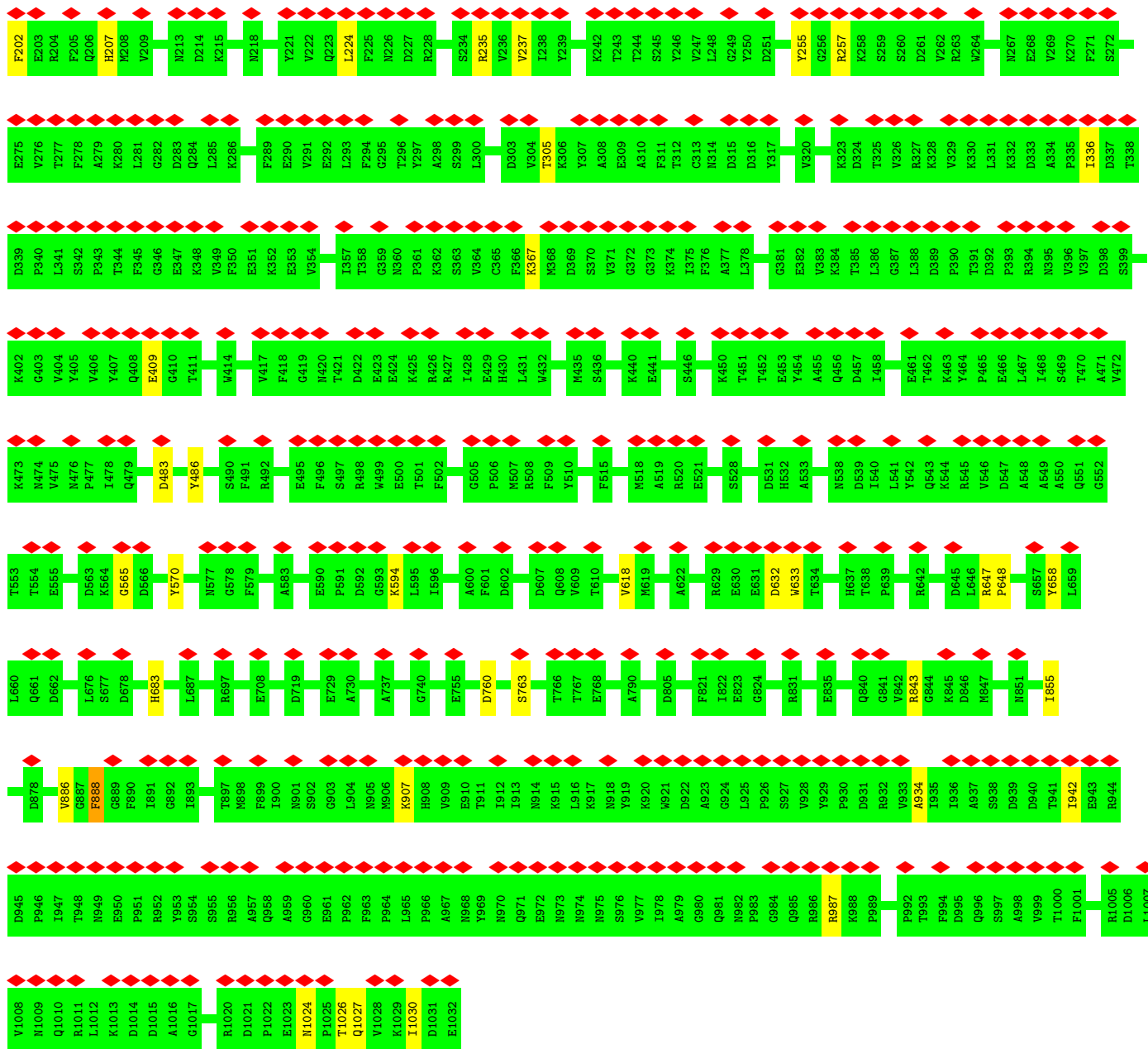
• Molecule 5: Baseplate wedge protein gp7





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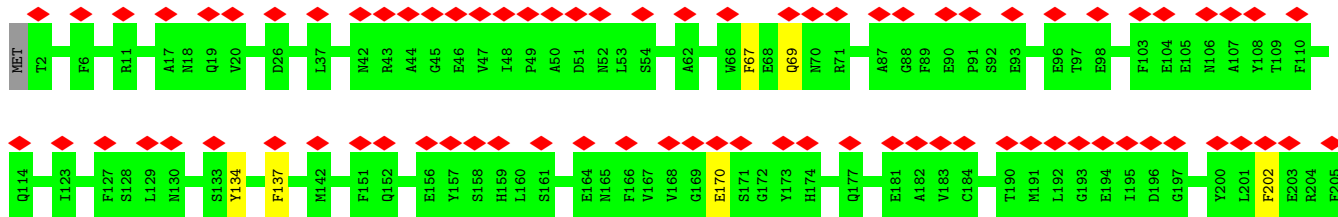


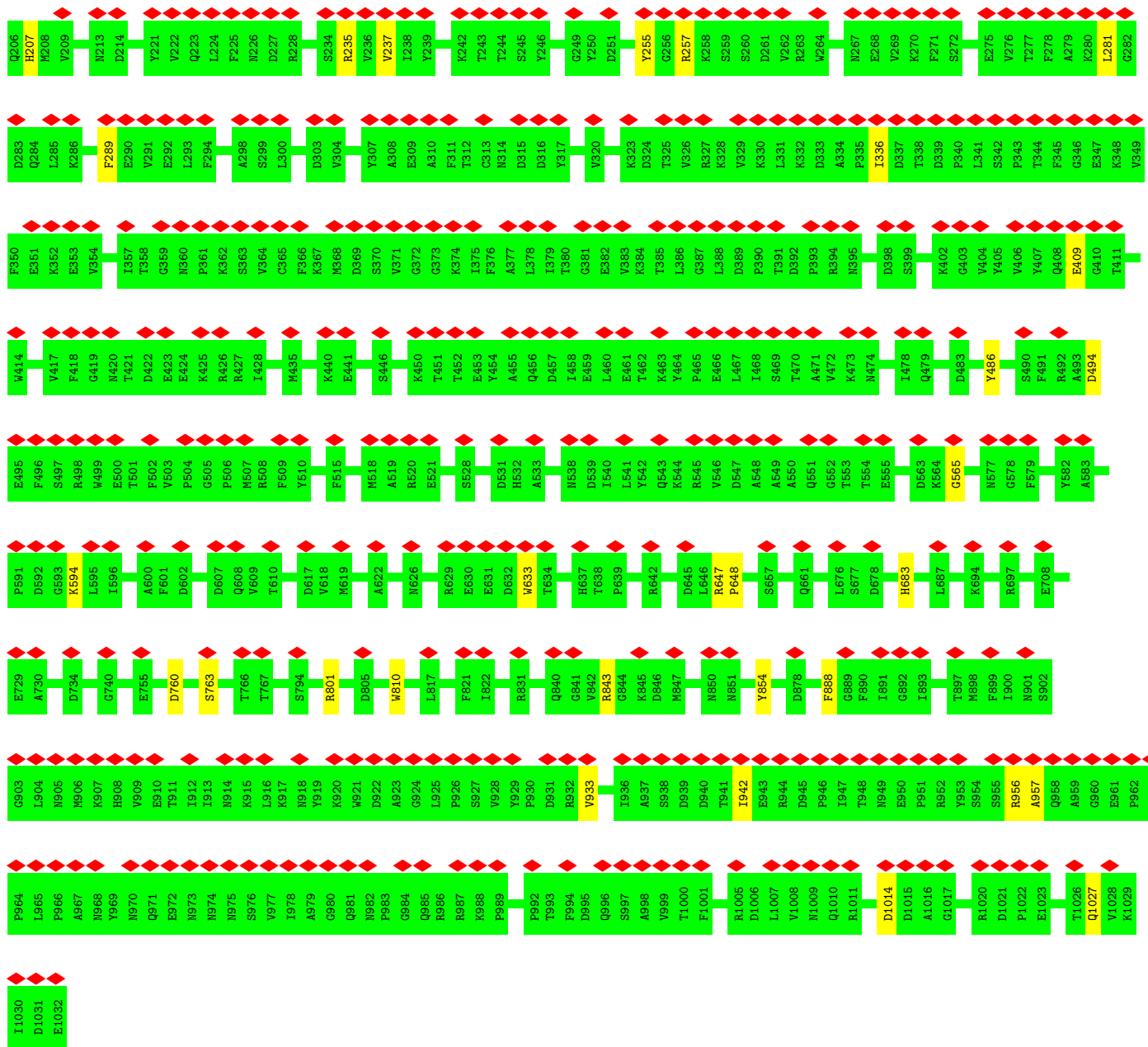


• Molecule 5: Baseplate wedge protein gp7

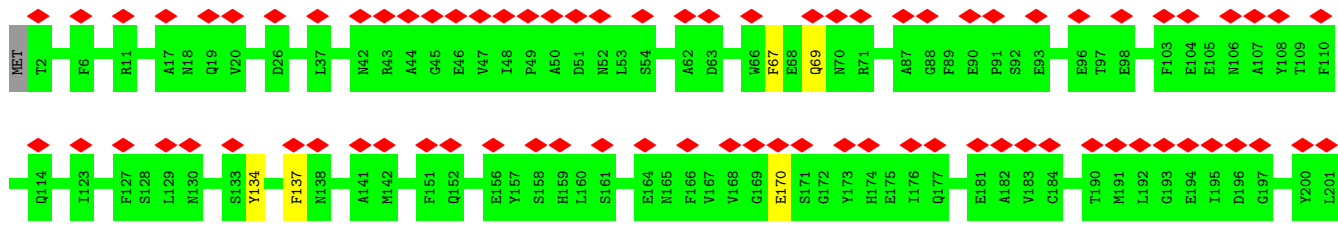


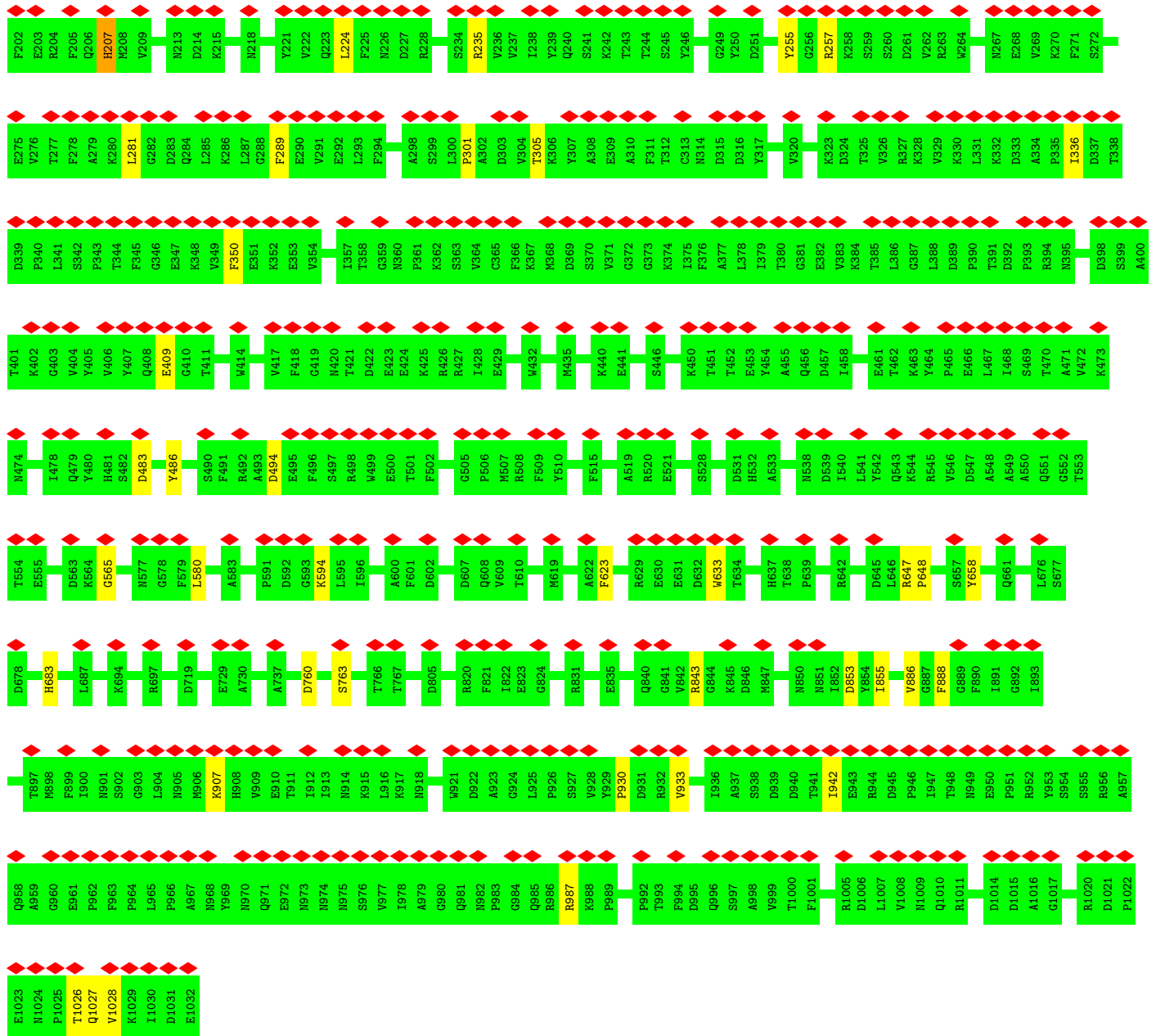
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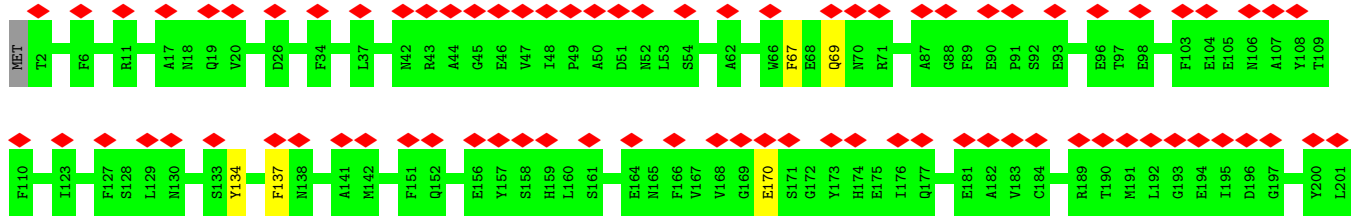


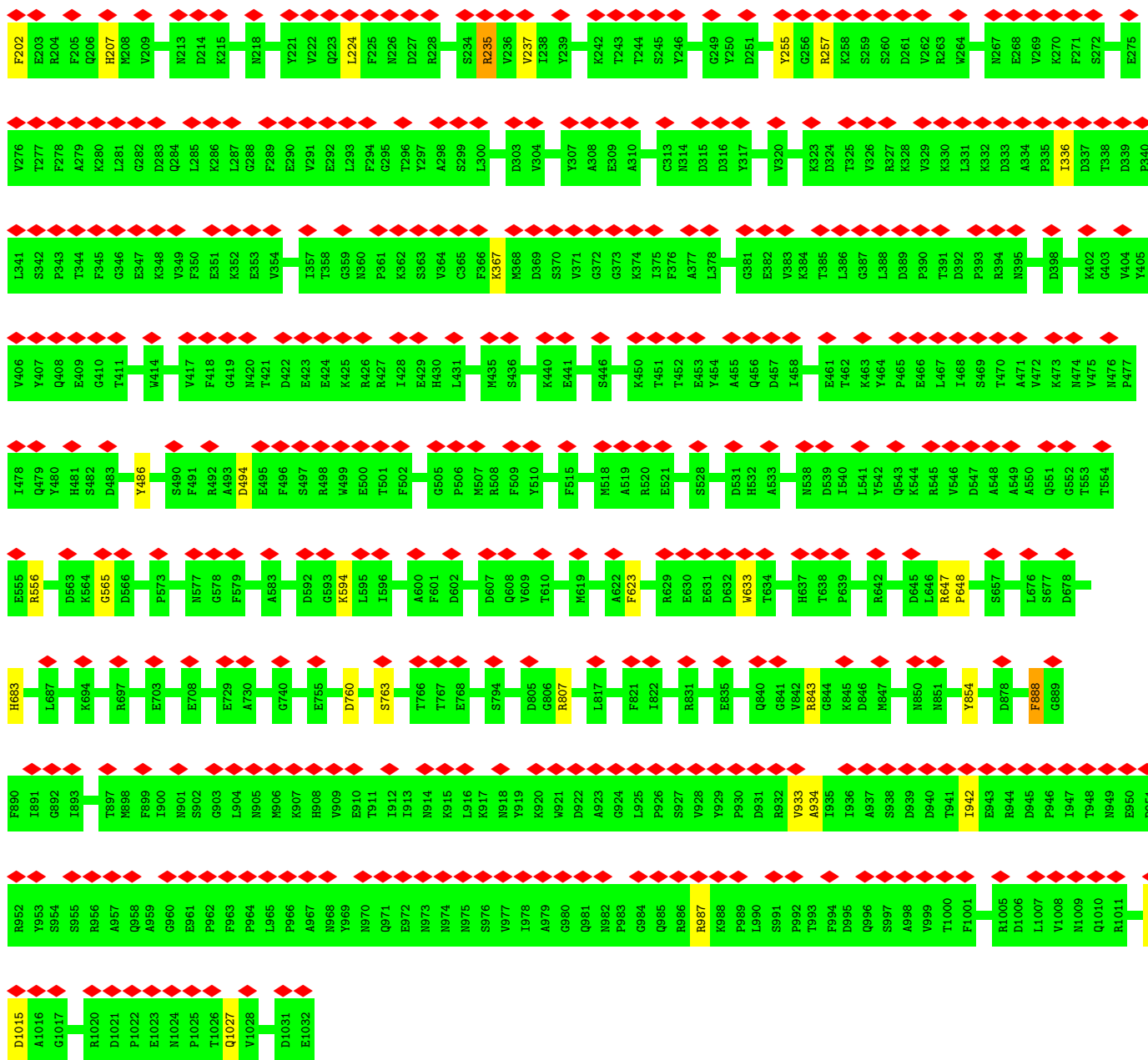
• Molecule 5: Baseplate wedge protein gp7



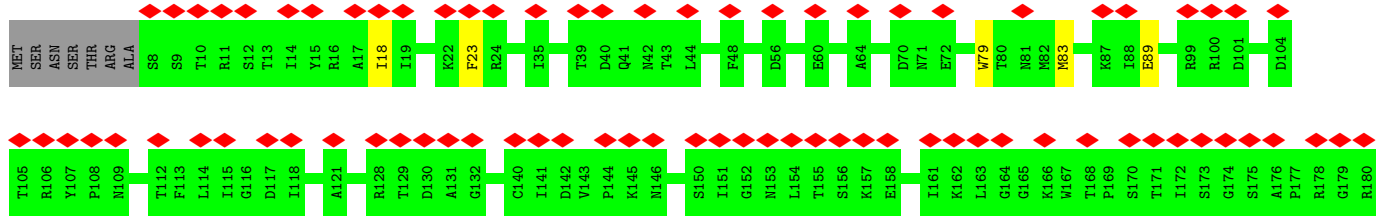
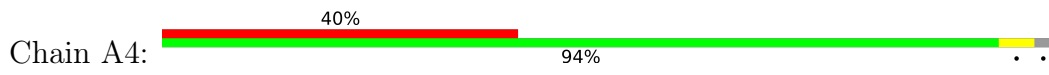


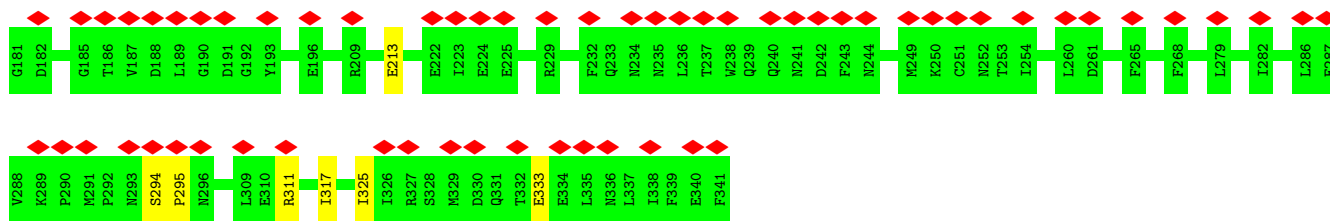
• Molecule 5: Baseplate wedge protein gp7



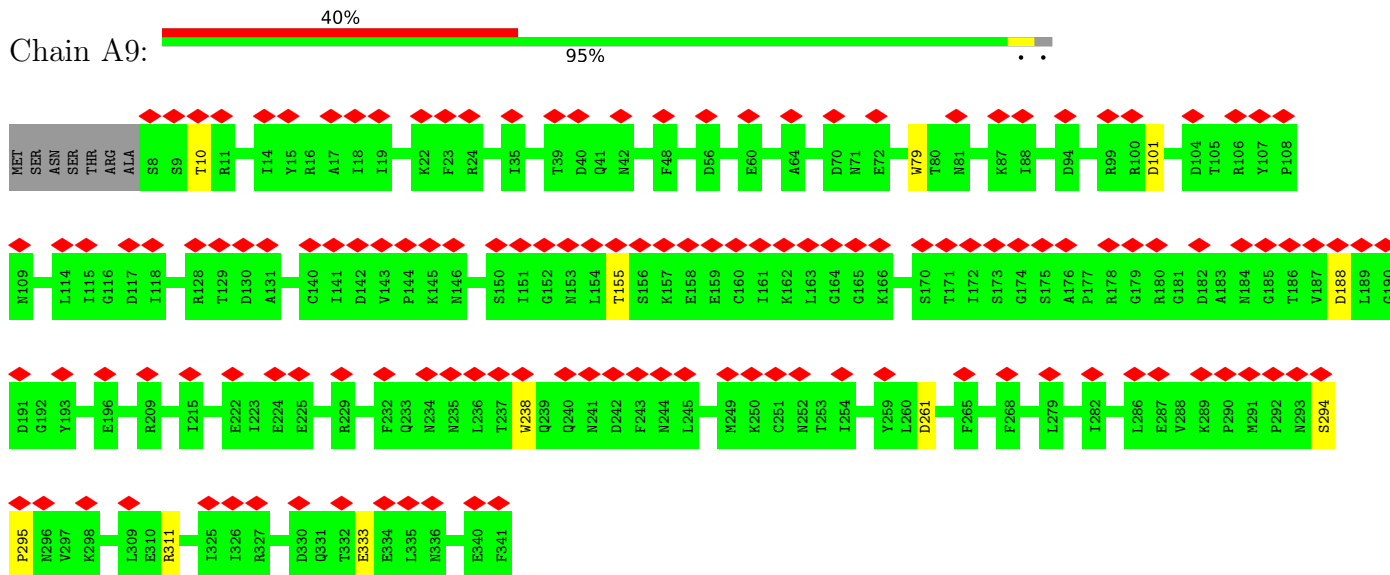


• Molecule 6: Baseplate wedge subunit

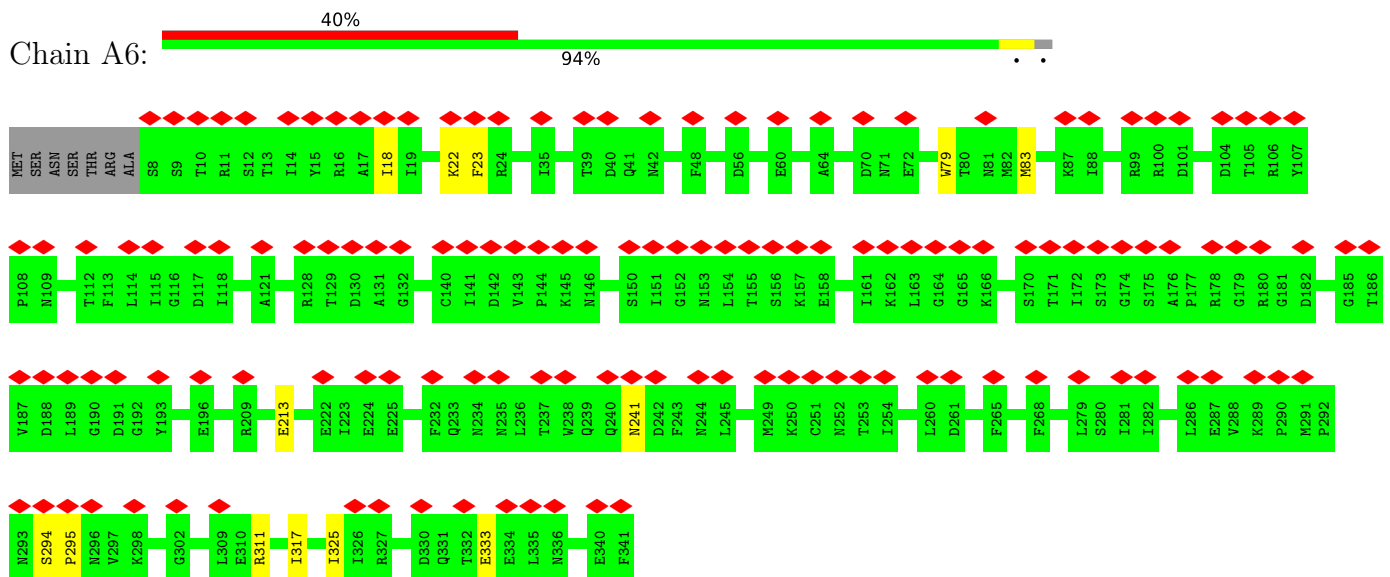




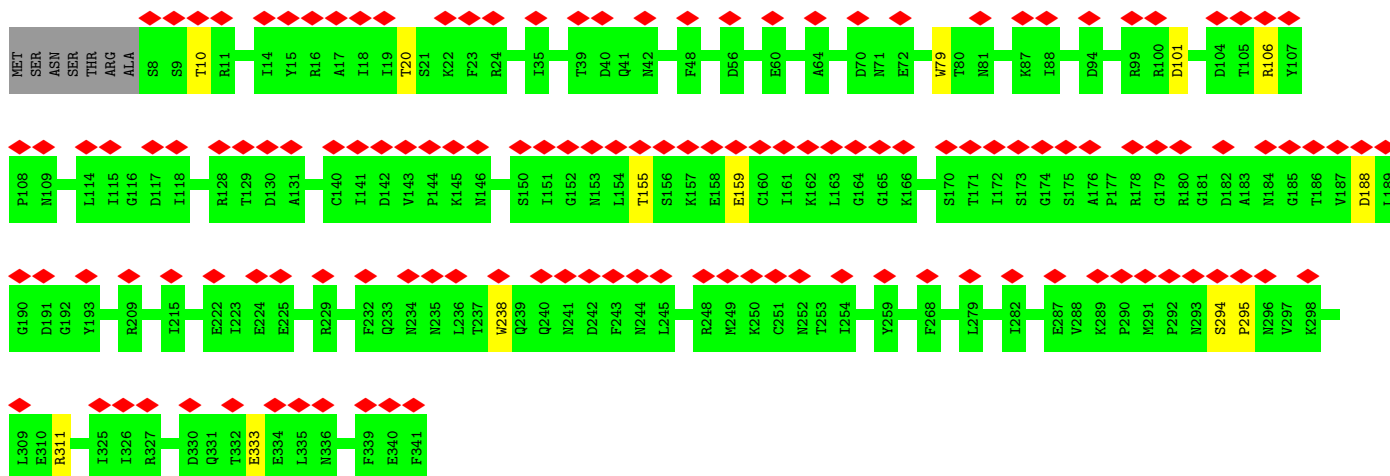
- Molecule 6: Baseplate wedge subunit



- Molecule 6: Baseplate wedge subunit

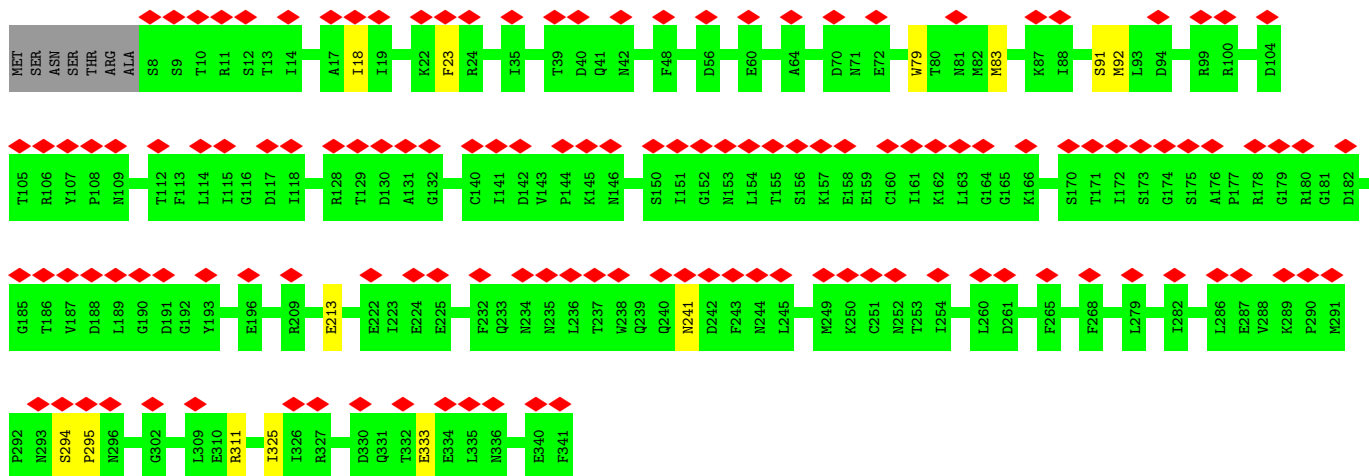


- Molecule 6: Baseplate wedge subunit



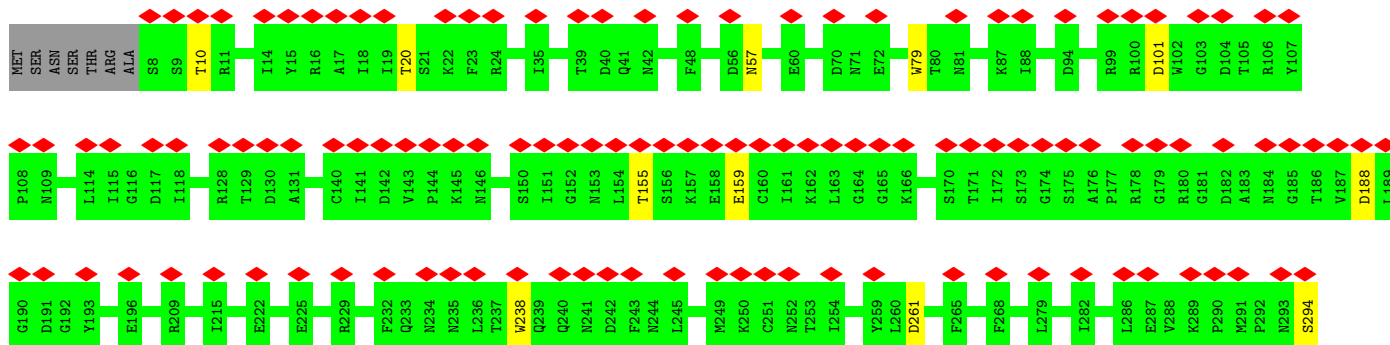
- Molecule 6: Baseplate wedge subunit

Chain A8: 39% 94%



- Molecule 6: Baseplate wedge subunit

Chain A7: 39% 94%

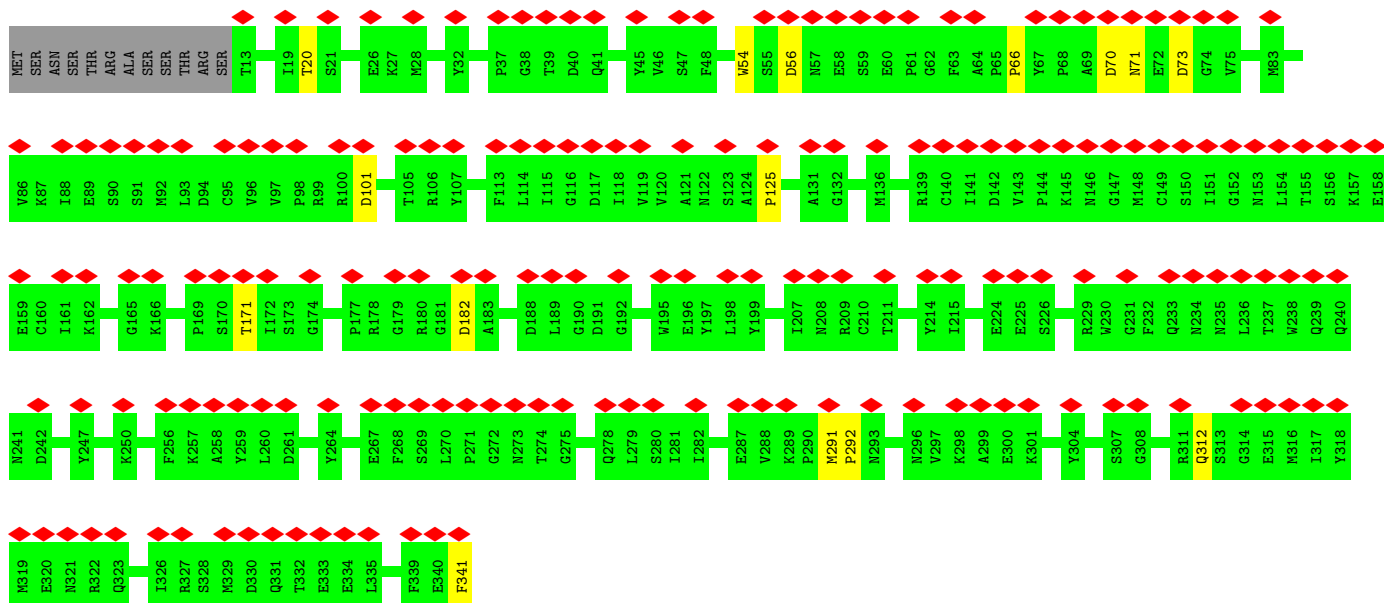




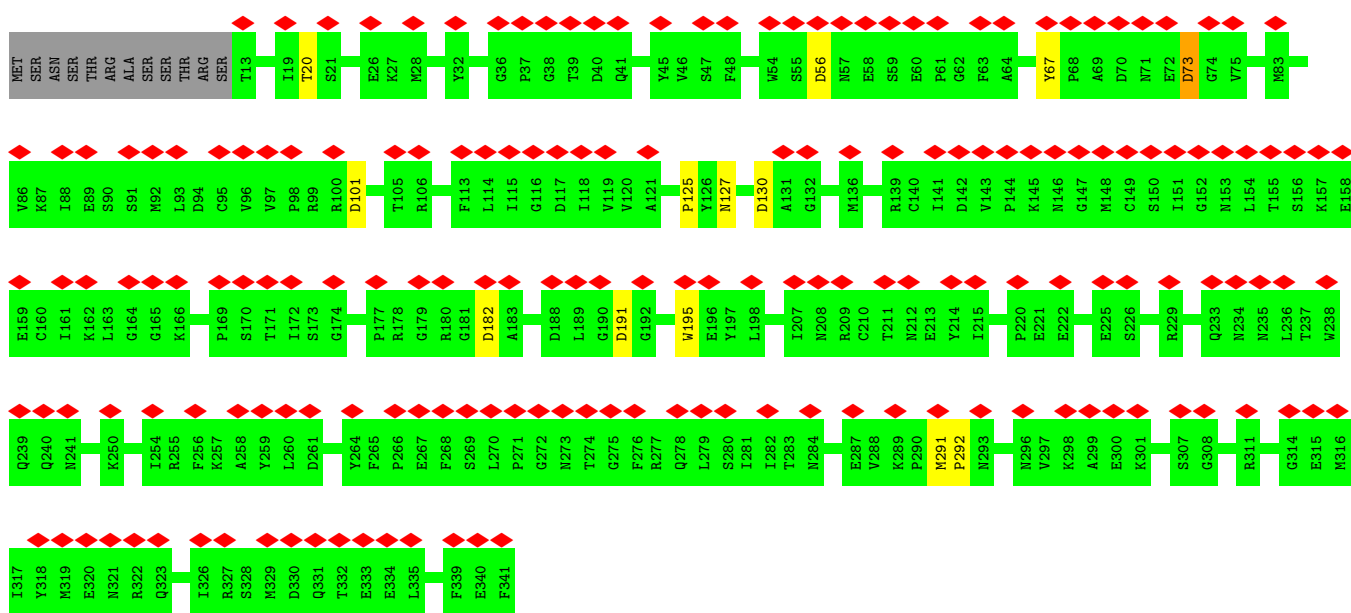
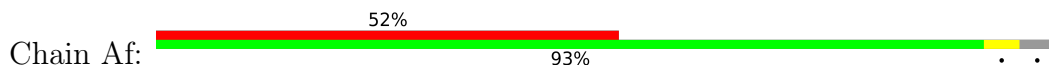
• Molecule 6: Baseplate wedge subunit



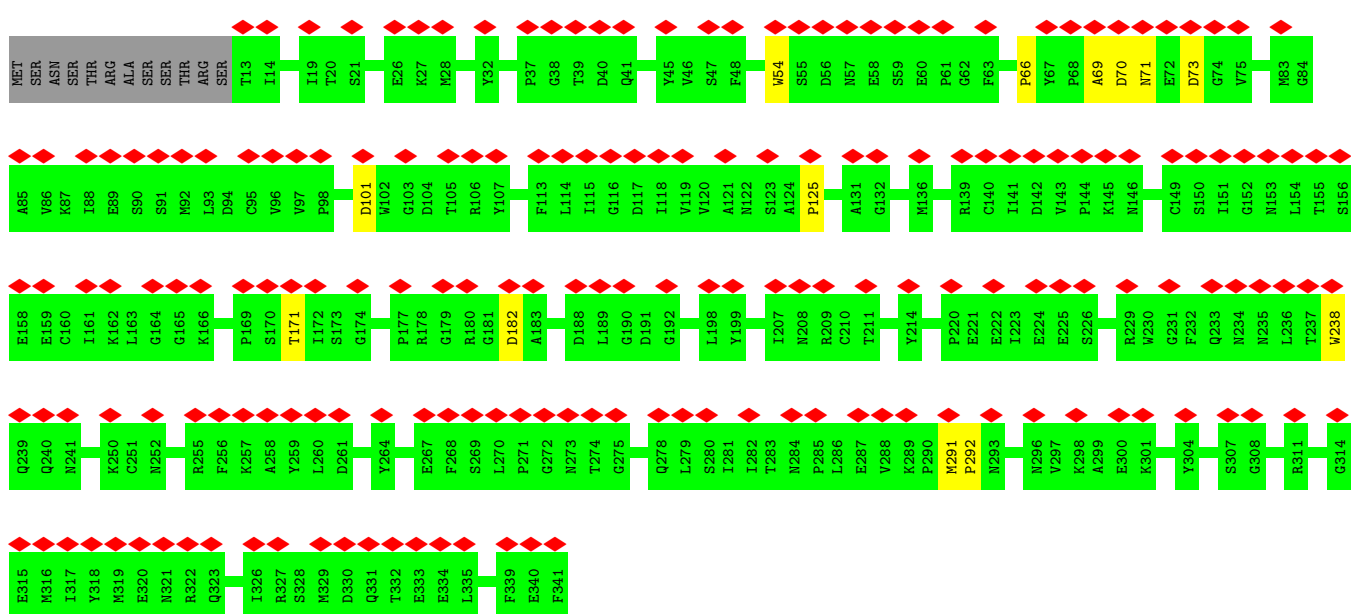
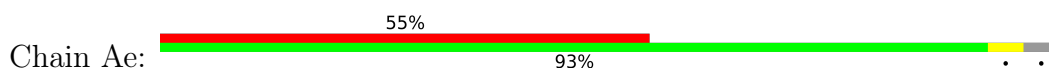
• Molecule 6: Baseplate wedge subunit



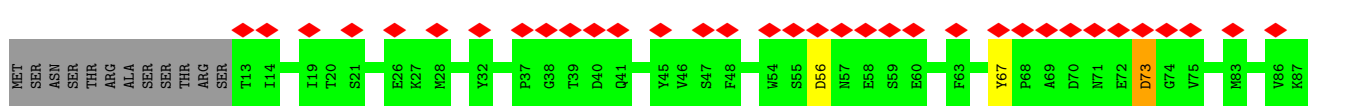
• Molecule 6: Baseplate wedge subunit

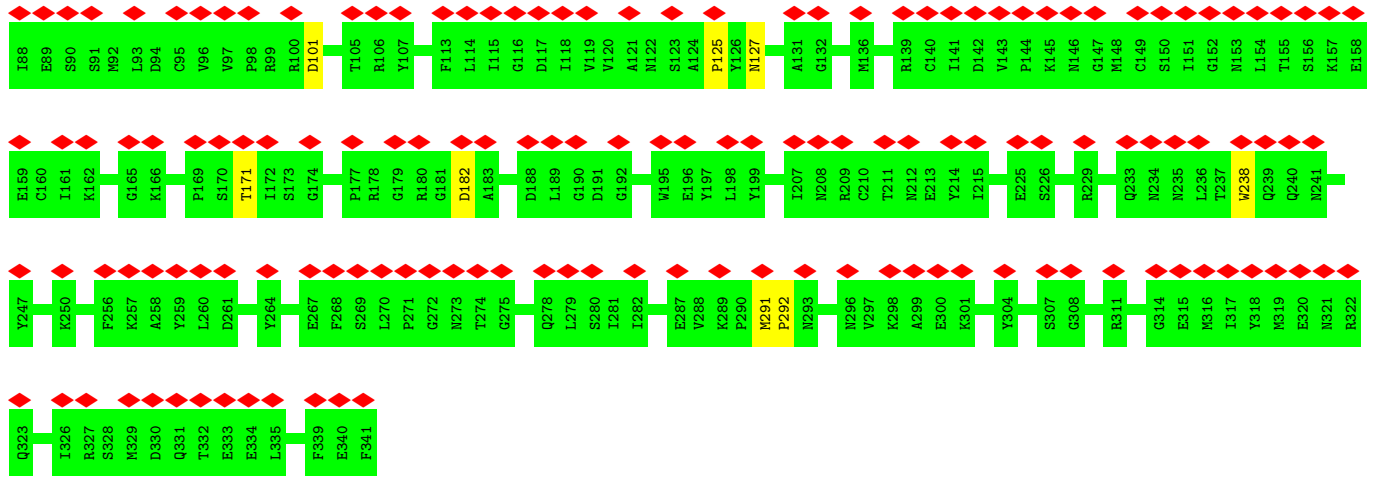


• Molecule 6: Baseplate wedge subunit

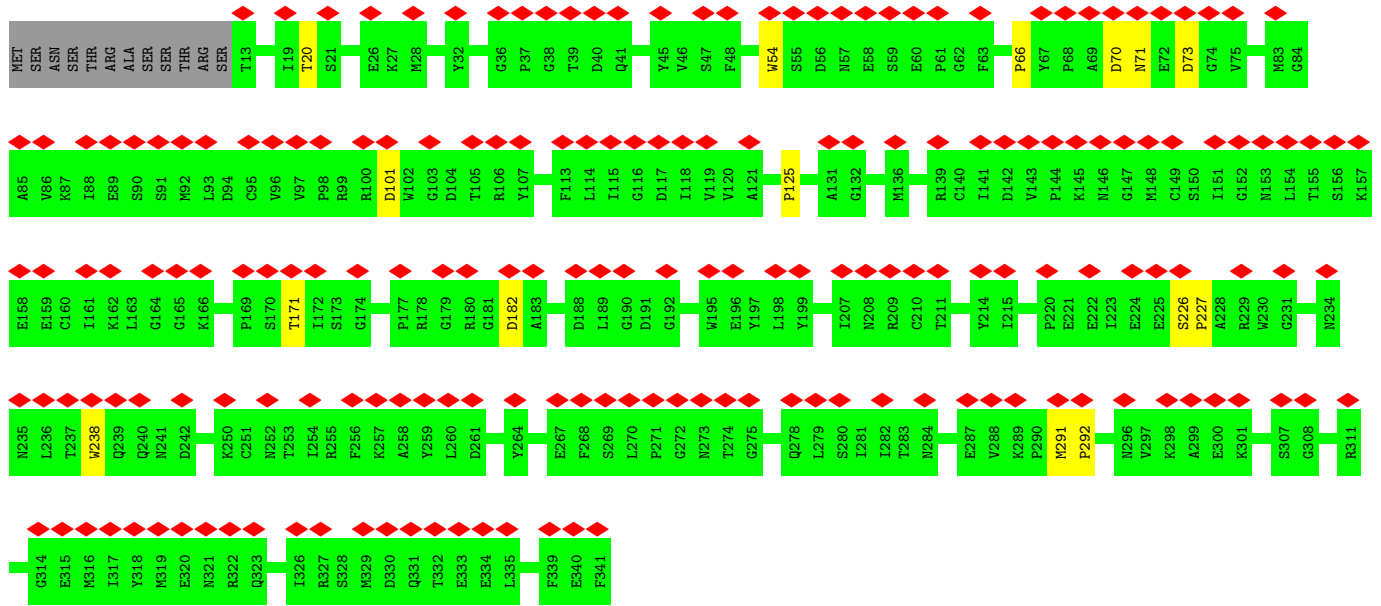
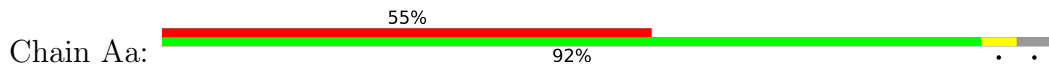


• Molecule 6: Baseplate wedge subunit

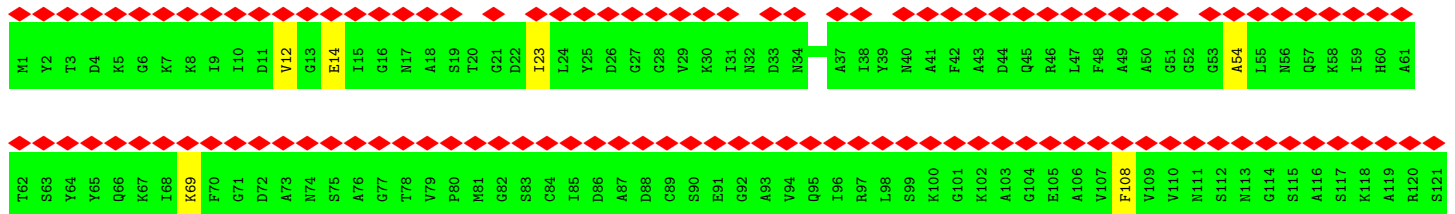


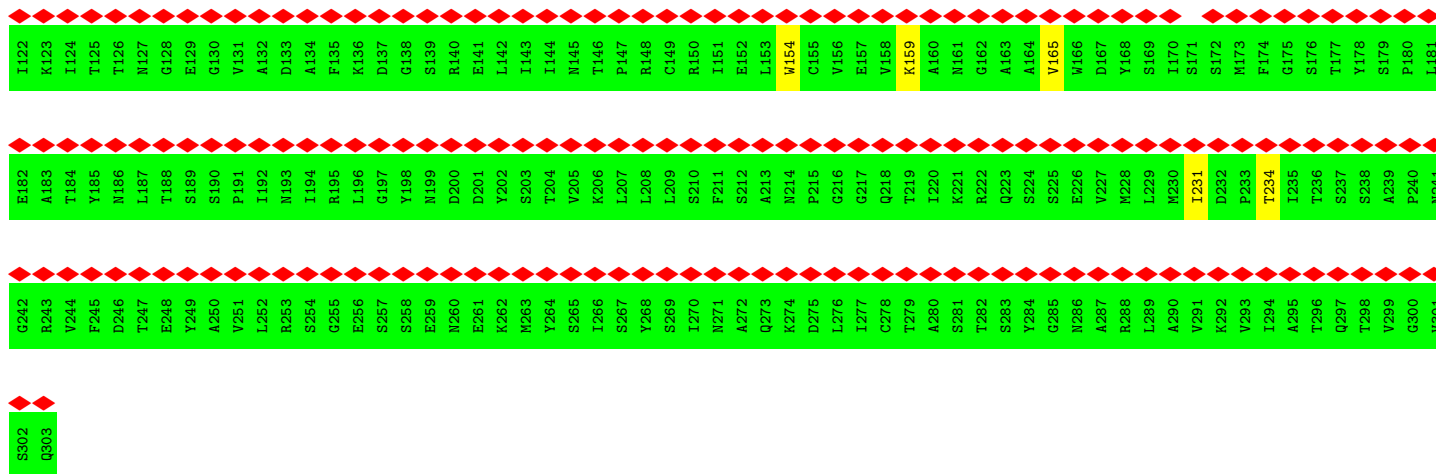


• Molecule 6: Baseplate wedge subunit

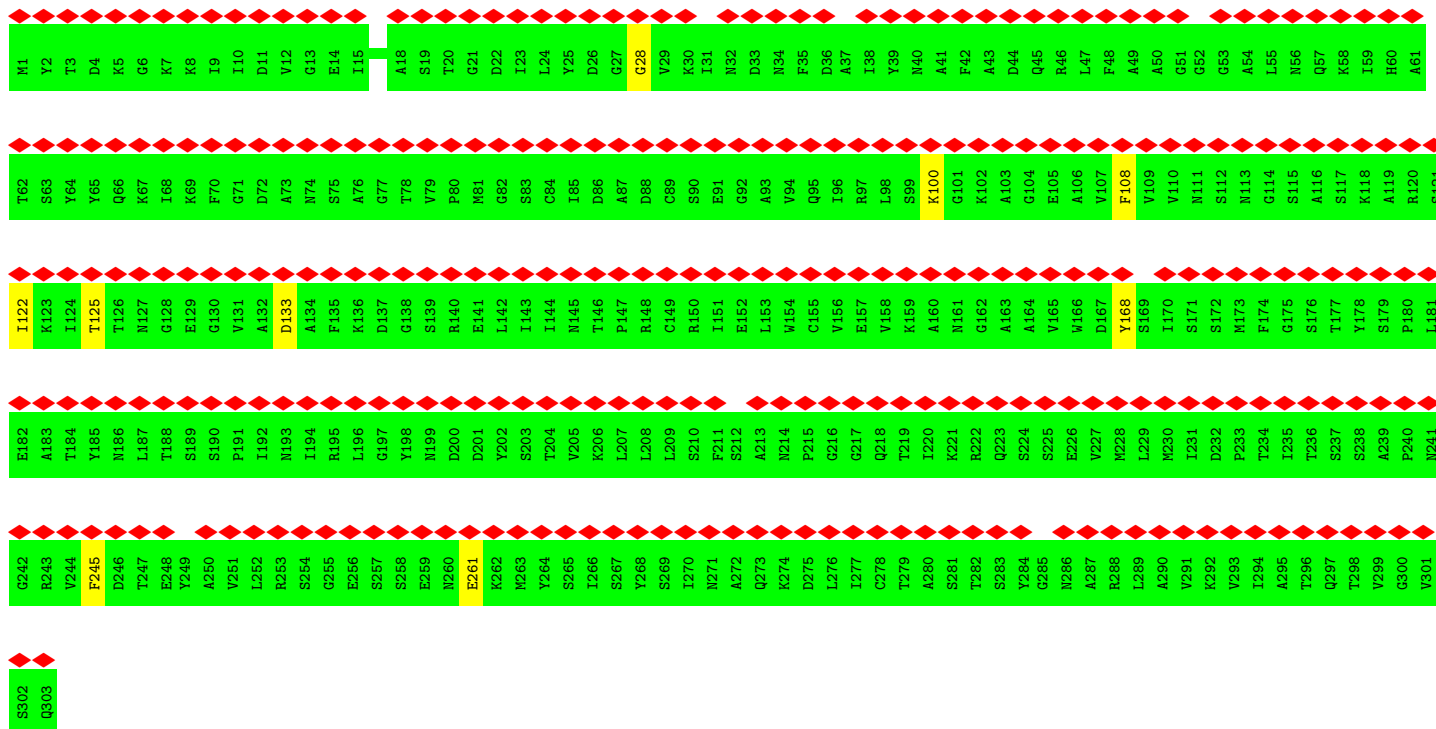


• Molecule 7: Baseplate wedge tail fiber connector



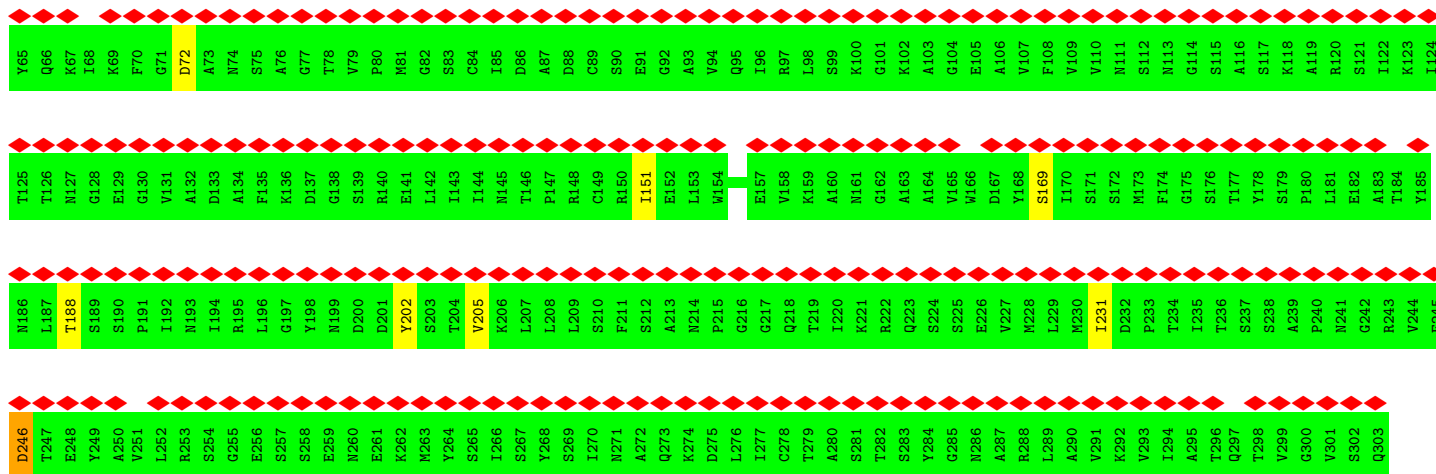


• Molecule 7: Baseplate wedge tail fiber connector

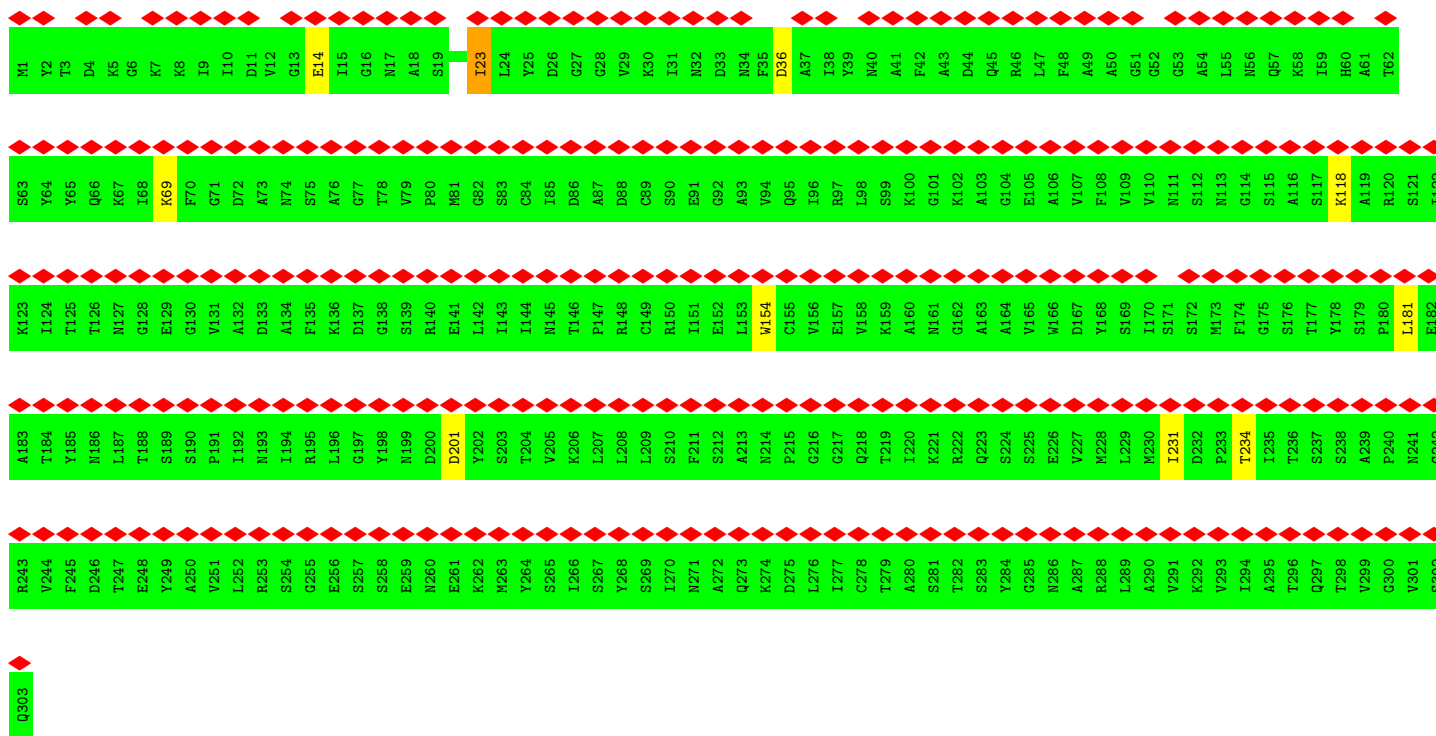


• Molecule 7: Baseplate wedge tail fiber connector

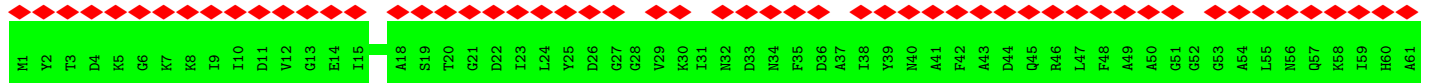


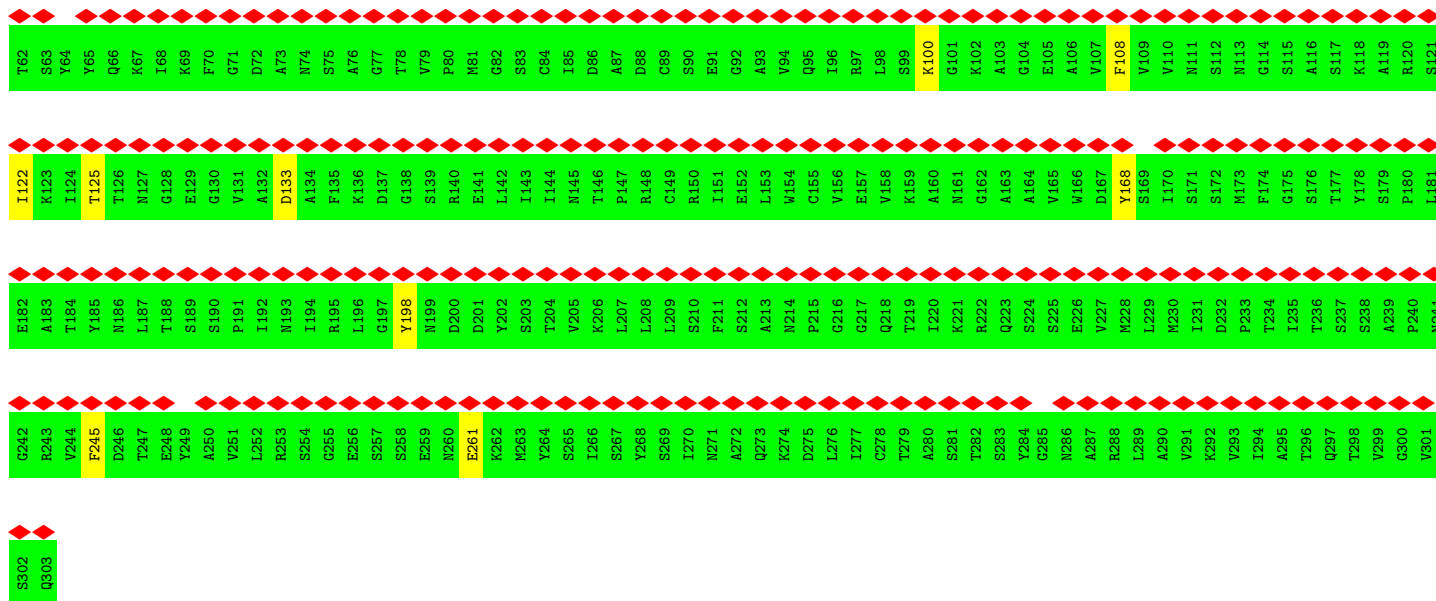


• Molecule 7: Baseplate wedge tail fiber connector

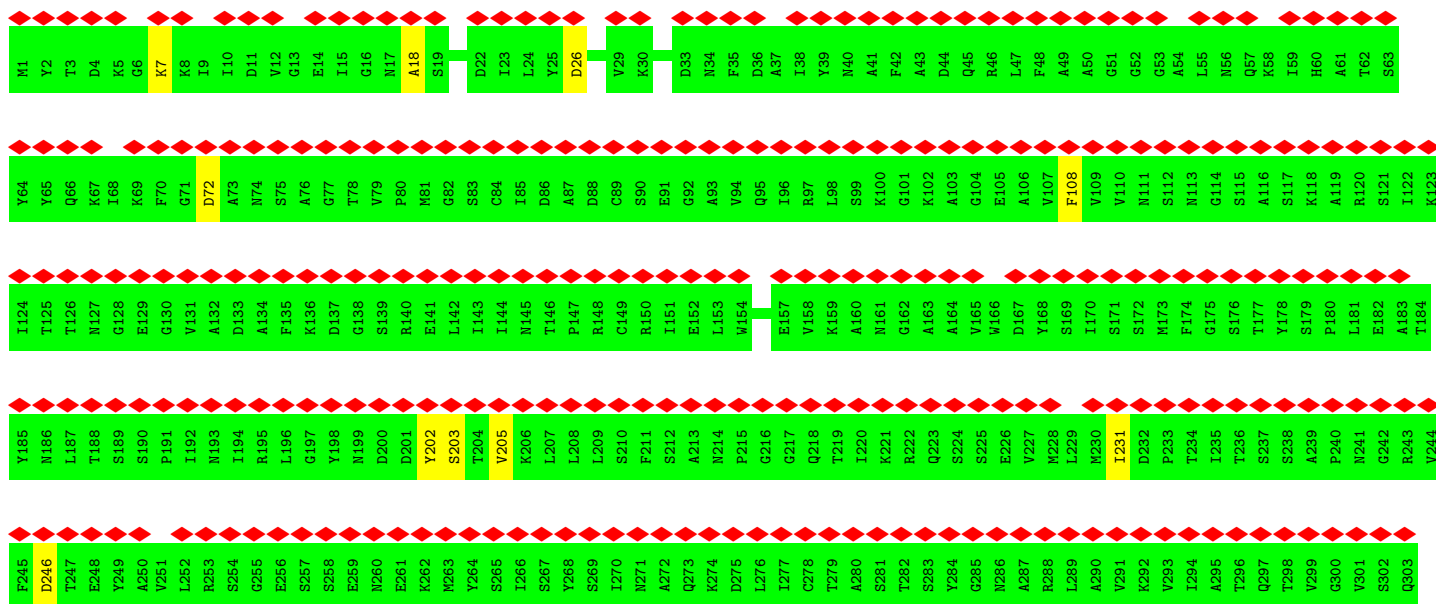


• Molecule 7: Baseplate wedge tail fiber connector

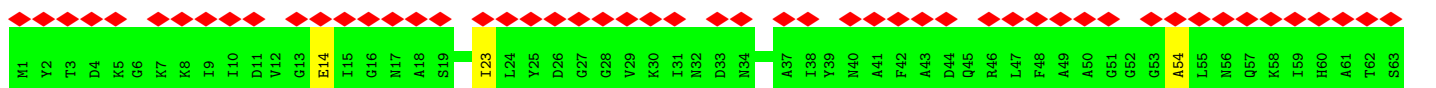


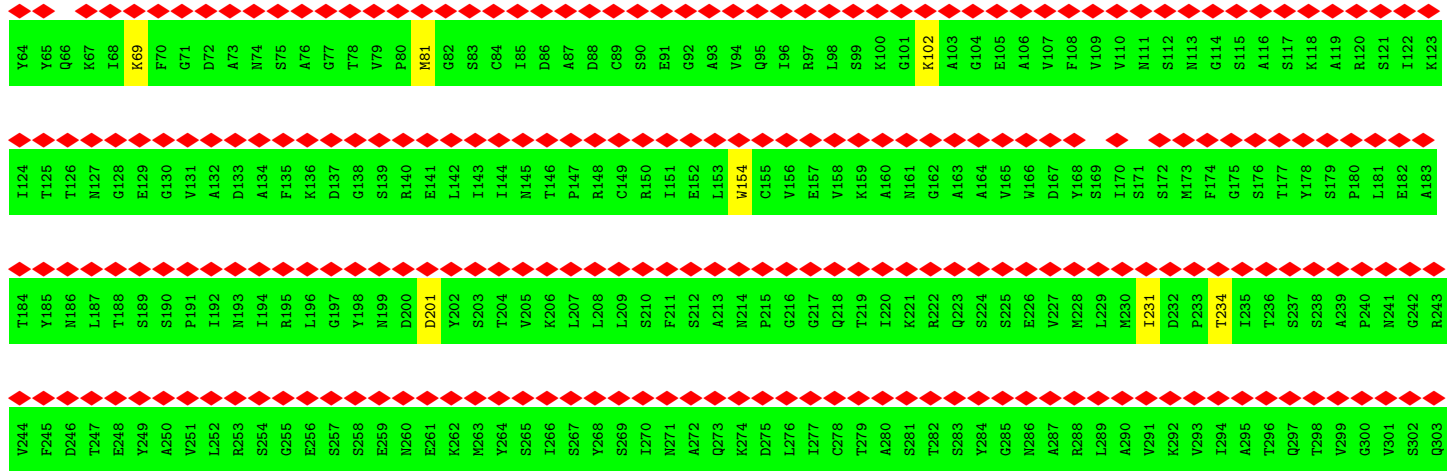


• Molecule 7: Baseplate wedge tail fiber connector

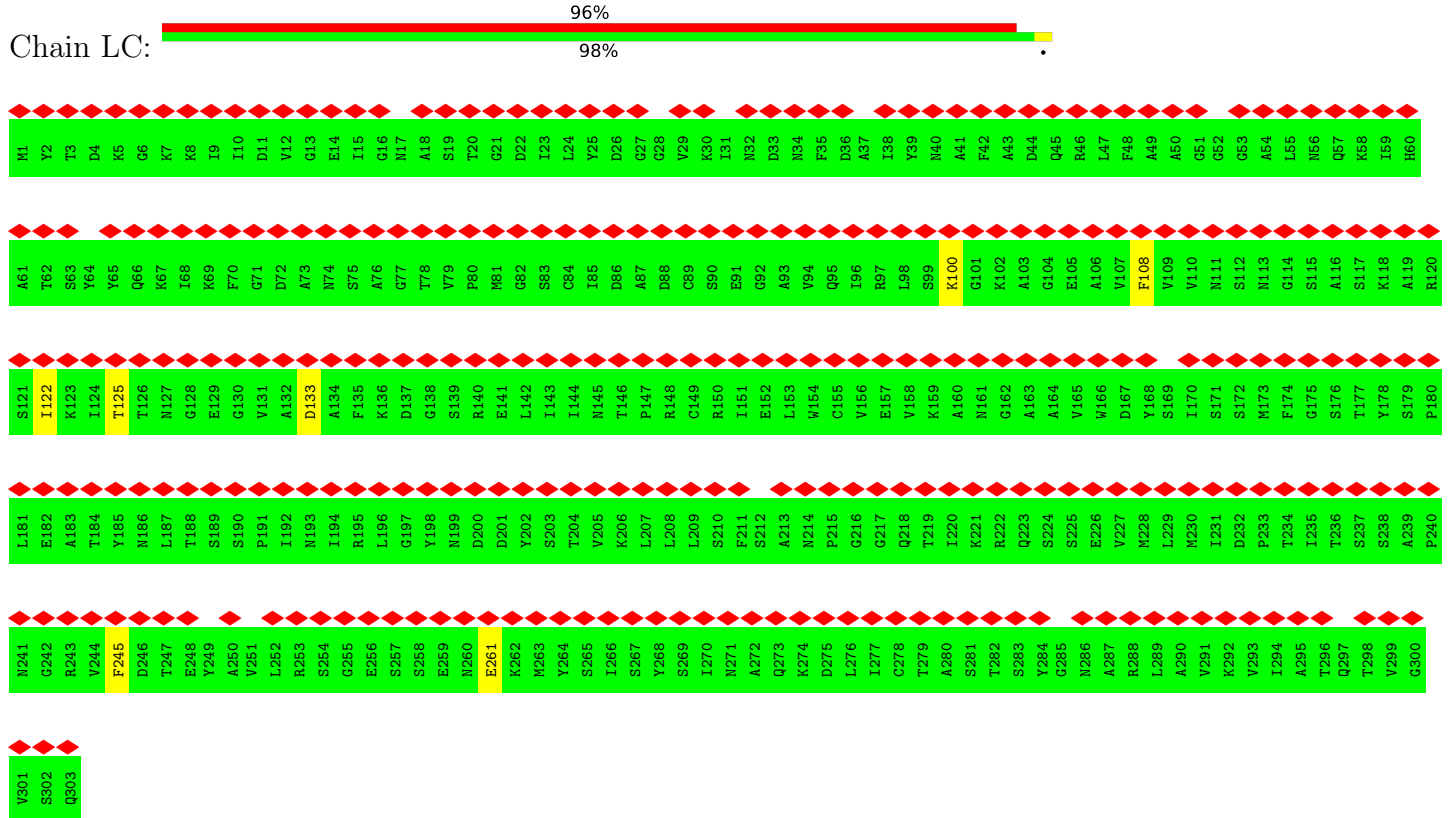


• Molecule 7: Baseplate wedge tail fiber connector

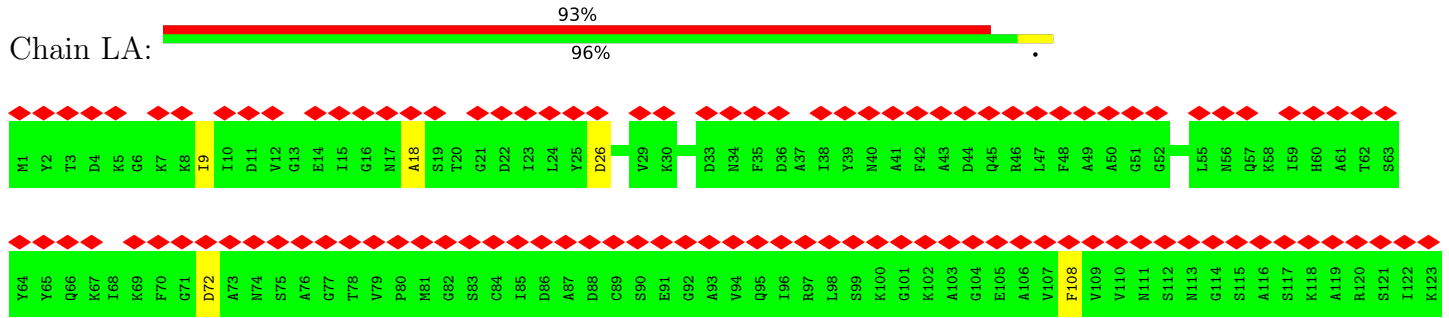


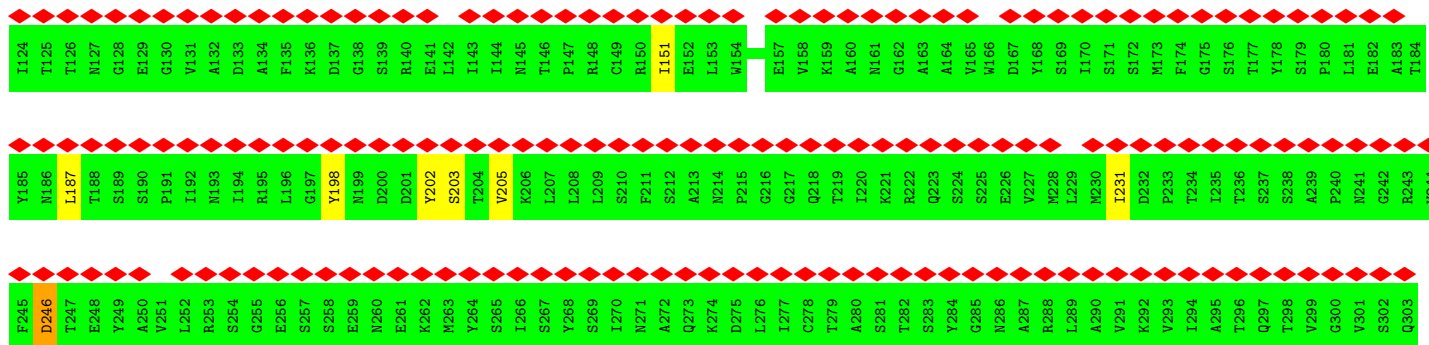


• Molecule 7: Baseplate wedge tail fiber connector

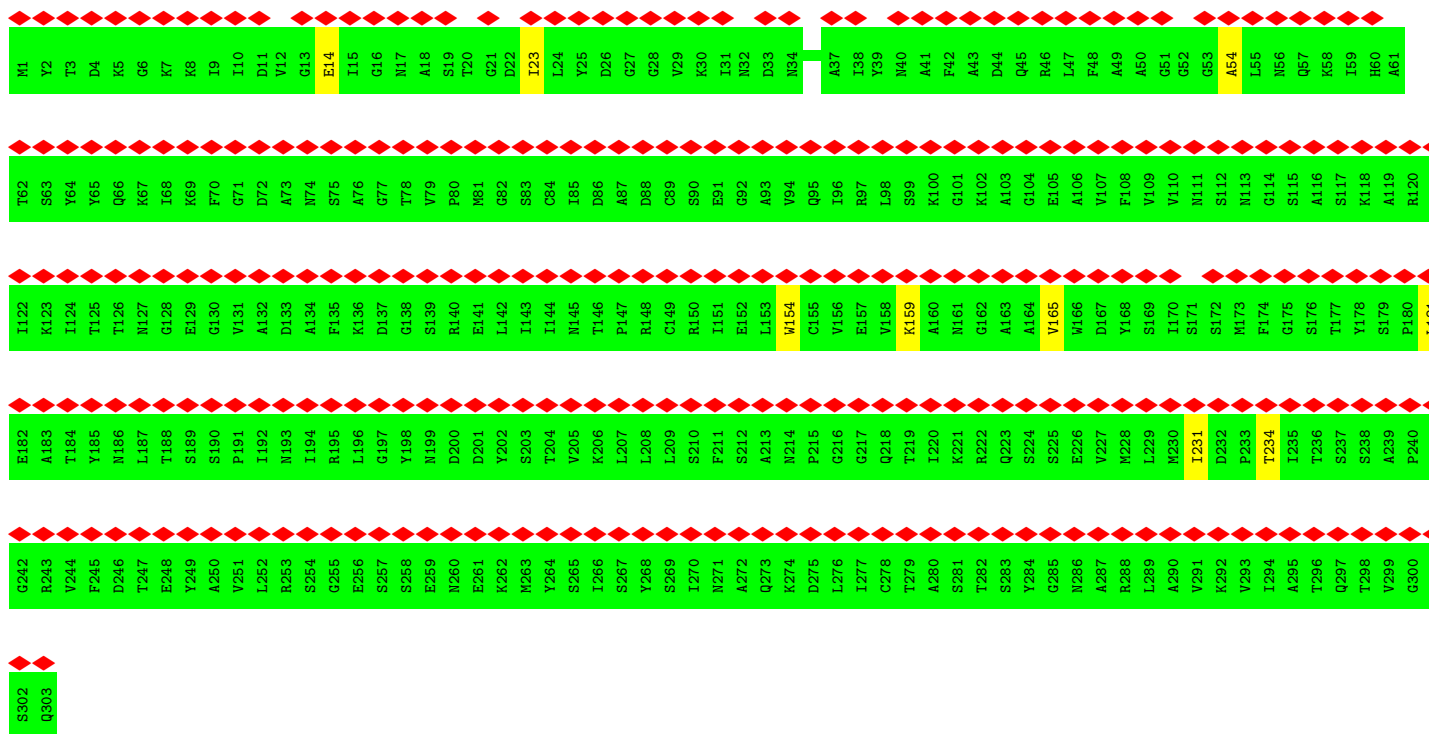


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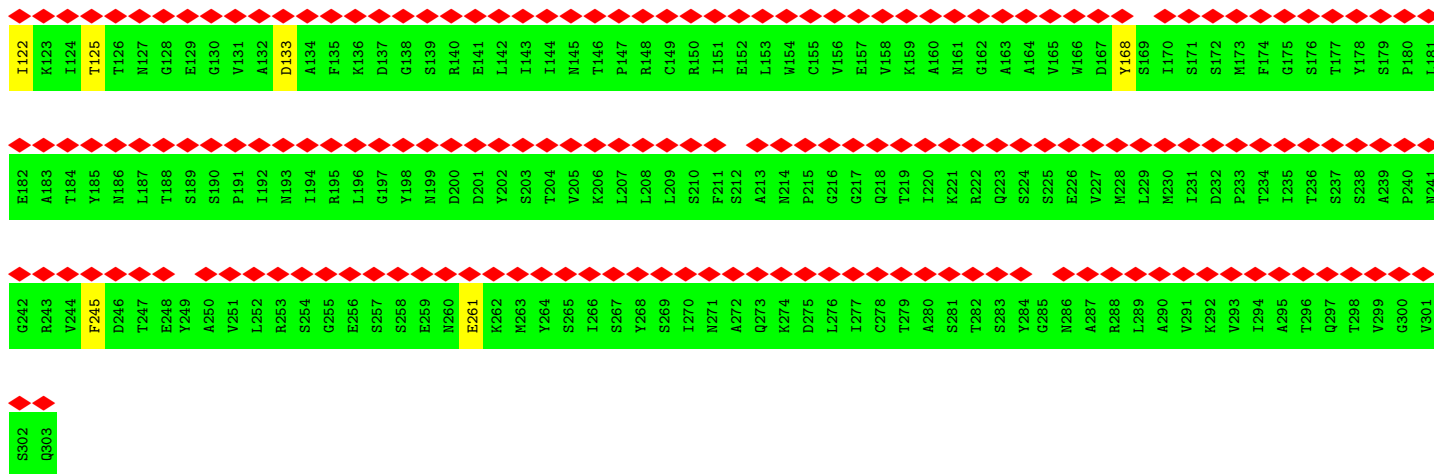


• Molecule 7: Baseplate wedge tail fiber connector

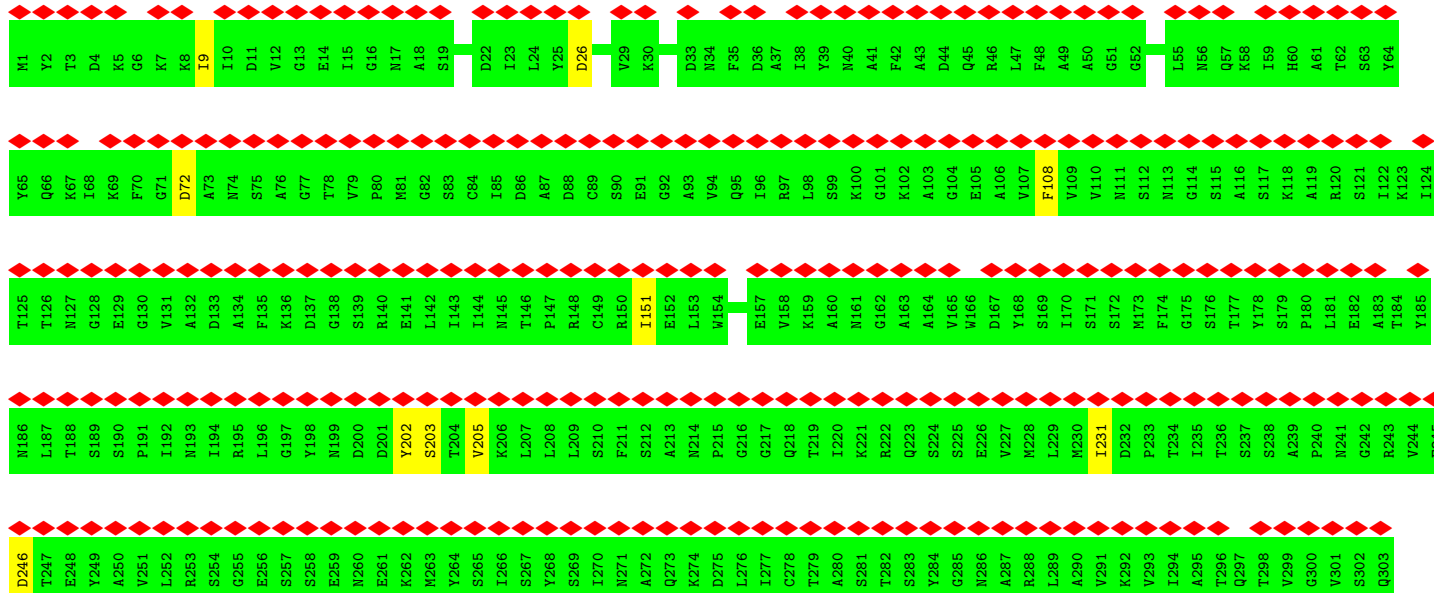


• Molecule 7: Baseplate wedge tail fiber connector

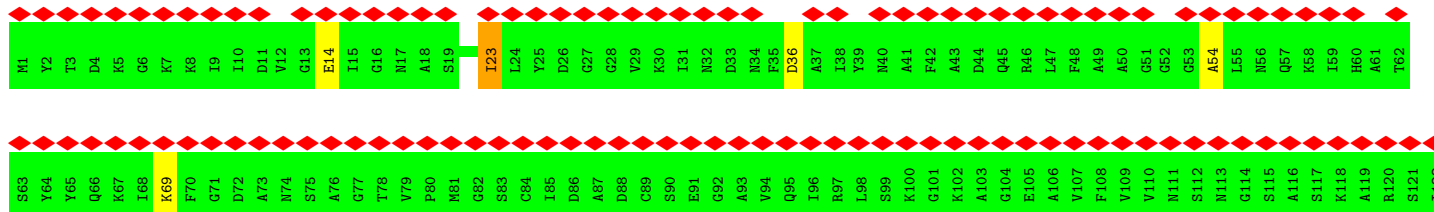


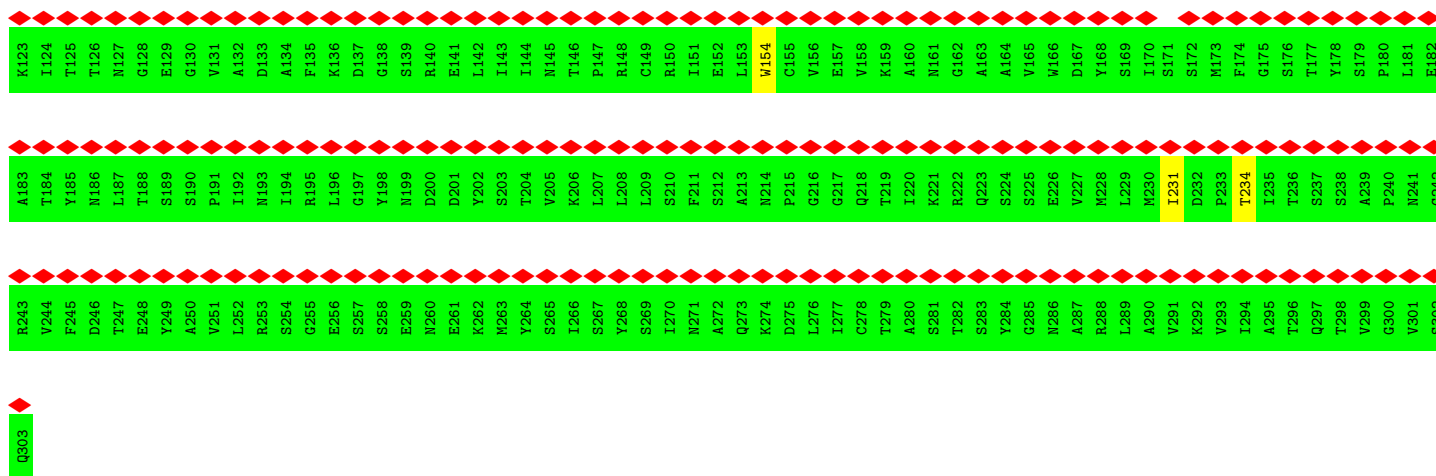


• Molecule 7: Baseplate wedge tail fiber connector

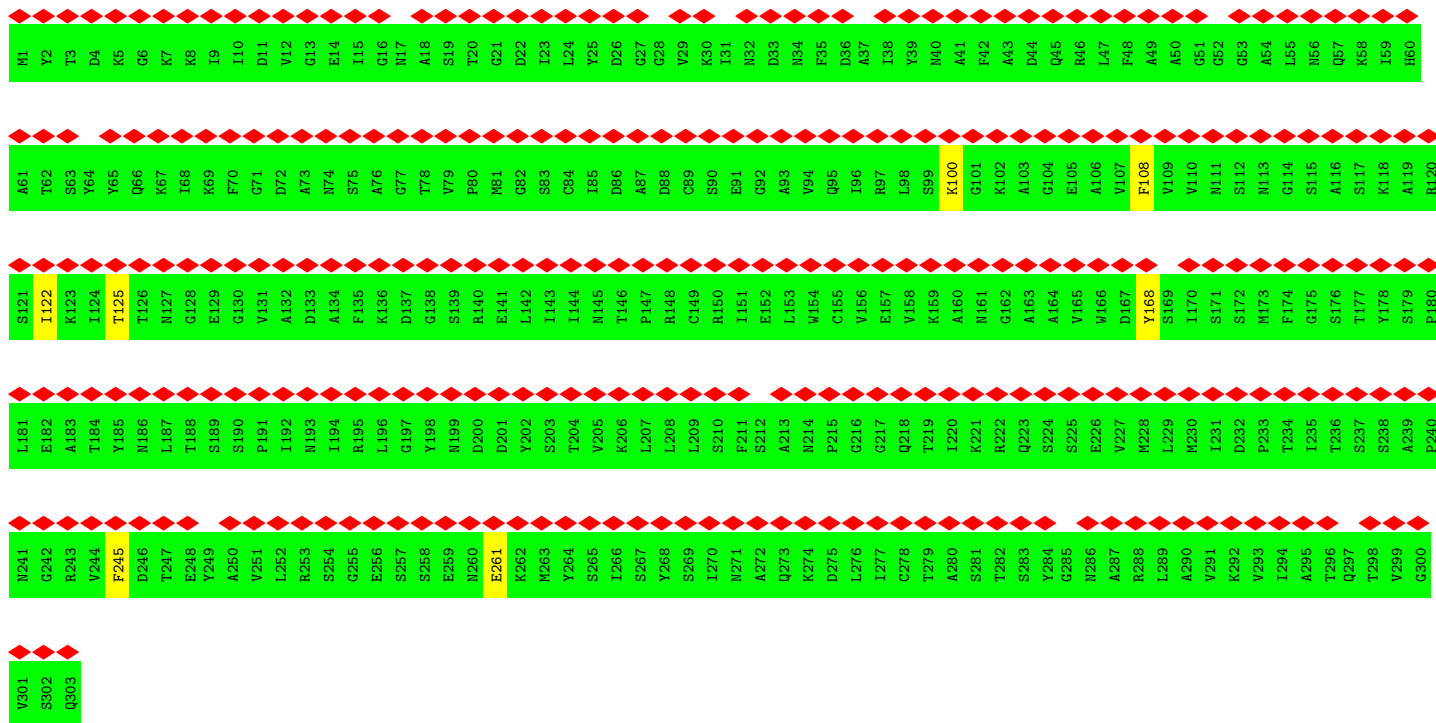


• Molecule 7: Baseplate wedge tail fiber connector

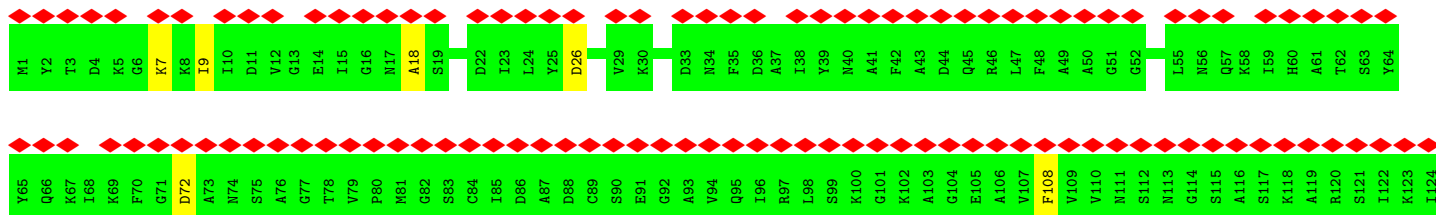


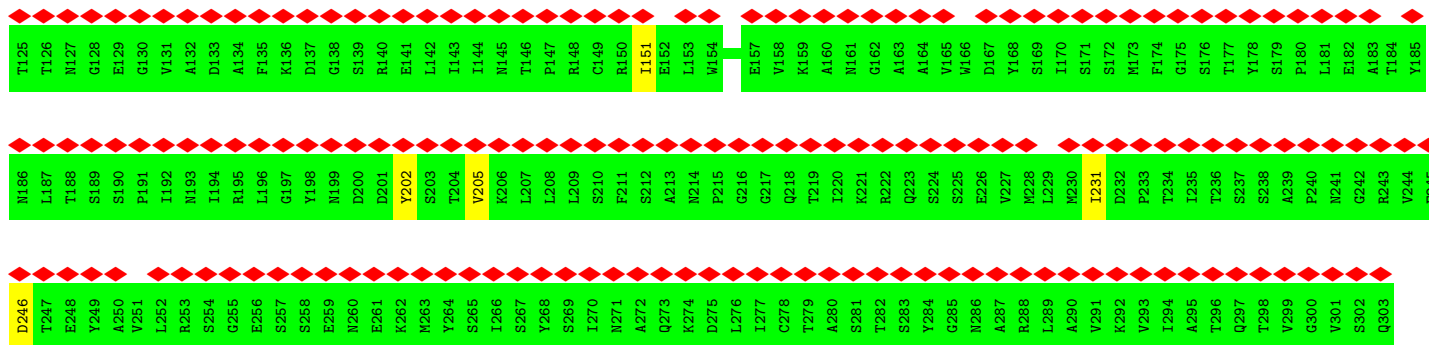


• Molecule 7: Baseplate wedge tail fiber connector



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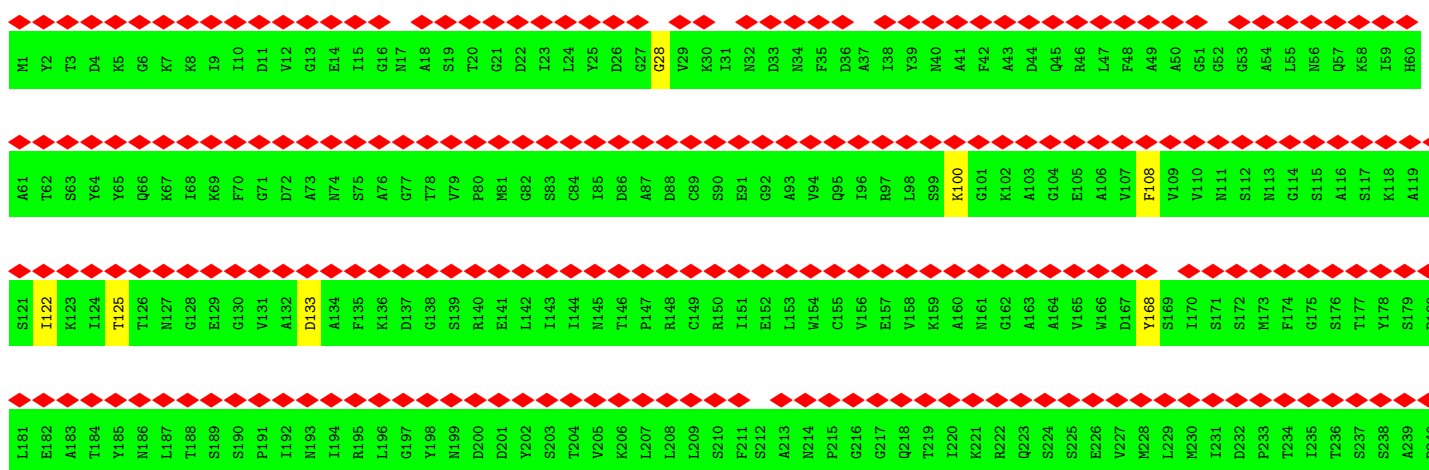


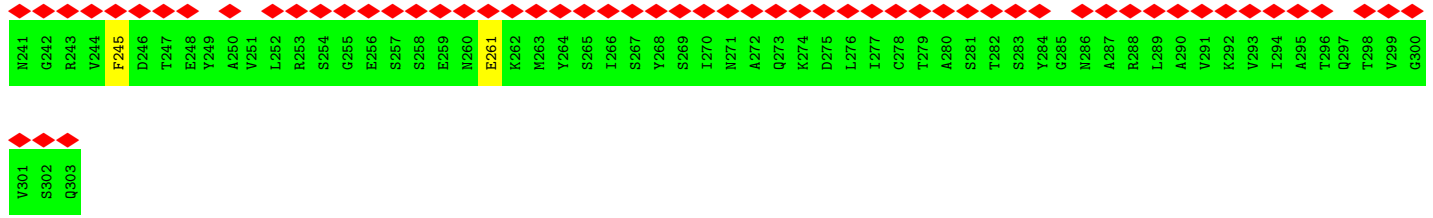


• Molecule 7: Baseplate wedge tail fiber connector

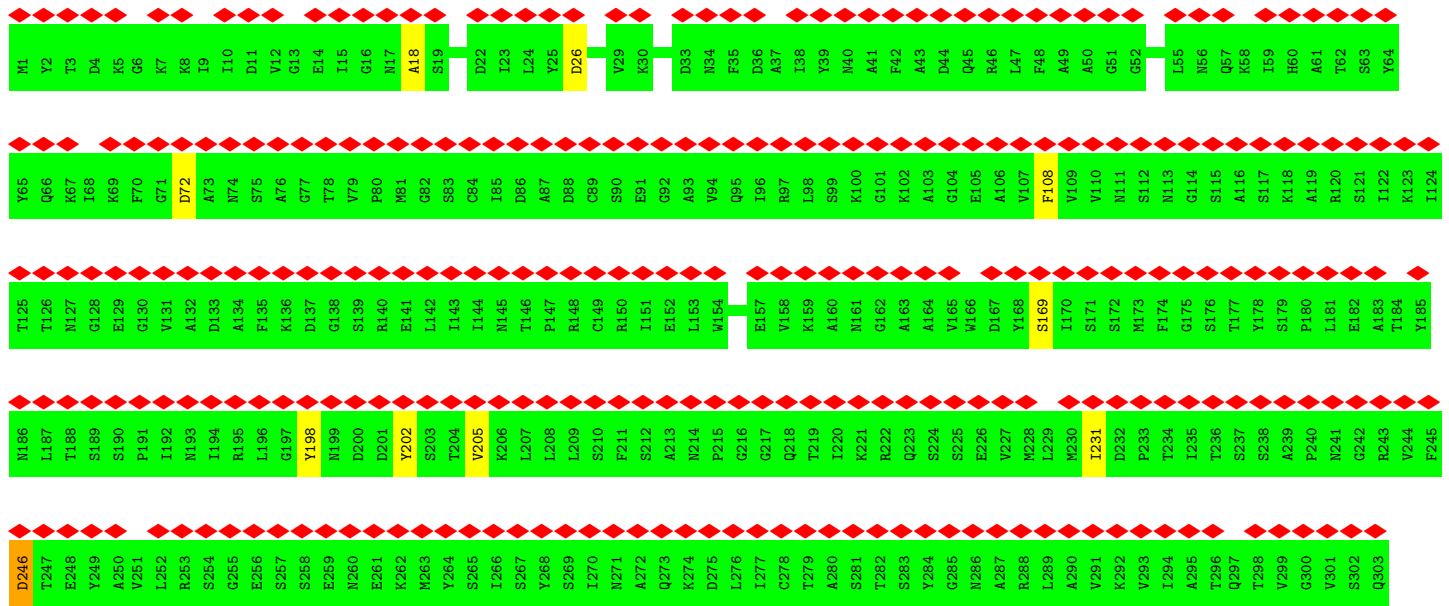


• Molecule 7: Baseplate wedge tail fiber connector





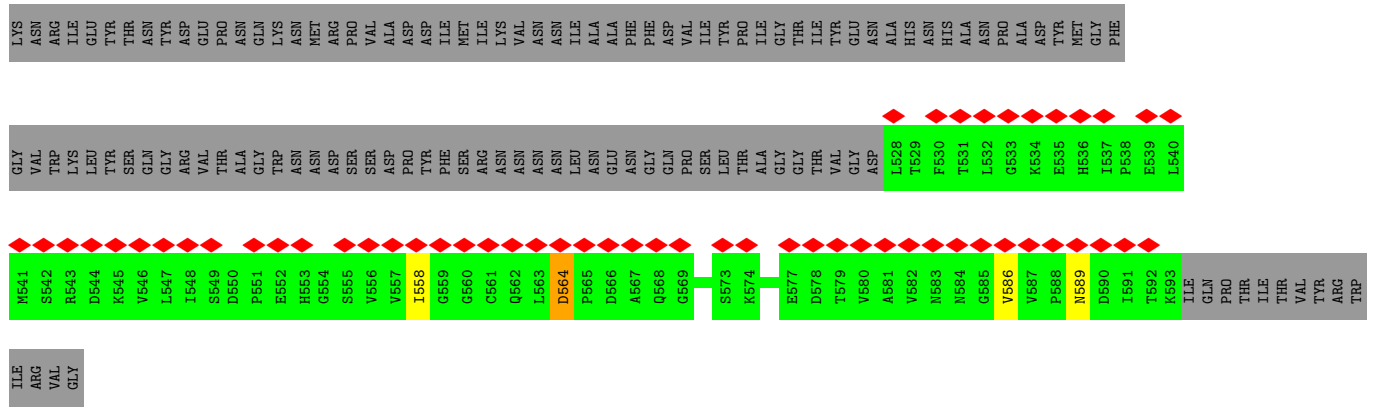
• Molecule 7: Baseplate wedge tail fiber connector



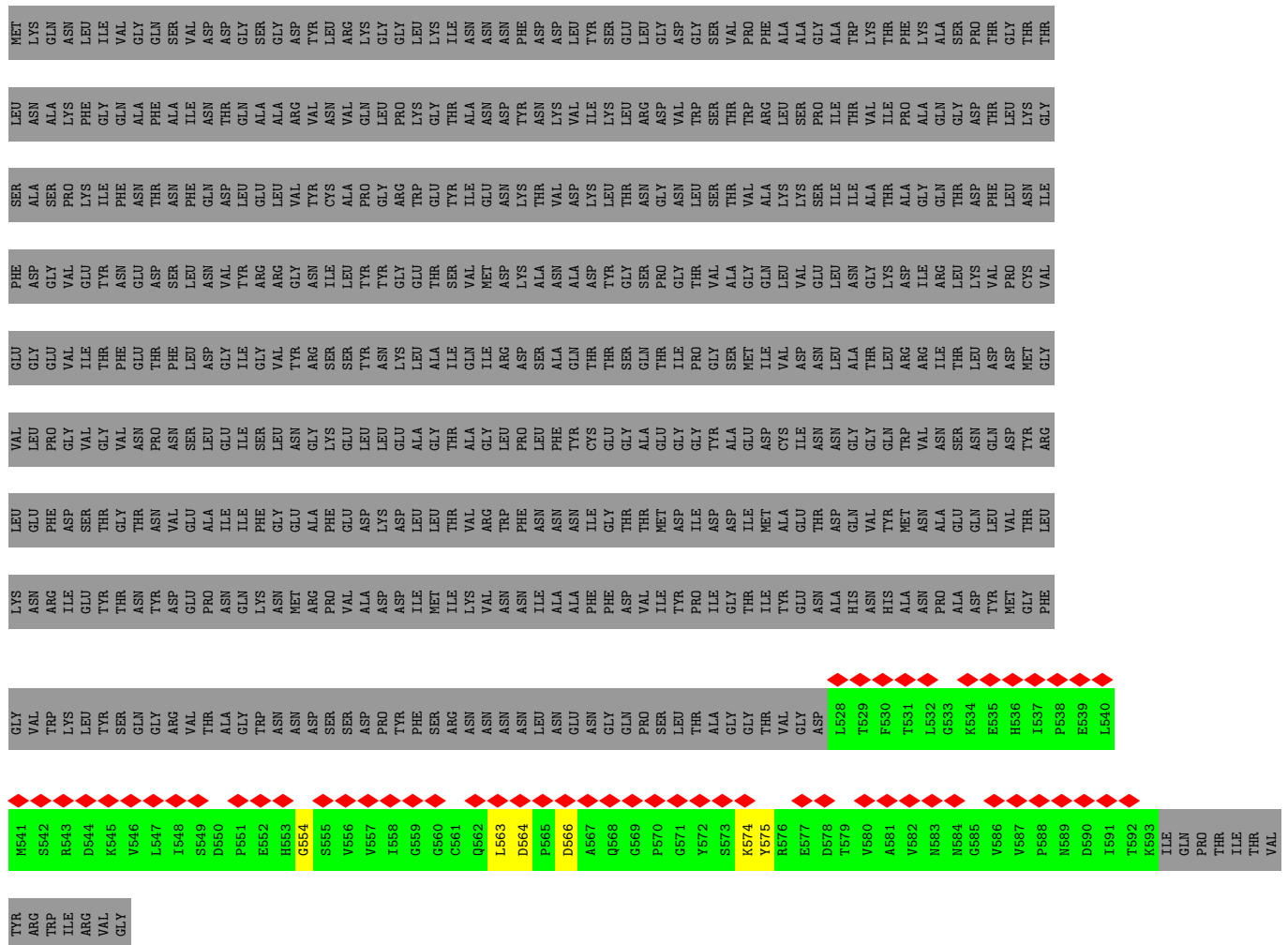
• Molecule 8: Baseplate wedge protein gp10



MET	LYS	GLN	ASN	ALA	LYS	GLY	ASP	PHE	GLU	VAL
LEU	ASN	ALA	LYS	PHE	LYS	VAL	GLY	LEU	ASN	ALA
SER	ALA	PRO	LYS	ILE	ASN	THR	ASP	THR	GLN	GLY
PHE	ASP	VAL	THR	THR	ASN	GLY	VAL	THR	THR	THR
GLU	GLY	VAL	THR	PHE	GLY	THR	THR	THR	THR	THR
VAL	LEU	PRO	GLY	ASN	GLY	THR	THR	THR	THR	THR
LEU	PHE	ASP	GLY	THR	THR	THR	THR	THR	THR	THR
GLU	ASP	VAL	THR	THR	THR	THR	THR	THR	THR	THR
LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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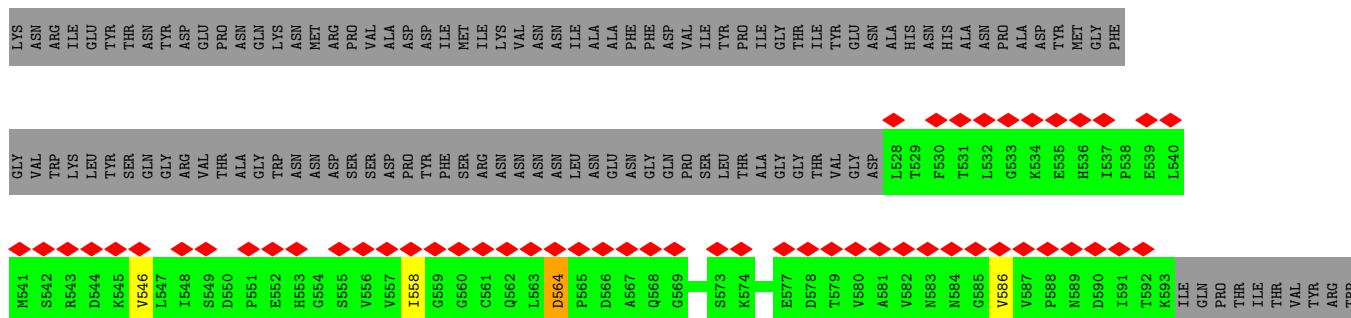


• Molecule 8: Baseplate wedge protein gp10

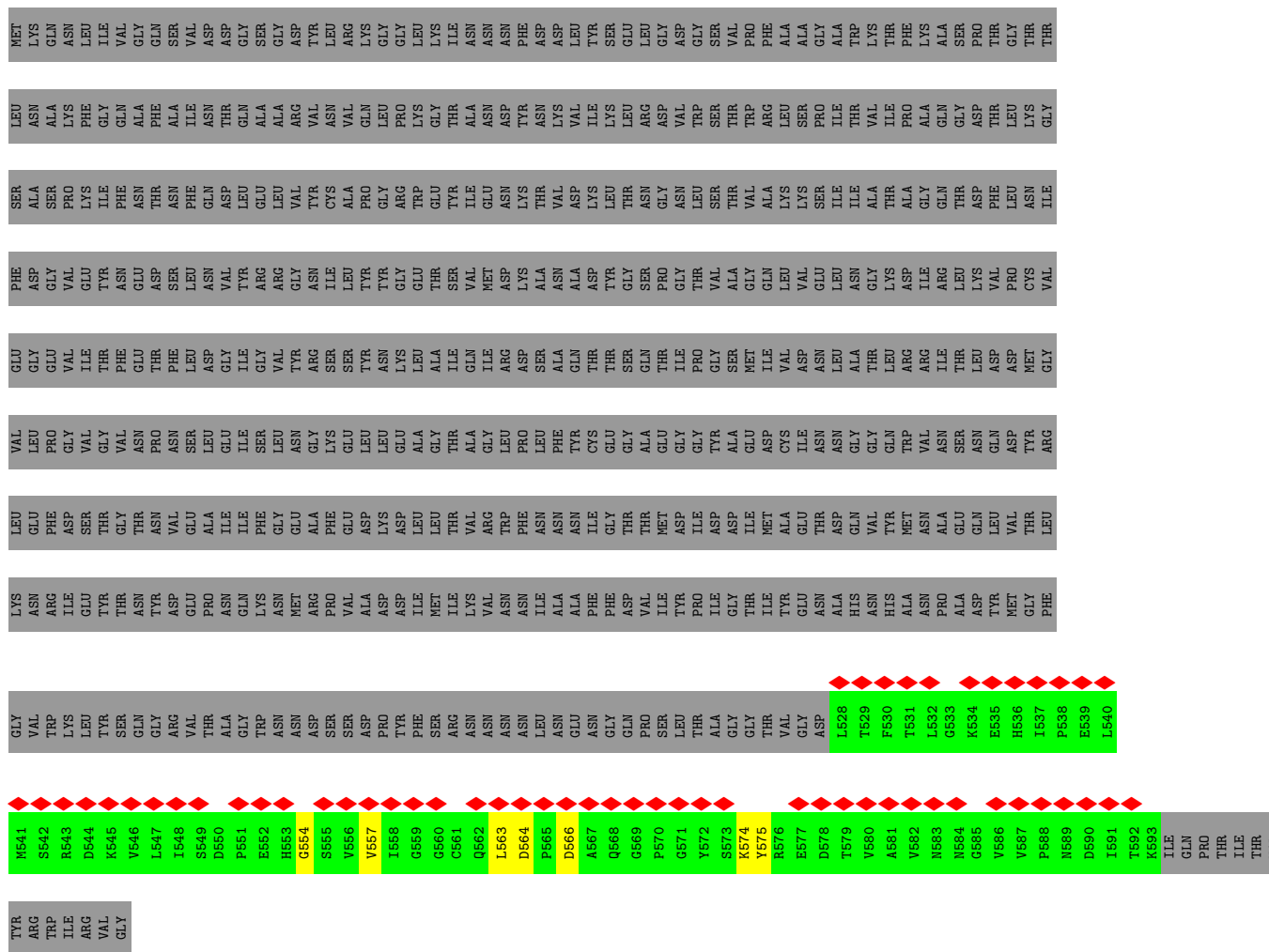


• Molecule 8: Baseplate wedge protein gp10



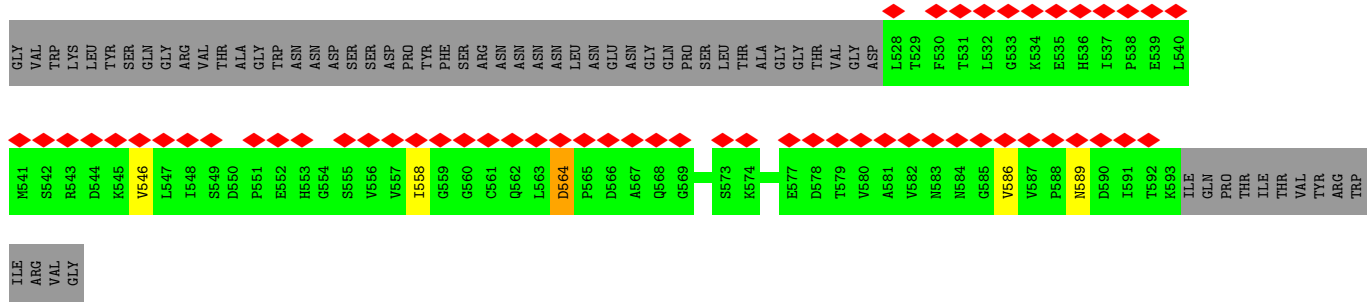


• Molecule 8: Baseplate wedge protein gp10

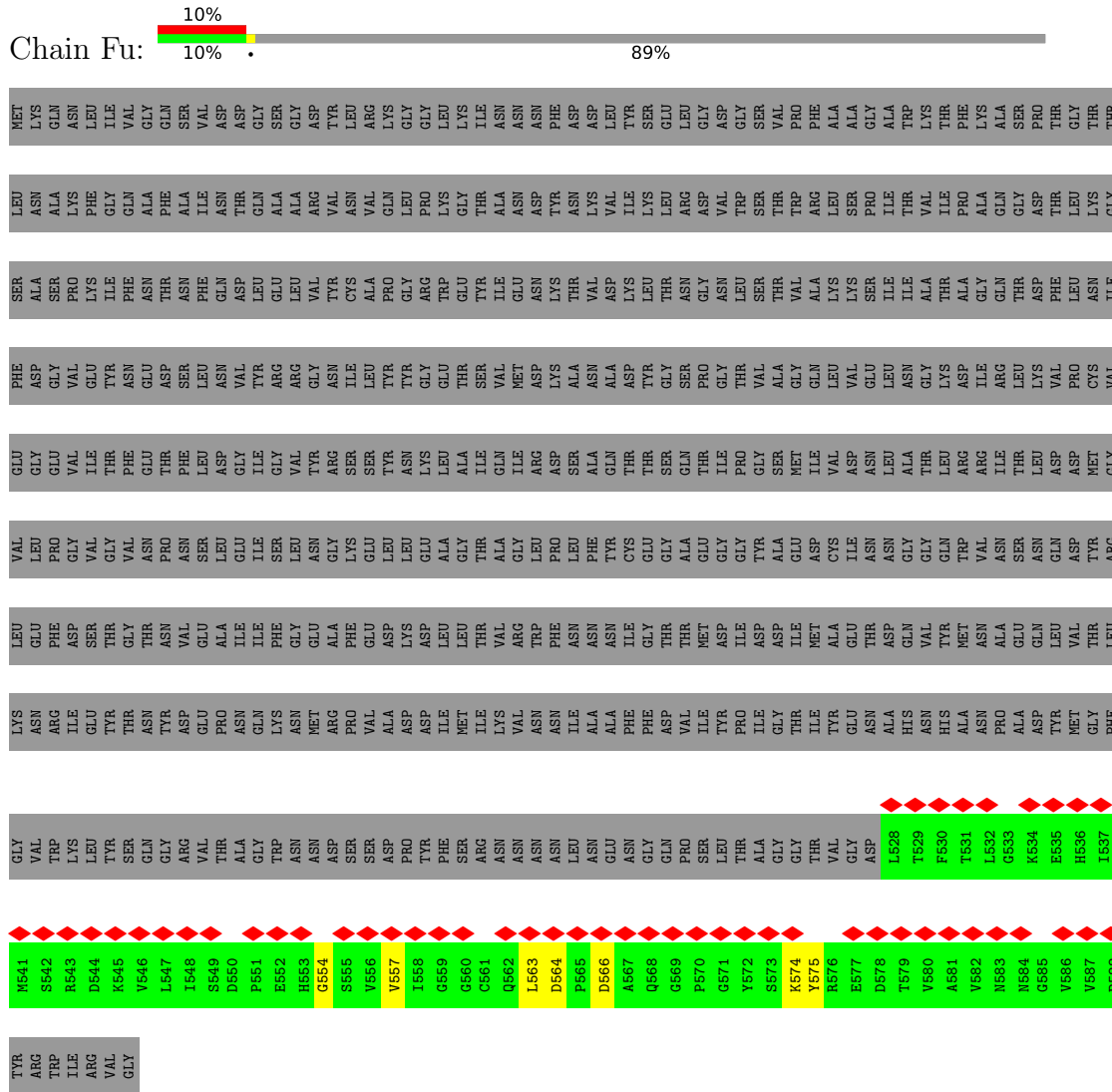


• Molecule 8: Baseplate wedge protein gp10

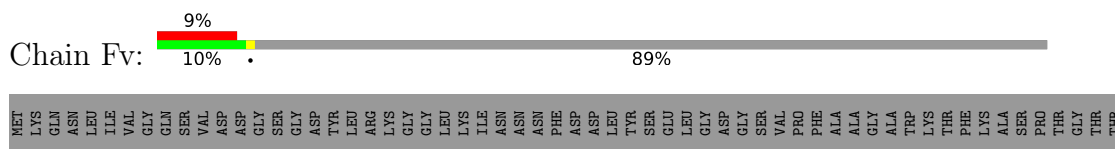


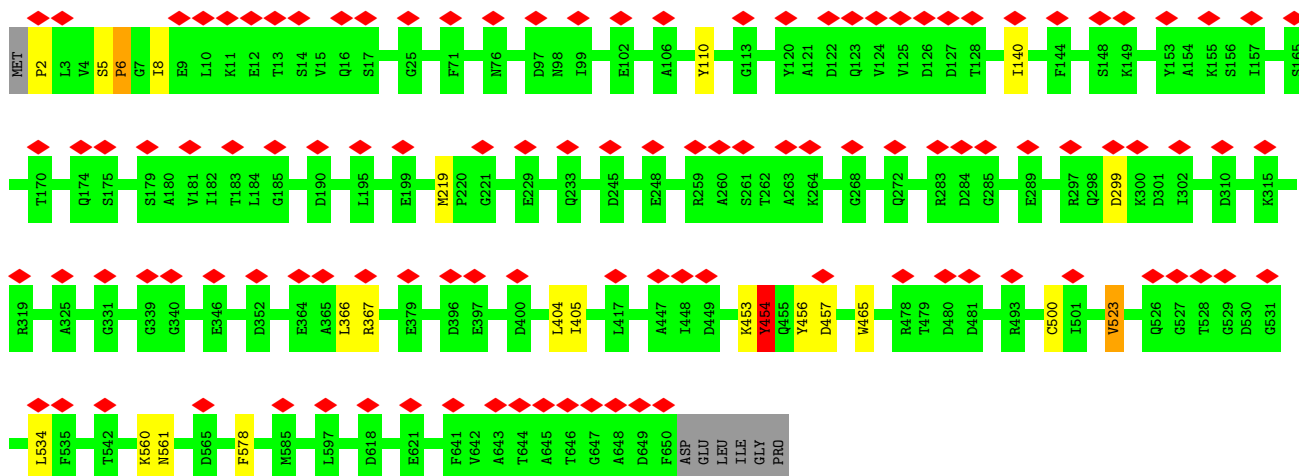


• Molecule 8: Baseplate wedge protein gp10

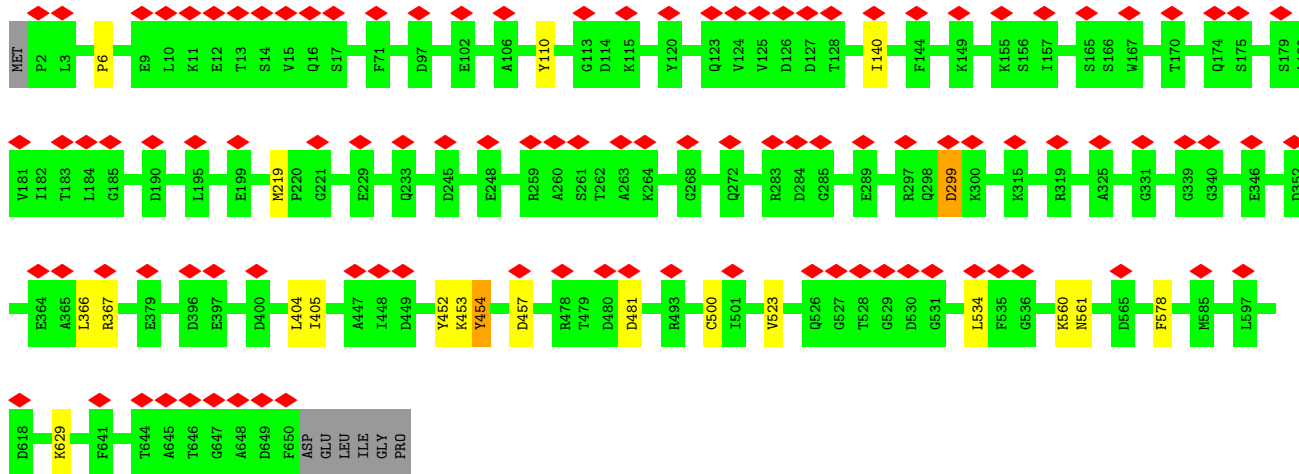


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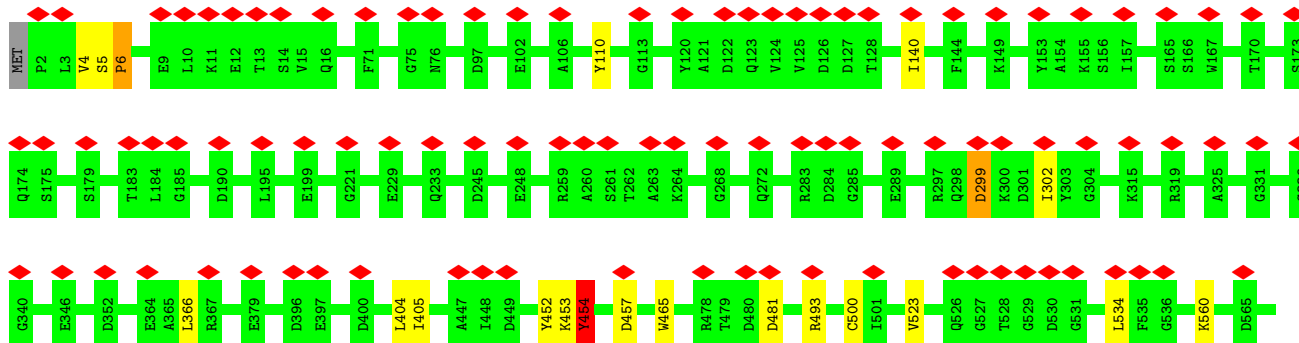


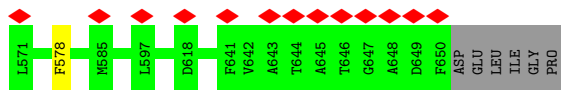


• Molecule 9: Tail sheath protein

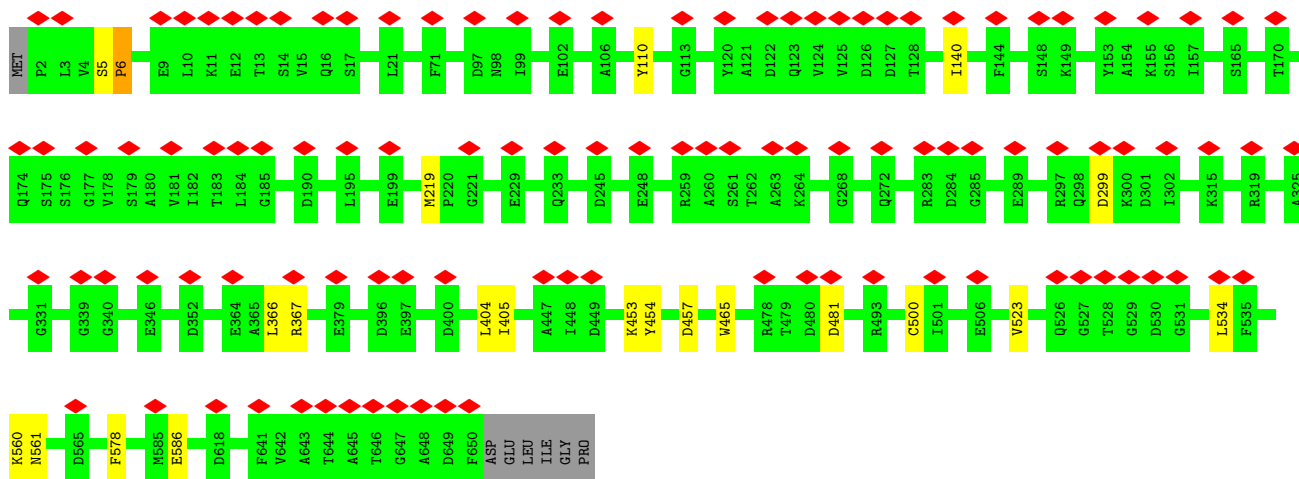


• Molecule 9: Tail sheath protein

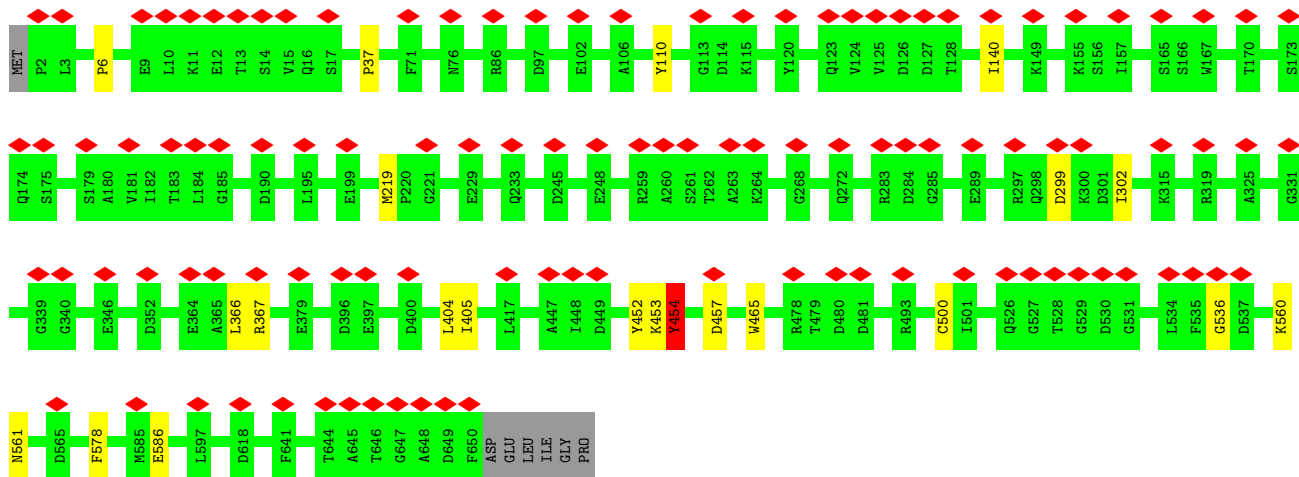




• Molecule 9: Tail sheath protein

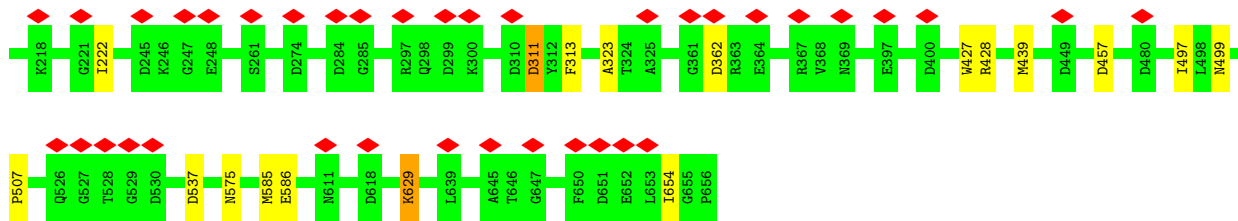


• Molecule 9: Tail sheath protein

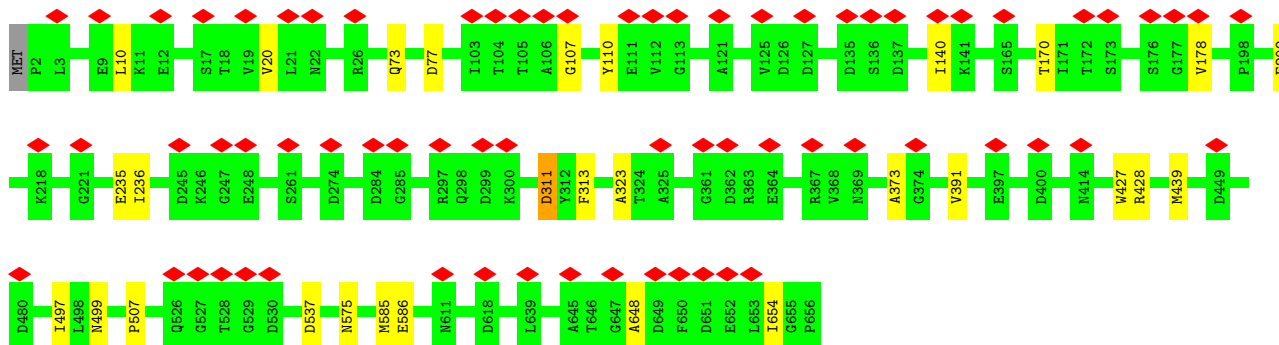


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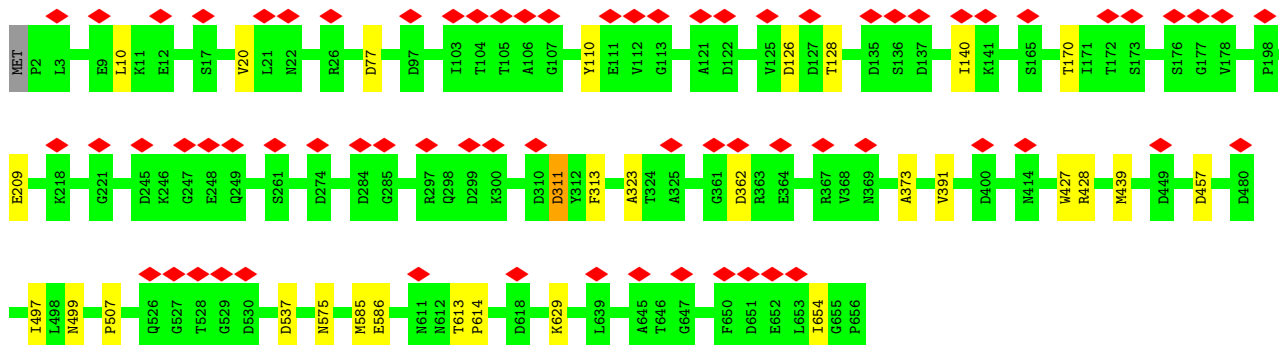




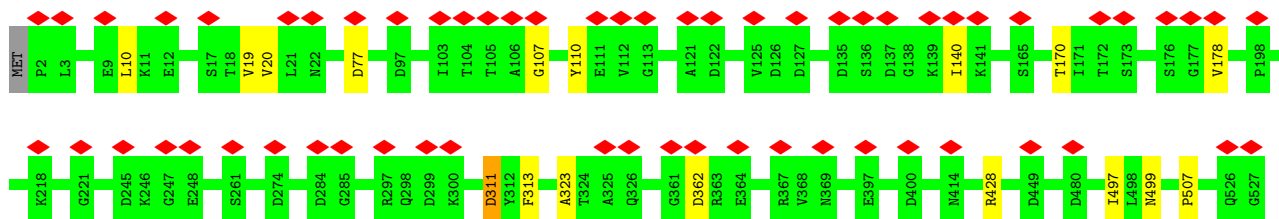
• Molecule 9: Tail sheath protein

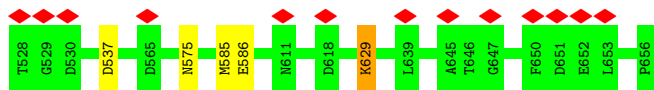


• Molecule 9: Tail sheath protein

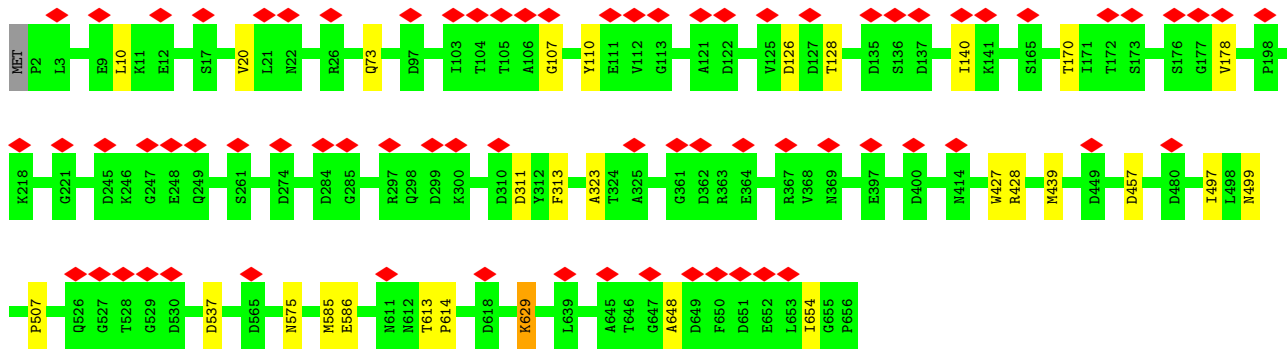


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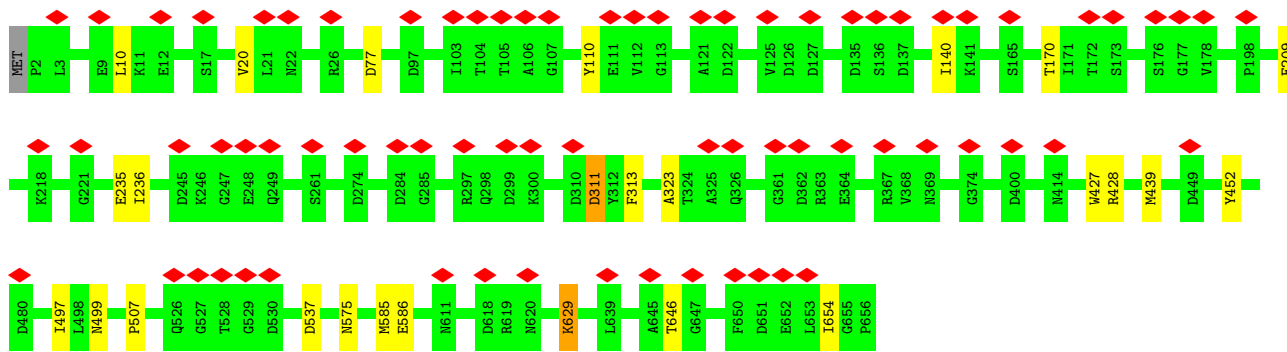




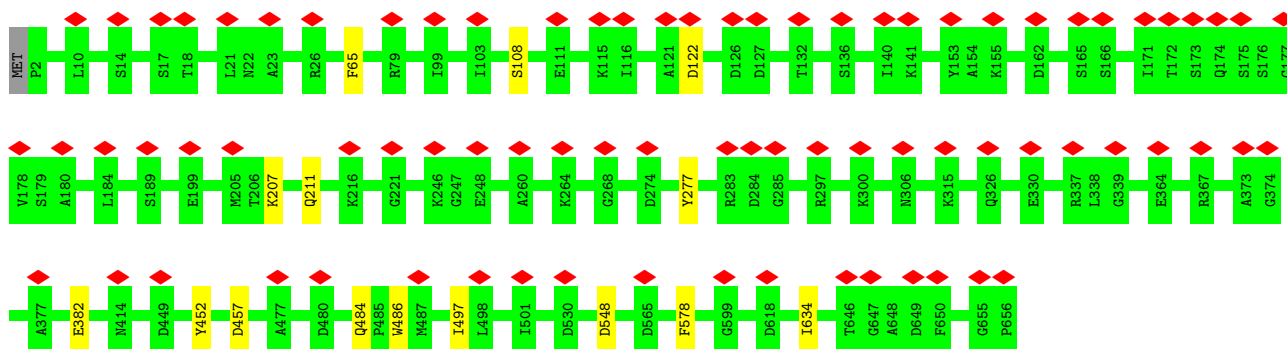
• Molecule 9: Tail sheath protein



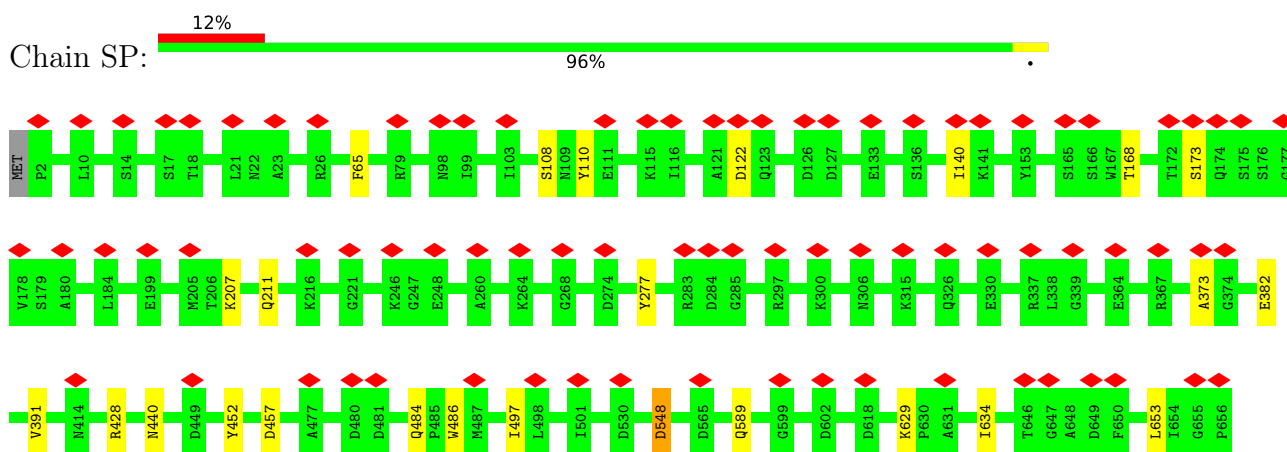
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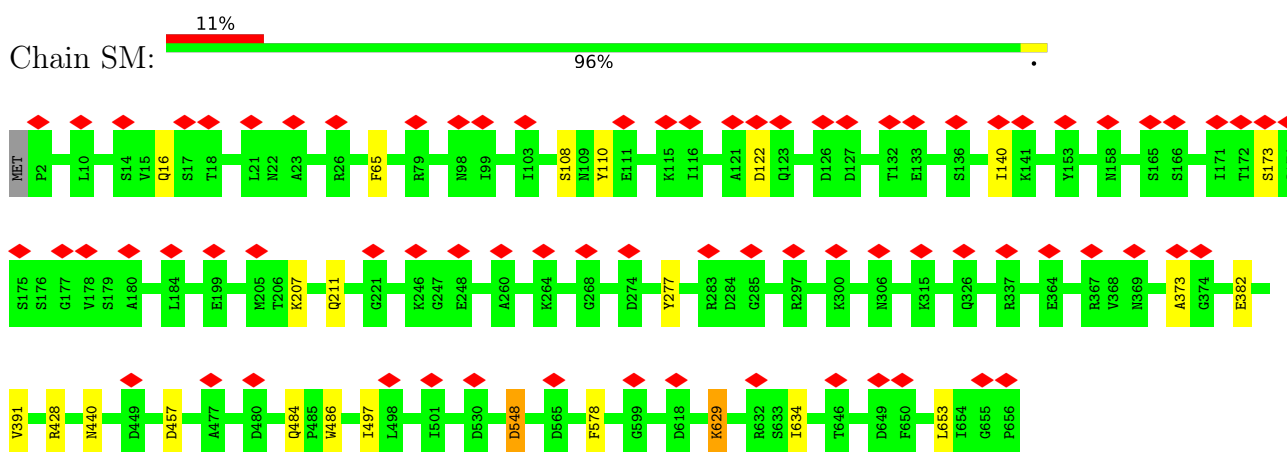
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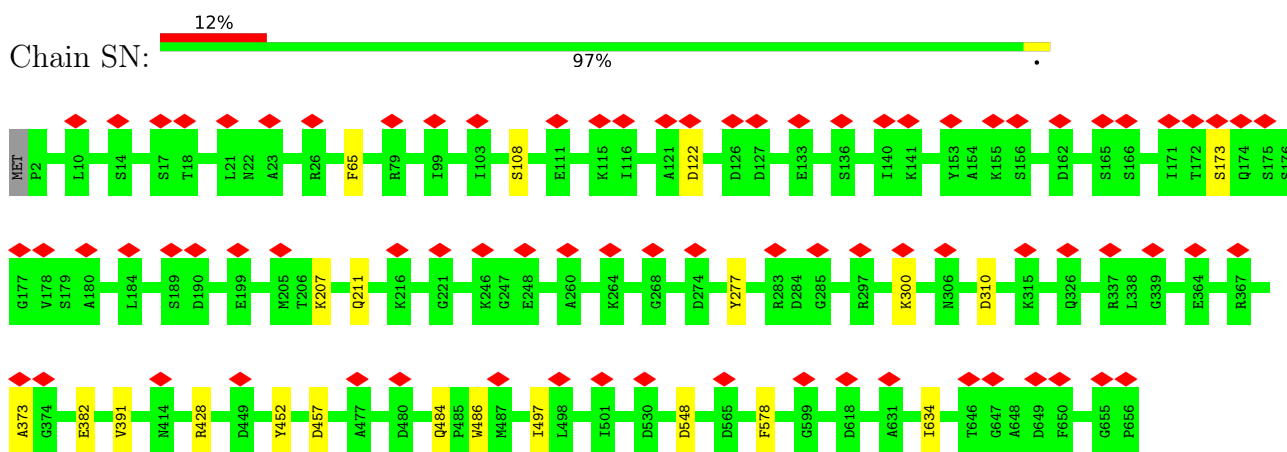
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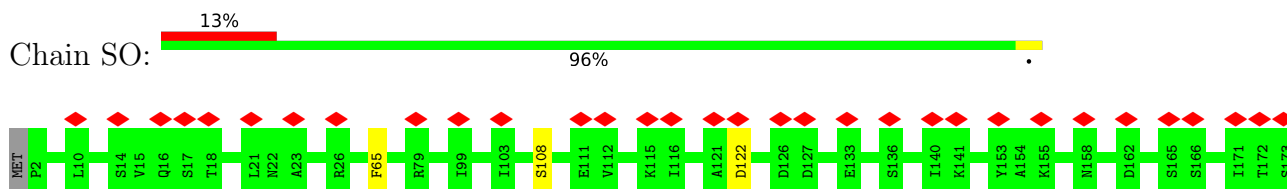
- Molecule 9: Tail sheath protein

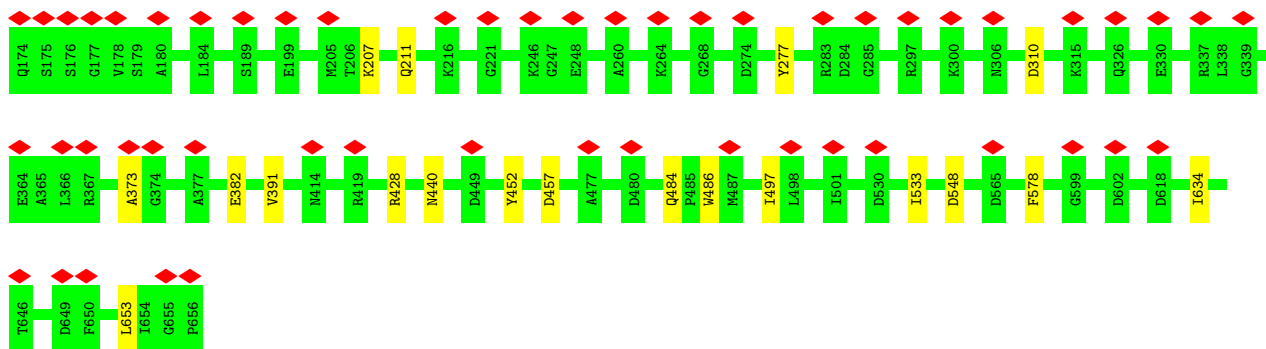


- Molecule 9: Tail sheath protein

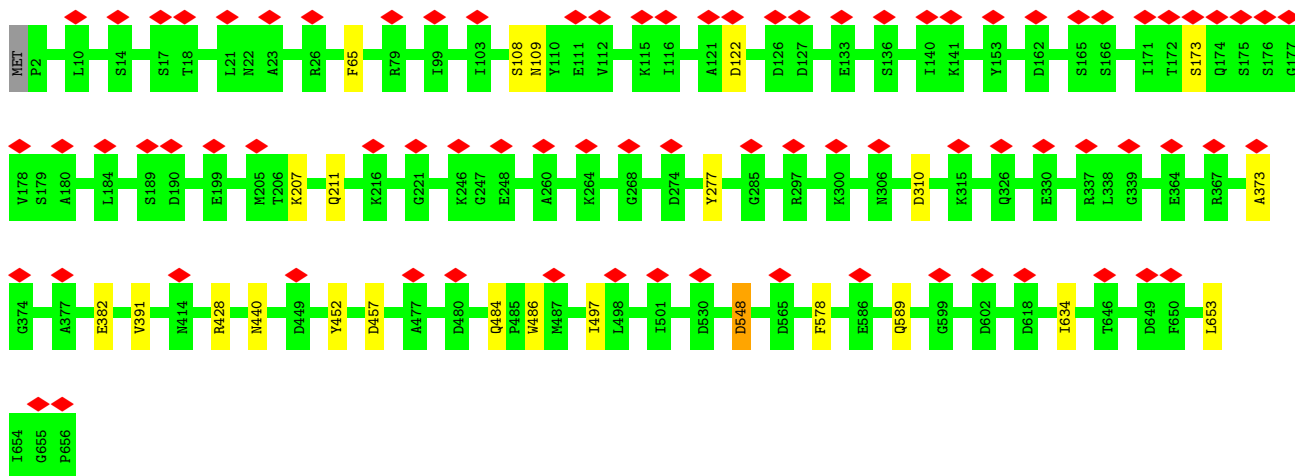


- Molecule 9: Tail sheath protein

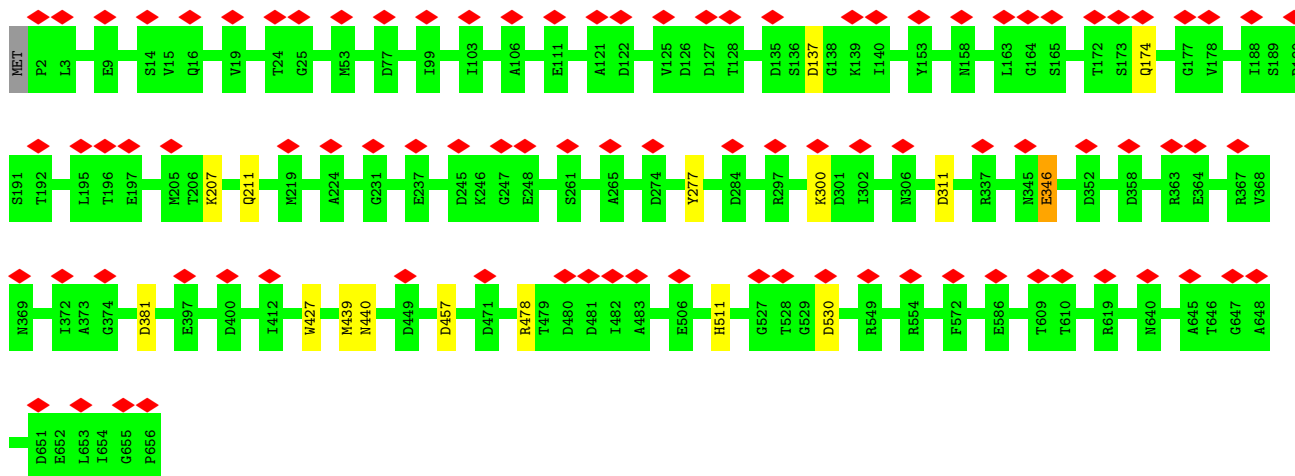




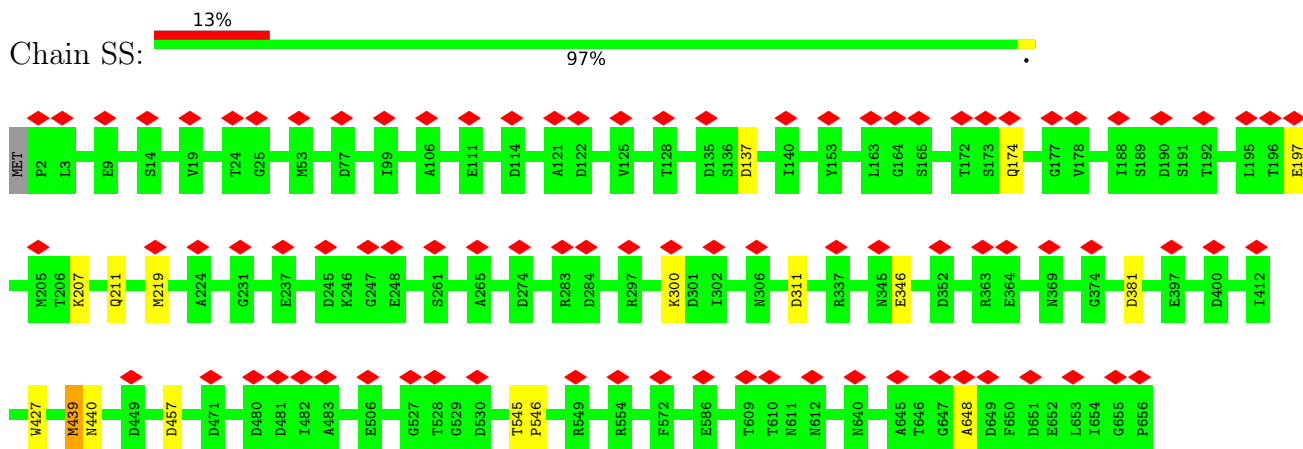
• Molecule 9: Tail sheath protein



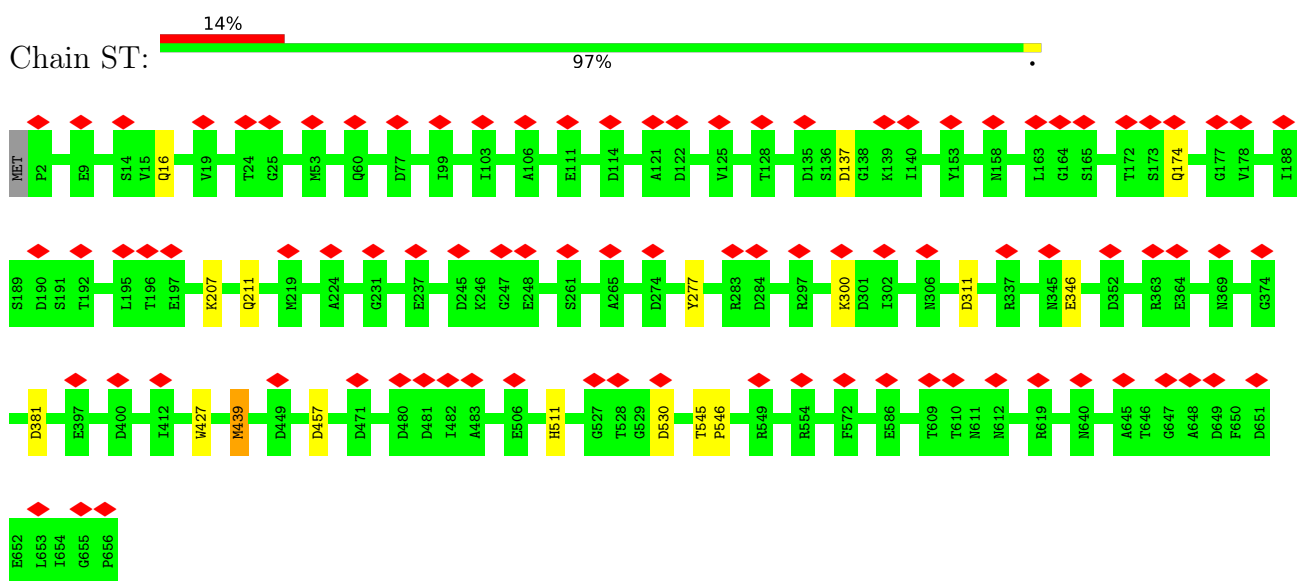
• Molecule 9: Tail sheath protein



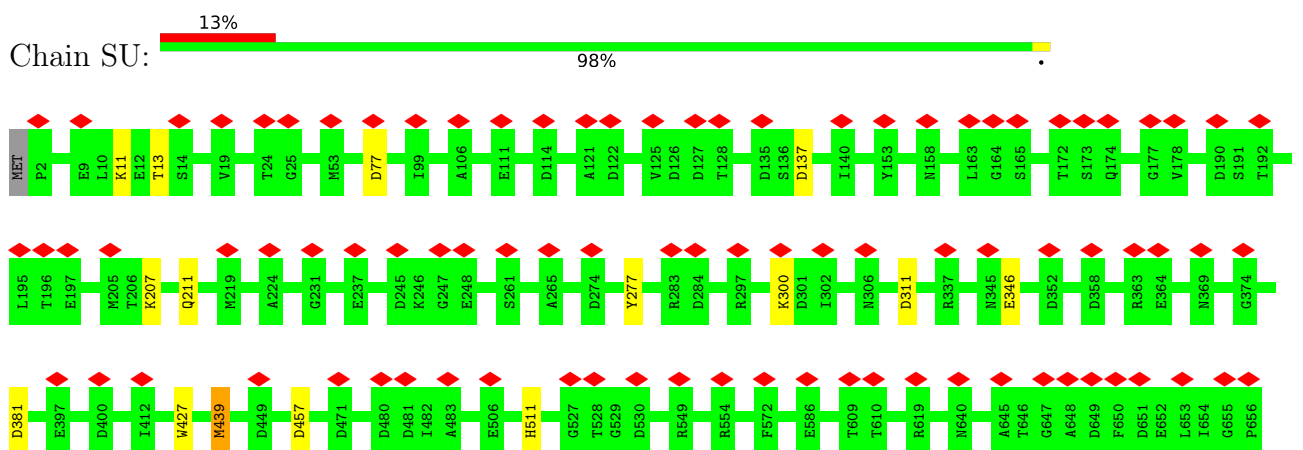
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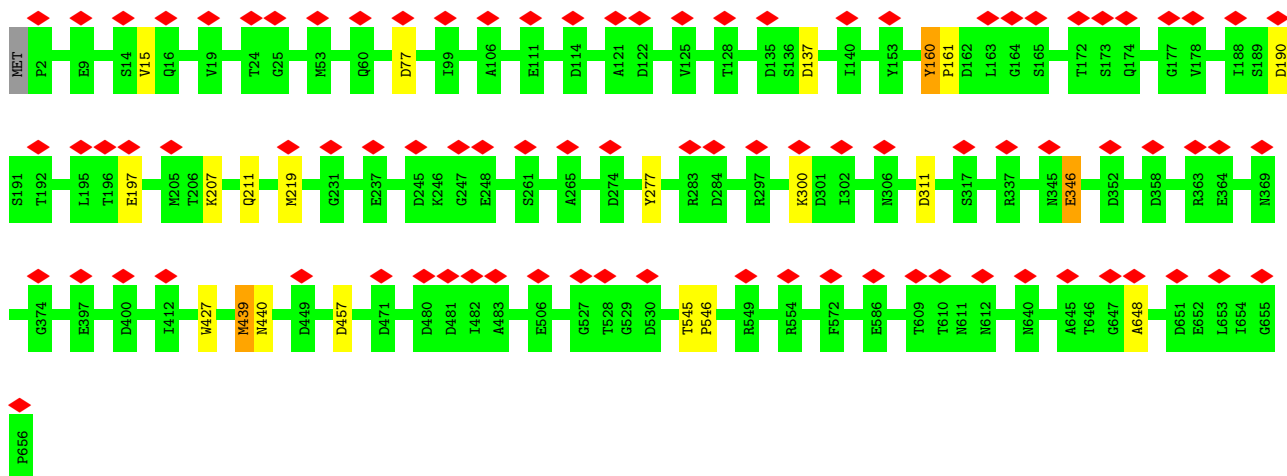


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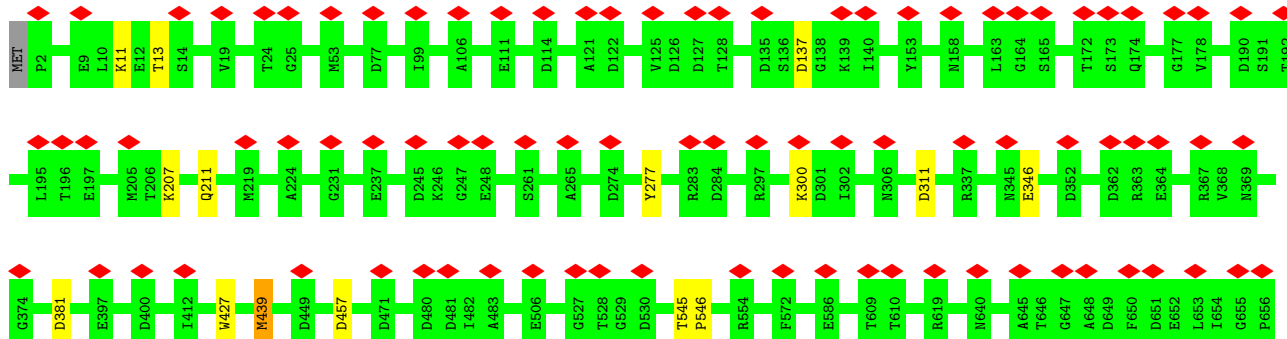


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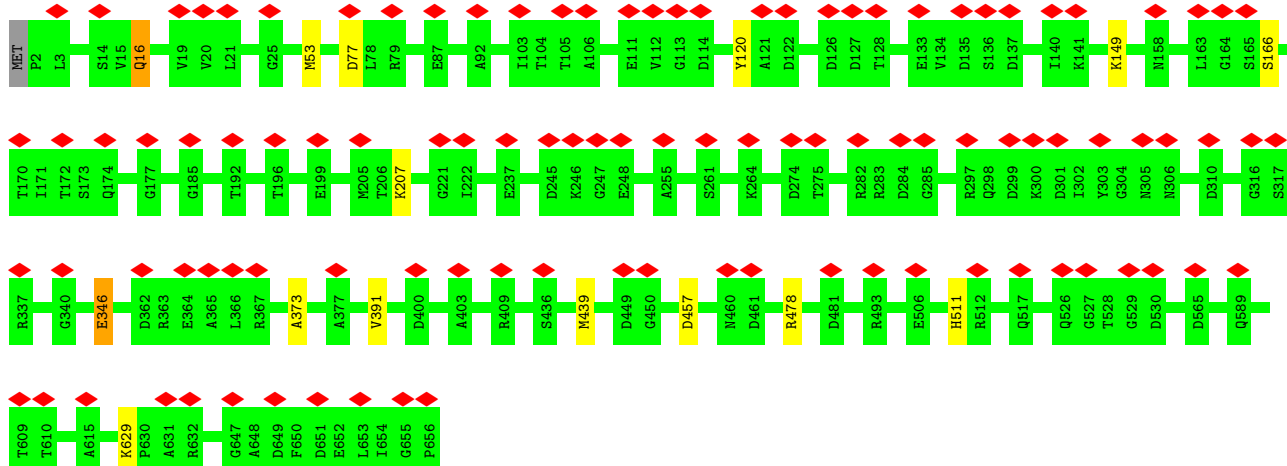




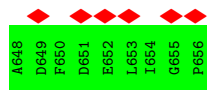
• Molecule 9: Tail sheath protein



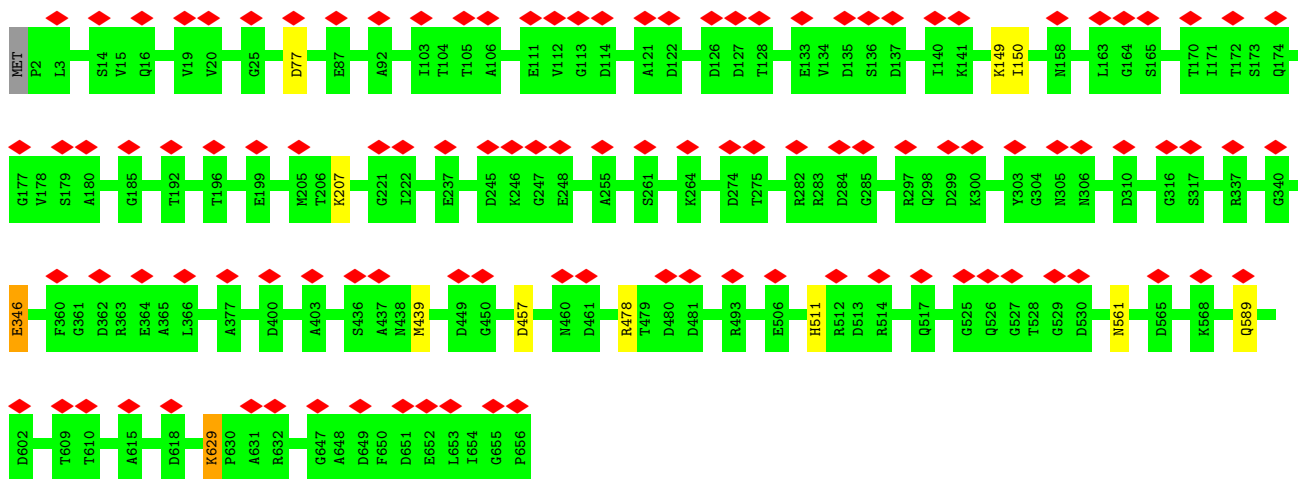
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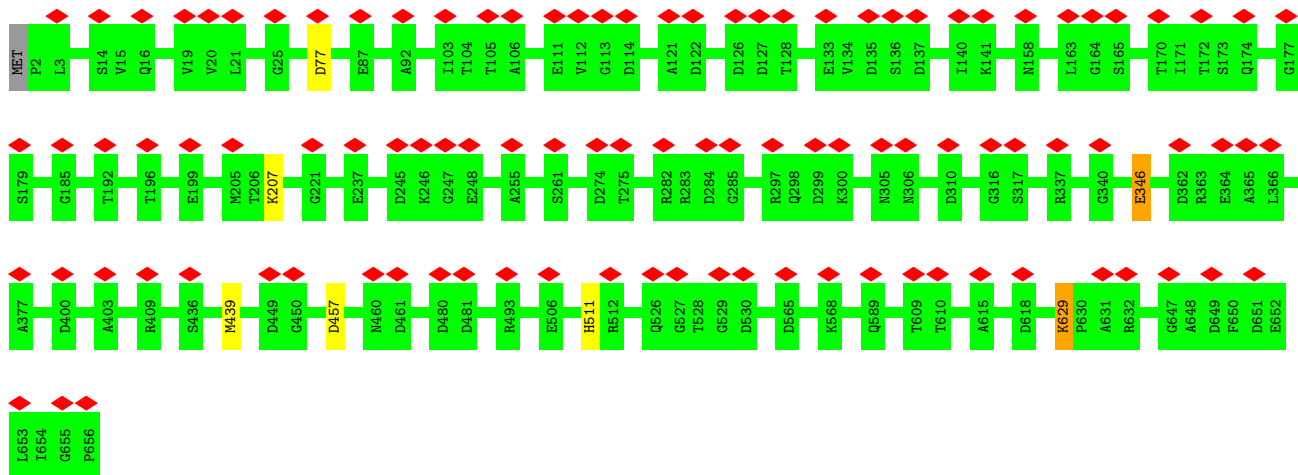
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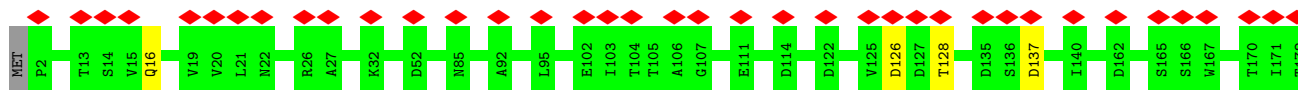
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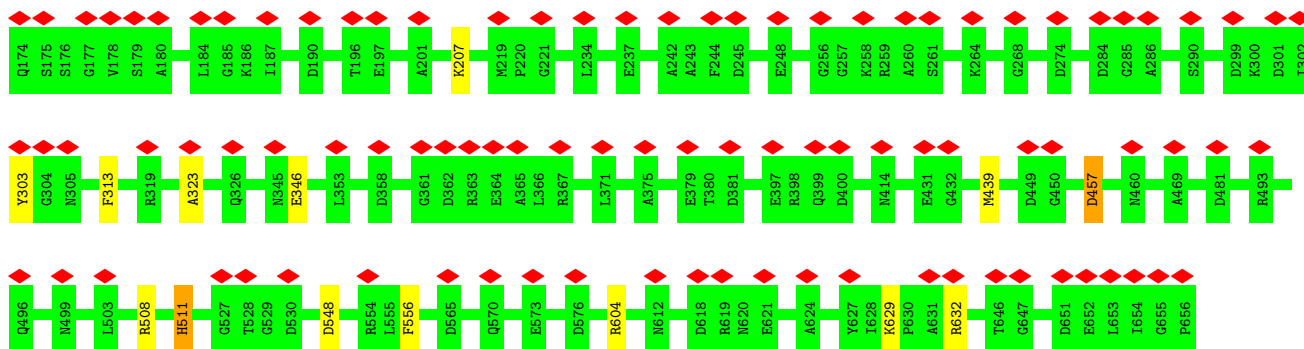


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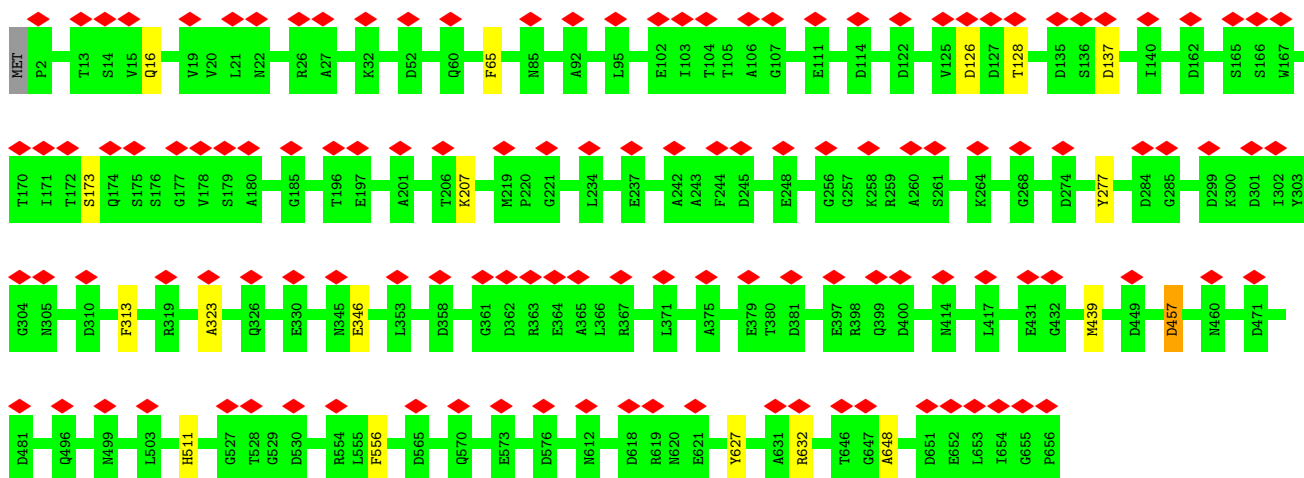


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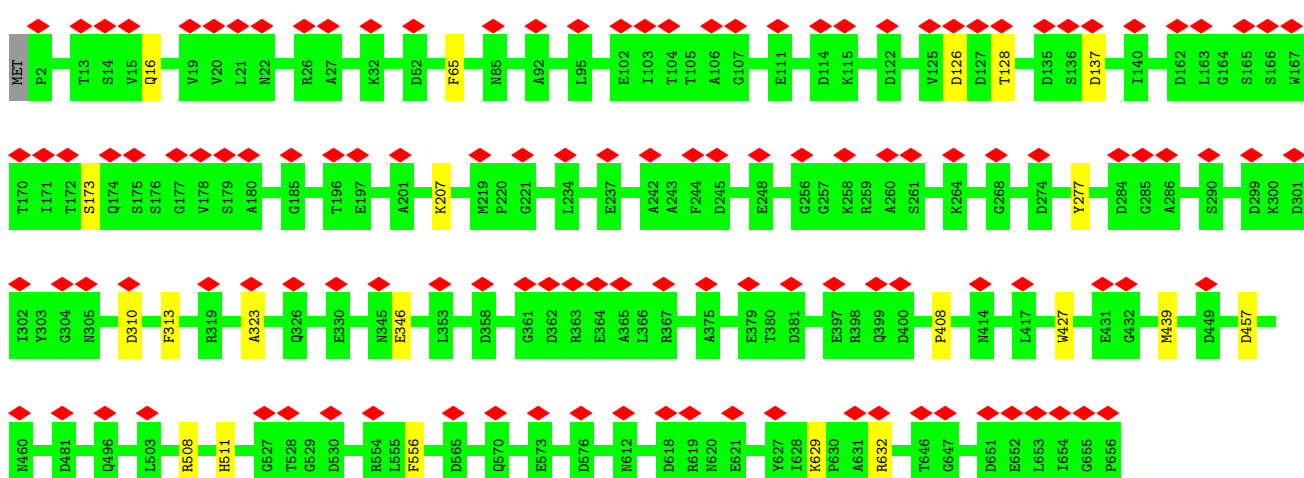




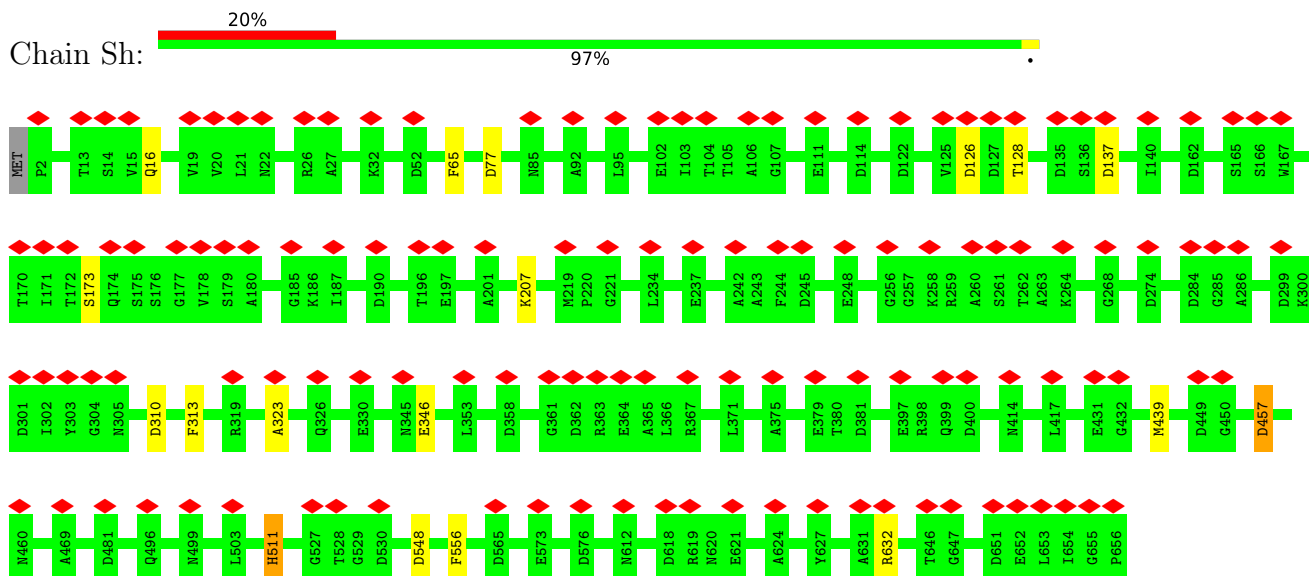
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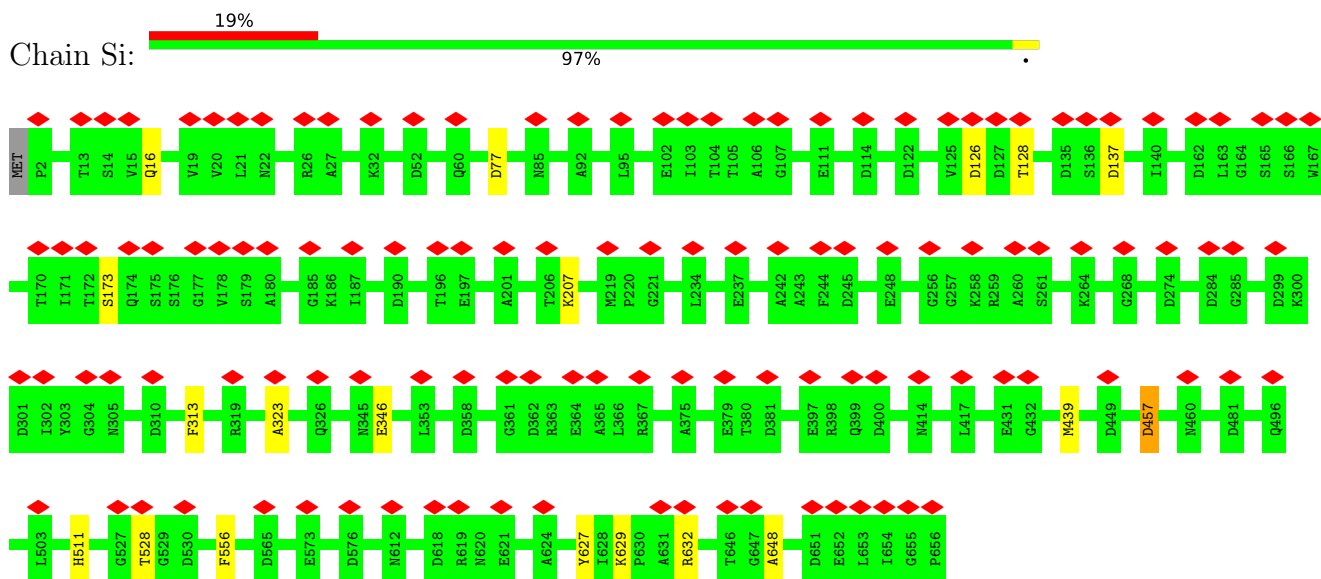
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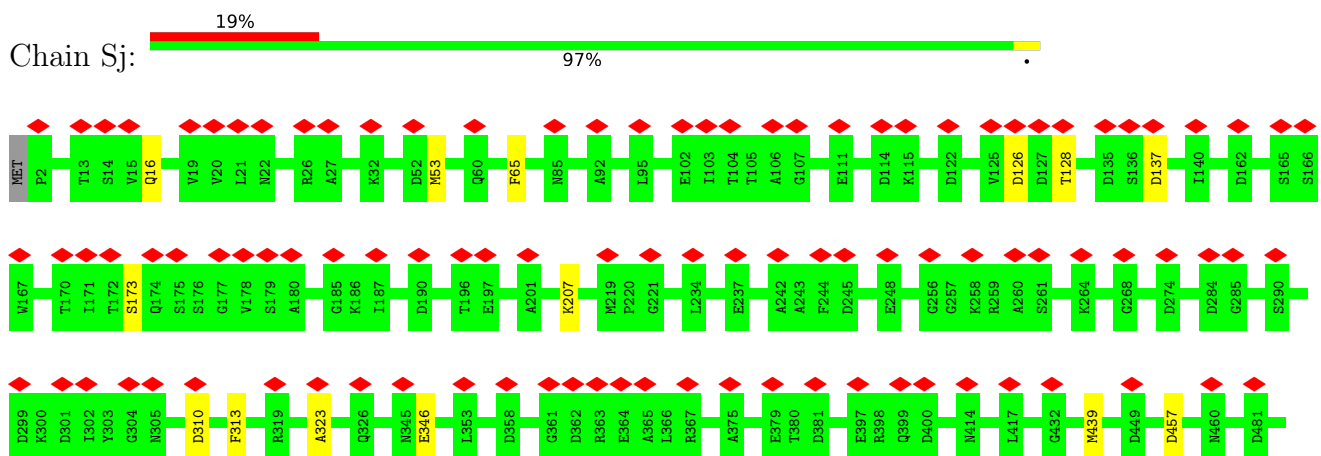
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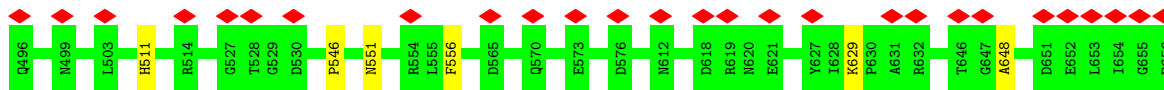


- Molecule 9: Tail sheath protein

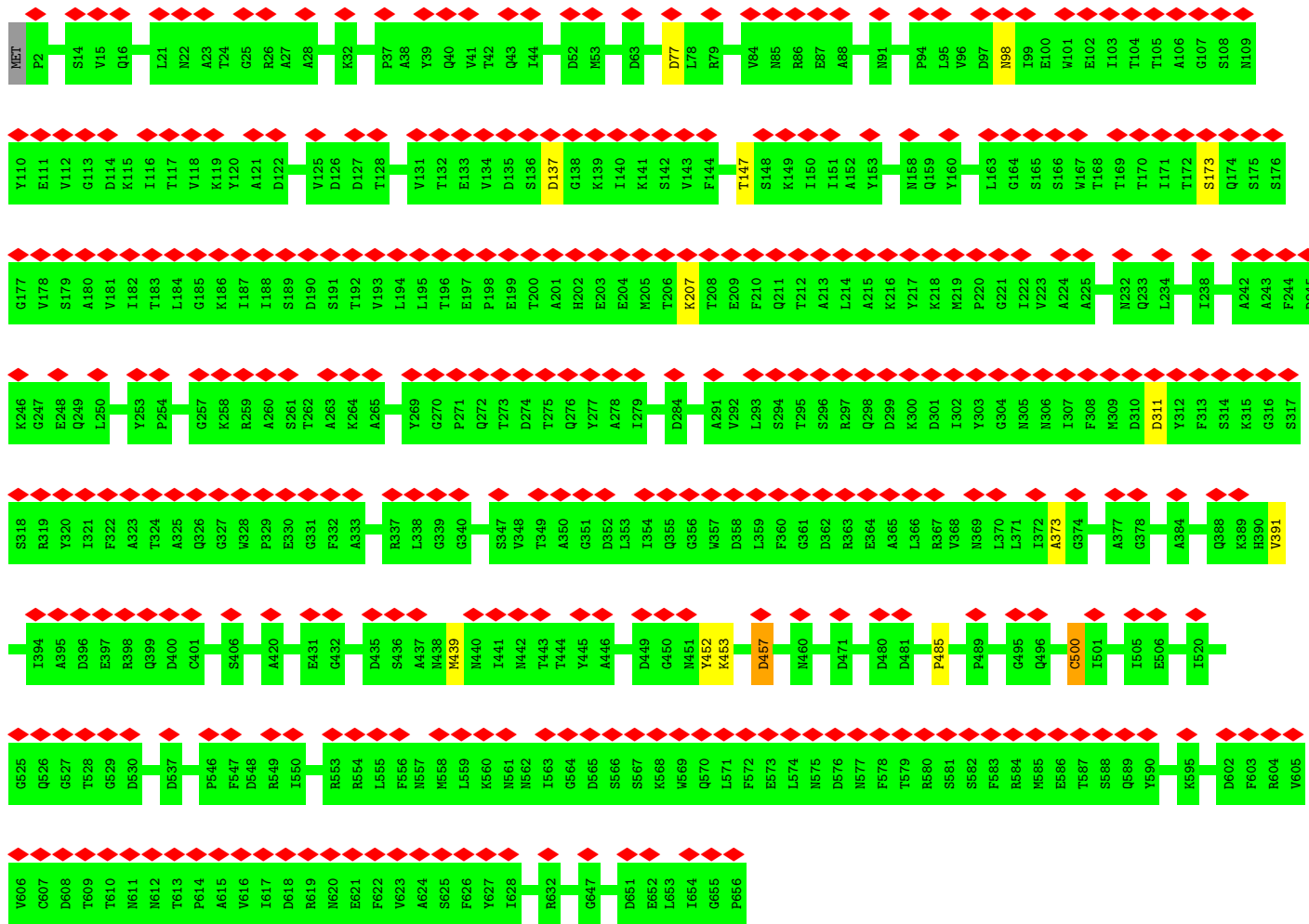


- Molecule 9: Tail sheath protein

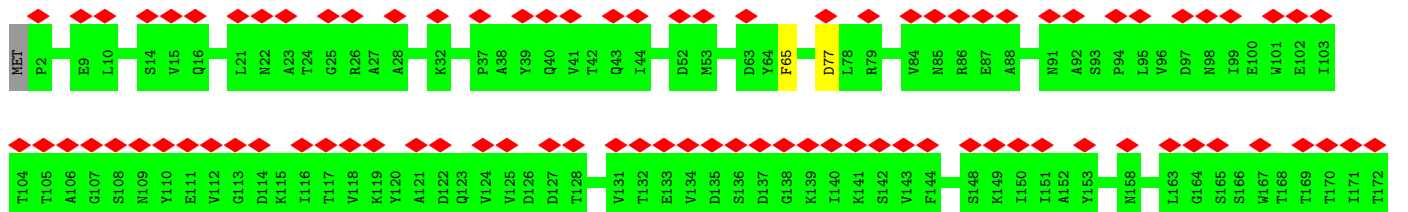


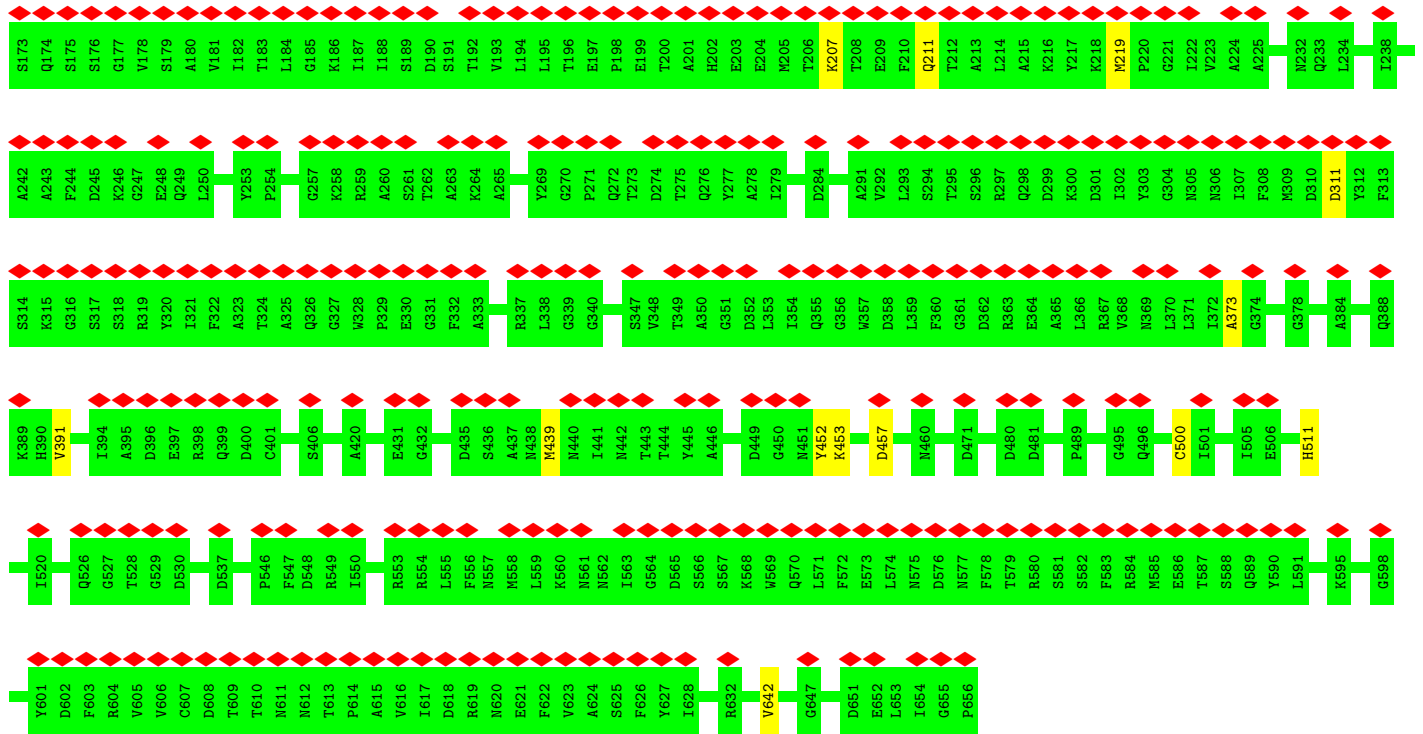


• Molecule 9: Tail sheath protein

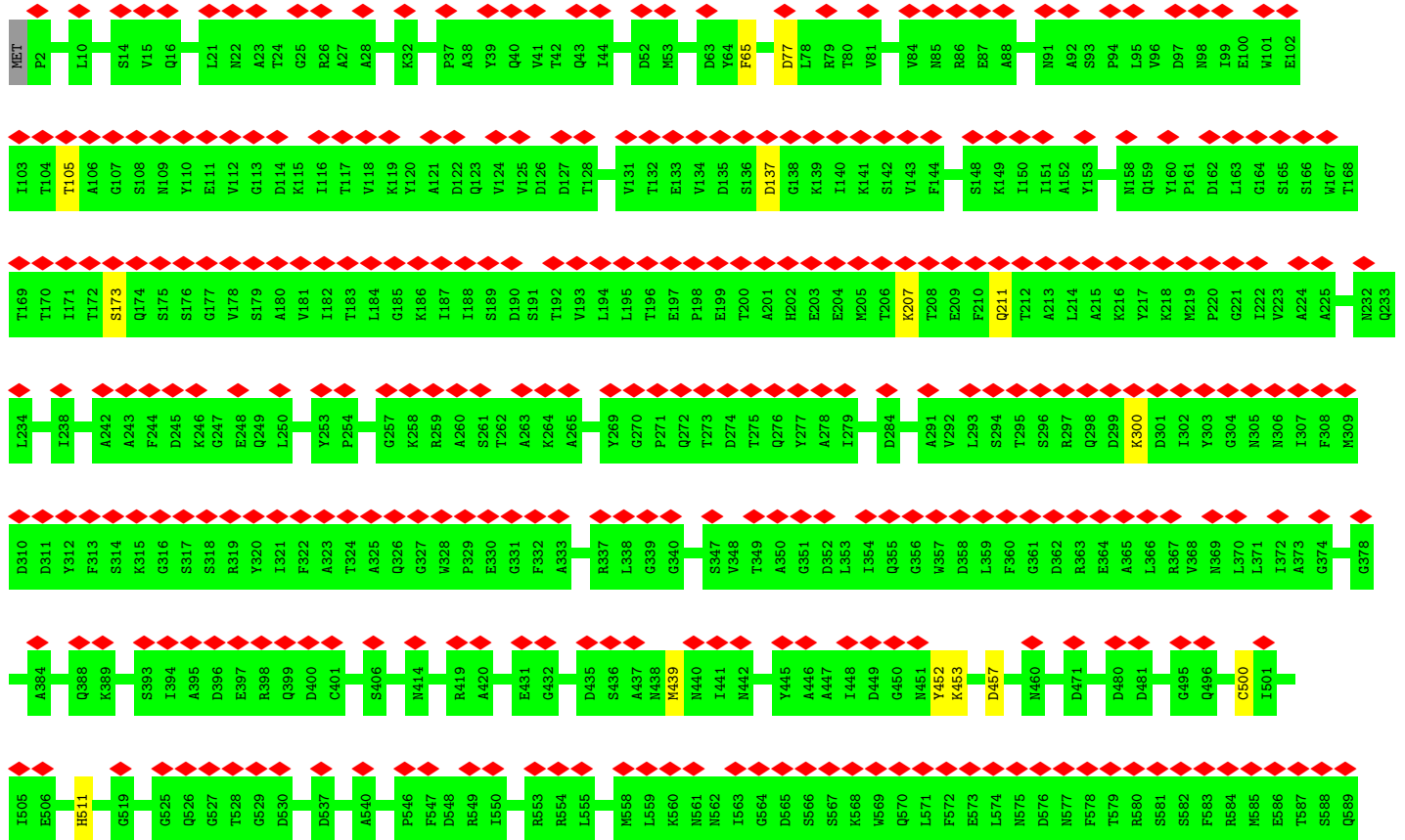


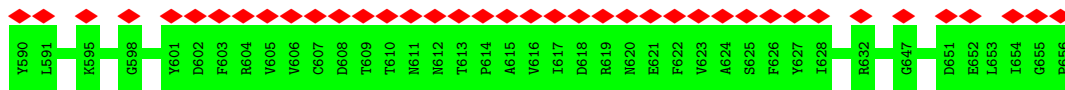
• Molecule 9: Tail sheath protein



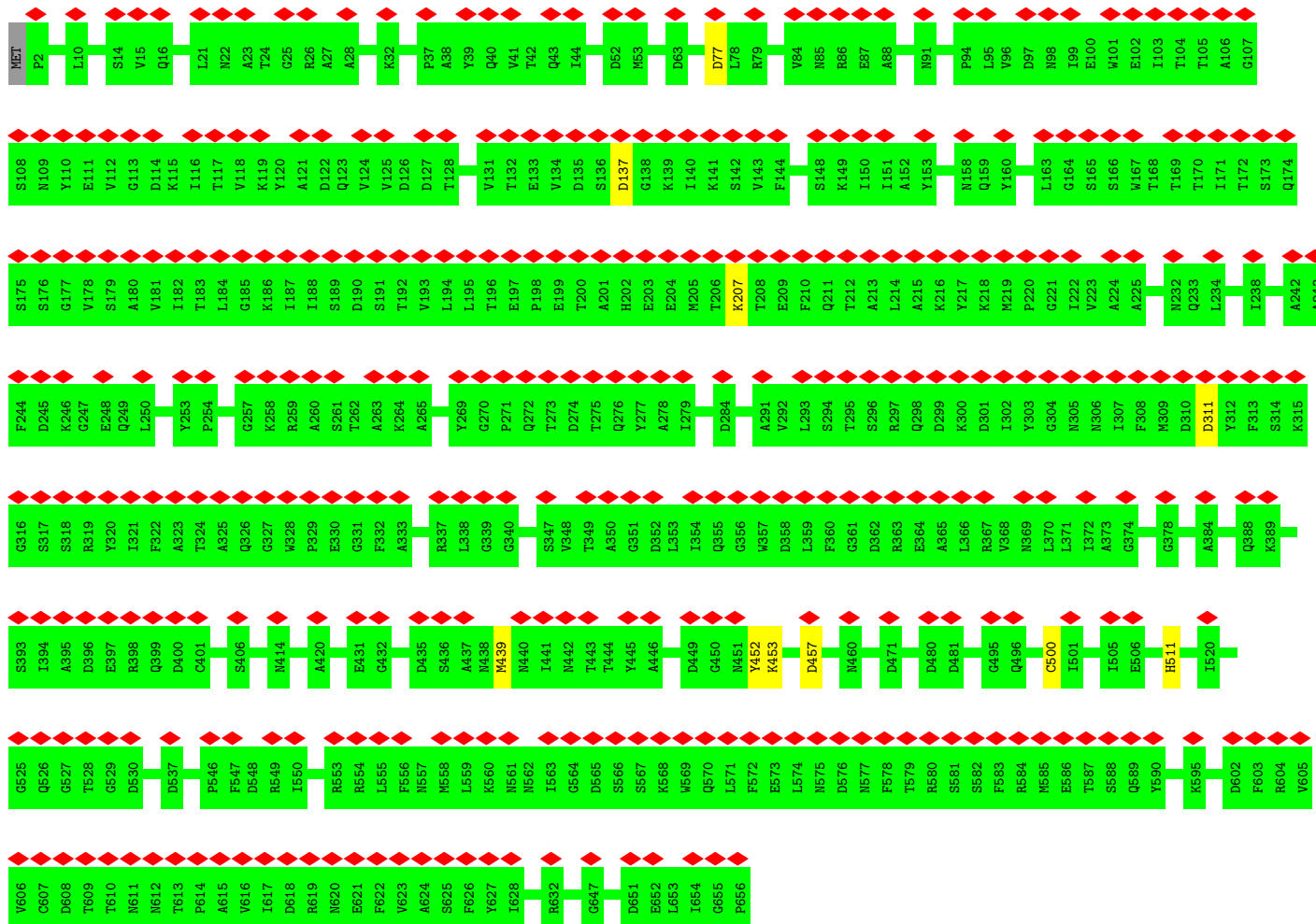


• Molecule 9: Tail sheath protein

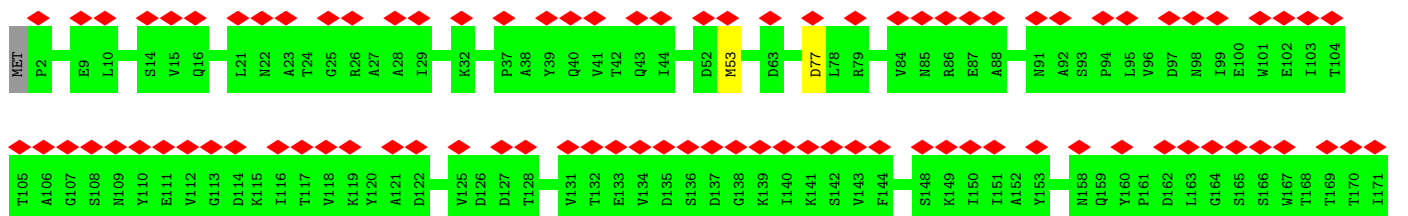


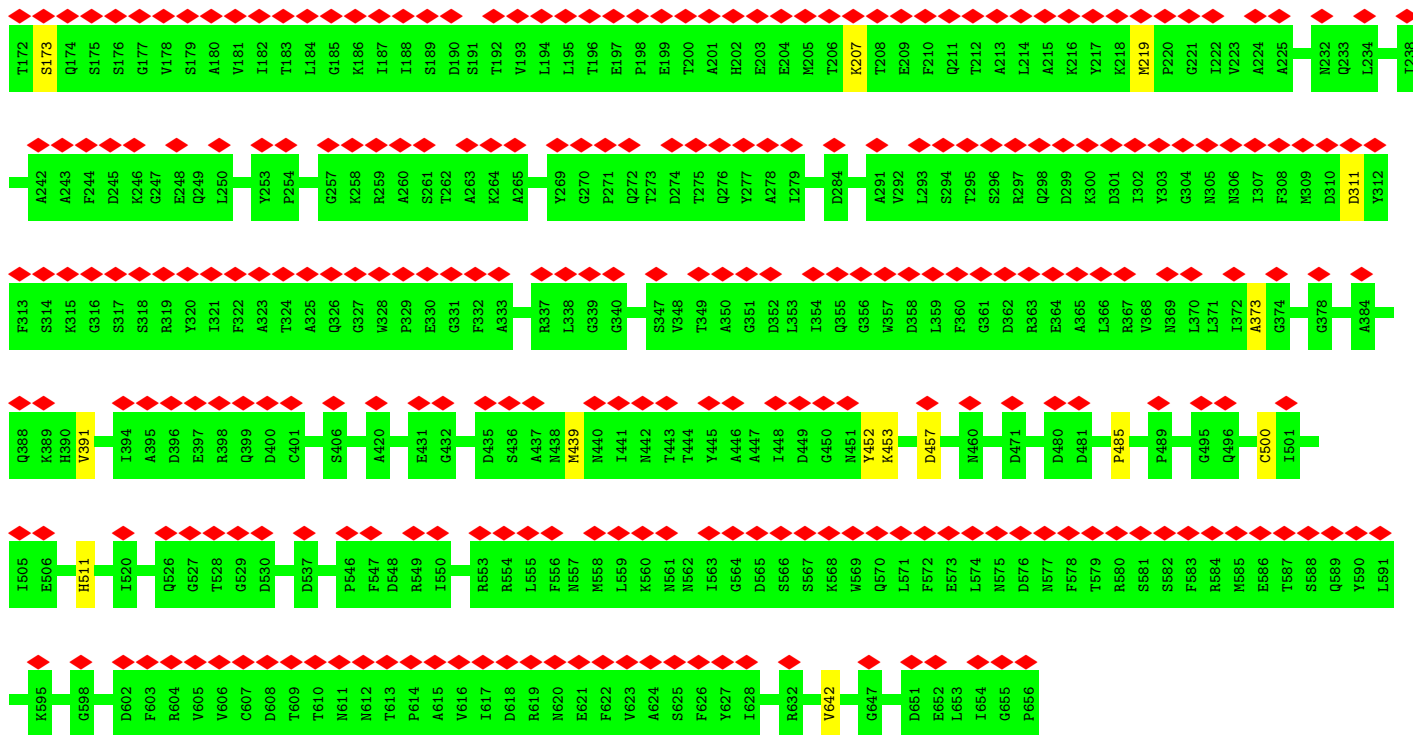


• Molecule 9: Tail sheath protein

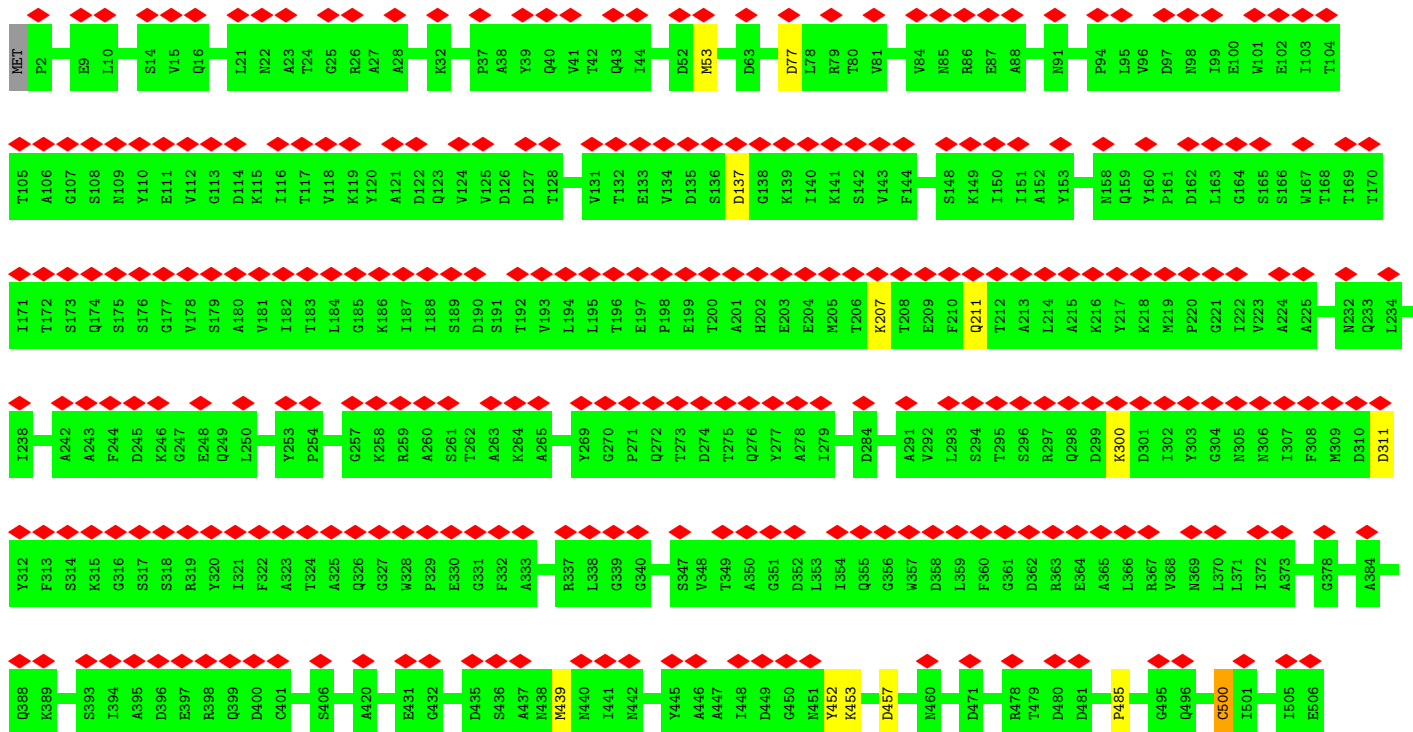


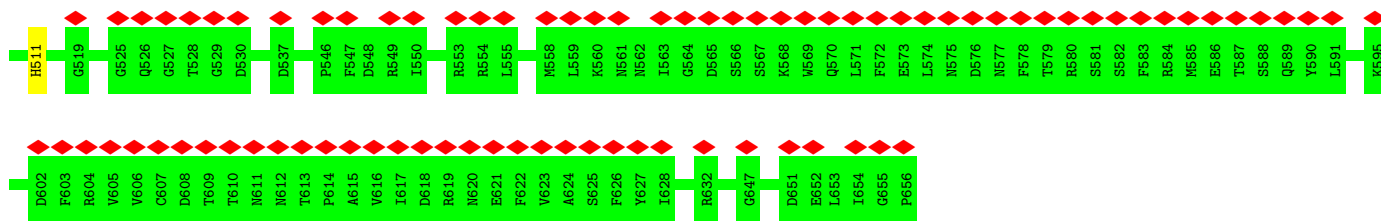
• Molecule 9: Tail sheath protein



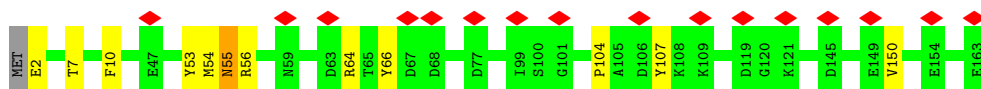
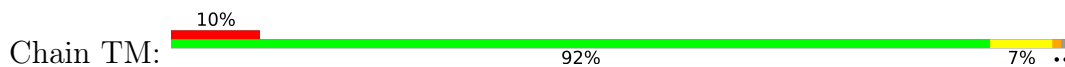


• Molecule 9: Tail sheath protein

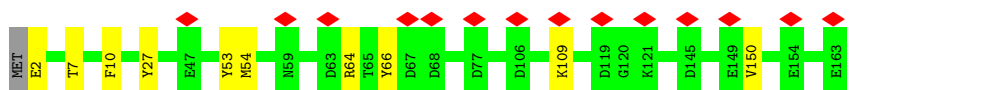




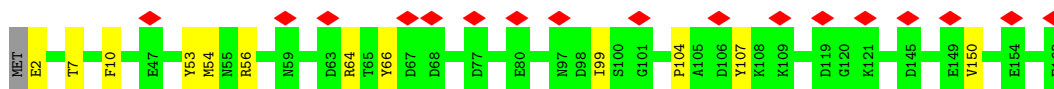
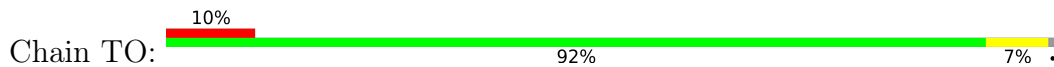
- Molecule 10: Tail tube protein



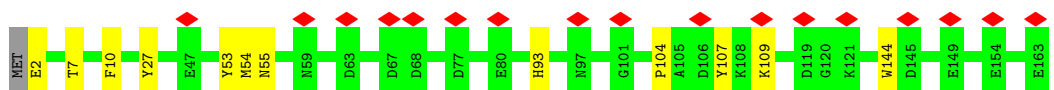
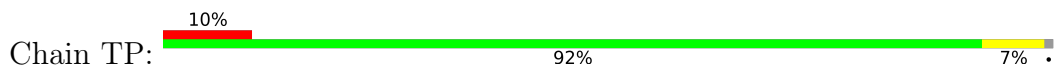
- Molecule 10: Tail tube protein



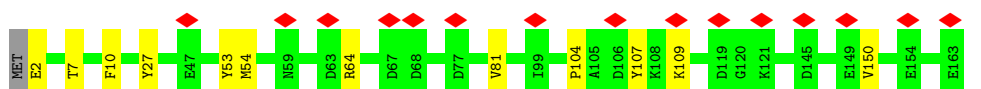
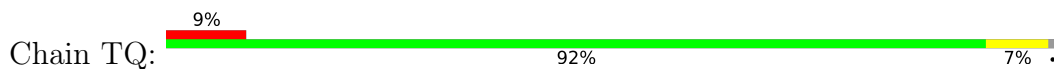
- Molecule 10: Tail tube protein



- Molecule 10: Tail tube protein



- Molecule 10: Tail tube protein

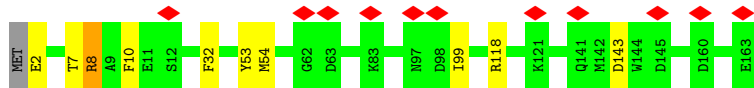


- Molecule 10: Tail tube protein

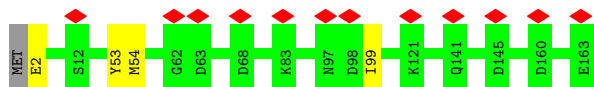




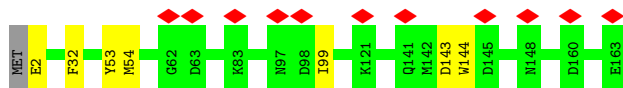
• Molecule 10: Tail tube protein



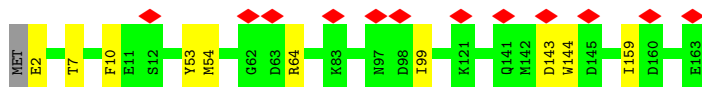
• Molecule 10: Tail tube protein



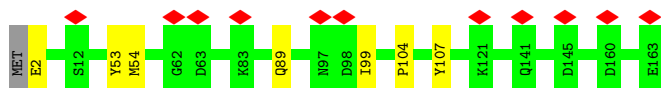
• Molecule 10: Tail tube protein



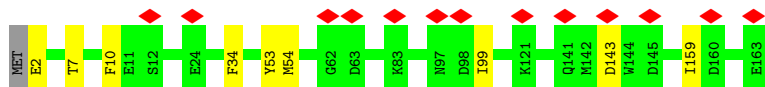
• Molecule 10: Tail tube protein



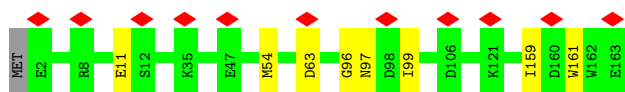
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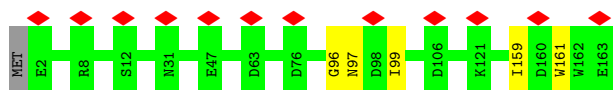
• Molecule 10: Tail tube protein



• Molecule 10: Tail tube protein



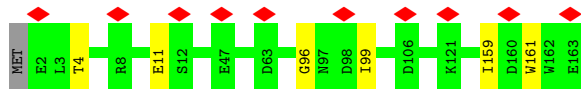
• Molecule 10: Tail tube protein



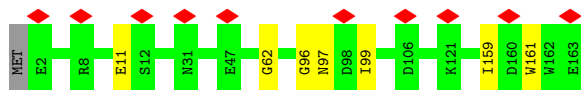
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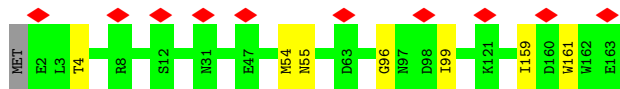
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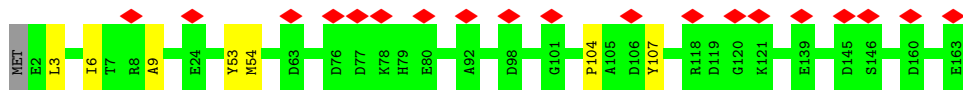
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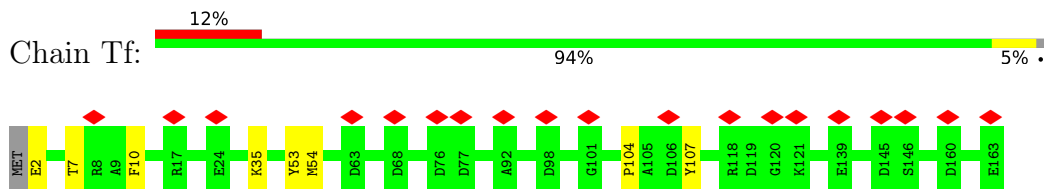
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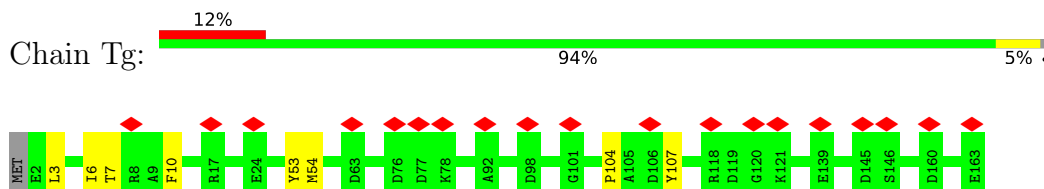
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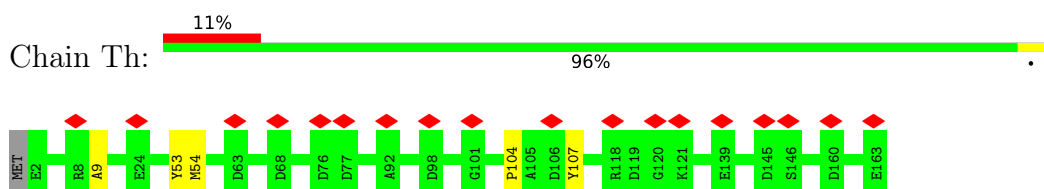
• Molecule 10: Tail tube protein



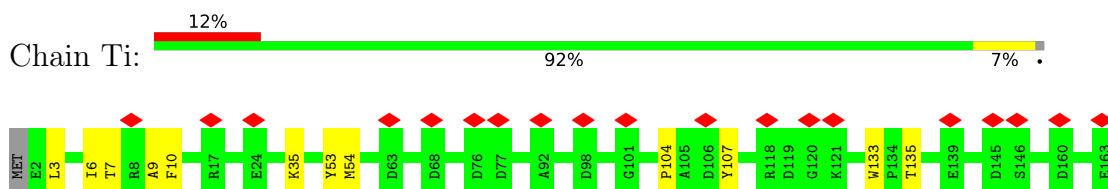
• Molecule 10: Tail tube protein



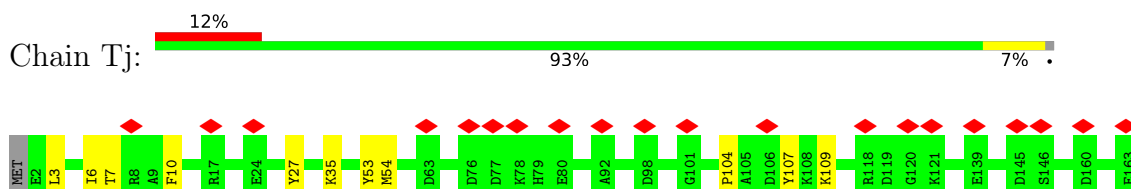
• Molecule 10: Tail tube protein



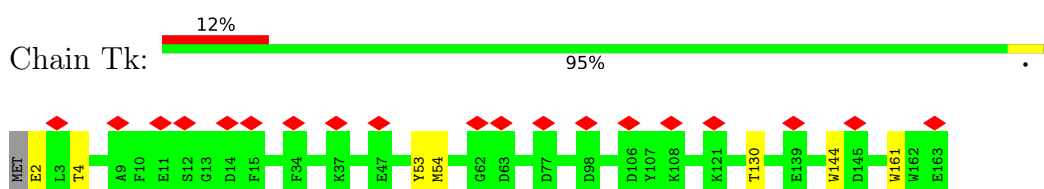
• Molecule 10: Tail tube protein



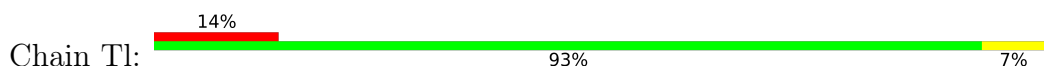
• Molecule 10: Tail tube protein



• Molecule 10: Tail tube protein

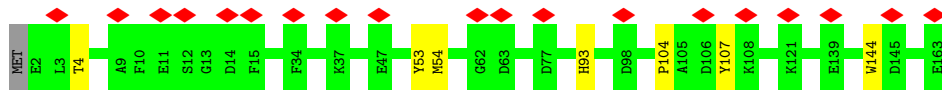


• Molecule 10: Tail tube protein

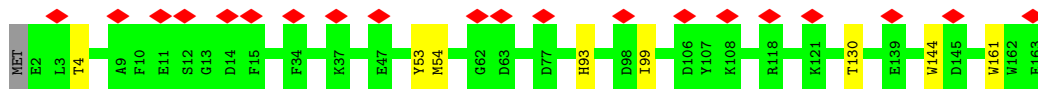




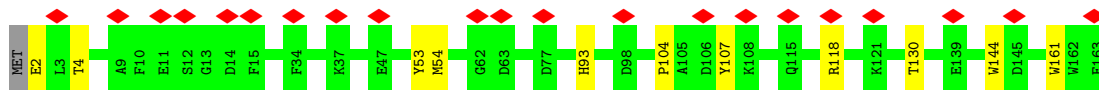
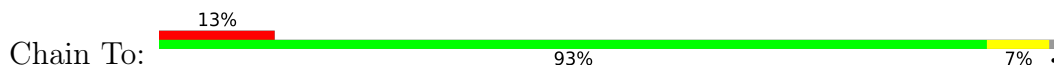
• Molecule 10: Tail tube protein



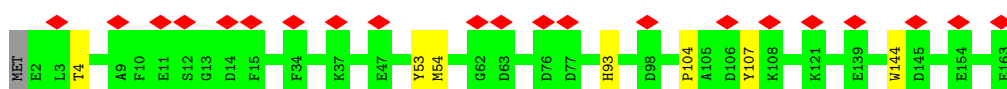
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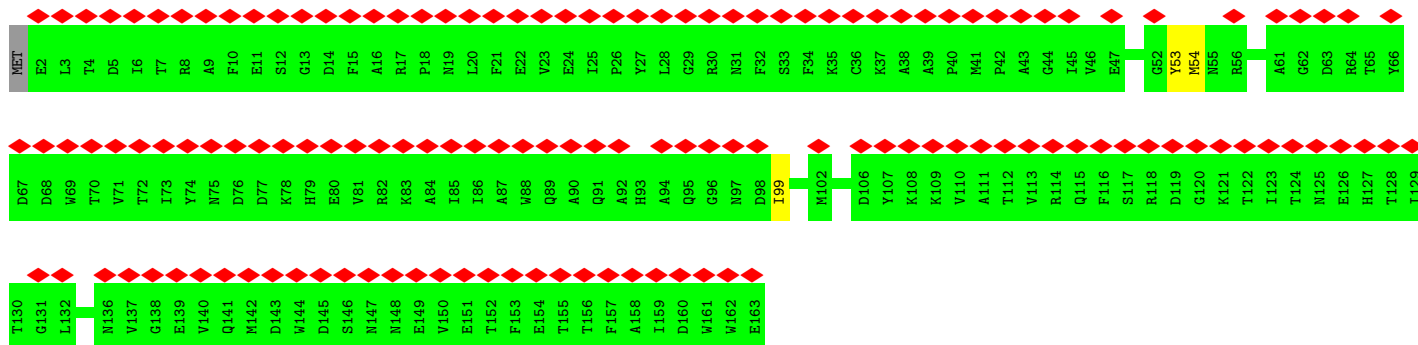
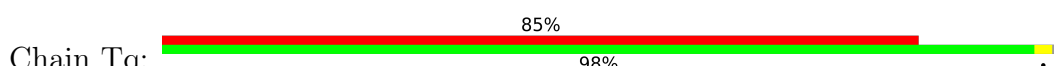
• Molecule 10: Tail tube protein



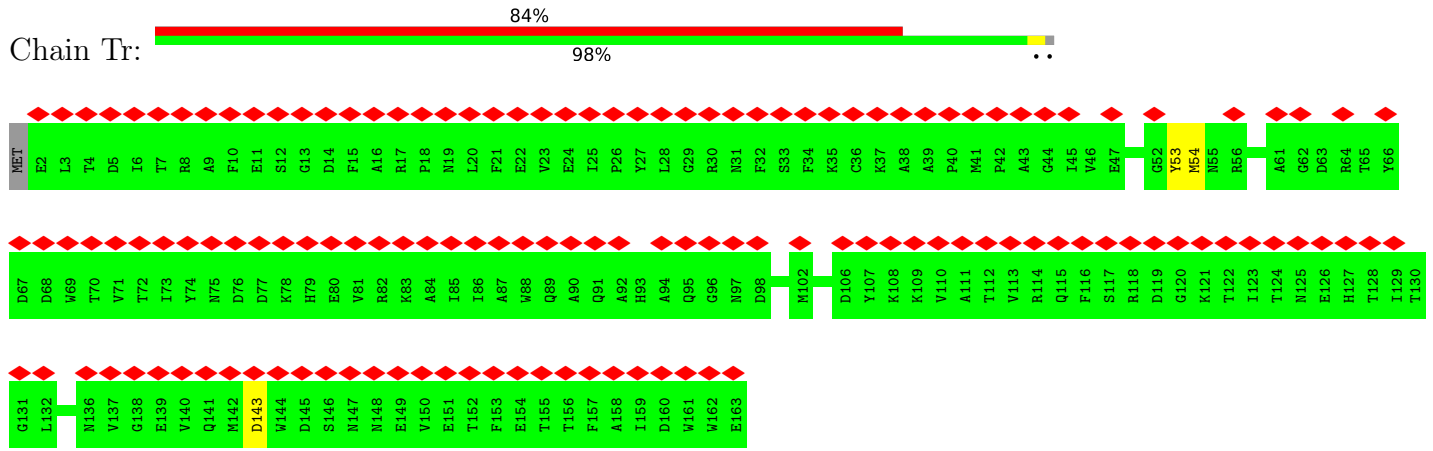
• Molecule 10: Tail tube protein



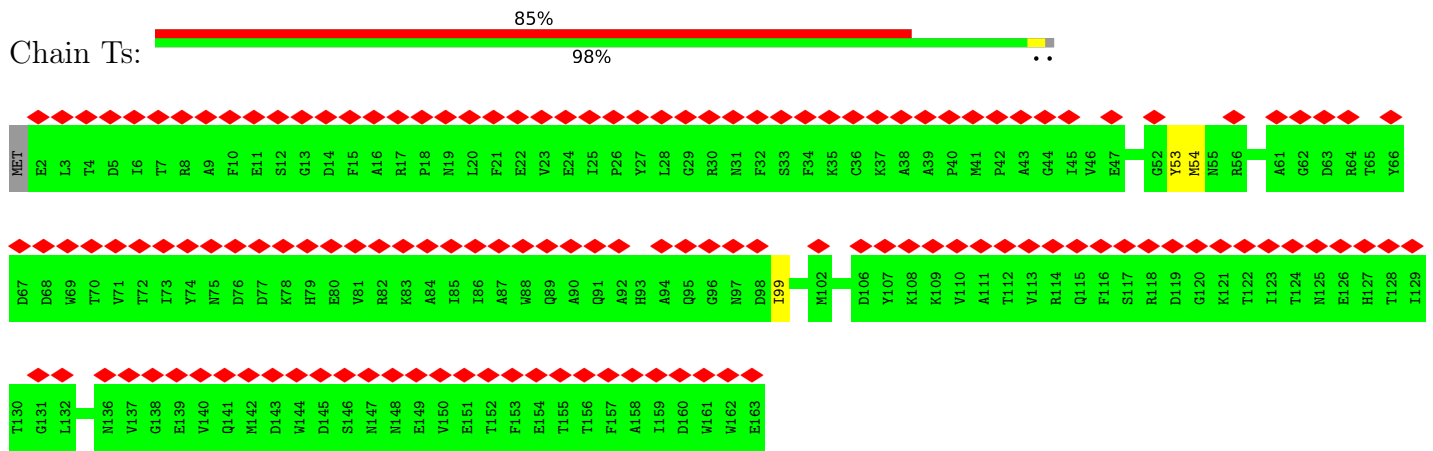
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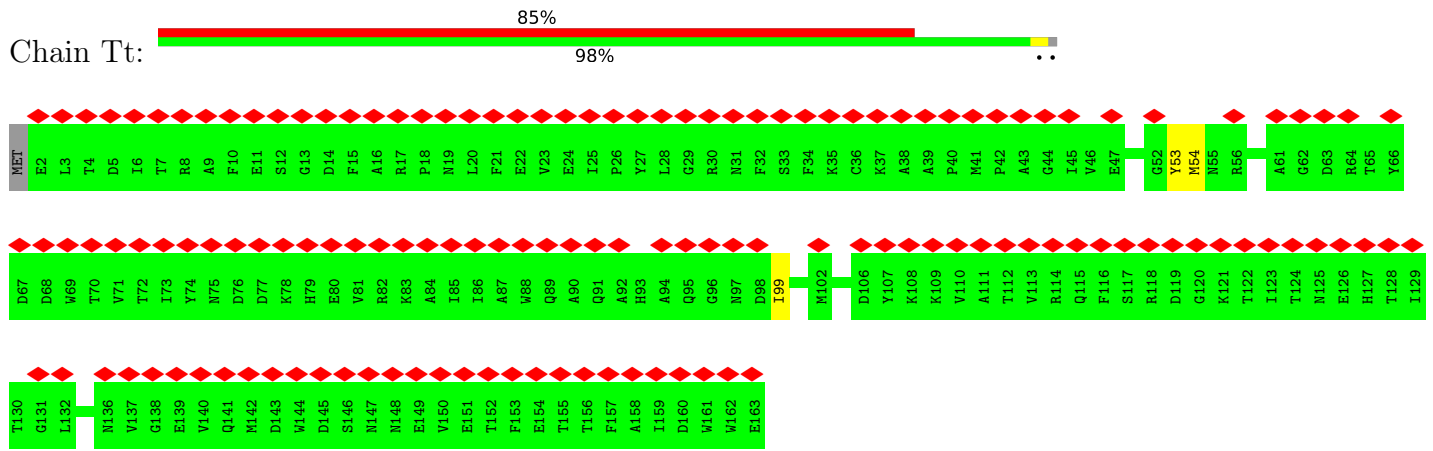
• Molecule 10: Tail tube protein



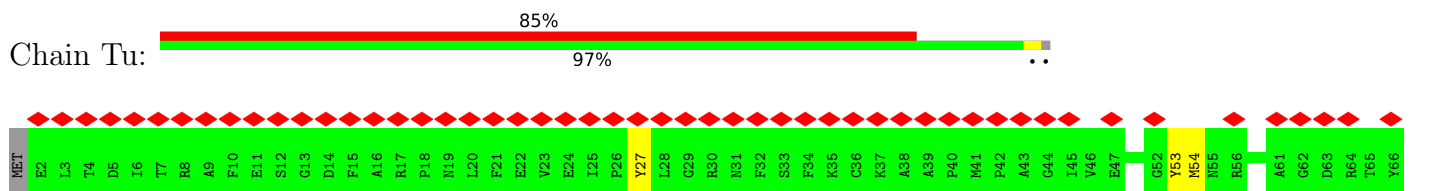
• Molecule 10: Tail tube protein

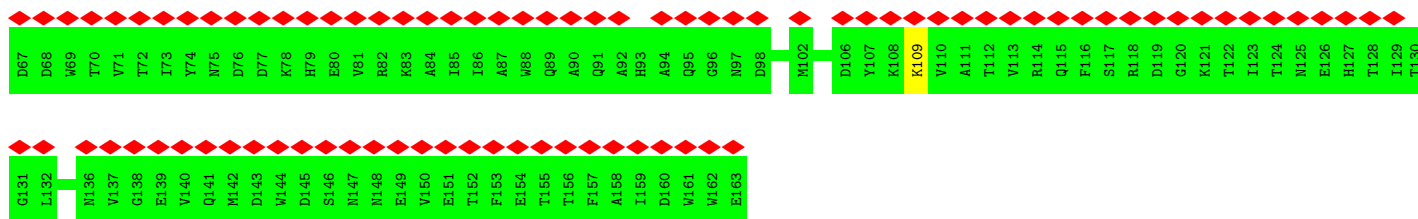


• Molecule 10: Tail tube protein

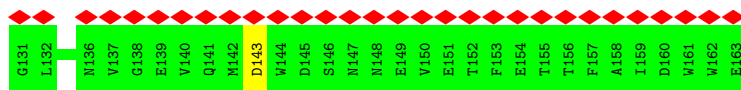
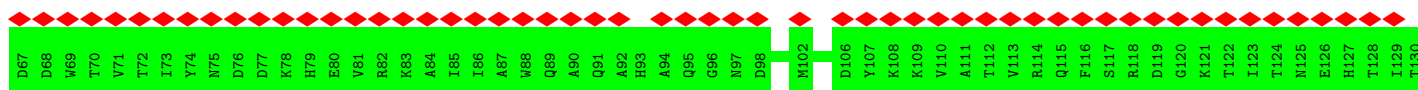
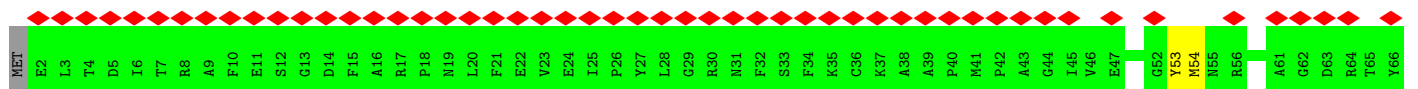
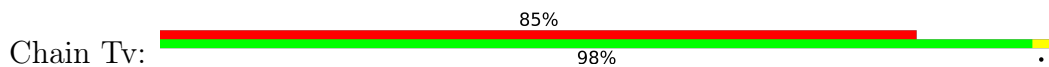


• Molecule 10: Tail tube protein

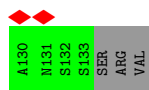




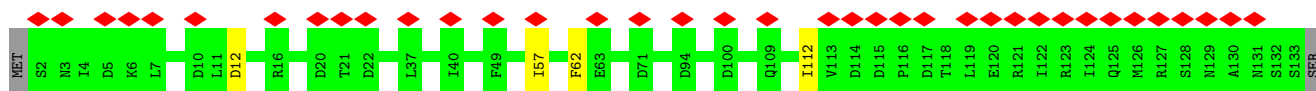
• Molecule 10: Tail tube protein



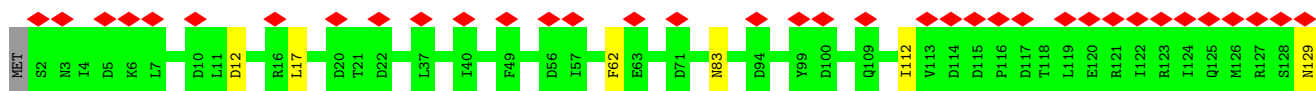
• Molecule 11: IraD/Gp25-like domain-containing protein

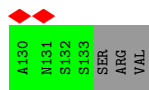


• Molecule 11: IraD/Gp25-like domain-containing protein



• Molecule 11: IraD/Gp25-like domain-containing protein

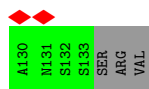
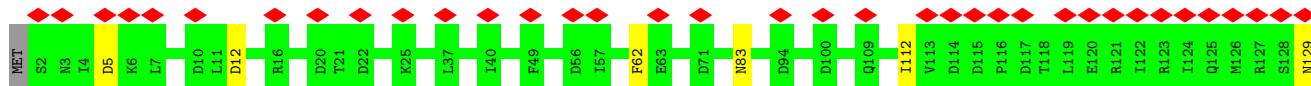




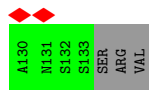
• Molecule 11: IraD/Gp25-like domain-containing protein



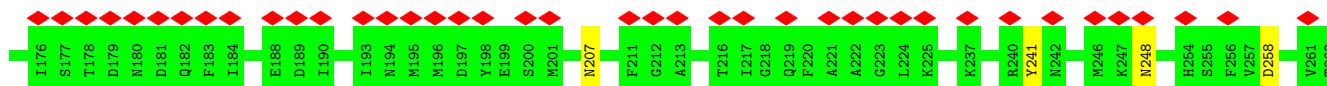
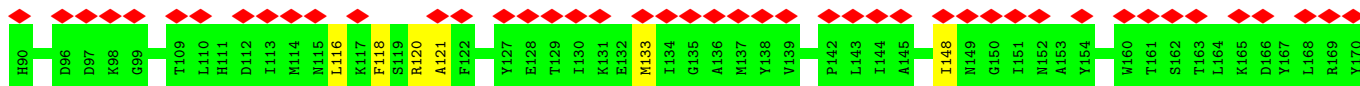
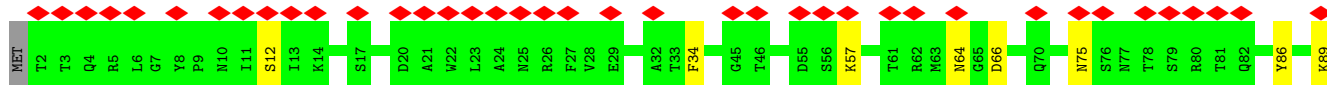
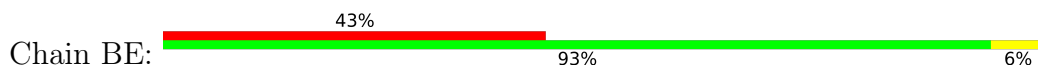
• Molecule 11: IraD/Gp25-like domain-containing protein

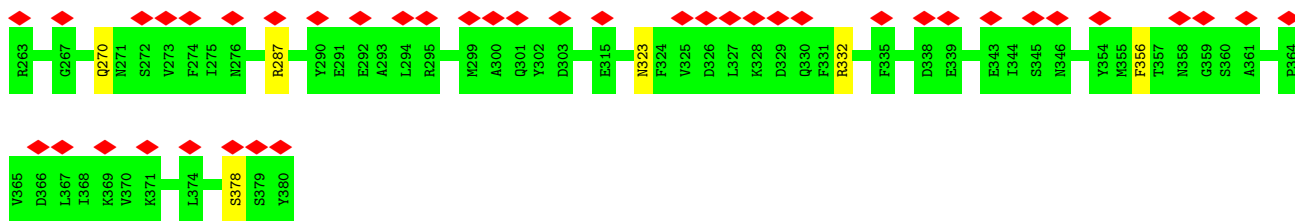


• Molecule 11: IraD/Gp25-like domain-containing protein

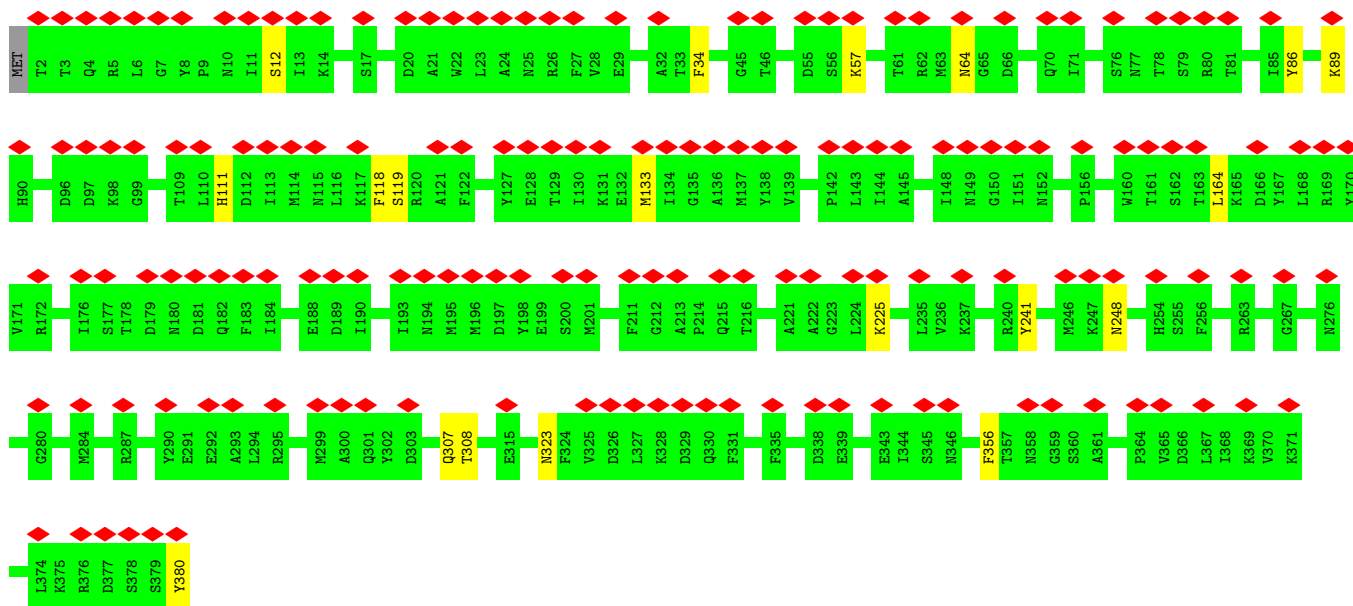
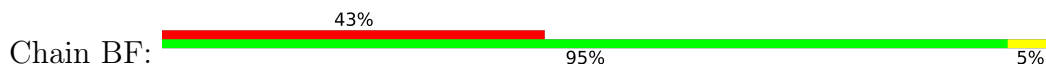


• Molecule 12: Putative baseplate hub subunit

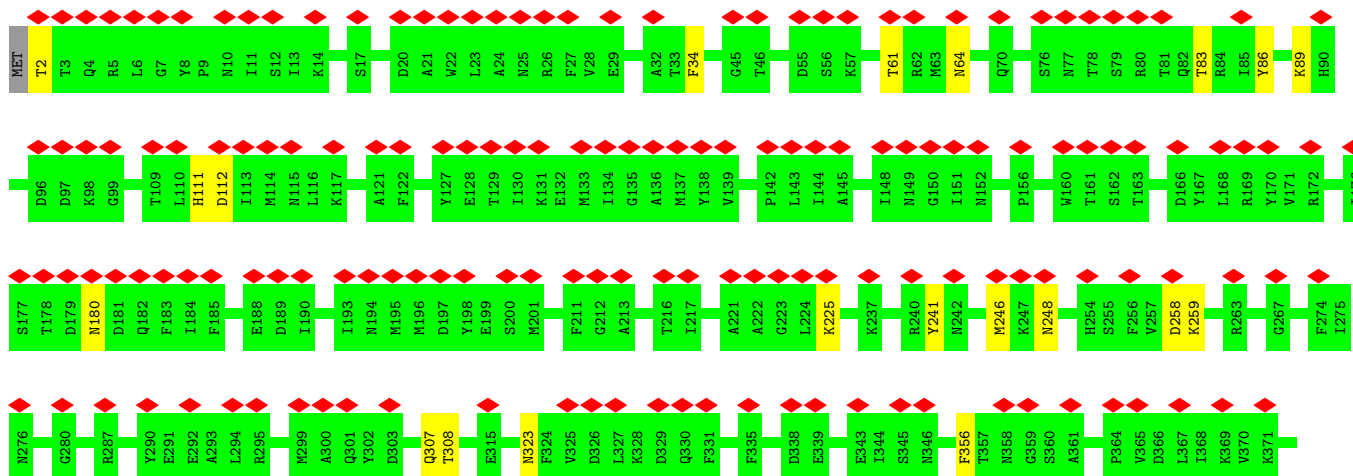
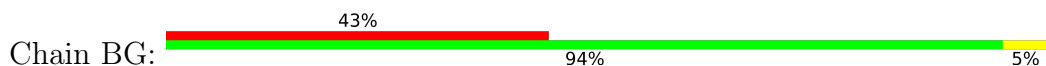


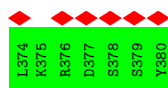


- Molecule 12: Putative baseplate hub subunit

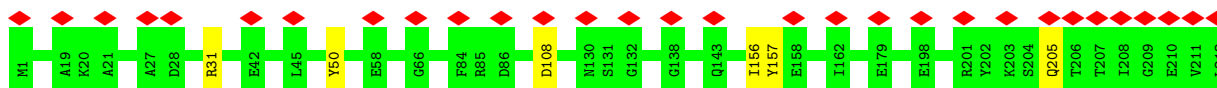


- Molecule 12: Putative baseplate hub subunit

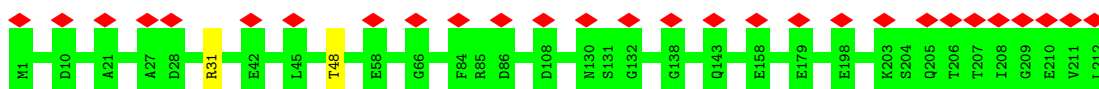




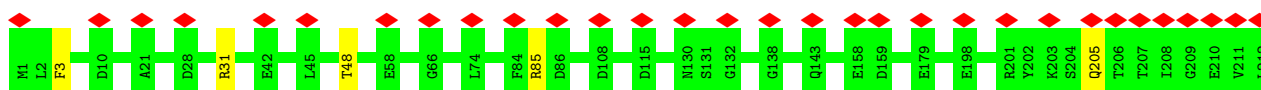
- Molecule 13: Baseplate wedge subunit



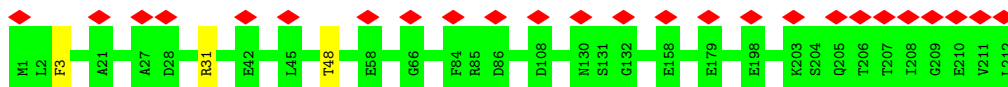
- Molecule 13: Baseplate wedge subunit



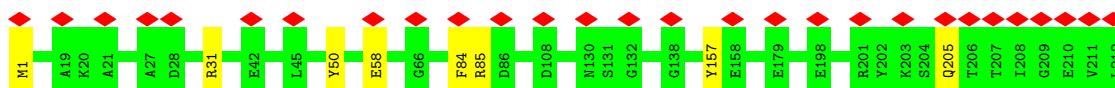
- Molecule 13: Baseplate wedge subunit



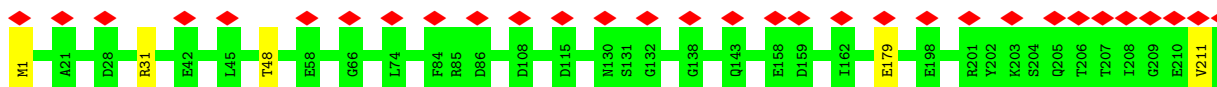
- Molecule 13: Baseplate wedge subunit



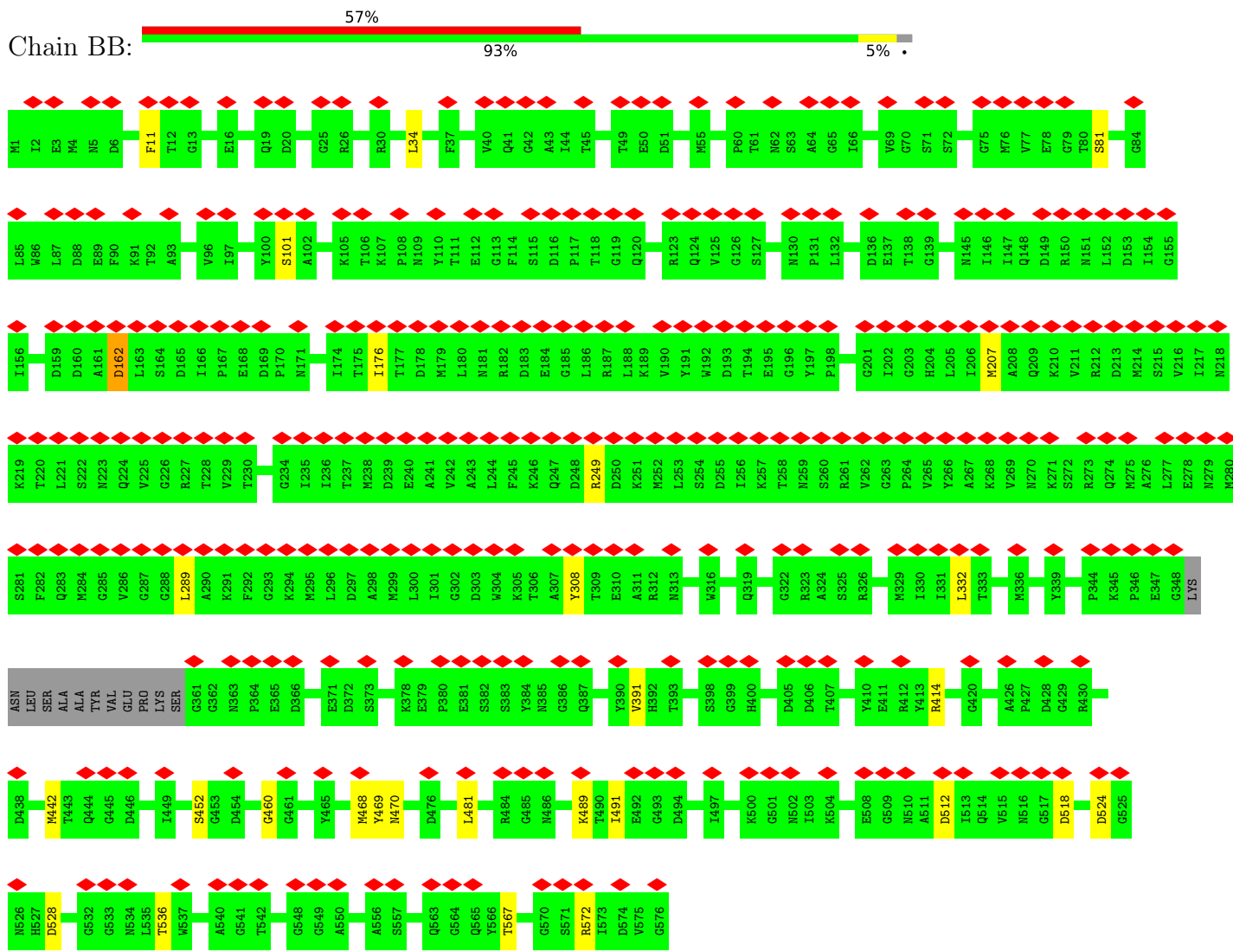
- Molecule 13: Baseplate wedge subunit



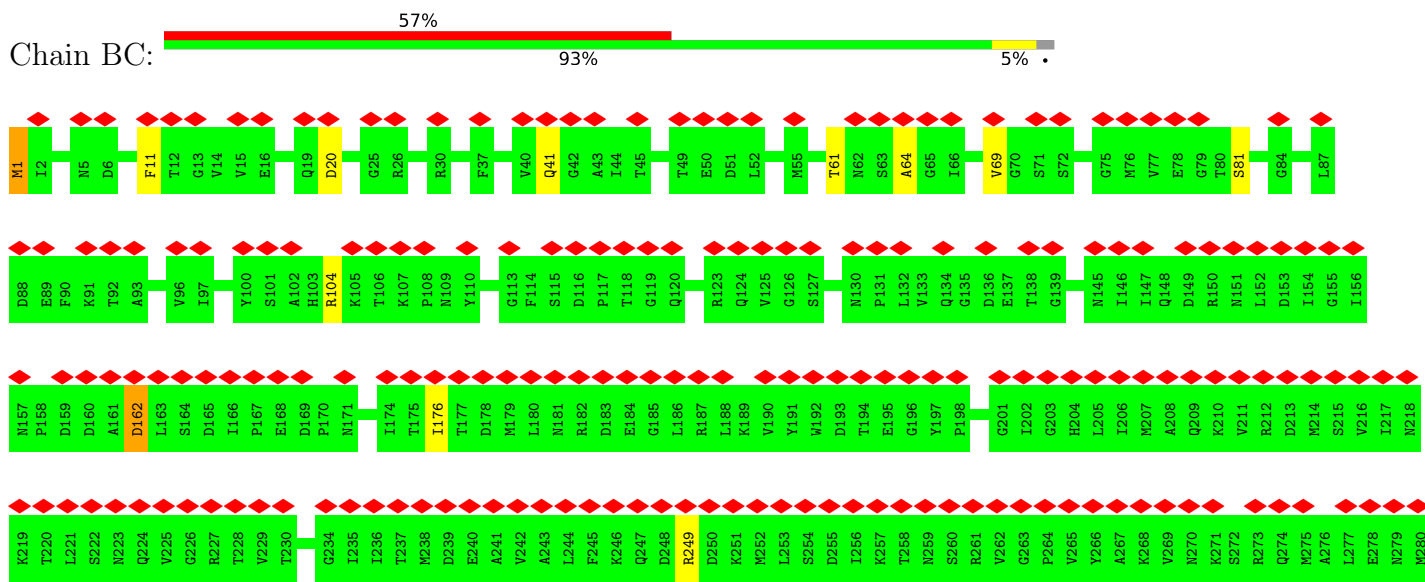
- Molecule 13: Baseplate wedge subunit

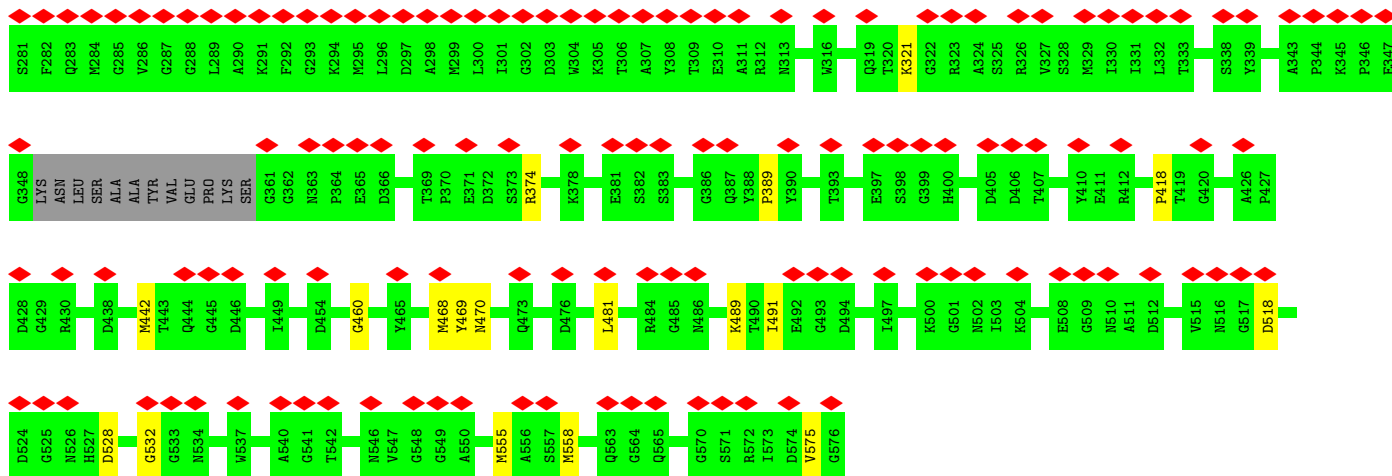


- Molecule 14: Baseplate central spike protein

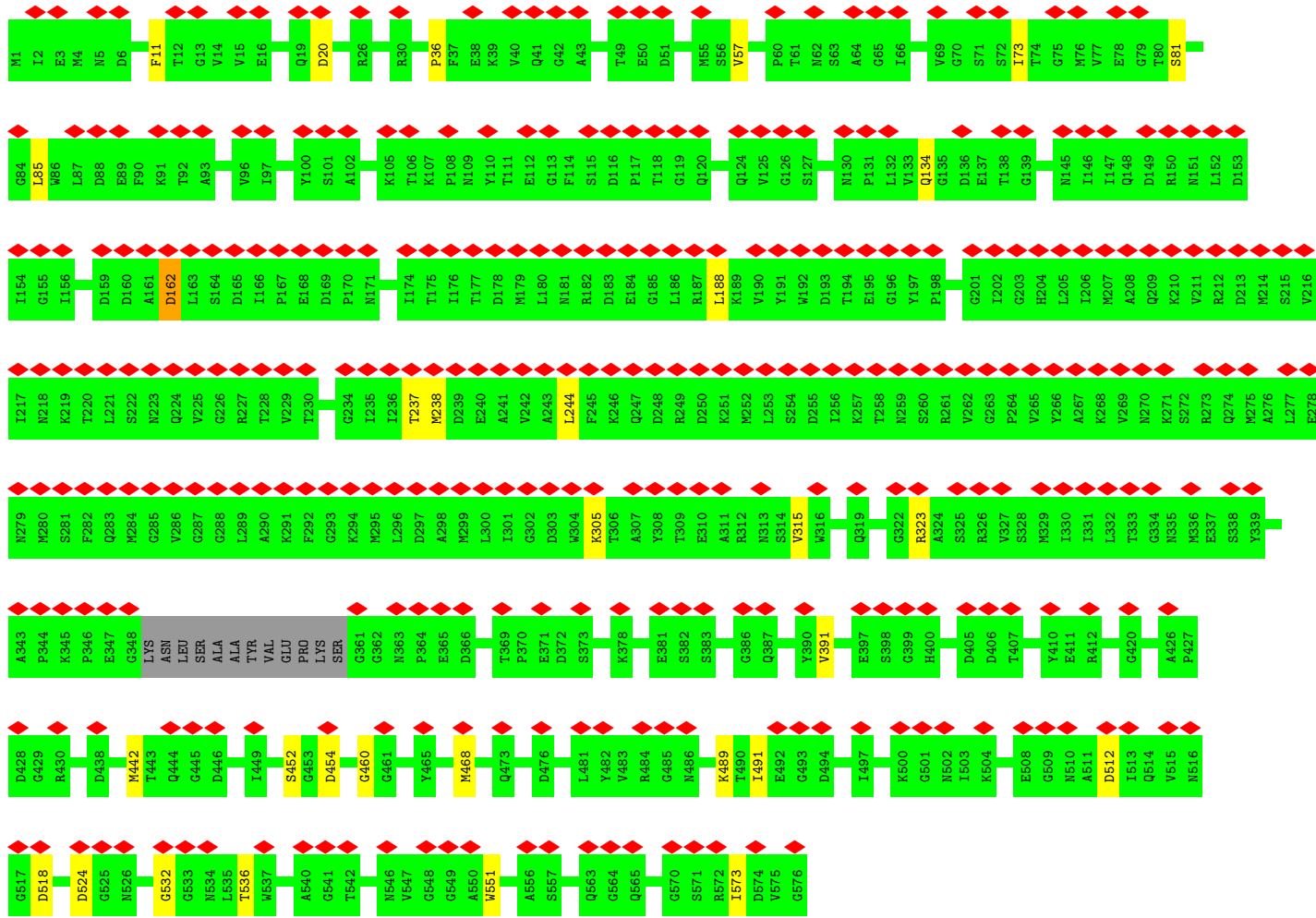


• Molecule 14: Baseplate central spike protein





• Molecule 14: Baseplate central spike protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	2415	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	83505	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.544	Depositor
Minimum map value	-0.295	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	546.304, 546.304, 546.304	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.067, 1.067, 1.067	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	LS	0.71	0/4832	1.21	8/6581 (0.1%)
1	LT	0.74	0/4832	1.27	14/6581 (0.2%)
1	LU	0.71	0/4832	1.23	5/6581 (0.1%)
1	LV	0.71	0/4832	1.21	7/6581 (0.1%)
1	LW	0.74	0/4832	1.28	10/6581 (0.2%)
1	LX	0.71	0/4832	1.23	6/6581 (0.1%)
1	LY	0.72	0/4832	1.21	6/6581 (0.1%)
1	LZ	0.74	0/4832	1.28	10/6581 (0.2%)
1	La	0.71	0/4832	1.22	7/6581 (0.1%)
1	Lb	0.72	0/4832	1.21	8/6581 (0.1%)
1	Lc	0.74	0/4832	1.27	11/6581 (0.2%)
1	Ld	0.71	0/4832	1.23	3/6581 (0.0%)
1	Le	0.71	0/4832	1.21	8/6581 (0.1%)
1	Lf	0.74	0/4832	1.28	11/6581 (0.2%)
1	Lg	0.71	0/4832	1.23	5/6581 (0.1%)
1	Lh	0.72	0/4832	1.21	6/6581 (0.1%)
1	Li	0.74	0/4832	1.28	9/6581 (0.1%)
1	Lj	0.71	0/4832	1.23	6/6581 (0.1%)
2	BK	0.64	0/2714	1.21	11/3681 (0.3%)
2	BL	0.61	0/2224	1.11	3/3011 (0.1%)
2	BM	0.64	0/2714	1.21	7/3681 (0.2%)
2	BN	0.61	0/2224	1.11	1/3011 (0.0%)
2	BO	0.64	0/2714	1.19	7/3681 (0.2%)
2	BP	0.62	0/2224	1.13	2/3011 (0.1%)
3	BQ	0.60	0/2309	1.10	4/3130 (0.1%)
3	BR	0.60	0/2309	1.10	3/3130 (0.1%)
3	BS	0.60	0/2309	1.11	5/3130 (0.2%)
3	BT	0.60	0/2309	1.09	4/3130 (0.1%)
3	BU	0.60	0/2309	1.09	3/3130 (0.1%)
3	BV	0.61	0/2309	1.09	4/3130 (0.1%)
4	AM	0.55	0/5307	1.02	3/7218 (0.0%)
4	AN	0.55	0/5307	1.01	3/7218 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	AO	0.56	0/5307	1.02	2/7218 (0.0%)
4	AP	0.55	0/5307	1.02	4/7218 (0.1%)
4	AQ	0.55	0/5307	1.02	4/7218 (0.1%)
4	AR	0.55	0/5307	1.02	2/7218 (0.0%)
4	AS	0.55	0/5260	1.03	6/7154 (0.1%)
4	AT	0.56	0/5239	1.05	8/7125 (0.1%)
4	AU	0.56	0/5260	1.02	6/7154 (0.1%)
4	AV	0.56	0/5239	1.05	9/7125 (0.1%)
4	AW	0.56	0/5260	1.03	5/7154 (0.1%)
4	AX	0.56	0/5239	1.04	7/7125 (0.1%)
5	A0	0.61	0/8656	1.12	11/11738 (0.1%)
5	A1	0.60	0/8656	1.11	10/11738 (0.1%)
5	A2	0.61	0/8656	1.12	15/11738 (0.1%)
5	A3	0.60	0/8656	1.12	12/11738 (0.1%)
5	AY	0.61	0/8656	1.12	13/11738 (0.1%)
5	AZ	0.60	0/8656	1.12	9/11738 (0.1%)
6	A4	0.60	0/2743	1.11	1/3730 (0.0%)
6	A5	0.61	0/2743	1.11	5/3730 (0.1%)
6	A6	0.61	0/2743	1.12	1/3730 (0.0%)
6	A7	0.61	0/2743	1.11	8/3730 (0.2%)
6	A8	0.61	0/2743	1.11	1/3730 (0.0%)
6	A9	0.61	0/2743	1.11	3/3730 (0.1%)
6	Aa	0.63	0/2707	1.17	4/3682 (0.1%)
6	Ab	0.63	0/2707	1.18	6/3682 (0.2%)
6	Ac	0.63	0/2707	1.17	5/3682 (0.1%)
6	Ad	0.64	0/2707	1.18	7/3682 (0.2%)
6	Ae	0.63	0/2707	1.19	6/3682 (0.2%)
6	Af	0.64	0/2707	1.18	8/3682 (0.2%)
7	LA	0.68	0/2304	1.12	3/3114 (0.1%)
7	LB	0.69	0/2304	1.12	2/3114 (0.1%)
7	LC	0.68	0/2304	1.16	4/3114 (0.1%)
7	LD	0.68	0/2304	1.12	2/3114 (0.1%)
7	LE	0.69	0/2304	1.12	0/3114
7	LF	0.68	0/2304	1.16	4/3114 (0.1%)
7	LG	0.67	0/2304	1.11	2/3114 (0.1%)
7	LH	0.68	0/2304	1.12	1/3114 (0.0%)
7	LI	0.67	0/2304	1.16	3/3114 (0.1%)
7	LJ	0.68	0/2304	1.12	3/3114 (0.1%)
7	LK	0.68	0/2304	1.11	2/3114 (0.1%)
7	LL	0.68	0/2304	1.16	4/3114 (0.1%)
7	LM	0.67	0/2304	1.12	2/3114 (0.1%)
7	LN	0.68	0/2304	1.12	2/3114 (0.1%)
7	LO	0.68	0/2304	1.16	4/3114 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	LP	0.67	0/2304	1.12	2/3114 (0.1%)
7	LQ	0.68	0/2304	1.12	2/3114 (0.1%)
7	LR	0.67	0/2304	1.15	4/3114 (0.1%)
8	FA	0.72	0/508	1.29	2/690 (0.3%)
8	FB	0.75	0/508	1.34	6/690 (0.9%)
8	FC	0.75	0/508	1.27	1/690 (0.1%)
8	FJ	0.72	0/508	1.28	2/690 (0.3%)
8	FK	0.75	0/508	1.36	6/690 (0.9%)
8	FL	0.74	0/508	1.28	2/690 (0.3%)
8	FS	0.71	0/508	1.26	1/690 (0.1%)
8	FT	0.76	0/508	1.38	6/690 (0.9%)
8	FU	0.75	0/508	1.26	0/690
8	Fb	0.71	0/508	1.28	1/690 (0.1%)
8	Fc	0.75	0/508	1.33	6/690 (0.9%)
8	Fd	0.75	0/508	1.25	2/690 (0.3%)
8	Fk	0.72	0/508	1.29	1/690 (0.1%)
8	Fl	0.74	0/508	1.30	2/690 (0.3%)
8	Fm	0.73	0/508	1.24	1/690 (0.1%)
8	Ft	0.71	0/508	1.27	2/690 (0.3%)
8	Fu	0.75	0/508	1.35	6/690 (0.9%)
8	Fv	0.73	0/508	1.25	1/690 (0.1%)
9	SA	0.58	0/5090	1.08	4/6921 (0.1%)
9	SB	0.57	0/5090	1.08	5/6921 (0.1%)
9	SC	0.58	0/5090	1.08	5/6921 (0.1%)
9	SD	0.57	0/5090	1.08	6/6921 (0.1%)
9	SE	0.57	0/5090	1.08	4/6921 (0.1%)
9	SF	0.57	0/5090	1.08	5/6921 (0.1%)
9	SG	0.57	0/5135	1.08	5/6983 (0.1%)
9	SH	0.57	0/5135	1.07	7/6983 (0.1%)
9	SI	0.57	0/5135	1.07	5/6983 (0.1%)
9	SJ	0.57	0/5135	1.07	6/6983 (0.1%)
9	SK	0.57	0/5135	1.07	8/6983 (0.1%)
9	SL	0.57	0/5135	1.08	7/6983 (0.1%)
9	SM	0.57	0/5135	1.08	4/6983 (0.1%)
9	SN	0.57	0/5135	1.08	3/6983 (0.0%)
9	SO	0.57	0/5135	1.08	3/6983 (0.0%)
9	SP	0.57	0/5135	1.08	4/6983 (0.1%)
9	SQ	0.57	0/5135	1.08	1/6983 (0.0%)
9	SR	0.57	0/5135	1.08	5/6983 (0.1%)
9	SS	0.58	0/5135	1.09	7/6983 (0.1%)
9	ST	0.57	0/5135	1.08	5/6983 (0.1%)
9	SU	0.58	0/5135	1.08	5/6983 (0.1%)
9	SV	0.58	0/5135	1.08	8/6983 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	SW	0.57	0/5135	1.08	6/6983 (0.1%)
9	SX	0.58	0/5135	1.07	4/6983 (0.1%)
9	SY	0.57	0/5135	1.05	3/6983 (0.0%)
9	SZ	0.57	0/5135	1.05	3/6983 (0.0%)
9	Sa	0.56	0/5135	1.05	4/6983 (0.1%)
9	Sb	0.57	0/5135	1.05	3/6983 (0.0%)
9	Sc	0.56	0/5135	1.06	3/6983 (0.0%)
9	Sd	0.57	0/5135	1.05	3/6983 (0.0%)
9	Se	0.56	0/5135	1.07	5/6983 (0.1%)
9	Sf	0.57	0/5135	1.07	5/6983 (0.1%)
9	Sg	0.57	0/5135	1.06	7/6983 (0.1%)
9	Sh	0.56	0/5135	1.07	8/6983 (0.1%)
9	Si	0.56	0/5135	1.07	7/6983 (0.1%)
9	Sj	0.56	0/5135	1.06	7/6983 (0.1%)
9	Sk	0.59	0/5135	1.11	7/6983 (0.1%)
9	Sl	0.59	0/5135	1.11	3/6983 (0.0%)
9	Sm	0.59	0/5135	1.10	5/6983 (0.1%)
9	Sn	0.59	0/5135	1.10	4/6983 (0.1%)
9	So	0.59	0/5135	1.10	6/6983 (0.1%)
9	Sp	0.59	0/5135	1.10	5/6983 (0.1%)
10	TM	0.60	0/1339	0.99	2/1821 (0.1%)
10	TN	0.59	0/1339	0.97	0/1821
10	TO	0.60	0/1339	1.00	1/1821 (0.1%)
10	TP	0.59	0/1339	0.99	0/1821
10	TQ	0.59	0/1339	0.98	0/1821
10	TR	0.59	0/1339	0.98	1/1821 (0.1%)
10	TS	0.58	0/1339	0.98	0/1821
10	TT	0.58	0/1339	0.99	2/1821 (0.1%)
10	TU	0.58	0/1339	0.99	1/1821 (0.1%)
10	TV	0.58	0/1339	0.98	0/1821
10	TW	0.68	2/1339 (0.1%)	1.00	3/1821 (0.2%)
10	TX	0.58	0/1339	0.99	1/1821 (0.1%)
10	TY	0.57	0/1339	0.99	0/1821
10	TZ	0.57	0/1339	0.99	0/1821
10	Ta	0.57	0/1339	0.99	0/1821
10	Tb	0.56	0/1339	0.98	0/1821
10	Tc	0.56	0/1339	0.99	0/1821
10	Td	0.56	0/1339	0.99	0/1821
10	Te	0.56	0/1339	0.96	0/1821
10	Tf	0.56	0/1339	0.96	0/1821
10	Tg	0.56	0/1339	0.98	0/1821
10	Th	0.56	0/1339	0.96	0/1821
10	Ti	0.56	0/1339	0.96	0/1821

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
10	Tj	0.56	0/1339	0.97	0/1821
10	Tk	0.52	0/1339	0.95	0/1821
10	Tl	0.52	0/1339	0.95	0/1821
10	Tm	0.52	0/1339	0.95	0/1821
10	Tn	0.52	0/1339	0.95	0/1821
10	To	0.52	0/1339	0.94	0/1821
10	Tp	0.52	0/1339	0.95	0/1821
10	Tq	0.60	0/1339	1.05	0/1821
10	Tr	0.61	0/1339	1.05	1/1821 (0.1%)
10	Ts	0.61	0/1339	1.04	0/1821
10	Tt	0.60	0/1339	1.04	0/1821
10	Tu	0.61	0/1339	1.04	0/1821
10	Tv	0.61	0/1339	1.03	1/1821 (0.1%)
11	AA	0.58	0/1059	1.15	5/1438 (0.3%)
11	AB	0.57	0/1059	1.13	2/1438 (0.1%)
11	AC	0.57	0/1059	1.16	4/1438 (0.3%)
11	AD	0.57	0/1059	1.13	3/1438 (0.2%)
11	AE	0.57	0/1059	1.16	4/1438 (0.3%)
11	AF	0.58	0/1059	1.17	5/1438 (0.3%)
12	BE	0.62	0/3125	1.21	7/4232 (0.2%)
12	BF	0.62	0/3125	1.18	5/4232 (0.1%)
12	BG	0.63	0/3125	1.20	6/4232 (0.1%)
13	AG	0.53	0/1794	1.00	1/2435 (0.0%)
13	AH	0.53	0/1794	0.98	1/2435 (0.0%)
13	AI	0.53	0/1794	0.99	0/2435
13	AJ	0.53	0/1794	0.98	1/2435 (0.0%)
13	AK	0.53	0/1794	0.98	0/2435
13	AL	0.53	0/1794	0.97	0/2435
14	BB	0.64	0/4441	1.19	5/6025 (0.1%)
14	BC	0.64	0/4441	1.16	6/6025 (0.1%)
14	BD	0.64	0/4441	1.17	5/6025 (0.1%)
All	All	0.61	2/617655 (0.0%)	1.11	755/839310 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	LS	0	3
1	LU	0	2
1	LV	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	LX	0	2
1	LY	0	5
1	LZ	0	1
1	La	0	2
1	Lb	0	3
1	Ld	0	1
1	Le	0	5
1	Lf	0	1
1	Lg	0	2
1	Lh	0	4
1	Lj	0	1
2	BM	0	1
2	BO	0	2
2	BP	0	1
3	BQ	0	1
3	BR	0	1
3	BS	0	2
3	BT	0	2
3	BU	0	1
3	BV	0	1
4	AM	0	1
4	AO	0	1
4	AQ	0	1
4	AS	0	1
5	A0	0	4
5	A1	0	2
5	A2	0	4
5	A3	0	3
5	AY	0	2
5	AZ	0	5
7	LE	0	1
7	LQ	0	1
8	FC	0	1
8	FL	0	1
8	FU	0	1
8	Fd	0	1
8	Fm	0	1
8	Fv	0	1
9	SM	0	1
9	SN	0	1
9	SO	0	1
9	SP	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	SQ	0	1
9	SR	0	2
9	ST	0	1
9	SU	0	1
9	SV	0	1
9	SW	0	1
9	SX	0	1
9	Se	0	1
9	Sf	0	2
9	Sg	0	2
9	Sh	0	1
9	Si	0	1
All	All	0	100

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	TW	8	ARG	CD-NE	9.59	1.59	1.46
10	TW	8	ARG	NE-CZ	7.99	1.41	1.33

The worst 5 of 755 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	SA	6	PRO	CB-CA-C	-8.81	99.44	110.98
2	BK	200	ARG	NE-CZ-NH1	-7.98	113.52	121.50
8	Fb	564	ASP	CA-CB-CG	7.70	120.30	112.60
8	FA	564	ASP	CA-CB-CG	7.67	120.27	112.60
12	BE	34	PHE	CA-CB-CG	7.59	121.39	113.80

There are no chirality outliers.

5 of 100 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Le	26	ALA	Peptide
1	Le	307	ARG	Peptide
1	Le	593	SER	Peptide
1	Le	605	ARG	Peptide
1	Le	92	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LS	4752	0	4730	5	0
1	LT	4752	0	4730	5	0
1	LU	4752	0	4730	3	0
1	LV	4752	0	4730	6	0
1	LW	4752	0	4730	4	0
1	LX	4752	0	4730	5	0
1	LY	4752	0	4730	7	0
1	LZ	4752	0	4730	3	0
1	La	4752	0	4730	4	0
1	Lb	4752	0	4730	5	0
1	Lc	4752	0	4730	4	0
1	Ld	4752	0	4730	4	0
1	Le	4752	0	4730	4	0
1	Lf	4752	0	4730	4	0
1	Lg	4752	0	4730	5	0
1	Lh	4752	0	4730	6	0
1	Li	4752	0	4730	5	0
1	Lj	4752	0	4730	4	0
2	BK	2664	0	2609	3	0
2	BL	2180	0	2138	7	0
2	BM	2664	0	2609	5	0
2	BN	2180	0	2138	7	0
2	BO	2664	0	2609	2	0
2	BP	2180	0	2138	11	0
3	BQ	2263	0	2203	9	0
3	BR	2263	0	2203	8	0
3	BS	2263	0	2203	7	0
3	BT	2263	0	2203	7	0
3	BU	2263	0	2203	8	0
3	BV	2263	0	2203	8	0
4	AM	5191	0	5061	5	0
4	AN	5191	0	5061	4	0
4	AO	5191	0	5061	7	0
4	AP	5191	0	5061	3	0
4	AQ	5191	0	5061	3	0
4	AR	5191	0	5061	5	0
4	AS	5145	0	5008	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AT	5125	0	4993	6	0
4	AU	5145	0	5008	3	0
4	AV	5125	0	4993	8	0
4	AW	5145	0	5008	0	0
4	AX	5125	0	4993	8	0
5	A0	8438	0	8098	13	0
5	A1	8438	0	8098	8	0
5	A2	8438	0	8098	11	0
5	A3	8438	0	8098	8	0
5	AY	8438	0	8098	14	0
5	AZ	8438	0	8098	10	0
6	A4	2669	0	2557	4	0
6	A5	2669	0	2557	3	0
6	A6	2669	0	2557	5	0
6	A7	2669	0	2557	4	0
6	A8	2669	0	2557	4	0
6	A9	2669	0	2557	3	0
6	Aa	2633	0	2522	5	0
6	Ab	2633	0	2522	3	0
6	Ac	2633	0	2522	5	0
6	Ad	2633	0	2522	7	0
6	Ae	2633	0	2522	4	0
6	Af	2633	0	2522	4	0
7	LA	2270	0	2236	3	0
7	LB	2270	0	2236	2	0
7	LC	2270	0	2236	1	0
7	LD	2270	0	2236	2	0
7	LE	2270	0	2236	2	0
7	LF	2270	0	2236	1	0
7	LG	2270	0	2236	4	0
7	LH	2270	0	2236	3	0
7	LI	2270	0	2236	1	0
7	LJ	2270	0	2236	2	0
7	LK	2270	0	2236	1	0
7	LL	2270	0	2236	2	0
7	LM	2270	0	2236	2	0
7	LN	2270	0	2236	3	0
7	LO	2270	0	2236	2	0
7	LP	2270	0	2236	4	0
7	LQ	2270	0	2236	4	0
7	LR	2270	0	2236	2	0
8	FA	499	0	490	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	FB	499	0	490	2	0
8	FC	499	0	490	3	0
8	FJ	499	0	490	0	0
8	FK	499	0	490	1	0
8	FL	499	0	490	0	0
8	FS	499	0	490	0	0
8	FT	499	0	490	2	0
8	FU	499	0	490	1	0
8	Fb	499	0	490	0	0
8	Fc	499	0	490	2	0
8	Fd	499	0	490	1	0
8	Fk	499	0	490	1	0
8	Fl	499	0	490	2	0
8	Fm	499	0	490	3	0
8	Ft	499	0	490	0	0
8	Fu	499	0	490	2	0
8	Fv	499	0	490	1	0
9	SA	4993	0	4889	13	0
9	SB	4993	0	4889	13	0
9	SC	4993	0	4889	8	0
9	SD	4993	0	4889	9	0
9	SE	4993	0	4889	9	0
9	SF	4993	0	4889	10	0
9	SG	5037	0	4931	11	0
9	SH	5037	0	4931	7	0
9	SI	5037	0	4931	10	0
9	SJ	5037	0	4931	9	0
9	SK	5037	0	4931	9	0
9	SL	5037	0	4931	10	0
9	SM	5037	0	4931	11	0
9	SN	5037	0	4931	8	0
9	SO	5037	0	4931	9	0
9	SP	5037	0	4931	10	0
9	SQ	5037	0	4931	6	0
9	SR	5037	0	4931	9	0
9	SS	5037	0	4931	4	0
9	ST	5037	0	4931	2	0
9	SU	5037	0	4931	2	0
9	SV	5037	0	4931	7	0
9	SW	5037	0	4931	2	0
9	SX	5037	0	4931	4	0
9	SY	5037	0	4931	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	SZ	5037	0	4931	4	0
9	Sa	5037	0	4931	3	0
9	Sb	5037	0	4931	2	0
9	Sc	5037	0	4931	3	0
9	Sd	5037	0	4931	2	0
9	Se	5037	0	4931	3	0
9	Sf	5037	0	4931	6	0
9	Sg	5037	0	4931	4	0
9	Sh	5037	0	4931	3	0
9	Si	5037	0	4931	6	0
9	Sj	5037	0	4931	5	0
9	Sk	5037	0	4931	4	0
9	Sl	5037	0	4931	7	0
9	Sm	5037	0	4931	3	0
9	Sn	5037	0	4931	2	0
9	So	5037	0	4931	7	0
9	Sp	5037	0	4931	3	0
10	TM	1305	0	1235	9	0
10	TN	1305	0	1235	6	0
10	TO	1305	0	1235	9	0
10	TP	1305	0	1235	10	0
10	TQ	1305	0	1235	7	0
10	TR	1305	0	1235	7	0
10	TS	1305	0	1235	5	0
10	TT	1305	0	1235	6	0
10	TU	1305	0	1235	9	0
10	TV	1305	0	1235	7	0
10	TW	1305	0	1235	7	0
10	TX	1305	0	1235	8	0
10	TY	1305	0	1235	7	0
10	TZ	1305	0	1235	5	0
10	Ta	1305	0	1235	4	0
10	Tb	1305	0	1235	4	0
10	Tc	1305	0	1235	6	0
10	Td	1305	0	1235	7	0
10	Te	1305	0	1235	4	0
10	Tf	1305	0	1235	5	0
10	Tg	1305	0	1235	4	0
10	Th	1305	0	1235	3	0
10	Ti	1305	0	1235	7	0
10	Tj	1305	0	1235	6	0
10	Tk	1305	0	1235	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	Tl	1305	0	1235	5	0
10	Tm	1305	0	1235	3	0
10	Tn	1305	0	1235	4	0
10	To	1305	0	1235	5	0
10	Tp	1305	0	1235	3	0
10	Tq	1305	0	1235	3	0
10	Tr	1305	0	1235	2	0
10	Ts	1305	0	1235	3	0
10	Tt	1305	0	1235	3	0
10	Tu	1305	0	1235	3	0
10	Tv	1305	0	1235	2	0
11	AA	1044	0	1042	1	0
11	AB	1044	0	1042	4	0
11	AC	1044	0	1042	7	0
11	AD	1044	0	1042	1	0
11	AE	1044	0	1042	1	0
11	AF	1044	0	1042	1	0
12	BE	3055	0	2962	9	0
12	BF	3055	0	2962	7	0
12	BG	3055	0	2962	7	0
13	AG	1747	0	1652	0	0
13	AH	1747	0	1652	3	0
13	AI	1747	0	1652	0	0
13	AJ	1747	0	1652	3	0
13	AK	1747	0	1652	0	0
13	AL	1747	0	1652	2	0
14	BB	4354	0	4218	7	0
14	BC	4354	0	4218	15	0
14	BD	4354	0	4218	15	0
15	BB	1	0	0	0	0
All	All	605128	0	590112	710	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 1.

The worst 5 of 710 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)
12:BG:246:MET:HE1	14:BC:1:MET:HE1	1.56	0.86
10:TP:2:GLU:CG	10:TX:99:ILE:HD12	2.14	0.77
5:A3:235:ARG:NH2	6:Ad:291:MET:HE1	2.01	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:TM:2:GLU:CG	10:TU:99:ILE:HD12	2.18	0.74
5:A0:235:ARG:NH2	6:Ae:291:MET:HE1	2.03	0.73

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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	LS	525/1065 (49%)	518 (99%)	7 (1%)	61	72
1	LT	525/1065 (49%)	518 (99%)	7 (1%)	61	72
1	LU	525/1065 (49%)	511 (97%)	14 (3%)	39	60
1	LV	525/1065 (49%)	516 (98%)	9 (2%)	53	68
1	LW	525/1065 (49%)	519 (99%)	6 (1%)	65	74
1	LX	525/1065 (49%)	512 (98%)	13 (2%)	42	62
1	LY	525/1065 (49%)	517 (98%)	8 (2%)	57	70
1	LZ	525/1065 (49%)	518 (99%)	7 (1%)	61	72
1	La	525/1065 (49%)	513 (98%)	12 (2%)	44	64
1	Lb	525/1065 (49%)	518 (99%)	7 (1%)	61	72
1	Lc	525/1065 (49%)	518 (99%)	7 (1%)	61	72
1	Ld	525/1065 (49%)	513 (98%)	12 (2%)	44	64
1	Le	525/1065 (49%)	517 (98%)	8 (2%)	57	70
1	Lf	525/1065 (49%)	516 (98%)	9 (2%)	53	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Lg	525/1065 (49%)	511 (97%)	14 (3%)	39	60
1	Lh	525/1065 (49%)	516 (98%)	9 (2%)	53	68
1	Li	525/1065 (49%)	517 (98%)	8 (2%)	57	70
1	Lj	525/1065 (49%)	511 (97%)	14 (3%)	39	60
2	BK	294/297 (99%)	291 (99%)	3 (1%)	68	76
2	BL	239/297 (80%)	237 (99%)	2 (1%)	73	77
2	BM	294/297 (99%)	287 (98%)	7 (2%)	43	63
2	BN	239/297 (80%)	233 (98%)	6 (2%)	42	62
2	BO	294/297 (99%)	288 (98%)	6 (2%)	48	66
2	BP	239/297 (80%)	235 (98%)	4 (2%)	53	68
3	BQ	243/256 (95%)	239 (98%)	4 (2%)	55	69
3	BR	243/256 (95%)	236 (97%)	7 (3%)	37	58
3	BS	243/256 (95%)	239 (98%)	4 (2%)	55	69
3	BT	243/256 (95%)	237 (98%)	6 (2%)	42	62
3	BU	243/256 (95%)	238 (98%)	5 (2%)	47	65
3	BV	243/256 (95%)	239 (98%)	4 (2%)	55	69
4	AM	570/571 (100%)	560 (98%)	10 (2%)	51	67
4	AN	570/571 (100%)	556 (98%)	14 (2%)	42	62
4	AO	570/571 (100%)	560 (98%)	10 (2%)	51	67
4	AP	570/571 (100%)	559 (98%)	11 (2%)	50	67
4	AQ	570/571 (100%)	558 (98%)	12 (2%)	47	65
4	AR	570/571 (100%)	556 (98%)	14 (2%)	42	62
4	AS	565/571 (99%)	558 (99%)	7 (1%)	63	73
4	AT	563/571 (99%)	554 (98%)	9 (2%)	55	69
4	AU	565/571 (99%)	555 (98%)	10 (2%)	51	67
4	AV	563/571 (99%)	553 (98%)	10 (2%)	51	67
4	AW	565/571 (99%)	555 (98%)	10 (2%)	51	67
4	AX	563/571 (99%)	555 (99%)	8 (1%)	59	71
5	A0	923/924 (100%)	909 (98%)	14 (2%)	57	70
5	A1	923/924 (100%)	911 (99%)	12 (1%)	61	72
5	A2	923/924 (100%)	908 (98%)	15 (2%)	55	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A3	923/924 (100%)	908 (98%)	15 (2%)	55	69
5	AY	923/924 (100%)	912 (99%)	11 (1%)	63	73
5	AZ	923/924 (100%)	910 (99%)	13 (1%)	59	71
6	A4	293/299 (98%)	288 (98%)	5 (2%)	53	68
6	A5	293/299 (98%)	289 (99%)	4 (1%)	59	71
6	A6	293/299 (98%)	288 (98%)	5 (2%)	53	68
6	A7	293/299 (98%)	290 (99%)	3 (1%)	68	76
6	A8	293/299 (98%)	287 (98%)	6 (2%)	48	66
6	A9	293/299 (98%)	290 (99%)	3 (1%)	68	76
6	Aa	288/299 (96%)	284 (99%)	4 (1%)	59	71
6	Ab	288/299 (96%)	285 (99%)	3 (1%)	68	76
6	Ac	288/299 (96%)	284 (99%)	4 (1%)	59	71
6	Ad	288/299 (96%)	285 (99%)	3 (1%)	68	76
6	Ae	288/299 (96%)	284 (99%)	4 (1%)	59	71
6	Af	288/299 (96%)	286 (99%)	2 (1%)	76	79
7	LA	245/245 (100%)	238 (97%)	7 (3%)	37	58
7	LB	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LC	245/245 (100%)	242 (99%)	3 (1%)	63	73
7	LD	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LE	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LF	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LG	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LH	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LI	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LJ	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LK	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LL	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LM	245/245 (100%)	239 (98%)	6 (2%)	43	63
7	LN	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LO	245/245 (100%)	241 (98%)	4 (2%)	55	69
7	LP	245/245 (100%)	241 (98%)	4 (2%)	55	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LQ	245/245 (100%)	240 (98%)	5 (2%)	48	66
7	LR	245/245 (100%)	241 (98%)	4 (2%)	55	69
8	FA	57/509 (11%)	54 (95%)	3 (5%)	20	45
8	FB	57/509 (11%)	57 (100%)	0	100	100
8	FC	57/509 (11%)	55 (96%)	2 (4%)	32	54
8	FJ	57/509 (11%)	54 (95%)	3 (5%)	20	45
8	FK	57/509 (11%)	57 (100%)	0	100	100
8	FL	57/509 (11%)	55 (96%)	2 (4%)	32	54
8	FS	57/509 (11%)	54 (95%)	3 (5%)	20	45
8	FT	57/509 (11%)	57 (100%)	0	100	100
8	FU	57/509 (11%)	55 (96%)	2 (4%)	32	54
8	Fb	57/509 (11%)	53 (93%)	4 (7%)	14	39
8	Fc	57/509 (11%)	57 (100%)	0	100	100
8	Fd	57/509 (11%)	55 (96%)	2 (4%)	32	54
8	Fk	57/509 (11%)	53 (93%)	4 (7%)	14	39
8	Fl	57/509 (11%)	57 (100%)	0	100	100
8	Fm	57/509 (11%)	54 (95%)	3 (5%)	20	45
8	Ft	57/509 (11%)	53 (93%)	4 (7%)	14	39
8	Fu	57/509 (11%)	57 (100%)	0	100	100
8	Fv	57/509 (11%)	55 (96%)	2 (4%)	32	54
9	SA	534/540 (99%)	529 (99%)	5 (1%)	70	76
9	SB	534/540 (99%)	530 (99%)	4 (1%)	76	79
9	SC	534/540 (99%)	529 (99%)	5 (1%)	70	76
9	SD	534/540 (99%)	529 (99%)	5 (1%)	70	76
9	SE	534/540 (99%)	531 (99%)	3 (1%)	78	81
9	SF	534/540 (99%)	528 (99%)	6 (1%)	65	74
9	SG	539/540 (100%)	529 (98%)	10 (2%)	50	67
9	SH	539/540 (100%)	529 (98%)	10 (2%)	50	67
9	SI	539/540 (100%)	529 (98%)	10 (2%)	50	67
9	SJ	539/540 (100%)	528 (98%)	11 (2%)	48	66
9	SK	539/540 (100%)	528 (98%)	11 (2%)	48	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	SL	539/540 (100%)	529 (98%)	10 (2%)	50	67
9	SM	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SN	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SO	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SP	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SQ	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	SR	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SS	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	ST	539/540 (100%)	531 (98%)	8 (2%)	57	70
9	SU	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	SV	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	SW	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	SX	539/540 (100%)	534 (99%)	5 (1%)	70	76
9	SY	539/540 (100%)	531 (98%)	8 (2%)	57	70
9	SZ	539/540 (100%)	530 (98%)	9 (2%)	53	68
9	Sa	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Sb	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Sc	539/540 (100%)	531 (98%)	8 (2%)	57	70
9	Sd	539/540 (100%)	535 (99%)	4 (1%)	76	79
9	Se	539/540 (100%)	530 (98%)	9 (2%)	53	68
9	Sf	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	Sg	539/540 (100%)	533 (99%)	6 (1%)	65	74
9	Sh	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Si	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Sj	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Sk	539/540 (100%)	534 (99%)	5 (1%)	70	76
9	Sl	539/540 (100%)	534 (99%)	5 (1%)	70	76
9	Sm	539/540 (100%)	532 (99%)	7 (1%)	61	72
9	Sn	539/540 (100%)	535 (99%)	4 (1%)	76	79
9	So	539/540 (100%)	534 (99%)	5 (1%)	70	76
9	Sp	539/540 (100%)	531 (98%)	8 (2%)	57	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	TM	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	TN	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	TO	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	TP	138/139 (99%)	138 (100%)	0	100	100
10	TQ	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	TR	138/139 (99%)	138 (100%)	0	100	100
10	TS	138/139 (99%)	138 (100%)	0	100	100
10	TT	138/139 (99%)	138 (100%)	0	100	100
10	TU	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	TV	138/139 (99%)	138 (100%)	0	100	100
10	TW	138/139 (99%)	138 (100%)	0	100	100
10	TX	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	TY	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	TZ	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	Ta	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	Tb	138/139 (99%)	135 (98%)	3 (2%)	45	64
10	Tc	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	Td	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	Te	138/139 (99%)	138 (100%)	0	100	100
10	Tf	138/139 (99%)	138 (100%)	0	100	100
10	Tg	138/139 (99%)	138 (100%)	0	100	100
10	Th	138/139 (99%)	138 (100%)	0	100	100
10	Ti	138/139 (99%)	138 (100%)	0	100	100
10	Tj	138/139 (99%)	138 (100%)	0	100	100
10	Tk	138/139 (99%)	137 (99%)	1 (1%)	76	79
10	Tl	138/139 (99%)	135 (98%)	3 (2%)	45	64
10	Tm	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	Tn	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	To	138/139 (99%)	135 (98%)	3 (2%)	45	64
10	Tp	138/139 (99%)	136 (99%)	2 (1%)	59	71
10	Tq	138/139 (99%)	138 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Tr	138/139 (99%)	138 (100%)	0	100	100
10	Ts	138/139 (99%)	138 (100%)	0	100	100
10	Tt	138/139 (99%)	138 (100%)	0	100	100
10	Tu	138/139 (99%)	138 (100%)	0	100	100
10	Tv	138/139 (99%)	138 (100%)	0	100	100
11	AA	122/126 (97%)	119 (98%)	3 (2%)	42	62
11	AB	122/126 (97%)	122 (100%)	0	100	100
11	AC	122/126 (97%)	118 (97%)	4 (3%)	33	56
11	AD	122/126 (97%)	120 (98%)	2 (2%)	55	69
11	AE	122/126 (97%)	121 (99%)	1 (1%)	73	77
11	AF	122/126 (97%)	119 (98%)	3 (2%)	42	62
12	BE	333/334 (100%)	325 (98%)	8 (2%)	43	63
12	BF	333/334 (100%)	325 (98%)	8 (2%)	43	63
12	BG	333/334 (100%)	323 (97%)	10 (3%)	36	57
13	AG	184/184 (100%)	180 (98%)	4 (2%)	45	64
13	AH	184/184 (100%)	180 (98%)	4 (2%)	45	64
13	AI	184/184 (100%)	182 (99%)	2 (1%)	65	74
13	AJ	184/184 (100%)	182 (99%)	2 (1%)	65	74
13	AK	184/184 (100%)	181 (98%)	3 (2%)	55	69
13	AL	184/184 (100%)	181 (98%)	3 (2%)	55	69
14	BB	474/484 (98%)	459 (97%)	15 (3%)	34	56
14	BC	474/484 (98%)	464 (98%)	10 (2%)	47	65
14	BD	474/484 (98%)	462 (98%)	12 (2%)	42	62
All	All	65604/84042 (78%)	64593 (98%)	1011 (2%)	55	70

5 of 1011 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	Ac	20	THR
10	TN	150	VAL
8	FS	558	ILE
9	Sp	53	MET
12	BG	61	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 693 such sidechains are listed below:

Mol	Chain	Res	Type
9	SJ	589	GLN
9	Sk	59	ASN
9	SN	463	ASN
9	SJ	570	GLN
9	Sb	570	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

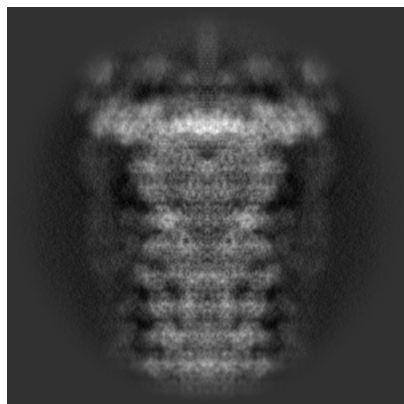
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50186. These allow visual inspection of the internal detail of the map and identification of artifacts.

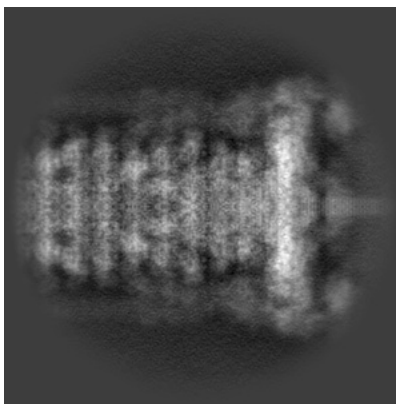
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

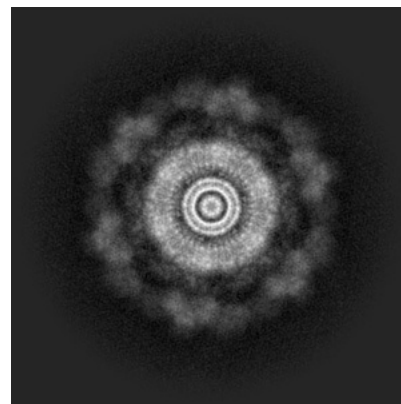
6.1.1 Primary map



X

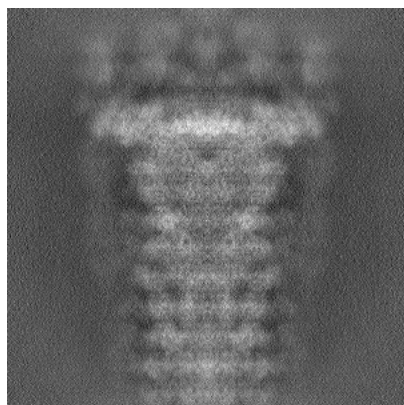


Y

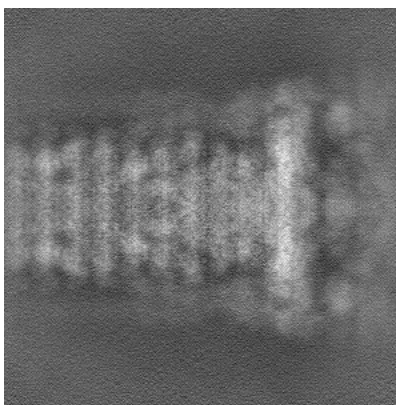


Z

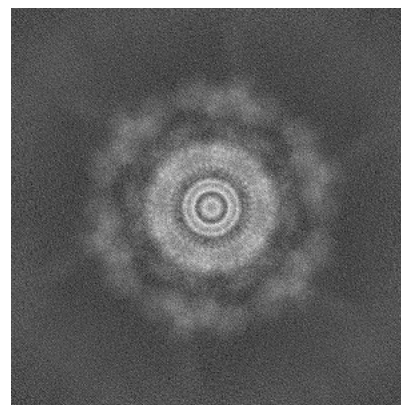
6.1.2 Raw map



X



Y

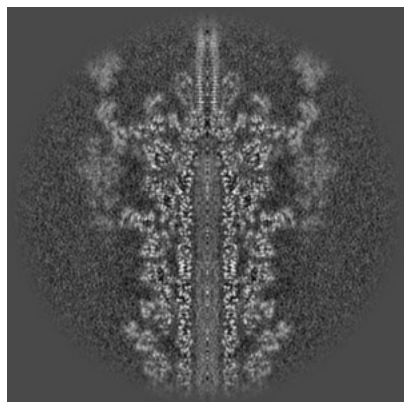


Z

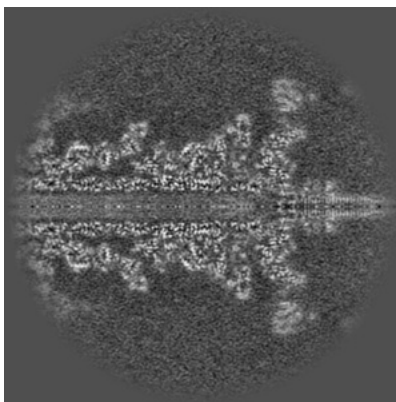
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

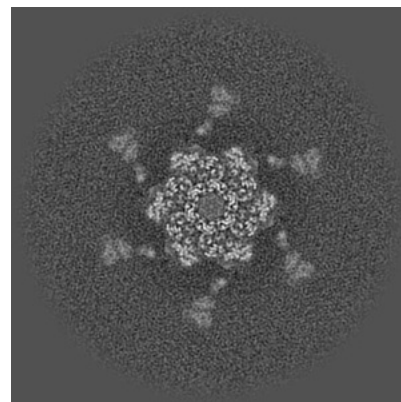
6.2.1 Primary map



X Index: 256

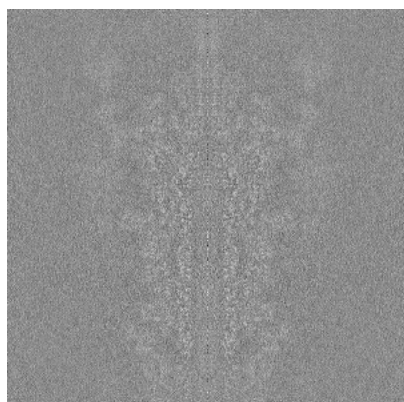


Y Index: 256

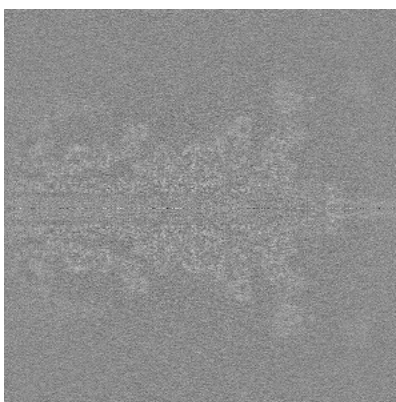


Z Index: 256

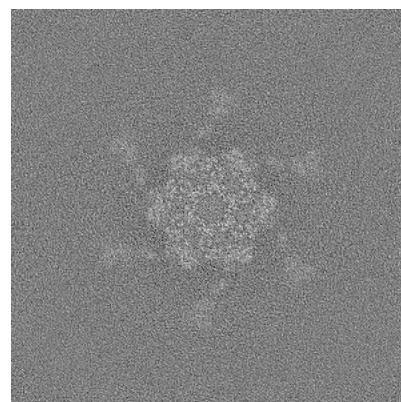
6.2.2 Raw map



X Index: 256



Y Index: 256

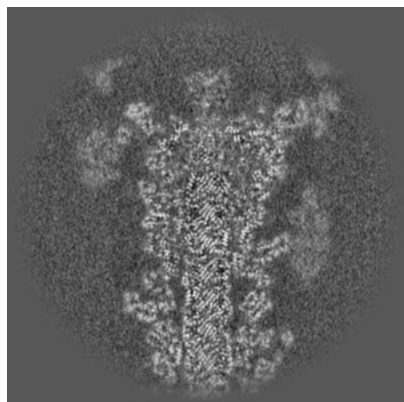


Z Index: 256

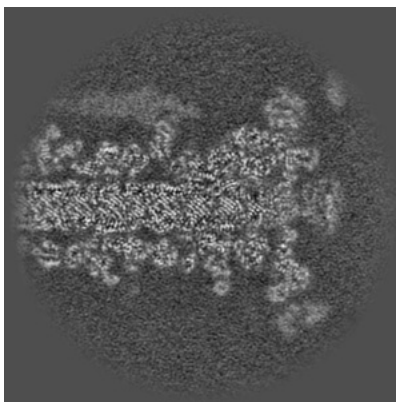
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

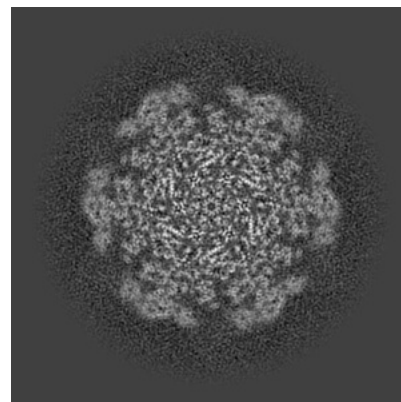
6.3.1 Primary map



X Index: 279

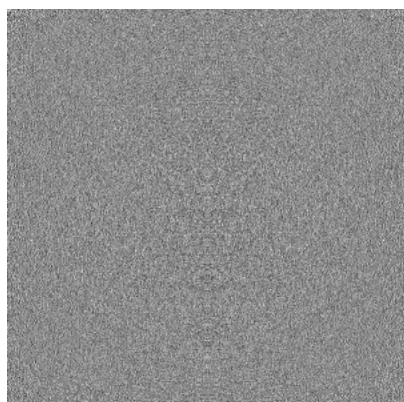


Y Index: 278

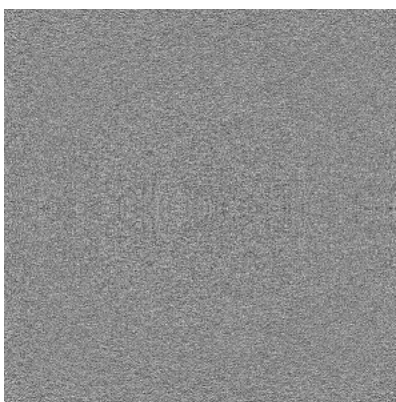


Z Index: 356

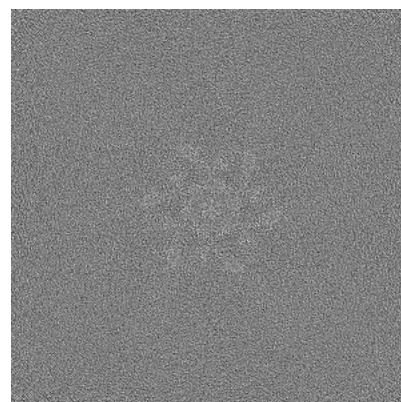
6.3.2 Raw map



X Index: 0



Y Index: 0

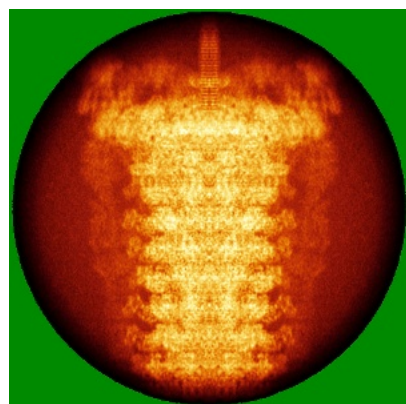


Z Index: 0

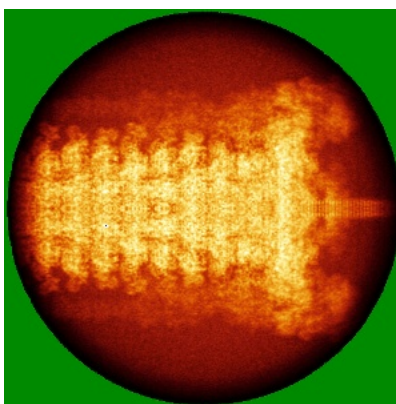
The images above show the largest variance slices of the map in three orthogonal directions.

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

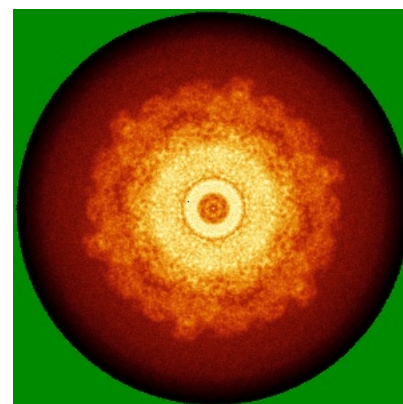
6.4.1 Primary map



X

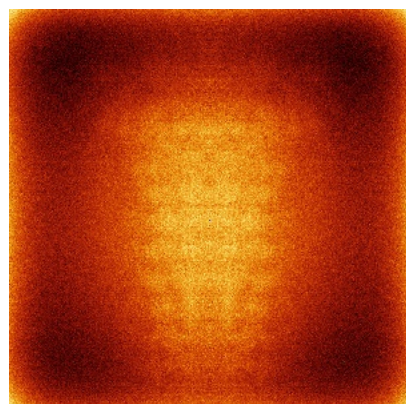


Y

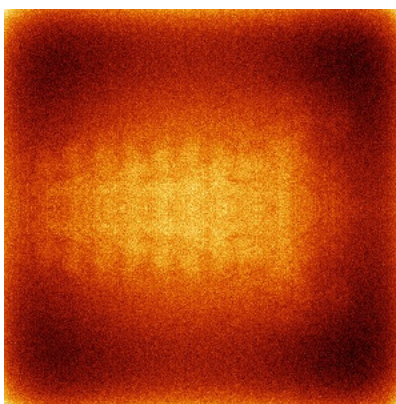


Z

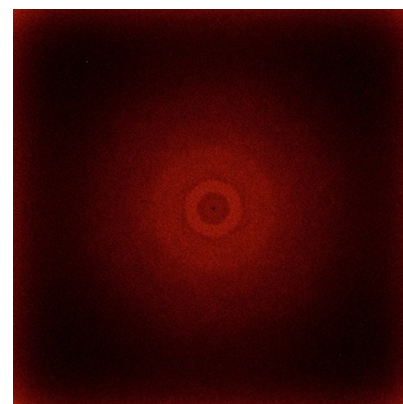
6.4.2 Raw map



X



Y

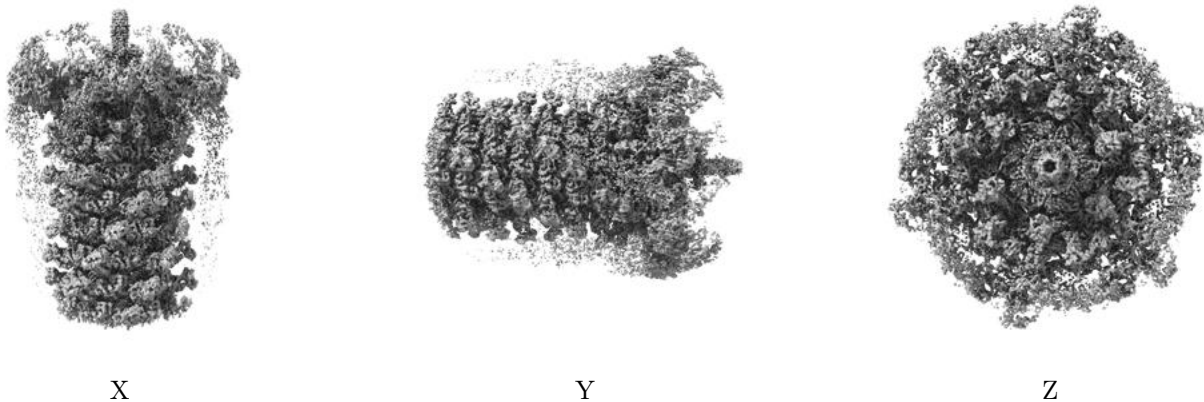


Z

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.

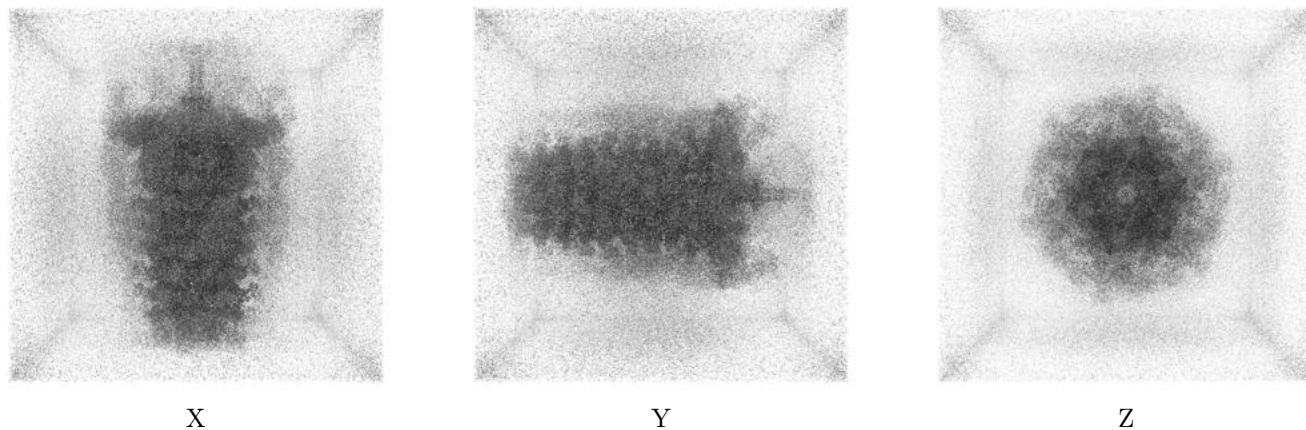
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

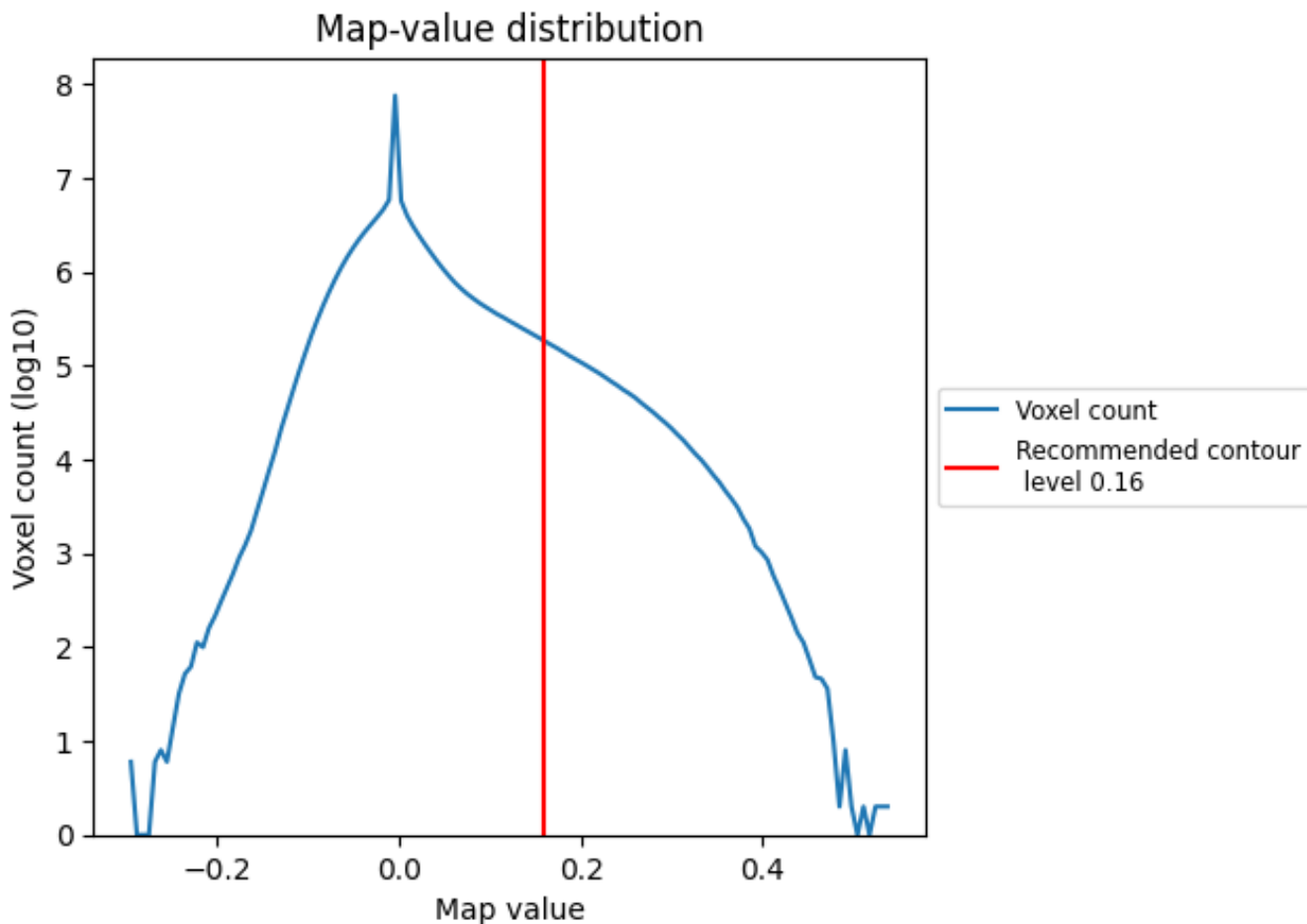
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

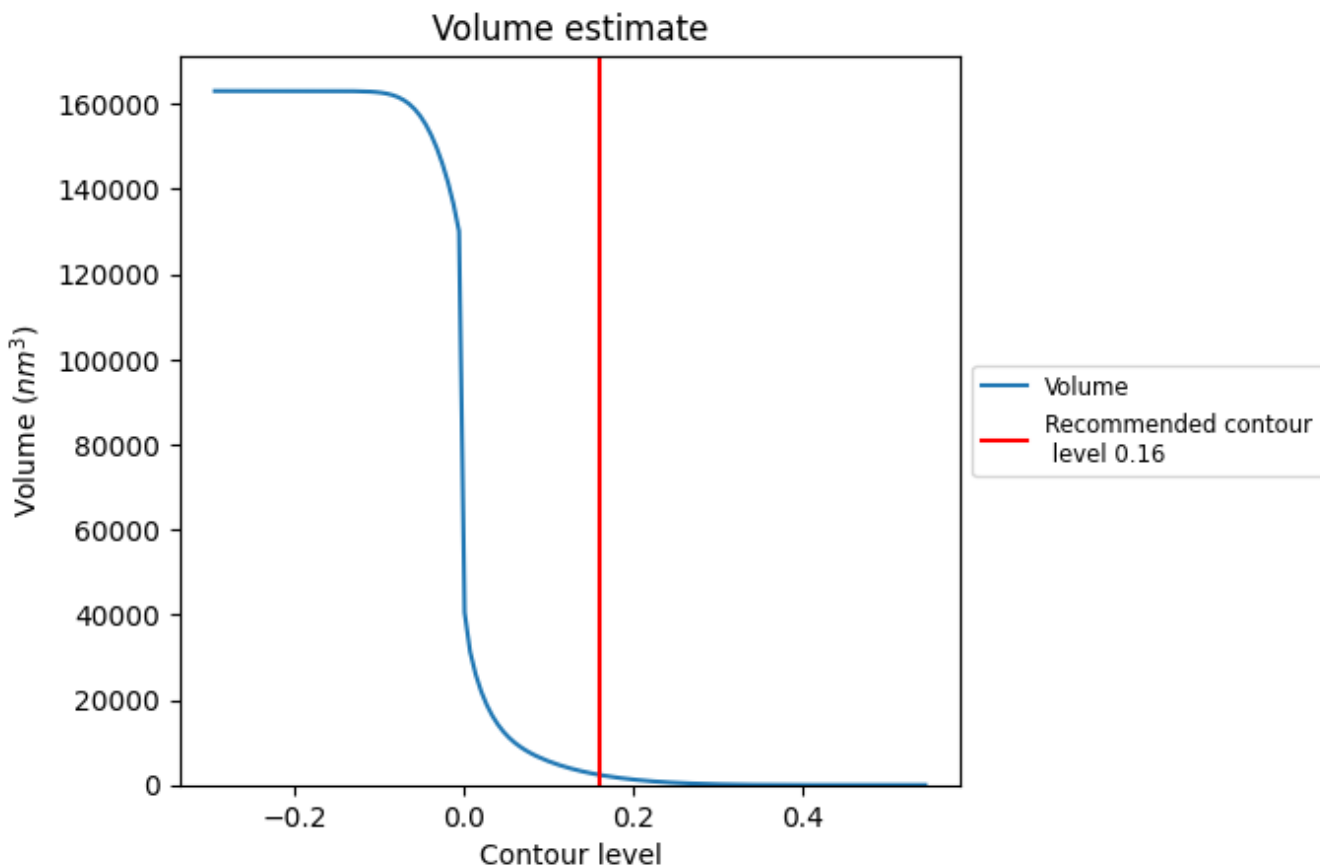
This section contains the results of statistical analysis of the map.

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.

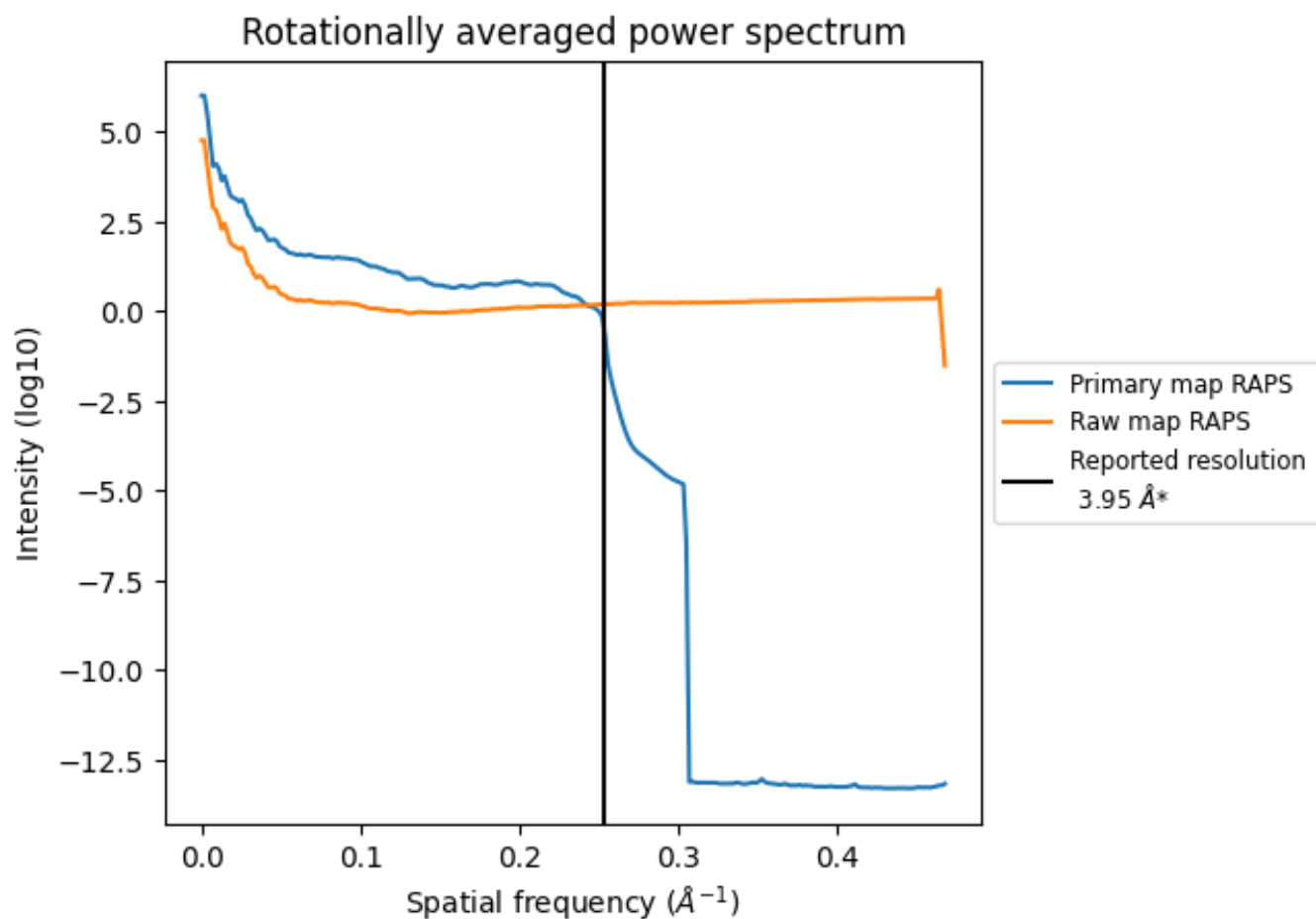
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 23520 nm³; this corresponds to an approximate mass of 2125 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 [i](#)

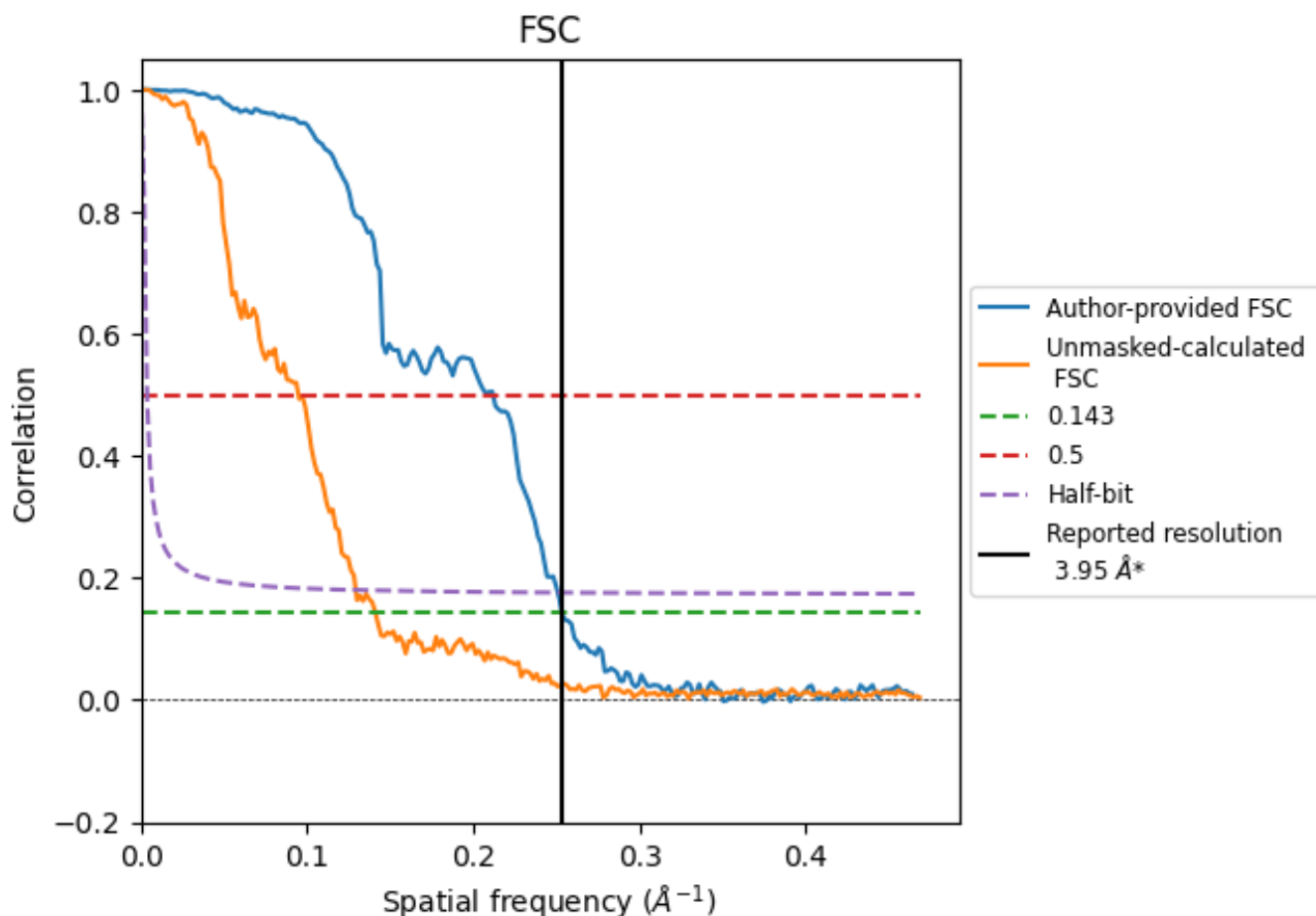


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

8.2 Resolution estimates [i](#)

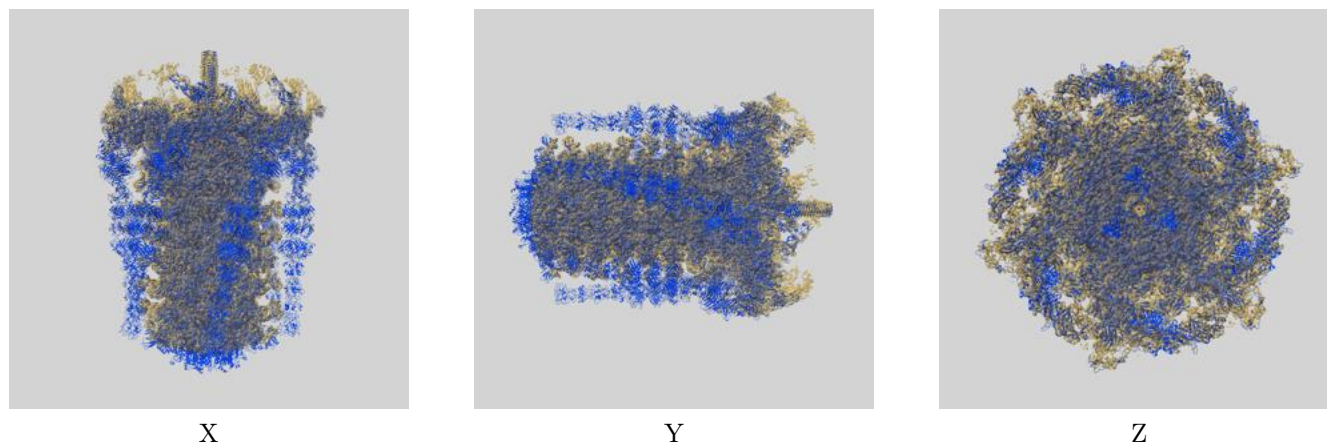
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.95	-	-
Author-provided FSC curve	3.95	4.72	3.99
Unmasked-calculated*	7.09	10.56	7.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.09 differs from the reported value 3.95 by more than 10 %

9 Map-model fit [i](#)

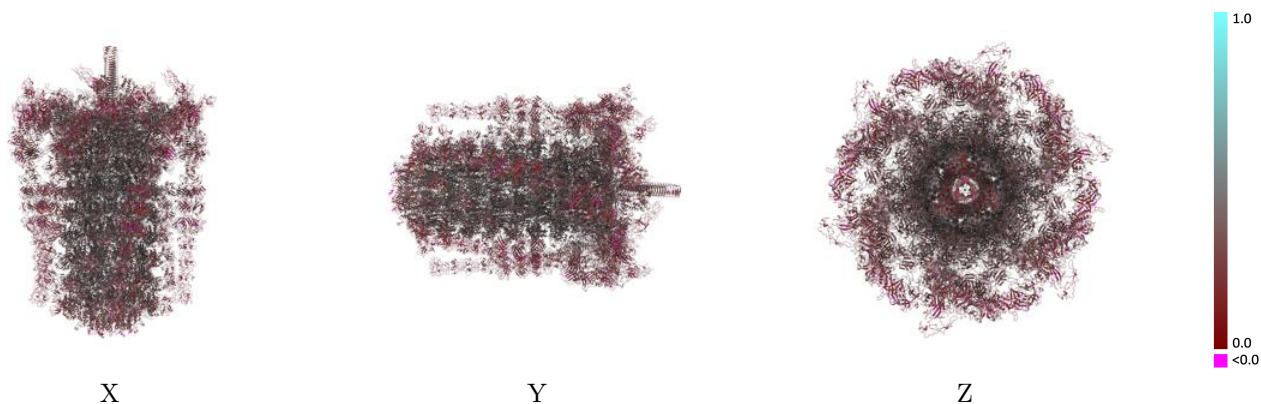
This section contains information regarding the fit between EMDB map EMD-50186 and PDB model 9F4A. Per-residue inclusion information can be found in section 3 on page 31.

9.1 Map-model overlay [i](#)



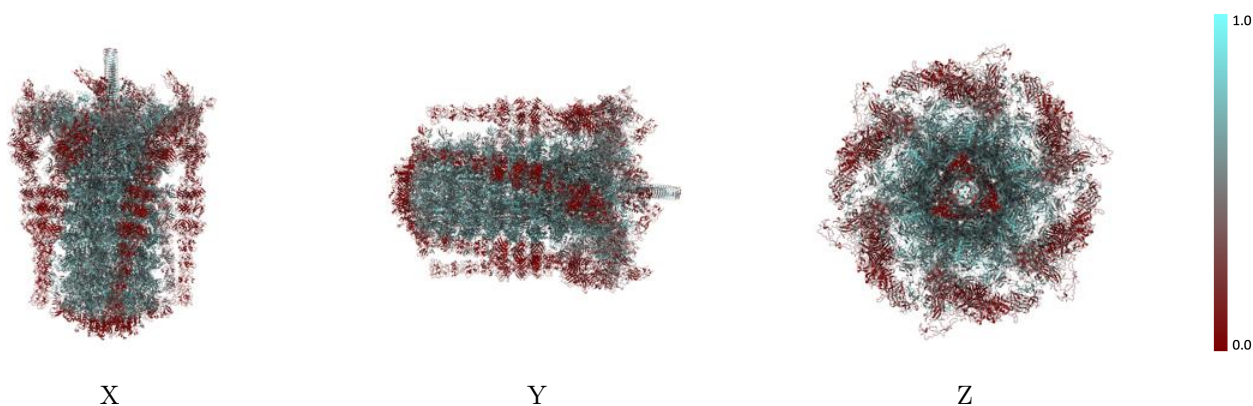
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



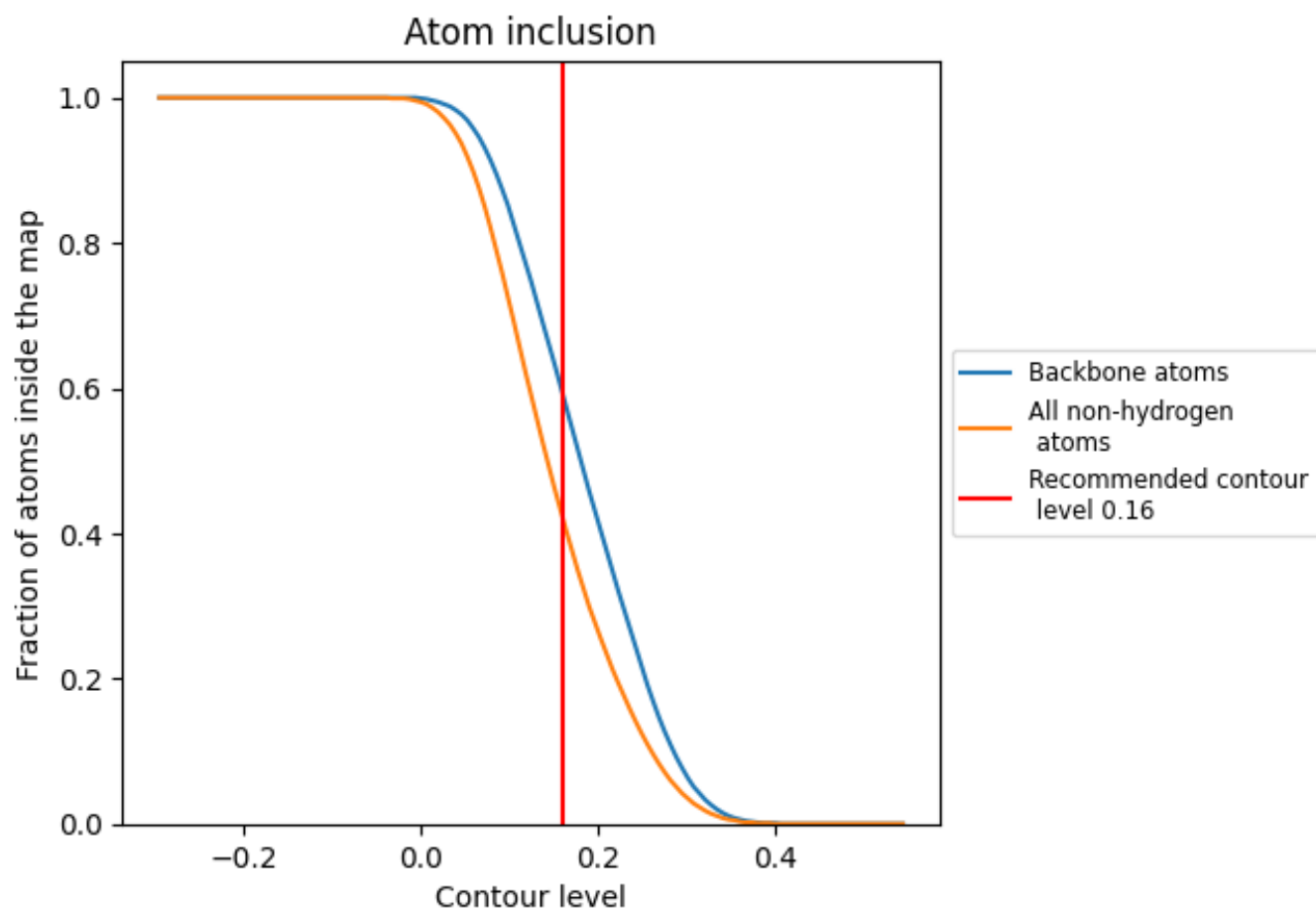
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 42% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4220	0.3380
A0	0.4220	0.2960
A1	0.4250	0.2950
A2	0.4270	0.2950
A3	0.4200	0.2950
A4	0.4580	0.3220
A5	0.4560	0.3200
A6	0.4630	0.3220
A7	0.4600	0.3210
A8	0.4620	0.3200
A9	0.4670	0.3200
AA	0.4760	0.3900
AB	0.4730	0.3910
AC	0.4740	0.3920
AD	0.4740	0.3910
AE	0.4700	0.3910
AF	0.4740	0.3970
AG	0.5890	0.4020
AH	0.5870	0.4020
AI	0.5890	0.4010
AJ	0.5890	0.3990
AK	0.5890	0.3960
AL	0.5870	0.4010
AM	0.6240	0.3900
AN	0.6280	0.3900
AO	0.6250	0.3890
AP	0.6270	0.3910
AQ	0.6270	0.3900
AR	0.6290	0.3890
AS	0.5990	0.3760
AT	0.6050	0.3790
AU	0.6000	0.3770
AV	0.6070	0.3780
AW	0.6030	0.3770
AX	0.6030	0.3790



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Chain	Atom inclusion	Q-score
AY	0.4240	0.2960
AZ	0.4280	0.2960
Aa	0.3770	0.2560
Ab	0.3810	0.2550
Ac	0.3800	0.2520
Ad	0.3720	0.2510
Ae	0.3730	0.2520
Af	0.3760	0.2530
BB	0.3640	0.3020
BC	0.3600	0.3010
BD	0.3600	0.3000
BE	0.4220	0.3580
BF	0.4260	0.3590
BG	0.4230	0.3600
BK	0.4090	0.3770
BL	0.4670	0.3840
BM	0.4090	0.3740
BN	0.4680	0.3860
BO	0.4070	0.3720
BP	0.4690	0.3860
BQ	0.5340	0.4280
BR	0.5290	0.4300
BS	0.5330	0.4300
BT	0.5310	0.4300
BU	0.5310	0.4310
BV	0.5330	0.4280
FA	0.1640	0.2180
FB	0.1580	0.2200
FC	0.1800	0.2390
FJ	0.1540	0.2200
FK	0.1680	0.2180
FL	0.1740	0.2340
FS	0.1540	0.2180
FT	0.1540	0.2190
FU	0.1760	0.2370
Fb	0.1680	0.2240
Fc	0.1640	0.2200
Fd	0.1850	0.2400
Fk	0.1600	0.2210
Fl	0.1680	0.2210
Fm	0.1700	0.2390
Ft	0.1500	0.2220





















































































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Chain	Atom inclusion	Q-score
Fu	0.1540	0.2180
Fv	0.1780	0.2350
LA	0.0870	0.2620
LB	0.0650	0.2510
LC	0.0630	0.2530
LD	0.0890	0.2620
LE	0.0600	0.2500
LF	0.0610	0.2540
LG	0.0870	0.2610
LH	0.0630	0.2530
LI	0.0620	0.2530
LJ	0.0880	0.2630
LK	0.0660	0.2510
LL	0.0610	0.2520
LM	0.0840	0.2630
LN	0.0570	0.2520
LO	0.0600	0.2540
LP	0.0890	0.2620
LQ	0.0620	0.2520
LR	0.0610	0.2540
LS	0.0130	0.2710
LT	0.0120	0.2410
LU	0.0220	0.2630
LV	0.0130	0.2730
LW	0.0120	0.2410
LX	0.0230	0.2620
LY	0.0130	0.2710
LZ	0.0120	0.2390
La	0.0260	0.2600
Lb	0.0130	0.2710
Lc	0.0130	0.2380
Ld	0.0220	0.2620
Le	0.0150	0.2710
Lf	0.0130	0.2400
Lg	0.0230	0.2620
Lh	0.0130	0.2690
Li	0.0120	0.2400
Lj	0.0250	0.2610
SA	0.5870	0.4010
SB	0.5870	0.4010
SC	0.5900	0.4010
SD	0.5880	0.4010

































































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Chain	Atom inclusion	Q-score
SE	 0.5860	 0.4010
SF	 0.5860	 0.4010
SG	 0.6340	 0.3990
SH	 0.6340	 0.3990
SI	 0.6300	 0.3990
SJ	 0.6320	 0.3990
SK	 0.6330	 0.3980
SL	 0.6320	 0.3980
SM	 0.6200	 0.3850
SN	 0.6190	 0.3850
SO	 0.6160	 0.3850
SP	 0.6190	 0.3850
SQ	 0.6190	 0.3840
SR	 0.6180	 0.3850
SS	 0.6100	 0.3800
ST	 0.6090	 0.3790
SU	 0.6110	 0.3790
SV	 0.6130	 0.3800
SW	 0.6110	 0.3800
SX	 0.6110	 0.3800
SY	 0.5940	 0.3600
SZ	 0.5930	 0.3600
Sa	 0.5950	 0.3590
Sb	 0.5970	 0.3610
Sc	 0.5910	 0.3600
Sd	 0.5950	 0.3610
Se	 0.5670	 0.3440
Sf	 0.5730	 0.3430
Sg	 0.5710	 0.3440
Sh	 0.5700	 0.3430
Si	 0.5730	 0.3440
Sj	 0.5700	 0.3440
Sk	 0.3440	 0.3000
Sl	 0.3440	 0.3000
Sm	 0.3430	 0.3000
Sn	 0.3450	 0.3000
So	 0.3420	 0.3010
Sp	 0.3440	 0.3000
TM	 0.6350	 0.4510
TN	 0.6400	 0.4490
TO	 0.6350	 0.4480
TP	 0.6410	 0.4500

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Chain	Atom inclusion	Q-score
TQ	 0.6420	 0.4500
TR	 0.6320	 0.4490
TS	 0.6450	 0.4420
TT	 0.6440	 0.4430
TU	 0.6520	 0.4440
TV	 0.6480	 0.4440
TW	 0.6470	 0.4450
TX	 0.6490	 0.4430
TY	 0.6500	 0.4440
TZ	 0.6470	 0.4420
Ta	 0.6500	 0.4440
Tb	 0.6560	 0.4460
Tc	 0.6500	 0.4440
Td	 0.6530	 0.4440
Te	 0.6340	 0.4360
Tf	 0.6310	 0.4370
Tg	 0.6290	 0.4370
Th	 0.6310	 0.4360
Ti	 0.6270	 0.4350
Tj	 0.6310	 0.4350
Tk	 0.6170	 0.4040
Tl	 0.6190	 0.4030
Tm	 0.6190	 0.4050
Tn	 0.6210	 0.4050
To	 0.6200	 0.4030
Tp	 0.6150	 0.4060
Tq	 0.1420	 0.2930
Tr	 0.1430	 0.2900
Ts	 0.1450	 0.2900
Tt	 0.1420	 0.2900
Tu	 0.1420	 0.2920
Tv	 0.1450	 0.2920