



wwPDB EM Validation Summary Report ⓘ

May 5, 2025 – 10:46 pm BST

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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

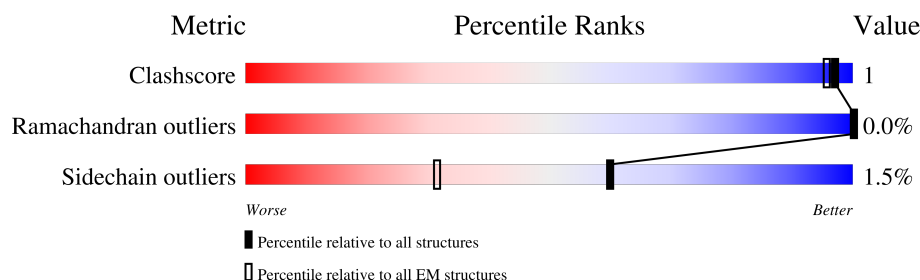
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LT	1281	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LU	1281	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LV	1281	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LW	1281	<div> <div>48%</div> <div>47%</div> <div>52%</div> </div>
1	LX	1281	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LY	1281	<div> <div>48%</div> <div>46%</div> <div>52%</div> </div>
1	LZ	1281	<div> <div>48%</div> <div>47%</div> <div>52%</div> </div>

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Mol	Chain	Length	Quality of chain
1	La	1281	<div>48%</div> <div>46% 52%</div>
1	Lb	1281	<div>48%</div> <div>46% 52%</div>
1	Lc	1281	<div>48%</div> <div>46% 52%</div>
1	Ld	1281	<div>48%</div> <div>47% 52%</div>
1	Le	1281	<div>48%</div> <div>46% 52%</div>
1	Lf	1281	<div>48%</div> <div>46% 52%</div>
1	Lg	1281	<div>48%</div> <div>46% 52%</div>
1	Lh	1281	<div>48%</div> <div>46% 52%</div>
1	Li	1281	<div>48%</div> <div>46% 52%</div>
1	Lj	1281	<div>48%</div> <div>46% 52%</div>
2	BK	350	<div>47%</div> <div>95%</div>
2	BL	350	<div>28%</div> <div>76% 21%</div>
2	BM	350	<div>46%</div> <div>94% 5%</div>
2	BN	350	<div>27%</div> <div>75% 21%</div>
2	BO	350	<div>45%</div> <div>95%</div>
2	BP	350	<div>27%</div> <div>74% 5% 21%</div>
3	BQ	308	<div>19%</div> <div>90% 5%</div>
3	BR	308	<div>18%</div> <div>90% 5%</div>
3	BS	308	<div>19%</div> <div>91% 5%</div>
3	BT	308	<div>19%</div> <div>90% 5%</div>
3	BU	308	<div>19%</div> <div>90% 5%</div>
3	BV	308	<div>18%</div> <div>91% 5%</div>
4	AM	655	<div>12%</div> <div>97%</div>
4	AN	655	<div>11%</div> <div>97%</div>
4	AO	655	<div>12%</div> <div>96%</div>

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Mol	Chain	Length	Quality of chain
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% ..
6	Ab	341	52% 93% ...
6	Ac	341	54% 92% ..
6	Ad	341	54% 92% ..

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Mol	Chain	Length	Quality of chain
6	Ae	341	<div>55%</div> <div>93%</div>
6	Af	341	<div>52%</div> <div>93%</div>
7	LA	303	<div>93%</div> <div>96%</div>
7	LB	303	<div>95%</div> <div>97%</div>
7	LC	303	<div>96%</div> <div>98%</div>
7	LD	303	<div>93%</div> <div>97%</div>
7	LE	303	<div>97%</div> <div>97%</div>
7	LF	303	<div>97%</div> <div>97%</div>
7	LG	303	<div>93%</div> <div>96%</div>
7	LH	303	<div>97%</div> <div>97%</div>
7	LI	303	<div>96%</div> <div>98%</div>
7	LJ	303	<div>93%</div> <div>97%</div>
7	LK	303	<div>96%</div> <div>98%</div>
7	LL	303	<div>96%</div> <div>97%</div>
7	LM	303	<div>93%</div> <div>97%</div>
7	LN	303	<div>97%</div> <div>96%</div>
7	LO	303	<div>97%</div> <div>97%</div>
7	LP	303	<div>94%</div> <div>97%</div>
7	LQ	303	<div>96%</div> <div>97%</div>
7	LR	303	<div>97%</div> <div>97%</div>
8	FA	607	<div>9%</div> <div>10%</div> <div>89%</div>
8	FB	607	<div>9%</div> <div>10%</div> <div>89%</div>
8	FC	607	<div>8%</div> <div>10%</div> <div>89%</div>
8	FJ	607	<div>9%</div> <div>10%</div> <div>89%</div>
8	FK	607	<div>9%</div> <div>10%</div> <div>89%</div>

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Mol	Chain	Length	Quality of chain
8	FL	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	FS	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	FT	607	<div> <div>10%</div> <div>10%</div> <div>89%</div> </div>
8	FU	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Fb	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Fc	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Fd	607	<div> <div>8%</div> <div>10%</div> <div>89%</div> </div>
8	Fk	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Fl	607	<div> <div>10%</div> <div>10%</div> <div>89%</div> </div>
8	Fm	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Ft	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
8	Fu	607	<div> <div>10%</div> <div>10%</div> <div>89%</div> </div>
8	Fv	607	<div> <div>9%</div> <div>10%</div> <div>89%</div> </div>
9	SA	656	<div> <div>16%</div> <div>95%</div> </div>
9	SB	656	<div> <div>17%</div> <div>95%</div> </div>
9	SC	656	<div> <div>16%</div> <div>96%</div> </div>
9	SD	656	<div> <div>17%</div> <div>96%</div> </div>
9	SE	656	<div> <div>16%</div> <div>96%</div> </div>
9	SF	656	<div> <div>17%</div> <div>96%</div> </div>
9	SG	656	<div> <div>11%</div> <div>95%</div> </div>
9	SH	656	<div> <div>11%</div> <div>96%</div> </div>
9	SI	656	<div> <div>11%</div> <div>95%</div> </div>
9	SJ	656	<div> <div>11%</div> <div>96%</div> </div>
9	SK	656	<div> <div>11%</div> <div>96%</div> </div>
9	SL	656	<div> <div>11%</div> <div>95%</div> </div>

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Mol	Chain	Length	Quality of chain
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% .
9	Si	656	19% 97% .
9	Sj	656	19% 97% .
9	Sk	656	55% 98% .

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Mol	Chain	Length	Quality of chain
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% 7% ..
10	TN	163	9% 93% 6% .
10	TO	163	10% 92% 7% .
10	TP	163	10% 92% 7% .
10	TQ	163	9% 92% 7% .
10	TR	163	10% 93% 6% .
10	TS	163	7% 97% ..
10	TT	163	7% 95% ..
10	TU	163	7% 93% 6% .
10	TV	163	7% 95% ..
10	TW	163	7% 93% 6% ..
10	TX	163	8% 94% 6% .
10	TY	163	7% 94% 5% .
10	TZ	163	7% 96% ..
10	Ta	163	6% 96% ..
10	Tb	163	6% 96% ..
10	Tc	163	6% 95% ..
10	Td	163	6% 95% ..
10	Te	163	12% 95% ..
10	Tf	163	12% 94% 5% .

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Mol	Chain	Length	Quality of chain
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% .
12	BE	380	43% 93% 6%
12	BF	380	43% 95% 5%
12	BG	380	43% 94% 5%

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Mol	Chain	Length	Quality of chain
13	AG	212	<div> <div>15%</div> <div>98%</div> <div>.</div> </div>
13	AH	212	<div> <div>13%</div> <div>96%</div> <div>.</div> </div>
13	AI	212	<div> <div>13%</div> <div>99%</div> <div>.</div> </div>
13	AJ	212	<div> <div>15%</div> <div>98%</div> <div>.</div> </div>
13	AK	212	<div> <div>12%</div> <div>99%</div> <div>.</div> </div>
13	AL	212	<div> <div>14%</div> <div>97%</div> <div>.</div> </div>
14	BB	576	<div> <div>57%</div> <div>93%</div> <div>5% .</div> </div>
14	BC	576	<div> <div>57%</div> <div>93%</div> <div>5% .</div> </div>
14	BD	576	<div> <div>57%</div> <div>93%</div> <div>5% .</div> </div>

2 Entry composition

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
1	Ld	617	Total	C	N	O	S	0	0
			4752	2963	834	947	8		

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
5	AZ	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		
5	A0	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		
5	A1	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		
5	A2	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		
5	A3	1031	Total	C	N	O	S	0	0
			8438	5377	1416	1617	28		

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
6	A4	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		
6	A9	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		
6	A6	334	Total	C	N	O	S	0	0
			2669	1693	446	513	17		

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

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

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
10	TM	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	TN	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	TO	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
10	TP	162	Total	C	N	O	S	0	0
			1305	825	222	253	5		
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	TW	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		

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

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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		

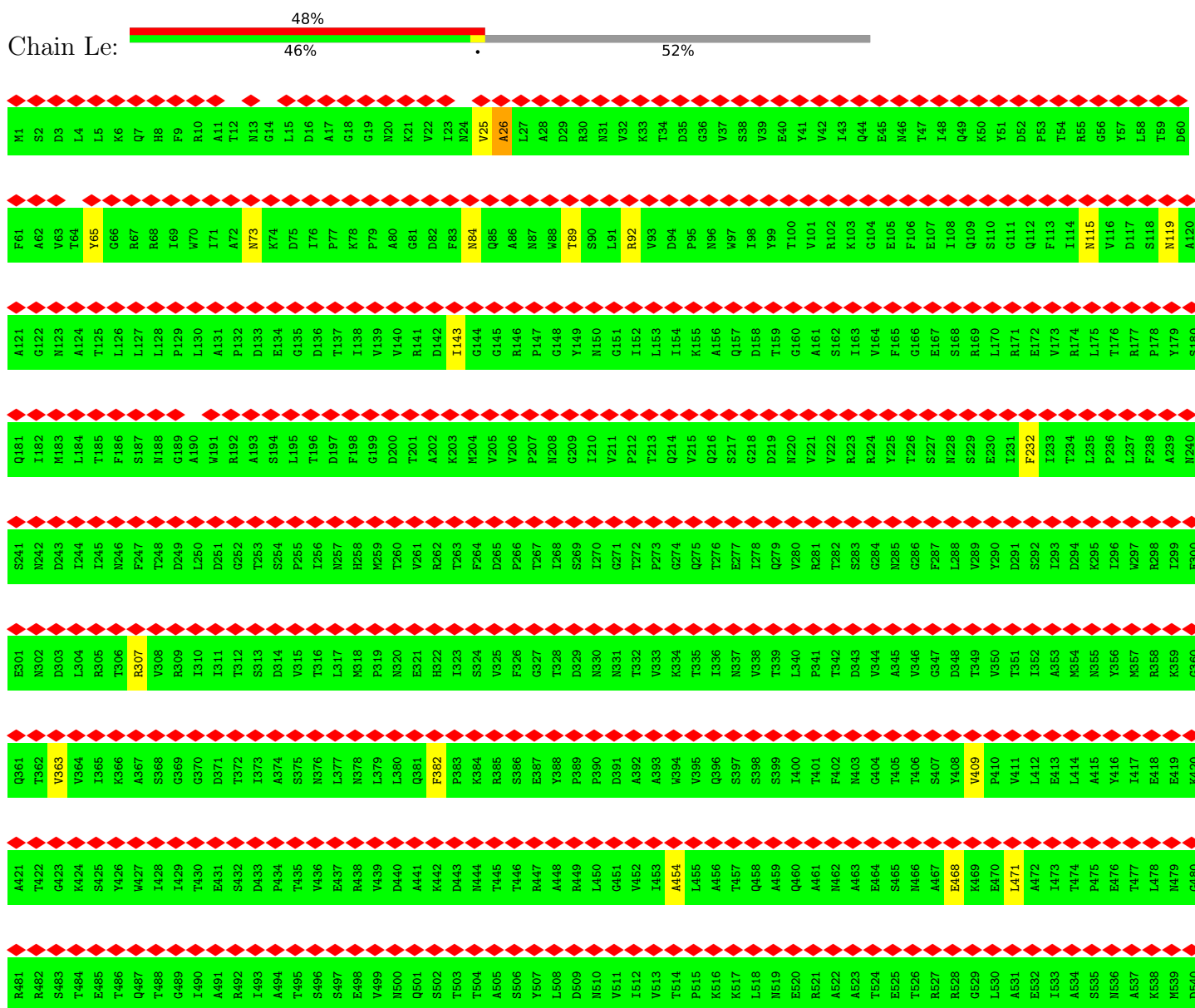
- Molecule 15 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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



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	G574	A575	P576	N577	T578	T579	N580	D581	R582	S583	S584	A585	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	K612	Q613	S614	G615	I616	V617	TRP	LEU	ALA	THR	ASP	SER	GLY	VAL	ARG	ASN	GLY	THR	PRO	THR	SER	ASN	ILE	THR	VAL	THR	GLN	GLU	ALA	THR	LEU	HIS	LYS	VAL	VAL	ALA	THR	ASP	ASP	LYS	ALA	GLY	THR	ILE	GLN	ILE	ALA																																																																																																																																																																																																																																																																																																																																																						
THR	GLN	THR	GLU	ASN	ALA	GLY	VAL	ASN	LYS	ALA	VAL	PRO	LYS	THR	LEU	ASN	ARG	THR	ALA	THR	ASN	THR	VAL	ILE	GLY	ALA	ARG	PHE	PRO	SER	PRO	GLY	ALA	THR	PHE	GLY	THR	VAL	SER	THR	LYS	VAL	THR	ASN	PRO	LYS	GLY	ALA	LEU	ILE	PHE																																																																																																																																																																																																																																																																																																																																																												
ASP	LYS	PHE	ALA	THR	GLY	ILE	GLN	VAL	THR	SER	GLY	LEU	THR	ILE	GLY	THR	LEU	TRP	ASP	HIS	THR	ASN	ILE	GLN	GLU	ALA	ARG	THR	GLN	GLN	THR	LEU	PHE	VAL	ALA	THR	THR	ALA	ARG	GLY	THR	ASP	ALA	LYS	LYS	ILE	VAL																																																																																																																																																																																																																																																																																																																																																																
THR	ALA	THR	LEU	HIS	LYS	THR	ALA	THR	GLY	ALA	ILE	LEU	ALA	GLN	TYR	THR	THR	ALA	VAL	GLN	ASP	THR	LEU	SER	ASP	ARG	ILE	VAL	PRO	ALA	ALA	TYR	GLN	THR	THR	ILE	THR	LYS	TRP	GLN	ALA	THR	VAL	THR	ARG	GLY	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																												
VAL	ARG	LEU	THR	GLY	ASP	THR	TRP	GLY	ASN	THR	ASP	GLY	SER	THR	THR	THR	GLY	TYR	ALA	VAL	LYS	VAL	ALA	VAL	SER	PRO	TYR	GLU	LYS	THR	LYS	THR	THR	THR	THR	THR	THR	THR	THR	LYS	ALA	THR	MET	LEU	GLY	GLN																																																																																																																																																																																																																																																																																																																																																																	
THR	PRO	ASP	TYR	ALA	ARG	ASP	ILE	GLN	THR	ILE	SER	GLY	TRP	SER	PHE	THR	THR	SER	PHE	ASN	ASN	ILE	SER	VAL	GLN	ASN	ILE	THR	VAL	ALA	GLY	GLY	LYS	THR	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																										
ARG	ASP	GLY	GLU	ARG	GLY	ILE	THR	ALA	PRO	GLN	THR	SER	ALA	GLY	THR	GLY	VAL	VAL	LYS	ASN	GLY	THR	THR	THR	ALA	ALA	GLN	GLN	THR	GLN	GLY	GLY	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																								
GLY	ASN	ALA	VAL	GLY	THR	VAL	VAL	VAL	ASP	VAL	GLN	LEU	ALA	VAL	GLU	VAL	ASN	SER	ILE	PHE	GLY	GLN	SER	GLN	ALA	PHE	ARG	THR	ARG	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																						
TYR	ALA	ARG	ALA	ASP	ARG	TYR	VAL	LYS	ALA	GLY	THR	GLY	THR	THR	ASN	GLY	ASN	SER	SER	TYR	ALA	ILE	THR	GLY	ALA	SER	GLU	SER	TRP	VAL	THR	GLU	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																				
LYS	GLY	LEU	GLY	MET	VAL	PRO	ILE	THR	PRO	ILE	PRO	ASN	PRO	SER	THR	VAL	VAL	THR	GLY	GLY	GLU	LYS	THR	ALA	GLY	GLY	GLY	VAL	LEU	THR	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																
ALA	ASP	LYS	PHE	HIS	THR	VAL	THR	MET	ILE	THR	ASN	LEU	ASN	ASN	PHE	THR	MET	THR	ARG	VAL	VAL	SER	ALA	THR	PRO	THR	ALA	VAL	ALA	THR	GLY	VAL	THR	SER	SER	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

● Molecule 1: Long tail fiber proximal subunit



M1	S2	D3	L4	L5	K6	Q7	H8	F9	R10	A11	T12	N13	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	I43	Q44	E45	N46	T47	I48	Q49	K50	Y51	D52	P53	T54	R55	G56	Y57	L58	T59	D60	
F61	A62	V63	T64	Y65	G66	R67	R68	I69	W70	I71	A72	N73	K74	D75	I76	P77	K78	P79	A80	G81	D82	F83	N84	Q85	A86	N87	W88	T89	S90	L91	R92	V93	D94	P95	N96	W97	I98	Y99	T100	V101	R102	K103	G104	E105	F106	E107	I108	Q109	L110	G111	Q112	F113	I114	N115	V116	D117	N118	N119	A120	
A121	G122	N123	A124	T125	L126	L127	L128	P129	L130	A131	P132	D133	E134	G135	D136	T137	I138	V139	V140	R141	D142	I143	G144	G145	R146	P147	G148	Y149	N150	G151	I152	L153	I154	K155	A156	Q157	D158	T159	G160	A161	I162	V163	I163	V164	F165	G166	E167	S168	R169	L170	R171	E172	V173	R174	L175	T176	R177	P178	Y179	S180



ALA ASP
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● Molecule 1: Long tail fiber proximal subunit



P601	K602	T603	L604	R605	E606	Y607	K608	A609	T610	V611	N612	T613	S614	G615	I616	V617	TRP	LEU	THR	ALA	THR	ASP	SER	GLU	VAL	ARG	ASN	GLY	THR	PRO	ALA	SER	ASN	V570	N510	V511	I512	THR	G573	G574	VAL	THR	THR	PRO	GLU	LEU	ALA	ALA	LYS	THR	THR	ASP	GLY	ALA	ILE	GLY	LEU	ILE	GLN	ALA
R481	R482	S483	T484	E485	T486	Q487	T488	G489	I490	A491	R492	I493	A494	T495	S496	S497	E498	T499	N500	Q501	S502	T503	T504	A505	S506	Y507	L508	ALA	Q569	L569	V570	ASN	V511	I512	THR	G573	G574	VAL	THR	THR	PRO	GLU	LEU	ALA	ALA	LYS	THR	THR	ASP	GLY	ALA	ILE	GLY	LEU	ILE	GLN	ALA			
A541	G542	T543	D544	E545	F546	T547	I548	V549	T550	P551	K552	T553	L554	L555	Y556	R557	T558	T559	S560	D561	S562	R563	L564	G565	V566	V567	Q568	ALA	Q569	L569	V570	ASN	V511	I512	THR	G573	G574	VAL	THR	THR	PRO	GLU	LEU	ALA	ALA	LYS	THR	THR	ASP	GLY	ALA	ILE	GLY	LEU	ILE	GLN	ALA			
A421	T422	G423	K424	S425	Y426	W427	I428	A429	T430	E431	S432	D433	P434	T435	V436	E437	R438	V439	D440	A441	K442	D443	N444	T445	V446	R447	A448	R449	L450	N450	V451	G452	V453	A454	L455	A456	T457	Q458	A459	Q460	A461	W462	A463	E464	S465	N466	A467	E468	G469	E470	L471	A472	I473	T474	P475	E476	T477	N478	G480	
Q361	T362	V363	V364	T365	K366	A367	S368	G369	G370	D371	T372	I373	A374	S375	N376	L377	N378	L379	L380	Q381	F382	P383	K384	R385	S386	E387	Y388	P389	D390	D391	A392	A393	V394	V395	Q396	S397	S398	S399	I400	T401	F402	N403	G404	T405	T406	S407	Y408	V409	P410	V411	L412	E413	L414	A415	Y416	I417	E418	E419	K420	
E301	N302	D303	L304	S305	T306	R307	V308	R309	T310	T311	T312	S313	D314	V315	T316	L317	N318	P319	N320	E321	H322	I323	S324	R325	F326	G327	T328	D329	N330	N331	T332	V333	K334	T335	I336	N337	V338	T339	L340	P341	T342	D343	G344	A345	V346	G347	D348	T349	V350	T351	I352	A353	M354	N355	Y356	N357	E358	K359	G360	
S241	N242	D243	T244	N245	N246	F247	T248	D249	L250	D251	G252	T253	S254	P255	T256	N257	M258	M259	T260	R261	S262	T263	F264	D265	P266	T267	T268	S269	T270	G271	T272	P273	Q274	Q275	T276	E277	T278	Q279	V280	R281	T282	S283	G284	N285	G286	F287	L288	V289	D290	D291	S292	T293	D294	K295	T296	W297	R298	T299	F300	
I181	I182	M183	L184	T185	F186	S187	H188	A189	G190	W191	R192	S193	S194	L195	T196	D197	F198	G199	D200	T201	A202	K203	H204	V205	V206	P207	T208	G209	T210	V211	P212	T213	Q214	V215	Q216	S217	G218	D219	N220	V221	V222	R223	R224	V225	T226	S227	N228	S229	T230	I231	F232	T233	T234	L235	P236	L237	F238	A239	N240	
A121	G122	M123	A124	T125	L126	L127	L128	P129	L130	A131	P132	D133	E134	G135	D136	T137	T138	V139	V140	R141	D142	I143	G144	G145	R146	P147	G148	V149	N150	G151	I152	L153	I154	K155	A156	Q157	D158	T159	G160	A161	S162	I163	V164	F165	G166	E167	S168	L169	L170	R171	E172	V173	L174	L175	T176	R177	Y178	S180		
F61	A62	V63	T64	V65	G66	R67	R68	L69	W70	I71	A72	M73	K74	D75	I76	P77	K78	P79	A80	G81	D82	F83	N84	Q85	A86	N87	W88	T89	S90	L91	R92	V93	D94	P95	N96	W97	I98	Y99	T100	V101	R102	K103	G104	E105	F106	E107	I108	Q109	S110	G111	Q112	F113	T114	N115	V116	D117	S118	N119	A120	

[illegible]

- Molecule 1: Long tail fiber proximal subunit



E301	S241	Q181	A121	F61	M1
N302	N242	I182	G122	A62	S2
D303	D243	M183	P123	V63	D3
L304	L244	L184	A124	T64	L4
R305	T245	T185	T125	Y65	L5
T306	N246	F186	L126	G66	K6
R307	T247	S187	L127	R67	Q7
V308	T248	N188	L128	R68	H8
R309	D249	G189	P129	I69	F9
I310	L250	A190	L130	W70	R10
I311	D251	W191	A131	I71	A11
T312	G252	W192	P132	A72	T12
S313	T253	A193	D133	N73	M13
D314	S254	S194	E134	K74	G14
V315	P255	L195	G135	D75	L15
T316	L256	T196	D136	I76	D16
L317	N257	D197	T137	F77	A17
M318	H258	F198	I138	K78	G18
P319	M259	G199	V139	F79	G19
N320	T260	D200	V140	A80	N20
E321	V261	T201	R141	G81	K21
H322	R262	A202	D142	D82	V22
I323	T263	K203	I143	F83	T23
S324	F264	M204	G144	N84	N24
V325	D265	V205	G145	K85	V25
F326	P266	V206	R146	A86	A26
G327	T267	P207	P147	N87	L27
T328	L268	N208	G148	W88	A28
D329	S269	G209	Y149	T89	D29
N330	L270	I210	N150	S90	R30
N331	G271	V211	G151	L91	N31
T332	T272	P212	I152	R92	V32
V333	P273	T213	L153	V93	K33
K334	G274	Q214	I154	D94	T34
T335	Q275	V215	K155	P95	D35
I336	T276	Q216	A156	N96	G36
N337	E277	S217	Q157	W97	V37
V338	L278	G218	D158	I98	S38
T339	Q279	D219	T159	Y99	V39
L340	R280	N220	G160	T100	E40
P341	N281	V221	A161	V101	Y41
T342	T282	V222	S162	R102	V42
D343	S283	R223	I163	K103	I43
V344	G284	R224	V164	G104	O44
A345	N285	Y225	F165	E105	E45
V346	G286	T226	G166	F106	N46
G347	F287	S227	E167	E107	T47
D348	L288	N228	S168	I108	I48
T349	V289	S229	R169	Q109	Q49
V350	Y290	E230	L170	S110	K50
T351	D291	I231	R171	G111	Y51
I352	S292	F232	E172	Q112	D52
A353	L293	T233	V173	F113	P53
M354	D294	T234	R174	I114	T54
N355	K295	L235	R175	N115	R55
Y356	T296	P236	T176	V116	G56
M357	W297	L237	R177	D117	Y57
R358	R298	F238	P178	S118	L58
K359	L299	A239	Y179	N119	T59
T360	T300	N240	G180	A120	D60

- Molecule 1: Long tail fiber proximal subunit

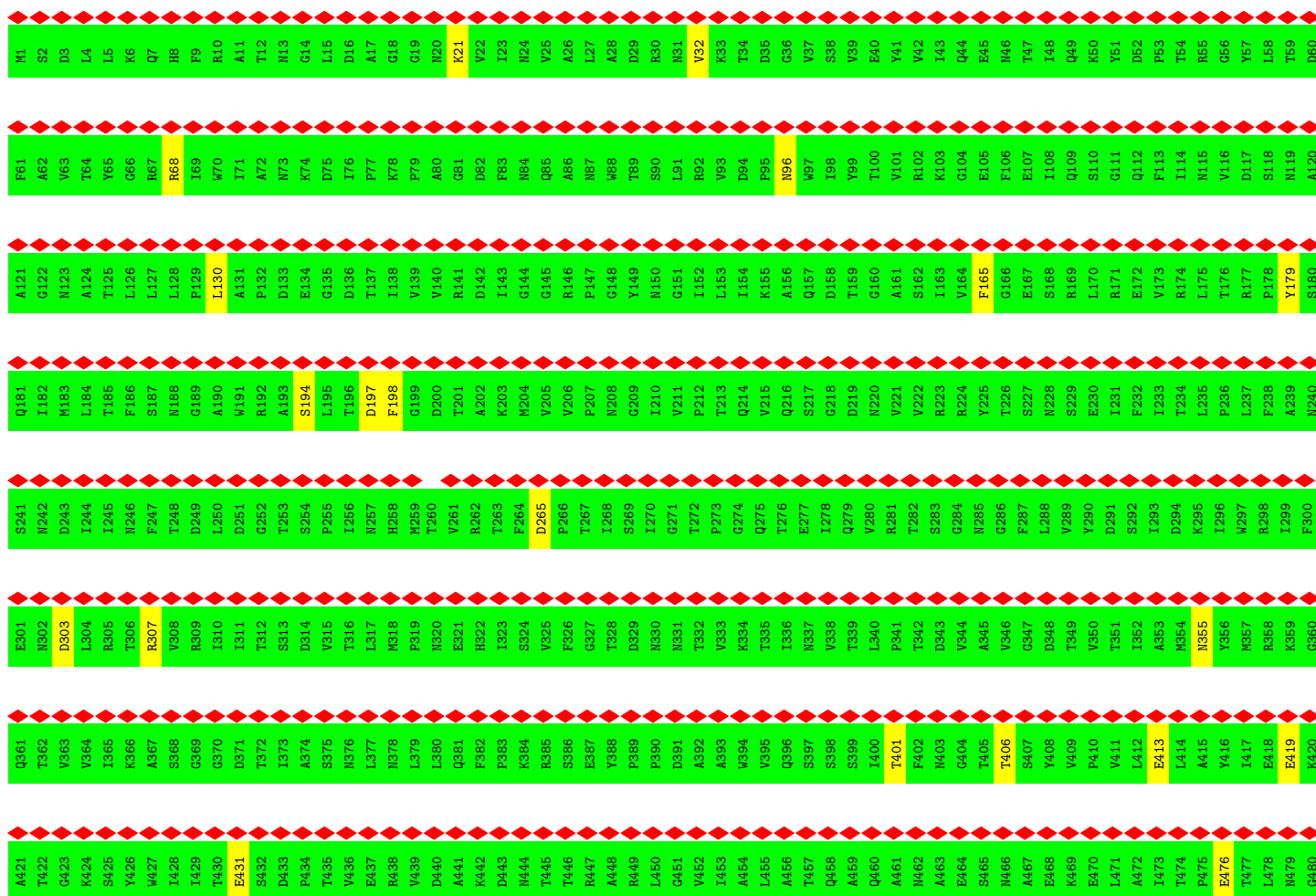


[illegible]

[illegible]

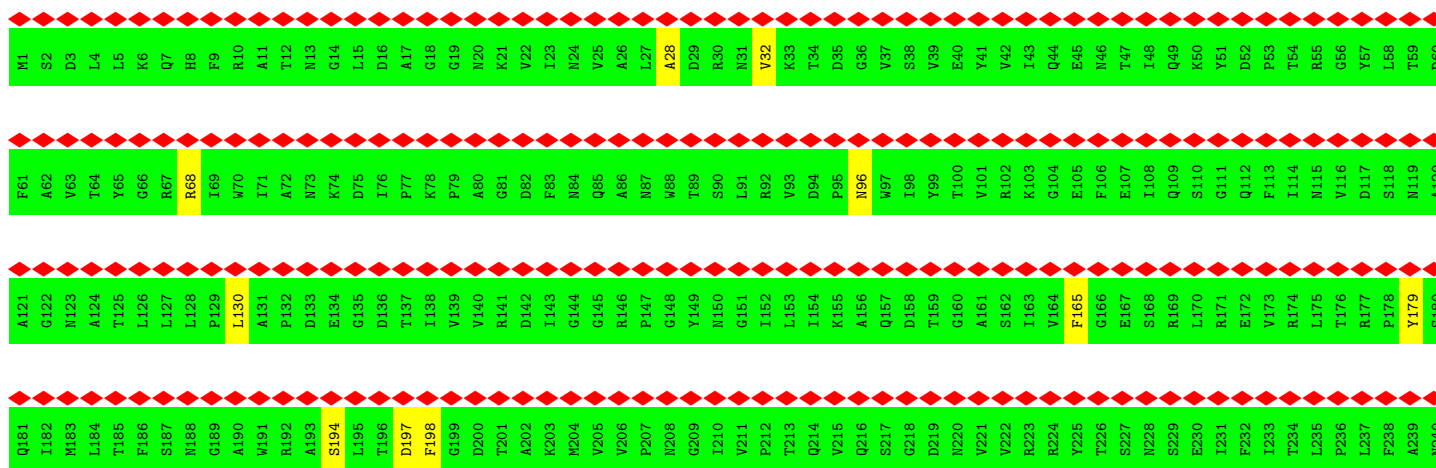
- Molecule 1: Long tail fiber proximal subunit

Chain Lj:  48% 46% 52%

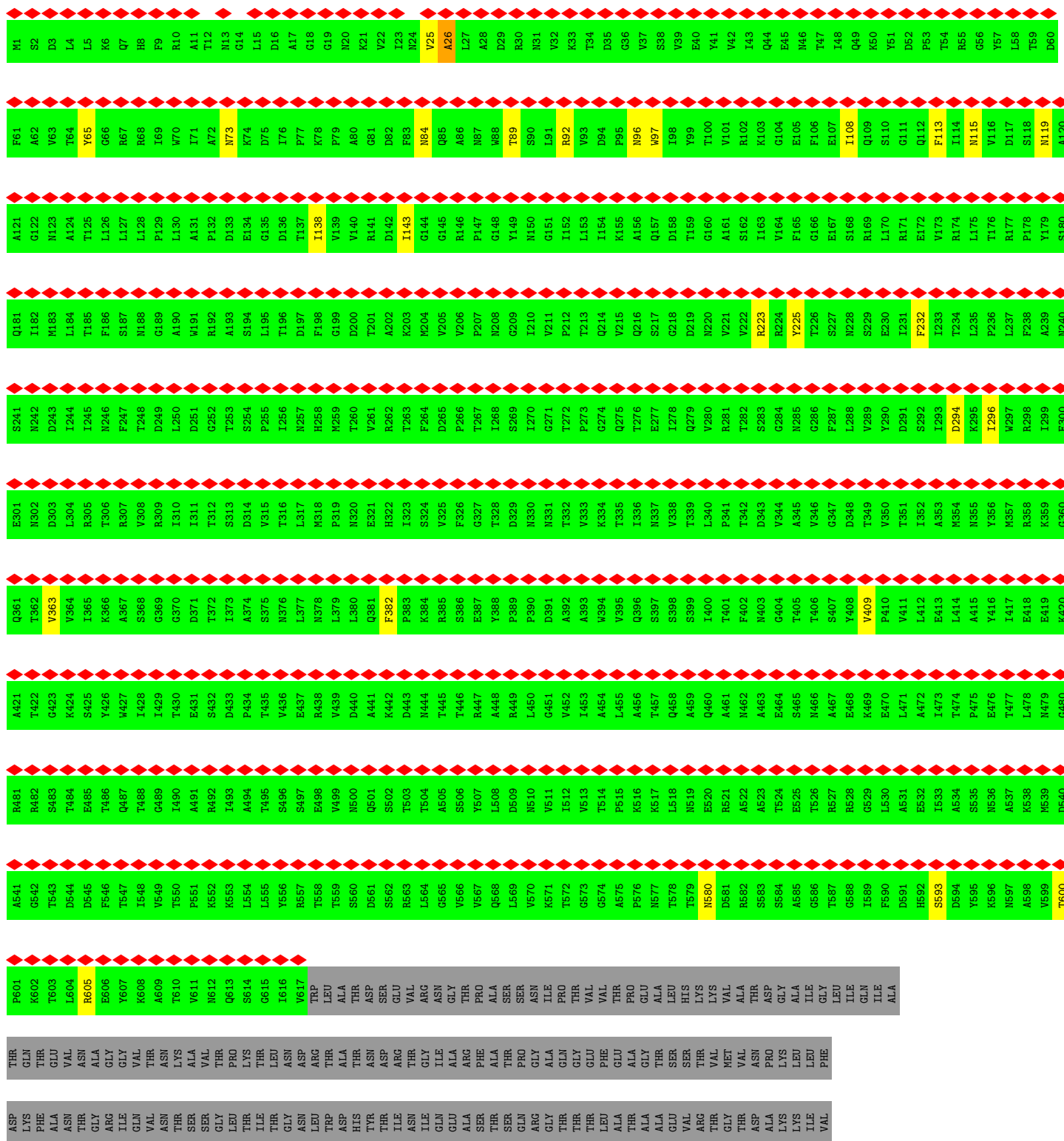












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- Molecule 1: Long tail fiber proximal subunit

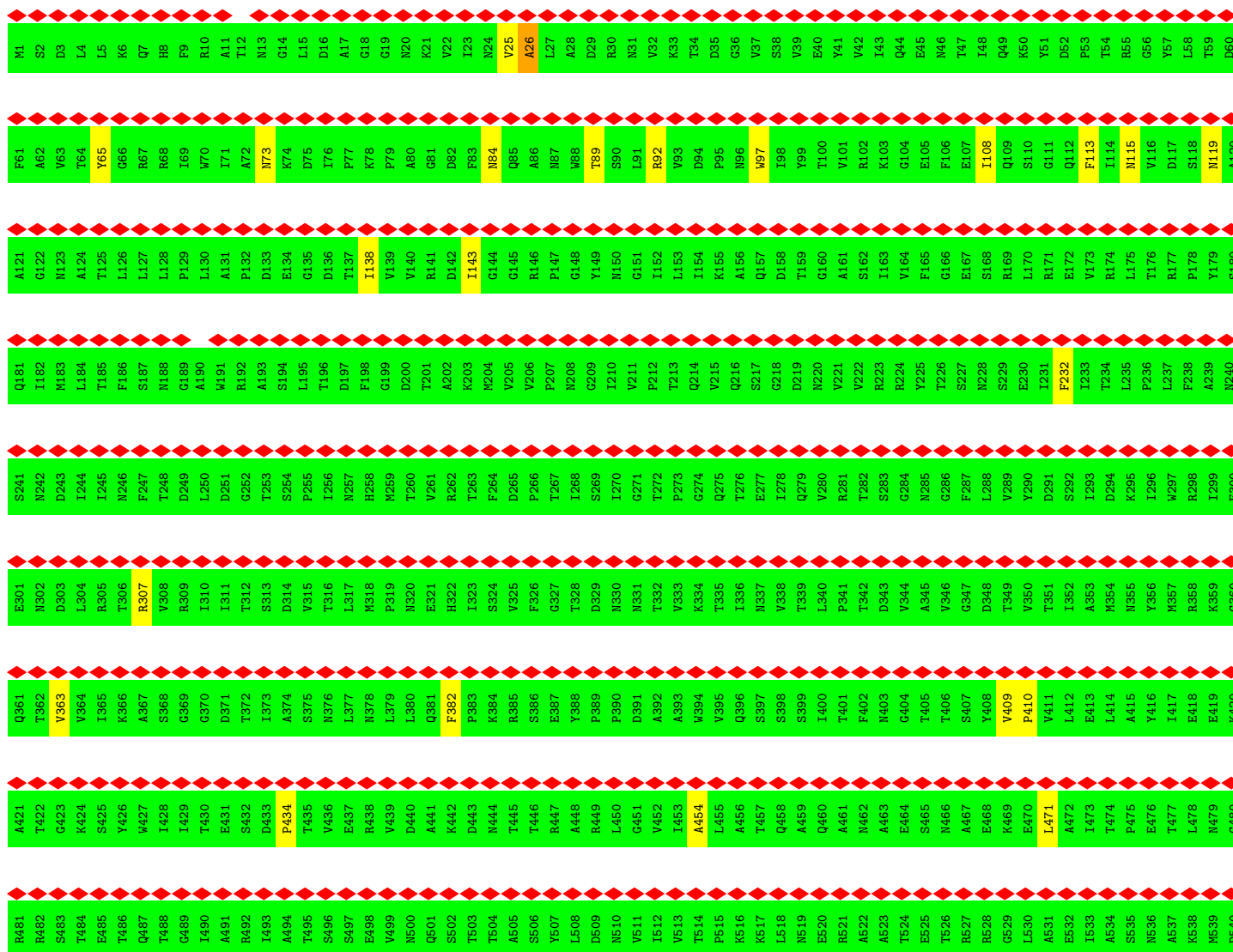


E301	Q361	S241	Q181	A121	F61	M1
	T362	N242	I182	G122	A62	S2
	V363	D243	M183	D243	W63	D3
	V364	I244	L184	A124	T64	I4
	I365	I245	L185	T125	V65	L5
	K366	N246	F186	L126	G66	K6
	A367	F247	S187	L127	B67	Q7
	S368	T248	N188	L128	R68	H8
	G369	R249	G189	P129	T69	F9
	G370	L250	A190	L130	W70	R10
E311	D371	D251	W191	A131	I71	A11
	T372	G252	R192	P132	A72	T12
	I373	T253	A193	D133	W73	N13
	A374	S254	S194	E134	K74	G14
	S375	P255	L195	G135	D75	L15
	N376	I256	T196	D136	T76	D16
	L377	N257	D197	T137	P77	A17
	M318	H258	F198	I138	K78	G18
	L379	M259	G199	V139	P79	G19
	L380	T260	D200	V140	A80	N20
E321	Q381	V261	T201	R141	C81	K21
	H322	R262	A202	D142	D82	V22
	I323	T263	K203	I143	F83	T23
	S324	F264	W204	G144	N84	N24
	R385	V265	V205	G145	K85	V25
	F386	P266	V206	R146	A86	A26
	E387	T267	P207	P147	N87	L27
	L388	I268	N208	G148	W88	A28
	R389	D269	G209	Y149	T89	D29
	P390	L270	T210	N150	S90	R30
E331	D391	G271	V211	G151	L91	N31
	A392	T272	P212	I152	R92	V32
	A393	T273	T213	L153	W93	K33
	K394	G274	Q214	I154	D94	T34
	V395	Q275	V215	K155	P95	D35
	Q396	T276	Q216	A156	N96	D36
	S397	E277	S217	Q157	W97	G36
	S398	L278	G218	D158	I98	V37
	S399	Q279	D219	T159	Y99	S38
	I400	V280	N220	G160	T100	V39
E341	T401	R281	V221	A161	V101	E40
	F402	T282	V222	S162	R102	V42
	M403	S283	R223	I163	K103	I43
	G404	G284	R224	V164	G104	Q44
	T405	N285	Y225	F165	E105	E45
	T406	G286	T226	G166	F106	M46
	S407	F287	S227	E167	E107	T47
	Y408	L288	N228	S168	I108	I48
	V409	T289	S229	R169	Q109	V49
	P410	Y290	E230	L170	S110	K50
E351	V411	D291	I231	R171	G111	V51
	L412	S292	F232	E172	Q112	D52
	A413	I293	T233	V173	F113	P53
	L414	D294	T234	R174	I114	T54
	A415	K295	L235	L175	N115	R55
	Y416	I296	P236	T176	V116	G56
	I417	W297	L237	R177	D117	V57
	E418	R298	F238	P178	S118	L58
	E419	K299	I239	A179	A119	T59
	A420	T290	W400	S180	L120	V60

- Molecule 1: Long tail fiber proximal subunit



- Molecule 1: Long tail fiber proximal subunit



GLY	PRO	PRO	GLY	ASP	ALA	LYS	TYR	GLY	ARG	THR	VAL	THR	ASP	THR	P601
LEU	VAL	VAL	LYS	ARG	LYS	LEU	ARG	GLY	ASP	ALA	LEU	ALA	LYS	GLN	G602
ILE	ILE	ILE	PHE	ARG	GLY	ARG	ALA	GLU	TYR	THR	THR	THR	ALA	GLU	T603
TRP	ALA	TRP	ALA	TYR	MET	TYR	GLY	GLY	ARG	HIS	GLY	THR	THR	ASN	L604
PRO	MET	MET	GLY	GLY	GLY	ILE	ILE	ILE	ARG	ALA	ASP	GLY	GLY	ALA	R605
ASP	THR	THR	VAL	VAL	THR	VAL	VAL	VAL	ASP	LYS	GLY	LYS	ILE	GLY	E606
PRO	ARG	PRO	TRP	ILE	PRO	ILE	VAL	ASP	ILE	THR	THR	THR	ILE	THR	T607
ARG	TRP	TRP	ILE	VAL	TRP	VAL	VAL	VAL	ASP	ALA	GLN	ALA	GLN	VAL	G608
GLN	MET	ARG	THR	LYS	THR	GLY	LYS	VAL	ALA	THR	GLY	ASN	VAL	THR	LYS
ASN	ARG	THR	ASN	LYS	PRO	PRO	ALA	PRO	THR	GLY	ASN	THR	THR	LYS	T610
THR	ILE	ILE	TYR	GLY	ILE	GLN	GLY	THR	ILE	ALA	ASP	SER	SER	ALA	V611
LEU	LYS	LYS	ASN	ASP	ASN	THR	ASP	THR	SER	THR	THR	THR	THR	VAL	P612
PHE	PRO	PRO	PRO	ALA	ALA	ALA	GLY	GLY	GLY	LEU	LEU	LEU	GLY	THR	ASN
GLU	GLU	GLU	ASN	ALA	THR	SER	ALA	ALA	ALA	LEU	LEU	LEU	THR	PRO	Q613
TRP	LEU	ASN	THR	THR	ALA	ALA	TRP	SER	TRP	ALA	SER	THR	THR	LYS	S614
VAL	VAL	PRO	VAL	GLY	VAL	VAL	GLY	VAL	THR	THR	THR	THR	ILE	THR	L615
ASP	LYS	SER	PHE	ASN	GLY	GLY	THR	THR	PHE	TYR	LEU	THR	GLY	LEU	T616
TRP	PHE	THR	THR	GLY	GLY	GLY	THR	THR	ASN	GLN	LEU	ASP	ASP	ASN	G617
VAL	ASP	VAL	ASP	VAL	VAL	VAL	ASN	ASN	THR	ALA	GLY	LEU	ARG	THR	TRP
ASN	THR	THR	THR	THR	THR	THR	ASN	THR	SER	GLY	ALA	TRP	THR	ALA	LEU
LYS	THR	THR	GLY	GLY	GLY	GLY	VAL	VAL	PHE	GLN	VAL	HIS	ASP	THR	ALA
THR	TYR	TYR	VAL	ALA	LYS	ASN	SER	SER	ASN	VAL	ASP	ASP	TYR	ASN	S661
LEU	GLY	GLY	ILE	ILE	GLY	GLY	ILE	ILE	SER	ALA	LYS	THR	THR	ASP	S662
LYS	GLY	GLY	THR	THR	THR	THR	THR	THR	ASN	THR	GLY	THR	THR	VAL	R663
PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L664
GLU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G665
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V666
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T667
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	Q668
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L669
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V670
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	K671
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T672
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G673
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V674
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	A675
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	P676
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	N677
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T678
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T679
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	H680
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL
THR	THR	THR	THR	THR	THR	THR	THR	THR							

- Molecule 1: Long tail fiber proximal subunit



A121	G122	M123	A124	L126	L127	L128	P129	L130	A131	P132	D133	E134	G135	D136	T137	I138	V139	F140	R141	D142	I143	G144	G145	R146	P147	G148	Y149	M150	G151	I152	L153	I154	K155	A156	Q157	D158	T159	G160	A161	S162	L163	V164	F165	G166	E167	S168	R169	L170	R171	E172	V173	R174	L175	T176	R177	P178	Y179	H180	
F61	A62	V63	T64	Y65	G66	R67	R68	I69	W70	A71	A72	N73	K74	D75	I76	P77	K78	P79	A80	G81	D82	F83	N84	Q85	A86	N87	W88	T89	S90	L91	R92	V93	D94	P95	N96	W97	I98	Y99	T100	A101	R102	K103	G104	E105	F106	E107	I108	Q109	S110	G111	Q112	F113	I114	N115	V116	D117	S118	N119	A120
M1	S2	D3	L4	L5	K6	Q7	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	I43	Q44	E45	N46	T47	I48	Q49	K50	Y51	D52	P53	T54	R55	G56	Y57	L58	T59	D60

LYS	TYR	GLY	ARG	THR	VAL	THR	ASP	THR	THR	P601	A541	R481	A421	Q361	E301	S241	Q181
GLY	ALA	ASN	ASP	PRO	ARG	ALA	LYS	THR	GLN	K602	G542	R482	T422	T362	N302	N242	I182
LEU	ARG	ALA	GLY	THR	LEU	ALA	THR	THR	THR	T603	T543	S483	G423	V363	N303	D243	M183
GLY	THR	VAL	THR	TYR	THR	GLY	ASN	ASN	VAL	L604	D544	T484	K424	V364	L304	I244	L184
GLY	GLY	GLY	GLY	ARG	ALA	ALA	GLY	GLY	ALA	R605	D545	E485	S425	I365	R305	I245	T185
THR	ARG	THR	THR	ARG	ASP	GLY	GLY	GLY	GLY	E606	F546	T486	Y426	K366	T306	N246	F186
ILE	ASP	THR	ILE	ASP	THR	THR	ILE	THR	THR	Y607	T547	Q487	Y427	A367	R307	F247	S187
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	K608	I548	T488	I428	S368	V308	T248	N188
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	A609	V549	G489	I429	G369	R309	D249	G189
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	T610	T550	T490	T430	G370	I310	L250	A190
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	V611	P551	A491	E431	D371	I311	D251	W191
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	N612	K552	R492	S432	T372	T312	G252	R192
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	Q613	K553	I493	D433	I373	S313	T253	A193
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	S614	L554	A494	P434	A374	D314	S254	S194
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G615	L555	T495	T435	S375	V315	P255	L195
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	T616	V556	S496	V436	N376	T316	I256	T196
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V617	R557	S497	E437	L377	L317	N257	F197
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	TRP	T558	E498	R438	N378	M318	H258	D198
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	T559	V499	V439	L379	P319	M259	G199
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	S560	N500	D440	L380	N320	T260	D200
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D561	Q501	A441	Q381	E321	V261	T201
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	THR	S562	S502	K442	F382	H322	R262	A202
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R563	T503	D443	P383	I323	T263	K203
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L564	T504	M444	K384	S324	F264	M204
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G565	A505	T445	R385	V325	D265	V205
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLY	V566	S506	T446	S386	F326	P266	V206
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	THR	V567	Y507	R447	E387	G327	T267	P207
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ALA	Q568	L508	A448	P388	T328	I268	N208
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L569	D509	R449	P389	D329	S269	G209
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	V570	N510	L450	P390	N330	I270	I210
LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ILE	K571	V511	G451	D391	N331	G271	V211
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	PRO	T572	I512	V452	A392	T332	T272	P212
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G573	V513	I453	A393	V333	P273	T213
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL	G574	T514	A454	W394	K334	G274	Q214
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	A575	P515	L455	V395	T335	Q275	V215
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	P576	K516	A456	Q396	I336	Q216	V216
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ALA	N577	K517	T457	S397	I337	T276	Q217
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	T578	L518	Q458	S398	S217	E277	S217
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T579	N519	A459	S399	V338	G218	G218
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS	N580	E520	Q460	I400	T339	D219	D219
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LYS	D581	R521	A461	T401	L340	V220	N220
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL	R582	A522	M462	F402	P341	R281	V221
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ALA	S583	A523	A463	N403	D343	S283	R223
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ASP	S584	T524	E464	G404	V344	G284	R224
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	GLY	E585	T525	S465	T405	A345	N285	Y225
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ALA	G586	T526	M466	T406	V346	G286	T226
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	GLY	T587	R527	A467	S407	G347	F287	S227
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	G588	R528	E468	Y408	L288	L288	N228
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ILE	I589	G529	K469	Y409	T349	V289	S229
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ILE	F590	L530	E470	P410	V290	E230	E230
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D591	A531	L471	V411	D291	I231	I231
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	H592	E532	A472	L412	S292	F232	F232
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S593	I533	I473	E413	I293	I233	I233
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D594	A534	T474	L414	D294	T234	T234
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	Y595	S535	F475	A415	N355	L235	L235
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	K596	N536	E476	Y416	I296	P236	P236
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	N597	A537	T477	I417	W297	L237	L237
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	A598	K538	L478	E418	R298	F238	F238
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V599	M539	M479	E419	A239	A239	A239
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T600	D540	G480	K420	G360	N240	N240

GLY
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- Molecule 1: Long tail fiber proximal subunit



F61	A62	V63	T64	Y65	G66	R67	R68	I69	W70	I71	A72	N73	K74	D75	I76	P77	K78	P79	A80	G81	D82	F83	N84	Q85	A86	N87	W88	T89	S90	L91	R92	V93	D94	P95	N96	W97	I98	Y99	T100	V101	R102	K103	G104	E105	F106	E107	I108	Q109	S110	G111	Q112	F113	I114	N115	V116	D117	S118	N119	A120
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A121	G122	N123	A124	T125	L126	L127	L128	P129	L130	A131	P132	D133	E134	G135	D136	T137	L138	V139	V140	R141	D142	I143	G144	G145	R146	P147	G148	Y149	N150	G151	I152	L153	I154	K155	A156	Q157	D158	T159	G160	A161	G162	S162	I163	V164	F165	G166	E167	S168	R169	L170	R171	E172	V173	R174	L175	T176	R177	P178	Y179	S180
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Q181	I182	M183	L184	T185	F186	S187	N188	G189	A190	W191	R192	A193	S194	L195	T196	D197	F198	G199	D200	T201	A202	K203	M204	V205	V206	P207	N208	G209	I210	V211	P212	T213	Q214	V215	Q216	S217	G218	D219	N220	V221	V222	R223	R224	Y225	T226	S227	N228	S229	E230	I231	F232	I233	T234	L235	P236	T237	F238	A239	N240
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S241	N242	D243	I244	I245	N246	F247	T248	D249	L250	D251	G252	T253	S254	P255	I256	N257	H258	M259	T260	V261	R262	T263	T264	D265	P266	T267	I268	S269	I270	G271	T272	P273	G274	Q275	T276	E277	I278	Q279	V280	R281	T282	S283	G284	N285	G286	F287	L288	V289	Y290	D291	S292	I293	D294	K295	I296	W297	R298	I299	F300
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E301	E302	E303	E304	E305	E306	E307	E308	E309	E310	E311	E312	E313	E314	E315	E316	E317	E318	E319	E320	E321	E322	E323	E324	E325	E326	E327	E328	E329	E330	E331	E332	E333	E334	E335	E336	E337	E338	E339	E340	E341	E342	E343	E344	E345	E346	E347	E348	E349	E350	E351	E352	E353	E354	E355	E356	E357	E358	E359	E360
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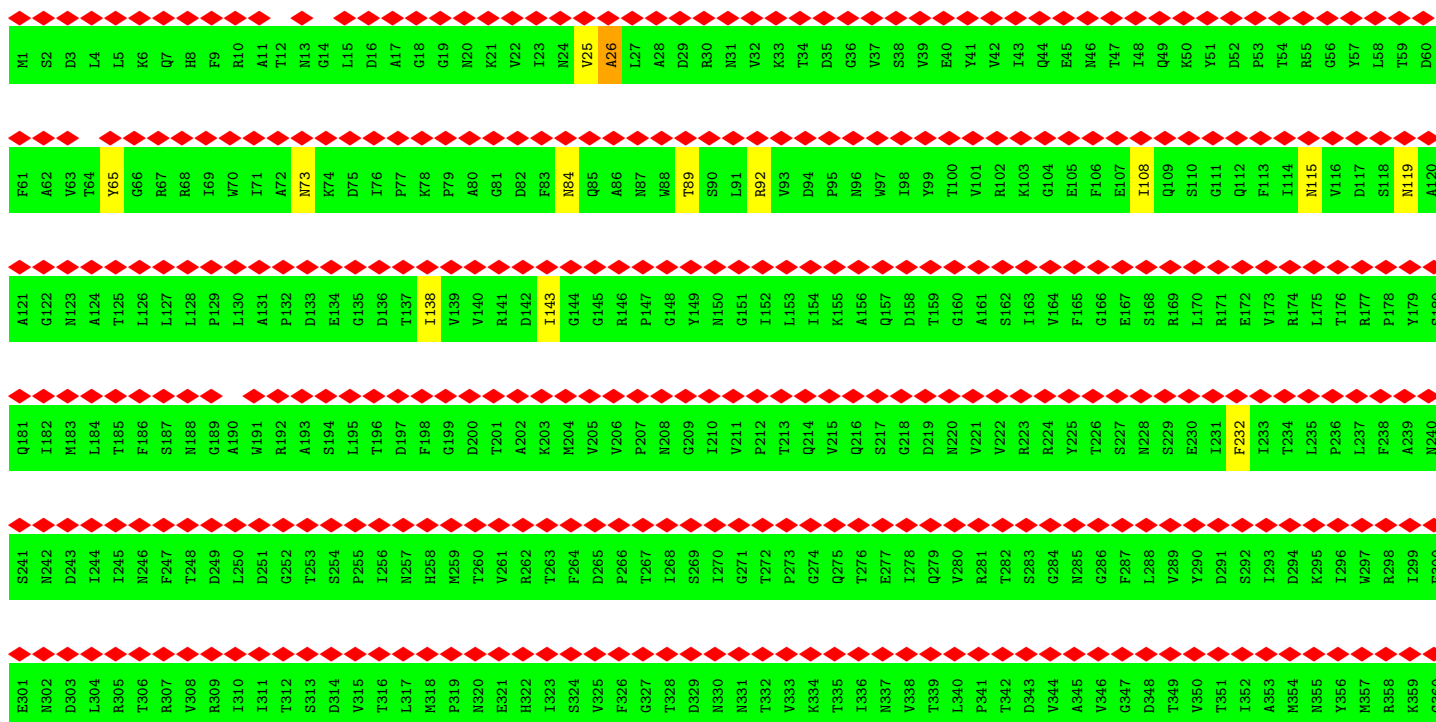
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P601	K602	T603	L604	R605	E606	Y607	K608	A609	T610	V611	N612	Q613	S614	G615	L616	V617	TRP	LEU	ALA	THR	ASP	SER	GLU	VAL	ARG	ASN	GLY	THR	PRO	ALA	SER	SER	ASN	ILE	PRO	THR	VAL	THR	PRO	GLU	ALA	LEU	HIS	LYS	LYS	VAL	ALA	THR	ASP	GLY	ALA	ILE	GLY	LEU	ILE	GLN	ILE	ALA
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THR	GLN	THR	GLU	VAL	ASN	ALA	GLY	GLY	VAL	THR	ASN	LYS	ALA	VAL	THR	PRO	THR	LYS	THR	LEU	ASN	ASP	ARG	THR	ALA	ASN	ASP	ARG	THR	GLY	ILE	ALA	ALA	ARG	ALA	PHE	ALA	THR	PRO	GLY	GLY	ALA	GLN	GLY	GLU	PHE	GLU	GLU	ALA	GLY	THR	THR	SER	SER	THR	THR	VAL	VAL	VAL	ASN	PRO	LYS	LEU	LEU	PHE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

- Molecule 1: Long tail fiber proximal subunit



- Molecule 1: Long tail fiber proximal subunit



VAL	ARG	ALA	ASP	THR	THR	GLN	THR	P601	A541	R481	A421	Q361	E301	S241	Q181	A121	F61	M1
LEU	LEU	ALA	PHE	THR	THR	GLN	THR	K602	G642	R482	T422	T362	N302	N242	I182	G122	A62	S2
THR	THR	ALA	ALA	THR	THR	GLU	THR	T603	T642	S483	G423	V363	D303	D243	M183	N123	V63	D3
GLY	GLY	THR	THR	THR	THR	ASN	VAL	L604	D644	T484	K424	V364	L304	I244	L184	A124	T64	L4
ASP	ASP	ALA	GLY	THR	THR	ASN	ALA	R605	D545	E485	S425	K365	R305	I245	T185	L125	V65	L5
GLY	GLY	THR	ARG	THR	THR	GLY	GLY	E606	F646	T486	Y426	K366	T306	T246	F186	L126	G66	K6
THR	THR	THR	ILE	THR	THR	GLY	GLY	Y607	T547	Q487	W427	A367	R307	F247	S187	L127	R67	Q7
TRP	TRP	VAL	VAL	THR	THR	VAL	VAL	K608	I648	T488	I428	S368	V308	T248	H188	L128	H68	H8
GLN	GLN	THR	VAL	THR	THR	ASN	THR	A609	V549	G489	I429	G369	R309	D249	G189	L129	I69	F9
ASN	ASN	THR	THR	THR	THR	ASN	THR	T610	T550	I490	T430	G370	I310	L250	A190	L130	W70	R10
ASP	ASP	ALA	SER	THR	THR	ALA	ALA	V611	P561	A491	E431	D371	I311	D251	W191	A131	I71	A11
THR	THR	THR	VAL	THR	THR	VAL	VAL	N612	K652	R492	S432	T372	T312	G252	R192	P132	A72	T12
GLY	GLY	THR	THR	THR	THR	PRO	THR	Q613	K563	I493	D433	I373	S313	T253	A193	D133	M73	N13
LEU	LEU	THR	LEU	THR	THR	LYS	THR	P614	L564	A494	P434	A374	D314	S254	S194	E134	K74	G14
ILE	ILE	THR	ILE	THR	THR	GLN	THR	G615	L565	T495	T435	S375	V315	P255	L195	G135	D75	L15
THR	THR	THR	THR	THR	THR	LEU	LEU	I616	Y656	S496	V436	N376	T316	I256	T196	I76	I76	D16
PRO	PRO	ALA	THR	THR	THR	ASN	ASP	V617	R567	S497	E437	L377	L317	N257	D197	T137	P77	A17
ASP	ASP	THR	ASN	THR	THR	ARG	ASP	TRP	T568	E498	R438	L378	M318	H258	F198	K78	K78	G18
GLY	GLY	THR	LEU	THR	THR	ARG	THR	ALA	V569	V499	V439	L379	P319	M259	G199	V139	P79	G19
ASP	ASP	ALA	THR	THR	THR	ALA	ALA	ALA	S660	N500	D440	L380	N320	T260	D200	V140	A80	N20
THR	THR	THR	HIS	THR	THR	THR	THR	ASP	D561	Q501	A441	Q381	H322	R262	T201	R141	G81	K21
TYR	TYR	GLN	THR	THR	THR	ASN	THR	ASP	S662	Q502	K442	F382	I323	T263	A202	D142	D82	V22
ALA	ALA	VAL	THR	THR	THR	ILE	THR	VAL	R563	T503	D443	P383	T323	T264	K203	I143	F83	I23
LEU	LEU	THR	ASN	THR	THR	GLY	THR	VAL	L564	T504	N444	K384	S324	F264	M204	G144	N84	N24
ILE	ILE	THR	ILE	THR	THR	GLY	THR	ASN	G565	A505	T445	R385	V325	D265	V205	G145	Q85	V25
GLN	GLN	THR	GLN	THR	THR	ILE	THR	ASN	V566	S506	T446	S386	F326	P266	V206	R146	A86	A26
ASP	ASP	THR	THR	THR	THR	ALA	THR	GLY	V567	Y507	R447	E387	G327	T267	P207	P147	N87	L27
SER	SER	THR	THR	THR	THR	ALA	THR	ALA	Q668	L508	A448	Y388	T328	I268	N208	G148	W88	A28
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THR	THR	THR	THR	THR	THR	ALA	THR	ILE	T572	I512	V462	A392	T332	T272	P212	I152	R92	V32
LEU	LEU	THR	THR	THR	THR	GLN	THR	PRO	G573	V513	I463	A393	V333	P273	T213	L153	D93	V32
HIS	HIS	THR	THR	THR	THR	THR	THR	VAL	G574	T514	A464	W394	K334	G274	Q214	I154	Y93	K33
THR	THR	THR	THR	THR	THR	PHE	THR	VAL	A575	P515	I465	V395	T335	Q275	V215	K155	P95	T34
LEU	LEU	THR	ALA	THR	THR	GLU	THR	THR	P576	K516	A466	Q396	I336	T276	Q216	K156	N96	D35
PRO	PRO	VAL	THR	THR	THR	ALA	THR	ALA	V577	K517	T467	S397	I337	E277	S217	A156	G36	G36
GLY	GLY	THR	ALA	THR	THR	ALA	THR	ALA	T578	L518	Q468	S398	V338	I278	G218	D158	W97	V37
LEU	LEU	THR	THR	THR	THR	SER	THR	THR	V579	N519	A469	S399	V339	Q279	D219	T159	I98	S38
LYS	LYS	THR	VAL	THR	THR	THR	THR	LYS	N680	E520	Q460	T400	T339	Q279	D219	T159	Y99	V39
ARG	ARG	THR	ARG	THR	THR	THR	THR	LYS	D681	R521	A461	T401	P341	R281	N220	G160	T100	E40
THR	THR	THR	GLY	THR	THR	VAL	THR	VAL	R682	A522	N462	F402	T342	T282	V222	G161	V101	E41
ALA	ALA	THR	THR	THR	THR	ALA	THR	ALA	S683	A523	A463	N403	D343	S283	R223	S162	R102	V42
ASP	ASP	THR	ASP	THR	THR	ASN	THR	THR	T524	E464	V344	G404	R224	G284	R224	I163	K103	I43
LYS	LYS	THR	LYS	THR	THR	LYS	THR	GLY	E525	S465	A345	T405	V346	N285	Y225	F165	G104	O44
LEU	LEU	THR	LEU	THR	THR	LEU	THR	ALA	V526	N466	V346	T406	V346	G286	T226	F166	E105	E45
ILE	ILE	THR	ILE	THR	THR	ILE	THR	GLY	T527	A467	G347	T407	G347	F287	S227	E107	F106	E46
GLY	GLY	THR	GLY	THR	THR	GLY	THR	THR	R528	E468	D348	Y408	D348	V289	N228	E167	E107	T47
LEU	LEU	THR	THR	THR	THR	ILE	THR	LEU	G529	K469	T349	V409	T349	V289	R169	S168	I108	I48
THR	THR	THR	THR	THR	THR	GLN	THR	THR	F590	E470	V350	P410	V350	Y290	S229	G169	Q109	Q49
ALA	ALA	THR	THR	THR	THR	ILE	THR	ALA	V411	T351	I352	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	L412	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	E413	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	L414	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	E415	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	Y416	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	I417	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	E418	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	E419	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	K420	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	G460	I352	F232	S292	D291	D291	I231	R171	G111	K50
THR	THR	THR	THR	THR	THR	THR	THR	THR	D540	I352	F232	S292	D291	D291	I231	R171	G111	K50
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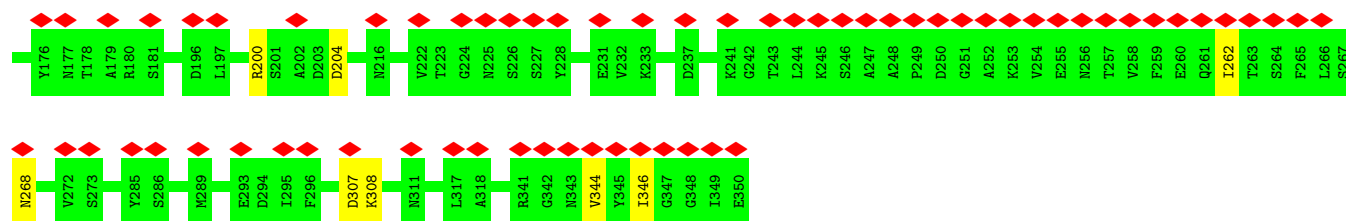
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- Molecule 1: Long tail fiber proximal subunit

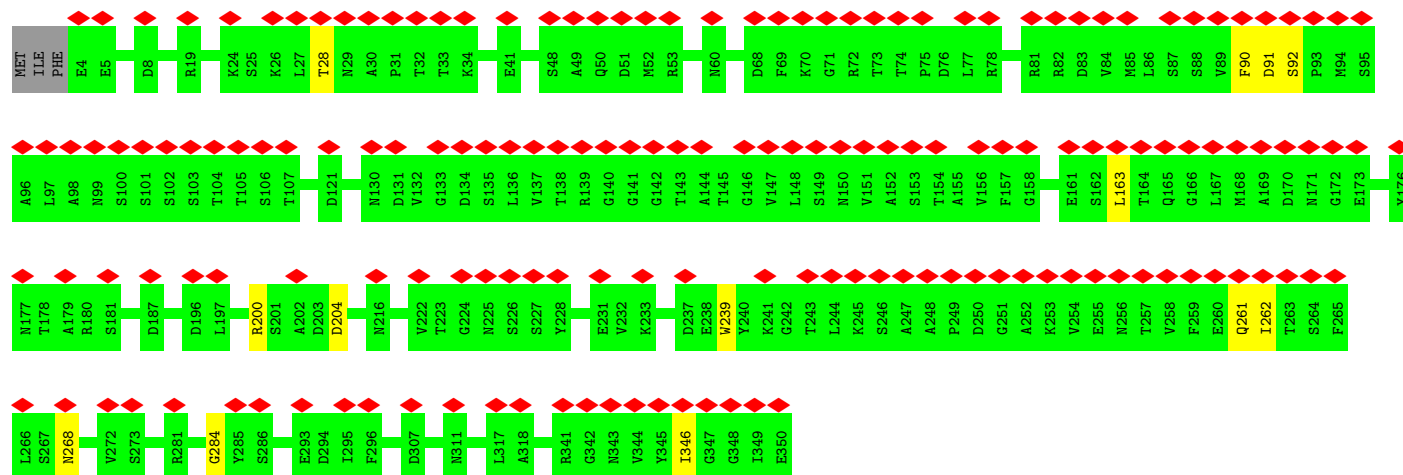


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G423	G424	V364	V364	T362	N302	N242	I182	G122	A62
S425	A426	T366	T366	T362	D303	D243	M183	G123	V63
W427	Y426	A367	T306	T366	L304	I244	L184	A124	T64
L428	L428	S368	V308	T366	T306	N246	F186	L126	G66
L429	T430	G369	V308	T366	R307	F247	N188	L128	R68
T430	E431	G370	T310	T366	T310	D249	G189	P129	T69
S432	D433	D371	T311	T366	T311	L250	A190	L130	W70
D433	A374	T372	T312	T366	T312	D251	W191	A131	I71
P434	S375	T373	T313	T366	T313	G252	R192	P132	A72
T435	S376	A374	D314	T366	T314	T253	A193	D133	N73
V436	N376	S375	V315	T366	V315	S254	S194	E134	K74
E437	L377	N376	T316	T366	T316	T256	T196	G135	D75
R438	N378	L377	L317	T366	L317	N257	D197	D136	I76
V439	N378	N378	N318	T366	N318	H258	F198	T137	P77
D440	P319	L380	P319	T366	P319	M259	G199	I138	K78
D440	L380	N320	N320	T366	N320	T260	D200	V140	P79
K441	Q381	E321	E321	T366	E321	V261	T201	R141	A80
K442	F382	H322	H322	T366	H322	R262	A202	D142	G81
D443	T383	T323	T323	T366	T323	K263	M204	T143	D82
N444	K384	S324	S324	T366	S324	T264	K204	G144	F83
T445	R385	V325	V325	T366	V325	D265	V205	G145	N84
T446	S386	F326	F326	T366	F326	P266	V206	R146	Q85
R447	E387	G327	G327	T366	G327	T267	P207	P147	A86
A448	X388	T328	T328	T366	T328	I268	N208	G148	N87
R449	P389	D329	D329	T366	P389	S269	G209	Y149	W88
L450	P390	N330	N330	T366	N330	I270	I210	N150	T89
G451	D391	N331	N331	T366	D391	G271	V211	G151	S90
A452	A392	T332	T332	T366	T332	T272	P212	I152	R91
I453	A393	V333	V333	T366	V333	P273	T213	L153	A92
A454	W394	K334	K334	T366	K334	G274	Q214	I154	V93
L455	V395	T335	T335	T366	T335	Q275	V215	K155	D94
A456	Q396	T336	T336	T366	T336	T276	Q216	A156	P95
T457	S397	N337	N337	T366	N337	E277	S217	Q157	N96
Q458	S398	V338	V338	T366	V338	I278	G218	D158	V97
A459	S399	T339	T339	T366	T339	Q279	D219	T159	I98
Q460	T400	L340	L340	T366	L340	V280	N220	G160	V39
A461	T401	P341	P341	T366	P341	R281	V221	A161	E40
N462	F402	T342	T342	T366	T342	T282	V222	S162	Y41
A463	N403	S403	S403	T366	N403	S283	R223	I163	R102
E464	G404	V444	V444	T366	G404	G284	R224	V164	K103
S465	T405	A345	A345	T366	A345	N285	Y225	F165	G104
N466	T406	V346	V346	T366	V346	G286	T226	G166	E105
A467	S407	G347	G347	T366	S407	T287	S227	E167	F106
E468	Y408	D348	D348	T366	D348	L288	N228	S168	T47
K469	V409	T349	T349	T366	V409	V289	S229	R169	I108
E470	P410	V350	V350	T366	P410	Y290	E230	L170	Q109
L471	L471	T351	T351	T366	T351	D291	I231	R171	K50
A472	A472	L412	L412	T366	L412	S292	F232	E172	G111
I473	I473	E413	A353	T366	A353	T293	I233	V173	Q112
T474	T474	L414	K354	T366	L414	D294	T234	R174	F113
P475	P475	A415	N355	T366	N355	K296	L235	I175	I114
E476	E476	Y416	T356	T366	Y416	T296	T236	T176	M15
T477	T477	I417	N357	T366	I417	W297	L237	R177	N115
L478	L478	E418	N358	T366	E418	R298	F238	P178	D117
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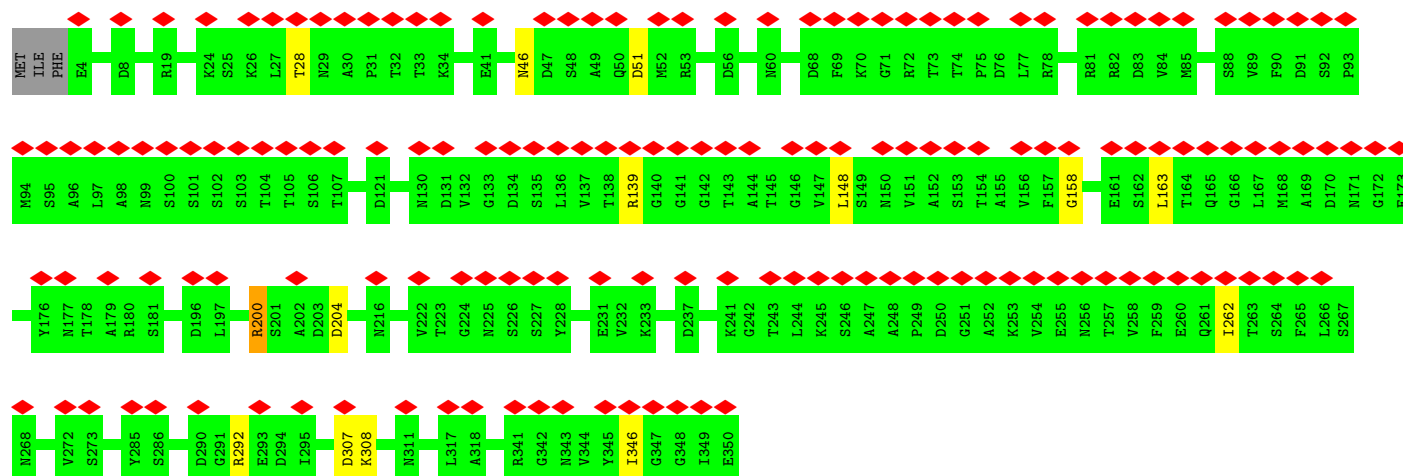




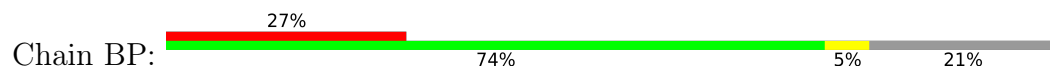
• Molecule 2: Baseplate tail tube cap

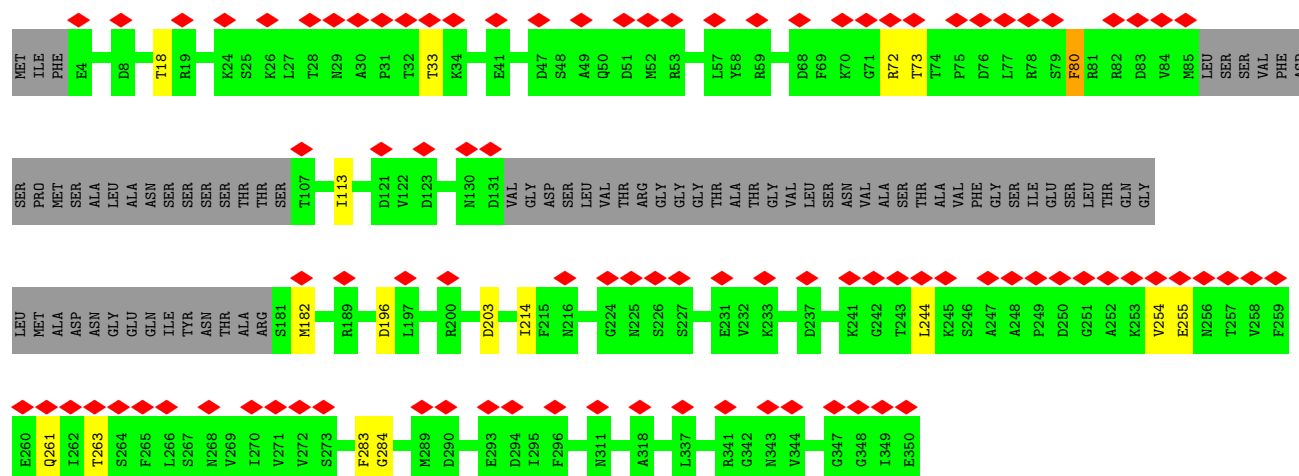


• Molecule 2: Baseplate tail tube cap

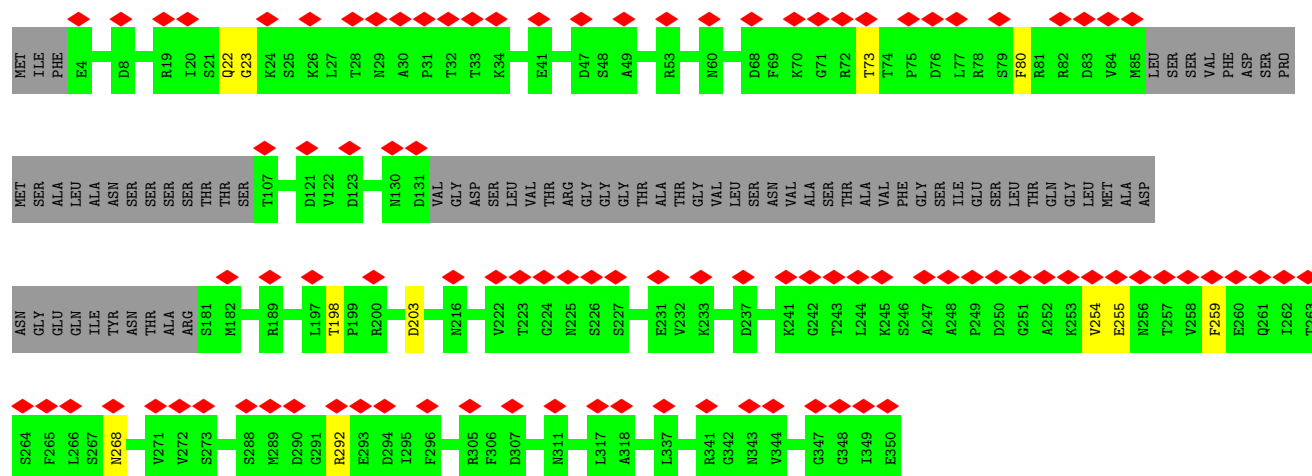
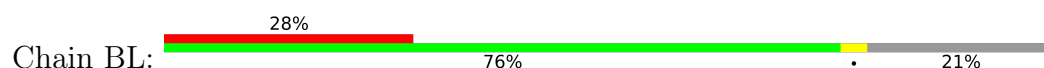


• Molecule 2: Baseplate tail tube cap

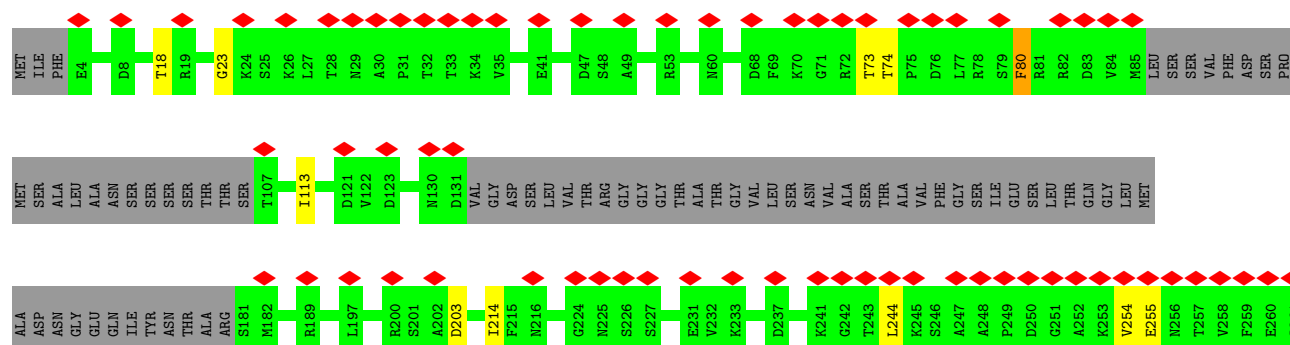
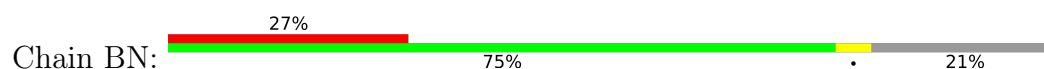


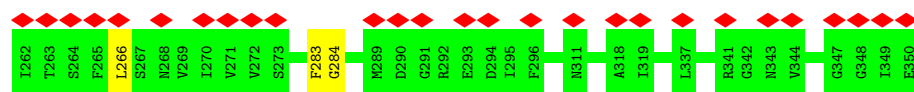


• Molecule 2: Baseplate tail tube cap

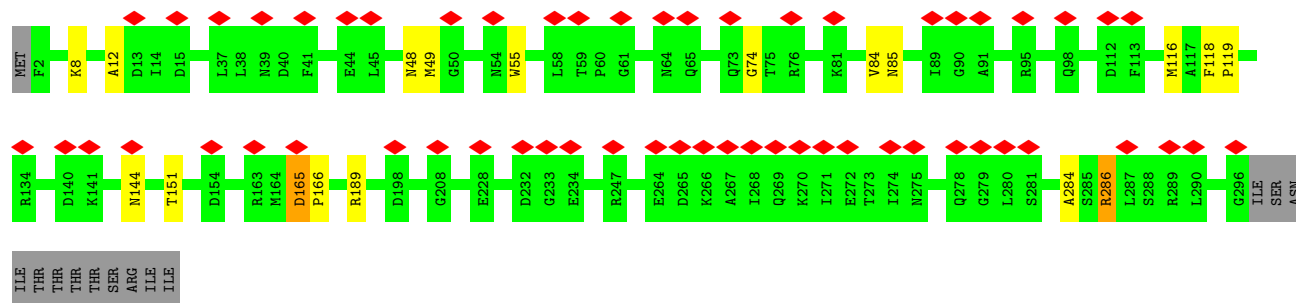
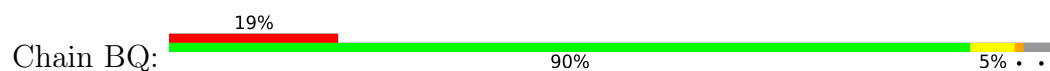


• Molecule 2: Baseplate tail tube cap

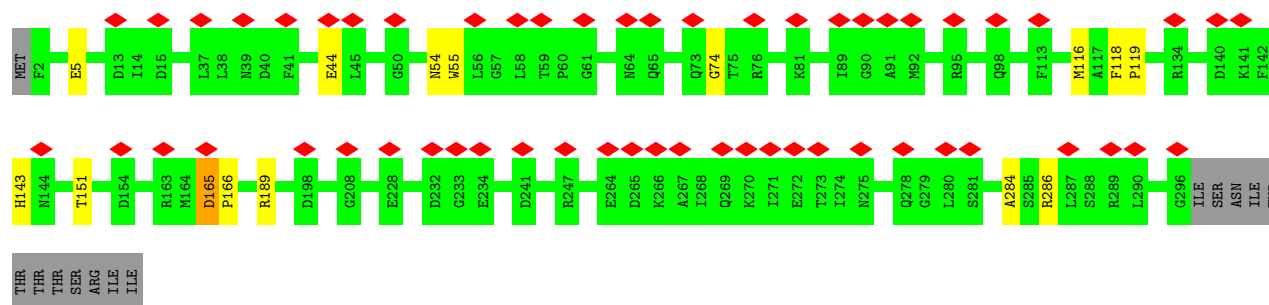
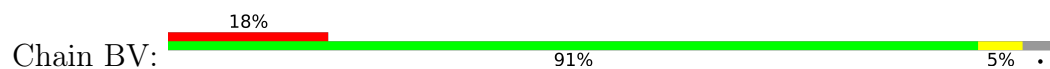




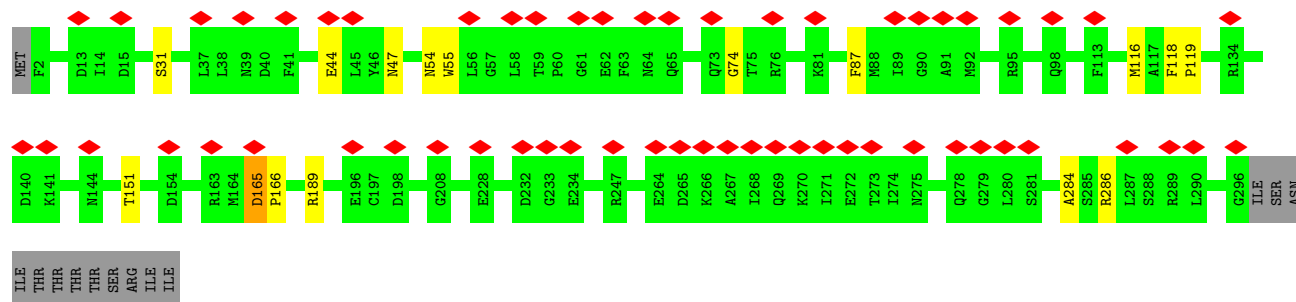
• Molecule 3: Baseplate subunit



• Molecule 3: Baseplate subunit

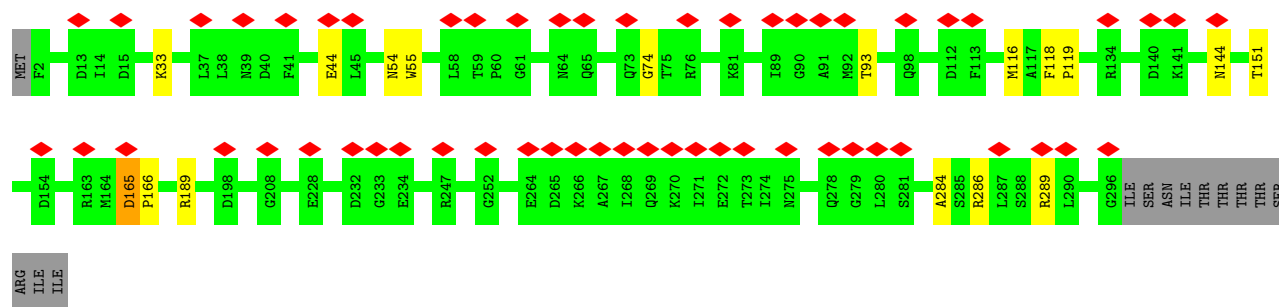


• Molecule 3: Baseplate subunit

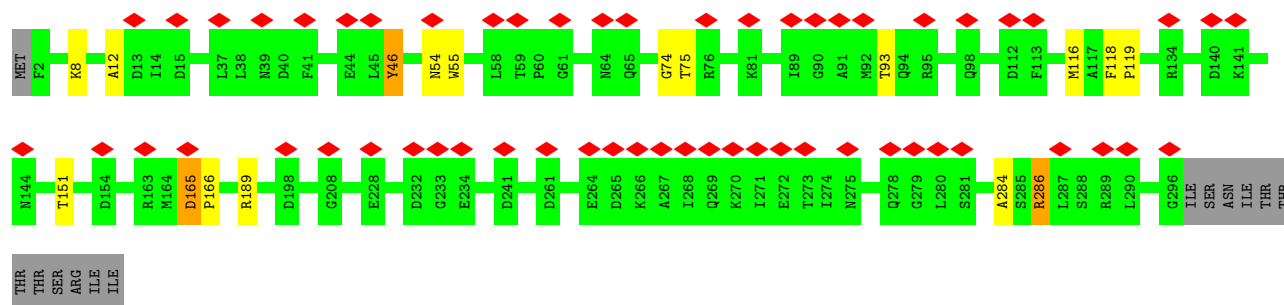


• Molecule 3: Baseplate subunit

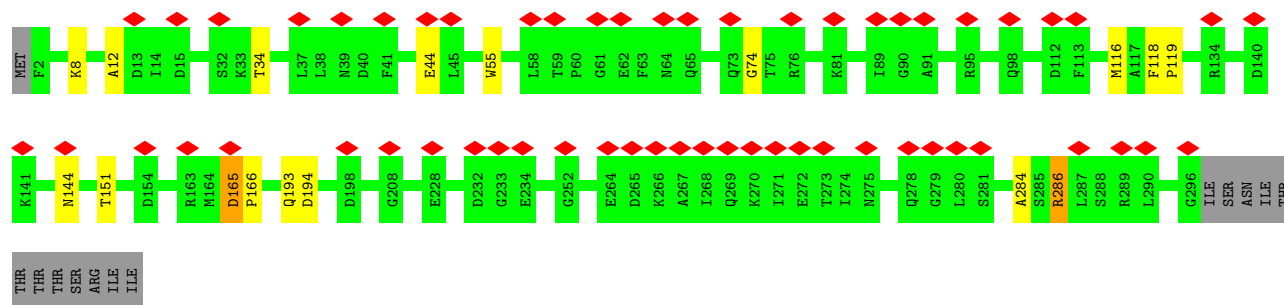




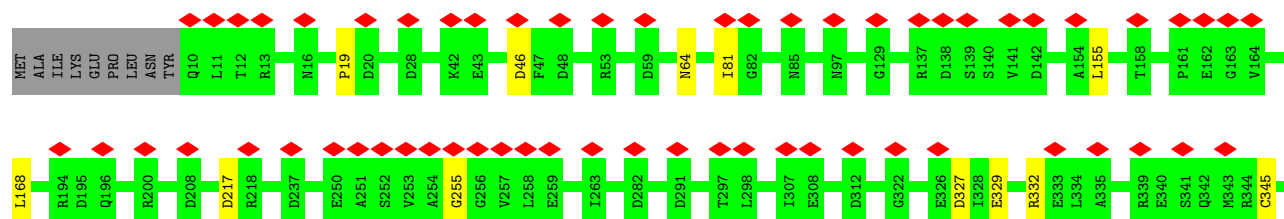
• Molecule 3: Baseplate subunit

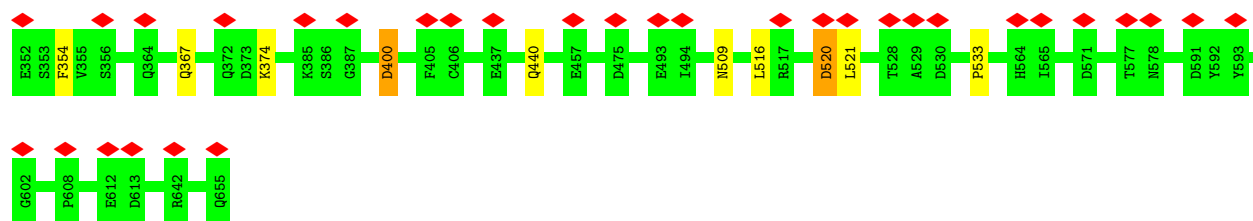


• Molecule 3: Baseplate subunit

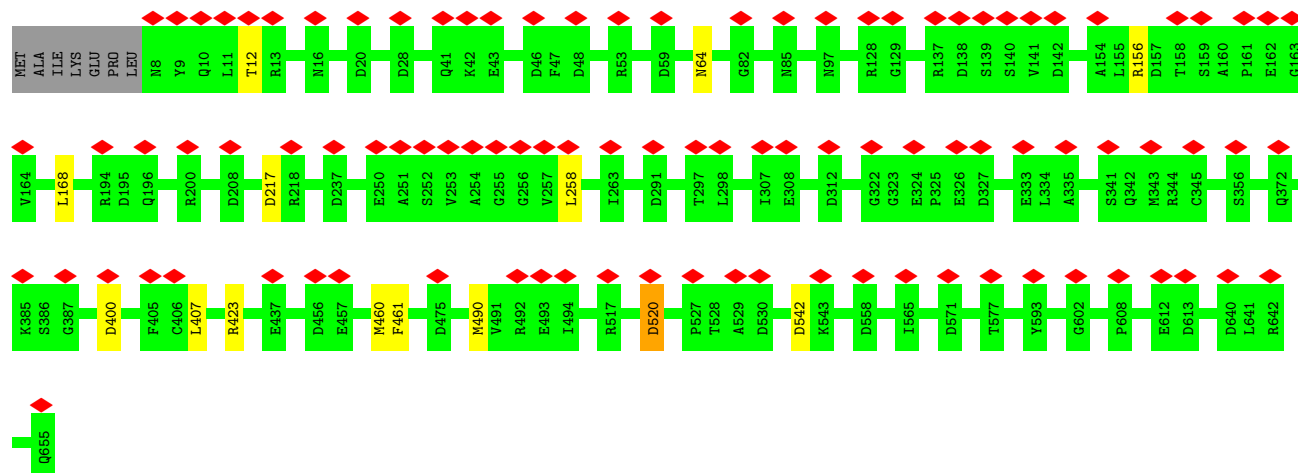


• Molecule 4: Baseplate wedge protein gp6

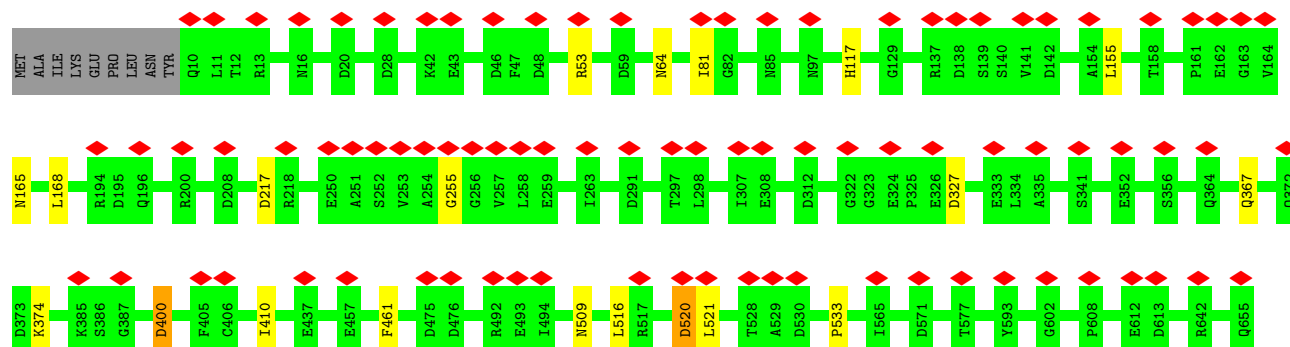




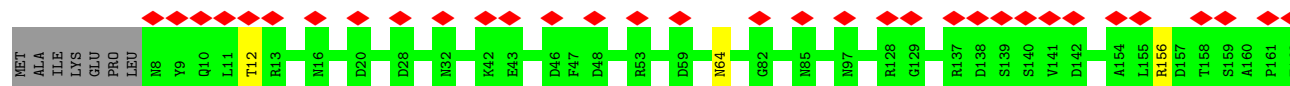
• Molecule 4: Baseplate wedge protein gp6

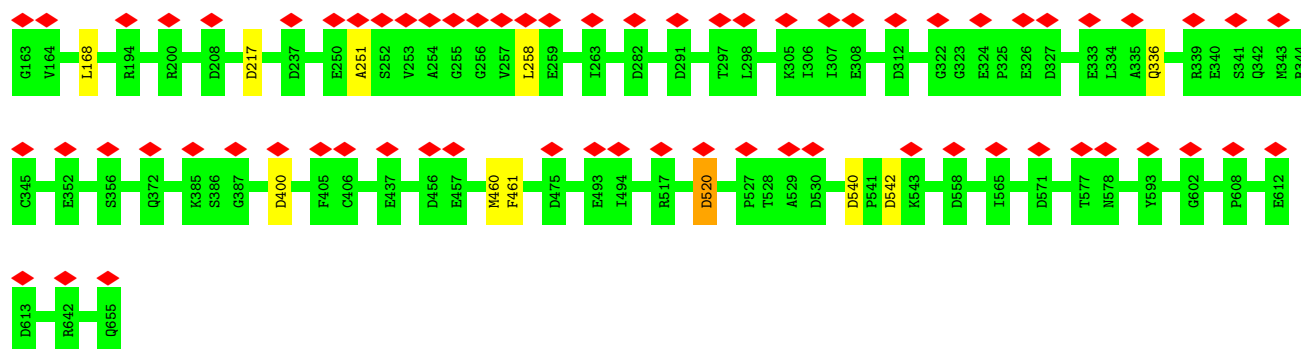


• Molecule 4: Baseplate wedge protein gp6

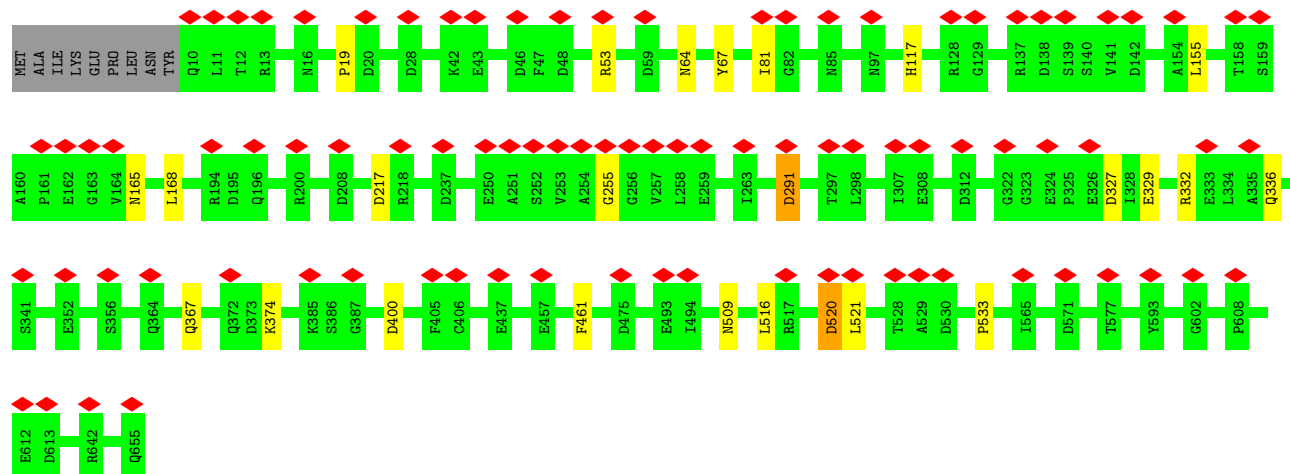


• Molecule 4: Baseplate wedge protein gp6

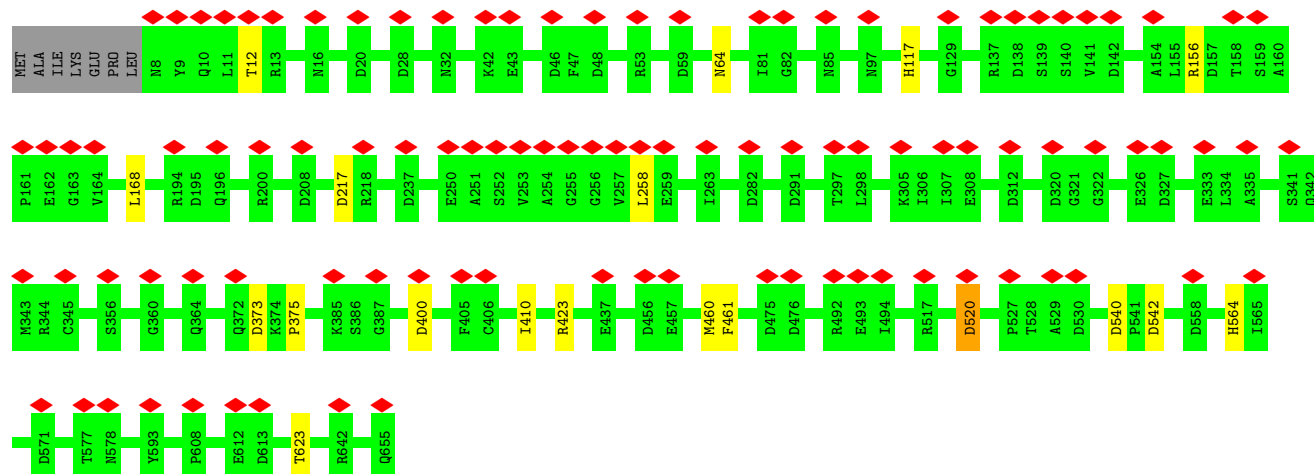




• Molecule 4: Baseplate wedge protein gp6

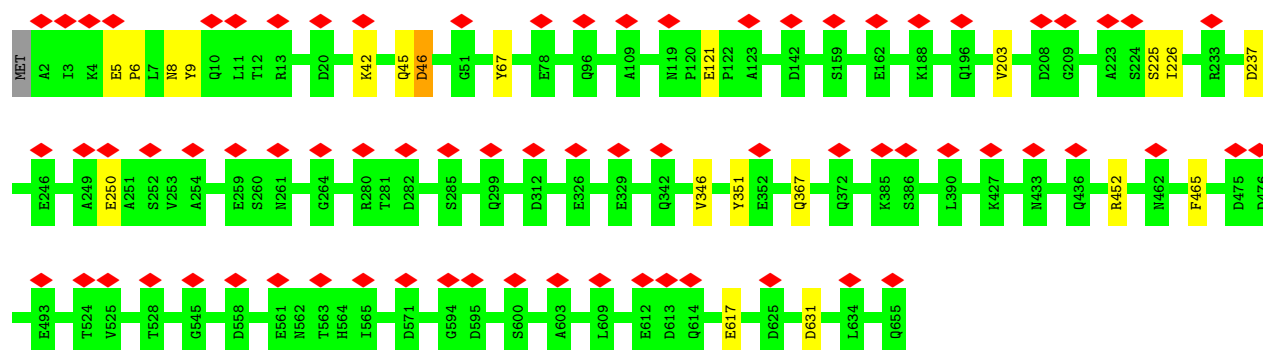


• Molecule 4: Baseplate wedge protein gp6



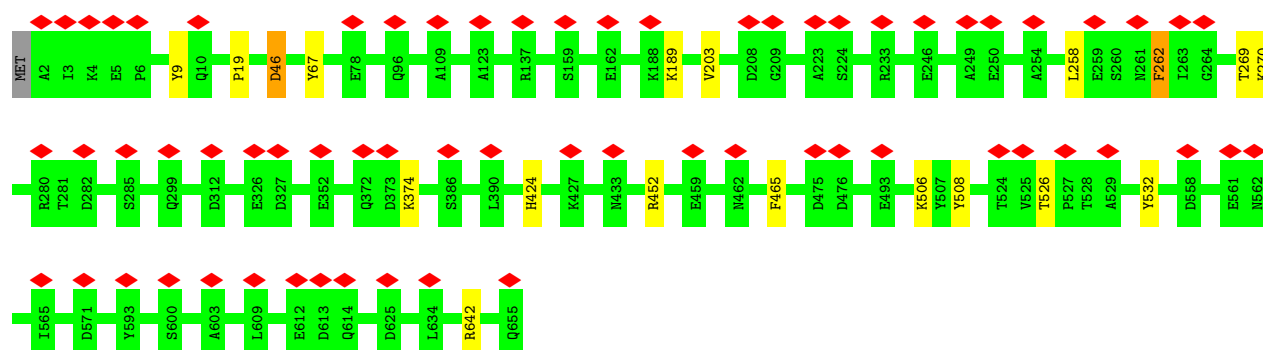
• Molecule 4: Baseplate wedge protein gp6

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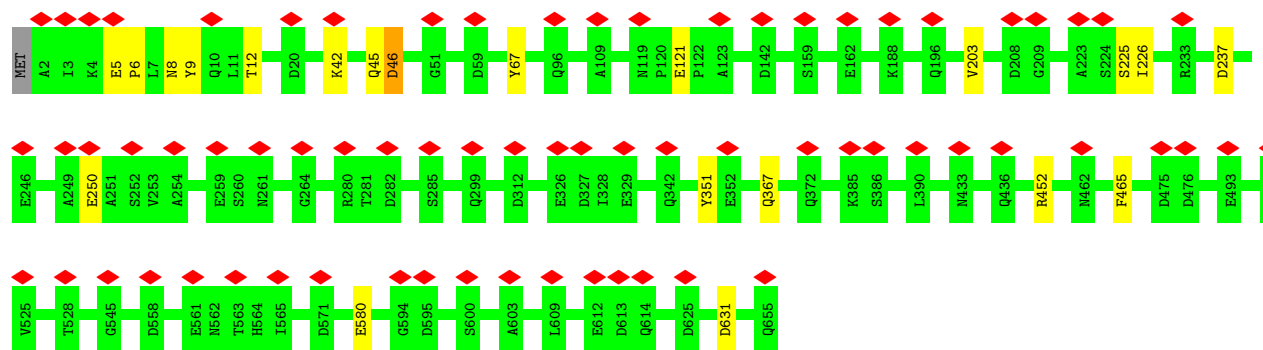
• Molecule 4: Baseplate wedge protein gp6

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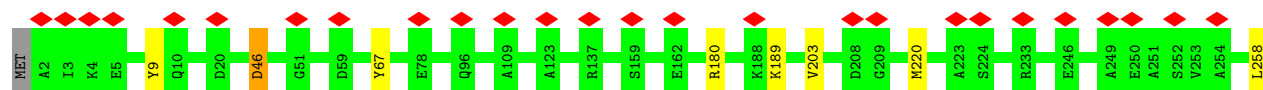
• Molecule 4: Baseplate wedge protein gp6

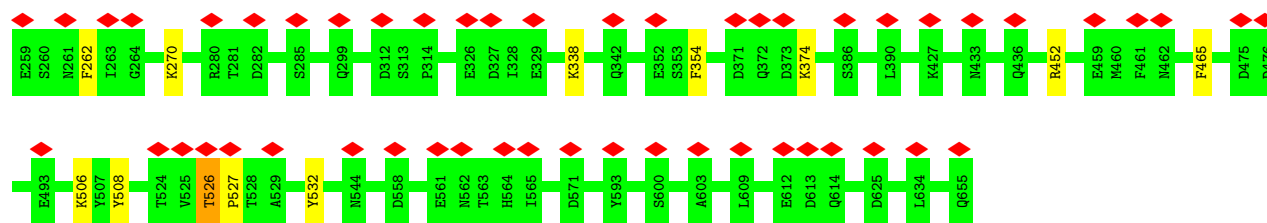
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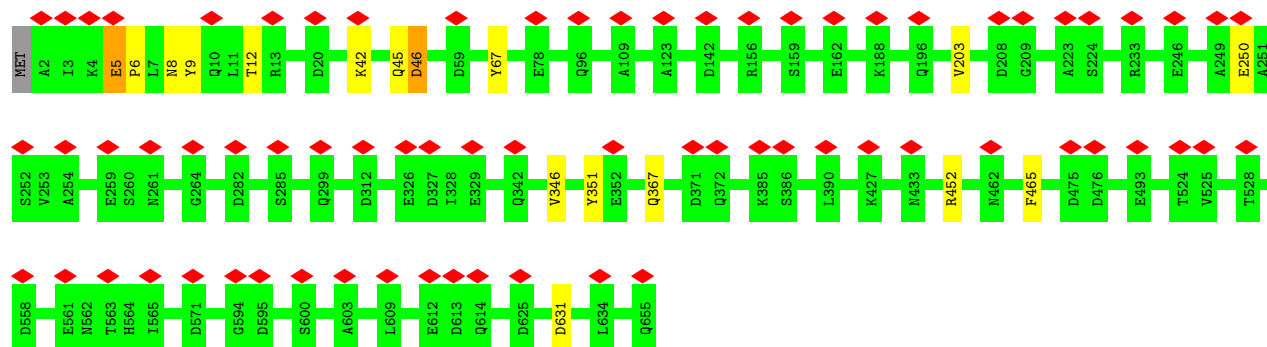
• Molecule 4: Baseplate wedge protein gp6

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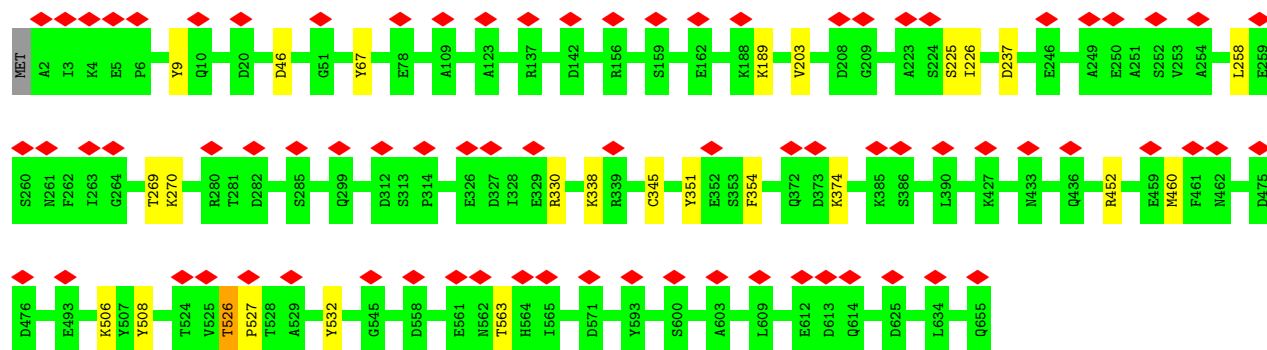




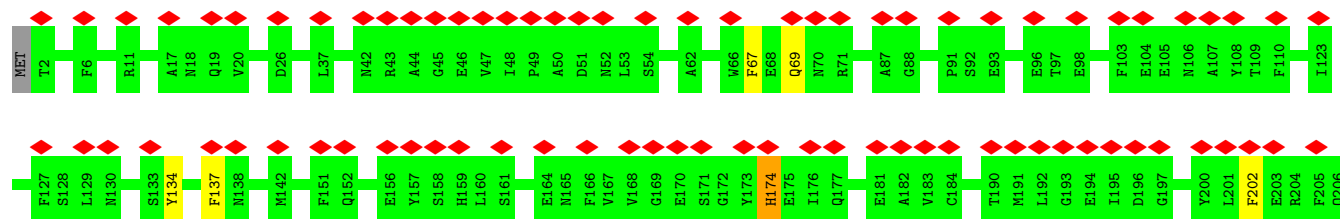
• Molecule 4: Baseplate wedge protein gp6



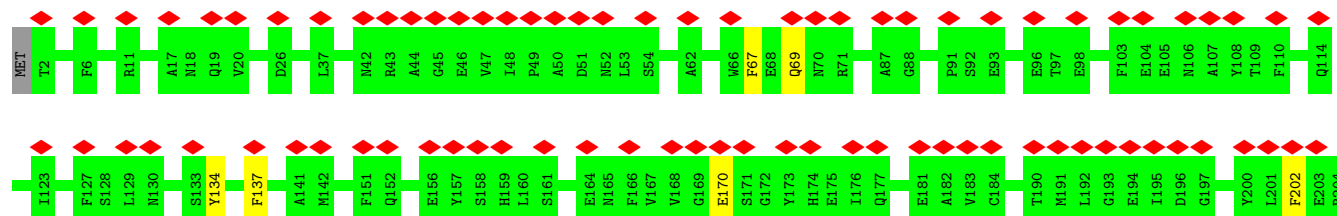
• Molecule 4: Baseplate wedge protein gp6

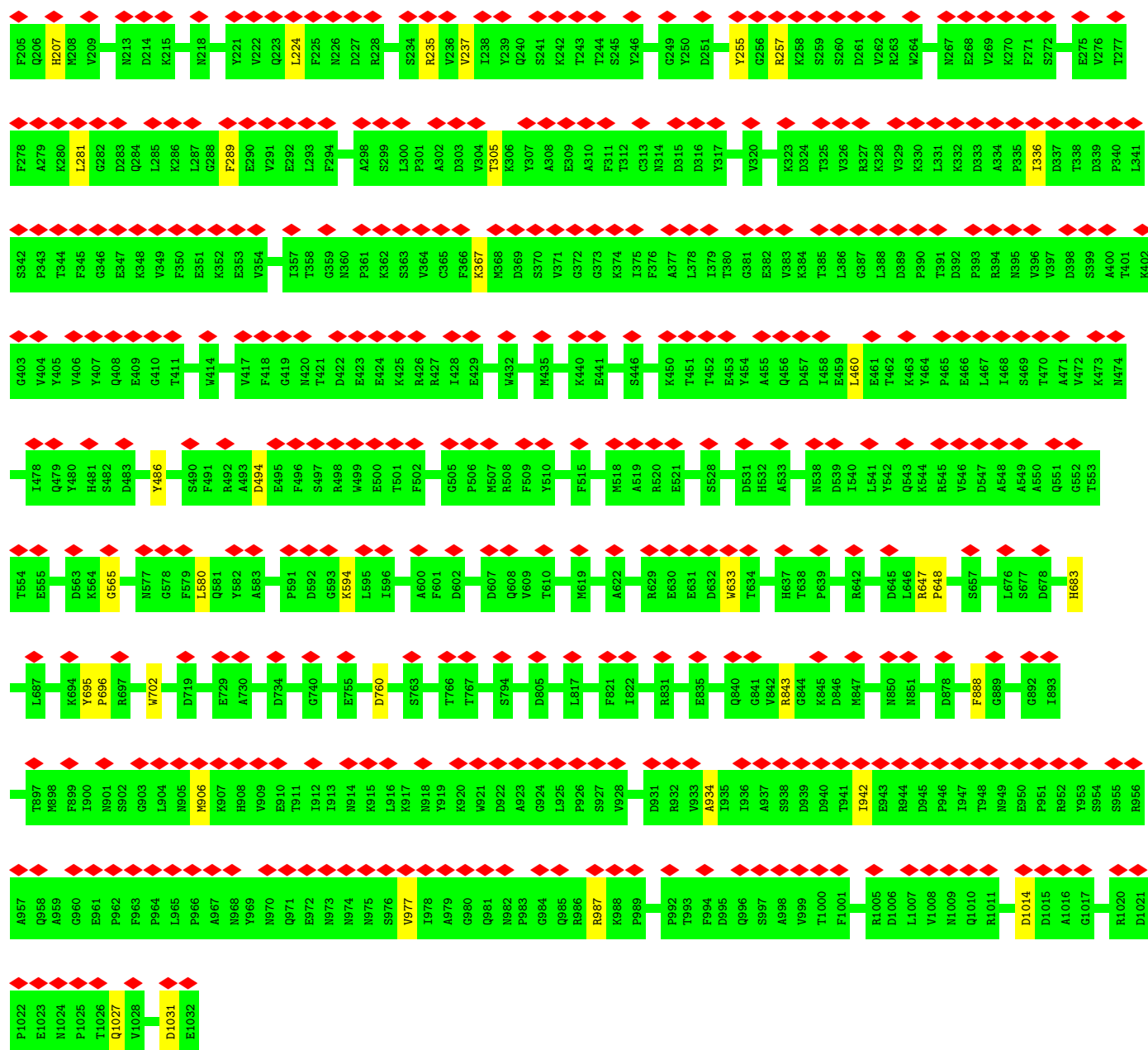


• Molecule 5: Baseplate wedge protein gp7



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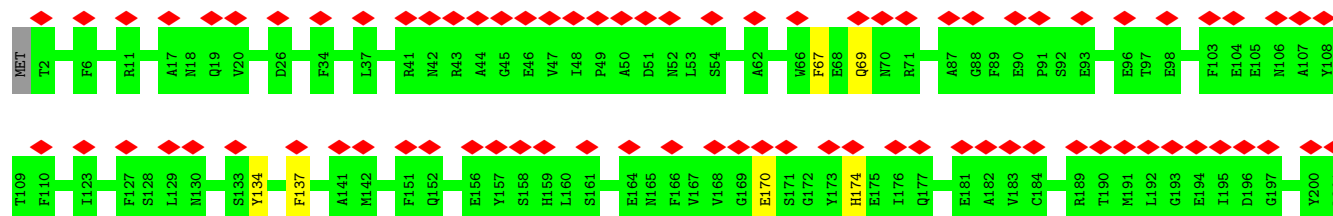


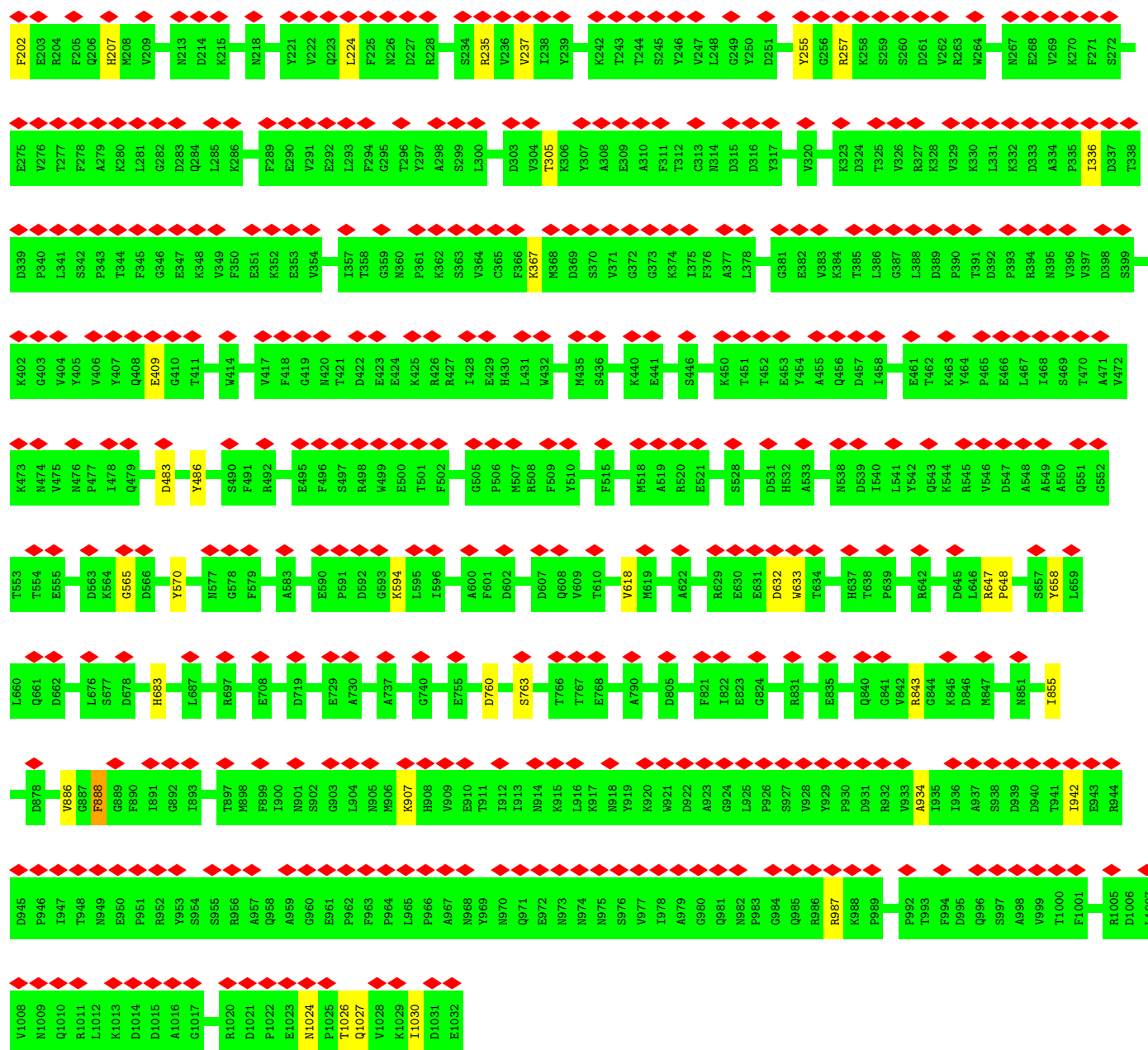


• Molecule 5: Baseplate wedge protein gp7

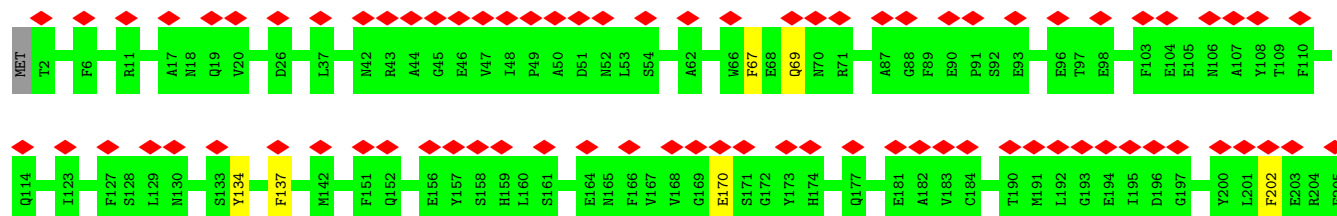


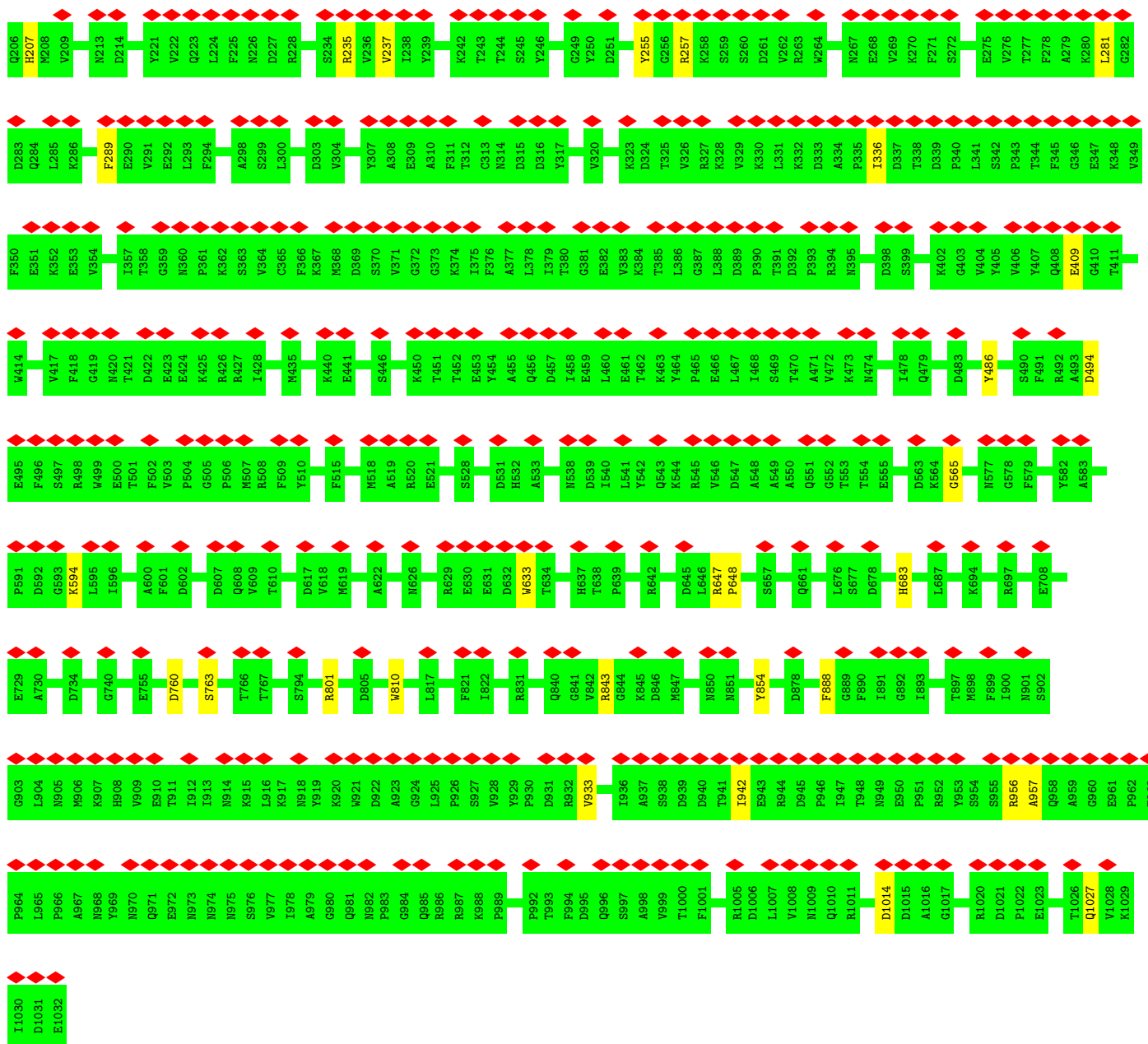
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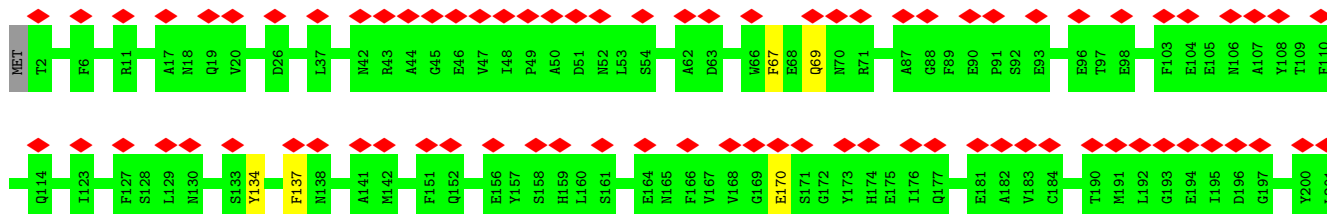


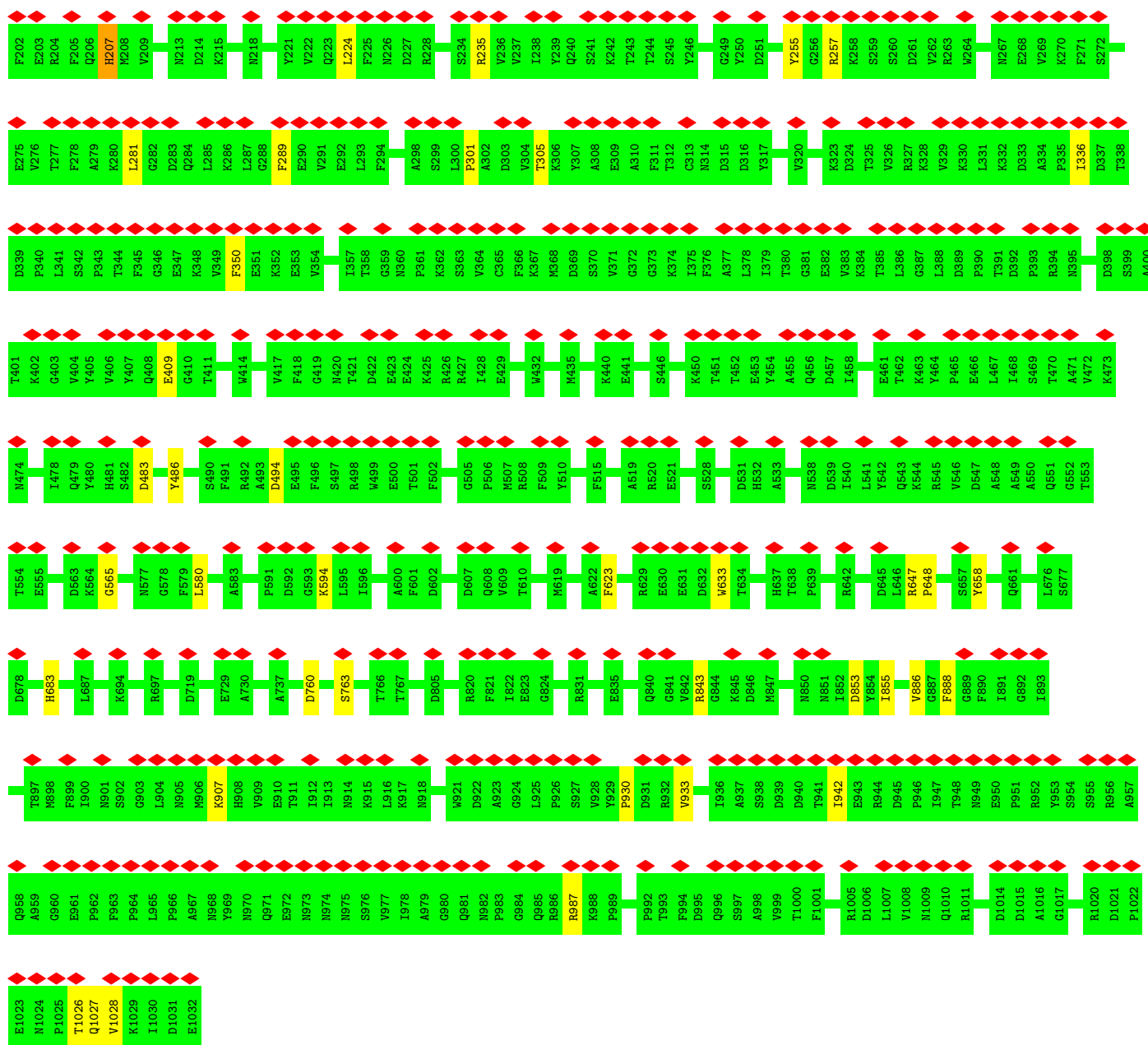
• Molecule 5: Baseplate wedge protein gp7





• Molecule 5: Baseplate wedge protein gp7

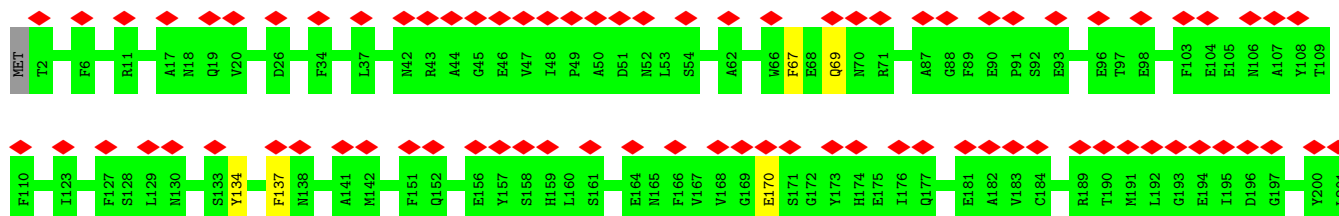


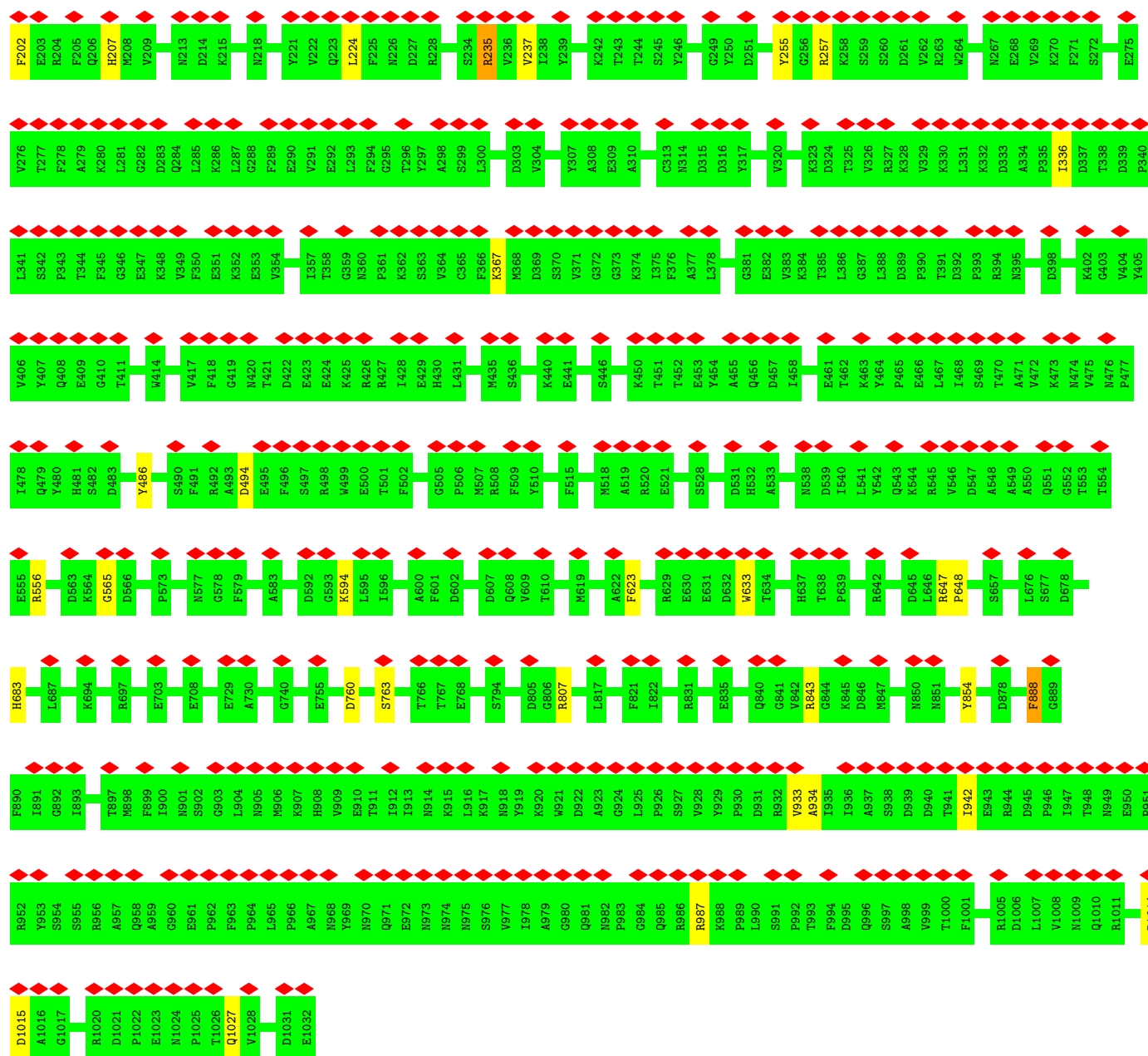


• Molecule 5: Baseplate wedge protein gp7

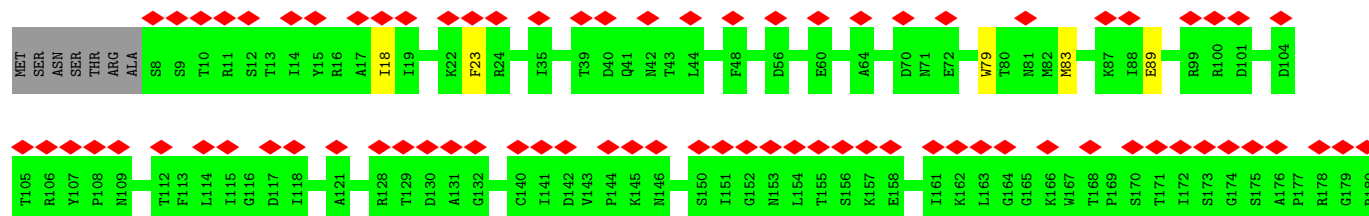
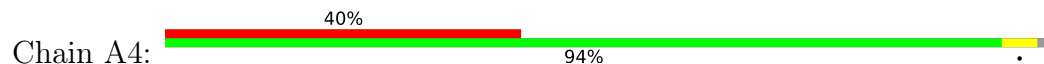


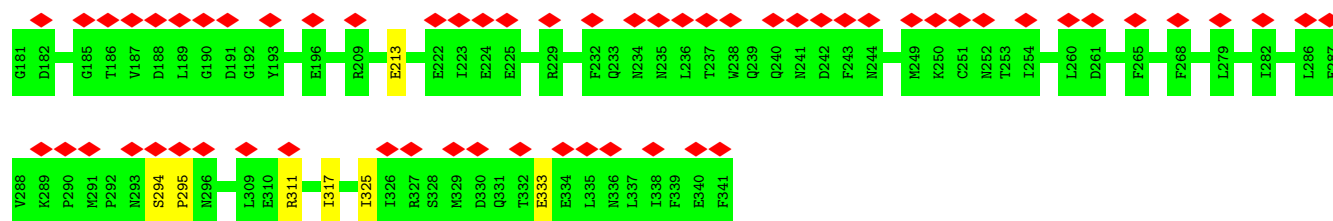
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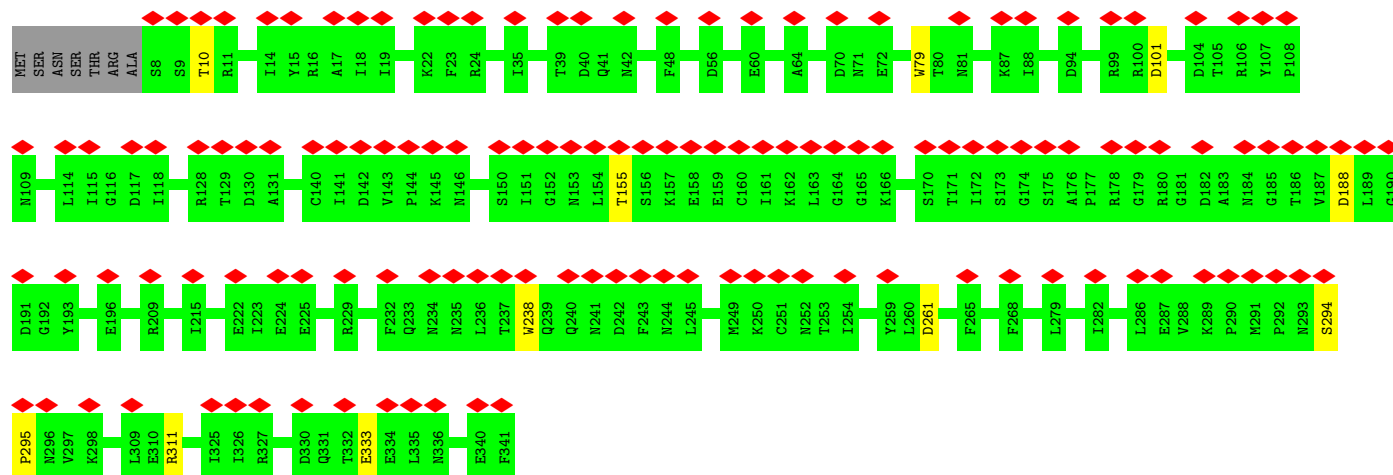
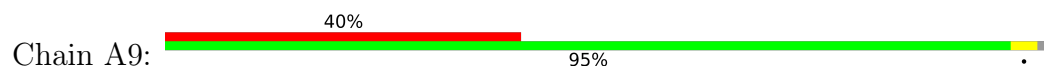


• Molecule 6: Baseplate wedge subunit

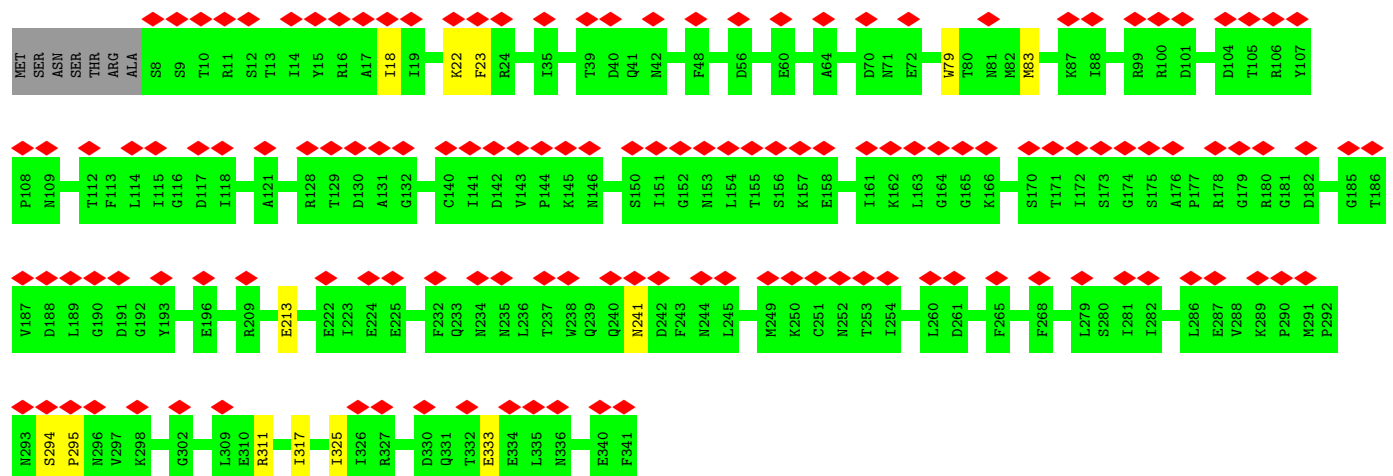
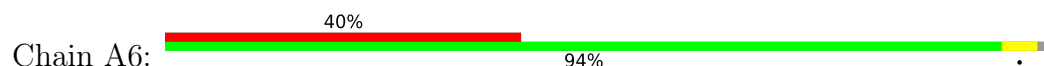




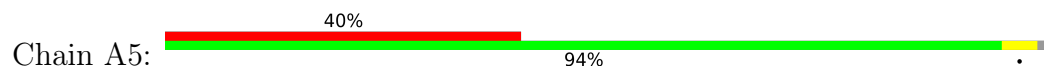
• Molecule 6: Baseplate wedge subunit

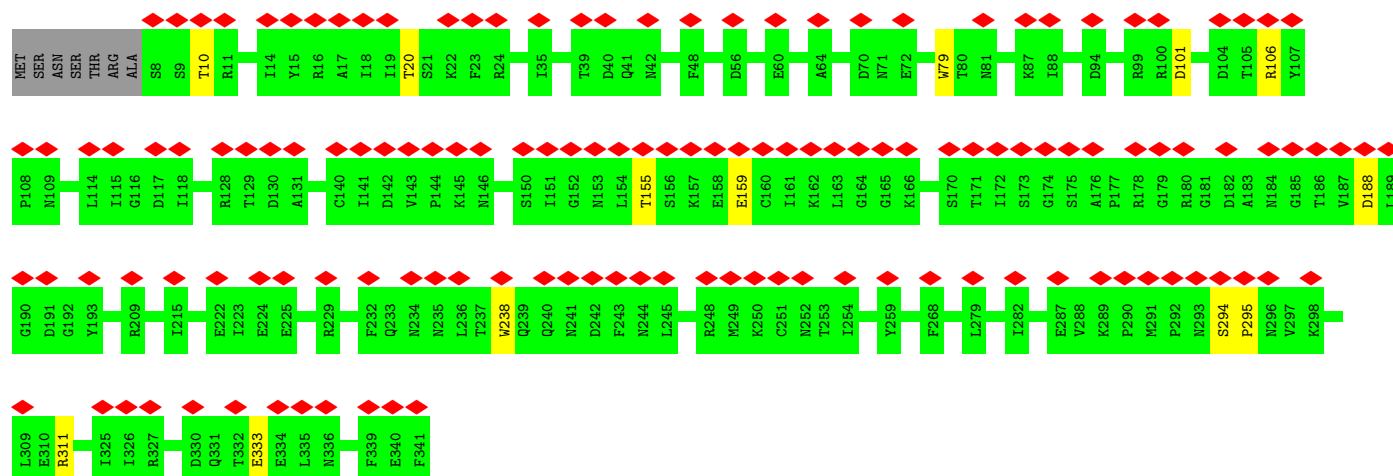


• Molecule 6: Baseplate wedge subunit

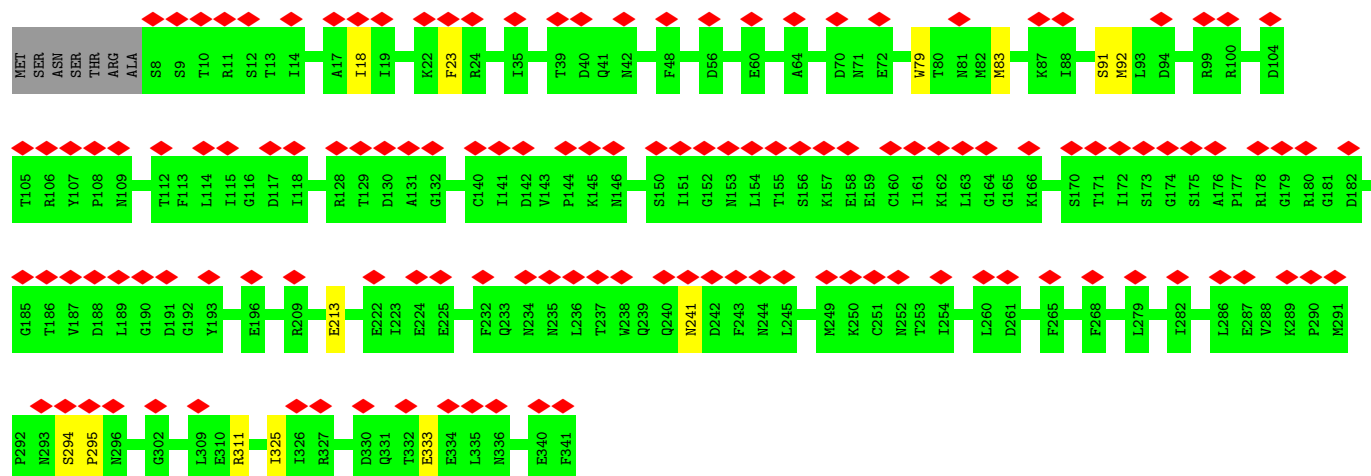


• Molecule 6: Baseplate wedge subunit

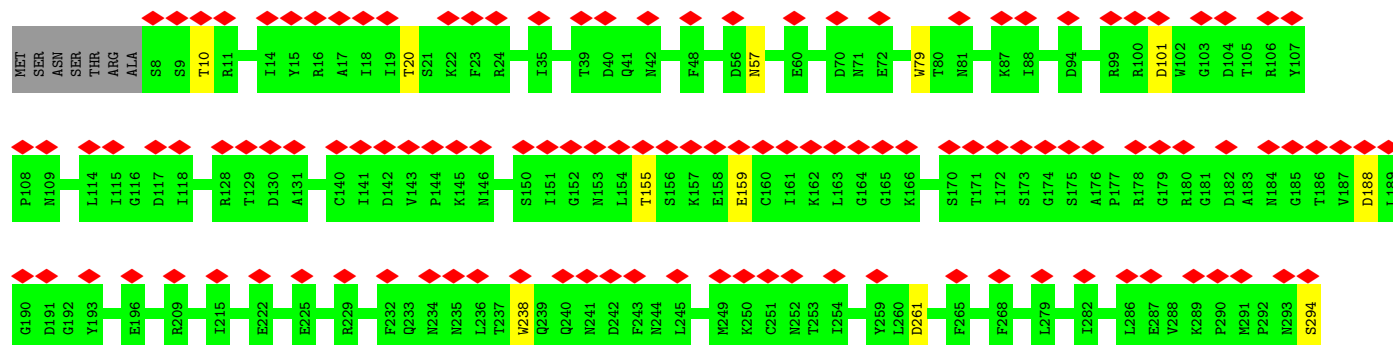
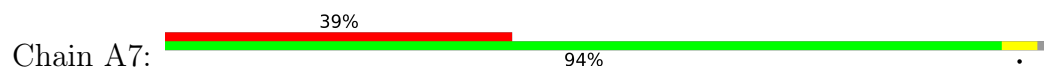




• Molecule 6: Baseplate wedge subunit

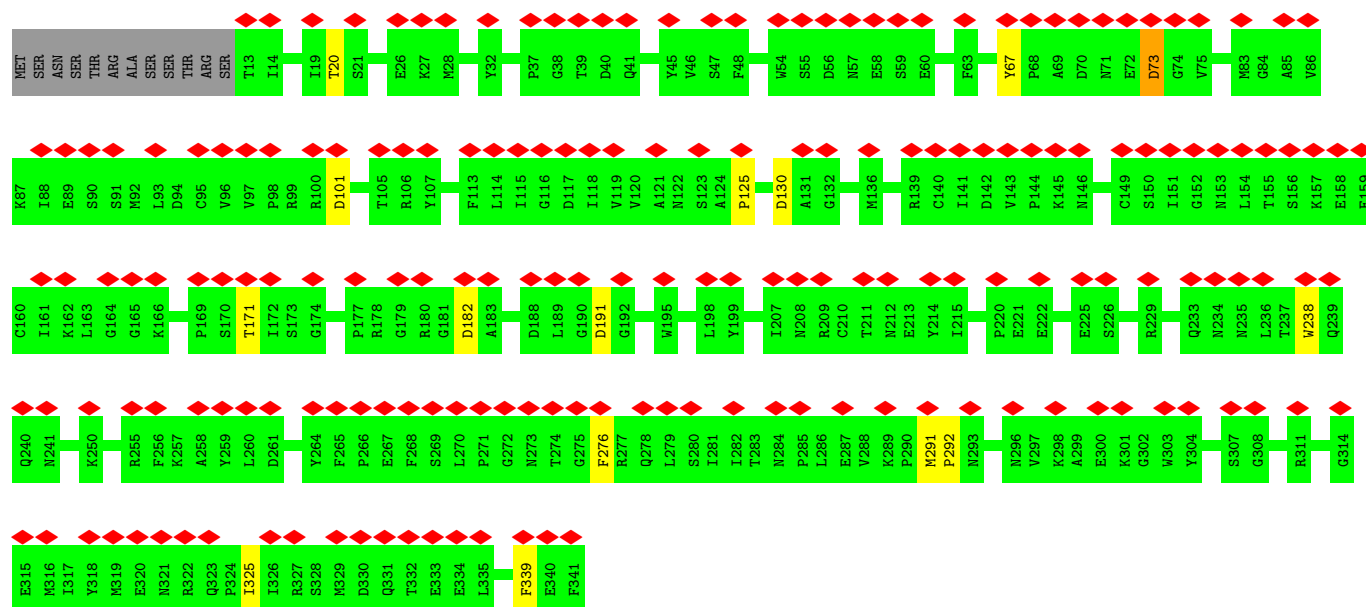


• Molecule 6: Baseplate wedge subunit

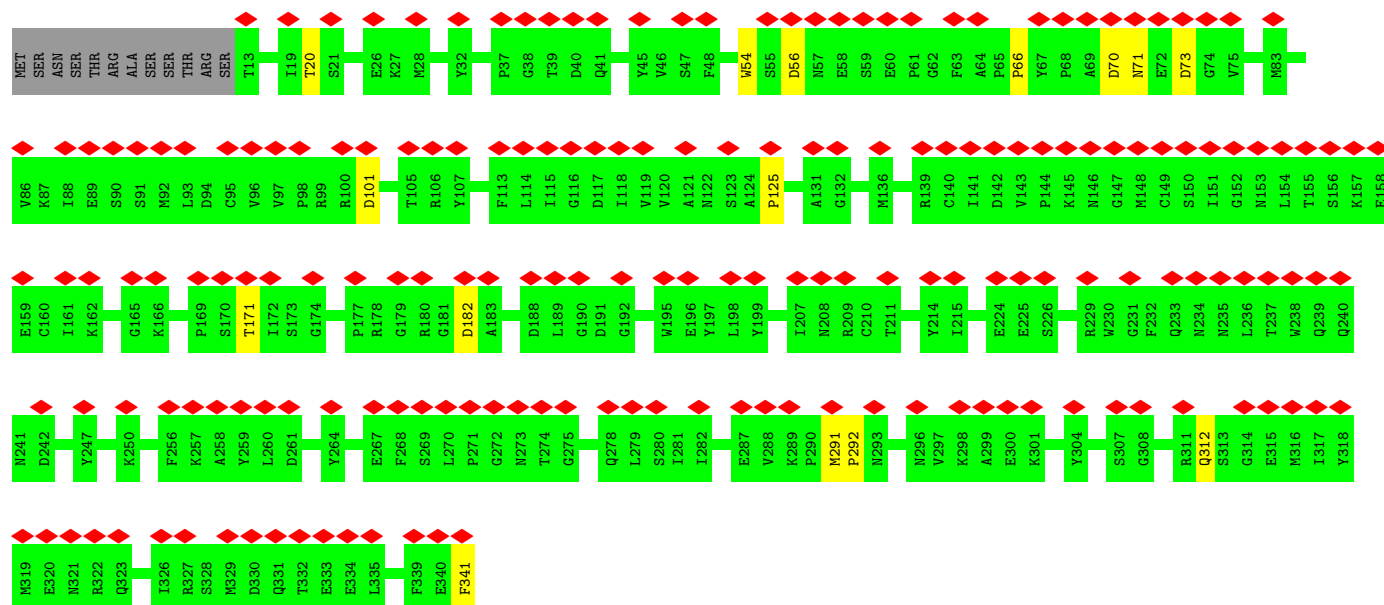
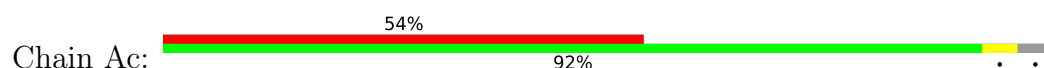




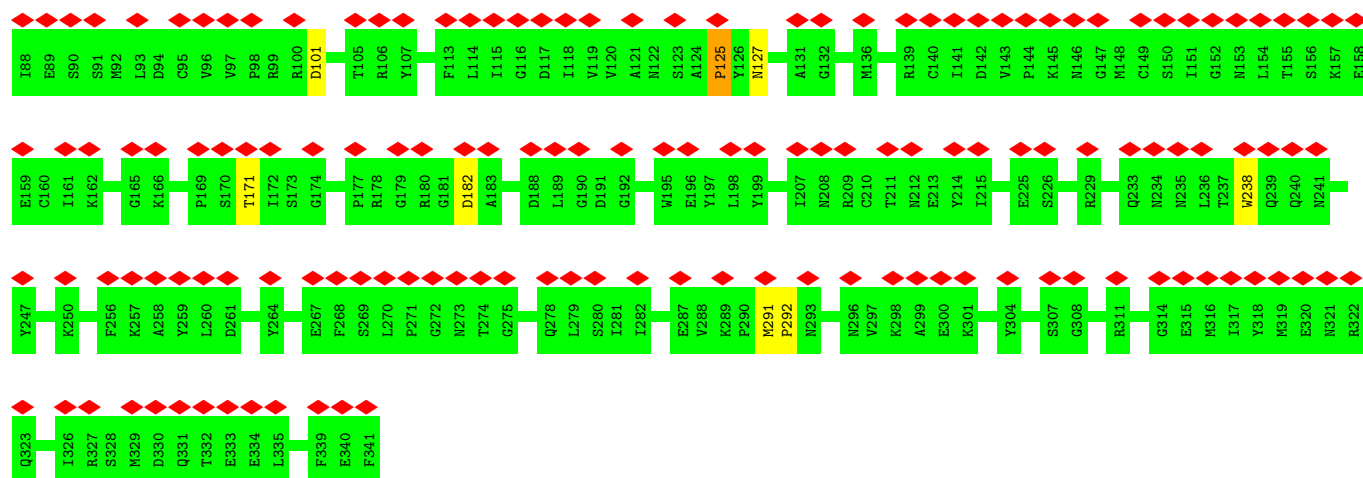
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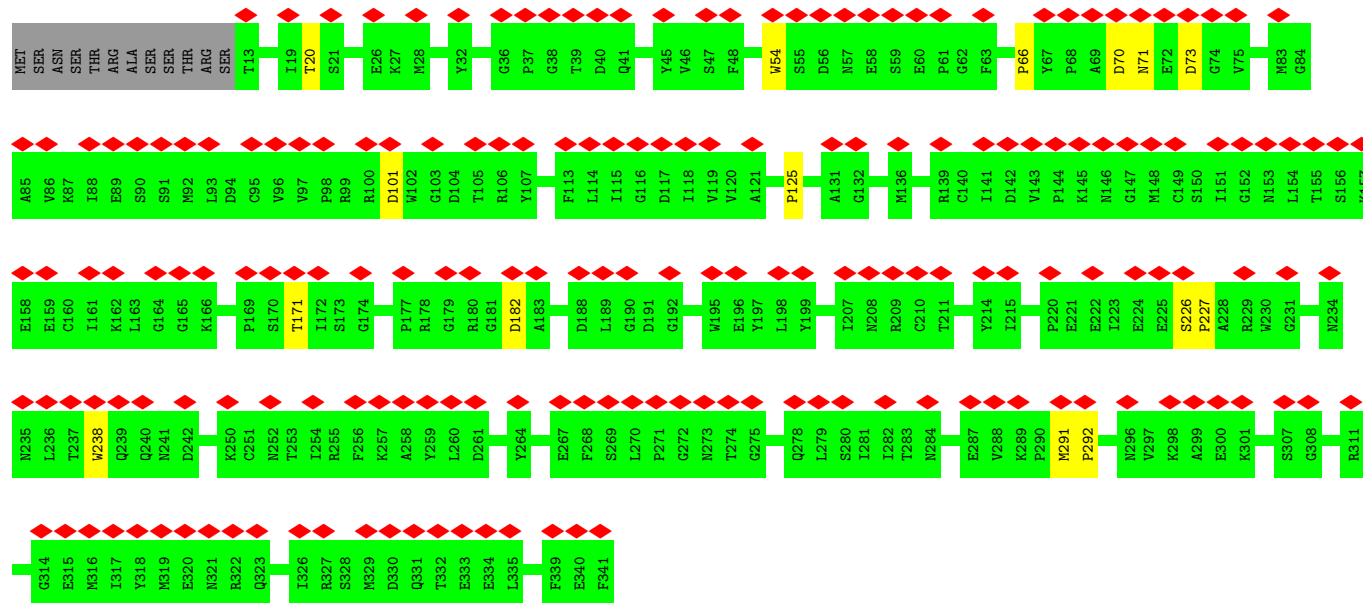
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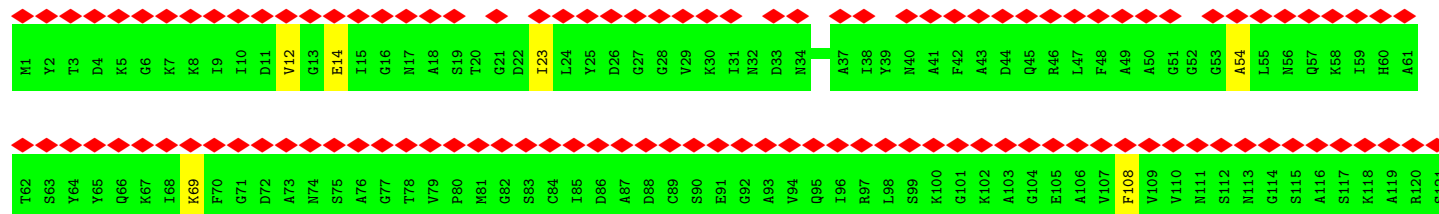
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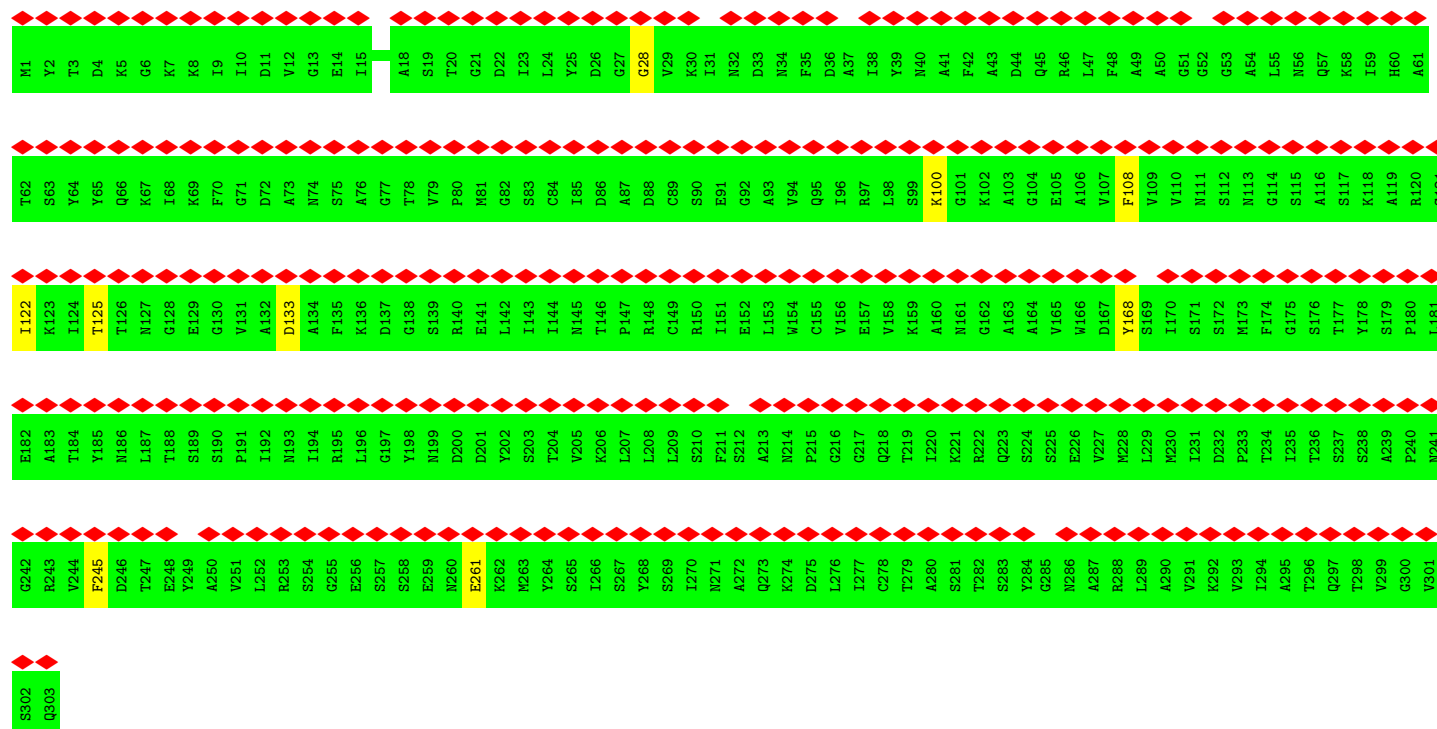
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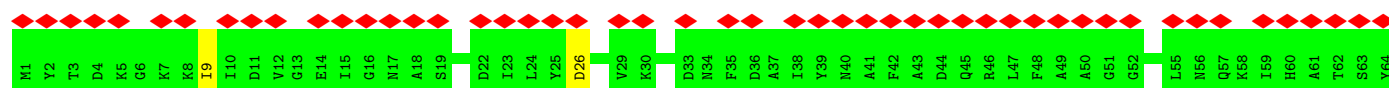
• Molecule 7: Baseplate wedge tail fiber connector

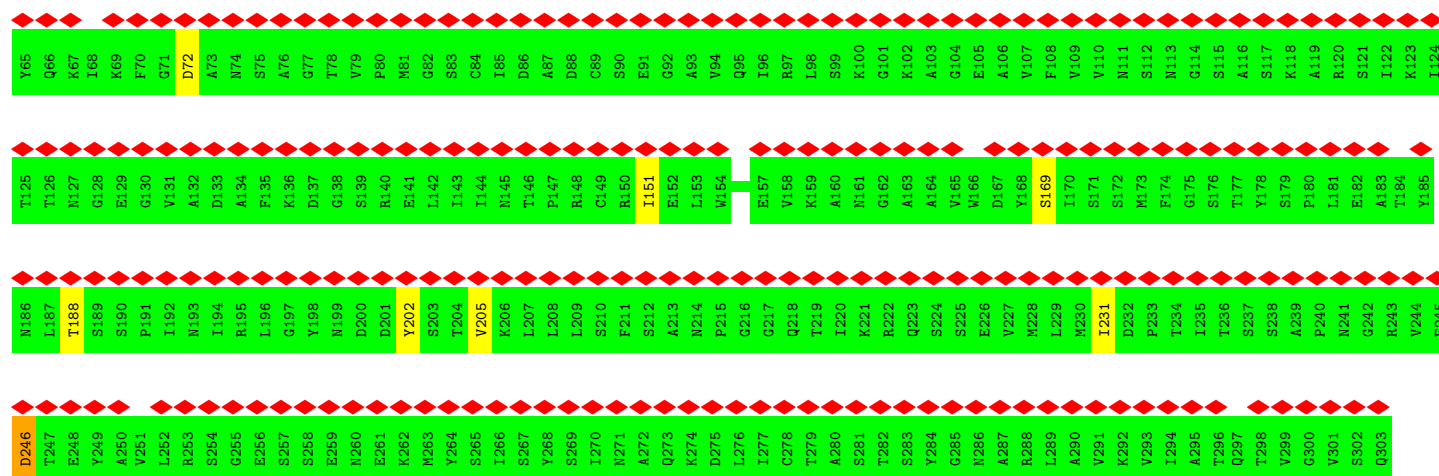


- Molecule 7: Baseplate wedge tail fiber connector

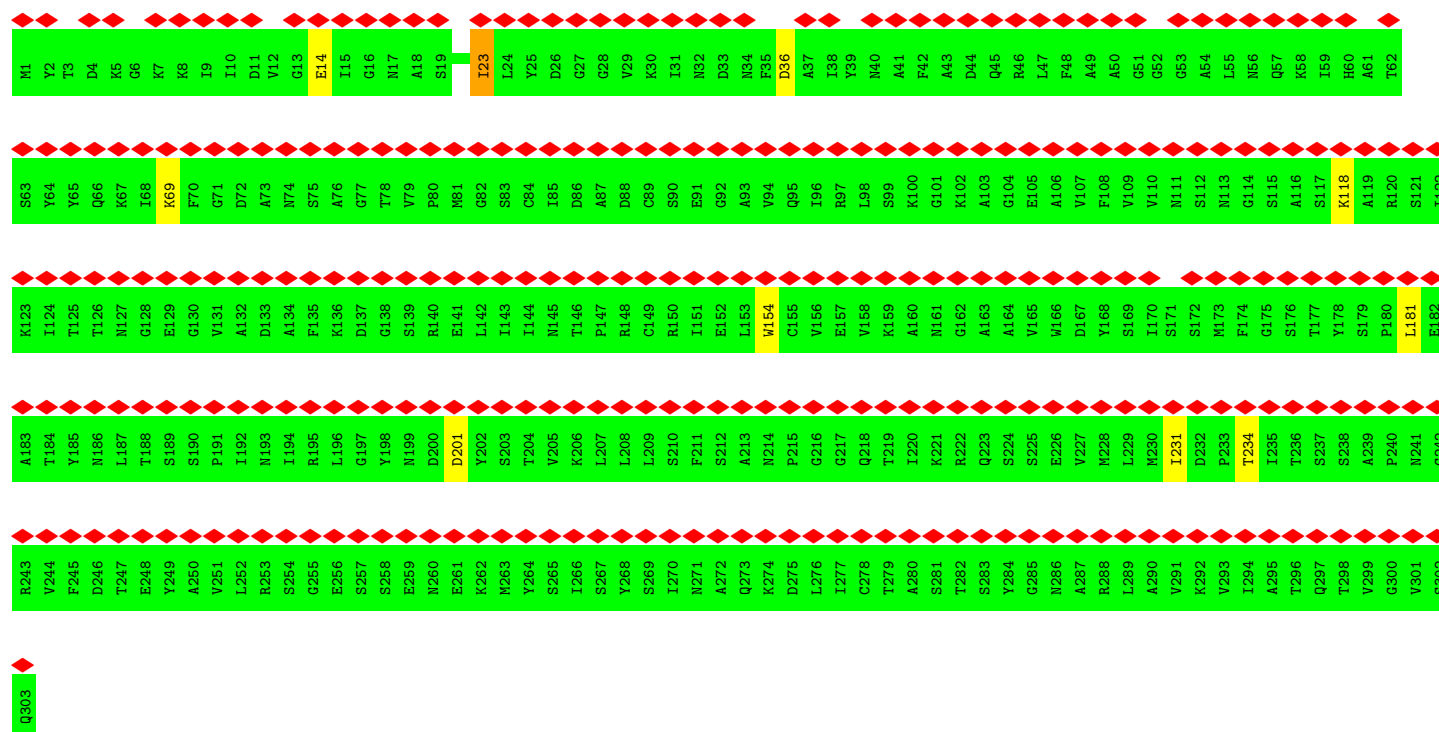


- Molecule 7: Baseplate wedge tail fiber connector

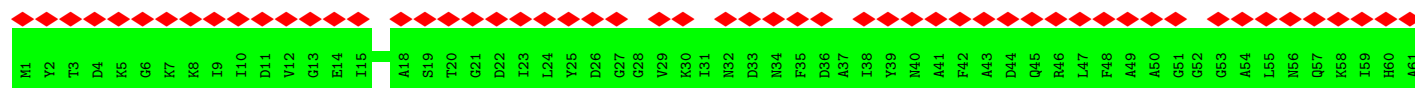


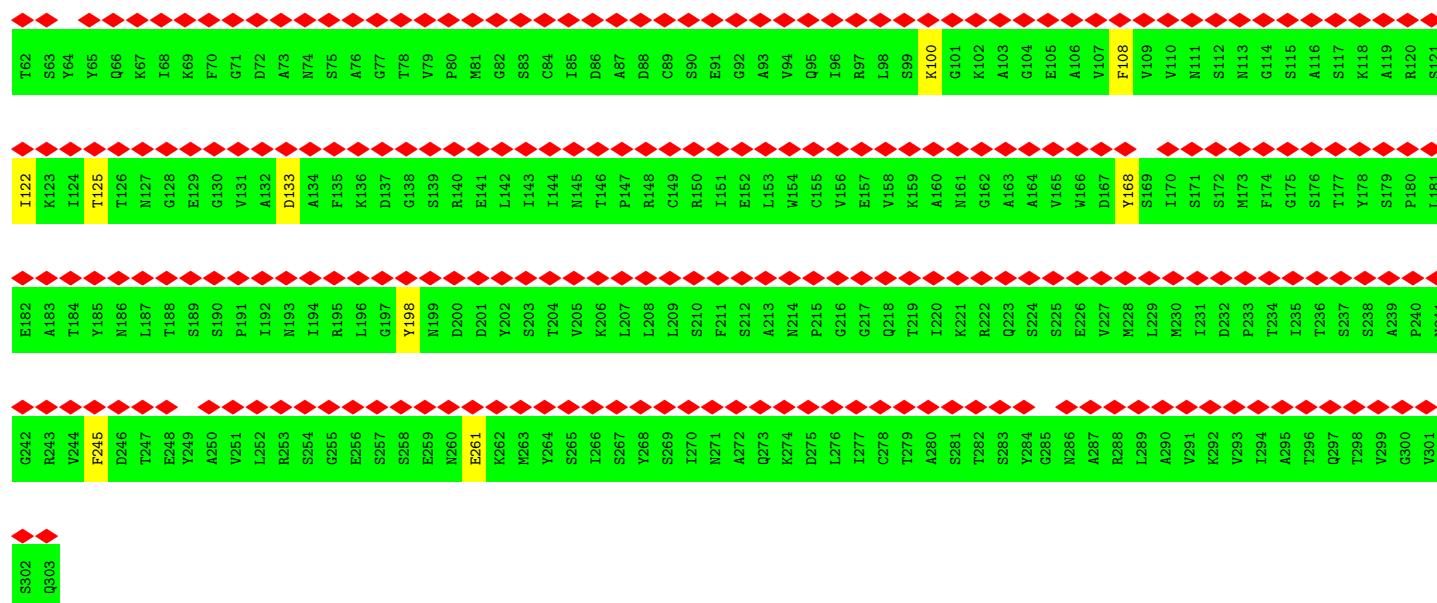


• Molecule 7: Baseplate wedge tail fiber connector

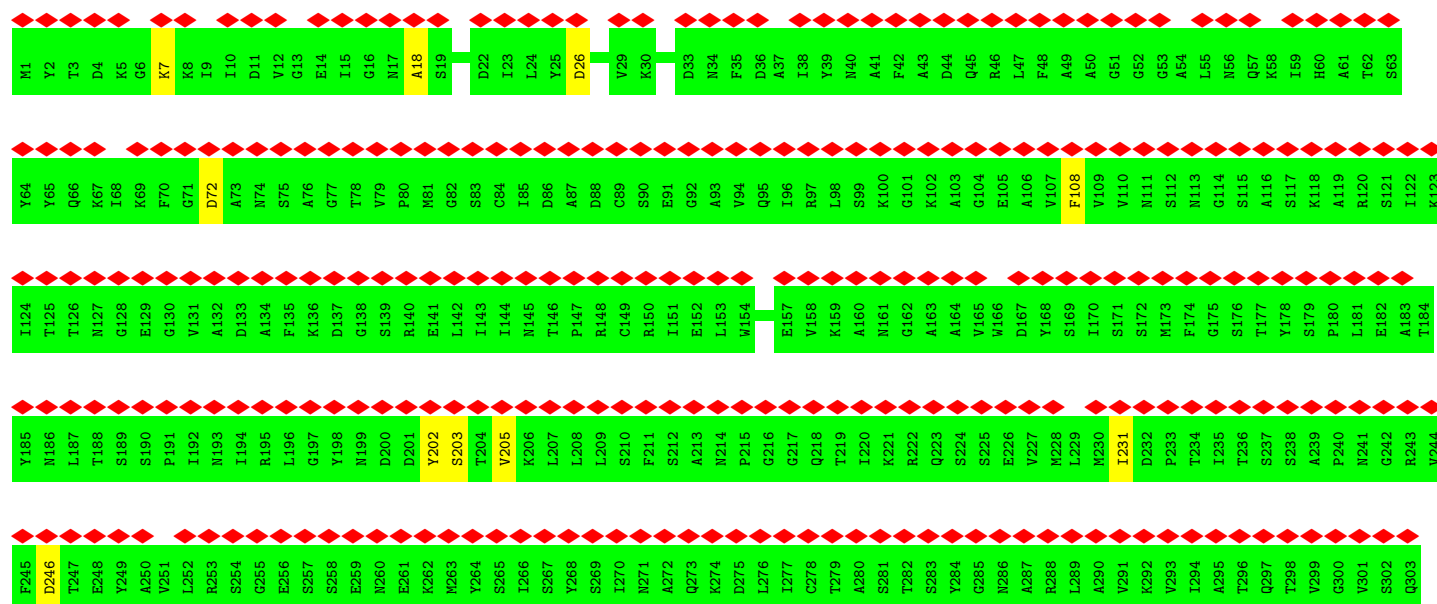


• Molecule 7: Baseplate wedge tail fiber connector

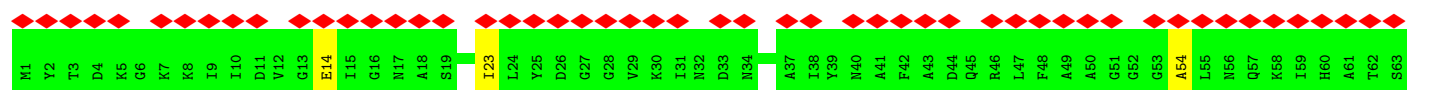


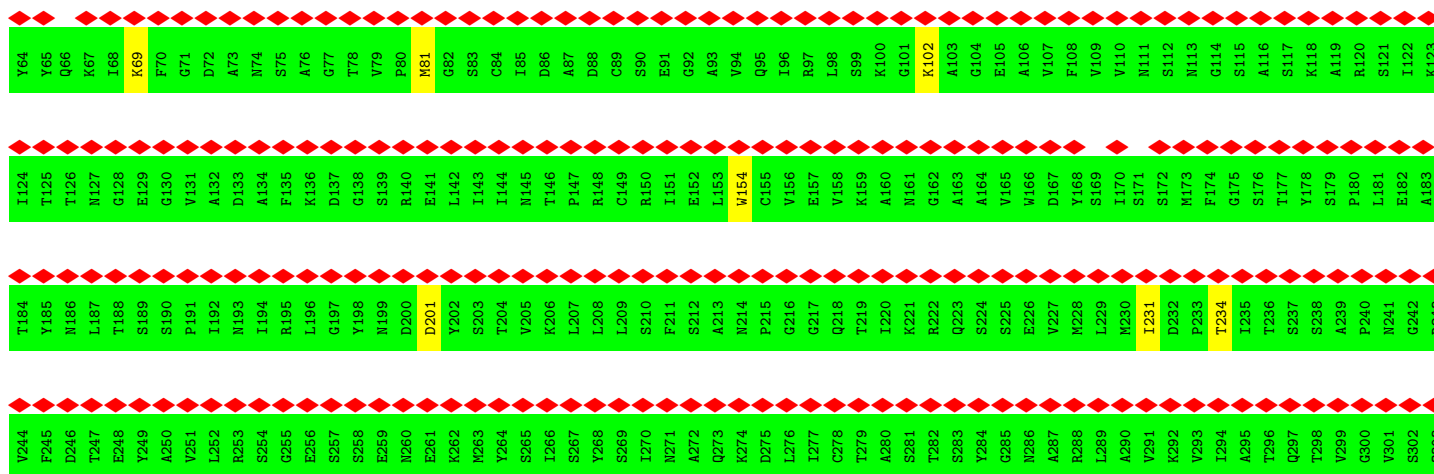


- Molecule 7: Baseplate wedge tail fiber connector

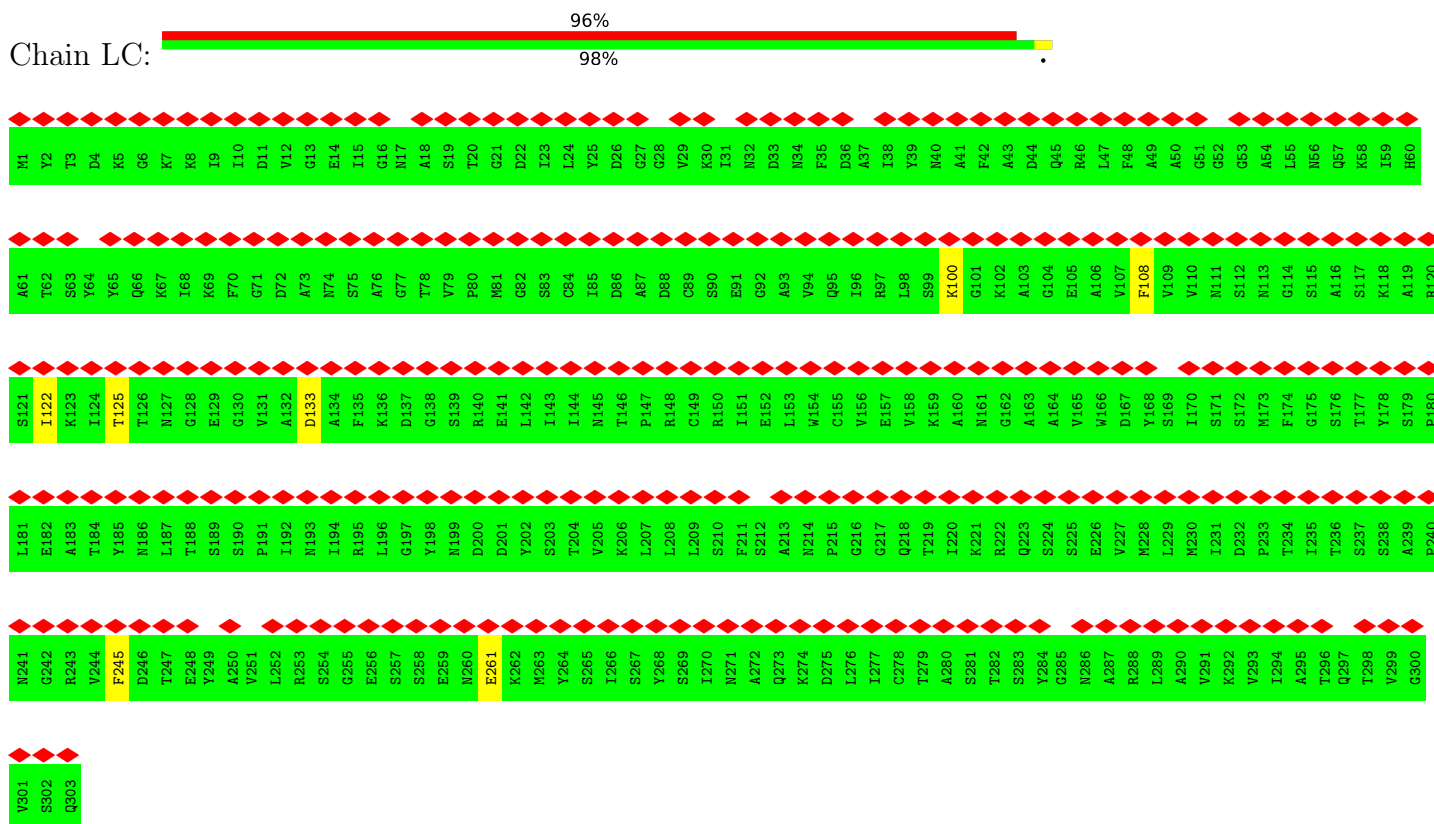


- Molecule 7: Baseplate wedge tail fiber connector

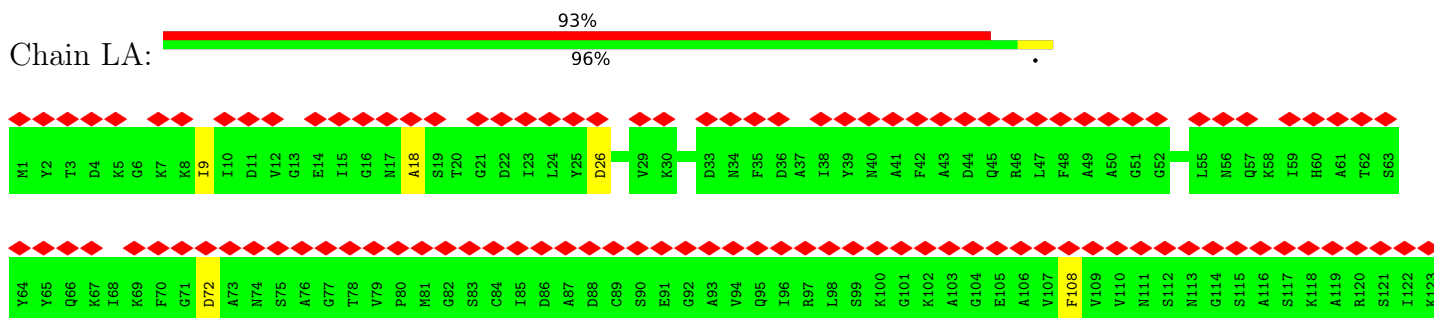


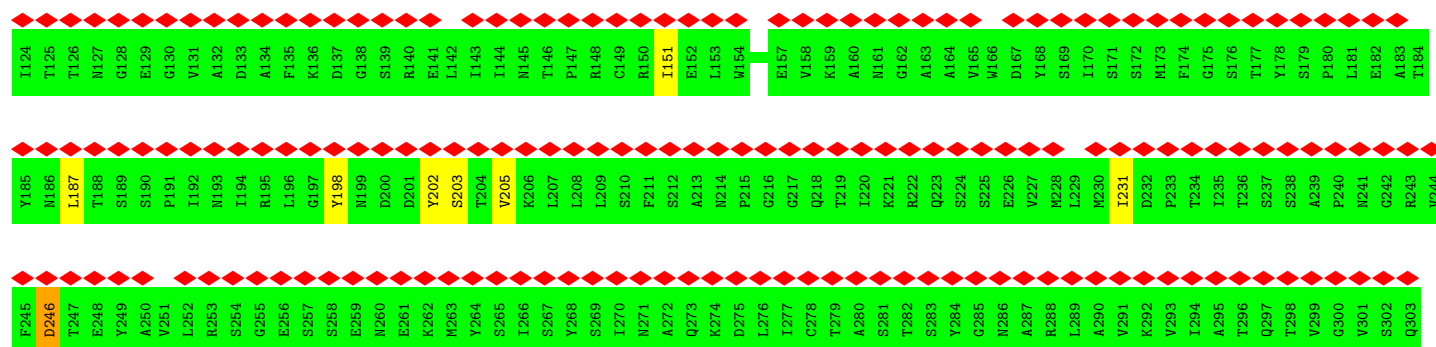


• Molecule 7: Baseplate wedge tail fiber connector

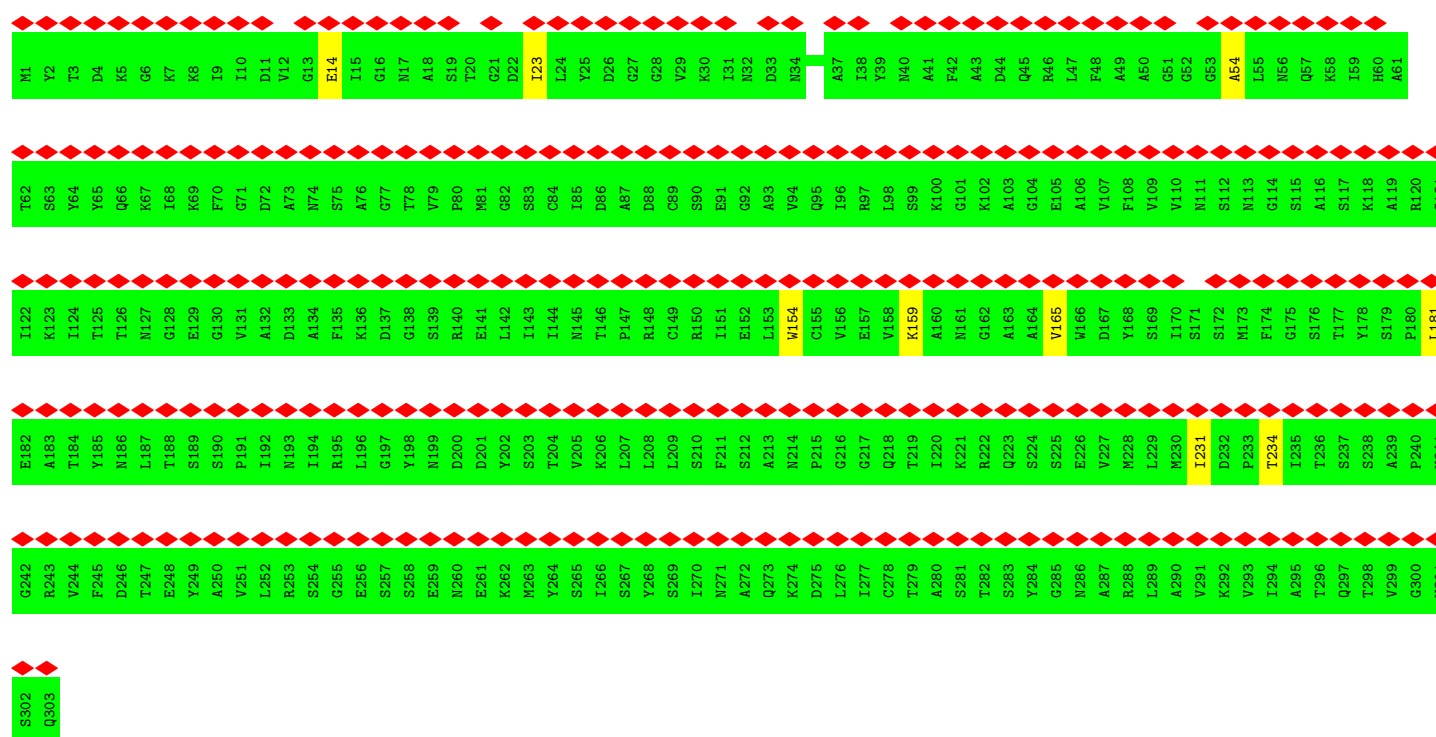


• Molecule 7: Baseplate wedge tail fiber connector



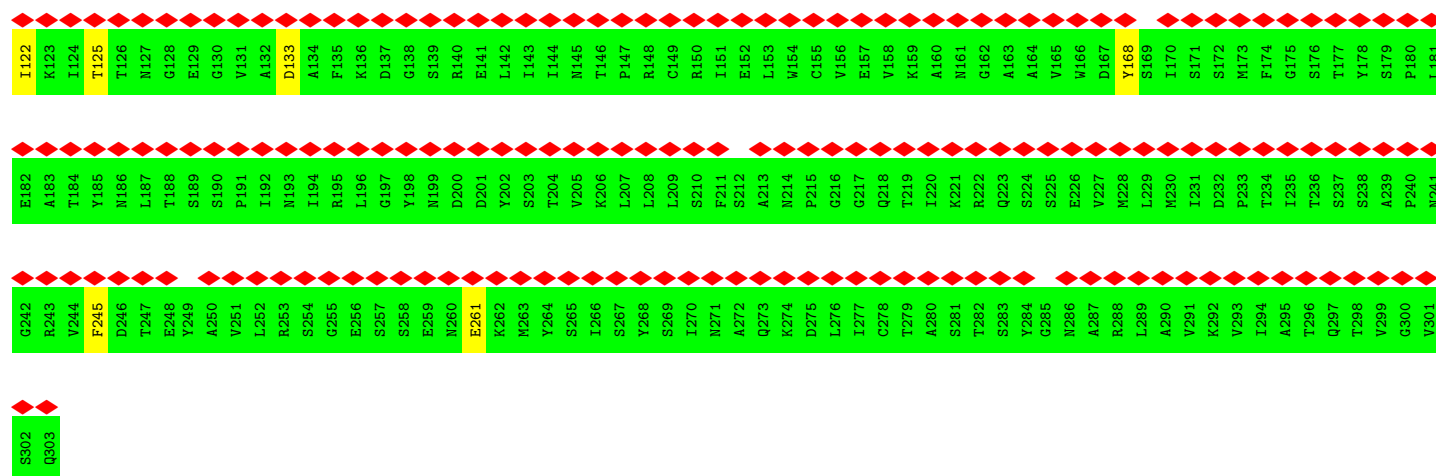


• Molecule 7: Baseplate wedge tail fiber connector

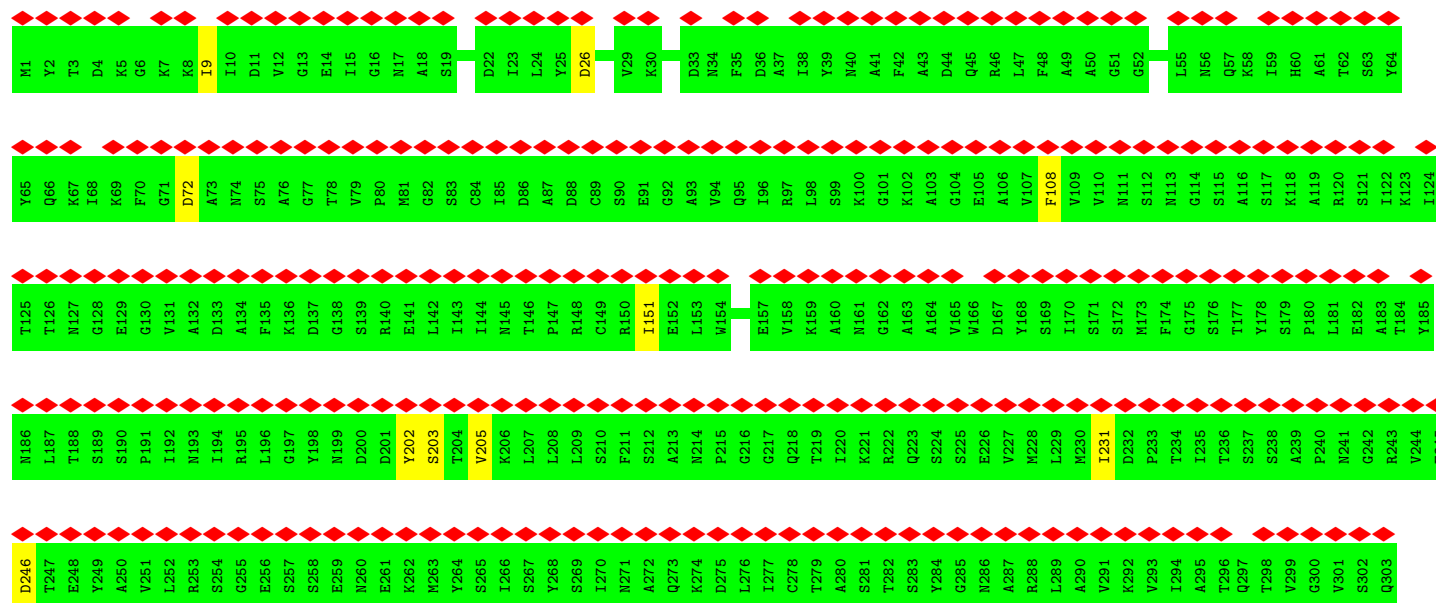


• Molecule 7: Baseplate wedge tail fiber connector

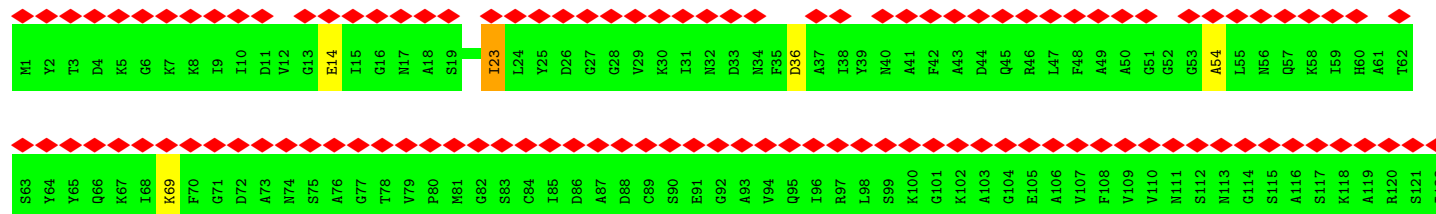


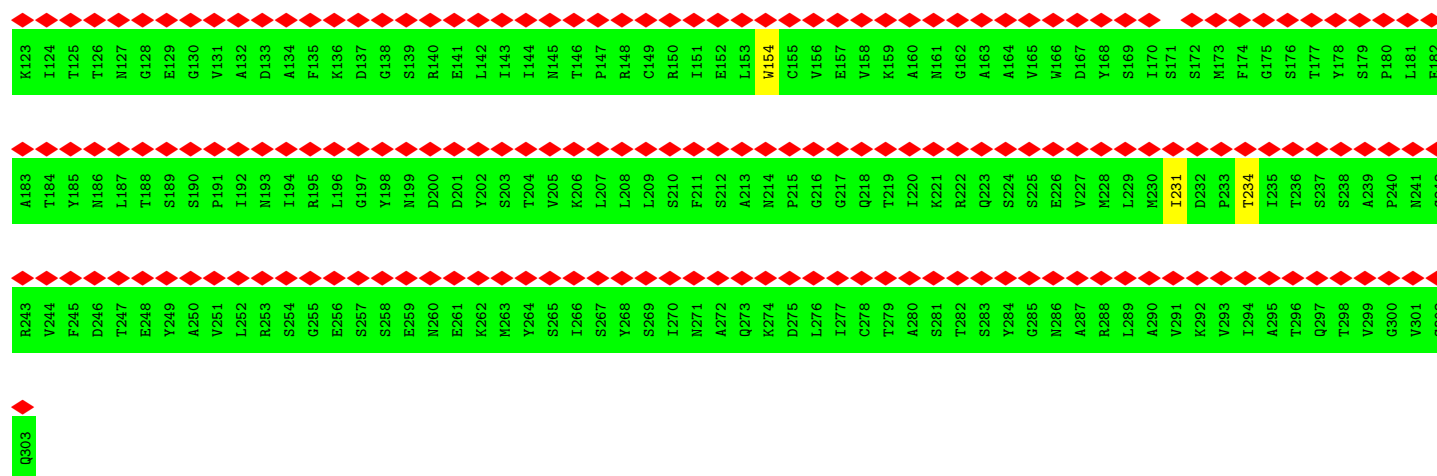


• Molecule 7: Baseplate wedge tail fiber connector

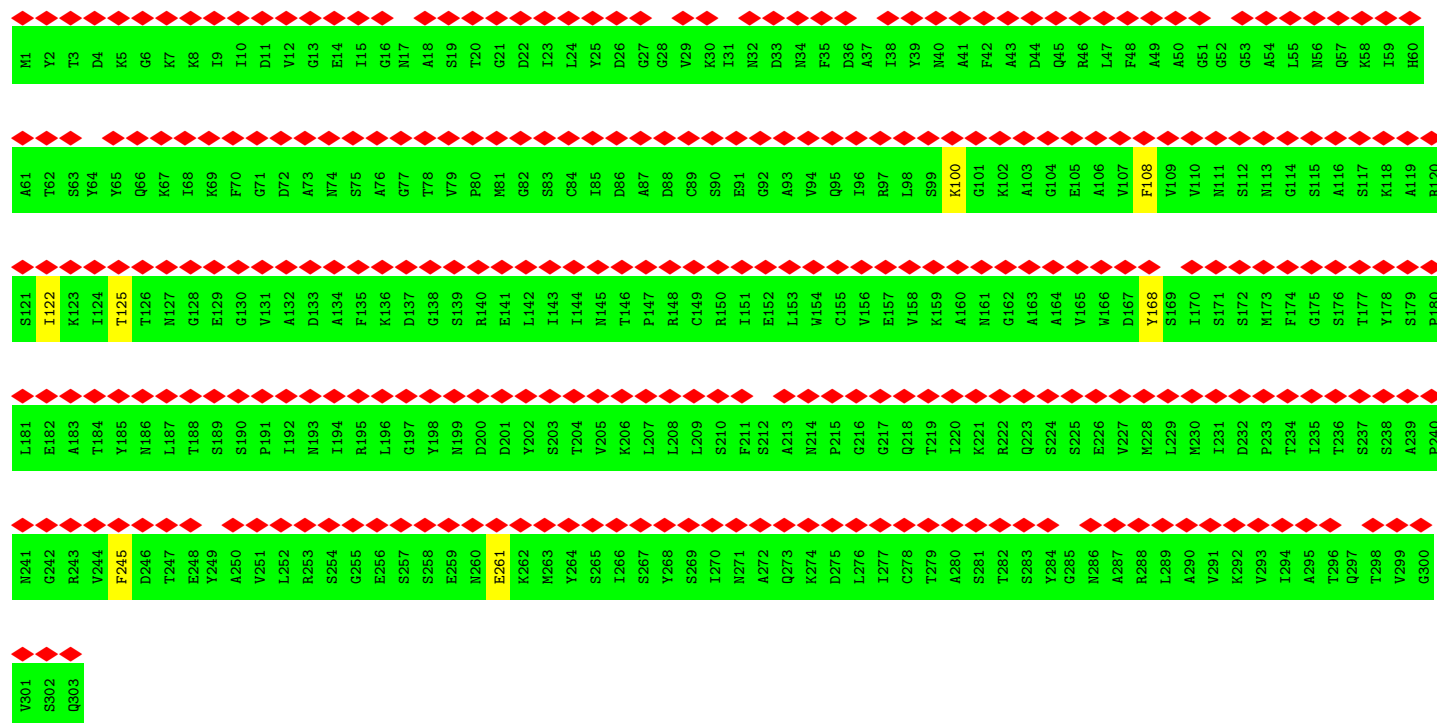


• Molecule 7: Baseplate wedge tail fiber connector

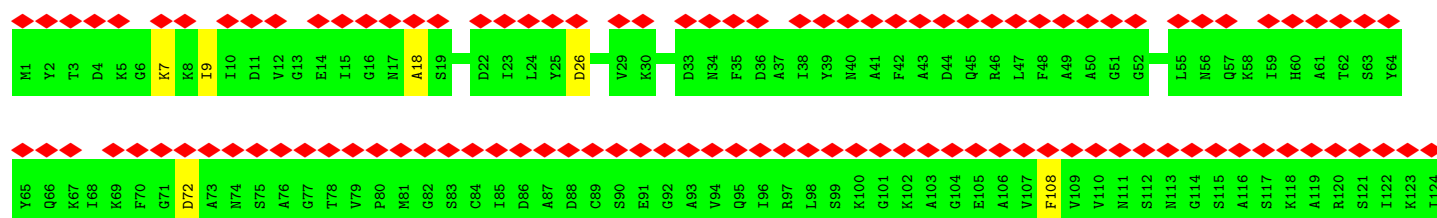


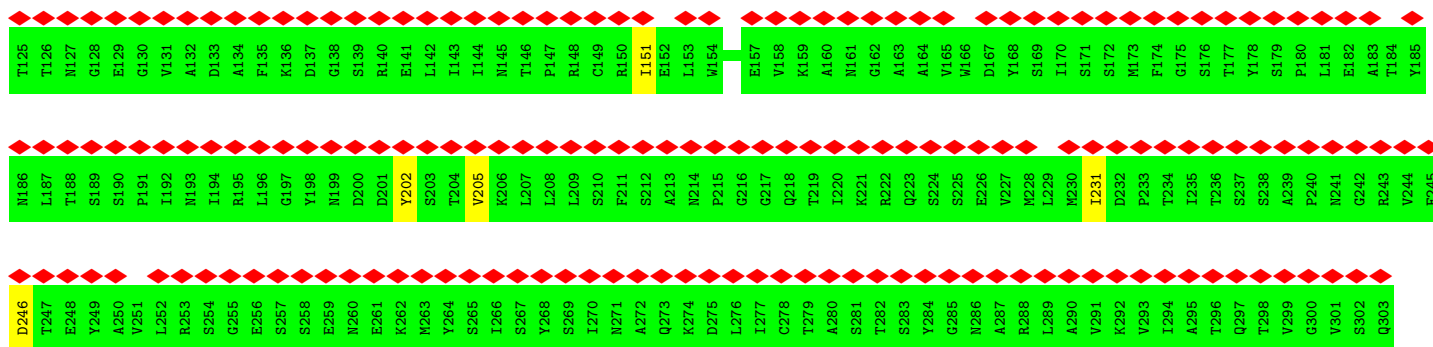


- Molecule 7: Baseplate wedge tail fiber connector



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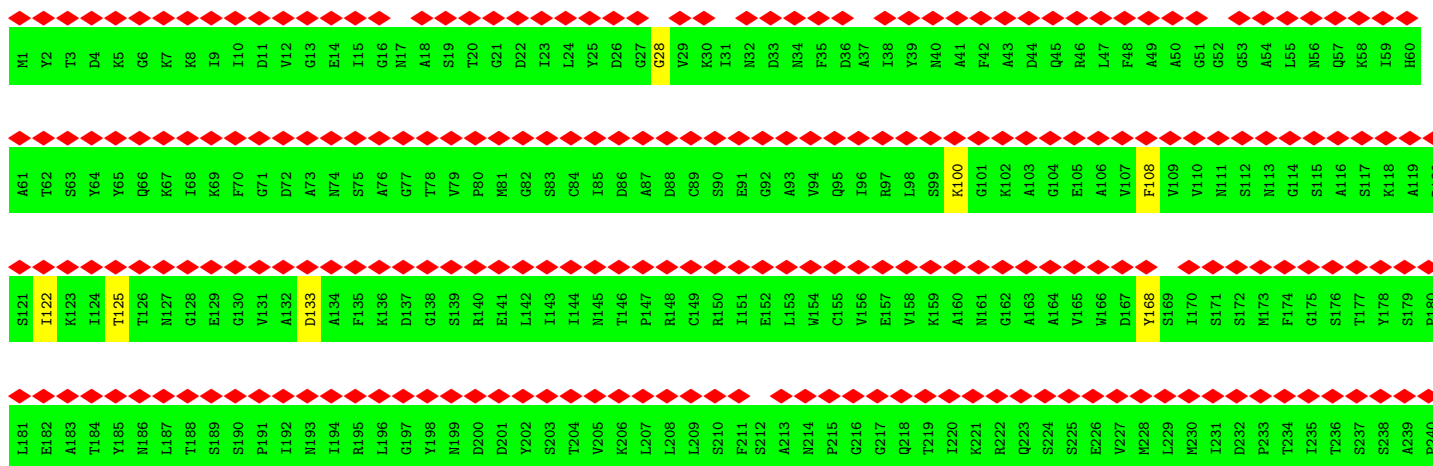


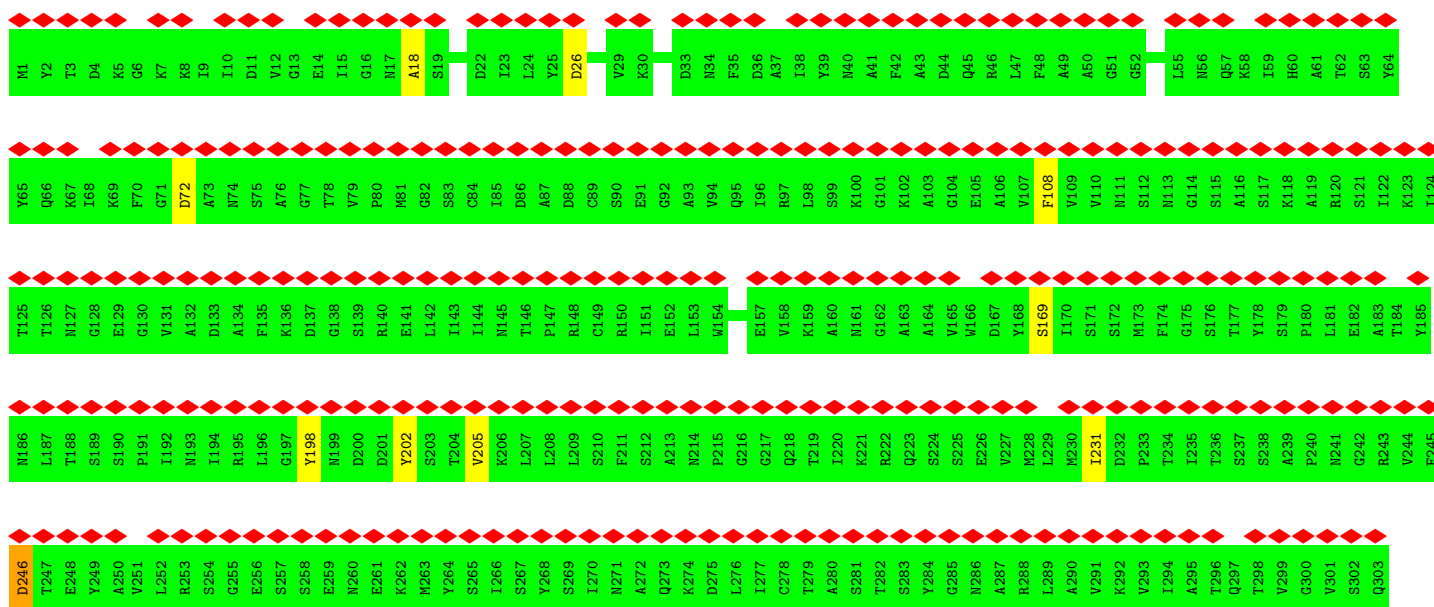
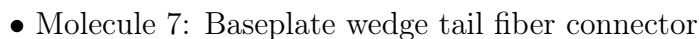


• Molecule 7: Baseplate wedge tail fiber connector

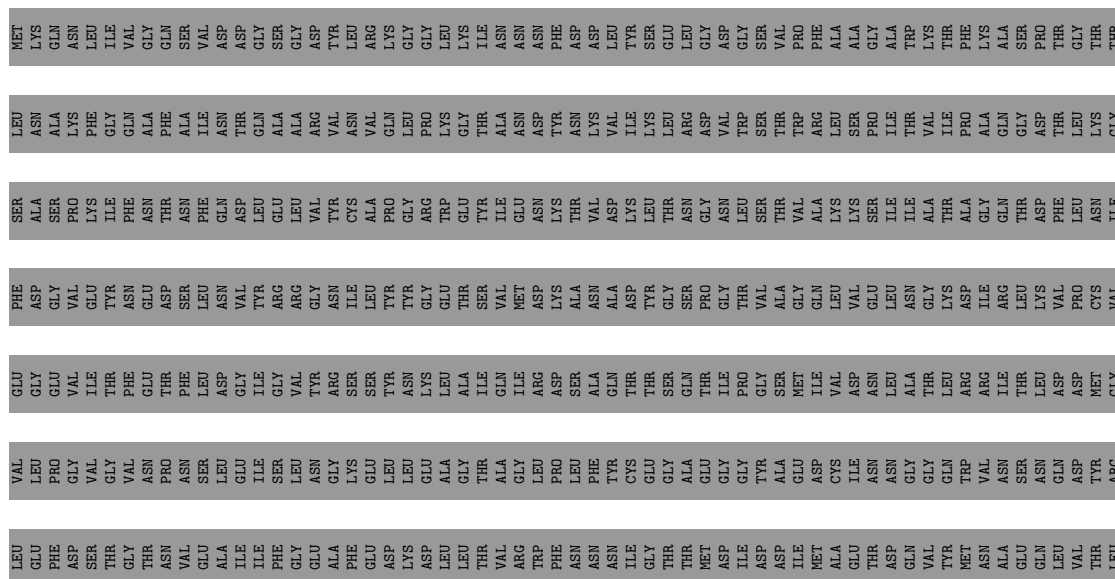


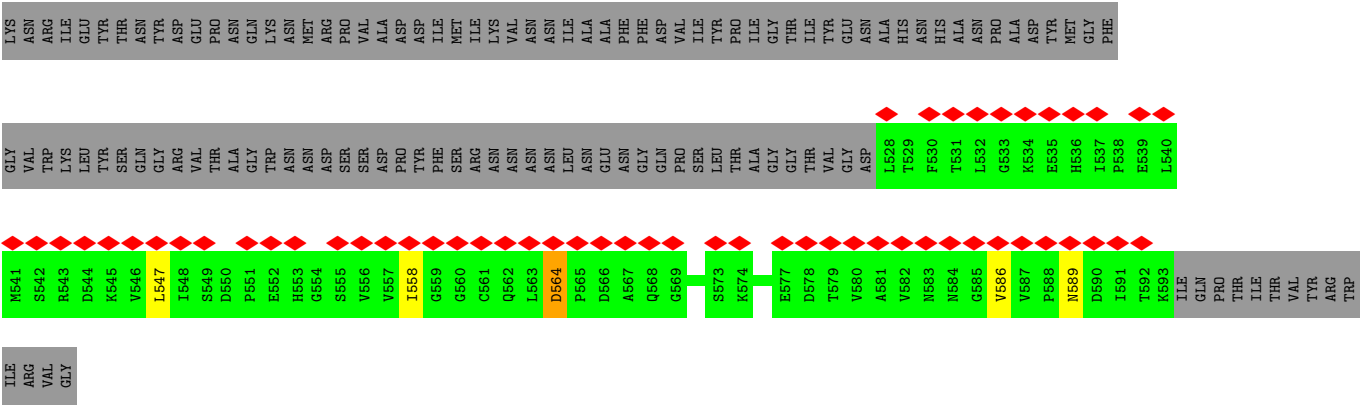
• Molecule 7: Baseplate wedge tail fiber connector



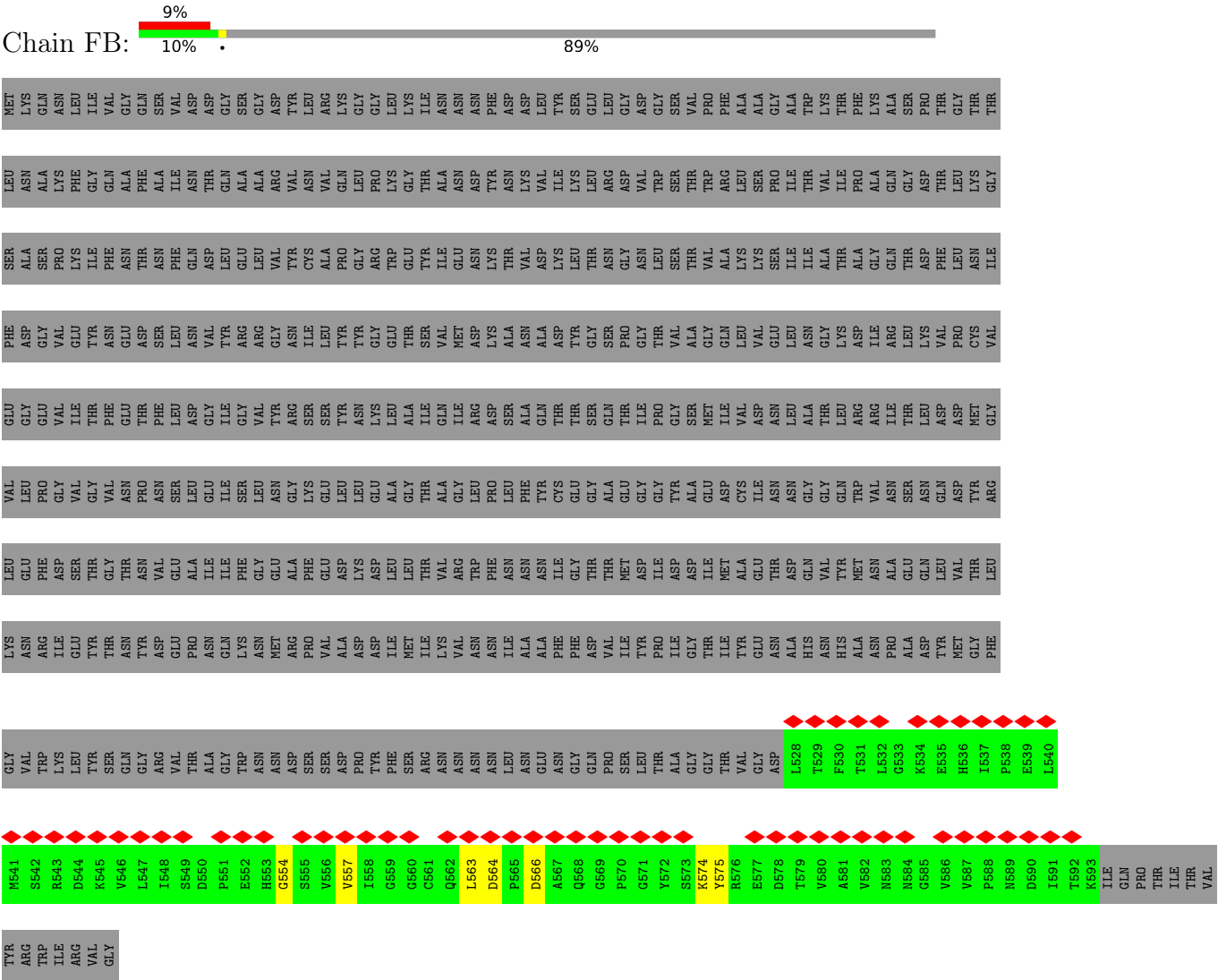


- Molecule 8: Baseplate wedge protein gp10

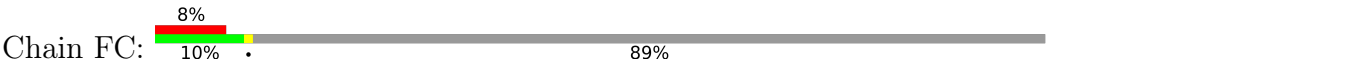




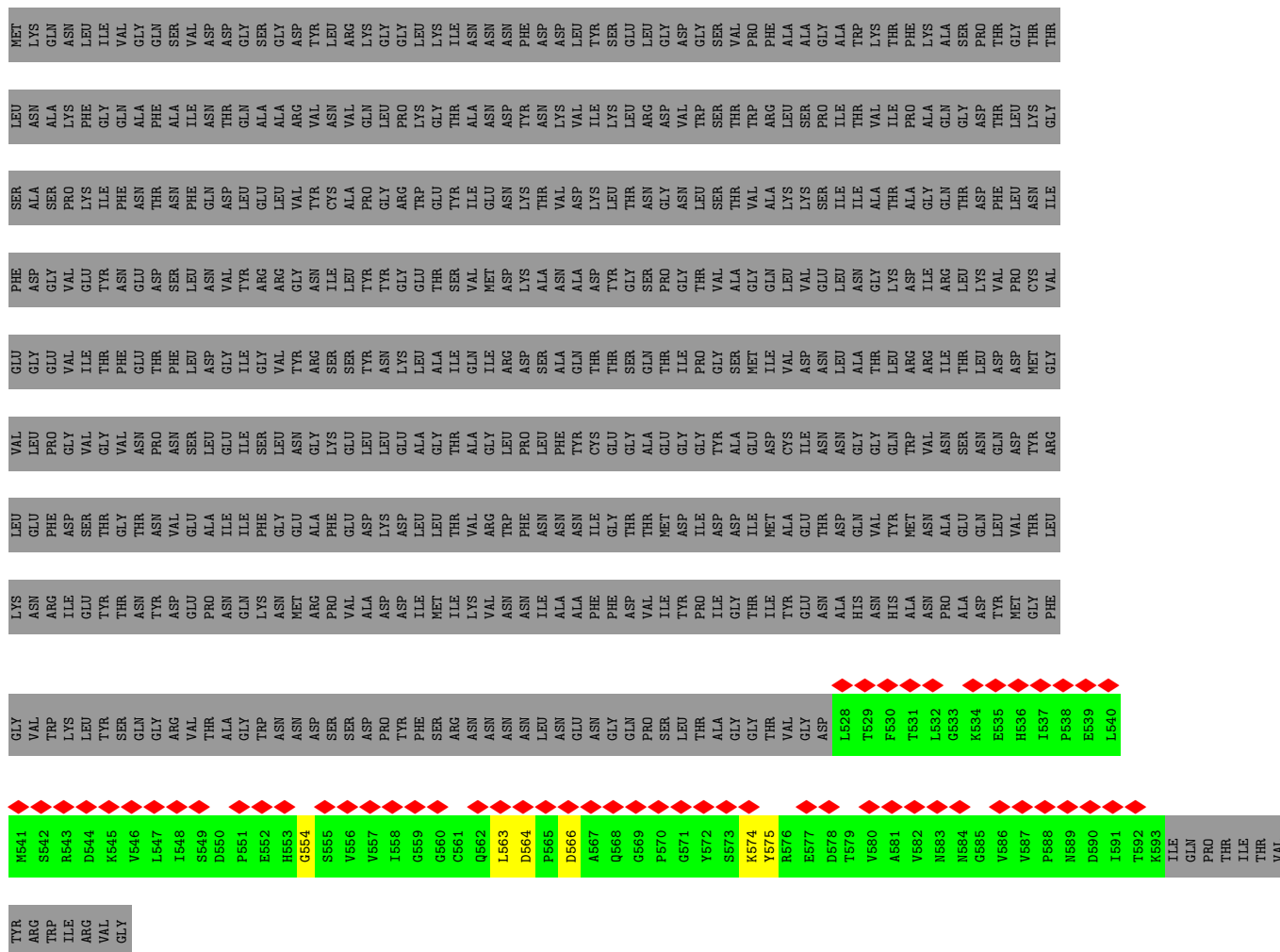
• Molecule 8: Baseplate wedge protein gp10



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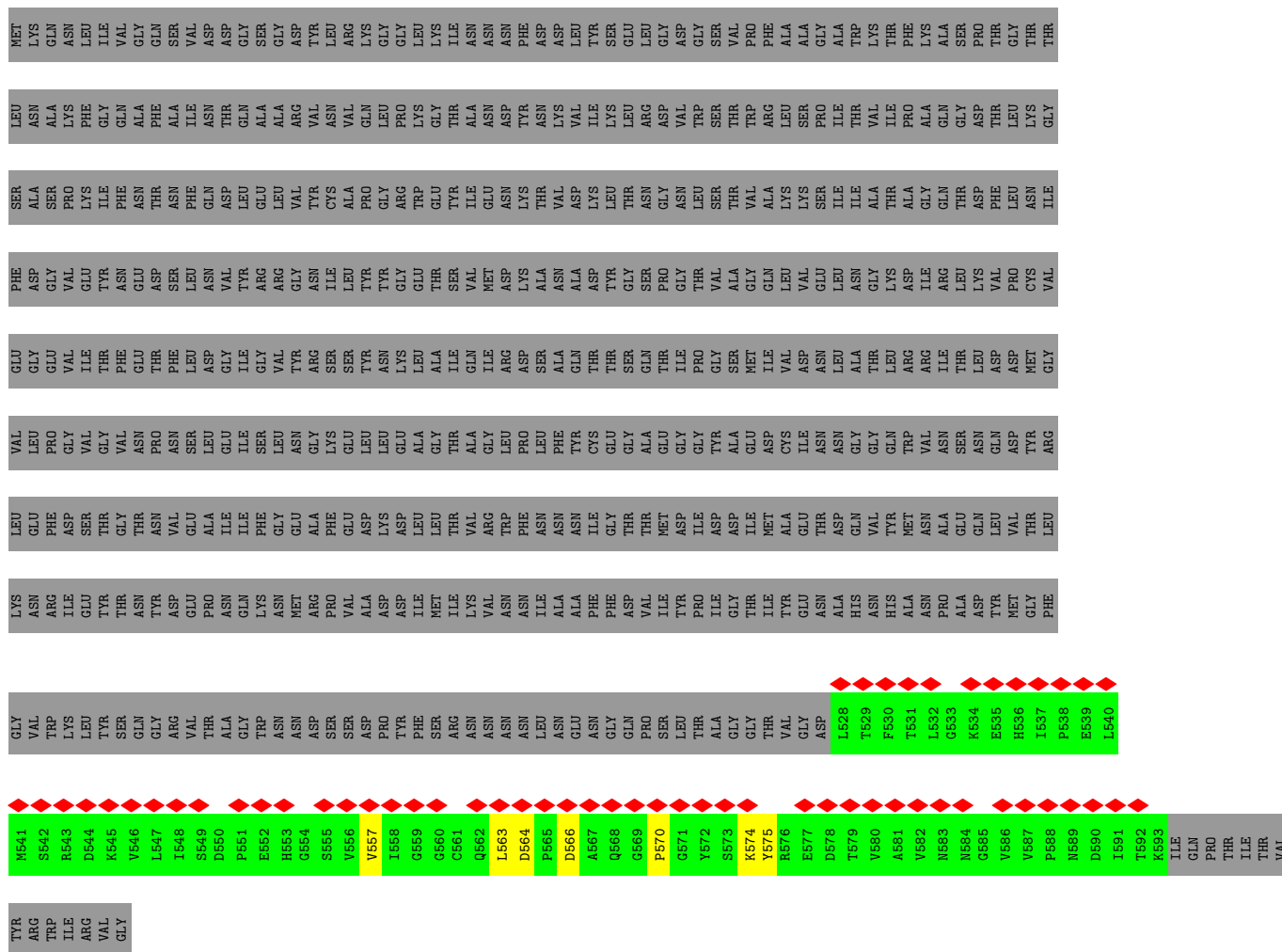
- Molecule 8: Baseplate wedge protein gp10



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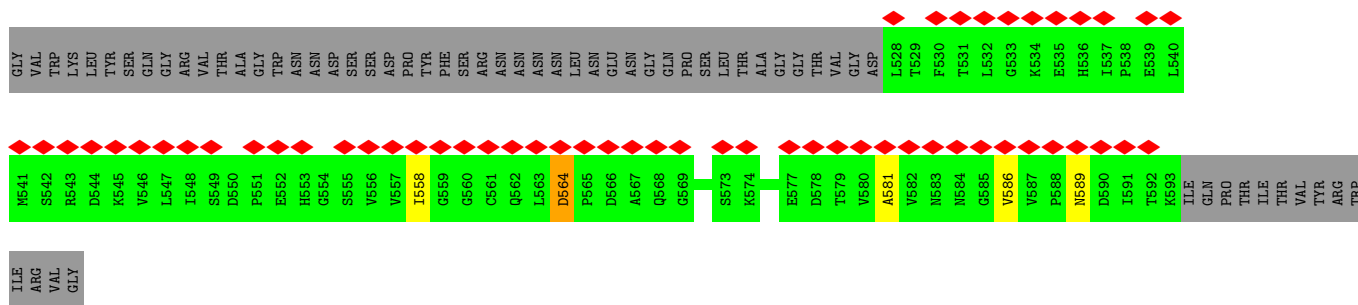


- Molecule 8: Baseplate wedge protein gp10

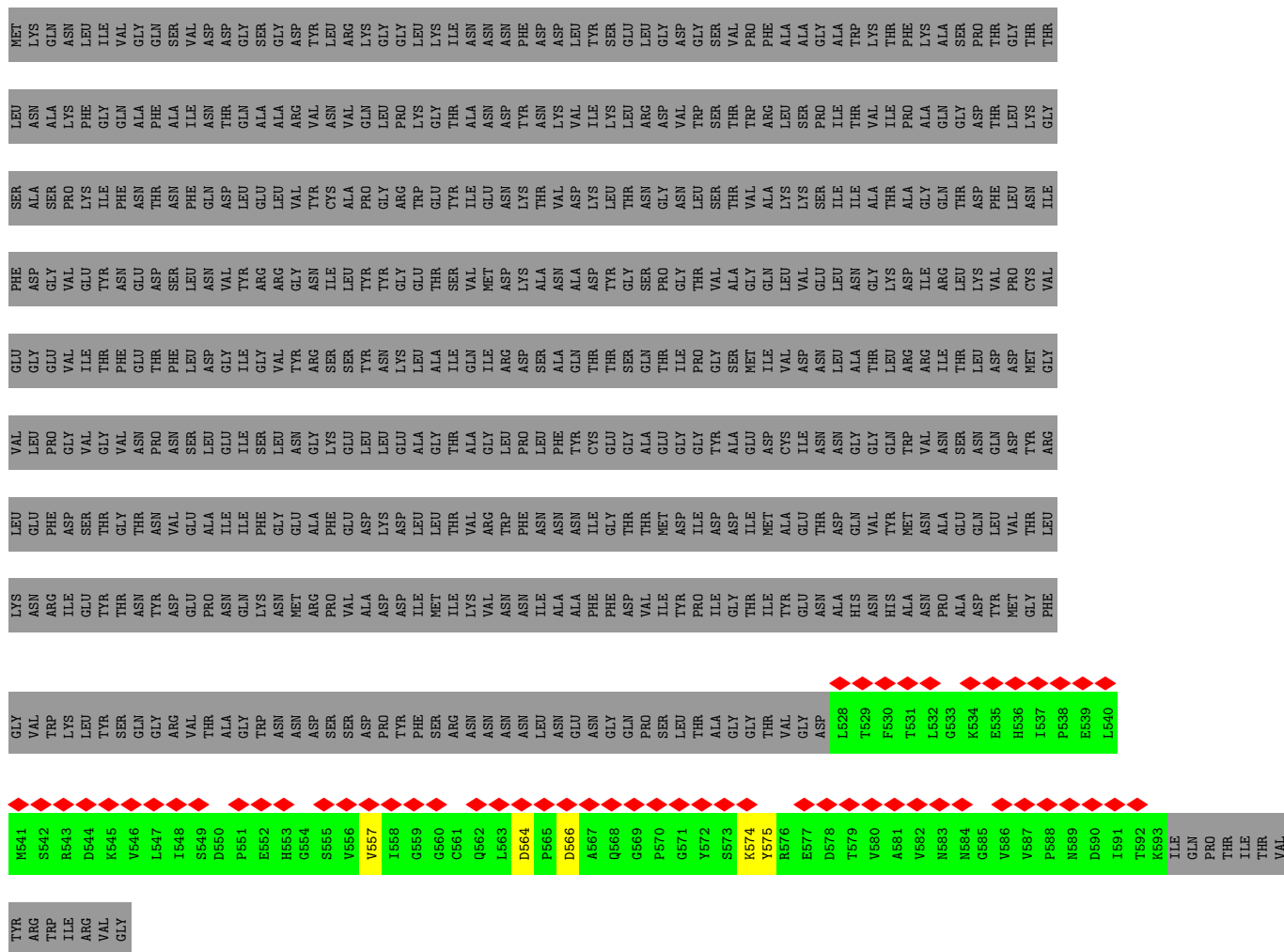


- Molecule 8: Baseplate wedge protein gp10





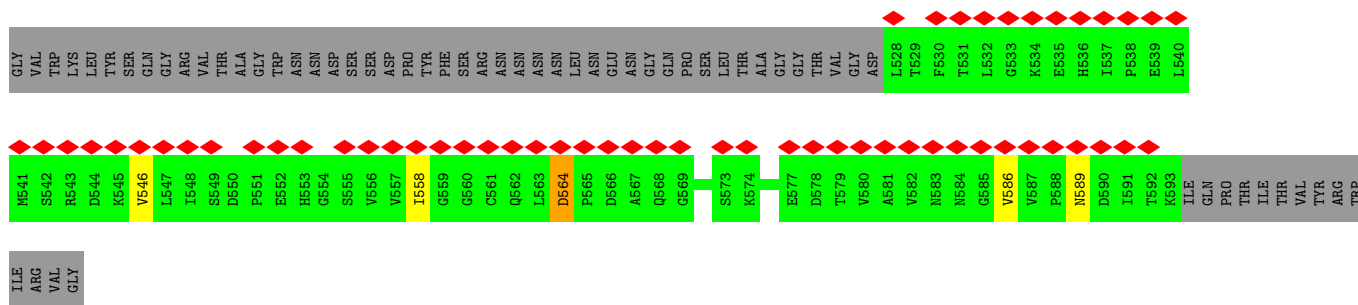
- Molecule 8: Baseplate wedge protein gp10



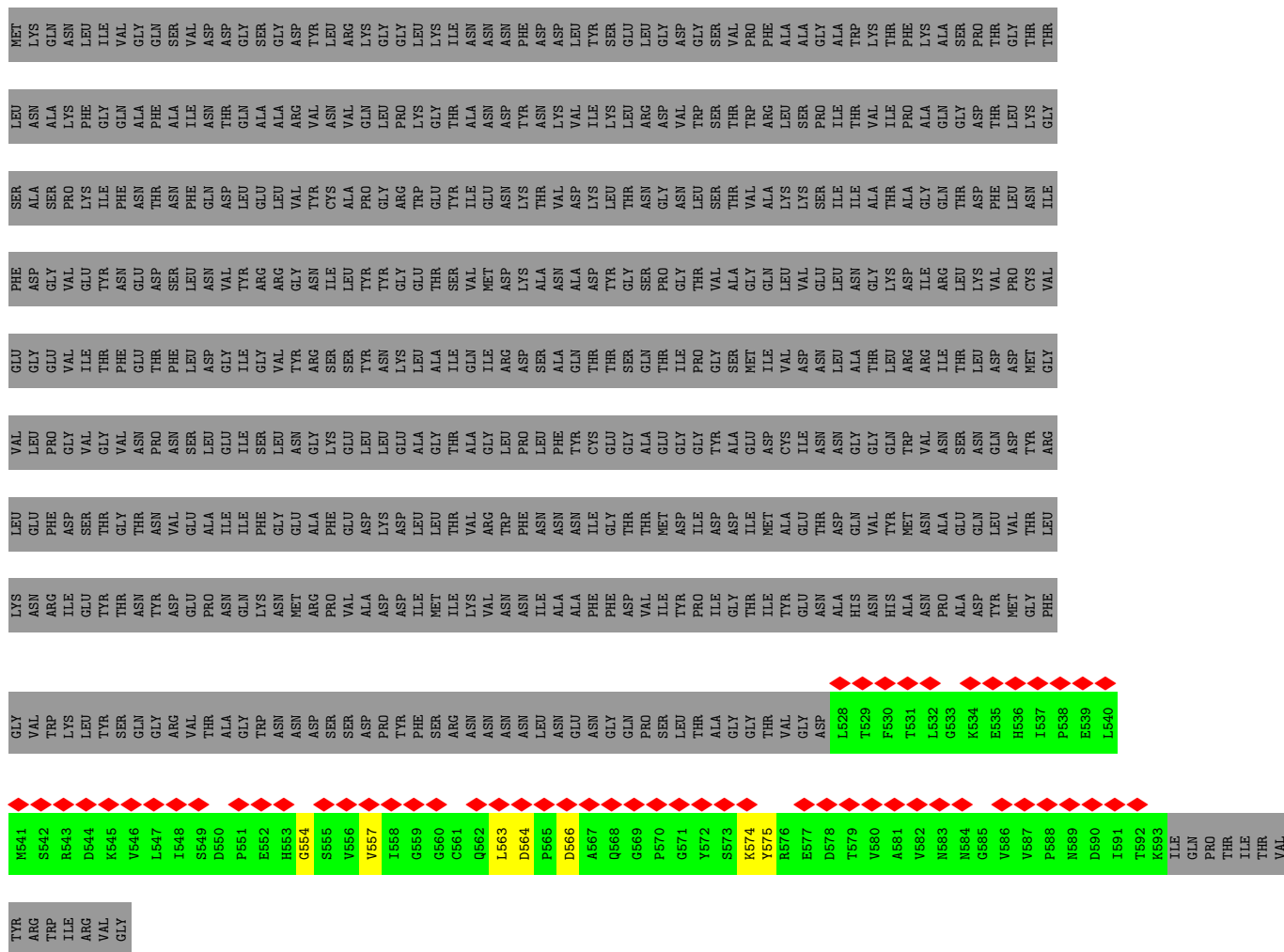
- Molecule 8: Baseplate wedge protein gp10





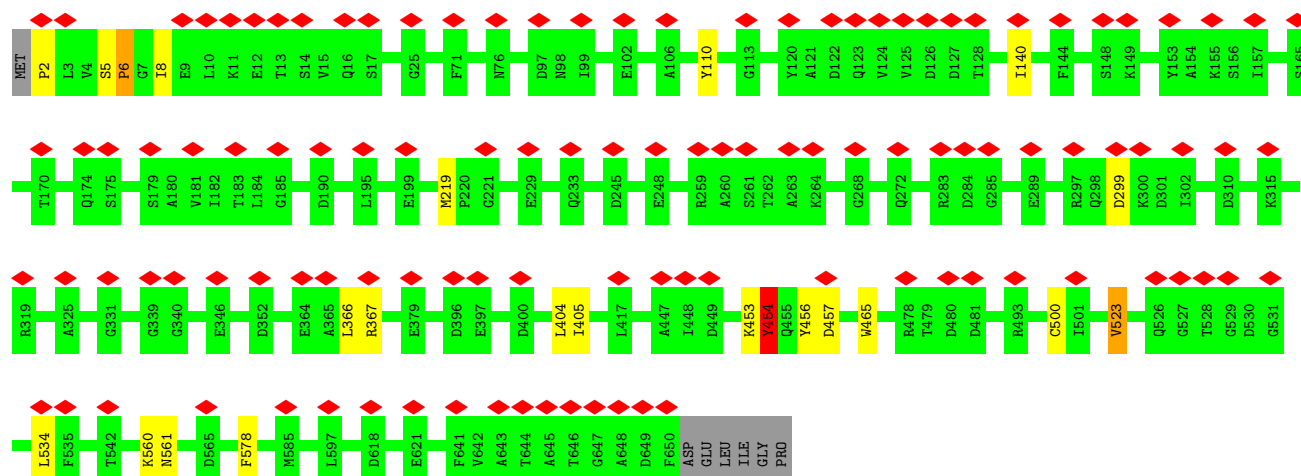


- Molecule 8: Baseplate wedge protein gp10

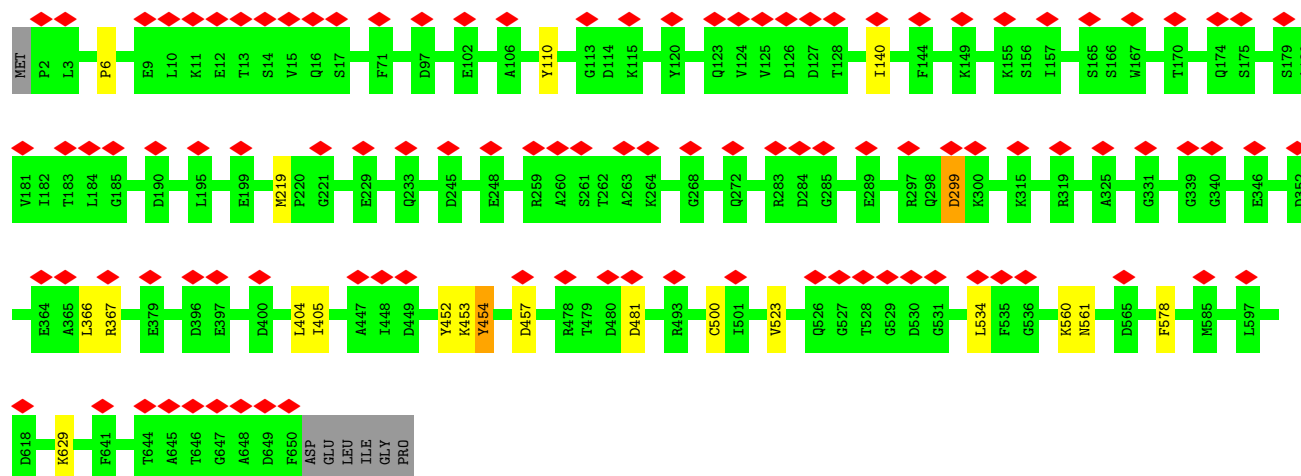


- Molecule 8: Baseplate wedge protein gp10

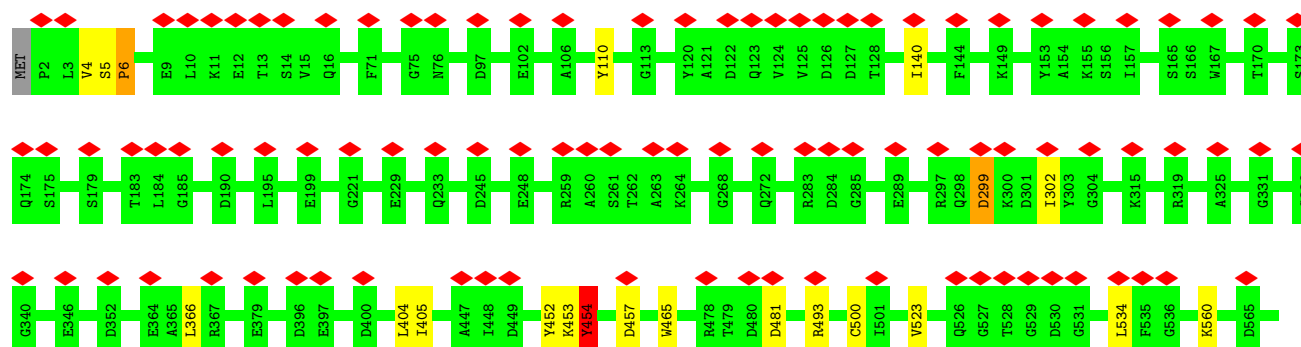


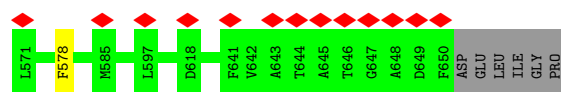


• Molecule 9: Tail sheath protein

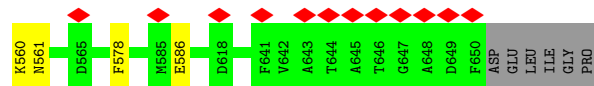
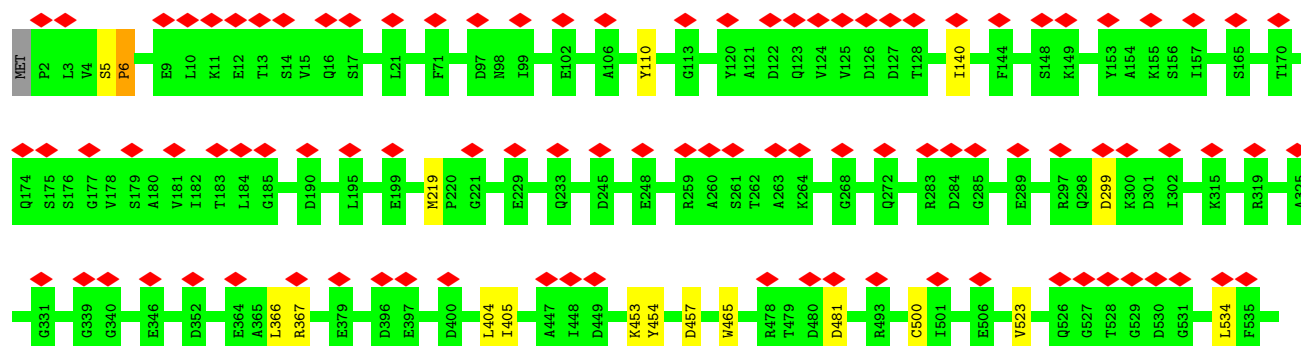


• Molecule 9: Tail sheath protein

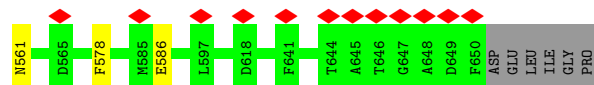
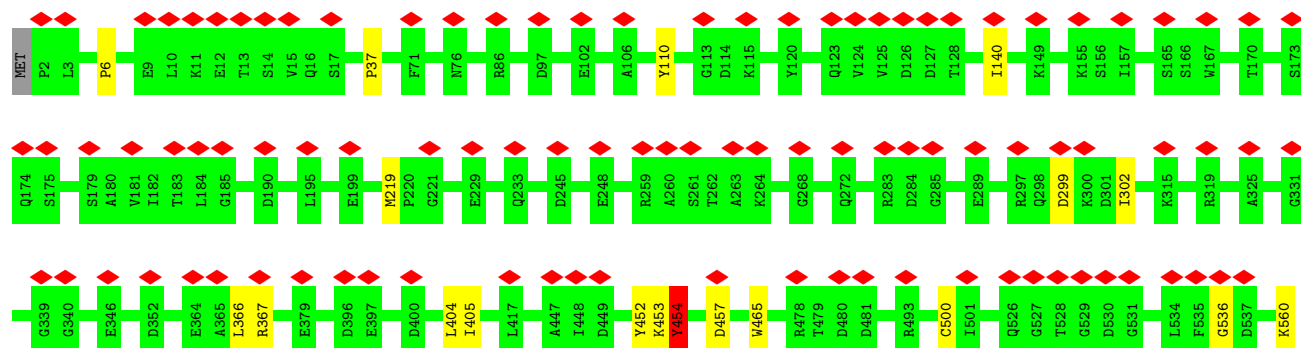




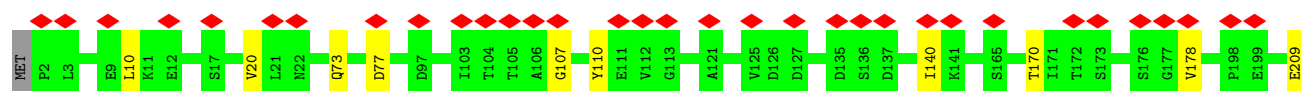
• Molecule 9: Tail sheath protein

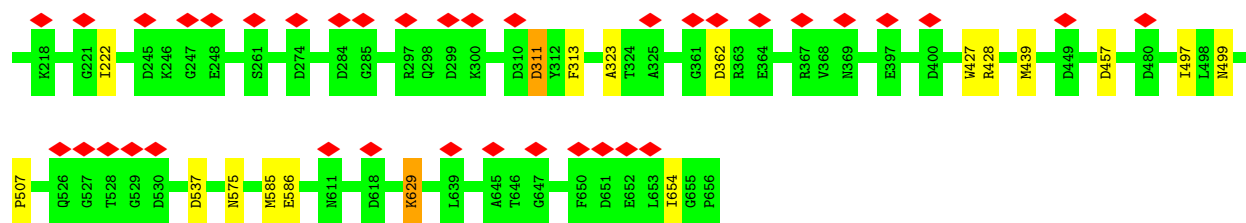


• Molecule 9: Tail sheath protein



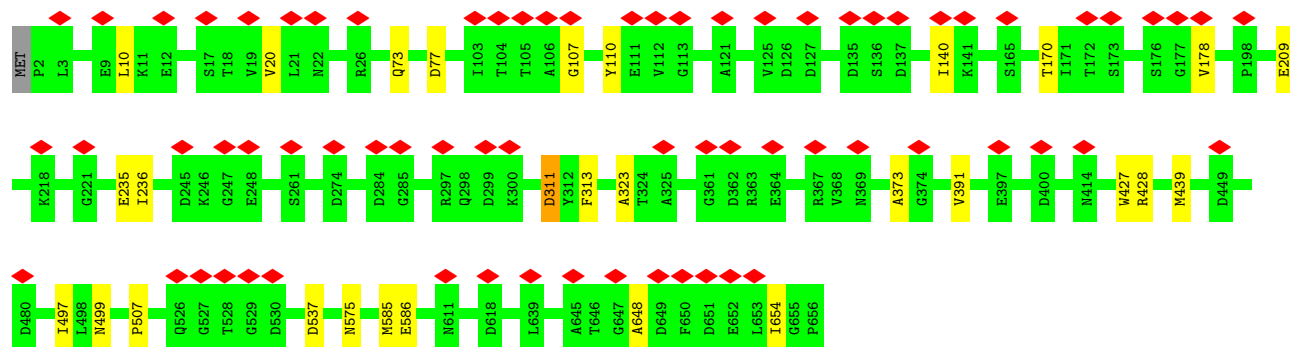
• Molecule 9: Tail sheath protein





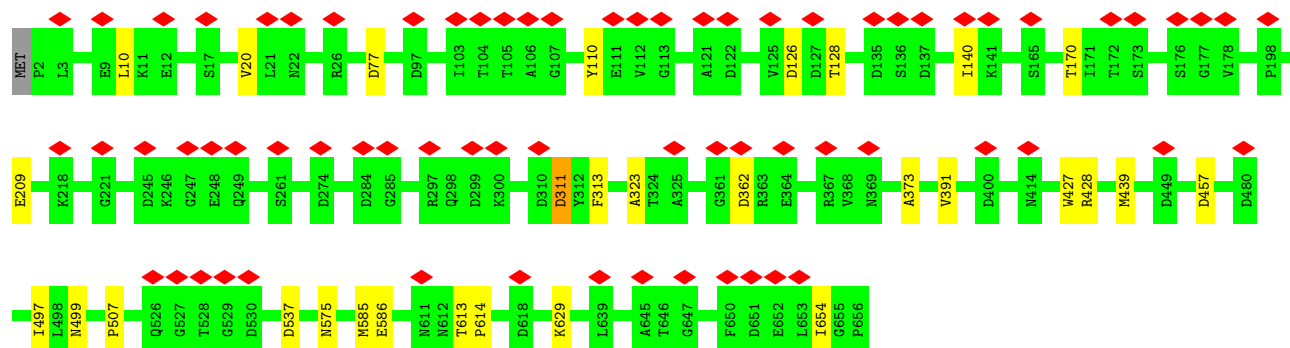
• Molecule 9: Tail sheath protein

Chain SG: 11% 95%



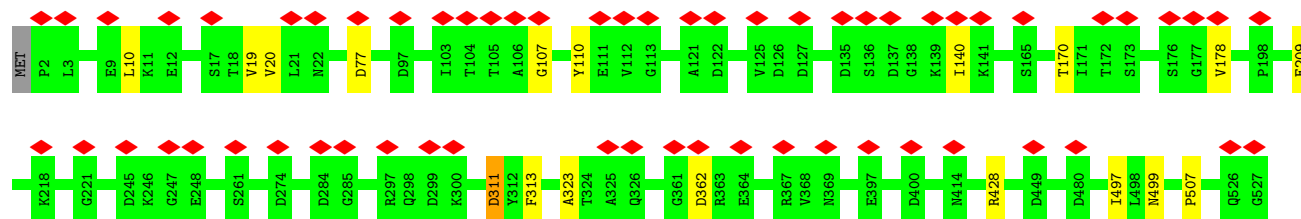
• Molecule 9: Tail sheath protein

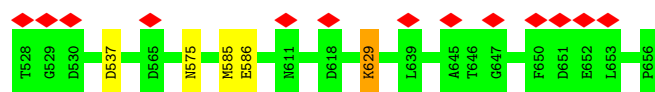
Chain SL: 11% 95%



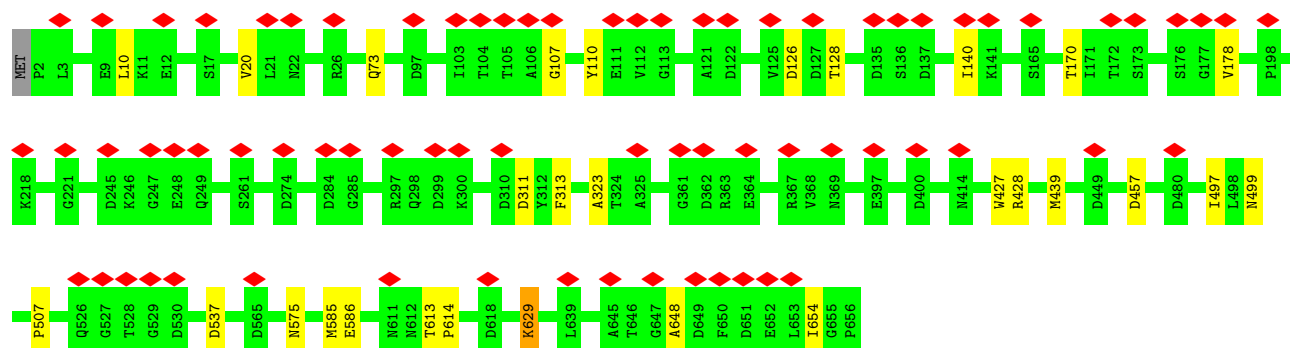
• Molecule 9: Tail sheath protein

Chain SH: 11% 96%

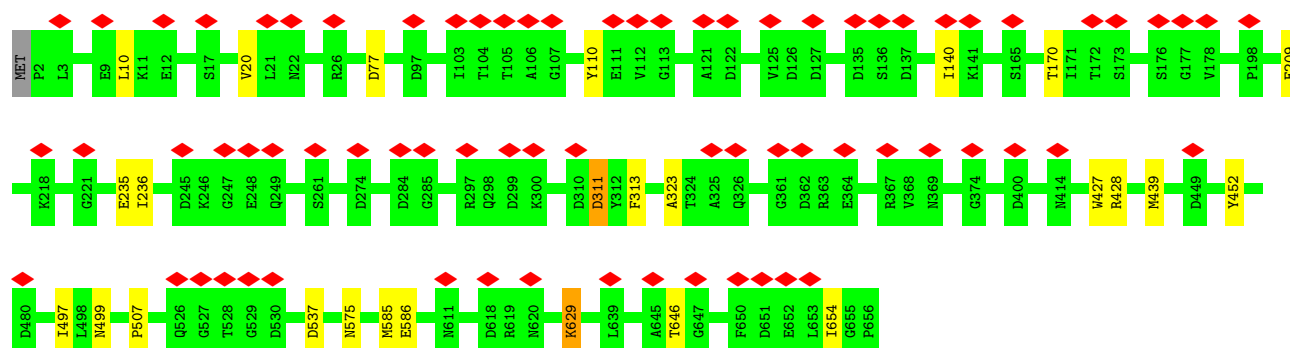




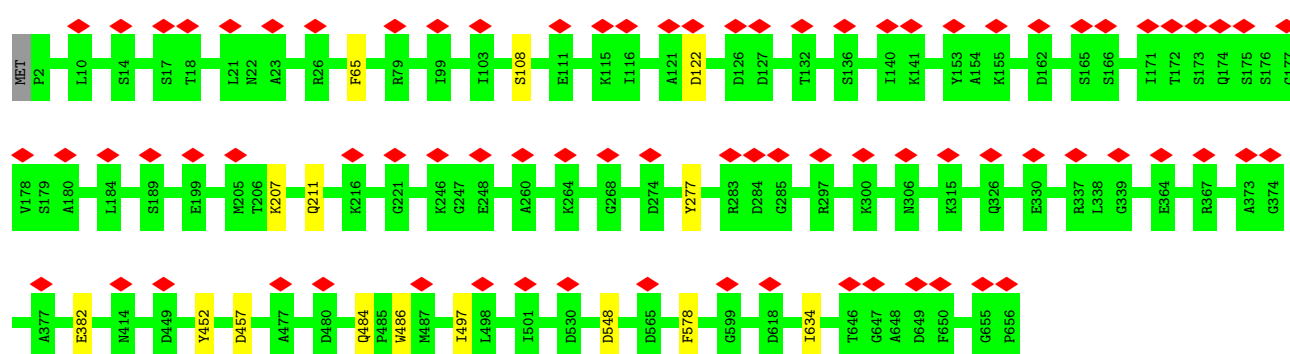
- Molecule 9: Tail sheath protein



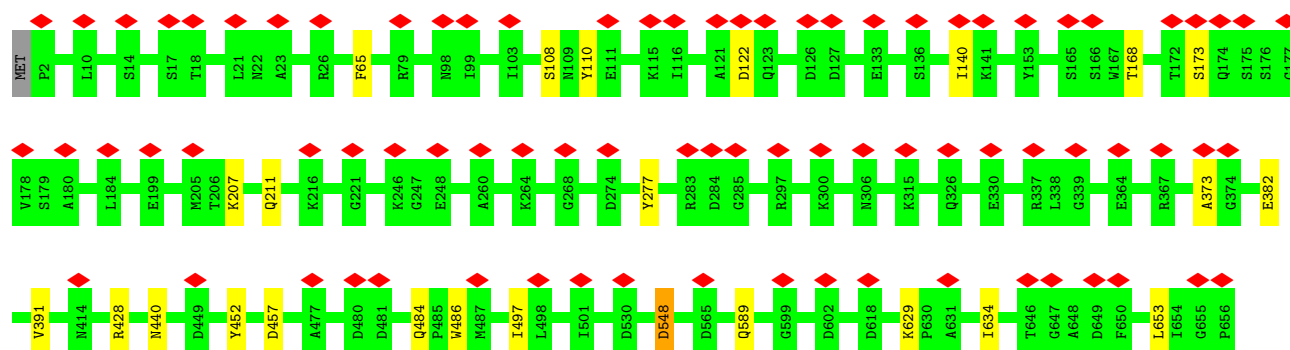
- Molecule 9: Tail sheath protein



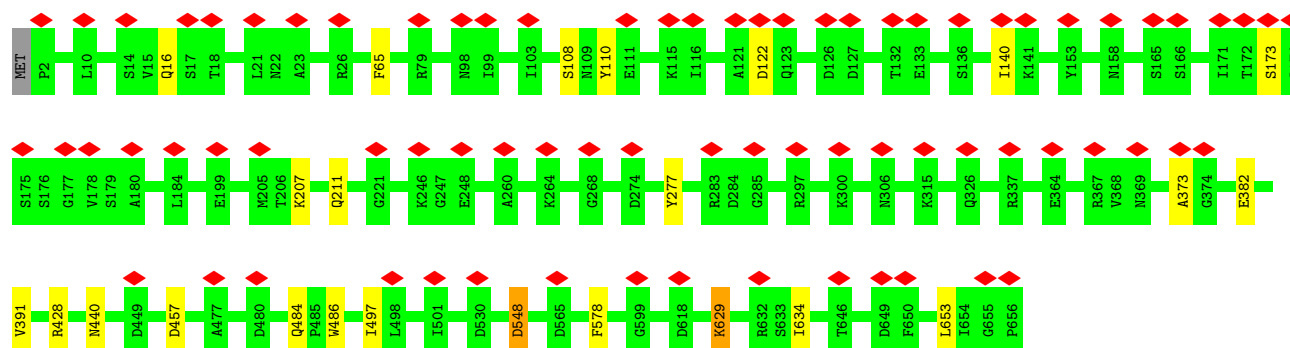
- Molecule 9: Tail sheath protein



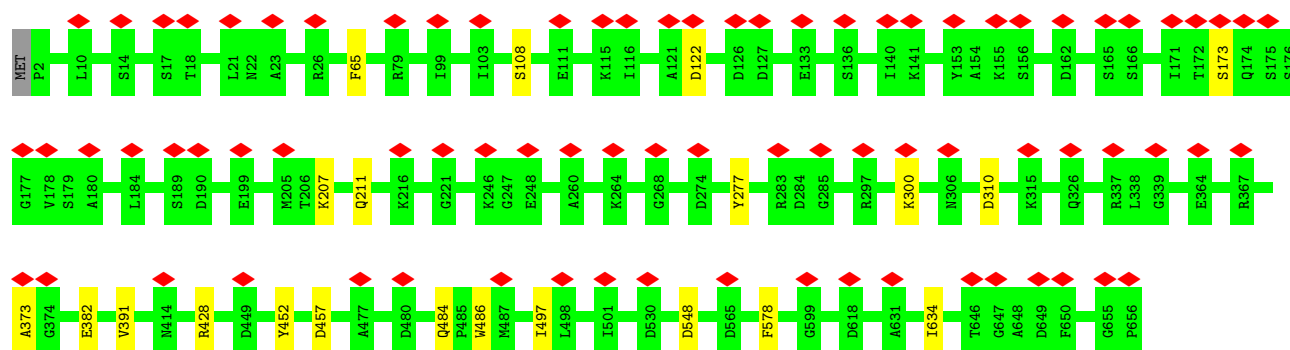
- Molecule 9: Tail sheath protein



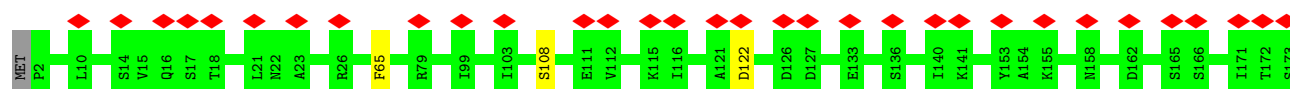
• Molecule 9: Tail sheath protein

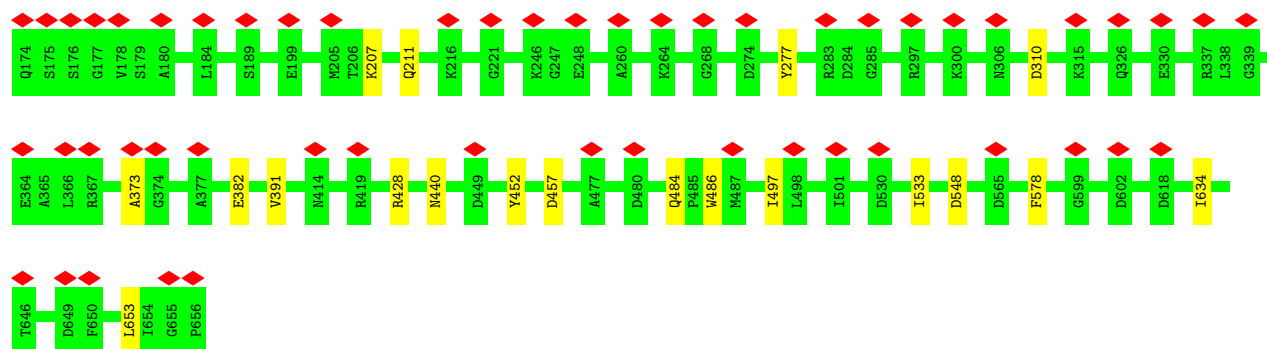


• Molecule 9: Tail sheath protein



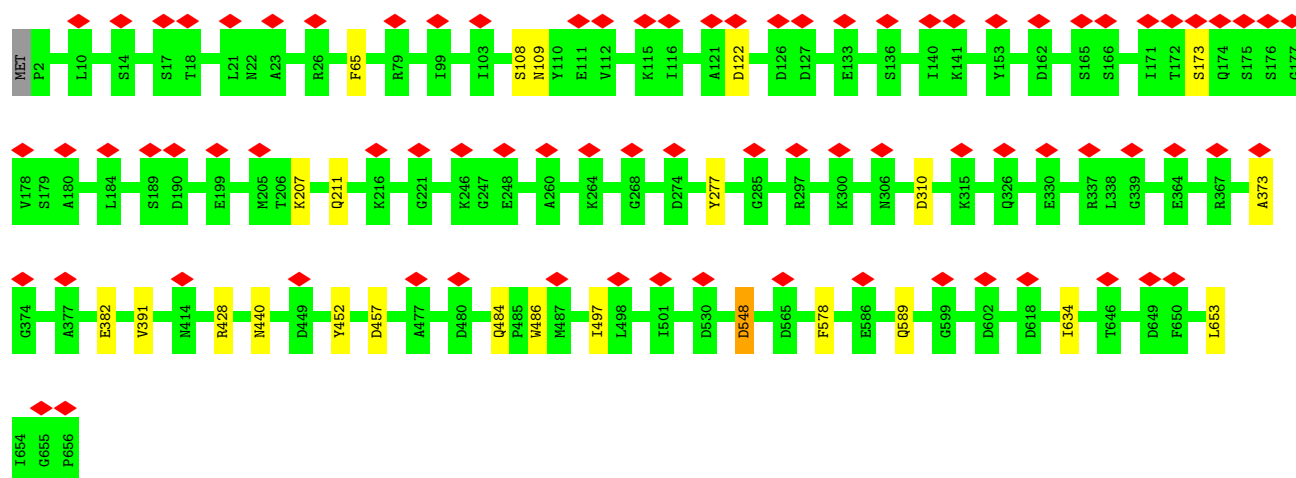
• Molecule 9: Tail sheath protein





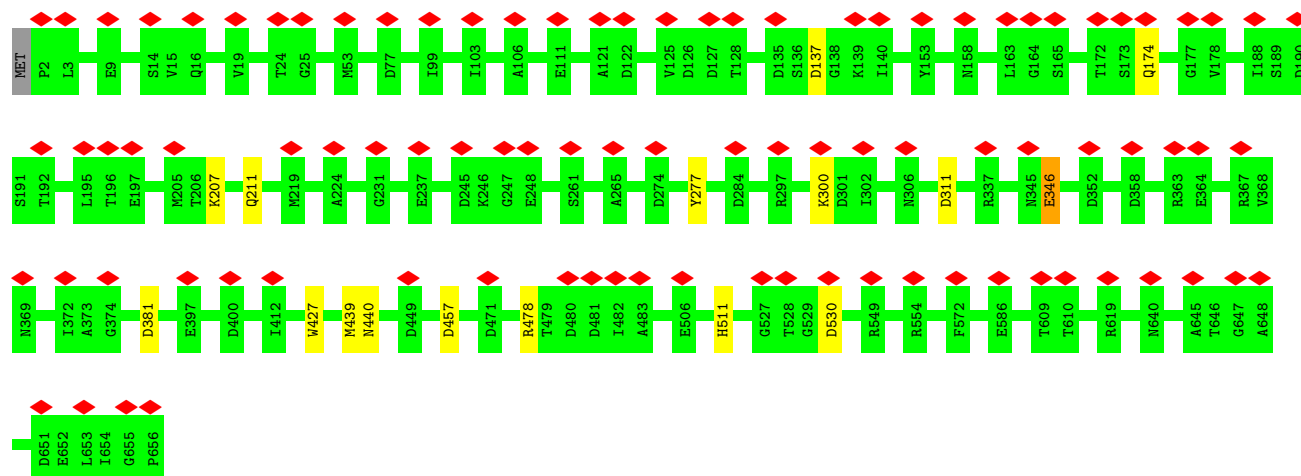
- Molecule 9: Tail sheath protein

Chain SR: 12% 96%

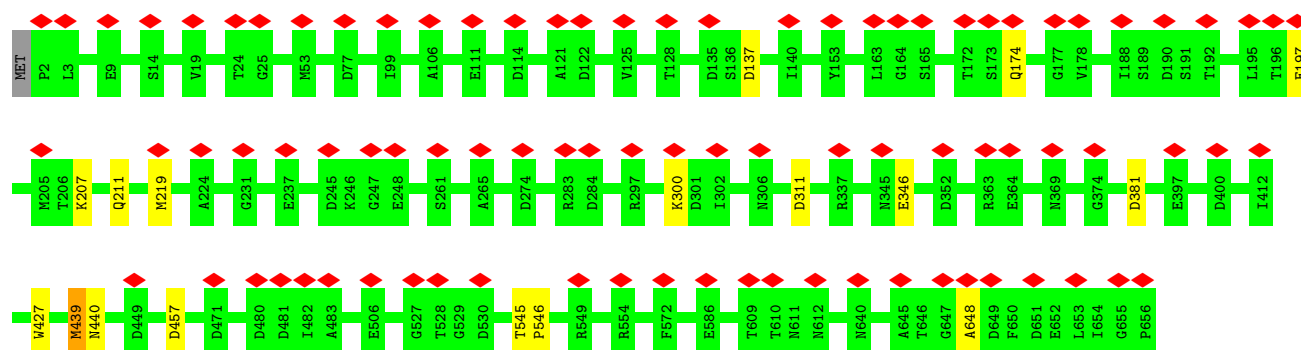


- Molecule 9: Tail sheath protein

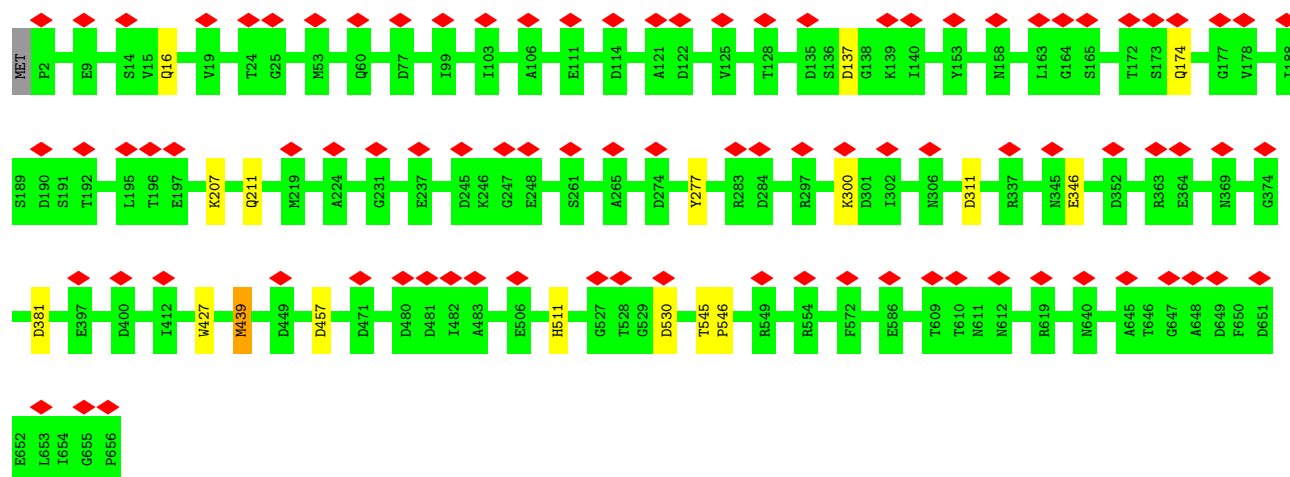
Chain SW: 14% 97%



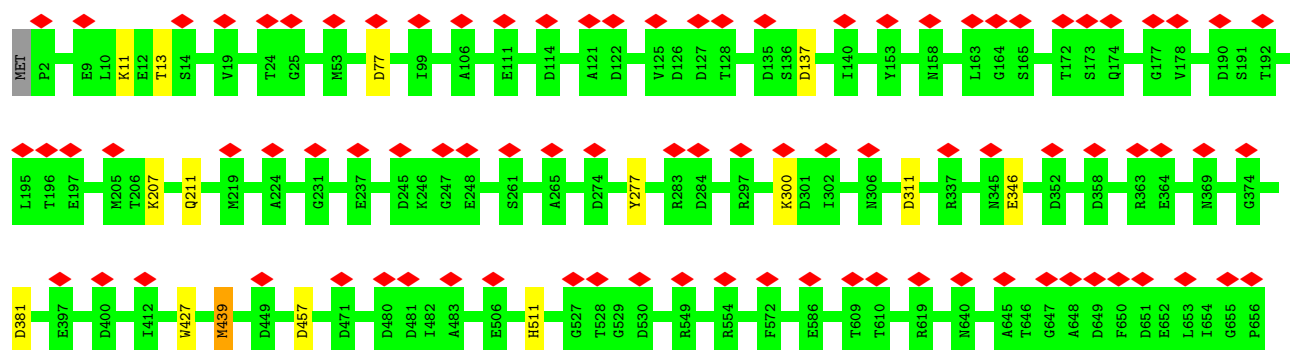
- Molecule 9: Tail sheath protein



- Molecule 9: Tail sheath protein

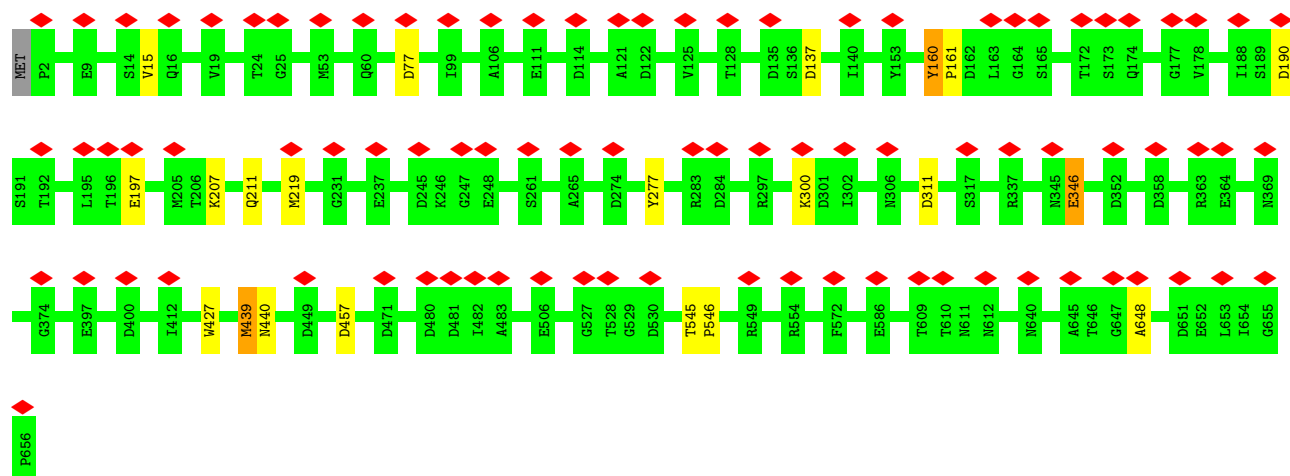


- Molecule 9: Tail sheath protein

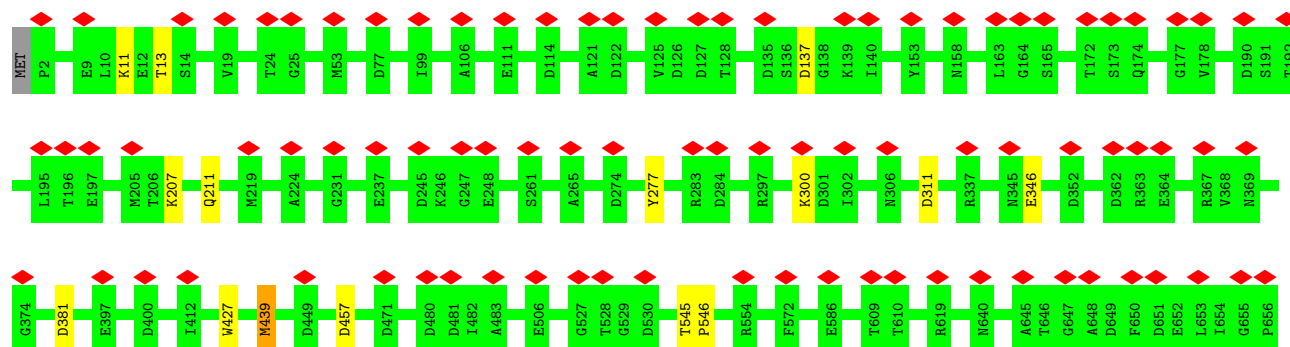


- Molecule 9: Tail sheath protein

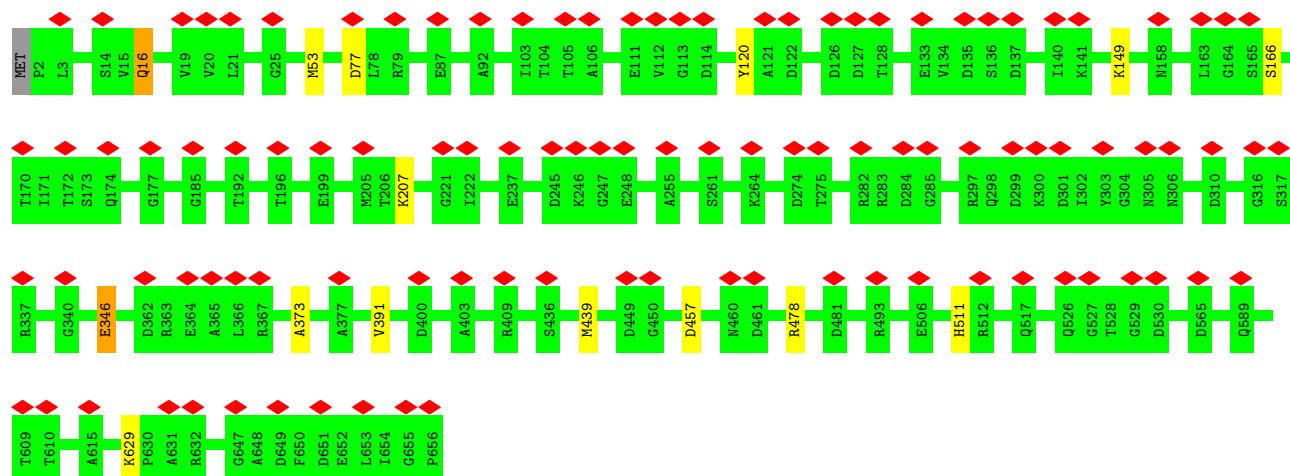




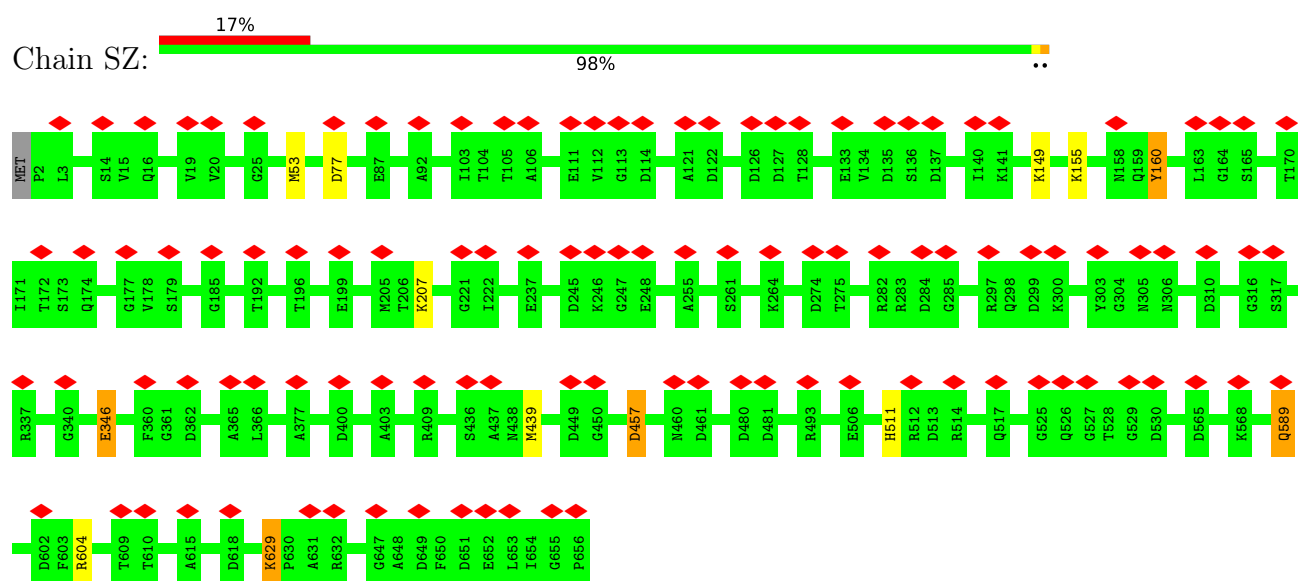
- Molecule 9: Tail sheath protein



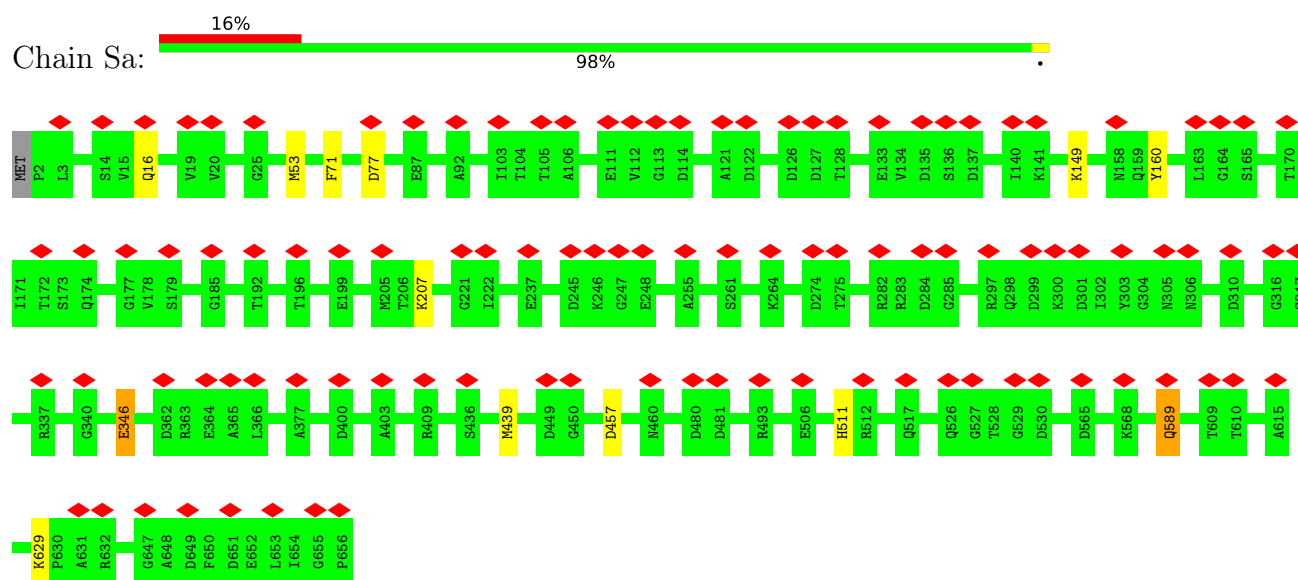
- Molecule 9: Tail sheath protein



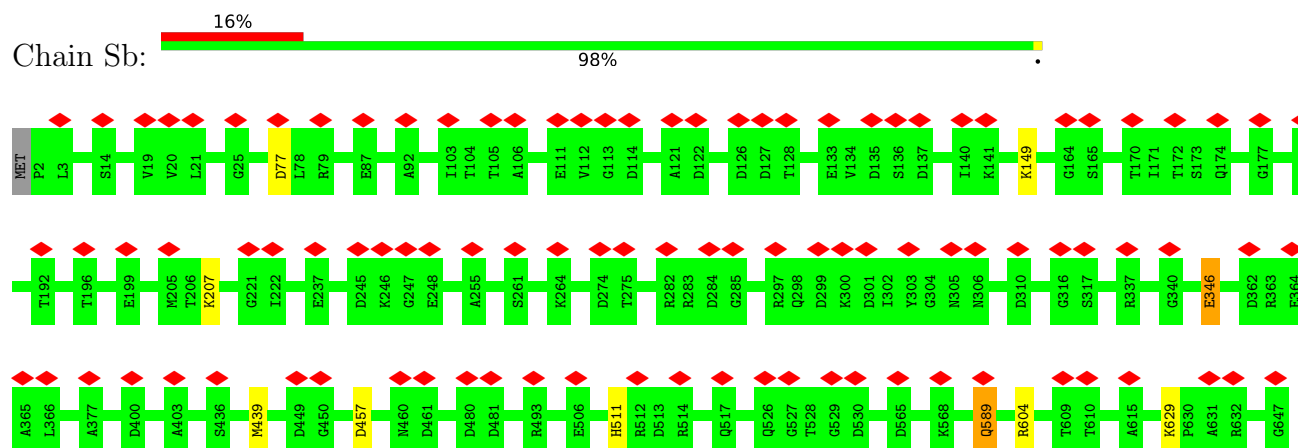
- Molecule 9: Tail sheath protein

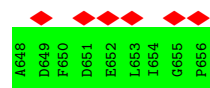


• Molecule 9: Tail sheath protein

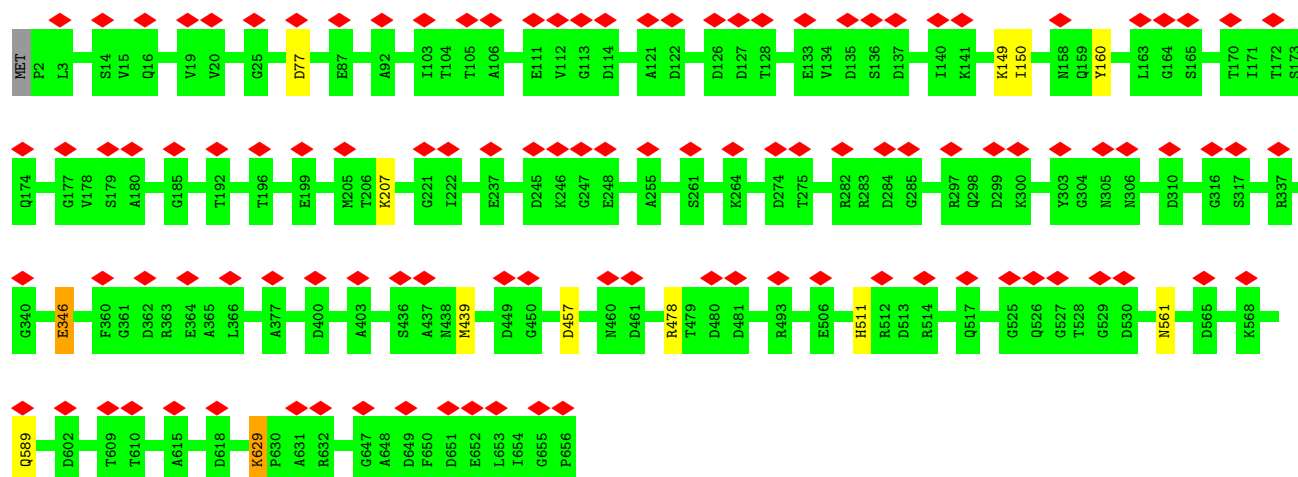


• Molecule 9: Tail sheath protein

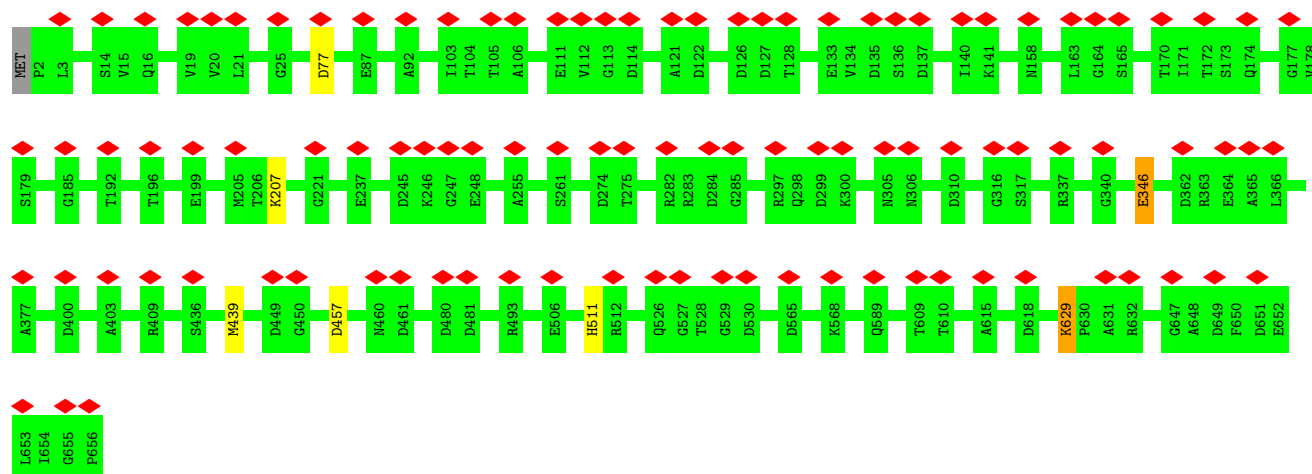




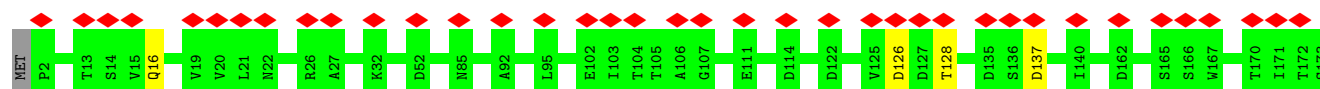
• Molecule 9: Tail sheath protein

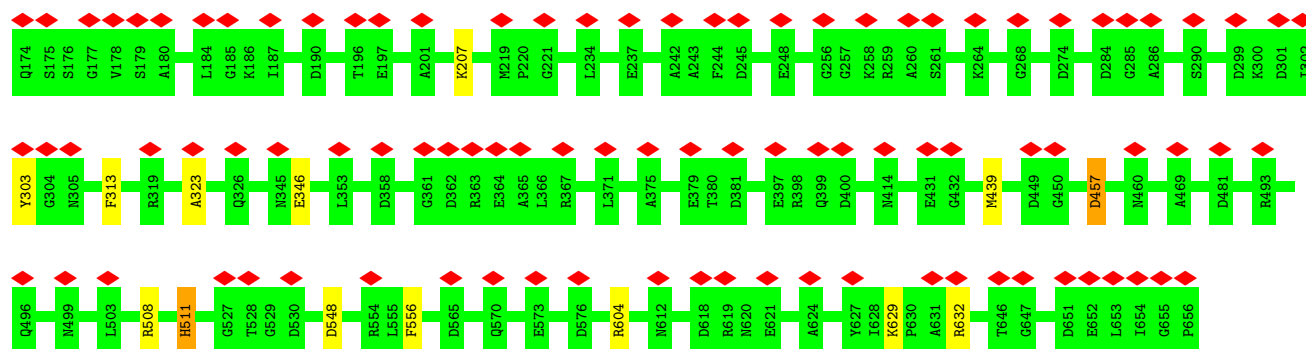


• Molecule 9: Tail sheath protein

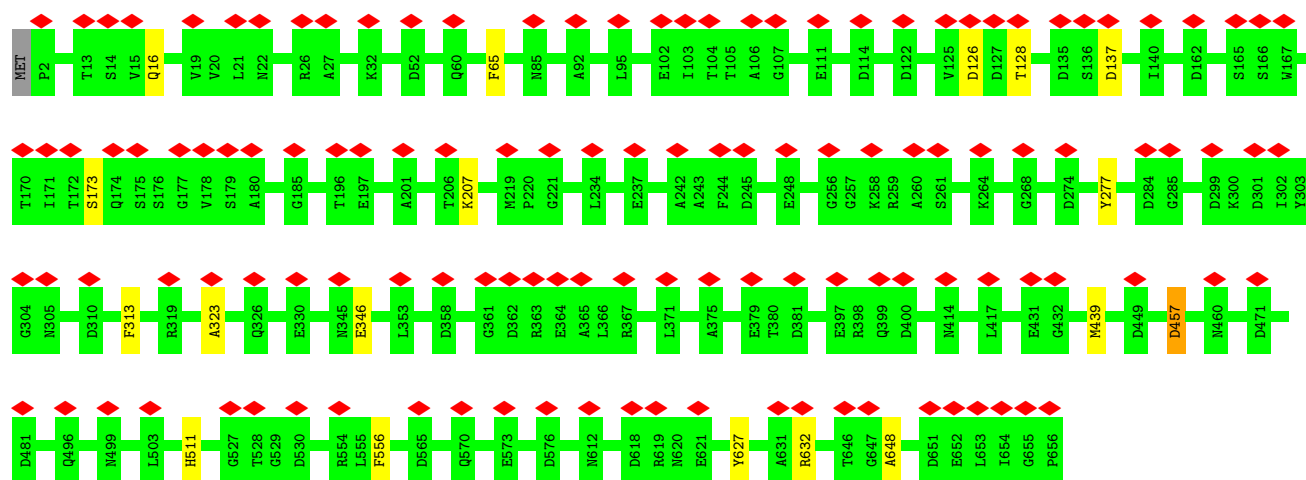


• Molecule 9: Tail sheath protein

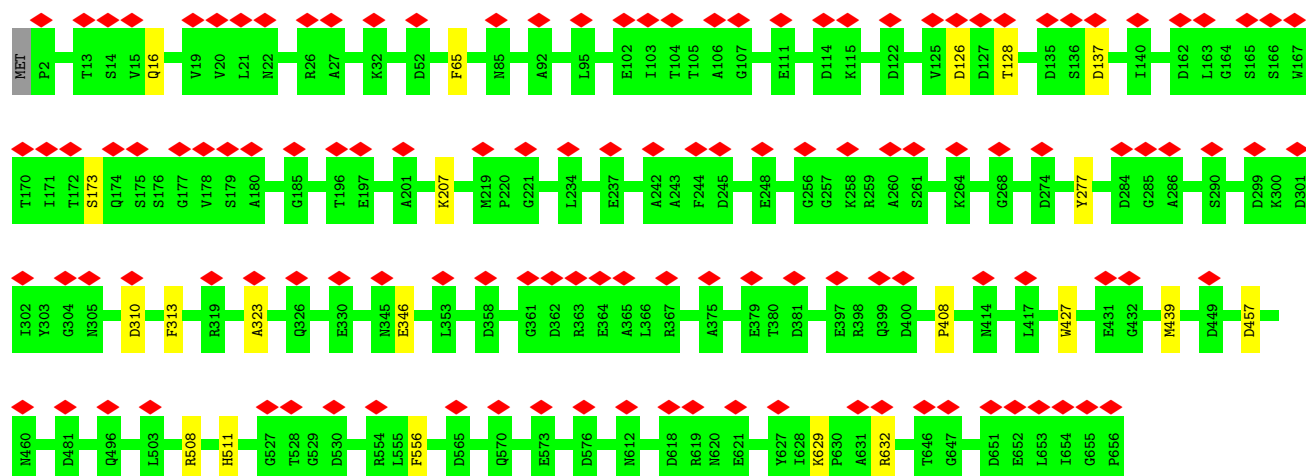




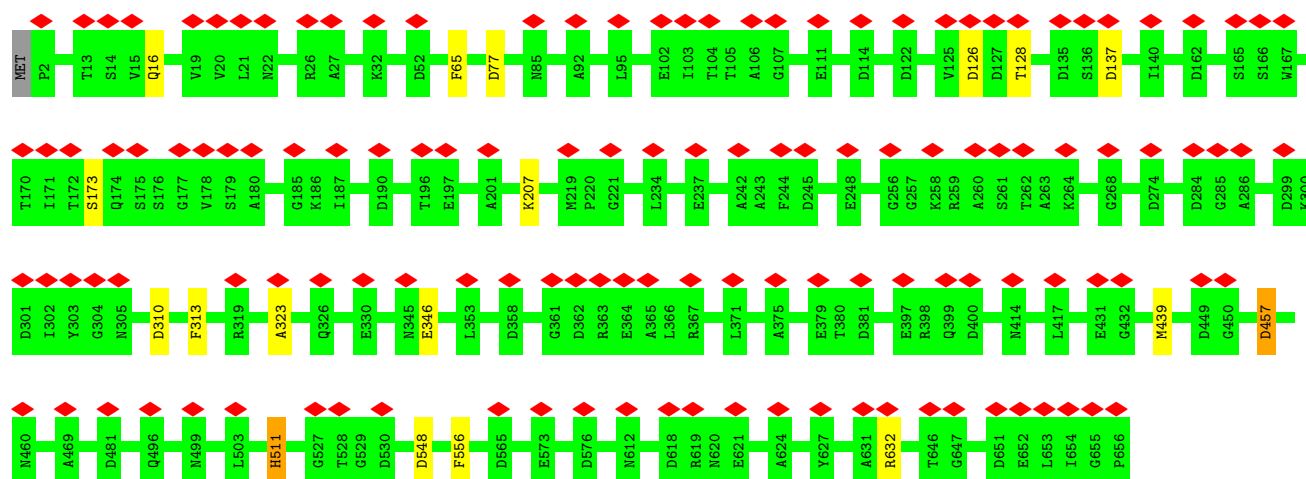
• Molecule 9: Tail sheath protein



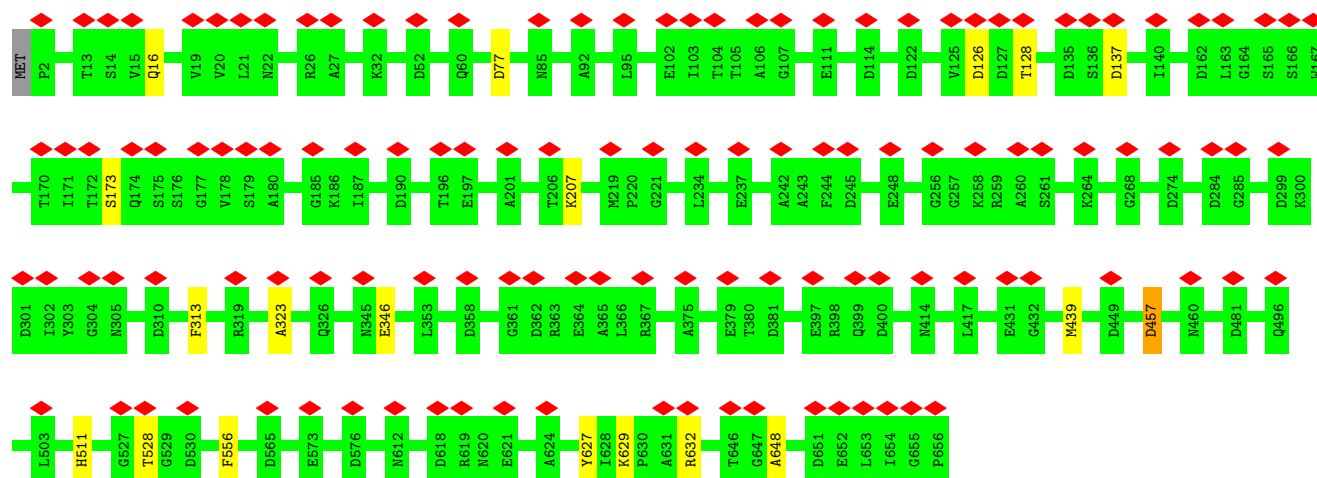
• Molecule 9: Tail sheath protein



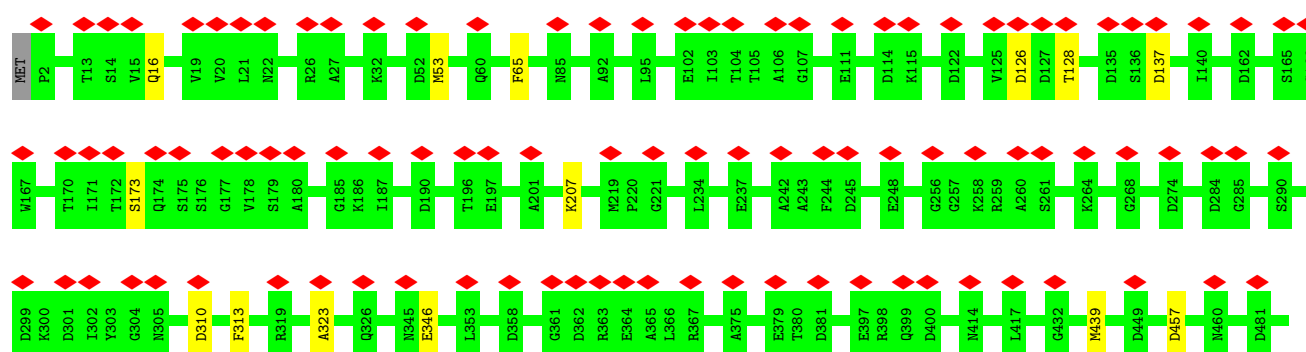
• Molecule 9: Tail sheath protein

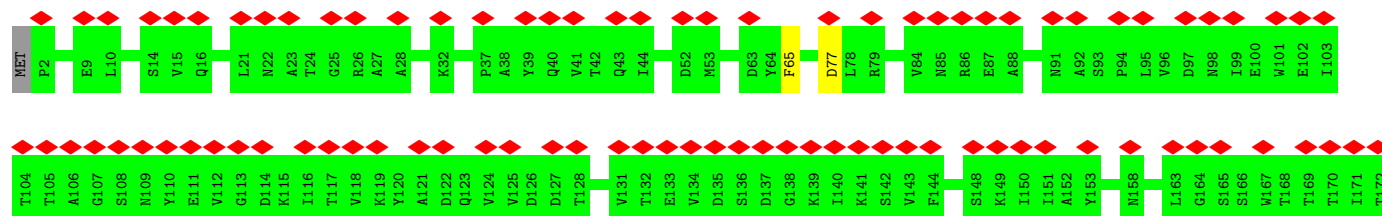


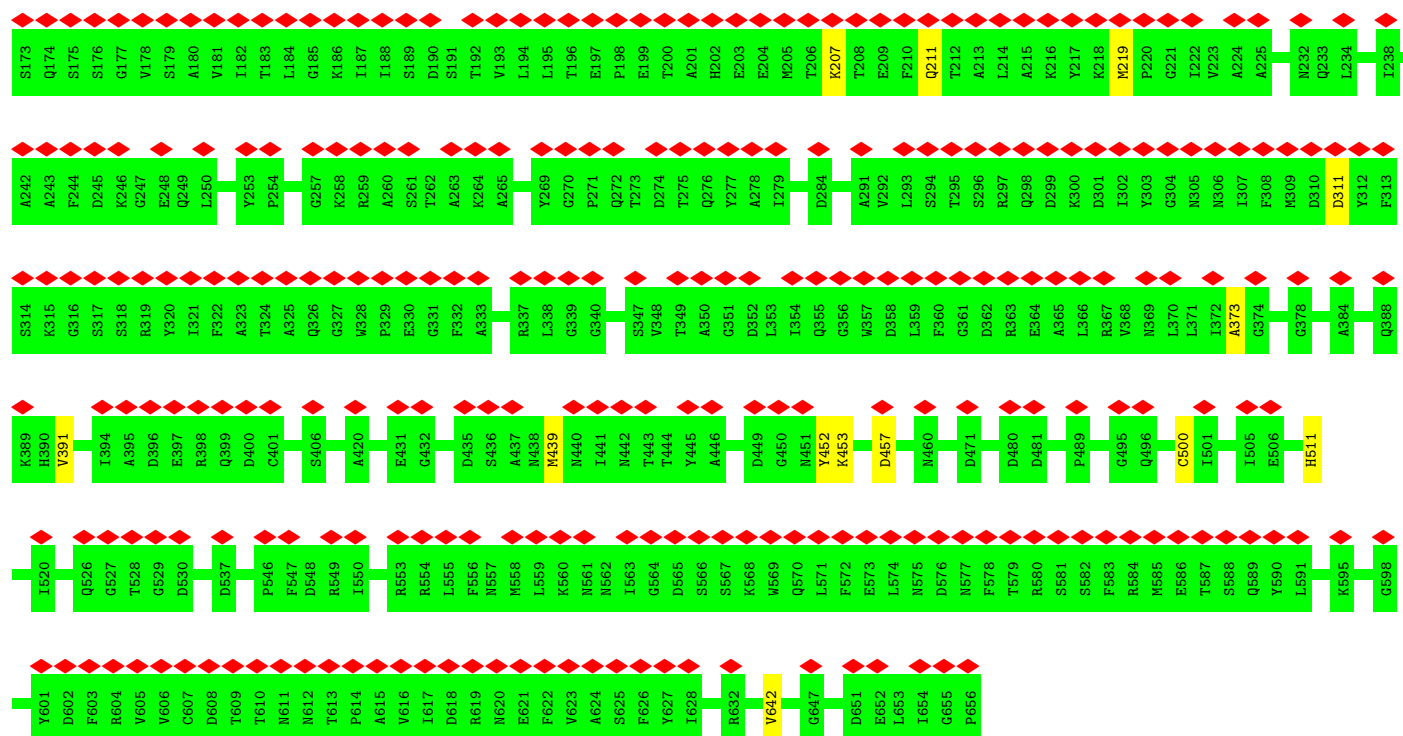
• Molecule 9: Tail sheath protein



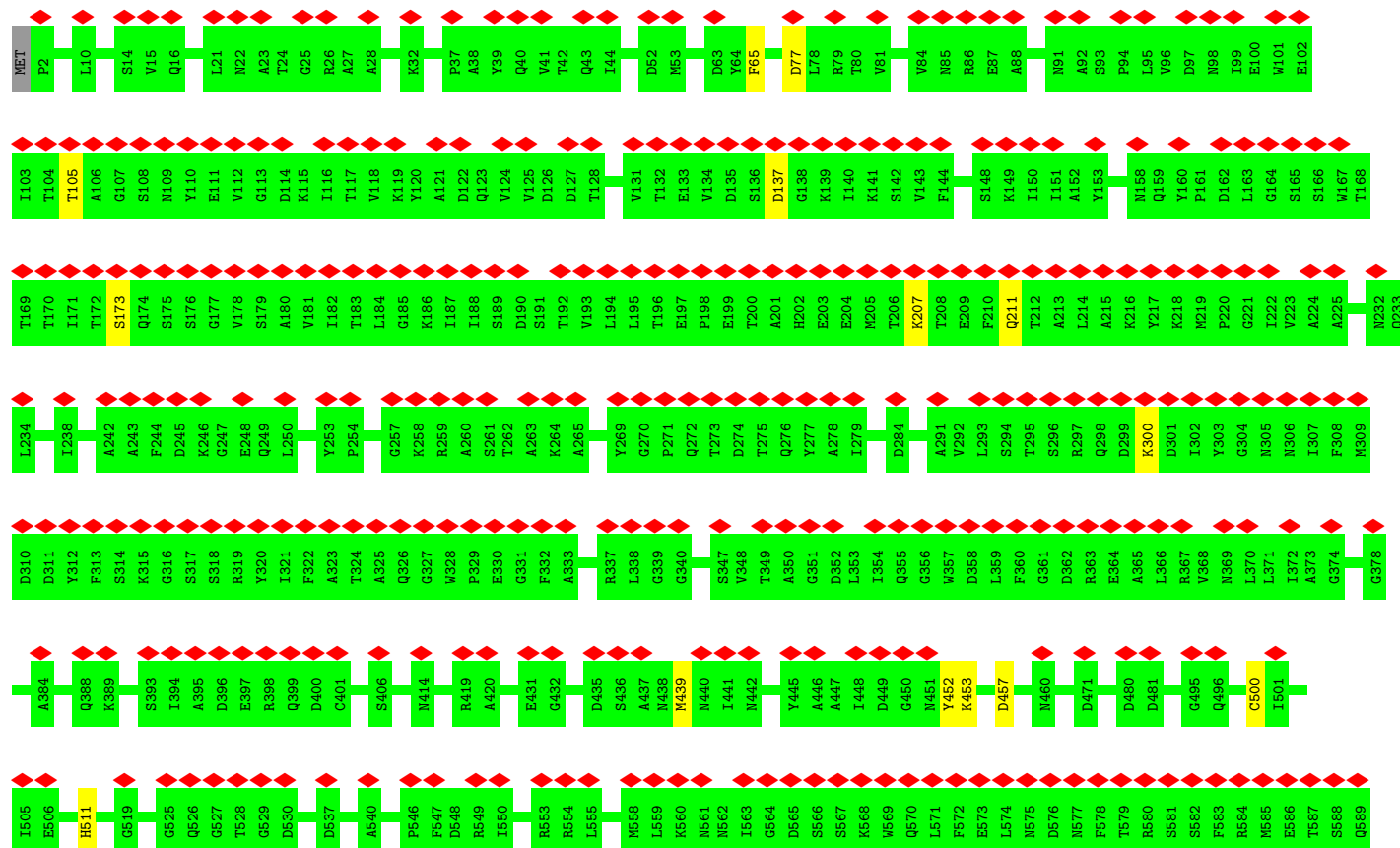
• Molecule 9: Tail sheath protein

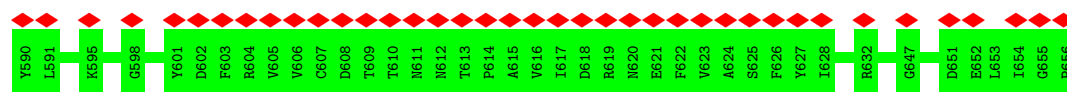






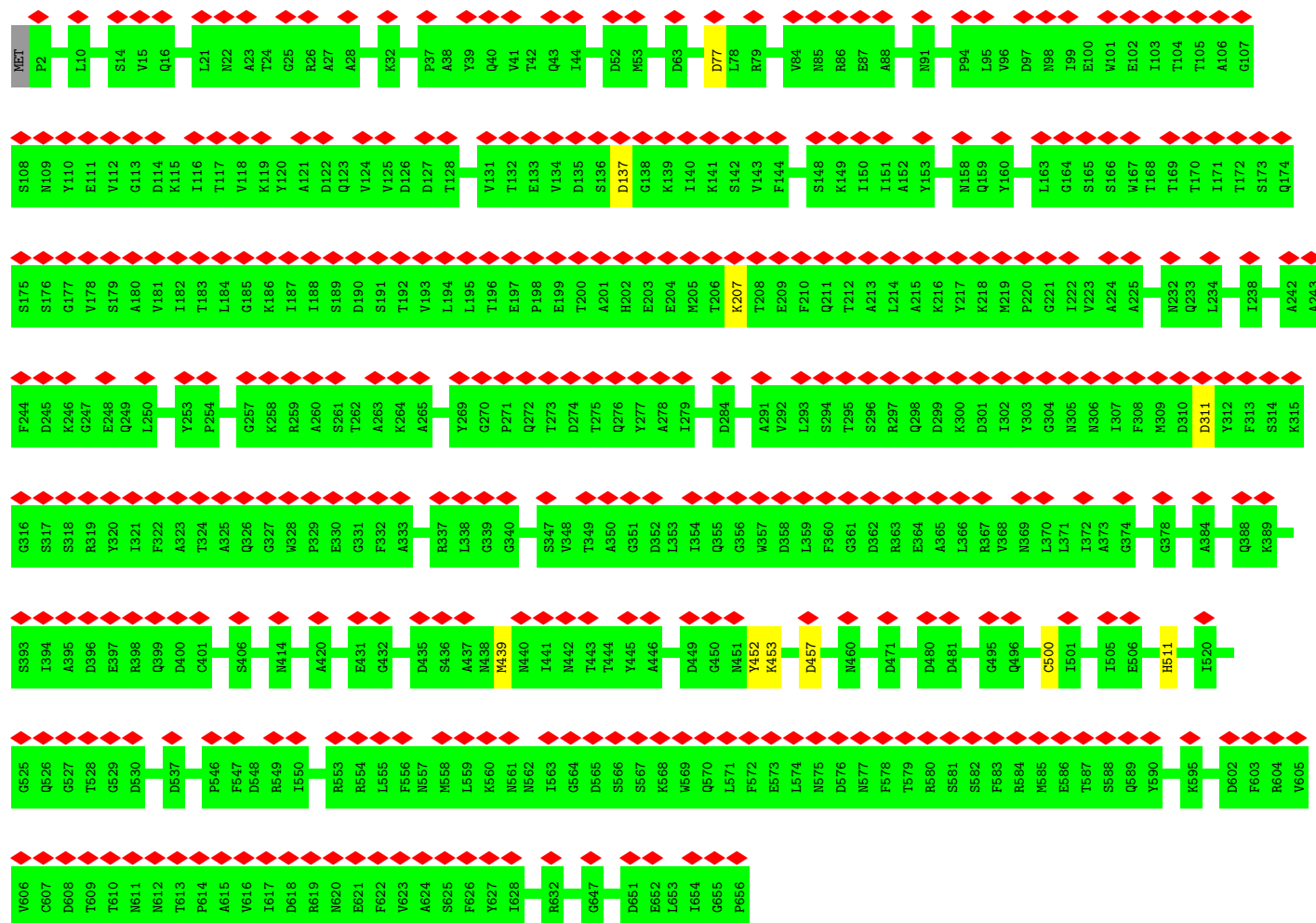
• Molecule 9: Tail sheath protein





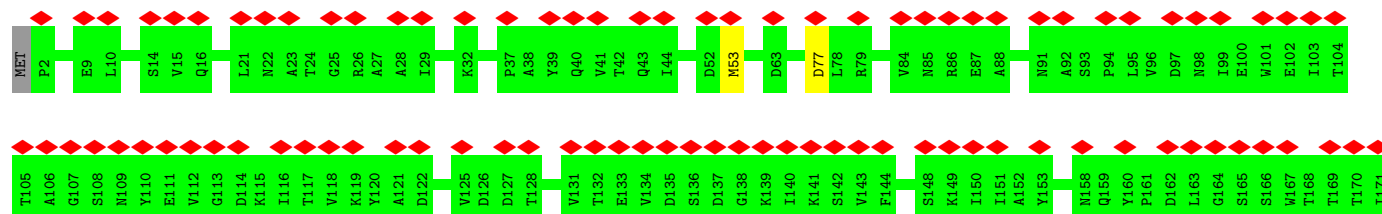
• Molecule 9: Tail sheath protein

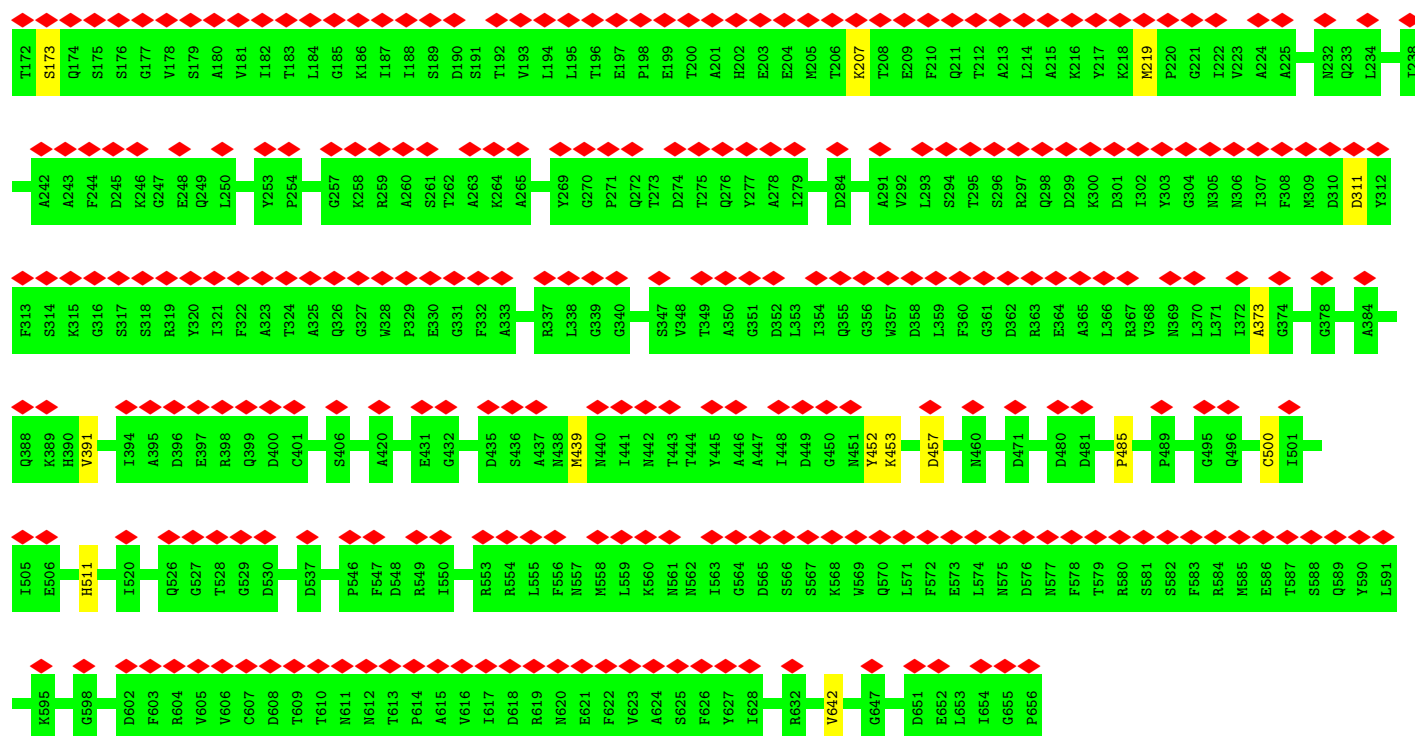
Chain Sn: 55% 98%



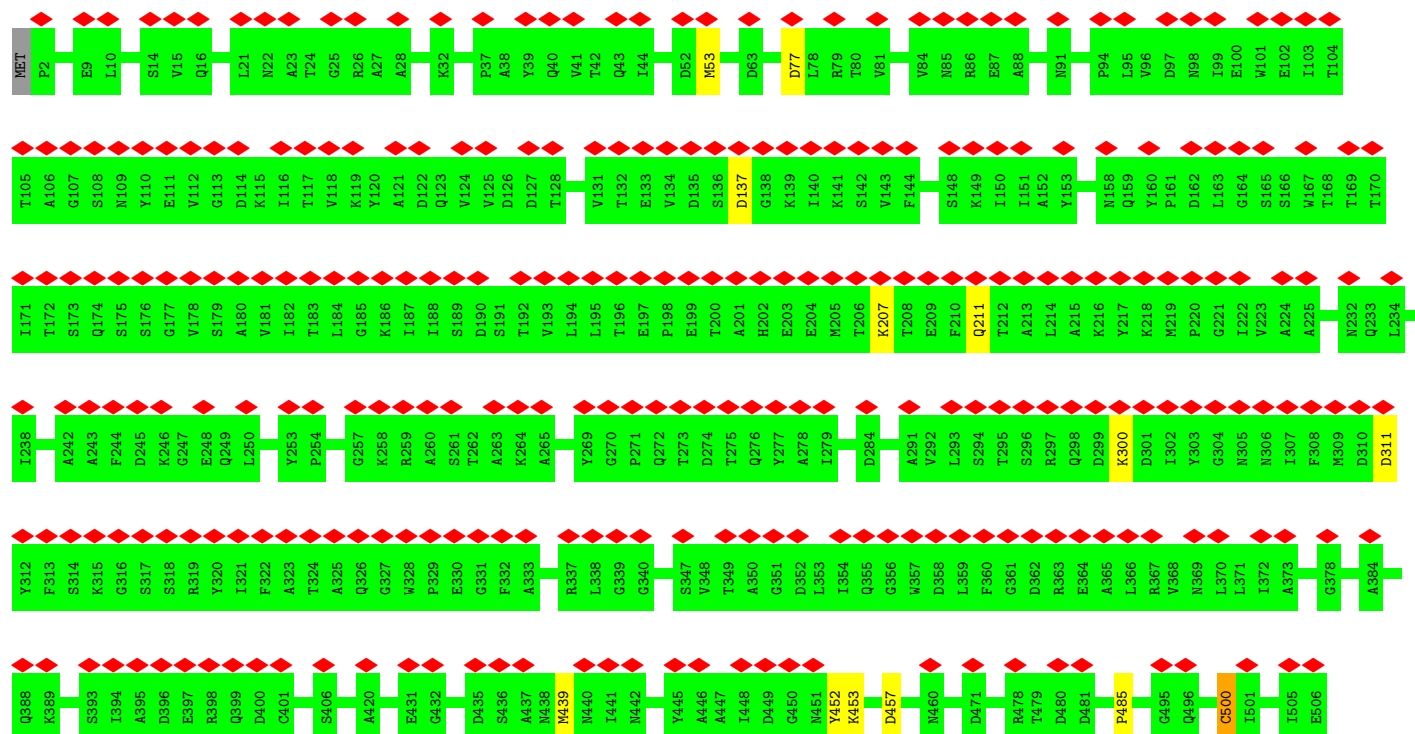
• Molecule 9: Tail sheath protein

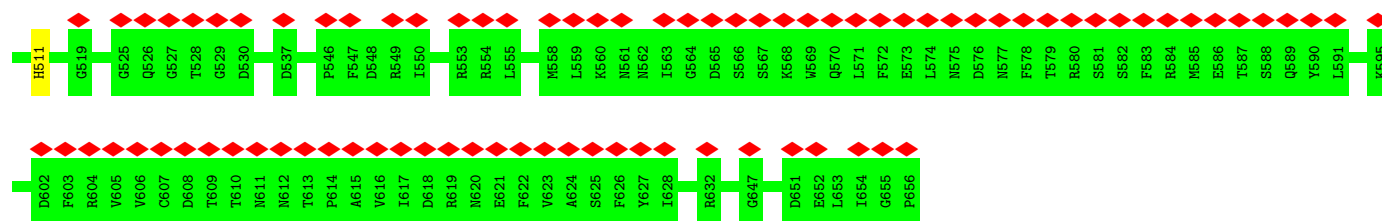
Chain So: 56% 97%



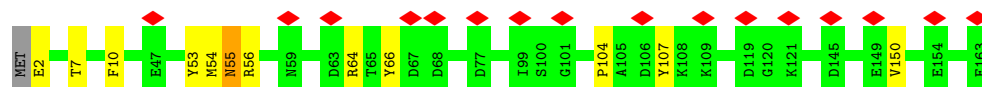


• Molecule 9: Tail sheath protein

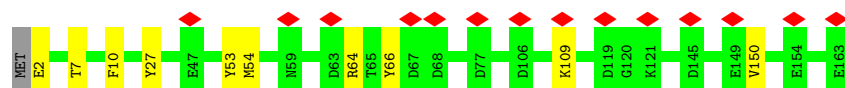




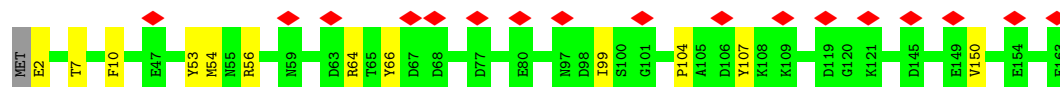
- Molecule 10: Tail tube protein



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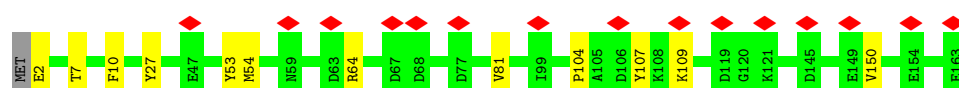
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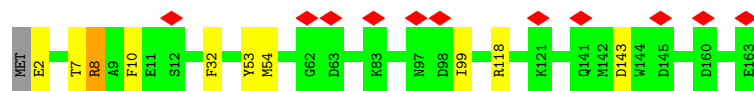


- Molecule 10: Tail tube protein

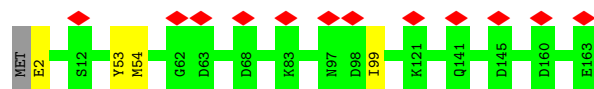




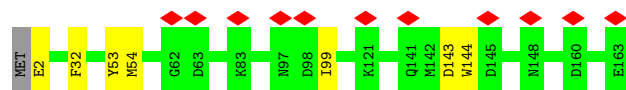
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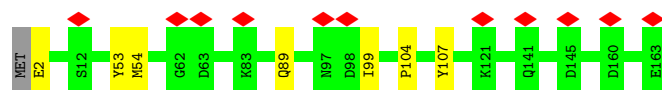
- Molecule 10: Tail tube protein



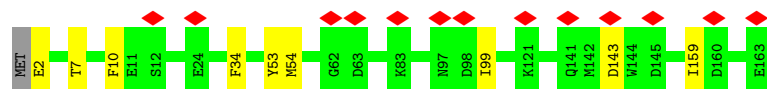
- Molecule 10: Tail tube protein



- Molecule 10: Tail tube protein

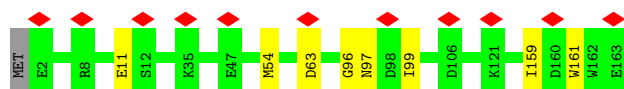


- Molecule 10: Tail tube protein



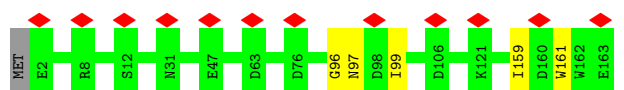
- Molecule 10: Tail tube protein

Chain TY:  7% 94% 5%



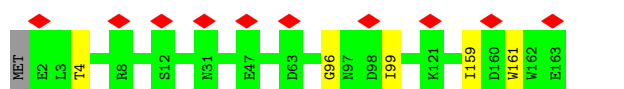
- Molecule 10: Tail tube protein

Chain TZ:  7% 96%



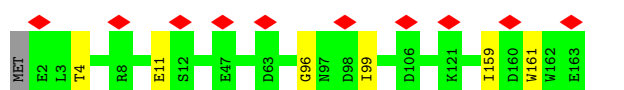
- Molecule 10: Tail tube protein

Chain Ta:  6% 96%



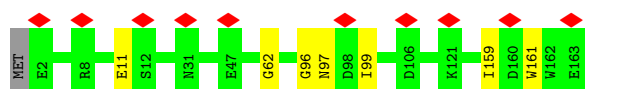
- Molecule 10: Tail tube protein

Chain Tb:  6% 96%



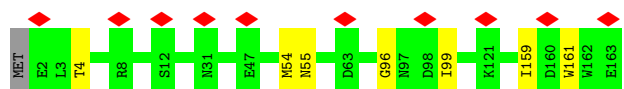
- Molecule 10: Tail tube protein

Chain Tc:  6% 95%



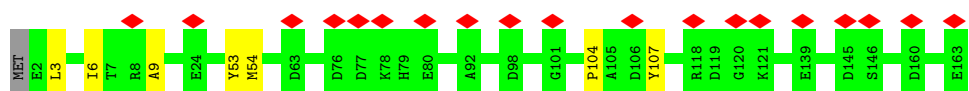
- Molecule 10: Tail tube protein

Chain Td:  6% 95%

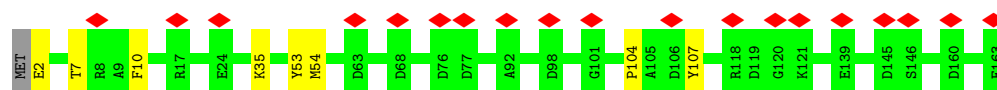
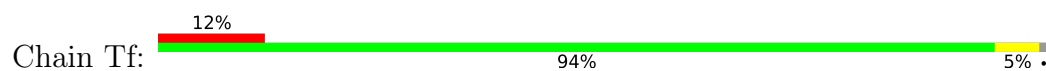


- Molecule 10: Tail tube protein

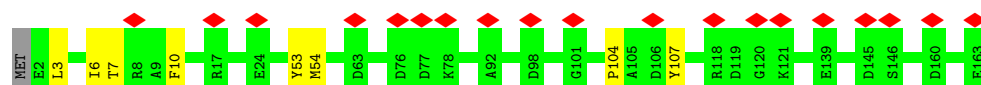
Chain Te:  12% 95%



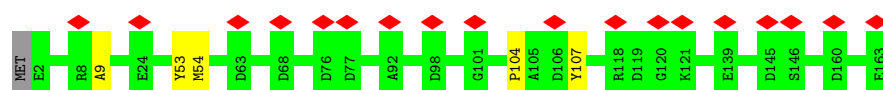
• Molecule 10: Tail tube protein



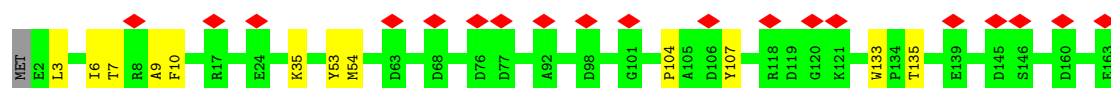
• Molecule 10: Tail tube protein



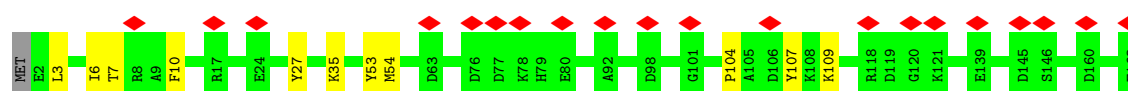
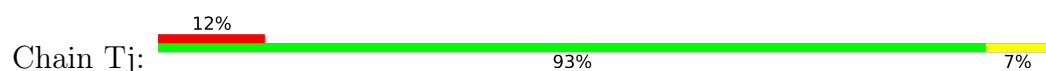
• Molecule 10: Tail tube protein



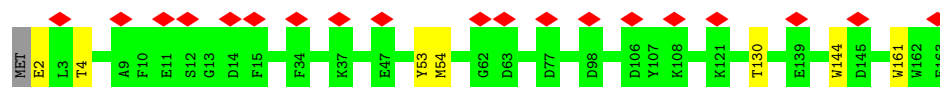
• Molecule 10: Tail tube protein



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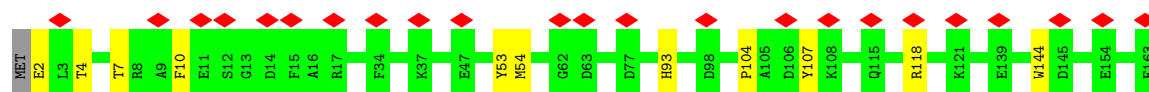


• Molecule 10: Tail tube protein

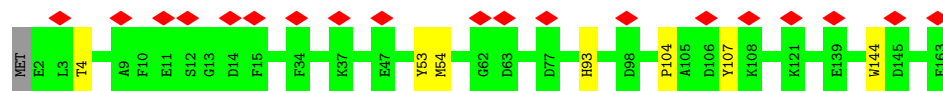


• Molecule 10: Tail tube protein

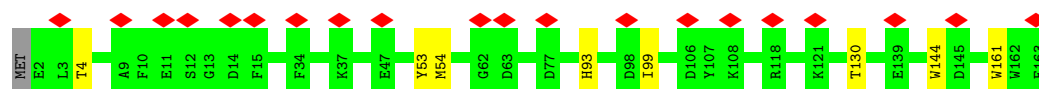




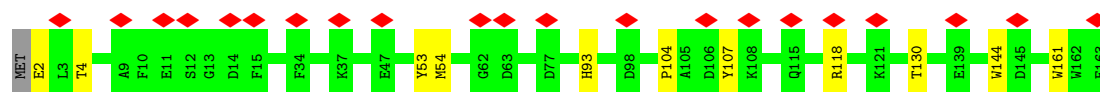
- Molecule 10: Tail tube protein



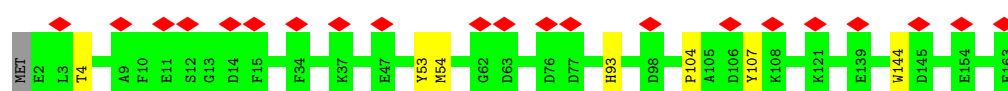
- Molecule 10: Tail tube protein



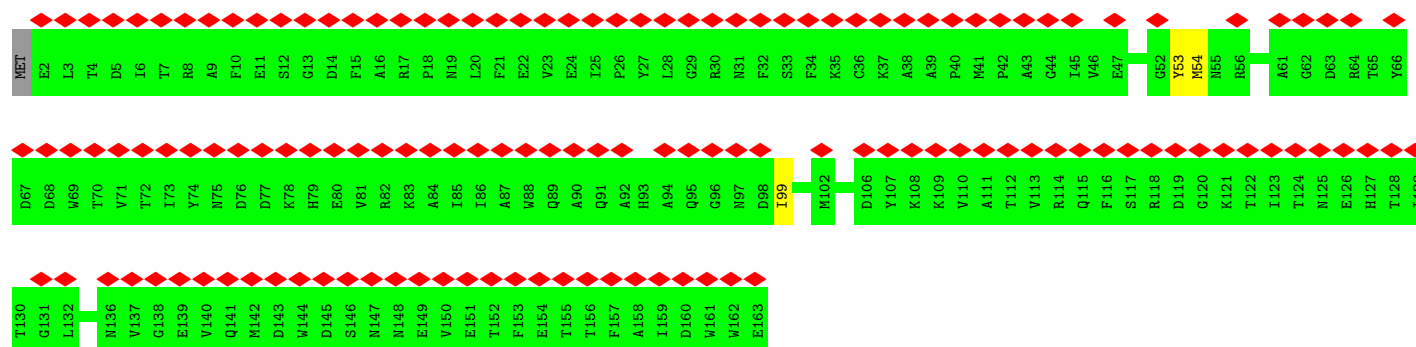
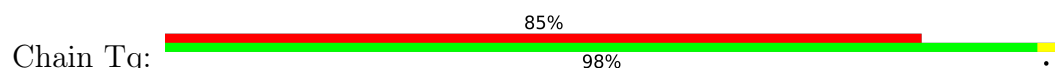
- Molecule 10: Tail tube protein



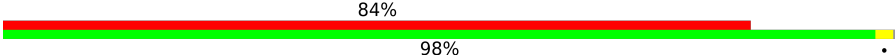
- Molecule 10: Tail tube protein

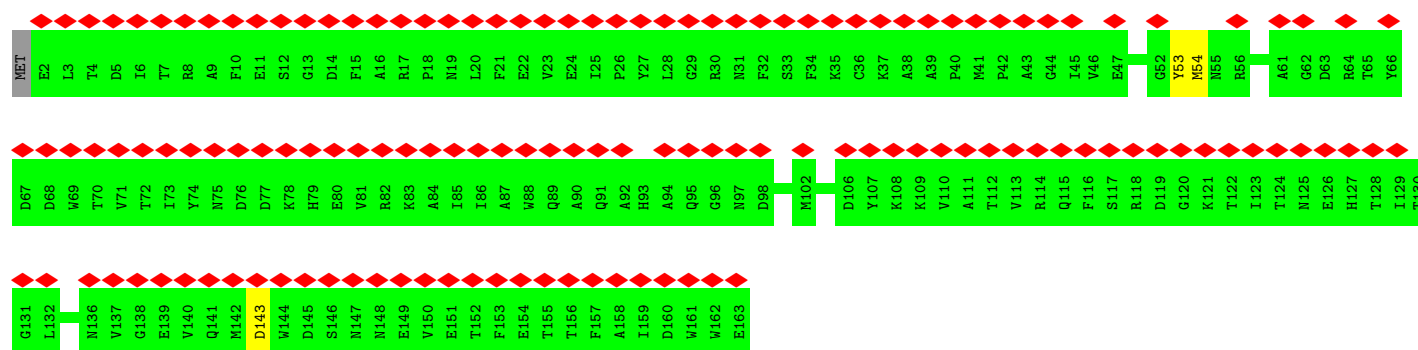


- Molecule 10: Tail tube protein

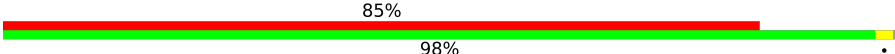


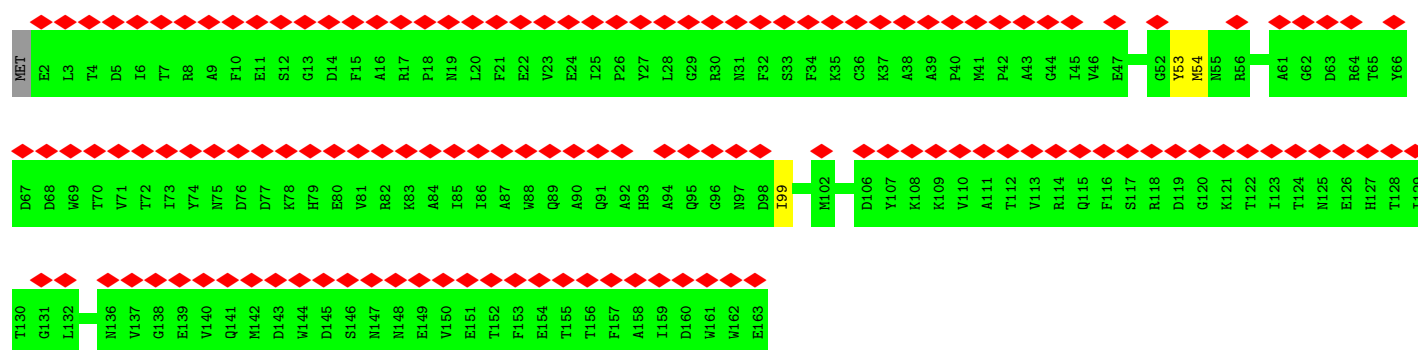
- Molecule 10: Tail tube protein

Chain Tr: 

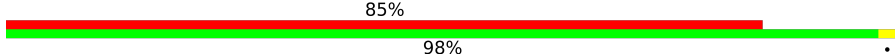


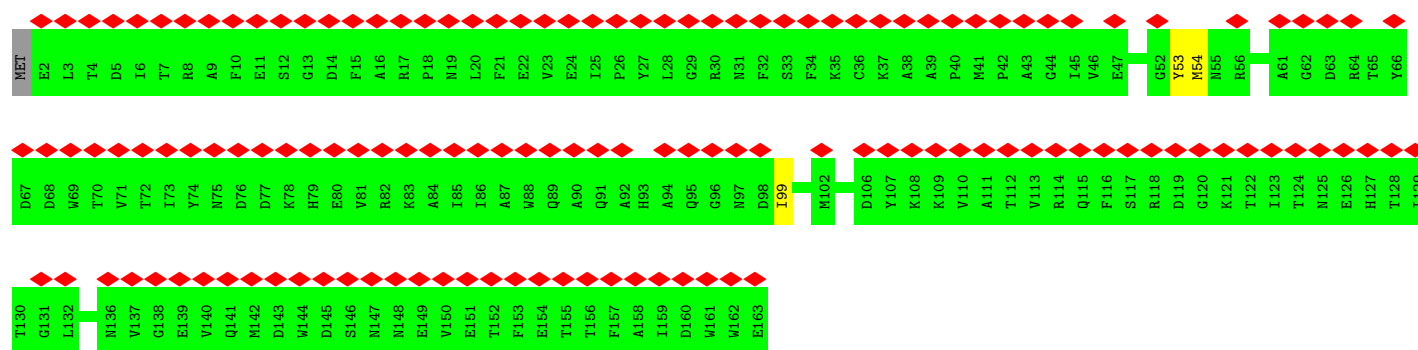
• Molecule 10: Tail tube protein

Chain Ts: 

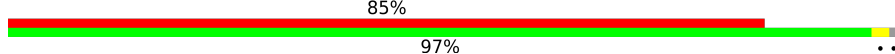


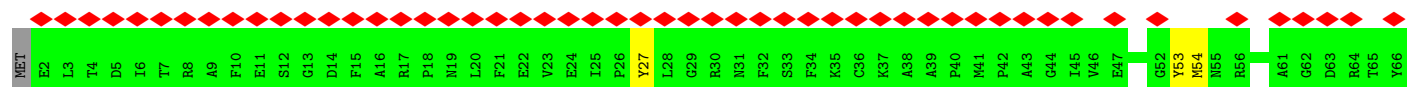
• Molecule 10: Tail tube protein

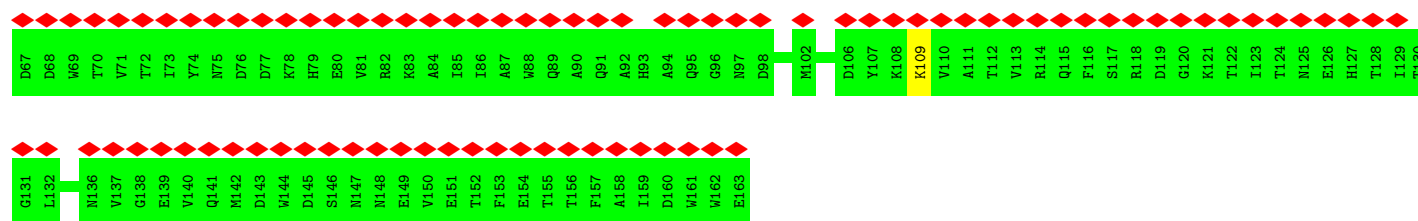
Chain Tt: 



• Molecule 10: Tail tube protein

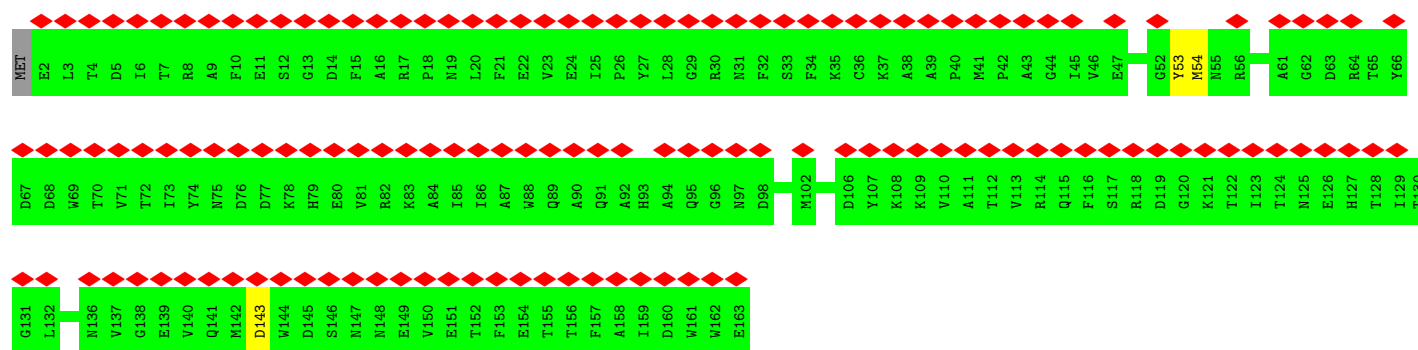
Chain Tu: 





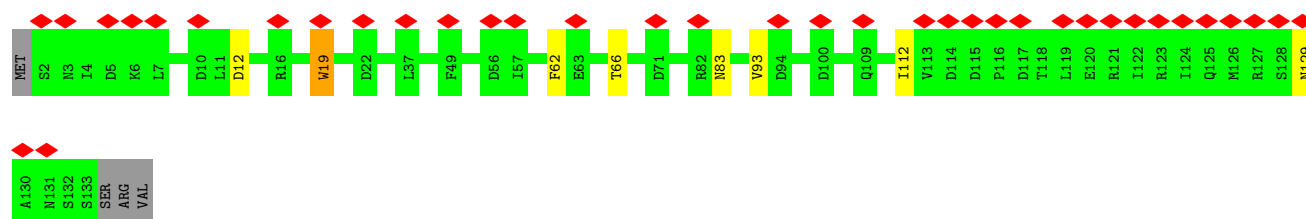
• Molecule 10: Tail tube protein

Chain Tv: 85% 98%



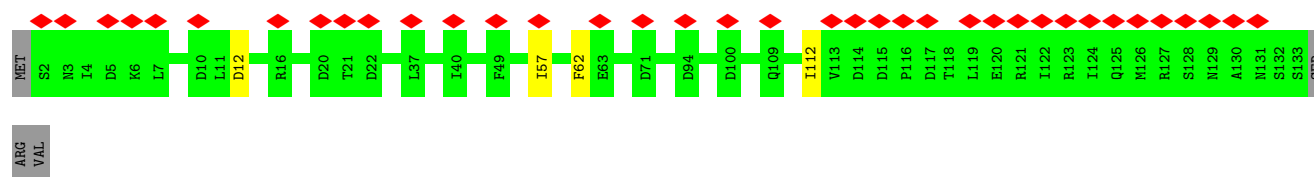
• Molecule 11: IraD/Gp25-like domain-containing protein

Chain AA: 27% 91% 5%



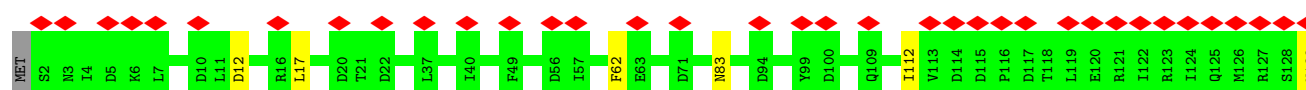
• Molecule 11: IraD/Gp25-like domain-containing protein

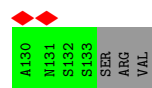
Chain AB: 27% 94%



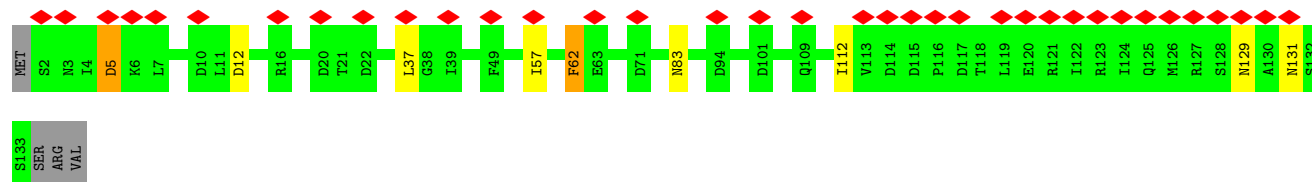
• Molecule 11: IraD/Gp25-like domain-containing protein

Chain AD: 28% 93%

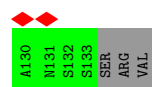




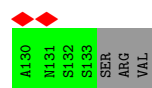
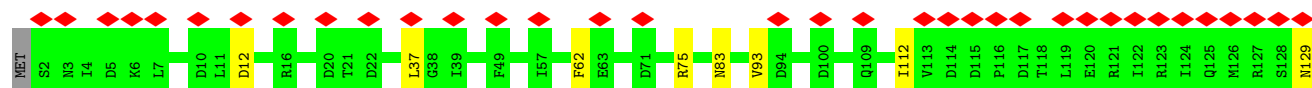
- Molecule 11: IraD/Gp25-like domain-containing protein



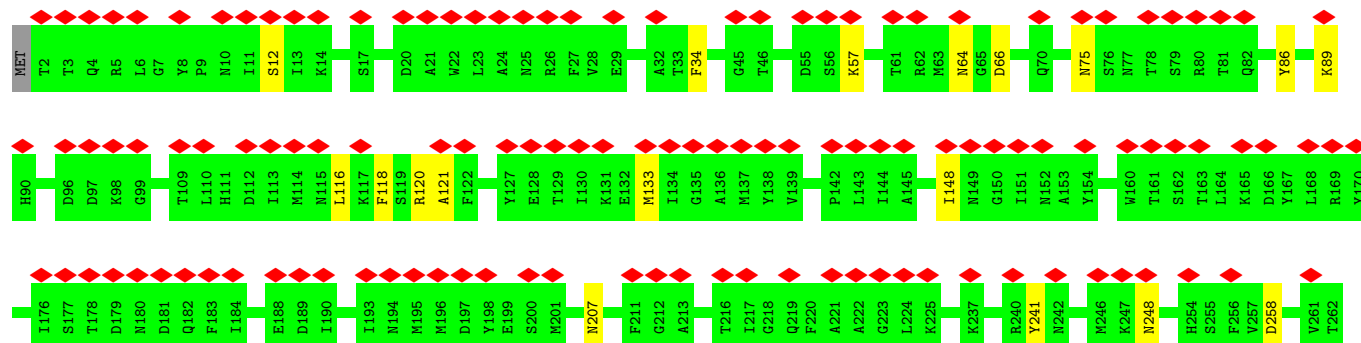
- Molecule 11: IraD/Gp25-like domain-containing protein

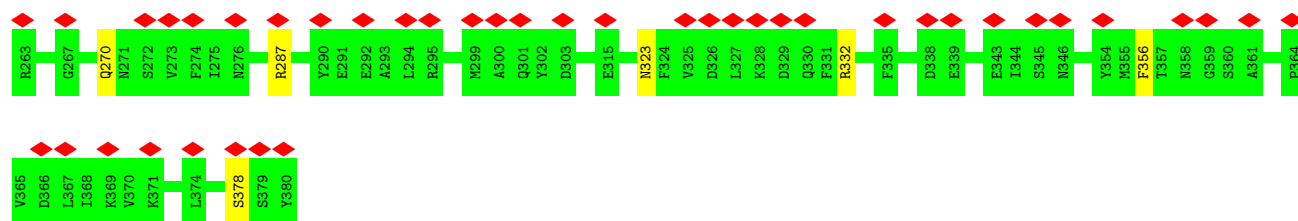


- Molecule 11: IraD/Gp25-like domain-containing protein

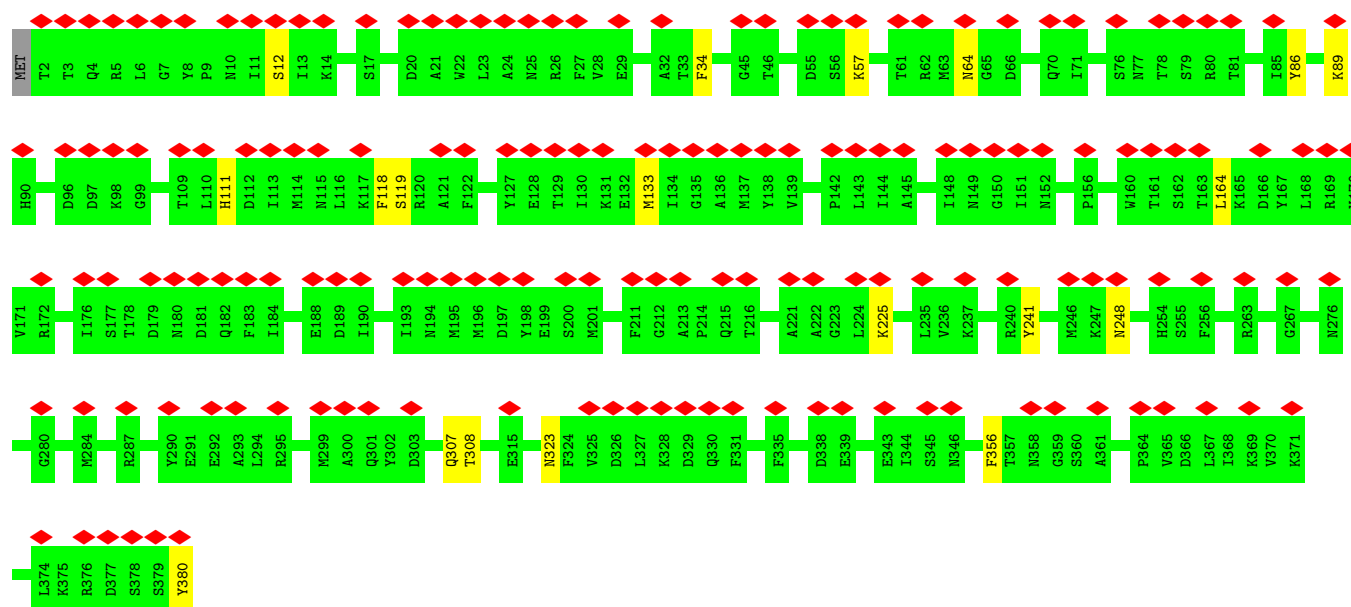
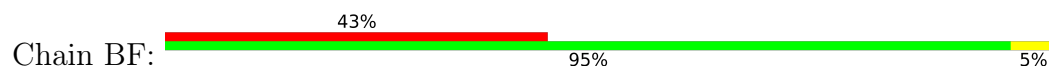


- Molecule 12: Putative baseplate hub subunit

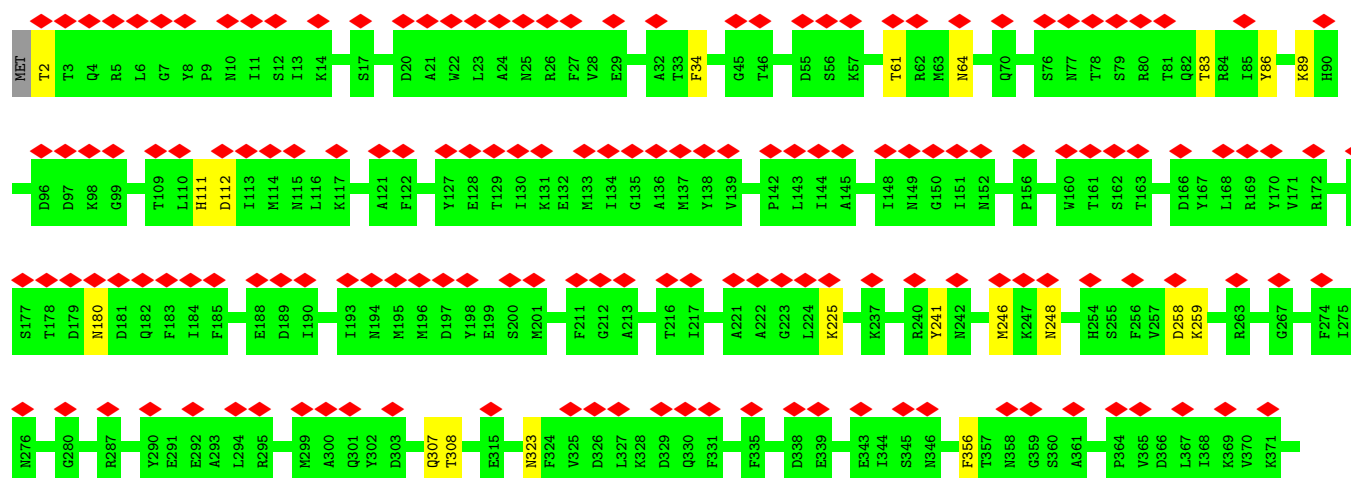
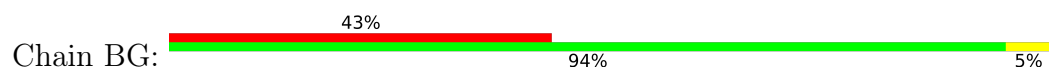


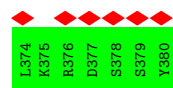


• Molecule 12: Putative baseplate hub subunit

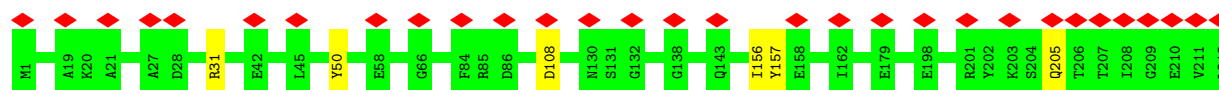


• Molecule 12: Putative baseplate hub subunit

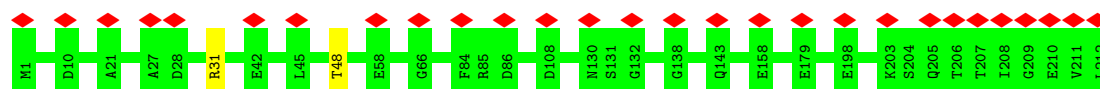




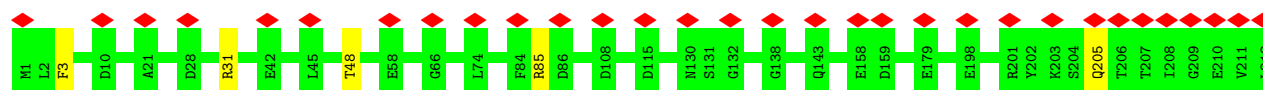
- Molecule 13: Baseplate wedge subunit



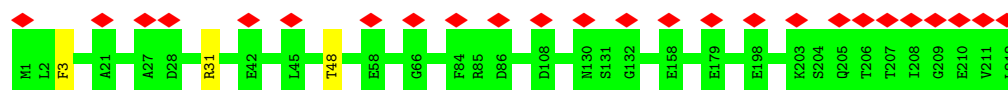
- Molecule 13: Baseplate wedge subunit



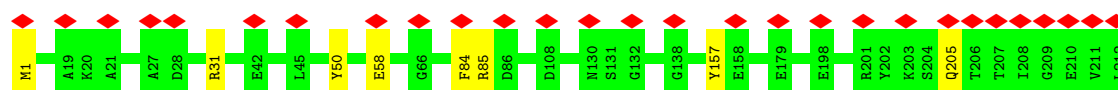
- Molecule 13: Baseplate wedge subunit



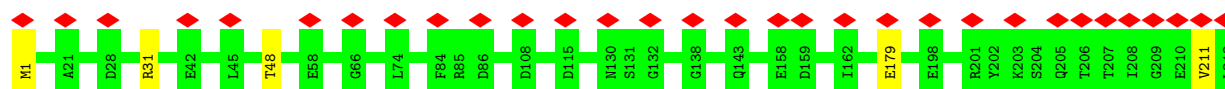
- Molecule 13: Baseplate wedge subunit



- Molecule 13: Baseplate wedge subunit

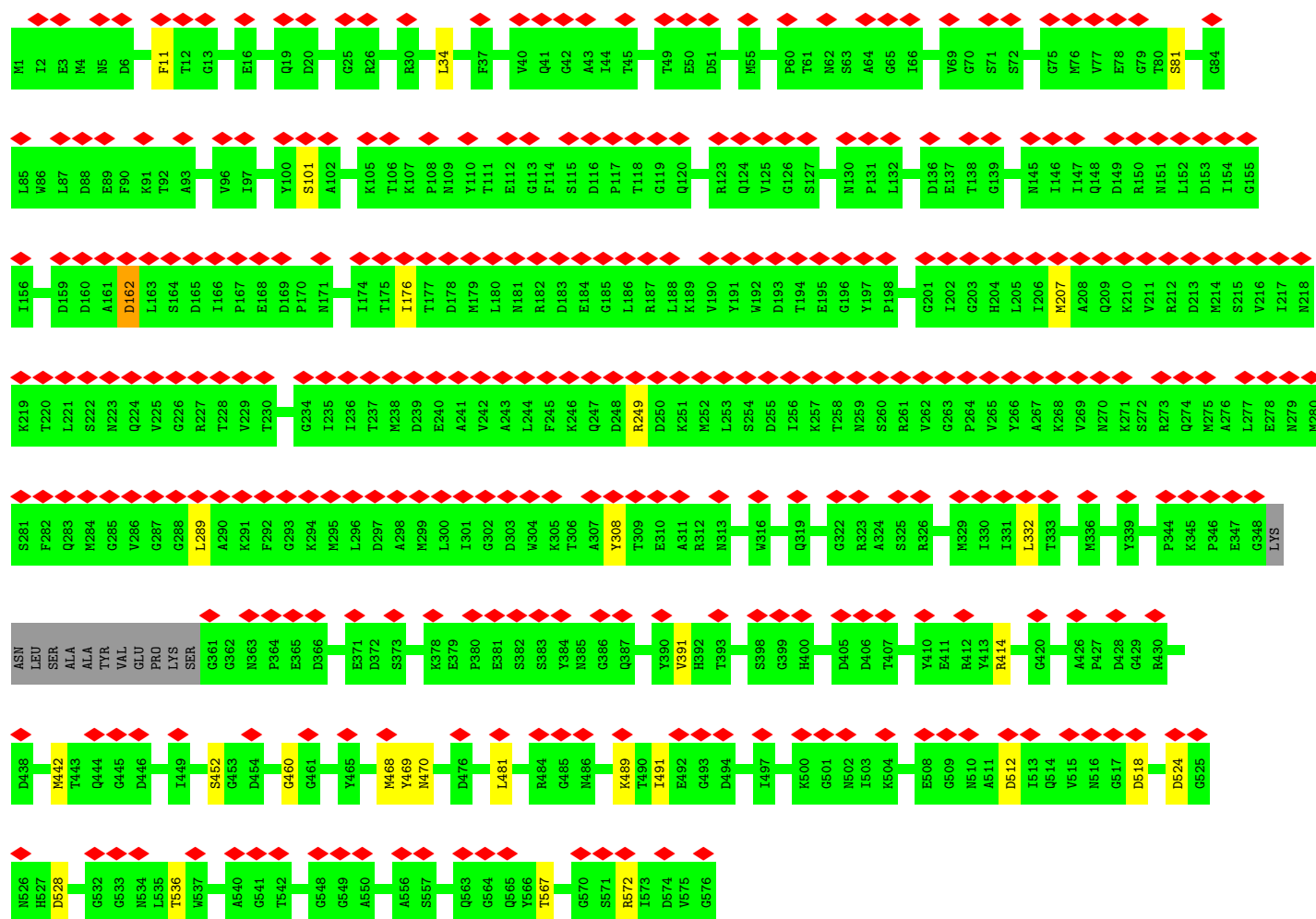


- Molecule 13: Baseplate wedge subunit



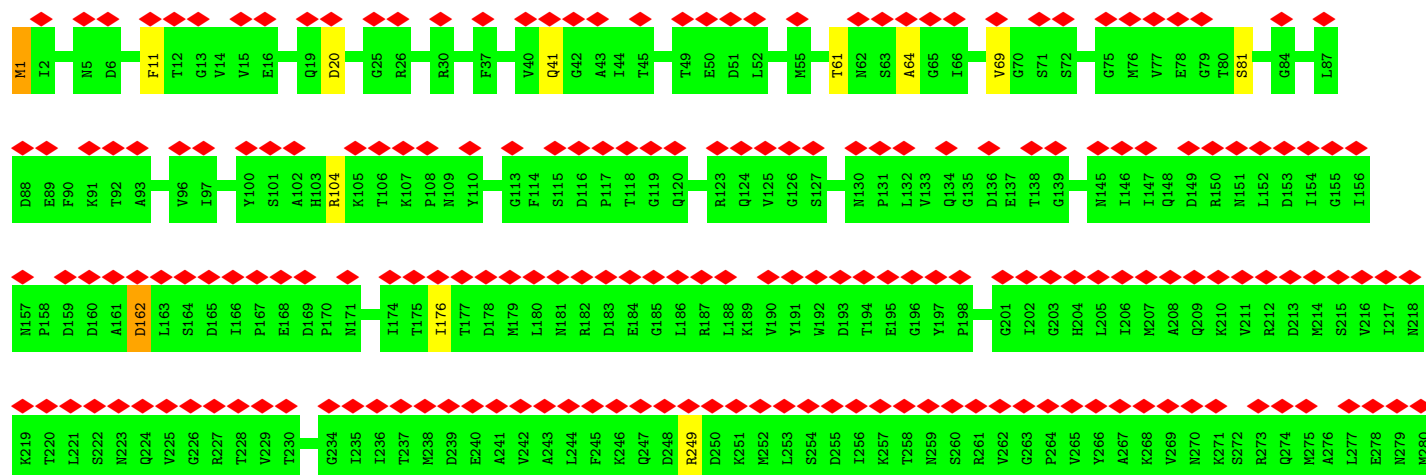
- Molecule 14: Baseplate central spike protein

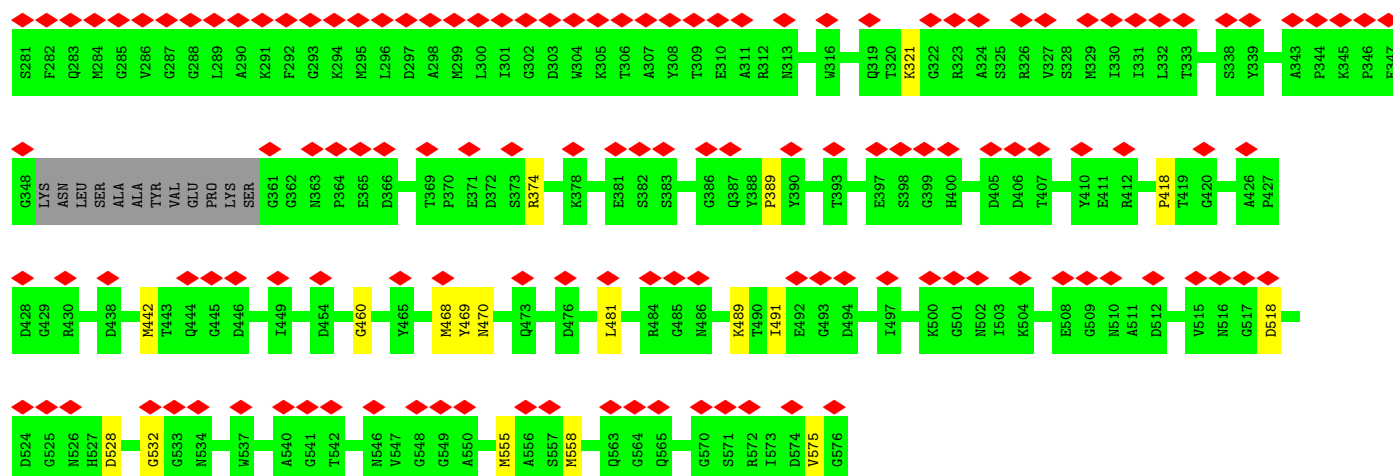
Chain BB: 



• Molecule 14: Baseplate central spike protein

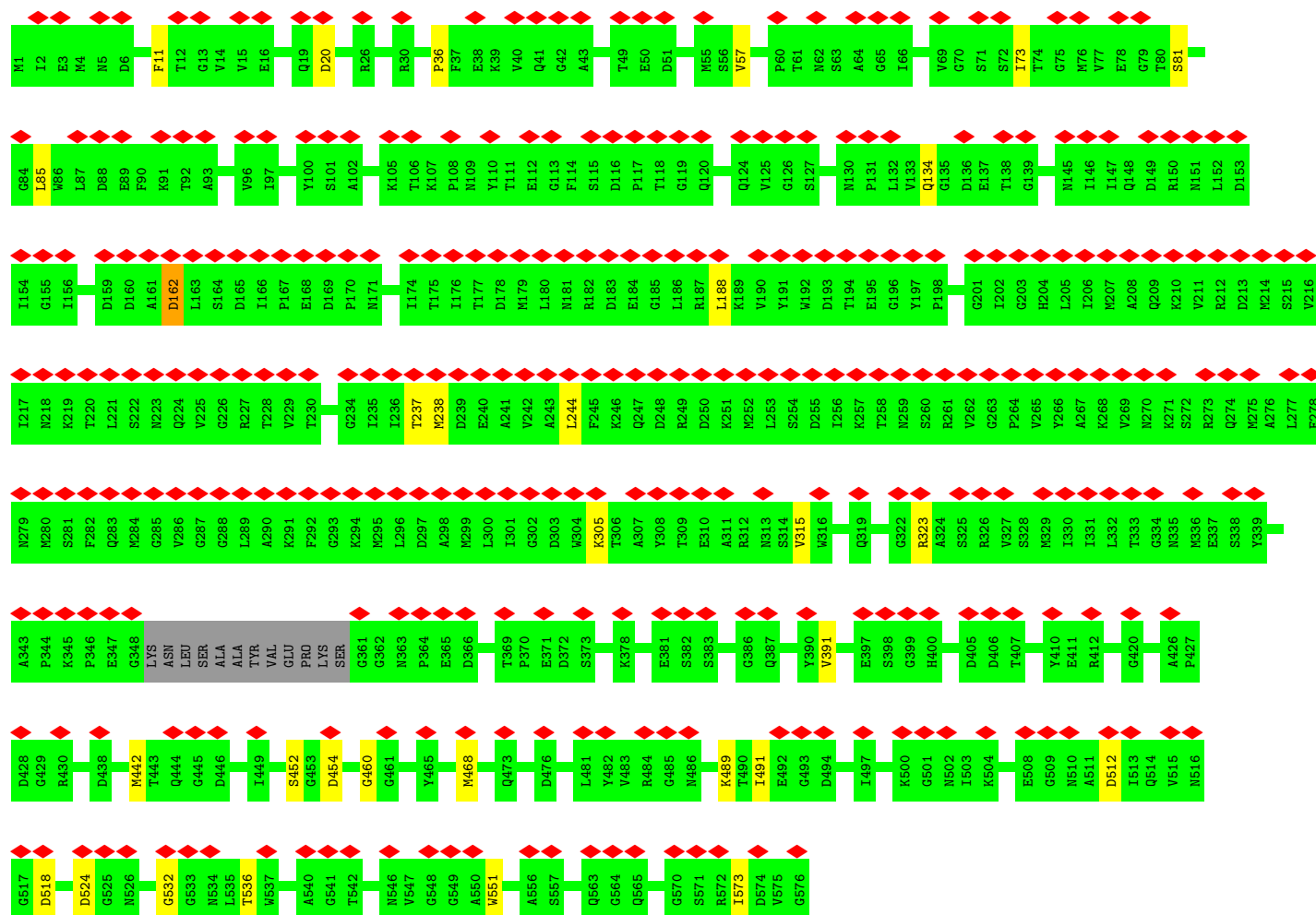
Chain BC: 





• Molecule 14: Baseplate central spike protein

Chain BD: 57% 93% 5% •



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

5.1 Standard geometry

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 ⓘ

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](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LS	615/1281 (48%)	553 (90%)	62 (10%)	0	100	100
1	LT	615/1281 (48%)	555 (90%)	60 (10%)	0	100	100
1	LU	615/1281 (48%)	554 (90%)	61 (10%)	0	100	100
1	LV	615/1281 (48%)	555 (90%)	60 (10%)	0	100	100
1	LW	615/1281 (48%)	551 (90%)	64 (10%)	0	100	100
1	LX	615/1281 (48%)	557 (91%)	58 (9%)	0	100	100
1	LY	615/1281 (48%)	554 (90%)	61 (10%)	0	100	100
1	LZ	615/1281 (48%)	561 (91%)	54 (9%)	0	100	100
1	La	615/1281 (48%)	552 (90%)	63 (10%)	0	100	100
1	Lb	615/1281 (48%)	554 (90%)	61 (10%)	0	100	100
1	Lc	615/1281 (48%)	558 (91%)	57 (9%)	0	100	100
1	Ld	615/1281 (48%)	562 (91%)	53 (9%)	0	100	100
1	Le	615/1281 (48%)	548 (89%)	67 (11%)	0	100	100
1	Lf	615/1281 (48%)	560 (91%)	55 (9%)	0	100	100
1	Lg	615/1281 (48%)	552 (90%)	63 (10%)	0	100	100
1	Lh	615/1281 (48%)	554 (90%)	61 (10%)	0	100	100
1	Li	615/1281 (48%)	556 (90%)	59 (10%)	0	100	100
1	Lj	615/1281 (48%)	550 (89%)	65 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	BK	345/350 (99%)	304 (88%)	41 (12%)	0	100	100
2	BL	271/350 (77%)	236 (87%)	35 (13%)	0	100	100
2	BM	345/350 (99%)	301 (87%)	44 (13%)	0	100	100
2	BN	271/350 (77%)	239 (88%)	32 (12%)	0	100	100
2	BO	345/350 (99%)	307 (89%)	38 (11%)	0	100	100
2	BP	271/350 (77%)	233 (86%)	38 (14%)	0	100	100
3	BQ	293/308 (95%)	265 (90%)	28 (10%)	0	100	100
3	BR	293/308 (95%)	266 (91%)	27 (9%)	0	100	100
3	BS	293/308 (95%)	268 (92%)	25 (8%)	0	100	100
3	BT	293/308 (95%)	266 (91%)	27 (9%)	0	100	100
3	BU	293/308 (95%)	274 (94%)	19 (6%)	0	100	100
3	BV	293/308 (95%)	271 (92%)	22 (8%)	0	100	100
4	AM	652/655 (100%)	624 (96%)	28 (4%)	0	100	100
4	AN	652/655 (100%)	617 (95%)	35 (5%)	0	100	100
4	AO	652/655 (100%)	624 (96%)	28 (4%)	0	100	100
4	AP	652/655 (100%)	616 (94%)	36 (6%)	0	100	100
4	AQ	652/655 (100%)	618 (95%)	34 (5%)	0	100	100
4	AR	652/655 (100%)	617 (95%)	35 (5%)	0	100	100
4	AS	646/655 (99%)	606 (94%)	40 (6%)	0	100	100
4	AT	644/655 (98%)	611 (95%)	33 (5%)	0	100	100
4	AU	646/655 (99%)	607 (94%)	39 (6%)	0	100	100
4	AV	644/655 (98%)	609 (95%)	35 (5%)	0	100	100
4	AW	646/655 (99%)	608 (94%)	38 (6%)	0	100	100
4	AX	644/655 (98%)	609 (95%)	35 (5%)	0	100	100
5	A0	1029/1032 (100%)	952 (92%)	77 (8%)	0	100	100
5	A1	1029/1032 (100%)	951 (92%)	78 (8%)	0	100	100
5	A2	1029/1032 (100%)	950 (92%)	79 (8%)	0	100	100
5	A3	1029/1032 (100%)	952 (92%)	77 (8%)	0	100	100
5	AY	1029/1032 (100%)	954 (93%)	75 (7%)	0	100	100
5	AZ	1029/1032 (100%)	941 (91%)	88 (9%)	0	100	100
6	A4	332/341 (97%)	302 (91%)	30 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A5	332/341 (97%)	308 (93%)	24 (7%)	0	100	100
6	A6	332/341 (97%)	300 (90%)	32 (10%)	0	100	100
6	A7	332/341 (97%)	308 (93%)	24 (7%)	0	100	100
6	A8	332/341 (97%)	304 (92%)	28 (8%)	0	100	100
6	A9	332/341 (97%)	308 (93%)	24 (7%)	0	100	100
6	Aa	327/341 (96%)	300 (92%)	27 (8%)	0	100	100
6	Ab	327/341 (96%)	299 (91%)	27 (8%)	1 (0%)	37	70
6	Ac	327/341 (96%)	300 (92%)	27 (8%)	0	100	100
6	Ad	327/341 (96%)	301 (92%)	26 (8%)	0	100	100
6	Ae	327/341 (96%)	297 (91%)	30 (9%)	0	100	100
6	Af	327/341 (96%)	302 (92%)	25 (8%)	0	100	100
7	LA	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LB	301/303 (99%)	278 (92%)	23 (8%)	0	100	100
7	LC	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LD	301/303 (99%)	291 (97%)	10 (3%)	0	100	100
7	LE	301/303 (99%)	281 (93%)	20 (7%)	0	100	100
7	LF	301/303 (99%)	290 (96%)	11 (4%)	0	100	100
7	LG	301/303 (99%)	288 (96%)	13 (4%)	0	100	100
7	LH	301/303 (99%)	279 (93%)	22 (7%)	0	100	100
7	LI	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LJ	301/303 (99%)	291 (97%)	10 (3%)	0	100	100
7	LK	301/303 (99%)	277 (92%)	24 (8%)	0	100	100
7	LL	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LM	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LN	301/303 (99%)	278 (92%)	23 (8%)	0	100	100
7	LO	301/303 (99%)	290 (96%)	11 (4%)	0	100	100
7	LP	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
7	LQ	301/303 (99%)	279 (93%)	22 (7%)	0	100	100
7	LR	301/303 (99%)	289 (96%)	12 (4%)	0	100	100
8	FA	64/607 (10%)	57 (89%)	7 (11%)	0	100	100
8	FB	64/607 (10%)	61 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	FC	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	FJ	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	FK	64/607 (10%)	59 (92%)	5 (8%)	0	100	100
8	FL	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	FS	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	FT	64/607 (10%)	60 (94%)	4 (6%)	0	100	100
8	FU	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	Fb	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	Fc	64/607 (10%)	60 (94%)	4 (6%)	0	100	100
8	Fd	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	Fk	64/607 (10%)	57 (89%)	7 (11%)	0	100	100
8	Fl	64/607 (10%)	60 (94%)	4 (6%)	0	100	100
8	Fm	64/607 (10%)	59 (92%)	5 (8%)	0	100	100
8	Ft	64/607 (10%)	58 (91%)	6 (9%)	0	100	100
8	Fu	64/607 (10%)	60 (94%)	4 (6%)	0	100	100
8	Fv	64/607 (10%)	59 (92%)	5 (8%)	0	100	100
9	SA	647/656 (99%)	607 (94%)	40 (6%)	0	100	100
9	SB	647/656 (99%)	607 (94%)	40 (6%)	0	100	100
9	SC	647/656 (99%)	609 (94%)	38 (6%)	0	100	100
9	SD	647/656 (99%)	608 (94%)	39 (6%)	0	100	100
9	SE	647/656 (99%)	609 (94%)	38 (6%)	0	100	100
9	SF	647/656 (99%)	608 (94%)	39 (6%)	0	100	100
9	SG	653/656 (100%)	606 (93%)	47 (7%)	0	100	100
9	SH	653/656 (100%)	612 (94%)	41 (6%)	0	100	100
9	SI	653/656 (100%)	609 (93%)	44 (7%)	0	100	100
9	SJ	653/656 (100%)	605 (93%)	48 (7%)	0	100	100
9	SK	653/656 (100%)	604 (92%)	49 (8%)	0	100	100
9	SL	653/656 (100%)	604 (92%)	49 (8%)	0	100	100
9	SM	653/656 (100%)	616 (94%)	37 (6%)	0	100	100
9	SN	653/656 (100%)	617 (94%)	36 (6%)	0	100	100
9	SO	653/656 (100%)	614 (94%)	39 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	SP	653/656 (100%)	615 (94%)	38 (6%)	0	100	100
9	SQ	653/656 (100%)	616 (94%)	37 (6%)	0	100	100
9	SR	653/656 (100%)	613 (94%)	40 (6%)	0	100	100
9	SS	653/656 (100%)	618 (95%)	35 (5%)	0	100	100
9	ST	653/656 (100%)	618 (95%)	35 (5%)	0	100	100
9	SU	653/656 (100%)	616 (94%)	37 (6%)	0	100	100
9	SV	653/656 (100%)	620 (95%)	33 (5%)	0	100	100
9	SW	653/656 (100%)	621 (95%)	32 (5%)	0	100	100
9	SX	653/656 (100%)	615 (94%)	38 (6%)	0	100	100
9	SY	653/656 (100%)	621 (95%)	32 (5%)	0	100	100
9	SZ	653/656 (100%)	620 (95%)	32 (5%)	1 (0%)	44	76
9	Sa	653/656 (100%)	622 (95%)	30 (5%)	1 (0%)	44	76
9	Sb	653/656 (100%)	623 (95%)	30 (5%)	0	100	100
9	Sc	653/656 (100%)	620 (95%)	32 (5%)	1 (0%)	44	76
9	Sd	653/656 (100%)	621 (95%)	32 (5%)	0	100	100
9	Se	653/656 (100%)	620 (95%)	33 (5%)	0	100	100
9	Sf	653/656 (100%)	620 (95%)	33 (5%)	0	100	100
9	Sg	653/656 (100%)	619 (95%)	34 (5%)	0	100	100
9	Sh	653/656 (100%)	616 (94%)	37 (6%)	0	100	100
9	Si	653/656 (100%)	617 (94%)	36 (6%)	0	100	100
9	Sj	653/656 (100%)	620 (95%)	33 (5%)	0	100	100
9	Sk	653/656 (100%)	624 (96%)	29 (4%)	0	100	100
9	Sl	653/656 (100%)	621 (95%)	32 (5%)	0	100	100
9	Sm	653/656 (100%)	621 (95%)	32 (5%)	0	100	100
9	Sn	653/656 (100%)	627 (96%)	26 (4%)	0	100	100
9	So	653/656 (100%)	627 (96%)	26 (4%)	0	100	100
9	Sp	653/656 (100%)	625 (96%)	28 (4%)	0	100	100
10	TM	160/163 (98%)	152 (95%)	8 (5%)	0	100	100
10	TN	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
10	TO	160/163 (98%)	151 (94%)	9 (6%)	0	100	100
10	TP	160/163 (98%)	151 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	TQ	160/163 (98%)	152 (95%)	8 (5%)	0	100	100
10	TR	160/163 (98%)	152 (95%)	8 (5%)	0	100	100
10	TS	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	TT	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
10	TU	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	TV	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	TW	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
10	TX	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	TY	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
10	TZ	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
10	Ta	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Tb	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
10	Tc	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Td	160/163 (98%)	152 (95%)	8 (5%)	0	100	100
10	Te	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Tf	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
10	Tg	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Th	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Ti	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
10	Tj	160/163 (98%)	157 (98%)	3 (2%)	0	100	100
10	Tk	160/163 (98%)	150 (94%)	10 (6%)	0	100	100
10	Tl	160/163 (98%)	151 (94%)	9 (6%)	0	100	100
10	Tm	160/163 (98%)	151 (94%)	9 (6%)	0	100	100
10	Tn	160/163 (98%)	151 (94%)	9 (6%)	0	100	100
10	To	160/163 (98%)	151 (94%)	9 (6%)	0	100	100
10	Tp	160/163 (98%)	149 (93%)	11 (7%)	0	100	100
10	Tq	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
10	Tr	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
10	Ts	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
10	Tt	160/163 (98%)	157 (98%)	3 (2%)	0	100	100
10	Tu	160/163 (98%)	156 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	Tv	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
11	AA	130/136 (96%)	119 (92%)	11 (8%)	0	100	100
11	AB	130/136 (96%)	122 (94%)	8 (6%)	0	100	100
11	AC	130/136 (96%)	119 (92%)	11 (8%)	0	100	100
11	AD	130/136 (96%)	121 (93%)	9 (7%)	0	100	100
11	AE	130/136 (96%)	118 (91%)	12 (9%)	0	100	100
11	AF	130/136 (96%)	117 (90%)	13 (10%)	0	100	100
12	BE	377/380 (99%)	342 (91%)	35 (9%)	0	100	100
12	BF	377/380 (99%)	352 (93%)	25 (7%)	0	100	100
12	BG	377/380 (99%)	346 (92%)	31 (8%)	0	100	100
13	AG	210/212 (99%)	201 (96%)	9 (4%)	0	100	100
13	AH	210/212 (99%)	203 (97%)	7 (3%)	0	100	100
13	AI	210/212 (99%)	199 (95%)	11 (5%)	0	100	100
13	AJ	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
13	AK	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
13	AL	210/212 (99%)	204 (97%)	6 (3%)	0	100	100
14	BB	560/576 (97%)	531 (95%)	29 (5%)	0	100	100
14	BC	560/576 (97%)	531 (95%)	29 (5%)	0	100	100
14	BD	560/576 (97%)	536 (96%)	24 (4%)	0	100	100
All	All	77157/99906 (77%)	72069 (93%)	5084 (7%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	Ab	125	PRO
9	Sa	160	TYR
9	SZ	160	TYR
9	Sc	160	TYR

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LS	525/1065 (49%)	518 (99%)	7 (1%)	65	76
1	LT	525/1065 (49%)	518 (99%)	7 (1%)	65	76
1	LU	525/1065 (49%)	511 (97%)	14 (3%)	40	60
1	LV	525/1065 (49%)	516 (98%)	9 (2%)	56	72
1	LW	525/1065 (49%)	519 (99%)	6 (1%)	70	79
1	LX	525/1065 (49%)	512 (98%)	13 (2%)	42	61
1	LY	525/1065 (49%)	517 (98%)	8 (2%)	60	74
1	LZ	525/1065 (49%)	518 (99%)	7 (1%)	65	76
1	La	525/1065 (49%)	513 (98%)	12 (2%)	45	63
1	Lb	525/1065 (49%)	518 (99%)	7 (1%)	65	76
1	Lc	525/1065 (49%)	518 (99%)	7 (1%)	65	76
1	Ld	525/1065 (49%)	513 (98%)	12 (2%)	45	63
1	Le	525/1065 (49%)	517 (98%)	8 (2%)	60	74
1	Lf	525/1065 (49%)	516 (98%)	9 (2%)	56	72
1	Lg	525/1065 (49%)	511 (97%)	14 (3%)	40	60
1	Lh	525/1065 (49%)	516 (98%)	9 (2%)	56	72
1	Li	525/1065 (49%)	517 (98%)	8 (2%)	60	74
1	Lj	525/1065 (49%)	511 (97%)	14 (3%)	40	60
2	BK	294/297 (99%)	291 (99%)	3 (1%)	73	81
2	BL	239/297 (80%)	237 (99%)	2 (1%)	79	84
2	BM	294/297 (99%)	287 (98%)	7 (2%)	44	62
2	BN	239/297 (80%)	233 (98%)	6 (2%)	42	61
2	BO	294/297 (99%)	288 (98%)	6 (2%)	50	68
2	BP	239/297 (80%)	235 (98%)	4 (2%)	56	72
3	BQ	243/256 (95%)	239 (98%)	4 (2%)	58	73
3	BR	243/256 (95%)	236 (97%)	7 (3%)	37	58
3	BS	243/256 (95%)	239 (98%)	4 (2%)	58	73
3	BT	243/256 (95%)	237 (98%)	6 (2%)	42	61
3	BU	243/256 (95%)	238 (98%)	5 (2%)	48	66
3	BV	243/256 (95%)	239 (98%)	4 (2%)	58	73
4	AM	570/571 (100%)	560 (98%)	10 (2%)	54	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AN	570/571 (100%)	556 (98%)	14 (2%)	42	61
4	AO	570/571 (100%)	560 (98%)	10 (2%)	54	71
4	AP	570/571 (100%)	559 (98%)	11 (2%)	52	69
4	AQ	570/571 (100%)	558 (98%)	12 (2%)	48	66
4	AR	570/571 (100%)	556 (98%)	14 (2%)	42	61
4	AS	565/571 (99%)	558 (99%)	7 (1%)	67	78
4	AT	563/571 (99%)	554 (98%)	9 (2%)	58	73
4	AU	565/571 (99%)	555 (98%)	10 (2%)	54	71
4	AV	563/571 (99%)	553 (98%)	10 (2%)	54	71
4	AW	565/571 (99%)	555 (98%)	10 (2%)	54	71
4	AX	563/571 (99%)	555 (99%)	8 (1%)	62	75
5	A0	923/924 (100%)	909 (98%)	14 (2%)	60	74
5	A1	923/924 (100%)	911 (99%)	12 (1%)	65	76
5	A2	923/924 (100%)	908 (98%)	15 (2%)	58	73
5	A3	923/924 (100%)	908 (98%)	15 (2%)	58	73
5	AY	923/924 (100%)	912 (99%)	11 (1%)	67	78
5	AZ	923/924 (100%)	910 (99%)	13 (1%)	62	75
6	A4	293/299 (98%)	288 (98%)	5 (2%)	56	72
6	A5	293/299 (98%)	289 (99%)	4 (1%)	62	75
6	A6	293/299 (98%)	288 (98%)	5 (2%)	56	72
6	A7	293/299 (98%)	290 (99%)	3 (1%)	73	81
6	A8	293/299 (98%)	287 (98%)	6 (2%)	50	68
6	A9	293/299 (98%)	290 (99%)	3 (1%)	73	81
6	Aa	288/299 (96%)	284 (99%)	4 (1%)	62	75
6	Ab	288/299 (96%)	285 (99%)	3 (1%)	73	81
6	Ac	288/299 (96%)	284 (99%)	4 (1%)	62	75
6	Ad	288/299 (96%)	285 (99%)	3 (1%)	73	81
6	Ae	288/299 (96%)	284 (99%)	4 (1%)	62	75
6	Af	288/299 (96%)	286 (99%)	2 (1%)	81	86
7	LA	245/245 (100%)	238 (97%)	7 (3%)	37	58
7	LB	245/245 (100%)	240 (98%)	5 (2%)	50	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LC	245/245 (100%)	242 (99%)	3 (1%)	67	78
7	LD	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LE	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LF	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LG	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LH	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LI	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LJ	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LK	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LL	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LM	245/245 (100%)	239 (98%)	6 (2%)	44	62
7	LN	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LO	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LP	245/245 (100%)	241 (98%)	4 (2%)	58	73
7	LQ	245/245 (100%)	240 (98%)	5 (2%)	50	68
7	LR	245/245 (100%)	241 (98%)	4 (2%)	58	73
8	FA	57/509 (11%)	54 (95%)	3 (5%)	19	42
8	FB	57/509 (11%)	57 (100%)	0	100	100
8	FC	57/509 (11%)	55 (96%)	2 (4%)	31	52
8	FJ	57/509 (11%)	54 (95%)	3 (5%)	19	42
8	FK	57/509 (11%)	57 (100%)	0	100	100
8	FL	57/509 (11%)	55 (96%)	2 (4%)	31	52
8	FS	57/509 (11%)	54 (95%)	3 (5%)	19	42
8	FT	57/509 (11%)	57 (100%)	0	100	100
8	FU	57/509 (11%)	55 (96%)	2 (4%)	31	52
8	Fb	57/509 (11%)	53 (93%)	4 (7%)	12	35
8	Fc	57/509 (11%)	57 (100%)	0	100	100
8	Fd	57/509 (11%)	55 (96%)	2 (4%)	31	52
8	Fk	57/509 (11%)	53 (93%)	4 (7%)	12	35
8	Fl	57/509 (11%)	57 (100%)	0	100	100
8	Fm	57/509 (11%)	54 (95%)	3 (5%)	19	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Ft	57/509 (11%)	53 (93%)	4 (7%)	12	35
8	Fu	57/509 (11%)	57 (100%)	0	100	100
8	Fv	57/509 (11%)	55 (96%)	2 (4%)	31	52
9	SA	534/540 (99%)	529 (99%)	5 (1%)	75	83
9	SB	534/540 (99%)	530 (99%)	4 (1%)	81	86
9	SC	534/540 (99%)	529 (99%)	5 (1%)	75	83
9	SD	534/540 (99%)	529 (99%)	5 (1%)	75	83
9	SE	534/540 (99%)	531 (99%)	3 (1%)	84	88
9	SF	534/540 (99%)	528 (99%)	6 (1%)	70	79
9	SG	539/540 (100%)	529 (98%)	10 (2%)	52	69
9	SH	539/540 (100%)	529 (98%)	10 (2%)	52	69
9	SI	539/540 (100%)	529 (98%)	10 (2%)	52	69
9	SJ	539/540 (100%)	528 (98%)	11 (2%)	50	68
9	SK	539/540 (100%)	528 (98%)	11 (2%)	50	68
9	SL	539/540 (100%)	529 (98%)	10 (2%)	52	69
9	SM	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SN	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SO	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SP	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SQ	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	SR	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SS	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	ST	539/540 (100%)	531 (98%)	8 (2%)	60	74
9	SU	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	SV	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	SW	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	SX	539/540 (100%)	534 (99%)	5 (1%)	75	83
9	SY	539/540 (100%)	531 (98%)	8 (2%)	60	74
9	SZ	539/540 (100%)	530 (98%)	9 (2%)	56	72
9	Sa	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	Sb	539/540 (100%)	532 (99%)	7 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Sc	539/540 (100%)	531 (98%)	8 (2%)	60	74
9	Sd	539/540 (100%)	535 (99%)	4 (1%)	81	86
9	Se	539/540 (100%)	530 (98%)	9 (2%)	56	72
9	Sf	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	Sg	539/540 (100%)	533 (99%)	6 (1%)	70	79
9	Sh	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	Si	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	Sj	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	Sk	539/540 (100%)	534 (99%)	5 (1%)	75	83
9	Sl	539/540 (100%)	534 (99%)	5 (1%)	75	83
9	Sm	539/540 (100%)	532 (99%)	7 (1%)	65	76
9	Sn	539/540 (100%)	535 (99%)	4 (1%)	81	86
9	So	539/540 (100%)	534 (99%)	5 (1%)	75	83
9	Sp	539/540 (100%)	531 (98%)	8 (2%)	60	74
10	TM	138/139 (99%)	137 (99%)	1 (1%)	81	86
10	TN	138/139 (99%)	137 (99%)	1 (1%)	81	86
10	TO	138/139 (99%)	137 (99%)	1 (1%)	81	86
10	TP	138/139 (99%)	138 (100%)	0	100	100
10	TQ	138/139 (99%)	136 (99%)	2 (1%)	62	75
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%)	81	86
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%)	81	86
10	TY	138/139 (99%)	136 (99%)	2 (1%)	62	75
10	TZ	138/139 (99%)	137 (99%)	1 (1%)	81	86
10	Ta	138/139 (99%)	136 (99%)	2 (1%)	62	75
10	Tb	138/139 (99%)	135 (98%)	3 (2%)	47	65
10	Tc	138/139 (99%)	136 (99%)	2 (1%)	62	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Td	138/139 (99%)	136 (99%)	2 (1%)	62	75
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%)	81	86
10	Tl	138/139 (99%)	135 (98%)	3 (2%)	47	65
10	Tm	138/139 (99%)	136 (99%)	2 (1%)	62	75
10	Tn	138/139 (99%)	136 (99%)	2 (1%)	62	75
10	To	138/139 (99%)	135 (98%)	3 (2%)	47	65
10	Tp	138/139 (99%)	136 (99%)	2 (1%)	62	75
10	Tq	138/139 (99%)	138 (100%)	0	100	100
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	61
11	AB	122/126 (97%)	122 (100%)	0	100	100
11	AC	122/126 (97%)	118 (97%)	4 (3%)	33	54
11	AD	122/126 (97%)	120 (98%)	2 (2%)	58	73
11	AE	122/126 (97%)	121 (99%)	1 (1%)	79	84
11	AF	122/126 (97%)	119 (98%)	3 (2%)	42	61
12	BE	333/334 (100%)	325 (98%)	8 (2%)	44	62
12	BF	333/334 (100%)	325 (98%)	8 (2%)	44	62
12	BG	333/334 (100%)	323 (97%)	10 (3%)	36	57
13	AG	184/184 (100%)	180 (98%)	4 (2%)	47	65
13	AH	184/184 (100%)	180 (98%)	4 (2%)	47	65
13	AI	184/184 (100%)	182 (99%)	2 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	AJ	184/184 (100%)	182 (99%)	2 (1%)	70	79
13	AK	184/184 (100%)	181 (98%)	3 (2%)	58	73
13	AL	184/184 (100%)	181 (98%)	3 (2%)	58	73
14	BB	474/484 (98%)	459 (97%)	15 (3%)	34	55
14	BC	474/484 (98%)	464 (98%)	10 (2%)	48	66
14	BD	474/484 (98%)	462 (98%)	12 (2%)	42	61
All	All	65604/84042 (78%)	64593 (98%)	1011 (2%)	60	74

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 ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

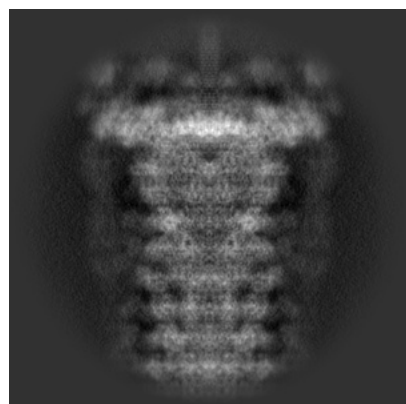
6 Map visualisation [i](#)

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.

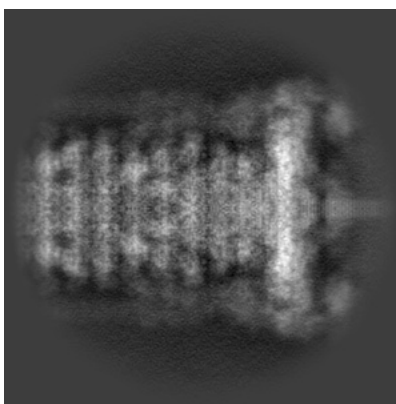
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

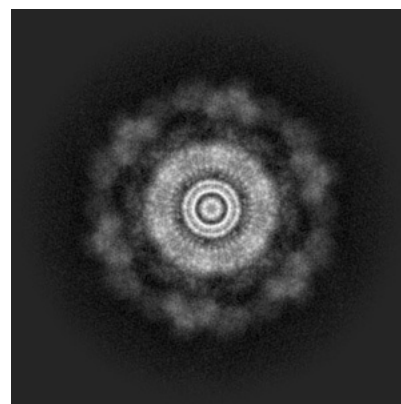
6.1.1 Primary map



X

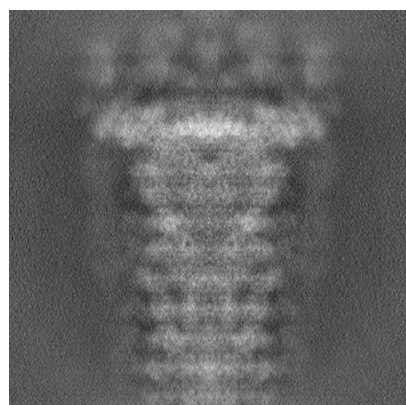


Y

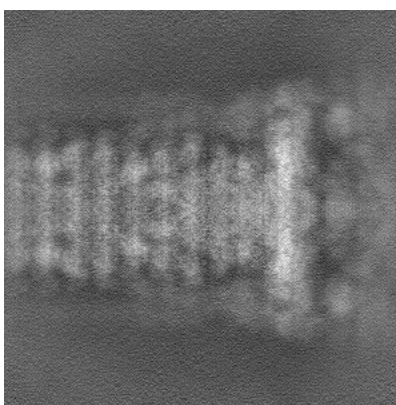


Z

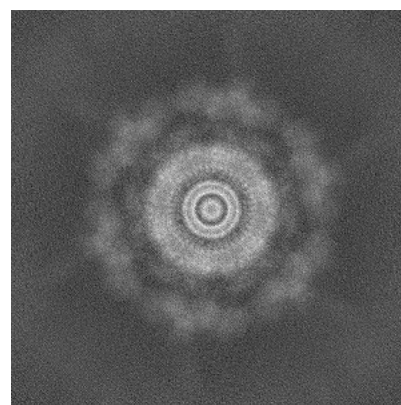
6.1.2 Raw map



X



Y

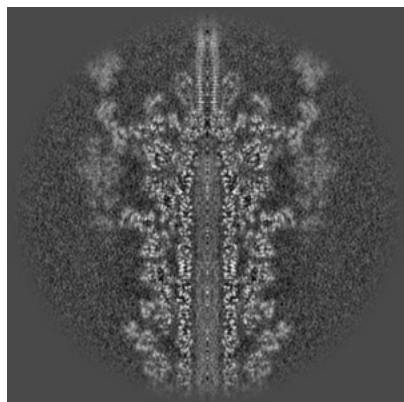


Z

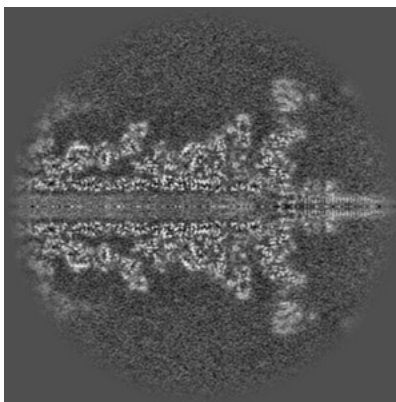
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

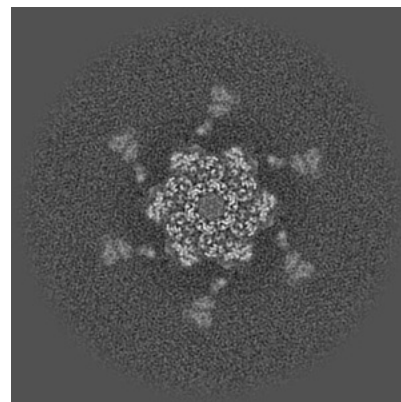
6.2.1 Primary map



X Index: 256

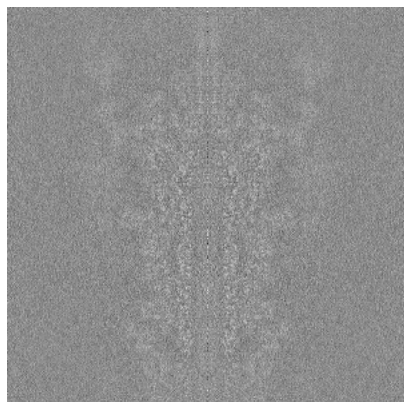


Y Index: 256

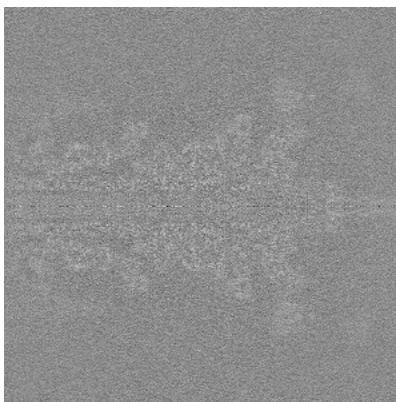


Z Index: 256

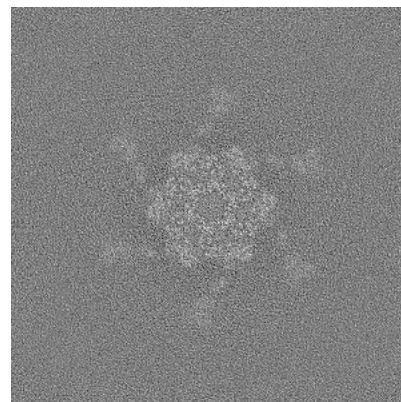
6.2.2 Raw map



X Index: 256



Y Index: 256

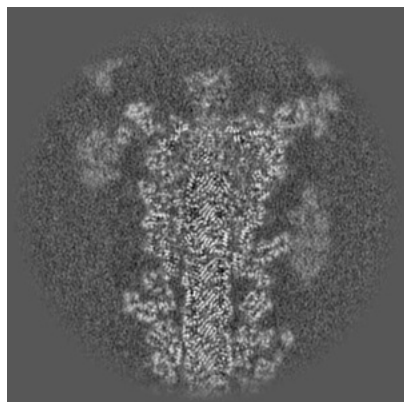


Z Index: 256

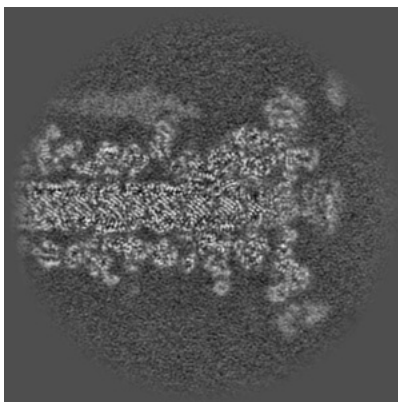
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

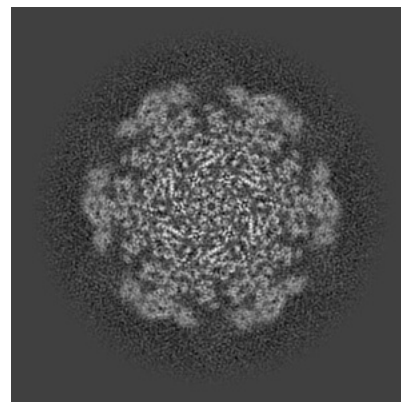
6.3.1 Primary map



X Index: 279

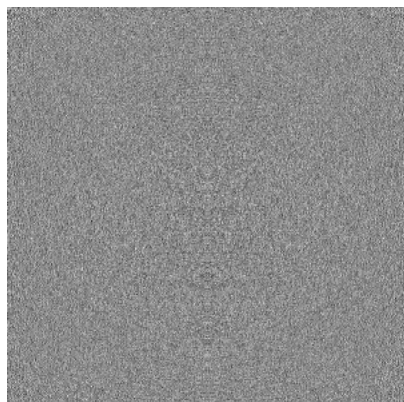


Y Index: 278

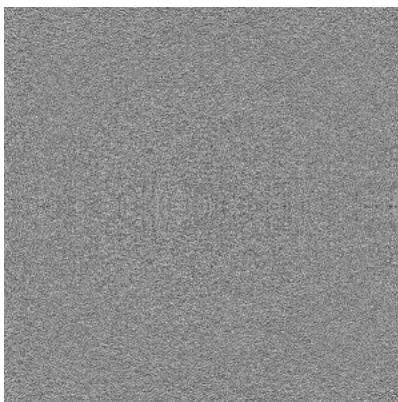


Z Index: 356

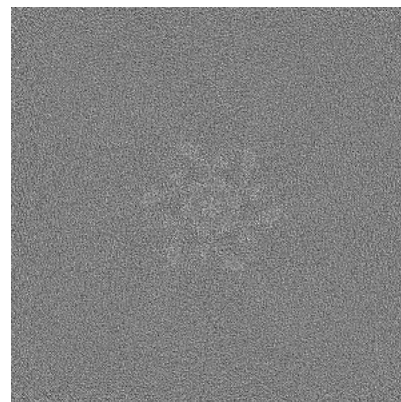
6.3.2 Raw map



X Index: 0



Y Index: 0

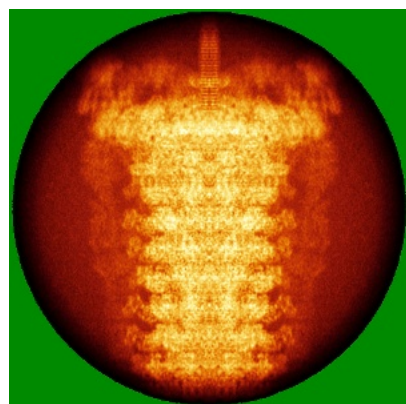


Z Index: 0

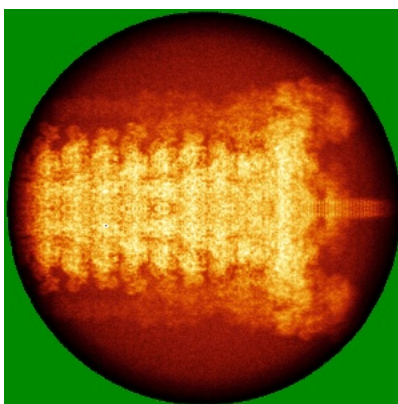
The images above show the largest variance slices of the map in three orthogonal directions.

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

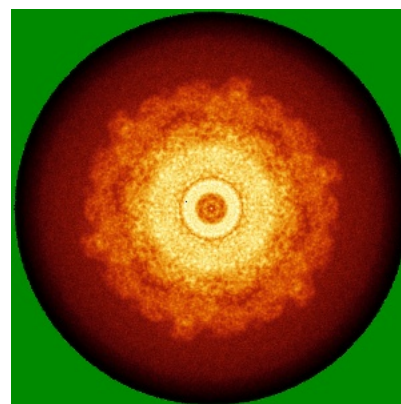
6.4.1 Primary map



X

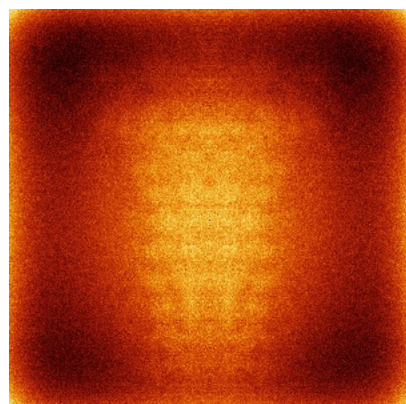


Y

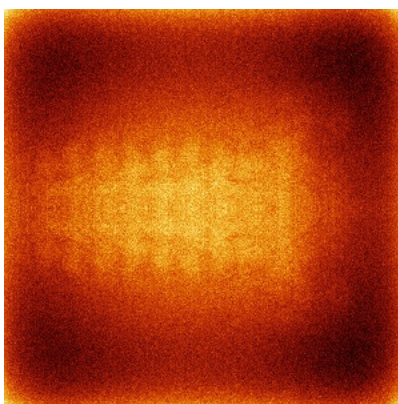


Z

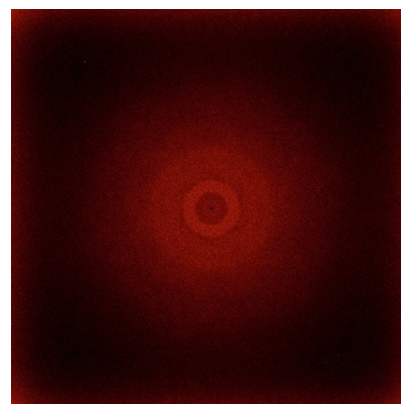
6.4.2 Raw map



X



Y

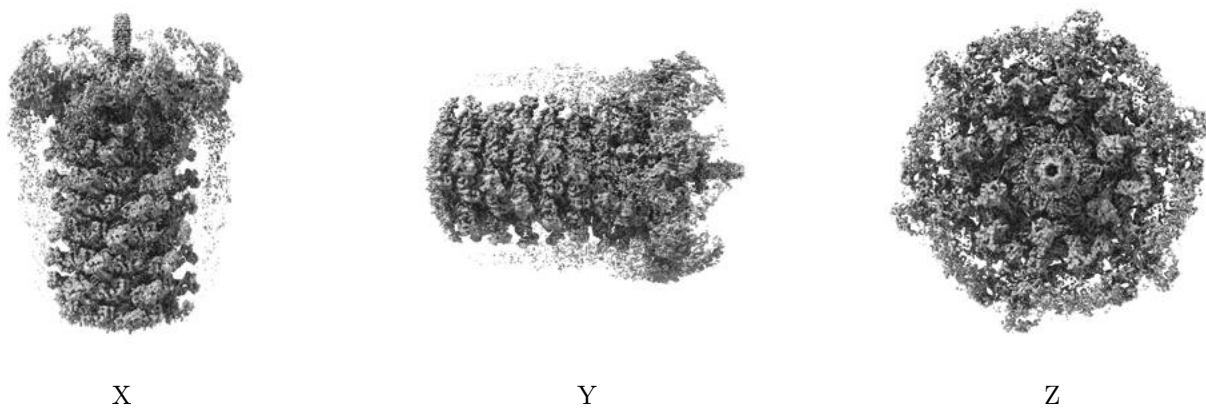


Z

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.

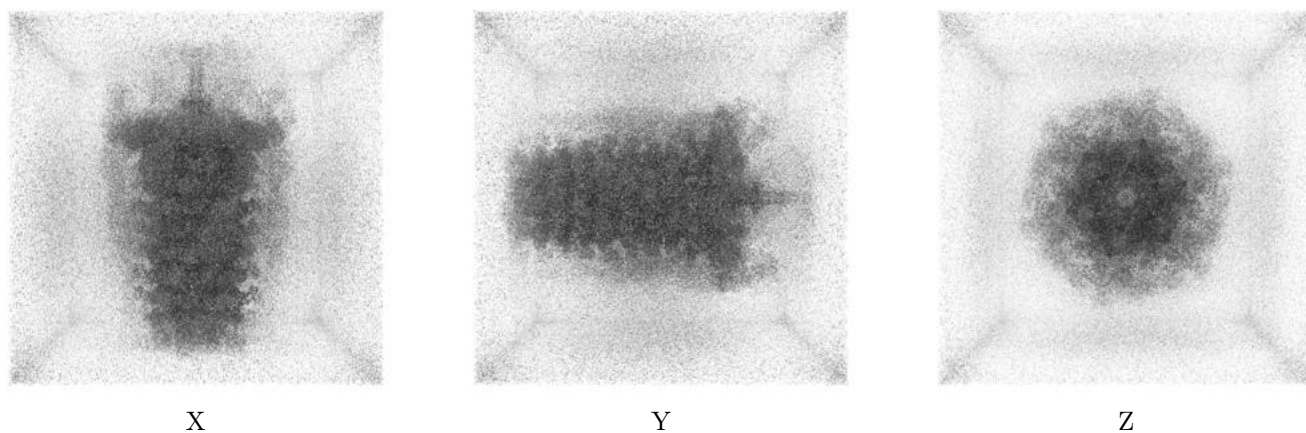
6.5 Orthogonal surface views [i](#)

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.

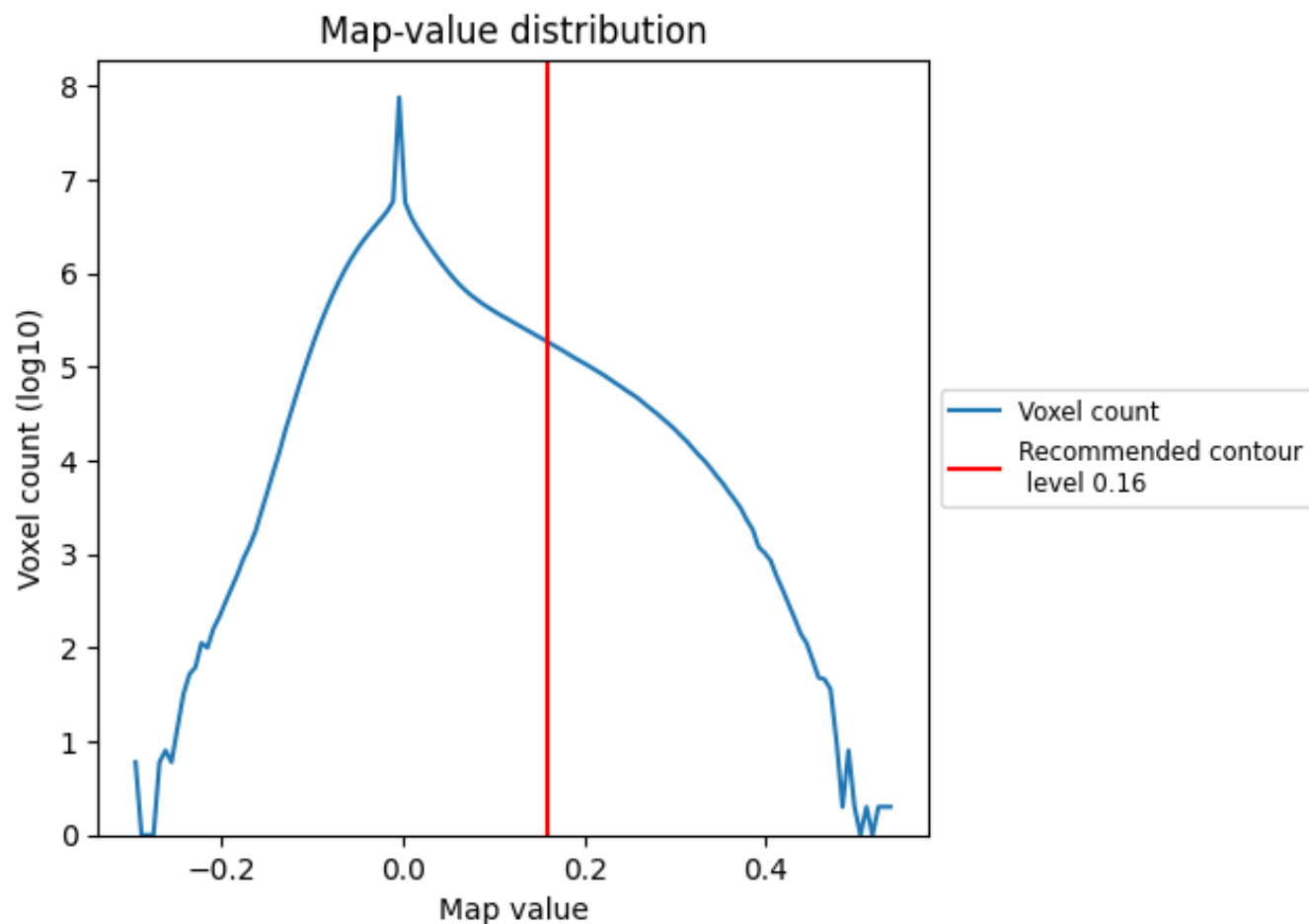
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

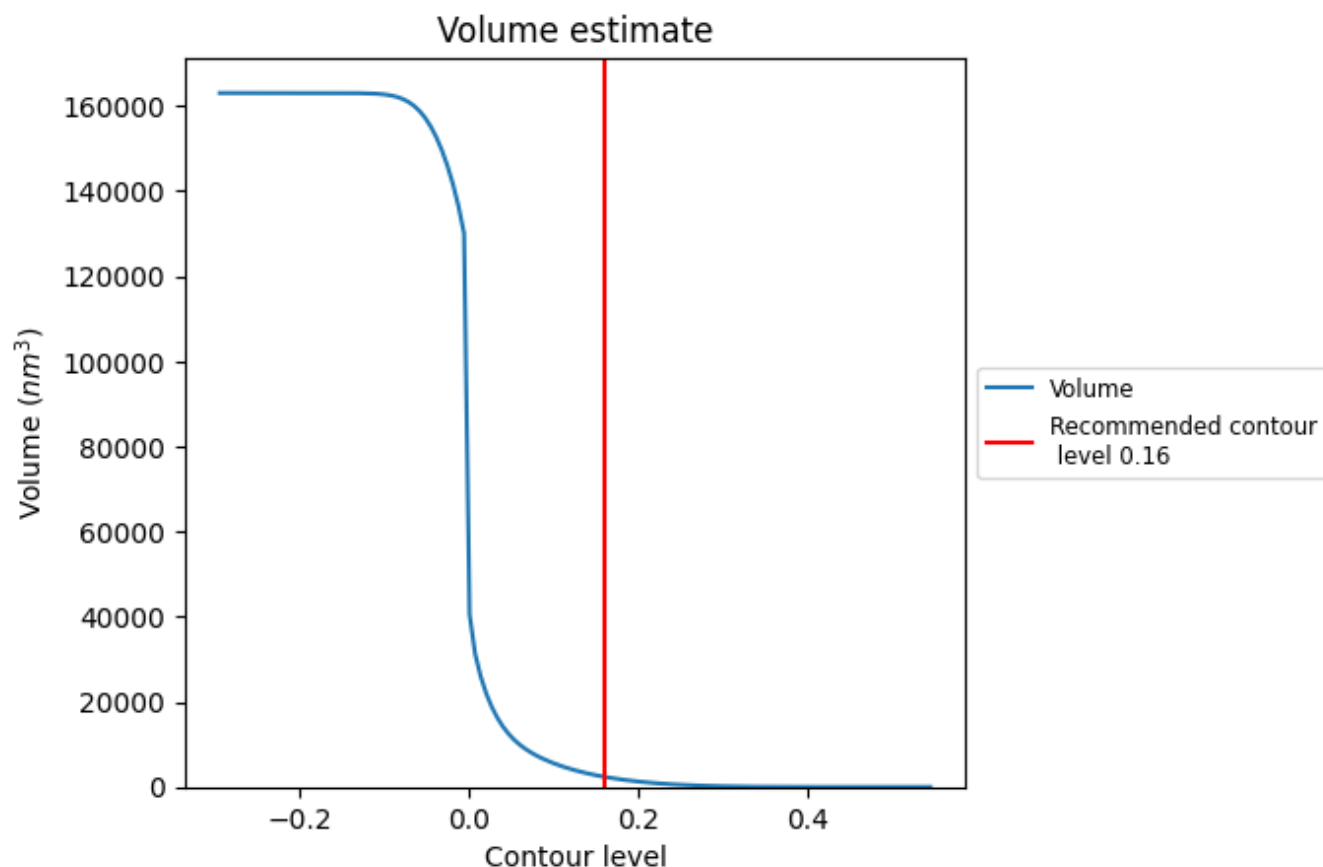
This section contains the results of statistical analysis of the map.

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.

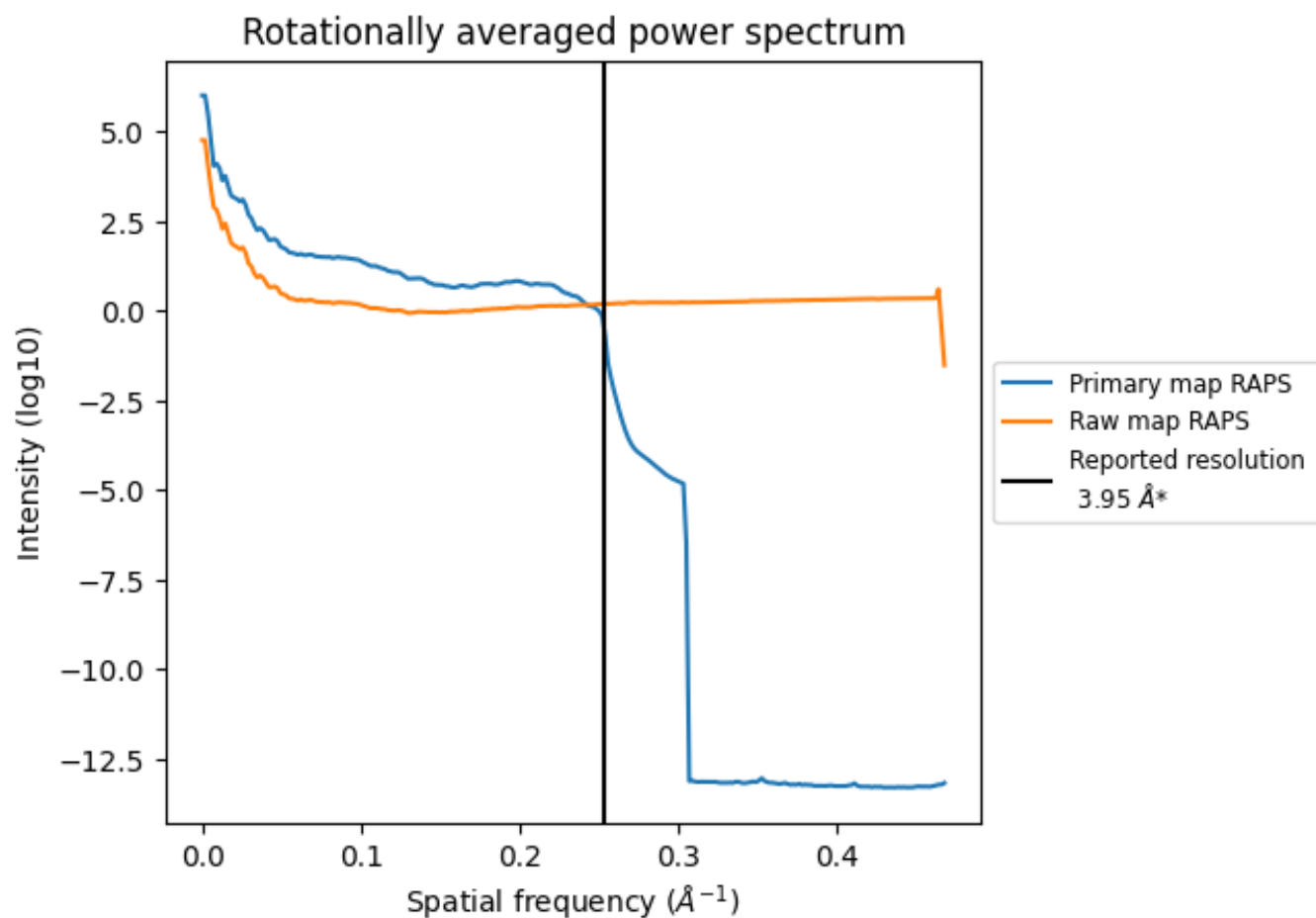
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2352 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 ⓘ

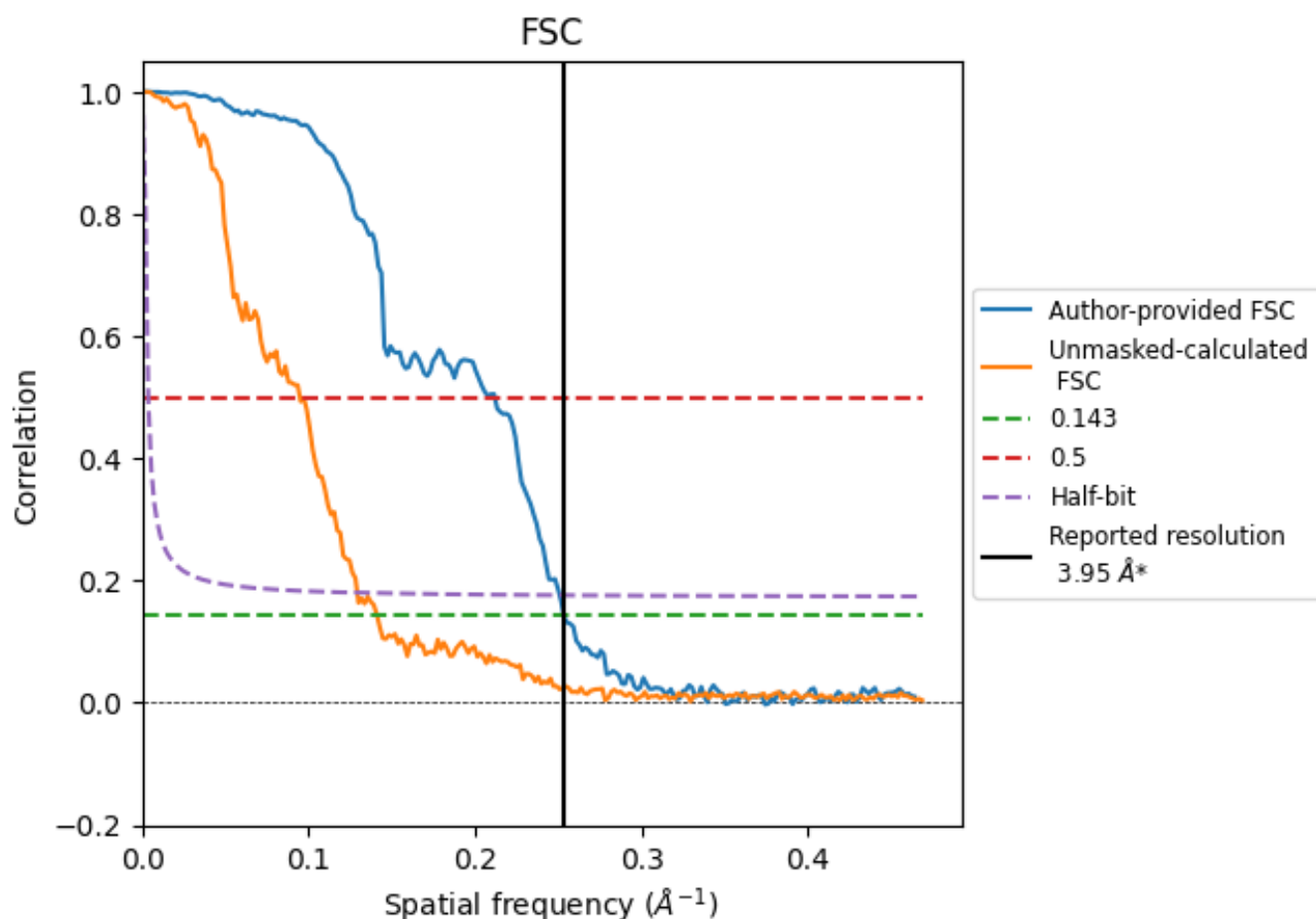


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

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](#)

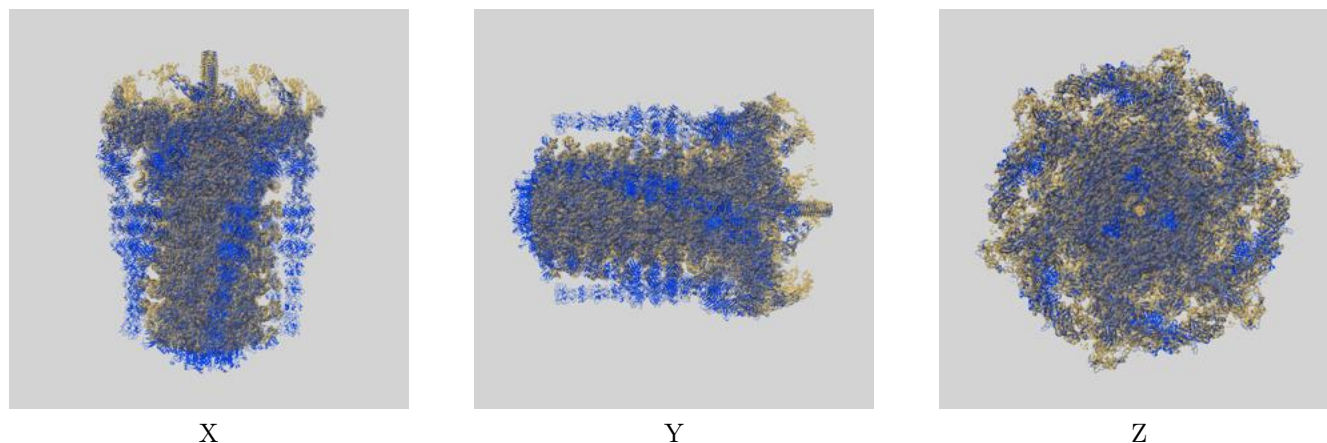
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.95	-	-
Author-provided FSC curve	3.95	4.72	3.99
Unmasked-calculated*	7.09	10.56	7.74

*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](#)

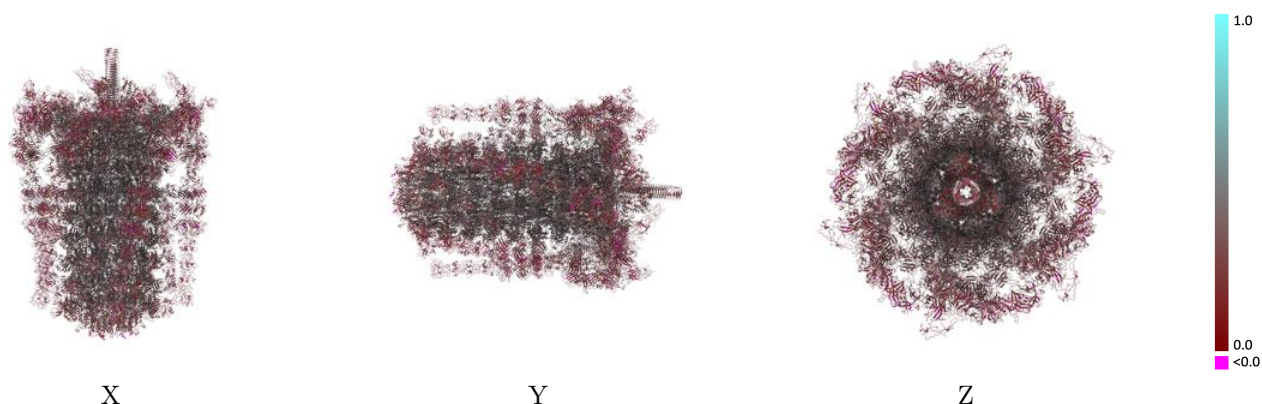
This section contains information regarding the fit between EMDB map EMD-50186 and PDB model 9F4A. Per-residue inclusion information can be found in section [3](#) on page [31](#).

9.1 Map-model overlay [i](#)



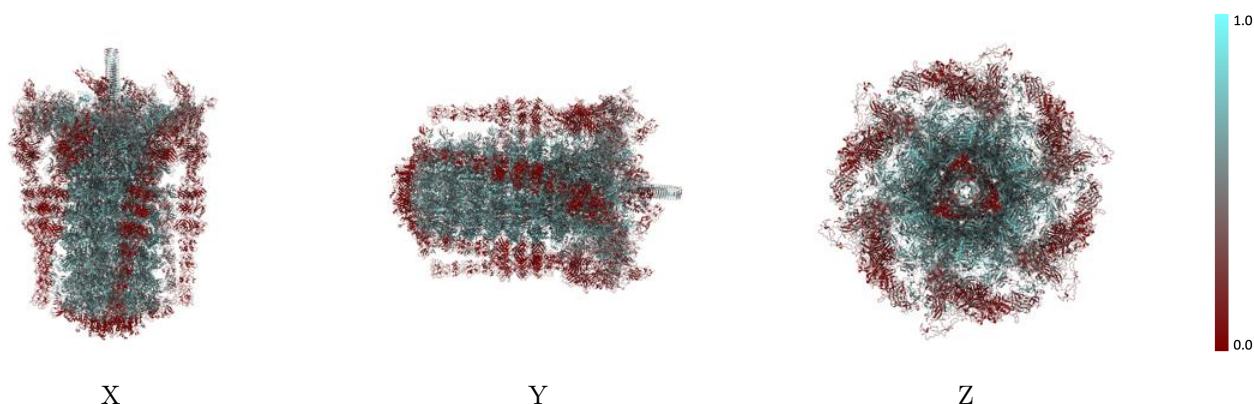
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



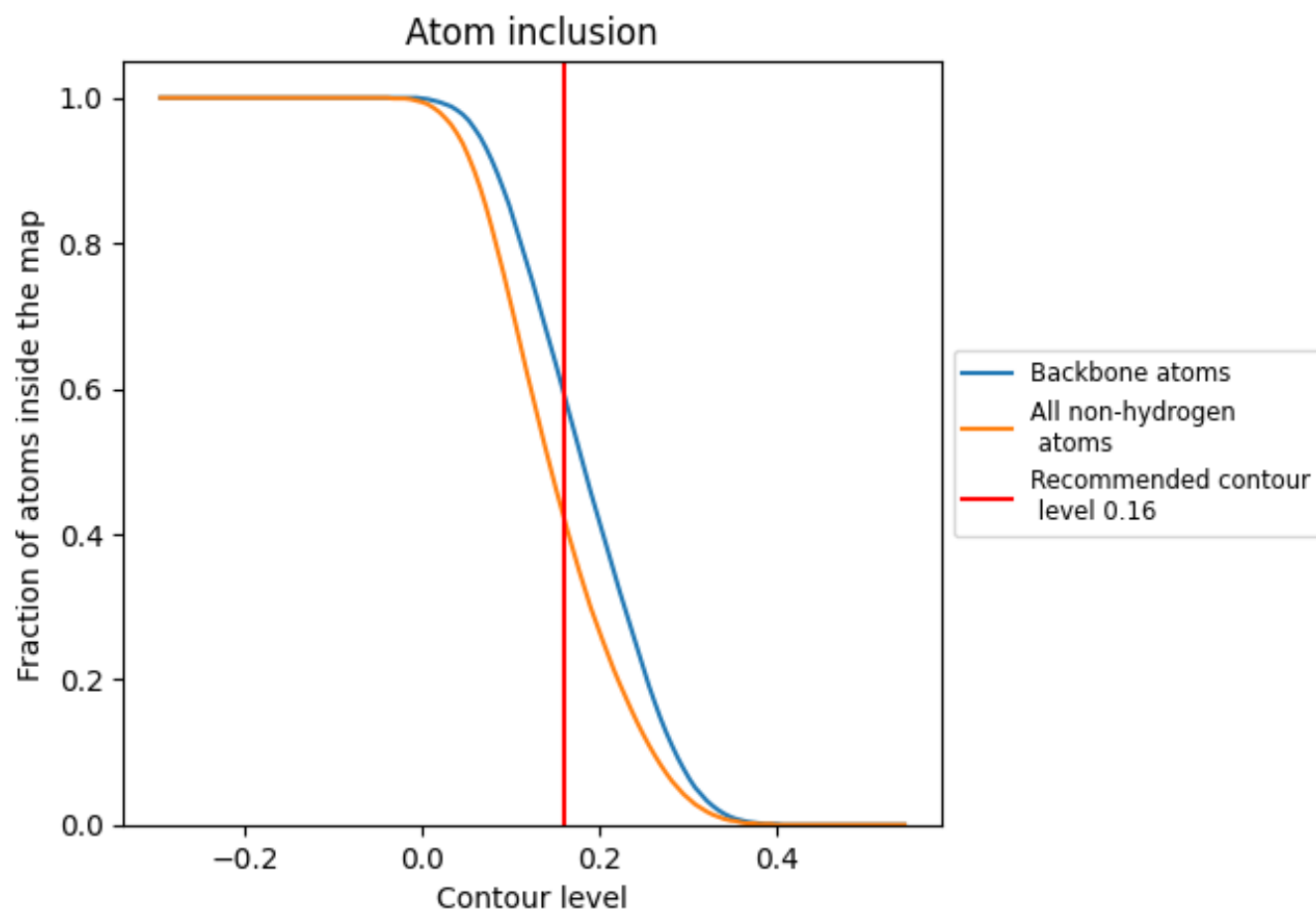
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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