wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 03:45 PM EST

PDB ID	:	7MUS
EMDB ID	:	EMD-24020
Title	:	Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 2
Authors	:	Sheedlo, M.J.; Durie, C.L.; Swanson, M.; Lacy, D.B.; Ohi, M.D.
Deposited on	:	2021-05-14
Resolution	:	4.60 Å(reported)

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

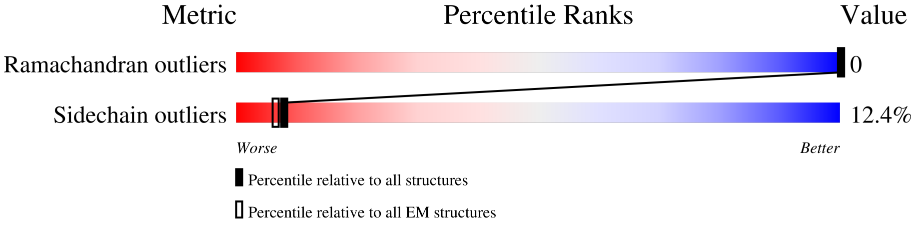
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

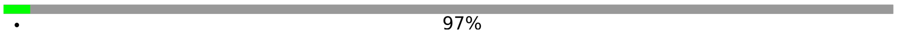
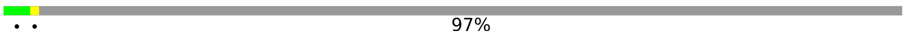
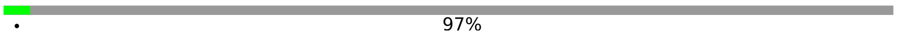
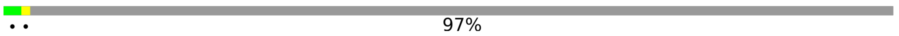
The reported resolution of this entry is 4.60 Å.

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	AG	1048	
1	Ag	1048	
1	BG	1048	
1	Bg	1048	
1	CG	1048	
1	Cg	1048	
1	DG	1048	
1	Dg	1048	
1	EG	1048	

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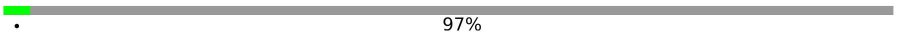
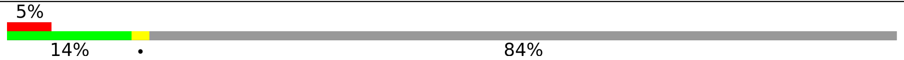
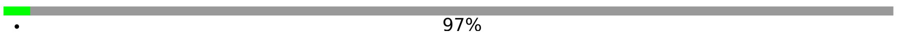
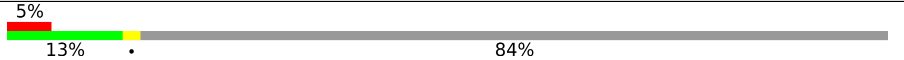
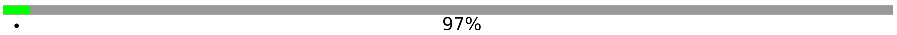
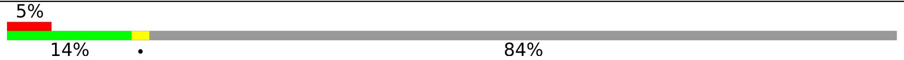
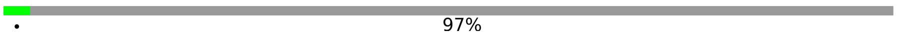
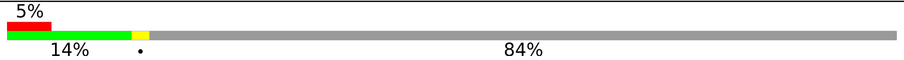
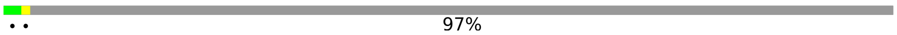
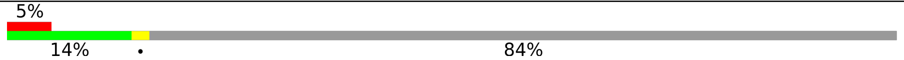
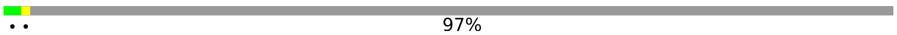
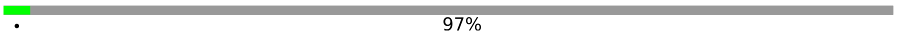
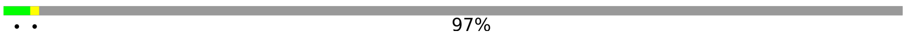
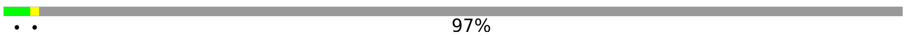
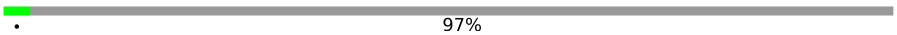
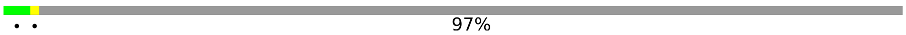
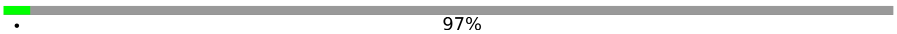
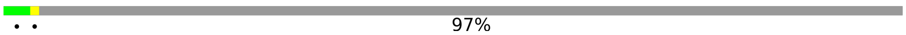
Mol	Chain	Length	Quality of chain
1	Eg	1048	
1	FG	1048	
1	Fg	1048	
1	GG	1048	
1	Gg	1048	
1	HG	1048	
1	Hg	1048	
1	IG	1048	
1	Ig	1048	
1	JG	1048	
1	Jg	1048	
1	KG	1048	
1	Kg	1048	
1	LG	1048	
1	Lg	1048	
1	MG	1048	
1	Mg	1048	
1	NG	1048	
1	OG	1048	
1	PG	1048	
1	VG	1048	
1	WG	1048	
1	XG	1048	
1	YG	1048	
1	ZG	1048	

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Mol	Chain	Length	Quality of chain
2	AD	163	75% 10% 14%
2	Ad	163	74% 10% 16%
2	BD	163	77% 9% 14%
2	Bd	163	78% 6% 16%
2	CD	163	74% 12% 14%
2	Cd	163	77% 7% 16%
2	DD	163	80% 6% 14%
2	Dd	163	77% 7% 16%
2	ED	163	78% 8% 14%
2	Ed	163	77% 7% 16%
2	FD	163	77% 9% 14%
2	Fd	163	75% 9% 16%
2	GD	163	77% 9% 14%
2	Gd	163	76% 8% 16%
2	HD	163	79% 7% 14%
2	Hd	163	75% 9% 16%
2	ID	163	76% 10% 14%
2	Id	163	74% 10% 16%
2	JD	163	77% 9% 14%
2	Jd	163	74% 10% 16%
2	KD	163	• 82% • 14%
2	Kd	163	76% 8% 16%
2	LD	163	76% 10% 14%
2	Ld	163	76% 8% 16%
2	MD	163	77% 9% 14%

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Mol	Chain	Length	Quality of chain
2	Md	163	77% 7% 16%
3	AF	269	22% 77%
3	Af	269	20% 78%
3	BF	269	21% 77%
3	Bf	269	19% 78%
3	CF	269	22% 77%
3	Cf	269	19% 78%
3	DF	269	22% 77%
3	Df	269	20% 78%
3	EF	269	22% 77%
3	Ef	269	20% 78%
3	FF	269	20% 77%
3	Ff	269	20% 78%
3	GF	269	22% 77%
3	Gf	269	21% 78%
3	HF	269	21% 77%
3	Hf	269	19% 78%
3	IF	269	21% 77%
3	If	269	19% 78%
3	JF	269	23% 77%
3	Jf	269	20% 78%
3	KF	269	20% 77%
3	Kf	269	20% 78%
3	LF	269	21% 77%
3	Lf	269	20% 78%

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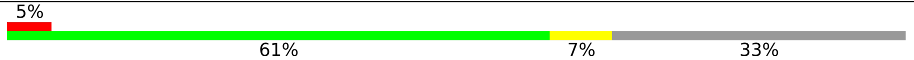
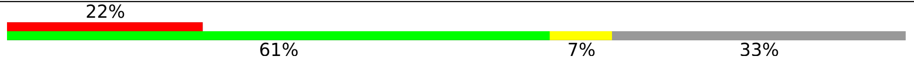
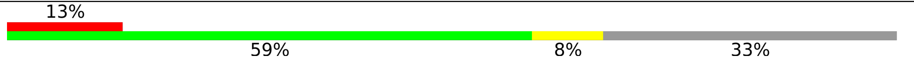
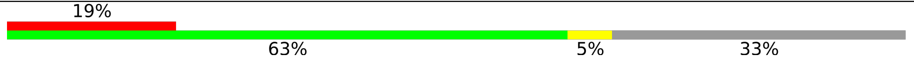
Mol	Chain	Length	Quality of chain
3	MF	269	
3	Mf	269	
3	VF	269	
3	WF	269	
3	XF	269	
3	YF	269	
3	ZF	269	
4	AH	361	
4	BH	361	
4	CH	361	
4	DH	361	
4	EH	361	
4	FH	361	
4	GH	361	
4	HH	361	
4	IH	361	
4	JH	361	
4	KH	361	
4	LH	361	
4	MH	361	
4	VH	361	
4	WH	361	
4	XH	361	
4	YH	361	
4	ZH	361	

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Mol	Chain	Length	Quality of chain
5	AK	189	 70% 10% 20%
5	BK	189	 70% 10% 20%
5	CK	189	 70% 10% 20%
5	DK	189	 72% 8% 20%
5	EK	189	 73% 7% 20%
5	FK	189	 72% 7% 20%
5	GK	189	 71% 8% 20%
5	HK	189	 71% 9% 20%
5	IK	189	 72% 8% 20%
5	JK	189	 72% 8% 20%
5	KK	189	 72% 8% 20%
5	LK	189	 70% 10% 20%
5	MK	189	 74% 6% 20%
6	AL	249	 65% 5% 31%
6	BL	249	 63% 7% 31%
6	CL	249	 61% 8% 31%
6	DL	249	 63% 6% 31%
6	EL	249	 61% 8% 31%
6	FL	249	 65% • 31%
6	GL	249	 63% 6% 31%
6	HL	249	 64% 5% 31%
6	IL	249	 64% 5% 31%
6	JL	249	 63% 6% 31%
6	KL	249	 64% 6% 31%
6	LL	249	 61% 8% 31%

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Mol	Chain	Length	Quality of chain
6	ML	249	63% 6% 31%
7	AM	320	57% 8% 35%
7	BM	320	58% 7% 35%
7	CM	320	58% 7% 35%
7	DM	320	57% 8% 35%
7	EM	320	58% 7% 35%
7	FM	320	58% 7% 35%
7	GM	320	57% 8% 35%
7	HM	320	58% 7% 35%
7	IM	320	58% 8% 35%
7	JM	320	55% 10% 35%
7	KM	320	58% 7% 35%
7	LM	320	58% 8% 35%
7	MM	320	58% 7% 35%
8	AN	124	56% 6% 37%
8	BN	124	58% 5% 37%
8	CN	124	56% 7% 37%
8	DN	124	60% • 37%
8	EN	124	56% 7% 37%
8	FN	124	54% 9% 37%
8	GN	124	57% 6% 37%
8	HN	124	56% 7% 37%
8	IN	124	54% 9% 37%
8	JN	124	57% 6% 37%
8	KN	124	52% 10% 37%

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Mol	Chain	Length	Quality of chain
8	LN	124	• 52% 10% 37%
8	MN	124	• 53% 10% 37%
9	AU	9	100%
9	BU	9	100%
9	CU	9	100%
9	DU	9	100%
9	EU	9	100%
9	FU	9	100%
9	GU	9	100%
9	HU	9	100%
9	IU	9	100%
9	JU	9	100%
9	KU	9	100%
9	LU	9	100%
9	MU	9	100%
10	AX	48	15% 100%
10	BX	48	21% 100%
10	CX	48	• 100%
10	DX	48	19% 100%
10	EX	48	19% 100%
10	FX	48	17% 100%
10	GX	48	23% 100%
10	HX	48	15% 100%
10	IX	48	10% 100%
10	JX	48	17% 100%

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Mol	Chain	Length	Quality of chain
10	KX	48	15% 100%
10	LX	48	6% 100%
10	MX	48	15% 100%
10	VX	48	10% 100%
10	WX	48	10% 100%
10	XX	48	10% 100%
10	YX	48	17% 100%
10	ZX	48	6% 100%
11	AC	303	59% 10% 31%
11	BC	303	61% 8% 31%
11	CC	303	60% 9% 31%
11	DC	303	• 71% 10% 20%
11	EC	303	• 61% 8% 31%
11	FC	303	63% 6% 31%
11	GC	303	62% 7% 31%
11	HC	303	• 71% 9% 20%
11	IC	303	• 70% 10% 20%
11	JC	303	64% 5% 31%
11	KC	303	63% 6% 31%
11	LC	303	• 72% 8% 20%
11	MC	303	• 71% 10% 20%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 192370 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 IcmE protein.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	AG	165	Total C N O S 1229 780 203 242 4	0	0
1	Gg	34	Total C N O S 276 168 47 60 1	0	0
1	Hg	34	Total C N O S 276 168 47 60 1	0	0
1	Bg	34	Total C N O S 276 168 47 60 1	0	0
1	BG	165	Total C N O S 1229 780 203 242 4	0	0
1	Ig	34	Total C N O S 276 168 47 60 1	0	0
1	Jg	34	Total C N O S 276 168 47 60 1	0	0
1	CG	165	Total C N O S 1229 780 203 242 4	0	0
1	Kg	34	Total C N O S 276 168 47 60 1	0	0
1	Ag	34	Total C N O S 276 168 47 60 1	0	0
1	Lg	34	Total C N O S 276 168 47 60 1	0	0
1	DG	165	Total C N O S 1229 780 203 242 4	0	0
1	Cg	34	Total C N O S 276 168 47 60 1	0	0
1	Mg	34	Total C N O S 276 168 47 60 1	0	0
1	VG	34	Total C N O S 276 168 47 60 1	0	0
1	WG	34	Total C N O S 276 168 47 60 1	0	0
1	XG	34	Total C N O S 276 168 47 60 1	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
1	EG	165	Total C N O S 1229 780 203 242 4	0	0
1	YG	34	Total C N O S 276 168 47 60 1	0	0
1	ZG	34	Total C N O S 276 168 47 60 1	0	0
1	FG	165	Total C N O S 1229 780 203 242 4	0	0
1	Dg	34	Total C N O S 276 168 47 60 1	0	0
1	GG	165	Total C N O S 1229 780 203 242 4	0	0
1	Eg	34	Total C N O S 276 168 47 60 1	0	0
1	Fg	34	Total C N O S 276 168 47 60 1	0	0
1	HG	165	Total C N O S 1229 780 203 242 4	0	0
1	IG	165	Total C N O S 1229 780 203 242 4	0	0
1	JG	165	Total C N O S 1229 780 203 242 4	0	0
1	KG	165	Total C N O S 1229 780 203 242 4	0	0
1	LG	165	Total C N O S 1229 780 203 242 4	0	0
1	MG	165	Total C N O S 1229 780 203 242 4	0	0
1	NG	165	Total C N O S 1229 780 203 242 4	0	0
1	OG	165	Total C N O S 1229 780 203 242 4	0	0
1	PG	165	Total C N O S 1229 780 203 242 4	0	0

- Molecule 2 is a protein called DotD.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	GD	140	Total C N O S 1086 692 185 206 3	0	0
2	Gd	137	Total C N O S 1058 672 182 202 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Dd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	Hd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	ID	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Id	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	JD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Jd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	KD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Kd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	LD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	CD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Ld	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	MD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Md	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	AD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Ad	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	BD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Bd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	ED	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Cd	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	DD	140	Total 1086	C 692	N 185	O 206	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ed	137	Total 1058	C 672	N 182	O 202	S 2	0	0
2	FD	140	Total 1086	C 692	N 185	O 206	S 3	0	0
2	Fd	137	Total 1058	C 672	N 182	O 202	S 2	0	0

- Molecule 3 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	GF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Gf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	HF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Hf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	IF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	If	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	JF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Jf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	KF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Kf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	LF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Lf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	MF	63	Total 483	C 308	N 84	O 90	S 1	0	0
3	Df	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	Mf	59	Total 449	C 290	N 77	O 81	S 1	0	0
3	VF	63	Total 483	C 308	N 84	O 90	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	WF	63	483	308	84	90	1	0	0
3	XF	63	483	308	84	90	1	0	0
3	CF	63	483	308	84	90	1	0	0
3	YF	63	483	308	84	90	1	0	0
3	ZF	63	483	308	84	90	1	0	0
3	Af	59	449	290	77	81	1	0	0
3	BF	63	483	308	84	90	1	0	0
3	Bf	59	449	290	77	81	1	0	0
3	Cf	59	449	290	77	81	1	0	0
3	DF	63	483	308	84	90	1	0	0
3	EF	63	483	308	84	90	1	0	0
3	Ef	59	449	290	77	81	1	0	0
3	FF	63	483	308	84	90	1	0	0
3	Ff	59	449	290	77	81	1	0	0
3	AF	63	483	308	84	90	1	0	0

- Molecule 4 is a protein called Type IV secretion protein IcmK.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	GH	258	1983	1268	336	371	8	0	0
4	HH	258	1983	1268	336	371	8	0	0
4	IH	258	1983	1268	336	371	8	0	0
4	JH	258	1983	1268	336	371	8	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
4	AH	258	Total C N O S 1983 1268 336 371 8	0	0
4	KH	258	Total C N O S 1983 1268 336 371 8	0	0
4	LH	258	Total C N O S 1983 1268 336 371 8	0	0
4	MH	258	Total C N O S 1983 1268 336 371 8	0	0
4	VH	243	Total C N O S 1875 1201 319 348 7	0	0
4	WH	243	Total C N O S 1875 1201 319 348 7	0	0
4	XH	243	Total C N O S 1875 1201 319 348 7	0	0
4	YH	243	Total C N O S 1875 1201 319 348 7	0	0
4	ZH	243	Total C N O S 1875 1201 319 348 7	0	0
4	BH	258	Total C N O S 1983 1268 336 371 8	0	0
4	CH	258	Total C N O S 1983 1268 336 371 8	0	0
4	DH	258	Total C N O S 1983 1268 336 371 8	0	0
4	EH	258	Total C N O S 1983 1268 336 371 8	0	0
4	FH	258	Total C N O S 1983 1268 336 371 8	0	0

- Molecule 5 is a protein called Inner membrane lipoprotein YiaD.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	GK	151	Total C N O S 1175 747 209 215 4	0	0
5	HK	151	Total C N O S 1175 747 209 215 4	0	0
5	IK	151	Total C N O S 1175 747 209 215 4	0	0
5	JK	151	Total C N O S 1175 747 209 215 4	0	0
5	KK	151	Total C N O S 1175 747 209 215 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	LK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	AK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	MK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	BK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	CK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	DK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	EK	151	Total 1175	C 747	N 209	O 215	S 4	0	0
5	FK	151	Total 1175	C 747	N 209	O 215	S 4	0	0

- Molecule 6 is a protein called Outer membrane protein, OmpA family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	GL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	HL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	IL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	JL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	KL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	LL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	ML	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	AL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	BL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	CL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	DL	173	Total 1388	C 877	N 253	O 253	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	EL	173	Total 1388	C 877	N 253	O 253	S 5	0	0
6	FL	173	Total 1388	C 877	N 253	O 253	S 5	0	0

- Molecule 7 is a protein called DUF2807 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	GM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	HM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	IM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	JM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	KM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	LM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	MM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	AM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	BM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	CM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	DM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	EM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0
7	FM	208	Total 1650	C 1046	N 293	O 308	S 3	0	0

- Molecule 8 is a protein called Neurogenic locus notch.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	HN	78	Total 582	C 357	N 99	O 113	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	IN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	JN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	KN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	LN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	MN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	AN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	BN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	CN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	DN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	EN	78	Total 582	C 357	N 99	O 113	S 13	0	0
8	FN	78	Total 582	C 357	N 99	O 113	S 13	0	0

- Molecule 9 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	GU	9	Total 45	C 27	N 9	O 9	0	0
9	HU	9	Total 45	C 27	N 9	O 9	0	0
9	IU	9	Total 45	C 27	N 9	O 9	0	0
9	JU	9	Total 45	C 27	N 9	O 9	0	0
9	KU	9	Total 45	C 27	N 9	O 9	0	0
9	LU	9	Total 45	C 27	N 9	O 9	0	0
9	MU	9	Total 45	C 27	N 9	O 9	0	0
9	AU	9	Total 45	C 27	N 9	O 9	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
9	BU	9	Total C N O 45 27 9 9	0	0
9	CU	9	Total C N O 45 27 9 9	0	0
9	DU	9	Total C N O 45 27 9 9	0	0
9	EU	9	Total C N O 45 27 9 9	0	0
9	FU	9	Total C N O 45 27 9 9	0	0

- Molecule 10 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms	AltConf	Trace
10	GX	48	Total C N O 240 144 48 48	0	0
10	HX	48	Total C N O 240 144 48 48	0	0
10	IX	48	Total C N O 240 144 48 48	0	0
10	JX	48	Total C N O 240 144 48 48	0	0
10	KX	48	Total C N O 240 144 48 48	0	0
10	LX	48	Total C N O 240 144 48 48	0	0
10	MX	48	Total C N O 240 144 48 48	0	0
10	VX	48	Total C N O 240 144 48 48	0	0
10	WX	48	Total C N O 240 144 48 48	0	0
10	XX	48	Total C N O 240 144 48 48	0	0
10	YX	48	Total C N O 240 144 48 48	0	0
10	ZX	48	Total C N O 240 144 48 48	0	0
10	AX	48	Total C N O 240 144 48 48	0	0
10	BX	48	Total C N O 240 144 48 48	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	CX	48	240	144	48	48	0	0
10	DX	48	240	144	48	48	0	0
10	EX	48	240	144	48	48	0	0
10	FX	48	240	144	48	48	0	0

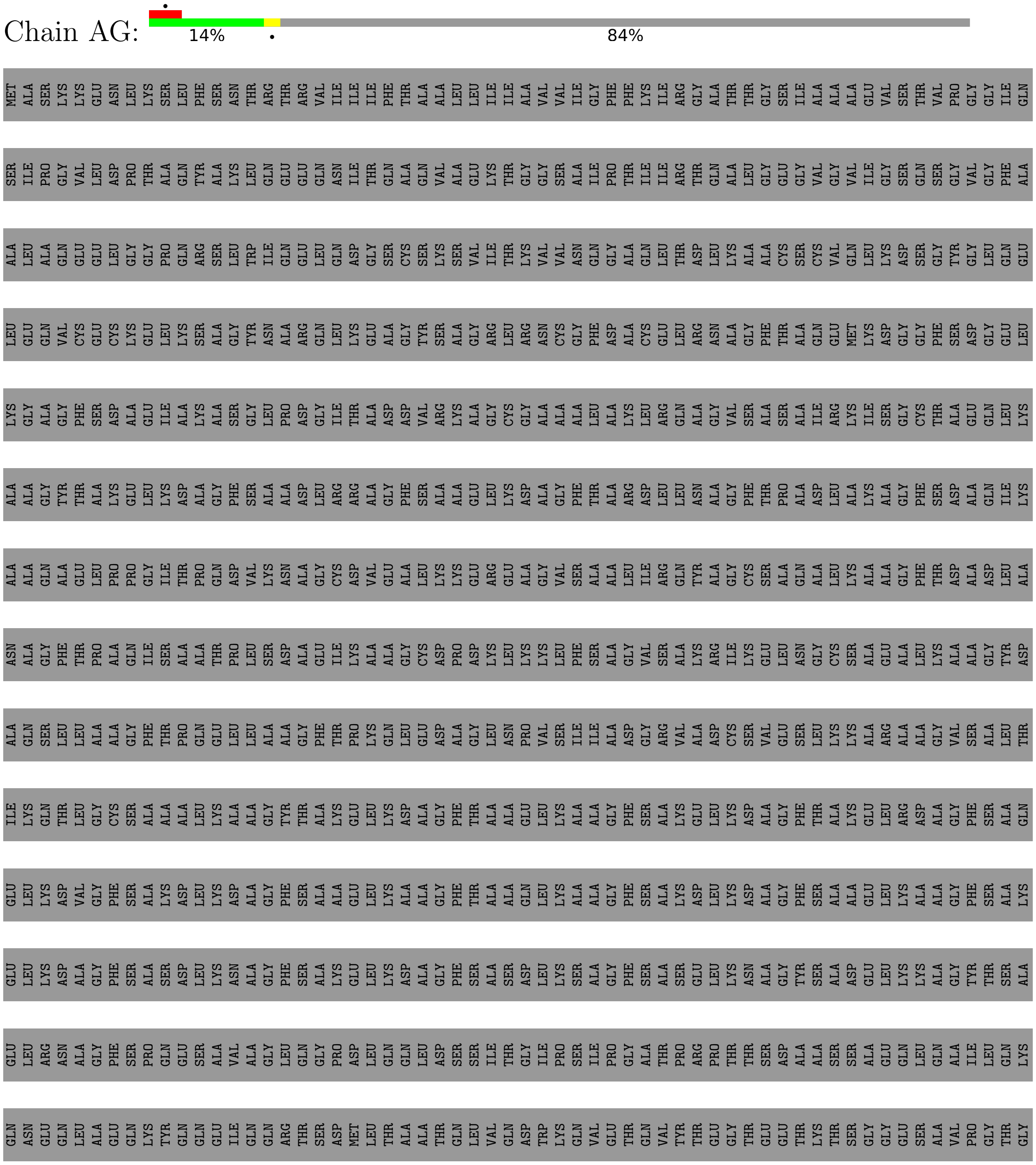
- Molecule 11 is a protein called DotC.

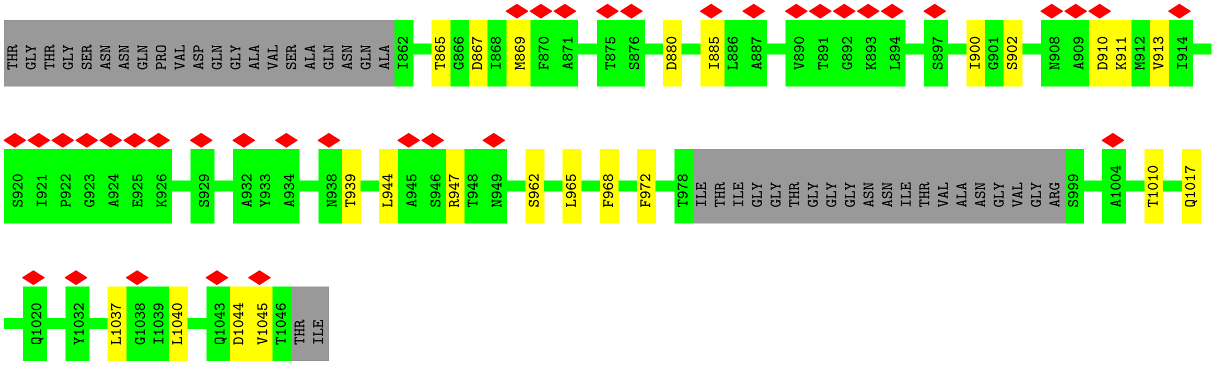
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	CC	209	1667	1061	292	309	5	0	0
11	EC	209	1667	1061	292	309	5	0	0
11	FC	209	1667	1061	292	309	5	0	0
11	DC	243	1921	1216	340	357	8	0	0
11	GC	209	1667	1061	292	309	5	0	0
11	HC	243	1921	1216	340	357	8	0	0
11	MC	243	1921	1216	340	357	8	0	0
11	JC	209	1667	1061	292	309	5	0	0
11	KC	209	1667	1061	292	309	5	0	0
11	LC	243	1921	1216	340	357	8	0	0
11	AC	209	1667	1061	292	309	5	0	0
11	BC	209	1667	1061	292	309	5	0	0
11	IC	243	1921	1216	340	357	8	0	0

3 Residue-property plots ⓘ

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

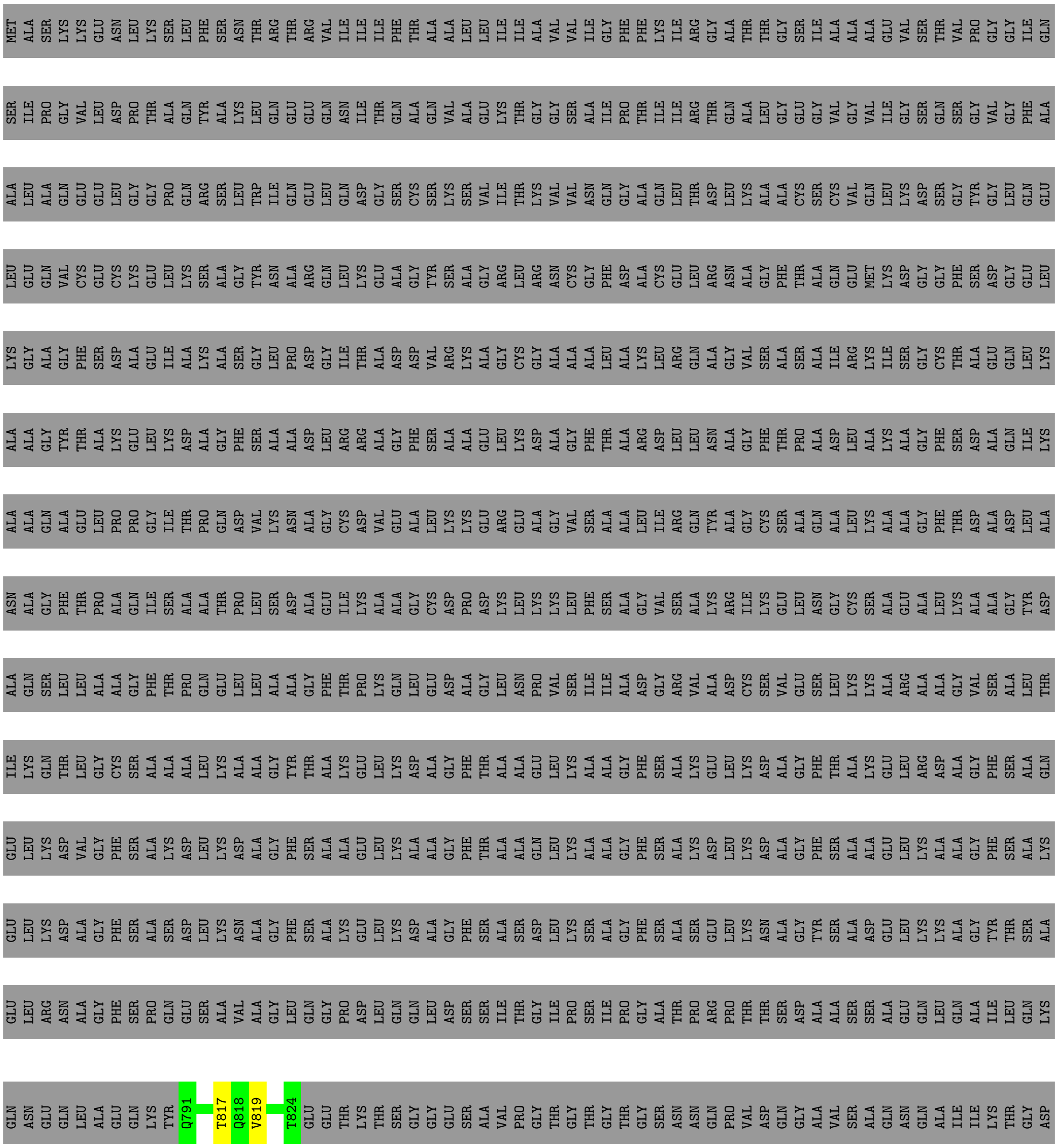
- Molecule 1: IcmE protein





- Molecule 1: IcmE protein

Chain Gg:



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

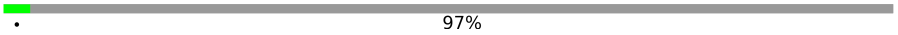
ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN THR THR ILE THR ILE GLY GLY THR GLY GLY GLY

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

ILE

- Molecule 1: IcmE protein

Chain Hg:



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

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

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

ALA ALA GLN ALA GLU LEU PRO PRO GLY ILE THR PRO GLN ASP VAL LYS ASN ALA GLY CYS ASP VAL GLU ALA LEU LYS GLU ARG GLU ALA GLY VAL SER ALA ALA LEU ILE ARG GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ASP ALA ASP LEU ALA

ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

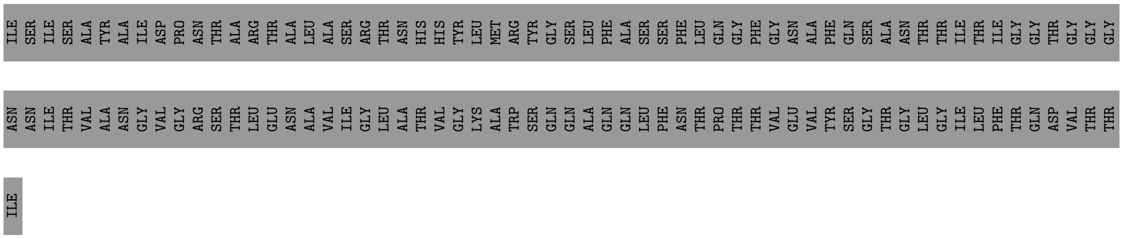
GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

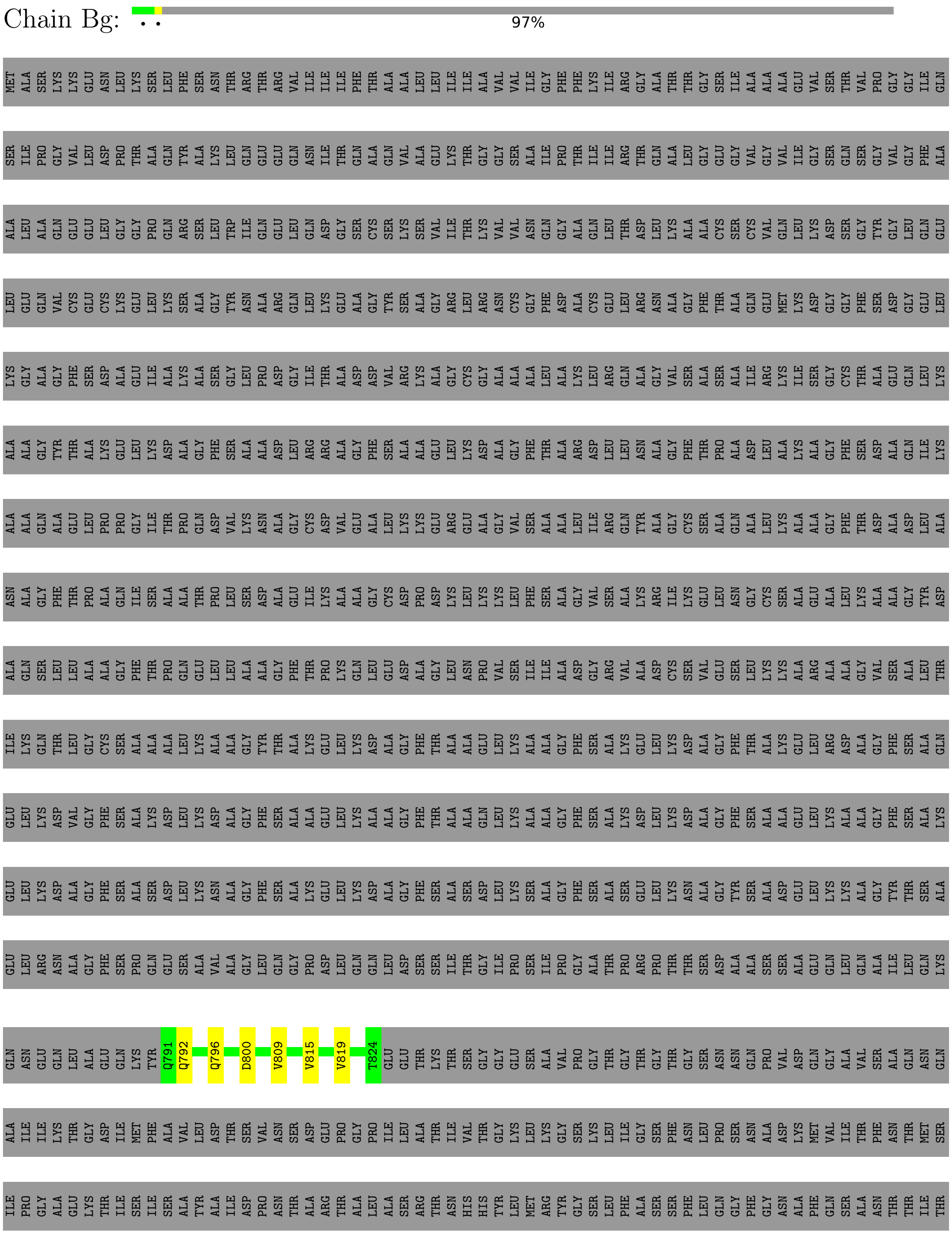
GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 D800 Y820 T824 GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA ILE LYS THR GLY ASP

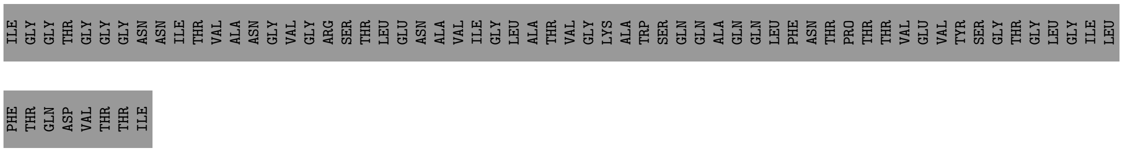
ILE MET PHE ALA VAL LEU ASP THR SER VAL ASN SER ASP GLU PRO GLY PRO ILE LEU ALA THR ILE VAL THR GLY LYS LEU LYS GLY SER LYS LEU ILE GLY SER PHE ASN LEU PRO SER ASN ALA ASP LYS MET VAL ILE THR PHE ASN THR MET SER ILE PRO GLY ALA GLU LYS THR



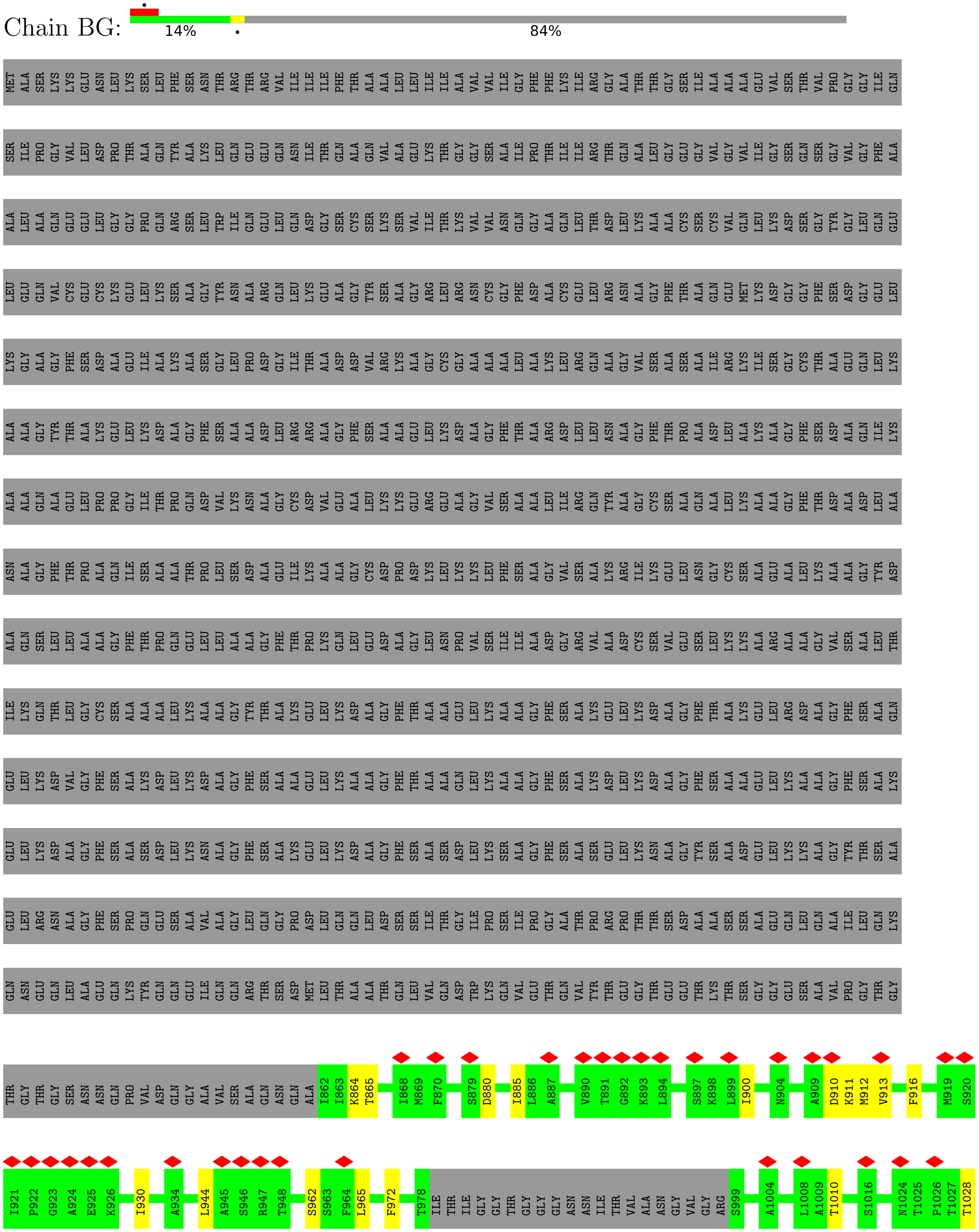
- Molecule 1: IcmE protein

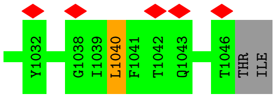
Chain Bg:



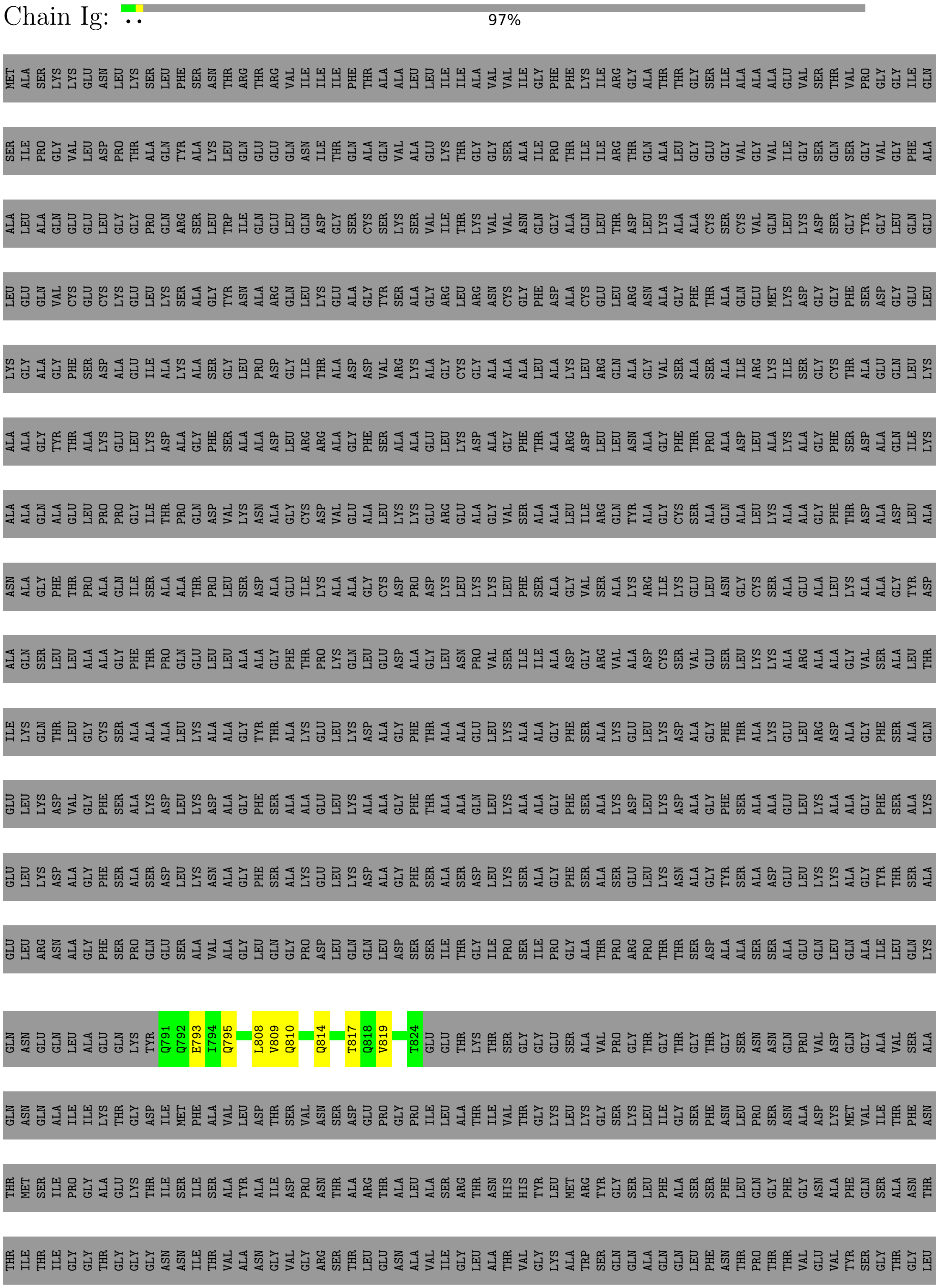


- Molecule 1: IcmE protein





- Molecule 1: IcmE protein



GLY ILE LEU PHE THR GLN ASP VAL THR THR ILE

- Molecule 1: IcmE protein

Chain Jg:

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

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

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

ALA ALA GLN ALA GLU LEU PRO PRO GLY ILE THR PRO GLN ASP VAL LYS ASN ALA GLY CYS ASP VAL GLU ALA LEU LYS LYS GLU ARG GLU ALA GLY VAL SER ALA ALA LEU ILE ARG GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ASP ALA ASP LEU ALA

ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 D800 M801 L802 L808 V809 Q814 T817 Q818 V819 Y820 T821 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER

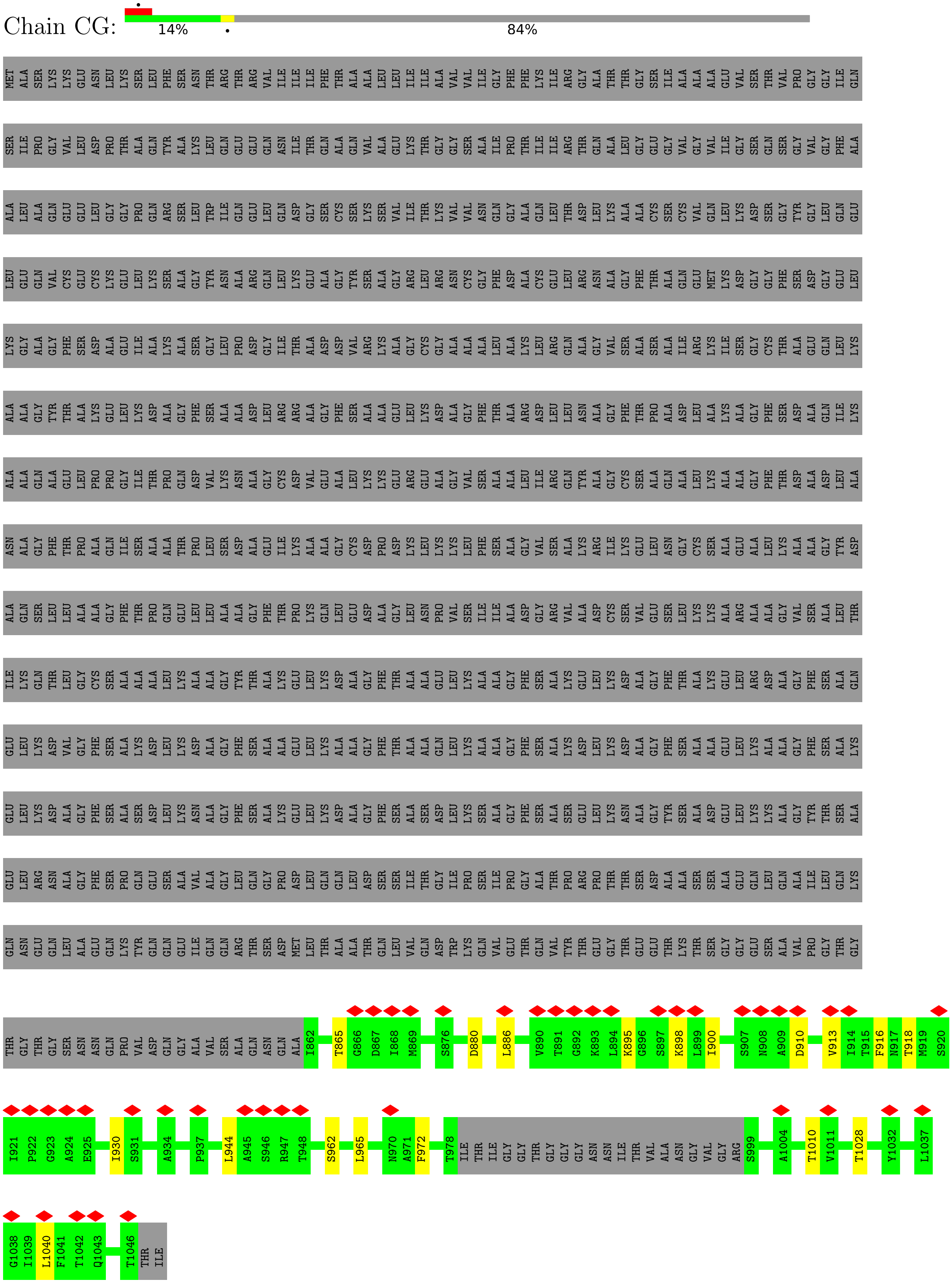
ALA GLN ASN GLN ALA ILE ILE LYS THR GLY ASP ILE MET PHE ALA VAL LEU ASP THR SER VAL ASN SER ASP GLU PRO GLY PRO ILE LEU ALA THR ILE VAL THR GLY LYS LEU LYS GLY SER LYS LEU ILE GLY SER PHE ASN LEU PRO SER ASN ALA ASP LYS MET VAL ILE THR PHE

ASN THR MET SER ILE PRO GLY ALA GLU LYS THR ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN

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

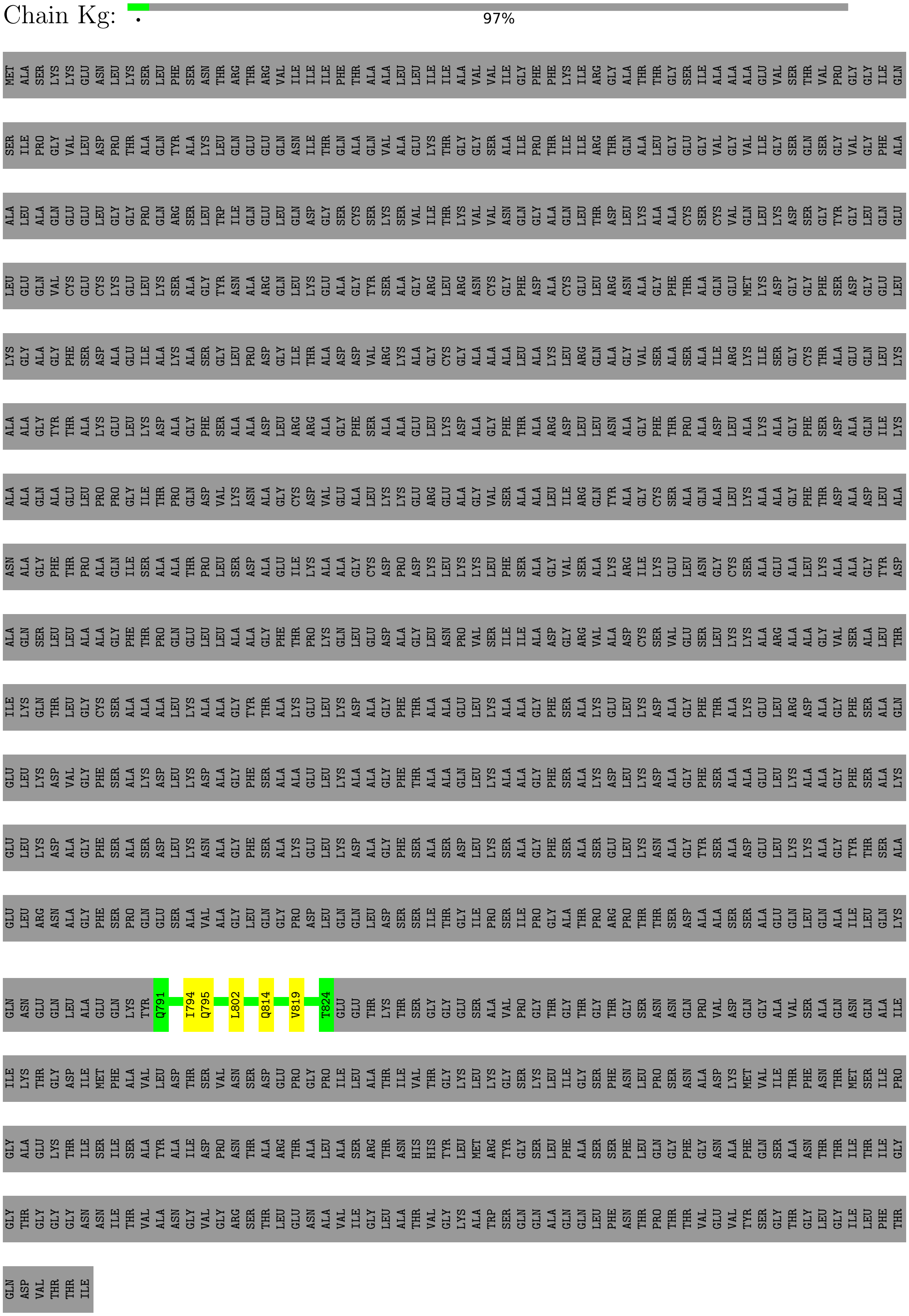
LEU GLY ILE LEU PHE THR GLN ASP VAL THR THR ILE

- Molecule 1: IcmE protein



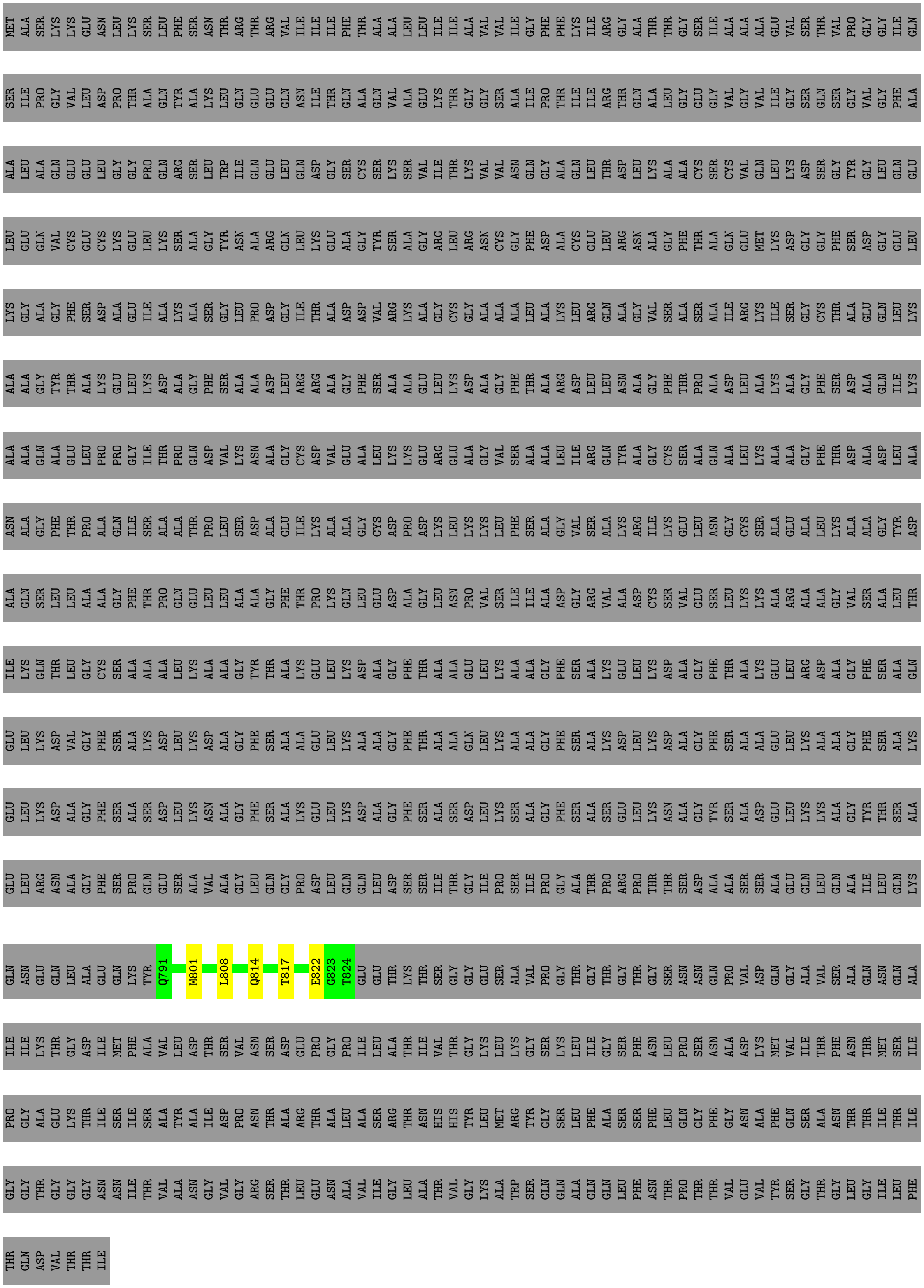
- Molecule 1: IcmE protein

Chain Kg:



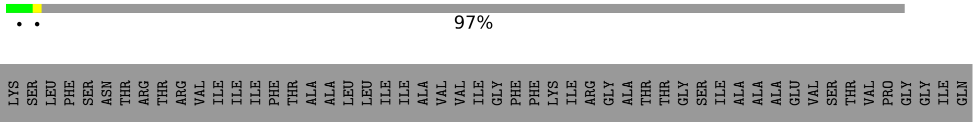
- Molecule 1: IcmE protein

Chain Ag:



- Molecule 1: IcmE protein

Chain Lg:



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

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

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ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 Q792 E793 I794 Q795 L808 Q814 V815 T821 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN

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

ILE PRO GLY ALA GLU LYS THR ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN THR THR ILE THR

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

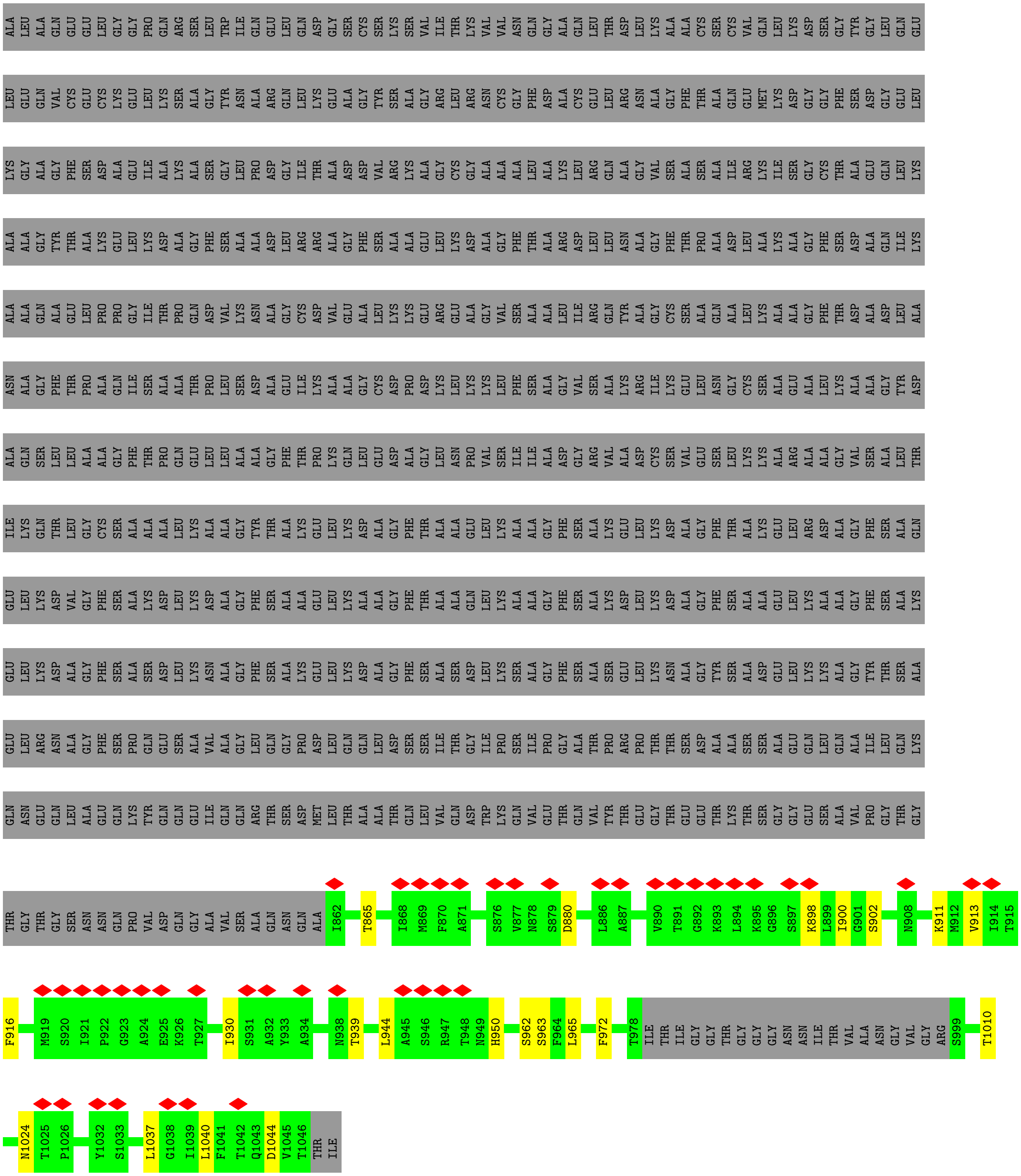
PHE THR GLN ASP VAL THR THR ILE

- Molecule 1: IcmE protein

Chain DG:

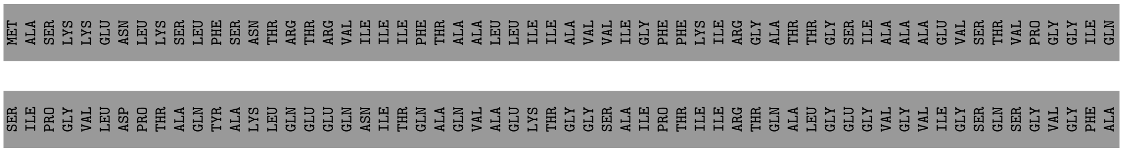
MET ALA SER LYS LYS GLU ASN LEU LYS SER LEU PHE SER ASN THR ARG THR ARG VAL ILE ILE ILE PHE THR ALA ALA LEU LEU ILE ALA VAL VAL ILE GLY PHE PHE LYS ILE ARG GLY ALA THR THR GLY SER ILE ALA ALA ALA GLU VAL SER THR VAL PRO GLY GLY ILE GLN

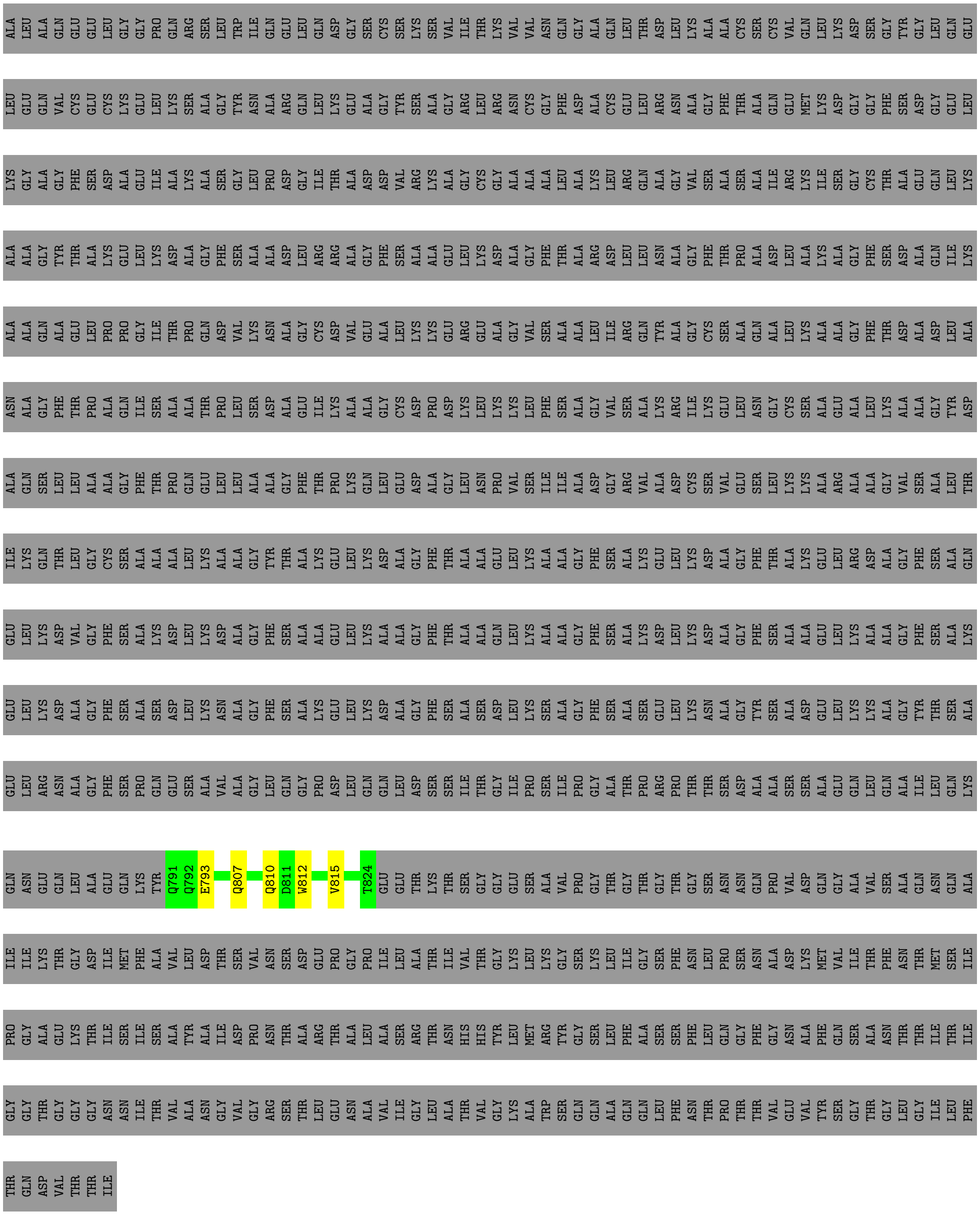
SER ILE PRO GLY VAL LEU ASP PRO THR ALA GLN TYR ALA LYS LEU GLN GLU GLU GLN ASN ILE THR GLN ALA GLN VAL ALA GLU LYS THR GLY GLY SER ALA ILE PRO THR ILE ILE ARG THR GLN ALA LEU GLY GLU GLY VAL GLY VAL ILE GLY SER GLN SER GLY VAL GLY PHE ALA



- Molecule 1: IcmE protein

Chain Cg:





ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

ALA ALA GLN ALA GLU LEU PRO PRO GLY ILE THR PRO GLN ASP VAL LYS ASN ALA GLY CYS ASP VAL GLU ALA LEU LYS LYS GLU ARG GLU ALA GLY VAL SER ALA ALA LEU ILE ARG GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ASP ALA ASP LEU ALA

ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 Q792 E793 Q807 Q810 D811 W812 V815 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA

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

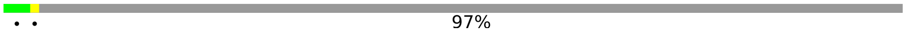
PRO GLY ALA GLU LYS THR ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN THR THR ILE THR ILE

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

THR GLN ASP VAL THR THR ILE

- Molecule 1: IcmE protein

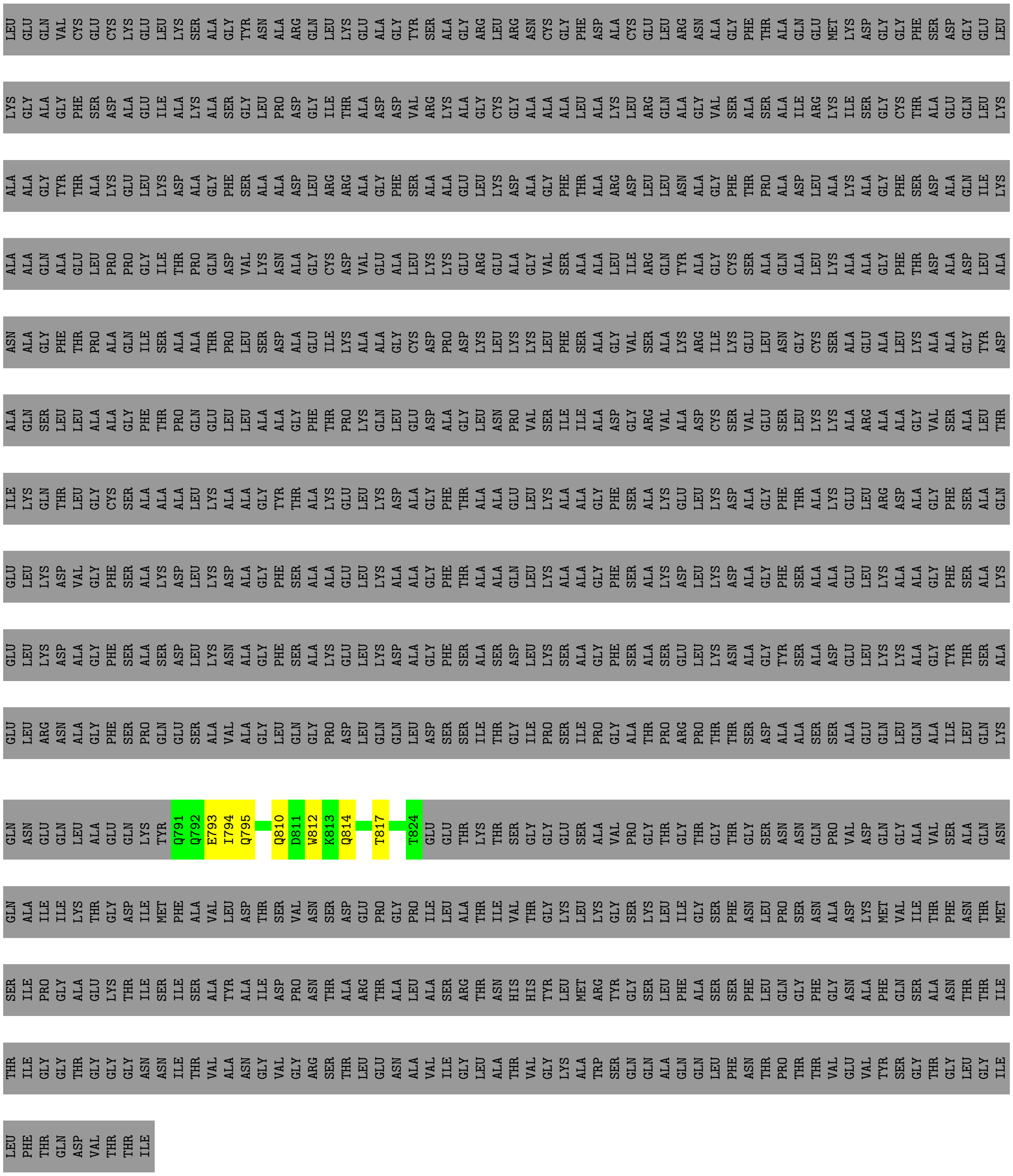
Chain Mg:



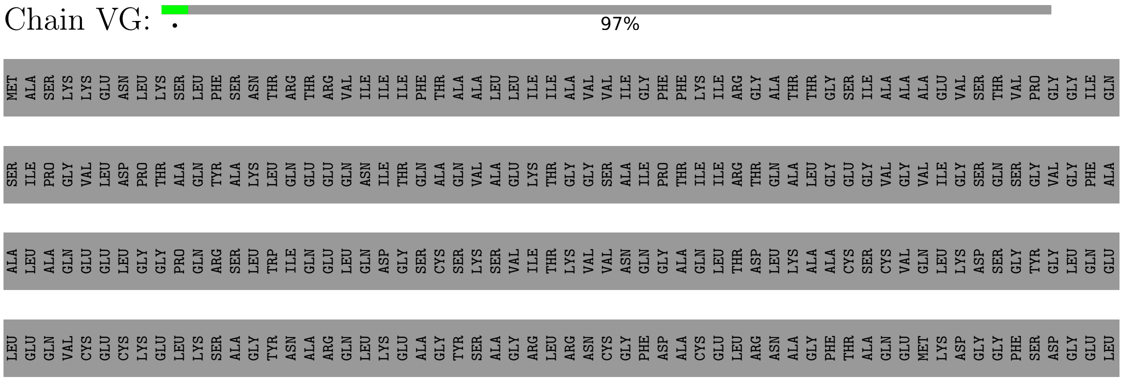
MET ALA SER LYS LYS GLU ASN LEU LYS SER LEU PHE SER ASN THR ARG THR ARG VAL ILE ILE ILE PHE THR ALA ALA LEU LEU ILE ILE ALA VAL VAL ILE GLY PHE PHE LYS ILE ARG GLY ALA THR THR GLY SER ILE ALA ALA ALA GLU VAL SER THR VAL PRO GLY GLY ILE GLN

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

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU



- Molecule 1: IcmE protein



LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

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ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 Q792 E793 K813 Q818 V819 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA ILE ILE LYS

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

GLU LYS THR ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN THR THR ILE THR ILE GLY GLY THR

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

VAL THR THR ILE

- Molecule 1: IcmE protein

Chain WG:

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

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

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

ALA ALA GLN ALA GLU LEU PRO PRO GLY ILE THR PRO GLN ASP VAL LYS ASN ALA GLY CYS ASP VAL GLU ALA LEU LYS LYS GLU ARG GLU ALA GLY VAL SER ALA ALA LEU ILE ARG GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ASP ALA ASP LEU ALA

ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 I794 D800 M801 L802 E816 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA ILE ILE

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

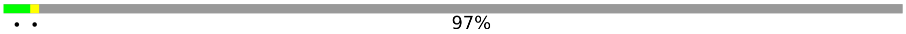
ALA GLU LYS THR ILE SER ILE SER ALA TYR ALA ILE ASP PRO ASN THR ALA ARG THR ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA SER SER PHE LEU GLN GLY PHE GLY ASN ALA PHE GLN SER ALA ASN THR THR ILE THR ILE GLY GLY

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

ASP VAL THR THR ILE

- Molecule 1: IcmE protein

Chain XG:



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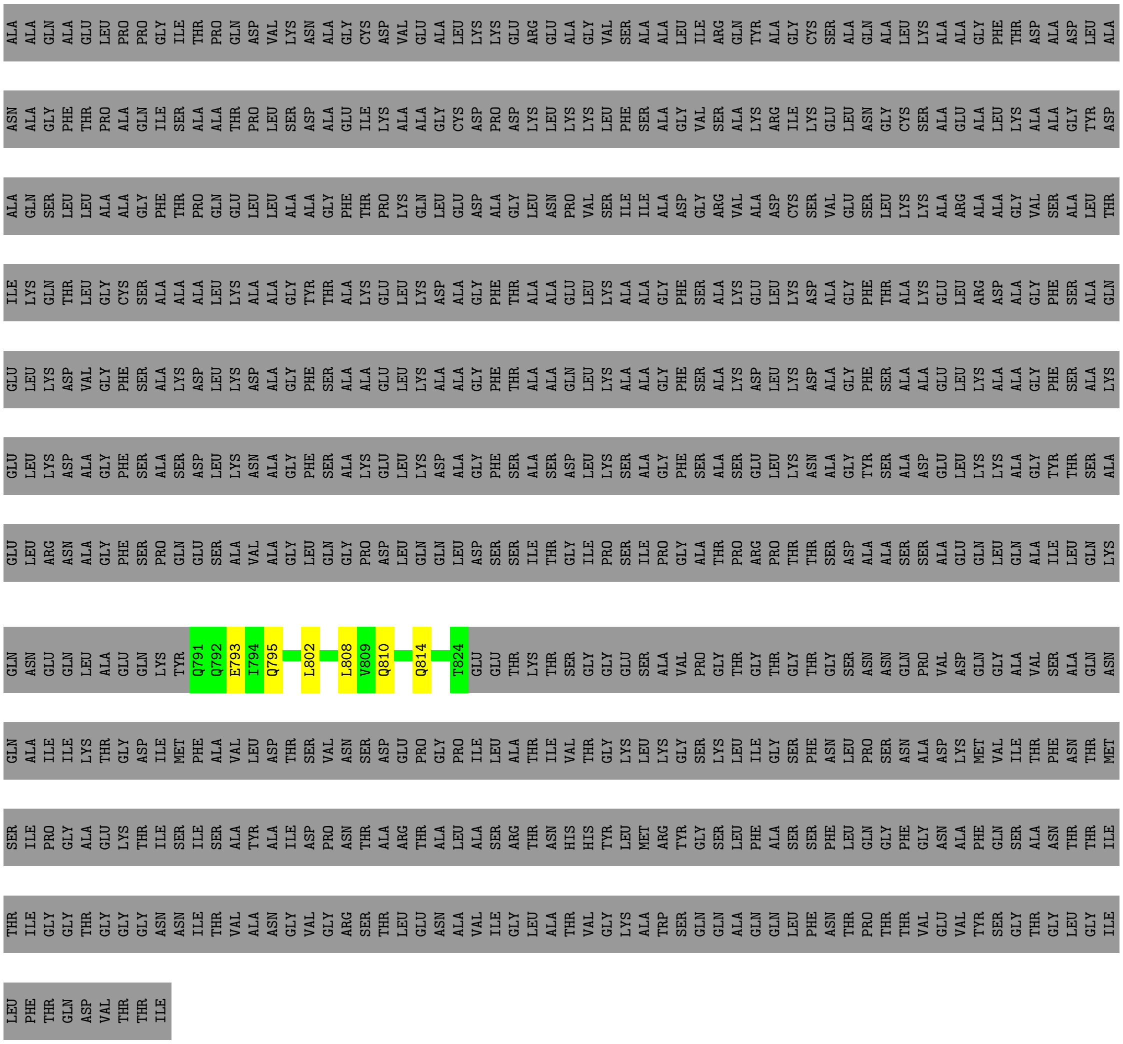
SER ILE PRO GLY VAL LEU ASP PRO THR ALA GLN TYR ALA LYS LEU GLN GLU GLU GLN ASN ILE THR GLN ALA GLN VAL ALA GLU LYS THR GLY GLY SER ALA ILE PRO THR ILE ILE ARG THR GLN ALA LEU GLY GLU GLY VAL GLY VAL ILE GLY SER GLN SER GLY VAL GLY PHE ALA

ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

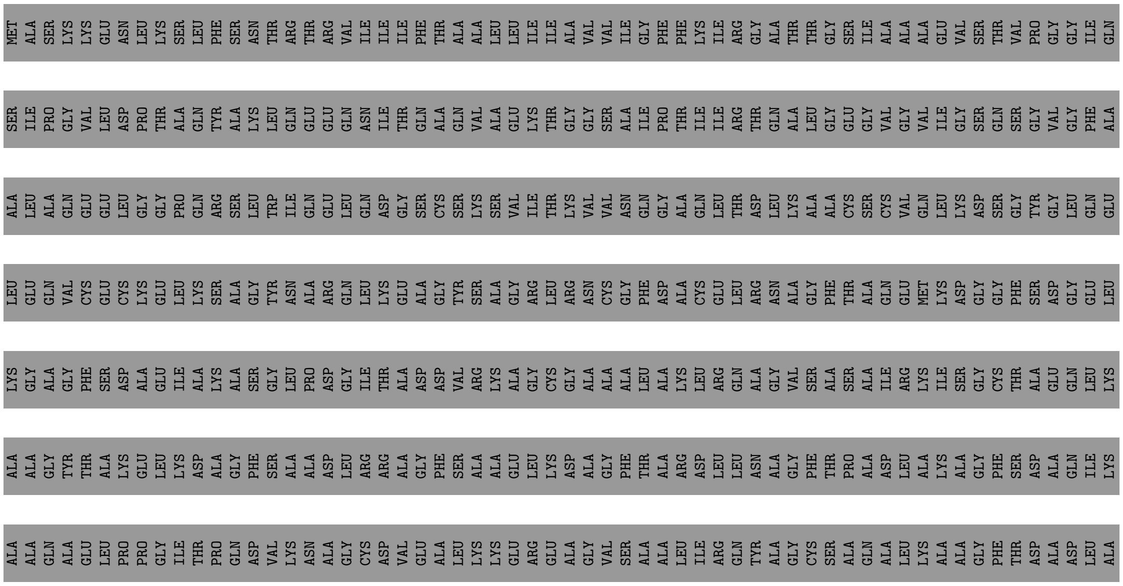
LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

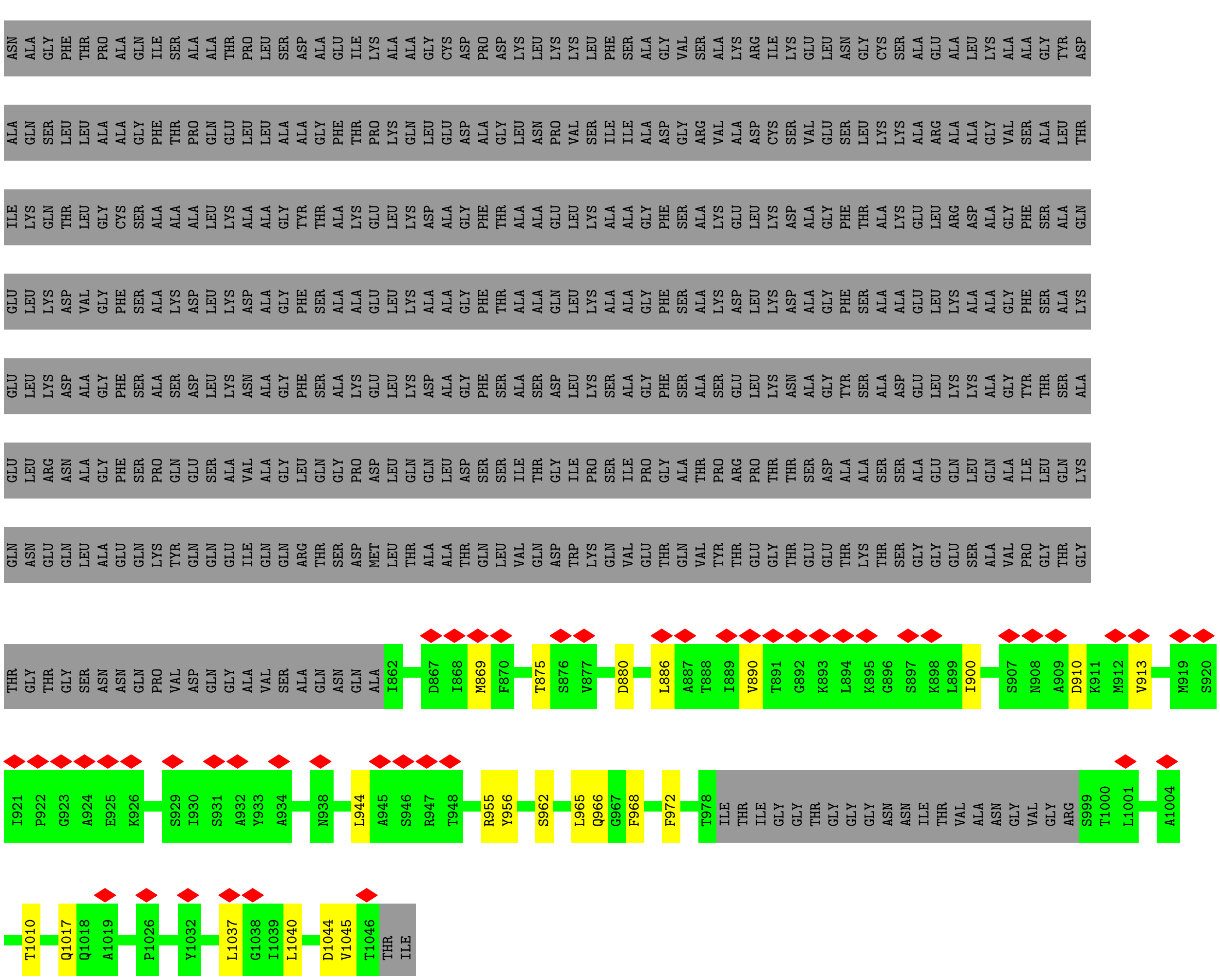
ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS



- Molecule 1: IcmE protein

Chain EG:





ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LEU LYS LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU LYS ALA ALA GLY TYR ASP

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

ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLY PHE SER ALA GLN

GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA GLN LEU LYS ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS

GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA GLY PHE SER ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ASP GLU LEU LYS LYS ALA GLY TYR THR SER ALA

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

GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR GLN GLN GLU ILE GLN GLN ARG THR SER ASP MET LEU THR ALA ALA THR GLN LEU VAL GLN ASP TRP LYS GLN VAL GLU THR GLN VAL TYR THR GLU GLY THR GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO GLY THR GLY

THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA I862 D867 I868 M869 F870 T875 S876 V877 D880 L886 A887 T888 I889 V890 T891 G892 K893 L894 K895 G896 S897 K898 L899 I900 S907 N908 A909 D910 K911 M912 V913 M919 S920

I921 P922 G923 A924 E925 K926 S929 I930 S931 A932 Y933 A934 N938 L944 A945 S946 R947 T948 R955 Y956 S962 L965 Q966 G967 F968 F972 T978 ILE THR ILE GLY GLY THR GLY GLY GLY ASN ASN ILE THR VAL ALA ASN GLY VAL GLY ARG S999 T1000 L1001 A1004

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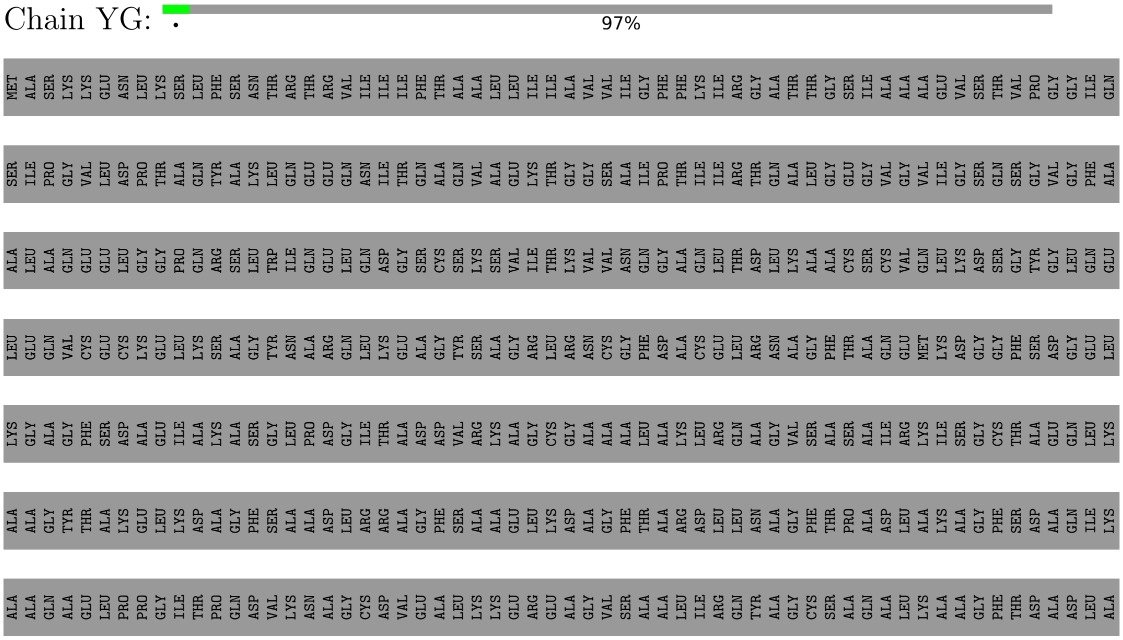
- Molecule 1: IcmE protein

Chain YG:



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

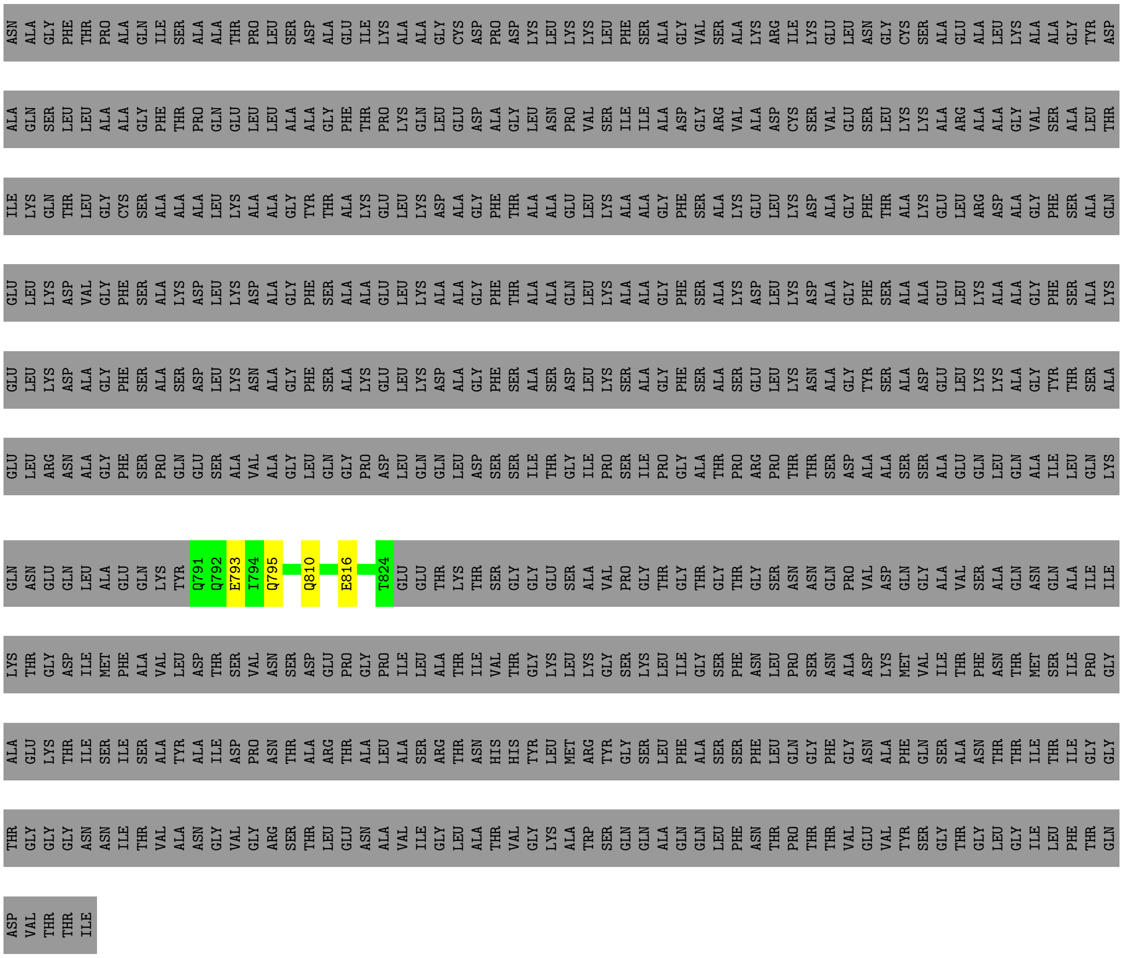
ALA LEU ALA GLN GLU GLU LEU GLY GLY PRO GLN ARG SER LEU TRP ILE GLN GLU LEU GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY LEU GLN GLU

LEU GLU GLN VAL CYS GLU CYS LYS GLU LEU LYS SER ALA GLY TYR ASN ALA ARG GLN LEU LYS GLU ALA GLY TYR SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA CYS GLU LEU ARG ASN ALA GLY PHE THR ALA GLN GLU MET LYS ASP GLY GLY PHE SER ASP GLY GLU LEU

LYS GLY ALA GLY PHE SER ASP ALA GLU ILE ALA LYS ALA SER GLY LEU PRO ASP GLY ILE THR ALA ASP ASP VAL ARG LYS ALA GLY CYS GLY ALA ALA ALA LEU ALA LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN LEU LYS

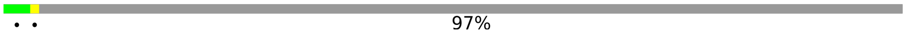
ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ASP LEU ARG ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA ARG ASP LEU LEU ASN ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ALA GLY PHE SER ASP ALA GLN ILE LYS

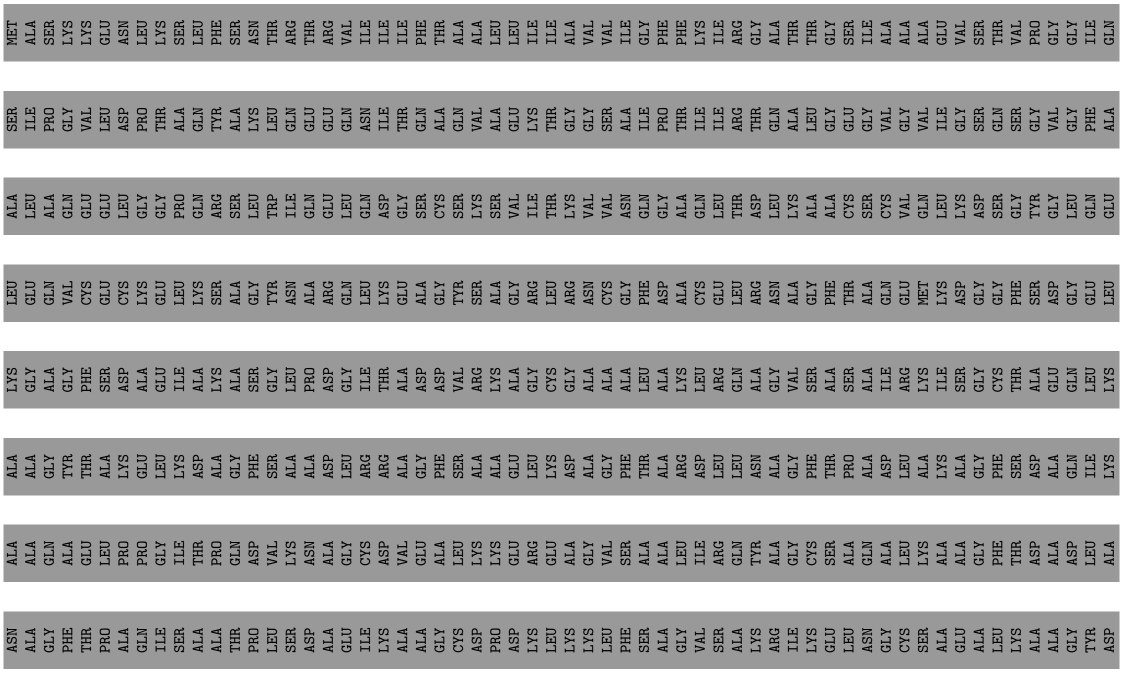
ALA ALA GLN ALA GLU LEU PRO PRO GLY ILE THR PRO GLN ASP VAL LYS ASN ALA GLY CYS ASP VAL GLU ALA LEU LYS LYS GLU ARG GLU ALA GLY VAL SER ALA ALA LEU ILE ARG GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ASP ALA ASP LEU ALA

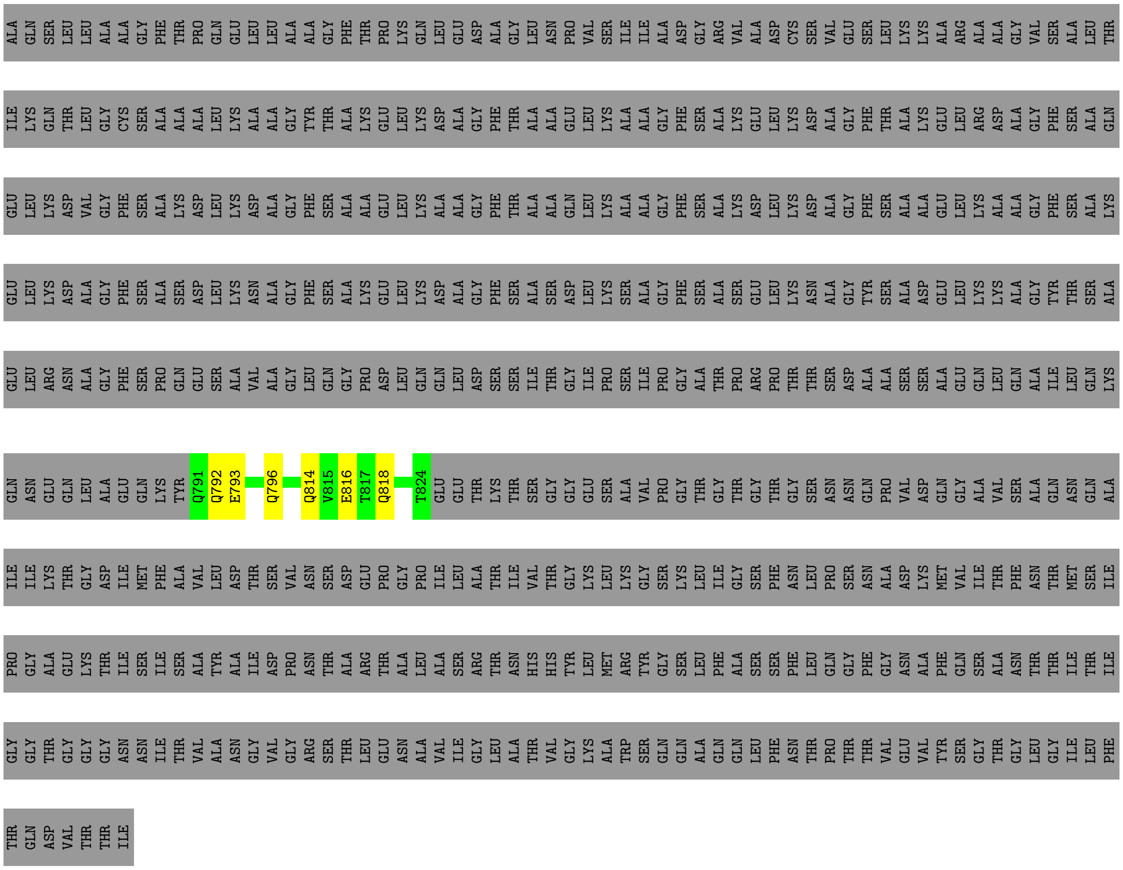


- Molecule 1: IcmE protein

Chain ZG:

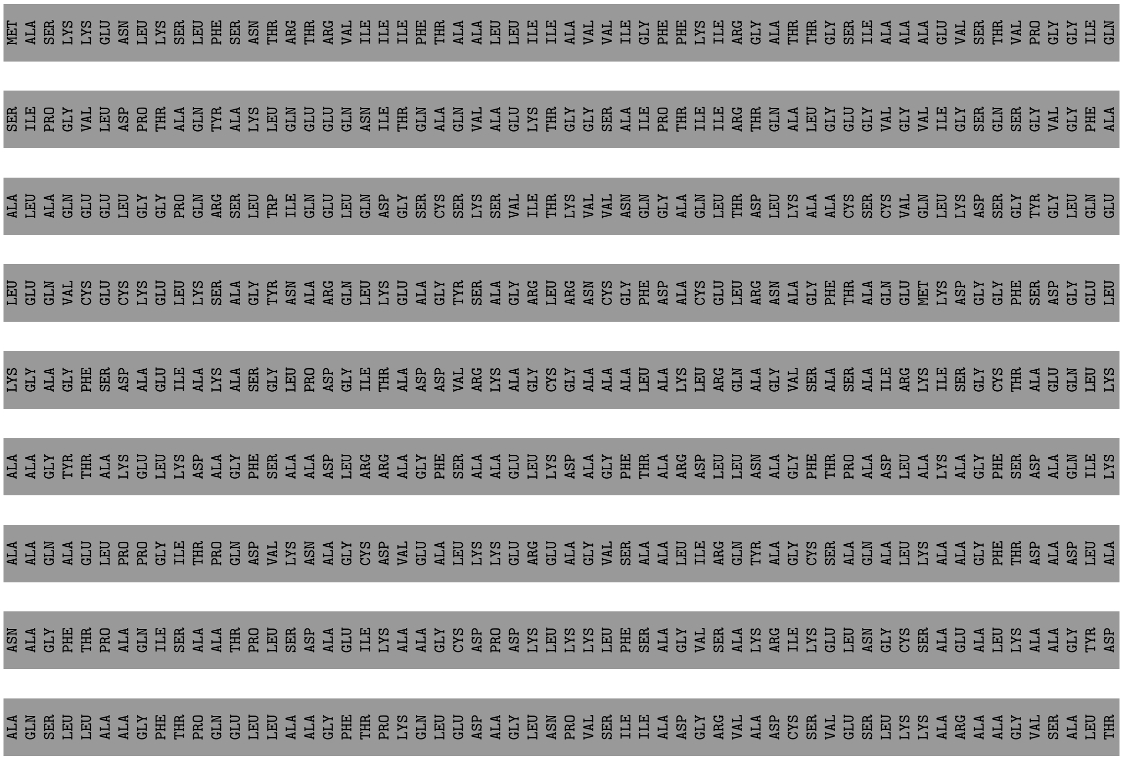


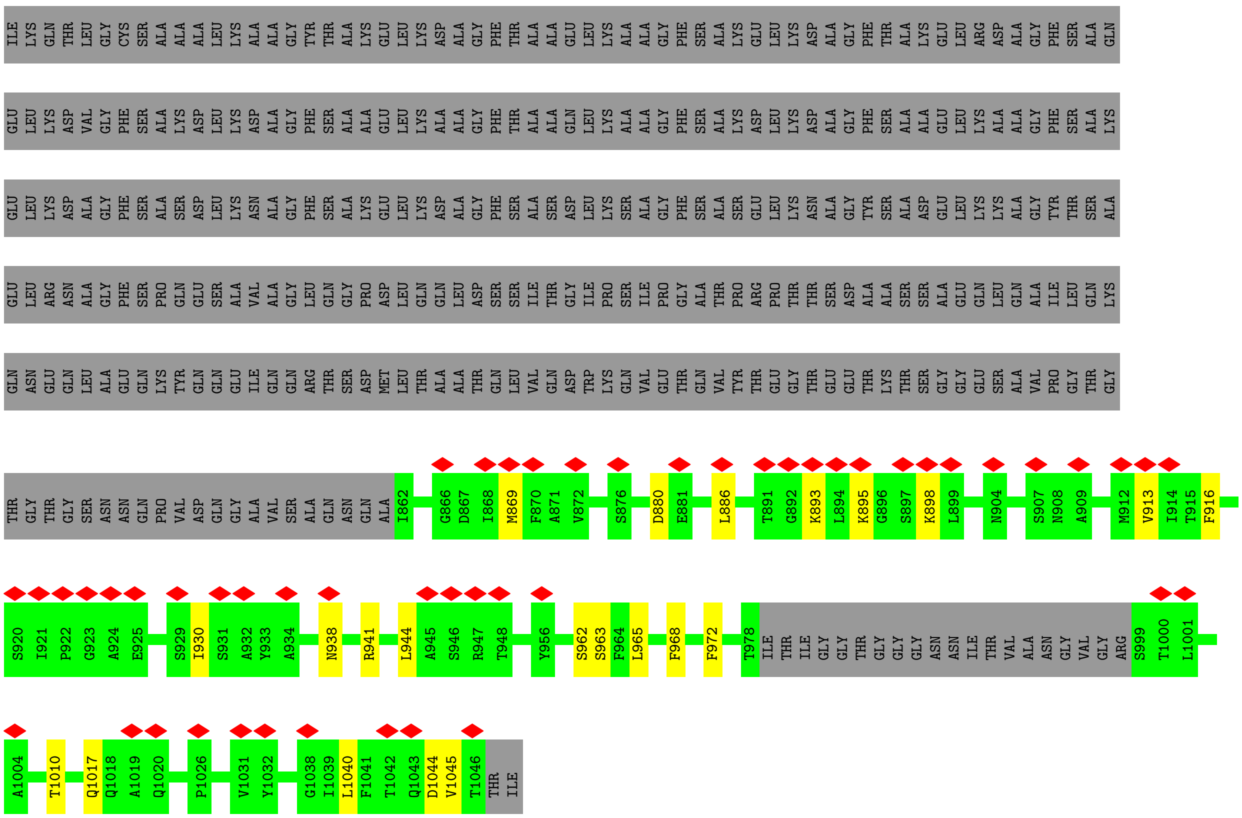




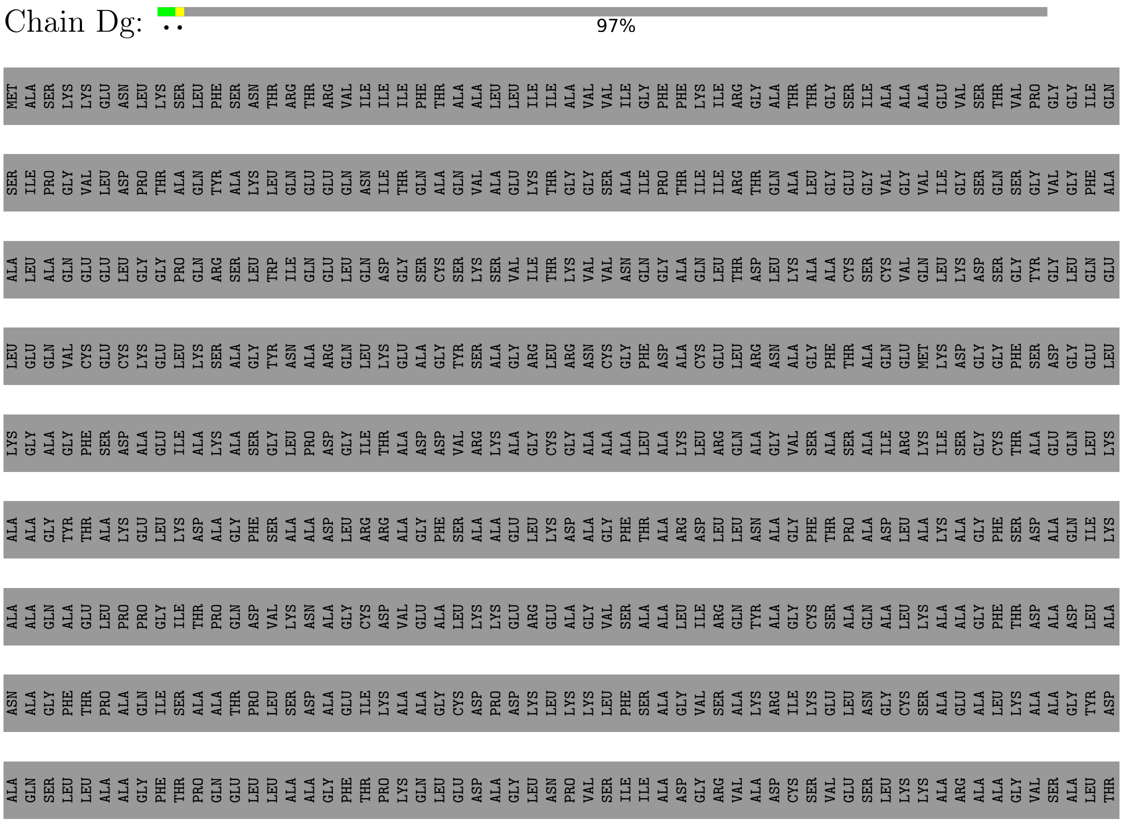
- Molecule 1: IcmE protein

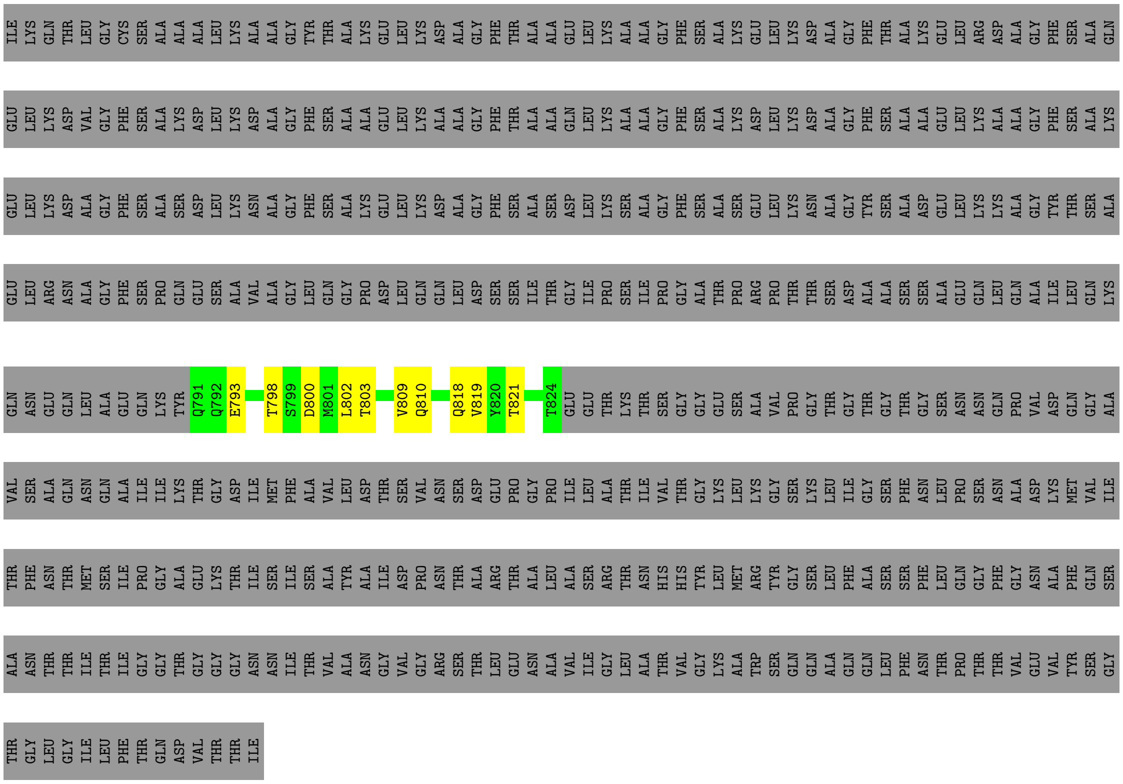
Chain FG:





- Molecule 1: IcmE protein





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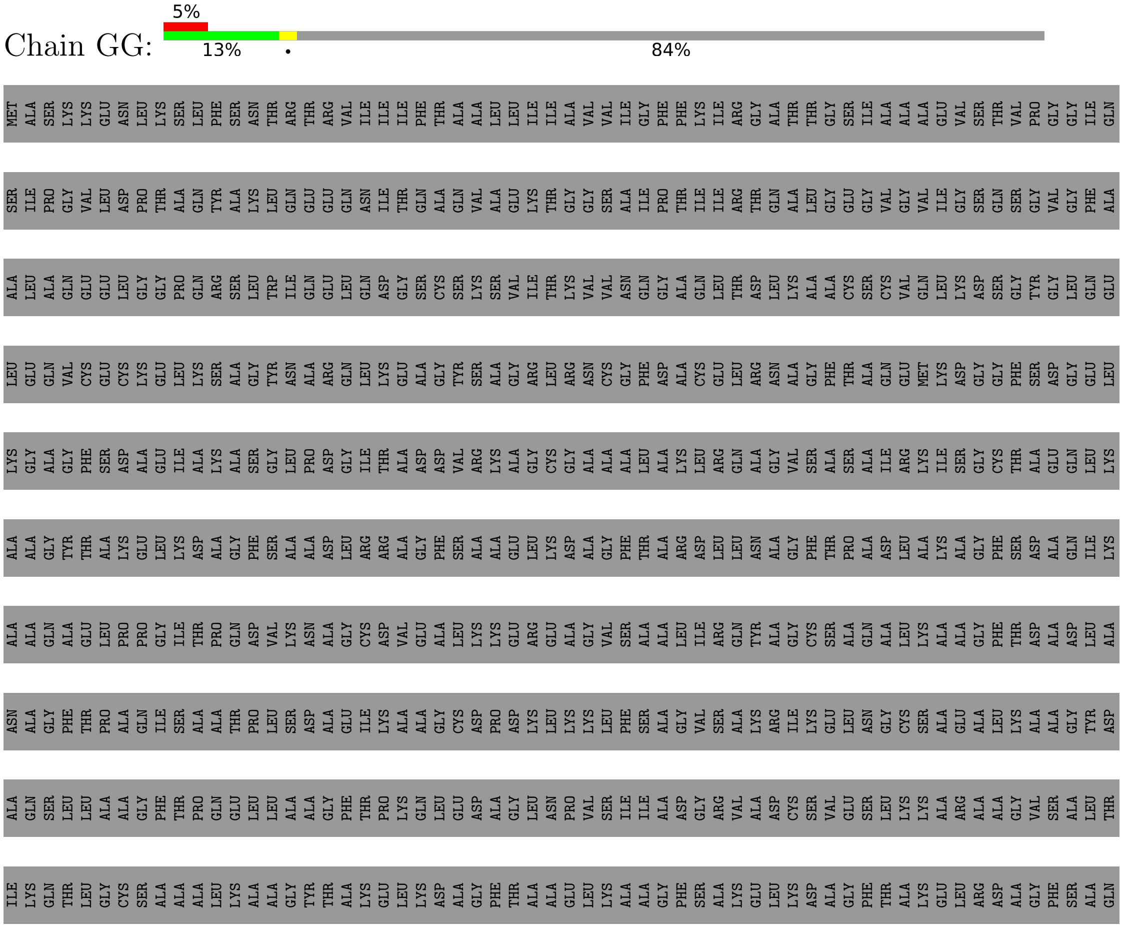
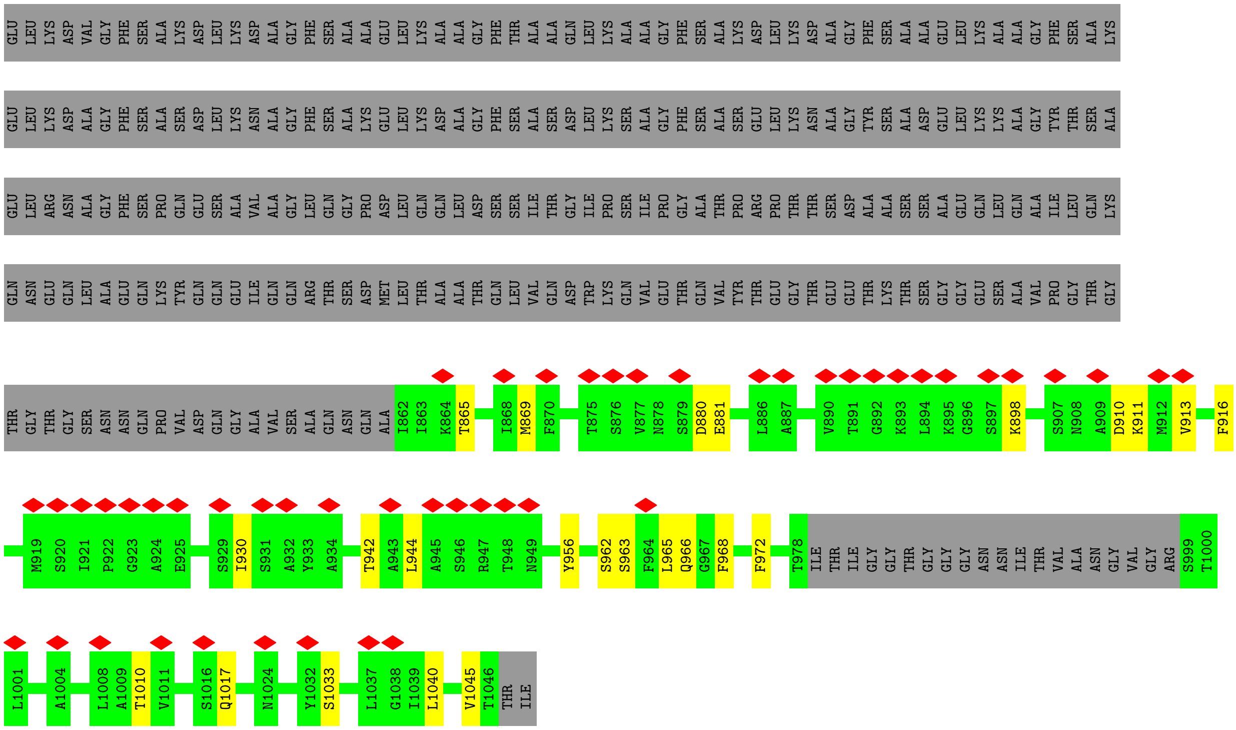
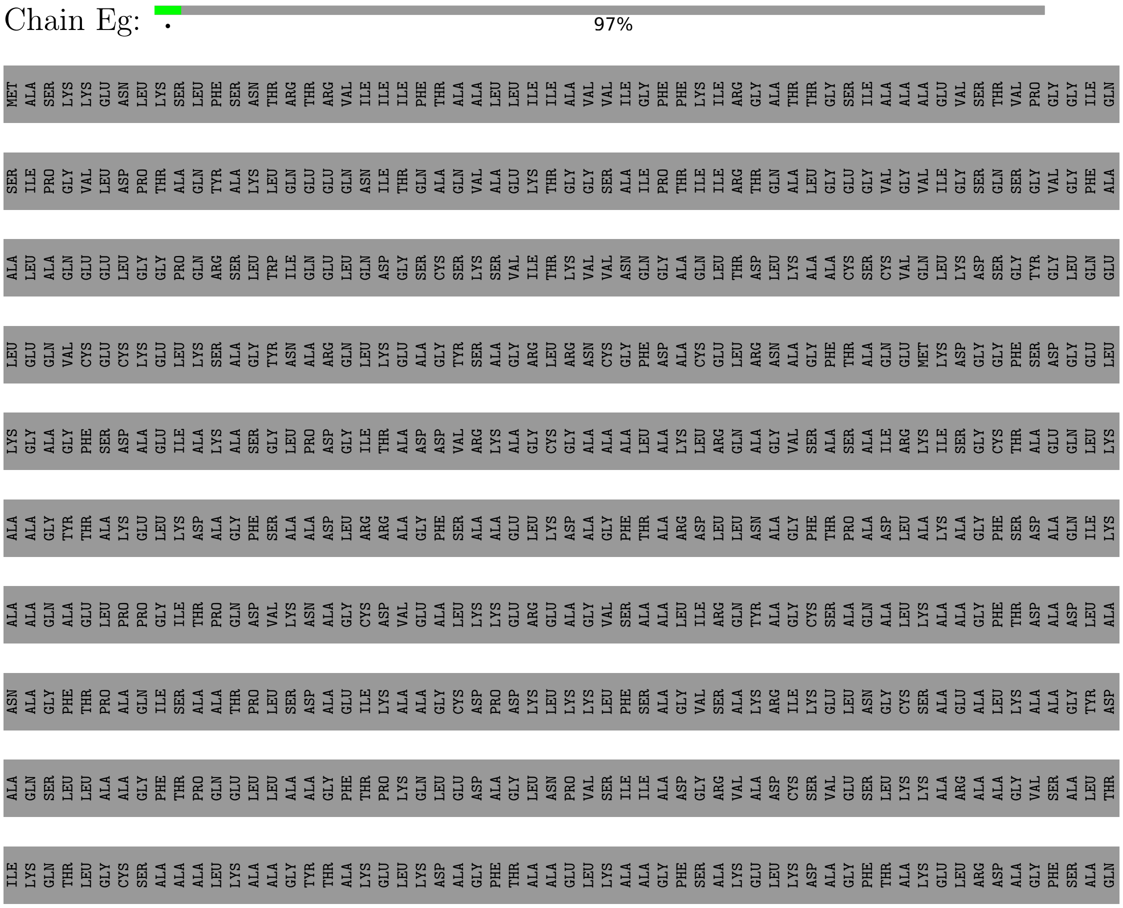
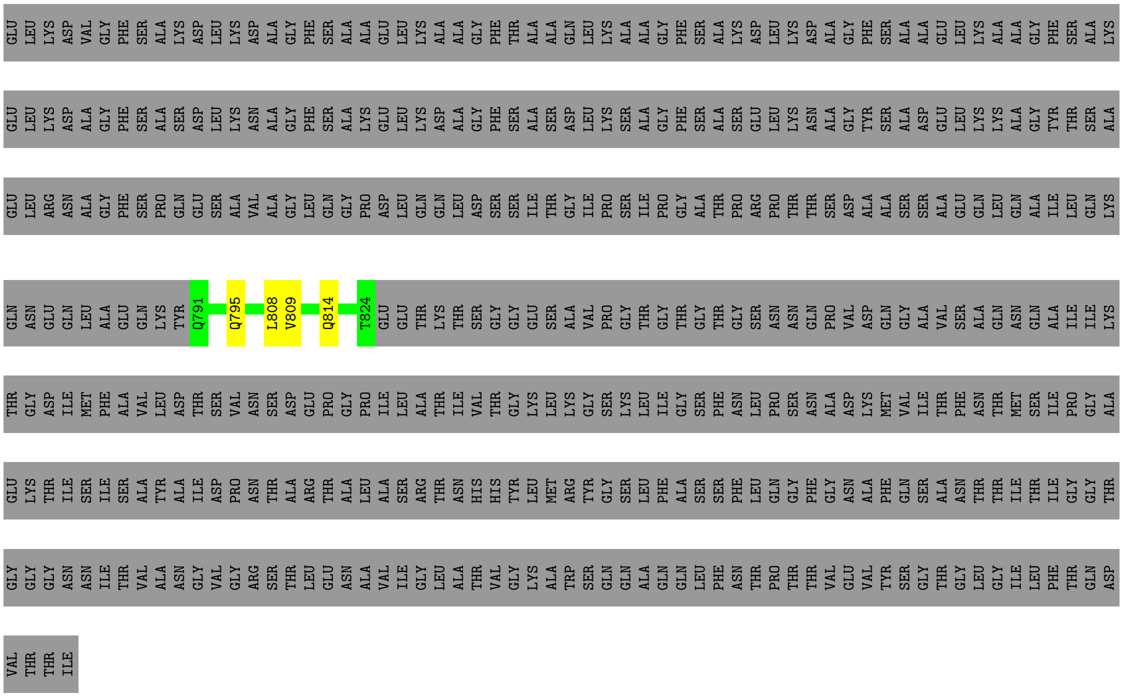




- Molecule 1: IcmE protein

Chain Eg:





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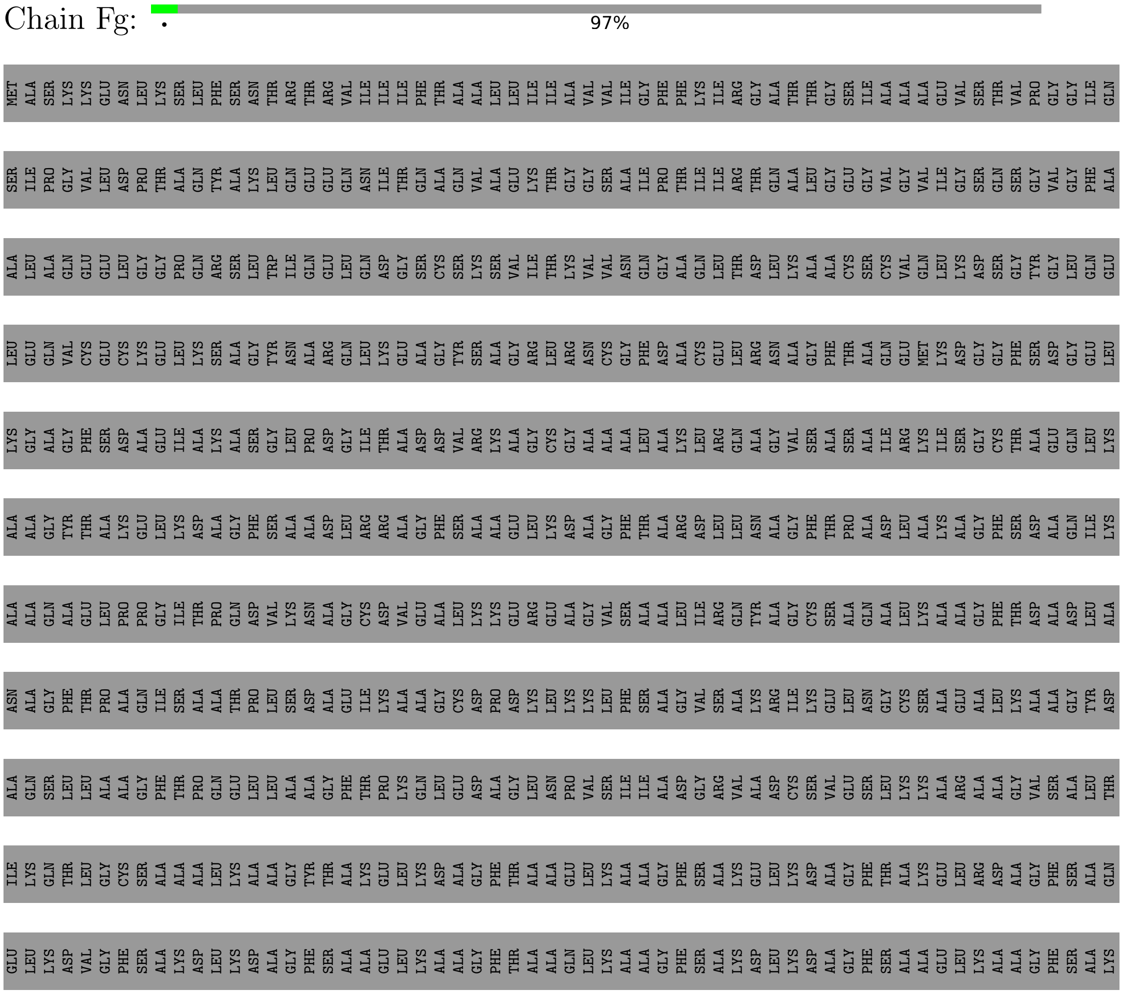

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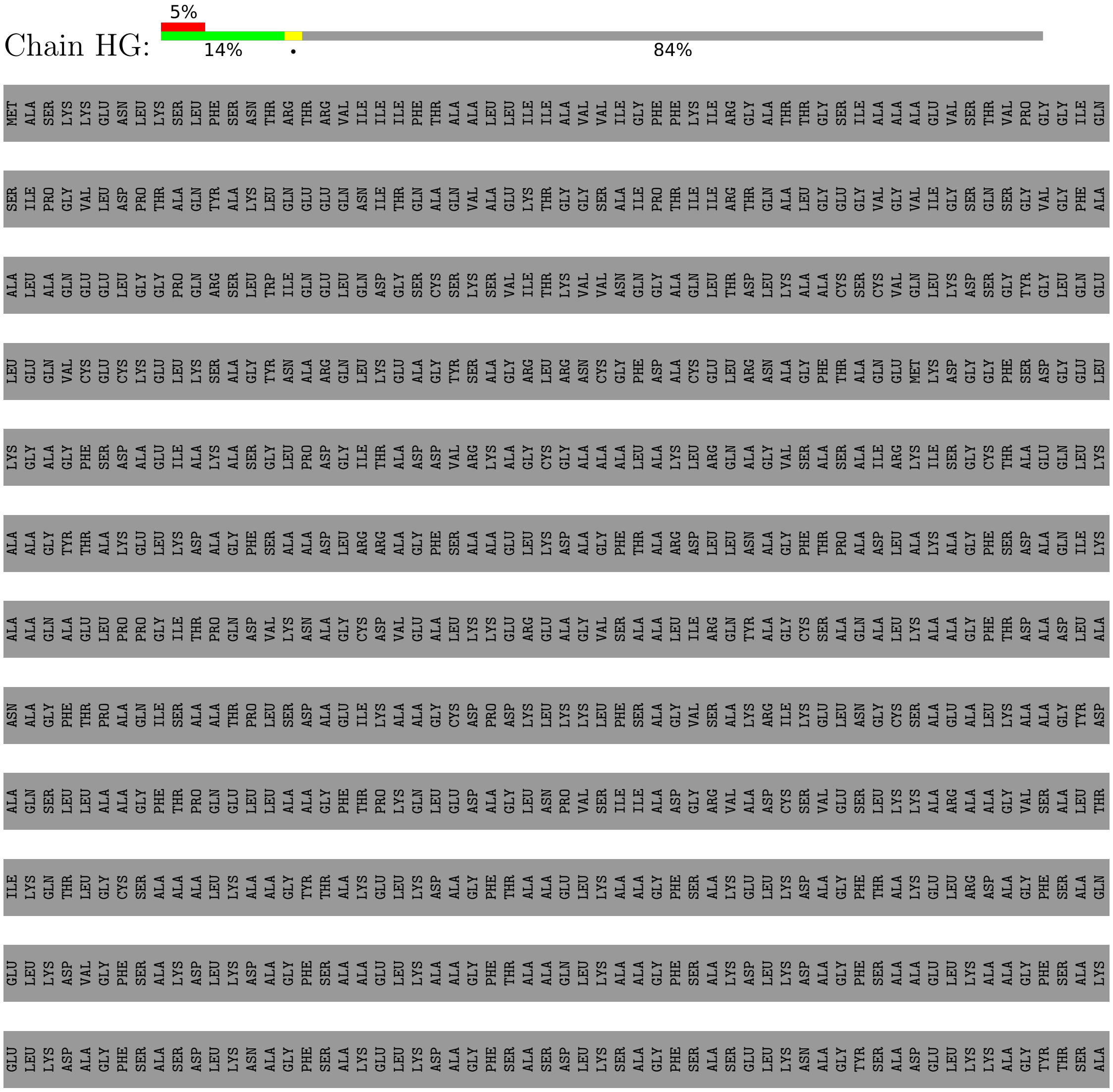

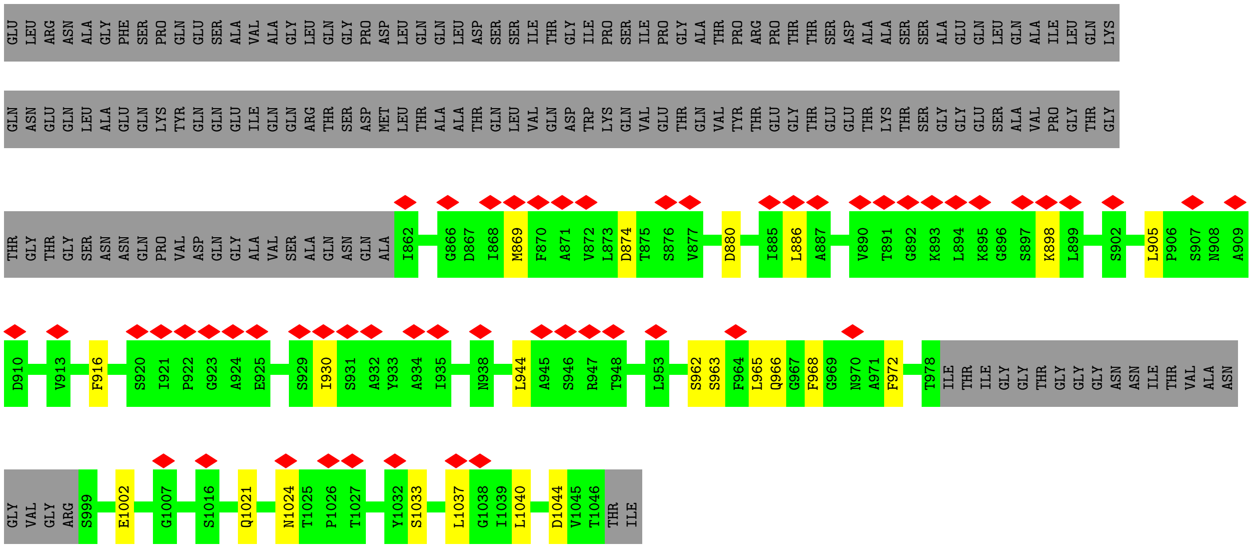

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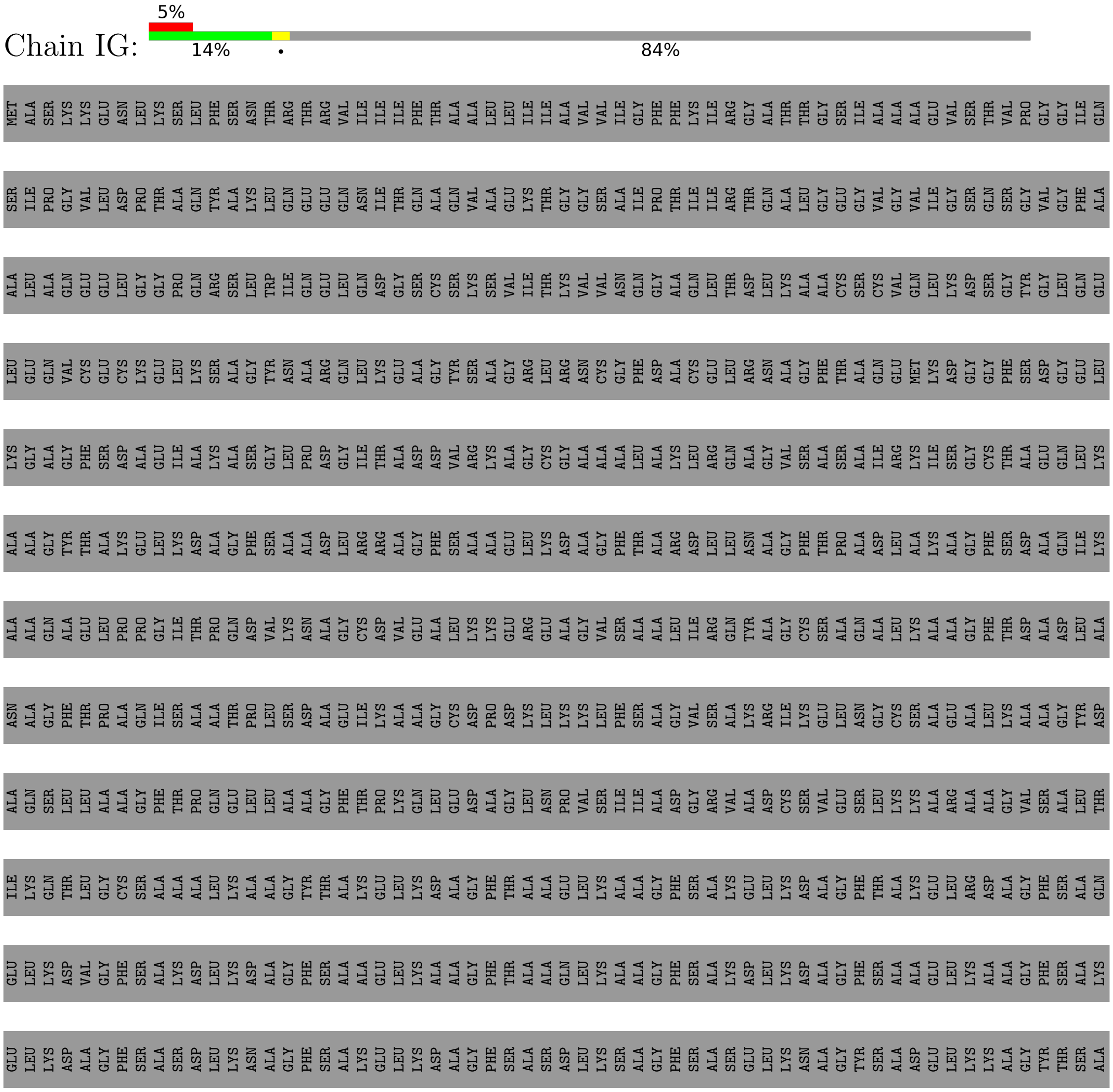

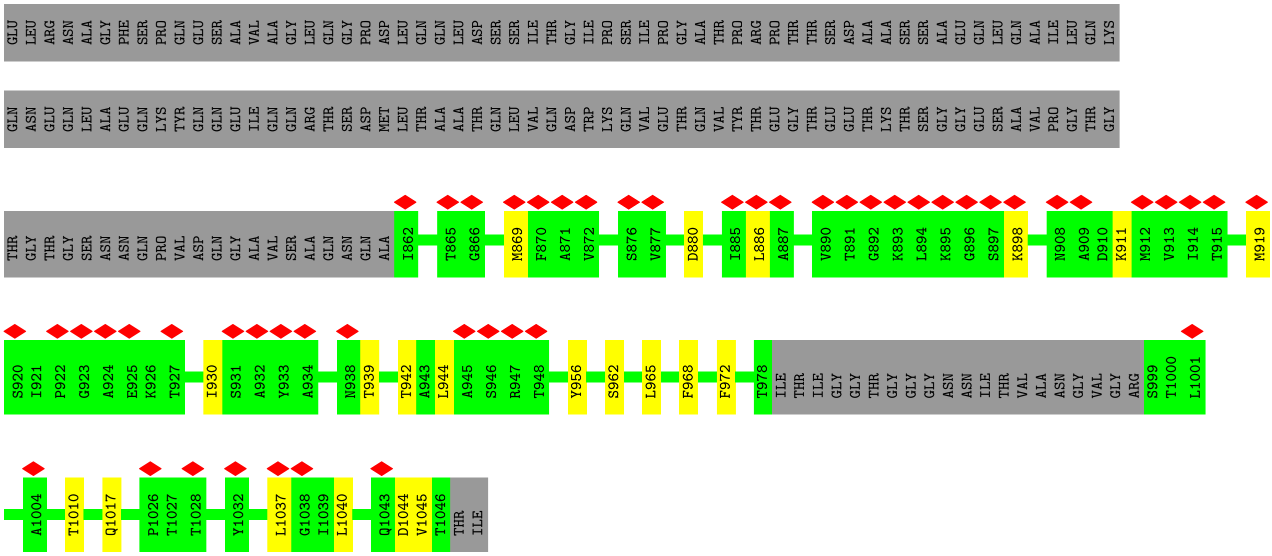

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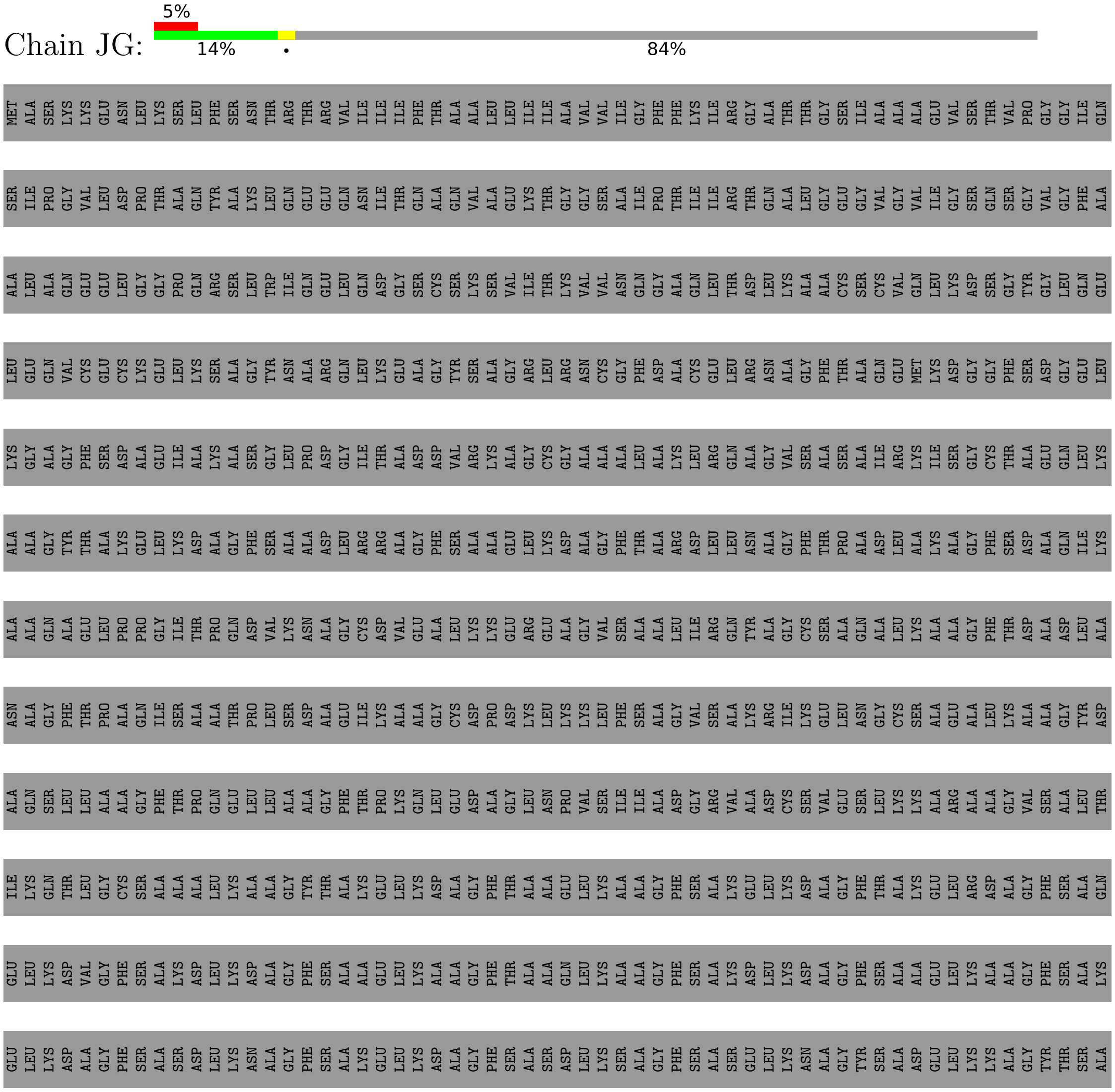

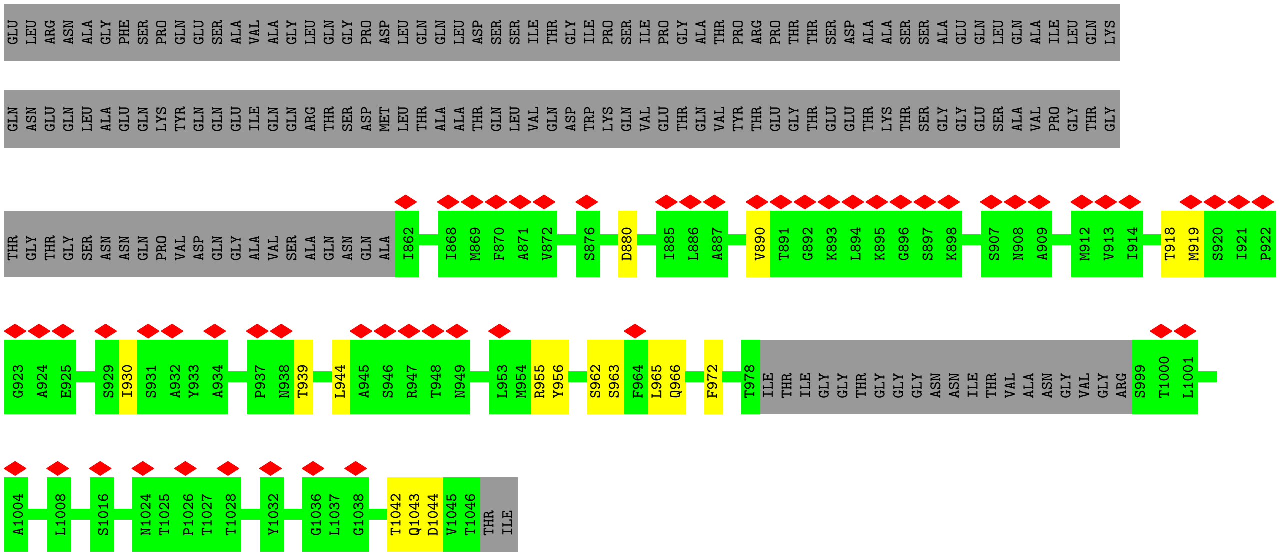

- Molecule 1: IcmE protein

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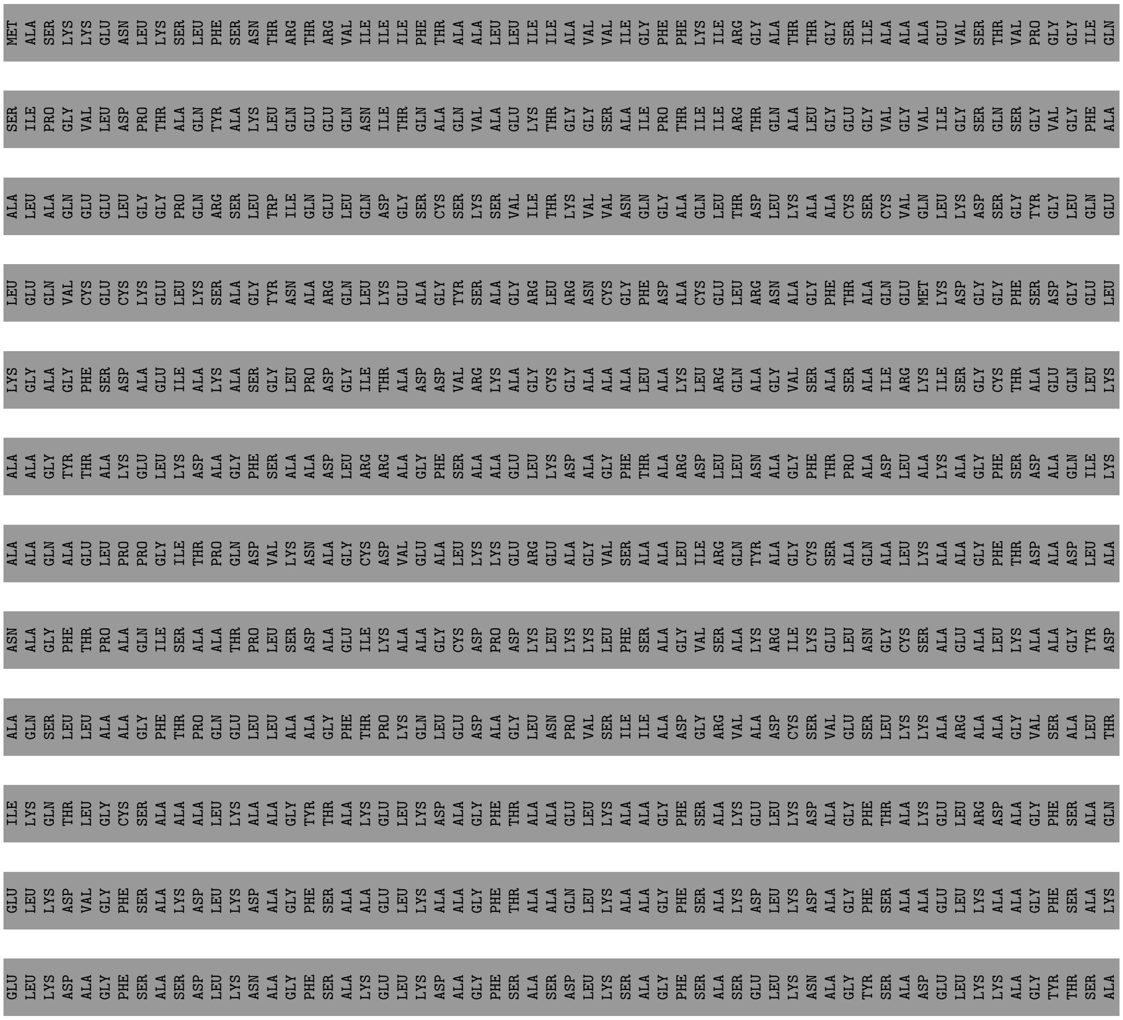
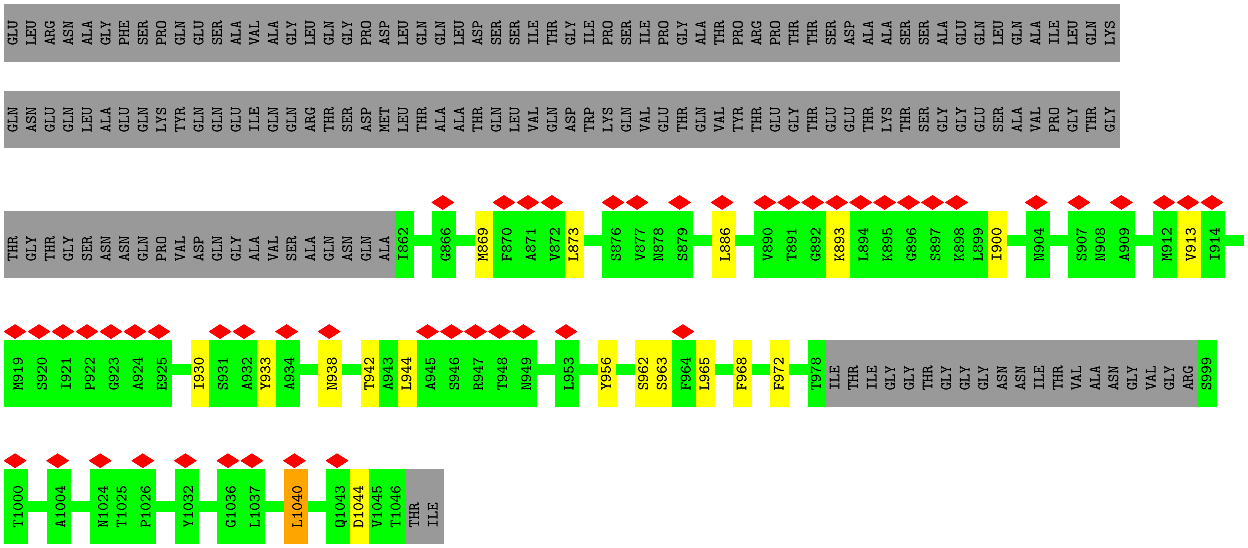
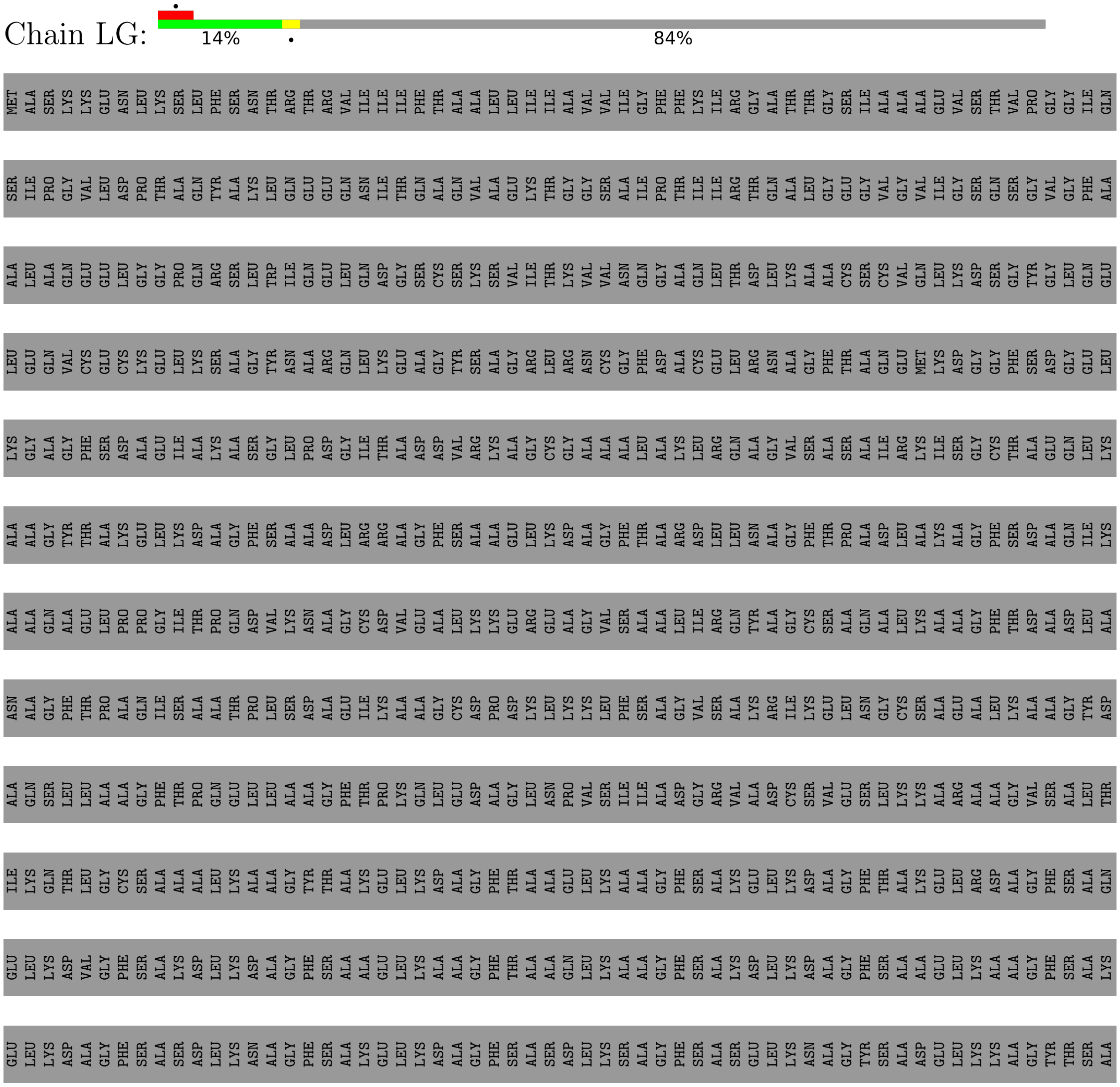
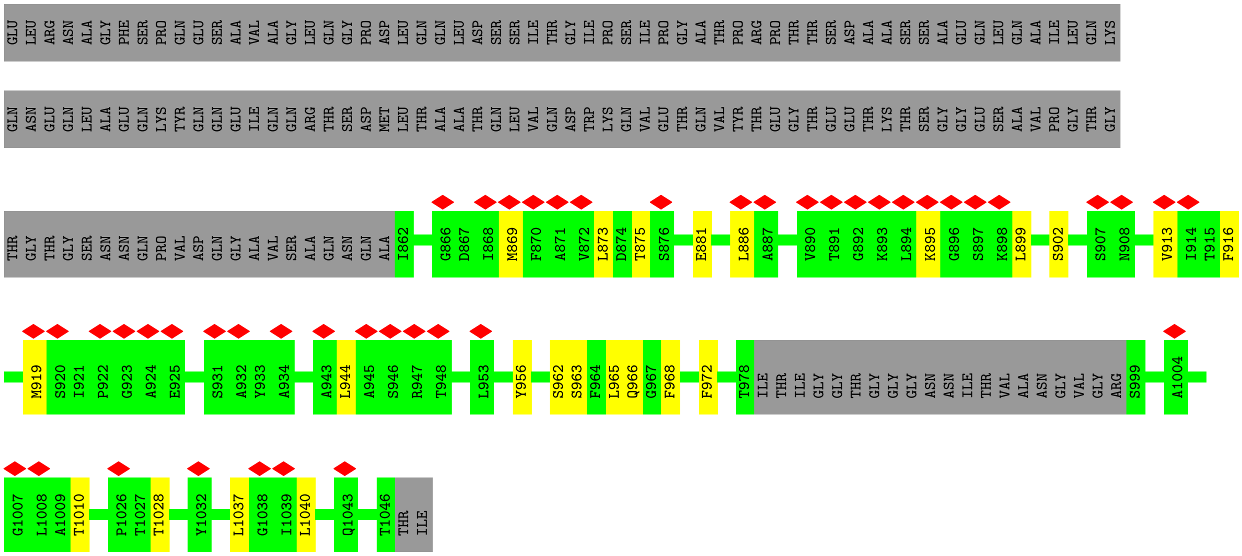




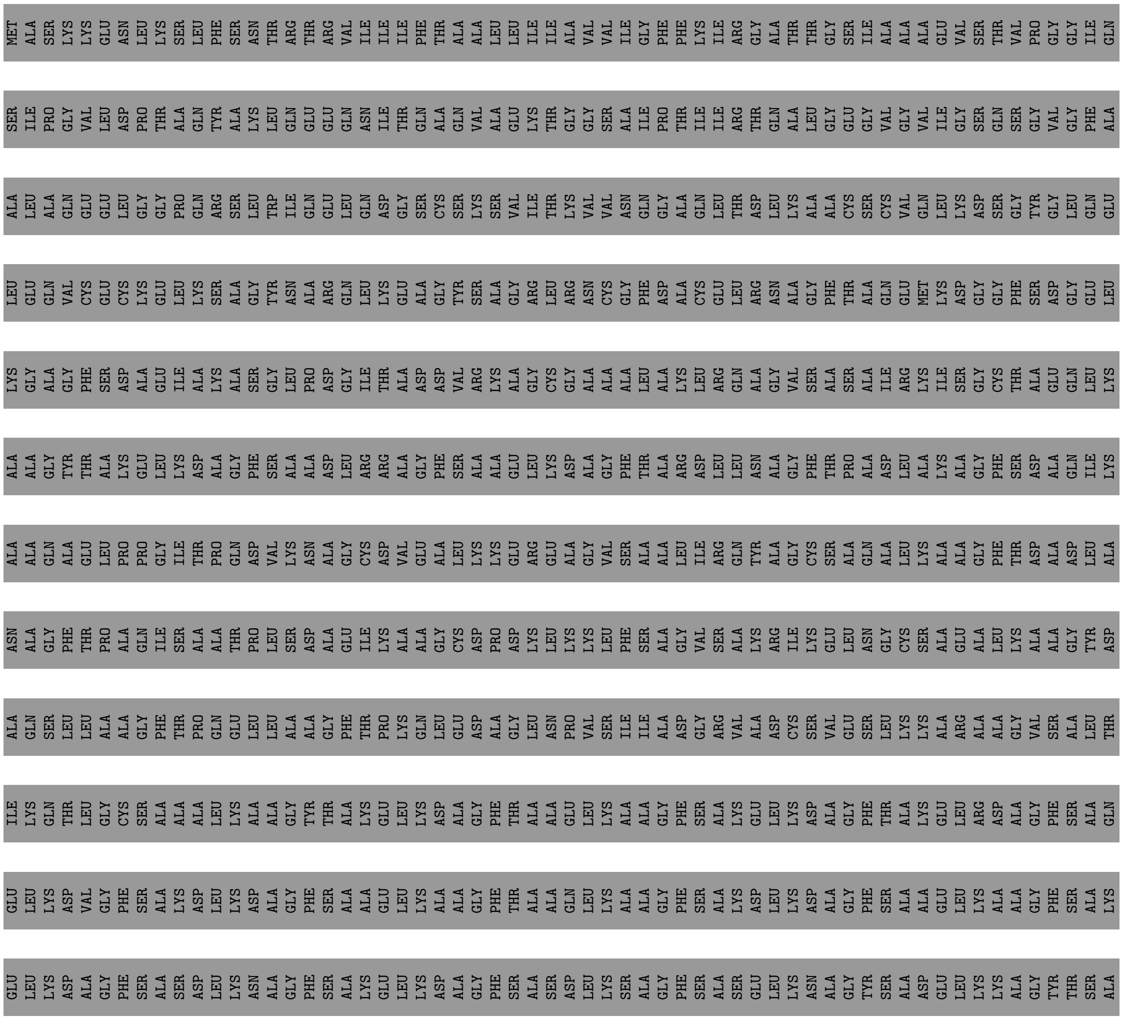
• Molecule 1: IcmE protein

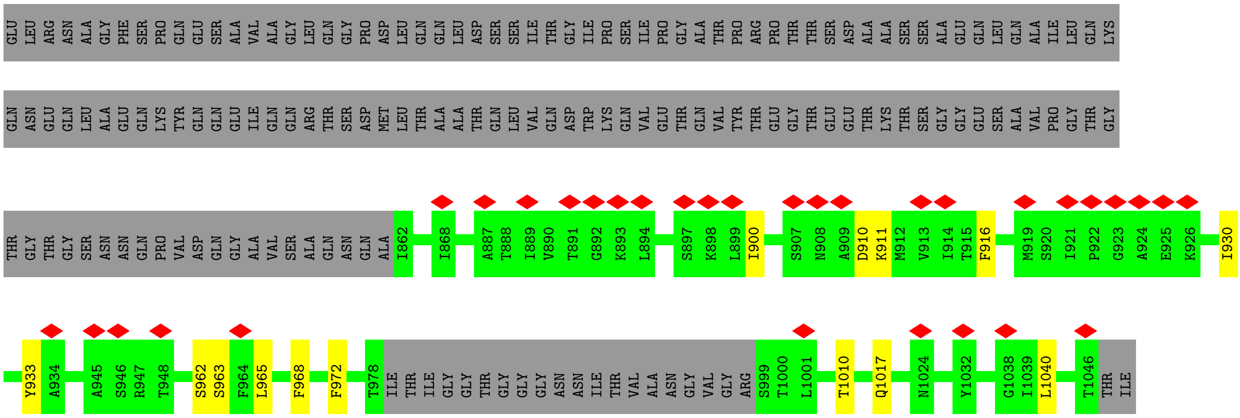




- Molecule 1: IcmE protein

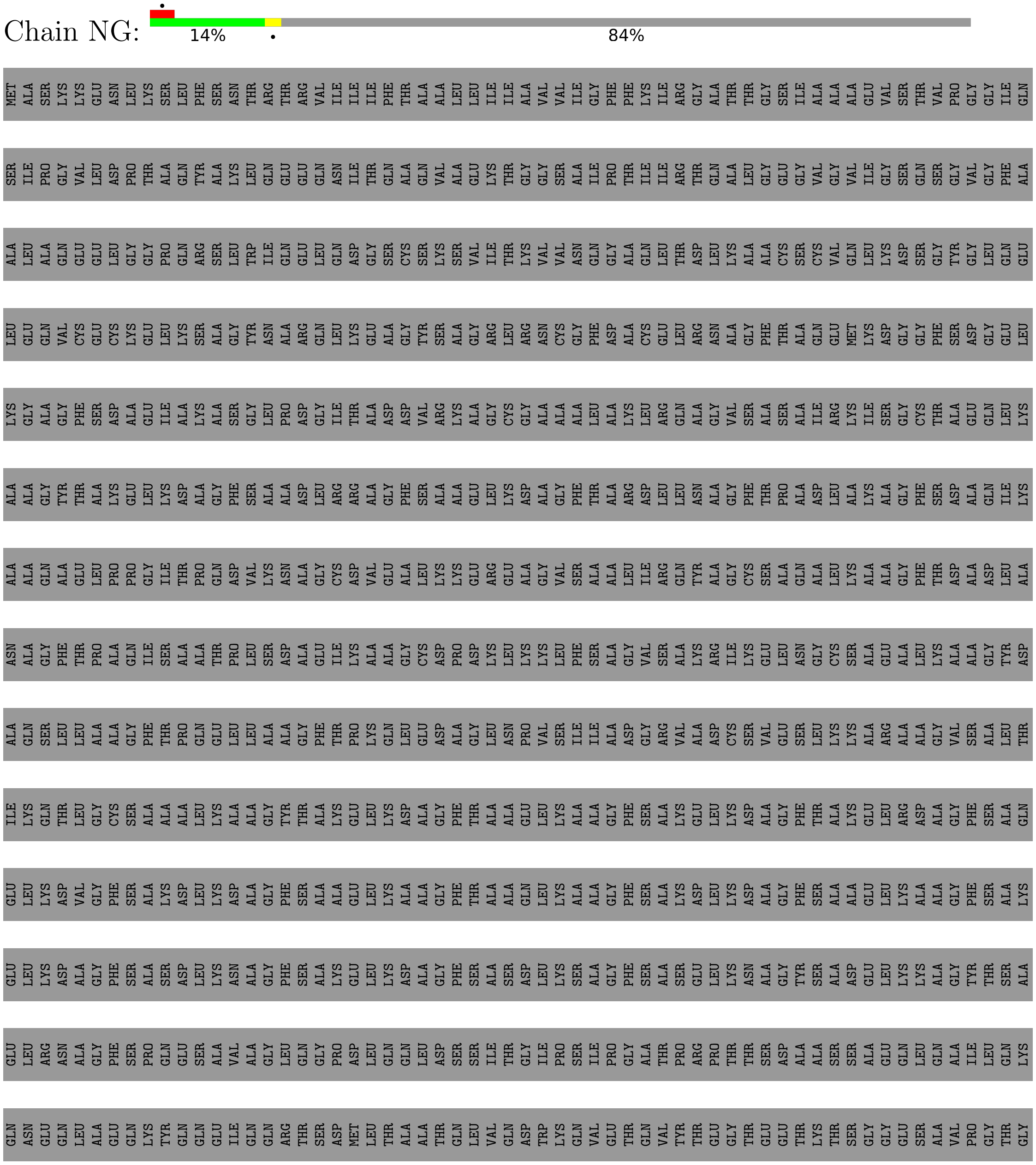
Chain MG:

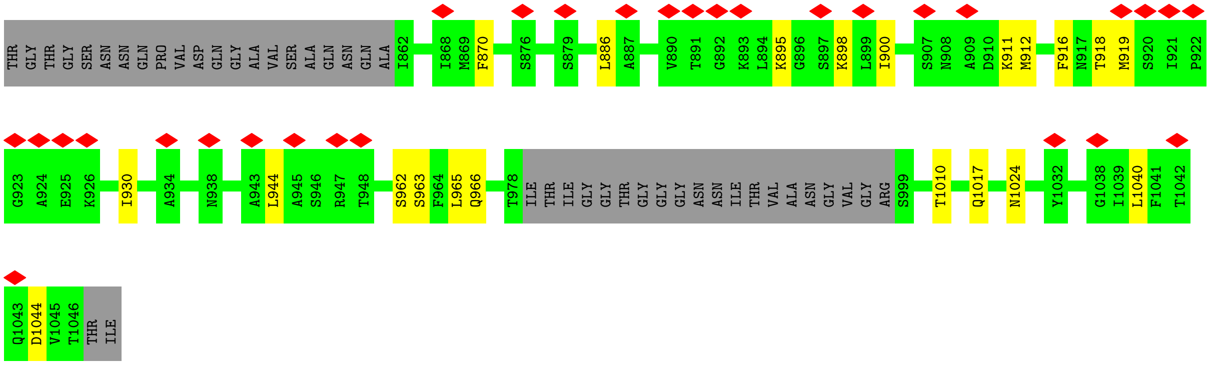




- Molecule 1: IcmE protein

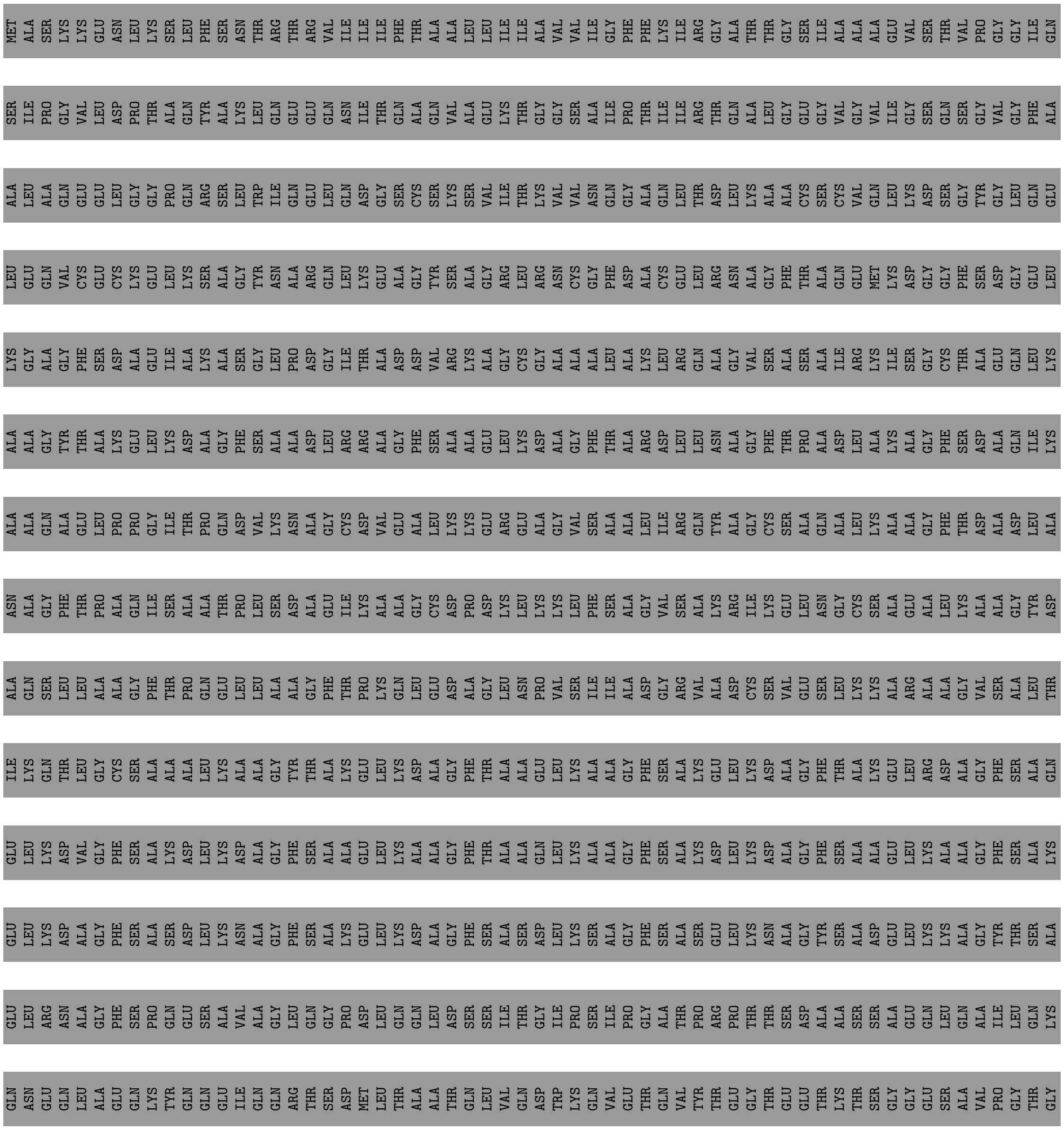
Chain NG:

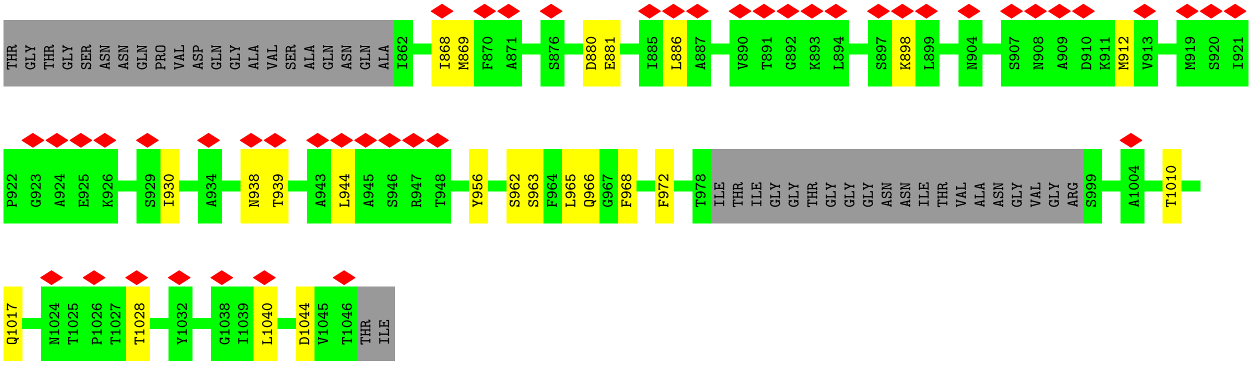




- Molecule 1: IcmE protein

Chain OG:





• Molecule 1: IcmE protein

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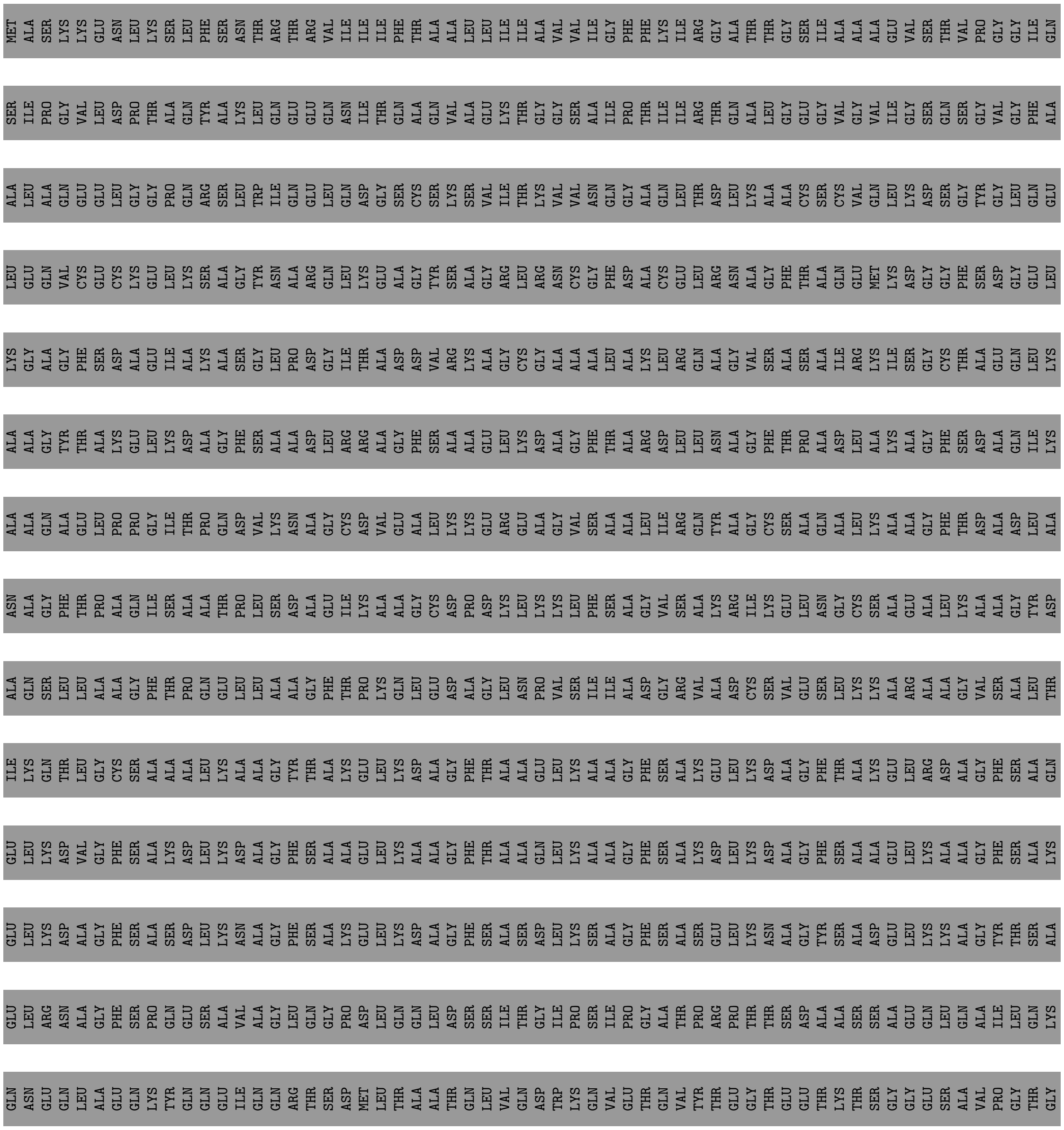
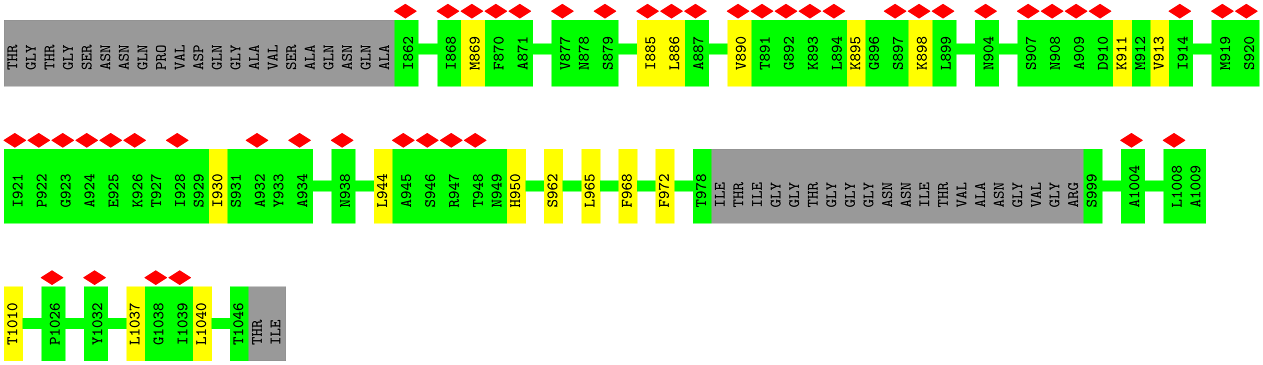
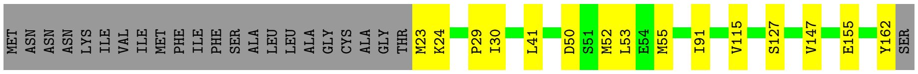




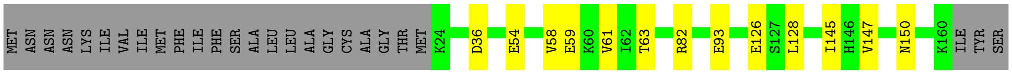
- Molecule 2: DotD

Chain GD:



- Molecule 2: DotD

Chain Gd:



- Molecule 2: DotD

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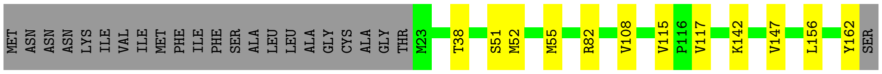
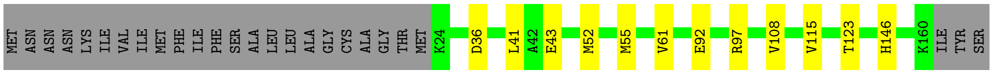


- Molecule 2: DotD

Chain Dd:



- Molecule 2: DotD

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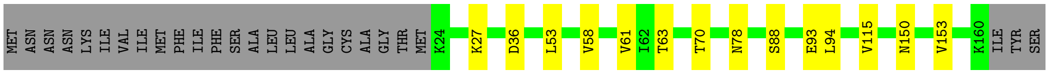

- Molecule 2: DotD

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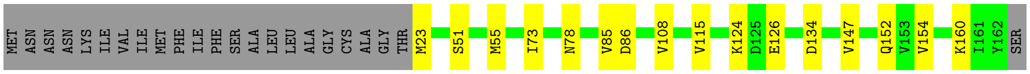

• Molecule 2: DotD

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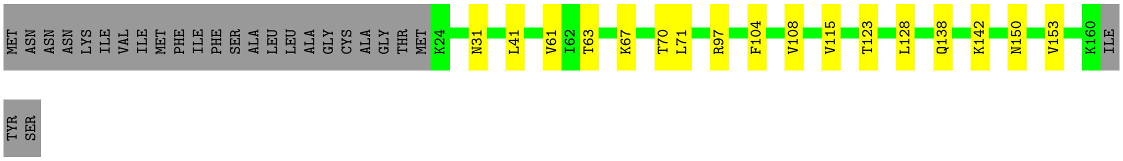

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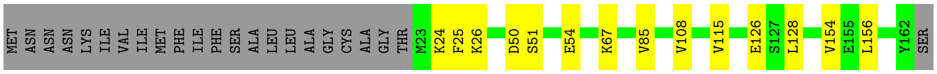

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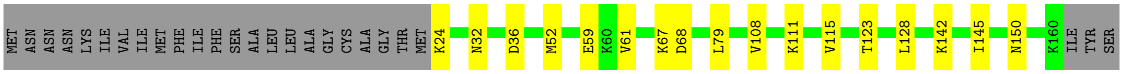

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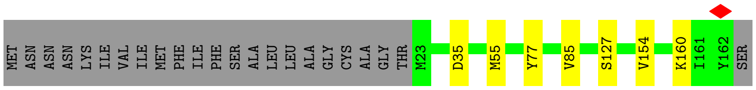

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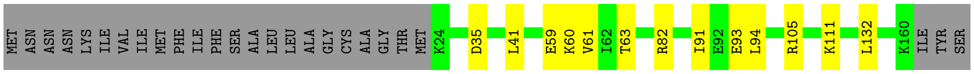

• Molecule 2: DotD

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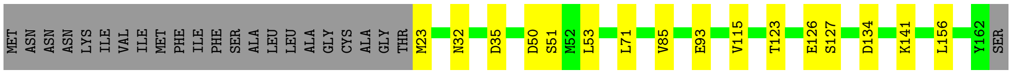

• Molecule 2: DotD

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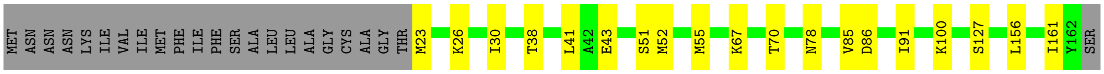

- Molecule 2: DotD

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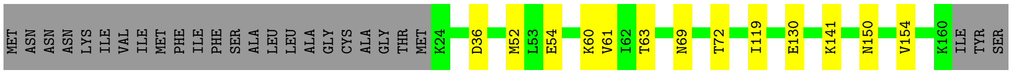

- Molecule 2: DotD

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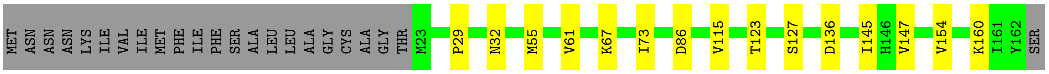

- Molecule 2: DotD

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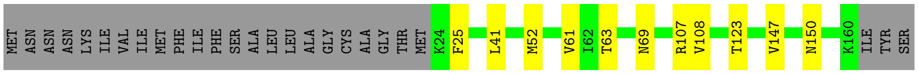

- Molecule 2: DotD

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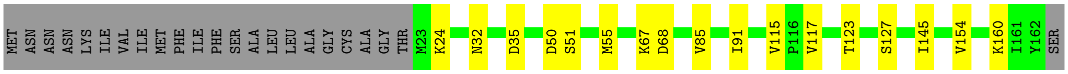

- Molecule 2: DotD

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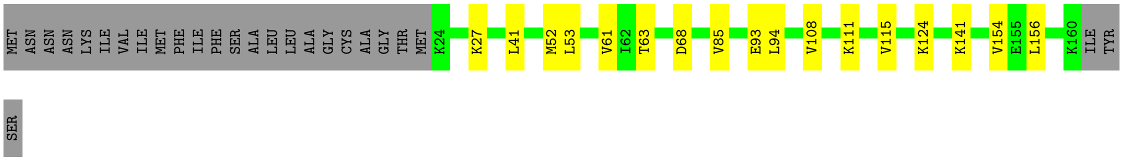
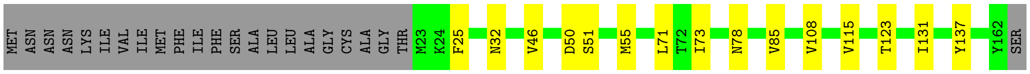


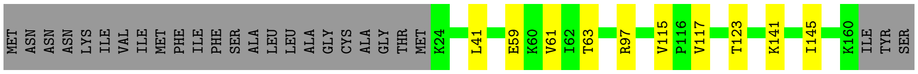
- Molecule 2: DotD

Chain BD:



- Molecule 2: DotD

Chain Bd:



- Molecule 2: DotD

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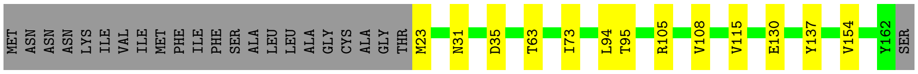
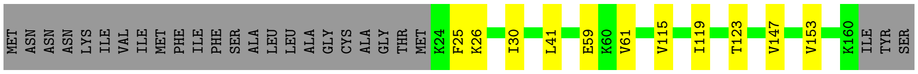


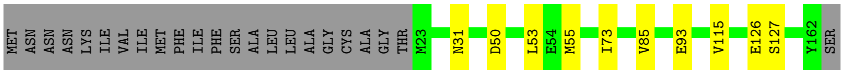
- Molecule 2: DotD

Chain Cd:



- Molecule 2: DotD

Chain DD:

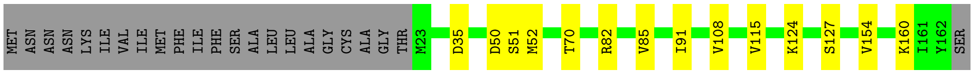


- Molecule 2: DotD

Chain Ed:

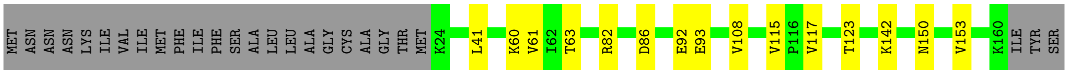
- Molecule 2: DotD

Chain FD:



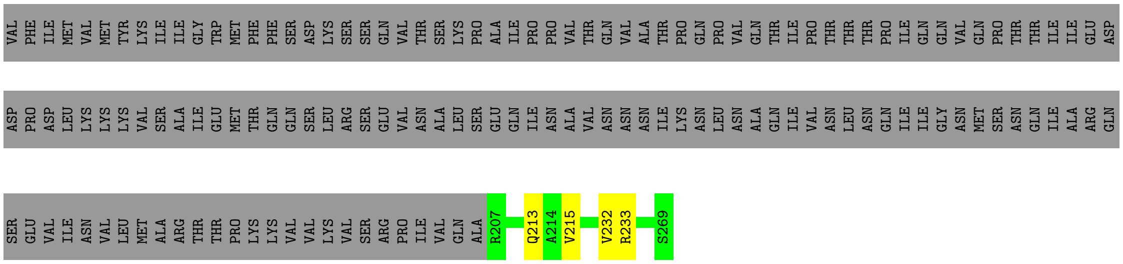
- Molecule 2: DotD

Chain Fd:



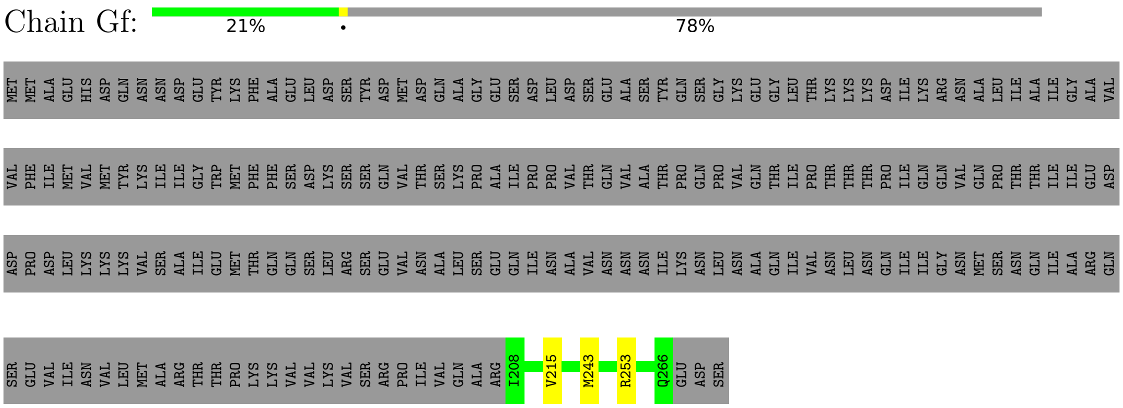
- Molecule 3: DotF

Chain GF:



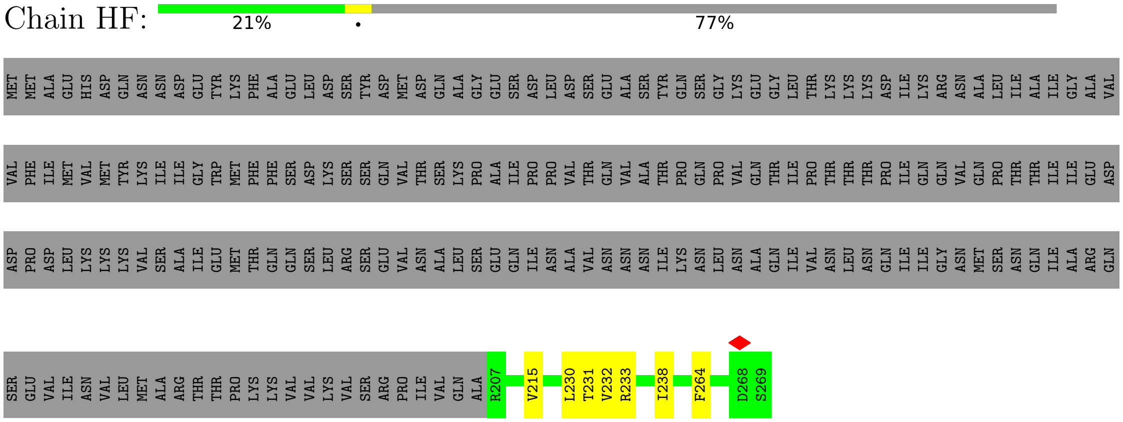
- Molecule 3: DotF

Chain Gf:



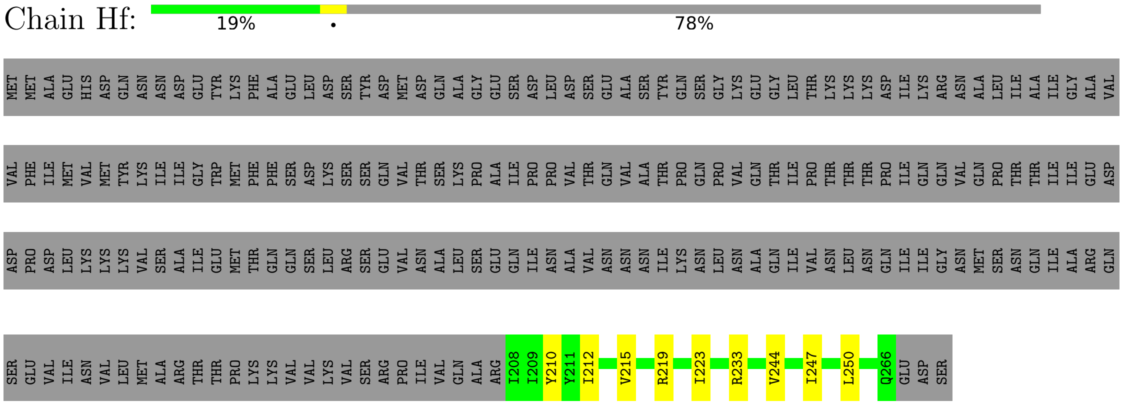
- Molecule 3: DotF

Chain HF:



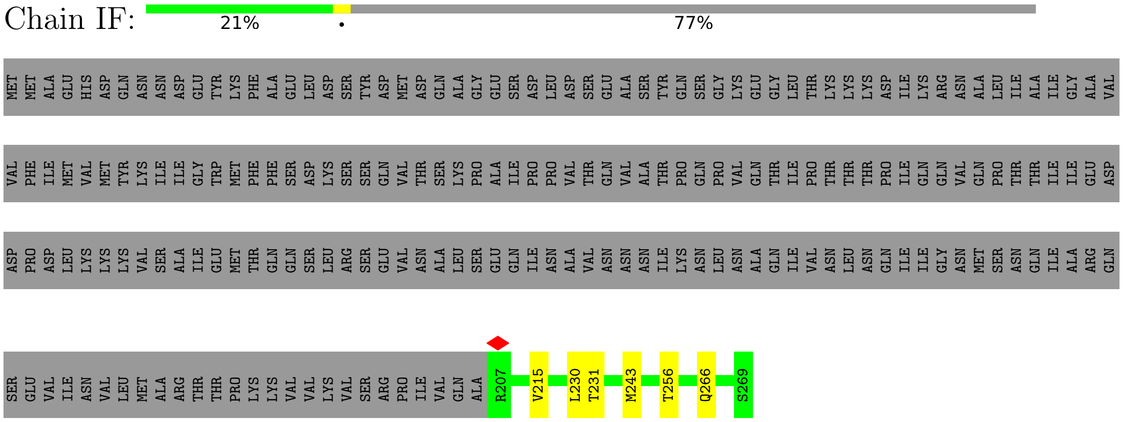
- Molecule 3: DotF

Chain Hf:



- Molecule 3: DotF

Chain IF:



- Molecule 3: DotF

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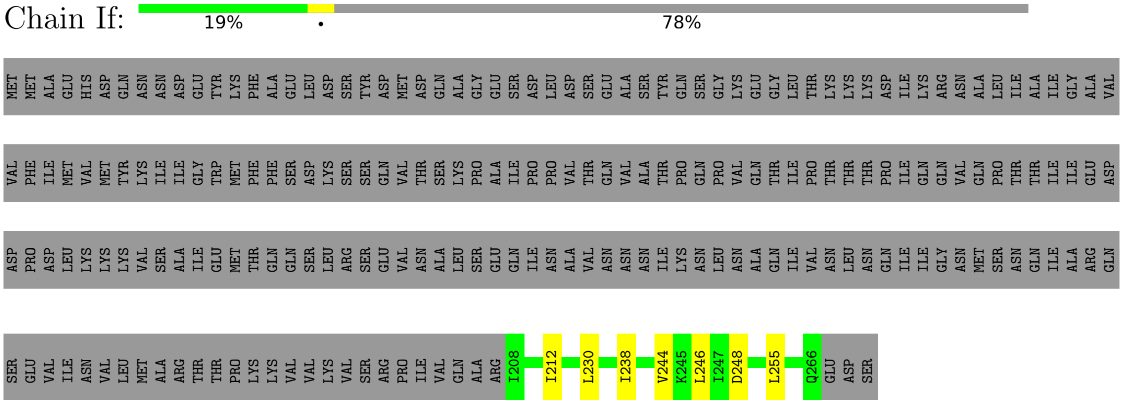
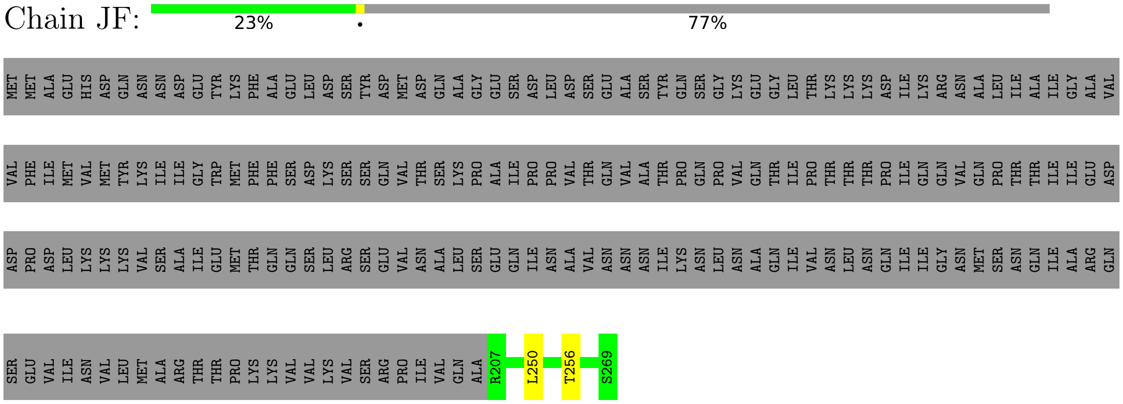


- Molecule 3: DotF

Chain JF:



- Molecule 3: DotF

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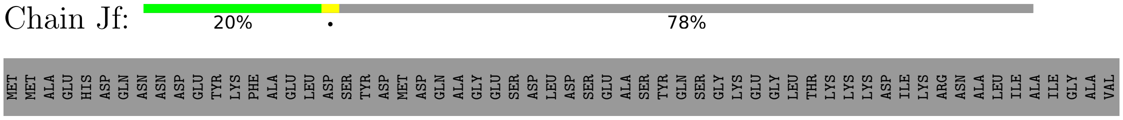

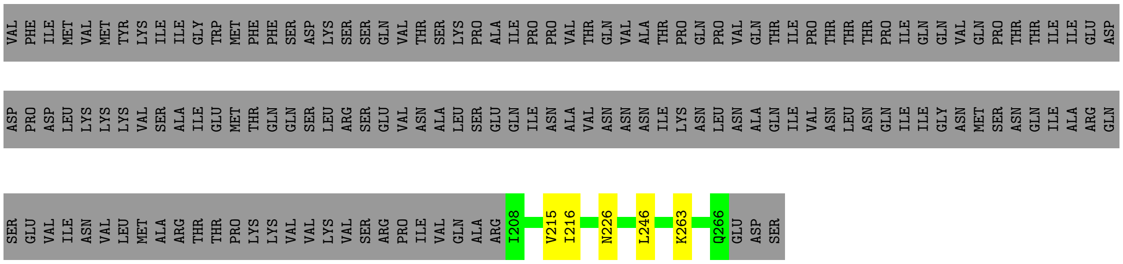

- Molecule 3: DotF

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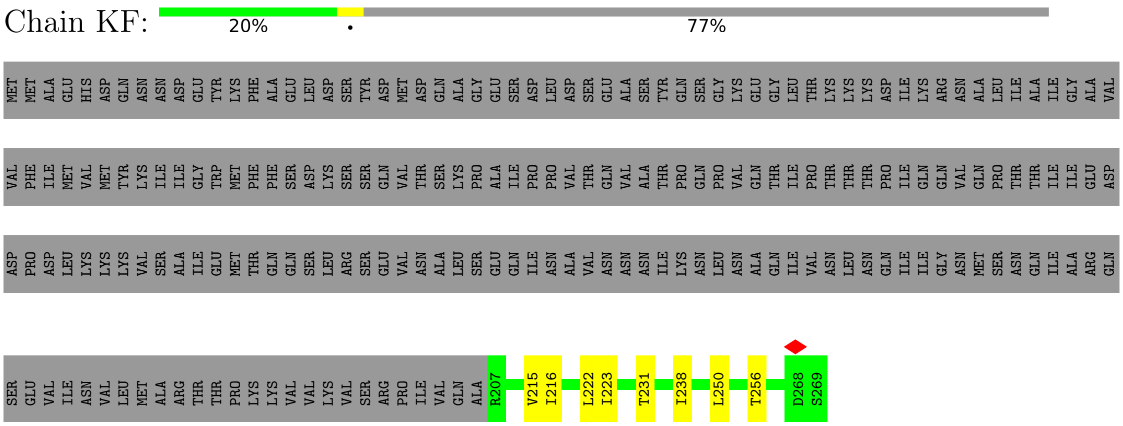

- Molecule 3: DotF

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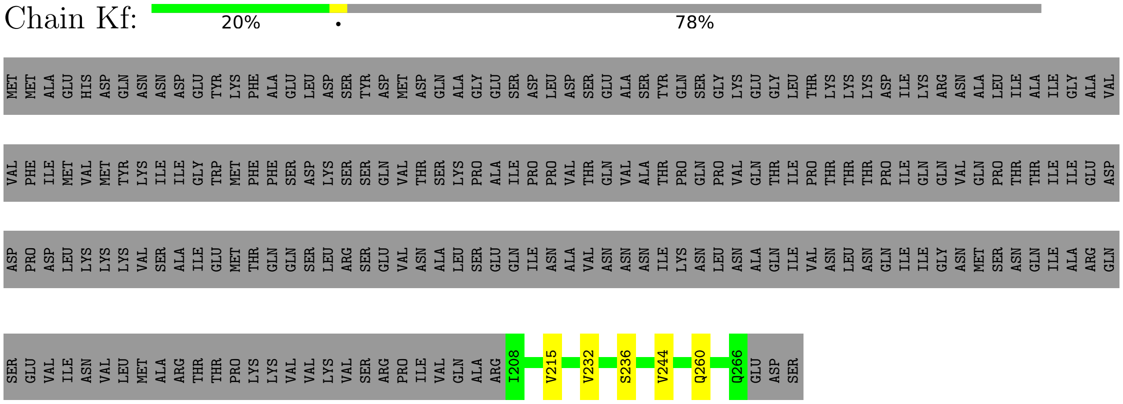
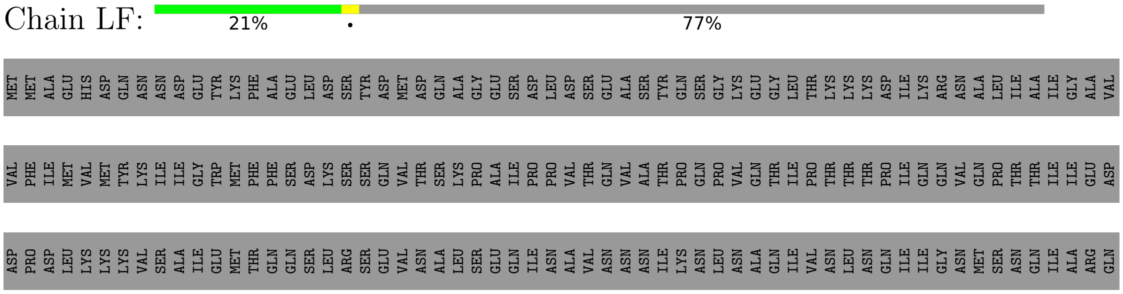
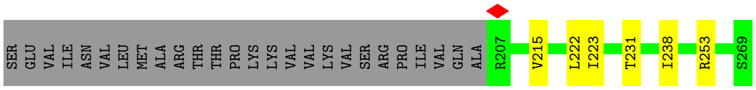


- Molecule 3: DotF

Chain LF:





- Molecule 3: DotF

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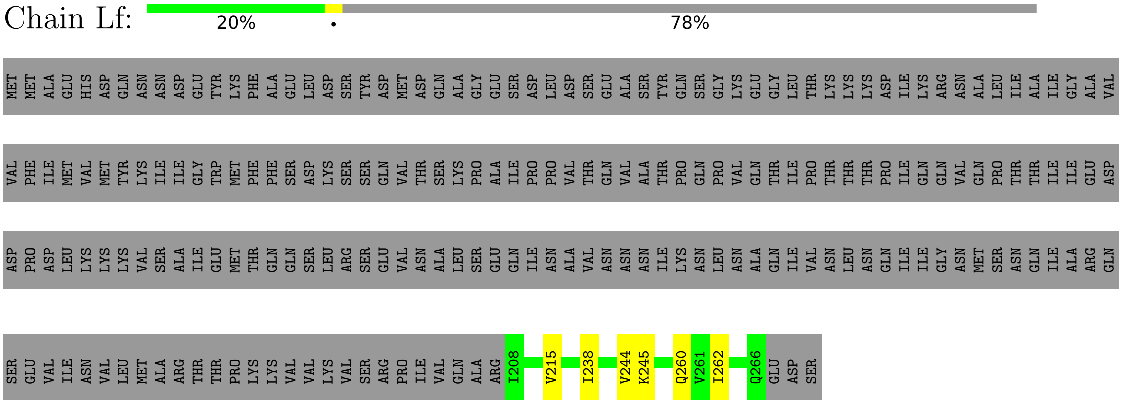

- Molecule 3: DotF

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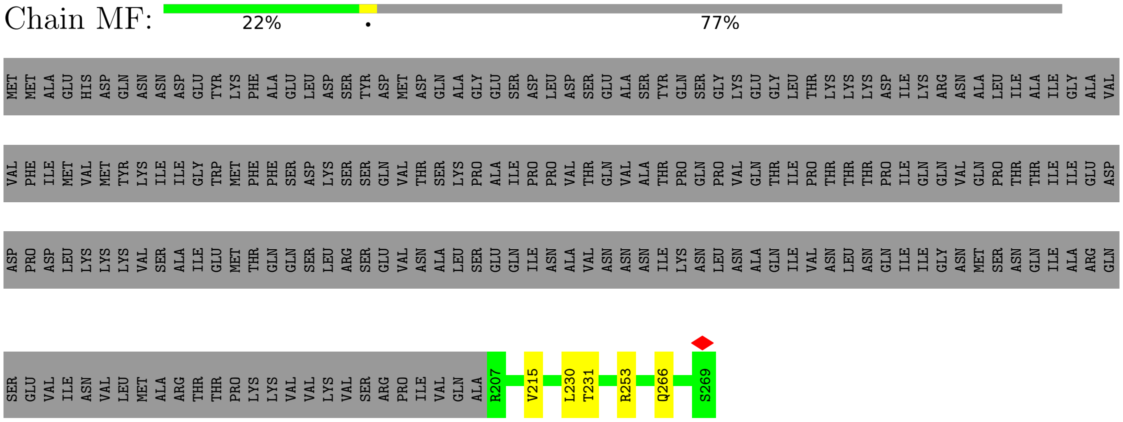
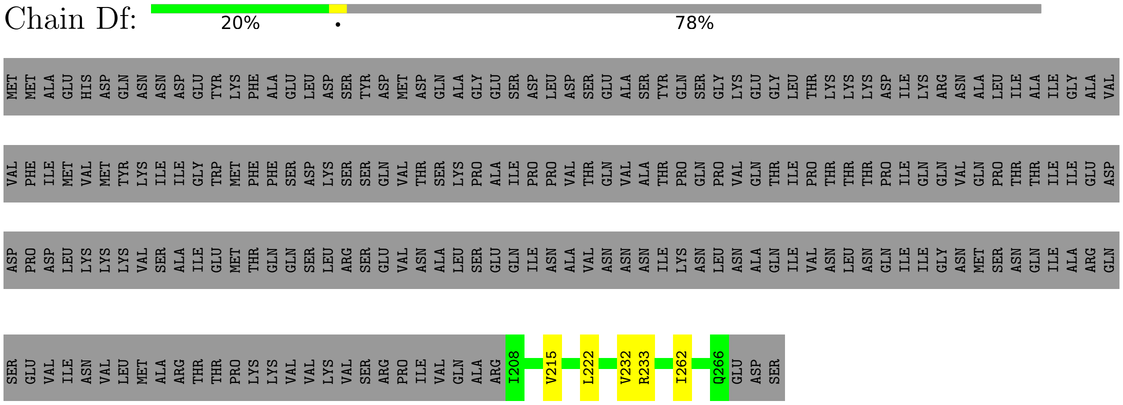


- Molecule 3: DotF

Chain Df:



- Molecule 3: DotF

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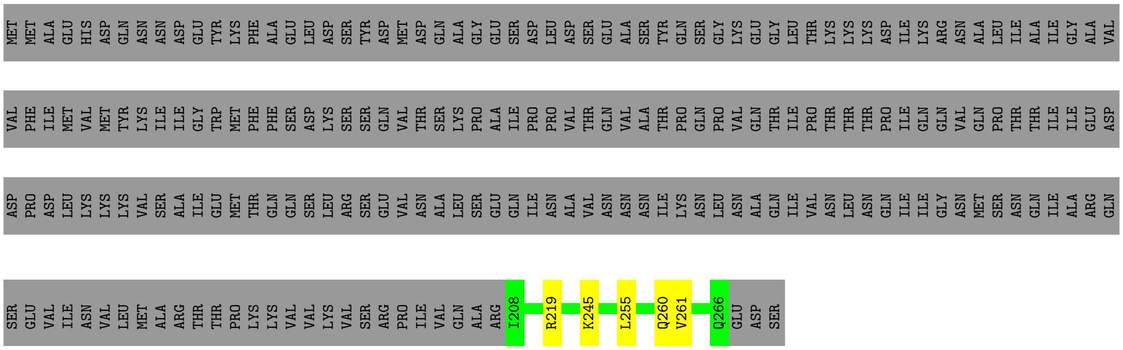

- Molecule 3: DotF

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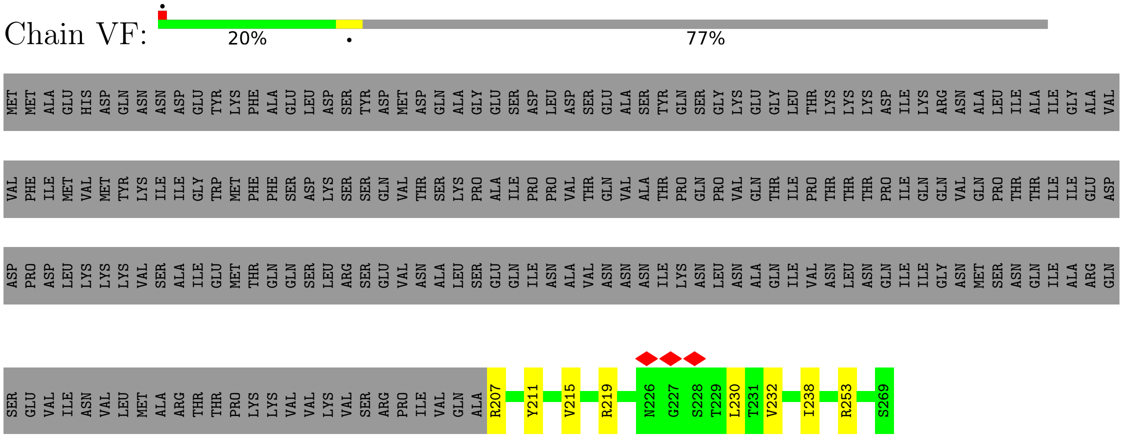
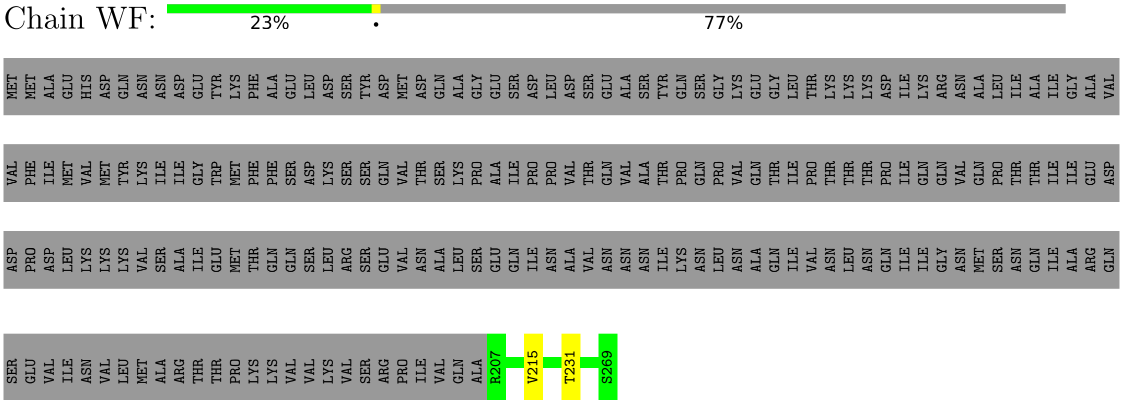


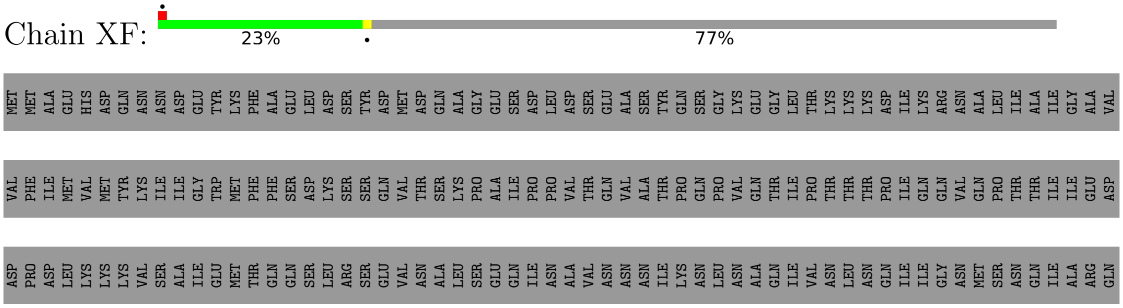
- Molecule 3: DotF

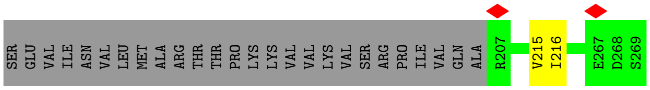
Chain WF:



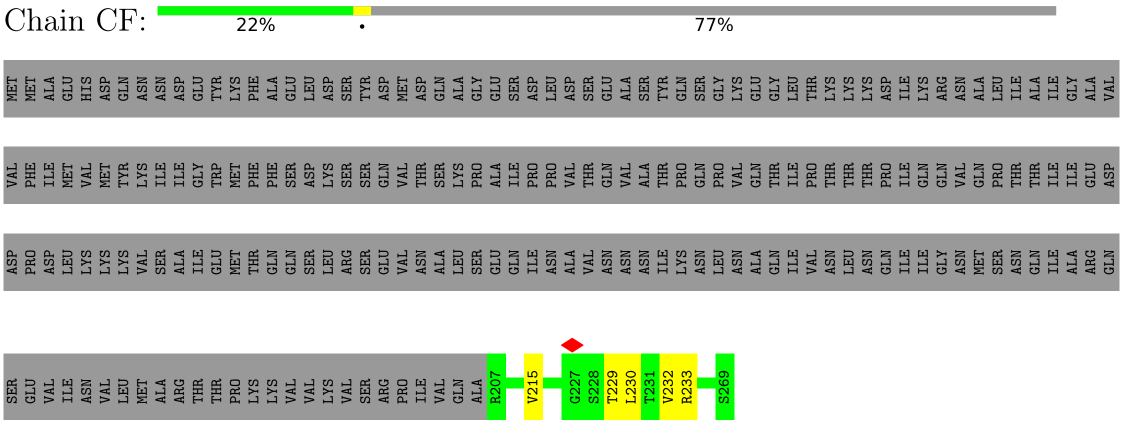
- Molecule 3: DotF

Chain XF:

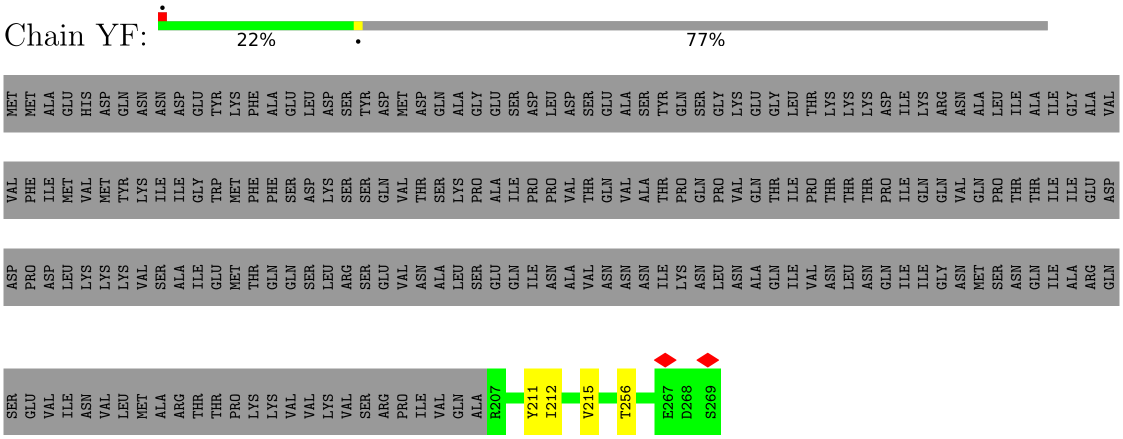




- Molecule 3: DotF



- Molecule 3: DotF



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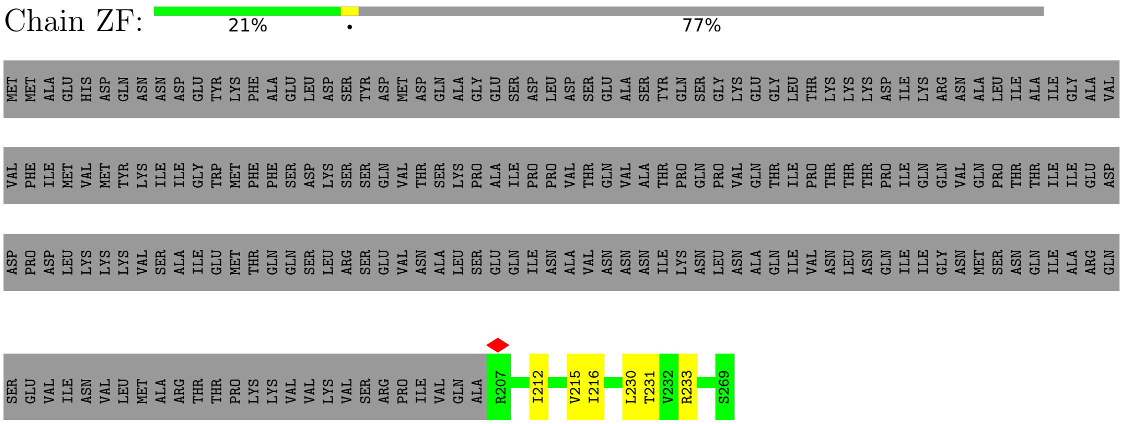

- Molecule 3: DotF

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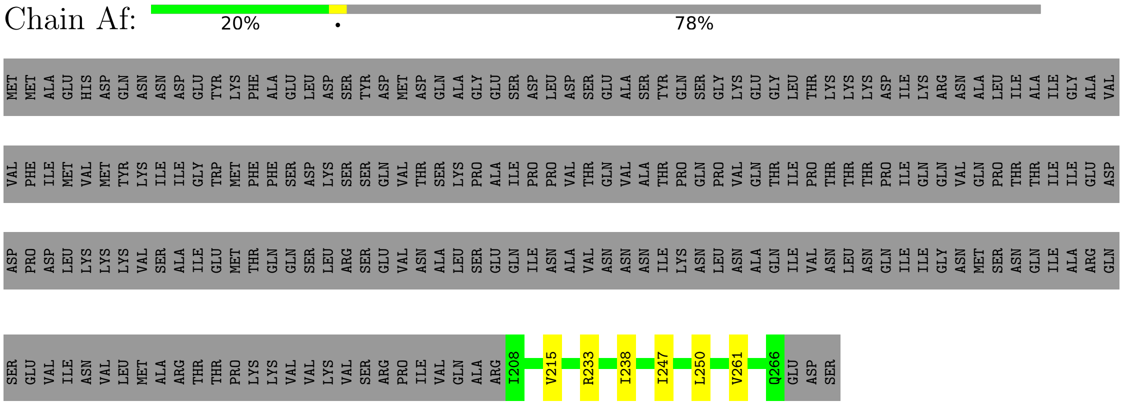

- Molecule 3: DotF

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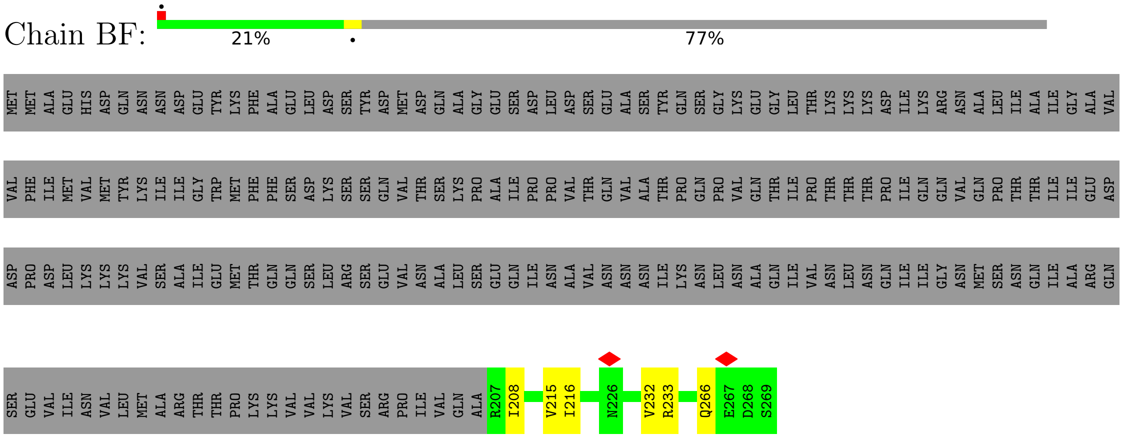
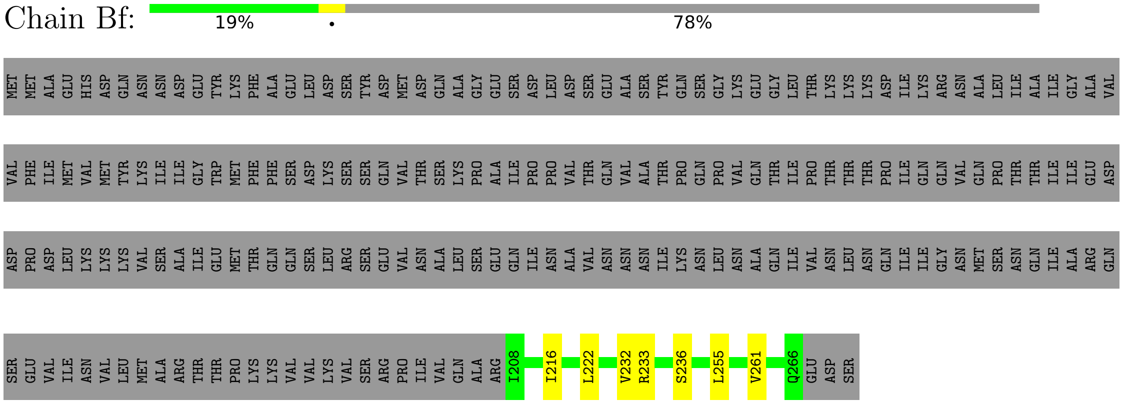


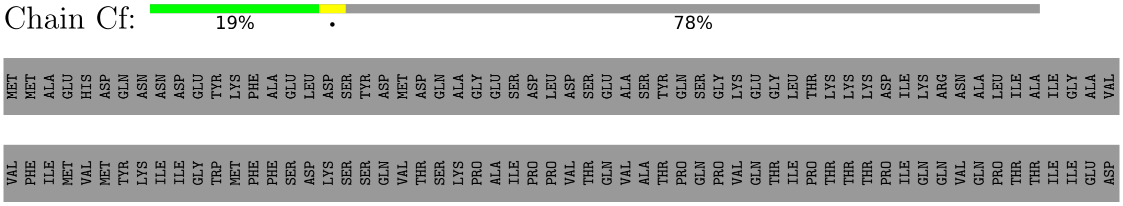
- Molecule 3: DotF

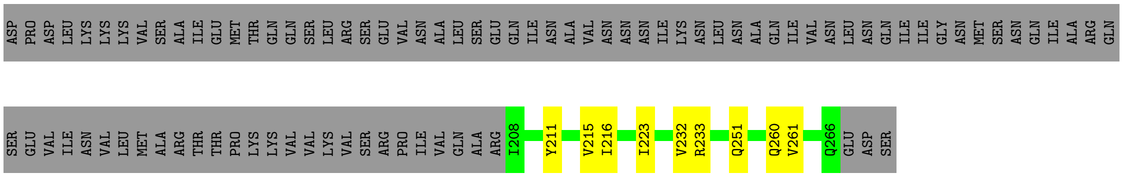
Chain Bf:



- Molecule 3: DotF

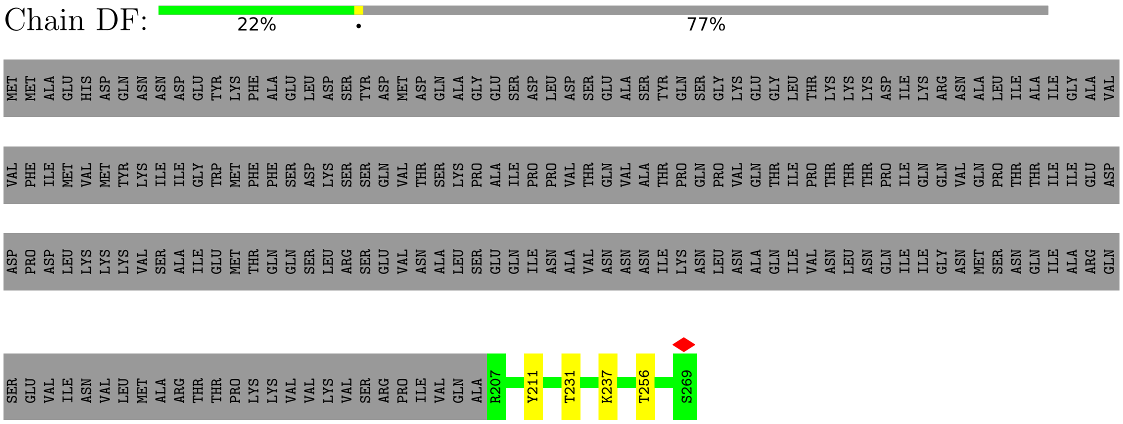
Chain Cf:





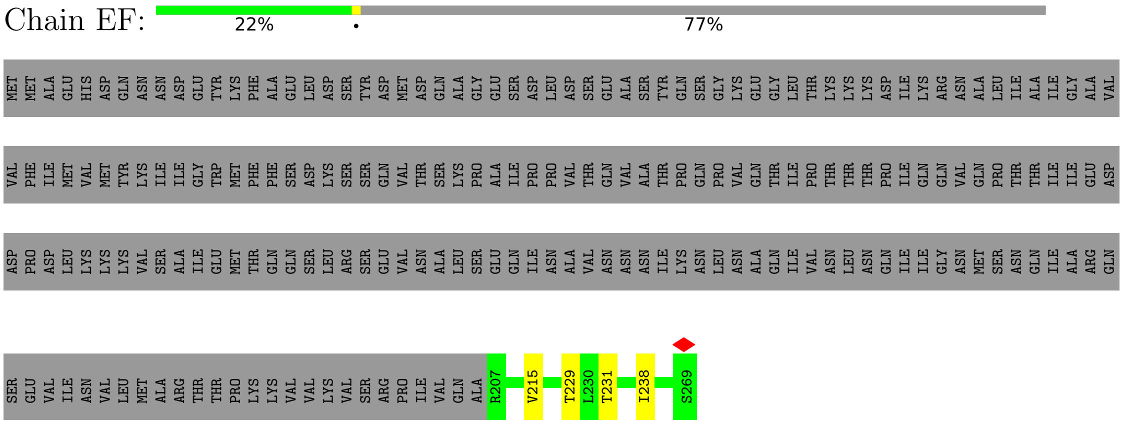
- Molecule 3: DotF

Chain DF:



- Molecule 3: DotF

Chain EF:



- Molecule 3: DotF

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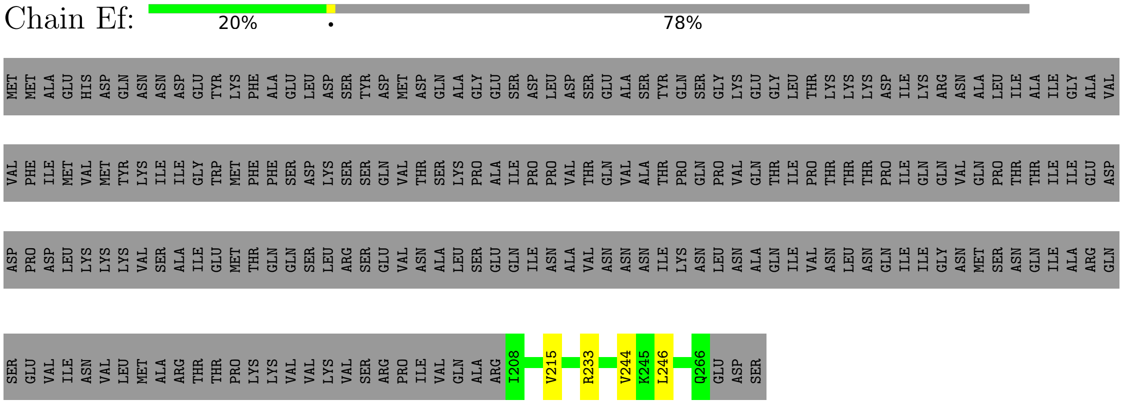

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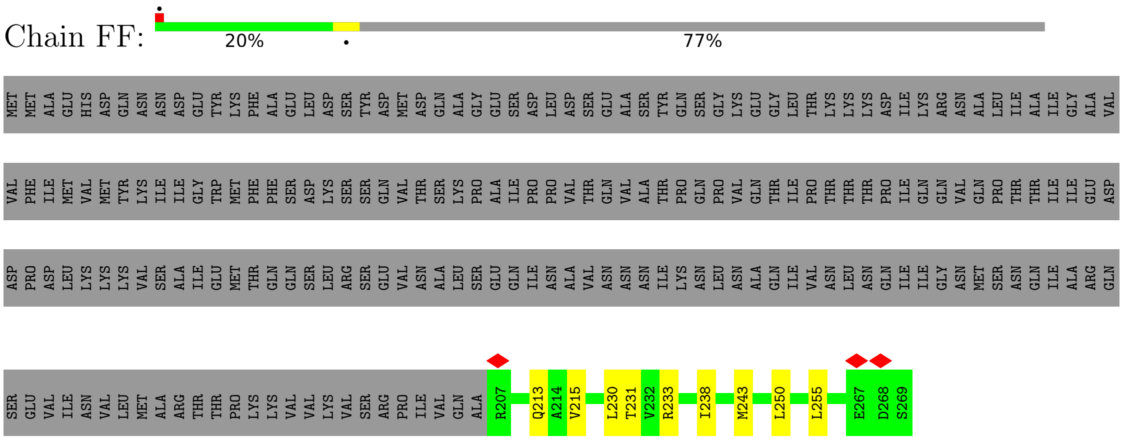
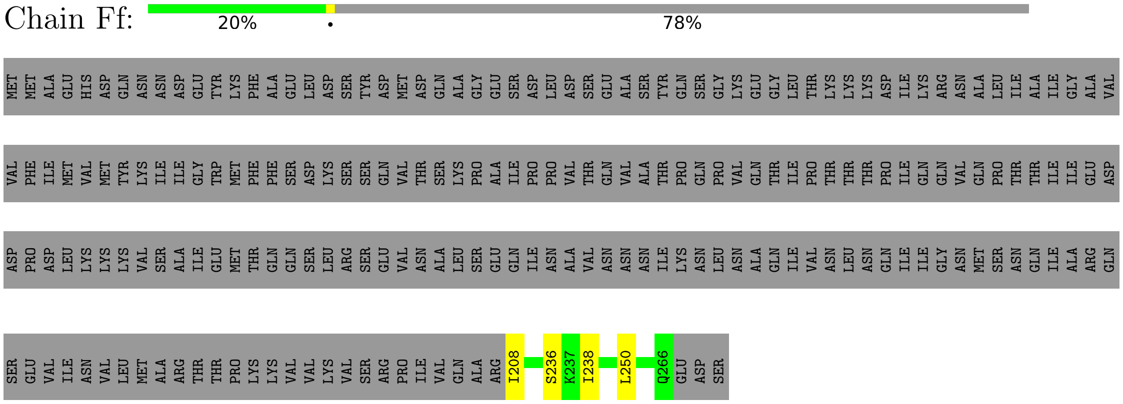
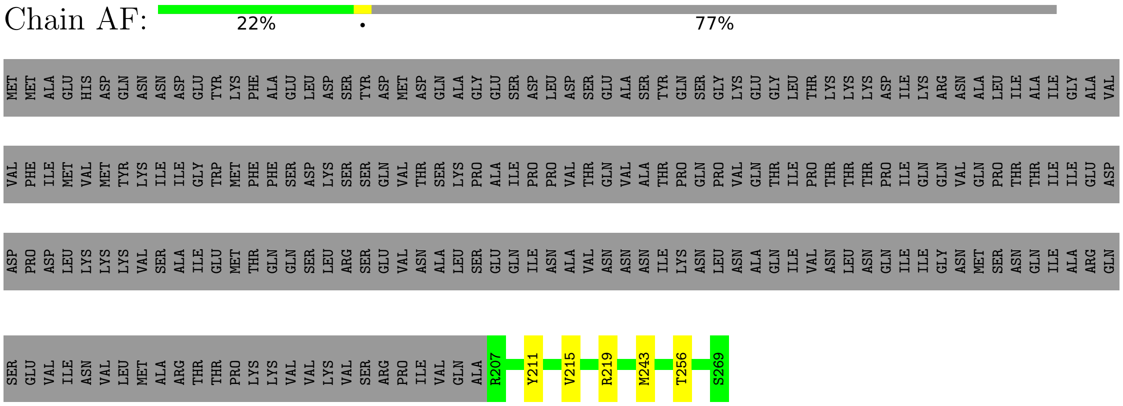


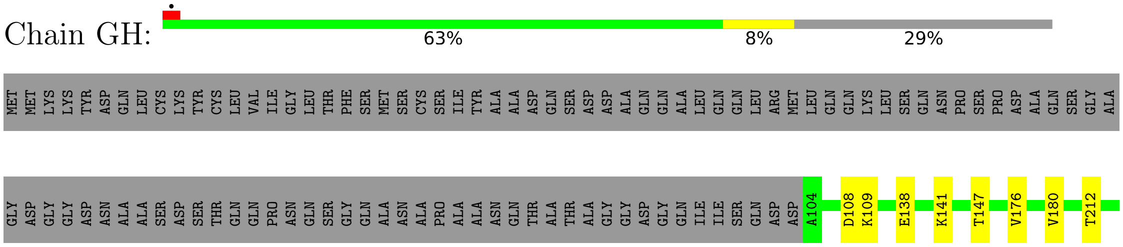
- Molecule 3: DotF

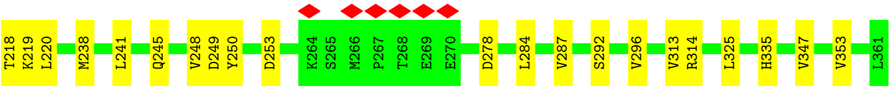


- Molecule 3: DotF

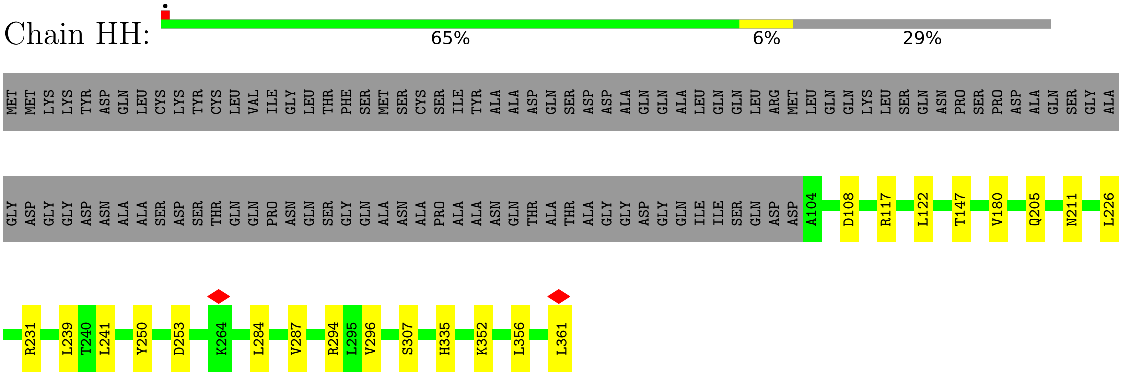


- Molecule 4: Type IV secretion protein IcmK

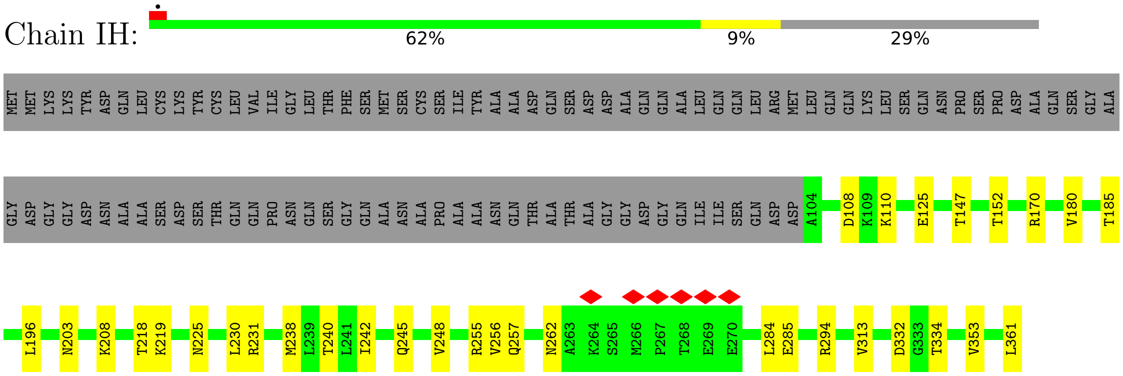




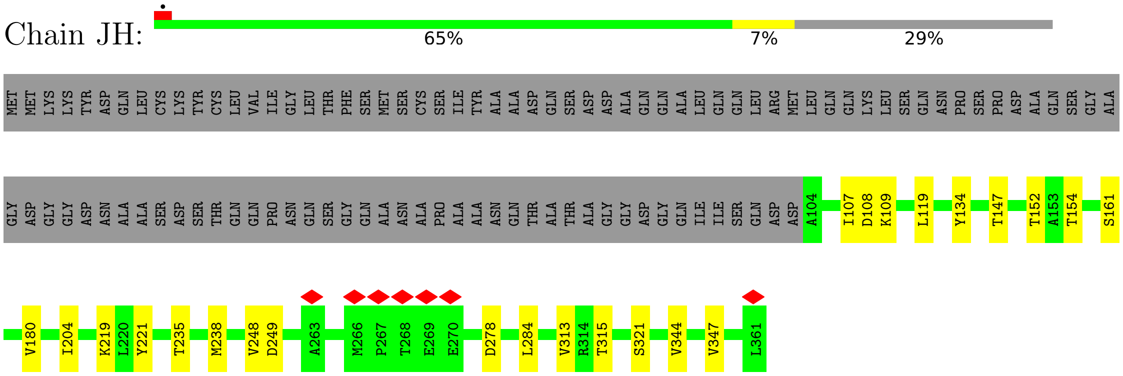
- Molecule 4: Type IV secretion protein IcmK



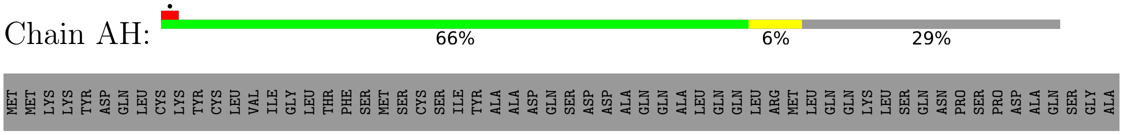
- Molecule 4: Type IV secretion protein IcmK

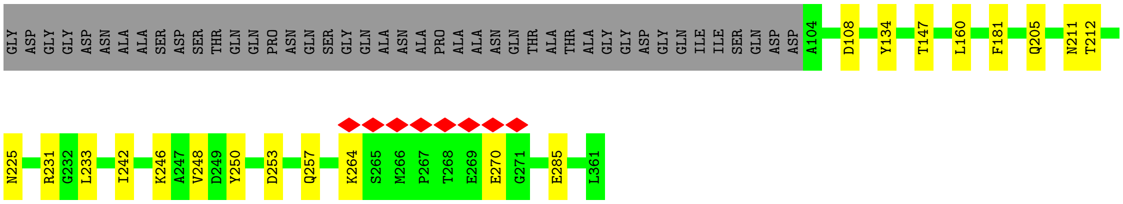


- Molecule 4: Type IV secretion protein IcmK



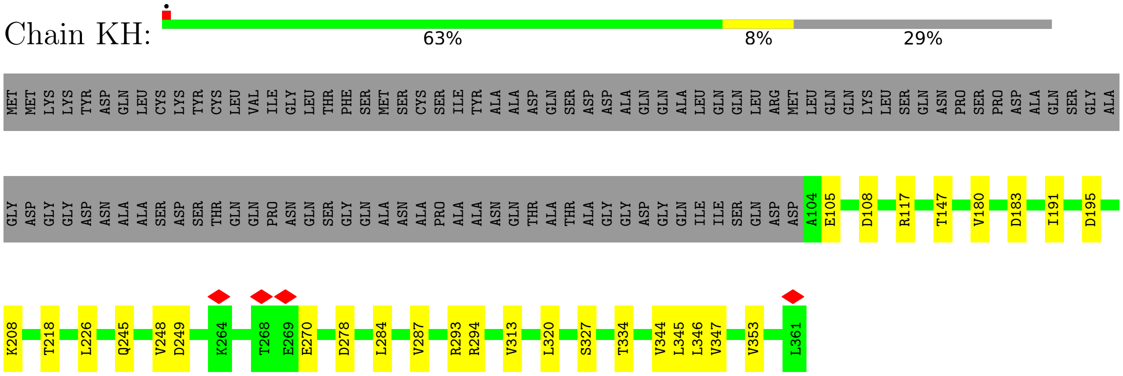
- Molecule 4: Type IV secretion protein IcmK





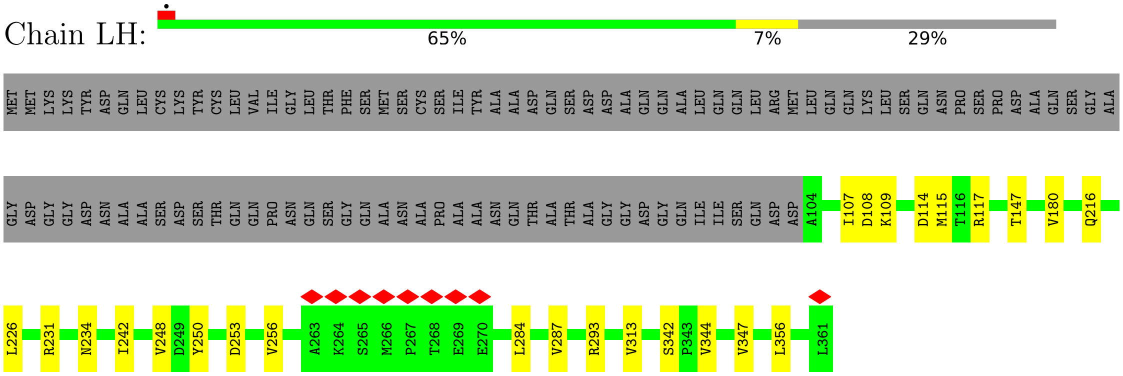
- Molecule 4: Type IV secretion protein IcmK

Chain KH:



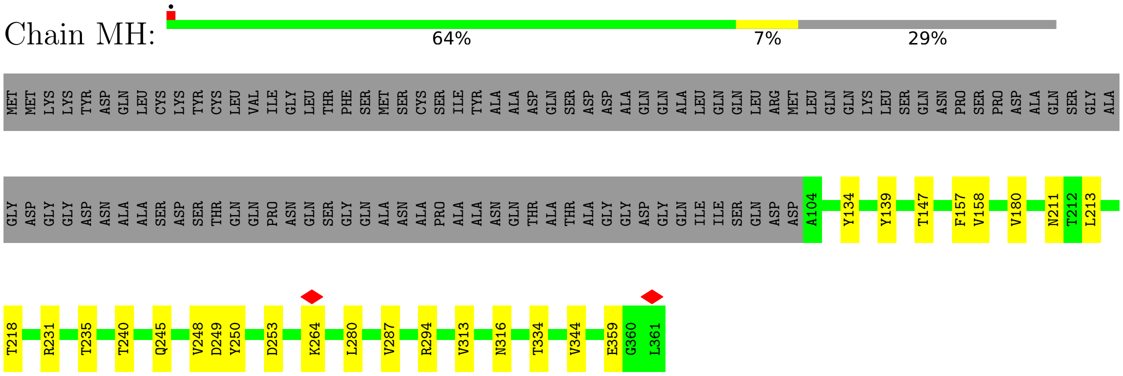
- Molecule 4: Type IV secretion protein IcmK

Chain LH:



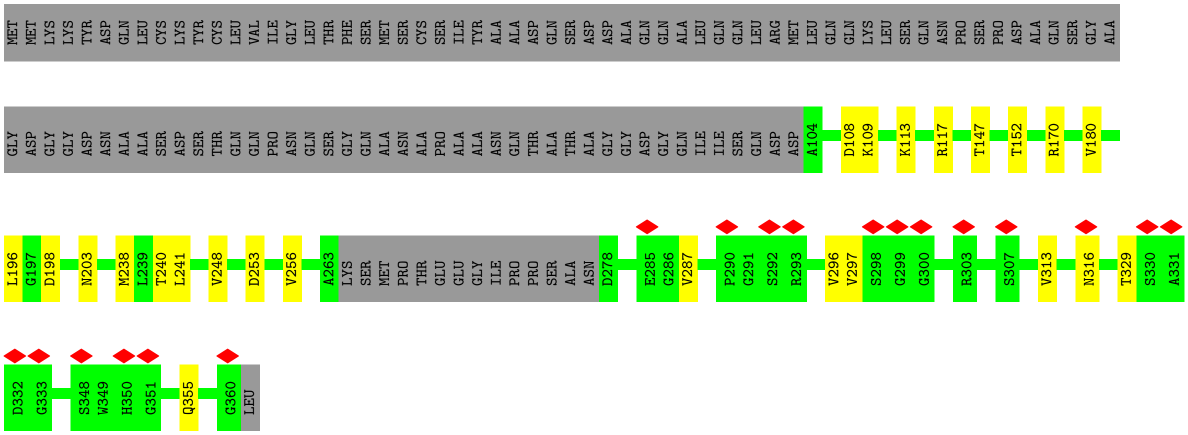
- Molecule 4: Type IV secretion protein IcmK

Chain MH:

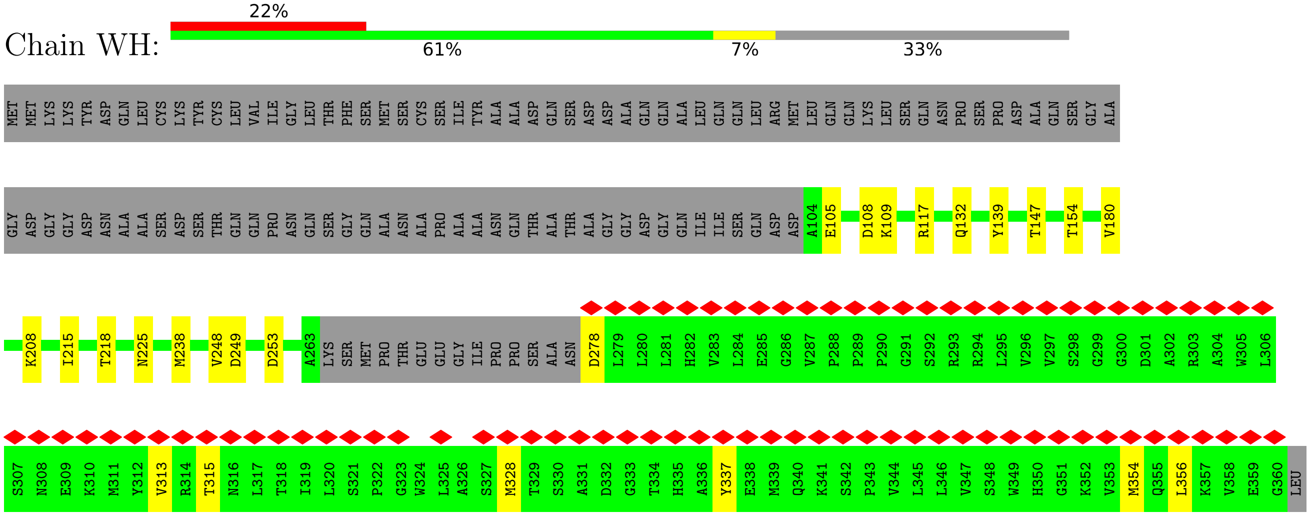


- Molecule 4: Type IV secretion protein IcmK

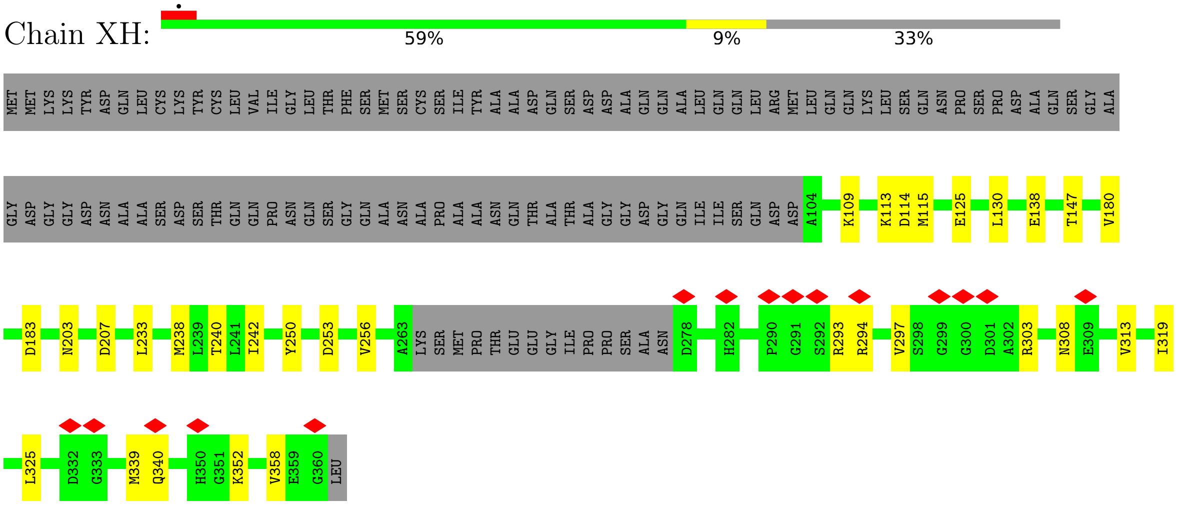
Chain VH:



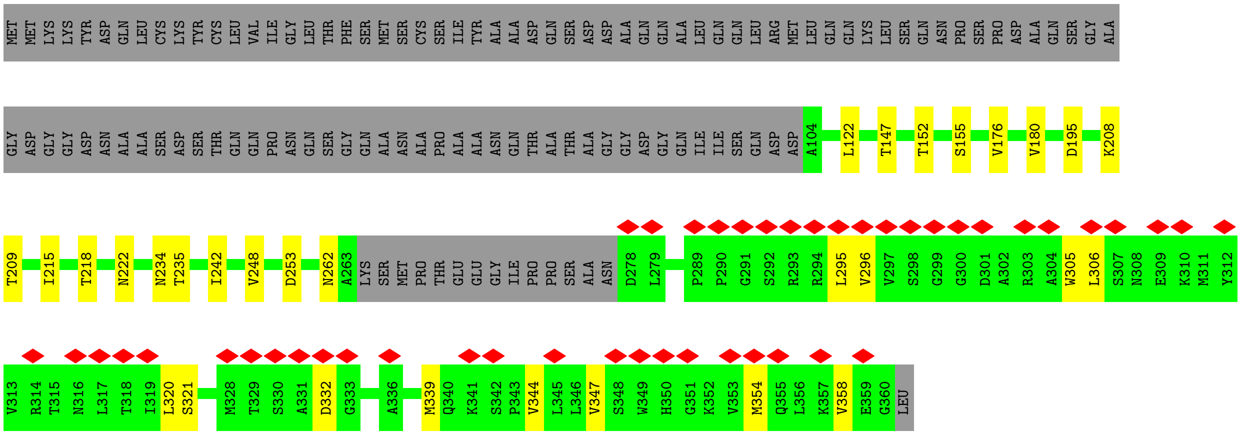
• Molecule 4: Type IV secretion protein IcmK



• Molecule 4: Type IV secretion protein IcmK

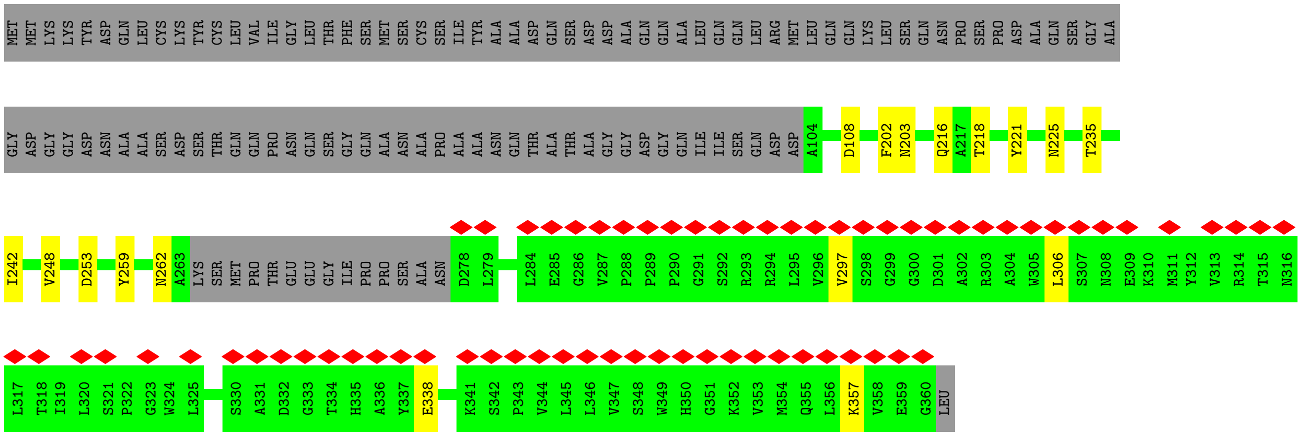


• Molecule 4: Type IV secretion protein IcmK



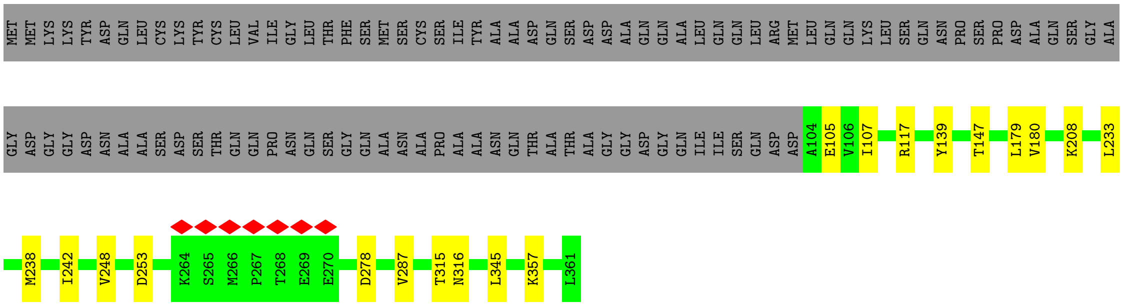
- Molecule 4: Type IV secretion protein IcmK

Chain ZH:



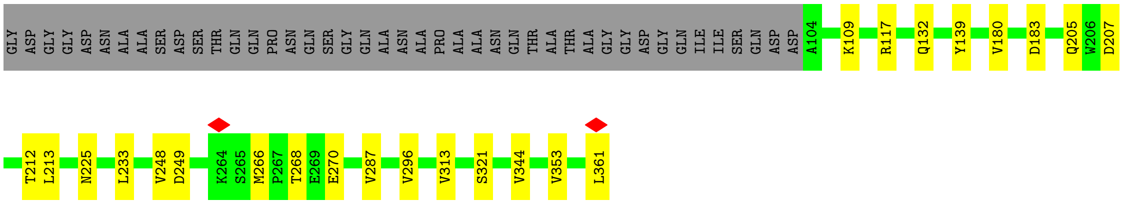
- Molecule 4: Type IV secretion protein IcmK

Chain BH:



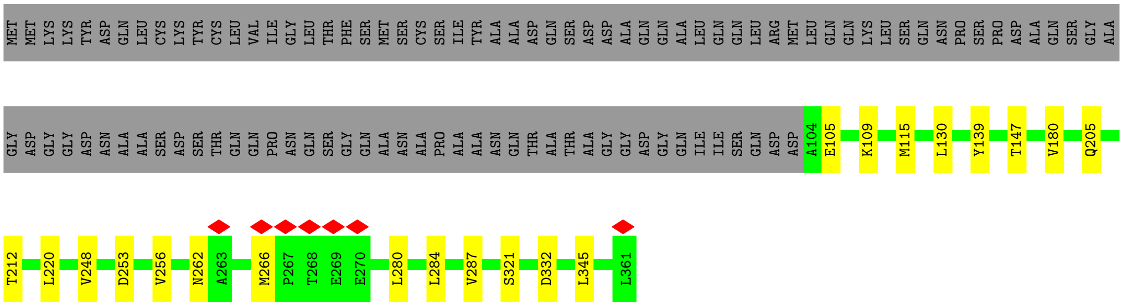
- Molecule 4: Type IV secretion protein IcmK

Chain CH:



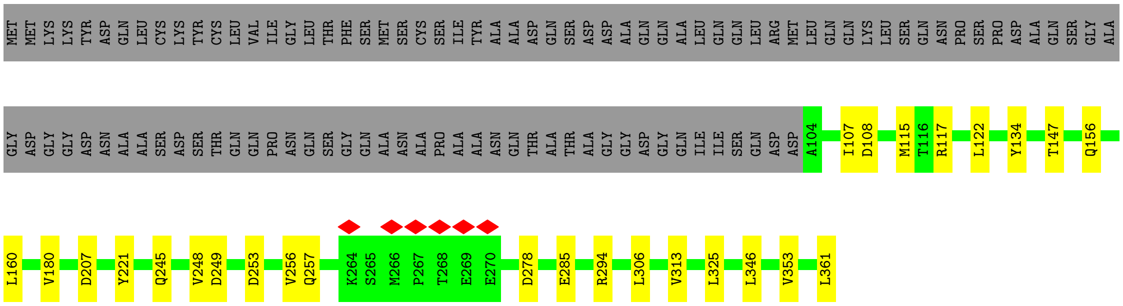
- Molecule 4: Type IV secretion protein IcmK

Chain DH:



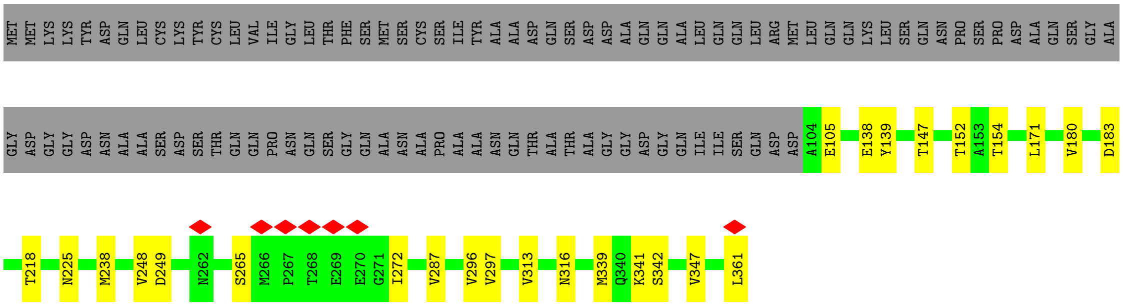
- Molecule 4: Type IV secretion protein IcmK

Chain EH:



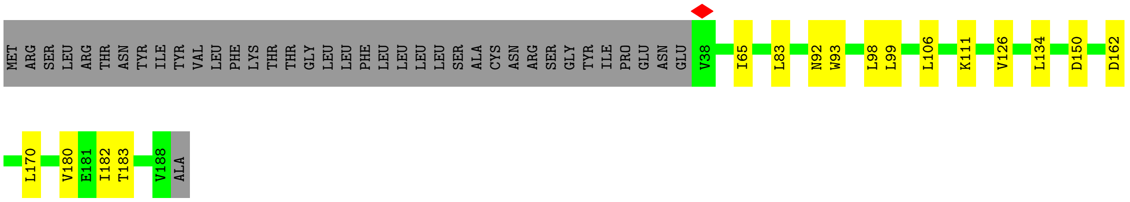
- Molecule 4: Type IV secretion protein IcmK

Chain FH:



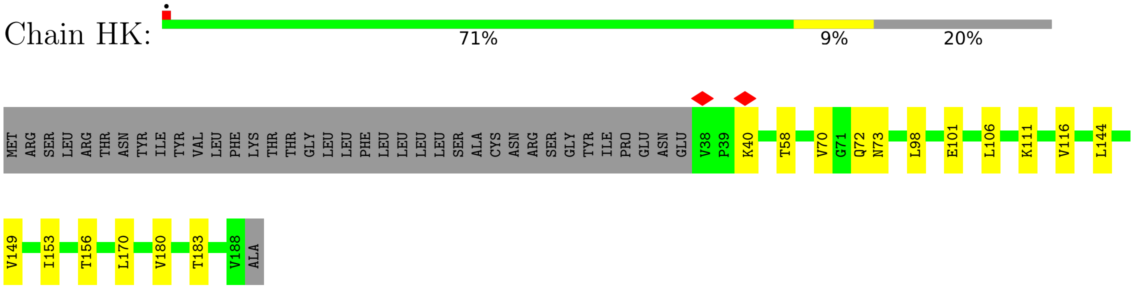
- Molecule 5: Inner membrane lipoprotein YiaD

Chain GK:



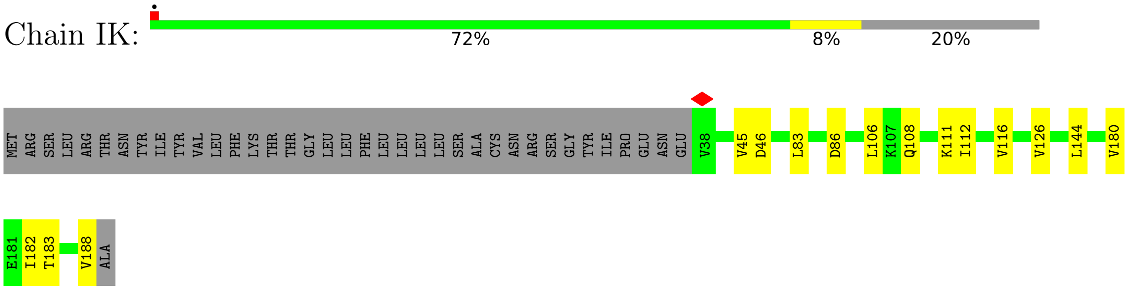
- Molecule 5: Inner membrane lipoprotein YiaD

Chain HK:



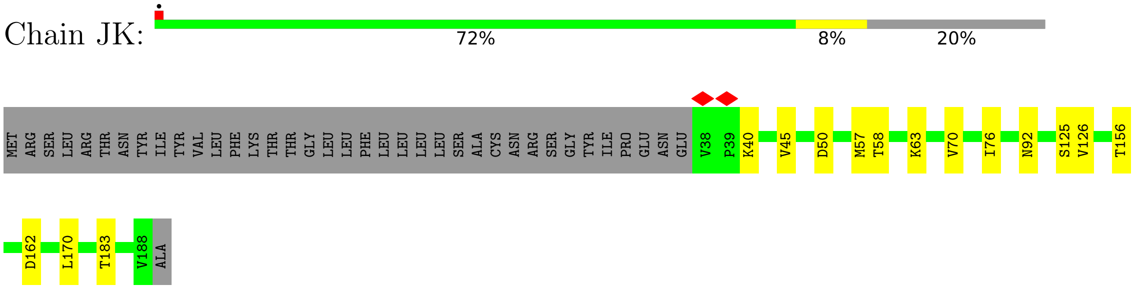
- Molecule 5: Inner membrane lipoprotein YiaD

Chain IK:



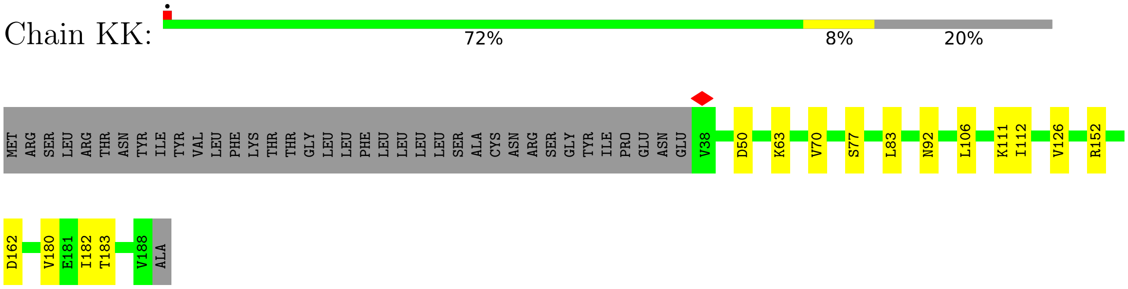
- Molecule 5: Inner membrane lipoprotein YiaD

Chain JK:



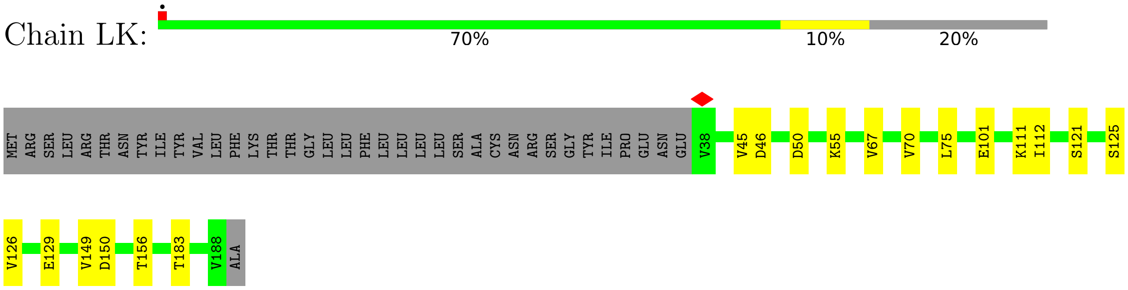
- Molecule 5: Inner membrane lipoprotein YiaD

Chain KK:



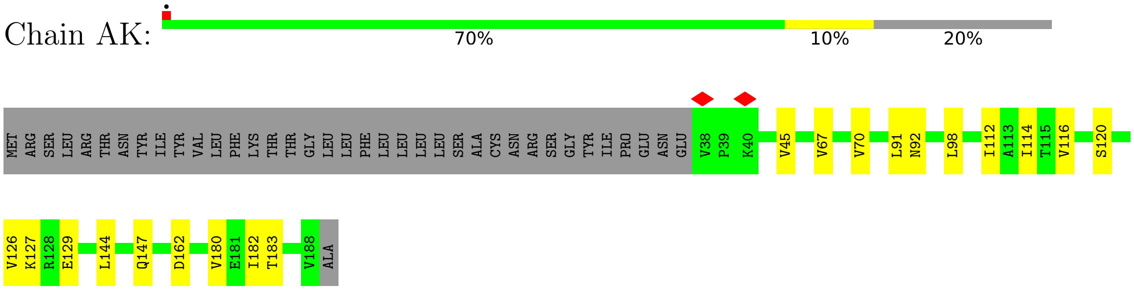
- Molecule 5: Inner membrane lipoprotein YiaD

Chain LK:



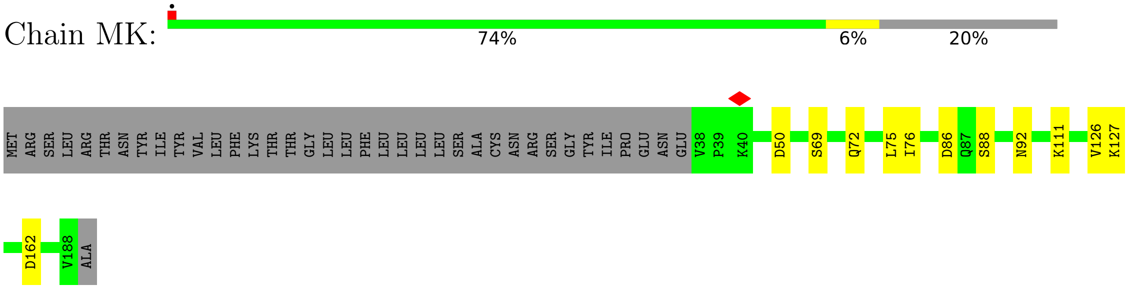
• Molecule 5: Inner membrane lipoprotein YiaD

Chain AK:



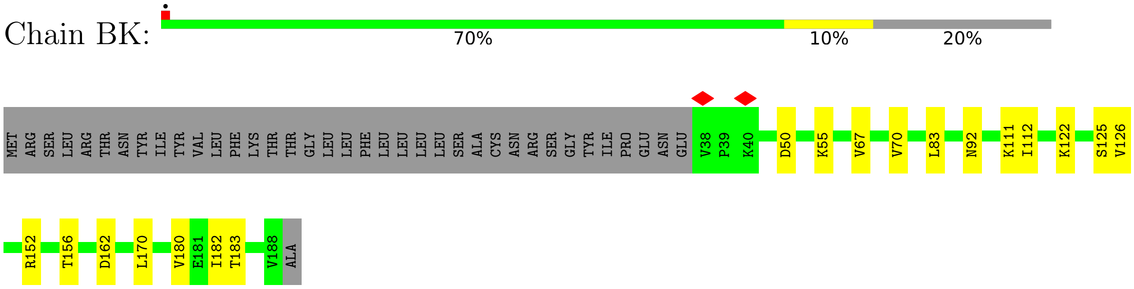
• Molecule 5: Inner membrane lipoprotein YiaD

Chain MK:



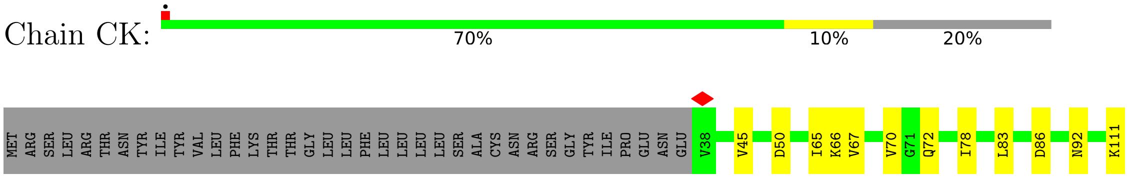
• Molecule 5: Inner membrane lipoprotein YiaD

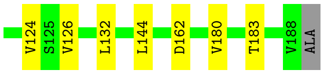
Chain BK:



• Molecule 5: Inner membrane lipoprotein YiaD

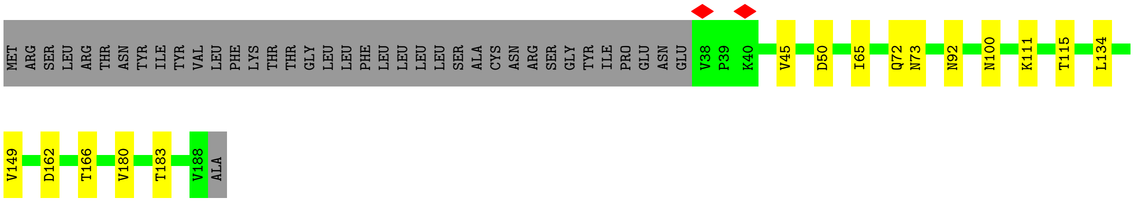
Chain CK:





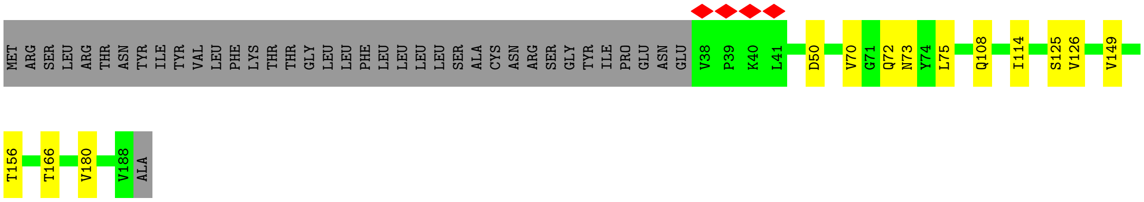
- Molecule 5: Inner membrane lipoprotein YiaD

Chain DK:



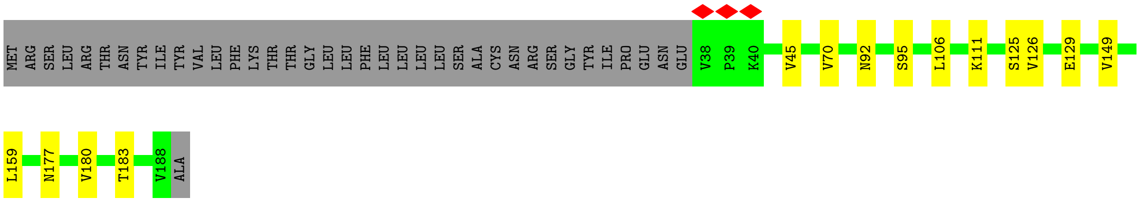
- Molecule 5: Inner membrane lipoprotein YiaD

Chain EK:



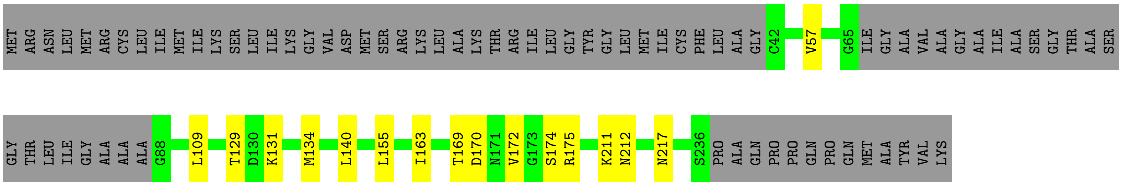
- Molecule 5: Inner membrane lipoprotein YiaD

Chain FK:



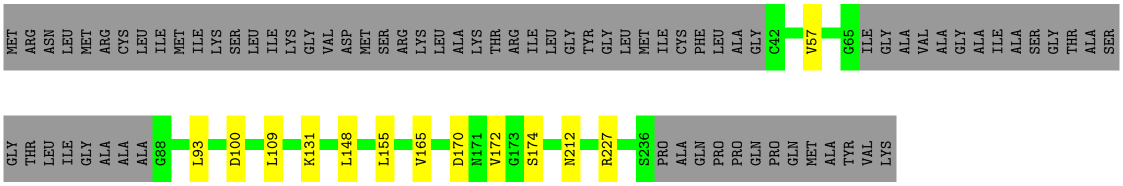
- Molecule 6: Outer membrane protein, OmpA family protein

Chain GL:



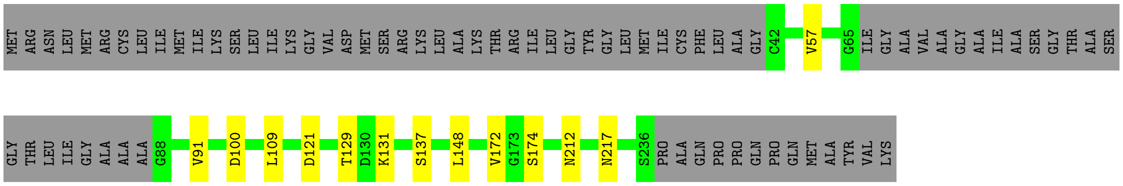
- Molecule 6: Outer membrane protein, OmpA family protein

Chain HL:



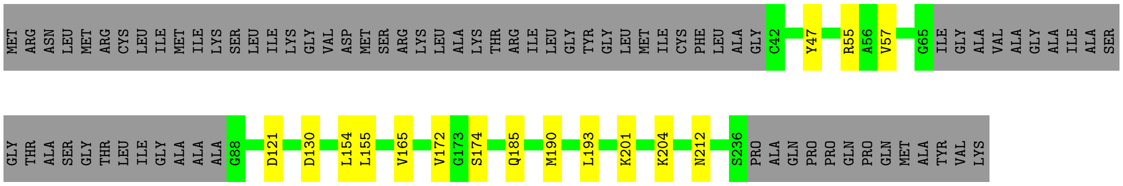
- Molecule 6: Outer membrane protein, OmpA family protein

Chain IL:



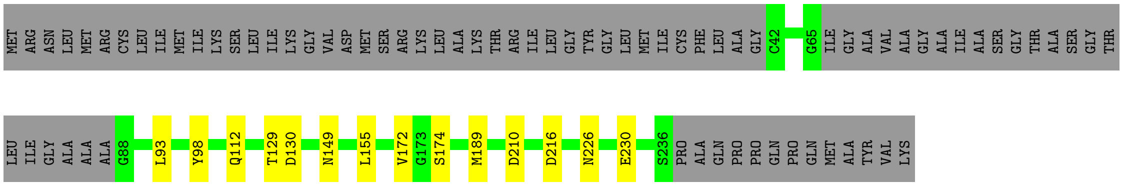
- Molecule 6: Outer membrane protein, OmpA family protein

Chain JL:



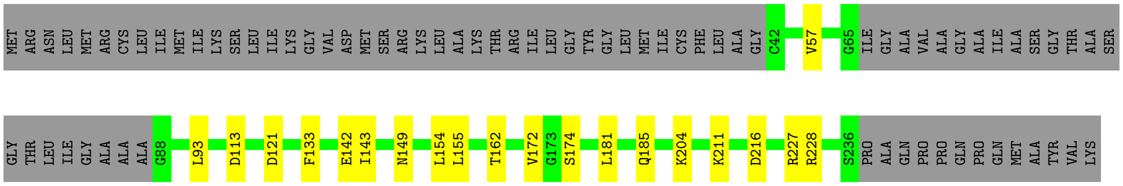
- Molecule 6: Outer membrane protein, OmpA family protein

Chain KL:



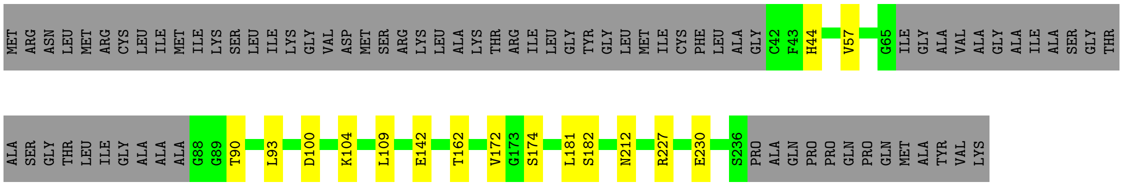
- Molecule 6: Outer membrane protein, OmpA family protein

Chain LL:



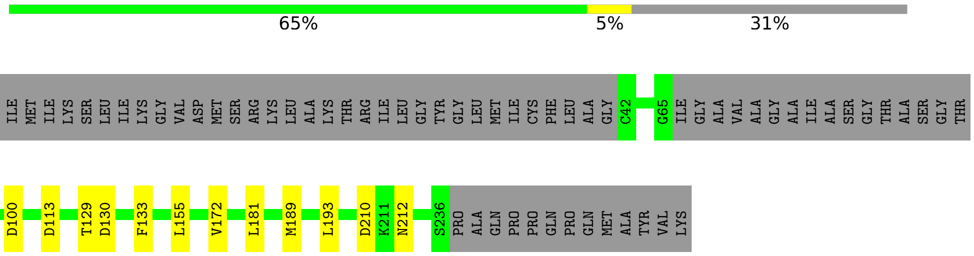
- Molecule 6: Outer membrane protein, OmpA family protein

Chain ML:



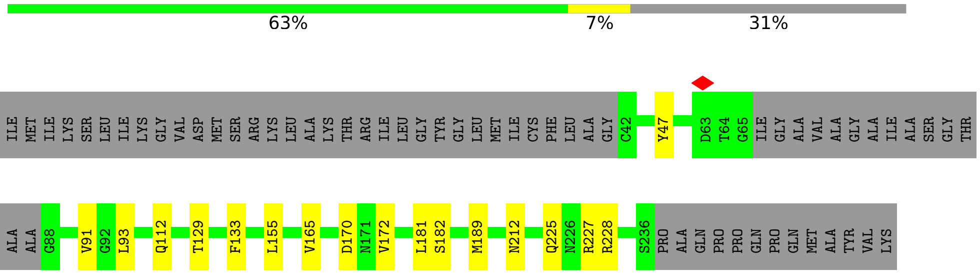
- Molecule 6: Outer membrane protein, OmpA family protein

Chain AL:



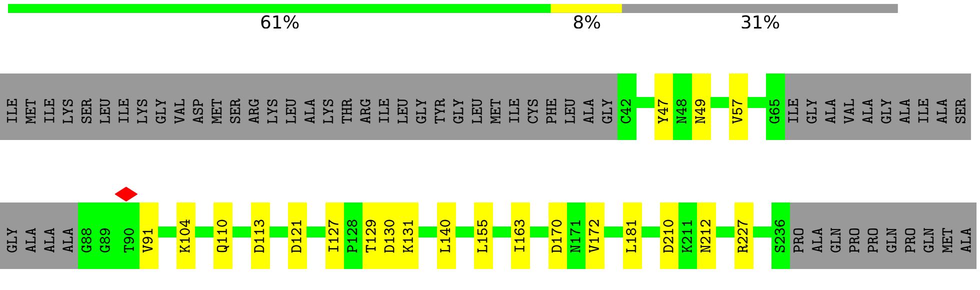
- Molecule 6: Outer membrane protein, OmpA family protein

Chain BL:



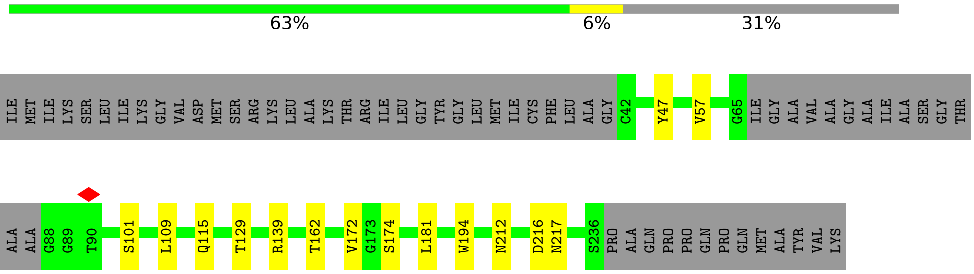
- Molecule 6: Outer membrane protein, OmpA family protein

Chain CL:

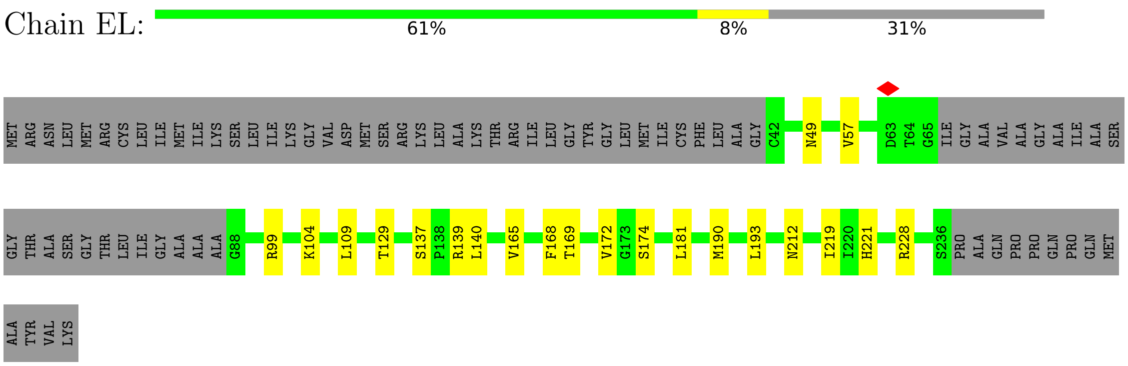


- Molecule 6: Outer membrane protein, OmpA family protein

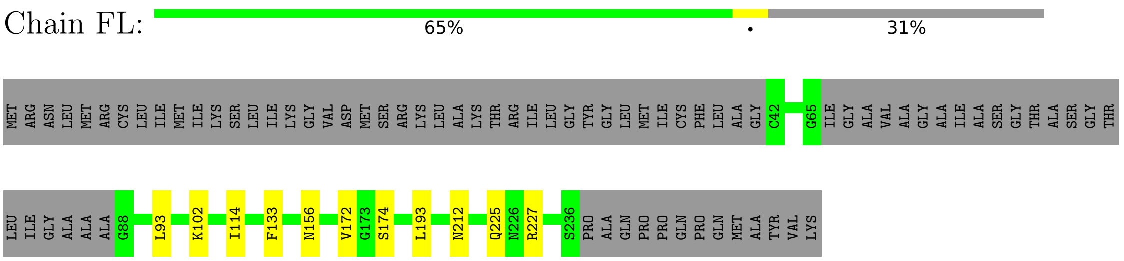
Chain DL:



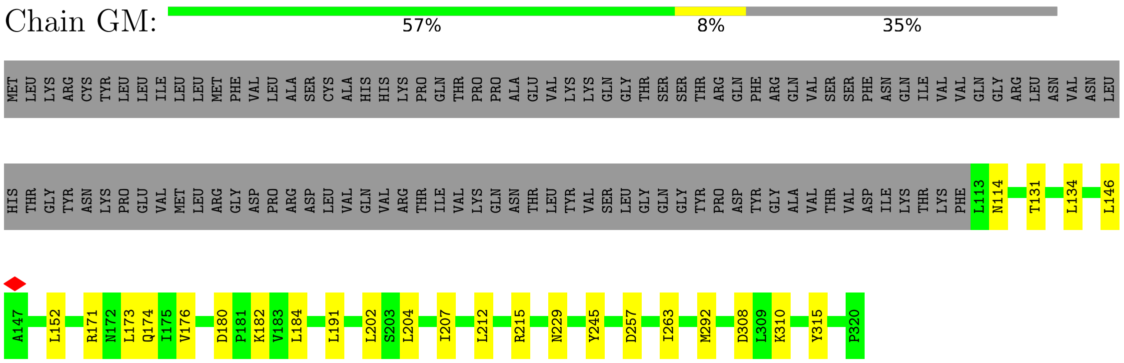
- Molecule 6: Outer membrane protein, OmpA family protein



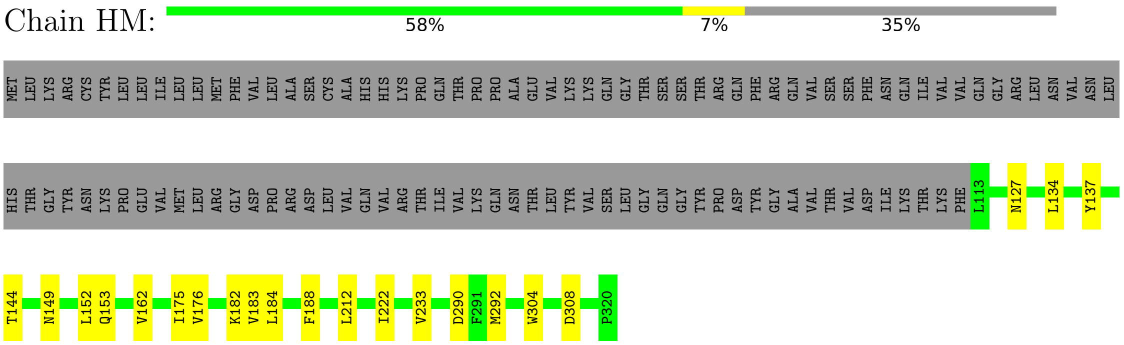
- Molecule 6: Outer membrane protein, OmpA family protein



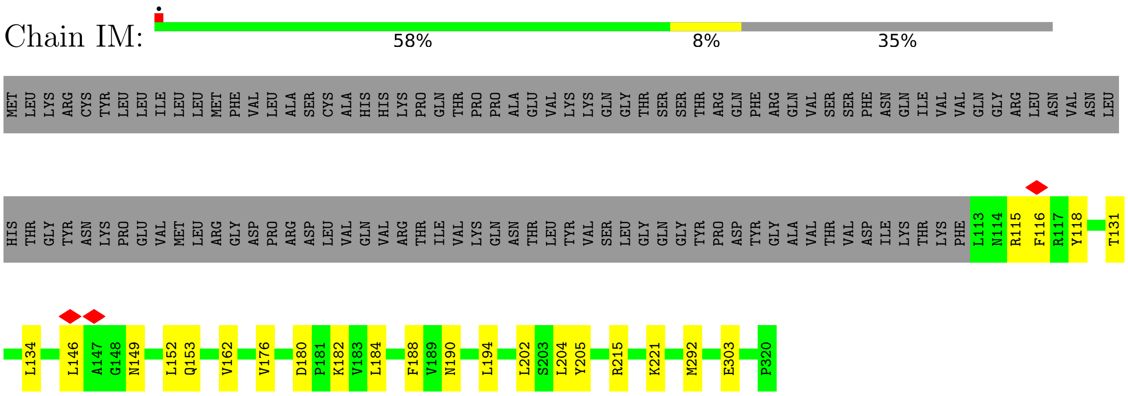
- Molecule 7: DUF2807 domain-containing protein



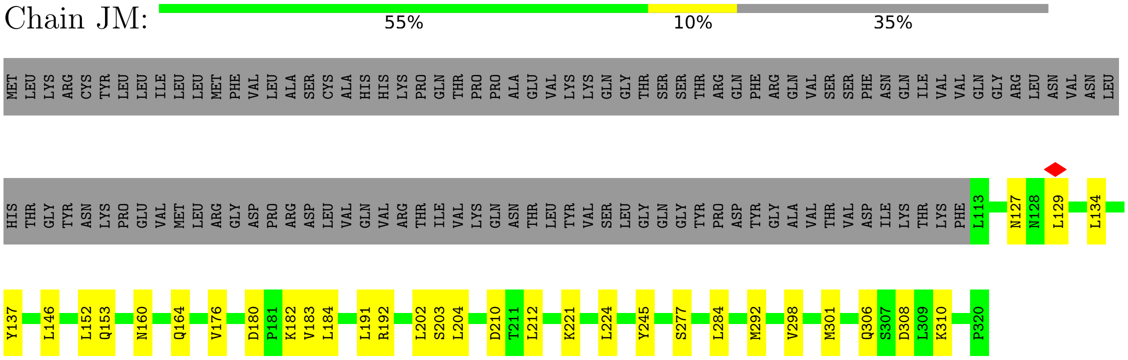
- Molecule 7: DUF2807 domain-containing protein



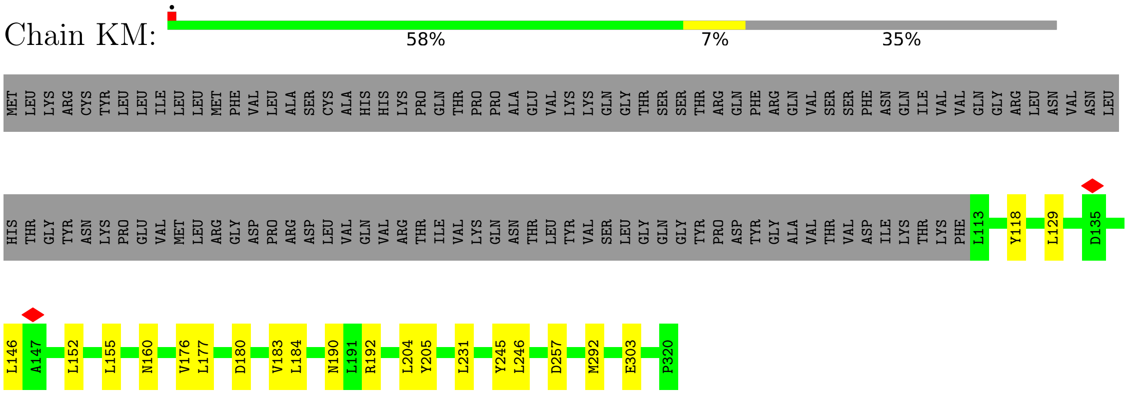
- Molecule 7: DUF2807 domain-containing protein



- Molecule 7: DUF2807 domain-containing protein



- Molecule 7: DUF2807 domain-containing protein



- Molecule 7: DUF2807 domain-containing protein

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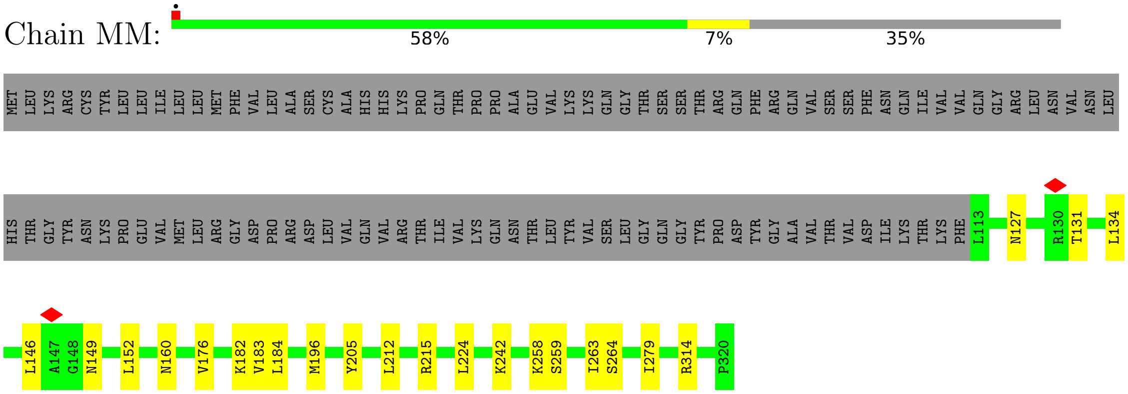
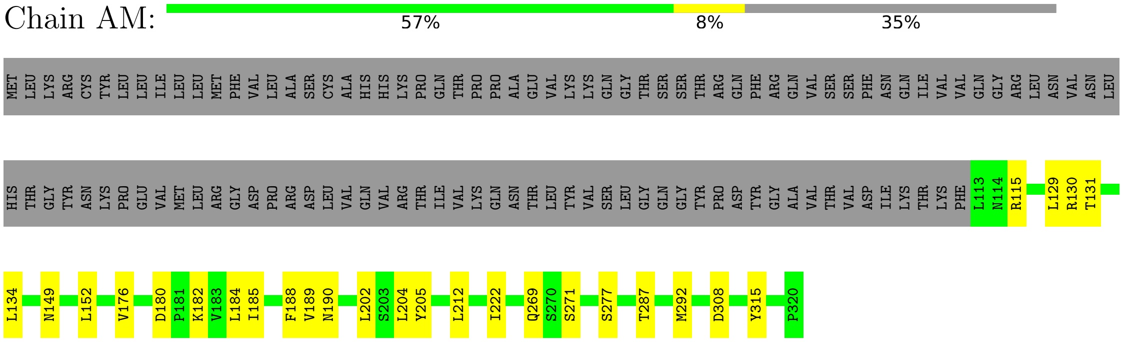
Chain MM:



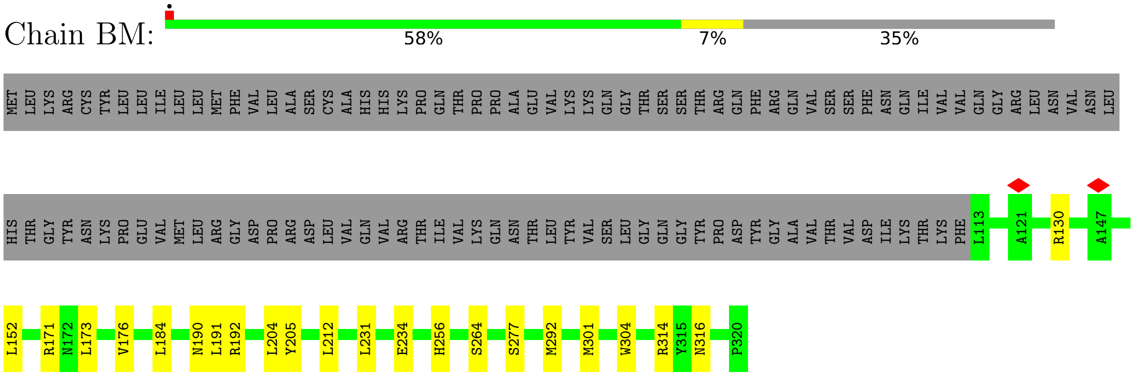
- Molecule 7: DUF2807 domain-containing protein

Chain AM:



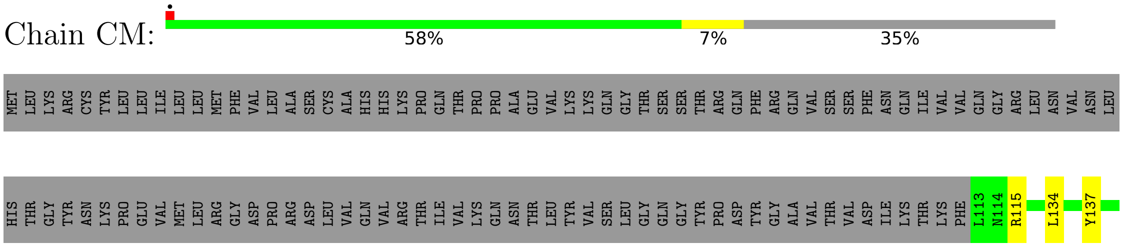
- Molecule 7: DUF2807 domain-containing protein

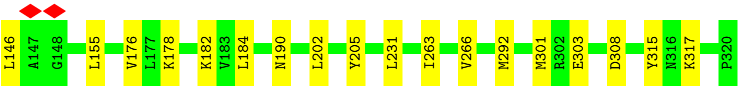
Chain BM:



- Molecule 7: DUF2807 domain-containing protein

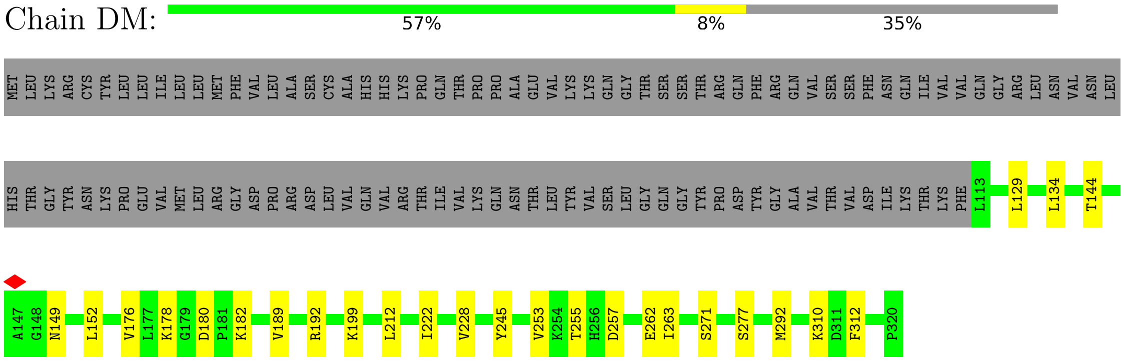
Chain CM:





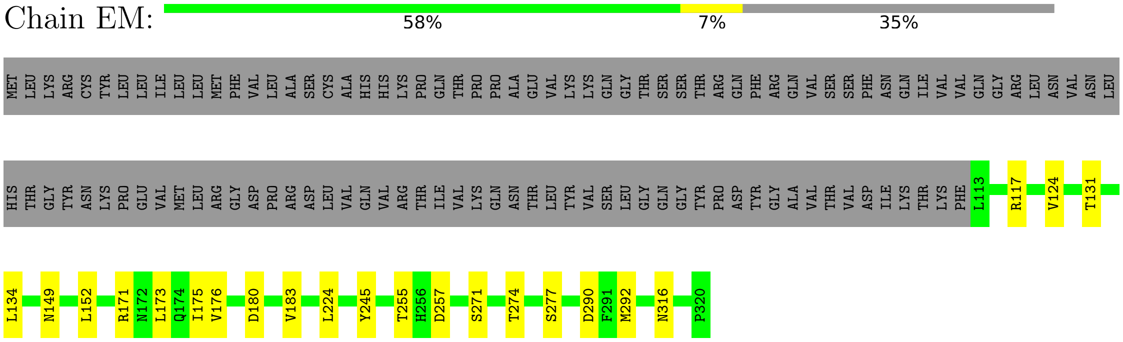
- Molecule 7: DUF2807 domain-containing protein

Chain DM:



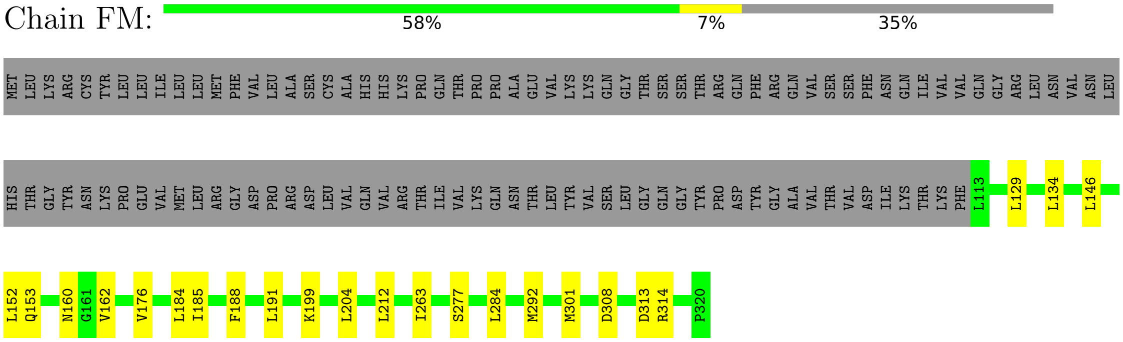
- Molecule 7: DUF2807 domain-containing protein

Chain EM:



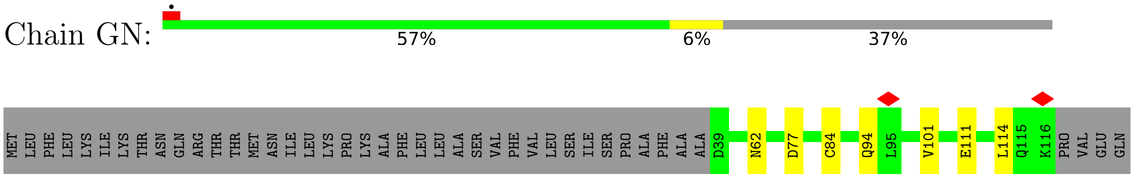
- Molecule 7: DUF2807 domain-containing protein

Chain FM:



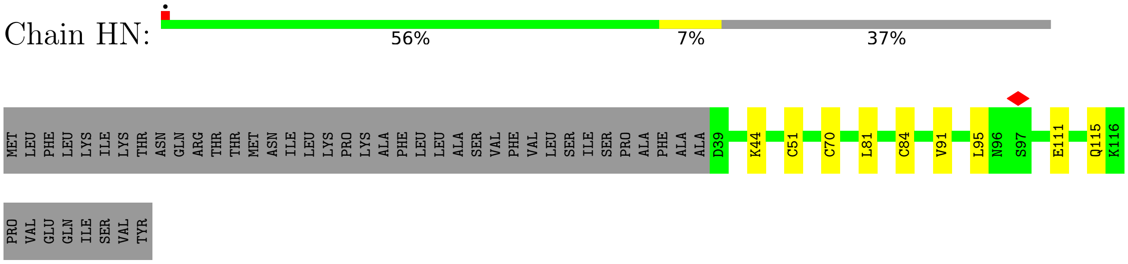
- Molecule 8: Neurogenic locus notch

Chain GN:



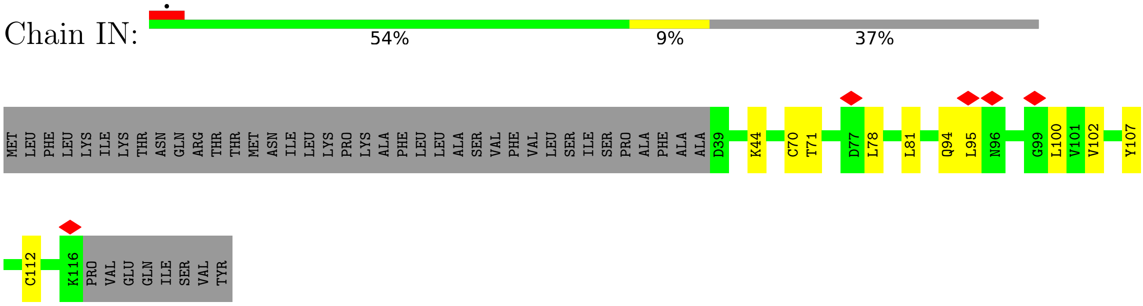
- Molecule 8: Neurogenic locus notch

Chain HN:



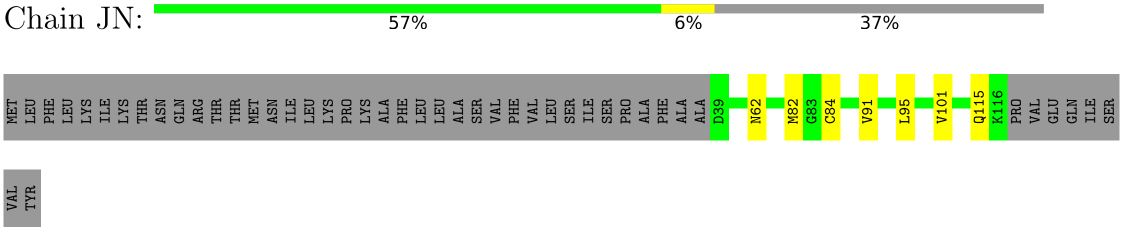
- Molecule 8: Neurogenic locus notch

Chain IN:



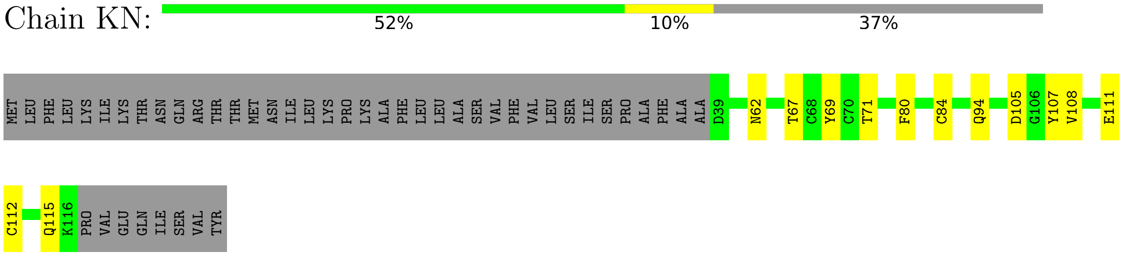
- Molecule 8: Neurogenic locus notch

Chain JN:



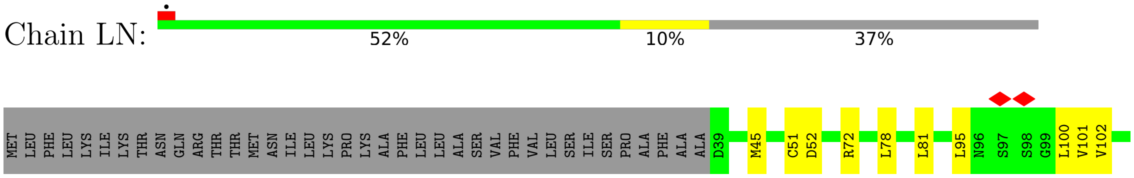
- Molecule 8: Neurogenic locus notch

Chain KN:



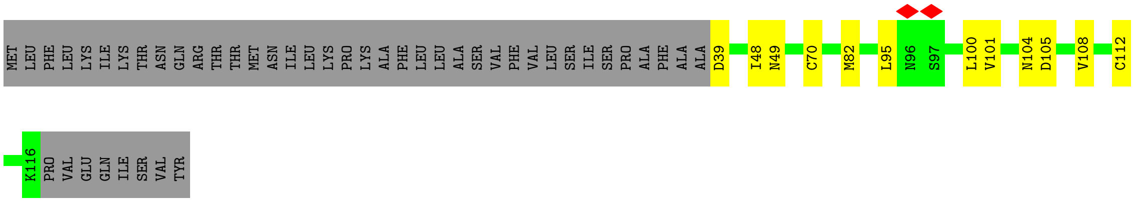
- Molecule 8: Neurogenic locus notch

Chain LN:



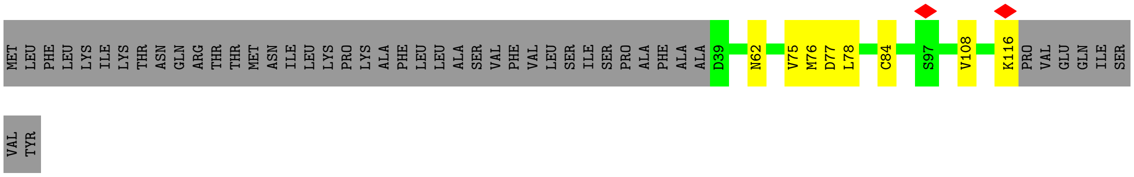
- Molecule 8: Neurogenic locus notch

Chain MN:



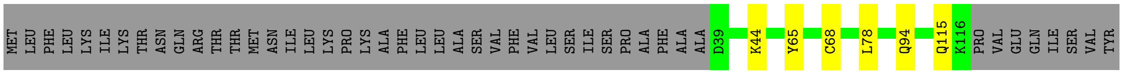
- Molecule 8: Neurogenic locus notch

Chain AN:



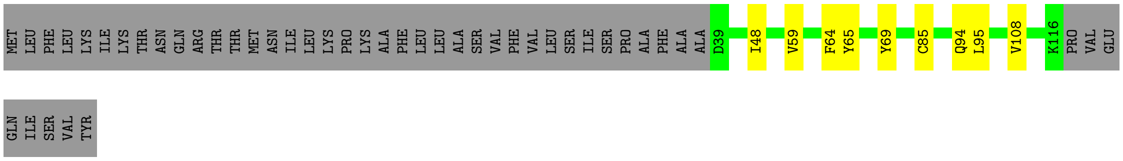
- Molecule 8: Neurogenic locus notch

Chain BN:



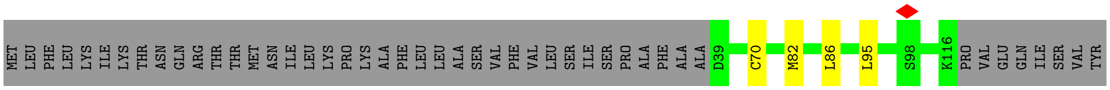
- Molecule 8: Neurogenic locus notch

Chain CN:



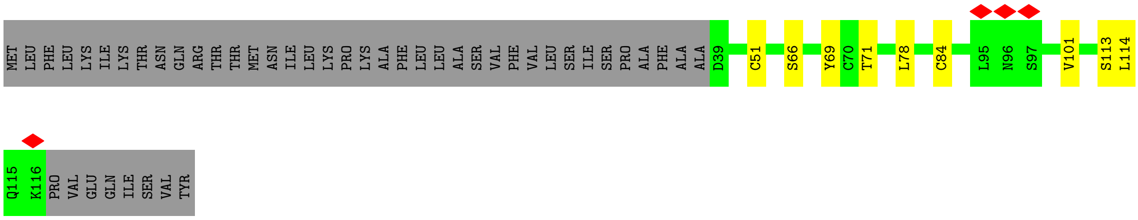
- Molecule 8: Neurogenic locus notch

Chain DN:



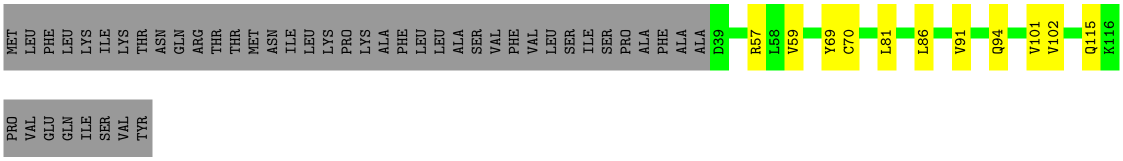
- Molecule 8: Neurogenic locus notch

Chain EN:



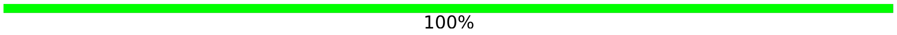
- Molecule 8: Neurogenic locus notch

Chain FN:



- Molecule 9: Unknown protein fragment

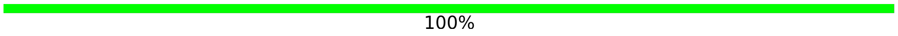
Chain GU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

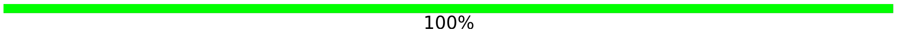
Chain HU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

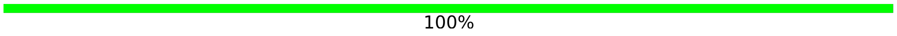
Chain IU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain JU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain KU:

There are no outlier residues recorded for this chain.

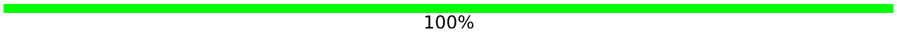
- Molecule 9: Unknown protein fragment

Chain LU:

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

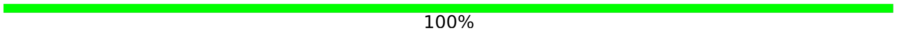
Chain MU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain AU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain BU:

There are no outlier residues recorded for this chain.

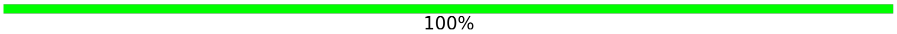
- Molecule 9: Unknown protein fragment

Chain CU:

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

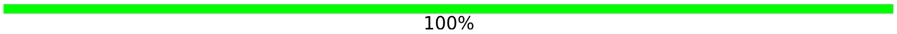
Chain DU:



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain EU:



There are no outlier residues recorded for this chain.

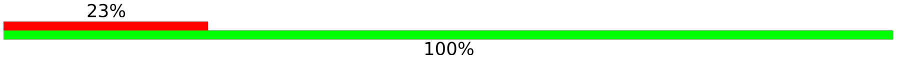
- Molecule 9: Unknown protein fragment

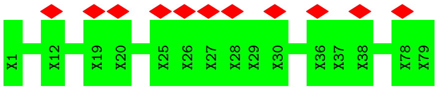
Chain FU:

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment

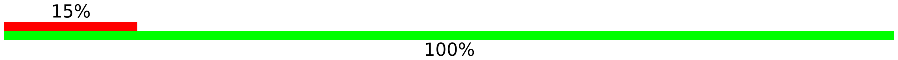
Chain GX:

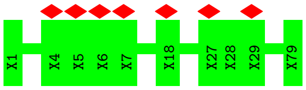




- Molecule 10: Unknown protein fragment

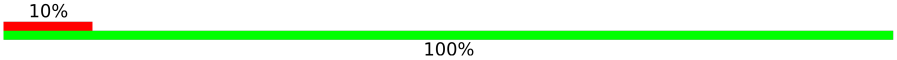
Chain HX:

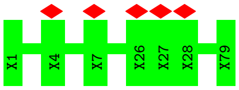




- Molecule 10: Unknown protein fragment

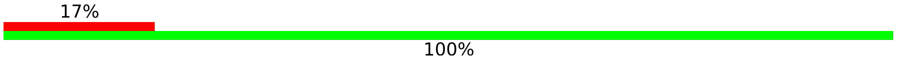
Chain IX:

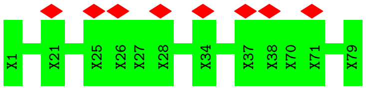




- Molecule 10: Unknown protein fragment

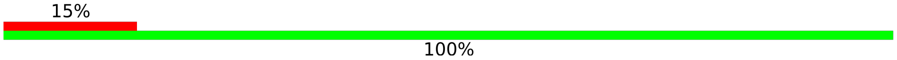
Chain JX:

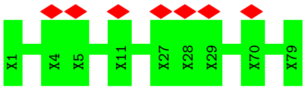




- Molecule 10: Unknown protein fragment

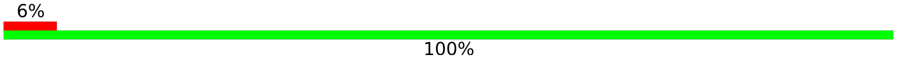
Chain KX:

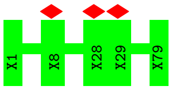




- Molecule 10: Unknown protein fragment

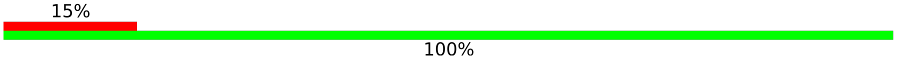
Chain LX:

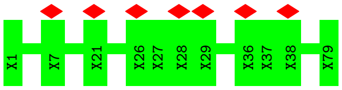




- Molecule 10: Unknown protein fragment

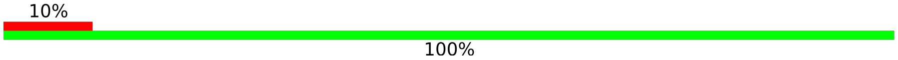
Chain MX:

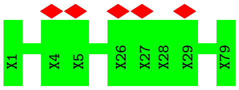




- Molecule 10: Unknown protein fragment

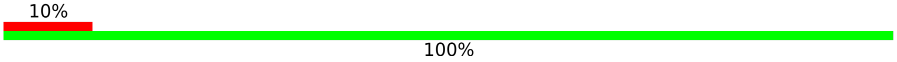
Chain VX:

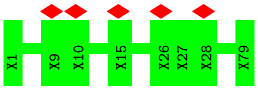




- Molecule 10: Unknown protein fragment

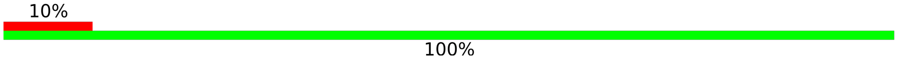
Chain WX:

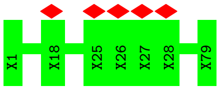




- Molecule 10: Unknown protein fragment

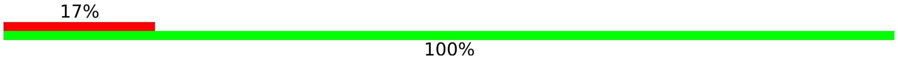
Chain XX:

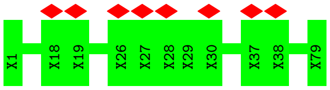




- Molecule 10: Unknown protein fragment

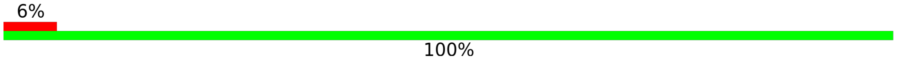
Chain YX:

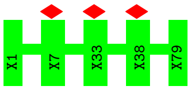




- Molecule 10: Unknown protein fragment

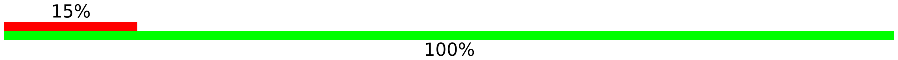
Chain ZX:

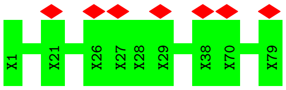




- Molecule 10: Unknown protein fragment

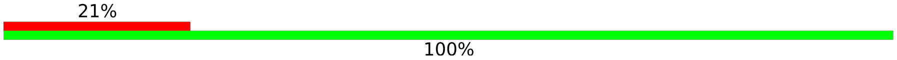
Chain AX:

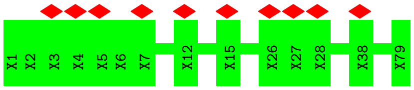




- Molecule 10: Unknown protein fragment

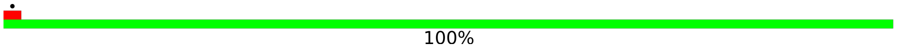
Chain BX:

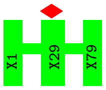




- Molecule 10: Unknown protein fragment

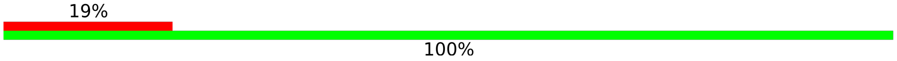
Chain CX:

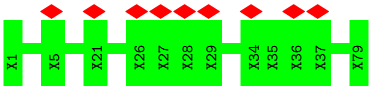




- Molecule 10: Unknown protein fragment

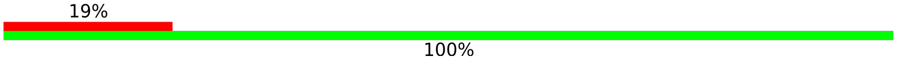
Chain DX:

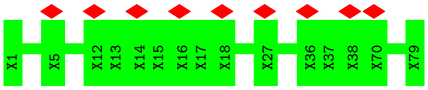




- Molecule 10: Unknown protein fragment

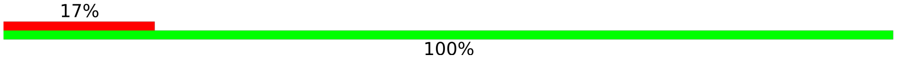
Chain EX:

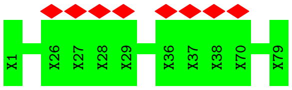




- Molecule 10: Unknown protein fragment

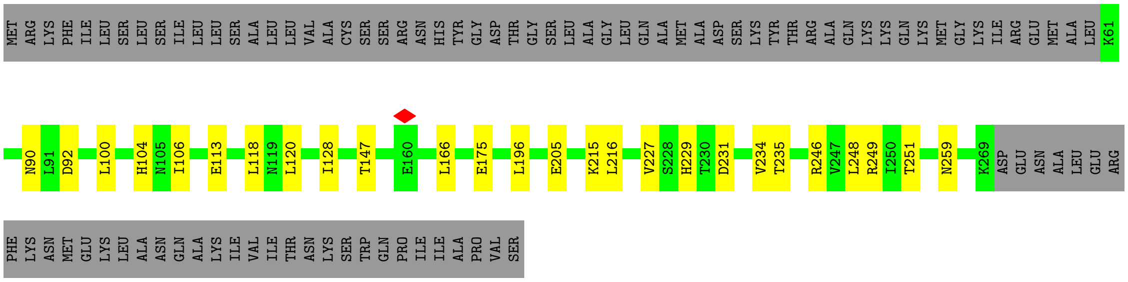
Chain FX:





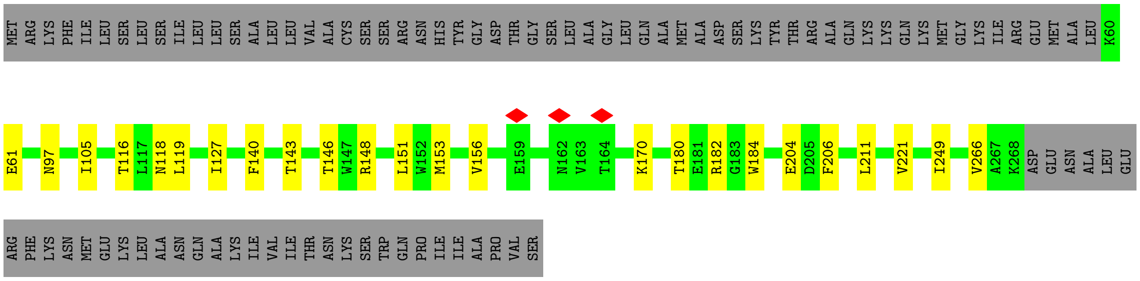
- Molecule 11: DotC

Chain CC:

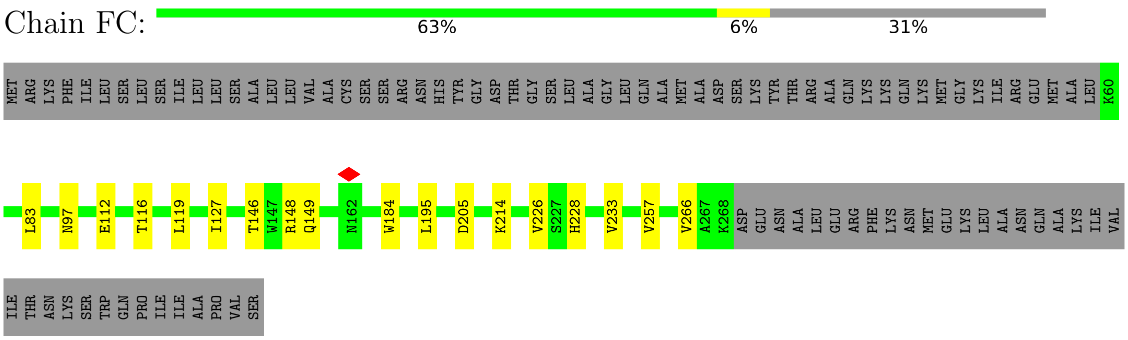


- Molecule 11: DotC

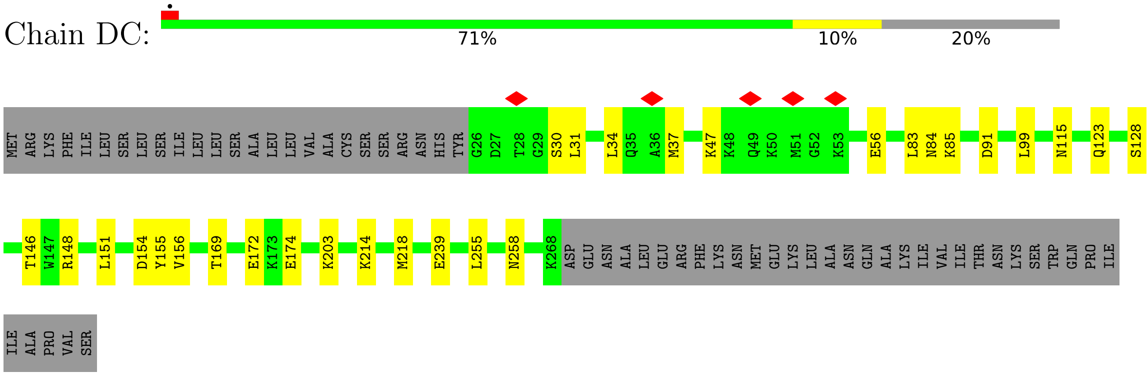
Chain EC:



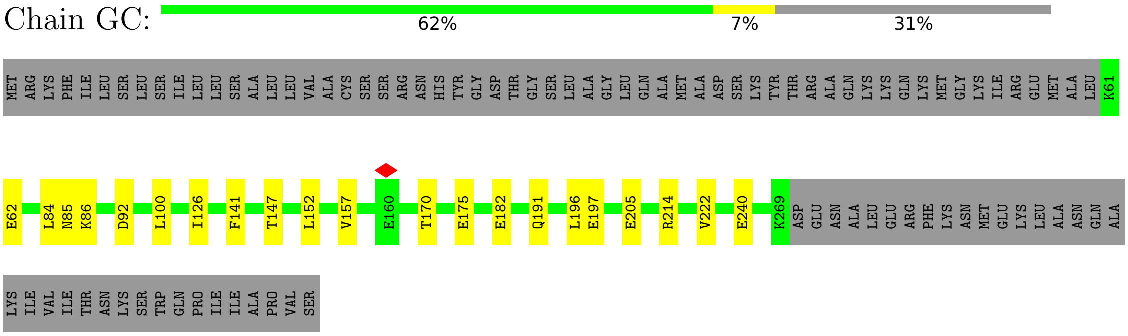
- Molecule 11: DotC



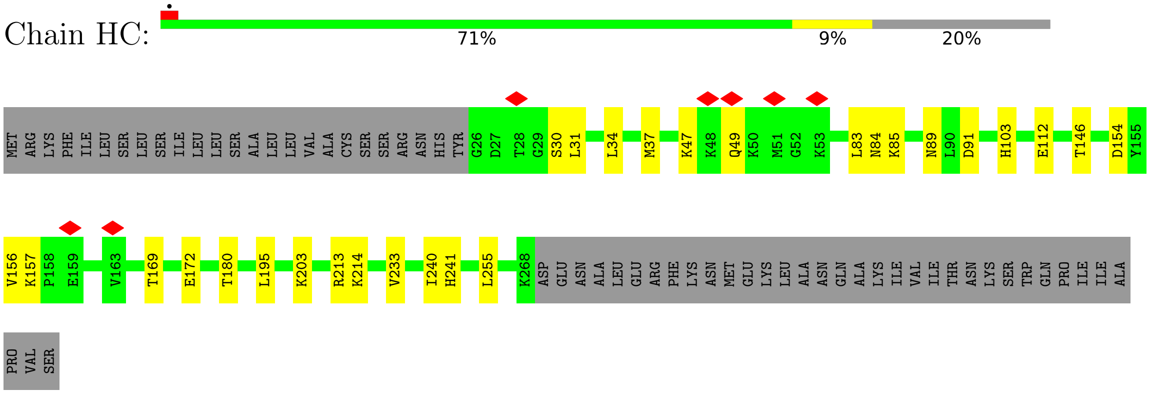
- Molecule 11: DotC



- Molecule 11: DotC

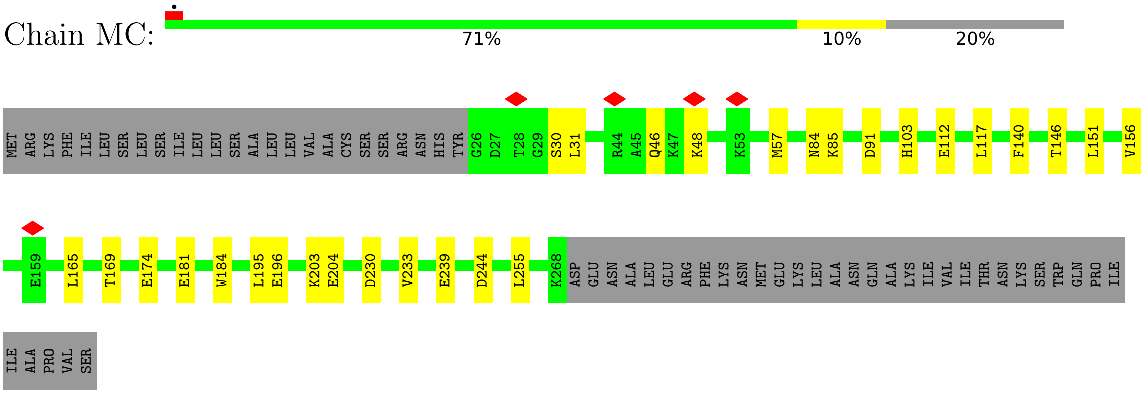


- Molecule 11: DotC



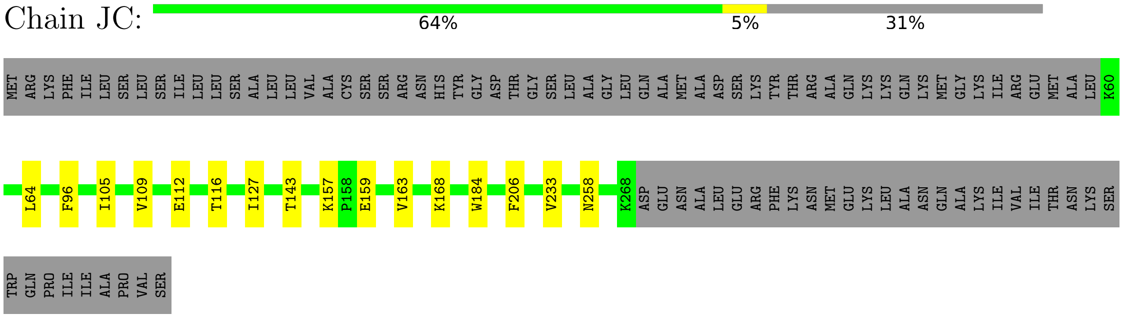
- Molecule 11: DotC

Chain MC:



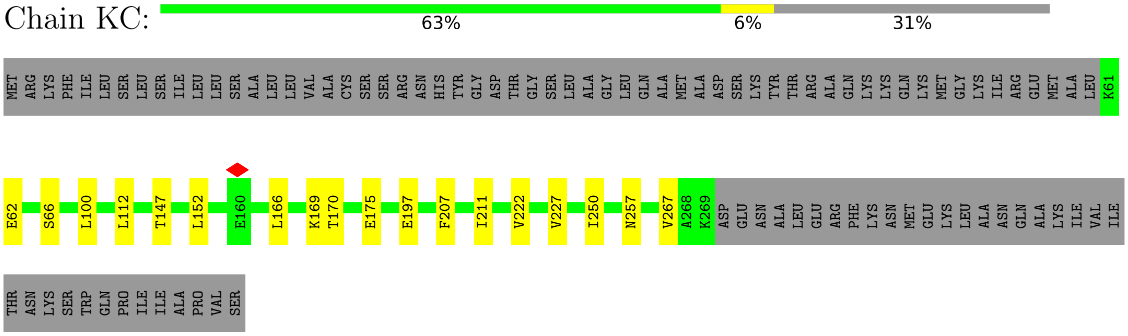
- Molecule 11: DotC

Chain JC:



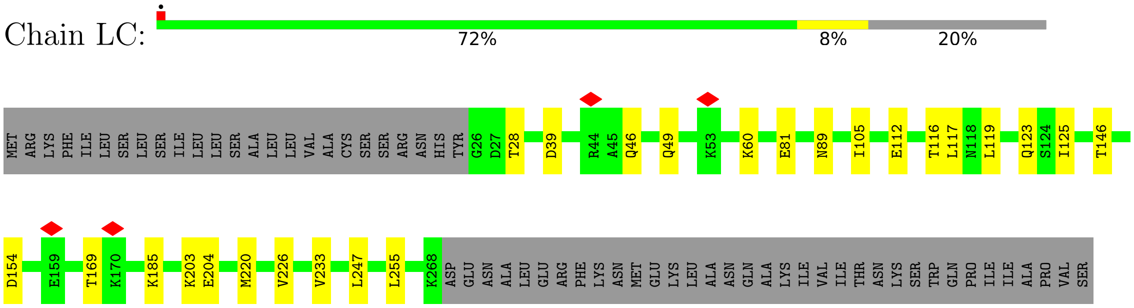
- Molecule 11: DotC

Chain KC:



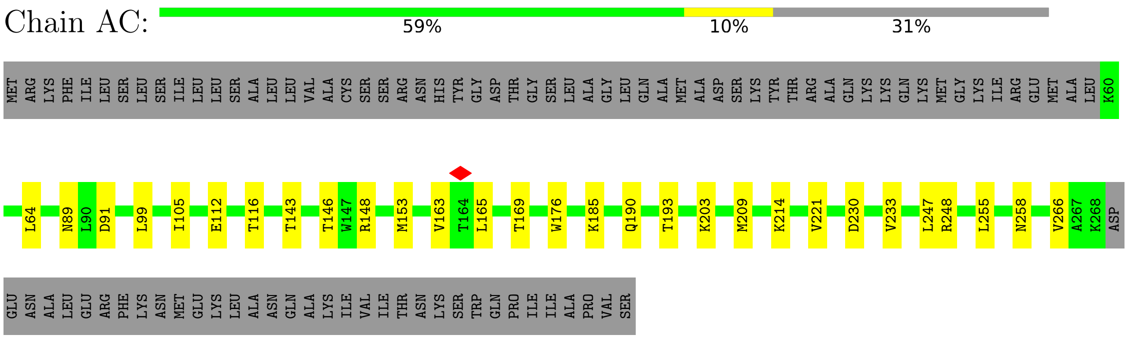
- Molecule 11: DotC

Chain LC:



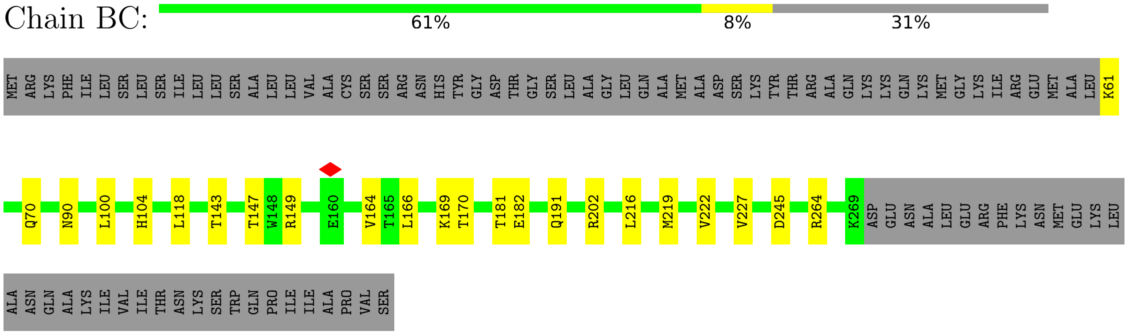
- Molecule 11: DotC

Chain AC:



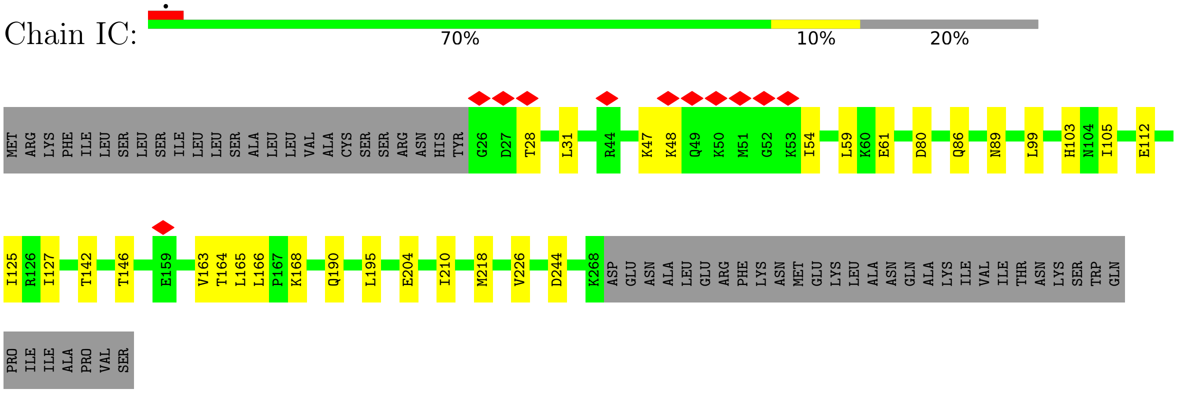
- Molecule 11: DotC

Chain BC:



- Molecule 11: DotC

Chain IC:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75959	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.010	Depositor
Minimum map value	-4.020	Depositor
Average map value	0.091	Depositor
Map value standard deviation	0.547	Depositor
Recommended contour level	2.0	Depositor
Map size (Å)	561.0, 561.0, 561.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.244, 2.244, 2.244	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	AG	0.29	0/1250	0.59	1/1699 (0.1%)
1	Ag	0.26	0/278	0.51	0/377
1	BG	0.30	0/1250	0.60	1/1699 (0.1%)
1	Bg	0.29	0/278	0.49	0/377
1	CG	0.30	0/1250	0.58	1/1699 (0.1%)
1	Cg	0.28	0/278	0.46	0/377
1	DG	0.30	0/1250	0.62	1/1699 (0.1%)
1	Dg	0.27	0/278	0.45	0/377
1	EG	0.29	0/1250	0.57	1/1699 (0.1%)
1	Eg	0.27	0/278	0.48	0/377
1	FG	0.30	0/1250	0.60	1/1699 (0.1%)
1	Fg	0.27	0/278	0.50	0/377
1	GG	0.30	0/1250	0.60	1/1699 (0.1%)
1	Gg	0.29	0/278	0.47	0/377
1	HG	0.29	0/1250	0.59	1/1699 (0.1%)
1	Hg	0.29	0/278	0.50	0/377
1	IG	0.30	0/1250	0.60	1/1699 (0.1%)
1	Ig	0.30	0/278	0.50	0/377
1	JG	0.31	0/1250	0.59	0/1699
1	Jg	0.29	0/278	0.48	0/377
1	KG	0.29	0/1250	0.60	1/1699 (0.1%)
1	Kg	0.28	0/278	0.47	0/377
1	LG	0.30	0/1250	0.59	1/1699 (0.1%)
1	Lg	0.26	0/278	0.47	0/377
1	MG	0.29	0/1250	0.58	0/1699
1	Mg	0.29	0/278	0.49	0/377
1	NG	0.30	0/1250	0.59	0/1699
1	OG	0.29	0/1250	0.60	1/1699 (0.1%)
1	PG	0.30	0/1250	0.59	1/1699 (0.1%)
1	VG	0.31	0/278	0.57	0/377
1	WG	0.28	0/278	0.53	0/377
1	XG	0.28	0/278	0.54	0/377
1	YG	0.29	0/278	0.54	0/377
1	ZG	0.29	0/278	0.55	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	AD	0.33	0/1107	0.53	0/1502
2	Ad	0.32	0/1078	0.51	0/1463
2	BD	0.33	0/1107	0.54	0/1502
2	Bd	0.34	0/1078	0.54	0/1463
2	CD	0.34	0/1107	0.54	0/1502
2	Cd	0.31	0/1078	0.51	0/1463
2	DD	0.33	0/1107	0.55	0/1502
2	Dd	0.31	0/1078	0.50	0/1463
2	ED	0.34	0/1107	0.55	0/1502
2	Ed	0.31	0/1078	0.51	0/1463
2	FD	0.33	0/1107	0.54	0/1502
2	Fd	0.32	0/1078	0.50	0/1463
2	GD	0.33	0/1107	0.56	0/1502
2	Gd	0.32	0/1078	0.54	0/1463
2	HD	0.33	0/1107	0.56	0/1502
2	Hd	0.32	0/1078	0.49	0/1463
2	ID	0.33	0/1107	0.55	0/1502
2	Id	0.31	0/1078	0.50	0/1463
2	JD	0.34	0/1107	0.55	0/1502
2	Jd	0.33	0/1078	0.51	0/1463
2	KD	0.33	0/1107	0.56	0/1502
2	Kd	0.31	0/1078	0.53	0/1463
2	LD	0.34	0/1107	0.55	0/1502
2	Ld	0.34	0/1078	0.52	0/1463
2	MD	0.34	0/1107	0.53	0/1502
2	Md	0.31	0/1078	0.51	0/1463
3	AF	0.27	0/490	0.54	0/660
3	Af	0.29	0/456	0.53	0/615
3	BF	0.28	0/490	0.55	0/660
3	Bf	0.29	0/456	0.53	0/615
3	CF	0.28	0/490	0.55	0/660
3	Cf	0.30	0/456	0.55	0/615
3	DF	0.28	0/490	0.57	0/660
3	Df	0.30	0/456	0.53	0/615
3	EF	0.29	0/490	0.52	0/660
3	Ef	0.29	0/456	0.53	0/615
3	FF	0.28	0/490	0.56	0/660
3	Ff	0.30	0/456	0.52	0/615
3	GF	0.28	0/490	0.57	0/660
3	Gf	0.29	0/456	0.53	0/615
3	HF	0.28	0/490	0.55	0/660
3	Hf	0.28	0/456	0.52	0/615
3	IF	0.29	0/490	0.57	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	If	0.28	0/456	0.53	0/615
3	JF	0.27	0/490	0.56	0/660
3	Jf	0.30	0/456	0.52	0/615
3	KF	0.28	0/490	0.54	0/660
3	Kf	0.29	0/456	0.56	0/615
3	LF	0.28	0/490	0.56	0/660
3	Lf	0.30	0/456	0.53	0/615
3	MF	0.28	0/490	0.58	0/660
3	Mf	0.29	0/456	0.54	0/615
3	VF	0.28	0/490	0.53	0/660
3	WF	0.28	0/490	0.55	0/660
3	XF	0.27	0/490	0.55	0/660
3	YF	0.27	0/490	0.56	0/660
3	ZF	0.28	0/490	0.55	0/660
4	AH	0.32	0/2033	0.56	0/2775
4	BH	0.32	0/2033	0.54	0/2775
4	CH	0.31	0/2033	0.54	0/2775
4	DH	0.31	0/2033	0.52	0/2775
4	EH	0.31	0/2033	0.55	0/2775
4	FH	0.31	0/2033	0.54	0/2775
4	GH	0.32	0/2033	0.56	0/2775
4	HH	0.32	0/2033	0.53	0/2775
4	IH	0.32	0/2033	0.53	0/2775
4	JH	0.32	0/2033	0.53	0/2775
4	KH	0.32	0/2033	0.55	0/2775
4	LH	0.32	0/2033	0.56	0/2775
4	MH	0.31	0/2033	0.56	0/2775
4	VH	0.29	0/1921	0.53	0/2620
4	WH	0.28	0/1921	0.51	0/2620
4	XH	0.29	0/1921	0.54	0/2620
4	YH	0.28	0/1921	0.53	0/2620
4	ZH	0.29	0/1921	0.55	0/2620
5	AK	0.34	0/1195	0.54	0/1616
5	BK	0.35	0/1195	0.55	0/1616
5	CK	0.33	0/1195	0.55	0/1616
5	DK	0.34	0/1195	0.55	0/1616
5	EK	0.34	0/1195	0.54	0/1616
5	FK	0.34	0/1195	0.56	0/1616
5	GK	0.33	0/1195	0.56	0/1616
5	HK	0.34	0/1195	0.55	0/1616
5	IK	0.32	0/1195	0.53	0/1616
5	JK	0.33	0/1195	0.55	0/1616
5	KK	0.34	0/1195	0.54	0/1616

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	LK	0.32	0/1195	0.56	0/1616
5	MK	0.33	0/1195	0.56	0/1616
6	AL	0.32	0/1417	0.57	0/1912
6	BL	0.34	0/1417	0.57	0/1912
6	CL	0.34	0/1417	0.56	0/1912
6	DL	0.33	0/1417	0.56	0/1912
6	EL	0.33	0/1417	0.56	0/1912
6	FL	0.33	0/1417	0.57	0/1912
6	GL	0.33	0/1417	0.56	0/1912
6	HL	0.33	0/1417	0.57	0/1912
6	IL	0.33	0/1417	0.58	0/1912
6	JL	0.33	0/1417	0.60	0/1912
6	KL	0.33	0/1417	0.57	0/1912
6	LL	0.33	0/1417	0.57	0/1912
6	ML	0.35	0/1417	0.56	0/1912
7	AM	0.31	0/1678	0.58	0/2262
7	BM	0.31	0/1678	0.61	0/2262
7	CM	0.31	0/1678	0.60	0/2262
7	DM	0.32	0/1678	0.59	0/2262
7	EM	0.31	0/1678	0.59	0/2262
7	FM	0.31	0/1678	0.59	0/2262
7	GM	0.32	0/1678	0.58	0/2262
7	HM	0.31	0/1678	0.56	0/2262
7	IM	0.30	0/1678	0.57	0/2262
7	JM	0.32	0/1678	0.60	0/2262
7	KM	0.32	0/1678	0.58	0/2262
7	LM	0.31	0/1678	0.57	0/2262
7	MM	0.31	0/1678	0.59	0/2262
8	AN	0.34	0/593	0.55	0/799
8	BN	0.36	0/593	0.54	0/799
8	CN	0.35	0/593	0.55	0/799
8	DN	0.37	0/593	0.56	0/799
8	EN	0.35	0/593	0.52	0/799
8	FN	0.34	0/593	0.55	0/799
8	GN	0.36	0/593	0.52	0/799
8	HN	0.37	0/593	0.52	0/799
8	IN	0.35	0/593	0.53	0/799
8	JN	0.35	0/593	0.54	0/799
8	KN	0.36	0/593	0.54	0/799
8	LN	0.36	0/593	0.53	0/799
8	MN	0.32	0/593	0.52	0/799
11	AC	0.34	0/1702	0.55	0/2315
11	BC	0.33	0/1702	0.53	0/2315

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
11	CC	0.34	0/1702	0.53	0/2315
11	DC	0.33	0/1957	0.53	0/2651
11	EC	0.33	0/1702	0.53	0/2315
11	FC	0.34	0/1702	0.52	0/2315
11	GC	0.33	0/1702	0.53	0/2315
11	HC	0.33	0/1957	0.52	0/2651
11	IC	0.31	0/1957	0.54	0/2651
11	JC	0.35	0/1702	0.54	0/2315
11	KC	0.34	0/1702	0.54	0/2315
11	LC	0.34	0/1957	0.53	0/2651
11	MC	0.33	0/1957	0.53	0/2651
All	All	0.32	0/191071	0.55	13/258997 (0.0%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KG	1040	LEU	CA-CB-CG	6.51	130.27	115.30
1	IG	1040	LEU	CA-CB-CG	5.88	128.83	115.30
1	FG	1040	LEU	CA-CB-CG	5.83	128.71	115.30
1	GG	1040	LEU	CA-CB-CG	5.81	128.67	115.30
1	BG	1040	LEU	CA-CB-CG	5.73	128.49	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	AG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Ag	32/1048 (3%)	32 (100%)	0	0	100	100
1	BG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	CG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Cg	32/1048 (3%)	32 (100%)	0	0	100	100
1	DG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Dg	32/1048 (3%)	32 (100%)	0	0	100	100
1	EG	161/1048 (15%)	157 (98%)	4 (2%)	0	100	100
1	Eg	32/1048 (3%)	32 (100%)	0	0	100	100
1	FG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Gg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	HG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Hg	32/1048 (3%)	29 (91%)	3 (9%)	0	100	100
1	IG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Ig	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	JG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Jg	32/1048 (3%)	32 (100%)	0	0	100	100
1	KG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Kg	32/1048 (3%)	32 (100%)	0	0	100	100
1	LG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Lg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	MG	161/1048 (15%)	158 (98%)	3 (2%)	0	100	100
1	Mg	32/1048 (3%)	32 (100%)	0	0	100	100
1	NG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	OG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	PG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	VG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	WG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	XG	32/1048 (3%)	32 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	YG	32/1048 (3%)	32 (100%)	0	0	100	100
1	ZG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
2	AD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Ad	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	BD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Bd	135/163 (83%)	132 (98%)	3 (2%)	0	100	100
2	CD	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
2	Cd	135/163 (83%)	132 (98%)	3 (2%)	0	100	100
2	DD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Dd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ED	138/163 (85%)	135 (98%)	3 (2%)	0	100	100
2	Ed	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
2	FD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Fd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	GD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Gd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
2	HD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Hd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	ID	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
2	Id	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	JD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Jd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	KD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Kd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
2	LD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Ld	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	MD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Md	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
3	AF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Af	57/269 (21%)	56 (98%)	1 (2%)	0	100	100
3	BF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Bf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	CF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Cf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
3	DF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Df	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	EF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Ef	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	FF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Ff	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	GF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Gf	57/269 (21%)	50 (88%)	7 (12%)	0	100	100
3	HF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Hf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	IF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	JF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Jf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	KF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Kf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	LF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Lf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	MF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Mf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	VF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	WF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	XF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	YF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	ZF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
4	AH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
4	BH	256/361 (71%)	243 (95%)	13 (5%)	0	100	100
4	CH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	DH	256/361 (71%)	237 (93%)	19 (7%)	0	100	100
4	EH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
4	FH	256/361 (71%)	248 (97%)	8 (3%)	0	100	100
4	GH	256/361 (71%)	237 (93%)	19 (7%)	0	100	100
4	HH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
4	IH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	JH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	KH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	LH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	MH	256/361 (71%)	235 (92%)	21 (8%)	0	100	100
4	VH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	WH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
4	XH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	YH	239/361 (66%)	222 (93%)	17 (7%)	0	100	100
4	ZH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	AK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	BK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	CK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	DK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	EK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	FK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	GK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	HK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	IK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	JK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	KK	149/189 (79%)	137 (92%)	12 (8%)	0	100	100
5	LK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	MK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
6	AL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	BL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	CL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	DL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	EL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	FL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	GL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	HL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	IL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	JL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	KL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	LL	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
6	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	AM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
7	BM	206/320 (64%)	183 (89%)	23 (11%)	0	100	100
7	CM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
7	DM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
7	EM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	FM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	GM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	HM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	JM	206/320 (64%)	183 (89%)	23 (11%)	0	100	100
7	KM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	LM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	MM	206/320 (64%)	181 (88%)	25 (12%)	0	100	100
8	AN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
8	BN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
8	CN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
8	DN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	EN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
8	FN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
8	GN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	HN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	IN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	JN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
8	KN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
8	LN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	MN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
11	AC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
11	BC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
11	CC	207/303 (68%)	197 (95%)	10 (5%)	0	100	100
11	DC	241/303 (80%)	225 (93%)	16 (7%)	0	100	100
11	EC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	FC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
11	GC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
11	HC	241/303 (80%)	227 (94%)	14 (6%)	0	100	100
11	IC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	JC	207/303 (68%)	196 (95%)	11 (5%)	0	100	100
11	KC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
11	LC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	MC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
All	All	23724/70112 (34%)	22355 (94%)	1369 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	AG	135/765 (18%)	113 (84%)	22 (16%)	2	14
1	Ag	31/765 (4%)	26 (84%)	5 (16%)	2	15
1	BG	135/765 (18%)	117 (87%)	18 (13%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Bg	31/765 (4%)	25 (81%)	6 (19%)	1 9
1	CG	135/765 (18%)	118 (87%)	17 (13%)	4 21
1	Cg	31/765 (4%)	26 (84%)	5 (16%)	2 15
1	DG	135/765 (18%)	115 (85%)	20 (15%)	3 17
1	Dg	31/765 (4%)	21 (68%)	10 (32%)	0 2
1	EG	135/765 (18%)	114 (84%)	21 (16%)	2 16
1	Eg	31/765 (4%)	27 (87%)	4 (13%)	4 20
1	FG	135/765 (18%)	114 (84%)	21 (16%)	2 16
1	Fg	31/765 (4%)	27 (87%)	4 (13%)	4 20
1	GG	135/765 (18%)	112 (83%)	23 (17%)	2 13
1	Gg	31/765 (4%)	29 (94%)	2 (6%)	17 44
1	HG	135/765 (18%)	114 (84%)	21 (16%)	2 16
1	Hg	31/765 (4%)	29 (94%)	2 (6%)	17 44
1	IG	135/765 (18%)	115 (85%)	20 (15%)	3 17
1	Ig	31/765 (4%)	23 (74%)	8 (26%)	0 4
1	JG	135/765 (18%)	118 (87%)	17 (13%)	4 21
1	Jg	31/765 (4%)	23 (74%)	8 (26%)	0 4
1	KG	135/765 (18%)	116 (86%)	19 (14%)	3 18
1	Kg	31/765 (4%)	26 (84%)	5 (16%)	2 15
1	LG	135/765 (18%)	113 (84%)	22 (16%)	2 14
1	Lg	31/765 (4%)	25 (81%)	6 (19%)	1 9
1	MG	135/765 (18%)	121 (90%)	14 (10%)	7 27
1	Mg	31/765 (4%)	24 (77%)	7 (23%)	1 6
1	NG	135/765 (18%)	114 (84%)	21 (16%)	2 16
1	OG	135/765 (18%)	113 (84%)	22 (16%)	2 14
1	PG	135/765 (18%)	118 (87%)	17 (13%)	4 21
1	VG	31/765 (4%)	27 (87%)	4 (13%)	4 20
1	WG	31/765 (4%)	27 (87%)	4 (13%)	4 20
1	XG	31/765 (4%)	25 (81%)	6 (19%)	1 9
1	YG	31/765 (4%)	27 (87%)	4 (13%)	4 20
1	ZG	31/765 (4%)	25 (81%)	6 (19%)	1 9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AD	121/139 (87%)	104 (86%)	17 (14%)	3	19
2	Ad	118/139 (85%)	101 (86%)	17 (14%)	3	18
2	BD	121/139 (87%)	106 (88%)	15 (12%)	4	21
2	Bd	118/139 (85%)	108 (92%)	10 (8%)	10	36
2	CD	121/139 (87%)	102 (84%)	19 (16%)	2	15
2	Cd	118/139 (85%)	107 (91%)	11 (9%)	9	30
2	DD	121/139 (87%)	111 (92%)	10 (8%)	11	36
2	Dd	118/139 (85%)	106 (90%)	12 (10%)	7	27
2	ED	121/139 (87%)	108 (89%)	13 (11%)	6	26
2	Ed	118/139 (85%)	106 (90%)	12 (10%)	7	27
2	FD	121/139 (87%)	107 (88%)	14 (12%)	5	23
2	Fd	118/139 (85%)	103 (87%)	15 (13%)	4	21
2	GD	121/139 (87%)	106 (88%)	15 (12%)	4	21
2	Gd	118/139 (85%)	105 (89%)	13 (11%)	6	25
2	HD	121/139 (87%)	109 (90%)	12 (10%)	8	28
2	Hd	118/139 (85%)	104 (88%)	14 (12%)	5	22
2	ID	121/139 (87%)	105 (87%)	16 (13%)	4	20
2	Id	118/139 (85%)	101 (86%)	17 (14%)	3	18
2	JD	121/139 (87%)	107 (88%)	14 (12%)	5	23
2	Jd	118/139 (85%)	101 (86%)	17 (14%)	3	18
2	KD	121/139 (87%)	114 (94%)	7 (6%)	20	47
2	Kd	118/139 (85%)	105 (89%)	13 (11%)	6	25
2	LD	121/139 (87%)	105 (87%)	16 (13%)	4	20
2	Ld	118/139 (85%)	105 (89%)	13 (11%)	6	25
2	MD	121/139 (87%)	106 (88%)	15 (12%)	4	21
2	Md	118/139 (85%)	107 (91%)	11 (9%)	9	30
3	AF	53/237 (22%)	48 (91%)	5 (9%)	8	30
3	Af	49/237 (21%)	43 (88%)	6 (12%)	5	22
3	BF	53/237 (22%)	47 (89%)	6 (11%)	6	24
3	Bf	49/237 (21%)	42 (86%)	7 (14%)	3	18
3	CF	53/237 (22%)	48 (91%)	5 (9%)	8	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Cf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	DF	53/237 (22%)	49 (92%)	4 (8%)	13	40
3	Df	49/237 (21%)	44 (90%)	5 (10%)	7	27
3	EF	53/237 (22%)	49 (92%)	4 (8%)	13	40
3	Ef	49/237 (21%)	45 (92%)	4 (8%)	11	36
3	FF	53/237 (22%)	44 (83%)	9 (17%)	2	13
3	Ff	49/237 (21%)	45 (92%)	4 (8%)	11	36
3	GF	53/237 (22%)	49 (92%)	4 (8%)	13	40
3	Gf	49/237 (21%)	46 (94%)	3 (6%)	18	46
3	HF	53/237 (22%)	46 (87%)	7 (13%)	4	20
3	Hf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	IF	53/237 (22%)	47 (89%)	6 (11%)	6	24
3	If	49/237 (21%)	42 (86%)	7 (14%)	3	18
3	JF	53/237 (22%)	51 (96%)	2 (4%)	33	58
3	Jf	49/237 (21%)	44 (90%)	5 (10%)	7	27
3	KF	53/237 (22%)	45 (85%)	8 (15%)	3	16
3	Kf	49/237 (21%)	44 (90%)	5 (10%)	7	27
3	LF	53/237 (22%)	47 (89%)	6 (11%)	6	24
3	Lf	49/237 (21%)	43 (88%)	6 (12%)	5	22
3	MF	53/237 (22%)	48 (91%)	5 (9%)	8	30
3	Mf	49/237 (21%)	44 (90%)	5 (10%)	7	27
3	VF	53/237 (22%)	45 (85%)	8 (15%)	3	16
3	WF	53/237 (22%)	51 (96%)	2 (4%)	33	58
3	XF	53/237 (22%)	51 (96%)	2 (4%)	33	58
3	YF	53/237 (22%)	49 (92%)	4 (8%)	13	40
3	ZF	53/237 (22%)	47 (89%)	6 (11%)	6	24
4	AH	220/300 (73%)	200 (91%)	20 (9%)	9	31
4	BH	220/300 (73%)	201 (91%)	19 (9%)	10	35
4	CH	220/300 (73%)	196 (89%)	24 (11%)	6	25
4	DH	220/300 (73%)	199 (90%)	21 (10%)	8	29
4	EH	220/300 (73%)	193 (88%)	27 (12%)	4	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	FH	220/300 (73%)	194 (88%)	26 (12%)	5	23
4	GH	220/300 (73%)	191 (87%)	29 (13%)	4	20
4	HH	220/300 (73%)	198 (90%)	22 (10%)	7	28
4	IH	220/300 (73%)	187 (85%)	33 (15%)	3	16
4	JH	220/300 (73%)	196 (89%)	24 (11%)	6	25
4	KH	220/300 (73%)	191 (87%)	29 (13%)	4	20
4	LH	220/300 (73%)	195 (89%)	25 (11%)	5	24
4	MH	220/300 (73%)	194 (88%)	26 (12%)	5	23
4	VH	207/300 (69%)	183 (88%)	24 (12%)	5	23
4	WH	207/300 (69%)	183 (88%)	24 (12%)	5	23
4	XH	207/300 (69%)	176 (85%)	31 (15%)	3	16
4	YH	207/300 (69%)	177 (86%)	30 (14%)	3	17
4	ZH	207/300 (69%)	190 (92%)	17 (8%)	11	36
5	AK	129/163 (79%)	110 (85%)	19 (15%)	3	17
5	BK	129/163 (79%)	111 (86%)	18 (14%)	3	19
5	CK	129/163 (79%)	110 (85%)	19 (15%)	3	17
5	DK	129/163 (79%)	114 (88%)	15 (12%)	5	23
5	EK	129/163 (79%)	116 (90%)	13 (10%)	7	27
5	FK	129/163 (79%)	115 (89%)	14 (11%)	6	25
5	GK	129/163 (79%)	113 (88%)	16 (12%)	4	21
5	HK	129/163 (79%)	112 (87%)	17 (13%)	4	20
5	IK	129/163 (79%)	114 (88%)	15 (12%)	5	23
5	JK	129/163 (79%)	114 (88%)	15 (12%)	5	23
5	KK	129/163 (79%)	114 (88%)	15 (12%)	5	23
5	LK	129/163 (79%)	111 (86%)	18 (14%)	3	19
5	MK	129/163 (79%)	117 (91%)	12 (9%)	9	30
6	AL	148/203 (73%)	136 (92%)	12 (8%)	11	37
6	BL	148/203 (73%)	131 (88%)	17 (12%)	5	23
6	CL	148/203 (73%)	127 (86%)	21 (14%)	3	18
6	DL	148/203 (73%)	133 (90%)	15 (10%)	7	27
6	EL	148/203 (73%)	127 (86%)	21 (14%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	FL	148/203 (73%)	137 (93%)	11 (7%)	13	40
6	GL	148/203 (73%)	132 (89%)	16 (11%)	6	26
6	HL	148/203 (73%)	135 (91%)	13 (9%)	10	33
6	IL	148/203 (73%)	135 (91%)	13 (9%)	10	33
6	JL	148/203 (73%)	132 (89%)	16 (11%)	6	26
6	KL	148/203 (73%)	134 (90%)	14 (10%)	8	29
6	LL	148/203 (73%)	128 (86%)	20 (14%)	4	19
6	ML	148/203 (73%)	132 (89%)	16 (11%)	6	26
7	AM	175/276 (63%)	148 (85%)	27 (15%)	2	16
7	BM	175/276 (63%)	153 (87%)	22 (13%)	4	21
7	CM	175/276 (63%)	154 (88%)	21 (12%)	5	22
7	DM	175/276 (63%)	149 (85%)	26 (15%)	3	16
7	EM	175/276 (63%)	153 (87%)	22 (13%)	4	21
7	FM	175/276 (63%)	152 (87%)	23 (13%)	4	20
7	GM	175/276 (63%)	149 (85%)	26 (15%)	3	16
7	HM	175/276 (63%)	154 (88%)	21 (12%)	5	22
7	IM	175/276 (63%)	151 (86%)	24 (14%)	3	19
7	JM	175/276 (63%)	143 (82%)	32 (18%)	1	11
7	KM	175/276 (63%)	154 (88%)	21 (12%)	5	22
7	LM	175/276 (63%)	151 (86%)	24 (14%)	3	19
7	MM	175/276 (63%)	152 (87%)	23 (13%)	4	20
8	AN	66/107 (62%)	58 (88%)	8 (12%)	5	22
8	BN	66/107 (62%)	60 (91%)	6 (9%)	9	31
8	CN	66/107 (62%)	57 (86%)	9 (14%)	3	19
8	DN	66/107 (62%)	62 (94%)	4 (6%)	18	46
8	EN	66/107 (62%)	57 (86%)	9 (14%)	3	19
8	FN	66/107 (62%)	55 (83%)	11 (17%)	2	14
8	GN	66/107 (62%)	59 (89%)	7 (11%)	6	26
8	HN	66/107 (62%)	57 (86%)	9 (14%)	3	19
8	IN	66/107 (62%)	55 (83%)	11 (17%)	2	14
8	JN	66/107 (62%)	59 (89%)	7 (11%)	6	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	KN	66/107 (62%)	53 (80%)	13 (20%)	1	9
8	LN	66/107 (62%)	53 (80%)	13 (20%)	1	9
8	MN	66/107 (62%)	54 (82%)	12 (18%)	1	11
11	AC	178/257 (69%)	149 (84%)	29 (16%)	2	14
11	BC	178/257 (69%)	155 (87%)	23 (13%)	4	20
11	CC	178/257 (69%)	152 (85%)	26 (15%)	3	17
11	DC	203/257 (79%)	174 (86%)	29 (14%)	3	18
11	EC	178/257 (69%)	154 (86%)	24 (14%)	4	19
11	FC	178/257 (69%)	160 (90%)	18 (10%)	7	27
11	GC	178/257 (69%)	157 (88%)	21 (12%)	5	23
11	HC	203/257 (79%)	175 (86%)	28 (14%)	3	19
11	IC	203/257 (79%)	173 (85%)	30 (15%)	3	17
11	JC	178/257 (69%)	162 (91%)	16 (9%)	9	32
11	KC	178/257 (69%)	160 (90%)	18 (10%)	7	27
11	LC	203/257 (79%)	178 (88%)	25 (12%)	4	22
11	MC	203/257 (79%)	174 (86%)	29 (14%)	3	18
All	All	20484/55449 (37%)	17938 (88%)	2546 (12%)	8	21

5 of 2546 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	CL	57	VAL
1	KG	873	LEU
2	Cd	115	VAL
6	CL	47	TYR
5	EK	114	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
8	AN	61	ASN
1	KG	1017	GLN
11	GC	193	ASN
1	JG	1017	GLN
8	FN	115	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	IX	1
10	GX	1
10	AX	1
10	ZX	1
10	CX	1
10	WX	1
10	YX	1
10	EX	1
10	MX	1
10	HX	1
10	LX	1
10	VX	1
10	BX	1
10	KX	1
10	JX	1
10	FX	1

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Mol	Chain	Number of breaks
10	DX	1
10	XX	1

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	IX	38:UNK	C	70:UNK	N	26.35
1	GX	38:UNK	C	70:UNK	N	25.37
1	AX	38:UNK	C	70:UNK	N	25.35
1	ZX	38:UNK	C	70:UNK	N	24.93
1	CX	38:UNK	C	70:UNK	N	24.93

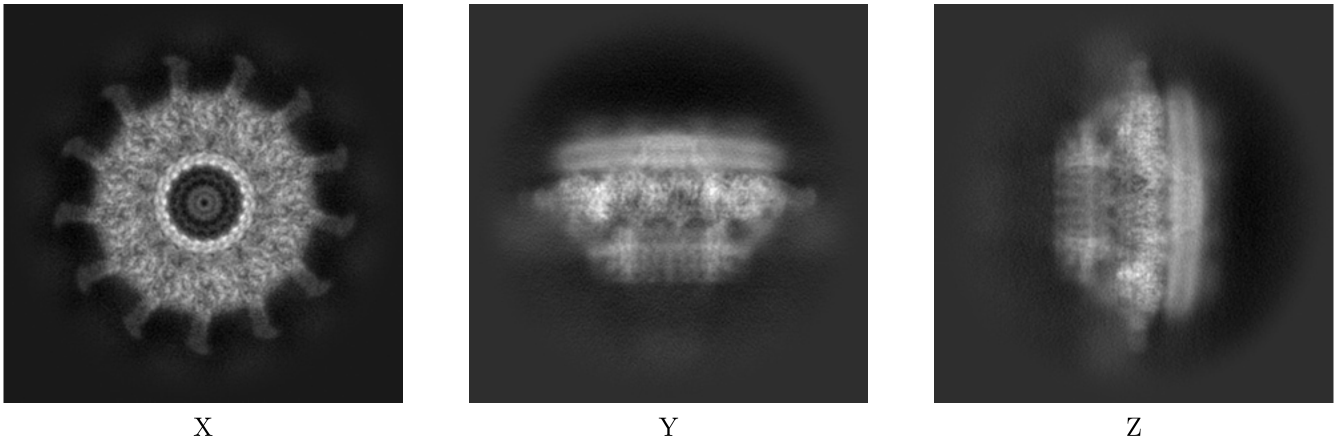
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24020. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

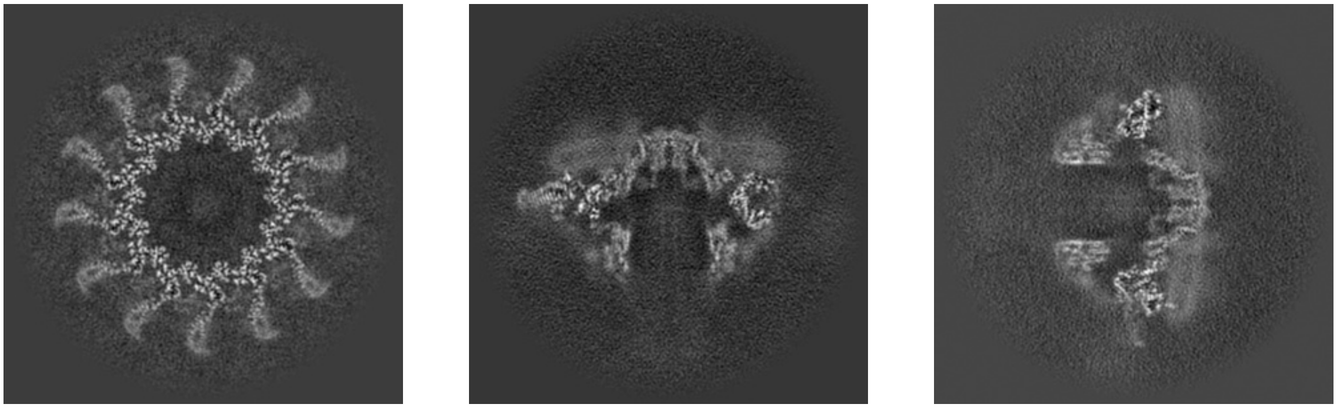
6.1.1 Primary map



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

6.2 Central slices

6.2.1 Primary map

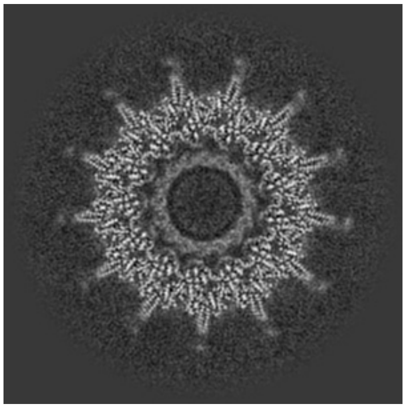


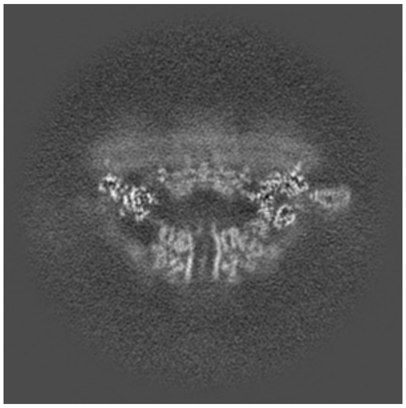
X Index: 125 Y Index: 125 Z Index: 125

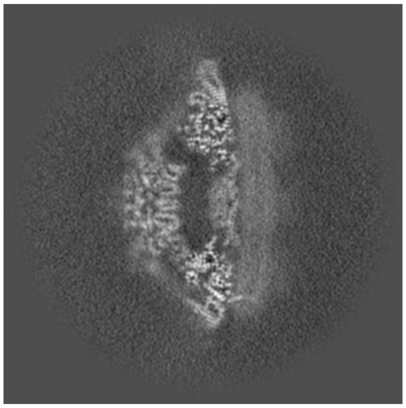
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

6.3.1 Primary map


X Index: 134


Y Index: 149

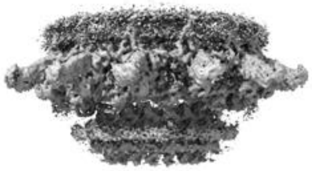

Z Index: 152

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

6.4 Orthogonal surface views

6.4.1 Primary map


X


Y


Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

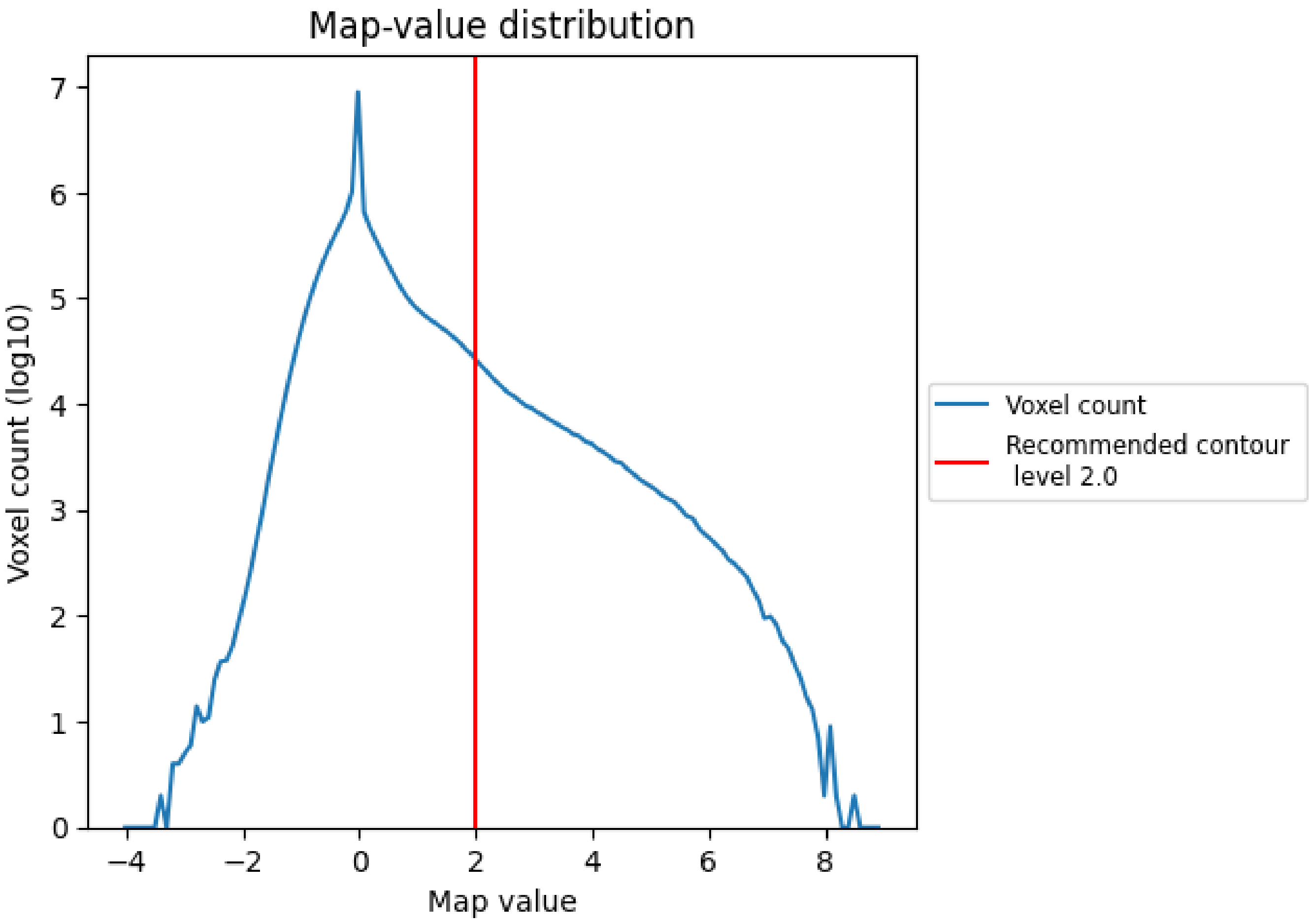
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

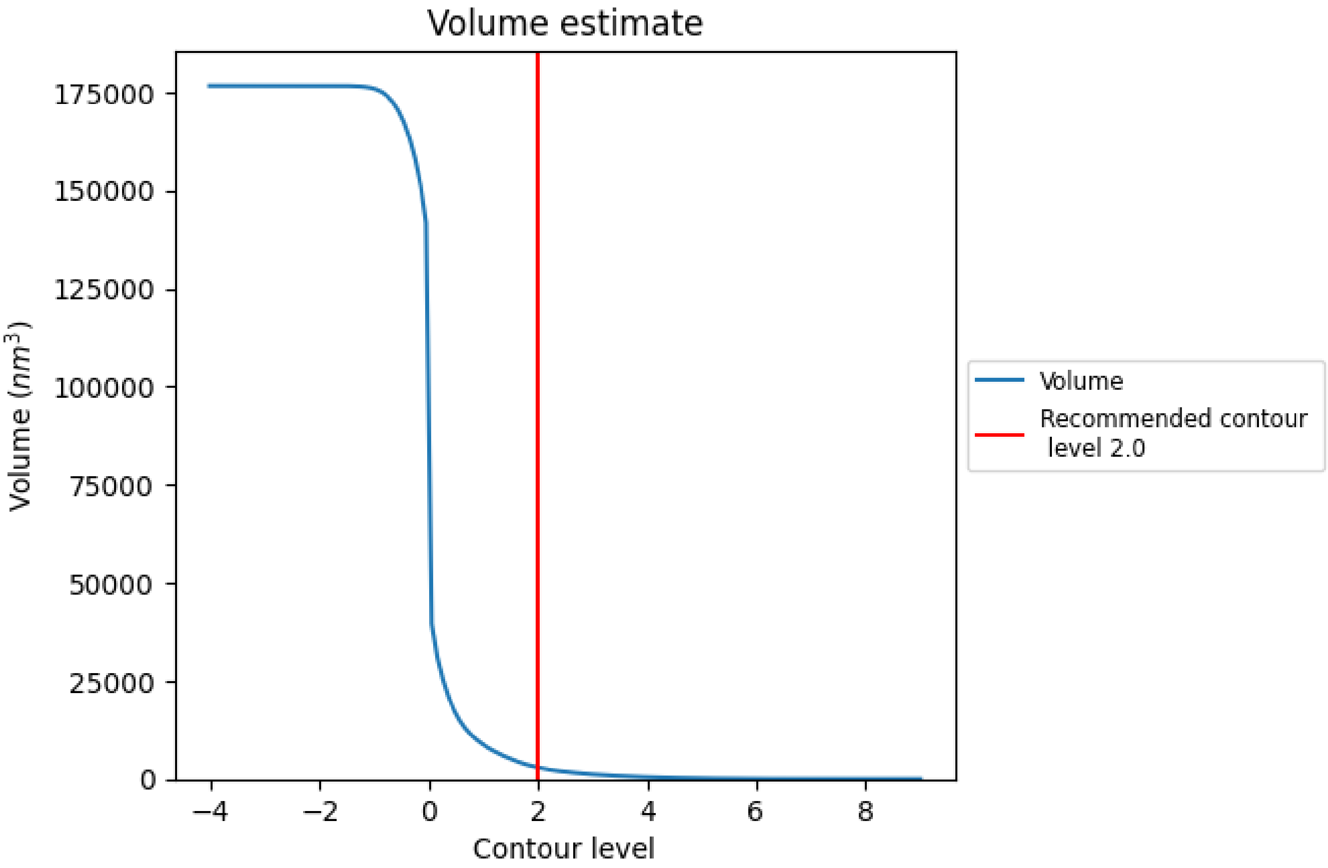
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

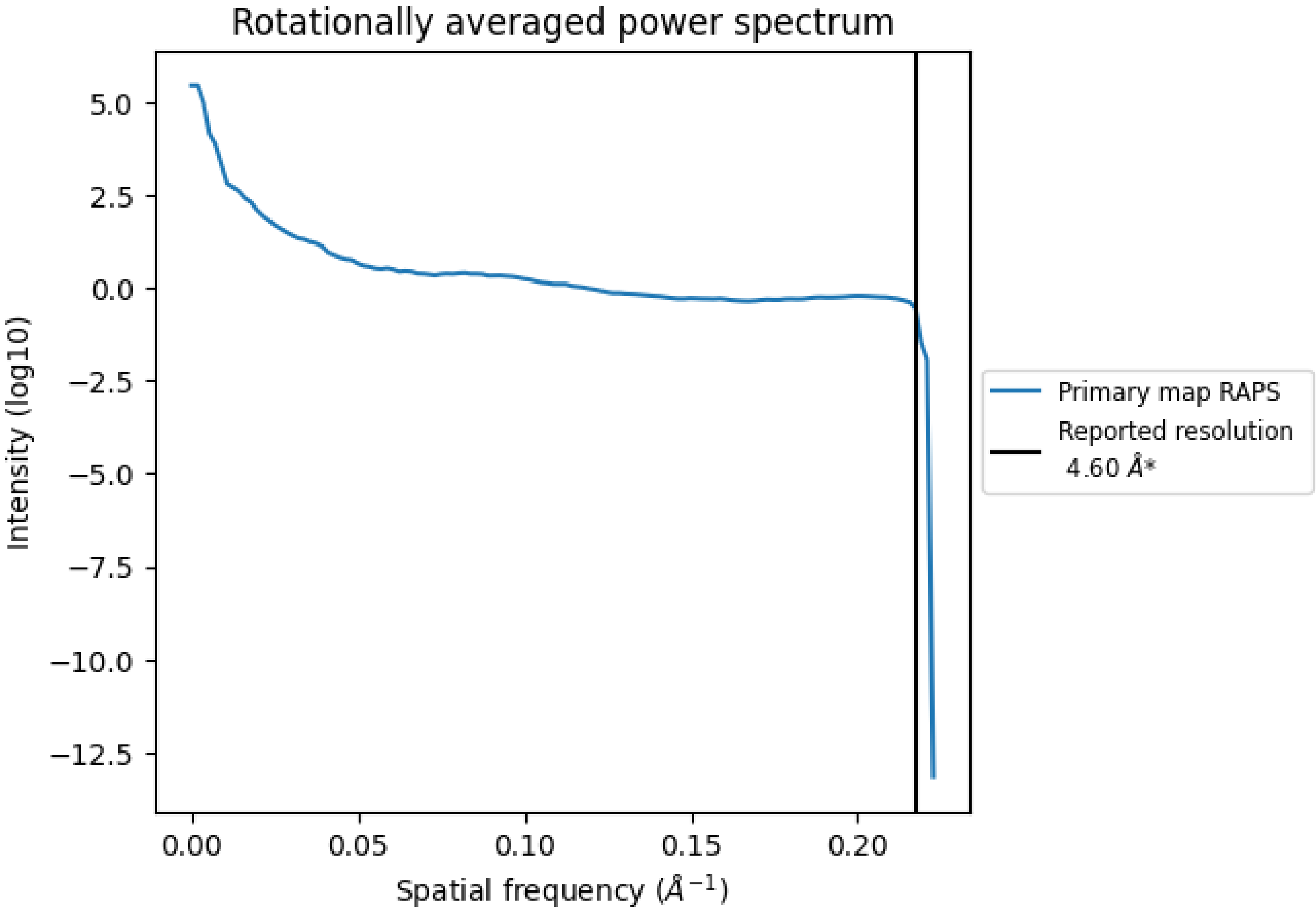
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 2956 nm^3; this corresponds to an approximate mass of 2670 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 0.217 Å^{-1}

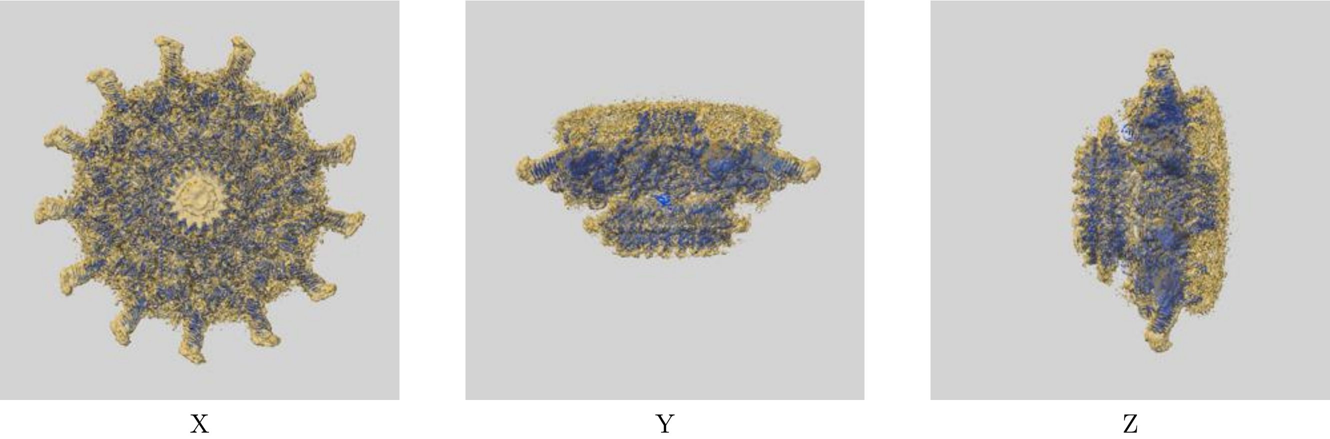
8 Fourier-Shell correlation (i)

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

9 Map-model fit ⓘ

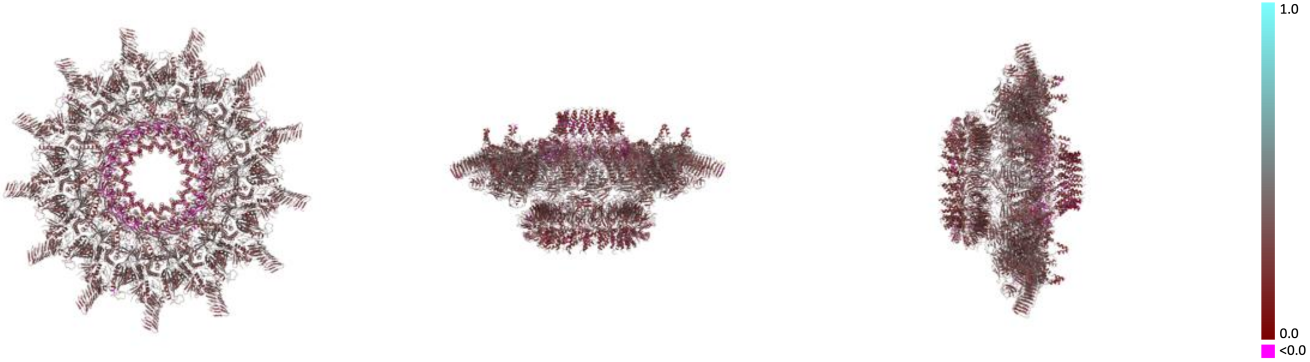
This section contains information regarding the fit between EMDB map EMD-24020 and PDB model 7MUS. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay ⓘ



The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

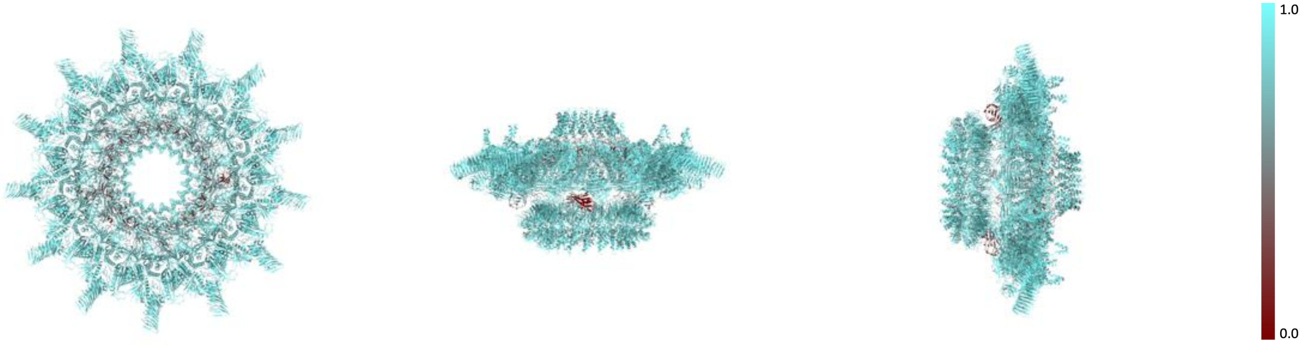
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

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.

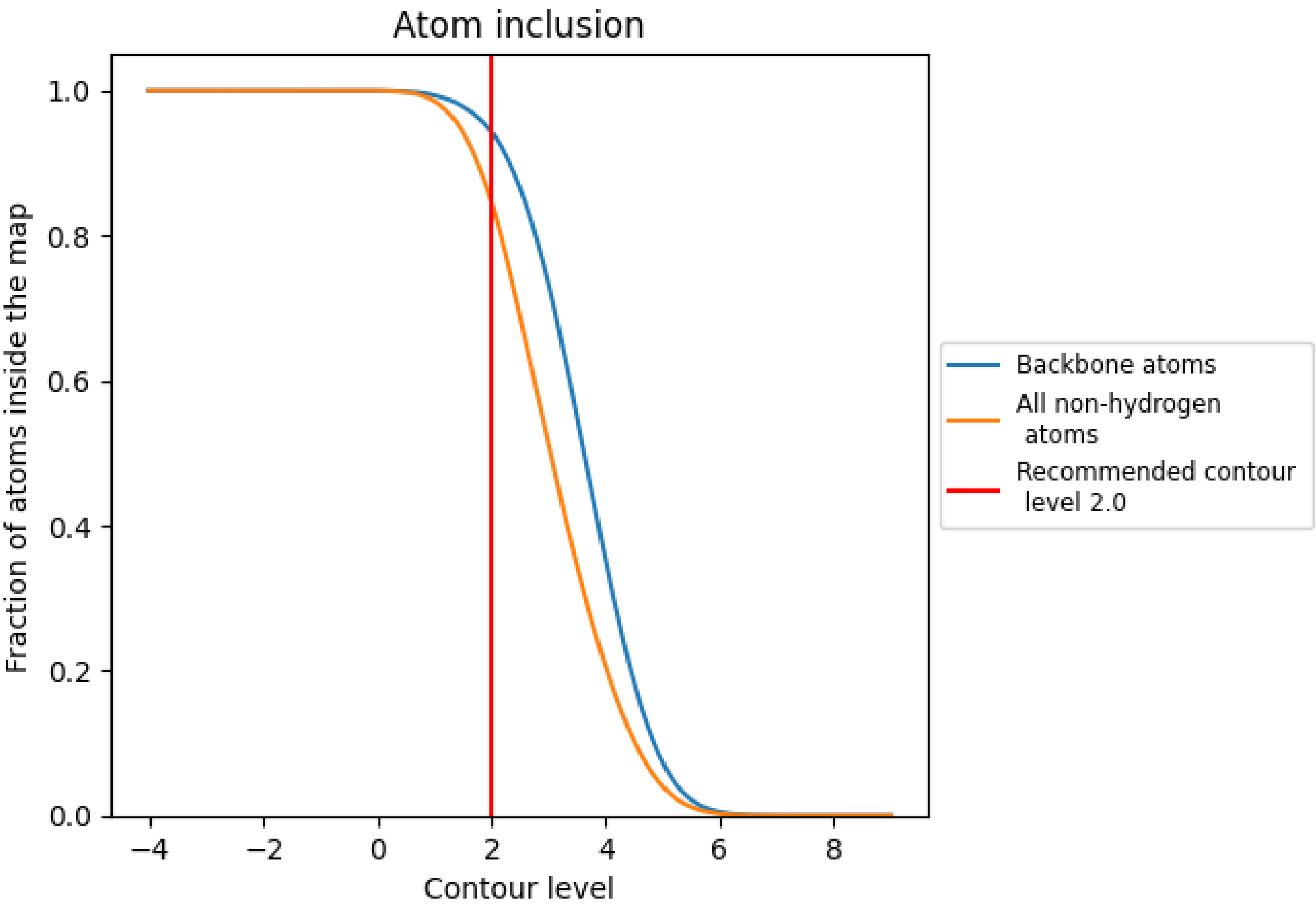
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

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 (2.0).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 85% 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 (2.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8461	0.3050
AC	0.8871	0.3340
AD	0.8839	0.3450
AF	0.8854	0.2740
AG	0.6667	0.1580
AH	0.8727	0.3080
AK	0.8898	0.3440
AL	0.8925	0.3310
AM	0.8963	0.3180
AN	0.8776	0.3560
AU	1.0000	0.4820
AX	0.7458	0.2770
Ad	0.8809	0.3330
Af	0.9157	0.3180
Ag	0.9044	0.2670
BC	0.8773	0.3380
BD	0.8727	0.3400
BF	0.8514	0.2650
BG	0.6675	0.1480
BH	0.8686	0.3090
BK	0.8845	0.3480
BL	0.8962	0.3300
BM	0.8783	0.3330
BN	0.8934	0.3620
BU	1.0000	0.5020
BX	0.7708	0.2630
Bd	0.8876	0.3350
Bf	0.8474	0.3060
Bg	0.9118	0.2750
CC	0.8742	0.3420
CD	0.8933	0.3380
CF	0.8577	0.2620
CG	0.6585	0.1580
CH	0.8701	0.3140
CK	0.8933	0.3450

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Chain	Atom inclusion	Q-score
CL	0.8933	0.3230
CM	0.8845	0.3280
CN	0.8741	0.3690
CU	1.0000	0.4640
CX	0.9083	0.3150
Cd	0.8895	0.3380
Cf	0.9089	0.3330
Cg	0.9007	0.2640
DC	0.8526	0.3270
DD	0.8764	0.3520
DF	0.9087	0.2730
DG	0.6478	0.1630
DH	0.8686	0.3050
DK	0.8976	0.3500
DL	0.8925	0.3280
DM	0.9056	0.3280
DN	0.8654	0.3550
DU	1.0000	0.4930
DX	0.8208	0.2710
Dd	0.8847	0.3290
Df	0.8975	0.3220
Dg	0.9338	0.2730
EC	0.8675	0.3290
ED	0.8727	0.3480
EF	0.8896	0.2630
EG	0.6133	0.1540
EH	0.8676	0.3130
EK	0.8679	0.3470
EL	0.8977	0.3210
EM	0.8901	0.3270
EN	0.8217	0.3610
EU	1.0000	0.4890
EX	0.7750	0.2630
Ed	0.8742	0.3280
Ef	0.8884	0.3140
Eg	0.9081	0.2710
FC	0.8767	0.3360
FD	0.8848	0.3540
FF	0.8726	0.2570
FG	0.6141	0.1400
FH	0.8506	0.3120
FK	0.8836	0.3530

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Chain	Atom inclusion	Q-score
FL	0.8984	0.3280
FM	0.8864	0.3250
FN	0.8986	0.3660
FU	0.9778	0.4360
FX	0.7125	0.3110
Fd	0.8934	0.3350
Ff	0.8679	0.3000
Fg	0.9154	0.2540
GC	0.8761	0.3370
GD	0.8923	0.3570
GF	0.8726	0.2720
GG	0.6429	0.1470
GH	0.8593	0.3090
GK	0.8933	0.3460
GL	0.9014	0.3270
GM	0.9038	0.3290
GN	0.8724	0.3520
GU	1.0000	0.4720
GX	0.7250	0.2490
Gd	0.8742	0.3380
Gf	0.8679	0.3190
Gg	0.9007	0.2890
HC	0.8510	0.3210
HD	0.8783	0.3500
HF	0.8641	0.2590
HG	0.6125	0.1320
HH	0.8978	0.3230
HK	0.8898	0.3510
HL	0.9118	0.3350
HM	0.8802	0.3240
HN	0.8636	0.3590
HU	1.0000	0.4480
HX	0.8292	0.2900
Hd	0.8857	0.3380
Hf	0.8747	0.3050
Hg	0.9007	0.2850
IC	0.8446	0.3220
ID	0.8811	0.3400
IF	0.8790	0.2550
IG	0.5895	0.1260
IH	0.8681	0.3160
IK	0.8880	0.3510

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Chain	Atom inclusion	Q-score
IL	0.8999	0.3280
IM	0.8814	0.3330
IN	0.8199	0.3590
IU	1.0000	0.4820
IX	0.8500	0.2470
Id	0.8982	0.3360
If	0.8861	0.2960
Ig	0.9154	0.2920
JC	0.8804	0.3360
JD	0.8699	0.3430
JF	0.9002	0.2540
JG	0.5911	0.1270
JH	0.8634	0.3200
JK	0.8871	0.3490
JL	0.9036	0.3290
JM	0.8908	0.3290
JN	0.8794	0.3670
JU	1.0000	0.4660
JX	0.8125	0.2640
Jd	0.8732	0.3350
Jf	0.8702	0.3140
Jg	0.8897	0.2910
KC	0.8896	0.3370
KD	0.8642	0.3500
KF	0.8854	0.2420
KG	0.6190	0.1290
KH	0.8604	0.3080
KK	0.8906	0.3510
KL	0.9133	0.3310
KM	0.8883	0.3320
KN	0.8934	0.3620
KU	1.0000	0.4740
KX	0.7917	0.2790
Kd	0.8722	0.3340
Kf	0.8724	0.3060
Kg	0.9228	0.2820
LC	0.8536	0.3280
LD	0.8876	0.3540
LF	0.8832	0.2480
LG	0.6445	0.1470
LH	0.8511	0.2990
LK	0.8863	0.3420

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Chain	Atom inclusion	Q-score
LL	0.8940	0.3250
LM	0.8678	0.3300
LN	0.8706	0.3570
LU	0.9778	0.4540
LX	0.8708	0.2500
Ld	0.8895	0.3440
Lf	0.8519	0.3100
Lg	0.9301	0.2840
MC	0.8425	0.3130
MD	0.8727	0.3530
MF	0.8769	0.2620
MG	0.6897	0.1860
MH	0.8747	0.3080
MK	0.9003	0.3540
ML	0.9185	0.3380
MM	0.8963	0.3260
MN	0.8462	0.3680
MU	0.9778	0.4600
MX	0.8208	0.2570
Md	0.9020	0.3410
Mf	0.8998	0.3340
Mg	0.8971	0.2710
NG	0.7167	0.1890
OG	0.6453	0.1520
PG	0.6363	0.1390
VF	0.8854	0.2410
VG	0.8860	0.2540
VH	0.7935	0.2830
VX	0.8167	0.2590
WF	0.8981	0.2750
WG	0.8971	0.2680
WH	0.5886	0.2720
WX	0.8000	0.2850
XF	0.8386	0.2520
XG	0.9007	0.2810
XH	0.7967	0.2930
XX	0.8375	0.2630
YF	0.8493	0.2570
YG	0.8603	0.2550
YH	0.7092	0.2860
YX	0.7833	0.2410
ZF	0.8641	0.2570

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Chain	**Atom inclusion**	**Q-score**
ZG	0.8934	0.2640
ZH	0.6571	0.2640
ZX	0.8500	0.2450