wwPDB EM Validation Summary Report (i)

Mar 8, 2026 – 03:59 PM UTC

PDB ID	:	7MUV / pdb_00007muv
EMDB ID	:	EMD-24023
Title	:	Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 3
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)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

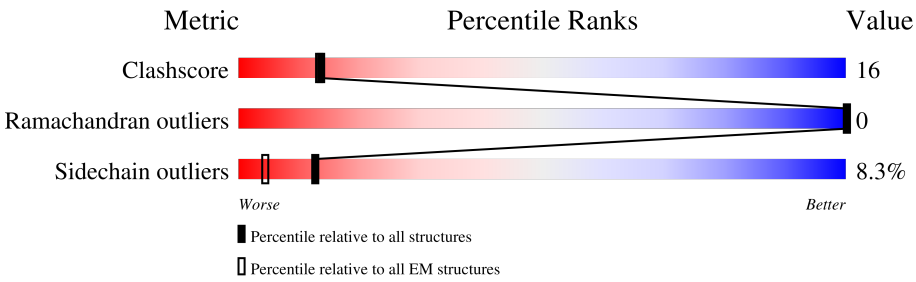
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

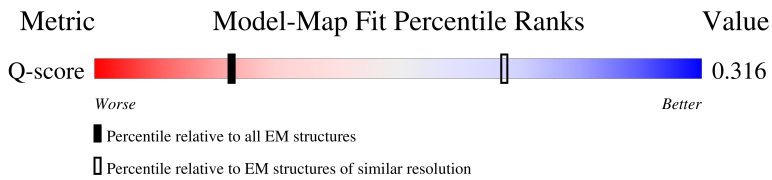
1 Overall quality at a glance (i)

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	9% 6% 84%
1	Ag	1048	97%
1	BG	1048	10% 6% 84%
1	Bg	1048	97%

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Mol	Chain	Length	Quality of chain
1	CG	1048	9% 6% 84%
1	Cg	1048	97%
1	DG	1048	9% 6% 84%
1	Dg	1048	97%
1	EG	1048	9% 6% 84%
1	Eg	1048	97%
1	FG	1048	9% 6% 84%
1	Fg	1048	97%
1	GG	1048	9% 6% 84%
1	Gg	1048	97%
1	HG	1048	8% 7% 84%
1	Hg	1048	97%
1	IG	1048	8% 7% 84%
1	Ig	1048	97%
1	JG	1048	9% 6% 84%
1	Jg	1048	97%
1	KG	1048	9% 6% 84%
1	Kg	1048	97%
1	LG	1048	9% 6% 84%
1	Lg	1048	97%
1	MG	1048	10% 6% 84%
1	Mg	1048	97%
1	NG	1048	8% 7% 84%
1	OG	1048	8% 7% 84%
1	PG	1048	9% 6% 84%

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Mol	Chain	Length	Quality of chain
1	VG	1048	97%
1	WG	1048	97%
1	XG	1048	97%
1	YG	1048	97%
1	ZG	1048	97%
2	AH	361	44% 24% 29%
2	BH	361	43% 26% 29%
2	CH	361	48% 22% 29%
2	DH	361	45% 25% 29%
2	EH	361	41% 26% 29%
2	FH	361	45% 25% 29%
2	GH	361	47% 23% 29%
2	HH	361	47% 23% 29%
2	IH	361	47% 22% 29%
2	JH	361	49% 19% 29%
2	KH	361	47% 21% 29%
2	LH	361	44% 24% 29%
2	MH	361	45% 24% 29%
2	VH	361	12% 41% 24% 33%
2	WH	361	23% 44% 20% 33%
2	XH	361	9% 43% 22% 33%
2	YH	361	23% 41% 24% 33%
2	ZH	361	14% 44% 22% 33%
3	AK	189	52% 26% 20%
3	BK	189	53% 25% 20%

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Mol	Chain	Length	Quality of chain
3	CK	189	58% 20% 20%
3	DK	189	52% 25% 20%
3	EK	189	56% 21% 20%
3	FK	189	48% 31% 20%
3	GK	189	49% 28% 20%
3	HK	189	51% 26% 20%
3	IK	189	50% 28% 20%
3	JK	189	49% 28% 20%
3	KK	189	46% 32% 20%
3	LK	189	51% 25% 20%
3	MK	189	46% 28% 6% 20%
4	AL	249	45% 23% 31%
4	BL	249	43% 23% 31%
4	CL	249	47% 21% 31%
4	DL	249	43% 25% 31%
4	EL	249	43% 24% 31%
4	FL	249	44% 23% 31%
4	GL	249	41% 27% 31%
4	HL	249	42% 26% 31%
4	IL	249	43% 24% 31%
4	JL	249	43% 23% 31%
4	KL	249	40% 26% 31%
4	LL	249	42% 26% 31%
4	ML	249	45% 22% 31%
5	AN	124	5% 39% 22% 37%

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Mol	Chain	Length	Quality of chain
5	BN	124	7% 35% 27% • 37%
5	CN	124	• 36% 26% • 37%
5	DN	124	• 44% 18% • 37%
5	EN	124	• 41% 21% • 37%
5	FN	124	5% 44% 19% • 37%
5	GN	124	• 40% 20% • 37%
5	HN	124	• 43% 19% • 37%
5	IN	124	• 38% 23% • 37%
5	JN	124	• 33% 28% • 37%
5	KN	124	• 44% 18% • 37%
5	LN	124	• 38% 23% • 37%
5	MN	124	• 38% 23% • 37%
6	AU	9	89% 11%
6	BU	9	100%
6	CU	9	100%
6	DU	9	89% 11%
6	EU	9	89% 11%
6	FU	9	78% 22%
6	GU	9	89% 11%
6	HU	9	89% 11%
6	IU	9	89% 11%
6	JU	9	89% 11%
6	KU	9	89% 11%
6	LU	9	89% 11%
6	MU	9	100%

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Mol	Chain	Length	Quality of chain
7	AX	48	31% 92% 8%
7	BX	48	35% 85% 15%
7	CX	48	40% 96%
7	DX	48	42% 98%
7	EX	48	46% 100%
7	FX	48	29% 100%
7	GX	48	33% 100%
7	HX	48	44% 96%
7	IX	48	46% 98%
7	JX	48	31% 96%
7	KX	48	42% 98%
7	LX	48	29% 100%
7	MX	48	31% 90% 10%
7	VX	48	42% 98%
7	WX	48	40% 96%
7	XX	48	29% 98%
7	YX	48	40% 88% 12%
7	ZX	48	38% 96%
8	AD	163	51% 33% 14%
8	Ad	163	52% 30% 16%
8	BD	163	58% 27% 14%
8	Bd	163	56% 26% 16%
8	CD	163	63% 22% 14%
8	Cd	163	54% 28% 16%
8	DD	163	55% 29% 14%

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Mol	Chain	Length	Quality of chain
8	Dd	163	61% 21% 16%
8	ED	163	56% 29% 14%
8	Ed	163	54% 26% 16%
8	FD	163	50% 32% 14%
8	Fd	163	50% 32% 16%
8	GD	163	54% 29% 14%
8	Gd	163	55% 29% 16%
8	HD	163	61% 21% 14%
8	Hd	163	56% 23% 16%
8	ID	163	60% 24% 14%
8	Id	163	61% 23% 16%
8	JD	163	58% 25% 14%
8	Jd	163	60% 23% 16%
8	KD	163	58% 26% 14%
8	Kd	163	60% 22% 16%
8	LD	163	55% 28% 14%
8	Ld	163	55% 26% 16%
8	MD	163	64% 20% 14%
8	Md	163	55% 27% 16%
9	AF	269	13% 10% 77%
9	Af	269	15% 7% 78%
9	BF	269	16% 7% 77%
9	Bf	269	12% 9% 78%
9	CF	269	10% 13% 77%
9	Cf	269	13% 9% 78%

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Mol	Chain	Length	Quality of chain
9	DF	269	13% 10% 77%
9	Df	269	13% 8% 78%
9	EF	269	14% 9% 77%
9	Ef	269	12% 9% 78%
9	FF	269	13% 10% 77%
9	Ff	269	12% 10% 78%
9	GF	269	13% 9% 77%
9	Gf	269	16% 5% 78%
9	HF	269	14% 9% 77%
9	Hf	269	16% 5% 78%
9	IF	269	16% 7% 77%
9	If	269	12% 8% 78%
9	JF	269	14% 9% 77%
9	Jf	269	15% 6% 78%
9	KF	269	13% 10% 77%
9	Kf	269	12% 10% 78%
9	LF	269	15% 7% 77%
9	Lf	269	13% 8% 78%
9	MF	269	14% 8% 77%
9	Mf	269	14% 8% 78%
9	VF	269	13% 10% 77%
9	WF	269	13% 10% 77%
9	XF	269	12% 12% 77%
9	YF	269	13% 9% 77%
9	ZF	269	17% 6% 77%

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Mol	Chain	Length	Quality of chain
10	AC	303	5% 46% 33% 20%
10	BC	303	52% 25% 20%
10	CC	303	37% 29% 31%
10	DC	303	42% 25% 31%
10	EC	303	40% 26% 31%
10	FC	303	53% 23% 20%
10	GC	303	36% 30% 31%
10	HC	303	43% 23% 31%
10	IC	303	39% 27% 31%
10	JC	303	52% 25% 20%
10	KC	303	50% 27% 20%
10	LC	303	42% 22% 5% 31%
10	MC	303	40% 25% 31%
11	AM	320	36% 28% 35%
11	BM	320	32% 31% 35%
11	CM	320	38% 25% 35%
11	DM	320	42% 21% 35%
11	EM	320	34% 29% 35%
11	FM	320	31% 31% 35%
11	GM	320	35% 28% 35%
11	HM	320	39% 24% 35%
11	IM	320	41% 21% 35%
11	JM	320	33% 30% 35%
11	KM	320	38% 24% 35%
11	LM	320	41% 22% 35%

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Mol	Chain	Length	Quality of chain
11	MM	320	38% 26% 35%

2 Entry composition (i)

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
			Total	C	N	O	S		
1	AG	165	1229	780	203	242	4	0	0
1	Fg	34	276	168	47	60	1	0	0
1	Gg	34	276	168	47	60	1	0	0
1	BG	165	1229	780	203	242	4	0	0
1	Hg	34	276	168	47	60	1	0	0
1	Bg	34	276	168	47	60	1	0	0
1	Ig	34	276	168	47	60	1	0	0
1	CG	165	1229	780	203	242	4	0	0
1	Jg	34	276	168	47	60	1	0	0
1	Kg	34	276	168	47	60	1	0	0
1	DG	165	1229	780	203	242	4	0	0
1	Lg	34	276	168	47	60	1	0	0
1	Mg	34	276	168	47	60	1	0	0
1	EG	165	1229	780	203	242	4	0	0
1	VG	34	276	168	47	60	1	0	0
1	WG	34	276	168	47	60	1	0	0
1	XG	34	276	168	47	60	1	0	0

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

- Molecule 2 is a protein called Type IV secretion protein IcmK.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	EH	258	1983	1268	336	371	8	0	0
			Total	C	N	O	S		
2	FH	258	1983	1268	336	371	8	0	0

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

- Molecule 3 is a protein called Inner membrane lipoprotein YiaD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	EK	151	1175	747	209	215	4	0	0
3	FK	151	1175	747	209	215	4	0	0
3	GK	151	1175	747	209	215	4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	HK	151	1175	747	209	215	4	0	0
3	IK	151	1175	747	209	215	4	0	0
3	JK	151	1175	747	209	215	4	0	0
3	KK	151	1175	747	209	215	4	0	0
3	LK	151	1175	747	209	215	4	0	0
3	AK	151	1175	747	209	215	4	0	0
3	MK	151	1175	747	209	215	4	0	0
3	BK	151	1175	747	209	215	4	0	0
3	CK	151	1175	747	209	215	4	0	0
3	DK	151	1175	747	209	215	4	0	0

- Molecule 4 is a protein called Outer membrane protein, OmpA family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	EL	173	1388	877	253	253	5	0	0
4	FL	173	1388	877	253	253	5	0	0
4	GL	173	1388	877	253	253	5	0	0
4	HL	173	1388	877	253	253	5	0	0
4	IL	173	1388	877	253	253	5	0	0
4	JL	173	1388	877	253	253	5	0	0
4	KL	173	1388	877	253	253	5	0	0
4	LL	173	1388	877	253	253	5	0	0
4	ML	173	1388	877	253	253	5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AL	173	1388	877	253	253	5	0	0
4	BL	173	1388	877	253	253	5	0	0
4	CL	173	1388	877	253	253	5	0	0
4	DL	173	1388	877	253	253	5	0	0

- Molecule 5 is a protein called Neurogenic locus notch.

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

- Molecule 6 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	EU	9	45	27	9	9	0	0
6	FU	9	45	27	9	9	0	0
6	GU	9	45	27	9	9	0	0
6	HU	9	45	27	9	9	0	0
6	IU	9	45	27	9	9	0	0
6	JU	9	45	27	9	9	0	0
6	KU	9	45	27	9	9	0	0
6	LU	9	45	27	9	9	0	0
6	MU	9	45	27	9	9	0	0
6	AU	9	45	27	9	9	0	0
6	BU	9	45	27	9	9	0	0
6	CU	9	45	27	9	9	0	0
6	DU	9	45	27	9	9	0	0

- Molecule 7 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	EX	48	240	144	48	48	0	0
7	FX	48	240	144	48	48	0	0
7	GX	48	240	144	48	48	0	0
7	HX	48	240	144	48	48	0	0
7	IX	48	240	144	48	48	0	0
7	JX	48	240	144	48	48	0	0
7	KX	48	240	144	48	48	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	LX	48	240	144	48	48	0	0
7	MX	48	240	144	48	48	0	0
7	VX	48	240	144	48	48	0	0
7	WX	48	240	144	48	48	0	0
7	XX	48	240	144	48	48	0	0
7	YX	48	240	144	48	48	0	0
7	ZX	48	240	144	48	48	0	0
7	AX	48	240	144	48	48	0	0
7	BX	48	240	144	48	48	0	0
7	CX	48	240	144	48	48	0	0
7	DX	48	240	144	48	48	0	0

- Molecule 8 is a protein called DotD.

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

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

- Molecule 9 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	Ef	59	449	290	77	81	1	0	0

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	YF	63	483	308	84	90	1	0	0
9	ZF	63	483	308	84	90	1	0	0
9	Af	59	449	290	77	81	1	0	0
9	BF	63	483	308	84	90	1	0	0
9	Bf	59	449	290	77	81	1	0	0
9	Cf	59	449	290	77	81	1	0	0
9	DF	63	483	308	84	90	1	0	0
9	Df	59	449	290	77	81	1	0	0
9	EF	63	483	308	84	90	1	0	0

- Molecule 10 is a protein called DotC.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LC	209	1667	1061	292	309	5	0	0
			Total	C	N	O	S		
10	MC	209	1667	1061	292	309	5	0	0
			Total	C	N	O	S		
10	AC	243	1921	1216	340	357	8	0	0

- Molecule 11 is a protein called DUF2807 domain-containing protein.

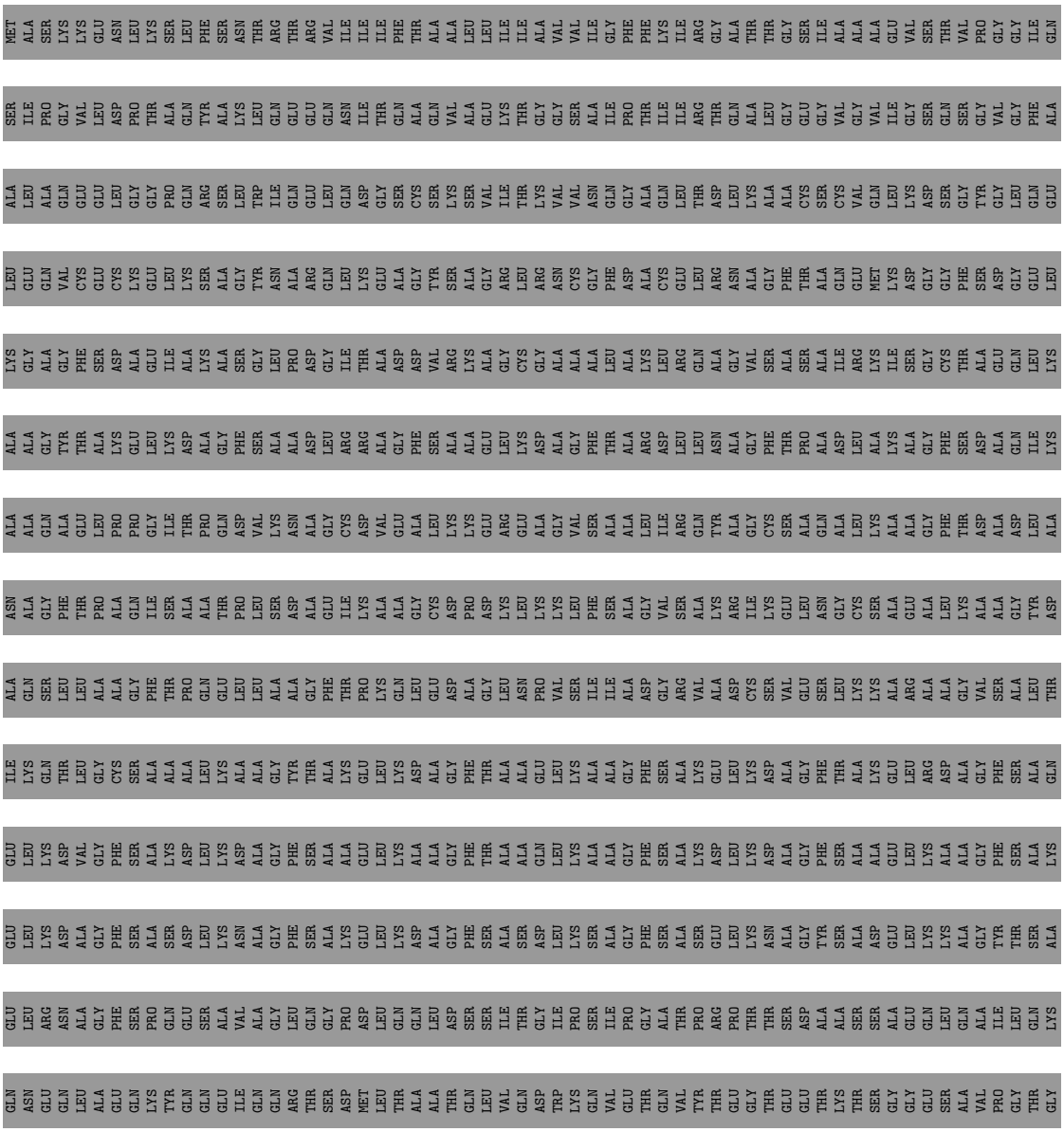
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	HM	208	1650	1046	293	308	3	0	0
			Total	C	N	O	S		
11	IM	208	1650	1046	293	308	3	0	0
			Total	C	N	O	S		
11	KM	208	1650	1046	293	308	3	0	0
			Total	C	N	O	S		
11	LM	208	1650	1046	293	308	3	0	0
			Total	C	N	O	S		
11	MM	208	1650	1046	293	308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

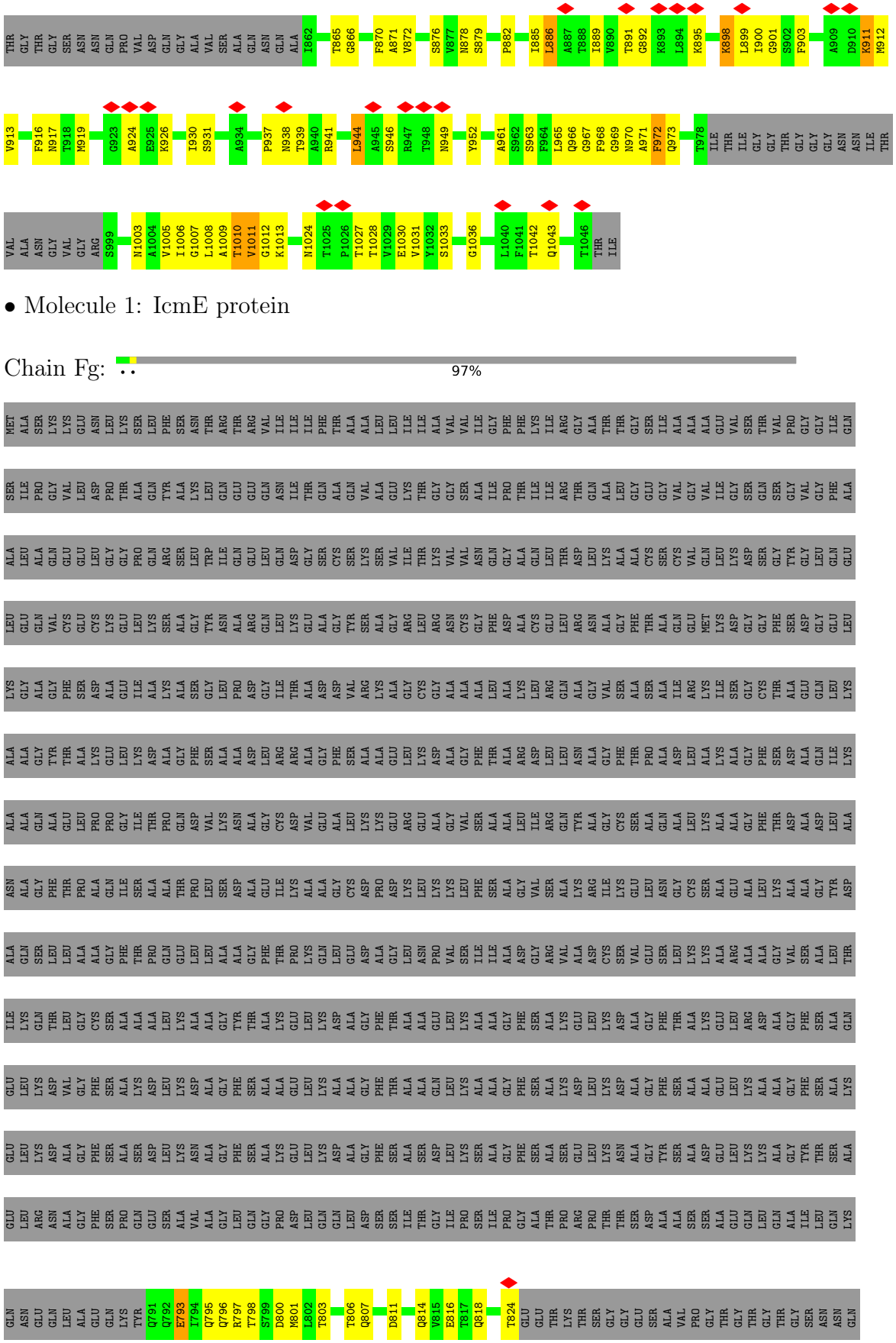
3 Residue-property plots (i)

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

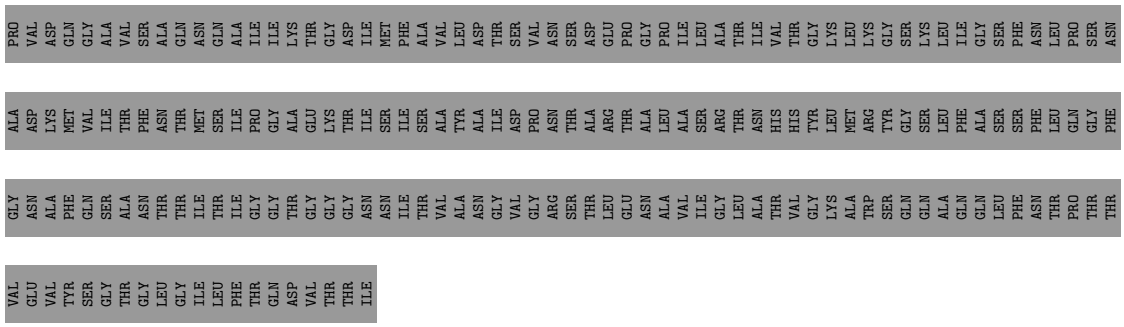
Chain AG:





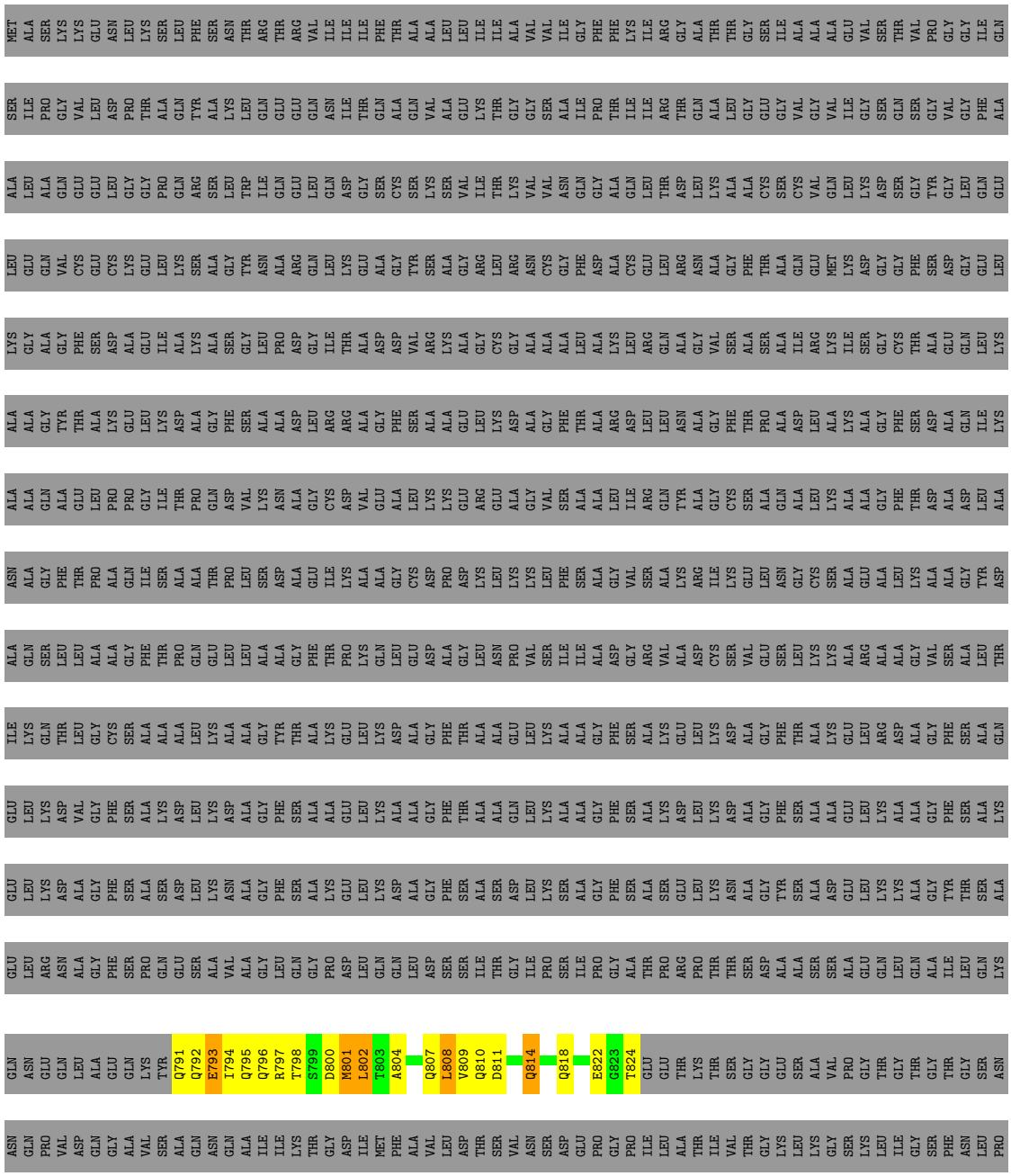
- Molecule 1: IcmE protein

Chain Fg: 97%



- Molecule 1: IcmE protein

Chain Gg: 97%



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 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 BG: 10% 6% • 84%

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

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 ASP

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

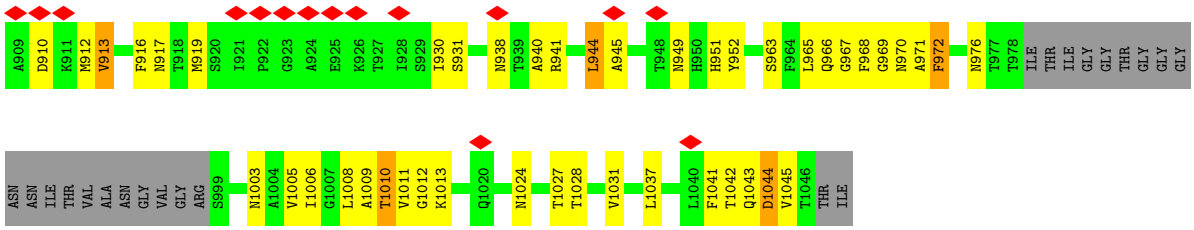
GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA ALA GLY PHE SER ALA ALA ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA ALA GLN LEU LYS ASP ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA LYS ALA

GLU LEU LYS ASP ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA SER GLU LEU LYS ASP ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA

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

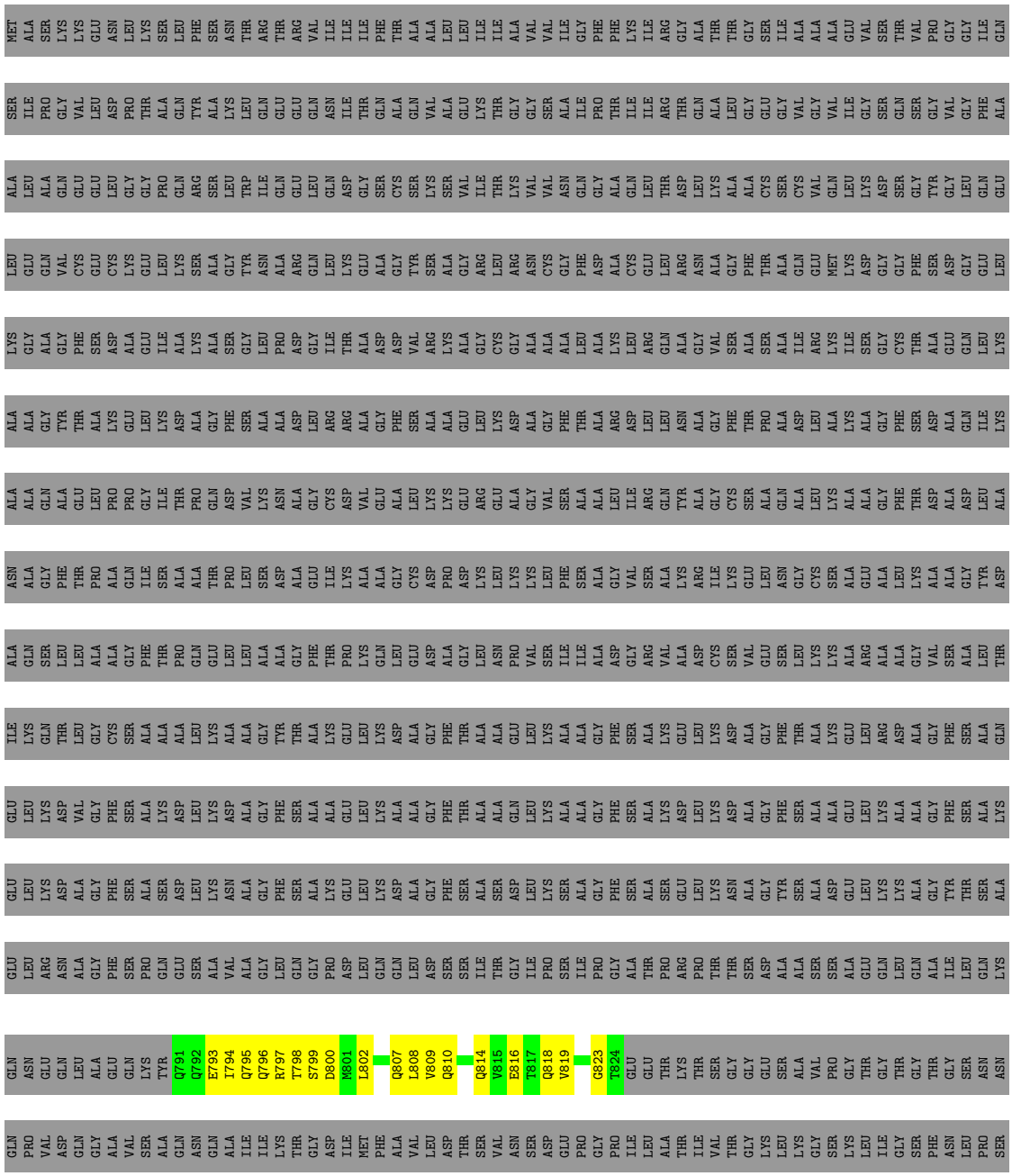
GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR GLN GLN GLU ILE GLN VAL ALA VAL SER ALA GLN ARG THR SER ASP MET LEU THR ALA ALA THR GLN LEU VAL ASP TRP LYS GLN VAL GLU THR GLN VAL TYR THR GLU GLY THR THR GLU THR LYS THR SER GLY GLU GLU SER ALA ALA GLN GLY THR GLY

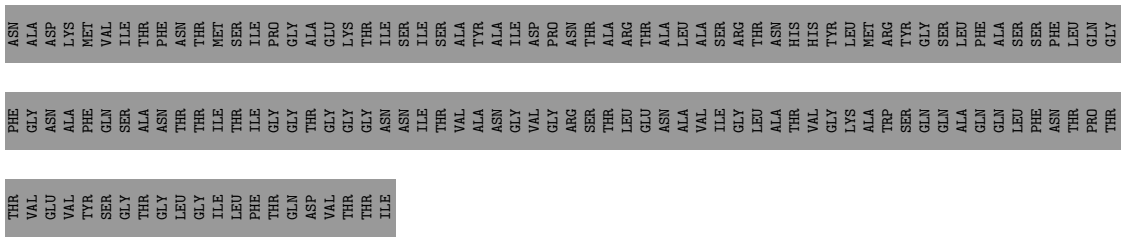
THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA I862 I863 G866 D867 I868 M869 F870 A871 V872 L873 S876 V877 N878 S879 P882 L886 A887 T888 I889 V890 T891 G892 K893 L894 K898 L899 I900 G901 S902 F903 N904 L905 N908



- Molecule 1: IcmE protein

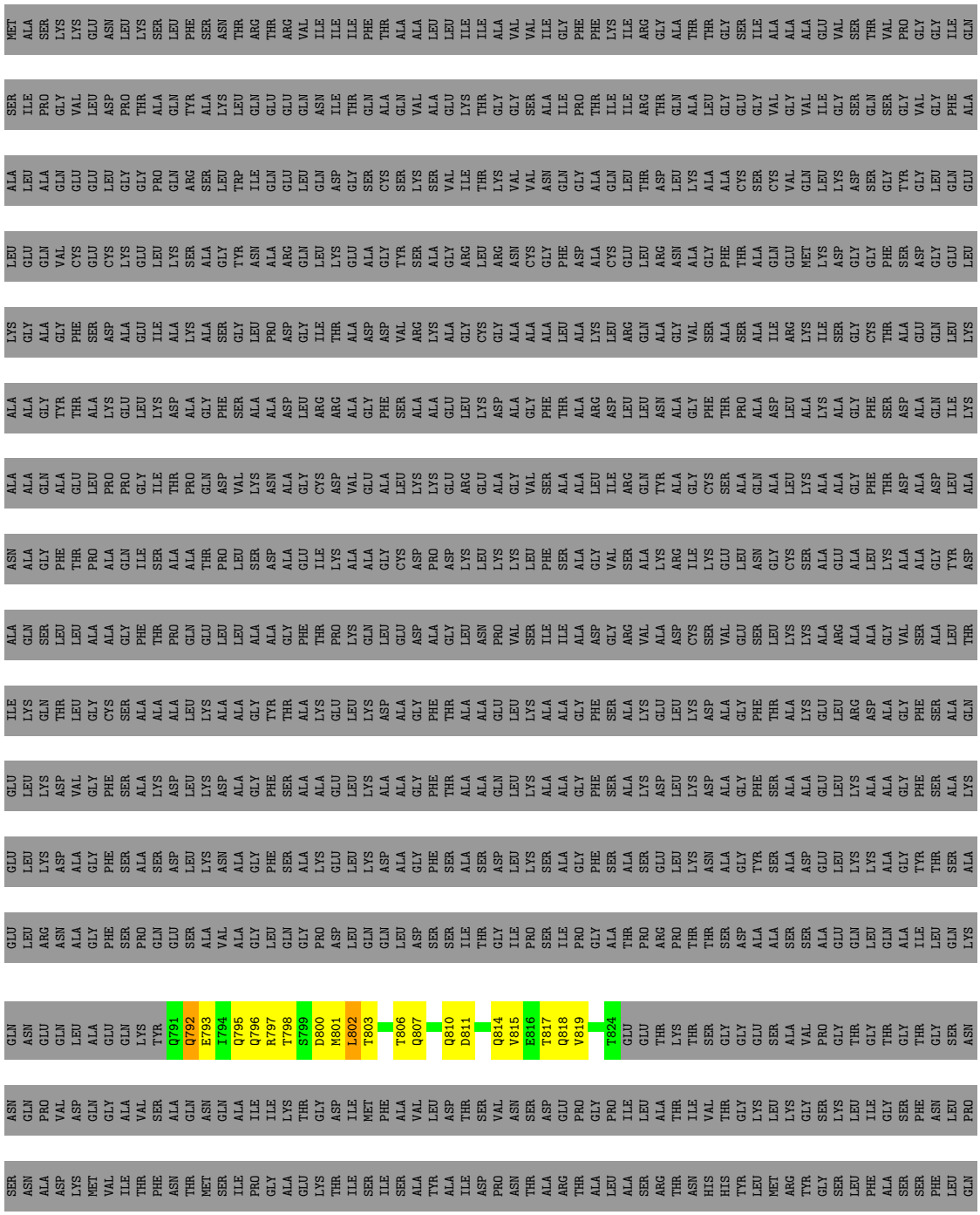
Chain Hg: 97%

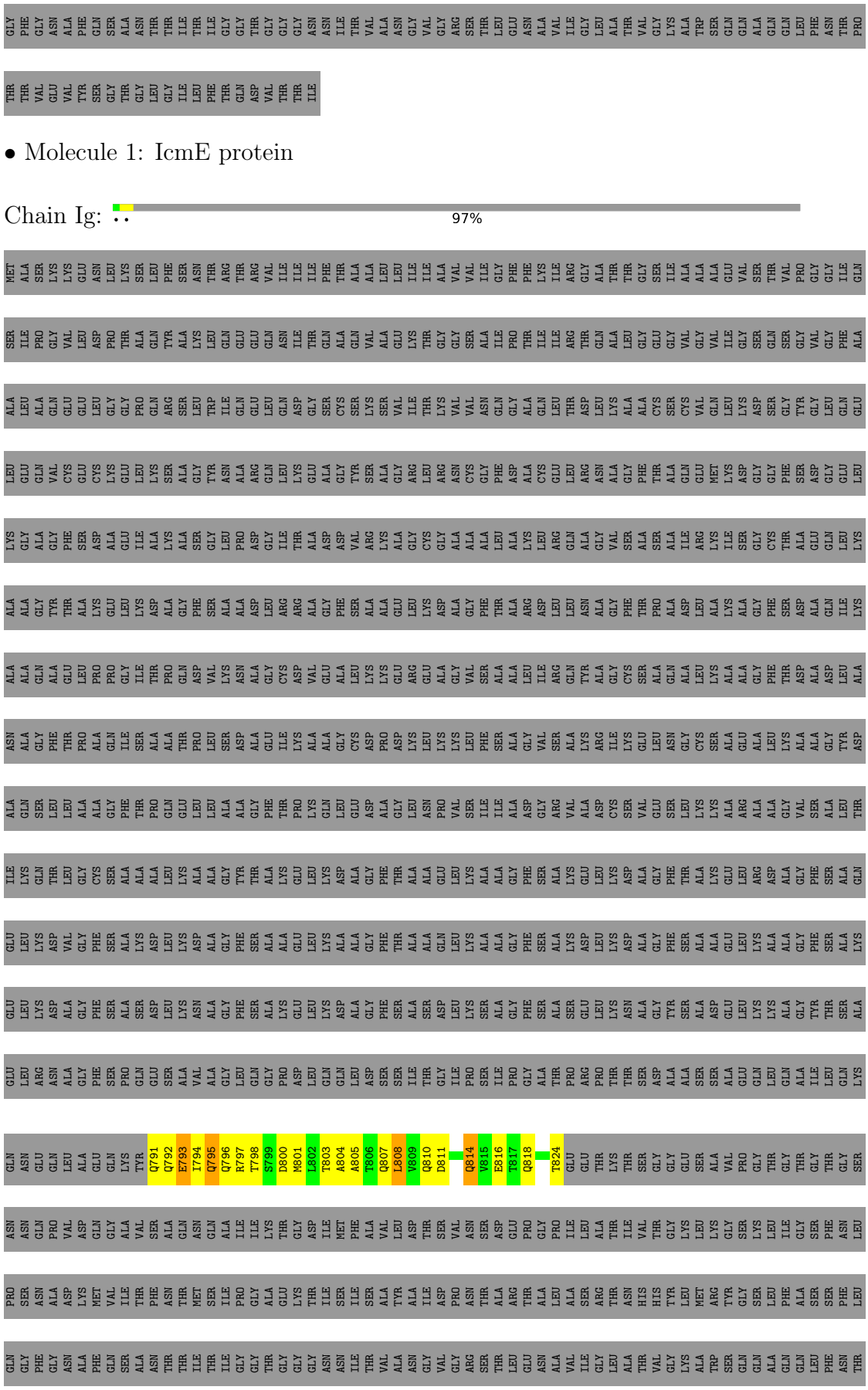




• Molecule 1: IcmE protein

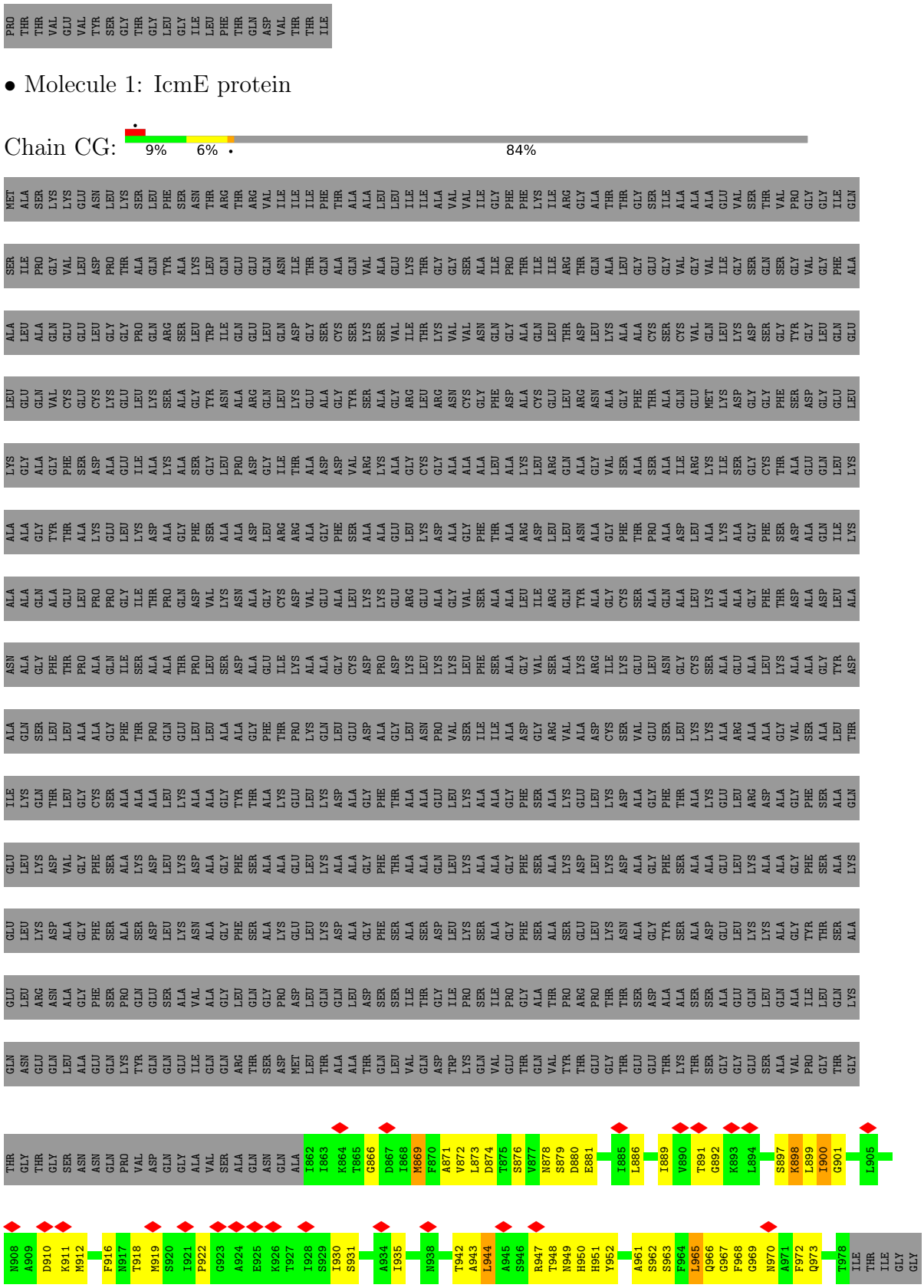
Chain Bg: 97%

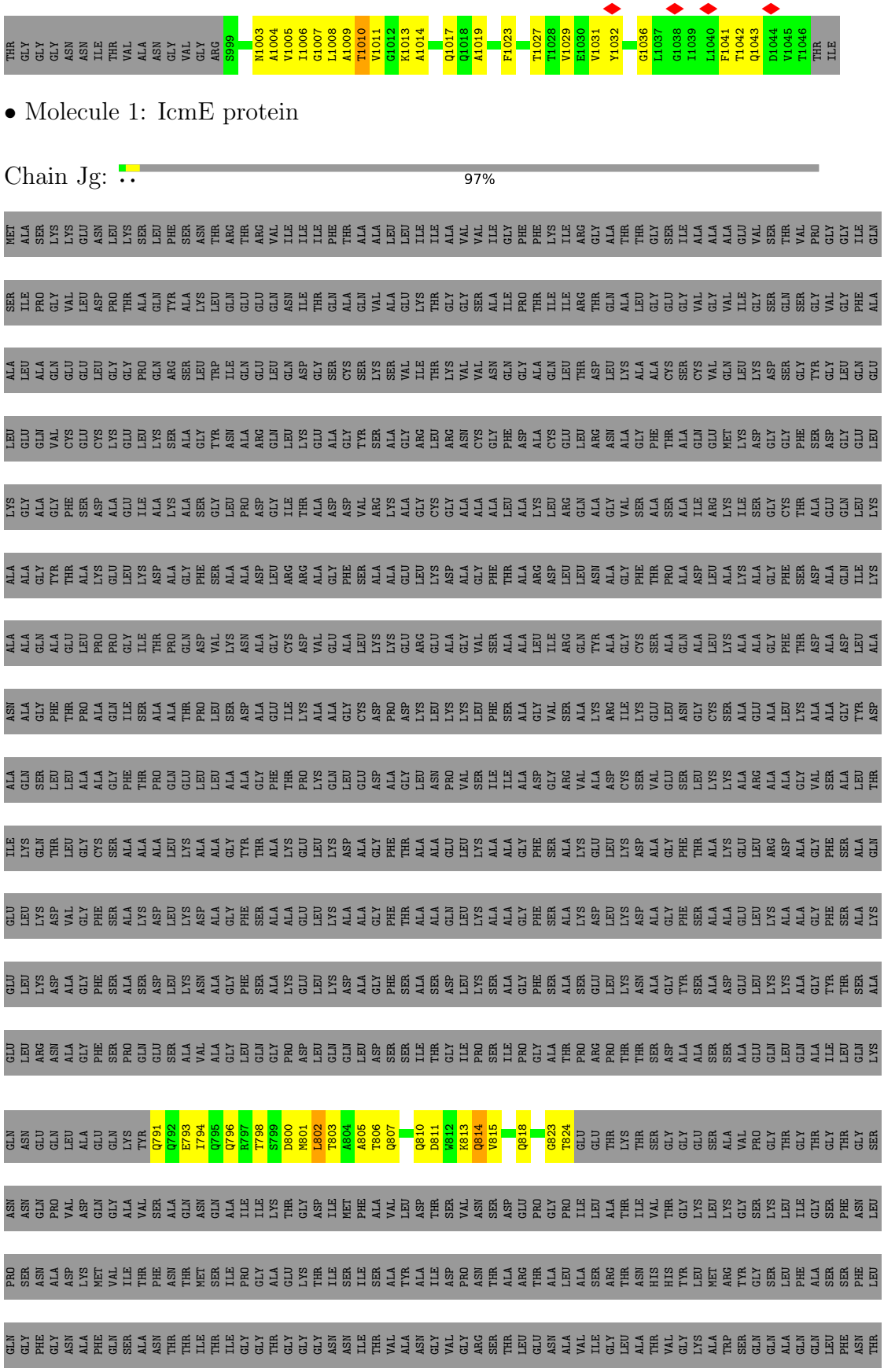




• Molecule 1: IcmE protein

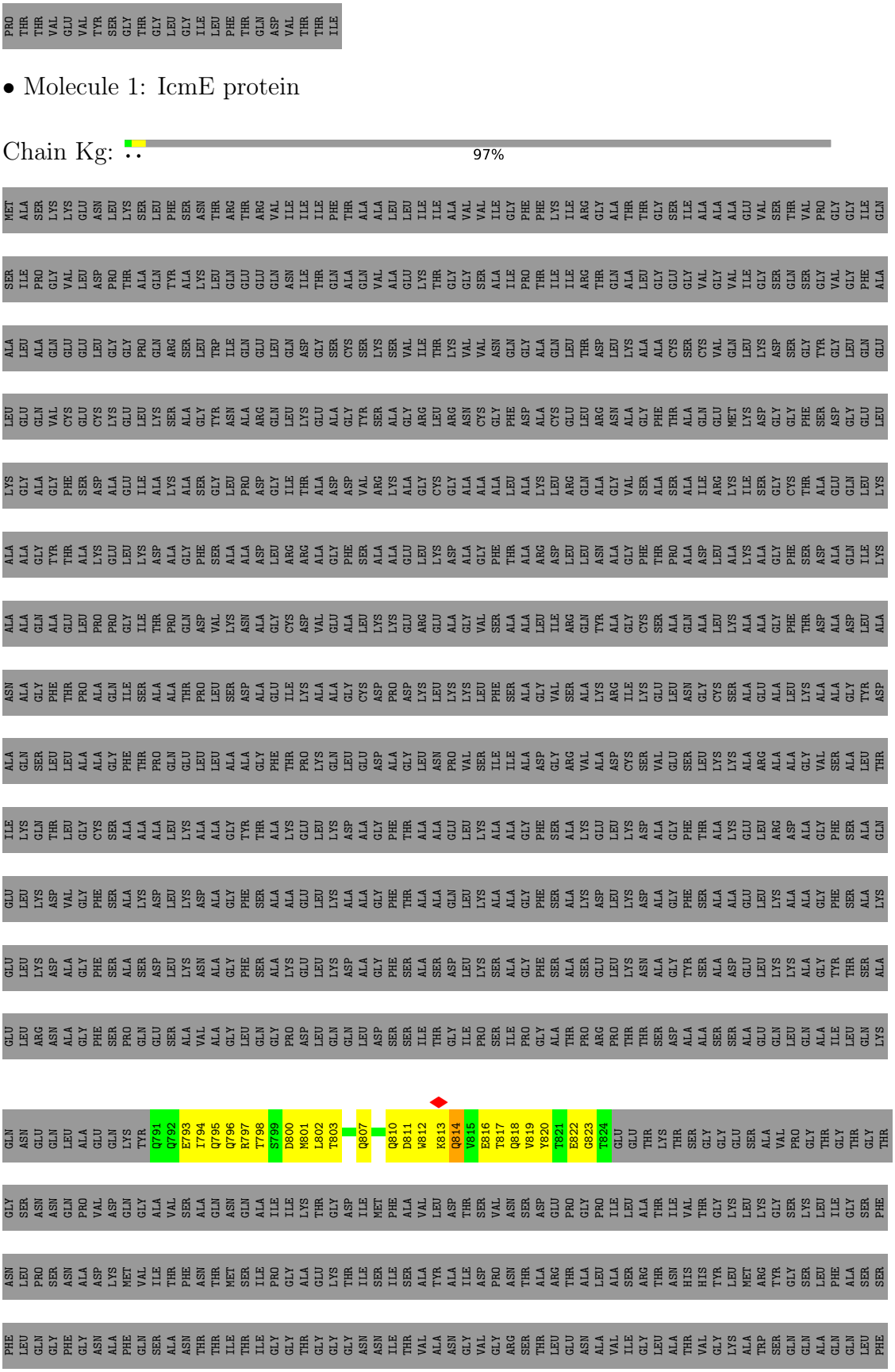
Chain Ig: 97%

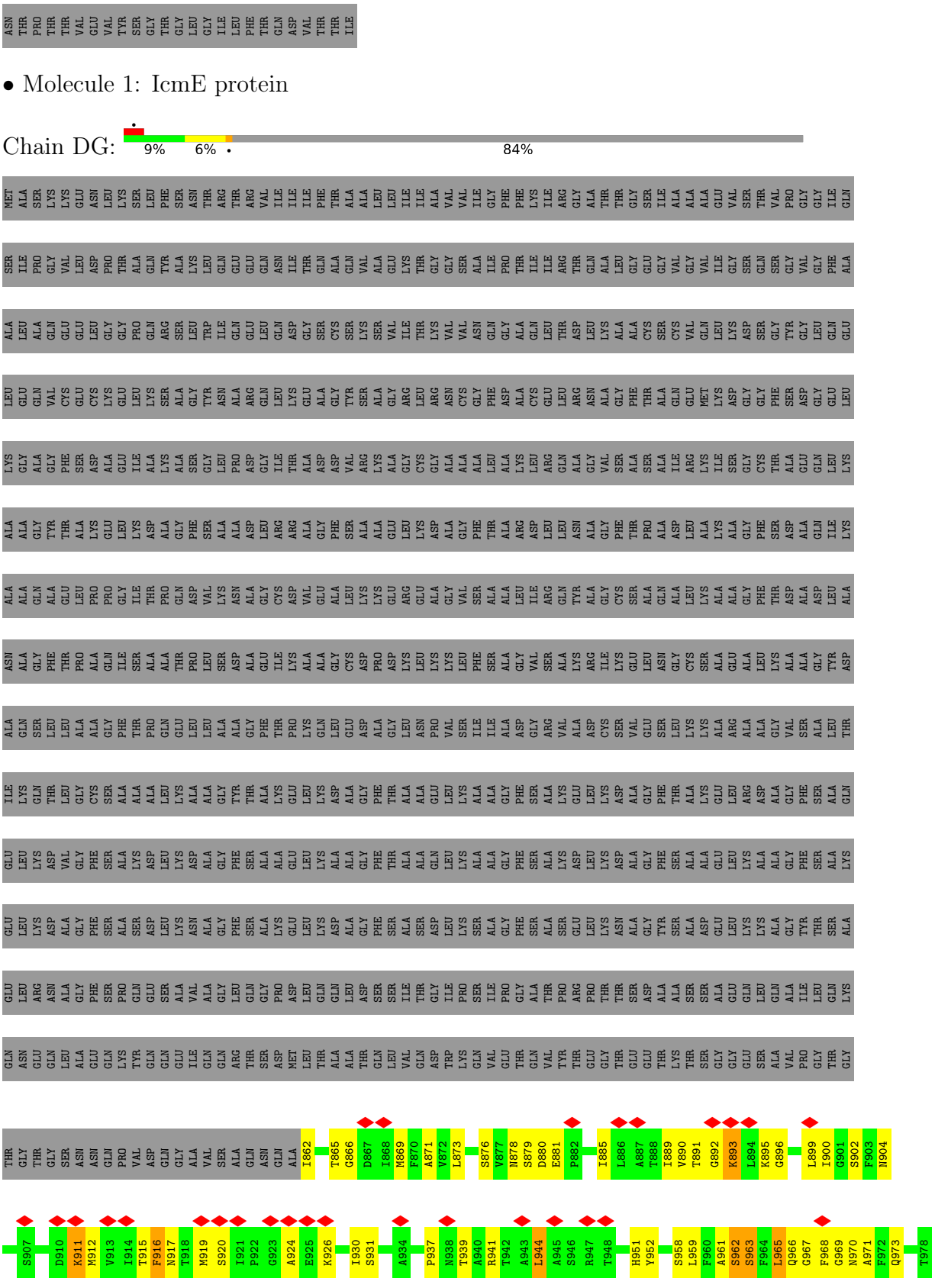

PRO THR THR VAL GLU VAL TYR SER GLY THR GLY LEU GLY ILE LEU PHE THR GLN ASP VAL THR THR ILE
• Molecule 1: IcmE protein
Chain CG:
9%
6%
84%
MET ALA SER LYS LYS GLU ASN LEU LYS SER LEU PHE SER ASN THR ARG THR ARG VAL ILE ILE ILE PHE THR ALA ALA LEU LEU LEU ILE ILE ALA VAL VAL ILE GLY PHE PHE LYS ILE ARG 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 ILE ARG THR GLN ALA LEU GLY GLU 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 ILE 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 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 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 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 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 GLN TYR ALA GLY CYS SER ALA GLN ALA LEU LYS ALA ALA GLY PHE THR ALA LYS ALA LEU
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 GLU LEU PHE SER ALA ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU ALA LEU 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 ALA GLY VAL SER ALA LEU THR
ILE LYS GLN THR LEU GLY CYS SER ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS ASP ALA GLY PHE THR ALA ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS ASP ALA GLY PHE THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA 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 ASP ALA GLY PHE THR ALA ALA ALA GLN LEU LEU LYS ASP ALA GLY PHE THR ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA ALA LYS
GLU LEU LYS ASP ALA GLY PHE SER ALA LYS ASP LEU LYS ASN ALA GLY PHE SER ALA LYS GLU LEU LYS ASN ALA GLY PHE SER ALA ALA ALA SER GLU LEU LYS ASN ALA GLY TYR SER ALA ALA ASP GLU LEU LYS LYS GLY PHE SER ALA ALA ALA GLY PHE 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 GLU THR THR SER ASP ALA ALA ALA SER GLU ILE LEU GLN LYS
GLN ASN GLU GLN GLN LYS TYR GLN GLN GLU ILE GLN THR GLN MET LEU THR ALA ALA THR GLN LEU GLN ASP TRP LYS GLN VAL GLU THR GLN VAL TYR THR GLU GLY THR THR GLU GLU THR LYS THR SER ALA GLY GLU GLU SER ILE ALA ALA GLY THR THR GLY
THR GLY THR GLY SER ASN ASN GLN PRO VAL ASP GLN GLY ALA VAL SER ALA GLN ASN GLN ALA I862 I863 K864 T865 G866 D867 I868 M869 F870 A871 V872 L873 D874 T875 S876 V877 N878 S879 D880 E881 I885 L886 I889 V890 T891 G892 K893 L894 S897 K898 L899 I900 G901 L905
N908 A909 D910 K911 M912 F916 N917 T918 M919 S920 I921 P922 G923 A924 E925 K926 T927 I928 S929 I930 S931 A934 I935 N938 T942 A943 L944 A945 S946 R947 T948 N949 H950 H951 Y952 A961 S962 S963 F964 L965 Q966 G967 F968 G969 N970 A971 F972 Q973 T978
ILE THR ILE GLY GLY



• Molecule 1: IcmE protein

Chain Jg: 97%


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 Kg:
97%
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 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 GLN ASN ILE THR GLN 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 GLU 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 LEU ARG ALA GLY PHE SER ALA ALA GLU LEU LYS ASP 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 GLU LEU LYS ALA ALA ALA LEU LEU 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 SER ASP PRO ASP LYS LEU LYS ASP LYS LEU PHE SER ALA GLY VAL SER ALA LYS ARG GLY CYS SER ALA GLU LEU ASN GLY CYS CYS SER ALA GLU ALA LYS LEU LYS ALA GLY PHE SER ASP ALA GLY 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 ASP ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA ALA ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA ALA GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU ARG ASP ALA GLN
GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA ALA GLY PHE THR ALA ALA ALA GLN LEU LYS ASP 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 ALA
GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA ALA GLY PHE SER ALA ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA ALA SER GLU LEU LYS ASP ALA GLY TYR THR 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 PHE SER ALA 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 GLN LEU GLN ALA ILE LEU GLN LYS
GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 Q792 E793 I794 Q795 Q796 R797 T798 S799 D800 M801 L802 T803 Q807 Q810 D811 W812 K813 Q814 W815 E816 T817 Q818 V819 Y820 T821 E822 G823 T824 GLU GLU THR LYS THR SER GLY GLY GLU SER ALA VAL PRO 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 ILE LEU ALA THR ILE VAL THR GLY GLY LYS LEU 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 THR THR ILE SER ILE ILE ASP PRO ASN THR ALA ARG THR ALA ALA LEU ALA SER ARG THR ASN HIS HIS TYR LEU MET ARG TYR GLY SER LEU PHE ALA ALA 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 LYS GLN GLN GLN LEU GLN GLN


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:
9%
6%
84%
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 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 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 ALA ILE GLN GLY ALA GLN LEU THR ASP LEU LYS ALA ALA CYS SER CYS VAL GLN LEU LYS ASP SER GLY TYR GLY VAL 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 ALA SER ALA GLY TYR SER 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 GLN 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 LYS LYS LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG ALA GLY CYS THR ALA GLU GLN 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 VAL SER ALA ILE ARG LYS ILE SER GLY 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 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 ALA GLY VAL SER ALA LYS ARG ILE LYS GLU LEU ASN GLY CYS SER ALA GLU GLU ALA LEU LYS ASP GLY GLY ALA LEU LYS ARG 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 ALA GLY VAL SER ALA LEU THR
ILE LYS GLN THR LEU GLY CYS SER ALA ALA LEU LYS ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA ALA GLY PHE THR ALA ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA LYS GLU LEU 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 ASP ALA ALA GLY PHE THR ALA ALA ALA GLN LEU LEU LYS ASP ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA 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 GLU LEU LYS ASP ALA GLY PHE THR ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA SER ASP LEU LYS ASN ALA GLY TYR SER ALA ALA ASP GLU LEU LEU LYS ALA ALA GLY PHE SER ALA LYS
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GLN ASN GLU GLN GLN LEU ALA LYS TYR GLN GLN GLN LYS GLU ILE 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 GLU GLN SER ALA VAL PRO GLY THR GLY
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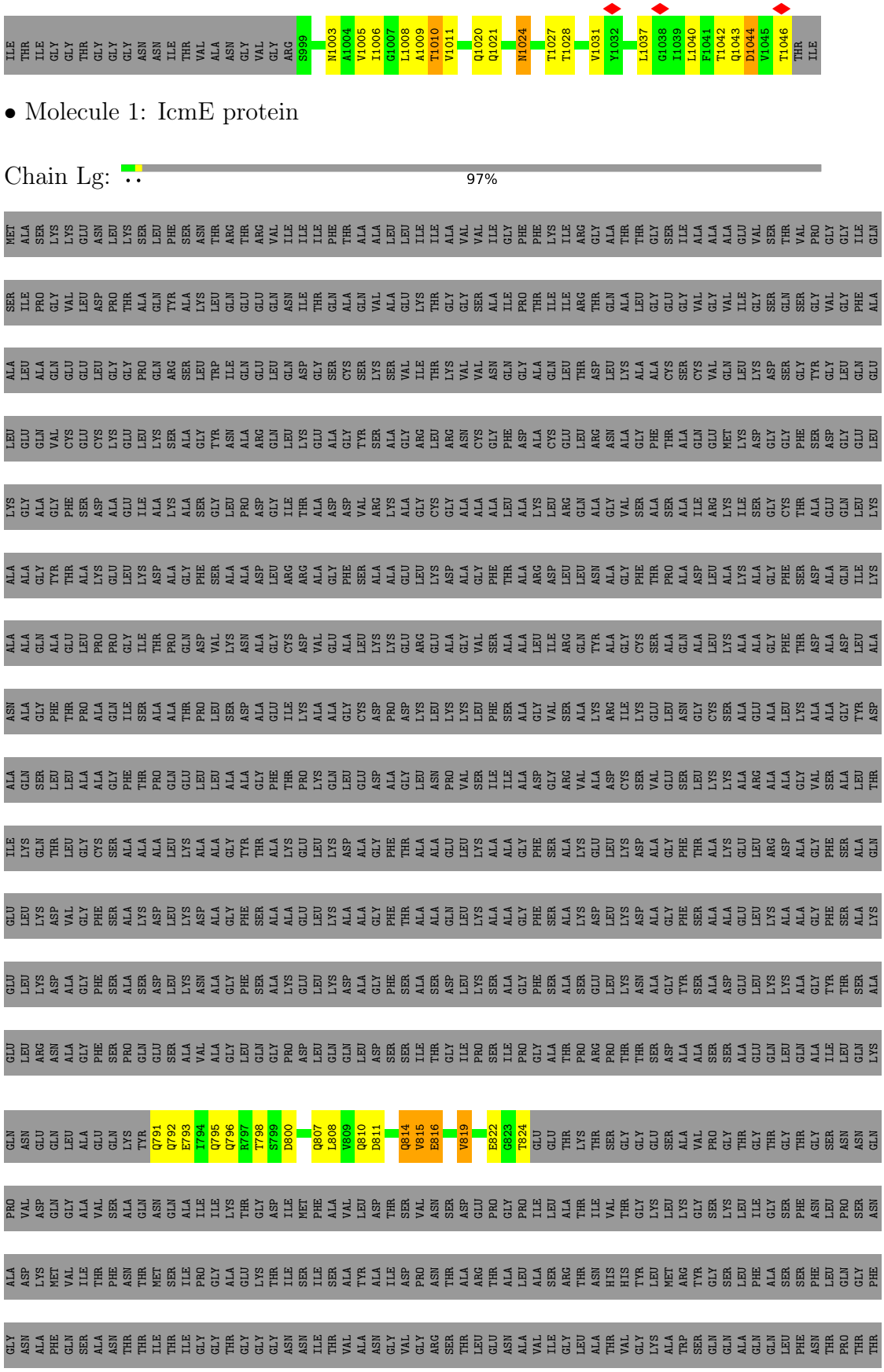
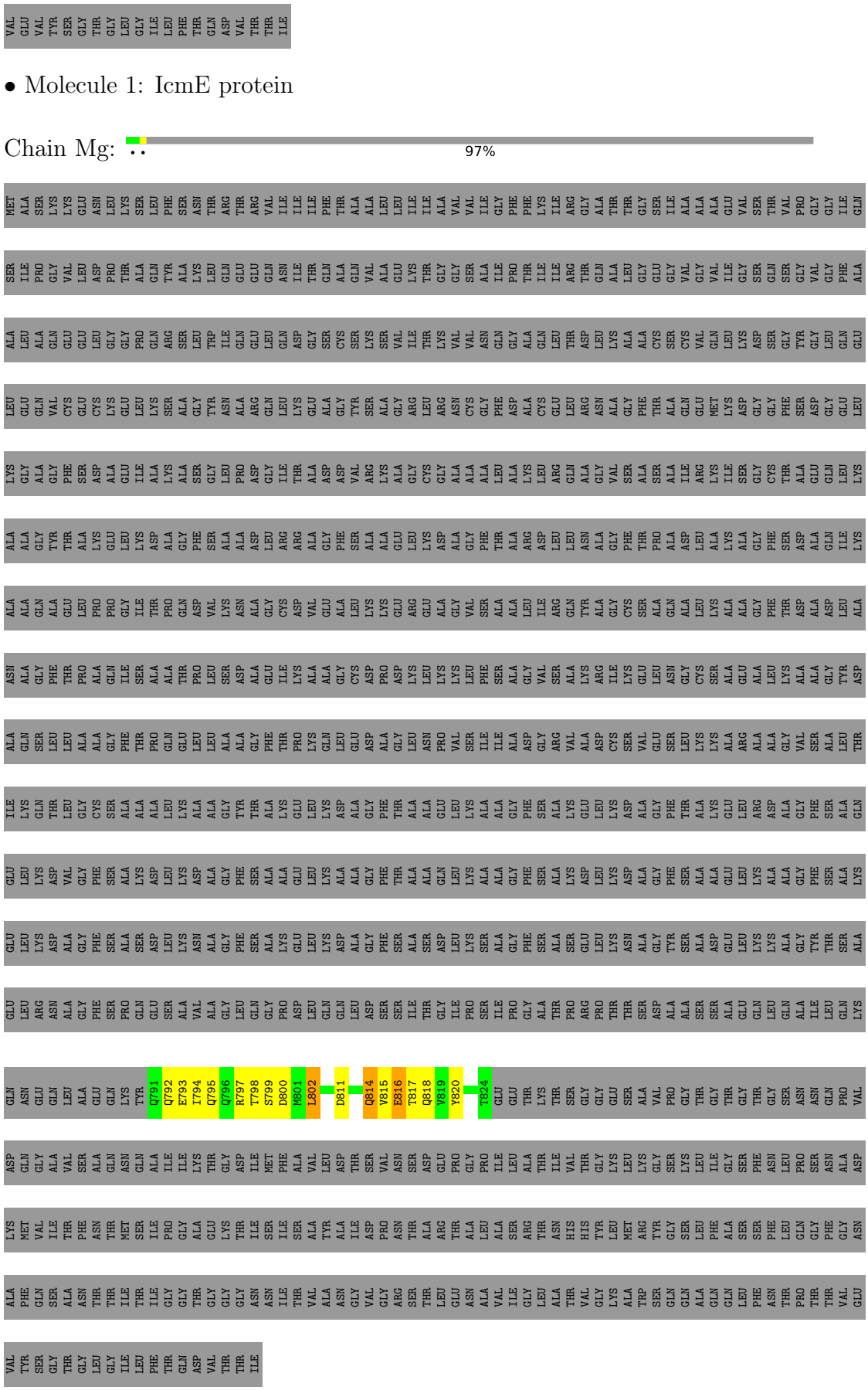


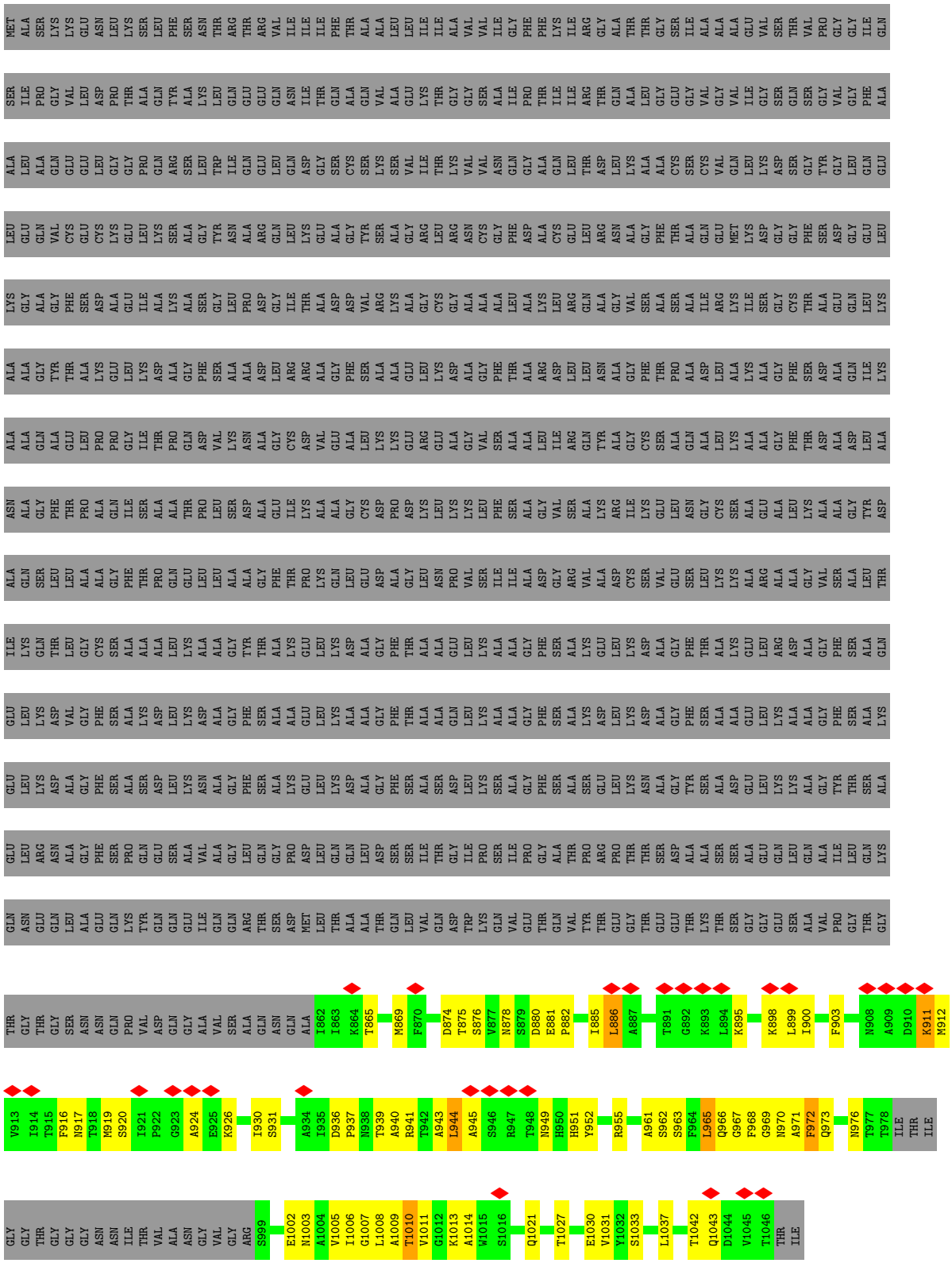
• Molecule 1: IcmE protein

Chain Lg: 97%


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:
97%
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 GLN ASP GLY SER CYS SER LYS SER VAL ILE THR LYS VAL VAL ASN GLN GLY ALA GLN LEU THR ARG 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 SER ALA GLY PHE THR ALA ALA 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 ILE 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 ALA LEU ILE ARG GLN ALA LYS ARG CYS ILE LYS GLU LEU ASN GLY CYS CYS SER ALA GLU ALA LEU LYS LYS GLY ALA GLY
ALA GLN SER LEU LEU ALA ALA GLY PHE THR PRO GLN GLU LEU LEU ALA GLY PHE THR PRO LYS GLN LEU GLU ASP ALA GLY LEU 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 ALA GLY
ILE LYS GLN THR LEU GLY CYS SER ALA ALA ALA LEU LYS ALA ALA LYS GLU LEU LYS ASP ALA GLY PHE THR ALA ALA ALA GLU LEU LYS ALA ALA GLY PHE SER ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA LEU LEU ARG ASP ALA GLY PHE SER ALA GLN
GLU LEU LYS ASP VAL GLY PHE SER ALA LYS ASP LEU LYS ASP ALA ALA ALA ALA GLN LEU LYS ALA ALA GLY PHE THR ALA ALA ALA GLU 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 SER ALA ALA SER ASP LEU LYS ASN ALA GLY PHE SER ALA SER ALA GLU LEU LYS ASP ALA GLY TYR SER ALA ALA ASP 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 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 ALA ILE ILE LEU GLN LEU GLN ALA ILE LEU GLN LYS
GLN ASN GLU GLN LEU ALA GLU GLN LYS TYR Q791 Q792 E793 I794 Q795 Q796 R797 T798 S799 D800 M801 L802 D811 Q814 V815 E816 T817 Q818 V819 Y820 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

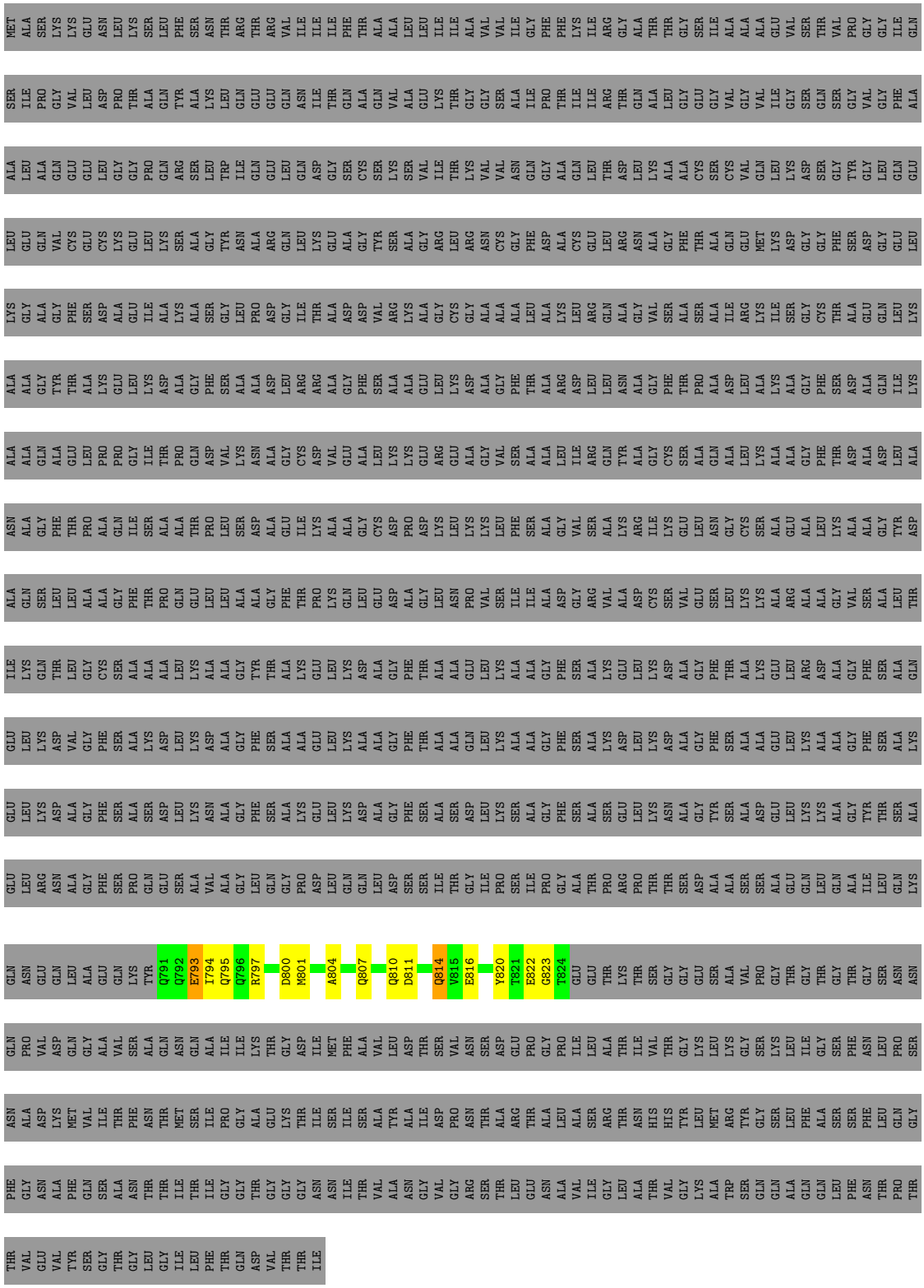
- Molecule 1: IcmE protein

Chain EG: 9% 6% 84%



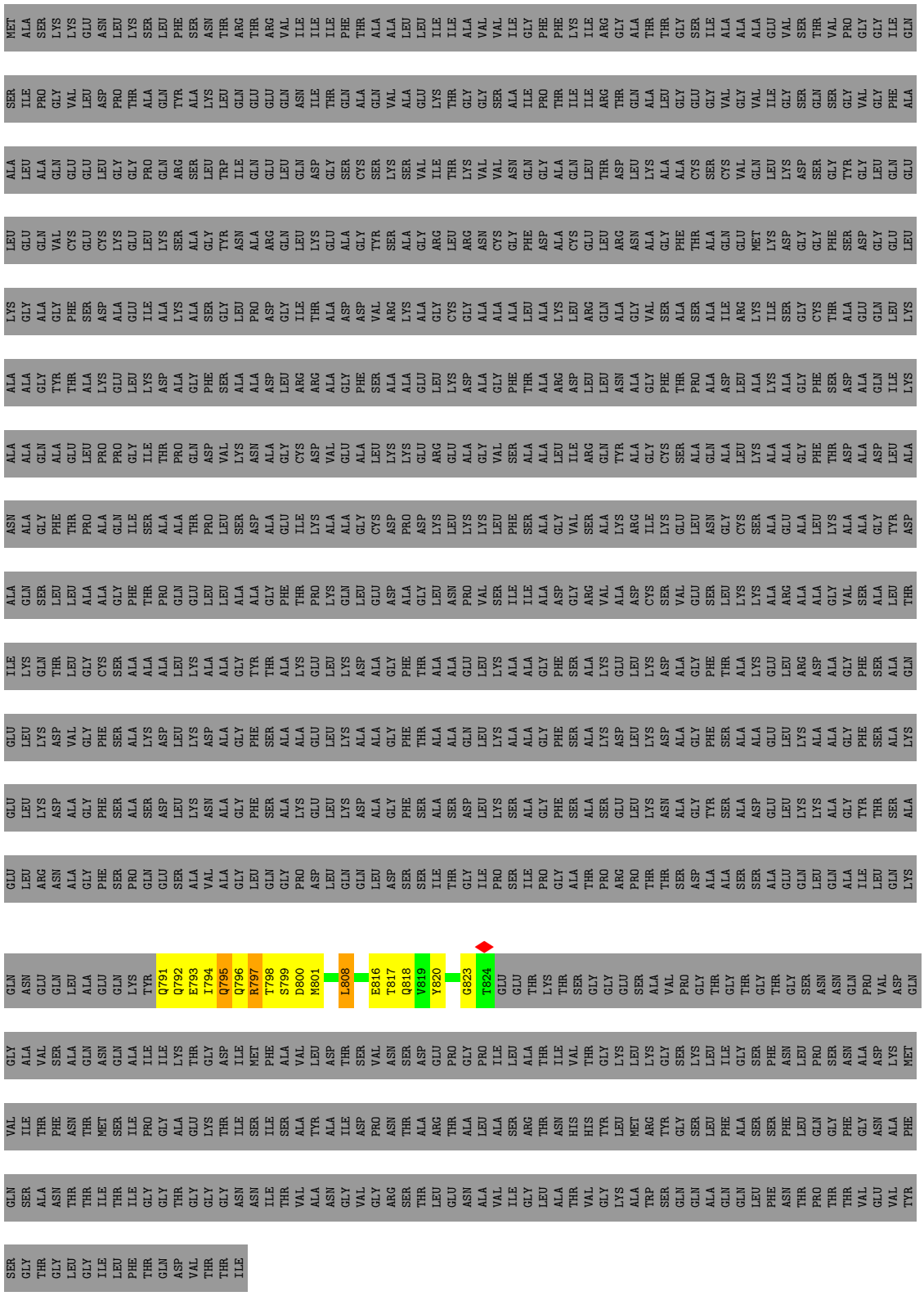
- Molecule 1: IcmE protein

Chain VG: 97%



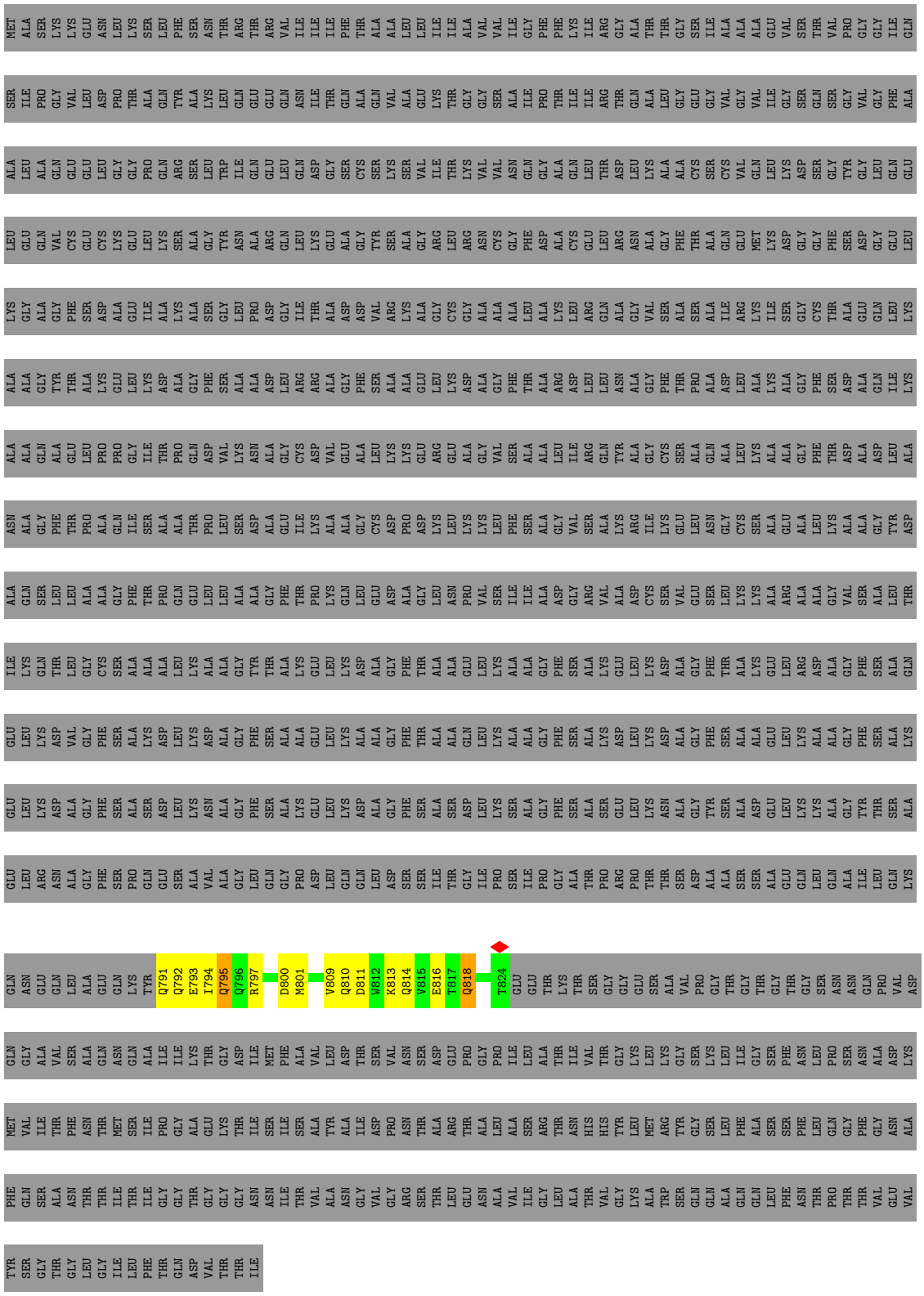
• Molecule 1: IcmE protein

Chain WG: 97%



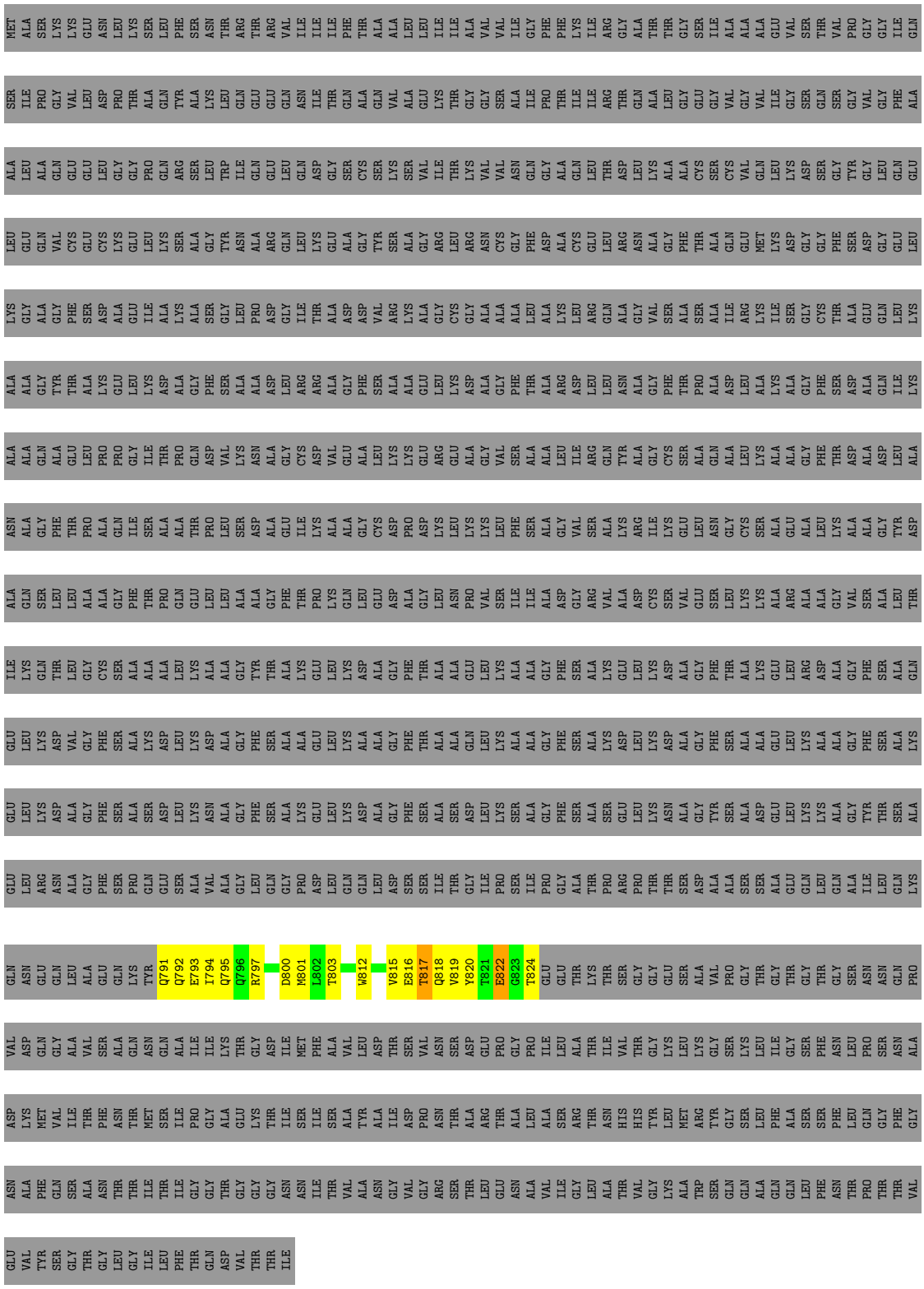
- Molecule 1: IcmE protein

Chain XG: 97%



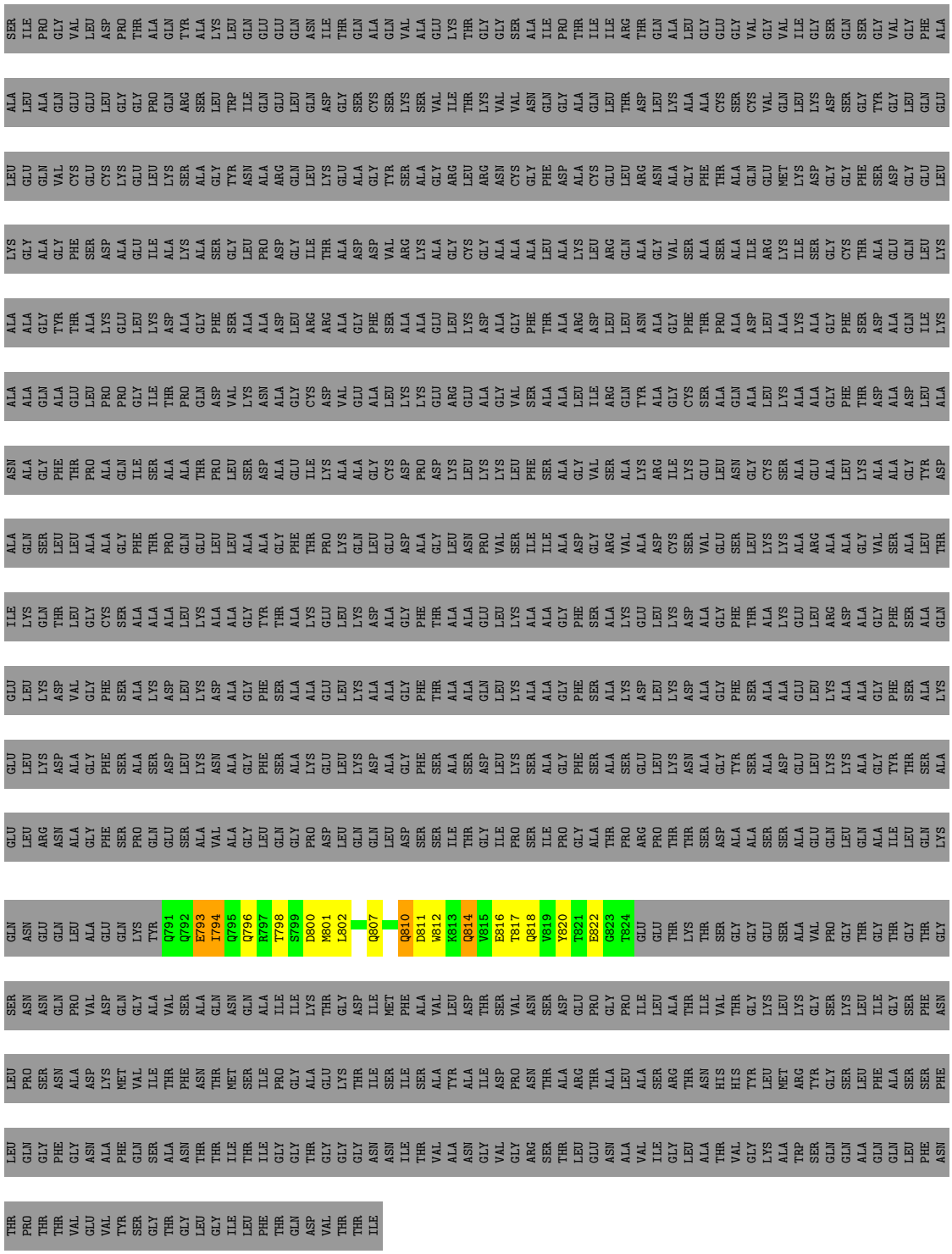
- Molecule 1: IcmE protein

Chain YG: 97%



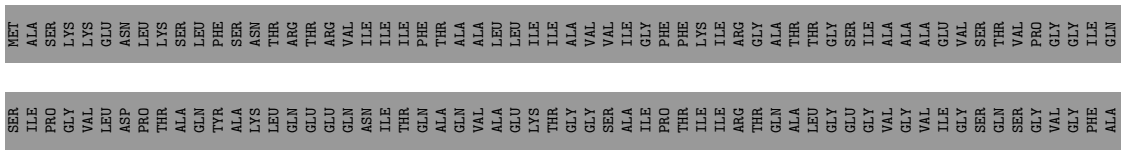
- Molecule 1: IcmE protein

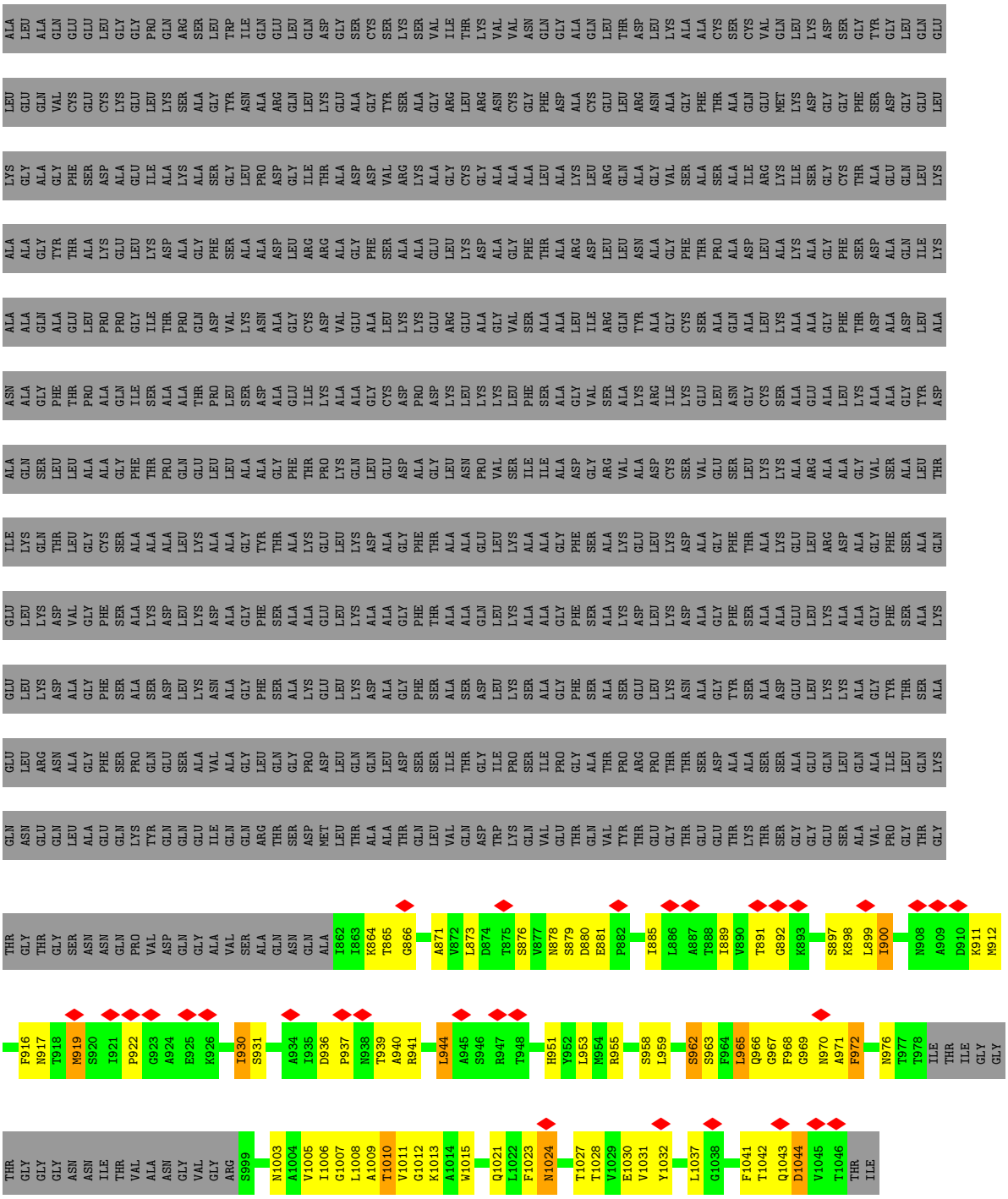
Chain ZG: 97%



• Molecule 1: IcmE protein

Chain FG: 9% 6% • 84%

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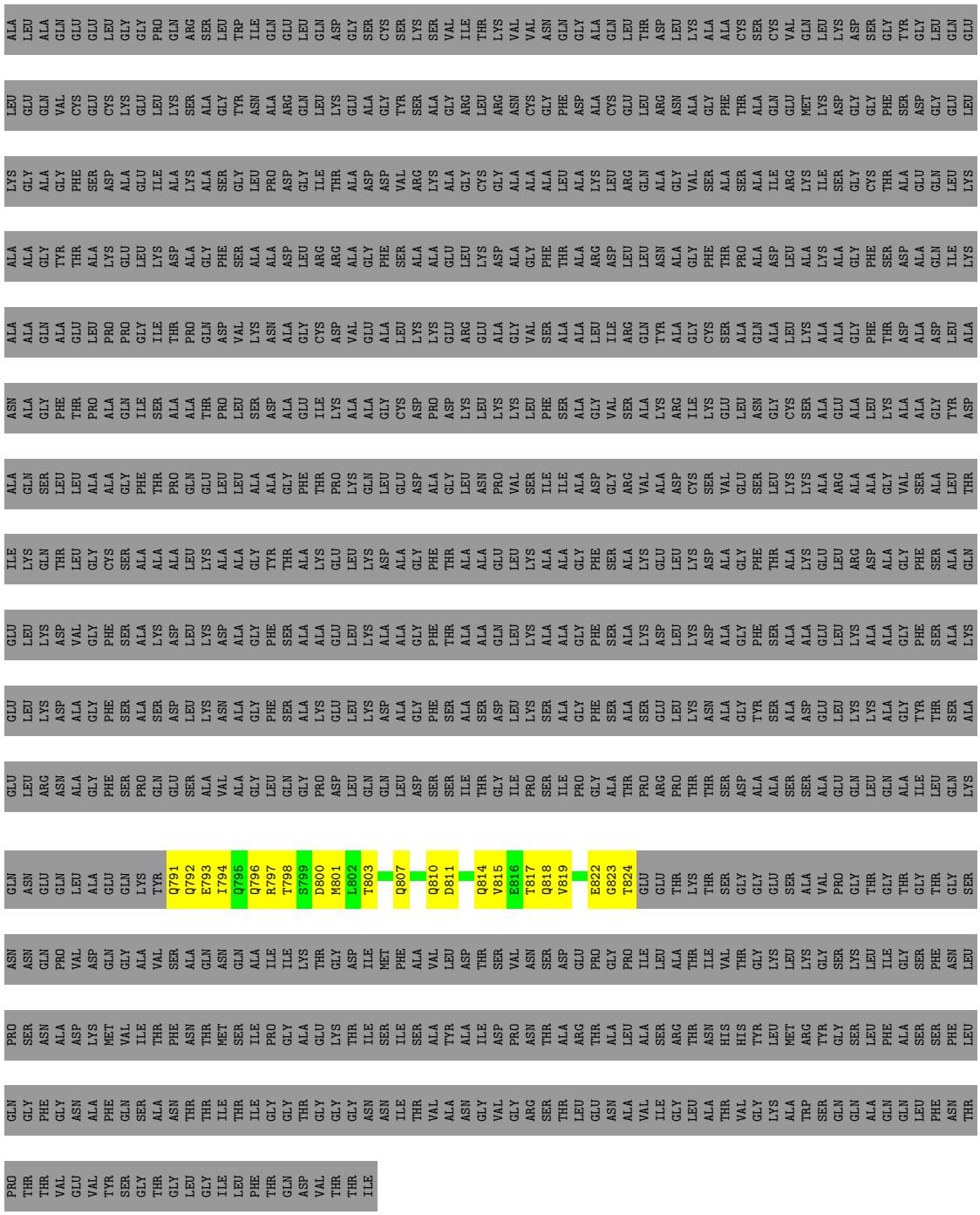
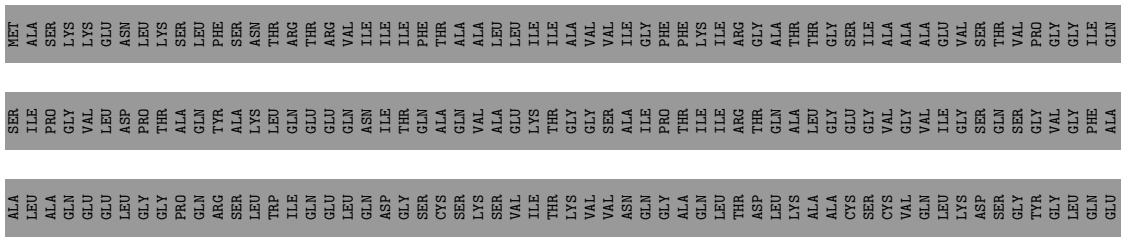
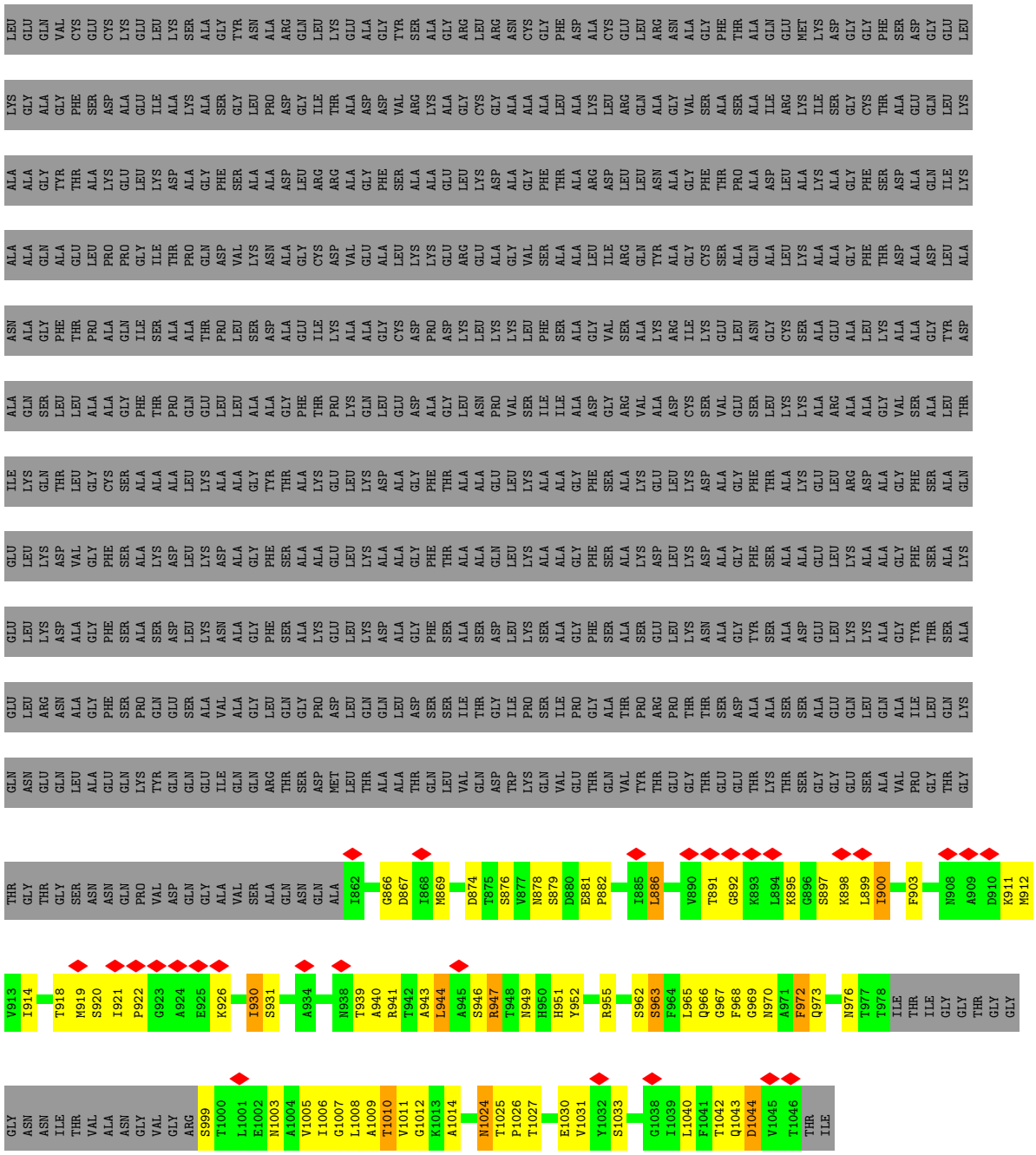
GLU LEU ARG ASN ALA GLY PHE SER PRO GLN GLU SER ALA VAL ALA GLY LEU GLN GLN GLN ASP SER SER ILE THR GLY ILE PRO GLY ALA THR PRO ARG PRO THR THR SER ASP ALA ALA SER GLN LEU GLN ALA ILE LEU GLN LYS
GLU LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS ASP ALA GLY PHE SER ALA SER ASP LEU LYS SER ALA ALA GLY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



• Molecule 1: IcmE protein

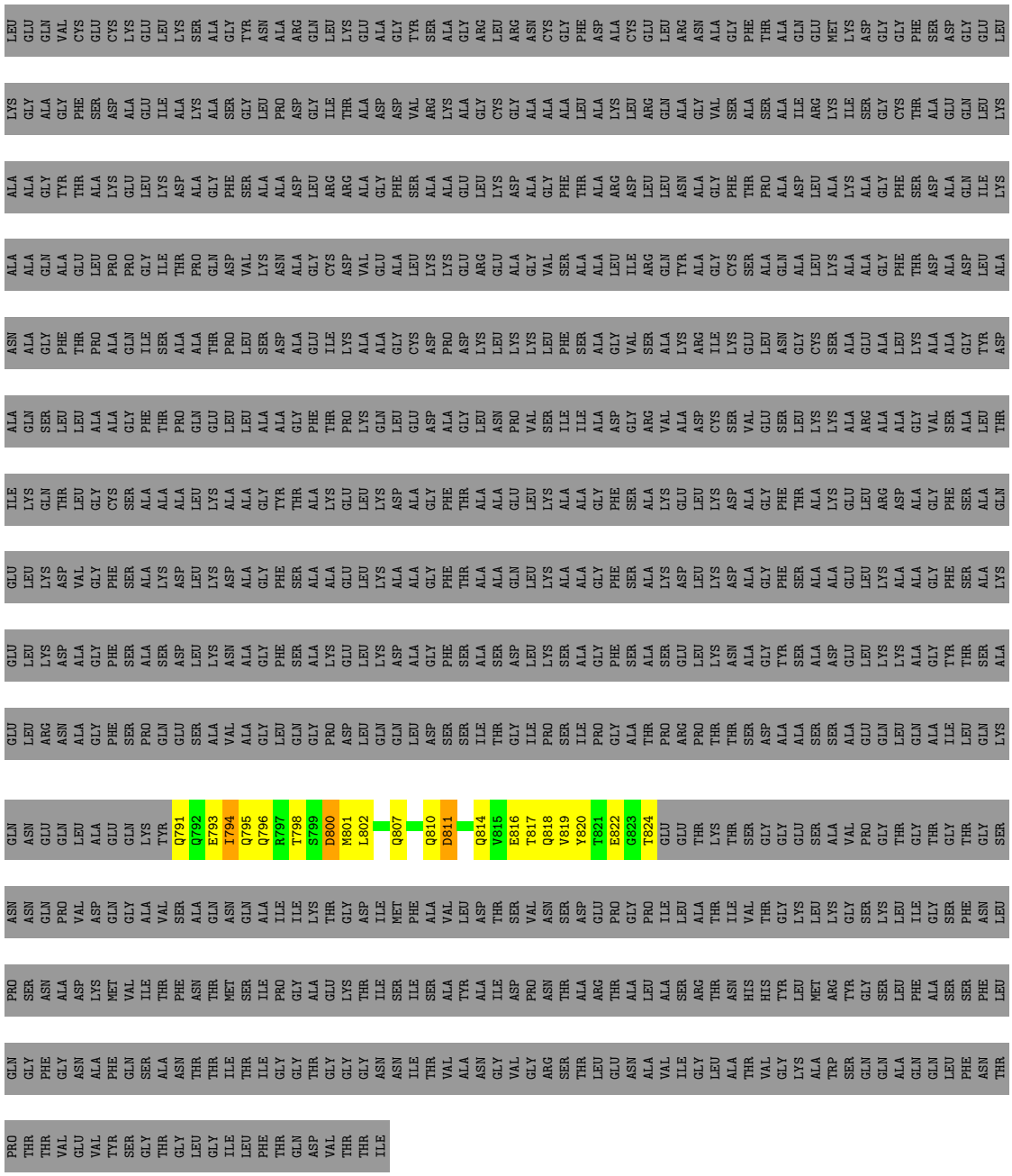
Chain GG:





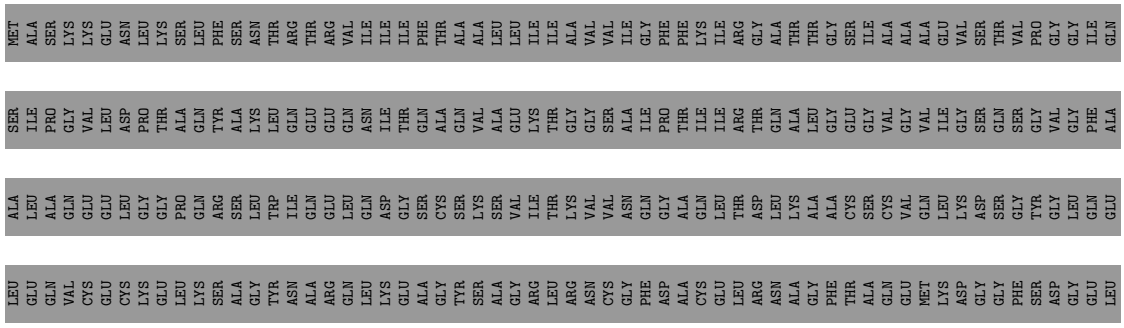
• Molecule 1: IcmE protein

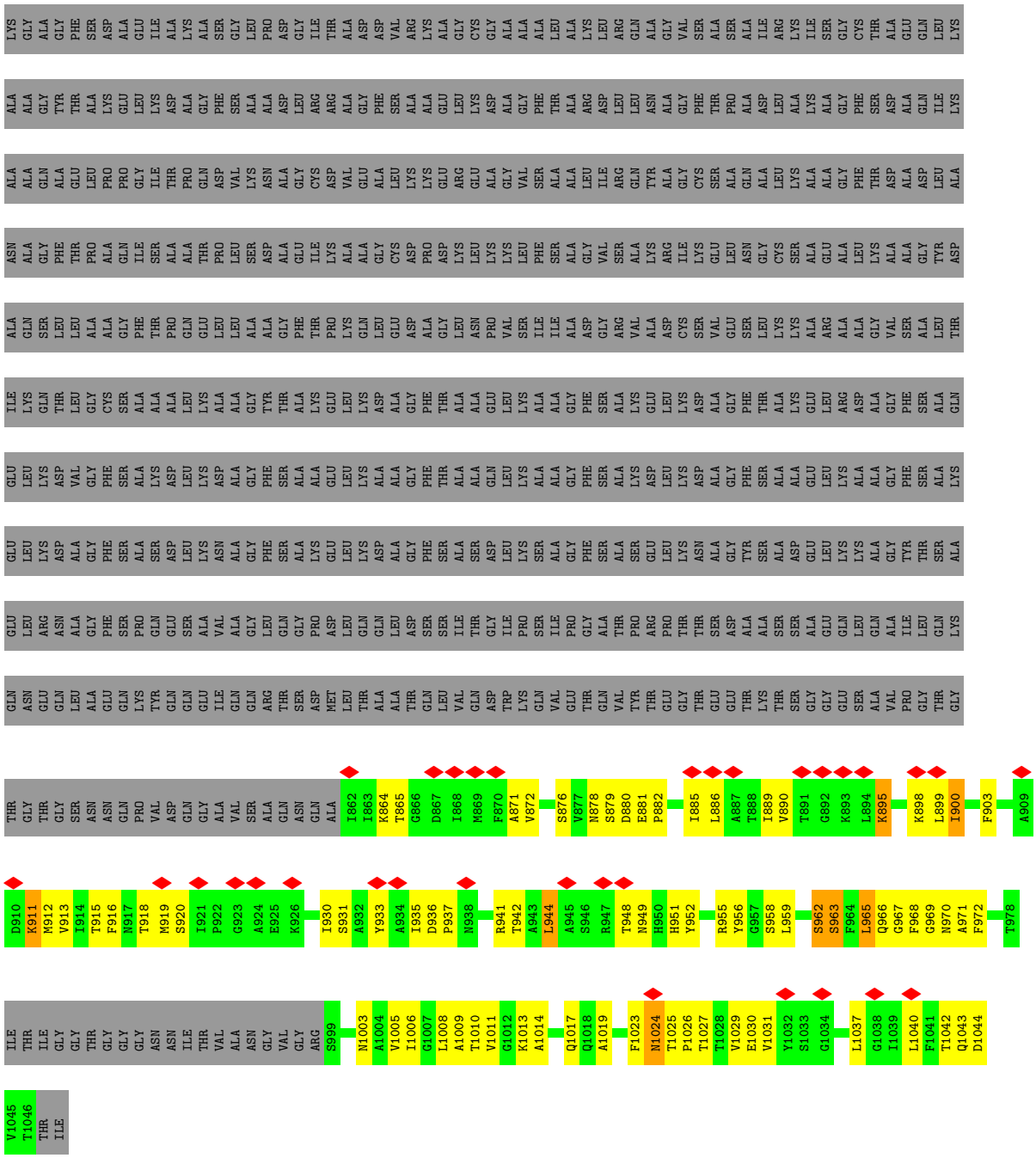
Chain Dg: 97%



• Molecule 1: IcmE protein

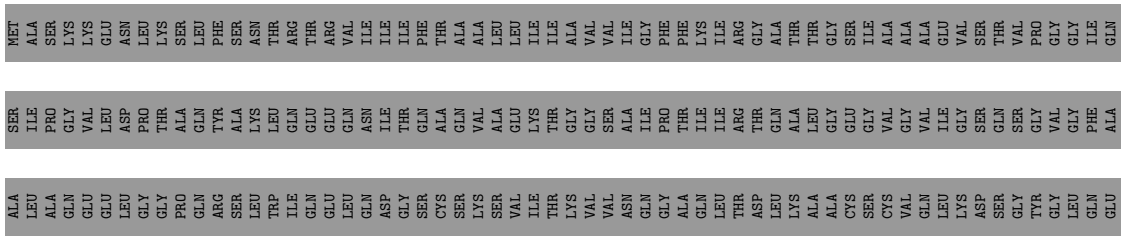
Chain HG:

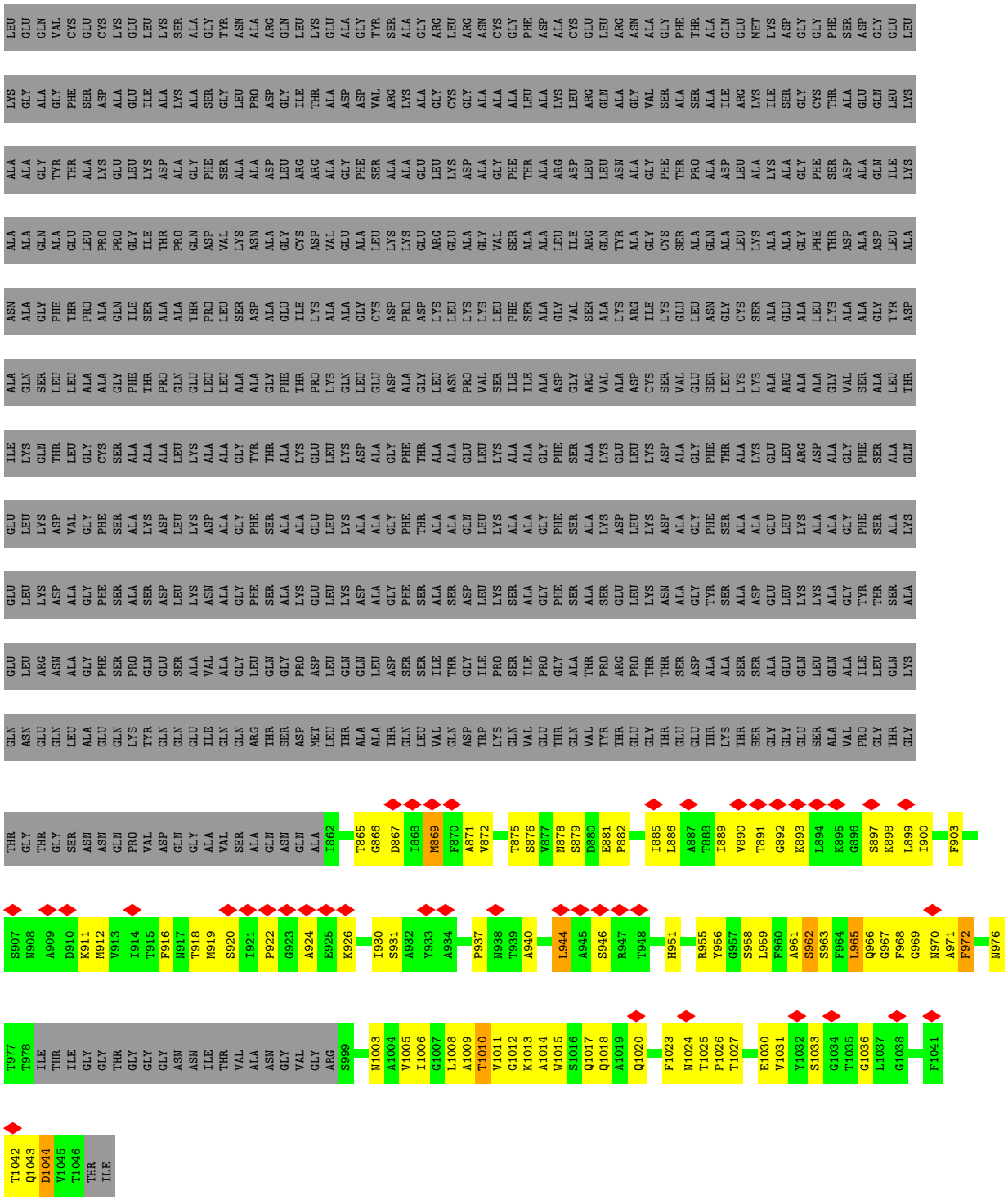




• Molecule 1: IcmE protein

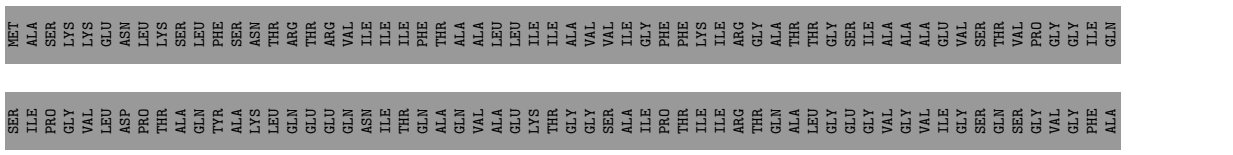
Chain IG: 8% 7% • 84%

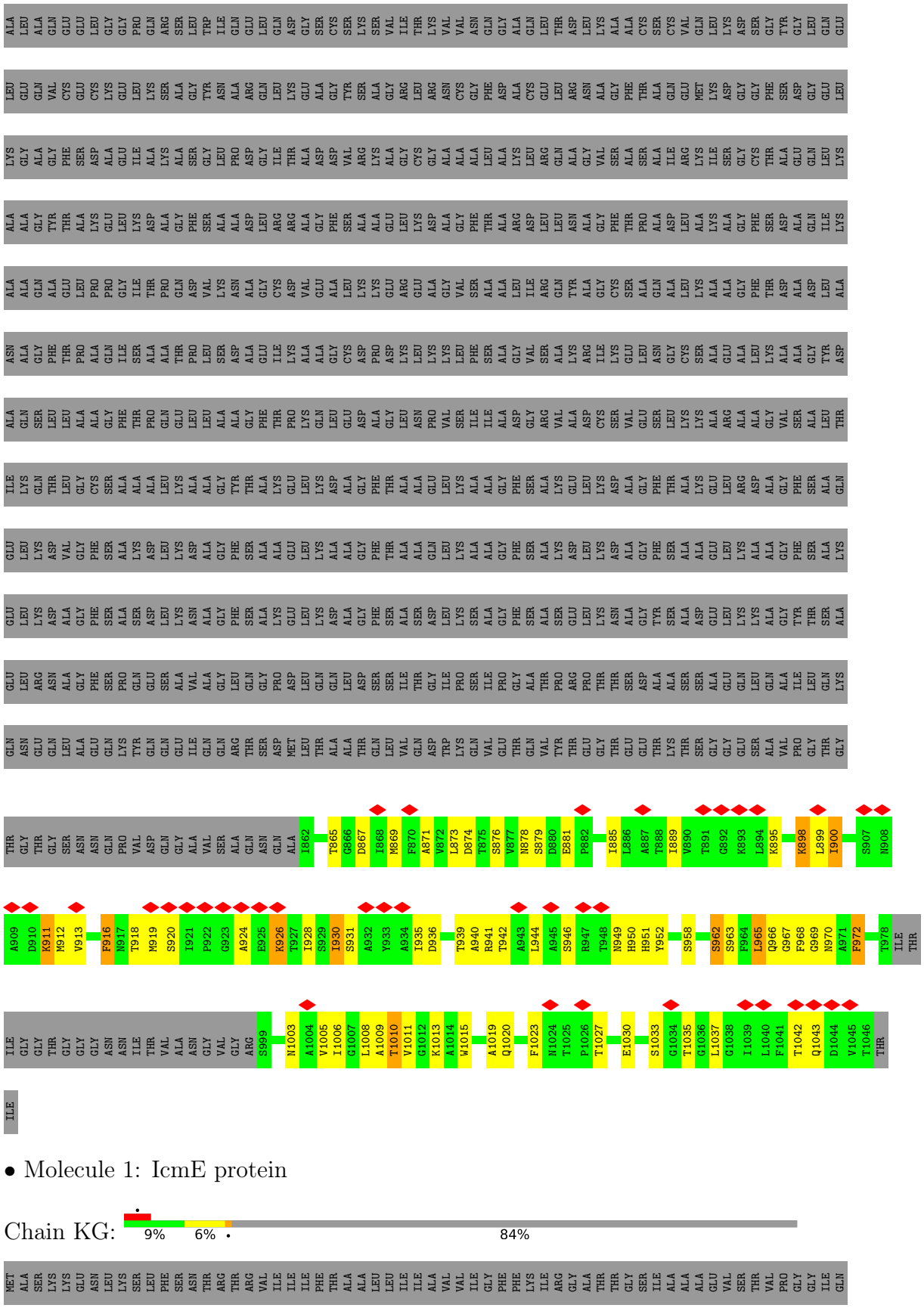




• Molecule 1: IcmE protein

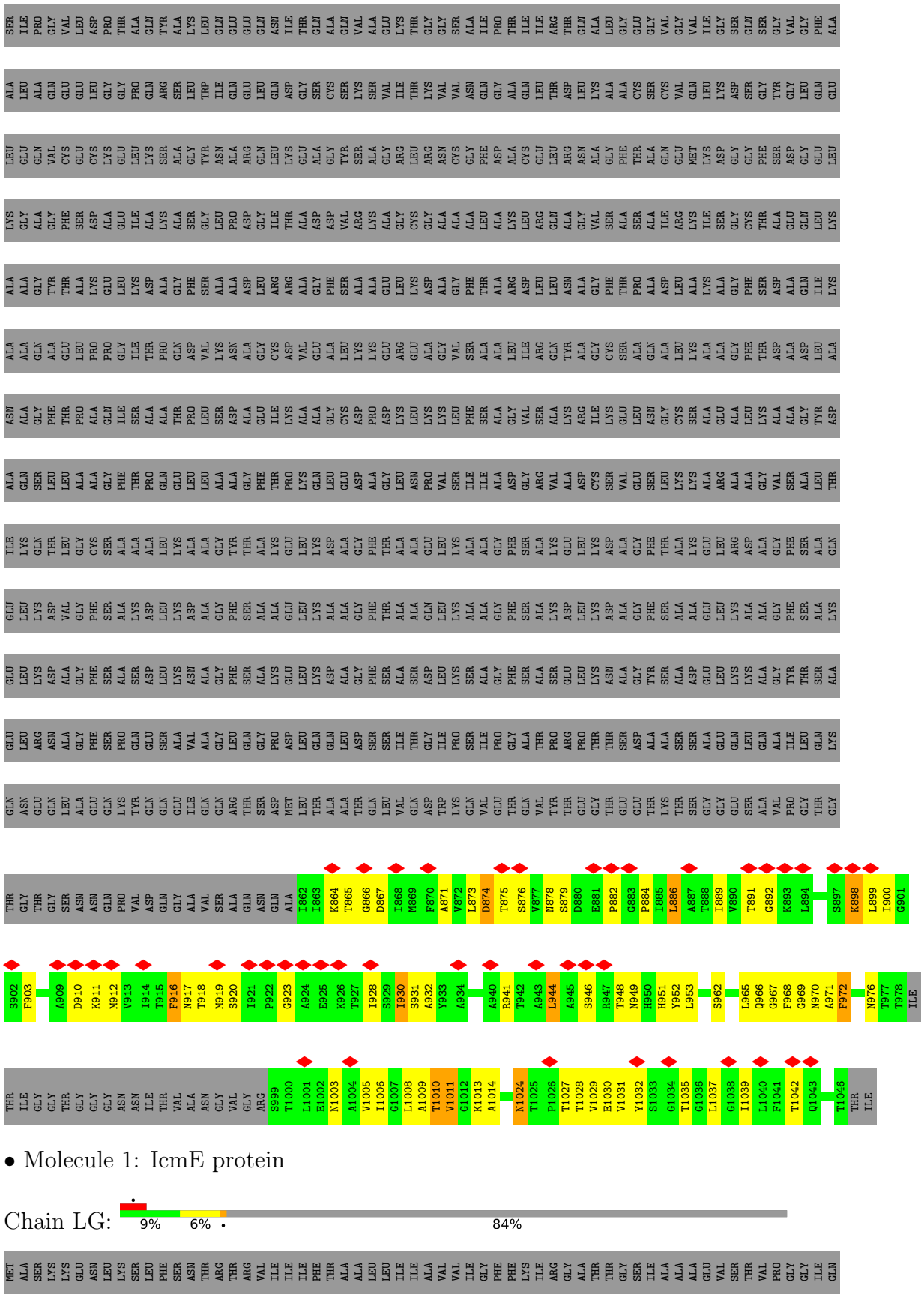
Chain JG: 9% 6% 84%





- Molecule 1: IcmE protein

Chain KG: 9% 6% 84%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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 SER ALA GLY ARG LEU ARG ASN CYS GLY PHE ASP ALA GLN 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 ALA ALA LEU ARG GLN ALA GLY VAL SER ALA SER ALA ILE ARG LYS ILE SER GLY CYS THR ALA GLU GLN ILE LYS
ALA ALA GLY TYR THR ALA LYS GLU LEU LYS ASP ALA GLY PHE SER ALA ALA ALA GLU GLU LEU LYS ASP ALA GLY PHE THR PRO ALA ASP LEU ALA LYS ASP LEU ASN ALA GLY PHE THR PRO ALA GLN ALA GLY PHE SER ALA GLY PHE SER ASP ALA GLN ILE LYS
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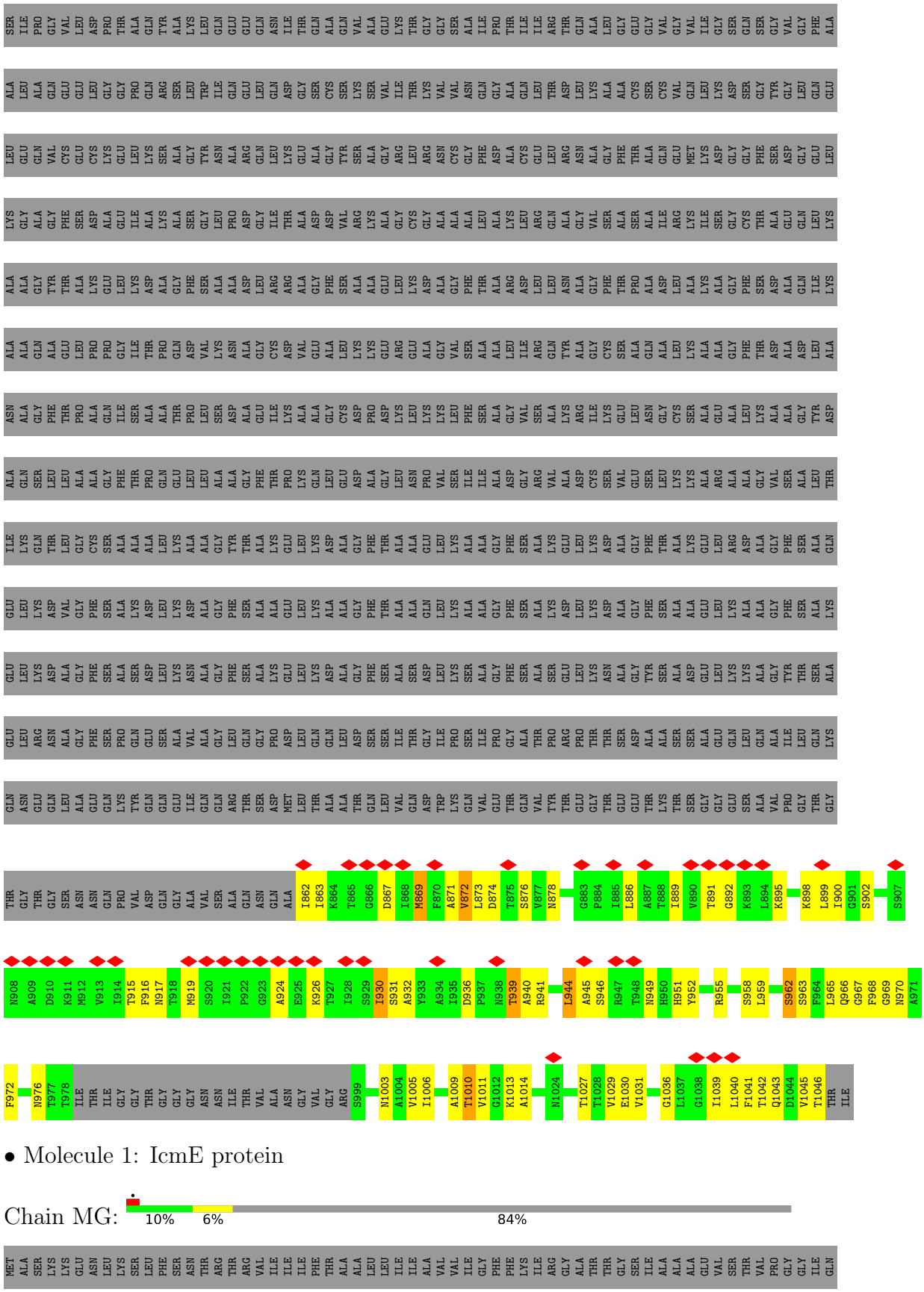
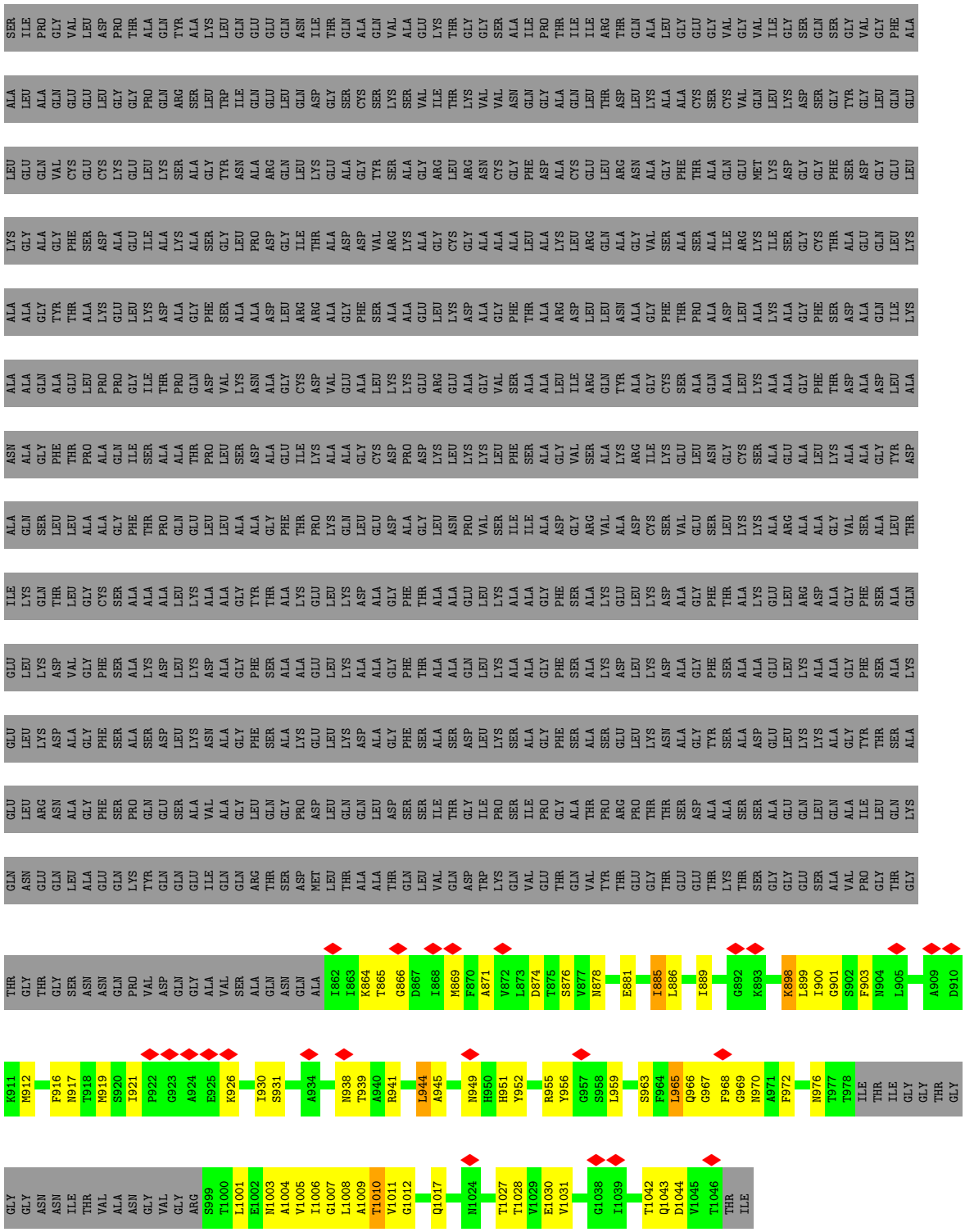
ASN ALA GLY PHE THR PRO ALA GLN ILE SER ALA ALA THR PRO LEU SER ASP ALA GLU ILE LYS ALA ALA GLY CYS ASP PRO ASP LYS LYS LEU PHE SER ALA ALA GLY VAL SER ALA LYS ARG ILE LYS GLU SER ALA GLU GLU ALA ALA ALA LEU LYS ALA ALA GLY TYR ASP
ALA GLN SER LEU LEU ALA ALA GLY PHE THR PRO GLN GLU LEU LEU ALA ALA GLY 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 ALA LEU LYS ALA GLY 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 ALA GLU LEU LYS ASP ALA GLY PHE SER ALA LYS ALA 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 ALA GLU LEU LYS ALA ALA GLY PHE THR ALA ALA ALA GLN LEU LYS ASP ALA GLY PHE SER ALA LYS ASP LEU LYS ASP ALA GLY PHE SER ALA 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 ALA ALA ASP LYS LEU LYS ASN ALA GLY PHE SER ALA ALA GLU LEU LYS ALA ALA GLY TYR THR SER ALA
GLU LEU ARG ASN ALA GLY PHE SER PRO GLN GLU GLN SER ALA VAL ALA GLY LEU GLN GLY PRO ASP LEU SER ILE THR GLY ILE PRO SER ILE PRO GLY ALA THR PRO ARG PRO THR THR SER ASP GLU GLN LEU ALA ILE LEU GLN GLN LYS
GLN ASN GLU GLN GLN LEU ALA GLU GLN 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 ALA 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 I863 K864 T865 G866 D867 I868 M869 F870 A871 V872 L873 D874 T875 S876 V877 N878 S879 D880 E881 P882 G883 P884 I885 L886 A887 T888 I889 V890 T891 G892 K893 L894 S897 K898 L899 I900 G901
S902 F903 A909 D910 K911 M912 V913 I914 T915 F916 N917 T918 M919 S920 I921 P922 G923 A924 E925 K926 T927 I928 S929 I930 S931 A932 Y933 A934 A940 R941 T942 A943 L944 A945 S946 R947 T948 N949 H950 Y952 L953 S962 L965 Q966 G967 F968 G969 N970 A971 F972 N976 T977 T978 ILE
THR ILE GLY GLY THR GLY GLY GLY ASN ASN ILE THR VAL ALA ASN GLY VAL GLY ARG S999 T1000 L1001 E1002 N1003 A1004 V1005 I1006 G1007 L1008 A1009 T1010 V1011 G1012 K1013 A1014 N1024 T1025 P1026 T1027 T1028 V1029 E1030 V1031 Y1032 S1033 G1034 T1035 G1036 L1037 G1038 I1039 L1040 F1041 T1042 Q1043 T1046 THR ILE
• Molecule 1: IcmE protein
Chain LG: 9% 6% • 84%
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



- Molecule 1: IcmE protein

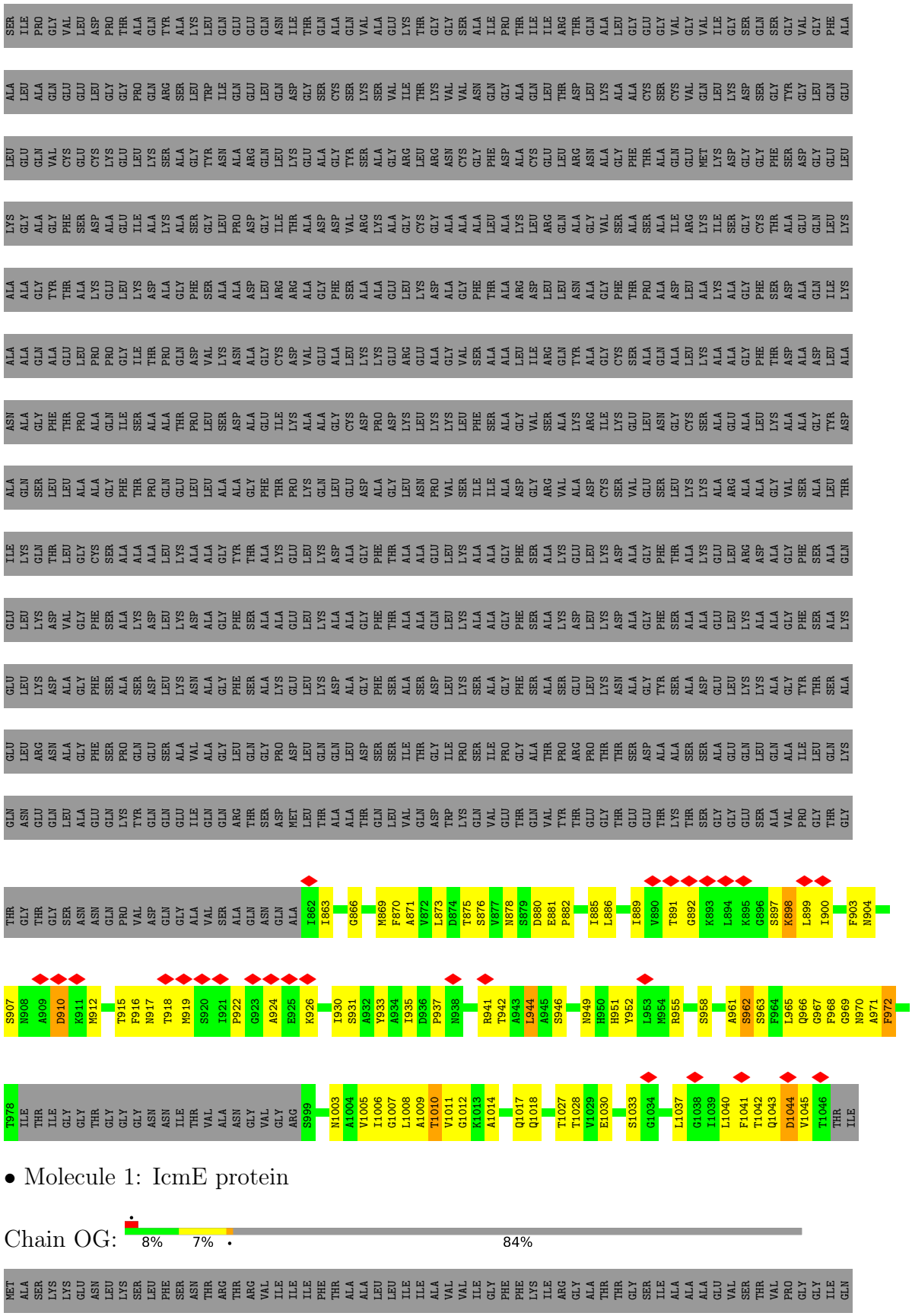
Chain MG: 10% 6% 84%

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



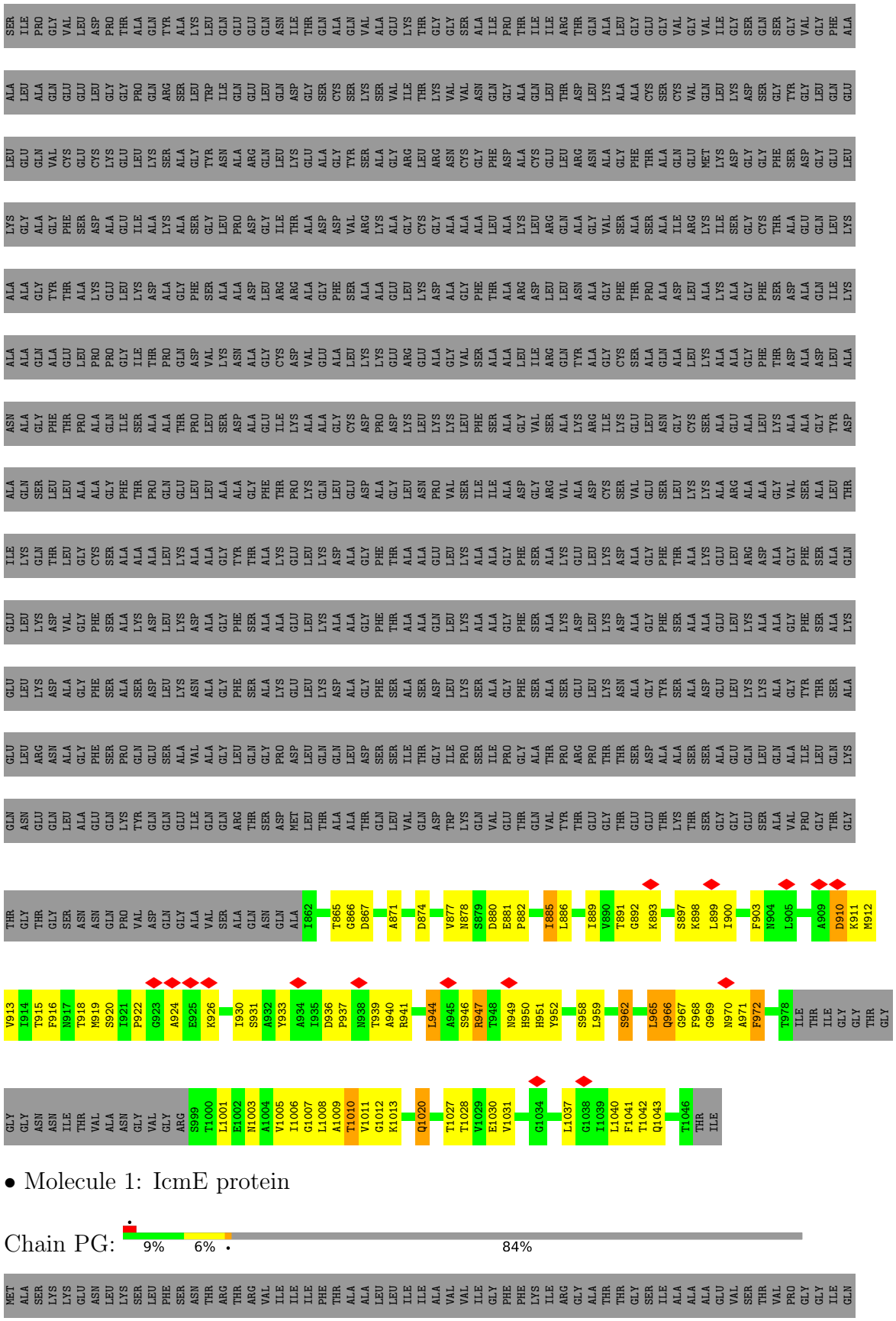
- Molecule 1: IcmE protein

Chain NG: 8% 7% • 84%



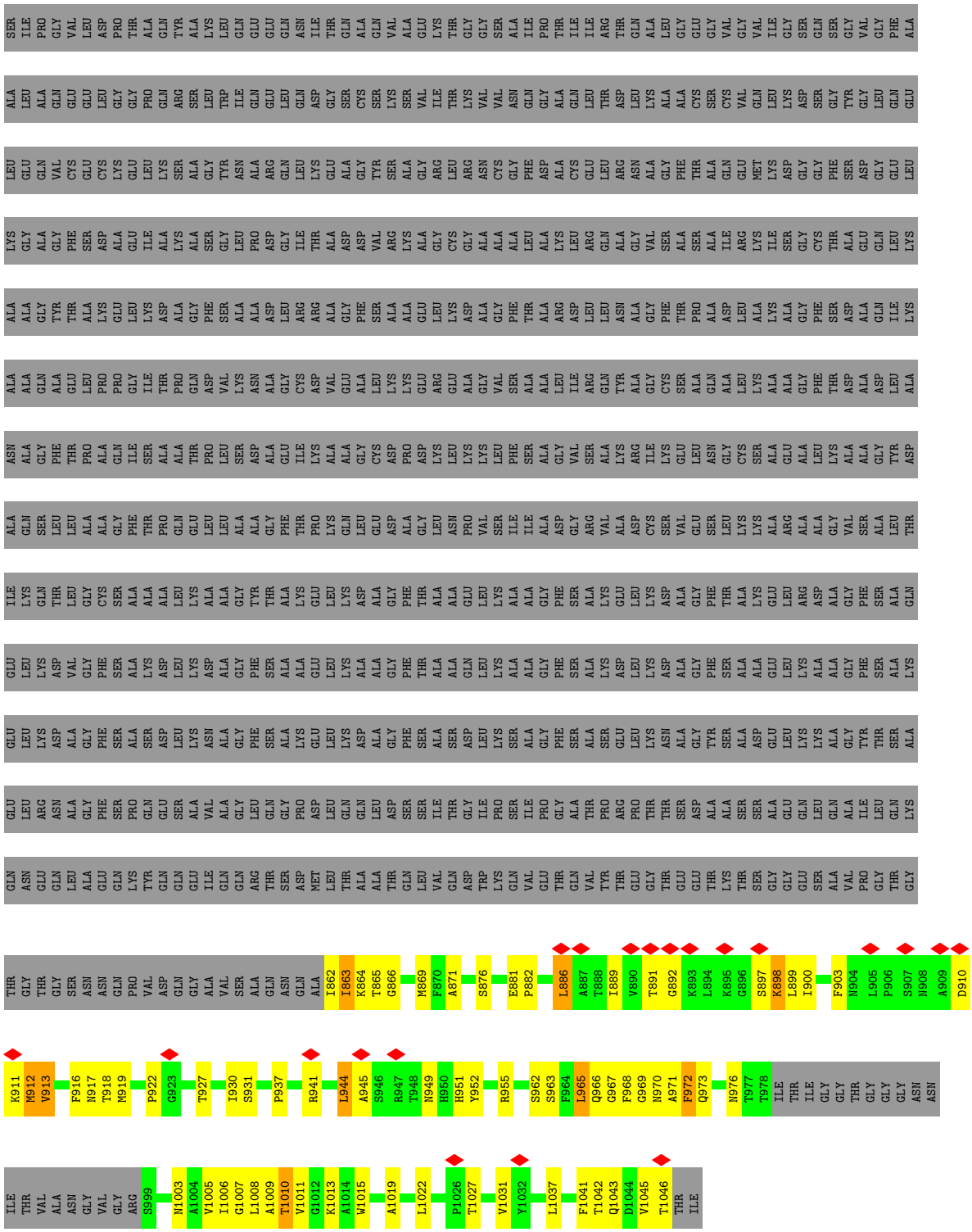
- Molecule 1: IcmE protein

Chain OG: 8% 7% • 84%



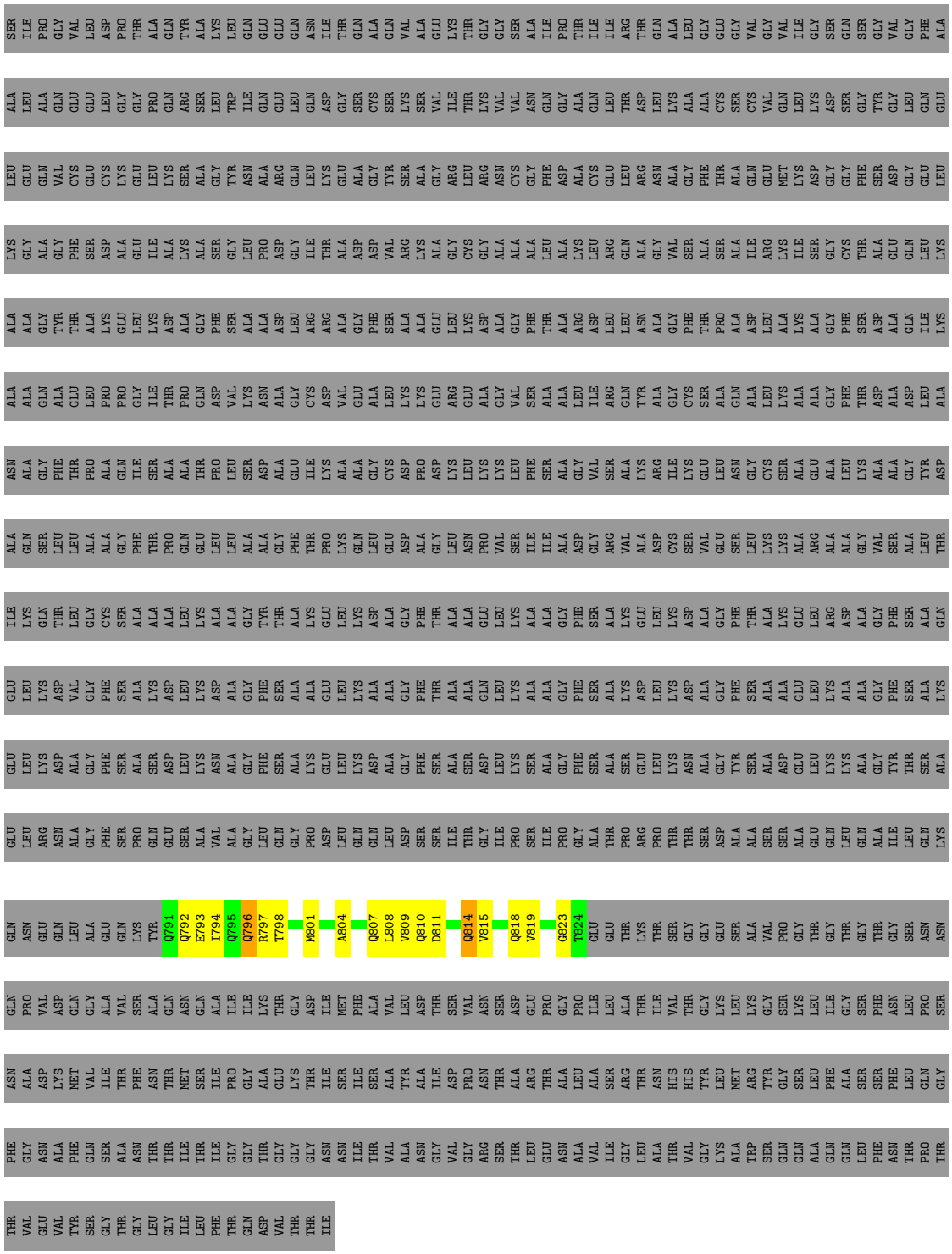
- Molecule 1: IcmE protein

Chain PG:



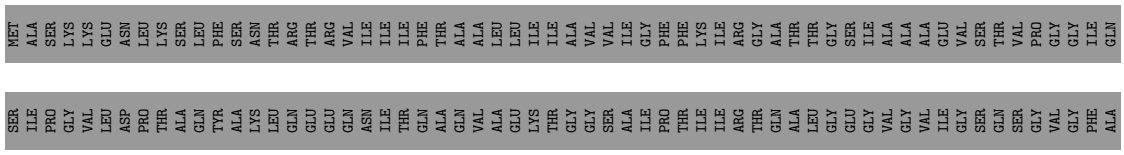
- Molecule 1: IcmE protein

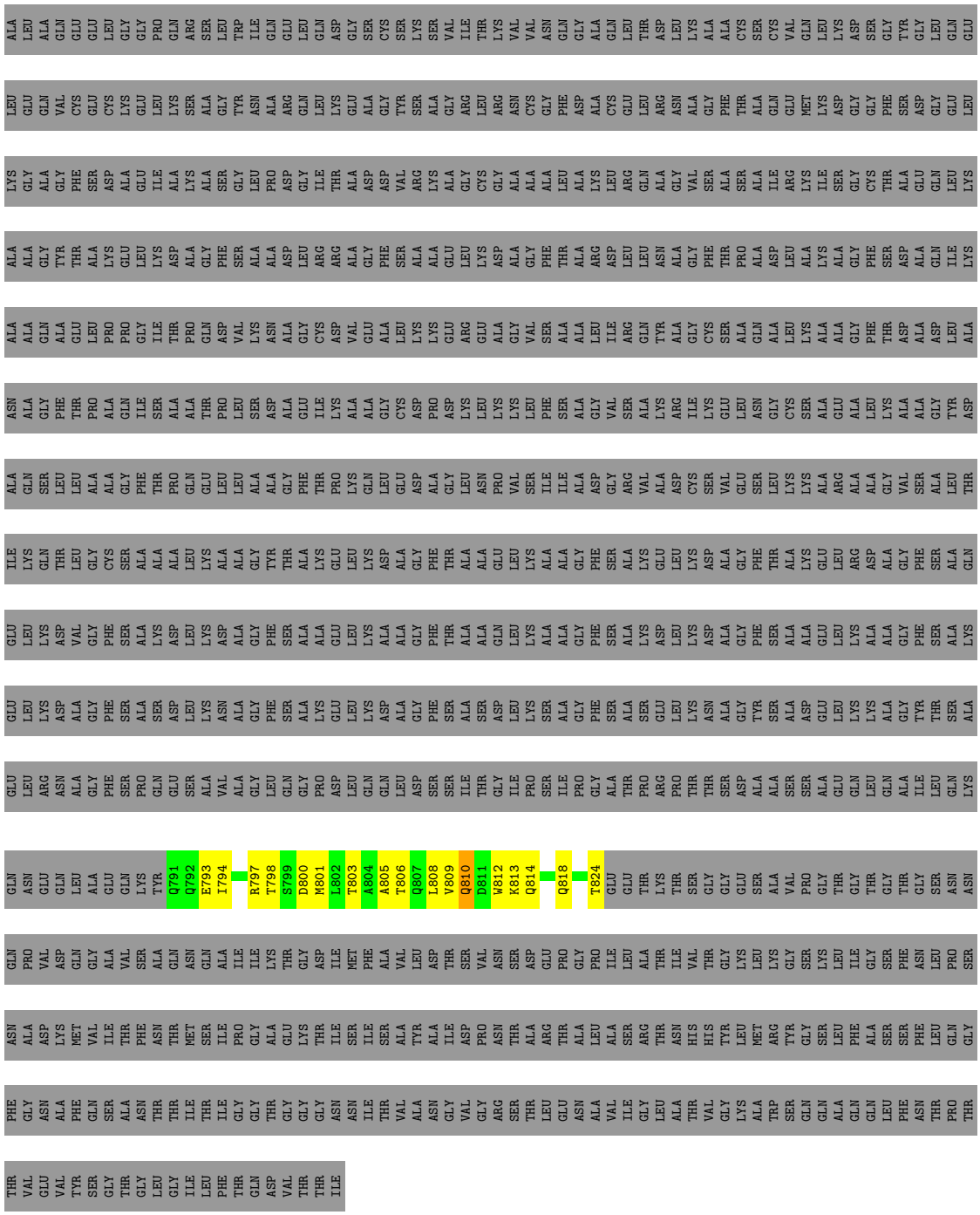
Chain Ag: 97%



• Molecule 1: IcmE protein

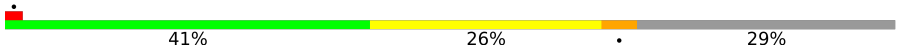
Chain Eg: 97%

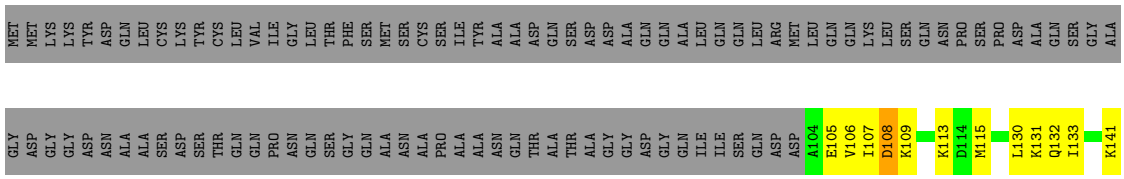


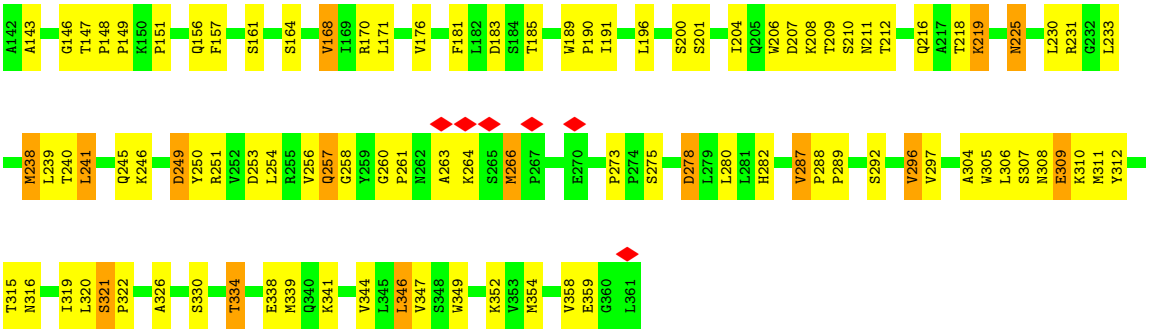


• Molecule 2: Type IV secretion protein IcmK

Chain EH:

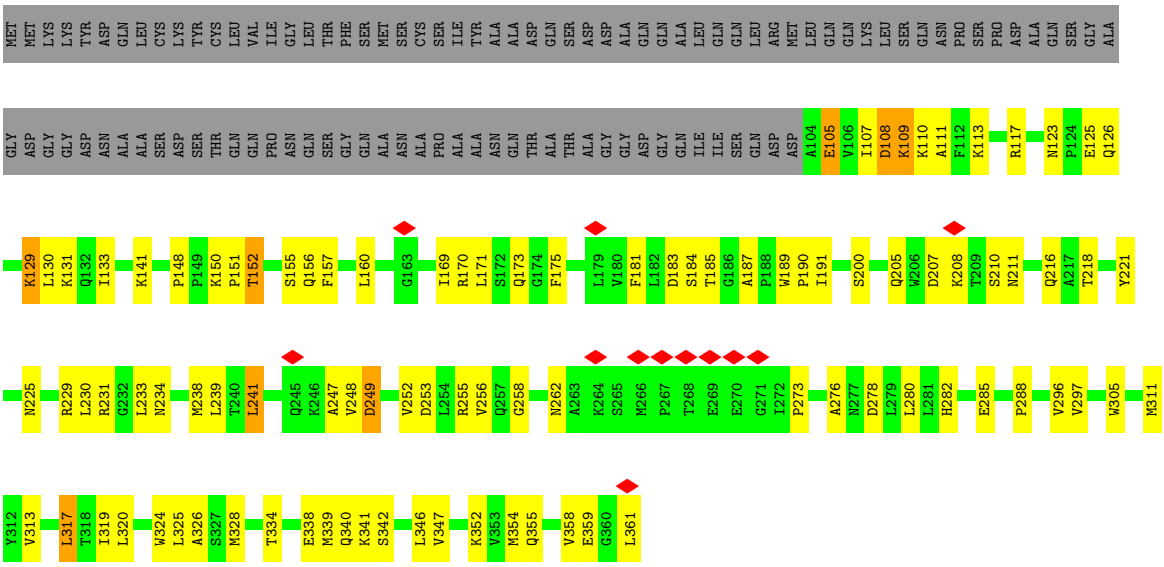






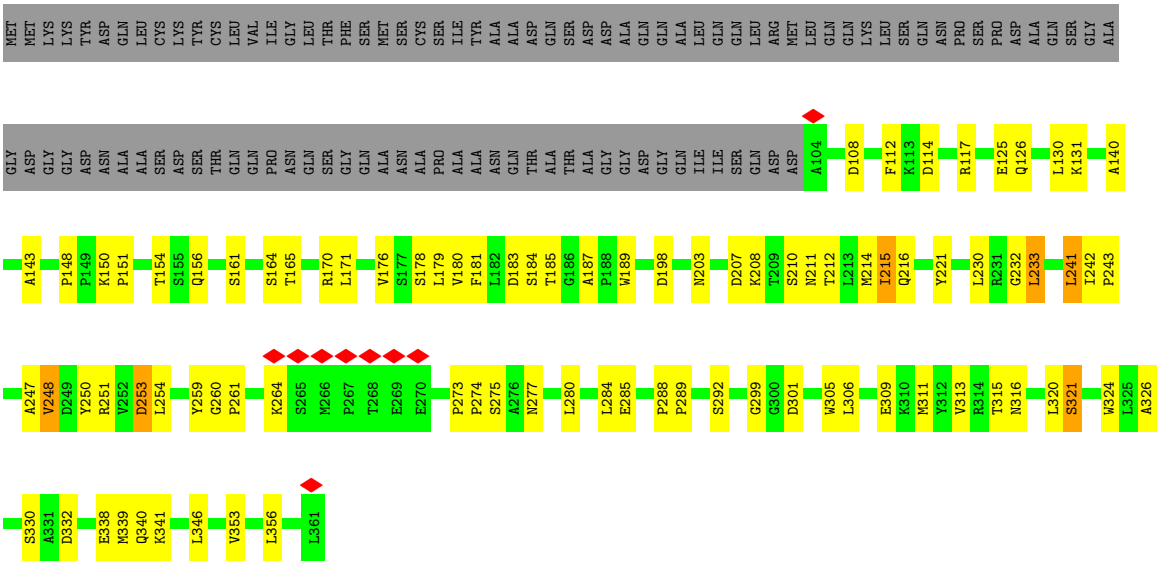
- Molecule 2: Type IV secretion protein IcmK

Chain FH:



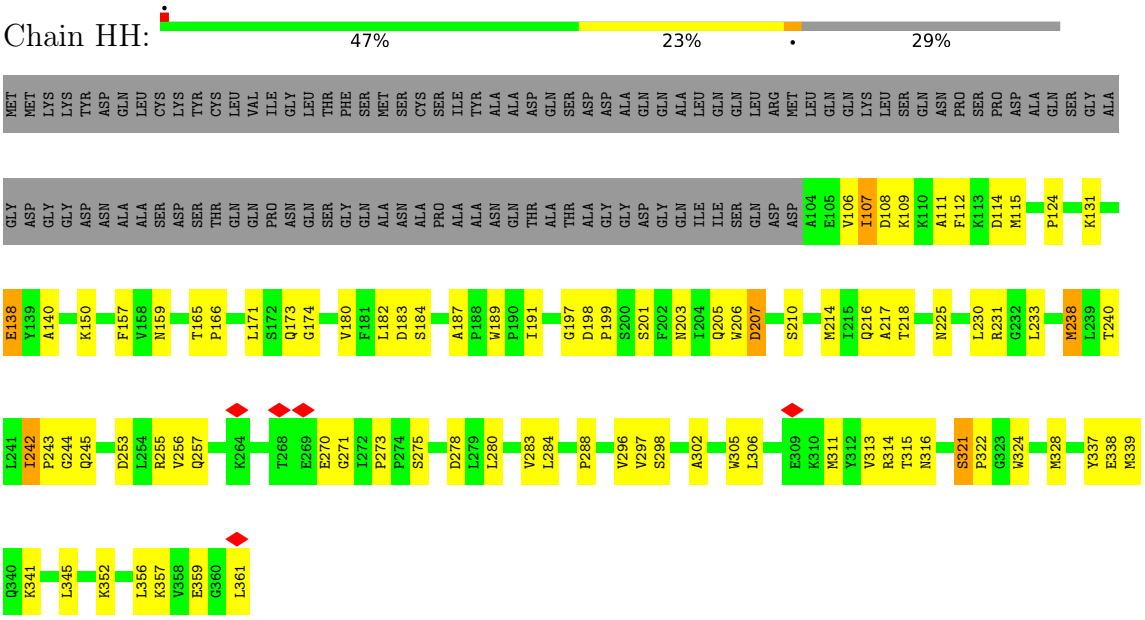
- Molecule 2: Type IV secretion protein IcmK

Chain GH:



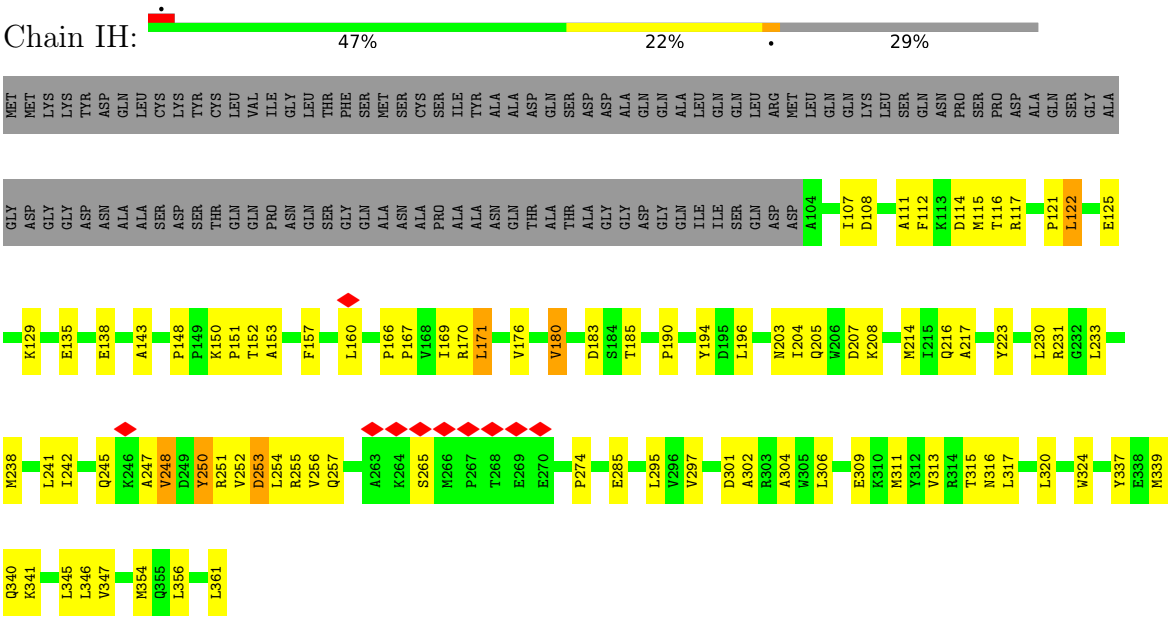
• Molecule 2: Type IV secretion protein IcmK

Chain HH:



• Molecule 2: Type IV secretion protein IcmK

Chain IH:



• Molecule 2: Type IV secretion protein IcmK

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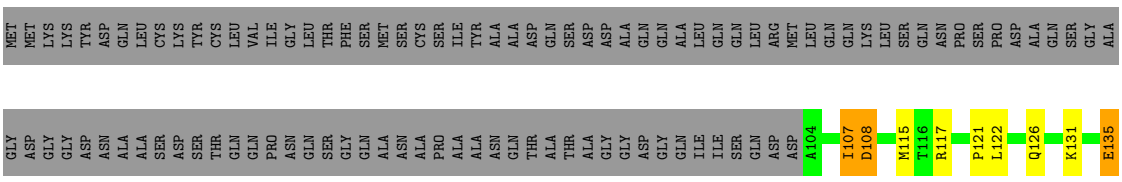
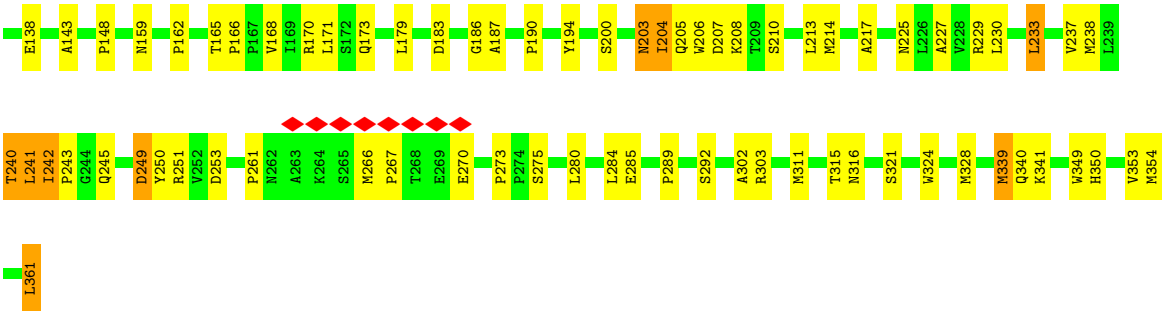
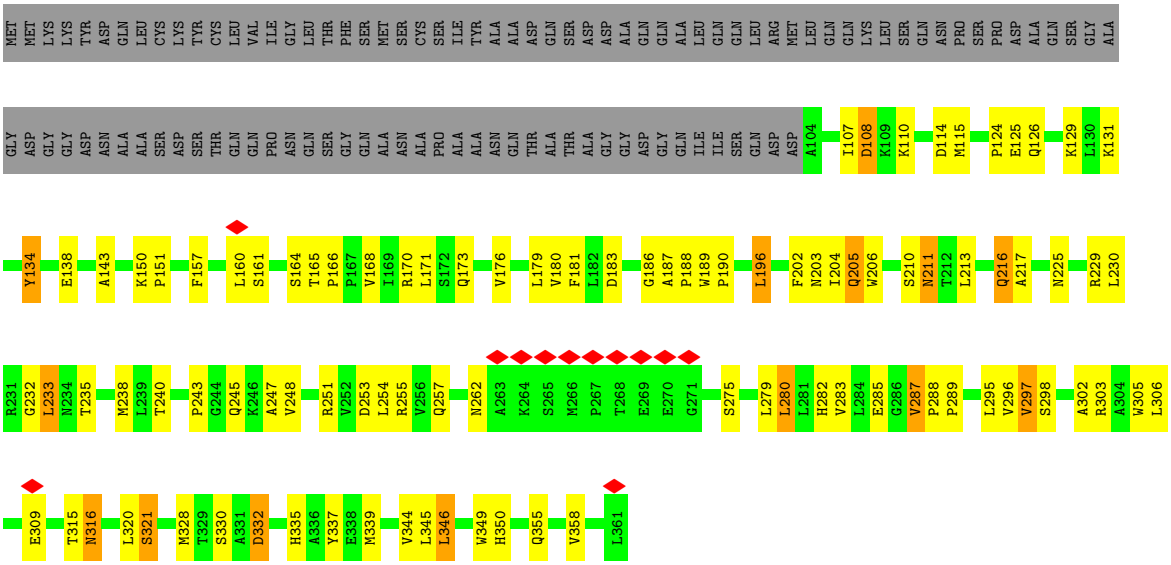




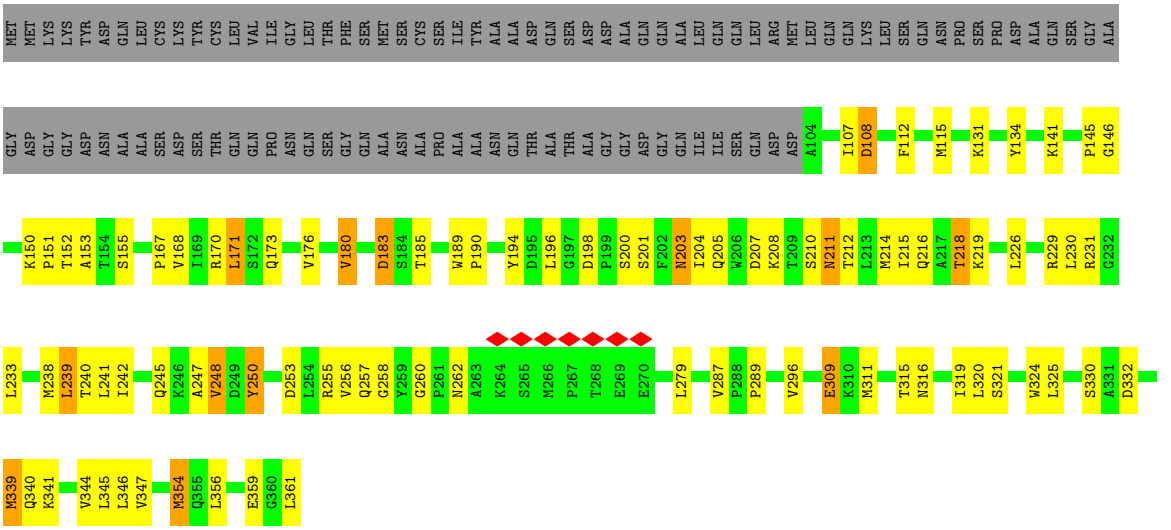
- Molecule 2: Type IV secretion protein IcmK

Chain AH:



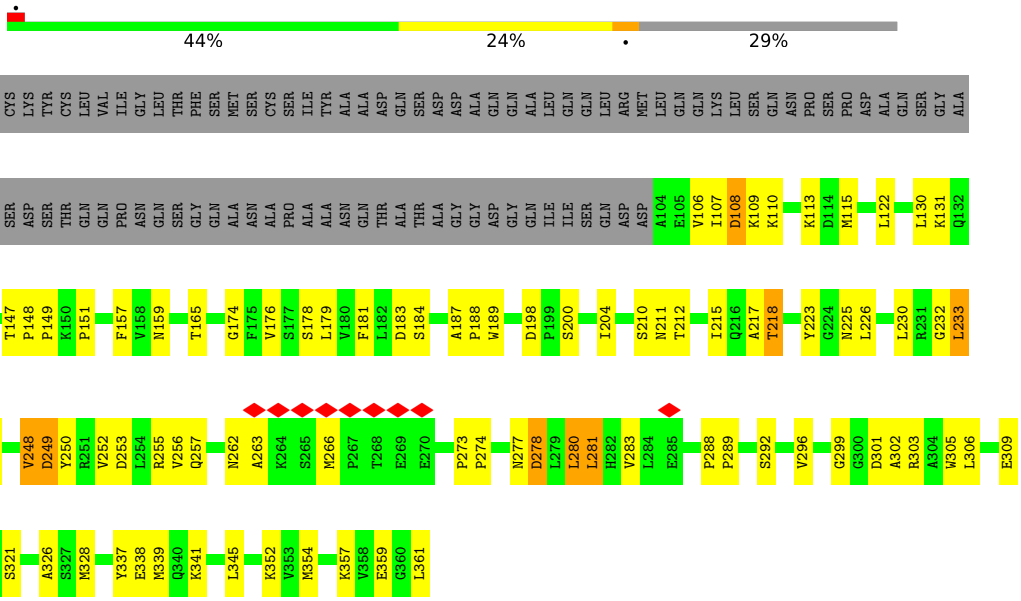
- Molecule 2: Type IV secretion protein IcmK

Chain KH:



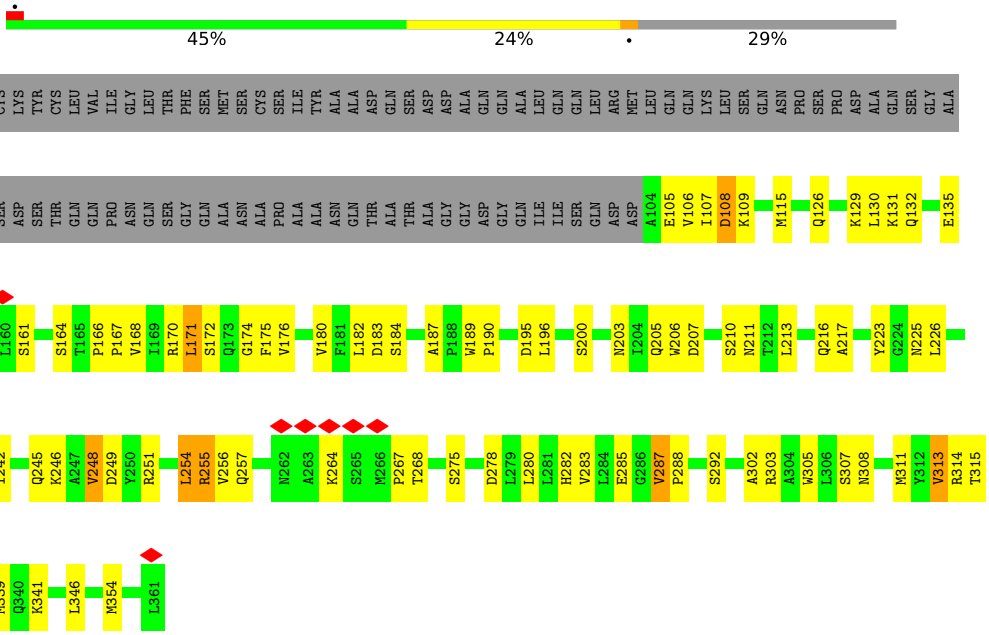
- Molecule 2: Type IV secretion protein IcmK

Chain LH:



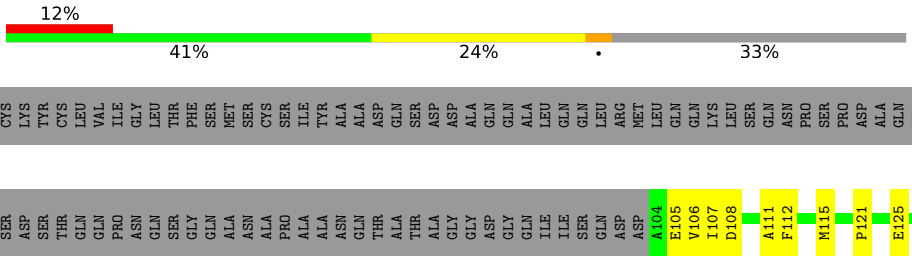
- Molecule 2: Type IV secretion protein IcmK

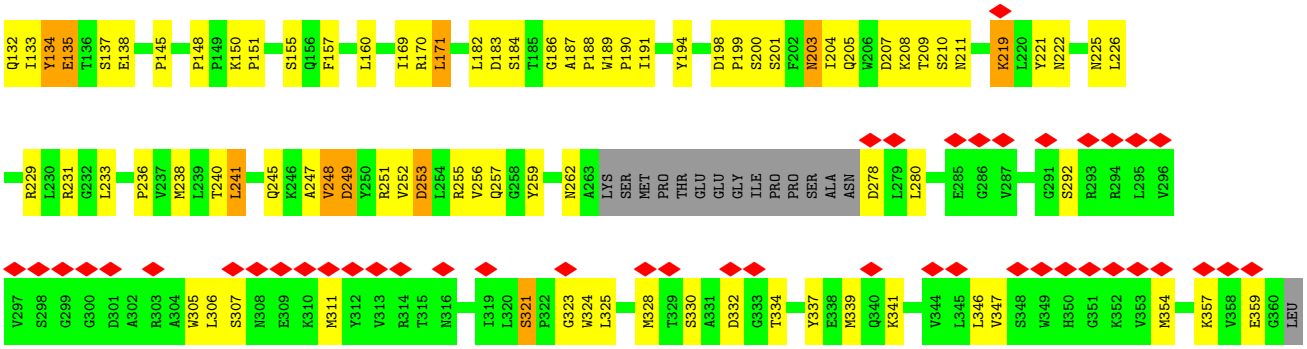
Chain MH:



- Molecule 2: Type IV secretion protein IcmK

Chain VH:





- Molecule 2: Type IV secretion protein IcmK

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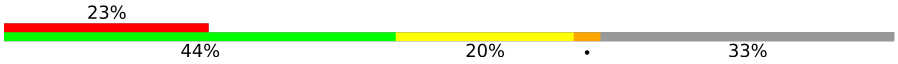
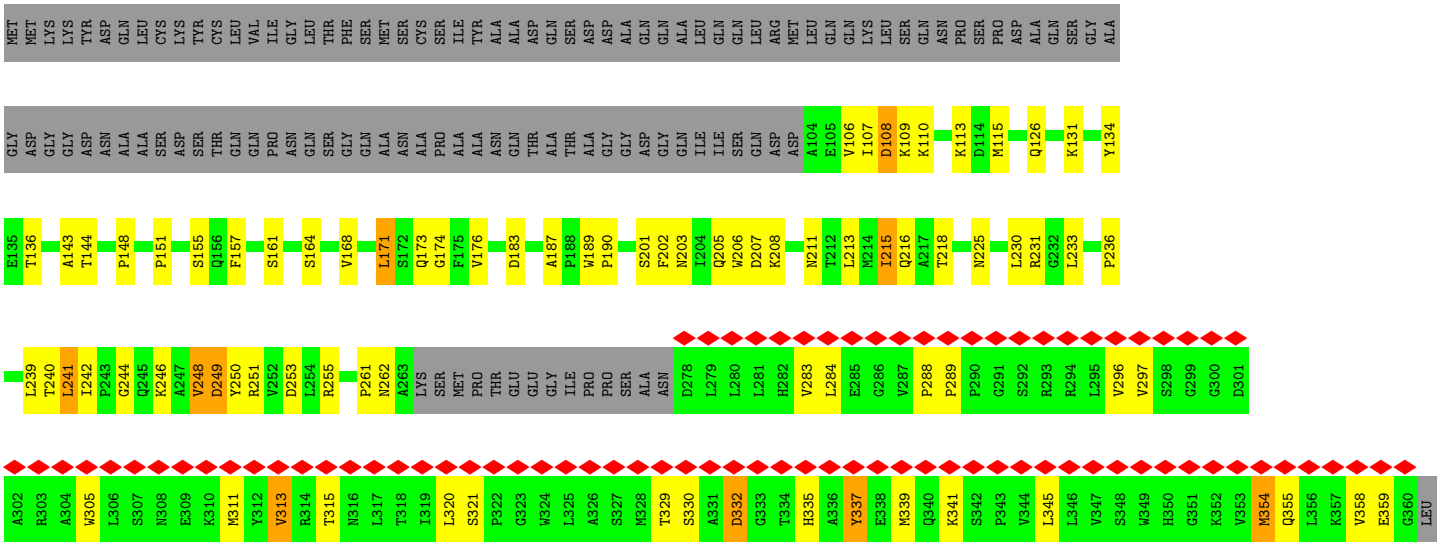
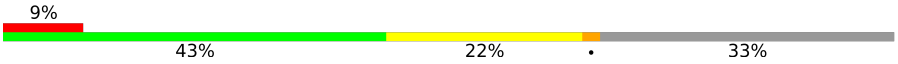
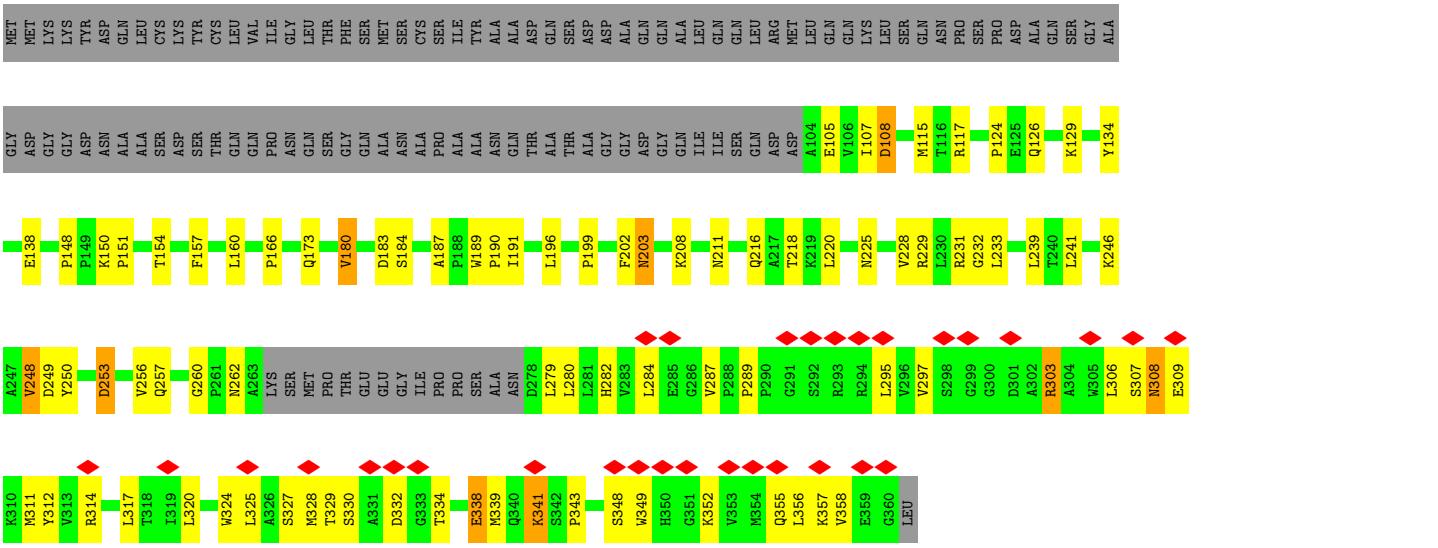




- Molecule 2: Type IV secretion protein IcmK

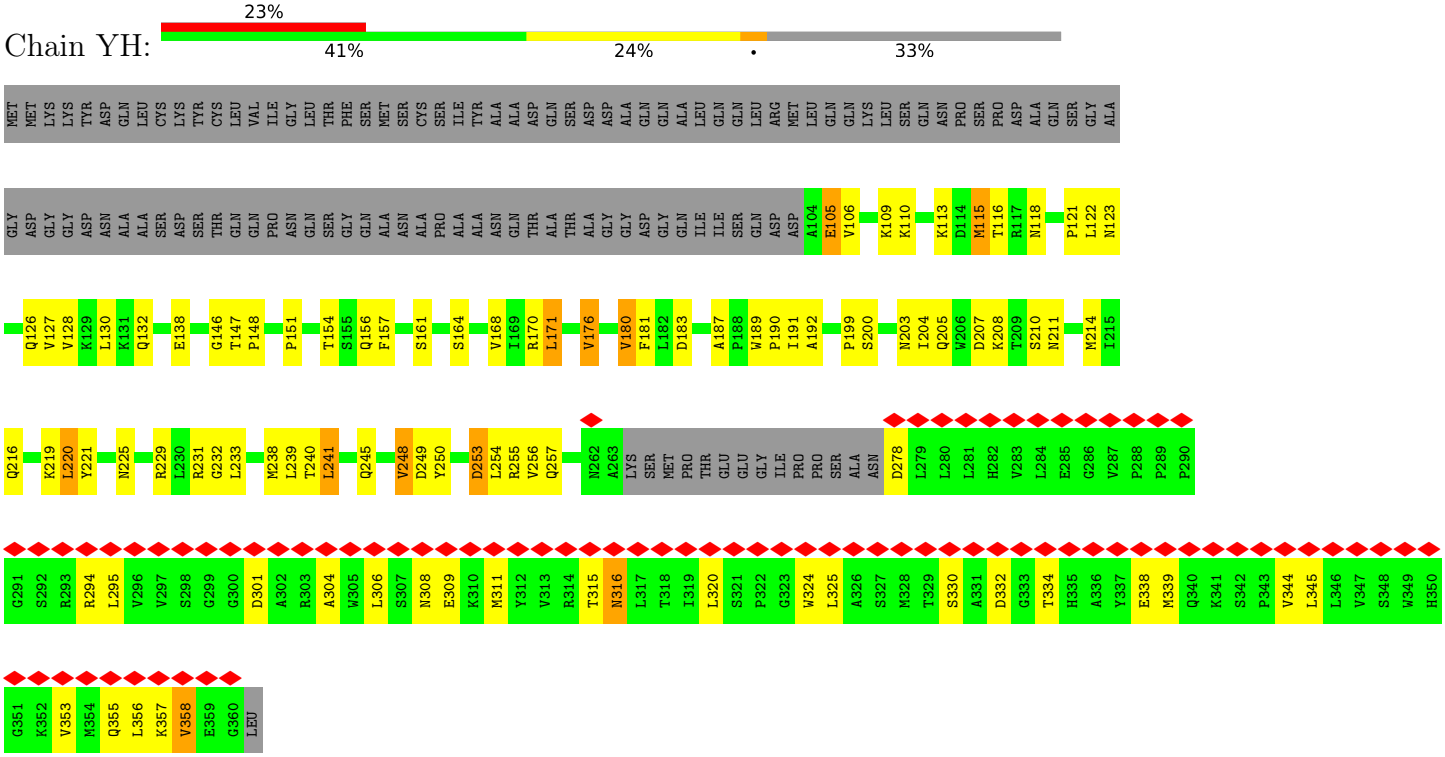
Chain XH:





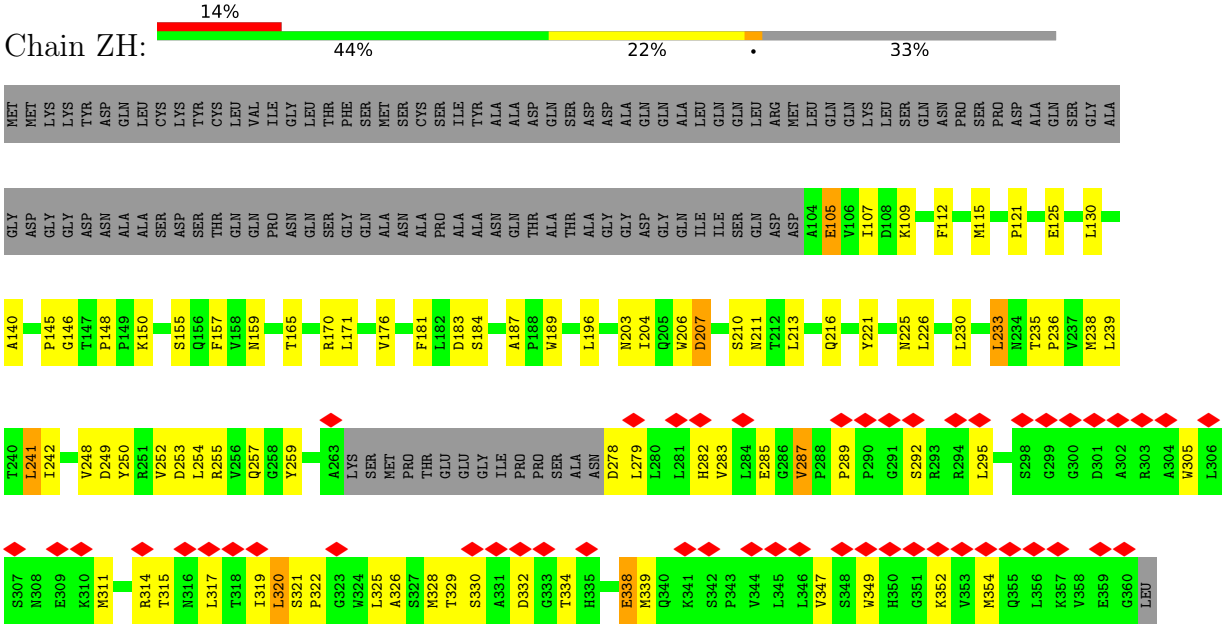
- Molecule 2: Type IV secretion protein IcmK

Chain YH:



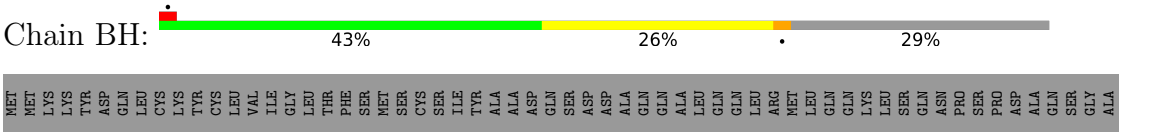
- Molecule 2: Type IV secretion protein IcmK

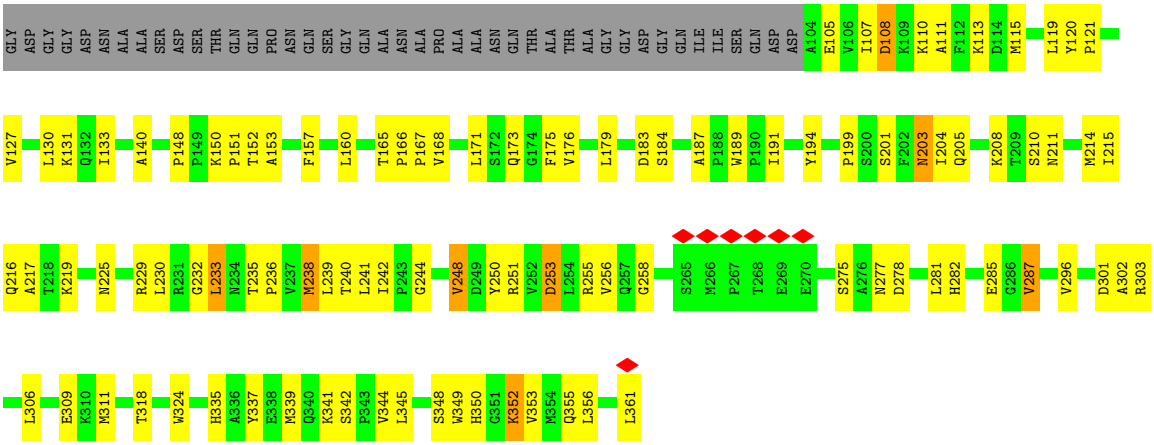
Chain ZH:



- Molecule 2: Type IV secretion protein IcmK

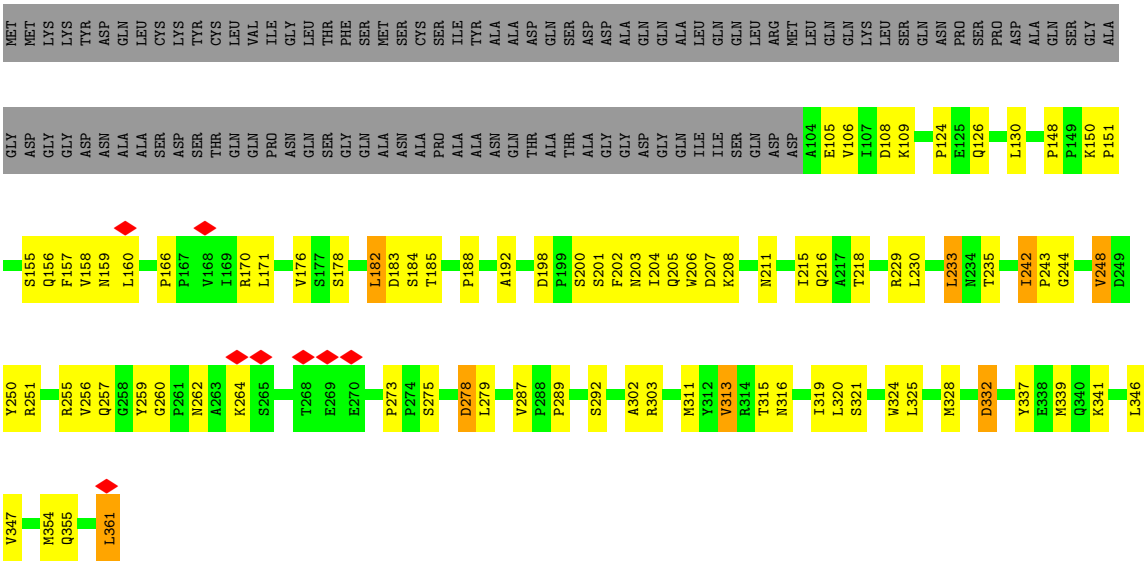
Chain BH:





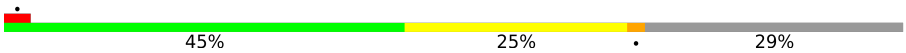
- Molecule 2: Type IV secretion protein IcmK

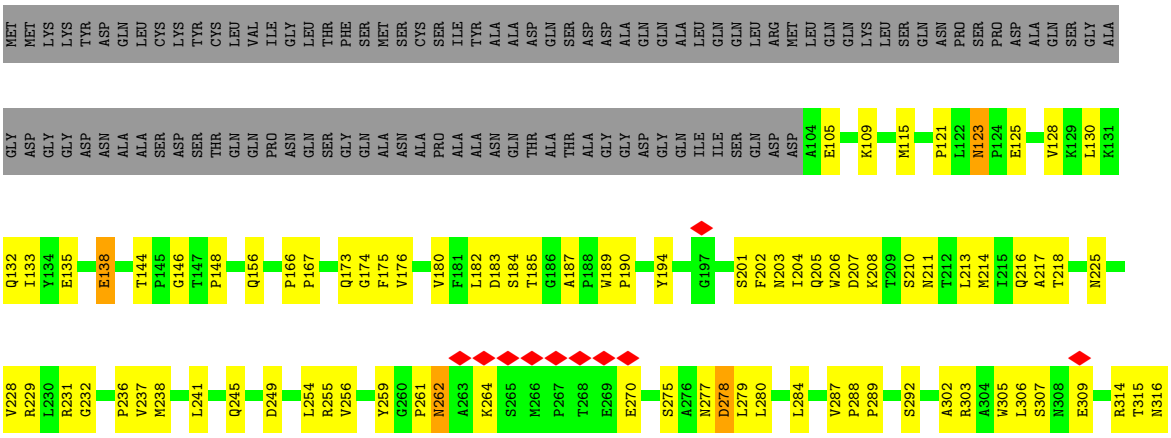
Chain CH:

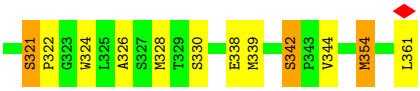


- Molecule 2: Type IV secretion protein IcmK

Chain DH:

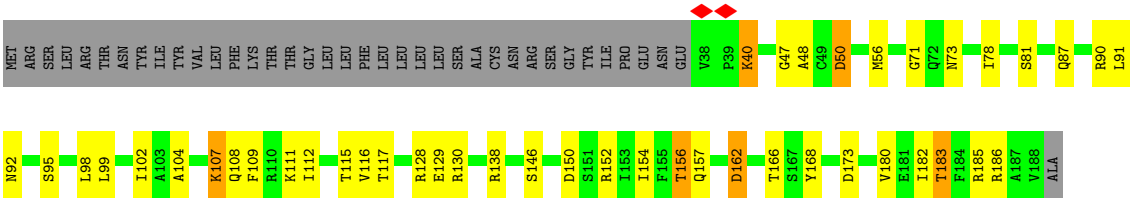






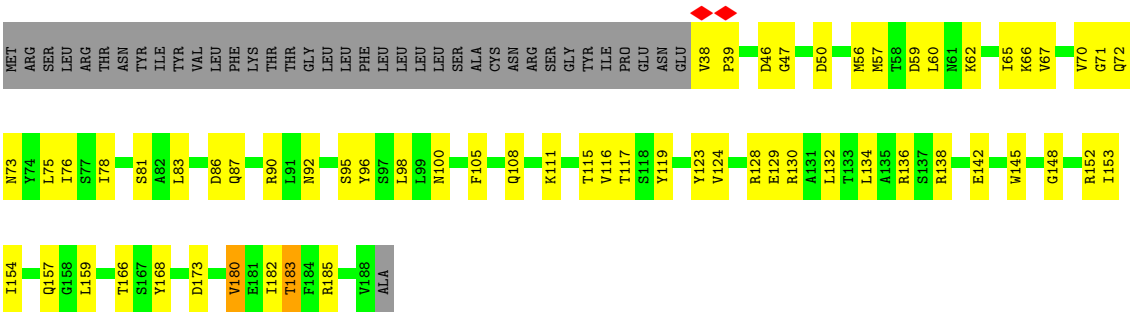
• Molecule 3: Inner membrane lipoprotein YiaD

Chain EK:



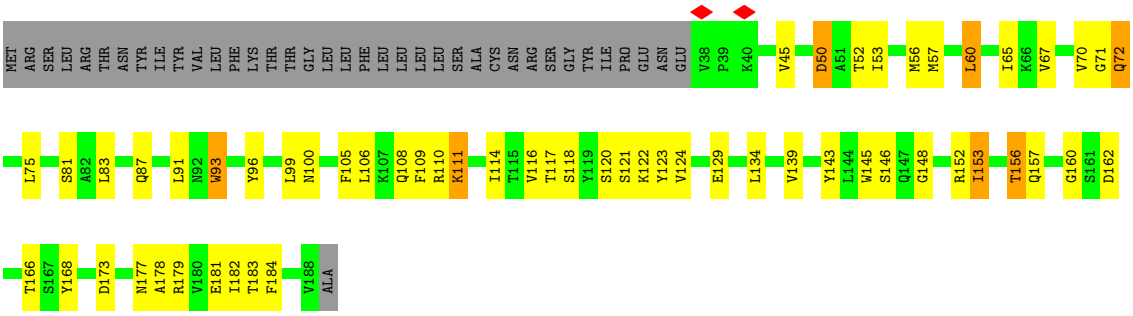
• Molecule 3: Inner membrane lipoprotein YiaD

Chain FK:



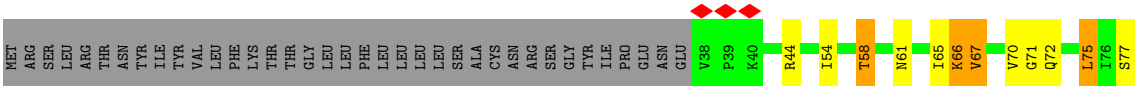
• Molecule 3: Inner membrane lipoprotein YiaD

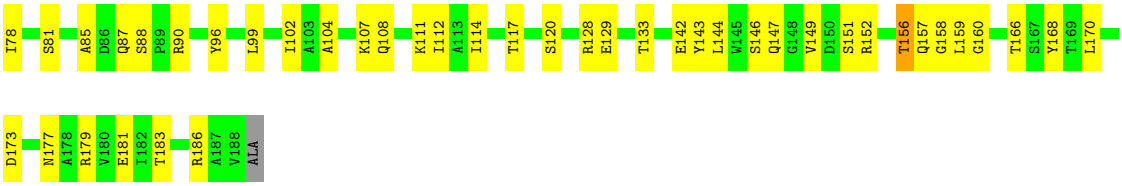
Chain GK:



• Molecule 3: Inner membrane lipoprotein YiaD

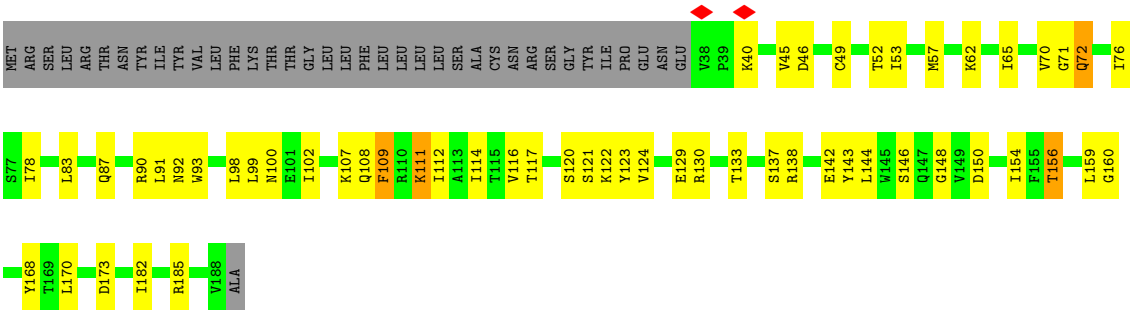
Chain HK:





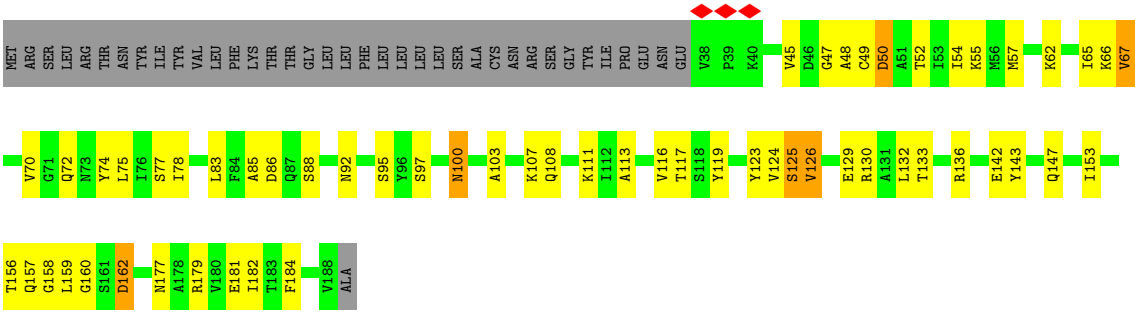
• Molecule 3: Inner membrane lipoprotein YiaD

Chain IK:



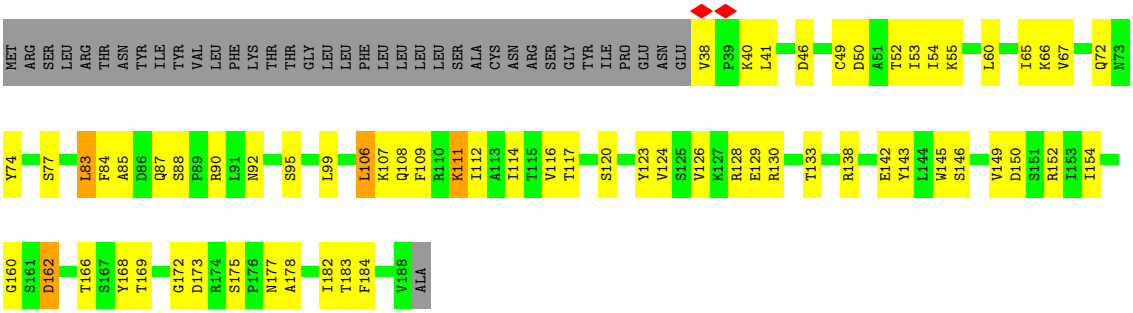
• Molecule 3: Inner membrane lipoprotein YiaD

Chain JK:



• Molecule 3: Inner membrane lipoprotein YiaD

Chain KK:



• Molecule 3: Inner membrane lipoprotein YiaD

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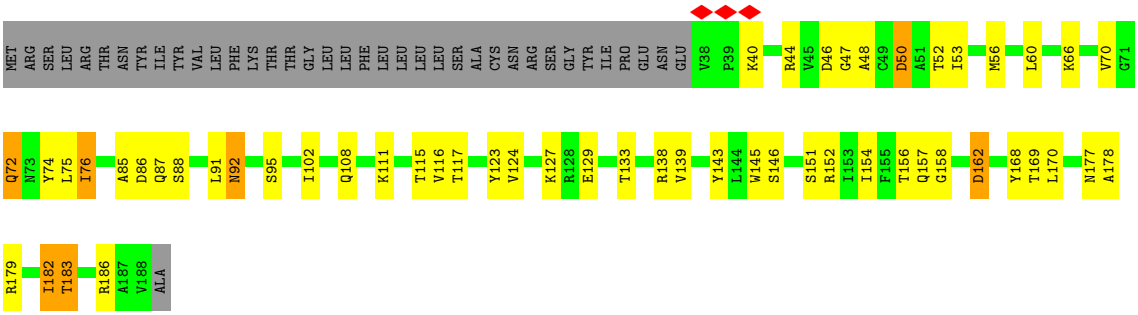
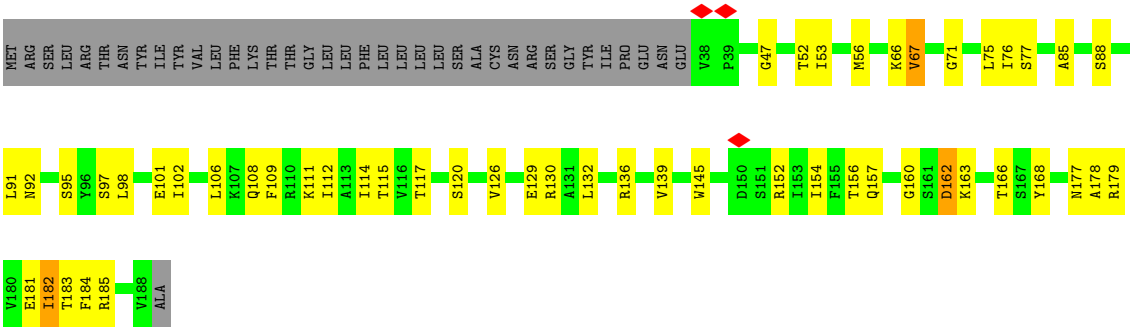


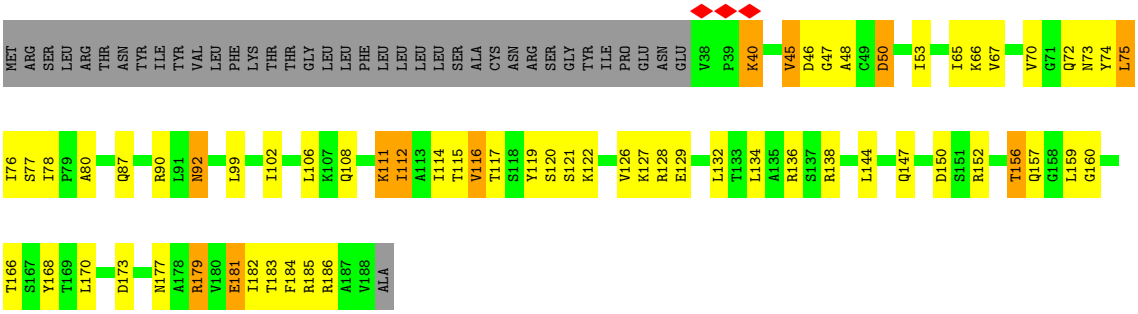
- Molecule 3: Inner membrane lipoprotein YiaD

Chain AK:



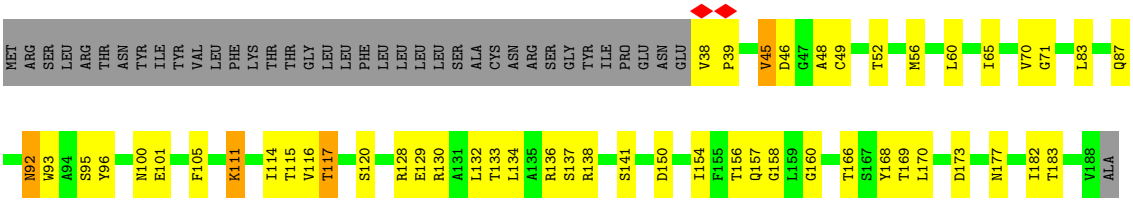
- Molecule 3: Inner membrane lipoprotein YiaD

Chain MK:



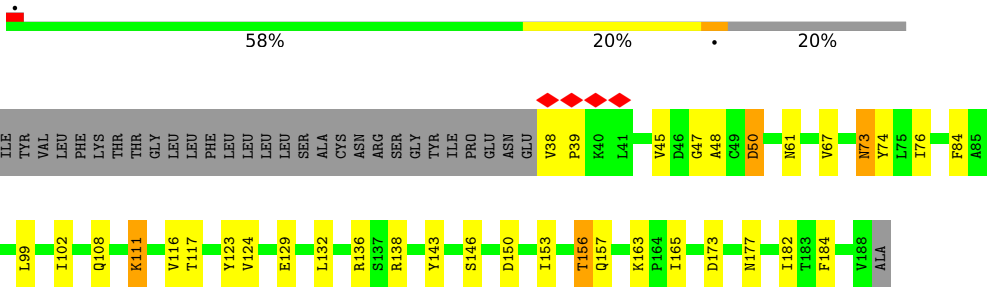
- Molecule 3: Inner membrane lipoprotein YiaD

Chain BK:



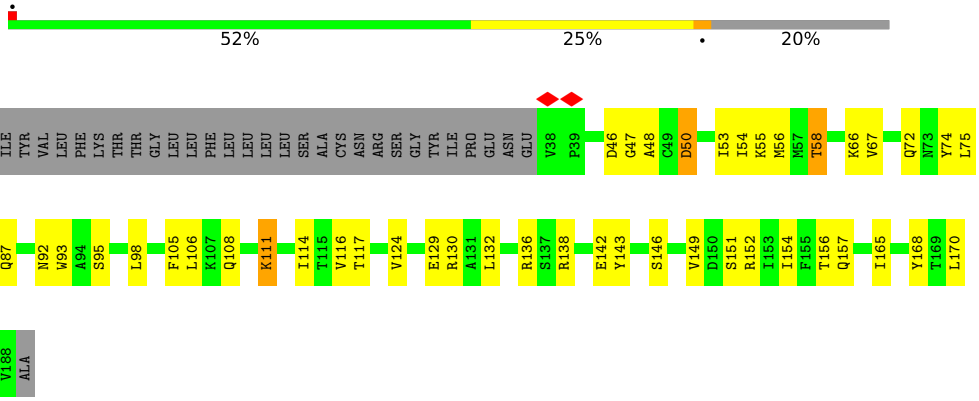
• Molecule 3: Inner membrane lipoprotein YiaD

Chain CK:



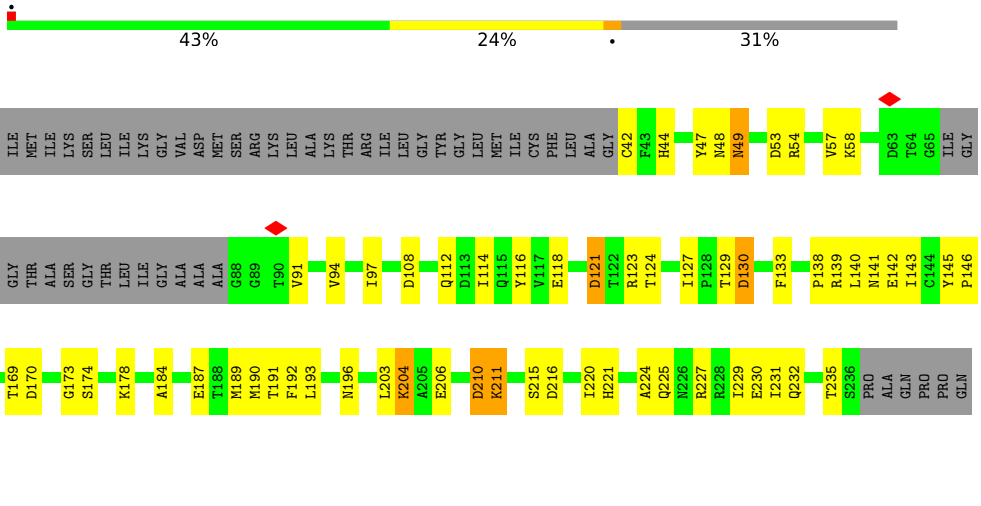
• Molecule 3: Inner membrane lipoprotein YiaD

Chain DK:



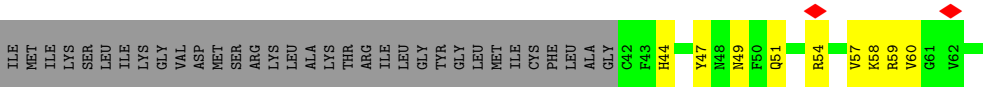
• Molecule 4: Outer membrane protein, OmpA family protein

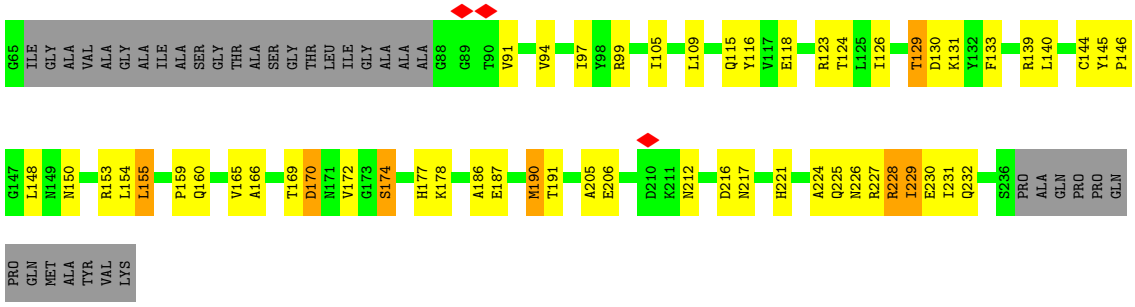
Chain EL:



• Molecule 4: Outer membrane protein, OmpA family protein

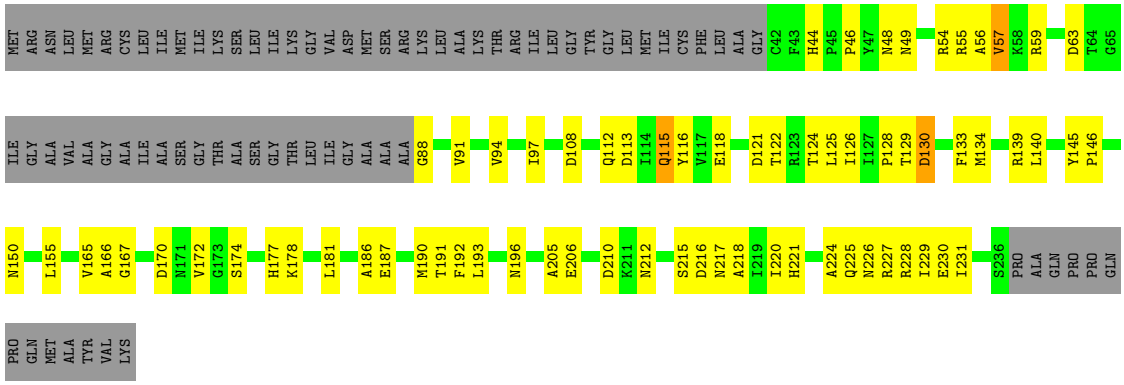
Chain FL:





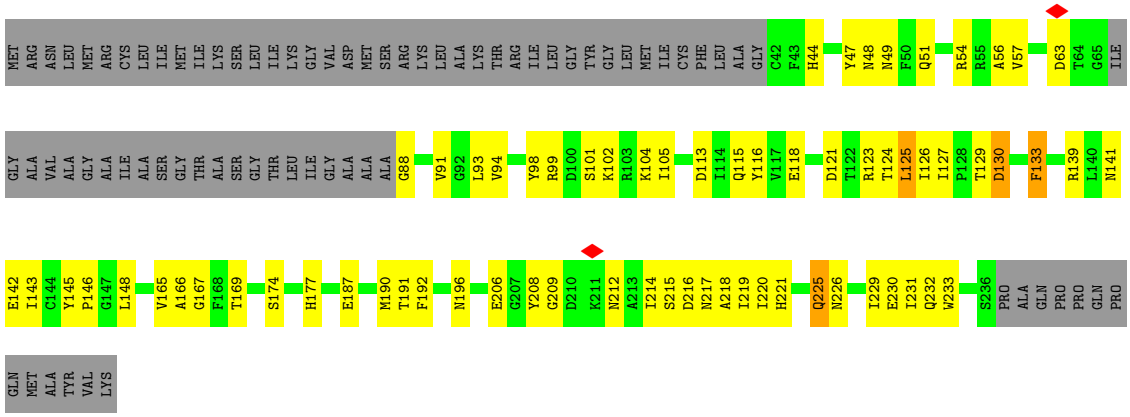
• Molecule 4: Outer membrane protein, OmpA family protein

Chain GL: 41% 27% • 31%



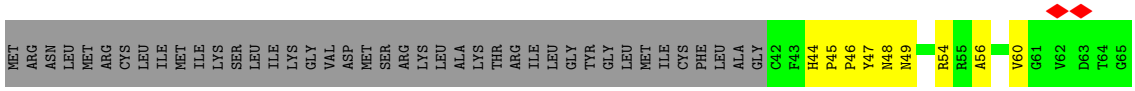
• Molecule 4: Outer membrane protein, OmpA family protein

Chain HL: 42% 26% • 31%



• Molecule 4: Outer membrane protein, OmpA family protein

Chain IL: 43% 24% • 31%



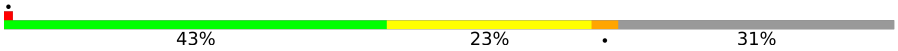
ILE GLY ALA VAL ALA GLY ALA ILE ALA SER GLY THR ALA SER GLY THR LEU ILE GLY ALA ALA ALA G88 V91 G92 L93 V94 I97 K102 I105 I106 L109 Q110 D113 I114 E118 D121 T122 R123 T124 L125 I126 I127 P128 T129 D130 K131 E142 Y145 P146

G147 L148 N149 N150 R153 L154 T162 V165 A166 T169 D170 N171 V172 G173 S174 R175 S176 H177 K178 R179 M189 M190 T191 F192 N196 E206 D210 S215 D216 N217 I220 H221 G222 S223 A224 Q225 N226 R227 R228 I229 E230 I231 Q232 W233 S236 PRO ALA GLN PRO

PRO GLN PRO GLN MET ALA TYR VAL LYS

- Molecule 4: Outer membrane protein, OmpA family protein

Chain JL:



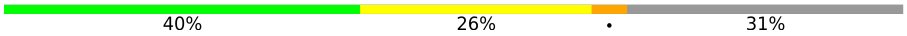
MET ARG ASN LEU MET ARG CYS LEU ILE MET ILE LYS SER LEU ILE LYS GLY VAL ASP MET SER ARG LYS LEU ALA LYS THR ARG ILE LEU GLY TYR GLY LEU MET ILE CYS PHE LEU ALA GLY C42 F43 H44 Y47 N48 N49 R59 D63 T64 G65 ILE GLY ALA VAL ALA GLY

ALA ILE ALA SER GLY THR ALA SER GLY THR LEU ILE GLY ALA ALA ALA G88 G89 T90 V91 V94 I97 D113 I114 Q115 Y116 V117 E118 D121 T122 R123 T124 L125 I126 I127 P128 T129 D130 F133 M134 R139 Y145 P146 N150 R153 Y164 V165 A166 D170

N171 V172 G173 S174 R175 S176 H177 K178 L181 Q185 A186 E187 M190 T191 A200 K204 A205 E206 N212 A213 I214 S215 D216 N217 A218 I219 I220 H221 G222 S223 A224 Q225 N226 R227 E230 I231 Q232 T235 S236 PRO ALA GLN PRO PRO GLN PRO GLN MET ALA TYR VAL LYS

- Molecule 4: Outer membrane protein, OmpA family protein

Chain KL:



MET ARG ASN LEU MET ARG CYS LEU ILE MET ILE LYS SER LEU ILE LYS GLY VAL ASP MET SER ARG LYS LEU ALA LYS THR ARG ILE LEU GLY TYR GLY LEU MET ILE CYS PHE LEU ALA GLY C42 F43 H44 Y47 N48 N49 R54 V57 V60 G65 ILE GLY ALA VAL

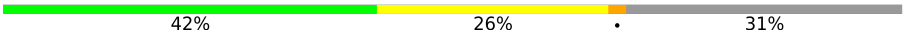
ALA GLY ALA ILE ALA SER GLY THR ALA SER GLY THR LEU ILE GLY ALA ALA ALA G88 L93 V94 I97 L109 Q112 D113 I114 Q115 Y116 T124 L125 I126 T129 D130 K131 Y132 F133 M134 F135 S136 S137 P138 R139 L140 N141 E142 I143 C144 Y145 P146 N150 L155

P159 Q160 V165 A166 G167 F168 T169 D170 N171 V172 G173 S174 R175 S176 H177 K178 R179 K180 Q183 A184 Q185 T188 T191 A199 R202 L203 E206 G207 Y208 G209 D210 K211 D216 N217 A218 I219 I220 H221 A224 Q225 N226 R227 R228 I229 E230 I231 Q232 W233 S236 PRO

ALA GLN PRO PRO GLN PRO GLN MET ALA TYR VAL LYS

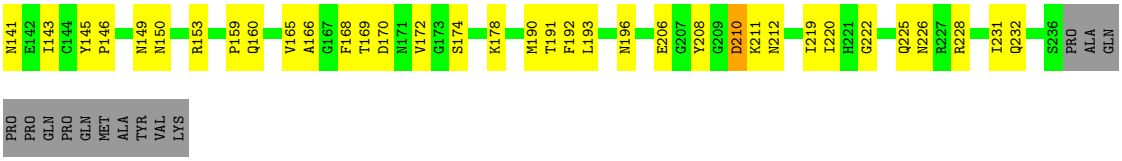
- Molecule 4: Outer membrane protein, OmpA family protein

Chain LL:



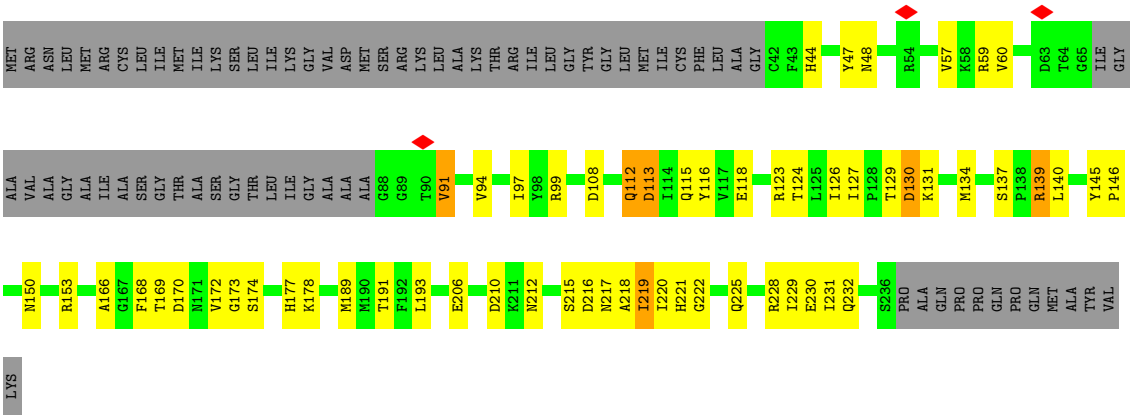
MET ARG ASN LEU MET ARG CYS LEU ILE MET ILE LYS SER LEU ILE LYS GLY VAL ASP MET SER ARG LYS LEU ALA LYS THR ARG ILE LEU GLY TYR GLY LEU MET ILE CYS PHE LEU ALA GLY C42 F43 H44 P45 P46 Y47 N48 N49 F50 Q51 P52 D53 R54 V57 K58 R59 D63

T64 G65 ILE GLY ALA VAL ALA GLY ALA ILE ALA SER GLY THR ALA SER GLY THR LEU ILE GLY ALA ALA ALA G88 V91 V94 I97 Y98 R99 K104 I105 L109 Q115 Y116 V117 E118 T124 L125 I126 I127 P128 T129 D130 K131 Y132 F133 M134 S137 P138 R139 L140



• Molecule 4: Outer membrane protein, OmpA family protein

Chain ML:



• Molecule 4: Outer membrane protein, OmpA family protein

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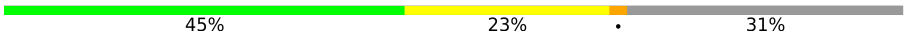
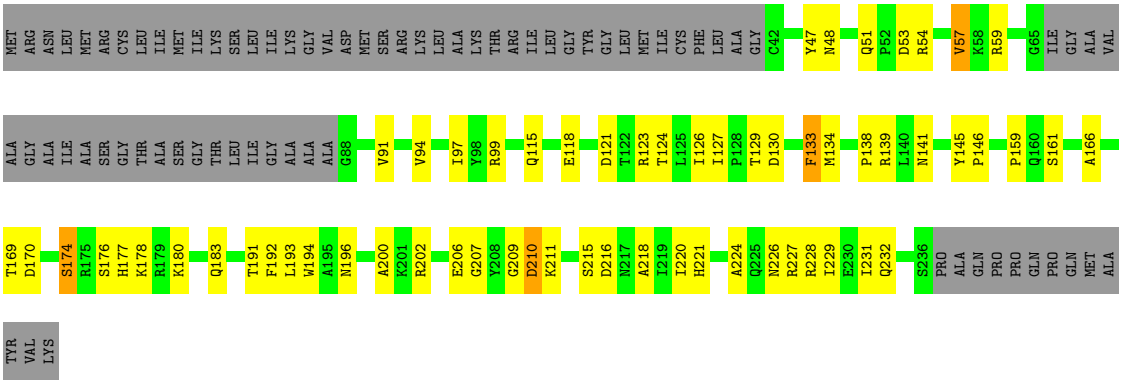
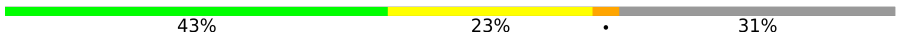
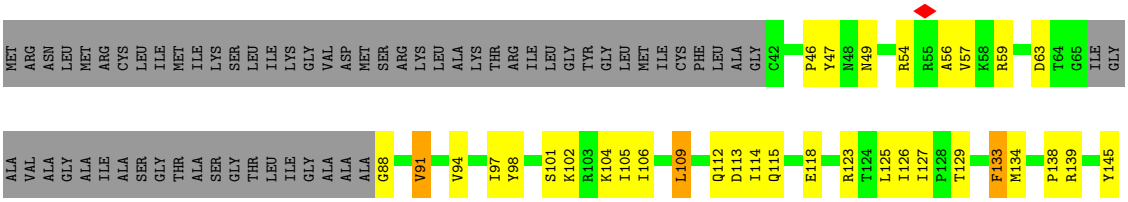


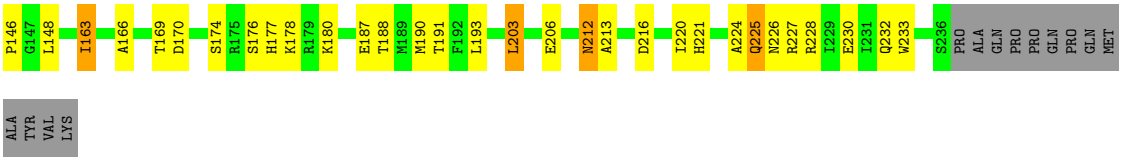


• Molecule 4: Outer membrane protein, OmpA family protein

Chain BL:







• Molecule 4: Outer membrane protein, OmpA family protein

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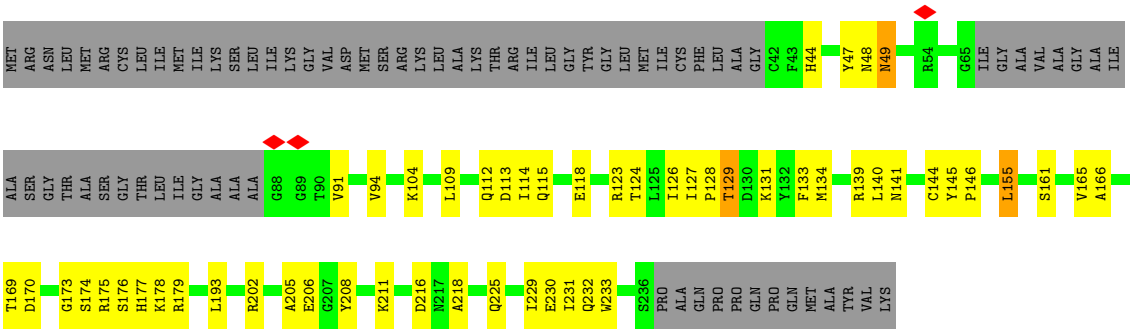
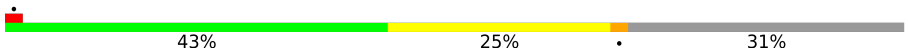
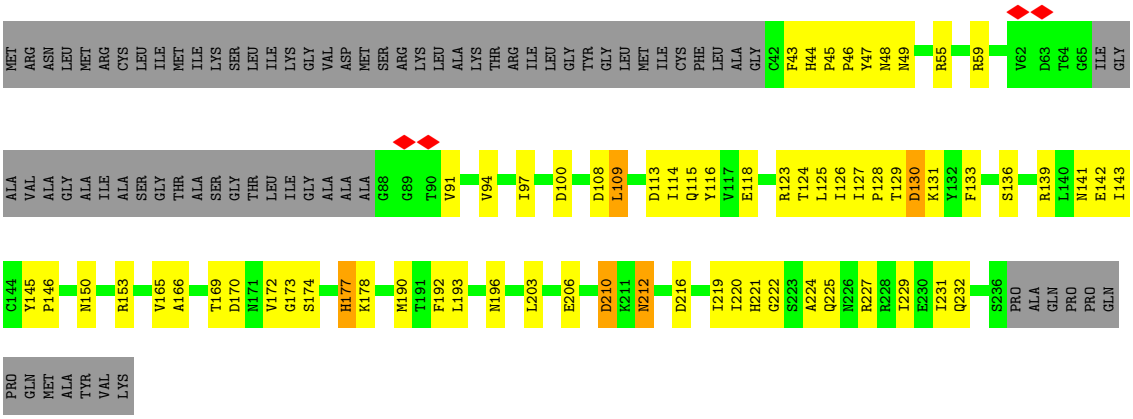


• Molecule 4: Outer membrane protein, OmpA family protein

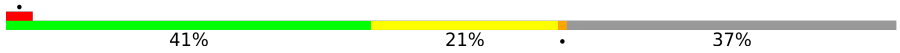
Chain DL:

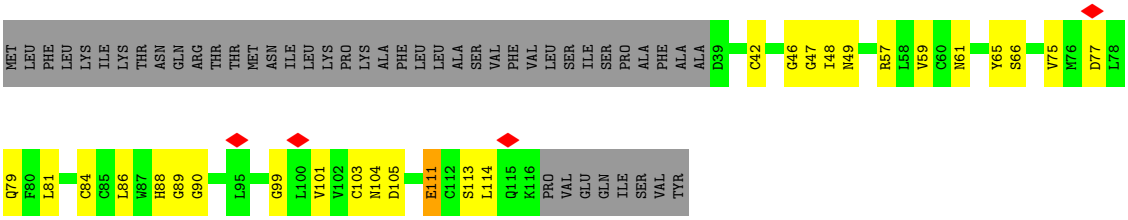




• Molecule 5: Neurogenic locus notch

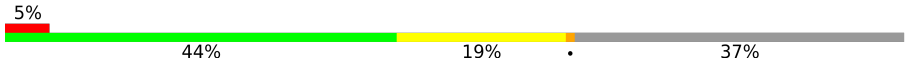
Chain EN:

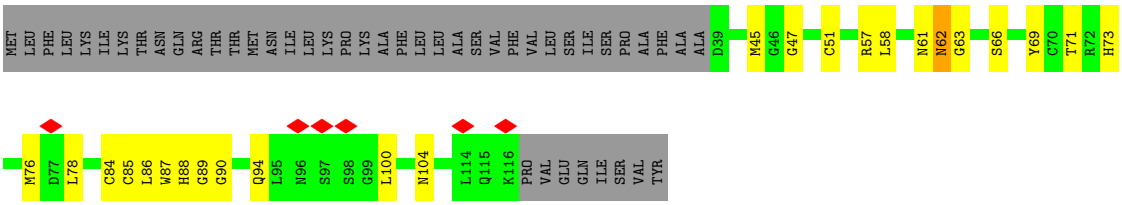




• Molecule 5: Neurogenic locus notch

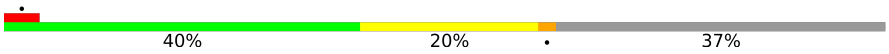
Chain FN:





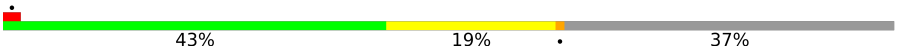
- Molecule 5: Neurogenic locus notch

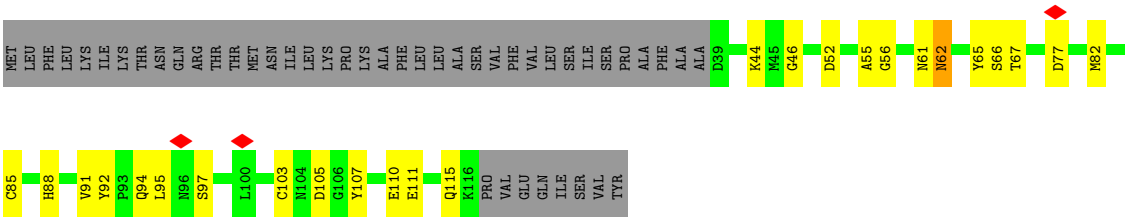
Chain GN:



- Molecule 5: Neurogenic locus notch

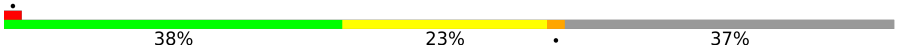
Chain HN:

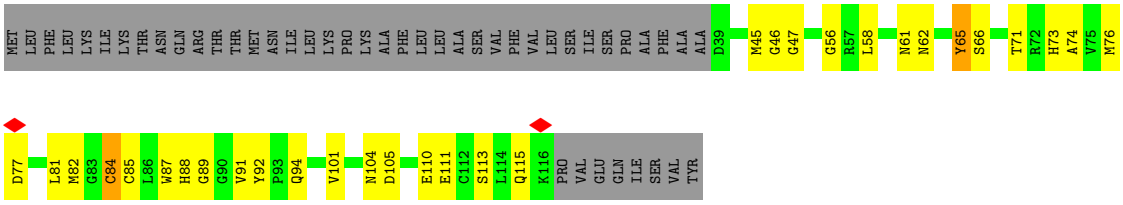




- Molecule 5: Neurogenic locus notch

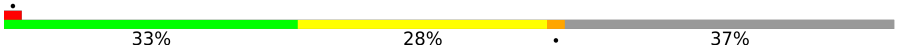
Chain IN:

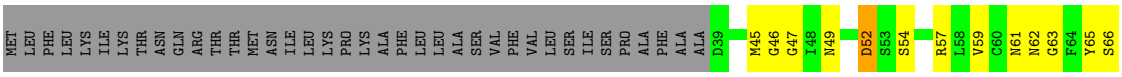


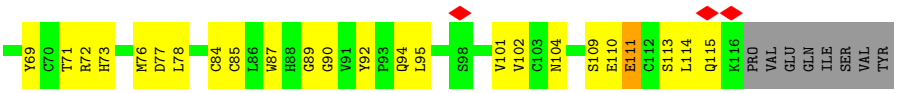


- Molecule 5: Neurogenic locus notch

Chain JN:

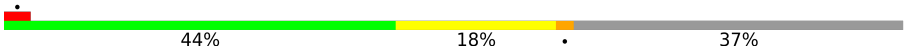


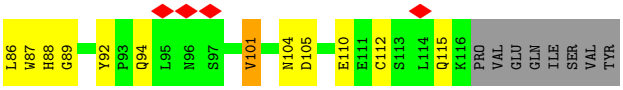




• Molecule 5: Neurogenic locus notch

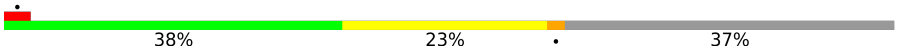
Chain KN:

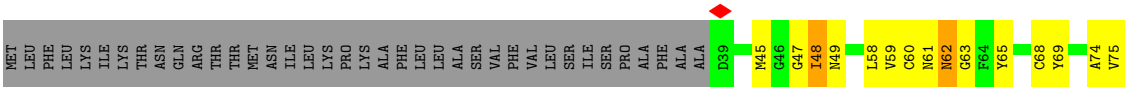


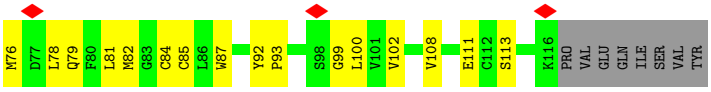


• Molecule 5: Neurogenic locus notch

Chain LN:

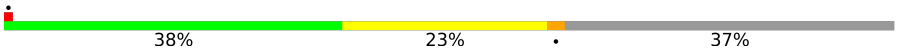


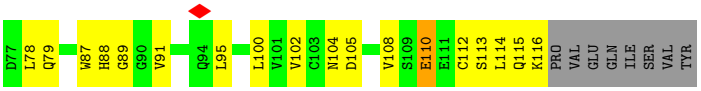




• Molecule 5: Neurogenic locus notch

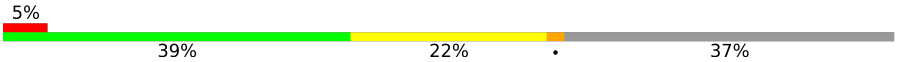
Chain MN:

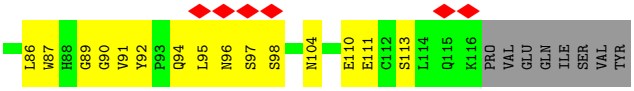




• Molecule 5: Neurogenic locus notch

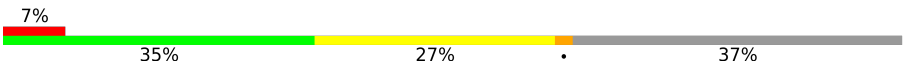
Chain AN:

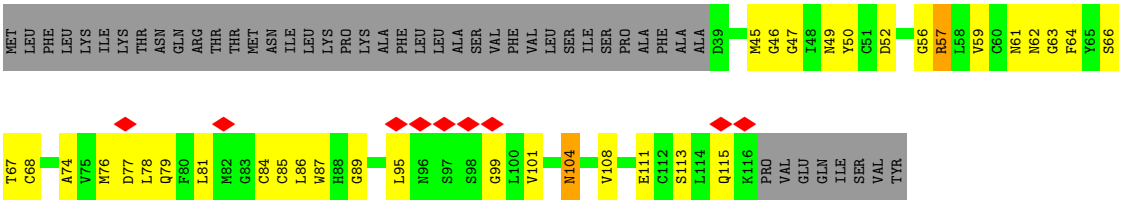




• Molecule 5: Neurogenic locus notch

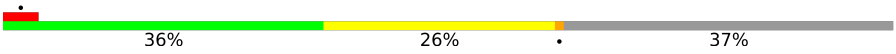
Chain BN:

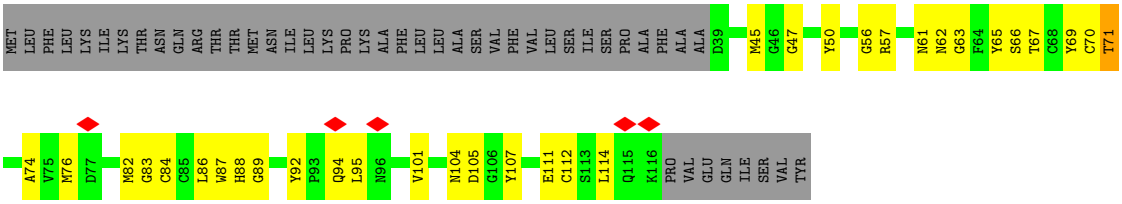




• Molecule 5: Neurogenic locus notch

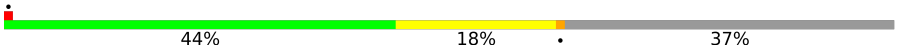
Chain CN:

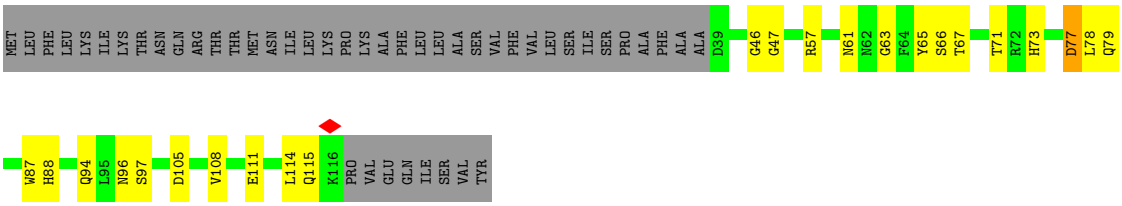




• Molecule 5: Neurogenic locus notch

Chain DN:





• Molecule 6: Unknown protein fragment

Chain EU:

• Molecule 6: Unknown protein fragment

Chain FU:

• Molecule 6: Unknown protein fragment

Chain GU:

• Molecule 6: Unknown protein fragment

Chain HU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain IU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain JU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain KU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain LU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain MU: 100%

There are no outlier residues recorded for this chain.

• Molecule 6: Unknown protein fragment

Chain AU: 89% 11%

X122 X127 X130

• Molecule 6: Unknown protein fragment

Chain BU: 100%

There are no outlier residues recorded for this chain.

• Molecule 6: Unknown protein fragment

Chain CU: 100%

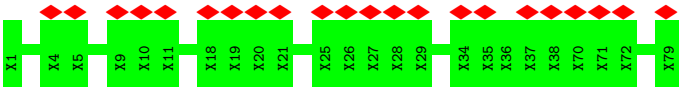
There are no outlier residues recorded for this chain.

• Molecule 6: Unknown protein fragment

Chain DU: 89% 11%

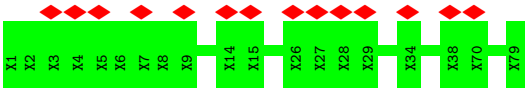
• Molecule 7: Unknown protein fragment

Chain EX: 46% 100%



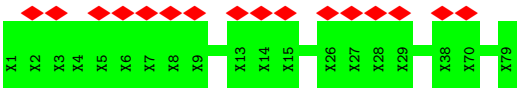
• Molecule 7: Unknown protein fragment

Chain FX: 29% 100%



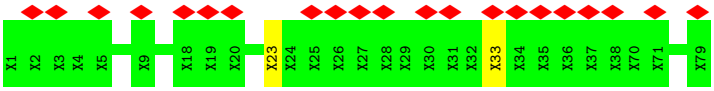
• Molecule 7: Unknown protein fragment

Chain GX: 33% 100%



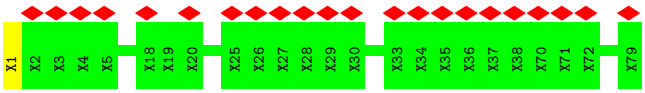
• Molecule 7: Unknown protein fragment

Chain HX: 44% 96%



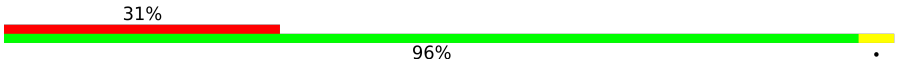
• Molecule 7: Unknown protein fragment

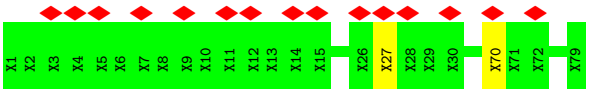
Chain IX: 46% 98%



• Molecule 7: Unknown protein fragment

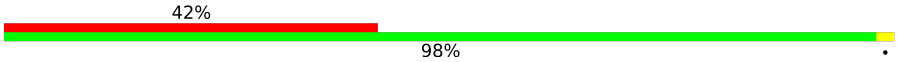
Chain JX:

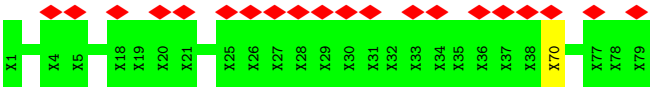




• Molecule 7: Unknown protein fragment

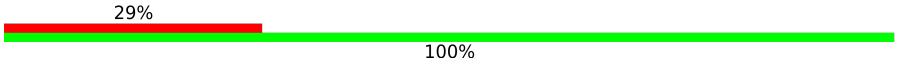
Chain KX:

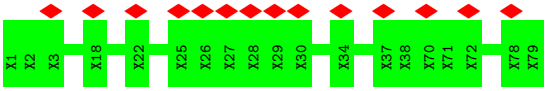




• Molecule 7: Unknown protein fragment

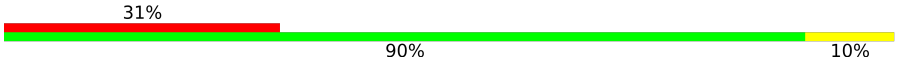
Chain LX:

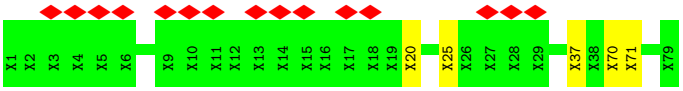




• Molecule 7: Unknown protein fragment

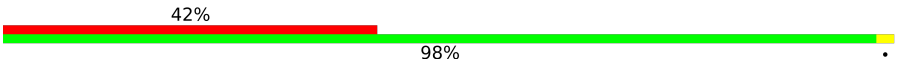
Chain MX:

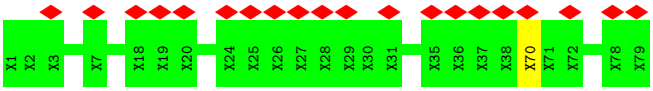




• Molecule 7: Unknown protein fragment

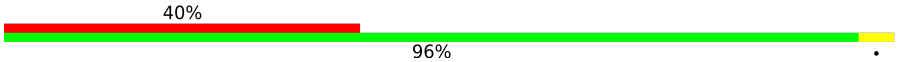
Chain VX:

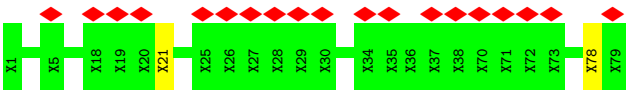




• Molecule 7: Unknown protein fragment

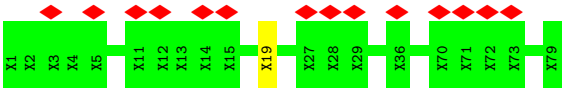
Chain WX:





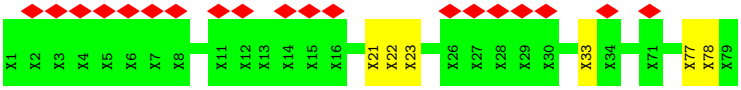
• Molecule 7: Unknown protein fragment

Chain XX: 29% 98%



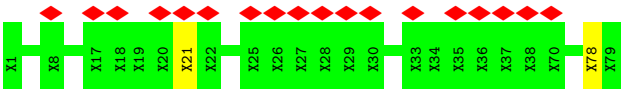
• Molecule 7: Unknown protein fragment

Chain YX: 40% 88% 12%



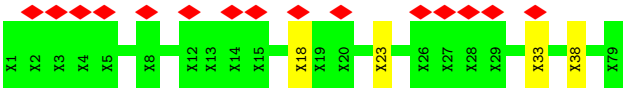
• Molecule 7: Unknown protein fragment

Chain ZX: 38% 96%



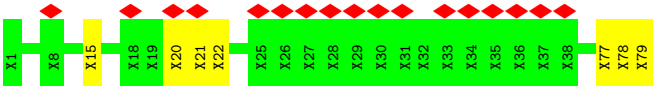
• Molecule 7: Unknown protein fragment

Chain AX: 31% 92% 8%



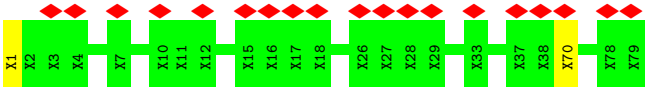
• Molecule 7: Unknown protein fragment

Chain BX: 35% 85% 15%



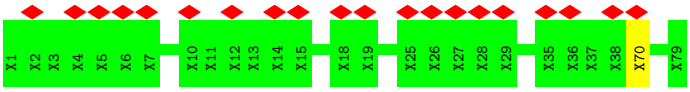
• Molecule 7: Unknown protein fragment

Chain CX: 40% 96%



• Molecule 7: Unknown protein fragment

Chain DX: 42% 98%



- Molecule 8: DotD

Chain Ed: 54% 26% • 16%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR MET K24 P29 N32 P33 S34 D35 D36 A37 T38 I39 K40 L41 L53 E54 M55 A56 K57 K60 V61 S66 K67 T70 I73 P74 N75 A76 Y77 N78 L79 Q80

A81 S84 V85 D86 E92 R97 R105 F106 R107 V108 K111 V115 E126 S127 L128 A129 E130 I131 L132 Y137 Q138 K142 I145 H146 V147 Y148 P149 N150 S151 Q152 V153 L156 K160 ILE TYR SER

- Molecule 8: DotD

Chain FD: 50% 32% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K27 P28 P29 I30 D35 D36 A37 T38 L41 A42 E43 A44 V48 V58 V61 I62 T63 N69 T70 L71 T72 I73 Y77 A81 V85 D86 W87

S88 G89 E92 E93 L94 I98 R105 V108 L109 L118 I119 S120 I121 K124 S127 L128 A129 E130 R133 D136 Y137 Q138 V147 Y148 P149 N150 S151 Q152 V153 V154 E155 L156 R157 Y158 A159 K160 I161 Y162 SER

- Molecule 8: DotD

Chain Fd: 50% 32% • 16%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR MET K24 P25 K26 P29 I30 N31 N32 P33 D36 I39 K40 L41 V48 M52 L53 E54 M55 E59 K60 V61 I62 T63 P64 K67 L71 T72 I73 P74 N75

A76 Y77 N78 L79 Q80 A81 R82 A83 W87 S88 E92 E93 R97 F104 R105 L109 G110 K111 V115 P116 I119 E126 S127 L128 A129 R133 Y137 K142 I145 Y148 P149 N150 S151 Q152 V153 V154 E155 K160 ILE TYR SER

- Molecule 8: DotD

Chain GD: 54% 29% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K27 P28 P29 I30 N31 N32 D35 T38 I39 S47 D50 S51 M52 L53 E54 M55 A56 K57 V61 I62 T63 P64 P65 S66 K67 D68 N69 I73 N78

L79 R82 W87 S88 G89 L94 T95 F106 R107 V108 K111 L118 K124 D125 E126 S127 R133 D136 Y137 G140 K141 K142 Y148 P149 Q152 V153 V154 Y158 A159 K160 I161 Y162 SER

- Molecule 8: DotD

Chain Gd: 55% 29% 16%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR MET K24 P25 K26 K27 P28 P29 I30 N31 N32 P33 S34 D35 D36 A37 T38 I39 S49 M52 K57 V58 E59 K60 V61 I62 L71 Q80 A81 R82 W87 I91

L94 I98 A99 K100 V108 L109 G110 K111 L118 I119 R133 Y137 Q138 A139 K142 A143 S144 V147 Y148 P149 N150 S151 Q152 V153 V154 E155 L156 R157 Y158 A159 K160 ILE TYR SER

- Molecule 8: DotD

Chain HD: 61% 21% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K27 P28 P29 I30 D35 T38 I39 K40 L41 M52 M55 A56 E59 I62 Y77 N78 R82 D86 W87 S88 G89 P90 I91 L94 T95

I98 R105 F106 R107 V108 L109 V115 K124 D125 E126 E130 I131 L132 R133 D136 N150 S151 Q152 V153 V154 E155 L156 R157 Y158 Y162 SER

- Molecule 8: DotD

Chain Hd: 56% 23% • 16%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR MET K24 F25 K26 P29 I30 N31 N32 P33 S34 D35 D36 A37 T38 I39 V48 M55 E59 K60 V61 L71 P74 N75 A76 Y77 N78 L79 Q80 A81 S84 V85

D86 W87 P90 I91 E92 E93 R97 K100 V115 S120 I121 S122 T123 L128 R133 Y137 I145 H146 V147 Y148 P149 N150 S151 Q152 V153 Y158 A159 K160 ILE TYR SER

- Molecule 8: DotD

Chain ID: 60% 24% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K26 K27 P28 P29 I30 N31 D35 D36 A37 T38 I39 K40 L41 A44 V48 D68 N69 T70 I73 Y77 R82 A83 S84 V85 D86 W87 S88 G89

E92 T95 I98 R105 F106 R107 V115 I119 T123 K124 D125 L132 R133 D134 I135 D136 Y137 I145 H146 V147 V153 V154 E155 Y158 A159 K160 I161 Y162 SER

- Molecule 8: DotD

Chain Id: 61% 23% • 16%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR MET K24 F25 K26 P33 S34 D35 D36 A37 T38 I39 V48 K57 K60 P64 K67 D68 I73 P74 N75 A76 L79 Q80 A81 S84 W87 E93

L94 I98 F104 R107 V108 V115 T123 E126 S127 L128 A129 E130 Y137 Y148 S151 Q152 V153 V154 E155 K160 ILE TYR SER

- Molecule 8: DotD

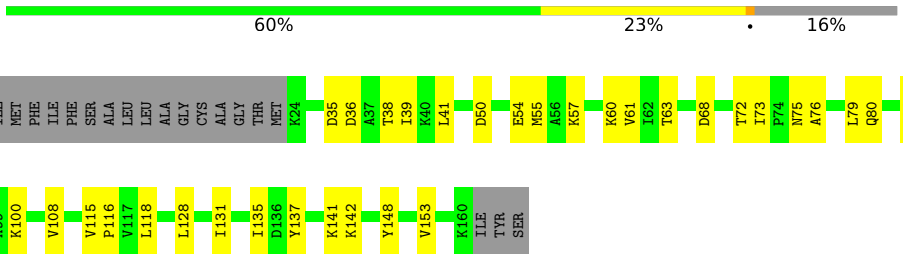
Chain JD: 58% 25% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K24 K27 P28 P29 D35 D36 A37 T38 I39 K40 L41 D50 M55 E59 T63 N69 T70 L71 T72 I73 A76 L79 R82 D86 W87 S88

G89 P90 I91 E92 E93 L94 I98 R107 V115 T123 K124 D125 E126 L132 R133 Y137 G140 H146 P149 Q152 E155 L156 R157 Y158 A159 K160 I161 Y162 SER

- Molecule 8: DotD

Chain Jd:



- Molecule 8: DotD

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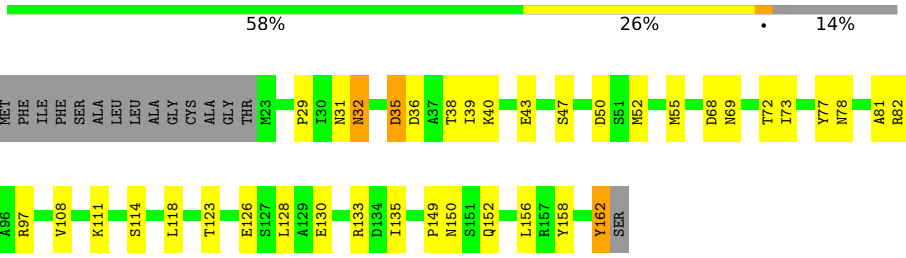
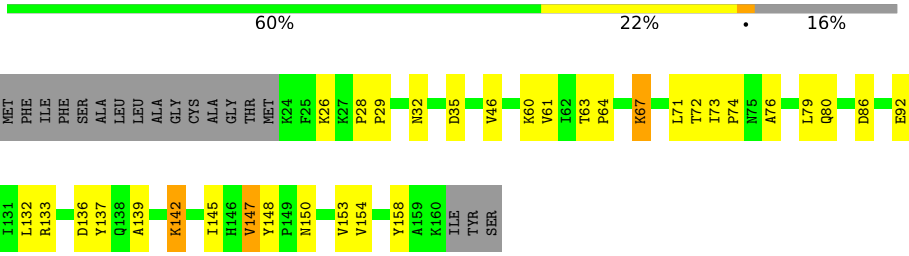


- Molecule 8: DotD

Chain Kd:



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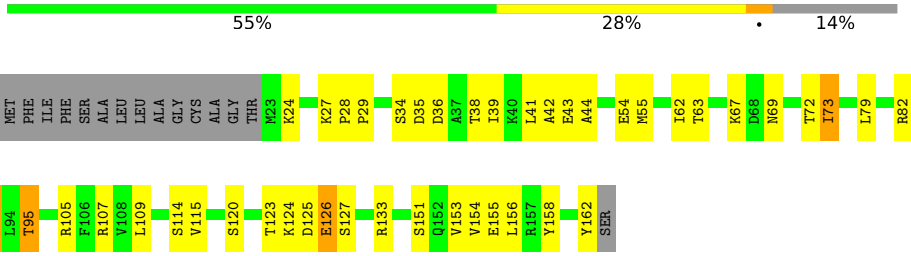
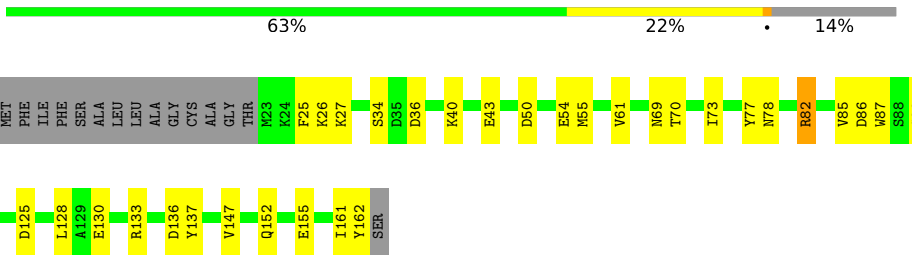
Chain LD:



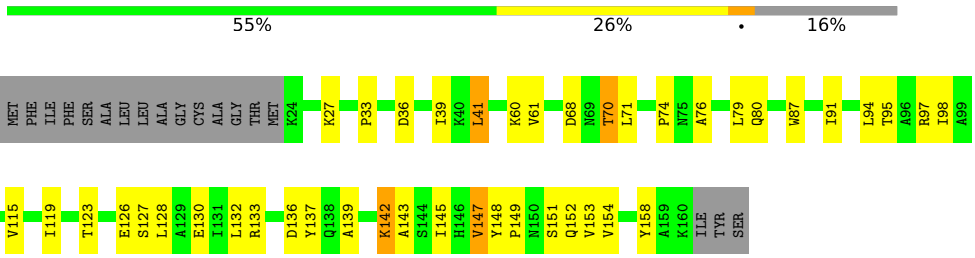
- Molecule 8: DotD

Chain CD:



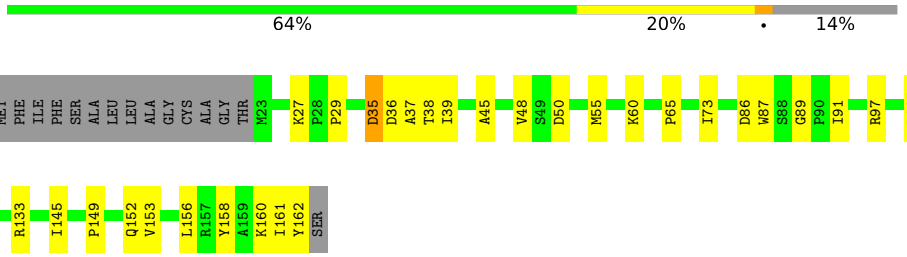
- Molecule 8: DotD

Chain Ld:



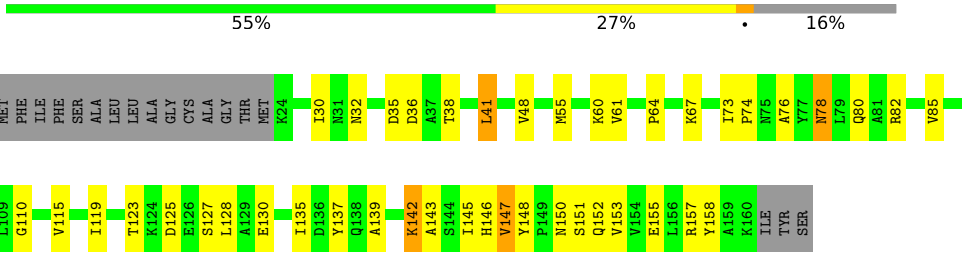
- Molecule 8: DotD

Chain MD:



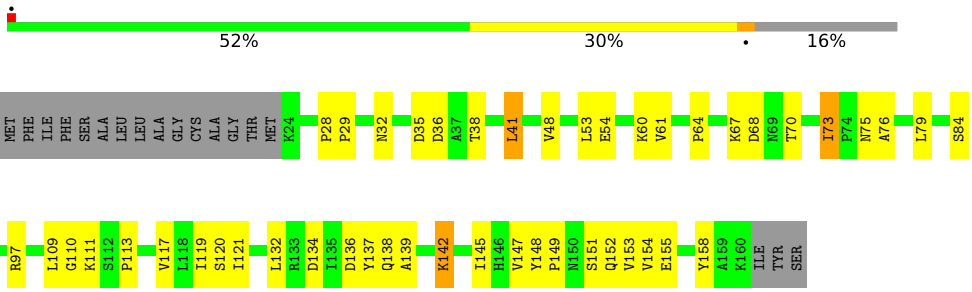
- Molecule 8: DotD

Chain Md:



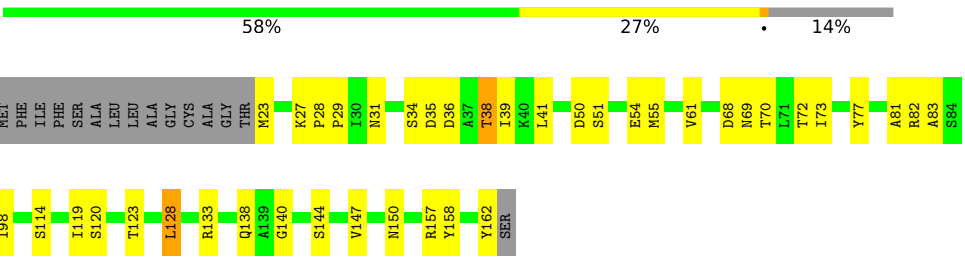
- Molecule 8: DotD

Chain Ad:



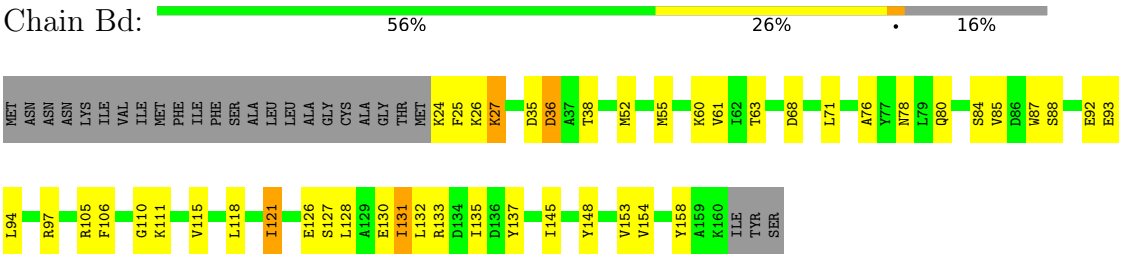
- Molecule 8: DotD

Chain BD:



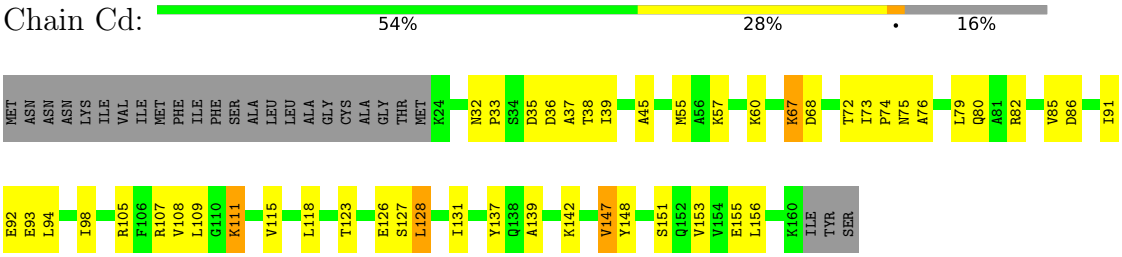
- Molecule 8: DotD

Chain Bd:



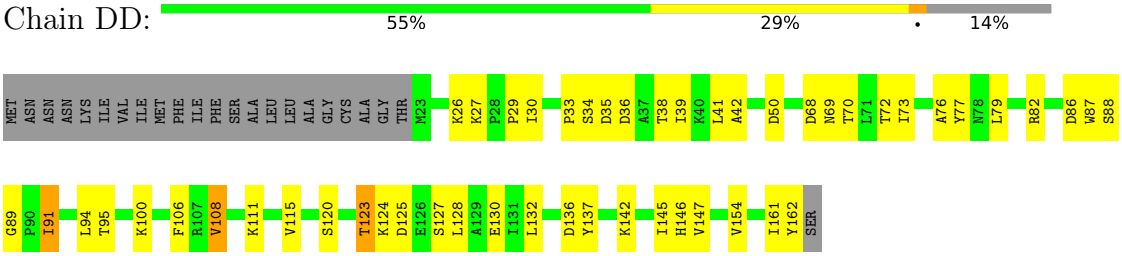
- Molecule 8: DotD

Chain Cd:



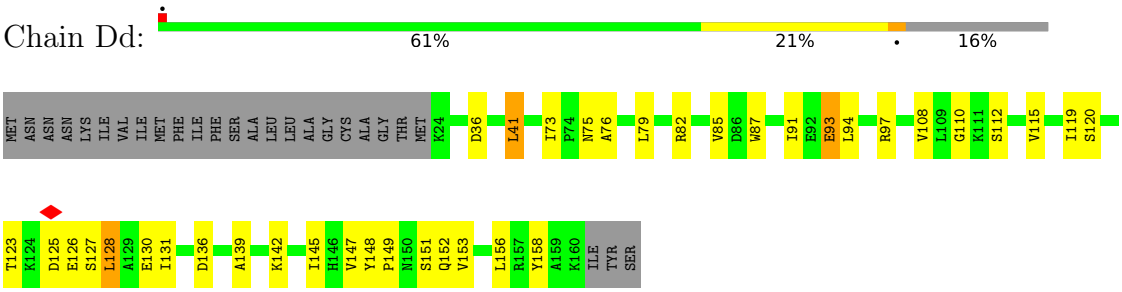
- Molecule 8: DotD

Chain DD:



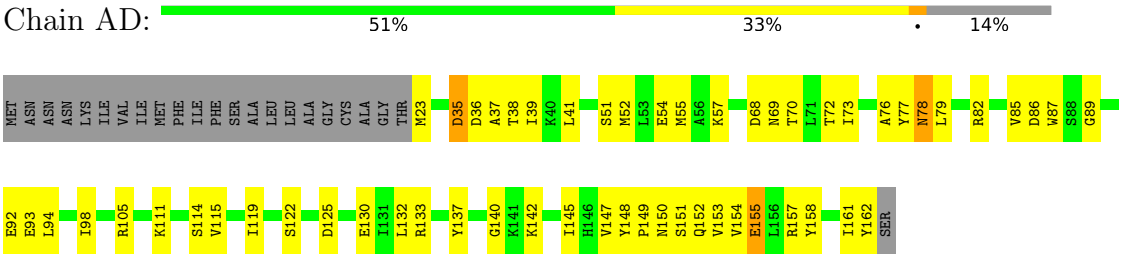
- Molecule 8: DotD

Chain Dd:



- Molecule 8: DotD

Chain AD:



- Molecule 8: DotD

Chain ED: 56% 29% • 14%

MET ASN ASN ASN LYS ILE VAL ILE MET PHE ILE PHE SER ALA LEU LEU ALA GLY CYS ALA GLY THR M23 K27 P28 P29 N32 D35 D36 I39 A42 D50 M55 V58 V61 D68 N69 Y77 N78 L79 R82 A83 S84 W87 S88 G89 P90

I91 E92 T95 A96 R97 R105 F106 R107 K111 S114 V115 K124 D125 E126 S127 L128 A129 E130 I131 L132 R133 Y137 G140 N150 S151 Q152 V153 V154 E155 L156 R157 Y158 I161 Y162 SER

- Molecule 9: DotF

Chain Ef: 12% 9% • 78%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 I209 Y210 Y211 I212 Q213 I216 P217 G218 R219 L222 I223 V232 R233 E234 G235 S236 K237 I238 Y241 G242 M243 V244 K245 L246 I247 L250

R253 I254 L255 T256 S257 S258 G259 Q260 V261 I262 K263 Q266 GLU ASP SER

- Molecule 9: DotF

Chain FF: 13% 10% • 77%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

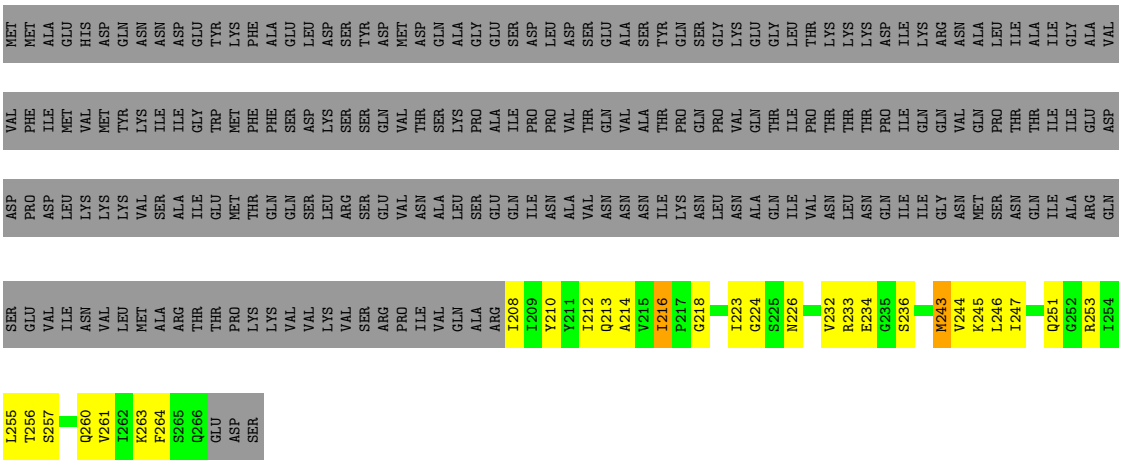
ASP PRO ASP LEU LYS LYS LYS VAL SER ALA ILE GLU MET THR GLN GLN SER LEU ARG SER GLU VAL ASN ALA LEU SER GLU GLN ILE ASN ALA VAL ASN ASN ASN ILE LYS ASN LEU ASN ALA GLN ILE VAL ASN LEU ASN ASN GLN ILE ILE GLY ASN MET SER ASN GLN ILE ALA ARG GLN

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA R207 I208 I209 Y210 Q213 A214 V215 R219 I223 G224 S225 N226 G227 S228 T229 L230 T231 V232 R233 S236 K237 I238 P239 G240 Y241 K245 G252 R253

I254 L255 T256 S257 S258 G259 Q260 V261 I262 K263 F264 S265 Q266 E267 D268 S269

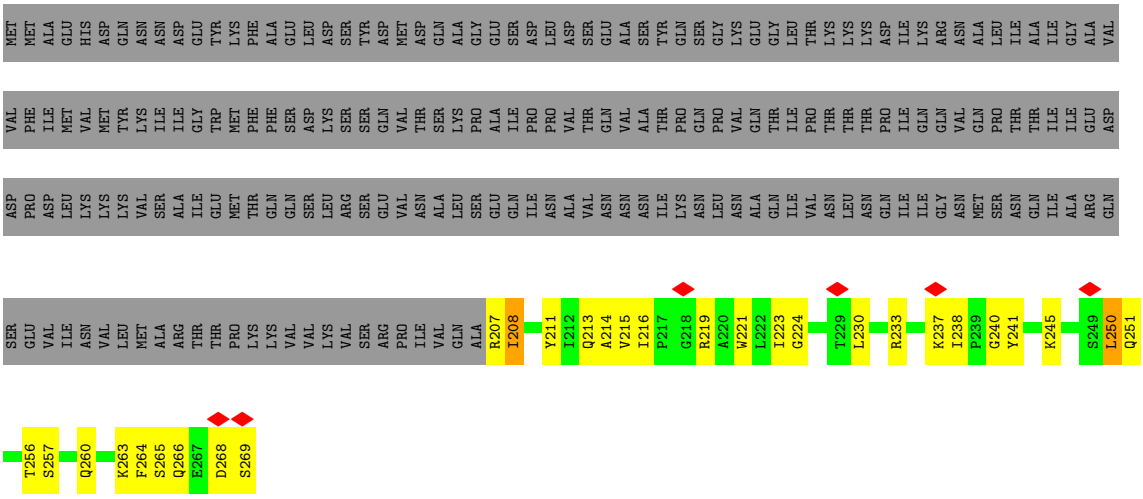
- Molecule 9: DotF

Chain Ff: 12% 10% • 78%



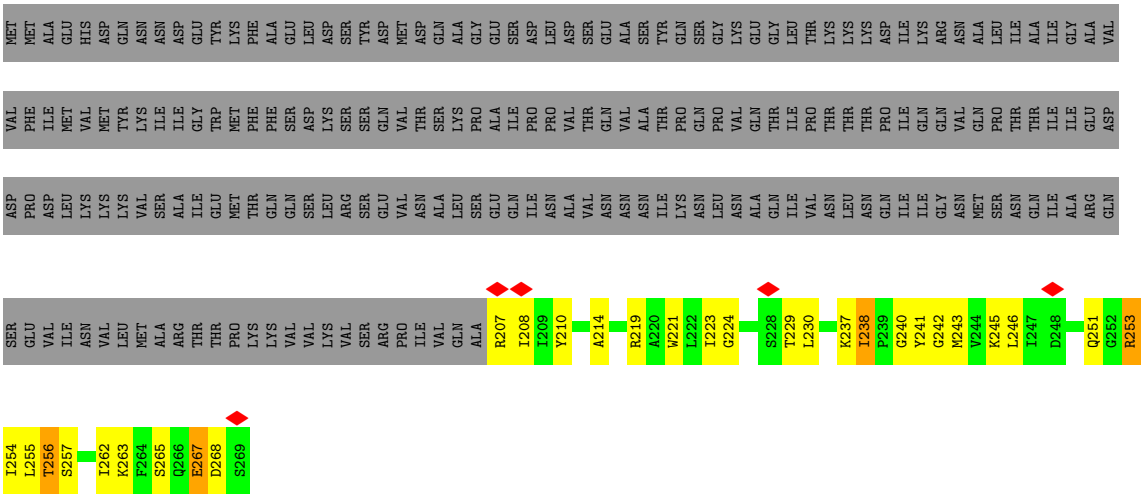
- Molecule 9: DotF

Chain AF:



- Molecule 9: DotF

Chain GF:



- Molecule 9: DotF

Chain Gf: 16% 5% • 78%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 V215 I216 P217 G218 R219 R233 S236 Y241 G242 M243 V244 K245 L246 I247 L255 T256 S257 F264 S265 Q266 GLU ASP SER

- Molecule 9: DotF

Chain HF: 14% 9% 77%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA R207 I208 I209 I212 Q213 A214 V215 I216 R219 A220 W221 L222 I223 G224 S225 N226 L230 T231 V232 R233 K237 I238 P239 G240 K245 I254 S257

I262 K263 F264 S269

- Molecule 9: DotF

Chain Hf: 16% 5% • 78%

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

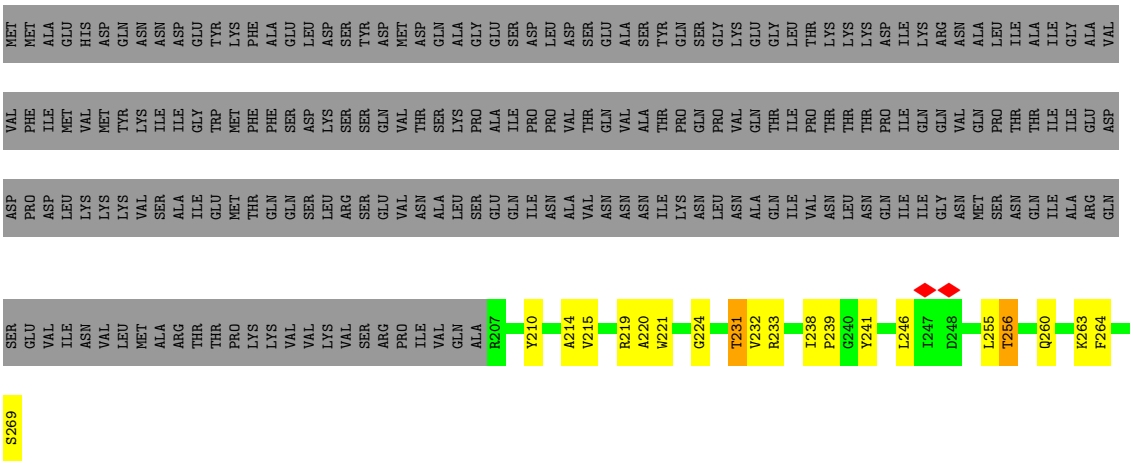
VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 I209 Y210 Q213 A214 V215 I216 P217 W221 L222 S225 N226 G227 R233 E234 G235 Y241 G242 M243 V244 T256 S257 Q266 GLU ASP SER

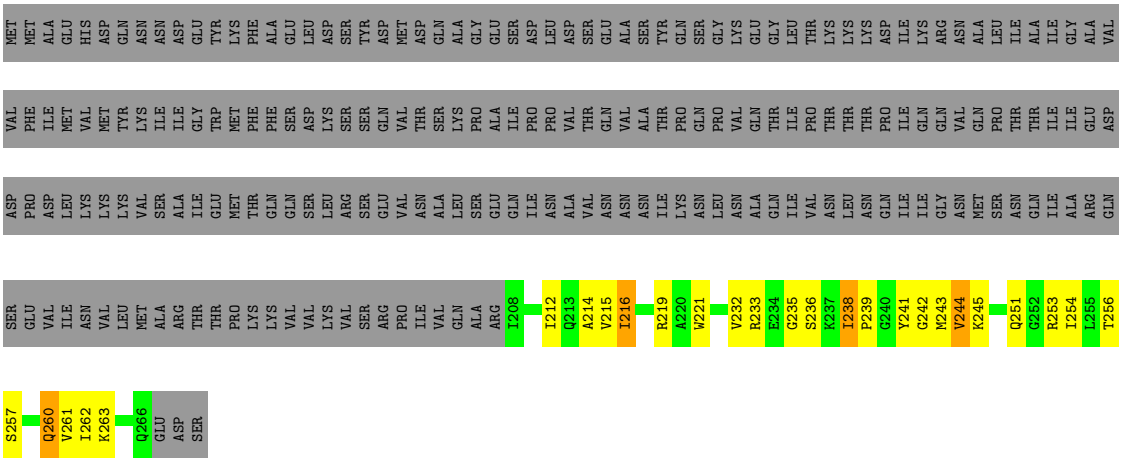
- Molecule 9: DotF

Chain IF: 16% 7% • 77%



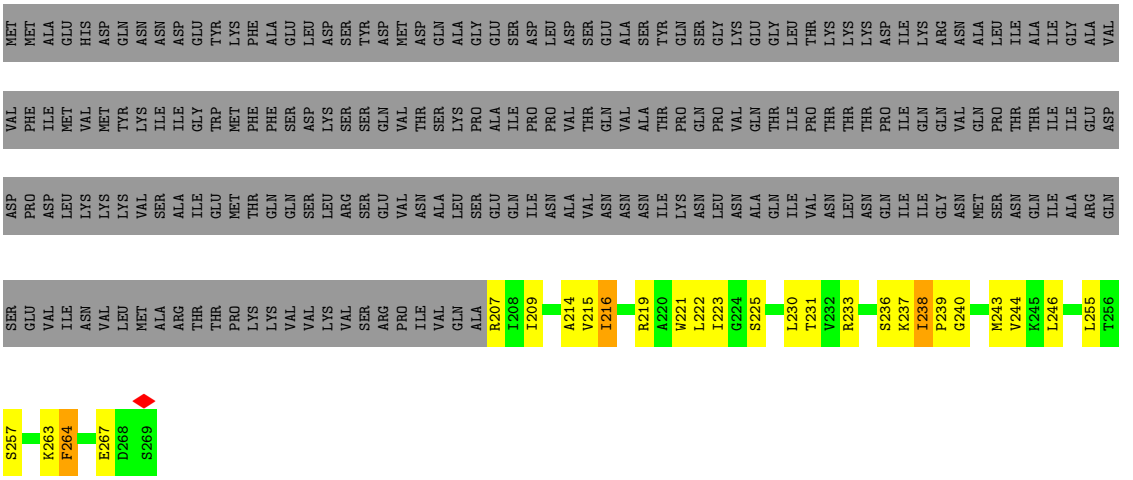
- Molecule 9: DotF

Chain If: 12% 8% • 78%



- Molecule 9: DotF

Chain JF: 14% 9% • 77%



- Molecule 9: DotF

Chain Jf: 15% 6% • 78%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 A214 V215 I216 P217 A220 W221 L222 I223 L230 T231 V232 G235 I238 Y241 G242 M243 V244 K245 L246 L255 T256 K263 Q266

GLU ASP SER

• Molecule 9: DotF

Chain KF: 13% 10% • 77%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

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

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA R207 I208 I209 Y210 Y211 V215 R219 I223 G224 S225 N226 G227 L230 T231 V232 R233 E234 G235 I238 P239 G240 Y241 G242 M243 V244 K245 L250 Q251

T256 S257 S258 G259 Q260 V261 I262 K263 F264 D268 S269

• Molecule 9: DotF

Chain Kf: 12% 10% 78%

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

VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP

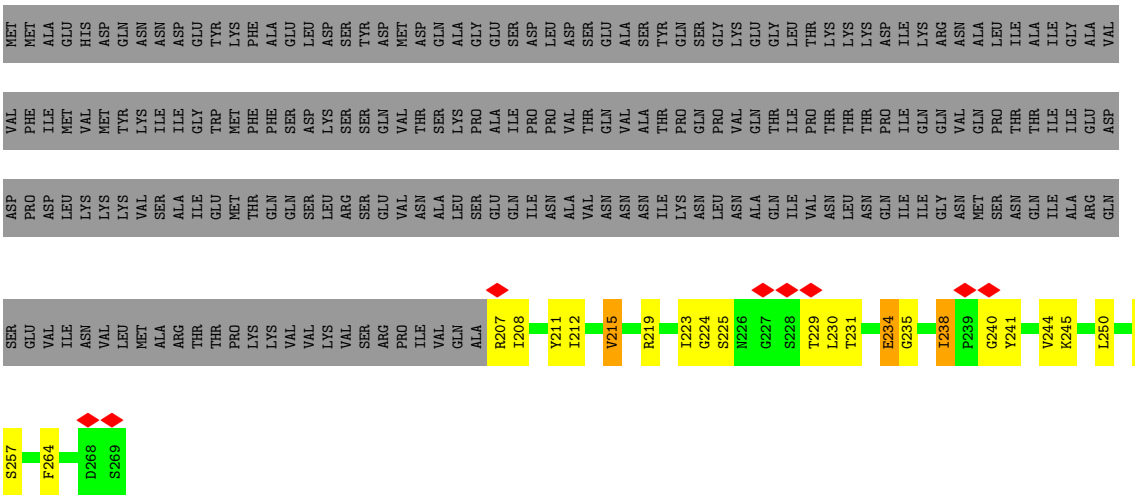
ASP PRO ASP LEU LYS LYS LYS VAL SER ALA ILE GLU MET THR GLN GLN SER LEU ARG SER GLU VAL ASN ALA LEU SER GLU GLN ILE ASN ALA VAL ASN ASN ILE LYS ASN LEU ASN ALA GLN ILE VAL ASN LEU ASN GLN ILE ILE GLY ASN MET SER ASN GLN ILE ALA ARG GLN

SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 I209 Y210 Y211 A214 V215 I216 P217 G218 R219 A220 W221 L222 I223 G224 S225 T229 V232 R233 K237 I238 Y241 G242 M243 V244 K245 L246

L250 L255 T256 S257 S258 G259 Q260 S265 Q266 GLU ASP SER

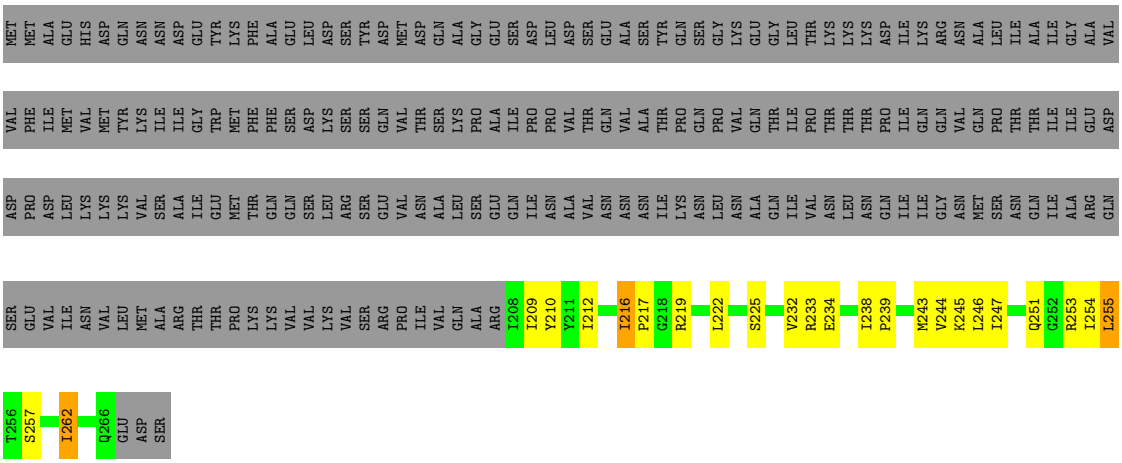
- Molecule 9: DotF

Chain LF:



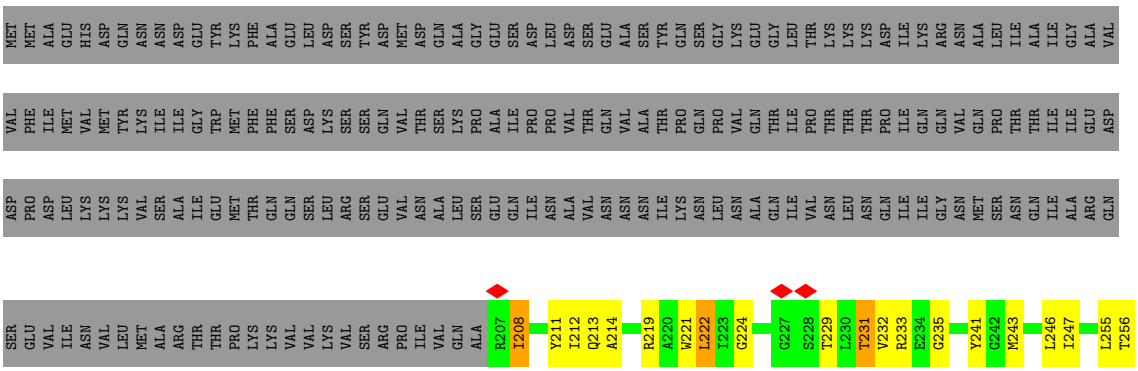
- Molecule 9: DotF

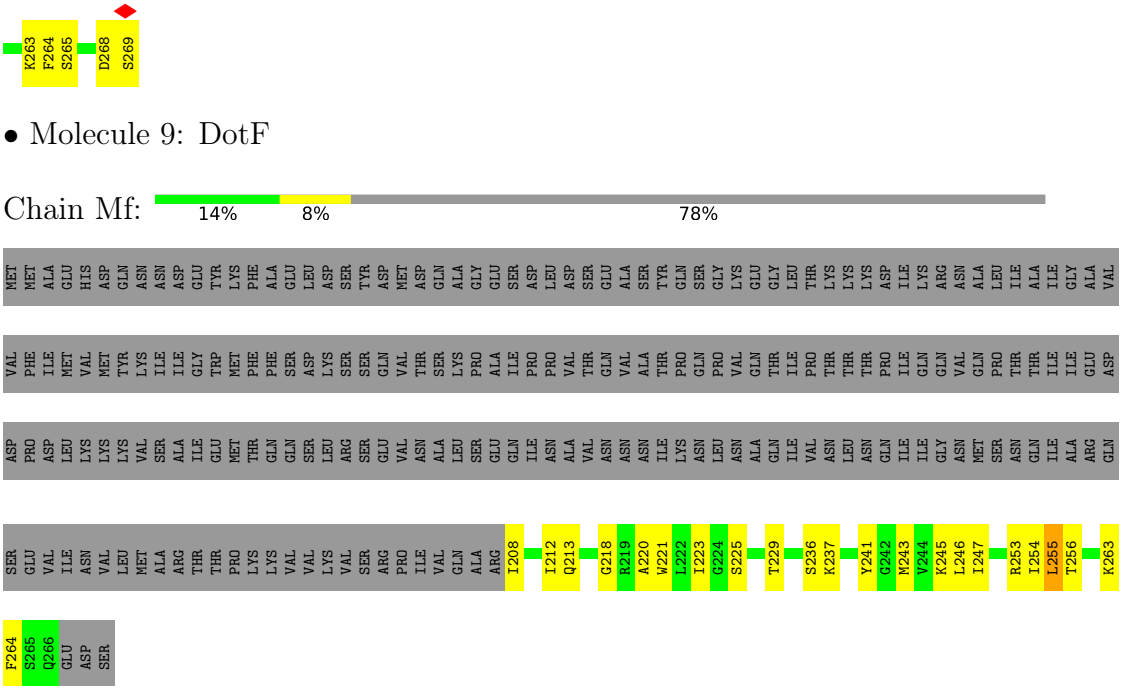
Chain Lf:

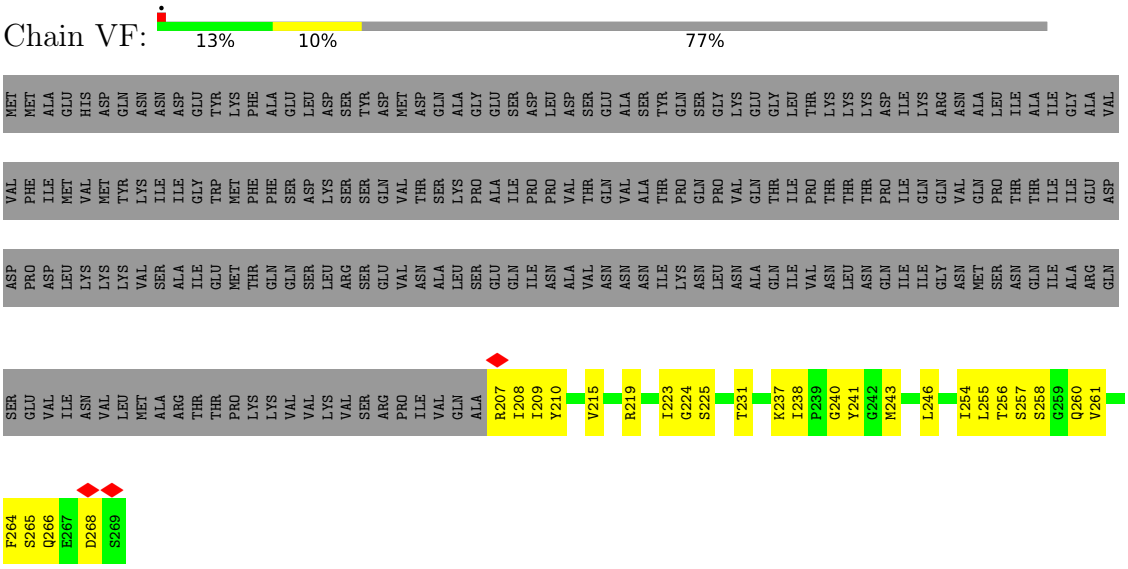


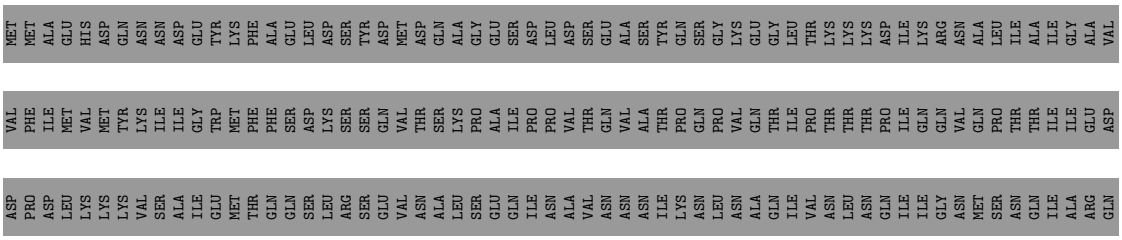
- Molecule 9: DotF

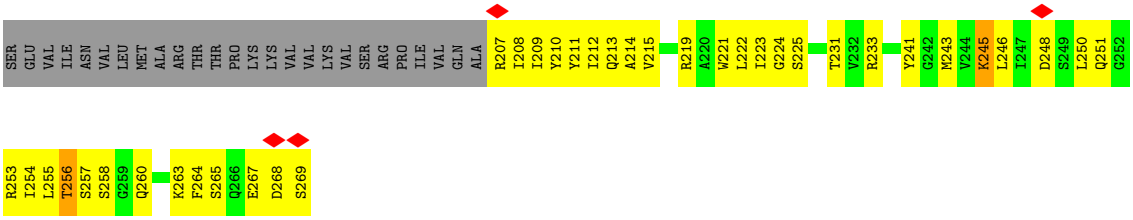
Chain MF:




K263 F264 S265 D268 S269
• Molecule 9: DotF
Chain Mf:
14% 8% 78%
MET MET ALA GLU HIS ASP GLN ASN ASN ASP GLU TYR LYS PHE ALA GLU LEU ASP SER TYR ASP MET ASP GLN ALA GLY GLU SER ASP LEU ASP SER GLU ALA SER TYR GLN SER GLY LYS GLU GLY LEU THR LYS LYS LYS ASP ILE LYS ARG ASN ALA LEU ILE ALA ILE GLY ALA VAL
VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP
ASP PRO ASP LEU LYS LYS LYS VAL SER ALA ILE GLU MET THR GLN GLN SER LEU ARG SER GLU VAL ASN ALA LEU SER GLU GLN ILE ASN ALA VAL ASN ASN ASN ILE LYS ASN LEU ASN ALA GLN ILE VAL ASN LEU ASN MET SER ASN GLN ILE ALA ARG GLN
SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA ARG I208 I212 Q213 G218 R219 A220 W221 L222 I223 G224 S225 T229 S236 K237 Y241 G242 M243 V244 K245 L246 I247 R253 I254 L255 T256 K263
F264 S265 Q266 GLU ASP SER

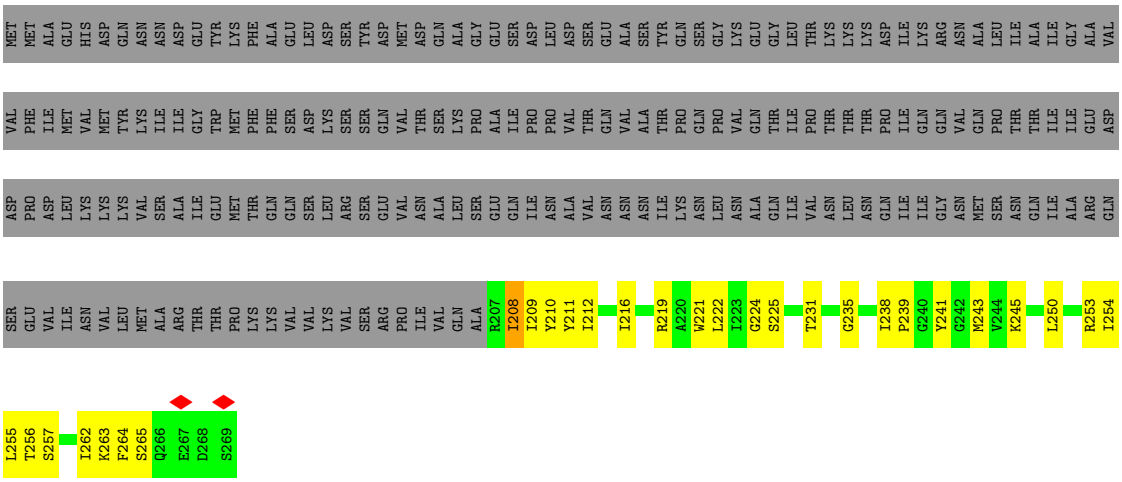

• Molecule 9: DotF
Chain VF:
13% 10% 77%
MET MET ALA GLU HIS ASP GLN ASN ASN ASP GLU TYR LYS PHE ALA GLU LEU ASP SER TYR ASP MET ASP GLN ALA GLY GLU SER ASP LEU ASP SER GLU ALA SER TYR GLN SER GLY LYS GLU GLY LEU THR LYS LYS LYS ASP ILE LYS ARG ASN ALA LEU ILE ALA ILE GLY ALA VAL
VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP
ASP PRO ASP LEU LYS LYS LYS VAL SER ALA ILE GLU MET THR GLN GLN SER LEU ARG SER GLU VAL ASN ALA LEU SER GLU GLN ILE ASN ALA VAL ASN ASN ASN ILE LYS ASN LEU ASN ALA GLN ILE VAL ASN LEU ASN MET SER ASN GLN ILE ALA ARG GLN
SER GLU VAL ILE ASN VAL LEU MET ALA ARG THR THR PRO LYS LYS VAL VAL LYS VAL SER ARG PRO ILE VAL GLN ALA R207 I208 I209 Y210 V215 R219 I223 G224 S225 T231 K237 I238 P239 G240 Y241 G242 M243 L246 I254 L255 T256 S257 S258 G259 Q260 V261
F264 S265 Q266 E267 D268 S269


• Molecule 9: DotF
Chain CF:
10% 13% 77%
MET MET ALA GLU HIS ASP GLN ASN ASN ASP GLU TYR LYS PHE ALA GLU LEU ASP SER TYR ASP MET ASP GLN ALA GLY GLU SER ASP LEU ASP SER GLU ALA SER TYR GLN SER GLY LYS GLU GLY LEU THR LYS LYS LYS ASP ILE LYS ARG ASN ALA LEU ILE ALA ILE GLY ALA VAL
VAL PHE ILE MET VAL MET TYR LYS ILE ILE GLY TRP MET PHE PHE SER ASP LYS SER SER GLN VAL THR SER LYS PRO ALA ILE PRO PRO VAL THR GLN VAL ALA THR PRO GLN PRO VAL GLN THR ILE PRO THR THR THR PRO ILE GLN GLN VAL GLN PRO THR THR ILE ILE GLU ASP
ASP PRO ASP LEU LYS LYS LYS VAL SER ALA ILE GLU MET THR GLN GLN SER LEU ARG SER GLU VAL ASN ALA LEU SER GLU GLN ILE ASN ALA VAL ASN ASN ASN ILE LYS ASN LEU ASN ALA GLN ILE VAL ASN LEU ASN MET SER ASN GLN ILE ALA ARG GLN



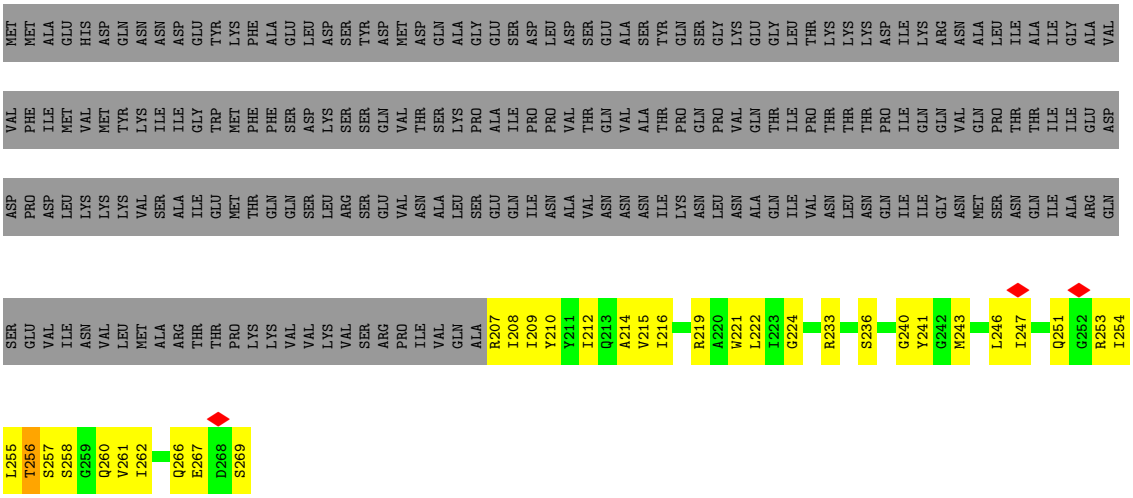
• Molecule 9: DotF

Chain WF:



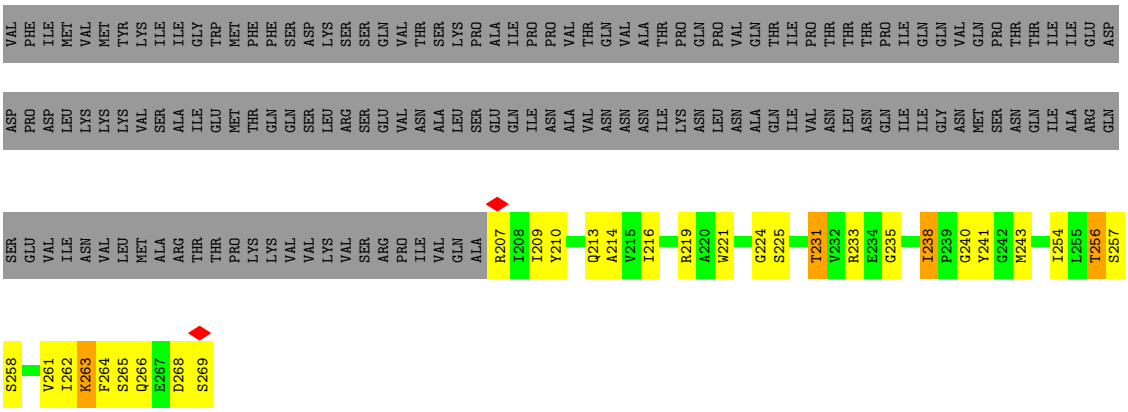
• Molecule 9: DotF

Chain XF:



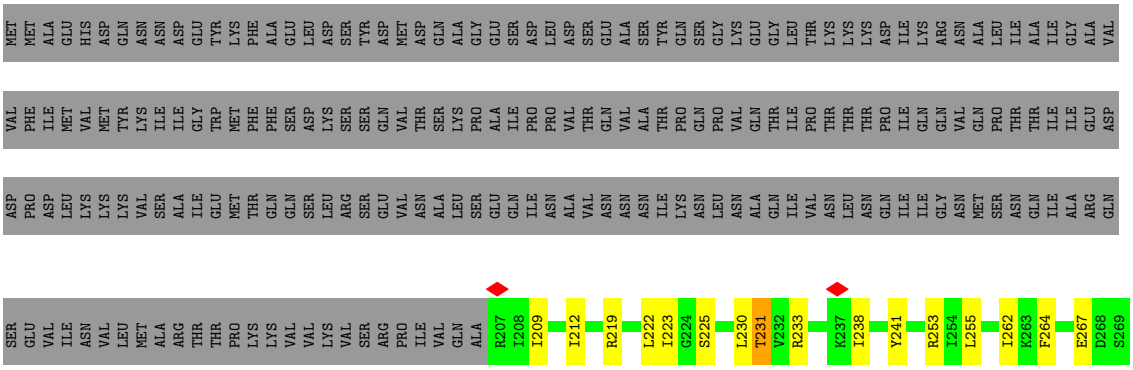
• Molecule 9: DotF

Chain YF:



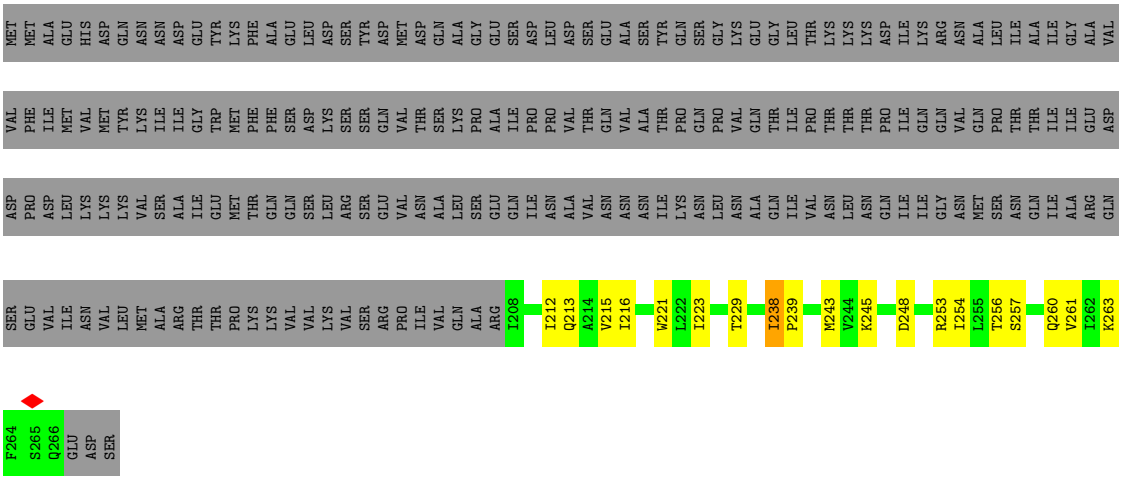
• Molecule 9: DotF

Chain ZF:



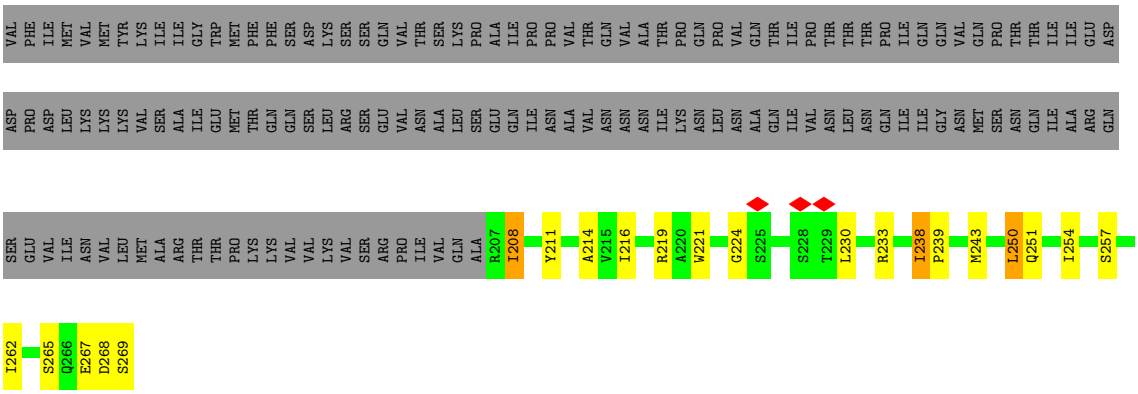
• Molecule 9: DotF

Chain Af:



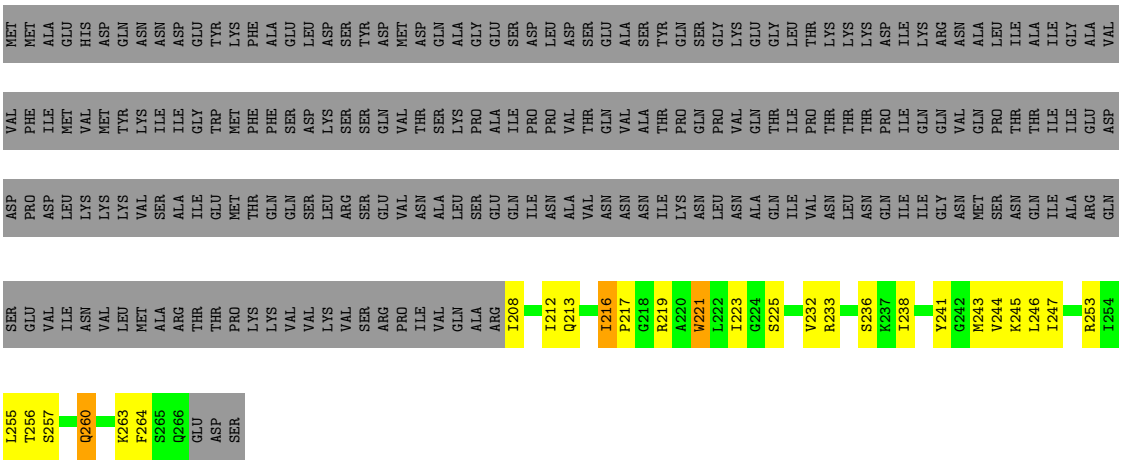
• Molecule 9: DotF

Chain BF:



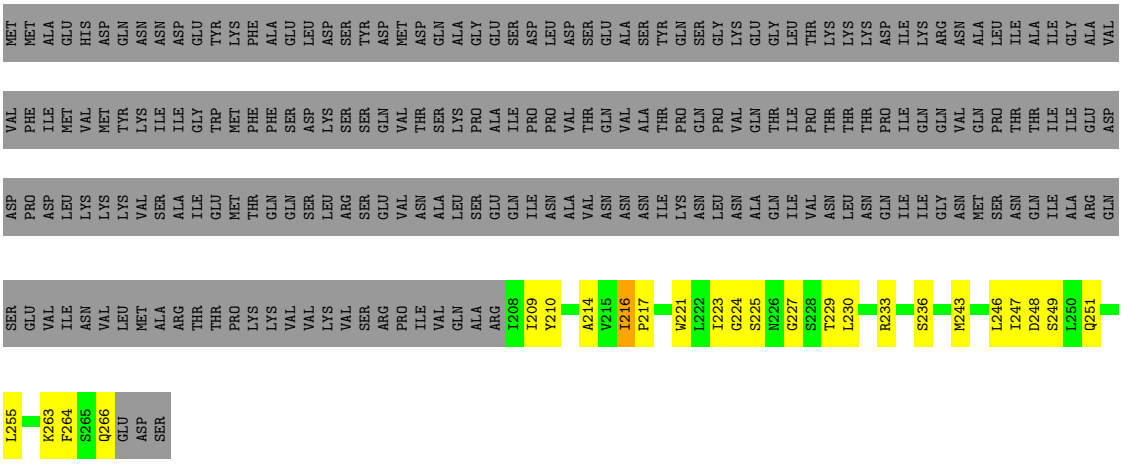
• Molecule 9: DotF

Chain Bf: 12% 9% • 78%



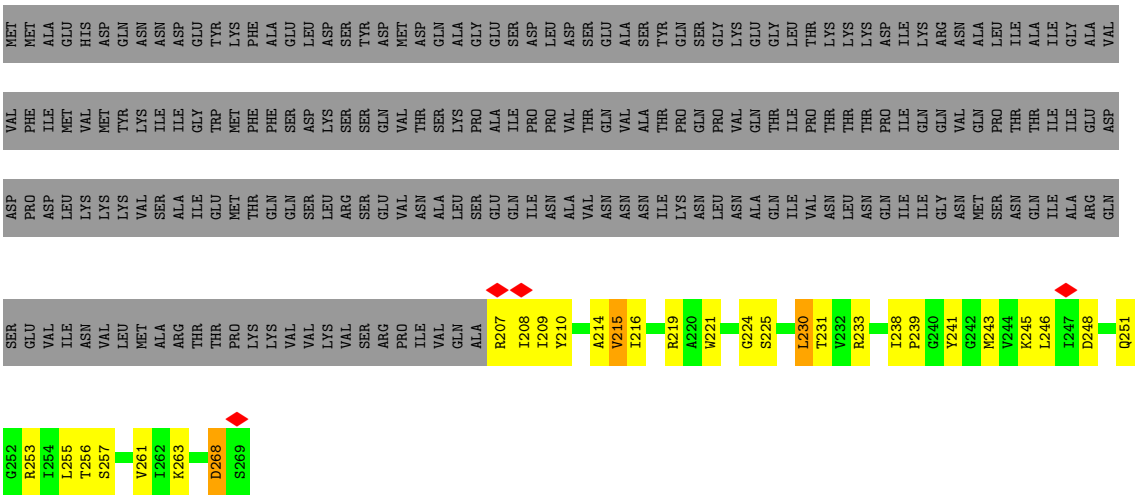
• Molecule 9: DotF

Chain Cf: 13% 9% 78%



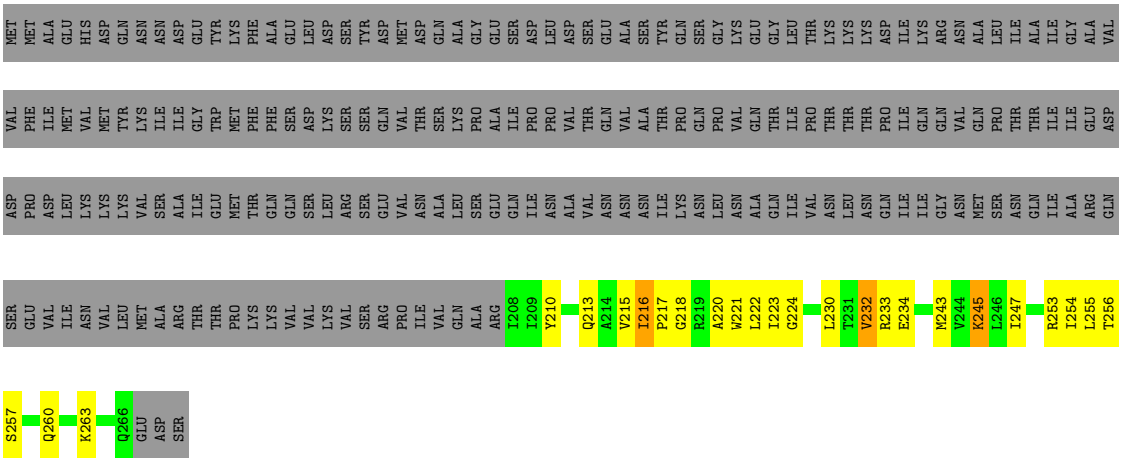
• Molecule 9: DotF

Chain DF: 13% 10% • 77%



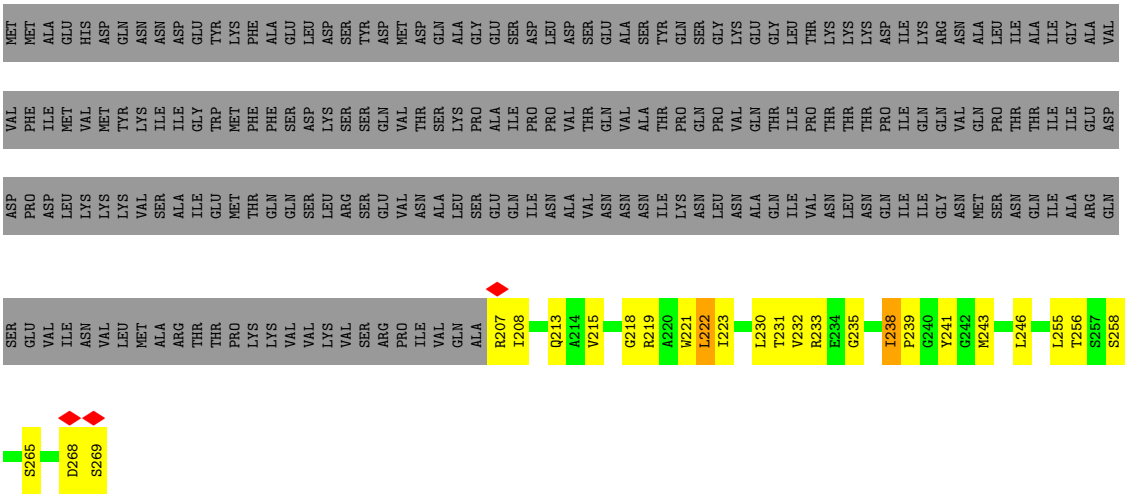
- Molecule 9: DotF

Chain Df:



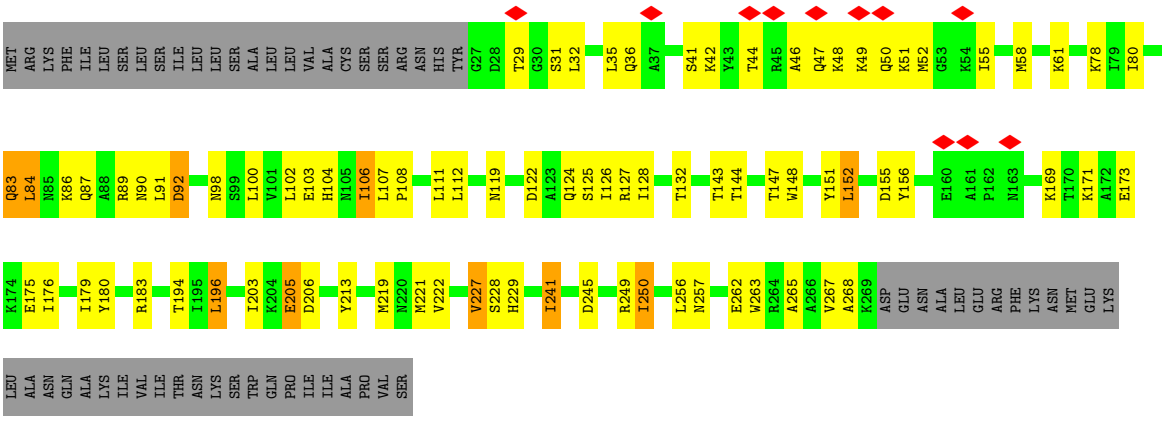
- Molecule 9: DotF

Chain EF:



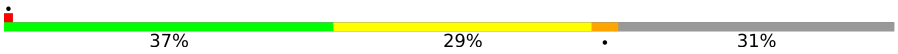
- Molecule 10: DotC

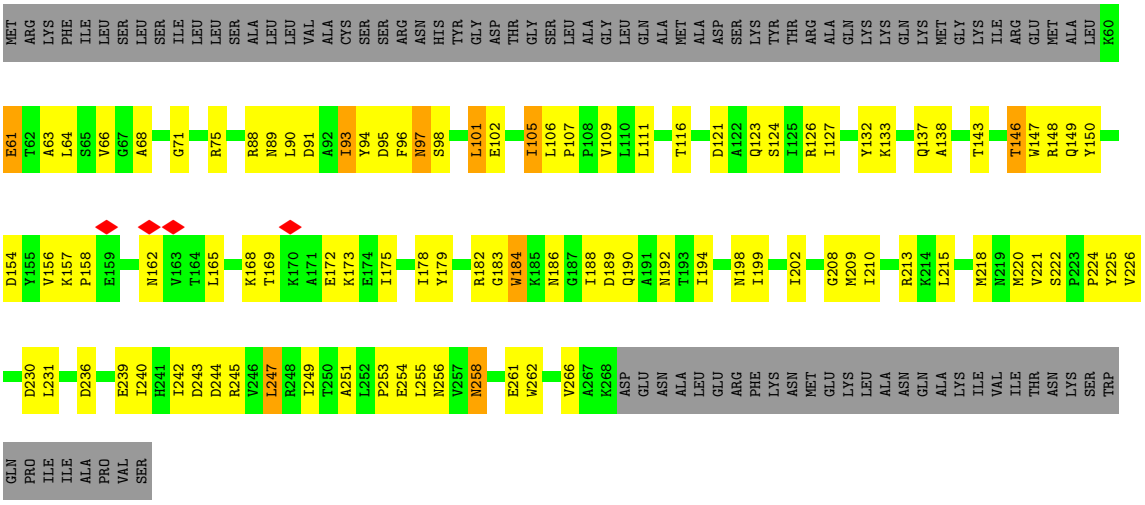
Chain BC:



- Molecule 10: DotC

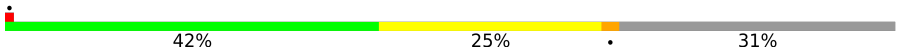
Chain CC:

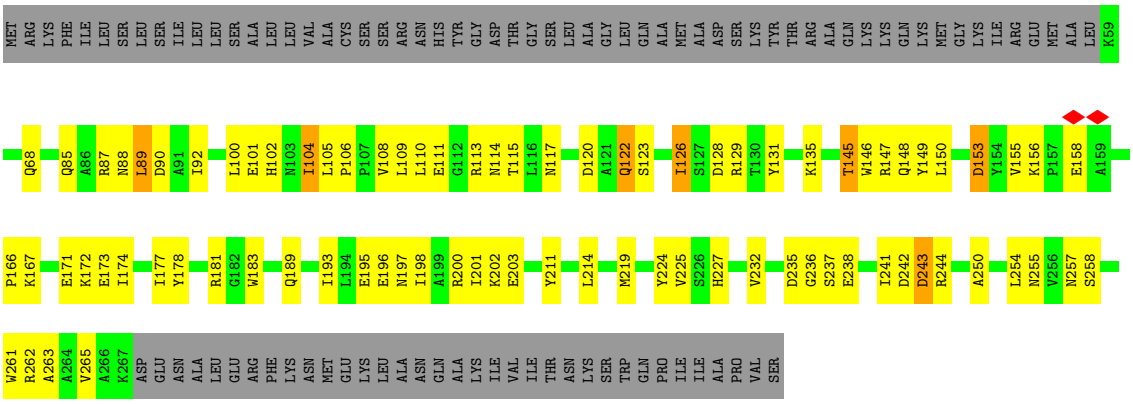




- Molecule 10: DotC

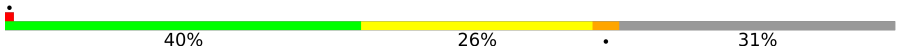
Chain DC:

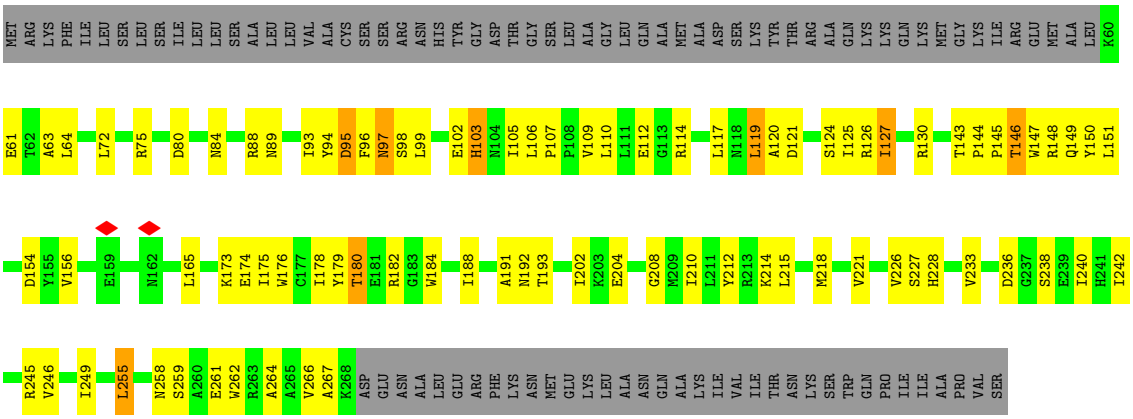




- Molecule 10: DotC

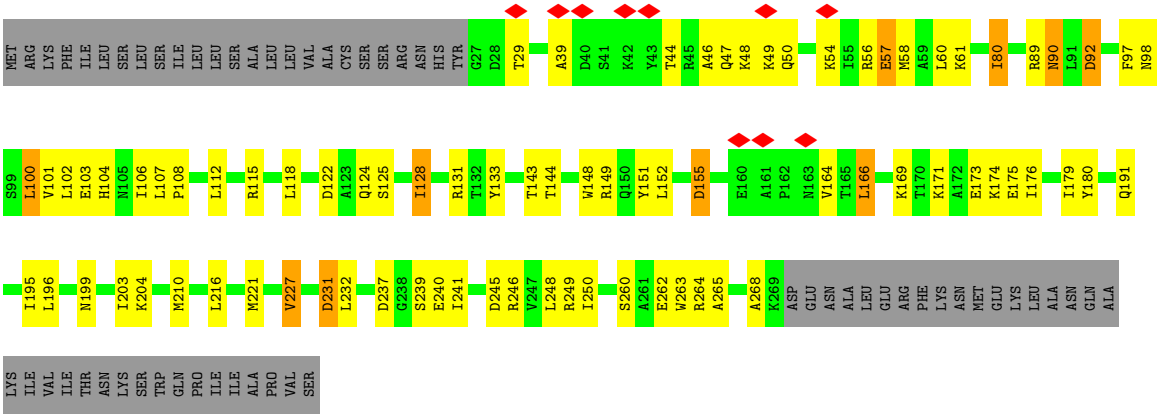
Chain EC:





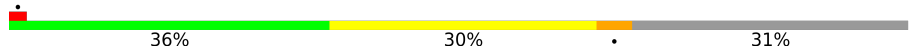
- Molecule 10: DotC

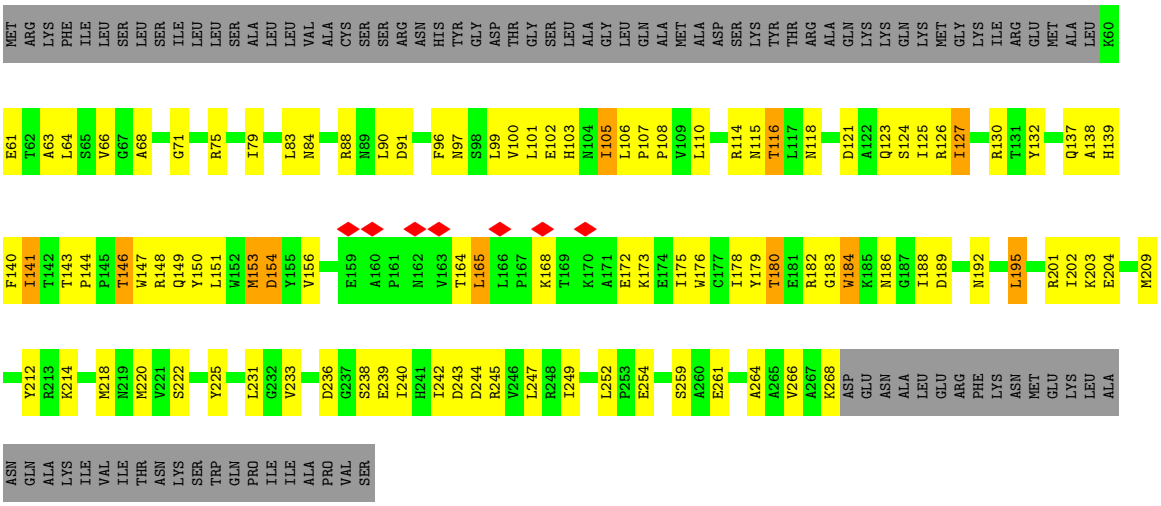
Chain FC:



- Molecule 10: DotC

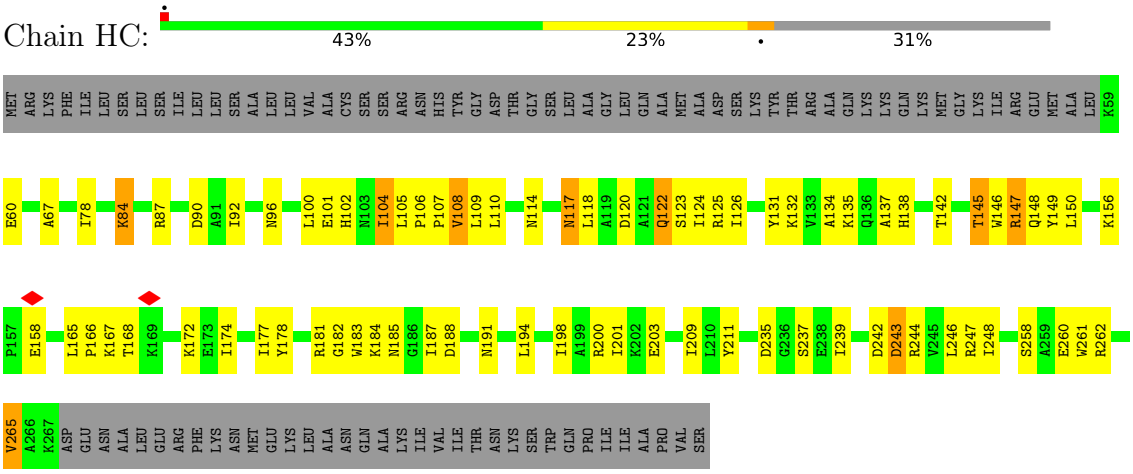
Chain GC:





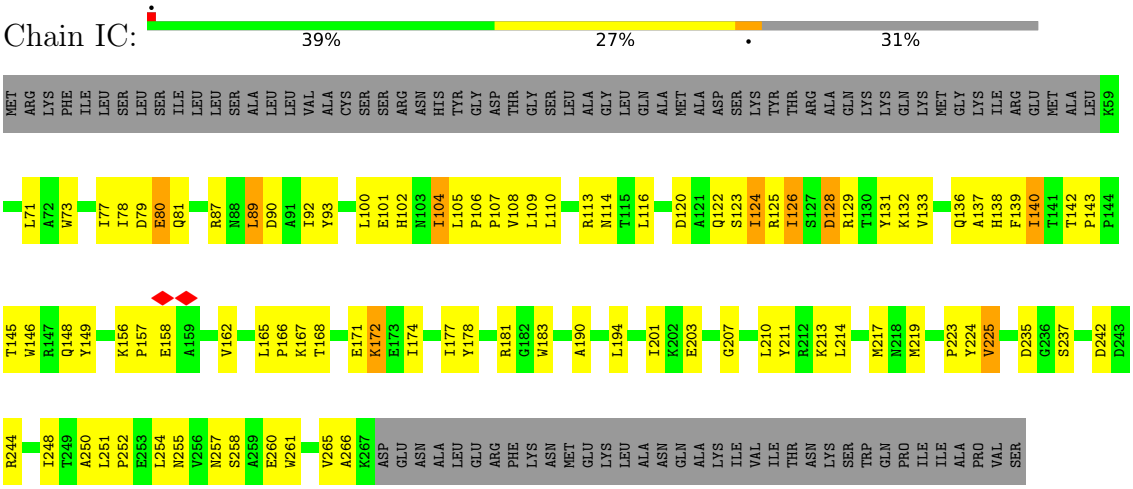
- Molecule 10: DotC

Chain HC:



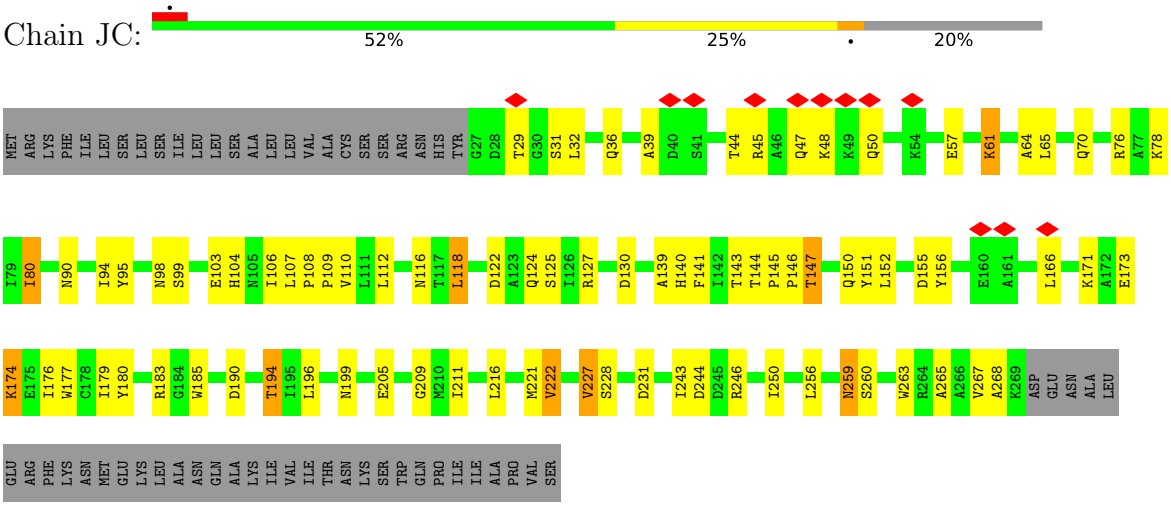
- Molecule 10: DotC

Chain IC:



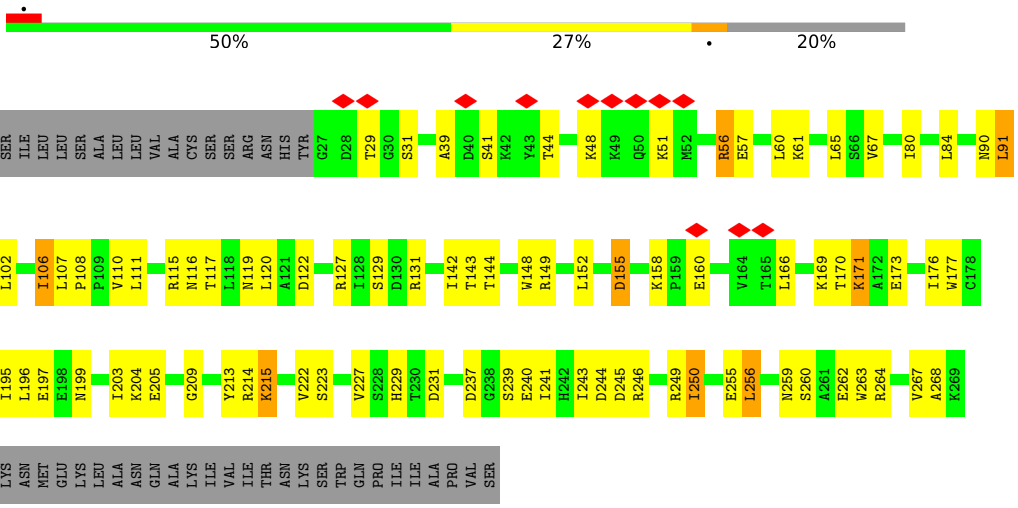
- Molecule 10: DotC

Chain JC:



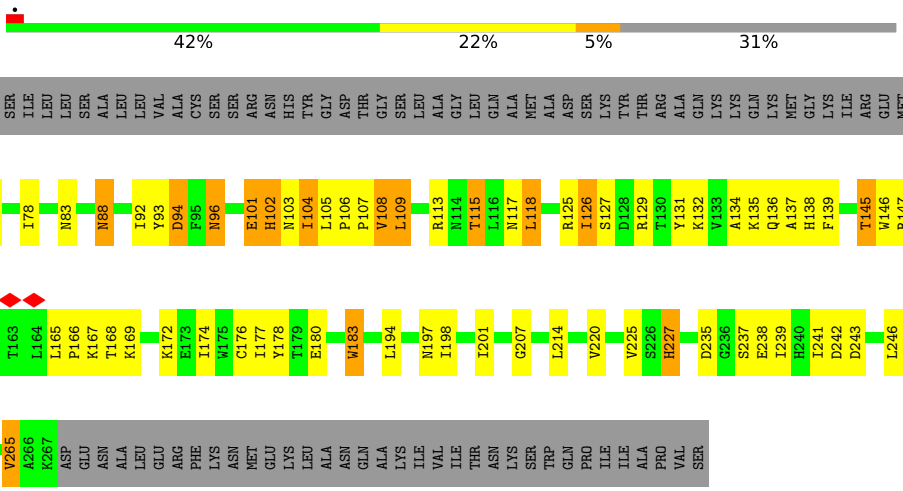
- Molecule 10: DotC

Chain KC:



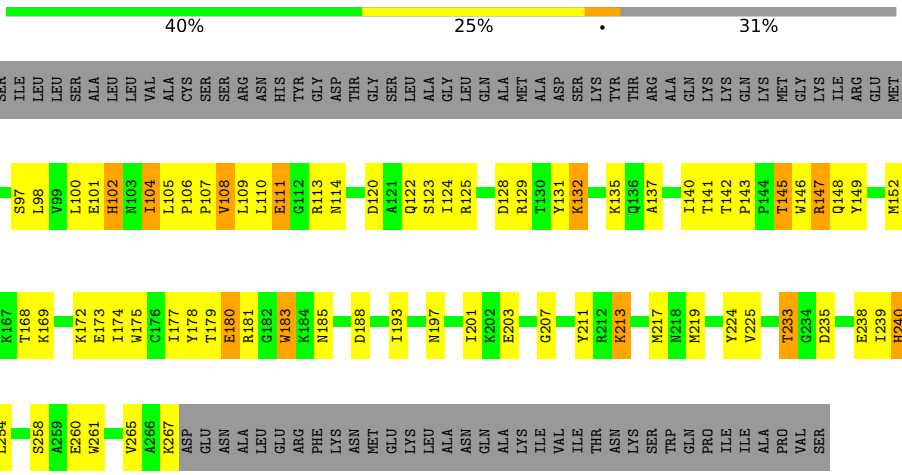
- Molecule 10: DotC

Chain LC:



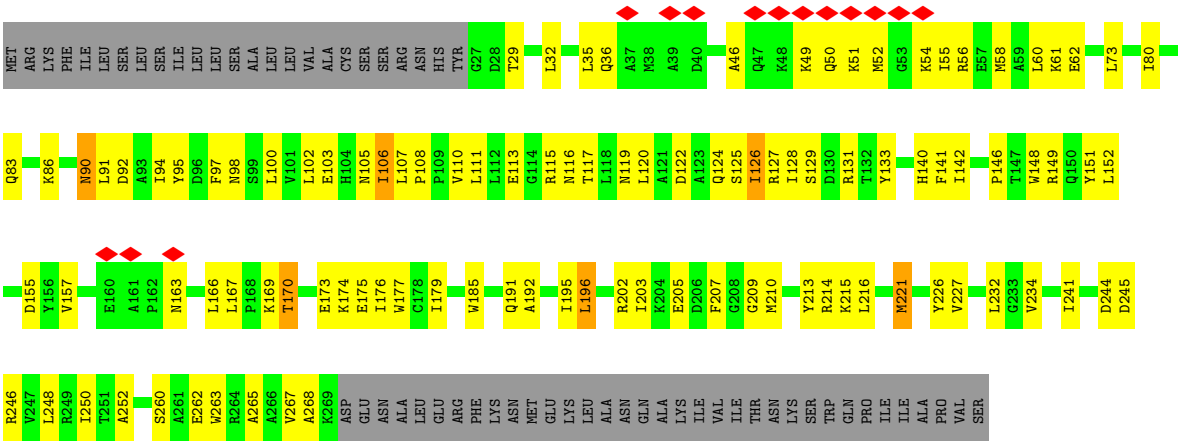
- Molecule 10: DotC

Chain MC:



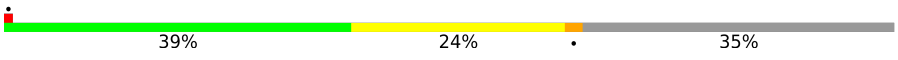
- Molecule 10: DotC

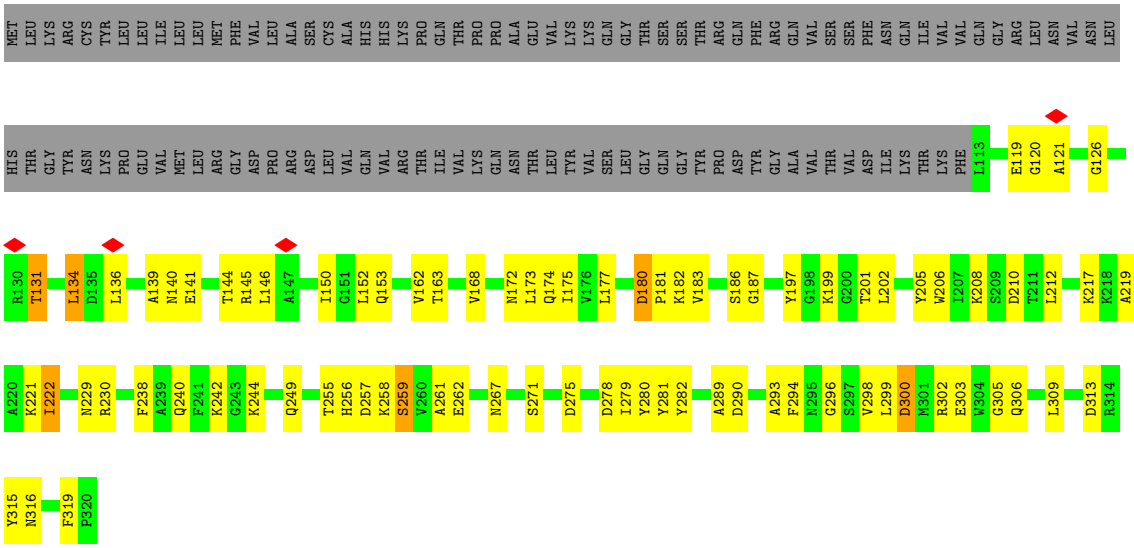
Chain AC:



• Molecule 11: DUF2807 domain-containing protein

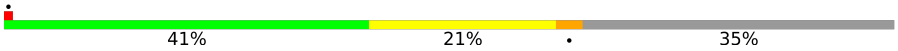
Chain HM:

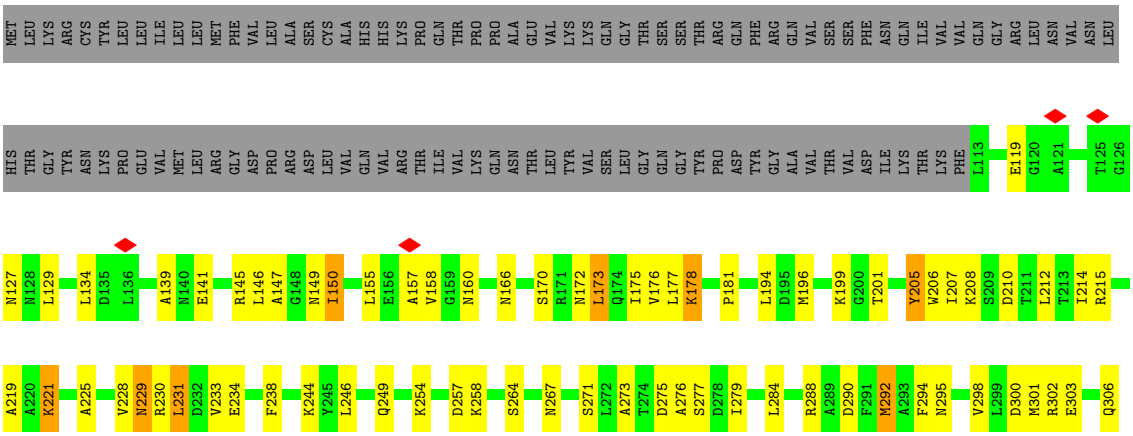


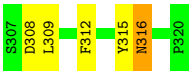


• Molecule 11: DUF2807 domain-containing protein

Chain IM:

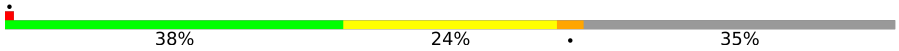


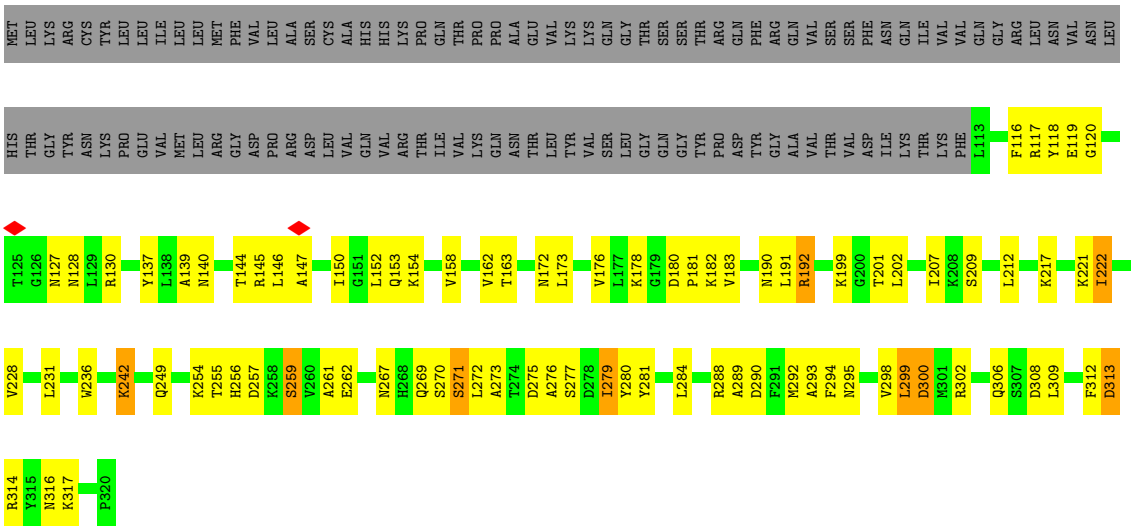




• Molecule 11: DUF2807 domain-containing protein

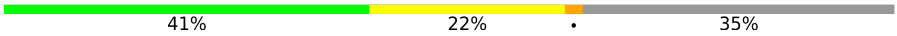
Chain KM:

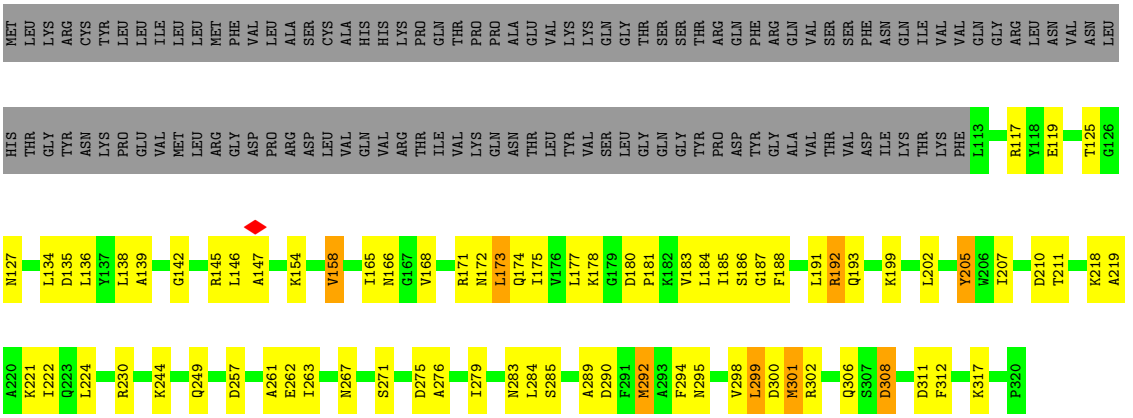




• Molecule 11: DUF2807 domain-containing protein

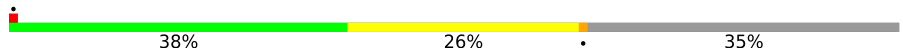
Chain LM:

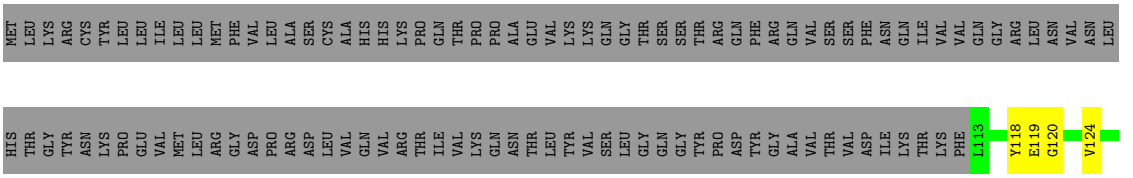


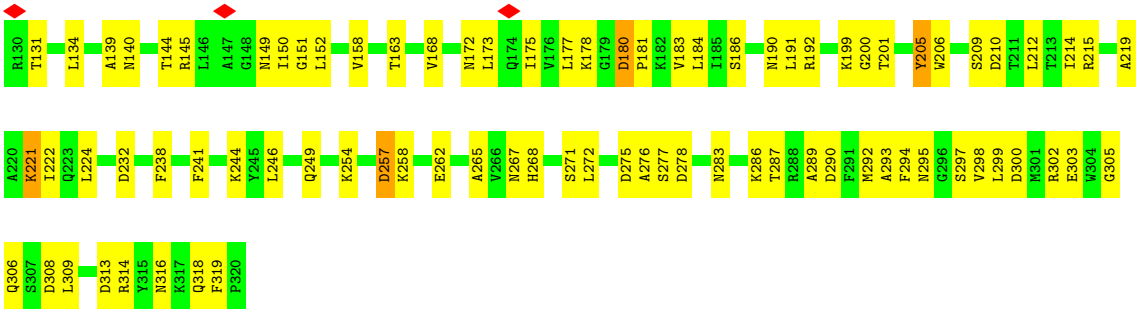


• Molecule 11: DUF2807 domain-containing protein

Chain MM:

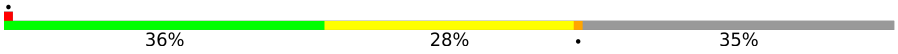


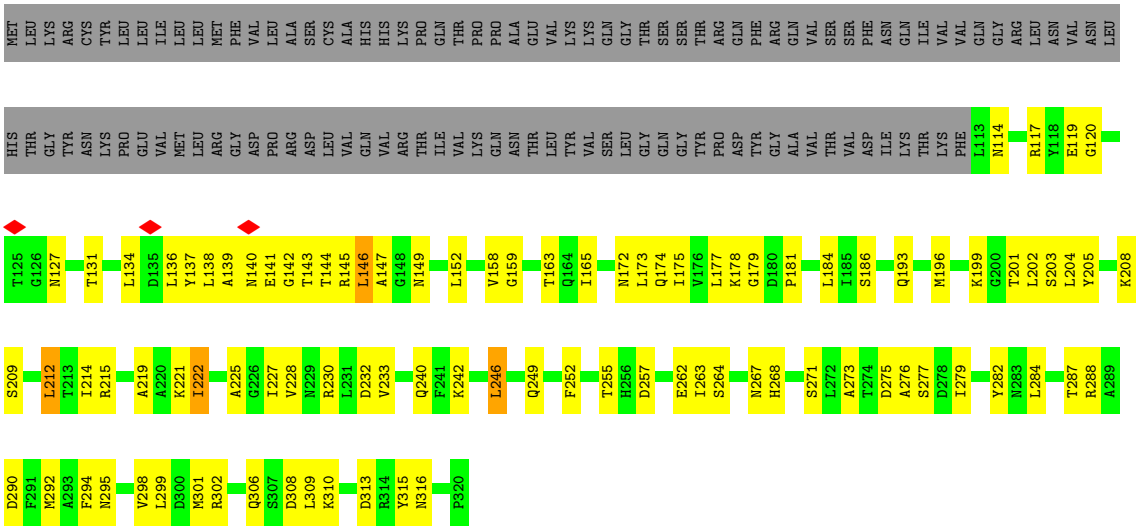




- Molecule 11: DUF2807 domain-containing protein

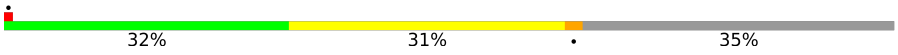
Chain AM:

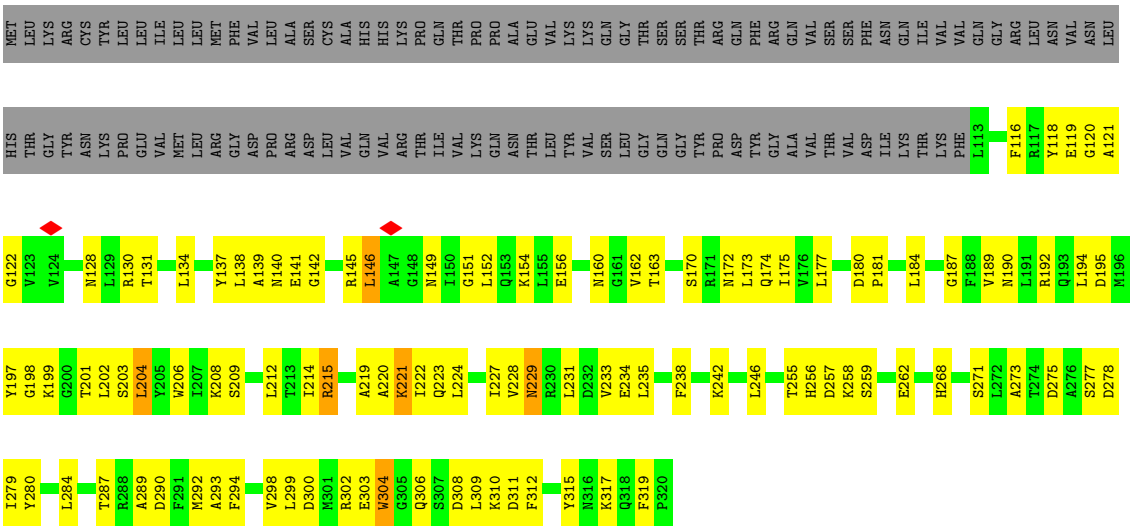




- Molecule 11: DUF2807 domain-containing protein

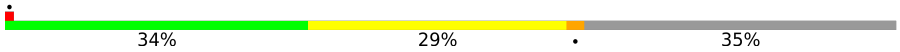
Chain BM:

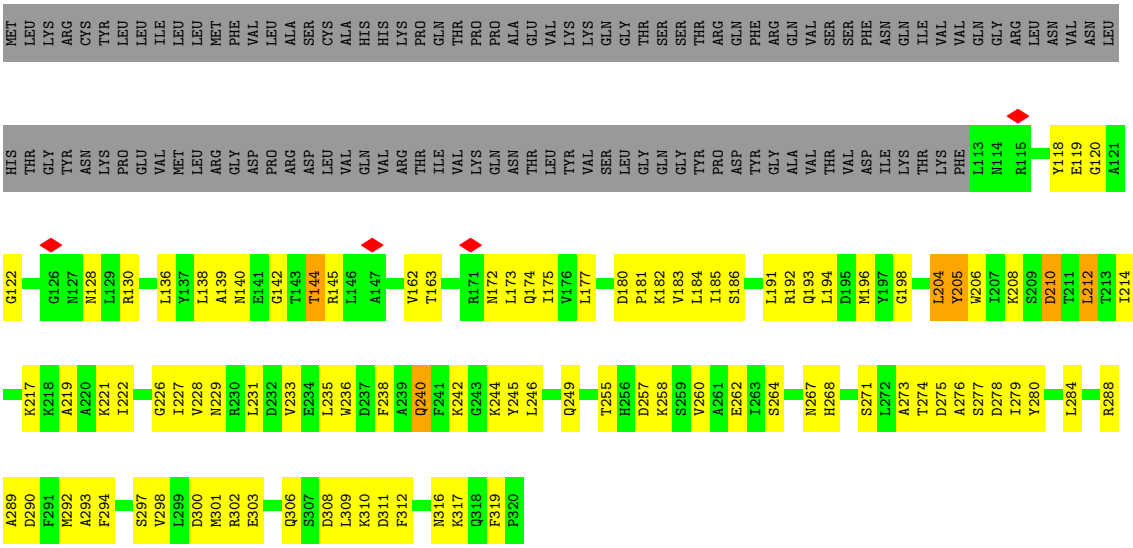




- Molecule 11: DUF2807 domain-containing protein

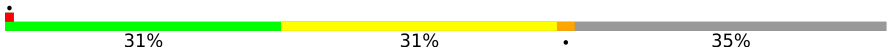
Chain EM:

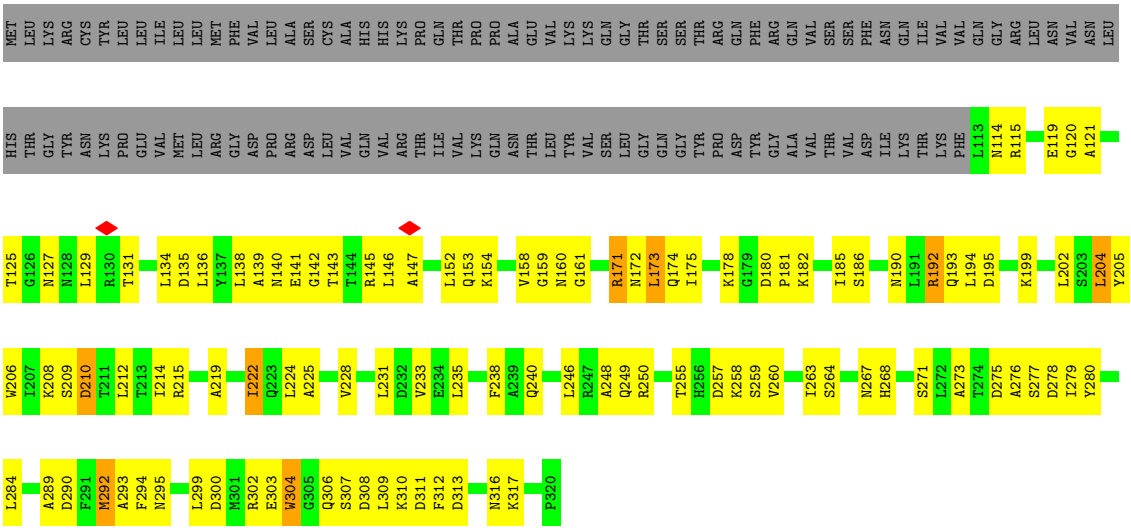




- Molecule 11: DUF2807 domain-containing protein

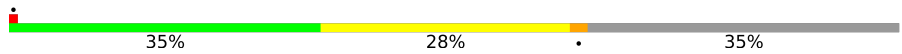
Chain FM:

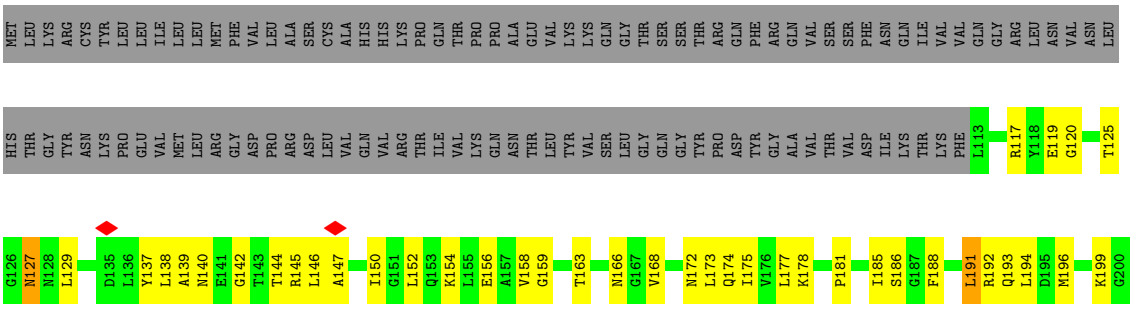


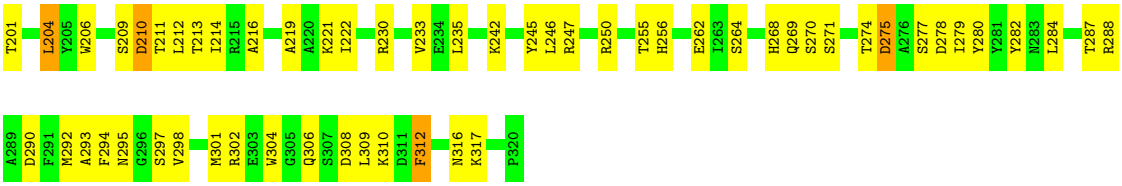


- Molecule 11: DUF2807 domain-containing protein

Chain GM:

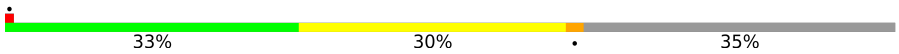


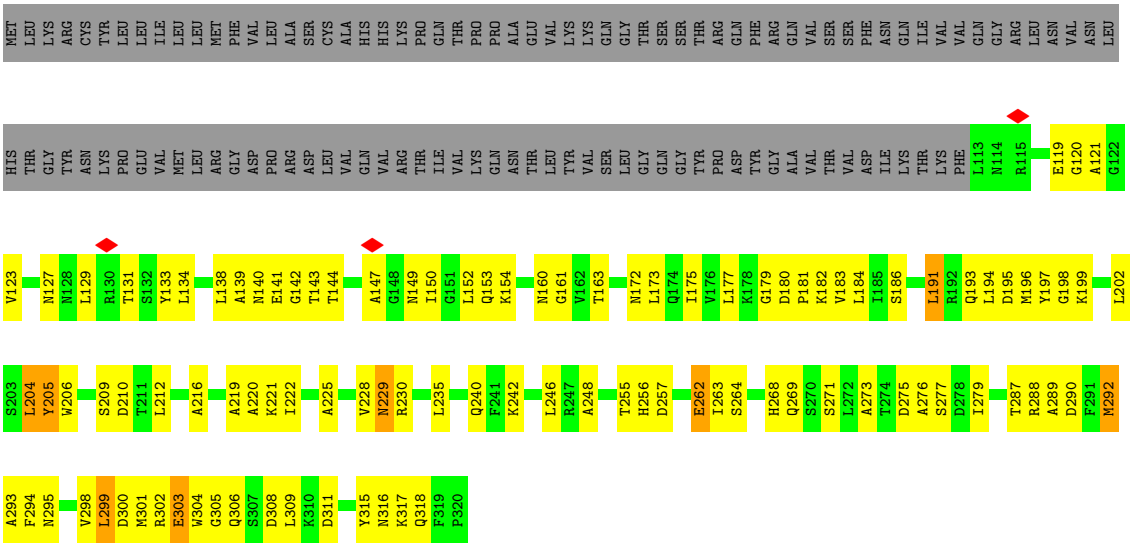




• Molecule 11: DUF2807 domain-containing protein

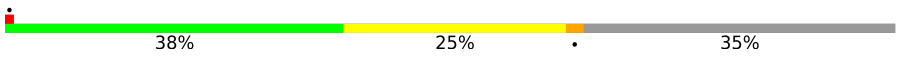
Chain JM:

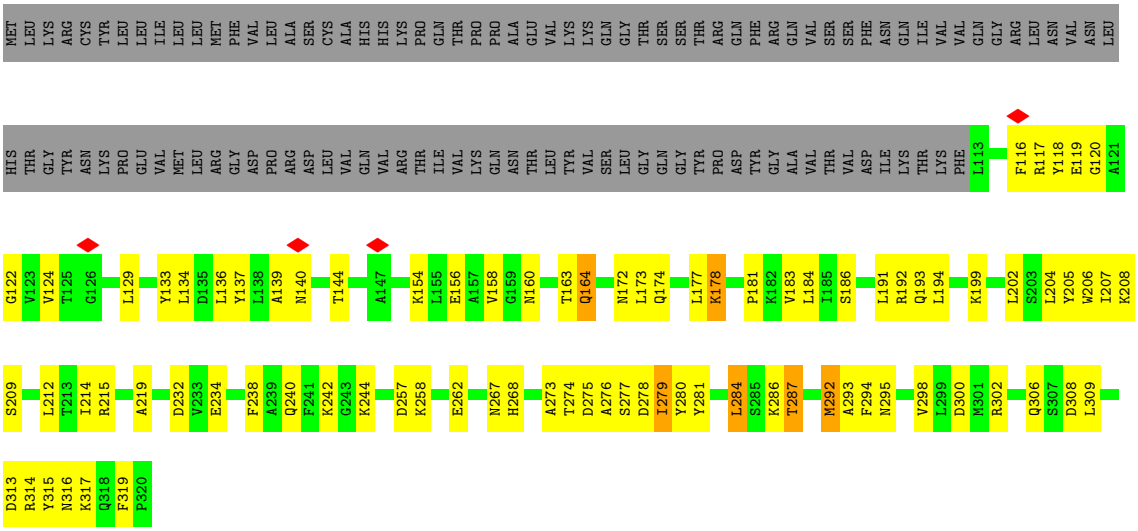




• Molecule 11: DUF2807 domain-containing protein

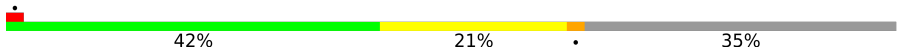
Chain CM:

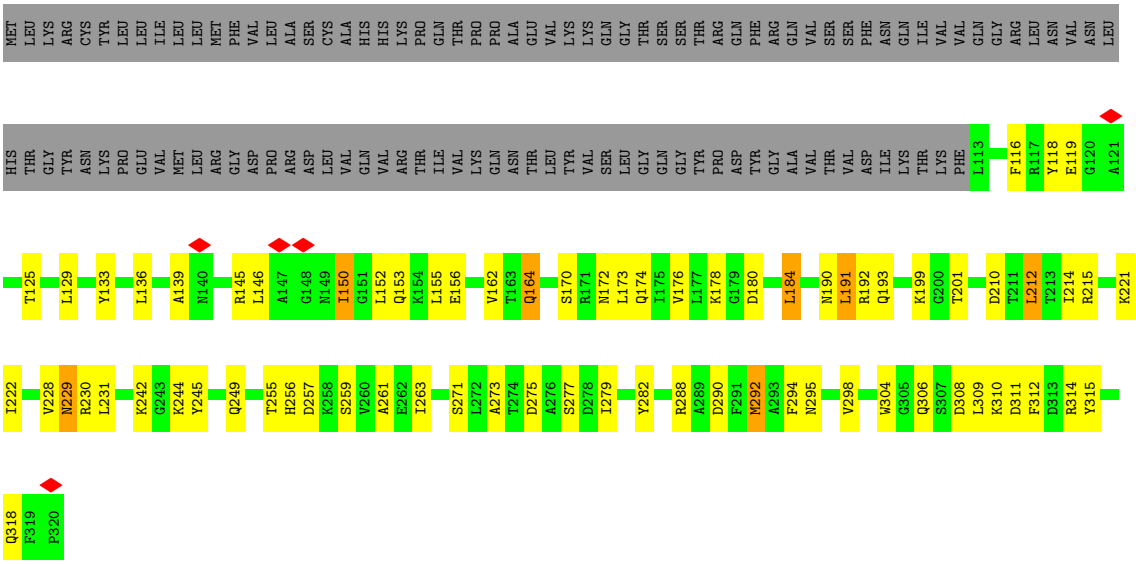




• Molecule 11: DUF2807 domain-containing protein

Chain DM:




MET LEU LYS ARG CYS TYR LEU LEU ILE LEU LEU MET PHE VAL LEU ALA SER CYS ALA HIS HIS LYS PRO GLN THR PRO PRO ALA GLU VAL LYS LYS GLN GLY THR SER SER THR ARG GLN PHE ARG GLN VAL SER SER PHE ASN GLN ILE VAL VAL GLN GLY ARG LEU ASN VAL ASN LEU
HIS THR GLY TYR ASN LYS PRO GLU VAL MET LEU ARG GLY ASP PRO ARG ASP LEU VAL GLN VAL ARG THR ILE VAL LYS GLN ASN THR LEU TYR VAL SER LEU GLY GLN GLY TYR PRO ASP TYR GLY ALA VAL THR VAL ASP ILE LYS THR LYS PHE L113 F116 R117 Y118 E119 G120 A121
T125 L129 Y133 L136 A139 M140 R145 L146 A147 G148 N149 T150 G151 L152 Q153 K154 L155 E156 V162 T163 Q164 S170 R171 N172 L173 Q174 I175 V176 L177 K178 G179 D180 L184 N190 L191 R192 Q193 K199 G200 T201 D210 T211 L212 T213 I214 R215 K221
I222 V228 N229 R230 L231 K242 G243 K244 Y245 Q249 T255 H256 D257 K258 S259 V260 A261 E262 I263 S271 L272 A273 T274 D275 A276 S277 D278 I279 Y282 R288 A289 D290 F291 M292 A293 F294 N295 V298 W304 G305 Q306 S307 D308 L309 K310 D311 F312 D313 R314 Y315
Q318 F319 P320

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64698	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 ($e^-/Å^2$)	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	9.229	Depositor
Minimum map value	-3.621	Depositor
Average map value	0.091	Depositor
Map value standard deviation	0.546	Depositor
Recommended contour level	2.25	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	0.15	0/1250	0.38	0/1699
1	Ag	0.12	0/278	0.23	0/377
1	BG	0.16	0/1250	0.40	0/1699
1	Bg	0.12	0/278	0.23	0/377
1	CG	0.16	0/1250	0.40	0/1699
1	Cg	0.11	0/278	0.24	0/377
1	DG	0.16	0/1250	0.40	0/1699
1	Dg	0.12	0/278	0.28	0/377
1	EG	0.16	0/1250	0.39	0/1699
1	Eg	0.12	0/278	0.25	0/377
1	FG	0.17	0/1250	0.43	0/1699
1	Fg	0.11	0/278	0.24	0/377
1	GG	0.17	0/1250	0.42	0/1699
1	Gg	0.11	0/278	0.26	0/377
1	HG	0.16	0/1250	0.40	0/1699
1	Hg	0.11	0/278	0.24	0/377
1	IG	0.16	0/1250	0.42	0/1699
1	Ig	0.11	0/278	0.26	0/377
1	JG	0.16	0/1250	0.40	0/1699
1	Jg	0.11	0/278	0.24	0/377
1	KG	0.16	0/1250	0.39	0/1699
1	Kg	0.11	0/278	0.27	0/377
1	LG	0.16	0/1250	0.42	0/1699
1	Lg	0.11	0/278	0.26	0/377
1	MG	0.17	0/1250	0.38	0/1699
1	Mg	0.11	0/278	0.26	0/377
1	NG	0.16	0/1250	0.39	0/1699
1	OG	0.16	0/1250	0.39	0/1699
1	PG	0.16	0/1250	0.39	0/1699
1	VG	0.12	0/278	0.32	0/377
1	WG	0.13	0/278	0.31	0/377
1	XG	0.15	0/278	0.36	0/377
1	YG	0.13	0/278	0.32	0/377
1	ZG	0.14	0/278	0.29	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	AH	0.15	0/2033	0.33	0/2775
2	BH	0.15	0/2033	0.32	0/2775
2	CH	0.14	0/2033	0.30	0/2775
2	DH	0.14	0/2033	0.30	0/2775
2	EH	0.15	0/2033	0.31	0/2775
2	FH	0.15	0/2033	0.31	0/2775
2	GH	0.14	0/2033	0.30	0/2775
2	HH	0.13	0/2033	0.27	0/2775
2	IH	0.14	0/2033	0.31	0/2775
2	JH	0.14	0/2033	0.29	0/2775
2	KH	0.14	0/2033	0.29	0/2775
2	LH	0.14	0/2033	0.33	0/2775
2	MH	0.14	0/2033	0.30	0/2775
2	VH	0.11	0/1921	0.29	0/2620
2	WH	0.11	0/1921	0.29	0/2620
2	XH	0.11	0/1921	0.29	0/2620
2	YH	0.11	0/1921	0.29	0/2620
2	ZH	0.12	0/1921	0.30	0/2620
3	AK	0.18	0/1195	0.31	0/1616
3	BK	0.18	0/1195	0.30	0/1616
3	CK	0.16	0/1195	0.32	0/1616
3	DK	0.16	0/1195	0.29	0/1616
3	EK	0.15	0/1195	0.29	0/1616
3	FK	0.16	0/1195	0.30	0/1616
3	GK	0.16	0/1195	0.32	0/1616
3	HK	0.16	0/1195	0.31	0/1616
3	IK	0.15	0/1195	0.30	0/1616
3	JK	0.16	0/1195	0.29	0/1616
3	KK	0.16	0/1195	0.30	0/1616
3	LK	0.16	0/1195	0.30	0/1616
3	MK	0.16	0/1195	0.30	0/1616
4	AL	0.14	0/1417	0.30	0/1912
4	BL	0.16	0/1417	0.34	0/1912
4	CL	0.15	0/1417	0.32	0/1912
4	DL	0.15	0/1417	0.32	0/1912
4	EL	0.15	0/1417	0.36	0/1912
4	FL	0.15	0/1417	0.32	0/1912
4	GL	0.15	0/1417	0.34	0/1912
4	HL	0.15	0/1417	0.34	0/1912
4	IL	0.15	0/1417	0.33	0/1912
4	JL	0.15	0/1417	0.33	0/1912
4	KL	0.15	0/1417	0.31	0/1912
4	LL	0.15	0/1417	0.31	0/1912

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	ML	0.15	0/1417	0.32	0/1912
5	AN	0.15	0/593	0.31	0/799
5	BN	0.13	0/593	0.27	0/799
5	CN	0.14	0/593	0.30	0/799
5	DN	0.15	0/593	0.29	0/799
5	EN	0.14	0/593	0.29	0/799
5	FN	0.15	0/593	0.27	0/799
5	GN	0.15	0/593	0.28	0/799
5	HN	0.13	0/593	0.26	0/799
5	IN	0.15	0/593	0.29	0/799
5	JN	0.13	0/593	0.27	0/799
5	KN	0.13	0/593	0.29	0/799
5	LN	0.14	0/593	0.29	0/799
5	MN	0.13	0/593	0.27	0/799
8	AD	0.16	0/1107	0.32	0/1502
8	Ad	0.15	0/1078	0.31	0/1463
8	BD	0.17	0/1107	0.33	0/1502
8	Bd	0.15	0/1078	0.27	0/1463
8	CD	0.15	0/1107	0.34	0/1502
8	Cd	0.14	0/1078	0.30	0/1463
8	DD	0.15	0/1107	0.32	0/1502
8	Dd	0.15	0/1078	0.30	0/1463
8	ED	0.16	0/1107	0.35	0/1502
8	Ed	0.14	0/1078	0.27	0/1463
8	FD	0.16	0/1107	0.36	0/1502
8	Fd	0.14	0/1078	0.28	0/1463
8	GD	0.16	0/1107	0.35	0/1502
8	Gd	0.16	0/1078	0.30	0/1463
8	HD	0.17	0/1107	0.34	0/1502
8	Hd	0.14	0/1078	0.27	0/1463
8	ID	0.16	0/1107	0.34	0/1502
8	Id	0.15	0/1078	0.28	0/1463
8	JD	0.15	0/1107	0.33	0/1502
8	Jd	0.14	0/1078	0.27	0/1463
8	KD	0.15	0/1107	0.34	0/1502
8	Kd	0.14	0/1078	0.27	0/1463
8	LD	0.16	0/1107	0.32	0/1502
8	Ld	0.15	0/1078	0.28	0/1463
8	MD	0.16	0/1107	0.33	0/1502
8	Md	0.14	0/1078	0.30	0/1463
9	AF	0.11	0/490	0.26	0/660
9	Af	0.11	0/456	0.31	0/615
9	BF	0.11	0/490	0.23	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
9	Bf	0.12	0/456	0.30	0/615
9	CF	0.11	0/490	0.30	0/660
9	Cf	0.11	0/456	0.24	0/615
9	DF	0.12	0/490	0.23	0/660
9	Df	0.13	0/456	0.28	0/615
9	EF	0.10	0/490	0.24	0/660
9	Ef	0.10	0/456	0.25	0/615
9	FF	0.10	0/490	0.25	0/660
9	Ff	0.12	0/456	0.30	0/615
9	GF	0.10	0/490	0.26	0/660
9	Gf	0.11	0/456	0.25	0/615
9	HF	0.11	0/490	0.28	0/660
9	Hf	0.12	0/456	0.32	0/615
9	IF	0.10	0/490	0.28	0/660
9	If	0.10	0/456	0.26	0/615
9	JF	0.10	0/490	0.27	0/660
9	Jf	0.11	0/456	0.26	0/615
9	KF	0.09	0/490	0.26	0/660
9	Kf	0.11	0/456	0.29	0/615
9	LF	0.10	0/490	0.30	0/660
9	Lf	0.12	0/456	0.25	0/615
9	MF	0.10	0/490	0.30	0/660
9	Mf	0.13	0/456	0.32	0/615
9	VF	0.12	0/490	0.26	0/660
9	WF	0.09	0/490	0.25	0/660
9	XF	0.11	0/490	0.26	0/660
9	YF	0.10	0/490	0.29	0/660
9	ZF	0.10	0/490	0.25	0/660
10	AC	0.15	0/1957	0.30	0/2651
10	BC	0.16	0/1957	0.31	0/2651
10	CC	0.17	0/1702	0.30	0/2315
10	DC	0.17	0/1702	0.32	0/2315
10	EC	0.17	0/1702	0.32	0/2315
10	FC	0.16	0/1957	0.30	0/2651
10	GC	0.16	0/1702	0.31	0/2315
10	HC	0.16	0/1702	0.30	0/2315
10	IC	0.16	0/1702	0.29	0/2315
10	JC	0.16	0/1957	0.32	0/2651
10	KC	0.16	0/1957	0.31	0/2651
10	LC	0.16	0/1702	0.30	0/2315
10	MC	0.17	0/1702	0.30	0/2315
11	AM	0.14	0/1678	0.32	0/2262
11	BM	0.13	0/1678	0.34	0/2262

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
11	CM	0.14	0/1678	0.32	0/2262
11	DM	0.14	0/1678	0.32	0/2262
11	EM	0.14	0/1678	0.32	0/2262
11	FM	0.13	0/1678	0.35	0/2262
11	GM	0.14	0/1678	0.33	0/2262
11	HM	0.14	0/1678	0.31	0/2262
11	IM	0.14	0/1678	0.33	0/2262
11	JM	0.14	0/1678	0.32	0/2262
11	KM	0.13	0/1678	0.31	0/2262
11	LM	0.14	0/1678	0.33	0/2262
11	MM	0.13	0/1678	0.32	0/2262
All	All	0.15	0/191071	0.32	0/258997

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	1229	0	1231	65	0
1	Ag	276	0	263	12	0
1	BG	1229	0	1231	59	0
1	Bg	276	0	263	18	0
1	CG	1229	0	1231	66	0
1	Cg	276	0	263	19	0
1	DG	1229	0	1231	65	0
1	Dg	276	0	263	18	0
1	EG	1229	0	1231	55	0
1	Eg	276	0	263	21	0
1	FG	1229	0	1231	55	0
1	Fg	276	0	263	15	0
1	GG	1229	0	1231	66	0
1	Gg	276	0	263	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HG	1229	0	1231	64	0
1	Hg	276	0	263	12	0
1	IG	1229	0	1231	67	0
1	Ig	276	0	263	23	0
1	JG	1229	0	1231	60	0
1	Jg	276	0	263	17	0
1	KG	1229	0	1231	64	0
1	Kg	276	0	263	22	0
1	LG	1229	0	1231	50	0
1	Lg	276	0	263	18	0
1	MG	1229	0	1231	56	0
1	Mg	276	0	263	18	0
1	NG	1229	0	1231	72	0
1	OG	1229	0	1231	76	0
1	PG	1229	0	1231	63	0
1	VG	276	0	263	16	0
1	WG	276	0	263	17	0
1	XG	276	0	263	16	0
1	YG	276	0	263	16	0
1	ZG	276	0	263	17	0
2	AH	1983	0	2009	78	0
2	BH	1983	0	2009	82	0
2	CH	1983	0	2009	65	0
2	DH	1983	0	2009	80	0
2	EH	1983	0	2009	85	0
2	FH	1983	0	2009	74	0
2	GH	1983	0	2009	56	0
2	HH	1983	0	2009	72	0
2	IH	1983	0	2009	70	0
2	JH	1983	0	2009	65	0
2	KH	1983	0	2009	69	0
2	LH	1983	0	2009	73	0
2	MH	1983	0	2009	66	0
2	VH	1875	0	1900	70	0
2	WH	1875	0	1900	51	0
2	XH	1875	0	1900	68	0
2	YH	1875	0	1900	72	0
2	ZH	1875	0	1900	63	0
3	AK	1175	0	1221	29	0
3	BK	1175	0	1221	35	0
3	CK	1175	0	1221	27	0
3	DK	1175	0	1221	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	EK	1175	0	1221	34	0
3	FK	1175	0	1221	47	0
3	GK	1175	0	1221	40	0
3	HK	1175	0	1221	38	0
3	IK	1175	0	1221	39	0
3	JK	1175	0	1221	35	0
3	KK	1175	0	1221	43	0
3	LK	1175	0	1221	39	0
3	MK	1175	0	1221	42	0
4	AL	1388	0	1378	41	0
4	BL	1388	0	1378	48	0
4	CL	1388	0	1378	33	0
4	DL	1388	0	1378	51	0
4	EL	1388	0	1378	47	0
4	FL	1388	0	1378	40	0
4	GL	1388	0	1378	56	0
4	HL	1388	0	1378	52	0
4	IL	1388	0	1378	46	0
4	JL	1388	0	1378	48	0
4	KL	1388	0	1378	57	0
4	LL	1388	0	1378	49	0
4	ML	1388	0	1378	39	0
5	AN	582	0	530	21	0
5	BN	582	0	530	27	0
5	CN	582	0	530	19	0
5	DN	582	0	530	20	0
5	EN	582	0	530	19	0
5	FN	582	0	530	17	0
5	GN	582	0	530	17	0
5	HN	582	0	530	19	0
5	IN	582	0	530	24	0
5	JN	582	0	530	25	0
5	KN	582	0	530	16	0
5	LN	582	0	530	25	0
5	MN	582	0	530	20	0
6	AU	45	0	12	1	0
6	BU	45	0	12	0	0
6	CU	45	0	12	0	0
6	DU	45	0	12	1	0
6	EU	45	0	12	1	0
6	FU	45	0	12	1	0
6	GU	45	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	HU	45	0	12	1	0
6	IU	45	0	12	1	0
6	JU	45	0	13	1	0
6	KU	45	0	13	1	0
6	LU	45	0	12	1	0
6	MU	45	0	12	0	0
7	AX	240	0	56	2	0
7	BX	240	0	57	5	0
7	CX	240	0	57	2	0
7	DX	240	0	56	2	0
7	EX	240	0	55	0	0
7	FX	240	0	54	0	0
7	GX	240	0	54	0	0
7	HX	240	0	55	1	0
7	IX	240	0	55	1	0
7	JX	240	0	57	2	0
7	KX	240	0	55	1	0
7	LX	240	0	55	0	0
7	MX	240	0	58	3	0
7	VX	240	0	54	1	0
7	WX	240	0	52	1	0
7	XX	240	0	54	1	0
7	YX	240	0	55	4	0
7	ZX	240	0	54	1	0
8	AD	1086	0	1121	44	0
8	Ad	1058	0	1092	36	0
8	BD	1086	0	1121	37	0
8	Bd	1058	0	1092	36	0
8	CD	1086	0	1121	34	0
8	Cd	1058	0	1092	40	0
8	DD	1086	0	1121	42	0
8	Dd	1058	0	1092	23	0
8	ED	1086	0	1121	38	0
8	Ed	1058	0	1092	38	0
8	FD	1086	0	1121	44	0
8	Fd	1058	0	1092	46	0
8	GD	1086	0	1121	41	0
8	Gd	1058	0	1092	31	0
8	HD	1086	0	1121	37	0
8	Hd	1058	0	1092	33	0
8	ID	1086	0	1121	34	0
8	Id	1058	0	1092	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	JD	1086	0	1121	32	0
8	Jd	1058	0	1092	30	0
8	KD	1086	0	1121	36	0
8	Kd	1058	0	1092	28	0
8	LD	1086	0	1121	33	0
8	Ld	1058	0	1092	34	0
8	MD	1086	0	1121	25	0
8	Md	1058	0	1092	28	0
9	AF	483	0	502	23	0
9	Af	449	0	474	11	0
9	BF	483	0	502	15	0
9	Bf	449	0	474	15	0
9	CF	483	0	502	23	0
9	Cf	449	0	474	14	0
9	DF	483	0	502	22	0
9	Df	449	0	474	18	0
9	EF	483	0	502	17	0
9	Ef	449	0	474	17	0
9	FF	483	0	502	17	0
9	Ff	449	0	474	19	0
9	GF	483	0	502	20	0
9	Gf	449	0	474	12	0
9	HF	483	0	502	18	0
9	Hf	449	0	474	12	0
9	IF	483	0	502	15	0
9	If	449	0	474	26	0
9	JF	483	0	502	16	0
9	Jf	449	0	474	11	0
9	KF	483	0	502	18	0
9	Kf	449	0	474	19	0
9	LF	483	0	502	13	0
9	Lf	449	0	474	15	0
9	MF	483	0	502	18	0
9	Mf	449	0	474	11	0
9	VF	483	0	502	22	0
9	WF	483	0	502	20	0
9	XF	483	0	502	22	0
9	YF	483	0	502	21	0
9	ZF	483	0	502	10	0
10	AC	1921	0	1952	84	0
10	BC	1921	0	1952	63	0
10	CC	1667	0	1682	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	DC	1667	0	1682	70	0
10	EC	1667	0	1682	56	0
10	FC	1921	0	1952	65	0
10	GC	1667	0	1682	74	0
10	HC	1667	0	1682	53	0
10	IC	1667	0	1682	74	0
10	JC	1921	0	1952	65	0
10	KC	1921	0	1952	77	0
10	LC	1667	0	1682	67	0
10	MC	1667	0	1682	66	0
11	AM	1650	0	1658	65	0
11	BM	1650	0	1658	72	0
11	CM	1650	0	1658	57	0
11	DM	1650	0	1658	46	0
11	EM	1650	0	1658	68	0
11	FM	1650	0	1658	73	0
11	GM	1650	0	1658	67	0
11	HM	1650	0	1658	59	0
11	IM	1650	0	1658	51	0
11	JM	1650	0	1658	72	0
11	KM	1650	0	1658	64	0
11	LM	1650	0	1658	45	0
11	MM	1650	0	1658	54	0
All	All	192370	0	190612	6122	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

The worst 5 of 6122 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EM:198:GLY:O	11:EM:219:ALA:HB3	1.66	0.96
1:ZG:798:THR:HA	2:BH:115:MET:HE1	1.50	0.92
11:JM:275:ASP:HB3	11:JM:294:PHE:HB2	1.50	0.91
5:LN:78:LEU:H	2:MH:354:MET:HE1	1.43	0.83
4:DL:166:ALA:HA	4:DL:206:GLU:O	1.77	0.83

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	Ag	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	BG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	CG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Cg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	DG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Dg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	EG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Eg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	FG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Gg	32/1048 (3%)	32 (100%)	0	0	100	100
1	HG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Hg	32/1048 (3%)	32 (100%)	0	0	100	100
1	IG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Ig	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	JG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Jg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	KG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Kg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	LG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Lg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	MG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Mg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	NG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	OG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	PG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	VG	32/1048 (3%)	32 (100%)	0	0	100	100
1	WG	32/1048 (3%)	32 (100%)	0	0	100	100
1	XG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	YG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
2	BH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	CH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
2	DH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
2	EH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
2	FH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
2	GH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
2	HH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
2	IH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	JH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
2	KH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	LH	256/361 (71%)	243 (95%)	13 (5%)	0	100	100
2	MH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	VH	239/361 (66%)	227 (95%)	12 (5%)	0	100	100
2	WH	239/361 (66%)	235 (98%)	4 (2%)	0	100	100
2	XH	239/361 (66%)	234 (98%)	5 (2%)	0	100	100
2	YH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
2	ZH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
3	AK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	BK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	CK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	DK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	EK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	FK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	GK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	HK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
3	IK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	JK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	KK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	LK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
3	MK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
4	AL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	BL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
4	CL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	DL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	EL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	FL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	GL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	HL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	IL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	JL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	KL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
4	LL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
5	AN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	BN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	CN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
5	DN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
5	EN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
5	FN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	GN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	HN	76/124 (61%)	73 (96%)	3 (4%)	0	100	100
5	IN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	JN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	KN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	LN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	MN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	AD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Ad	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	BD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Bd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	CD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
8	Cd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	DD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Dd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
8	ED	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Ed	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
8	FD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
8	Fd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	GD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Gd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
8	HD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Hd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
8	ID	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Id	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
8	JD	138/163 (85%)	128 (93%)	10 (7%)	0	100	100
8	Jd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	KD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Kd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
8	LD	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
8	Ld	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	MD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Md	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	AF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	Af	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	BF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Bf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	CF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
9	Cf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	DF	61/269 (23%)	61 (100%)	0	0	100	100
9	Df	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	EF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Ef	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	FF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
9	Ff	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	GF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Gf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	HF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Hf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	IF	61/269 (23%)	53 (87%)	8 (13%)	0	100	100
9	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	JF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Jf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	KF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
9	Kf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
9	LF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
9	Lf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	MF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Mf	57/269 (21%)	56 (98%)	1 (2%)	0	100	100
9	VF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
9	WF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	XF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
9	YF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
9	ZF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	AC	241/303 (80%)	225 (93%)	16 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	BC	241/303 (80%)	229 (95%)	12 (5%)	0	100	100
10	CC	207/303 (68%)	191 (92%)	16 (8%)	0	100	100
10	DC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
10	EC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
10	FC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
10	GC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
10	HC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
10	IC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
10	JC	241/303 (80%)	227 (94%)	14 (6%)	0	100	100
10	KC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
10	LC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
10	MC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	AM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
11	BM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
11	CM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
11	DM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	EM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
11	FM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	GM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
11	HM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
11	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
11	JM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	KM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
11	LM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
11	MM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
All	All	23724/70112 (34%)	22448 (95%)	1276 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Ag	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	BG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Bg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	CG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	Cg	31/765 (4%)	30 (97%)	1 (3%)	34	55
1	DG	135/765 (18%)	120 (89%)	15 (11%)	6	20
1	Dg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	EG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Eg	31/765 (4%)	29 (94%)	2 (6%)	15	37
1	FG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Fg	31/765 (4%)	30 (97%)	1 (3%)	34	55
1	GG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Gg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	HG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	Hg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	IG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	Ig	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	JG	135/765 (18%)	121 (90%)	14 (10%)	7	22
1	Jg	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	KG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Kg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	LG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	Lg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	MG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Mg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	NG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	OG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	PG	135/765 (18%)	124 (92%)	11 (8%)	11	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	VG	31/765 (4%)	29 (94%)	2 (6%)	15	37
1	WG	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	XG	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	YG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	ZG	31/765 (4%)	25 (81%)	6 (19%)	1	8
2	AH	220/300 (73%)	196 (89%)	24 (11%)	6	21
2	BH	220/300 (73%)	203 (92%)	17 (8%)	12	32
2	CH	220/300 (73%)	204 (93%)	16 (7%)	13	34
2	DH	220/300 (73%)	205 (93%)	15 (7%)	14	36
2	EH	220/300 (73%)	200 (91%)	20 (9%)	9	28
2	FH	220/300 (73%)	206 (94%)	14 (6%)	16	37
2	GH	220/300 (73%)	206 (94%)	14 (6%)	16	37
2	HH	220/300 (73%)	209 (95%)	11 (5%)	22	43
2	IH	220/300 (73%)	212 (96%)	8 (4%)	31	52
2	JH	220/300 (73%)	202 (92%)	18 (8%)	10	31
2	KH	220/300 (73%)	201 (91%)	19 (9%)	10	29
2	LH	220/300 (73%)	203 (92%)	17 (8%)	12	32
2	MH	220/300 (73%)	200 (91%)	20 (9%)	9	28
2	VH	207/300 (69%)	190 (92%)	17 (8%)	10	31
2	WH	207/300 (69%)	184 (89%)	23 (11%)	6	20
2	XH	207/300 (69%)	186 (90%)	21 (10%)	7	23
2	YH	207/300 (69%)	184 (89%)	23 (11%)	6	20
2	ZH	207/300 (69%)	190 (92%)	17 (8%)	10	31
3	AK	129/163 (79%)	119 (92%)	10 (8%)	11	32
3	BK	129/163 (79%)	120 (93%)	9 (7%)	14	36
3	CK	129/163 (79%)	121 (94%)	8 (6%)	16	38
3	DK	129/163 (79%)	118 (92%)	11 (8%)	10	29
3	EK	129/163 (79%)	122 (95%)	7 (5%)	20	42
3	FK	129/163 (79%)	122 (95%)	7 (5%)	20	42
3	GK	129/163 (79%)	115 (89%)	14 (11%)	6	21
3	HK	129/163 (79%)	122 (95%)	7 (5%)	20	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	IK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	JK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	KK	129/163 (79%)	120 (93%)	9 (7%)	14	36
3	LK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	MK	129/163 (79%)	111 (86%)	18 (14%)	3	15
4	AL	148/203 (73%)	140 (95%)	8 (5%)	20	42
4	BL	148/203 (73%)	136 (92%)	12 (8%)	11	31
4	CL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	DL	148/203 (73%)	138 (93%)	10 (7%)	14	36
4	EL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	FL	148/203 (73%)	134 (90%)	14 (10%)	8	25
4	GL	148/203 (73%)	141 (95%)	7 (5%)	23	45
4	HL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	IL	148/203 (73%)	137 (93%)	11 (7%)	13	33
4	JL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	KL	148/203 (73%)	132 (89%)	16 (11%)	6	22
4	LL	148/203 (73%)	141 (95%)	7 (5%)	23	45
4	ML	148/203 (73%)	135 (91%)	13 (9%)	9	29
5	AN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	BN	66/107 (62%)	60 (91%)	6 (9%)	9	28
5	CN	66/107 (62%)	59 (89%)	7 (11%)	6	22
5	DN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	EN	66/107 (62%)	62 (94%)	4 (6%)	17	39
5	FN	66/107 (62%)	62 (94%)	4 (6%)	17	39
5	GN	66/107 (62%)	60 (91%)	6 (9%)	9	28
5	HN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	IN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	JN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	KN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	LN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	MN	66/107 (62%)	56 (85%)	10 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Ad	118/139 (85%)	108 (92%)	10 (8%)	10	29
8	BD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Bd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	CD	121/139 (87%)	118 (98%)	3 (2%)	42	62
8	Cd	118/139 (85%)	111 (94%)	7 (6%)	18	40
8	DD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Dd	118/139 (85%)	110 (93%)	8 (7%)	14	36
8	ED	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Ed	118/139 (85%)	104 (88%)	14 (12%)	5	19
8	FD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Fd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	GD	121/139 (87%)	110 (91%)	11 (9%)	9	28
8	Gd	118/139 (85%)	111 (94%)	7 (6%)	18	40
8	HD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Hd	118/139 (85%)	108 (92%)	10 (8%)	10	29
8	ID	121/139 (87%)	113 (93%)	8 (7%)	15	37
8	Id	118/139 (85%)	114 (97%)	4 (3%)	32	54
8	JD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Jd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	KD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Kd	118/139 (85%)	112 (95%)	6 (5%)	21	43
8	LD	121/139 (87%)	106 (88%)	15 (12%)	4	18
8	Ld	118/139 (85%)	110 (93%)	8 (7%)	14	36
8	MD	121/139 (87%)	113 (93%)	8 (7%)	15	37
8	Md	118/139 (85%)	107 (91%)	11 (9%)	8	26
9	AF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Af	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	BF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	Bf	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	CF	53/237 (22%)	48 (91%)	5 (9%)	8	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Cf	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	DF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	Df	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	EF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Ef	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	FF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Ff	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	GF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Gf	49/237 (21%)	47 (96%)	2 (4%)	27	49
9	HF	53/237 (22%)	48 (91%)	5 (9%)	8	26
9	Hf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	IF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	If	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	JF	53/237 (22%)	46 (87%)	7 (13%)	4	16
9	Jf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	KF	53/237 (22%)	45 (85%)	8 (15%)	3	13
9	Kf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	LF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Lf	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	MF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Mf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	VF	53/237 (22%)	52 (98%)	1 (2%)	50	66
9	WF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	XF	53/237 (22%)	51 (96%)	2 (4%)	29	51
9	YF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	ZF	53/237 (22%)	48 (91%)	5 (9%)	8	26
10	AC	203/257 (79%)	188 (93%)	15 (7%)	13	33
10	BC	203/257 (79%)	176 (87%)	27 (13%)	4	16
10	CC	178/257 (69%)	159 (89%)	19 (11%)	6	22
10	DC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	EC	178/257 (69%)	155 (87%)	23 (13%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	FC	203/257 (79%)	189 (93%)	14 (7%)	14	36
10	GC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	HC	178/257 (69%)	158 (89%)	20 (11%)	6	20
10	IC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	JC	203/257 (79%)	189 (93%)	14 (7%)	14	36
10	KC	203/257 (79%)	185 (91%)	18 (9%)	9	28
10	LC	178/257 (69%)	157 (88%)	21 (12%)	5	19
10	MC	178/257 (69%)	156 (88%)	22 (12%)	4	18
11	AM	175/276 (63%)	163 (93%)	12 (7%)	14	36
11	BM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	CM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	DM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	EM	175/276 (63%)	160 (91%)	15 (9%)	10	29
11	FM	175/276 (63%)	157 (90%)	18 (10%)	7	23
11	GM	175/276 (63%)	161 (92%)	14 (8%)	11	31
11	HM	175/276 (63%)	168 (96%)	7 (4%)	28	49
11	IM	175/276 (63%)	156 (89%)	19 (11%)	6	21
11	JM	175/276 (63%)	155 (89%)	20 (11%)	5	20
11	KM	175/276 (63%)	161 (92%)	14 (8%)	11	31
11	LM	175/276 (63%)	158 (90%)	17 (10%)	8	25
11	MM	175/276 (63%)	162 (93%)	13 (7%)	13	33
All	All	20484/55449 (37%)	18791 (92%)	1693 (8%)	12	30

5 of 1693 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	XH	233	LEU
8	Ad	97	ARG
1	MG	930	ILE
1	YG	815	VAL
2	XH	220	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 206 such sidechains are listed below:

Mol	Chain	Res	Type
1	ZG	818	GLN
4	BL	225	GLN
1	PG	1017	GLN
2	ZH	205	GLN
11	FM	174	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	EX	1
7	GX	1
7	YX	1
7	VX	1
7	CX	1
7	AX	1
7	FX	1
7	JX	1

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Mol	Chain	Number of breaks
7	KX	1
7	MX	1
7	WX	1
7	XX	1
7	LX	1
7	BX	1
7	HX	1
7	ZX	1
7	IX	1
7	DX	1

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	EX	38:UNK	C	70:UNK	N	24.84
1	GX	38:UNK	C	70:UNK	N	24.65
1	YX	38:UNK	C	70:UNK	N	24.61
1	VX	38:UNK	C	70:UNK	N	24.52
1	CX	38:UNK	C	70:UNK	N	24.52

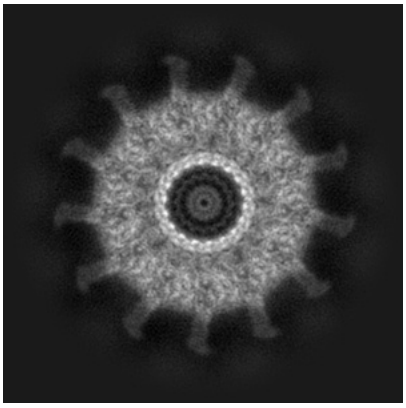
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24023. These allow visual inspection of the internal detail of the map and identification of artifacts.

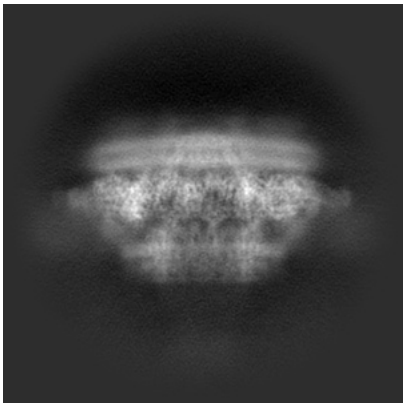
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

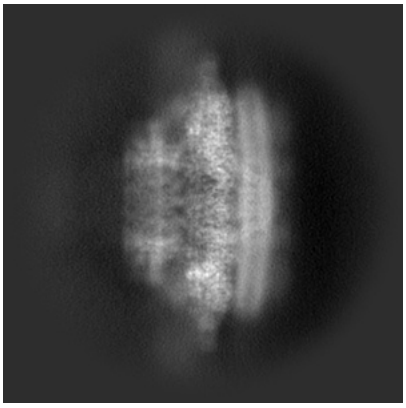
6.1.1 Primary map



X



Y

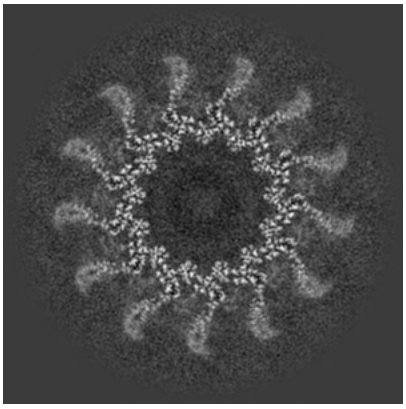


Z

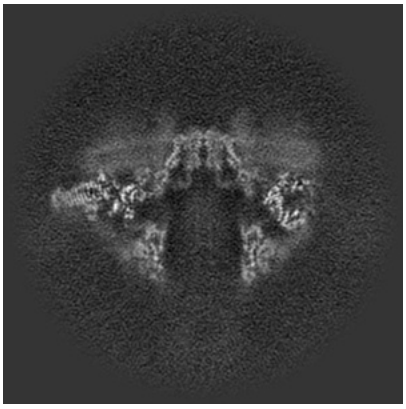
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 125



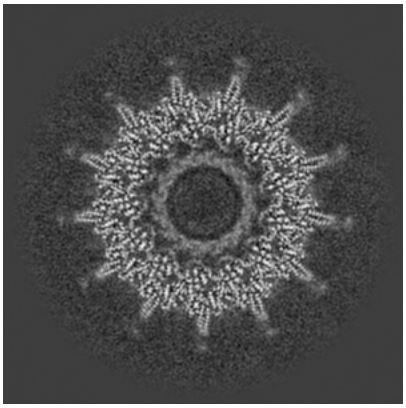
Y Index: 125

Z Index: 125

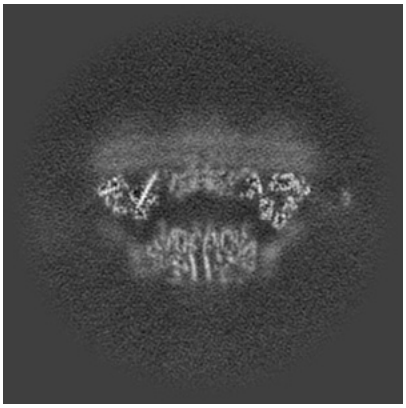
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

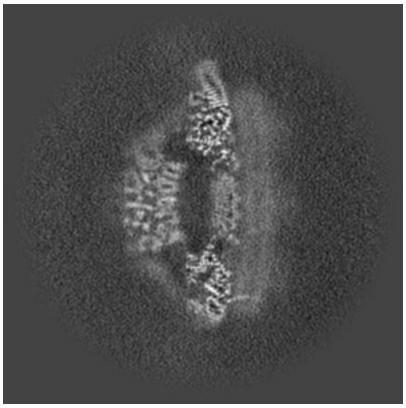
6.3.1 Primary map



X Index: 134



Y Index: 101

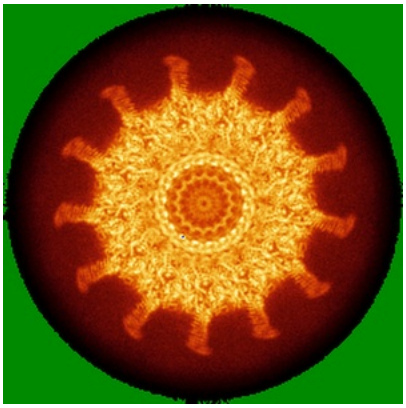


Z Index: 151

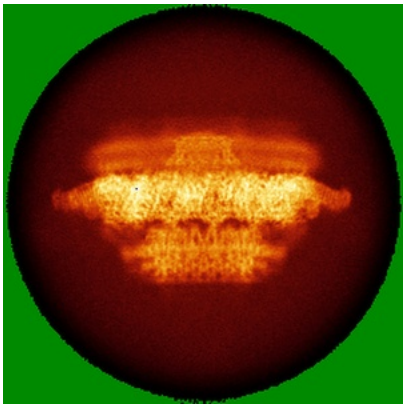
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

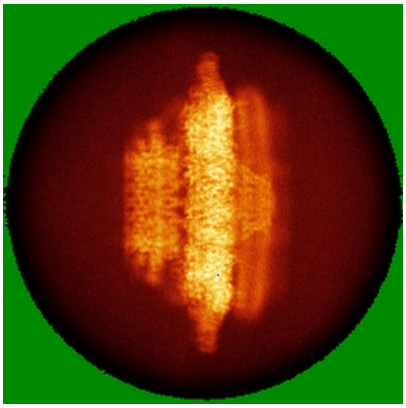
6.4.1 Primary map



X



Y

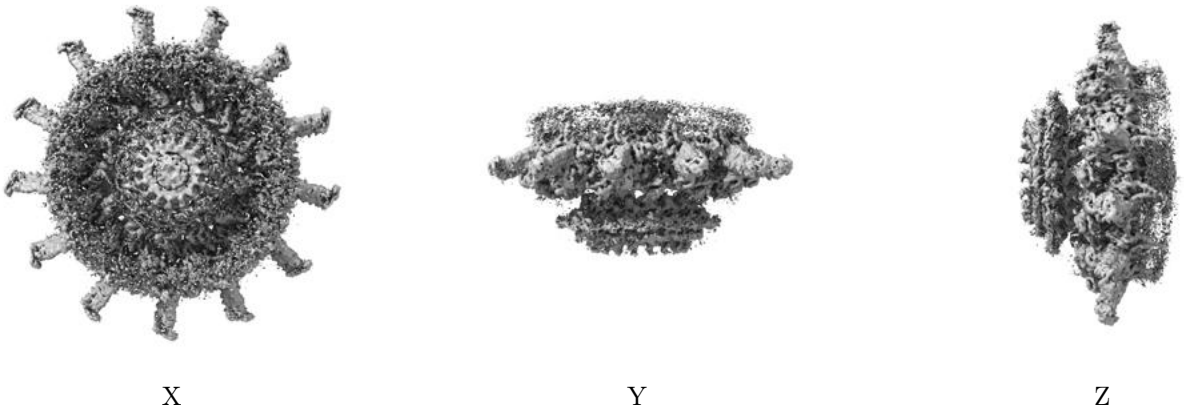


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

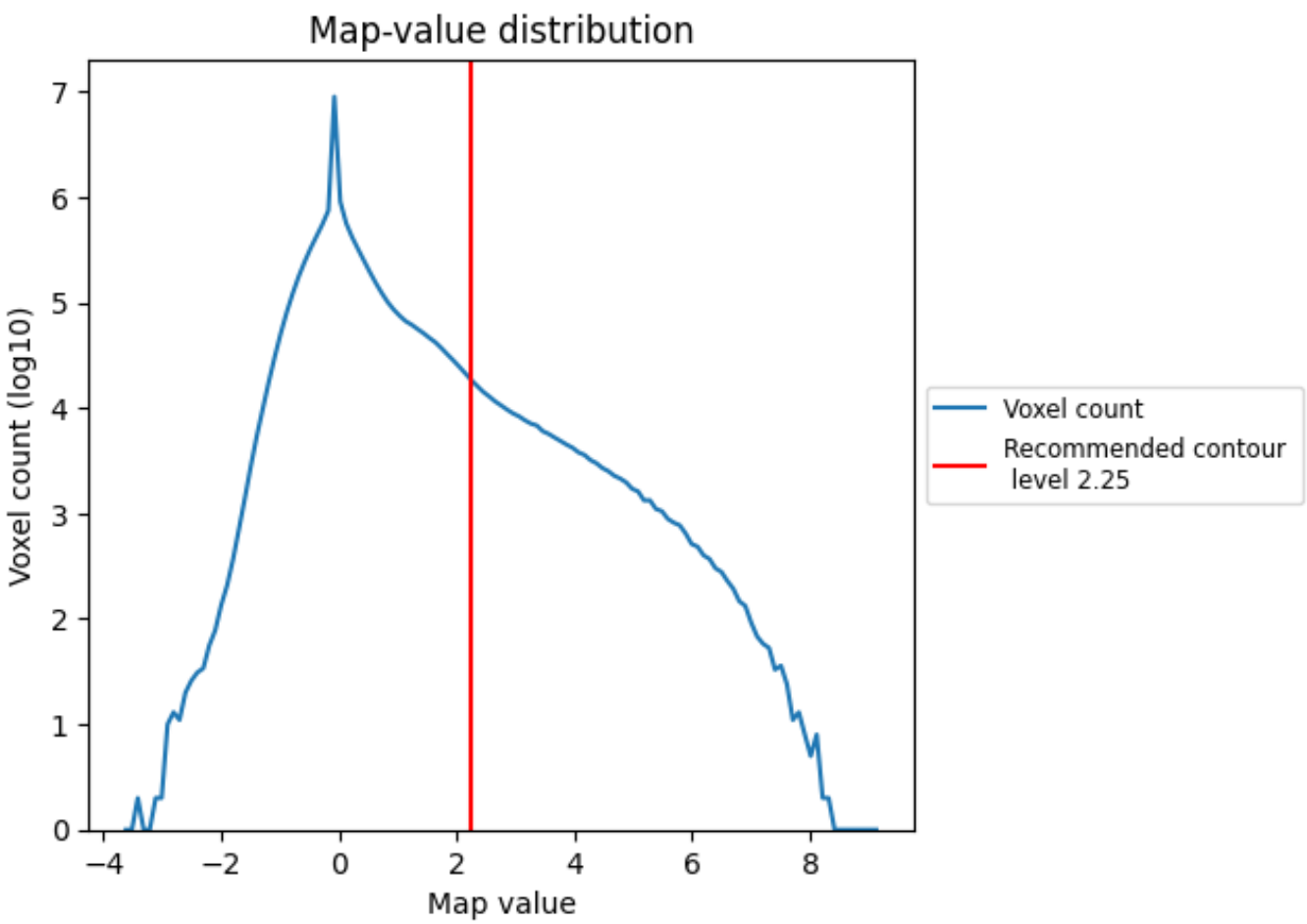
6.6 Mask visualisation (i)

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

7 Map analysis (i)

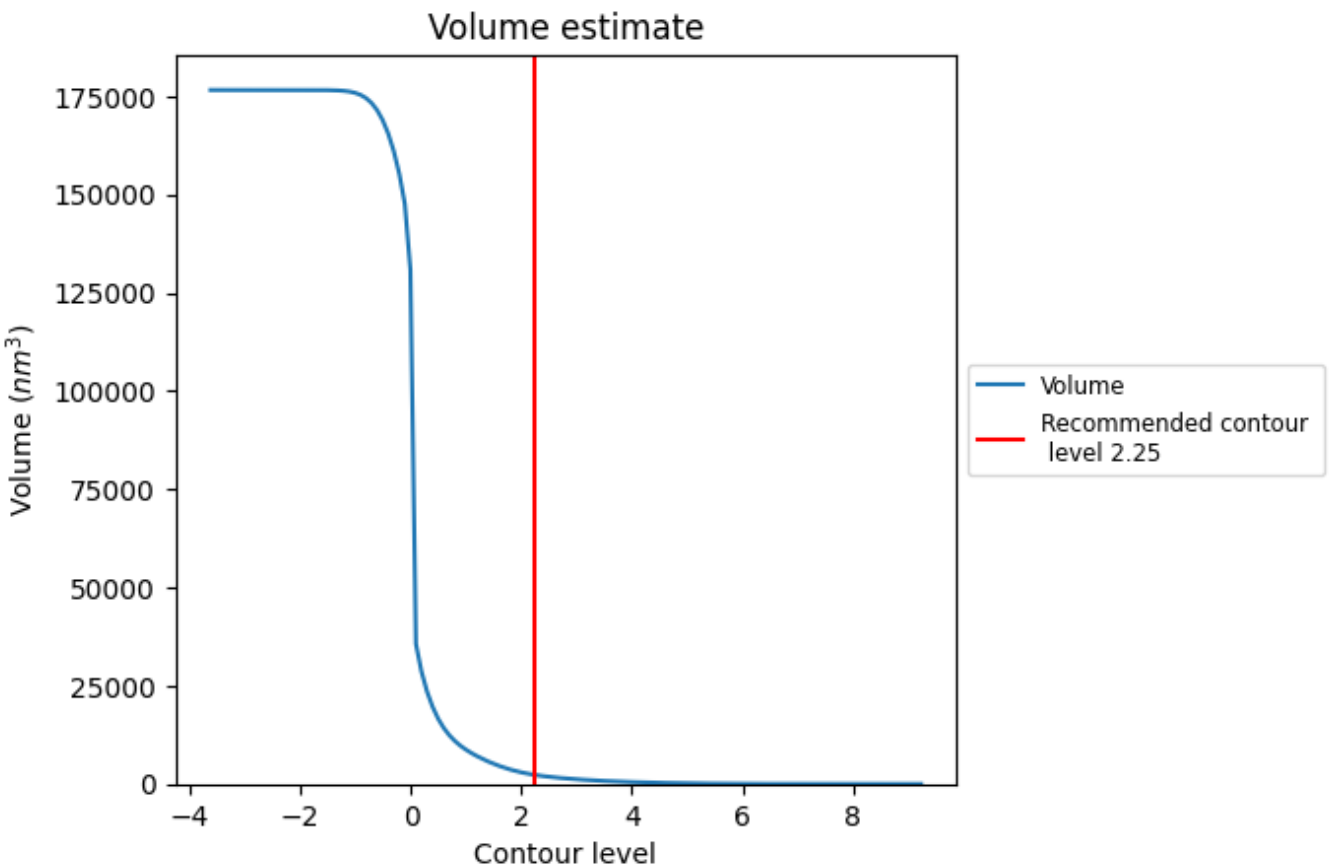
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

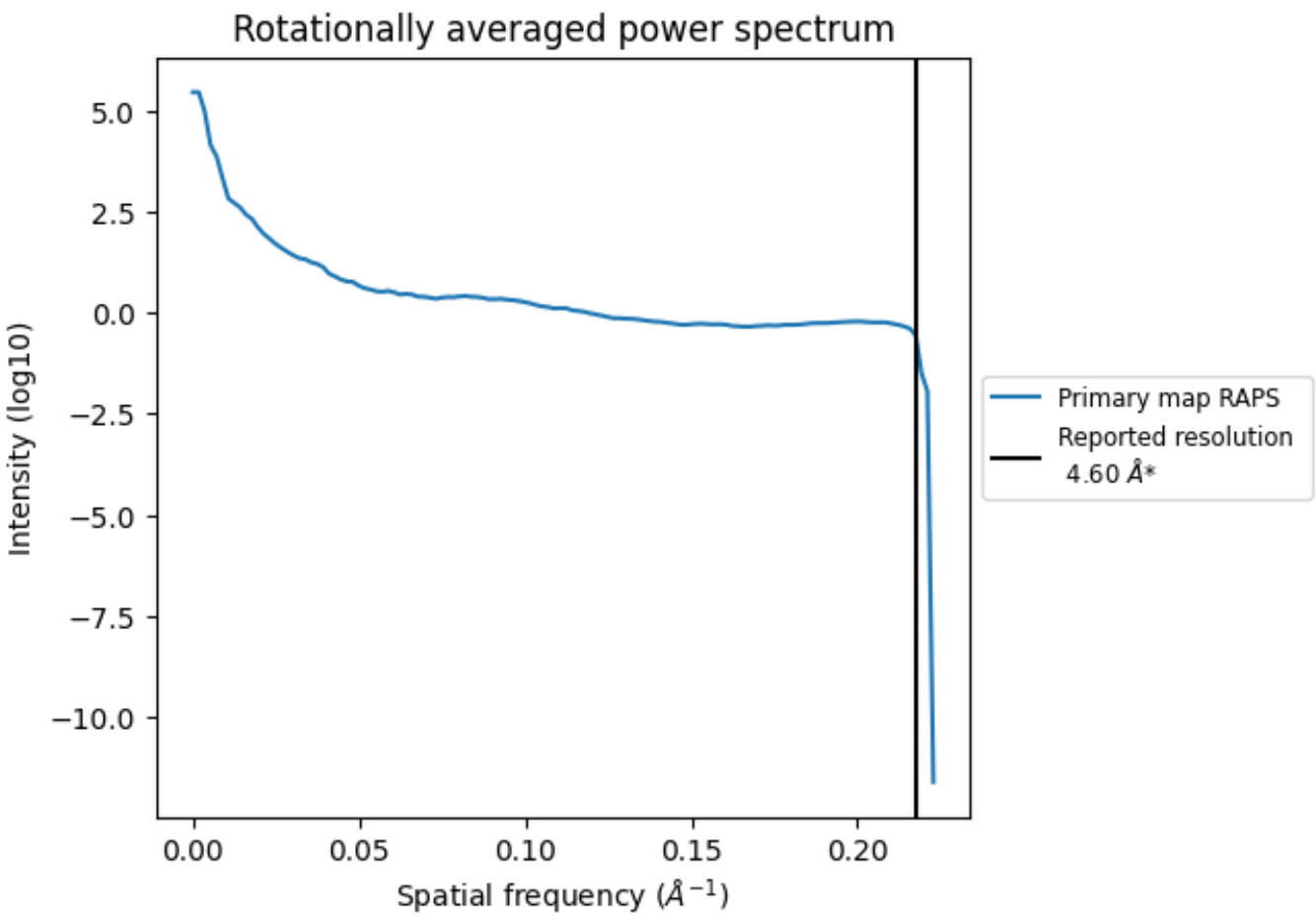
7.2 Volume estimate (i)



The volume at the recommended contour level is 2290 nm^3; this corresponds to an approximate mass of 2069 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.217 Å^{-1}

8 Fourier-Shell correlation (i)

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

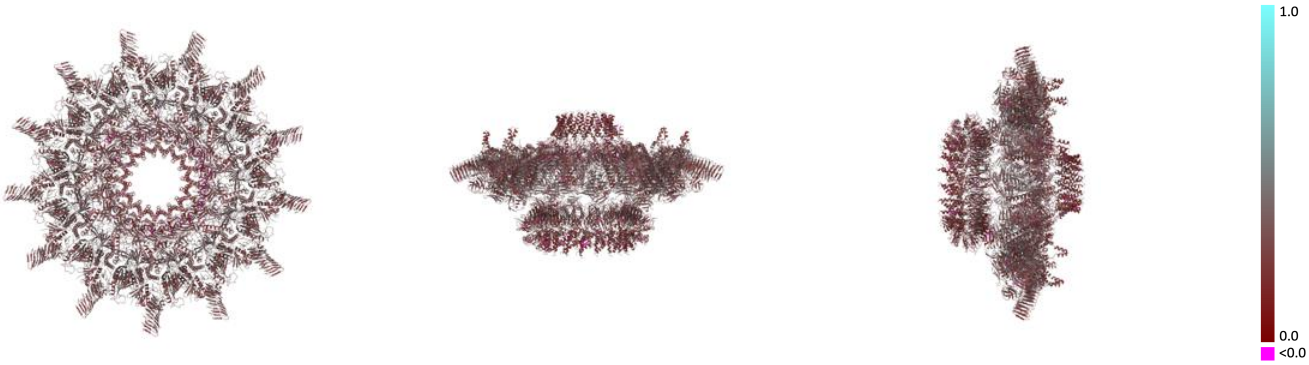
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24023 and PDB model 7MUV. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay (i)

This section was not generated.

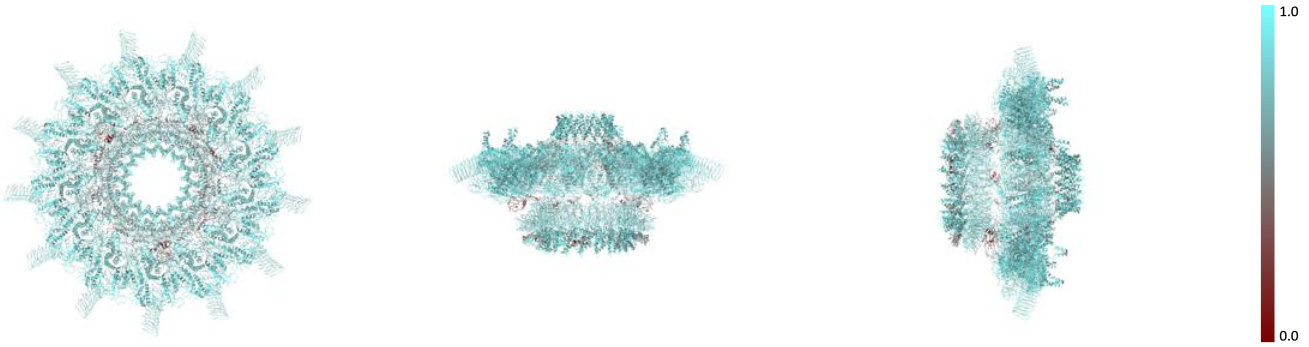
9.2 Q-score mapped to coordinate model (i)



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.

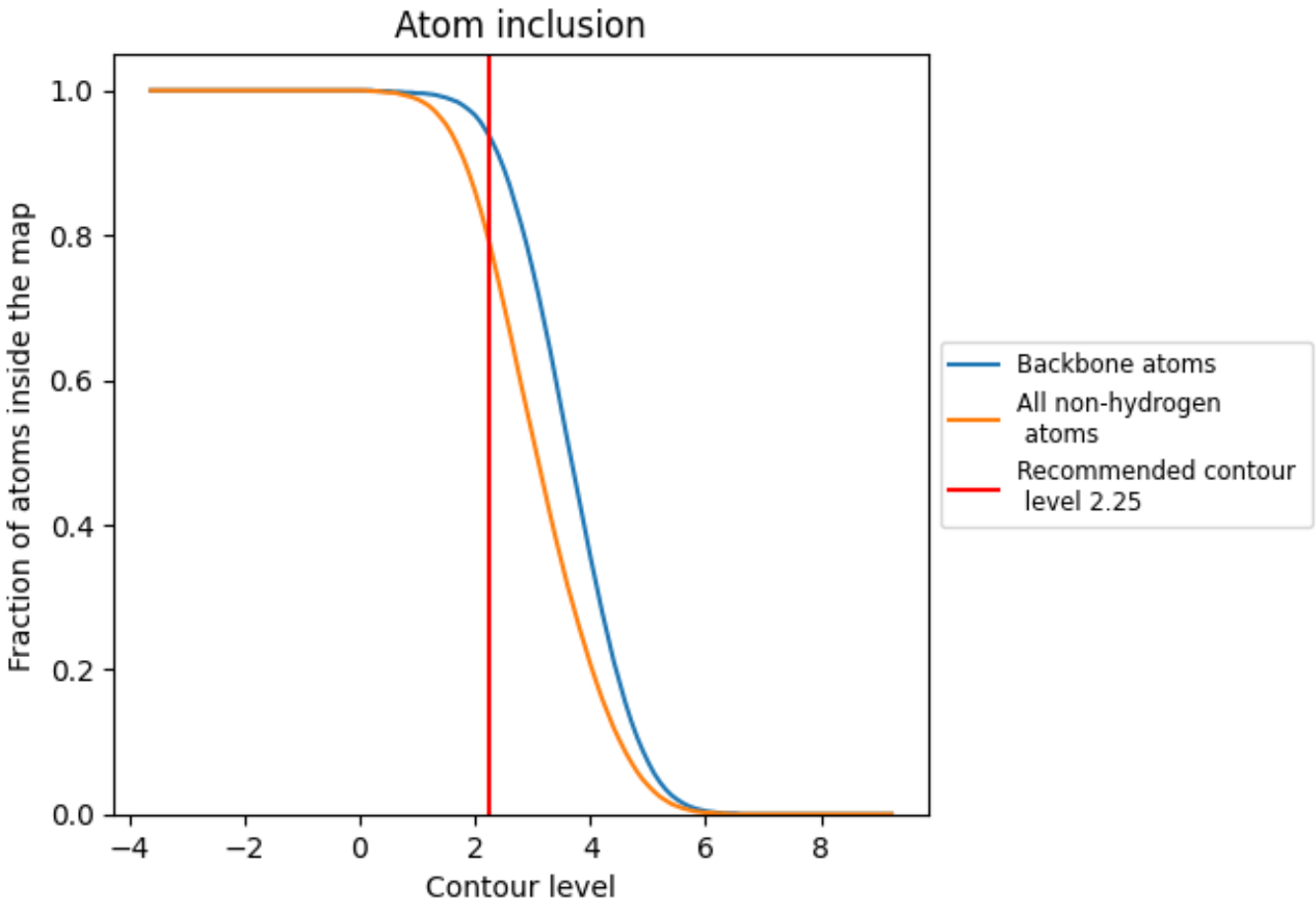
9.3 Atom inclusion mapped to coordinate model (i)



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 (2.25).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (2.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7900	0.3160
AC	0.7910	0.3300
AD	0.8170	0.3540
AF	0.7810	0.2420
AG	0.6540	0.2680
AH	0.8060	0.3150
AK	0.8390	0.3520
AL	0.8400	0.3280
AM	0.8120	0.3270
AN	0.7920	0.3720
AU	0.9780	0.4790
AX	0.6210	0.2160
Ad	0.8370	0.3450
Af	0.7950	0.3120
Ag	0.8310	0.2930
BC	0.7890	0.3280
BD	0.8170	0.3640
BF	0.7880	0.2480
BG	0.6470	0.2540
BH	0.7950	0.3180
BK	0.8320	0.3460
BL	0.8350	0.3320
BM	0.8190	0.3220
BN	0.7670	0.3530
BU	1.0000	0.4510
BX	0.5710	0.2670
Bd	0.8310	0.3400
Bf	0.8180	0.3170
Bg	0.8310	0.2720
CC	0.8250	0.3270
CD	0.8240	0.3540
CF	0.7220	0.2560
CG	0.6560	0.2470
CH	0.8150	0.3260
CK	0.8350	0.3520

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Chain	Atom inclusion	Q-score
CL	0.8490	0.3310
CM	0.8060	0.3270
CN	0.7710	0.3610
CU	1.0000	0.4840
CX	0.6330	0.3280
Cd	0.8370	0.3330
Cf	0.7860	0.3050
Cg	0.8050	0.2830
DC	0.8530	0.3310
DD	0.8330	0.3500
DF	0.7900	0.2560
DG	0.6650	0.2520
DH	0.8020	0.3090
DK	0.8520	0.3550
DL	0.8430	0.3320
DM	0.8000	0.3230
DN	0.8090	0.3700
DU	0.9560	0.4600
DX	0.6000	0.2440
Dd	0.8240	0.3380
Df	0.7900	0.3130
Dg	0.8490	0.2700
EC	0.8360	0.3380
ED	0.8120	0.3470
EF	0.7920	0.2660
EG	0.6560	0.2530
EH	0.8160	0.3140
EK	0.8390	0.3450
EL	0.8470	0.3380
EM	0.8230	0.3300
EN	0.8040	0.3600
EU	1.0000	0.4750
EX	0.5330	0.2410
Ed	0.8380	0.3450
Ef	0.7930	0.3120
Eg	0.8710	0.2920
FC	0.7930	0.3300
FD	0.8320	0.3460
FF	0.7620	0.2750
FG	0.6910	0.2440
FH	0.7920	0.3080
FK	0.8280	0.3490

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Chain	Atom inclusion	Q-score
FL	0.8580	0.3350
FM	0.8190	0.3170
FN	0.7850	0.3610
FU	0.9330	0.4430
FX	0.6620	0.2630
Fd	0.8400	0.3330
Ff	0.7810	0.3070
Fg	0.8640	0.2760
GC	0.8310	0.3350
GD	0.8190	0.3590
GF	0.7660	0.2370
GG	0.6690	0.2290
GH	0.8110	0.3180
GK	0.8410	0.3520
GL	0.8440	0.3350
GM	0.8420	0.3320
GN	0.7710	0.3580
GU	1.0000	0.4310
GX	0.6210	0.2760
Gd	0.8340	0.3420
Gf	0.7490	0.3190
Gg	0.8270	0.2770
HC	0.8490	0.3370
HD	0.8240	0.3560
HF	0.7920	0.2750
HG	0.6470	0.2210
HH	0.8060	0.3160
HK	0.8490	0.3450
HL	0.8490	0.3290
HM	0.8400	0.3300
HN	0.8250	0.3720
HU	0.9560	0.4740
HX	0.5330	0.2320
Hd	0.8470	0.3440
Hf	0.8430	0.3040
Hg	0.8090	0.2740
IC	0.8410	0.3450
ID	0.8390	0.3520
IF	0.8020	0.2490
IG	0.6130	0.2190
IH	0.8020	0.3150
IK	0.8500	0.3530

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Chain	Atom inclusion	Q-score
IL	0.8360	0.3350
IM	0.8140	0.3230
IN	0.8250	0.3640
IU	0.9780	0.4440
IX	0.5460	0.2540
Id	0.8420	0.3400
If	0.8130	0.2930
Ig	0.8460	0.2780
JC	0.7810	0.3290
JD	0.8290	0.3430
JF	0.7750	0.2470
JG	0.6050	0.2030
JH	0.8210	0.3110
JK	0.8500	0.3450
JL	0.8510	0.3270
JM	0.8310	0.3370
JN	0.7970	0.3470
JU	1.0000	0.4940
JX	0.6540	0.2890
Jd	0.8310	0.3310
Jf	0.7930	0.3150
Jg	0.8380	0.2510
KC	0.7800	0.3320
KD	0.8290	0.3440
KF	0.7620	0.2430
KG	0.6030	0.1930
KH	0.8140	0.3070
KK	0.8530	0.3620
KL	0.8500	0.3270
KM	0.8350	0.3340
KN	0.7760	0.3630
KU	0.9560	0.4680
KX	0.5670	0.2750
Kd	0.8520	0.3390
Kf	0.8020	0.3060
Kg	0.8350	0.2850
LC	0.8370	0.3450
LD	0.8400	0.3450
LF	0.7640	0.2590
LG	0.6220	0.1990
LH	0.8190	0.3190
LK	0.8510	0.3500

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Chain	Atom inclusion	Q-score
LL	0.8410	0.3350
LM	0.8200	0.3280
LN	0.7880	0.3650
LU	0.9780	0.4900
LX	0.6710	0.2650
Ld	0.8210	0.3420
Lf	0.8060	0.3300
Lg	0.8600	0.2730
MC	0.8440	0.3440
MD	0.8250	0.3510
MF	0.7600	0.2660
MG	0.6780	0.2680
MH	0.8180	0.3190
MK	0.8430	0.3510
ML	0.8410	0.3290
MM	0.8130	0.3180
MN	0.8510	0.3560
MU	1.0000	0.4940
MX	0.6250	0.2650
Md	0.8440	0.3390
Mf	0.8130	0.3070
Mg	0.8310	0.2970
NG	0.6620	0.2630
OG	0.7310	0.2650
PG	0.6860	0.2770
VF	0.8130	0.2690
VG	0.8420	0.2760
VH	0.6680	0.2990
VX	0.5210	0.2560
WF	0.7640	0.2630
WG	0.8160	0.2840
WH	0.5420	0.2340
WX	0.5880	0.2760
XF	0.7880	0.2710
XG	0.7900	0.2520
XH	0.6960	0.2910
XX	0.6420	0.2460
YF	0.7750	0.2460
YG	0.8460	0.2770
YH	0.5510	0.2760
YX	0.6370	0.2940
ZF	0.7960	0.2710

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Chain	Atom inclusion	Q-score
ZG	0.8120	0.2820
ZH	0.6650	0.3070
ZX	0.5500	0.2810