



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:38 AM UTC

PDB ID : 7MUY / pdb_00007muy
EMDB ID : EMD-24026
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 5
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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

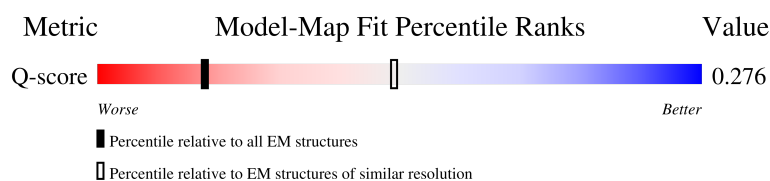
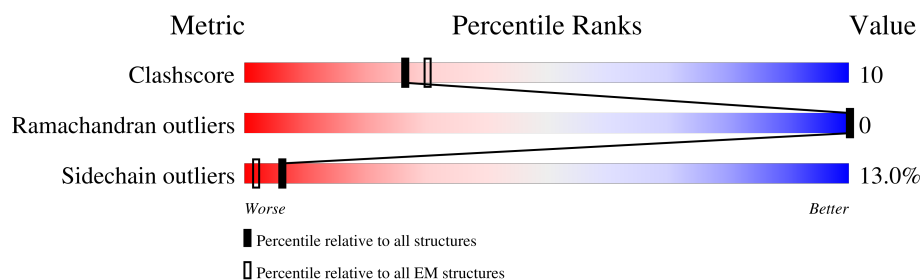
1 Overall quality at a glance i

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AG	1048	 10% 5% 84%
1	Ag	1048	 97%
1	BG	1048	 9% 6% 84%
1	Bg	1048	 97%

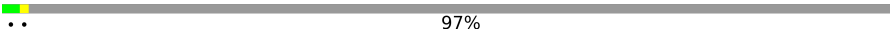
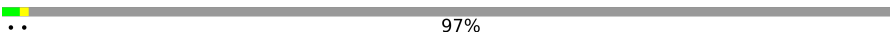
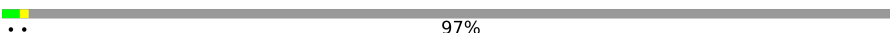
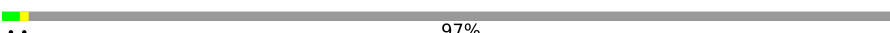
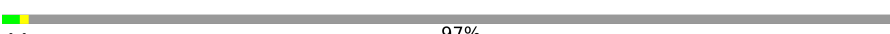
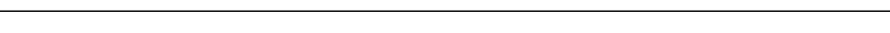
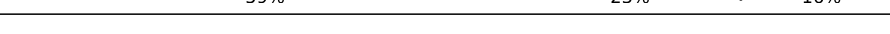
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Mol	Chain	Length	Quality of chain
1	CG	1048	
1	Cg	1048	
1	DG	1048	
1	Dg	1048	
1	EG	1048	
1	Eg	1048	
1	FG	1048	
1	Fg	1048	
1	GG	1048	
1	Gg	1048	
1	HG	1048	
1	Hg	1048	
1	IG	1048	
1	Ig	1048	
1	JG	1048	
1	Jg	1048	
1	KG	1048	
1	Kg	1048	
1	LG	1048	
1	Lg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

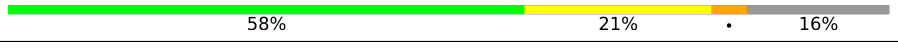
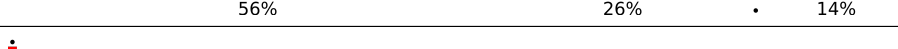
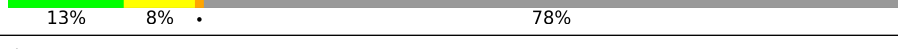
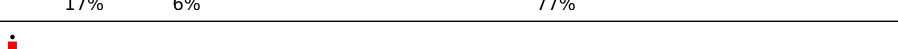
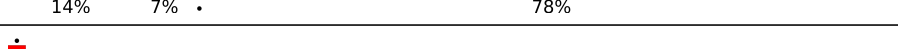
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AD	163	 58% 24% 14%
2	Ad	163	 57% 23% 16%
2	BD	163	 63% 21% 14%
2	Bd	163	 65% 14% 5% 16%
2	CD	163	 54% 27% 5% 14%
2	Cd	163	 63% 20% 16%
2	DD	163	 62% 24% 14%
2	Dd	163	 60% 23% 16%
2	ED	163	 65% 19% 14%
2	Ed	163	 59% 23% 16%
2	FD	163	 62% 21% 14%
2	Fd	163	 60% 22% 16%
2	GD	163	 60% 23% 14%
2	Gd	163	 61% 20% 16%
2	HD	163	 63% 21% 14%
2	Hd	163	 64% 18% 16%
2	ID	163	 58% 26% 14%
2	Id	163	 64% 18% 16%
2	JD	163	 55% 28% 14%
2	Jd	163	 64% 20% 16%

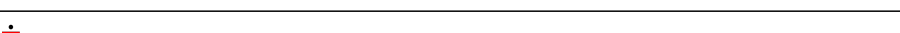
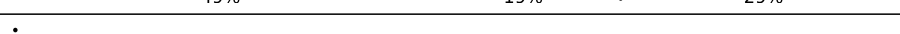
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Mol	Chain	Length	Quality of chain
2	KD	163	
2	Kd	163	
2	LD	163	
2	Ld	163	
2	MD	163	
2	Md	163	
3	AF	269	
3	Af	269	
3	BF	269	
3	Bf	269	
3	CF	269	
3	Cf	269	
3	DF	269	
3	Df	269	
3	EF	269	
3	Ef	269	
3	FF	269	
3	Ff	269	
3	GF	269	
3	Gf	269	
3	HF	269	
3	Hf	269	
3	IF	269	
3	If	269	
3	JF	269	

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Mol	Chain	Length	Quality of chain
3	Jf	269	
3	KF	269	
3	Kf	269	
3	LF	269	
3	Lf	269	
3	MF	269	
3	Mf	269	
3	VF	269	
3	WF	269	
3	XF	269	
3	YF	269	
3	ZF	269	
4	AH	361	
4	BH	361	
4	CH	361	
4	DH	361	
4	EH	361	
4	FH	361	
4	GH	361	
4	HH	361	
4	IH	361	
4	JH	361	
4	KH	361	
4	LH	361	
4	MH	361	

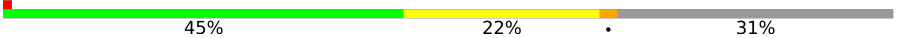
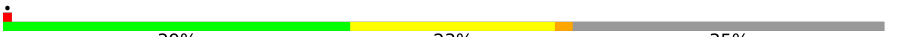
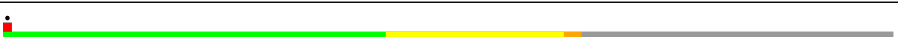
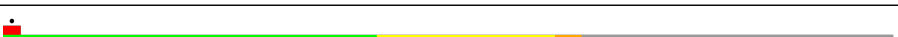
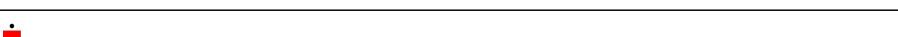
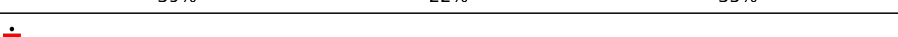
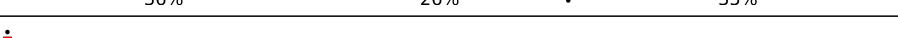
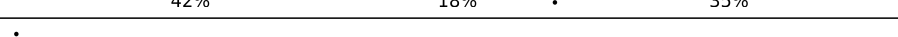
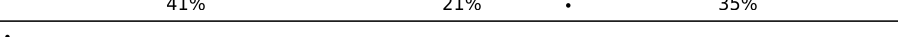
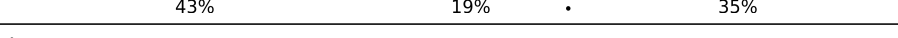
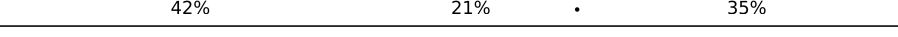
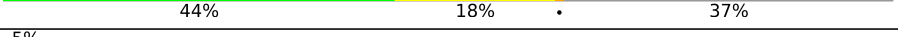
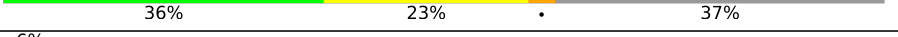
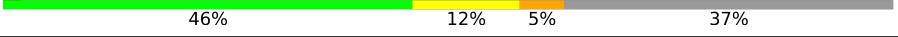
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Mol	Chain	Length	Quality of chain
4	VH	361	
4	WH	361	
4	XH	361	
4	YH	361	
4	ZH	361	
5	AK	189	
5	BK	189	
5	CK	189	
5	DK	189	
5	EK	189	
5	FK	189	
5	GK	189	
5	HK	189	
5	IK	189	
5	JK	189	
5	KK	189	
5	LK	189	
5	MK	189	
6	AL	249	
6	BL	249	
6	CL	249	
6	DL	249	
6	EL	249	
6	FL	249	
6	GL	249	

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Mol	Chain	Length	Quality of chain
6	HL	249	
6	IL	249	
6	JL	249	
6	KL	249	
6	LL	249	
6	ML	249	
7	AM	320	
7	BM	320	
7	CM	320	
7	DM	320	
7	EM	320	
7	FM	320	
7	GM	320	
7	HM	320	
7	IM	320	
7	JM	320	
7	KM	320	
7	LM	320	
7	MM	320	
8	AN	124	
8	BN	124	
8	CN	124	
8	DN	124	
8	EN	124	
8	FN	124	

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Mol	Chain	Length	Quality of chain
8	GN	124	
8	HN	124	
8	IN	124	
8	JN	124	
8	KN	124	
8	LN	124	
8	MN	124	
9	AU	9	
9	BU	9	
9	CU	9	
9	DU	9	
9	EU	9	
9	FU	9	
9	GU	9	
9	HU	9	
9	IU	9	
9	JU	9	
9	KU	9	
9	LU	9	
9	MU	9	
10	AX	48	
10	BX	48	
10	CX	48	
10	DX	48	
10	EX	48	

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Mol	Chain	Length	Quality of chain
10	FX	48	27% 96% .
10	GX	48	17% 100%
10	HX	48	33% 96% .
10	IX	48	42% 96% .
10	JX	48	40% 92% 8%
10	KX	48	38% 100%
10	LX	48	46% 100%
10	MX	48	29% 96% .
10	VX	48	38% 88% 12%
10	WX	48	33% 100%
10	XX	48	21% 100%
10	YX	48	27% 96% .
10	ZX	48	35% 92% 8%
11	AC	303	. 48% 18% . 31%
11	BC	303	. 60% 19% . 20%
11	CC	303	5% 60% 18% . 20%
11	DC	303	. 45% 22% . 31%
11	EC	303	. 50% 17% . 31%
11	FC	303	. 57% 21% . 20%
11	GC	303	6% 55% 23% . 20%
11	HC	303	. 49% 17% . 31%
11	IC	303	. 44% 20% 5% 31%
11	JC	303	. 51% 16% . 31%
11	KC	303	6% 57% 19% 5% 20%
11	LC	303	. 50% 17% . 31%

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Mol	Chain	Length	Quality of chain
11	MC	303	46% 20% . 31%

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

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

- Molecule 2 is a protein called DotD.

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

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

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

- Molecule 3 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	EF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Ef	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	FF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Ff	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	AF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	GF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Gf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	HF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Hf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	IF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	If	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	JF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Jf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	KF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Kf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	LF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Lf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	MF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Mf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	VF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	WF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	XF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	YF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	ZF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Af	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	BF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Bf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	CF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Cf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	DF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Df	59	Total	C	N	O	S	0	0
			449	290	77	81	1		

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

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

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

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

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

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

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

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

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

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

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

- Molecule 8 is a protein called Neurogenic locus notch.

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

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

- Molecule 9 is a protein called Unknown protein fragment.

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

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

- Molecule 10 is a protein called Unknown protein fragment.

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

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

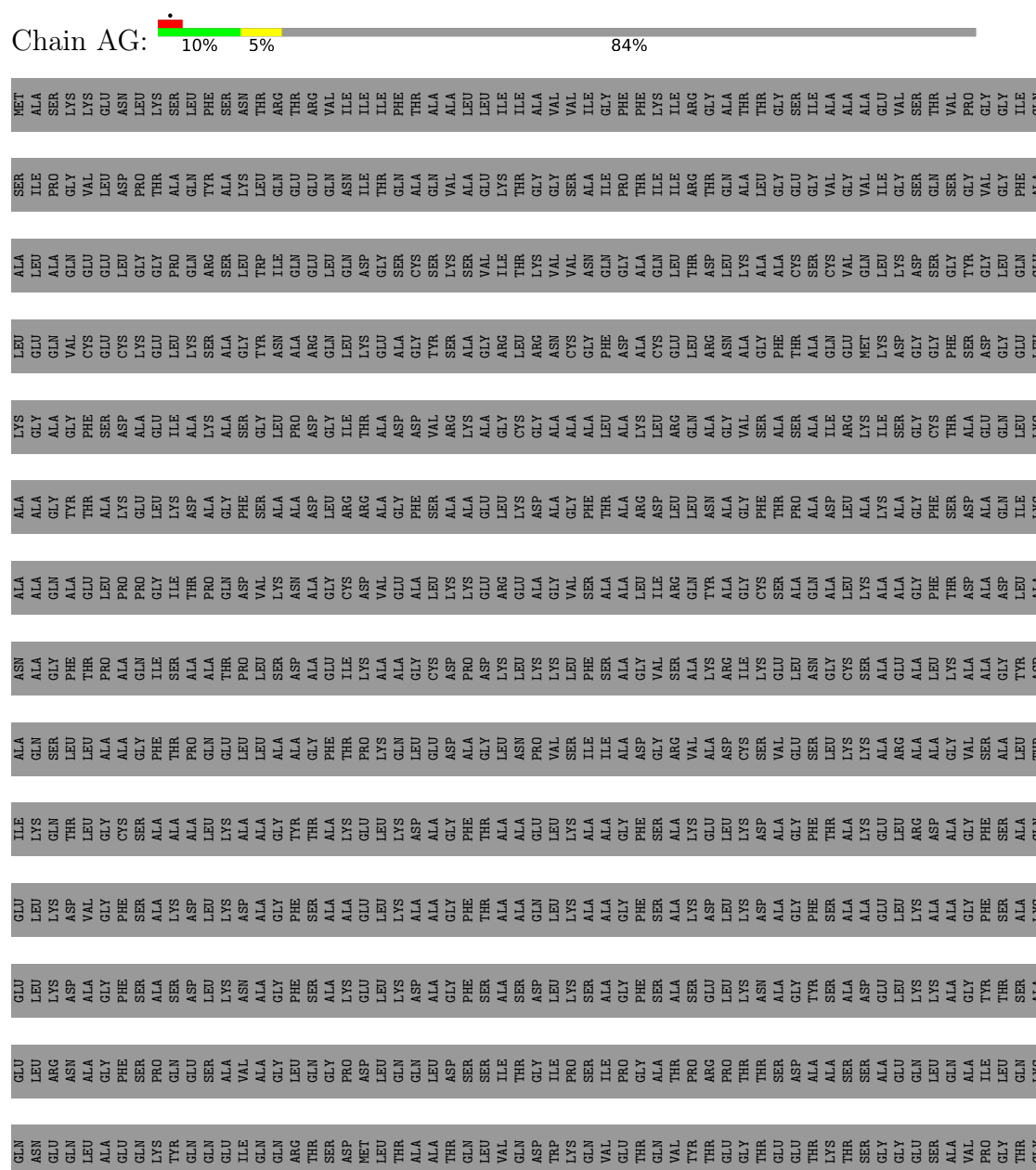
- Molecule 11 is a protein called DotC.

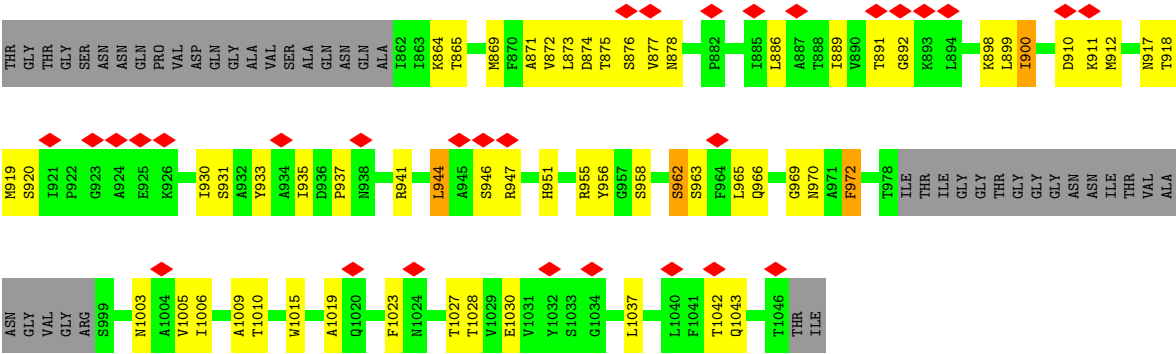
Mol	Chain	Residues	Atoms					AltConf	Trace
11	CC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	BC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	GC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	KC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	DC	209	Total	C	N	O	S	0	0
			1667	1061	292	309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

3 Residue-property plots

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

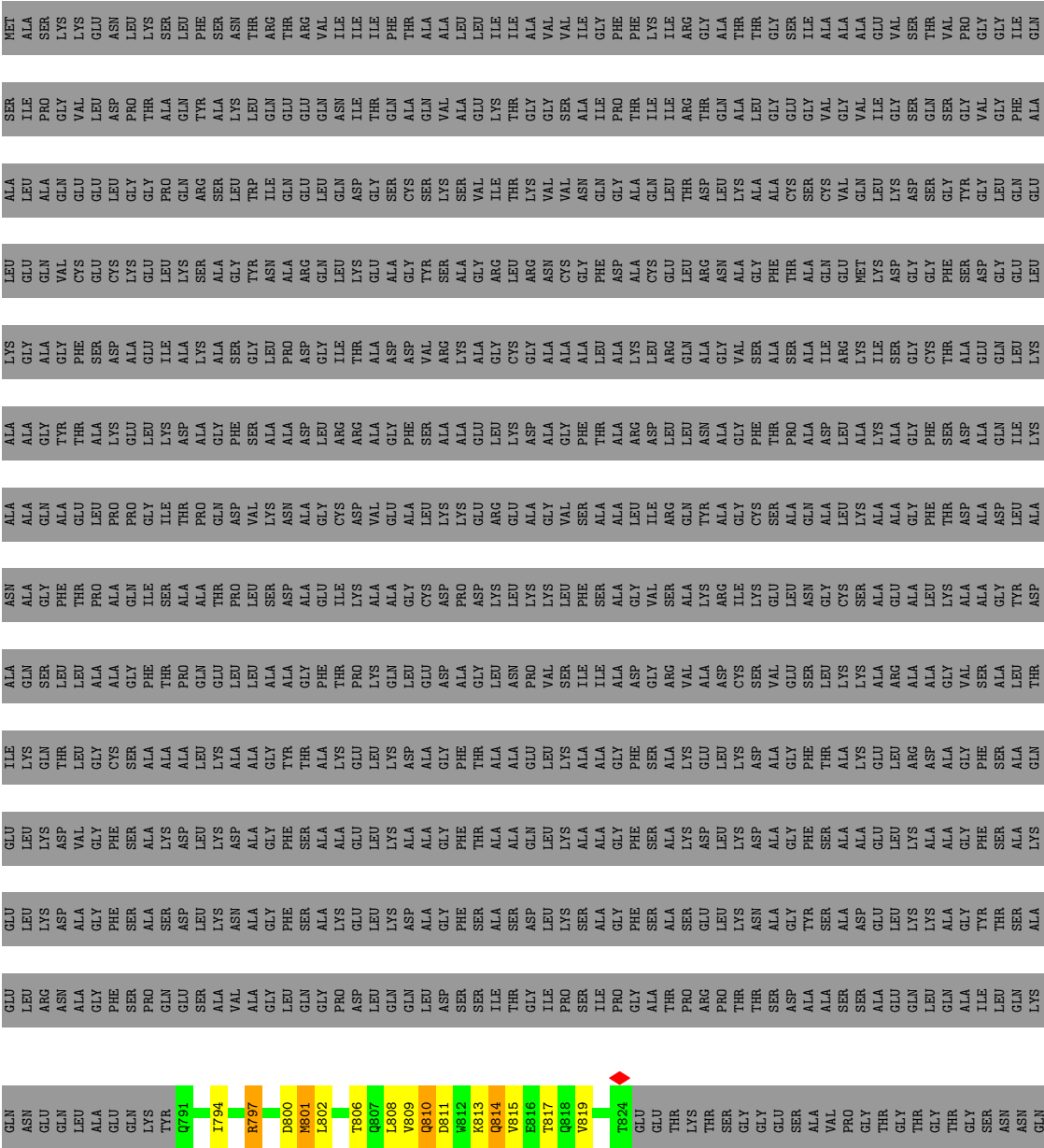
- Molecule 1: IcmE protein





● Molecule 1: IcmE protein

Chain Eg: .. 97%



[illegible]

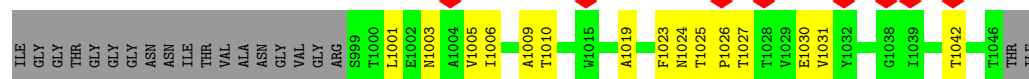
- Molecule 1: IcmE protein

Chain Fg: 97%

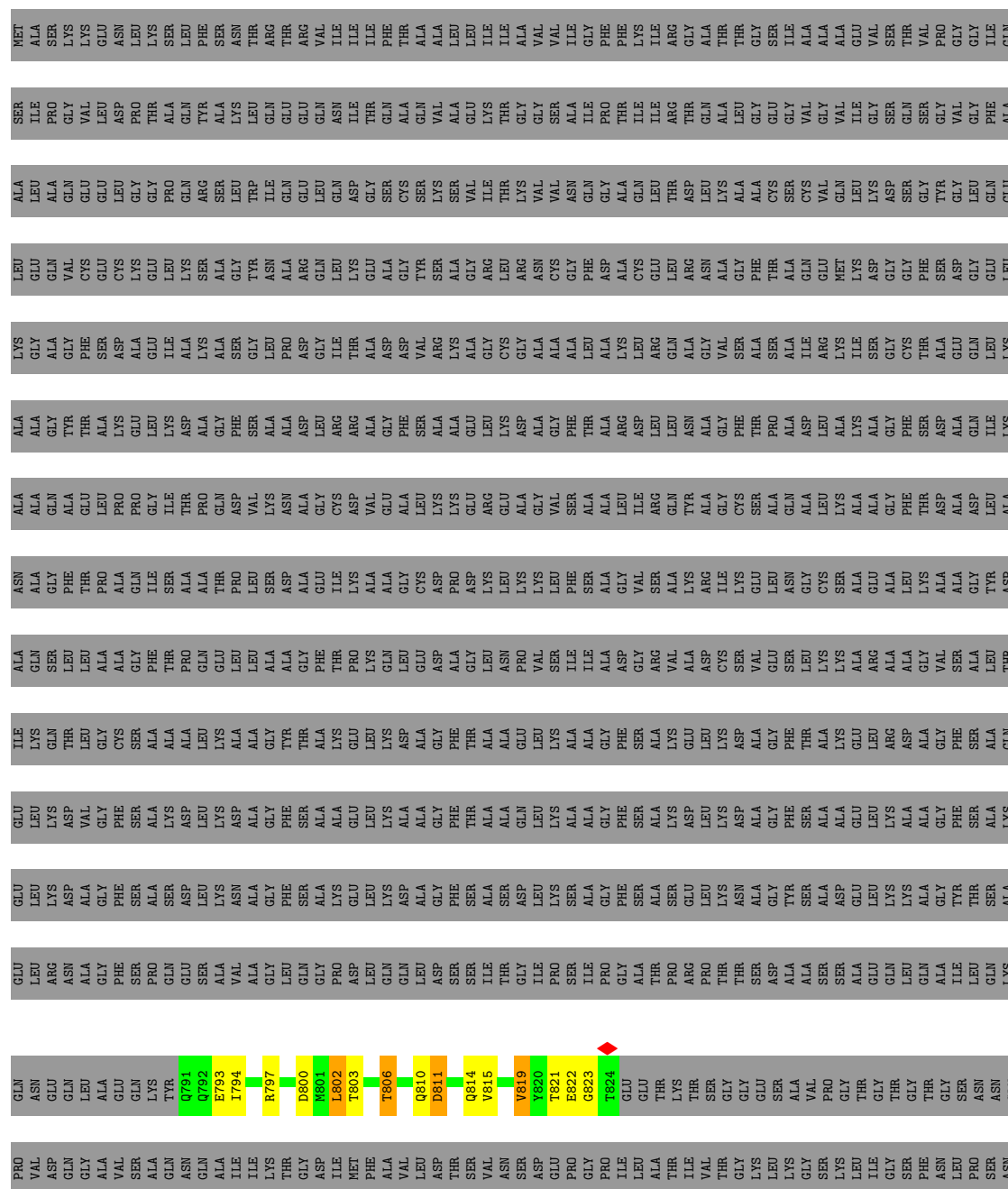
[illegible]

- Molecule 1: IcmE protein

[illegible]



Chain Gg: 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 Hg: 97%

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

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

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

LIE	LYS	GLN	THR	LEU	GLY	CYS	SER	ALA	ALA	ALA	ALA	LEU	LYS	ALA	ALA	GLY	TYR	THR	ALA	LYS	GLU	LEU	LYS	ASP	ALA	ASP	GLY	PHE	THR	THR	ALA	ALA	GLU	LEU	LYS	ALA	ALA	GLY	PHE	SER	LYS	GLU	LEU	LYS	ASP	ALA	ALA	GLY	PHE	SER	LYS	ALA	GLN
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GLU LEU LEU LYS ASP ASP GLY PHE SER SER ALA ALA ASP ASP LYS ASN ASN ALA ALA SER ALA SER ASP ASP LEU LEU LYS LYS ASP ASP ALA ALA GLY PHE SER SER SER SER LEU LEU LYS LYS LYS LYS TYR TYR SER SER ASP ASP GLU GLU LEU LEU LYS LYS ALA ALA GLY PHE SER SER SER SER GLU GLU LEU LYS LYS LYS LYS TYR TYR THR THR SER SER

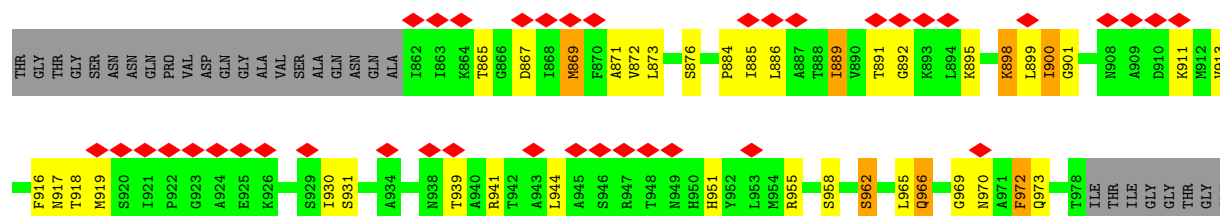
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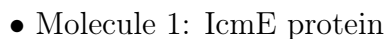


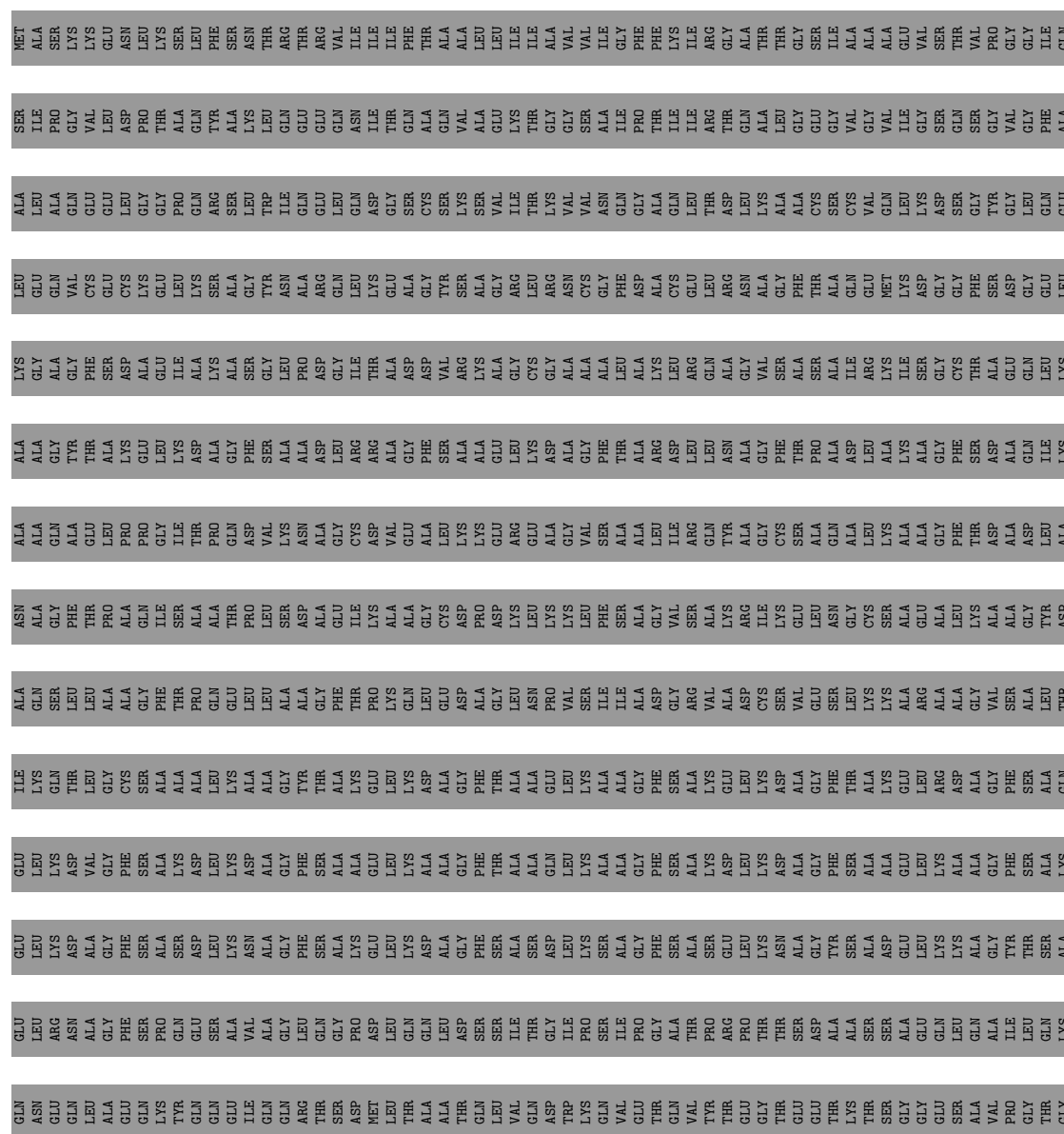
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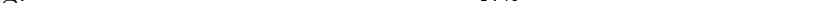
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Chain Jg: .. 97%



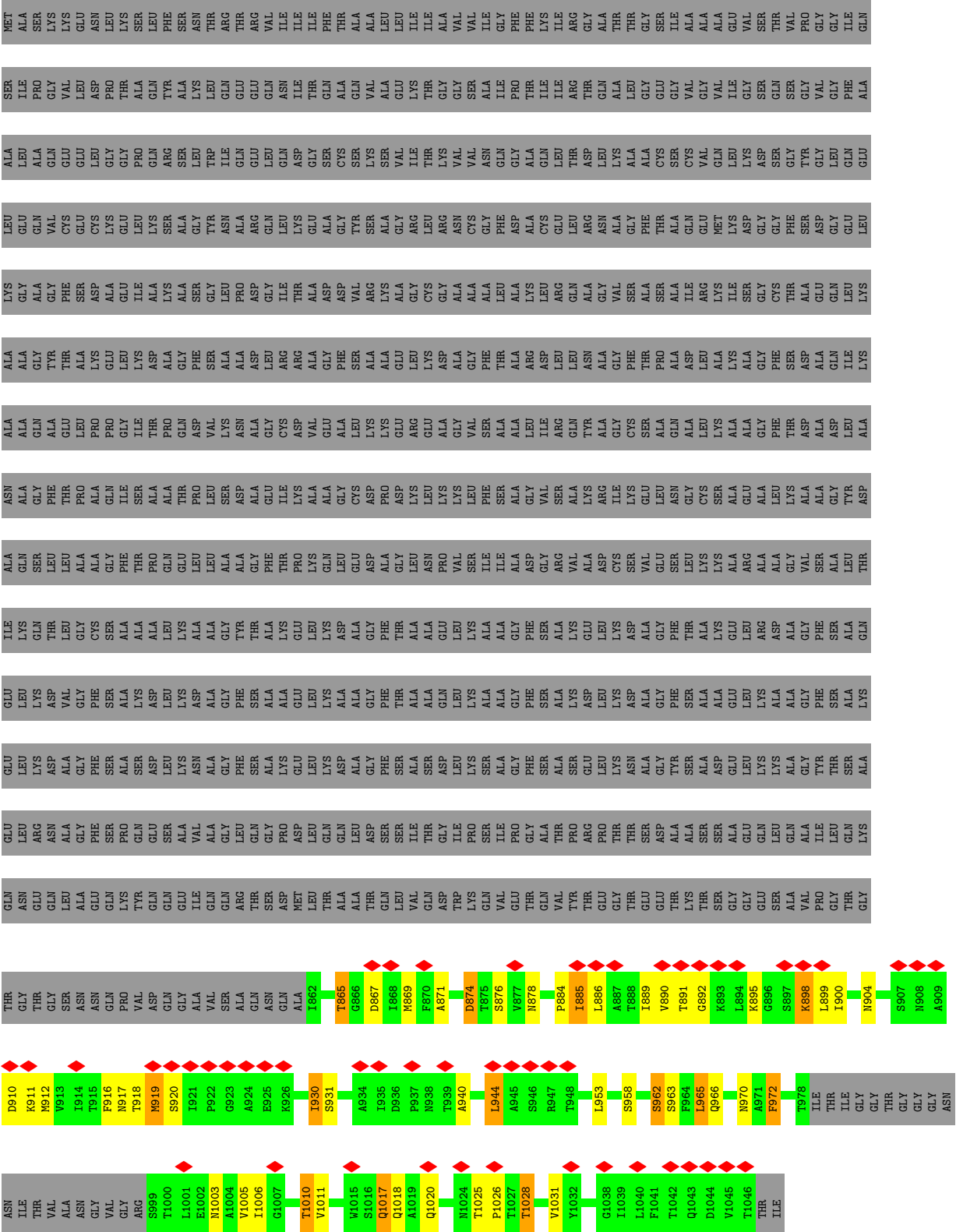


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Chain Lg:  97%



• Molecule 1: IcmE protein



• Molecule 1: IcmE protein

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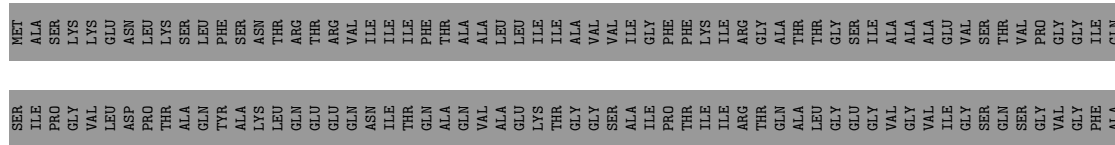
- Molecule 1: IcmE protein

97%

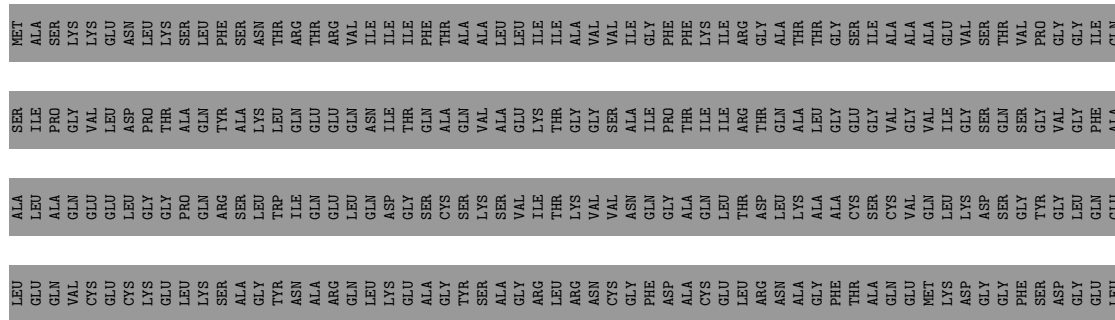
- Molecule 1: IcmE protein



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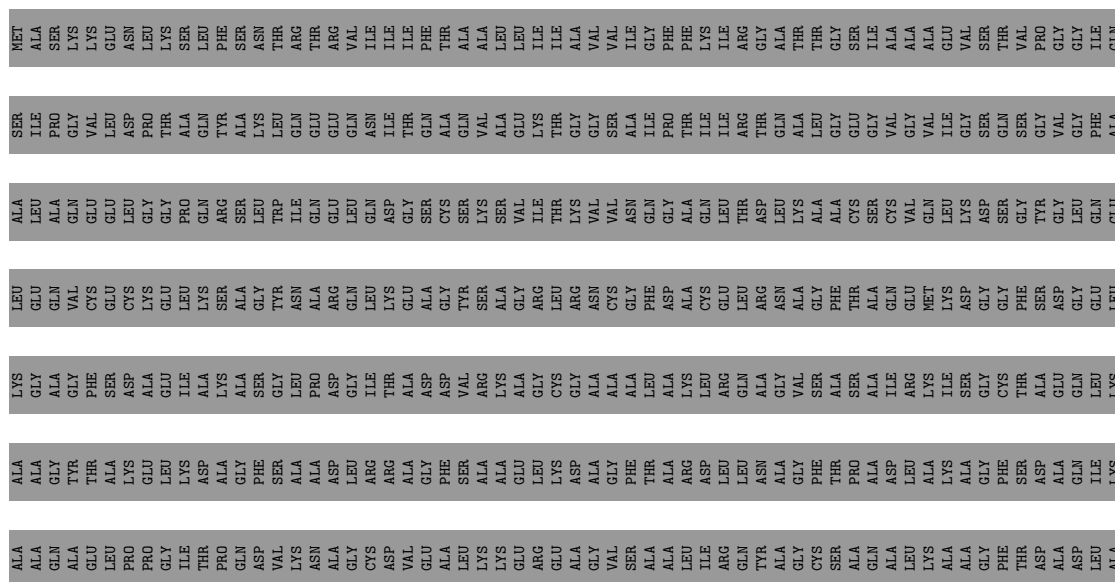
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[illegible]



[illegible]

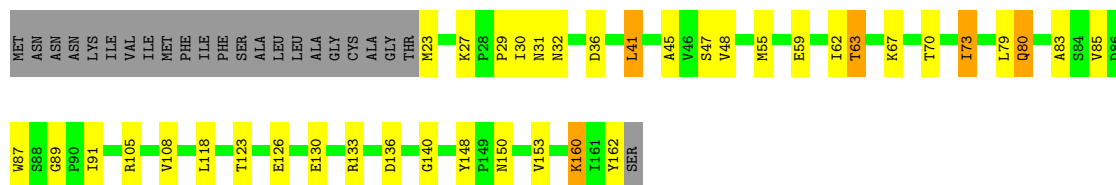


- Molecule 1: IcmE protein

[illegible]

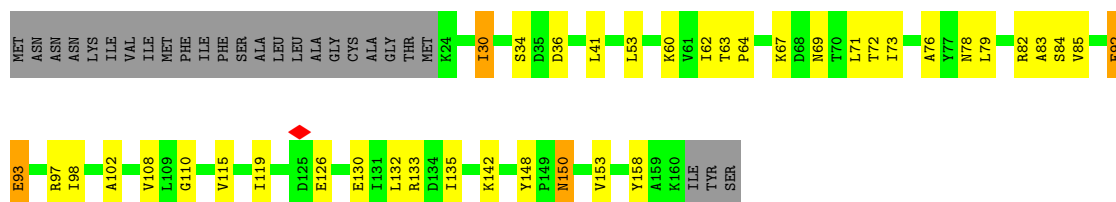


Chain FD:  62% 21% 14%



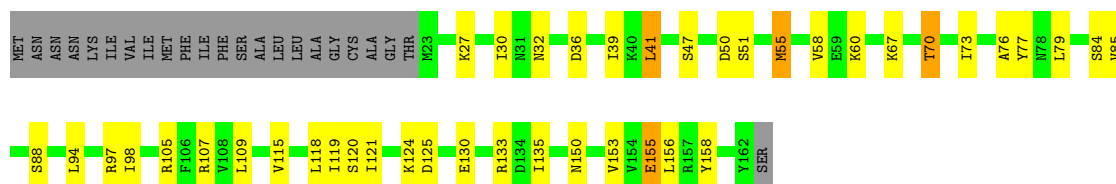
• Molecule 2: DotD

Chain Fd:  60% 22% 16%



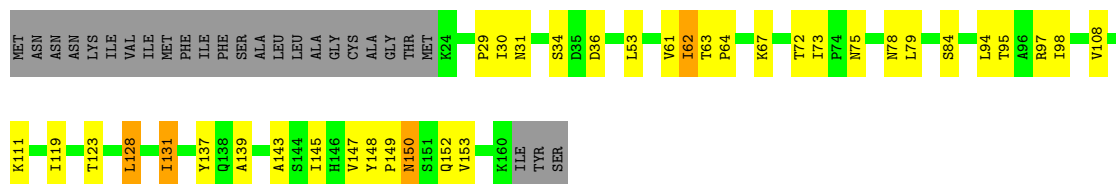
• Molecule 2: DotD

Chain GD:  60% 23% 14%



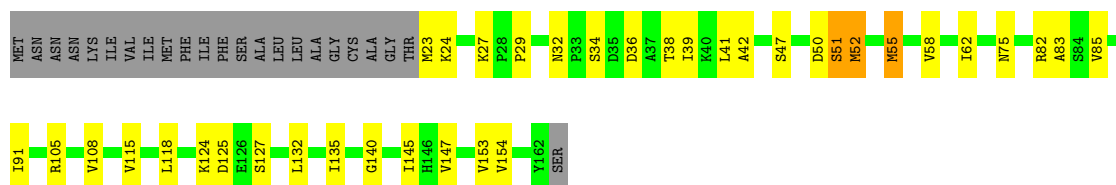
• Molecule 2: DotD

Chain Gd:  61% 20% 16%



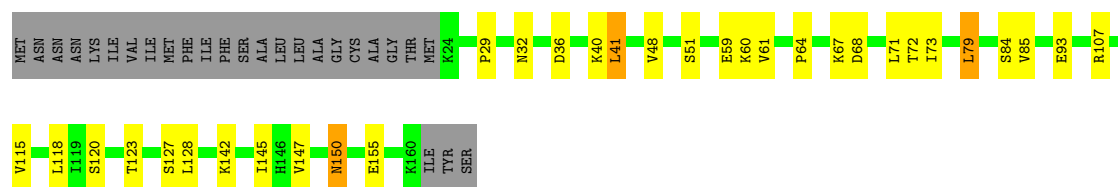
• Molecule 2: DotD

Chain HD:  63% 21% 14%



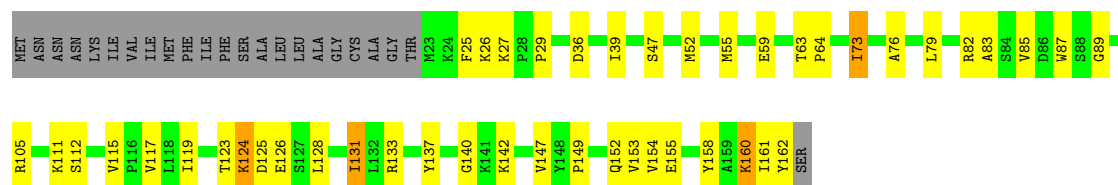
• Molecule 2: DotD

Chain Hd:  64% 18% 16%



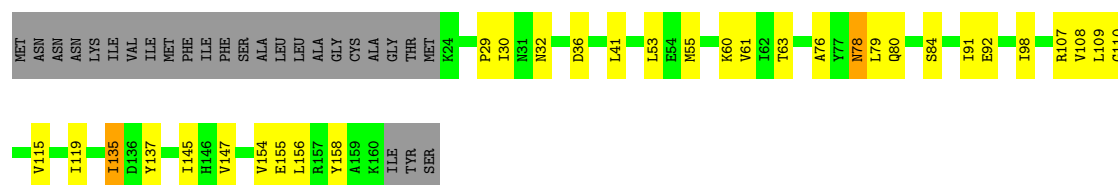
• Molecule 2: DotD

Chain ID:  58% 26% 14%



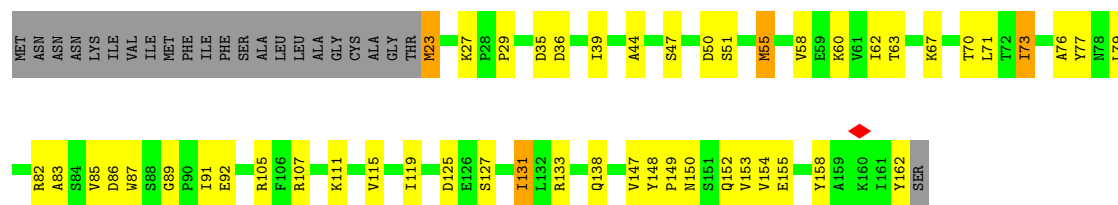
• Molecule 2: DotD

Chain Id:  64% 18% 16%



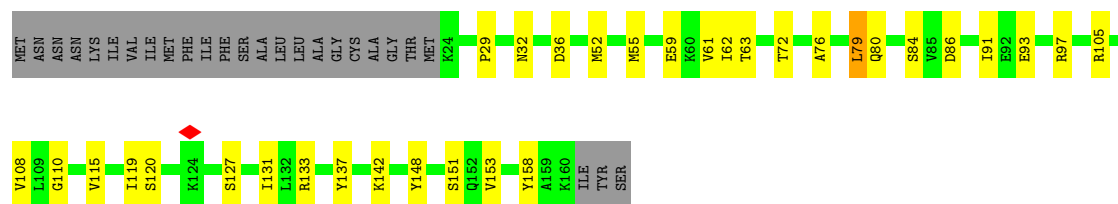
• Molecule 2: DotD

Chain JD:  55% 28% 14%



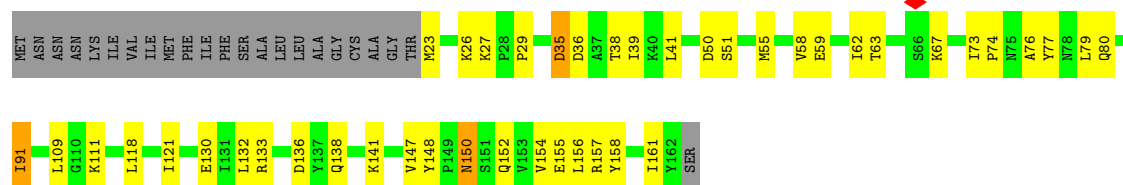
• Molecule 2: DotD

Chain Jd:  64% 20% 16%



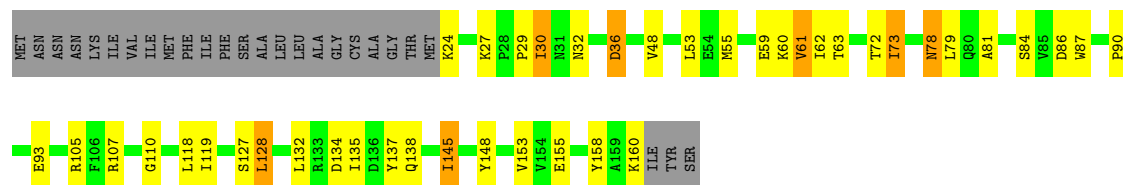
• Molecule 2: DotD

Chain KD:  59% 25% 14%



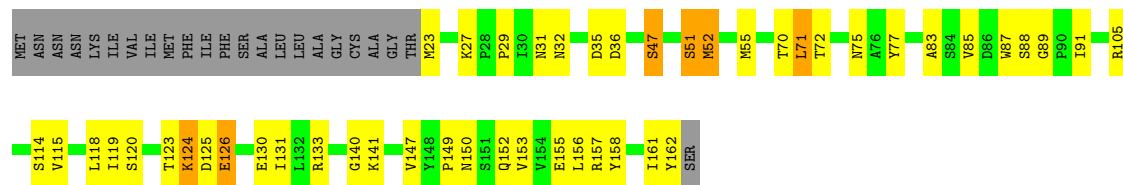
• Molecule 2: DotD

Chain Kd:  58% 21% 16%



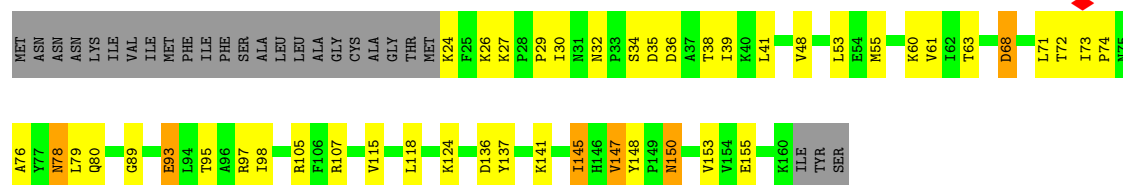
• Molecule 2: DotD

Chain LD:  56% 26% 14%



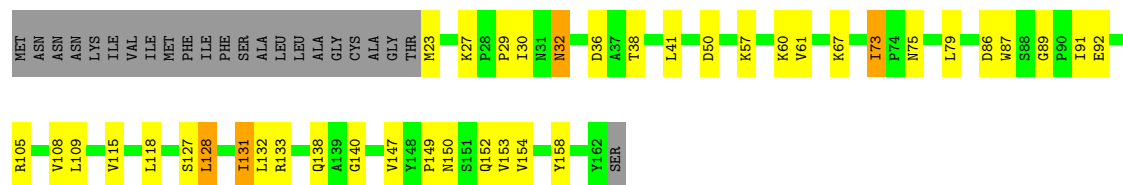
• Molecule 2: DotD

Chain Ld:  56% 25% 16%



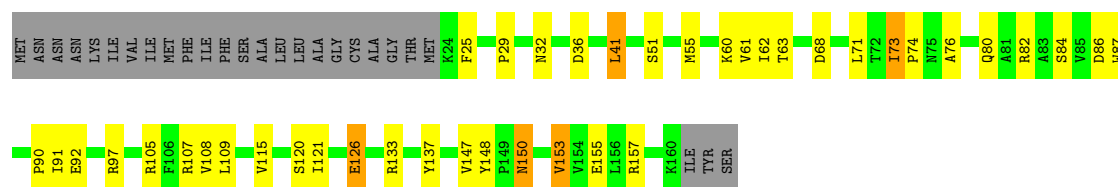
• Molecule 2: DotD

Chain MD:  61% 22% 14%



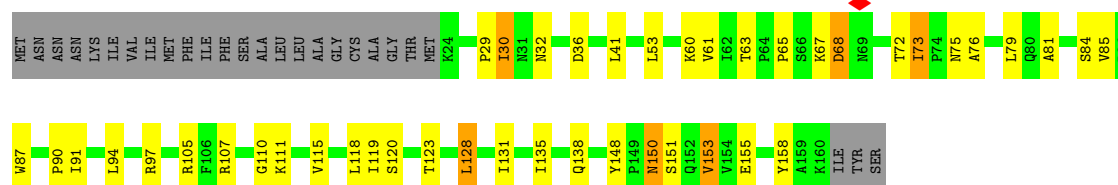
• Molecule 2: DotD

Chain Md:  59% 22% 16%



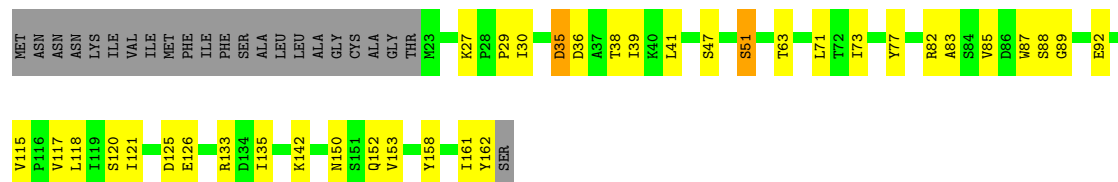
• Molecule 2: DotD

Chain Ad:  57% 23% 16%



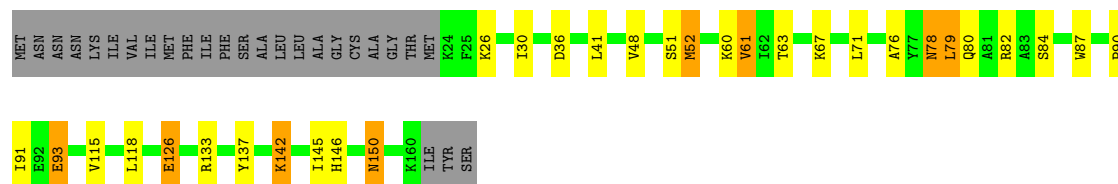
• Molecule 2: DotD

Chain BD:  63% 21% 14%



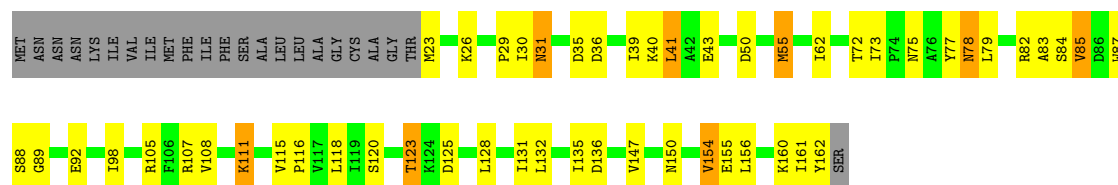
• Molecule 2: DotD

Chain Bd:  65% 14% 5% 16%



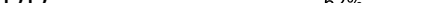
• Molecule 2: DotD

Chain CD:  54% 27% 5% 14%

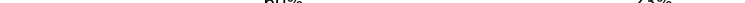


• Molecule 2: DotD

L109	G110	V115	E126	I131	D136	A139	K142	A143	S144	I145	H146	V147	Y148	P149	M150	V153	Y158	A159	K160	I16	TYR	SER																				
MET	ASN	ASN	ASN	I16	VAL	I16	MET	PHE	TLE	PHE	SER	LEU	ALA	ALA	GLY	GLY	THR	MET	K24	I30	D35	D36	A37	T38	I39	K40	L41	S51	E59	K60	V61	I62	D68	A76	L79	S84	I91	L94	K97	I98	R105	V109

Chain DD:  62% 24% 14%

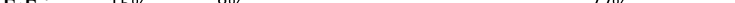
I119	S120	T123	K124	D125	E126	S127	E130	I131	L132	R133	D136	I145	M150	V154	Y158	I161	Y162	SER																									
MET	ASN	ASN	LYS	ILE	VAL	ILE	MET	PHE	ILE	PHE	SER	LEU	ALA	LEU	GLY	CYS	ALA	ALA	GLY	THR	K23	K26	K27	I30	D36	L41	S51	M52	M55	T63	S66	I73	R82	A83	S84	D86	W87	S88	G89	I98	V108	Y115	Y116

Chain Dd: 

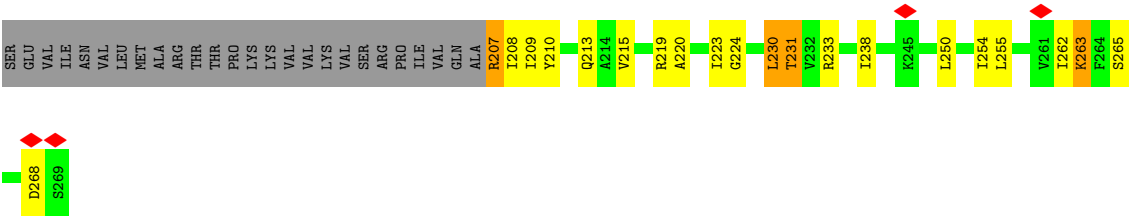
V108	V109	G110		V115		L118	L119	S120	PHE	L121	S122		E126	S127	L128		R133		D136	Y137		K142		L145	R146	V147	Y148	P149	N150		V153	V154	E155	L156	R157	Y158	A159	K160	L161	L162	TYR	SER		V108	V109	ASN	ASN	ASN	LYS	ILE	VAL	ILE	MET	PHE	PHE	SER	LEU	ALA	LEU	ALA	GLY	CYS	ALA	GLY	THR	MET	G24	P29	N31	N32	D36	L41	V48	M52	L53	E54	K60	V61		L71	N78		A81	V85	D86	W87		E92	R97	I98		R105
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Chain AD:

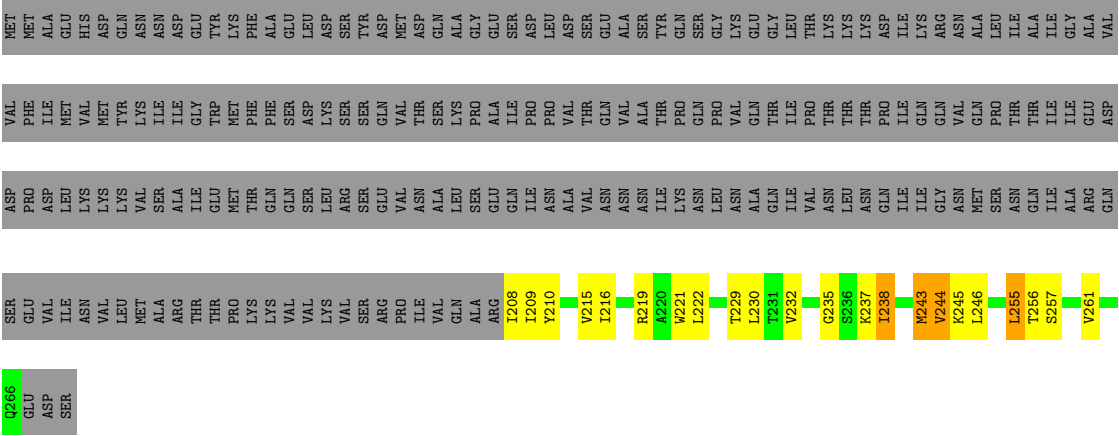
S88	G89	I98	R105	V115	P116	V117	L118	I119	S120	I121	S122	T123	K124	L132	R133	Q138	A139	G140	I145	H146	V147	Y148	F149	M150	S151	Q152	V153	V154	E155	L156	Y162	SER									
MET	ASN	ASN	LYS	ILE	VAL	ILE	PHE	PHE	SER	LEU	ALA	ALA	GLY	THR	K23	K24	K27	P28	P29	M32	P33	S34	D35	D36	I39	S47	S51	E54	M55	I62	D68	M69	T70	L71	T72	I73	A76	Q80	V85	D86	I87

Chain EF: 

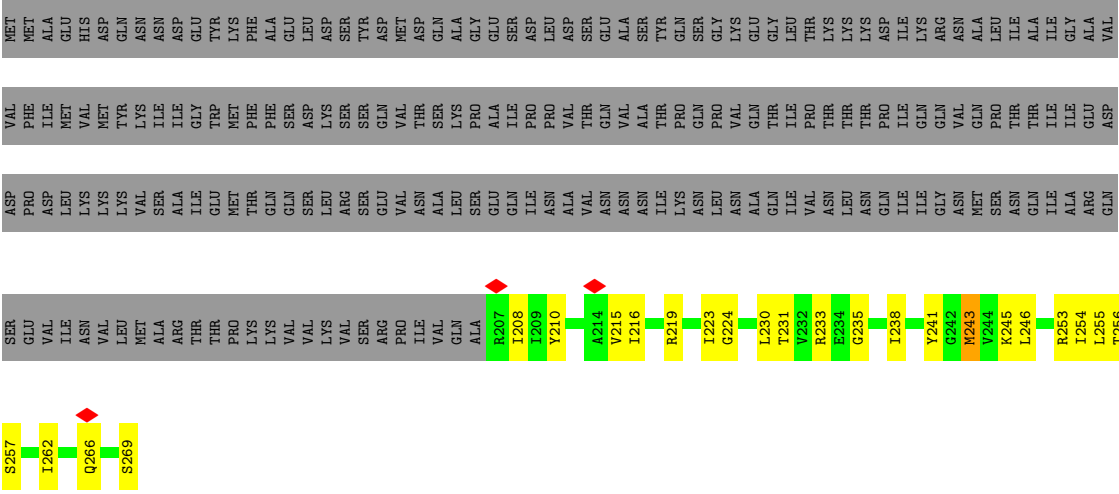
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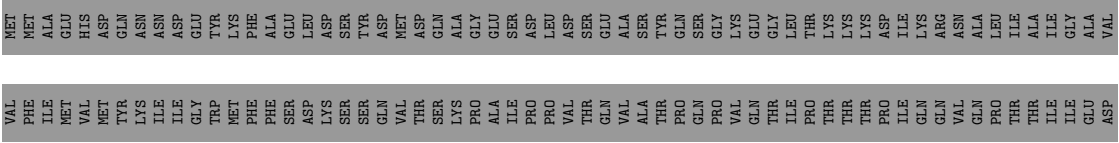
• Molecule 3: DotF



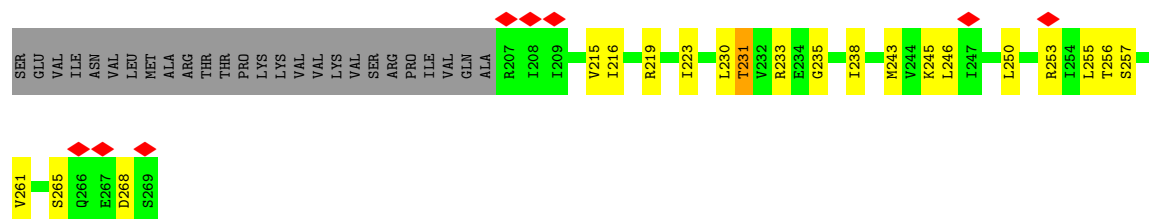
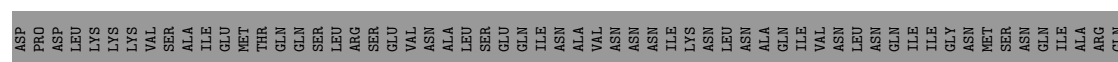
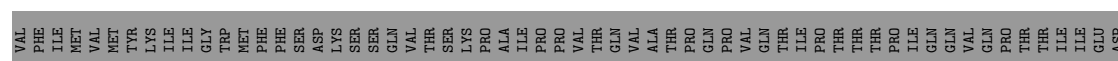
• Molecule 3: DotF



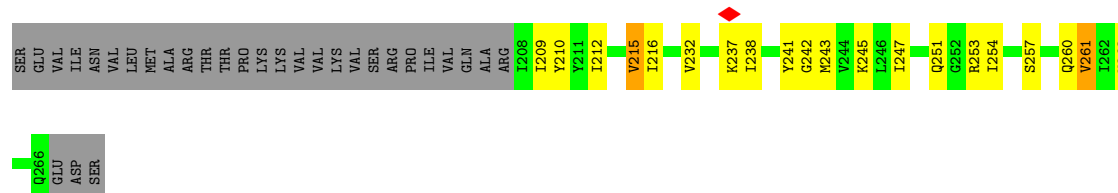
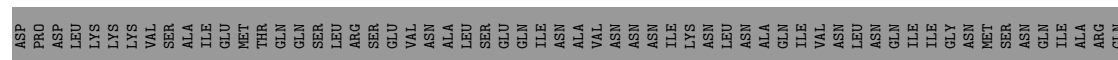
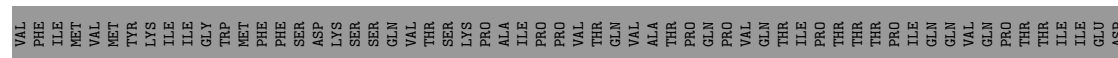
• Molecule 3: DotF



- Molecule 3: DotF



- Molecule 3: DotF

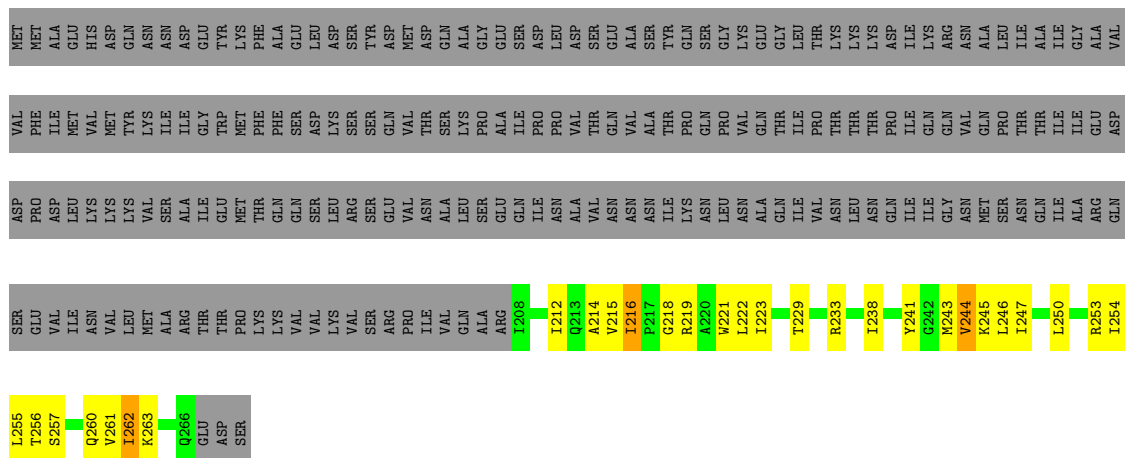


- Molecule 3: DotF

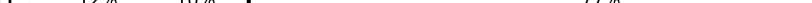


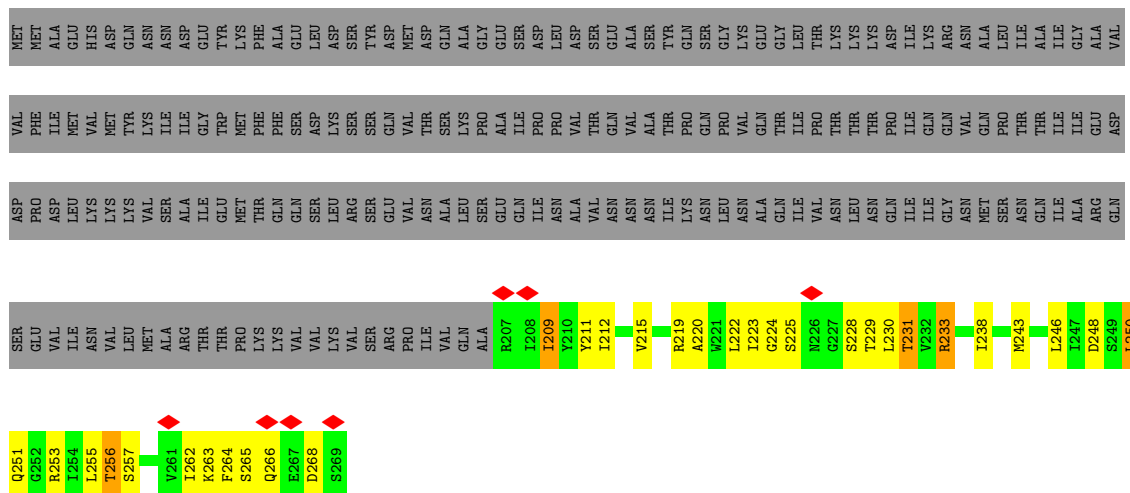
- Molecule 3: DotF

Chain Lf: 12% 9% . 78%



- Molecule 3: DotF

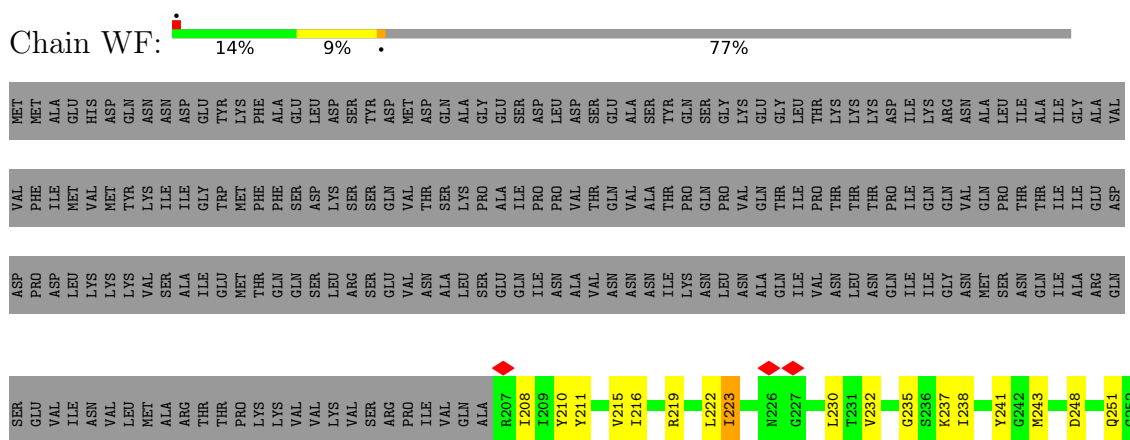
Chain MF:  12% 10% . 77%



- Molecule 3: DotF

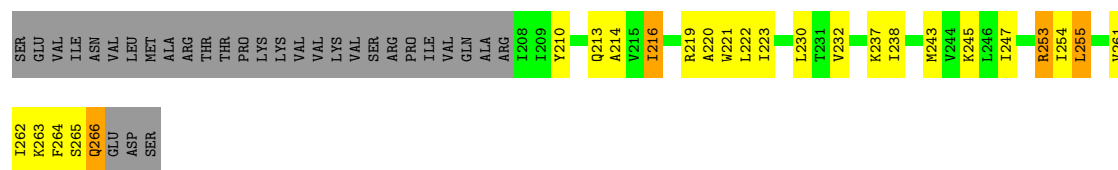
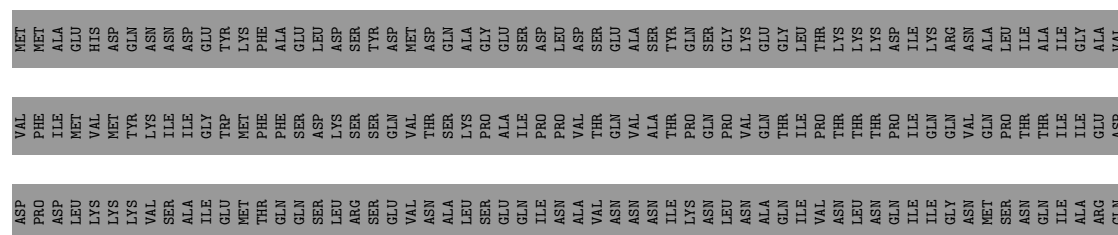
- Molecule 3: DotF

- Molecule 3: DotF

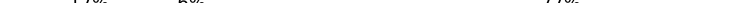


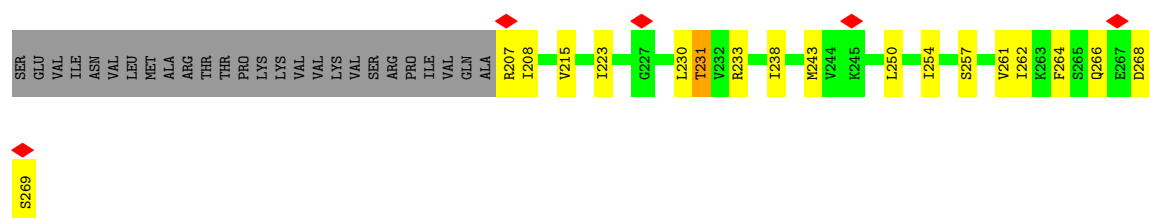
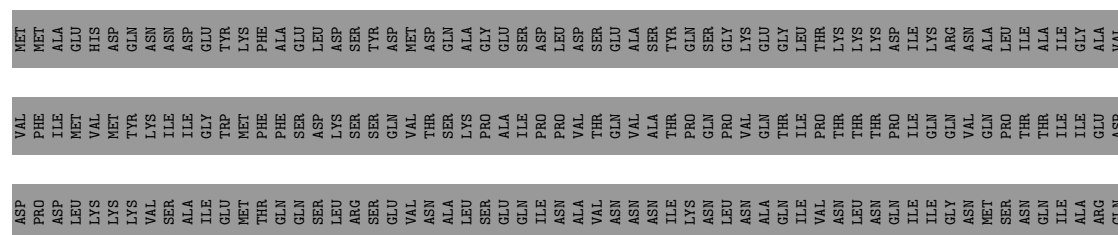
- Molecule 3: DotF

Chain Af: 13% 8% . 78%



- Molecule 3: DotF

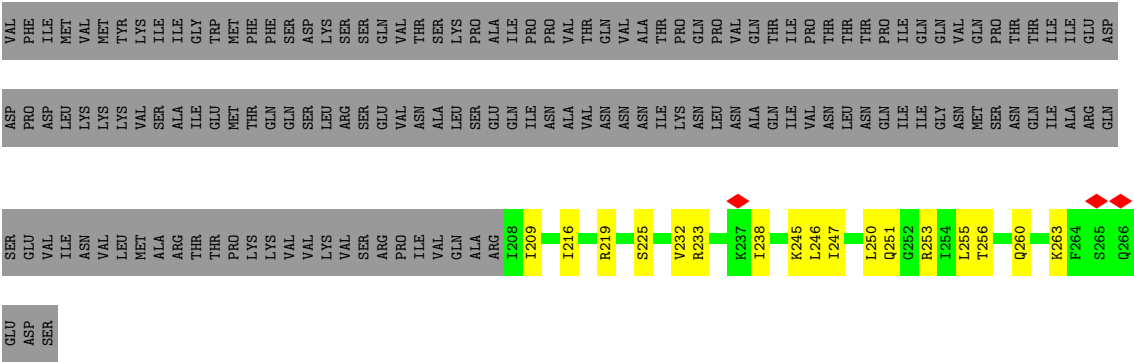
Chain BF: 



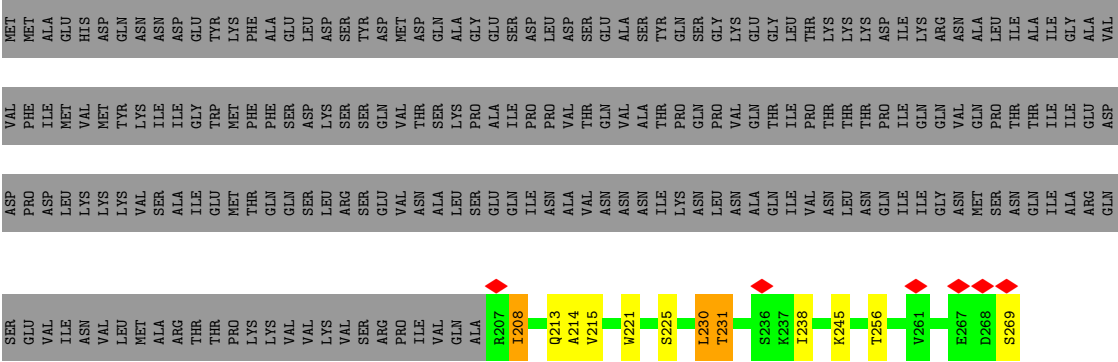
- Molecule 3: DotF

Chain Bf:

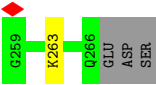
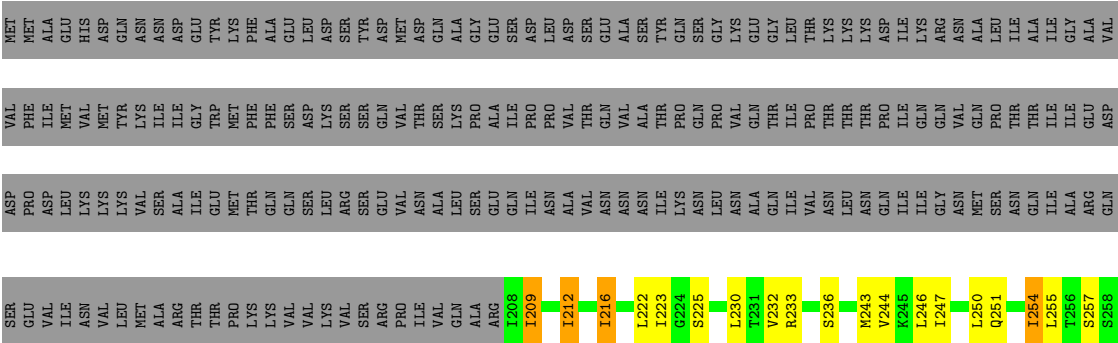




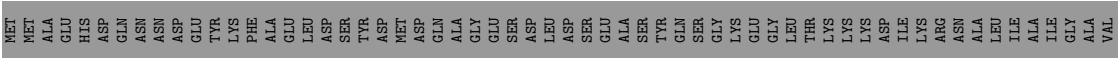
• Molecule 3: DotF



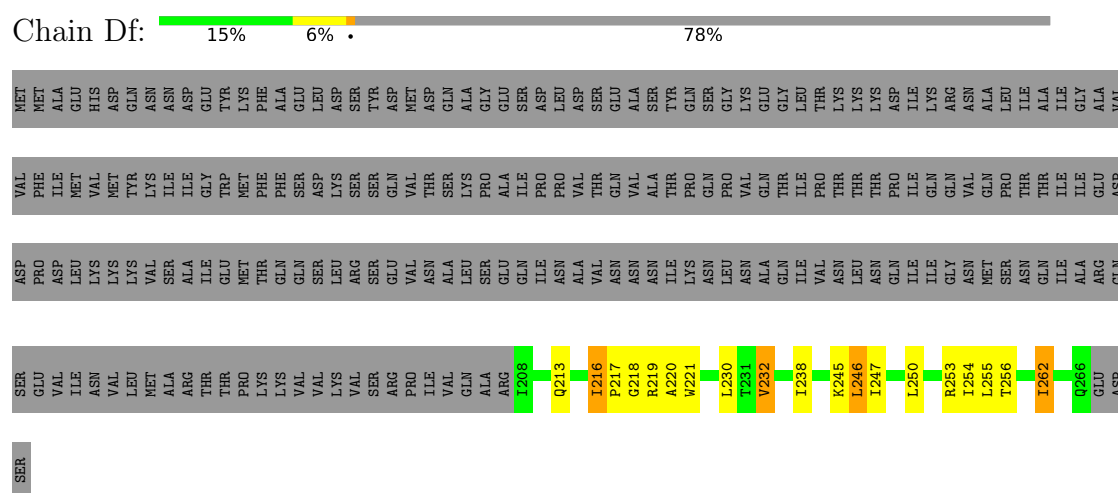
• Molecule 3: DotF



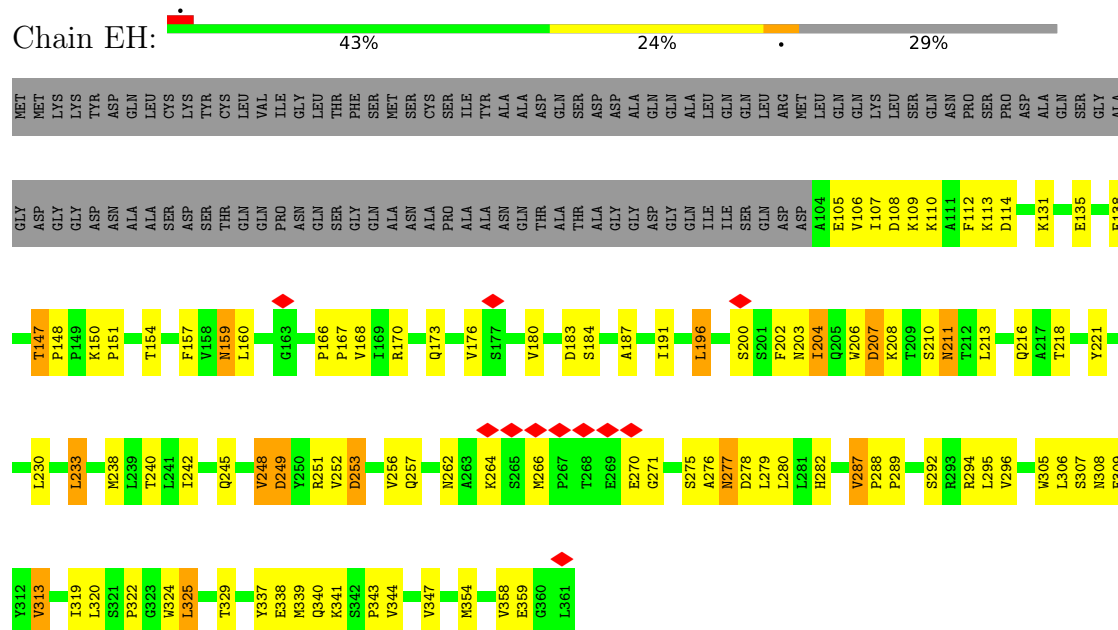
• Molecule 3: DotF



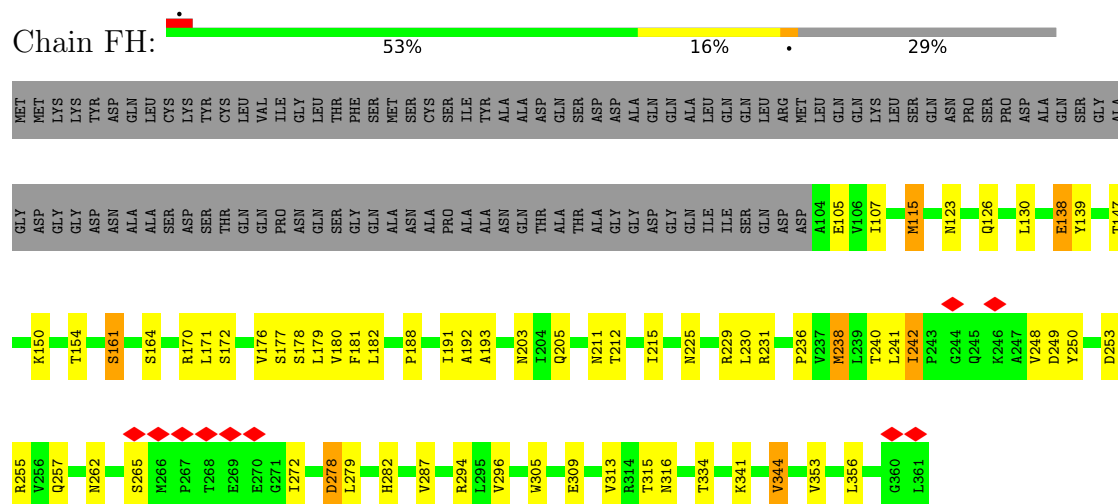
- Molecule 3: DotF



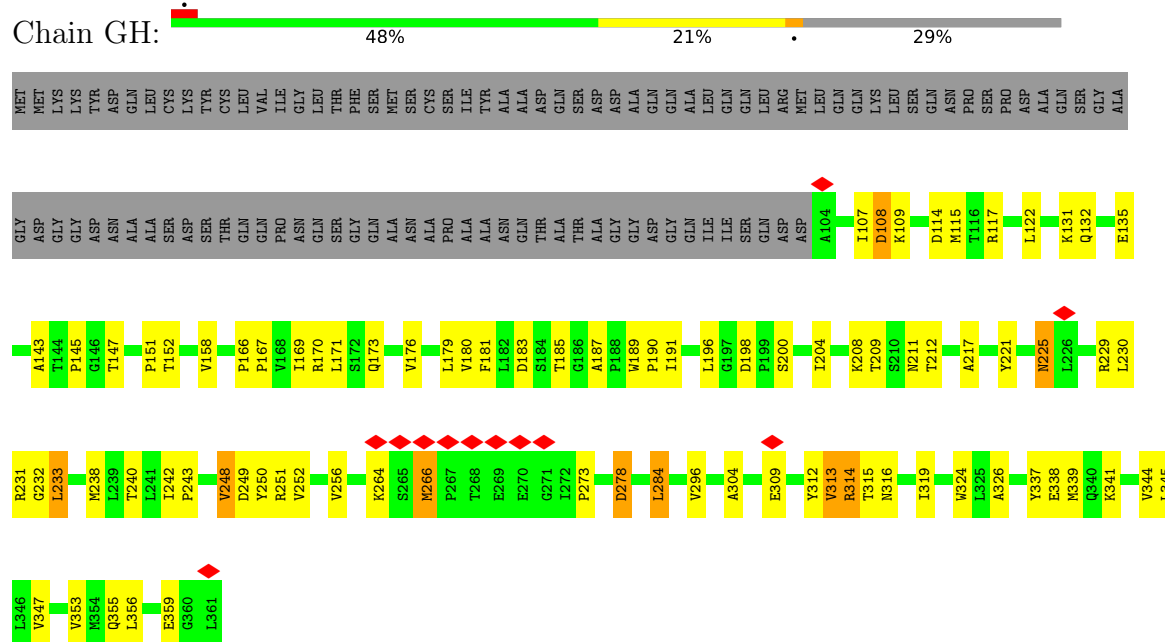
- Molecule 4: Type IV secretion protein IcmK



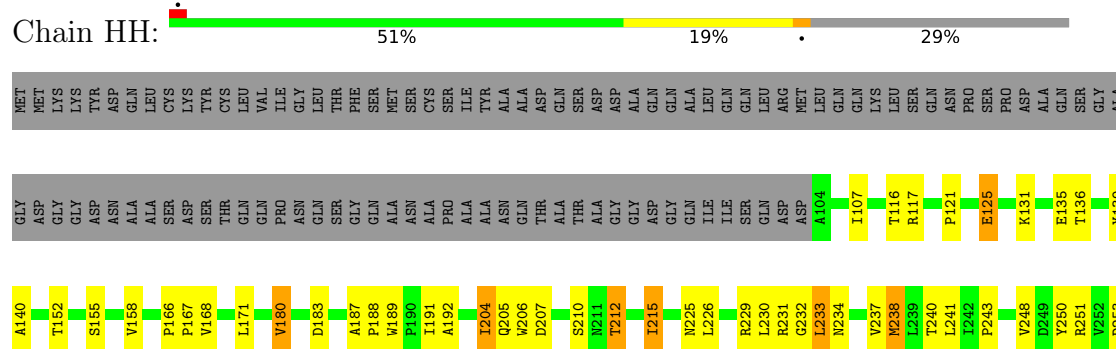
- Molecule 4: Type IV secretion protein IcmK



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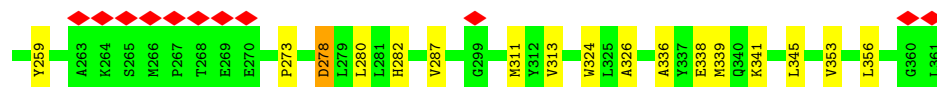
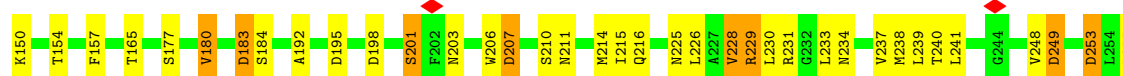
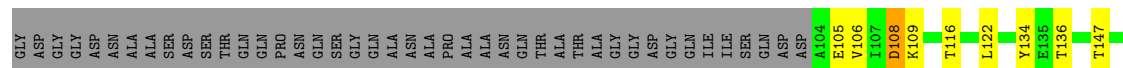
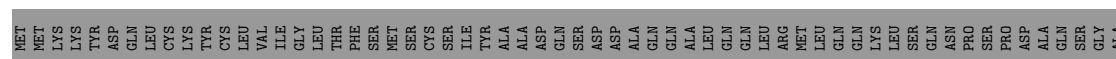
• Molecule 4: Type IV secretion protein IcmK





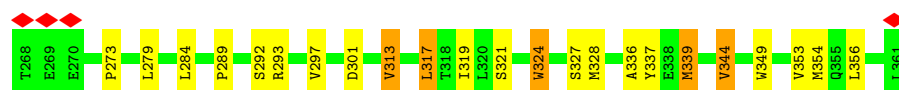
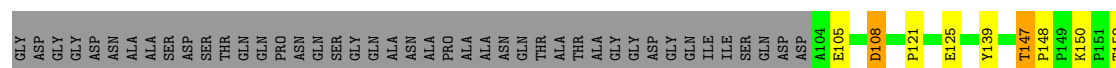
• Molecule 4: Type IV secretion protein IcmK

Chain IH: 54% 15% 29%



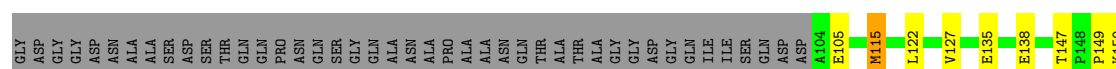
• Molecule 4: Type IV secretion protein IcmK

Chain JH: 53% 14% 29%

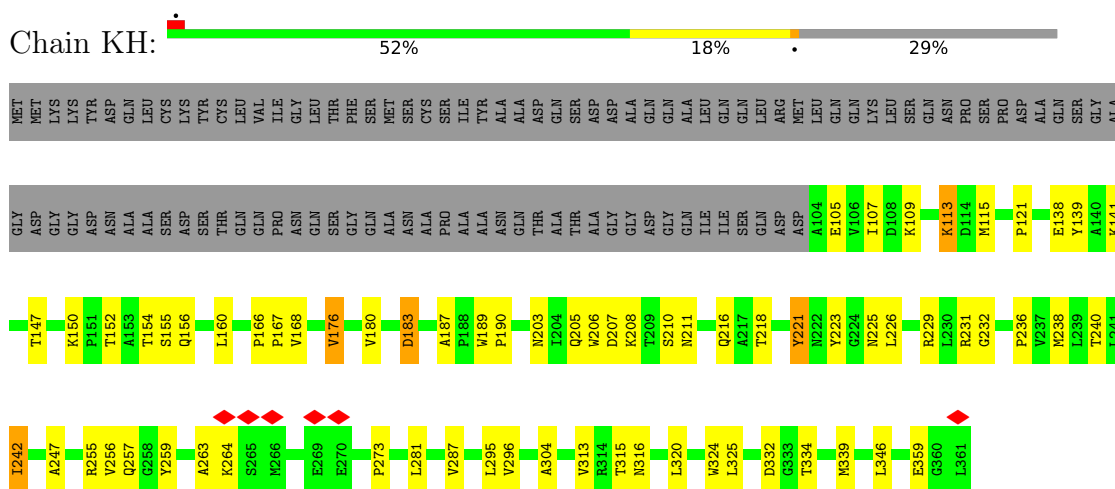


• Molecule 4: Type IV secretion protein IcmK

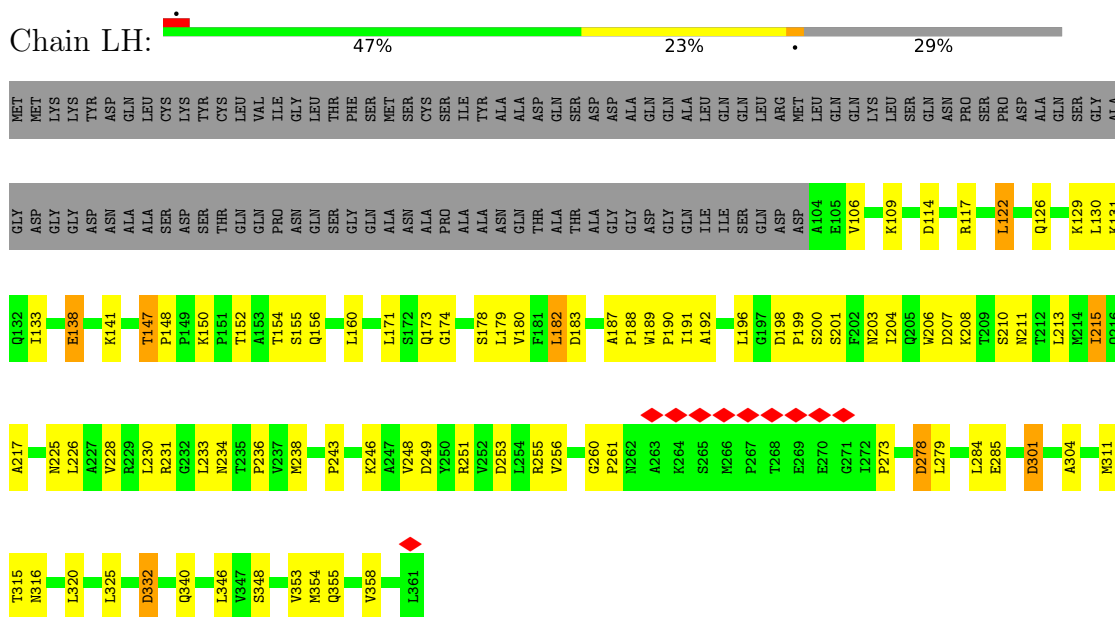
Chain AH: 47% 22% 29%



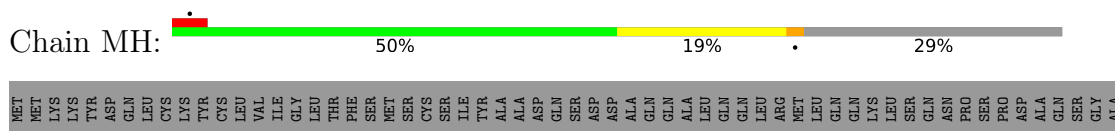
- Molecule 4: Type IV secretion protein IcmK

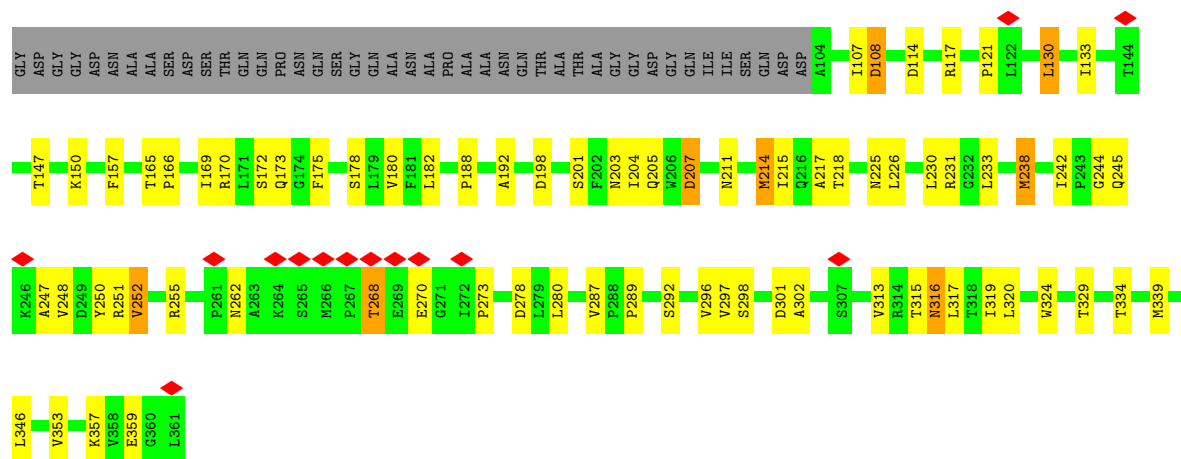


- Molecule 4: Type IV secretion protein IcmK

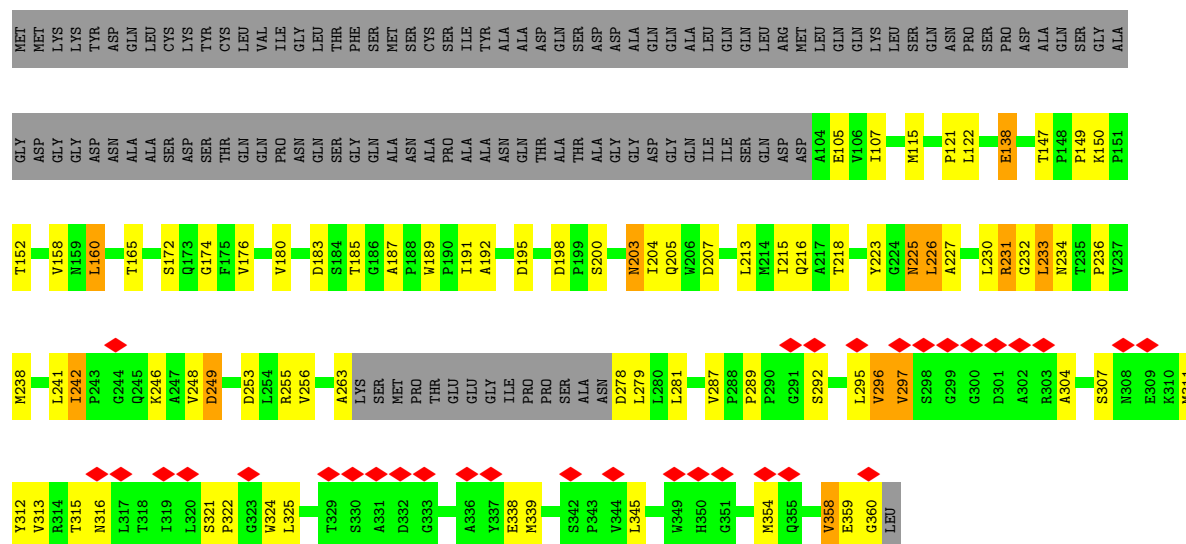


- Molecule 4: Type IV secretion protein IcmK

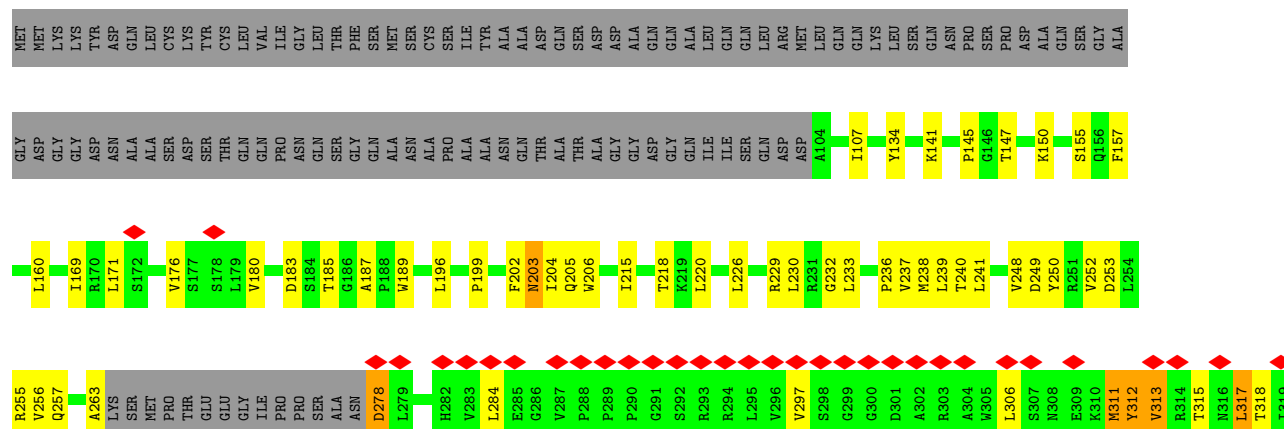




• Molecule 4: Type IV secretion protein IcmK

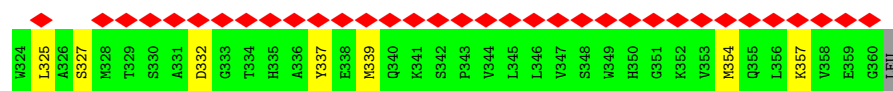
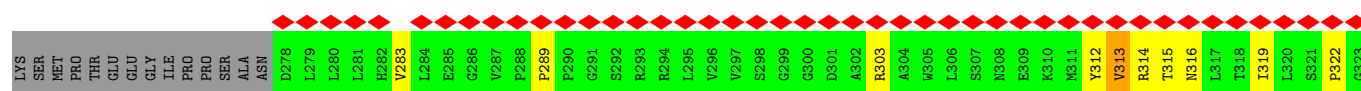
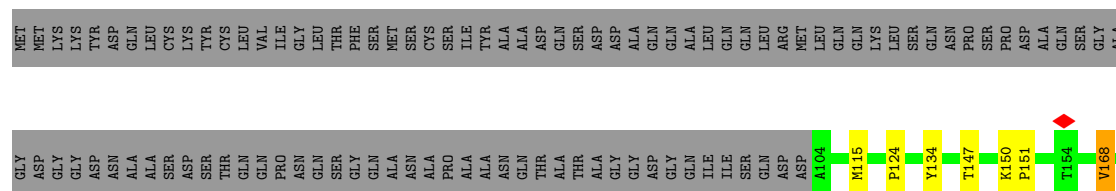


• Molecule 4: Type IV secretion protein IcmK

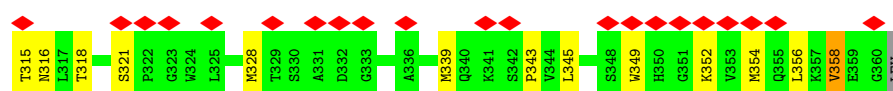
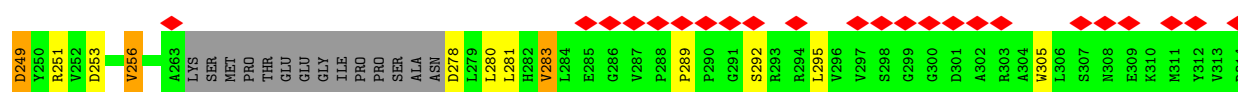
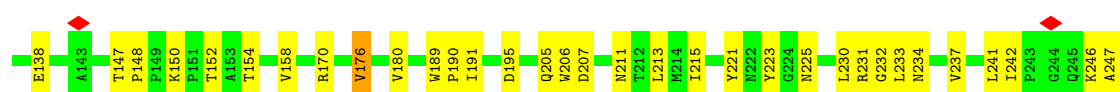
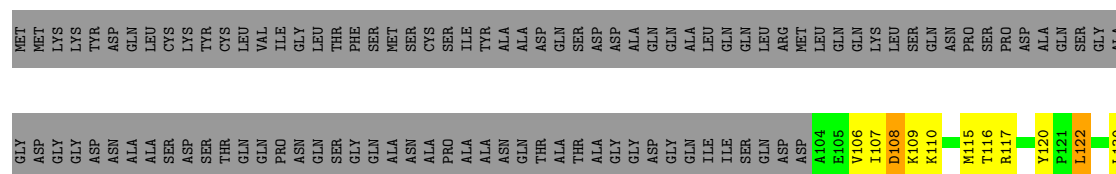




• Molecule 4: Type IV secretion protein IcmK

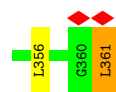


• Molecule 4: Type IV secretion protein IcmK



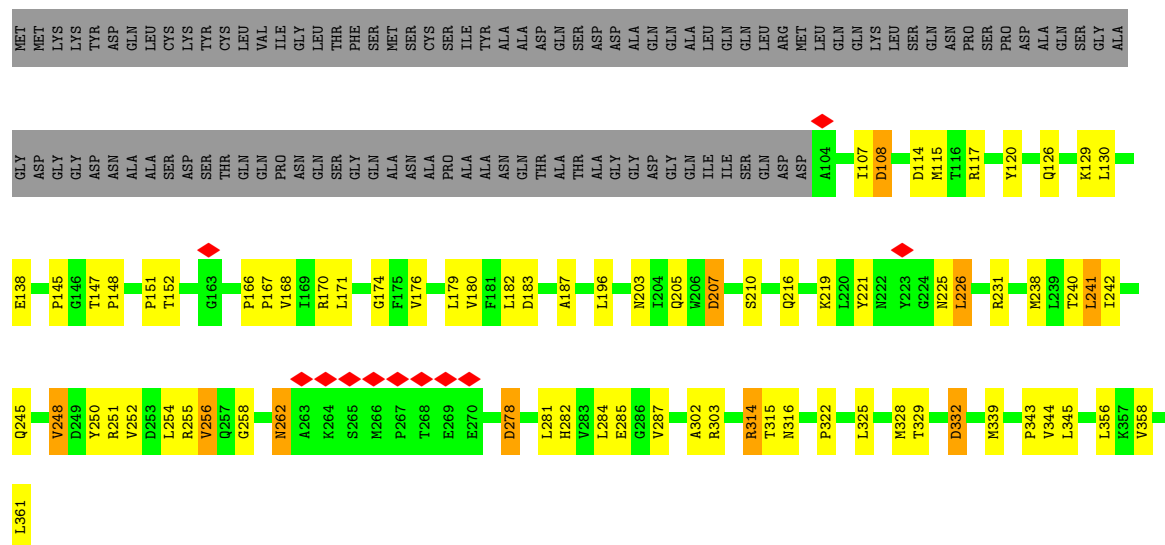
• Molecule 4: Type IV secretion protein IcmK





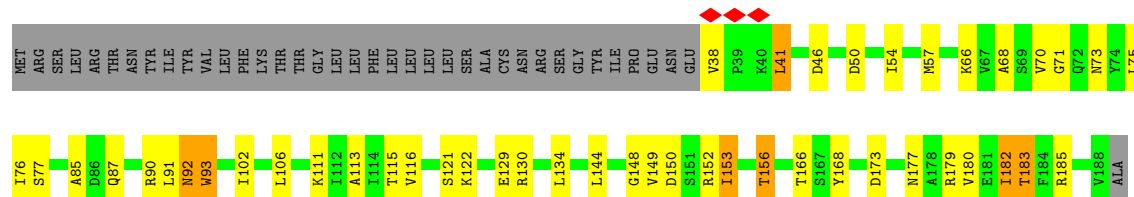
• Molecule 4: Type IV secretion protein IcmK

Chain DH: 51% 18% 29%



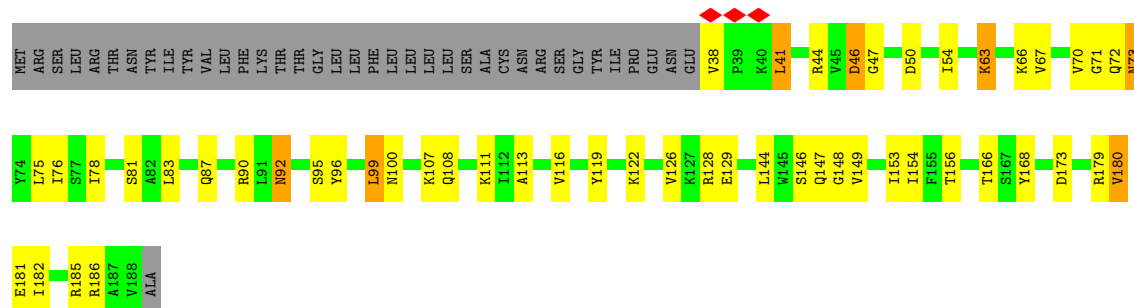
• Molecule 5: Inner membrane lipoprotein YiaD

Chain EK: 55% 21% 20%

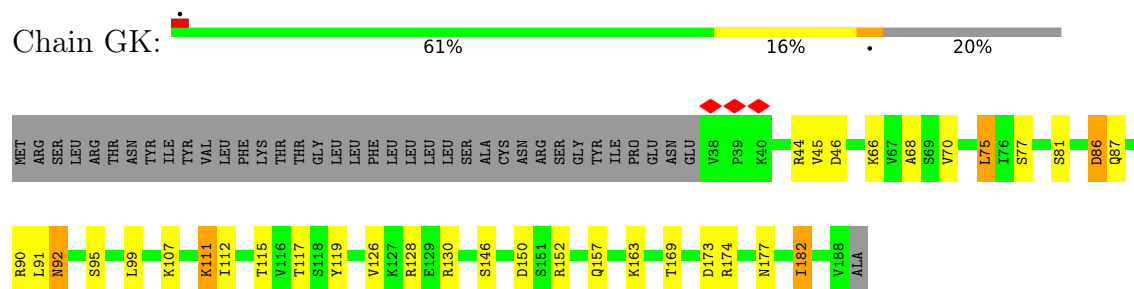


• Molecule 5: Inner membrane lipoprotein YiaD

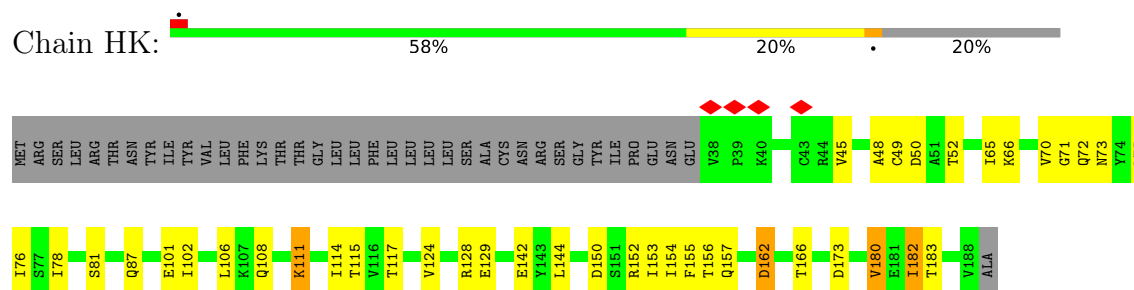
Chain FK: 52% 24% 20%



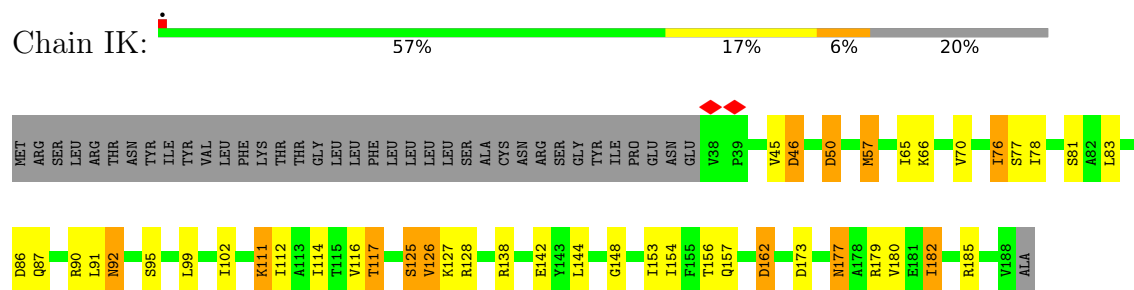
• Molecule 5: Inner membrane lipoprotein YiaD



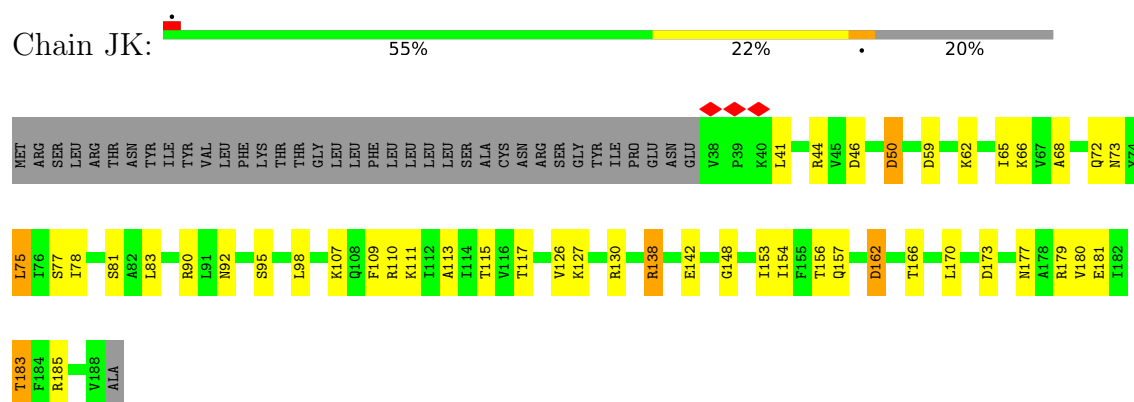
- Molecule 5: Inner membrane lipoprotein YiaD



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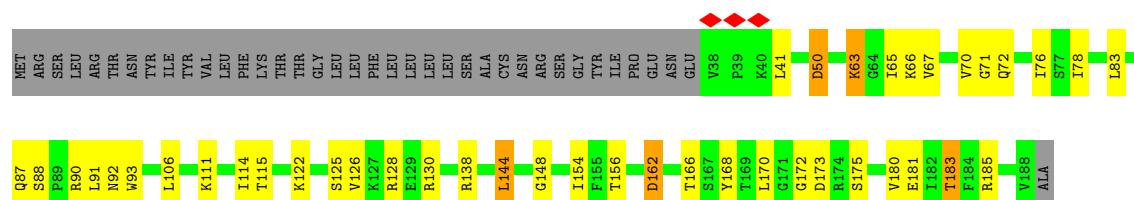


- Molecule 5: Inner membrane lipoprotein YiaD

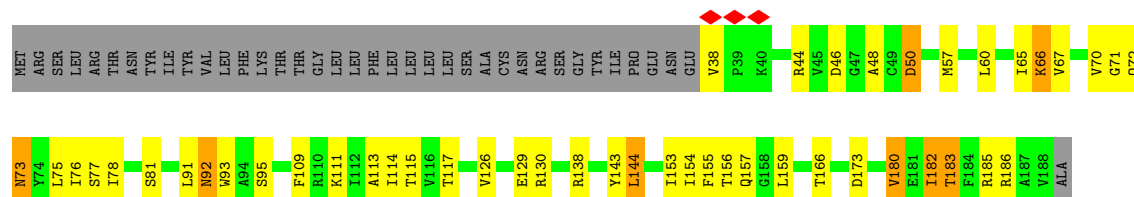


- Molecule 5: Inner membrane lipoprotein YiaD

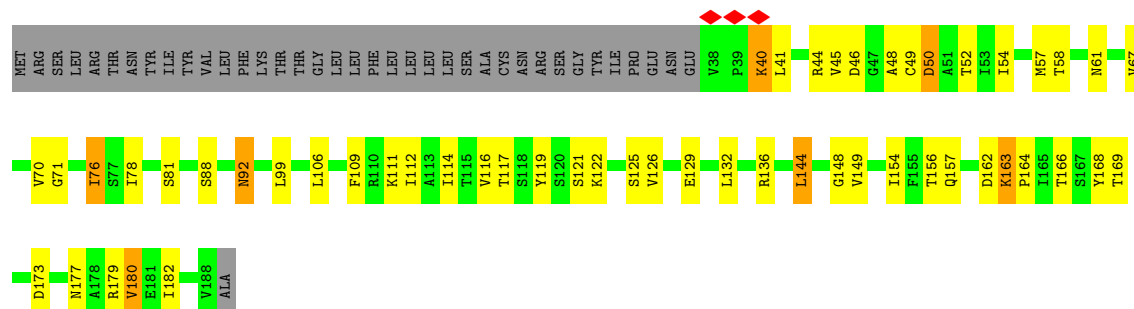




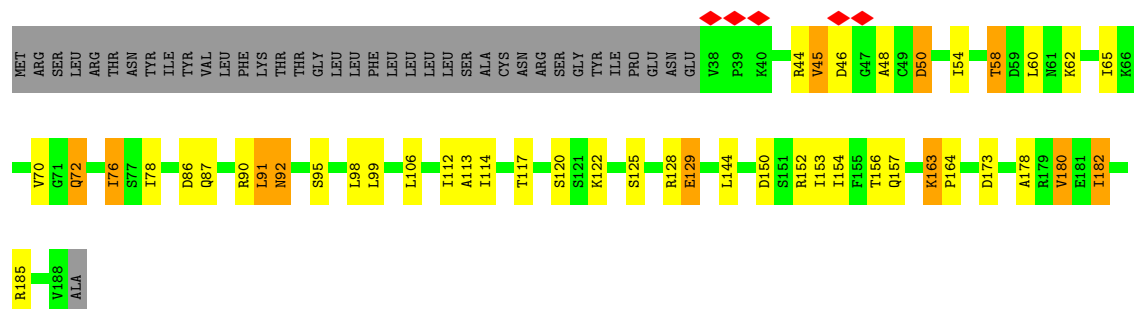
• Molecule 5: Inner membrane lipoprotein YiaD



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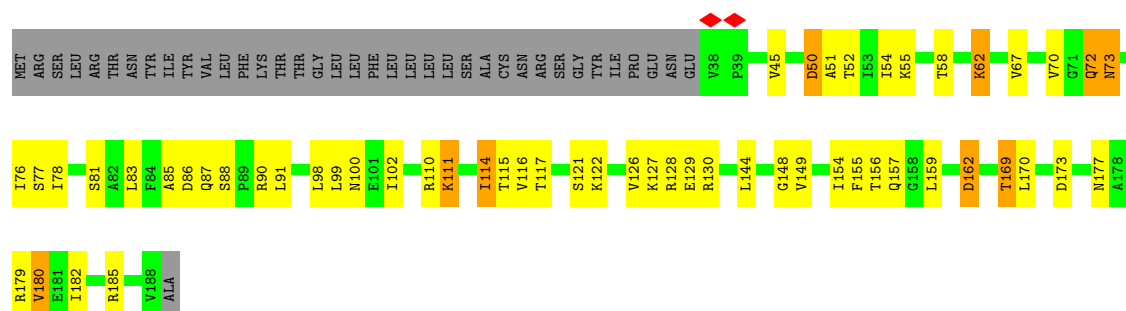


• Molecule 5: Inner membrane lipoprotein YiaD

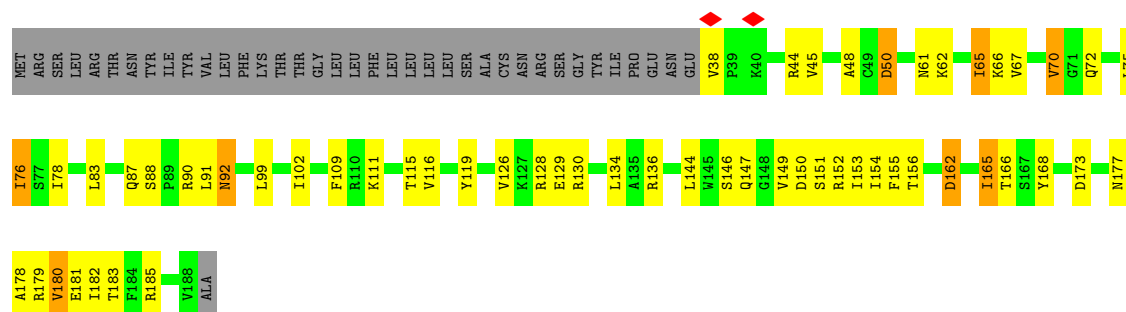


• Molecule 5: Inner membrane lipoprotein YiaD

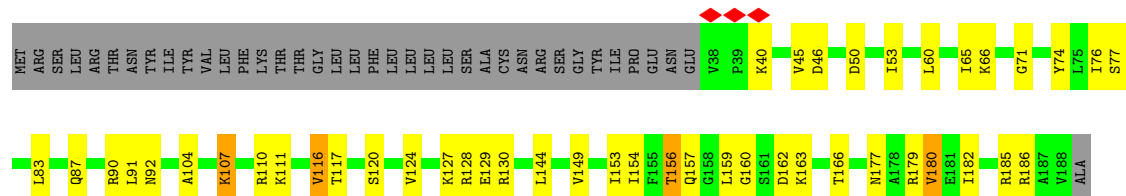




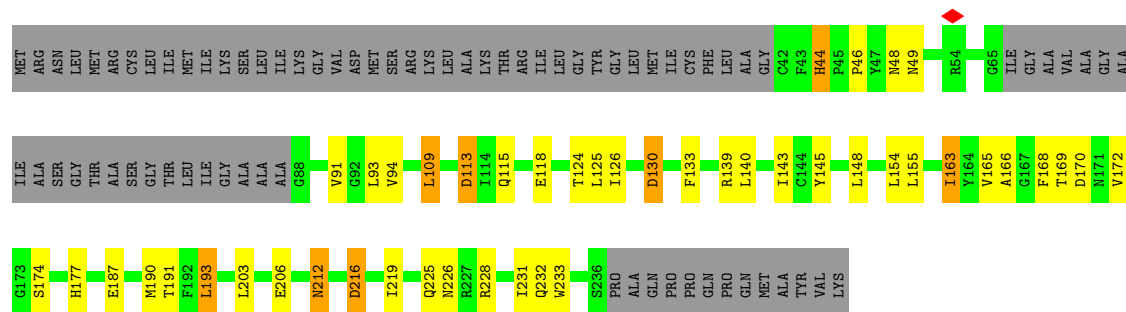
- Molecule 5: Inner membrane lipoprotein YiaD



- Molecule 5: Inner membrane lipoprotein YiaD

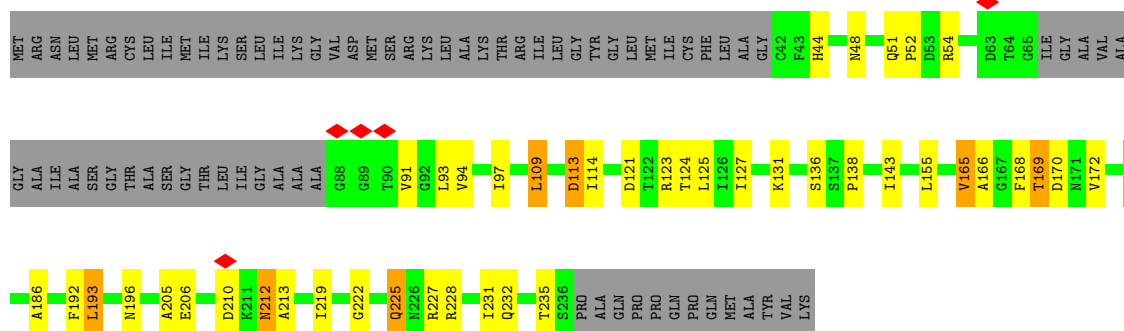


- Molecule 6: Outer membrane protein, OmpA family protein



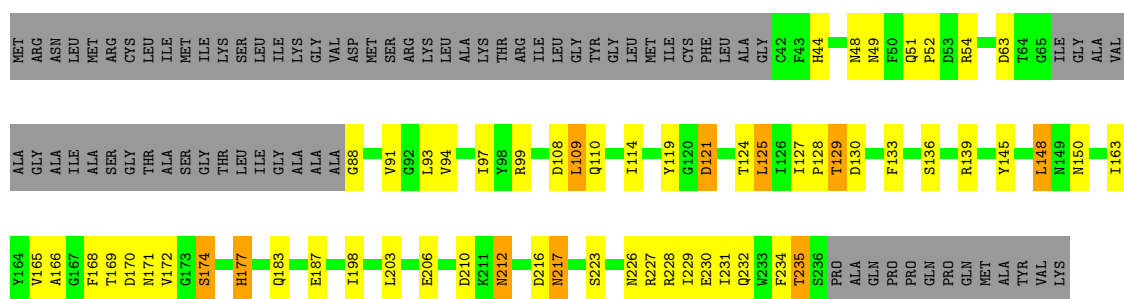
- Molecule 6: Outer membrane protein, OmpA family protein

Chain FL:  51% 15% 31%



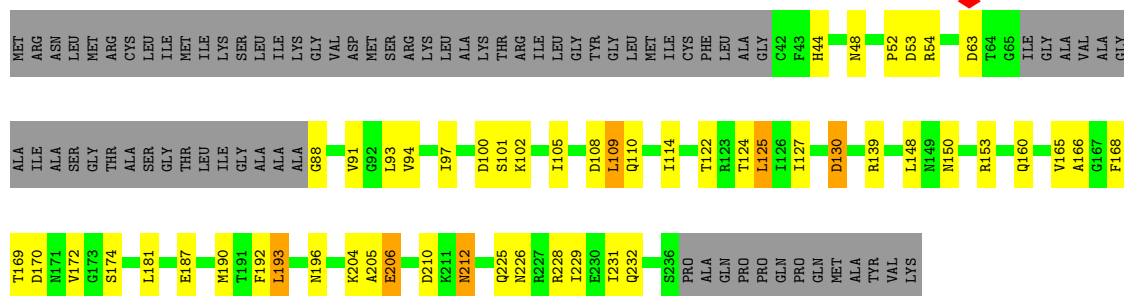
- Molecule 6: Outer membrane protein, OmpA family protein

Chain GL:  45% 20% 31%



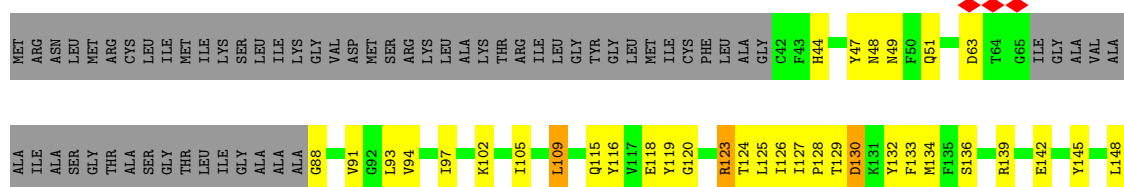
- Molecule 6: Outer membrane protein, OmpA family protein

Chain HL:  48% 19% 31%



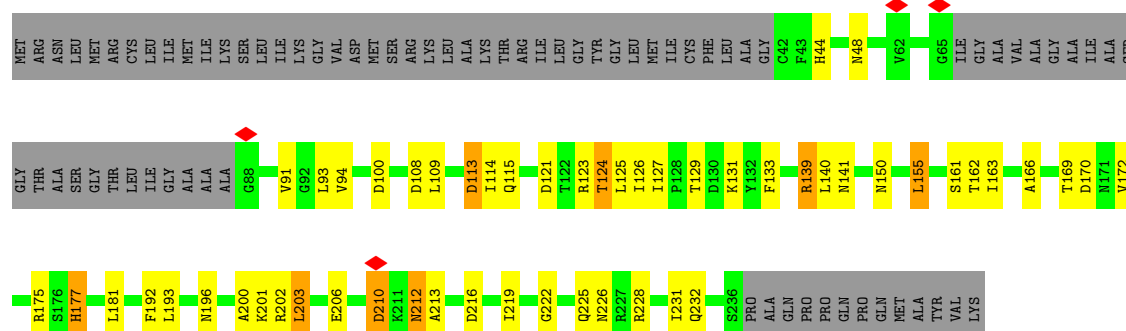
- Molecule 6: Outer membrane protein, OmpA family protein

Chain IL:  45% 22% 31%

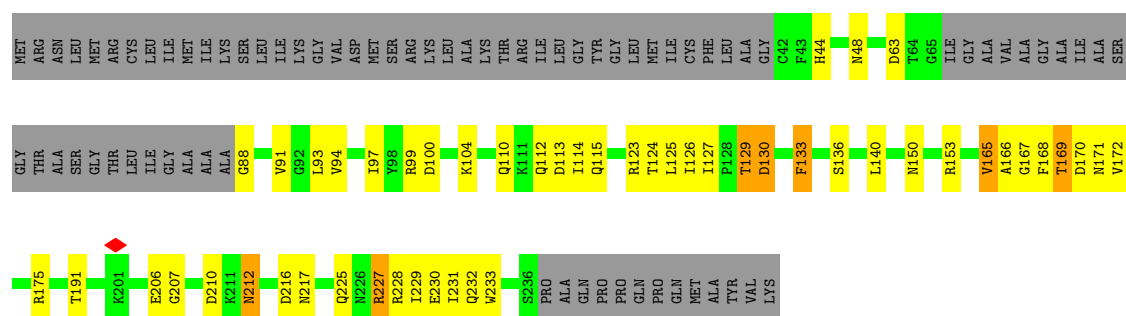




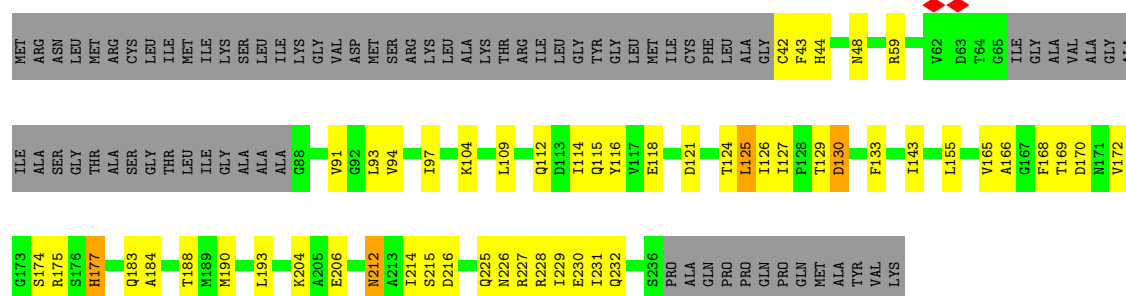
- Molecule 6: Outer membrane protein, OmpA family protein



- Molecule 6: Outer membrane protein, OmpA family protein

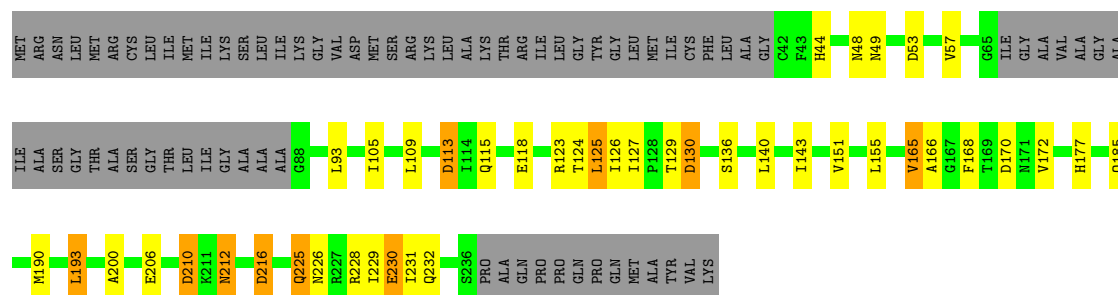


- Molecule 6: Outer membrane protein, OmpA family protein

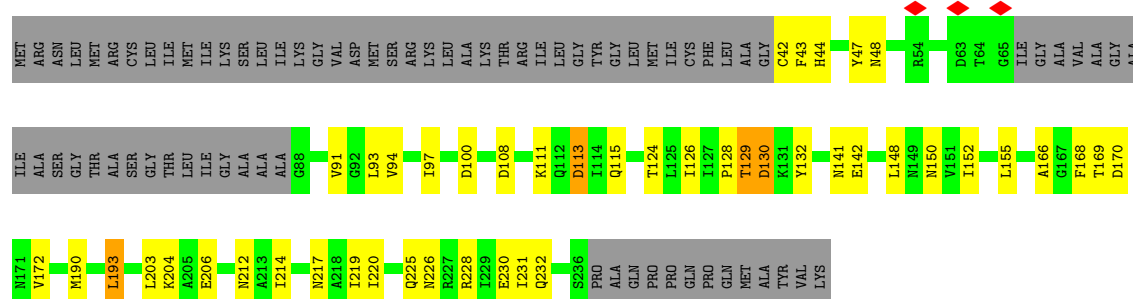


- Molecule 6: Outer membrane protein, OmpA family protein

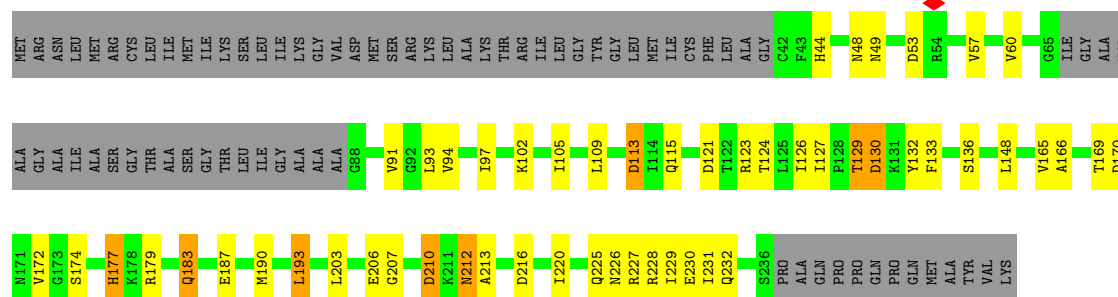




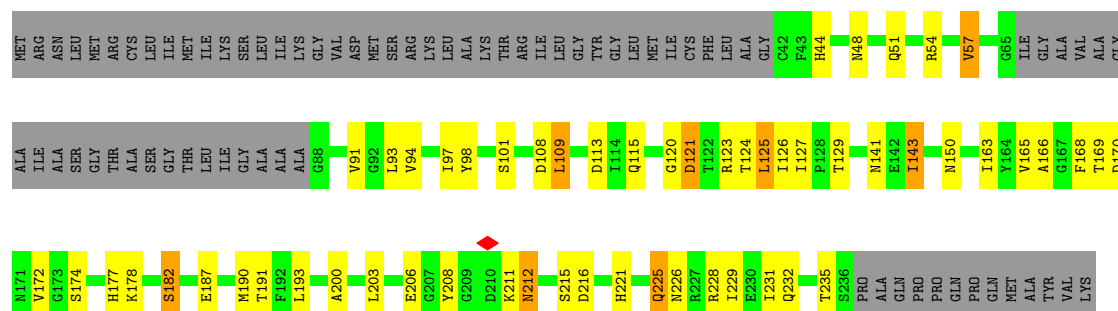
- Molecule 6: Outer membrane protein, OmpA family protein

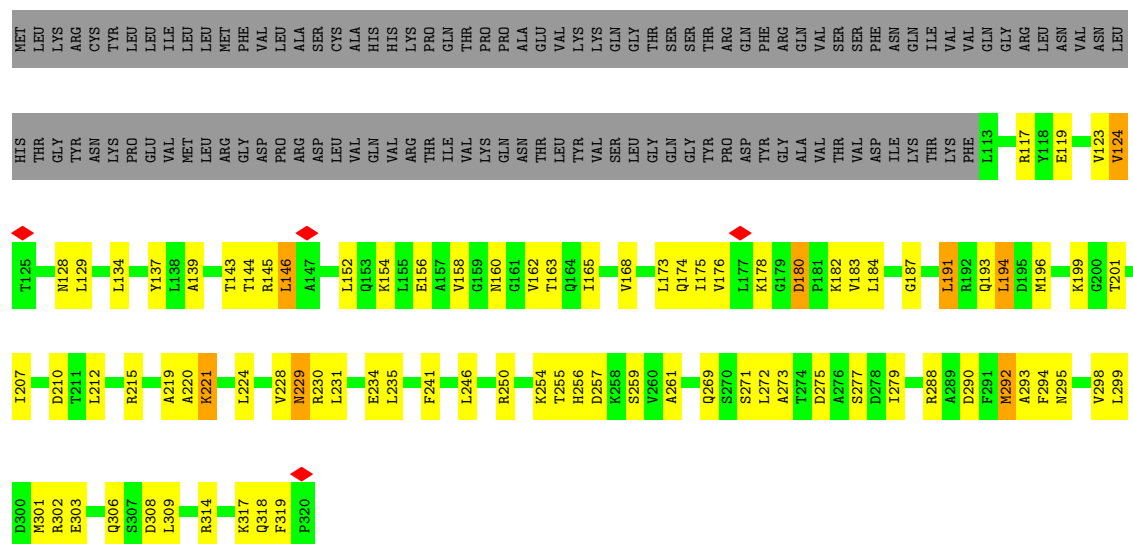


- Molecule 6: Outer membrane protein, OmpA family protein



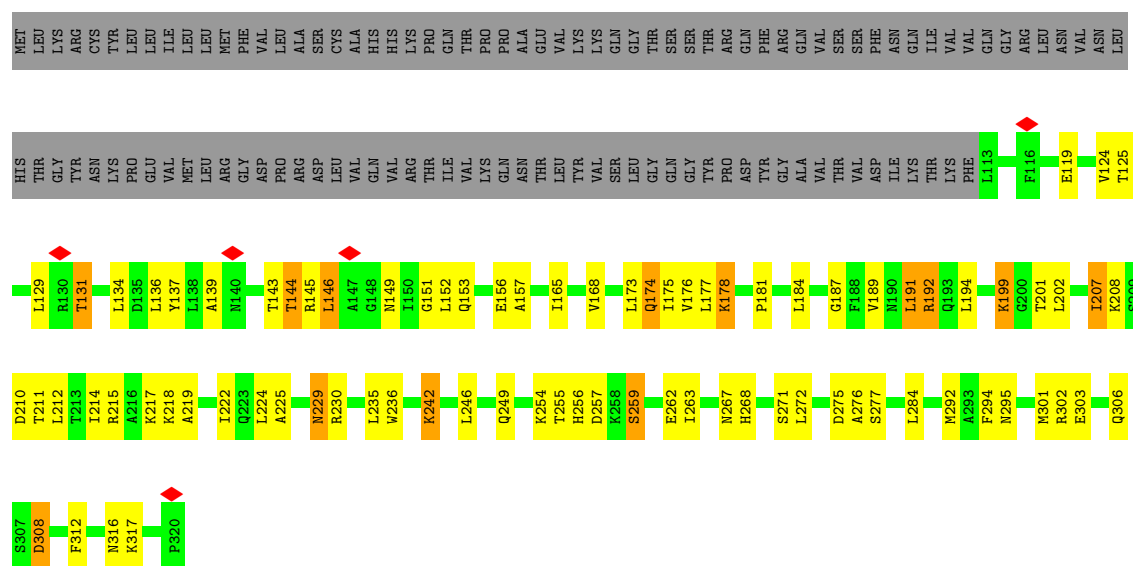
- Molecule 6: Outer membrane protein, OmpA family protein





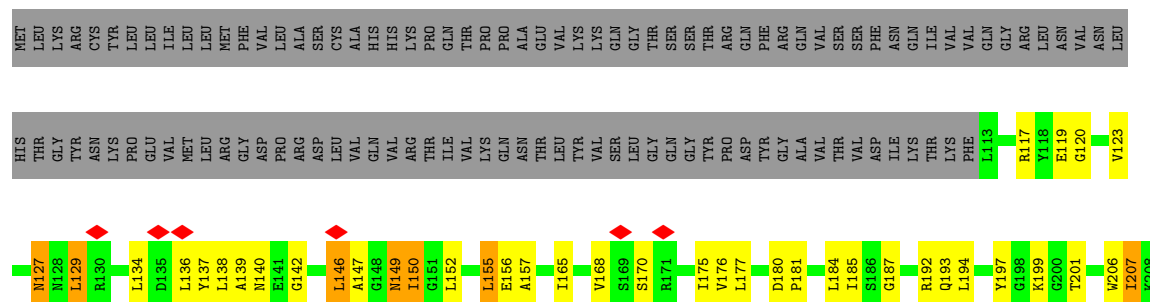
• Molecule 7: DUF2807 domain-containing protein

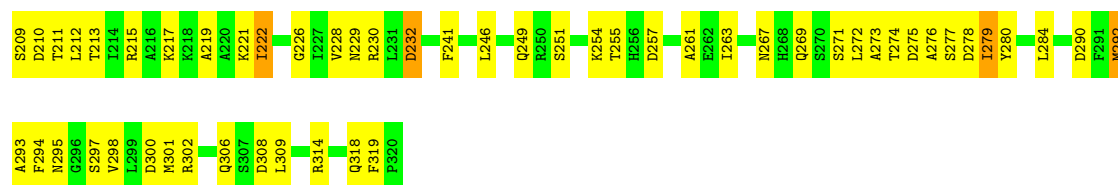
Chain HM: 39% 22% 35%



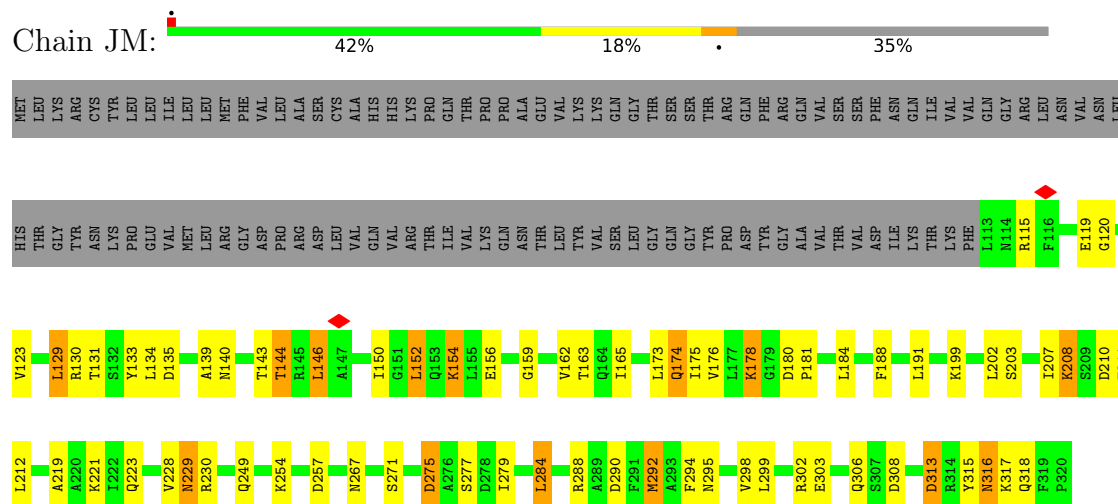
• Molecule 7: DUF2807 domain-containing protein

Chain IM: 36% 26% 35%

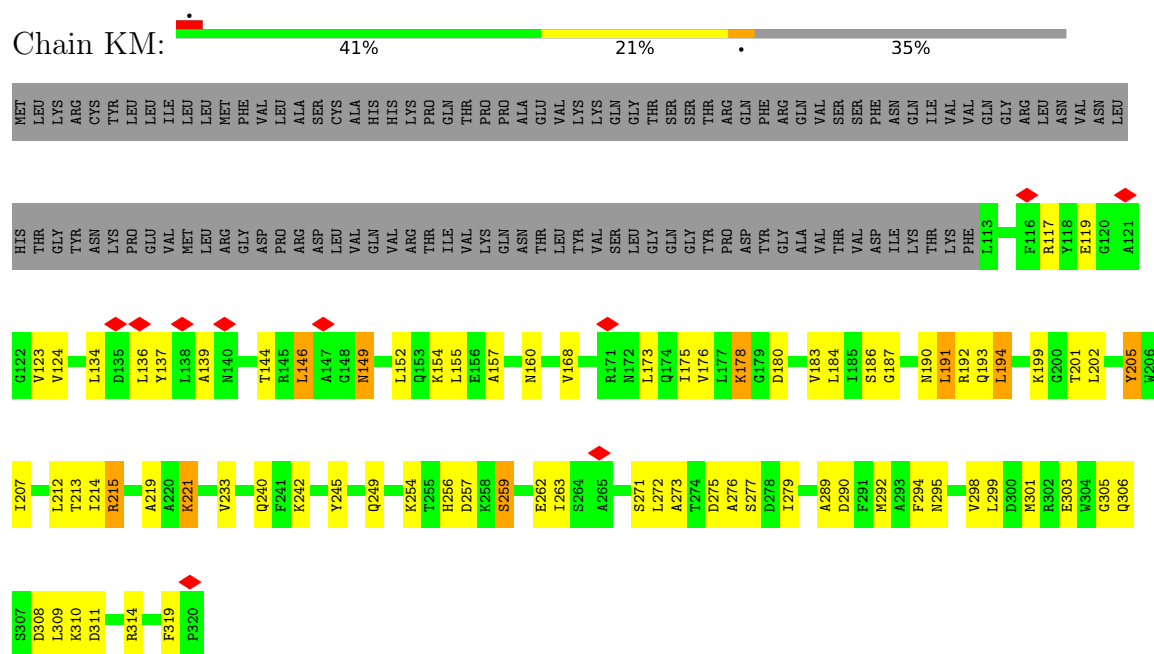




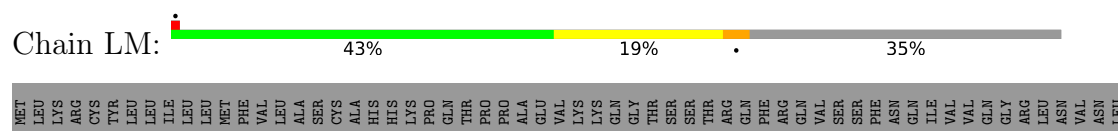
• Molecule 7: DUF2807 domain-containing protein

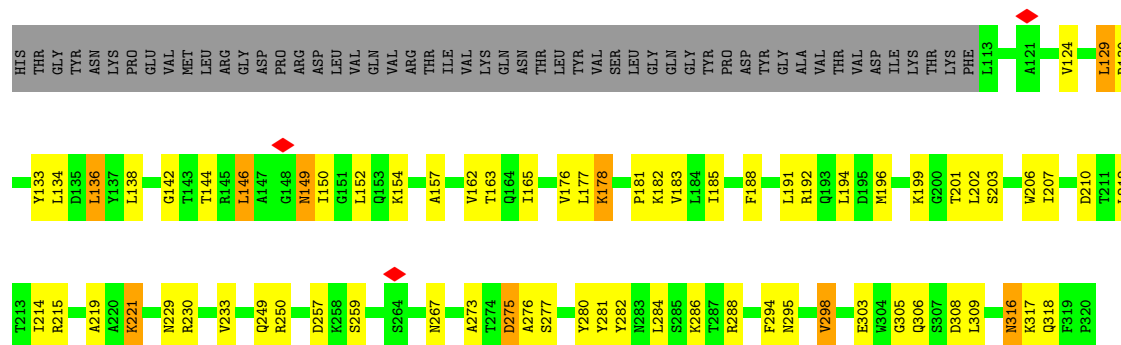


• Molecule 7: DUF2807 domain-containing protein

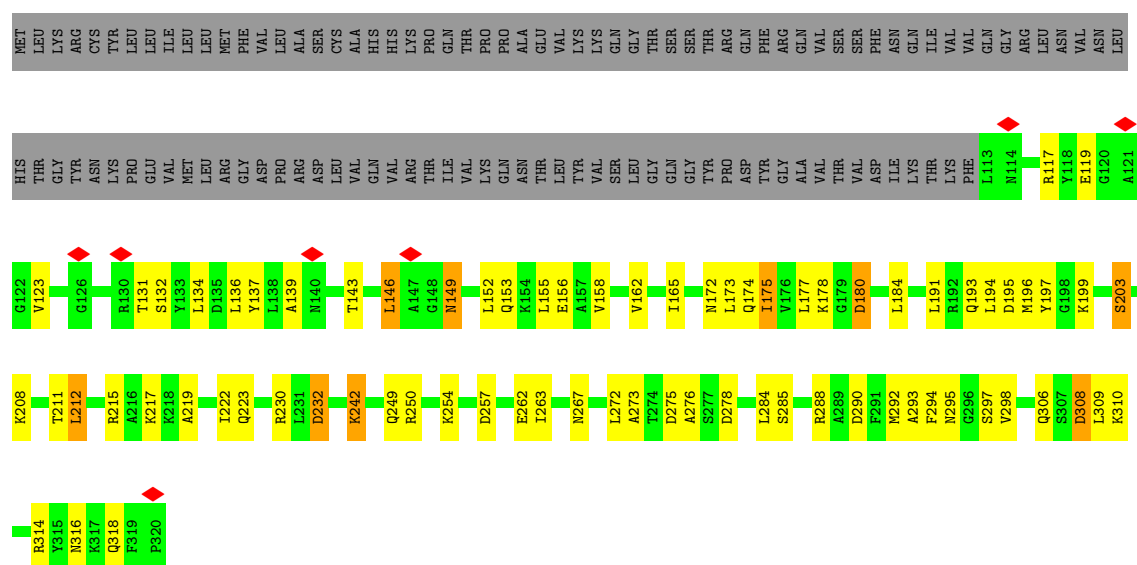


• Molecule 7: DUF2807 domain-containing protein

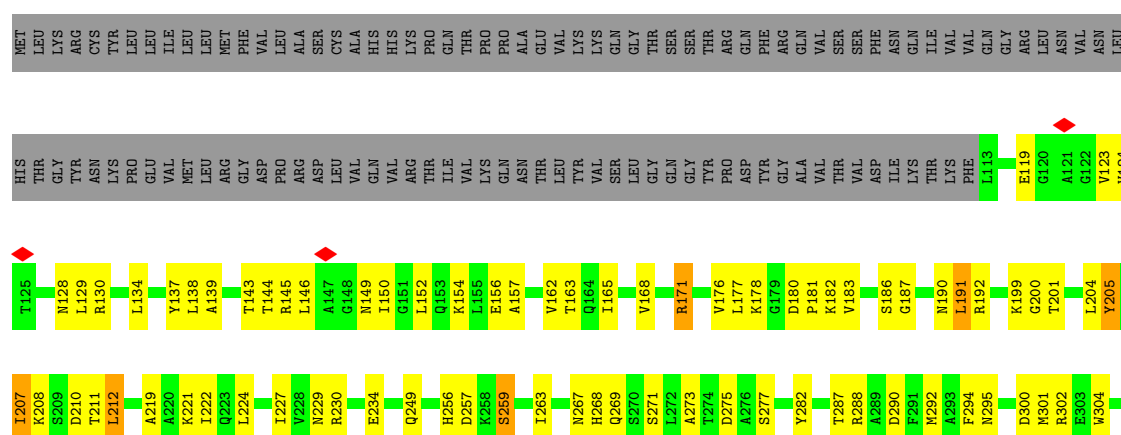


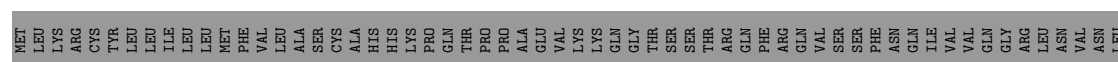


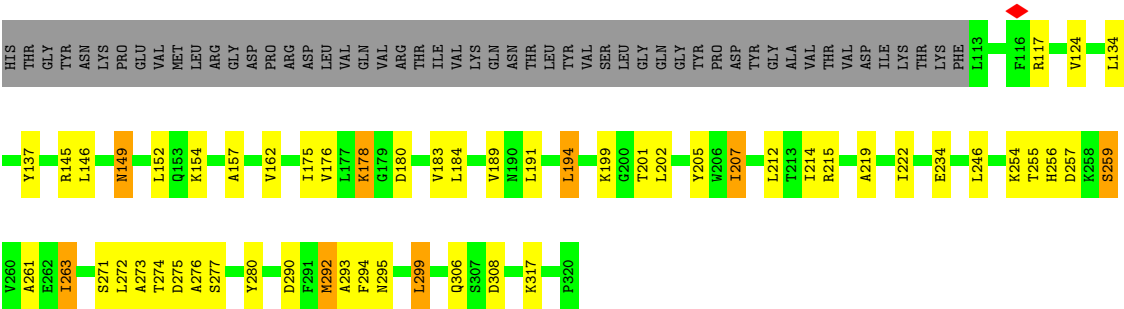
• Molecule 7: DUF2807 domain-containing protein



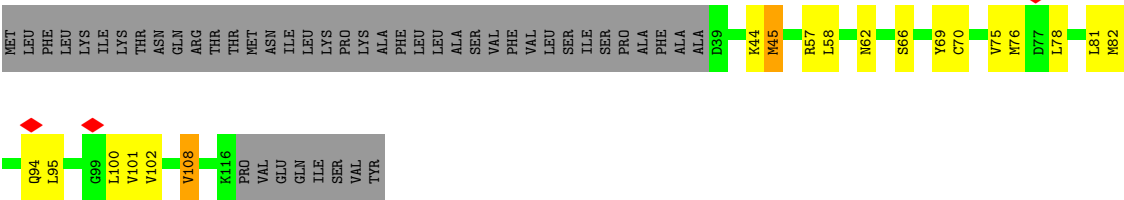
• Molecule 7: DUF2807 domain-containing protein



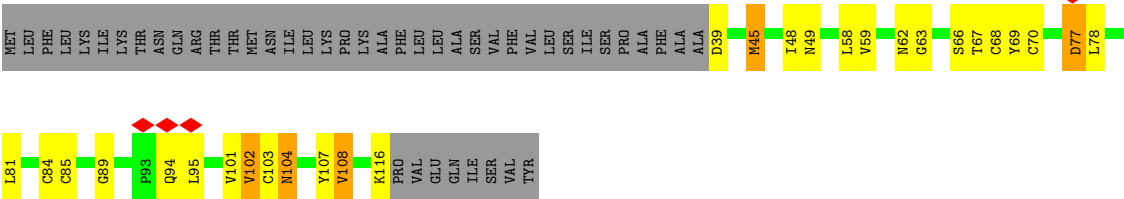




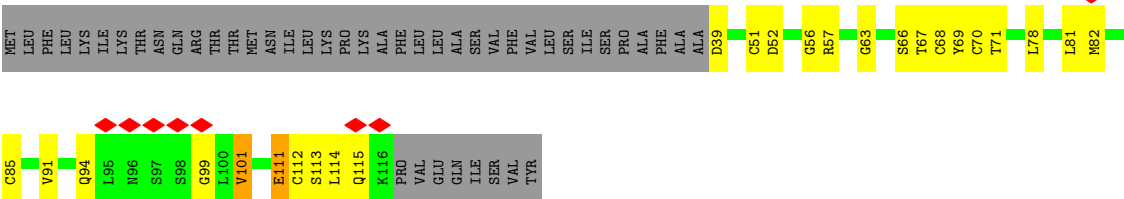
• Molecule 8: Neurogenic locus notch



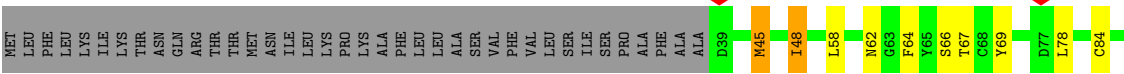
• Molecule 8: Neurogenic locus notch



• Molecule 8: Neurogenic locus notch

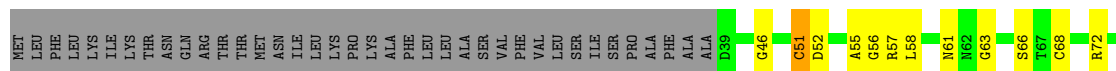


• Molecule 8: Neurogenic locus notch

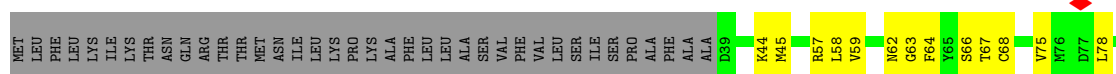




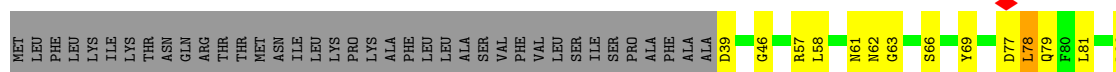
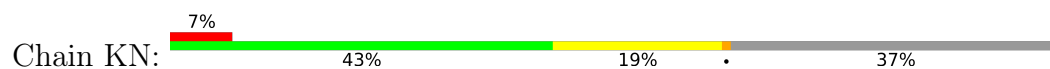
- Molecule 8: Neurogenic locus notch



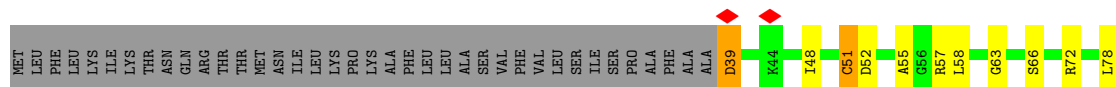
- Molecule 8: Neurogenic locus notch



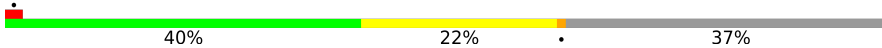
- Molecule 8: Neurogenic locus notch

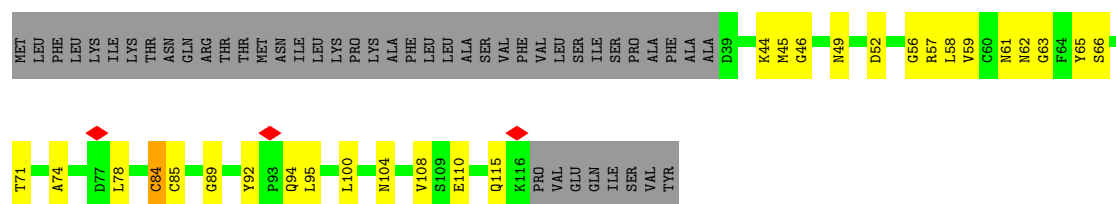


- Molecule 8: Neurogenic locus notch

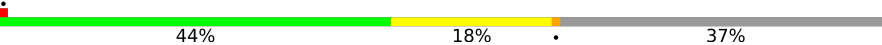


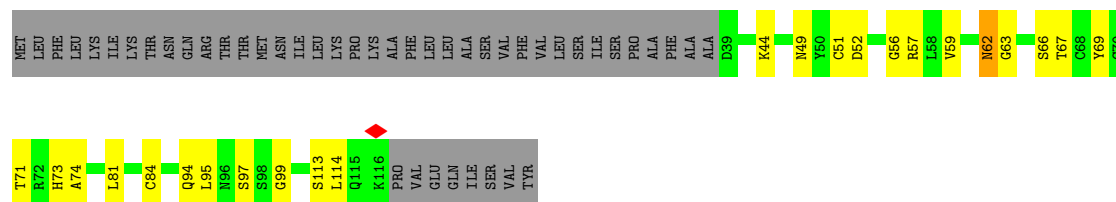
- Molecule 8: Neurogenic locus notch

Chain MN: 

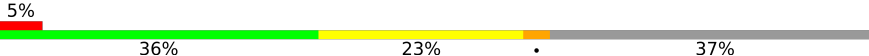


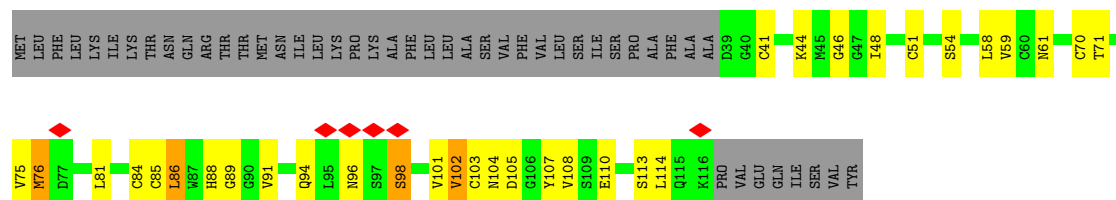
- Molecule 8: Neurogenic locus notch

Chain AN: 



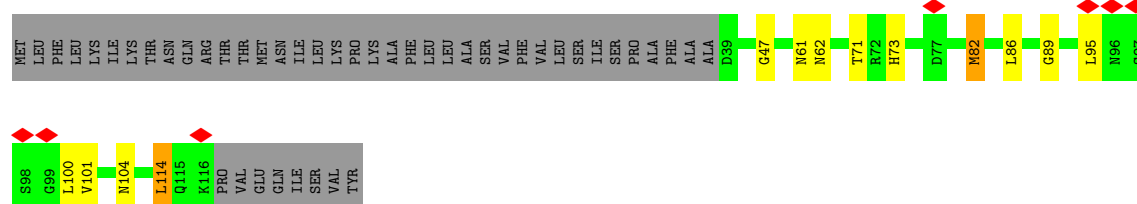
- Molecule 8: Neurogenic locus notch

Chain BN: 

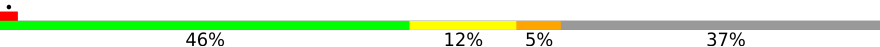


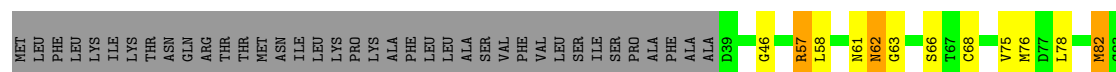
- Molecule 8: Neurogenic locus notch

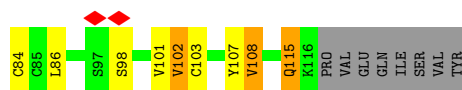
Chain CN: 



- Molecule 8: Neurogenic locus notch

Chain DN: 





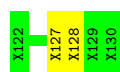
- Molecule 9: Unknown protein fragment

Chain EU: 89% 11%



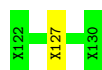
- Molecule 9: Unknown protein fragment

Chain FU: 78% 22%



- Molecule 9: Unknown protein fragment

Chain GU: 89% 11%



- Molecule 9: Unknown protein fragment

Chain HU: 100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain IU: 89% 11%



- Molecule 9: Unknown protein fragment

Chain JU: 78% 22%



- Molecule 9: Unknown protein fragment

Chain KU: 100%

There are no outlier residues recorded for this chain.

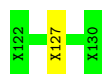
- Molecule 9: Unknown protein fragment

Chain LU:  100%

There are no outlier residues recorded for this chain.

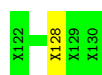
- Molecule 9: Unknown protein fragment

Chain MU:  89% 11%



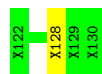
- Molecule 9: Unknown protein fragment

Chain AU:  89% 11%

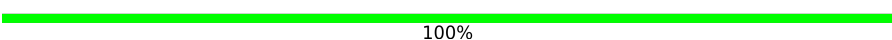


- Molecule 9: Unknown protein fragment

Chain BU:  89% 11%



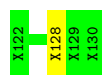
- Molecule 9: Unknown protein fragment

Chain CU:  100%

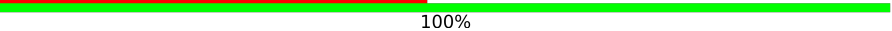
There are no outlier residues recorded for this chain.

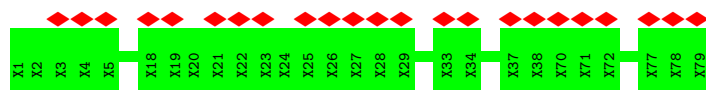
- Molecule 9: Unknown protein fragment

Chain DU:  89% 11%

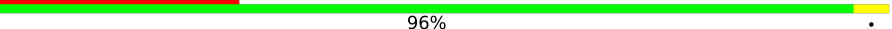


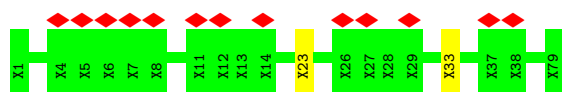
- Molecule 10: Unknown protein fragment

Chain EX:  48%  100%

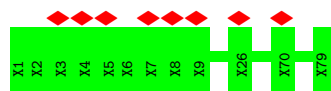


- Molecule 10: Unknown protein fragment

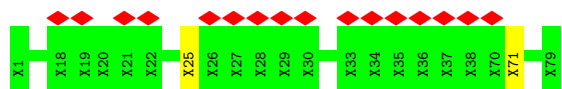
Chain FX:  27%  96%



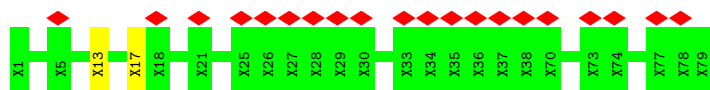
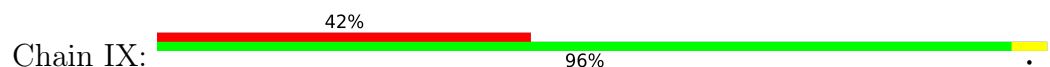
- Molecule 10: Unknown protein fragment



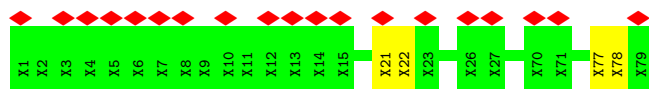
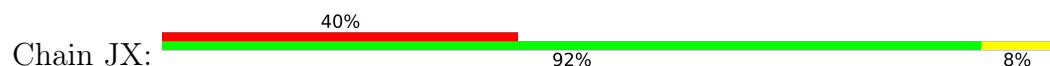
- Molecule 10: Unknown protein fragment



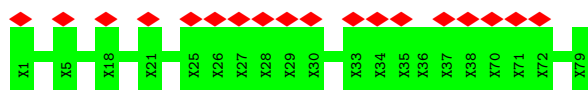
- Molecule 10: Unknown protein fragment



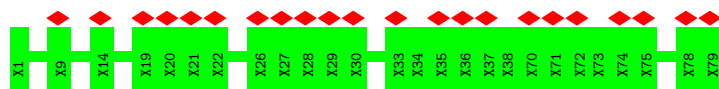
- Molecule 10: Unknown protein fragment



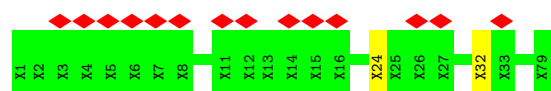
- Molecule 10: Unknown protein fragment



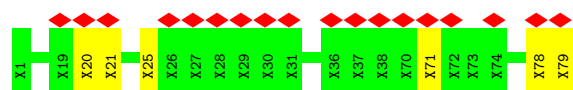
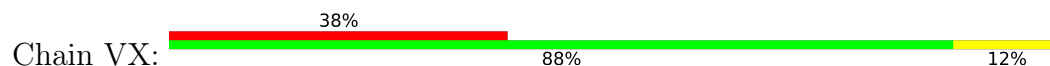
- Molecule 10: Unknown protein fragment



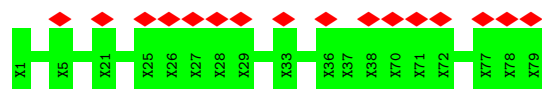
- Molecule 10: Unknown protein fragment



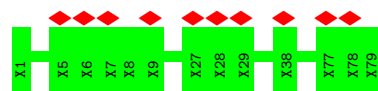
- Molecule 10: Unknown protein fragment



- Molecule 10: Unknown protein fragment



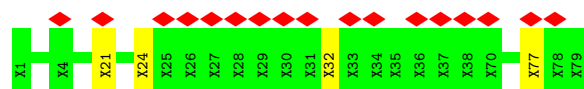
- Molecule 10: Unknown protein fragment



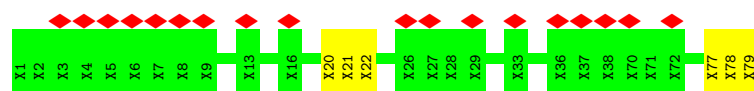
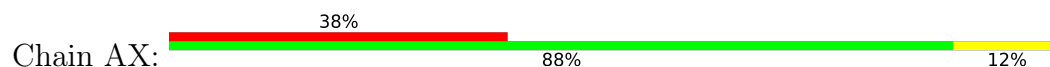
- Molecule 10: Unknown protein fragment



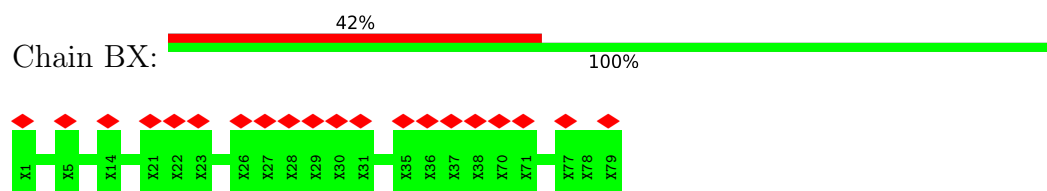
- Molecule 10: Unknown protein fragment



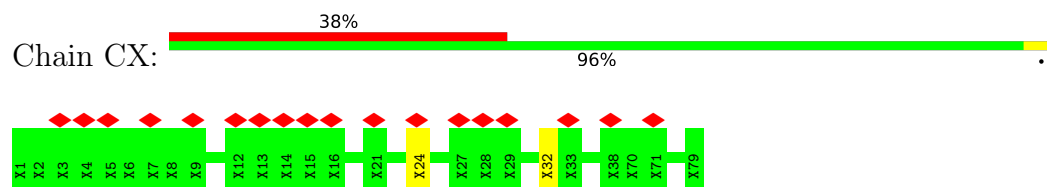
- Molecule 10: Unknown protein fragment



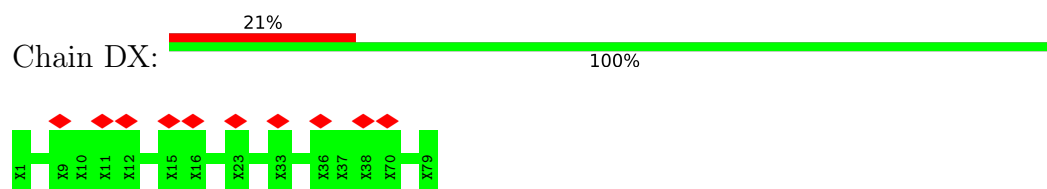
- Molecule 10: Unknown protein fragment



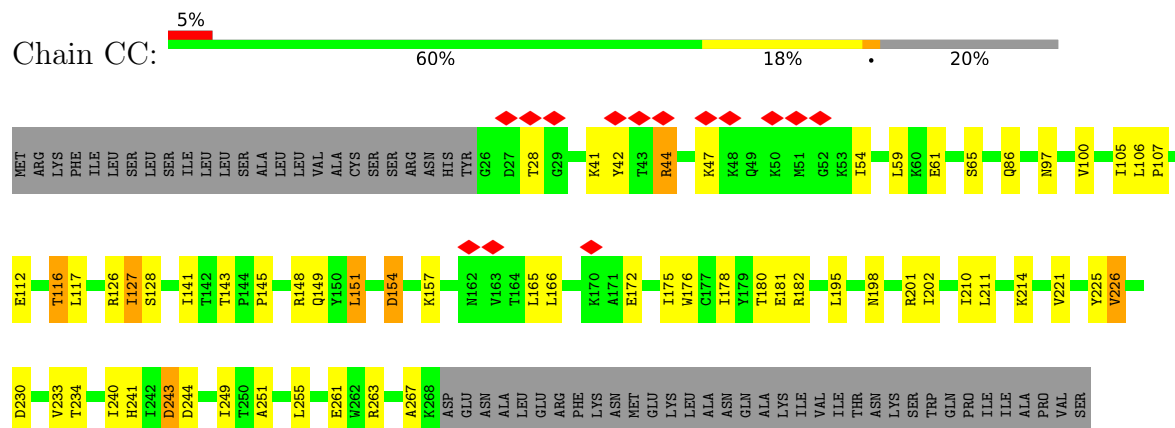
- Molecule 10: Unknown protein fragment



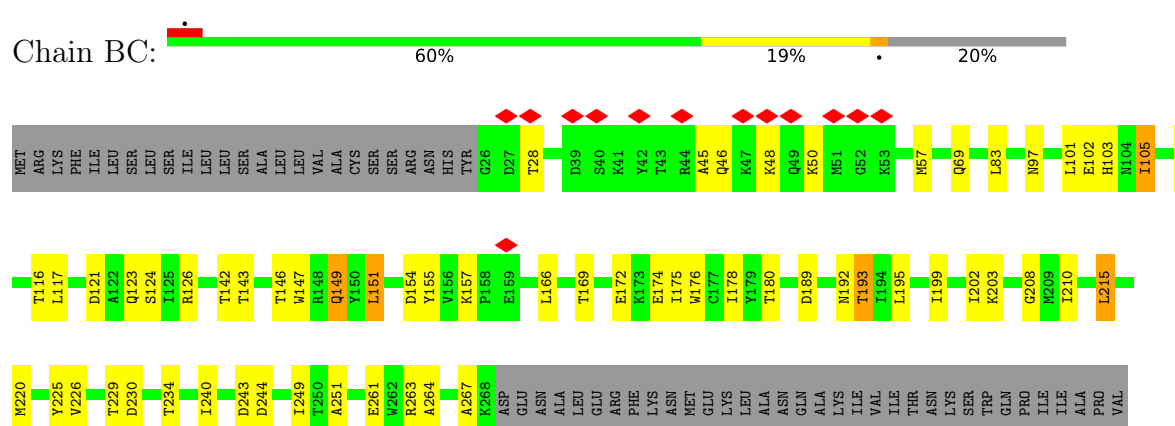
- Molecule 10: Unknown protein fragment



- Molecule 11: DotC

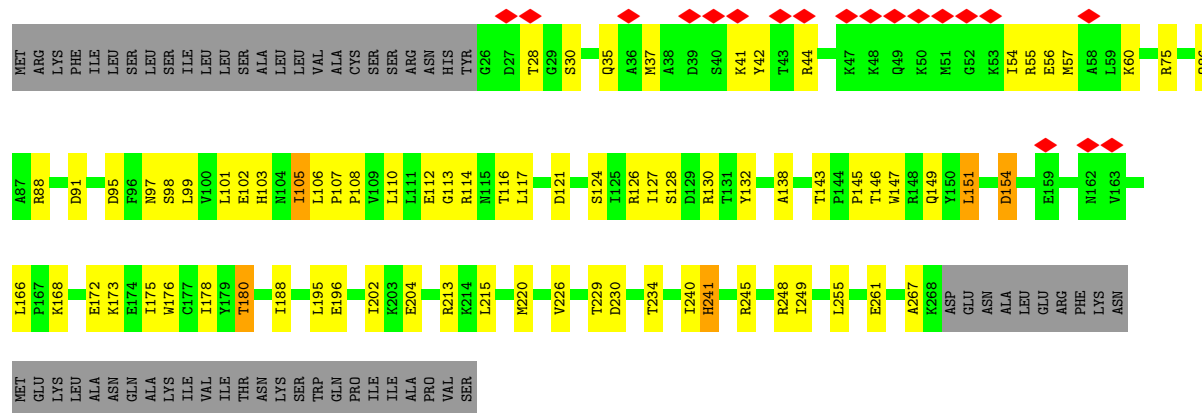


- Molecule 11: DotC

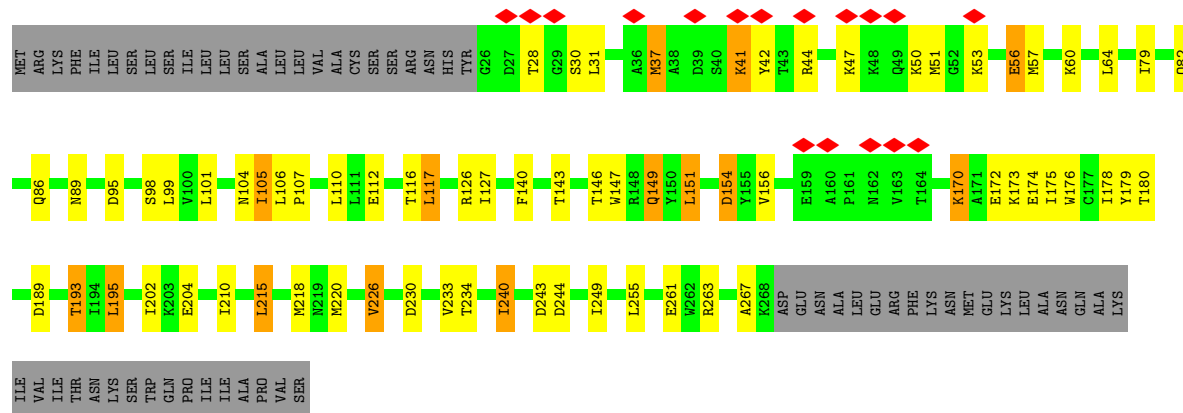


SER

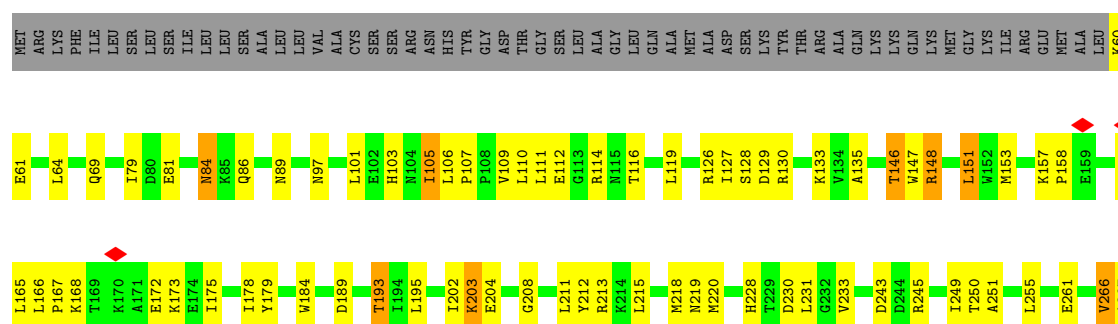
• Molecule 11: DotC



• Molecule 11: DotC



• Molecule 11: DotC



K268
ASP
GLU
ASN
ALA
LEU
GLU
ARG
PHE
LYS
ASN
MET
GLU
LYS
LEU
ALA
ASN
GLN
ALA
LYS
ILE
VAL
ILE
THR
ASN
LYS
SER
TRP
GLN
PRO
ILE
ILE
ALA
PRO
VAL
SER

• Molecule 11: DotC



MET	ARG	LYS	PHE	VAL	ILE	LEU	SER	LEU	SER	LEU	ILE	LEU	ASN	MET	GLU	LYS	ALA	LEU	VAL	ALA	GLN	ASN	LYS	GLN	ALA	VAL	SER	K61
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Q70	W75	I80	K86	R89	D92	L100	E103	H104	N105	I106	L107	P108	SER	T117	L118	D122	S125	V247	I126	R127	I128	T147	W148	R149	L152	D155	K158	P159	E160	A161	V164	L167	P168	K169	E173	K174	E175	I176	W177	C178	I179	W185
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D190	N199	R202	T203	K204	E205	R214	K215	L216	M221	V222	Y226	V227	S228	H229	T230	D231	I241	R246	V247	L248	A252	L256	N257	V258	N259	E262	A266	V267	A268	K269	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	LYS	ASN	MET	GLU	LYS	LEU	ALA	ASN	GLN
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ALA	LYS	ILE	VAL	ILE	THR	ASN	LYS	TRP	PRO	PRO	ILE	ALA	PRO	VAL	SER
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• Molecule 11: DotC



MET	ARG	LYS	PHE	ILE	LEU	SER	LEU	ILE	LEU	LEU	SER	ALA	LEU	VAL	ALA	CYS	SER	SER	ARG	ASN	HIS	T266	D27	T28	G29	S30	L31	L34	Q35	A36	K37	A38	D39	S40	R44	K47	K48	Q49	K50	M51	G52	K53	F54	R55	E56	I93	N97	L101	E102	H103
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N104	I105	L106	P107	V109	L110	L111	E112	G113	R114	N115	T116	L119	I125	R126	R130	T142	T143	T146	W147	Y150	L151	W152	M153	E159	V163	T169	E172	K173	E174	I175	W176	T180	W184	D189	T193	I194	L195	N198	I199	I202	G208
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Y212	R213	N221	Y225	V226	D230	L231	G232	V233	T234	E239	I240	H241	I242	D243	D244	R245	L255	R263	A267	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	LYS	ASN	MET	GLU	LYS	LEU	ALA	ASN	GLN	ALA	LYS	ILE	VAL	ILE	THR	ASN	LYS	TRP	GLN	PRO	ILE
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ILE	ALA	PRO	VAL	SER
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• Molecule 11: DotC



MET	ARG	LYS	PHE	LEU	SER	LEU	ILE	LEU	LEU	SER	ALA	LEU	VAL	ALA	CYS	SER	SER	ARG	ASN	HIS	TYR	GLY	ASP	THR	GLY	LEU	ALA	GLY	LEU	GLN	ALA	MET	ALA	ASP	SER	LYS	TYR	THR	ARG	ALA	GLN	LYS	GLN	LYS	MET	GLY	LYS	ILE	ALA	ARG	GLU	MET	ALA	LEU	PRO	K60
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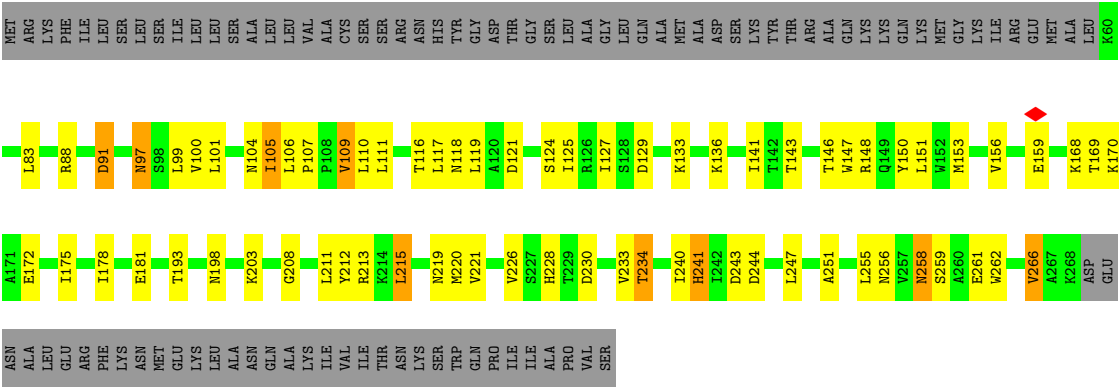
L64	Q86	A87	R88	N89	L90	D91	N97	S98	L99	I105	V109	L110	L111	M115	T116	L117	N118	L119	Q123	R126	I127	K133	H139	F140	T143	W147	L151	D154	K157	P158	E159	A160	P161	N162	V163	L166	P167	K168	T169	K170	A171	E172
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K173	E174	I175	I178	R182	K185	L195	E196	I202	G208	Y212	R213	K214	L215	M220	Y225	V226	V233	H241	T242	D243	R245	I249	T250	A251	L255	N256	E261	Y262	R263	A264	A265	V266	A267	K268	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	T169	LYS	ASN
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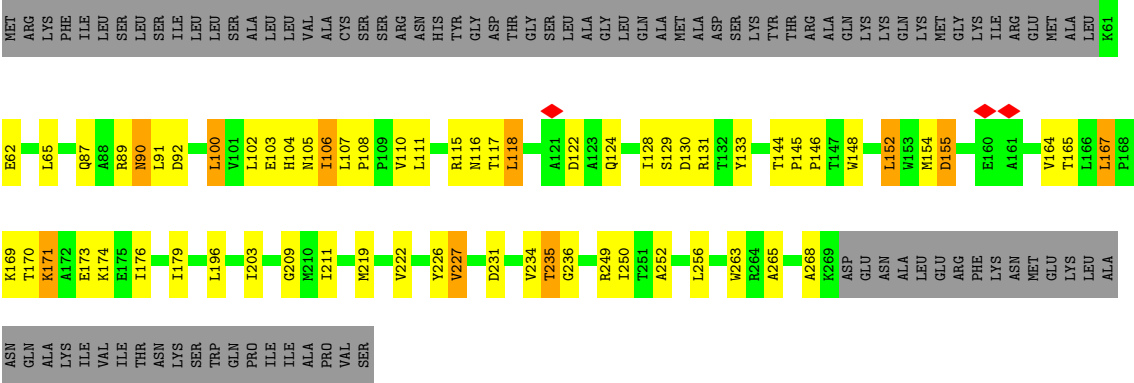
MET	GLU	LYS	LEU	ALA	ASN	GLN	ALA	LYS	THR	ASN	LYS	SER	TRP	GLN	PRO	ILE	ILE	ALA	PRO	VAL	SER
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[illegible][illegible][illegible]

WORLD WIDE
PDB
PROTEIN DATA BANK



● Molecule 11: DotC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41057	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	7.797	Depositor
Minimum map value	-2.782	Depositor
Average map value	0.094	Depositor
Map value standard deviation	0.545	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	0.22	0/1250	0.53	0/1699
1	Ag	0.16	0/278	0.36	0/377
1	BG	0.23	0/1250	0.57	1/1699 (0.1%)
1	Bg	0.16	0/278	0.35	0/377
1	CG	0.22	0/1250	0.54	0/1699
1	Cg	0.16	0/278	0.40	0/377
1	DG	0.21	0/1250	0.55	1/1699 (0.1%)
1	Dg	0.17	0/278	0.34	0/377
1	EG	0.21	0/1250	0.53	0/1699
1	Eg	0.17	0/278	0.36	0/377
1	FG	0.22	0/1250	0.54	0/1699
1	Fg	0.17	0/278	0.38	0/377
1	GG	0.22	0/1250	0.57	1/1699 (0.1%)
1	Gg	0.17	0/278	0.32	0/377
1	HG	0.22	0/1250	0.54	0/1699
1	Hg	0.16	0/278	0.33	0/377
1	IG	0.22	0/1250	0.53	0/1699
1	Ig	0.16	0/278	0.39	0/377
1	JG	0.22	0/1250	0.57	1/1699 (0.1%)
1	Jg	0.17	0/278	0.36	0/377
1	KG	0.22	0/1250	0.54	0/1699
1	Kg	0.16	0/278	0.35	0/377
1	LG	0.22	0/1250	0.55	0/1699
1	Lg	0.16	0/278	0.36	0/377
1	MG	0.21	0/1250	0.53	0/1699
1	Mg	0.17	0/278	0.36	0/377
1	NG	0.22	0/1250	0.53	0/1699
1	OG	0.21	0/1250	0.54	0/1699
1	PG	0.22	0/1250	0.53	0/1699
1	VG	0.20	0/278	0.53	0/377
1	WG	0.17	0/278	0.47	0/377
1	XG	0.18	0/278	0.45	0/377
1	YG	0.19	0/278	0.44	0/377
1	ZG	0.20	0/278	0.47	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AD	0.21	0/1107	0.47	0/1502
2	Ad	0.19	0/1078	0.38	0/1463
2	BD	0.22	0/1107	0.49	0/1502
2	Bd	0.18	0/1078	0.36	0/1463
2	CD	0.20	0/1107	0.46	0/1502
2	Cd	0.19	0/1078	0.42	0/1463
2	DD	0.21	0/1107	0.46	0/1502
2	Dd	0.20	0/1078	0.38	0/1463
2	ED	0.23	0/1107	0.53	0/1502
2	Ed	0.20	0/1078	0.41	0/1463
2	FD	0.22	0/1107	0.48	0/1502
2	Fd	0.18	0/1078	0.40	0/1463
2	GD	0.21	0/1107	0.48	0/1502
2	Gd	0.19	0/1078	0.43	0/1463
2	HD	0.20	0/1107	0.47	0/1502
2	Hd	0.19	0/1078	0.40	0/1463
2	ID	0.22	0/1107	0.50	0/1502
2	Id	0.18	0/1078	0.41	0/1463
2	JD	0.21	0/1107	0.48	0/1502
2	Jd	0.18	0/1078	0.38	0/1463
2	KD	0.21	0/1107	0.47	0/1502
2	Kd	0.19	0/1078	0.40	0/1463
2	LD	0.21	0/1107	0.48	0/1502
2	Ld	0.19	0/1078	0.42	0/1463
2	MD	0.21	0/1107	0.52	0/1502
2	Md	0.19	0/1078	0.39	0/1463
3	AF	0.17	0/490	0.36	0/660
3	Af	0.16	0/456	0.39	0/615
3	BF	0.16	0/490	0.34	0/660
3	Bf	0.16	0/456	0.41	0/615
3	CF	0.14	0/490	0.33	0/660
3	Cf	0.16	0/456	0.36	0/615
3	DF	0.15	0/490	0.35	0/660
3	Df	0.16	0/456	0.36	0/615
3	EF	0.15	0/490	0.35	0/660
3	Ef	0.15	0/456	0.31	0/615
3	FF	0.16	0/490	0.34	0/660
3	Ff	0.16	0/456	0.31	0/615
3	GF	0.15	0/490	0.35	0/660
3	Gf	0.15	0/456	0.37	0/615
3	HF	0.15	0/490	0.35	0/660
3	Hf	0.16	0/456	0.34	0/615
3	IF	0.14	0/490	0.34	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	If	0.15	0/456	0.35	0/615
3	JF	0.13	0/490	0.32	0/660
3	Jf	0.15	0/456	0.33	0/615
3	KF	0.16	0/490	0.40	0/660
3	Kf	0.15	0/456	0.33	0/615
3	LF	0.15	0/490	0.34	0/660
3	Lf	0.16	0/456	0.33	0/615
3	MF	0.16	0/490	0.32	0/660
3	Mf	0.16	0/456	0.31	0/615
3	VF	0.18	0/490	0.41	0/660
3	WF	0.18	0/490	0.40	0/660
3	XF	0.15	0/490	0.34	0/660
3	YF	0.14	0/490	0.35	0/660
3	ZF	0.16	0/490	0.32	0/660
4	AH	0.18	0/2033	0.40	0/2775
4	BH	0.19	0/2033	0.39	0/2775
4	CH	0.19	0/2033	0.38	0/2775
4	DH	0.18	0/2033	0.38	0/2775
4	EH	0.18	0/2033	0.39	0/2775
4	FH	0.18	0/2033	0.38	0/2775
4	GH	0.19	0/2033	0.41	0/2775
4	HH	0.19	0/2033	0.40	0/2775
4	IH	0.19	0/2033	0.41	0/2775
4	JH	0.18	0/2033	0.38	0/2775
4	KH	0.19	0/2033	0.39	0/2775
4	LH	0.20	0/2033	0.42	0/2775
4	MH	0.19	0/2033	0.40	0/2775
4	VH	0.16	0/1921	0.37	0/2620
4	WH	0.16	0/1921	0.41	0/2620
4	XH	0.17	0/1921	0.39	0/2620
4	YH	0.16	0/1921	0.38	0/2620
4	ZH	0.16	0/1921	0.39	0/2620
5	AK	0.20	0/1195	0.41	0/1616
5	BK	0.22	0/1195	0.43	0/1616
5	CK	0.20	0/1195	0.39	0/1616
5	DK	0.21	0/1195	0.42	0/1616
5	EK	0.20	0/1195	0.40	0/1616
5	FK	0.20	0/1195	0.40	0/1616
5	GK	0.21	0/1195	0.39	0/1616
5	HK	0.23	0/1195	0.41	0/1616
5	IK	0.20	0/1195	0.39	0/1616
5	JK	0.20	0/1195	0.38	0/1616
5	KK	0.21	0/1195	0.41	0/1616

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	LK	0.21	0/1195	0.42	0/1616
5	MK	0.20	0/1195	0.40	0/1616
6	AL	0.19	0/1417	0.43	0/1912
6	BL	0.21	0/1417	0.45	0/1912
6	CL	0.20	0/1417	0.43	0/1912
6	DL	0.21	0/1417	0.43	0/1912
6	EL	0.21	0/1417	0.43	0/1912
6	FL	0.20	0/1417	0.46	0/1912
6	GL	0.20	0/1417	0.45	0/1912
6	HL	0.21	0/1417	0.44	0/1912
6	IL	0.19	0/1417	0.45	0/1912
6	JL	0.20	0/1417	0.43	0/1912
6	KL	0.20	0/1417	0.47	0/1912
6	LL	0.21	0/1417	0.42	0/1912
6	ML	0.21	0/1417	0.45	0/1912
7	AM	0.18	0/1678	0.42	0/2262
7	BM	0.19	0/1678	0.42	0/2262
7	CM	0.18	0/1678	0.42	0/2262
7	DM	0.18	0/1678	0.43	0/2262
7	EM	0.18	0/1678	0.40	0/2262
7	FM	0.18	0/1678	0.43	0/2262
7	GM	0.18	0/1678	0.41	0/2262
7	HM	0.19	0/1678	0.45	0/2262
7	IM	0.19	0/1678	0.43	0/2262
7	JM	0.19	0/1678	0.39	0/2262
7	KM	0.18	0/1678	0.43	0/2262
7	LM	0.18	0/1678	0.43	0/2262
7	MM	0.18	0/1678	0.41	0/2262
8	AN	0.20	0/593	0.44	0/799
8	BN	0.20	0/593	0.46	0/799
8	CN	0.19	0/593	0.37	0/799
8	DN	0.19	0/593	0.40	0/799
8	EN	0.20	0/593	0.40	0/799
8	FN	0.20	0/593	0.38	0/799
8	GN	0.19	0/593	0.41	0/799
8	HN	0.18	0/593	0.40	0/799
8	IN	0.18	0/593	0.38	0/799
8	JN	0.19	0/593	0.39	0/799
8	KN	0.19	0/593	0.36	0/799
8	LN	0.21	0/593	0.37	0/799
8	MN	0.20	0/593	0.39	0/799
11	AC	0.21	0/1702	0.41	0/2315
11	BC	0.20	0/1957	0.41	0/2651

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CC	0.20	0/1957	0.39	0/2651
11	DC	0.21	0/1702	0.43	0/2315
11	EC	0.22	0/1702	0.40	0/2315
11	FC	0.21	0/1957	0.39	0/2651
11	GC	0.20	0/1957	0.39	0/2651
11	HC	0.21	0/1702	0.39	0/2315
11	IC	0.21	0/1702	0.42	0/2315
11	JC	0.22	0/1702	0.40	0/2315
11	KC	0.20	0/1957	0.41	0/2651
11	LC	0.21	0/1702	0.45	0/2315
11	MC	0.21	0/1702	0.42	0/2315
All	All	0.20	0/191071	0.43	4/258997 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	JG	939	THR	N-CA-C	-6.04	106.24	113.97
1	BG	939	THR	N-CA-C	-5.96	106.99	114.56
1	DG	939	THR	N-CA-C	-5.72	107.30	114.56
1	GG	939	THR	N-CA-C	-5.56	107.15	114.04

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	34	0
1	Ag	276	0	263	9	0
1	BG	1229	0	1231	34	0
1	Bg	276	0	263	12	0
1	CG	1229	0	1231	34	0
1	Cg	276	0	263	11	0
1	DG	1229	0	1231	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Dg	276	0	263	8	0
1	EG	1229	0	1231	33	0
1	Eg	276	0	263	9	0
1	FG	1229	0	1231	38	0
1	Fg	276	0	263	9	0
1	GG	1229	0	1231	35	0
1	Gg	276	0	263	10	0
1	HG	1229	0	1231	35	0
1	Hg	276	0	263	7	0
1	IG	1229	0	1231	26	0
1	Ig	276	0	263	10	0
1	JG	1229	0	1231	33	0
1	Jg	276	0	263	9	0
1	KG	1229	0	1231	30	0
1	Kg	276	0	263	8	0
1	LG	1229	0	1231	23	0
1	Lg	276	0	263	6	0
1	MG	1229	0	1231	31	0
1	Mg	276	0	263	8	0
1	NG	1229	0	1231	28	0
1	OG	1229	0	1231	33	0
1	PG	1229	0	1231	26	0
1	VG	276	0	263	6	0
1	WG	276	0	263	7	0
1	XG	276	0	263	6	0
1	YG	276	0	263	10	0
1	ZG	276	0	263	7	0
2	AD	1086	0	1121	28	0
2	Ad	1058	0	1092	27	0
2	BD	1086	0	1121	26	0
2	Bd	1058	0	1092	17	0
2	CD	1086	0	1121	28	0
2	Cd	1058	0	1092	19	0
2	DD	1086	0	1121	25	0
2	Dd	1058	0	1092	21	0
2	ED	1086	0	1121	24	0
2	Ed	1058	0	1092	20	0
2	FD	1086	0	1121	25	0
2	Fd	1058	0	1092	23	0
2	GD	1086	0	1121	32	0
2	Gd	1058	0	1092	21	0
2	HD	1086	0	1121	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Hd	1058	0	1092	17	0
2	ID	1086	0	1121	30	0
2	Id	1058	0	1092	17	0
2	JD	1086	0	1121	33	0
2	Jd	1058	0	1092	18	0
2	KD	1086	0	1121	28	0
2	Kd	1058	0	1092	25	0
2	LD	1086	0	1121	30	0
2	Ld	1058	0	1092	31	0
2	MD	1086	0	1121	22	0
2	Md	1058	0	1092	22	0
3	AF	483	0	502	9	0
3	Af	449	0	474	13	0
3	BF	483	0	502	8	0
3	Bf	449	0	474	8	0
3	CF	483	0	502	8	0
3	Cf	449	0	474	12	0
3	DF	483	0	502	10	0
3	Df	449	0	474	10	0
3	EF	483	0	502	8	0
3	Ef	449	0	474	5	0
3	FF	483	0	502	18	0
3	Ff	449	0	474	15	0
3	GF	483	0	502	9	0
3	Gf	449	0	474	12	0
3	HF	483	0	502	9	0
3	Hf	449	0	474	8	0
3	IF	483	0	502	12	0
3	If	449	0	474	11	0
3	JF	483	0	502	10	0
3	Jf	449	0	474	9	0
3	KF	483	0	502	10	0
3	Kf	449	0	474	10	0
3	LF	483	0	502	15	0
3	Lf	449	0	474	13	0
3	MF	483	0	502	21	0
3	Mf	449	0	474	15	0
3	VF	483	0	502	15	0
3	WF	483	0	502	14	0
3	XF	483	0	502	13	0
3	YF	483	0	502	15	0
3	ZF	483	0	502	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AH	1983	0	2009	51	0
4	BH	1983	0	2009	41	0
4	CH	1983	0	2009	51	0
4	DH	1983	0	2009	41	0
4	EH	1983	0	2009	55	0
4	FH	1983	0	2009	34	0
4	GH	1983	0	2009	50	0
4	HH	1983	0	2009	45	0
4	IH	1983	0	2009	31	0
4	JH	1983	0	2009	40	0
4	KH	1983	0	2009	40	0
4	LH	1983	0	2009	55	0
4	MH	1983	0	2009	42	0
4	VH	1875	0	1900	50	0
4	WH	1875	0	1900	36	0
4	XH	1875	0	1900	35	0
4	YH	1875	0	1900	37	0
4	ZH	1875	0	1900	43	0
5	AK	1175	0	1221	28	0
5	BK	1175	0	1221	31	0
5	CK	1175	0	1221	32	0
5	DK	1175	0	1221	31	0
5	EK	1175	0	1221	28	0
5	FK	1175	0	1221	32	0
5	GK	1175	0	1221	25	0
5	HK	1175	0	1221	25	0
5	IK	1175	0	1221	27	0
5	JK	1175	0	1221	31	0
5	KK	1175	0	1221	23	0
5	LK	1175	0	1221	29	0
5	MK	1175	0	1221	24	0
6	AL	1388	0	1378	28	0
6	BL	1388	0	1378	34	0
6	CL	1388	0	1378	33	0
6	DL	1388	0	1378	28	0
6	EL	1388	0	1378	29	0
6	FL	1388	0	1378	30	0
6	GL	1388	0	1378	38	0
6	HL	1388	0	1378	32	0
6	IL	1388	0	1378	39	0
6	JL	1388	0	1378	31	0
6	KL	1388	0	1378	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	LL	1388	0	1378	34	0
6	ML	1388	0	1378	30	0
7	AM	1650	0	1658	43	0
7	BM	1650	0	1658	44	0
7	CM	1650	0	1658	48	0
7	DM	1650	0	1658	28	0
7	EM	1650	0	1658	33	0
7	FM	1650	0	1658	41	0
7	GM	1650	0	1658	51	0
7	HM	1650	0	1658	43	0
7	IM	1650	0	1658	51	0
7	JM	1650	0	1658	35	0
7	KM	1650	0	1658	42	0
7	LM	1650	0	1658	33	0
7	MM	1650	0	1658	46	0
8	AN	582	0	530	12	0
8	BN	582	0	530	19	0
8	CN	582	0	530	6	0
8	DN	582	0	530	11	0
8	EN	582	0	530	7	0
8	FN	582	0	530	16	0
8	GN	582	0	530	13	0
8	HN	582	0	530	6	0
8	IN	582	0	530	8	0
8	JN	582	0	530	19	0
8	KN	582	0	530	12	0
8	LN	582	0	530	13	0
8	MN	582	0	530	15	0
9	AU	45	0	12	1	0
9	BU	45	0	12	1	0
9	CU	45	0	13	0	0
9	DU	45	0	12	1	0
9	EU	45	0	12	1	0
9	FU	45	0	12	2	0
9	GU	45	0	12	1	0
9	HU	45	0	12	0	0
9	IU	45	0	12	1	0
9	JU	45	0	13	2	0
9	KU	45	0	12	0	0
9	LU	45	0	13	0	0
9	MU	45	0	12	1	0
10	AX	240	0	55	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	BX	240	0	56	0	0
10	CX	240	0	54	1	0
10	DX	240	0	56	0	0
10	EX	240	0	56	0	0
10	FX	240	0	57	1	0
10	GX	240	0	53	0	0
10	HX	240	0	56	1	0
10	IX	240	0	56	1	0
10	JX	240	0	56	2	0
10	KX	240	0	56	0	0
10	LX	240	0	53	0	0
10	MX	240	0	55	1	0
10	VX	240	0	58	3	0
10	WX	240	0	58	0	0
10	XX	240	0	55	0	0
10	YX	240	0	55	1	0
10	ZX	240	0	57	2	0
11	AC	1667	0	1682	41	0
11	BC	1921	0	1952	33	0
11	CC	1921	0	1952	33	0
11	DC	1667	0	1682	43	0
11	EC	1667	0	1682	38	0
11	FC	1921	0	1952	45	0
11	GC	1921	0	1952	50	0
11	HC	1667	0	1682	39	0
11	IC	1667	0	1682	43	0
11	JC	1667	0	1682	28	0
11	KC	1921	0	1952	39	0
11	LC	1667	0	1682	32	0
11	MC	1667	0	1682	41	0
All	All	192370	0	190622	3839	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 10.

The worst 5 of 3839 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)
6:DL:129:THR:O	6:DL:133:PHE:HB2	1.71	0.91
6:KL:129:THR:O	6:KL:133:PHE:HB2	1.73	0.89
6:BL:166:ALA:HA	6:BL:206:GLU:O	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:KL:166:ALA:HA	6:KL:206:GLU:O	1.76	0.85
6:JL:166:ALA:HA	6:JL:206:GLU:O	1.77	0.85

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%)	154 (96%)	7 (4%)	0	100	100
1	Ag	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	BG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	CG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Cg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	DG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Dg	32/1048 (3%)	32 (100%)	0	0	100	100
1	EG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Eg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	FG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Fg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	GG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Gg	32/1048 (3%)	32 (100%)	0	0	100	100
1	HG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Hg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	IG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Ig	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	JG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Jg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	KG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Kg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	LG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	Lg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	MG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
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%)	157 (98%)	4 (2%)	0	100	100
1	PG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	VG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	WG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	XG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	YG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AD	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
2	Ad	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
2	BD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Bd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	CD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Cd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	DD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Dd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ED	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Ed	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	FD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Fd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	GD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Gd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
2	HD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Hd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ID	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
2	Id	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	JD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
2	Jd	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
2	KD	138/163 (85%)	126 (91%)	12 (9%)	0	100	100
2	Kd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	LD	138/163 (85%)	134 (97%)	4 (3%)	0	100	100
2	Ld	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	MD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Md	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
3	AF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Af	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	BF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Bf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	CF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Cf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	DF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Df	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	EF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Ef	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	FF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Ff	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	GF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Gf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	HF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Hf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
3	IF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	If	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	JF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Jf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	KF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Kf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	LF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Lf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	MF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Mf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	VF	61/269 (23%)	61 (100%)	0	0	100	100
3	WF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	XF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	YF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	ZF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
4	AH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
4	BH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	CH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
4	DH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
4	EH	256/361 (71%)	248 (97%)	8 (3%)	0	100	100
4	FH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
4	GH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	HH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	IH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	JH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
4	KH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	LH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	MH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	VH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	WH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
4	XH	239/361 (66%)	232 (97%)	7 (3%)	0	100	100
4	YH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	ZH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	AK	149/189 (79%)	145 (97%)	4 (3%)	0	100	100
5	BK	149/189 (79%)	145 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	DK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	EK	149/189 (79%)	146 (98%)	3 (2%)	0	100	100
5	FK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	GK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	HK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	IK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	JK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	KK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	LK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	MK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
6	AL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
6	BL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	CL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	DL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	EL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	FL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	GL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	HL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	IL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	JL	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
6	KL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	LL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	AM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
7	BM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	CM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
7	DM	206/320 (64%)	196 (95%)	10 (5%)	0	100	100
7	EM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
7	FM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	GM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	HM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	JM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
7	KM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
7	LM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
7	MM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
8	AN	76/124 (61%)	66 (87%)	10 (13%)	0	100	100
8	BN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	CN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	DN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	EN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	FN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	GN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	HN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	IN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	JN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	KN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	LN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	MN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
11	AC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
11	BC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
11	CC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	DC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
11	EC	207/303 (68%)	202 (98%)	5 (2%)	0	100	100
11	FC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	GC	241/303 (80%)	234 (97%)	7 (3%)	0	100	100
11	HC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	IC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
11	JC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
11	KC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	LC	207/303 (68%)	190 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	MC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
All	All	23724/70112 (34%)	22457 (95%)	1267 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Ag	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	BG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Bg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	CG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Cg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	DG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Dg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	EG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Eg	31/765 (4%)	21 (68%)	10 (32%)	0	2
1	FG	135/765 (18%)	121 (90%)	14 (10%)	7	22
1	Fg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	GG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Gg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	HG	135/765 (18%)	118 (87%)	17 (13%)	4	17
1	Hg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	IG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Ig	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	JG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Jg	31/765 (4%)	24 (77%)	7 (23%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	KG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Kg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	LG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Lg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	MG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Mg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	NG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	OG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	PG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	VG	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	WG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	XG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	YG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	ZG	31/765 (4%)	27 (87%)	4 (13%)	4	17
2	AD	121/139 (87%)	104 (86%)	17 (14%)	3	15
2	Ad	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	BD	121/139 (87%)	112 (93%)	9 (7%)	13	33
2	Bd	118/139 (85%)	101 (86%)	17 (14%)	3	14
2	CD	121/139 (87%)	101 (84%)	20 (16%)	2	12
2	Cd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	DD	121/139 (87%)	111 (92%)	10 (8%)	10	30
2	Dd	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	ED	121/139 (87%)	112 (93%)	9 (7%)	13	33
2	Ed	118/139 (85%)	102 (86%)	16 (14%)	3	15
2	FD	121/139 (87%)	106 (88%)	15 (12%)	4	18
2	Fd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	GD	121/139 (87%)	109 (90%)	12 (10%)	7	24
2	Gd	118/139 (85%)	104 (88%)	14 (12%)	5	19
2	HD	121/139 (87%)	108 (89%)	13 (11%)	6	22
2	Hd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	ID	121/139 (87%)	112 (93%)	9 (7%)	13	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Id	118/139 (85%)	106 (90%)	12 (10%)	7	23
2	JD	121/139 (87%)	109 (90%)	12 (10%)	7	24
2	Jd	118/139 (85%)	108 (92%)	10 (8%)	10	29
2	KD	121/139 (87%)	110 (91%)	11 (9%)	9	28
2	Kd	118/139 (85%)	106 (90%)	12 (10%)	7	23
2	LD	121/139 (87%)	103 (85%)	18 (15%)	3	14
2	Ld	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	MD	121/139 (87%)	102 (84%)	19 (16%)	2	12
2	Md	118/139 (85%)	102 (86%)	16 (14%)	3	15
3	AF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Af	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	BF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Bf	49/237 (21%)	44 (90%)	5 (10%)	7	23
3	CF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Cf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	DF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Df	49/237 (21%)	42 (86%)	7 (14%)	3	14
3	EF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Ef	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	FF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Ff	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	GF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Gf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	HF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Hf	49/237 (21%)	45 (92%)	4 (8%)	10	31
3	IF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	If	49/237 (21%)	39 (80%)	10 (20%)	1	7
3	JF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Jf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	KF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Kf	49/237 (21%)	40 (82%)	9 (18%)	1	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	LF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Lf	49/237 (21%)	38 (78%)	11 (22%)	1	6
3	MF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Mf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	VF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	WF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	XF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	YF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	ZF	53/237 (22%)	47 (89%)	6 (11%)	5	20
4	AH	220/300 (73%)	191 (87%)	29 (13%)	4	16
4	BH	220/300 (73%)	201 (91%)	19 (9%)	10	29
4	CH	220/300 (73%)	194 (88%)	26 (12%)	5	19
4	DH	220/300 (73%)	189 (86%)	31 (14%)	3	15
4	EH	220/300 (73%)	185 (84%)	35 (16%)	2	12
4	FH	220/300 (73%)	196 (89%)	24 (11%)	6	21
4	GH	220/300 (73%)	197 (90%)	23 (10%)	6	22
4	HH	220/300 (73%)	193 (88%)	27 (12%)	4	18
4	IH	220/300 (73%)	194 (88%)	26 (12%)	5	19
4	JH	220/300 (73%)	192 (87%)	28 (13%)	4	17
4	KH	220/300 (73%)	200 (91%)	20 (9%)	9	28
4	LH	220/300 (73%)	198 (90%)	22 (10%)	7	24
4	MH	220/300 (73%)	193 (88%)	27 (12%)	4	18
4	VH	207/300 (69%)	180 (87%)	27 (13%)	4	16
4	WH	207/300 (69%)	176 (85%)	31 (15%)	3	13
4	XH	207/300 (69%)	185 (89%)	22 (11%)	6	22
4	YH	207/300 (69%)	181 (87%)	26 (13%)	4	17
4	ZH	207/300 (69%)	179 (86%)	28 (14%)	4	15
5	AK	129/163 (79%)	109 (84%)	20 (16%)	2	13
5	BK	129/163 (79%)	107 (83%)	22 (17%)	2	11
5	CK	129/163 (79%)	111 (86%)	18 (14%)	3	15
5	DK	129/163 (79%)	118 (92%)	11 (8%)	10	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	EK	129/163 (79%)	113 (88%)	16 (12%)	4	18
5	FK	129/163 (79%)	112 (87%)	17 (13%)	4	16
5	GK	129/163 (79%)	120 (93%)	9 (7%)	14	36
5	HK	129/163 (79%)	115 (89%)	14 (11%)	6	21
5	IK	129/163 (79%)	108 (84%)	21 (16%)	2	12
5	JK	129/163 (79%)	116 (90%)	13 (10%)	7	23
5	KK	129/163 (79%)	110 (85%)	19 (15%)	3	14
5	LK	129/163 (79%)	112 (87%)	17 (13%)	4	16
5	MK	129/163 (79%)	107 (83%)	22 (17%)	2	11
6	AL	148/203 (73%)	135 (91%)	13 (9%)	9	29
6	BL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	CL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	DL	148/203 (73%)	136 (92%)	12 (8%)	11	31
6	EL	148/203 (73%)	129 (87%)	19 (13%)	4	17
6	FL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	GL	148/203 (73%)	129 (87%)	19 (13%)	4	17
6	HL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	IL	148/203 (73%)	134 (90%)	14 (10%)	8	25
6	JL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	KL	148/203 (73%)	135 (91%)	13 (9%)	9	29
6	LL	148/203 (73%)	134 (90%)	14 (10%)	8	25
6	ML	148/203 (73%)	130 (88%)	18 (12%)	5	18
7	AM	175/276 (63%)	154 (88%)	21 (12%)	5	18
7	BM	175/276 (63%)	148 (85%)	27 (15%)	2	13
7	CM	175/276 (63%)	147 (84%)	28 (16%)	2	12
7	DM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	EM	175/276 (63%)	150 (86%)	25 (14%)	3	14
7	FM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	GM	175/276 (63%)	153 (87%)	22 (13%)	4	17
7	HM	175/276 (63%)	147 (84%)	28 (16%)	2	12
7	IM	175/276 (63%)	146 (83%)	29 (17%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	JM	175/276 (63%)	144 (82%)	31 (18%)	2	10
7	KM	175/276 (63%)	148 (85%)	27 (15%)	2	13
7	LM	175/276 (63%)	152 (87%)	23 (13%)	4	16
7	MM	175/276 (63%)	158 (90%)	17 (10%)	8	25
8	AN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	BN	66/107 (62%)	54 (82%)	12 (18%)	2	10
8	CN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	DN	66/107 (62%)	55 (83%)	11 (17%)	2	11
8	EN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	FN	66/107 (62%)	53 (80%)	13 (20%)	1	8
8	GN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	HN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	IN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	JN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	KN	66/107 (62%)	58 (88%)	8 (12%)	5	18
8	LN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	MN	66/107 (62%)	57 (86%)	9 (14%)	3	15
11	AC	178/257 (69%)	157 (88%)	21 (12%)	5	19
11	BC	203/257 (79%)	181 (89%)	22 (11%)	6	22
11	CC	203/257 (79%)	176 (87%)	27 (13%)	4	16
11	DC	178/257 (69%)	155 (87%)	23 (13%)	4	17
11	EC	178/257 (69%)	159 (89%)	19 (11%)	6	22
11	FC	203/257 (79%)	183 (90%)	20 (10%)	7	24
11	GC	203/257 (79%)	178 (88%)	25 (12%)	4	18
11	HC	178/257 (69%)	157 (88%)	21 (12%)	5	19
11	IC	178/257 (69%)	146 (82%)	32 (18%)	2	10
11	JC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	KC	203/257 (79%)	170 (84%)	33 (16%)	2	12
11	LC	178/257 (69%)	156 (88%)	22 (12%)	4	18
11	MC	178/257 (69%)	150 (84%)	28 (16%)	2	12
All	All	20484/55449 (37%)	17824 (87%)	2660 (13%)	6	16

5 of 2660 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	BD	85	VAL
8	CN	114	LEU
6	BL	93	LEU
2	BD	63	THR
11	IC	157	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 259 such sidechains are listed below:

Mol	Chain	Res	Type
1	IG	1043	GLN
1	OG	976	ASN
1	DG	1020	GLN
8	JN	61	ASN
11	AC	85	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

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

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	JX	38:UNK	C	70:UNK	N	25.78
1	WX	38:UNK	C	70:UNK	N	25.34
1	YX	38:UNK	C	70:UNK	N	25.23
1	XX	38:UNK	C	70:UNK	N	25.08
1	GX	38:UNK	C	70:UNK	N	24.81

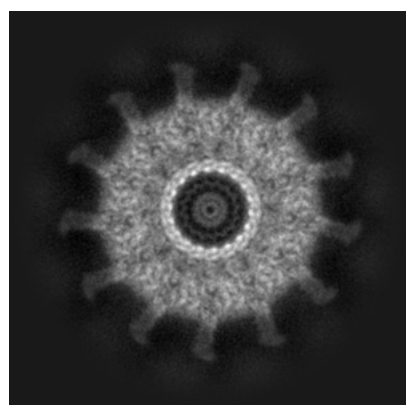
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24026. These allow visual inspection of the internal detail of the map and identification of artifacts.

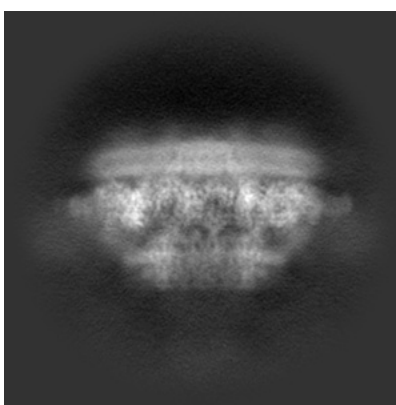
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

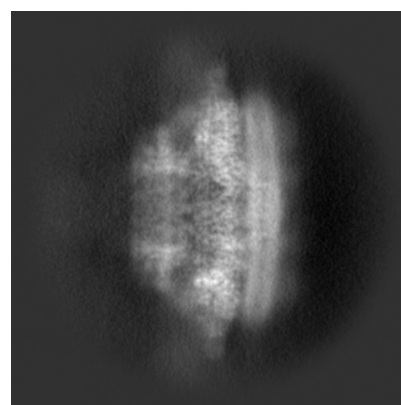
6.1.1 Primary map



X



Y

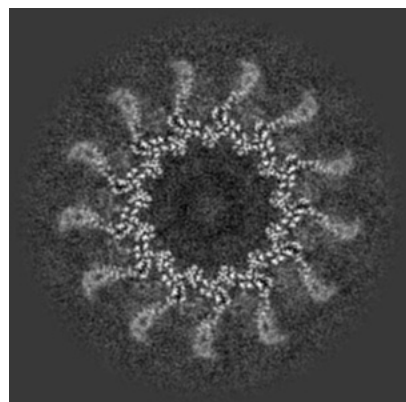


Z

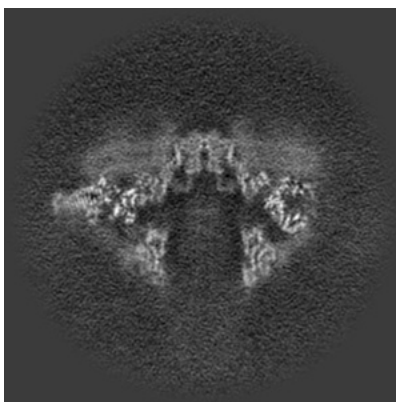
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

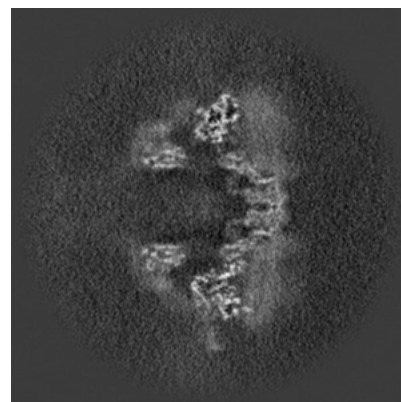
6.2.1 Primary map



X Index: 125



Y Index: 125

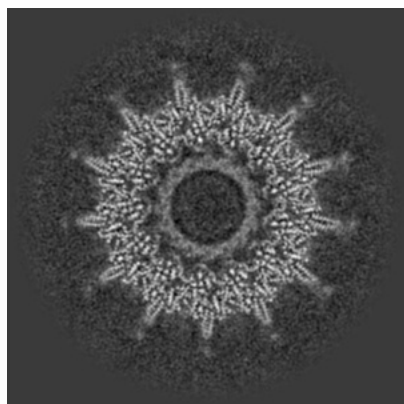


Z Index: 125

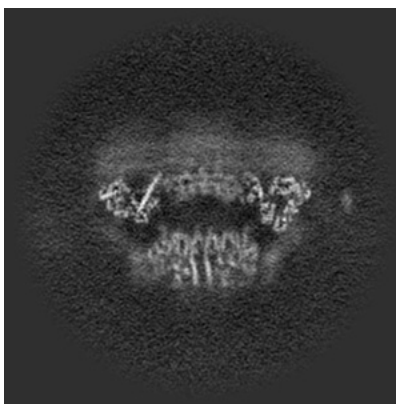
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

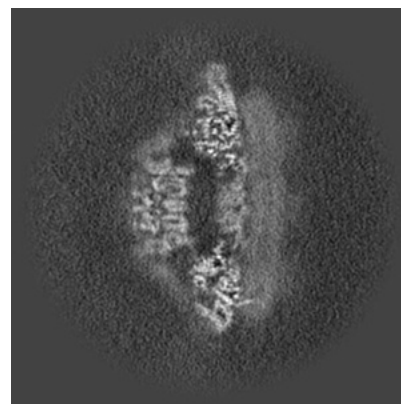
6.3.1 Primary map



X Index: 134



Y Index: 101

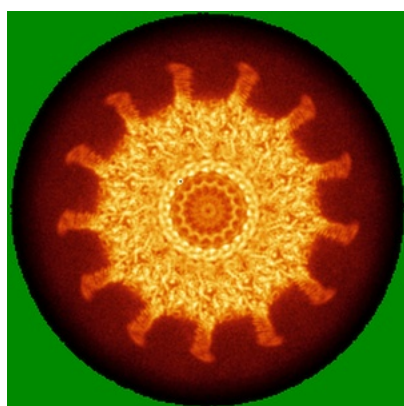


Z Index: 152

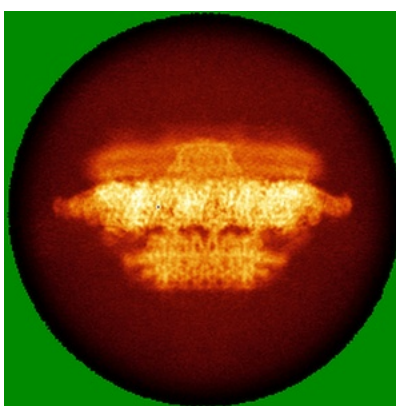
The images above show the largest variance slices of the map in three orthogonal directions.

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

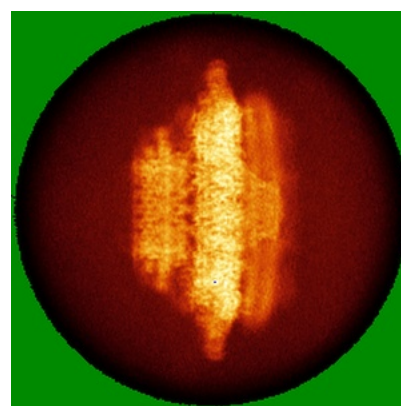
6.4.1 Primary map



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

This section was not generated.

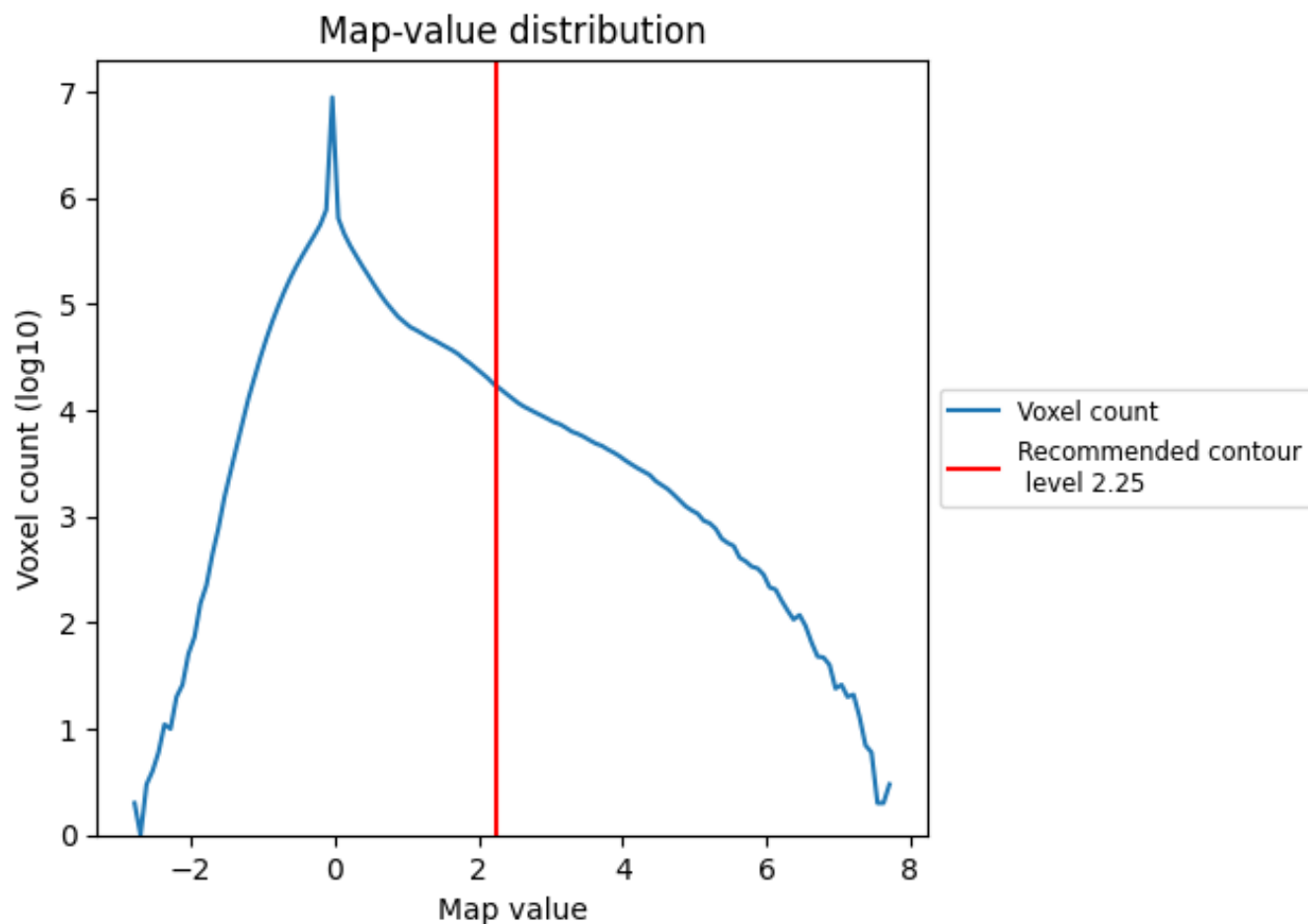
6.6 Mask visualisation

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

7 Map analysis [i](#)

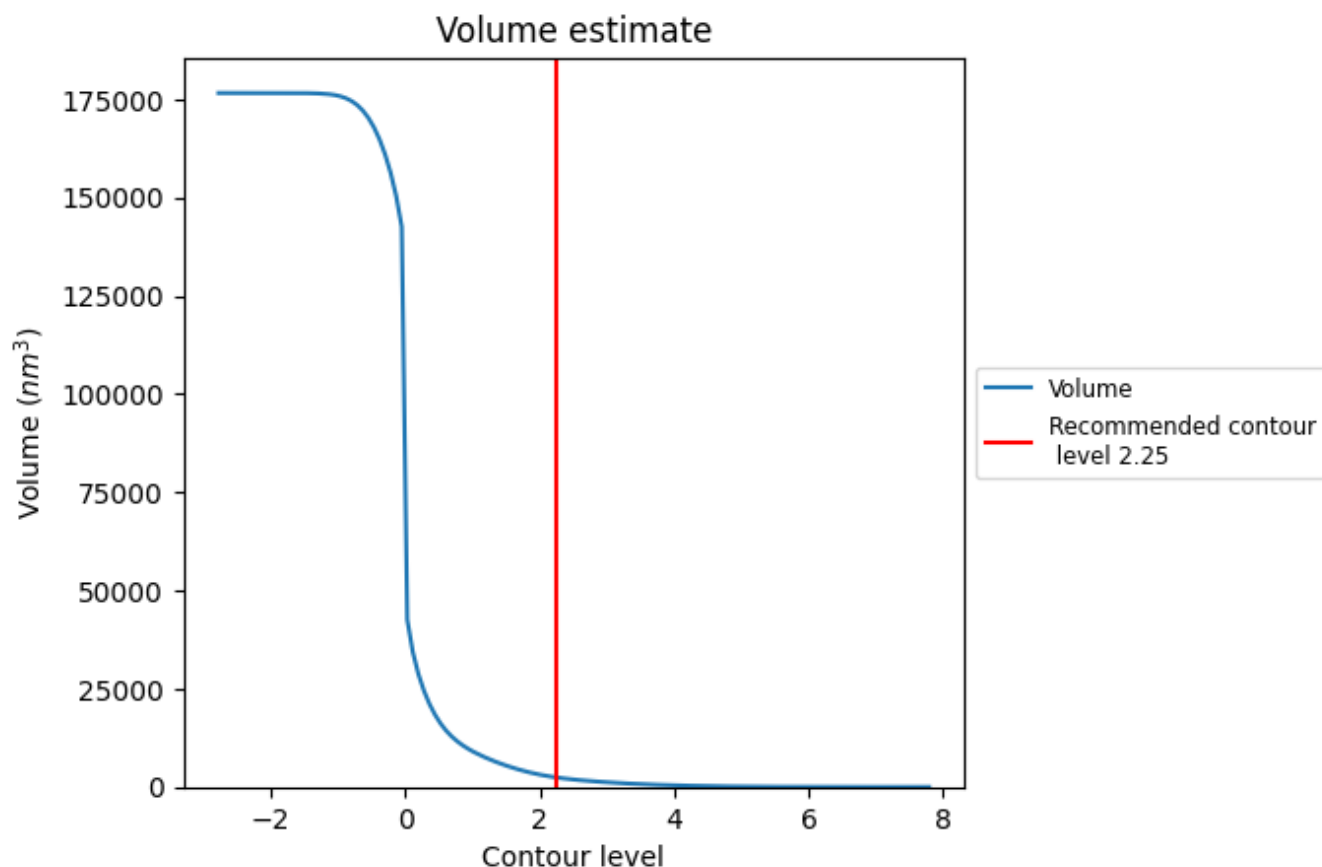
This section contains the results of statistical analysis of the map.

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.

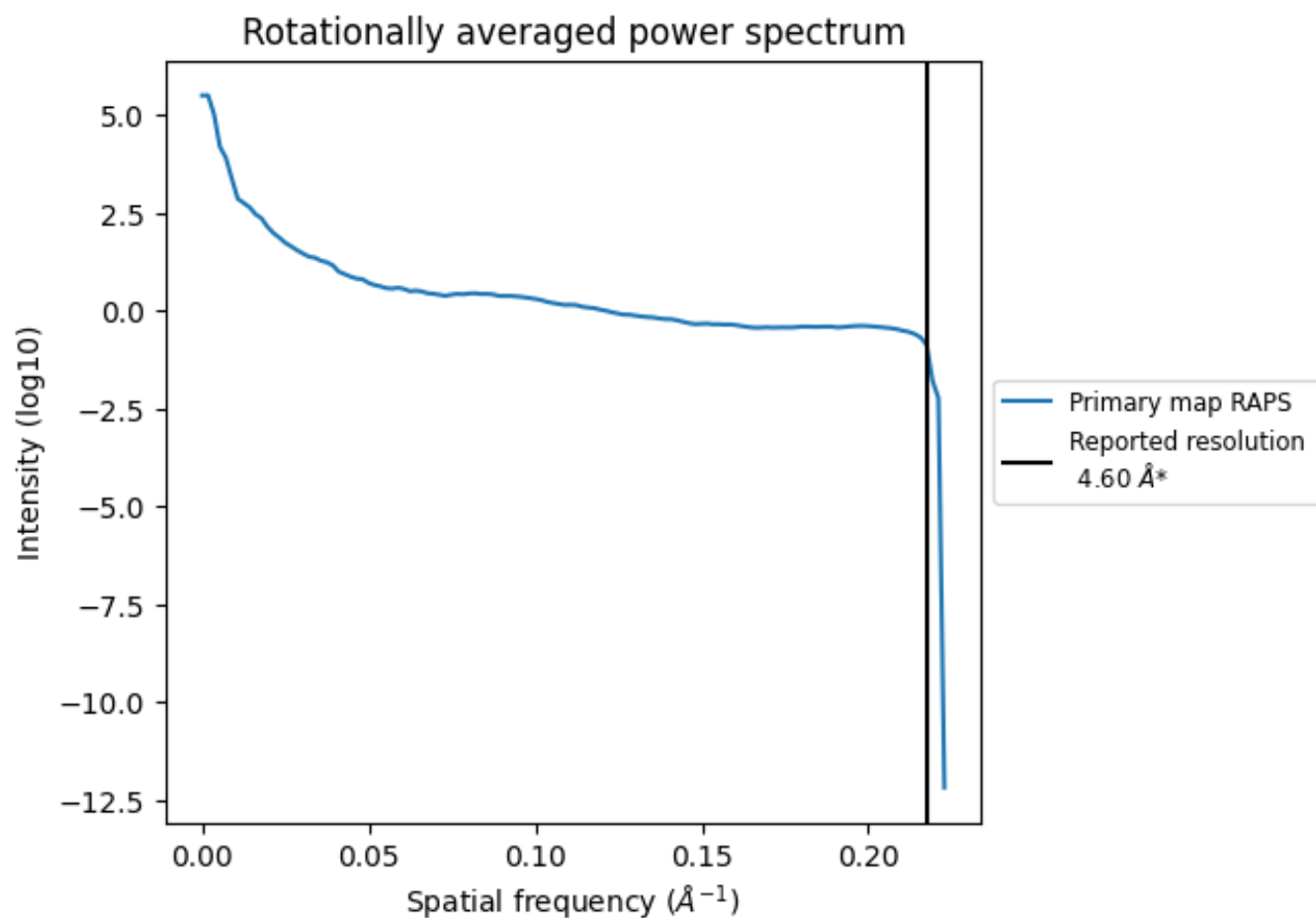
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2412 nm^3 ; this corresponds to an approximate mass of 2179 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

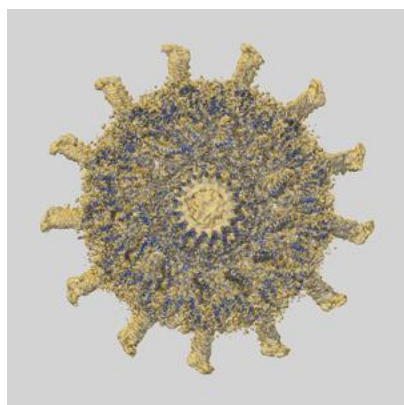
8 Fourier-Shell correlation ⓘ

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

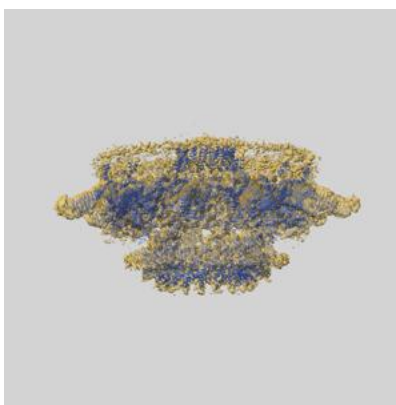
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24026 and PDB model 7MUY. Per-residue inclusion information can be found in section [3](#) on page [23](#).

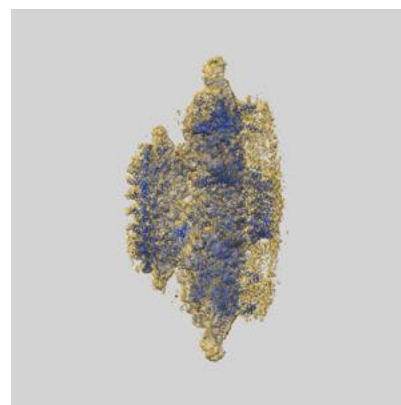
9.1 Map-model overlay [i](#)



X



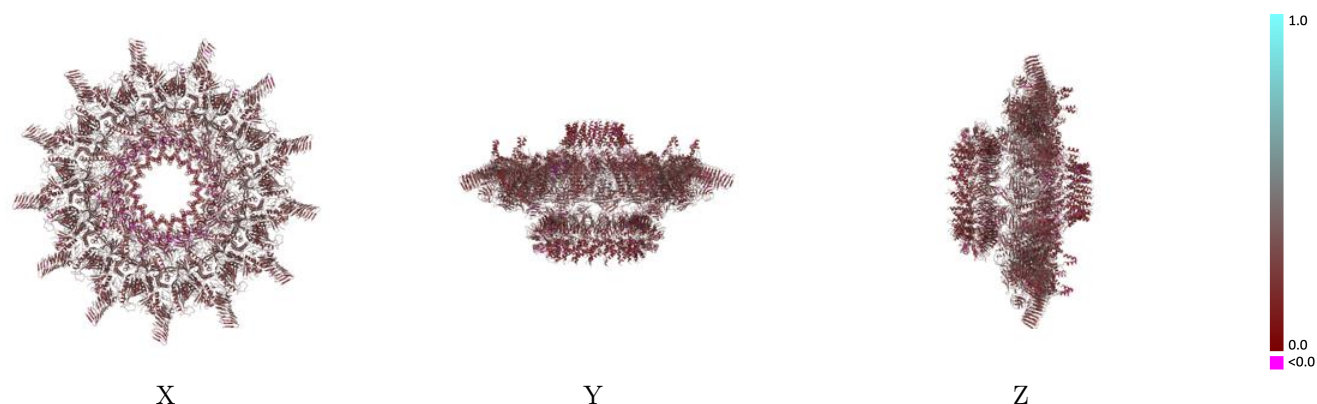
Y



Z

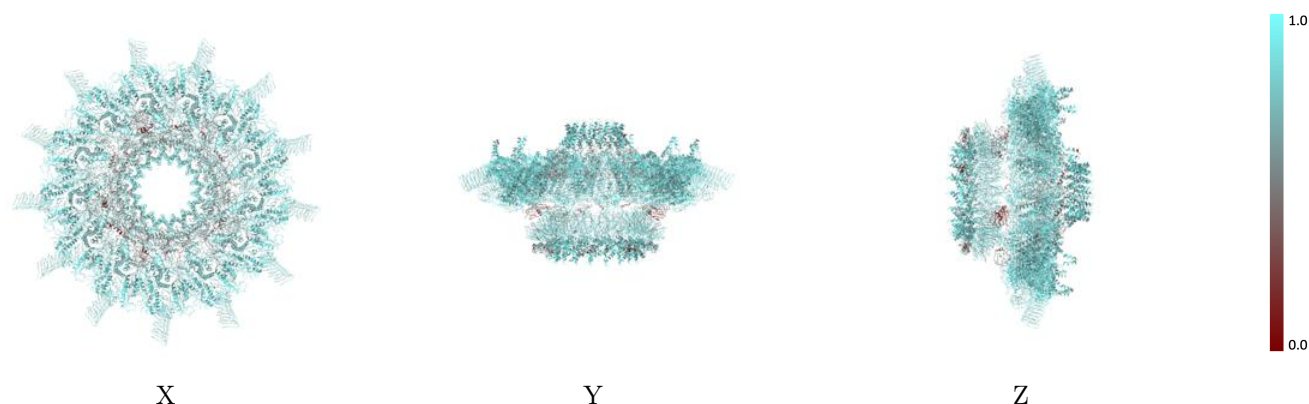
The images above show the 3D surface view of the map at the recommended contour level 2.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



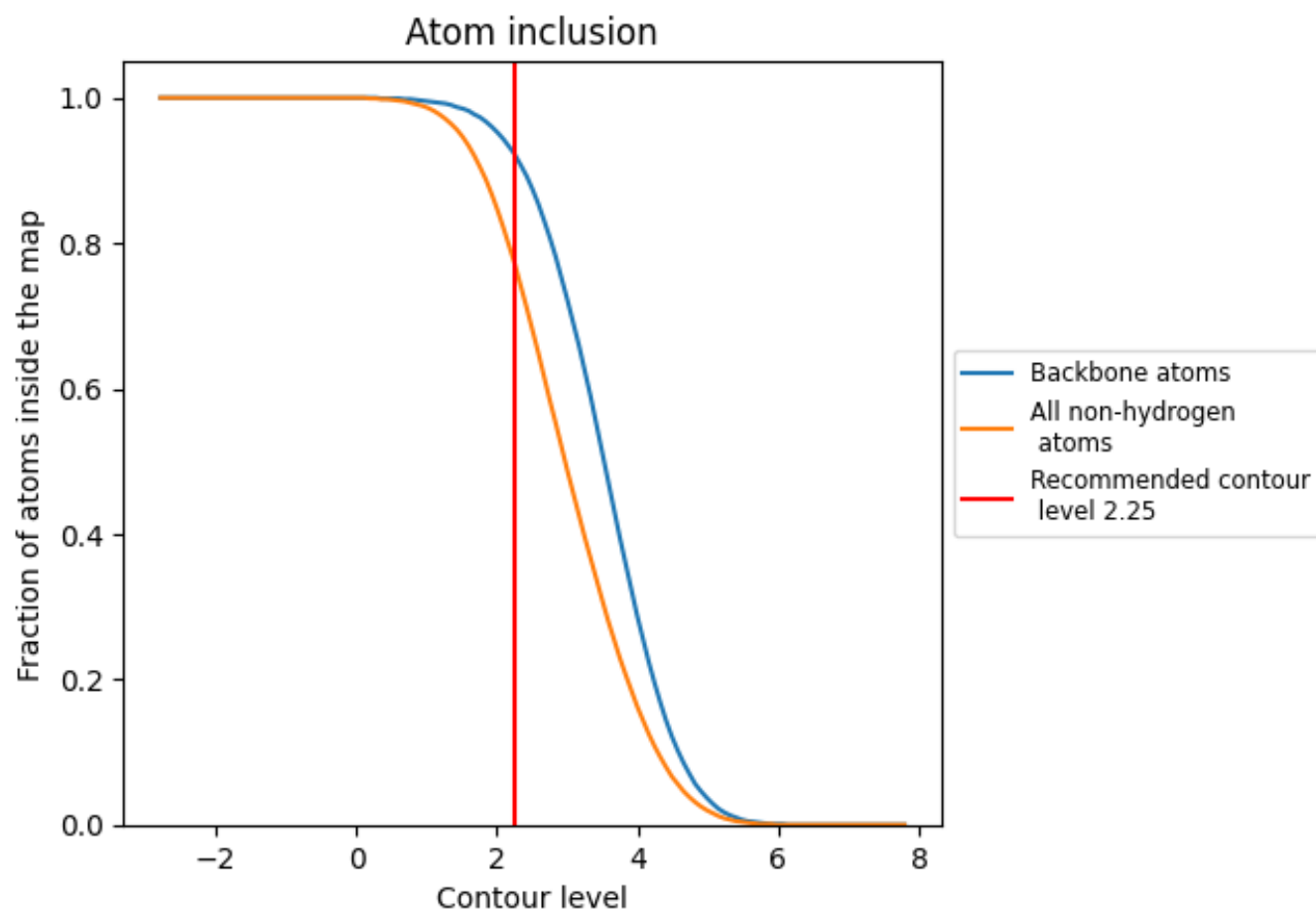
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.7730	 0.2760
AC	 0.8090	 0.3010
AD	 0.8300	 0.3070
AF	 0.8070	 0.2390
AG	 0.6780	 0.1990
AH	 0.7930	 0.2780
AK	 0.8240	 0.3060
AL	 0.8320	 0.2870
AM	 0.8110	 0.2930
AN	 0.8060	 0.3290
AU	 0.9780	 0.4800
AX	 0.5620	 0.1910
Ad	 0.8360	 0.3050
Af	 0.8410	 0.2840
Ag	 0.8680	 0.2400
BC	 0.7680	 0.3000
BD	 0.8110	 0.3100
BF	 0.8000	 0.2210
BG	 0.5760	 0.1780
BH	 0.8040	 0.2840
BK	 0.8440	 0.3160
BL	 0.8480	 0.2920
BM	 0.8370	 0.2960
BN	 0.7730	 0.3370
BU	 1.0000	 0.4440
BX	 0.5170	 0.1940
Bd	 0.8270	 0.3040
Bf	 0.7950	 0.2670
Bg	 0.8420	 0.2520
CC	 0.7450	 0.2840
CD	 0.8220	 0.3190
CF	 0.7370	 0.2400
CG	 0.5850	 0.1750
CH	 0.8050	 0.2760
CK	 0.8270	 0.3190



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Chain	Atom inclusion	Q-score
CL	 0.8290	 0.2950
CM	 0.8100	 0.2900
CN	 0.7410	 0.3380
CU	 0.9780	 0.4570
CX	 0.6040	 0.2160
Cd	 0.8280	 0.2950
Cf	 0.8020	 0.2600
Cg	 0.8600	 0.2560
DC	 0.8220	 0.2960
DD	 0.8010	 0.3120
DF	 0.8000	 0.2370
DG	 0.5670	 0.1720
DH	 0.7900	 0.2790
DK	 0.8100	 0.3170
DL	 0.8220	 0.2850
DM	 0.8230	 0.2840
DN	 0.8110	 0.3340
DU	 0.8670	 0.4170
DX	 0.6920	 0.2460
Dd	 0.8110	 0.3070
Df	 0.7680	 0.2910
Dg	 0.8420	 0.2580
EC	 0.8140	 0.3010
ED	 0.8030	 0.3060
EF	 0.7660	 0.2310
EG	 0.5670	 0.1690
EH	 0.7830	 0.2780
EK	 0.8360	 0.3140
EL	 0.8290	 0.2990
EM	 0.8360	 0.2900
EN	 0.8080	 0.3250
EU	 1.0000	 0.4630
EX	 0.5000	 0.2210
Ed	 0.8310	 0.3090
Ef	 0.8060	 0.2840
Eg	 0.8090	 0.2370
FC	 0.7650	 0.2860
FD	 0.8060	 0.3090
FF	 0.7790	 0.2250
FG	 0.5720	 0.1640
FH	 0.7880	 0.2810
FK	 0.8230	 0.3110

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Chain	Atom inclusion	Q-score
FL	 0.8180	 0.2830
FM	 0.8110	 0.2900
FN	 0.7920	 0.3320
FU	 0.8890	 0.4460
FX	 0.6830	 0.2640
Fd	 0.8220	 0.3010
Ff	 0.7630	 0.2770
Fg	 0.8200	 0.2510
GC	 0.7540	 0.2760
GD	 0.8070	 0.3110
GF	 0.7940	 0.2330
GG	 0.5490	 0.1540
GH	 0.7890	 0.2720
GK	 0.8290	 0.3170
GL	 0.8460	 0.2970
GM	 0.8060	 0.2900
GN	 0.7600	 0.3230
GU	 0.9780	 0.4930
GX	 0.7540	 0.2280
Gd	 0.8160	 0.3040
Gf	 0.7810	 0.2770
Gg	 0.8120	 0.2400
HC	 0.8190	 0.2870
HD	 0.7990	 0.3110
HF	 0.7560	 0.2290
HG	 0.5740	 0.1470
HH	 0.7900	 0.2830
HK	 0.8130	 0.3070
HL	 0.8350	 0.2900
HM	 0.8270	 0.2810
HN	 0.7430	 0.3150
HU	 0.9780	 0.4660
HX	 0.6330	 0.2130
Hd	 0.8340	 0.3130
Hf	 0.8090	 0.2770
Hg	 0.8240	 0.2530
IC	 0.8120	 0.3000
ID	 0.8130	 0.3190
IF	 0.7920	 0.2090
IG	 0.5890	 0.1470
IH	 0.7770	 0.2780
IK	 0.8200	 0.3100

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Chain	Atom inclusion	Q-score
IL	 0.8190	 0.2860
IM	 0.8040	 0.2980
IN	 0.8200	 0.3340
IU	 0.9330	 0.4130
IX	 0.5330	 0.2020
Id	 0.8360	 0.3110
If	 0.7770	 0.2870
Ig	 0.8380	 0.2560
JC	 0.8140	 0.3040
JD	 0.8010	 0.3240
JF	 0.7920	 0.2260
JG	 0.5470	 0.1340
JH	 0.7970	 0.2810
JK	 0.8020	 0.3110
JL	 0.8260	 0.2990
JM	 0.8160	 0.2980
JN	 0.7760	 0.3380
JU	 0.9560	 0.4960
JX	 0.5920	 0.1790
Jd	 0.8250	 0.3120
Jf	 0.7860	 0.2530
Jg	 0.8380	 0.2630
KC	 0.7720	 0.2850
KD	 0.8220	 0.3120
KF	 0.7560	 0.2180
KG	 0.5580	 0.1490
KH	 0.8070	 0.2800
KK	 0.8140	 0.3140
KL	 0.8070	 0.2920
KM	 0.8060	 0.2860
KN	 0.7500	 0.3350
KU	 0.9560	 0.4320
KX	 0.6000	 0.2380
Kd	 0.8400	 0.3020
Kf	 0.8220	 0.2720
Kg	 0.8420	 0.2560
LC	 0.8150	 0.2930
LD	 0.8180	 0.3060
LF	 0.8090	 0.2360
LG	 0.6230	 0.1850
LH	 0.7910	 0.2780
LK	 0.8290	 0.3050

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Chain	Atom inclusion	Q-score
LL	 0.8360	 0.2980
LM	 0.8290	 0.2920
LN	 0.7920	 0.3200
LU	 0.9780	 0.4390
LX	 0.5710	 0.2220
Ld	 0.8140	 0.2990
Lf	 0.8180	 0.2670
Lg	 0.8380	 0.2540
MC	 0.8260	 0.3020
MD	 0.8240	 0.3130
MF	 0.7620	 0.2100
MG	 0.6430	 0.2100
MH	 0.7800	 0.2660
MK	 0.8150	 0.3140
ML	 0.8480	 0.2960
MM	 0.8180	 0.2790
MN	 0.8040	 0.3250
MU	 0.9560	 0.4300
MX	 0.7210	 0.2410
Md	 0.8450	 0.3040
Mf	 0.7520	 0.2790
Mg	 0.8090	 0.2380
NG	 0.6150	 0.1880
OG	 0.6430	 0.2060
PG	 0.6460	 0.1920
VF	 0.7880	 0.2260
VG	 0.8270	 0.2320
VH	 0.6910	 0.2720
VX	 0.5580	 0.2250
WF	 0.7580	 0.2210
WG	 0.7940	 0.2310
WH	 0.6340	 0.2520
WX	 0.6040	 0.2630
XF	 0.7330	 0.2210
XG	 0.8380	 0.2520
XH	 0.5360	 0.2570
XX	 0.7580	 0.2450
YF	 0.7880	 0.2220
YG	 0.8120	 0.2310
YH	 0.6780	 0.2530
YX	 0.6880	 0.2570
ZF	 0.7450	 0.2220

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Chain	Atom inclusion	Q-score
ZG	 0.8310	 0.2490
ZH	 0.5510	 0.2250
ZX	 0.6000	 0.2180