



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:27 AM UTC

PDB ID : 7MUW / pdb_00007muw
EMDB ID : EMD-24024
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 4
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:

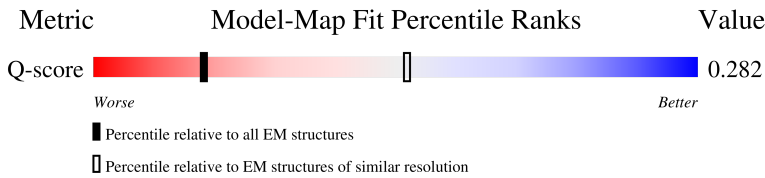
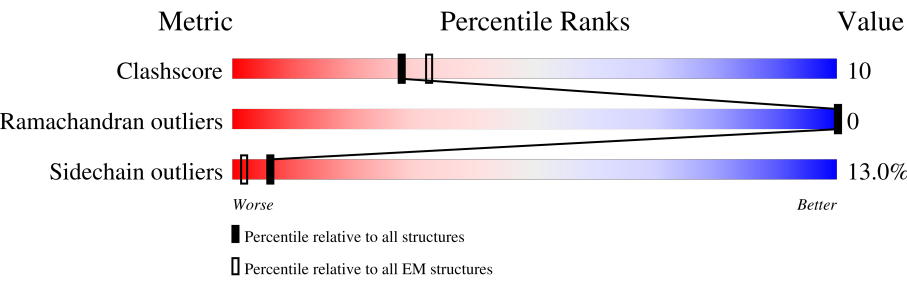
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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



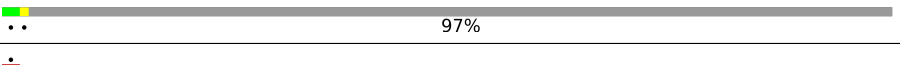
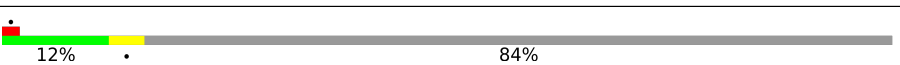
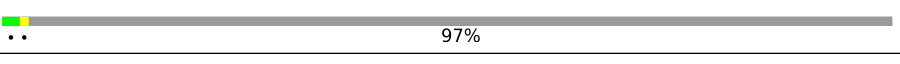
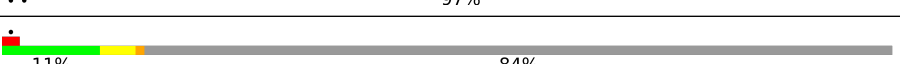
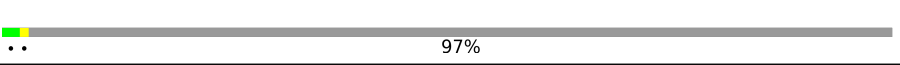
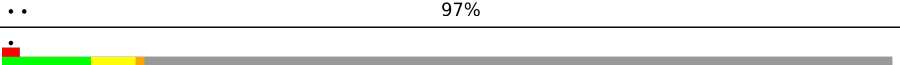
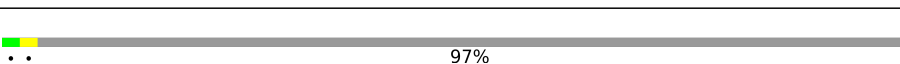
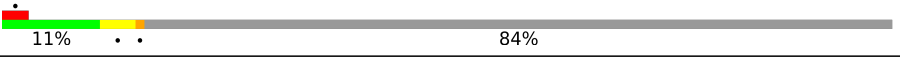
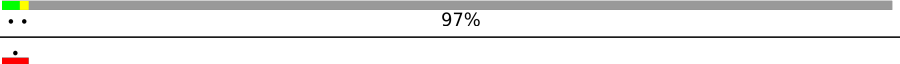
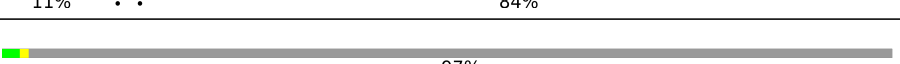
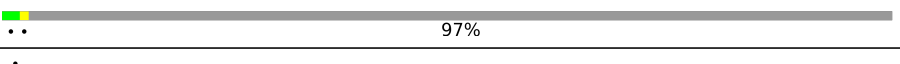
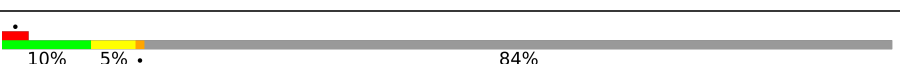
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	11% . 84%
1	Ag	1048	.. 97%
1	BG	1048	10% 5% . 84%
1	Bg	1048	.. 97%

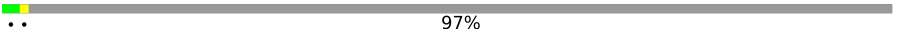
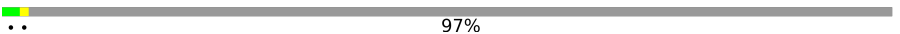
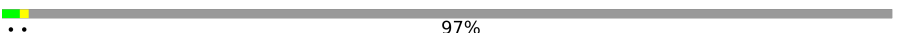
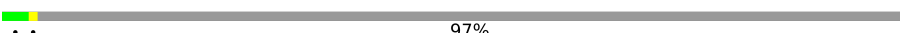
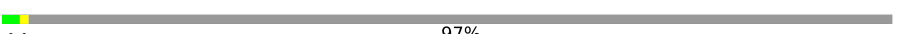
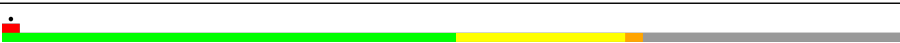
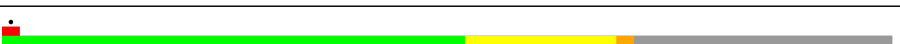
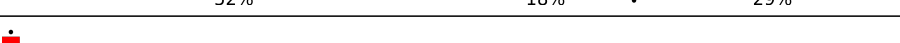
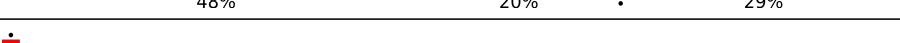
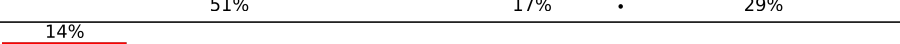
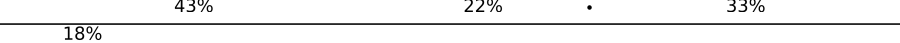
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Mol	Chain	Length	Quality of chain
1	CG	1048	 12% 5% 84%
1	Cg	1048	 97%
1	DG	1048	 10% 5% 84%
1	Dg	1048	 97%
1	EG	1048	 12% 5% 84%
1	Eg	1048	 97%
1	FG	1048	 11% 5% 84%
1	Fg	1048	 97%
1	GG	1048	 11% 5% 84%
1	Gg	1048	 97%
1	HG	1048	 11% 5% 84%
1	Hg	1048	 97%
1	IG	1048	 10% 5% 84%
1	Ig	1048	 97%
1	JG	1048	 11% 5% 84%
1	Jg	1048	 97%
1	KG	1048	 11% 5% 84%
1	Kg	1048	 97%
1	LG	1048	 10% 5% 84%
1	Lg	1048	 97%
1	MG	1048	 11% 5% 84%
1	Mg	1048	 97%
1	NG	1048	 10% 5% 84%
1	OG	1048	11% 5% 84%
1	PG	1048	11% 5% 84%

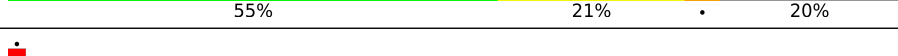
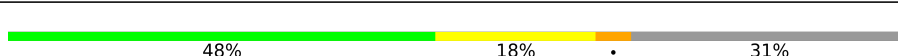
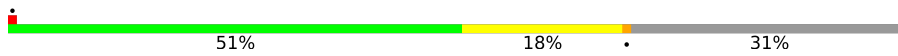
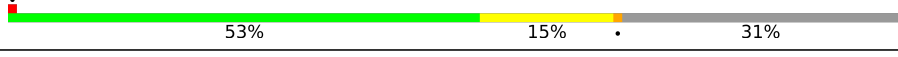
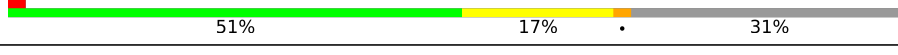
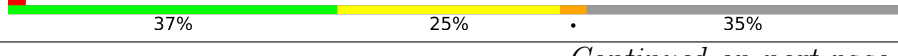
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AH	361	 49% 20% 29%
2	BH	361	 50% 20% 29%
2	CH	361	 51% 18% 29%
2	DH	361	 50% 19% 29%
2	EH	361	 51% 17% 29%
2	FH	361	 49% 19% 29%
2	GH	361	 51% 19% 29%
2	HH	361	 52% 17% 29%
2	IH	361	 51% 19% 29%
2	JH	361	 48% 19% 29%
2	KH	361	 52% 18% 29%
2	LH	361	 48% 20% 29%
2	MH	361	 51% 17% 29%
2	VH	361	 14% 43% 22% 33%
2	WH	361	 18% 48% 17% 33%
2	XH	361	 21% 47% 17% 33%
2	YH	361	 10% 46% 18% 33%
2	ZH	361	 23% 52% 13% 33%
3	AK	189	 57% 19% 20%
3	BK	189	 57% 21% 20%

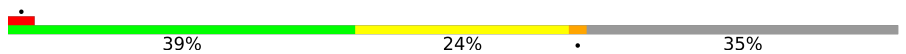
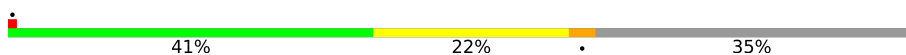
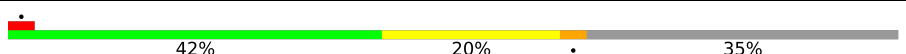
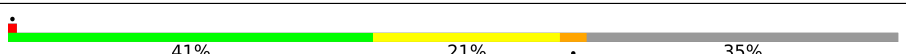
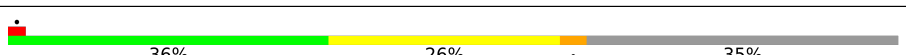
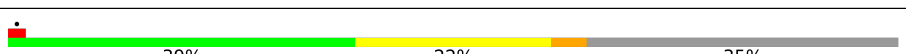
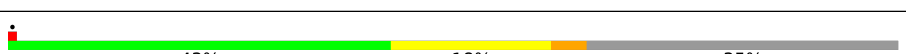
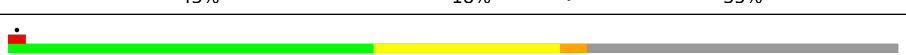
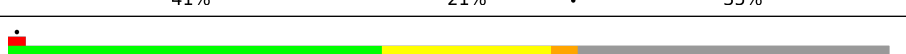
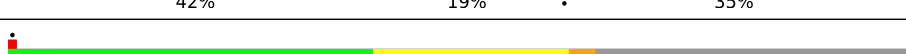
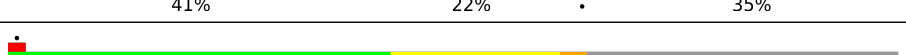
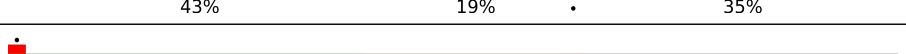
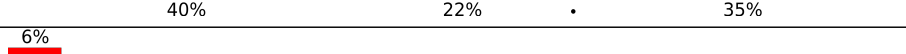
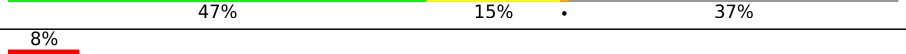
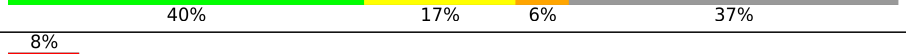
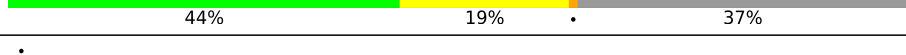
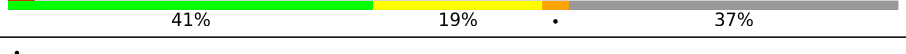
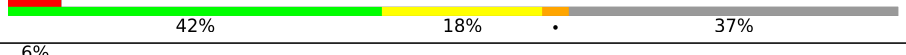
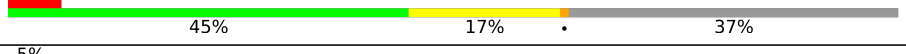
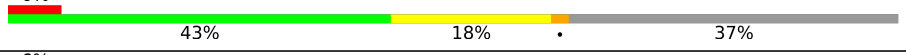
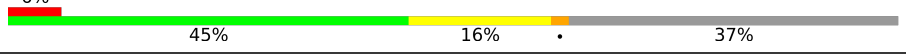
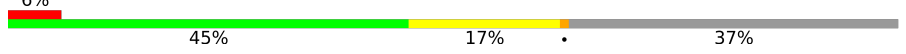
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Mol	Chain	Length	Quality of chain
3	CK	189	
3	DK	189	
3	EK	189	
3	FK	189	
3	GK	189	
3	HK	189	
3	IK	189	
3	JK	189	
3	KK	189	
3	LK	189	
3	MK	189	
4	AL	249	
4	BL	249	
4	CL	249	
4	DL	249	
4	EL	249	
4	FL	249	
4	GL	249	
4	HL	249	
4	IL	249	
4	JL	249	
4	KL	249	
4	LL	249	
4	ML	249	
5	AM	320	

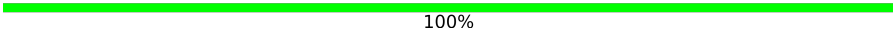
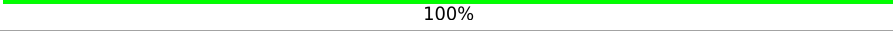
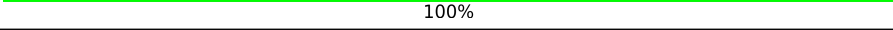
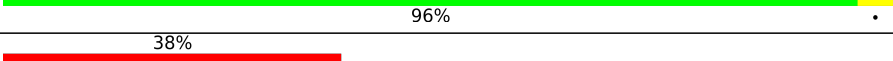
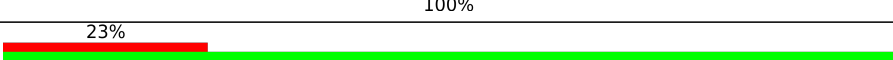
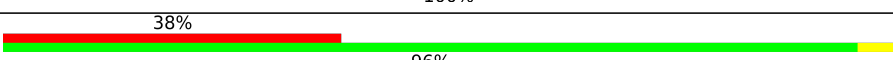
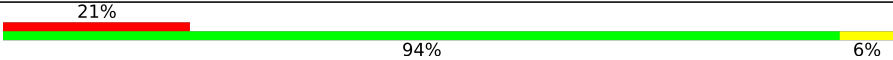
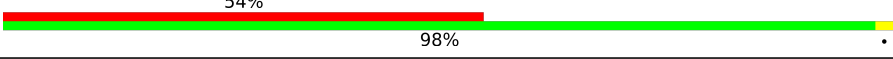
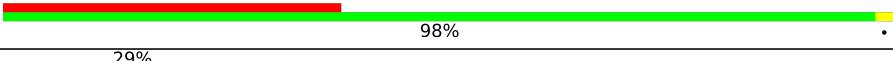
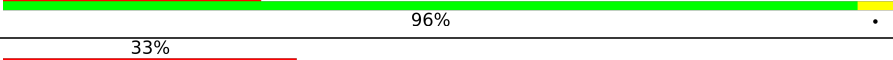
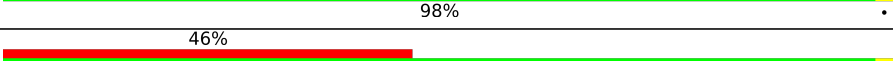
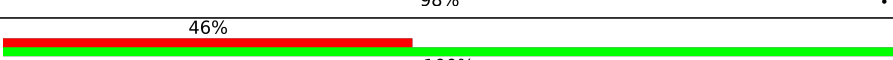
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Mol	Chain	Length	Quality of chain
5	BM	320	
5	CM	320	
5	DM	320	
5	EM	320	
5	FM	320	
5	GM	320	
5	HM	320	
5	IM	320	
5	JM	320	
5	KM	320	
5	LM	320	
5	MM	320	
6	AN	124	
6	BN	124	
6	CN	124	
6	DN	124	
6	EN	124	
6	FN	124	
6	GN	124	
6	HN	124	
6	IN	124	
6	JN	124	
6	KN	124	
6	LN	124	
6	MN	124	

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Mol	Chain	Length	Quality of chain
7	AU	9	
7	BU	9	
7	CU	9	
7	DU	9	
7	EU	9	
7	FU	9	
7	GU	9	
7	HU	9	
7	IU	9	
7	JU	9	
7	KU	9	
7	LU	9	
7	MU	9	
8	AX	48	
8	BX	48	
8	CX	48	
8	DX	48	
8	EX	48	
8	FX	48	
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8	HX	48	
8	IX	48	
8	JX	48	
8	KX	48	
8	LX	48	

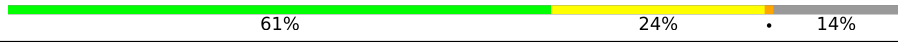
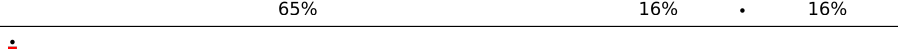
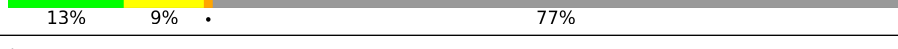
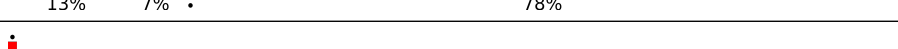
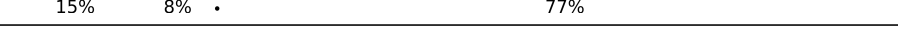
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Mol	Chain	Length	Quality of chain
8	MX	48	40% 100%
8	VX	48	33% 100%
8	WX	48	31% 100%
8	XX	48	29% 100%
8	YX	48	33% 98%
8	ZX	48	46% 98%
9	AD	163	64% 20% 14%
9	Ad	163	59% 23% 16%
9	BD	163	66% 19% 14%
9	Bd	163	53% 29% 16%
9	CD	163	64% 20% 14%
9	Cd	163	58% 23% 16%
9	DD	163	61% 21% 14%
9	Dd	163	65% 17% 16%
9	ED	163	60% 23% 14%
9	Ed	163	58% 25% 16%
9	FD	163	63% 21% 14%
9	Fd	163	64% 17% 16%
9	GD	163	60% 23% 14%
9	Gd	163	58% 23% 16%
9	HD	163	58% 25% 14%
9	Hd	163	62% 20% 16%
9	ID	163	63% 20% 14%
9	Id	163	63% 18% 16%
9	JD	163	63% 22% 14%

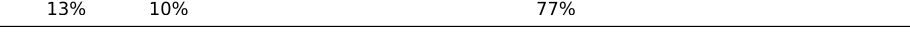
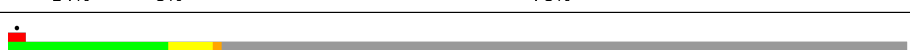
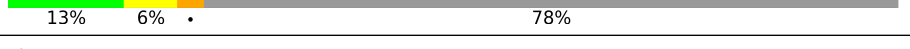
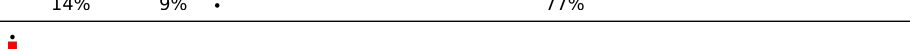
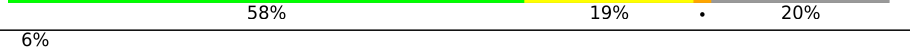
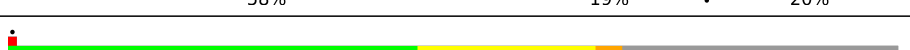
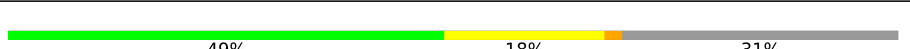
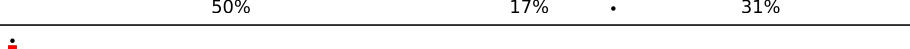
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Mol	Chain	Length	Quality of chain
9	Jd	163	
9	KD	163	
9	Kd	163	
9	LD	163	
9	Ld	163	
9	MD	163	
9	Md	163	
10	AF	269	
10	Af	269	
10	BF	269	
10	Bf	269	
10	CF	269	
10	Cf	269	
10	DF	269	
10	Df	269	
10	EF	269	
10	Ef	269	
10	FF	269	
10	Ff	269	
10	GF	269	
10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

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Mol	Chain	Length	Quality of chain
10	JF	269	
10	Jf	269	
10	KF	269	
10	Kf	269	
10	LF	269	
10	Lf	269	
10	MF	269	
10	Mf	269	
10	VF	269	
10	WF	269	
10	XF	269	
10	YF	269	
10	ZF	269	
11	AC	303	
11	BC	303	
11	CC	303	
11	DC	303	
11	EC	303	
11	FC	303	
11	GC	303	
11	HC	303	
11	IC	303	
11	JC	303	
11	KC	303	
11	LC	303	

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Mol	Chain	Length	Quality of chain
11	MC	303	47% 19% . 31%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 192116 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	Fg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Gg	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	Hg	34	Total 276	C 168	N 47	O 60	S 1	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	CG	165	Total 1229	C 780	N 203	O 242	S 4	0	0
1	Jg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Kg	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	Lg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Mg	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	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
1	XG	34	Total 276	C 168	N 47	O 60	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	YG	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	ZG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Cg	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	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		
1	Eg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

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

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

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

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

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

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

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

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

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

- Molecule 5 is a protein called DUF2807 domain-containing protein.

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

- Molecule 6 is a protein called Neurogenic locus notch.

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

- Molecule 7 is a protein called Unknown protein fragment.

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

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

- Molecule 8 is a protein called Unknown protein fragment.

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

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

- Molecule 9 is a protein called DotD.

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

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

- Molecule 10 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ef	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
10	FF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
10	Ff	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
10	AF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
10	GF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
10	Gf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
10	HF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	Hf	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	IF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	If	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	JF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	Jf	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	KF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	Kf	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	LF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	Lf	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	MF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	CF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	Mf	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	VF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	WF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	XF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	YF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	ZF	63	Total 483	C 308	N 84	O 90	S 1	0	0
10	Af	59	Total 449	C 290	N 77	O 81	S 1	0	0
10	BF	63	Total 483	C 308	N 84	O 90	S 1	0	0
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10	Cf	59	Total 449	C 290	N 77	O 81	S 1	0	0

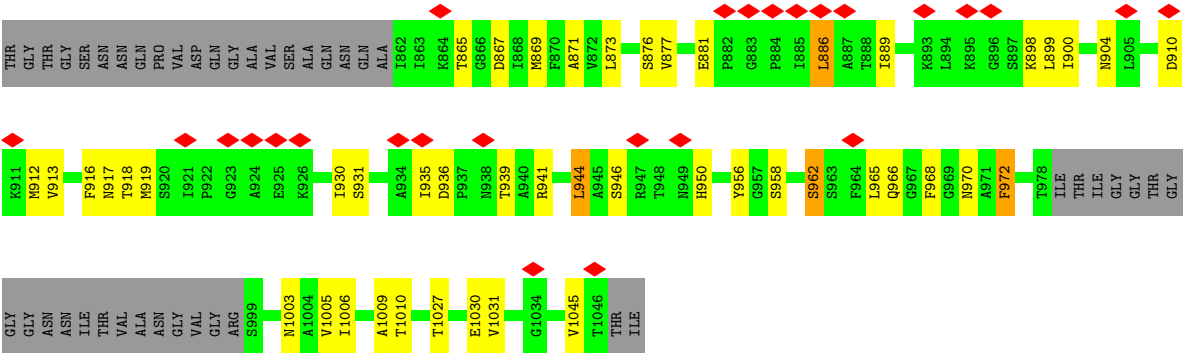
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Mol	Chain	Residues	Atoms					AltConf	Trace
10	DF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
10	Df	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
10	EF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

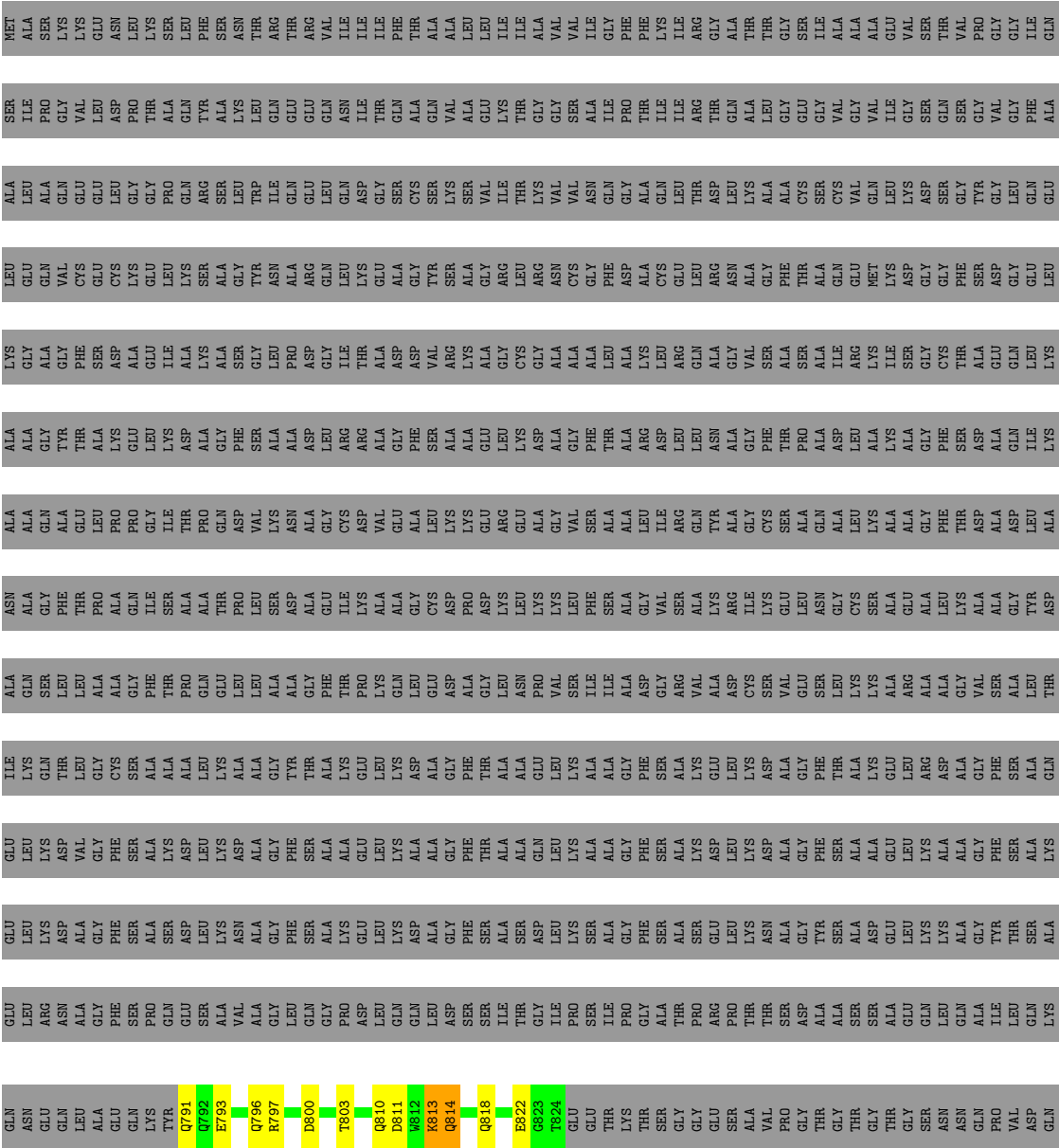
- Molecule 11 is a protein called DotC.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	CC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
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	GC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
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	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
11	KC	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	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		



● Molecule 1: IcmE protein

Chain Fg: .. 97%

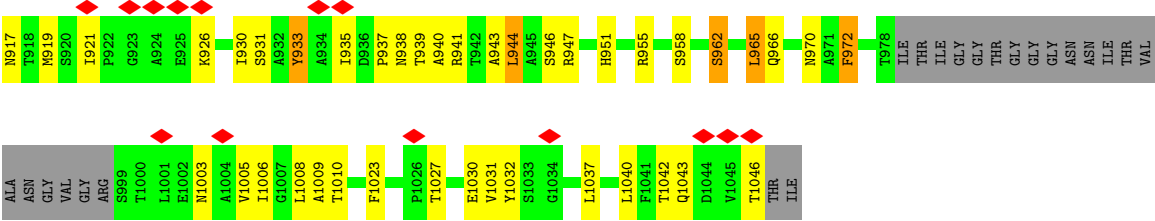


SER	GLN	VAL	GLY
GLY	SER	ILE	VAL
THR	ALA	THR	ALA
LEU	ASN	PHE	SER
GLY	THR	ASN	ALA
ILE	THR	MET	GLN
LEU	THR	SER	ASN
PHE	ILE	PRO	GLN
THR	GLY	ILE	ILE
GLN	THR	GLY	ILE
ASP	GLY	ALA	LYS
VAL	GLY	GLU	THR
THR	GLY	LYS	GLY
THR	ASN	ILE	ASP
ILE	ASN	ILE	ILE
	ILE	ILE	PHE
	THR	SER	ALA
	VAL	ALA	VAL
	ASN	TYR	LEU
	GLY	ILE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

- Molecule 1: IcmE protein

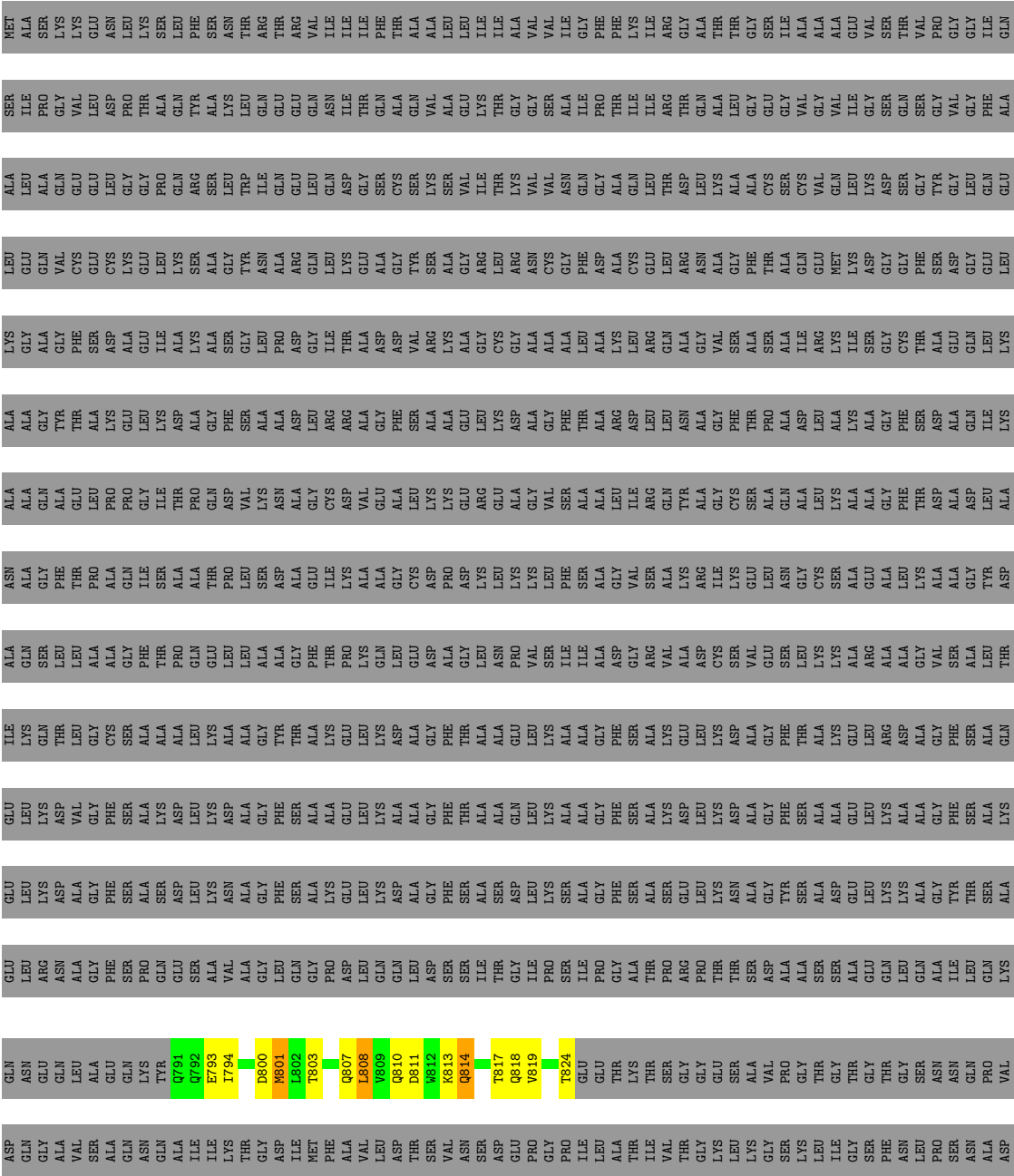
Chain Gg: 97%

[illegible]



● Molecule 1: IcmE protein

Chain Hg: .. 97%



[illegible]

- Molecule 1: IcmE protein

Chain Bg: 97%

[illegible]

84%

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

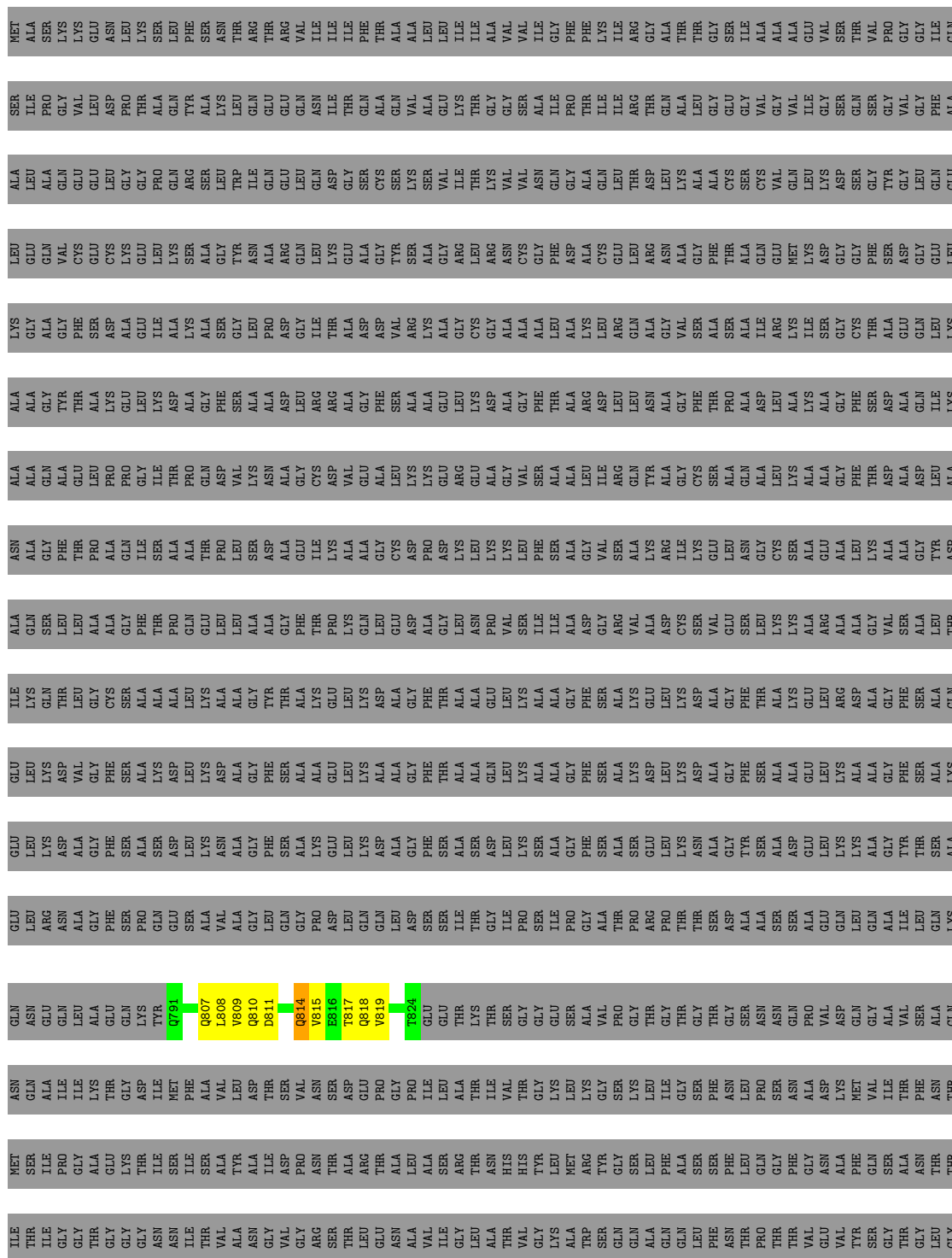
[illegible]

- Molecule 1: IcmE protein

Chain Kg: 

- Molecule 1: IcmE protein

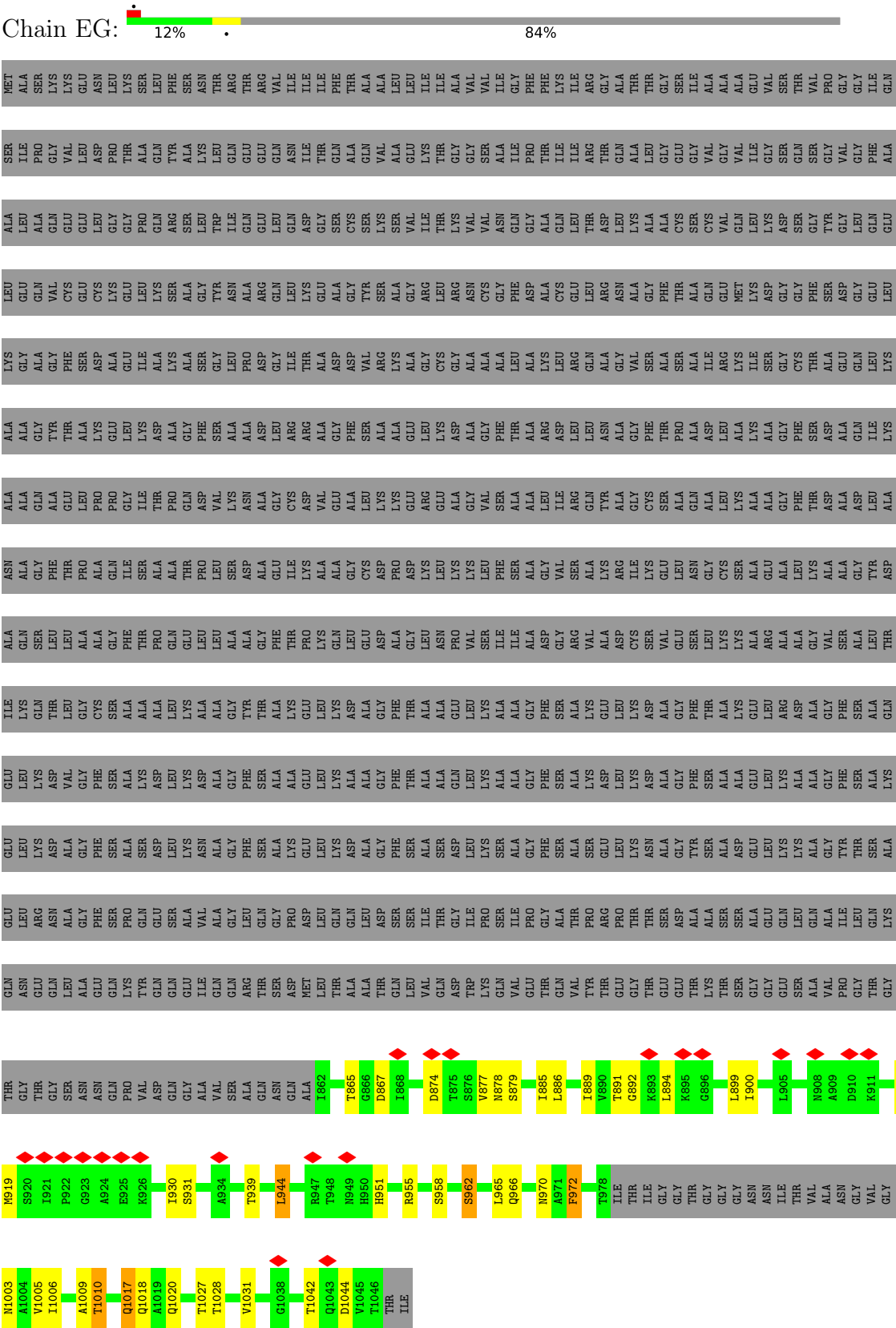
Chain Lg: 97%



Chain Mg: .. 97%



● Molecule 1: IcmE protein



● Molecule 1: IcmE protein

97%

- Molecule 1: IcmE protein

97%

- Molecule 1: IcmE protein

- Molecule 1: IcmE protein

Chain ZG: ..

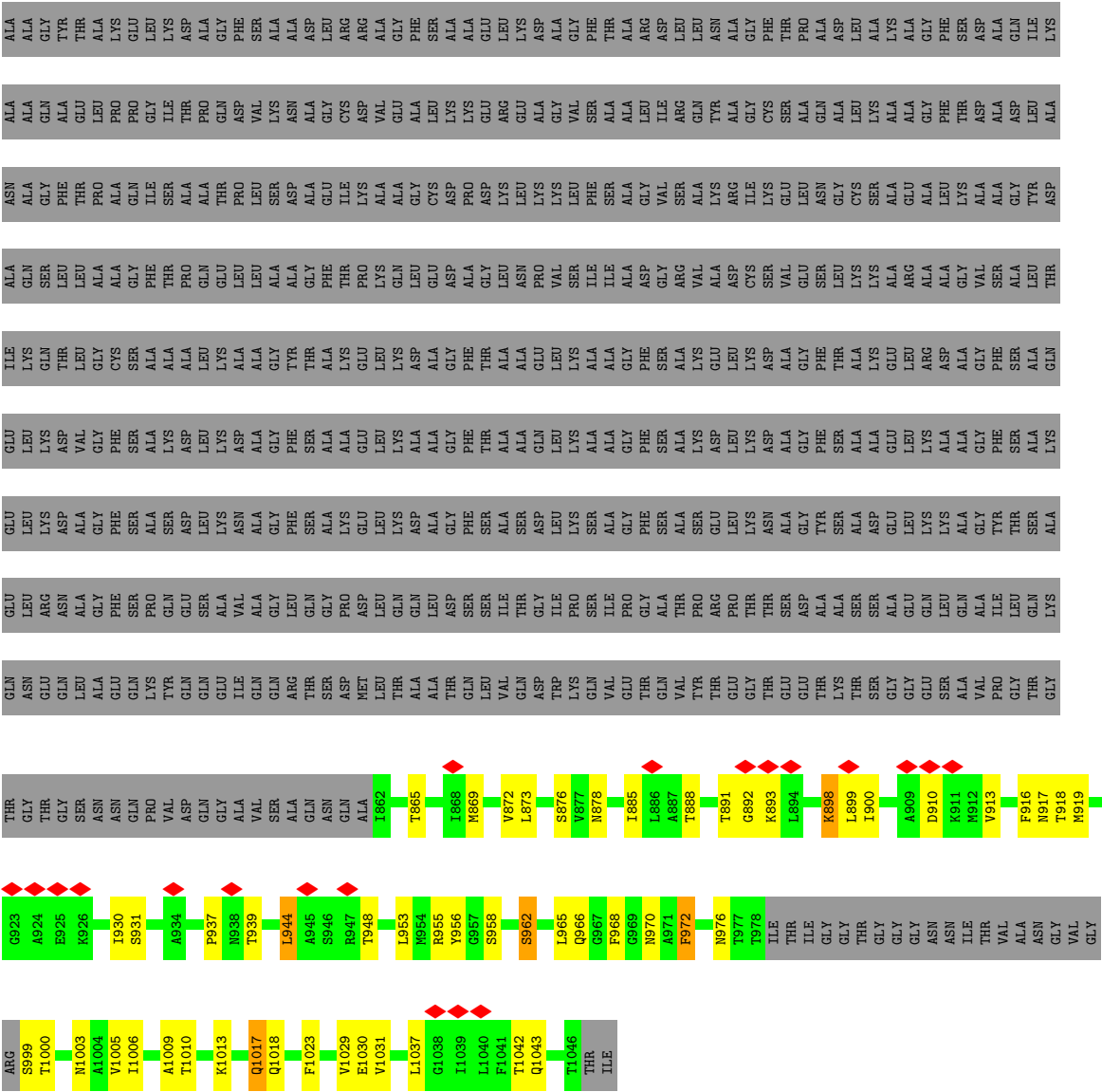
97%

[illegible]

- Molecule 1: IcmE protein

[illegible]





● Molecule 1: IcmE protein

- Molecule 1: IcmE protein

[illegible]

- Molecule 1: IcmE protein

[illegible]







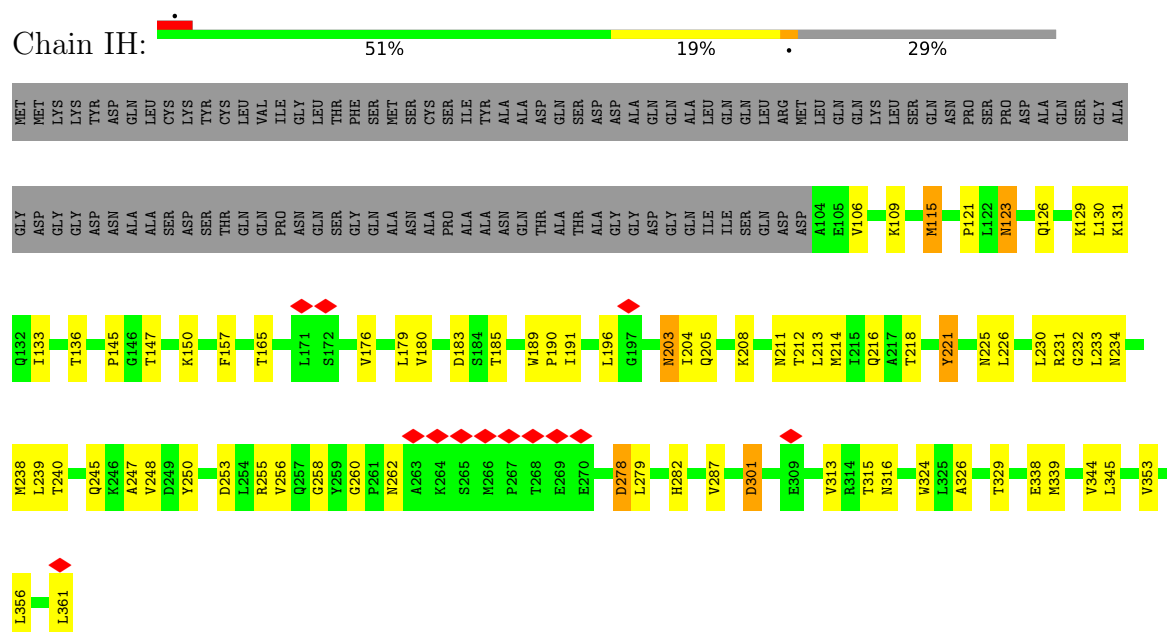
Chain Eg: 97%





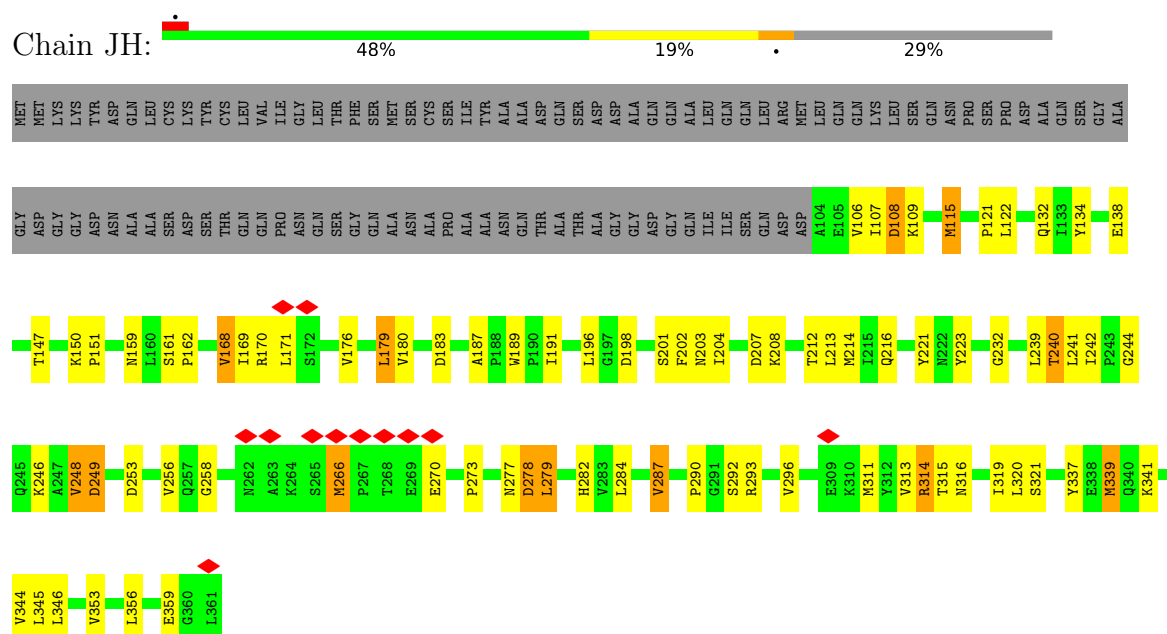
• Molecule 2: Type IV secretion protein IcmK

Chain IH:



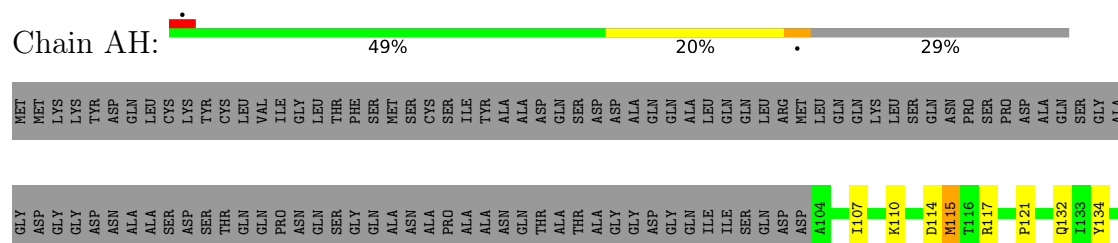
• Molecule 2: Type IV secretion protein IcmK

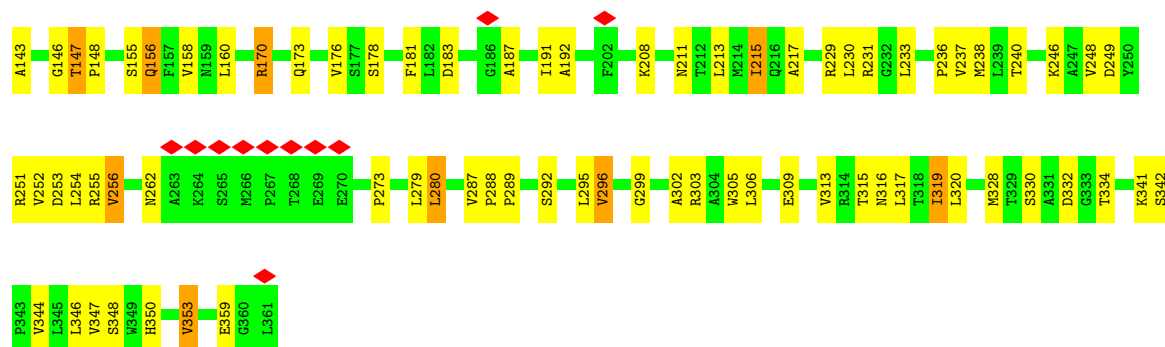
Chain JH:



• Molecule 2: Type IV secretion protein IcmK

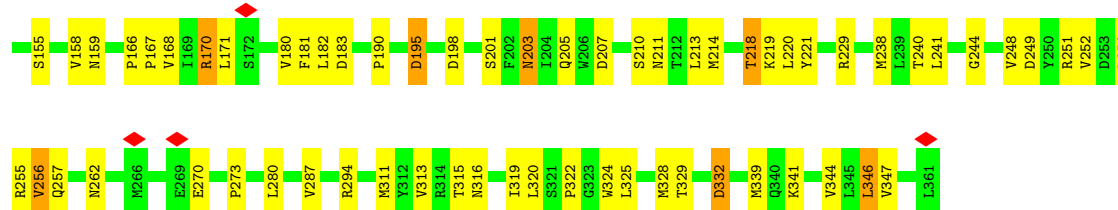
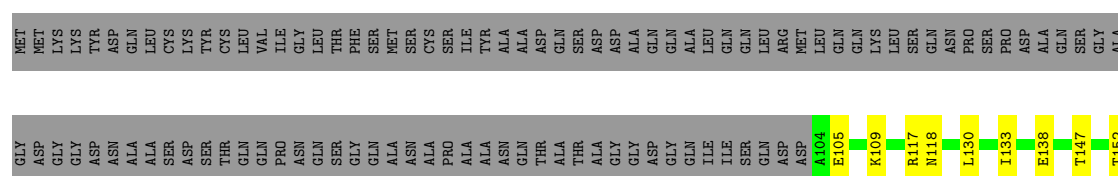
Chain AH:





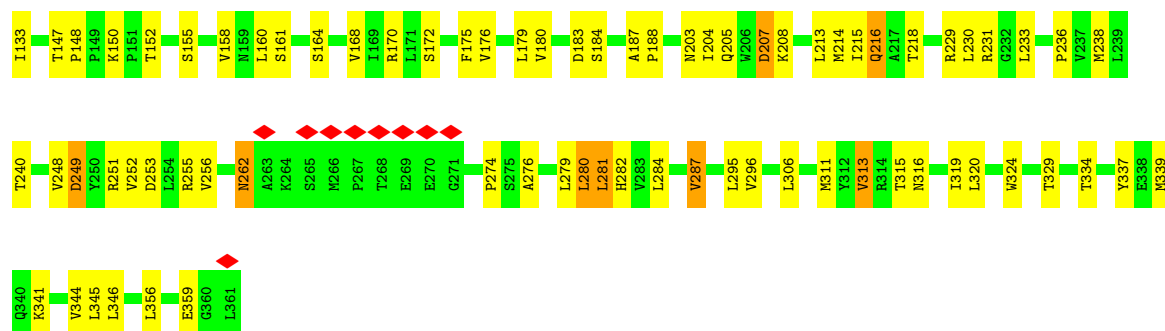
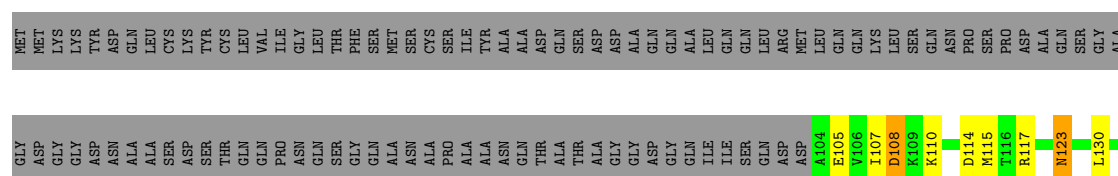
• Molecule 2: Type IV secretion protein IcmK

Chain KH: 52% 18% 29%



• Molecule 2: Type IV secretion protein IcmK

Chain LH: 48% 20% 29%

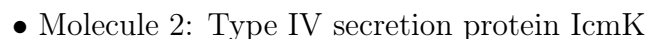


• Molecule 2: Type IV secretion protein IcmK

Frequency	Percentage
Daily	51%
Weekly	17%
Monthly	29%
Other	3%

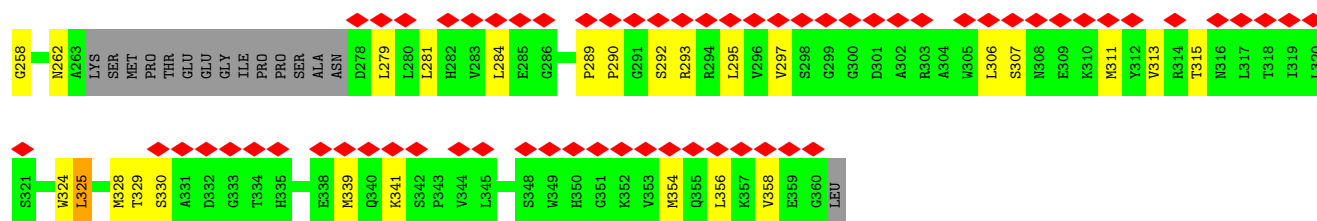


Frequency	Percentage
Daily	14%
Often	43%
Sometimes	22%
Never	33%

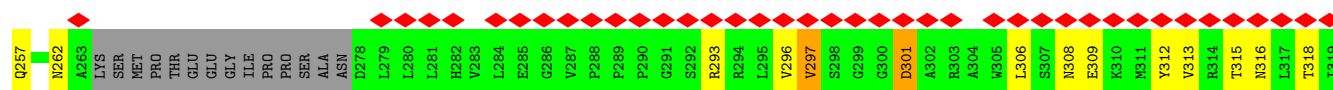
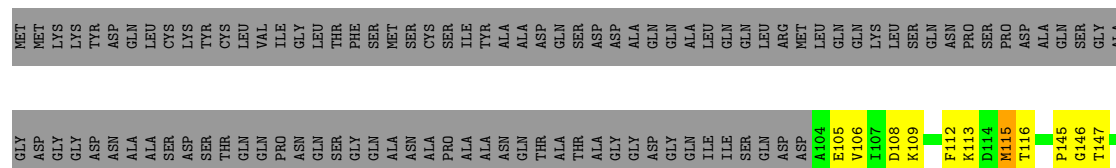


Frequency	Percentage
Very often	18%
Often	48%
Sometimes	17%
Never	33%

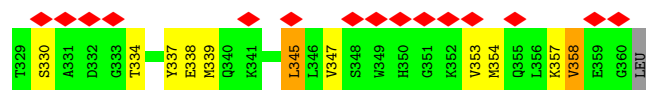
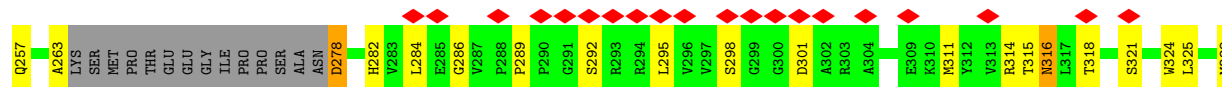
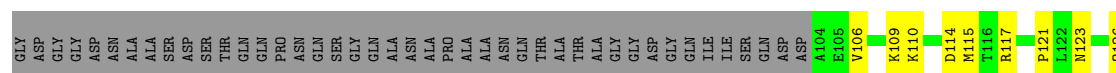




• Molecule 2: Type IV secretion protein IcmK

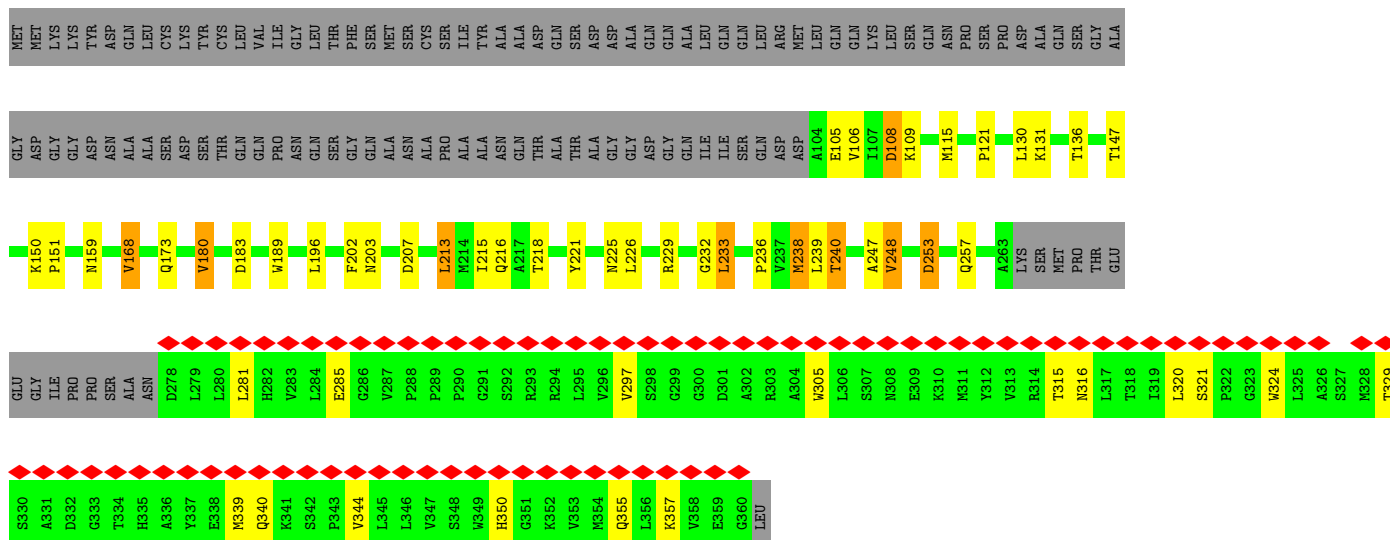


• Molecule 2: Type IV secretion protein IcmK

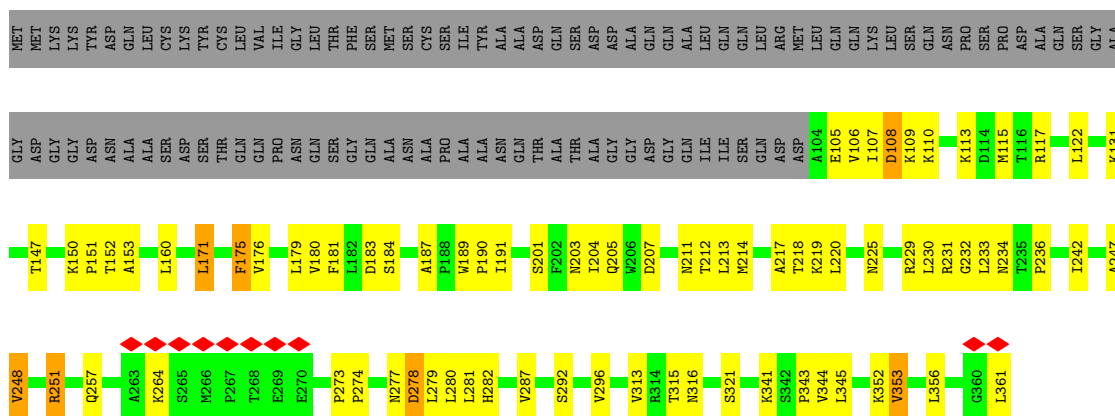


• Molecule 2: Type IV secretion protein IcmK

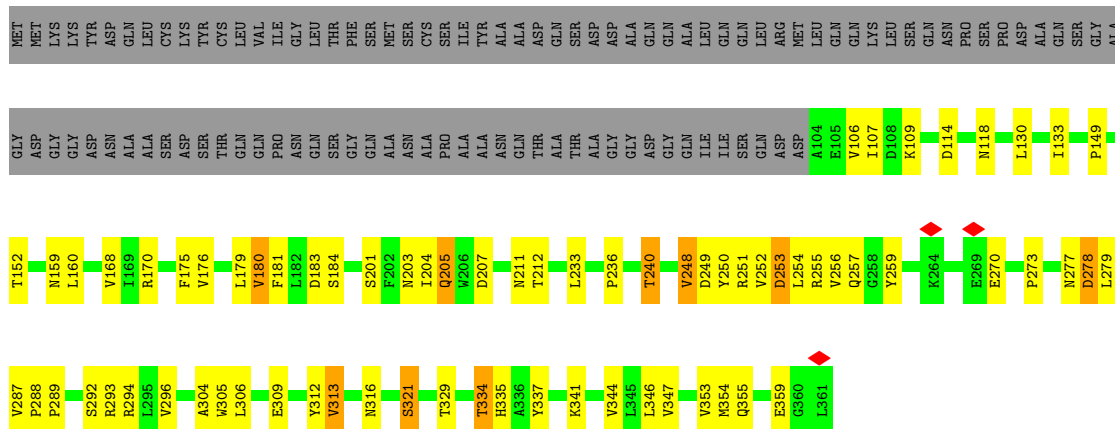




- Molecule 2: Type IV secretion protein IcmK



- Molecule 2: Type IV secretion protein IcmK

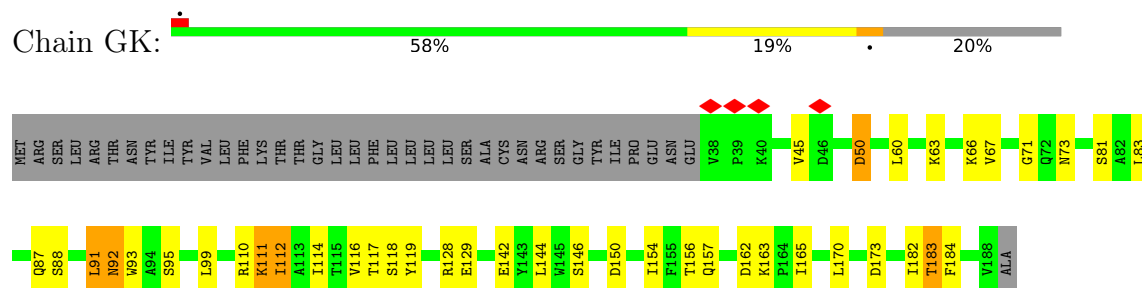


- Molecule 2: Type IV secretion protein IcmK

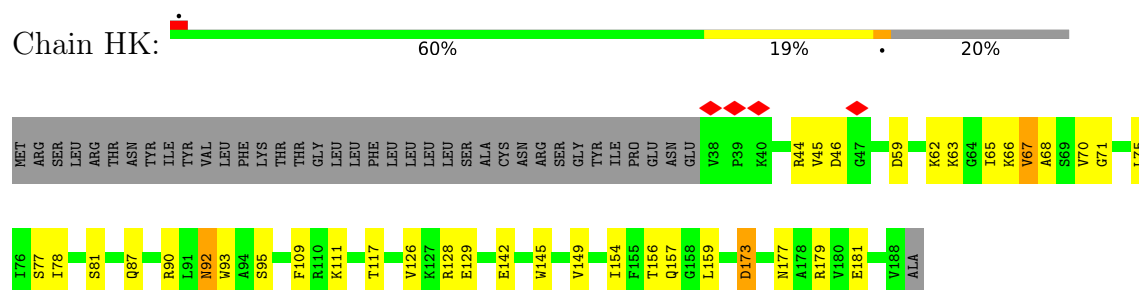
- Molecule 3: Inner membrane lipoprotein YiaD

- Molecule 3: Inner membrane lipoprotein YiaD

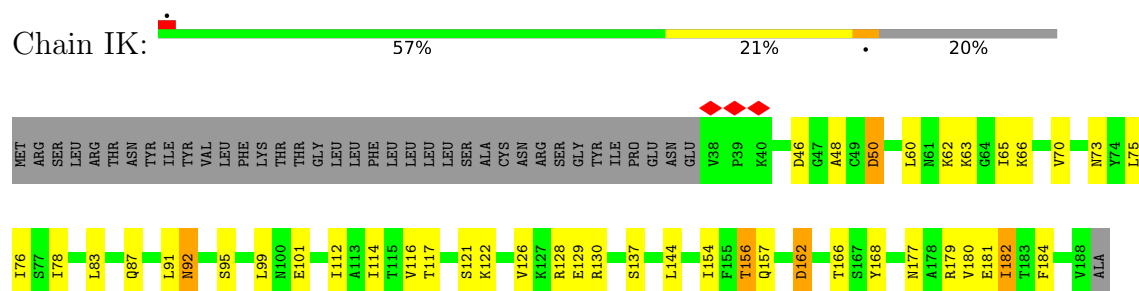
- Molecule 3: Inner membrane lipoprotein YiaD



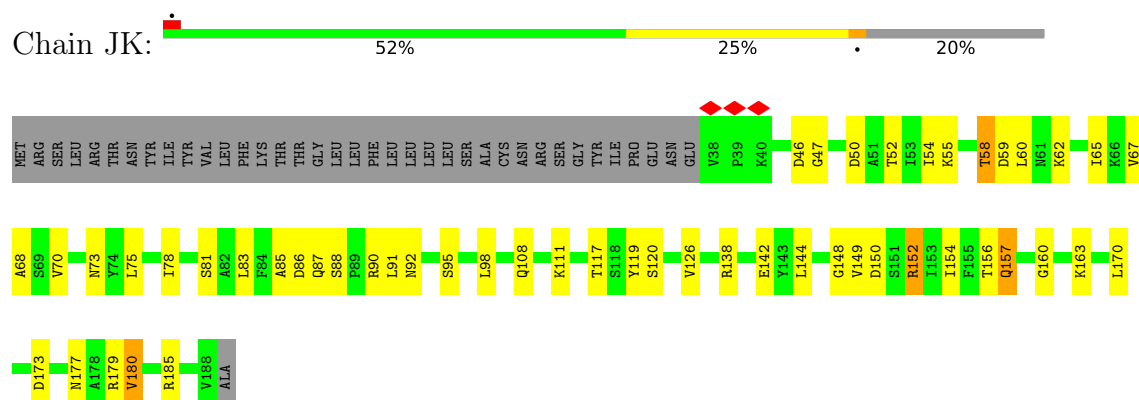
- Molecule 3: Inner membrane lipoprotein YiaD



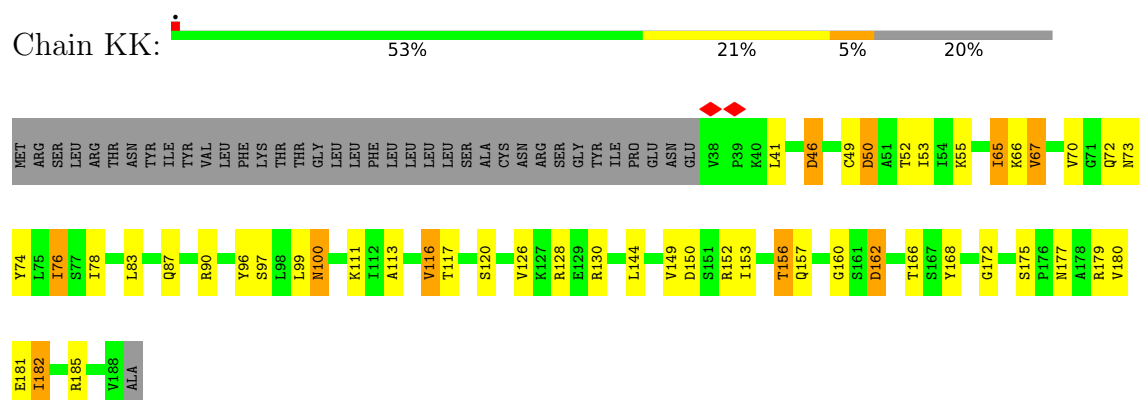
- Molecule 3: Inner membrane lipoprotein YiaD



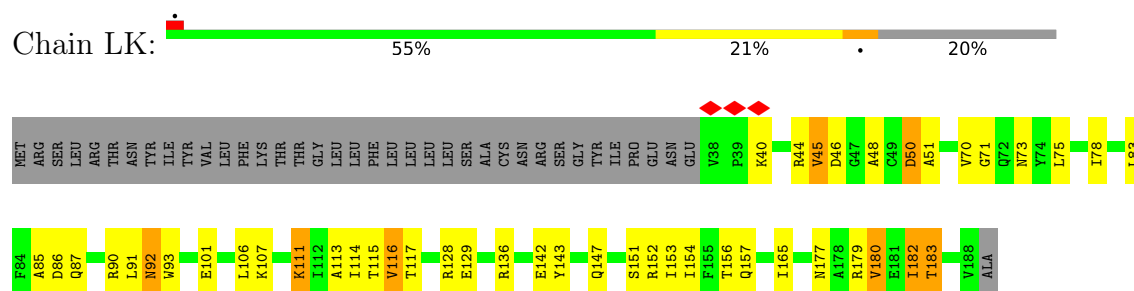
- Molecule 3: Inner membrane lipoprotein YiaD



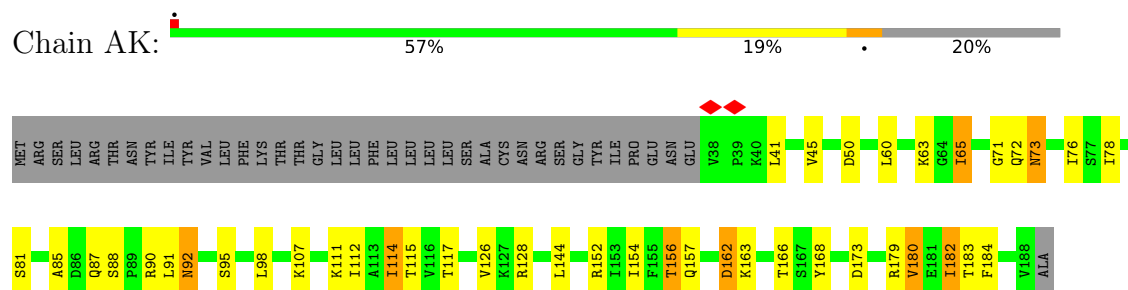
- Molecule 3: Inner membrane lipoprotein YiaD



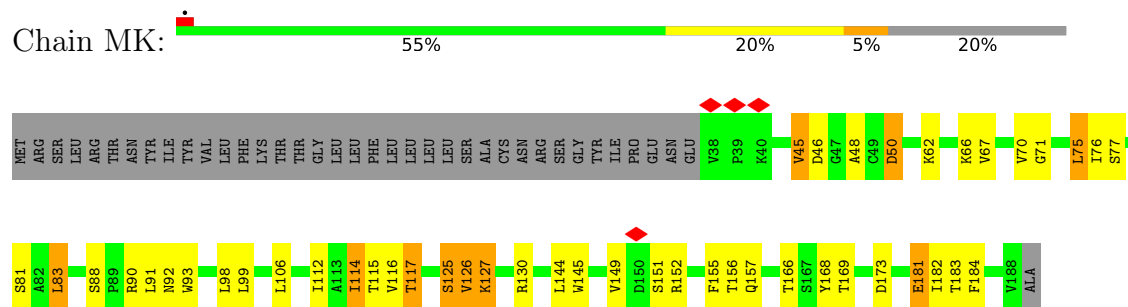
- Molecule 3: Inner membrane lipoprotein YiaD



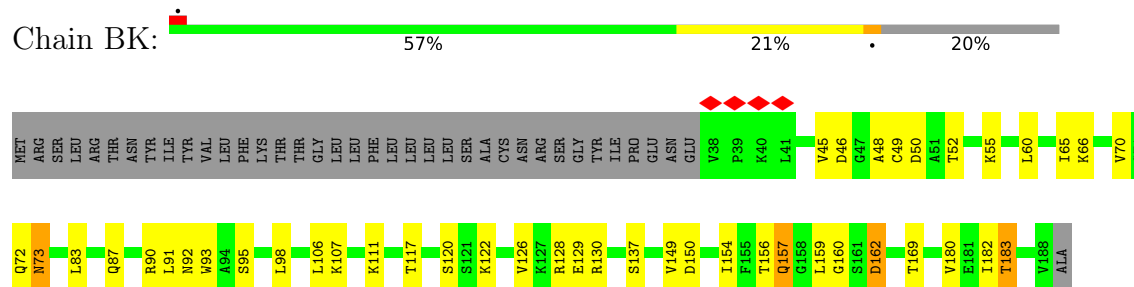
- Molecule 3: Inner membrane lipoprotein YiaD



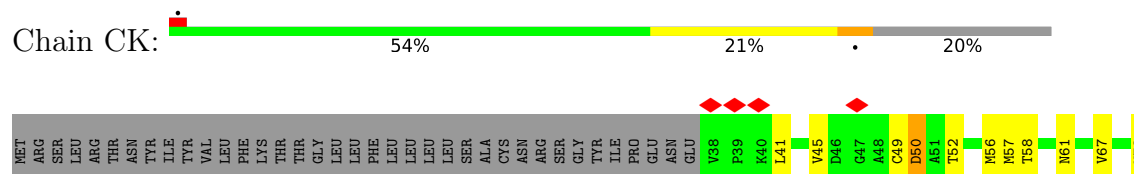
- Molecule 3: Inner membrane lipoprotein YiaD

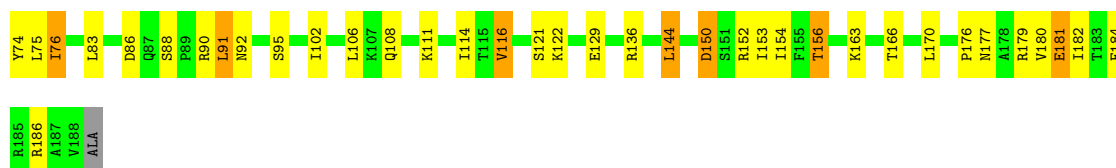


- Molecule 3: Inner membrane lipoprotein YiaD

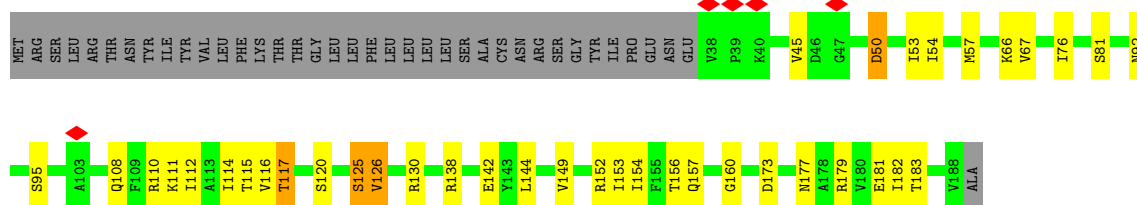


- Molecule 3: Inner membrane lipoprotein YiaD

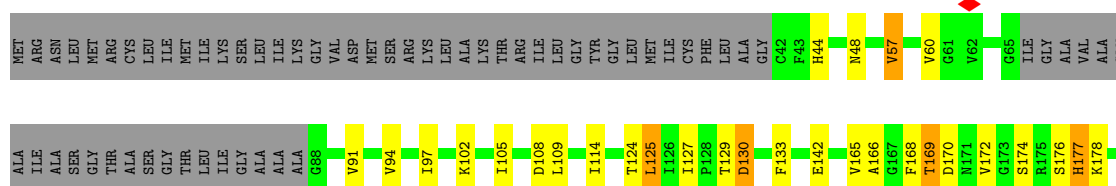




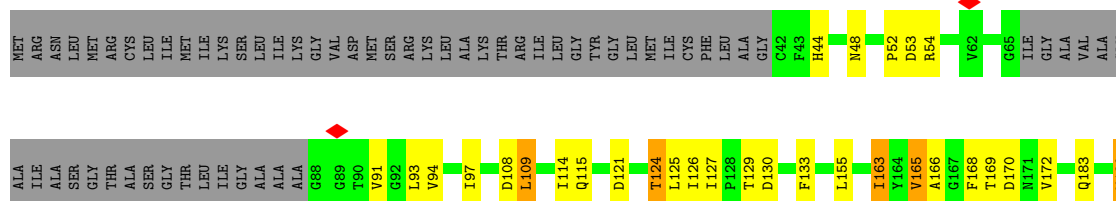
- Molecule 3: Inner membrane lipoprotein YiaD



- Molecule 4: Outer membrane protein, OmpA family protein

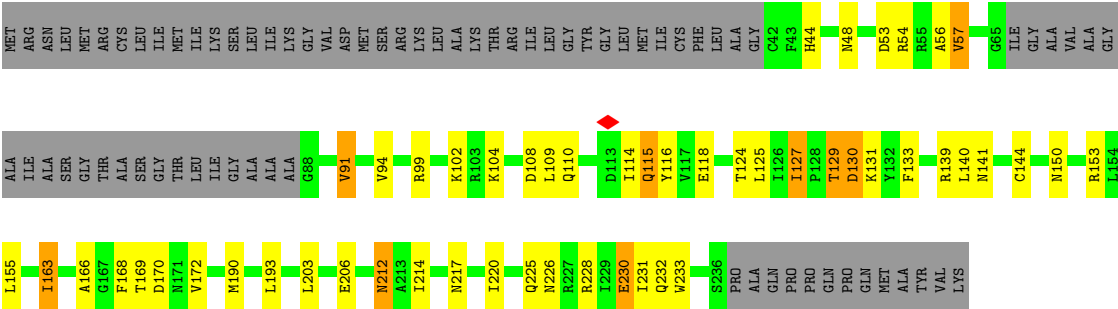


- Molecule 4: Outer membrane protein, OmpA family protein

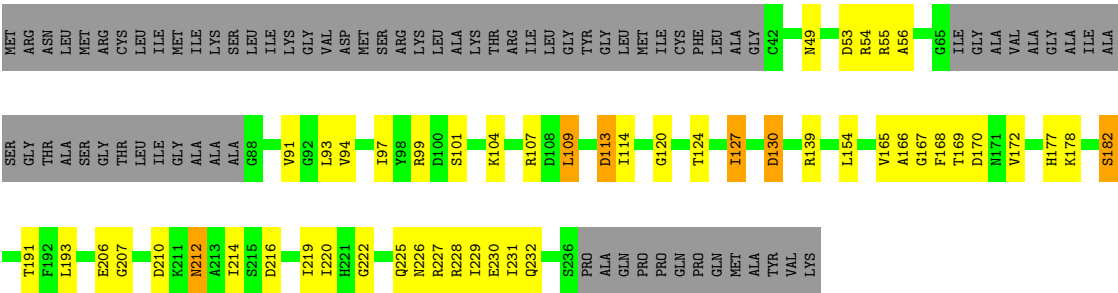


- Molecule 4: Outer membrane protein, OmpA family protein

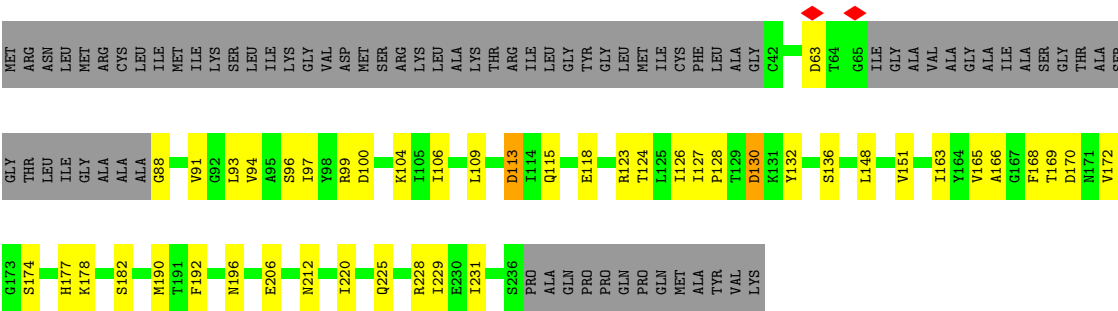




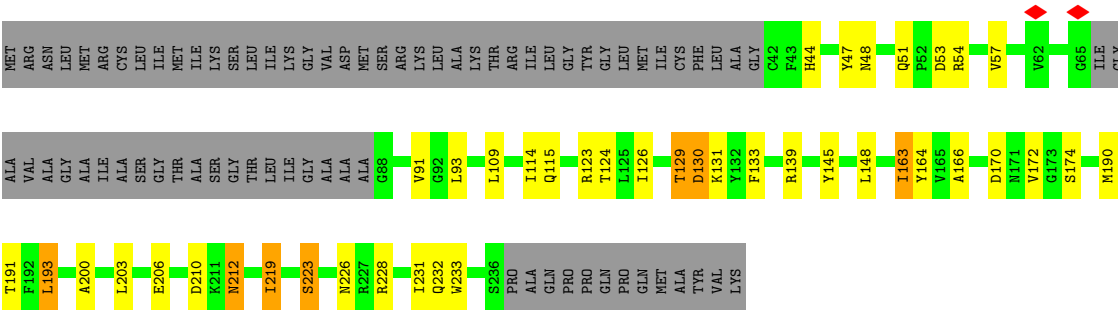
• Molecule 4: Outer membrane protein, OmpA family protein



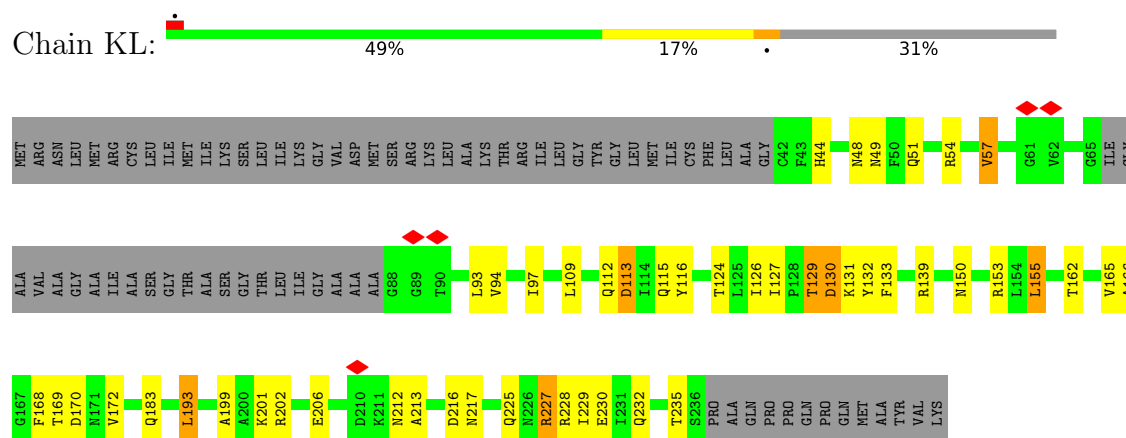
• Molecule 4: Outer membrane protein, OmpA family protein



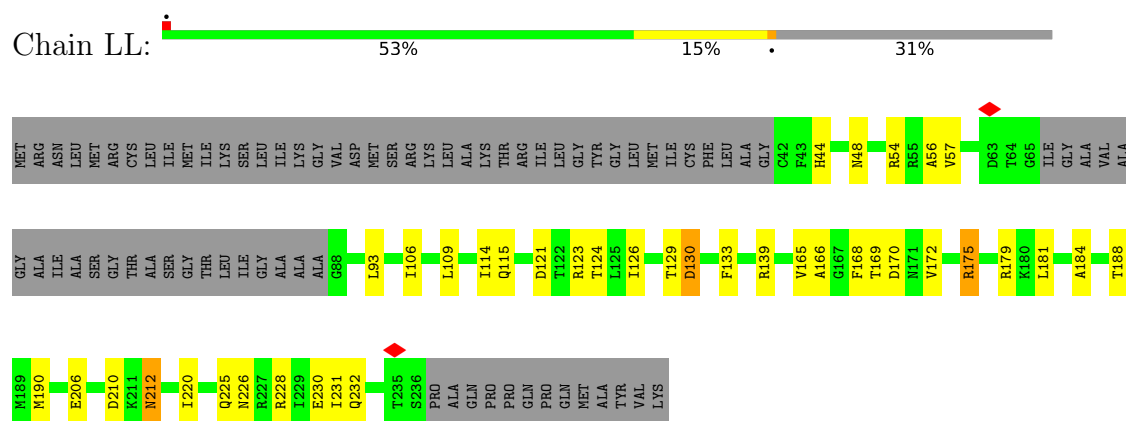
• Molecule 4: Outer membrane protein, OmpA family protein



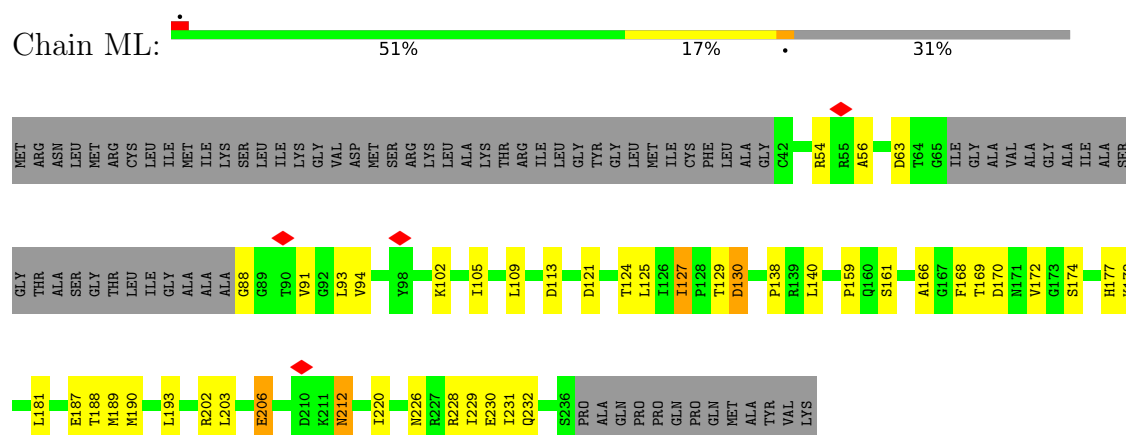
- Molecule 4: Outer membrane protein, OmpA family protein



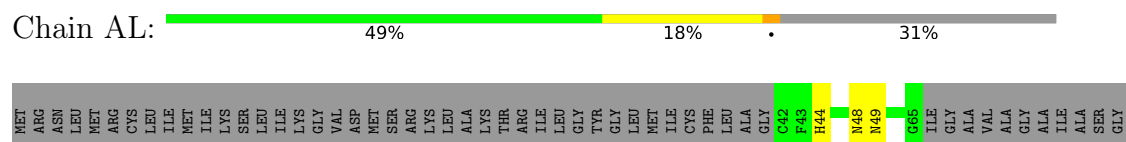
- Molecule 4: Outer membrane protein, OmpA family protein

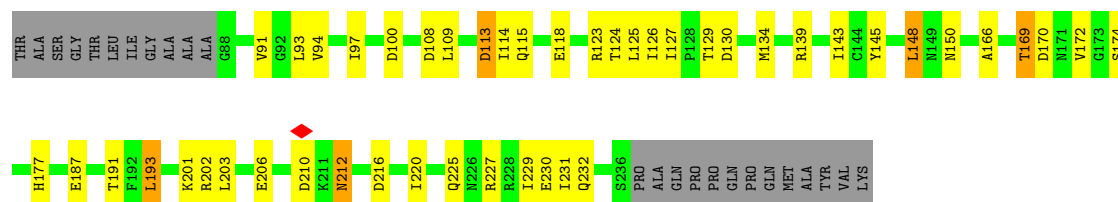


- Molecule 4: Outer membrane protein, OmpA family protein

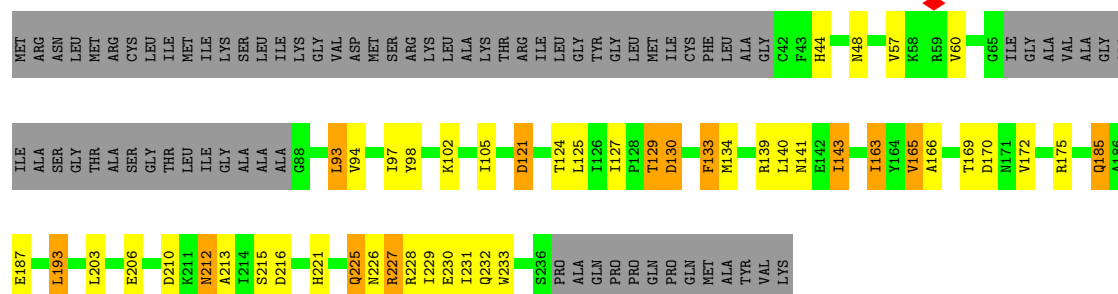


- Molecule 4: Outer membrane protein, OmpA family protein

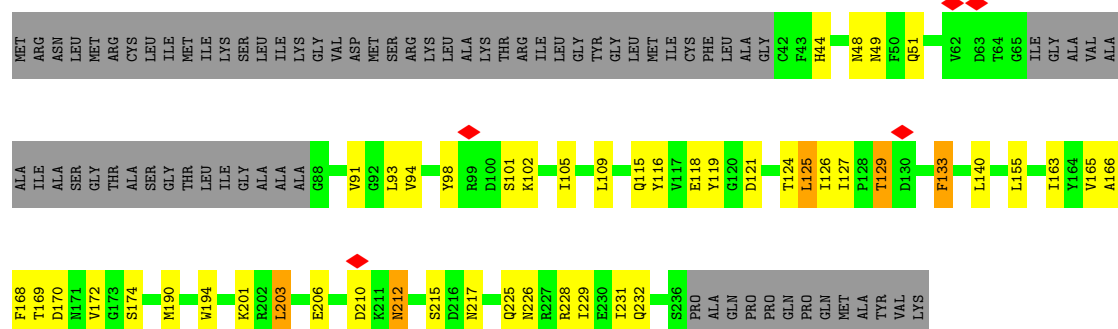




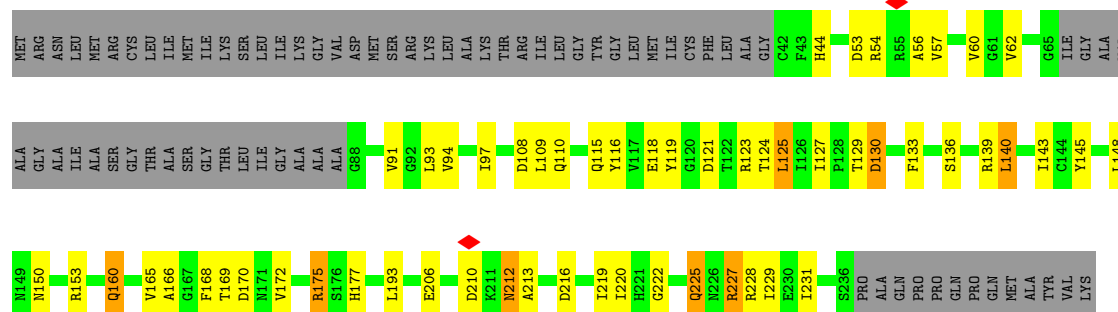
- Molecule 4: Outer membrane protein, OmpA family protein



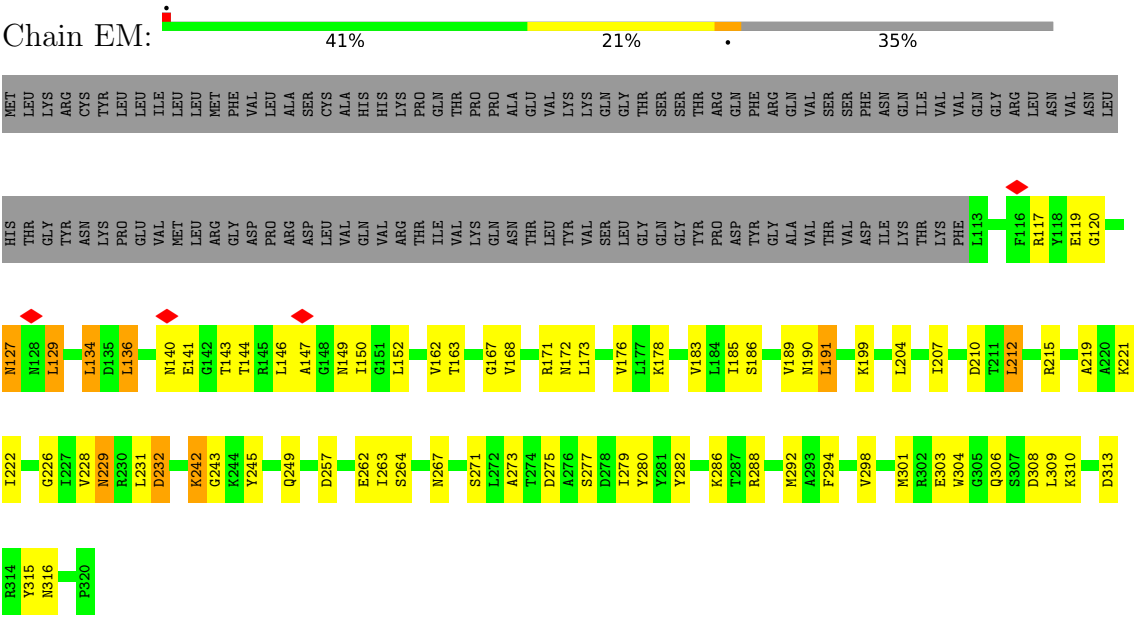
- Molecule 4: Outer membrane protein, OmpA family protein



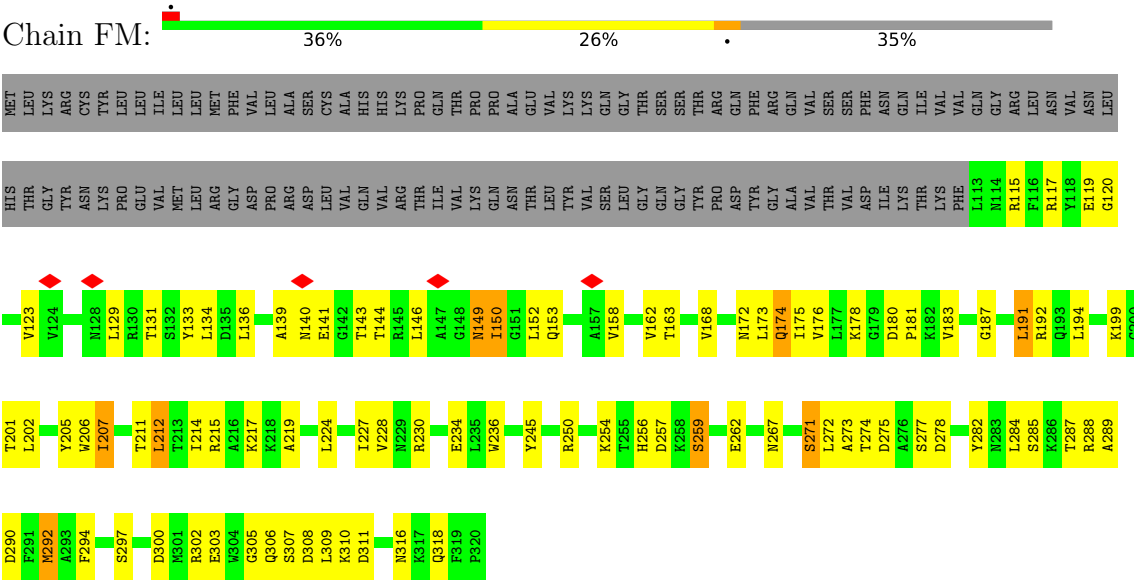
- Molecule 4: Outer membrane protein, OmpA family protein



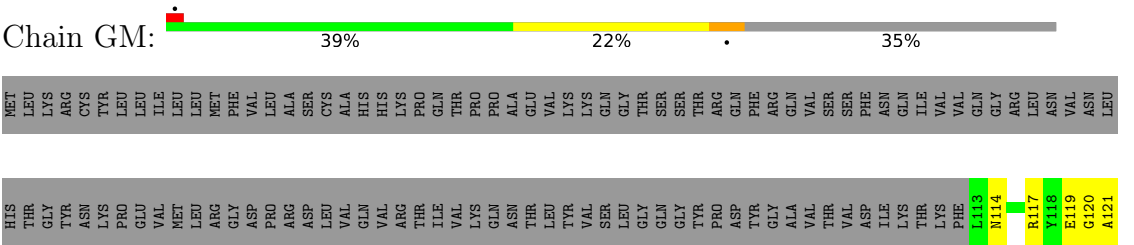
• Molecule 5: DUF2807 domain-containing protein

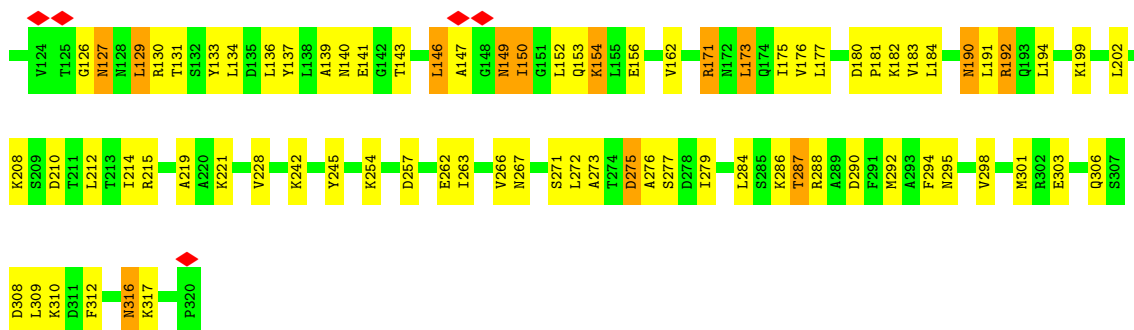


• Molecule 5: DUF2807 domain-containing protein

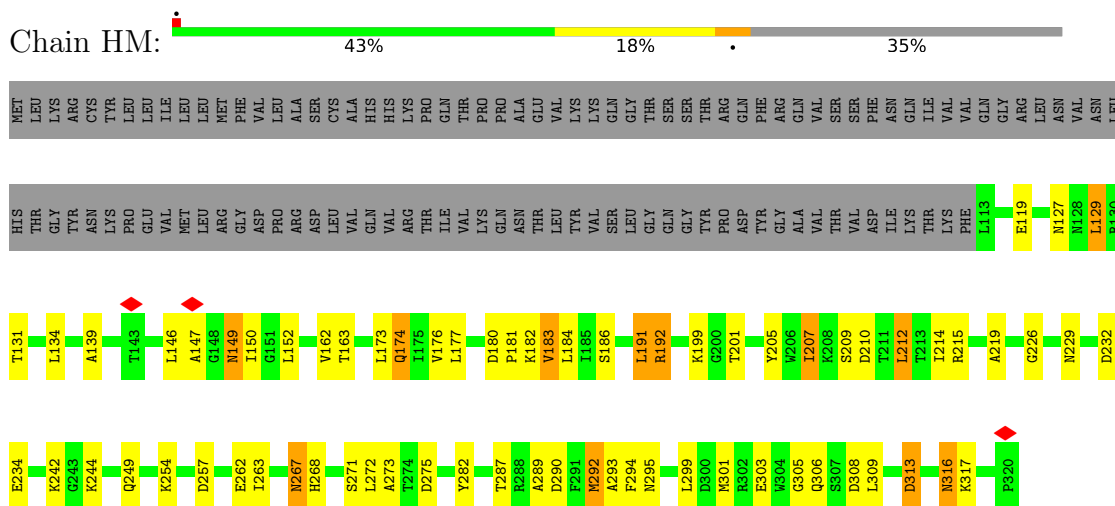


• Molecule 5: DUF2807 domain-containing protein

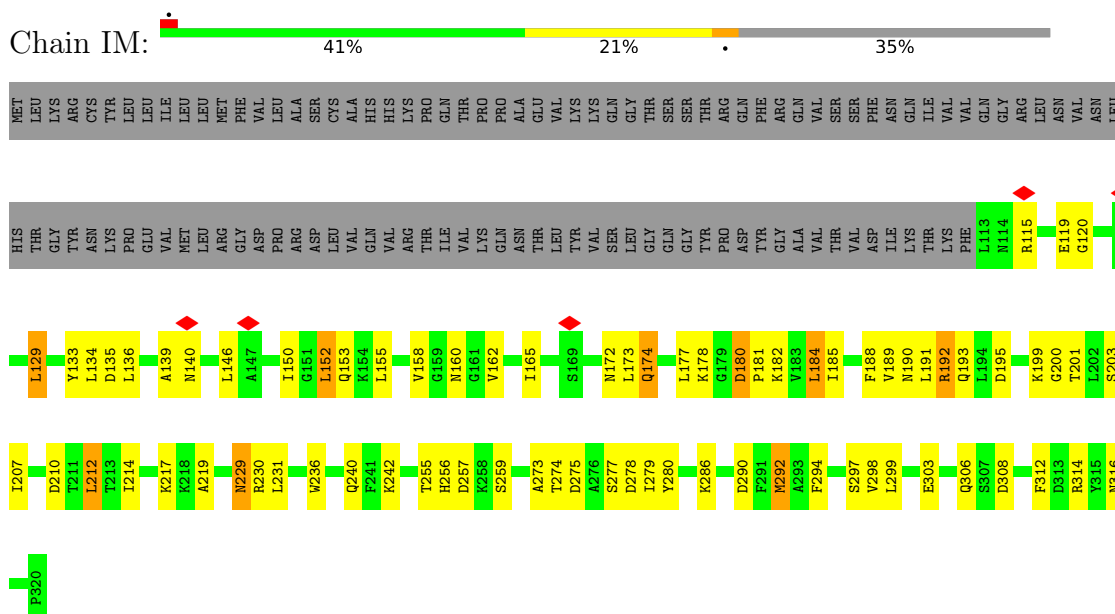




- Molecule 5: DUF2807 domain-containing protein

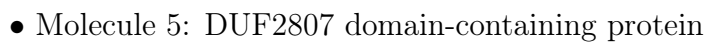


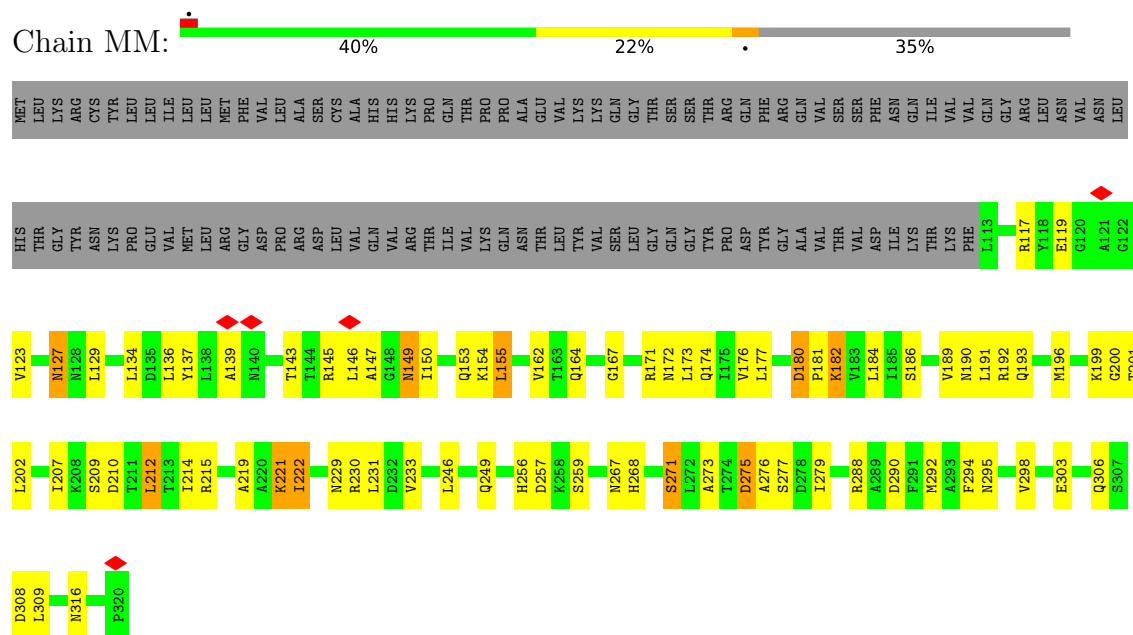
- Molecule 5: DUF2807 domain-containing protein



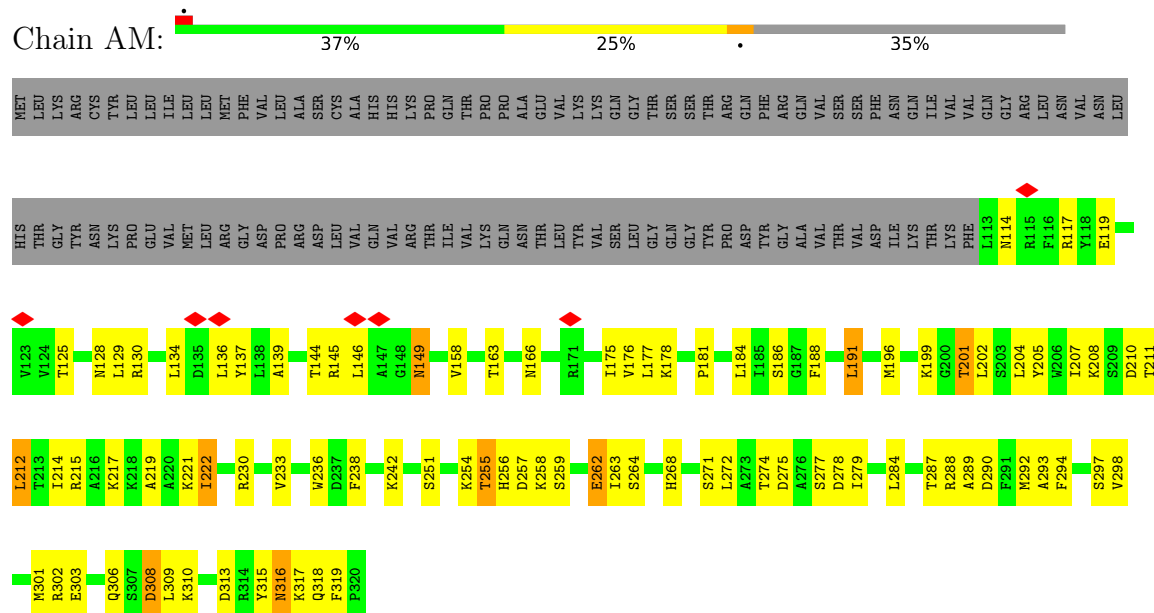
- Molecule 5: DUF2807 domain-containing protein



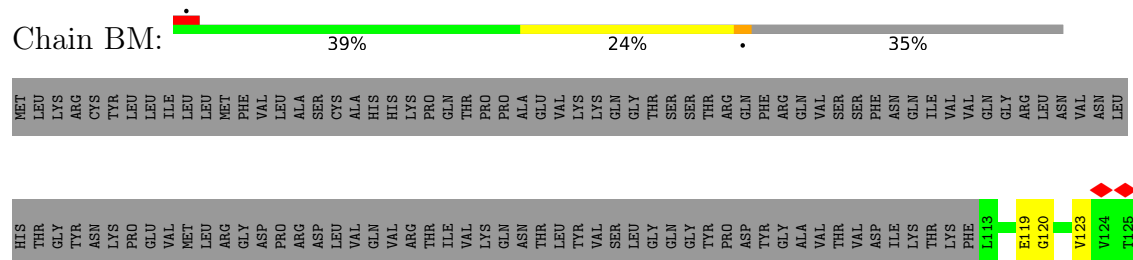


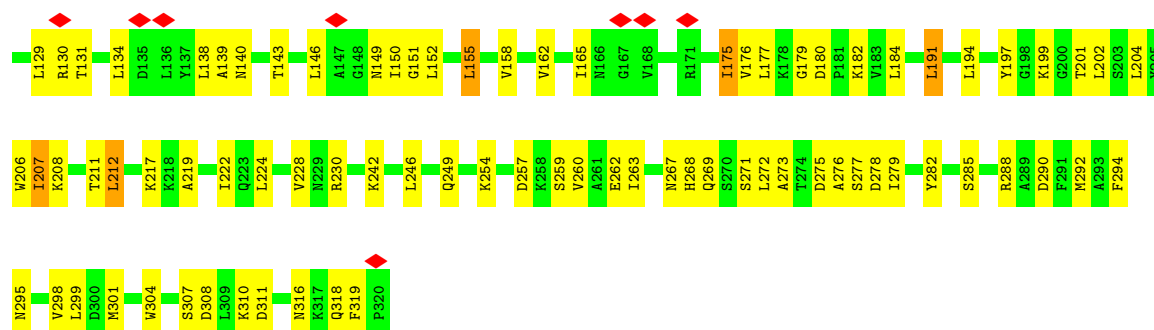


- Molecule 5: DUF2807 domain-containing protein

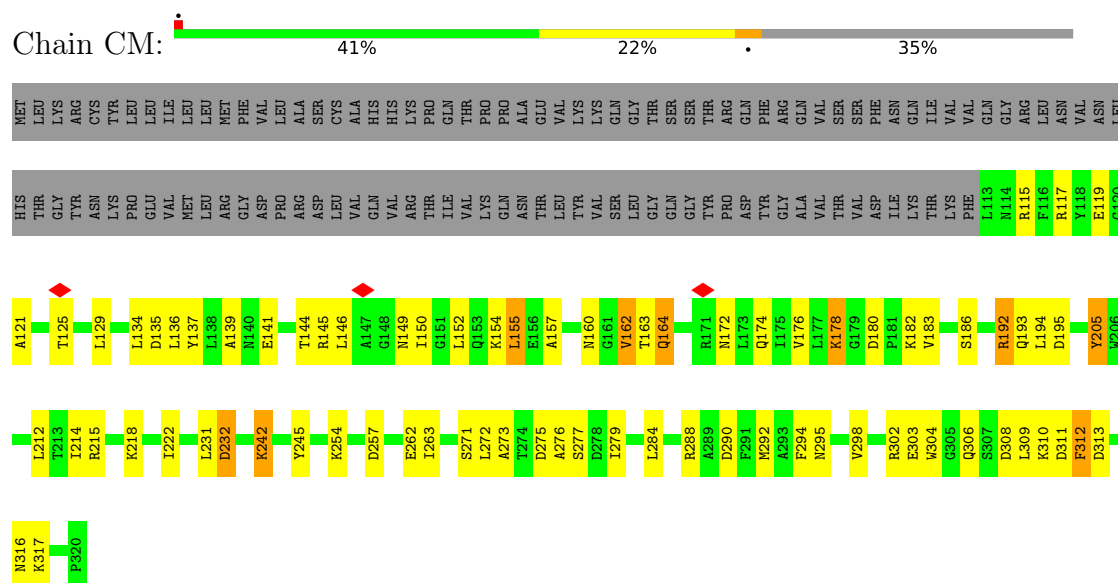


- Molecule 5: DUF2807 domain-containing protein

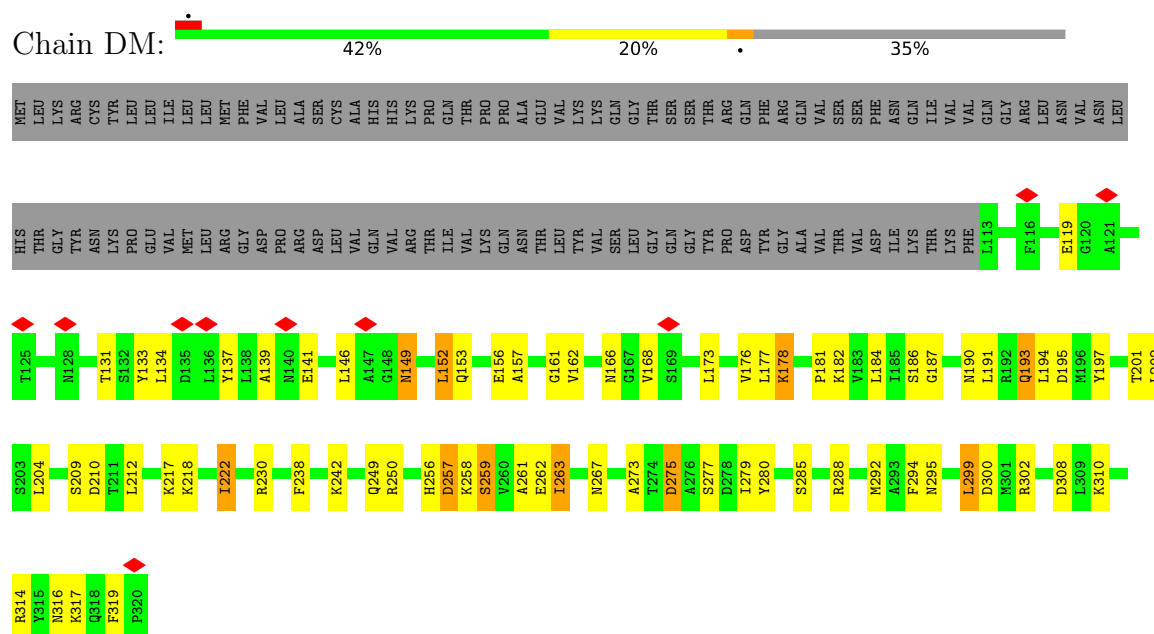




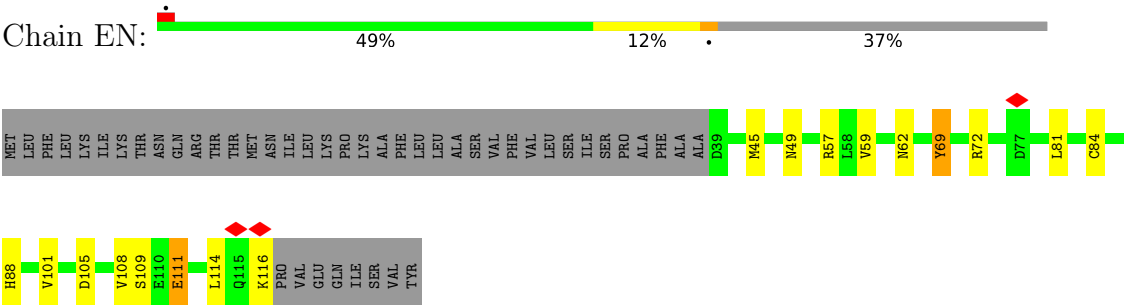
• Molecule 5: DUF2807 domain-containing protein



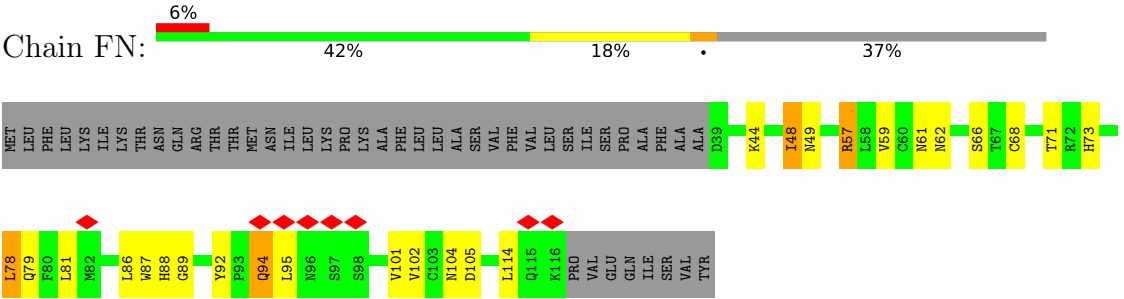
• Molecule 5: DUF2807 domain-containing protein



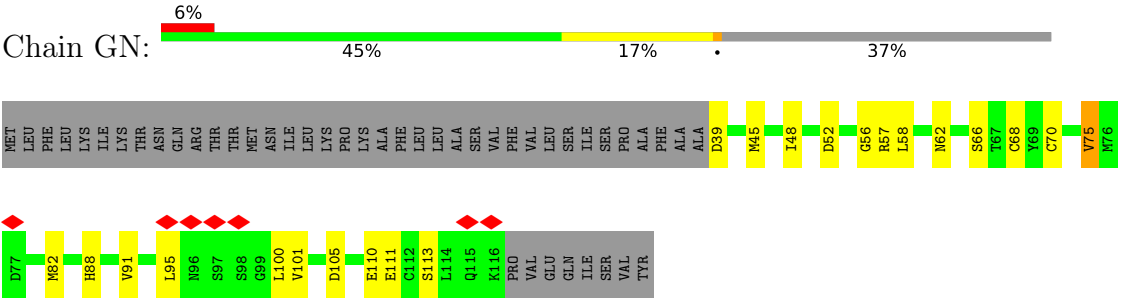
• Molecule 6: Neurogenic locus notch



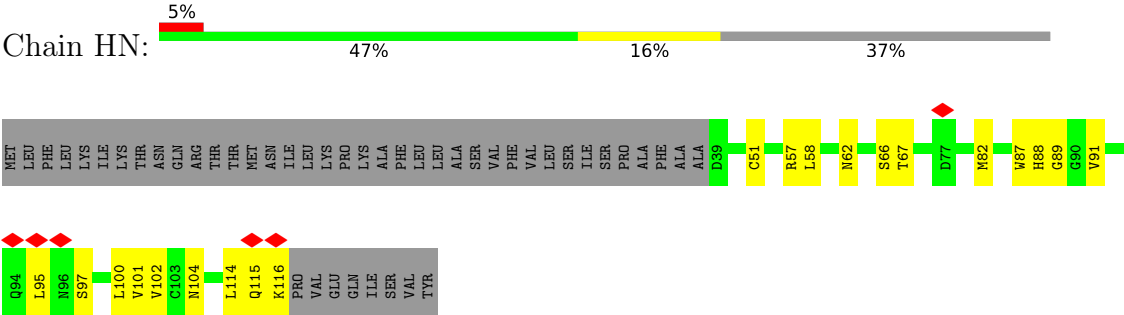
• Molecule 6: Neurogenic locus notch



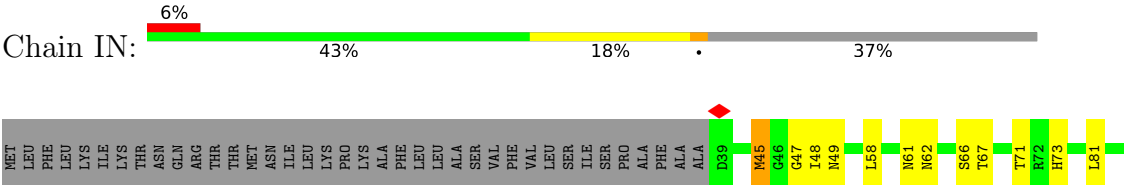
• Molecule 6: Neurogenic locus notch

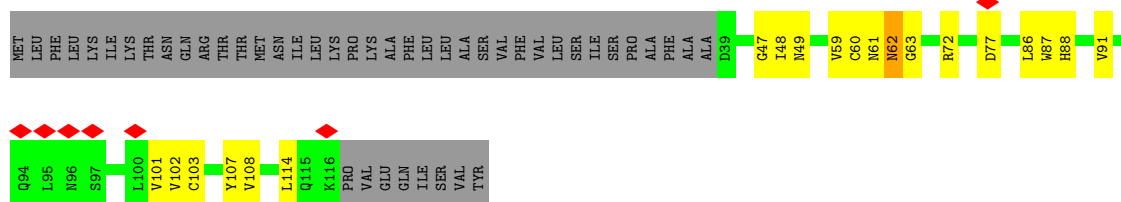


• Molecule 6: Neurogenic locus notch

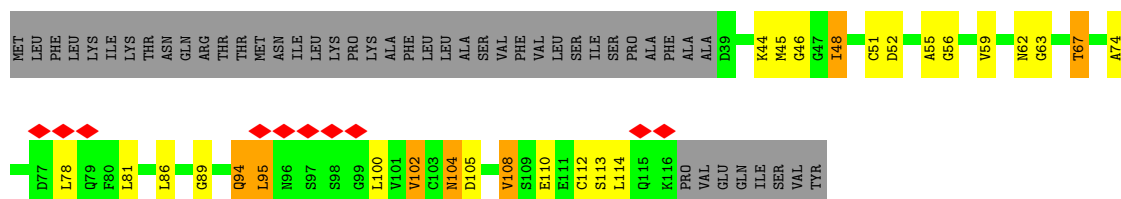


• Molecule 6: Neurogenic locus notch

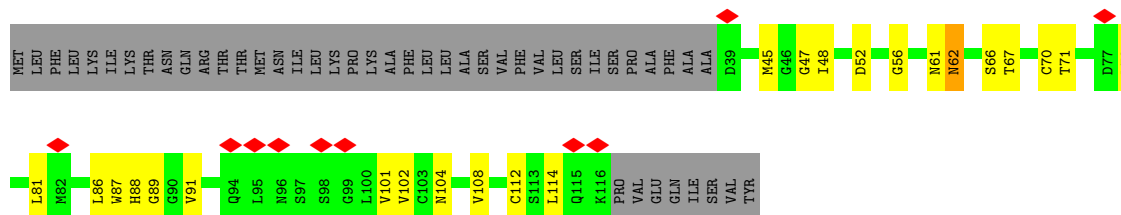




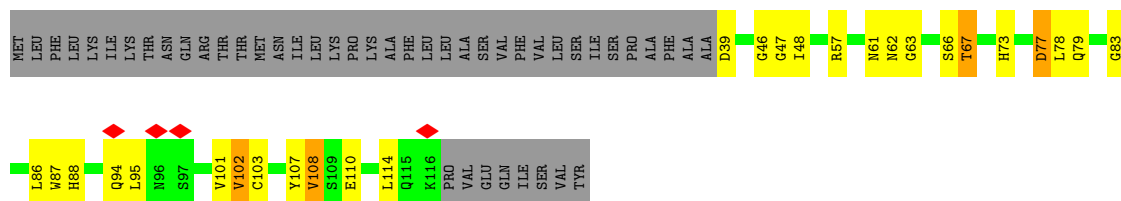
- Molecule 6: Neurogenic locus notch



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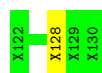


- Molecule 7: Unknown protein fragment



- Molecule 7: Unknown protein fragment

Chain FU:  89% 11%



- Molecule 7: Unknown protein fragment

Chain GU:  78% 22%

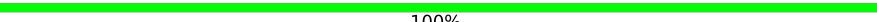


- Molecule 7: Unknown protein fragment

Chain HU:  100%

There are no outlier residues recorded for this chain.

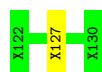
- Molecule 7: Unknown protein fragment

Chain IU:  100%

There are no outlier residues recorded for this chain.

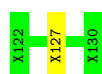
- Molecule 7: Unknown protein fragment

Chain JU:  89% 11%



- Molecule 7: Unknown protein fragment

Chain KU:  89% 11%



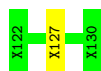
- Molecule 7: Unknown protein fragment

Chain LU:  89% 11%

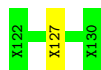


- Molecule 7: Unknown protein fragment

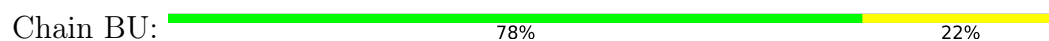
Chain MU:  89% 11%



- Molecule 7: Unknown protein fragment



- Molecule 7: Unknown protein fragment



- Molecule 7: Unknown protein fragment

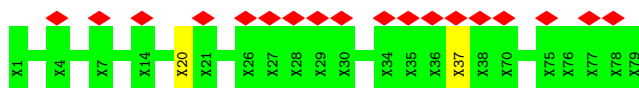
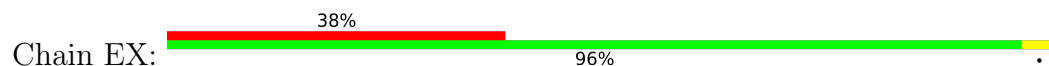


There are no outlier residues recorded for this chain.

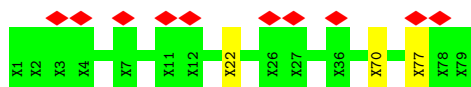
- Molecule 7: Unknown protein fragment



- Molecule 8: Unknown protein fragment

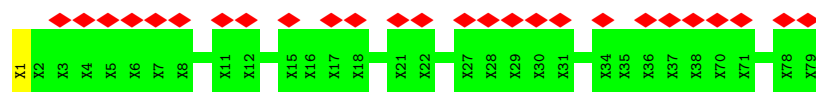


- Molecule 8: Unknown protein fragment

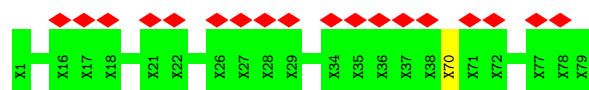
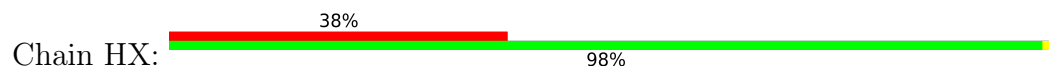


- Molecule 8: Unknown protein fragment

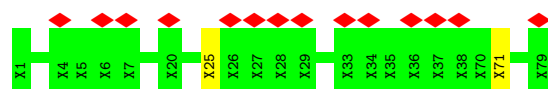




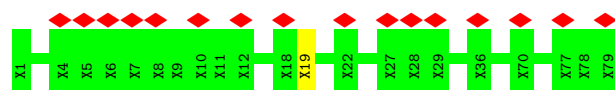
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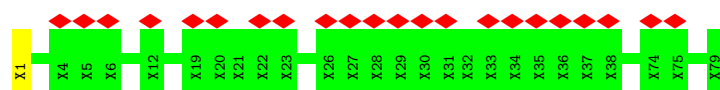
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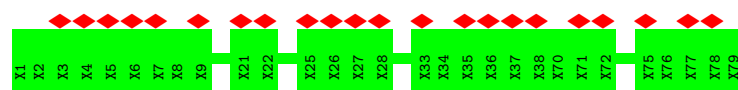
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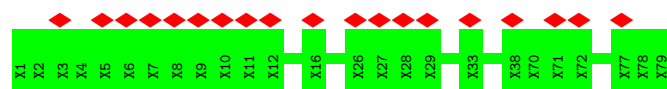
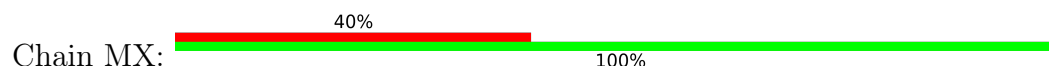
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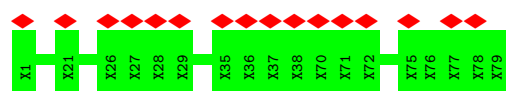
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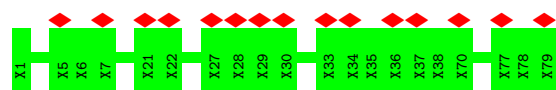
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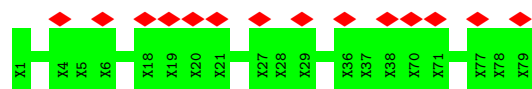
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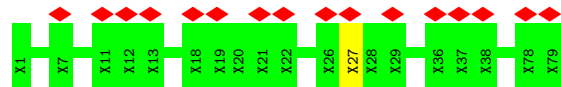
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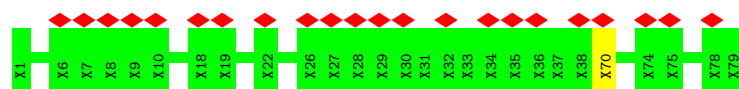
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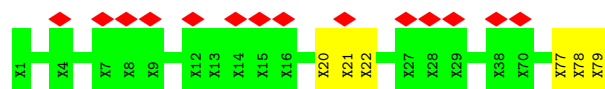
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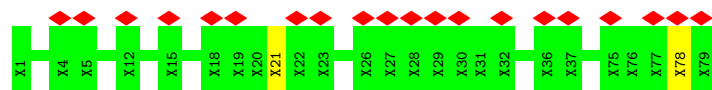
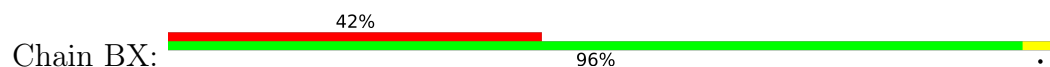
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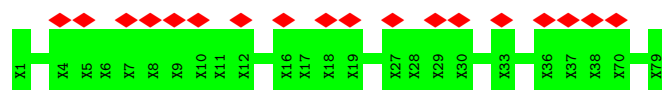
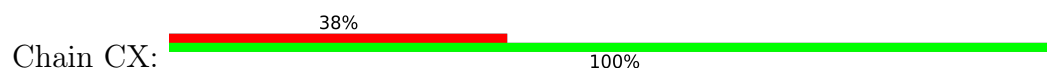
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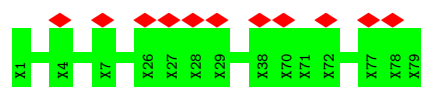
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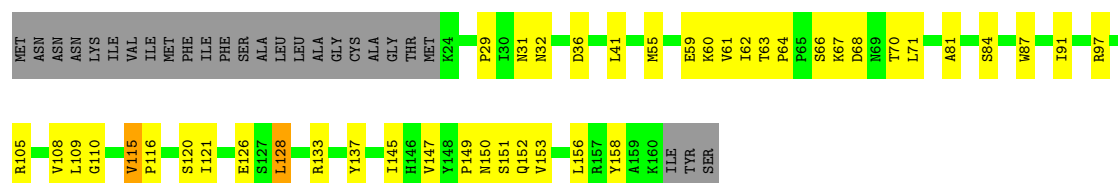
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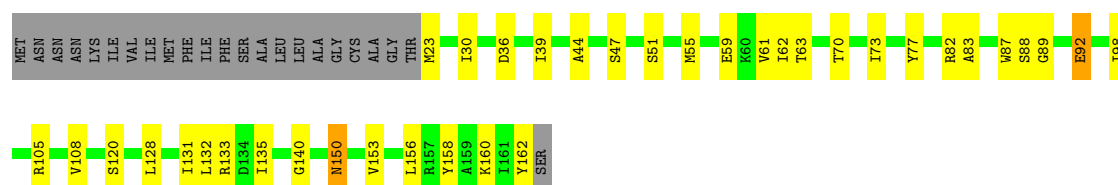
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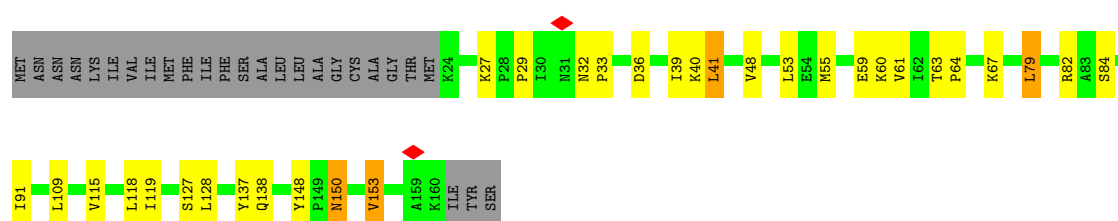
- Molecule 9: DotD



- Molecule 9: DotD

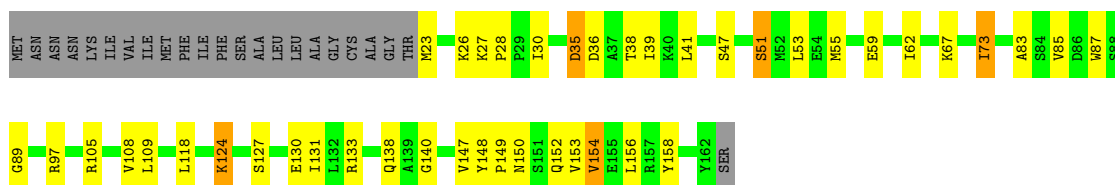


- Molecule 9: DotD

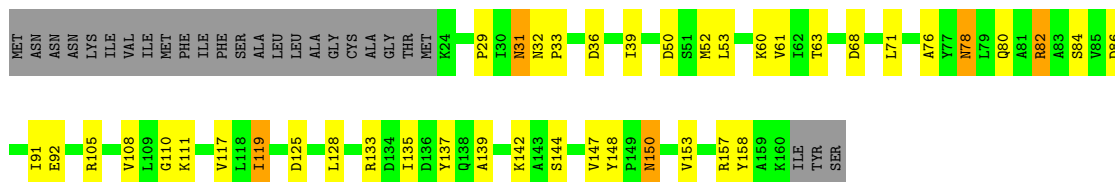


- Molecule 9: DotD

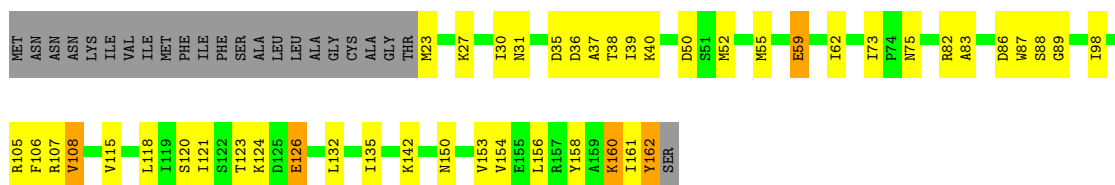




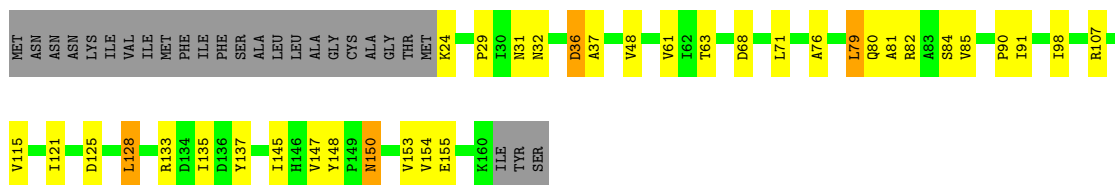
• Molecule 9: DotD



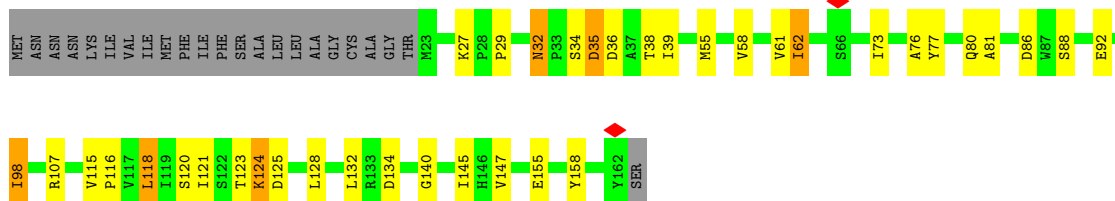
• Molecule 9: DotD



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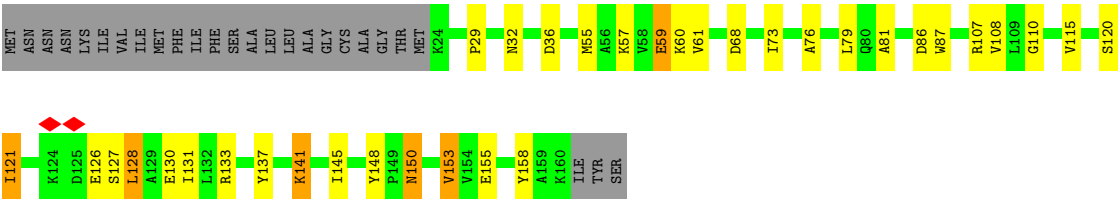


• Molecule 9: DotD

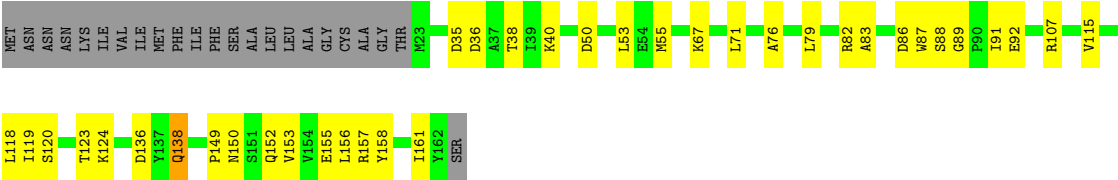


• Molecule 9: DotD

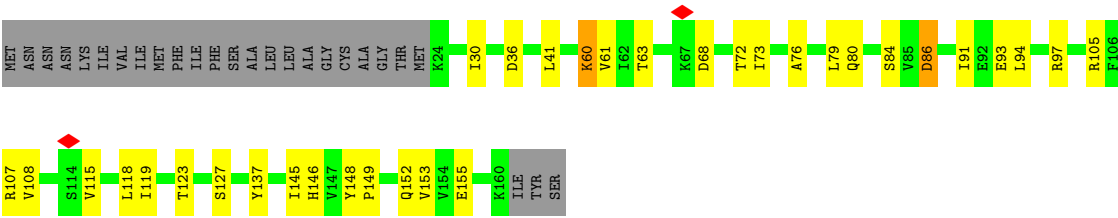




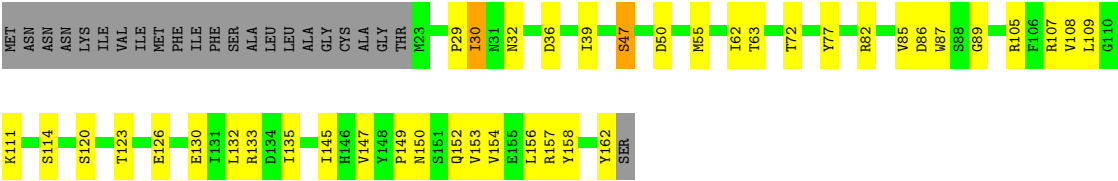
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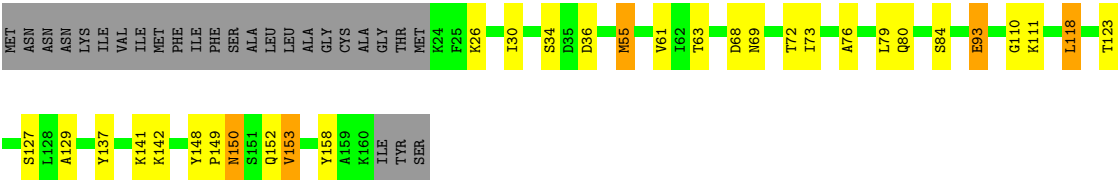
• Molecule 9: DotD



• Molecule 9: DotD

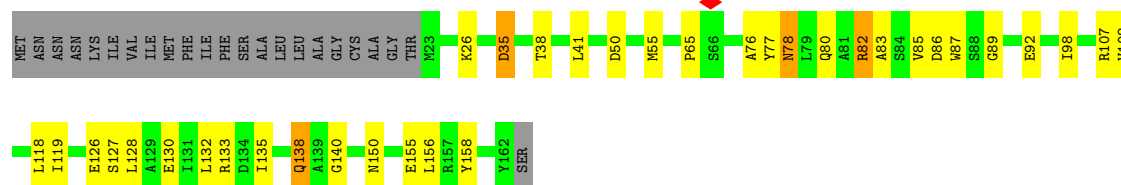


• Molecule 9: DotD



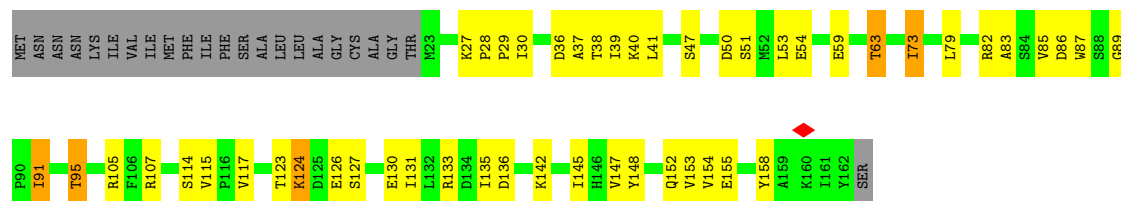
• Molecule 9: DotD

Chain CD: 



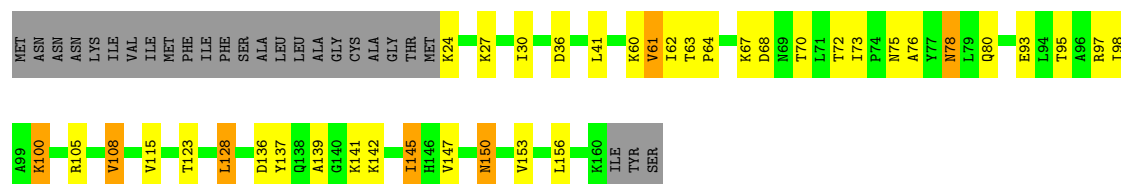
• Molecule 9: DotD

Chain LD: 



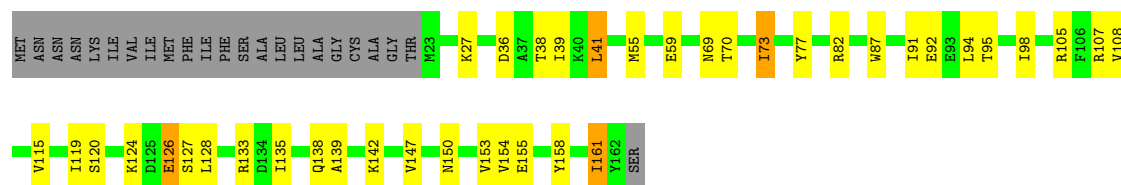
• Molecule 9: DotD

Chain Ld: 



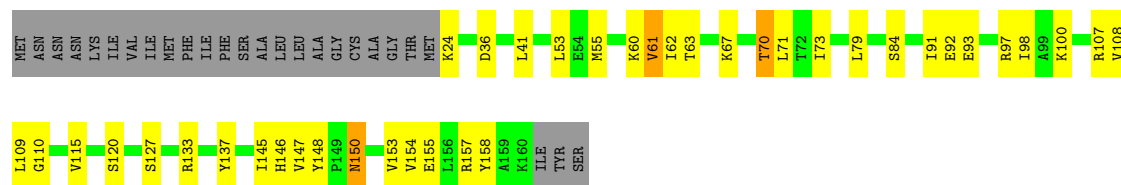
• Molecule 9: DotD

Chain MD: 



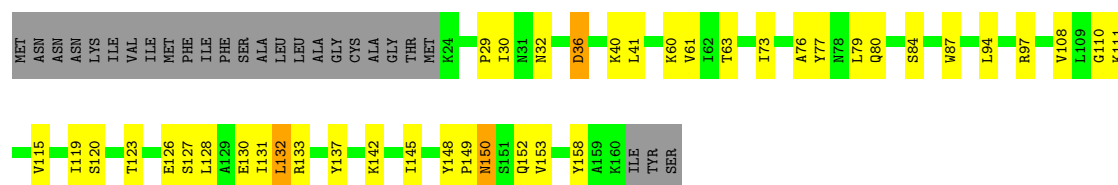
• Molecule 9: DotD

Chain Md: 



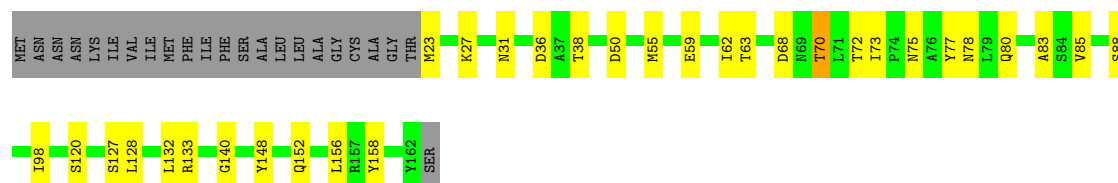
• Molecule 9: DotD

Chain Ad:  59% 23% 16%



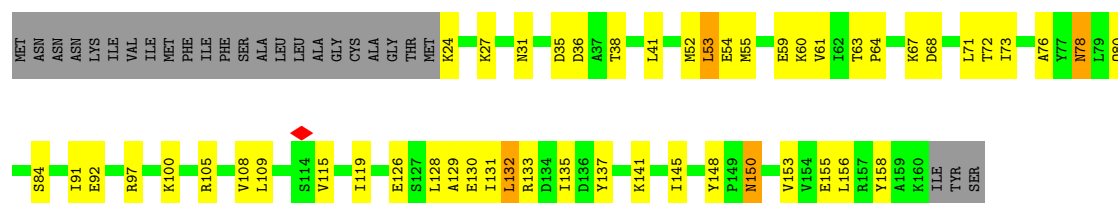
• Molecule 9: DotD

Chain BD:  66% 19% 14%



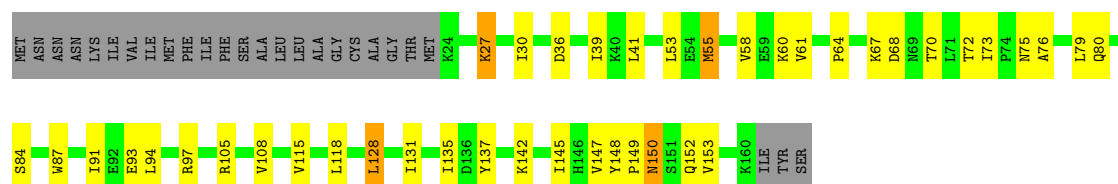
• Molecule 9: DotD

Chain Bd:  53% 29% 16%



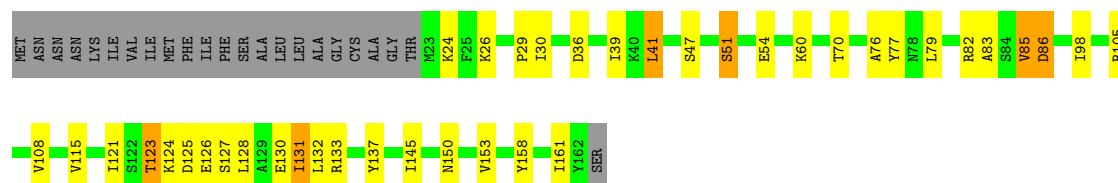
• Molecule 9: DotD

Chain Cd:  58% 23% 16%



• Molecule 9: DotD

Chain DD:  61% 21% 14%



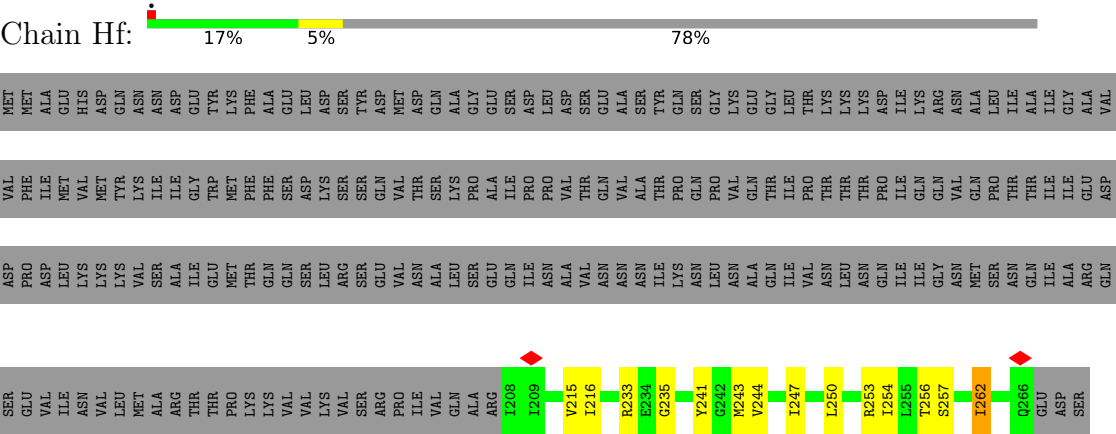
• Molecule 9: DotD



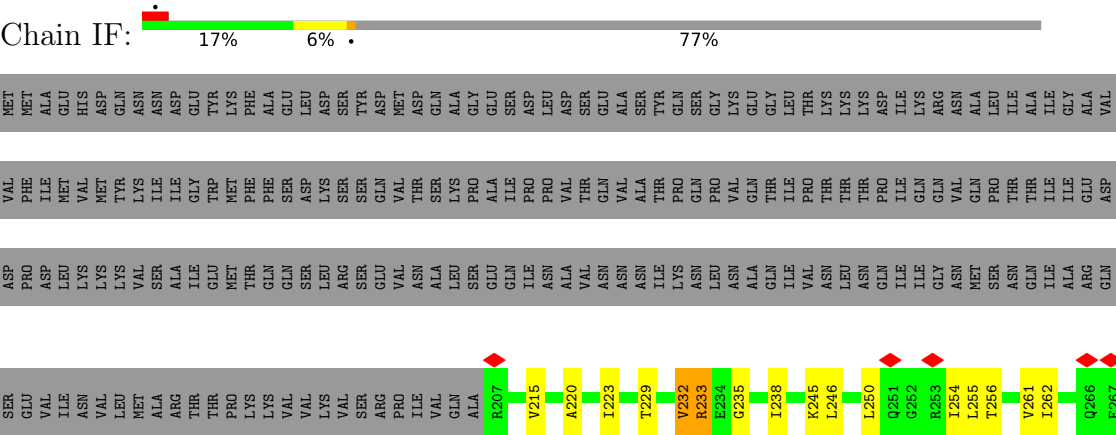
WORLD WIDE
PDB
PROTEIN DATA BANK



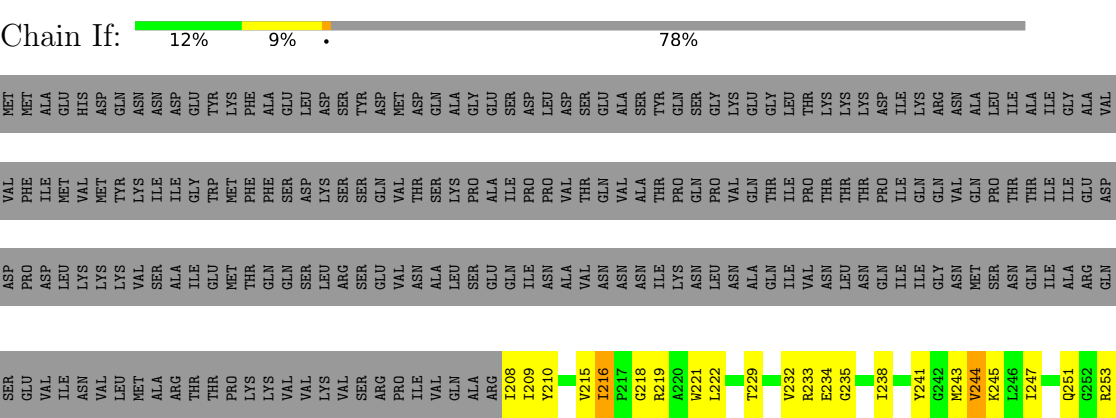
• Molecule 10: DotF

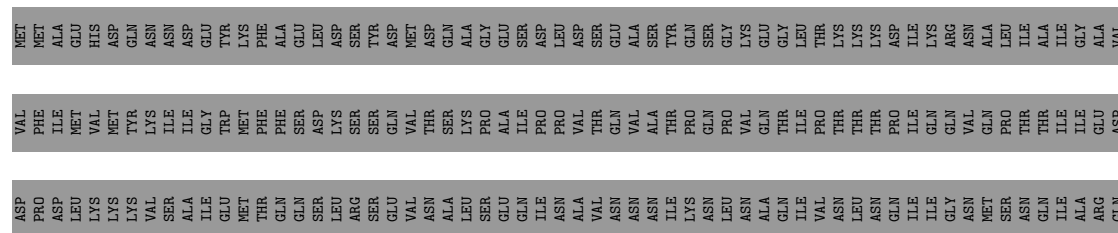


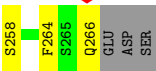
• Molecule 10: DotF



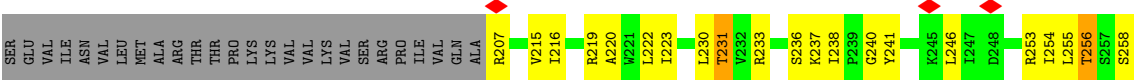
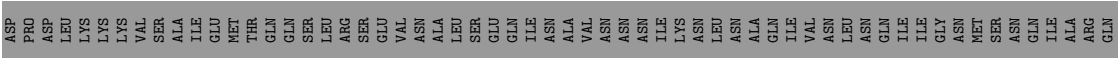
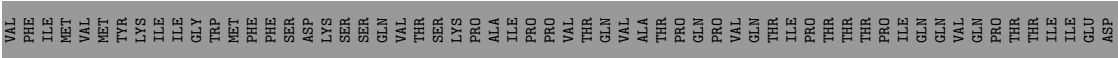
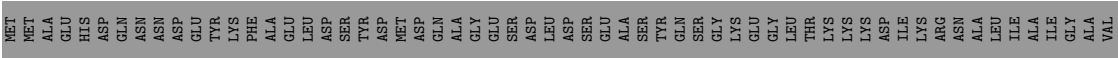
• Molecule 10: DotF



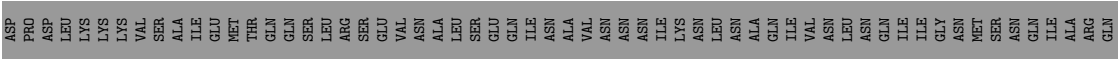
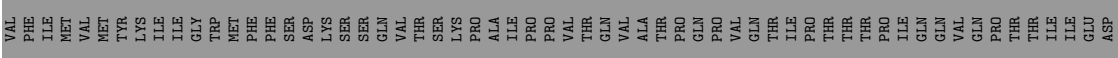
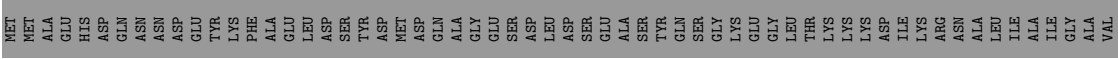




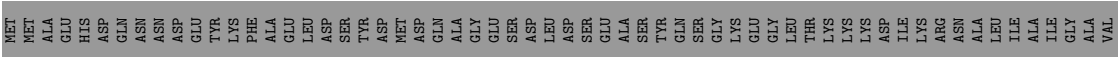
• Molecule 10: DotF

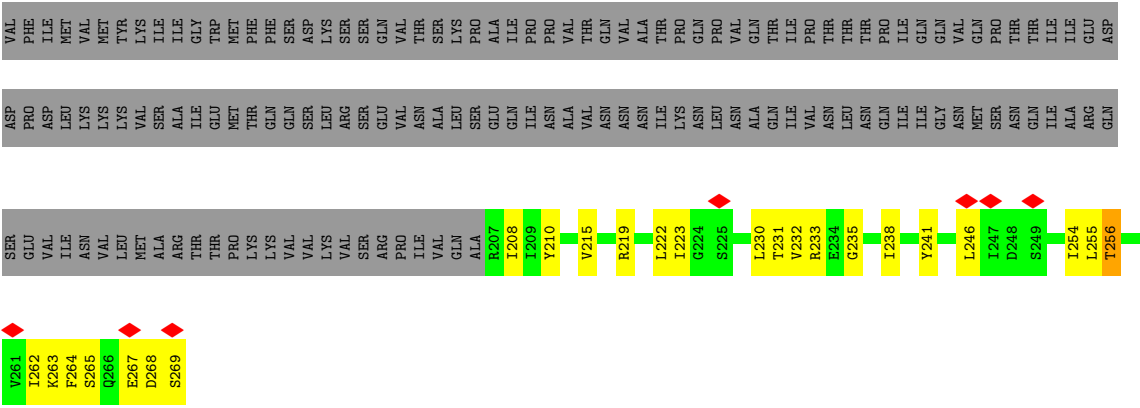


• Molecule 10: DotF

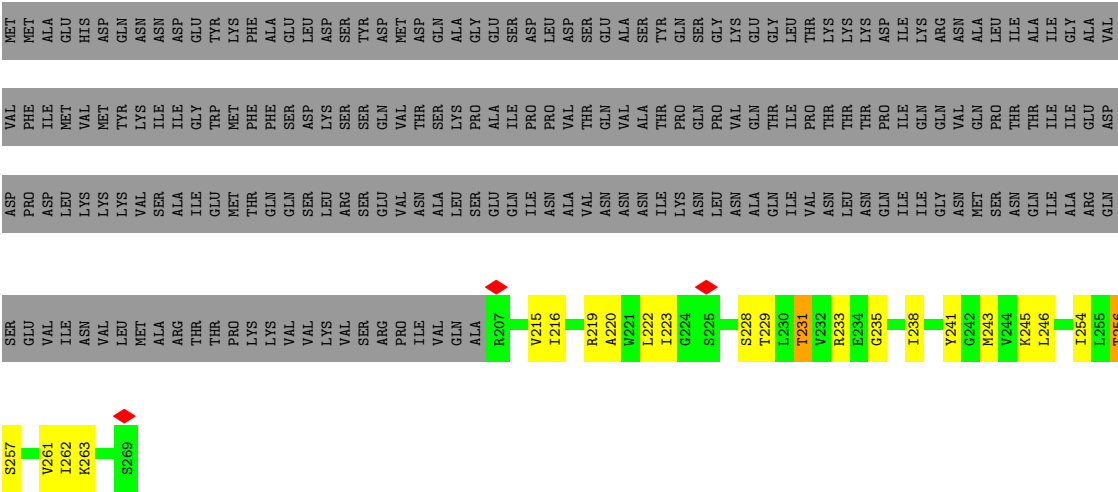


• Molecule 10: DotF

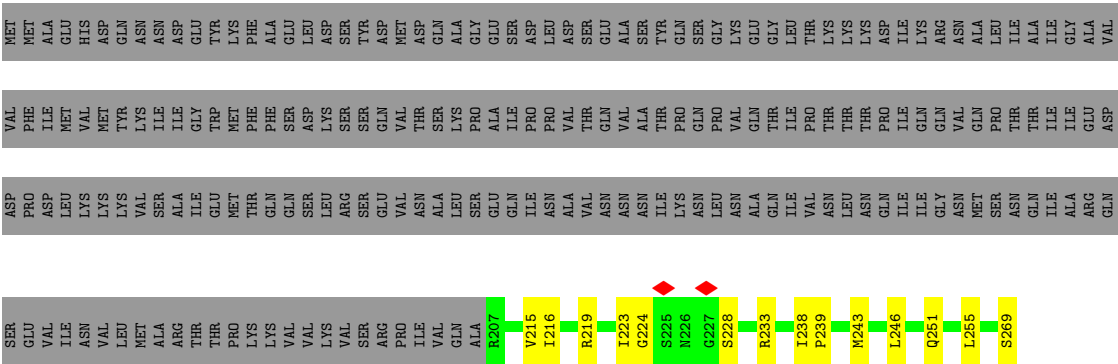




● Molecule 10: DotF



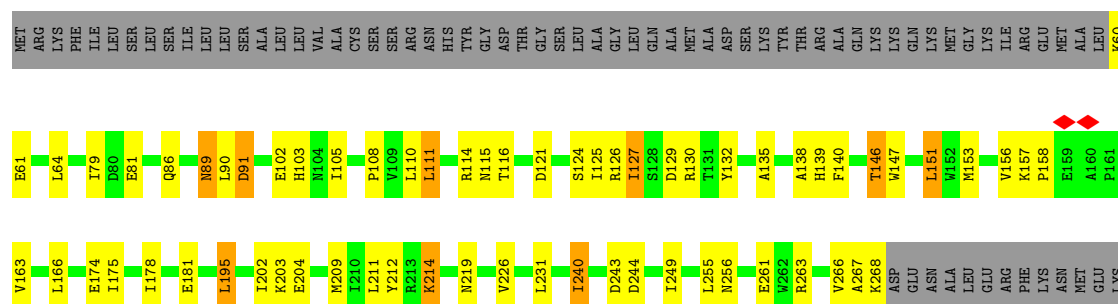
● Molecule 10: DotF



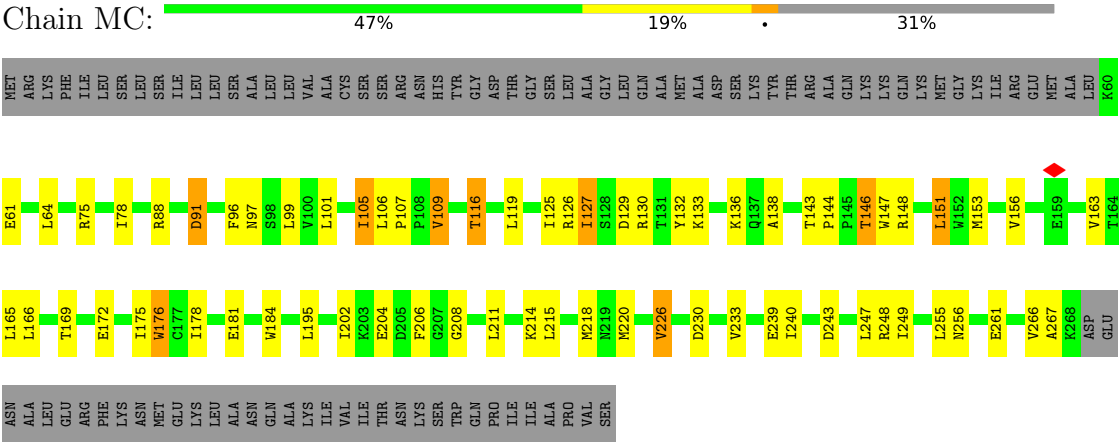
● Molecule 10: DotF



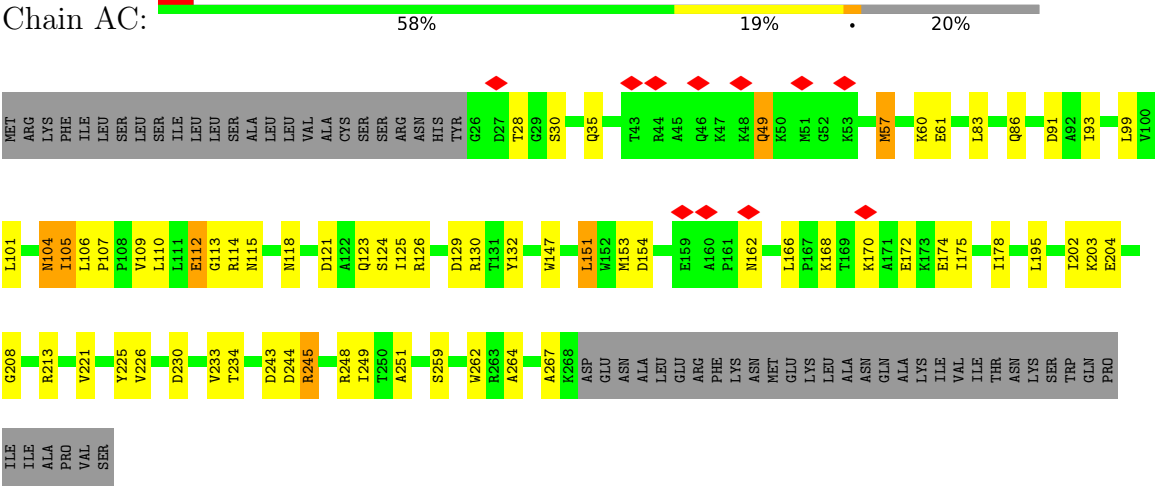




• Molecule 11: DotC



• Molecule 11: DotC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42013	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	7.809	Depositor
Minimum map value	-3.314	Depositor
Average map value	0.095	Depositor
Map value standard deviation	0.541	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	0.52	0/1699
1	Ag	0.14	0/278	0.31	0/377
1	BG	0.22	0/1250	0.54	1/1699 (0.1%)
1	Bg	0.18	0/278	0.35	0/377
1	CG	0.22	0/1250	0.54	0/1699
1	Cg	0.15	0/278	0.32	0/377
1	DG	0.22	0/1250	0.54	0/1699
1	Dg	0.18	0/278	0.34	0/377
1	EG	0.21	0/1250	0.52	1/1699 (0.1%)
1	Eg	0.16	0/278	0.36	0/377
1	FG	0.22	0/1250	0.51	0/1699
1	Fg	0.14	0/278	0.33	0/377
1	GG	0.22	0/1250	0.53	0/1699
1	Gg	0.17	0/278	0.38	0/377
1	HG	0.22	0/1250	0.55	0/1699
1	Hg	0.15	0/278	0.33	0/377
1	IG	0.21	0/1250	0.52	0/1699
1	Ig	0.16	0/278	0.32	0/377
1	JG	0.21	0/1250	0.55	1/1699 (0.1%)
1	Jg	0.16	0/278	0.35	0/377
1	KG	0.23	0/1250	0.55	2/1699 (0.1%)
1	Kg	0.17	0/278	0.34	0/377
1	LG	0.21	0/1250	0.53	1/1699 (0.1%)
1	Lg	0.16	0/278	0.36	0/377
1	MG	0.21	0/1250	0.50	0/1699
1	Mg	0.16	0/278	0.36	0/377
1	NG	0.21	0/1250	0.55	0/1699
1	OG	0.21	0/1250	0.53	0/1699
1	PG	0.21	0/1250	0.53	0/1699
1	VG	0.17	0/278	0.47	0/377
1	WG	0.17	0/278	0.36	0/377
1	XG	0.19	0/278	0.53	0/377
1	YG	0.18	0/278	0.43	0/377
1	ZG	0.18	0/278	0.45	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AH	0.19	0/2033	0.41	0/2775
2	BH	0.19	0/2033	0.41	0/2775
2	CH	0.18	0/2033	0.40	0/2775
2	DH	0.19	0/2033	0.40	0/2775
2	EH	0.18	0/2033	0.40	0/2775
2	FH	0.18	0/2033	0.40	0/2775
2	GH	0.19	0/2033	0.40	0/2775
2	HH	0.18	0/2033	0.39	0/2775
2	IH	0.18	0/2033	0.41	0/2775
2	JH	0.17	0/2033	0.38	0/2775
2	KH	0.18	0/2033	0.40	0/2775
2	LH	0.22	0/2033	0.44	0/2775
2	MH	0.18	0/2033	0.39	0/2775
2	VH	0.16	0/1921	0.40	0/2620
2	WH	0.16	0/1921	0.39	0/2620
2	XH	0.16	0/1921	0.40	0/2620
2	YH	0.17	0/1921	0.41	0/2620
2	ZH	0.16	0/1921	0.40	0/2620
3	AK	0.20	0/1195	0.41	0/1616
3	BK	0.20	0/1195	0.42	0/1616
3	CK	0.20	0/1195	0.38	0/1616
3	DK	0.20	0/1195	0.39	0/1616
3	EK	0.20	0/1195	0.40	0/1616
3	FK	0.20	0/1195	0.41	0/1616
3	GK	0.20	0/1195	0.41	0/1616
3	HK	0.20	0/1195	0.38	0/1616
3	IK	0.21	0/1195	0.40	0/1616
3	JK	0.20	0/1195	0.41	0/1616
3	KK	0.20	0/1195	0.40	0/1616
3	LK	0.20	0/1195	0.41	0/1616
3	MK	0.19	0/1195	0.37	0/1616
4	AL	0.20	0/1417	0.45	0/1912
4	BL	0.20	0/1417	0.44	0/1912
4	CL	0.20	0/1417	0.43	0/1912
4	DL	0.20	0/1417	0.45	0/1912
4	EL	0.20	0/1417	0.44	0/1912
4	FL	0.20	0/1417	0.43	0/1912
4	GL	0.20	0/1417	0.45	0/1912
4	HL	0.20	0/1417	0.44	0/1912
4	IL	0.20	0/1417	0.44	0/1912
4	JL	0.19	0/1417	0.46	0/1912
4	KL	0.20	0/1417	0.44	0/1912
4	LL	0.20	0/1417	0.46	0/1912

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ML	0.20	0/1417	0.42	0/1912
5	AM	0.18	0/1678	0.44	0/2262
5	BM	0.18	0/1678	0.42	0/2262
5	CM	0.18	0/1678	0.43	0/2262
5	DM	0.18	0/1678	0.42	0/2262
5	EM	0.18	0/1678	0.41	0/2262
5	FM	0.18	0/1678	0.42	0/2262
5	GM	0.17	0/1678	0.39	0/2262
5	HM	0.18	0/1678	0.43	0/2262
5	IM	0.19	0/1678	0.45	0/2262
5	JM	0.17	0/1678	0.43	0/2262
5	KM	0.18	0/1678	0.43	0/2262
5	LM	0.17	0/1678	0.41	0/2262
5	MM	0.18	0/1678	0.41	0/2262
6	AN	0.19	0/593	0.36	0/799
6	BN	0.19	0/593	0.38	0/799
6	CN	0.18	0/593	0.40	0/799
6	DN	0.18	0/593	0.37	0/799
6	EN	0.19	0/593	0.39	0/799
6	FN	0.18	0/593	0.37	0/799
6	GN	0.18	0/593	0.40	0/799
6	HN	0.18	0/593	0.38	0/799
6	IN	0.19	0/593	0.39	0/799
6	JN	0.19	0/593	0.37	0/799
6	KN	0.19	0/593	0.38	0/799
6	LN	0.19	0/593	0.38	0/799
6	MN	0.20	0/593	0.42	0/799
9	AD	0.22	0/1107	0.49	0/1502
9	Ad	0.18	0/1078	0.37	0/1463
9	BD	0.19	0/1107	0.46	0/1502
9	Bd	0.17	0/1078	0.37	0/1463
9	CD	0.20	0/1107	0.47	0/1502
9	Cd	0.17	0/1078	0.38	0/1463
9	DD	0.21	0/1107	0.48	0/1502
9	Dd	0.18	0/1078	0.42	0/1463
9	ED	0.20	0/1107	0.49	0/1502
9	Ed	0.17	0/1078	0.37	0/1463
9	FD	0.21	0/1107	0.49	0/1502
9	Fd	0.18	0/1078	0.40	0/1463
9	GD	0.21	0/1107	0.49	0/1502
9	Gd	0.18	0/1078	0.39	0/1463
9	HD	0.21	0/1107	0.50	0/1502
9	Hd	0.17	0/1078	0.40	0/1463

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	ID	0.21	0/1107	0.51	0/1502
9	Id	0.18	0/1078	0.41	0/1463
9	JD	0.20	0/1107	0.47	0/1502
9	Jd	0.18	0/1078	0.36	0/1463
9	KD	0.20	0/1107	0.48	0/1502
9	Kd	0.17	0/1078	0.36	0/1463
9	LD	0.21	0/1107	0.47	0/1502
9	Ld	0.18	0/1078	0.39	0/1463
9	MD	0.21	0/1107	0.48	0/1502
9	Md	0.18	0/1078	0.42	0/1463
10	AF	0.14	0/490	0.34	0/660
10	Af	0.17	0/456	0.50	0/615
10	BF	0.14	0/490	0.30	0/660
10	Bf	0.15	0/456	0.33	0/615
10	CF	0.15	0/490	0.32	0/660
10	Cf	0.16	0/456	0.35	0/615
10	DF	0.15	0/490	0.38	0/660
10	Df	0.14	0/456	0.35	0/615
10	EF	0.14	0/490	0.35	0/660
10	Ef	0.15	0/456	0.34	0/615
10	FF	0.15	0/490	0.34	0/660
10	Ff	0.15	0/456	0.33	0/615
10	GF	0.14	0/490	0.35	0/660
10	Gf	0.15	0/456	0.35	0/615
10	HF	0.16	0/490	0.39	0/660
10	Hf	0.15	0/456	0.36	0/615
10	IF	0.16	0/490	0.33	0/660
10	If	0.15	0/456	0.36	0/615
10	JF	0.14	0/490	0.39	0/660
10	Jf	0.14	0/456	0.31	0/615
10	KF	0.14	0/490	0.36	0/660
10	Kf	0.15	0/456	0.34	0/615
10	LF	0.17	0/490	0.39	0/660
10	Lf	0.16	0/456	0.38	0/615
10	MF	0.16	0/490	0.34	0/660
10	Mf	0.14	0/456	0.31	0/615
10	VF	0.13	0/490	0.33	0/660
10	WF	0.15	0/490	0.33	0/660
10	XF	0.14	0/490	0.31	0/660
10	YF	0.14	0/490	0.34	0/660
10	ZF	0.14	0/490	0.33	0/660
11	AC	0.20	0/1957	0.40	0/2651
11	BC	0.20	0/1957	0.39	0/2651

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CC	0.20	0/1702	0.40	0/2315
11	DC	0.20	0/1702	0.39	0/2315
11	EC	0.21	0/1702	0.43	0/2315
11	FC	0.20	0/1957	0.39	0/2651
11	GC	0.21	0/1702	0.42	0/2315
11	HC	0.20	0/1702	0.40	0/2315
11	IC	0.20	0/1702	0.40	0/2315
11	JC	0.20	0/1957	0.40	0/2651
11	KC	0.20	0/1702	0.39	0/2315
11	LC	0.20	0/1702	0.42	0/2315
11	MC	0.21	0/1702	0.42	0/2315
All	All	0.19	0/190816	0.42	6/258661 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	BH	0	1
2	JH	0	1
2	MH	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	LG	939	THR	N-CA-C	-6.46	106.36	114.56
1	KG	1009	ALA	CA-C-N	-5.36	113.32	122.11
1	KG	1009	ALA	C-N-CA	-5.36	113.32	122.11
1	BG	939	THR	N-CA-C	-5.35	107.77	114.56
1	EG	939	THR	N-CA-C	-5.22	107.93	114.56

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	BH	321	SER	Peptide
2	JH	321	SER	Peptide
2	MH	321	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	1229	0	1231	25	0
1	Ag	276	0	263	10	0
1	BG	1229	0	1231	36	0
1	Bg	276	0	263	10	0
1	CG	1229	0	1231	27	0
1	Cg	276	0	263	4	0
1	DG	1229	0	1231	33	0
1	Dg	276	0	263	7	0
1	EG	1229	0	1231	25	0
1	Eg	276	0	263	7	0
1	FG	1229	0	1231	23	0
1	Fg	276	0	263	9	0
1	GG	1229	0	1231	30	0
1	Gg	276	0	263	15	0
1	HG	1229	0	1231	29	0
1	Hg	276	0	263	8	0
1	IG	1229	0	1231	31	0
1	Ig	276	0	263	11	0
1	JG	1229	0	1231	28	0
1	Jg	276	0	263	8	0
1	KG	1229	0	1231	32	0
1	Kg	276	0	263	11	0
1	LG	1229	0	1231	33	0
1	Lg	276	0	263	4	0
1	MG	1229	0	1231	27	0
1	Mg	276	0	263	8	0
1	NG	1229	0	1231	34	0
1	OG	1229	0	1231	27	0
1	PG	1229	0	1231	26	0
1	VG	276	0	263	7	0
1	WG	276	0	263	2	0
1	XG	276	0	263	5	0
1	YG	276	0	263	3	0
1	ZG	276	0	263	6	0
2	AH	1983	0	2009	43	0
2	BH	1983	0	2009	43	0
2	CH	1983	0	2009	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	DH	1983	0	2009	44	0
2	EH	1983	0	2009	46	0
2	FH	1983	0	2009	46	0
2	GH	1983	0	2009	42	0
2	HH	1983	0	2009	42	0
2	IH	1983	0	2009	38	0
2	JH	1983	0	2009	48	0
2	KH	1983	0	2009	42	0
2	LH	1983	0	2009	51	0
2	MH	1983	0	2009	37	0
2	VH	1875	0	1900	38	0
2	WH	1875	0	1900	35	0
2	XH	1875	0	1900	47	0
2	YH	1875	0	1900	45	0
2	ZH	1875	0	1900	30	0
3	AK	1175	0	1221	26	0
3	BK	1175	0	1221	22	0
3	CK	1175	0	1221	27	0
3	DK	1175	0	1221	23	0
3	EK	1175	0	1221	23	0
3	FK	1175	0	1221	25	0
3	GK	1175	0	1221	23	0
3	HK	1175	0	1221	22	0
3	IK	1175	0	1221	23	0
3	JK	1175	0	1221	28	0
3	KK	1175	0	1221	30	0
3	LK	1175	0	1221	31	0
3	MK	1175	0	1221	25	0
4	AL	1388	0	1378	31	0
4	BL	1388	0	1378	32	0
4	CL	1388	0	1378	25	0
4	DL	1388	0	1378	36	0
4	EL	1388	0	1378	33	0
4	FL	1388	0	1378	27	0
4	GL	1388	0	1378	29	0
4	HL	1388	0	1378	32	0
4	IL	1388	0	1378	24	0
4	JL	1388	0	1378	24	0
4	KL	1388	0	1378	30	0
4	LL	1388	0	1378	26	0
4	ML	1388	0	1378	28	0
5	AM	1650	0	1658	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	BM	1650	0	1658	44	0
5	CM	1650	0	1658	41	0
5	DM	1650	0	1658	39	0
5	EM	1650	0	1658	43	0
5	FM	1650	0	1658	52	0
5	GM	1650	0	1658	44	0
5	HM	1650	0	1658	41	0
5	IM	1650	0	1658	44	0
5	JM	1650	0	1658	41	0
5	KM	1650	0	1658	42	0
5	LM	1650	0	1658	36	0
5	MM	1650	0	1658	46	0
6	AN	582	0	530	9	0
6	BN	582	0	530	14	0
6	CN	582	0	530	10	0
6	DN	582	0	530	14	0
6	EN	582	0	530	6	0
6	FN	582	0	530	14	0
6	GN	582	0	530	10	0
6	HN	582	0	530	10	0
6	IN	582	0	530	12	0
6	JN	582	0	530	11	0
6	KN	582	0	530	9	0
6	LN	582	0	530	7	0
6	MN	582	0	530	6	0
7	AU	45	0	12	1	0
7	BU	45	0	12	2	0
7	CU	45	0	12	0	0
7	DU	45	0	12	1	0
7	EU	45	0	12	1	0
7	FU	45	0	12	1	0
7	GU	45	0	12	2	0
7	HU	45	0	12	0	0
7	IU	45	0	12	0	0
7	JU	45	0	12	1	0
7	KU	45	0	13	1	0
7	LU	45	0	12	1	0
7	MU	45	0	12	1	0
8	AX	240	0	54	3	0
8	BX	240	0	57	2	0
8	CX	240	0	58	0	0
8	DX	240	0	55	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	EX	240	0	56	1	0
8	FX	240	0	57	2	0
8	GX	240	0	55	1	0
8	HX	240	0	55	1	0
8	IX	240	0	56	1	0
8	JX	240	0	59	1	0
8	KX	240	0	56	1	0
8	LX	240	0	59	0	0
8	MX	240	0	52	0	0
8	VX	240	0	57	0	0
8	WX	240	0	58	0	0
8	XX	240	0	54	0	0
8	YX	240	0	54	1	0
8	ZX	240	0	55	1	0
9	AD	1086	0	1121	20	0
9	Ad	1058	0	1092	19	0
9	BD	1086	0	1121	20	0
9	Bd	1058	0	1092	28	0
9	CD	1086	0	1121	17	0
9	Cd	1058	0	1092	24	0
9	DD	1086	0	1121	30	0
9	Dd	1058	0	1092	14	0
9	ED	1086	0	1121	26	0
9	Ed	1058	0	1092	23	0
9	FD	1086	0	1121	22	0
9	Fd	1058	0	1092	19	0
9	GD	1086	0	1121	24	0
9	Gd	1058	0	1092	23	0
9	HD	1086	0	1121	31	0
9	Hd	1058	0	1092	22	0
9	ID	1086	0	1121	23	0
9	Id	1058	0	1092	22	0
9	JD	1086	0	1121	21	0
9	Jd	1058	0	1092	17	0
9	KD	1086	0	1121	25	0
9	Kd	1058	0	1092	16	0
9	LD	1086	0	1121	28	0
9	Ld	1058	0	1092	22	0
9	MD	1086	0	1121	24	0
9	Md	1058	0	1092	21	0
10	AF	483	0	502	13	0
10	Af	449	0	474	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	BF	483	0	502	8	0
10	Bf	449	0	474	11	0
10	CF	483	0	502	12	0
10	Cf	449	0	474	10	0
10	DF	483	0	502	14	0
10	Df	449	0	474	8	0
10	EF	483	0	502	11	0
10	Ef	449	0	474	11	0
10	FF	483	0	502	11	0
10	Ff	449	0	474	13	0
10	GF	483	0	502	14	0
10	Gf	449	0	474	14	0
10	HF	483	0	502	10	0
10	Hf	449	0	474	8	0
10	IF	483	0	502	8	0
10	If	449	0	474	17	0
10	JF	483	0	502	14	0
10	Jf	449	0	474	8	0
10	KF	483	0	502	13	0
10	Kf	449	0	474	8	0
10	LF	483	0	502	6	0
10	Lf	449	0	474	10	0
10	MF	483	0	502	14	0
10	Mf	449	0	474	15	0
10	VF	483	0	502	14	0
10	WF	483	0	502	13	0
10	XF	483	0	502	11	0
10	YF	483	0	502	13	0
10	ZF	483	0	502	7	0
11	AC	1921	0	1952	39	0
11	BC	1921	0	1952	42	0
11	CC	1667	0	1682	44	0
11	DC	1667	0	1682	31	0
11	EC	1667	0	1682	33	0
11	FC	1921	0	1952	44	0
11	GC	1667	0	1682	33	0
11	HC	1667	0	1682	24	0
11	IC	1667	0	1682	35	0
11	JC	1921	0	1952	35	0
11	KC	1667	0	1682	39	0
11	LC	1667	0	1682	33	0
11	MC	1667	0	1682	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	192116	0	190355	3684	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 3684 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)
4:JL:129:THR:O	4:JL:133:PHE:HB2	1.63	0.98
4:FL:129:THR:O	4:FL:133:PHE:HB2	1.72	0.88
4:CL:166:ALA:HA	4:CL:206:GLU:O	1.77	0.85
4:GL:166:ALA:HA	4:GL:206:GLU:O	1.76	0.84
4:HL:166:ALA:HA	4:HL:206:GLU:O	1.78	0.84

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%)	153 (95%)	8 (5%)	0	100	100
1	Ag	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	BG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Bg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	CG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Cg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	DG	161/1048 (15%)	157 (98%)	4 (2%)	0	100	100
1	Dg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	EG	161/1048 (15%)	158 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Eg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	FG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Gg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	HG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Hg	32/1048 (3%)	32 (100%)	0	0	100	100
1	IG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Ig	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	JG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Jg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	KG	161/1048 (15%)	157 (98%)	4 (2%)	0	100	100
1	Kg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	LG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Lg	32/1048 (3%)	32 (100%)	0	0	100	100
1	MG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Mg	32/1048 (3%)	29 (91%)	3 (9%)	0	100	100
1	NG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	OG	161/1048 (15%)	158 (98%)	3 (2%)	0	100	100
1	PG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	VG	32/1048 (3%)	32 (100%)	0	0	100	100
1	WG	32/1048 (3%)	32 (100%)	0	0	100	100
1	XG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	YG	32/1048 (3%)	32 (100%)	0	0	100	100
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	BH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
2	CH	256/361 (71%)	247 (96%)	9 (4%)	0	100	100
2	DH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
2	EH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
2	FH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	GH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
2	HH	256/361 (71%)	247 (96%)	9 (4%)	0	100	100
2	IH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	JH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	KH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	LH	256/361 (71%)	243 (95%)	13 (5%)	0	100	100
2	MH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	VH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
2	WH	239/361 (66%)	232 (97%)	7 (3%)	0	100	100
2	XH	239/361 (66%)	232 (97%)	7 (3%)	0	100	100
2	YH	239/361 (66%)	231 (97%)	8 (3%)	0	100	100
2	ZH	239/361 (66%)	231 (97%)	8 (3%)	0	100	100
3	AK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
3	BK	149/189 (79%)	145 (97%)	4 (3%)	0	100	100
3	CK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	DK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	EK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	FK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	GK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	HK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	IK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	JK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	KK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
3	LK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	MK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
4	AL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
4	BL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	CL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	DL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	EL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
4	FL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	GL	169/249 (68%)	164 (97%)	5 (3%)	0	100	100
4	HL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	IL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	JL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	KL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
4	LL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	ML	169/249 (68%)	164 (97%)	5 (3%)	0	100	100
5	AM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
5	BM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
5	CM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
5	DM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
5	EM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
5	FM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
5	GM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
5	HM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
5	IM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
5	JM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
5	KM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
5	LM	206/320 (64%)	197 (96%)	9 (4%)	0	100	100
5	MM	206/320 (64%)	195 (95%)	11 (5%)	0	100	100
6	AN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
6	BN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
6	CN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
6	DN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
6	EN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
6	FN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
6	GN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
6	HN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
6	IN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
6	JN	76/124 (61%)	73 (96%)	3 (4%)	0	100	100
6	KN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	LN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
6	MN	76/124 (61%)	73 (96%)	3 (4%)	0	100	100
9	AD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
9	Ad	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
9	BD	138/163 (85%)	134 (97%)	4 (3%)	0	100	100
9	Bd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
9	CD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
9	Cd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
9	DD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
9	Dd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
9	ED	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
9	Ed	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
9	FD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
9	Fd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	GD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
9	Gd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
9	HD	138/163 (85%)	135 (98%)	3 (2%)	0	100	100
9	Hd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
9	ID	138/163 (85%)	134 (97%)	4 (3%)	0	100	100
9	Id	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	JD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
9	Jd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	KD	138/163 (85%)	134 (97%)	4 (3%)	0	100	100
9	Kd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	LD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
9	Ld	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
9	MD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
9	Md	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
10	AF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	Af	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
10	BF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	Bf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
10	CF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
10	Cf	57/269 (21%)	50 (88%)	7 (12%)	0	100	100
10	DF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
10	Df	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
10	EF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
10	Ef	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
10	FF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
10	Ff	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
10	GF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	Gf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
10	HF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
10	Hf	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
10	IF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
10	JF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
10	Jf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
10	KF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
10	Kf	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
10	LF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
10	Lf	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
10	MF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	Mf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
10	VF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
10	WF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	XF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	YF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
10	ZF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
11	AC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
11	BC	241/303 (80%)	236 (98%)	5 (2%)	0	100	100
11	CC	207/303 (68%)	191 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	DC	207/303 (68%)	196 (95%)	11 (5%)	0	100	100
11	EC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
11	FC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
11	GC	207/303 (68%)	196 (95%)	11 (5%)	0	100	100
11	HC	207/303 (68%)	196 (95%)	11 (5%)	0	100	100
11	IC	207/303 (68%)	189 (91%)	18 (9%)	0	100	100
11	JC	241/303 (80%)	229 (95%)	12 (5%)	0	100	100
11	KC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
11	LC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
11	MC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
All	All	23690/70112 (34%)	22525 (95%)	1165 (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%)	115 (85%)	20 (15%)	3	14
1	Ag	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	BG	135/765 (18%)	120 (89%)	15 (11%)	6	20
1	Bg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	CG	135/765 (18%)	120 (89%)	15 (11%)	6	20
1	Cg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	DG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Dg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	EG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	Eg	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	FG	135/765 (18%)	119 (88%)	16 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Fg	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	GG	135/765 (18%)	121 (90%)	14 (10%)	7	22
1	Gg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	HG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Hg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	IG	135/765 (18%)	120 (89%)	15 (11%)	6	20
1	Ig	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	JG	135/765 (18%)	118 (87%)	17 (13%)	4	17
1	Jg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	KG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Kg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	LG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Lg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	MG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Mg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	NG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	OG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	PG	135/765 (18%)	111 (82%)	24 (18%)	2	10
1	VG	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	WG	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	XG	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	YG	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	ZG	31/765 (4%)	28 (90%)	3 (10%)	8	25
2	AH	220/300 (73%)	190 (86%)	30 (14%)	3	15
2	BH	220/300 (73%)	193 (88%)	27 (12%)	4	18
2	CH	220/300 (73%)	197 (90%)	23 (10%)	6	22
2	DH	220/300 (73%)	195 (89%)	25 (11%)	5	20
2	EH	220/300 (73%)	188 (86%)	32 (14%)	3	14
2	FH	220/300 (73%)	190 (86%)	30 (14%)	3	15
2	GH	220/300 (73%)	195 (89%)	25 (11%)	5	20
2	HH	220/300 (73%)	200 (91%)	20 (9%)	9	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	IH	220/300 (73%)	192 (87%)	28 (13%)	4	17
2	JH	220/300 (73%)	191 (87%)	29 (13%)	4	16
2	KH	220/300 (73%)	197 (90%)	23 (10%)	6	22
2	LH	220/300 (73%)	193 (88%)	27 (12%)	4	18
2	MH	220/300 (73%)	186 (84%)	34 (16%)	2	13
2	VH	207/300 (69%)	172 (83%)	35 (17%)	2	11
2	WH	207/300 (69%)	181 (87%)	26 (13%)	4	17
2	XH	207/300 (69%)	183 (88%)	24 (12%)	5	19
2	YH	207/300 (69%)	182 (88%)	25 (12%)	5	18
2	ZH	207/300 (69%)	180 (87%)	27 (13%)	4	16
3	AK	129/163 (79%)	111 (86%)	18 (14%)	3	15
3	BK	129/163 (79%)	110 (85%)	19 (15%)	3	14
3	CK	129/163 (79%)	109 (84%)	20 (16%)	2	13
3	DK	129/163 (79%)	118 (92%)	11 (8%)	10	29
3	EK	129/163 (79%)	111 (86%)	18 (14%)	3	15
3	FK	129/163 (79%)	114 (88%)	15 (12%)	5	19
3	GK	129/163 (79%)	111 (86%)	18 (14%)	3	15
3	HK	129/163 (79%)	115 (89%)	14 (11%)	6	21
3	IK	129/163 (79%)	115 (89%)	14 (11%)	6	21
3	JK	129/163 (79%)	112 (87%)	17 (13%)	4	16
3	KK	129/163 (79%)	110 (85%)	19 (15%)	3	14
3	LK	129/163 (79%)	113 (88%)	16 (12%)	4	18
3	MK	129/163 (79%)	107 (83%)	22 (17%)	2	11
4	AL	148/203 (73%)	133 (90%)	15 (10%)	7	23
4	BL	148/203 (73%)	128 (86%)	20 (14%)	4	15
4	CL	148/203 (73%)	131 (88%)	17 (12%)	5	19
4	DL	148/203 (73%)	131 (88%)	17 (12%)	5	19
4	EL	148/203 (73%)	133 (90%)	15 (10%)	7	23
4	FL	148/203 (73%)	132 (89%)	16 (11%)	6	22
4	GL	148/203 (73%)	127 (86%)	21 (14%)	3	15
4	HL	148/203 (73%)	132 (89%)	16 (11%)	6	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	IL	148/203 (73%)	136 (92%)	12 (8%)	11	31
4	JL	148/203 (73%)	133 (90%)	15 (10%)	7	23
4	KL	148/203 (73%)	132 (89%)	16 (11%)	6	22
4	LL	148/203 (73%)	138 (93%)	10 (7%)	14	36
4	ML	148/203 (73%)	133 (90%)	15 (10%)	7	23
5	AM	175/276 (63%)	147 (84%)	28 (16%)	2	12
5	BM	175/276 (63%)	153 (87%)	22 (13%)	4	17
5	CM	175/276 (63%)	148 (85%)	27 (15%)	2	13
5	DM	175/276 (63%)	153 (87%)	22 (13%)	4	17
5	EM	175/276 (63%)	152 (87%)	23 (13%)	4	16
5	FM	175/276 (63%)	151 (86%)	24 (14%)	3	15
5	GM	175/276 (63%)	142 (81%)	33 (19%)	1	9
5	HM	175/276 (63%)	151 (86%)	24 (14%)	3	15
5	IM	175/276 (63%)	156 (89%)	19 (11%)	6	21
5	JM	175/276 (63%)	153 (87%)	22 (13%)	4	17
5	KM	175/276 (63%)	152 (87%)	23 (13%)	4	16
5	LM	175/276 (63%)	152 (87%)	23 (13%)	4	16
5	MM	175/276 (63%)	155 (89%)	20 (11%)	5	20
6	AN	66/107 (62%)	57 (86%)	9 (14%)	3	15
6	BN	66/107 (62%)	49 (74%)	17 (26%)	0	4
6	CN	66/107 (62%)	55 (83%)	11 (17%)	2	11
6	DN	66/107 (62%)	53 (80%)	13 (20%)	1	8
6	EN	66/107 (62%)	58 (88%)	8 (12%)	5	18
6	FN	66/107 (62%)	57 (86%)	9 (14%)	3	15
6	GN	66/107 (62%)	58 (88%)	8 (12%)	5	18
6	HN	66/107 (62%)	58 (88%)	8 (12%)	5	18
6	IN	66/107 (62%)	58 (88%)	8 (12%)	5	18
6	JN	66/107 (62%)	55 (83%)	11 (17%)	2	11
6	KN	66/107 (62%)	55 (83%)	11 (17%)	2	11
6	LN	66/107 (62%)	57 (86%)	9 (14%)	3	15
6	MN	66/107 (62%)	54 (82%)	12 (18%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AD	121/139 (87%)	109 (90%)	12 (10%)	7	24
9	Ad	118/139 (85%)	102 (86%)	16 (14%)	3	15
9	BD	121/139 (87%)	113 (93%)	8 (7%)	15	37
9	Bd	118/139 (85%)	100 (85%)	18 (15%)	3	13
9	CD	121/139 (87%)	105 (87%)	16 (13%)	4	16
9	Cd	118/139 (85%)	103 (87%)	15 (13%)	4	17
9	DD	121/139 (87%)	109 (90%)	12 (10%)	7	24
9	Dd	118/139 (85%)	105 (89%)	13 (11%)	6	21
9	ED	121/139 (87%)	108 (89%)	13 (11%)	6	22
9	Ed	118/139 (85%)	106 (90%)	12 (10%)	7	23
9	FD	121/139 (87%)	110 (91%)	11 (9%)	9	28
9	Fd	118/139 (85%)	105 (89%)	13 (11%)	6	21
9	GD	121/139 (87%)	105 (87%)	16 (13%)	4	16
9	Gd	118/139 (85%)	103 (87%)	15 (13%)	4	17
9	HD	121/139 (87%)	106 (88%)	15 (12%)	4	18
9	Hd	118/139 (85%)	105 (89%)	13 (11%)	6	21
9	ID	121/139 (87%)	109 (90%)	12 (10%)	7	24
9	Id	118/139 (85%)	107 (91%)	11 (9%)	8	26
9	JD	121/139 (87%)	111 (92%)	10 (8%)	10	30
9	Jd	118/139 (85%)	104 (88%)	14 (12%)	5	19
9	KD	121/139 (87%)	109 (90%)	12 (10%)	7	24
9	Kd	118/139 (85%)	104 (88%)	14 (12%)	5	19
9	LD	121/139 (87%)	102 (84%)	19 (16%)	2	12
9	Ld	118/139 (85%)	103 (87%)	15 (13%)	4	17
9	MD	121/139 (87%)	109 (90%)	12 (10%)	7	24
9	Md	118/139 (85%)	102 (86%)	16 (14%)	3	15
10	AF	53/237 (22%)	44 (83%)	9 (17%)	2	11
10	Af	49/237 (21%)	41 (84%)	8 (16%)	2	12
10	BF	53/237 (22%)	45 (85%)	8 (15%)	3	13
10	Bf	49/237 (21%)	40 (82%)	9 (18%)	1	10
10	CF	53/237 (22%)	46 (87%)	7 (13%)	4	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Cf	49/237 (21%)	42 (86%)	7 (14%)	3	14
10	DF	53/237 (22%)	45 (85%)	8 (15%)	3	13
10	Df	49/237 (21%)	38 (78%)	11 (22%)	1	6
10	EF	53/237 (22%)	42 (79%)	11 (21%)	1	7
10	Ef	49/237 (21%)	40 (82%)	9 (18%)	1	10
10	FF	53/237 (22%)	45 (85%)	8 (15%)	3	13
10	Ff	49/237 (21%)	40 (82%)	9 (18%)	1	10
10	GF	53/237 (22%)	47 (89%)	6 (11%)	5	20
10	Gf	49/237 (21%)	42 (86%)	7 (14%)	3	14
10	HF	53/237 (22%)	47 (89%)	6 (11%)	5	20
10	Hf	49/237 (21%)	44 (90%)	5 (10%)	7	23
10	IF	53/237 (22%)	47 (89%)	6 (11%)	5	20
10	If	49/237 (21%)	41 (84%)	8 (16%)	2	12
10	JF	53/237 (22%)	46 (87%)	7 (13%)	4	16
10	Jf	49/237 (21%)	43 (88%)	6 (12%)	5	18
10	KF	53/237 (22%)	43 (81%)	10 (19%)	1	9
10	Kf	49/237 (21%)	39 (80%)	10 (20%)	1	7
10	LF	53/237 (22%)	45 (85%)	8 (15%)	3	13
10	Lf	49/237 (21%)	45 (92%)	4 (8%)	10	31
10	MF	53/237 (22%)	46 (87%)	7 (13%)	4	16
10	Mf	49/237 (21%)	40 (82%)	9 (18%)	1	10
10	VF	53/237 (22%)	47 (89%)	6 (11%)	5	20
10	WF	53/237 (22%)	44 (83%)	9 (17%)	2	11
10	XF	53/237 (22%)	46 (87%)	7 (13%)	4	16
10	YF	53/237 (22%)	48 (91%)	5 (9%)	8	26
10	ZF	53/237 (22%)	49 (92%)	4 (8%)	12	33
11	AC	203/257 (79%)	177 (87%)	26 (13%)	4	17
11	BC	203/257 (79%)	178 (88%)	25 (12%)	4	18
11	CC	178/257 (69%)	154 (86%)	24 (14%)	4	15
11	DC	178/257 (69%)	152 (85%)	26 (15%)	3	14
11	EC	178/257 (69%)	155 (87%)	23 (13%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	FC	203/257 (79%)	180 (89%)	23 (11%)	5	20
11	GC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	HC	178/257 (69%)	152 (85%)	26 (15%)	3	14
11	IC	178/257 (69%)	151 (85%)	27 (15%)	3	13
11	JC	203/257 (79%)	171 (84%)	32 (16%)	2	12
11	KC	178/257 (69%)	161 (90%)	17 (10%)	8	25
11	LC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	MC	178/257 (69%)	149 (84%)	29 (16%)	2	12
All	All	20459/55449 (37%)	17802 (87%)	2657 (13%)	6	16

5 of 2657 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	BL	175	ARG
10	DF	223	ILE
9	Bd	91	ILE
4	BL	165	VAL
11	JC	184	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 248 such sidechains are listed below:

Mol	Chain	Res	Type
10	MF	226	ASN
1	IG	1043	GLN
2	XH	159	ASN
1	IG	938	ASN
11	AC	84	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

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

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	HX	38:UNK	C	70:UNK	N	26.96
1	JX	38:UNK	C	70:UNK	N	26.39
1	VX	38:UNK	C	70:UNK	N	26.34

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	ZX	38:UNK	C	70:UNK	N	26.34
1	BX	38:UNK	C	70:UNK	N	25.84

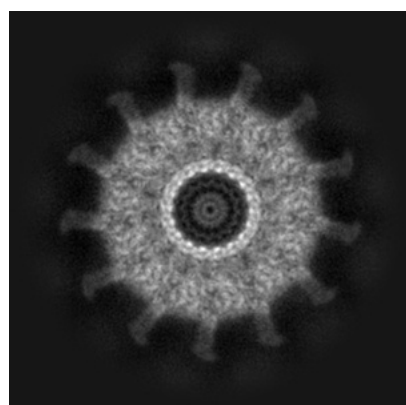
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24024. These allow visual inspection of the internal detail of the map and identification of artifacts.

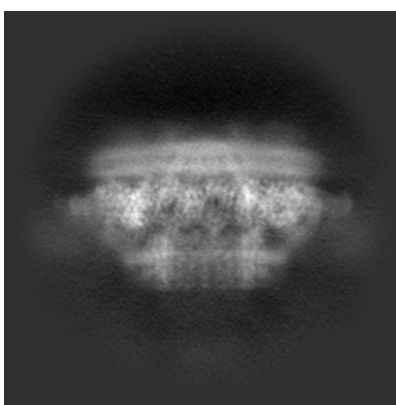
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

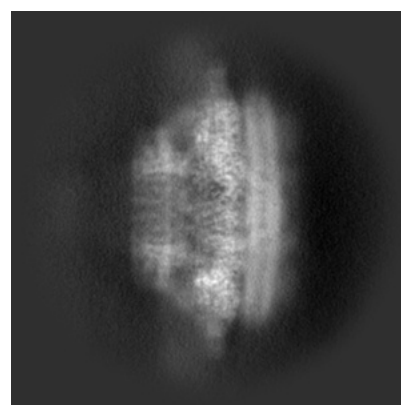
6.1.1 Primary map



X



Y

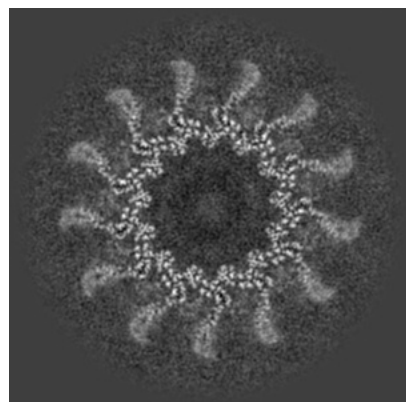


Z

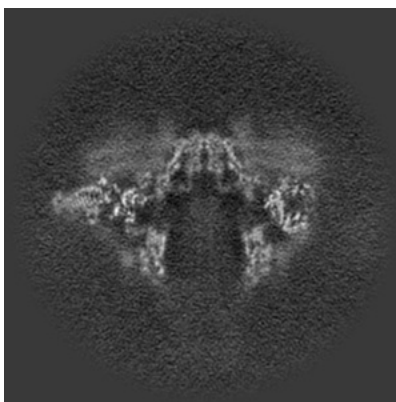
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

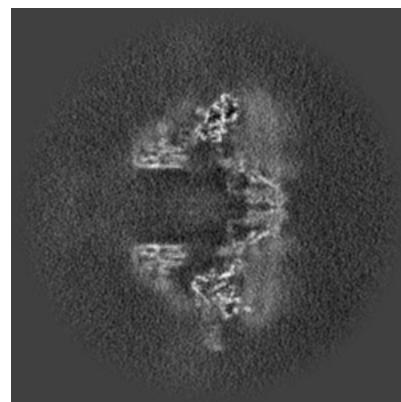
6.2.1 Primary map



X Index: 125



Y Index: 125

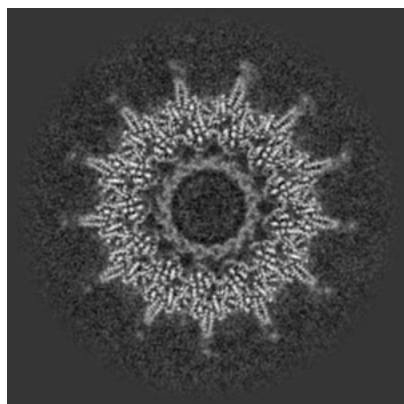


Z Index: 125

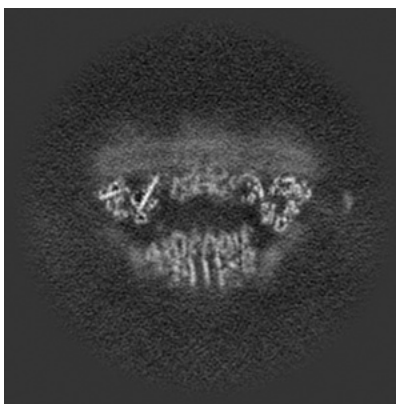
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

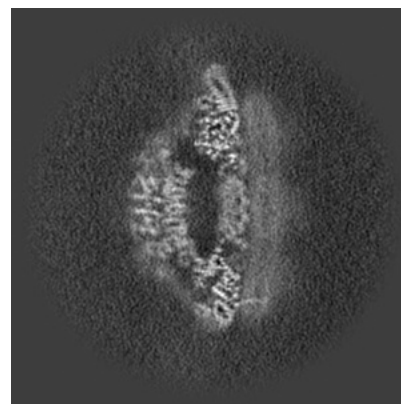
6.3.1 Primary map



X Index: 134



Y Index: 101

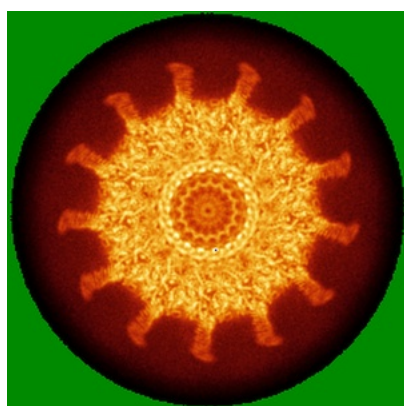


Z Index: 151

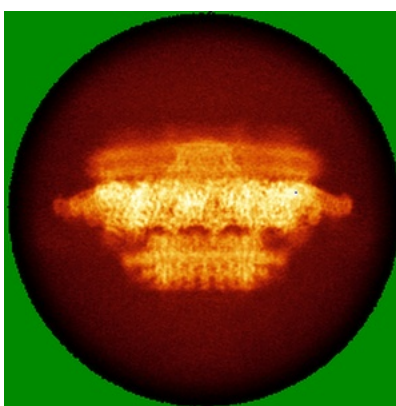
The images above show the largest variance slices of the map in three orthogonal directions.

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

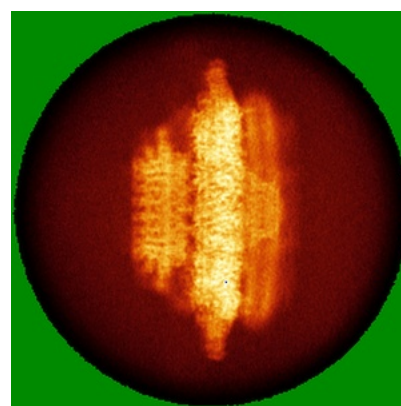
6.4.1 Primary map



X



Y

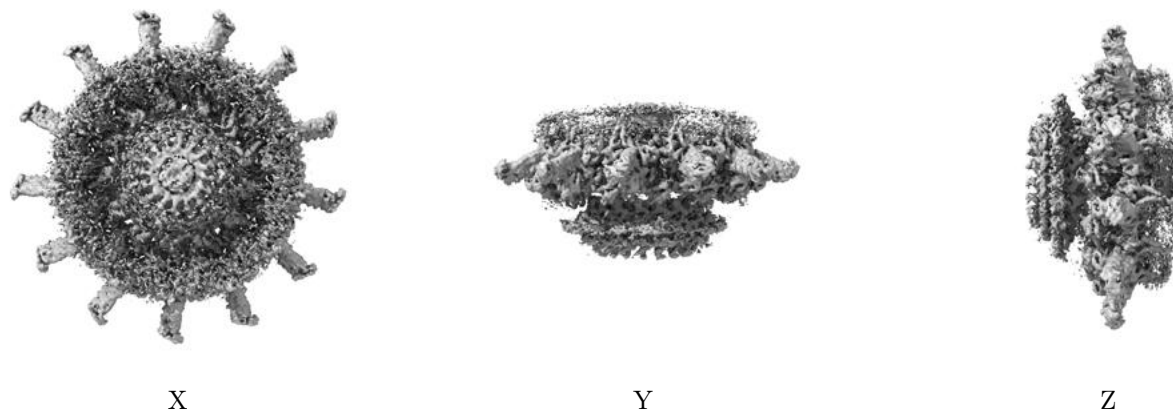


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

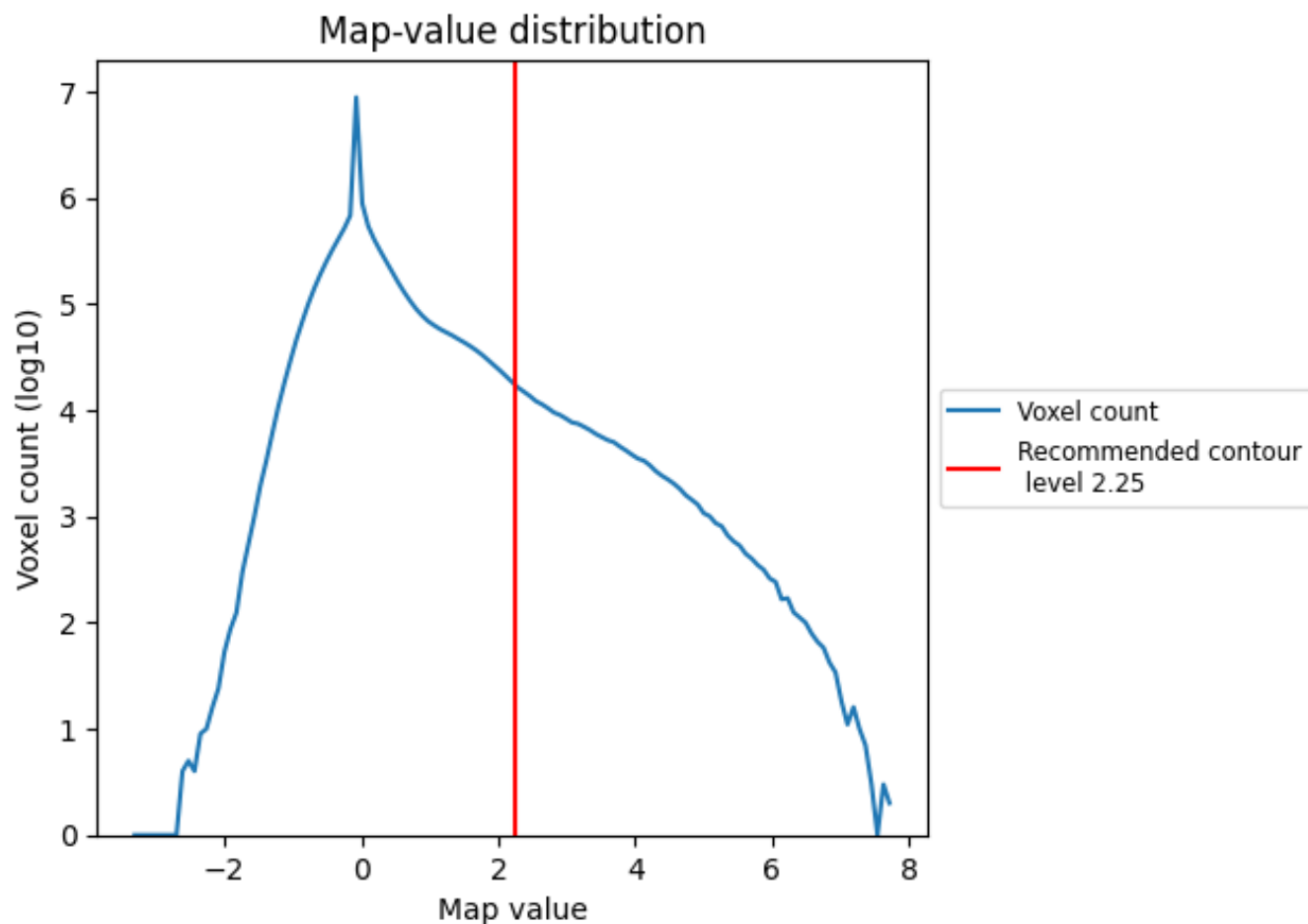
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

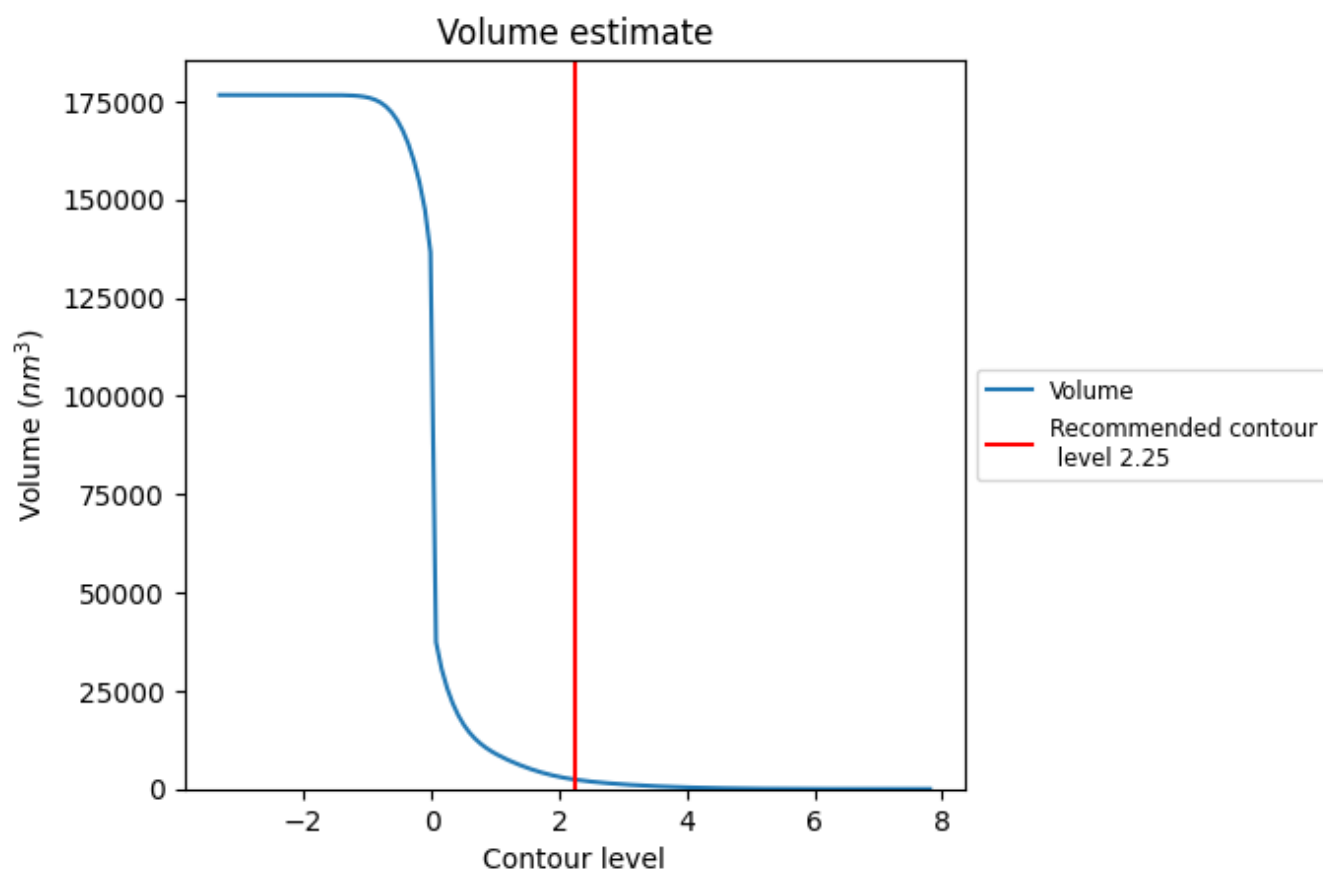
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

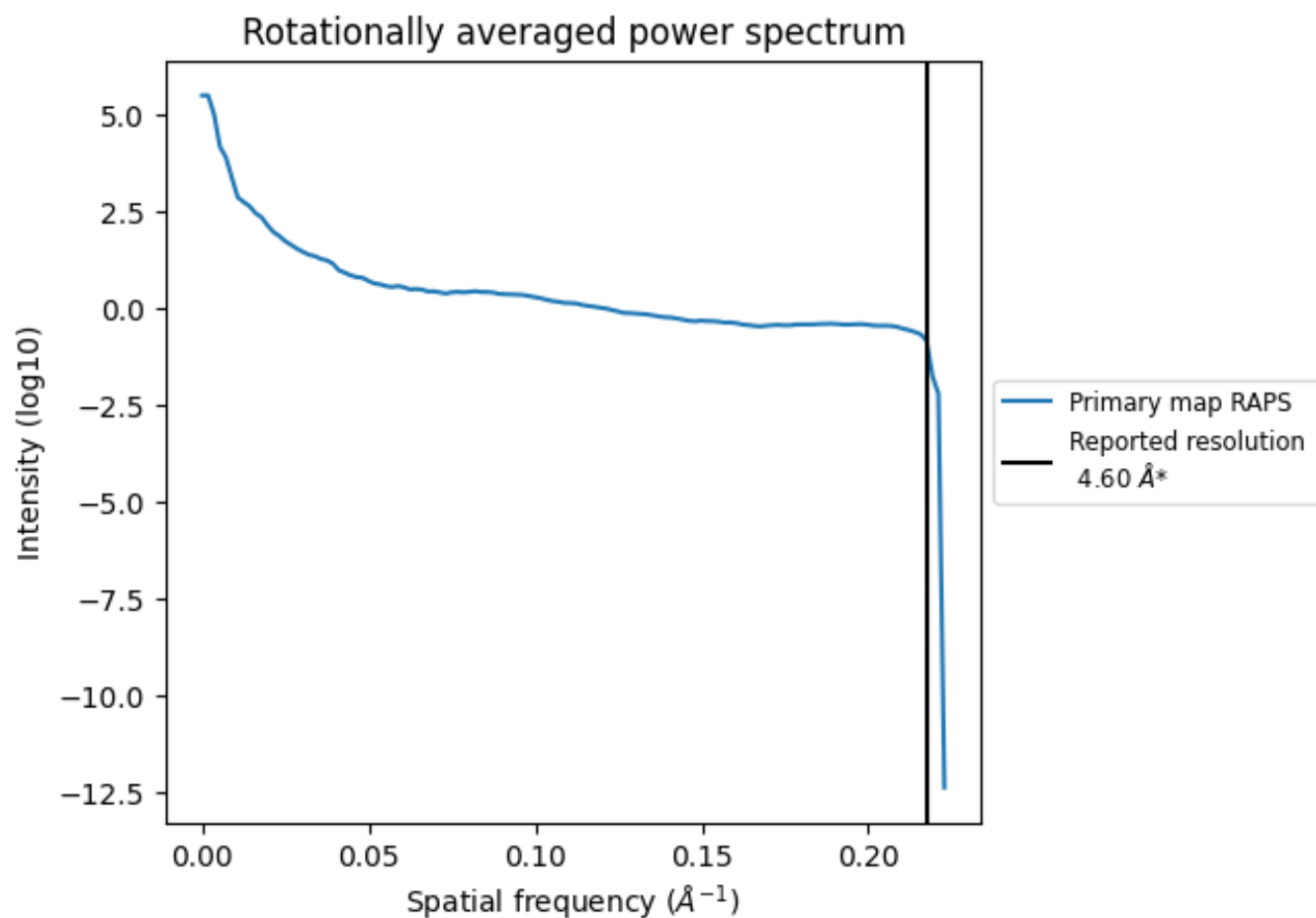
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2386 nm³; this corresponds to an approximate mass of 2155 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 $\text{\AA}^{-1}$

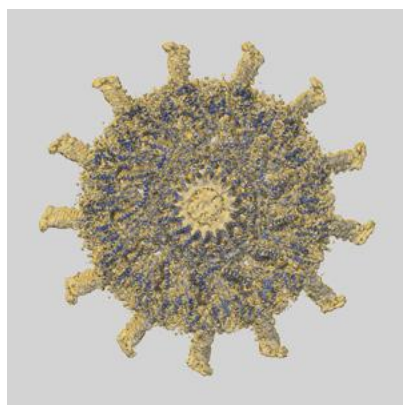
8 Fourier-Shell correlation

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

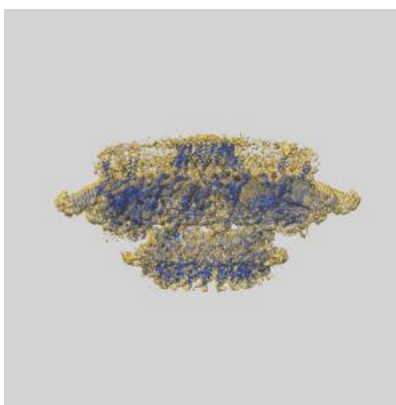
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24024 and PDB model 7MUW. Per-residue inclusion information can be found in section 3 on page 23.

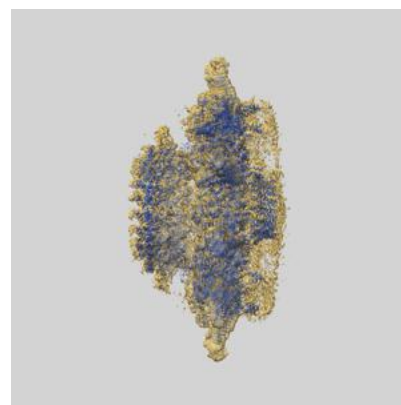
9.1 Map-model overlay [i](#)



X



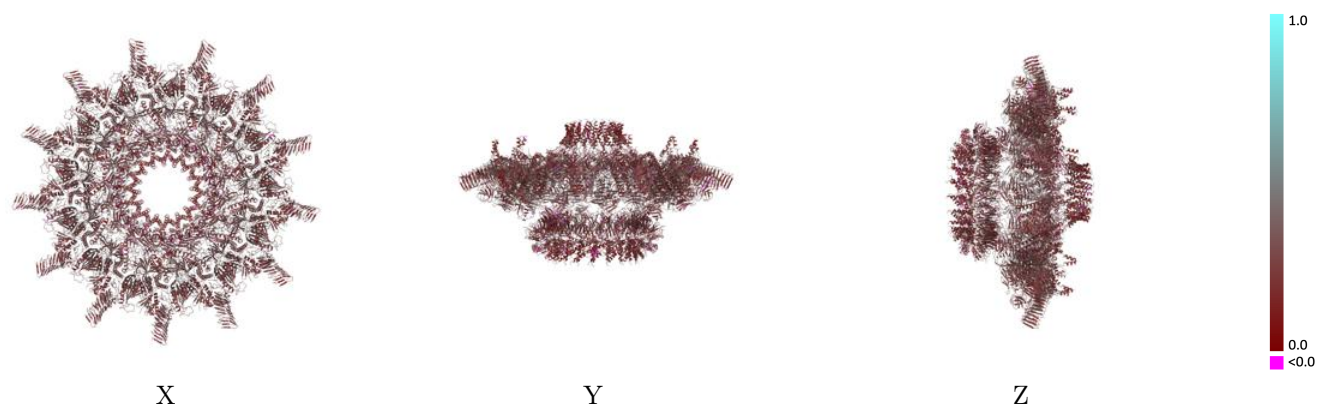
Y



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](#)

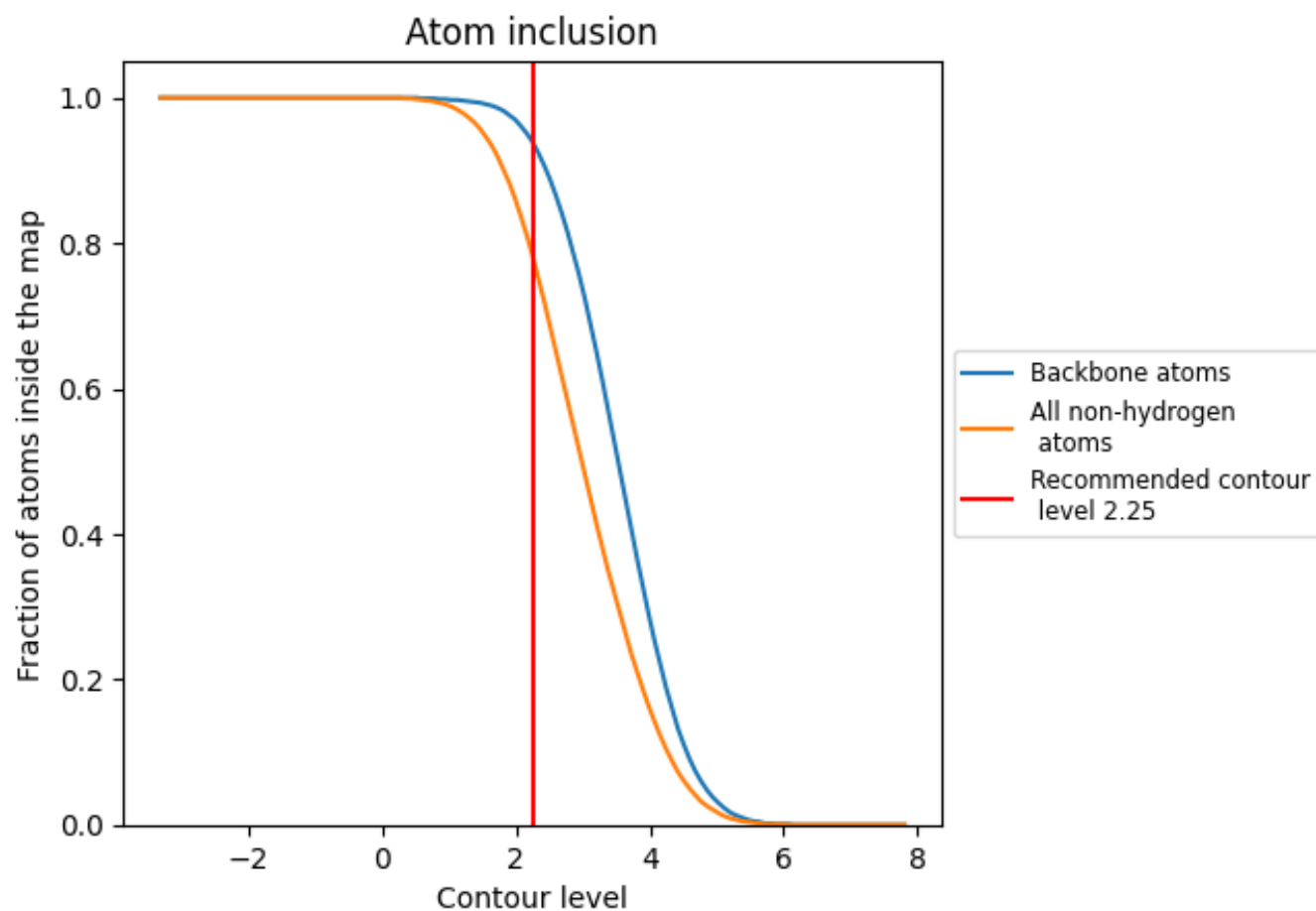


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 78% 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	 0.7820	 0.2820
AC	 0.7720	 0.2930
AD	 0.8080	 0.3200
AF	 0.7980	 0.2290
AG	 0.6910	 0.2430
AH	 0.7820	 0.2740
AK	 0.8110	 0.3060
AL	 0.8200	 0.2840
AM	 0.7870	 0.2930
AN	 0.7600	 0.3330
AU	 0.9560	 0.4410
AX	 0.6540	 0.2400
Ad	 0.8240	 0.3120
Af	 0.7930	 0.2740
Ag	 0.8120	 0.2550
BC	 0.7590	 0.2830
BD	 0.8090	 0.3110
BF	 0.7790	 0.2220
BG	 0.6550	 0.2250
BH	 0.7930	 0.2730
BK	 0.8300	 0.3040
BL	 0.8300	 0.2900
BM	 0.7990	 0.2910
BN	 0.7330	 0.3180
BU	 0.9780	 0.4590
BX	 0.5670	 0.2260
Bd	 0.8140	 0.3090
Bf	 0.7790	 0.2820
Bg	 0.8640	 0.2740
CC	 0.8140	 0.2900
CD	 0.8110	 0.3160
CF	 0.7130	 0.2400
CG	 0.6570	 0.2330
CH	 0.8090	 0.2930
CK	 0.8240	 0.3160



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Chain	Atom inclusion	Q-score
CL	 0.8430	 0.2900
CM	 0.8110	 0.2840
CN	 0.7410	 0.3220
CU	 0.9780	 0.4900
CX	 0.5880	 0.2190
Cd	 0.8350	 0.2900
Cf	 0.7740	 0.2780
Cg	 0.8570	 0.2580
DC	 0.8250	 0.2920
DD	 0.8160	 0.3020
DF	 0.7730	 0.2310
DG	 0.7180	 0.2500
DH	 0.7960	 0.2850
DK	 0.8110	 0.3100
DL	 0.8490	 0.2920
DM	 0.7850	 0.2850
DN	 0.7730	 0.3330
DU	 1.0000	 0.4410
DX	 0.7330	 0.2560
Dd	 0.8140	 0.3120
Df	 0.7200	 0.2600
Dg	 0.8380	 0.2790
EC	 0.8170	 0.3040
ED	 0.8050	 0.3150
EF	 0.7980	 0.2270
EG	 0.6690	 0.2430
EH	 0.7890	 0.2790
EK	 0.8290	 0.3130
EL	 0.8450	 0.2940
EM	 0.8090	 0.2850
EN	 0.7810	 0.3230
EU	 0.9560	 0.4260
EX	 0.5420	 0.2110
Ed	 0.8210	 0.3010
Ef	 0.7880	 0.2840
Eg	 0.8530	 0.2540
FC	 0.7840	 0.2970
FD	 0.8130	 0.3080
FF	 0.7980	 0.2380
FG	 0.6900	 0.2290
FH	 0.8060	 0.2820
FK	 0.8030	 0.3050

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Chain	Atom inclusion	Q-score
FL	 0.8320	 0.2990
FM	 0.8140	 0.3010
FN	 0.7550	 0.3230
FU	 1.0000	 0.4520
FX	 0.7420	 0.2780
Fd	 0.8290	 0.3060
Ff	 0.8180	 0.2950
Fg	 0.8490	 0.2650
GC	 0.8110	 0.3010
GD	 0.8100	 0.3150
GF	 0.7770	 0.2370
GG	 0.7040	 0.2260
GH	 0.7970	 0.2810
GK	 0.8060	 0.3080
GL	 0.8240	 0.2930
GM	 0.8220	 0.2920
GN	 0.7600	 0.3200
GU	 0.9560	 0.4710
GX	 0.4750	 0.2200
Gd	 0.8220	 0.3050
Gf	 0.7740	 0.2860
Gg	 0.8530	 0.2540
HC	 0.8220	 0.2950
HD	 0.8220	 0.3190
HF	 0.7710	 0.2330
HG	 0.7040	 0.2250
HH	 0.8080	 0.2820
HK	 0.8190	 0.3070
HL	 0.8340	 0.2900
HM	 0.8290	 0.2940
HN	 0.7920	 0.3310
HU	 0.9560	 0.4480
HX	 0.5580	 0.2450
Hd	 0.8470	 0.2990
Hf	 0.8110	 0.2690
Hg	 0.7980	 0.2550
IC	 0.8140	 0.3000
ID	 0.8110	 0.3060
IF	 0.7830	 0.2030
IG	 0.7100	 0.2390
IH	 0.7910	 0.2720
IK	 0.8360	 0.3120

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Chain	Atom inclusion	Q-score
IL	 0.8350	 0.2950
IM	 0.8110	 0.2800
IN	 0.7850	 0.3260
IU	 0.9330	 0.4260
IX	 0.6540	 0.2380
Id	 0.8420	 0.3010
If	 0.8290	 0.2920
Ig	 0.8600	 0.2490
JC	 0.7810	 0.2900
JD	 0.8010	 0.3070
JF	 0.7790	 0.2370
JG	 0.6590	 0.2230
JH	 0.8040	 0.2750
JK	 0.8140	 0.3050
JL	 0.8410	 0.2920
JM	 0.8100	 0.2950
JN	 0.7410	 0.3150
JU	 0.9780	 0.4640
JX	 0.6460	 0.2330
Jd	 0.8000	 0.3030
Jf	 0.8060	 0.2840
Jg	 0.8570	 0.2560
KC	 0.7850	 0.2970
KD	 0.8070	 0.3070
KF	 0.7560	 0.2220
KG	 0.6730	 0.2060
KH	 0.8070	 0.2820
KK	 0.8250	 0.3130
KL	 0.8300	 0.2990
KM	 0.8300	 0.2920
KN	 0.7520	 0.3300
KU	 0.9780	 0.4760
KX	 0.5540	 0.2180
Kd	 0.8290	 0.3060
Kf	 0.8090	 0.2910
Kg	 0.8350	 0.2420
LC	 0.8180	 0.3000
LD	 0.8080	 0.3160
LF	 0.8020	 0.2350
LG	 0.6570	 0.1890
LH	 0.7970	 0.2680
LK	 0.8260	 0.3160

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Chain	Atom inclusion	Q-score
LL	 0.8270	 0.2960
LM	 0.8040	 0.2770
LN	 0.8110	 0.3390
LU	 0.9780	 0.4700
LX	 0.5500	 0.2410
Ld	 0.8290	 0.2960
Lf	 0.8130	 0.2690
Lg	 0.8530	 0.2520
MC	 0.8190	 0.3040
MD	 0.7860	 0.3160
MF	 0.8130	 0.2280
MG	 0.6760	 0.2120
MH	 0.8000	 0.2760
MK	 0.8040	 0.3160
ML	 0.8090	 0.2910
MM	 0.7940	 0.2850
MN	 0.7760	 0.3210
MU	 0.9110	 0.4900
MX	 0.6330	 0.2400
Md	 0.8170	 0.2970
Mf	 0.8110	 0.2730
Mg	 0.8600	 0.2570
NG	 0.6620	 0.2190
OG	 0.6830	 0.2440
PG	 0.7070	 0.2390
VF	 0.7410	 0.2360
VG	 0.8200	 0.2480
VH	 0.6660	 0.2670
VX	 0.6580	 0.2130
WF	 0.7810	 0.2360
WG	 0.8380	 0.2530
WH	 0.6180	 0.2580
WX	 0.6540	 0.2510
XF	 0.7710	 0.2190
XG	 0.7980	 0.2540
XH	 0.5890	 0.2530
XX	 0.6670	 0.2320
YF	 0.7940	 0.2290
YG	 0.8090	 0.2510
YH	 0.7010	 0.2540
YX	 0.6210	 0.2590
ZF	 0.8340	 0.2440

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Chain	Atom inclusion	Q-score
ZG	 0.7720	 0.2470
ZH	 0.5400	 0.2220
ZX	 0.5620	 0.2240