



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 12:13 AM EST

PDB ID : 7MUW
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:

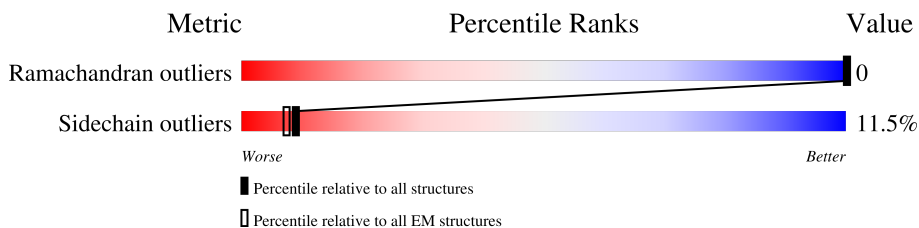
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



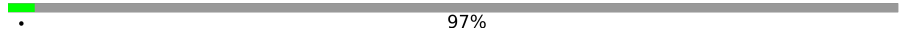

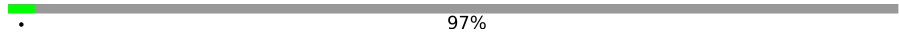

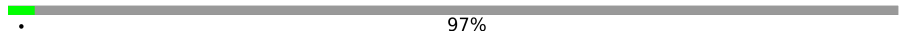

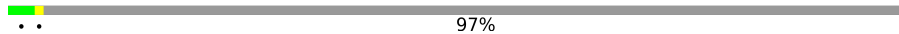

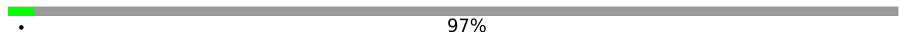

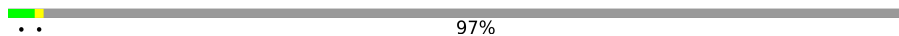

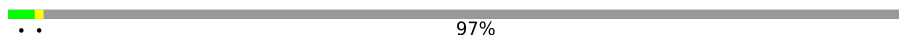

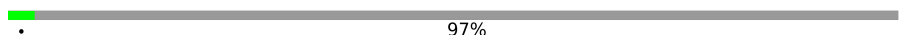

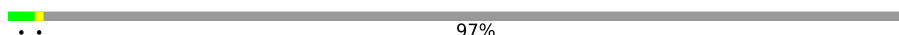



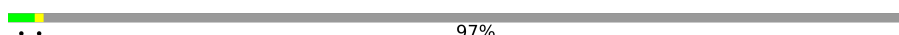
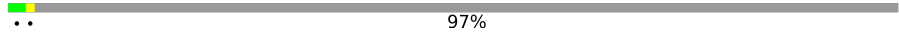
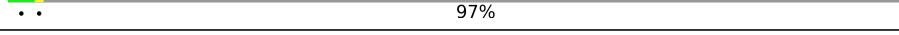
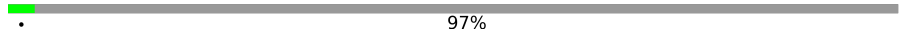
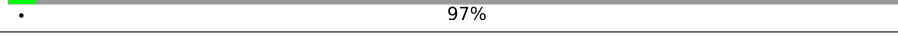
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	14% . 84%
1	Ag	1048	. . 97%
1	BG	1048	14% . 84%
1	Bg	1048	. . 97%
1	CG	1048	14% . 84%
1	Cg	1048	. . 97%
1	DG	1048	14% . 84%
1	Dg	1048	. . 97%
1	EG	1048	14% . 84%

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Mol	Chain	Length	Quality of chain
1	Eg	1048	 97%
1	FG	1048	 14% 84%
1	Fg	1048	 97%
1	GG	1048	 14% 84%
1	Gg	1048	 97%
1	HG	1048	 14% 84%
1	Hg	1048	 97%
1	IG	1048	 14% 84%
1	Ig	1048	 97%
1	JG	1048	 15% 84%
1	Jg	1048	 97%
1	KG	1048	 15% 84%
1	Kg	1048	 97%
1	LG	1048	 14% 84%
1	Lg	1048	 97%
1	MG	1048	 14% 84%
1	Mg	1048	 97%
1	NG	1048	 14% 84%
1	OG	1048	 14% 84%
1	PG	1048	 14% 84%
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%

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Mol	Chain	Length	Quality of chain
2	AH	361	64% 8% 29%
2	BH	361	64% 7% 29%
2	CH	361	65% 6% 29%
2	DH	361	65% 7% 29%
2	EH	361	63% 8% 29%
2	FH	361	64% 7% 29%
2	GH	361	66% 6% 29%
2	HH	361	67% 5% 29%
2	IH	361	65% 6% 29%
2	JH	361	63% 8% 29%
2	KH	361	66% 6% 29%
2	LH	361	65% 7% 29%
2	MH	361	64% 8% 29%
2	VH	361	14% 60% 7% 33%
2	WH	361	18% 60% 7% 33%
2	XH	361	21% 61% 7% 33%
2	YH	361	10% 60% 7% 33%
2	ZH	361	23% 60% 8% 33%
3	AK	189	72% 8% 20%
3	BK	189	71% 9% 20%
3	CK	189	72% 8% 20%
3	DK	189	76% 6% 20%
3	EK	189	74% 6% 20%
3	FK	189	74% 6% 20%
3	GK	189	74% 6% 20%













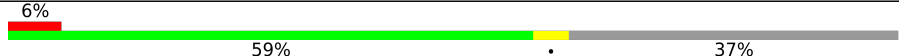
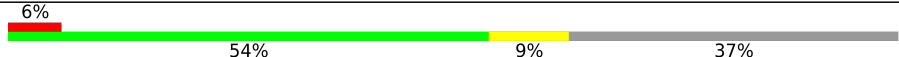
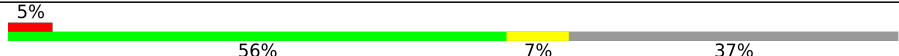

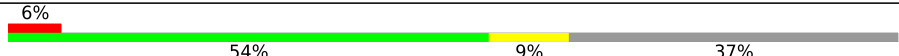
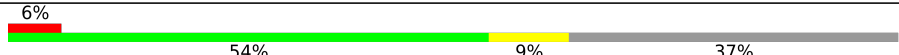
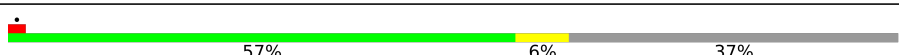
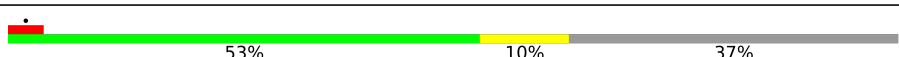
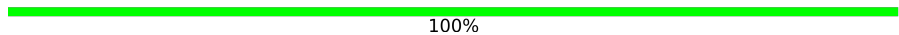
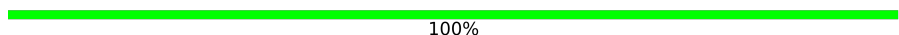
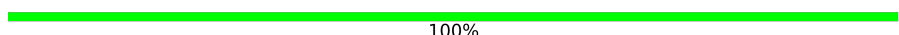
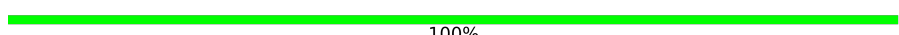
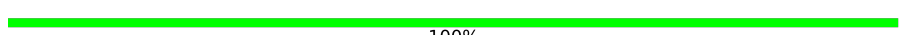
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Mol	Chain	Length	Quality of chain
3	HK	189	74% 6% 20%
3	IK	189	74% 6% 20%
3	JK	189	73% 7% 20%
3	KK	189	70% 10% 20%
3	LK	189	74% 6% 20%
3	MK	189	70% 10% 20%
4	AL	249	65% . 31%
4	BL	249	62% 8% 31%
4	CL	249	65% . 31%
4	DL	249	64% 6% 31%
4	EL	249	63% 6% 31%
4	FL	249	63% 6% 31%
4	GL	249	62% 7% 31%
4	HL	249	65% 5% 31%
4	IL	249	65% . 31%
4	JL	249	65% . 31%
4	KL	249	63% 6% 31%
4	LL	249	66% . 31%
4	ML	249	65% . 31%
5	AM	320	55% 10% 35%
5	BM	320	59% 6% 35%
5	CM	320	57% 8% 35%
5	DM	320	59% 6% 35%
5	EM	320	58% 7% 35%
5	FM	320	57% 8% 35%










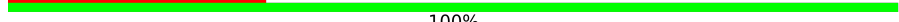

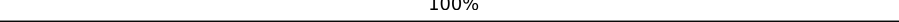





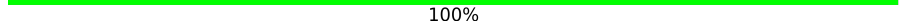

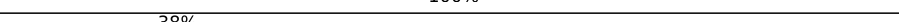


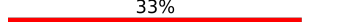


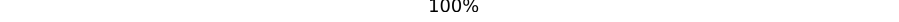







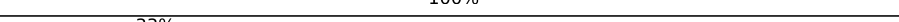







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Mol	Chain	Length	Quality of chain
5	GM	320	 55% 10% 35%
5	HM	320	 58% 7% 35%
5	IM	320	 60% 5% 35%
5	JM	320	 57% 8% 35%
5	KM	320	 58% 7% 35%
5	LM	320	 59% 6% 35%
5	MM	320	 59% 6% 35%
6	AN	124	 6% 54% 9% 37%
6	BN	124	 8% 52% 10% 37%
6	CN	124	 8% 53% 10% 37%
6	DN	124	 55% 8% 37%
6	EN	124	 56% 6% 37%
6	FN	124	 6% 59% 37%
6	GN	124	 6% 54% 9% 37%
6	HN	124	 5% 56% 7% 37%
6	IN	124	 6% 55% 8% 37%
6	JN	124	 6% 54% 9% 37%
6	KN	124	 6% 54% 9% 37%
6	LN	124	 57% 6% 37%
6	MN	124	 6% 53% 10% 37%
7	AU	9	 100%
7	BU	9	 100%
7	CU	9	 100%
7	DU	9	 100%
7	EU	9	 100%

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Mol	Chain	Length	Quality of chain
7	FU	9	 100%
7	GU	9	 100%
7	HU	9	 100%
7	IU	9	 100%
7	JU	9	 100%
7	KU	9	 100%
7	LU	9	 100%
7	MU	9	 100%
8	AX	48	 29%  100%
8	BX	48	 42%  100%
8	CX	48	 38%  100%
8	DX	48	 23%  100%
8	EX	48	 38%  100%
8	FX	48	 21%  100%
8	GX	48	 54%  100%
8	HX	48	 38%  100%
8	IX	48	 29%  100%
8	JX	48	 33%  100%
8	KX	48	 46%  100%
8	LX	48	 46%  100%
8	MX	48	 40%  100%
8	VX	48	 33%  100%
8	WX	48	 31%  100%
8	XX	48	 29%  100%
8	YX	48	 33% 100%

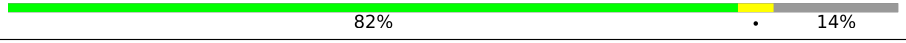















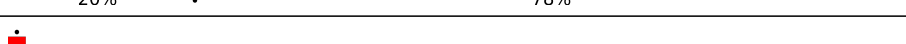
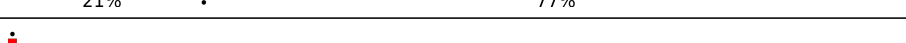







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Mol	Chain	Length	Quality of chain
8	ZX	48	
9	AD	163	
9	Ad	163	
9	BD	163	
9	Bd	163	
9	CD	163	
9	Cd	163	
9	DD	163	
9	Dd	163	
9	ED	163	
9	Ed	163	
9	FD	163	
9	Fd	163	
9	GD	163	
9	Gd	163	
9	HD	163	
9	Hd	163	
9	ID	163	
9	Id	163	
9	JD	163	
9	Jd	163	
9	KD	163	
9	Kd	163	
9	LD	163	
9	Ld	163	











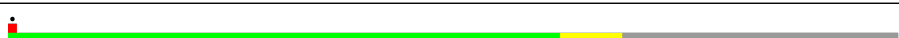

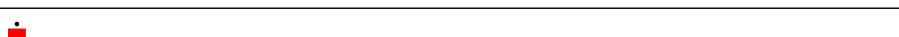
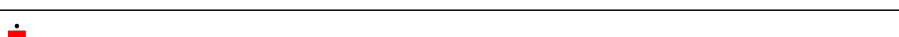
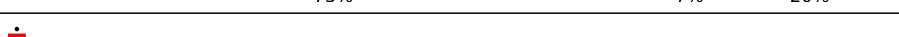
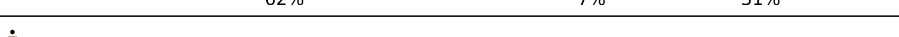

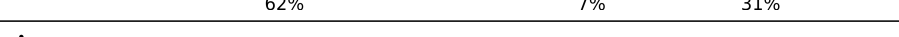

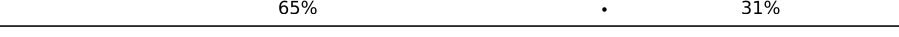
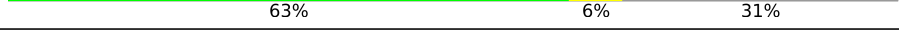
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Mol	Chain	Length	Quality of chain
9	MD	163	 82% 14%
9	Md	163	 74% 10% 16%
10	AF	269	 21% 77%
10	Af	269	 20% 78%
10	BF	269	 21% 77%
10	Bf	269	 20% 78%
10	CF	269	 21% 77%
10	Cf	269	 19% 78%
10	DF	269	 21% 77%
10	Df	269	 19% 78%
10	EF	269	 20% 77%
10	Ef	269	 20% 78%
10	FF	269	 21% 77%
10	Ff	269	 19% 78%
10	GF	269	 22% 77%
10	Gf	269	 20% 78%
10	HF	269	 21% 77%
10	Hf	269	 21% 78%
10	IF	269	 22% 77%
10	If	269	 20% 78%
10	JF	269	 22% 77%
10	Jf	269	 20% 78%
10	KF	269	 20% 77%
10	Kf	269	 20% 78%
10	LF	269	 21% 77%

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Mol	Chain	Length	Quality of chain
10	Lf	269	 21% 78%
10	MF	269	 21% 77%
10	Mf	269	 19% 78%
10	VF	269	 22% 77%
10	WF	269	 21% 77%
10	XF	269	 21% 77%
10	YF	269	 21% 77%
10	ZF	269	 22% 77%
11	AC	303	 73% 7% 20%
11	BC	303	 6% 73% 8% 20%
11	CC	303	 62% 7% 31%
11	DC	303	 62% 7% 31%
11	EC	303	 62% 7% 31%
11	FC	303	 73% 7% 20%
11	GC	303	 62% 7% 31%
11	HC	303	 61% 8% 31%
11	IC	303	 62% 7% 31%
11	JC	303	 71% 9% 20%
11	KC	303	 65% 31%
11	LC	303	 63% 6% 31%
11	MC	303	 60% 9% 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
			Total	C	N	O	S		
1	AG	165	1229	780	203	242	4	0	0
1	Fg	34	276	168	47	60	1	0	0
1	Gg	34	276	168	47	60	1	0	0
1	BG	165	1229	780	203	242	4	0	0
1	Hg	34	276	168	47	60	1	0	0
1	Bg	34	276	168	47	60	1	0	0
1	Ig	34	276	168	47	60	1	0	0
1	CG	165	1229	780	203	242	4	0	0
1	Jg	34	276	168	47	60	1	0	0
1	Kg	34	276	168	47	60	1	0	0
1	DG	165	1229	780	203	242	4	0	0
1	Lg	34	276	168	47	60	1	0	0
1	Mg	34	276	168	47	60	1	0	0
1	EG	165	1229	780	203	242	4	0	0
1	VG	34	276	168	47	60	1	0	0
1	WG	34	276	168	47	60	1	0	0
1	XG	34	276	168	47	60	1	0	0

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

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

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

- Molecule 6 is a protein called Neurogenic locus notch.

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

- Molecule 7 is a protein called Unknown protein fragment.

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

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

- Molecule 8 is a protein called Unknown protein fragment.

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

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

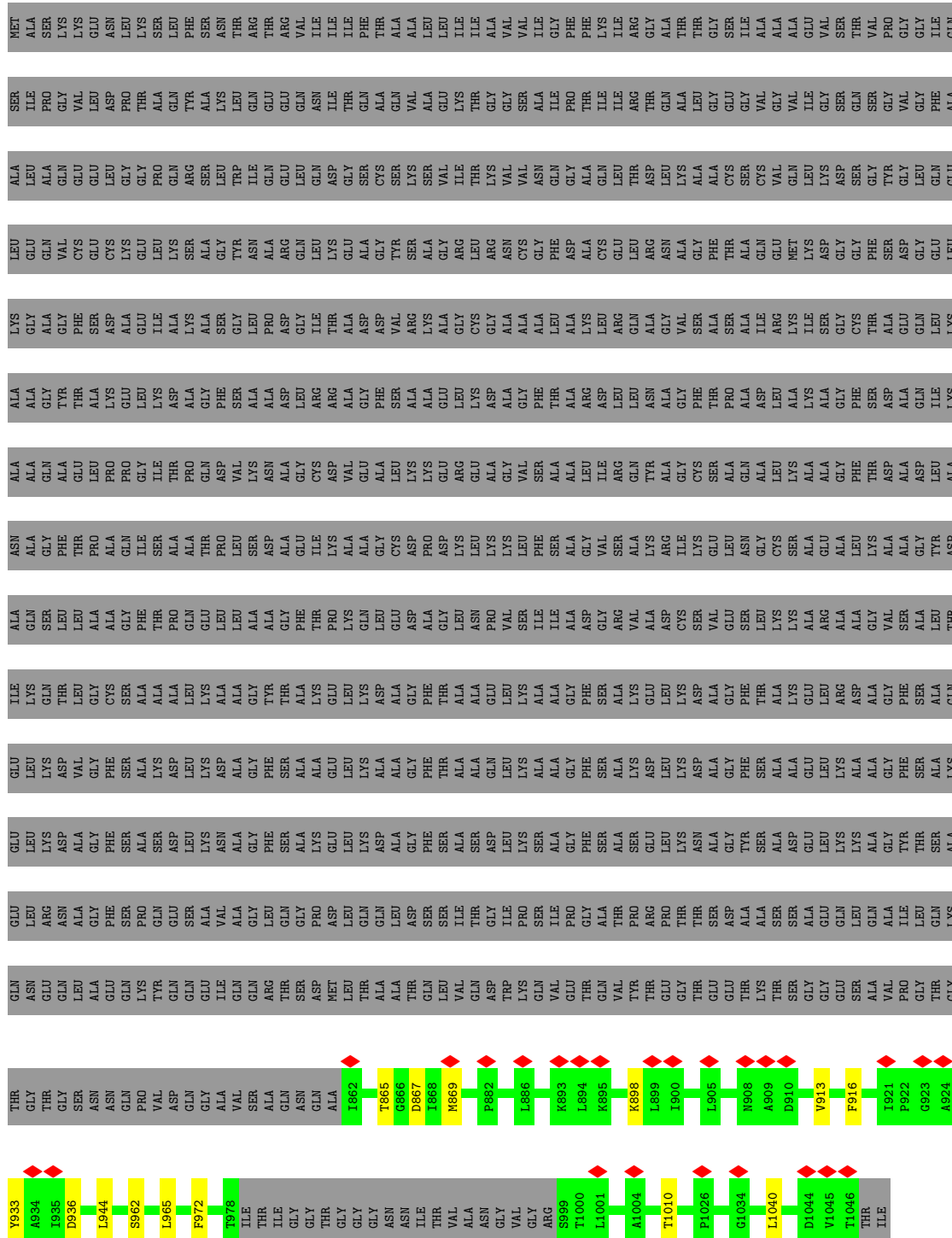
- Molecule 11 is a protein called DotC.

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		

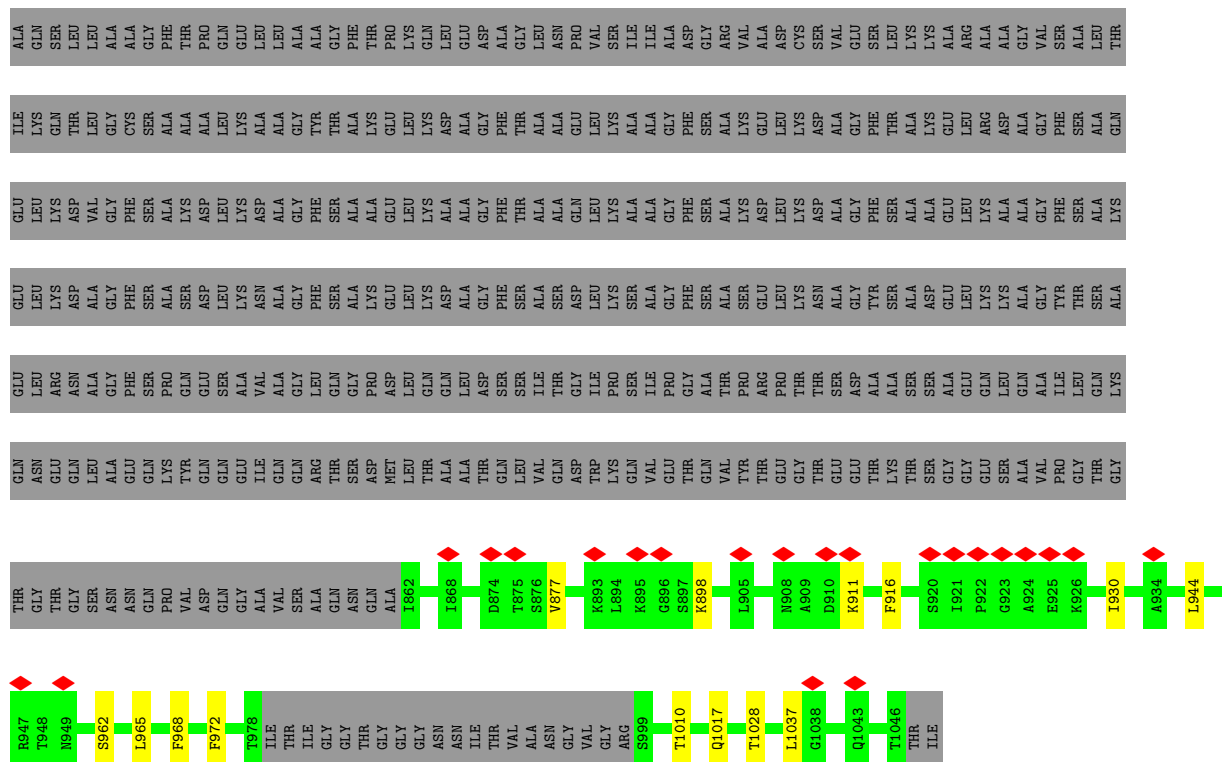
THR
THR
ILE

Molecule 1: IcmE protein

Chain BG:  14% 84%

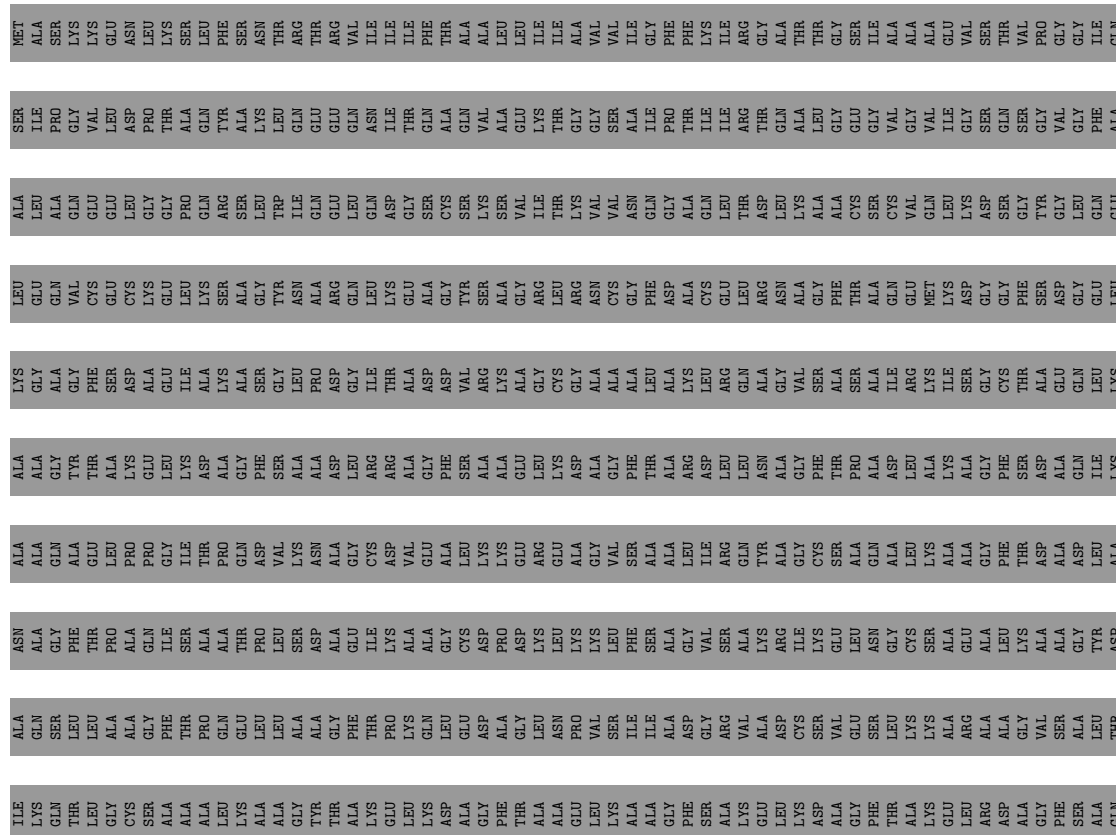


Molecule 1: IcmE protein



• Molecule 1: IcmE protein

Chain VG:  97%



ILE SER
THR VAL
ALA TYR
ASN ALA
GLY ILE
VAL ASP
GLY PRO
ASN ASN

ILE THR
VAL VAL
ALA ALA
ASN ALA
GLY VAL
VAL VAL
ASN ASN

• Molecule 1: IcmE protein

Chain Cg:  97%

MET ALA
SER SER
ILE THR
PRO VAL
GLY TYR
VAL THR
LEU ALA
ASP ASP
THR THR
PRO THR
ALA THR

SER ILE
PRO PRO
GLY VAL
THR THR
VAL THR
LEU THR
ASP THR
THR THR

ALA LEU
SER SER
GLY VAL
CYS THR
GLY THR
LEU THR
GLY THR
GLY THR

LEU LEU
GLY VAL
GLN THR
CYS THR
CYS THR
CYS THR
CYS THR
CYS THR

LYS GLY
ALA VAL
SER THR
ASP THR
ALA THR
SER THR
SER THR
SER THR

ALA GLY
SER THR
PHE THR
GLY THR
PHE THR
PHE THR
PHE THR
PHE THR

ALA GLN
SER THR
PHE THR
GLY THR
PHE THR
PHE THR
PHE THR
PHE THR

ASN ALA
SER THR
PHE THR
GLY THR
PHE THR
PHE THR
PHE THR
PHE THR

ALA GLN
SER THR
PHE THR
GLY THR
PHE THR
PHE THR
PHE THR
PHE THR

ILE LYS
SER THR
THR THR
GLY THR
CYS THR
CYS THR
CYS THR
CYS THR

GLU LEU
LYS THR
ASP THR
VAL THR
PHE THR
SER THR
SER THR
SER THR

GLU LEU
LYS THR
ASP THR
VAL THR
PHE THR
SER THR
SER THR
SER THR

GLU LEU
ARG THR
ASN THR
ALA THR
PHE THR
SER THR
SER THR
SER THR

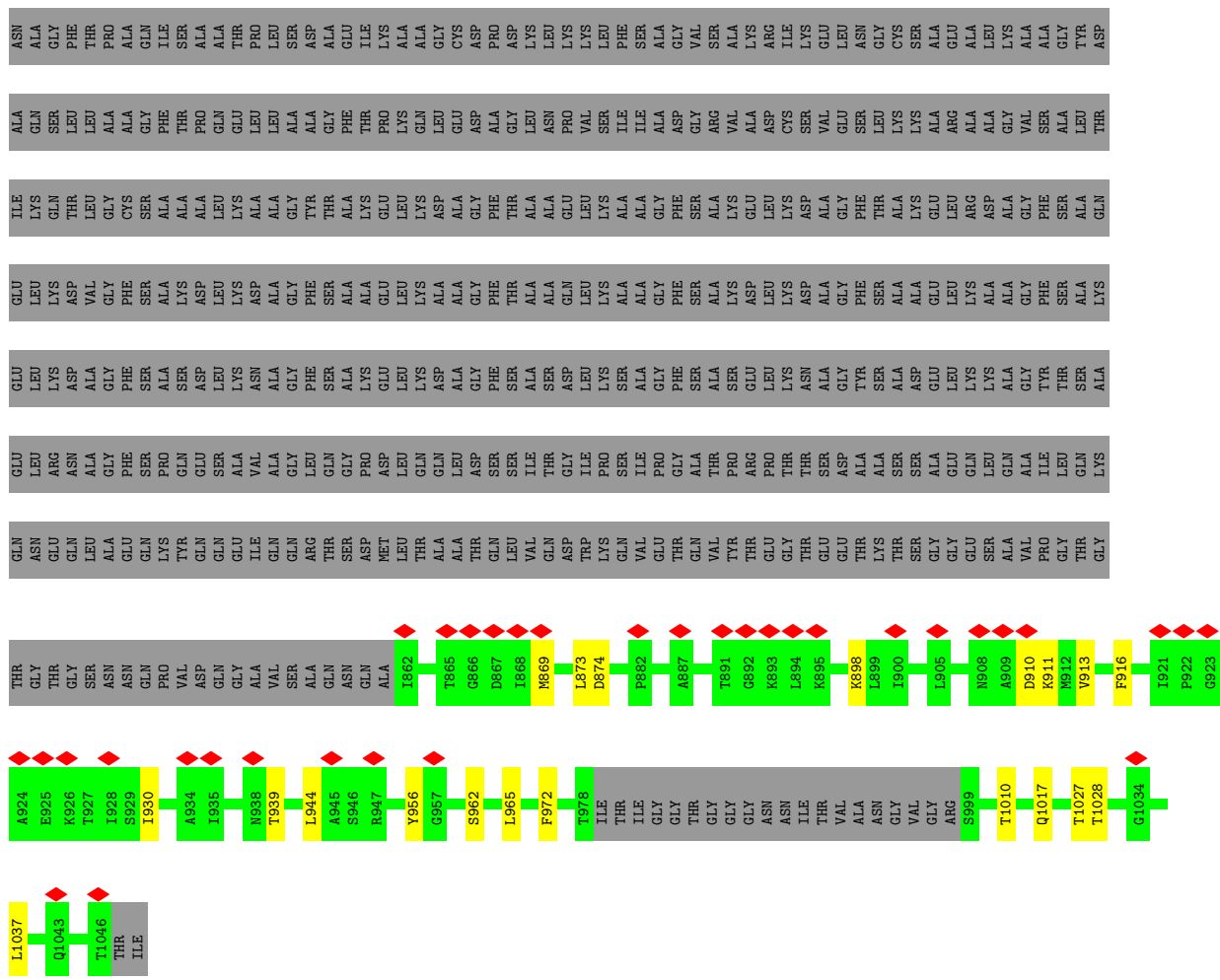
GLN ASN
SER THR
GLY THR
VAL THR
PHE THR
SER THR
SER THR
SER THR

ILE LYS
THR THR
GLY THR
ASP THR
MET THR
PHE THR
PHE THR
PHE THR

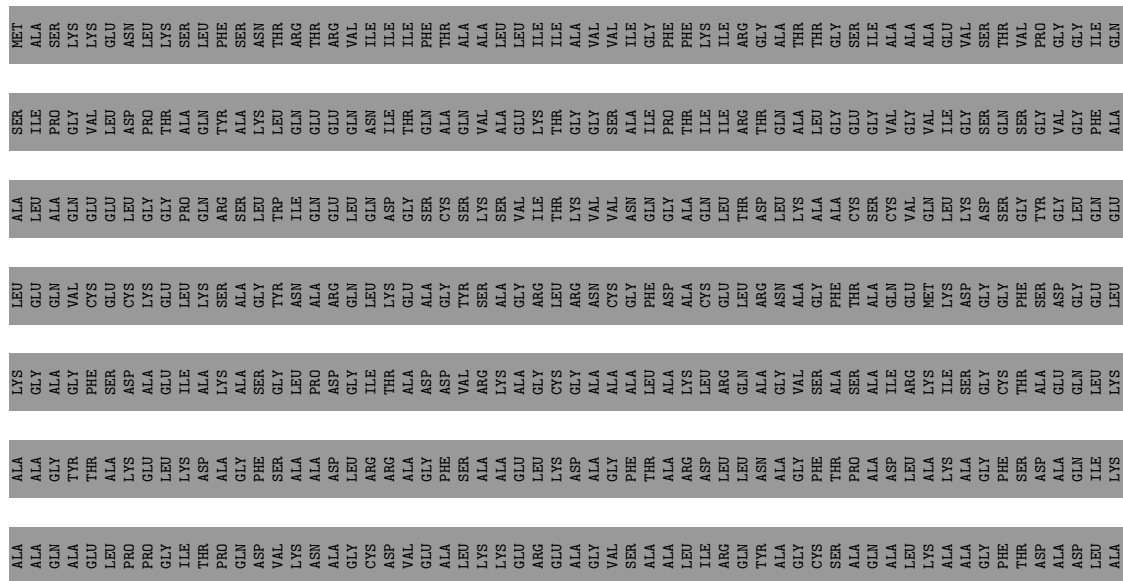
GLY ALA
SER THR
LYS THR
THR THR
ILE THR
SER THR
SER THR
SER THR

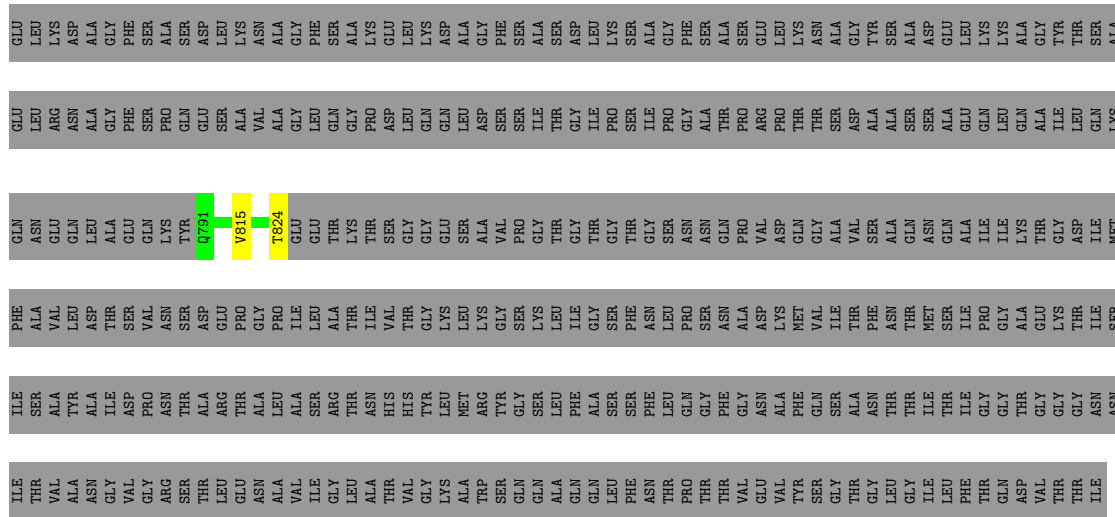
GLY THR
SER THR
SER THR
SER THR
SER THR
SER THR
SER THR
SER THR

THR VAL
GLY THR
SER THR
SER THR
SER THR
SER THR
SER THR
SER THR

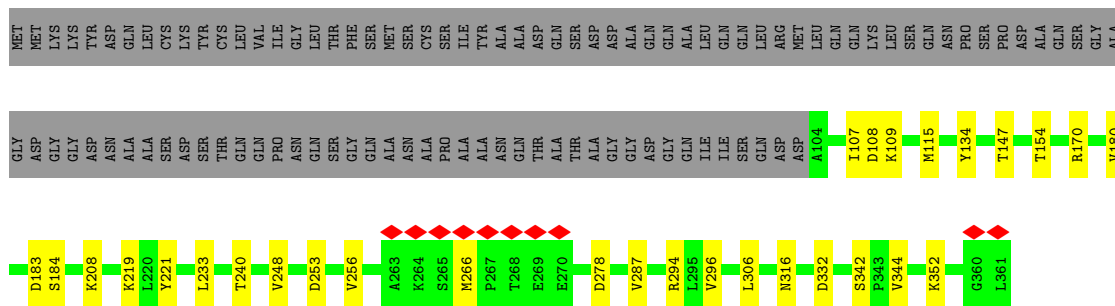


● Molecule 1: IcmE protein

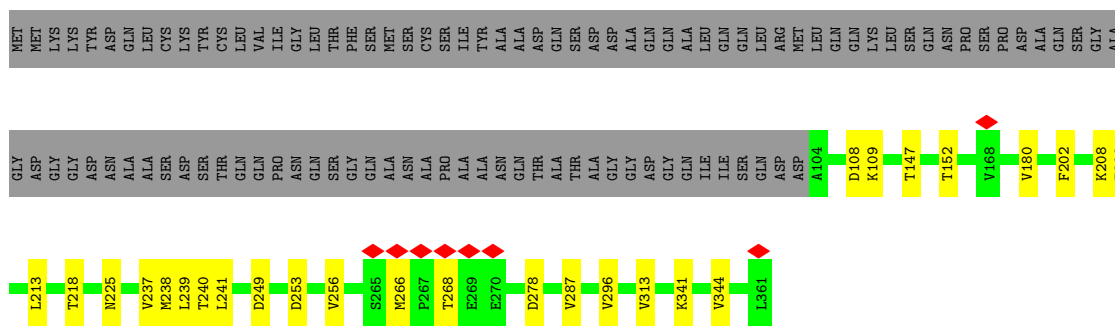




• Molecule 2: Type IV secretion protein IcmK

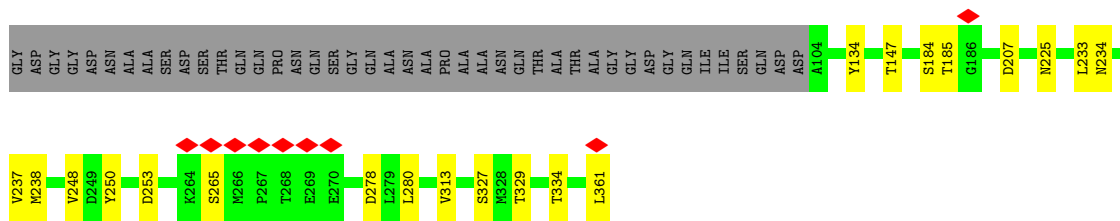


• Molecule 2: Type IV secretion protein IcmK

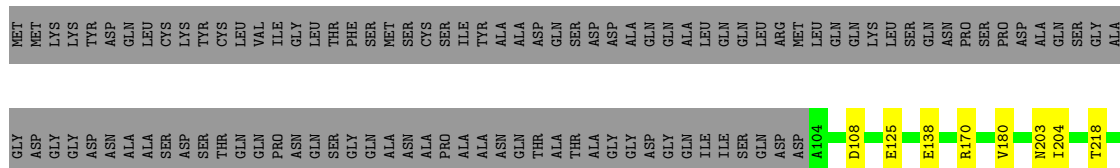


• Molecule 2: Type IV secretion protein IcmK

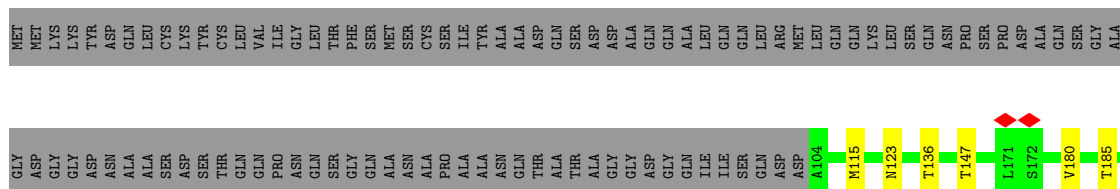




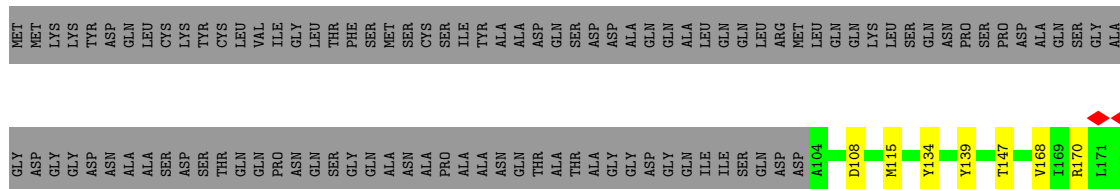
• Molecule 2: Type IV secretion protein IcmK



• Molecule 2: Type IV secretion protein IcmK



• Molecule 2: Type IV secretion protein IcmK



• Molecule 2: Type IV secretion protein IcmK

Chain AH:



MET MET LYS LYS TYR ASP GLN LEU CYS TYR CYS TYR CYS VAL ILE ILE GLN THR THR PHE SER MET MET CYS TYR SER SER ILE TYR TYR ALA ALA ALA ASP THR ALA GLN ASP ASP THR ALA GLN TYR LEU LEU LEU LEU LEU LEU LEU LEU MET ASP LEU GLN LYS LEU SER ASN PRO SER ASP ALA GLN TYR SER ASP MET LEU GLN ASP GLY R170 G186 F202 L213 L233 V237 M238 L239 T240 V248 D249 Y250 D253 V256 N262 A263 K264 S265 M266 P267 T268 E269 E270 L280 V287 V296 V313 S342 H350 V353 L361

GLY ASP MET LYS LYS TYR ASP ASP ALA ALA LEU CYS TYR CYS TYR CYS VAL ILE ILE GLN THR THR PHE SER MET MET CYS TYR SER SER ILE TYR TYR ALA ALA ALA ASP THR ALA GLN ASP ASP THR ALA GLN TYR LEU LEU LEU LEU LEU LEU LEU MET ASP LEU GLN LYS LEU SER ASN PRO SER ASP ALA GLN TYR SER ASP MET LEU GLN ASP GLY K109 D114 M115 T116 R117 Q132 I133 Y134 T147 Q156

- Molecule 2: Type IV secretion protein IcmK

Chain KH:



MET MET LYS LYS TYR ASP GLN LEU CYS TYR CYS TYR CYS VAL ILE ILE GLN THR THR PHE SER MET MET CYS TYR SER SER ILE TYR TYR ALA ALA ALA ASP THR ALA GLN ASP ASP THR ALA GLN TYR LEU LEU LEU LEU LEU LEU MET ASP LEU GLN LYS LEU SER ASN PRO SER ASP ALA GLN TYR SER ASP MET LEU GLN ASP GLY T218 M238 L241 V248 D249 Y250 M266 E269 E270 V287 V313 T329 D332 V344 L346 L361

GLY ASP MET LYS LYS TYR ASP ASP ALA ALA LEU CYS TYR CYS TYR CYS VAL ILE ILE GLN THR THR PHE SER MET MET CYS TYR SER SER ILE TYR TYR ALA ALA ALA ASP THR ALA GLN ASP ASP THR ALA GLN TYR LEU LEU LEU LEU LEU LEU MET ASP LEU GLN LYS LEU SER ASN PRO SER ASP ALA GLN TYR SER ASP MET LEU GLN ASP GLY A104 E105 T147 R170 L171 S172 V180 D183 D195 S210

- Molecule 2: Type IV secretion protein IcmK

Chain LH:



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GLY ASP MET LYS LYS TYR ASP ASP ALA ALA LEU CYS TYR CYS TYR CYS VAL ILE ILE GLN THR THR PHE SER MET MET CYS TYR SER SER ILE TYR TYR ALA ALA ALA ASP THR ALA GLN ASP ASP THR ALA GLN TYR LEU LEU LEU LEU LEU LEU MET ASP LEU GLN LYS LEU SER ASN PRO SER ASP ALA GLN TYR SER ASP MET LEU GLN ASP GLY A104 E105 V106 I107 D108 H123 T147 T152 L160 R170 V176

- Molecule 2: Type IV secretion protein IcmK

Chain MH:



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• Molecule 2: Type IV secretion protein IcmK



MET MET LYS LYS TYR ASP GLN LEU CYS TYR TYR CYS LEU VAL ILE LEU GLY LEU THR PHE SER MET MET CYS TYR TYR CYS LEU TYR TYR ALA ASP ALA ASP ALA ASP THR ASN SER ASP ASP ALA GLN ALA LEU GLN GLN LEU GLN ARG ASP MET LEU GLN LYS SER LEU ASN PRO PRO PRO ASP ALA GLN SER SER THR ASP ASP K109 K113 D114 M115 Y134 T147 L160 R170 F175

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V176 V180 V185 T185 L204 T240 V248 D249 Y250 D253 A263 LYS SER MET THR ALA THR ASN D278 H282 V283 L284 E285 P288 P289 P290 G291 S292 R293 R294 L295 V296 V297 S298 G299 D299 D300 A302 R303 A304 E309 K310 M311 Y312

V313 N316 L317 T318 S321 S330 A331 D332 G333 M339 Q340 K341 L345 S348 W349 H350 G351 K352 V353 M354 Q355 K357 V358 E359 G360 LEU

• Molecule 2: Type IV secretion protein IcmK



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GLY ASP GLY TYR ASN ALA SER ASP THR GLN PRO ASN GLN THR ALA THR ALA GLY GLN ILE ILE SER LEU ASP ASP A104 E105 D108 M115 L130 T136 T147 V180 D183

L213 Y221 L233 M238 L239 T240 V248 D253 A263 LYS SER MET THR ALA THR ASN D278 L279 L280 L281 H282 V283 L284 E285 G286 V287 P288 P289 P290 G291 S292 R293 R294 L295 V296 V297 S299 G299 G300 D301 A302 R303 A304 W305 L306 S307 N308

E309 K310 M311 V312 V313 R314 T315 N316 L317 T318 I319 L320 S321 P322 G323 W324 L325 A326 S327 M328 T329 S330 A331 D332 G333 T334 H335 A336 V337 E338 M339 Q340 K341 S342 P343 V344 L345 L346 V347 W349 H350 G351 K352 V353 M354 Q355 L356 K357 E359 G360 LEU

• Molecule 2: Type IV secretion protein IcmK



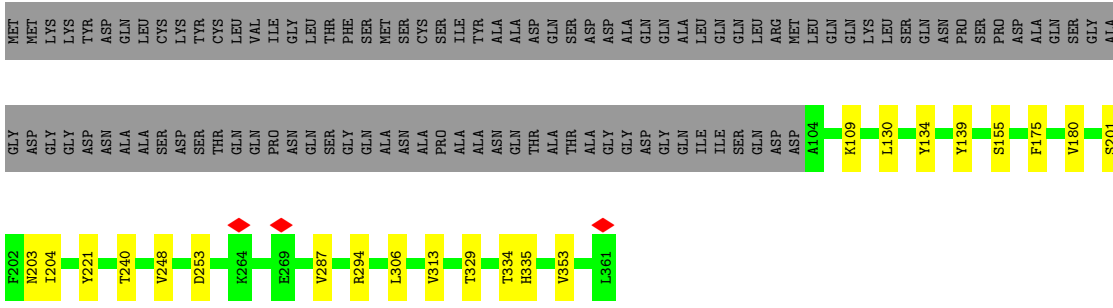
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GLY ASP GLY TYR ASN ALA SER ASP THR GLN PRO ASN GLN THR ALA THR ALA GLY GLN ILE ILE SER LEU ASP ASP A104 I107 D108 K109 T147 L160 R170 L171 F175 V176 V180

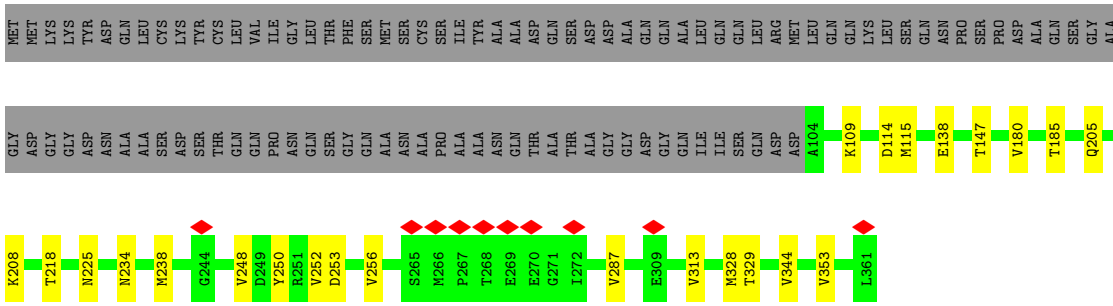
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• Molecule 2: Type IV secretion protein IcmK

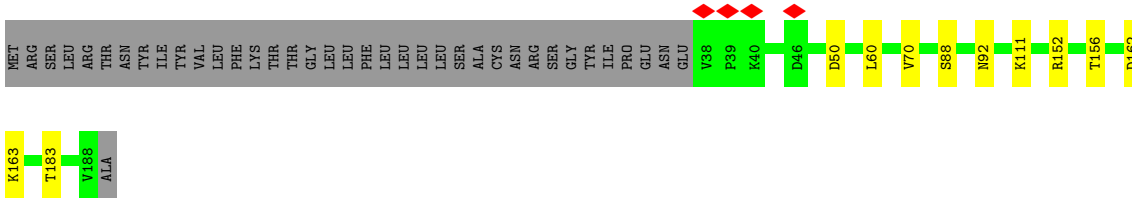
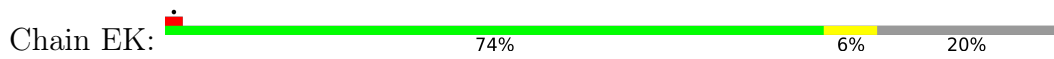




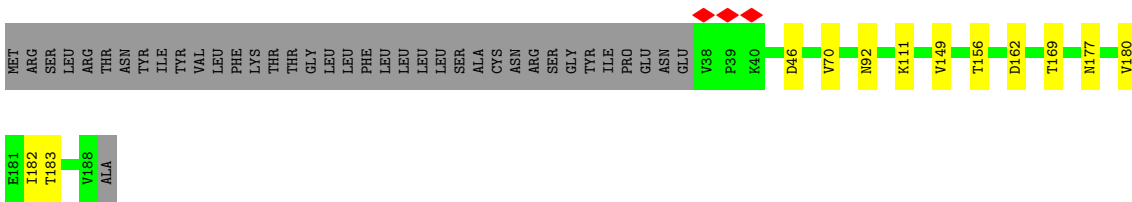
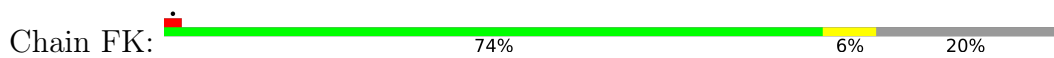
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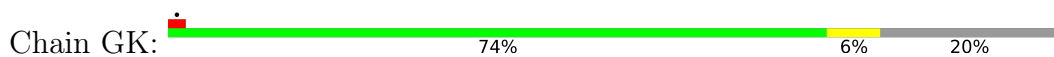
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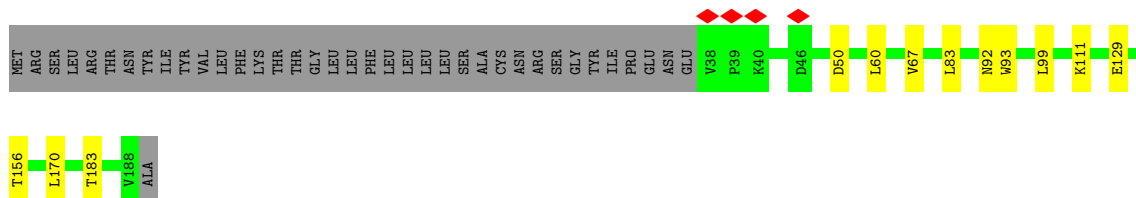


• Molecule 3: Inner membrane lipoprotein YiaD

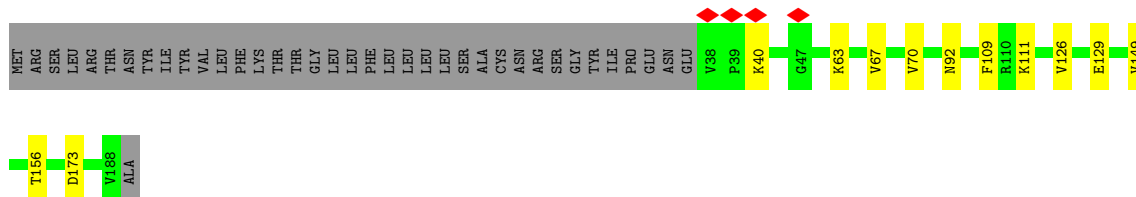
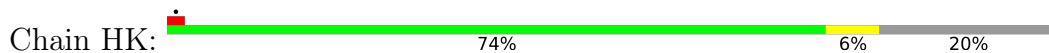


• Molecule 3: Inner membrane lipoprotein YiaD

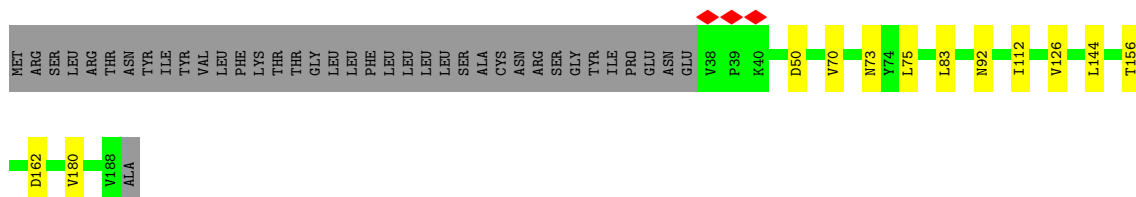
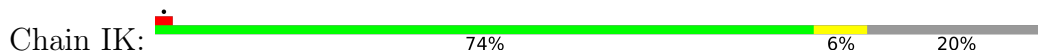




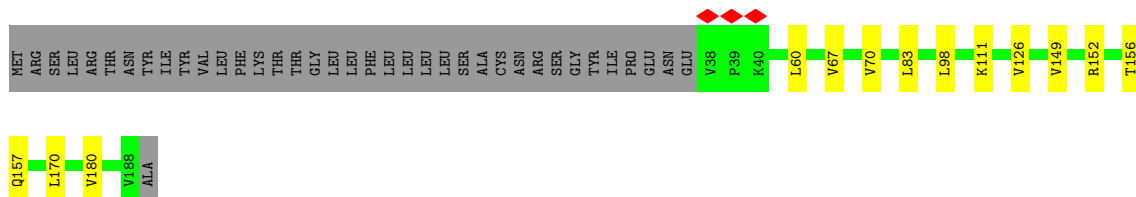
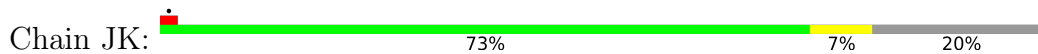
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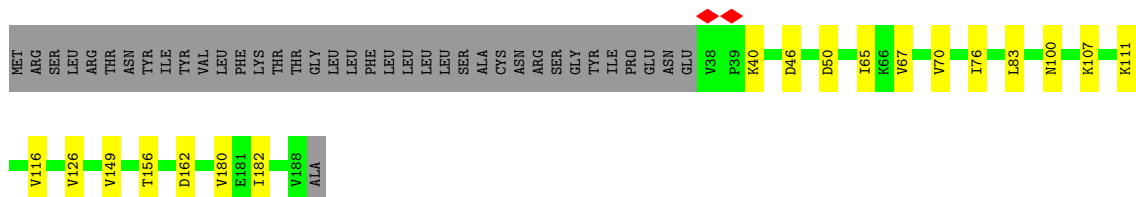
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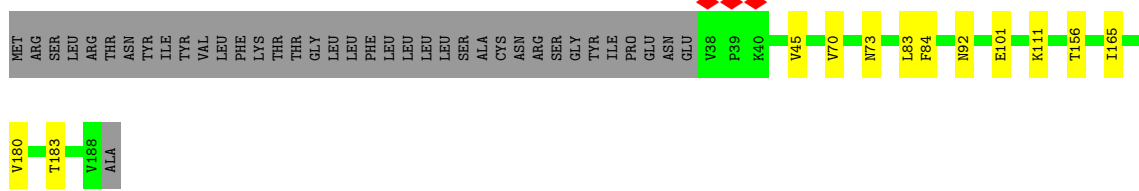
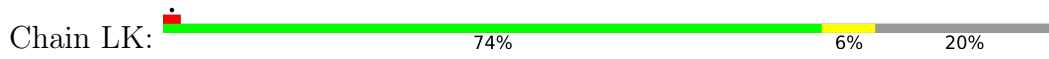
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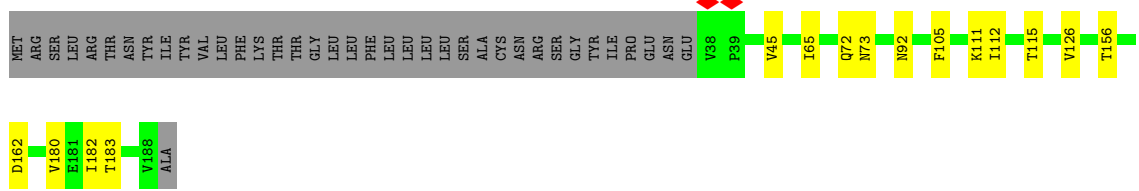
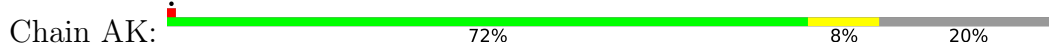
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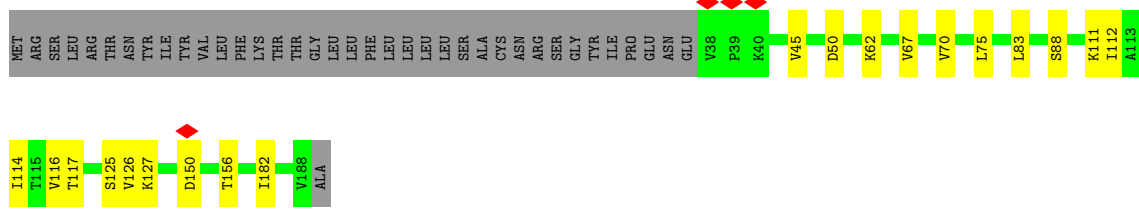
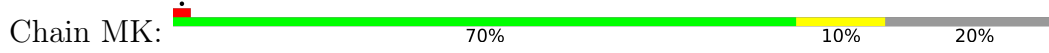
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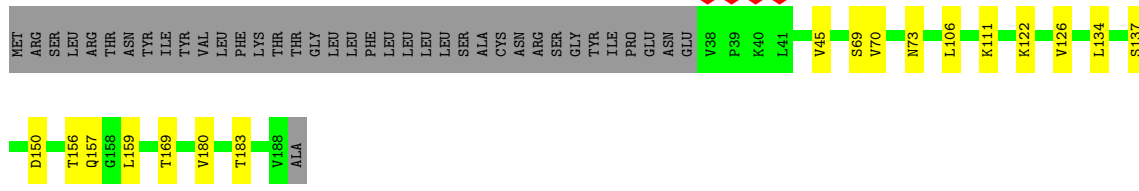
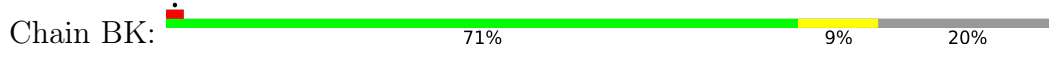
- Molecule 3: Inner membrane lipoprotein YiaD



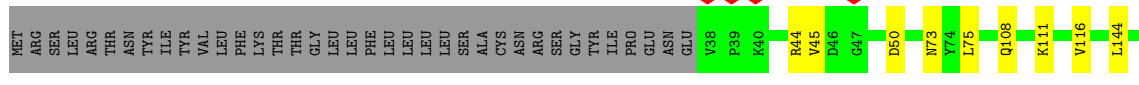
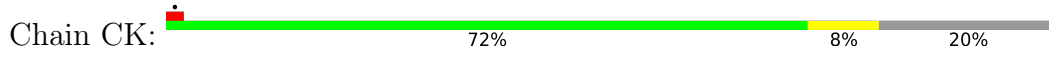
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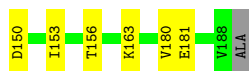


- Molecule 3: Inner membrane lipoprotein YiaD

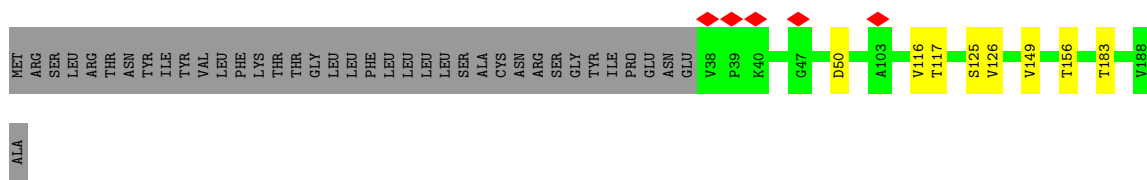
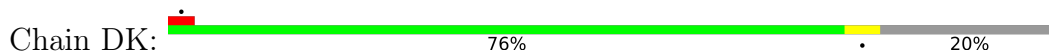


- Molecule 3: Inner membrane lipoprotein YiaD

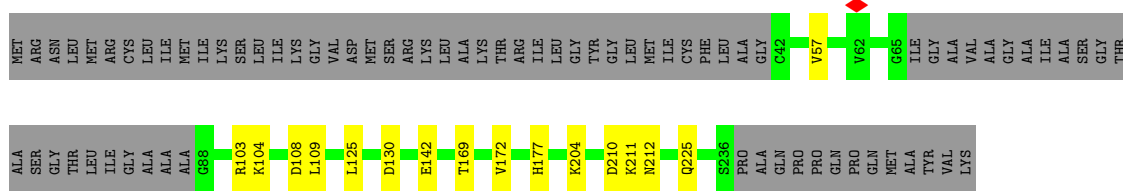




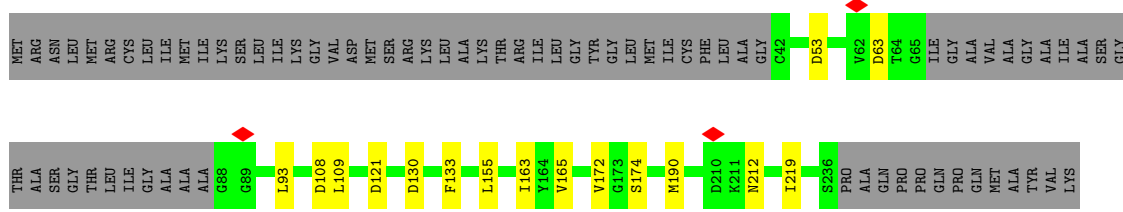
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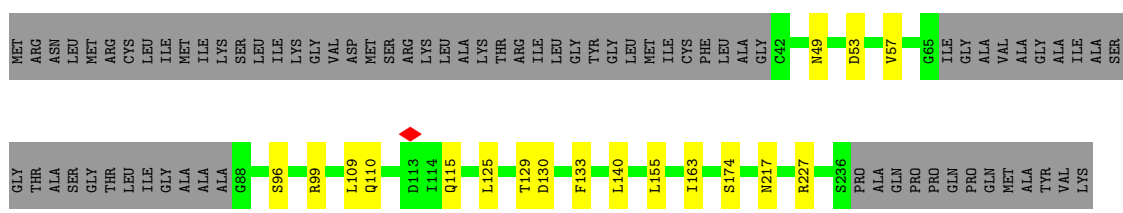
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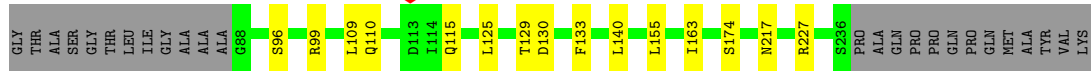
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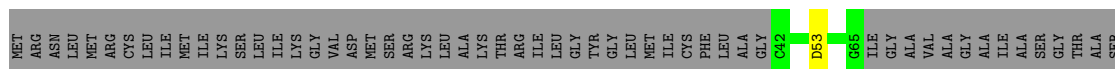


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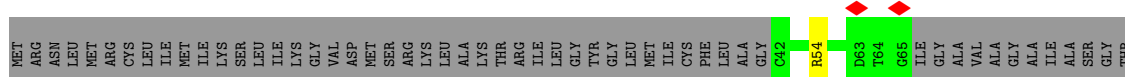


- Molecule 4: Outer membrane protein, OmpA family protein

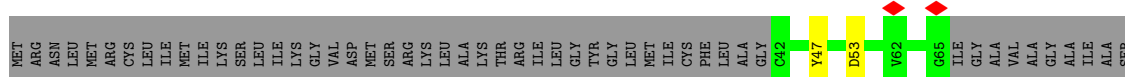




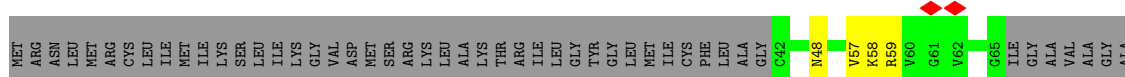
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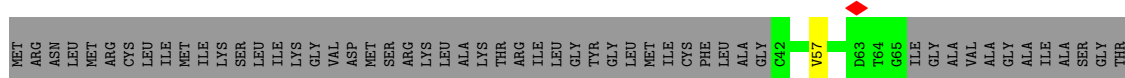
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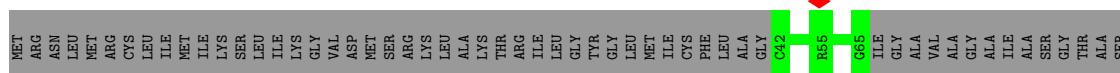
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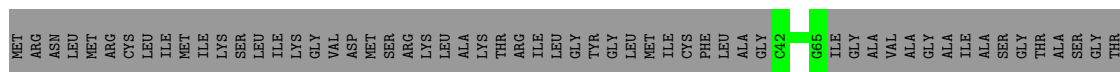
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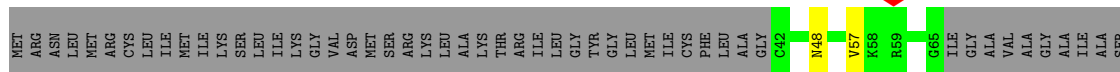
● Molecule 4: Outer membrane protein, OmpA family protein



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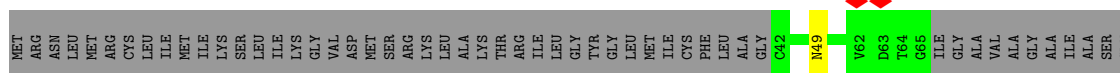


● Molecule 4: Outer membrane protein, OmpA family protein



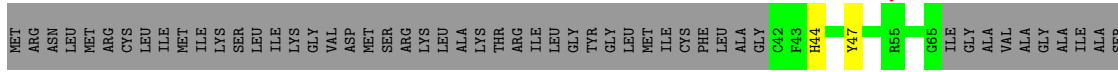
LYS

● Molecule 4: Outer membrane protein, OmpA family protein

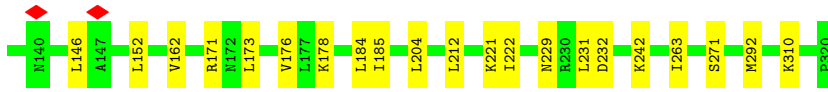
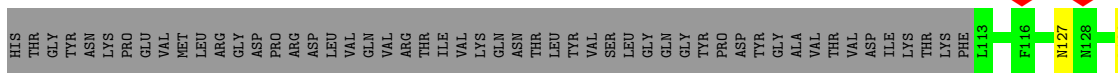
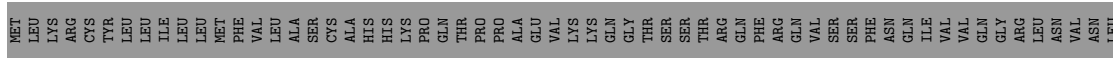


● Molecule 4: Outer membrane protein, OmpA family protein

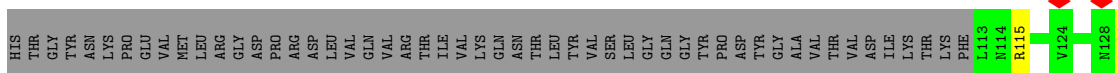
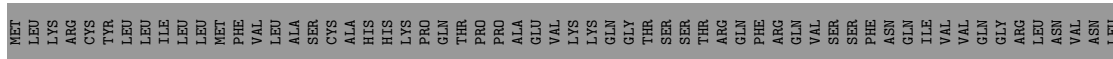




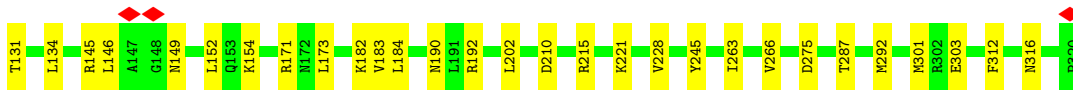
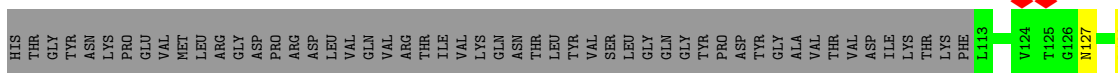
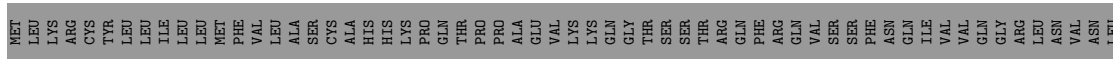
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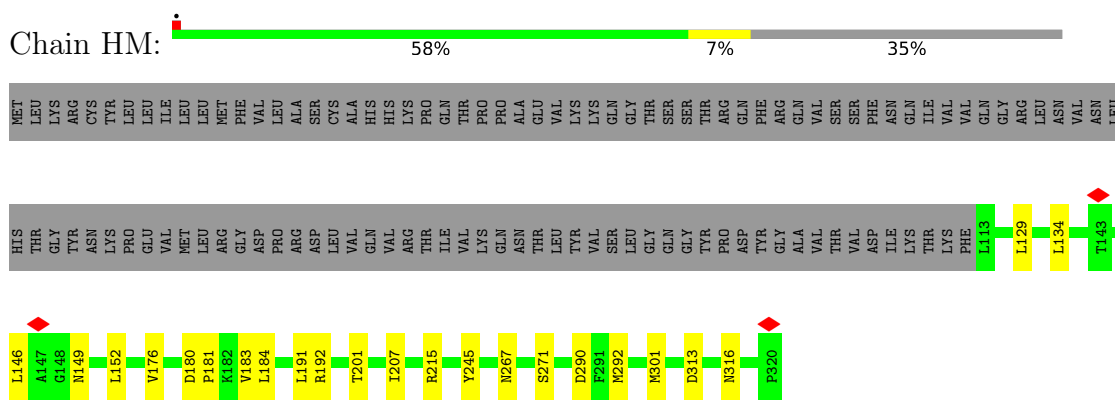
• Molecule 5: DUF2807 domain-containing protein



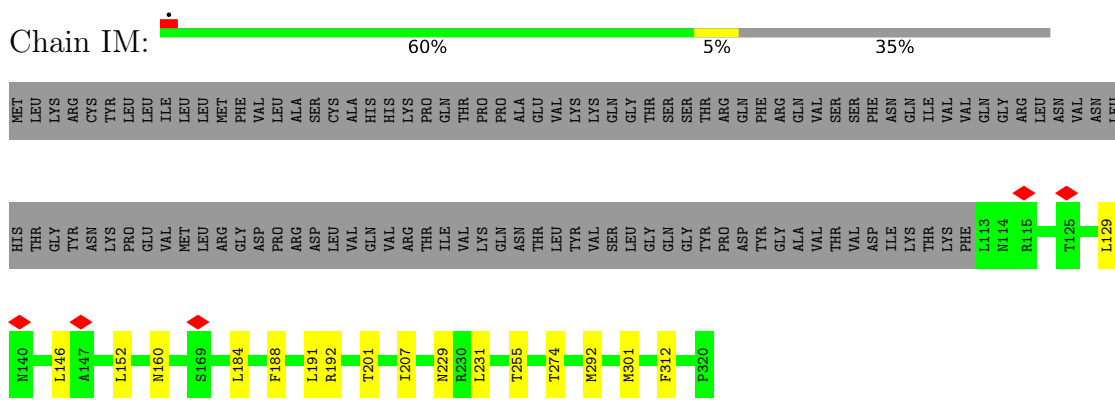
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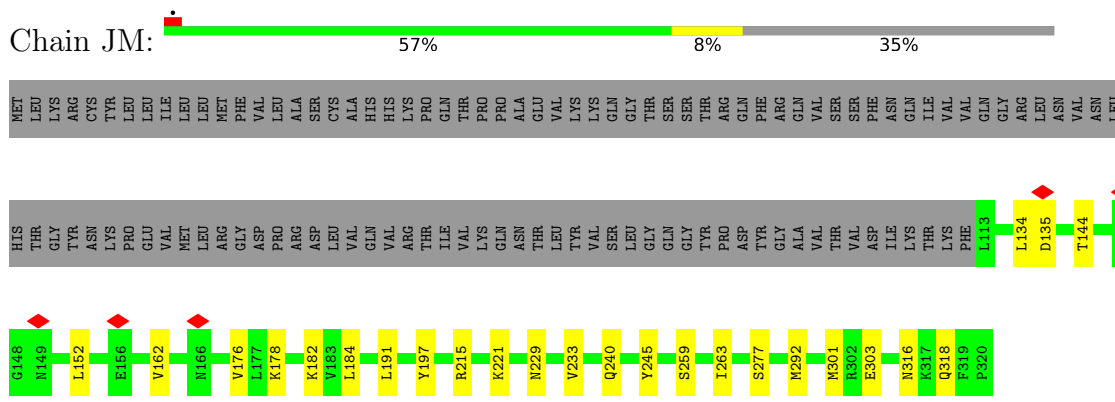
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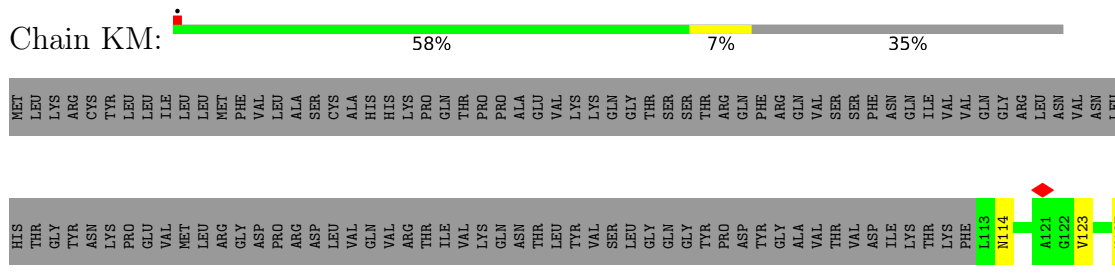
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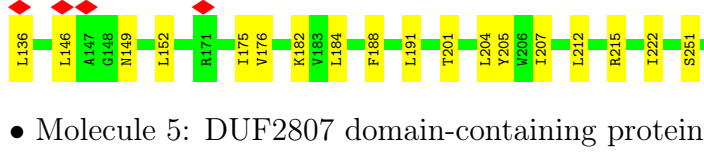
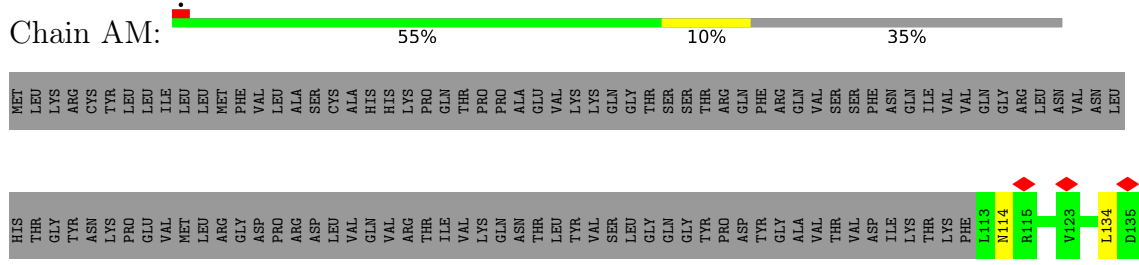
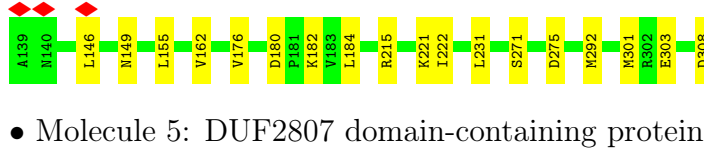
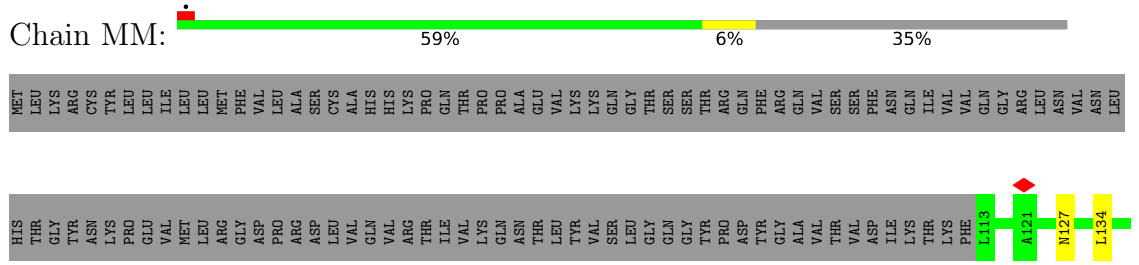
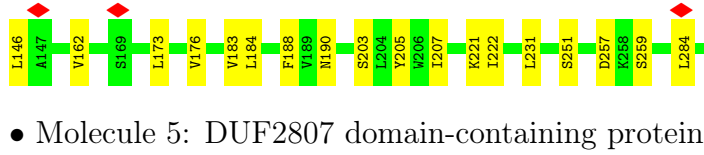
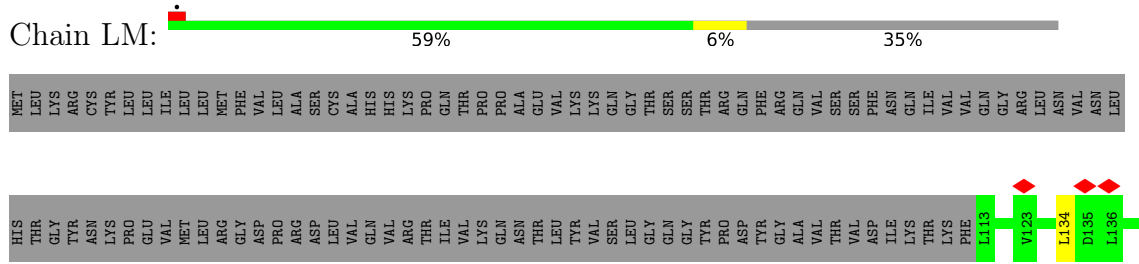
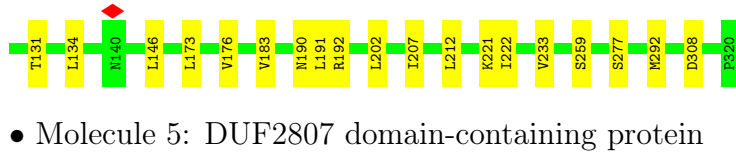


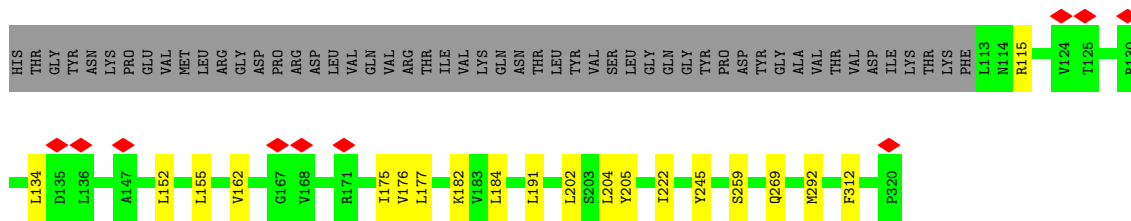
• Molecule 5: DUF2807 domain-containing protein



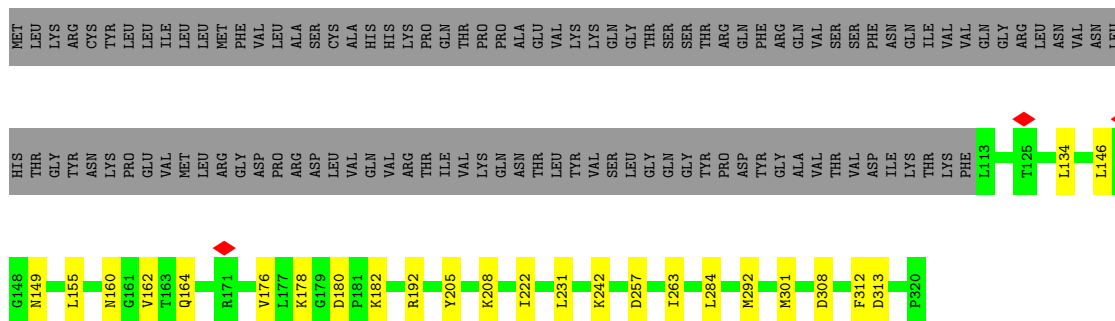
• Molecule 5: DUF2807 domain-containing protein



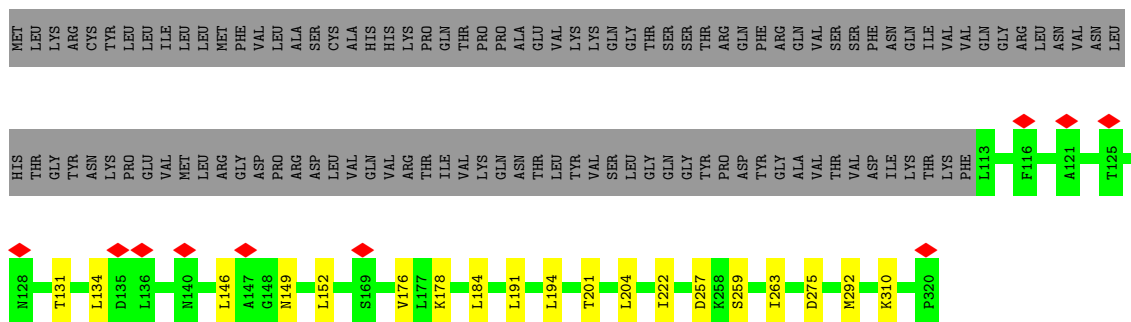




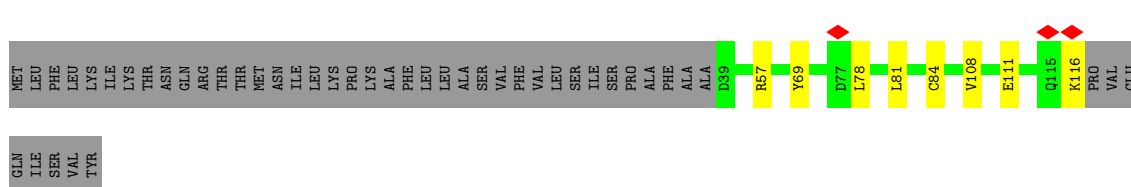
• Molecule 5: DUF2807 domain-containing protein



• Molecule 5: DUF2807 domain-containing protein

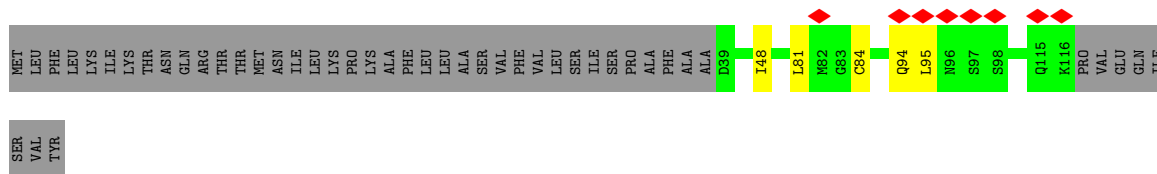


• Molecule 6: Neurogenic locus notch

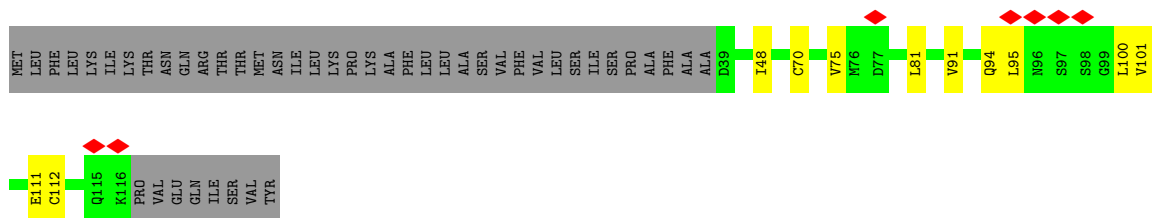


• Molecule 6: Neurogenic locus notch

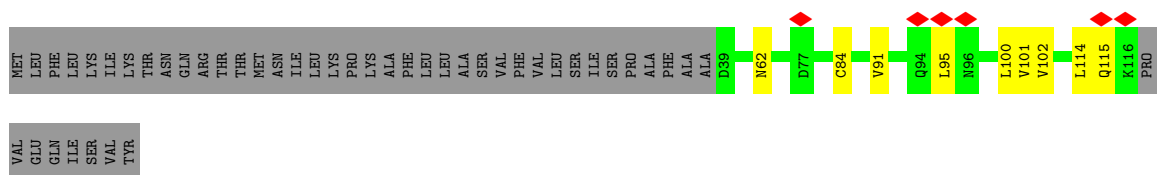




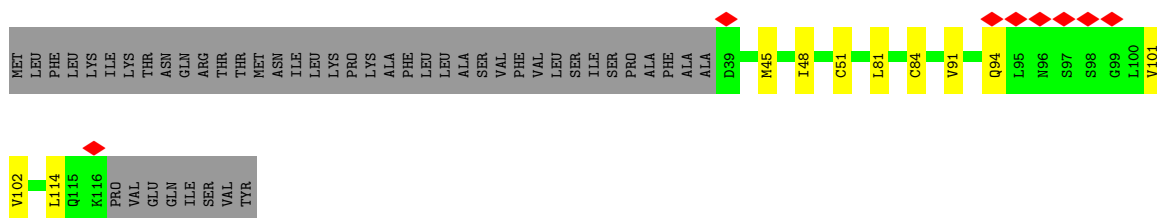
• Molecule 6: Neurogenic locus notch



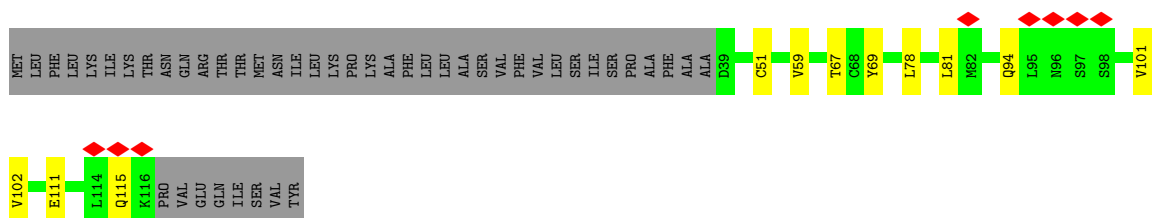
• Molecule 6: Neurogenic locus notch



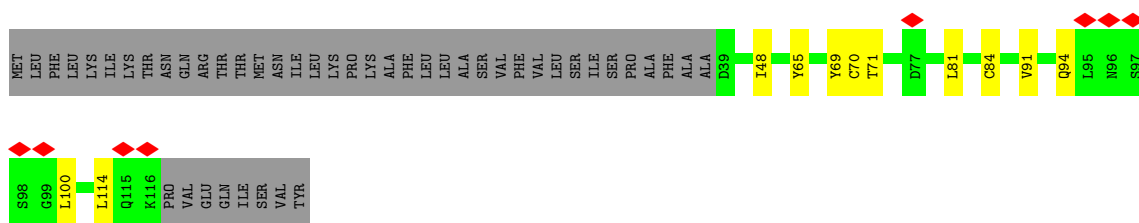
• Molecule 6: Neurogenic locus notch



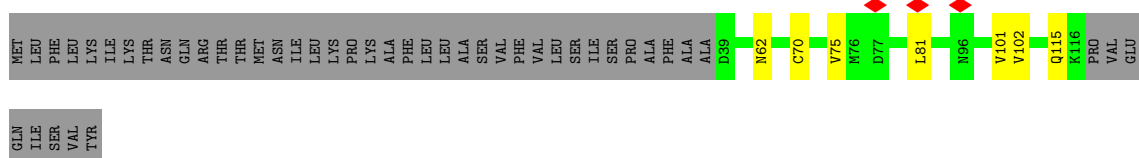
• Molecule 6: Neurogenic locus notch



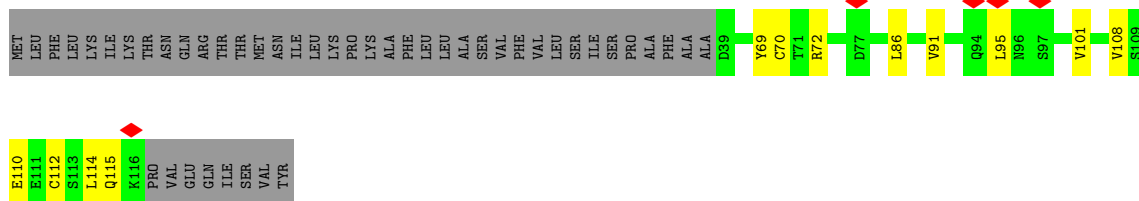
• Molecule 6: Neurogenic locus notch



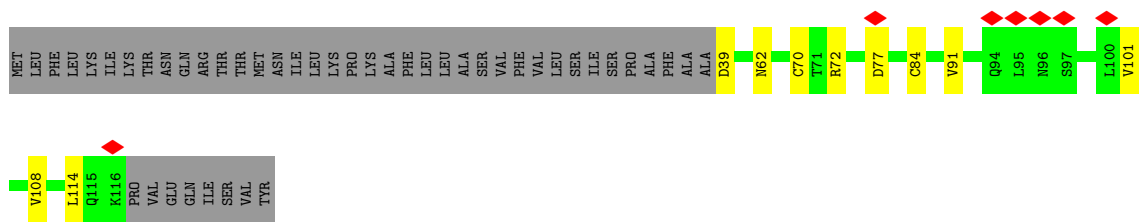
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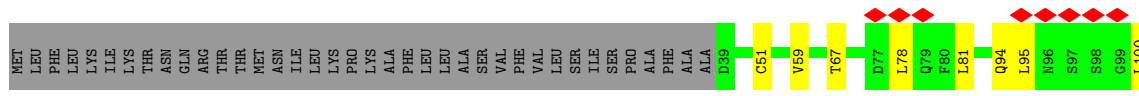
• Molecule 6: Neurogenic locus notch

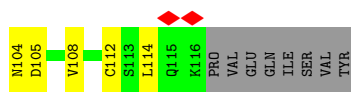


• Molecule 6: Neurogenic locus notch

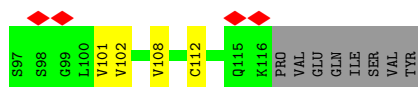
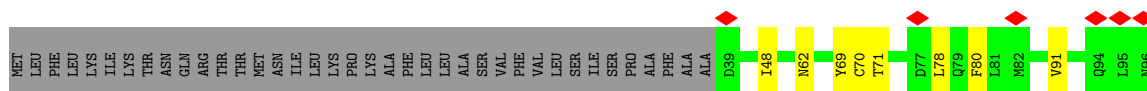


• Molecule 6: Neurogenic locus notch

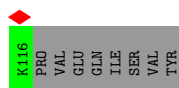
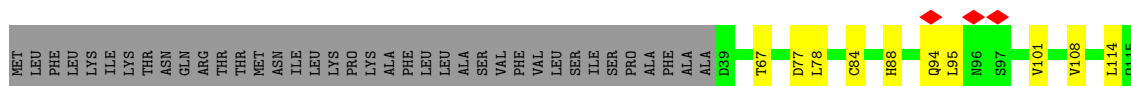




- Molecule 6: Neurogenic locus notch



- Molecule 6: Neurogenic locus notch



- Molecule 7: Unknown protein fragment



There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment



There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment



There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment



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:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain KU:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain LU:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain MU:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain AU:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain BU:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

Chain CU:  100%

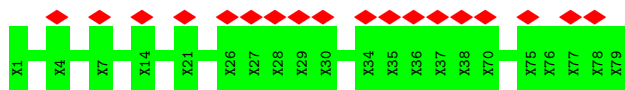
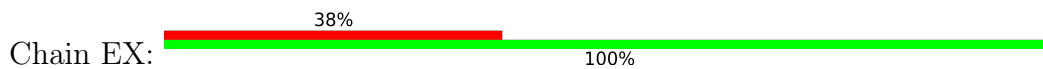
There are no outlier residues recorded for this chain.

- Molecule 7: Unknown protein fragment

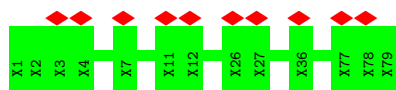
Chain DU:  100%

There are no outlier residues recorded for this chain.

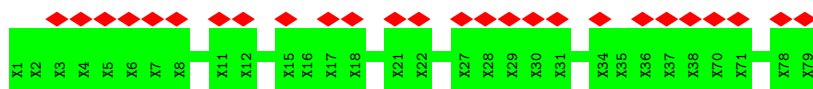
- Molecule 8: Unknown protein fragment



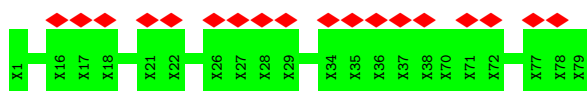
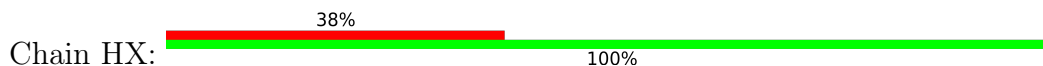
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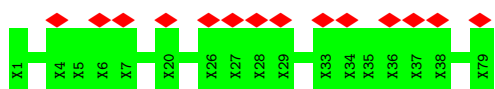
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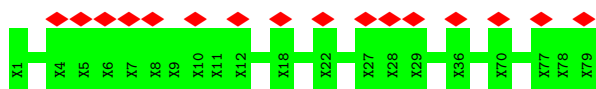
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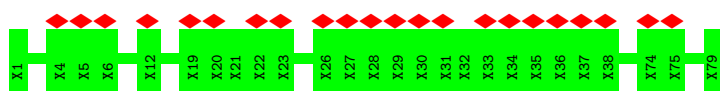
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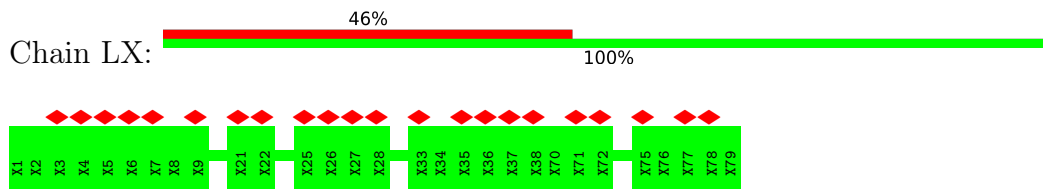
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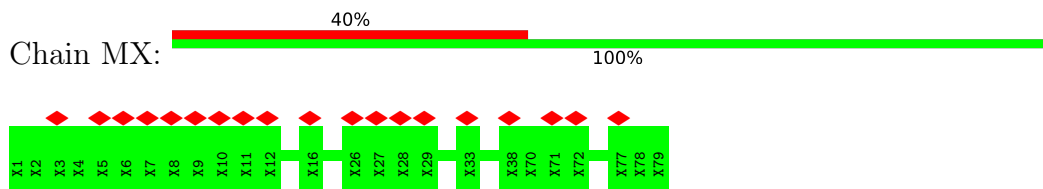
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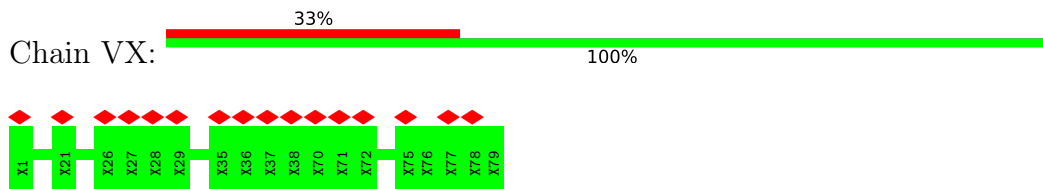
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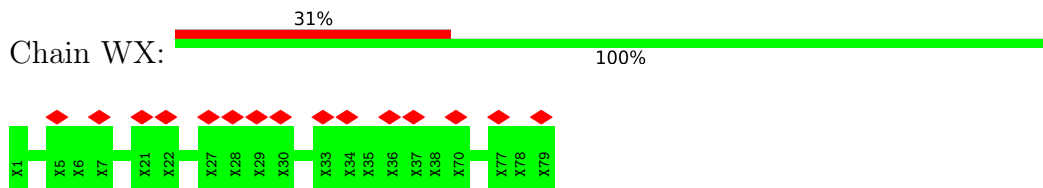
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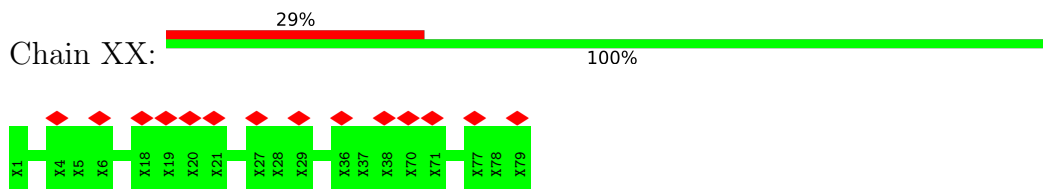
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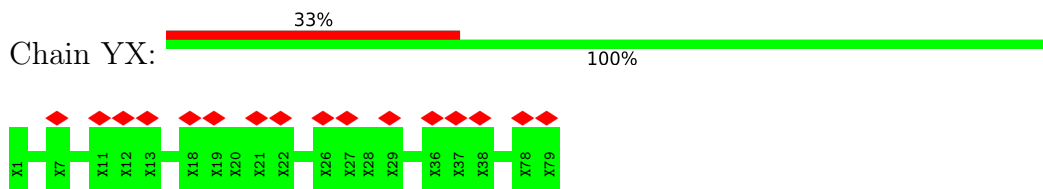
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- Molecule 8: Unknown protein fragment

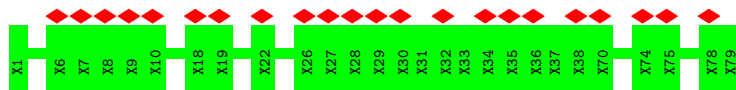


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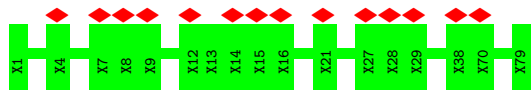


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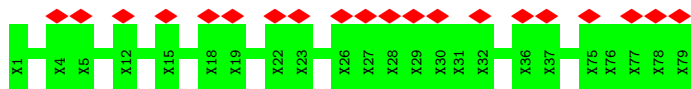
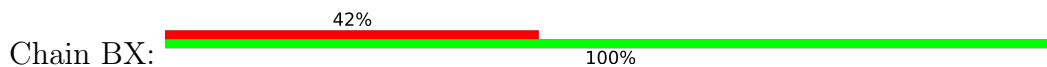




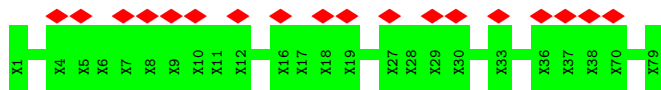
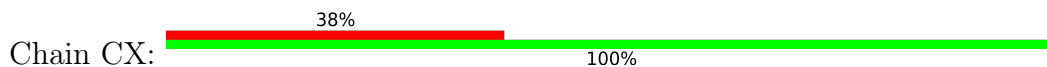
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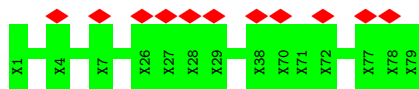
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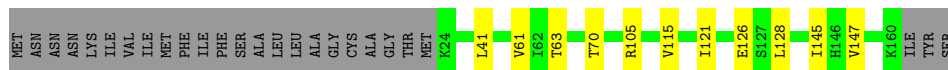
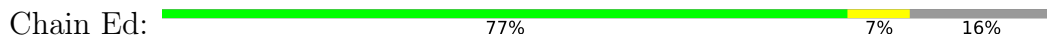
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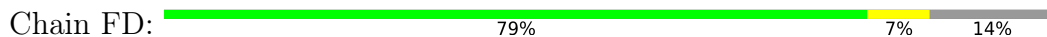
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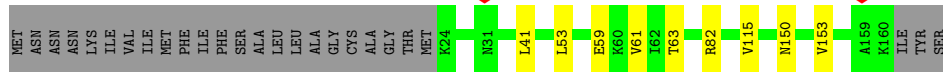
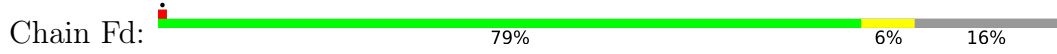
• Molecule 9: DotD



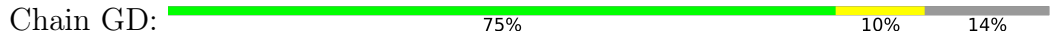
• Molecule 9: DotD



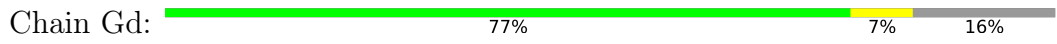
• Molecule 9: DotD



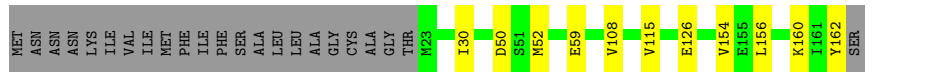
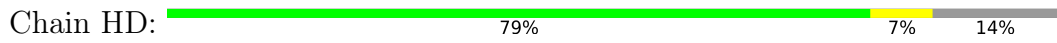
● Molecule 9: DotD



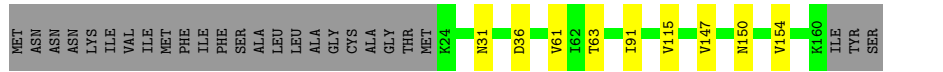
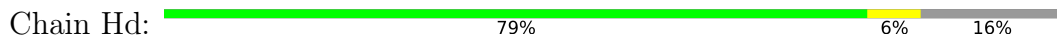
● Molecule 9: DotD



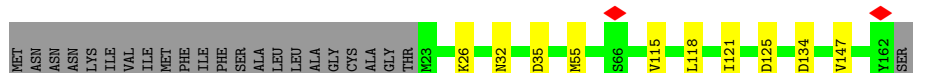
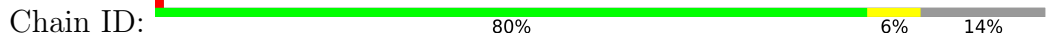
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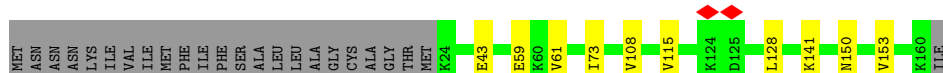
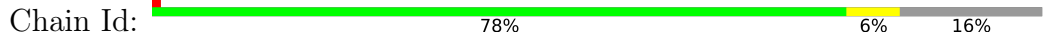
● Molecule 9: DotD



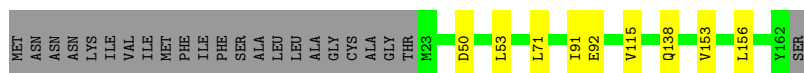
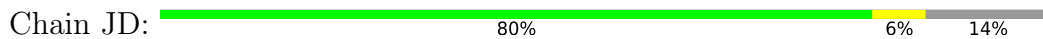
● Molecule 9: DotD



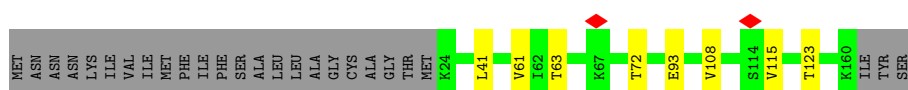
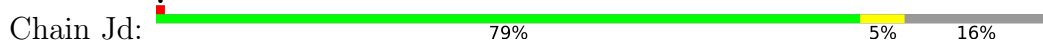
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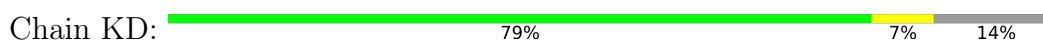
● Molecule 9: DotD



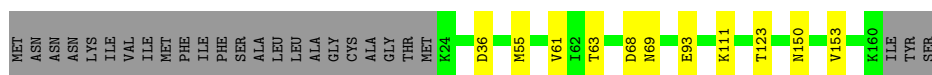
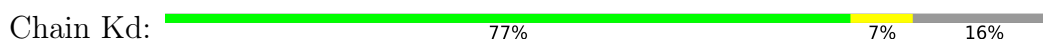
● Molecule 9: DotD



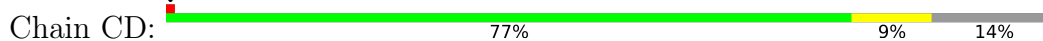
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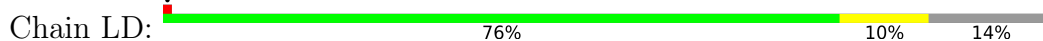
● Molecule 9: DotD



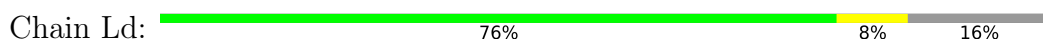
● Molecule 9: DotD



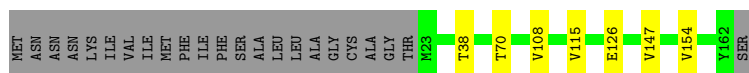
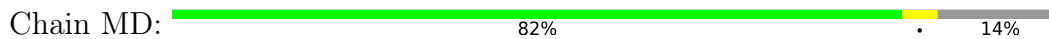
● Molecule 9: DotD



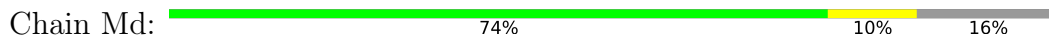
● Molecule 9: DotD



● Molecule 9: DotD

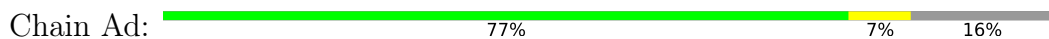


● Molecule 9: DotD

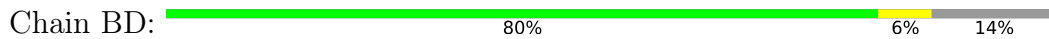


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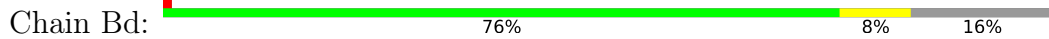
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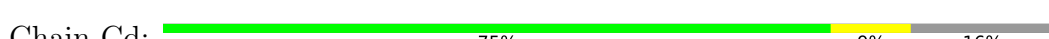
● Molecule 9: DotD



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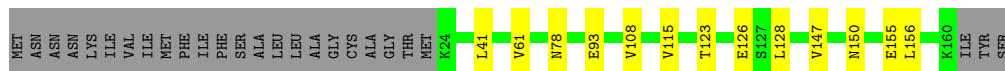
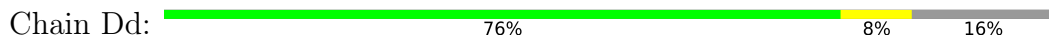
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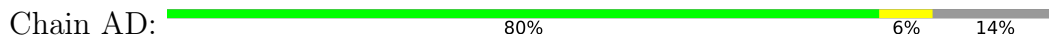
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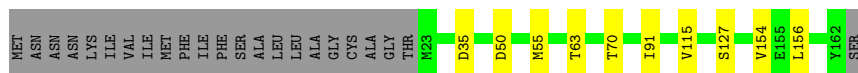
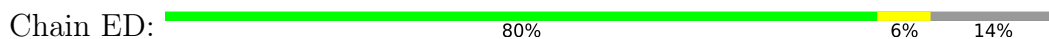
● Molecule 9: DotD



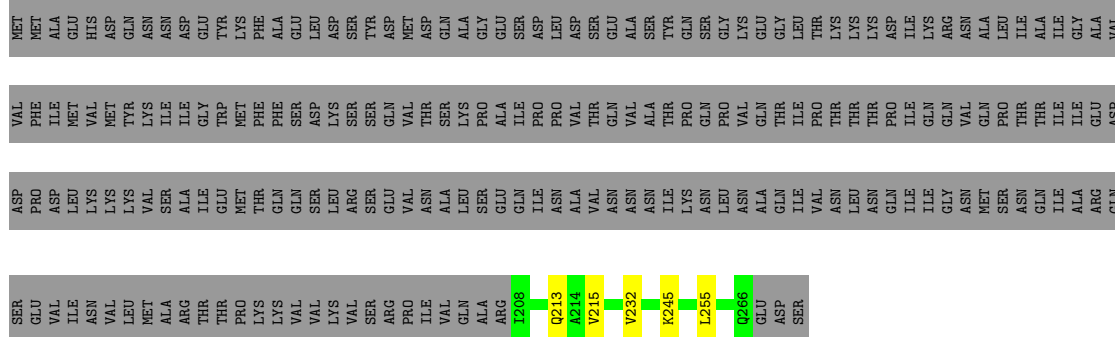
● Molecule 9: DotD



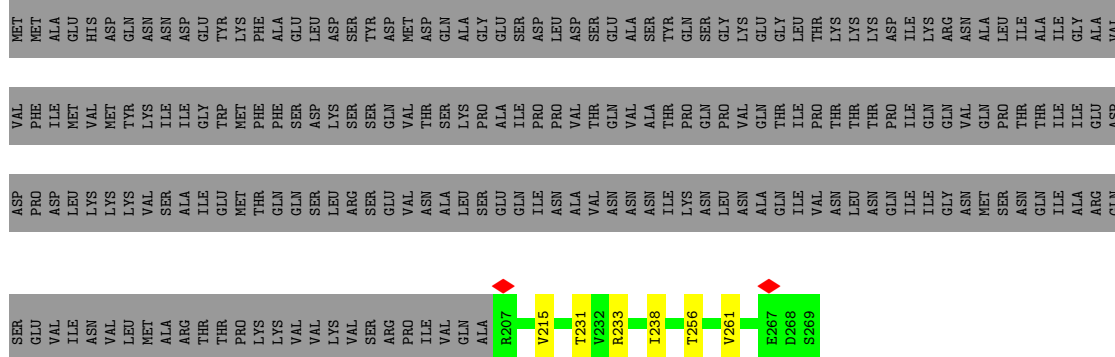
● Molecule 9: DotD



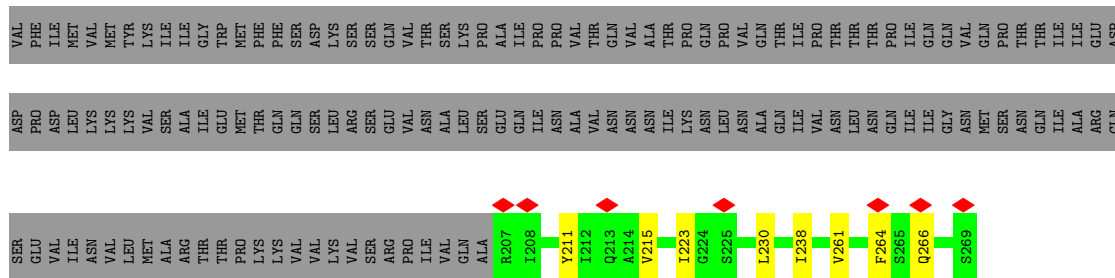
● Molecule 10: DotF



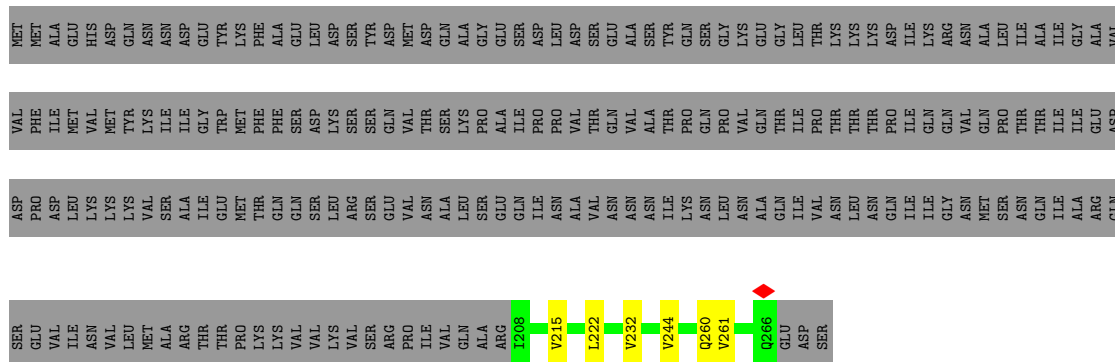
● Molecule 10: DotF



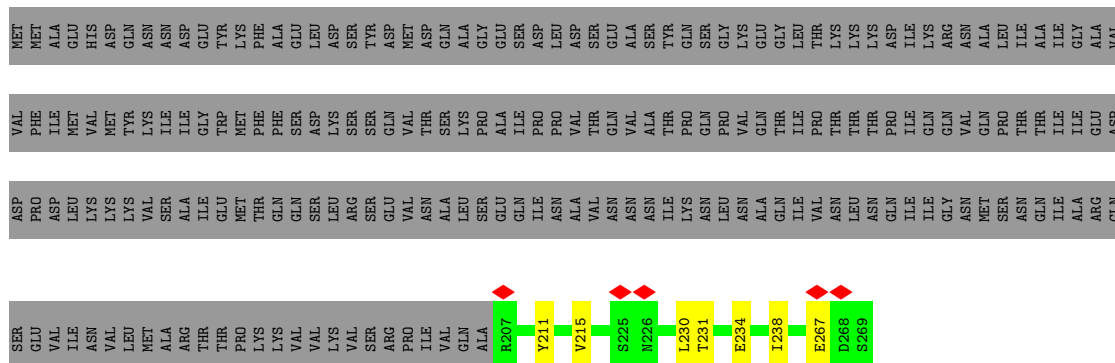
● Molecule 10: DotF



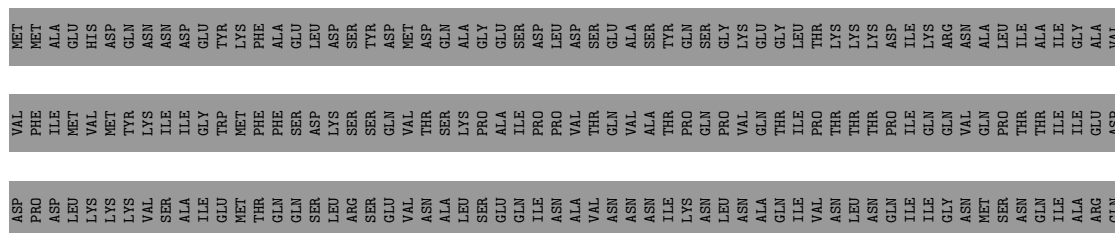
● Molecule 10: DotF



● Molecule 10: DotF



● Molecule 10: DotF



Chain VF:  22% . 77%

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

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	TRP	MET	LYS	THR	PRO	PHE	LYS	THR	VAL	VAL	VAL	SER	SER	ARG	GLU	ASP	PRO	THR	ILE	ASN	GLN	ALA	LEU	SER	ALA	
R207	V215	L230	T231	K245	D248	T256	V261	E267	D268	S269																										

• Molecule 10: DotF

Chain WF:  21% . 77%

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

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	TRP	MET	LYS	THR	PRO	PHE	LYS	THR	VAL	VAL	VAL	SER	SER	ARG	GLU	ASP	PRO	THR	ILE	ASN	GLN	ALA	LEU	SER	ALA	
R207	V215	T231	T238	K245	D251	T256	V261	F264	S269																											

• Molecule 10: DotF

Chain XF:  21% . 77%

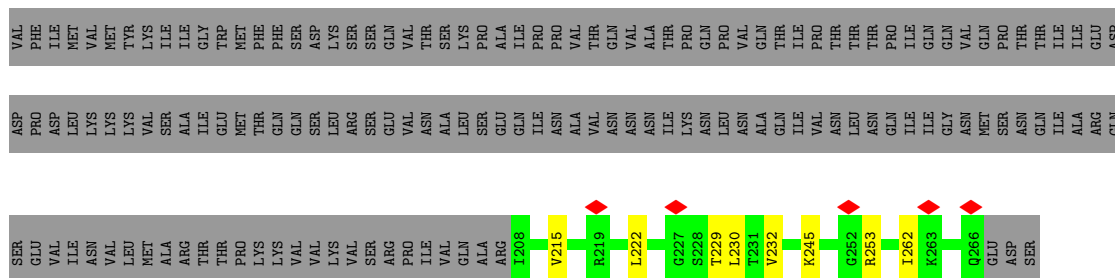
MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	ASP	TYR	TRP	GLY	ASP	GLU	GLU	LEU	ASP	SER	TYR	ASP	GLN	ASP	MET	THR	ASN	LEU	GLN	ALA	GLY	GLU	VAL							
VAL	PHE	ILE	MET	VAL	MET	TYR	LYS	ILE	TRP	PHE	PHE	ALA	GLN	SER	ASP	SER	SER	GLN	VAL	VAL	THR	THR	SER	PRO	LEU	SER	PRO	ALA	ALA	GLU	SER	PRO	ALA	ILE	SER	GLN	
ASP	PRO	ASP	LEU	LYS	LYS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

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	TRP	MET	LYS	THR	PRO	PHE	LYS	THR	VAL	VAL	VAL	SER	SER	ARG	GLU	ASP	PRO	THR	ILE	ASN	GLN	ALA	LEU	SER	ALA	
R207	L208	V215	S225	L230	T231	V232	R233	L246	L247	D248	S249	T256	V261	E267	D268	S269																				

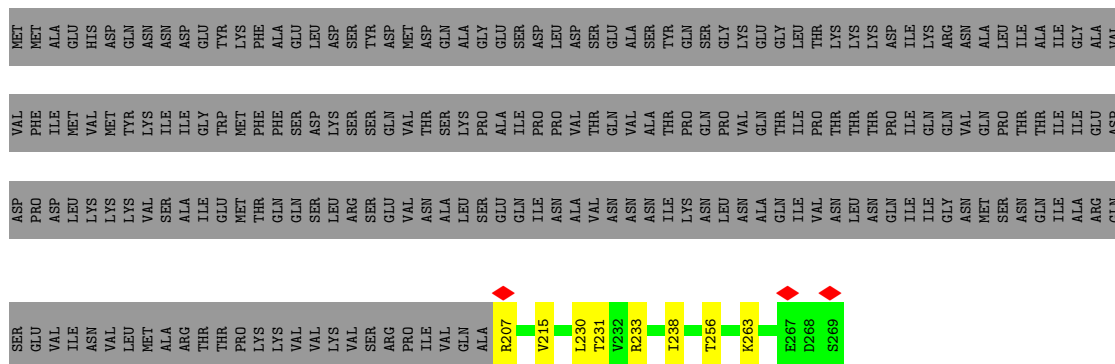
• Molecule 10: DotF

Chain YF:  21% . 77%

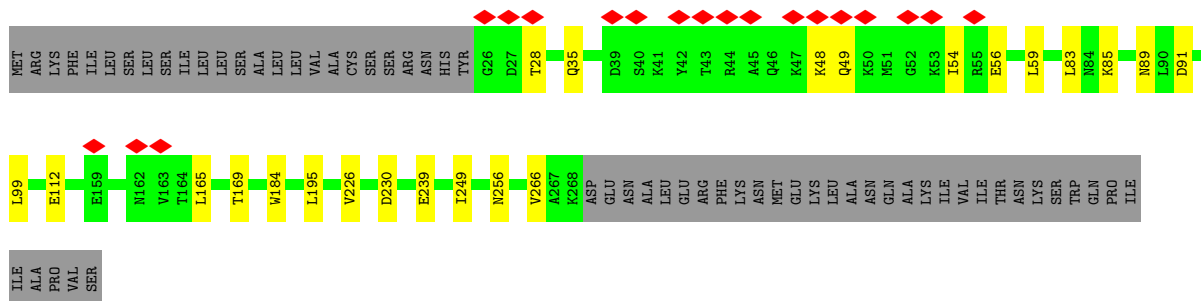
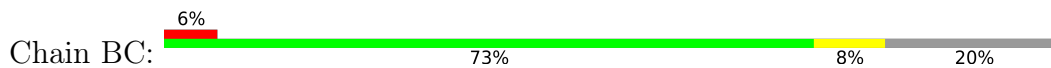
MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	ASP	TYR	TRP	GLY	ASP	GLU	GLU	LEU	ASP	SER	TYR	ASP	GLN	ASP	MET	THR	ASN	LEU	GLN	ALA	GLY	GLU	VAL							
VAL	PHE	ILE	MET	VAL	MET	TYR	LYS	ILE	TRP	PHE	PHE	ALA	GLN	SER	ASP	SER	SER	GLN	VAL	VAL	THR	THR	SER	PRO	LEU	SER	PRO	ALA	ALA	GLU	SER	PRO	ALA	ILE	SER	GLN	
ASP	PRO	ASP	LEU	LYS	LYS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



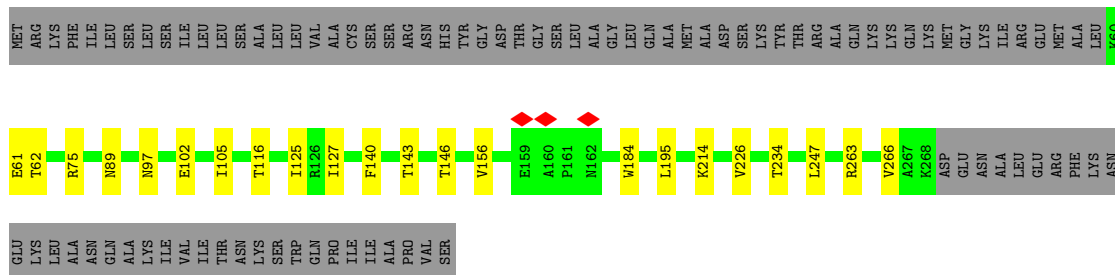
• Molecule 10: DotF



• Molecule 11: DotC

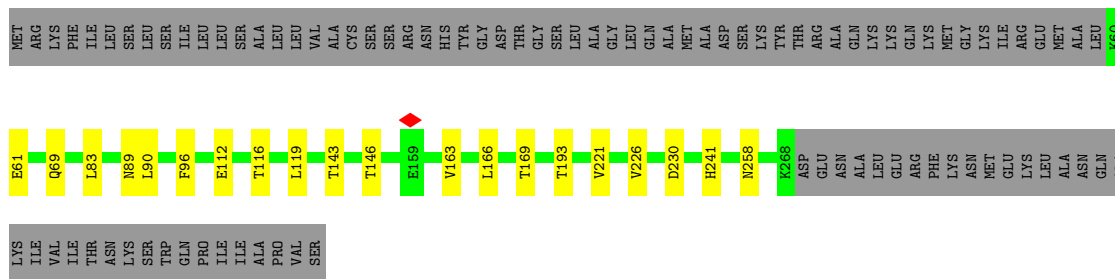


• Molecule 11: DotC



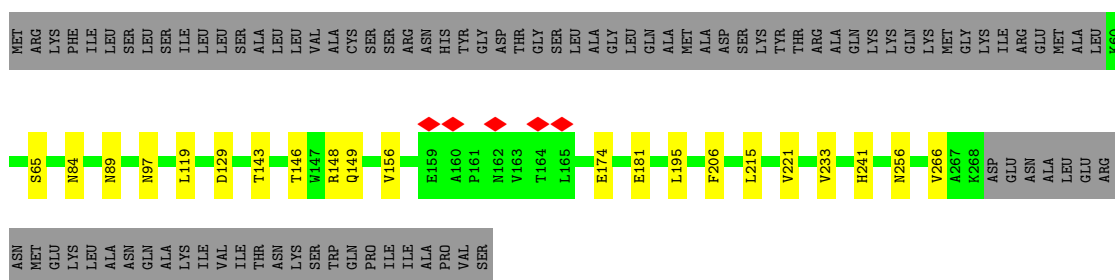
• Molecule 11: DotC

Chain DC: 62% 7% 31%



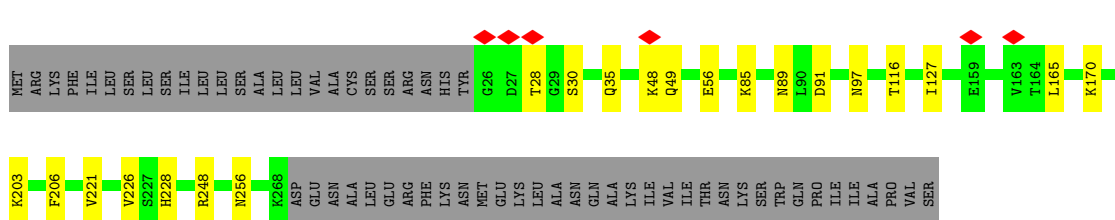
● Molecule 11: DotC

Chain EC: 62% 7% 31%



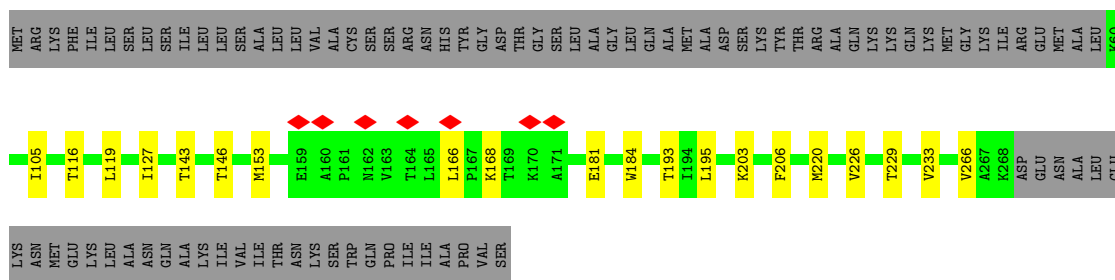
● Molecule 11: DotC

Chain FC: 73% 7% 20%



● Molecule 11: DotC

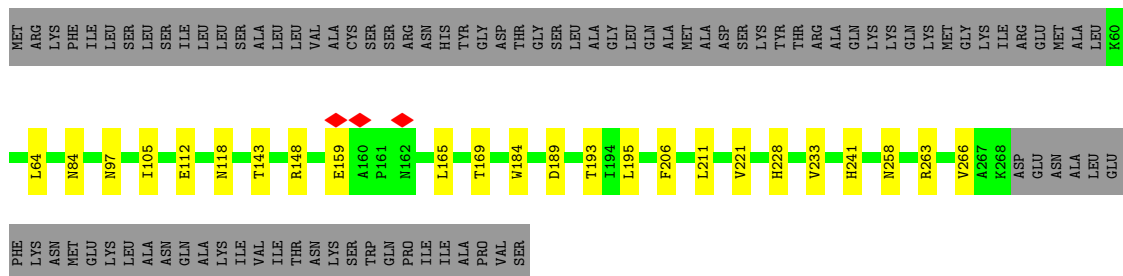
Chain GC: 62% 7% 31%



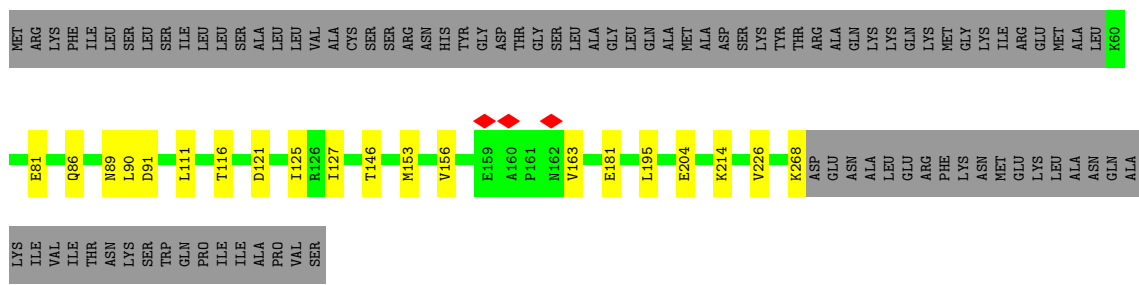
● Molecule 11: DotC

Chain HC: 61% 8% 31%

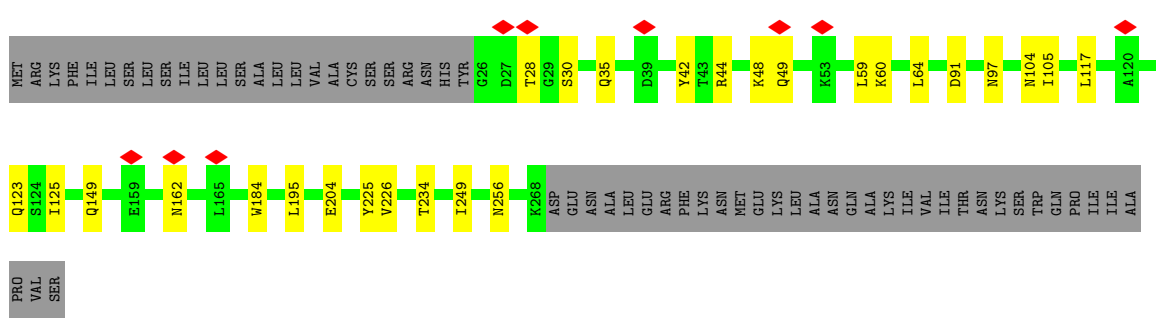
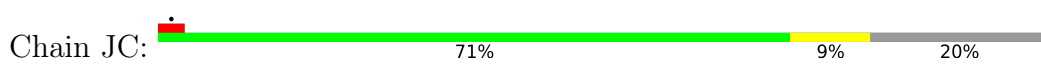




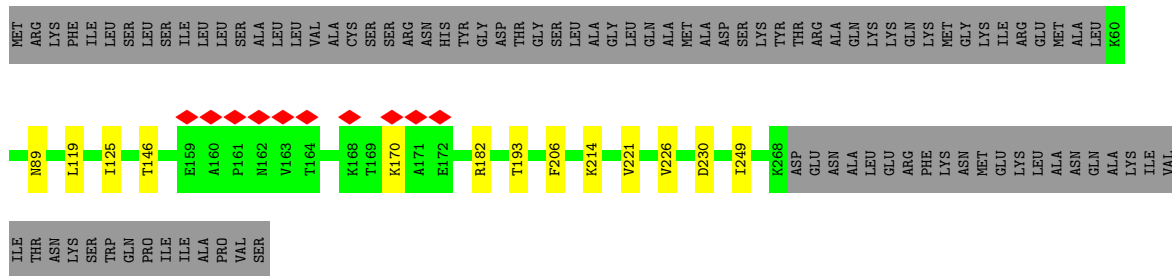
• Molecule 11: DotC



• Molecule 11: DotC

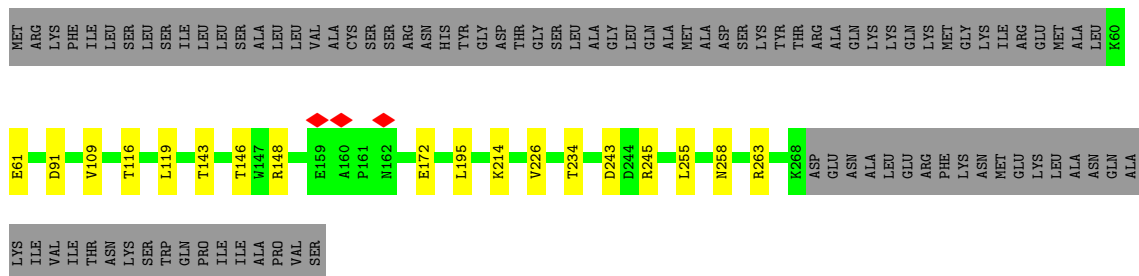


• Molecule 11: DotC

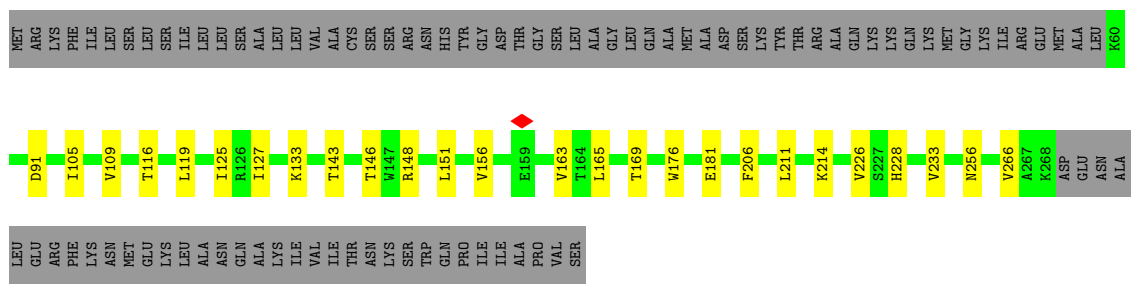


• Molecule 11: DotC

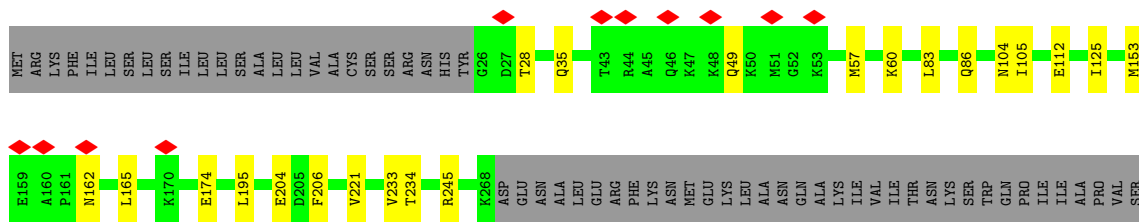




• Molecule 11: DotC



• 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 (\AA)	561.0, 561.0, 561.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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	0.30	0/1250	0.54	0/1699
1	Ag	0.25	0/278	0.45	0/377
1	BG	0.29	0/1250	0.55	0/1699
1	Bg	0.28	0/278	0.46	0/377
1	CG	0.29	0/1250	0.55	0/1699
1	Cg	0.26	0/278	0.44	0/377
1	DG	0.29	0/1250	0.56	0/1699
1	Dg	0.28	0/278	0.50	0/377
1	EG	0.30	0/1250	0.54	0/1699
1	Eg	0.25	0/278	0.47	0/377
1	FG	0.29	0/1250	0.55	0/1699
1	Fg	0.26	0/278	0.46	0/377
1	GG	0.30	0/1250	0.55	0/1699
1	Gg	0.26	0/278	0.49	0/377
1	HG	0.29	0/1250	0.55	0/1699
1	Hg	0.26	0/278	0.46	0/377
1	IG	0.29	0/1250	0.56	0/1699
1	Ig	0.25	0/278	0.44	0/377
1	JG	0.29	0/1250	0.54	0/1699
1	Jg	0.26	0/278	0.46	0/377
1	KG	0.30	0/1250	0.56	0/1699
1	Kg	0.26	0/278	0.46	0/377
1	LG	0.29	0/1250	0.56	0/1699
1	Lg	0.25	0/278	0.45	0/377
1	MG	0.28	0/1250	0.55	0/1699
1	Mg	0.26	0/278	0.47	0/377
1	NG	0.28	0/1250	0.57	1/1699 (0.1%)
1	OG	0.29	0/1250	0.56	1/1699 (0.1%)
1	PG	0.29	0/1250	0.55	0/1699
1	VG	0.26	0/278	0.53	0/377
1	WG	0.27	0/278	0.46	0/377
1	XG	0.26	0/278	0.55	0/377
1	YG	0.28	0/278	0.50	0/377
1	ZG	0.28	0/278	0.53	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AH	0.29	0/2033	0.53	0/2775
2	BH	0.29	0/2033	0.53	0/2775
2	CH	0.29	0/2033	0.52	0/2775
2	DH	0.29	0/2033	0.52	0/2775
2	EH	0.28	0/2033	0.52	0/2775
2	FH	0.28	0/2033	0.51	0/2775
2	GH	0.29	0/2033	0.53	0/2775
2	HH	0.29	0/2033	0.51	0/2775
2	IH	0.28	0/2033	0.52	0/2775
2	JH	0.28	0/2033	0.51	0/2775
2	KH	0.29	0/2033	0.53	0/2775
2	LH	0.30	0/2033	0.55	0/2775
2	MH	0.28	0/2033	0.51	0/2775
2	VH	0.27	0/1921	0.53	0/2620
2	WH	0.28	0/1921	0.52	0/2620
2	XH	0.28	0/1921	0.53	0/2620
2	YH	0.27	0/1921	0.52	0/2620
2	ZH	0.27	0/1921	0.54	0/2620
3	AK	0.29	0/1195	0.54	0/1616
3	BK	0.29	0/1195	0.55	0/1616
3	CK	0.31	0/1195	0.53	0/1616
3	DK	0.29	0/1195	0.53	0/1616
3	EK	0.29	0/1195	0.53	0/1616
3	FK	0.30	0/1195	0.53	0/1616
3	GK	0.30	0/1195	0.54	0/1616
3	HK	0.29	0/1195	0.52	0/1616
3	IK	0.30	0/1195	0.55	0/1616
3	JK	0.30	0/1195	0.54	0/1616
3	KK	0.30	0/1195	0.53	0/1616
3	LK	0.30	0/1195	0.54	0/1616
3	MK	0.29	0/1195	0.52	0/1616
4	AL	0.30	0/1417	0.54	0/1912
4	BL	0.30	0/1417	0.54	0/1912
4	CL	0.30	0/1417	0.53	0/1912
4	DL	0.30	0/1417	0.55	0/1912
4	EL	0.29	0/1417	0.55	0/1912
4	FL	0.29	0/1417	0.54	0/1912
4	GL	0.30	0/1417	0.55	0/1912
4	HL	0.29	0/1417	0.55	0/1912
4	IL	0.29	0/1417	0.55	0/1912
4	JL	0.29	0/1417	0.54	0/1912
4	KL	0.29	0/1417	0.54	0/1912
4	LL	0.30	0/1417	0.54	0/1912

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ML	0.30	0/1417	0.54	0/1912
5	AM	0.28	0/1678	0.57	0/2262
5	BM	0.28	0/1678	0.56	0/2262
5	CM	0.29	0/1678	0.58	0/2262
5	DM	0.29	0/1678	0.56	0/2262
5	EM	0.29	0/1678	0.56	0/2262
5	FM	0.29	0/1678	0.57	0/2262
5	GM	0.28	0/1678	0.55	0/2262
5	HM	0.28	0/1678	0.57	0/2262
5	IM	0.29	0/1678	0.60	0/2262
5	JM	0.28	0/1678	0.59	0/2262
5	KM	0.29	0/1678	0.58	0/2262
5	LM	0.28	0/1678	0.57	0/2262
5	MM	0.28	0/1678	0.57	0/2262
6	AN	0.32	0/593	0.51	0/799
6	BN	0.31	0/593	0.52	0/799
6	CN	0.30	0/593	0.50	0/799
6	DN	0.30	0/593	0.51	0/799
6	EN	0.31	0/593	0.53	0/799
6	FN	0.31	0/593	0.51	0/799
6	GN	0.30	0/593	0.52	0/799
6	HN	0.30	0/593	0.50	0/799
6	IN	0.31	0/593	0.53	0/799
6	JN	0.30	0/593	0.53	0/799
6	KN	0.32	0/593	0.53	0/799
6	LN	0.32	0/593	0.52	0/799
6	MN	0.30	0/593	0.54	0/799
9	AD	0.32	0/1107	0.53	0/1502
9	Ad	0.28	0/1078	0.49	0/1463
9	BD	0.28	0/1107	0.51	0/1502
9	Bd	0.28	0/1078	0.50	0/1463
9	CD	0.29	0/1107	0.52	0/1502
9	Cd	0.28	0/1078	0.48	0/1463
9	DD	0.30	0/1107	0.52	0/1502
9	Dd	0.28	0/1078	0.51	0/1463
9	ED	0.29	0/1107	0.52	0/1502
9	Ed	0.28	0/1078	0.49	0/1463
9	FD	0.30	0/1107	0.53	0/1502
9	Fd	0.28	0/1078	0.51	0/1463
9	GD	0.29	0/1107	0.54	0/1502
9	Gd	0.28	0/1078	0.50	0/1463
9	HD	0.29	0/1107	0.54	0/1502
9	Hd	0.27	0/1078	0.50	0/1463

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	ID	0.29	0/1107	0.54	0/1502
9	Id	0.29	0/1078	0.48	0/1463
9	JD	0.30	0/1107	0.50	0/1502
9	Jd	0.29	0/1078	0.49	0/1463
9	KD	0.30	0/1107	0.52	0/1502
9	Kd	0.28	0/1078	0.48	0/1463
9	LD	0.29	0/1107	0.51	0/1502
9	Ld	0.28	0/1078	0.50	0/1463
9	MD	0.30	0/1107	0.53	0/1502
9	Md	0.29	0/1078	0.49	0/1463
10	AF	0.26	0/490	0.55	0/660
10	Af	0.28	0/456	0.57	0/615
10	BF	0.27	0/490	0.53	0/660
10	Bf	0.27	0/456	0.51	0/615
10	CF	0.27	0/490	0.53	0/660
10	Cf	0.27	0/456	0.52	0/615
10	DF	0.27	0/490	0.57	0/660
10	Df	0.27	0/456	0.53	0/615
10	EF	0.26	0/490	0.53	0/660
10	Ef	0.27	0/456	0.51	0/615
10	FF	0.27	0/490	0.55	0/660
10	Ff	0.27	0/456	0.53	0/615
10	GF	0.26	0/490	0.53	0/660
10	Gf	0.26	0/456	0.54	0/615
10	HF	0.27	0/490	0.56	0/660
10	Hf	0.28	0/456	0.54	0/615
10	IF	0.27	0/490	0.55	0/660
10	If	0.27	0/456	0.53	0/615
10	JF	0.26	0/490	0.54	0/660
10	Jf	0.26	0/456	0.52	0/615
10	KF	0.26	0/490	0.55	0/660
10	Kf	0.27	0/456	0.51	0/615
10	LF	0.26	0/490	0.54	0/660
10	Lf	0.28	0/456	0.52	0/615
10	MF	0.27	0/490	0.53	0/660
10	Mf	0.27	0/456	0.53	0/615
10	VF	0.26	0/490	0.53	0/660
10	WF	0.26	0/490	0.55	0/660
10	XF	0.26	0/490	0.53	0/660
10	YF	0.27	0/490	0.53	0/660
10	ZF	0.27	0/490	0.55	0/660
11	AC	0.29	0/1957	0.51	0/2651
11	BC	0.28	0/1957	0.51	0/2651

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CC	0.29	0/1702	0.52	0/2315
11	DC	0.30	0/1702	0.51	0/2315
11	EC	0.30	0/1702	0.52	0/2315
11	FC	0.29	0/1957	0.51	0/2651
11	GC	0.29	0/1702	0.52	0/2315
11	HC	0.29	0/1702	0.51	0/2315
11	IC	0.30	0/1702	0.50	0/2315
11	JC	0.28	0/1957	0.51	0/2651
11	KC	0.29	0/1702	0.51	0/2315
11	LC	0.29	0/1702	0.52	0/2315
11	MC	0.29	0/1702	0.51	0/2315
All	All	0.29	0/190816	0.53	2/258661 (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.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	NG	965	LEU	CA-CB-CG	5.15	127.15	115.30
1	OG	965	LEU	CA-CB-CG	5.01	126.81	115.30

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 [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AG	161/1048 (15%)	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	135/765 (18%)	113 (84%)	22 (16%)	2	14
1	Ag	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	BG	135/765 (18%)	120 (89%)	15 (11%)	6	25
1	Bg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	CG	135/765 (18%)	120 (89%)	15 (11%)	6	25
1	Cg	31/765 (4%)	26 (84%)	5 (16%)	2	15
1	DG	135/765 (18%)	116 (86%)	19 (14%)	3	18
1	Dg	31/765 (4%)	27 (87%)	4 (13%)	4	20
1	EG	135/765 (18%)	121 (90%)	14 (10%)	7	27
1	Eg	31/765 (4%)	29 (94%)	2 (6%)	17	44
1	FG	135/765 (18%)	118 (87%)	17 (13%)	4	21
1	Fg	31/765 (4%)	30 (97%)	1 (3%)	39	62
1	GG	135/765 (18%)	120 (89%)	15 (11%)	6	25
1	Gg	31/765 (4%)	28 (90%)	3 (10%)	8	29
1	HG	135/765 (18%)	115 (85%)	20 (15%)	3	17
1	Hg	31/765 (4%)	25 (81%)	6 (19%)	1	9
1	IG	135/765 (18%)	121 (90%)	14 (10%)	7	27
1	Ig	31/765 (4%)	26 (84%)	5 (16%)	2	15
1	JG	135/765 (18%)	122 (90%)	13 (10%)	8	29
1	Jg	31/765 (4%)	25 (81%)	6 (19%)	1	9
1	KG	135/765 (18%)	123 (91%)	12 (9%)	9	33
1	Kg	31/765 (4%)	25 (81%)	6 (19%)	1	9
1	LG	135/765 (18%)	115 (85%)	20 (15%)	3	17
1	Lg	31/765 (4%)	27 (87%)	4 (13%)	4	20
1	MG	135/765 (18%)	114 (84%)	21 (16%)	2	16
1	Mg	31/765 (4%)	25 (81%)	6 (19%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	NG	135/765 (18%)	114 (84%)	21 (16%)	2	16
1	OG	135/765 (18%)	112 (83%)	23 (17%)	2	13
1	PG	135/765 (18%)	114 (84%)	21 (16%)	2	16
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%)	24 (77%)	7 (23%)	1	6
1	YG	31/765 (4%)	28 (90%)	3 (10%)	8	29
1	ZG	31/765 (4%)	30 (97%)	1 (3%)	39	62
2	AH	220/300 (73%)	192 (87%)	28 (13%)	4	21
2	BH	220/300 (73%)	194 (88%)	26 (12%)	5	23
2	CH	220/300 (73%)	198 (90%)	22 (10%)	7	28
2	DH	220/300 (73%)	196 (89%)	24 (11%)	6	25
2	EH	220/300 (73%)	190 (86%)	30 (14%)	3	19
2	FH	220/300 (73%)	193 (88%)	27 (12%)	4	22
2	GH	220/300 (73%)	199 (90%)	21 (10%)	8	29
2	HH	220/300 (73%)	203 (92%)	17 (8%)	13	39
2	IH	220/300 (73%)	198 (90%)	22 (10%)	7	28
2	JH	220/300 (73%)	192 (87%)	28 (13%)	4	21
2	KH	220/300 (73%)	200 (91%)	20 (9%)	9	31
2	LH	220/300 (73%)	196 (89%)	24 (11%)	6	25
2	MH	220/300 (73%)	193 (88%)	27 (12%)	4	22
2	VH	207/300 (69%)	182 (88%)	25 (12%)	5	22
2	WH	207/300 (69%)	182 (88%)	25 (12%)	5	22
2	XH	207/300 (69%)	183 (88%)	24 (12%)	5	23
2	YH	207/300 (69%)	181 (87%)	26 (13%)	4	21
2	ZH	207/300 (69%)	179 (86%)	28 (14%)	4	19
3	AK	129/163 (79%)	114 (88%)	15 (12%)	5	23
3	BK	129/163 (79%)	112 (87%)	17 (13%)	4	20
3	CK	129/163 (79%)	114 (88%)	15 (12%)	5	23
3	DK	129/163 (79%)	121 (94%)	8 (6%)	18	45
3	EK	129/163 (79%)	118 (92%)	11 (8%)	10	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	FK	129/163 (79%)	117 (91%)	12 (9%)	9	30
3	GK	129/163 (79%)	117 (91%)	12 (9%)	9	30
3	HK	129/163 (79%)	117 (91%)	12 (9%)	9	30
3	IK	129/163 (79%)	117 (91%)	12 (9%)	9	30
3	JK	129/163 (79%)	116 (90%)	13 (10%)	7	27
3	KK	129/163 (79%)	111 (86%)	18 (14%)	3	19
3	LK	129/163 (79%)	117 (91%)	12 (9%)	9	30
3	MK	129/163 (79%)	110 (85%)	19 (15%)	3	17
4	AL	148/203 (73%)	137 (93%)	11 (7%)	13	40
4	BL	148/203 (73%)	129 (87%)	19 (13%)	4	21
4	CL	148/203 (73%)	137 (93%)	11 (7%)	13	40
4	DL	148/203 (73%)	134 (90%)	14 (10%)	8	29
4	EL	148/203 (73%)	132 (89%)	16 (11%)	6	26
4	FL	148/203 (73%)	132 (89%)	16 (11%)	6	26
4	GL	148/203 (73%)	130 (88%)	18 (12%)	5	22
4	HL	148/203 (73%)	136 (92%)	12 (8%)	11	37
4	IL	148/203 (73%)	137 (93%)	11 (7%)	13	40
4	JL	148/203 (73%)	137 (93%)	11 (7%)	13	40
4	KL	148/203 (73%)	132 (89%)	16 (11%)	6	26
4	LL	148/203 (73%)	140 (95%)	8 (5%)	22	49
4	ML	148/203 (73%)	138 (93%)	10 (7%)	16	42
5	AM	175/276 (63%)	144 (82%)	31 (18%)	2	12
5	BM	175/276 (63%)	155 (89%)	20 (11%)	5	24
5	CM	175/276 (63%)	150 (86%)	25 (14%)	3	18
5	DM	175/276 (63%)	156 (89%)	19 (11%)	6	25
5	EM	175/276 (63%)	152 (87%)	23 (13%)	4	20
5	FM	175/276 (63%)	150 (86%)	25 (14%)	3	18
5	GM	175/276 (63%)	144 (82%)	31 (18%)	2	12
5	HM	175/276 (63%)	152 (87%)	23 (13%)	4	20
5	IM	175/276 (63%)	158 (90%)	17 (10%)	8	29
5	JM	175/276 (63%)	150 (86%)	25 (14%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	KM	175/276 (63%)	153 (87%)	22 (13%)	4	21
5	LM	175/276 (63%)	155 (89%)	20 (11%)	5	24
5	MM	175/276 (63%)	155 (89%)	20 (11%)	5	24
6	AN	66/107 (62%)	55 (83%)	11 (17%)	2	14
6	BN	66/107 (62%)	53 (80%)	13 (20%)	1	9
6	CN	66/107 (62%)	54 (82%)	12 (18%)	1	11
6	DN	66/107 (62%)	56 (85%)	10 (15%)	3	16
6	EN	66/107 (62%)	58 (88%)	8 (12%)	5	22
6	FN	66/107 (62%)	61 (92%)	5 (8%)	13	39
6	GN	66/107 (62%)	55 (83%)	11 (17%)	2	14
6	HN	66/107 (62%)	57 (86%)	9 (14%)	3	19
6	IN	66/107 (62%)	56 (85%)	10 (15%)	3	16
6	JN	66/107 (62%)	55 (83%)	11 (17%)	2	14
6	KN	66/107 (62%)	55 (83%)	11 (17%)	2	14
6	LN	66/107 (62%)	59 (89%)	7 (11%)	6	26
6	MN	66/107 (62%)	54 (82%)	12 (18%)	1	11
9	AD	121/139 (87%)	112 (93%)	9 (7%)	13	40
9	Ad	118/139 (85%)	106 (90%)	12 (10%)	7	27
9	BD	121/139 (87%)	111 (92%)	10 (8%)	11	36
9	Bd	118/139 (85%)	105 (89%)	13 (11%)	6	25
9	CD	121/139 (87%)	106 (88%)	15 (12%)	4	21
9	Cd	118/139 (85%)	103 (87%)	15 (13%)	4	21
9	DD	121/139 (87%)	110 (91%)	11 (9%)	9	31
9	Dd	118/139 (85%)	105 (89%)	13 (11%)	6	25
9	ED	121/139 (87%)	111 (92%)	10 (8%)	11	36
9	Ed	118/139 (85%)	107 (91%)	11 (9%)	9	30
9	FD	121/139 (87%)	110 (91%)	11 (9%)	9	31
9	Fd	118/139 (85%)	109 (92%)	9 (8%)	13	39
9	GD	121/139 (87%)	104 (86%)	17 (14%)	3	19
9	Gd	118/139 (85%)	106 (90%)	12 (10%)	7	27
9	HD	121/139 (87%)	110 (91%)	11 (9%)	9	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Hd	118/139 (85%)	109 (92%)	9 (8%)	13	39
9	ID	121/139 (87%)	111 (92%)	10 (8%)	11	36
9	Id	118/139 (85%)	108 (92%)	10 (8%)	10	36
9	JD	121/139 (87%)	112 (93%)	9 (7%)	13	40
9	Jd	118/139 (85%)	110 (93%)	8 (7%)	16	42
9	KD	121/139 (87%)	110 (91%)	11 (9%)	9	31
9	Kd	118/139 (85%)	107 (91%)	11 (9%)	9	30
9	LD	121/139 (87%)	105 (87%)	16 (13%)	4	20
9	Ld	118/139 (85%)	105 (89%)	13 (11%)	6	25
9	MD	121/139 (87%)	114 (94%)	7 (6%)	20	47
9	Md	118/139 (85%)	102 (86%)	16 (14%)	3	19
10	AF	53/237 (22%)	46 (87%)	7 (13%)	4	20
10	Af	49/237 (21%)	44 (90%)	5 (10%)	7	27
10	BF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	Bf	49/237 (21%)	43 (88%)	6 (12%)	5	22
10	CF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	Cf	49/237 (21%)	42 (86%)	7 (14%)	3	18
10	DF	53/237 (22%)	46 (87%)	7 (13%)	4	20
10	Df	49/237 (21%)	41 (84%)	8 (16%)	2	14
10	EF	53/237 (22%)	45 (85%)	8 (15%)	3	16
10	Ef	49/237 (21%)	44 (90%)	5 (10%)	7	27
10	FF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	Ff	49/237 (21%)	42 (86%)	7 (14%)	3	18
10	GF	53/237 (22%)	48 (91%)	5 (9%)	8	30
10	Gf	49/237 (21%)	44 (90%)	5 (10%)	7	27
10	HF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	Hf	49/237 (21%)	46 (94%)	3 (6%)	18	46
10	IF	53/237 (22%)	48 (91%)	5 (9%)	8	30
10	If	49/237 (21%)	43 (88%)	6 (12%)	5	22
10	JF	53/237 (22%)	49 (92%)	4 (8%)	13	40
10	Jf	49/237 (21%)	44 (90%)	5 (10%)	7	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	KF	53/237 (22%)	45 (85%)	8 (15%)	3	16
10	Kf	49/237 (21%)	43 (88%)	6 (12%)	5	22
10	LF	53/237 (22%)	46 (87%)	7 (13%)	4	20
10	Lf	49/237 (21%)	47 (96%)	2 (4%)	30	56
10	MF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	Mf	49/237 (21%)	42 (86%)	7 (14%)	3	18
10	VF	53/237 (22%)	49 (92%)	4 (8%)	13	40
10	WF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	XF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	YF	53/237 (22%)	47 (89%)	6 (11%)	6	24
10	ZF	53/237 (22%)	50 (94%)	3 (6%)	20	47
11	AC	203/257 (79%)	181 (89%)	22 (11%)	6	26
11	BC	203/257 (79%)	180 (89%)	23 (11%)	6	24
11	CC	178/257 (69%)	156 (88%)	22 (12%)	4	21
11	DC	178/257 (69%)	158 (89%)	20 (11%)	6	24
11	EC	178/257 (69%)	157 (88%)	21 (12%)	5	23
11	FC	203/257 (79%)	181 (89%)	22 (11%)	6	26
11	GC	178/257 (69%)	158 (89%)	20 (11%)	6	24
11	HC	178/257 (69%)	154 (86%)	24 (14%)	4	19
11	IC	178/257 (69%)	158 (89%)	20 (11%)	6	24
11	JC	203/257 (79%)	176 (87%)	27 (13%)	4	20
11	KC	178/257 (69%)	165 (93%)	13 (7%)	14	40
11	LC	178/257 (69%)	160 (90%)	18 (10%)	7	27
11	MC	178/257 (69%)	152 (85%)	26 (15%)	3	17
All	All	20459/55449 (37%)	18110 (88%)	2349 (12%)	9	23

5 of 2349 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	KC	214	LYS
9	Dd	41	LEU
2	CH	180	VAL
11	KC	193	THR
5	DM	152	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
10	BF	251	GLN
5	CM	164	GLN
5	BM	249	GLN
1	GG	1020	GLN
5	DM	267	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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

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Mol	Chain	Number of breaks
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
1	ZX	38:UNK	C	70:UNK	N	26.34
1	BX	38:UNK	C	70:UNK	N	25.84

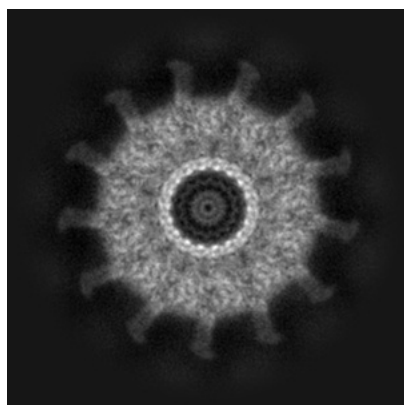
6 Map visualisation [i](#)

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.

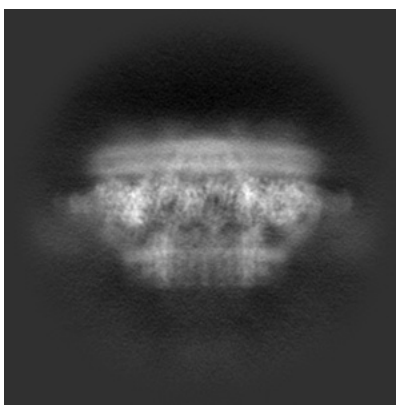
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

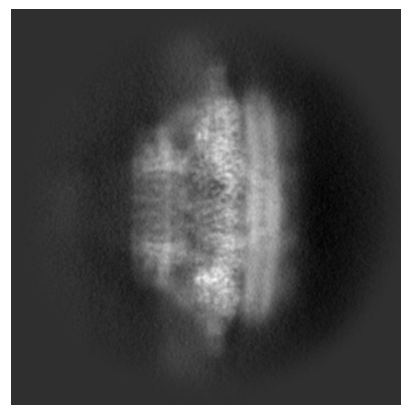
6.1.1 Primary map



X



Y

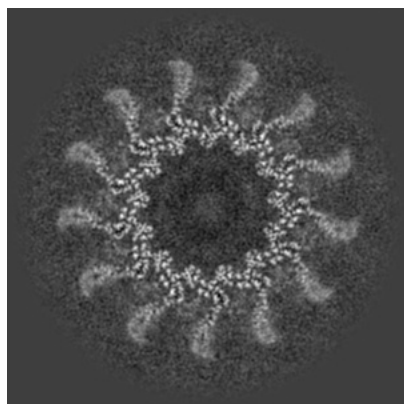


Z

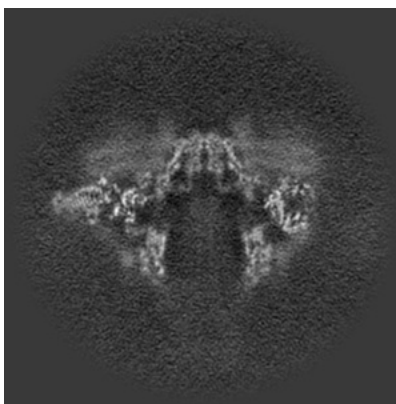
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

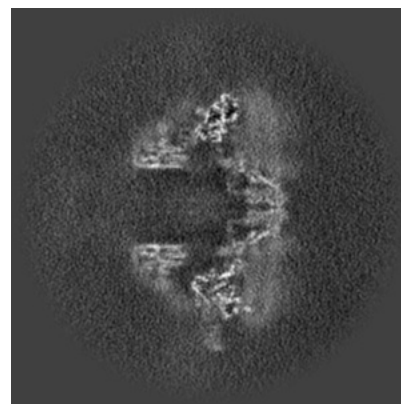
6.2.1 Primary map



X Index: 125



Y Index: 125

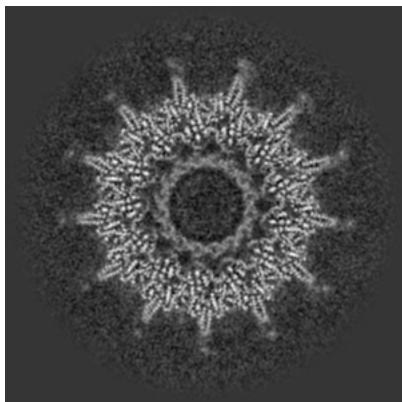


Z Index: 125

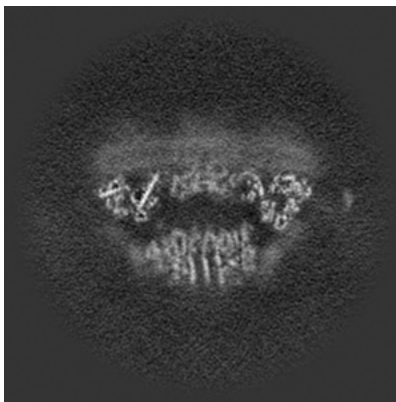
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

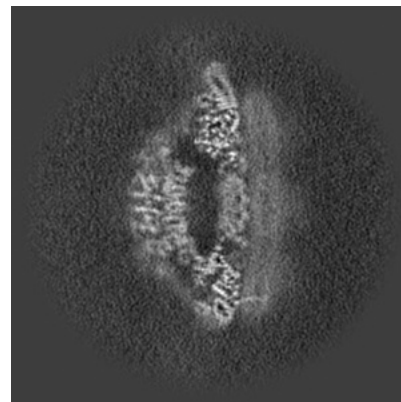
6.3.1 Primary map



X Index: 134



Y Index: 101

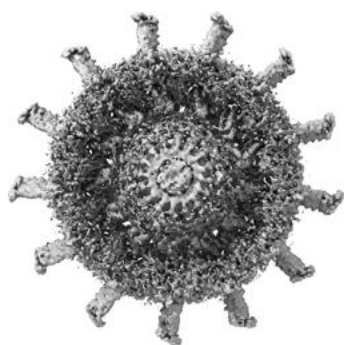


Z Index: 151

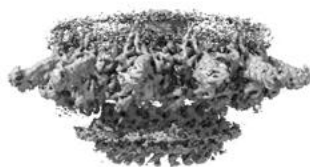
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

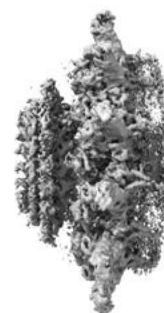
6.4.1 Primary map



X



Y



Z

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

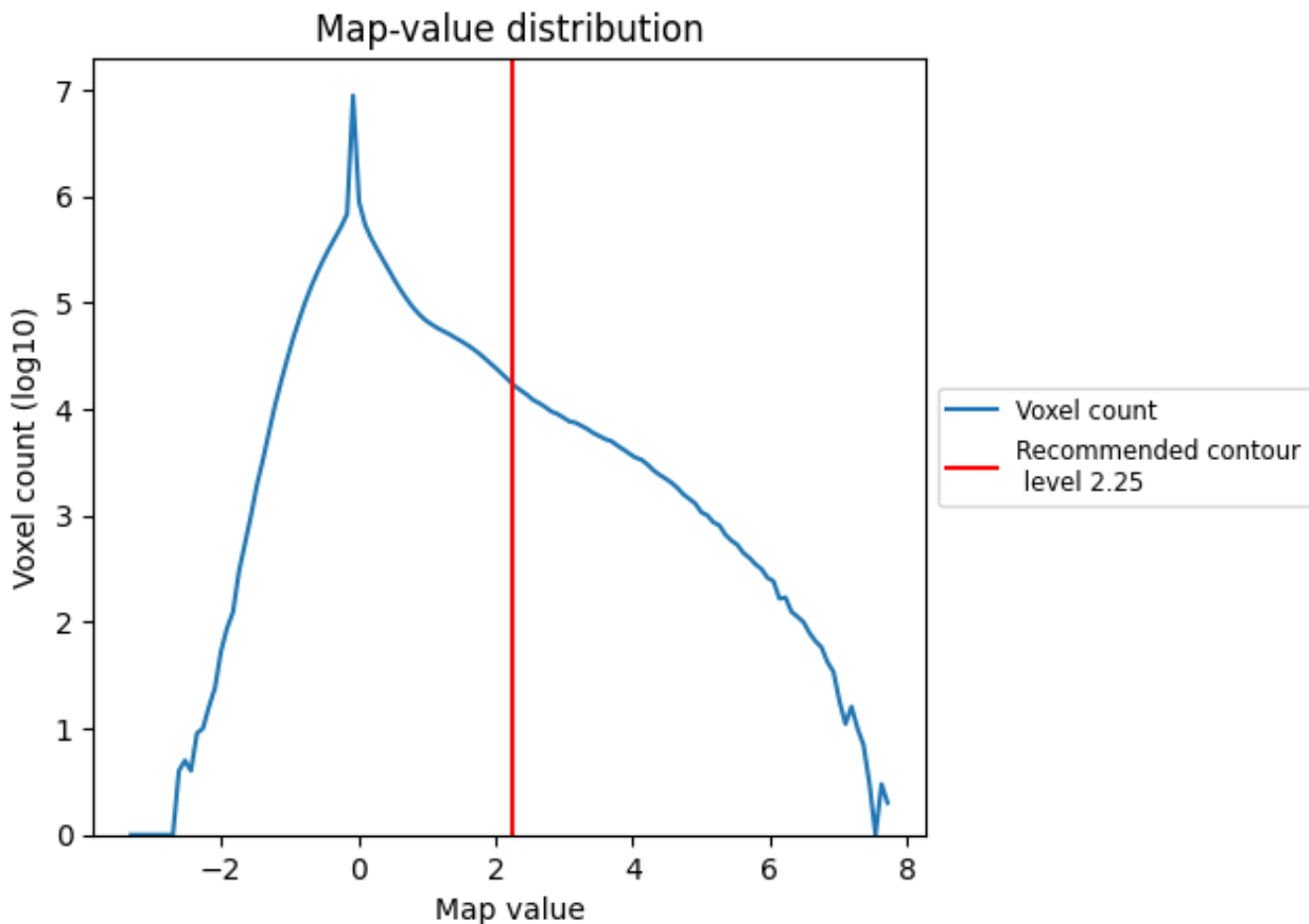
6.5 Mask visualisation

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

7 Map analysis [i](#)

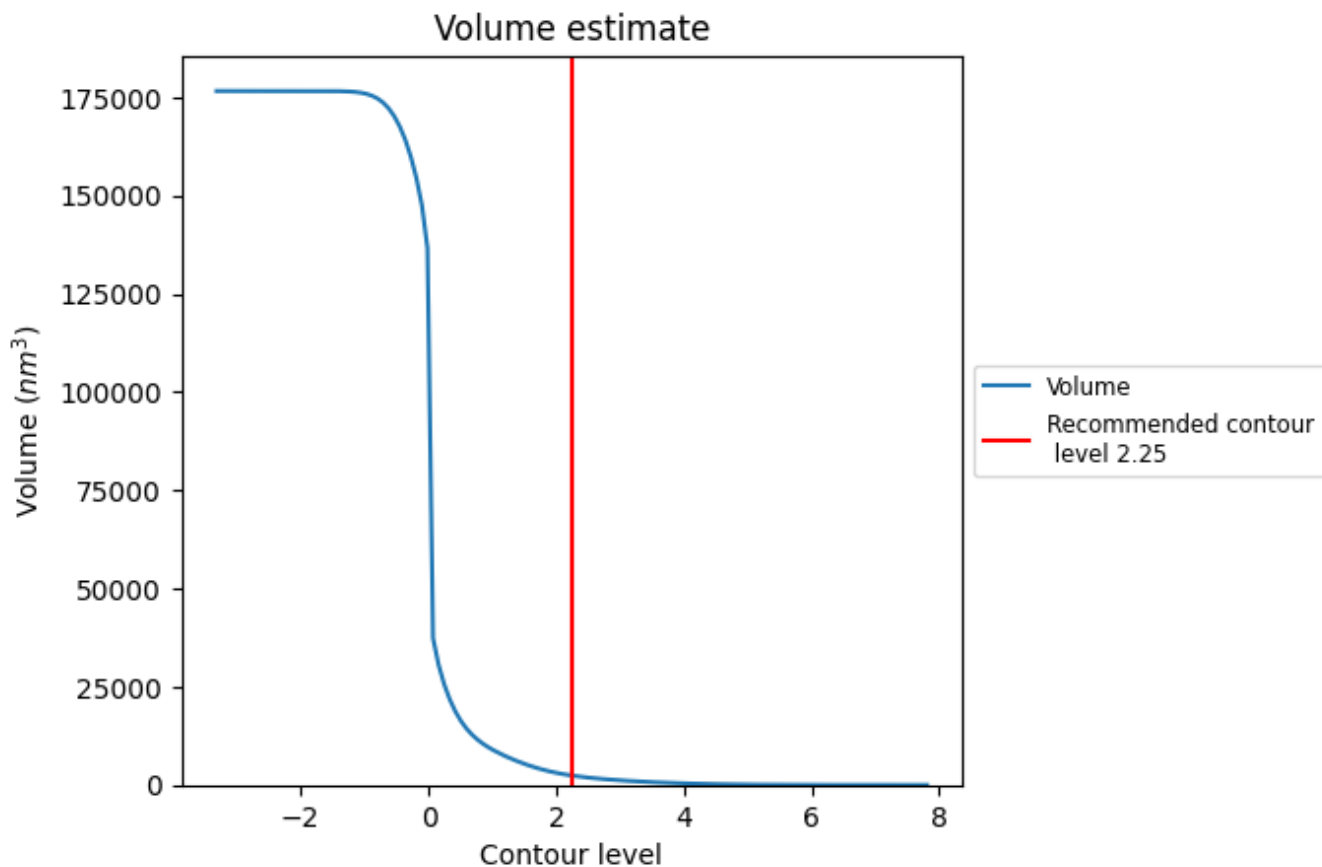
This section contains the results of statistical analysis of the map.

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.

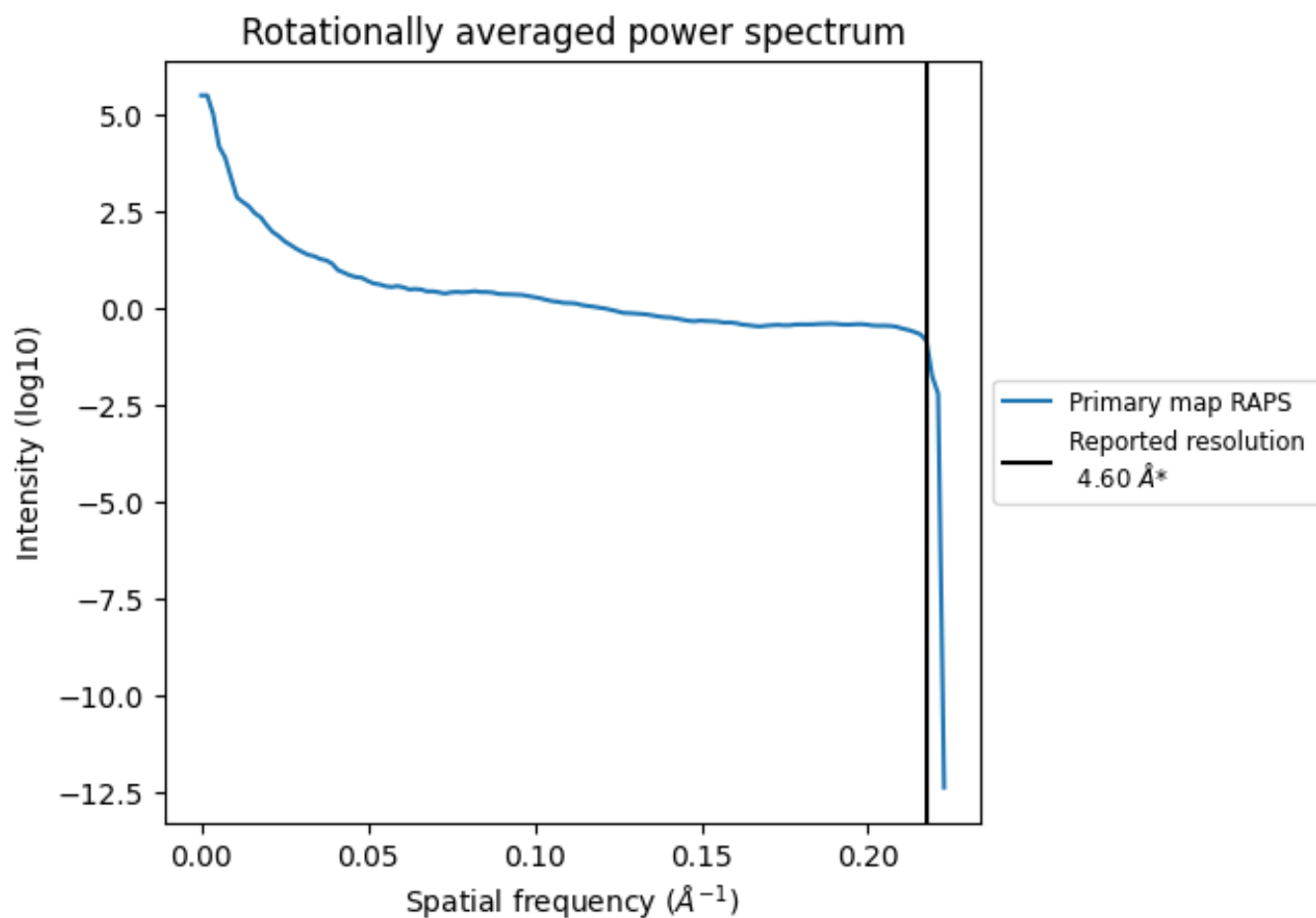
7.2 Volume estimate [\(i\)](#)



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 [i](#)



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

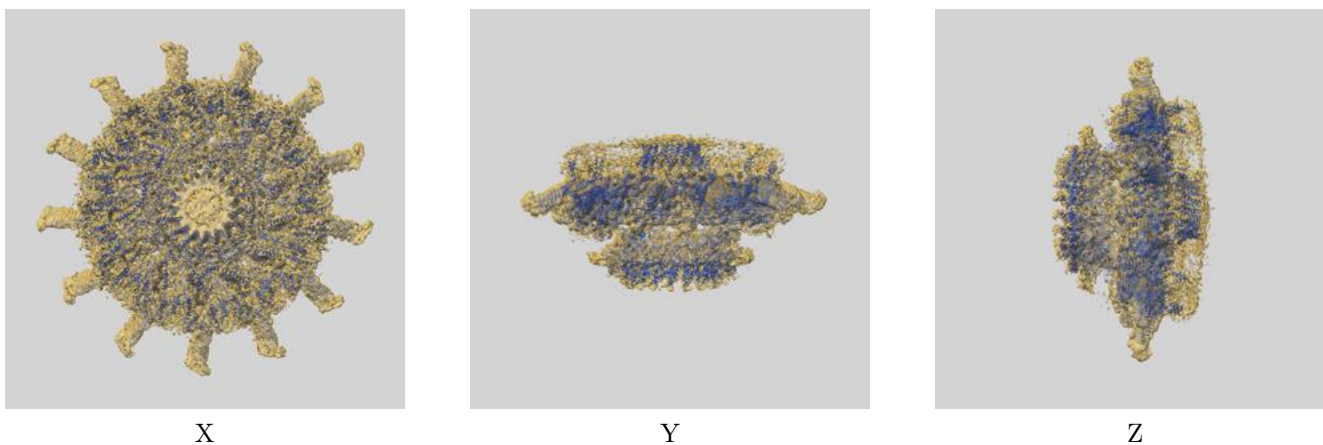
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

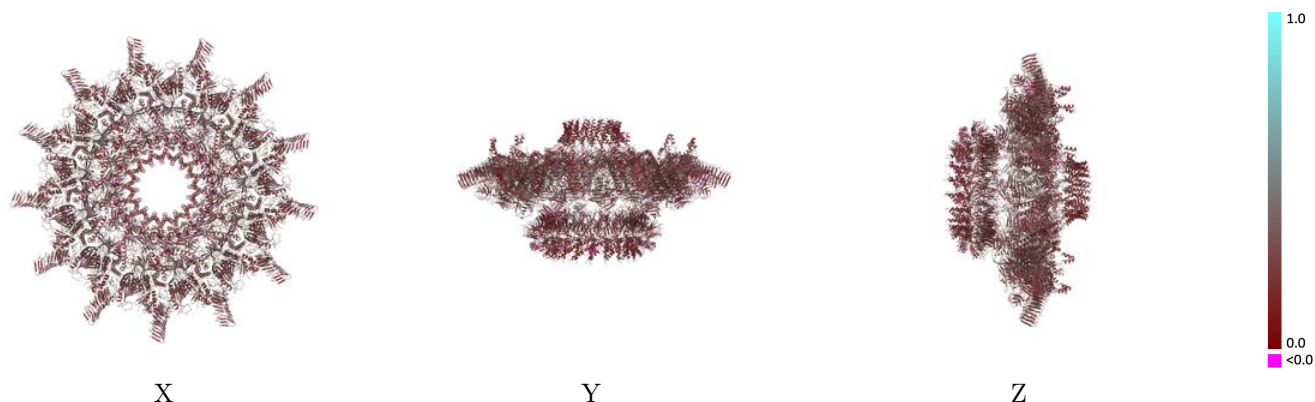
This section contains information regarding the fit between EMDB map EMD-24024 and PDB model 7MUW. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



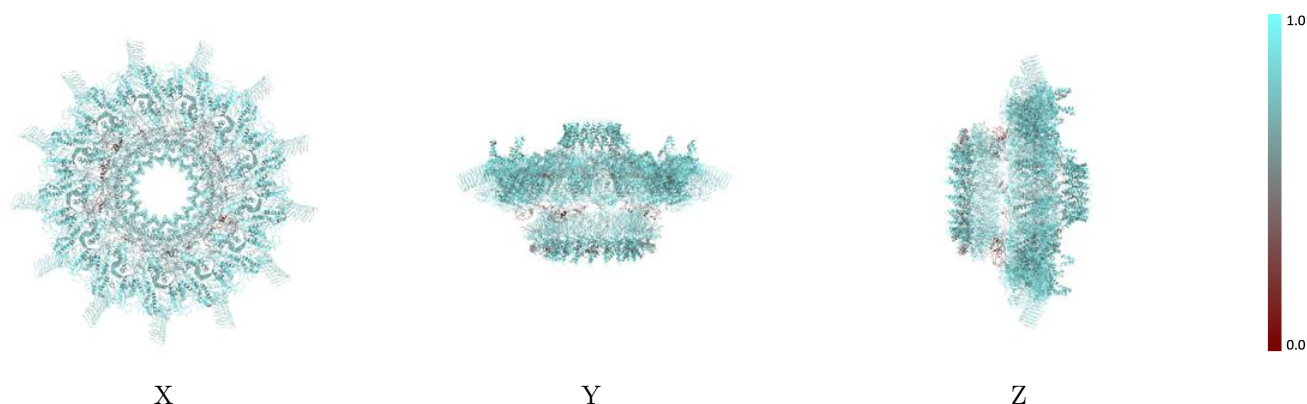
The images above show the 3D surface view of the map at the recommended contour level 2.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



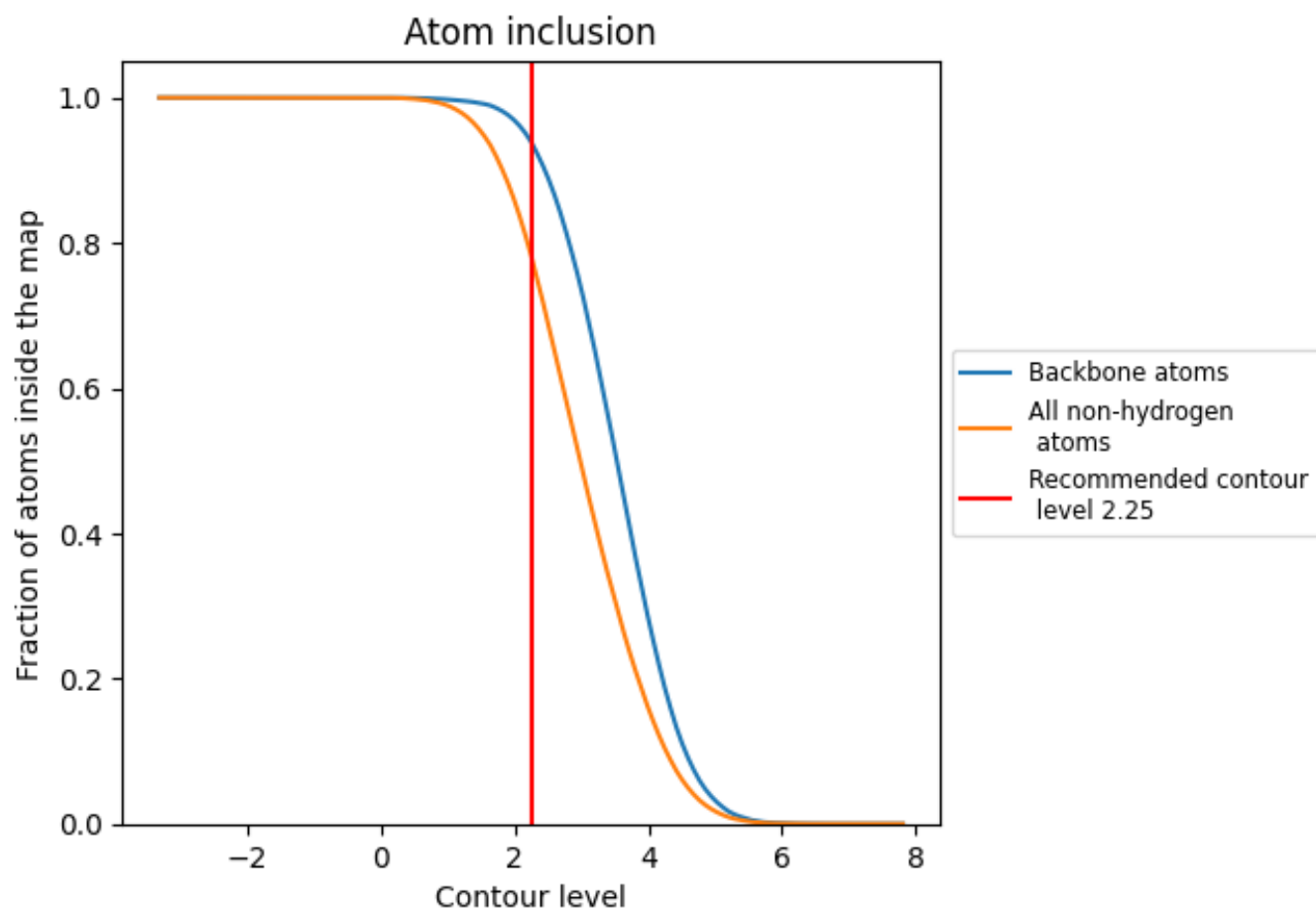
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 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	 0.7815	 0.2820
AC	 0.7717	 0.2930
AD	 0.8081	 0.3200
AF	 0.7983	 0.2290
AG	 0.6913	 0.2430
AH	 0.7818	 0.2740
AK	 0.8110	 0.3060
AL	 0.8199	 0.2840
AM	 0.7871	 0.2930
AN	 0.7605	 0.3330
AU	 0.9556	 0.4410
AX	 0.6542	 0.2400
Ad	 0.8242	 0.3120
Af	 0.7927	 0.2740
Ag	 0.8125	 0.2550
BC	 0.7589	 0.2830
BD	 0.8090	 0.3110
BF	 0.7792	 0.2220
BG	 0.6552	 0.2250
BH	 0.7931	 0.2730
BK	 0.8303	 0.3040
BL	 0.8302	 0.2900
BM	 0.7989	 0.2910
BN	 0.7325	 0.3180
BU	 0.9778	 0.4590
BX	 0.5667	 0.2260
Bd	 0.8136	 0.3090
Bf	 0.7790	 0.2820
Bg	 0.8640	 0.2740
CC	 0.8135	 0.2900
CD	 0.8109	 0.3160
CF	 0.7134	 0.2400
CG	 0.6568	 0.2330
CH	 0.8090	 0.2930
CK	 0.8241	 0.3160























































































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Chain	Atom inclusion	Q-score
CL	 0.8428	 0.2900
CM	 0.8107	 0.2840
CN	 0.7413	 0.3220
CU	 0.9778	 0.4900
CX	 0.5875	 0.2190
Cd	 0.8348	 0.2900
Cf	 0.7745	 0.2780
Cg	 0.8566	 0.2580
DC	 0.8252	 0.2920
DD	 0.8155	 0.3020
DF	 0.7728	 0.2310
DG	 0.7184	 0.2500
DH	 0.7957	 0.2850
DK	 0.8110	 0.3100
DL	 0.8488	 0.2920
DM	 0.7846	 0.2850
DN	 0.7727	 0.3330
DU	 1.0000	 0.4410
DX	 0.7333	 0.2560
Dd	 0.8136	 0.3120
Df	 0.7198	 0.2590
Dg	 0.8382	 0.2790
EC	 0.8172	 0.3040
ED	 0.8052	 0.3150
EF	 0.7983	 0.2260
EG	 0.6691	 0.2430
EH	 0.7890	 0.2790
EK	 0.8294	 0.3130
EL	 0.8451	 0.2940
EM	 0.8094	 0.2850
EN	 0.7815	 0.3230
EU	 0.9556	 0.4260
EX	 0.5417	 0.2110
Ed	 0.8213	 0.3000
Ef	 0.7882	 0.2840
Eg	 0.8529	 0.2540
FC	 0.7839	 0.2970
FD	 0.8127	 0.3080
FF	 0.7983	 0.2380
FG	 0.6897	 0.2290
FH	 0.8060	 0.2820
FK	 0.8031	 0.3050





















































































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Chain	Atom inclusion	Q-score
FL	 0.8317	 0.2990
FM	 0.8144	 0.3010
FN	 0.7552	 0.3230
FU	 1.0000	 0.4520
FX	 0.7417	 0.2780
Fd	 0.8290	 0.3060
Ff	 0.8178	 0.2950
Fg	 0.8493	 0.2650
GC	 0.8110	 0.3010
GD	 0.8099	 0.3150
GF	 0.7771	 0.2370
GG	 0.7044	 0.2260
GH	 0.7967	 0.2810
GK	 0.8058	 0.3080
GL	 0.8236	 0.2930
GM	 0.8218	 0.2920
GN	 0.7605	 0.3200
GU	 0.9556	 0.4710
GX	 0.4750	 0.2200
Gd	 0.8223	 0.3050
Gf	 0.7745	 0.2860
Gg	 0.8529	 0.2540
HC	 0.8221	 0.2950
HD	 0.8221	 0.3190
HF	 0.7707	 0.2330
HG	 0.7044	 0.2250
HH	 0.8080	 0.2820
HK	 0.8189	 0.3070
HL	 0.8340	 0.2900
HM	 0.8287	 0.2940
HN	 0.7920	 0.3310
HU	 0.9556	 0.4480
HX	 0.5583	 0.2450
Hd	 0.8473	 0.2990
Hf	 0.8109	 0.2690
Hg	 0.7978	 0.2550
IC	 0.8135	 0.3000
ID	 0.8109	 0.3060
IF	 0.7834	 0.2030
IG	 0.7102	 0.2390
IH	 0.7911	 0.2720
IK	 0.8364	 0.3120





















































































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Chain	Atom inclusion	Q-score
IL	 0.8347	 0.2950
IM	 0.8113	 0.2800
IN	 0.7850	 0.3260
IU	 0.9333	 0.4260
IX	 0.6542	 0.2380
Id	 0.8415	 0.3010
If	 0.8292	 0.2920
Ig	 0.8603	 0.2490
JC	 0.7807	 0.2900
JD	 0.8015	 0.3070
JF	 0.7792	 0.2370
JG	 0.6593	 0.2230
JH	 0.8044	 0.2750
JK	 0.8136	 0.3050
JL	 0.8406	 0.2920
JM	 0.8101	 0.2950
JN	 0.7413	 0.3150
JU	 0.9778	 0.4640
JX	 0.6458	 0.2330
Jd	 0.8002	 0.3030
Jf	 0.8064	 0.2840
Jg	 0.8566	 0.2550
KC	 0.7853	 0.2970
KD	 0.8071	 0.3070
KF	 0.7558	 0.2220
KG	 0.6732	 0.2060
KH	 0.8075	 0.2820
KK	 0.8250	 0.3130
KL	 0.8302	 0.2990
KM	 0.8299	 0.2920
KN	 0.7517	 0.3300
KU	 0.9778	 0.4760
KX	 0.5542	 0.2180
Kd	 0.8290	 0.3060
Kf	 0.8087	 0.2910
Kg	 0.8346	 0.2420
LC	 0.8178	 0.3000
LD	 0.8081	 0.3160
LF	 0.8025	 0.2350
LG	 0.6568	 0.1890
LH	 0.7972	 0.2680
LK	 0.8259	 0.3160



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Chain	Atom inclusion	Q-score
LL	 0.8265	 0.2960
LM	 0.8038	 0.2770
LN	 0.8112	 0.3390
LU	 0.9778	 0.4700
LX	 0.5500	 0.2410
Ld	 0.8290	 0.2960
Lf	 0.8132	 0.2690
Lg	 0.8529	 0.2520
MC	 0.8190	 0.3040
MD	 0.7856	 0.3160
MF	 0.8132	 0.2280
MG	 0.6765	 0.2120
MH	 0.8003	 0.2760
MK	 0.8040	 0.3160
ML	 0.8095	 0.2910
MM	 0.7939	 0.2850
MN	 0.7762	 0.3210
MU	 0.9111	 0.4900
MX	 0.6333	 0.2400
Md	 0.8165	 0.2970
Mf	 0.8109	 0.2730
Mg	 0.8603	 0.2570
NG	 0.6617	 0.2190
OG	 0.6831	 0.2440
PG	 0.7069	 0.2390
VF	 0.7410	 0.2360
VG	 0.8199	 0.2480
VH	 0.6663	 0.2670
VX	 0.6583	 0.2130
WF	 0.7813	 0.2360
WG	 0.8382	 0.2530
WH	 0.6179	 0.2580
WX	 0.6542	 0.2510
XF	 0.7707	 0.2190
XG	 0.7978	 0.2540
XH	 0.5891	 0.2530
XX	 0.6667	 0.2320
YF	 0.7941	 0.2290
YG	 0.8088	 0.2510
YH	 0.7005	 0.2540
YX	 0.6208	 0.2590
ZF	 0.8344	 0.2440

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Chain	Atom inclusion	Q-score
ZG	 0.7721	 0.2470
ZH	 0.5397	 0.2220
ZX	 0.5625	 0.2240