



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 02:40 AM EST

PDB ID : 6X65
EMDB ID : EMD-22070
Title : Legionella pneumophila Dot/Icm T4SS
Authors : Durie, C.L.; Sheedlo, M.J.; Chung, J.M.; Byrne, B.G.; Su, M.; Knight, T.; Swanson, M.S.; Lacy, D.B.; Ohi, M.D.
Deposited on : 2020-05-27
Resolution : 3.70 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 : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

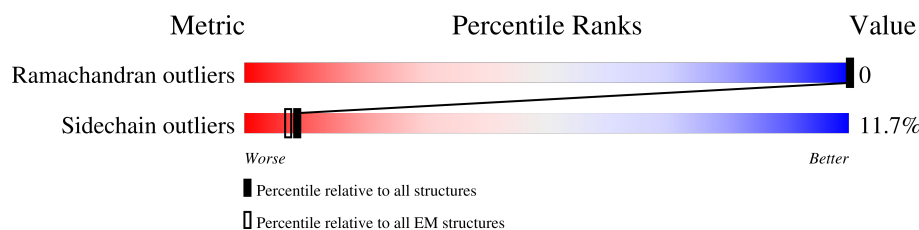
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY



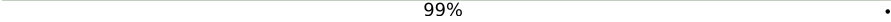




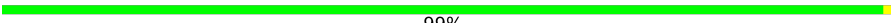


The reported resolution of this entry is 3.70 Å.

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.





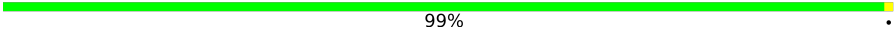




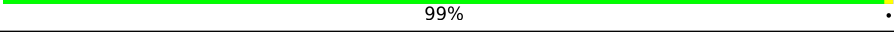




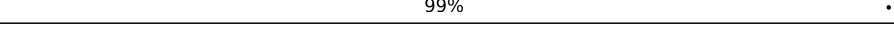




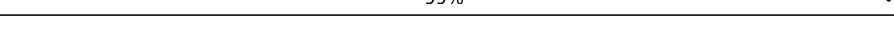

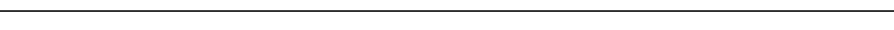

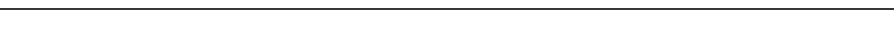
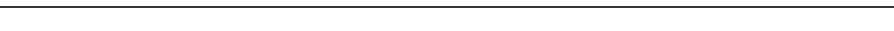


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	AV	228	 63% 37%
1	AW	228	 14% 86%
1	AX	228	 99% .
1	AY	228	 23% 77%
1	AZ	228	 30% . 69%
1	BV	228	 62% . 37%
1	BW	228	 14% 86%
1	BX	228	 99% .
1	BY	228	 23% 77%
1	BZ	228	 30% . 69%



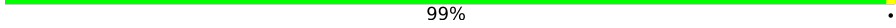

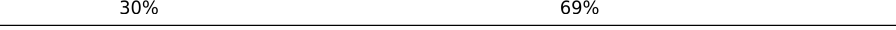
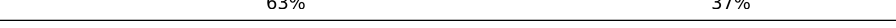

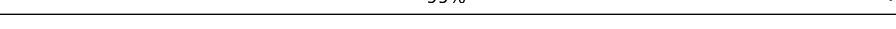
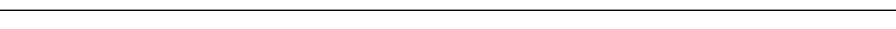
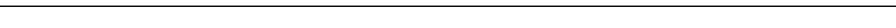






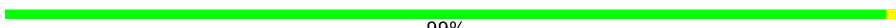




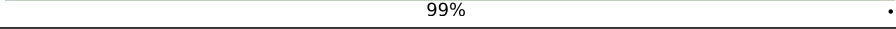



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Mol	Chain	Length	Quality of chain
1	CV	228	 63% 37%
1	CW	228	 14% 86%
1	CX	228	 99% .
1	CY	228	 23% 77%
1	CZ	228	 30% 69%
1	DV	228	 63% 37%
1	DW	228	 14% 86%
1	DX	228	 99% .
1	DY	228	 23% 77%
1	DZ	228	 30% . 69%
1	EV	228	 63% 37%
1	EW	228	 14% 86%
1	EX	228	 99% .
1	EY	228	 23% 77%
1	EZ	228	 30% 69%
1	FV	228	 63% 37%
1	FW	228	 14% 86%
1	FX	228	 99% .
1	FY	228	 23% 77%
1	FZ	228	 30% 69%
1	GV	228	 63% 37%
1	GW	228	 14% 86%
1	GX	228	 99% .
1	GY	228	 23% 77%
1	GZ	228	 30% 69%



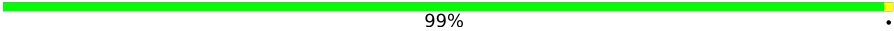








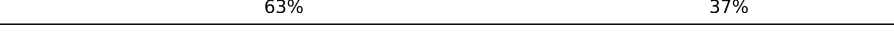







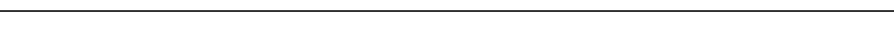

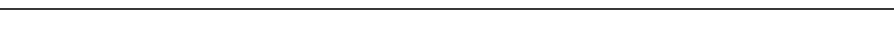
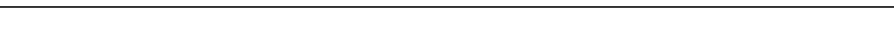


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Mol	Chain	Length	Quality of chain
1	HV	228	 63% 37%
1	HW	228	 14% 86%
1	HX	228	 99% .
1	HY	228	 23% 77%
1	HZ	228	 30% 69%
1	IV	228	 63% 37%
1	IW	228	 14% 86%
1	IX	228	 99% .
1	IY	228	 23% 77%
1	IZ	228	 30% 69%
1	JV	228	 63% 37%
1	JW	228	 14% 86%
1	JX	228	 99% .
1	JY	228	 23% 77%
1	JZ	228	 30% 69%
1	KV	228	 63% 37%
1	KW	228	 14% 86%
1	KX	228	 99% .
1	KY	228	 23% 77%
1	KZ	228	 30% 69%
1	LV	228	 63% 37%
1	LW	228	 14% 86%
1	LX	228	 99% .
1	LY	228	 23% 77%
1	LZ	228	 30% . 69%

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Mol	Chain	Length	Quality of chain
1	MV	228	 63% 37%
1	MW	228	 14% 86%
1	MX	228	 99% .
1	MY	228	 23% 77%
1	MZ	228	 30% 69%
1	NV	228	 63% 37%
1	NW	228	 14% 86%
1	OV	228	 62% . 37%
1	OW	228	 14% 86%
1	PV	228	 63% 37%
1	PW	228	 14% 86%
1	QV	228	 63% 37%
1	QW	228	 14% 86%
1	RV	228	 63% 37%
1	RW	228	 14% 86%
2	AC	303	 62% . 34%
2	BC	303	 60% 6% 34%
2	CC	303	 60% 6% 34%
2	DC	303	 59% 7% 34%
2	EC	303	 60% 6% 34%
2	FC	303	 61% 5% 34%
2	GC	303	 60% 6% 34%
2	HC	303	 61% 5% 34%
2	IC	303	 60% 6% 34%
2	JC	303	 61% . 34%


























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Mol	Chain	Length	Quality of chain
2	KC	303	
2	LC	303	
2	MC	303	
3	AD	163	
3	Ad	163	
3	BD	163	
3	Bd	163	
3	CD	163	
3	Cd	163	
3	DD	163	
3	Dd	163	
3	ED	163	
3	Ed	163	
3	FD	163	
3	Fd	163	
3	GD	163	
3	Gd	163	
3	HD	163	
3	Hd	163	
3	ID	163	
3	Id	163	
3	JD	163	
3	Jd	163	
3	KD	163	
3	Kd	163	







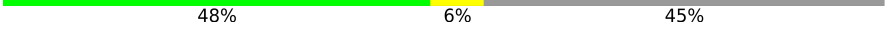

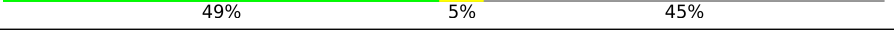

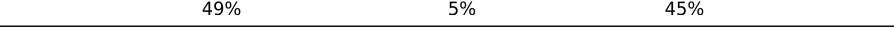
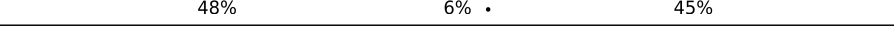
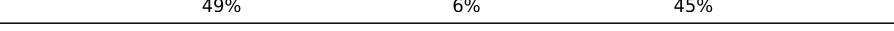
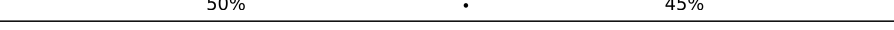



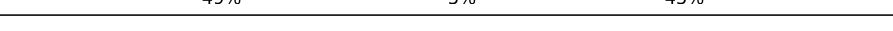
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Mol	Chain	Length	Quality of chain
3	LD	163	
3	Ld	163	
3	MD	163	
3	Md	163	
4	AH	361	
4	BH	361	
4	CH	361	
4	DH	361	
4	EH	361	
4	FH	361	
4	GH	361	
4	HH	361	
4	IH	361	
4	JH	361	
4	KH	361	
4	LH	361	
4	MH	361	
5	AK	189	
5	BK	189	
5	CK	189	
5	DK	189	
5	EK	189	
5	FK	189	
5	GK	189	
5	HK	189	

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Mol	Chain	Length	Quality of chain
5	IK	189	 71%7%22%
5	JK	189	 69%9%22%
5	KK	189	 70%8%22%
5	LK	189	 70%8%22%
5	MK	189	 71%7%22%
6	N	249	 50%. .45%
6	O	249	 48%6%45%
6	P	249	 51%.45%
6	Q	249	 49%5%45%
6	R	249	 51%.45%
6	S	249	 49%5%45%
6	T	249	 48%6%.45%
6	U	249	 49%6%45%
6	V	249	 50%.45%
6	W	249	 50%.45%
6	X	249	 50%.45%
6	Y	249	 51%. .45%
6	Z	249	 49%5%45%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 124910 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 Type IV secretion system unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	AV	144	Total	C	N	O	0	0
			720	432	144	144		
1	AW	32	Total	C	N	O	0	0
			160	96	32	32		
1	BV	144	Total	C	N	O	0	0
			720	432	144	144		
1	BW	32	Total	C	N	O	0	0
			160	96	32	32		
1	CV	144	Total	C	N	O	0	0
			720	432	144	144		
1	CW	32	Total	C	N	O	0	0
			160	96	32	32		
1	DV	144	Total	C	N	O	0	0
			720	432	144	144		
1	DW	32	Total	C	N	O	0	0
			160	96	32	32		
1	EV	144	Total	C	N	O	0	0
			720	432	144	144		
1	EW	32	Total	C	N	O	0	0
			160	96	32	32		
1	FV	144	Total	C	N	O	0	0
			720	432	144	144		
1	FW	32	Total	C	N	O	0	0
			160	96	32	32		
1	GV	144	Total	C	N	O	0	0
			720	432	144	144		
1	GW	32	Total	C	N	O	0	0
			160	96	32	32		
1	HV	144	Total	C	N	O	0	0
			720	432	144	144		
1	HW	32	Total	C	N	O	0	0
			160	96	32	32		
1	IV	144	Total	C	N	O	0	0
			720	432	144	144		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	IW	32	Total	C	N	O	0	0
			160	96	32	32		
1	JV	144	Total	C	N	O	0	0
			720	432	144	144		
1	JW	32	Total	C	N	O	0	0
			160	96	32	32		
1	KV	144	Total	C	N	O	0	0
			720	432	144	144		
1	KW	32	Total	C	N	O	0	0
			160	96	32	32		
1	LV	144	Total	C	N	O	0	0
			720	432	144	144		
1	LW	32	Total	C	N	O	0	0
			160	96	32	32		
1	MV	144	Total	C	N	O	0	0
			720	432	144	144		
1	MW	32	Total	C	N	O	0	0
			160	96	32	32		
1	NV	144	Total	C	N	O	0	0
			720	432	144	144		
1	NW	32	Total	C	N	O	0	0
			160	96	32	32		
1	OV	144	Total	C	N	O	0	0
			720	432	144	144		
1	OW	32	Total	C	N	O	0	0
			160	96	32	32		
1	PV	144	Total	C	N	O	0	0
			720	432	144	144		
1	PW	32	Total	C	N	O	0	0
			160	96	32	32		
1	QV	144	Total	C	N	O	0	0
			720	432	144	144		
1	QW	32	Total	C	N	O	0	0
			160	96	32	32		
1	RV	144	Total	C	N	O	0	0
			720	432	144	144		
1	RW	32	Total	C	N	O	0	0
			160	96	32	32		
1	AX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	AY	52	Total	C	N	O	0	0
			260	156	52	52		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	AZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	BX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	BY	52	Total	C	N	O	0	0
			260	156	52	52		
1	BZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	CX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	CY	52	Total	C	N	O	0	0
			260	156	52	52		
1	CZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	DX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	DY	52	Total	C	N	O	0	0
			260	156	52	52		
1	DZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	EX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	EY	52	Total	C	N	O	0	0
			260	156	52	52		
1	EZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	FX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	FY	52	Total	C	N	O	0	0
			260	156	52	52		
1	FZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	GX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	GY	52	Total	C	N	O	0	0
			260	156	52	52		
1	GZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	HX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	HY	52	Total	C	N	O	0	0
			260	156	52	52		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	HZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	IX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	IY	52	Total	C	N	O	0	0
			260	156	52	52		
1	IZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	JX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	JY	52	Total	C	N	O	0	0
			260	156	52	52		
1	JZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	KX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	KY	52	Total	C	N	O	0	0
			260	156	52	52		
1	KZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	LX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	LY	52	Total	C	N	O	0	0
			260	156	52	52		
1	LZ	70	Total	C	N	O	0	0
			350	210	70	70		
1	MX	228	Total	C	N	O	0	0
			1140	684	228	228		
1	MY	52	Total	C	N	O	0	0
			260	156	52	52		
1	MZ	70	Total	C	N	O	0	0
			350	210	70	70		

- Molecule 2 is a protein called DotC.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	BC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	CC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	EC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	FC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	GC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	HC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	IC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	JC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	KC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	LC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		
2	MC	200	Total	C	N	O	S	0	0
			1596	1016	280	295	5		

- Molecule 3 is a protein called DotD.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Ad	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	BD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Bd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	CD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Cd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	DD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Dd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	ED	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ed	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	FD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Fd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	GD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Gd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	HD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Hd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	ID	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Id	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	JD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Jd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	KD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Kd	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	LD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Ld	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		
3	MD	135	Total	C	N	O	S	0	0
			1040	660	178	200	2		
3	Md	138	Total	C	N	O	S	0	0
			1066	678	183	203	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AH	89	Total	C	N	O	S	0	0
			678	432	119	123	4		
4	BH	89	Total	C	N	O	S	0	0
			678	432	119	123	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	CH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	DH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	EH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	FH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	GH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	HH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	IH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	JH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	KH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	LH	89	Total 678	C 432	N 119	O 123	S 4	0	0
4	MH	89	Total 678	C 432	N 119	O 123	S 4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	BK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	CK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	DK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	EK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	FK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	GK	148	Total 1152	C 731	N 205	O 212	S 4	0	0
5	HK	148	Total 1152	C 731	N 205	O 212	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	IK	148	Total	C	N	O	S	0	0
			1152	731	205	212	4		
5	JK	148	Total	C	N	O	S	0	0
			1152	731	205	212	4		
5	KK	148	Total	C	N	O	S	0	0
			1152	731	205	212	4		
5	LK	148	Total	C	N	O	S	0	0
			1152	731	205	212	4		
5	MK	148	Total	C	N	O	S	0	0
			1152	731	205	212	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	O	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	P	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	Q	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	R	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	S	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	T	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	U	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	V	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	W	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	X	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	Y	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		
6	Z	136	Total	C	N	O	S	0	0
			1108	701	201	202	4		

3 Residue-property plots [i](#)

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

- Molecule 1: Type IV secretion system unknown protein fragment

Chain AV:  63% 37%



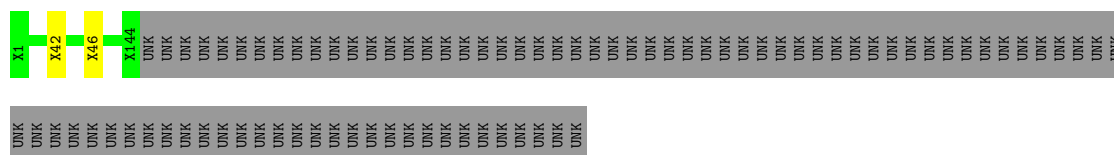
- Molecule 1: Type IV secretion system unknown protein fragment

Chain AW:  14% 86%



- Molecule 1: Type IV secretion system unknown protein fragment

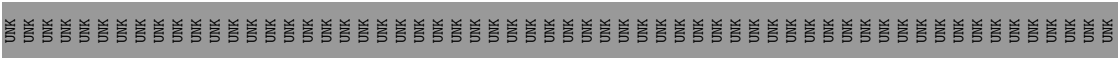
Chain BV:  62% 37%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain BW:  14% 86%

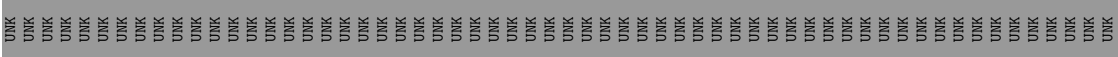
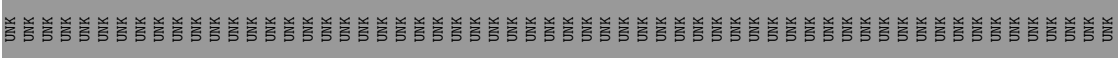




• Molecule 1: Type IV secretion system unknown protein fragment



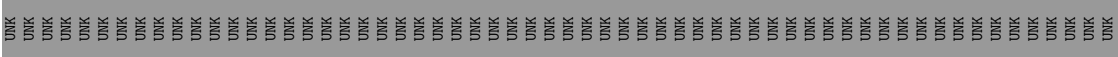
• Molecule 1: Type IV secretion system unknown protein fragment

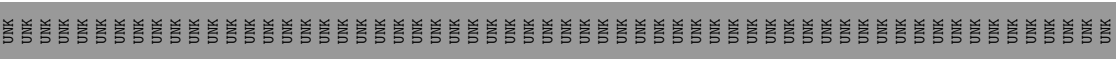


• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment

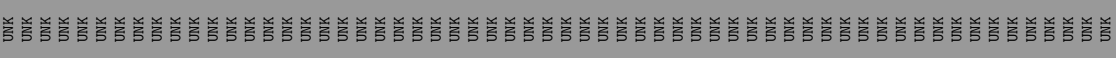
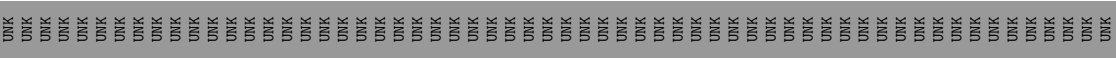




● Molecule 1: Type IV secretion system unknown protein fragment



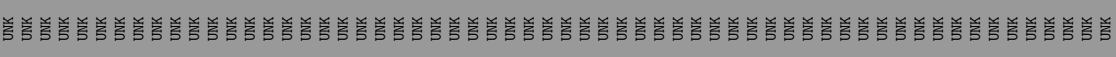
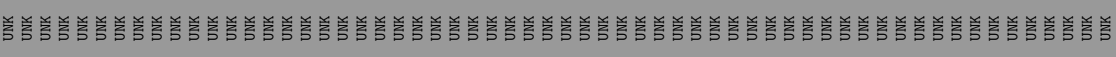
● Molecule 1: Type IV secretion system unknown protein fragment



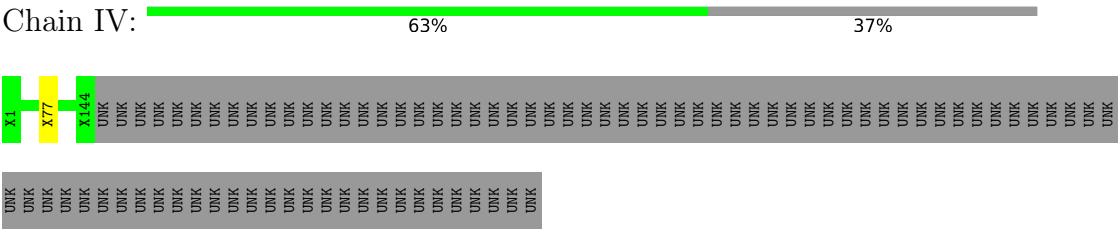
● Molecule 1: Type IV secretion system unknown protein fragment



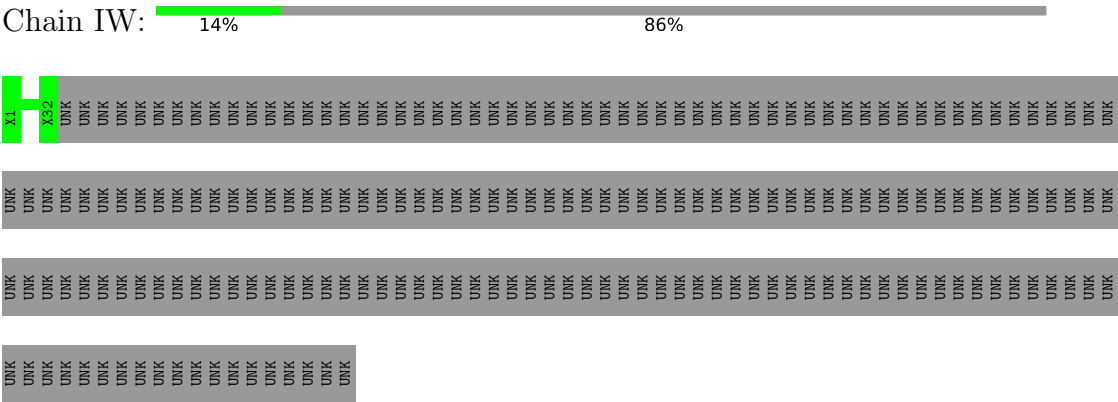
● Molecule 1: Type IV secretion system unknown protein fragment



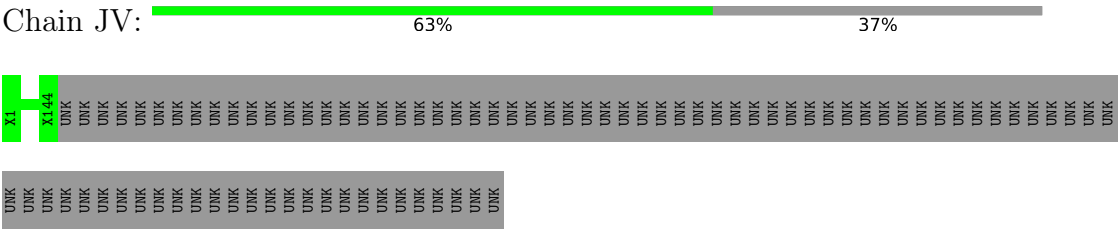
• Molecule 1: Type IV secretion system unknown protein fragment



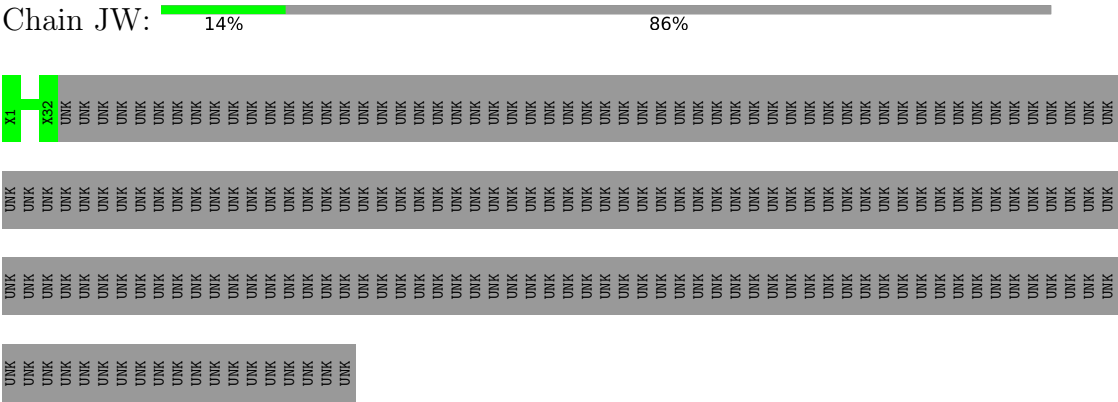
• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment

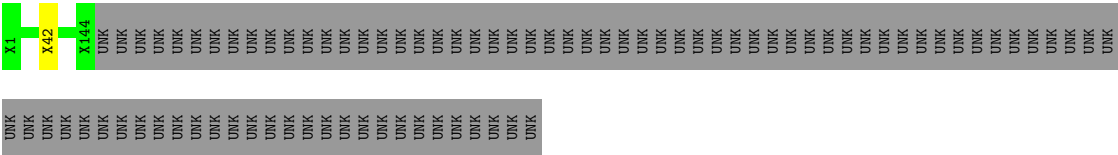


• Molecule 1: Type IV secretion system unknown protein fragment

Chain KV:

63%

37%

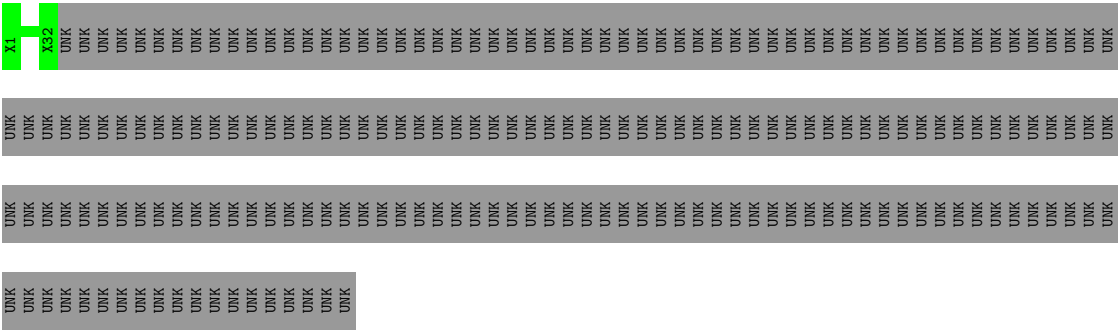


• Molecule 1: Type IV secretion system unknown protein fragment

Chain KW:

14%

86%

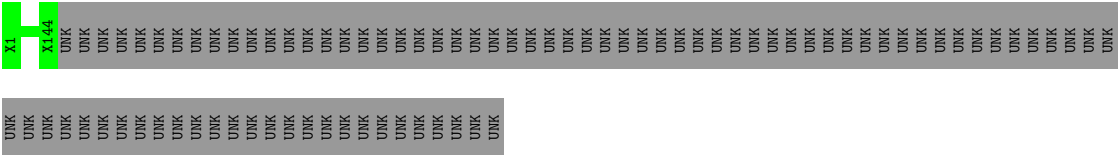


• Molecule 1: Type IV secretion system unknown protein fragment

Chain LV:

63%

37%

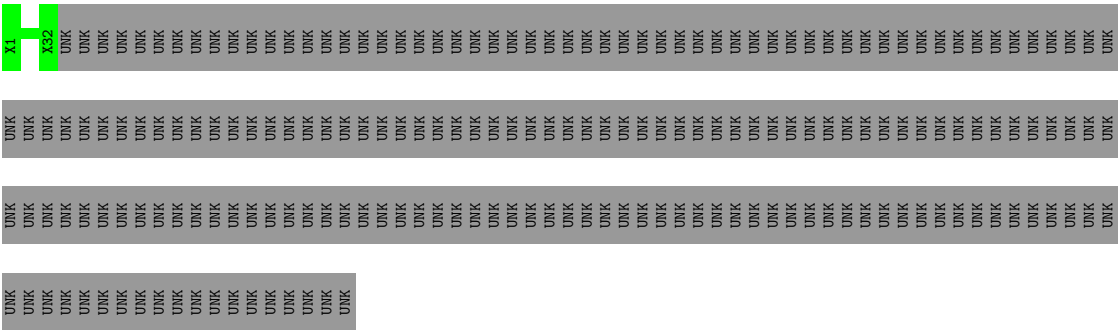


• Molecule 1: Type IV secretion system unknown protein fragment

Chain LW:

14%

86%



• Molecule 1: Type IV secretion system unknown protein fragment

Chain MV:

63%

37%

- Molecule 1: Type IV secretion system unknown protein fragment



- Molecule 1: Type IV secretion system unknown protein fragment

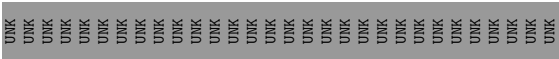


- Molecule 1: Type IV secretion system unknown protein fragment

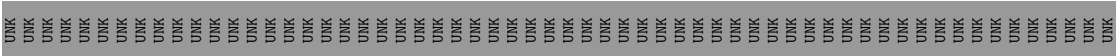
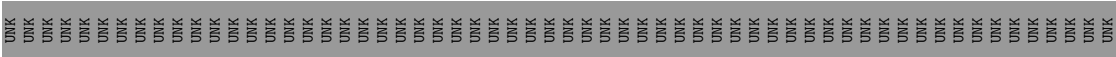


- Molecule 1: Type IV secretion system unknown protein fragment

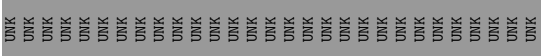




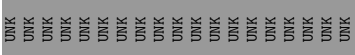
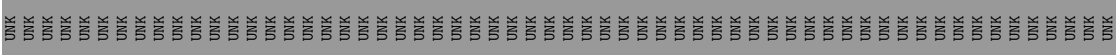
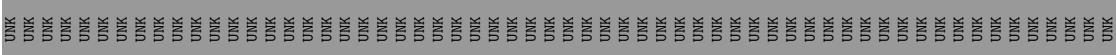
• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment

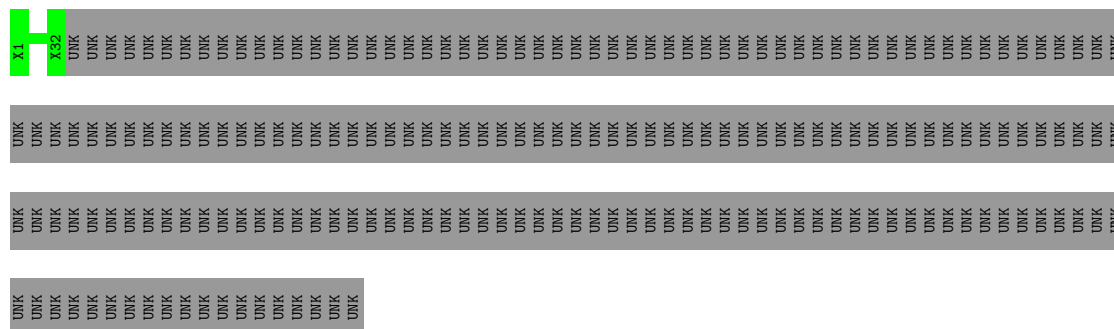


• Molecule 1: Type IV secretion system unknown protein fragment



- Molecule 1: Type IV secretion system unknown protein fragment

Chain QW:  14% 86%



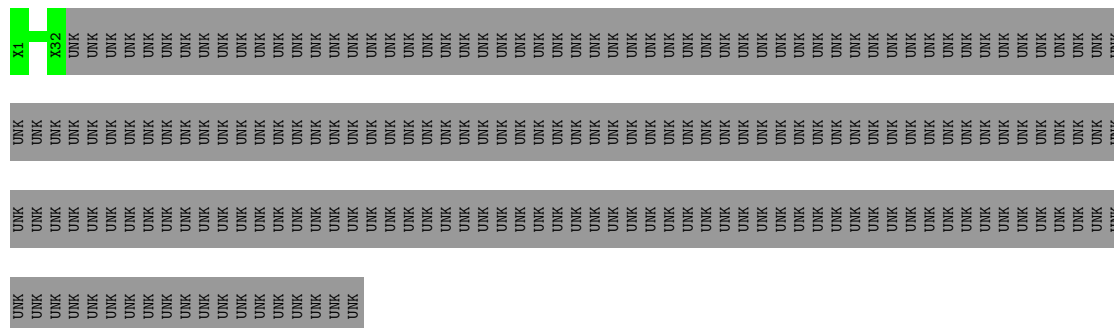
- Molecule 1: Type IV secretion system unknown protein fragment

Chain RV:  63% 37%



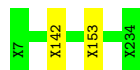
- Molecule 1: Type IV secretion system unknown protein fragment

Chain RW:  14% 86%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain AX:  99%

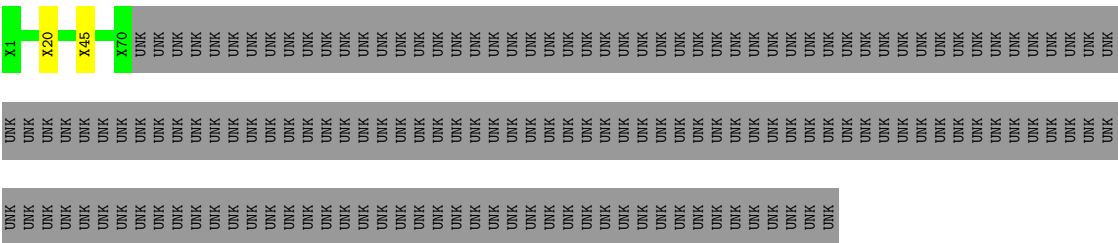


- Molecule 1: Type IV secretion system unknown protein fragment

Chain AY:  23% 77%



• Molecule 1: Type IV secretion system unknown protein fragment



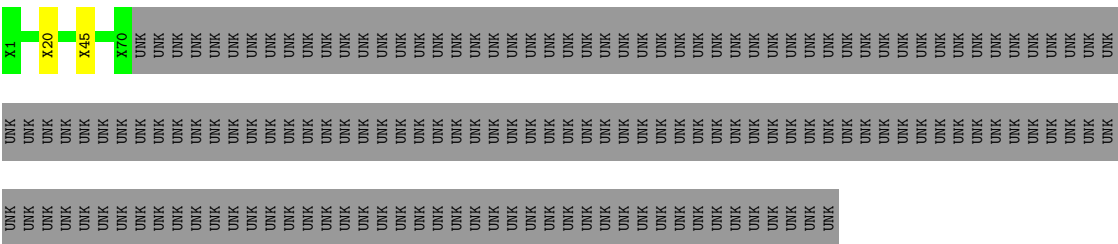
• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment

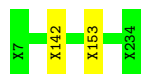


• Molecule 1: Type IV secretion system unknown protein fragment



- Molecule 1: Type IV secretion system unknown protein fragment

Chain CX:  99%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain CY:  23%  77%



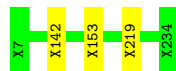
- Molecule 1: Type IV secretion system unknown protein fragment

Chain CZ:  30%  69%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain DX:  99%

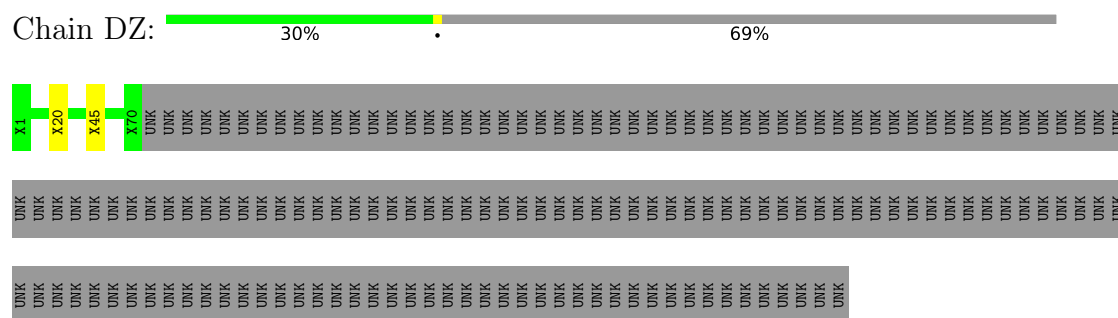


- Molecule 1: Type IV secretion system unknown protein fragment

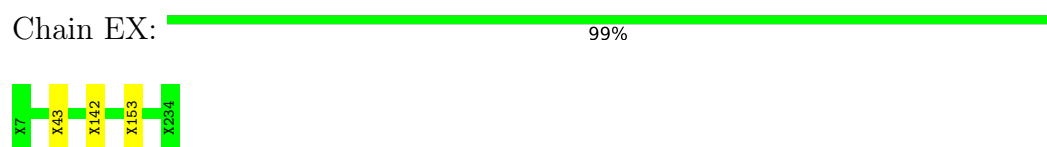
Chain DY:  23%  77%



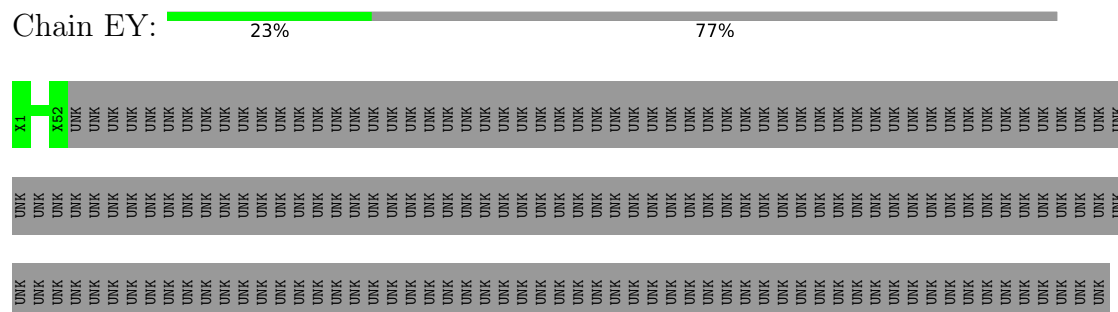
- Molecule 1: Type IV secretion system unknown protein fragment



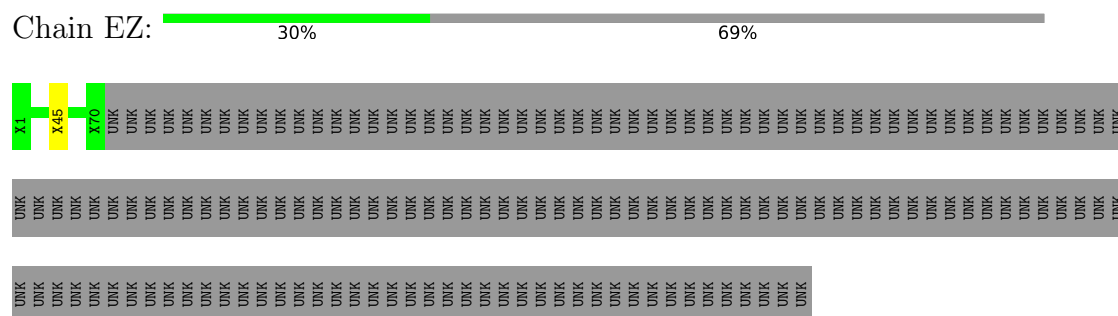
- Molecule 1: Type IV secretion system unknown protein fragment



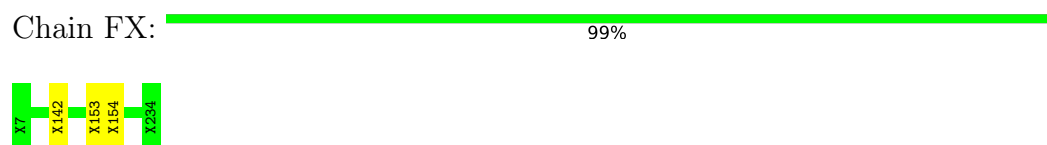
- Molecule 1: Type IV secretion system unknown protein fragment



- Molecule 1: Type IV secretion system unknown protein fragment

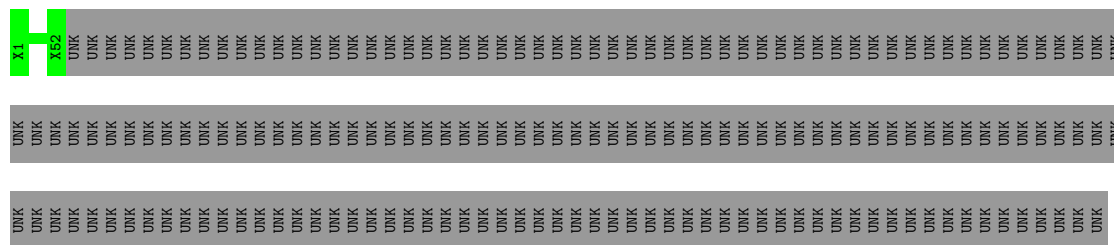


- Molecule 1: Type IV secretion system unknown protein fragment



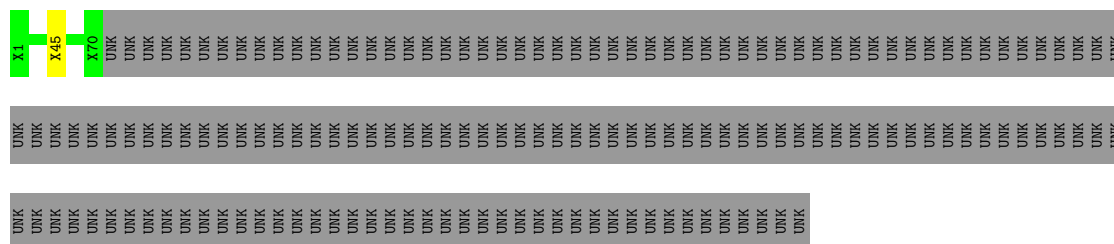
- Molecule 1: Type IV secretion system unknown protein fragment

Chain FY:  23% 77%



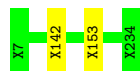
- Molecule 1: Type IV secretion system unknown protein fragment

Chain FZ:  30% 69%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain GX:  99%



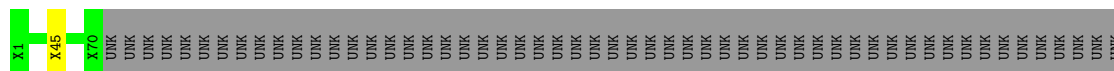
- Molecule 1: Type IV secretion system unknown protein fragment

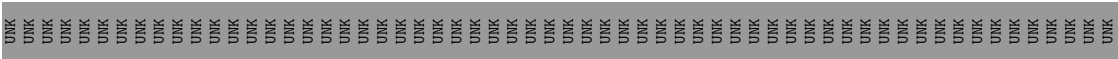
Chain GY:  23% 77%



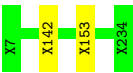
- Molecule 1: Type IV secretion system unknown protein fragment

Chain GZ:  30% 69%

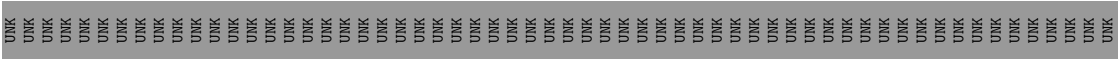




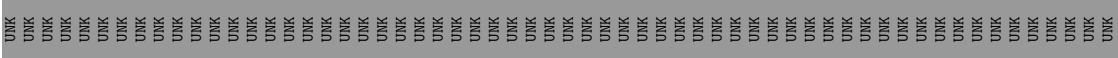
● Molecule 1: Type IV secretion system unknown protein fragment



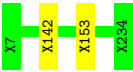
● Molecule 1: Type IV secretion system unknown protein fragment



● Molecule 1: Type IV secretion system unknown protein fragment



● Molecule 1: Type IV secretion system unknown protein fragment

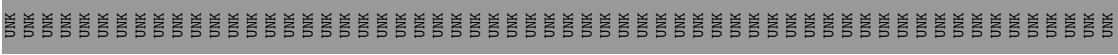


● Molecule 1: Type IV secretion system unknown protein fragment

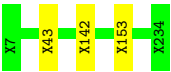




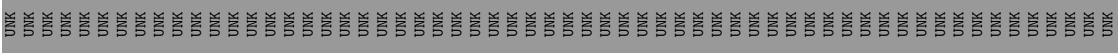
• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment



• Molecule 1: Type IV secretion system unknown protein fragment

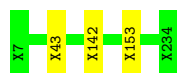


• Molecule 1: Type IV secretion system unknown protein fragment



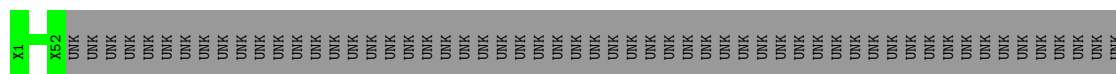
• Molecule 1: Type IV secretion system unknown protein fragment

Chain KX:  99%



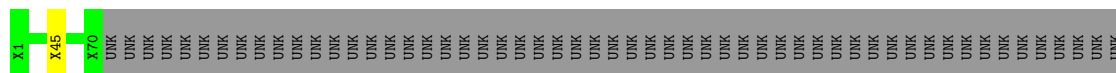
- Molecule 1: Type IV secretion system unknown protein fragment

Chain KY:  23%  77%



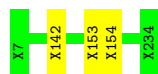
- Molecule 1: Type IV secretion system unknown protein fragment

Chain KZ:  30%  69%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain LX:  99%



- Molecule 1: Type IV secretion system unknown protein fragment

Chain LY:  23%  77%



- Molecule 1: Type IV secretion system unknown protein fragment

[illegible]

- Chain MX:  99%

A diagram showing a sequence of five nodes connected by horizontal lines. The nodes are labeled X7, X43, X142, X153, and X234. X7 and X234 are green, while X43, X142, and X153 are yellow.

- Chain MY:

[illegible]

- Chain MZ:  30% 69%

[illegible]

- Chain AC: 

[illegible]

SER
TRP
GLN
PRO
ILE
ILE
ALA
PRO
VAL
SER

● Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU SER ILE LEU LEU SER VAL ALA LEU LEU VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA GLY LEU LEU GLN ALA MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET MET GLY LYS ILE ARG GLU MET A58 I79

R126 R127 S128 T143 R148 P161 VAL THR LEU PRO LYS THR LYS ALA GLU K173 E174 C177 T180 D189 V221 H228 T229 V233 D243 V246 N256 V257 N258 S259 K268 ASP GLU ASN ALA LEU GLU ARG PHE LYS ASN MET MET GLU LYS

LEU ALA ASN GLN ALA LYS ILE VAL ILE ILE THR ASN SER TRP GLN PRO ILE ILE ALA PRO VAL SER

● Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU SER ILE LEU LEU SER VAL ALA LEU LEU VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA GLY LEU LEU GLN ALA MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET MET GLY LYS ILE ARG GLU MET A58 L72

D91 M104 L117 R126 P161 VAL THR LEU PRO LYS THR LYS ALA GLU K173 C177 T180 D189 Q190 V221 H228 T229 T234 E239 D243 V246 K268 ASP GLU ASN ALA LEU GLU ARG PHE LYS ASN MET MET GLY LYS ILE ARG GLU MET MET LEU ALA ASN

GLN ALA LYS ILE VAL ILE THR ASN SER TRP GLN PRO ILE ILE ALA PRO VAL SER

● Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU SER ILE LEU LEU SER VAL ALA LEU LEU VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA GLY LEU LEU GLN ALA MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET MET GLY LYS ILE ARG GLU MET A58 T62

L72 D91 S98 N104 L119 R126 S128 F140 T143 K157 P161 VAL THR LEU PRO LYS THR LYS ALA GLU K173 C177 Q190 L231 T234 V246 N256 V257 N258 K268 ASP GLU ASN ALA LEU GLU ARG PHE LYS ASN

MET GLU LYS LEU ALA ASN GLN ALA LYS ILE ILE VAL ILE THR ASN LYS TRP GLN PRO ILE ILE ALA PRO VAL SER

● Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU SER ILE LEU LEU SER VAL ALA LEU LEU VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA GLY LEU LEU GLN ALA MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET MET GLY LYS ILE ARG GLU MET A58 E61

L72 E81 N97 E102 I105 L117 R126 H139 P161 ASN VAL THR LEU LEU PRO LYS THR LYS ALA GLU K173 C177 D189 I199 H228 T229 S238 D244 E245 V246 K268 ASP GLU ASN ALA LEU GLU ARG PHE LYS ASN MET MET GLU LYS

LEU
ALA
ASN
GLN
ALA
LYS
ILE
ILE
VAL
THR
ASN
LEU
LYS
SER
TRP
GLN
LEU
ILE
ILE
ALA
PRO
VAL
SER

• Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU LEU ILE ILE THR ASN LEU LEU SER ALA LEU LEU VAL VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA LEU LEU GLN MET MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET GLN LYS MET GLY ILE ILE ARG GLU MET A58 E61

L90 T143 Q149 P161 VAL THR LEU LEU PRO LYS THR LYS ALA CYS K173 C177 T180 E181 D189 L211 H228 T229 V246 N258 K268 ASP GLU ASN LYS ALA LEU LEU ARG PHE LYS ASN MET GLU LYS LEU LEU ASN ASN ALA LYS ILE VAL ILE

THR ASN LYS SER TRP GLN PRO ILE ILE ALA PRO VAL SER

• Molecule 2: DotC



MET ARG LYS PHE ILE SER LEU SER ILE ILE LEU LEU SER ALA LEU LEU VAL VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA LEU GLY GLN MET MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET GLU LYS MET ILE ILE ARG GLU MET A58 E61

L64 K85 R130 H139 K157 P161 ASN VAL THR LEU LEU PRO LYS THR LYS ALA CYS K173 C177 T180 Q190 H228 E239 D243 V246 N256 V257 N258 V266 K267 K268 ASP GLU ASN ALA LEU ARG PHE ILE ILE ASN MET GLU LYS LEU

ALA ASN GLN ALA LYS ILE VAL THR ASN LYS SER TRP GLN PRO ILE ILE ALA PRO VAL SER

• Molecule 2: DotC



MET ARG LYS PHE ILE LEU SER LEU SER ILE ILE LEU LEU SER ALA LEU LEU VAL VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA LEU GLY GLN MET MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET GLU LYS MET ILE ILE ARG GLU MET A58 E81

N104 T116 V134 M153 P161 ASN VAL THR LEU LEU PRO LYS THR LYS ALA CYS K173 C177 T180 D189 V221 H228 T229 D243 D244 R245 V246 N256 K268 ASP GLU ASN ALA LEU LEU ARG PHE LYS ASN MET GLU LYS LEU ALA ASN GLN ALA


LYS ILE VAL ILE THR ASN LYS SER TRP GLN PRO ILE ILE ALA PRO VAL SER

• Molecule 2: DotC



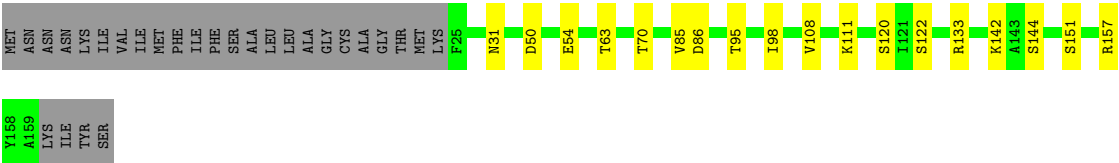
MET ARG LYS PHE ILE LEU SER LEU SER ILE ILE LEU LEU SER ALA LEU LEU VAL VAL ALA CYS SER SER ARG ASN HIS TYR GLY ASP THR GLY SER LEU ALA LEU LEU GLN MET MET ALA ASP SER LYS TYR THR ARG ALA GLN LYS LYS MET GLU LYS LEU LEU ILE ILE ARG GLU MET A58 L72

D91 R126 V134 T143 P161 ASN VAL THR LEU LEU PRO LYS THR LYS ALA CYS K173 C177 L211 H228 T229 D243 V246 L255 N258 K268 ASP GLU ASN LYS ALA LEU LEU ARG PHE LYS LYS MET GLU LYS LEU LEU ILE ILE ASN ASN ALA LYS ILE VAL

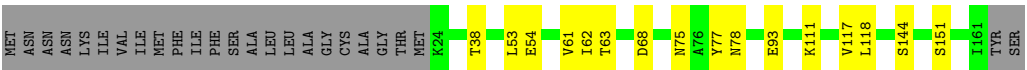
Chain Cd:  77% 7% 15%



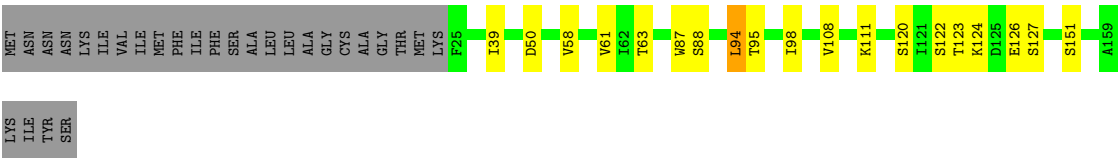
• Molecule 3: DotD



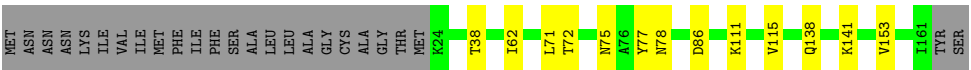
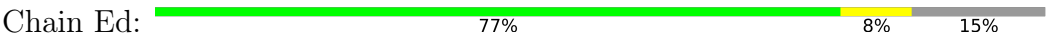
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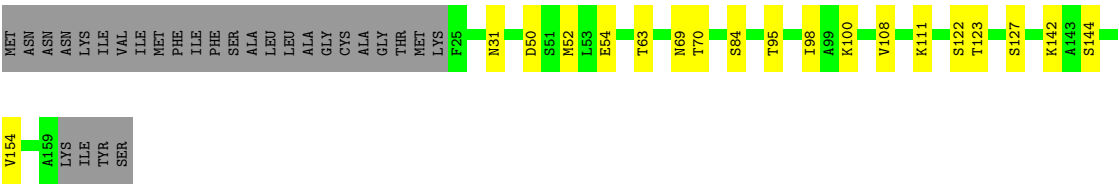
• Molecule 3: DotD



• Molecule 3: DotD

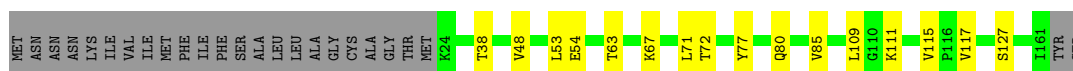


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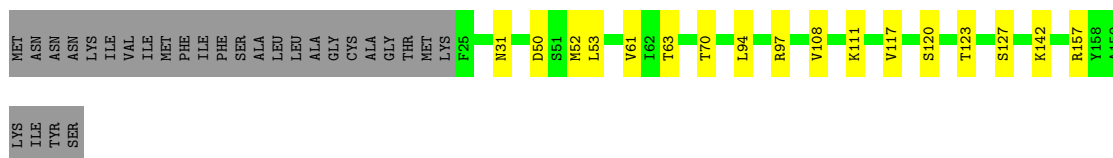
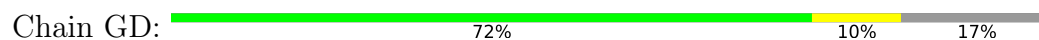


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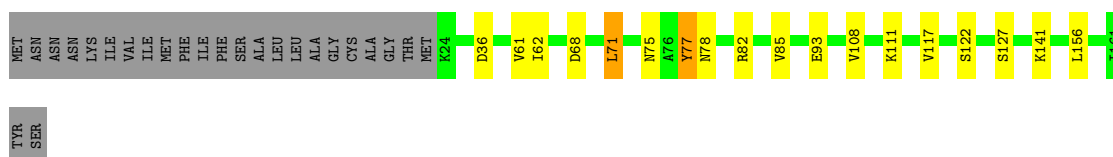
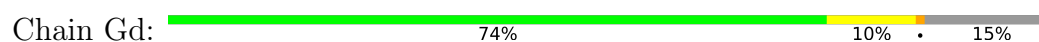




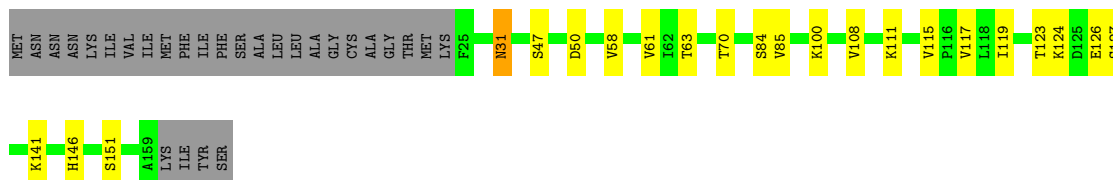
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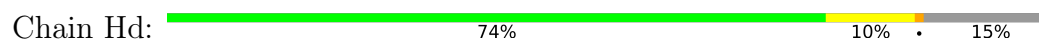
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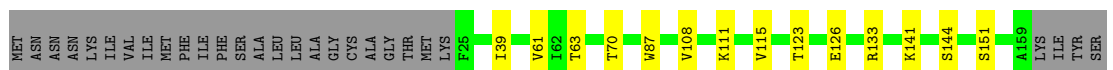
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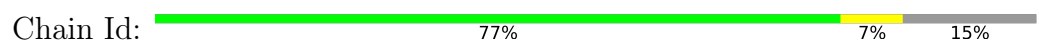
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- Molecule 3: DotD

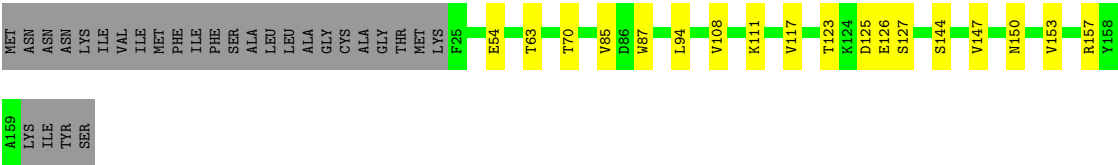


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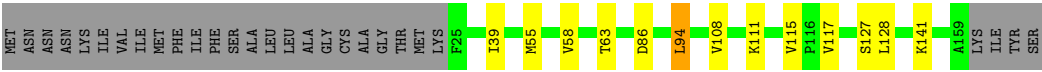
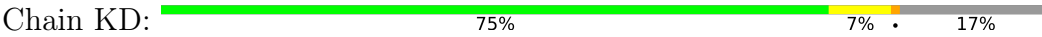
• Molecule 3: DotD



• Molecule 3: DotD



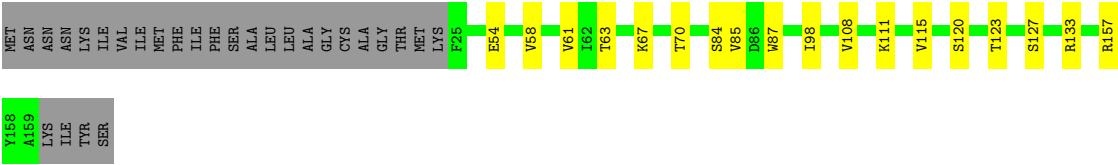
• Molecule 3: DotD



• Molecule 3: DotD



• Molecule 3: DotD



• Molecule 3: DotD





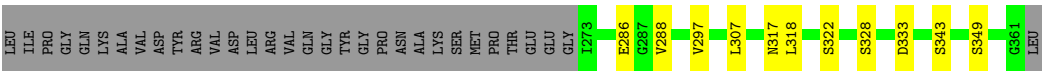
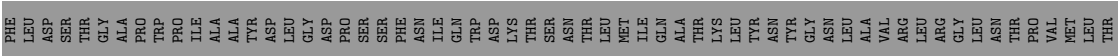
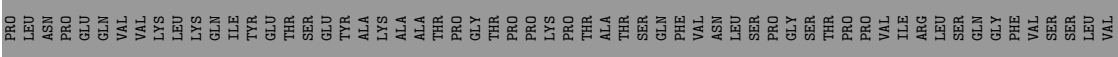
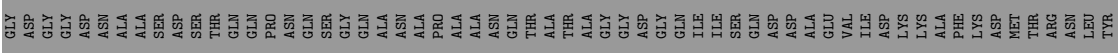
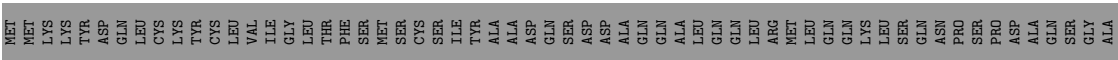
● Molecule 3: DotD



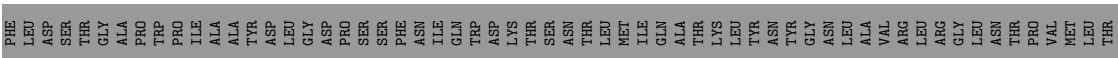
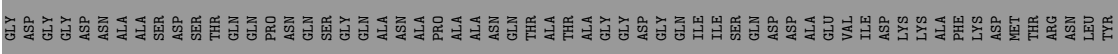
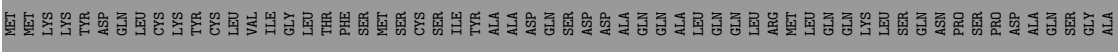
● Molecule 3: DotD

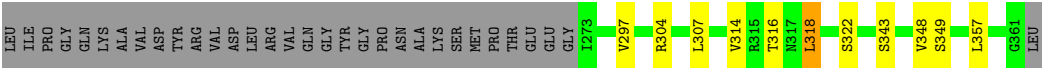


● Molecule 4: Type IV secretion protein IcmK

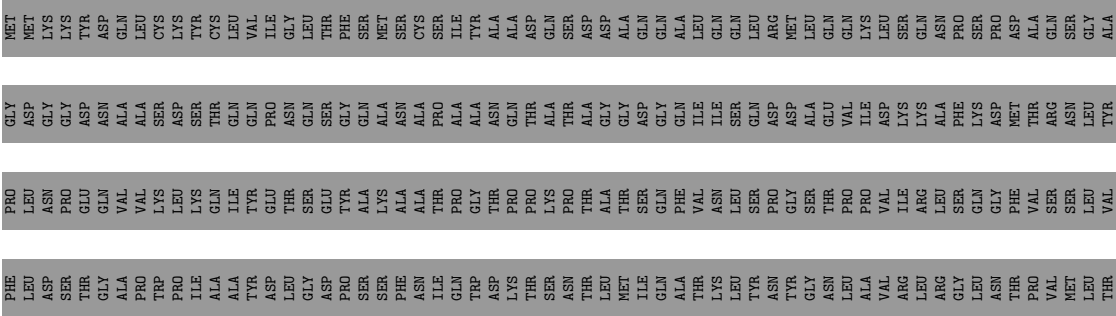


● Molecule 4: Type IV secretion protein IcmK

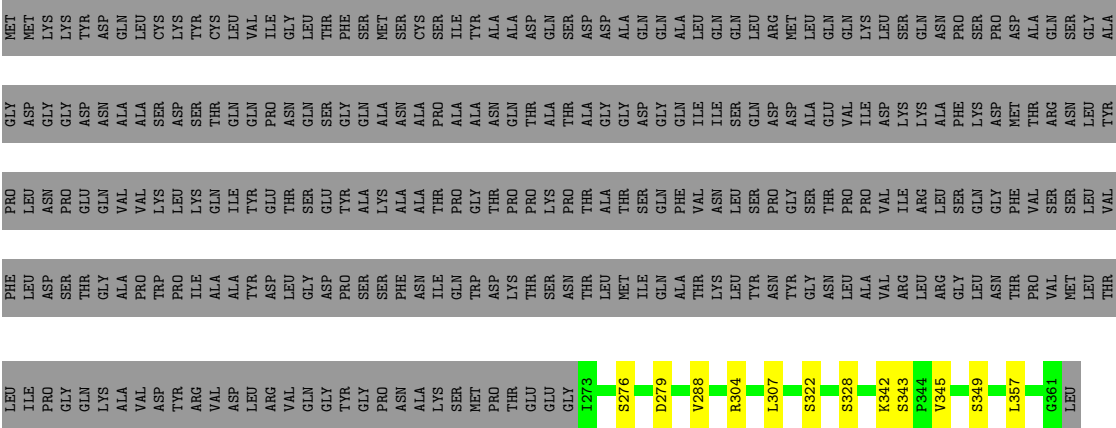




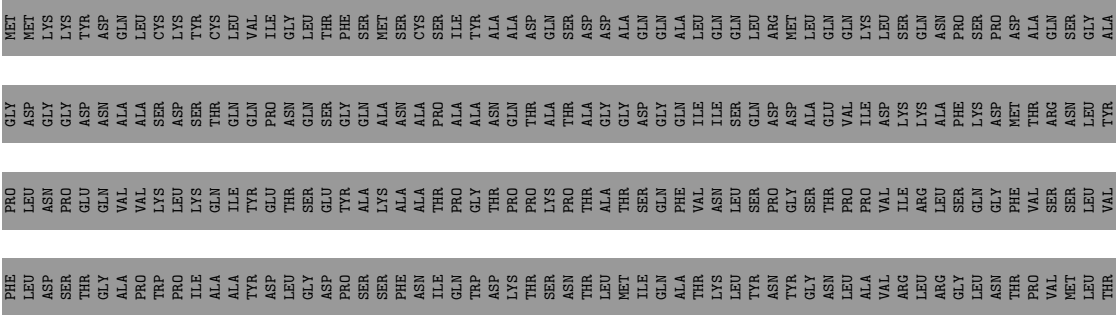
• Molecule 4: Type IV secretion protein IcmK

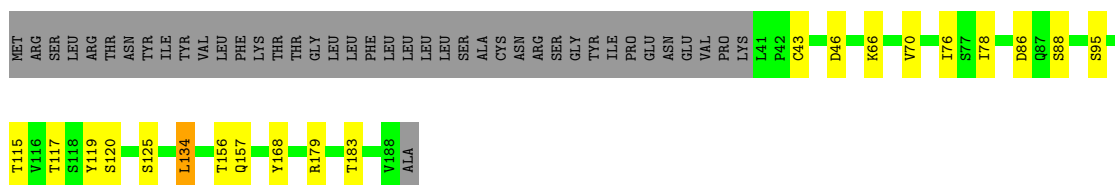


• Molecule 4: Type IV secretion protein IcmK



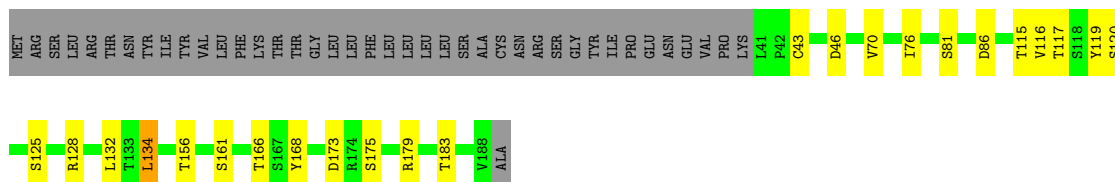
• Molecule 4: Type IV secretion protein IcmK





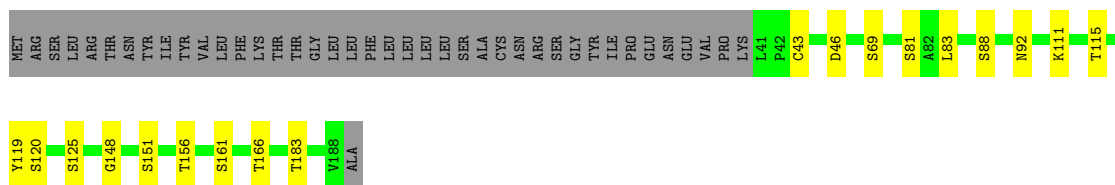
- Molecule 5: Inner membrane lipoprotein YiaD

Chain CK: 66% 12% 22%



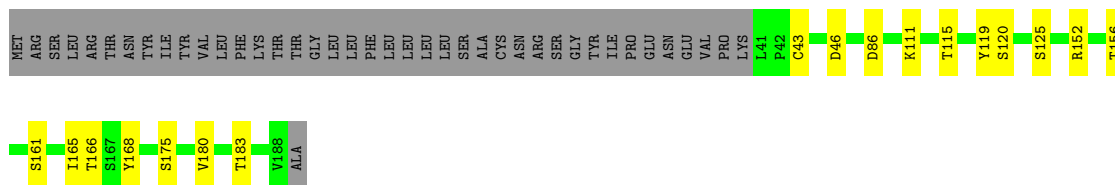
- Molecule 5: Inner membrane lipoprotein YiaD

Chain DK: 69% 10% 22%



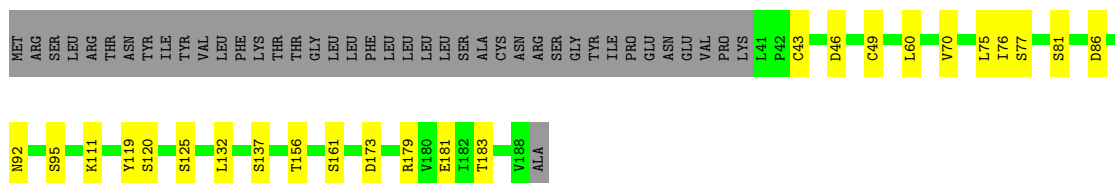
- Molecule 5: Inner membrane lipoprotein YiaD

Chain EK: 69% 9% 22%



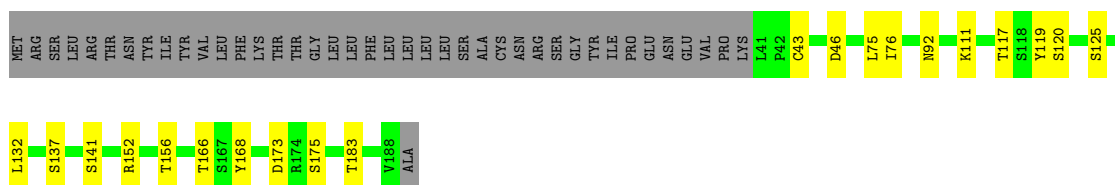
- Molecule 5: Inner membrane lipoprotein YiaD

Chain FK: 66% 13% 22%



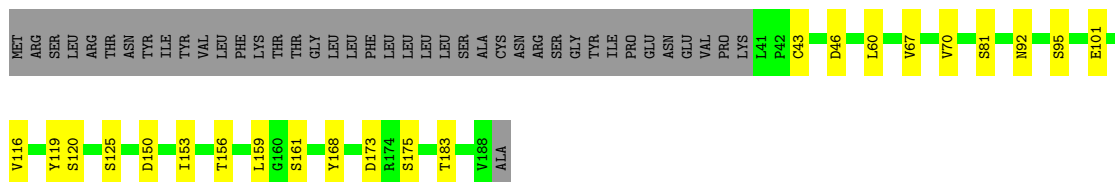
- Molecule 5: Inner membrane lipoprotein YiaD

Chain GK: 68% 11% 22%



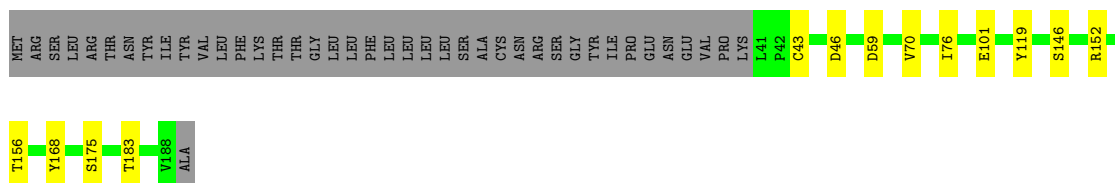
- Molecule 5: Inner membrane lipoprotein YiaD

Chain HK: 67% 12% 22%



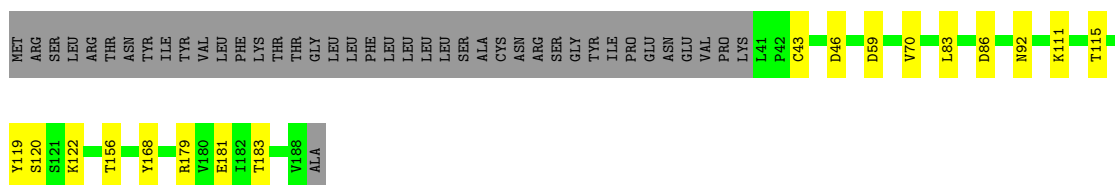
- Molecule 5: Inner membrane lipoprotein YiaD

Chain IK: 71% 7% 22%



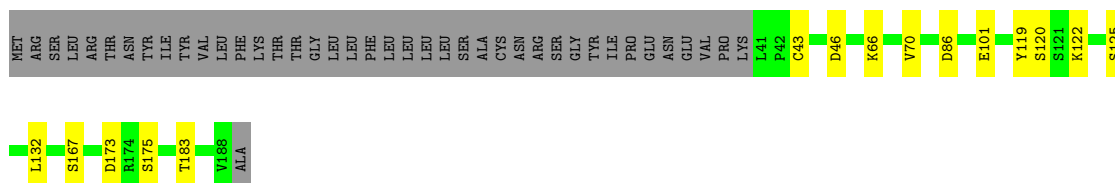
- Molecule 5: Inner membrane lipoprotein YiaD

Chain JK: 69% 9% 22%



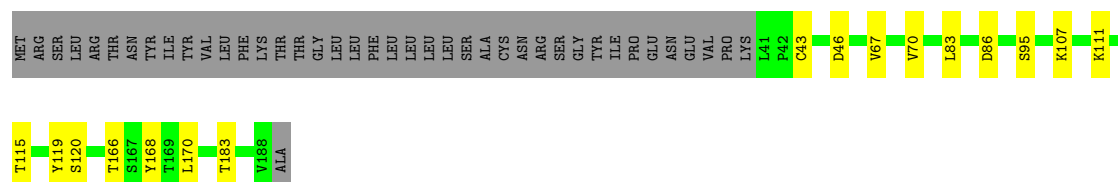
- Molecule 5: Inner membrane lipoprotein YiaD

Chain KK: 70% 8% 22%

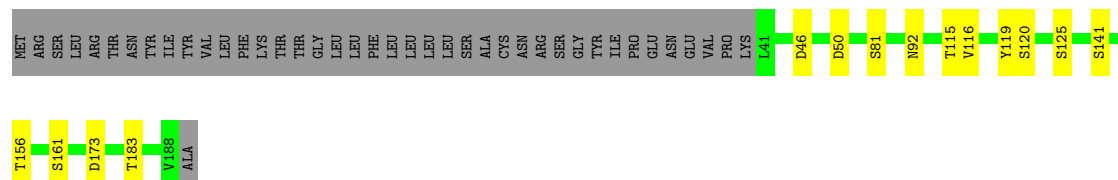
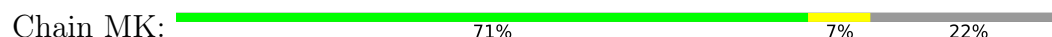


- Molecule 5: Inner membrane lipoprotein YiaD

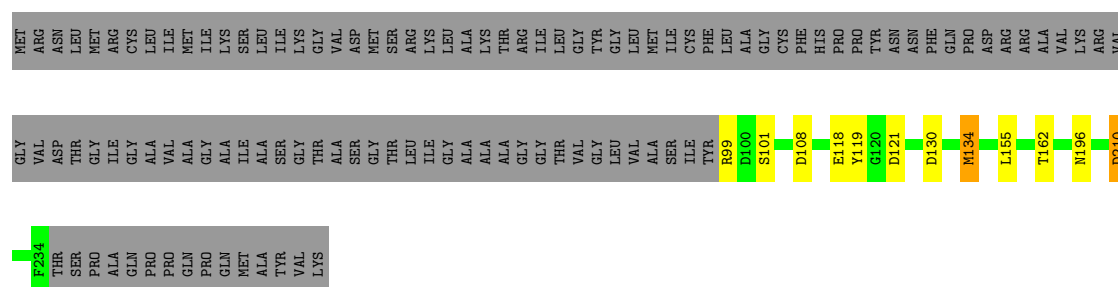
Chain LK: 70% 8% 22%



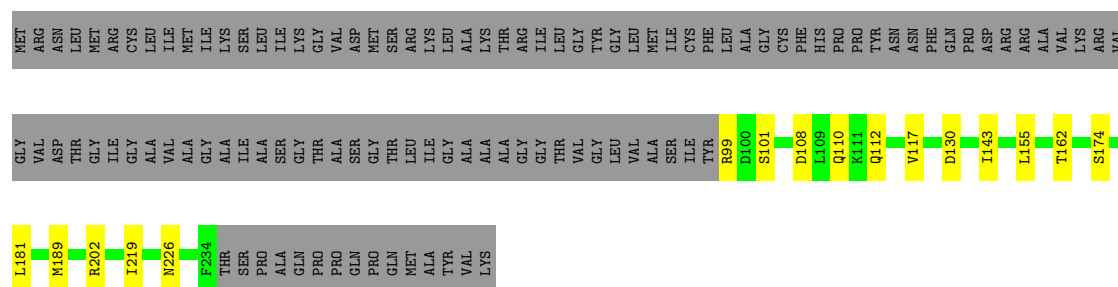
- Molecule 5: Inner membrane lipoprotein YiaD



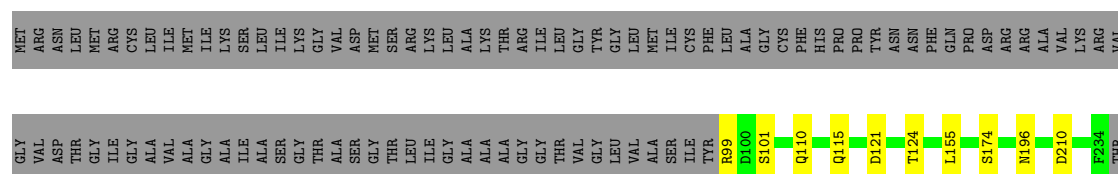
- Molecule 6: Outer membrane protein, OmpA family protein



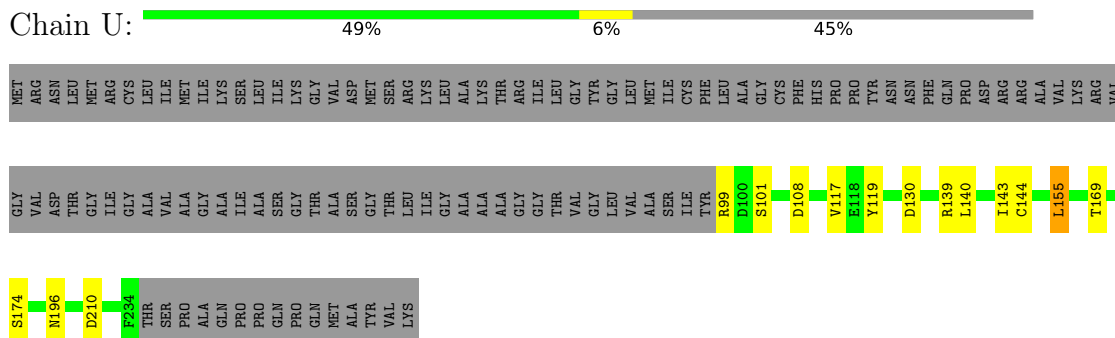
- Molecule 6: Outer membrane protein, OmpA family protein



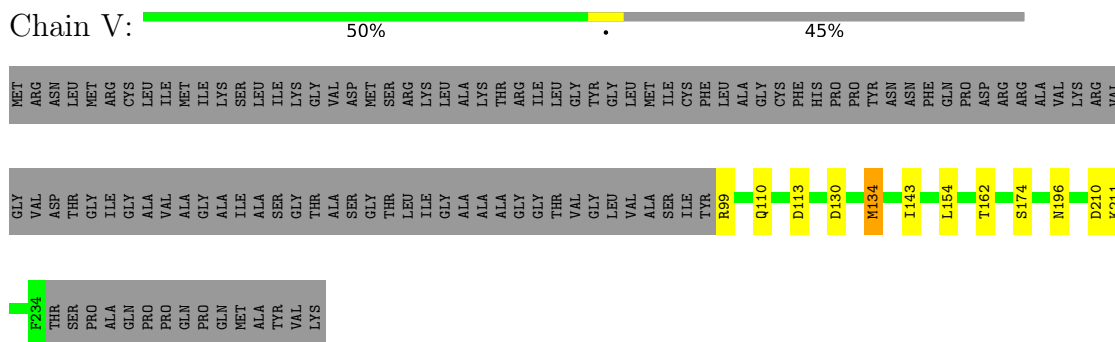
- Molecule 6: Outer membrane protein, OmpA family protein



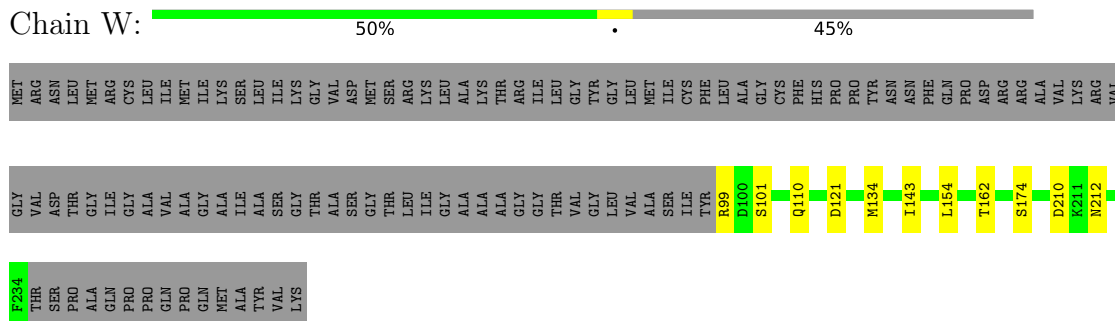
- Molecule 6: Outer membrane protein, OmpA family protein



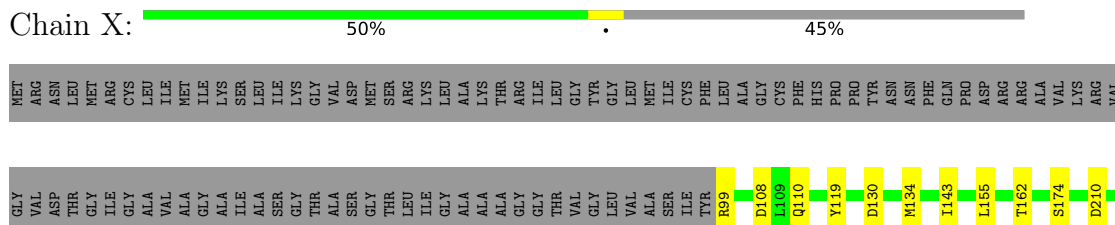
- Molecule 6: Outer membrane protein, OmpA family protein



- Molecule 6: Outer membrane protein, OmpA family protein



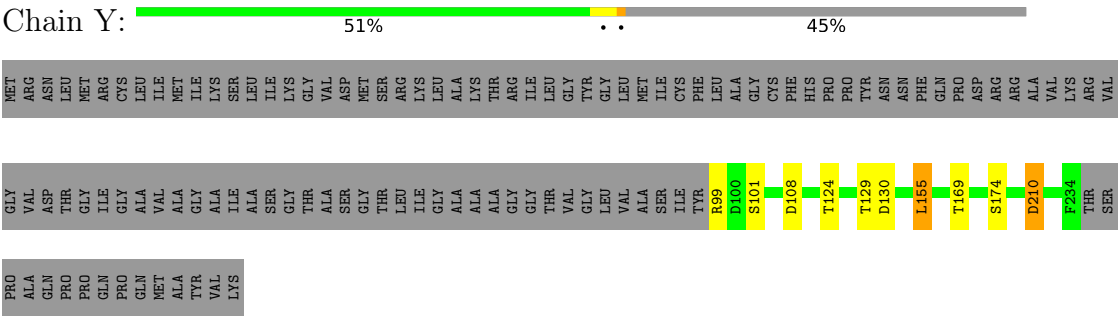
- Molecule 6: Outer membrane protein, OmpA family protein



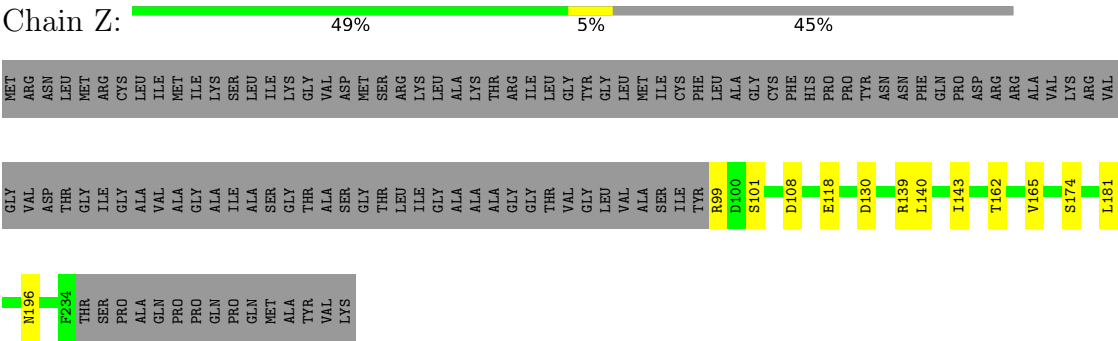
F234

THR
SER
PRO
LEU
ALA
GLN
PRO
PRO
PRO
PRO
GLN
GLN
MET
ALA
TYR
VAL
LYS

- Molecule 6: Outer membrane protein, OmpA family protein



- Molecule 6: Outer membrane protein, OmpA family protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12200	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 ($e^-/\text{\AA}^2$)	58.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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
2	AC	0.51	0/1629	0.67	0/2214
2	BC	0.51	0/1629	0.70	1/2214 (0.0%)
2	CC	0.52	0/1629	0.73	2/2214 (0.1%)
2	DC	0.49	0/1629	0.67	0/2214
2	EC	0.53	0/1629	0.74	2/2214 (0.1%)
2	FC	0.52	0/1629	0.71	2/2214 (0.1%)
2	GC	0.52	0/1629	0.78	3/2214 (0.1%)
2	HC	0.52	0/1629	0.79	3/2214 (0.1%)
2	IC	0.52	0/1629	0.74	2/2214 (0.1%)
2	JC	0.51	0/1629	0.74	2/2214 (0.1%)
2	KC	0.53	0/1629	0.75	1/2214 (0.0%)
2	LC	0.53	0/1629	0.71	1/2214 (0.0%)
2	MC	0.53	0/1629	0.73	3/2214 (0.1%)
3	AD	0.49	0/1060	0.76	3/1441 (0.2%)
3	Ad	0.50	0/1086	0.81	2/1474 (0.1%)
3	BD	0.50	0/1060	0.80	3/1441 (0.2%)
3	Bd	0.52	0/1086	0.78	1/1474 (0.1%)
3	CD	0.50	0/1060	0.80	1/1441 (0.1%)
3	Cd	0.53	1/1086 (0.1%)	0.82	2/1474 (0.1%)
3	DD	0.50	0/1060	0.78	2/1441 (0.1%)
3	Dd	0.53	0/1086	0.80	1/1474 (0.1%)
3	ED	0.52	0/1060	0.77	2/1441 (0.1%)
3	Ed	0.51	0/1086	0.77	1/1474 (0.1%)
3	FD	0.52	0/1060	0.75	1/1441 (0.1%)
3	Fd	0.55	0/1086	0.78	2/1474 (0.1%)
3	GD	0.50	0/1060	0.79	2/1441 (0.1%)
3	Gd	0.49	0/1086	0.78	2/1474 (0.1%)
3	HD	0.56	1/1060 (0.1%)	0.78	1/1441 (0.1%)
3	Hd	0.53	0/1086	0.82	2/1474 (0.1%)
3	ID	0.49	0/1060	0.76	0/1441
3	Id	0.52	0/1086	0.82	2/1474 (0.1%)
3	JD	0.49	0/1060	0.75	2/1441 (0.1%)
3	Jd	0.54	0/1086	0.82	2/1474 (0.1%)
3	KD	0.51	0/1060	0.77	3/1441 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	Kd	0.52	0/1086	0.77	1/1474 (0.1%)
3	LD	0.55	0/1060	0.80	1/1441 (0.1%)
3	Ld	0.51	0/1086	0.77	2/1474 (0.1%)
3	MD	0.51	0/1060	0.76	2/1441 (0.1%)
3	Md	0.53	0/1086	0.77	1/1474 (0.1%)
4	AH	0.61	0/695	0.79	0/947
4	BH	0.59	0/695	0.82	0/947
4	CH	0.59	0/695	0.78	0/947
4	DH	0.57	0/695	0.77	0/947
4	EH	0.61	0/695	0.79	1/947 (0.1%)
4	FH	0.59	0/695	0.76	0/947
4	GH	0.58	0/695	0.77	2/947 (0.2%)
4	HH	0.55	0/695	0.72	0/947
4	IH	0.57	0/695	0.76	1/947 (0.1%)
4	JH	0.64	0/695	0.79	1/947 (0.1%)
4	KH	0.59	0/695	0.81	1/947 (0.1%)
4	LH	0.62	0/695	0.80	1/947 (0.1%)
4	MH	0.59	0/695	0.78	0/947
5	AK	0.54	0/1171	0.70	0/1583
5	BK	0.52	0/1171	0.73	1/1583 (0.1%)
5	CK	0.52	0/1171	0.75	3/1583 (0.2%)
5	DK	0.53	0/1171	0.70	1/1583 (0.1%)
5	EK	0.53	0/1171	0.71	0/1583
5	FK	0.51	0/1171	0.73	1/1583 (0.1%)
5	GK	0.54	0/1171	0.74	1/1583 (0.1%)
5	HK	0.52	0/1171	0.70	0/1583
5	IK	0.53	0/1171	0.71	1/1583 (0.1%)
5	JK	0.53	0/1171	0.76	1/1583 (0.1%)
5	KK	0.53	0/1171	0.71	1/1583 (0.1%)
5	LK	0.53	0/1171	0.68	1/1583 (0.1%)
5	MK	0.50	0/1171	0.69	0/1583
6	N	0.52	0/1130	0.75	2/1522 (0.1%)
6	O	0.52	0/1130	0.71	0/1522
6	P	0.52	0/1130	0.74	0/1522
6	Q	0.49	0/1130	0.69	0/1522
6	R	0.50	0/1130	0.77	1/1522 (0.1%)
6	S	0.51	0/1130	0.71	0/1522
6	T	0.54	0/1130	0.74	1/1522 (0.1%)
6	U	0.49	0/1130	0.74	2/1522 (0.1%)
6	V	0.51	0/1130	0.77	1/1522 (0.1%)
6	W	0.52	0/1130	0.71	0/1522
6	X	0.53	0/1130	0.75	1/1522 (0.1%)
6	Y	0.54	0/1130	0.74	2/1522 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	Z	0.50	0/1130	0.69	0/1522
All	All	0.53	2/88023 (0.0%)	0.75	94/119353 (0.1%)

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
1	AX	0	2
1	AZ	0	2
1	BV	0	2
1	BX	0	2
1	BZ	0	2
1	CV	0	1
1	CX	0	2
1	CZ	0	1
1	DX	0	3
1	DZ	0	2
1	EX	0	3
1	EZ	0	1
1	FV	0	1
1	FX	0	3
1	FZ	0	1
1	GV	0	1
1	GX	0	2
1	GZ	0	1
1	HV	0	1
1	HX	0	2
1	HZ	0	1
1	IV	0	1
1	IX	0	2
1	IZ	0	1
1	JX	0	3
1	JZ	0	1
1	KV	0	1
1	KX	0	3
1	KZ	0	1
1	LX	0	3
1	LZ	0	2
1	MX	0	3
1	MZ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	NV	0	1
1	OV	0	2
1	PV	0	1
1	RV	0	1
2	BC	0	1
3	Bd	0	1
3	Ed	0	1
3	Fd	0	1
3	Id	0	1
3	Jd	0	1
3	Kd	0	1
3	Md	0	1
4	AH	0	1
4	BH	0	1
4	DH	0	2
4	EH	0	1
4	FH	0	1
4	GH	0	1
4	HH	0	1
4	IH	0	1
4	JH	0	1
4	KH	0	1
4	LH	0	1
5	DK	0	1
6	N	0	2
6	O	0	2
6	Q	0	2
6	T	0	1
6	V	0	2
6	W	0	1
6	X	0	1
6	Z	0	1
All	All	0	96

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Cd	58	VAL	CB-CG1	-5.97	1.40	1.52
3	HD	31	ASN	C-N	-5.41	1.21	1.34

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	JK	59	ASP	CB-CG-OD2	10.30	127.58	118.30
2	HC	117	LEU	CA-CB-CG	10.27	138.92	115.30
6	X	155	LEU	CA-CB-CG	9.98	138.26	115.30
6	V	113	ASP	CB-CG-OD1	9.90	127.21	118.30
2	GC	117	LEU	CA-CB-CG	9.13	136.30	115.30

There are no chirality outliers.

5 of 96 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BV	42	UNK	Peptide
1	BV	46	UNK	Peptide
1	CV	77	UNK	Peptide
1	FV	42	UNK	Peptide
1	GV	77	UNK	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	
2	AC	196/303 (65%)	190 (97%)	6 (3%)	0	100	100
2	BC	196/303 (65%)	189 (96%)	7 (4%)	0	100	100
2	CC	196/303 (65%)	189 (96%)	7 (4%)	0	100	100
2	DC	196/303 (65%)	187 (95%)	9 (5%)	0	100	100
2	EC	196/303 (65%)	187 (95%)	9 (5%)	0	100	100
2	FC	196/303 (65%)	187 (95%)	9 (5%)	0	100	100
2	GC	196/303 (65%)	189 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	HC	196/303 (65%)	190 (97%)	6 (3%)	0	100	100
2	IC	196/303 (65%)	191 (97%)	5 (3%)	0	100	100
2	JC	196/303 (65%)	187 (95%)	9 (5%)	0	100	100
2	KC	196/303 (65%)	189 (96%)	7 (4%)	0	100	100
2	LC	196/303 (65%)	188 (96%)	8 (4%)	0	100	100
2	MC	196/303 (65%)	191 (97%)	5 (3%)	0	100	100
3	AD	133/163 (82%)	127 (96%)	6 (4%)	0	100	100
3	Ad	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	BD	133/163 (82%)	125 (94%)	8 (6%)	0	100	100
3	Bd	136/163 (83%)	125 (92%)	11 (8%)	0	100	100
3	CD	133/163 (82%)	128 (96%)	5 (4%)	0	100	100
3	Cd	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	DD	133/163 (82%)	126 (95%)	7 (5%)	0	100	100
3	Dd	136/163 (83%)	127 (93%)	9 (7%)	0	100	100
3	ED	133/163 (82%)	125 (94%)	8 (6%)	0	100	100
3	Ed	136/163 (83%)	129 (95%)	7 (5%)	0	100	100
3	FD	133/163 (82%)	126 (95%)	7 (5%)	0	100	100
3	Fd	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	GD	133/163 (82%)	125 (94%)	8 (6%)	0	100	100
3	Gd	136/163 (83%)	128 (94%)	8 (6%)	0	100	100
3	HD	133/163 (82%)	128 (96%)	5 (4%)	0	100	100
3	Hd	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	ID	133/163 (82%)	129 (97%)	4 (3%)	0	100	100
3	Id	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	JD	133/163 (82%)	126 (95%)	7 (5%)	0	100	100
3	Jd	136/163 (83%)	127 (93%)	9 (7%)	0	100	100
3	KD	133/163 (82%)	127 (96%)	6 (4%)	0	100	100
3	Kd	136/163 (83%)	130 (96%)	6 (4%)	0	100	100
3	LD	133/163 (82%)	126 (95%)	7 (5%)	0	100	100
3	Ld	136/163 (83%)	126 (93%)	10 (7%)	0	100	100
3	MD	133/163 (82%)	128 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Md	136/163 (83%)	129 (95%)	7 (5%)	0	100	100
4	AH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	BH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	CH	87/361 (24%)	77 (88%)	10 (12%)	0	100	100
4	DH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	EH	87/361 (24%)	76 (87%)	11 (13%)	0	100	100
4	FH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	GH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	HH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	IH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	JH	87/361 (24%)	78 (90%)	9 (10%)	0	100	100
4	KH	87/361 (24%)	79 (91%)	8 (9%)	0	100	100
4	LH	87/361 (24%)	77 (88%)	10 (12%)	0	100	100
4	MH	87/361 (24%)	78 (90%)	9 (10%)	0	100	100
5	AK	146/189 (77%)	142 (97%)	4 (3%)	0	100	100
5	BK	146/189 (77%)	138 (94%)	8 (6%)	0	100	100
5	CK	146/189 (77%)	138 (94%)	8 (6%)	0	100	100
5	DK	146/189 (77%)	138 (94%)	8 (6%)	0	100	100
5	EK	146/189 (77%)	139 (95%)	7 (5%)	0	100	100
5	FK	146/189 (77%)	137 (94%)	9 (6%)	0	100	100
5	GK	146/189 (77%)	140 (96%)	6 (4%)	0	100	100
5	HK	146/189 (77%)	138 (94%)	8 (6%)	0	100	100
5	IK	146/189 (77%)	140 (96%)	6 (4%)	0	100	100
5	JK	146/189 (77%)	141 (97%)	5 (3%)	0	100	100
5	KK	146/189 (77%)	137 (94%)	9 (6%)	0	100	100
5	LK	146/189 (77%)	139 (95%)	7 (5%)	0	100	100
5	MK	146/189 (77%)	136 (93%)	10 (7%)	0	100	100
6	N	134/249 (54%)	123 (92%)	11 (8%)	0	100	100
6	O	134/249 (54%)	124 (92%)	10 (8%)	0	100	100
6	P	134/249 (54%)	126 (94%)	8 (6%)	0	100	100
6	Q	134/249 (54%)	127 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	R	134/249 (54%)	126 (94%)	8 (6%)	0	100	100
6	S	134/249 (54%)	127 (95%)	7 (5%)	0	100	100
6	T	134/249 (54%)	126 (94%)	8 (6%)	0	100	100
6	U	134/249 (54%)	128 (96%)	6 (4%)	0	100	100
6	V	134/249 (54%)	126 (94%)	8 (6%)	0	100	100
6	W	134/249 (54%)	124 (92%)	10 (8%)	0	100	100
6	X	134/249 (54%)	125 (93%)	9 (7%)	0	100	100
6	Y	134/249 (54%)	125 (93%)	9 (7%)	0	100	100
6	Z	134/249 (54%)	126 (94%)	8 (6%)	0	100	100
All	All	10816/18564 (58%)	10205 (94%)	611 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AC	169/257 (66%)	157 (93%)	12 (7%)	14	45
2	BC	169/257 (66%)	153 (90%)	16 (10%)	8	34
2	CC	169/257 (66%)	154 (91%)	15 (9%)	9	37
2	DC	169/257 (66%)	149 (88%)	20 (12%)	5	26
2	EC	169/257 (66%)	152 (90%)	17 (10%)	7	31
2	FC	169/257 (66%)	155 (92%)	14 (8%)	11	40
2	GC	169/257 (66%)	153 (90%)	16 (10%)	8	34
2	HC	169/257 (66%)	156 (92%)	13 (8%)	13	43
2	IC	169/257 (66%)	152 (90%)	17 (10%)	7	31
2	JC	169/257 (66%)	156 (92%)	13 (8%)	13	43
2	KC	169/257 (66%)	154 (91%)	15 (9%)	9	37
2	LC	169/257 (66%)	154 (91%)	15 (9%)	9	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	MC	169/257 (66%)	157 (93%)	12 (7%)	14	45
3	AD	116/139 (84%)	101 (87%)	15 (13%)	4	22
3	Ad	119/139 (86%)	105 (88%)	14 (12%)	5	26
3	BD	116/139 (84%)	99 (85%)	17 (15%)	3	18
3	Bd	119/139 (86%)	106 (89%)	13 (11%)	6	29
3	CD	116/139 (84%)	93 (80%)	23 (20%)	1	8
3	Cd	119/139 (86%)	109 (92%)	10 (8%)	11	40
3	DD	116/139 (84%)	100 (86%)	16 (14%)	3	21
3	Dd	119/139 (86%)	104 (87%)	15 (13%)	4	23
3	ED	116/139 (84%)	98 (84%)	18 (16%)	2	17
3	Ed	119/139 (86%)	108 (91%)	11 (9%)	9	36
3	FD	116/139 (84%)	98 (84%)	18 (16%)	2	17
3	Fd	119/139 (86%)	106 (89%)	13 (11%)	6	29
3	GD	116/139 (84%)	101 (87%)	15 (13%)	4	22
3	Gd	119/139 (86%)	101 (85%)	18 (15%)	3	17
3	HD	116/139 (84%)	95 (82%)	21 (18%)	1	11
3	Hd	119/139 (86%)	102 (86%)	17 (14%)	3	19
3	ID	116/139 (84%)	102 (88%)	14 (12%)	5	24
3	Id	119/139 (86%)	110 (92%)	9 (8%)	13	43
3	JD	116/139 (84%)	100 (86%)	16 (14%)	3	21
3	Jd	119/139 (86%)	105 (88%)	14 (12%)	5	26
3	KD	116/139 (84%)	105 (90%)	11 (10%)	8	34
3	Kd	119/139 (86%)	100 (84%)	19 (16%)	2	15
3	LD	116/139 (84%)	99 (85%)	17 (15%)	3	18
3	Ld	119/139 (86%)	103 (87%)	16 (13%)	4	21
3	MD	116/139 (84%)	102 (88%)	14 (12%)	5	24
3	Md	119/139 (86%)	97 (82%)	22 (18%)	1	10
4	AH	75/300 (25%)	65 (87%)	10 (13%)	4	22
4	BH	75/300 (25%)	64 (85%)	11 (15%)	3	18
4	CH	75/300 (25%)	67 (89%)	8 (11%)	6	30
4	DH	75/300 (25%)	65 (87%)	10 (13%)	4	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	EH	75/300 (25%)	65 (87%)	10 (13%)	4	22
4	FH	75/300 (25%)	69 (92%)	6 (8%)	12	42
4	GH	75/300 (25%)	66 (88%)	9 (12%)	5	25
4	HH	75/300 (25%)	69 (92%)	6 (8%)	12	42
4	IH	75/300 (25%)	65 (87%)	10 (13%)	4	22
4	JH	75/300 (25%)	64 (85%)	11 (15%)	3	18
4	KH	75/300 (25%)	67 (89%)	8 (11%)	6	30
4	LH	75/300 (25%)	64 (85%)	11 (15%)	3	18
4	MH	75/300 (25%)	64 (85%)	11 (15%)	3	18
5	AK	126/163 (77%)	108 (86%)	18 (14%)	3	19
5	BK	126/163 (77%)	106 (84%)	20 (16%)	2	16
5	CK	126/163 (77%)	105 (83%)	21 (17%)	2	14
5	DK	126/163 (77%)	110 (87%)	16 (13%)	4	23
5	EK	126/163 (77%)	109 (86%)	17 (14%)	4	21
5	FK	126/163 (77%)	103 (82%)	23 (18%)	1	10
5	GK	126/163 (77%)	107 (85%)	19 (15%)	3	17
5	HK	126/163 (77%)	104 (82%)	22 (18%)	2	12
5	IK	126/163 (77%)	114 (90%)	12 (10%)	8	34
5	JK	126/163 (77%)	110 (87%)	16 (13%)	4	23
5	KK	126/163 (77%)	112 (89%)	14 (11%)	6	28
5	LK	126/163 (77%)	111 (88%)	15 (12%)	5	25
5	MK	126/163 (77%)	112 (89%)	14 (11%)	6	28
6	N	118/203 (58%)	108 (92%)	10 (8%)	10	40
6	O	118/203 (58%)	104 (88%)	14 (12%)	5	25
6	P	118/203 (58%)	108 (92%)	10 (8%)	10	40
6	Q	118/203 (58%)	107 (91%)	11 (9%)	9	35
6	R	118/203 (58%)	108 (92%)	10 (8%)	10	40
6	S	118/203 (58%)	105 (89%)	13 (11%)	6	29
6	T	118/203 (58%)	102 (86%)	16 (14%)	3	21
6	U	118/203 (58%)	104 (88%)	14 (12%)	5	25
6	V	118/203 (58%)	108 (92%)	10 (8%)	10	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	W	118/203 (58%)	108 (92%)	10 (8%)	10	40
6	X	118/203 (58%)	109 (92%)	9 (8%)	13	43
6	Y	118/203 (58%)	108 (92%)	10 (8%)	10	40
6	Z	118/203 (58%)	106 (90%)	12 (10%)	7	31
All	All	9399/15613 (60%)	8301 (88%)	1098 (12%)	9	26

5 of 1098 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	MK	183	THR
6	N	119	TYR
5	MK	173	ASP
6	U	143	ILE
3	FD	52	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
6	V	212	ASN
6	W	177	HIS
6	Z	112	GLN
2	JC	241	HIS
2	JC	103	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-22070. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.