



wwPDB EM Validation Summary Report ⓘ

Feb 25, 2024 – 08:06 AM EST

PDB ID : 6X6K
EMDB ID : EMD-22076
Title : Cryo-EM Structure of the Helicobacter pylori dCag3 OMC
Authors : Sheedlo, M.J.; Chung, J.M.; Sawhney, N.; Durie, C.L.; Cover, T.L.; Ohi, M.D.;
Lacy, D.B.
Deposited on : 2020-05-28
Resolution : 3.10 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:

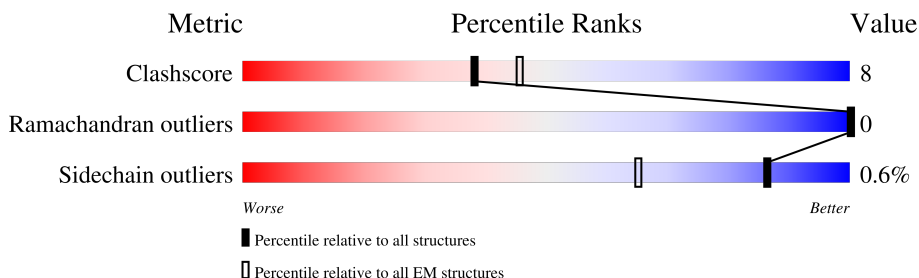
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 3.10 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.






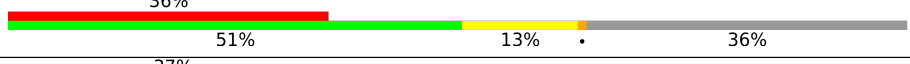

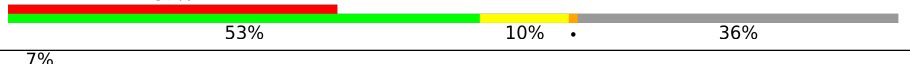
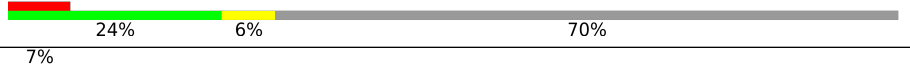







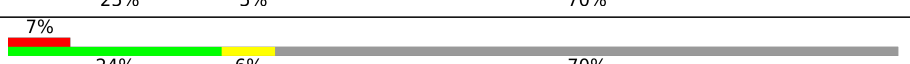


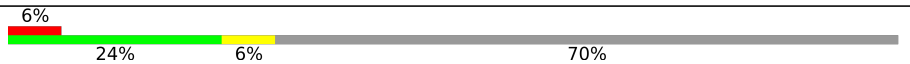



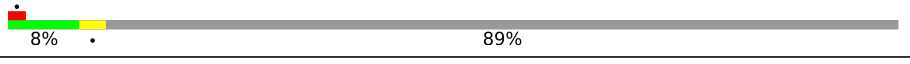
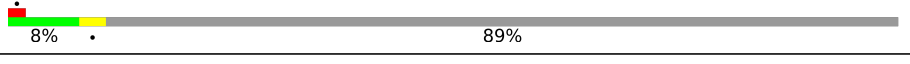
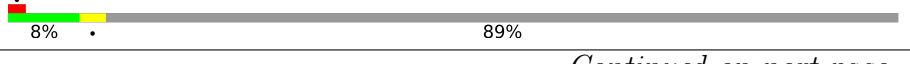

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	AT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">38%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">53%</div> <div style="text-align: center;">11%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	BT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">36%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">12%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	CT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">36%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">51%</div> <div style="text-align: center;">12%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	DT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">37%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">12%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	ET	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">36%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">53%</div> <div style="text-align: center;">11%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	FT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">37%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">51%</div> <div style="text-align: center;">13%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	GT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">38%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">53%</div> <div style="text-align: center;">10%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>
1	HT	278	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">37%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">12%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">36%</div> </div>










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Mol	Chain	Length	Quality of chain
1	IT	278	
1	JT	278	
1	KT	278	
1	LT	278	
1	MT	278	
1	NT	278	
2	AX	522	
2	BX	522	
2	CX	522	
2	DX	522	
2	EX	522	
2	FX	522	
2	GX	522	
2	HX	522	
2	IX	522	
2	JX	522	
2	KX	522	
2	LX	522	
2	MX	522	
2	NX	522	
3	AY	1927	
3	BY	1927	
3	CY	1927	
3	DY	1927	
3	EY	1927	

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Mol	Chain	Length	Quality of chain
3	FY	1927	 8% 89%
3	GY	1927	 8% 89%
3	HY	1927	 8% 89%
3	IY	1927	 8% 89%
3	JY	1927	 8% 89%
3	KY	1927	 8% 89%
3	LY	1927	 8% 89%
3	MY	1927	 8% 89%
3	NY	1927	 8% 89%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 60970 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 Cag pathogenicity island protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AT	179	1502	957	261	282	2	0	0
1	BT	179	1502	957	261	282	2	0	0
1	CT	179	1502	957	261	282	2	0	0
1	DT	179	1502	957	261	282	2	0	0
1	ET	179	1502	957	261	282	2	0	0
1	FT	179	1502	957	261	282	2	0	0
1	GT	179	1502	957	261	282	2	0	0
1	HT	179	1502	957	261	282	2	0	0
1	IT	179	1502	957	261	282	2	0	0
1	JT	179	1502	957	261	282	2	0	0
1	KT	179	1502	957	261	282	2	0	0
1	LT	179	1502	957	261	282	2	0	0
1	MT	179	1502	957	261	282	2	0	0
1	NT	179	1502	957	261	282	2	0	0

- Molecule 2 is a protein called Type IV secretion system apparatus protein CagX.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AX	155	1275	819	222	231	3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	CX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	DX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	EX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	FX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	GX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	HX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	IX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	JX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	KX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	LX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	MX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		
2	NX	155	Total	C	N	O	S	0	0
			1275	819	222	231	3		

- Molecule 3 is a protein called Cag pathogenicity island protein (Cag7).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	BY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	CY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	DY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	EY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	FY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		

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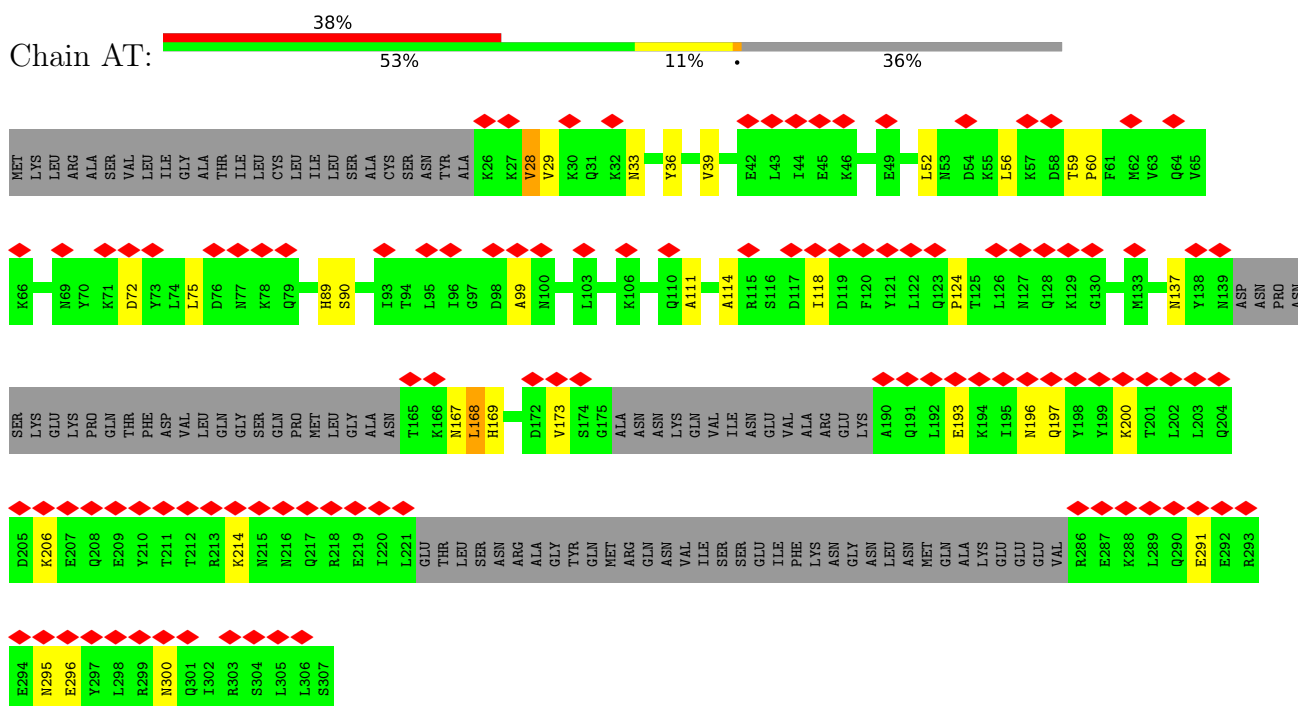
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	GY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	HY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	IY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	JY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	KY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	LY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	MY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		
3	NY	209	Total	C	N	O	S	0	0
			1578	1014	255	300	9		

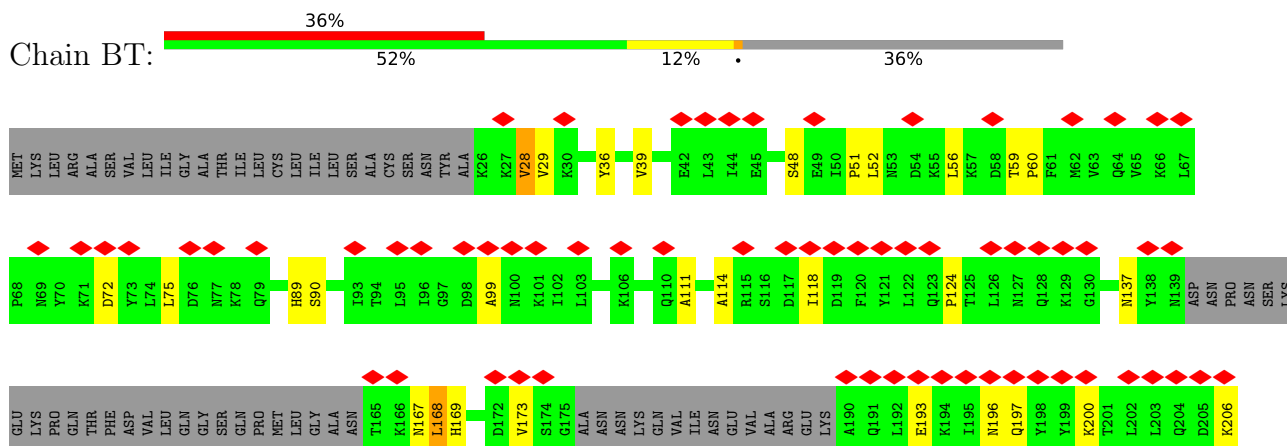
3 Residue-property plots

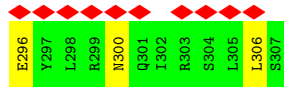
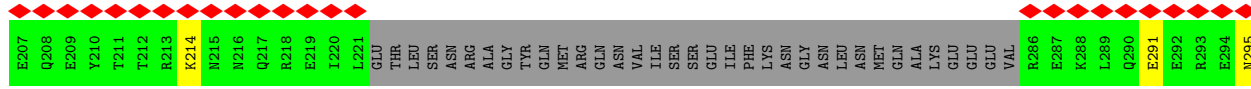
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Cag pathogenicity island protein

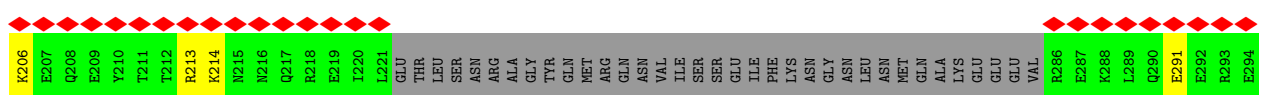
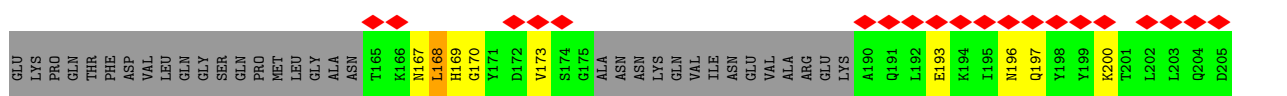
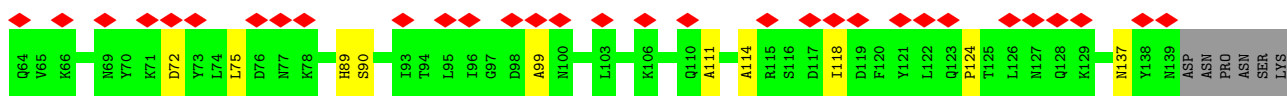
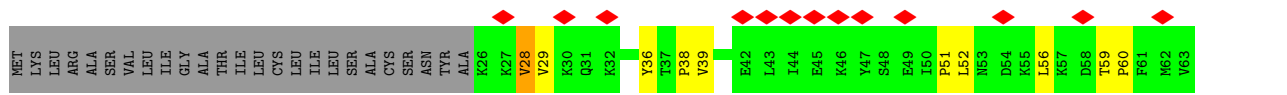


- Molecule 1: Cag pathogenicity island protein

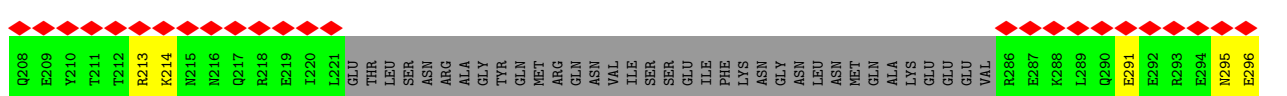
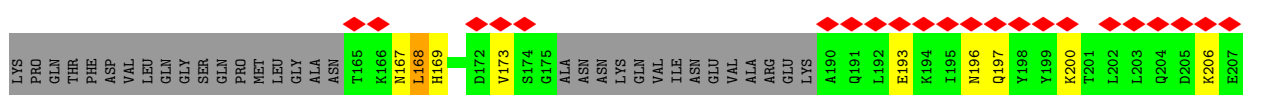
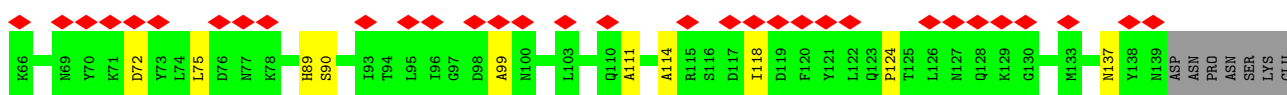
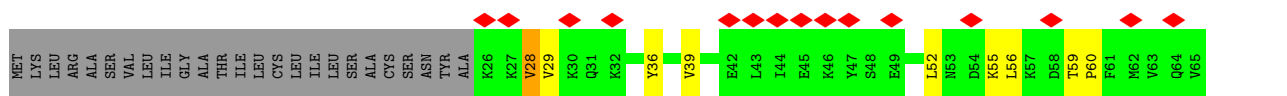


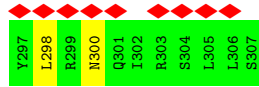


• Molecule 1: Cag pathogenicity island protein

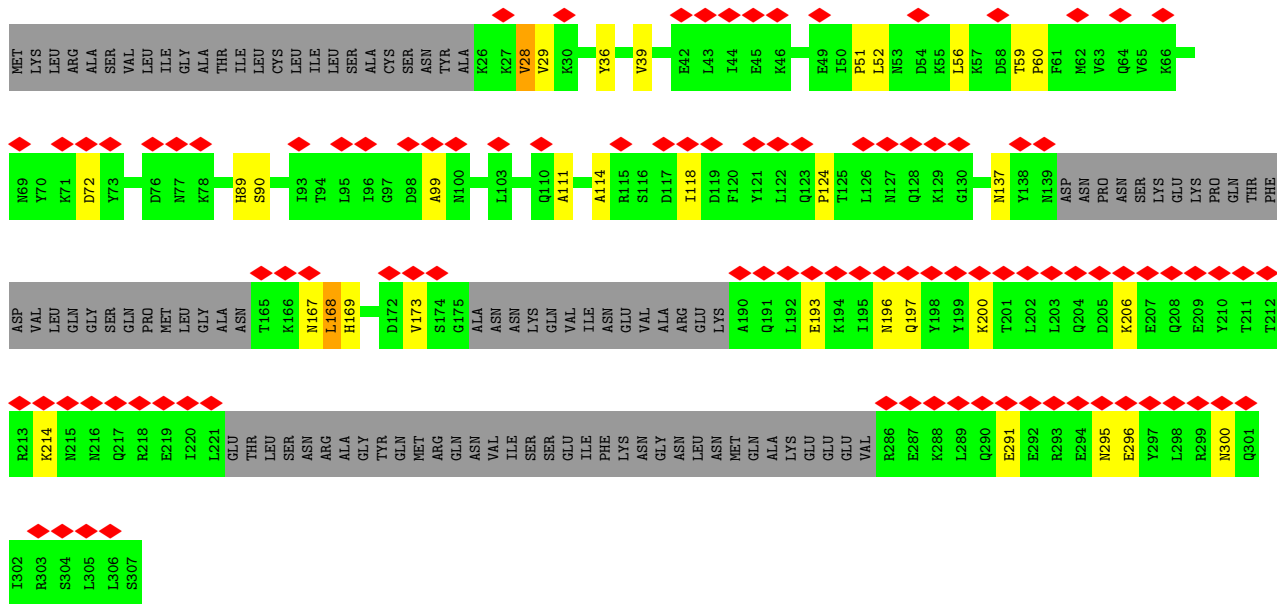


• Molecule 1: Cag pathogenicity island protein

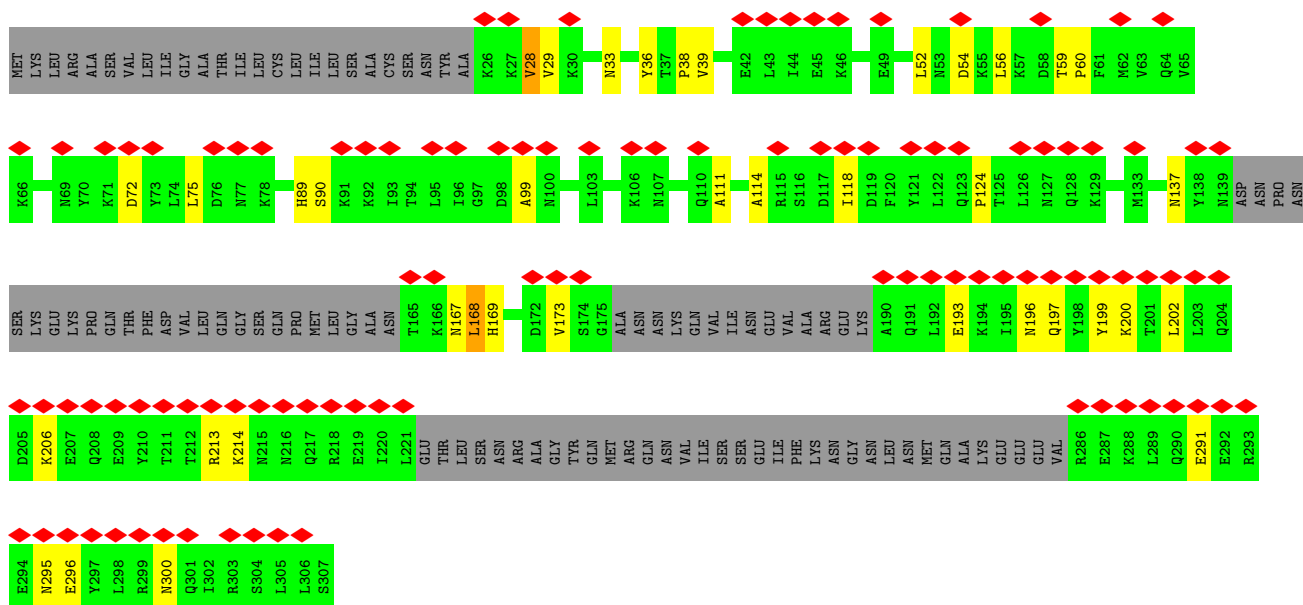




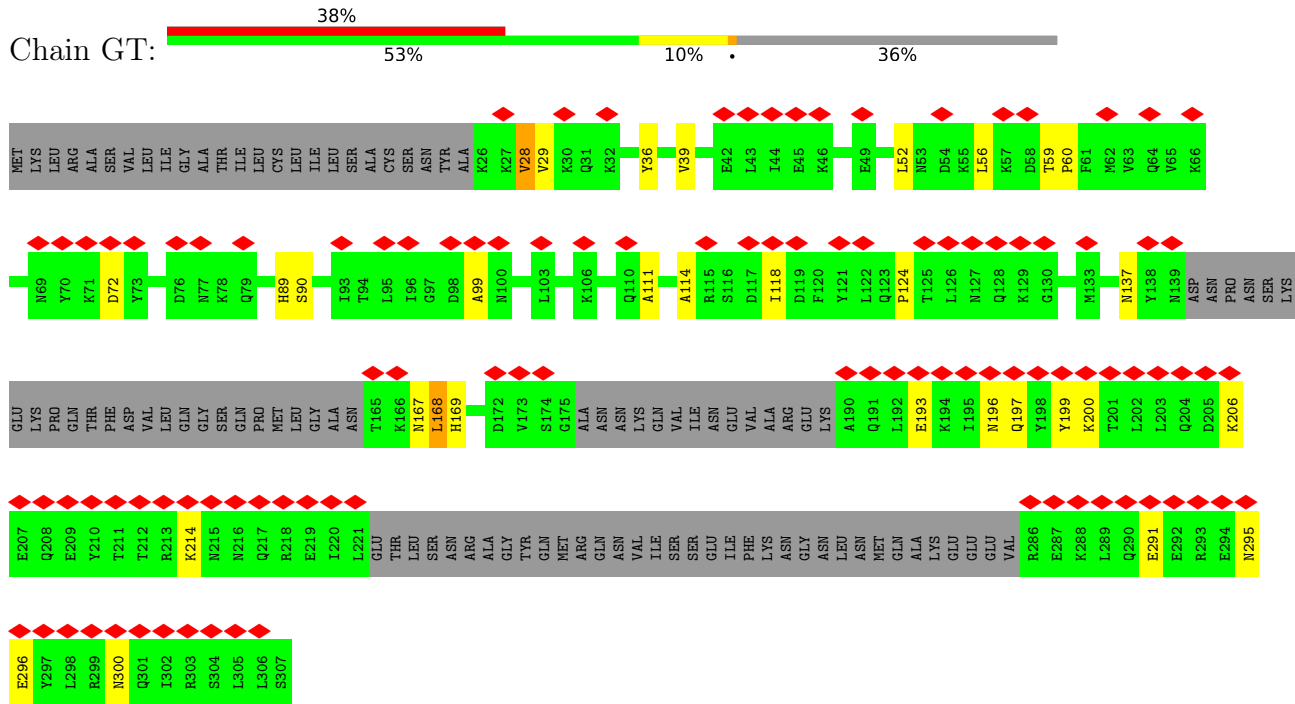
• Molecule 1: Cag pathogenicity island protein



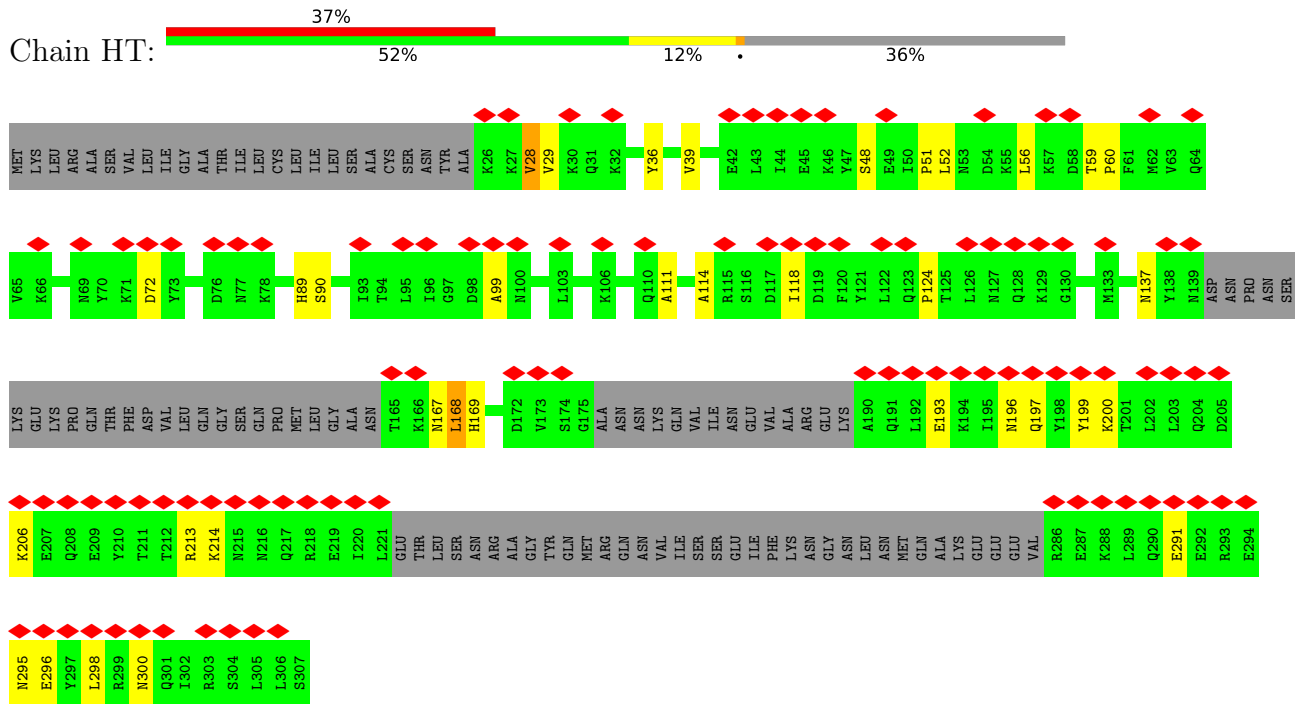
• Molecule 1: Cag pathogenicity island protein



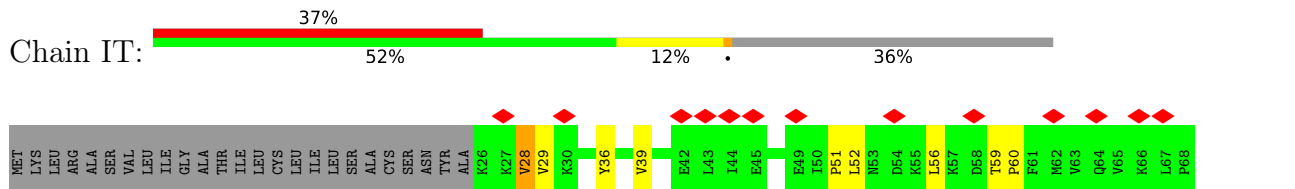
• Molecule 1: Cag pathogenicity island protein

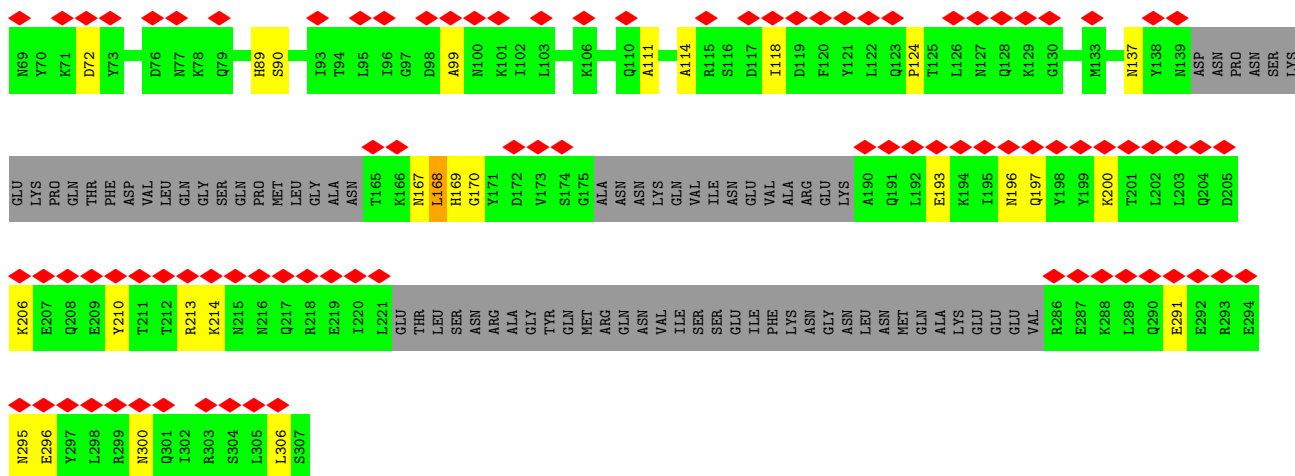


• Molecule 1: Cag pathogenicity island protein

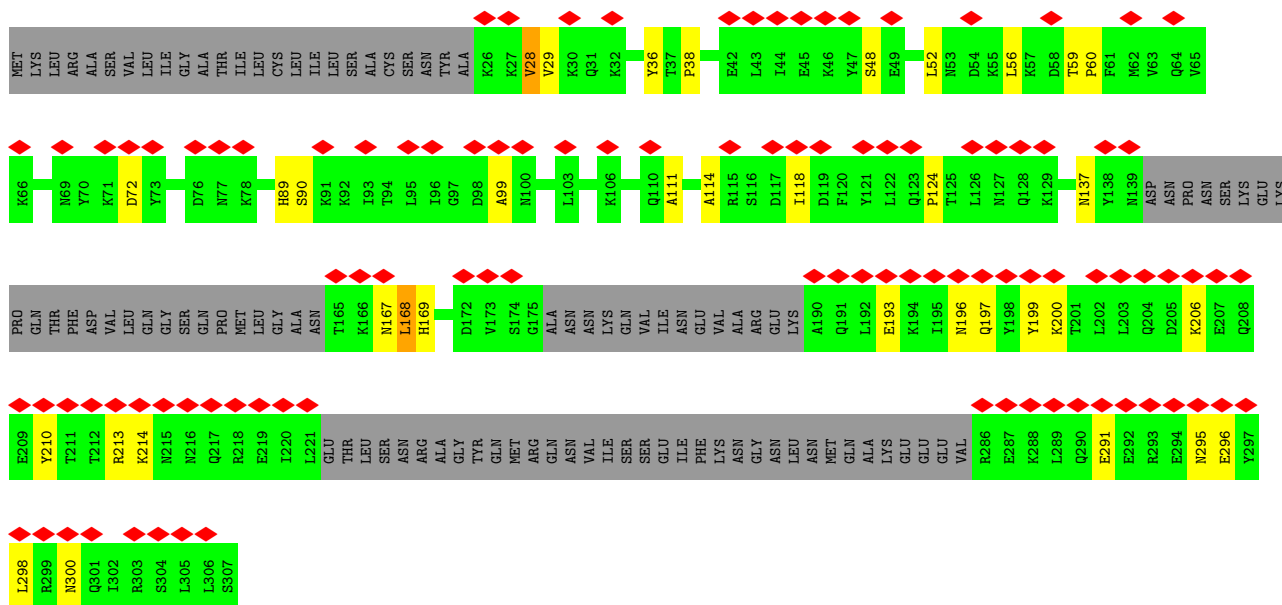


• Molecule 1: Cag pathogenicity island protein

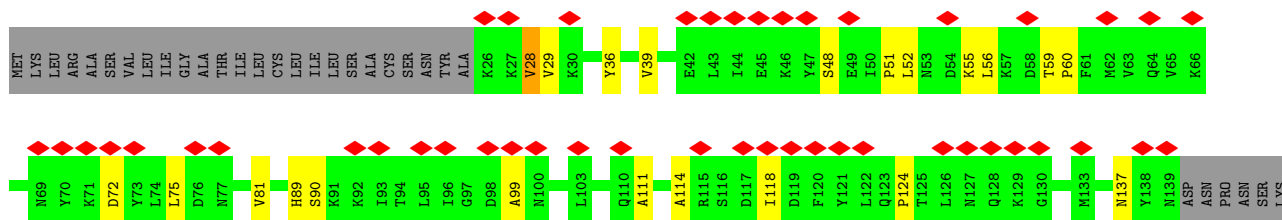
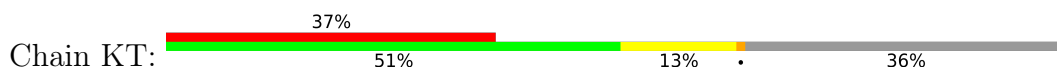


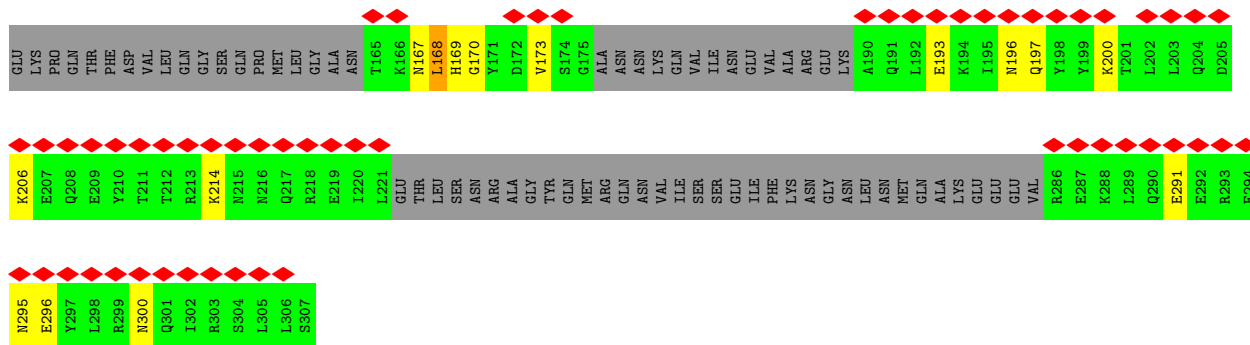


• Molecule 1: Cag pathogenicity island protein

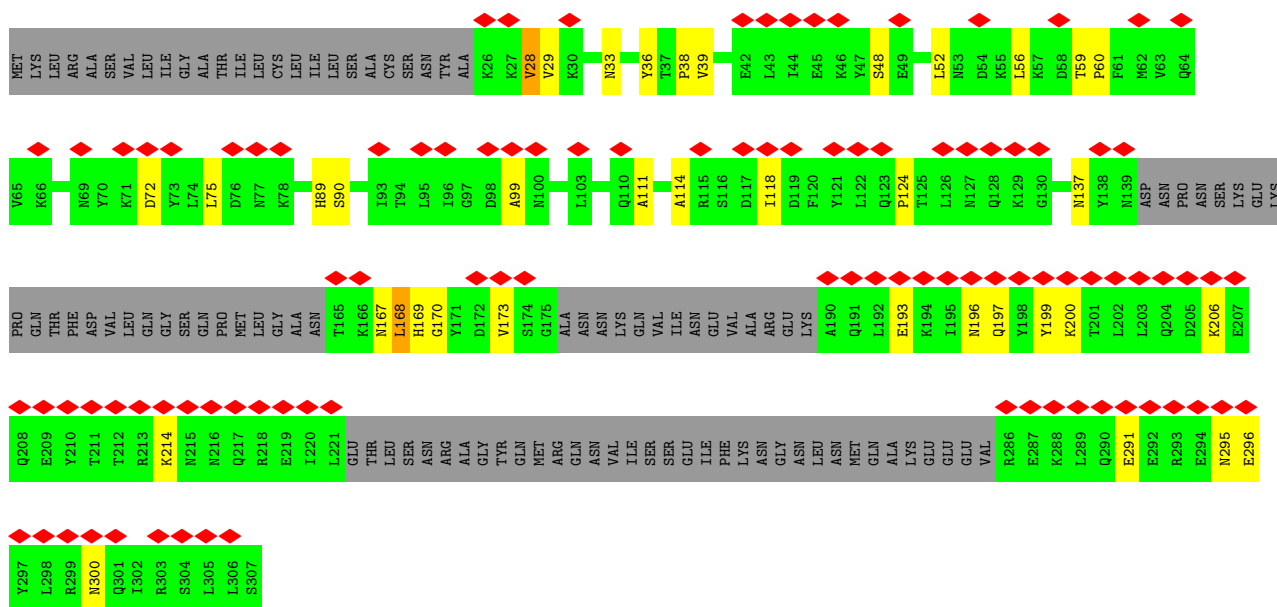


• Molecule 1: Cag pathogenicity island protein

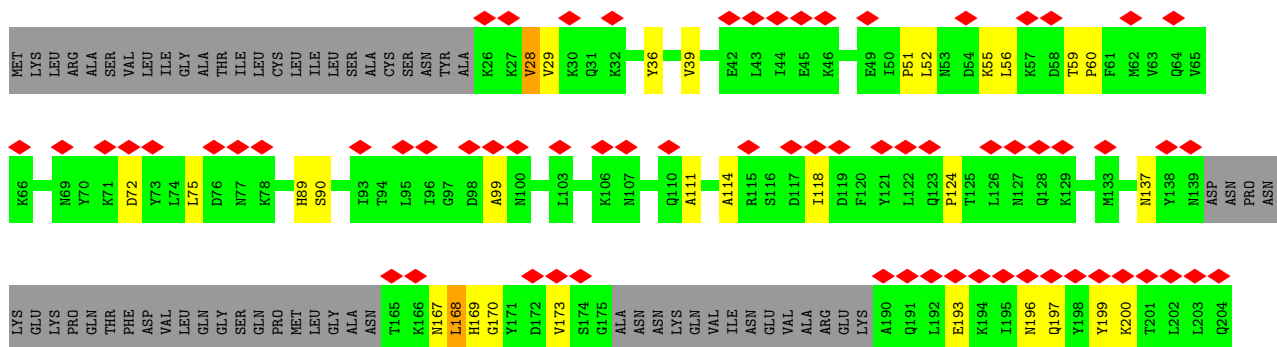
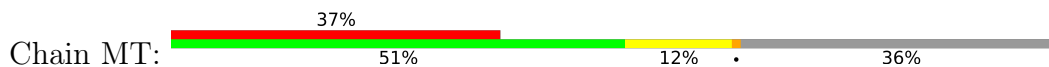


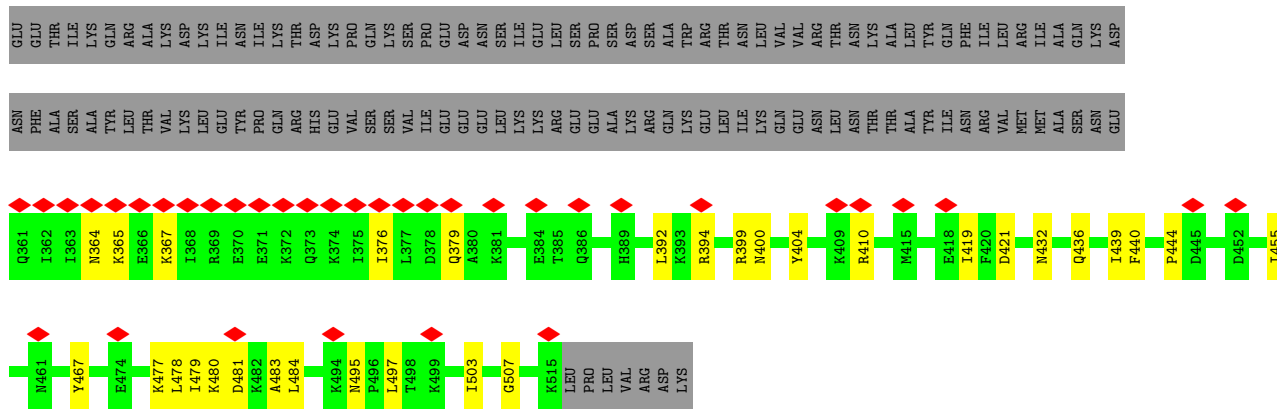


• Molecule 1: Cag pathogenicity island protein

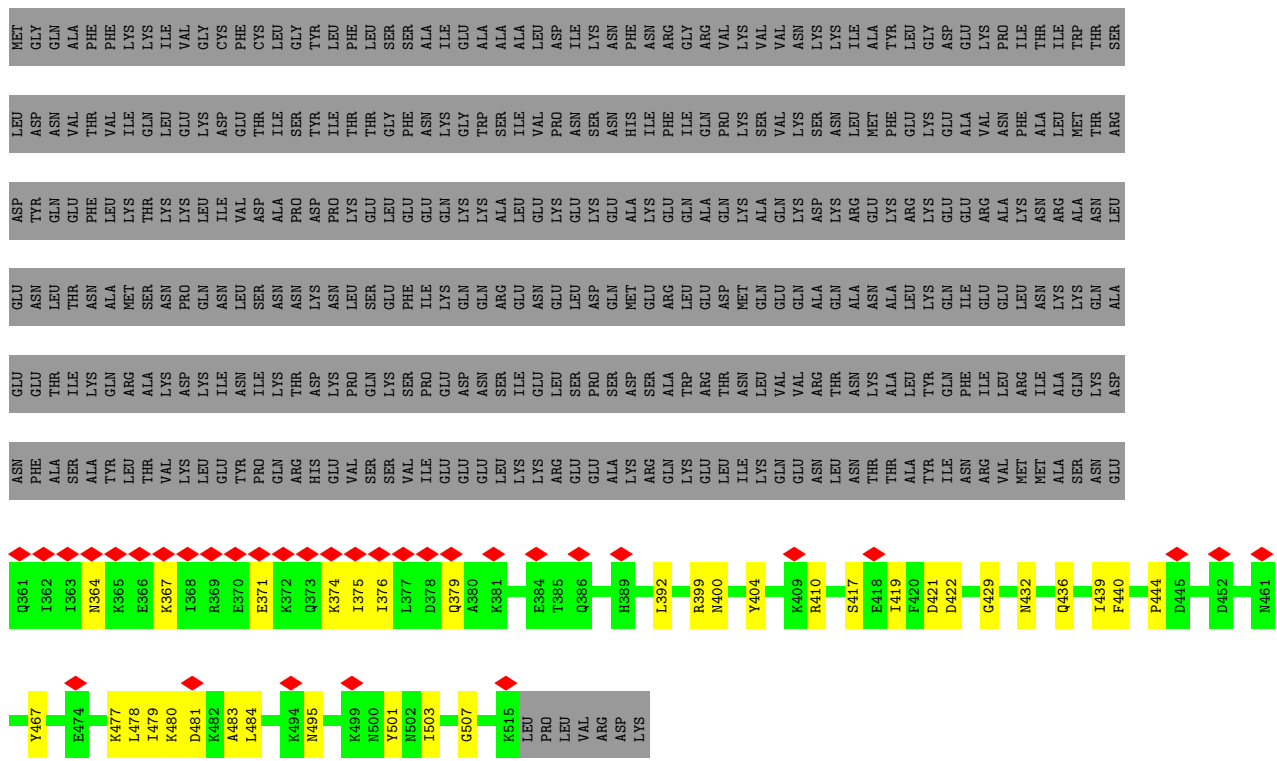


• Molecule 1: Cag pathogenicity island protein

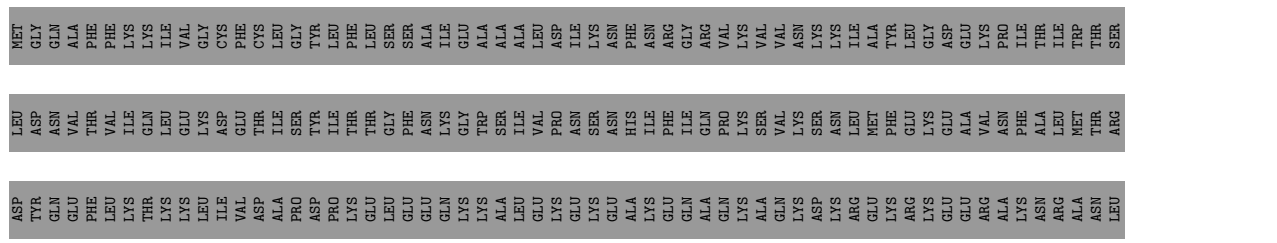


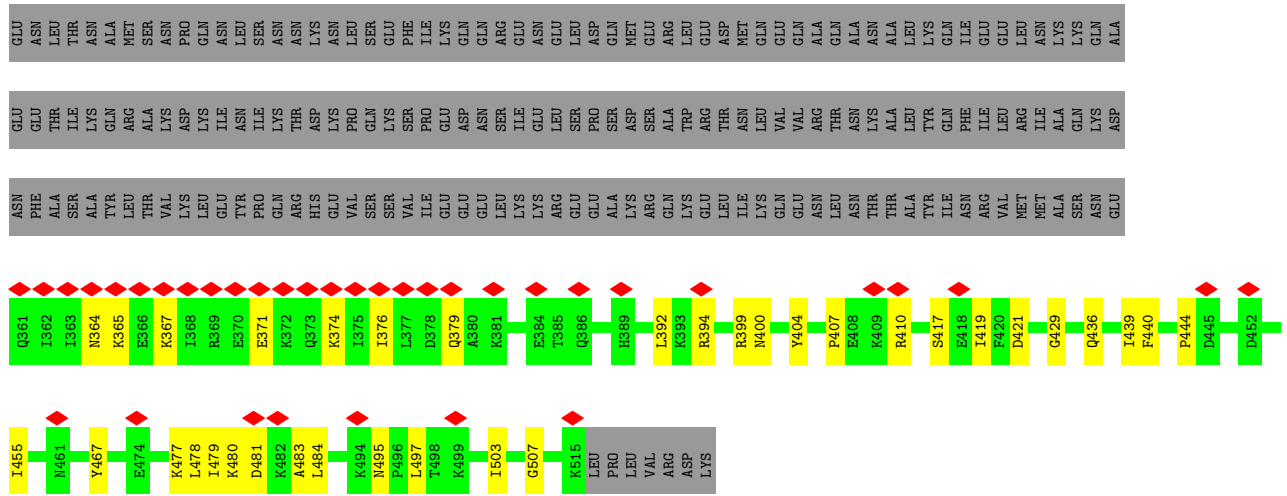


• Molecule 2: Type IV secretion system apparatus protein CagX

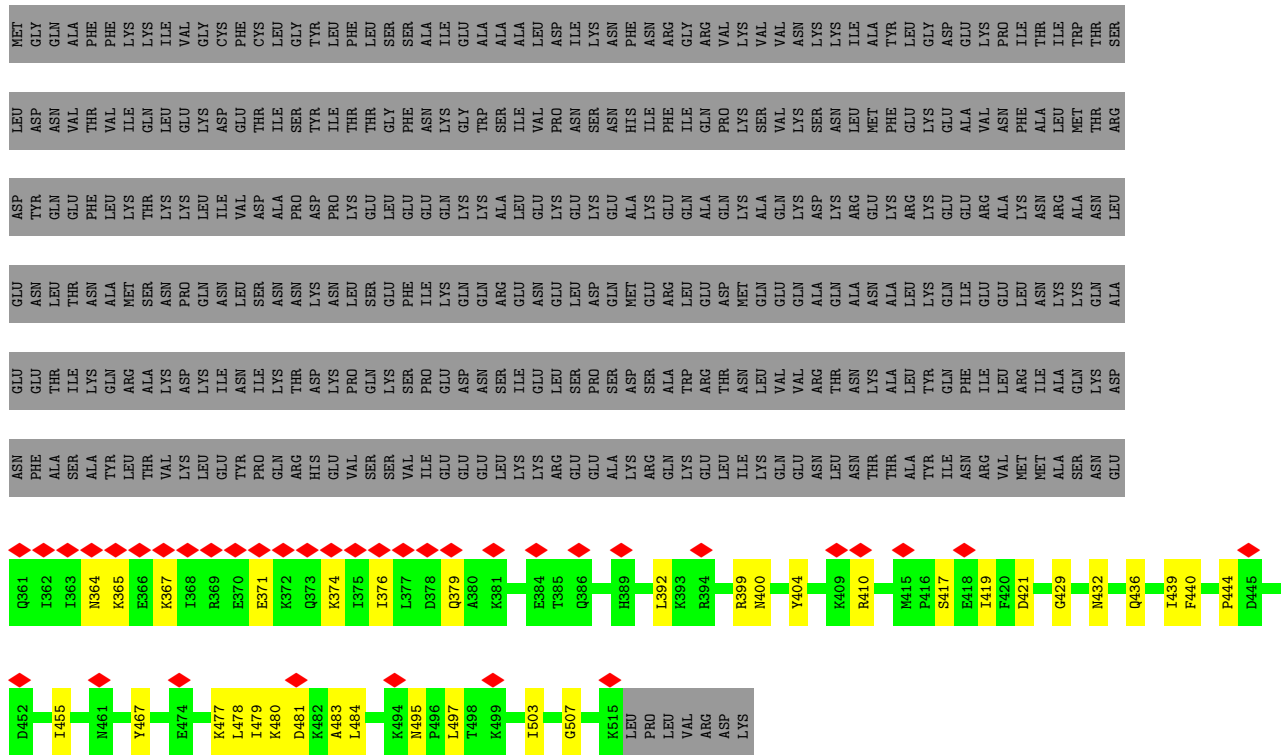


• Molecule 2: Type IV secretion system apparatus protein CagX

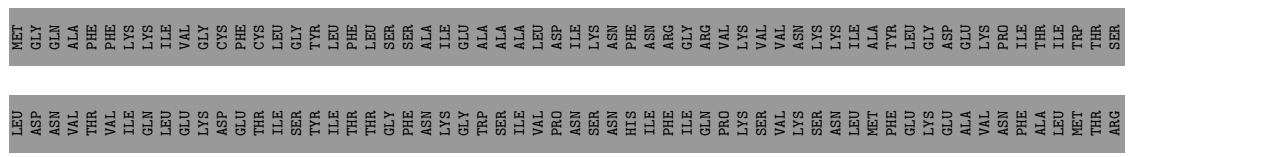


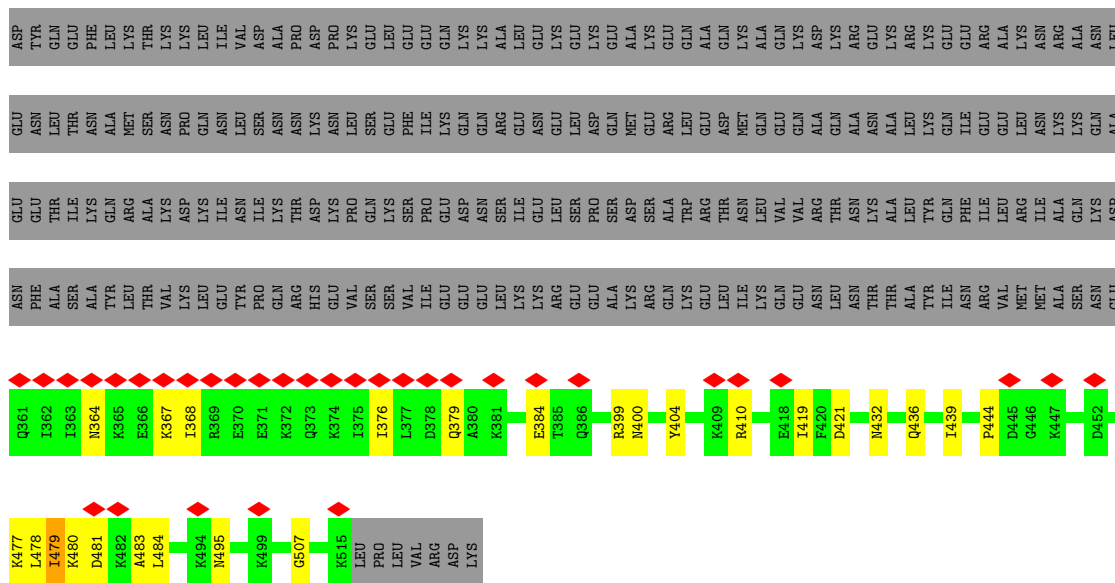


• Molecule 2: Type IV secretion system apparatus protein CagX

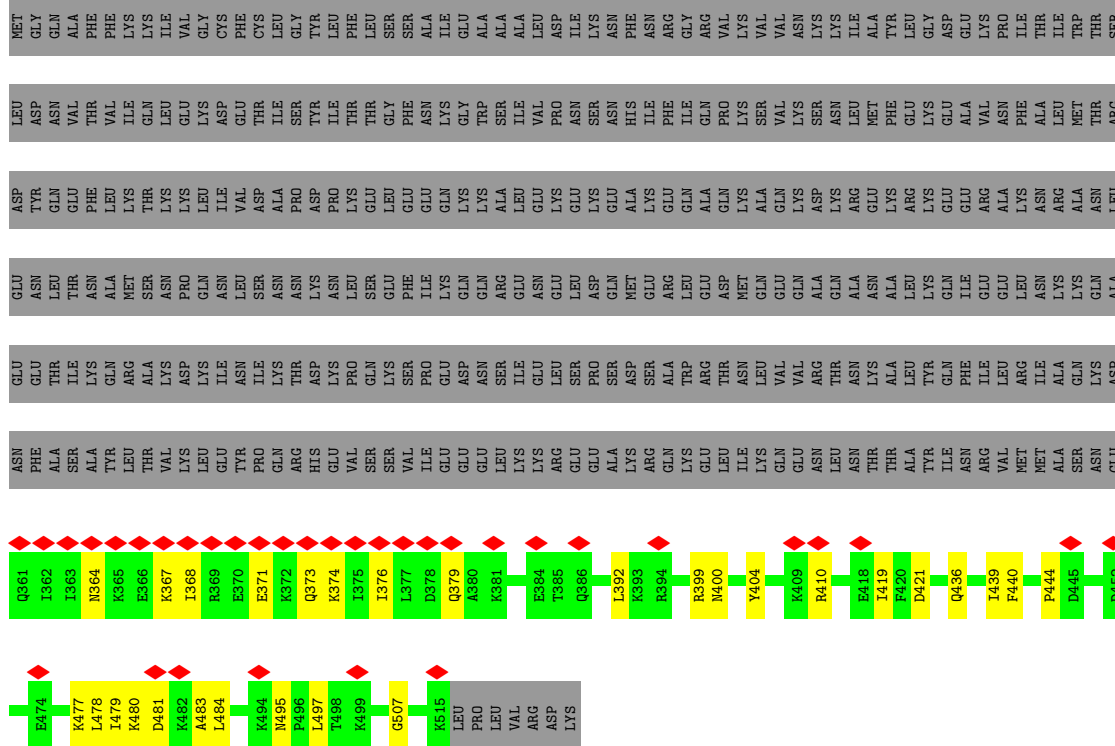


• Molecule 2: Type IV secretion system apparatus protein CagX



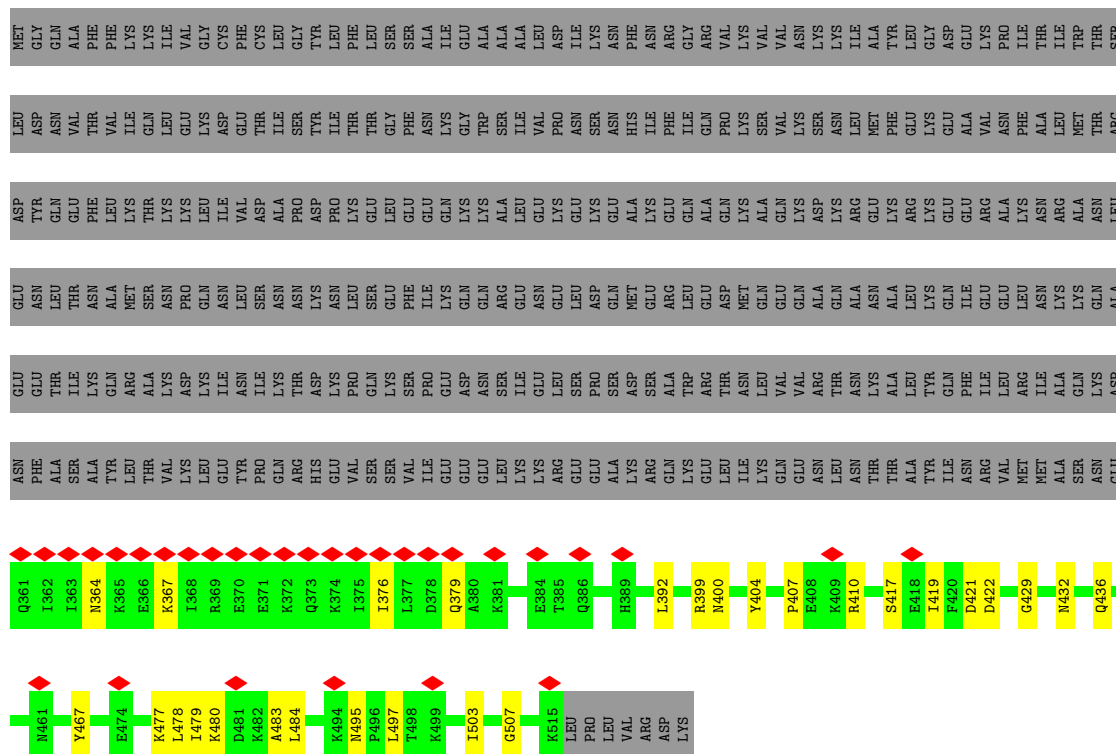


• Molecule 2: Type IV secretion system apparatus protein CagX

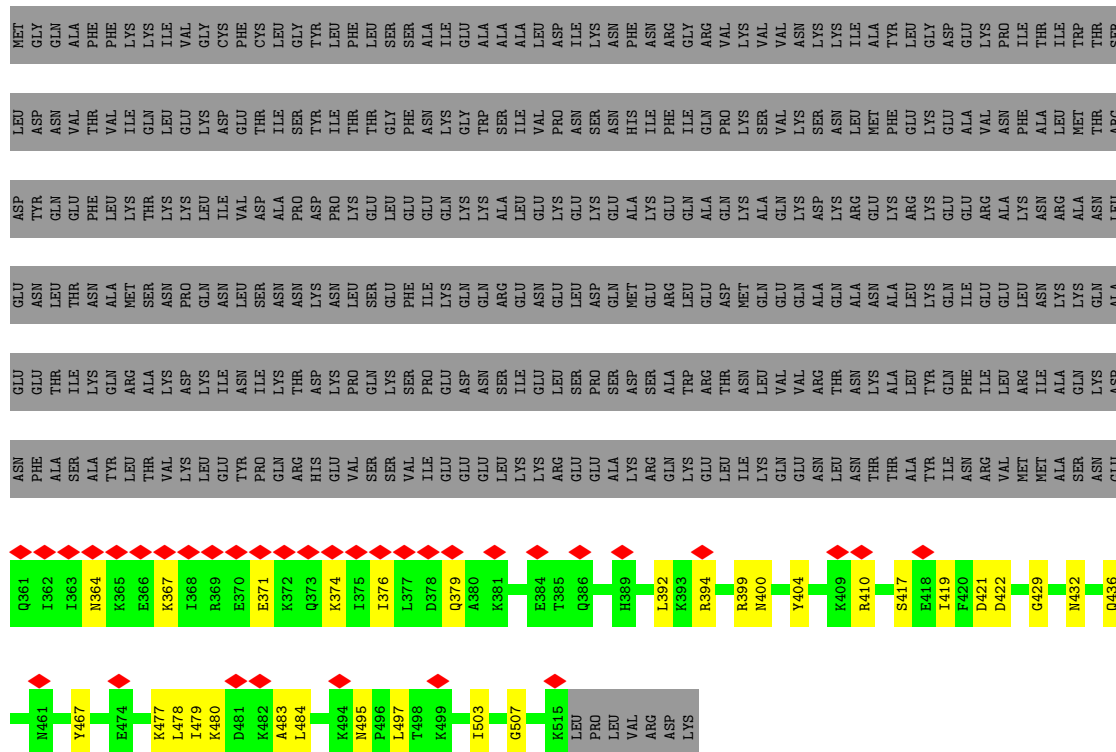


• Molecule 2: Type IV secretion system apparatus protein CagX

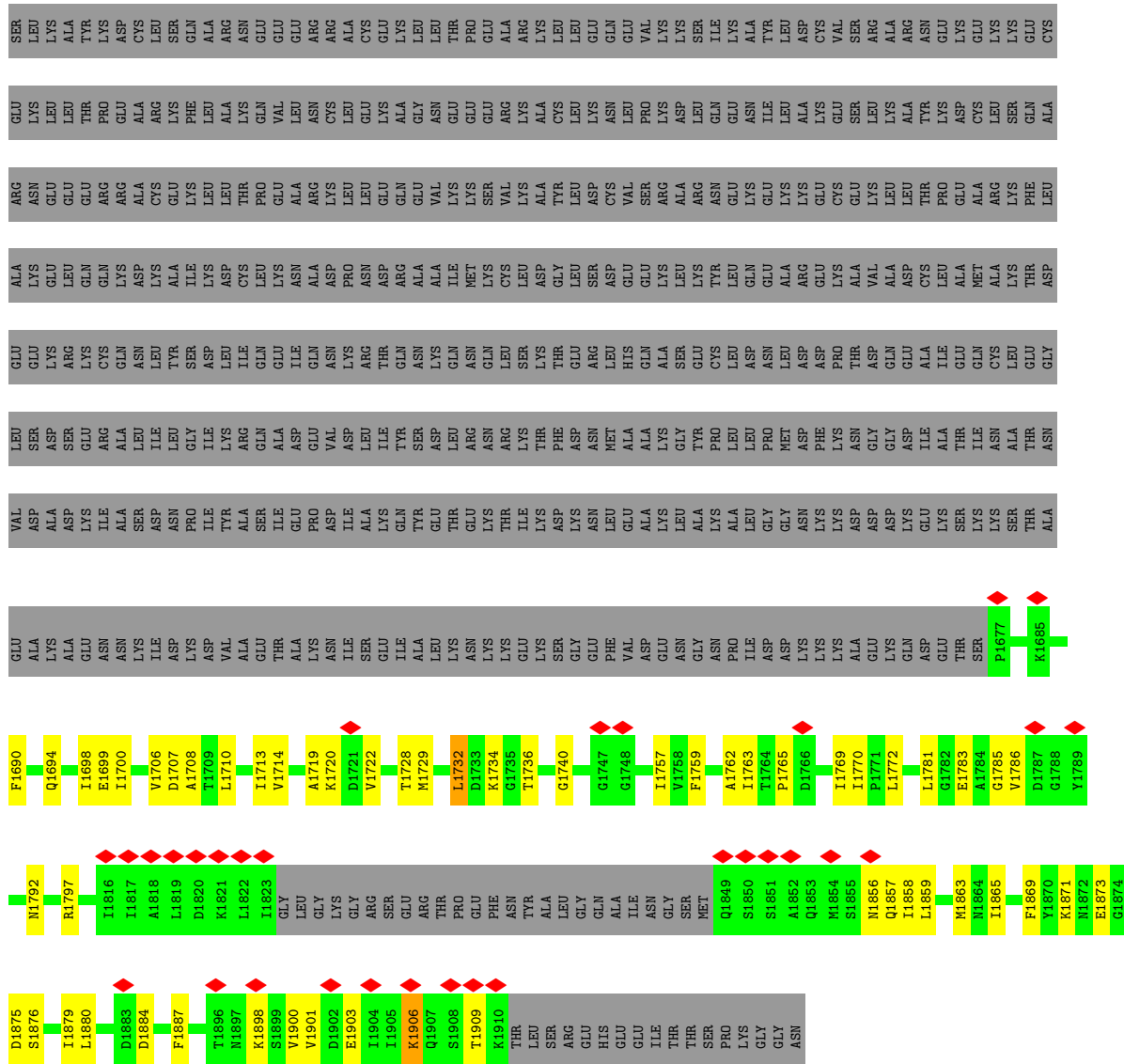




• Molecule 2: Type IV secretion system apparatus protein CagX



• Molecule 3: Cag pathogenicity island protein (Cag7)



● Molecule 3: Cag pathogenicity island protein (Cag7)

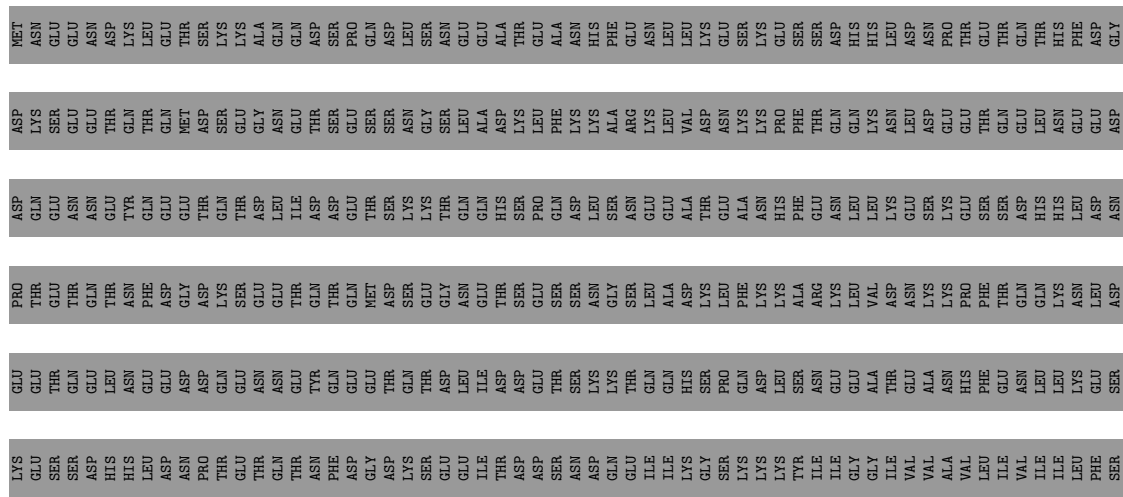
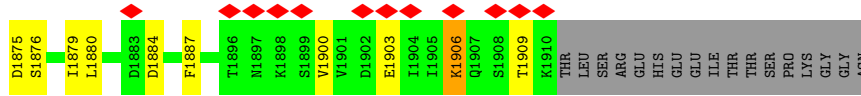


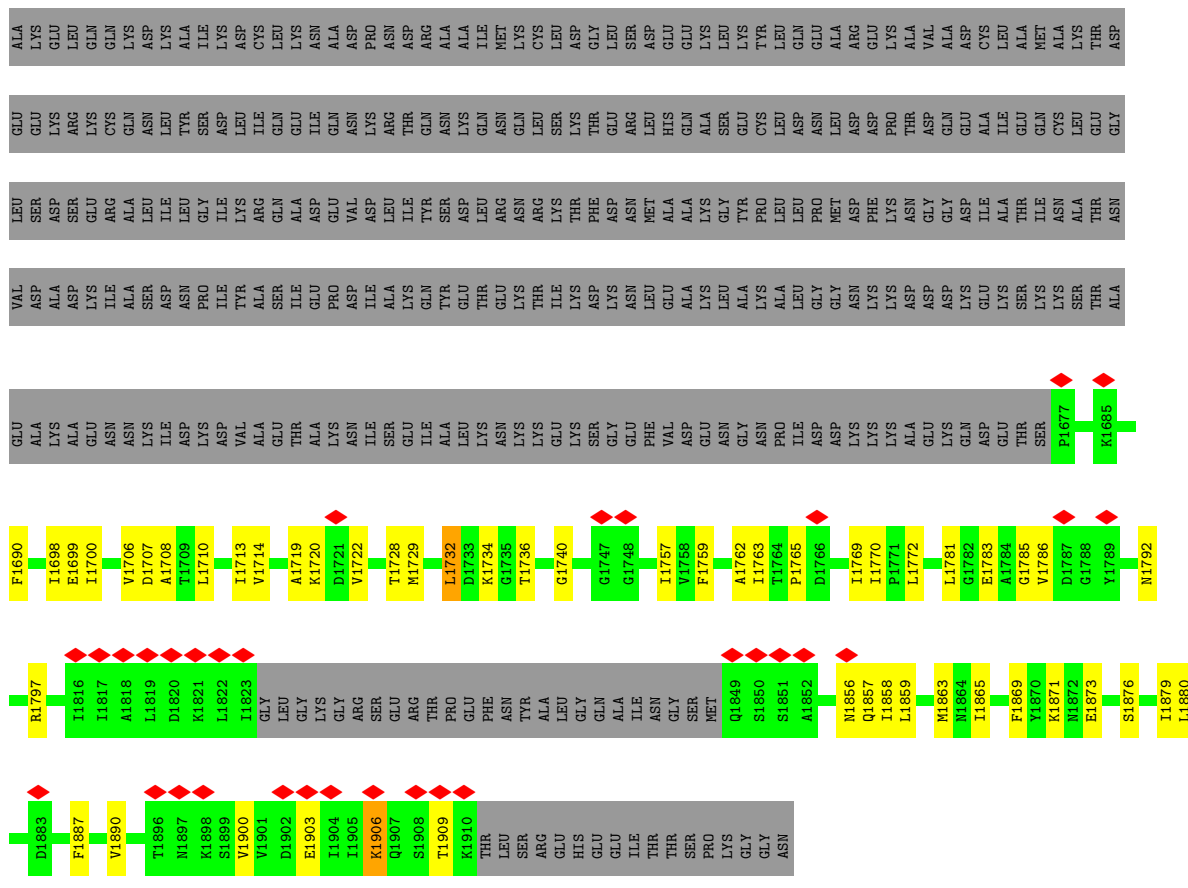
Table of amino acid residues and their corresponding three-letter codes, arranged in multiple rows. Some residues are highlighted in green or yellow, and others are marked with red diamonds. The highlighted residues include: K1685, F1690, Q1694, I1698, E1699, I1700, V1706, D1707, A1708, L1710, I1713, V1714, A1719, K1720, D1721, V1722, T1728, M1729, L1732, D1733, K1734, G1735, T1736, G1740, G1747, G1748, I1757, V1758, F1759, A1762, I1763, T1764, P1765, D1766, I1769, I1770, I1771, L1772, L1781, G1782, E1783, A1784, G1785, V1786, D1787, G1788, Y1789, M1792, R1797, I1816, I1817, A1818, L1819, D1820, K1821, L1822, I1823, M1856, Q1857, I1858, L1859, M1863, M1864, I1865, F1869, Y1870, K1871, M1872, E1873, G1874. Residues marked with red diamonds include: K1685, A1719, D1721, V1722, T1728, M1729, L1732, D1733, K1734, G1735, T1736, G1740, G1747, G1748, I1757, V1758, F1759, A1762, I1763, T1764, P1765, D1766, I1769, I1770, I1771, L1772, L1781, G1782, E1783, A1784, G1785, V1786, D1787, G1788, Y1789, M1792, R1797, I1816, I1817, A1818, L1819, D1820, K1821, L1822, I1823, M1856, Q1857, I1858, L1859, M1863, M1864, I1865, F1869, Y1870, K1871, M1872, E1873, G1874.



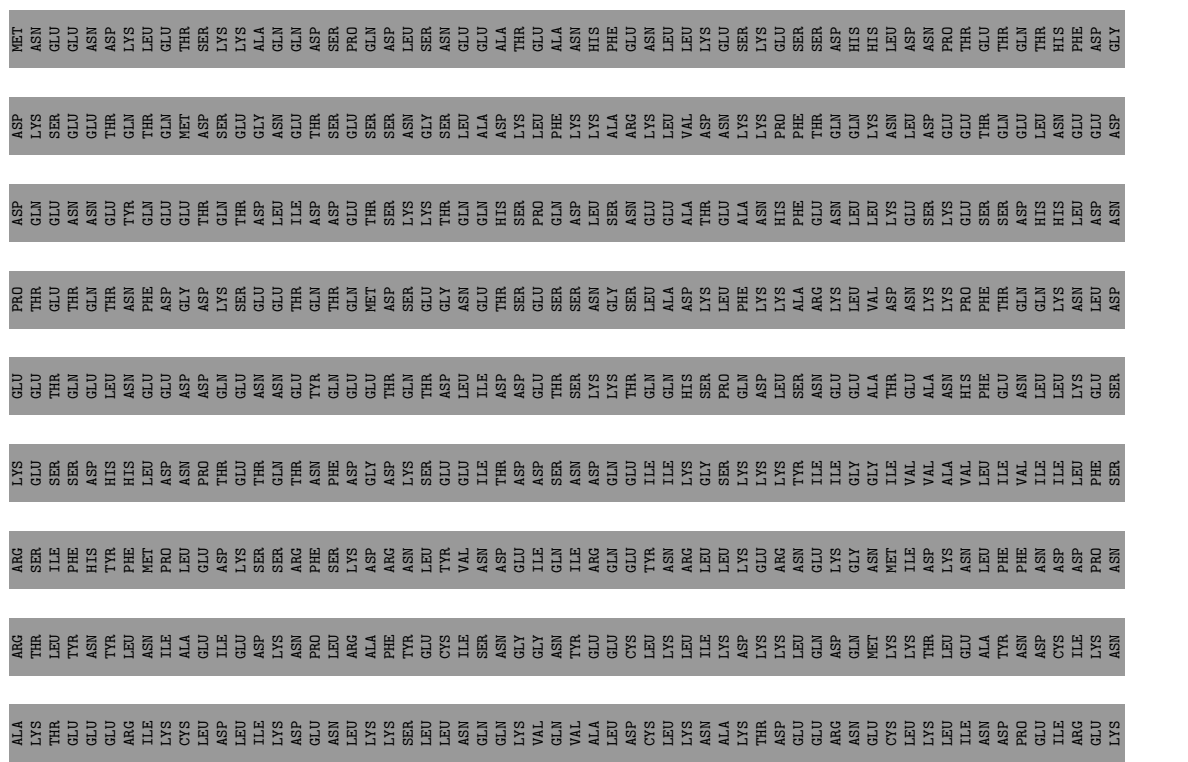
• Molecule 3: Cag pathogenicity island protein (Cag7)

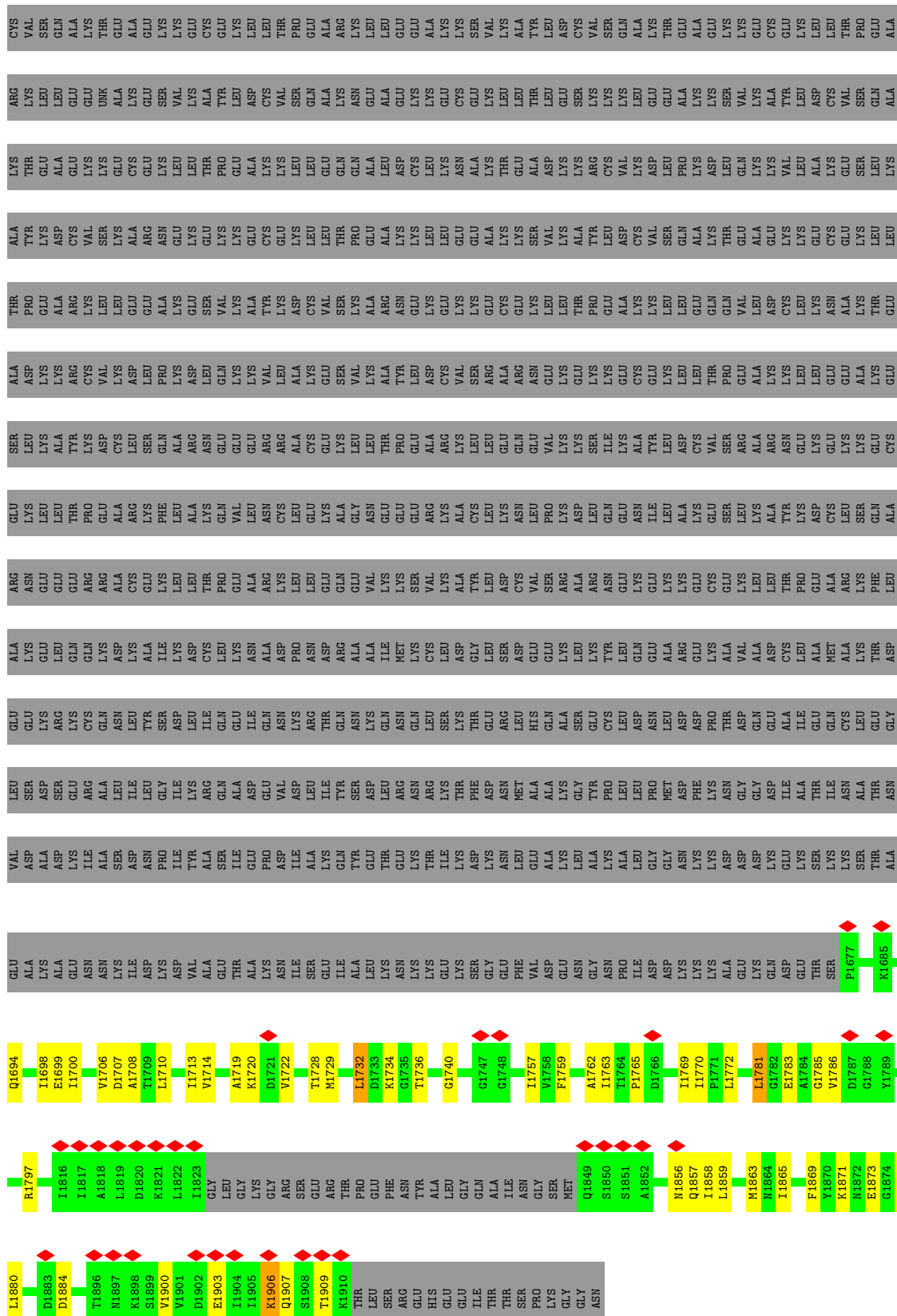


MET	ASN	GLU	LEU	THR	LYS	ALA	GLN	ASP	SER	PRO	GLN	ASP	LEU	THR	HIS	PHE	ARG	GLU	HIS	LEU	LEU	LEU	ILE	THR	THR	SER	PRO	LYS	GLY	GLY	ASN	
ASP	LYS	SER	GLU	ASN	GLU	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR	GLN	THR
ASP	GLN	GLU	ASN	ASN	ASN	TYR	GLN	THR	GLN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



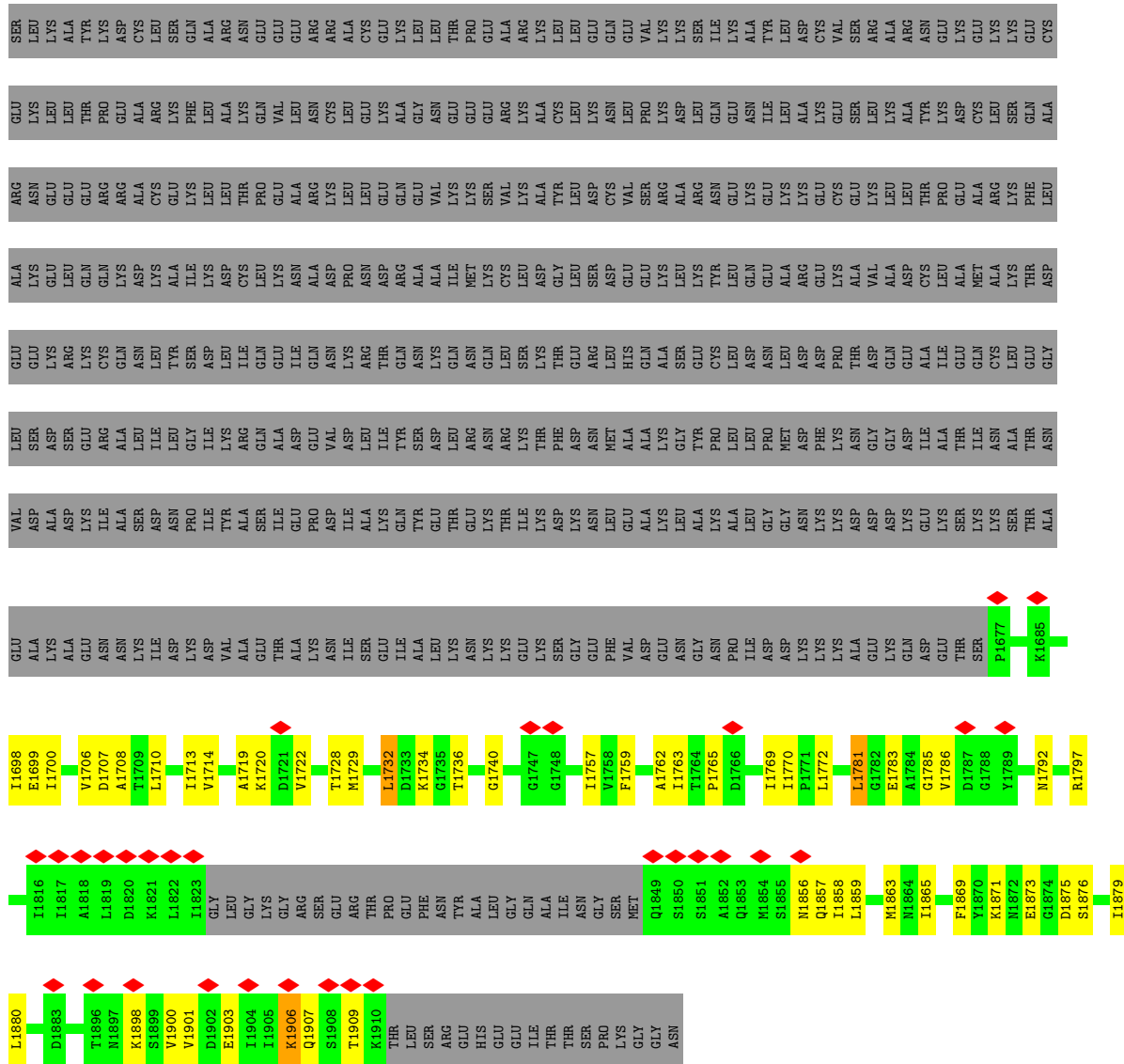
● Molecule 3: Cag pathogenicity island protein (Cag7)



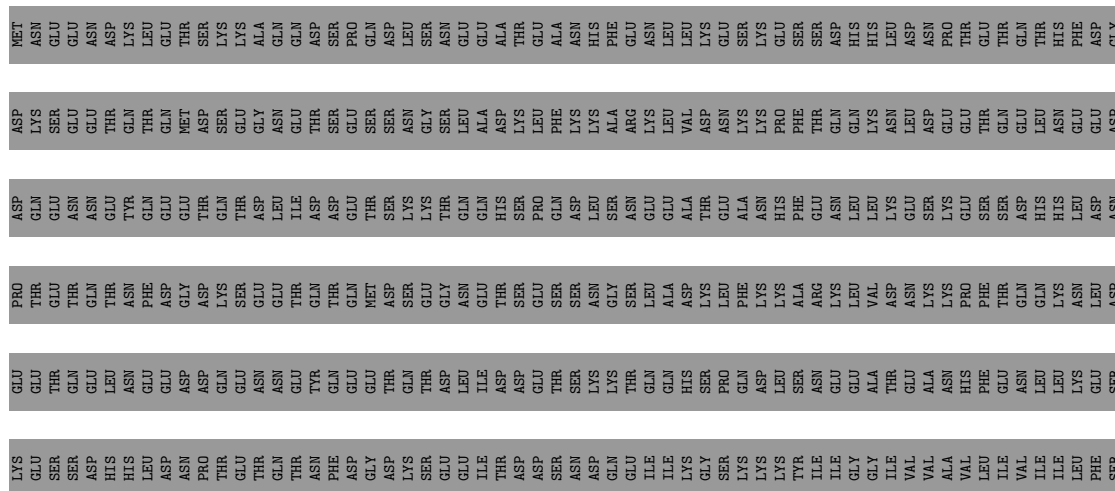


● Molecule 3: Cag pathogenicity island protein (Cag7)





• Molecule 3: Cag pathogenicity island protein (Cag7)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C14	Depositor
Number of particles used	7337	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 ($e^-/\text{\AA}^2$)	59.7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.049	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	510.0, 510.0, 510.0	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	AT	0.41	0/1525	0.71	4/2049 (0.2%)
1	BT	0.41	0/1525	0.71	4/2049 (0.2%)
1	CT	0.41	0/1525	0.71	4/2049 (0.2%)
1	DT	0.41	0/1525	0.71	4/2049 (0.2%)
1	ET	0.41	0/1525	0.71	4/2049 (0.2%)
1	FT	0.41	0/1525	0.71	4/2049 (0.2%)
1	GT	0.41	0/1525	0.71	4/2049 (0.2%)
1	HT	0.41	0/1525	0.71	4/2049 (0.2%)
1	IT	0.41	0/1525	0.71	4/2049 (0.2%)
1	JT	0.41	0/1525	0.71	4/2049 (0.2%)
1	KT	0.41	0/1525	0.71	4/2049 (0.2%)
1	LT	0.41	0/1525	0.71	4/2049 (0.2%)
1	MT	0.41	0/1525	0.71	4/2049 (0.2%)
1	NT	0.41	0/1525	0.71	4/2049 (0.2%)
2	AX	0.54	0/1301	0.69	0/1752
2	BX	0.54	0/1301	0.69	0/1752
2	CX	0.54	0/1301	0.69	0/1752
2	DX	0.54	0/1301	0.69	0/1752
2	EX	0.54	0/1301	0.69	0/1752
2	FX	0.54	0/1301	0.69	1/1752 (0.1%)
2	GX	0.54	0/1301	0.69	0/1752
2	HX	0.54	0/1301	0.69	0/1752
2	IX	0.54	0/1301	0.69	0/1752
2	JX	0.54	0/1301	0.69	0/1752
2	KX	0.54	0/1301	0.69	1/1752 (0.1%)
2	LX	0.54	0/1301	0.69	1/1752 (0.1%)
2	MX	0.54	0/1301	0.69	1/1752 (0.1%)
2	NX	0.54	0/1301	0.69	1/1752 (0.1%)
3	AY	0.55	0/1602	0.72	3/2170 (0.1%)
3	BY	0.55	0/1602	0.72	4/2170 (0.2%)
3	CY	0.55	0/1602	0.72	4/2170 (0.2%)
3	DY	0.55	0/1602	0.72	3/2170 (0.1%)
3	EY	0.55	0/1602	0.72	3/2170 (0.1%)
3	FY	0.55	0/1602	0.72	4/2170 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	GY	0.55	0/1602	0.72	4/2170 (0.2%)
3	HY	0.55	0/1602	0.72	4/2170 (0.2%)
3	IY	0.55	0/1602	0.72	4/2170 (0.2%)
3	JY	0.55	0/1602	0.72	4/2170 (0.2%)
3	KY	0.55	0/1602	0.72	4/2170 (0.2%)
3	LY	0.55	0/1602	0.72	3/2170 (0.1%)
3	MY	0.55	0/1602	0.72	4/2170 (0.2%)
3	NY	0.55	0/1602	0.72	4/2170 (0.2%)
All	All	0.50	0/61992	0.71	113/83594 (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
2	AX	0	1
2	BX	0	1
2	CX	0	1
2	DX	0	1
2	EX	0	1
2	FX	0	1
2	GX	0	1
2	HX	0	1
2	IX	0	1
2	JX	0	1
2	KX	0	1
2	LX	0	1
2	MX	0	1
2	NX	0	1
All	All	0	14

There are no bond length outliers.

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	MY	1772	LEU	CA-CB-CG	7.79	133.22	115.30
3	CY	1772	LEU	CA-CB-CG	7.79	133.21	115.30
3	KY	1772	LEU	CA-CB-CG	7.78	133.20	115.30
3	AY	1772	LEU	CA-CB-CG	7.78	133.19	115.30
3	HY	1772	LEU	CA-CB-CG	7.78	133.20	115.30

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AX	479	ILE	Peptide
2	BX	479	ILE	Peptide
2	CX	479	ILE	Peptide
2	DX	479	ILE	Peptide
2	EX	479	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AT	1502	0	1525	21	0
1	BT	1502	0	1525	23	0
1	CT	1502	0	1525	23	0
1	DT	1502	0	1525	23	0
1	ET	1502	0	1525	20	0
1	FT	1502	0	1525	27	0
1	GT	1502	0	1525	21	0
1	HT	1502	0	1525	23	0
1	IT	1502	0	1525	23	0
1	JT	1502	0	1525	23	0
1	KT	1502	0	1525	26	0
1	LT	1502	0	1525	26	0
1	MT	1502	0	1525	24	0
1	NT	1502	0	1525	20	0
2	AX	1275	0	1309	26	0
2	BX	1275	0	1309	28	0
2	CX	1275	0	1309	26	0
2	DX	1275	0	1309	24	0
2	EX	1275	0	1309	27	0
2	FX	1275	0	1309	29	0
2	GX	1275	0	1309	31	0
2	HX	1275	0	1309	29	0
2	IX	1275	0	1309	25	0
2	JX	1275	0	1309	27	0
2	KX	1275	0	1309	21	0
2	LX	1275	0	1309	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	MX	1275	0	1309	27	0
2	NX	1275	0	1309	28	0
3	AY	1578	0	1637	45	0
3	BY	1578	0	1637	45	0
3	CY	1578	0	1637	48	0
3	DY	1578	0	1637	43	0
3	EY	1578	0	1637	42	0
3	FY	1578	0	1637	45	0
3	GY	1578	0	1637	44	0
3	HY	1578	0	1637	44	0
3	IY	1578	0	1637	46	0
3	JY	1578	0	1637	42	0
3	KY	1578	0	1637	42	0
3	LY	1578	0	1637	41	0
3	MY	1578	0	1637	43	0
3	NY	1578	0	1637	42	0
All	All	60970	0	62594	984	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 984 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BX:444:PRO:O	2:CX:410:ARG:NH2	2.22	0.73
2:HX:444:PRO:O	2:IX:410:ARG:NH2	2.21	0.73
3:AY:1722:VAL:HB	3:AY:1732:LEU:HB2	1.72	0.72
3:DY:1722:VAL:HB	3:DY:1732:LEU:HB2	1.72	0.72
3:FY:1722:VAL:HB	3:FY:1732:LEU:HB2	1.72	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	BT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	CT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	DT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	ET	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	FT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	GT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	HT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	IT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	JT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	KT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	LT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	MT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
1	NT	171/278 (62%)	160 (94%)	11 (6%)	0	100	100
2	AX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	BX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	CX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	DX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	EX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	FX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	GX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	HX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	IX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	JX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	KX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	LX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	MX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
2	NX	153/522 (29%)	145 (95%)	8 (5%)	0	100	100
3	AY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	BY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	DY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	EY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	FY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	GY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	HY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	IY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	JY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	KY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	LY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	MY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
3	NY	205/1927 (11%)	195 (95%)	10 (5%)	0	100	100
All	All	7406/38178 (19%)	7000 (94%)	406 (6%)	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	AT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	BT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	CT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	DT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	ET	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	FT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	GT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	HT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	IT	169/254 (66%)	167 (99%)	2 (1%)	71	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	JT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	KT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	LT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	MT	169/254 (66%)	167 (99%)	2 (1%)	71	88
1	NT	169/254 (66%)	167 (99%)	2 (1%)	71	88
2	AX	139/470 (30%)	139 (100%)	0	100	100
2	BX	139/470 (30%)	139 (100%)	0	100	100
2	CX	139/470 (30%)	139 (100%)	0	100	100
2	DX	139/470 (30%)	139 (100%)	0	100	100
2	EX	139/470 (30%)	139 (100%)	0	100	100
2	FX	139/470 (30%)	139 (100%)	0	100	100
2	GX	139/470 (30%)	139 (100%)	0	100	100
2	HX	139/470 (30%)	139 (100%)	0	100	100
2	IX	139/470 (30%)	139 (100%)	0	100	100
2	JX	139/470 (30%)	139 (100%)	0	100	100
2	KX	139/470 (30%)	139 (100%)	0	100	100
2	LX	139/470 (30%)	139 (100%)	0	100	100
2	MX	139/470 (30%)	139 (100%)	0	100	100
2	NX	139/470 (30%)	139 (100%)	0	100	100
3	AY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	BY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	CY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	DY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	EY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	FY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	GY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	HY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	IY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	JY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	KY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	LY	177/1724 (10%)	176 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	MY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
3	NY	177/1724 (10%)	176 (99%)	1 (1%)	86	94
All	All	6790/34272 (20%)	6748 (99%)	42 (1%)	86	94

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	JT	214	LYS
3	LY	1906	LYS
3	JY	1906	LYS
3	KY	1906	LYS
1	MT	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

There are no chain breaks in this entry.

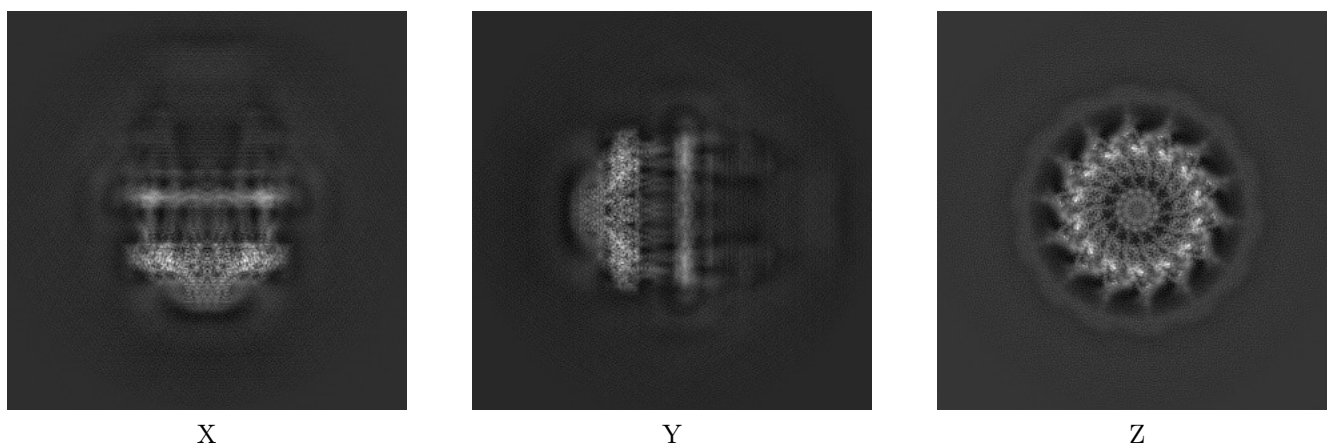
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22076. 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](#)

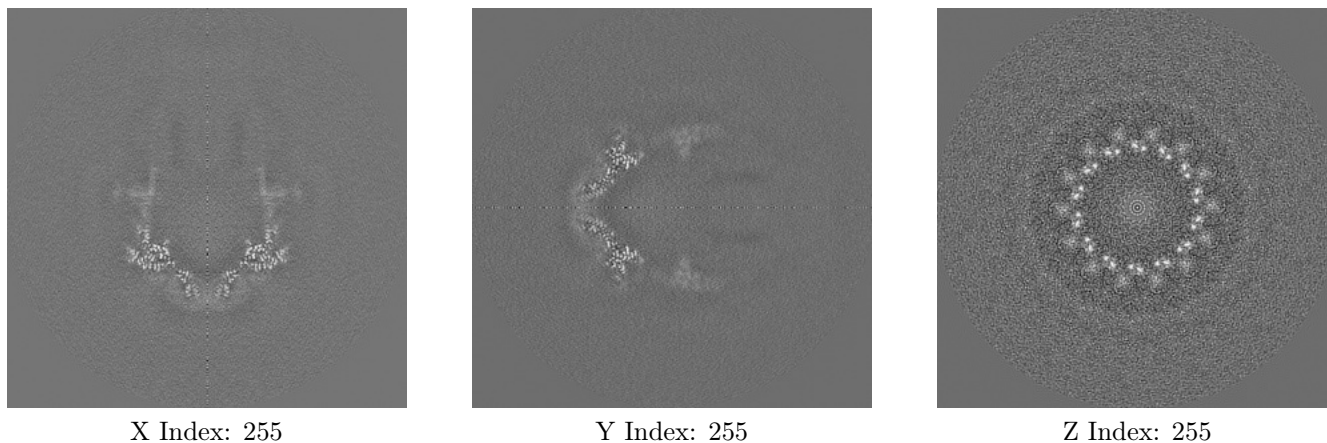
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



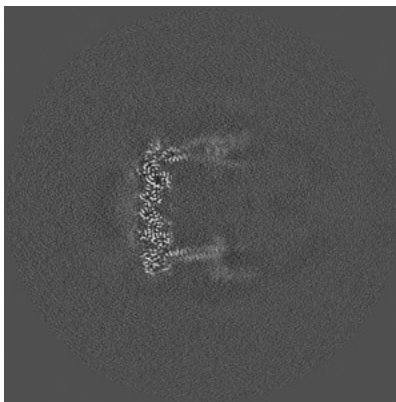
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

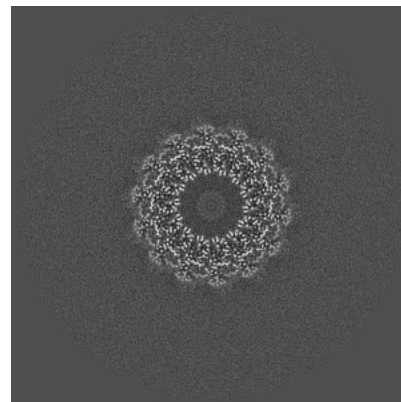
6.3.1 Primary map



X Index: 224



Y Index: 303

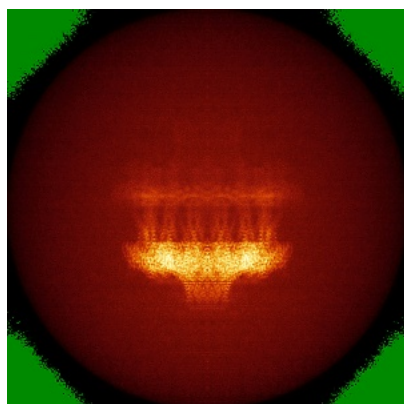


Z Index: 188

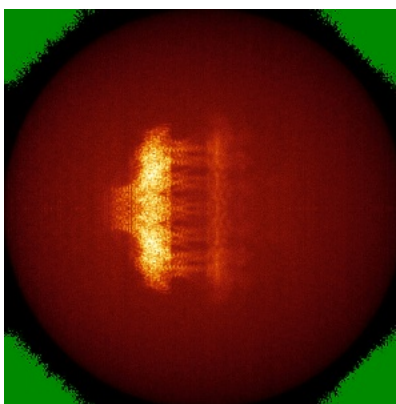
The images above show the largest variance slices of the map in three orthogonal directions.

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

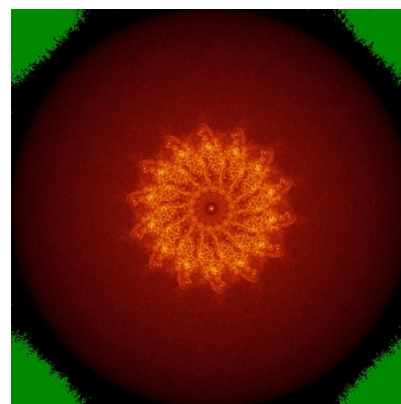
6.4.1 Primary map



X



Y

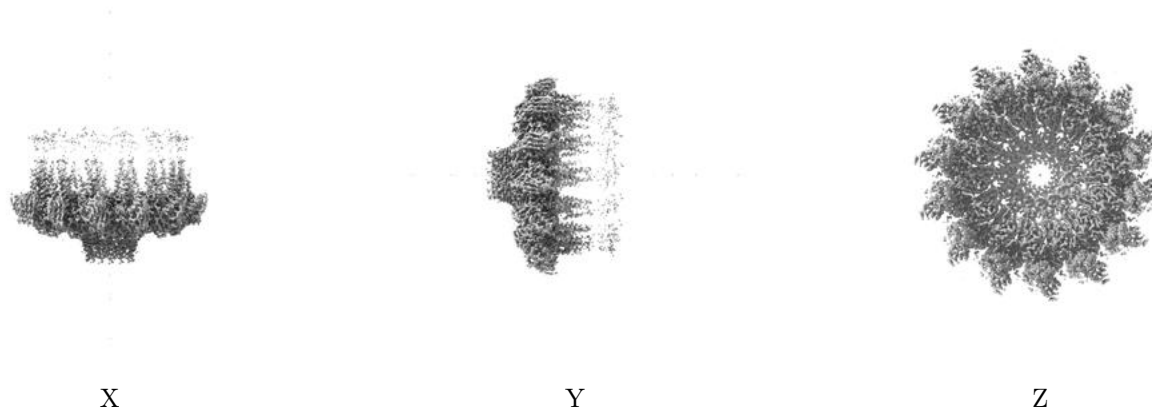


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

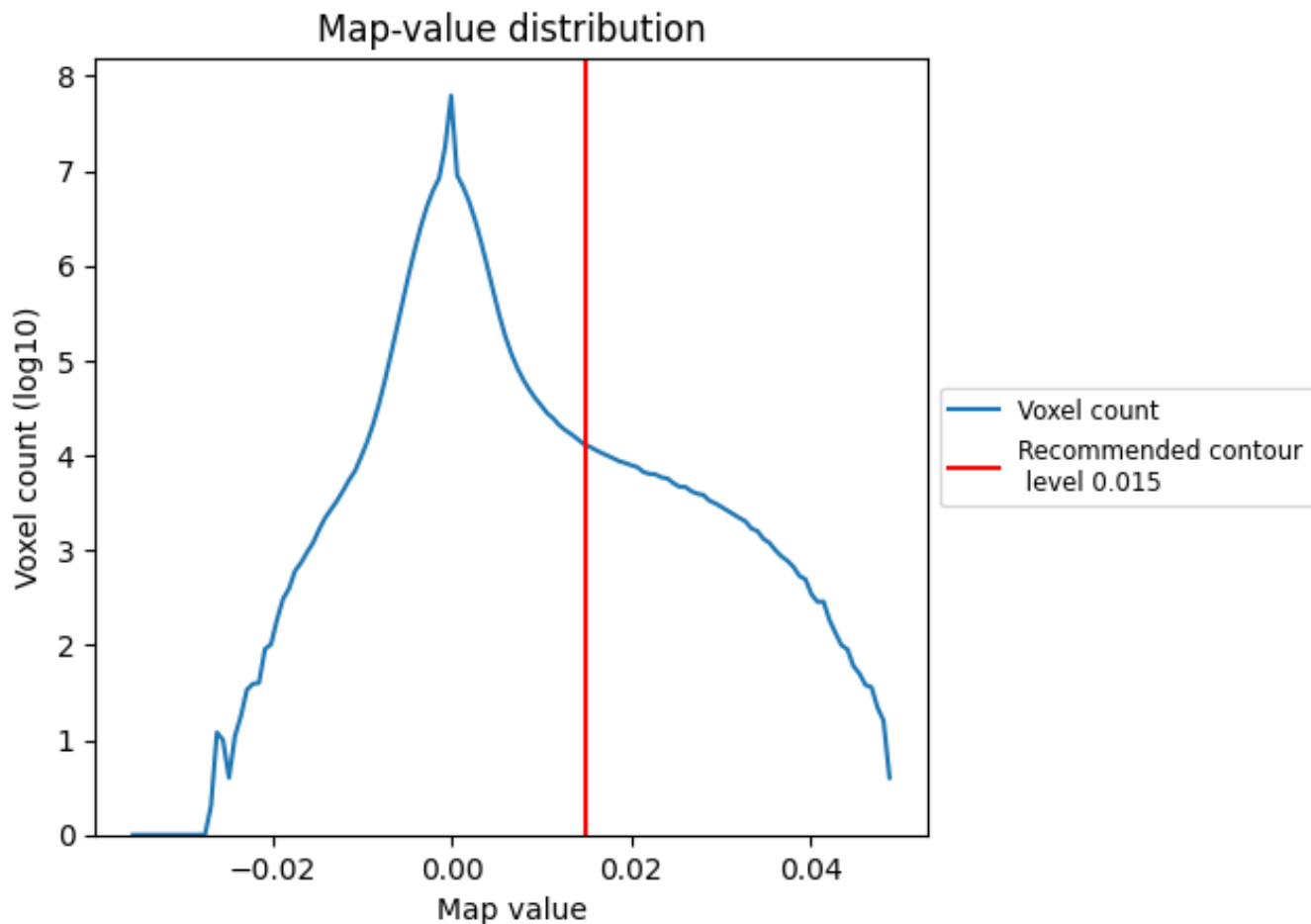
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

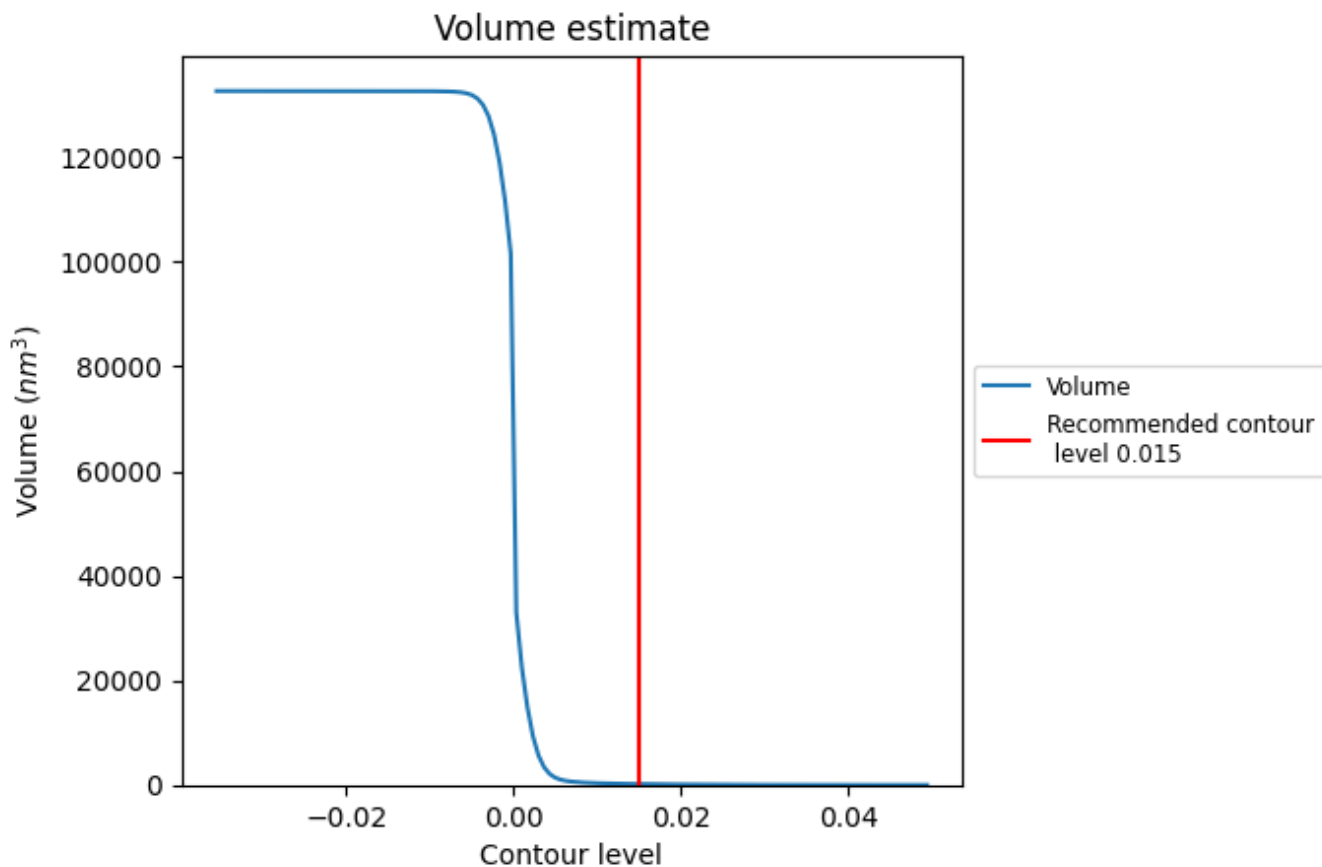
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

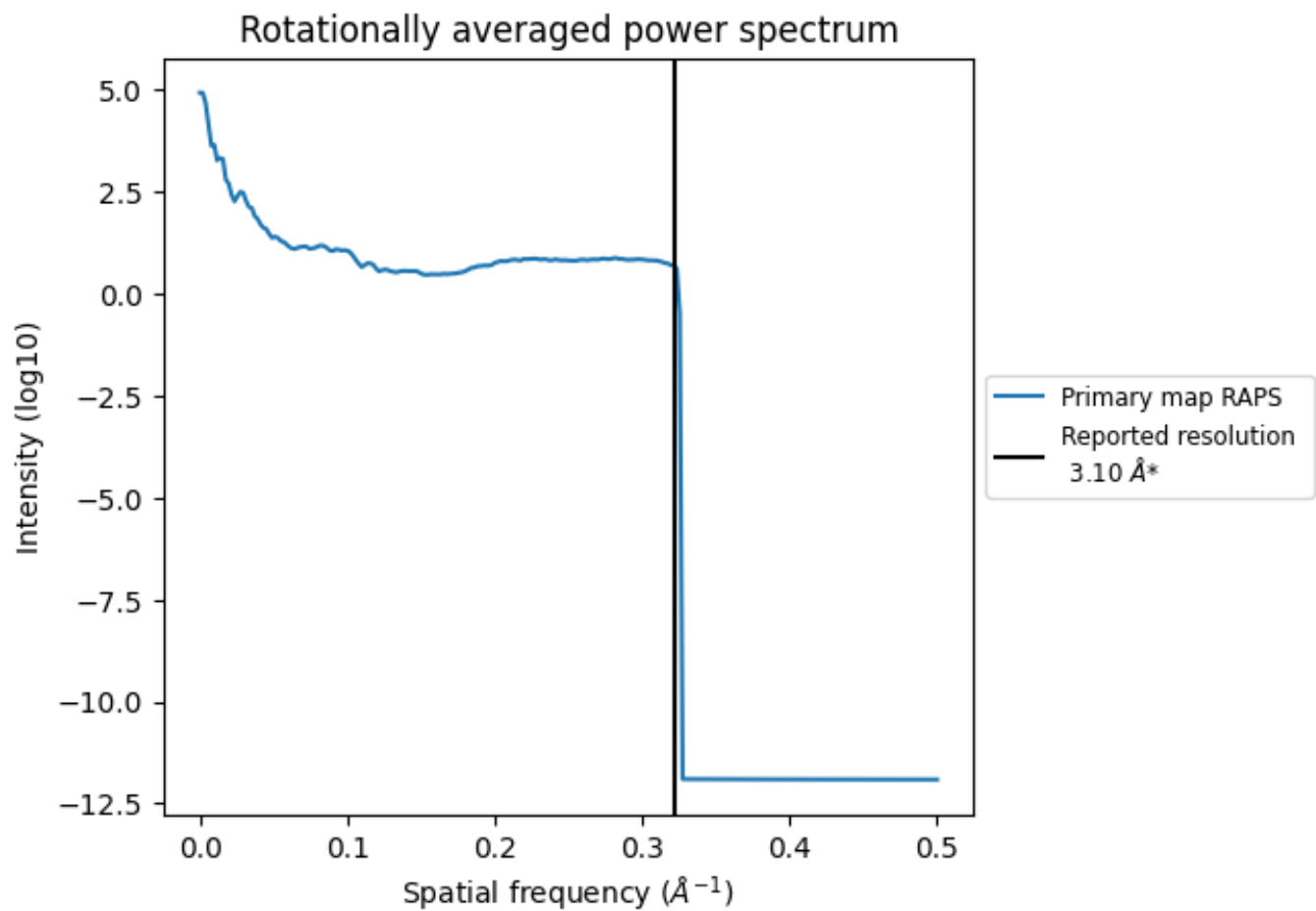
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm³; this corresponds to an approximate mass of 163 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](#)

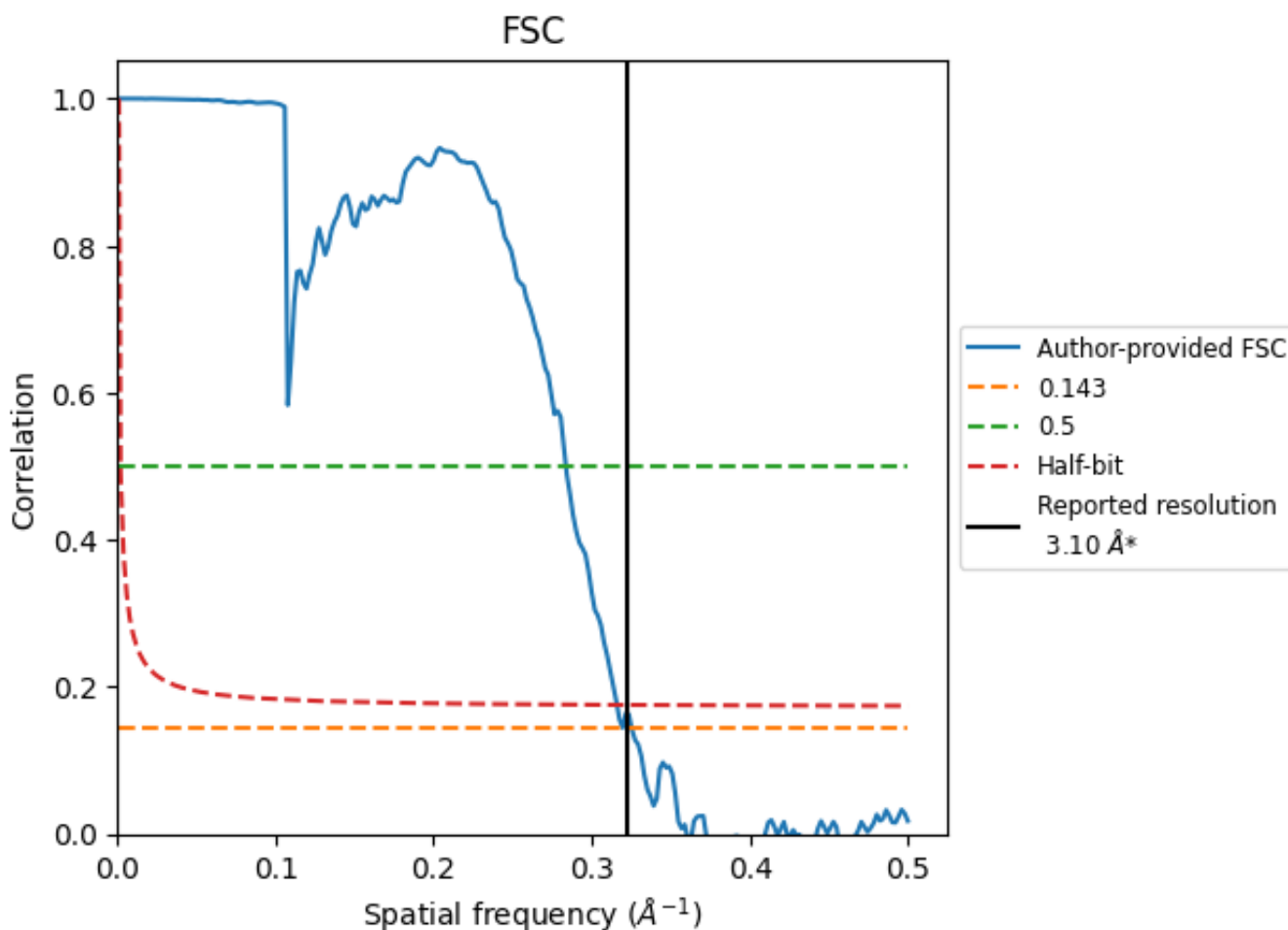


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

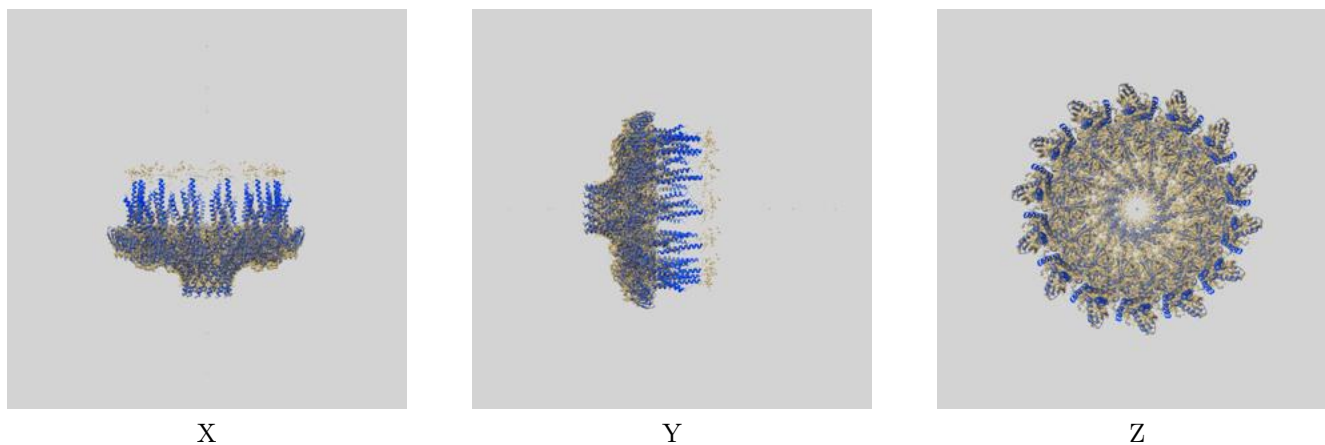
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.52	3.16
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

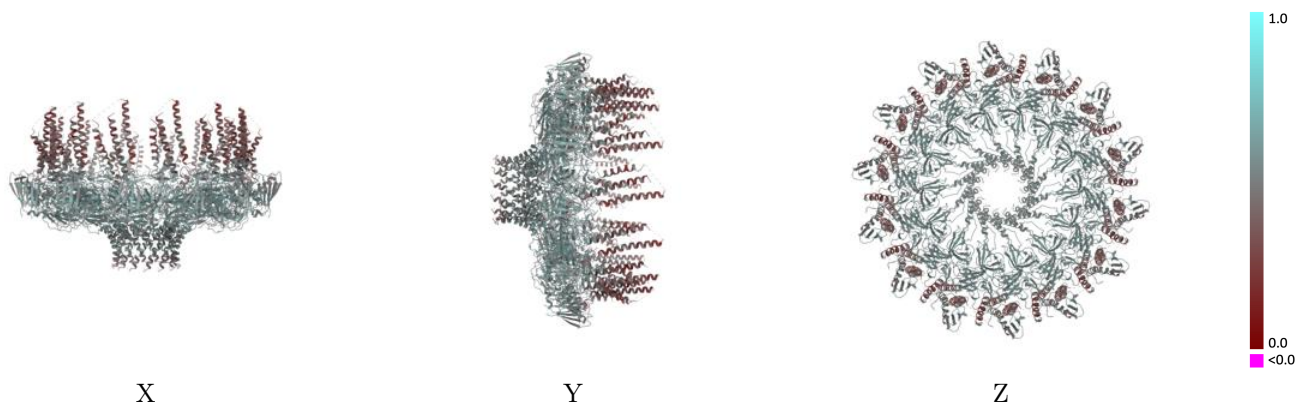
This section contains information regarding the fit between EMDB map EMD-22076 and PDB model 6X6K. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



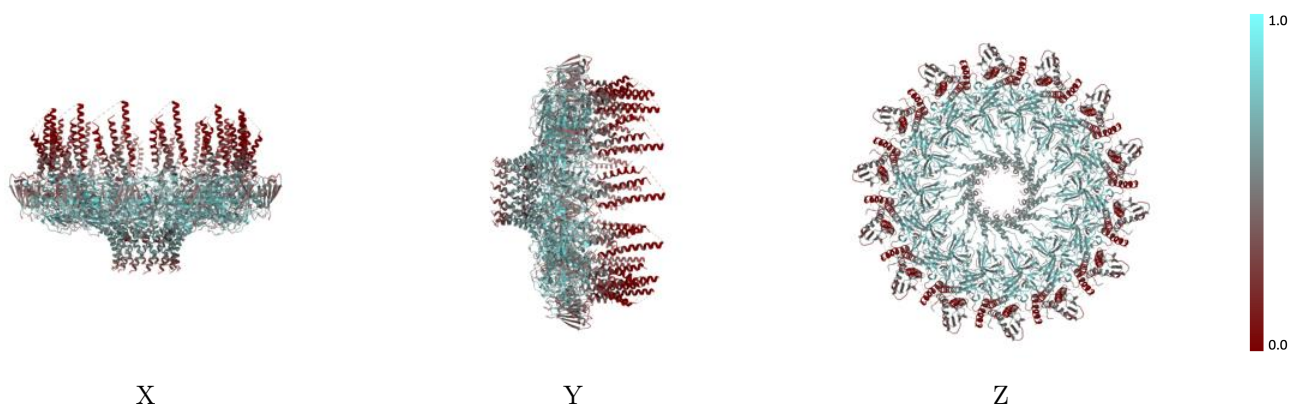
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



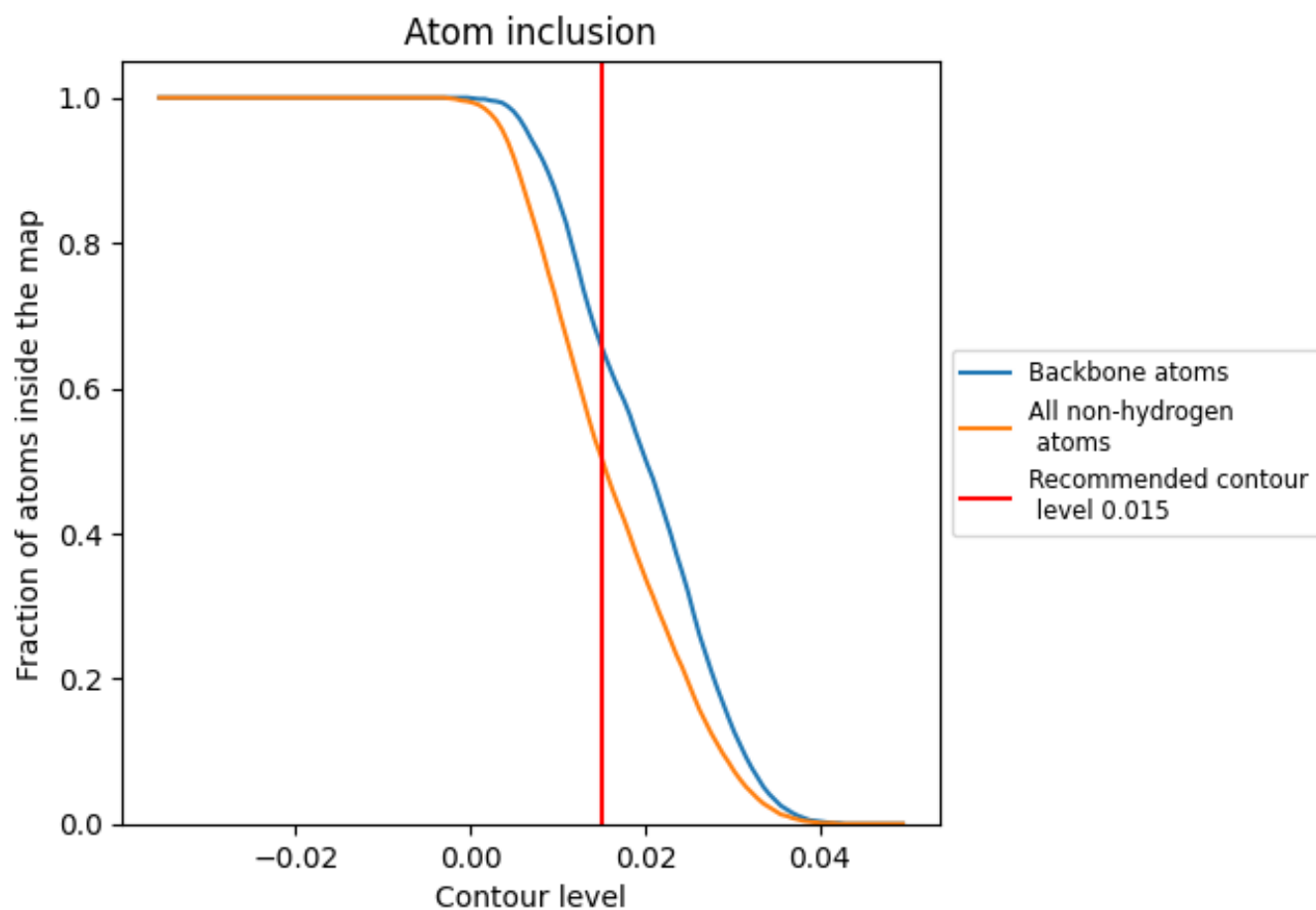
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 50% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5050	0.5040
AT	0.3380	0.4550
AX	0.5770	0.5170
AY	0.6070	0.5400
BT	0.3390	0.4580
BX	0.5750	0.5160
BY	0.6070	0.5410
CT	0.3350	0.4550
CX	0.5740	0.5180
CY	0.6040	0.5410
DT	0.3390	0.4550
DX	0.5720	0.5190
DY	0.6020	0.5420
ET	0.3400	0.4550
EX	0.5790	0.5170
EY	0.6040	0.5430
FT	0.3360	0.4540
FX	0.5780	0.5190
FY	0.6050	0.5400
GT	0.3330	0.4530
GX	0.5800	0.5190
GY	0.6090	0.5410
HT	0.3370	0.4560
HX	0.5770	0.5170
HY	0.6060	0.5400
IT	0.3370	0.4560
IX	0.5710	0.5190
IY	0.6070	0.5400
JT	0.3350	0.4520
JX	0.5740	0.5170
JY	0.6050	0.5390
KT	0.3360	0.4550
KX	0.5730	0.5170
KY	0.6020	0.5400
LT	0.3370	0.4560



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Chain	Atom inclusion	Q-score
LX	 0.5790	 0.5170
LY	 0.6050	 0.5390
MT	 0.3350	 0.4570
MX	 0.5770	 0.5190
MY	 0.6050	 0.5390
NT	 0.3390	 0.4560
NX	 0.5790	 0.5170
NY	 0.6090	 0.5400