



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jan 7, 2020 – 01:44 PM EST

PDB ID : 6L7C
EMDB ID: : EMD-0842
Title : CsgFG complex with substrate CsgAN6 peptide in Curli biogenesis system
Authors : Yan, Z.F.; Yin, M.; Chen, J.N.; Li, X.M.
Deposited on : 2019-11-01
Resolution : 3.34 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

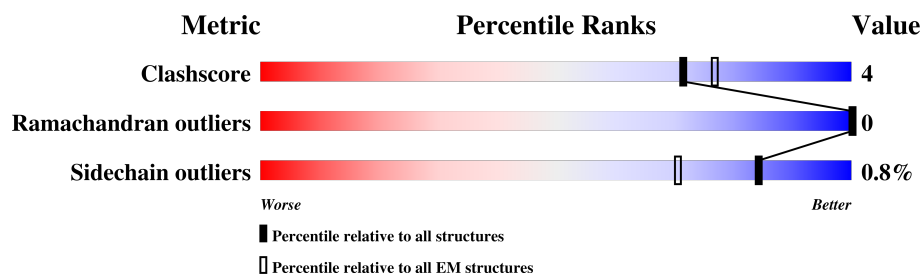
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.34 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.













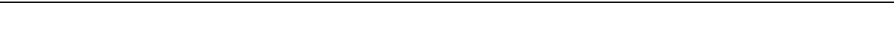

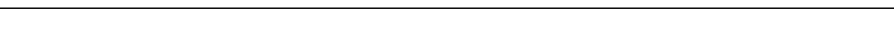
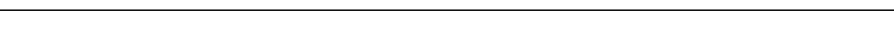
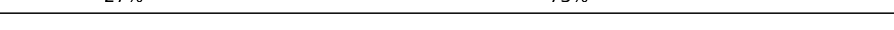



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	A	277	80% 11% 9%
1	B	277	80% 11% 9%
1	C	277	82% 9% 9%
1	D	277	81% 10% 9%
1	E	277	80% 11% 9%
1	F	277	81% 10% 9%
1	G	277	80% 11% 9%
1	H	277	81% 10% 9%
1	I	277	82% 9% 9%

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Mol	Chain	Length	Quality of chain	
2	J	138		
2	K	138		
2	L	138		
2	M	138		
2	N	138		
2	O	138		
2	P	138		
2	Q	138		
2	R	138		
3	S	22		
3	T	22		
3	U	22		
3	V	22		
3	W	22		
3	X	22		
3	Y	22		
3	Z	22		
3	a	22		

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 20601 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 Curli production assembly/transport protein CsgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	B	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	C	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	D	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	E	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	F	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	G	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	H	253	Total 1968	C 1244	N 341	O 376	S 7	0	0
1	I	253	Total 1968	C 1244	N 341	O 376	S 7	0	0

- Molecule 2 is a protein called CsgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	36	Total 275	C 170	N 50	O 54	S 1	0	0
2	K	36	Total 275	C 170	N 50	O 54	S 1	0	0
2	L	36	Total 275	C 170	N 50	O 54	S 1	0	0
2	M	36	Total 275	C 170	N 50	O 54	S 1	0	0
2	N	36	Total 275	C 170	N 50	O 54	S 1	0	0
2	O	36	Total 275	C 170	N 50	O 54	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	36	Total	C	N	O	S	0	0
			275	170	50	54	1		
2	Q	36	Total	C	N	O	S	0	0
			275	170	50	54	1		
2	R	36	Total	C	N	O	S	0	0
			275	170	50	54	1		

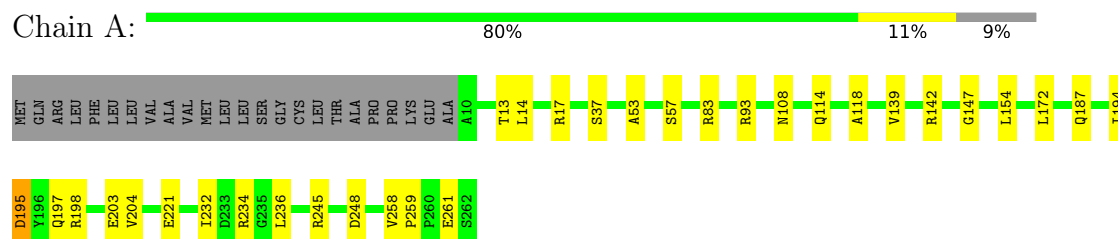
- Molecule 3 is a protein called Major curlin subunit CsgA.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	S	6	Total	C	N	O	0	0
			46	31	7	8		
3	T	6	Total	C	N	O	0	0
			46	31	7	8		
3	U	6	Total	C	N	O	0	0
			46	31	7	8		
3	V	6	Total	C	N	O	0	0
			46	31	7	8		
3	W	6	Total	C	N	O	0	0
			46	31	7	8		
3	X	6	Total	C	N	O	0	0
			46	31	7	8		
3	Y	6	Total	C	N	O	0	0
			46	31	7	8		
3	Z	6	Total	C	N	O	0	0
			46	31	7	8		
3	a	6	Total	C	N	O	0	0
			46	31	7	8		

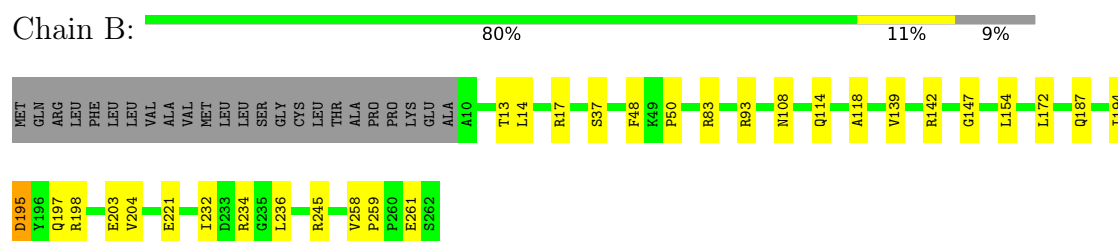
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

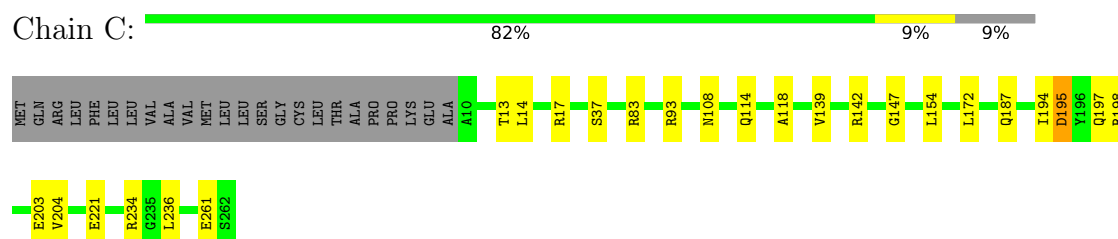
- Molecule 1: Curli production assembly/transport protein CsgG



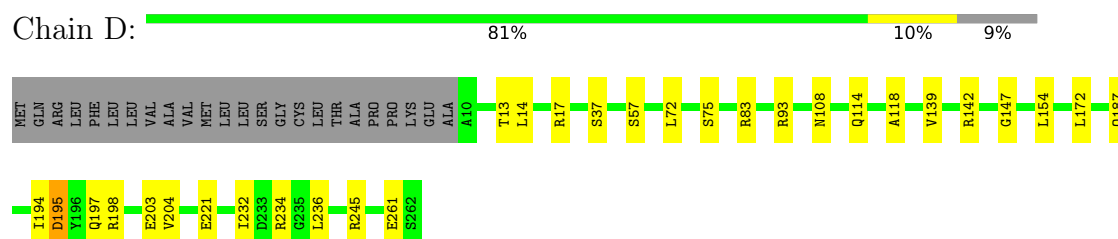
- Molecule 1: Curli production assembly/transport protein CsgG



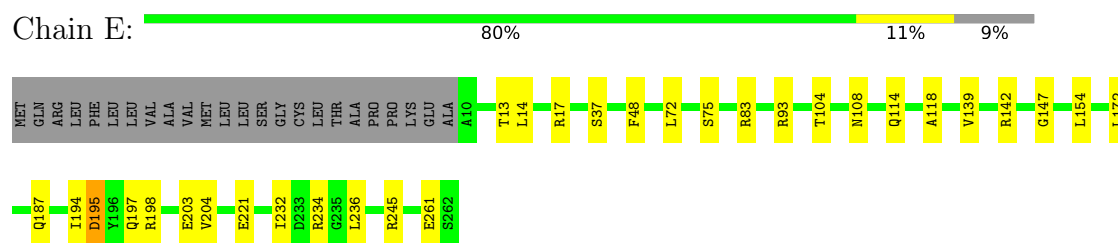
- Molecule 1: Curli production assembly/transport protein CsgG



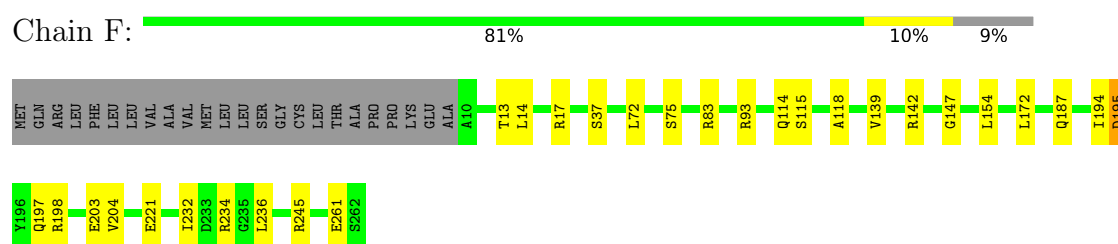
- Molecule 1: Curli production assembly/transport protein CsgG



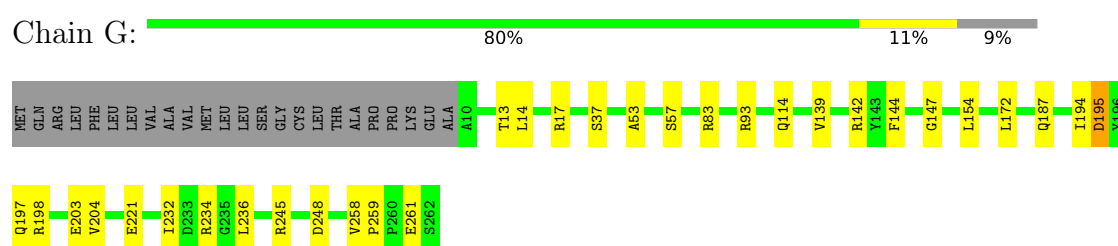
- Molecule 1: Curli production assembly/transport protein CsgG



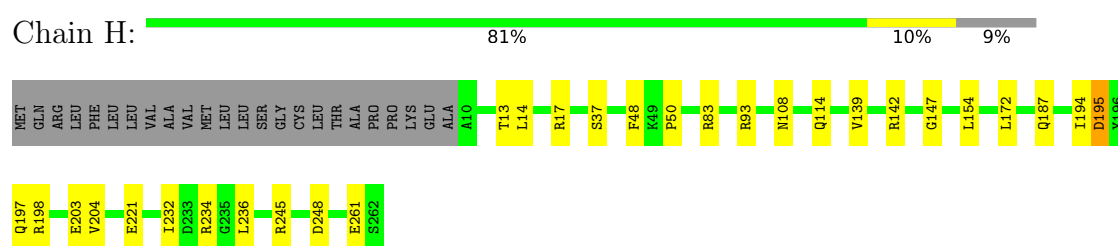
- Molecule 1: Curli production assembly/transport protein CsgG



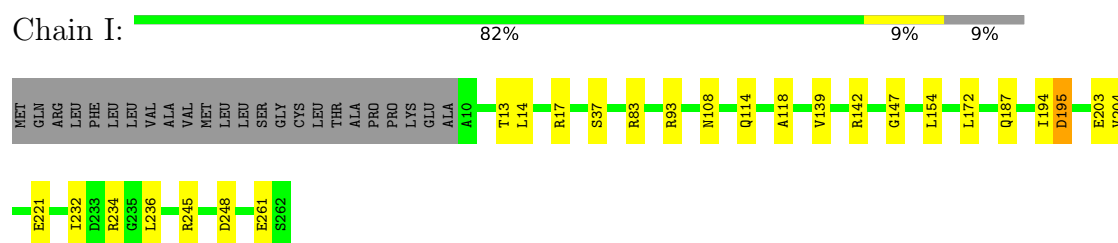
- Molecule 1: Curli production assembly/transport protein CsgG



- Molecule 1: Curli production assembly/transport protein CsgG



- Molecule 1: Curli production assembly/transport protein CsgG



- Molecule 2: CsgF

Chain J:  22% 74%

MET	ARG	VAL	LYS	HIS	ALA	VAL	VAL	LEU	LEU	MET	LEU	ILE	SER	PRO	LEU	SER	TRP	ALA	GLY	T4	P10	P16	R17	N18	K33	S36	TYR	ASN	ASP	ARG	LYS	PHE	GLY	ILE	GLU	THR	PRO	SER	ALA	LEU	ASP	ASN	PHE	THR	GLN	ALA	ILE	SER	ASP	GLN	ILE	LEU	GLY	LEU
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LEU	SER	ASN	ILE	THR	GLY	LYS	PRO	GLY	ARG	MET	VAL	THR	ASP	TYR	ILE	VAL	ASP	ILE	ALA	ASN	ARG	ASP	GLY	GLN	LEU	GLN	LEU	ASN	VAL	THR	ASN	ASP	ARG	LYS	THR	GLY	GLN	THR	SER	THR	ILE	GLN	VAL	SER	GLY	ASN	LEU	PHE	THR	GLN	ASN	ASP	PHE
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• Molecule 2: CsgF

Chain K:  22% 74%

MET	ARG	VAL	LYS	HIS	ALA	VAL	VAL	LEU	LEU	MET	LEU	ILE	SER	PRO	LEU	SER	TRP	ALA	GLY	T4	P10	P16	R17	N18	K33	S36	TYR	ASN	ASP	ARG	LYS	PHE	GLY	ILE	GLU	THR	PRO	SER	ALA	LEU	ASP	ASN	PHE	THR	GLN	ALA	ILE	SER	ASP	GLN	ILE	LEU	GLY	LEU
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LEU	SER	ASN	ILE	THR	GLY	LYS	PRO	GLY	ARG	MET	VAL	THR	ASP	TYR	ILE	VAL	ASP	ILE	ALA	ASN	ARG	ASP	GLY	GLN	LEU	GLN	LEU	ASN	VAL	THR	ASN	ASP	ARG	LYS	THR	GLY	GLN	THR	SER	THR	ILE	GLN	VAL	SER	GLY	ASN	LEU	PHE	THR	GLN	ASN	ASP	PHE
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• Molecule 2: CsgF

Chain L:  22% 74%

MET	ARG	VAL	LYS	HIS	ALA	VAL	VAL	LEU	LEU	MET	LEU	ILE	SER	PRO	LEU	SER	TRP	ALA	GLY	T4	P10	P16	R17	N18	K33	S36	TYR	ASN	ASP	ARG	LYS	PHE	GLY	ILE	GLU	THR	PRO	SER	ALA	LEU	ASP	ASN	PHE	THR	GLN	ALA	ILE	SER	ASP	GLN	ILE	LEU	GLY	LEU
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LEU	SER	ASN	ILE	THR	GLY	LYS	PRO	GLY	ARG	MET	VAL	THR	ASP	TYR	ILE	VAL	ASP	ILE	ALA	ASN	ARG	ASP	GLY	GLN	LEU	GLN	LEU	ASN	VAL	THR	ASN	ASP	ARG	LYS	THR	GLY	GLN	THR	SER	THR	ILE	GLN	VAL	SER	GLY	ASN	LEU	PHE	THR	GLN	ASN	ASP	PHE
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• Molecule 2: CsgF

Chain M:  23% 74%

MET	ARG	VAL	LYS	HIS	ALA	VAL	VAL	LEU	LEU	MET	LEU	ILE	SER	PRO	LEU	SER	TRP	ALA	GLY	T4	P10	P16	R17	N18	S36	TYR	ASN	ASP	PHE	GLY	ILE	GLU	THR	PRO	ALA	SER	ASP	ASN	PHE	THR	GLN	ASN	GLN	ILE	SER	THR	ASP	GLY	LEU	LEU	SER
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ASN	ILE	THR	GLY	LYS	PRO	GLY	ARG	MET	VAL	THR	ASN	ASP	TYR	ILE	VAL	ASP	ILE	ALA	ASN	ARG	ASP	GLY	GLN	LEU	GLN	LEU	ASN	VAL	THR	ASP	ARG	LYS	THR	GLY	THR	SER	THR	ILE	GLN	VAL	SER	GLY	LEU	GLN	ASN	ASN	SER	THR	ASP	PHE
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• Molecule 2: CsgF

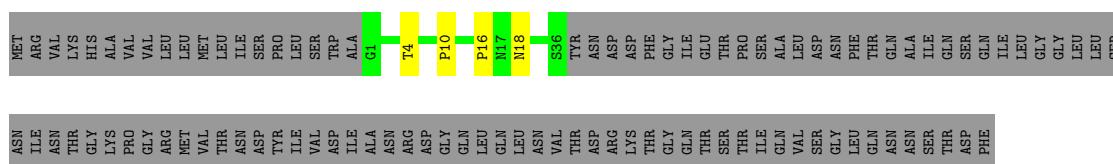
Chain N:  22% 74%

MET	ARG	VAL	LYS	HIS	ALA	VAL	VAL	LEU	LEU	MET	LEU	ILE	SER	PRO	LEU	SER	TRP	ALA	GLY	T4	P10	P16	R17	N18	K33	S36	TYR	ASN	ASP	ARG	LYS	PHE	GLY	ILE	GLU	THR	PRO	ALA	SER	ASP	ASN	PHE	THR	GLN	ALA	ILE	SER	ASP	GLN	ILE	LEU	GLY	LEU
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LEU	SER	ASN	ILE	THR	GLY	LYS	PRO	GLY	ARG	MET	VAL	THR	ASP	TYR	ILE	VAL	ASP	ILE	ALA	ASN	ARG	ASP	GLY	GLN	LEU	GLN	LEU	ASN	VAL	THR	ASN	ASP	ARG	LYS	THR	GLY	GLN	THR	SER	THR	ILE	GLN	VAL	SER	GLY	ASN	LEU	PHE	THR	GLN	ASN	ASP	PHE
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• Molecule 2: CsgF

Chain O:  23% 74%



- Molecule 2: CsgF



- Molecule 2: CsgF



- Molecule 3: Major curlin subunit CsgA

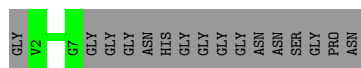


- Molecule 3: Major curlin subunit CsgA



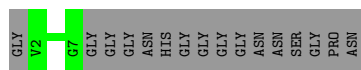
- Molecule 3: Major curlin subunit CsgA

Chain U:  27% 73%



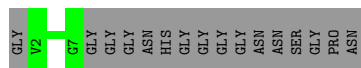
- Molecule 3: Major curlin subunit CsgA

Chain V:  27% 73%



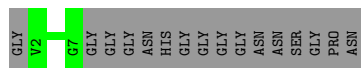
- Molecule 3: Major curlin subunit CsgA

Chain W:  27% 73%



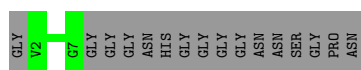
- Molecule 3: Major curlin subunit CsgA

Chain X:  27% 73%



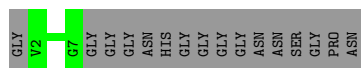
- Molecule 3: Major curlin subunit CsgA

Chain Y:  27% 73%



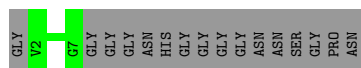
- Molecule 3: Major curlin subunit CsgA

Chain Z:  27% 73%



- Molecule 3: Major curlin subunit CsgA

Chain a:  27% 73%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	139702	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI/PHILIPS CM300FEG/HE	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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 >2	RMSZ	# Z >2
1	A	0.32	0/2003	0.54	1/2720 (0.0%)
1	B	0.32	0/2003	0.54	1/2720 (0.0%)
1	C	0.32	0/2003	0.54	1/2720 (0.0%)
1	D	0.32	0/2003	0.54	1/2720 (0.0%)
1	E	0.32	0/2003	0.54	1/2720 (0.0%)
1	F	0.32	0/2003	0.54	1/2720 (0.0%)
1	G	0.32	0/2003	0.54	1/2720 (0.0%)
1	H	0.32	0/2003	0.54	1/2720 (0.0%)
1	I	0.32	0/2003	0.54	1/2720 (0.0%)
2	J	0.29	0/282	0.45	0/381
2	K	0.29	0/282	0.45	0/381
2	L	0.29	0/282	0.45	0/381
2	M	0.29	0/282	0.45	0/381
2	N	0.30	0/282	0.45	0/381
2	O	0.29	0/282	0.45	0/381
2	P	0.29	0/282	0.45	0/381
2	Q	0.29	0/282	0.45	0/381
2	R	0.29	0/282	0.46	0/381
3	S	0.32	0/47	0.44	0/64
3	T	0.33	0/47	0.44	0/64
3	U	0.32	0/47	0.44	0/64
3	V	0.32	0/47	0.44	0/64
3	W	0.32	0/47	0.44	0/64
3	X	0.33	0/47	0.44	0/64
3	Y	0.32	0/47	0.44	0/64
3	Z	0.32	0/47	0.44	0/64
3	a	0.33	0/47	0.44	0/64
All	All	0.31	0/20988	0.53	9/28485 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	154	LEU	CA-CB-CG	5.25	127.39	115.30
1	D	154	LEU	CA-CB-CG	5.25	127.38	115.30
1	E	154	LEU	CA-CB-CG	5.25	127.38	115.30
1	C	154	LEU	CA-CB-CG	5.25	127.36	115.30
1	H	154	LEU	CA-CB-CG	5.24	127.36	115.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	ASP	Peptide
1	B	195	ASP	Peptide
1	C	195	ASP	Peptide
1	D	195	ASP	Peptide
1	E	195	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1968	0	1979	19	0
1	B	1968	0	1979	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1968	0	1979	14	0
1	D	1968	0	1979	17	0
1	E	1968	0	1979	19	0
1	F	1968	0	1979	16	0
1	G	1968	0	1979	18	0
1	H	1968	0	1979	17	0
1	I	1968	0	1979	15	0
2	J	275	0	251	4	0
2	K	275	0	251	4	0
2	L	275	0	251	4	0
2	M	275	0	251	3	0
2	N	275	0	251	4	0
2	O	275	0	251	3	0
2	P	275	0	251	4	0
2	Q	275	0	251	4	0
2	R	275	0	251	3	0
3	S	46	0	44	0	0
3	T	46	0	44	0	0
3	U	46	0	44	0	0
3	V	46	0	44	0	0
3	W	46	0	44	0	0
3	X	46	0	44	0	0
3	Y	46	0	44	0	0
3	Z	46	0	44	0	0
3	a	46	0	44	0	0
All	All	20601	0	20466	154	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 4.

The worst 5 of 154 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:K:16:PRO:HB3	2:L:18:ASN:HB3	1.75	0.67
2:J:18:ASN:HB3	2:R:16:PRO:HB3	1.77	0.67
2:M:16:PRO:HB3	2:N:18:ASN:HB3	1.76	0.65
2:J:16:PRO:HB3	2:K:18:ASN:HB3	1.81	0.62
2:L:16:PRO:HB3	2:M:18:ASN:HB3	1.83	0.60

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	B	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	C	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	D	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	E	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	F	251/277 (91%)	239 (95%)	12 (5%)	0	100	100
1	G	251/277 (91%)	239 (95%)	12 (5%)	0	100	100
1	H	251/277 (91%)	240 (96%)	11 (4%)	0	100	100
1	I	251/277 (91%)	239 (95%)	12 (5%)	0	100	100
2	J	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	K	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	L	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	M	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	N	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	O	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	P	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	Q	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
2	R	34/138 (25%)	33 (97%)	1 (3%)	0	100	100
3	S	4/22 (18%)	4 (100%)	0	0	100	100
3	T	4/22 (18%)	4 (100%)	0	0	100	100
3	U	4/22 (18%)	4 (100%)	0	0	100	100
3	V	4/22 (18%)	4 (100%)	0	0	100	100
3	W	4/22 (18%)	4 (100%)	0	0	100	100
3	X	4/22 (18%)	4 (100%)	0	0	100	100
3	Y	4/22 (18%)	4 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Z	4/22 (18%)	4 (100%)	0	0	100	100
3	a	4/22 (18%)	4 (100%)	0	0	100	100
All	All	2601/3933 (66%)	2490 (96%)	111 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	B	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	C	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	D	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	E	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	F	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	G	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	H	216/236 (92%)	215 (100%)	1 (0%)	90	95
1	I	216/236 (92%)	215 (100%)	1 (0%)	90	95
2	J	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	K	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	L	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	M	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	N	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	O	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	P	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	Q	29/118 (25%)	28 (97%)	1 (3%)	40	71
2	R	29/118 (25%)	28 (97%)	1 (3%)	40	71
3	S	5/12 (42%)	5 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	T	5/12 (42%)	5 (100%)	0	100	100
3	U	5/12 (42%)	5 (100%)	0	100	100
3	V	5/12 (42%)	5 (100%)	0	100	100
3	W	5/12 (42%)	5 (100%)	0	100	100
3	X	5/12 (42%)	5 (100%)	0	100	100
3	Y	5/12 (42%)	5 (100%)	0	100	100
3	Z	5/12 (42%)	5 (100%)	0	100	100
3	a	5/12 (42%)	5 (100%)	0	100	100
All	All	2250/3294 (68%)	2232 (99%)	18 (1%)	84	91

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	261	GLU
2	J	4	THR
2	O	4	THR
1	G	261	GLU
1	H	261	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	17	ASN
2	L	17	ASN
2	P	17	ASN
2	J	17	ASN
2	O	17	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.