



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:42 AM UTC

PDB ID : 4JDO / pdb\_00004jdo  
Title : Secreted chlamydial protein pgp3, coiled-coil deletion  
Authors : Galaledeen, A.; Taylor, A.B.; Chen, D.; Holloway, S.P.; Zhong, G.; Hart, P.J.  
Deposited on : 2013-02-25  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

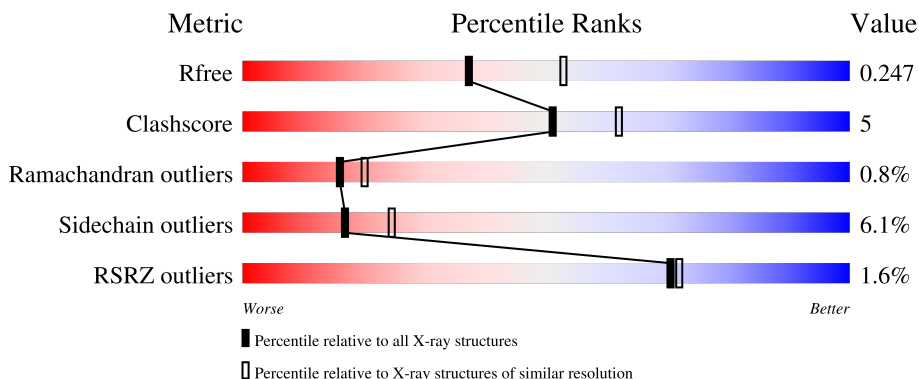
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	219	 86% 11% ..
1	B	219	 83% 17%
1	C	219	 84% 15% ..
1	D	219	 83% 14% ..
1	E	219	 80% 16% ..

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Mol	Chain	Length	Quality of chain
1	F	219	 84% 12% ..
1	G	219	 2% 81% 16% ..
1	H	219	 83% 12% ..
1	I	219	 % 84% 13% ..

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15034 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Virulence plasmid protein pGP3-D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	215	Total 1578	C 990	N 261	O 319	S 4	Se 4	0	0	0
1	B	218	Total 1603	C 1006	N 264	O 323	S 4	Se 6	0	1	0
1	C	217	Total 1593	C 999	N 263	O 322	S 4	Se 5	0	0	0
1	D	217	Total 1593	C 998	N 264	O 323	S 4	Se 4	0	0	0
1	E	215	Total 1580	C 992	N 261	O 318	S 4	Se 5	0	0	0
1	F	217	Total 1598	C 1003	N 263	O 322	S 4	Se 6	0	1	0
1	G	217	Total 1593	C 999	N 263	O 322	S 4	Se 5	0	0	0
1	H	216	Total 1586	C 995	N 262	O 320	S 4	Se 5	0	0	0
1	I	217	Total 1593	C 999	N 263	O 322	S 4	Se 5	0	0	0

There are 414 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
A	?	-	GLY	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	ALA	deletion	UNP A0A0E9CJA7
A	?	-	GLU	deletion	UNP A0A0E9CJA7
A	?	-	LYS	deletion	UNP A0A0E9CJA7
A	?	-	ALA	deletion	UNP A0A0E9CJA7
A	?	-	TYR	deletion	UNP A0A0E9CJA7
A	?	-	GLN	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
A	?	-	GLU	deletion	UNP A0A0E9CJA7
A	?	-	LYS	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
A	?	-	GLY	deletion	UNP A0A0E9CJA7
A	?	-	ASN	deletion	UNP A0A0E9CJA7
A	?	-	GLN	deletion	UNP A0A0E9CJA7
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	GLY	deletion	UNP A0A0E9CJA7
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	ALA	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	THR	deletion	UNP A0A0E9CJA7
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	VAL	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	SER	deletion	UNP A0A0E9CJA7
A	?	-	THR	deletion	UNP A0A0E9CJA7
A	?	-	VAL	deletion	UNP A0A0E9CJA7
A	?	-	GLN	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	LYS	deletion	UNP A0A0E9CJA7
A	?	-	ILE	deletion	UNP A0A0E9CJA7
A	?	-	THR	deletion	UNP A0A0E9CJA7
A	?	-	THR	deletion	UNP A0A0E9CJA7
A	?	-	ASP	deletion	UNP A0A0E9CJA7
A	?	-	PRO	deletion	UNP A0A0E9CJA7
A	?	-	SER	deletion	UNP A0A0E9CJA7
A	?	-	LEU	deletion	UNP A0A0E9CJA7
B	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
B	?	-	GLY	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	ALA	deletion	UNP A0A0E9CJA7
B	?	-	GLU	deletion	UNP A0A0E9CJA7
B	?	-	LYS	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ALA	deletion	UNP A0A0E9CJA7
B	?	-	TYR	deletion	UNP A0A0E9CJA7
B	?	-	GLN	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	GLU	deletion	UNP A0A0E9CJA7
B	?	-	LYS	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	GLY	deletion	UNP A0A0E9CJA7
B	?	-	ASN	deletion	UNP A0A0E9CJA7
B	?	-	GLN	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	GLY	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	ALA	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	THR	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	VAL	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	SER	deletion	UNP A0A0E9CJA7
B	?	-	THR	deletion	UNP A0A0E9CJA7
B	?	-	VAL	deletion	UNP A0A0E9CJA7
B	?	-	GLN	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	LYS	deletion	UNP A0A0E9CJA7
B	?	-	ILE	deletion	UNP A0A0E9CJA7
B	?	-	THR	deletion	UNP A0A0E9CJA7
B	?	-	THR	deletion	UNP A0A0E9CJA7
B	?	-	ASP	deletion	UNP A0A0E9CJA7
B	?	-	PRO	deletion	UNP A0A0E9CJA7
B	?	-	SER	deletion	UNP A0A0E9CJA7
B	?	-	LEU	deletion	UNP A0A0E9CJA7
C	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
C	?	-	GLY	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	ALA	deletion	UNP A0A0E9CJA7
C	?	-	GLU	deletion	UNP A0A0E9CJA7
C	?	-	LYS	deletion	UNP A0A0E9CJA7
C	?	-	ALA	deletion	UNP A0A0E9CJA7
C	?	-	TYR	deletion	UNP A0A0E9CJA7
C	?	-	GLN	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7
C	?	-	GLU	deletion	UNP A0A0E9CJA7
C	?	-	LYS	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7
C	?	-	GLY	deletion	UNP A0A0E9CJA7
C	?	-	ASN	deletion	UNP A0A0E9CJA7
C	?	-	GLN	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	GLY	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	ALA	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	THR	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	VAL	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	SER	deletion	UNP A0A0E9CJA7
C	?	-	THR	deletion	UNP A0A0E9CJA7
C	?	-	VAL	deletion	UNP A0A0E9CJA7
C	?	-	GLN	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	LEU	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	LYS	deletion	UNP A0A0E9CJA7
C	?	-	ILE	deletion	UNP A0A0E9CJA7
C	?	-	THR	deletion	UNP A0A0E9CJA7
C	?	-	THR	deletion	UNP A0A0E9CJA7
C	?	-	ASP	deletion	UNP A0A0E9CJA7
C	?	-	PRO	deletion	UNP A0A0E9CJA7
C	?	-	SER	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	LEU	deletion	UNP A0A0E9CJA7
D	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
D	?	-	GLY	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	ALA	deletion	UNP A0A0E9CJA7
D	?	-	GLU	deletion	UNP A0A0E9CJA7
D	?	-	LYS	deletion	UNP A0A0E9CJA7
D	?	-	ALA	deletion	UNP A0A0E9CJA7
D	?	-	TYR	deletion	UNP A0A0E9CJA7
D	?	-	GLN	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	GLU	deletion	UNP A0A0E9CJA7
D	?	-	LYS	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	GLY	deletion	UNP A0A0E9CJA7
D	?	-	ASN	deletion	UNP A0A0E9CJA7
D	?	-	GLN	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	GLY	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	ALA	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	THR	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	VAL	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	SER	deletion	UNP A0A0E9CJA7
D	?	-	THR	deletion	UNP A0A0E9CJA7
D	?	-	VAL	deletion	UNP A0A0E9CJA7
D	?	-	GLN	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	LYS	deletion	UNP A0A0E9CJA7
D	?	-	ILE	deletion	UNP A0A0E9CJA7
D	?	-	THR	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	THR	deletion	UNP A0A0E9CJA7
D	?	-	ASP	deletion	UNP A0A0E9CJA7
D	?	-	PRO	deletion	UNP A0A0E9CJA7
D	?	-	SER	deletion	UNP A0A0E9CJA7
D	?	-	LEU	deletion	UNP A0A0E9CJA7
E	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
E	?	-	GLY	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	ALA	deletion	UNP A0A0E9CJA7
E	?	-	GLU	deletion	UNP A0A0E9CJA7
E	?	-	LYS	deletion	UNP A0A0E9CJA7
E	?	-	ALA	deletion	UNP A0A0E9CJA7
E	?	-	TYR	deletion	UNP A0A0E9CJA7
E	?	-	GLN	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
E	?	-	GLU	deletion	UNP A0A0E9CJA7
E	?	-	LYS	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
E	?	-	GLY	deletion	UNP A0A0E9CJA7
E	?	-	ASN	deletion	UNP A0A0E9CJA7
E	?	-	GLN	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	GLY	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	ALA	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	THR	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	VAL	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	SER	deletion	UNP A0A0E9CJA7
E	?	-	THR	deletion	UNP A0A0E9CJA7
E	?	-	VAL	deletion	UNP A0A0E9CJA7
E	?	-	GLN	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	LYS	deletion	UNP A0A0E9CJA7
E	?	-	ILE	deletion	UNP A0A0E9CJA7
E	?	-	THR	deletion	UNP A0A0E9CJA7
E	?	-	THR	deletion	UNP A0A0E9CJA7
E	?	-	ASP	deletion	UNP A0A0E9CJA7
E	?	-	PRO	deletion	UNP A0A0E9CJA7
E	?	-	SER	deletion	UNP A0A0E9CJA7
E	?	-	LEU	deletion	UNP A0A0E9CJA7
F	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
F	?	-	GLY	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	ALA	deletion	UNP A0A0E9CJA7
F	?	-	GLU	deletion	UNP A0A0E9CJA7
F	?	-	LYS	deletion	UNP A0A0E9CJA7
F	?	-	ALA	deletion	UNP A0A0E9CJA7
F	?	-	TYR	deletion	UNP A0A0E9CJA7
F	?	-	GLN	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	GLU	deletion	UNP A0A0E9CJA7
F	?	-	LYS	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	GLY	deletion	UNP A0A0E9CJA7
F	?	-	ASN	deletion	UNP A0A0E9CJA7
F	?	-	GLN	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	GLY	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	ALA	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	THR	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	VAL	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	SER	deletion	UNP A0A0E9CJA7
F	?	-	THR	deletion	UNP A0A0E9CJA7
F	?	-	VAL	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLN	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	LYS	deletion	UNP A0A0E9CJA7
F	?	-	ILE	deletion	UNP A0A0E9CJA7
F	?	-	THR	deletion	UNP A0A0E9CJA7
F	?	-	THR	deletion	UNP A0A0E9CJA7
F	?	-	ASP	deletion	UNP A0A0E9CJA7
F	?	-	PRO	deletion	UNP A0A0E9CJA7
F	?	-	SER	deletion	UNP A0A0E9CJA7
F	?	-	LEU	deletion	UNP A0A0E9CJA7
G	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
G	?	-	GLY	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	ALA	deletion	UNP A0A0E9CJA7
G	?	-	GLU	deletion	UNP A0A0E9CJA7
G	?	-	LYS	deletion	UNP A0A0E9CJA7
G	?	-	ALA	deletion	UNP A0A0E9CJA7
G	?	-	TYR	deletion	UNP A0A0E9CJA7
G	?	-	GLN	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	GLU	deletion	UNP A0A0E9CJA7
G	?	-	LYS	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	GLY	deletion	UNP A0A0E9CJA7
G	?	-	ASN	deletion	UNP A0A0E9CJA7
G	?	-	GLN	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	GLY	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	ALA	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	THR	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	VAL	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	SER	deletion	UNP A0A0E9CJA7
G	?	-	THR	deletion	UNP A0A0E9CJA7
G	?	-	VAL	deletion	UNP A0A0E9CJA7
G	?	-	GLN	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	LYS	deletion	UNP A0A0E9CJA7
G	?	-	ILE	deletion	UNP A0A0E9CJA7
G	?	-	THR	deletion	UNP A0A0E9CJA7
G	?	-	THR	deletion	UNP A0A0E9CJA7
G	?	-	ASP	deletion	UNP A0A0E9CJA7
G	?	-	PRO	deletion	UNP A0A0E9CJA7
G	?	-	SER	deletion	UNP A0A0E9CJA7
G	?	-	LEU	deletion	UNP A0A0E9CJA7
H	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
H	?	-	GLY	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	ALA	deletion	UNP A0A0E9CJA7
H	?	-	GLU	deletion	UNP A0A0E9CJA7
H	?	-	LYS	deletion	UNP A0A0E9CJA7
H	?	-	ALA	deletion	UNP A0A0E9CJA7
H	?	-	TYR	deletion	UNP A0A0E9CJA7
H	?	-	GLN	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	GLU	deletion	UNP A0A0E9CJA7
H	?	-	LYS	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	GLY	deletion	UNP A0A0E9CJA7
H	?	-	ASN	deletion	UNP A0A0E9CJA7
H	?	-	GLN	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	GLY	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	ALA	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	THR	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	VAL	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	SER	deletion	UNP A0A0E9CJA7
H	?	-	THR	deletion	UNP A0A0E9CJA7
H	?	-	VAL	deletion	UNP A0A0E9CJA7
H	?	-	GLN	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	LYS	deletion	UNP A0A0E9CJA7
H	?	-	ILE	deletion	UNP A0A0E9CJA7
H	?	-	THR	deletion	UNP A0A0E9CJA7
H	?	-	THR	deletion	UNP A0A0E9CJA7
H	?	-	ASP	deletion	UNP A0A0E9CJA7
H	?	-	PRO	deletion	UNP A0A0E9CJA7
H	?	-	SER	deletion	UNP A0A0E9CJA7
H	?	-	LEU	deletion	UNP A0A0E9CJA7
I	1	MSE	-	initiating methionine	UNP A0A0E9CJA7
I	?	-	GLY	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	ALA	deletion	UNP A0A0E9CJA7
I	?	-	GLU	deletion	UNP A0A0E9CJA7
I	?	-	LYS	deletion	UNP A0A0E9CJA7
I	?	-	ALA	deletion	UNP A0A0E9CJA7
I	?	-	TYR	deletion	UNP A0A0E9CJA7
I	?	-	GLN	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7
I	?	-	GLU	deletion	UNP A0A0E9CJA7
I	?	-	LYS	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7
I	?	-	GLY	deletion	UNP A0A0E9CJA7
I	?	-	ASN	deletion	UNP A0A0E9CJA7
I	?	-	GLN	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7

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Chain	Residue	Modelled	Actual	Comment	Reference
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	GLY	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	ALA	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	THR	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	VAL	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	SER	deletion	UNP A0A0E9CJA7
I	?	-	THR	deletion	UNP A0A0E9CJA7
I	?	-	VAL	deletion	UNP A0A0E9CJA7
I	?	-	GLN	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	LYS	deletion	UNP A0A0E9CJA7
I	?	-	ILE	deletion	UNP A0A0E9CJA7
I	?	-	THR	deletion	UNP A0A0E9CJA7
I	?	-	THR	deletion	UNP A0A0E9CJA7
I	?	-	ASP	deletion	UNP A0A0E9CJA7
I	?	-	PRO	deletion	UNP A0A0E9CJA7
I	?	-	SER	deletion	UNP A0A0E9CJA7
I	?	-	LEU	deletion	UNP A0A0E9CJA7

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	D	1	Total Na 1 1	0	0
2	G	1	Total Na 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	71	Total O 71 71	0	0

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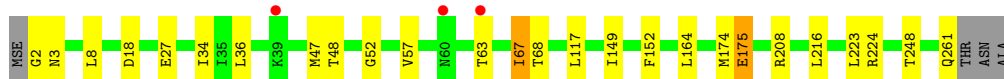
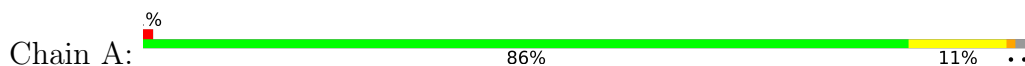
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	B	65	Total 65	O 65	0	0
3	C	77	Total 77	O 77	0	0
3	D	85	Total 85	O 85	0	0
3	E	71	Total 71	O 71	0	0
3	F	87	Total 87	O 87	0	0
3	G	78	Total 78	O 78	0	0
3	H	84	Total 84	O 84	0	0
3	I	96	Total 96	O 96	0	0

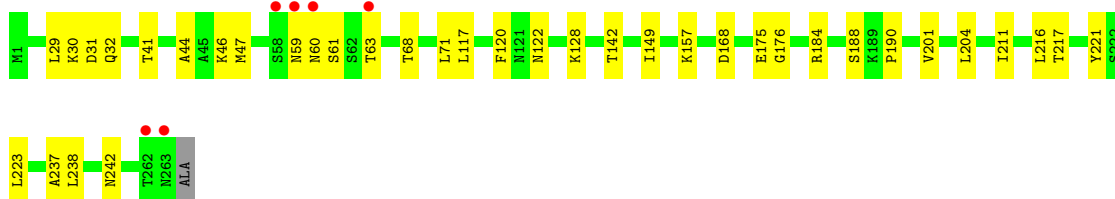
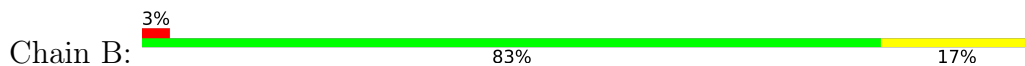
### 3 Residue-property plots [i](#)

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 and electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

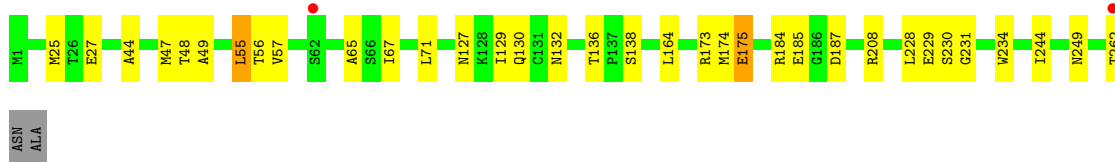
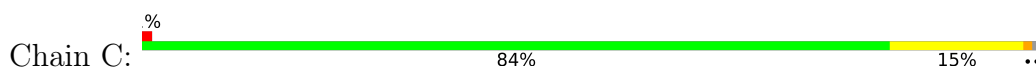
- Molecule 1: Virulence plasmid protein pGP3-D



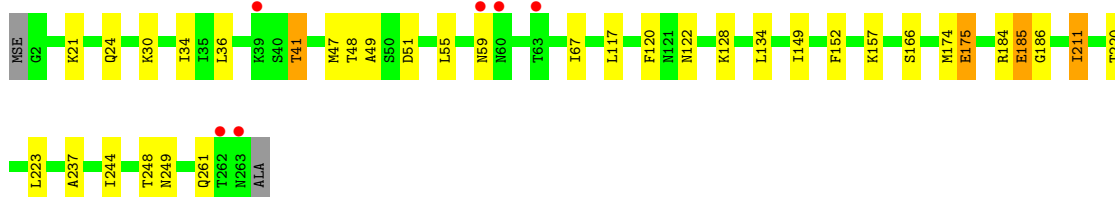
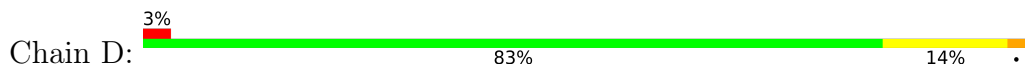
- Molecule 1: Virulence plasmid protein pGP3-D



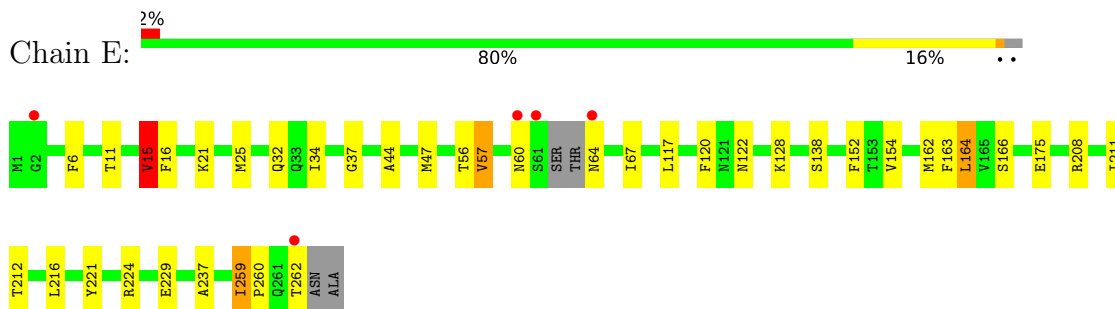
- Molecule 1: Virulence plasmid protein pGP3-D



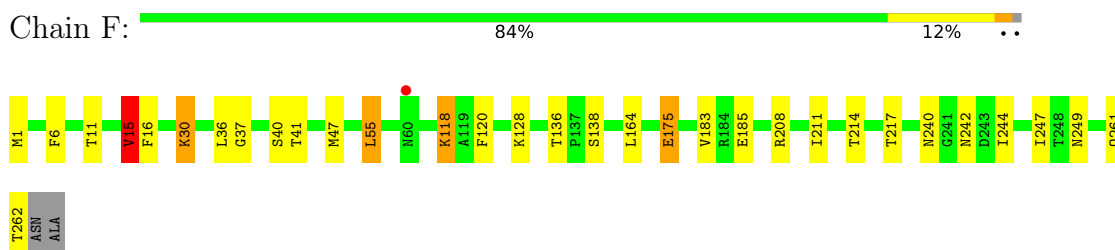
- Molecule 1: Virulence plasmid protein pGP3-D



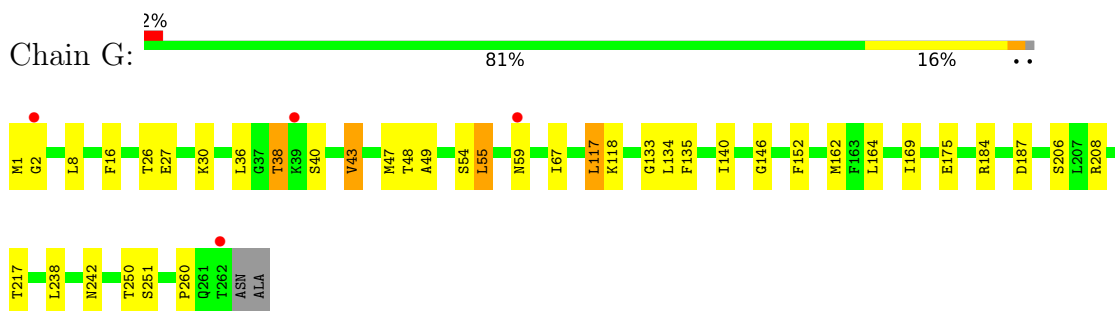
- Molecule 1: Virulence plasmid protein pGP3-D



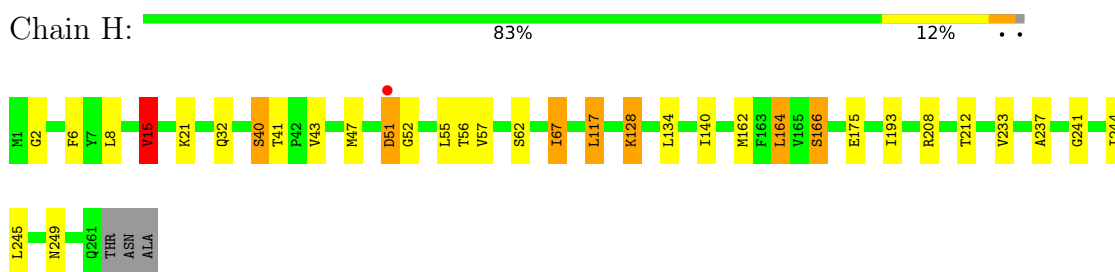
- Molecule 1: Virulence plasmid protein pGP3-D



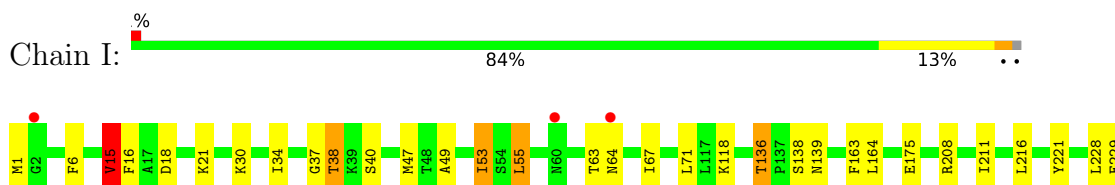
- Molecule 1: Virulence plasmid protein pGP3-D

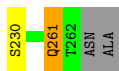


- Molecule 1: Virulence plasmid protein pGP3-D



- Molecule 1: Virulence plasmid protein pGP3-D





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.24Å 146.24Å 161.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.46 – 2.30 29.46 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.46-2.30) 99.7 (29.46-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 2.31Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.184 , 0.242 0.189 , 0.247	Depositor DCC
$R_{free}$ test set	4312 reflections (2.53%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.0	Xtrriage
Anisotropy	0.189	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 32.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.031 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15034	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.00 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6973e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
NA

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	A	0.54	0/1597	0.83	0/2166
1	B	0.51	0/1625	0.91	3/2203 (0.1%)
1	C	0.51	0/1612	0.86	0/2186
1	D	0.59	0/1612	0.90	1/2187 (0.0%)
1	E	0.56	0/1598	0.90	4/2165 (0.2%)
1	F	0.54	0/1620	0.90	1/2196 (0.0%)
1	G	0.58	0/1612	0.89	1/2186 (0.0%)
1	H	0.59	0/1605	0.91	1/2176 (0.0%)
1	I	0.58	0/1612	0.90	1/2186 (0.0%)
All	All	0.56	0/14493	0.89	12/19651 (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	G	0	1

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	2	GLY	N-CA-C	-8.31	104.40	115.21
1	F	15	VAL	CB-CA-C	-7.96	100.03	111.34
1	I	15	VAL	CB-CA-C	-6.78	102.27	111.63
1	E	15	VAL	CB-CA-C	-6.11	102.85	111.28
1	B	41	THR	CA-C-N	-6.05	114.38	120.31

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	1	MSE	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	1578	0	1590	15	0
1	B	1603	0	1620	18	0
1	C	1593	0	1609	23	0
1	D	1593	0	1603	17	0
1	E	1580	0	1596	23	0
1	F	1598	0	1619	20	0
1	G	1593	0	1609	22	0
1	H	1586	0	1602	20	0
1	I	1593	0	1609	23	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
2	G	1	0	0	0	0
3	A	71	0	0	1	0
3	B	65	0	0	2	0
3	C	77	0	0	0	0
3	D	85	0	0	0	0
3	E	71	0	0	2	0
3	F	87	0	0	0	0
3	G	78	0	0	0	0
3	H	84	0	0	0	0
3	I	96	0	0	1	0
All	All	15034	0	14457	149	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 5.

The worst 5 of 149 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)
1:F:136:THR:HG22	1:F:138:SER:H	1.33	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:162:MSE:HE2	1:E:260:PRO:HB3	1.52	0.92
1:E:128:LYS:HG2	1:E:237:ALA:HB2	1.57	0.85
1:H:128:LYS:HG2	1:H:237:ALA:HB2	1.60	0.82
1:G:118:LYS:HE2	1:I:261:GLN:HA	1.60	0.81

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 X-ray entries followed by that with respect to entries of similar resolution.

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	213/219 (97%)	202 (95%)	10 (5%)	1 (0%)	24	31
1	B	217/219 (99%)	207 (95%)	8 (4%)	2 (1%)	14	17
1	C	215/219 (98%)	206 (96%)	7 (3%)	2 (1%)	14	17
1	D	215/219 (98%)	200 (93%)	14 (6%)	1 (0%)	24	31
1	E	211/219 (96%)	203 (96%)	7 (3%)	1 (0%)	24	31
1	F	216/219 (99%)	207 (96%)	8 (4%)	1 (0%)	24	31
1	G	215/219 (98%)	205 (95%)	8 (4%)	2 (1%)	14	17
1	H	214/219 (98%)	205 (96%)	6 (3%)	3 (1%)	9	9
1	I	215/219 (98%)	204 (95%)	9 (4%)	2 (1%)	14	17
All	All	1931/1971 (98%)	1839 (95%)	77 (4%)	15 (1%)	16	20

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	229	GLU
1	H	51	ASP
1	B	175	GLU
1	F	175	GLU
1	A	175	GLU

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	182/180 (101%)	174 (96%)	8 (4%)	25	38
1	B	185/180 (103%)	179 (97%)	6 (3%)	34	51
1	C	184/180 (102%)	179 (97%)	5 (3%)	39	58
1	D	184/180 (102%)	174 (95%)	10 (5%)	20	29
1	E	182/180 (101%)	165 (91%)	17 (9%)	8	11
1	F	185/180 (103%)	168 (91%)	17 (9%)	8	11
1	G	184/180 (102%)	172 (94%)	12 (6%)	15	22
1	H	183/180 (102%)	170 (93%)	13 (7%)	13	19
1	I	184/180 (102%)	172 (94%)	12 (6%)	15	22
All	All	1653/1620 (102%)	1553 (94%)	100 (6%)	17	25

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	211	ILE
1	G	134	LEU
1	I	261	GLN
1	F	217	THR
1	G	27	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	121	ASN
1	G	59	ASN
1	H	132	ASN
1	F	249	ASN
1	G	60	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	211/219 (96%)	-0.19	3 (1%) 73 75	18, 28, 43, 53	0
1	B	213/219 (97%)	0.01	6 (2%) 55 57	20, 32, 49, 66	0
1	C	212/219 (96%)	-0.02	2 (0%) 81 82	21, 31, 46, 53	0
1	D	213/219 (97%)	-0.12	6 (2%) 55 57	17, 26, 37, 58	0
1	E	210/219 (95%)	0.08	5 (2%) 59 62	18, 29, 42, 63	0
1	F	212/219 (96%)	-0.10	1 (0%) 87 87	17, 28, 40, 44	0
1	G	212/219 (96%)	-0.11	4 (1%) 66 68	16, 26, 43, 53	0
1	H	211/219 (96%)	-0.14	1 (0%) 87 87	15, 25, 42, 57	0
1	I	212/219 (96%)	-0.25	3 (1%) 73 75	15, 25, 38, 48	0
All	All	1906/1971 (96%)	-0.09	31 (1%) 70 72	15, 28, 43, 66	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	61	SER	4.4
1	D	263	ASN	4.3
1	B	60	ASN	3.6
1	E	262	THR	3.6
1	D	60	ASN	3.5

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NA	G	301	1/1	0.91	0.17	29,29,29,29	0
2	NA	D	301	1/1	0.94	0.06	32,32,32,32	0
2	NA	A	301	1/1	0.94	0.07	31,31,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.