wwPDB X-ray Structure Validation Summary Report (i)

Jun 16, 2024 – 11:56 AM EDT

PDB ID	:	5ED0
Title	:	Structure of the Shigella flexneri VapC mutant D7N
Authors	:	Xu, K.; Dedic, E.; Brodersen, D.E.
Deposited on	:	2015-10-20
Resolution	:	2.10 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

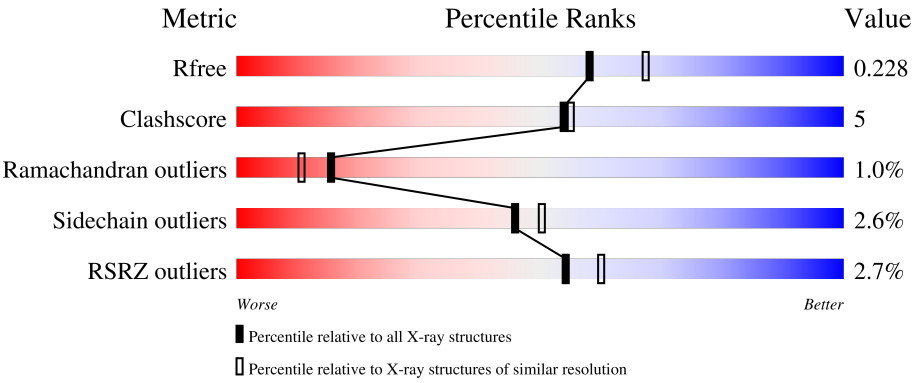
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 >=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 <=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	138	91% 5%
1	B	138	% 82% 12%
1	C	138	3% 86% 7%
1	D	138	6% 80% 14%
1	E	138	% 83% 8%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	138	6% 83% 12%
1	G	138	4% 85% 11%
1	H	138	% 85% 10%
1	I	138	4% 78% 14%
1	J	138	2% 79% 14%
1	K	138	% 86% 9%
1	L	138	2% 77% 16%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13853 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 tRNA(fMet)-specific endonuclease VapC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	0	1	0
			1041	650	192	191	8			
1	B	132	Total	C	N	O	S	0	0	0
			1033	645	191	190	7			
1	C	132	Total	C	N	O	S	0	0	0
			1024	641	187	189	7			
1	D	132	Total	C	N	O	S	0	1	0
			1043	652	193	190	8			
1	E	132	Total	C	N	O	S	0	0	0
			1033	645	191	190	7			
1	F	132	Total	C	N	O	S	0	0	0
			1022	640	187	188	7			
1	G	132	Total	C	N	O	S	0	0	0
			1025	641	188	189	7			
1	H	132	Total	C	N	O	S	0	0	0
			1031	645	192	187	7			
1	I	132	Total	C	N	O	S	0	2	0
			1040	650	190	192	8			
1	J	132	Total	C	N	O	S	0	1	0
			1025	642	186	190	7			
1	K	132	Total	C	N	O	S	0	0	0
			1031	645	192	187	7			
1	L	132	Total	C	N	O	S	0	1	0
			1029	645	186	191	7			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP O06662
A	-4	HIS	-	expression tag	UNP O06662
A	-3	HIS	-	expression tag	UNP O06662
A	-2	HIS	-	expression tag	UNP O06662
A	-1	HIS	-	expression tag	UNP O06662

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP O06662
A	1	HIS	-	expression tag	UNP O06662
A	7	ASN	ASP	engineered mutation	UNP O06662
B	-5	MET	-	initiating methionine	UNP O06662
B	-4	HIS	-	expression tag	UNP O06662
B	-3	HIS	-	expression tag	UNP O06662
B	-2	HIS	-	expression tag	UNP O06662
B	-1	HIS	-	expression tag	UNP O06662
B	0	HIS	-	expression tag	UNP O06662
B	1	HIS	-	expression tag	UNP O06662
B	7	ASN	ASP	engineered mutation	UNP O06662
C	-5	MET	-	initiating methionine	UNP O06662
C	-4	HIS	-	expression tag	UNP O06662
C	-3	HIS	-	expression tag	UNP O06662
C	-2	HIS	-	expression tag	UNP O06662
C	-1	HIS	-	expression tag	UNP O06662
C	0	HIS	-	expression tag	UNP O06662
C	1	HIS	-	expression tag	UNP O06662
C	7	ASN	ASP	engineered mutation	UNP O06662
D	-5	MET	-	initiating methionine	UNP O06662
D	-4	HIS	-	expression tag	UNP O06662
D	-3	HIS	-	expression tag	UNP O06662
D	-2	HIS	-	expression tag	UNP O06662
D	-1	HIS	-	expression tag	UNP O06662
D	0	HIS	-	expression tag	UNP O06662
D	1	HIS	-	expression tag	UNP O06662
D	7	ASN	ASP	engineered mutation	UNP O06662
E	-5	MET	-	initiating methionine	UNP O06662
E	-4	HIS	-	expression tag	UNP O06662
E	-3	HIS	-	expression tag	UNP O06662
E	-2	HIS	-	expression tag	UNP O06662
E	-1	HIS	-	expression tag	UNP O06662
E	0	HIS	-	expression tag	UNP O06662
E	1	HIS	-	expression tag	UNP O06662
E	7	ASN	ASP	engineered mutation	UNP O06662
F	-5	MET	-	initiating methionine	UNP O06662
F	-4	HIS	-	expression tag	UNP O06662
F	-3	HIS	-	expression tag	UNP O06662
F	-2	HIS	-	expression tag	UNP O06662
F	-1	HIS	-	expression tag	UNP O06662
F	0	HIS	-	expression tag	UNP O06662
F	1	HIS	-	expression tag	UNP O06662

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	7	ASN	ASP	engineered mutation	UNP O06662
G	-5	MET	-	initiating methionine	UNP O06662
G	-4	HIS	-	expression tag	UNP O06662
G	-3	HIS	-	expression tag	UNP O06662
G	-2	HIS	-	expression tag	UNP O06662
G	-1	HIS	-	expression tag	UNP O06662
G	0	HIS	-	expression tag	UNP O06662
G	1	HIS	-	expression tag	UNP O06662
G	7	ASN	ASP	engineered mutation	UNP O06662
H	-5	MET	-	initiating methionine	UNP O06662
H	-4	HIS	-	expression tag	UNP O06662
H	-3	HIS	-	expression tag	UNP O06662
H	-2	HIS	-	expression tag	UNP O06662
H	-1	HIS	-	expression tag	UNP O06662
H	0	HIS	-	expression tag	UNP O06662
H	1	HIS	-	expression tag	UNP O06662
H	7	ASN	ASP	engineered mutation	UNP O06662
I	-5	MET	-	initiating methionine	UNP O06662
I	-4	HIS	-	expression tag	UNP O06662
I	-3	HIS	-	expression tag	UNP O06662
I	-2	HIS	-	expression tag	UNP O06662
I	-1	HIS	-	expression tag	UNP O06662
I	0	HIS	-	expression tag	UNP O06662
I	1	HIS	-	expression tag	UNP O06662
I	7	ASN	ASP	engineered mutation	UNP O06662
J	-5	MET	-	initiating methionine	UNP O06662
J	-4	HIS	-	expression tag	UNP O06662
J	-3	HIS	-	expression tag	UNP O06662
J	-2	HIS	-	expression tag	UNP O06662
J	-1	HIS	-	expression tag	UNP O06662
J	0	HIS	-	expression tag	UNP O06662
J	1	HIS	-	expression tag	UNP O06662
J	7	ASN	ASP	engineered mutation	UNP O06662
K	-5	MET	-	initiating methionine	UNP O06662
K	-4	HIS	-	expression tag	UNP O06662
K	-3	HIS	-	expression tag	UNP O06662
K	-2	HIS	-	expression tag	UNP O06662
K	-1	HIS	-	expression tag	UNP O06662
K	0	HIS	-	expression tag	UNP O06662
K	1	HIS	-	expression tag	UNP O06662
K	7	ASN	ASP	engineered mutation	UNP O06662
L	-5	MET	-	initiating methionine	UNP O06662

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	-4	HIS	-	expression tag	UNP O06662
L	-3	HIS	-	expression tag	UNP O06662
L	-2	HIS	-	expression tag	UNP O06662
L	-1	HIS	-	expression tag	UNP O06662
L	0	HIS	-	expression tag	UNP O06662
L	1	HIS	-	expression tag	UNP O06662
L	7	ASN	ASP	engineered mutation	UNP O06662

- Molecule 2 is water.

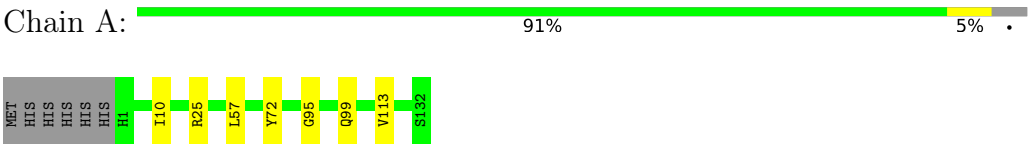
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	143	Total O 143 143	0	0
2	B	123	Total O 123 123	0	0
2	C	116	Total O 116 116	0	0
2	D	148	Total O 148 148	0	0
2	E	137	Total O 137 137	0	0
2	F	103	Total O 103 103	0	0
2	G	127	Total O 127 127	0	0
2	H	122	Total O 122 122	0	0
2	I	116	Total O 116 116	0	0
2	J	102	Total O 102 102	0	0
2	K	139	Total O 139 139	0	0
2	L	100	Total O 100 100	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.

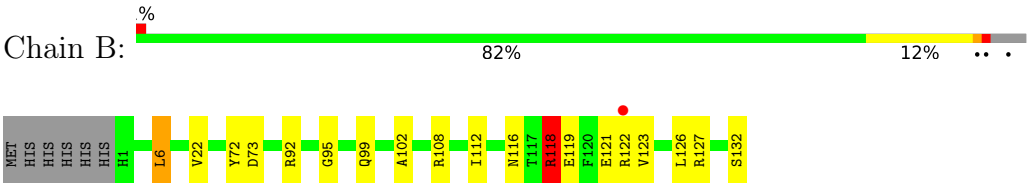
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain A:



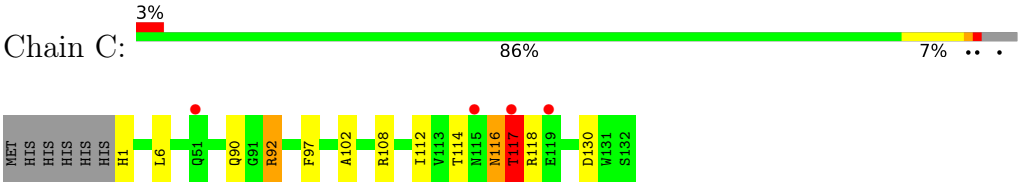
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain B:



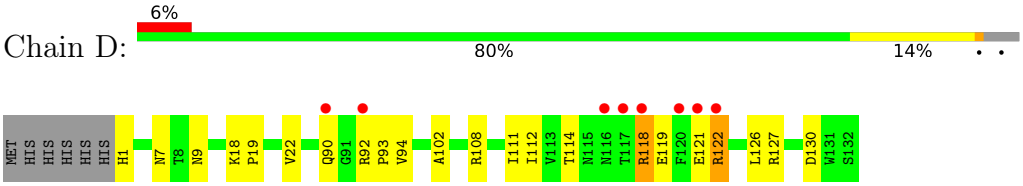
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain C:



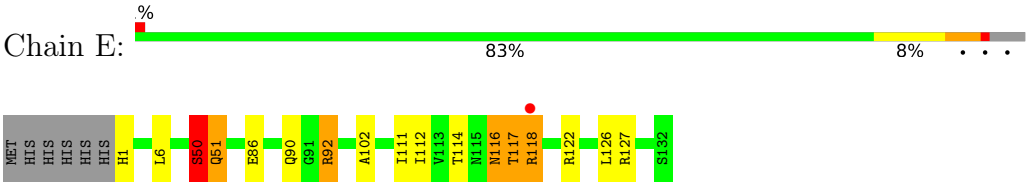
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain D:



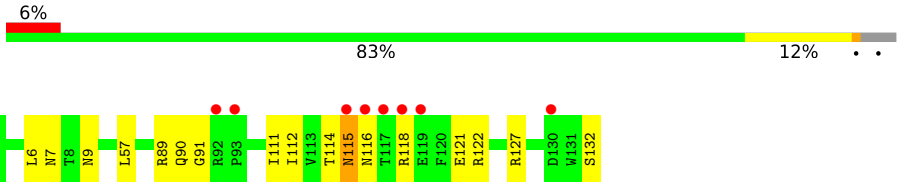
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain E:



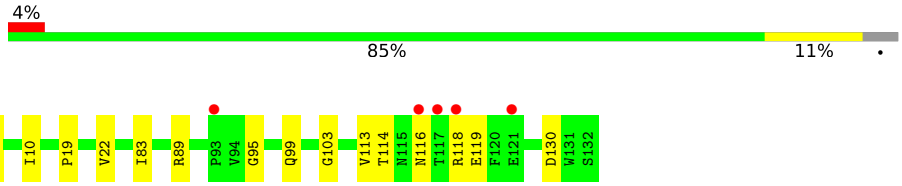
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain F:



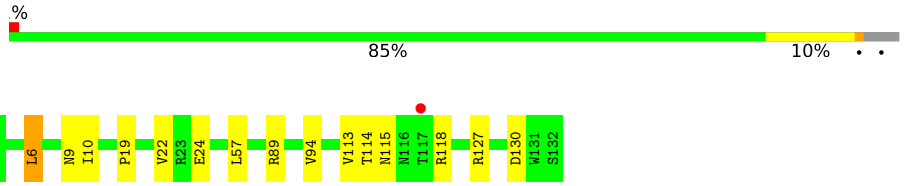
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain G:



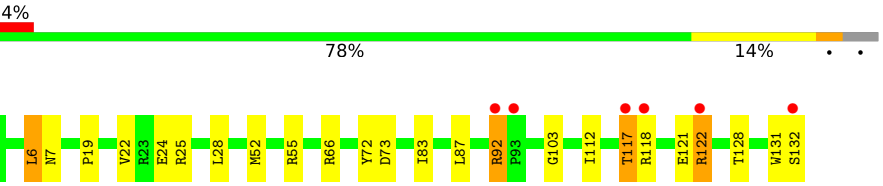
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain H:



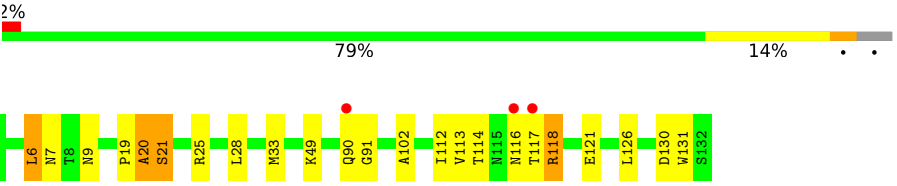
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain I:



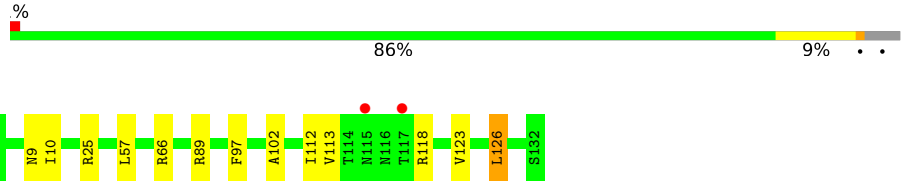
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain J:



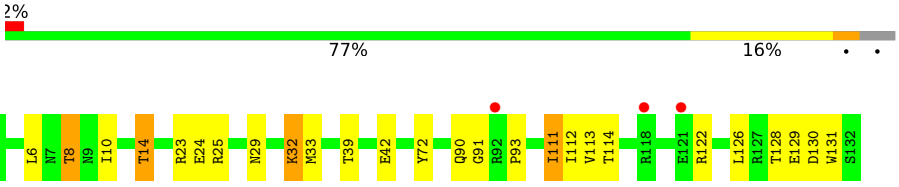
• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain K:



• Molecule 1: tRNA(fMet)-specific endonuclease VapC

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	160.55Å 185.46Å 146.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.41 – 2.10 48.53 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.41-2.10) 99.7 (48.53-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.42 (at 2.10Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.177 , 0.225 0.184 , 0.228	Depositor DCC
R_{free} test set	2000 reflections (1.58%)	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13853	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.44	0/1056	0.57	0/1422
1	B	0.41	0/1048	0.60	1/1411 (0.1%)
1	C	0.41	0/1039	0.64	1/1400 (0.1%)
1	D	0.48	0/1059	0.66	1/1426 (0.1%)
1	E	0.42	0/1048	0.69	2/1411 (0.1%)
1	F	0.38	0/1037	0.64	0/1397
1	G	0.41	0/1040	0.57	0/1401
1	H	0.40	0/1047	0.57	1/1410 (0.1%)
1	I	0.44	0/1055	0.68	5/1422 (0.4%)
1	J	0.38	0/1040	0.74	4/1402 (0.3%)
1	K	0.42	0/1047	0.61	0/1410
1	L	0.40	0/1044	0.57	0/1408
All	All	0.42	0/12560	0.63	15/16920 (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	E	0	1
1	F	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	92	ARG	NE-CZ-NH1	-7.35	116.63	120.30
1	J	20	ALA	N-CA-C	7.06	130.06	111.00
1	I	28	LEU	CA-CB-CG	7.00	131.41	115.30
1	J	20	ALA	C-N-CA	6.66	138.35	121.70
1	C	117	THR	C-N-CA	6.53	138.02	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	50	SER	Peptide
1	F	115	ASN	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	1041	0	1054	4	0
1	B	1033	0	1045	13	0
1	C	1024	0	1030	7	0
1	D	1043	0	1055	19	0
1	E	1033	0	1045	13	0
1	F	1022	0	1025	10	0
1	G	1025	0	1029	9	0
1	H	1031	0	1042	6	0
1	I	1040	0	1044	18	0
1	J	1025	0	1021	17	0
1	K	1031	0	1042	6	0
1	L	1029	0	1033	15	0
2	A	143	0	0	2	0
2	B	123	0	0	2	0
2	C	116	0	0	2	0
2	D	148	0	0	4	0
2	E	137	0	0	2	0
2	F	103	0	0	0	0
2	G	127	0	0	1	0
2	H	122	0	0	1	0
2	I	116	0	0	3	0
2	J	102	0	0	0	0
2	K	139	0	0	1	0
2	L	100	0	0	0	0
All	All	13853	0	12465	131	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 131 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:E:50:SER:HB2	1:E:51:GLN:HB2	1.60	0.82
1:B:92:ARG:HH12	1:B:122:ARG:HB2	1.49	0.77
1:L:6:LEU:HD11	1:L:33:MET:HE2	1.67	0.76
1:D:92:ARG:HH22	1:D:122:ARG:HD3	1.51	0.74
1:D:121:GLU:HG3	1:D:122:ARG:HG3	1.69	0.74

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	131/138 (95%)	129 (98%)	2 (2%)	0	100	100
1	B	130/138 (94%)	127 (98%)	2 (2%)	1 (1%)	19	15
1	C	130/138 (94%)	125 (96%)	2 (2%)	3 (2%)	6	2
1	D	131/138 (95%)	129 (98%)	1 (1%)	1 (1%)	19	15
1	E	130/138 (94%)	124 (95%)	3 (2%)	3 (2%)	6	2
1	F	130/138 (94%)	126 (97%)	4 (3%)	0	100	100
1	G	130/138 (94%)	128 (98%)	2 (2%)	0	100	100
1	H	130/138 (94%)	128 (98%)	1 (1%)	1 (1%)	19	15
1	I	132/138 (96%)	129 (98%)	2 (2%)	1 (1%)	19	15
1	J	131/138 (95%)	126 (96%)	2 (2%)	3 (2%)	6	2
1	K	130/138 (94%)	128 (98%)	1 (1%)	1 (1%)	19	15
1	L	131/138 (95%)	127 (97%)	3 (2%)	1 (1%)	19	15
All	All	1566/1656 (95%)	1526 (97%)	25 (2%)	15 (1%)	15	11

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	118	ARG
1	C	116	ASN
1	D	118	ARG
1	E	117	THR
1	I	117	THR

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	111/117 (95%)	110 (99%)	1 (1%)	78	84
1	B	110/117 (94%)	108 (98%)	2 (2%)	59	65
1	C	108/117 (92%)	106 (98%)	2 (2%)	57	63
1	D	111/117 (95%)	109 (98%)	2 (2%)	59	65
1	E	110/117 (94%)	108 (98%)	2 (2%)	59	65
1	F	107/117 (92%)	103 (96%)	4 (4%)	34	35
1	G	108/117 (92%)	108 (100%)	0	100	100
1	H	109/117 (93%)	105 (96%)	4 (4%)	34	35
1	I	110/117 (94%)	107 (97%)	3 (3%)	44	48
1	J	107/117 (92%)	103 (96%)	4 (4%)	34	35
1	K	109/117 (93%)	105 (96%)	4 (4%)	34	35
1	L	109/117 (93%)	101 (93%)	8 (7%)	14	11
All	All	1309/1404 (93%)	1273 (97%)	36 (3%)	46	47

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	8	THR
1	L	126	LEU
1	L	14	THR
1	L	90	GLN
1	F	132	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	7	ASN
1	K	9	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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^{th} 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^2)	Q<0.9
1	A	132/138 (95%)	-0.21	0 100 100	15, 21, 41, 49	0
1	B	132/138 (95%)	-0.22	1 (0%) 86 88	16, 24, 47, 92	0
1	C	132/138 (95%)	-0.21	4 (3%) 50 56	15, 23, 54, 113	0
1	D	132/138 (95%)	-0.11	8 (6%) 21 26	16, 21, 55, 88	0
1	E	132/138 (95%)	-0.27	1 (0%) 86 88	18, 24, 57, 79	0
1	F	132/138 (95%)	0.02	8 (6%) 21 26	18, 27, 62, 92	0
1	G	132/138 (95%)	-0.17	5 (3%) 40 46	15, 23, 51, 90	0
1	H	132/138 (95%)	-0.26	1 (0%) 86 88	17, 24, 51, 76	0
1	I	132/138 (95%)	-0.16	6 (4%) 33 38	15, 25, 61, 86	0
1	J	132/138 (95%)	-0.16	3 (2%) 60 65	17, 29, 60, 96	0
1	K	132/138 (95%)	-0.24	2 (1%) 73 77	16, 21, 51, 77	0
1	L	132/138 (95%)	-0.14	3 (2%) 60 65	18, 27, 66, 98	0
All	All	1584/1656 (95%)	-0.18	42 (2%) 54 60	15, 24, 57, 113	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	117	THR	6.2
1	G	93	PRO	5.7
1	G	118	ARG	5.1
1	J	117	THR	4.9
1	C	117	THR	4.9

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.