WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 6, 2024 – 11:03 AM EST

PDB ID	:	2GJV
Title	:	Crystal Structure of a Protein of Unknown Function from Salmonella typhimurium
Authors	:	Minasov, G.; Shuvalova, L.; Brunzelle, J.S.; Vorontsov, I.I.; Collart, F.R.; Joachimiak, A.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2006-03-31
Resolution	:	2.39 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

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 2.39 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.
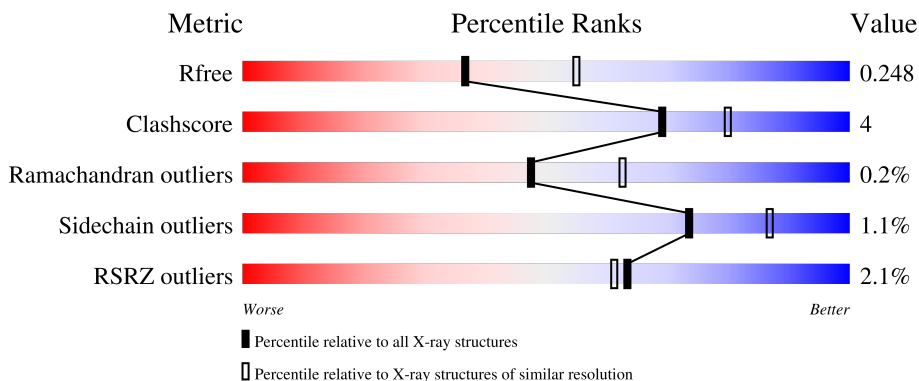
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	175	
1	B	175	
1	C	175	
1	D	175	
1	E	175	

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Mol	Chain	Length	Quality of chain
1	F	175	

%
68%   10%   22%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 6971 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 putative cytoplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0
1	B	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0
1	C	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0
1	D	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0
1	E	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0
1	F	136	Total 1058	C 663	N 182	O 207	S 6	0	0	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	cloning artifact	UNP Q8ZKJ0
A	-22	HIS	-	expression tag	UNP Q8ZKJ0
A	-21	HIS	-	expression tag	UNP Q8ZKJ0
A	-20	HIS	-	expression tag	UNP Q8ZKJ0
A	-19	HIS	-	expression tag	UNP Q8ZKJ0
A	-18	HIS	-	expression tag	UNP Q8ZKJ0
A	-17	HIS	-	expression tag	UNP Q8ZKJ0
A	-16	SER	-	cloning artifact	UNP Q8ZKJ0
A	-15	SER	-	cloning artifact	UNP Q8ZKJ0
A	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
A	-13	VAL	-	cloning artifact	UNP Q8ZKJ0
A	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
A	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
A	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
A	-9	THR	-	cloning artifact	UNP Q8ZKJ0
A	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
A	-7	ASN	-	cloning artifact	UNP Q8ZKJ0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
A	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
A	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
A	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
A	-2	SER	-	cloning artifact	UNP Q8ZKJ0
A	-1	ASN	-	cloning artifact	UNP Q8ZKJ0
A	0	ALA	-	cloning artifact	UNP Q8ZKJ0
B	-23	MET	-	cloning artifact	UNP Q8ZKJ0
B	-22	HIS	-	expression tag	UNP Q8ZKJ0
B	-21	HIS	-	expression tag	UNP Q8ZKJ0
B	-20	HIS	-	expression tag	UNP Q8ZKJ0
B	-19	HIS	-	expression tag	UNP Q8ZKJ0
B	-18	HIS	-	expression tag	UNP Q8ZKJ0
B	-17	HIS	-	expression tag	UNP Q8ZKJ0
B	-16	SER	-	cloning artifact	UNP Q8ZKJ0
B	-15	SER	-	cloning artifact	UNP Q8ZKJ0
B	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
B	-13	VAL	-	cloning artifact	UNP Q8ZKJ0
B	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
B	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
B	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
B	-9	THR	-	cloning artifact	UNP Q8ZKJ0
B	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
B	-7	ASN	-	cloning artifact	UNP Q8ZKJ0
B	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
B	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
B	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
B	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
B	-2	SER	-	cloning artifact	UNP Q8ZKJ0
B	-1	ASN	-	cloning artifact	UNP Q8ZKJ0
B	0	ALA	-	cloning artifact	UNP Q8ZKJ0
C	-23	MET	-	cloning artifact	UNP Q8ZKJ0
C	-22	HIS	-	expression tag	UNP Q8ZKJ0
C	-21	HIS	-	expression tag	UNP Q8ZKJ0
C	-20	HIS	-	expression tag	UNP Q8ZKJ0
C	-19	HIS	-	expression tag	UNP Q8ZKJ0
C	-18	HIS	-	expression tag	UNP Q8ZKJ0
C	-17	HIS	-	expression tag	UNP Q8ZKJ0
C	-16	SER	-	cloning artifact	UNP Q8ZKJ0
C	-15	SER	-	cloning artifact	UNP Q8ZKJ0
C	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
C	-13	VAL	-	cloning artifact	UNP Q8ZKJ0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
C	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
C	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
C	-9	THR	-	cloning artifact	UNP Q8ZKJ0
C	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
C	-7	ASN	-	cloning artifact	UNP Q8ZKJ0
C	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
C	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
C	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
C	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
C	-2	SER	-	cloning artifact	UNP Q8ZKJ0
C	-1	ASN	-	cloning artifact	UNP Q8ZKJ0
C	0	ALA	-	cloning artifact	UNP Q8ZKJ0
D	-23	MET	-	cloning artifact	UNP Q8ZKJ0
D	-22	HIS	-	expression tag	UNP Q8ZKJ0
D	-21	HIS	-	expression tag	UNP Q8ZKJ0
D	-20	HIS	-	expression tag	UNP Q8ZKJ0
D	-19	HIS	-	expression tag	UNP Q8ZKJ0
D	-18	HIS	-	expression tag	UNP Q8ZKJ0
D	-17	HIS	-	expression tag	UNP Q8ZKJ0
D	-16	SER	-	cloning artifact	UNP Q8ZKJ0
D	-15	SER	-	cloning artifact	UNP Q8ZKJ0
D	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
D	-13	VAL	-	cloning artifact	UNP Q8ZKJ0
D	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
D	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
D	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
D	-9	THR	-	cloning artifact	UNP Q8ZKJ0
D	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
D	-7	ASN	-	cloning artifact	UNP Q8ZKJ0
D	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
D	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
D	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
D	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
D	-2	SER	-	cloning artifact	UNP Q8ZKJ0
D	-1	ASN	-	cloning artifact	UNP Q8ZKJ0
D	0	ALA	-	cloning artifact	UNP Q8ZKJ0
E	-23	MET	-	cloning artifact	UNP Q8ZKJ0
E	-22	HIS	-	expression tag	UNP Q8ZKJ0
E	-21	HIS	-	expression tag	UNP Q8ZKJ0
E	-20	HIS	-	expression tag	UNP Q8ZKJ0
E	-19	HIS	-	expression tag	UNP Q8ZKJ0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	HIS	-	expression tag	UNP Q8ZKJ0
E	-17	HIS	-	expression tag	UNP Q8ZKJ0
E	-16	SER	-	cloning artifact	UNP Q8ZKJ0
E	-15	SER	-	cloning artifact	UNP Q8ZKJ0
E	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
E	-13	VAL	-	cloning artifact	UNP Q8ZKJ0
E	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
E	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
E	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
E	-9	THR	-	cloning artifact	UNP Q8ZKJ0
E	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
E	-7	ASN	-	cloning artifact	UNP Q8ZKJ0
E	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
E	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
E	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
E	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
E	-2	SER	-	cloning artifact	UNP Q8ZKJ0
E	-1	ASN	-	cloning artifact	UNP Q8ZKJ0
E	0	ALA	-	cloning artifact	UNP Q8ZKJ0
F	-23	MET	-	cloning artifact	UNP Q8ZKJ0
F	-22	HIS	-	expression tag	UNP Q8ZKJ0
F	-21	HIS	-	expression tag	UNP Q8ZKJ0
F	-20	HIS	-	expression tag	UNP Q8ZKJ0
F	-19	HIS	-	expression tag	UNP Q8ZKJ0
F	-18	HIS	-	expression tag	UNP Q8ZKJ0
F	-17	HIS	-	expression tag	UNP Q8ZKJ0
F	-16	SER	-	cloning artifact	UNP Q8ZKJ0
F	-15	SER	-	cloning artifact	UNP Q8ZKJ0
F	-14	GLY	-	cloning artifact	UNP Q8ZKJ0
F	-13	VAL	-	cloning artifact	UNP Q8ZKJ0
F	-12	ASP	-	cloning artifact	UNP Q8ZKJ0
F	-11	LEU	-	cloning artifact	UNP Q8ZKJ0
F	-10	GLY	-	cloning artifact	UNP Q8ZKJ0
F	-9	THR	-	cloning artifact	UNP Q8ZKJ0
F	-8	GLU	-	cloning artifact	UNP Q8ZKJ0
F	-7	ASN	-	cloning artifact	UNP Q8ZKJ0
F	-6	LEU	-	cloning artifact	UNP Q8ZKJ0
F	-5	TYR	-	cloning artifact	UNP Q8ZKJ0
F	-4	PHE	-	cloning artifact	UNP Q8ZKJ0
F	-3	GLN	-	cloning artifact	UNP Q8ZKJ0
F	-2	SER	-	cloning artifact	UNP Q8ZKJ0
F	-1	ASN	-	cloning artifact	UNP Q8ZKJ0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	cloning artifact	UNP Q8ZKJ0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Cl 1	0	0
2	B	1	Total 1	Cl 1	0	0
2	C	1	Total 1	Cl 1	0	0
2	D	1	Total 1	Cl 1	0	0
2	E	1	Total 1	Cl 1	0	0
2	F	1	Total 1	Cl 1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Ca 2	0	0
3	B	1	Total 1	Ca 1	0	0
3	C	1	Total 1	Ca 1	0	0
3	D	2	Total 2	Ca 2	0	0
3	E	1	Total 1	Ca 1	0	0
3	F	1	Total 1	Ca 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total 110	O 110	0	0
4	B	116	Total 116	O 116	0	0

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	92	Total 92	O 92	0	0
4	D	108	Total 108	O 108	0	0
4	E	86	Total 86	O 86	0	0
4	F	97	Total 97	O 97	0	0

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 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.
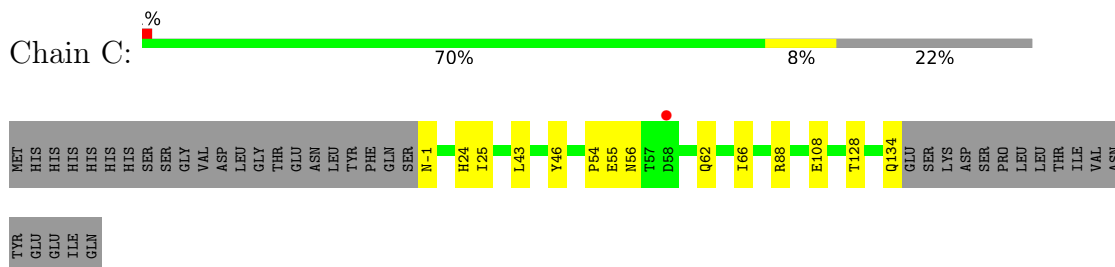
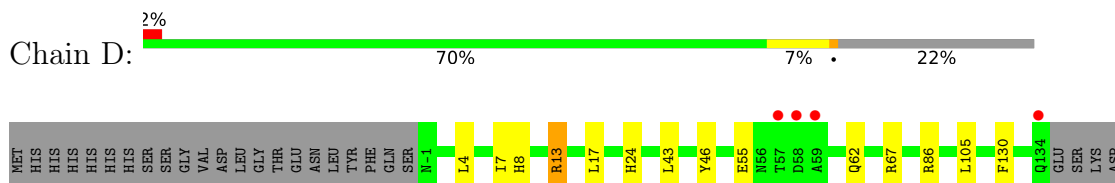• Molecule 1: putative cytoplasmic protein
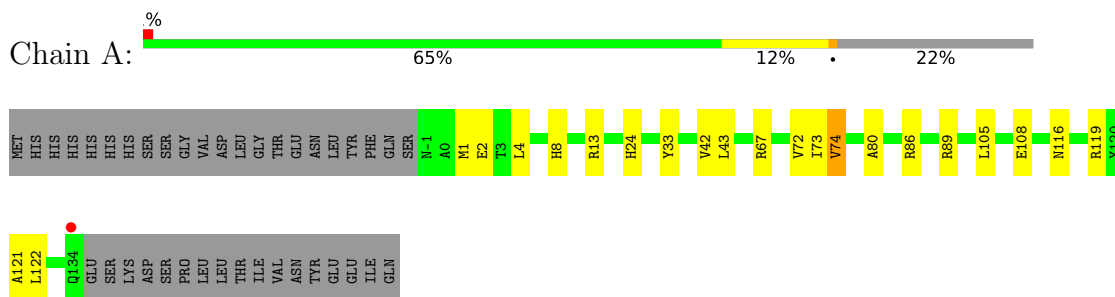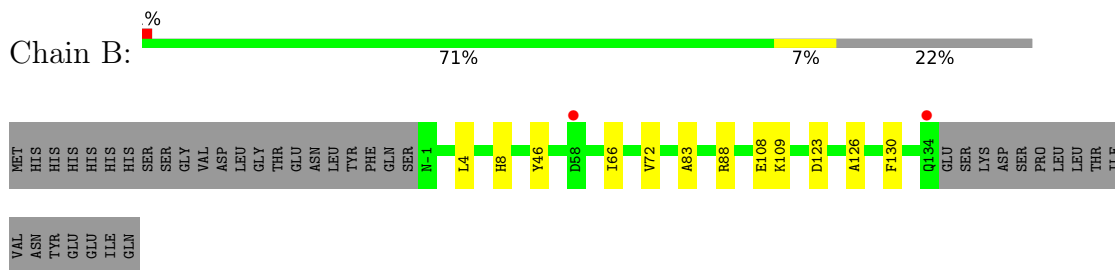
Chain A:

• Molecule 1: putative cytoplasmic protein

Chain B:

• Molecule 1: putative cytoplasmic protein

Chain C:

• Molecule 1: putative cytoplasmic protein

Chain D:

SER PRO LEU LEU THR ILE VAL ASN TYR GLU GLU ILE GLN

• Molecule 1: putative cytoplasmic protein

Chain E:

4%

71%   6% •   22%

MET HIS HIS HIS HIS HIS SER SER GLY VAL ASP LEU GLY THR GLU ASN LEU TYR PHE GLN SER N-1 L4 H8 L14 I23 H24 I25 T36 G37 Q38 I44 N56 T57 D58 A59 Q62 R88 L105 C118 E133 Q134 GLU SER LYS ASP SER

PRO LEU LEU THR ILE VAL ASN TYR GLU GLU ILE GLN

• Molecule 1: putative cytoplasmic protein

Chain F:

%

68%   10%   22%

MET HIS HIS HIS HIS HIS SER SER GLY VAL ASP LEU GLY THR GLU ASN LEU TYR PHE GLN SER N-1 A0 M1 E2 T3 L4 H8 L14 D20 I23 T36 I77 D85 R88 R89 L96 R101 P102 L103 W104 L105 C118 S127 Q134 GLU

SER LYS ASP SER PRO LEU LEU THR ILE VAL ASN TYR GLU GLU ILE GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	134.14Å 77.00Å 85.11Å 90.00° 109.25° 90.00°	Depositor
Resolution (Å)	27.90 – 2.39 27.90 – 2.39	Depositor EDS
% Data completeness (in resolution range)	93.5 (27.90-2.39) 93.5 (27.90-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	7.83 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.168 , 0.249 0.167 , 0.248	Depositor DCC
R_{free} test set	1520 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	27.2	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.2	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6971	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1   Standard geometry (i)

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

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	0/1075	0.75	0/1464
1	B	0.51	0/1075	0.75	0/1464
1	C	0.52	0/1075	0.78	1/1464 (0.1%)
1	D	0.50	0/1075	0.75	0/1464
1	E	0.54	1/1075 (0.1%)	0.76	0/1464
1	F	0.48	0/1075	0.76	0/1464
All	All	0.52	1/6450 (0.0%)	0.76	1/8784 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	118	CYS	CB-SG	-5.54	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	25	ILE	N-CA-C	-5.00	97.50	111.00

There are no chirality outliers.

There are no planarity outliers.

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	1058	0	1057	12	0
1	B	1058	0	1057	7	0
1	C	1058	0	1057	7	0
1	D	1058	0	1057	10	0
1	E	1058	0	1057	9	0
1	F	1058	0	1057	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	1	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	110	0	0	1	0
4	B	116	0	0	0	0
4	C	92	0	0	0	0
4	D	108	0	0	2	0
4	E	86	0	0	0	0
4	F	97	0	0	0	0
All	All	6971	0	6342	47	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 47 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:C:62:GLN:HE22	1:D:105:LEU:H	1.23	0.86
1:E:62:GLN:HE22	1:F:105:LEU:H	1.28	0.82
1:D:62:GLN:HE22	1:E:105:LEU:H	1.28	0.77
1:F:14:LEU:HB3	1:F:23:ILE:HD13	1.72	0.71
1:B:88:ARG:HD3	1:B:108:GLU:OE2	1.90	0.71

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	134/175 (77%)	134 (100%)	0	0	100	100
1	B	134/175 (77%)	132 (98%)	2 (2%)	0	100	100
1	C	134/175 (77%)	132 (98%)	1 (1%)	1 (1%)	22	32
1	D	134/175 (77%)	131 (98%)	2 (2%)	1 (1%)	22	32
1	E	134/175 (77%)	132 (98%)	2 (2%)	0	100	100
1	F	134/175 (77%)	129 (96%)	5 (4%)	0	100	100
All	All	804/1050 (77%)	790 (98%)	12 (2%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	55	GLU
1	C	55	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	118/155 (76%)	115 (98%)	3 (2%)	47	67
1	B	118/155 (76%)	118 (100%)	0	100	100
1	C	118/155 (76%)	116 (98%)	2 (2%)	60	78
1	D	118/155 (76%)	116 (98%)	2 (2%)	60	78
1	E	118/155 (76%)	117 (99%)	1 (1%)	81	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	118/155 (76%)	118 (100%)	0	100	100
All	All	708/930 (76%)	700 (99%)	8 (1%)	73	87

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	88	ARG
1	D	86	ARG
1	C	134	GLN
1	C	-1	ASN
1	D	13	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	62	GLN
1	E	116	ASN
1	F	134	GLN
1	E	134	GLN
1	E	76	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 14 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 95th 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(Å²)	Q<0.9
1	A	136/175 (77%)	-0.25	1 (0%)	87	86	21, 28, 35, 39	0
1	B	136/175 (77%)	-0.24	2 (1%)	73	72	22, 28, 35, 38	0
1	C	136/175 (77%)	-0.22	1 (0%)	87	86	20, 28, 35, 36	0
1	D	136/175 (77%)	-0.19	4 (2%)	51	50	21, 29, 34, 36	0
1	E	136/175 (77%)	-0.06	7 (5%)	28	26	21, 28, 35, 40	0
1	F	136/175 (77%)	-0.09	2 (1%)	73	72	21, 28, 35, 38	0
All	All	816/1050 (77%)	-0.18	17 (2%)	63	61	20, 28, 35, 40	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	56	ASN	3.8
1	E	58	ASP	3.6
1	E	38	GLN	3.6
1	E	134	GLN	3.0
1	A	134	GLN	2.9

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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^2)	Q<0.9
3	CA	D	154	1/1	0.90	0.17	56,56,56,56	1
3	CA	B	153	1/1	0.91	0.22	31,31,31,31	1
3	CA	F	153	1/1	0.91	0.19	29,29,29,29	1
3	CA	A	154	1/1	0.94	0.12	44,44,44,44	1
3	CA	C	153	1/1	0.94	0.12	27,27,27,27	1
2	CL	E	152	1/1	0.96	0.20	38,38,38,38	0
2	CL	F	152	1/1	0.96	0.24	54,54,54,54	0
3	CA	A	153	1/1	0.96	0.08	32,32,32,32	1
2	CL	D	152	1/1	0.96	0.25	48,48,48,48	0
2	CL	A	152	1/1	0.97	0.10	40,40,40,40	0
2	CL	B	152	1/1	0.98	0.25	44,44,44,44	0
3	CA	E	153	1/1	0.98	0.12	48,48,48,48	0
3	CA	D	153	1/1	0.98	0.08	58,58,58,58	0
2	CL	C	152	1/1	0.99	0.15	35,35,35,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.