



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 10:16 pm BST

PDB ID : 4DAM
Title : Crystal structure of small single-stranded DNA-binding protein from *Streptomyces coelicolor*
Authors : Filic, Z.; Herron, P.; Ivic, N.; Luic, M.; Manjasetty, B.A.; Paradzik, T.; Vujaklija, D.
Deposited on : 2012-01-13
Resolution : 1.70 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 ⓘ symbol.

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	:	2.11
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)	:	2.11

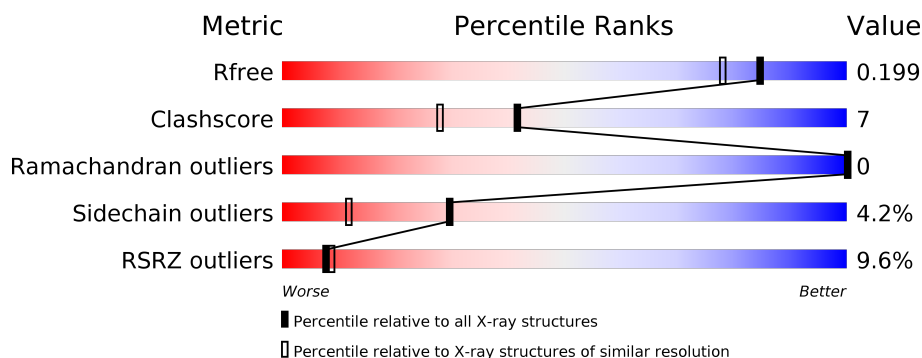
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 on 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 $\leq 5\%$. 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	128	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>14%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	128	<div> <div>12%</div> <div> <div></div> <div>70%</div> <div>15%</div> <div></div> <div>16%</div> </div> </div>
1	C	128	<div> <div>9%</div> <div> <div></div> <div>65%</div> <div>11%</div> <div>•</div> <div>22%</div> </div> </div>
1	D	128	<div> <div>5%</div> <div> <div></div> <div>70%</div> <div>16%</div> <div></div> <div>15%</div> </div> </div>
1	E	128	<div> <div>8%</div> <div> <div></div> <div>77%</div> <div>11%</div> <div></div> <div>13%</div> </div> </div>
1	F	128	<div> <div>13%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>•</div> <div>14%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	128	<div><div></div><div>5%</div><div>66%</div><div>9%</div><div>23%</div></div>
1	H	128	<div><div></div><div>5%</div><div>71%</div><div>13%</div><div>16%</div></div>
1	I	128	<div><div></div><div>13%</div><div>74%</div><div>11%</div><div>14%</div></div>
1	J	128	<div><div></div><div>7%</div><div>77%</div><div>7%</div><div>16%</div></div>
1	K	128	<div><div></div><div>7%</div><div>77%</div><div>10%</div><div>13%</div></div>
1	L	128	<div><div></div><div>8%</div><div>68%</div><div>9%</div><div>22%</div></div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11106 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 Single-stranded DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	113	Total	C	N	O	S	0	8	0
			879	547	161	166	5			
1	B	108	Total	C	N	O	S	0	7	0
			860	533	162	161	4			
1	C	100	Total	C	N	O	S	0	12	0
			838	524	156	152	6			
1	D	109	Total	C	N	O	S	0	10	0
			900	558	169	169	4			
1	E	112	Total	C	N	O	S	0	10	0
			923	569	176	172	6			
1	F	110	Total	C	N	O	S	0	5	0
			876	542	167	162	5			
1	G	98	Total	C	N	O	S	0	8	0
			785	491	148	141	5			
1	H	108	Total	C	N	O	S	0	6	0
			850	530	157	159	4			
1	I	110	Total	C	N	O	S	0	5	0
			866	536	164	161	5			
1	J	108	Total	C	N	O	S	0	7	0
			865	535	164	161	5			
1	K	111	Total	C	N	O	S	1	5	0
			868	538	162	162	6			
1	L	100	Total	C	N	O	S	0	7	0
			788	496	144	144	4			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
A	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
A	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
A	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
A	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
A	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
A	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
A	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
A	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
A	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
A	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
A	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
B	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
B	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
B	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
B	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
B	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
B	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
B	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
B	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
C	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
C	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
C	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
C	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
C	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
C	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
C	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
C	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
D	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
D	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
D	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
D	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
D	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
D	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
D	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
D	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
D	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
D	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
D	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
D	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
E	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
E	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
E	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
E	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
E	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
E	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
E	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
E	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
F	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
F	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
F	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
F	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
F	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
F	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
F	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
F	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
G	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
G	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
G	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
G	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
G	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
G	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
G	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
H	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
H	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
H	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
H	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
H	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
H	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
H	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
H	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
I	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
I	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
I	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
I	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
I	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
I	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
I	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
I	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
J	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
J	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
J	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
J	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
J	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
J	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
J	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
J	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
K	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
K	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
K	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
K	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
K	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
K	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
K	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9
L	-11	MET	-	EXPRESSION TAG	UNP Q9KYI9
L	-10	ARG	-	EXPRESSION TAG	UNP Q9KYI9
L	-9	GLY	-	EXPRESSION TAG	UNP Q9KYI9
L	-8	SER	-	EXPRESSION TAG	UNP Q9KYI9
L	-7	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-6	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-5	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-4	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-3	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-2	HIS	-	EXPRESSION TAG	UNP Q9KYI9
L	-1	GLY	-	EXPRESSION TAG	UNP Q9KYI9
L	0	SER	-	EXPRESSION TAG	UNP Q9KYI9
L	4	ILE	THR	ENGINEERED MUTATION	UNP Q9KYI9

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	79	Total O 79 79	0	0
2	B	58	Total O 58 58	0	0
2	C	57	Total O 57 57	0	0
2	D	91	Total O 91 91	0	0
2	E	89	Total O 89 89	0	0
2	F	52	Total O 52 52	0	0
2	G	43	Total O 43 43	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	83	Total 83	O 83	0	0
2	I	53	Total 53	O 53	0	0
2	J	78	Total 78	O 78	0	0
2	K	77	Total 77	O 77	0	0
2	L	48	Total 48	O 48	0	0

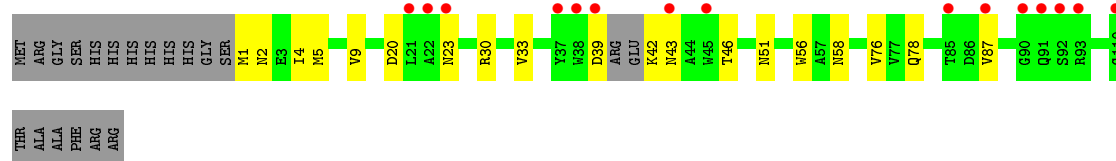
3 Residue-property plots [i](#)

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 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.

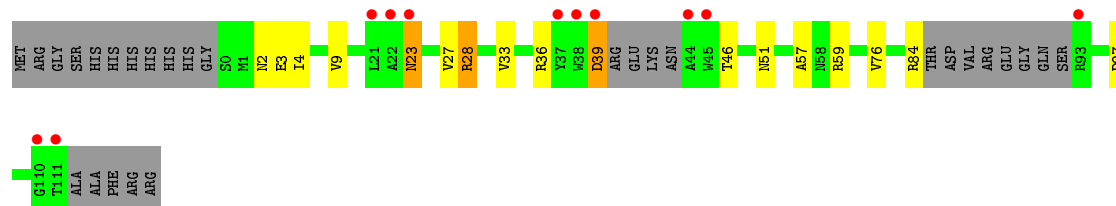
- Molecule 1: Single-stranded DNA-binding protein 1



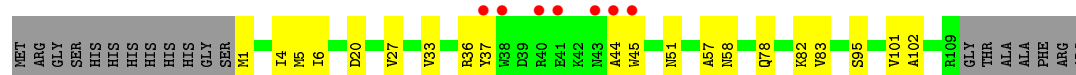
- Molecule 1: Single-stranded DNA-binding protein 1



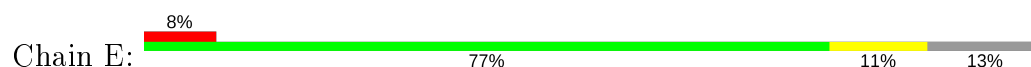
- Molecule 1: Single-stranded DNA-binding protein 1



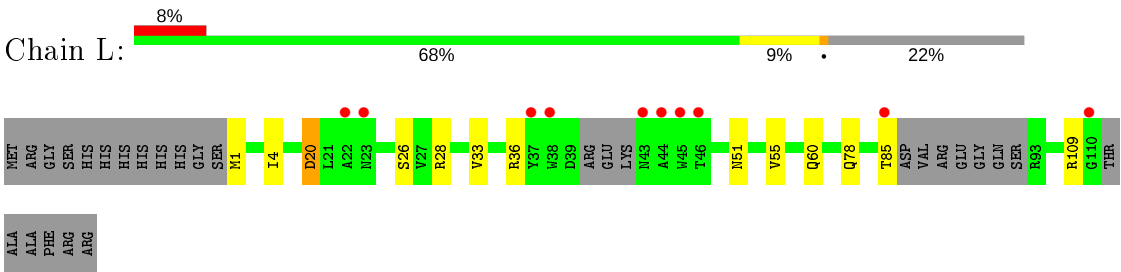
- Molecule 1: Single-stranded DNA-binding protein 1



- Molecule 1: Single-stranded DNA-binding protein 1



● Molecule 1: Single-stranded DNA-binding protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	150.00 Å 150.00 Å 54.70 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.70 36.54 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.70) 99.9 (36.54-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.89 (at 1.70 Å)	Xtriage
Refinement program	REFMAC 5.6.0116	Depositor
R, R_{free}	0.153 , 0.192 0.167 , 0.199	Depositor DCC
R_{free} test set	7555 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 31.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l 0.018 for h,-h-k,-l 0.116 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11106	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.89 % 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 9.2985e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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

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	0.66	0/918	0.85	1/1256 (0.1%)
1	B	0.67	1/884 (0.1%)	0.82	0/1203
1	C	0.69	1/863 (0.1%)	0.92	2/1173 (0.2%)
1	D	0.67	0/924	0.84	0/1259
1	E	0.68	0/953	0.86	1/1295 (0.1%)
1	F	0.67	1/895 (0.1%)	0.84	2/1217 (0.2%)
1	G	0.71	1/813 (0.1%)	0.85	0/1104
1	H	0.70	0/871	0.88	2/1187 (0.2%)
1	I	0.67	0/888	0.88	3/1208 (0.2%)
1	J	0.72	0/883	0.84	0/1202
1	K	0.72	1/898 (0.1%)	0.91	1/1223 (0.1%)
1	L	0.74	2/813 (0.2%)	0.82	2/1108 (0.2%)
All	All	0.69	7/10603 (0.1%)	0.86	14/14435 (0.1%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	56	TRP	CD2-CE2	5.91	1.48	1.41
1	L	26[A]	SER	CB-OG	-5.63	1.34	1.42
1	L	26[B]	SER	CB-OG	-5.63	1.34	1.42
1	F	56	TRP	CD2-CE2	5.27	1.47	1.41
1	G	45	TRP	CD2-CE2	5.09	1.47	1.41

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	59	ARG	NE-CZ-NH1	8.56	124.58	120.30
1	A	86	ASP	CB-CG-OD2	7.24	124.82	118.30
1	H	86	ASP	CB-CG-OD1	-6.89	112.09	118.30
1	I	19	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	I	19	ARG	NE-CZ-NH2	-6.47	117.06	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	879	0	860	22	0
1	B	860	0	832	19	0
1	C	838	0	826	19	0
1	D	900	0	879	31	0
1	E	923	0	909	16	0
1	F	876	0	860	16	0
1	G	785	0	787	14	0
1	H	850	0	825	19	0
1	I	866	0	847	15	0
1	J	865	0	845	11	0
1	K	868	0	846	14	0
1	L	788	0	765	18	0
2	A	79	0	0	1	0
2	B	58	0	0	1	0
2	C	57	0	0	3	0
2	D	91	0	0	6	0
2	E	89	0	0	2	0
2	F	52	0	0	0	0
2	G	43	0	0	0	0
2	H	83	0	0	0	0
2	I	53	0	0	0	0
2	J	78	0	0	0	0
2	K	77	0	0	4	0
2	L	48	0	0	1	0
All	All	11106	0	10081	144	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 7.

The worst 5 of 144 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:51:ASN:HD22	1:G:4:ILE:HD12	1.13	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ASN:HD22	1:C:4[A]:ILE:HD12	1.13	1.09
1:I:51:ASN:HD22	1:L:4[A]:ILE:HD12	1.14	1.07
1:E:4[A]:ILE:HD12	1:H:51:ASN:HD22	1.19	1.04
1:E:51:ASN:HD22	1:H:4:ILE:HD12	1.24	1.02

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 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	120/128 (94%)	119 (99%)	1 (1%)	0	100	100
1	B	111/128 (87%)	109 (98%)	2 (2%)	0	100	100
1	C	107/128 (84%)	106 (99%)	1 (1%)	0	100	100
1	D	117/128 (91%)	113 (97%)	4 (3%)	0	100	100
1	E	121/128 (94%)	116 (96%)	5 (4%)	0	100	100
1	F	113/128 (88%)	112 (99%)	1 (1%)	0	100	100
1	G	101/128 (79%)	100 (99%)	1 (1%)	0	100	100
1	H	110/128 (86%)	109 (99%)	1 (1%)	0	100	100
1	I	112/128 (88%)	111 (99%)	1 (1%)	0	100	100
1	J	111/128 (87%)	109 (98%)	2 (2%)	0	100	100
1	K	115/128 (90%)	112 (97%)	3 (3%)	0	100	100
1	L	101/128 (79%)	99 (98%)	2 (2%)	0	100	100
All	All	1339/1536 (87%)	1315 (98%)	24 (2%)	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 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	94/101 (93%)	89 (95%)	5 (5%)	22	7
1	B	89/101 (88%)	83 (93%)	6 (7%)	16	4
1	C	89/101 (88%)	85 (96%)	4 (4%)	27	10
1	D	96/101 (95%)	92 (96%)	4 (4%)	30	12
1	E	100/101 (99%)	98 (98%)	2 (2%)	55	38
1	F	92/101 (91%)	87 (95%)	5 (5%)	22	7
1	G	84/101 (83%)	81 (96%)	3 (4%)	35	16
1	H	88/101 (87%)	83 (94%)	5 (6%)	20	6
1	I	90/101 (89%)	85 (94%)	5 (6%)	21	7
1	J	91/101 (90%)	87 (96%)	4 (4%)	28	11
1	K	92/101 (91%)	90 (98%)	2 (2%)	52	34
1	L	81/101 (80%)	79 (98%)	2 (2%)	47	29
All	All	1086/1212 (90%)	1039 (96%)	47 (4%)	30	11

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	20	ASP
1	G	23	ASN
1	K	20	ASP
1	F	46	THR
1	G	37	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	2	ASN
1	G	11	ASN
1	L	51	ASN
1	F	78	GLN

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Mol	Chain	Res	Type
1	G	78	GLN

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 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.

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, 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(Å ²)	Q<0.9
1	A	113/128 (88%)	0.14	6 (5%) 26 29	14, 22, 70, 94	4 (3%)
1	B	108/128 (84%)	0.33	15 (13%) 2 3	16, 25, 70, 85	1 (0%)
1	C	100/128 (78%)	0.33	11 (11%) 5 6	15, 23, 66, 87	0
1	D	109/128 (85%)	0.26	7 (6%) 19 21	13, 20, 75, 108	2 (1%)
1	E	112/128 (87%)	0.17	10 (8%) 9 11	13, 21, 73, 107	1 (0%)
1	F	110/128 (85%)	0.50	17 (15%) 2 2	16, 26, 76, 94	3 (2%)
1	G	98/128 (76%)	0.18	7 (7%) 16 18	14, 23, 61, 78	0
1	H	108/128 (84%)	-0.03	6 (5%) 24 27	12, 20, 51, 80	0
1	I	110/128 (85%)	0.58	17 (15%) 2 2	16, 26, 72, 102	0
1	J	108/128 (84%)	0.05	9 (8%) 11 13	13, 20, 57, 77	1 (0%)
1	K	111/128 (86%)	0.11	9 (8%) 12 14	13, 20, 70, 100	3 (2%)
1	L	100/128 (78%)	0.35	10 (10%) 7 8	14, 23, 67, 85	2 (2%)
All	All	1287/1536 (83%)	0.25	124 (9%) 8 9	12, 22, 70, 108	17 (1%)

The worst 5 of 124 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	22	ALA	12.6
1	D	40	ARG	7.7
1	I	40	ARG	7.7
1	G	37	TYR	7.5
1	G	45	TRP	7.3

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 carbohydrates 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.