wwPDB X-ray Structure Validation Summary Report (i)

Oct 21, 2024 – 03:22 PM EDT

PDB ID	:	3DL3
Title	:	Crystal structure of the tellurite resistance protein TehB. Northeast Structural Genomics Consortium target VfR98 .
Authors	:	Kuzin, A.P.; Su, M.; Seetharaman, J.; Wang, D.; Mao, L.; Maglaqui, M.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2008-06-26
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*
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:

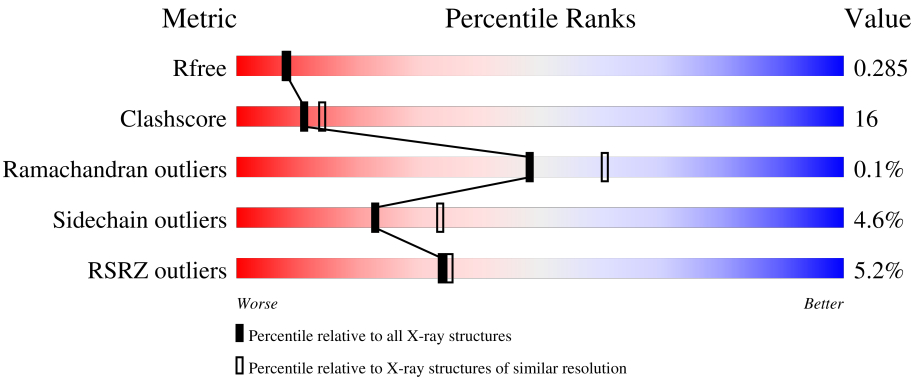
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (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 >=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	119	3% 61% 19% 19%
1	B	119	4% 54% 26% • 19%
1	D	119	6% 57% 23% • 19%
1	E	119	4% 64% 26% • 8%

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Mol	Chain	Length	Quality of chain
1	F	119	4% 66% 26% 8%
1	G	119	6% 53% 23% 21%
1	H	119	5% 57% 20% 20%
1	I	119	2% 46% 39% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6572 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 Tellurite resistance protein B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	Se	0	0	0
			778	499	130	147	1	1			
1	B	96	Total	C	N	O	S	Se	0	0	0
			777	500	129	146	1	1			
1	D	96	Total	C	N	O	S	Se	0	0	0
			777	500	129	146	1	1			
1	E	110	Total	C	N	O	S	Se	0	0	0
			890	569	151	167	1	2			
1	G	94	Total	C	N	O	S	Se	0	0	0
			758	488	124	144	1	1			
1	H	95	Total	C	N	O	S	Se	0	0	0
			769	494	128	145	1	1			
1	F	110	Total	C	N	O	S	Se	0	0	0
			890	569	151	167	1	2			
1	I	105	Total	C	N	O	S	Se	0	0	0
			849	543	144	159	1	2			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	112	LEU	-	expression tag	UNP Q5E3X2
A	113	GLU	-	expression tag	UNP Q5E3X2
A	114	HIS	-	expression tag	UNP Q5E3X2
A	115	HIS	-	expression tag	UNP Q5E3X2
A	116	HIS	-	expression tag	UNP Q5E3X2
A	117	HIS	-	expression tag	UNP Q5E3X2
A	118	HIS	-	expression tag	UNP Q5E3X2
A	119	HIS	-	expression tag	UNP Q5E3X2
B	112	LEU	-	expression tag	UNP Q5E3X2
B	113	GLU	-	expression tag	UNP Q5E3X2
B	114	HIS	-	expression tag	UNP Q5E3X2
B	115	HIS	-	expression tag	UNP Q5E3X2
B	116	HIS	-	expression tag	UNP Q5E3X2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	117	HIS	-	expression tag	UNP Q5E3X2
B	118	HIS	-	expression tag	UNP Q5E3X2
B	119	HIS	-	expression tag	UNP Q5E3X2
D	112	LEU	-	expression tag	UNP Q5E3X2
D	113	GLU	-	expression tag	UNP Q5E3X2
D	114	HIS	-	expression tag	UNP Q5E3X2
D	115	HIS	-	expression tag	UNP Q5E3X2
D	116	HIS	-	expression tag	UNP Q5E3X2
D	117	HIS	-	expression tag	UNP Q5E3X2
D	118	HIS	-	expression tag	UNP Q5E3X2
D	119	HIS	-	expression tag	UNP Q5E3X2
E	112	LEU	-	expression tag	UNP Q5E3X2
E	113	GLU	-	expression tag	UNP Q5E3X2
E	114	HIS	-	expression tag	UNP Q5E3X2
E	115	HIS	-	expression tag	UNP Q5E3X2
E	116	HIS	-	expression tag	UNP Q5E3X2
E	117	HIS	-	expression tag	UNP Q5E3X2
E	118	HIS	-	expression tag	UNP Q5E3X2
E	119	HIS	-	expression tag	UNP Q5E3X2
G	112	LEU	-	expression tag	UNP Q5E3X2
G	113	GLU	-	expression tag	UNP Q5E3X2
G	114	HIS	-	expression tag	UNP Q5E3X2
G	115	HIS	-	expression tag	UNP Q5E3X2
G	116	HIS	-	expression tag	UNP Q5E3X2
G	117	HIS	-	expression tag	UNP Q5E3X2
G	118	HIS	-	expression tag	UNP Q5E3X2
G	119	HIS	-	expression tag	UNP Q5E3X2
H	112	LEU	-	expression tag	UNP Q5E3X2
H	113	GLU	-	expression tag	UNP Q5E3X2
H	114	HIS	-	expression tag	UNP Q5E3X2
H	115	HIS	-	expression tag	UNP Q5E3X2
H	116	HIS	-	expression tag	UNP Q5E3X2
H	117	HIS	-	expression tag	UNP Q5E3X2
H	118	HIS	-	expression tag	UNP Q5E3X2
H	119	HIS	-	expression tag	UNP Q5E3X2
F	112	LEU	-	expression tag	UNP Q5E3X2
F	113	GLU	-	expression tag	UNP Q5E3X2
F	114	HIS	-	expression tag	UNP Q5E3X2
F	115	HIS	-	expression tag	UNP Q5E3X2
F	116	HIS	-	expression tag	UNP Q5E3X2
F	117	HIS	-	expression tag	UNP Q5E3X2
F	118	HIS	-	expression tag	UNP Q5E3X2

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Chain	Residue	Modelled	Actual	Comment	Reference
F	119	HIS	-	expression tag	UNP Q5E3X2
I	112	LEU	-	expression tag	UNP Q5E3X2
I	113	GLU	-	expression tag	UNP Q5E3X2
I	114	HIS	-	expression tag	UNP Q5E3X2
I	115	HIS	-	expression tag	UNP Q5E3X2
I	116	HIS	-	expression tag	UNP Q5E3X2
I	117	HIS	-	expression tag	UNP Q5E3X2
I	118	HIS	-	expression tag	UNP Q5E3X2
I	119	HIS	-	expression tag	UNP Q5E3X2

- Molecule 2 is water.

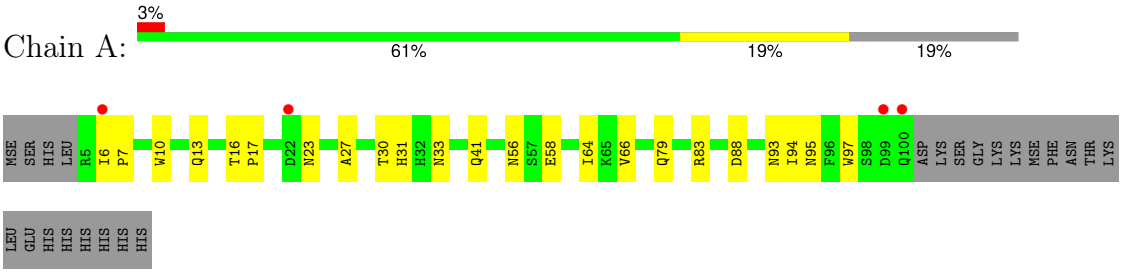
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	11	Total O 11 11	0	0
2	B	5	Total O 5 5	0	0
2	D	10	Total O 10 10	0	0
2	E	5	Total O 5 5	0	0
2	G	5	Total O 5 5	0	0
2	H	29	Total O 29 29	0	0
2	F	6	Total O 6 6	0	0
2	I	13	Total O 13 13	0	0

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.

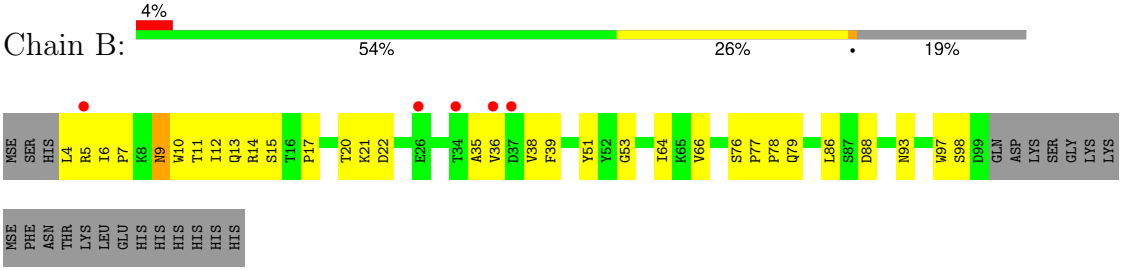
• Molecule 1: Tellurite resistance protein B

Chain A:



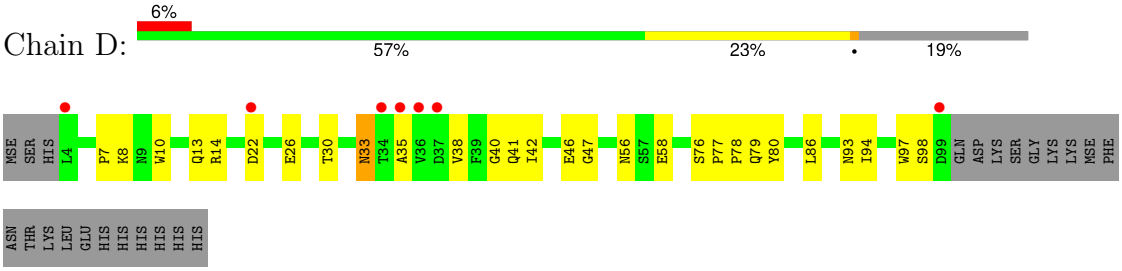
• Molecule 1: Tellurite resistance protein B

Chain B:



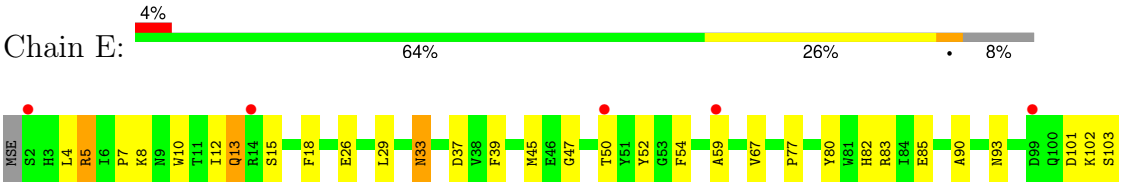
• Molecule 1: Tellurite resistance protein B

Chain D:



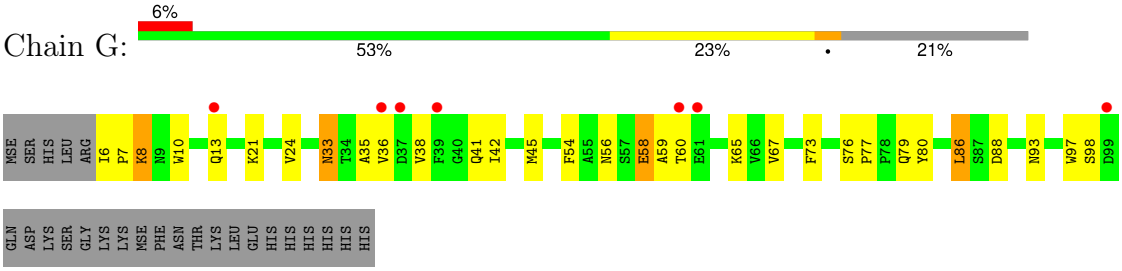
• Molecule 1: Tellurite resistance protein B

Chain E:



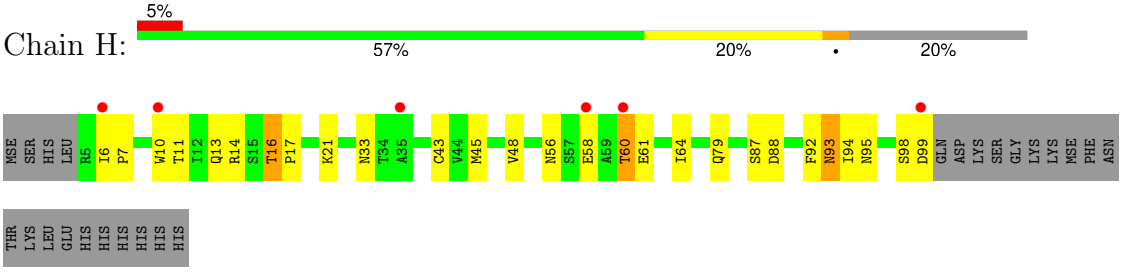
• Molecule 1: Tellurite resistance protein B

Chain G:



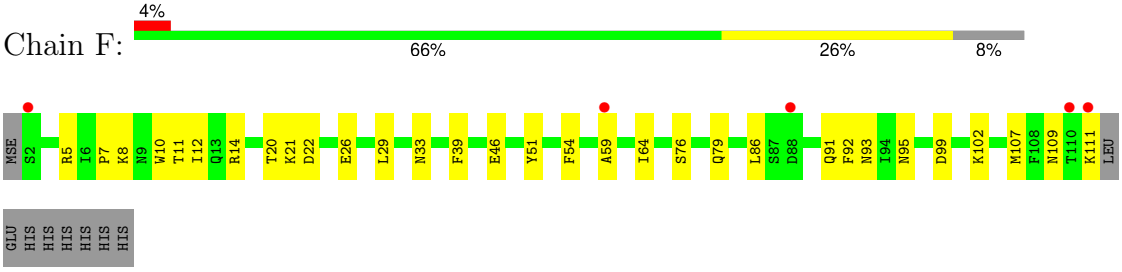
• Molecule 1: Tellurite resistance protein B

Chain H:



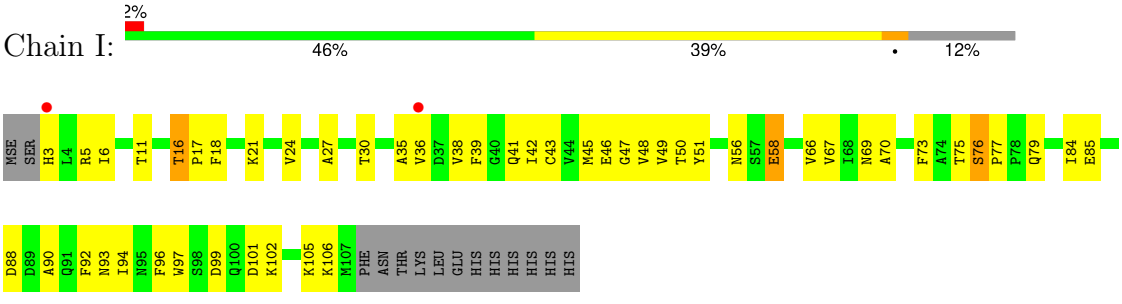
• Molecule 1: Tellurite resistance protein B

Chain F:



• Molecule 1: Tellurite resistance protein B

Chain I:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	43.57Å 205.02Å 56.36Å 90.00° 110.21° 90.00°	Depositor
Resolution (Å)	19.90 – 2.30 19.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	91.5 (19.90-2.30) 95.9 (19.90-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.53 (at 2.26Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.232 , 0.274 0.241 , 0.285	Depositor DCC
R_{free} test set	1982 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	43.4	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.056 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6572	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% 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	0.46	0/801	0.62	0/1094
1	B	0.43	0/800	0.59	0/1093
1	D	0.44	0/800	0.62	0/1093
1	E	0.41	0/914	0.61	0/1240
1	F	0.42	0/914	0.60	0/1240
1	G	0.41	0/781	0.57	0/1068
1	H	0.43	0/792	0.56	0/1082
1	I	0.43	0/872	0.59	0/1184
All	All	0.43	0/6674	0.59	0/9094

There are no bond length outliers.

There are no bond angle outliers.

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	778	0	730	19	0
1	B	777	0	733	30	0
1	D	777	0	733	18	0
1	E	890	0	848	30	0
1	F	890	0	848	22	0
1	G	758	0	709	21	0
1	H	769	0	722	26	0
1	I	849	0	808	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	11	0	0	1	0
2	B	5	0	0	1	0
2	D	10	0	0	0	0
2	E	5	0	0	0	0
2	F	6	0	0	0	0
2	G	5	0	0	0	0
2	H	29	0	0	0	0
2	I	13	0	0	2	0
All	All	6572	0	6131	203	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 16.

The worst 5 of 203 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:I:42:ILE:CD1	1:I:84:ILE:HD11	1.78	1.11
1:I:42:ILE:HD13	1:I:84:ILE:HD11	1.34	1.04
1:G:13:GLN:HE21	1:G:98:SER:HB3	1.30	0.95
1:I:42:ILE:HD13	1:I:84:ILE:CD1	1.95	0.95
1:D:56:ASN:HD22	1:D:58:GLU:H	1.06	0.94

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	94/119 (79%)	91 (97%)	3 (3%)	0	100	100
1	B	94/119 (79%)	93 (99%)	1 (1%)	0	100	100
1	D	94/119 (79%)	88 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	E	108/119 (91%)	105 (97%)	2 (2%)	1 (1%)	14 17
1	F	108/119 (91%)	105 (97%)	3 (3%)	0	100 100
1	G	92/119 (77%)	90 (98%)	2 (2%)	0	100 100
1	H	93/119 (78%)	90 (97%)	3 (3%)	0	100 100
1	I	103/119 (87%)	101 (98%)	2 (2%)	0	100 100
All	All	786/952 (83%)	763 (97%)	22 (3%)	1 (0%)	48 60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	103	SER

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	85/104 (82%)	82 (96%)	3 (4%)	31 46
1	B	85/104 (82%)	83 (98%)	2 (2%)	44 61
1	D	85/104 (82%)	81 (95%)	4 (5%)	22 32
1	E	98/104 (94%)	92 (94%)	6 (6%)	15 22
1	F	98/104 (94%)	96 (98%)	2 (2%)	50 68
1	G	83/104 (80%)	76 (92%)	7 (8%)	9 11
1	H	84/104 (81%)	79 (94%)	5 (6%)	16 23
1	I	93/104 (89%)	89 (96%)	4 (4%)	25 36
All	All	711/832 (86%)	678 (95%)	33 (5%)	23 33

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	39	PHE
1	I	16	THR

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Mol	Chain	Res	Type
1	I	93	ASN
1	E	37	ASP
1	E	33	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	95	ASN
1	I	95	ASN
1	G	33	ASN
1	F	95	ASN
1	G	31	HIS

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)

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	95/119 (79%)	0.21	4 (4%)	41	42	27, 39, 55, 73	0
1	B	95/119 (79%)	0.59	5 (5%)	33	34	28, 47, 72, 87	0
1	D	95/119 (79%)	0.37	7 (7%)	22	23	28, 43, 72, 83	0
1	E	108/119 (90%)	0.49	5 (4%)	38	39	28, 45, 68, 86	1 (0%)
1	F	108/119 (90%)	0.35	5 (4%)	38	39	30, 44, 72, 78	0
1	G	93/119 (78%)	0.58	7 (7%)	22	23	32, 50, 68, 72	0
1	H	94/119 (78%)	0.47	6 (6%)	27	28	18, 46, 69, 84	1 (1%)
1	I	103/119 (86%)	0.39	2 (1%)	66	67	30, 44, 78, 89	0
All	All	791/952 (83%)	0.43	41 (5%)	34	35	18, 45, 71, 89	2 (0%)

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	13	GLN	3.5
1	E	14	ARG	3.3
1	H	58	GLU	3.3
1	F	2	SER	3.3
1	A	22	ASP	3.1

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.