



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 06:43 am BST

PDB ID : 4FQB
Title : crystal structure of toxic effector Tse1 in complex with immune protein Tsi1
Authors : Wang, T.; Li, L.; Zhang, W.
Deposited on : 2012-06-25
Resolution : 2.69 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

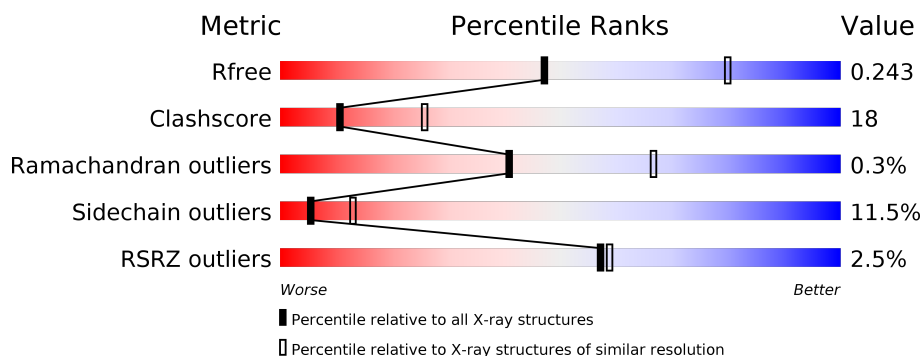
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	162	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>19%</div> <div>••</div> <div>10%</div> </div> </div>
1	C	162	<div> <div>3%</div> <div> <div></div> <div>59%</div> <div>26%</div> <div>6%</div> <div>10%</div> </div> </div>
1	E	162	<div> <div>2%</div> <div> <div></div> <div>57%</div> <div>25%</div> <div>6%</div> <div>•</div> <div>10%</div> </div> </div>
1	G	162	<div> <div>7%</div> <div> <div></div> <div>64%</div> <div>20%</div> <div>6%</div> <div>10%</div> </div> </div>
2	B	162	<div> <div>%</div> <div> <div></div> <div>62%</div> <div>25%</div> <div>•</div> <div>9%</div> </div> </div>
2	D	162	<div> <div></div> <div> <div></div> <div>69%</div> <div>19%</div> <div>•</div> <div>9%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	162	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>68%</div><div>18%</div><div>6%</div><div>9%</div></div></div>
2	H	162	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>69%</div><div>19%</div><div>• •</div><div>9%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9004 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 toxic effector Tse1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	146	Total	C	N	O	S	1	0	0
			1091	682	195	205	9			
1	C	146	Total	C	N	O	S	0	0	0
			1091	682	195	205	9			
1	E	146	Total	C	N	O	S	0	0	0
			1091	682	195	205	9			
1	G	146	Total	C	N	O	S	0	0	0
			1091	682	195	205	9			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	155	LEU	-	EXPRESSION TAG	UNP Q9I2Q1
A	156	GLU	-	EXPRESSION TAG	UNP Q9I2Q1
A	157	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
A	158	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
A	159	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
A	160	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
A	161	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
A	162	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	155	LEU	-	EXPRESSION TAG	UNP Q9I2Q1
C	156	GLU	-	EXPRESSION TAG	UNP Q9I2Q1
C	157	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	158	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	159	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	160	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	161	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
C	162	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
E	155	LEU	-	EXPRESSION TAG	UNP Q9I2Q1
E	156	GLU	-	EXPRESSION TAG	UNP Q9I2Q1
E	157	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
E	158	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
E	159	HIS	-	EXPRESSION TAG	UNP Q9I2Q1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	160	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
E	161	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
E	162	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	155	LEU	-	EXPRESSION TAG	UNP Q9I2Q1
G	156	GLU	-	EXPRESSION TAG	UNP Q9I2Q1
G	157	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	158	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	159	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	160	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	161	HIS	-	EXPRESSION TAG	UNP Q9I2Q1
G	162	HIS	-	EXPRESSION TAG	UNP Q9I2Q1

- Molecule 2 is a protein called immune protein Tsi1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	148	Total	C	N	O	S	0	0	0
			1142	701	202	230	9			
2	D	148	Total	C	N	O	S	0	0	0
			1142	701	202	230	9			
2	F	148	Total	C	N	O	S	0	0	0
			1142	701	202	230	9			
2	H	148	Total	C	N	O	S	0	0	0
			1142	701	202	230	9			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	19	MET	-	EXPRESSION TAG	UNP Q9I2Q0
B	173	LEU	-	EXPRESSION TAG	UNP Q9I2Q0
B	174	GLU	-	EXPRESSION TAG	UNP Q9I2Q0
B	175	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
B	176	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
B	177	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
B	178	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
B	179	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
B	180	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
D	19	MET	-	EXPRESSION TAG	UNP Q9I2Q0
D	173	LEU	-	EXPRESSION TAG	UNP Q9I2Q0
D	174	GLU	-	EXPRESSION TAG	UNP Q9I2Q0
D	175	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
D	176	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
D	177	HIS	-	EXPRESSION TAG	UNP Q9I2Q0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	178	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
D	179	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
D	180	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	19	MET	-	EXPRESSION TAG	UNP Q9I2Q0
F	173	LEU	-	EXPRESSION TAG	UNP Q9I2Q0
F	174	GLU	-	EXPRESSION TAG	UNP Q9I2Q0
F	175	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	176	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	177	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	178	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	179	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
F	180	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	19	MET	-	EXPRESSION TAG	UNP Q9I2Q0
H	173	LEU	-	EXPRESSION TAG	UNP Q9I2Q0
H	174	GLU	-	EXPRESSION TAG	UNP Q9I2Q0
H	175	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	176	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	177	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	178	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	179	HIS	-	EXPRESSION TAG	UNP Q9I2Q0
H	180	HIS	-	EXPRESSION TAG	UNP Q9I2Q0

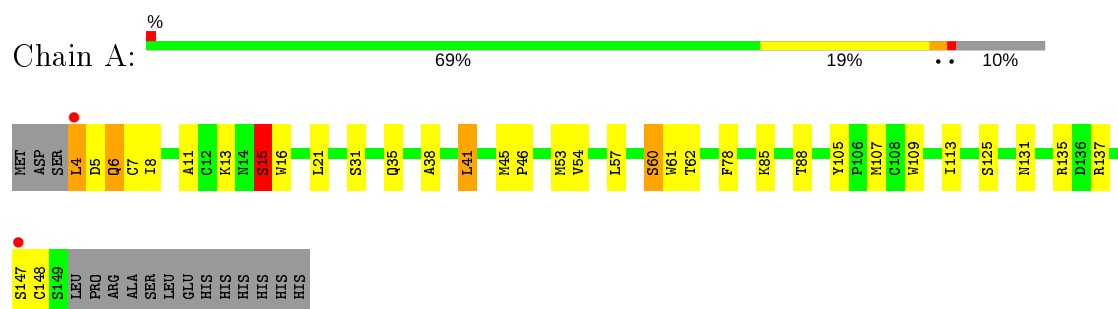
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	9	Total O 9 9	0	0
3	B	17	Total O 17 17	0	0
3	C	5	Total O 5 5	0	0
3	D	15	Total O 15 15	0	0
3	E	2	Total O 2 2	0	0
3	F	14	Total O 14 14	0	0
3	G	1	Total O 1 1	0	0
3	H	9	Total O 9 9	0	0

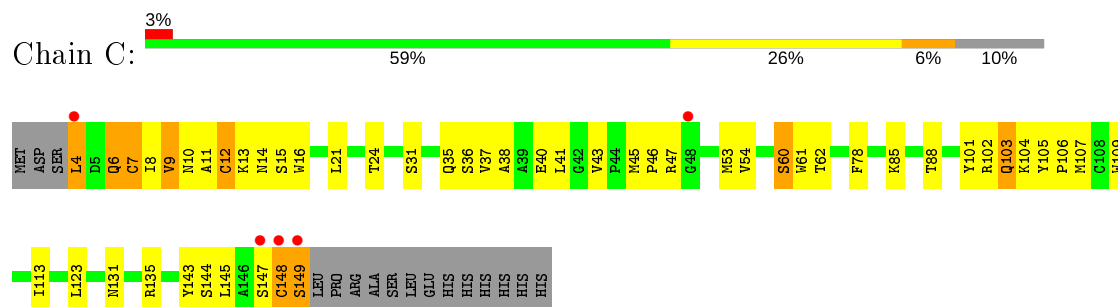
3 Residue-property plots [i](#)

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.

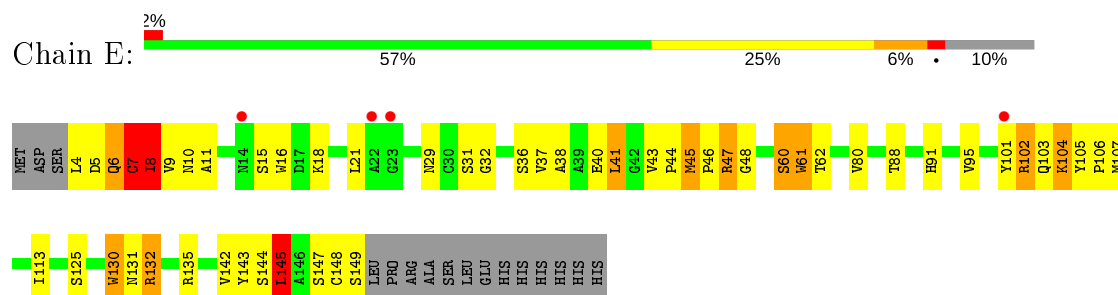
- Molecule 1: toxic effector Tse1



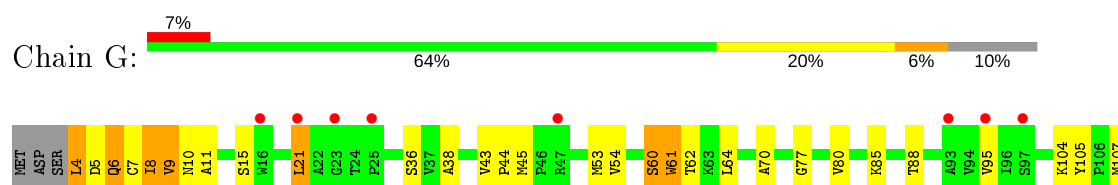
- Molecule 1: toxic effector Tse1



- Molecule 1: toxic effector Tse1



- Molecule 1: toxic effector Tse1



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.71Å 97.71Å 293.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.69 29.77 – 2.69	Depositor EDS
% Data completeness (in resolution range)	93.6 (30.00-2.69) 93.7 (29.77-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.201 , 0.245 0.207 , 0.243	Depositor DCC
R_{free} test set	2201 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	69.8	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9004	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.83	3/1113 (0.3%)	0.87	2/1508 (0.1%)
1	C	0.79	2/1113 (0.2%)	0.86	3/1508 (0.2%)
1	E	0.79	3/1113 (0.3%)	0.80	1/1508 (0.1%)
1	G	0.70	1/1113 (0.1%)	0.75	0/1508
2	B	1.03	3/1166 (0.3%)	1.06	4/1575 (0.3%)
2	D	1.02	1/1166 (0.1%)	0.94	1/1575 (0.1%)
2	F	0.90	0/1166	0.96	4/1575 (0.3%)
2	H	0.92	2/1166 (0.2%)	1.12	6/1575 (0.4%)
All	All	0.88	15/9116 (0.2%)	0.93	21/12332 (0.2%)

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
2	B	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	134	TRP	CD2-CE2	6.98	1.49	1.41
2	B	28	GLU	CD-OE1	6.85	1.33	1.25
1	C	16	TRP	CD2-CE2	5.68	1.48	1.41
2	H	118	SER	CB-OG	-5.37	1.35	1.42
1	A	16	TRP	CD2-CE2	5.37	1.47	1.41

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	145	GLN	CB-CA-C	-19.52	71.35	110.40
2	H	146	LYS	N-CA-C	-11.42	80.15	111.00
1	C	148	CYS	N-CA-CB	-10.22	92.20	110.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	145	GLN	N-CA-C	9.14	135.69	111.00
2	B	85	GLY	N-CA-C	-8.87	90.92	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	90	GLY	Peptide

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	1091	0	1069	34	0
1	C	1091	0	1069	57	0
1	E	1091	0	1069	62	0
1	G	1091	0	1069	50	0
2	B	1142	0	1061	35	0
2	D	1142	0	1061	23	1
2	F	1142	0	1061	41	0
2	H	1142	0	1061	27	0
3	A	9	0	0	0	0
3	B	17	0	0	2	0
3	C	5	0	0	0	0
3	D	15	0	0	0	0
3	E	2	0	0	0	0
3	F	14	0	0	3	0
3	G	1	0	0	0	0
3	H	9	0	0	1	0
All	All	9004	0	8520	321	1

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 18.

The worst 5 of 321 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:G:144:SER:C	1:G:145:LEU:HD12	1.38	1.44
1:E:45:MET:CE	1:E:46:PRO:HD2	1.58	1.32
1:E:45:MET:HA	1:E:45:MET:CE	1.67	1.24
2:F:152:VAL:HG12	3:F:213:HOH:O	1.45	1.15
1:E:45:MET:HE1	1:E:46:PRO:HD2	1.21	1.13

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:33:PHE:O	2:D:35:SER:OG[4_555]	2.12	0.08

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	144/162 (89%)	133 (92%)	11 (8%)	0	100	100
1	C	144/162 (89%)	134 (93%)	10 (7%)	0	100	100
1	E	144/162 (89%)	134 (93%)	8 (6%)	2 (1%)	11	28
1	G	144/162 (89%)	128 (89%)	16 (11%)	0	100	100
2	B	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
2	D	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
2	F	146/162 (90%)	138 (94%)	8 (6%)	0	100	100
2	H	146/162 (90%)	138 (94%)	7 (5%)	1 (1%)	22	46
All	All	1160/1296 (90%)	1089 (94%)	68 (6%)	3 (0%)	41	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	7	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	8	ILE
2	H	146	LYS

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	113/128 (88%)	102 (90%)	11 (10%)	8	19
1	C	113/128 (88%)	95 (84%)	18 (16%)	2	6
1	E	113/128 (88%)	94 (83%)	19 (17%)	2	5
1	G	113/128 (88%)	100 (88%)	13 (12%)	5	13
2	B	127/139 (91%)	114 (90%)	13 (10%)	7	17
2	D	127/139 (91%)	113 (89%)	14 (11%)	6	14
2	F	127/139 (91%)	118 (93%)	9 (7%)	14	34
2	H	127/139 (91%)	114 (90%)	13 (10%)	7	17
All	All	960/1068 (90%)	850 (88%)	110 (12%)	5	13

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	137	ASP
1	E	31	SER
2	H	137	ASP
2	D	151	SER
2	D	169	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	132	GLN
2	D	168	GLN
1	G	10	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	14	ASN
1	E	6	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	146/162 (90%)	-0.12	2 (1%) 75 77	46, 80, 124, 149	1 (0%)
1	C	146/162 (90%)	0.02	5 (3%) 45 45	55, 91, 139, 168	0
1	E	146/162 (90%)	-0.06	4 (2%) 54 55	57, 97, 140, 175	0
1	G	146/162 (90%)	0.21	11 (7%) 14 12	63, 102, 149, 175	0
2	B	148/162 (91%)	-0.31	1 (0%) 87 89	42, 63, 98, 160	0
2	D	148/162 (91%)	-0.36	0 100 100	43, 63, 92, 153	0
2	F	148/162 (91%)	-0.13	3 (2%) 65 67	45, 69, 121, 146	0
2	H	148/162 (91%)	-0.13	3 (2%) 65 67	44, 68, 134, 168	0
All	All	1176/1296 (90%)	-0.11	29 (2%) 57 59	42, 78, 137, 175	1 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	149	SER	5.4
1	E	23	GLY	4.9
1	C	4	LEU	4.1
1	C	147	SER	4.0
2	H	156	ALA	3.7

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.