



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:07 PM UTC

PDB ID : 2BSQ / pdb_00002bsq
Title : FitAB bound to DNA
Authors : Mattison, K.; Wilbur, J.S.; So, M.; Brennan, R.G.
Deposited on : 2005-05-23
Resolution : 3.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

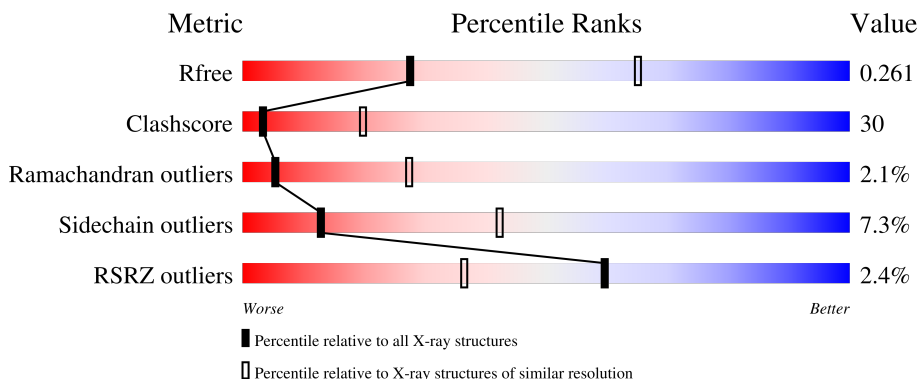
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 $\leq 5\%$. 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	146	 4% 60% 32% 6%
1	B	146	 65% 28%
1	C	146	 2% 64% 30% 5%
1	D	146	 0% 55% 36% 5%
2	E	77	 3% 44% 35% 10% 10%

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Mol	Chain	Length	Quality of chain
2	F	77	<p>%</p> <p>44% 36% 16%</p>
2	G	77	<p>3%</p> <p>45% 35% 6% 12%</p>
2	H	77	<p>3%</p> <p>44% 30% 9% 17%</p>
3	I	36	<p>6%</p> <p>14% 78% 8%</p>
4	J	36	<p>8%</p> <p>89% 11%</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	5IU	J	52	-	-	X	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7910 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 TRAFFICKING PROTEIN B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	144	1122	720	196	202	4	0	0	1
1	B	141	1092	702	187	199	4	0	0	1
1	C	144	1122	720	196	202	4	0	0	1
1	D	141	1092	702	187	199	4	0	0	1

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	139	LEU	ASP	engineered mutation	UNP Q5F882
B	139	LEU	ASP	engineered mutation	UNP Q5F882
C	139	LEU	ASP	engineered mutation	UNP Q5F882
D	139	LEU	ASP	engineered mutation	UNP Q5F882

- Molecule 2 is a protein called TRAFFICKING PROTEIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	69	510	311	100	98	1	0	0	1
2	F	65	480	294	93	92	1	0	0	1
2	G	68	506	309	99	97	1	0	0	1
2	H	64	471	289	92	89	1	0	0	1

- Molecule 3 is a DNA chain called IR36, FORWARD STRAND.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	I	N	O	P			
3	I	36	732	356	1	114	226	35	0	0	0

- Molecule 4 is a DNA chain called IR36, REVERSE STRAND.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	I	N	O	P			
4	J	36	738	354	1	146	202	35	0	0	0

- Molecule 5 is water.

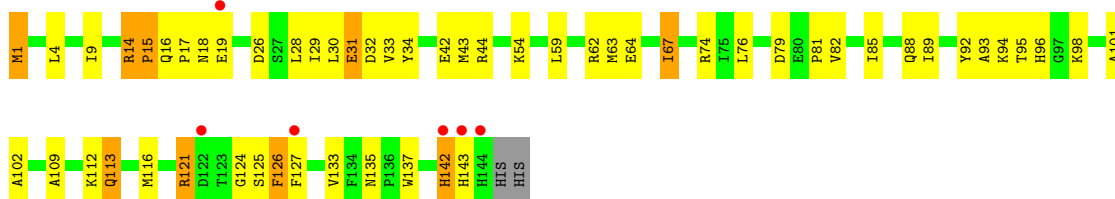
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total 7	O 7	0	0
5	B	2	Total 2	O 2	0	0
5	C	12	Total 12	O 12	0	0
5	D	1	Total 1	O 1	0	0
5	E	8	Total 8	O 8	0	0
5	F	3	Total 3	O 3	0	0
5	G	4	Total 4	O 4	0	0
5	H	5	Total 5	O 5	0	0
5	I	3	Total 3	O 3	0	0

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.

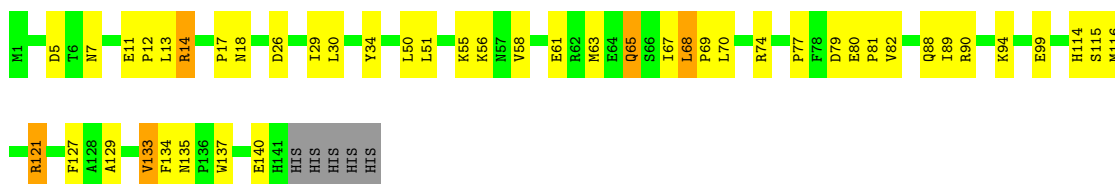
- Molecule 1: TRAFFICKING PROTEIN B

Chain A: 



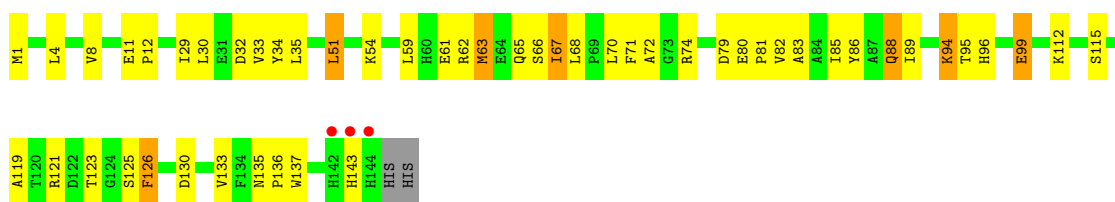
- Molecule 1: TRAFFICKING PROTEIN B

Chain B: 



- Molecule 1: TRAFFICKING PROTEIN B

Chain C: 



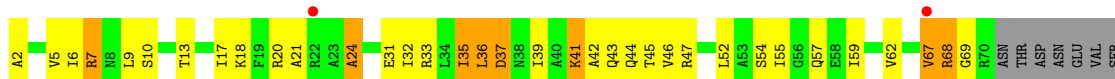
- Molecule 1: TRAFFICKING PROTEIN B

Chain D: 



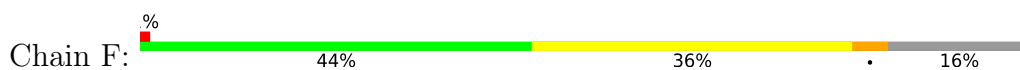


- Molecule 2: TRAFFICKING PROTEIN A



LEU

- Molecule 2: TRAFFICKING PROTEIN A



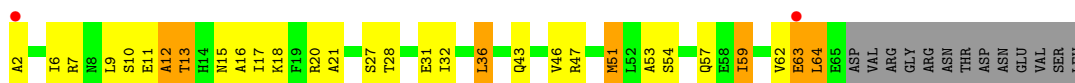
LEU

- Molecule 2: TRAFFICKING PROTEIN A

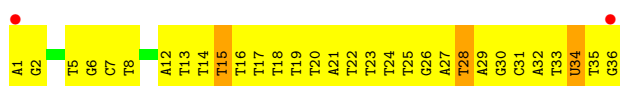


LEU

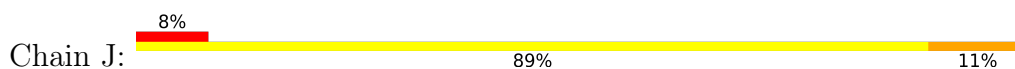
- Molecule 2: TRAFFICKING PROTEIN A



- Molecule 3: IR36, FORWARD STRAND



- Molecule 4: IR36, REVERSE STRAND



C57
A38
A39
A40
T41
G42
C43
T44
A45
T46
C47
A48
A49
A50
A51
U52
A53
A54
A55
A56
A57
A58
A59
A60
T61
G62
A63
T64
A65
G66
C67
A68
A69
T70
C71
T72

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.04Å 82.40Å 135.50Å 90.00° 94.19° 90.00°	Depositor
Resolution (Å)	70.36 – 3.00 70.36 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (70.36-3.00) 99.9 (70.36-3.00)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.213 , 0.271 0.207 , 0.261	Depositor DCC
R_{free} test set	3316 reflections (9.94%)	wwPDB-VP
Wilson B-factor (Å ²)	45.4	Xtrriage
Anisotropy	0.816	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7910	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5IU

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	0.58	1/1148 (0.1%)	0.96	7/1563 (0.4%)
1	B	0.61	1/1115 (0.1%)	1.03	3/1518 (0.2%)
1	C	0.53	1/1148 (0.1%)	0.92	0/1563
1	D	0.54	1/1115 (0.1%)	1.00	3/1518 (0.2%)
2	E	0.63	1/511 (0.2%)	1.01	2/686 (0.3%)
2	F	0.68	1/481 (0.2%)	0.91	0/646
2	G	0.65	1/507 (0.2%)	0.92	0/681
2	H	0.60	1/472 (0.2%)	1.07	2/634 (0.3%)
3	I	0.37	0/793	0.92	1/1221 (0.1%)
4	J	0.37	0/809	0.87	2/1243 (0.2%)
All	All	0.55	8/8099 (0.1%)	0.96	20/11273 (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
3	I	0	1
4	J	0	1
All	All	0	2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	64	LEU	C-N	-5.76	1.25	1.33
1	A	143	HIS	C-N	-5.72	1.25	1.33
2	E	69	GLY	C-N	-5.64	1.25	1.33
1	B	140	GLU	C-N	-5.64	1.25	1.33
2	G	68	ARG	C-N	-5.54	1.25	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	13	THR	N-CA-C	-11.40	98.86	111.28
2	E	24	ALA	N-CA-C	-8.85	99.11	110.53
1	B	14	ARG	CA-C-N	7.13	126.65	119.24
1	B	14	ARG	C-N-CA	7.13	126.65	119.24
1	A	76	LEU	N-CA-C	6.10	118.45	109.42

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	I	28	DT	Sidechain
4	J	61	DT	Sidechain

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	1122	0	1132	52	0
1	B	1092	0	1111	41	0
1	C	1122	0	1132	47	0
1	D	1092	0	1111	70	0
2	E	510	0	529	53	0
2	F	480	0	500	41	0
2	G	506	0	526	32	0
2	H	471	0	494	52	0
3	I	732	0	415	66	0
4	J	738	0	403	87	0
5	A	7	0	0	1	0
5	B	2	0	0	0	0
5	C	12	0	0	0	0
5	D	1	0	0	0	0
5	E	8	0	0	0	0
5	F	3	0	0	2	0
5	G	4	0	0	0	0
5	H	5	0	0	0	0
5	I	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7910	0	7353	456	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 30.

The worst 5 of 456 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)
3:I:26:DG:H2''	3:I:27:DA:H5'	1.27	1.15
4:J:52:5IU:H2''	4:J:53:DA:H5'	1.26	1.15
3:I:13:DT:H2''	3:I:14:DT:H5''	1.27	1.12
4:J:52:5IU:H2''	4:J:53:DA:C5'	1.79	1.10
3:I:21:DA:H2''	3:I:22:DT:H5'	1.39	1.03

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	142/146 (97%)	123 (87%)	15 (11%)	4 (3%)	4	21
1	B	139/146 (95%)	127 (91%)	12 (9%)	0	100	100
1	C	142/146 (97%)	123 (87%)	17 (12%)	2 (1%)	9	36
1	D	139/146 (95%)	120 (86%)	17 (12%)	2 (1%)	9	36
2	E	67/77 (87%)	61 (91%)	4 (6%)	2 (3%)	3	19
2	F	63/77 (82%)	52 (82%)	11 (18%)	0	100	100
2	G	66/77 (86%)	58 (88%)	3 (4%)	5 (8%)	1	4
2	H	62/77 (80%)	55 (89%)	5 (8%)	2 (3%)	3	18
All	All	820/892 (92%)	719 (88%)	84 (10%)	17 (2%)	5	27

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ILE
2	G	68	ARG
2	H	12	ALA
1	C	67	ILE
1	C	126	PHE

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	118/121 (98%)	112 (95%)	6 (5%)	21	55
1	B	115/121 (95%)	109 (95%)	6 (5%)	21	55
1	C	118/121 (98%)	109 (92%)	9 (8%)	12	41
1	D	115/121 (95%)	109 (95%)	6 (5%)	21	55
2	E	52/61 (85%)	47 (90%)	5 (10%)	8	31
2	F	49/61 (80%)	43 (88%)	6 (12%)	5	21
2	G	52/61 (85%)	46 (88%)	6 (12%)	5	24
2	H	48/61 (79%)	43 (90%)	5 (10%)	7	28
All	All	667/728 (92%)	618 (93%)	49 (7%)	13	42

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	35	ILE
2	F	51	MET
2	E	36	LEU
2	F	20	ARG
2	F	64	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	113	GLN
2	E	15	ASN
1	D	138	HIS
2	E	38	ASN
1	B	138	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	5IU	I	34	3,4	18,21,22	4.38	1 (5%)	25,30,33	0.47	0
4	5IU	J	52	4,3	18,21,22	4.25	1 (5%)	25,30,33	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	5IU	I	34	3,4	-	0/7/21/22	0/2/2/2
4	5IU	J	52	4,3	-	1/7/21/22	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	34	5IU	C5-I5	-18.43	1.56	2.08
4	J	52	5IU	C5-I5	-17.85	1.58	2.08

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	52	5IU	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	34	5IU	6	0
4	J	52	5IU	9	0

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 [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	144/146 (98%)	-0.14	6 (4%) 40 22	20, 36, 61, 88	0
1	B	141/146 (96%)	-0.43	0 100 100	17, 28, 43, 64	0
1	C	144/146 (98%)	-0.05	3 (2%) 63 40	25, 40, 67, 93	0
1	D	141/146 (96%)	-0.09	1 (0%) 84 66	23, 38, 68, 79	0
2	E	69/77 (89%)	-0.11	2 (2%) 53 31	26, 38, 56, 60	0
2	F	65/77 (84%)	-0.22	1 (1%) 72 49	21, 30, 52, 62	0
2	G	68/77 (88%)	-0.13	2 (2%) 53 31	16, 30, 59, 66	0
2	H	64/77 (83%)	0.01	2 (3%) 51 30	25, 37, 65, 71	0
3	I	35/36 (97%)	0.58	2 (5%) 29 15	23, 45, 71, 103	0
4	J	35/36 (97%)	0.75	3 (8%) 16 8	23, 46, 73, 107	0
All	All	906/964 (93%)	-0.09	22 (2%) 59 36	16, 36, 65, 107	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	J	72	DT	4.6
1	A	143	HIS	4.5
1	A	144	HIS	4.1
3	I	36	DG	3.8
2	G	22	ARG	3.7

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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(\AA^2)	Q<0.9
4	5IU	J	52	20/21	0.77	0.20	61,78,93,109	0
3	5IU	I	34	20/21	0.84	0.17	78,94,108,119	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.