Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:26 AM UTC

PDB ID	:	8EWH / pdb_00008ewh
Title	:	Salmonella typhimurium GTPase BIPA
Authors	:	Brown, R.S.; deLivron, M.A.; Robinson, V.L.
Deposited on	:	2022-10-23
Resolution	:	2.33 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

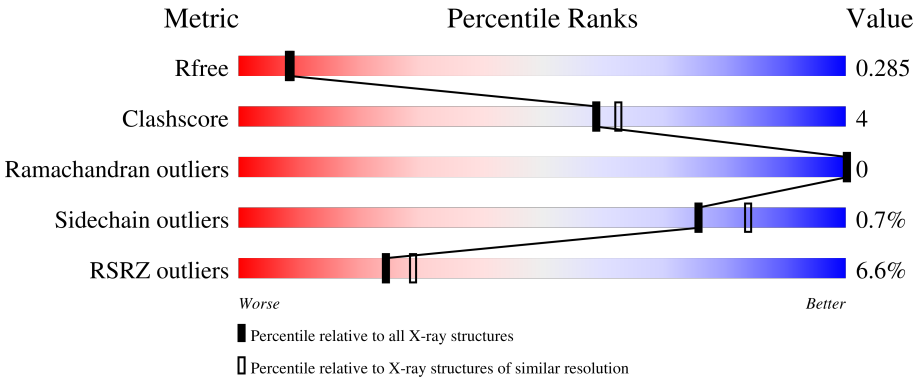
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.33 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	607	5% 86% 10% .
1	B	607	7% 82% 14% .

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9158 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 50S ribosomal subunit assembly factor BipA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4522	2831	801	873	17			
1	B	581	Total	C	N	O	S	0	0	0
			4522	2831	801	873	17			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Na	0	0
			2	2		
2	B	2	Total	Na	0	0
			2	2		

- Molecule 3 is water.

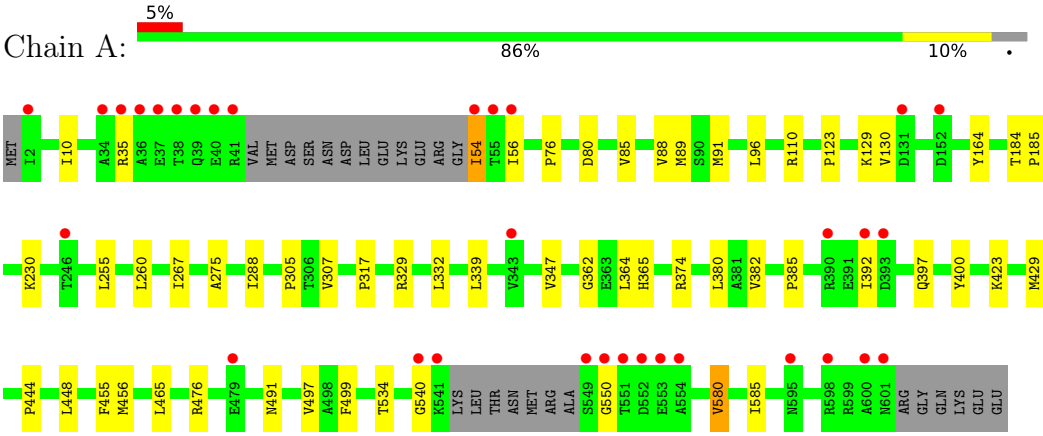
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	70	Total	O	0	0
			70	70		
3	B	40	Total	O	0	0
			40	40		

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.

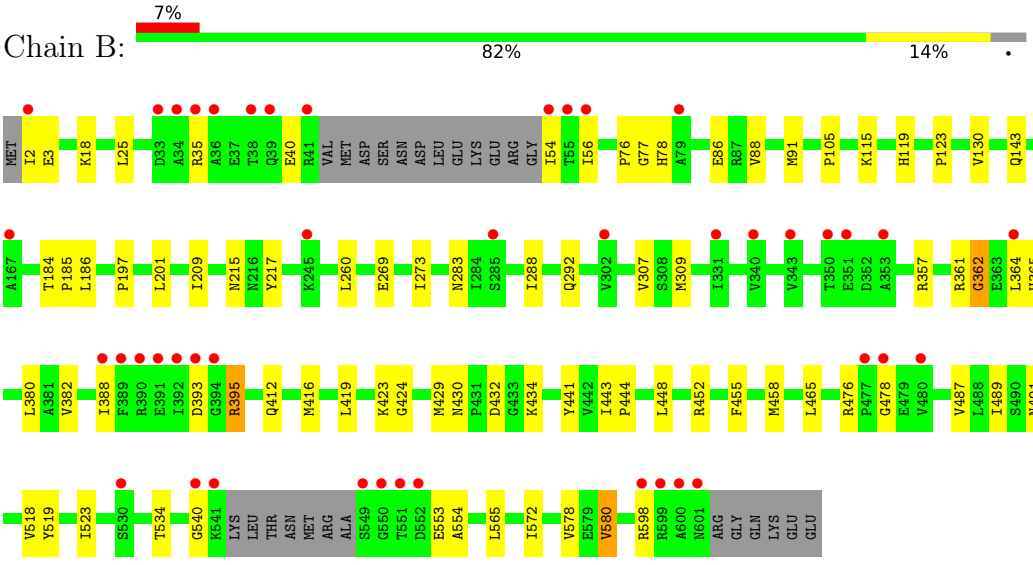
• Molecule 1: 50S ribosomal subunit assembly factor BipA

Chain A:



• Molecule 1: 50S ribosomal subunit assembly factor BipA

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	89.41Å 83.70Å 95.41Å 90.00° 105.77° 90.00°	Depositor
Resolution (Å)	29.78 – 2.33 29.78 – 2.33	Depositor EDS
% Data completeness (in resolution range)	90.6 (29.78-2.33) 90.7 (29.78-2.33)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.54 (at 2.34Å)	Xtriage
Refinement program	REFMAC v5.8.0267	Depositor
R, R_{free}	0.231 , 0.283 0.234 , 0.285	Depositor DCC
R_{free} test set	2551 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å^2)	30.0	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 32.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	9158	wwPDB-VP
Average B, all atoms (Å^2)	36.0	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 20.69 % 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 8.2334e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

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

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	1.22	9/4593 (0.2%)	1.30	2/6213 (0.0%)
1	B	1.22	6/4593 (0.1%)	1.30	8/6213 (0.1%)
All	All	1.22	15/9186 (0.2%)	1.30	10/12426 (0.1%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	123	PRO	C-O	-7.97	1.15	1.23
1	A	123	PRO	C-O	-6.38	1.16	1.23
1	B	283	ASN	C-O	6.08	1.31	1.23
1	A	431	PRO	C-O	-6.00	1.17	1.23
1	A	305	PRO	C-O	-5.87	1.19	1.24
1	A	129	LYS	C-O	-5.74	1.16	1.23
1	A	385	PRO	C-O	-5.70	1.17	1.23
1	A	550	GLY	N-CA	5.56	1.49	1.44
1	A	317	PRO	C-O	-5.53	1.16	1.24
1	B	197	PRO	C-O	-5.50	1.17	1.23
1	B	105	PRO	C-O	-5.13	1.18	1.23
1	B	78	HIS	CE1-NE2	5.10	1.37	1.32
1	B	77	GLY	C-O	-5.08	1.19	1.24
1	A	465	LEU	C-O	-5.06	1.18	1.24
1	A	585	ILE	C-O	5.04	1.29	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	478	GLY	CA-C-O	-6.12	118.01	122.23
1	B	18	LYS	CA-C-N	5.63	127.75	120.44
1	B	18	LYS	C-N-CA	5.63	127.75	120.44
1	A	497	VAL	CA-C-N	5.28	127.66	120.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	497	VAL	C-N-CA	5.28	127.66	120.54
1	B	362	GLY	CA-C-O	-5.18	117.73	122.24
1	B	497	VAL	CA-C-N	5.12	127.46	120.54
1	B	497	VAL	C-N-CA	5.12	127.46	120.54
1	B	424	GLY	CA-C-O	-5.09	116.64	120.76
1	B	432	ASP	CA-CB-CG	5.08	117.68	112.60

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	4522	0	4514	35	0
1	B	4522	0	4514	46	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	70	0	0	0	0
3	B	40	0	0	0	0
All	All	9158	0	9028	79	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.

All (79) 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:A:423:LYS:HB3	1:A:476:ARG:HD3	1.77	0.65
1:A:80:ASP:OD2	1:A:364:LEU:HD21	1.97	0.65
1:B:35:ARG:HD3	1:B:260:LEU:HD22	1.79	0.65
1:A:429:MET:HE1	1:B:429:MET:SD	2.38	0.63
1:A:380:LEU:HD13	1:A:382:VAL:HG13	1.80	0.63
1:A:91:MET:HG3	1:A:225:ARG:HB2	1.83	0.60
1:A:91:MET:CG	1:A:225:ARG:HB2	2.32	0.59
1:B:455:PHE:HA	1:B:458:MET:HE3	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:553:GLU:HG3	1:B:554:ALA:H	1.67	0.58
1:B:412:GLN:O	1:B:416:MET:HG3	2.02	0.58
1:B:491:ASN:HB3	1:B:534:THR:HG22	1.85	0.58
1:A:429:MET:HE1	1:B:429:MET:CE	2.35	0.57
1:B:393:ASP:O	1:B:395:ARG:HG2	2.06	0.56
1:A:491:ASN:HB3	1:A:534:THR:HG22	1.87	0.56
1:B:553:GLU:HG3	1:B:554:ALA:N	2.21	0.56
1:A:455:PHE:CD2	1:A:456:MET:HE2	2.41	0.55
1:A:329:ARG:NH1	1:A:332:LEU:HD23	2.21	0.55
1:A:380:LEU:HD12	1:A:380:LEU:C	2.31	0.55
1:B:54:ILE:HG13	1:B:56:ILE:HG12	1.89	0.53
1:A:380:LEU:CD1	1:A:382:VAL:HG13	2.37	0.53
1:B:292:GLN:O	1:B:292:GLN:HG3	2.08	0.53
1:B:184:THR:HB	1:B:185:PRO:HD3	1.89	0.53
1:B:86:GLU:HG2	1:B:119:HIS:NE2	2.24	0.52
1:B:25:LEU:HD21	1:B:186:LEU:HD23	1.92	0.51
1:B:419:LEU:HD13	1:B:441:TYR:CD1	2.45	0.51
1:A:499:PHE:HD2	1:A:540:GLY:HA3	1.74	0.51
1:B:423:LYS:HB3	1:B:476:ARG:HD3	1.92	0.51
1:B:91:MET:HE2	1:B:273:ILE:HG12	1.92	0.51
1:A:307:VAL:HG11	1:A:362:GLY:C	2.36	0.50
1:B:307:VAL:HG11	1:B:362:GLY:C	2.36	0.50
1:B:54:ILE:CG1	1:B:56:ILE:HG12	2.42	0.50
1:A:35:ARG:CZ	1:A:260:LEU:HD22	2.41	0.50
1:B:380:LEU:CD1	1:B:382:VAL:HG13	2.42	0.49
1:B:380:LEU:C	1:B:380:LEU:HD12	2.38	0.49
1:A:230:LYS:HD2	1:A:267:ILE:HD11	1.96	0.48
1:A:110:ARG:HD2	1:A:438:ARG:CZ	2.44	0.48
1:B:487:VAL:HG21	1:B:523:ILE:HD12	1.96	0.48
1:A:130:VAL:HG11	1:A:164:TYR:HB3	1.96	0.47
1:B:518:VAL:HG12	1:B:519:TYR:N	2.29	0.47
1:A:423:LYS:HB3	1:A:476:ARG:CD	2.45	0.47
1:B:201:LEU:CD1	1:B:269:GLU:HB3	2.45	0.47
1:A:184:THR:HB	1:A:185:PRO:HD3	1.97	0.46
1:B:76:PRO:HD3	1:B:88:VAL:HG21	1.97	0.46
1:B:309:MET:HE2	1:B:382:VAL:HB	1.96	0.46
1:B:419:LEU:HD13	1:B:441:TYR:CE1	2.51	0.46
1:A:54:ILE:HG23	1:A:56:ILE:HG12	1.98	0.46
1:B:130:VAL:HG11	1:B:164:TYR:HB3	1.97	0.46
1:B:2:ILE:HG23	1:B:3:GLU:OE1	2.17	0.45
1:B:452:ARG:NH1	1:B:465:LEU:HB3	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:380:LEU:HD13	1:B:382:VAL:HG13	1.98	0.45
1:A:339:LEU:HD13	1:A:347:VAL:HG23	1.98	0.45
1:B:215:ASN:OD1	1:B:217:TYR:HB2	2.17	0.45
1:B:572:ILE:HD13	1:B:578:VAL:HG23	1.98	0.45
1:A:400:TYR:HA	1:A:444:PRO:HA	1.99	0.44
1:A:455:PHE:HD2	1:A:456:MET:HE2	1.83	0.44
1:B:361:ARG:H	1:B:365:HIS:HD2	1.65	0.44
1:A:392:ILE:HG23	1:A:397:GLN:NE2	2.33	0.43
1:A:430:ASN:OD1	1:A:430:ASN:C	2.62	0.43
1:B:143:GLN:OE1	1:B:434:LYS:NZ	2.51	0.42
1:B:499:PHE:HD2	1:B:540:GLY:HA3	1.84	0.42
1:B:489:ILE:HG12	1:B:523:ILE:HD13	2.00	0.42
1:A:10:ILE:HD12	1:A:96:LEU:HD23	2.02	0.42
1:A:76:PRO:HD3	1:A:88:VAL:HG21	2.02	0.41
1:B:357:ARG:HD3	1:B:388:ILE:HD11	2.01	0.41
1:B:448:LEU:HD12	1:B:448:LEU:HA	1.88	0.41
1:B:374:ARG:CD	1:B:580:VAL:HG13	2.50	0.41
1:A:209:ILE:HD11	1:A:288:ILE:HD11	2.02	0.41
1:A:364:LEU:HD12	1:A:365:HIS:N	2.35	0.41
1:A:491:ASN:HB3	1:A:534:THR:CG2	2.49	0.41
1:B:209:ILE:HD11	1:B:288:ILE:HD11	2.01	0.41
1:A:448:LEU:HD12	1:A:448:LEU:HA	1.89	0.41
1:A:85:VAL:O	1:A:89:MET:HG2	2.20	0.41
1:B:430:ASN:OD1	1:B:430:ASN:C	2.62	0.41
1:B:371:GLU:HG2	1:B:565:LEU:HD23	2.03	0.41
1:B:443:ILE:HG13	1:B:444:PRO:HD2	2.02	0.41
1:B:374:ARG:HD2	1:B:580:VAL:HG13	2.03	0.41
1:A:374:ARG:CD	1:A:580:VAL:HG13	2.51	0.40
1:A:255:LEU:HB2	1:A:275:ALA:HB3	2.03	0.40
1:B:115:LYS:O	1:B:119:HIS:HD2	2.05	0.40

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	575/607 (95%)	555 (96%)	20 (4%)	0	100	100
1	B	575/607 (95%)	555 (96%)	20 (4%)	0	100	100
All	All	1150/1214 (95%)	1110 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	496/519 (96%)	494 (100%)	2 (0%)	84	89
1	B	496/519 (96%)	491 (99%)	5 (1%)	68	79
All	All	992/1038 (96%)	985 (99%)	7 (1%)	76	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ILE
1	A	580	VAL
1	B	40	GLU
1	B	364	LEU
1	B	395	ARG
1	B	580	VAL
1	B	598	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	71	ASN
1	A	216	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	266	ASN
1	A	591	HIS
1	B	13	HIS
1	B	71	ASN
1	B	169	ASN
1	B	234	ASN
1	B	293	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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 (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, 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	581/607 (95%)	0.50	32 (5%)	30	36	18, 32, 59, 109	0
1	B	581/607 (95%)	0.61	45 (7%)	19	23	20, 34, 65, 101	1 (0%)
All	All	1162/1214 (95%)	0.55	77 (6%)	24	29	18, 33, 64, 109	1 (0%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	54	ILE	6.0
1	A	56	ILE	5.8
1	B	34	ALA	5.4
1	B	38	THR	5.3
1	B	54	ILE	5.1
1	B	549	SER	4.8
1	A	549	SER	4.7
1	A	36	ALA	4.7
1	B	56	ILE	4.6
1	A	55	THR	4.5
1	B	478	GLY	4.5
1	A	2	ILE	4.3
1	A	551	THR	4.1
1	A	600	ALA	4.1
1	A	38	THR	4.1
1	B	36	ALA	4.0
1	A	550	GLY	4.0
1	B	2	ILE	4.0
1	B	392	ILE	3.9
1	B	41	ARG	3.8
1	B	152	ASP	3.7
1	B	550	GLY	3.6
1	A	552	ASP	3.6
1	A	34	ALA	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	390	ARG	3.6
1	B	551	THR	3.6
1	B	55	THR	3.3
1	A	392	ILE	3.3
1	B	39	GLN	3.3
1	A	41	ARG	3.2
1	A	39	GLN	3.2
1	B	388	ILE	3.1
1	A	37	GLU	3.1
1	B	340	VAL	3.0
1	B	343	VAL	3.0
1	A	35	ARG	3.0
1	A	541	LYS	3.0
1	B	477	PRO	2.9
1	B	552	ASP	2.8
1	B	364	LEU	2.8
1	B	600	ALA	2.8
1	B	33	ASP	2.8
1	A	152	ASP	2.7
1	B	540	GLY	2.7
1	B	353	ALA	2.6
1	B	35	ARG	2.6
1	A	393	ASP	2.6
1	B	390	ARG	2.5
1	B	285	SER	2.5
1	B	350	THR	2.5
1	B	601	ASN	2.5
1	B	393	ASP	2.4
1	A	554	ALA	2.4
1	B	351	GLU	2.4
1	A	40	GLU	2.3
1	B	394	GLY	2.3
1	A	343	VAL	2.3
1	B	302	VAL	2.2
1	A	131	ASP	2.2
1	B	480	VAL	2.2
1	A	595	ASN	2.2
1	A	479	GLU	2.2
1	A	601	ASN	2.1
1	A	540	GLY	2.1
1	B	167	ALA	2.1
1	B	389	PHE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	79	ALA	2.1
1	B	530	SER	2.1
1	B	331	ILE	2.1
1	B	391	GLU	2.1
1	A	598	ARG	2.1
1	B	599	ARG	2.1
1	B	245	LYS	2.0
1	A	246	THR	2.0
1	A	553	GLU	2.0
1	B	541	LYS	2.0
1	B	598	ARG	2.0

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 oligosaccharides in this entry.

6.4 Ligands (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(Å^2)	Q<0.9
2	NA	B	701	1/1	0.70	0.23	28,28,28,28	0
2	NA	A	701	1/1	0.84	0.11	31,31,31,31	0
2	NA	B	702	1/1	0.86	0.10	36,36,36,36	0
2	NA	A	702	1/1	0.93	0.07	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.