



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 04:21 AM GMT

PDB ID : 1XA7
Title : Crystal structure of the benzylpenicillin-acylatedBlaR1 sensor domain from Staphylococcus aureus
Authors : Wilke, M.S.; Hills, T.L.; Zhang, H.Z.; Chambers, H.F.; Strynadka, N.C.
Deposited on : 2004-08-25
Resolution : 2.40 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

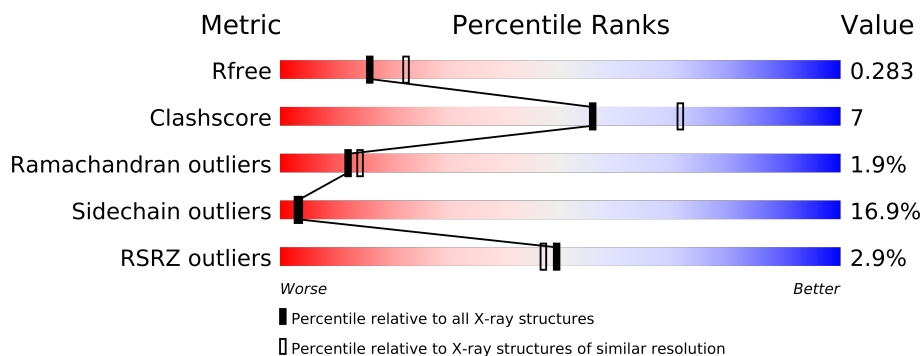
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	255	
1	B	255	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4106 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Regulatory protein blaR1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	Se	0	0	0
			2036	1304	341	381	1	9			
1	B	240	Total	C	N	O	S	Se	0	0	0
			2029	1301	341	377	1	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	38	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	59	PG1	SER	MODIFIED RESIDUE	UNP P18357
A	67	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	82	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	104	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	146	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	164	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	165	MSE	MET	MODIFIED RESIDUE	UNP P18357
A	249	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	35	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	38	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	59	PG1	SER	MODIFIED RESIDUE	UNP P18357
B	67	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	82	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	104	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	146	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	164	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	165	MSE	MET	MODIFIED RESIDUE	UNP P18357
B	249	MSE	MET	MODIFIED RESIDUE	UNP P18357

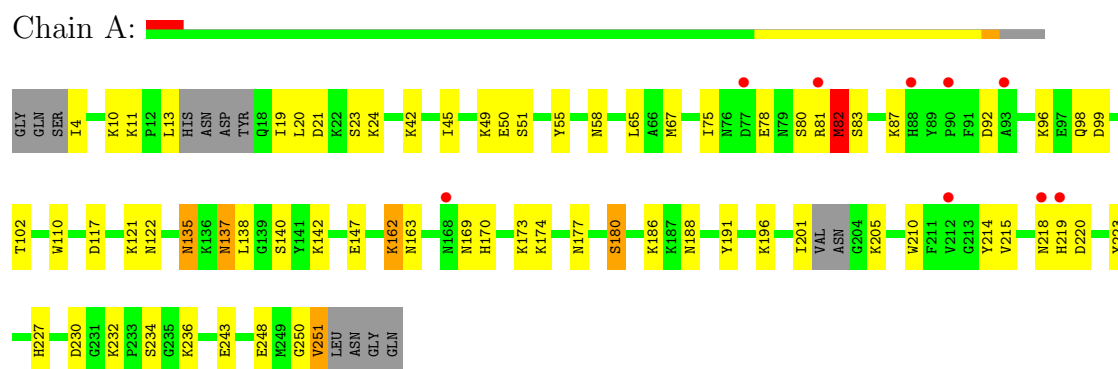
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	21	Total 21	O 21	0	0
2	B	20	Total 20	O 20	0	0

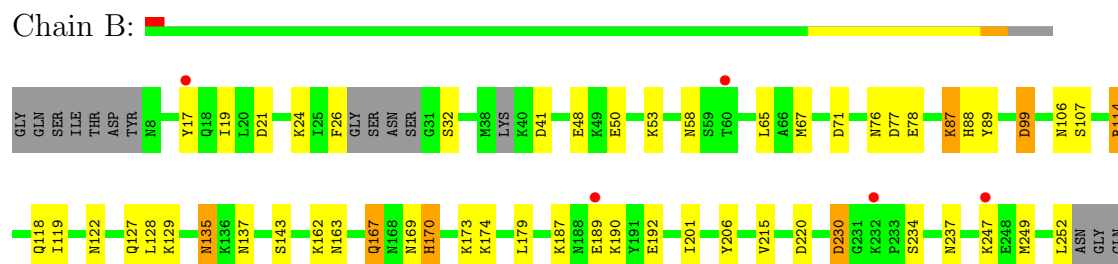
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Regulatory protein blaR1



- Molecule 1: Regulatory protein blaR1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	88.39Å 88.39Å 125.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 30.32 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.00-2.40) 99.1 (30.32-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.220 , 0.275 0.225 , 0.283	Depositor DCC
R_{free} test set	973 reflections (5.15%)	DCC
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 33840 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4106	wwPDB-VP
Average B, all atoms (Å ²)	46.0	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.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PG1

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	0.92	3/2045 (0.1%)	0.96	6/2727 (0.2%)
1	B	0.87	1/2039 (0.0%)	0.92	8/2721 (0.3%)
All	All	0.89	4/4084 (0.1%)	0.94	14/5448 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	249	MSE	CG-SE	-5.85	1.75	1.95
1	A	223	TYR	CD2-CE2	-5.44	1.31	1.39
1	A	210	TRP	CB-CG	-5.37	1.40	1.50
1	A	67	MSE	SE-CE	-5.03	1.65	1.95

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	ASP	CB-CG-OD2	8.42	125.88	118.30
1	B	220	ASP	CB-CG-OD2	7.86	125.38	118.30
1	A	21	ASP	CB-CG-OD2	7.25	124.83	118.30
1	A	230	ASP	CB-CG-OD2	7.19	124.77	118.30
1	A	220	ASP	CB-CG-OD2	6.56	124.20	118.30
1	B	71	ASP	CB-CG-OD2	6.53	124.18	118.30
1	B	21	ASP	CB-CG-OD2	5.93	123.64	118.30
1	B	230	ASP	CB-CG-OD2	5.89	123.60	118.30
1	B	99	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	77	ASP	CB-CG-OD2	5.45	123.21	118.30
1	A	92	ASP	CB-CG-OD2	5.44	123.20	118.30
1	B	41	ASP	CB-CG-OD2	5.44	123.20	118.30
1	A	117	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	114	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2036	0	0	16	0
1	B	2029	0	0	11	0
2	A	21	0	0	4	0
2	B	20	0	0	2	0
All	All	4106	0	0	27	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (27) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:82:MSE:SE	2:A:271:HOH:O	2.36	0.92
1:A:98:GLN:NE2	1:A:102:THR:CG2	2.41	0.84
1:B:190:LYS:NZ	1:B:252:LEU:O	2.15	0.78
1:B:187:LYS:NZ	1:B:192:GLU:OE2	2.25	0.69
1:B:106:ASN:ND2	2:B:263:HOH:O	2.25	0.69
1:A:55:TYR:CD2	1:A:227:HIS:CE1	2.82	0.68
1:A:180:SER:OG	1:A:214:TYR:OH	2.12	0.67
1:A:137:ASN:ND2	1:A:138:LEU:O	2.31	0.63
1:A:188:ASN:ND2	1:A:191:TYR:CE1	2.72	0.58
1:B:67:MSE:CE	1:B:179:LEU:CD2	2.83	0.56
1:A:55:TYR:CE2	1:A:227:HIS:CE1	2.94	0.55
1:A:173:LYS:O	1:A:177:ASN:ND2	2.41	0.54
1:B:163:ASN:OD1	1:B:167:GLN:OE1	2.25	0.54
1:B:118:GLN:CG	2:B:270:HOH:O	2.56	0.53
1:A:196:LYS:NZ	2:A:261:HOH:O	2.43	0.51
1:A:162:LYS:NZ	1:A:163:ASN:OD1	2.45	0.50
1:A:137:ASN:ND2	1:A:137:ASN:C	2.67	0.47
1:B:206:TYR:CD2	1:B:206:TYR:N	2.84	0.45
1:A:121:LYS:NZ	2:A:258:HOH:O	2.49	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:163:ASN:OD1	1:B:167:GLN:CD	2.56	0.44
1:A:250:GLY:O	1:A:251:VAL:O	2.35	0.44
1:A:186:LYS:NZ	1:A:243:GLU:OE2	2.51	0.43
1:B:114:ARG:O	1:B:118:GLN:NE2	2.52	0.43
1:A:82:MSE:CG	2:A:271:HOH:O	2.67	0.43
1:B:87:LYS:O	1:B:89:TYR:N	2.52	0.42
1:A:98:GLN:CG	1:A:110:TRP:CZ2	3.02	0.41
1:B:127:GLN:OE1	1:B:170:HIS:NE2	2.54	0.40

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	235/255 (92%)	210 (89%)	19 (8%)	6 (3%)	8	8
1	B	233/255 (91%)	213 (91%)	17 (7%)	3 (1%)	18	24
All	All	468/510 (92%)	423 (90%)	36 (8%)	9 (2%)	12	14

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	ASN
1	A	23	SER
1	B	58	ASN
1	A	51	SER
1	A	58	ASN
1	A	82	MSE
1	B	88	HIS
1	A	147	GLU
1	B	135	ASN

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	220/222 (99%)	180 (82%)	40 (18%)	2	3
1	B	219/222 (99%)	185 (84%)	34 (16%)	4	4
All	All	439/444 (99%)	365 (83%)	74 (17%)	3	3

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	10	LYS
1	A	11	LYS
1	A	13	LEU
1	A	19	ILE
1	A	20	LEU
1	A	24	LYS
1	A	42	LYS
1	A	45	ILE
1	A	49	LYS
1	A	50	GLU
1	A	65	LEU
1	A	75	ILE
1	A	78	GLU
1	A	80	SER
1	A	81	ARG
1	A	82	MSE
1	A	83	SER
1	A	87	LYS
1	A	96	LYS
1	A	122	ASN
1	A	135	ASN
1	A	137	ASN
1	A	140	SER
1	A	142	LYS
1	A	162	LYS
1	A	169	ASN
1	A	170	HIS
1	A	174	LYS

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Mol	Chain	Res	Type
1	A	180	SER
1	A	201	ILE
1	A	205	LYS
1	A	215	VAL
1	A	218	ASN
1	A	219	HIS
1	A	232	LYS
1	A	234	SER
1	A	236	LYS
1	A	248	GLU
1	A	251	VAL
1	B	17	TYR
1	B	19	ILE
1	B	24	LYS
1	B	26	PHE
1	B	32	SER
1	B	48	GLU
1	B	50	GLU
1	B	53	LYS
1	B	65	LEU
1	B	76	ASN
1	B	78	GLU
1	B	87	LYS
1	B	99	ASP
1	B	107	SER
1	B	119	ILE
1	B	122	ASN
1	B	128	LEU
1	B	129	LYS
1	B	135	ASN
1	B	137	ASN
1	B	143	SER
1	B	162	LYS
1	B	167	GLN
1	B	169	ASN
1	B	170	HIS
1	B	173	LYS
1	B	174	LYS
1	B	189	GLU
1	B	201	ILE
1	B	215	VAL
1	B	230	ASP

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Mol	Chain	Res	Type
1	B	234	SER
1	B	237	ASN
1	B	247	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	PG1	A	59	1	27,30,31	7.57	4 (14%)	36,42,44	2.29	11 (30%)
1	PG1	B	59	1	27,30,31	9.08	6 (22%)	36,42,44	1.92	13 (36%)

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
1	PG1	A	59	1	-	0/18/42/44	0/2/2/2
1	PG1	B	59	1	-	0/18/42/44	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	59	PG1	O-C	46.40	1.43	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	59	PG1	O-C	38.47	1.38	1.11
1	B	59	PG1	OG-C7	5.62	1.45	1.33
1	A	59	PG1	OG-C7	4.76	1.43	1.33
1	A	59	PG1	C2-S1	-3.74	1.77	1.85
1	A	59	PG1	C3-N4	-3.63	1.42	1.46
1	B	59	PG1	C2-S1	-3.60	1.78	1.85
1	B	59	PG1	C5-S1	-2.83	1.76	1.85
1	B	59	PG1	CA-C	2.26	1.52	1.48
1	B	59	PG1	C3-N4	-2.01	1.44	1.46

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59	PG1	C11-C3-N4	-6.37	109.44	111.82
1	A	59	PG1	C6-C5-N4	-5.72	101.08	112.79
1	A	59	PG1	OG-C7-C6	5.18	119.29	111.27
1	B	59	PG1	OG-C7-C6	4.88	118.83	111.27
1	A	59	PG1	C5-N4-C3	4.25	119.76	109.62
1	B	59	PG1	C5-N4-C3	4.13	119.47	109.62
1	B	59	PG1	C6-C5-N4	-3.71	105.20	112.79
1	B	59	PG1	C11-C3-N4	-3.54	110.50	111.82
1	A	59	PG1	C6-C5-S1	3.20	118.51	110.22
1	A	59	PG1	OG-C7-O8	-3.17	117.56	124.03
1	B	59	PG1	C2-S1-C5	2.85	100.15	94.01
1	A	59	PG1	C5-C6-N14	2.78	114.52	109.11
1	A	59	PG1	C17-C15-N14	2.39	119.47	115.56
1	B	59	PG1	S1-C5-N4	-2.38	103.45	106.66
1	B	59	PG1	OG-C7-O8	-2.34	119.25	124.03
1	B	59	PG1	C5-C6-N14	2.29	113.57	109.11
1	B	59	PG1	C9-C2-C3	-2.28	106.81	112.05
1	A	59	PG1	C5-C6-C7	-2.24	106.75	110.80
1	B	59	PG1	C17-C15-N14	2.22	119.19	115.56
1	A	59	PG1	O16-C15-N14	-2.19	119.28	123.08
1	A	59	PG1	C2-S1-C5	2.18	98.71	94.01
1	B	59	PG1	C10-C2-S1	2.12	112.75	109.15
1	B	59	PG1	C5-C6-C7	-2.02	107.15	110.80
1	B	59	PG1	C18-C17-C15	-2.02	106.23	113.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	242/255 (94%)	0.07	9 (3%)	39 38	22, 44, 66, 85	0
1	B	240/255 (94%)	0.18	5 (2%)	60 58	24, 47, 71, 81	0
All	All	482/510 (94%)	0.13	14 (2%)	49 47	22, 46, 68, 85	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	77	ASP	4.6
1	B	232	LYS	3.1
1	A	218	ASN	3.1
1	A	219	HIS	3.0
1	B	17	TYR	2.9
1	B	247	LYS	2.9
1	A	88	HIS	2.9
1	A	90	PRO	2.9
1	A	81	ARG	2.8
1	B	60	THR	2.5
1	A	212	VAL	2.2
1	A	93	ALA	2.1
1	A	168	ASN	2.1
1	B	189	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	PG1	A	59	29/30	0.14	-0.42	23,34,46,48	0
1	PG1	B	59	29/30	0.14	-0.87	23,32,42,45	0

6.3 Carbohydrates

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.