



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 09:26 pm BST

PDB ID : 2ARZ
Title : Crystal Structure of Protein of Unknown Function from *Pseudomonas aeruginosa*
Authors : Nocek, B.; Xu, X.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2005-08-22
Resolution : 2.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
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

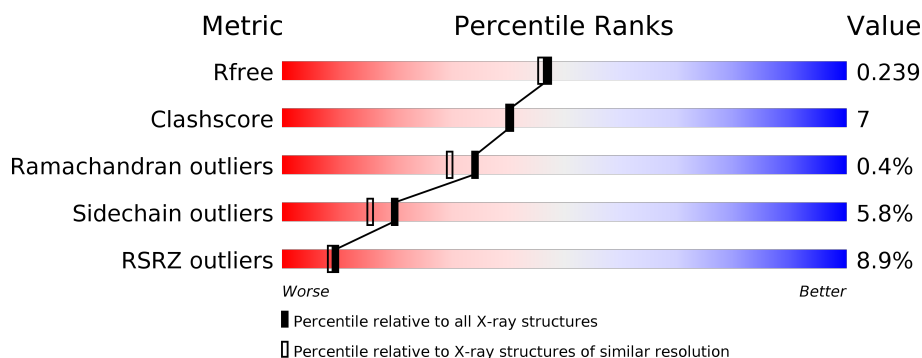
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	247	<div> <div>13%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• • •</div> </div> </div>
1	B	247	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>• 5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4042 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 hypothetical protein PA4388.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	238	Total	C	N	O	S	0	1	0
			1874	1195	345	328	6			
1	B	235	Total	C	N	O	S	0	0	0
			1836	1173	335	321	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	CLONING ARTIFACT	UNP Q9HW16
A	-1	ASN	-	CLONING ARTIFACT	UNP Q9HW16
A	0	SER	-	CLONING ARTIFACT	UNP Q9HW16
B	-2	ALA	-	CLONING ARTIFACT	UNP Q9HW16
B	-1	ASN	-	CLONING ARTIFACT	UNP Q9HW16
B	0	SER	-	CLONING ARTIFACT	UNP Q9HW16

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cl	0	0
			3	3		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

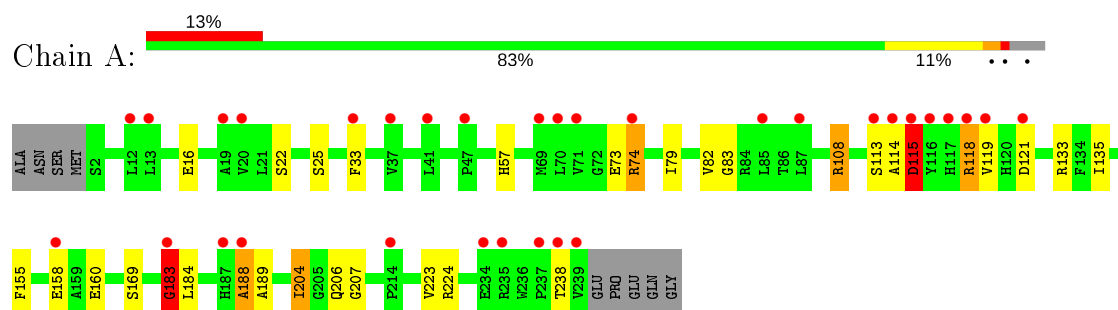
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	154	Total	O	0	0
			154	154		
4	B	163	Total	O	0	0
			163	163		

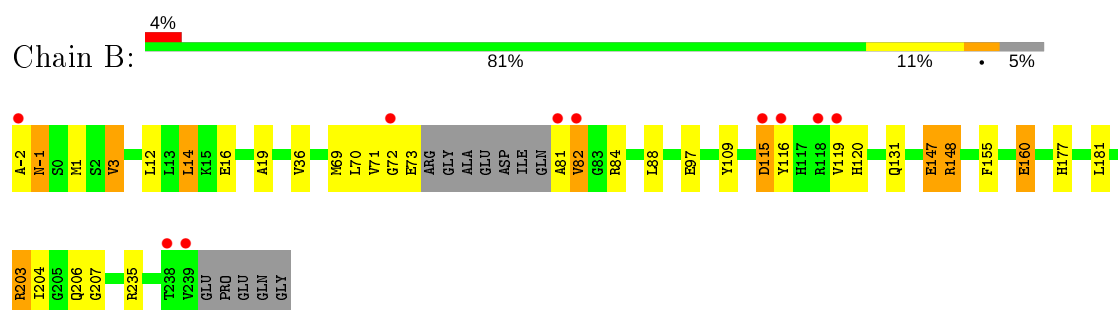
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: hypothetical protein PA4388



- Molecule 1: hypothetical protein PA4388



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.27Å 79.78Å 99.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.56 – 2.00 33.55 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.56-2.00) 99.8 (33.55-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.195 , 0.240 0.195 , 0.239	Depositor DCC
R_{free} test set	1946 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4042	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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

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

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	0.67	0/1928	0.79	2/2624 (0.1%)
1	B	0.77	1/1889 (0.1%)	0.79	6/2571 (0.2%)
All	All	0.72	1/3817 (0.0%)	0.79	8/5195 (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
1	A	0	4
1	B	1	0
All	All	1	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	160	GLU	CB-CG	-5.59	1.41	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	148	ARG	NE-CZ-NH2	-6.92	116.84	120.30
1	B	206	GLN	N-CA-C	6.22	127.81	111.00
1	A	206	GLN	N-CA-C	6.07	127.38	111.00
1	B	14	LEU	CB-CG-CD1	6.01	121.21	111.00
1	B	148	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	108	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	B	206	GLN	CA-C-N	5.73	127.66	116.20
1	B	203	ARG	NE-CZ-NH1	5.32	122.96	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	81	ALA	CA

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ARG	Peptide
1	A	183	GLY	Peptide
1	A	188	ALA	Peptide
1	A	204	ILE	Peptide

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	1874	0	1821	26	0
1	B	1836	0	1786	29	1
2	A	3	0	0	0	0
3	A	12	0	16	1	0
4	A	154	0	0	1	1
4	B	163	0	0	1	2
All	All	4042	0	3623	53	2

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 7.

All (53) 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:B:81:ALA:CB	1:B:82:VAL:HA	1.46	1.33
1:B:81:ALA:HB1	1:B:82:VAL:CA	1.60	1.30
1:A:79:ILE:HD12	1:B:36:VAL:HG12	1.29	1.11
1:B:16:GLU:HG2	4:B:378:HOH:O	1.53	1.09
1:A:115:ASP:O	1:A:119:VAL:HG12	1.56	1.04
1:A:74[A]:ARG:HG2	1:A:74[A]:ARG:HH21	1.34	0.90
1:A:79:ILE:HD12	1:B:36:VAL:CG1	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:VAL:HA	1:B:148:ARG:HH22	1.42	0.84
1:A:74[A]:ARG:HH21	1:A:74[A]:ARG:CG	1.95	0.79
1:A:73:GLU:HG3	1:A:82:VAL:HB	1.70	0.74
1:A:74[A]:ARG:HG2	1:A:74[A]:ARG:NH2	2.02	0.70
1:B:12:LEU:HD11	1:B:72:GLY:O	1.96	0.65
1:B:147:GLU:CD	1:B:147:GLU:H	2.00	0.65
1:A:204:ILE:O	1:A:207:GLY:HA3	1.97	0.64
1:B:-2:ALA:H2	1:B:-1:ASN:HA	1.63	0.64
1:B:81:ALA:CB	1:B:82:VAL:CA	2.34	0.60
1:A:108:ARG:HH22	1:A:160:GLU:CD	2.06	0.58
1:B:109:TYR:O	1:B:203:ARG:NH1	2.36	0.58
1:A:115:ASP:O	1:A:119:VAL:CG1	2.44	0.57
1:B:116:TYR:CD1	1:B:120:HIS:HD2	2.24	0.56
1:B:70:LEU:HD11	1:B:84:ARG:HG2	1.88	0.55
1:B:116:TYR:CD1	1:B:120:HIS:CD2	2.96	0.54
1:A:113:SER:O	1:A:114:ALA:C	2.46	0.53
1:B:81:ALA:HB1	1:B:82:VAL:HA	0.63	0.53
1:B:115:ASP:O	1:B:119:VAL:HG12	2.09	0.52
1:B:155:PHE:O	1:B:160:GLU:HB2	2.10	0.51
1:A:118:ARG:NE	1:A:118:ARG:HA	2.25	0.51
1:B:177:HIS:CD2	1:B:181:LEU:HD22	2.46	0.51
1:B:19:ALA:HB1	1:B:69:MET:HG2	1.93	0.50
1:B:12:LEU:HD11	1:B:72:GLY:C	2.32	0.50
1:A:73:GLU:CG	1:A:82:VAL:HB	2.41	0.49
1:A:155:PHE:O	1:A:160:GLU:HB2	2.13	0.48
1:A:108:ARG:NH2	1:A:160:GLU:CD	2.67	0.48
1:B:73:GLU:OE1	1:B:81:ALA:CB	2.62	0.47
1:B:12:LEU:HD11	1:B:73:GLU:HA	1.97	0.46
1:A:113:SER:O	1:A:114:ALA:O	2.34	0.45
1:B:12:LEU:CD1	1:B:73:GLU:HA	2.46	0.45
3:A:2647:GOL:C3	3:A:2648:GOL:H32	2.46	0.45
1:A:183:GLY:HA3	1:A:184:LEU:HG	1.98	0.45
1:B:204:ILE:O	1:B:207:GLY:HA3	2.15	0.45
1:A:33:PHE:CE1	1:B:88:LEU:HD21	2.51	0.45
1:A:16:GLU:OE1	1:A:74[A]:ARG:HD3	2.17	0.45
1:A:25:SER:HB2	1:A:33:PHE:CD1	2.51	0.45
1:B:-2:ALA:N	1:B:-1:ASN:HA	2.30	0.44
1:B:73:GLU:OE1	1:B:81:ALA:HB3	2.17	0.44
1:A:74[B]:ARG:HD3	4:A:2670:HOH:O	2.19	0.43
1:A:83:GLY:HA2	1:A:135:ILE:O	2.19	0.43
1:A:74[A]:ARG:NH2	1:A:74[A]:ARG:CG	2.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-2:ALA:N	1:B:-1:ASN:CA	2.82	0.42
1:B:116:TYR:HA	1:B:120:HIS:HD2	1.85	0.42
1:A:115:ASP:OD1	1:A:115:ASP:N	2.54	0.41
1:A:188:ALA:HB1	1:A:189:ALA:HB3	2.03	0.41
1:A:22:SER:HA	1:A:33:PHE:O	2.21	0.41

All (2) 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)
1:B:-1:ASN:ND2	4:B:325:HOH:O[4_556]	1.87	0.33
4:A:2790:HOH:O	4:B:402:HOH:O[2_564]	2.18	0.02

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	237/247 (96%)	228 (96%)	7 (3%)	2 (1%)	19	13
1	B	231/247 (94%)	227 (98%)	4 (2%)	0	100	100
All	All	468/494 (95%)	455 (97%)	11 (2%)	2 (0%)	34	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	183	GLY
1	A	115	ASP

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	182/188 (97%)	171 (94%)	11 (6%)	19	14
1	B	179/188 (95%)	168 (94%)	11 (6%)	18	14
All	All	361/376 (96%)	339 (94%)	22 (6%)	20	14

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	HIS
1	A	74[A]	ARG
1	A	74[B]	ARG
1	A	115	ASP
1	A	121	ASP
1	A	133	ARG
1	A	158	GLU
1	A	169	SER
1	A	223	VAL
1	A	224	ARG
1	A	238	THR
1	B	-1	ASN
1	B	1	MET
1	B	3	VAL
1	B	14	LEU
1	B	71	VAL
1	B	82	VAL
1	B	97	GLU
1	B	115	ASP
1	B	131	GLN
1	B	147	GLU
1	B	235	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	62	GLN
1	A	120	HIS
1	A	142	HIS

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Mol	Chain	Res	Type
1	A	171	HIS
1	B	8	ASN
1	B	24	HIS
1	B	120	HIS
1	B	225	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](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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	GOL	A	2647	-	5,5,5	0.31	0	5,5,5	0.68	0
3	GOL	A	2648	-	5,5,5	0.36	0	5,5,5	0.94	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	GOL	A	2647	-	-	4/4/4/4	-
3	GOL	A	2648	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2647	GOL	C1-C2-C3-O3
3	A	2648	GOL	O1-C1-C2-C3
3	A	2648	GOL	C1-C2-C3-O3
3	A	2648	GOL	O2-C2-C3-O3
3	A	2648	GOL	O1-C1-C2-O2
3	A	2647	GOL	O1-C1-C2-C3
3	A	2647	GOL	O2-C2-C3-O3
3	A	2647	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2647	GOL	1	0
3	A	2648	GOL	1	0

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, 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	238/247 (96%)	0.57	32 (13%) 3 2	24, 37, 60, 72	0
1	B	235/247 (95%)	0.04	10 (4%) 35 34	24, 31, 50, 62	0
All	All	473/494 (95%)	0.31	42 (8%) 9 8	24, 34, 56, 72	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	ALA	9.2
1	A	119	VAL	6.6
1	B	82	VAL	5.4
1	A	238	THR	4.9
1	B	118	ARG	4.5
1	A	187	HIS	4.5
1	A	114	ALA	4.2
1	A	118	ARG	4.0
1	A	116	TYR	3.9
1	A	74[A]	ARG	3.9
1	A	121	ASP	3.6
1	B	119	VAL	3.4
1	A	235	ARG	3.1
1	A	239	VAL	3.1
1	A	183	GLY	3.0
1	A	13	LEU	2.9
1	A	71	VAL	2.9
1	A	70	LEU	2.9
1	B	116	TYR	2.8
1	A	188	ALA	2.8
1	A	85	LEU	2.7
1	A	158	GLU	2.7
1	A	115	ASP	2.6
1	B	72	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	87	LEU	2.5
1	A	20	VAL	2.5
1	B	238	THR	2.4
1	A	41	LEU	2.4
1	B	239	VAL	2.4
1	A	234	GLU	2.4
1	A	69	MET	2.4
1	A	237	PRO	2.3
1	A	12	LEU	2.3
1	A	19	ALA	2.2
1	A	33	PHE	2.2
1	A	37	VAL	2.1
1	A	47	PRO	2.1
1	A	113	SER	2.0
1	A	214	PRO	2.0
1	A	117	HIS	2.0
1	B	115	ASP	2.0
1	B	-2	ALA	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 carbohydrates 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(\AA^2)	Q<0.9
3	GOL	A	2648	6/6	0.76	0.23	43,52,53,54	0
3	GOL	A	2647	6/6	0.85	0.20	48,51,51,52	0
2	CL	A	501	1/1	0.98	0.05	34,34,34,34	0
2	CL	A	401	1/1	0.99	0.05	25,25,25,25	0
2	CL	A	601	1/1	0.99	0.04	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.