



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:35 PM GMT

PDB ID : 3BCG
Title : Conformational changes of the AcrR regulator reveal a mechanism of induction
Authors : Gu, R.; Li, M.; Su, C.C.; Long, F.; Yang, F.; McDermott, G.; Yu, E.Y.
Deposited on : 2007-11-12
Resolution : 2.48 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>

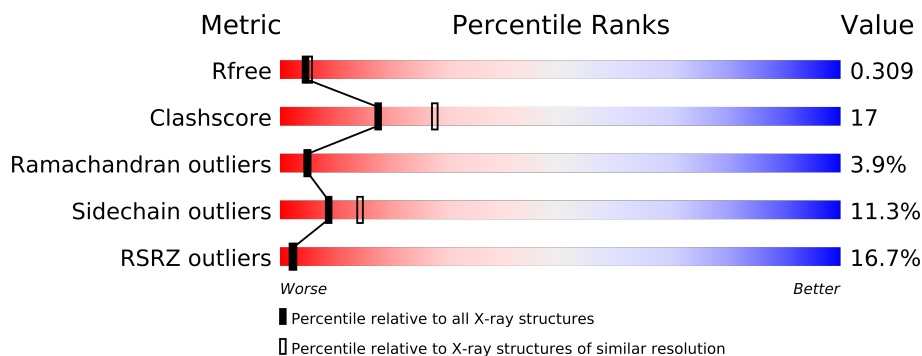
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.48 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	3277 (2.50-2.46)
Clashscore	79885	4136 (2.50-2.46)
Ramachandran outliers	78287	4052 (2.50-2.46)
Sidechain outliers	78261	4054 (2.50-2.46)
RSRZ outliers	66119	3279 (2.50-2.46)

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	215	
1	B	215	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3428 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 HTH-type transcriptional regulator acrR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1672	1065	287	309	11			
1	B	207	Total	C	N	O	S	0	0	0
			1672	1065	287	309	11			

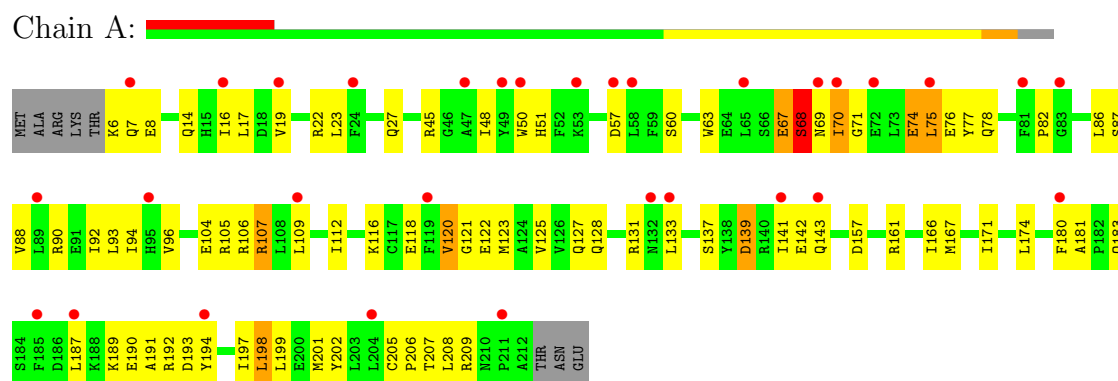
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	42	Total	O	0	0
			42	42		
2	B	42	Total	O	0	0
			42	42		

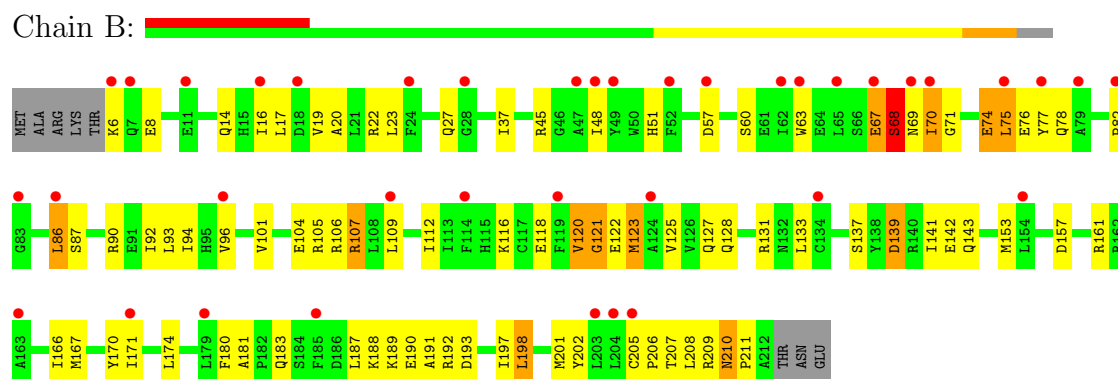
3 Residue-property plots

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: HTH-type transcriptional regulator acrR



- Molecule 1: HTH-type transcriptional regulator acrR



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	46.66Å 46.66Å 166.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.48 40.41 – 2.69	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.48) 97.7 (40.41-2.69)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	12.14 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.214 , 0.268 0.304 , 0.309	Depositor DCC
R_{free} test set	521 reflections (4.77%)	DCC
Wilson B-factor (Å ²)	64.6	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.9	EDS
Estimated twinning fraction	0.479 for -h,-k,l 0.088 for h,-h-k,-l 0.086 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 10952 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3428	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.35	0/1702	0.56	0/2295
1	B	0.35	0/1702	0.56	0/2295
All	All	0.35	0/3404	0.56	0/4590

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	68	SER	Peptide
1	B	68	SER	Peptide

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	1672	0	1688	72	0
1	B	1672	0	1688	66	0
2	A	42	0	0	0	0
2	B	42	0	0	0	0
All	All	3428	0	3376	117	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 17.

All (117) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:201:MET:CE	1:B:201:MET:CE	1.97	1.40
1:A:201:MET:CE	1:B:201:MET:HE2	1.52	1.32
1:A:201:MET:HE2	1:B:201:MET:CE	1.53	1.27
1:A:201:MET:HE1	1:B:201:MET:CE	1.88	1.02
1:A:201:MET:CE	1:B:201:MET:HE1	1.91	0.96
1:B:107:ARG:HB3	1:B:107:ARG:HH11	1.35	0.90
1:A:87:SER:HB2	1:A:90:ARG:HH21	1.52	0.74
1:A:208:LEU:HG	1:B:197:ILE:HD12	1.69	0.73
1:A:197:ILE:HD12	1:B:208:LEU:HG	1.74	0.70
1:A:118:GLU:HG3	1:B:118:GLU:HG3	1.73	0.69
1:A:201:MET:HE2	1:B:201:MET:HE2	0.73	0.68
1:A:107:ARG:HH11	1:A:107:ARG:CG	2.06	0.68
1:B:67:GLU:O	1:B:69:ASN:N	2.26	0.67
1:A:94:ILE:HD12	1:A:192:ARG:HA	1.75	0.67
1:B:193:ASP:O	1:B:197:ILE:HG12	1.96	0.66
1:B:94:ILE:HD12	1:B:192:ARG:HA	1.78	0.64
1:B:87:SER:HB2	1:B:90:ARG:HH21	1.60	0.63
1:A:67:GLU:O	1:A:69:ASN:N	2.27	0.62
1:A:193:ASP:O	1:A:197:ILE:HG12	1.98	0.62
1:A:201:MET:CE	1:B:201:MET:HE3	2.24	0.62
1:A:107:ARG:HH11	1:A:107:ARG:CB	2.13	0.61
1:A:107:ARG:HH11	1:A:107:ARG:HG2	1.64	0.61
1:B:167:MET:HB2	1:B:202:TYR:HH	1.67	0.60
1:A:201:MET:HE1	1:B:201:MET:HE3	1.81	0.59
1:A:75:LEU:HD13	1:A:76:GLU:HG2	1.84	0.59
1:A:93:LEU:HD22	1:A:171:ILE:HG13	1.84	0.59
1:B:107:ARG:CB	1:B:107:ARG:HH11	2.12	0.58
1:A:14:GLN:HA	1:A:17:LEU:HD12	1.86	0.56
1:B:167:MET:HB2	1:B:202:TYR:OH	2.06	0.56
1:A:78:GLN:HG2	1:A:88:VAL:HG21	1.89	0.55
1:A:107:ARG:HB3	1:A:107:ARG:HH11	1.72	0.55
1:A:187:LEU:O	1:A:191:ALA:HB2	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:14:GLN:HA	1:B:17:LEU:HD12	1.90	0.53
1:A:70:ILE:HG22	1:A:96:VAL:HG12	1.89	0.53
1:A:181:ALA:HB2	1:B:131:ARG:HG2	1.91	0.53
1:A:69:ASN:HA	1:A:70:ILE:C	2.28	0.53
1:B:69:ASN:HA	1:B:70:ILE:C	2.29	0.53
1:B:93:LEU:HD22	1:B:171:ILE:HG13	1.90	0.53
1:A:57:ASP:HA	1:A:60:SER:HB2	1.89	0.53
1:A:201:MET:HE3	1:B:201:MET:HE1	1.87	0.52
1:A:122:GLU:O	1:A:125:VAL:HG22	2.09	0.52
1:B:187:LEU:O	1:B:191:ALA:HB2	2.08	0.52
1:A:139:ASP:HA	1:A:142:GLU:HB2	1.90	0.52
1:B:139:ASP:HA	1:B:142:GLU:HB2	1.91	0.52
1:A:107:ARG:NH1	1:A:107:ARG:HG2	2.25	0.52
1:B:122:GLU:O	1:B:125:VAL:HG22	2.10	0.52
1:B:57:ASP:HA	1:B:60:SER:HB2	1.92	0.52
1:A:104:GLU:HA	1:A:107:ARG:HB2	1.92	0.52
1:A:131:ARG:HG2	1:B:181:ALA:HB2	1.91	0.51
1:A:94:ILE:CD1	1:A:192:ARG:HA	2.39	0.51
1:B:121:GLY:C	1:B:123:MET:H	2.14	0.51
1:B:70:ILE:HG22	1:B:96:VAL:HG12	1.93	0.51
1:A:157:ASP:O	1:A:209:ARG:HA	2.11	0.50
1:B:75:LEU:HD13	1:B:76:GLU:HG2	1.95	0.49
1:A:206:PRO:C	1:A:208:LEU:H	2.16	0.49
1:B:70:ILE:HG13	1:B:71:GLY:H	1.78	0.49
1:A:201:MET:O	1:A:205:CYS:HB2	2.12	0.49
1:B:139:ASP:O	1:B:143:GLN:HG2	2.13	0.48
1:A:139:ASP:O	1:A:143:GLN:HG2	2.13	0.48
1:B:206:PRO:C	1:B:208:LEU:H	2.16	0.48
1:A:23:LEU:O	1:A:27:GLN:HG2	2.13	0.47
1:B:112:ILE:HA	1:B:116:LYS:HB2	1.96	0.47
1:A:93:LEU:HA	1:A:96:VAL:HG22	1.95	0.47
1:A:112:ILE:HA	1:A:116:LYS:HB2	1.97	0.47
1:A:167:MET:HB2	1:A:202:TYR:OH	2.13	0.47
1:A:167:MET:HA	1:A:198:LEU:HD11	1.97	0.47
1:B:86:LEU:HD12	1:B:153:MET:HB3	1.97	0.47
1:A:16:ILE:HD12	1:A:51:HIS:CD2	2.49	0.47
1:B:23:LEU:O	1:B:27:GLN:HG2	2.15	0.47
1:A:201:MET:HE1	1:B:201:MET:HE1	1.71	0.46
1:A:92:ILE:O	1:A:96:VAL:HG13	2.14	0.46
1:B:74:GLU:O	1:B:78:GLN:N	2.36	0.46
1:A:137:SER:O	1:A:141:ILE:HG12	2.15	0.46
1:B:104:GLU:HA	1:B:107:ARG:HB2	1.97	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:201:MET:HE3	1:B:201:MET:CE	2.27	0.45
1:B:104:GLU:C	1:B:106:ARG:H	2.20	0.45
1:B:137:SER:O	1:B:141:ILE:HG12	2.16	0.45
1:A:121:GLY:C	1:A:123:MET:H	2.18	0.45
1:B:157:ASP:O	1:B:209:ARG:HA	2.17	0.45
1:B:93:LEU:HA	1:B:96:VAL:HG22	1.98	0.45
1:A:93:LEU:HD21	1:A:167:MET:HE2	1.99	0.45
1:B:69:ASN:HA	1:B:70:ILE:O	2.18	0.44
1:A:104:GLU:C	1:A:106:ARG:H	2.21	0.44
1:A:141:ILE:HD12	1:A:167:MET:HE1	1.99	0.44
1:B:93:LEU:HD21	1:B:167:MET:CE	2.48	0.44
1:A:69:ASN:HA	1:A:70:ILE:O	2.16	0.44
1:B:167:MET:HA	1:B:198:LEU:HD11	1.99	0.44
1:A:74:GLU:O	1:A:78:GLN:N	2.39	0.44
1:A:166:ILE:HD13	1:B:174:LEU:HD21	1.99	0.44
1:B:94:ILE:CD1	1:B:192:ARG:HA	2.46	0.44
1:A:90:ARG:HA	1:A:199:LEU:HD11	2.00	0.43
1:B:205:CYS:HA	1:B:206:PRO:HD2	1.90	0.43
1:A:7:GLN:HG3	1:A:7:GLN:O	2.18	0.43
1:A:127:GLN:HG3	1:B:180:PHE:CZ	2.53	0.43
1:A:68:SER:O	1:A:71:GLY:N	2.52	0.43
1:A:107:ARG:NH1	1:A:107:ARG:CG	2.73	0.43
1:B:92:ILE:O	1:B:96:VAL:HG13	2.19	0.43
1:B:93:LEU:HD21	1:B:167:MET:HE2	2.01	0.42
1:A:194:TYR:CD1	1:B:166:ILE:HD11	2.55	0.42
1:A:93:LEU:HD21	1:A:167:MET:CE	2.49	0.42
1:B:68:SER:O	1:B:71:GLY:N	2.53	0.42
1:A:70:ILE:HG13	1:A:71:GLY:H	1.84	0.41
1:B:20:ALA:HA	1:B:37:ILE:HD12	2.01	0.41
1:A:180:PHE:CZ	1:B:127:GLN:HG3	2.56	0.41
1:B:166:ILE:O	1:B:170:TYR:N	2.52	0.41
1:A:87:SER:HA	1:A:90:ARG:HE	1.84	0.41
1:A:48:ILE:C	1:A:50:TRP:H	2.24	0.41
1:B:16:ILE:HD12	1:B:51:HIS:CD2	2.55	0.41
1:B:210:ASN:HA	1:B:211:PRO:HD3	1.85	0.41
1:A:107:ARG:HB3	1:A:107:ARG:NH1	2.36	0.41
1:B:16:ILE:HD13	1:B:48:ILE:HG13	2.02	0.41
1:A:174:LEU:HD21	1:B:166:ILE:HD13	2.02	0.41
1:A:205:CYS:HA	1:A:206:PRO:HD2	1.87	0.40
1:B:128:GLN:HA	1:B:131:ARG:HB2	2.04	0.40
1:A:128:GLN:HA	1:A:131:ARG:HB2	2.02	0.40
1:B:101:VAL:HG11	1:B:188:LYS:HB2	2.02	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:50:TRP:HE3	1:A:51:HIS:CE1	2.38	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	205/215 (95%)	182 (89%)	16 (8%)	7 (3%)	6	6
1	B	205/215 (95%)	180 (88%)	16 (8%)	9 (4%)	4	4
All	All	410/430 (95%)	362 (88%)	32 (8%)	16 (4%)	5	5

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	SER
1	A	70	ILE
1	A	74	GLU
1	B	68	SER
1	B	70	ILE
1	B	74	GLU
1	B	121	GLY
1	B	207	THR
1	A	207	THR
1	A	105	ARG
1	B	105	ARG
1	B	82	PRO
1	A	120	VAL
1	A	82	PRO
1	B	120	VAL
1	B	210	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	181/188 (96%)	161 (89%)	20 (11%)	9	15
1	B	181/188 (96%)	160 (88%)	21 (12%)	8	13
All	All	362/376 (96%)	321 (89%)	41 (11%)	9	14

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	8	GLU
1	A	19	VAL
1	A	22	ARG
1	A	45	ARG
1	A	63	TRP
1	A	67	GLU
1	A	75	LEU
1	A	77	TYR
1	A	86	LEU
1	A	107	ARG
1	A	109	LEU
1	A	120	VAL
1	A	133	LEU
1	A	139	ASP
1	A	161	ARG
1	A	183	GLN
1	A	189	LYS
1	A	190	GLU
1	A	198	LEU
1	B	6	LYS
1	B	8	GLU
1	B	19	VAL
1	B	22	ARG
1	B	45	ARG
1	B	63	TRP
1	B	67	GLU
1	B	75	LEU
1	B	77	TYR

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Mol	Chain	Res	Type
1	B	86	LEU
1	B	107	ARG
1	B	109	LEU
1	B	120	VAL
1	B	123	MET
1	B	133	LEU
1	B	139	ASP
1	B	161	ARG
1	B	183	GLN
1	B	189	LYS
1	B	190	GLU
1	B	198	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	HIS
1	B	51	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 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	207/215 (96%)	1.15	31 (14%)	3 3	45, 69, 93, 99	0
1	B	207/215 (96%)	1.22	38 (18%)	2 2	45, 70, 96, 102	0
All	All	414/430 (96%)	1.18	69 (16%)	2 2	45, 70, 95, 102	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	LEU	4.6
1	A	70	ILE	4.5
1	B	70	ILE	4.5
1	B	65	LEU	4.0
1	B	16	ILE	4.0
1	B	119	PHE	3.9
1	A	185	PHE	3.6
1	B	203	LEU	3.6
1	B	6	LYS	3.5
1	B	75	LEU	3.4
1	A	119	PHE	3.3
1	B	96	VAL	3.3
1	A	187	LEU	3.2
1	A	83	GLY	3.1
1	A	16	ILE	3.1
1	B	7	GLN	3.0
1	A	57	ASP	2.9
1	A	75	LEU	2.8
1	A	58	LEU	2.8
1	B	204	LEU	2.8
1	A	19	VAL	2.8
1	B	83	GLY	2.8
1	B	11	GLU	2.7
1	A	194	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	69	ASN	2.7
1	B	47	ALA	2.7
1	A	7	GLN	2.6
1	A	132	ASN	2.6
1	A	50	TRP	2.6
1	B	57	ASP	2.6
1	A	72	GLU	2.5
1	B	114	PHE	2.5
1	A	49	TYR	2.5
1	B	79	ALA	2.5
1	A	141	ILE	2.5
1	B	185	PHE	2.5
1	B	109	LEU	2.4
1	B	154	LEU	2.4
1	A	81	PHE	2.4
1	B	52	PHE	2.4
1	B	69	ASN	2.4
1	A	109	LEU	2.4
1	B	28	GLY	2.4
1	B	171	ILE	2.4
1	B	134	CYS	2.3
1	B	86	LEU	2.3
1	A	95	HIS	2.3
1	B	124	ALA	2.3
1	B	82	PRO	2.3
1	B	163	ALA	2.3
1	B	67	GLU	2.3
1	A	204	LEU	2.3
1	B	179	LEU	2.2
1	A	89	LEU	2.2
1	A	53	LYS	2.2
1	B	205	CYS	2.2
1	A	24	PHE	2.2
1	B	48	ILE	2.2
1	B	24	PHE	2.1
1	B	49	TYR	2.1
1	B	18	ASP	2.1
1	A	143	GLN	2.1
1	A	133	LEU	2.1
1	A	180	PHE	2.1
1	A	211	PRO	2.0
1	B	77	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	63	TRP	2.0
1	A	47	ALA	2.0
1	B	62	ILE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

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.