Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:57 PM GMT

PDB ID	:	5BQT
Title	:	Structure of TrmBL2, an archaeal chromatin protein, shows a novel mode of DNA binding.
Authors	:	Ahmad, M.U.; Diederichs, K.; Welte, W.
Deposited on	:	2015-05-29
Resolution	:	3.00 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

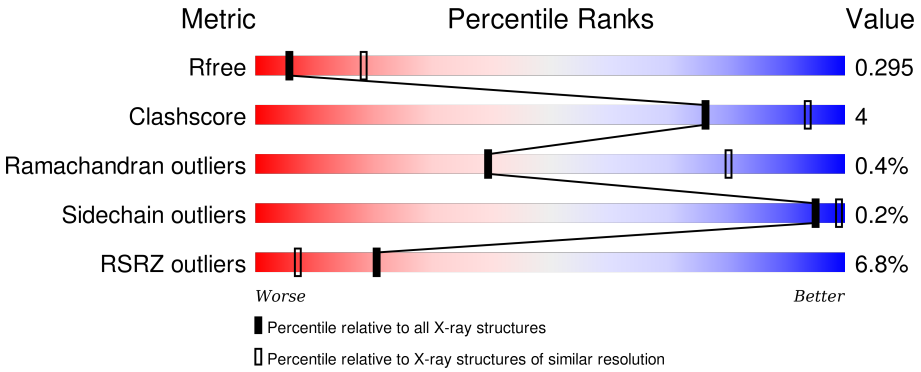
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	262	8% 89% 10%
1	B	262	5% 84% 12%
1	C	262	10% 89% 10%
1	D	262	5% 93% 6%

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
2	CA	B	301	-	-	-	X

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 17203 atoms, of which 8719 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 Putative HTH-type transcriptional regulator TrmBL2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	261	Total	C	H	N	O	S	0	0	0
			4320	1379	2187	353	395	6			
1	B	253	Total	C	H	N	O	S	0	0	0
			4197	1336	2132	342	381	6			
1	C	262	Total	C	H	N	O	S	0	0	0
			4342	1385	2200	355	396	6			
1	D	262	Total	C	H	N	O	S	0	0	0
			4342	1385	2200	355	396	6			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

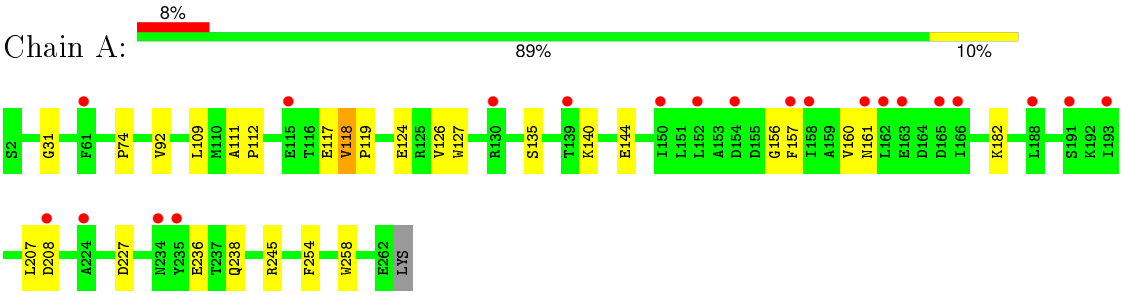
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

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 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.

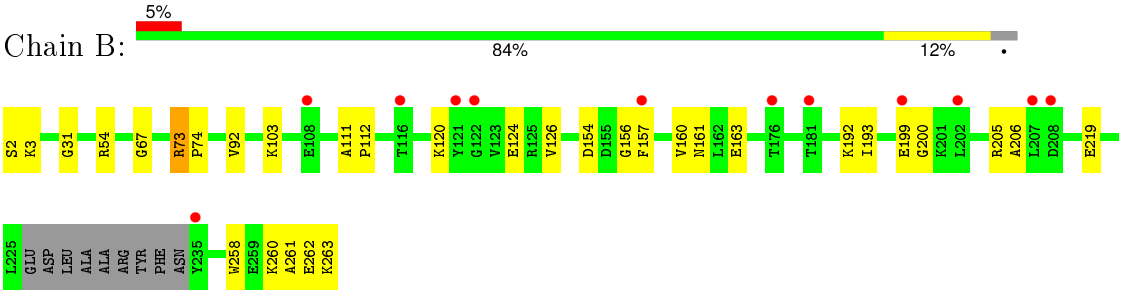
- Molecule 1: Putative HTH-type transcriptional regulator TrmBL2

Chain A:



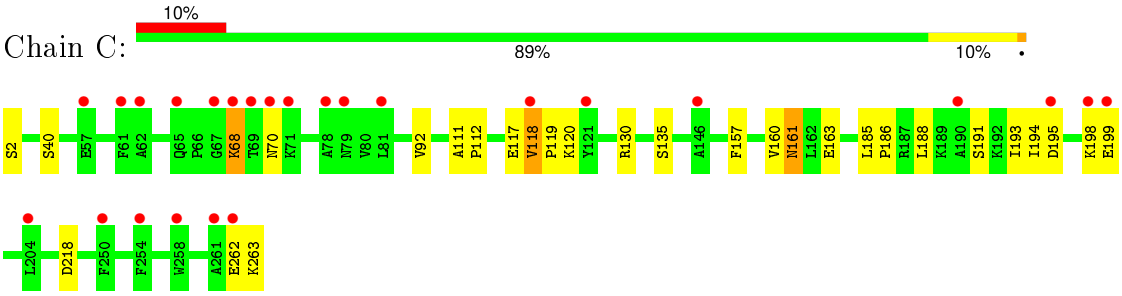
- Molecule 1: Putative HTH-type transcriptional regulator TrmBL2

Chain B:



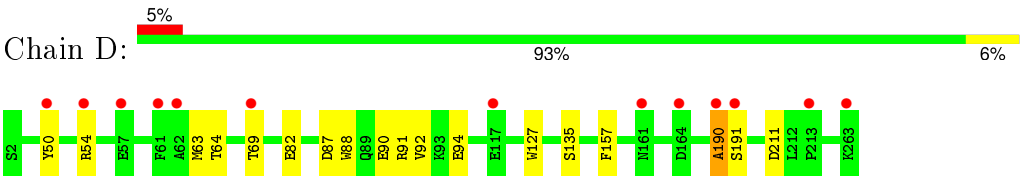
- Molecule 1: Putative HTH-type transcriptional regulator TrmBL2

Chain C:



- Molecule 1: Putative HTH-type transcriptional regulator TrmBL2

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	82.30Å 235.14Å 63.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.84 – 3.00 47.84 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.84-3.00) 99.5 (47.84-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 3.01Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.233 , 0.289 0.236 , 0.295	Depositor DCC
R_{free} test set	1246 reflections (4.91%)	DCC
Wilson B-factor (Å^2)	112.0	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 93.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	1 of 25410 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	17203	wwPDB-VP
Average B, all atoms (Å^2)	146.0	wwPDB-VP

Xtriage'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.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA

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	0.26	0/2173	0.47	0/2932
1	B	0.25	0/2102	0.47	0/2833
1	C	0.31	1/2182 (0.0%)	0.54	2/2943 (0.1%)
1	D	0.28	0/2182	0.51	0/2943
All	All	0.28	1/8639 (0.0%)	0.50	2/11651 (0.0%)

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	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	68	LYS	CG-CD	-5.47	1.33	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	68	LYS	CD-CE-NZ	-8.49	92.17	111.70
1	C	118	VAL	C-N-CD	-5.78	107.89	120.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	190	ALA	Peptide

5.2 Too-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 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	2133	2187	2186	20	0
1	B	2065	2132	2130	21	0
1	C	2142	2200	2199	19	11
1	D	2142	2200	2199	14	11
2	B	1	0	0	0	0
2	D	1	0	0	0	0
All	All	8484	8719	8714	66	11

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 (66) 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:C:68:LYS:HG2	1:C:68:LYS:O	1.97	0.65
1:B:54:ARG:NH1	1:C:40:SER:OG	2.31	0.63
1:A:157:PHE:CG	1:A:157:PHE:O	2.53	0.62
1:C:117:GLU:N	1:C:118:VAL:HA	2.15	0.61
1:D:135:SER:OG	1:D:157:PHE:O	2.18	0.61
1:C:135:SER:OG	1:C:157:PHE:O	2.15	0.60
1:D:190:ALA:HB3	1:D:191:SER:HA	1.87	0.56
1:A:135:SER:HB2	1:A:236:GLU:OE2	2.08	0.54
1:B:92:VAL:HG11	1:D:92:VAL:HG11	1.91	0.52
1:A:118:VAL:HB	1:A:119:PRO:HD3	1.92	0.51
1:A:124:GLU:OE2	1:A:126:VAL:O	2.29	0.51
1:D:50:TYR:CD2	1:D:50:TYR:C	2.85	0.50
1:B:154:ASP:OD1	1:B:156:GLY:N	2.38	0.50
1:A:92:VAL:HG11	1:C:92:VAL:HG11	1.94	0.49
1:C:119:PRO:O	1:C:120:LYS:HB2	2.12	0.49
1:B:103:LYS:NZ	1:D:82:GLU:OE1	2.46	0.49
1:B:199:GLU:N	1:B:200:GLY:HA2	2.28	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:VAL:O	1:C:161:ASN:HB2	2.14	0.48
1:C:185:LEU:HB2	1:C:186:PRO:HD3	1.96	0.48
1:A:140:LYS:O	1:A:144:GLU:HG3	2.15	0.47
1:C:160:VAL:O	1:C:161:ASN:CB	2.63	0.47
1:D:190:ALA:H	1:D:191:SER:HB3	1.80	0.47
1:A:182:LYS:HE3	1:A:207:LEU:HA	1.97	0.47
1:D:90:GLU:O	1:D:94:GLU:HG2	2.15	0.47
1:B:156:GLY:CA	1:B:157:PHE:HB2	2.46	0.46
1:A:254:PHE:O	1:A:258:TRP:N	2.45	0.46
1:A:111:ALA:HB3	1:A:112:PRO:HD3	1.99	0.45
1:C:68:LYS:O	1:C:68:LYS:CG	2.64	0.45
1:C:188:LEU:O	1:C:191:SER:HB3	2.17	0.45
1:D:64:THR:OG1	1:D:69:THR:HB	2.18	0.44
1:B:2:SER:OG	1:B:3:LYS:N	2.50	0.44
1:C:68:LYS:O	1:C:70:ASN:N	2.50	0.44
1:A:127:TRP:CE2	1:B:67:GLY:HA2	2.53	0.44
1:A:182:LYS:HD2	1:A:208:ASP:OD1	2.18	0.44
1:C:188:LEU:O	1:C:194:ILE:CD1	2.66	0.44
1:D:87:ASP:O	1:D:91:ARG:HG3	2.18	0.43
1:B:260:LYS:O	1:B:261:ALA:HB2	2.18	0.43
1:A:117:GLU:HG3	1:A:117:GLU:O	2.18	0.43
1:B:258:TRP:O	1:B:260:LYS:HA	2.17	0.43
1:B:205:ARG:HB3	1:B:261:ALA:HB3	2.00	0.43
1:C:163:GLU:HB2	1:C:193:ILE:HG13	2.00	0.43
1:B:31:GLY:O	1:B:74:PRO:HD3	2.17	0.43
1:C:111:ALA:N	1:C:112:PRO:HD2	2.34	0.43
1:B:163:GLU:OE2	1:B:192:LYS:N	2.51	0.43
1:B:111:ALA:HB3	1:B:112:PRO:HD3	2.01	0.43
1:A:245:ARG:HD2	1:D:211:ASP:O	2.18	0.43
1:B:206:ALA:H	1:B:261:ALA:HB3	1.83	0.42
1:A:31:GLY:O	1:A:74:PRO:HD3	2.19	0.42
1:D:190:ALA:HB3	1:D:191:SER:CA	2.50	0.42
1:A:236:GLU:OE2	1:A:238:GLN:CD	2.57	0.42
1:A:156:GLY:CA	1:A:157:PHE:HB3	2.50	0.42
1:B:163:GLU:HG3	1:B:193:ILE:HG13	2.02	0.41
1:B:124:GLU:HG3	1:B:126:VAL:H	1.85	0.41
1:D:63:MET:HG2	1:D:64:THR:O	2.19	0.41
1:C:188:LEU:O	1:C:194:ILE:HD12	2.21	0.41
1:A:236:GLU:OE2	1:A:238:GLN:NE2	2.53	0.41
1:D:88:TRP:HA	1:D:91:ARG:HD3	2.03	0.41
1:A:160:VAL:HA	1:A:161:ASN:HA	1.82	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:ARG:HB2	1:D:127:TRP:CH2	2.56	0.41
1:A:109:LEU:HD22	1:C:2:SER:OG	2.21	0.41
1:B:120:LYS:NZ	1:B:219:GLU:OE1	2.53	0.41
1:B:160:VAL:HA	1:B:161:ASN:HA	1.85	0.40
1:A:135:SER:CB	1:A:236:GLU:OE2	2.70	0.40
1:C:195:ASP:O	1:C:199:GLU:HG3	2.21	0.40
1:B:262:GLU:HB2	1:B:263:LYS:HB2	2.03	0.40
1:C:262:GLU:O	1:C:263:LYS:C	2.59	0.40

All (11) 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:C:199:GLU:HG3	1:D:50:TYR:HH[1_554]	0.87	0.73
1:C:198:LYS:HE3	1:D:54:ARG:HH21[1_554]	1.17	0.43
1:C:195:ASP:OD1	1:D:54:ARG:HH11[1_554]	1.25	0.35
1:C:199:GLU:HG2	1:D:50:TYR:HE1[1_554]	1.27	0.33
1:C:195:ASP:OD1	1:D:54:ARG:HH12[1_554]	1.31	0.29
1:C:199:GLU:OE2	1:D:50:TYR:CE1[1_554]	1.92	0.28
1:C:199:GLU:OE2	1:D:50:TYR:CZ[1_554]	1.94	0.26
1:C:199:GLU:CG	1:D:50:TYR:HH[1_554]	1.44	0.16
1:C:198:LYS:HE3	1:D:54:ARG:NH2[1_554]	1.47	0.13
1:C:199:GLU:HG3	1:D:50:TYR:OH[1_554]	1.54	0.06
1:C:199:GLU:CG	1:D:50:TYR:OH[1_554]	2.15	0.05

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	259/262 (99%)	241 (93%)	16 (6%)	2 (1%)	24 66
1	B	249/262 (95%)	238 (96%)	11 (4%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	260/262 (99%)	243 (94%)	15 (6%)	2 (1%)	24 66
1	D	260/262 (99%)	245 (94%)	15 (6%)	0	100 100
All	All	1028/1048 (98%)	967 (94%)	57 (6%)	4 (0%)	39 80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	ASP
1	A	118	VAL
1	C	161	ASN
1	C	218	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	229/230 (100%)	229 (100%)	0	100 100
1	B	223/230 (97%)	222 (100%)	1 (0%)	93 98
1	C	230/230 (100%)	229 (100%)	1 (0%)	93 98
1	D	230/230 (100%)	230 (100%)	0	100 100
All	All	912/920 (99%)	910 (100%)	2 (0%)	95 99

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	73	ARG
1	C	130	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	238	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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

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, 95^{th} 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	261/262 (99%)	0.56	21 (8%)	15	5	77, 128, 195, 281	0
1	B	253/262 (96%)	0.41	12 (4%)	35	14	73, 128, 194, 268	0
1	C	262/262 (100%)	0.61	25 (9%)	10	4	84, 130, 204, 278	0
1	D	262/262 (100%)	0.62	13 (4%)	32	13	78, 122, 207, 316	0
All	All	1038/1048 (99%)	0.55	71 (6%)	20	7	73, 127, 201, 316	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	235	TYR	9.6
1	A	157	PHE	8.5
1	C	118	VAL	5.6
1	A	162	LEU	5.3
1	A	234	ASN	4.6
1	C	261	ALA	4.6
1	A	165	ASP	4.6
1	C	79	ASN	4.3
1	B	208	ASP	4.1
1	B	157	PHE	4.1
1	D	117	GLU	4.1
1	C	62	ALA	4.0
1	C	198	LYS	3.9
1	C	67	GLY	3.8
1	C	61	PHE	3.8
1	A	193	ILE	3.7
1	A	163	GLU	3.7
1	D	161	ASN	3.7
1	B	116	THR	3.5
1	A	235	TYR	3.5
1	C	81	LEU	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	191	SER	3.3
1	A	161	ASN	3.2
1	C	146	ALA	3.2
1	B	121	TYR	3.2
1	C	190	ALA	3.1
1	C	254	PHE	3.1
1	D	61	PHE	3.1
1	A	154	ASP	3.1
1	B	199	GLU	3.0
1	C	262	GLU	3.0
1	D	164	ASP	3.0
1	C	195	ASP	2.9
1	C	78	ALA	2.9
1	C	199	GLU	2.8
1	D	263	LYS	2.8
1	A	158	ILE	2.7
1	C	69	THR	2.7
1	B	122	GLY	2.6
1	A	188	LEU	2.6
1	C	70	ASN	2.6
1	A	152	LEU	2.6
1	A	208	ASP	2.5
1	A	115	GLU	2.5
1	D	57	GLU	2.5
1	C	121	TYR	2.4
1	D	62	ALA	2.4
1	D	54	ARG	2.4
1	C	250	PHE	2.4
1	B	176	THR	2.4
1	D	50	TYR	2.4
1	C	71	LYS	2.4
1	D	69	THR	2.3
1	B	202	LEU	2.3
1	D	190	ALA	2.3
1	C	68	LYS	2.3
1	A	150	ILE	2.2
1	B	181	THR	2.2
1	A	130	ARG	2.2
1	C	204	LEU	2.2
1	D	191	SER	2.1
1	A	224	ALA	2.1
1	C	258	TRP	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	65	GLN	2.1
1	B	207	LEU	2.1
1	C	57	GLU	2.1
1	B	108	GLU	2.1
1	D	213	PRO	2.1
1	A	139	THR	2.0
1	A	61	PHE	2.0
1	A	166	ILE	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. 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, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
2	CA	B	301	1/1	-0.03	0.42	2.12	776,776,776,776	0
2	CA	D	301	1/1	0.23	1.20	-	214,214,214,214	0

6.5 Other polymers (i)

There are no such residues in this entry.