Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 02:36 pm BST

PDB ID	:	5OKJ
Title	:	Non-conservatively refined structure of Gan1D-WT, a putative 6-phospho-bet a-galactosidase from Geobacillus stearothermophilus, in the C2 spacegroup
Authors	:	Lansky, S.; Zehavi, A.; Shoham, Y.; Shoham, G.
Deposited on	:	2017-07-25
Resolution	:	1.76 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 ①) were used in the production of this report:

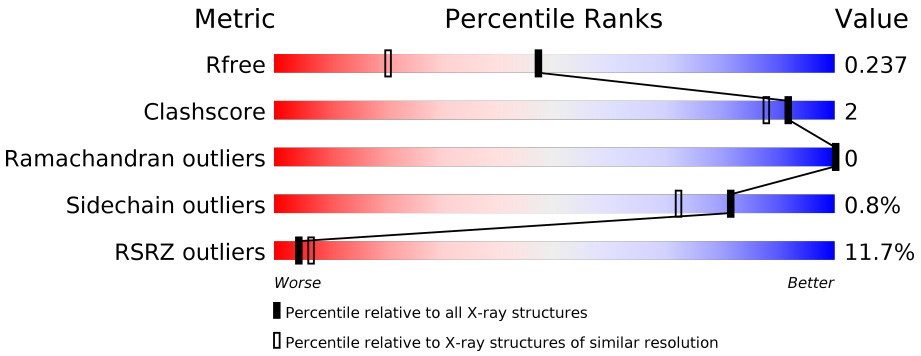
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 <=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	485	7% 94%
1	B	485	16% 92% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8349 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.

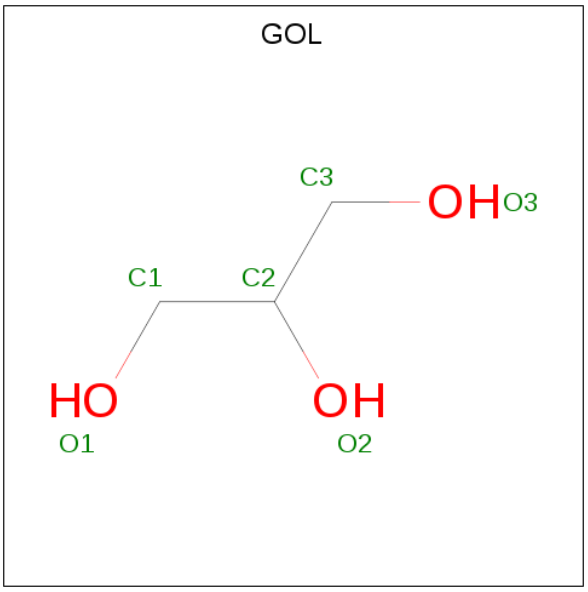
- Molecule 1 is a protein called Putative 6-phospho-beta-galactobiosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	9	0
			3921	2519	674	717	11			
1	B	474	Total	C	N	O	S	0	3	0
			3884	2494	664	715	11			

There are 16 discrepancies between the modelled and reference sequences:

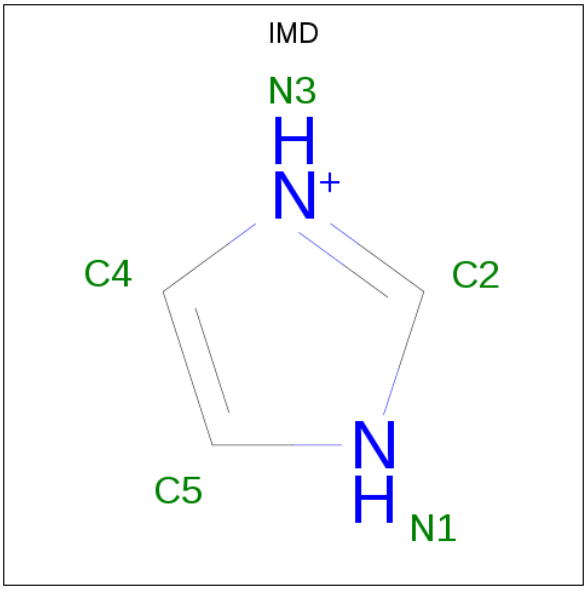
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP W8QF82
A	-5	ILE	-	expression tag	UNP W8QF82
A	-4	HIS	-	expression tag	UNP W8QF82
A	-3	HIS	-	expression tag	UNP W8QF82
A	-2	HIS	-	expression tag	UNP W8QF82
A	-1	HIS	-	expression tag	UNP W8QF82
A	0	HIS	-	expression tag	UNP W8QF82
A	1	HIS	-	expression tag	UNP W8QF82
B	-6	MET	-	initiating methionine	UNP W8QF82
B	-5	ILE	-	expression tag	UNP W8QF82
B	-4	HIS	-	expression tag	UNP W8QF82
B	-3	HIS	-	expression tag	UNP W8QF82
B	-2	HIS	-	expression tag	UNP W8QF82
B	-1	HIS	-	expression tag	UNP W8QF82
B	0	HIS	-	expression tag	UNP W8QF82
B	1	HIS	-	expression tag	UNP W8QF82

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

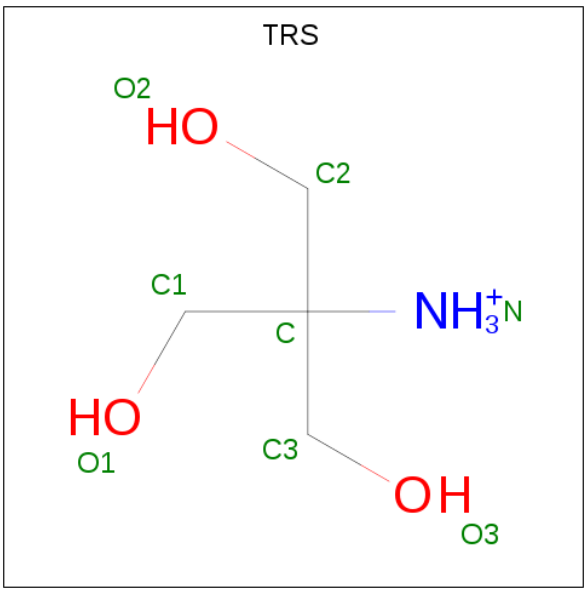
- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 5 3 2	0	0
3	A	1	Total C N 5 3 2	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code:

TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	8	4	1	3	0	0

- Molecule 5 is water.

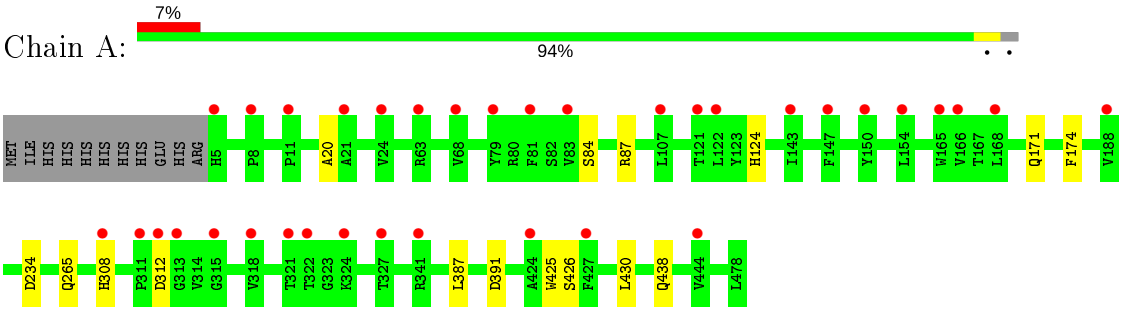
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	355	355	355	0	0
			Total	O		
5	B	165	165	165	0	0

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 (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.

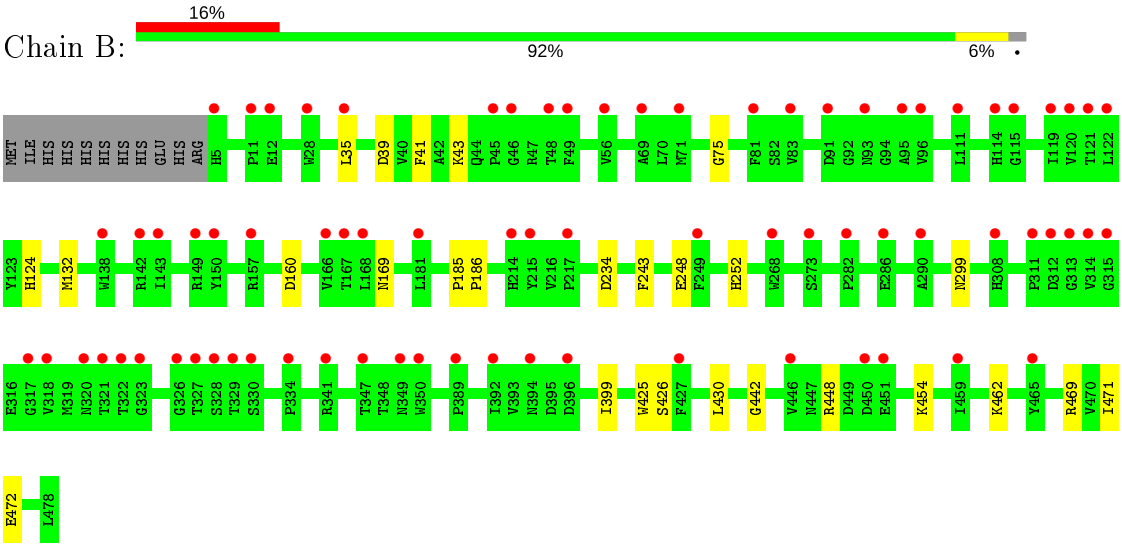
- Molecule 1: Putative 6-phospho-beta-galactobiosidase

Chain A:



- Molecule 1: Putative 6-phospho-beta-galactobiosidase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	108.02Å 68.81Å 152.77Å 90.00° 100.74° 90.00°	Depositor
Resolution (Å)	25.59 – 1.76 25.59 – 1.76	Depositor EDS
% Data completeness (in resolution range)	90.9 (25.59-1.76) 90.2 (25.59-1.76)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 1.76Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.203 , 0.241 0.201 , 0.237	Depositor DCC
R_{free} test set	4936 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	25.8	Xtriage
Anisotropy	0.940	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 40.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8349	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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, 0.333 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, TRS, IMD

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	0.44	0/4069	0.57	0/5534
1	B	0.42	0/4014	0.54	0/5463
All	All	0.43	0/8083	0.55	0/10997

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3921	0	3745	9	0
1	B	3884	0	3678	17	0
2	A	6	0	8	1	0
3	A	10	0	10	0	0
4	A	8	0	12	0	0
5	A	355	0	0	0	0
5	B	165	0	0	0	0
All	All	8349	0	7453	25	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 2.

All (25) 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:132:MET:CE	1:B:186:PRO:HB3	2.09	0.81
1:B:132:MET:HE2	1:B:186:PRO:HB3	1.76	0.67
1:B:132:MET:HE1	1:B:186:PRO:HB3	1.79	0.64
1:B:124:HIS:CE1	1:B:169:ASN:HD22	2.19	0.61
1:B:39:ASP:O	1:B:43:LYS:HD2	2.10	0.51
1:B:41:PHE:CG	1:B:185:PRO:HD3	2.46	0.49
1:B:35:LEU:H	1:B:35:LEU:HD12	1.75	0.49
1:B:124:HIS:CE1	1:B:169:ASN:ND2	2.81	0.48
1:A:84:SER:HB3	1:A:87:ARG:HG3	1.96	0.48
1:B:41:PHE:CD2	1:B:185:PRO:HD3	2.51	0.46
1:B:248:GLU:HA	1:B:252:HIS:HB2	1.97	0.46
1:A:387:LEU:HD11	1:A:391:ASP:HA	1.98	0.45
1:A:312:ASP:OD1	1:A:312:ASP:N	2.49	0.45
1:A:234:ASP:HA	1:B:234:ASP:HA	1.98	0.45
1:A:265:GLN:OE1	2:A:501:GOL:H11	2.18	0.44
1:A:171:GLN:HA	1:A:174:PHE:CE2	2.54	0.43
1:B:425:TRP:HA	1:B:426:SER:HA	1.62	0.42
1:B:426:SER:O	1:B:442:GLY:HA2	2.19	0.42
1:B:469:ARG:HA	1:B:472:GLU:HG2	2.02	0.42
1:A:308:HIS:C	1:A:308:HIS:ND1	2.74	0.41
1:B:75:GLY:O	1:B:471:ILE:HG21	2.21	0.41
1:B:448:ARG:HA	1:B:454:LYS:HD2	2.03	0.40
1:A:425:TRP:HA	1:A:426:SER:HA	1.83	0.40
1:A:20:ALA:HB2	1:A:124:HIS:CE1	2.57	0.40
1:B:399:ILE:HD11	1:B:462:LYS:HG2	2.04	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	481/485 (99%)	465 (97%)	16 (3%)	0	100	100
1	B	475/485 (98%)	455 (96%)	20 (4%)	0	100	100
All	All	956/970 (99%)	920 (96%)	36 (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	409/412 (99%)	407 (100%)	2 (0%)	88	83
1	B	402/412 (98%)	398 (99%)	4 (1%)	76	63
All	All	811/824 (98%)	805 (99%)	6 (1%)	81	75

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	430	LEU
1	A	438	GLN
1	B	160	ASP
1	B	243	PHE
1	B	299	ASN
1	B	430	LEU

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	438	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)

4 ligands 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	$\#\|Z\| > 2$
3	IMD	A	502	-	3,5,5	0.39	0	4,5,5	0.57	0
4	TRS	A	504	-	7,7,7	0.30	0	9,9,9	0.93	0
3	IMD	A	503	-	3,5,5	0.41	0	4,5,5	0.55	0
2	GOL	A	501	-	5,5,5	0.31	0	5,5,5	0.83	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	IMD	A	502	-	-	-	0/1/1/1
4	TRS	A	504	-	-	6/9/9/9	-
3	IMD	A	503	-	-	-	0/1/1/1
2	GOL	A	501	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	504	TRS	C2-C-C1-O1
4	A	504	TRS	C3-C-C1-O1
4	A	504	TRS	N-C-C1-O1
4	A	504	TRS	C3-C-C2-O2
4	A	504	TRS	N-C-C2-O2
4	A	504	TRS	C1-C-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	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, 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	474/485 (97%)	0.59	35 (7%) 14 19	18, 27, 49, 70	0
1	B	474/485 (97%)	0.92	76 (16%) 1 3	25, 36, 55, 75	0
All	All	948/970 (97%)	0.76	111 (11%) 4 6	18, 32, 53, 75	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	HIS	7.4
1	B	5	HIS	6.5
1	A	321	THR	6.1
1	B	326	GLY	5.4
1	B	321	THR	5.4
1	B	95	ALA	5.0
1	B	322	THR	4.8
1	B	122	LEU	4.7
1	A	312	ASP	4.6
1	B	312	ASP	4.4
1	A	313	GLY	4.4
1	B	83	VAL	4.3
1	B	315	GLY	4.2
1	A	311	PRO	4.1
1	B	311	PRO	3.9
1	B	28	TRP	3.8
1	B	327	THR	3.8
1	B	290	ALA	3.8
1	A	318	VAL	3.8
1	B	320	ASN	3.8
1	B	465	TYR	3.6
1	A	122	LEU	3.6
1	B	318	VAL	3.5
1	B	349	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	168	LEU	3.4
1	A	83	VAL	3.4
1	B	119	ILE	3.4
1	A	8	PRO	3.3
1	A	154	LEU	3.3
1	B	56	VAL	3.3
1	B	120	VAL	3.3
1	B	392	ILE	3.2
1	B	35	LEU	3.1
1	B	46	GLY	3.1
1	B	149	ARG	3.1
1	B	328	SER	3.1
1	A	81	PHE	3.0
1	B	93	ASN	3.0
1	A	11	PRO	2.9
1	B	121	THR	2.9
1	A	147	PHE	2.9
1	A	168	LEU	2.8
1	B	181	LEU	2.8
1	B	317	GLY	2.8
1	B	313	GLY	2.8
1	B	157	ARG	2.8
1	B	334	PRO	2.8
1	B	451	GLU	2.7
1	B	138	TRP	2.7
1	B	314	VAL	2.7
1	B	81	PHE	2.7
1	B	11	PRO	2.7
1	B	215	TYR	2.7
1	A	444	VAL	2.7
1	B	142	ARG	2.7
1	A	63[A]	ARG	2.6
1	B	347	THR	2.6
1	A	327	THR	2.6
1	A	21	ALA	2.6
1	A	150	TYR	2.6
1	B	115	GLY	2.5
1	B	396	ASP	2.5
1	B	49	PHE	2.5
1	A	24	VAL	2.5
1	B	48	THR	2.5
1	B	111	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	121	THR	2.5
1	A	341	ARG	2.5
1	B	350	TRP	2.5
1	B	308	HIS	2.4
1	B	91	ASP	2.4
1	B	389	PRO	2.4
1	B	114	HIS	2.4
1	A	322	THR	2.3
1	B	427	PHE	2.3
1	A	424	ALA	2.3
1	B	45	PRO	2.3
1	B	282	PRO	2.3
1	A	315	GLY	2.3
1	A	143	ILE	2.3
1	B	167	THR	2.3
1	B	330	SER	2.3
1	B	150	TYR	2.3
1	A	166	VAL	2.2
1	A	188	VAL	2.2
1	B	217	PRO	2.2
1	A	79	TYR	2.2
1	A	68	VAL	2.2
1	A	324	LYS	2.2
1	B	166	VAL	2.2
1	B	459	ILE	2.2
1	B	341	ARG	2.2
1	B	394	ASN	2.2
1	B	96	VAL	2.2
1	A	107	LEU	2.2
1	B	329	THR	2.2
1	B	249	PHE	2.1
1	A	308	HIS	2.1
1	B	446	VAL	2.1
1	B	286	GLU	2.1
1	B	268	TRP	2.1
1	B	273	SER	2.1
1	B	143	ILE	2.1
1	B	450	ASP	2.1
1	A	427	PHE	2.1
1	B	69	ALA	2.1
1	B	214	HIS	2.1
1	B	323	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	165	TRP	2.0
1	B	71	MET	2.0
1	B	12	GLU	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, 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	B-factors(Å^2)	Q<0.9
4	TRS	A	504	8/8	0.73	0.19	26,37,44,44	0
3	IMD	A	502	5/5	0.85	0.23	33,37,45,47	0
3	IMD	A	503	5/5	0.89	0.16	31,31,34,34	0
2	GOL	A	501	6/6	0.89	0.23	41,44,54,54	0

6.5 Other polymers (i)

There are no such residues in this entry.