



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 05:55 PM EDT

PDB ID : 6ZJV  
Title : Cold-adapted beta-D-galactosidase from *Arthrobacter* sp. 32cB mutant D207A  
Authors : Rutkiewicz, M.; Bujacz, A.; Bujacz, G.  
Deposited on : 2020-06-29  
Resolution : 2.25 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

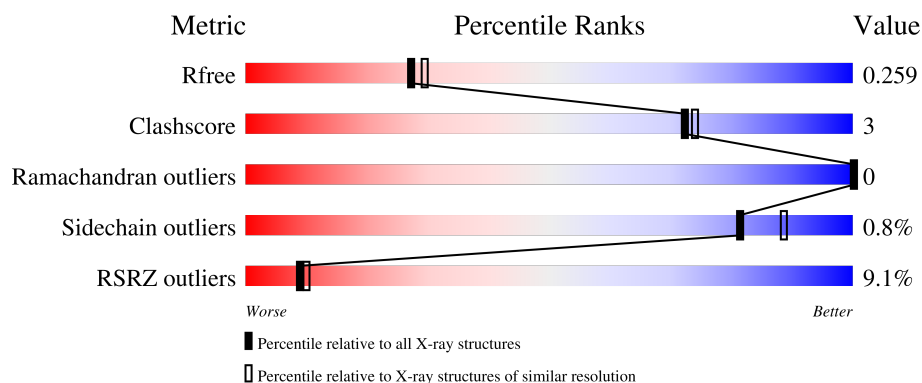
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1010	<div> <div>9%</div> <div>89%</div> <div>9%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7839 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.

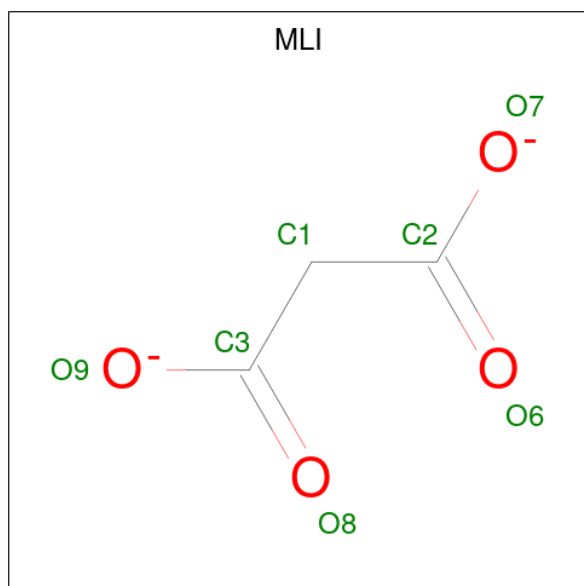
- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	989	7690	4840	1376	1453	21	0	12	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	ALA	ASP	engineered mutation	UNP A0A023UGN9

- Molecule 2 is MALONATE ION (three-letter code: MLI) (formula:  $C_3H_2O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	7	3	4	0	0

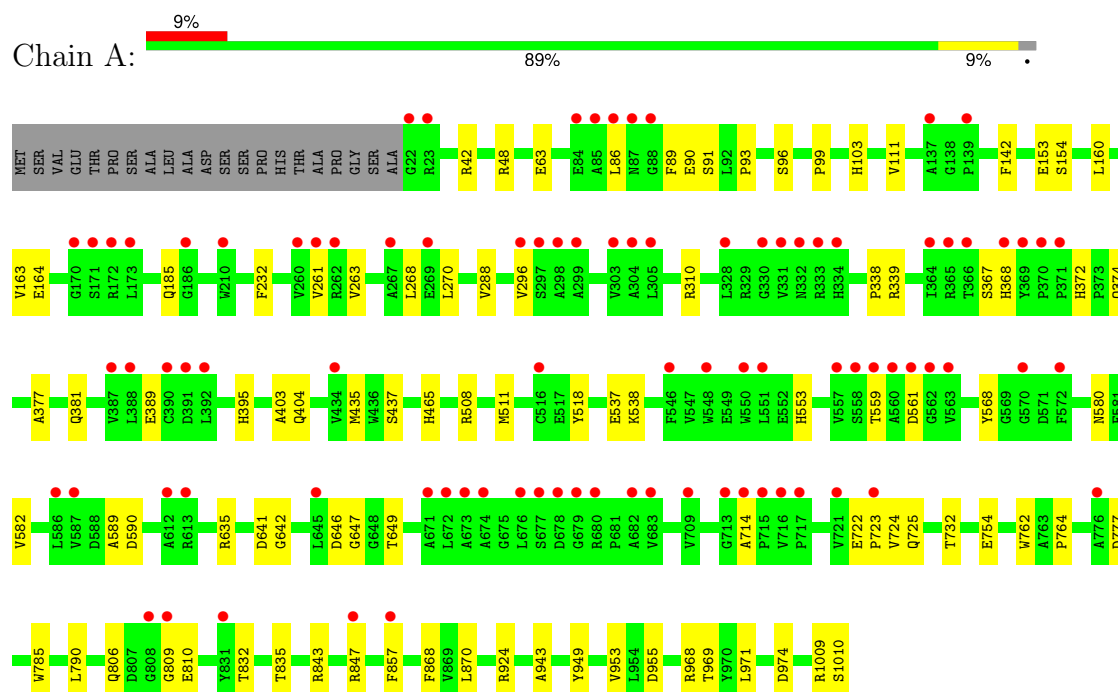
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	142	Total 142	O 142	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Beta-galactosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.45Å 139.45Å 127.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.12 – 2.25 47.12 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.12-2.25) 99.5 (47.12-2.25)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, $R_{free}$	0.236 , 0.260 0.239 , 0.259	Depositor DCC
$R_{free}$ test set	1095 reflections (1.60%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.2	Xtriage
Anisotropy	0.688	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7839	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.34	0/7910	0.55	0/10776

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 [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	7690	0	7407	51	0
2	A	7	0	2	0	0
3	A	142	0	0	1	0
All	All	7839	0	7409	51	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 3.

All (51) 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:A:263:VAL:HG22	1:A:268:LEU:HB2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:HIS:HB2	1:A:582:VAL:HG22	1.71	0.71
1:A:537:GLU:O	1:A:538:LYS:HB3	2.03	0.58
1:A:949:TYR:HB2	1:A:953:VAL:HG21	1.85	0.58
1:A:99:PRO:HA	1:A:103:HIS:O	2.04	0.57
1:A:261:VAL:HG22	1:A:270:LEU:HG	1.87	0.56
1:A:263:VAL:HG23	1:A:263:VAL:O	2.07	0.55
1:A:372:HIS:ND1	1:A:374:GLN:HG2	2.24	0.53
1:A:764:PRO:HD2	1:A:955:ASP:OD1	2.08	0.52
1:A:288:VAL:HG23	1:A:288:VAL:O	2.09	0.52
1:A:646:ASP:OD1	1:A:647:GLY:N	2.43	0.52
1:A:42:ARG:NH2	1:A:164:GLU:OE2	2.41	0.52
1:A:553:HIS:CB	1:A:582:VAL:HG22	2.39	0.50
1:A:389:GLU:HG3	1:A:437:SER:HB3	1.93	0.49
1:A:635:ARG:HG2	1:A:649:THR:HG22	1.94	0.49
1:A:641:ASP:OD1	1:A:642:GLY:N	2.45	0.49
1:A:160:LEU:O	1:A:163:VAL:HG12	2.14	0.48
1:A:153:GLU:HA	1:A:154:SER:HA	1.69	0.48
1:A:943:ALA:HB3	1:A:974:ASP:HB2	1.96	0.47
1:A:339:ARG:NH2	3:A:1204:HOH:O	2.46	0.47
1:A:725:GLN:HG2	1:A:732:THR:HB	1.97	0.46
1:A:868:PHE:HB2	1:A:971:LEU:HB3	1.97	0.46
1:A:90:GLU:CD	1:A:103:HIS:HE1	2.19	0.46
1:A:949:TYR:HB2	1:A:953:VAL:CG2	2.44	0.46
1:A:806:GLN:O	1:A:809:GLY:N	2.43	0.45
1:A:754:GLU:OE1	1:A:968:ARG:NE	2.47	0.45
1:A:338:PRO:HG3	1:A:589:ALA:HB1	1.99	0.45
1:A:63:GLU:OE2	1:A:91:SER:CB	2.65	0.45
1:A:722:GLU:HB2	1:A:835:THR:HG23	1.97	0.44
1:A:559:THR:OG1	1:A:561:ASP:OD1	2.31	0.44
1:A:832:THR:OG1	1:A:843:ARG:HB3	2.17	0.44
1:A:338:PRO:HG2	1:A:590:ASP:OD1	2.16	0.44
1:A:870:LEU:HB2	1:A:969:THR:HB	1.99	0.43
1:A:435[B]:MET:HE1	1:A:465:HIS:HB2	2.00	0.43
1:A:724:VAL:HG23	1:A:810:GLU:HG3	1.99	0.43
1:A:377:ALA:O	1:A:381:GLN:HG3	2.19	0.43
1:A:785:TRP:CD1	1:A:790:LEU:HD12	2.54	0.43
1:A:111:VAL:HG13	1:A:395:HIS:CD2	2.54	0.42
1:A:723:PRO:HA	1:A:810:GLU:HG2	1.99	0.42
1:A:93:PRO:O	1:A:96:SER:HB3	2.20	0.42
1:A:568:TYR:HB2	1:A:580:ASN:HA	2.02	0.42
1:A:1009:ARG:O	1:A:1010:SER:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:714:ALA:HA	1:A:924:ARG:HH22	1.85	0.42
1:A:261:VAL:HG12	1:A:296:VAL:HG23	2.02	0.41
1:A:367:SER:HA	1:A:368:HIS:HA	1.83	0.41
1:A:508:ARG:HA	1:A:511:MET:SD	2.61	0.41
1:A:142:PHE:CE2	1:A:185:GLN:HG2	2.55	0.41
1:A:777:ASP:HB2	1:A:857:PHE:CD1	2.55	0.41
1:A:263:VAL:HG21	1:A:268:LEU:HD12	2.02	0.41
1:A:86:LEU:HD11	1:A:89:PHE:HB2	2.03	0.41
1:A:403:ALA:O	1:A:404:GLN:HB2	2.22	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	999/1010 (99%)	972 (97%)	27 (3%)	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	787/792 (99%)	781 (99%)	6 (1%)	81	88

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

Mol	Chain	Res	Type
1	A	48	ARG
1	A	232	PHE
1	A	310	ARG
1	A	518	TYR
1	A	762	TRP
1	A	847	ARG

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

Mol	Chain	Res	Type
1	A	103	HIS
1	A	440	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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
2	MLI	A	1101	-	6,6,6	1.44	0	7,7,7	1.25	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
2	MLI	A	1101	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	MLI	C3-C1-C2-O6
2	A	1101	MLI	C3-C1-C2-O7
2	A	1101	MLI	C2-C1-C3-O8
2	A	1101	MLI	C2-C1-C3-O9

There are no ring outliers.

No monomer is involved in short contacts.

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	989/1010 (97%)	0.55	90 (9%) 9 10	46, 73, 112, 142	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	560	ALA	7.1
1	A	85	ALA	6.9
1	A	716	VAL	6.9
1	A	676	LEU	6.0
1	A	369	TYR	5.4
1	A	559	THR	5.1
1	A	298	ALA	4.2
1	A	561	ASP	4.2
1	A	714	ALA	4.2
1	A	562	GLY	4.0
1	A	390	CYS	3.7
1	A	776	ALA	3.7
1	A	713	GLY	3.6
1	A	563	VAL	3.6
1	A	366	THR	3.5
1	A	365	ARG	3.3
1	A	299	ALA	3.3
1	A	808	GLY	3.3
1	A	715	PRO	3.3
1	A	613[A]	ARG	3.2
1	A	86	LEU	3.1
1	A	87	ASN	3.1
1	A	516	CYS	3.0
1	A	857	PHE	3.0
1	A	682	ALA	3.0
1	A	22	GLY	3.0
1	A	139	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	548	TRP	2.9
1	A	671	ALA	2.9
1	A	721	VAL	2.9
1	A	332	ASN	2.8
1	A	677	SER	2.8
1	A	388	LEU	2.8
1	A	387	VAL	2.7
1	A	391	ASP	2.7
1	A	260	VAL	2.7
1	A	847	ARG	2.7
1	A	645	LEU	2.7
1	A	717	PRO	2.7
1	A	23	ARG	2.6
1	A	210	TRP	2.6
1	A	674	ALA	2.6
1	A	173	LEU	2.6
1	A	328	LEU	2.6
1	A	709	VAL	2.5
1	A	368	HIS	2.5
1	A	371	PRO	2.5
1	A	551	LEU	2.5
1	A	172	ARG	2.5
1	A	570	GLY	2.5
1	A	434	VAL	2.5
1	A	262	ARG	2.5
1	A	84	GLU	2.5
1	A	683	VAL	2.5
1	A	809	GLY	2.5
1	A	392	LEU	2.4
1	A	831	TYR	2.4
1	A	673	ALA	2.4
1	A	334	HIS	2.4
1	A	723	PRO	2.4
1	A	679	GLY	2.4
1	A	170	GLY	2.4
1	A	572	PHE	2.3
1	A	364	ILE	2.3
1	A	297	SER	2.3
1	A	303	VAL	2.3
1	A	330	GLY	2.3
1	A	586	LEU	2.3
1	A	296	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	331	VAL	2.2
1	A	370	PRO	2.2
1	A	305	LEU	2.2
1	A	333	ARG	2.2
1	A	550	TRP	2.2
1	A	612	ALA	2.2
1	A	267	ALA	2.2
1	A	678	ASP	2.2
1	A	557	VAL	2.1
1	A	137	ALA	2.1
1	A	171	SER	2.1
1	A	672	LEU	2.1
1	A	269	GLU	2.1
1	A	558	SER	2.1
1	A	587	VAL	2.1
1	A	88	GLY	2.0
1	A	304	ALA	2.0
1	A	546	PHE	2.0
1	A	680	ARG	2.0
1	A	261	VAL	2.0
1	A	186	GLY	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 monosaccharides 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	MLI	A	1101	7/7	0.83	0.22	86,87,88,88	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.