



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:22 PM UTC

PDB ID : 3RRA / pdb_00003rra
Title : Crystal structure of enolase PRK14017 (target EFI-500653) from *Ralstonia pickettii* 12J with magnesium bound
Authors : Patskovsky, Y.; Ramagopal, U.A.; Hillerich, B.; Seidel, R.D.; Zencheck, W.D.; Toro, R.; Imker, H.J.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on : 2011-04-29
Resolution : 2.30 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 types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

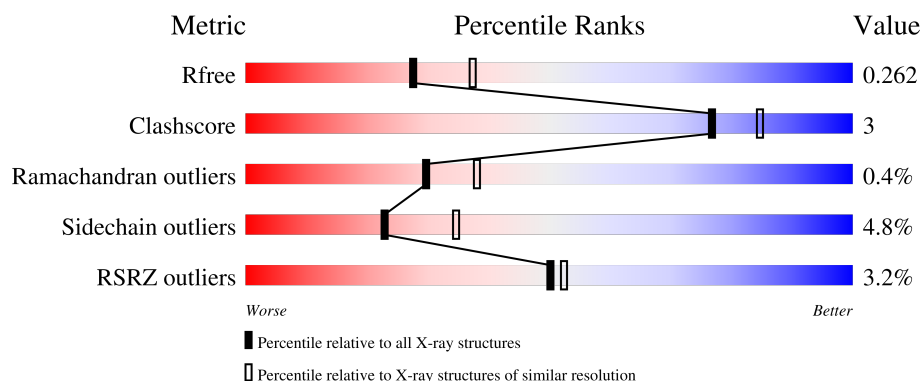
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 ≥ 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	405	
1	B	405	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5970 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 D-galactonate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	1	0
			2891	1847	502	528	14			
1	B	379	Total	C	N	O	S	0	6	0
			2939	1877	514	534	14			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP B2UCA8
A	1	VAL	-	expression tag	UNP B2UCA8
A	383	ALA	-	expression tag	UNP B2UCA8
A	384	GLU	-	expression tag	UNP B2UCA8
A	385	ASN	-	expression tag	UNP B2UCA8
A	386	LEU	-	expression tag	UNP B2UCA8
A	387	TYR	-	expression tag	UNP B2UCA8
A	388	PHE	-	expression tag	UNP B2UCA8
A	389	GLN	-	expression tag	UNP B2UCA8
A	390	SER	-	expression tag	UNP B2UCA8
A	391	HIS	-	expression tag	UNP B2UCA8
A	392	HIS	-	expression tag	UNP B2UCA8
A	393	HIS	-	expression tag	UNP B2UCA8
A	394	HIS	-	expression tag	UNP B2UCA8
A	395	HIS	-	expression tag	UNP B2UCA8
A	396	HIS	-	expression tag	UNP B2UCA8
A	397	TRP	-	expression tag	UNP B2UCA8
A	398	SER	-	expression tag	UNP B2UCA8
A	399	HIS	-	expression tag	UNP B2UCA8
A	400	PRO	-	expression tag	UNP B2UCA8
A	401	GLN	-	expression tag	UNP B2UCA8
A	402	PHE	-	expression tag	UNP B2UCA8
A	403	GLU	-	expression tag	UNP B2UCA8
A	404	LYS	-	expression tag	UNP B2UCA8
B	0	MET	-	expression tag	UNP B2UCA8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	VAL	-	expression tag	UNP B2UCA8
B	383	ALA	-	expression tag	UNP B2UCA8
B	384	GLU	-	expression tag	UNP B2UCA8
B	385	ASN	-	expression tag	UNP B2UCA8
B	386	LEU	-	expression tag	UNP B2UCA8
B	387	TYR	-	expression tag	UNP B2UCA8
B	388	PHE	-	expression tag	UNP B2UCA8
B	389	GLN	-	expression tag	UNP B2UCA8
B	390	SER	-	expression tag	UNP B2UCA8
B	391	HIS	-	expression tag	UNP B2UCA8
B	392	HIS	-	expression tag	UNP B2UCA8
B	393	HIS	-	expression tag	UNP B2UCA8
B	394	HIS	-	expression tag	UNP B2UCA8
B	395	HIS	-	expression tag	UNP B2UCA8
B	396	HIS	-	expression tag	UNP B2UCA8
B	397	TRP	-	expression tag	UNP B2UCA8
B	398	SER	-	expression tag	UNP B2UCA8
B	399	HIS	-	expression tag	UNP B2UCA8
B	400	PRO	-	expression tag	UNP B2UCA8
B	401	GLN	-	expression tag	UNP B2UCA8
B	402	PHE	-	expression tag	UNP B2UCA8
B	403	GLU	-	expression tag	UNP B2UCA8
B	404	LYS	-	expression tag	UNP B2UCA8

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0

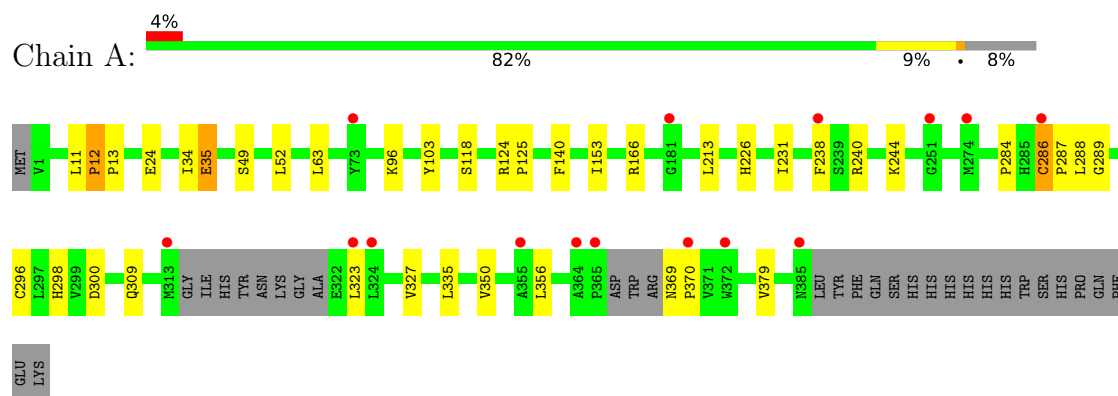
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total 57	O 57	0	0
4	B	79	Total 79	O 79	0	0

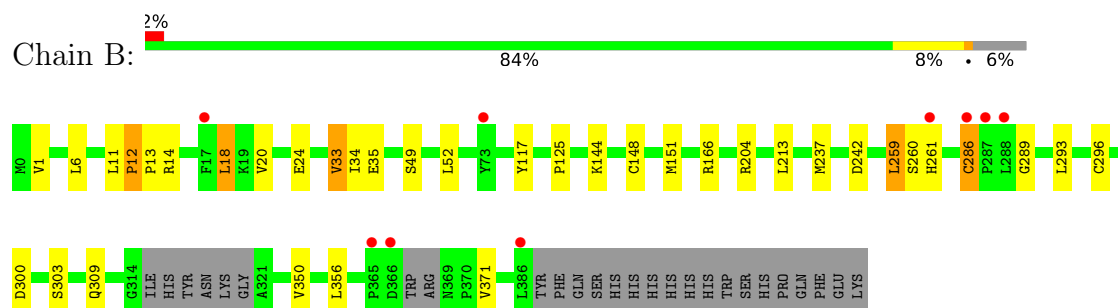
3 Residue-property plots

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: Putative D-galactonate dehydratase



• Molecule 1: Putative D-galactonate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	117.34Å 117.34Å 113.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 50.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-2.30) 94.6 (50.00-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.206 , 0.263 0.205 , 0.262	Depositor DCC
R_{free} test set	1036 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h 0.000 for -l,-k,-h 0.000 for -h,-l,-k 0.000 for -h,l,k 0.027 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5970	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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: MG, 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	0.57	0/2962	0.91	3/4023 (0.1%)
1	B	0.58	1/3024 (0.0%)	0.92	3/4105 (0.1%)
All	All	0.57	1/5986 (0.0%)	0.92	6/8128 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	33	VAL	CA-CB	-5.49	1.47	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	11	LEU	CA-C-N	9.78	130.46	120.38
1	A	11	LEU	C-N-CA	9.78	130.46	120.38
1	A	12	PRO	N-CA-C	8.45	121.01	110.70
1	B	12	PRO	N-CA-C	7.69	120.08	110.70
1	B	289	GLY	CA-C-N	5.24	124.74	119.19
1	B	289	GLY	C-N-CA	5.24	124.74	119.19

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	2891	0	2862	13	0
1	B	2939	0	2924	20	0
2	A	1	0	0	1	0
2	B	1	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	57	0	0	2	0
4	B	79	0	0	0	0
All	All	5970	0	5786	34	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 (34) 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:34:ILE:O	1:B:35:GLU:C	2.38	0.67
1:B:259:LEU:HD13	1:B:296:CYS:HA	1.75	0.67
1:A:34:ILE:O	1:A:35:GLU:C	2.38	0.66
1:A:226[A]:HIS:HE1	4:A:460:HOH:O	1.81	0.62
1:B:125:PRO:HG3	1:B:166[A]:ARG:HG3	1.90	0.53
1:B:12:PRO:HB2	1:B:13:PRO:HD3	1.90	0.53
1:B:11:LEU:HB3	1:B:12:PRO:HD2	1.92	0.52
1:B:33:VAL:HG13	1:B:260:SER:HB3	1.92	0.51
1:A:103:TYR:H	1:A:298:HIS:CD2	2.28	0.51
1:A:125:PRO:HG3	1:A:166:ARG:HG3	1.92	0.50
2:A:405:CL:CL	2:B:405:CL:CL	3.04	0.50
1:A:286:CYS:HB2	1:A:296:CYS:SG	2.52	0.49
1:B:125:PRO:HG3	1:B:166[B]:ARG:HG3	1.95	0.48
1:B:33:VAL:HG13	1:B:260:SER:CB	2.42	0.48
1:B:117:TYR:HE1	1:B:144:LYS:HB2	1.79	0.48
1:B:12:PRO:C	1:B:14:ARG:H	2.22	0.48
1:B:49[B]:SER:HA	1:B:52:LEU:HD12	1.97	0.47
1:A:284:PRO:HB2	1:A:309:GLN:HE22	1.80	0.45
1:B:286:CYS:SG	1:B:293:LEU:HA	2.57	0.45
1:B:6:LEU:HG	1:B:20:VAL:HG22	1.99	0.44
1:B:117:TYR:CE1	1:B:144:LYS:HB2	2.52	0.44
1:B:49[A]:SER:HA	1:B:52:LEU:HD12	1.99	0.44
1:A:288:LEU:HB3	1:A:289:GLY:H	1.53	0.44
1:B:300:ASP:OD1	1:B:309:GLN:NE2	2.49	0.44
1:A:140:PHE:HZ	1:A:335:LEU:HD13	1.83	0.44
1:A:96:LYS:NZ	4:A:443:HOH:O	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:HD23	1:A:63:LEU:HD22	2.00	0.43
1:A:369:ASN:HA	1:A:370:PRO:HD3	1.82	0.42
1:B:237:MET:HG2	1:B:242:ASP:HB3	2.01	0.42
1:A:300:ASP:OD1	1:A:309:GLN:NE2	2.52	0.42
1:B:1:VAL:HG13	1:B:24:GLU:HG3	2.02	0.42
1:A:49:SER:HA	1:A:52:LEU:HD12	2.02	0.41
1:B:6:LEU:HD23	1:B:18:LEU:HD21	2.03	0.40
1:B:11:LEU:HA	1:B:12:PRO:HD3	1.93	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	369/405 (91%)	354 (96%)	12 (3%)	3 (1%)	16	20
1	B	379/405 (94%)	369 (97%)	10 (3%)	0	100	100
All	All	748/810 (92%)	723 (97%)	22 (3%)	3 (0%)	30	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	PRO
1	A	287	PRO
1	A	12	PRO

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	294/323 (91%)	278 (95%)	16 (5%)	20	29
1	B	299/323 (93%)	287 (96%)	12 (4%)	28	42
All	All	593/646 (92%)	565 (95%)	28 (5%)	23	35

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	35	GLU
1	A	118	SER
1	A	124	ARG
1	A	153	ILE
1	A	213	LEU
1	A	231	ILE
1	A	238	PHE
1	A	240	ARG
1	A	244	LYS
1	A	286	CYS
1	A	323	LEU
1	A	327	VAL
1	A	350	VAL
1	A	356	LEU
1	A	379	VAL
1	B	18	LEU
1	B	148	CYS
1	B	151	MET
1	B	204	ARG
1	B	213	LEU
1	B	259	LEU
1	B	261	HIS
1	B	286	CYS
1	B	303	SER
1	B	350	VAL
1	B	356	LEU
1	B	371	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	285	HIS
1	A	298	HIS
1	A	309	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [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	374/405 (92%)	0.29	15 (4%) 42 44	39, 66, 100, 119	1 (0%)
1	B	379/405 (93%)	0.23	9 (2%) 59 62	26, 61, 97, 131	6 (1%)
All	All	753/810 (92%)	0.26	24 (3%) 50 52	26, 64, 99, 131	7 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	73	TYR	5.3
1	B	366	ASP	4.4
1	A	324	LEU	4.0
1	B	386	LEU	3.5
1	A	323	LEU	2.8
1	A	313	MET	2.7
1	B	17	PHE	2.7
1	A	365	PRO	2.7
1	B	287	PRO	2.7
1	A	181	GLY	2.5
1	A	364	ALA	2.5
1	A	355	ALA	2.3
1	A	73	TYR	2.3
1	A	251	GLY	2.2
1	B	261	HIS	2.2
1	A	372	TRP	2.1
1	B	288	LEU	2.1
1	A	370	PRO	2.1
1	B	365	PRO	2.1
1	A	286	CYS	2.1
1	B	286	CYS	2.1
1	A	385	ASN	2.1
1	A	274	MET	2.1
1	A	238	PHE	2.1

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	MG	B	406	1/1	0.90	0.08	96,96,96,96	0
3	MG	A	406	1/1	0.94	0.06	83,83,83,83	0
2	CL	A	405	1/1	0.95	0.10	68,68,68,68	0
2	CL	B	405	1/1	0.96	0.09	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.