



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 02:57 PM GMT

PDB ID : 2POD
Title : Crystal structure of a member of enolase superfamily from Burkholderia pseudomallei K96243
Authors : Patskovsky, Y.; Bonanno, J.; Sauder, J.M.; Gilmore, J.M.; Iizuka, M.; Ozyurt, S.; Wasserman, S.R.; Smith, D.; Gerlt, J.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-04-26
Resolution : 2.34 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>

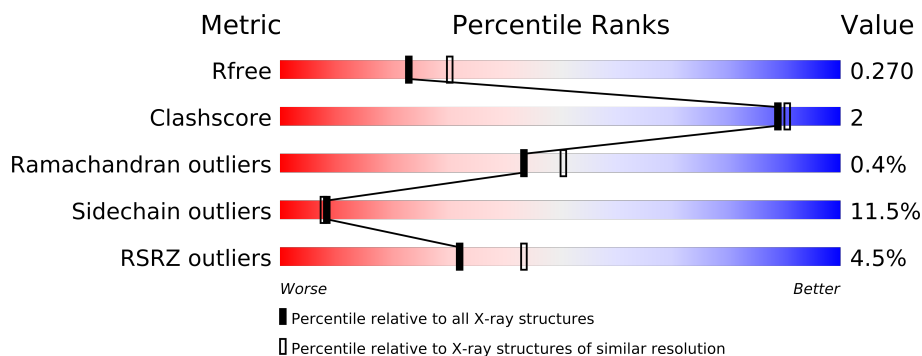
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.34 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	4049 (2.38-2.30)
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)
RSRZ outliers	66119	4050 (2.38-2.30)

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 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	410	
1	B	410	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6132 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 Mandelate racemase / muconate lactonizing enzyme.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	Se	0	1	0
			2987	1900	516	557	6	8			
1	B	380	Total	C	N	O	S	Se	0	1	0
			2991	1901	514	562	6	8			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	CLONING ARTIFACT	UNP Q63IJ7
A	0	SER	-	CLONING ARTIFACT	UNP Q63IJ7
A	1	LEU	-	CLONING ARTIFACT	UNP Q63IJ7
A	81	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	173	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	213	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	216	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	249	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	291	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	309	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	383	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
A	401	GLU	-	CLONING ARTIFACT	UNP Q63IJ7
A	402	GLY	-	CLONING ARTIFACT	UNP Q63IJ7
A	403	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
A	404	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
A	405	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
A	406	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
A	407	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
A	408	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	-1	MSE	-	CLONING ARTIFACT	UNP Q63IJ7
B	0	SER	-	CLONING ARTIFACT	UNP Q63IJ7
B	1	LEU	-	CLONING ARTIFACT	UNP Q63IJ7
B	81	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	173	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	213	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	216	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	249	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	291	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	309	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	383	MSE	MET	MODIFIED RESIDUE	UNP Q63IJ7
B	401	GLU	-	CLONING ARTIFACT	UNP Q63IJ7
B	402	GLY	-	CLONING ARTIFACT	UNP Q63IJ7
B	403	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	404	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	405	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	406	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	407	HIS	-	CLONING ARTIFACT	UNP Q63IJ7
B	408	HIS	-	CLONING ARTIFACT	UNP Q63IJ7

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is water.

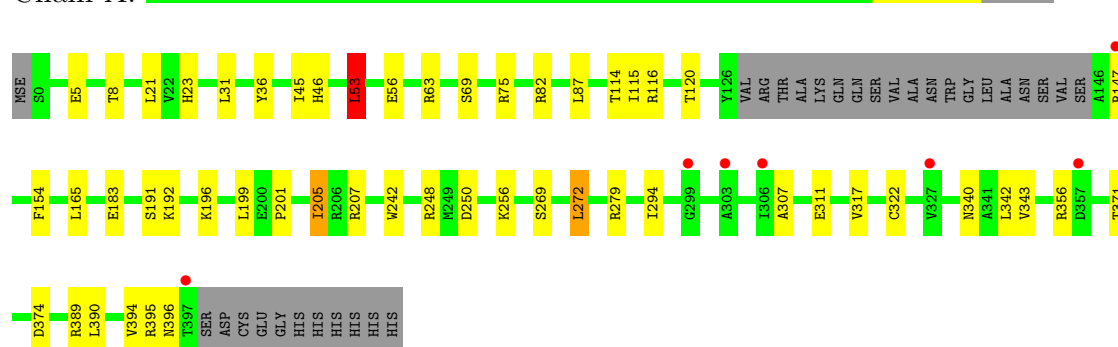
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	88	Total O 88 88	0	0
3	B	64	Total O 64 64	0	0

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 ($\text{RSRZ} > 2$). 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.

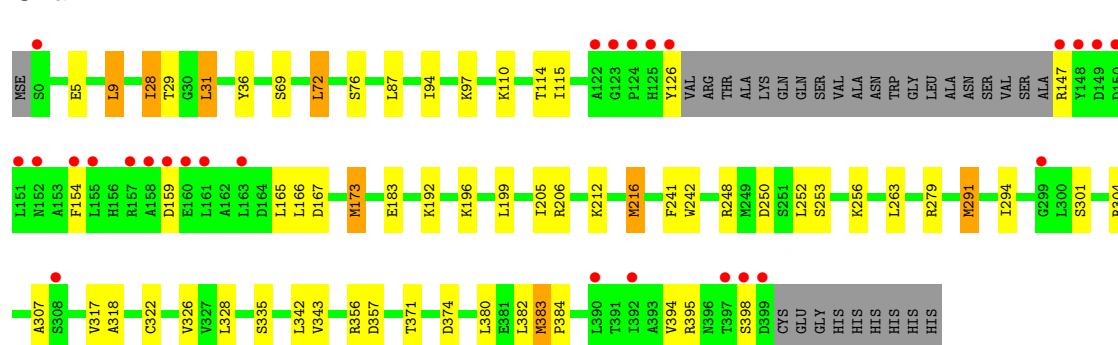
- Molecule 1: Mandelate racemase / muconate lactonizing enzyme

Chain A:



- Molecule 1: Mandelate racemase / muconate lactonizing enzyme

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	146.77Å 146.77Å 85.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.34 46.41 – 2.34	Depositor EDS
% Data completeness (in resolution range)	90.7 (20.00-2.34) 90.7 (46.41-2.34)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.3.0034	Depositor
R, R_{free}	0.209 , 0.275 0.206 , 0.270	Depositor DCC
R_{free} test set	1077 reflections (3.20%)	DCC
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.431	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 28.7	EDS
Estimated twinning fraction	0.011 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	1 of 34781 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6132	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.39	0/3056	0.63	1/4144 (0.0%)
1	B	0.40	0/3060	0.63	1/4150 (0.0%)
All	All	0.40	0/6116	0.63	2/8294 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	LEU	CA-CB-CG	5.86	128.77	115.30
1	B	9	LEU	CA-CB-CG	5.25	127.37	115.30

There are no chirality outliers.

There are no planarity outliers.

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	2987	0	2931	12	0
1	B	2991	0	2927	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	88	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	64	0	0	0	0
All	All	6132	0	5858	27	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 2.

All (27) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:8:THR:OG1	1:A:46:HIS:HE1	1.86	0.58
1:B:216:MSE:HE2	1:B:241:PHE:HB3	1.89	0.55
1:B:28:ILE:HD11	1:B:94:ILE:HA	1.89	0.54
1:A:75:ARG:HB3	1:B:76[A]:SER:HB3	1.92	0.50
1:A:307:ALA:HA	1:A:317:VAL:HG21	1.92	0.50
1:B:165:LEU:HD13	1:B:173:MSE:HG2	1.95	0.49
1:B:291:MSE:HG2	1:B:318:ALA:O	2.13	0.49
1:A:56:GLU:OE1	1:A:63:ARG:NH2	2.46	0.48
1:B:115:ILE:HD13	1:B:335:SER:HB3	1.95	0.48
1:B:114:THR:HG22	1:B:371:THR:HB	1.95	0.47
1:B:5:GLU:HG3	1:B:398:SER:HB3	1.95	0.47
1:A:114:THR:HG22	1:A:371:THR:HB	1.97	0.46
1:B:31:LEU:HD11	1:B:382:LEU:HG	1.98	0.46
1:A:120:THR:HG21	1:A:322:CYS:SG	2.56	0.45
1:B:383:MSE:HA	1:B:384:PRO:HD3	1.89	0.45
1:A:311:GLU:HG3	1:A:340:ASN:HB3	1.99	0.44
1:A:82:ARG:HD3	1:B:72:LEU:HD23	1.98	0.44
1:B:166:LEU:HD21	1:B:212:LYS:HD2	1.99	0.43
1:A:201:PRO:O	1:A:205:ILE:HG23	2.19	0.43
1:B:307:ALA:HA	1:B:317:VAL:HG21	2.00	0.43
1:B:28:ILE:HD13	1:B:97:LYS:HB2	2.01	0.43
1:A:5:GLU:HB3	1:A:23:HIS:HD2	1.84	0.42
1:B:301:SER:HA	1:B:304:ARG:HH11	1.85	0.42
1:A:269:SER:HB3	1:A:272:LEU:HD22	2.01	0.42
1:B:9:LEU:HD22	1:B:394:VAL:HG12	2.02	0.41
1:B:326:VAL:HG22	1:B:380:LEU:HD11	2.01	0.41
1:A:53:LEU:HA	1:A:56:GLU:HG3	2.01	0.41

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	376/410 (92%)	364 (97%)	11 (3%)	1 (0%)	50	60
1	B	377/410 (92%)	357 (95%)	18 (5%)	2 (0%)	38	44
All	All	753/820 (92%)	721 (96%)	29 (4%)	3 (0%)	43	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	TYR
1	B	36	TYR
1	B	322	CYS

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	312/328 (95%)	278 (89%)	34 (11%)	9	9
1	B	314/328 (96%)	276 (88%)	38 (12%)	7	6
All	All	626/656 (95%)	554 (88%)	72 (12%)	8	8

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	31	LEU
1	A	45	ILE
1	A	53	LEU
1	A	69	SER
1	A	87	LEU

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Mol	Chain	Res	Type
1	A	115	ILE
1	A	116	ARG
1	A	147	ARG
1	A	154	PHE
1	A	165	LEU
1	A	183	GLU
1	A	191	SER
1	A	192	LYS
1	A	196	LYS
1	A	199	LEU
1	A	205	ILE
1	A	207	ARG
1	A	242	TRP
1	A	248	ARG
1	A	250	ASP
1	A	256	LYS
1	A	272	LEU
1	A	279	ARG
1	A	294	ILE
1	A	342	LEU
1	A	343	VAL
1	A	356	ARG
1	A	374	ASP
1	A	389	ARG
1	A	390	LEU
1	A	394	VAL
1	A	395	ARG
1	A	396	ASN
1	B	28	ILE
1	B	29	THR
1	B	31	LEU
1	B	69	SER
1	B	72	LEU
1	B	87	LEU
1	B	110	LYS
1	B	126	TYR
1	B	147	ARG
1	B	154	PHE
1	B	159	ASP
1	B	167	ASP
1	B	173	MSE
1	B	183	GLU

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Mol	Chain	Res	Type
1	B	192	LYS
1	B	196	LYS
1	B	199	LEU
1	B	205	ILE
1	B	206	ARG
1	B	216	MSE
1	B	242	TRP
1	B	248	ARG
1	B	250	ASP
1	B	252	LEU
1	B	253	SER
1	B	256	LYS
1	B	263	LEU
1	B	279	ARG
1	B	291	MSE
1	B	294	ILE
1	B	328	LEU
1	B	342	LEU
1	B	343	VAL
1	B	356	ARG
1	B	357	ASP
1	B	374	ASP
1	B	383	MSE
1	B	395	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	A	125	HIS
1	A	396	ASN
1	B	16	ASN
1	B	125	HIS
1	B	344	GLN

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 ⓘ

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.

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	379/410 (92%)	0.14	7 (1%) 65 75	32, 47, 71, 104	0
1	B	380/410 (92%)	0.38	27 (7%) 16 23	34, 50, 75, 109	0
All	All	759/820 (92%)	0.26	34 (4%) 32 43	32, 48, 74, 109	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	126	TYR	7.0
1	B	147	ARG	6.2
1	B	123	GLY	5.4
1	B	398	SER	4.3
1	B	399	ASP	4.2
1	B	148	TYR	4.2
1	B	161	LEU	4.1
1	B	149	ASP	3.9
1	A	147	ARG	3.9
1	B	397	THR	3.7
1	B	151	LEU	3.5
1	B	160	GLU	3.5
1	B	390	LEU	3.2
1	B	154	PHE	3.1
1	B	124	PRO	3.1
1	A	357	ASP	3.1
1	B	159	ASP	3.0
1	B	163	LEU	2.9
1	B	0	SER	2.9
1	B	158	ALA	2.9
1	B	150	ASP	2.9
1	B	155	LEU	2.8
1	A	299	GLY	2.6
1	B	157	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	125	HIS	2.5
1	B	122	ALA	2.5
1	B	392	ILE	2.2
1	B	299	GLY	2.2
1	A	303	ALA	2.2
1	A	397	THR	2.1
1	B	152	ASN	2.1
1	B	308	SER	2.1
1	A	327	VAL	2.1
1	A	306	ILE	2.1

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 ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NA	B	409	1/1	0.12	0.55	66,66,66,66	0
2	NA	A	409	1/1	0.12	-0.43	73,73,73,73	0

6.5 Other polymers ⓘ

There are no such residues in this entry.