

Full wwPDB X-ray Structure Validation Report (i)

Dec 12, 2023 – 06:14 pm GMT

PDB ID : 4AY3

Title : Crystal structure of Bacillus anthracis PurE

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Deposited on : 2012-06-18

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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

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)

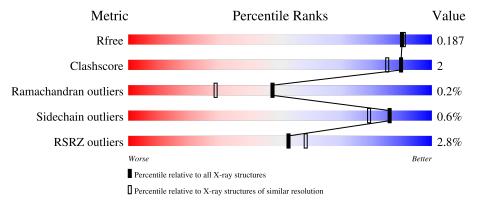
 $Validation\ Pipeline\ (wwPDB-VP) \quad : \quad 2.36$

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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
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 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 <=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	181	84%	•	12%
1	В	181	81%	8%	12%
1	С	181	85%		13%
1	D	181	83%	•	14%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5253 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 N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE MUTASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	160	Total	С	N	О	S	7	3	0
1	A	100	1200	757	203	234	6	1	3	U
1	В	160	Total	С	N	О	S	7	3	0
1	Б	100	1203	760	204	233	6	1	3	0
1	С	158	Total	С	N	О	S	10	1	0
1		198	1175	741	201	226	7	10	1	U
1	D	156	Total	С	N	О	S	5	2	0
1	ט	150	1163	734	199	224	6		2	U

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q81ZH8
A	-18	GLY	-	expression tag	UNP Q81ZH8
A	-17	SER	-	expression tag	UNP Q81ZH8
A	-16	SER	-	expression tag	UNP Q81ZH8
A	-15	HIS	-	expression tag	UNP Q81ZH8
A	-14	HIS	-	expression tag	UNP Q81ZH8
A	-13	HIS	-	expression tag	UNP Q81ZH8
A	-12	HIS	-	expression tag	UNP Q81ZH8
A	-11	HIS	-	expression tag	UNP Q81ZH8
A	-10	HIS	-	expression tag	UNP Q81ZH8
A	-9	SER	-	expression tag	UNP Q81ZH8
A	-8	SER	-	expression tag	UNP Q81ZH8
A	-7	GLY	-	expression tag	UNP Q81ZH8
A	-6	LEU	-	expression tag	UNP Q81ZH8
A	-5	VAL	-	expression tag	UNP Q81ZH8
A	-4	PRO	-	expression tag	UNP Q81ZH8
A	-3	ARG	-	expression tag	UNP Q81ZH8
A	-2	GLY		expression tag	UNP Q81ZH8
A	-1	SER	-	expression tag	UNP Q81ZH8
A	0	HIS	-	expression tag	UNP Q81ZH8



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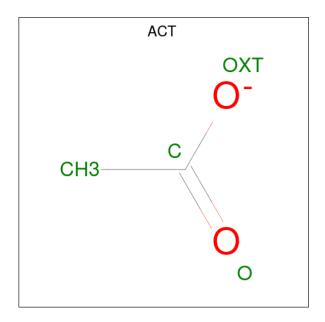
Chain	Residue	Modelled Modelled	Actual	Comment	Reference
В	-19	MET	-	expression tag	UNP Q81ZH8
В	-18	GLY	-	expression tag	UNP Q81ZH8
В	-17	SER	-	expression tag	UNP Q81ZH8
В	-16	SER	-	expression tag	UNP Q81ZH8
В	-15	HIS	-	expression tag	UNP Q81ZH8
В	-14	HIS	_	expression tag	UNP Q81ZH8
В	-13	HIS	-	expression tag	UNP Q81ZH8
В	-12	HIS	-	expression tag	UNP Q81ZH8
В	-11	HIS	-	expression tag	UNP Q81ZH8
В	-10	HIS	-	expression tag	UNP Q81ZH8
В	-9	SER	-	expression tag	UNP Q81ZH8
В	-8	SER	-	expression tag	UNP Q81ZH8
В	-7	GLY	-	expression tag	UNP Q81ZH8
В	-6	LEU	-	expression tag	UNP Q81ZH8
В	-5	VAL	-	expression tag	UNP Q81ZH8
В	-4	PRO	_	expression tag	UNP Q81ZH8
В	-3	ARG	-	expression tag	UNP Q81ZH8
В	-2	GLY	-	expression tag	UNP Q81ZH8
В	-1	SER	-	expression tag	UNP Q81ZH8
В	0	HIS	-	expression tag	UNP Q81ZH8
С	-19	MET	-	expression tag	UNP Q81ZH8
С	-18	GLY	-	expression tag	UNP Q81ZH8
С	-17	SER	-	expression tag	UNP Q81ZH8
С	-16	SER	-	expression tag	UNP Q81ZH8
С	-15	HIS	-	expression tag	UNP Q81ZH8
С	-14	HIS	-	expression tag	UNP Q81ZH8
С	-13	HIS	-	expression tag	UNP Q81ZH8
С	-12	HIS	-	expression tag	UNP Q81ZH8
С	-11	HIS	-	expression tag	UNP Q81ZH8
С	-10	HIS	-	expression tag	UNP Q81ZH8
С	-9	SER	-	expression tag	UNP Q81ZH8
С	-8	SER	-	expression tag	UNP Q81ZH8
С	-7	GLY	-	expression tag	UNP Q81ZH8
С	-6	LEU	-	expression tag	UNP Q81ZH8
С	-5	VAL	_	expression tag	UNP Q81ZH8
С	-4	PRO	-	expression tag	UNP Q81ZH8
С	-3	ARG	-	expression tag	UNP Q81ZH8
С	-2	GLY	-	expression tag	UNP Q81ZH8
С	-1	SER	-	expression tag	UNP Q81ZH8
С	0	HIS	-	expression tag	UNP Q81ZH8
D	-19	MET	-	expression tag	UNP Q81ZH8
D	-18	GLY	_	expression tag	UNP Q81ZH8



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Chain	Residue	Modelled	Actual	Comment	Reference
D	-17	SER	-	expression tag	UNP Q81ZH8
D	-16	SER	-	expression tag	UNP Q81ZH8
D	-15	HIS	-	expression tag	UNP Q81ZH8
D	-14	HIS	-	expression tag	UNP Q81ZH8
D	-13	HIS	_	expression tag	UNP Q81ZH8
D	-12	HIS	-	expression tag	UNP Q81ZH8
D	-11	HIS	-	expression tag	UNP Q81ZH8
D	-10	HIS	-	expression tag	UNP Q81ZH8
D	-9	SER	-	expression tag	UNP Q81ZH8
D	-8	SER	-	expression tag	UNP Q81ZH8
D	-7	GLY	-	expression tag	UNP Q81ZH8
D	-6	LEU	-	expression tag	UNP Q81ZH8
D	-5	VAL	-	expression tag	UNP Q81ZH8
D	-4	PRO	-	expression tag	UNP Q81ZH8
D	-3	ARG	-	expression tag	UNP Q81ZH8
D	-2	GLY	-	expression tag	UNP Q81ZH8
D	-1	SER	-	expression tag	UNP Q81ZH8
D	0	HIS	-	expression tag	UNP Q81ZH8

 \bullet Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $\mathrm{C_2H_3O_2}).$



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



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total C O 4 2 2	0	0
2	С	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0

• Molecule 3 is water.

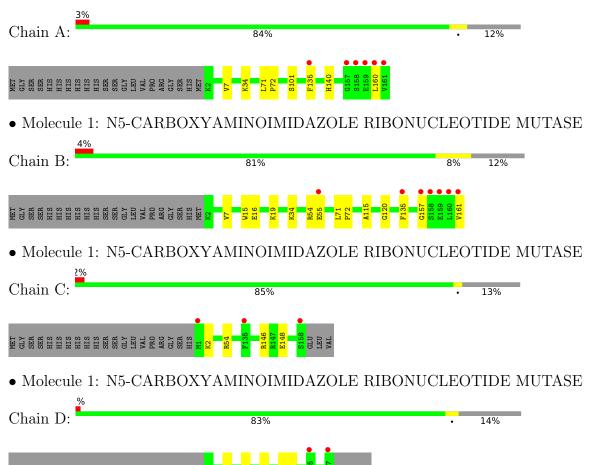
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	155	Total O 155 155	0	0
3	В	100	Total O 100 100	0	0
3	С	145	Total O 145 145	0	0
3	D	92	Total O 92 92	0	0



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: N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE MUTASE





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	86.88Å 86.88Å 131.37Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.53 - 1.76	Depositor
rtesolution (A)	49.48 - 1.76	EDS
% Data completeness	99.9 (49.53-1.76)	Depositor
(in resolution range)	99.9 (49.48-1.76)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	6.24 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.7.0027	Depositor
υ .	0.152 , 0.178	Depositor
R, R_{free}	0.164 , 0.187	DCC
R_{free} test set	2920 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 47.2	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5253	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.43% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: ACT

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		
IVIOI	Moi Chain		ISZ $\# Z > 5$		# Z > 5	
1	A	0.56	$1/1227 \ (0.1\%)$	0.69	0/1661	
1	В	0.52	0/1230	0.72	0/1664	
1	С	0.62	0/1196	0.75	1/1619 (0.1%)	
1	D	0.52	0/1187	0.71	0/1608	
All	All	0.56	1/4840 (0.0%)	0.72	$1/6552 \ (0.0\%)$	

All (1) bond length outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	101	SER	CB-OG	-6.78	1.33	1.42

All (1) bond angle outliers are listed below:

ľ	Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
	1	С	146	ARG	NE-CZ-NH2	-5.18	117.71	120.30

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	1200	0	1224	4	0
1	В	1203	0	1232	9	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	С	1175	0	1201	2	0
1	D	1163	0	1187	3	0
2	A	8	0	6	1	0
2	В	4	0	3	0	0
2	С	4	0	3	0	0
2	D	4	0	3	0	0
3	A	155	0	0	0	0
3	В	100	0	0	2	0
3	С	145	0	0	2	0
3	D	92	0	0	1	0
All	All	5253	0	4859	17	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 2.

All (17) 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:15:TRP:CE2	1:B:19[A]:LYS:HB2	2.30	0.66
1:B:15:TRP:CZ2	1:B:19[A]:LYS:HB2	2.32	0.65
1:B:55:GLU:HG3	3:B:2048:HOH:O	1.97	0.63
1:B:16:GLU:HG2	3:B:2008:HOH:O	2.00	0.61
2:A:1162:ACT:H3	2:A:1163:ACT:H1	1.85	0.58
1:C:54:ARG:NH1	3:C:2075:HOH:O	2.39	0.56
1:A:140:HIS:CE1	1:B:54:ARG:HD2	2.46	0.51
1:D:55:GLU:HG3	3:D:2033:HOH:O	2.11	0.51
1:C:148[B]:GLU:HG3	3:C:2129:HOH:O	2.13	0.47
1:D:7:VAL:O	1:D:34:LYS:HA	2.15	0.46
1:B:71:LEU:HB3	1:B:72:PRO:HD3	1.98	0.44
1:B:7:VAL:O	1:B:34:LYS:HA	2.19	0.42
1:D:71:LEU:HB3	1:D:72:PRO:HD3	2.02	0.41
1:A:135:PHE:HB3	1:B:135:PHE:CD1	2.56	0.41
1:A:71:LEU:HB3	1:A:72:PRO:HD3	2.02	0.41
1:B:115:ALA:O	1:B:120:GLY:HA3	2.21	0.41
1:A:7:VAL:O	1:A:34:LYS:HA	2.21	0.41

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	Perce	entiles
1	A	161/181 (89%)	157 (98%)	4 (2%)	0	100	100
1	В	161/181 (89%)	158 (98%)	2 (1%)	1 (1%)	25	10
1	С	157/181~(87%)	154 (98%)	3 (2%)	0	100	100
1	D	156/181~(86%)	155 (99%)	1 (1%)	0	100	100
All	All	635/724~(88%)	624 (98%)	10 (2%)	1 (0%)	47	29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	157	GLY

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	Percer	ntiles
1	A	128/143 (90%)	127 (99%)	1 (1%)	81	72
1	В	128/143 (90%)	127 (99%)	1 (1%)	81	72
1	С	124/143 (87%)	123 (99%)	1 (1%)	81	72
1	D	123/143 (86%)	123 (100%)	0	100	100
All	All	503/572 (88%)	500 (99%)	3 (1%)	86	79

All (3) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	160	LEU
1	В	161	VAL
1	С	2	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

5 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		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACT	A	1163	-	3,3,3	0.85	0	3,3,3	0.95	0
2	ACT	В	1162	-	3,3,3	0.79	0	3,3,3	0.96	0
2	ACT	С	1159	-	3,3,3	0.72	0	3,3,3	0.85	0
2	ACT	D	1158	-	3,3,3	0.76	0	3,3,3	0.72	0
2	ACT	A	1162	-	3,3,3	0.78	0	3,3,3	0.60	0

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.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1163	ACT	1	0
2	A	1162	ACT	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 (i)

6.1 Protein, DNA and RNA chains (i)

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>	$\#\mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	160/181 (88%)	-0.20	6 (3%) 40 47	12, 21, 43, 73	2 (1%)
1	В	160/181 (88%)	-0.18	7 (4%) 34 40	13, 25, 43, 61	2 (1%)
1	С	158/181 (87%)	-0.25	3 (1%) 66 74	10, 17, 33, 66	5 (3%)
1	D	156/181 (86%)	-0.23	2 (1%) 77 83	16, 27, 43, 53	1 (0%)
All	All	634/724 (87%)	-0.21	18 (2%) 53 58	10, 22, 43, 73	10 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	158	SER	5.3
1	A	135	PHE	4.8
1	В	135	PHE	4.2
1	A	161	VAL	3.9
1	A	157	GLY	3.6
1	A	159	GLU	3.3
1	В	160	LEU	3.2
1	В	161	VAL	3.1
1	A	160	LEU	3.0
1	С	1	MET	2.9
1	В	158	SER	2.8
1	В	55	GLU	2.5
1	С	135	PHE	2.4
1	A	158	SER	2.3
1	D	135	PHE	2.3
1	В	157	GLY	2.3
1	В	159	GLU	2.1
1	D	157	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^{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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	ACT	A	1163	4/4	0.56	0.37	37,39,40,40	0
2	ACT	В	1162	4/4	0.61	0.23	45,45,47,50	0
2	ACT	A	1162	4/4	0.68	0.25	38,43,45,50	0
2	ACT	D	1158	4/4	0.82	0.18	42,44,45,49	0
2	ACT	С	1159	4/4	0.89	0.14	40,41,43,44	0

6.5 Other polymers (i)

There are no such residues in this entry.

