



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2OB3 / pdb_00002ob3
Title : Structure of Phosphotriesterase mutant H257Y/L303T
Authors : Kim, J.; Ramagopal, U.A.; Tsai, P.; Raushel, F.M.; Almo, S.C.
Deposited on : 2006-12-18
Resolution : 1.04 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

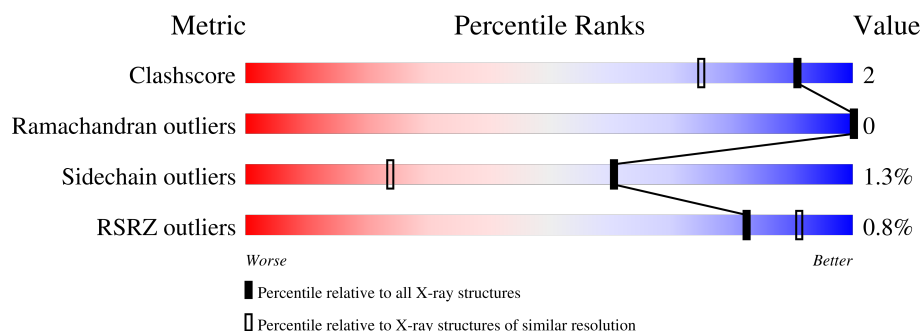
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.04 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))
Clashscore	190562	1063 (1.06-1.02)
Ramachandran outliers	187476	1034 (1.06-1.02)
Sidechain outliers	187428	1035 (1.06-1.02)
RSRZ outliers	180081	1035 (1.06-1.02)

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	330	 92% 6% •
1	B	330	 91% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6065 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 Parathion hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	11	0
			2615	1652	464	492	7			
1	B	330	Total	C	N	O	S	0	4	0
			2563	1618	454	484	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	TYR	HIS	engineered mutation	UNP P0A434
A	303	THR	LEU	engineered mutation	UNP P0A434
B	257	TYR	HIS	engineered mutation	UNP P0A434
B	303	THR	LEU	engineered mutation	UNP P0A434

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	423	Total	O	0	0
			423	423		
4	B	432	Total	O	0	0
			432	432		

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: Parathion hydrolase



- Molecule 1: Parathion hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.36Å 45.37Å 79.21Å 104.86° 93.27° 97.81°	Depositor
Resolution (Å)	30.00 – 1.04 30.00 – 1.04	Depositor EDS
% Data completeness (in resolution range)	95.0 (30.00-1.04) 80.6 (30.00-1.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.00 (at 1.04Å)	Xtriage
Refinement program	SHELX	Depositor
R, R_{free}	0.105 , 0.127 (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	6.0	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	6065	wwPDB-VP
Average B, all atoms (Å ²)	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.76% 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: KCX, BTB, ZN

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	0.93	2/2651 (0.1%)	1.25	22/3600 (0.6%)
1	B	0.94	4/2598 (0.2%)	1.29	24/3527 (0.7%)
All	All	0.94	6/5249 (0.1%)	1.27	46/7127 (0.6%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	356	ARG	CD-NE	-6.08	1.37	1.46
1	B	140	LEU	CB-CG	6.07	1.65	1.53
1	B	152	ARG	NE-CZ	-5.81	1.26	1.33
1	B	162	GLY	C-N	-5.61	1.26	1.33
1	B	249	LEU	CB-CG	5.60	1.64	1.53
1	A	364	ALA	C-OXT	5.48	1.34	1.23

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	140	LEU	CD1-CG-CD2	14.23	142.12	110.80
1	B	139	ARG	CG-CD-NE	12.39	139.26	112.00
1	B	264	ASP	CA-CB-CG	11.24	123.84	112.60
1	A	148	GLN	OE1-CD-NE2	-8.90	113.70	122.60
1	A	356	ARG	NE-CZ-NH2	8.88	127.19	119.20
1	B	118	ARG	NE-CZ-NH2	8.55	126.90	119.20
1	A	356	ARG	CD-NE-CZ	8.18	135.85	124.40
1	A	356	ARG	NE-CZ-NH1	-8.04	113.46	121.50
1	B	249	LEU	CD1-CG-CD2	7.96	128.31	110.80
1	A	139	ARG	CA-CB-CG	7.56	129.22	114.10
1	B	162	GLY	CA-C-N	7.46	132.24	121.80
1	B	162	GLY	C-N-CA	7.46	132.24	121.80
1	A	337	ARG	CD-NE-CZ	7.39	134.75	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	35	ASP	CA-CB-CG	7.20	119.80	112.60
1	A	77	LYS	CA-C-N	6.92	129.43	120.44
1	A	77	LYS	C-N-CA	6.92	129.43	120.44
1	A	88	ARG	NE-CZ-NH1	6.48	127.98	121.50
1	A	131	TRP	CA-CB-CG	6.43	125.81	113.60
1	B	131	TRP	CA-CB-CG	6.43	125.81	113.60
1	A	89[A]	ARG	NE-CZ-NH2	6.42	124.97	119.20
1	A	89[B]	ARG	NE-CZ-NH2	6.42	124.97	119.20
1	B	77	LYS	CA-C-N	6.38	128.82	120.28
1	B	77	LYS	C-N-CA	6.38	128.82	120.28
1	A	132[A]	PHE	CB-CA-C	6.29	120.82	111.06
1	A	132[B]	PHE	CB-CA-C	6.29	120.82	111.06
1	A	230	HIS	CE1-NE2-CD2	-6.26	102.73	109.00
1	A	164	ARG	CD-NE-CZ	5.96	132.74	124.40
1	B	356	ARG	CD-NE-CZ	5.82	132.55	124.40
1	B	207	ARG	CD-NE-CZ	5.69	132.37	124.40
1	A	41	ARG	NE-CZ-NH1	-5.60	115.90	121.50
1	B	38	ASN	CA-CB-CG	-5.58	107.02	112.60
1	B	337	ARG	CG-CD-NE	-5.55	99.78	112.00
1	B	162	GLY	O-C-N	-5.41	115.53	122.39
1	B	55	HIS	CG-CD2-NE2	5.36	112.56	107.20
1	A	36	ARG	CA-C-O	5.33	127.38	121.56
1	B	230	HIS	CE1-NE2-CD2	-5.33	103.67	109.00
1	B	264	ASP	OD1-CG-OD2	5.31	135.65	122.90
1	A	89[A]	ARG	CB-CG-CD	5.23	123.33	111.30
1	A	89[B]	ARG	CB-CG-CD	5.23	123.33	111.30
1	B	67	ARG	NE-CZ-NH2	5.18	123.86	119.20
1	A	118	ARG	NE-CZ-NH2	-5.17	114.54	119.20
1	A	77	LYS	O-C-N	-5.10	116.82	122.07
1	B	55	HIS	CE1-NE2-CD2	-5.09	103.91	109.00
1	B	356	ARG	NE-CZ-NH2	-5.07	114.63	119.20
1	B	290	GLN	OE1-CD-NE2	5.07	127.67	122.60
1	B	41	ARG	NE-CZ-NH1	-5.02	116.48	121.50

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	2615	0	2623	13	0
1	B	2563	0	2573	5	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	14	0	19	0	0
3	B	14	0	18	0	0
4	A	423	0	0	8	0
4	B	432	0	0	2	0
All	All	6065	0	5233	18	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 (18) 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:293:MET:HE3	4:B:1336:HOH:O	1.91	0.70
1:A:35:ASP:HA	4:A:1190:HOH:O	1.92	0.69
1:A:338:GLU:HG3	4:A:1280:HOH:O	2.04	0.56
1:A:89[A]:ARG:NH1	4:A:1093:HOH:O	2.49	0.46
1:A:115:GLU:HG2	4:A:1132:HOH:O	2.15	0.46
1:A:88:ARG:NH2	4:A:1252:HOH:O	2.49	0.45
1:A:131:TRP:CG	1:A:132[B]:PHE:H	2.35	0.44
1:B:335:PHE:CZ	1:B:339:LYS:HE3	2.52	0.44
1:A:302:TRP:CH2	1:A:321:ASN:HB3	2.51	0.44
1:A:89[B]:ARG:NH2	4:A:1092:HOH:O	2.49	0.44
1:B:35:ASP:OD1	1:B:36:ARG:NH1	2.50	0.44
1:A:164:ARG:NH2	4:A:1310:HOH:O	2.50	0.43
1:B:81:GLU:HG3	4:B:1070:HOH:O	2.18	0.43
1:A:139:ARG:HA	1:A:179:PHE:CE1	2.53	0.43
1:B:302:TRP:CH2	1:B:321:ASN:HB3	2.54	0.43
1:A:298[B]:VAL:CG1	1:A:328:ILE:HD12	2.50	0.42
1:A:88:ARG:NH1	4:A:1150:HOH:O	2.49	0.40
1:A:314:MET:HE3	1:A:314:MET:HA	2.03	0.40

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	339/330 (103%)	330 (97%)	9 (3%)	0	100	100
1	B	333/330 (101%)	323 (97%)	10 (3%)	0	100	100
All	All	672/660 (102%)	653 (97%)	19 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	276/264 (104%)	271 (98%)	5 (2%)	51	14
1	B	270/264 (102%)	266 (98%)	4 (2%)	57	18
All	All	546/528 (103%)	537 (98%)	9 (2%)	61	17

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89[A]	ARG
1	A	89[B]	ARG
1	A	274	ILE
1	A	299[A]	SER
1	A	299[B]	SER
1	B	35	ASP
1	B	206	GLN
1	B	264	ASP

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Mol	Chain	Res	Type
1	B	299	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	206	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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$
1	KCX	B	169	1,2	10,11,12	1.75	1 (10%)	6,12,14	1.83	1 (16%)
1	KCX	A	169	1,2	10,11,12	2.16	2 (20%)	6,12,14	2.17	1 (16%)

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
1	KCX	B	169	1,2	-	0/9/10/12	-
1	KCX	A	169	1,2	-	0/9/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	169	KCX	OQ1-CX	5.14	1.31	1.21
1	B	169	KCX	OQ1-CX	4.70	1.30	1.21
1	A	169	KCX	CB-CA	4.08	1.59	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	OQ1-CX-NZ	-5.21	117.01	124.92
1	B	169	KCX	OQ1-CX-NZ	-4.34	118.33	124.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	BTB	A	906	-	13,13,13	3.14	4 (30%)	7,16,16	1.32	1 (14%)
3	BTB	B	905	-	13,13,13	2.41	3 (23%)	7,16,16	1.04	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	BTB	A	906	-	-	0/21/21/21	-
3	BTB	B	905	-	-	0/21/21/21	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	906	BTB	C3-C2	9.18	1.64	1.53
3	B	905	BTB	C7-N	7.04	1.57	1.48
3	A	906	BTB	C5-N	4.10	1.53	1.48
3	A	906	BTB	C2-N	3.22	1.54	1.48
3	B	905	BTB	C2-N	3.22	1.54	1.48
3	A	906	BTB	C4-C2	-3.04	1.49	1.53
3	B	905	BTB	C5-N	2.22	1.51	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	906	BTB	O3-C3-C2	-2.77	104.88	111.40

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 [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, 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	329/330 (99%)	-0.33	3 (0%) 81 90	2, 7, 15, 44	11 (3%)
1	B	329/330 (99%)	-0.36	2 (0%) 85 93	3, 7, 15, 32	4 (1%)
All	All	658/660 (99%)	-0.35	5 (0%) 82 91	2, 7, 16, 44	15 (2%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	35	ASP	3.9
1	B	264	ASP	3.1
1	A	35	ASP	2.9
1	A	338	GLU	2.1
1	A	364	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	KCX	A	169	12/13	0.99	0.04	4,5,6,7	0
1	KCX	B	169	12/13	0.99	0.03	4,5,5,6	0

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	BTB	B	905	14/14	0.98	0.04	6,7,10,13	0
3	BTB	A	906	14/14	0.99	0.04	6,7,12,14	0
2	ZN	B	903	1/1	1.00	0.03	4,4,4,4	0
2	ZN	B	904	1/1	1.00	0.03	7,7,7,7	0
2	ZN	A	901	1/1	1.00	0.03	5,5,5,5	0
2	ZN	A	902	1/1	1.00	0.03	7,7,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.