



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 6G49 / pdb_00006g49
Title : Crystal structure of the periplasmic domain of TgpA from *Pseudomonas aeruginosa*
Authors : Milani, M.; Mastrangelo, E.; Uruburu, M.
Deposited on : 2018-03-27
Resolution : 1.60 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

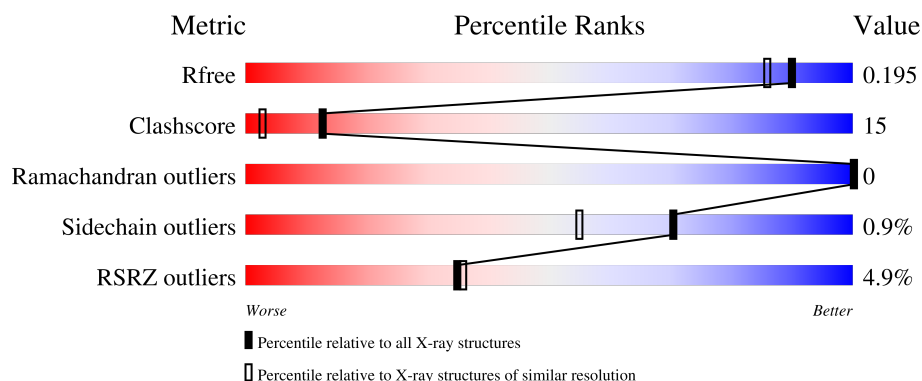
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	338	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2832 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 Protein-glutamine gamma-glutamyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	288	2487	1590	454	433	10	0	26	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	162	MET	-	initiating methionine	UNP Q9HZX3
A	163	GLY	-	expression tag	UNP Q9HZX3
A	164	SER	-	expression tag	UNP Q9HZX3
A	165	ASP	-	expression tag	UNP Q9HZX3
A	166	LYS	-	expression tag	UNP Q9HZX3
A	167	ILE	-	expression tag	UNP Q9HZX3
A	168	HIS	-	expression tag	UNP Q9HZX3
A	169	HIS	-	expression tag	UNP Q9HZX3
A	170	HIS	-	expression tag	UNP Q9HZX3
A	171	HIS	-	expression tag	UNP Q9HZX3
A	172	HIS	-	expression tag	UNP Q9HZX3
A	173	HIS	-	expression tag	UNP Q9HZX3
A	174	HIS	-	expression tag	UNP Q9HZX3
A	175	HIS	-	expression tag	UNP Q9HZX3
A	176	HIS	-	expression tag	UNP Q9HZX3
A	177	HIS	-	expression tag	UNP Q9HZX3
A	178	GLY	-	expression tag	UNP Q9HZX3
A	179	VAL	-	expression tag	UNP Q9HZX3

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	287	Total	O	1	24
			309	309		

- Molecule 1: Protein-glutamine gamma-glutamyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.64Å 71.64Å 164.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.50 – 1.60 43.50 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.50-1.60) 99.9 (43.50-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.160 , 0.194 (Not available) , 0.195	Depositor DCC
R_{free} test set	2869 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2832	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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: CL, PO4

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	1.02	3/2637 (0.1%)	1.05	1/3582 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	HIS	N-CA	-6.57	1.38	1.46
1	A	477	GLY	N-CA	5.20	1.51	1.45
1	A	313	LEU	N-CA	-5.04	1.40	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	ASP	CA-CB-CG	5.27	117.87	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	245[A]	ARG	Sidechain
1	A	245[B]	ARG	Sidechain
1	A	473[A]	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	473[B]	ARG	Sidechain

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	2487	0	2468	74	0
2	A	35	0	0	2	0
3	A	1	0	0	0	0
4	A	309	0	0	18	0
All	All	2832	0	2468	76	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 15.

All (76) 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:235[B]:ARG:HD2	1:A:286[B]:ASP:OD1	1.40	1.19
1:A:334:ARG:NH1	4:A:772[B]:HOH:O	1.78	1.15
1:A:230:GLU:HG2	4:A:651:HOH:O	1.48	1.12
1:A:235[B]:ARG:CD	1:A:286[B]:ASP:OD1	2.01	1.07
2:A:502:PO4:O2	4:A:758[B]:HOH:O	1.71	1.05
1:A:245[B]:ARG:HH11	1:A:245[B]:ARG:HG3	1.31	0.93
1:A:202[A]:MET:CE	1:A:405:ALA:HB2	2.01	0.91
1:A:306[A]:ARG:CZ	4:A:603:HOH:O	2.20	0.88
1:A:286[B]:ASP:OD2	4:A:842[B]:HOH:O	1.91	0.87
1:A:202[A]:MET:CE	1:A:405:ALA:CB	2.57	0.83
1:A:245[B]:ARG:HG3	1:A:245[B]:ARG:NH1	1.88	0.81
1:A:226:LEU:HD11	1:A:440[A]:LEU:HD11	1.67	0.77
1:A:202[A]:MET:HE3	1:A:405:ALA:CB	2.16	0.76
1:A:479[B]:GLU:HG3	1:A:480:GLN:HE22	1.50	0.75
1:A:342:MET:HE3	1:A:343:HIS:CE1	2.21	0.75
1:A:202[A]:MET:HE3	1:A:405:ALA:HB2	1.68	0.74
1:A:479[B]:GLU:CG	1:A:480:GLN:HE22	2.00	0.74
1:A:202[A]:MET:HE1	1:A:405:ALA:HB2	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235[B]:ARG:HD3	1:A:286[B]:ASP:OD1	1.88	0.71
1:A:384:PRO:HB3	1:A:402:GLY:HA2	1.72	0.70
1:A:479[B]:GLU:HG3	1:A:480:GLN:NE2	2.07	0.69
1:A:219:ARG:NH2	4:A:601:HOH:O	2.20	0.69
1:A:306[A]:ARG:NH2	4:A:603:HOH:O	2.22	0.68
1:A:235[B]:ARG:HD2	1:A:286[B]:ASP:CG	2.17	0.67
1:A:250:ALA:O	1:A:252[B]:GLN:NE2	2.28	0.67
1:A:342:MET:HE3	1:A:343:HIS:NE2	2.10	0.65
1:A:445:PHE:O	1:A:478[B]:LEU:HD22	1.98	0.64
1:A:243:ASP:OD1	1:A:245[A]:ARG:HG3	2.00	0.61
1:A:226:LEU:HD11	1:A:440[A]:LEU:CD1	2.32	0.60
1:A:239[B]:MET:HE1	1:A:426:ALA:HB2	1.85	0.59
1:A:202[A]:MET:CE	1:A:405:ALA:HB1	2.34	0.57
1:A:256[B]:GLU:OE2	1:A:296:ARG:CG	2.52	0.57
1:A:411[B]:MET:HE1	1:A:463[B]:VAL:HG11	1.86	0.57
1:A:306[A]:ARG:HD2	4:A:603:HOH:O	2.03	0.57
1:A:371[A]:GLN:NE2	4:A:607:HOH:O	2.37	0.57
1:A:245[B]:ARG:HH11	1:A:245[B]:ARG:CG	2.10	0.57
1:A:478[A]:LEU:CD1	1:A:482:LEU:HB2	2.36	0.56
1:A:256[B]:GLU:CD	1:A:296:ARG:HG3	2.31	0.56
1:A:316:ARG:NH1	4:A:609[B]:HOH:O	2.39	0.56
1:A:371[B]:GLN:CG	1:A:375:HIS:CE1	2.91	0.53
1:A:479[B]:GLU:CD	1:A:480:GLN:HE22	2.17	0.53
1:A:306[A]:ARG:CD	4:A:603:HOH:O	2.57	0.52
1:A:371[B]:GLN:HG3	1:A:375:HIS:CE1	2.44	0.52
1:A:345:ASN:O	1:A:349[B]:ARG:HG3	2.09	0.52
1:A:479[B]:GLU:HG3	1:A:480:GLN:CD	2.35	0.52
1:A:479[B]:GLU:HG3	1:A:480:GLN:OE1	2.10	0.52
1:A:342:MET:CE	1:A:343:HIS:NE2	2.74	0.51
1:A:370:LEU:HD11	1:A:463[A]:VAL:HG21	1.94	0.50
1:A:243:ASP:OD1	1:A:245[A]:ARG:CG	2.60	0.49
1:A:306[A]:ARG:NE	4:A:603:HOH:O	2.35	0.49
1:A:466[A]:THR:HG23	4:A:656:HOH:O	2.11	0.49
1:A:202[A]:MET:HE3	1:A:405:ALA:HB1	1.91	0.49
1:A:478[A]:LEU:HD11	1:A:482:LEU:HB2	1.95	0.48
1:A:480:GLN:CD	1:A:480:GLN:N	2.71	0.48
1:A:371[B]:GLN:CD	1:A:375:HIS:CE1	2.94	0.46
1:A:202[A]:MET:SD	1:A:207:ILE:HD11	2.56	0.46
1:A:299:SER:HB2	4:A:811:HOH:O	2.17	0.44
2:A:505:PO4:O1	4:A:602:HOH:O	2.21	0.44
1:A:202[B]:MET:HE3	1:A:239[B]:MET:SD	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256[B]:GLU:OE2	1:A:296:ARG:HG2	2.18	0.43
1:A:372:ARG:HD2	4:A:680:HOH:O	2.18	0.43
1:A:478[A]:LEU:HD11	1:A:482:LEU:HD12	2.01	0.43
1:A:236:ALA:HB1	1:A:281[B]:TRP:CD1	2.54	0.43
1:A:256[B]:GLU:CD	1:A:296:ARG:CG	2.92	0.43
1:A:479[B]:GLU:OE1	1:A:480:GLN:NE2	2.48	0.43
1:A:254:SER:OG	1:A:256[B]:GLU:OE2	2.32	0.42
1:A:202[A]:MET:HG2	1:A:239[A]:MET:SD	2.59	0.41
1:A:470:ALA:O	1:A:473[A]:ARG:HB3	2.20	0.41
1:A:371[B]:GLN:HG3	1:A:375:HIS:ND1	2.35	0.41
1:A:226:LEU:CD2	4:A:610[B]:HOH:O	2.68	0.40
1:A:230:GLU:CG	1:A:475[A]:GLU:OE1	2.69	0.40
1:A:257:ASP:OD1	1:A:260:HIS:HB2	2.20	0.40
1:A:371[B]:GLN:HE21	1:A:371[B]:GLN:HA	1.86	0.40
1:A:226:LEU:HD23	4:A:610[B]:HOH:O	2.21	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	312/338 (92%)	304 (97%)	8 (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	259/274 (94%)	256 (99%)	3 (1%)	63 43

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

Mol	Chain	Res	Type
1	A	274	MET
1	A	306[A]	ARG
1	A	306[B]	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	375	HIS
1	A	480	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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
2	PO4	A	502	-	4,4,4	0.44	0	6,6,6	2.06	2 (33%)
2	PO4	A	506	-	4,4,4	0.36	0	6,6,6	1.15	1 (16%)
2	PO4	A	501	-	4,4,4	1.08	0	6,6,6	0.88	0
2	PO4	A	505	-	4,4,4	0.75	0	6,6,6	1.63	3 (50%)
2	PO4	A	504	-	4,4,4	0.60	0	6,6,6	1.07	0
2	PO4	A	507	-	4,4,4	1.47	1 (25%)	6,6,6	1.48	1 (16%)
2	PO4	A	503	-	4,4,4	0.70	0	6,6,6	2.60	3 (50%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	507	PO4	P-O1	2.72	1.56	1.50

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	503	PO4	O4-P-O2	5.32	124.47	107.91
2	A	502	PO4	O4-P-O3	3.35	118.34	107.91
2	A	502	PO4	O3-P-O1	-3.00	100.33	110.95
2	A	505	PO4	O4-P-O2	2.43	115.48	107.91
2	A	507	PO4	O4-P-O2	-2.42	100.38	107.91
2	A	503	PO4	O4-P-O3	-2.34	100.63	107.91
2	A	503	PO4	O2-P-O1	-2.23	103.08	110.95
2	A	506	PO4	O4-P-O3	2.21	114.79	107.91
2	A	505	PO4	O3-P-O2	-2.07	101.49	107.91
2	A	505	PO4	O4-P-O1	-2.04	103.75	110.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	PO4	1	0
2	A	505	PO4	1	0

5.7 Other polymers [i](#)

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 [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	288/338 (85%)	0.07	14 (4%) 35 36	11, 25, 45, 73	27 (9%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	259	LEU	8.0
1	A	254	SER	4.3
1	A	195	VAL	4.2
1	A	482	LEU	4.2
1	A	253	TRP	3.9
1	A	258	ALA	3.6
1	A	306[A]	ARG	3.1
1	A	245[A]	ARG	2.9
1	A	255	GLY	2.8
1	A	256[A]	GLU	2.8
1	A	260	HIS	2.8
1	A	257	ASP	2.7
1	A	196	THR	2.5
1	A	353	ASP	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
2	PO4	A	506	5/5	0.75	0.15	59,76,88,106	0
2	PO4	A	503	5/5	0.82	0.12	44,50,67,93	0
2	PO4	A	505	5/5	0.86	0.39	32,71,85,85	5
2	PO4	A	502	5/5	0.89	0.13	49,63,70,103	0
2	PO4	A	504	5/5	0.89	0.09	43,55,70,70	0
2	PO4	A	507	5/5	0.90	0.23	38,44,62,68	5
2	PO4	A	501	5/5	0.92	0.11	35,41,47,49	5
3	CL	A	508	1/1	0.98	0.06	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.