



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4J05
Title : Crystal structure of a eukaryotic phosphate transporter
Authors : Pedersen, B.P.; Kumar, H.; Waight, A.B.; Risenmay, A.J.; Roe-Zurz, Z.; Chau, B.H.; Schlessinger, A.; Bonomi, M.; Harries, W.; Sali, A.; Johri, A.K.; Stroud, R.M.
Deposited on : 2013-01-30
Resolution : 2.90 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>

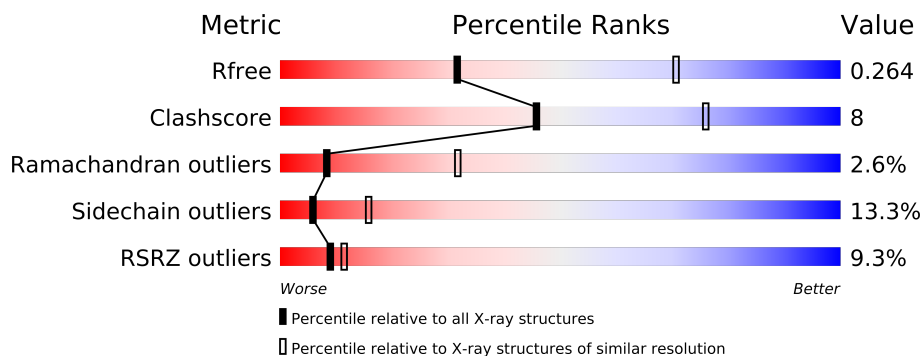
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.90 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	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

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	530	
1	B	530	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	PO4	A	600	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6590 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 Phosphate transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	422	Total	C	N	O	S	0	0	0
			3290	2173	543	558	16			
1	B	422	Total	C	N	O	S	0	0	0
			3290	2173	543	558	16			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP A8N031
A	0	PRO	-	EXPRESSION TAG	UNP A8N031
A	523	GLY	-	EXPRESSION TAG	UNP A8N031
A	524	GLY	-	EXPRESSION TAG	UNP A8N031
A	525	LEU	-	EXPRESSION TAG	UNP A8N031
A	526	VAL	-	EXPRESSION TAG	UNP A8N031
A	527	PRO	-	EXPRESSION TAG	UNP A8N031
A	528	ARG	-	EXPRESSION TAG	UNP A8N031
B	-1	GLY	-	EXPRESSION TAG	UNP A8N031
B	0	PRO	-	EXPRESSION TAG	UNP A8N031
B	523	GLY	-	EXPRESSION TAG	UNP A8N031
B	524	GLY	-	EXPRESSION TAG	UNP A8N031
B	525	LEU	-	EXPRESSION TAG	UNP A8N031
B	526	VAL	-	EXPRESSION TAG	UNP A8N031
B	527	PRO	-	EXPRESSION TAG	UNP A8N031
B	528	ARG	-	EXPRESSION TAG	UNP A8N031

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

ILE
PRO
GLY
GLY
LEU
VAL
PRO
ARG

4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	174.51Å 174.51Å 173.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	69.00 – 2.90 75.21 – 2.90	Depositor EDS
% Data completeness (in resolution range)	93.6 (69.00-2.90) 93.7 (75.21-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1069)	Depositor
R, R_{free}	0.222 , 0.259 0.231 , 0.264	Depositor DCC
R_{free} test set	1980 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	81.2	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 96.4	EDS
Estimated twinning fraction	0.043 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 40756 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6590	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: 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	0.57	0/3373	0.70	0/4567
1	B	0.53	0/3373	0.68	0/4567
All	All	0.55	0/6746	0.69	0/9134

There are no bond length outliers.

There are no bond angle outliers.

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	3290	0	22	24	0
1	B	3290	0	22	32	0
2	A	5	0	0	2	0
2	B	5	0	0	1	0
All	All	6590	0	44	55	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 8.

All (55) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:85:CYS:SG	1:A:459:LYS:NZ	2.45	0.89
1:A:335:SER:O	1:A:337:VAL:N	2.12	0.82
1:B:335:SER:O	1:B:337:VAL:N	2.17	0.78
1:B:335:SER:OG	1:B:336:VAL:N	2.21	0.74
1:A:335:SER:OG	1:A:336:VAL:N	2.22	0.71
1:A:117:ILE:O	1:A:121:SER:OG	2.08	0.70
1:B:159:ASP:OD2	1:B:444:THR:OG1	2.10	0.68
1:B:94:VAL:O	1:B:98:SER:N	2.27	0.68
1:B:103:PHE:O	1:B:105:TYR:N	2.27	0.68
1:A:301:VAL:O	1:A:305:SER:OG	2.12	0.68
1:B:117:ILE:O	1:B:121:SER:OG	2.15	0.65
1:B:105:TYR:O	1:B:107:LYS:N	2.30	0.65
1:B:376:THR:OG1	1:B:428:PHE:O	2.14	0.65
1:A:158:SER:OG	1:A:447:ARG:NH1	2.32	0.63
1:A:103:PHE:O	1:A:105:TYR:N	2.30	0.63
1:A:431:ASN:ND2	2:A:600:PO4:O1	2.31	0.63
1:A:177:GLN:OE1	1:A:373:TYR:OH	2.17	0.63
1:B:108:GLU:OE1	1:B:108:GLU:N	2.35	0.59
1:B:440:GLU:OE1	1:B:502:THR:OG1	2.19	0.58
1:A:105:TYR:O	1:A:107:LYS:N	2.36	0.58
1:B:85:CYS:SG	1:B:459:LYS:NZ	2.77	0.58
1:A:177:GLN:NE2	2:A:600:PO4:O4	2.37	0.56
1:A:376:THR:OG1	1:A:428:PHE:O	2.24	0.56
1:B:338:LEU:O	1:B:340:GLN:N	2.38	0.56
1:A:168:THR:OG1	1:A:381:ASP:OD2	2.23	0.56
1:A:108:GLU:N	1:A:108:GLU:OE1	2.39	0.56
1:B:158:SER:OG	1:B:447:ARG:NH1	2.41	0.54
1:B:208:ASP:OD1	1:B:211:TRP:NE1	2.40	0.54
1:B:301:VAL:O	1:B:305:SER:OG	2.25	0.53
1:A:338:LEU:O	1:A:340:GLN:N	2.42	0.52
1:A:335:SER:C	1:A:337:VAL:N	2.64	0.52
1:A:121:SER:O	1:B:227:TYR:OH	2.28	0.50
1:A:440:GLU:OE1	1:A:502:THR:OG1	2.30	0.49
1:B:335:SER:C	1:B:337:VAL:N	2.67	0.48
1:B:330:ILE:O	1:B:334:GLN:N	2.47	0.48
1:B:122:ALA:O	1:B:212:ARG:NH1	2.47	0.47
1:B:215:ILE:O	1:B:218:SER:OG	2.31	0.47
1:A:330:ILE:O	1:A:334:GLN:N	2.47	0.47
1:A:385:ARG:NH2	1:A:440:GLU:OE2	2.49	0.46
1:B:119:GLN:OE1	1:B:139:ARG:NH1	2.50	0.45
1:B:177:GLN:OE1	1:B:373:TYR:OH	2.36	0.44
1:B:100:GLY:O	1:B:107:LYS:NZ	2.51	0.44
1:A:122:ALA:O	1:A:212:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:338:LEU:C	1:B:340:GLN:N	2.73	0.42
1:A:196:LYS:CB	1:A:351:TYR:CD1	3.03	0.42
1:B:168:THR:OG1	1:B:381:ASP:OD2	2.38	0.42
1:B:485:PHE:O	1:B:488:THR:OG1	2.38	0.42
1:B:312:ASN:ND2	1:B:500:ASP:OD2	2.53	0.41
1:B:385:ARG:NE	1:B:440:GLU:OE1	2.53	0.41
1:A:311:ARG:NH1	1:A:500:ASP:OD1	2.54	0.41
1:B:328:TYR:OH	2:B:600:PO4:O3	2.39	0.41
1:B:196:LYS:CB	1:B:351:TYR:CD1	3.05	0.40
1:A:208:ASP:OD1	1:A:211:TRP:NE1	2.54	0.40
1:B:158:SER:O	1:B:162:ASN:N	2.54	0.40
1:B:311:ARG:NH1	1:B:500:ASP:OD1	2.54	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	418/530 (79%)	374 (90%)	33 (8%)	11 (3%)	8	32
1	B	418/530 (79%)	374 (90%)	33 (8%)	11 (3%)	8	32
All	All	836/1060 (79%)	748 (90%)	66 (8%)	22 (3%)	8	32

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	VAL
1	A	336	VAL
1	A	343	PHE
1	B	104	VAL
1	B	336	VAL
1	A	101	ARG
1	A	443	PRO
1	B	343	PHE

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Mol	Chain	Res	Type
1	B	443	PRO
1	A	103	PHE
1	A	335	SER
1	A	339	ALA
1	B	101	ARG
1	B	335	SER
1	B	339	ALA
1	A	310	PHE
1	B	103	PHE
1	B	106	GLY
1	B	310	PHE
1	A	106	GLY
1	B	205	HIS
1	A	150	TYR

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	342/433 (79%)	298 (87%)	44 (13%)	6	17
1	B	342/433 (79%)	295 (86%)	47 (14%)	5	15
All	All	684/866 (79%)	593 (87%)	91 (13%)	6	16

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	VAL
1	A	42	PHE
1	A	45	ASP
1	A	51	ILE
1	A	52	ILE
1	A	54	GLN
1	A	99	PHE
1	A	101	ARG
1	A	104	VAL
1	A	112	ILE
1	A	119	GLN

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Mol	Chain	Res	Type
1	A	124	SER
1	A	126	TRP
1	A	127	ASP
1	A	130	ARG
1	A	136	THR
1	A	163	ILE
1	A	166	ARG
1	A	189	ILE
1	A	195	PHE
1	A	198	ARG
1	A	200	LYS
1	A	206	ASP
1	A	225	THR
1	A	305	SER
1	A	313	LEU
1	A	314	LEU
1	A	323	VAL
1	A	336	VAL
1	A	337	VAL
1	A	347	THR
1	A	370	LEU
1	A	380	ILE
1	A	387	LYS
1	A	395	MET
1	A	398	LEU
1	A	403	LEU
1	A	412	LYS
1	A	416	LEU
1	A	436	ILE
1	A	441	LEU
1	A	446	ILE
1	A	447	ARG
1	A	468	VAL
1	B	35	VAL
1	B	42	PHE
1	B	45	ASP
1	B	51	ILE
1	B	52	ILE
1	B	73	ARG
1	B	86	VAL
1	B	101	ARG
1	B	104	VAL

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Mol	Chain	Res	Type
1	B	112	ILE
1	B	119	GLN
1	B	124	SER
1	B	126	TRP
1	B	127	ASP
1	B	130	ARG
1	B	136	THR
1	B	160	ARG
1	B	163	ILE
1	B	166	ARG
1	B	189	ILE
1	B	195	PHE
1	B	198	ARG
1	B	200	LYS
1	B	225	THR
1	B	226	LEU
1	B	305	SER
1	B	313	LEU
1	B	314	LEU
1	B	323	VAL
1	B	330	ILE
1	B	336	VAL
1	B	337	VAL
1	B	347	THR
1	B	370	LEU
1	B	380	ILE
1	B	387	LYS
1	B	394	ILE
1	B	395	MET
1	B	398	LEU
1	B	403	LEU
1	B	412	LYS
1	B	416	LEU
1	B	436	ILE
1	B	441	LEU
1	B	446	ILE
1	B	447	ARG
1	B	468	VAL

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

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 ⓘ

2 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		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	A	600	-	4,4,4	0.23	0	6,6,6	0.31	0
2	PO4	B	600	-	4,4,4	0.24	0	6,6,6	0.31	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
2	PO4	A	600	-	-	0/0/0/0	0/0/0/0
2	PO4	B	600	-	-	0/0/0/0	0/0/0/0

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.

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	422/530 (79%)	0.74	31 (7%) 15 18	67, 97, 178, 212	0
1	B	422/530 (79%)	0.89	48 (11%) 6 7	71, 102, 190, 236	0
All	All	844/1060 (79%)	0.81	79 (9%) 9 11	67, 100, 183, 236	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	PHE	14.2
1	B	104	VAL	13.3
1	B	102	LYS	11.9
1	B	197	HIS	9.4
1	B	336	VAL	8.5
1	A	336	VAL	8.2
1	B	152	MET	7.8
1	A	197	HIS	7.4
1	B	101	ARG	7.2
1	B	105	TYR	6.7
1	A	196	LYS	6.3
1	B	196	LYS	6.0
1	B	154	ALA	6.0
1	B	35	VAL	5.5
1	B	155	THR	5.5
1	A	162	ASN	5.4
1	A	103	PHE	5.2
1	B	151	PRO	5.1
1	B	150	TYR	5.0
1	B	160	ARG	5.0
1	B	107	LYS	5.0
1	B	157	VAL	4.6
1	A	154	ALA	4.4
1	A	157	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	159	ASP	3.8
1	A	198	ARG	3.7
1	B	158	SER	3.6
1	A	160	ARG	3.6
1	B	156	VAL	3.5
1	B	518	ARG	3.5
1	A	151	PRO	3.3
1	B	110	ILE	3.3
1	A	340	GLN	3.2
1	B	100	GLY	3.1
1	B	394	ILE	3.0
1	A	153	SER	3.0
1	A	102	LYS	3.0
1	B	165	ARG	2.9
1	A	446	ILE	2.9
1	A	379	LEU	2.6
1	B	229	ARG	2.6
1	B	387	LYS	2.6
1	B	383	VAL	2.6
1	B	153	SER	2.6
1	B	30	PRO	2.6
1	A	164	HIS	2.5
1	B	198	ARG	2.5
1	A	104	VAL	2.5
1	B	340	GLN	2.5
1	A	207	VAL	2.4
1	B	33	LYS	2.4
1	B	307	TRP	2.4
1	B	34	LEU	2.4
1	A	165	ARG	2.4
1	A	398	LEU	2.4
1	B	338	LEU	2.3
1	A	497	PHE	2.3
1	A	338	LEU	2.3
1	A	387	LYS	2.3
1	B	493	PHE	2.3
1	B	164	HIS	2.3
1	B	515	ARG	2.3
1	A	61	GLN	2.2
1	A	499	ILE	2.2
1	A	35	VAL	2.2
1	B	512	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	394	ILE	2.2
1	B	169	LEU	2.1
1	A	105	TYR	2.1
1	B	31	GLN	2.1
1	B	435	PHE	2.1
1	B	148	GLY	2.1
1	B	337	VAL	2.1
1	B	98	SER	2.1
1	B	398	LEU	2.1
1	B	44	LEU	2.0
1	A	380	ILE	2.0
1	A	69	LEU	2.0
1	B	207	VAL	2.0

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	PO4	A	600	5/5	0.27	2.21	116,124,128,128	0
2	PO4	B	600	5/5	0.31	0.34	101,111,115,116	0

6.5 Other polymers ⓘ

There are no such residues in this entry.