Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	1V04
Title	:	SERUM PARAOXONASE BY DIRECTED EVOLUTION
Authors	:	Harel, M.; Aharoni, A.; Gaidukov, L.; Brumshtein, B.; Khersonsky, O.; Yagur, S.; Meged, R.; Dvir, H.; Ravelli, R.B.G.; Mccarthy, A.; Toker, L.; Silman, I.; Sussman, J.L.; Tawfik, D.S.
Deposited on	:	2004-03-22
Resolution	:	2.20 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

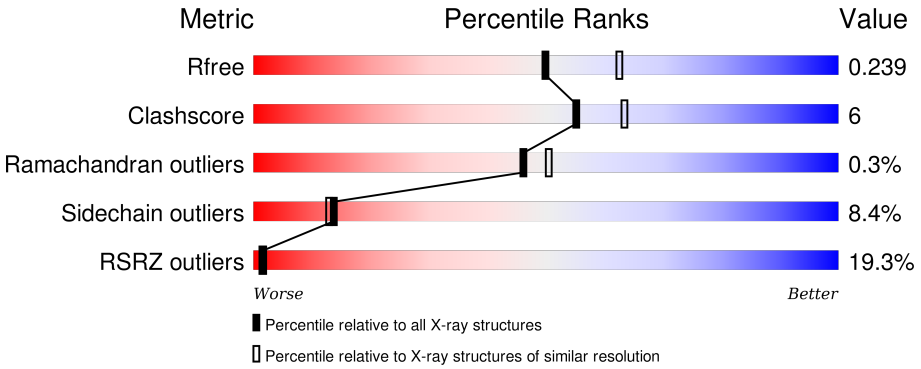
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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. 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	355	18%, 73%, 17%, 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2756 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.

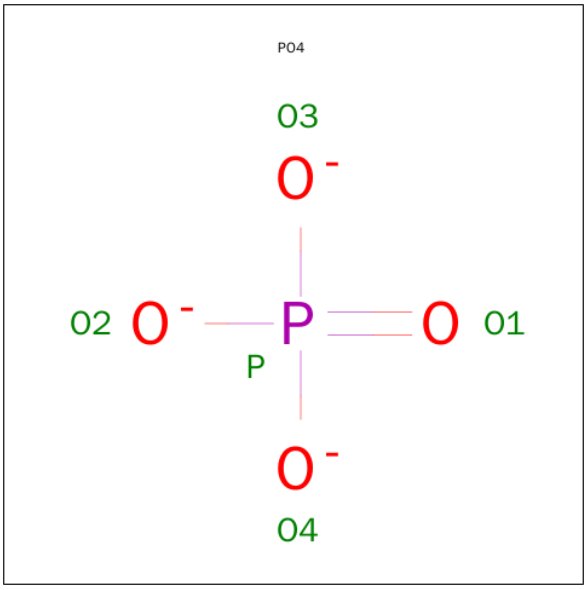
- Molecule 1 is a protein called SERUM PARAOXONASE/ARYLESTERASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	332	2634	1698	429	501	6	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	2	2	2	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 4 is water.

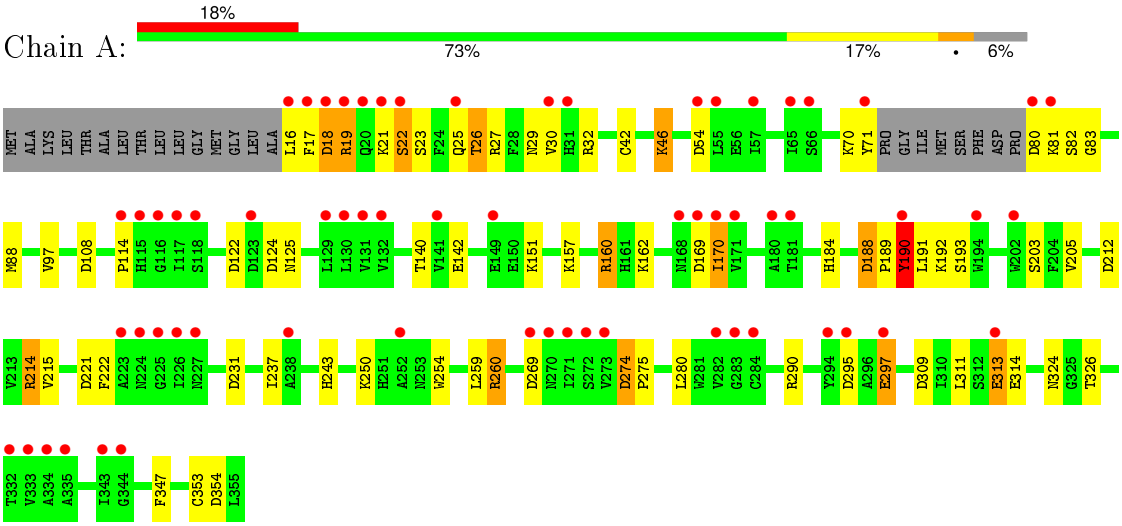
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	115	Total	O	0	0
			115	115		

3 Residue-property plots (i)

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 (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: SERUM PARAOXONASE/ARYLESTERASE 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	98.44Å 98.44Å 139.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 29.68 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-2.20) 99.7 (29.68-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.87 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.217 0.233 , 0.239	Depositor DCC
R_{free} test set	3516 reflections (9.96%)	DCC
Wilson B-factor (Å^2)	45.3	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 36.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 35311 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2756	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, 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	1.12	5/2701 (0.2%)	1.09	16/3678 (0.4%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	347	PHE	CE2-CZ	5.83	1.48	1.37
1	A	71	TYR	CB-CG	5.72	1.60	1.51
1	A	215	VAL	CB-CG1	5.71	1.64	1.52
1	A	142	GLU	CD-OE2	5.65	1.31	1.25
1	A	190	TYR	CD1-CE1	5.65	1.47	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	188	ASP	CB-CG-OD2	8.93	126.34	118.30
1	A	290	ARG	NE-CZ-NH2	-8.05	116.27	120.30
1	A	309	ASP	CB-CG-OD2	7.92	125.43	118.30
1	A	274	ASP	CB-CG-OD2	7.89	125.40	118.30
1	A	295	ASP	CB-CG-OD2	7.12	124.71	118.30
1	A	18	ASP	CB-CG-OD2	6.48	124.13	118.30
1	A	54	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	221	ASP	CB-CG-OD2	5.96	123.67	118.30
1	A	354	ASP	CB-CG-OD2	5.70	123.43	118.30
1	A	32	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	108	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	295	ASP	CB-CG-OD1	-5.40	113.44	118.30
1	A	231	ASP	CB-CG-OD2	5.38	123.14	118.30
1	A	269	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	214	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	212	ASP	CB-CG-OD2	5.06	122.85	118.30

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	2634	0	2579	32	0
2	A	2	0	0	0	0
3	A	5	0	0	0	0
4	A	115	0	0	4	0
All	All	2756	0	2579	32	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 6.

All (32) 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:190:TYR:CE2	4:A:2056:HOH:O	2.20	0.93
1:A:190:TYR:HE2	4:A:2056:HOH:O	1.52	0.92
1:A:324:ASN:OD1	1:A:326:THR:HG23	1.73	0.88
1:A:42:CYS:HG	1:A:353:CYS:HG	0.92	0.88
1:A:169:ASP:OD1	1:A:170:ILE:N	2.12	0.81
1:A:124:ASP:O	1:A:125:ASN:HB2	1.94	0.66
1:A:250:LYS:HE2	1:A:254:TRP:CZ3	2.34	0.62
1:A:274:ASP:OD1	1:A:275:PRO:HD2	1.99	0.62
1:A:27:ARG:O	1:A:243:HIS:HE1	1.83	0.61
1:A:140:THR:HG22	1:A:160:ARG:HD3	1.81	0.61
1:A:17:PHE:C	1:A:19:ARG:H	2.07	0.58
1:A:122:ASP:OD1	1:A:124:ASP:OD1	2.23	0.56
1:A:259:LEU:C	1:A:260:ARG:HG2	2.26	0.55
1:A:25:GLN:NE2	1:A:30:VAL:HG21	2.23	0.53
1:A:42:CYS:HG	1:A:353:CYS:CB	2.20	0.53
1:A:124:ASP:O	1:A:125:ASN:CB	2.58	0.52
1:A:160:ARG:NH1	4:A:2046:HOH:O	2.42	0.51
1:A:205:VAL:HG21	1:A:237:ILE:HD13	1.92	0.51
1:A:22:SER:O	1:A:26:THR:CG2	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:LYS:HE2	1:A:254:TRP:CE3	2.49	0.47
1:A:23:SER:O	1:A:27:ARG:HG3	2.14	0.47
1:A:21:LYS:O	1:A:25:GLN:HG3	2.16	0.45
1:A:184:HIS:CD2	1:A:192:LYS:HB2	2.52	0.45
1:A:280:LEU:HD12	1:A:280:LEU:N	2.32	0.43
1:A:88:MET:HG3	1:A:97:VAL:HG12	2.00	0.43
1:A:46:LYS:HB2	1:A:46:LYS:HE2	1.47	0.42
1:A:311:LEU:HD23	1:A:311:LEU:HA	1.77	0.41
1:A:297:GLU:HG2	4:A:2093:HOH:O	2.19	0.41
1:A:313:GLU:HG2	1:A:313:GLU:H	1.40	0.41
1:A:188:ASP:HA	1:A:189:PRO:HD3	1.94	0.41
1:A:27:ARG:O	1:A:243:HIS:CE1	2.70	0.40
1:A:83:GLY:HA3	1:A:114:PRO:HD3	2.03	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	328/355 (92%)	314 (96%)	13 (4%)	1 (0%)	46 50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASP

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	296/313 (95%)	271 (92%)	25 (8%)	14 13

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU
1	A	19	ARG
1	A	22	SER
1	A	26	THR
1	A	29	ASN
1	A	46	LYS
1	A	70	LYS
1	A	80	ASP
1	A	81	LYS
1	A	82	SER
1	A	151	LYS
1	A	157	LYS
1	A	160	ARG
1	A	162	LYS
1	A	170	ILE
1	A	190	TYR
1	A	191	LEU
1	A	193	SER
1	A	203	SER
1	A	214	ARG
1	A	222	PHE
1	A	260	ARG
1	A	297	GLU
1	A	313	GLU
1	A	314	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	50	ASN
1	A	91	ASN
1	A	147	GLN
1	A	197	HIS

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Mol	Chain	Res	Type
1	A	243	HIS
1	A	251	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	PO4	A	1358	2	4,4,4	0.82	0	6,6,6	0.26	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	PO4	A	1358	2	-	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.

No monomer is involved in short contacts.

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, 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>2	OWAB(Å^2)	Q<0.9
1	A	332/355 (93%)	0.73	64 (19%) 2 1	25, 36, 49, 61	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	71	TYR	11.1
1	A	17	PHE	8.1
1	A	16	LEU	7.2
1	A	18	ASP	7.1
1	A	80	ASP	6.3
1	A	55	LEU	5.4
1	A	20	GLN	5.2
1	A	294	TYR	5.1
1	A	190	TYR	4.9
1	A	19	ARG	4.7
1	A	117	ILE	4.6
1	A	226	ILE	4.6
1	A	81	LYS	4.5
1	A	333	VAL	4.4
1	A	271	ILE	4.4
1	A	31	HIS	4.4
1	A	194	TRP	4.3
1	A	170	ILE	4.2
1	A	21	LYS	4.1
1	A	116	GLY	3.8
1	A	123	ASP	3.7
1	A	270	ASN	3.7
1	A	335	ALA	3.5
1	A	169	ASP	3.4
1	A	171	VAL	3.4
1	A	225	GLY	3.4
1	A	334	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	149	GLU	3.4
1	A	132	VAL	3.3
1	A	272	SER	3.3
1	A	297	GLU	3.2
1	A	181	THR	3.2
1	A	65	ILE	3.1
1	A	238	ALA	3.1
1	A	282	VAL	3.0
1	A	168	ASN	3.0
1	A	25	GLN	2.9
1	A	224	ASN	2.9
1	A	332	THR	2.9
1	A	66	SER	2.8
1	A	131	VAL	2.8
1	A	54	ASP	2.8
1	A	118	SER	2.8
1	A	30	VAL	2.8
1	A	344	GLY	2.7
1	A	223	ALA	2.7
1	A	180	ALA	2.6
1	A	227	ASN	2.5
1	A	283	GLY	2.5
1	A	141	VAL	2.5
1	A	22	SER	2.4
1	A	115	HIS	2.4
1	A	295	ASP	2.4
1	A	313	GLU	2.3
1	A	269	ASP	2.3
1	A	284	CYS	2.3
1	A	343	ILE	2.2
1	A	57	ILE	2.2
1	A	130	LEU	2.2
1	A	129	LEU	2.1
1	A	202	TRP	2.1
1	A	273	VAL	2.1
1	A	252	ALA	2.0
1	A	114	PRO	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 carbohydrates 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. 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, 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	LLDF	B-factors(Å^2)	Q<0.9
3	PO4	A	1358	5/5	0.99	0.20	-1.16	41,43,47,49	0
2	CA	A	1356	1/1	0.97	0.28	-1.85	37,37,37,37	0
2	CA	A	1357	1/1	0.96	0.17	-4.50	37,37,37,37	0

6.5 Other polymers (i)

There are no such residues in this entry.