



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:33 AM GMT

PDB ID : 4D94
Title : Crystal Structure of TEP1r
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Deposited on : 2012-01-11
Resolution : 2.70 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>

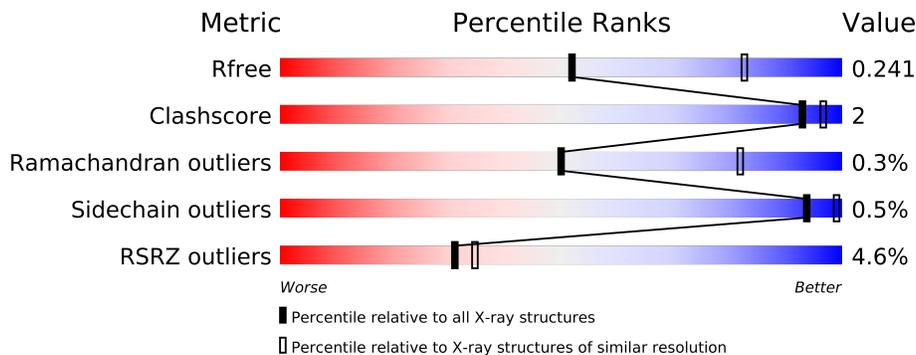
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.70 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	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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	1325	

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	NAG	A	2001	-	X
5	NA	A	2008	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 10466 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.

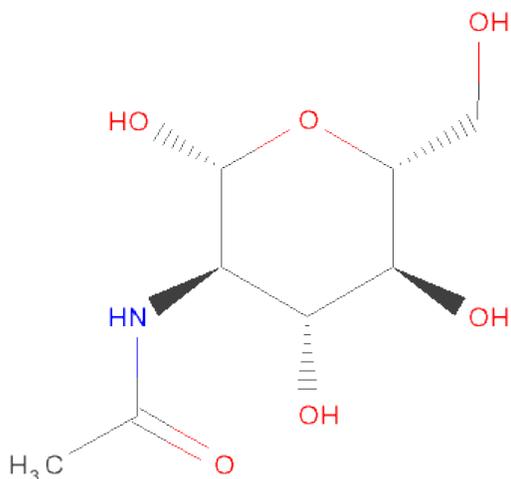
- Molecule 1 is a protein called Thioester-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1274	10246	6566	1708	1928	44	0	4	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1339	GLY	-	LINKER	UNP C9XI66
A	1340	GLY	-	LINKER	UNP C9XI66
A	1341	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1342	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1343	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1344	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1345	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1346	HIS	-	EXPRESSION TAG	UNP C9XI66

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1339	GLY	-	LINKER	UNP C9XI66
A	1340	GLY	-	LINKER	UNP C9XI66
A	1341	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1342	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1343	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1344	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1345	HIS	-	EXPRESSION TAG	UNP C9XI66
A	1346	HIS	-	EXPRESSION TAG	UNP C9XI66

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Na	0	0
			2	2		

- Molecule 6 is water.

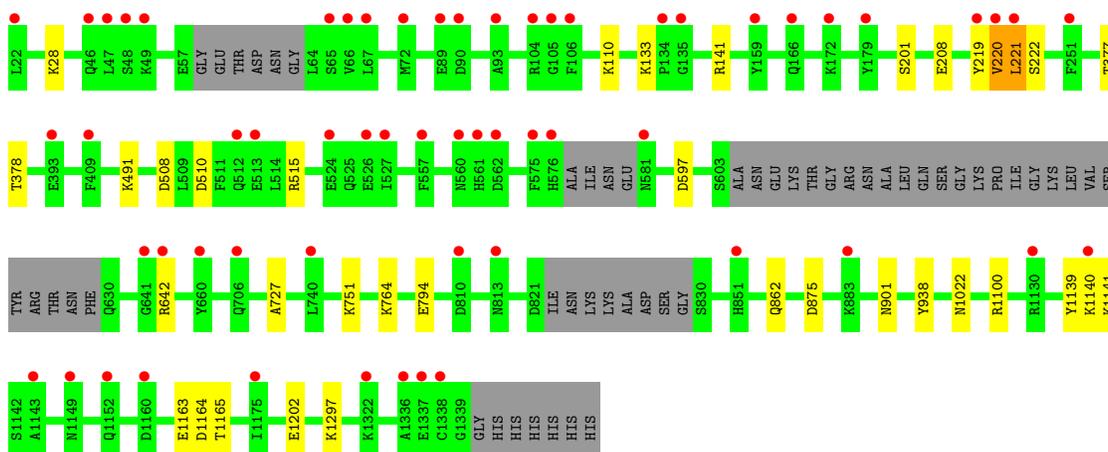
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	133	Total 133	O 133	0	0

3 Residue-property plots

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: Thioester-containing protein 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	150.51Å 150.51Å 226.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.87 – 2.70 43.87 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.87-2.70) 99.8 (43.87-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.219 , 0.244 0.218 , 0.241	Depositor DCC
R_{free} test set	3628 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	57.4	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 71857 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10466	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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: NA, NAG, CL

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	0.29	0/10455	0.54	1/14154 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	ARG	NE-CZ-NH1	5.93	123.26	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 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	10246	0	2	18	0
2	A	56	0	52	3	0
3	A	28	0	25	0	0
4	A	1	0	0	0	0
5	A	2	0	0	0	0
6	A	133	0	0	5	0
All	All	10466	0	79	18	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 2.

All (18) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:220:VAL:O	1:A:222:SER:N	2.33	0.62
1:A:110:LYS:NZ	1:A:597:ASP:OD1	2.33	0.61
1:A:1022:ASN:OD1	6:A:2279:HOH:O	2.16	0.61
1:A:491:LYS:NZ	1:A:508:ASP:OD2	2.35	0.59
1:A:1139:TYR:O	1:A:1141:LYS:N	2.35	0.58
1:A:727:ALA:O	1:A:764:LYS:NZ	2.37	0.57
1:A:219:TYR:O	1:A:221:LEU:N	2.38	0.56
1:A:510:ASP:OD1	1:A:515:ARG:NH1	2.40	0.55
1:A:901:ASN:ND2	6:A:2203:HOH:O	2.39	0.55
1:A:28:LYS:NZ	6:A:2227:HOH:O	2.39	0.54
1:A:377:THR:OG1	1:A:378:THR:N	2.45	0.50
1:A:201:SER:OG	2:A:2001:NAG:O6	2.33	0.46
1:A:208:GLU:CD	2:A:2001:NAG:H62	2.38	0.43
1:A:1100:ARG:NH2	6:A:2252:HOH:O	2.50	0.43
1:A:1297:LYS:NZ	6:A:2318:HOH:O	2.51	0.43
1:A:208:GLU:OE1	2:A:2001:NAG:H62	2.19	0.43
1:A:1163:GLU:O	1:A:1165:THR:N	2.52	0.42
1:A:875:ASP:OD1	1:A:938:TYR:OH	2.40	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	1268/1325 (96%)	1206 (95%)	58 (5%)	4 (0%)	50 82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	VAL
1	A	221	LEU

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Mol	Chain	Res	Type
1	A	1140	LYS
1	A	1164	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	1138/1174 (97%)	1132 (100%)	6 (0%)	94 99

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	LYS
1	A	642	ARG
1	A	751	LYS
1	A	794	GLU
1	A	862	GLN
1	A	1202	GLU

Some 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 chains 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](#)

2 carbohydrates 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
3	NAG	A	2004	1,3	12,14,15	1.01	1 (8%)	15,19,21	1.34	2 (13%)
3	NAG	A	2005	3	12,14,15	1.13	2 (16%)	15,19,21	1.41	3 (20%)

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	NAG	A	2004	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2005	3	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2005	NAG	C2-N2	-2.79	1.43	1.46
3	A	2005	NAG	O5-C5	-2.05	1.41	1.45
3	A	2004	NAG	C2-N2	-2.01	1.44	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2005	NAG	C3-C2-N2	-3.27	106.78	111.76
3	A	2005	NAG	C6-C5-C4	-2.29	107.47	113.00
3	A	2005	NAG	C2-N2-C7	-2.24	119.33	123.09
3	A	2004	NAG	C3-C2-N2	-2.17	108.46	111.76
3	A	2004	NAG	C6-C5-C4	-2.02	108.11	113.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	NAG	A	2001	1	12,14,15	0.47	0	15,19,21	0.83	1 (6%)
2	NAG	A	2002	1	12,14,15	0.48	0	15,19,21	0.84	1 (6%)
2	NAG	A	2003	1	12,14,15	0.47	0	15,19,21	0.83	1 (6%)
2	NAG	A	2006	1	12,14,15	0.47	0	15,19,21	0.82	1 (6%)

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	NAG	A	2001	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2002	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2003	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2006	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2002	NAG	O5-C5-C6	2.41	109.51	106.98
2	A	2001	NAG	O5-C5-C6	2.37	109.47	106.98
2	A	2006	NAG	O5-C5-C6	2.36	109.46	106.98
2	A	2003	NAG	O5-C5-C6	2.34	109.44	106.98

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	1274/1325 (96%)	0.28	59 (4%) 31 35	29, 64, 123, 181	1 (0%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1152	GLN	5.3
1	A	66	VAL	4.3
1	A	562	ASP	4.3
1	A	1130	ARG	4.2
1	A	172	LYS	3.9
1	A	47	LEU	3.8
1	A	104	ARG	3.8
1	A	1140	LYS	3.8
1	A	219	TYR	3.6
1	A	393	GLU	3.6
1	A	251	PHE	3.6
1	A	1338	CYS	3.4
1	A	1336	ALA	3.4
1	A	512	GLN	3.3
1	A	105	GLY	3.3
1	A	1175	ILE	3.2
1	A	557	PHE	3.2
1	A	135	GLY	3.2
1	A	813	ASN	3.1
1	A	46	GLN	3.0
1	A	524	GLU	2.9
1	A	1160	ASP	2.9
1	A	179	TYR	2.9
1	A	642	ARG	2.8
1	A	740	LEU	2.8
1	A	561	HIS	2.8
1	A	67	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	581	ASN	2.7
1	A	106	PHE	2.7
1	A	220	VAL	2.7
1	A	1149	ASN	2.6
1	A	72	MET	2.6
1	A	560	ASN	2.5
1	A	89	GLU	2.4
1	A	1322	LYS	2.4
1	A	513	GLU	2.4
1	A	1143	ALA	2.4
1	A	49	LYS	2.3
1	A	409	PHE	2.3
1	A	1337	GLU	2.3
1	A	90	ASP	2.3
1	A	576	HIS	2.3
1	A	706	GLN	2.3
1	A	159	TYR	2.3
1	A	526	GLU	2.3
1	A	93	ALA	2.2
1	A	65	SER	2.2
1	A	166	GLN	2.2
1	A	48	SER	2.2
1	A	575	PHE	2.2
1	A	660	TYR	2.2
1	A	851[A]	HIS	2.1
1	A	527	ILE	2.1
1	A	22	LEU	2.1
1	A	883	LYS	2.1
1	A	641	GLY	2.1
1	A	134	PRO	2.0
1	A	810	ASP	2.0
1	A	221	LEU	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](#)

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
3	NAG	A	2004	14/15	0.21	-0.14	89,100,109,117	0
3	NAG	A	2005	14/15	0.21	-	105,126,135,137	0

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
5	NA	A	2008	1/1	0.54	16.20	47,47,47,47	0
2	NAG	A	2001	14/15	0.32	2.55	94,115,124,124	0
2	NAG	A	2002	14/15	0.22	1.84	58,75,98,109	0
2	NAG	A	2003	14/15	0.17	0.71	57,75,86,88	0
5	NA	A	2009	1/1	0.19	-0.22	78,78,78,78	0
2	NAG	A	2006	14/15	0.17	-2.35	86,109,117,121	0
4	CL	A	2007	1/1	0.09	-2.50	43,43,43,43	0

6.5 Other polymers

There are no such residues in this entry.