



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:51 PM GMT

PDB ID : 2J0L
Title : CRYSTAL STRUCTURE OF A THE ACTIVE CONFORMATION OF THE KINASE DOMAIN OF FOCAL ADHESION KINASE WITH A PHOSPHORYLATED ACTIVATION LOOP.
Authors : Lietha, D.; Cai, X.; Li, Y.; Schaller, M.D.; Eck, M.J.
Deposited on : 2006-08-03
Resolution : 2.30 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>

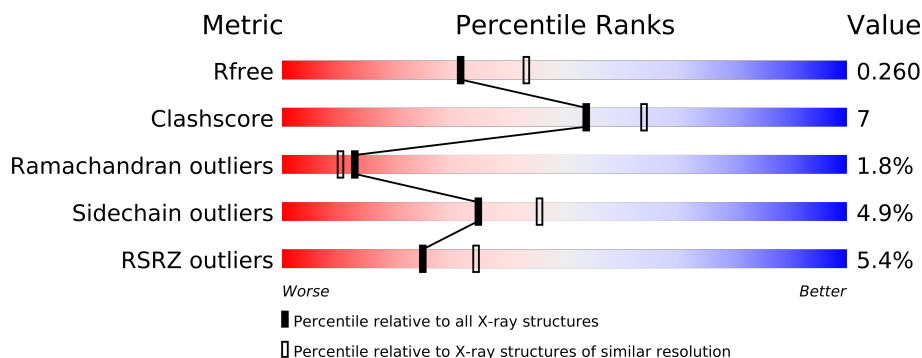
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.30 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	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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	276	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 2372 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 FOCAL ADHESION KINASE 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	276	2238	1421	385	411	2	19	67	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	556	SER	ALA	CONFLICT	UNP Q00944
A	557	ASN	THR	CONFLICT	UNP Q00944

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).

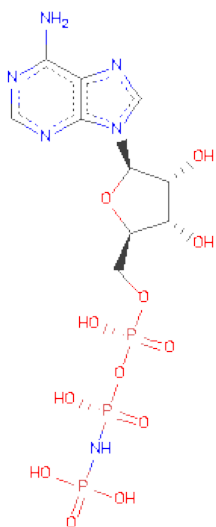


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

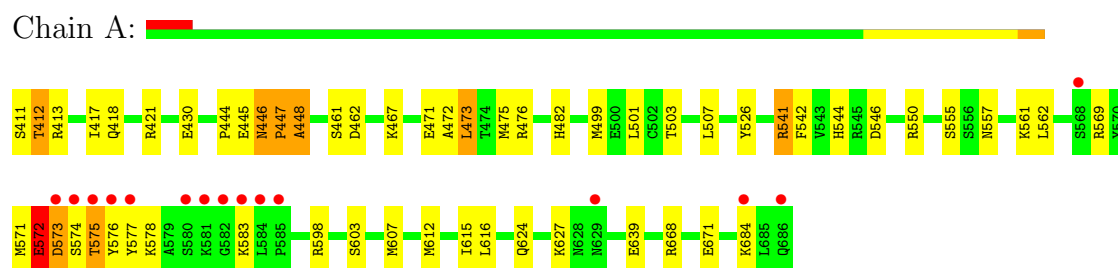
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	97	Total	O	0	0
			97	97		

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: FOCAL ADHESION KINASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.31Å 71.81Å 86.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.48 – 2.30 43.47 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.0 (43.48-2.30) 92.0 (43.47-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.263 0.207 , 0.260	Depositor DCC
R_{free} test set	568 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 11861 reflections (0.008%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2372	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.09% 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: MG, ANP, SO4, PTR

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	0.91	8/2256 (0.4%)	0.92	10/3043 (0.3%)

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	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	541	ARG	NE-CZ	-19.14	1.08	1.33
1	A	639	GLU	CG-CD	-17.70	1.25	1.51
1	A	671	GLU	CG-CD	-15.57	1.28	1.51
1	A	430	GLU	CG-CD	-12.82	1.32	1.51
1	A	627	LYS	CG-CD	-8.03	1.25	1.52
1	A	684	LYS	CD-CE	-6.29	1.35	1.51
1	A	572	GLU	CB-CG	6.00	1.63	1.52
1	A	578	LYS	CB-CG	-5.93	1.36	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	541	ARG	NE-CZ-NH2	-20.84	109.88	120.30
1	A	541	ARG	NE-CZ-NH1	16.03	128.31	120.30
1	A	684	LYS	CG-CD-CE	13.52	152.44	111.90
1	A	639	GLU	CB-CG-CD	13.43	150.47	114.20
1	A	671	GLU	CB-CG-CD	9.03	138.57	114.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	LYS	CG-CD-CE	7.13	133.31	111.90
1	A	639	GLU	CG-CD-OE2	6.62	131.54	118.30
1	A	639	GLU	CG-CD-OE1	-6.23	105.84	118.30
1	A	684	LYS	CD-CE-NZ	6.06	125.63	111.70
1	A	627	LYS	CB-CG-CD	5.96	127.08	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	541	ARG	Sidechain

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	2238	0	2236	30	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
4	A	31	0	13	0	0
5	A	97	0	0	1	0
All	All	2372	0	2249	30	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 7.

All (30) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:575:THR:HG22	1:A:576:PTR:HD2	1.50	0.91
1:A:575:THR:CG2	1:A:576:PTR:HD2	2.10	0.81
1:A:571:MET:C	1:A:573:ASP:H	1.93	0.72
1:A:576:PTR:HB2	1:A:598:ARG:HG2	1.79	0.65
1:A:546:ASP:OD2	1:A:550:ARG:NH2	2.30	0.64
1:A:501:LEU:HD23	1:A:503:THR:HG22	1.83	0.60
1:A:544:HIS:HD2	1:A:546:ASP:H	1.54	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:555:SER:OG	1:A:561:LYS:HE3	2.09	0.53
1:A:472:ALA:HA	1:A:475:MET:HE2	1.88	0.53
1:A:571:MET:C	1:A:573:ASP:N	2.61	0.53
1:A:612:MET:O	1:A:616:LEU:HD23	2.10	0.51
1:A:624:GLN:NE2	5:A:2068:HOH:O	2.39	0.50
1:A:575:THR:CG2	1:A:576:PTR:CD2	2.89	0.47
1:A:473:LEU:O	1:A:476:ARG:HG2	2.16	0.45
1:A:576:PTR:HB2	1:A:598:ARG:CG	2.45	0.45
1:A:411:SER:OG	1:A:412:THR:N	2.50	0.45
1:A:572:GLU:C	1:A:574:SER:H	2.20	0.44
1:A:507:LEU:HD21	1:A:615:ILE:HG12	1.99	0.44
1:A:482:HIS:HA	1:A:561:LYS:HG2	1.99	0.43
1:A:447:PRO:HB2	1:A:448:ALA:H	1.54	0.43
1:A:576:PTR:CE2	1:A:576:PTR:O1P	2.63	0.43
1:A:576:PTR:O1P	1:A:576:PTR:HE2	2.18	0.43
1:A:417:ILE:HG22	1:A:418:GLN:N	2.34	0.43
1:A:569:ARG:HG2	1:A:577:PTR:CE2	2.49	0.42
1:A:421:ARG:HH11	1:A:444:PRO:HD3	1.85	0.42
1:A:526:TYR:OH	1:A:557:ASN:O	2.30	0.42
1:A:446:ASN:CG	1:A:446:ASN:O	2.58	0.41
1:A:471:GLU:HG2	1:A:475:MET:CE	2.51	0.41
1:A:471:GLU:HG2	1:A:475:MET:HE1	2.03	0.41
1:A:603:SER:O	1:A:607:MET:HG3	2.22	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	273/276 (99%)	260 (95%)	8 (3%)	5 (2%)	13 10

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	412	THR
1	A	447	PRO
1	A	448	ALA
1	A	572	GLU
1	A	573	ASP

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	245/244 (100%)	233 (95%)	12 (5%)	35	45

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	413	ARG
1	A	445	GLU
1	A	446	ASN
1	A	461	SER
1	A	462	ASP
1	A	473	LEU
1	A	499	MET
1	A	542	PHE
1	A	562	LEU
1	A	575	THR
1	A	583	LYS
1	A	668	ARG

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	437	HIS
1	A	446	ASN
1	A	458	ASN
1	A	512	GLN
1	A	544	HIS
1	A	624	GLN

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Mol	Chain	Res	Type
1	A	637	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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	PTR	A	576	1	16,16,17	4.80	3 (18%)	20,22,24	1.01	1 (5%)
1	PTR	A	577	1	16,16,17	4.99	3 (18%)	20,22,24	1.33	1 (5%)

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	PTR	A	576	1	-	0/9/11/13	0/1/1/1
1	PTR	A	577	1	-	0/9/11/13	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	577	PTR	O-C	18.48	1.24	1.11
1	A	576	PTR	O-C	17.58	1.23	1.11
1	A	576	PTR	OH-CZ	-6.68	1.23	1.40
1	A	577	PTR	OH-CZ	-6.36	1.24	1.40
1	A	576	PTR	CA-C	3.63	1.55	1.48
1	A	577	PTR	CA-C	3.58	1.55	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	577	PTR	C-CA-N	-5.55	108.28	113.83
1	A	576	PTR	C-CA-N	3.81	117.63	113.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
2	SO4	A	1687	-	4,4,4	0.08	0	6,6,6	0.10	0
4	ANP	A	1689	3	33,33,33	3.40	9 (27%)	51,52,52	1.96	11 (21%)

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	SO4	A	1687	-	-	0/0/0/0	0/0/0/0
4	ANP	A	1689	3	-	1/18/38/38	0/1/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1689	ANP	PG-O1G	13.37	1.62	1.46
4	A	1689	ANP	PB-O1B	11.54	1.60	1.46
4	A	1689	ANP	O4'-C1'	4.08	1.47	1.41
4	A	1689	ANP	C4-N9	-3.03	1.33	1.37
4	A	1689	ANP	PA-O1A	2.37	1.60	1.51
4	A	1689	ANP	PG-O3G	-2.31	1.48	1.55
4	A	1689	ANP	C8-N9	-2.12	1.33	1.36
4	A	1689	ANP	PG-N3B	2.11	1.66	1.64
4	A	1689	ANP	PB-O2B	-2.04	1.49	1.55

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1689	ANP	N3-C2-N1	-8.44	121.65	128.71
4	A	1689	ANP	O4'-C1'-N9	4.27	112.42	108.44
4	A	1689	ANP	N3-C4-N9	4.27	133.15	125.43
4	A	1689	ANP	PB-N3B-PG	-4.19	123.02	130.07
4	A	1689	ANP	O2B-PB-N3B	3.10	115.02	106.61
4	A	1689	ANP	C5-C4-N3	-2.80	119.61	125.70
4	A	1689	ANP	O2G-PG-N3B	2.63	113.76	106.61
4	A	1689	ANP	O2G-PG-O1G	-2.60	106.93	113.60
4	A	1689	ANP	O1G-PG-N3B	-2.40	108.21	111.83
4	A	1689	ANP	C4-C5-N7	-2.16	107.67	109.52
4	A	1689	ANP	C2-N3-C4	2.16	120.15	114.01

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1689	ANP	O1G-PG-N3B-PB

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	276/276 (100%)	0.64	15 (5%)	25 34	26, 38, 63, 75	20 (7%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	582	GLY	11.8
1	A	575	THR	10.1
1	A	574	SER	10.0
1	A	581	LYS	8.0
1	A	573	ASP	7.4
1	A	580	SER	6.0
1	A	584	LEU	5.7
1	A	576	PTR	4.9
1	A	686	GLN	3.6
1	A	583	LYS	3.0
1	A	568	SER	2.5
1	A	684	LYS	2.3
1	A	629	ASN	2.3
1	A	585	PRO	2.3
1	A	577	PTR	2.1

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

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(\AA^2)	Q<0.9
1	PTR	A	576	16/17	0.45	0.69	73,74,75,76	0
1	PTR	A	577	16/17	0.28	-0.07	71,72,73,73	0

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(\AA^2)	Q<0.9
4	ANP	A	1689	31/31	0.10	-1.87	25,30,34,35	0
3	MG	A	1688	1/1	0.04	-3.07	37,37,37,37	0
2	SO4	A	1687	5/5	0.10	-3.67	102,102,102,102	0

6.5 Other polymers

There are no such residues in this entry.