



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2017 – 11:26 AM EDT

PDB ID : 5U6C
Title : Crystal structure of the Mer kinase domain in complex with a macrocyclic inhibitor
Authors : Gajiwala, K.S.; Ferre, R.A.
Deposited on : unknown
Resolution : 2.10 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

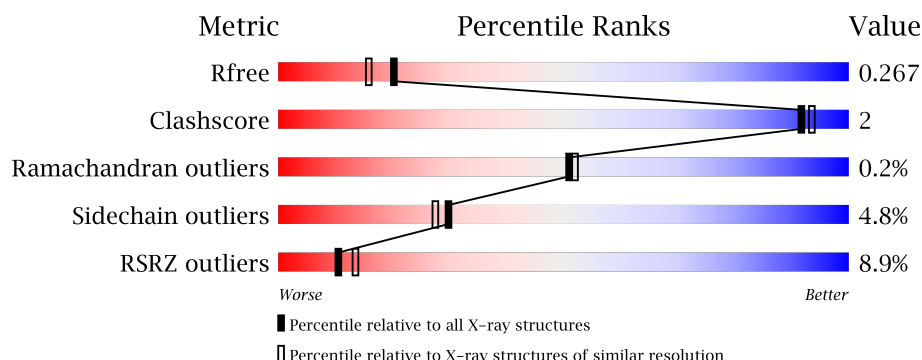
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 $\leq 5\%$. 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	315	
1	B	315	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4502 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 Tyrosine-protein kinase Mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	0	0
			2189	1399	363	406	21			
1	B	257	Total	C	N	O	S	0	1	0
			2075	1329	346	378	22			

There are 42 discrepancies between the modelled and reference sequences:

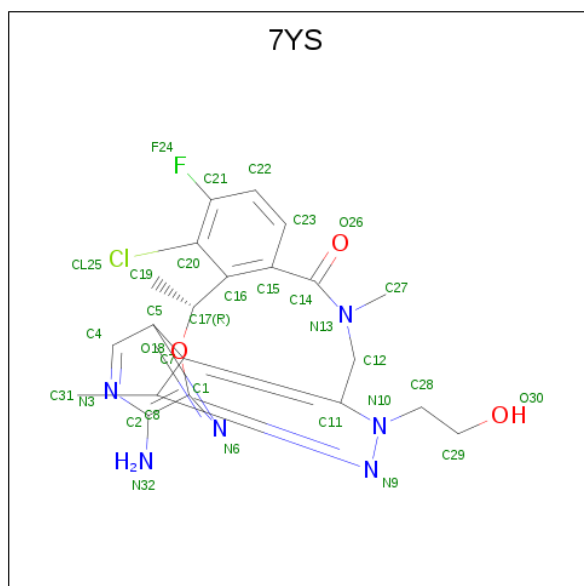
Chain	Residue	Modelled	Actual	Comment	Reference
A	550	MET	-	initiating methionine	UNP Q12866
A	551	GLY	-	expression tag	UNP Q12866
A	552	SER	-	expression tag	UNP Q12866
A	553	SER	-	expression tag	UNP Q12866
A	554	HIS	-	expression tag	UNP Q12866
A	555	HIS	-	expression tag	UNP Q12866
A	556	HIS	-	expression tag	UNP Q12866
A	557	HIS	-	expression tag	UNP Q12866
A	558	HIS	-	expression tag	UNP Q12866
A	559	HIS	-	expression tag	UNP Q12866
A	560	SER	-	expression tag	UNP Q12866
A	561	SER	-	expression tag	UNP Q12866
A	562	GLY	-	expression tag	UNP Q12866
A	563	GLU	-	expression tag	UNP Q12866
A	564	ASN	-	expression tag	UNP Q12866
A	565	LEU	-	expression tag	UNP Q12866
A	566	TYR	-	expression tag	UNP Q12866
A	567	PHE	-	expression tag	UNP Q12866
A	568	GLN	-	expression tag	UNP Q12866
A	569	GLY	-	expression tag	UNP Q12866
A	650	MET	ILE	conflict	UNP Q12866
B	550	MET	-	initiating methionine	UNP Q12866
B	551	GLY	-	expression tag	UNP Q12866
B	552	SER	-	expression tag	UNP Q12866
B	553	SER	-	expression tag	UNP Q12866

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Chain	Residue	Modelled	Actual	Comment	Reference
B	554	HIS	-	expression tag	UNP Q12866
B	555	HIS	-	expression tag	UNP Q12866
B	556	HIS	-	expression tag	UNP Q12866
B	557	HIS	-	expression tag	UNP Q12866
B	558	HIS	-	expression tag	UNP Q12866
B	559	HIS	-	expression tag	UNP Q12866
B	560	SER	-	expression tag	UNP Q12866
B	561	SER	-	expression tag	UNP Q12866
B	562	GLY	-	expression tag	UNP Q12866
B	563	GLU	-	expression tag	UNP Q12866
B	564	ASN	-	expression tag	UNP Q12866
B	565	LEU	-	expression tag	UNP Q12866
B	566	TYR	-	expression tag	UNP Q12866
B	567	PHE	-	expression tag	UNP Q12866
B	568	GLN	-	expression tag	UNP Q12866
B	569	GLY	-	expression tag	UNP Q12866
B	650	MET	ILE	conflict	UNP Q12866

- Molecule 2 is (10R)-7-amino-11-chloro-12-fluoro-1-(2-hydroxyethyl)-3,10,16-trimethyl-16,17-dihydro-1H-8,4-(azeno)pyrazolo[4,3-h][2,5,11]benzoxadiazacyclotetradecin-15(10H)-one (three-letter code: 7YS) (formula: C₂₁H₂₂ClFN₆O₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	F	N	O	0	0
			32	21	1	1	6	3		
2	B	1	Total	C	Cl	F	N	O	0	0
			32	21	1	1	6	3		

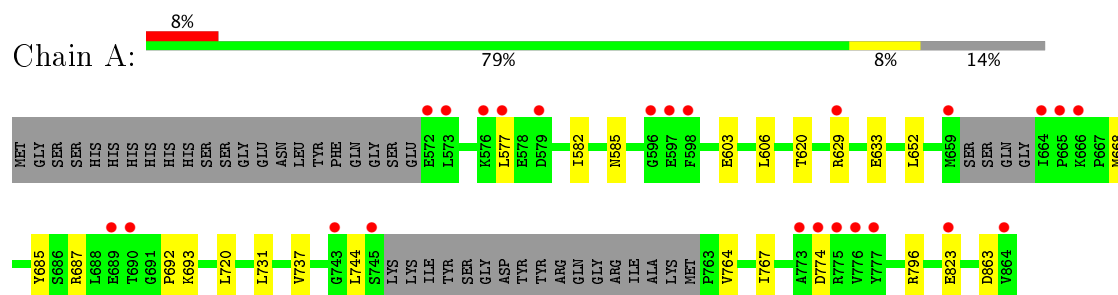
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	90	Total 90	O 90	0	0
3	B	84	Total 84	O 84	0	0

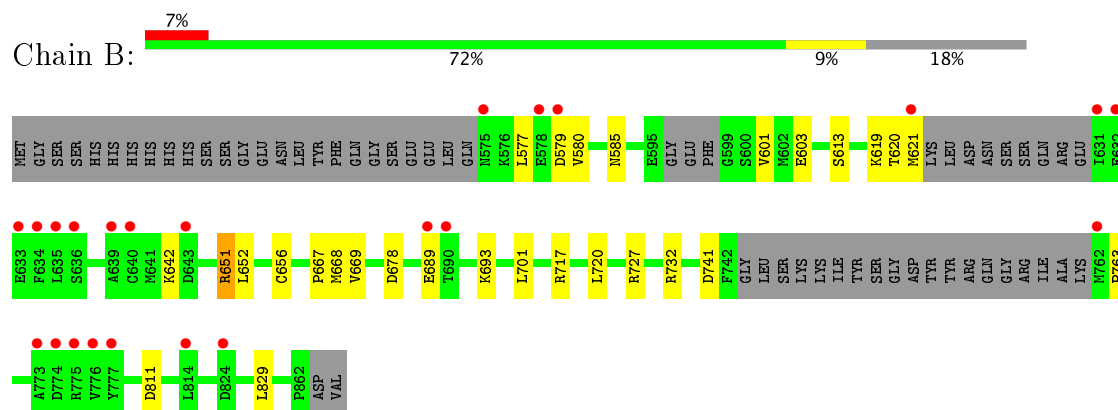
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Tyrosine-protein kinase Mer



• Molecule 1: Tyrosine-protein kinase Mer



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.69Å 92.33Å 69.27Å 90.00° 100.80° 90.00°	Depositor
Resolution (Å)	25.34 – 2.10 54.77 – 1.85	Depositor EDS
% Data completeness (in resolution range)	93.7 (25.34-2.10) 98.6 (54.77-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 1.86Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.211 , 0.257 0.221 , 0.267	Depositor DCC
R_{free} test set	1743 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4502	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 13.38% 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: 7YS

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	0.48	0/2233	0.63	0/3014
1	B	0.46	0/2117	0.61	0/2858
All	All	0.47	0/4350	0.62	0/5872

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2189	0	2196	7	0
1	B	2075	0	2090	10	0
2	A	32	0	0	0	0
2	B	32	0	0	0	0
3	A	90	0	0	0	0
3	B	84	0	0	0	0
All	All	4502	0	4286	16	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 2.

All (16) 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:B:652:LEU:HD13	1:B:669:VAL:HG13	1.84	0.59
1:A:823:GLU:HA	1:B:689:GLU:HG2	1.90	0.52
1:A:582:ILE:HG21	1:A:606:LEU:HD11	1.92	0.52
1:A:620:THR:HG22	1:A:668:MET:HG2	1.94	0.49
1:B:651[A]:ARG:HH12	1:B:732:ARG:HH12	1.59	0.48
1:B:621:MET:HB2	1:B:667:PRO:HG2	1.96	0.46
1:A:764:VAL:HA	1:A:767:ILE:HD12	1.97	0.46
1:A:685:TYR:HB3	1:A:692:PRO:HD2	1.98	0.45
1:B:620:THR:HG22	1:B:668:MET:HG2	1.98	0.44
1:B:727:ARG:HH22	1:B:763:PRO:HB3	1.81	0.44
1:B:601:VAL:HG22	1:B:619:LYS:HD3	1.99	0.43
1:B:701:LEU:HD21	1:B:829:LEU:HD13	1.99	0.43
1:B:580:VAL:HG23	1:B:642:LYS:HD2	2.02	0.41
1:A:731:LEU:HD23	1:A:737:VAL:HG22	2.01	0.41
1:A:687:ARG:HD2	1:A:796:ARG:HB3	2.03	0.41
1:B:651[A]:ARG:NH1	1:B:732:ARG:HH12	2.18	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	266/315 (84%)	261 (98%)	4 (2%)	1 (0%)	38	35
1	B	250/315 (79%)	244 (98%)	6 (2%)	0	100	100
All	All	516/630 (82%)	505 (98%)	10 (2%)	1 (0%)	51	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	744	LEU

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	246/282 (87%)	236 (96%)	10 (4%)	35	35
1	B	233/282 (83%)	219 (94%)	14 (6%)	22	19
All	All	479/564 (85%)	455 (95%)	24 (5%)	30	26

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	577	LEU
1	A	585	ASN
1	A	603	GLU
1	A	629	ARG
1	A	633	GLU
1	A	652	LEU
1	A	693	LYS
1	A	720	LEU
1	A	774	ASP
1	A	863	ASP
1	B	577	LEU
1	B	579	ASP
1	B	585	ASN
1	B	603	GLU
1	B	613	SER
1	B	651[A]	ARG
1	B	651[B]	ARG
1	B	656	CYS
1	B	678	ASP
1	B	693	LYS
1	B	717	ARG
1	B	720	LEU
1	B	741	ASP
1	B	811	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	585	ASN
1	A	628	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 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	7YS	A	9001	-	31,35,35	0.39	0	37,52,52	1.08	3 (8%)
2	7YS	B	9001	-	31,35,35	0.40	0	37,52,52	1.03	3 (8%)

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	7YS	A	9001	-	-	0/22/27/27	0/2/4/4
2	7YS	B	9001	-	-	0/22/27/27	0/2/4/4

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	9001	7YS	C27-N13-C14	-2.32	117.43	123.35
2	B	9001	7YS	C27-N13-C14	-2.05	118.10	123.35
2	A	9001	7YS	C8-N9-N10	2.05	106.14	104.43
2	B	9001	7YS	C8-N9-N10	2.08	106.17	104.43
2	B	9001	7YS	O18-C17-C16	2.15	110.68	107.45
2	A	9001	7YS	C12-N13-C14	2.31	125.78	119.92

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	272/315 (86%)	0.63	24 (8%) 11 14	20, 37, 77, 110	0
1	B	257/315 (81%)	0.63	23 (8%) 10 13	19, 37, 78, 104	0
All	All	529/630 (83%)	0.63	47 (8%) 10 13	19, 37, 77, 110	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	864	VAL	8.5
1	A	573	LEU	8.4
1	B	631	ILE	7.3
1	A	597	GLU	7.2
1	A	598	PHE	6.3
1	B	579	ASP	5.9
1	B	773	ALA	5.8
1	B	635	LEU	5.5
1	B	636	SER	5.4
1	A	572	GLU	5.2
1	B	775	ARG	4.8
1	B	634	PHE	4.6
1	A	775	ARG	4.6
1	B	777	TYR	4.6
1	A	665	PRO	3.9
1	B	690	THR	3.9
1	A	659	MET	3.9
1	B	640	CYS	3.8
1	B	621	MET	3.7
1	B	776	VAL	3.7
1	B	632	GLU	3.6
1	A	689	GLU	3.6
1	A	773	ALA	3.5
1	A	777	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	579	ASP	3.3
1	A	690	THR	3.2
1	A	823	GLU	3.1
1	B	774	ASP	3.1
1	A	745	SER	3.0
1	A	664	ILE	2.9
1	A	774	ASP	2.9
1	B	633	GLU	2.8
1	B	639	ALA	2.8
1	B	689	GLU	2.7
1	B	814	LEU	2.7
1	B	575	ASN	2.6
1	A	743	GLY	2.6
1	B	762	MET	2.5
1	A	596	GLY	2.4
1	B	824	ASP	2.4
1	A	576	LYS	2.3
1	B	578	GLU	2.3
1	A	629	ARG	2.3
1	A	776	VAL	2.2
1	B	643	ASP	2.2
1	A	577	LEU	2.1
1	A	666	LYS	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	7YS	B	9001	32/32	0.92	0.11	-0.94	23,29,32,41	0
2	7YS	A	9001	32/32	0.91	0.12	-1.10	21,28,30,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.