



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 9, 2017 – 10:50 am GMT

PDB ID : 5K9I
Title : Crystal structure of c-SRC in complex with a covalent lysine probe
Authors : Wan, X.; Ouyang, S.; Zhao, Q.; Taunton, J.
Deposited on : 2016-05-31
Resolution : 2.50 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 : recalc28906
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) : recalc28906

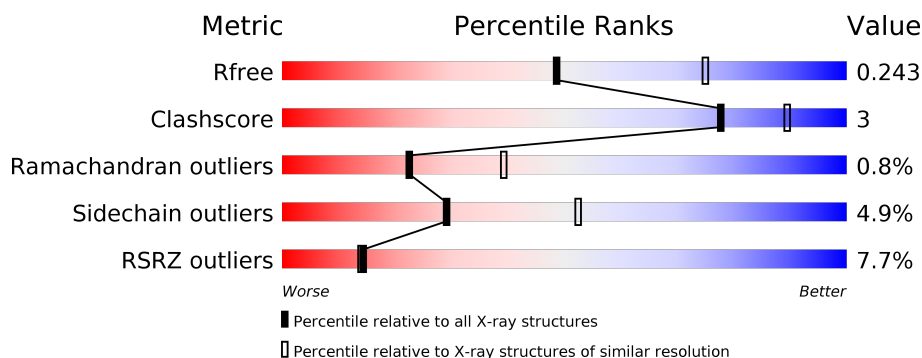
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	286	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div>10%</div> </div> </div>
1	B	286	<div> <div>9%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4347 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 Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	1	0
			2089	1344	347	381	17			
1	B	262	Total	C	N	O	S	0	1	0
			2118	1364	353	384	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	expression tag	UNP P00523
A	249	HIS	-	expression tag	UNP P00523
A	250	MET	-	expression tag	UNP P00523
B	248	GLY	-	expression tag	UNP P00523
B	249	HIS	-	expression tag	UNP P00523
B	250	MET	-	expression tag	UNP P00523

- Molecule 2 is 4-[(4-{4-[(3-cyclopropyl-1H-pyrazol-5-yl)amino]-6-[(prop-2-yn-1-yl)carbamoyl]pyrimidin-2-yl}piperazin-1-yl)methyl]benzene-1-sulfonyl fluoride (three-letter code: O44) (formula: C₂₅H₂₇FN₈O₃S).



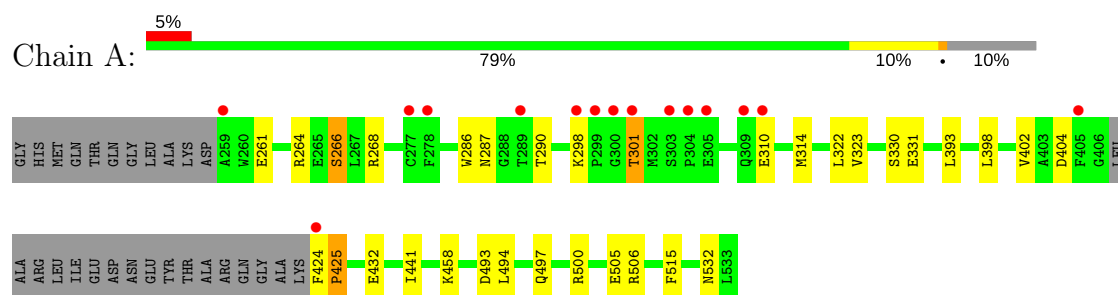
- Molecule 3 is water.



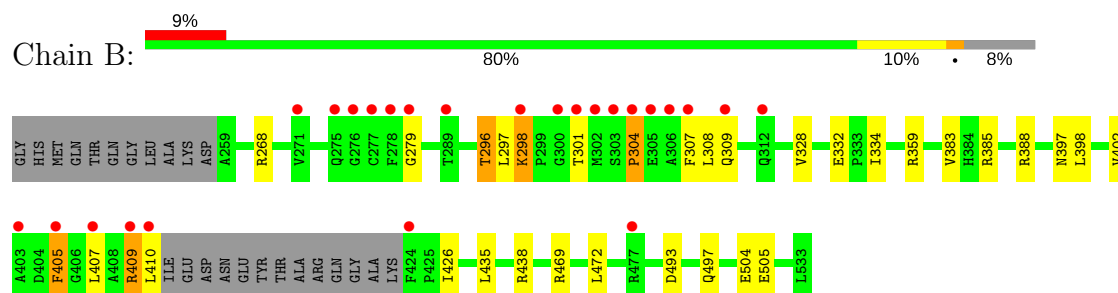
3 Residue-property plots [i](#)

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: Proto-oncogene tyrosine-protein kinase Src



• Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.01Å 63.31Å 73.77Å 78.85° 88.75° 89.93°	Depositor
Resolution (Å)	28.92 – 2.50 28.92 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (28.92-2.50) 90.7 (28.92-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.33 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.191 , 0.249 0.186 , 0.243	Depositor DCC
R_{free} test set	1129 reflections (4.52%)	DCC
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4347	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.17% 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: O44

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	0.42	0/2142	0.57	0/2900
1	B	0.42	0/2174	0.59	0/2943
All	All	0.42	0/4316	0.58	0/5843

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	2089	0	2067	14	0
1	B	2118	0	2108	13	1
2	A	37	0	0	1	0
2	B	37	0	0	1	0
3	A	35	0	0	0	0
3	B	31	0	0	0	0
All	All	4347	0	4175	29	1

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 3.

All (29) 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:500:ARG:HD3	1:A:505:GLU:HB3	1.71	0.72
1:B:297:LEU:HD13	1:B:334:ILE:H	1.63	0.63
1:A:298:LYS:O	1:A:301:THR:OG1	2.16	0.62
1:B:297:LEU:HD11	1:B:332:GLU:HG3	1.81	0.62
1:A:266:SER:OG	1:A:287:ASN:OD1	2.17	0.61
1:B:383:VAL:HG12	1:B:385:ARG:HG2	1.83	0.61
1:B:385:ARG:HD3	1:B:409:ARG:HD3	1.82	0.61
1:A:322:LEU:HD22	1:A:402:VAL:HB	1.84	0.58
1:A:432:GLU:OE2	1:A:506:ARG:NH2	2.37	0.57
1:B:304:PRO:HA	1:B:307:PHE:HB3	1.89	0.54
1:A:424:PHE:HD2	1:A:425:PRO:HD2	1.74	0.53
1:A:493:ASP:O	1:A:497:GLN:HG3	2.11	0.51
1:B:435:LEU:HD21	1:B:472:LEU:HD21	1.92	0.50
1:A:323:VAL:HG21	1:A:393:LEU:HD12	1.95	0.49
1:B:426:ILE:HD12	1:B:426:ILE:H	1.79	0.48
1:B:279:GLY:HA3	1:B:296:THR:O	2.14	0.47
1:A:261:GLU:OE1	1:A:330:SER:OG	2.32	0.46
1:A:458:LYS:NZ	1:A:532:ASN:O	2.48	0.46
2:B:601:O44:CAT	2:B:601:O44:OAU	2.65	0.45
1:B:297:LEU:HD22	1:B:334:ILE:N	2.34	0.43
1:A:264:ARG:NH2	1:A:331:GLU:O	2.52	0.43
1:A:286:TRP:HB3	1:A:290:THR:HB	2.02	0.42
1:B:359:ARG:HD3	1:B:359:ARG:HA	1.87	0.42
1:B:297:LEU:HD23	1:B:298:LYS:N	2.34	0.42
1:A:441:ILE:HD12	1:A:441:ILE:HA	1.93	0.41
1:A:494:LEU:HD22	1:A:515:PHE:CE1	2.55	0.41
2:A:601:O44:OAU	2:A:601:O44:CAT	2.67	0.41
1:B:493:ASP:O	1:B:497:GLN:HG3	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:397:ASN:OD1	1:B:438:ARG:NE[1_455]	2.18	0.02

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	255/286 (89%)	245 (96%)	8 (3%)	2 (1%)	22	39
1	B	259/286 (91%)	246 (95%)	11 (4%)	2 (1%)	22	39
All	All	514/572 (90%)	491 (96%)	19 (4%)	4 (1%)	22	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	304	PRO
1	A	404	ASP
1	B	298	LYS
1	A	425	PRO

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	225/245 (92%)	219 (97%)	6 (3%)	50	77
1	B	228/245 (93%)	211 (92%)	17 (8%)	16	29
All	All	453/490 (92%)	430 (95%)	23 (5%)	29	50

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	266	SER
1	A	268	ARG

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Mol	Chain	Res	Type
1	A	301	THR
1	A	310	GLU
1	A	314	MET
1	A	398	LEU
1	B	268	ARG
1	B	296	THR
1	B	301	THR
1	B	308	LEU
1	B	309	GLN
1	B	328	VAL
1	B	388	ARG
1	B	398	LEU
1	B	402	VAL
1	B	405[A]	PHE
1	B	405[B]	PHE
1	B	407	LEU
1	B	409	ARG
1	B	410	LEU
1	B	469	ARG
1	B	504	GLU
1	B	505	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 molecules 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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	O44	A	601	1	38,41,42	2.13	3 (7%)	46,57,60	2.60	19 (41%)
2	O44	B	601	1	38,41,42	2.23	4 (10%)	46,57,60	2.65	16 (34%)

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	O44	A	601	1	-	0/25/40/42	0/4/5/5
2	O44	B	601	1	-	0/25/40/42	0/4/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	O44	CBE-SBH	-11.62	1.60	1.80
2	A	601	O44	CBE-SBH	-11.18	1.61	1.80
2	B	601	O44	NAP-NAO	2.16	1.41	1.37
2	A	601	O44	C2-NAA	2.40	1.40	1.35
2	B	601	O44	C2-NAA	2.51	1.40	1.35
2	A	601	O44	CAT-CBL	4.59	1.28	1.18
2	B	601	O44	CAT-CBL	4.83	1.29	1.18

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	O44	CAM-CAL-CAK	-8.19	111.94	120.20
2	A	601	O44	CAN-CAL-CAK	-7.44	112.70	120.20
2	A	601	O44	CAM-CAL-CAK	-6.45	113.70	120.20
2	B	601	O44	CAJ-CAK-CAL	-6.19	119.78	129.30
2	B	601	O44	CAN-CAL-CAK	-5.53	114.62	120.20
2	A	601	O44	CAJ-CAK-CAL	-5.37	121.04	129.30
2	A	601	O44	CBA-NAX-CAY	-2.95	104.82	111.08
2	A	601	O44	N1-C2-N3	-2.87	121.52	126.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	O44	CAI-CAJ-CAK	-2.68	103.70	106.09
2	B	601	O44	CAZ-NAA-C2	-2.66	117.58	121.76
2	B	601	O44	N1-C2-N3	-2.47	122.19	126.32
2	A	601	O44	C5-C6-N1	-2.47	118.56	123.37
2	B	601	O44	C5-C4-N3	-2.40	118.11	123.41
2	B	601	O44	OAU-CAQ-C6	-2.37	116.05	121.13
2	A	601	O44	CBA-CBB-CBG	-2.34	116.32	120.78
2	A	601	O44	CBD-CBE-CBF	-2.31	118.87	121.58
2	A	601	O44	CAZ-NAA-C2	-2.23	118.25	121.76
2	B	601	O44	CBA-NAX-CAY	-2.16	106.49	111.08
2	A	601	O44	OAU-CAQ-C6	-2.12	116.58	121.13
2	B	601	O44	CAI-CAJ-CAK	-2.05	104.26	106.09
2	A	601	O44	N1-C2-NAA	2.01	119.35	117.11
2	B	601	O44	N3-C2-NAA	2.15	119.50	117.11
2	B	601	O44	NAH-C4-N3	2.26	123.31	117.00
2	A	601	O44	OBI-SBH-CBE	2.35	110.07	104.53
2	A	601	O44	CAQ-C6-N1	2.53	121.60	117.47
2	A	601	O44	OBJ-SBH-CBE	2.56	110.58	104.53
2	B	601	O44	OBJ-SBH-CBE	2.78	111.09	104.53
2	A	601	O44	C6-CAQ-NAR	3.19	119.88	115.52
2	B	601	O44	CAQ-C6-N1	3.23	122.74	117.47
2	A	601	O44	CBB-CBA-NAX	3.47	119.86	113.17
2	B	601	O44	C6-CAQ-NAR	4.71	121.97	115.52
2	A	601	O44	CAZ-NAA-CAV	4.86	121.86	111.57
2	B	601	O44	CAZ-NAA-CAV	5.18	122.55	111.57
2	A	601	O44	CAL-CAK-NAO	5.97	129.07	120.21
2	B	601	O44	CAL-CAK-NAO	6.62	130.05	120.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	O44	1	0
2	B	601	O44	1	0

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	258/286 (90%)	0.08	15 (5%) 24 24	19, 30, 65, 82	0
1	B	262/286 (91%)	0.24	25 (9%) 9 8	17, 32, 81, 112	0
All	All	520/572 (90%)	0.16	40 (7%) 14 14	17, 31, 69, 112	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	301	THR	11.4
1	B	300	GLY	8.5
1	B	405[A]	PHE	7.7
1	A	405[A]	PHE	7.2
1	B	302	MET	6.4
1	B	277	CYS	6.3
1	B	307	PHE	5.6
1	B	410	LEU	5.1
1	B	306	ALA	4.8
1	B	278	PHE	4.8
1	A	424	PHE	4.7
1	B	407	LEU	4.4
1	B	303	SER	4.2
1	A	300	GLY	4.1
1	B	424	PHE	4.0
1	A	305	GLU	3.9
1	B	305	GLU	3.3
1	B	409	ARG	3.2
1	B	279	GLY	3.1
1	A	304	PRO	3.1
1	A	259	ALA	2.9
1	A	303	SER	2.8
1	A	301	THR	2.8
1	B	276	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	275	GLN	2.5
1	A	310	GLU	2.4
1	B	304	PRO	2.4
1	A	298	LYS	2.3
1	B	271	VAL	2.3
1	B	289	THR	2.3
1	B	403	ALA	2.3
1	B	298	LYS	2.2
1	B	477	ARG	2.2
1	A	277	CYS	2.2
1	A	299	PRO	2.1
1	A	289	THR	2.1
1	B	309	GLN	2.1
1	A	309	GLN	2.1
1	B	312	GLN	2.1
1	A	278	PHE	2.1

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(Å ²)	Q<0.9
2	O44	A	601	37/38	0.94	0.14	-0.37	27,35,54,64	0
2	O44	B	601	37/38	0.93	0.18	-0.47	26,42,73,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.