



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:41 PM GMT

PDB ID : 3SC1
Title : Novel Isoquinolone PDK1 Inhibitors Discovered through Fragment-Based Lead
Discovery
Authors : Greasley, S.E.; Ferre, R.-A.; Krauss, M.; Cronin, C.
Deposited on : 2011-06-06
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>

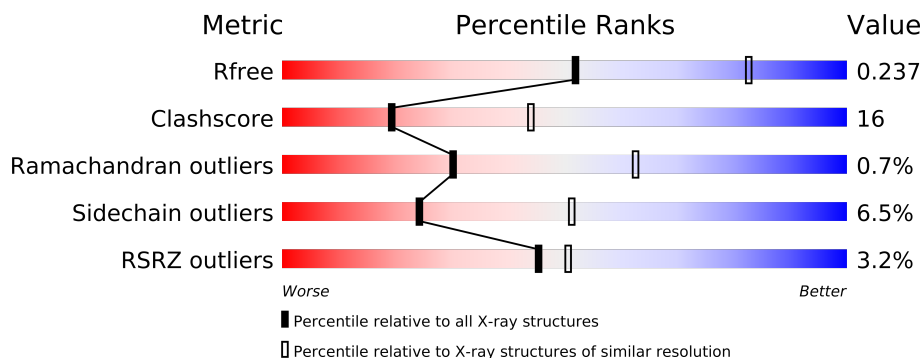
The following versions of software and data (see [references](#)) were used in the production of this report:

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	311	

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	3S1	A	900	-	X
3	SO4	A	901	-	X
3	SO4	A	903	-	X
4	GOL	A	905	-	X

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 2367 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.

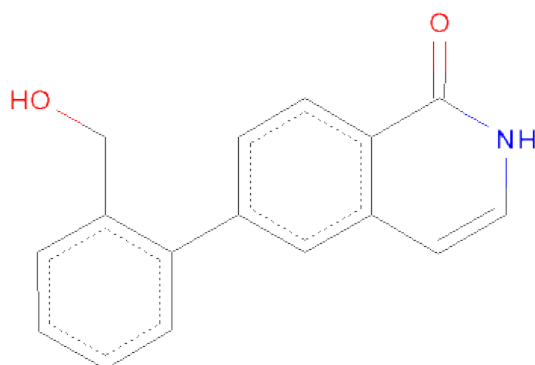
- Molecule 1 is a protein called 3-phosphoinositide-dependentprotein kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	279	2285	1483	378	416	1	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	GLY	-	EXPRESSION TAG	UNP O15530

- Molecule 2 is 6-[2-(HYDROXYMETHYL)PHENYL]ISOQUINOLIN-1(2H)-ONE (three-letter code: 3S1) (formula: C₁₆H₁₃NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	19	16	1	2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	123.71 Å 123.71 Å 47.30 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.70 43.27 – 2.64	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.70) 93.0 (43.27-2.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.65 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.200 , 0.237 0.200 , 0.237	Depositor DCC
R_{free} test set	537 reflections (4.89%)	DCC
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 25.1	EDS
Estimated twinning fraction	0.048 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 12465 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2367	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: GOL, 3S1, SO4, SEP

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	0.37	0/2329	0.51	0/3137

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2285	0	2300	76	1
2	A	19	0	13	0	0
3	A	20	0	0	0	0
4	A	12	0	16	0	0
5	A	31	0	0	2	0
All	All	2367	0	2329	76	1

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 16.

All (76) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:115:LYS:NZ	1:A:150:GLN:HE21	1.61	0.97
1:A:115:LYS:HZ3	1:A:150:GLN:HE21	1.12	0.96
1:A:243:VAL:HG12	1:A:244:GLY:H	1.43	0.79
1:A:243:VAL:HG12	1:A:244:GLY:N	2.05	0.72
1:A:284:ALA:HB1	1:A:289:LEU:HB3	1.71	0.71
1:A:240:ASN:HB2	1:A:257:LYS:O	1.95	0.66
1:A:202:ILE:HD11	1:A:261:LYS:HG2	1.77	0.66
1:A:93:PHE:CZ	1:A:123:LYS:HE3	2.32	0.65
1:A:113:LEU:HB3	1:A:118:ILE:HD11	1.79	0.63
1:A:115:LYS:HZ3	1:A:150:GLN:NE2	1.92	0.63
1:A:284:ALA:CB	1:A:289:LEU:HB3	2.29	0.62
1:A:202:ILE:HD12	1:A:261:LYS:HA	1.81	0.62
1:A:104:THR:O	1:A:105:SER:HB3	2.00	0.61
1:A:73:GLN:HG2	1:A:74:PRO:O	2.01	0.61
1:A:205:ASP:O	1:A:210:ASN:ND2	2.34	0.60
1:A:130:GLU:HB2	1:A:225:GLY:HA2	1.85	0.58
1:A:118:ILE:HD13	1:A:127:VAL:HG21	1.85	0.57
1:A:255:THR:HG22	1:A:256:GLU:HG3	1.87	0.57
1:A:297:LEU:HD13	1:A:319:LEU:CD1	2.35	0.57
1:A:164:ASN:OD1	1:A:215:GLU:HA	2.04	0.57
1:A:174:ILE:HD11	1:A:177:PHE:CD1	2.41	0.56
1:A:203:HIS:O	1:A:204:ARG:HB2	2.06	0.55
1:A:242:PHE:HD2	1:A:257:LYS:HZ3	1.52	0.54
1:A:202:ILE:CD1	1:A:261:LYS:HG2	2.37	0.54
1:A:118:ILE:HG23	1:A:123:LYS:HB2	1.90	0.53
1:A:163:LYS:HB3	1:A:215:GLU:HB3	1.90	0.53
1:A:262:SER:HB3	1:A:324:ARG:HH11	1.72	0.53
1:A:111:LYS:HD3	1:A:113:LEU:HD11	1.91	0.53
1:A:302:PRO:HB2	1:A:304:LYS:HD3	1.93	0.51
1:A:168:LEU:HB2	1:A:208:PRO:HB2	1.93	0.50
1:A:163:LYS:CB	1:A:215:GLU:HB3	2.42	0.49
1:A:286:ASN:O	1:A:290:ILE:HG13	2.14	0.48
1:A:113:LEU:HD12	1:A:113:LEU:N	2.29	0.47
1:A:177:PHE:HB3	1:A:181:CYS:HB2	1.97	0.47
1:A:216:ASP:O	1:A:217:MET:HB2	2.14	0.47
1:A:197:HIS:HB3	1:A:261:LYS:HD3	1.97	0.47
1:A:177:PHE:N	1:A:177:PHE:CD1	2.83	0.47
1:A:214:ASN:C	1:A:214:ASN:OD1	2.52	0.47
1:A:150:GLN:HG3	1:A:155:LEU:HD23	1.97	0.47
1:A:133:VAL:HG13	1:A:201:ILE:HD13	1.97	0.47
1:A:243:VAL:CG1	1:A:244:GLY:H	2.21	0.46
1:A:104:THR:O	1:A:105:SER:CB	2.64	0.46
1:A:174:ILE:HB	1:A:359:THR:HB	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:242:PHE:HD2	1:A:257:LYS:NZ	2.14	0.45
1:A:240:ASN:CB	1:A:257:LYS:O	2.64	0.45
1:A:301:PHE:CG	1:A:310:ARG:HG3	2.51	0.45
1:A:289:LEU:HD12	1:A:289:LEU:HA	1.80	0.45
1:A:75:ARG:HH21	1:A:76:LYS:H	1.65	0.45
1:A:151:ASP:OD1	1:A:154:LYS:N	2.44	0.45
1:A:79:PRO:HD2	1:A:80:GLU:OE2	2.17	0.45
1:A:330:MET:O	1:A:331:GLU:HB2	2.17	0.44
1:A:297:LEU:HD13	1:A:319:LEU:HD13	1.98	0.44
1:A:226:THR:HG23	5:A:17:HOH:O	2.17	0.44
1:A:209:GLU:N	1:A:209:GLU:OE1	2.41	0.44
1:A:94:SER:HB3	1:A:113:LEU:HG	2.00	0.44
1:A:183:ARG:HD3	1:A:341:PHE:O	2.18	0.44
1:A:222:THR:O	1:A:223:ASP:HB3	2.19	0.43
1:A:312:LEU:HB2	1:A:339:HIS:CE1	2.54	0.42
1:A:111:LYS:HE2	5:A:25:HOH:O	2.19	0.42
1:A:240:ASN:HD22	1:A:240:ASN:N	2.18	0.42
1:A:358:LEU:HD12	1:A:358:LEU:N	2.34	0.42
1:A:177:PHE:N	1:A:177:PHE:HD1	2.18	0.42
1:A:358:LEU:CD1	1:A:358:LEU:N	2.82	0.41
1:A:267:ALA:O	1:A:271:ILE:HG13	2.20	0.41
1:A:247:GLN:HG2	1:A:247:GLN:H	1.48	0.41
1:A:262:SER:HB3	1:A:324:ARG:NH1	2.35	0.41
1:A:293:LYS:HB3	1:A:298:GLU:HB3	2.02	0.41
1:A:306:PHE:HA	1:A:307:PRO:HD3	1.90	0.41
1:A:132:ASP:O	1:A:136:ARG:HG3	2.21	0.41
1:A:168:LEU:HD22	1:A:209:GLU:OE2	2.21	0.41
1:A:280:PRO:O	1:A:283:ARG:NH1	2.46	0.41
1:A:170:TYR:O	1:A:174:ILE:HG12	2.21	0.41
1:A:350:LEU:HD12	1:A:350:LEU:HA	1.89	0.41
1:A:256:GLU:HB2	1:A:258:SER:HB3	2.03	0.40
1:A:245:THR:O	1:A:249:VAL:HG23	2.20	0.40
1:A:252:GLU:HG2	1:A:253:LEU:N	2.37	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	Distance(Å)	Clash(Å)
1:A:303:GLU:OE2	1:A:303:GLU:OE2[5_555]	1.94	0.26

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	274/311 (88%)	261 (95%)	11 (4%)	2 (1%)	30 62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86	LYS
1	A	223	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	247/268 (92%)	231 (94%)	16 (6%)	24 51

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LEU
1	A	116	ARG
1	A	215	GLU
1	A	226	THR
1	A	230	LEU
1	A	240	ASN
1	A	242	PHE
1	A	247	GLN
1	A	253	LEU
1	A	289	LEU
1	A	300	ASP
1	A	304	LYS

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Mol	Chain	Res	Type
1	A	319	LEU
1	A	350	LEU
1	A	351	HIS
1	A	359	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	150	GLN
1	A	247	GLN
1	A	292	GLN
1	A	353	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	SEP	A	241	1	9,9,10	6.09	2 (22%)	10,12,14	3.25	7 (70%)

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	SEP	A	241	1	-	0/6/8/10	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	241	SEP	O-C	17.88	1.23	1.11
1	A	241	SEP	CA-C	2.74	1.53	1.48

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	SEP	P-OG-CB	-6.59	99.13	118.19
1	A	241	SEP	OG-P-O1P	-5.46	90.69	106.71
1	A	241	SEP	O3P-P-OG	-2.77	98.99	106.65
1	A	241	SEP	O3P-P-O2P	2.66	117.95	107.61
1	A	241	SEP	OG-CB-CA	2.39	112.08	108.69
1	A	241	SEP	O2P-P-O1P	2.38	118.22	110.44
1	A	241	SEP	O3P-P-O1P	2.33	118.06	110.44

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 ⓘ

7 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	3S1	A	900	-	21,21,21	2.09	10 (47%)	27,29,29	0.93	0
3	SO4	A	901	-	4,4,4	0.37	0	6,6,6	0.15	0
3	SO4	A	902	-	4,4,4	0.29	0	6,6,6	0.12	0
3	SO4	A	903	-	4,4,4	0.30	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	904	-	4,4,4	0.27	0	6,6,6	0.07	0
4	GOL	A	905	-	5,5,5	0.39	0	5,5,5	0.46	0
4	GOL	A	906	-	5,5,5	0.46	0	5,5,5	0.54	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
2	3S1	A	900	-	-	0/6/6/6	0/1/3/3
3	SO4	A	901	-	-	0/0/0/0	0/0/0/0
3	SO4	A	902	-	-	0/0/0/0	0/0/0/0
3	SO4	A	903	-	-	0/0/0/0	0/0/0/0
3	SO4	A	904	-	-	0/0/0/0	0/0/0/0
4	GOL	A	905	-	-	0/4/4/4	0/0/0/0
4	GOL	A	906	-	-	0/4/4/4	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	3S1	C7-C2	4.60	1.46	1.40
2	A	900	3S1	C6-C7	3.26	1.45	1.40
2	A	900	3S1	C12-C11	2.93	1.50	1.39
2	A	900	3S1	C14-C15	2.79	1.49	1.41
2	A	900	3S1	C13-N1	2.65	1.39	1.33
2	A	900	3S1	C10-C9	2.52	1.41	1.36
2	A	900	3S1	C3-C2	2.44	1.44	1.39
2	A	900	3S1	C16-C8	2.30	1.43	1.38
2	A	900	3S1	C9-C8	2.30	1.44	1.39
2	A	900	3S1	C12-N1	2.26	1.41	1.37

There are no bond angle outliers.

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	279/311 (89%)	-0.31	8 (2%) 49 55	18, 33, 61, 91	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	THR	4.6
1	A	242	PHE	3.5
1	A	231	SER	3.0
1	A	152	ASP	2.9
1	A	75	ARG	2.7
1	A	240	ASN	2.4
1	A	258	SER	2.3
1	A	73	GLN	2.2

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(Å ²)	Q<0.9
1	SEP	A	241	10/11	0.11	-1.66	86,88,90,90	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(Å ²)	Q<0.9
3	SO4	A	901	5/5	0.19	30.99	81,82,83,83	0
3	SO4	A	903	5/5	0.53	8.86	52,53,54,54	5
4	GOL	A	905	6/6	0.19	3.68	42,43,45,48	0
2	3S1	A	900	19/19	0.19	2.22	21,24,25,26	0
4	GOL	A	906	6/6	0.17	1.27	36,41,42,42	0
3	SO4	A	904	5/5	0.20	0.88	40,41,42,42	5
3	SO4	A	902	5/5	0.17	0.81	79,80,80,80	0

6.5 Other polymers ⓘ

There are no such residues in this entry.