Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:18 AM GMT

PDB ID	:	2WOZ
Title	:	THE NOVEL BETA-PROPELLER OF THE BTB-KELCH PROTEIN KRP1 PROVIDES THE BINDING SITE FOR LASP-1 THAT IS NECESSARY FOR PSEUDOPODIA EXTENSION
Authors	:	Gray, C.H.; Mcgarry, L.C.; Spence, H.J.; Riboldi-Tunnicliffe, A.; Ozanne, B.W.
Deposited on	:	2009-07-31
Resolution	:	2.00 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

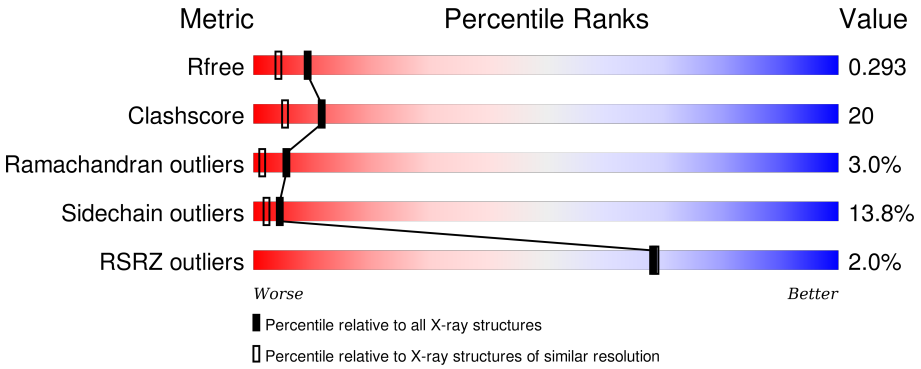
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 <=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	318	2% 63% 23% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2556 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 KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	307	2389	1533	393	449	14	0	0	0

- Molecule 2 is water.

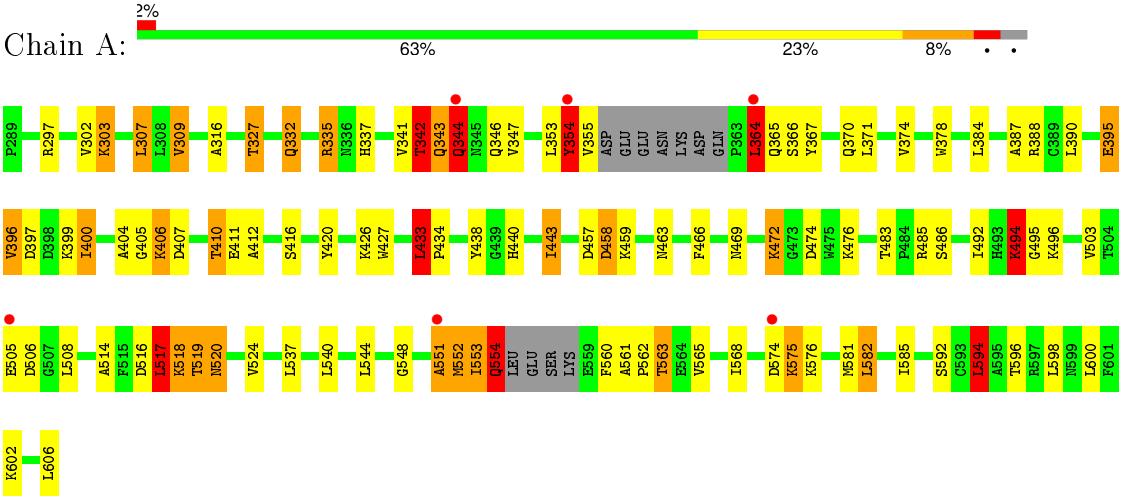
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	167	167	167	0	0

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 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: KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	66.11Å 98.53Å 46.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.50 – 2.00 42.40 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.1 (49.50-2.00) 96.5 (42.40-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.237 , 0.279 0.234 , 0.293	Depositor DCC
R_{free} test set	1057 reflections (5.39%)	DCC
Wilson B-factor (Å^2)	31.9	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	1 of 20683 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2556	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.82% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.68	1/2442 (0.0%)	0.90	7/3308 (0.2%)

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	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	395	GLU	CB-CG	-5.40	1.41	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	517	LEU	N-CA-C	7.12	130.22	111.00
1	A	495	GLY	N-CA-C	-6.91	95.83	113.10
1	A	594	LEU	CA-CB-CG	6.35	129.91	115.30
1	A	554	GLN	N-CA-C	-5.76	95.45	111.00
1	A	405	GLY	C-N-CA	5.71	135.99	121.70
1	A	494	LYS	N-CA-C	5.44	125.68	111.00
1	A	433	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	342	THR	Peptide
1	A	354	TYR	Peptide

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Mol	Chain	Res	Type	Group
1	A	494	LYS	Peptide
1	A	517	LEU	Peptide
1	A	519	THR	Peptide
1	A	553	ILE	Peptide

5.2 Too-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 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	2389	0	2379	97	0
2	A	167	0	0	17	0
All	All	2556	0	2379	97	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 20.

All (97) 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:551:ALA:HB1	1:A:552:MET:HA	1.16	1.09
1:A:551:ALA:HB2	1:A:562:PRO:HA	1.09	1.07
1:A:551:ALA:CB	1:A:562:PRO:HA	1.91	0.99
1:A:551:ALA:HB1	1:A:552:MET:CA	1.95	0.95
1:A:303:LYS:NZ	1:A:303:LYS:HB3	1.86	0.90
1:A:551:ALA:HB2	1:A:562:PRO:CA	2.01	0.86
1:A:516:ASP:OD1	1:A:518:LYS:HB3	1.77	0.85
1:A:303:LYS:HZ2	1:A:303:LYS:HB3	1.42	0.84
1:A:346:GLN:HE21	1:A:370:GLN:HE21	1.28	0.81
1:A:341:VAL:HG23	1:A:594:LEU:HG	1.63	0.80
1:A:551:ALA:CB	1:A:552:MET:HA	2.06	0.79
1:A:410:THR:HG21	2:A:2058:HOH:O	1.82	0.78
1:A:335:ARG:H	1:A:335:ARG:HD2	1.47	0.77
1:A:297:ARG:NH1	2:A:2007:HOH:O	2.17	0.77
1:A:342:THR:HG21	2:A:2055:HOH:O	1.85	0.75
1:A:516:ASP:OD1	1:A:518:LYS:CB	2.36	0.74
1:A:354:TYR:HB2	1:A:365:GLN:H	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:574:ASP:O	1:A:575:LYS:HB2	1.90	0.70
1:A:399:LYS:HE3	2:A:2054:HOH:O	1.92	0.69
1:A:505:GLU:HG2	2:A:2105:HOH:O	1.93	0.68
1:A:388:ARG:HD3	1:A:404:ALA:O	1.95	0.66
1:A:337:HIS:HE1	1:A:592:SER:OG	1.77	0.66
1:A:335:ARG:CD	1:A:335:ARG:H	2.09	0.65
1:A:517:LEU:N	1:A:518:LYS:HB2	2.13	0.64
1:A:520:ASN:ND2	1:A:520:ASN:H	1.97	0.62
1:A:346:GLN:HE21	1:A:370:GLN:NE2	1.98	0.62
1:A:426:LYS:HE3	2:A:2067:HOH:O	2.00	0.61
1:A:519:THR:N	1:A:520:ASN:HA	2.16	0.59
1:A:342:THR:HG23	1:A:344:GLN:N	2.16	0.59
1:A:355:VAL:HA	1:A:367:TYR:CE2	2.38	0.59
1:A:407:ASP:HB3	1:A:410:THR:HG22	1.84	0.59
1:A:548:GLY:HA2	1:A:565:VAL:O	2.03	0.59
1:A:433:LEU:HD22	1:A:434:PRO:HD2	1.84	0.58
1:A:364:LEU:HD13	1:A:387:ALA:CB	2.33	0.58
1:A:390:LEU:HD12	1:A:406:LYS:HG3	1.87	0.57
1:A:496:LYS:HE2	1:A:514:ALA:HB1	1.86	0.57
1:A:400:ILE:HB	2:A:2031:HOH:O	2.04	0.56
1:A:395:GLU:OE1	2:A:2052:HOH:O	2.17	0.56
1:A:582:LEU:HD13	1:A:585:ILE:HB	1.86	0.56
1:A:342:THR:HG23	1:A:344:GLN:H	1.70	0.55
1:A:303:LYS:HB2	1:A:600:LEU:HD21	1.88	0.55
1:A:496:LYS:HE2	1:A:514:ALA:CB	2.37	0.54
1:A:307:LEU:HD13	1:A:309:VAL:HG12	1.88	0.54
1:A:332:GLN:HE22	1:A:378:TRP:HB2	1.74	0.53
1:A:303:LYS:NZ	1:A:303:LYS:CB	2.63	0.53
1:A:594:LEU:HD13	2:A:2156:HOH:O	2.08	0.53
1:A:602:LYS:NZ	2:A:2163:HOH:O	2.41	0.53
1:A:341:VAL:HG22	1:A:347:VAL:HG22	1.91	0.52
1:A:552:MET:C	1:A:553:ILE:HG13	2.30	0.52
1:A:516:ASP:O	1:A:520:ASN:HA	2.11	0.51
1:A:576:LYS:HE2	2:A:2146:HOH:O	2.09	0.51
1:A:440:HIS:H	1:A:440:HIS:CD2	2.29	0.51
1:A:410:THR:HG22	1:A:412:ALA:H	1.76	0.51
1:A:316:ALA:HB2	1:A:327:THR:CG2	2.42	0.49
1:A:516:ASP:O	1:A:520:ASN:CB	2.59	0.49
1:A:551:ALA:CB	1:A:552:MET:CA	2.77	0.49
1:A:561:ALA:O	1:A:563:THR:HG22	2.12	0.48
1:A:457:ASP:C	1:A:458:ASP:O	2.50	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:ILE:HG22	1:A:554:GLN:N	2.28	0.48
1:A:466:PHE:HA	1:A:476:LYS:O	2.14	0.48
1:A:374:VAL:HG13	2:A:2163:HOH:O	2.13	0.48
1:A:364:LEU:HD13	1:A:387:ALA:HB3	1.95	0.47
1:A:406:LYS:HG2	1:A:438:TYR:CG	2.49	0.47
1:A:342:THR:O	1:A:344:GLN:O	2.33	0.47
1:A:443:ILE:HD13	1:A:492:ILE:HD11	1.96	0.47
1:A:516:ASP:OD1	1:A:518:LYS:HB2	2.14	0.47
1:A:341:VAL:HG23	1:A:594:LEU:CG	2.41	0.47
1:A:343:GLN:C	1:A:344:GLN:O	2.50	0.47
1:A:337:HIS:CE1	1:A:592:SER:OG	2.64	0.47
1:A:472:LYS:HD2	1:A:474:ASP:OD2	2.15	0.47
1:A:516:ASP:O	1:A:520:ASN:HB3	2.15	0.47
1:A:341:VAL:HG12	1:A:342:THR:O	2.14	0.47
1:A:483:THR:HB	1:A:485:ARG:HH21	1.80	0.46
1:A:420:TYR:HB2	1:A:427:TRP:CE3	2.50	0.46
1:A:552:MET:HE2	1:A:562:PRO:HG3	1.98	0.46
1:A:420:TYR:HB2	1:A:427:TRP:CZ3	2.51	0.46
1:A:568:ILE:CD1	1:A:585:ILE:HG21	2.46	0.45
1:A:344:GLN:HB3	1:A:346:GLN:HG2	1.99	0.45
1:A:354:TYR:O	1:A:366:SER:CA	2.65	0.45
1:A:574:ASP:O	1:A:575:LYS:CB	2.61	0.45
1:A:353:LEU:HA	1:A:354:TYR:HA	1.44	0.44
1:A:459:LYS:HB2	1:A:459:LYS:NZ	2.33	0.43
1:A:606:LEU:C	2:A:2166:HOH:O	2.56	0.42
1:A:303:LYS:HZ3	1:A:303:LYS:HB3	1.76	0.42
1:A:553:ILE:HG22	1:A:554:GLN:H	1.84	0.42
1:A:458:ASP:O	1:A:459:LYS:HG3	2.19	0.42
1:A:596:THR:HG23	1:A:598:LEU:HG	2.01	0.42
1:A:505:GLU:HG3	2:A:2097:HOH:O	2.18	0.42
1:A:486:SER:OG	1:A:503:VAL:HG12	2.19	0.42
1:A:520:ASN:HD22	1:A:520:ASN:H	1.64	0.41
1:A:486:SER:OG	1:A:503:VAL:CG1	2.68	0.41
1:A:400:ILE:CG2	2:A:2031:HOH:O	2.68	0.41
1:A:508:LEU:HD22	1:A:552:MET:HG2	2.02	0.41
1:A:554:GLN:HB2	1:A:560:PHE:CZ	2.55	0.41
1:A:396:VAL:HB	2:A:2050:HOH:O	2.20	0.40
1:A:517:LEU:CA	1:A:518:LYS:HB2	2.50	0.40
1:A:395:GLU:HG3	2:A:2031:HOH:O	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	301/318 (95%)	276 (92%)	16 (5%)	9 (3%)	5 1

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	GLN
1	A	458	ASP
1	A	518	LYS
1	A	406	LYS
1	A	494	LYS
1	A	551	ALA
1	A	575	LYS
1	A	344	GLN
1	A	364	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	260/272 (96%)	224 (86%)	36 (14%)	4 2

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	302	VAL
1	A	303	LYS

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Mol	Chain	Res	Type
1	A	307	LEU
1	A	309	VAL
1	A	327	THR
1	A	332	GLN
1	A	335	ARG
1	A	342	THR
1	A	344	GLN
1	A	354	TYR
1	A	364	LEU
1	A	371	LEU
1	A	384	LEU
1	A	396	VAL
1	A	397	ASP
1	A	400	ILE
1	A	410	THR
1	A	411	GLU
1	A	416	SER
1	A	433	LEU
1	A	443	ILE
1	A	463	ASN
1	A	469	ASN
1	A	472	LYS
1	A	506	ASP
1	A	520	ASN
1	A	524	VAL
1	A	537	LEU
1	A	540	LEU
1	A	544	LEU
1	A	552	MET
1	A	554	GLN
1	A	563	THR
1	A	581	MET
1	A	582	LEU
1	A	594	LEU

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	322	ASN
1	A	337	HIS
1	A	365	GLN
1	A	370	GLN

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Mol	Chain	Res	Type
1	A	440	HIS
1	A	463	ASN
1	A	520	ASN

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

There are no ligands in this entry.

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, 95^{th} 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	307/318 (96%)	0.24	6 (1%) 68 69	17, 28, 40, 46	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	354	TYR	3.9
1	A	344	GLN	2.8
1	A	505	GLU	2.3
1	A	364	LEU	2.1
1	A	574	ASP	2.1
1	A	551	ALA	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.