



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:22 AM UTC

PDB ID : 6UP2 / pdb_00006up2
Title : Crystal structure of the murine DHX36 helicase
Authors : Chuenchor, W.; Jiang, J.; Xiao, T.S.
Deposited on : 2019-10-16
Resolution : 1.97 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

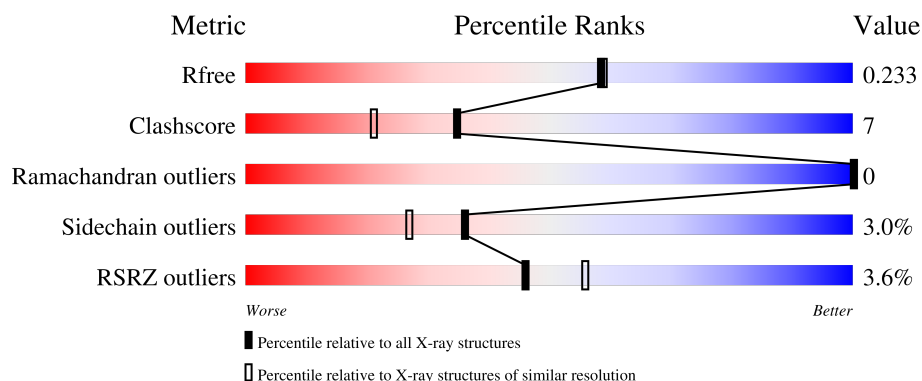
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

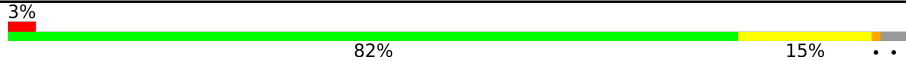
The reported resolution of this entry is 1.97 Å.

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}	180053	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	830	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	1002	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6779 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 Dhx36 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	809	6500	4141	1122	1204	33	0	1	0

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	272	Total 272	O 272	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.25Å 67.69Å 103.68Å 90.00° 92.49° 90.00°	Depositor
Resolution (Å)	45.39 – 1.97 45.39 – 1.97	Depositor EDS
% Data completeness (in resolution range)	98.6 (45.39-1.97) 98.6 (45.39-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.180 , 0.229 0.184 , 0.233	Depositor DCC
R_{free} test set	3002 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6779	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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: CL, GOL

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	0.55	1/6630 (0.0%)	0.92	12/8962 (0.1%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	533	PRO	N-CD	5.51	1.55	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	533	PRO	CA-C-N	-12.62	104.88	121.91
1	A	533	PRO	C-N-CA	-12.62	104.88	121.91
1	A	532	THR	CA-C-N	-10.94	109.11	120.38
1	A	532	THR	C-N-CA	-10.94	109.11	120.38
1	A	533	PRO	N-CA-C	9.42	122.19	110.70
1	A	915	LYS	CB-CA-C	-7.17	107.48	117.23
1	A	814	ASN	N-CA-C	6.34	120.72	112.92
1	A	492	ASN	N-CA-C	5.91	118.20	111.11
1	A	421	ARG	N-CA-C	-5.60	98.88	110.80
1	A	968	ASP	N-CA-C	-5.58	104.83	111.69
1	A	831	LEU	N-CA-C	5.49	120.04	113.23
1	A	706	CYS	CB-CA-C	-5.42	101.40	110.56

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	523	VAL	Peptide
1	A	706	CYS	Mainchain

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	6500	0	6614	97	0
2	A	6	0	8	1	0
3	A	1	0	0	4	0
4	A	272	0	0	4	0
All	All	6779	0	6622	98	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 7.

All (98) 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:736:ARG:NE	3:A:1002:CL:CL	2.32	0.99
1:A:395:GLU:O	1:A:398:ARG:NH1	1.97	0.98
1:A:531:LYS:HD2	1:A:532:THR:N	1.91	0.85
1:A:427:LYS:NZ	1:A:616:ASP:OD1	2.11	0.83
1:A:531:LYS:HD2	1:A:532:THR:H	1.47	0.79
1:A:967:ARG:HH11	1:A:967:ARG:HG3	1.49	0.77
1:A:420:ASN:ND2	1:A:581:GLU:OE2	2.18	0.76
1:A:531:LYS:NZ	1:A:536:VAL:HB	2.02	0.74
1:A:597:ARG:HH11	1:A:597:ARG:HG2	1.55	0.70
1:A:665[B]:HIS:ND1	4:A:1101:HOH:O	2.27	0.67
1:A:510:LYS:HA	1:A:536:VAL:HG22	1.78	0.66
1:A:519:LEU:HB2	1:A:785:MET:HE1	1.79	0.64
1:A:521:PRO:HB2	1:A:524:ASN:HB2	1.79	0.63
1:A:285:GLN:NE2	4:A:1103:HOH:O	2.30	0.62
1:A:885:ARG:NH1	1:A:889:ILE:HD11	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:967:ARG:HG3	1:A:967:ARG:NH1	2.14	0.62
1:A:488:PRO:HG3	1:A:563:LYS:HB2	1.82	0.61
1:A:517:HIS:HB3	1:A:520:MET:HE3	1.82	0.60
1:A:597:ARG:HH11	1:A:597:ARG:CG	2.14	0.60
1:A:736:ARG:NH2	3:A:1002:CL:CL	2.72	0.59
1:A:257:ARG:NH1	1:A:548:THR:HG21	2.18	0.58
1:A:420:ASN:HD22	1:A:581:GLU:CD	2.12	0.57
1:A:573:ASN:OD1	1:A:885:ARG:NH1	2.39	0.56
1:A:844:LYS:HD2	1:A:847:LYS:HD2	1.87	0.56
1:A:531:LYS:HE3	1:A:532:THR:O	2.05	0.55
1:A:736:ARG:CZ	3:A:1002:CL:CL	2.92	0.55
1:A:517:HIS:O	1:A:520:MET:HG2	2.07	0.55
1:A:838:ILE:HD11	1:A:878:LEU:HG	1.89	0.54
1:A:517:HIS:NE2	1:A:519:LEU:HB2	2.22	0.54
1:A:705:CYS:HG	1:A:961:TRP:CD1	2.25	0.54
1:A:391:GLU:HG3	1:A:454:LEU:HD13	1.91	0.53
1:A:726:PRO:HG2	1:A:729:LYS:HB2	1.90	0.53
1:A:760:GLU:HG2	1:A:764:ARG:NH1	2.24	0.53
2:A:1001:GOL:O1	3:A:1002:CL:CL	2.64	0.52
1:A:911:ILE:HD13	1:A:932:GLU:HG2	1.92	0.51
1:A:531:LYS:CE	1:A:536:VAL:HB	2.40	0.51
1:A:796:HIS:HE1	4:A:1307:HOH:O	1.94	0.51
1:A:526:THR:HG23	1:A:529:PHE:HE2	1.76	0.51
1:A:391:GLU:HG2	1:A:442:LEU:HD11	1.92	0.50
1:A:532:THR:O	1:A:533:PRO:C	2.50	0.50
1:A:954:GLU:OE1	1:A:954:GLU:N	2.36	0.50
1:A:223:GLU:HG2	1:A:380:GLY:HA3	1.93	0.50
1:A:268:VAL:O	1:A:272:ARG:HG3	2.12	0.50
1:A:512:LEU:HD21	1:A:529:PHE:HZ	1.77	0.50
1:A:533:PRO:C	1:A:535:GLY:H	2.20	0.49
1:A:435:TRP:HB3	1:A:436:PRO:HD3	1.94	0.49
1:A:843:GLY:HA2	1:A:845:LYS:NZ	2.28	0.49
1:A:863:PRO:HA	1:A:868:VAL:HG21	1.94	0.48
1:A:845:LYS:HE3	1:A:845:LYS:HA	1.95	0.48
1:A:760:GLU:OE2	1:A:764:ARG:NH2	2.37	0.48
1:A:365:LYS:HE3	1:A:366:PHE:CE2	2.50	0.47
1:A:760:GLU:HG2	1:A:764:ARG:HH12	1.78	0.47
1:A:316:ARG:HA	1:A:345:LEU:HD21	1.97	0.47
1:A:257:ARG:HD3	1:A:545:ILE:HB	1.96	0.47
1:A:245:LYS:HD3	1:A:245:LYS:HA	1.64	0.46
1:A:522:THR:O	1:A:525:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:966:SER:O	1:A:967:ARG:HB3	2.15	0.46
1:A:224:THR:HB	1:A:597:ARG:HH12	1.81	0.46
1:A:526:THR:HG23	1:A:529:PHE:CE2	2.50	0.46
1:A:531:LYS:HZ3	1:A:536:VAL:HB	1.79	0.46
1:A:843:GLY:HA2	1:A:845:LYS:HZ3	1.82	0.45
1:A:238:ASP:CG	1:A:272:ARG:HH22	2.25	0.45
1:A:329:HIS:CE1	1:A:359:ALA:HB3	2.52	0.45
1:A:257:ARG:HE	1:A:545:ILE:HG22	1.82	0.44
1:A:629:GLU:HB3	1:A:692:PRO:HG2	1.99	0.44
1:A:393:ILE:HD11	1:A:604:TYR:HB3	2.00	0.44
1:A:727:LEU:HA	1:A:730:GLU:OE2	2.18	0.43
1:A:226:CYS:HB2	1:A:378:ILE:HG22	1.99	0.43
1:A:916:ASP:OD1	1:A:916:ASP:N	2.50	0.43
1:A:531:LYS:NZ	1:A:532:THR:HB	2.32	0.43
1:A:845:LYS:N	1:A:845:LYS:HD2	2.33	0.43
1:A:583:VAL:HB	1:A:587:ASN:HB2	2.00	0.43
1:A:823:ILE:O	1:A:827:ILE:HG13	2.17	0.43
1:A:712:THR:N	1:A:790:LYS:HD3	2.34	0.42
1:A:819:ASN:HD21	1:A:980:LYS:HE3	1.83	0.42
1:A:523:VAL:C	1:A:525:GLN:N	2.77	0.42
1:A:212:ILE:CD1	1:A:236:ILE:HD11	2.50	0.42
1:A:527:GLN:OE1	1:A:552:ILE:HG12	2.20	0.42
1:A:215:HIS:CG	1:A:374:PRO:HG2	2.55	0.42
1:A:479:GLU:H	1:A:479:GLU:CD	2.25	0.42
1:A:223:GLU:OE1	1:A:223:GLU:N	2.50	0.41
1:A:554:ASP:HA	1:A:598:VAL:HG21	2.01	0.41
1:A:841:ASN:O	1:A:844:LYS:HE2	2.19	0.41
1:A:841:ASN:O	1:A:844:LYS:HG3	2.20	0.41
1:A:882:LEU:HB3	1:A:892:TYR:HB3	2.03	0.41
1:A:531:LYS:HD2	1:A:531:LYS:C	2.41	0.41
1:A:391:GLU:HG3	1:A:454:LEU:CD1	2.51	0.41
1:A:526:THR:CG2	1:A:529:PHE:HE2	2.32	0.41
1:A:532:THR:O	1:A:533:PRO:O	2.39	0.41
1:A:257:ARG:HH12	1:A:548:THR:HG21	1.83	0.41
1:A:521:PRO:HD2	1:A:524:ASN:HD22	1.86	0.41
1:A:705:CYS:HB3	1:A:815:ILE:HG12	2.03	0.41
1:A:884:MET:HE2	1:A:884:MET:HB3	1.85	0.41
1:A:911:ILE:HG21	1:A:932:GLU:HG3	2.03	0.41
1:A:785:MET:O	1:A:789:MET:HG3	2.22	0.40
1:A:533:PRO:C	1:A:535:GLY:N	2.80	0.40
1:A:668:GLU:OE1	4:A:1101:HOH:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:832:TYR:CG	1:A:833:PRO:HA	2.57	0.40

There are no symmetry-related clashes.

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	806/830 (97%)	790 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	729/747 (98%)	707 (97%)	22 (3%)	36	27

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	LEU
1	A	181	GLN
1	A	337	VAL
1	A	339	MET
1	A	404	LYS

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Mol	Chain	Res	Type
1	A	422	GLN
1	A	432	LYS
1	A	517	HIS
1	A	523	VAL
1	A	526	THR
1	A	532	THR
1	A	597	ARG
1	A	706	CYS
1	A	731	LYS
1	A	738	LYS
1	A	812	LYS
1	A	842	LEU
1	A	864	LYS
1	A	913	LYS
1	A	916	ASP
1	A	955	SER
1	A	967	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	HIS
1	A	420	ASN
1	A	881	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	GOL	A	1001	-	5,5,5	0.34	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	GOL	A	1001	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	GOL	C1-C2-C3-O3
2	A	1001	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	GOL	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	809/830 (97%)	0.17	29 (3%) 46 56	19, 43, 80, 159	1 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	526	THR	4.6
1	A	981	THR	4.5
1	A	523	VAL	4.2
1	A	766	PHE	3.7
1	A	400	VAL	3.6
1	A	529	PHE	3.6
1	A	536	VAL	3.5
1	A	528	VAL	3.3
1	A	525	GLN	3.2
1	A	842	LEU	3.1
1	A	534	PRO	3.0
1	A	550	ILE	2.9
1	A	535	GLY	2.9
1	A	420	ASN	2.8
1	A	527	GLN	2.7
1	A	194	ARG	2.5
1	A	346	LEU	2.5
1	A	519	LEU	2.4
1	A	719	PHE	2.3
1	A	957	HIS	2.3
1	A	845	LYS	2.3
1	A	421	ARG	2.3
1	A	964	THR	2.2
1	A	727	LEU	2.2
1	A	913	LYS	2.2
1	A	524	ASN	2.1
1	A	533	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	490	TRP	2.0
1	A	362	ASN	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	CL	A	1002	1/1	0.89	0.26	106,106,106,106	0
2	GOL	A	1001	6/6	0.91	0.10	40,52,59,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.