



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:00 PM GMT

PDB ID : 4WG5
Title : Calcium-Dependent Protein Kinase 1 from Toxoplasma gondii (TgCDPK1) in complex with inhibitor UW1647
Authors : Merritt, E.A.
Deposited on : 2014-09-17
Resolution : 2.30 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 (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

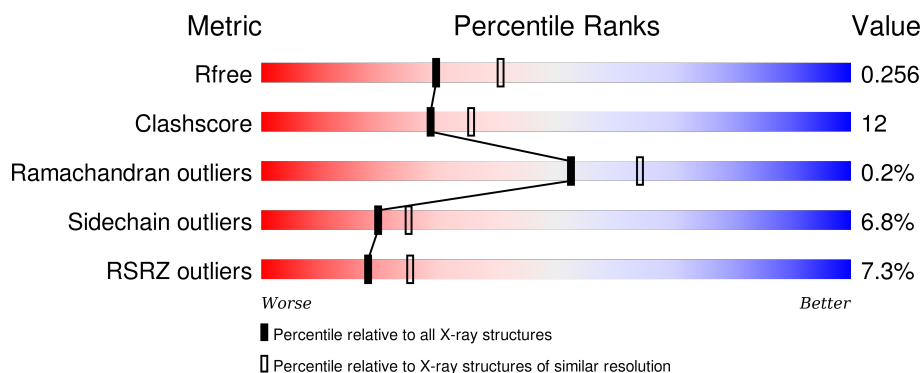
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	484	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3845 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.

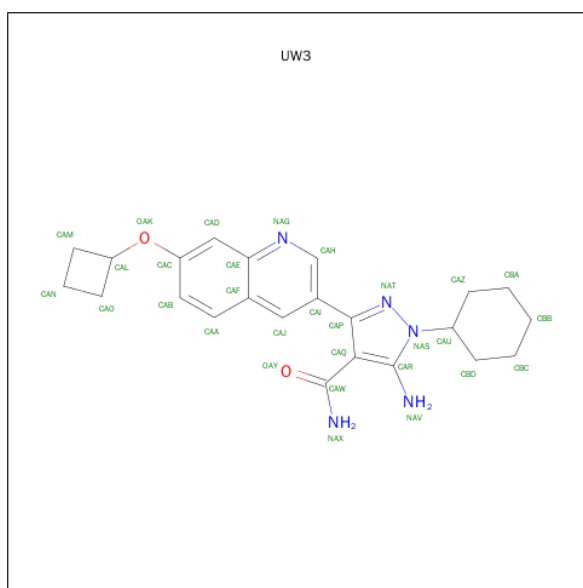
- Molecule 1 is a protein called Calmodulin-domain protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	464	Total	C	N	O	S	0	5	0
			3749	2374	627	728	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	expression tag	UNP Q9BJF5
A	25	PRO	-	expression tag	UNP Q9BJF5
A	26	GLY	-	expression tag	UNP Q9BJF5
A	27	SER	-	expression tag	UNP Q9BJF5
A	28	MET	-	expression tag	UNP Q9BJF5
A	29	MET	-	expression tag	UNP Q9BJF5

- Molecule 2 is 5-amino-3-[7-(cyclobutylloxy)quinolin-3-yl]-1-cyclohexyl-1H-pyrazole-4-carboxamide (three-letter code: UW3) (formula: C₂₃H₂₇N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			30	23	5	2		

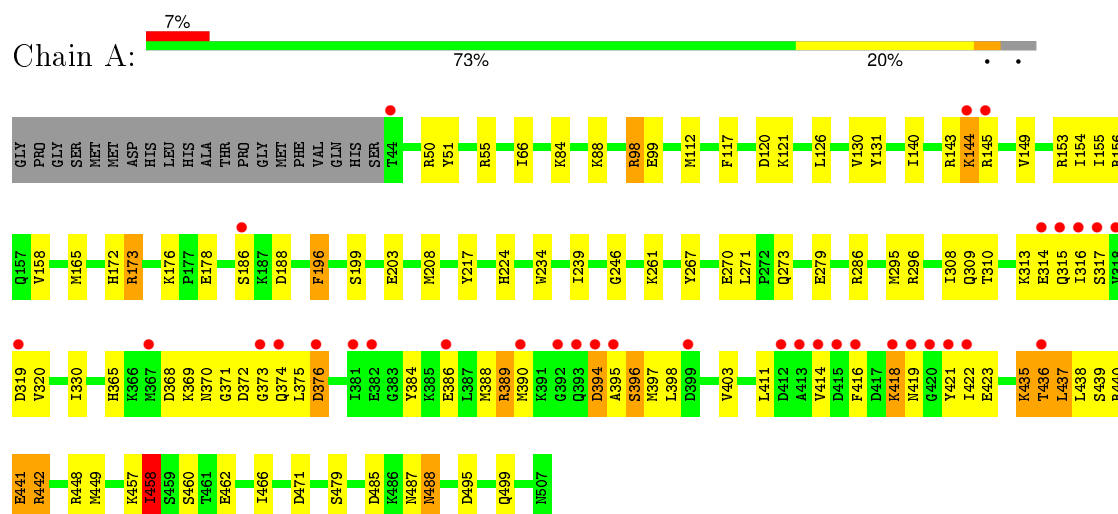
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	66	Total	O	0	0
			66	66		

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: Calmodulin-domain protein kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.19Å 72.95Å 67.88Å 90.00° 102.48° 90.00°	Depositor
Resolution (Å)	66.28 – 2.30 49.05 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.2 (66.28-2.30) 94.2 (49.05-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.220 , 0.259 0.225 , 0.256	Depositor DCC
R_{free} test set	936 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 19327 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3845	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.69% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UW3

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	0.94	2/3823 (0.1%)	0.94	8/5136 (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	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	217	TYR	CE1-CZ	-7.26	1.29	1.38
1	A	234	TRP	CE3-CZ3	6.65	1.49	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	ARG	NE-CZ-NH1	-7.72	116.44	120.30
1	A	296	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	A	448	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	A	458	ILE	CG1-CB-CG2	-5.60	99.08	111.40
1	A	156	ARG	NE-CZ-NH2	5.49	123.05	120.30
1	A	165	MET	CG-SD-CE	5.44	108.90	100.20
1	A	130	VAL	CB-CA-C	-5.20	101.53	111.40
1	A	55	ARG	NE-CZ-NH2	-5.11	117.75	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	414	VAL	Peptide
1	A	436	THR	Peptide

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	3749	0	3745	85	1
2	A	30	0	27	2	0
3	A	66	0	0	8	0
All	All	3845	0	3772	87	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 12.

All (87) 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:375:LEU:N	1:A:422:ILE:O	1.58	1.35
1:A:375:LEU:O	1:A:422:ILE:N	1.67	1.26
1:A:395:ALA:O	1:A:398:LEU:HG	1.60	1.02
1:A:384:TYR:CE2	1:A:388:MET:HE3	1.99	0.98
1:A:458:ILE:HD11	1:A:466:ILE:HD12	1.51	0.91
1:A:317:SER:O	1:A:320:VAL:HG22	1.74	0.88
1:A:394:ASP:OD1	1:A:396:SER:OG	1.91	0.86
1:A:436:THR:OG1	1:A:437:LEU:HD23	1.74	0.86
1:A:384:TYR:HE2	1:A:388:MET:HE3	1.42	0.84
1:A:319:ASP:O	1:A:320:VAL:HG13	1.80	0.82
1:A:397:MET:HE3	1:A:403:VAL:HA	1.63	0.81
1:A:458:ILE:CD1	1:A:466:ILE:HD12	2.11	0.81
1:A:375:LEU:C	1:A:422:ILE:H	1.85	0.80
1:A:384:TYR:CE2	1:A:388:MET:CE	2.65	0.78
1:A:186:SER:OG	1:A:188:ASP:OD1	2.03	0.77
1:A:438:LEU:O	1:A:438:LEU:HD13	1.83	0.76
1:A:375:LEU:O	1:A:422:ILE:CA	2.35	0.75
1:A:395:ALA:O	1:A:398:LEU:CG	2.36	0.74
1:A:386:GLU:HA	1:A:389:ARG:HE	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ARG:O	3:A:739:HOH:O	2.07	0.72
1:A:368:ASP:OD1	1:A:371:GLY:N	2.23	0.72
1:A:384:TYR:CD2	1:A:388:MET:HE3	2.25	0.72
1:A:458:ILE:CD1	1:A:466:ILE:CD1	2.67	0.72
1:A:411:LEU:HB2	1:A:418:LYS:HD2	1.80	0.64
1:A:384:TYR:HE2	1:A:388:MET:CE	2.07	0.62
1:A:178:GLU:HG3	3:A:751:HOH:O	2.00	0.60
1:A:370:ASN:HB3	1:A:372:ASP:HB2	1.82	0.60
1:A:458:ILE:HG13	1:A:462:GLU:HB2	1.84	0.59
1:A:224:HIS:HB2	3:A:717:HOH:O	2.03	0.59
1:A:376:ASP:HB3	1:A:421:TYR:CD1	2.38	0.58
1:A:196:PHE:HB2	3:A:731:HOH:O	2.02	0.58
1:A:270:GLU:O	1:A:271:LEU:HG	2.05	0.56
1:A:376:ASP:HA	1:A:422:ILE:HD12	1.87	0.55
1:A:397:MET:CE	1:A:403:VAL:HA	2.34	0.54
1:A:384:TYR:OH	1:A:435:LYS:NZ	2.36	0.54
1:A:375:LEU:CA	1:A:422:ILE:O	2.52	0.54
1:A:384:TYR:O	1:A:388:MET:HG2	2.09	0.53
1:A:112:MET:HG3	1:A:131:TYR:HE2	1.74	0.52
1:A:436:THR:O	1:A:438:LEU:N	2.42	0.51
1:A:246:GLY:HA2	1:A:330:ILE:HG13	1.92	0.51
1:A:317:SER:O	1:A:320:VAL:CG2	2.55	0.51
1:A:373:GLY:O	1:A:423:GLU:HA	2.11	0.51
1:A:375:LEU:O	1:A:422:ILE:CB	2.59	0.50
1:A:117:PHE:HD1	1:A:126:LEU:HD23	1.76	0.50
1:A:372:ASP:OD2	1:A:374:GLN:HG3	2.12	0.49
1:A:458:ILE:HD12	1:A:466:ILE:CD1	2.43	0.48
1:A:295[A]:MET:HE3	3:A:747:HOH:O	2.13	0.48
1:A:438:LEU:C	1:A:438:LEU:HD13	2.34	0.48
1:A:485:ASP:HB3	1:A:488:ASN:HB3	1.96	0.48
1:A:140:ILE:O	1:A:143:ARG:HB2	2.14	0.47
2:A:601:UW3:CAM	3:A:746:HOH:O	2.63	0.47
1:A:384:TYR:CD2	1:A:388:MET:CE	2.93	0.47
1:A:368:ASP:OD2	1:A:373:GLY:N	2.39	0.47
1:A:370:ASN:C	1:A:372:ASP:N	2.64	0.46
1:A:436:THR:O	1:A:439:SER:N	2.47	0.46
1:A:84:LYS:NZ	1:A:120:ASP:O	2.48	0.46
1:A:208:MET:CE	1:A:471[A]:ASP:OD2	2.63	0.46
1:A:375:LEU:O	1:A:422:ILE:HB	2.15	0.46
1:A:66:ILE:HD11	1:A:395:ALA:HB3	1.98	0.46
1:A:372:ASP:OD2	1:A:374:GLN:CG	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:ILE:HG13	1:A:462:GLU:CB	2.46	0.46
1:A:438:LEU:HD22	1:A:438:LEU:HA	1.82	0.45
1:A:440:ARG:HD3	1:A:440:ARG:O	2.17	0.45
1:A:149:VAL:O	1:A:153:ARG:HG3	2.15	0.45
2:A:601:UW3:H1	3:A:746:HOH:O	2.17	0.45
1:A:319:ASP:O	1:A:320:VAL:CG1	2.59	0.44
1:A:376:ASP:HB3	1:A:421:TYR:HD1	1.82	0.44
1:A:273:GLN:HB2	3:A:764:HOH:O	2.17	0.44
1:A:144:LYS:H	1:A:144:LYS:HG2	1.52	0.43
1:A:370:ASN:HB3	1:A:372:ASP:CB	2.47	0.43
1:A:154:ILE:O	1:A:158:VAL:HG23	2.19	0.43
1:A:50:ARG:HG2	1:A:51:TYR:CE2	2.55	0.42
1:A:316:ILE:O	1:A:316:ILE:HG13	2.19	0.42
1:A:308:ILE:O	1:A:309:GLN:C	2.56	0.42
1:A:279:GLU:OE2	1:A:286:ARG:NH1	2.48	0.42
1:A:495:ASP:OD2	1:A:499:GLN:NE2	2.51	0.42
1:A:155:ILE:HD13	1:A:155:ILE:HA	1.87	0.42
1:A:442:ARG:HG3	1:A:442:ARG:HH11	1.84	0.42
1:A:395:ALA:HA	1:A:398:LEU:HD21	2.02	0.41
1:A:437:LEU:O	1:A:441:GLU:HB2	2.20	0.41
1:A:176:LYS:HA	1:A:239:ILE:HD11	2.01	0.41
1:A:310:THR:O	1:A:313:LYS:HG2	2.20	0.41
1:A:374:GLN:O	1:A:375:LEU:HD23	2.20	0.41
1:A:314:GLU:HG2	1:A:314:GLU:O	2.20	0.41
1:A:267:TYR:CD1	1:A:267:TYR:N	2.88	0.41
1:A:172:HIS:O	1:A:173:ARG:CB	2.69	0.41
1:A:88:LYS:HB3	1:A:203:GLU:HB3	2.03	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:A:98:ARG:NH1	1:A:479:SER:OG[2_645]	2.02	0.18

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	467/484 (96%)	450 (96%)	16 (3%)	1 (0%)	52 64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	ARG

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	415/427 (97%)	387 (93%)	28 (7%)	20 26

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	ARG
1	A	99	GLU
1	A	121	LYS
1	A	144	LYS
1	A	196	PHE
1	A	199	SER
1	A	261	LYS
1	A	315	GLN
1	A	365	HIS
1	A	369	LYS
1	A	376	ASP
1	A	389	ARG
1	A	390	MET
1	A	394	ASP
1	A	396	SER
1	A	416	PHE

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Mol	Chain	Res	Type
1	A	418	LYS
1	A	419	ASN
1	A	435	LYS
1	A	437	LEU
1	A	441	GLU
1	A	442	ARG
1	A	449	MET
1	A	457	LYS
1	A	458	ILE
1	A	460	SER
1	A	487	ASN
1	A	488	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	370	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 ⓘ

1 ligand 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	$\# Z > 2$
2	UW3	A	601	-	31,34,34	3.45	8 (25%)	36,49,49	2.57	14 (38%)

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	UW3	A	601	-	-	0/8/30/30	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	UW3	CAI-CAP	-14.67	1.33	1.49
2	A	601	UW3	CAQ-CAW	-5.85	1.39	1.51
2	A	601	UW3	CAQ-CAP	-4.54	1.36	1.41
2	A	601	UW3	CAQ-CAR	-4.11	1.35	1.42
2	A	601	UW3	CAF-CAE	-3.91	1.36	1.42
2	A	601	UW3	CAE-NAG	-3.19	1.31	1.37
2	A	601	UW3	CAP-NAT	-2.20	1.33	1.35
2	A	601	UW3	CAH-NAG	5.04	1.40	1.31

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	UW3	OAY-CAW-NAX	-3.97	117.01	122.59
2	A	601	UW3	CAF-CAE-NAG	-3.13	117.61	122.08
2	A	601	UW3	CBD-CAU-NAS	-3.10	106.81	110.92
2	A	601	UW3	CAC-CAD-CAE	-2.81	117.46	119.14
2	A	601	UW3	CBB-CBC-CBD	-2.42	106.36	111.44
2	A	601	UW3	CAI-CAJ-CAF	-2.35	117.22	121.44
2	A	601	UW3	CAI-CAH-NAG	-2.23	122.64	125.46
2	A	601	UW3	CBB-CBA-CAZ	-2.03	107.19	111.44
2	A	601	UW3	CAJ-CAI-CAP	2.39	124.20	120.11
2	A	601	UW3	CAH-NAG-CAE	2.88	120.23	116.95
2	A	601	UW3	CAD-CAE-CAF	4.59	123.91	119.22
2	A	601	UW3	CAJ-CAF-CAE	4.97	124.20	118.28
2	A	601	UW3	CAN-CAO-CAL	5.16	92.95	88.17
2	A	601	UW3	CAN-CAM-CAL	7.05	94.70	88.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	UW3	2	0

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	464/484 (95%)	0.34	34 (7%) 18 25	21, 46, 101, 164	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	393	GLN	11.5
1	A	421	TYR	8.9
1	A	317	SER	7.7
1	A	420	GLY	7.7
1	A	419	ASN	6.9
1	A	415	ASP	5.2
1	A	316	ILE	5.1
1	A	315	GLN	4.8
1	A	318	VAL	4.6
1	A	367	MET	3.7
1	A	386	GLU	3.5
1	A	373	GLY	3.3
1	A	314	GLU	3.2
1	A	392	GLY	3.2
1	A	399	ASP	3.1
1	A	422	ILE	3.1
1	A	390	MET	3.1
1	A	395	ALA	3.0
1	A	319	ASP	2.9
1	A	394	ASP	2.8
1	A	413	ALA	2.5
1	A	376	ASP	2.5
1	A	436	THR	2.4
1	A	418	LYS	2.4
1	A	381	ILE	2.3
1	A	144	LYS	2.2
1	A	145	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	186	SER	2.1
1	A	416	PHE	2.1
1	A	374	GLN	2.1
1	A	382	GLU	2.1
1	A	412	ASP	2.1
1	A	44	THR	2.0
1	A	414	VAL	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	UW3	A	601	30/30	0.96	0.13	-0.15	16,26,37,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.