



Preliminary Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2020 – 12:29 AM EST

Deposition ID : D_1000253320

This is a Preliminary Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB Deposition System during initial deposition but before annotation of the structure.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

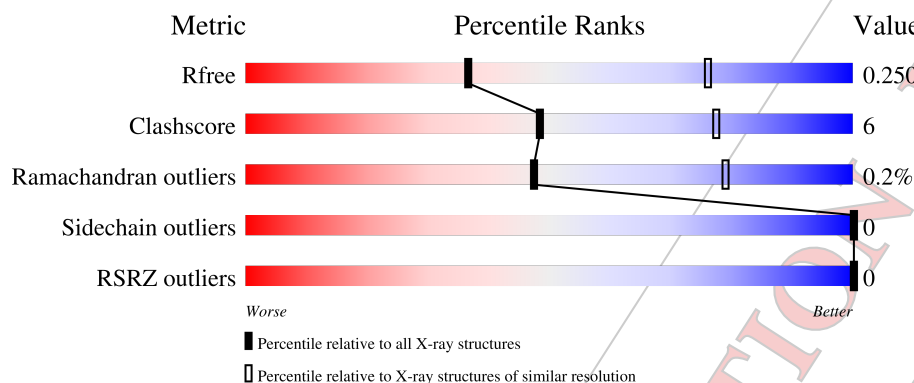
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 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	317	 70% 13% 17%
1	B	317	 66% 13% 21%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3991 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 SERINE/THREONINE-PROTEIN KINASE DCLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			1993	1293	324	367	9			
1	B	251	Total	C	N	O	S	0	0	0
			1928	1251	313	354	10			

- Molecule 2 is a ligand with the chemical component id XXX but its atom names do not match the existing wwPDB Chemical Component Dictionary definition for XXX. Consequently no firm identification of ligand chemistry can be made. Once the structure is annotated then an identification and diagram will be given here.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			35	26	7	2		
2	B	1	Total	C	N	O	0	0
			35	26	7	2		

i

- Molecule 1: SERINE/THREONINE-PROTEIN KINASE DCLK1



4 Data and refinement statistics [i](#)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.92Å 62.43Å 72.08Å 90.00° 96.07° 90.00°	Depositor
Resolution (Å)	71.68 – 3.10 71.68 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (71.68-3.10) 99.5 (71.68-3.10)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.193 , 0.251 0.192 , 0.250	Depositor DCC
R_{free} test set	562 reflections (5.25%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3991	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.27	0/2030	0.47	0/2763
1	B	0.27	0/1966	0.46	0/2675
All	All	0.27	0/3996	0.47	0/5438

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 [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	1993	0	1954	23	0
1	B	1928	0	1913	25	0
2	A	35	0	3	1	0
2	B	35	0	3	1	0
All	All	3991	0	3873	47	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 6.

All (47) 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:585:PRO:O	1:A:588:ARG:NH1	2.28	0.66
1:A:468:VAL:O	2:A:1:XXX:N2	2.34	0.61
1:B:567:LYS:O	1:B:635:ARG:NH1	2.36	0.58
1:B:434:GLN:HG3	1:B:461:LEU:HD22	1.85	0.58
1:A:551:PRO:HB3	1:A:598:PHE:HE1	1.69	0.57
1:B:454:GLU:OE1	1:B:454:GLU:N	2.37	0.57
1:B:572:ALA:O	1:B:576:ILE:HG13	2.07	0.55
1:B:468:VAL:O	2:B:1:XXX:N2	2.39	0.54
1:B:437:VAL:O	1:B:441:ARG:HG3	2.08	0.54
1:A:515:GLU:N	1:A:515:GLU:OE1	2.28	0.54
1:B:494:ASN:ND2	1:B:528:SER:HA	2.23	0.53
1:B:420:ILE:HG12	1:B:462:TYR:CE2	2.43	0.53
1:A:446:PRO:O	1:A:530:LYS:HE2	2.09	0.53
1:A:420:ILE:HG12	1:A:462:TYR:CE2	2.46	0.51
1:B:440:LEU:HA	1:B:443:VAL:HG22	1.93	0.51
1:B:495:LEU:HD13	1:B:517:LEU:HD21	1.92	0.50
1:A:511:ASP:HB2	1:A:536:LEU:HD12	1.94	0.50
1:A:457:VAL:HG13	1:A:458:PRO:HD2	1.93	0.50
1:A:423:LYS:NZ	1:A:456:ASP:OD1	2.26	0.49
1:B:459:THR:HG23	1:B:460:GLU:HG3	1.94	0.49
1:A:459:THR:OG1	1:A:460:GLU:OE1	2.27	0.49
1:B:450:LEU:H	1:B:466:GLU:HG2	1.77	0.49
1:A:419:LYS:NZ	1:A:436:GLU:OE2	2.42	0.48
1:A:437:VAL:HG21	1:A:461:LEU:HD21	1.96	0.48
1:A:466:GLU:OE2	1:A:530:LYS:NZ	2.36	0.47
1:B:446:PRO:O	1:B:530:LYS:HE2	2.15	0.47
1:A:550:THR:O	1:A:554:VAL:HG23	2.16	0.46
1:B:623:LEU:HB2	1:B:644:HIS:CE1	2.51	0.45
1:A:572:ALA:O	1:A:576:ILE:HG13	2.16	0.45
1:B:578:TYR:CG	1:B:586:PRO:HG3	2.52	0.45
1:A:426:CYS:HA	1:B:548:CYS:HB3	1.99	0.44
1:A:665:LYS:HE3	1:A:665:LYS:HB2	1.75	0.44
1:B:493:TYR:O	1:B:497:SER:OG	2.28	0.44
1:B:416:TYR:CE1	1:B:452:ILE:HG13	2.53	0.44
1:B:644:HIS:O	1:B:647:VAL:HG22	2.17	0.44
1:B:429:LYS:HB3	1:B:432:MET:HB2	2.00	0.43
1:A:383:PRO:HB2	1:A:385:THR:HG22	2.00	0.43
1:B:466:GLU:OE1	1:B:530:LYS:NZ	2.47	0.42
1:A:578:TYR:CG	1:A:586:PRO:HG3	2.55	0.42
1:A:411:SER:OG	1:A:412:THR:HG23	2.19	0.41
1:A:389:ARG:NH1	1:A:453:GLU:OE2	2.34	0.41
1:A:501:TYR:O	1:A:504:SER:OG	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:383:PRO:O	1:B:387:THR:HG23	2.21	0.41
1:B:582:CYS:HB2	1:B:584:PHE:CE2	2.55	0.41
1:A:492:LEU:HD13	1:A:577:THR:OG1	2.21	0.40
1:B:440:LEU:HD23	1:B:440:LEU:HA	1.90	0.40
1:B:492:LEU:HD13	1:B:577:THR:OG1	2.21	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	251/317 (79%)	243 (97%)	7 (3%)	1 (0%)	34	69
1	B	241/317 (76%)	236 (98%)	5 (2%)	0	100	100
All	All	492/634 (78%)	479 (97%)	12 (2%)	1 (0%)	47	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	665	LYS

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	208/272 (76%)	208 (100%)	0	100	100
1	B	205/272 (75%)	205 (100%)	0	100	100
All	All	413/544 (76%)	413 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	494	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

PRELIMINARY VALIDATION REPORT

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	263/317 (82%)	-0.30	0 100 100	13, 33, 69, 87	0
1	B	251/317 (79%)	-0.19	0 100 100	23, 42, 70, 87	0
All	All	514/634 (81%)	-0.25	0 100 100	13, 38, 70, 87	0

There are no RSRZ outliers to report.

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 monosaccharides in this entry.

6.4 Ligands [i](#)

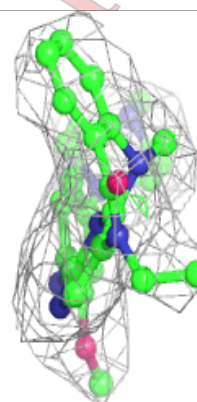
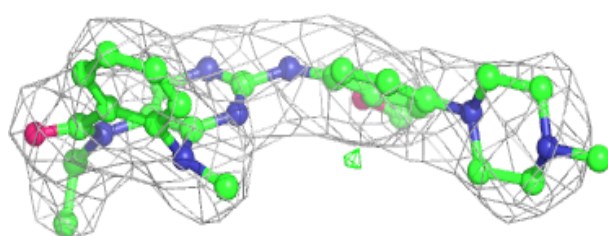
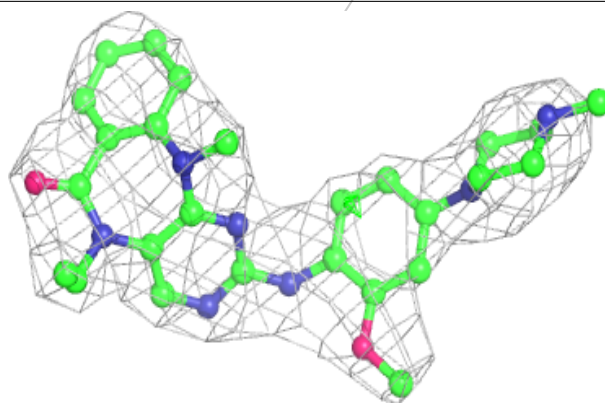
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
2	XXX	A	1	35/?	0.96	0.20	31,40,66,71	0
2	XXX	B	1	35/?	0.96	0.19	25,36,63,72	0

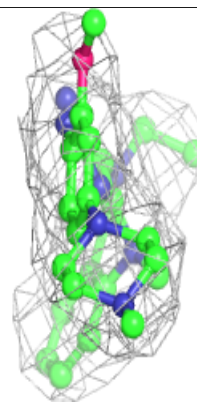
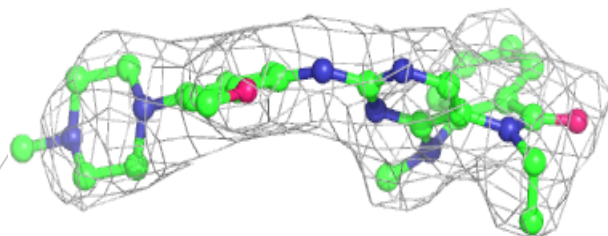
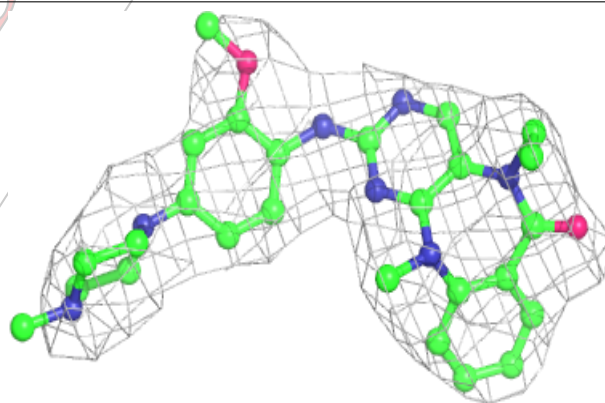
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around XXX A 1:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around XXX B 1:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.

PRELIMINARY VALIDATION REPORT