



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 14, 2020 – 05:28 AM BST

PDB ID : 6O5Z
Title : Crystal Structure of the human MLKL pseudokinase domain bound to compound 2
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Deposited on : 2019-03-04
Resolution : 2.29 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 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 : **FAILED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

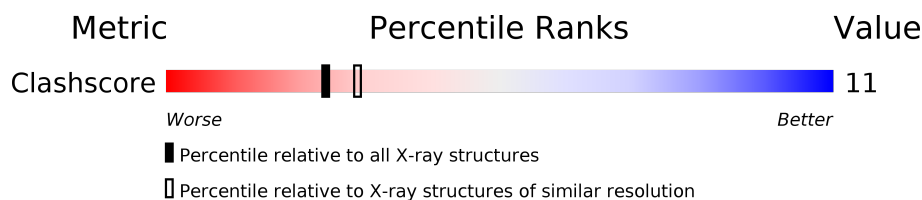
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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))
Clashscore	141614	7711 (2.30-2.26)

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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	287	 74% 21% 6%
1	B	287	 72% 19% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4482 atoms, of which 30 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 Mixed lineage kinase domain-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	0	0
			2184	1393	375	407	9			
1	B	260	Total	C	N	O	S	0	0	0
			2105	1342	363	392	8			

There are 10 discrepancies between the modelled and reference sequences:

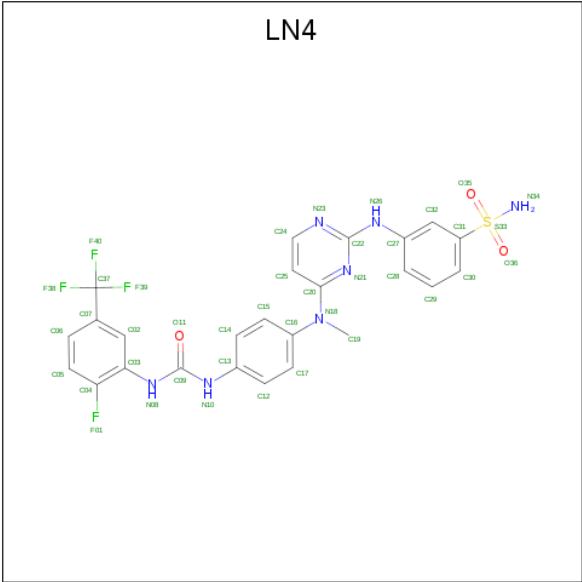
Chain	Residue	Modelled	Actual	Comment	Reference
A	185	GLY	-	expression tag	UNP Q8NB16
A	186	ALA	-	expression tag	UNP Q8NB16
A	187	MET	-	expression tag	UNP Q8NB16
A	188	GLY	-	expression tag	UNP Q8NB16
A	189	SER	-	expression tag	UNP Q8NB16
B	185	GLY	-	expression tag	UNP Q8NB16
B	186	ALA	-	expression tag	UNP Q8NB16
B	187	MET	-	expression tag	UNP Q8NB16
B	188	GLY	-	expression tag	UNP Q8NB16
B	189	SER	-	expression tag	UNP Q8NB16

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 3 is 1-[2-fluoranyl-5-(trifluoromethyl)phenyl]-3-[4-[methyl-2-[(3-sulfamoylphenyl)amino]pyrimidin-4-yl]amino]phenyl]urea (three-letter code: LN4) (formula: C₂₅H₂₁F₄N₇O₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	F	N	O	S	0	0
			40	25	4	7	3	1		

- Molecule 4 is water.

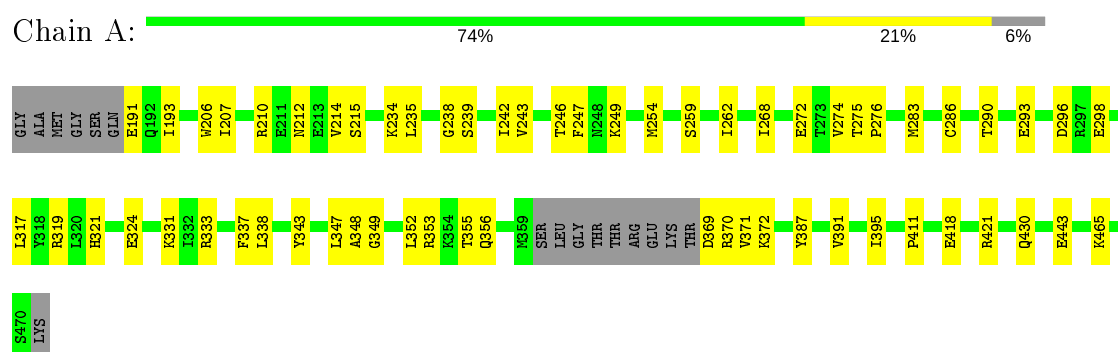
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	48	Total	O	0	0
			48	48		
4	B	55	Total	O	0	0
			55	55		

3 Residue-property plots [i](#)

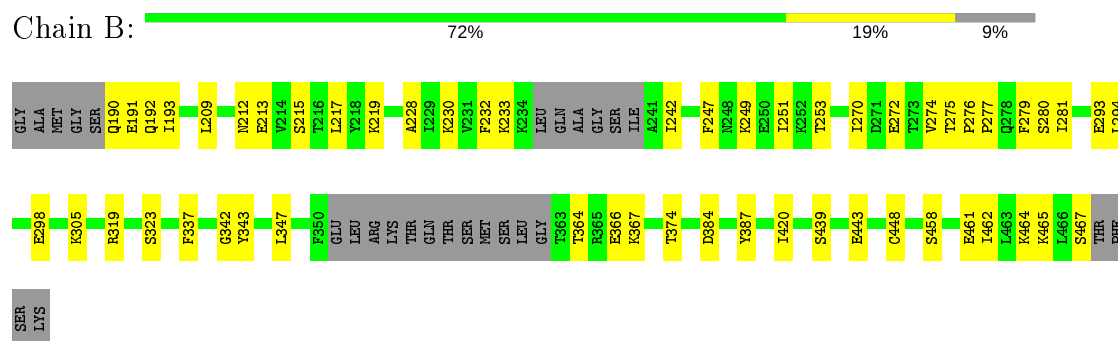
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS failed to run properly.

- Molecule 1: Mixed lineage kinase domain-like protein



- Molecule 1: Mixed lineage kinase domain-like protein



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.16 Å 118.84 Å 52.76 Å 90.00° 116.78° 90.00°	Depositor
Resolution (Å)	47.10 – 2.29	Depositor
% Data completeness (in resolution range)	98.8 (47.10-2.29)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.65 (at 2.29 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.183 , 0.232	Depositor
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.283	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.038 for h,-k,-h-l	Xtriage
Total number of atoms	4482	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: LN4, EDO

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	0.31	0/2223	0.47	0/2992
1	B	0.31	0/2142	0.49	0/2882
All	All	0.31	0/4365	0.48	0/5874

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

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	2184	0	2235	52	0
1	B	2105	0	2152	46	0
2	A	16	24	24	6	0
2	B	4	6	6	0	0
3	B	40	0	0	1	0
4	A	48	0	0	6	0
4	B	55	0	0	1	0
All	All	4452	30	4417	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 11.

The worst 5 of 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:331:LYS:HD2	1:A:353:ARG:HD3	1.37	1.02
1:A:430:GLN:NE2	4:A:602:HOH:O	2.00	0.94
1:A:331:LYS:HD2	1:A:353:ARG:CD	2.09	0.82
1:A:246:THR:HG23	1:A:352:LEU:HD13	1.69	0.74
1:B:215:SER:OG	1:B:230:LYS:NZ	2.20	0.74

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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](#)

6 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
3	LN4	B	501	-	43,43,43	1.60	9 (20%)	62,63,63	2.39	22 (35%)
2	EDO	B	502	-	3,3,3	0.43	0	2,2,2	0.38	0
2	EDO	A	502	-	3,3,3	0.54	0	2,2,2	0.17	0
2	EDO	A	501	-	3,3,3	0.50	0	2,2,2	0.25	0
2	EDO	A	504	-	3,3,3	0.44	0	2,2,2	0.35	0
2	EDO	A	503	-	3,3,3	0.53	0	2,2,2	0.31	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
3	LN4	B	501	-	-	7/32/32/32	0/4/4/4
2	EDO	B	502	-	-	0/1/1/1	-
2	EDO	A	502	-	-	1/1/1/1	-
2	EDO	A	501	-	-	0/1/1/1	-
2	EDO	A	504	-	-	0/1/1/1	-
2	EDO	A	503	-	-	0/1/1/1	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	LN4	C20-N21	3.38	1.39	1.34
3	B	501	LN4	C22-N26	3.24	1.43	1.36
3	B	501	LN4	C22-N23	3.22	1.39	1.34
3	B	501	LN4	C09-N08	3.13	1.44	1.37
3	B	501	LN4	C09-N10	2.76	1.43	1.37

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	LN4	C27-C32-C31	9.48	126.04	118.89
3	B	501	LN4	N10-C09-N08	6.28	123.47	112.49
3	B	501	LN4	C30-C31-C32	-5.34	114.06	120.62
3	B	501	LN4	C14-C13-C12	-3.76	113.89	119.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	LN4	N21-C20-N18	3.73	121.55	115.82

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

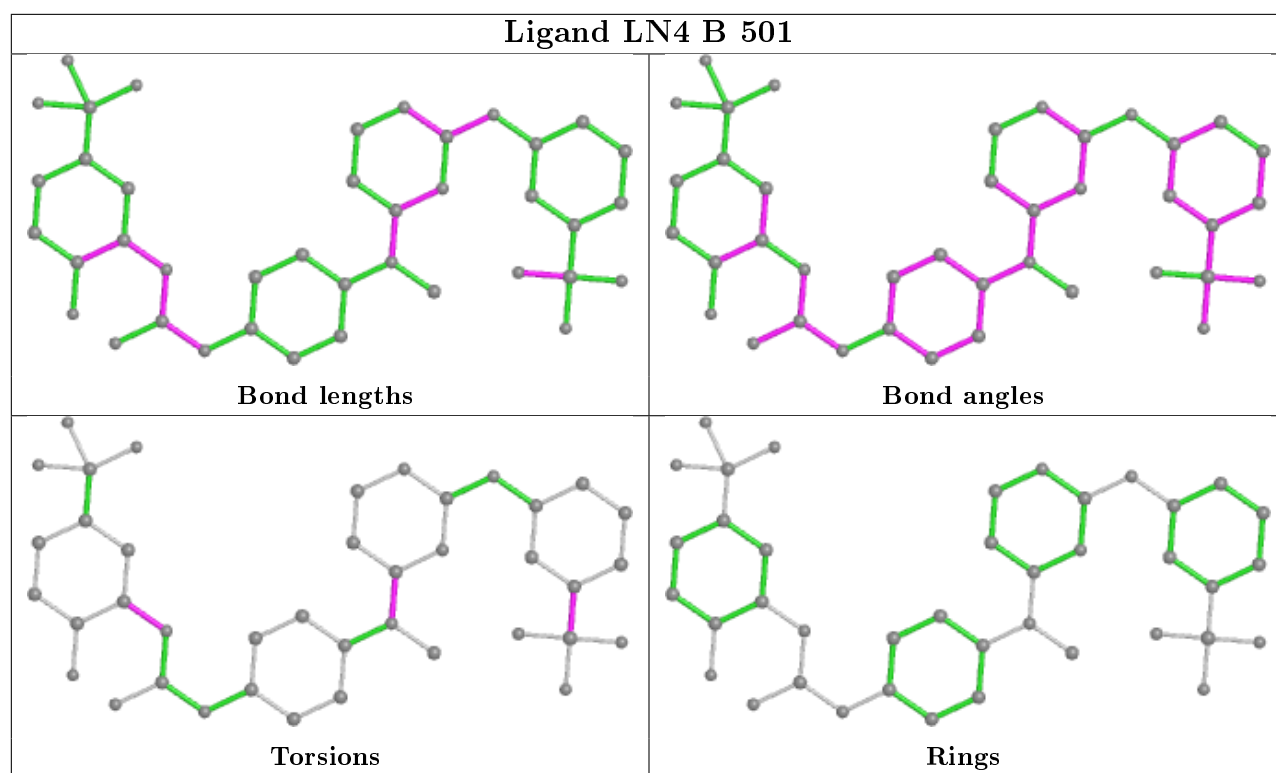
Mol	Chain	Res	Type	Atoms
2	A	502	EDO	O1-C1-C2-O2
3	B	501	LN4	C25-C20-N18-C16
3	B	501	LN4	C04-C03-N08-C09
3	B	501	LN4	C25-C20-N18-C19
3	B	501	LN4	N21-C20-N18-C16

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	LN4	1	0
2	A	502	EDO	3	0
2	A	501	EDO	2	0
2	A	504	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.