



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2021 – 12:10 PM JST

PDB ID : 6LN1
Title : A natural inhibitor of DYRK1A for treatment of diabetes mellitus
Authors : Li, H.; Chen, L.X.; Zheng, M.Z.; Zhang, Q.Z.; Zhang, C.L.; Wu, C.R.; Yang, K.Y.; Song, Z.R.; Wang, Q.Q.; Li, C.; Zhou, Y.R.; Chen, J.C.
Deposited on : 2019-12-28
Resolution : 2.70 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 : 2.23.2
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) : 2.23.2

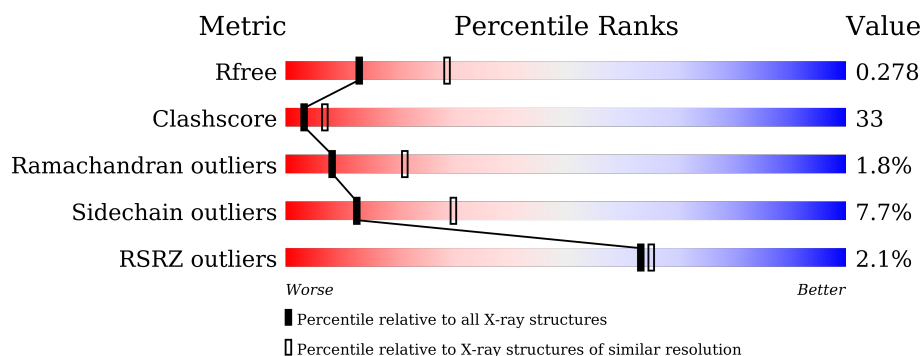
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 23%, yellow 23%, yellow 71%, green 71%, green 100%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 71% 23% • • </div> </div>
1	B	347	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 3%, orange 3%, orange 41%, yellow 41%, yellow 89%, green 89%, green 97%, green 100%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 3% 45% 41% 8% • 5% </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5626 atoms, of which 16 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.

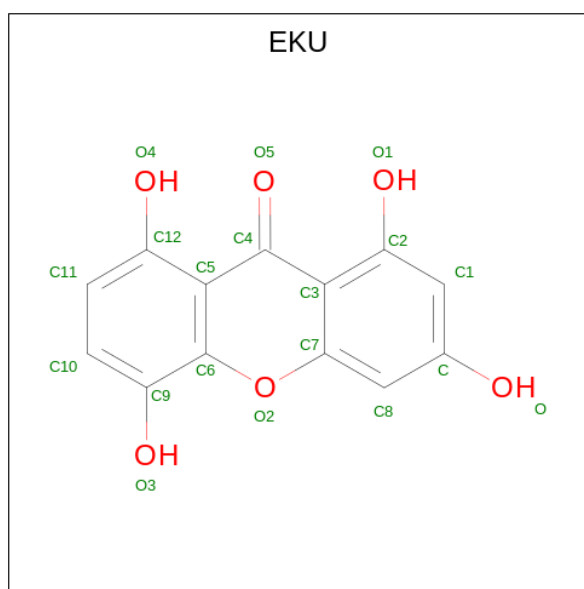
- Molecule 1 is a protein called Dual specificity tyrosine-phosphorylation-regulated kinase 1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	P	S	17	0	0
			2808	1809	481	500	1	17			
1	B	331	Total	C	N	O	P	S	18	0	0
			2720	1756	464	482	1	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	413	PHE	-	insertion	UNP Q13627
B	413	PHE	-	insertion	UNP Q13627

- Molecule 2 is 1,3,5,8-tetrakis(oxidanyl)xanthen-9-one (three-letter code: ECU) (formula: C₁₃H₈O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			27	13	8	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			27	13	8	6		

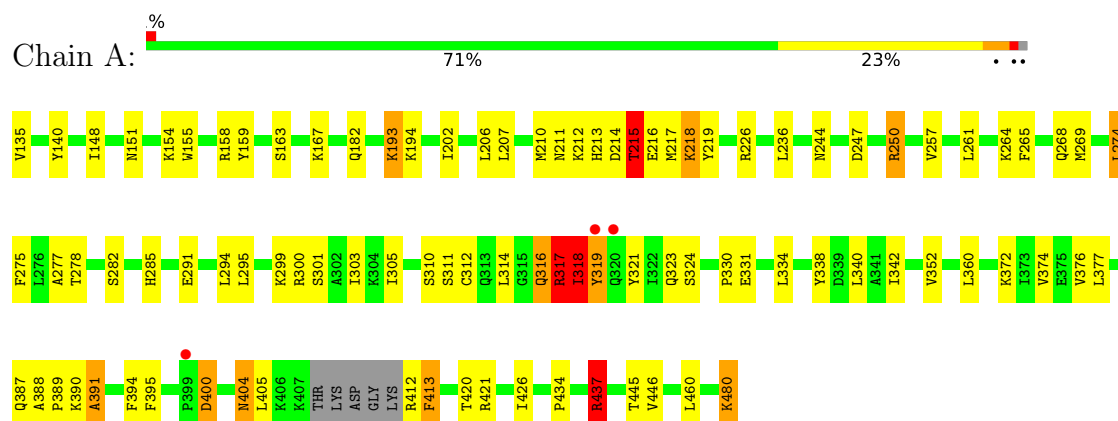
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total	O	0	0
			32	32		
3	B	12	Total	O	0	0
			12	12		

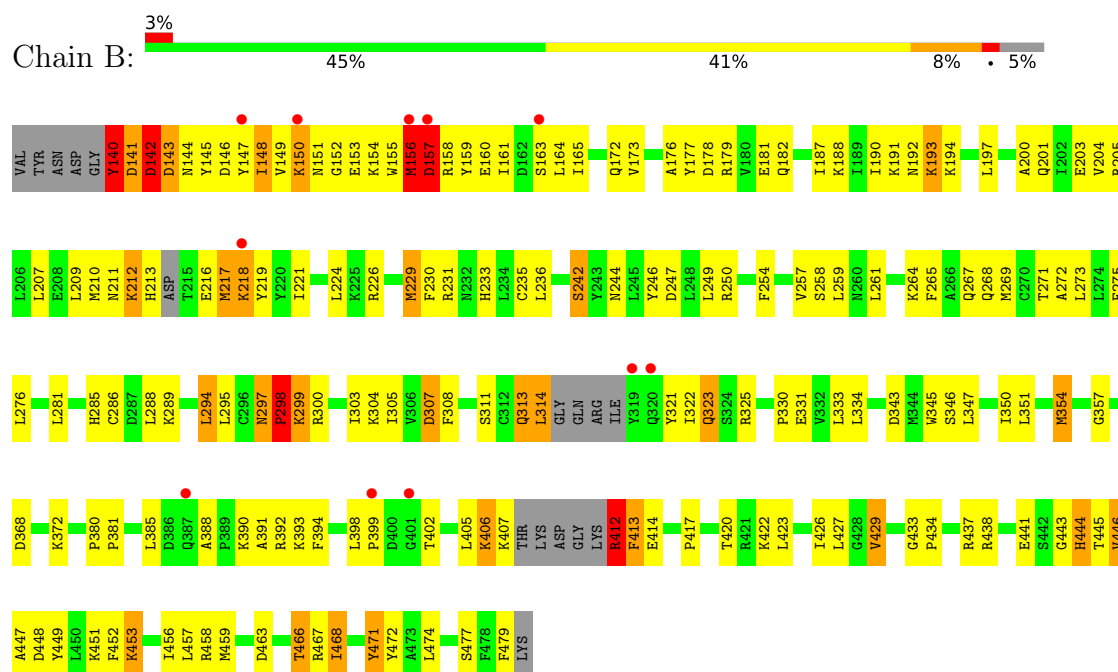
3 Residue-property plots

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 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: Dual specificity tyrosine-phosphorylation-regulated kinase 1A



- Molecule 1: Dual specificity tyrosine-phosphorylation-regulated kinase 1A



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	133.47Å 133.47Å 92.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.97 – 2.70 48.97 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.97-2.70) 99.9 (48.97-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.212 , 0.277 0.212 , 0.278	Depositor DCC
R_{free} test set	2015 reflections (7.80%)	wwPDB-VP
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5626	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: PTR, ECU

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	0.79	3/2857 (0.1%)	0.86	5/3850 (0.1%)
1	B	0.76	2/2766 (0.1%)	0.96	10/3725 (0.3%)
All	All	0.78	5/5623 (0.1%)	0.91	15/7575 (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	5
1	B	1	2
All	All	1	7

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	214	ASP	C-N	-19.16	0.90	1.34
1	B	313	GLN	C-N	8.42	1.53	1.34
1	A	317	ARG	C-N	-8.41	1.14	1.34
1	A	437	ARG	CG-CD	6.22	1.67	1.51
1	B	141	ASP	C-N	-5.23	1.22	1.34

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	142	ASP	N-CA-CB	-21.83	71.30	110.60
1	B	141	ASP	C-N-CA	-13.79	87.22	121.70
1	B	414	GLU	N-CA-C	-12.42	77.46	111.00
1	A	215	THR	CB-CA-C	-10.79	82.46	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	314	LEU	CB-CA-C	9.53	128.30	110.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	314	LEU	CA

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	215	THR	Peptide
1	A	317	ARG	Peptide,Mainchain
1	A	318	ILE	Peptide
1	A	319	TYR	Peptide
1	B	140	TYR	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	2808	0	2809	93	3
1	B	2720	0	2725	278	3
2	A	19	8	0	0	0
2	B	19	8	0	0	0
3	A	32	0	0	11	0
3	B	12	0	0	9	0
All	All	5610	16	5534	364	3

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 33.

The worst 5 of 364 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:B:438:ARG:HD2	1:B:444:HIS:CD2	1.47	1.47
1:B:151:ASN:HD21	1:B:163:SER:CA	1.35	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:313:GLN:O	1:B:314:LEU:HG	1.26	1.34
1:B:210:MET:HB3	1:B:218:LYS:NZ	1.42	1.30
1:B:438:ARG:HD2	1:B:444:HIS:NE2	1.48	1.28

All (3) 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:319:TYR:CD1	1:B:157:ASP:CB[3_655]	1.78	0.42
1:A:319:TYR:CE1	1:B:157:ASP:CB[3_655]	2.16	0.04
1:A:193:LYS:NZ	1:B:181:GLU:OE1[3_655]	2.19	0.01

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	337/347 (97%)	314 (93%)	20 (6%)	3 (1%)	17	40
1	B	322/347 (93%)	281 (87%)	32 (10%)	9 (3%)	5	11
All	All	659/694 (95%)	595 (90%)	52 (8%)	12 (2%)	8	21

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	ILE
1	B	157	ASP
1	B	406	LYS
1	B	413	PHE
1	B	156	MET

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	303/307 (99%)	283 (93%)	20 (7%)	16	38
1	B	294/307 (96%)	268 (91%)	26 (9%)	10	23
All	All	597/614 (97%)	551 (92%)	46 (8%)	13	30

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	212	LYS
1	B	354	MET
1	B	217	MET
1	B	258	SER
1	B	405	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	316	GLN
1	B	144	ASN
1	B	172	GLN
1	B	444	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	PTR	A	321	1	15,16,17	1.63	2 (13%)	19,22,24	0.72	0
1	PTR	B	321	1	15,16,17	1.13	1 (6%)	19,22,24	2.08	6 (31%)

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
1	PTR	A	321	1	-	0/10/11/13	0/1/1/1
1	PTR	B	321	1	-	2/10/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	PTR	OH-CZ	-4.97	1.29	1.40
1	B	321	PTR	P-OH	2.73	1.63	1.59
1	A	321	PTR	CB-CA	-2.01	1.49	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	321	PTR	CG-CB-CA	4.13	122.47	114.10
1	B	321	PTR	CE2-CZ-CE1	-3.86	114.23	120.18
1	B	321	PTR	CD2-CE2-CZ	3.67	124.23	119.73
1	B	321	PTR	P-OH-CZ	3.39	134.61	123.75
1	B	321	PTR	OH-CZ-CE1	2.87	127.76	119.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	321	PTR	N-CA-CB-CG
1	B	321	PTR	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
2	EKU	A	501	-	18,21,21	2.83	5 (27%)	26,32,32	1.89	7 (26%)
2	EKU	B	501	-	18,21,21	3.33	8 (44%)	26,32,32	2.20	6 (23%)

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	EKU	A	501	-	-	-	0/3/3/3
2	EKU	B	501	-	-	-	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	EKU	O5-C4	9.87	1.40	1.23
2	B	501	EKU	O2-C7	-8.42	1.23	1.36
2	B	501	EKU	O2-C6	-7.54	1.23	1.36
2	B	501	EKU	C12-C5	-4.03	1.35	1.43
2	B	501	EKU	C1-C	-3.76	1.33	1.39

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	EKU	C5-C4-C3	-6.59	115.52	123.40
2	B	501	EKU	C8-C7-C3	-5.31	117.17	123.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	EKU	C5-C4-C3	-4.43	118.11	123.40
2	A	501	EKU	O2-C6-C5	-4.14	116.61	120.87
2	B	501	EKU	O2-C7-C8	3.94	120.70	116.03

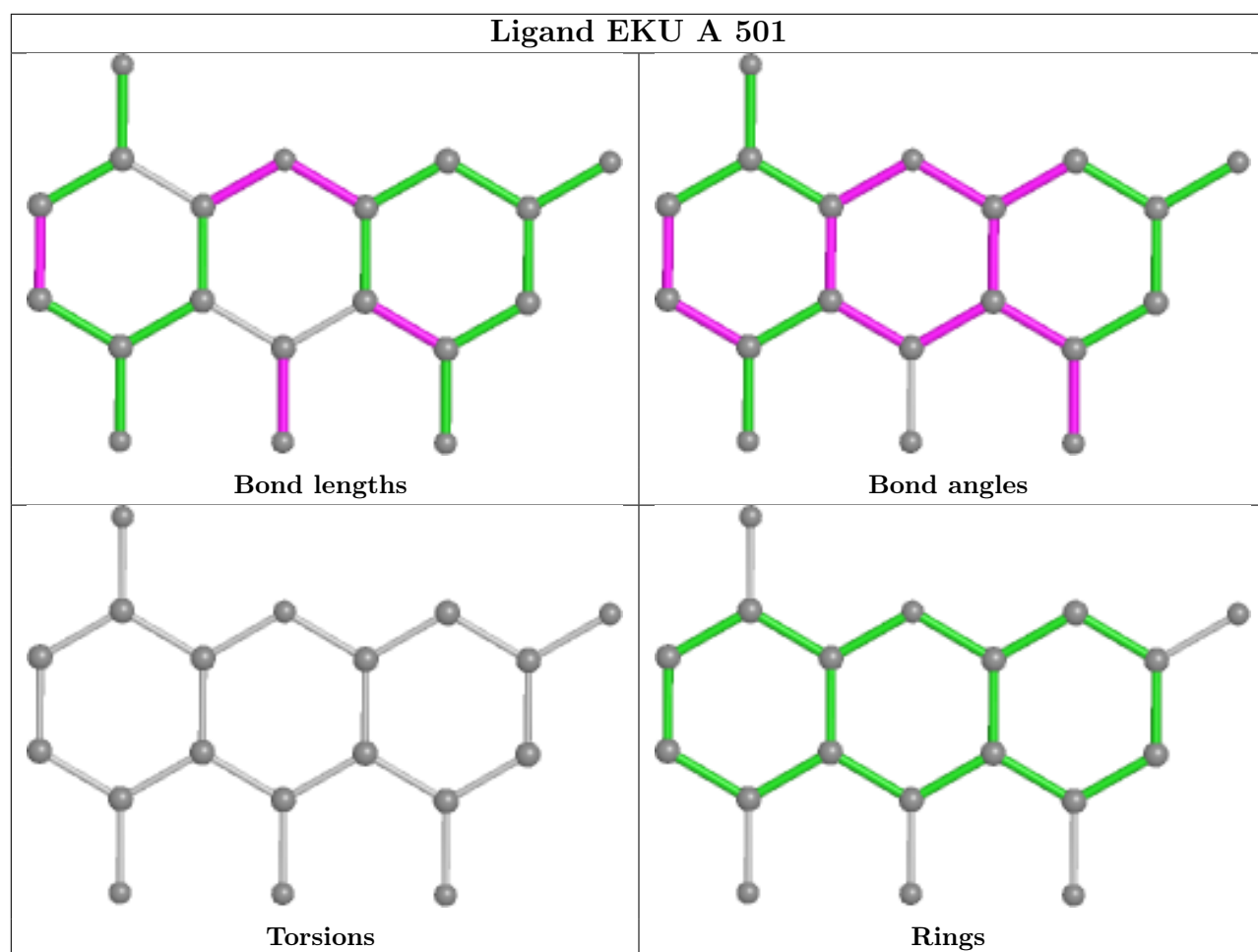
There are no chirality outliers.

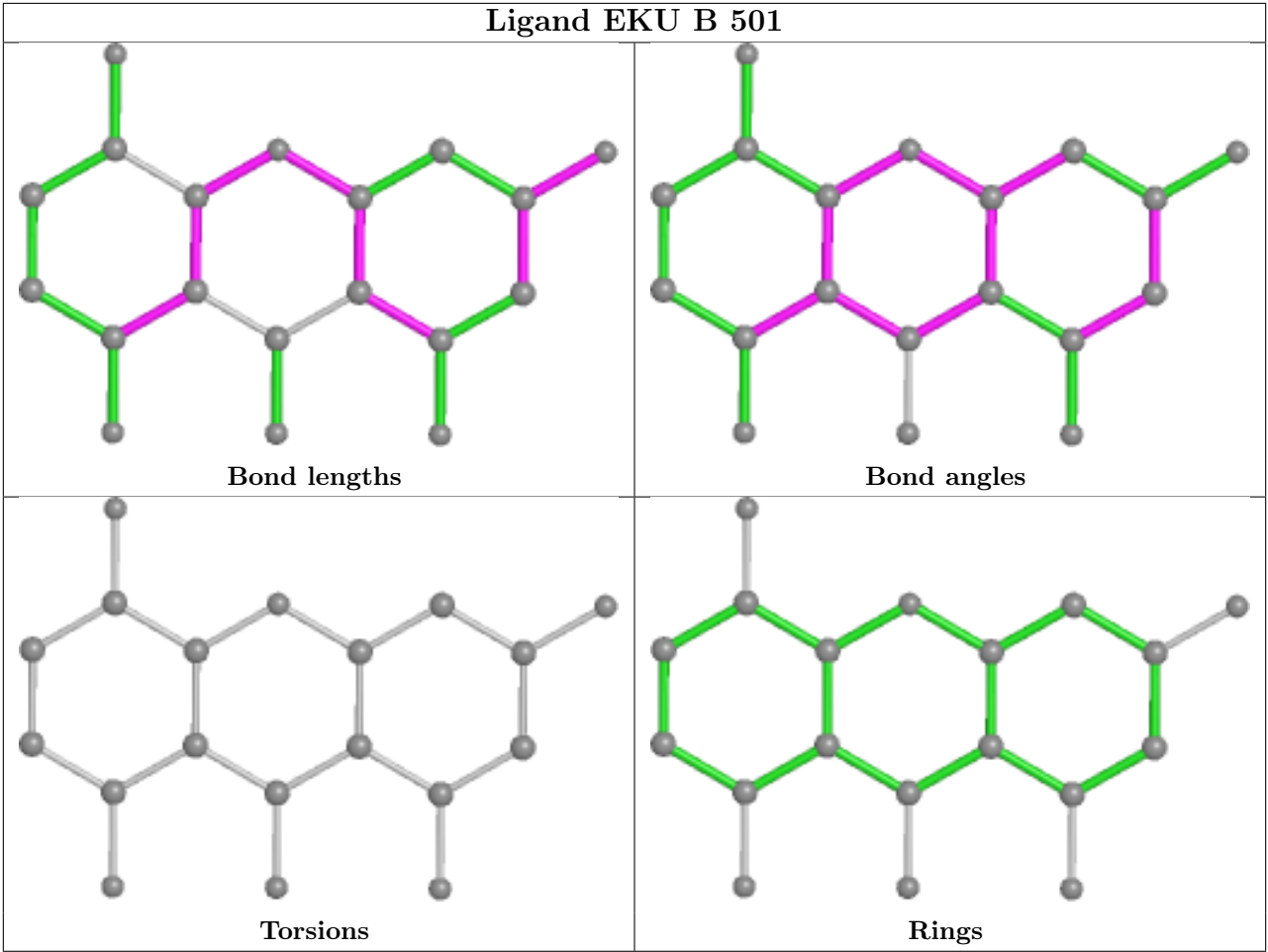
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	320:GLN	C	321:PTR	N	1.19
1	A	317:ARG	C	318:ILE	N	1.14
1	A	214:ASP	C	215:THR	N	0.90

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	341/347 (98%)	-0.28	3 (0%) 84 85	30, 46, 76, 107	1 (0%)
1	B	330/347 (95%)	0.14	11 (3%) 46 46	48, 81, 105, 117	0
All	All	671/694 (96%)	-0.07	14 (2%) 63 65	30, 64, 103, 117	1 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	319	TYR	5.0
1	B	401	GLY	3.6
1	B	218	LYS	3.5
1	B	147	TYR	3.3
1	B	156	MET	3.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

MODRES-RSR INFOmissingINFO

6.3 Carbohydrates [i](#)

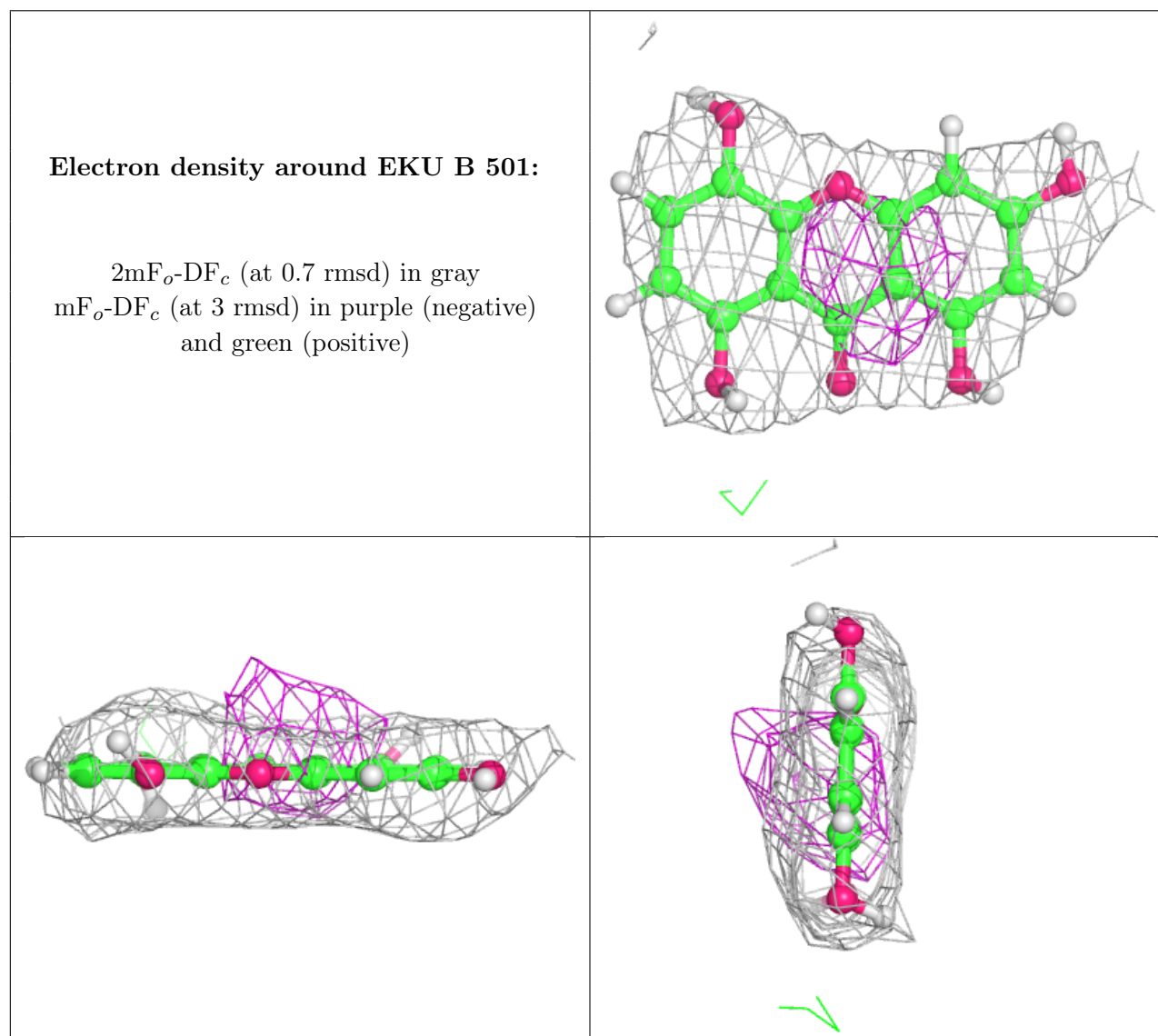
There are no monosaccharides in this entry.

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.

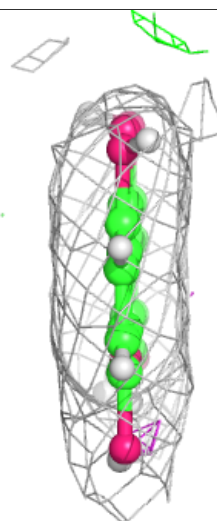
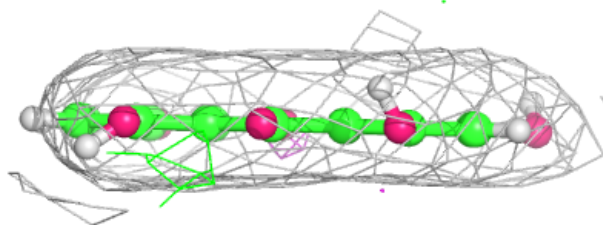
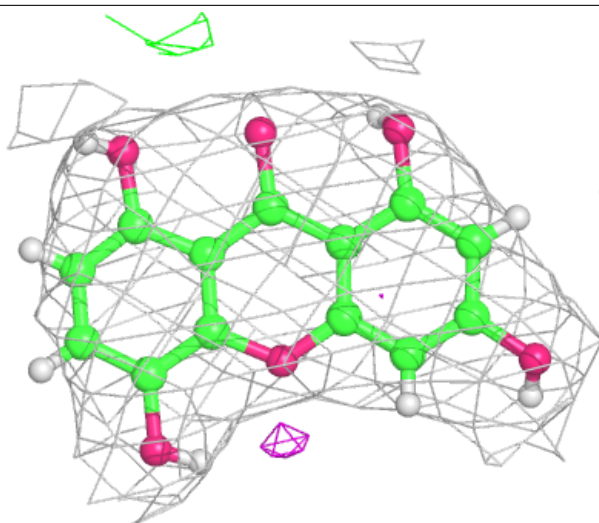
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EKU	B	501	19/19	0.87	0.22	64,74,89,91	0
2	EKU	A	501	19/19	0.96	0.17	34,42,50,53	0

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 EKV A 501:

$2mF_o-DF_c$ (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.