



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 07:48 AM UTC

PDB ID : 9CY5 / pdb\_00009cy5  
Title : Dyrk1a bound to a competitive inhibitor  
Authors : Montfort, W.R.  
Deposited on : 2024-08-01  
Resolution : 2.49 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](mailto: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>.

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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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

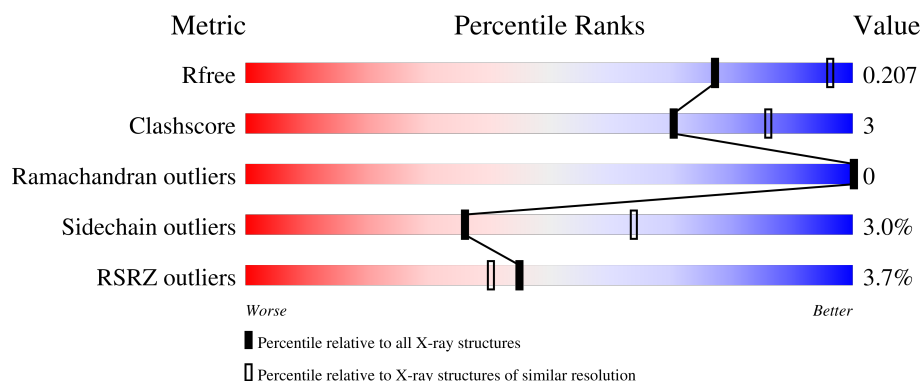
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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  $\geq 3$ , 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	365	
1	B	365	

## 2 Entry composition [i](#)

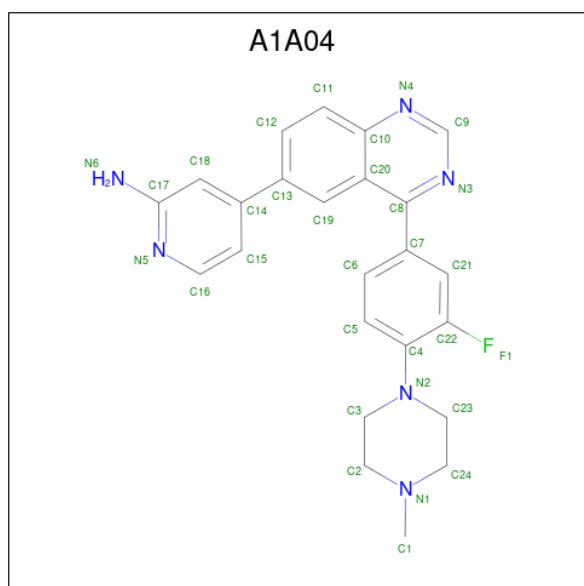
There are 4 unique types of molecules in this entry. The entry contains 5865 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dual specificity tyrosine-phosphorylation-regulated kinase 1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	P	S	0	5	0
			2829	1819	484	508	1	17			
1	B	342	Total	C	N	O	P	S	0	3	0
			2830	1819	487	506	1	17			

- Molecule 2 is (4P)-4-[(4M)-4-[3-fluoro-4-(4-methylpiperazin-1-yl)phenyl]quinazolin-6-yl]pyridin-2-amine (CCD ID: A1A04) (formula: C<sub>24</sub>H<sub>23</sub>FN<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	N	0	0
			31	24	1	6		
2	B	1	Total	C	F	N	0	0
			31	24	1	6		

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	8	5		

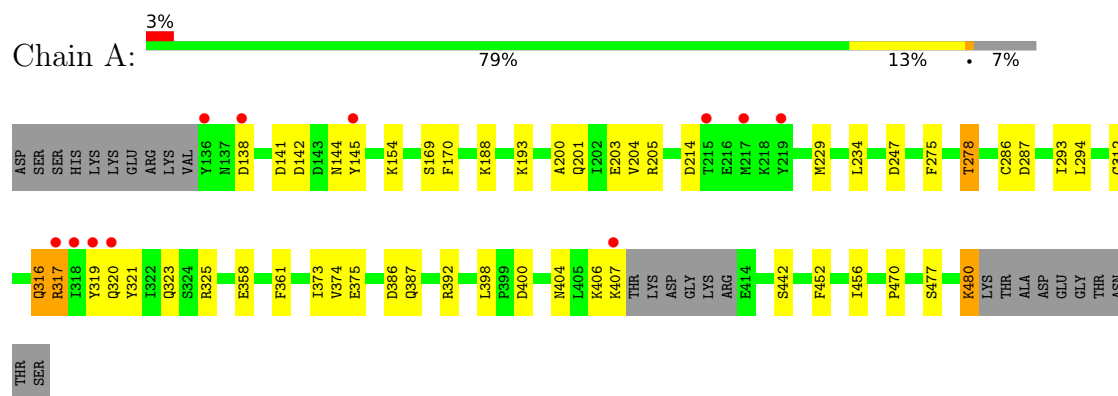
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	61	Total	O	0	0
			61	61		
4	B	70	Total	O	0	0
			70	70		

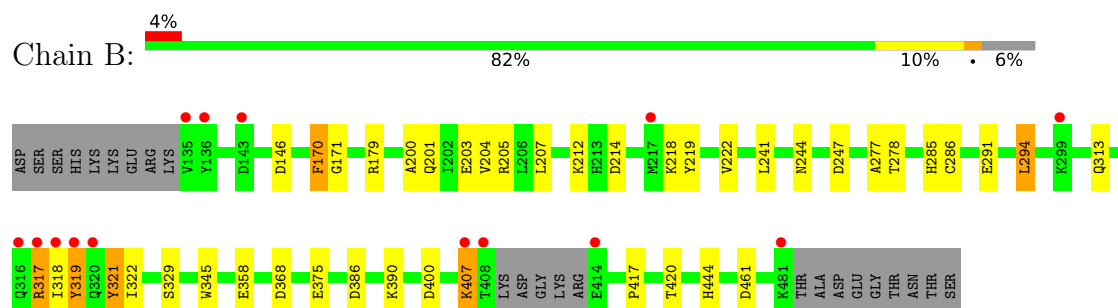
### 3 Residue-property plots [i](#)

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 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 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.89Å 84.65Å 148.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.81 – 2.49 24.81 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.1 (24.81-2.49) 99.3 (24.81-2.49)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.95 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.200 , 0.259 (Not available) , 0.207	Depositor DCC
$R_{free}$ test set	1472 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.3	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 20.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5865	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.61% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, A1A04, PG4

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	0.63	0/2878	1.17	9/3878 (0.2%)
1	B	0.62	0/2878	1.19	11/3878 (0.3%)
All	All	0.63	0/5756	1.18	20/7756 (0.3%)

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	3
1	B	0	2
All	All	0	5

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ASP	CA-CB-CG	7.43	120.03	112.60
1	B	368	ASP	CA-CB-CG	7.38	119.98	112.60
1	B	461	ASP	CA-CB-CG	7.22	119.82	112.60
1	B	212	LYS	CB-CA-C	-6.42	100.13	110.79
1	B	291	GLU	CB-CA-C	-6.17	100.19	110.68
1	A	142	ASP	CA-CB-CG	6.01	118.61	112.60
1	B	400	ASP	CA-CB-CG	6.00	118.60	112.60
1	A	141	ASP	CA-CB-CG	5.94	118.54	112.60
1	A	247	ASP	CA-CB-CG	5.91	118.50	112.60
1	A	287	ASP	CA-CB-CG	5.89	118.49	112.60
1	A	480	LYS	N-CA-CB	5.65	120.11	110.50
1	B	170	PHE	CA-CB-CG	-5.42	108.39	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	386	ASP	CA-CB-CG	5.38	117.98	112.60
1	A	400	ASP	CA-CB-CG	5.34	117.94	112.60
1	A	386	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	214	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	214	ASP	CA-CB-CG	5.29	117.89	112.60
1	B	375	GLU	CB-CA-C	-5.24	100.93	110.63
1	B	247	ASP	CA-CB-CG	5.16	117.76	112.60
1	B	212	LYS	N-CA-CB	5.15	117.69	110.12

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	205	ARG	Sidechain
1	A	325	ARG	Sidechain
1	A	392	ARG	Sidechain
1	B	179	ARG	Sidechain
1	B	317[A]	ARG	Sidechain

## 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	2829	0	2817	20	0
1	B	2830	0	2833	21	0
2	A	31	0	0	0	0
2	B	31	0	0	0	0
3	A	13	0	18	0	0
4	A	61	0	0	0	0
4	B	70	0	0	1	0
All	All	5865	0	5668	39	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 3.

All (39) 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:275:PHE:O	1:A:278:THR:HG23	1.73	0.87
1:A:201[B]:GLN:OE1	1:B:319:TYR:HB3	1.84	0.77
1:B:218:LYS:HD2	1:B:219:TYR:CE2	2.29	0.68
1:B:244:ASN:HB3	1:B:294:LEU:HD22	1.77	0.66
1:A:319:TYR:HA	1:B:201[A]:GLN:NE2	2.12	0.64
1:A:188:LYS:NZ	1:A:203:GLU:OE1	2.31	0.63
1:B:317[B]:ARG:O	1:B:317[B]:ARG:HG3	1.96	0.59
1:A:200:ALA:O	1:A:204:VAL:HG23	2.08	0.53
1:B:244:ASN:CB	1:B:294:LEU:HD22	2.40	0.52
1:A:319:TYR:O	1:A:320:GLN:NE2	2.43	0.50
1:A:312:CYS:HB2	1:A:316:GLN:HE21	1.76	0.50
1:B:205:ARG:NH2	1:B:313:GLN:OE1	2.45	0.50
1:B:417:PRO:HB2	1:B:420:THR:HG21	1.94	0.49
1:A:361:PHE:CE1	1:A:373:ILE:HA	2.47	0.49
1:B:203:GLU:HG2	1:B:207:LEU:HD12	1.94	0.49
1:B:222:VAL:HG23	1:B:241:LEU:HD11	1.97	0.47
1:B:146:ASP:OD1	1:B:171:GLY:HA2	2.15	0.47
1:B:285:HIS:O	1:B:286:CYS:HB2	2.13	0.47
1:A:145:TYR:CD2	1:A:193:LYS:HE2	2.49	0.47
1:B:170:PHE:C	1:B:170:PHE:CD1	2.92	0.47
1:A:317:ARG:O	1:A:320:GLN:NE2	2.49	0.46
1:B:218:LYS:HD2	1:B:219:TYR:CZ	2.51	0.46
1:B:200:ALA:O	1:B:204:VAL:HG23	2.16	0.46
1:B:407:LYS:HD2	1:B:407:LYS:H	1.81	0.45
1:A:229:MET:HE1	1:A:234:LEU:HD13	1.98	0.45
1:A:144:ASN:O	1:A:145:TYR:HB2	2.17	0.45
1:A:398:LEU:HD11	1:A:404:ASN:HD22	1.82	0.44
1:A:452:PHE:O	1:A:456:ILE:HG12	2.18	0.44
1:A:477:SER:HA	1:A:480:LYS:HG2	1.98	0.44
1:B:277:ALA:O	1:B:278:THR:C	2.60	0.44
1:A:170:PHE:CD1	1:A:170:PHE:C	2.97	0.42
1:B:321:PTR:O	1:B:321:PTR:CG	2.67	0.42
1:B:329:SER:HA	1:B:345:TRP:CD1	2.55	0.42
1:A:286:CYS:O	1:A:323:GLN:HA	2.20	0.41
1:A:312:CYS:HB2	1:A:316:GLN:NE2	2.35	0.41
1:A:293:ILE:C	1:A:294:LEU:HD12	2.46	0.41
1:A:374:VAL:O	1:A:375:GLU:C	2.64	0.41
1:B:203:GLU:HG2	1:B:207:LEU:CD1	2.51	0.41
1:B:444:HIS:CE1	4:B:641:HOH:O	2.75	0.40

There are no symmetry-related clashes.

## 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	339/365 (93%)	319 (94%)	20 (6%)	0	100	100
1	B	340/365 (93%)	320 (94%)	20 (6%)	0	100	100
All	All	679/730 (93%)	639 (94%)	40 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	305/323 (94%)	294 (96%)	11 (4%)	31	58
1	B	306/323 (95%)	299 (98%)	7 (2%)	44	72
All	All	611/646 (95%)	593 (97%)	18 (3%)	36	65

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	LYS
1	A	169	SER
1	A	278	THR
1	A	316	GLN
1	A	317	ARG
1	A	358	GLU
1	A	387	GLN
1	A	406	LYS

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Mol	Chain	Res	Type
1	A	407	LYS
1	A	442	SER
1	A	470	PRO
1	B	294	LEU
1	B	318	ILE
1	B	319	TYR
1	B	322	ILE
1	B	358	GLU
1	B	390	LYS
1	B	407	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	ASN
1	A	316	GLN
1	A	320	GLN
1	A	371	ASN
1	A	383	HIS
1	A	404	ASN
1	B	192	ASN
1	B	223	HIS
1	B	232	ASN
1	B	316	GLN
1	B	425	ASN
1	B	475	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	0.77	0	17,22,24	1.07	1 (5%)
1	PTR	B	321	1	15,16,17	0.92	0	17,22,24	1.09	1 (5%)

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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	321	PTR	OH-CZ-CE2	2.30	126.10	119.22
1	A	321	PTR	O3P-P-OH	2.09	111.50	105.32

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	321	PTR	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

3 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	A1A04	A	500	-	35,35,35	0.53	0	50,50,50	1.05	4 (8%)
2	A1A04	B	500	-	35,35,35	0.52	1 (2%)	50,50,50	1.08	3 (6%)
3	PG4	A	501	-	12,12,12	0.23	0	11,11,11	0.16	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	A1A04	A	500	-	-	2/12/22/22	0/5/5/5
2	A1A04	B	500	-	-	2/12/22/22	0/5/5/5
3	PG4	A	501	-	-	7/10/10/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	A1A04	C12-C13	2.07	1.43	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	A1A04	C20-C8-N3	-4.18	120.28	123.04
2	A	500	A1A04	C23-N2-C3	3.91	120.37	111.57
2	B	500	A1A04	C23-N2-C3	3.84	120.21	111.57
2	A	500	A1A04	C2-C3-N2	2.63	116.32	110.78
2	A	500	A1A04	C20-C8-N3	-2.23	121.57	123.04
2	A	500	A1A04	C23-N2-C4	2.04	121.03	116.19
2	B	500	A1A04	C14-C18-C17	2.00	119.39	117.35

There are no chirality outliers.

All (11) torsion outliers are listed below:

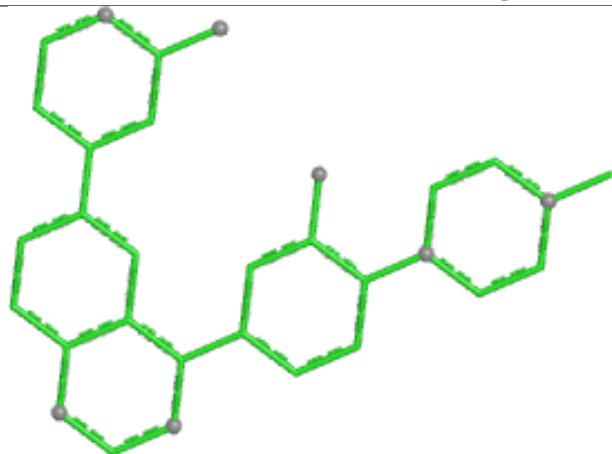
Mol	Chain	Res	Type	Atoms
2	A	500	A1A04	C22-C4-N2-C3
2	B	500	A1A04	C22-C4-N2-C23
3	A	501	PG4	O4-C7-C8-O5
3	A	501	PG4	C5-C6-O4-C7
3	A	501	PG4	C6-C5-O3-C4
3	A	501	PG4	C1-C2-O2-C3
2	B	500	A1A04	C5-C4-N2-C23
3	A	501	PG4	O1-C1-C2-O2
3	A	501	PG4	O2-C3-C4-O3
3	A	501	PG4	O3-C5-C6-O4
2	A	500	A1A04	C5-C4-N2-C3

There are no ring outliers.

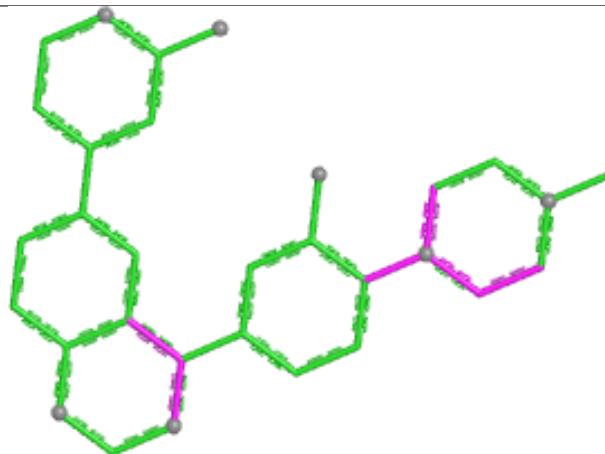
No monomer is involved in short contacts.

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.

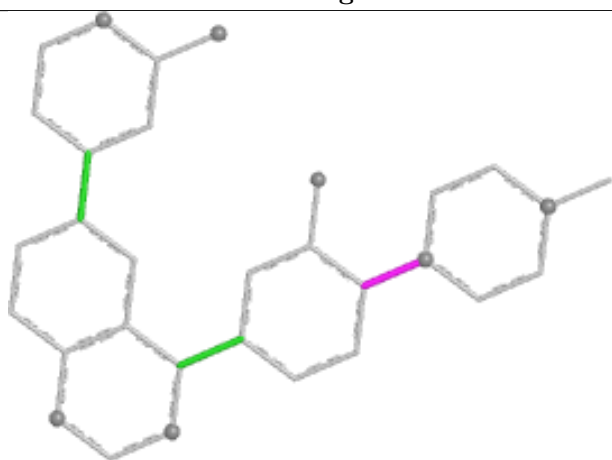
## Ligand A1A04 A 500



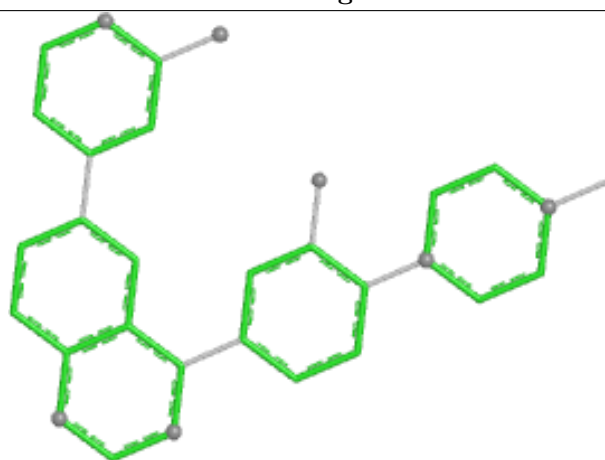
Bond lengths



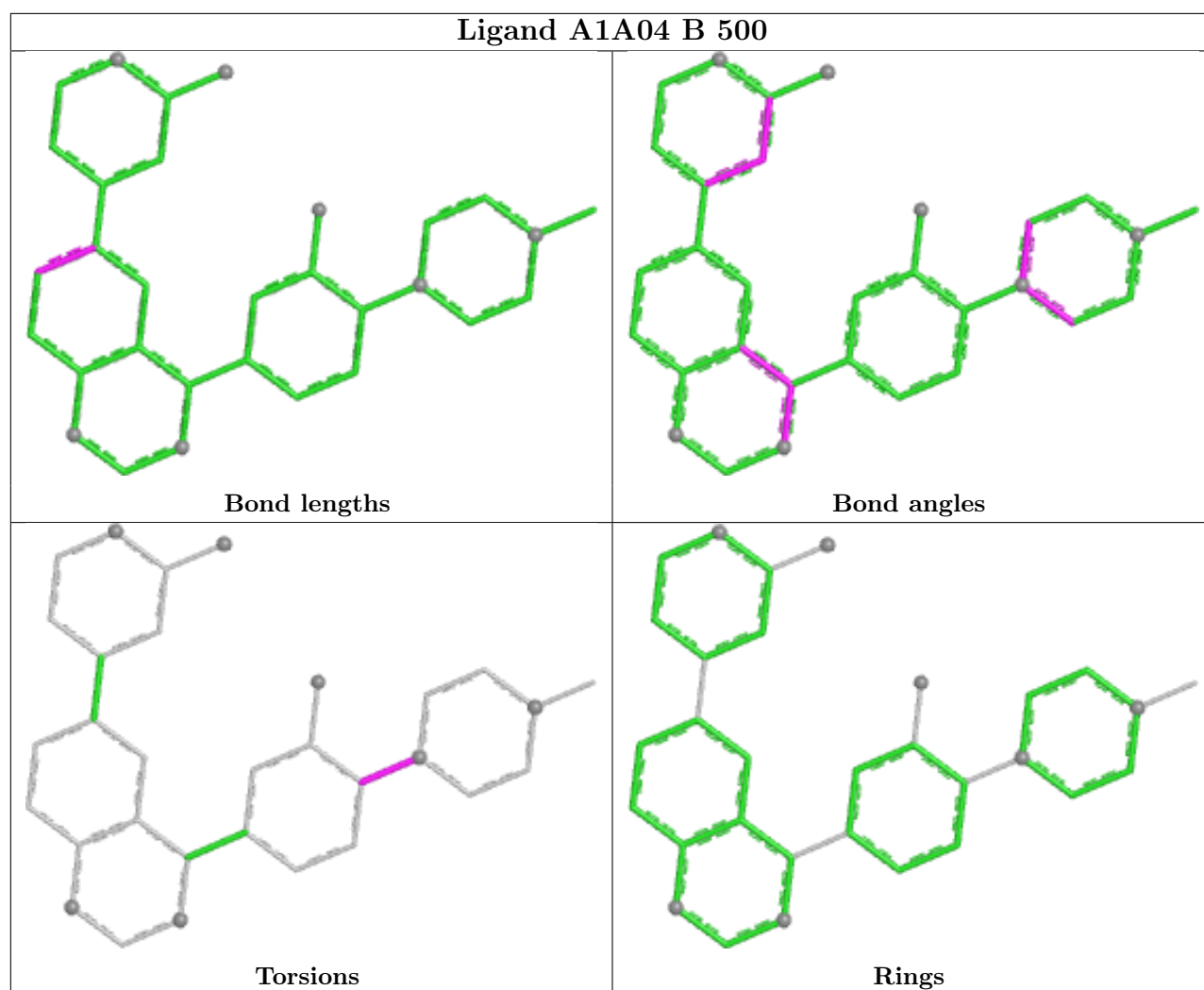
Bond angles



Torsions



Rings



## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	338/365 (92%)	-0.12	11 (3%)	49 45	3, 12, 45, 99	5 (1%)
1	B	341/365 (93%)	-0.12	14 (4%)	41 37	4, 12, 45, 92	3 (0%)
All	All	679/730 (93%)	-0.12	25 (3%)	45 40	3, 12, 45, 99	8 (1%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	318	ILE	7.8
1	A	318	ILE	6.6
1	B	317[A]	ARG	5.4
1	B	319	TYR	4.4
1	B	481	LYS	4.2
1	A	136	TYR	4.0
1	A	319	TYR	3.9
1	A	407	LYS	3.9
1	B	136	TYR	3.5
1	B	408	THR	3.4
1	A	317	ARG	3.3
1	B	135	VAL	3.1
1	A	145	TYR	3.1
1	A	320	GLN	3.0
1	B	299	LYS	2.9
1	A	138	ASP	2.7
1	B	320	GLN	2.6
1	B	407	LYS	2.5
1	A	219	TYR	2.5
1	B	316	GLN	2.4
1	A	217	MET	2.4
1	A	215	THR	2.3
1	B	414	GLU	2.3
1	B	143	ASP	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	217	MET	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PTR	B	321	16/17	0.86	0.18	28,42,49,49	0
1	PTR	A	321	16/17	0.95	0.09	13,16,20,24	0

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

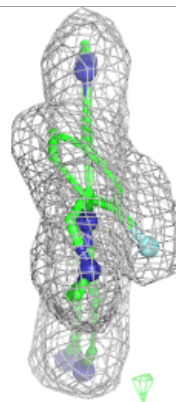
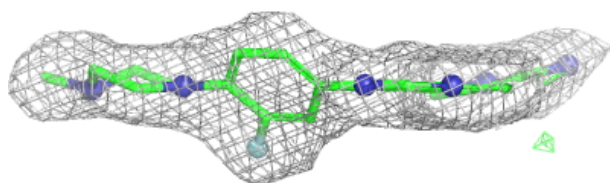
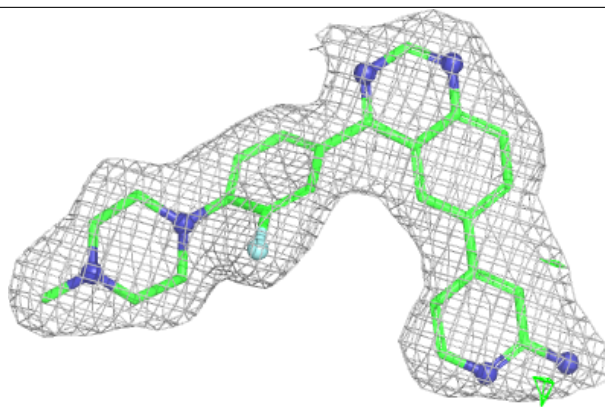
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PG4	A	501	13/13	0.89	0.12	29,34,43,44	0
2	A1A04	B	500	31/31	0.94	0.07	6,7,9,9	0
2	A1A04	A	500	31/31	0.95	0.07	6,7,8,8	0

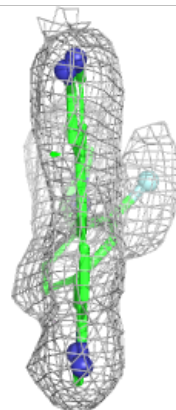
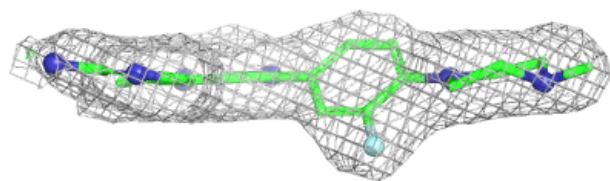
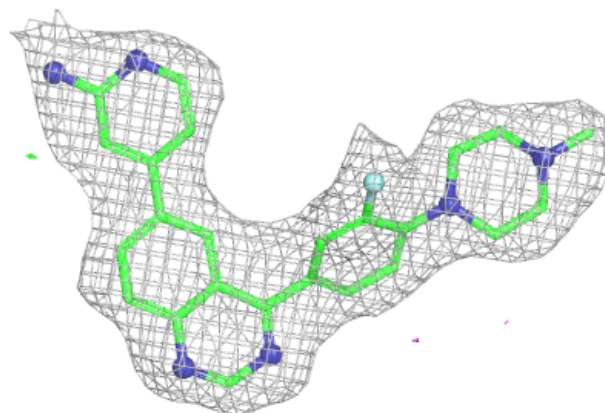
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1A04 B 500:**

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

**Electron density around A1A04 A 500:**

$2mF_o-DF_c$  (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.