



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2019 – 09:55 PM EDT

PDB ID : 4D2S  
Title : Human TTK in complex with a Dyrk1B inhibitor  
Authors : Debreczeni, J.E.; Kettle, J.G.; Ballard, P.; Bardelle, C.; Butterworth, S.; Colclough, N.; Critchlow, S.E.; Fairley, G.; Fillery, S.; Graham, M.A.; Goodwin, L.; Guichard, S.; Hudson, K.; Mahmood, A.; Vincent, J.; Ward, R.A.; Whittaker, D.  
Deposited on : 2014-05-12  
Resolution : 2.50 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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

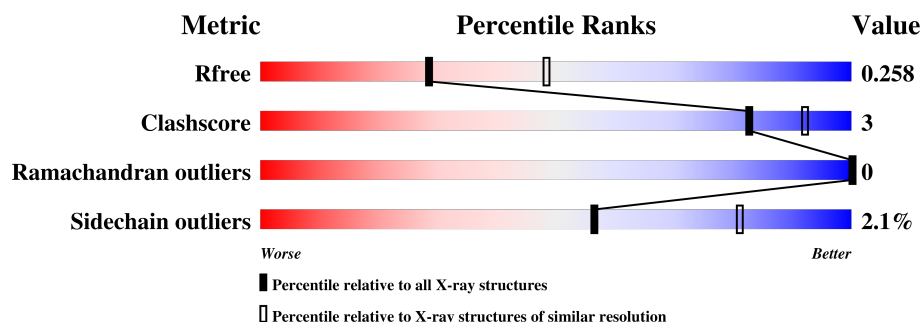
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	111664	4155 (2.50-2.50)
Clashscore	122126	4827 (2.50-2.50)
Ramachandran outliers	120053	4735 (2.50-2.50)
Sidechain outliers	120020	4737 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	284	

## 2 Entry composition [i](#)

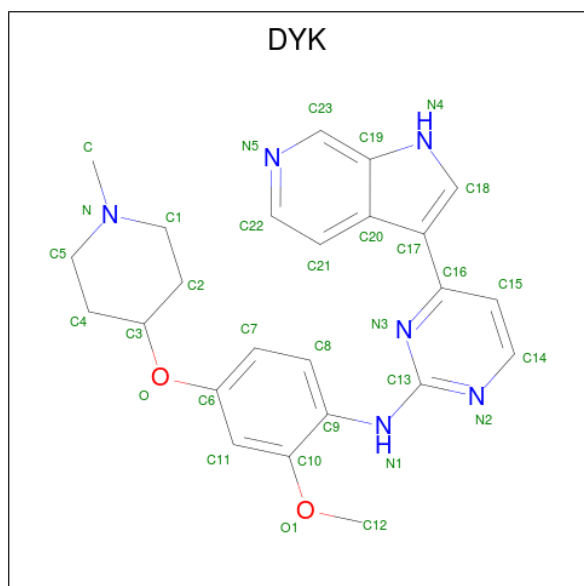
There are 3 unique types of molecules in this entry. The entry contains 1937 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN KINASE TTK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1903	1229	311	351	12			

- Molecule 2 is N-{2-methoxy-4-[(1-methylpiperidin-4-yl)oxy]phenyl}-4-(1H-pyrrolo[2,3-c]pyridin-3-yl)pyrimidin-2-amine (three-letter code: DYK) (formula: C<sub>24</sub>H<sub>26</sub>N<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			32	24	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		



• Molecule 1: DUAL SPECIFICITY PROTEIN KINASE TTK

GLY	ASP13	GLN	ASP14	GLN	ASP15	GLN	ASP16	GLN	ASP17	GLN	ASP18	GLN	ASP19	GLN	ASP20	GLN	ASP21	GLN	ASP22	GLN	ASP23	GLN	ASP24	GLN	ASP25	GLN	ASP26	GLN	ASP27	GLN	ASP28	GLN	ASP29	GLN	ASP30	GLN	ASP31	GLN	ASP32	GLN	ASP33	GLN	ASP34	GLN	ASP35	GLN	ASP36	GLN	ASP37	GLN	ASP38	GLN	ASP39	GLN	ASP40	GLN	ASP41	GLN	ASP42	GLN	ASP43	GLN	ASP44	GLN	ASP45	GLN	ASP46	GLN	ASP47	GLN	ASP48	GLN	ASP49	GLN	ASP50	GLN	ASP51	GLN	ASP52	GLN	ASP53	GLN	ASP54	GLN	ASP55	GLN	ASP56	GLN	ASP57	GLN	ASP58	GLN	ASP59	GLN	ASP60	GLN	ASP61	GLN	ASP62	GLN	ASP63	GLN	ASP64	GLN	ASP65	GLN	ASP66	GLN	ASP67	GLN	ASP68	GLN	ASP69	GLN	ASP70	GLN	ASP71	GLN	ASP72	GLN	ASP73	GLN	ASP74	GLN	ASP75	GLN	ASP76	GLN	ASP77	GLN	ASP78	GLN	ASP79	GLN	ASP80	GLN	ASP81	GLN	ASP82	GLN	ASP83	GLN	ASP84	GLN	ASP85	GLN	ASP86	GLN	ASP87	GLN	ASP88	GLN	ASP89	GLN	ASP90	GLN	ASP91	GLN	ASP92	GLN	ASP93	GLN	ASP94	GLN	ASP95	GLN	ASP96	GLN	ASP97	GLN	ASP98	GLN	ASP99	GLN	ASP100	GLN	ASP101	GLN	ASP102	GLN	ASP103	GLN	ASP104	GLN	ASP105	GLN	ASP106	GLN	ASP107	GLN	ASP108	GLN	ASP109	GLN	ASP110	GLN	ASP111	GLN	ASP112	GLN	ASP113	GLN	ASP114	GLN	ASP115	GLN	ASP116	GLN	ASP117	GLN	ASP118	GLN	ASP119	GLN	ASP120	GLN	ASP121	GLN	ASP122	GLN	ASP123	GLN	ASP124	GLN	ASP125	GLN	ASP126	GLN	ASP127	GLN	ASP128	GLN	ASP129	GLN	ASP130	GLN	ASP131	GLN	ASP132	GLN	ASP133	GLN	ASP134	GLN	ASP135	GLN	ASP136	GLN	ASP137	GLN	ASP138	GLN	ASP139	GLN	ASP140	GLN	ASP141	GLN	ASP142	GLN	ASP143	GLN	ASP144	GLN	ASP145	GLN	ASP146	GLN	ASP147	GLN	ASP148	GLN	ASP149	GLN	ASP150	GLN	ASP151	GLN	ASP152	GLN	ASP153	GLN	ASP154	GLN	ASP155	GLN	ASP156	GLN	ASP157	GLN	ASP158	GLN	ASP159	GLN	ASP160	GLN	ASP161	GLN	ASP162	GLN	ASP163	GLN	ASP164	GLN	ASP165	GLN	ASP166	GLN	ASP167	GLN	ASP168	GLN	ASP169	GLN	ASP170	GLN	ASP171	GLN	ASP172	GLN	ASP173	GLN	ASP174	GLN	ASP175	GLN	ASP176	GLN	ASP177	GLN	ASP178	GLN	ASP179	GLN	ASP180	GLN	ASP181	GLN	ASP182	GLN	ASP183	GLN	ASP184	GLN	ASP185	GLN	ASP186	GLN	ASP187	GLN	ASP188	GLN	ASP189	GLN	ASP190	GLN	ASP191	GLN	ASP192	GLN	ASP193	GLN	ASP194	GLN	ASP195	GLN	ASP196	GLN	ASP197	GLN	ASP198	GLN	ASP199	GLN	ASP200	GLN	ASP201	GLN	ASP202	GLN	ASP203	GLN	ASP204	GLN	ASP205	GLN	ASP206	GLN	ASP207	GLN	ASP208	GLN	ASP209	GLN	ASP210	GLN	ASP211	GLN	ASP212	GLN	ASP213	GLN	ASP214	GLN	ASP215	GLN	ASP216	GLN	ASP217	GLN	ASP218	GLN	ASP219	GLN	ASP220	GLN	ASP221	GLN	ASP222	GLN	ASP223	GLN	ASP224	GLN	ASP225	GLN	ASP226	GLN	ASP227	GLN	ASP228	GLN	ASP229	GLN	ASP230	GLN	ASP231	GLN	ASP232	GLN	ASP233	GLN	ASP234	GLN	ASP235	GLN	ASP236	GLN	ASP237	GLN	ASP238	GLN	ASP239	GLN	ASP240	GLN	ASP241	GLN	ASP242	GLN	ASP243	GLN	ASP244	GLN	ASP245	GLN	ASP246	GLN	ASP247	GLN	ASP248	GLN	ASP249	GLN	ASP250	GLN	ASP251	GLN	ASP252	GLN	ASP253	GLN	ASP254	GLN	ASP255	GLN	ASP256	GLN	ASP257	GLN	ASP258	GLN	ASP259	GLN	ASP260	GLN	ASP261	GLN	ASP262	GLN	ASP263	GLN	ASP264	GLN	ASP265	GLN	ASP266	GLN	ASP267	GLN	ASP268	GLN	ASP269	GLN	ASP270	GLN	ASP271	GLN	ASP272	GLN	ASP273</
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.01Å 113.35Å 71.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.58 – 2.50 26.07 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.6 (18.58-2.50) 89.0 (26.07-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.22 (at 2.50Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.179 , 0.221 0.226 , 0.258	Depositor DCC
$R_{free}$ test set	689 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.6	Xtriage
Anisotropy	0.634	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 67.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.041 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1937	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.80% 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: DYK

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	0.47	0/1944	0.65	0/2645

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	1903	0	1803	7	0
2	A	32	0	26	3	0
3	A	2	0	0	0	0
All	All	1937	0	1829	10	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 (10) 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:732:THR:HB	1:A:735:GLN:HB2	1.63	0.78

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1794:DYK:H21	2:A:1794:DYK:H15	1.85	0.57
1:A:574:TYR:CD1	1:A:643:ILE:HD11	2.43	0.53
1:A:529:LYS:HE2	1:A:531:ILE:HG22	1.90	0.53
1:A:688:ASN:HB3	1:A:732:THR:HG21	1.92	0.51
1:A:557:LEU:HD11	1:A:598:ILE:HG13	1.94	0.49
2:A:1794:DYK:C8	2:A:1794:DYK:N3	2.78	0.47
1:A:654:LEU:HB2	1:A:663:ILE:HD11	2.01	0.43
2:A:1794:DYK:N3	2:A:1794:DYK:H8	2.35	0.41
1:A:578:LEU:HD11	1:A:641:HIS:CG	2.57	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	241/284 (85%)	232 (96%)	9 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/260 (75%)	190 (98%)	4 (2%)	56	81

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	579	GLN
1	A	606	ASN
1	A	758	ASP
1	A	793	ILE

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	530	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	DYK	A	1794	-	34,36,36	0.68	1 (2%)	45,50,50	0.84	4 (8%)



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	DYK	A	1794	-	-	2/10/24/24	0/5/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1794	DYK	C21-C22	2.10	1.39	1.36

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1794	DYK	C6-O-C3	-2.88	113.38	119.05
2	A	1794	DYK	C22-C21-C20	-2.42	117.56	119.79
2	A	1794	DYK	O-C3-C4	2.27	113.32	108.31
2	A	1794	DYK	C16-C17-C20	2.01	127.83	123.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1794	DYK	C7-C6-O-C3
2	A	1794	DYK	C11-C6-O-C3

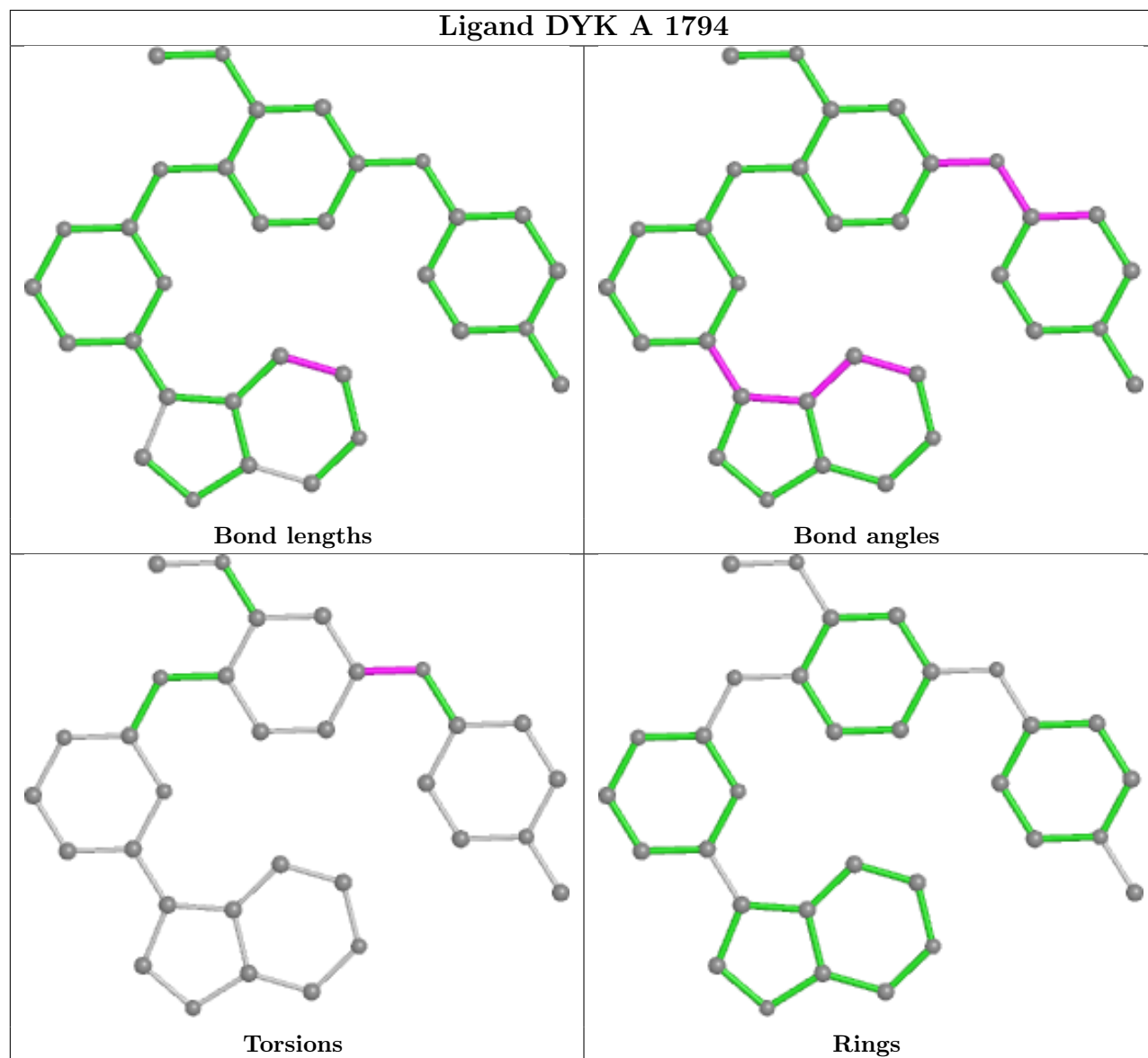
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1794	DYK	3	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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

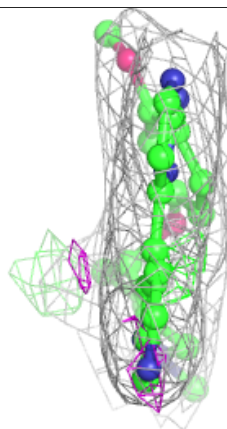
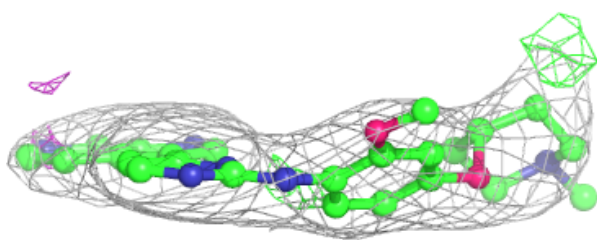
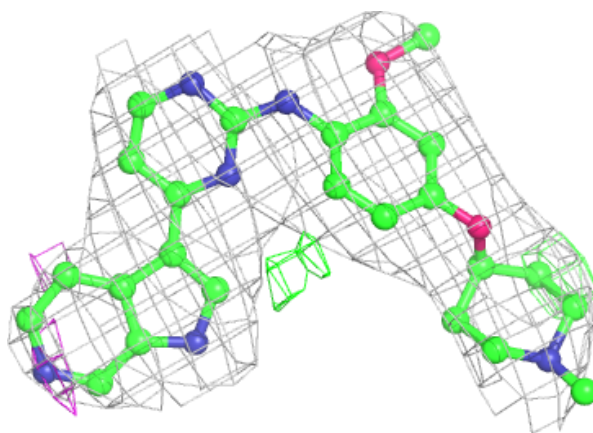
### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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 DYK A 1794:**

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



## 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.