



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 26, 2024 – 01:37 AM EDT

PDB ID : 6RA5  
Title : Human tnk in complex with compound 9  
Authors : Read, J.A.  
Deposited on : 2019-04-05  
Resolution : 2.90 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>.

---

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 : 2.37.1  
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) : 2.37.1

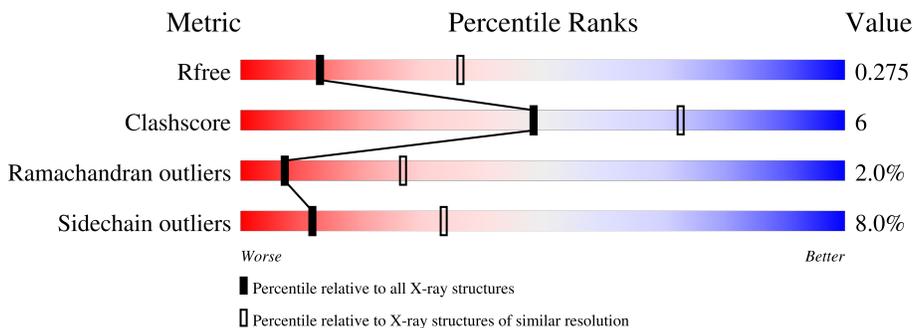
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	306	
1	B	306	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4384 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.

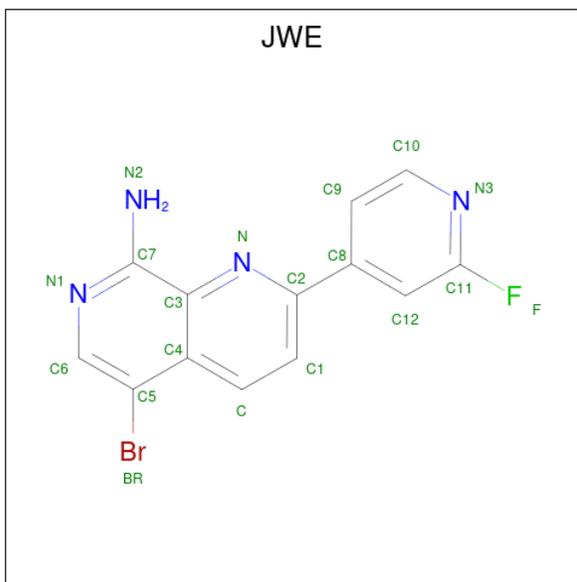
- Molecule 1 is a protein called TRAF2 and NCK-interacting protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	295	2271	1440	398	417	2	14	0	0	0
1	B	283	2040	1295	348	383	1	13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP Q9UKE5
A	10	SER	-	expression tag	UNP Q9UKE5
B	9	GLY	-	expression tag	UNP Q9UKE5
B	10	SER	-	expression tag	UNP Q9UKE5

- Molecule 2 is 5-bromanyl-2-(2-fluoranylpyridin-4-yl)-1,7-naphthyridin-8-amine (three-letter code: JWE) (formula: C<sub>13</sub>H<sub>8</sub>BrFN<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	F	N		
2	A	1	19	1	13	1	4	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	B	1	1	1	0	0

- Molecule 4 is water.

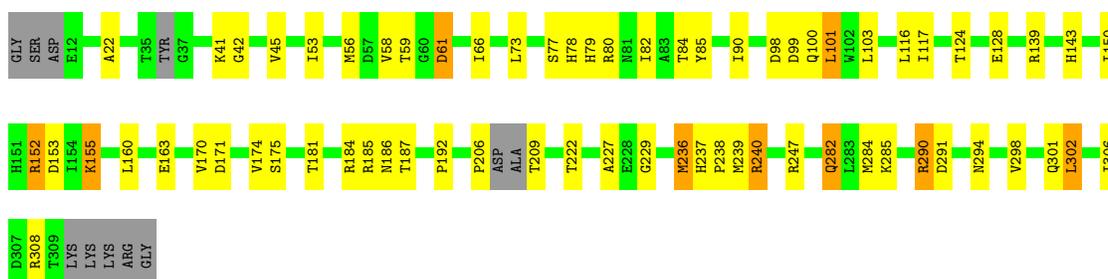
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	28	28	28	0	0
4	B	25	25	25	0	0

### 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. 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.

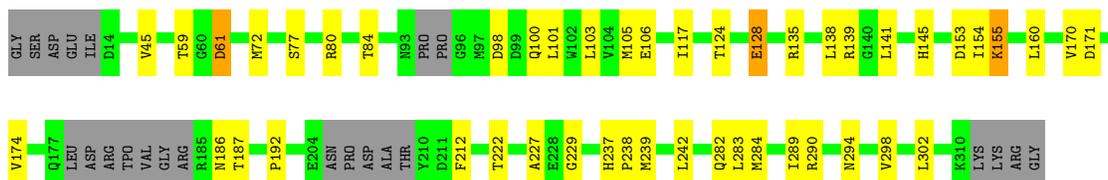
- Molecule 1: TRAF2 and NCK-interacting protein kinase

Chain A: 



- Molecule 1: TRAF2 and NCK-interacting protein kinase

Chain B: 



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.79Å 53.79Å 253.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.80 – 2.90 26.90 – 2.93	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.80-2.90) 97.8 (26.90-2.93)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 2.94Å)	Xtriage
Refinement program	BUSTER	Depositor
R, $R_{free}$	(Not available) , (Not available) 0.225 , 0.275	Depositor DCC
$R_{free}$ test set	783 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.9	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , 57.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.004 for -h,-k,l 0.071 for h,-h-k,-l 0.043 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4384	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, JWE, MG

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	0.50	0/2297	0.72	2/3112 (0.1%)
1	B	0.51	0/2073	0.72	1/2827 (0.0%)
All	All	0.50	0/4370	0.72	3/5939 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	290	ARG	CD-NE-CZ	5.36	131.10	123.60
1	A	290	ARG	CD-NE-CZ	5.18	130.85	123.60
1	A	41	LYS	N-CA-C	-5.17	97.05	111.00

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	2271	0	2169	31	0
1	B	2040	0	1797	19	0
2	A	19	0	0	0	0
3	B	1	0	0	0	0
4	A	28	0	0	0	0
4	B	25	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4384	0	3966	50	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 (50) 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:42:GLY:HA3	1:A:53:ILE:HD12	1.75	0.67
1:A:290:ARG:HD2	1:A:291:ASP:OD1	1.98	0.63
1:A:78:HIS:HE1	1:A:143:HIS:HE1	1.47	0.62
1:A:150:ILE:HG22	1:A:152:ARG:HG2	1.84	0.60
1:B:237:HIS:HD2	1:B:239:MET:H	1.49	0.59
1:A:237:HIS:HD2	1:A:239:MET:H	1.53	0.56
1:B:155:LYS:HA	1:B:222:THR:CG2	2.35	0.56
1:A:59:THR:HG22	1:A:61:ASP:H	1.71	0.56
1:B:59:THR:HG22	1:B:61:ASP:H	1.72	0.55
1:A:155:LYS:HA	1:A:222:THR:CG2	2.37	0.55
1:B:124:THR:HG22	1:B:227:ALA:O	2.07	0.54
1:A:124:THR:HG22	1:A:227:ALA:O	2.07	0.54
1:A:78:HIS:HE1	1:A:143:HIS:CE1	2.25	0.54
1:B:138:LEU:HD21	1:B:283:LEU:HD23	1.90	0.54
1:B:80:ARG:HH12	1:B:139:ARG:HD3	1.74	0.53
1:A:80:ARG:HH12	1:A:139:ARG:HD3	1.75	0.51
1:A:160:LEU:HD22	1:A:170:VAL:HG11	1.93	0.50
1:B:160:LEU:HD22	1:B:170:VAL:HG11	1.93	0.49
1:A:282:GLN:HA	1:A:285:LYS:HE2	1.93	0.49
1:A:236:MET:HG2	1:A:240:ARG:HD2	1.95	0.49
1:B:237:HIS:CD2	1:B:238:PRO:HD2	2.47	0.49
1:A:78:HIS:CE1	1:A:143:HIS:CE1	3.02	0.48
1:A:237:HIS:CD2	1:A:239:MET:HB2	2.49	0.48
1:A:77:SER:HB2	1:A:84:THR:HA	1.96	0.47
1:A:58:VAL:HG22	1:A:99:ASP:O	2.14	0.47
1:A:237:HIS:CD2	1:A:238:PRO:HD2	2.50	0.46
1:B:77:SER:HB2	1:B:84:THR:HA	1.98	0.46
1:A:236:MET:HB3	1:A:240:ARG:HB3	1.98	0.46
1:A:73:LEU:HD12	1:A:85:TYR:HB2	1.96	0.46
1:A:237:HIS:HD2	1:A:239:MET:HB2	1.81	0.45
1:A:117:ILE:HG21	1:A:229:GLY:HA2	1.99	0.44
1:B:141:LEU:HD21	1:B:154:ILE:HD11	2.00	0.44
1:B:155:LYS:HA	1:B:222:THR:HG21	2.00	0.43

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:ASP:HB2	1:A:174:VAL:CG2	2.48	0.43
1:B:117:ILE:HG21	1:B:229:GLY:HA2	2.00	0.43
1:B:145:HIS:CD2	1:B:212:PHE:HB2	2.54	0.43
1:B:135:ARG:HG3	1:B:289:ILE:HG23	2.01	0.42
1:B:153:ASP:HB2	1:B:174:VAL:CG2	2.49	0.42
1:A:116:LEU:HD13	1:A:306:ILE:HD13	2.00	0.42
1:A:302:LEU:O	1:A:306:ILE:HG12	2.19	0.42
1:A:56:MET:CE	1:A:66:ILE:HG12	2.50	0.42
1:A:152:ARG:HH21	1:A:185:ARG:HD2	1.85	0.42
1:A:206:PRO:C	1:A:209:THR:N	2.73	0.42
1:A:90:ILE:HG12	1:A:101:LEU:HB2	2.01	0.42
1:B:239:MET:HA	1:B:242:LEU:HD12	2.01	0.42
1:A:153:ASP:HB2	1:A:174:VAL:HG21	2.02	0.41
1:B:153:ASP:HB2	1:B:174:VAL:HG21	2.01	0.41
1:A:79:HIS:HB3	1:A:82:ILE:HD12	2.02	0.40
1:B:84:THR:H	1:B:106:GLU:HG2	1.86	0.40
1:B:128:GLU:H	1:B:128:GLU:HG3	1.71	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	287/306 (94%)	269 (94%)	12 (4%)	6 (2%)	7	26
1	B	274/306 (90%)	258 (94%)	11 (4%)	5 (2%)	8	29
All	All	561/612 (92%)	527 (94%)	23 (4%)	11 (2%)	7	27

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	ALA

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	186	ASN
1	A	294	ASN
1	B	294	ASN
1	A	308	ARG
1	B	45	VAL
1	B	171	ASP
1	A	171	ASP
1	A	45	VAL
1	A	192	PRO
1	B	192	PRO

### 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	228/264 (86%)	208 (91%)	20 (9%)	10	30
1	B	185/264 (70%)	172 (93%)	13 (7%)	15	41
All	All	413/528 (78%)	380 (92%)	33 (8%)	12	33

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ASP
1	A	98	ASP
1	A	100	GLN
1	A	101	LEU
1	A	103	LEU
1	A	128	GLU
1	A	152	ARG
1	A	155	LYS
1	A	163	GLU
1	A	175	SER
1	A	184	ARG
1	A	186	ASN
1	A	236	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	240	ARG
1	A	247	ARG
1	A	282	GLN
1	A	284	MET
1	A	298	VAL
1	A	301	GLN
1	A	302	LEU
1	B	61	ASP
1	B	72	MET
1	B	98	ASP
1	B	100	GLN
1	B	101	LEU
1	B	103	LEU
1	B	105	MET
1	B	128	GLU
1	B	155	LYS
1	B	282	GLN
1	B	284	MET
1	B	298	VAL
1	B	302	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	HIS
1	A	143	HIS
1	A	186	ASN
1	A	237	HIS
1	A	248	ASN
1	A	273	ASN
1	B	237	HIS
1	B	248	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](#)

3 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	TPO	A	181	1	8,10,11	1.07	1 (12%)	10,14,16	1.44	1 (10%)
1	TPO	A	187	1	8,10,11	1.64	2 (25%)	10,14,16	1.44	2 (20%)
1	TPO	B	187	1	8,10,11	2.05	3 (37%)	10,14,16	2.14	3 (30%)

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	TPO	A	181	1	-	3/9/11/13	-
1	TPO	A	187	1	-	2/9/11/13	-
1	TPO	B	187	1	-	0/9/11/13	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	187	TPO	CB-CA	3.48	1.61	1.53
1	A	187	TPO	P-OG1	-3.23	1.53	1.59
1	B	187	TPO	P-OG1	-3.11	1.53	1.59
1	B	187	TPO	CG2-CB	2.79	1.58	1.51
1	A	187	TPO	P-O1P	2.49	1.58	1.50
1	A	181	TPO	P-O1P	2.01	1.57	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	187	TPO	CG2-CB-CA	4.23	121.52	113.16
1	B	187	TPO	P-OG1-CB	-3.42	112.89	123.21
1	A	187	TPO	O-C-CA	-2.82	117.38	124.78
1	A	187	TPO	CG2-CB-CA	2.55	118.20	113.16
1	B	187	TPO	O-C-CA	-2.45	118.36	124.78
1	A	181	TPO	P-OG1-CB	-2.13	116.78	123.21

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	181	TPO	O-C-CA-CB
1	A	181	TPO	CB-OG1-P-O3P
1	A	187	TPO	O-C-CA-CB
1	A	187	TPO	CB-OG1-P-O1P
1	A	181	TPO	C-CA-CB-CG2

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	JWE	A	401	-	21,21,21	0.77	1 (4%)	27,30,30	1.06	1 (3%)

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	JWE	A	401	-	-	0/4/4/4	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	JWE	C12-C11	3.23	1.44	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	JWE	C7-C3-N	-4.42	116.92	120.33

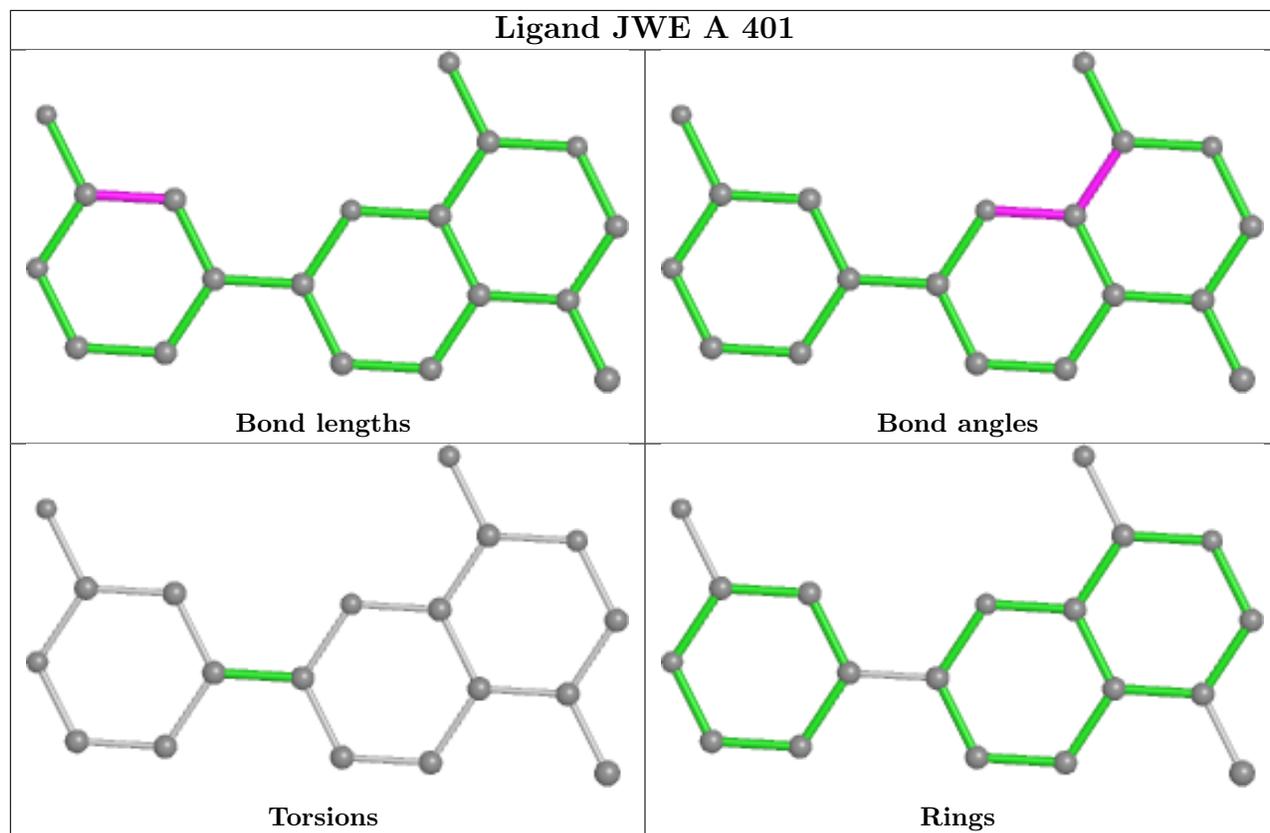
There are no chirality outliers.

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 [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 [i](#)

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

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

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

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

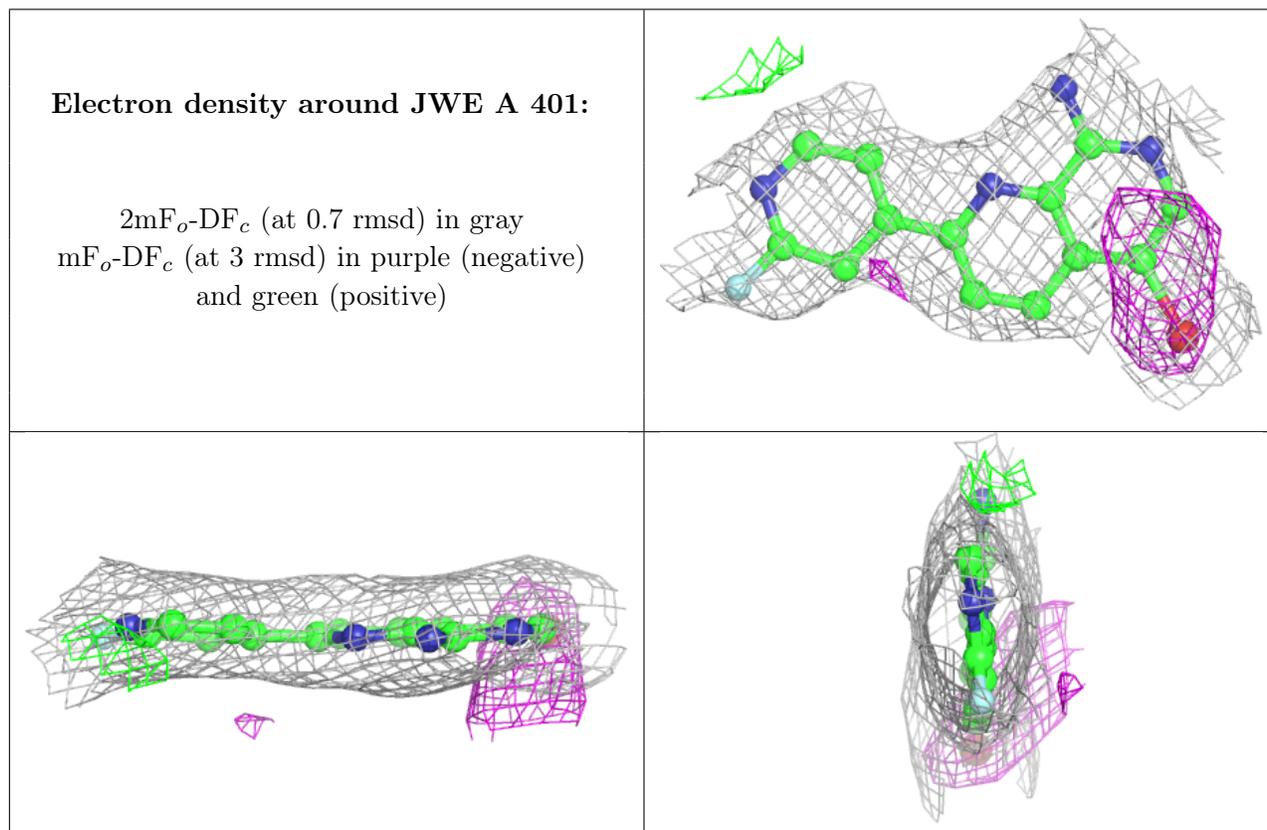
### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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.



## 6.5 Other polymers

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