



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 28, 2022 – 02:09 AM JST

PDB ID : 7VBT  
Title : Crystal structure of RIOK2 in complex with CQ211  
Authors : Zhu, C.; Zhang, Z.M.  
Deposited on : 2021-09-01  
Resolution : 2.54 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
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) : 2.29

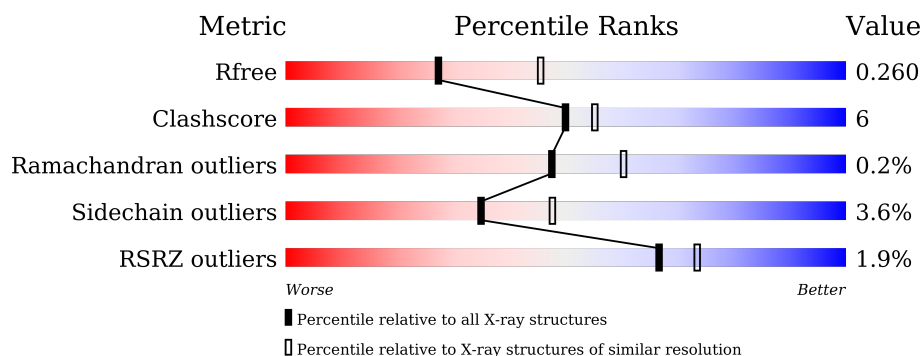
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.54 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	319	 2% 79% 14% • 6%
1	B	319	 2% 73% 16% • 10%

## 2 Entry composition [i](#)

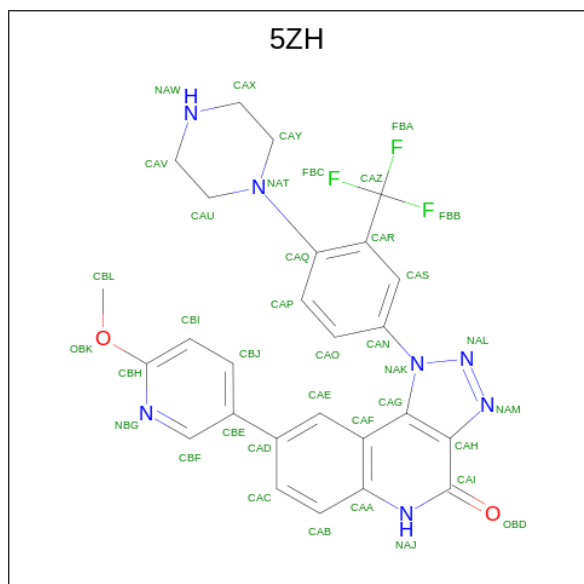
There are 3 unique types of molecules in this entry. The entry contains 4669 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	0	0
			2328	1494	393	426	15			
1	B	286	Total	C	N	O	S	0	0	0
			2242	1431	380	417	14			

- Molecule 2 is 8-(6-methoxypyridin-3-yl)-1-[4-piperazin-1-yl-3-(trifluoromethyl)phenyl]-5H-[1,2,3]triazolo[4,5-c]quinolin-4-one (three-letter code: 5ZH) (formula: C<sub>26</sub>H<sub>22</sub>F<sub>3</sub>N<sub>7</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			38	26	3	7	2		
2	B	1	Total	C	F	N	O	0	0
			38	26	3	7	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total 13	O 13	0	0
3	B	10	Total 10	O 10	0	0

- Molecule 1: Serine/threonine-protein kinase RIO2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.52Å 93.61Å 110.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.80 – 2.54 46.80 – 2.54	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.80-2.54) 99.7 (46.80-2.54)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.9_1692+SVN	Depositor
R, $R_{free}$	0.221 , 0.259 0.224 , 0.260	Depositor DCC
$R_{free}$ test set	1906 reflections (7.68%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.0	Xtriage
Anisotropy	0.680	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 37.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4669	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.76% 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: 5ZH

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	0.25	0/2380	0.46	0/3229
1	B	0.26	0/2289	0.44	0/3095
All	All	0.26	0/4669	0.45	0/6324

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	2328	0	2224	28	0
1	B	2242	0	2135	29	0
2	A	38	0	0	0	0
2	B	38	0	0	0	0
3	A	13	0	0	2	0
3	B	10	0	0	0	0
All	All	4669	0	4359	52	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 (52) 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:159:MET:HE1	1:A:310:GLN:HG3	1.57	0.86
1:A:292:ARG:NH1	3:A:502:HOH:O	2.09	0.86
1:B:159:MET:HE1	1:B:310:GLN:HG3	1.66	0.77
1:B:170:GLU:OE2	1:B:305:TYR:OH	2.04	0.75
1:A:284:PHE:O	3:A:501:HOH:O	2.07	0.72
1:A:105:LYS:NZ	1:A:249:GLN:OE1	2.23	0.71
1:B:105:LYS:NZ	1:B:249:GLN:OE1	2.24	0.70
1:A:271:ASP:OD2	1:B:267:LYS:NZ	2.26	0.69
1:B:31:GLU:OE2	1:B:147:ASN:N	2.28	0.67
1:B:202:VAL:HG21	1:B:208:VAL:HG21	1.80	0.63
1:A:228:ASP:O	1:A:233:ASN:ND2	2.36	0.58
1:A:87:THR:O	1:A:91:ARG:HG3	2.03	0.58
1:A:155:ARG:NH1	1:A:313:ASP:OD2	2.40	0.55
1:A:267:LYS:NZ	1:B:271:ASP:OD2	2.39	0.55
1:B:127:LEU:O	1:B:150:TRP:HA	2.07	0.55
1:A:24:GLU:OE2	1:A:155:ARG:NH2	2.39	0.54
1:A:222:HIS:ND1	1:A:297:ASP:OD1	2.39	0.54
1:B:235:ILE:HD12	1:B:245:ILE:HG21	1.89	0.54
1:B:89:SER:HA	1:B:94:VAL:O	2.10	0.52
1:B:226:HIS:NE2	1:B:246:ASP:O	2.37	0.52
1:B:92:GLN:HG3	1:B:115:GLU:OE2	2.10	0.51
1:B:82:TYR:CE2	1:B:86:LYS:HG3	2.45	0.51
1:B:93:VAL:HG21	1:B:180:ASP:OD2	2.11	0.50
1:B:204:ASP:HB3	1:B:207:SER:HB3	1.91	0.50
1:A:170:GLU:OE2	1:A:171:ARG:NH1	2.45	0.50
1:B:15:ASP:OD1	1:B:18:ARG:NH1	2.44	0.50
1:B:197:CYS:HB3	1:B:231:GLU:HG3	1.94	0.49
1:A:85:LEU:HD13	1:A:97:VAL:HG21	1.94	0.49
1:A:127:LEU:O	1:A:150:TRP:HA	2.13	0.49
1:A:197:CYS:HB3	1:A:231:GLU:HG3	1.95	0.47
1:A:292:ARG:HA	1:A:292:ARG:HD2	1.49	0.47
1:A:159:MET:HA	1:A:309:MET:HE1	1.97	0.47
1:B:202:VAL:HG22	1:B:240:ASP:OD2	2.14	0.47
1:A:261:TYR:OH	1:B:105:LYS:HD2	2.15	0.47
1:B:191:ILE:HG12	1:B:243:THR:HG21	1.96	0.46
1:A:105:LYS:HD2	1:B:261:TYR:OH	2.17	0.45
1:A:314:GLU:H	1:A:314:GLU:HG2	1.45	0.44
1:B:109:ILE:HG12	1:B:123:LYS:HG2	1.98	0.44
1:A:9:LEU:HD11	1:A:85:LEU:HB3	1.99	0.43
1:B:91:ARG:NH2	1:B:181:TYR:O	2.46	0.43
1:B:91:ARG:HH21	1:B:180:ASP:CG	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:MET:O	1:A:28:LYS:HG2	2.19	0.42
1:A:12:MET:HG2	1:A:16:ASP:HB2	2.00	0.42
1:A:230:ASN:HB3	1:B:260:TRP:CZ2	2.54	0.42
1:A:100:GLN:HB2	1:A:110:TYR:CE2	2.55	0.42
1:A:64:TRP:CH2	1:A:66:ARG:HB2	2.55	0.41
1:A:12:MET:HE3	1:A:17:PHE:HA	2.02	0.41
1:B:161:GLU:O	1:B:165:MET:HB2	2.21	0.41
1:A:75:LEU:HD21	1:A:83:LEU:HD12	2.01	0.41
1:B:166:LYS:O	1:B:170:GLU:HG3	2.21	0.40
1:B:291:ARG:HG3	1:B:292:ARG:N	2.37	0.40
1:B:12:MET:HG2	1:B:16:ASP:HB2	2.03	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	296/319 (93%)	289 (98%)	6 (2%)	1 (0%)	41	51
1	B	278/319 (87%)	272 (98%)	6 (2%)	0	100	100
All	All	574/638 (90%)	561 (98%)	12 (2%)	1 (0%)	47	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	GLU

### 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	239/284 (84%)	231 (97%)	8 (3%)	38	51
1	B	231/284 (81%)	222 (96%)	9 (4%)	32	44
All	All	470/568 (83%)	453 (96%)	17 (4%)	35	47

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	32	ILE
1	A	43	SER
1	A	80	TYR
1	A	207	SER
1	A	292	ARG
1	A	297	ASP
1	A	314	GLU
1	B	29	ASN
1	B	36	SER
1	B	60	LYS
1	B	92	GLN
1	B	149	SER
1	B	181	TYR
1	B	202	VAL
1	B	247	PHE
1	B	298	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

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	5ZH	B	401	-	42,43,43	3.46	21 (50%)	55,64,64	1.79	9 (16%)
2	5ZH	A	401	-	42,43,43	3.43	21 (50%)	55,64,64	1.79	13 (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	5ZH	B	401	-	-	3/20/28/28	0/6/6/6
2	5ZH	A	401	-	-	3/20/28/28	0/6/6/6

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	5ZH	OBD-CAI	10.73	1.45	1.23
2	A	401	5ZH	OBD-CAI	10.62	1.44	1.23
2	A	401	5ZH	OBK-CBH	10.05	1.51	1.35
2	B	401	5ZH	OBK-CBH	9.86	1.51	1.35
2	B	401	5ZH	CAQ-CAR	8.75	1.51	1.40
2	A	401	5ZH	CAQ-CAR	8.46	1.50	1.40
2	B	401	5ZH	CAS-CAN	4.36	1.44	1.38
2	B	401	5ZH	CAO-CAP	4.31	1.46	1.38
2	B	401	5ZH	CAY-CAX	4.16	1.61	1.51
2	A	401	5ZH	CAY-CAX	4.11	1.61	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	5ZH	CAO-CAP	3.96	1.46	1.38
2	A	401	5ZH	CAB-CAA	3.82	1.46	1.39
2	A	401	5ZH	CAS-CAN	3.75	1.43	1.38
2	B	401	5ZH	CAF-CAG	3.73	1.52	1.46
2	B	401	5ZH	CAE-CAF	3.71	1.46	1.39
2	A	401	5ZH	CAA-NAJ	3.71	1.46	1.39
2	A	401	5ZH	CAF-CAG	3.66	1.52	1.46
2	B	401	5ZH	CAB-CAA	3.66	1.45	1.39
2	B	401	5ZH	CAA-NAJ	3.57	1.46	1.39
2	B	401	5ZH	CBH-NBG	3.44	1.37	1.32
2	A	401	5ZH	CAE-CAF	3.43	1.45	1.39
2	A	401	5ZH	CBH-NBG	3.37	1.37	1.32
2	B	401	5ZH	CBI-CBJ	3.33	1.44	1.38
2	A	401	5ZH	CBI-CBJ	3.29	1.44	1.38
2	A	401	5ZH	CBI-CBH	-3.28	1.32	1.39
2	A	401	5ZH	CAU-CAV	3.26	1.59	1.51
2	B	401	5ZH	CBI-CBH	-3.23	1.32	1.39
2	B	401	5ZH	CAU-CAV	3.23	1.59	1.51
2	B	401	5ZH	CAO-CAN	2.93	1.44	1.38
2	A	401	5ZH	CBE-CAD	2.90	1.56	1.49
2	A	401	5ZH	CAC-CAD	2.86	1.45	1.39
2	B	401	5ZH	CBE-CAD	2.76	1.55	1.49
2	A	401	5ZH	CAO-CAN	2.75	1.43	1.38
2	B	401	5ZH	CAC-CAD	2.75	1.45	1.39
2	A	401	5ZH	CAP-CAQ	-2.61	1.35	1.39
2	A	401	5ZH	CAY-NAT	-2.60	1.42	1.46
2	B	401	5ZH	CBF-NBG	-2.51	1.29	1.34
2	B	401	5ZH	CAY-NAT	-2.49	1.42	1.46
2	A	401	5ZH	CBF-NBG	-2.48	1.29	1.34
2	B	401	5ZH	CAI-NAJ	-2.43	1.33	1.36
2	A	401	5ZH	CAI-NAJ	-2.34	1.34	1.36
2	B	401	5ZH	CAP-CAQ	-2.28	1.35	1.39

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	5ZH	CBF-NBG-CBH	6.55	122.39	116.63
2	A	401	5ZH	CBF-NBG-CBH	6.20	122.08	116.63
2	A	401	5ZH	NAM-NAL-NAK	4.54	111.42	106.37
2	B	401	5ZH	NAM-NAL-NAK	4.31	111.17	106.37
2	B	401	5ZH	CAH-CAI-NAJ	3.69	120.46	113.95
2	A	401	5ZH	CAH-CAI-NAJ	3.45	120.04	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	5ZH	CBL-OBK-CBH	-2.96	112.71	117.36
2	B	401	5ZH	CBE-CBF-NBG	-2.68	119.90	124.32
2	B	401	5ZH	CBL-OBK-CBH	-2.67	113.17	117.36
2	A	401	5ZH	FBC-CAZ-CAR	-2.57	108.23	112.70
2	B	401	5ZH	CAA-NAJ-CAI	-2.56	121.57	124.80
2	B	401	5ZH	CAG-CAF-CAA	-2.48	117.94	122.95
2	A	401	5ZH	CAG-CAF-CAA	-2.37	118.17	122.95
2	A	401	5ZH	CBE-CBF-NBG	-2.30	120.53	124.32
2	A	401	5ZH	FBA-CAZ-CAR	-2.27	108.75	112.70
2	B	401	5ZH	OBD-CAI-CAH	-2.22	120.03	124.37
2	A	401	5ZH	CAA-NAJ-CAI	-2.22	122.01	124.80
2	A	401	5ZH	CBI-CBH-NBG	-2.20	121.59	124.87
2	A	401	5ZH	FBB-CAZ-CAR	-2.18	108.91	112.70
2	A	401	5ZH	OBD-CAI-CAH	-2.06	120.35	124.37
2	B	401	5ZH	CAP-CAQ-NAT	-2.05	119.03	122.30
2	A	401	5ZH	CAE-CAF-CAA	2.01	119.77	118.46

There are no chirality outliers.

All (6) torsion outliers are listed below:

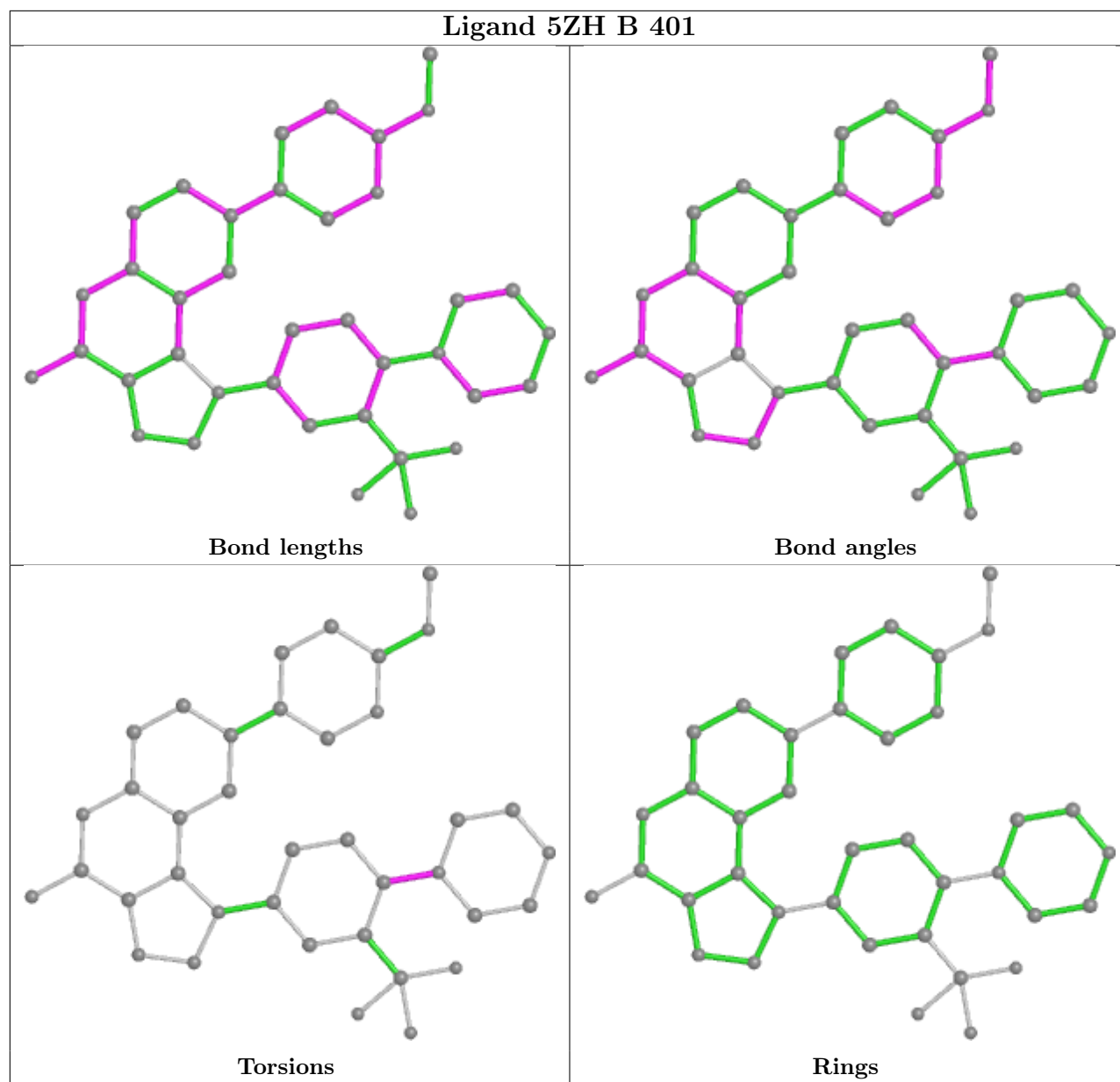
Mol	Chain	Res	Type	Atoms
2	B	401	5ZH	CAP-CAQ-NAT-CAU
2	A	401	5ZH	CAP-CAQ-NAT-CAU
2	B	401	5ZH	CAR-CAQ-NAT-CAU
2	B	401	5ZH	CAP-CAQ-NAT-CAY
2	A	401	5ZH	CAR-CAQ-NAT-CAU
2	A	401	5ZH	CAP-CAQ-NAT-CAY

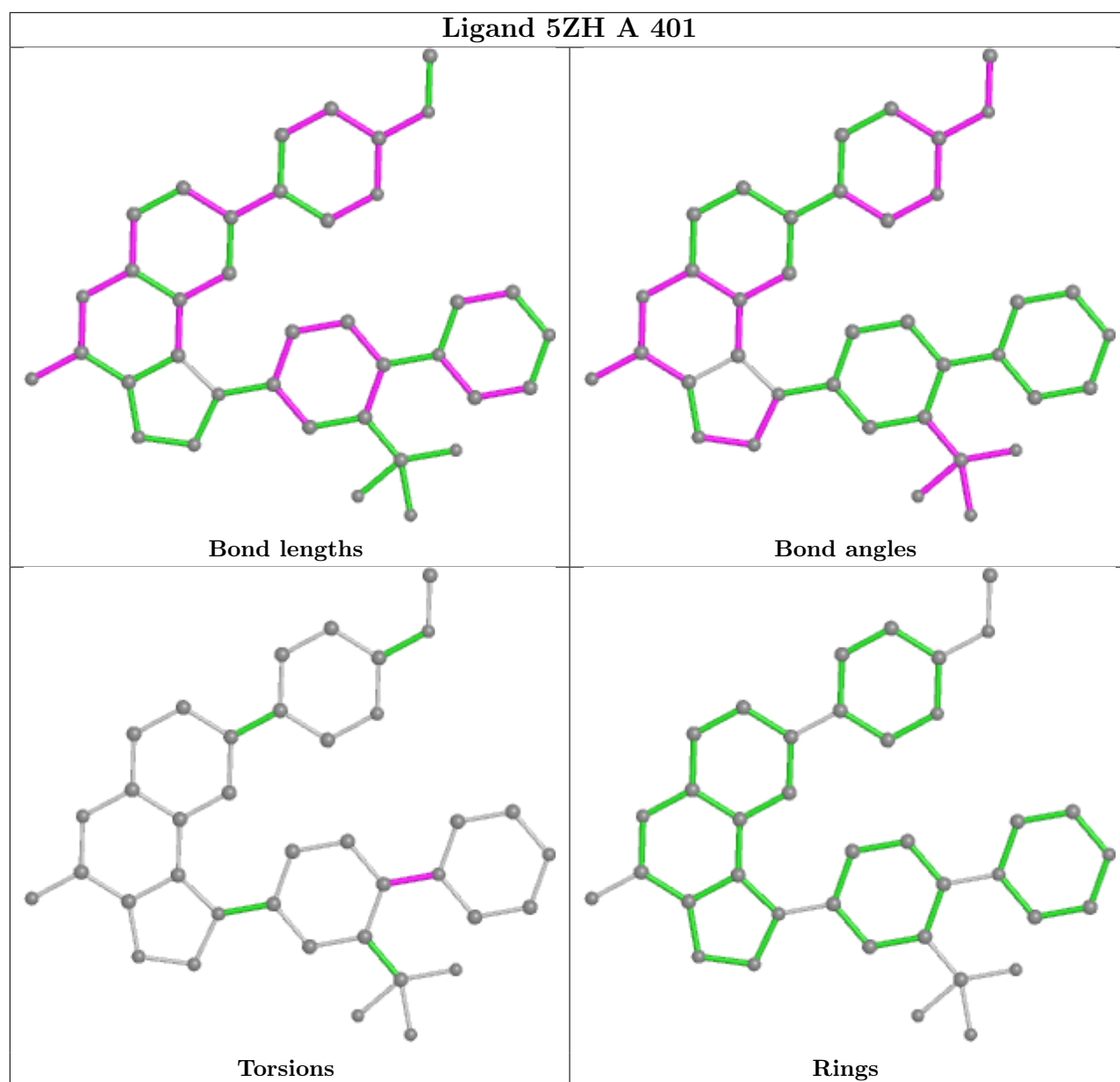
There are no ring outliers.

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](#)

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	300/319 (94%)	0.19	5 (1%) 70 76	46, 61, 90, 119	0
1	B	286/319 (89%)	0.21	6 (2%) 63 70	48, 66, 92, 105	0
All	All	586/638 (91%)	0.20	11 (1%) 66 73	46, 63, 91, 119	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	146	HIS	4.0
1	A	5	ASN	3.1
1	A	49	CYS	3.0
1	B	64	TRP	2.8
1	B	49	CYS	2.8
1	B	6	VAL	2.7
1	B	47	GLY	2.4
1	A	248	PRO	2.3
1	A	118	GLN	2.1
1	A	129	ARG	2.1
1	B	48	GLY	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

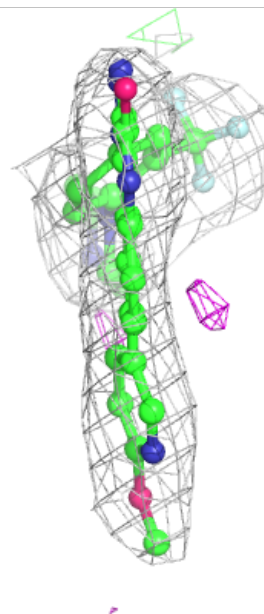
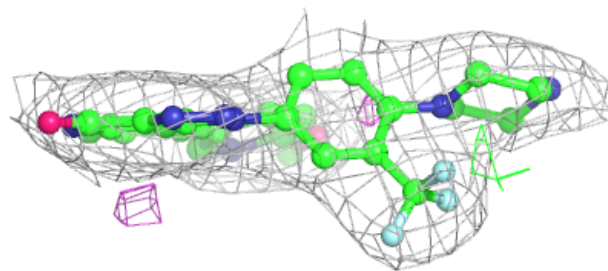
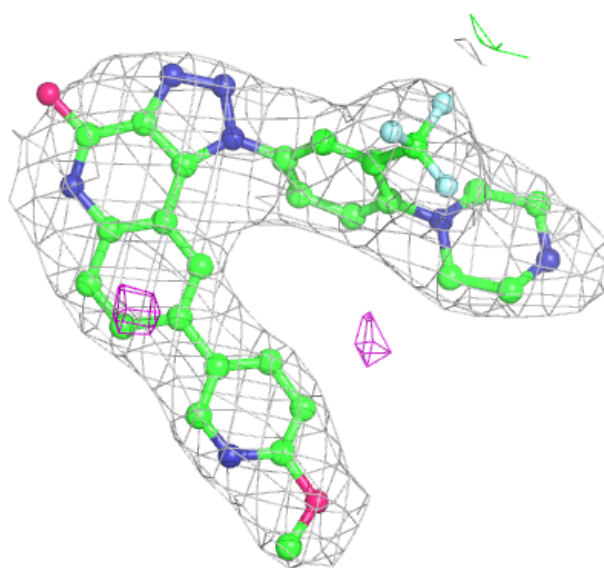
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	5ZH	A	401	38/38	0.94	0.14	47,72,91,98	0
2	5ZH	B	401	38/38	0.94	0.15	47,69,87,93	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.

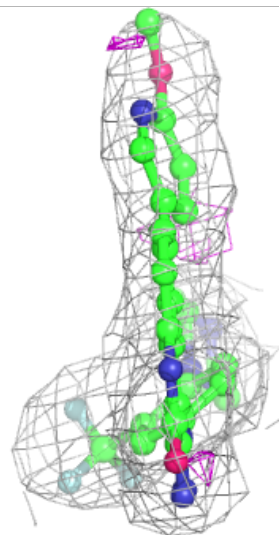
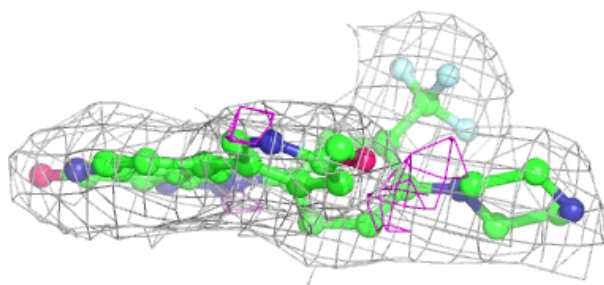
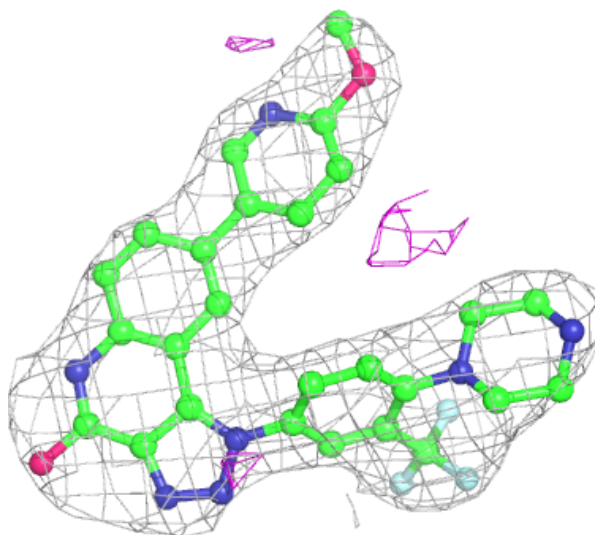
**Electron density around 5ZH A 401:**

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



**Electron density around 5ZH B 401:**

$2mF_o-DF_c$  (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.