



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2026 – 12:15 PM EDT

PDB ID : 11HQ / pdb\_000011hq  
Title : Type-III c-MET Inhibitor Enabled by Free-Energy Perturbation Calculations  
Authors : Eiler, D.R.; Abraham, N.; Kutter, S.; Kroeck, K.G.  
Deposited on : 2026-02-25  
Resolution : 2.65 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

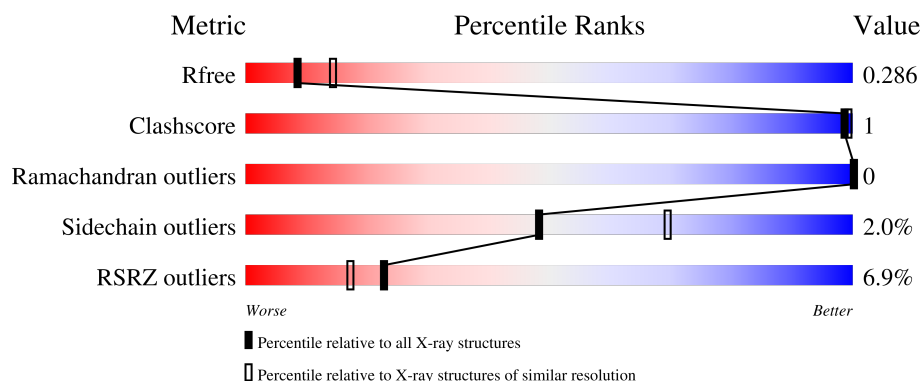
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	310	 3% 82% 14%
1	B	310	 5% 86% 10%
1	C	310	 10% 75% 6% 18%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13063 atoms, of which 6571 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.

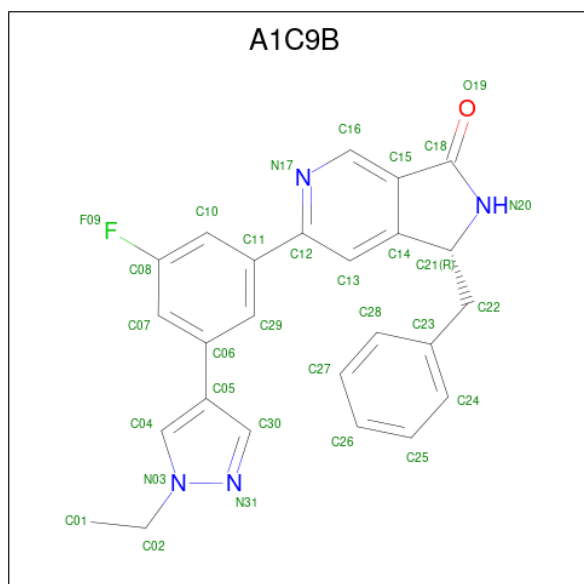
- Molecule 1 is a protein called Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	268	Total	C	H	N	O	S	0	0	0
			4279	1375	2154	361	375	14			
1	B	280	Total	C	H	N	O	S	0	0	0
			4496	1443	2263	378	397	15			
1	C	254	Total	C	H	N	O	S	0	0	0
			4093	1319	2065	343	352	14			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1272	VAL	LEU	engineered mutation	UNP P08581
B	1272	VAL	LEU	engineered mutation	UNP P08581
C	1272	VAL	LEU	engineered mutation	UNP P08581

- Molecule 2 is (1R,6M)-1-benzyl-6-[(3P)-3-(1-ethyl-1H-pyrazol-4-yl)-5-fluorophenyl]-1,2-dihydro-3H-pyrrolo[3,4-c]pyridin-3-one (CCD ID: A1C9B) (formula: C<sub>25</sub>H<sub>21</sub>FN<sub>4</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	0	0
			52	25	1	21	4	1		
2	B	1	Total	C	F	H	N	O	0	0
			52	25	1	21	4	1		
2	C	1	Total	C	F	H	N	O	0	0
			52	25	1	21	4	1		

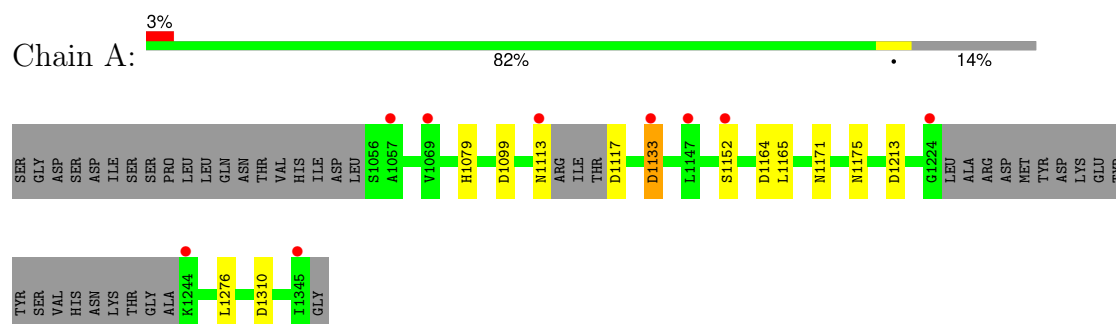
- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	6	Total	H	O	0	0
			18	12	6		
3	B	4	Total	H	O	0	0
			12	8	4		
3	C	3	Total	H	O	0	0
			9	6	3		

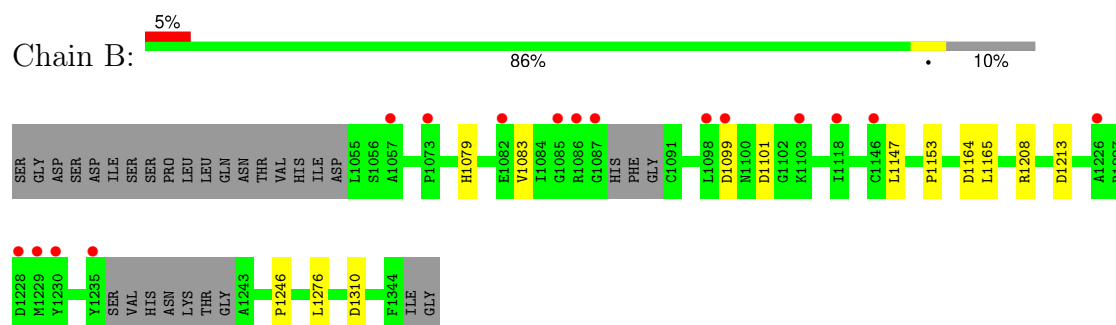
### 3 Residue-property plots [i](#)

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.

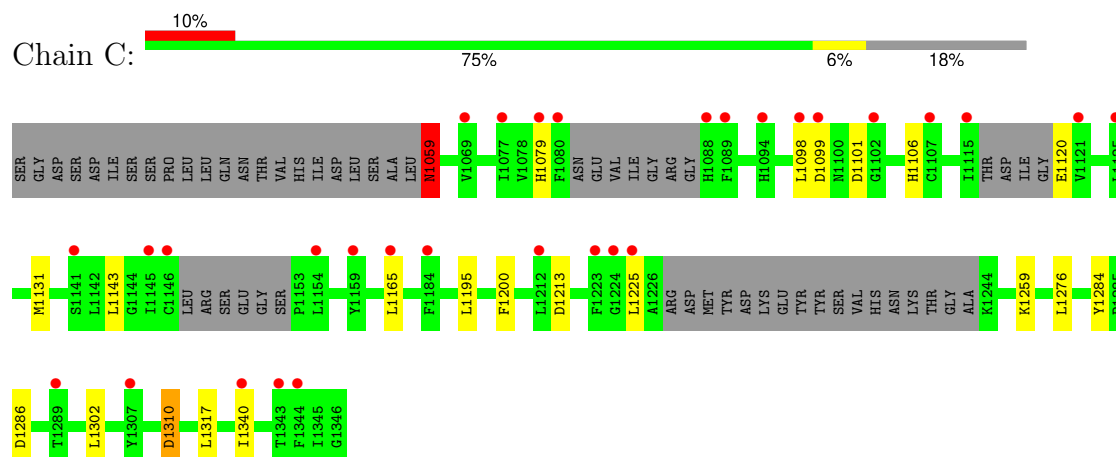
- Molecule 1: Hepatocyte growth factor receptor



- Molecule 1: Hepatocyte growth factor receptor



- Molecule 1: Hepatocyte growth factor receptor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.33Å 81.36Å 254.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.58 – 2.65 45.58 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.58-2.65) 99.4 (45.58-2.65)	Depositor EDS
$R_{merge}$	0.26	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.223 , 0.287 0.224 , 0.286	Depositor DCC
$R_{free}$ test set	1484 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.2	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 57.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13063	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: A1C9B

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	0.86	0/2177	1.45	10/2947 (0.3%)
1	B	0.87	0/2286	1.48	8/3094 (0.3%)
1	C	0.89	0/2078	1.46	8/2809 (0.3%)
All	All	0.88	0/6541	1.46	26/8850 (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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1117	ASP	CA-CB-CG	8.75	121.35	112.60
1	B	1213	ASP	CA-CB-CG	8.07	120.67	112.60
1	A	1213	ASP	CA-CB-CG	8.05	120.65	112.60
1	C	1213	ASP	CA-CB-CG	7.32	119.92	112.60
1	B	1101	ASP	CA-CB-CG	7.29	119.89	112.60
1	B	1099	ASP	CA-CB-CG	7.05	119.66	112.60
1	C	1310	ASP	CA-CB-CG	6.91	119.51	112.60
1	C	1286	ASP	CA-CB-CG	6.41	119.01	112.60
1	C	1059	ASN	CA-CB-CG	6.19	118.79	112.60
1	A	1099	ASP	CA-CB-CG	6.09	118.69	112.60
1	A	1113	ASN	CA-CB-CG	5.95	118.55	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1133	ASP	CA-CB-CG	5.91	118.51	112.60
1	C	1099	ASP	CA-CB-CG	5.80	118.40	112.60
1	A	1164	ASP	CA-C-N	5.58	127.76	120.28
1	A	1164	ASP	C-N-CA	5.58	127.76	120.28
1	A	1310	ASP	CA-CB-CG	5.44	118.04	112.60
1	B	1246	PRO	CA-C-N	5.36	127.51	120.60
1	B	1246	PRO	C-N-CA	5.36	127.51	120.60
1	B	1164	ASP	CA-CB-CG	5.28	117.88	112.60
1	A	1171	ASN	CA-CB-CG	5.24	117.84	112.60
1	A	1079	HIS	CE1-NE2-CD2	-5.20	103.81	109.00
1	B	1079	HIS	CE1-NE2-CD2	-5.18	103.82	109.00
1	C	1101	ASP	CA-CB-CG	5.17	117.77	112.60
1	B	1310	ASP	CA-CB-CG	5.14	117.74	112.60
1	C	1079	HIS	CA-CB-CG	5.07	118.87	113.80
1	C	1106	HIS	ND1-CE1-NE2	5.02	113.42	108.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1152	SER	Peptide
1	B	1153	PRO	Peptide

## 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	2125	2154	2151	1	0
1	B	2233	2263	2260	1	0
1	C	2028	2065	2060	5	0
2	A	31	21	0	0	0
2	B	31	21	0	0	0
2	C	31	21	0	0	0
3	A	6	12	0	0	0
3	B	4	8	0	0	0
3	C	3	6	0	0	0
All	All	6492	6571	6471	7	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 1.

All (7) 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:1165:LEU:HD21	1:A:1276:LEU:HD21	1.83	0.60
1:C:1165:LEU:HD21	1:C:1276:LEU:HD21	1.89	0.54
1:C:1195:LEU:HD12	1:C:1200:PHE:CD2	2.50	0.46
1:B:1165:LEU:HD21	1:B:1276:LEU:HD21	1.99	0.45
1:C:1284:TYR:H	1:C:1302:LEU:CD2	2.33	0.41
1:C:1059:ASN:HD22	1:C:1059:ASN:N	2.18	0.41
1:C:1225:LEU:HD12	1:C:1225:LEU:H	1.84	0.41

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	262/310 (84%)	256 (98%)	6 (2%)	0	100	100
1	B	274/310 (88%)	263 (96%)	11 (4%)	0	100	100
1	C	244/310 (79%)	239 (98%)	5 (2%)	0	100	100
All	All	780/930 (84%)	758 (97%)	22 (3%)	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	238/275 (86%)	236 (99%)	2 (1%)	73	85
1	B	249/275 (90%)	246 (99%)	3 (1%)	63	79
1	C	227/275 (82%)	218 (96%)	9 (4%)	28	47
All	All	714/825 (86%)	700 (98%)	14 (2%)	48	69

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1133	ASP
1	A	1175	ASN
1	B	1083	VAL
1	B	1147	LEU
1	B	1208	ARG
1	C	1059	ASN
1	C	1098	LEU
1	C	1120	GLU
1	C	1131	MET
1	C	1143	LEU
1	C	1259	LYS
1	C	1310	ASP
1	C	1317	LEU
1	C	1340	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1067	GLN

### 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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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	A1C9B	B	1401	-	35,35,35	0.69	0	47,50,50	1.44	4 (8%)
2	A1C9B	A	1401	-	35,35,35	0.68	0	47,50,50	1.39	4 (8%)
2	A1C9B	C	1401	-	35,35,35	0.68	0	47,50,50	1.44	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	A1C9B	B	1401	-	-	1/14/26/26	0/5/5/5
2	A1C9B	A	1401	-	-	0/14/26/26	0/5/5/5
2	A1C9B	C	1401	-	-	4/14/26/26	0/5/5/5

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1401	A1C9B	C15-C18-N20	-5.92	103.95	106.51
2	C	1401	A1C9B	C15-C18-N20	-5.50	104.13	106.51
2	A	1401	A1C9B	C15-C18-N20	-5.31	104.21	106.51
2	A	1401	A1C9B	C14-C15-C18	4.44	109.88	108.55
2	B	1401	A1C9B	C14-C15-C18	4.32	109.84	108.55
2	C	1401	A1C9B	C14-C15-C18	4.19	109.81	108.55
2	C	1401	A1C9B	C14-C21-N20	-3.25	100.61	101.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1401	A1C9B	C10-C08-C07	-2.84	120.05	123.50
2	B	1401	A1C9B	C14-C21-N20	-2.83	100.73	101.51
2	A	1401	A1C9B	C10-C08-C07	-2.81	120.08	123.50
2	C	1401	A1C9B	C10-C08-C07	-2.73	120.18	123.50
2	A	1401	A1C9B	C14-C21-N20	-2.10	100.93	101.51

There are no chirality outliers.

All (5) torsion outliers are listed below:

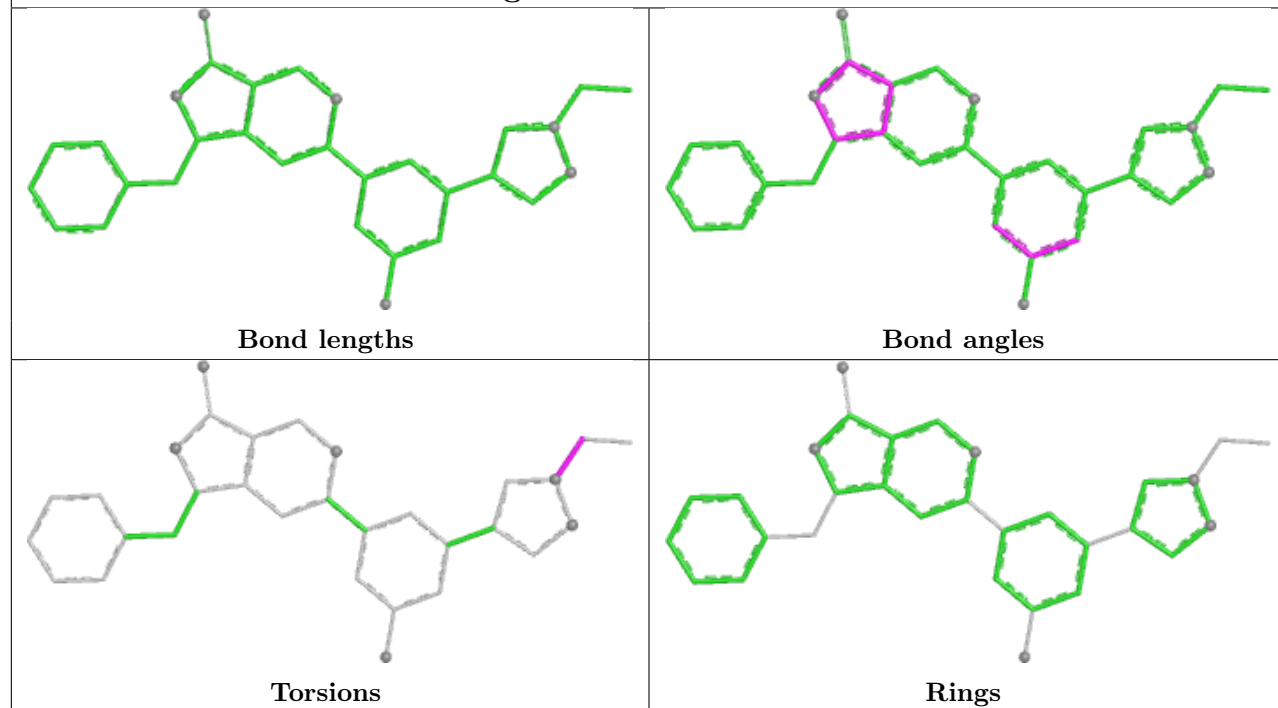
Mol	Chain	Res	Type	Atoms
2	C	1401	A1C9B	C04-C05-C06-C07
2	C	1401	A1C9B	C04-C05-C06-C29
2	C	1401	A1C9B	C30-C05-C06-C07
2	C	1401	A1C9B	C30-C05-C06-C29
2	B	1401	A1C9B	C01-C02-N03-N31

There are no ring outliers.

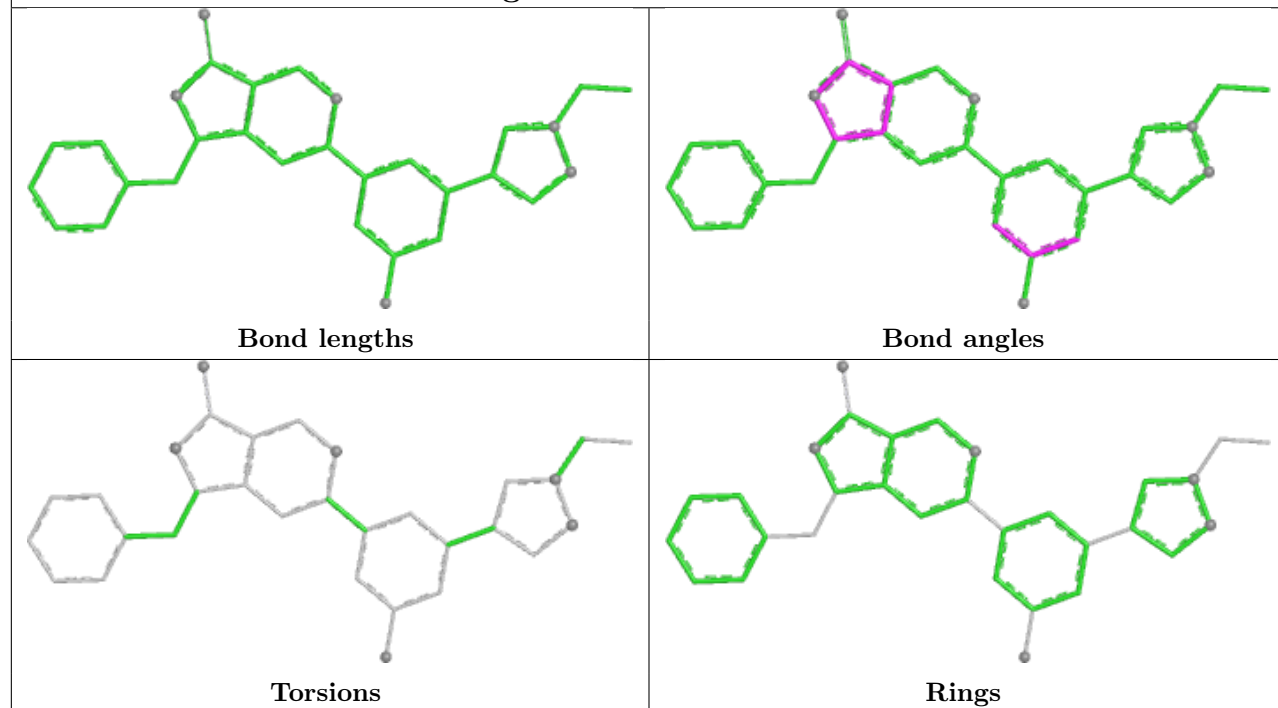
No monomer is involved in short contacts.

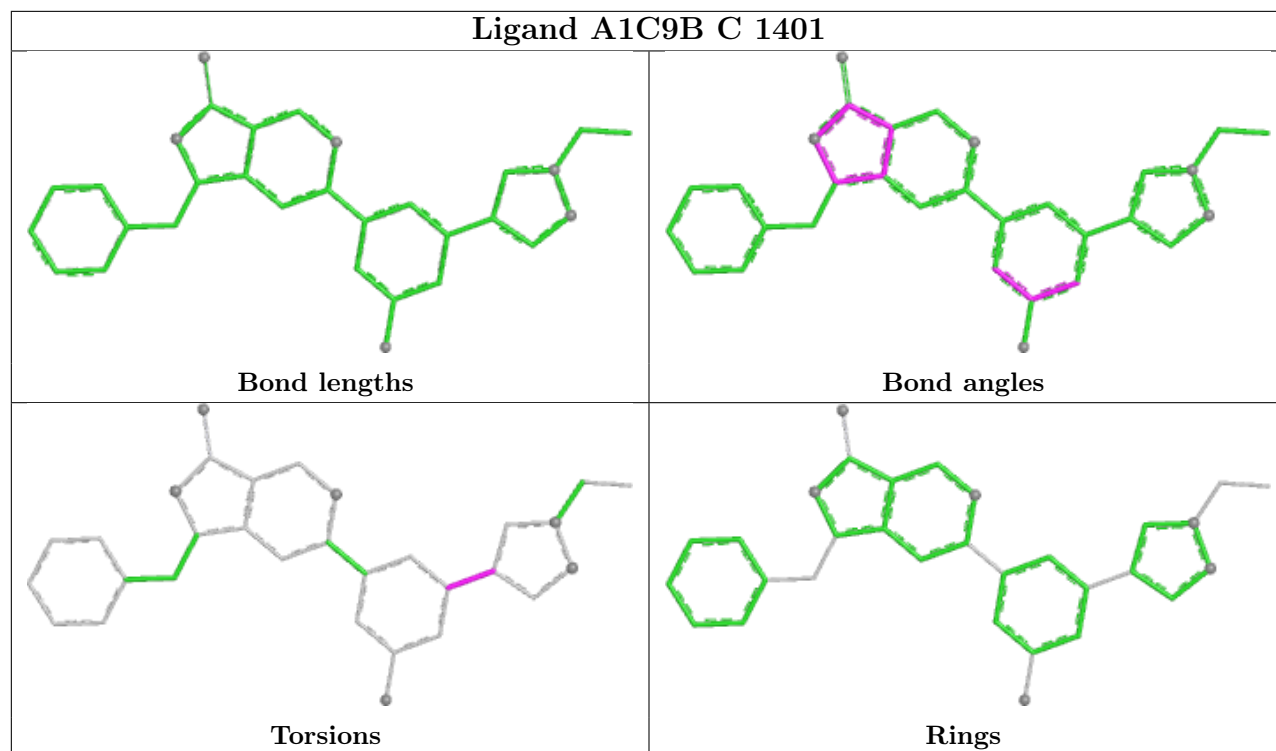
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 A1C9B B 1401



## Ligand A1C9B A 1401





## 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	268/310 (86%)	0.17	9 (3%)	48	40	34, 51, 96, 132	0
1	B	280/310 (90%)	0.36	16 (5%)	29	23	35, 60, 103, 144	0
1	C	254/310 (81%)	0.84	30 (11%)	9	7	47, 80, 124, 144	0
All	All	802/930 (86%)	0.45	55 (6%)	23	17	34, 63, 117, 144	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1057	ALA	4.7
1	C	1115	ILE	4.7
1	B	1087	GLY	4.6
1	C	1089	PHE	4.2
1	B	1226	ALA	3.5
1	C	1069	VAL	3.5
1	C	1146	CYS	3.4
1	B	1118	ILE	3.4
1	B	1230	TYR	3.4
1	A	1147	LEU	3.3
1	C	1165	LEU	3.2
1	C	1145	ILE	3.2
1	C	1225	LEU	3.2
1	C	1212	LEU	3.1
1	C	1088	HIS	3.1
1	B	1098	LEU	3.0
1	C	1121	VAL	3.0
1	C	1079	HIS	2.9
1	A	1069	VAL	2.8
1	B	1086	ARG	2.7
1	C	1344	PHE	2.7
1	C	1340	ILE	2.7
1	C	1094	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	1235	TYR	2.7
1	C	1289	THR	2.6
1	B	1085	GLY	2.6
1	C	1077	ILE	2.5
1	C	1223	PHE	2.5
1	A	1244	LYS	2.5
1	C	1307	TYR	2.5
1	C	1224	GLY	2.5
1	C	1141	SER	2.5
1	B	1099	ASP	2.5
1	C	1154	LEU	2.5
1	C	1184	PHE	2.5
1	B	1103	LYS	2.4
1	C	1080	PHE	2.4
1	C	1159	TYR	2.4
1	B	1228	ASP	2.4
1	C	1125	LEU	2.3
1	A	1224	GLY	2.3
1	B	1082	GLU	2.2
1	A	1152	SER	2.2
1	B	1073	PRO	2.2
1	B	1229	MET	2.2
1	C	1098	LEU	2.2
1	C	1343	THR	2.1
1	A	1345	ILE	2.1
1	B	1057	ALA	2.1
1	B	1146	CYS	2.1
1	C	1102	GLY	2.1
1	A	1133	ASP	2.1
1	C	1099	ASP	2.1
1	C	1107	CYS	2.1
1	A	1113	ASN	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 oligosaccharides in this entry.



## 6.4 Ligands ⓘ

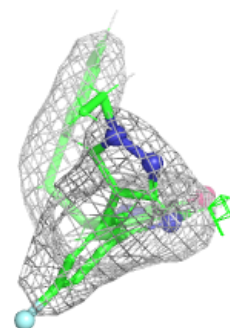
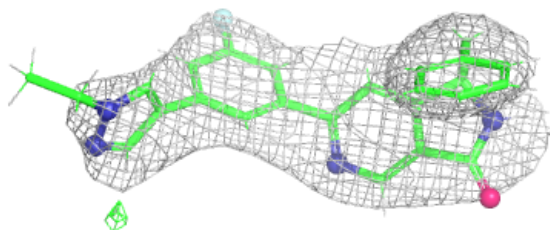
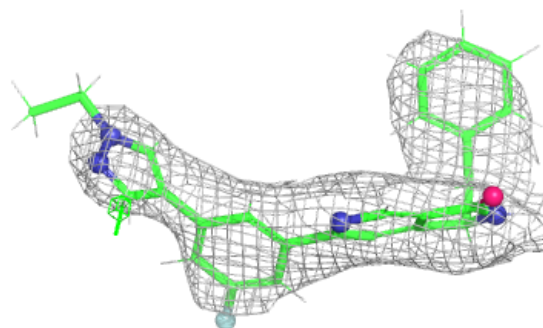
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	A1C9B	C	1401	31/31	0.82	0.16	60,81,110,111	0
2	A1C9B	B	1401	31/31	0.93	0.11	42,56,76,92	0
2	A1C9B	A	1401	31/31	0.93	0.10	38,57,83,86	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.

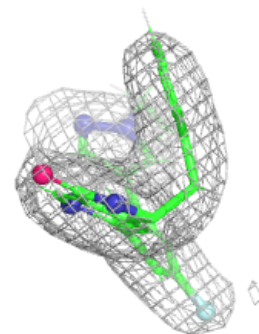
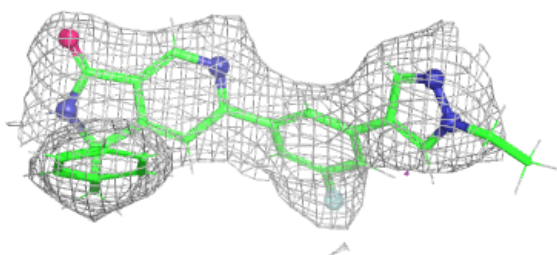
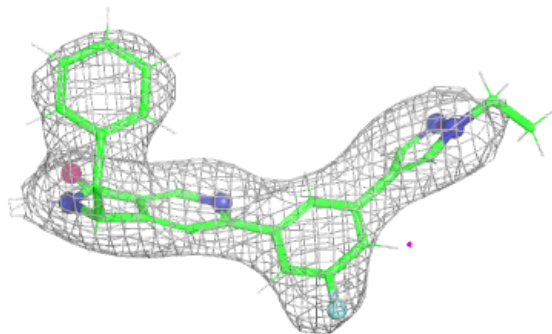
### Electron density around A1C9B C 1401:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
 mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
 and green (positive)

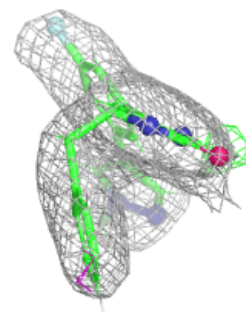
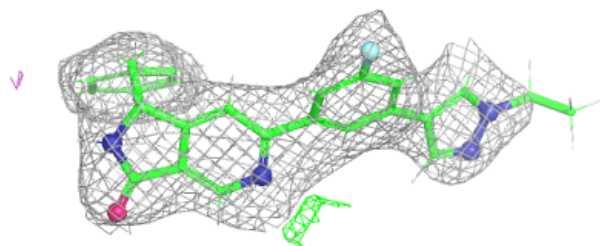
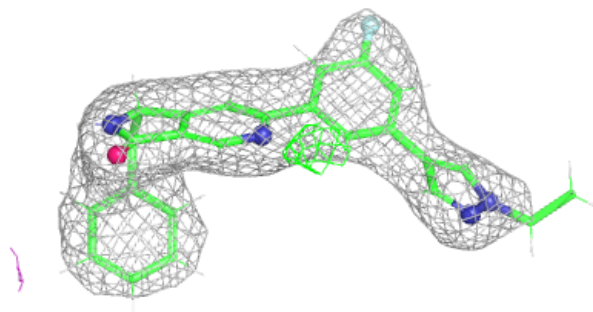


**Electron density around A1C9B B 1401:**

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

**Electron density around A1C9B A 1401:**

$2mF_o-DF_c$  (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.