



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2020 – 11:52 PM BST

PDB ID : 5J5F  
Title : X-Ray Crystal Structure of Acetylcholine Binding Protein (AChBP) in Complex with N4,N4-bis[(pyridin-2-yl)methyl]-6-(thiophen-3-yl)pyrimidine-2,4-diamine  
Authors : Kaczanowska, K.; Camacho Hernandez, G.A.; Harel, M.; Taylor, P.  
Deposited on : 2016-04-02  
Resolution : 2.04 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

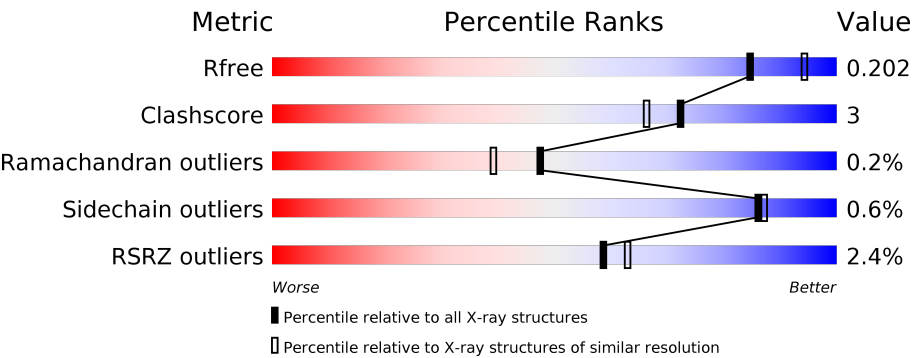
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.04 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.



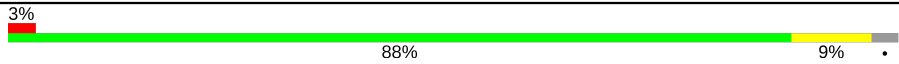

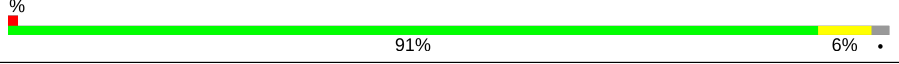

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 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	218	<div><div>91%6%</div></div>
1	B	218	<div><div>92%6%</div></div>
1	C	218	<div><div>91%7%</div></div>
1	D	218	<div><div>86%13%</div></div>
1	E	218	<div><div>93%7%</div></div>
1	F	218	<div><div>88%10%</div></div>

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Mol	Chain	Length	Quality of chain
1	G	218	
1	H	218	
1	I	218	
1	J	218	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	C	302	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19030 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 Acetylcholine-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	3	0
			1717	1073	290	349	5			
1	B	213	Total	C	N	O	S	0	2	0
			1715	1070	290	350	5			
1	C	213	Total	C	N	O	S	0	5	0
			1733	1081	290	357	5			
1	D	216	Total	C	N	O	S	0	2	0
			1740	1086	296	353	5			
1	E	218	Total	C	N	O	S	0	2	0
			1761	1098	300	358	5			
1	F	213	Total	C	N	O	S	0	2	0
			1717	1075	292	345	5			
1	G	212	Total	C	N	O	S	0	3	0
			1717	1072	292	348	5			
1	H	213	Total	C	N	O	S	0	4	0
			1730	1080	293	352	5			
1	I	213	Total	C	N	O	S	0	5	0
			1742	1088	298	351	5			
1	J	213	Total	C	N	O	S	0	1	0
			1711	1067	290	349	5			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ASP	-	expression tag	UNP P58154
A	-6	TYR	-	expression tag	UNP P58154
A	-5	LYS	-	expression tag	UNP P58154
A	-4	ASP	-	expression tag	UNP P58154
A	-3	ASP	-	expression tag	UNP P58154
A	-2	ASP	-	expression tag	UNP P58154
A	-1	ASP	-	expression tag	UNP P58154
A	0	LYS	-	expression tag	UNP P58154
B	-7	ASP	-	expression tag	UNP P58154

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	TYR	-	expression tag	UNP P58154
B	-5	LYS	-	expression tag	UNP P58154
B	-4	ASP	-	expression tag	UNP P58154
B	-3	ASP	-	expression tag	UNP P58154
B	-2	ASP	-	expression tag	UNP P58154
B	-1	ASP	-	expression tag	UNP P58154
B	0	LYS	-	expression tag	UNP P58154
C	-7	ASP	-	expression tag	UNP P58154
C	-6	TYR	-	expression tag	UNP P58154
C	-5	LYS	-	expression tag	UNP P58154
C	-4	ASP	-	expression tag	UNP P58154
C	-3	ASP	-	expression tag	UNP P58154
C	-2	ASP	-	expression tag	UNP P58154
C	-1	ASP	-	expression tag	UNP P58154
C	0	LYS	-	expression tag	UNP P58154
D	-7	ASP	-	expression tag	UNP P58154
D	-6	TYR	-	expression tag	UNP P58154
D	-5	LYS	-	expression tag	UNP P58154
D	-4	ASP	-	expression tag	UNP P58154
D	-3	ASP	-	expression tag	UNP P58154
D	-2	ASP	-	expression tag	UNP P58154
D	-1	ASP	-	expression tag	UNP P58154
D	0	LYS	-	expression tag	UNP P58154
E	-7	ASP	-	expression tag	UNP P58154
E	-6	TYR	-	expression tag	UNP P58154
E	-5	LYS	-	expression tag	UNP P58154
E	-4	ASP	-	expression tag	UNP P58154
E	-3	ASP	-	expression tag	UNP P58154
E	-2	ASP	-	expression tag	UNP P58154
E	-1	ASP	-	expression tag	UNP P58154
E	0	LYS	-	expression tag	UNP P58154
F	-7	ASP	-	expression tag	UNP P58154
F	-6	TYR	-	expression tag	UNP P58154
F	-5	LYS	-	expression tag	UNP P58154
F	-4	ASP	-	expression tag	UNP P58154
F	-3	ASP	-	expression tag	UNP P58154
F	-2	ASP	-	expression tag	UNP P58154
F	-1	ASP	-	expression tag	UNP P58154
F	0	LYS	-	expression tag	UNP P58154
G	-7	ASP	-	expression tag	UNP P58154
G	-6	TYR	-	expression tag	UNP P58154
G	-5	LYS	-	expression tag	UNP P58154

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-4	ASP	-	expression tag	UNP P58154
G	-3	ASP	-	expression tag	UNP P58154
G	-2	ASP	-	expression tag	UNP P58154
G	-1	ASP	-	expression tag	UNP P58154
G	0	LYS	-	expression tag	UNP P58154
H	-7	ASP	-	expression tag	UNP P58154
H	-6	TYR	-	expression tag	UNP P58154
H	-5	LYS	-	expression tag	UNP P58154
H	-4	ASP	-	expression tag	UNP P58154
H	-3	ASP	-	expression tag	UNP P58154
H	-2	ASP	-	expression tag	UNP P58154
H	-1	ASP	-	expression tag	UNP P58154
H	0	LYS	-	expression tag	UNP P58154
I	-7	ASP	-	expression tag	UNP P58154
I	-6	TYR	-	expression tag	UNP P58154
I	-5	LYS	-	expression tag	UNP P58154
I	-4	ASP	-	expression tag	UNP P58154
I	-3	ASP	-	expression tag	UNP P58154
I	-2	ASP	-	expression tag	UNP P58154
I	-1	ASP	-	expression tag	UNP P58154
I	0	LYS	-	expression tag	UNP P58154
J	-7	ASP	-	expression tag	UNP P58154
J	-6	TYR	-	expression tag	UNP P58154
J	-5	LYS	-	expression tag	UNP P58154
J	-4	ASP	-	expression tag	UNP P58154
J	-3	ASP	-	expression tag	UNP P58154
J	-2	ASP	-	expression tag	UNP P58154
J	-1	ASP	-	expression tag	UNP P58154
J	0	LYS	-	expression tag	UNP P58154

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		

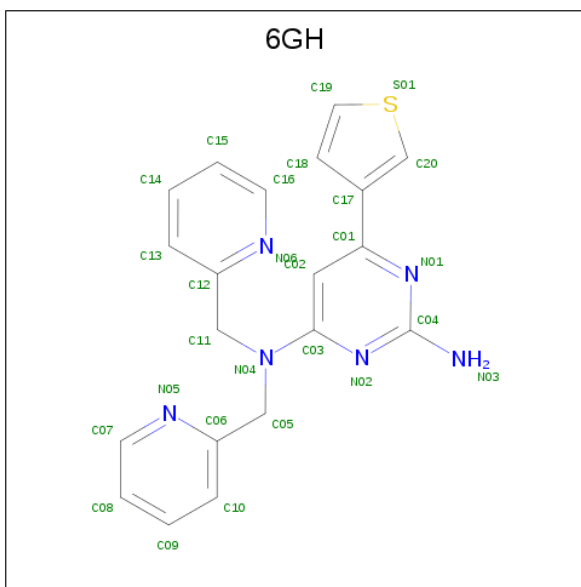
- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	H	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		
3	J	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is N 4 ,N 4 -bis[(pyridin-2-yl)methyl]-6-(thiophen-3-yl)pyrimidine-2,4-diamine (three-letter code: 6GH) (formula: C<sub>20</sub>H<sub>18</sub>N<sub>6</sub>S).





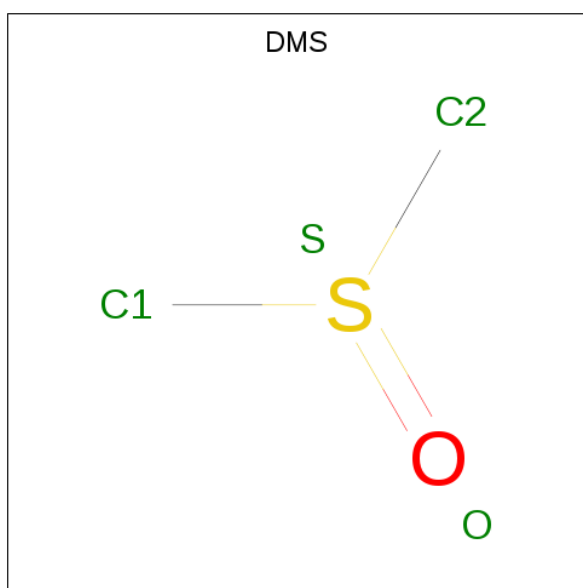
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			27	20	6	1		
4	B	1	Total	C	N	S	0	0
			27	20	6	1		
4	C	1	Total	C	N	S	0	0
			27	20	6	1		
4	D	1	Total	C	N	S	0	0
			27	20	6	1		
4	E	1	Total	C	N	S	0	0
			27	20	6	1		
4	F	1	Total	C	N	S	0	0
			27	20	6	1		
4	G	1	Total	C	N	S	0	0
			27	20	6	1		
4	H	1	Total	C	N	S	0	0
			27	20	6	1		
4	I	1	Total	C	N	S	0	0
			27	20	6	1		
4	J	1	Total	C	N	S	0	0
			27	20	6	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	F	1	Total	C	O	0	0
			6	3	3		
5	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula:  $C_2H_6OS$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	H	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	148	Total 148	O 148	0	0
7	B	129	Total 129	O 129	0	0
7	C	124	Total 124	O 124	0	0
7	D	111	Total 111	O 111	0	0
7	E	101	Total 101	O 101	0	0
7	F	111	Total 111	O 111	0	0
7	G	137	Total 137	O 137	0	0
7	H	146	Total 146	O 146	0	0
7	I	133	Total 133	O 133	0	0
7	J	126	Total 126	O 126	0	0

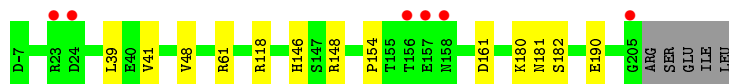
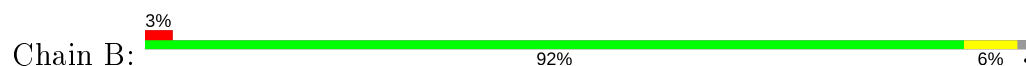
### 3 Residue-property plots [i](#)

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: Acetylcholine-binding protein



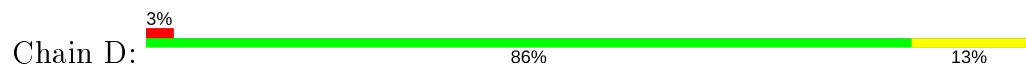
- Molecule 1: Acetylcholine-binding protein



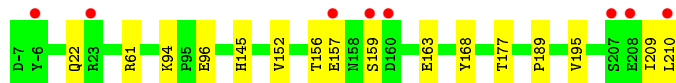
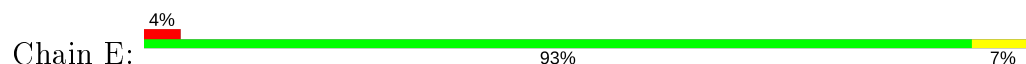
- Molecule 1: Acetylcholine-binding protein



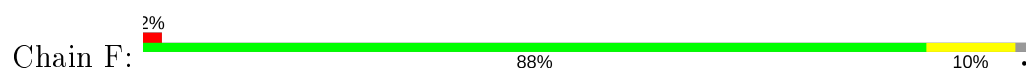
- Molecule 1: Acetylcholine-binding protein



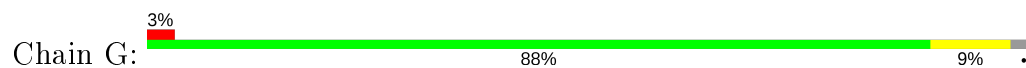
- Molecule 1: Acetylcholine-binding protein



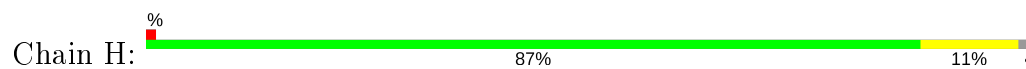
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



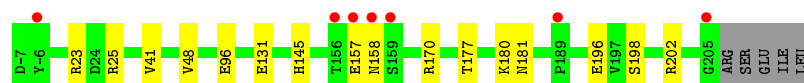
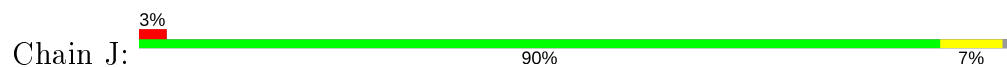
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.76Å 125.92Å 121.07Å 90.00° 110.03° 90.00°	Depositor
Resolution (Å)	49.83 – 2.04 49.83 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.83-2.04) 99.9 (49.83-2.04)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.57 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.166 , 0.202 0.167 , 0.202	Depositor DCC
$R_{free}$ test set	2013 reflections (1.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.4	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 52.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	19030	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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: GOL, PO4, DMS, 6GH, NAG

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	0.40	0/1763	0.53	0/2405
1	B	0.40	0/1758	0.54	0/2398
1	C	0.38	0/1785	0.56	0/2434
1	D	0.38	0/1782	0.54	0/2427
1	E	0.39	0/1801	0.54	0/2455
1	F	0.39	0/1759	0.56	0/2396
1	G	0.42	0/1762	0.58	0/2400
1	H	0.42	0/1779	0.58	0/2425
1	I	0.42	0/1791	0.54	0/2440
1	J	0.38	0/1751	0.53	0/2388
All	All	0.40	0/17731	0.55	0/24168

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	1717	0	1653	9	0
1	B	1715	0	1646	8	0
1	C	1733	0	1658	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1740	0	1676	20	0
1	E	1761	0	1695	10	0
1	F	1717	0	1664	16	0
1	G	1717	0	1653	14	0
1	H	1730	0	1667	17	0
1	I	1742	0	1685	11	0
1	J	1711	0	1639	12	0
2	A	5	0	0	1	0
2	B	15	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	F	10	0	0	1	0
2	H	5	0	0	0	0
2	I	10	0	0	1	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
3	D	14	0	13	0	0
3	E	14	0	13	0	0
3	F	14	0	13	2	0
3	G	14	0	13	0	0
3	H	14	0	13	0	0
3	I	14	0	13	0	0
3	J	14	0	13	0	0
4	A	27	0	0	0	0
4	B	27	0	0	0	0
4	C	27	0	0	0	0
4	D	27	0	0	0	0
4	E	27	0	0	1	0
4	F	27	0	0	0	0
4	G	27	0	0	0	0
4	H	27	0	0	0	0
4	I	27	0	0	0	0
4	J	27	0	0	0	0
5	F	6	0	8	0	0
5	H	6	0	8	0	0
6	H	4	0	6	0	0
7	A	148	0	0	3	0
7	B	129	0	0	1	0
7	C	124	0	0	2	0
7	D	111	0	0	0	0
7	E	101	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	F	111	0	0	1	0
7	G	137	0	0	5	0
7	H	146	0	0	2	0
7	I	133	0	0	1	0
7	J	126	0	0	0	0
All	All	19030	0	16788	116	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.

The worst 5 of 116 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:F:137:ARG:NH1	1:F:198:SER:OG	2.05	0.90
1:D:137:ARG:NH1	1:D:198:SER:OG	2.17	0.77
1:H:148:ARG:NH2	1:I:3:ASP:OD2	2.20	0.75
1:D:94:LYS:HE3	1:E:96:GLU:HG3	1.69	0.73
1:H:60:ASP:OD2	7:H:401:HOH:O	2.09	0.70

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	213/218 (98%)	213 (100%)	0	0	100	100
1	B	213/218 (98%)	211 (99%)	2 (1%)	0	100	100
1	C	216/218 (99%)	213 (99%)	3 (1%)	0	100	100
1	D	214/218 (98%)	213 (100%)	1 (0%)	0	100	100
1	E	218/218 (100%)	217 (100%)	0	1 (0%)	29	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	211/218 (97%)	210 (100%)	0	1 (0%)	29	18
1	G	211/218 (97%)	204 (97%)	5 (2%)	2 (1%)	17	8
1	H	215/218 (99%)	215 (100%)	0	0	100	100
1	I	216/218 (99%)	214 (99%)	1 (0%)	1 (0%)	29	18
1	J	212/218 (97%)	209 (99%)	3 (1%)	0	100	100
All	All	2139/2180 (98%)	2119 (99%)	15 (1%)	5 (0%)	47	39

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	23	ARG
1	E	189	PRO
1	F	161	ASP
1	G	24	ASP
1	I	190	GLU

### 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	202/204 (99%)	201 (100%)	1 (0%)	88	89
1	B	201/204 (98%)	201 (100%)	0	100	100
1	C	204/204 (100%)	203 (100%)	1 (0%)	88	89
1	D	204/204 (100%)	204 (100%)	0	100	100
1	E	206/204 (101%)	204 (99%)	2 (1%)	76	75
1	F	201/204 (98%)	200 (100%)	1 (0%)	88	89
1	G	201/204 (98%)	197 (98%)	4 (2%)	55	50
1	H	203/204 (100%)	200 (98%)	3 (2%)	65	63
1	I	204/204 (100%)	200 (98%)	4 (2%)	55	50
1	J	200/204 (98%)	200 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2026/2040 (99%)	2010 (99%)	16 (1%)	86	82

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	131[B]	GLU
1	G	162	SER
1	I	137[A]	ARG
1	G	131[A]	GLU
1	I	137[B]	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	158	ASN
1	G	158	ASN
1	H	9	ASN

### 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 ⓘ

34 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	PO4	B	302	-	4,4,4	0.85	0	6,6,6	0.58	0
6	DMS	H	305	-	3,3,3	2.02	2 (66%)	3,3,3	0.75	0
3	NAG	C	302	1	14,14,15	0.62	1 (7%)	17,19,21	1.38	1 (5%)
2	PO4	I	301	-	4,4,4	0.78	0	6,6,6	0.62	0
2	PO4	B	303	-	4,4,4	0.74	0	6,6,6	0.75	0
3	NAG	H	302	1	14,14,15	0.32	0	17,19,21	0.42	0
4	6GH	D	303	-	30,30,30	2.73	7 (23%)	36,40,40	2.75	13 (36%)
3	NAG	D	302	1	14,14,15	0.28	0	17,19,21	0.58	0
2	PO4	C	301	-	4,4,4	0.90	0	6,6,6	0.43	0
2	PO4	F	301	-	4,4,4	1.01	0	6,6,6	0.58	0
2	PO4	A	301	-	4,4,4	0.86	0	6,6,6	0.51	0
4	6GH	B	305	-	30,30,30	2.69	8 (26%)	36,40,40	2.73	12 (33%)
2	PO4	I	302	-	4,4,4	0.70	0	6,6,6	0.36	0
2	PO4	H	301	-	4,4,4	0.65	0	6,6,6	0.40	0
3	NAG	B	304	1	14,14,15	0.41	0	17,19,21	0.58	0
3	NAG	E	301	1	14,14,15	0.40	0	17,19,21	0.52	0
3	NAG	J	301	1	14,14,15	0.44	0	17,19,21	0.60	0
3	NAG	I	303	1	14,14,15	0.66	1 (7%)	17,19,21	1.04	1 (5%)
2	PO4	F	302	-	4,4,4	1.11	0	6,6,6	0.46	0
4	6GH	E	302	-	30,30,30	2.68	8 (26%)	36,40,40	2.82	14 (38%)
4	6GH	G	302	-	30,30,30	2.59	9 (30%)	36,40,40	2.89	12 (33%)
4	6GH	C	303	-	30,30,30	2.73	8 (26%)	36,40,40	2.77	13 (36%)
4	6GH	A	303	-	30,30,30	2.68	9 (30%)	36,40,40	2.78	14 (38%)
4	6GH	H	304	-	30,30,30	2.61	10 (33%)	36,40,40	2.79	14 (38%)
4	6GH	I	304	-	30,30,30	2.68	8 (26%)	36,40,40	2.90	14 (38%)
3	NAG	A	302	1	14,14,15	0.23	0	17,19,21	0.62	0
4	6GH	F	305	-	30,30,30	2.62	7 (23%)	36,40,40	2.98	13 (36%)
2	PO4	B	301	-	4,4,4	1.05	0	6,6,6	0.61	0
2	PO4	D	301	-	4,4,4	0.77	0	6,6,6	0.61	0
5	GOL	H	303	-	5,5,5	0.31	0	5,5,5	0.41	0
3	NAG	F	303	1	14,14,15	0.18	0	17,19,21	0.70	0
5	GOL	F	304	-	5,5,5	0.45	0	5,5,5	0.48	0
3	NAG	G	301	1	14,14,15	0.69	1 (7%)	17,19,21	0.74	0
4	6GH	J	302	-	30,30,30	2.64	8 (26%)	36,40,40	2.98	14 (38%)

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
3	NAG	C	302	1	-	3/6/23/26	0/1/1/1
3	NAG	H	302	1	-	2/6/23/26	0/1/1/1
4	6GH	D	303	-	-	0/12/16/16	0/4/4/4
3	NAG	D	302	1	-	2/6/23/26	0/1/1/1
4	6GH	B	305	-	-	0/12/16/16	0/4/4/4
3	NAG	B	304	1	-	0/6/23/26	0/1/1/1
4	6GH	F	305	-	-	0/12/16/16	0/4/4/4
3	NAG	J	301	1	-	1/6/23/26	0/1/1/1
3	NAG	I	303	1	-	1/6/23/26	0/1/1/1
4	6GH	E	302	-	-	0/12/16/16	0/4/4/4
4	6GH	G	302	-	-	0/12/16/16	0/4/4/4
4	6GH	C	303	-	-	0/12/16/16	0/4/4/4
4	6GH	A	303	-	-	0/12/16/16	0/4/4/4
4	6GH	H	304	-	-	0/12/16/16	0/4/4/4
4	6GH	I	304	-	-	0/12/16/16	0/4/4/4
3	NAG	A	302	1	-	3/6/23/26	0/1/1/1
3	NAG	E	301	1	-	0/6/23/26	0/1/1/1
5	GOL	H	303	-	-	2/4/4/4	-
3	NAG	F	303	1	-	4/6/23/26	0/1/1/1
5	GOL	F	304	-	-	2/4/4/4	-
3	NAG	G	301	1	-	2/6/23/26	0/1/1/1
4	6GH	J	302	-	-	0/12/16/16	0/4/4/4

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	303	6GH	C17-C01	-8.93	1.34	1.48
4	B	305	6GH	C17-C01	-8.89	1.34	1.48
4	E	302	6GH	C17-C01	-8.85	1.35	1.48
4	I	304	6GH	C17-C01	-8.83	1.35	1.48
4	J	302	6GH	C17-C01	-8.72	1.35	1.48

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	302	6GH	C01-N01-C04	10.31	122.22	116.34
4	A	303	6GH	C01-N01-C04	10.10	122.10	116.34
4	G	302	6GH	C01-N01-C04	9.64	121.84	116.34
4	I	304	6GH	C01-N01-C04	9.50	121.75	116.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	305	6GH	C01-N01-C04	9.49	121.75	116.34

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	304	GOL	O1-C1-C2-C3
3	A	302	NAG	O5-C5-C6-O6
3	F	303	NAG	O5-C5-C6-O6
3	C	302	NAG	O5-C5-C6-O6
3	A	302	NAG	C4-C5-C6-O6

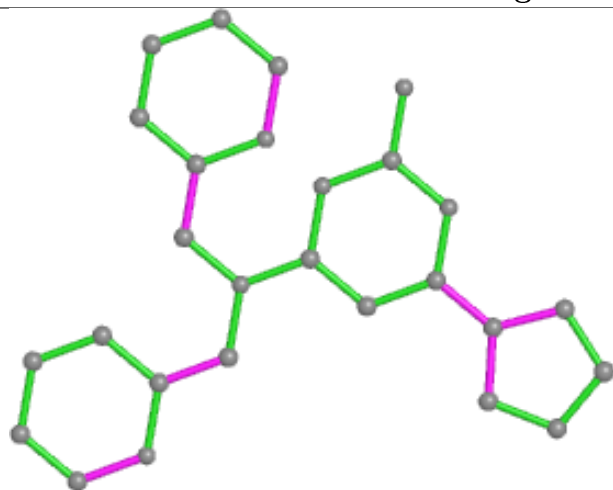
There are no ring outliers.

5 monomers are involved in 6 short contacts:

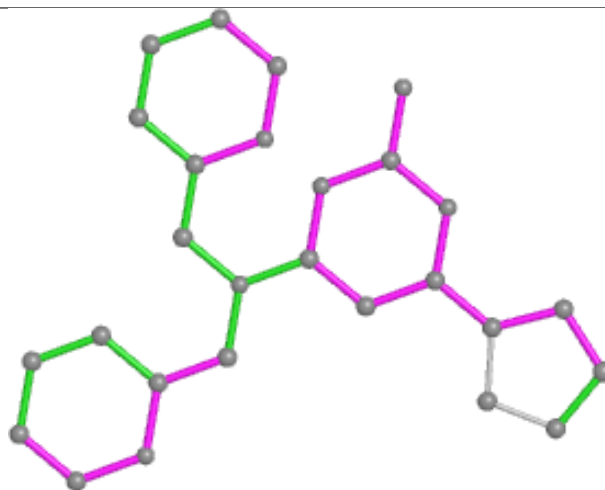
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	301	PO4	1	0
2	F	301	PO4	1	0
2	A	301	PO4	1	0
4	E	302	6GH	1	0
3	F	303	NAG	2	0

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.

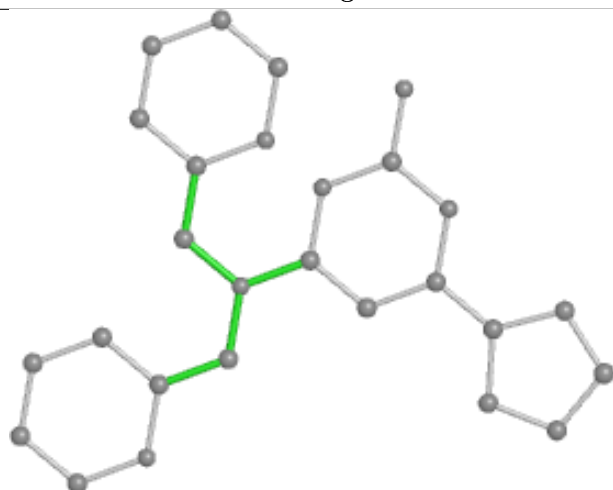
## Ligand 6GH D 303



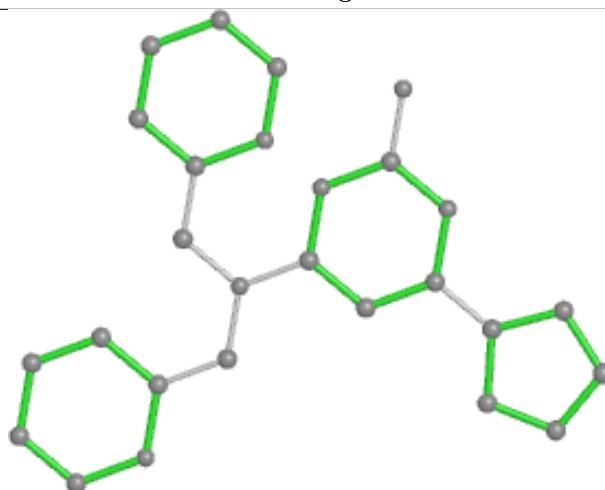
Bond lengths



Bond angles

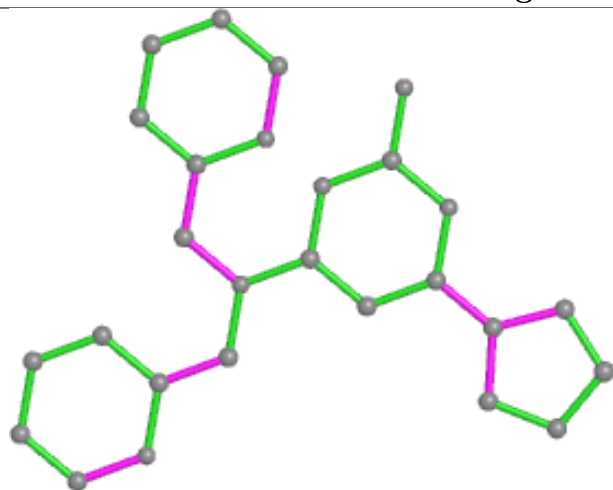


Torsions

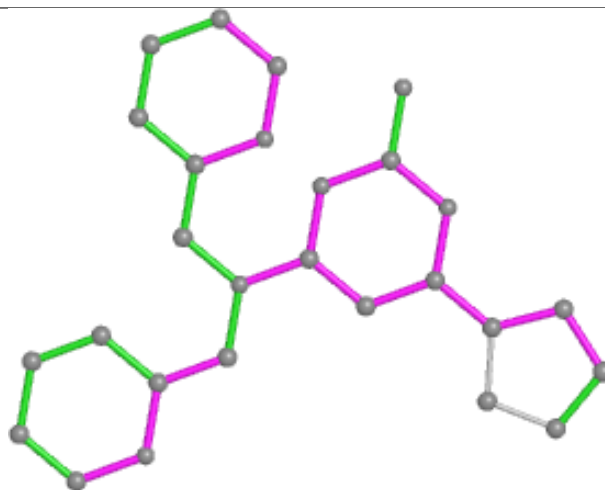


Rings

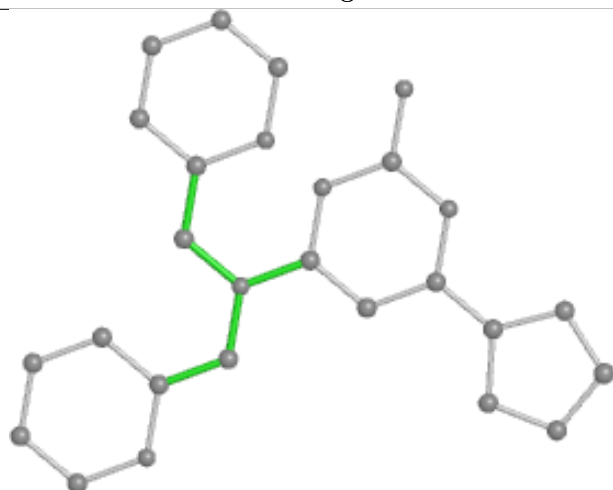
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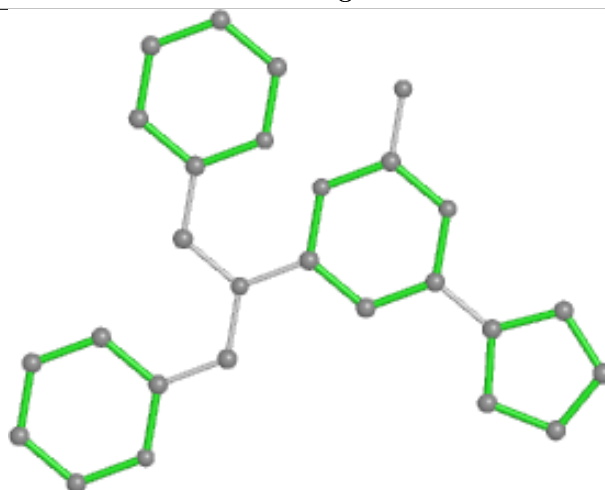
Bond lengths



Bond angles



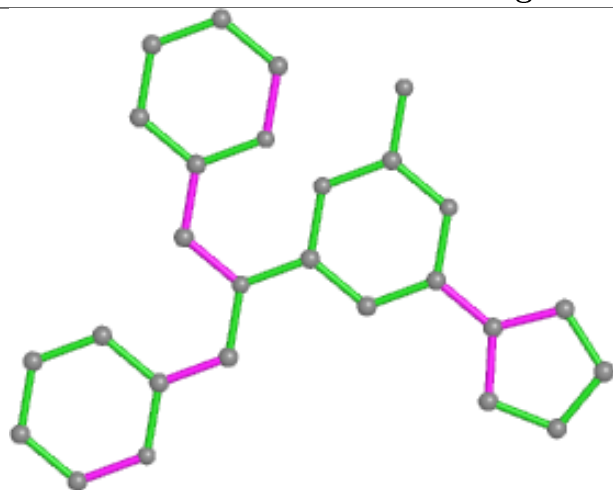
Torsions



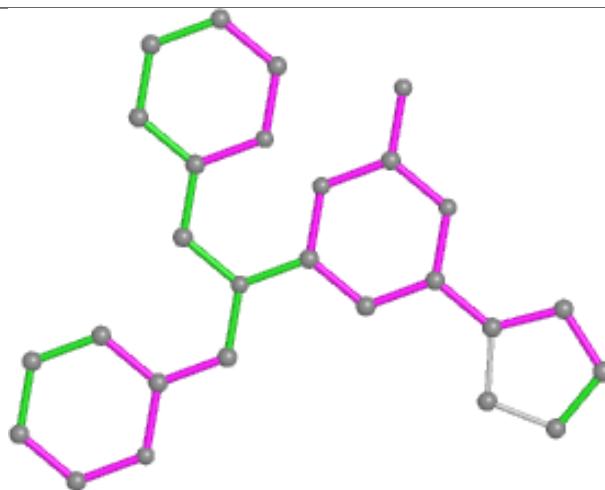
Rings



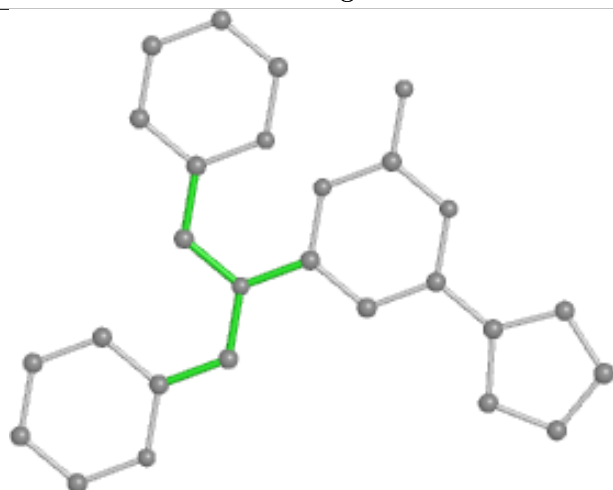
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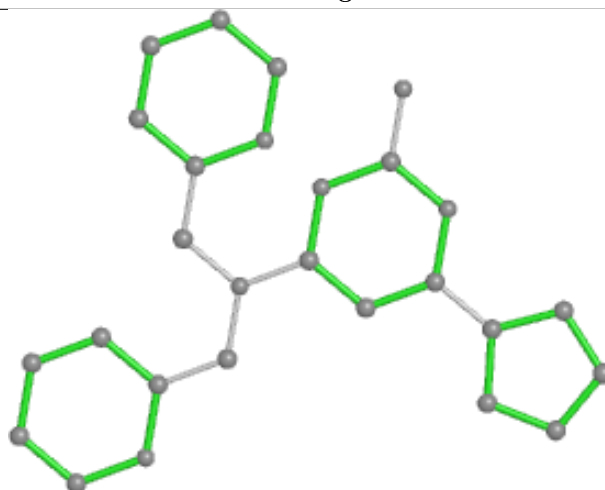
Bond lengths



Bond angles

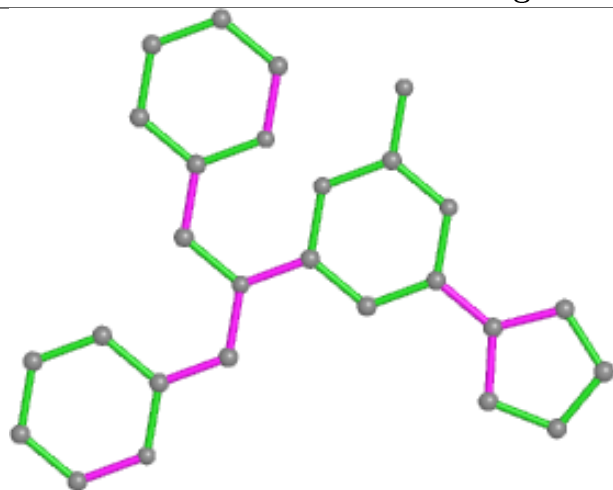


Torsions

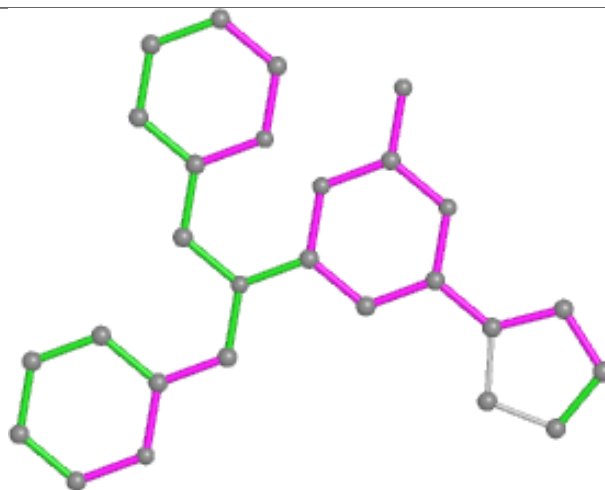


Rings

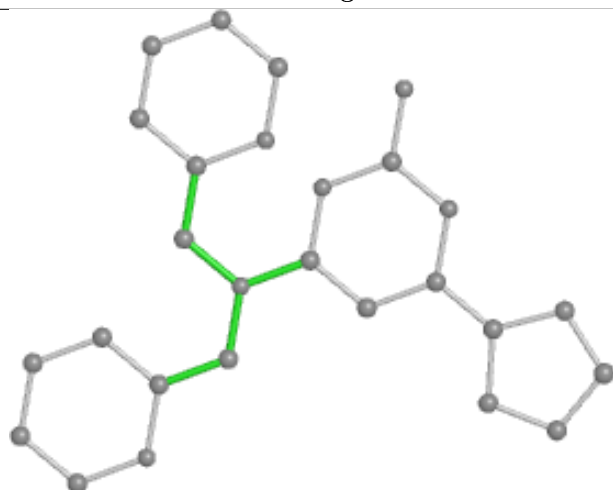
## Ligand 6GH G 302



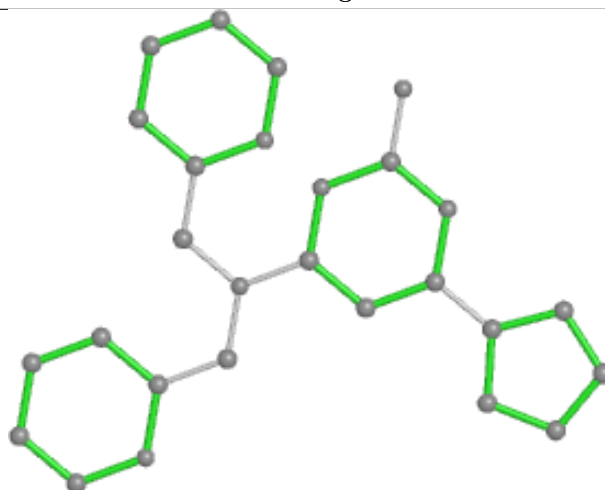
Bond lengths



Bond angles

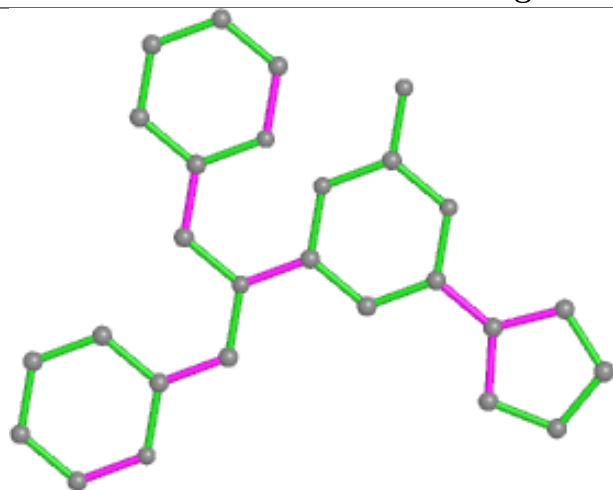


Torsions

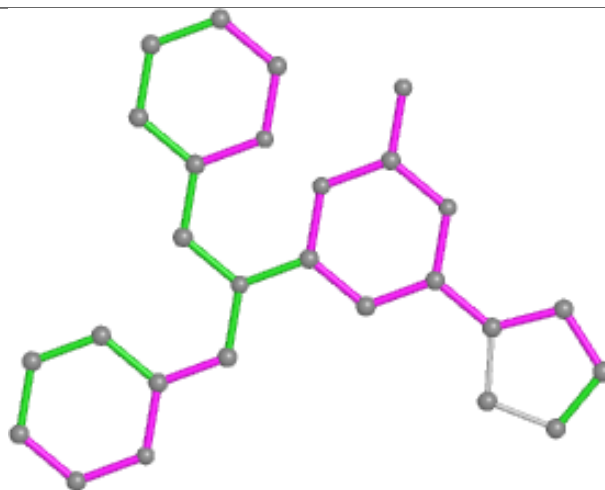


Rings

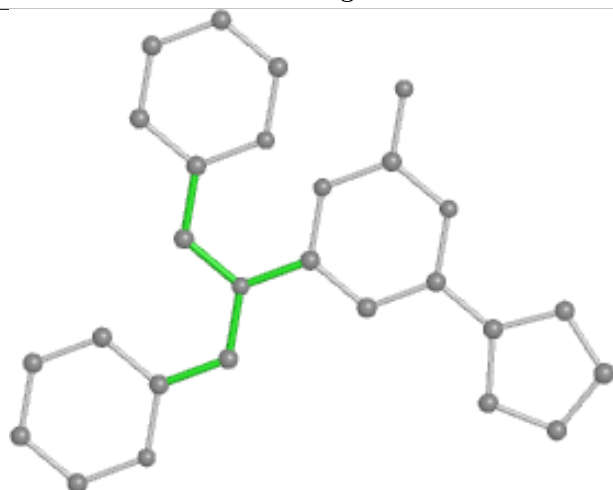
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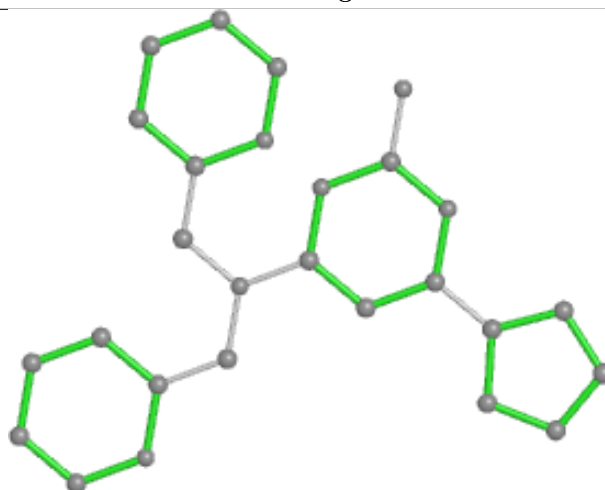
Bond lengths



Bond angles

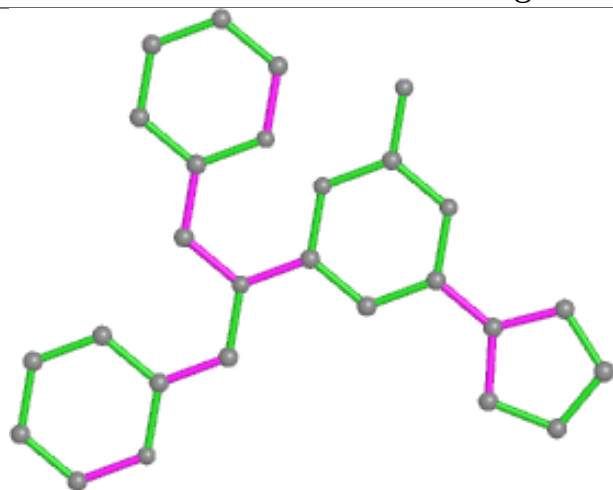


Torsions

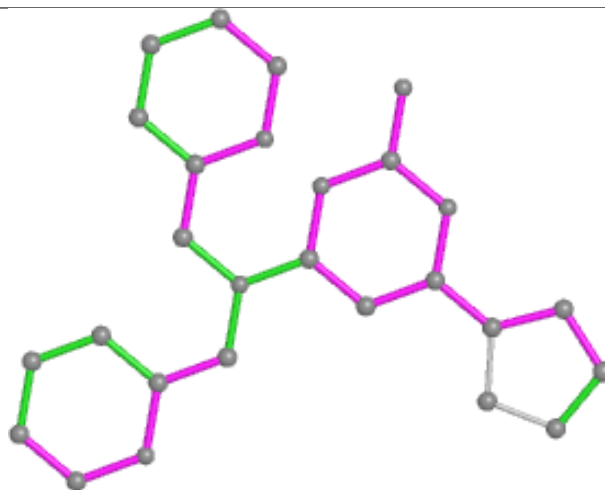


Rings

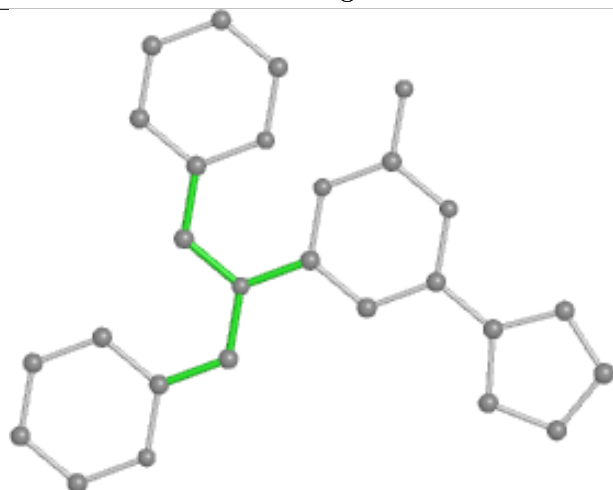
## Ligand 6GH A 303



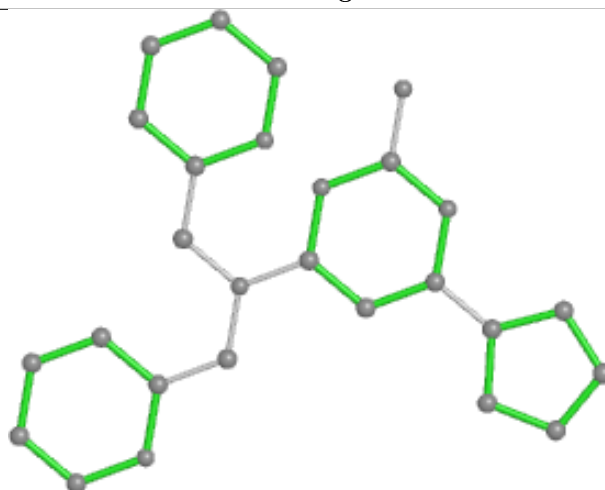
Bond lengths



Bond angles

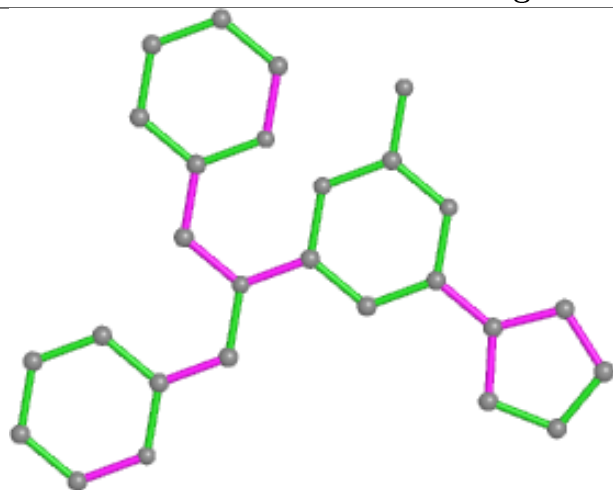


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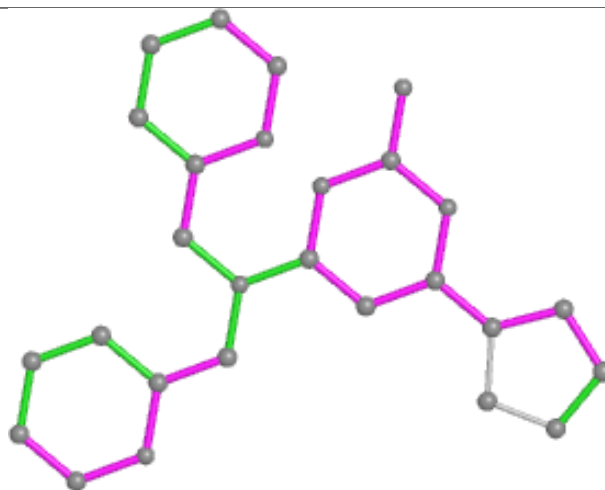


Rings

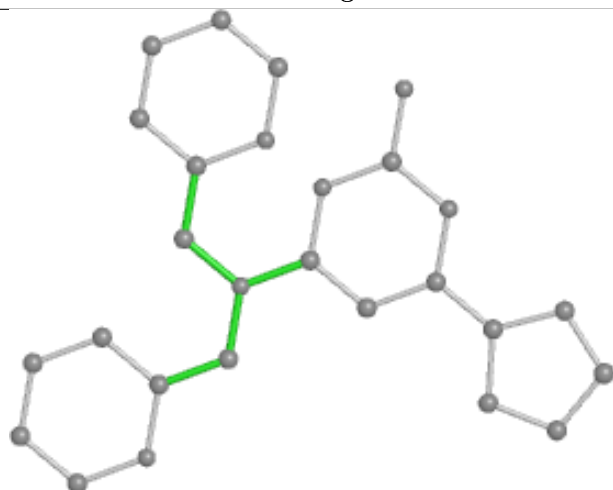
## Ligand 6GH H 304



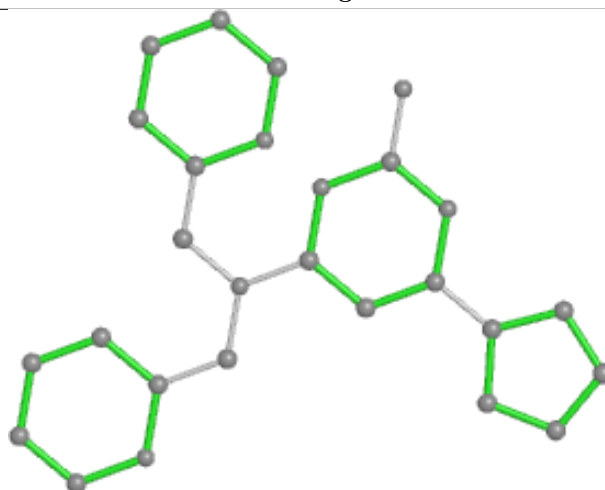
Bond lengths



Bond angles

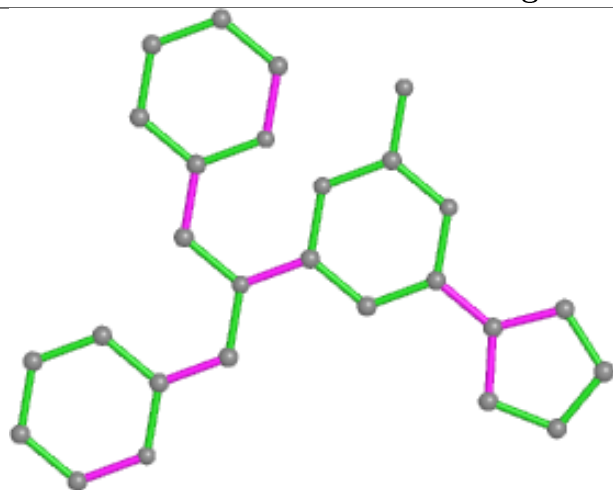


Torsions

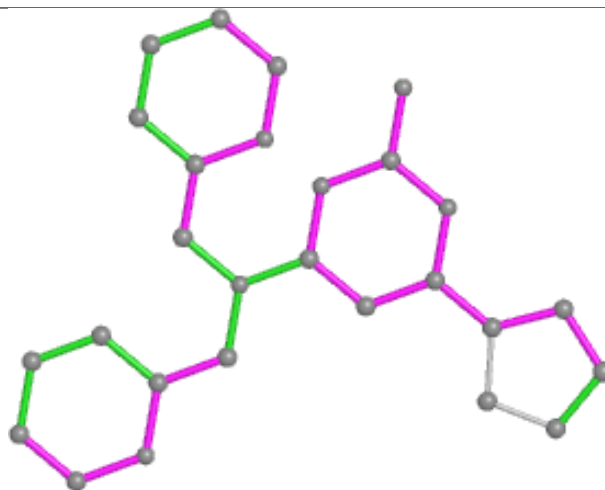


Rings

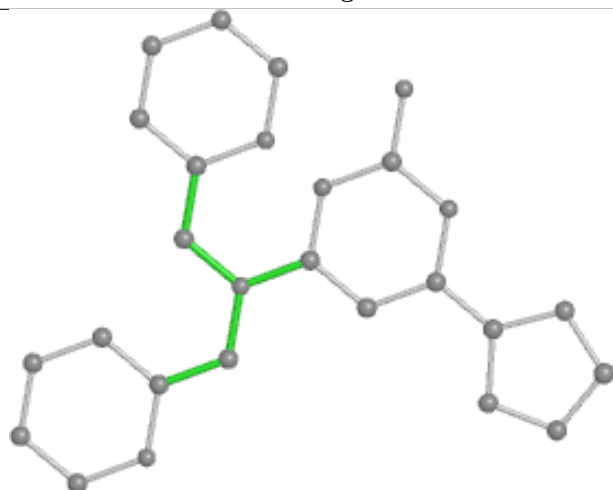
## Ligand 6GH I 304



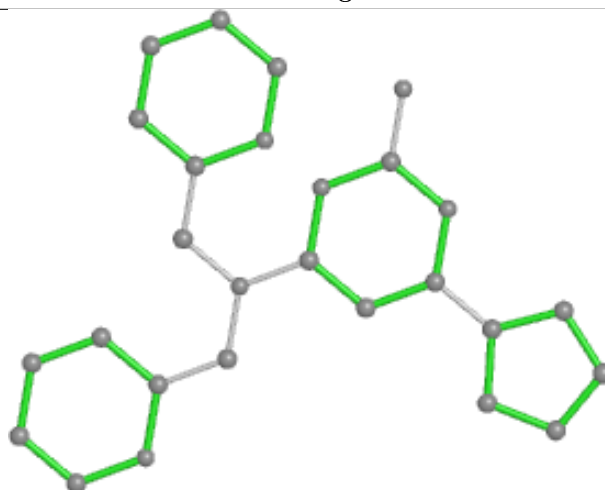
Bond lengths



Bond angles

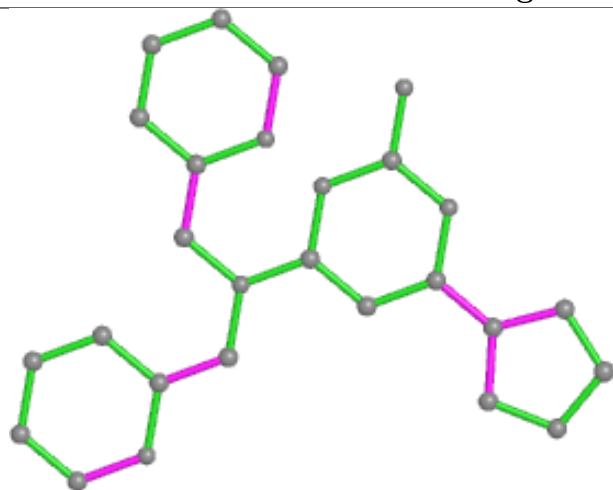


Torsions

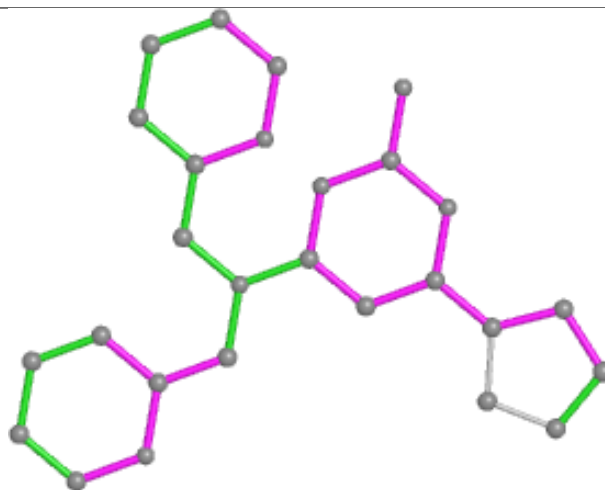


Rings

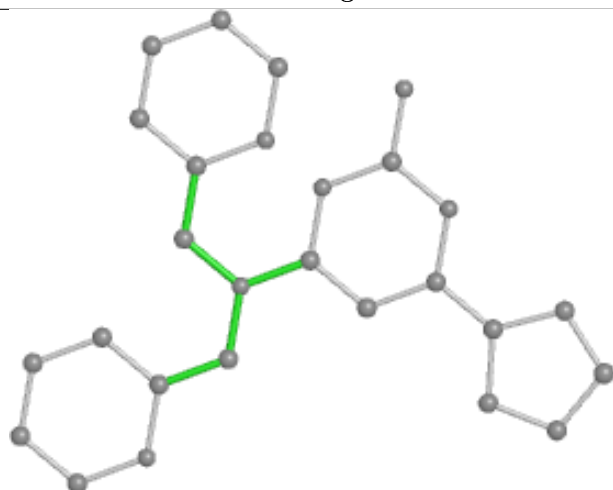
## Ligand 6GH F 305



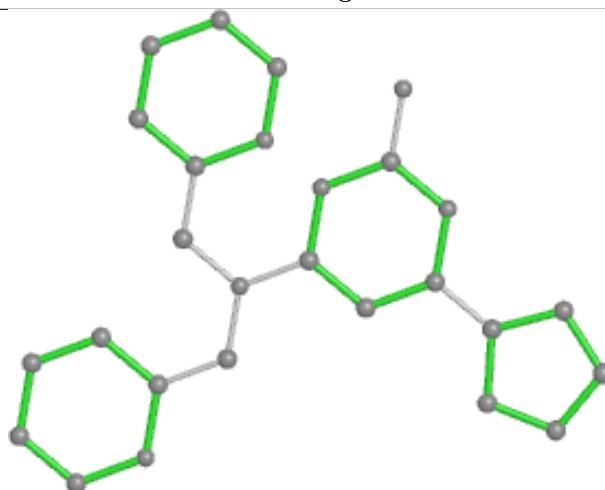
Bond lengths



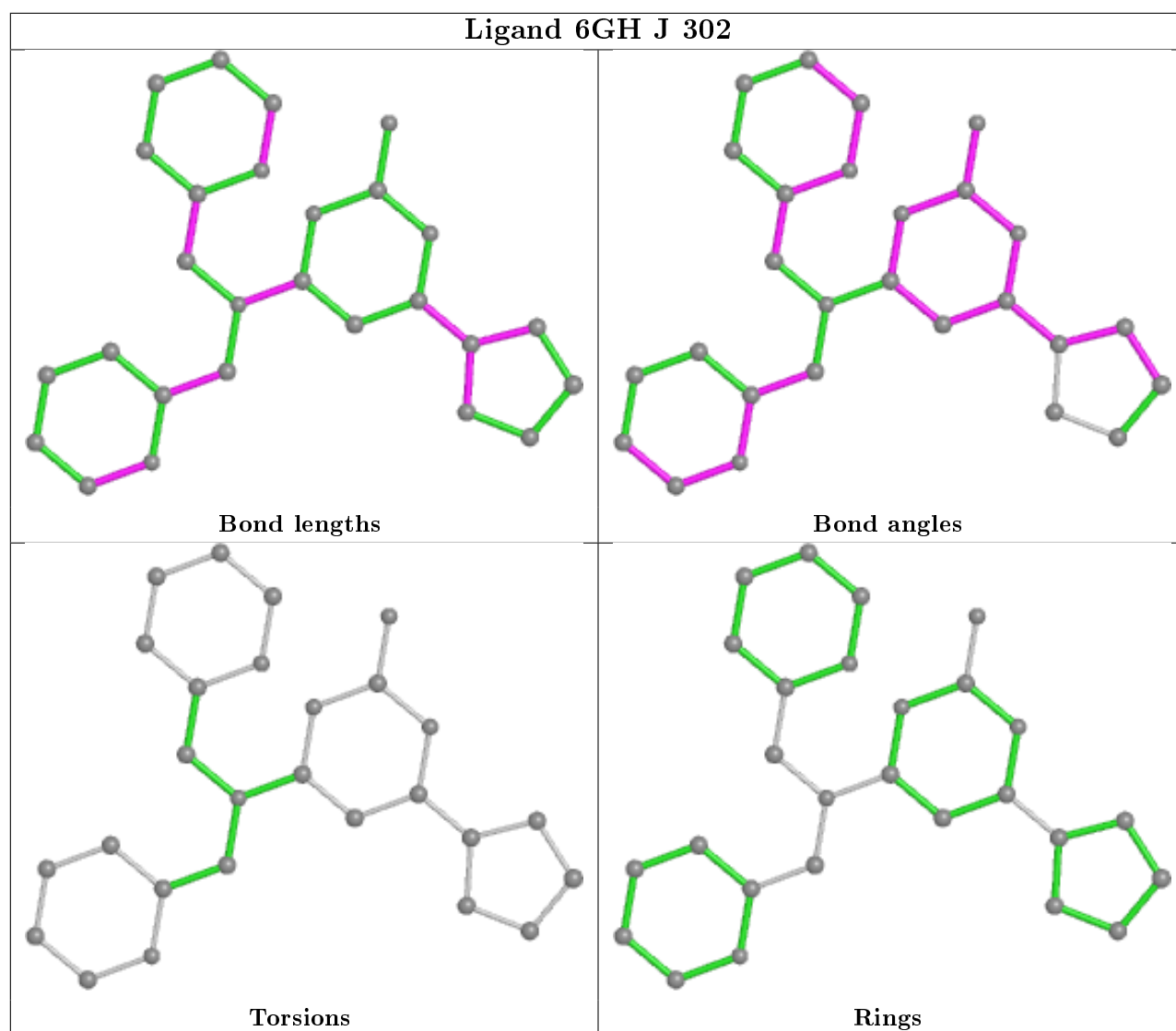
Bond angles



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	212/218 (97%)	-0.32	3 (1%) 75 78	13, 21, 39, 55	0
1	B	213/218 (97%)	-0.21	6 (2%) 53 58	11, 22, 44, 66	0
1	C	213/218 (97%)	-0.29	4 (1%) 66 71	13, 23, 44, 63	0
1	D	216/218 (99%)	-0.11	7 (3%) 47 52	13, 25, 44, 64	0
1	E	218/218 (100%)	-0.09	8 (3%) 41 45	13, 25, 49, 69	0
1	F	213/218 (97%)	-0.11	4 (1%) 66 71	12, 23, 46, 65	0
1	G	212/218 (97%)	-0.22	7 (3%) 46 50	10, 20, 44, 59	0
1	H	213/218 (97%)	-0.33	3 (1%) 75 78	10, 18, 37, 51	0
1	I	213/218 (97%)	-0.32	3 (1%) 75 78	11, 20, 38, 62	0
1	J	213/218 (97%)	-0.08	7 (3%) 46 50	12, 24, 47, 68	0
All	All	2136/2180 (97%)	-0.21	52 (2%) 59 63	10, 22, 45, 69	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	-6	TYR	5.0
1	G	156	THR	4.7
1	A	-6	TYR	4.7
1	D	158	ASN	4.5
1	G	-6	TYR	4.4

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

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

## 6.3 Carbohydrates ⓘ

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.

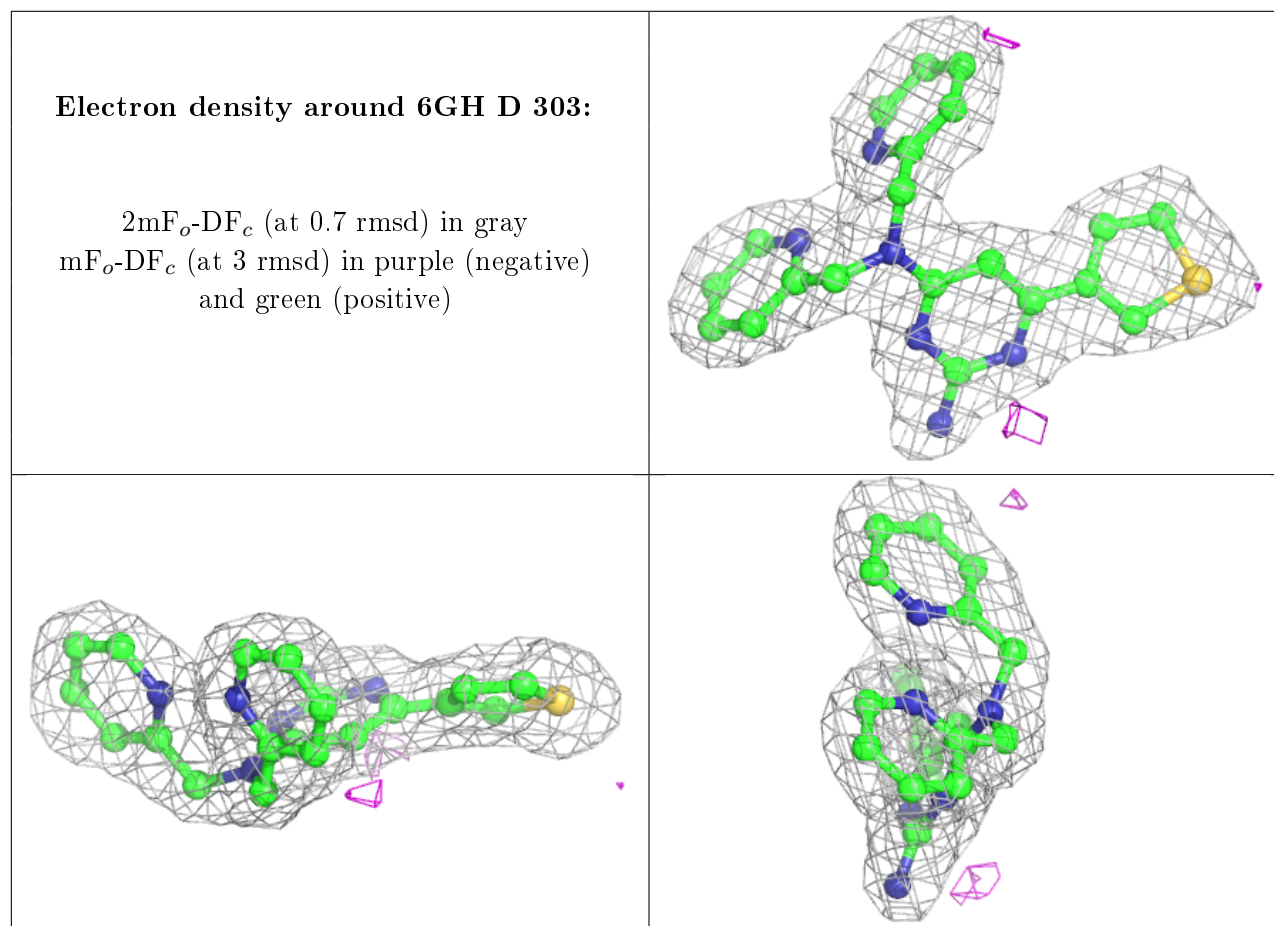
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	C	302	14/15	0.58	0.42	52,63,71,76	0
3	NAG	G	301	14/15	0.66	0.28	45,60,66,69	0
3	NAG	E	301	14/15	0.70	0.26	46,60,71,76	0
3	NAG	I	303	14/15	0.71	0.28	56,64,71,74	0
3	NAG	F	303	14/15	0.72	0.26	45,52,59,61	0
6	DMS	H	305	4/4	0.72	0.24	35,38,51,71	0
3	NAG	H	302	14/15	0.76	0.26	50,57,62,65	0
3	NAG	A	302	14/15	0.79	0.26	46,59,65,66	0
3	NAG	J	301	14/15	0.79	0.33	45,53,60,63	0
3	NAG	D	302	14/15	0.80	0.20	53,58,62,67	0
3	NAG	B	304	14/15	0.83	0.17	27,38,43,53	0
5	GOL	H	303	6/6	0.92	0.15	23,34,39,49	0
2	PO4	B	303	5/5	0.93	0.16	31,40,48,48	0
5	GOL	F	304	6/6	0.96	0.12	22,30,35,37	0
4	6GH	D	303	27/27	0.96	0.08	13,21,26,27	0
4	6GH	I	304	27/27	0.97	0.09	12,20,24,28	0
4	6GH	F	305	27/27	0.97	0.08	12,18,24,27	0
4	6GH	B	305	27/27	0.97	0.09	15,19,25,28	0
4	6GH	E	302	27/27	0.97	0.08	13,19,23,27	0
4	6GH	C	303	27/27	0.97	0.09	15,23,28,29	0
4	6GH	A	303	27/27	0.97	0.09	13,18,25,25	0
4	6GH	H	304	27/27	0.97	0.09	11,19,22,25	0
4	6GH	J	302	27/27	0.97	0.10	15,22,27,28	0
4	6GH	G	302	27/27	0.98	0.09	9,13,18,20	0
2	PO4	C	301	5/5	0.99	0.09	12,16,18,18	0
2	PO4	B	301	5/5	0.99	0.09	11,12,15,15	0
2	PO4	D	301	5/5	0.99	0.07	14,14,17,17	0
2	PO4	F	301	5/5	0.99	0.09	12,14,16,16	0
2	PO4	B	302	5/5	0.99	0.09	11,14,15,15	0
2	PO4	I	302	5/5	0.99	0.08	13,15,17,18	0
2	PO4	F	302	5/5	0.99	0.10	14,14,15,16	0
2	PO4	H	301	5/5	0.99	0.08	12,14,14,16	0

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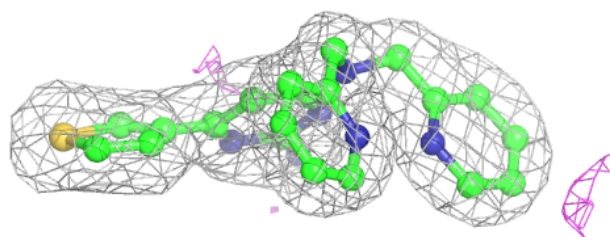
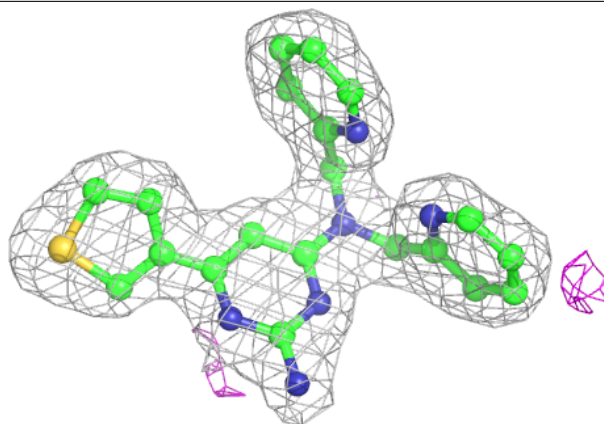
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	A	301	5/5	1.00	0.07	12,14,16,16	0
2	PO4	I	301	5/5	1.00	0.08	12,12,15,15	0

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.



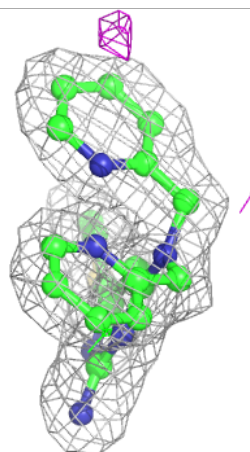
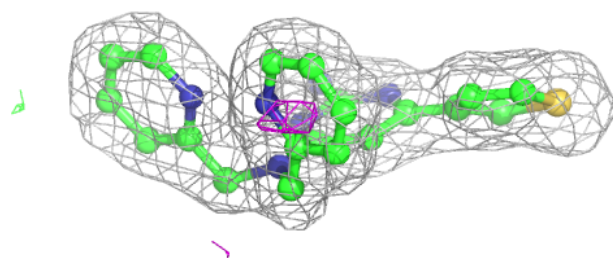
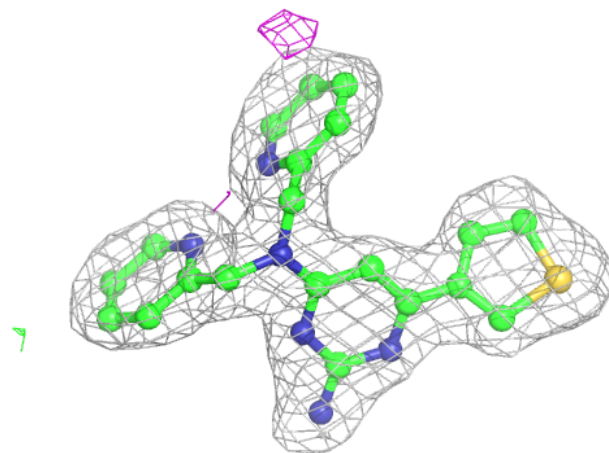
**Electron density around 6GH I 304:**

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



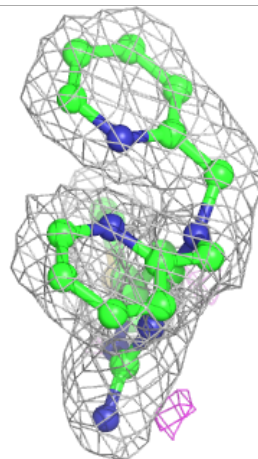
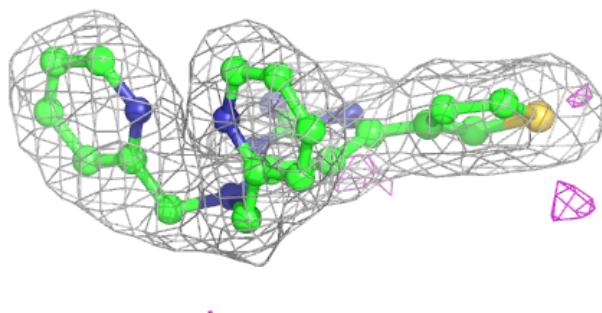
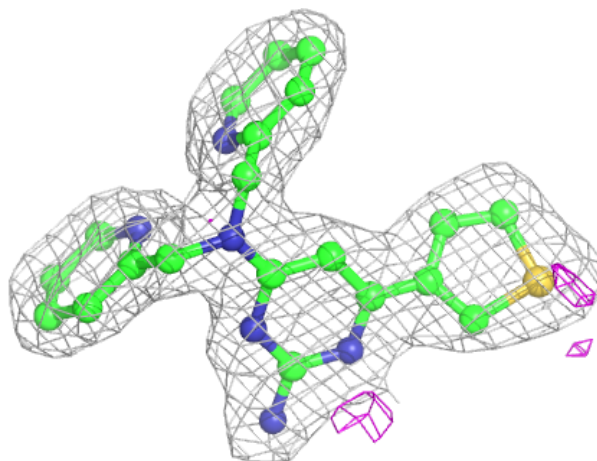
**Electron density around 6GH F 305:**

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



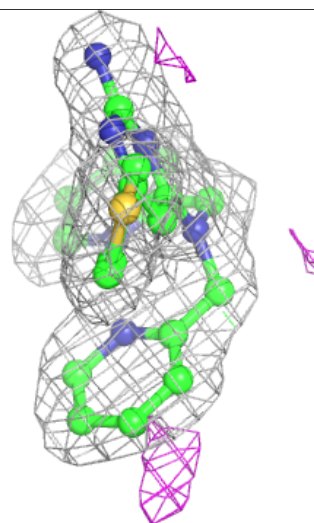
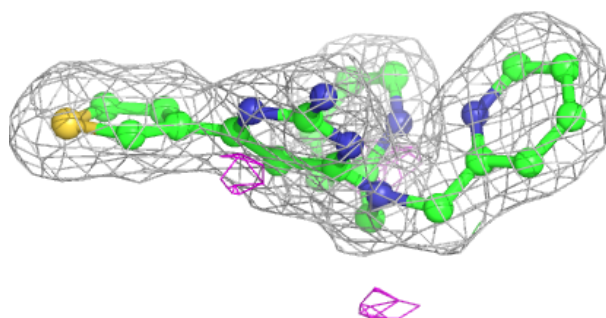
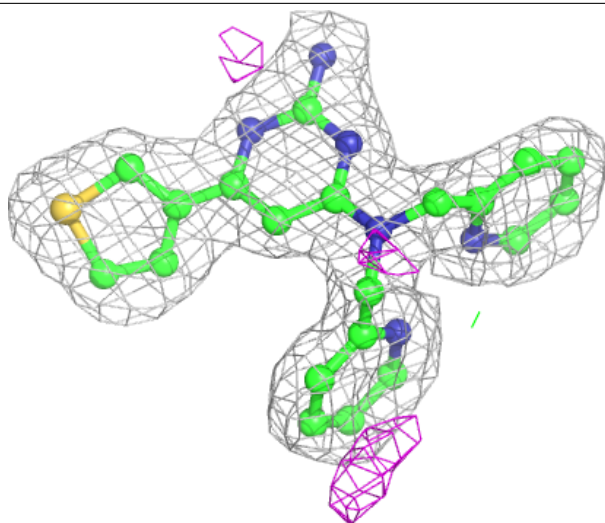
**Electron density around 6GH B 305:**

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



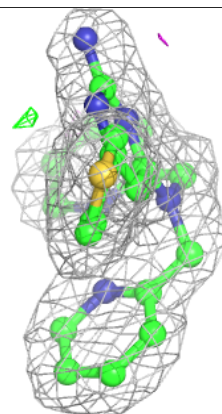
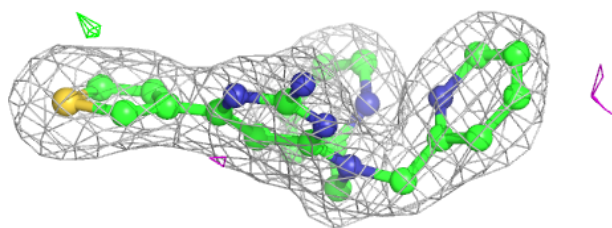
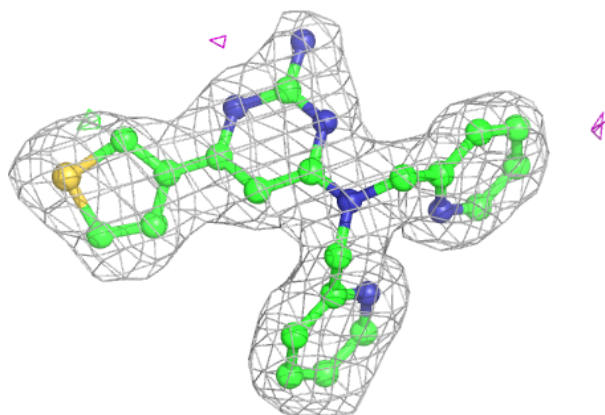
**Electron density around 6GH E 302:**

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



**Electron density around 6GH C 303:**

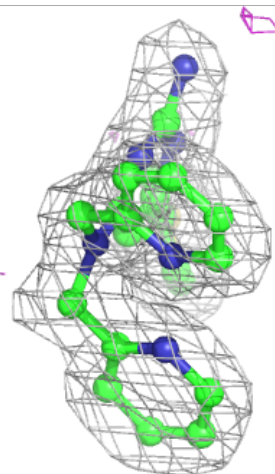
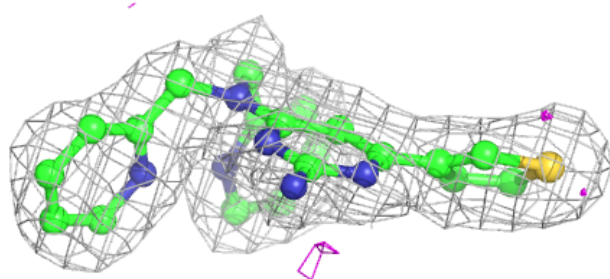
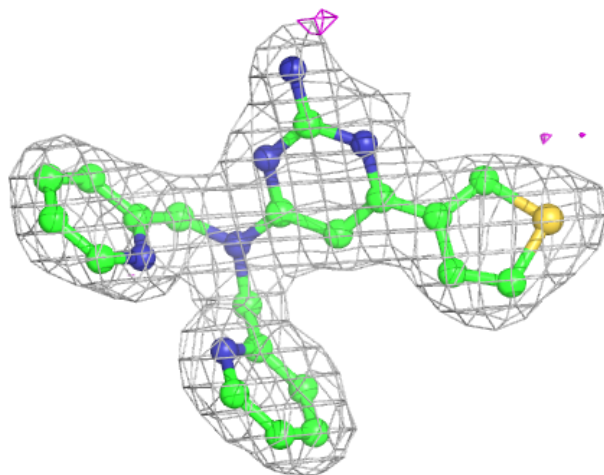
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





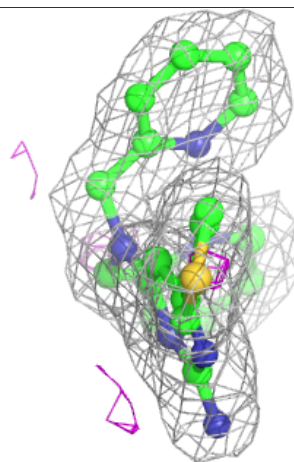
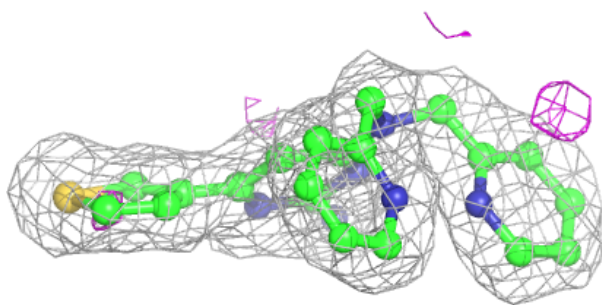
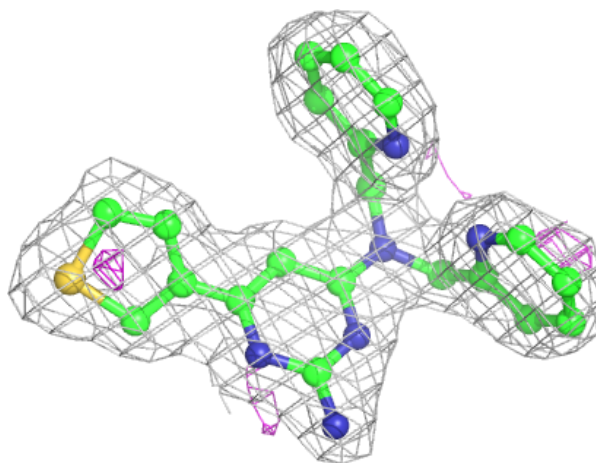
**Electron density around 6GH A 303:**

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



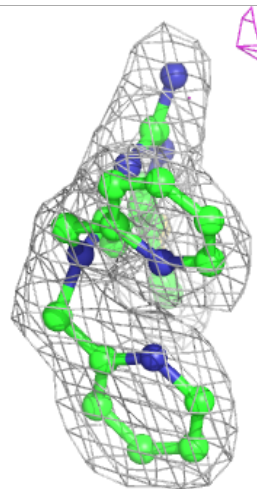
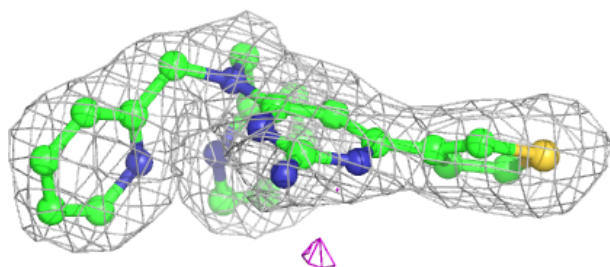
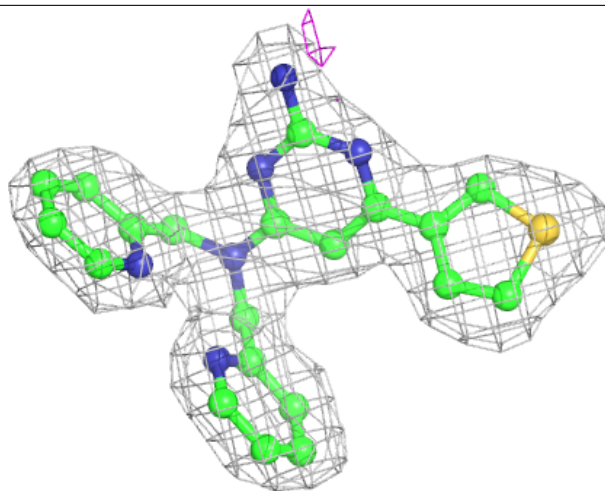
**Electron density around 6GH H 304:**

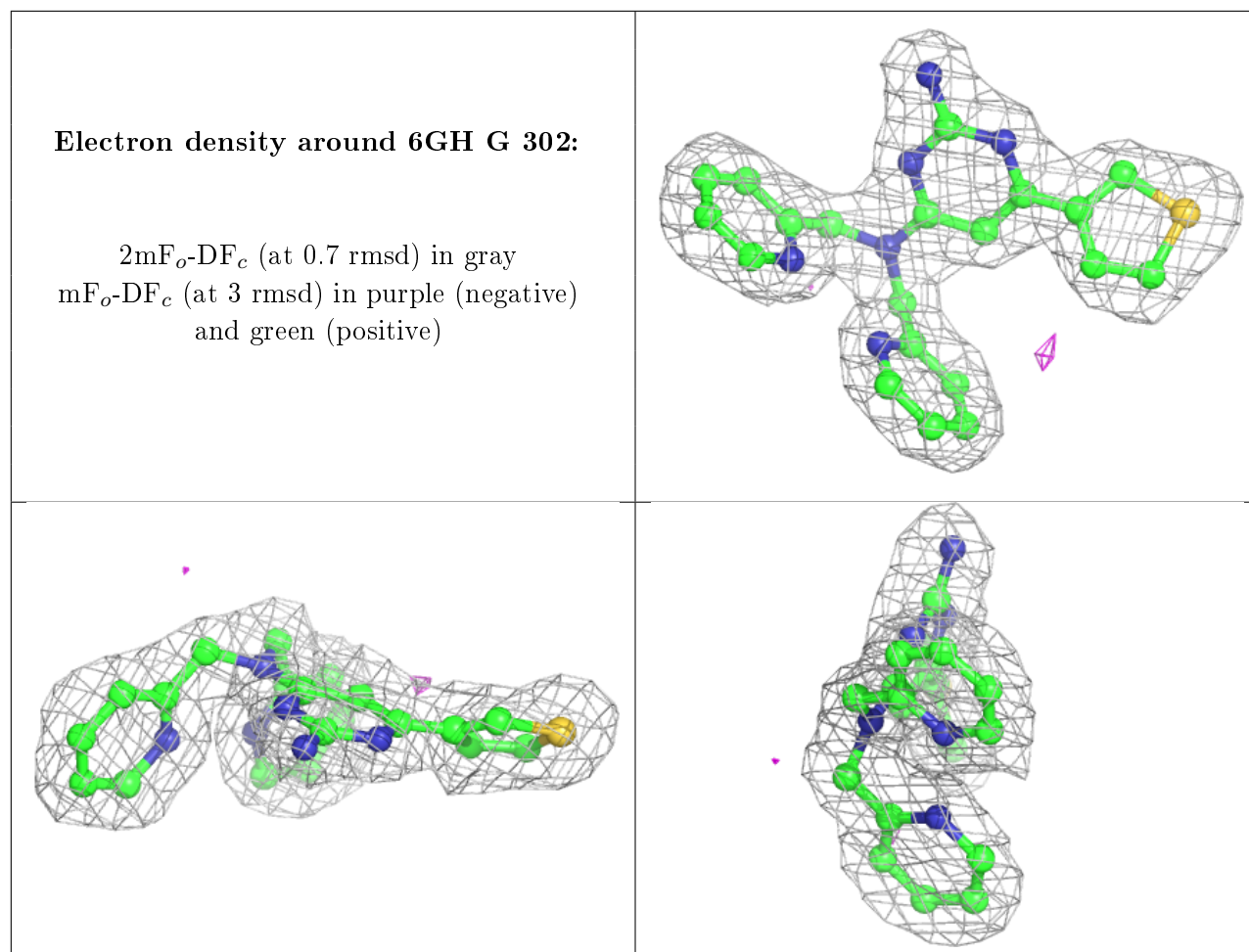
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 6GH J 302:**

$2mF_o-DF_c$  (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.