Full wwPDB X-ray Structure Validation Report ⓘ

Jun 5, 2023 – 07:03 PM EDT

PDB ID	:	7G00
Title	:	Crystal Structure of human FABP1 in complex with 2-[[3-(5-tert-butyl-1,2,4-oxadiazol-3-yl)-4,5,6,7-tetrahydro-1-benzothiophen-2-yl]carbamoyl]cyclopentene-1-carboxylic acid
Authors	:	Ehler, A.; Benz, J.; Obst, U.; Neidhart, W.; Rudolph, M.G.
Deposited on	:	2023-04-27
Resolution	:	2.60 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

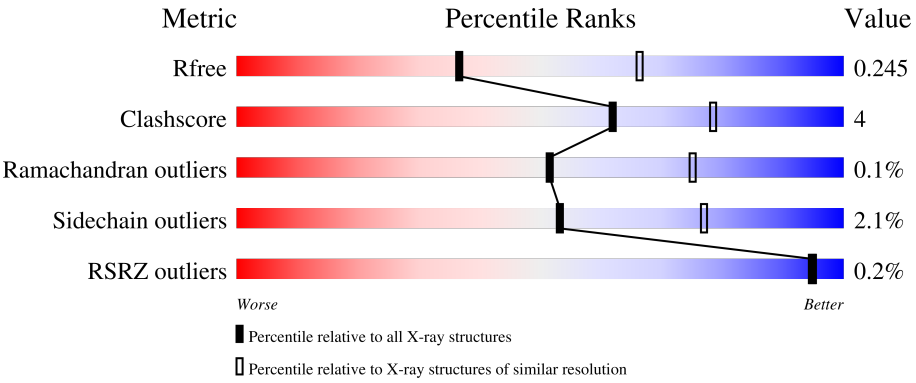
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.33
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 >=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 <=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	130	87% 11% •
1	B	130	83% 14% ••
1	C	130	92% 6% •
1	D	130	% 84% 13% ••

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Mol	Chain	Length	Quality of chain
1	E	130	
1	F	130	
1	G	130	
1	H	130	
1	I	130	
1	J	130	
1	K	130	
1	L	130	
1	M	130	
1	N	130	
1	O	130	
1	P	130	

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	SCN	E	501	-	-	-	X
3	SCN	M	501	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16781 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 Fatty acid-binding protein, liver.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	B	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	C	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	D	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	E	129	Total	C	N	O	S	0	0	0
			1011	640	168	198	5			
1	F	128	Total	C	N	O	S	0	0	0
			1005	637	167	196	5			
1	G	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	H	130	Total	C	N	O	S	0	0	0
			1015	642	169	199	5			
1	I	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	J	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	K	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	L	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	M	129	Total	C	N	O	S	0	0	0
			1011	640	168	198	5			
1	N	128	Total	C	N	O	S	0	0	0
			1005	637	167	196	5			
1	O	127	Total	C	N	O	S	0	0	0
			995	631	164	195	5			
1	P	129	Total	C	N	O	S	0	0	0
			1011	640	168	198	5			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P07148
A	-1	SER	-	expression tag	UNP P07148
A	0	HIS	-	expression tag	UNP P07148
B	-2	GLY	-	expression tag	UNP P07148
B	-1	SER	-	expression tag	UNP P07148
B	0	HIS	-	expression tag	UNP P07148
C	-2	GLY	-	expression tag	UNP P07148
C	-1	SER	-	expression tag	UNP P07148
C	0	HIS	-	expression tag	UNP P07148
D	-2	GLY	-	expression tag	UNP P07148
D	-1	SER	-	expression tag	UNP P07148
D	0	HIS	-	expression tag	UNP P07148
E	-2	GLY	-	expression tag	UNP P07148
E	-1	SER	-	expression tag	UNP P07148
E	0	HIS	-	expression tag	UNP P07148
F	-2	GLY	-	expression tag	UNP P07148
F	-1	SER	-	expression tag	UNP P07148
F	0	HIS	-	expression tag	UNP P07148
G	-2	GLY	-	expression tag	UNP P07148
G	-1	SER	-	expression tag	UNP P07148
G	0	HIS	-	expression tag	UNP P07148
H	-2	GLY	-	expression tag	UNP P07148
H	-1	SER	-	expression tag	UNP P07148
H	0	HIS	-	expression tag	UNP P07148
I	-2	GLY	-	expression tag	UNP P07148
I	-1	SER	-	expression tag	UNP P07148
I	0	HIS	-	expression tag	UNP P07148
J	-2	GLY	-	expression tag	UNP P07148
J	-1	SER	-	expression tag	UNP P07148
J	0	HIS	-	expression tag	UNP P07148
K	-2	GLY	-	expression tag	UNP P07148
K	-1	SER	-	expression tag	UNP P07148
K	0	HIS	-	expression tag	UNP P07148
L	-2	GLY	-	expression tag	UNP P07148
L	-1	SER	-	expression tag	UNP P07148
L	0	HIS	-	expression tag	UNP P07148
M	-2	GLY	-	expression tag	UNP P07148
M	-1	SER	-	expression tag	UNP P07148
M	0	HIS	-	expression tag	UNP P07148
N	-2	GLY	-	expression tag	UNP P07148
N	-1	SER	-	expression tag	UNP P07148
N	0	HIS	-	expression tag	UNP P07148

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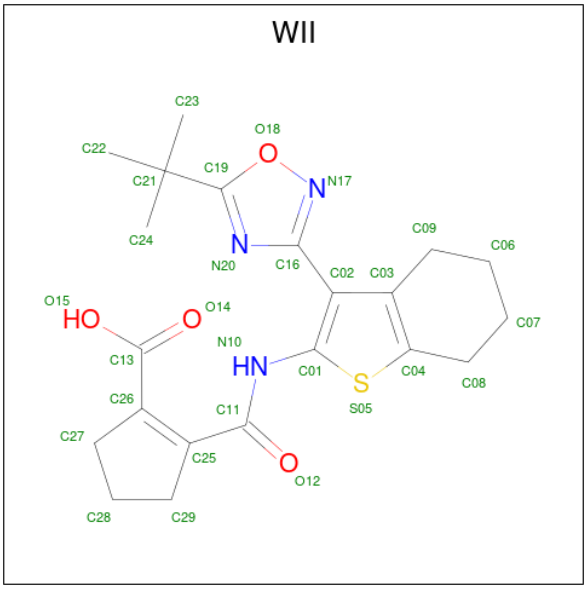
Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	GLY	-	expression tag	UNP P07148
O	-1	SER	-	expression tag	UNP P07148
O	0	HIS	-	expression tag	UNP P07148
P	-2	GLY	-	expression tag	UNP P07148
P	-1	SER	-	expression tag	UNP P07148
P	0	HIS	-	expression tag	UNP P07148

- Molecule 2 is 2-{[(3P)-3-(5-tert-butyl-1,2,4-oxadiazol-3-yl)-4,5,6,7-tetrahydro-1-benzothiophen-2-yl]carbamoyl}cyclopent-1-ene-1-carboxylic acid (three-letter code: WII) (formula: $C_{21}H_{25}N_3O_4S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	B	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	C	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	D	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	E	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	F	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	G	1	Total	C	N	O	S	0	0
			29	21	3	4	1		

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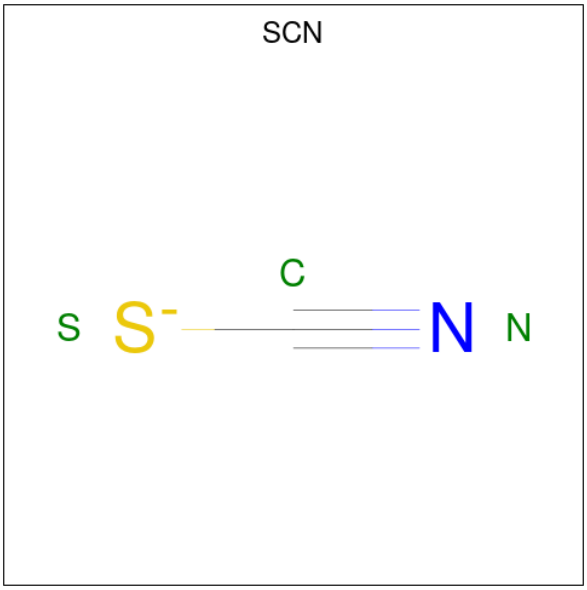
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	I	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	J	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	K	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	L	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	M	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	N	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	O	1	Total	C	N	O	S	0	0
			29	21	3	4	1		
2	P	1	Total	C	N	O	S	0	0
			29	21	3	4	1		

- Molecule 3 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	S	0	0
			3	1	1	1		
3	B	1	Total	C	N	S	0	0
			3	1	1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C N S 3 1 1 1	0	0
3	D	1	Total C N S 3 1 1 1	0	0
3	E	1	Total C N S 3 1 1 1	0	0
3	F	1	Total C N S 3 1 1 1	0	0
3	G	1	Total C N S 3 1 1 1	0	0
3	H	1	Total C N S 3 1 1 1	0	0
3	I	1	Total C N S 3 1 1 1	0	0
3	J	1	Total C N S 3 1 1 1	0	0
3	J	1	Total C N S 3 1 1 1	0	0
3	L	1	Total C N S 3 1 1 1	0	0
3	M	1	Total C N S 3 1 1 1	0	0
3	N	1	Total C N S 3 1 1 1	0	0
3	O	1	Total C N S 3 1 1 1	0	0
3	P	1	Total C N S 3 1 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	21	Total O 21 21	0	0
4	B	19	Total O 19 19	0	0
4	C	23	Total O 23 23	0	0
4	D	12	Total O 12 12	0	0
4	E	13	Total O 13 13	0	0

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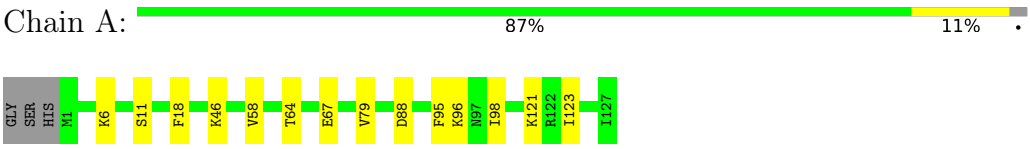
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	20	Total O 20 20	0	0
4	G	14	Total O 14 14	0	0
4	H	14	Total O 14 14	0	0
4	I	16	Total O 16 16	0	0
4	J	18	Total O 18 18	0	0
4	K	23	Total O 23 23	0	0
4	L	9	Total O 9 9	0	0
4	M	15	Total O 15 15	0	0
4	N	14	Total O 14 14	0	0
4	O	15	Total O 15 15	0	0
4	P	15	Total O 15 15	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.

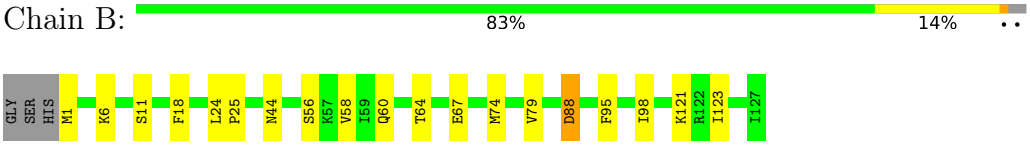
• Molecule 1: Fatty acid-binding protein, liver

Chain A:



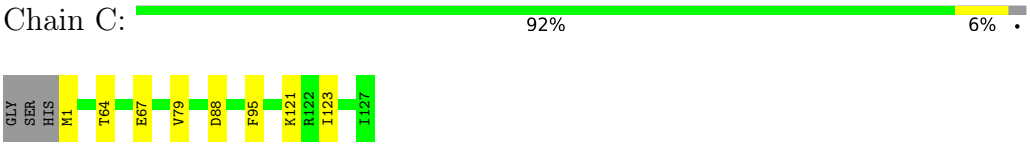
• Molecule 1: Fatty acid-binding protein, liver

Chain B:



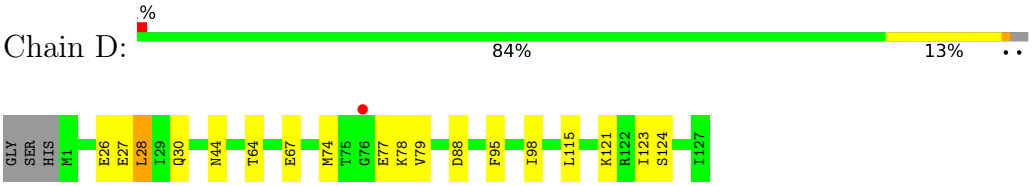
• Molecule 1: Fatty acid-binding protein, liver

Chain C:



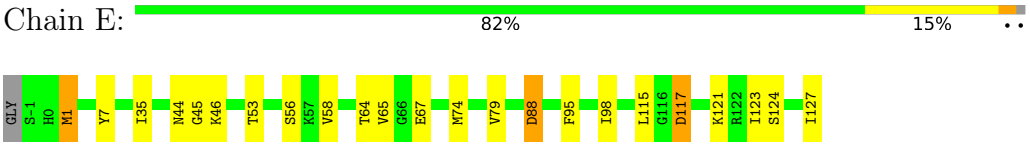
• Molecule 1: Fatty acid-binding protein, liver

Chain D:



• Molecule 1: Fatty acid-binding protein, liver

Chain E:



• Molecule 1: Fatty acid-binding protein, liver

Chain F:

• Molecule 1: Fatty acid-binding protein, liver

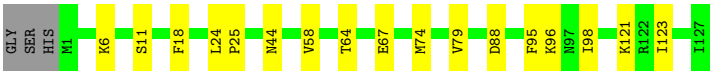
Chain G:

• Molecule 1: Fatty acid-binding protein, liver

Chain H:

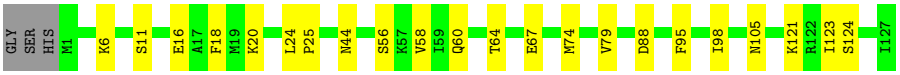
• Molecule 1: Fatty acid-binding protein, liver

Chain I:



• Molecule 1: Fatty acid-binding protein, liver

Chain J:

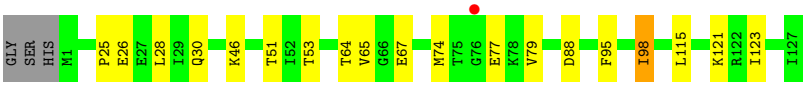


• Molecule 1: Fatty acid-binding protein, liver

Chain K:

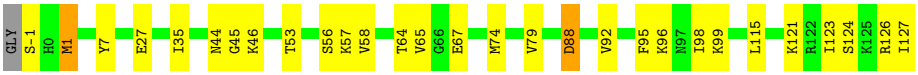
• Molecule 1: Fatty acid-binding protein, liver

Chain L:



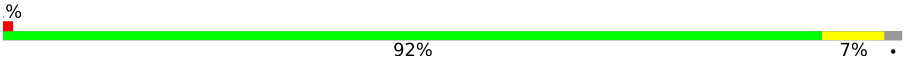
• Molecule 1: Fatty acid-binding protein, liver

Chain M:



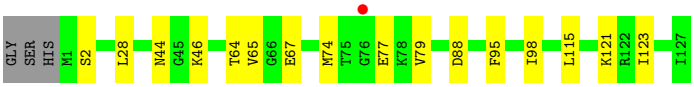
• Molecule 1: Fatty acid-binding protein, liver

Chain N:



• Molecule 1: Fatty acid-binding protein, liver

Chain O:



• Molecule 1: Fatty acid-binding protein, liver

Chain P:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	78.70Å 129.58Å 115.91Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	46.62 – 2.60 46.62 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.62-2.60) 94.3 (46.62-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 2.61Å)	Xtriage
Refinement program	PHENIX dev_989	Depositor
R, R_{free}	0.207 , 0.243 0.207 , 0.245	Depositor DCC
R_{free} test set	3585 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	51.4	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 25.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.470 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	16781	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1364e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SCN, WII

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	0.42	0/1005	0.57	0/1344
1	B	0.43	0/1005	0.57	0/1344
1	C	0.43	0/1005	0.58	0/1344
1	D	0.42	0/1005	0.58	0/1344
1	E	0.41	0/1022	0.57	0/1367
1	F	0.41	0/1016	0.56	0/1359
1	G	0.42	0/1005	0.57	0/1344
1	H	0.45	0/1026	1.05	3/1372 (0.2%)
1	I	0.43	0/1005	0.56	0/1344
1	J	0.43	0/1005	0.58	0/1344
1	K	0.43	0/1005	0.56	0/1344
1	L	0.42	0/1005	0.58	0/1344
1	M	0.44	0/1022	1.05	3/1367 (0.2%)
1	N	0.42	0/1016	0.57	0/1359
1	O	0.42	0/1005	0.58	0/1344
1	P	0.42	0/1022	0.56	0/1367
All	All	0.43	0/16174	0.65	6/21631 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	126	ARG	NE-CZ-NH1	-22.21	109.19	120.30
1	M	126	ARG	NE-CZ-NH1	-22.20	109.20	120.30
1	H	126	ARG	NE-CZ-NH2	22.18	131.39	120.30
1	M	126	ARG	NE-CZ-NH2	21.96	131.28	120.30
1	H	126	ARG	CD-NE-CZ	9.81	137.33	123.60
1	M	126	ARG	CD-NE-CZ	9.80	137.31	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	995	0	1028	10	0
1	B	995	0	1028	13	0
1	C	995	0	1028	3	0
1	D	995	0	1028	11	0
1	E	1011	0	1040	18	0
1	F	1005	0	1035	6	0
1	G	995	0	1028	12	0
1	H	1015	0	1043	13	0
1	I	995	0	1028	11	0
1	J	995	0	1028	16	0
1	K	995	0	1028	8	0
1	L	995	0	1028	11	0
1	M	1011	0	1040	19	0
1	N	1005	0	1035	5	0
1	O	995	0	1028	9	0
1	P	1011	0	1040	11	0
2	A	29	0	0	0	0
2	B	29	0	0	1	0
2	C	29	0	0	0	0
2	D	29	0	0	2	0
2	E	29	0	0	1	0
2	F	29	0	0	1	0
2	G	29	0	0	1	0
2	H	29	0	0	1	0
2	I	29	0	0	1	0
2	J	29	0	0	2	0
2	K	29	0	0	0	0
2	L	29	0	0	1	0
2	M	29	0	0	1	0
2	N	29	0	0	1	0
2	O	29	0	0	1	0
2	P	29	0	0	1	0
3	A	3	0	0	0	0
3	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
3	I	3	0	0	0	0
3	J	6	0	0	0	0
3	L	3	0	0	0	0
3	M	3	0	0	0	0
3	N	3	0	0	0	0
3	O	3	0	0	0	0
3	P	3	0	0	0	0
4	A	21	0	0	0	0
4	B	19	0	0	0	0
4	C	23	0	0	0	0
4	D	12	0	0	2	0
4	E	13	0	0	0	0
4	F	20	0	0	0	0
4	G	14	0	0	0	0
4	H	14	0	0	0	0
4	I	16	0	0	0	0
4	J	18	0	0	0	0
4	K	23	0	0	0	0
4	L	9	0	0	1	0
4	M	15	0	0	1	0
4	N	14	0	0	0	0
4	O	15	0	0	0	0
4	P	15	0	0	0	0
All	All	16781	0	16513	145	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 4.

All (145) 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:L:51:THR:OG1	4:L:601:HOH:O	2.01	0.78
1:J:58:VAL:HG21	1:M:53:THR:HG23	1.70	0.73
1:B:58:VAL:HG21	1:E:53:THR:HG23	1.72	0.72
1:P:98:ILE:HD13	1:P:115:LEU:HD13	1.77	0.66
1:I:6:LYS:HD2	1:P:127:ILE:HD12	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:53:THR:HG23	1:K:58:VAL:HG21	1.76	0.66
1:A:6:LYS:HD2	1:H:127:ILE:HD12	1.78	0.64
1:I:58:VAL:HG21	1:P:53:THR:HG23	1.81	0.63
1:H:79:VAL:HG21	1:H:95:PHE:HB2	1.81	0.62
1:E:79:VAL:HG21	1:E:95:PHE:HB2	1.82	0.62
1:M:79:VAL:HG21	1:M:95:PHE:HB2	1.82	0.62
1:P:79:VAL:HG21	1:P:95:PHE:HB2	1.82	0.61
1:I:79:VAL:HG21	1:I:95:PHE:HB2	1.84	0.60
1:A:58:VAL:HG21	1:H:53:THR:HG23	1.82	0.59
1:O:98:ILE:HD13	1:O:115:LEU:HB2	1.84	0.59
1:D:28:LEU:HD13	4:D:610:HOH:O	2.03	0.59
1:D:79:VAL:HG21	1:D:95:PHE:HB2	1.85	0.59
1:C:79:VAL:HG21	1:C:95:PHE:HB2	1.85	0.59
1:H:46:LYS:HB3	1:H:65:VAL:HG22	1.85	0.59
1:A:79:VAL:HG21	1:A:95:PHE:HB2	1.84	0.58
1:B:79:VAL:HG21	1:B:95:PHE:HB2	1.85	0.58
1:L:79:VAL:HG21	1:L:95:PHE:HB2	1.84	0.58
1:D:98:ILE:HG12	1:D:115:LEU:HD13	1.84	0.58
1:K:79:VAL:HG21	1:K:95:PHE:HB2	1.85	0.58
1:N:79:VAL:HG21	1:N:95:PHE:HB2	1.86	0.58
1:F:79:VAL:HG21	1:F:95:PHE:HB2	1.86	0.58
1:J:79:VAL:HG21	1:J:95:PHE:HB2	1.85	0.57
1:G:127:ILE:HD12	1:K:6:LYS:HD2	1.85	0.56
1:O:79:VAL:HG21	1:O:95:PHE:HB2	1.88	0.56
1:M:74:MET:HG2	2:M:500:WII:C07	2.35	0.56
1:G:98:ILE:HD13	1:G:115:LEU:HB2	1.88	0.56
1:M:1:MET:HG2	1:M:88:ASP:O	2.06	0.55
1:P:46:LYS:HB3	1:P:65:VAL:HG22	1.87	0.55
1:G:79:VAL:HG21	1:G:95:PHE:HB2	1.87	0.55
1:A:121:LYS:HE2	1:A:123:ILE:HD11	1.89	0.55
1:M:98:ILE:HD13	1:M:115:LEU:HD13	1.90	0.54
1:E:44:ASN:O	1:G:44:ASN:HB3	2.08	0.54
1:P:74:MET:HG2	2:P:500:WII:C07	2.38	0.54
1:E:74:MET:HG2	2:E:500:WII:C07	2.38	0.53
1:B:121:LYS:HE2	1:B:123:ILE:HD11	1.90	0.53
1:P:1:MET:HB3	1:P:88:ASP:OD2	2.08	0.53
1:B:6:LYS:HD2	1:E:127:ILE:HD12	1.90	0.53
1:D:26:GLU:OE2	1:D:30:GLN:NE2	2.37	0.53
1:E:1:MET:HG2	1:E:88:ASP:O	2.08	0.52
1:L:121:LYS:HE2	1:L:123:ILE:HD11	1.92	0.52
1:H:74:MET:HG2	2:H:500:WII:C07	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:121:LYS:HE2	1:J:123:ILE:HD11	1.92	0.52
1:J:16:GLU:O	1:J:20:LYS:HG3	2.10	0.52
1:O:74:MET:HG2	2:O:500:WII:C07	2.40	0.52
1:I:74:MET:HG2	2:I:500:WII:C07	2.40	0.51
1:D:121:LYS:HE2	1:D:123:ILE:HD11	1.92	0.51
1:G:121:LYS:HE2	1:G:123:ILE:HD11	1.93	0.51
1:J:6:LYS:HD2	1:M:127:ILE:HD12	1.93	0.51
1:D:124:SER:OG	2:D:500:WII:O15	2.22	0.50
1:I:18:PHE:HZ	1:I:98:ILE:HD13	1.76	0.50
1:H:121:LYS:HE2	1:H:123:ILE:HD11	1.93	0.49
1:D:74:MET:HG2	2:D:500:WII:C07	2.42	0.49
1:F:74:MET:HG2	2:F:502:WII:C07	2.42	0.49
1:I:121:LYS:HE2	1:I:123:ILE:HD11	1.94	0.49
1:L:74:MET:HG2	2:L:500:WII:C07	2.42	0.49
1:H:1:MET:HB2	1:H:88:ASP:OD2	2.12	0.49
1:J:11:SER:OG	1:L:77:GLU:HG3	2.13	0.49
1:E:98:ILE:HD13	1:E:115:LEU:HB2	1.95	0.49
1:H:25:PRO:O	1:H:29:ILE:HG13	2.13	0.48
1:J:18:PHE:HZ	1:J:98:ILE:HD13	1.78	0.48
1:E:117:ASP:OD1	1:E:117:ASP:N	2.43	0.48
1:H:98:ILE:HD13	1:H:115:LEU:HD13	1.95	0.48
1:G:74:MET:HG2	2:G:500:WII:C07	2.44	0.48
1:E:121:LYS:HE2	1:E:123:ILE:HD11	1.96	0.48
1:K:121:LYS:HE2	1:K:123:ILE:HD11	1.95	0.48
1:N:64:THR:HB	1:N:67:GLU:HG3	1.95	0.47
1:P:121:LYS:HE2	1:P:123:ILE:HD11	1.96	0.47
1:J:56:SER:HA	1:M:58:VAL:HB	1.96	0.47
1:K:18:PHE:HZ	1:K:98:ILE:HD13	1.79	0.47
1:B:11:SER:OG	1:D:77:GLU:HG3	2.14	0.47
1:F:64:THR:HB	1:F:67:GLU:HG3	1.96	0.47
1:O:121:LYS:HE2	1:O:123:ILE:HD11	1.97	0.47
1:A:18:PHE:HZ	1:A:98:ILE:HD13	1.79	0.47
1:M:57:LYS:NZ	4:M:601:HOH:O	2.45	0.47
1:E:44:ASN:HB3	1:G:44:ASN:O	2.16	0.46
1:I:11:SER:OG	1:O:77:GLU:HG3	2.16	0.46
1:P:64:THR:HB	1:P:67:GLU:HG3	1.98	0.46
1:A:58:VAL:HB	1:H:56:SER:HA	1.98	0.45
1:B:74:MET:HG2	2:B:201:WII:C07	2.46	0.45
1:C:64:THR:HB	1:C:67:GLU:HG3	1.98	0.45
1:F:58:VAL:HG21	1:L:53:THR:HG23	1.99	0.45
1:K:64:THR:HB	1:K:67:GLU:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:SER:OG	1:G:77:GLU:HG3	2.17	0.45
1:B:56:SER:HA	1:E:58:VAL:HB	1.97	0.45
1:D:64:THR:HB	1:D:67:GLU:HG3	1.98	0.45
1:J:74:MET:HG2	2:J:201:WII:C07	2.46	0.45
1:L:26:GLU:OE2	1:L:30:GLN:NE2	2.37	0.45
1:J:24:LEU:HG	1:J:25:PRO:HD2	1.99	0.45
1:M:121:LYS:HE2	1:M:123:ILE:HD11	1.99	0.45
1:J:24:LEU:HA	1:J:25:PRO:HD3	1.85	0.44
1:M:98:ILE:HD13	1:M:115:LEU:HB2	1.98	0.44
1:M:64:THR:HB	1:M:67:GLU:HG3	1.99	0.44
1:L:64:THR:HB	1:L:67:GLU:HG3	1.98	0.44
1:A:64:THR:HB	1:A:67:GLU:HG3	2.00	0.44
1:M:44:ASN:HB3	1:O:44:ASN:O	2.18	0.44
1:B:24:LEU:HA	1:B:25:PRO:HD3	1.85	0.44
1:C:121:LYS:HE2	1:C:123:ILE:HD11	1.98	0.44
1:F:121:LYS:HE2	1:F:123:ILE:HD11	1.99	0.44
1:J:124:SER:OG	2:J:201:WII:O15	2.27	0.44
1:N:74:MET:HG2	2:N:502:WII:C07	2.48	0.44
1:I:58:VAL:HB	1:P:56:SER:HA	2.00	0.43
1:B:58:VAL:HB	1:E:56:SER:HA	2.00	0.43
1:M:92:VAL:HG13	1:M:99:LYS:HE3	1.99	0.43
1:H:98:ILE:HD13	1:H:115:LEU:HB2	2.01	0.43
1:I:24:LEU:HA	1:I:25:PRO:HD3	1.86	0.43
1:A:46:LYS:O	1:A:64:THR:HA	2.18	0.43
1:B:18:PHE:HZ	1:B:98:ILE:HD13	1.83	0.43
1:I:64:THR:HB	1:I:67:GLU:HG3	2.01	0.43
1:E:1:MET:HB3	1:E:88:ASP:OD2	2.19	0.43
1:H:64:THR:HB	1:H:67:GLU:HG3	2.00	0.43
1:E:64:THR:HB	1:E:67:GLU:HG3	2.00	0.42
1:N:121:LYS:HE2	1:N:123:ILE:HD11	2.00	0.42
1:B:60:GLN:OE1	1:E:35:ILE:HG12	2.19	0.42
1:I:96:LYS:HE2	1:I:96:LYS:HB3	1.88	0.42
1:J:60:GLN:OE1	1:M:35:ILE:HG12	2.18	0.42
1:L:98:ILE:HD13	1:L:115:LEU:HB2	2.02	0.42
1:M:46:LYS:HB3	1:M:65:VAL:HG22	2.00	0.42
1:O:46:LYS:HB3	1:O:65:VAL:HG22	2.00	0.42
1:D:78:LYS:NZ	4:D:601:HOH:O	2.37	0.42
1:G:58:VAL:HB	1:K:56:SER:HA	2.02	0.42
1:G:64:THR:HB	1:G:67:GLU:HG3	2.00	0.42
1:E:46:LYS:HB3	1:E:65:VAL:HG22	2.01	0.42
1:G:25:PRO:O	1:G:29:ILE:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:7:TYR:HB3	1:M:124:SER:HB3	2.02	0.42
1:O:64:THR:HB	1:O:67:GLU:HG3	2.01	0.42
1:M:96:LYS:HB3	1:M:96:LYS:HE2	1.87	0.42
1:K:96:LYS:HB3	1:K:96:LYS:HE2	1.85	0.41
1:P:96:LYS:HE2	1:P:96:LYS:HB3	1.87	0.41
1:A:96:LYS:HA	1:F:96:LYS:HD2	2.03	0.41
1:B:64:THR:HB	1:B:67:GLU:HG3	2.03	0.41
1:J:64:THR:HB	1:J:67:GLU:HG3	2.03	0.41
1:L:46:LYS:HB3	1:L:65:VAL:HG22	2.03	0.41
1:M:44:ASN:O	1:O:44:ASN:HB3	2.20	0.41
1:E:44:ASN:O	1:E:46:LYS:N	2.54	0.41
1:N:96:LYS:HB3	1:N:96:LYS:HE2	1.87	0.41
1:E:7:TYR:HB3	1:E:124:SER:HB3	2.03	0.41
1:J:105:ASN:C	1:L:25:PRO:HG3	2.40	0.41
1:B:1:MET:N	1:B:88:ASP:OD2	2.54	0.40
1:D:44:ASN:HB3	1:H:44:ASN:O	2.21	0.40
1:J:58:VAL:HB	1:M:56:SER:HA	2.02	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	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
1	B	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
1	C	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
1	D	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
1	E	127/130 (98%)	123 (97%)	3 (2%)	1 (1%)	19	39
1	F	126/130 (97%)	124 (98%)	2 (2%)	0	100	100
1	G	125/130 (96%)	122 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	H	128/130 (98%)	125 (98%)	3 (2%)	0	100 100
1	I	125/130 (96%)	122 (98%)	3 (2%)	0	100 100
1	J	125/130 (96%)	122 (98%)	3 (2%)	0	100 100
1	K	125/130 (96%)	122 (98%)	3 (2%)	0	100 100
1	L	125/130 (96%)	122 (98%)	3 (2%)	0	100 100
1	M	127/130 (98%)	123 (97%)	3 (2%)	1 (1%)	19 39
1	N	126/130 (97%)	124 (98%)	2 (2%)	0	100 100
1	O	125/130 (96%)	122 (98%)	3 (2%)	0	100 100
1	P	127/130 (98%)	124 (98%)	3 (2%)	0	100 100
All	All	2011/2080 (97%)	1962 (98%)	47 (2%)	2 (0%)	51 75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	45	GLY
1	M	45	GLY

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	113/115 (98%)	112 (99%)	1 (1%)	78 91
1	B	113/115 (98%)	111 (98%)	2 (2%)	59 80
1	C	113/115 (98%)	111 (98%)	2 (2%)	59 80
1	D	113/115 (98%)	110 (97%)	3 (3%)	44 71
1	E	115/115 (100%)	112 (97%)	3 (3%)	46 72
1	F	114/115 (99%)	113 (99%)	1 (1%)	78 91
1	G	113/115 (98%)	110 (97%)	3 (3%)	44 71
1	H	115/115 (100%)	112 (97%)	3 (3%)	46 72
1	I	113/115 (98%)	111 (98%)	2 (2%)	59 80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	113/115 (98%)	111 (98%)	2 (2%)	59 80
1	K	113/115 (98%)	111 (98%)	2 (2%)	59 80
1	L	113/115 (98%)	110 (97%)	3 (3%)	44 71
1	M	115/115 (100%)	111 (96%)	4 (4%)	36 62
1	N	114/115 (99%)	113 (99%)	1 (1%)	78 91
1	O	113/115 (98%)	110 (97%)	3 (3%)	44 71
1	P	115/115 (100%)	112 (97%)	3 (3%)	46 72
All	All	1818/1840 (99%)	1780 (98%)	38 (2%)	53 77

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ASP
1	B	44	ASN
1	B	88	ASP
1	C	1	MET
1	C	88	ASP
1	D	27	GLU
1	D	28	LEU
1	D	88	ASP
1	E	1	MET
1	E	88	ASP
1	E	117	ASP
1	F	88	ASP
1	G	27	GLU
1	G	28	LEU
1	G	88	ASP
1	H	-1	SER
1	H	1	MET
1	H	88	ASP
1	I	44	ASN
1	I	88	ASP
1	J	44	ASN
1	J	88	ASP
1	K	1	MET
1	K	88	ASP
1	L	28	LEU
1	L	88	ASP
1	L	98	ILE
1	M	-1	SER

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Mol	Chain	Res	Type
1	M	1	MET
1	M	27	GLU
1	M	88	ASP
1	N	88	ASP
1	O	2	SER
1	O	28	LEU
1	O	88	ASP
1	P	0	HIS
1	P	1	MET
1	P	88	ASP

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

32 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	$\#\|Z\| > 2$
3	SCN	E	501	-	1,2,2	1.16	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	WII	E	500	-	26,32,32	3.53	12 (46%)	27,48,48	2.00	5 (18%)
2	WII	F	502	-	26,32,32	3.64	12 (46%)	27,48,48	2.03	6 (22%)
2	WII	H	500	-	26,32,32	3.64	12 (46%)	27,48,48	2.26	5 (18%)
2	WII	A	500	-	26,32,32	3.63	10 (38%)	27,48,48	2.25	6 (22%)
3	SCN	L	501	-	1,2,2	1.02	0	0,1,1	-	-
3	SCN	J	202	-	1,2,2	1.03	0	0,1,1	-	-
3	SCN	P	501	-	1,2,2	1.08	0	0,1,1	-	-
2	WII	M	500	-	26,32,32	3.63	11 (42%)	27,48,48	2.09	6 (22%)
2	WII	K	500	-	26,32,32	3.63	10 (38%)	27,48,48	2.13	6 (22%)
3	SCN	D	501	-	1,2,2	1.13	0	0,1,1	-	-
2	WII	O	500	-	26,32,32	3.75	12 (46%)	27,48,48	2.23	6 (22%)
3	SCN	F	501	-	1,2,2	0.83	0	0,1,1	-	-
3	SCN	I	501	-	1,2,2	0.90	0	0,1,1	-	-
2	WII	L	500	-	26,32,32	3.66	11 (42%)	27,48,48	2.19	8 (29%)
3	SCN	B	202	-	1,2,2	0.97	0	0,1,1	-	-
3	SCN	J	203	-	1,2,2	0.92	0	0,1,1	-	-
2	WII	P	500	-	26,32,32	3.68	12 (46%)	27,48,48	2.10	4 (14%)
2	WII	I	500	-	26,32,32	3.63	10 (38%)	27,48,48	2.36	7 (25%)
3	SCN	N	501	-	1,2,2	0.86	0	0,1,1	-	-
3	SCN	O	501	-	1,2,2	1.31	0	0,1,1	-	-
2	WII	N	502	-	26,32,32	3.64	12 (46%)	27,48,48	2.09	5 (18%)
3	SCN	H	501	-	1,2,2	1.07	0	0,1,1	-	-
2	WII	B	201	-	26,32,32	3.42	13 (50%)	27,48,48	2.03	5 (18%)
2	WII	J	201	-	26,32,32	3.40	13 (50%)	27,48,48	2.28	5 (18%)
3	SCN	G	501	-	1,2,2	1.34	0	0,1,1	-	-
2	WII	D	500	-	26,32,32	3.67	12 (46%)	27,48,48	2.03	6 (22%)
3	SCN	A	501	-	1,2,2	0.93	0	0,1,1	-	-
3	SCN	B	203	-	1,2,2	0.96	0	0,1,1	-	-
2	WII	C	500	-	26,32,32	3.70	12 (46%)	27,48,48	2.14	4 (14%)
2	WII	G	500	-	26,32,32	3.70	12 (46%)	27,48,48	2.03	4 (14%)
3	SCN	M	501	-	1,2,2	1.18	0	0,1,1	-	-

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	WII	E	500	-	-	4/13/39/39	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	WII	F	502	-	-	4/13/39/39	0/4/4/4
2	WII	L	500	-	-	4/13/39/39	0/4/4/4
2	WII	H	500	-	-	4/13/39/39	0/4/4/4
2	WII	O	500	-	-	4/13/39/39	0/4/4/4
2	WII	G	500	-	-	4/13/39/39	0/4/4/4
2	WII	A	500	-	-	4/13/39/39	0/4/4/4
2	WII	N	502	-	-	4/13/39/39	0/4/4/4
2	WII	C	500	-	-	4/13/39/39	0/4/4/4
2	WII	P	500	-	-	4/13/39/39	0/4/4/4
2	WII	J	201	-	-	4/13/39/39	0/4/4/4
2	WII	K	500	-	-	4/13/39/39	0/4/4/4
2	WII	B	201	-	-	4/13/39/39	0/4/4/4
2	WII	I	500	-	-	4/13/39/39	0/4/4/4
2	WII	M	500	-	-	4/13/39/39	0/4/4/4
2	WII	D	500	-	-	4/13/39/39	0/4/4/4

All (186) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	WII	C04-S05	-10.06	1.55	1.74
2	P	500	WII	C04-S05	-9.96	1.55	1.74
2	G	500	WII	C04-S05	-9.94	1.55	1.74
2	O	500	WII	C04-S05	-9.92	1.55	1.74
2	K	500	WII	C04-S05	-9.64	1.56	1.74
2	N	502	WII	C04-S05	-9.55	1.56	1.74
2	I	500	WII	C04-S05	-9.50	1.56	1.74
2	D	500	WII	C04-S05	-9.48	1.56	1.74
2	A	500	WII	C04-S05	-9.48	1.56	1.74
2	F	502	WII	C04-S05	-9.45	1.56	1.74
2	B	201	WII	C04-S05	-9.43	1.56	1.74
2	M	500	WII	C04-S05	-9.41	1.56	1.74
2	J	201	WII	C04-S05	-9.39	1.56	1.74
2	H	500	WII	C04-S05	-9.36	1.56	1.74
2	L	500	WII	C04-S05	-9.28	1.56	1.74
2	E	500	WII	C04-S05	-8.93	1.57	1.74
2	D	500	WII	C01-S05	-8.56	1.59	1.72
2	F	502	WII	C01-S05	-8.31	1.59	1.72
2	M	500	WII	C01-S05	-8.23	1.59	1.72
2	O	500	WII	C02-C03	8.04	1.59	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	500	WII	C01-S05	-8.00	1.60	1.72
2	A	500	WII	C01-S05	-8.00	1.60	1.72
2	C	500	WII	C02-C03	7.96	1.58	1.41
2	G	500	WII	C02-C03	7.86	1.58	1.41
2	N	502	WII	C01-S05	-7.83	1.60	1.72
2	G	500	WII	C01-S05	-7.79	1.60	1.72
2	K	500	WII	C02-C03	7.75	1.58	1.41
2	H	500	WII	C02-C03	7.74	1.58	1.41
2	I	500	WII	C01-S05	-7.73	1.60	1.72
2	P	500	WII	C02-C03	7.69	1.58	1.41
2	K	500	WII	C01-S05	-7.68	1.60	1.72
2	O	500	WII	C01-S05	-7.64	1.60	1.72
2	L	500	WII	C02-C03	7.63	1.58	1.41
2	N	502	WII	C02-C03	7.58	1.58	1.41
2	I	500	WII	C02-C03	7.58	1.58	1.41
2	A	500	WII	C02-C03	7.57	1.58	1.41
2	E	500	WII	C01-S05	-7.51	1.60	1.72
2	H	500	WII	C01-S05	-7.42	1.60	1.72
2	B	201	WII	C01-S05	-7.40	1.60	1.72
2	E	500	WII	C02-C03	7.39	1.57	1.41
2	M	500	WII	C02-C03	7.36	1.57	1.41
2	C	500	WII	C01-S05	-7.30	1.61	1.72
2	J	201	WII	C02-C03	7.23	1.57	1.41
2	F	502	WII	C02-C03	7.20	1.57	1.41
2	D	500	WII	C02-C03	7.19	1.57	1.41
2	B	201	WII	C02-C03	7.16	1.57	1.41
2	P	500	WII	C01-S05	-7.15	1.61	1.72
2	J	201	WII	C01-S05	-7.10	1.61	1.72
2	L	500	WII	C08-C04	6.01	1.55	1.50
2	O	500	WII	C08-C04	6.00	1.55	1.50
2	A	500	WII	C08-C04	5.96	1.55	1.50
2	I	500	WII	C08-C04	5.86	1.55	1.50
2	D	500	WII	C08-C04	5.85	1.55	1.50
2	M	500	WII	C08-C04	5.66	1.54	1.50
2	P	500	WII	C08-C04	5.59	1.54	1.50
2	C	500	WII	C08-C04	5.59	1.54	1.50
2	E	500	WII	C08-C04	5.39	1.54	1.50
2	G	500	WII	C08-C04	5.37	1.54	1.50
2	H	500	WII	C08-C04	5.33	1.54	1.50
2	N	502	WII	C08-C04	5.16	1.54	1.50
2	K	500	WII	C08-C04	4.96	1.54	1.50
2	F	502	WII	C08-C04	4.93	1.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	502	WII	O14-C13	4.86	1.35	1.22
2	K	500	WII	O14-C13	4.79	1.35	1.22
2	F	502	WII	O14-C13	4.79	1.35	1.22
2	H	500	WII	O14-C13	4.70	1.35	1.22
2	C	500	WII	O14-C13	4.64	1.35	1.22
2	P	500	WII	O14-C13	4.63	1.34	1.22
2	E	500	WII	O14-C13	4.62	1.34	1.22
2	I	500	WII	O14-C13	4.58	1.34	1.22
2	G	500	WII	O14-C13	4.54	1.34	1.22
2	A	500	WII	O14-C13	4.54	1.34	1.22
2	D	500	WII	O14-C13	4.47	1.34	1.22
2	B	201	WII	O14-C13	4.47	1.34	1.22
2	O	500	WII	O14-C13	4.43	1.34	1.22
2	J	201	WII	O14-C13	4.43	1.34	1.22
2	M	500	WII	O14-C13	4.40	1.34	1.22
2	L	500	WII	O14-C13	4.40	1.34	1.22
2	H	500	WII	C02-C01	4.38	1.50	1.41
2	E	500	WII	C09-C03	4.18	1.58	1.51
2	F	502	WII	C02-C01	4.15	1.50	1.41
2	P	500	WII	C09-C03	4.14	1.58	1.51
2	J	201	WII	C02-C01	4.10	1.50	1.41
2	P	500	WII	C02-C01	4.08	1.50	1.41
2	H	500	WII	C09-C03	4.01	1.58	1.51
2	C	500	WII	C02-C01	3.95	1.49	1.41
2	K	500	WII	C02-C01	3.91	1.49	1.41
2	N	502	WII	C02-C01	3.91	1.49	1.41
2	L	500	WII	C02-C01	3.89	1.49	1.41
2	G	500	WII	C09-C03	3.87	1.57	1.51
2	I	500	WII	C02-C01	3.84	1.49	1.41
2	O	500	WII	C09-C03	3.84	1.57	1.51
2	O	500	WII	C02-C01	3.84	1.49	1.41
2	A	500	WII	C02-C01	3.83	1.49	1.41
2	I	500	WII	C09-C03	3.83	1.57	1.51
2	M	500	WII	C09-C03	3.80	1.57	1.51
2	M	500	WII	C02-C01	3.78	1.49	1.41
2	B	201	WII	C02-C01	3.77	1.49	1.41
2	G	500	WII	C02-C01	3.75	1.49	1.41
2	A	500	WII	C09-C03	3.74	1.57	1.51
2	K	500	WII	C09-C03	3.65	1.57	1.51
2	B	201	WII	C09-C03	3.65	1.57	1.51
2	N	502	WII	C09-C03	3.65	1.57	1.51
2	E	500	WII	C02-C01	3.63	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	WII	C02-C01	3.62	1.49	1.41
2	F	502	WII	C09-C03	3.61	1.57	1.51
2	C	500	WII	C09-C03	3.61	1.57	1.51
2	L	500	WII	C09-C03	3.57	1.57	1.51
2	D	500	WII	C09-C03	3.53	1.57	1.51
2	J	201	WII	C09-C03	3.42	1.57	1.51
2	H	500	WII	O12-C11	-3.40	1.17	1.23
2	P	500	WII	O12-C11	-3.25	1.17	1.23
2	K	500	WII	O12-C11	-3.25	1.17	1.23
2	C	500	WII	O12-C11	-3.23	1.17	1.23
2	L	500	WII	O12-C11	-3.20	1.17	1.23
2	E	500	WII	O12-C11	-3.13	1.17	1.23
2	O	500	WII	O12-C11	-3.08	1.17	1.23
2	F	502	WII	O12-C11	-3.04	1.17	1.23
2	G	500	WII	O12-C11	-2.99	1.17	1.23
2	B	201	WII	C08-C04	2.96	1.52	1.50
2	M	500	WII	O12-C11	-2.94	1.18	1.23
2	J	201	WII	C08-C04	2.91	1.52	1.50
2	B	201	WII	O12-C11	-2.87	1.18	1.23
2	J	201	WII	O12-C11	-2.85	1.18	1.23
2	D	500	WII	C27-C26	-2.82	1.44	1.51
2	L	500	WII	C27-C26	-2.73	1.45	1.51
2	L	500	WII	C26-C25	2.73	1.42	1.36
2	N	502	WII	O12-C11	-2.69	1.18	1.23
2	O	500	WII	C26-C25	2.68	1.42	1.36
2	N	502	WII	C11-N10	2.64	1.41	1.35
2	D	500	WII	O12-C11	-2.57	1.18	1.23
2	I	500	WII	O12-C11	-2.55	1.18	1.23
2	G	500	WII	C27-C26	-2.51	1.45	1.51
2	K	500	WII	C27-C26	-2.46	1.45	1.51
2	E	500	WII	C27-C26	-2.43	1.45	1.51
2	M	500	WII	C27-C26	-2.43	1.45	1.51
2	F	502	WII	C11-N10	2.43	1.40	1.35
2	C	500	WII	C27-C26	-2.39	1.45	1.51
2	B	201	WII	C06-C09	-2.38	1.42	1.51
2	I	500	WII	C27-C26	-2.38	1.45	1.51
2	P	500	WII	C27-C26	-2.37	1.45	1.51
2	C	500	WII	C28-C27	2.37	1.61	1.52
2	O	500	WII	C27-C26	-2.36	1.45	1.51
2	J	201	WII	C28-C27	2.34	1.61	1.52
2	L	500	WII	C28-C27	2.33	1.61	1.52
2	A	500	WII	C27-C26	-2.33	1.45	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	500	WII	C11-N10	2.33	1.40	1.35
2	N	502	WII	C27-C26	-2.33	1.45	1.51
2	K	500	WII	C28-C27	2.32	1.61	1.52
2	C	500	WII	C26-C25	2.32	1.41	1.36
2	H	500	WII	C27-C26	-2.29	1.46	1.51
2	A	500	WII	C28-C27	2.29	1.61	1.52
2	J	201	WII	C06-C09	-2.27	1.43	1.51
2	D	500	WII	C28-C27	2.26	1.61	1.52
2	F	502	WII	C27-C26	-2.26	1.46	1.51
2	P	500	WII	C11-N10	2.25	1.40	1.35
2	B	201	WII	C27-C26	-2.25	1.46	1.51
2	I	500	WII	C28-C27	2.24	1.61	1.52
2	O	500	WII	C28-C27	2.24	1.61	1.52
2	C	500	WII	C11-N10	2.23	1.40	1.35
2	G	500	WII	C11-N10	2.23	1.40	1.35
2	N	502	WII	C28-C27	2.22	1.61	1.52
2	B	201	WII	C28-C27	2.20	1.61	1.52
2	D	500	WII	C26-C25	2.20	1.41	1.36
2	A	500	WII	O12-C11	-2.20	1.19	1.23
2	J	201	WII	C07-C06	-2.20	1.42	1.51
2	G	500	WII	C28-C27	2.18	1.61	1.52
2	B	201	WII	C26-C25	2.17	1.41	1.36
2	J	201	WII	C27-C26	-2.17	1.46	1.51
2	F	502	WII	C28-C27	2.14	1.61	1.52
2	M	500	WII	C28-C27	2.13	1.60	1.52
2	J	201	WII	C26-C25	2.11	1.41	1.36
2	P	500	WII	C28-C27	2.10	1.60	1.52
2	G	500	WII	C26-C25	2.09	1.41	1.36
2	D	500	WII	C06-C09	-2.09	1.43	1.51
2	H	500	WII	C06-C09	-2.08	1.43	1.51
2	B	201	WII	C07-C06	-2.07	1.43	1.51
2	H	500	WII	C28-C27	2.06	1.60	1.52
2	P	500	WII	C29-C25	-2.05	1.46	1.51
2	F	502	WII	C26-C25	2.04	1.40	1.36
2	E	500	WII	C06-C09	-2.04	1.44	1.51
2	E	500	WII	C28-C27	2.04	1.60	1.52
2	E	500	WII	C29-C25	-2.04	1.46	1.51
2	M	500	WII	C06-C09	-2.04	1.44	1.51
2	H	500	WII	C11-N10	2.02	1.40	1.35
2	N	502	WII	C06-C09	-2.00	1.44	1.51

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	201	WII	C02-C16-N17	8.92	129.33	115.88
2	H	500	WII	C02-C16-N17	8.65	128.93	115.88
2	C	500	WII	C02-C16-N17	8.08	128.06	115.88
2	I	500	WII	C02-C16-N17	8.06	128.03	115.88
2	P	500	WII	C02-C16-N17	7.90	127.80	115.88
2	K	500	WII	C02-C16-N17	7.62	127.37	115.88
2	A	500	WII	C02-C16-N17	7.58	127.31	115.88
2	B	201	WII	C02-C16-N17	7.49	127.18	115.88
2	F	502	WII	C02-C16-N17	7.31	126.90	115.88
2	M	500	WII	C02-C16-N17	7.24	126.80	115.88
2	N	502	WII	C02-C16-N17	6.96	126.37	115.88
2	L	500	WII	C02-C16-N17	6.59	125.82	115.88
2	D	500	WII	C02-C16-N17	6.31	125.39	115.88
2	O	500	WII	C21-C19-N20	6.19	128.57	122.93
2	G	500	WII	C02-C16-N17	6.02	124.96	115.88
2	E	500	WII	C02-C16-N17	5.95	124.85	115.88
2	O	500	WII	C02-C16-N17	5.74	124.53	115.88
2	G	500	WII	C21-C19-N20	5.10	127.58	122.93
2	H	500	WII	C16-N20-C19	4.80	108.18	101.38
2	J	201	WII	C16-N20-C19	4.64	107.96	101.38
2	A	500	WII	C16-N20-C19	4.47	107.72	101.38
2	L	500	WII	C21-C19-N20	4.44	126.97	122.93
2	C	500	WII	C16-N20-C19	4.40	107.61	101.38
2	I	500	WII	C16-N20-C19	4.33	107.51	101.38
2	A	500	WII	C21-C19-N20	4.19	126.75	122.93
2	P	500	WII	C16-N20-C19	4.18	107.30	101.38
2	D	500	WII	C21-C19-N20	4.17	126.73	122.93
2	B	201	WII	C16-N20-C19	4.13	107.22	101.38
2	K	500	WII	C16-N20-C19	4.09	107.18	101.38
2	M	500	WII	C16-N20-C19	4.08	107.16	101.38
2	O	500	WII	C16-N20-C19	3.94	106.97	101.38
2	E	500	WII	C21-C19-N20	3.88	126.47	122.93
2	I	500	WII	C21-C19-N20	3.82	126.41	122.93
2	G	500	WII	C16-N20-C19	3.78	106.73	101.38
2	E	500	WII	C16-N20-C19	3.68	106.60	101.38
2	L	500	WII	C16-N20-C19	3.64	106.54	101.38
2	I	500	WII	C07-C08-C04	3.64	119.50	113.53
2	D	500	WII	C16-N20-C19	3.52	106.37	101.38
2	N	502	WII	C16-N20-C19	3.51	106.35	101.38
2	N	502	WII	C07-C08-C04	3.39	119.11	113.53
2	F	502	WII	C16-N20-C19	3.36	106.14	101.38
2	F	502	WII	C22-C21-C19	-3.30	103.89	110.14
2	N	502	WII	C21-C19-N20	3.17	125.82	122.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	500	WII	C07-C08-C04	3.17	118.73	113.53
2	M	500	WII	C27-C26-C25	3.04	113.88	111.31
2	L	500	WII	C29-C25-C26	2.92	113.78	111.31
2	L	500	WII	C07-C08-C04	2.88	118.26	113.53
2	B	201	WII	C21-C19-N20	2.78	125.46	122.93
2	A	500	WII	C27-C26-C25	2.77	113.65	111.31
2	L	500	WII	C22-C21-C19	-2.76	104.92	110.14
2	D	500	WII	C27-C26-C25	2.75	113.63	111.31
2	M	500	WII	C21-C19-N20	2.74	125.43	122.93
2	I	500	WII	C27-C26-C25	2.74	113.62	111.31
2	C	500	WII	C21-C19-N20	2.67	125.36	122.93
2	A	500	WII	C07-C08-C04	2.66	117.89	113.53
2	K	500	WII	C21-C19-N20	2.60	125.30	122.93
2	F	502	WII	C27-C26-C25	2.58	113.49	111.31
2	C	500	WII	C29-C25-C26	2.56	113.47	111.31
2	N	502	WII	C27-C26-C25	2.53	113.45	111.31
2	P	500	WII	C27-C26-C25	2.50	113.43	111.31
2	A	500	WII	C06-C09-C03	2.47	117.91	112.84
2	K	500	WII	C29-C25-C26	2.43	113.36	111.31
2	J	201	WII	C27-C26-C25	2.41	113.35	111.31
2	B	201	WII	C27-C26-C25	2.38	113.32	111.31
2	I	500	WII	C06-C07-C08	2.37	123.08	112.55
2	M	500	WII	C07-C08-C04	2.36	117.41	113.53
2	D	500	WII	C22-C21-C19	-2.31	105.77	110.14
2	G	500	WII	C22-C21-C19	-2.25	105.88	110.14
2	J	201	WII	C11-C25-C26	-2.25	123.32	129.96
2	F	502	WII	C21-C19-N20	2.24	124.97	122.93
2	J	201	WII	O12-C11-N10	-2.19	119.24	123.92
2	O	500	WII	C22-C21-C19	-2.16	106.04	110.14
2	O	500	WII	C07-C08-C04	2.15	117.06	113.53
2	K	500	WII	C01-N10-C11	-2.15	121.32	126.64
2	O	500	WII	O15-C13-O14	-2.14	118.72	123.61
2	I	500	WII	C06-C09-C03	2.11	117.18	112.84
2	H	500	WII	C06-C07-C08	2.11	121.91	112.55
2	L	500	WII	C06-C07-C08	2.10	121.88	112.55
2	L	500	WII	O15-C13-O14	-2.10	118.81	123.61
2	E	500	WII	C06-C07-C08	2.06	121.71	112.55
2	D	500	WII	C07-C08-C04	2.05	116.90	113.53
2	H	500	WII	C27-C26-C25	2.04	113.04	111.31
2	P	500	WII	C11-C25-C26	-2.03	123.95	129.96
2	M	500	WII	O12-C11-C25	2.03	125.35	122.03
2	H	500	WII	C11-C25-C26	-2.02	124.00	129.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	K	500	WII	C11-C25-C26	-2.02	124.00	129.96
2	B	201	WII	C11-C25-C26	-2.01	124.02	129.96
2	F	502	WII	O14-C13-C26	-2.00	116.72	122.46

There are no chirality outliers.

All (64) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	WII	O14-C13-C26-C27
2	A	500	WII	O15-C13-C26-C25
2	B	201	WII	O14-C13-C26-C25
2	B	201	WII	O14-C13-C26-C27
2	B	201	WII	O15-C13-C26-C25
2	B	201	WII	O15-C13-C26-C27
2	C	500	WII	O14-C13-C26-C27
2	C	500	WII	O15-C13-C26-C25
2	D	500	WII	O14-C13-C26-C25
2	D	500	WII	O14-C13-C26-C27
2	D	500	WII	O15-C13-C26-C25
2	D	500	WII	O15-C13-C26-C27
2	E	500	WII	O14-C13-C26-C27
2	E	500	WII	O15-C13-C26-C25
2	F	502	WII	O14-C13-C26-C25
2	F	502	WII	O14-C13-C26-C27
2	F	502	WII	O15-C13-C26-C25
2	F	502	WII	O15-C13-C26-C27
2	G	500	WII	O14-C13-C26-C27
2	G	500	WII	O15-C13-C26-C25
2	H	500	WII	O14-C13-C26-C27
2	H	500	WII	O15-C13-C26-C25
2	I	500	WII	O14-C13-C26-C27
2	I	500	WII	O15-C13-C26-C25
2	J	201	WII	O14-C13-C26-C25
2	J	201	WII	O15-C13-C26-C25
2	K	500	WII	O14-C13-C26-C25
2	K	500	WII	O14-C13-C26-C27
2	K	500	WII	O15-C13-C26-C25
2	L	500	WII	O15-C13-C26-C27
2	M	500	WII	O14-C13-C26-C27
2	M	500	WII	O15-C13-C26-C25
2	N	502	WII	O14-C13-C26-C25
2	N	502	WII	O14-C13-C26-C27

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Mol	Chain	Res	Type	Atoms
2	N	502	WII	O15-C13-C26-C25
2	N	502	WII	O15-C13-C26-C27
2	O	500	WII	O14-C13-C26-C25
2	O	500	WII	O14-C13-C26-C27
2	O	500	WII	O15-C13-C26-C25
2	O	500	WII	O15-C13-C26-C27
2	P	500	WII	O14-C13-C26-C27
2	P	500	WII	O15-C13-C26-C25
2	L	500	WII	O14-C13-C26-C27
2	J	201	WII	O14-C13-C26-C27
2	A	500	WII	O14-C13-C26-C25
2	C	500	WII	O14-C13-C26-C25
2	E	500	WII	O14-C13-C26-C25
2	G	500	WII	O14-C13-C26-C25
2	H	500	WII	O14-C13-C26-C25
2	I	500	WII	O14-C13-C26-C25
2	L	500	WII	O14-C13-C26-C25
2	M	500	WII	O14-C13-C26-C25
2	P	500	WII	O14-C13-C26-C25
2	A	500	WII	O15-C13-C26-C27
2	C	500	WII	O15-C13-C26-C27
2	E	500	WII	O15-C13-C26-C27
2	G	500	WII	O15-C13-C26-C27
2	H	500	WII	O15-C13-C26-C27
2	I	500	WII	O15-C13-C26-C27
2	J	201	WII	O15-C13-C26-C27
2	K	500	WII	O15-C13-C26-C27
2	M	500	WII	O15-C13-C26-C27
2	P	500	WII	O15-C13-C26-C27
2	L	500	WII	O15-C13-C26-C25

There are no ring outliers.

13 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	500	WII	1	0
2	F	502	WII	1	0
2	H	500	WII	1	0
2	M	500	WII	1	0
2	O	500	WII	1	0
2	L	500	WII	1	0
2	P	500	WII	1	0

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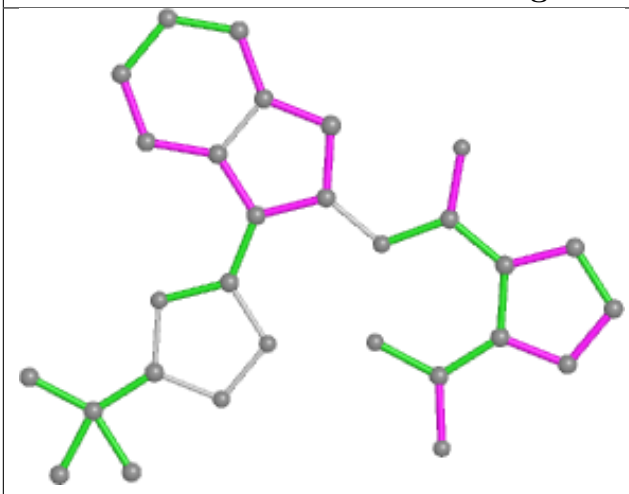
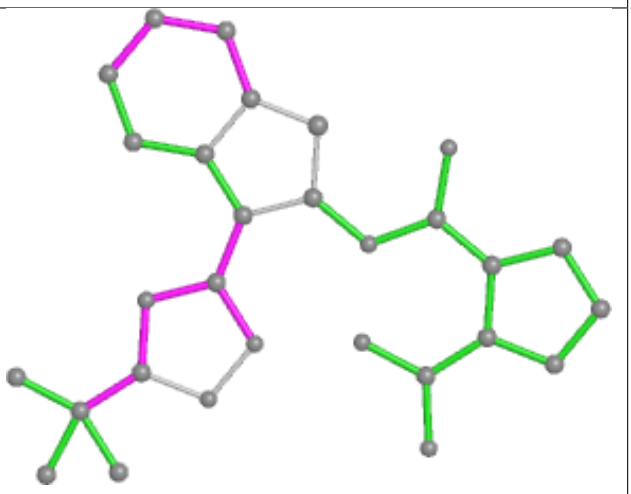
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	500	WII	1	0
2	N	502	WII	1	0
2	B	201	WII	1	0
2	J	201	WII	2	0
2	D	500	WII	2	0
2	G	500	WII	1	0

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 then 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.

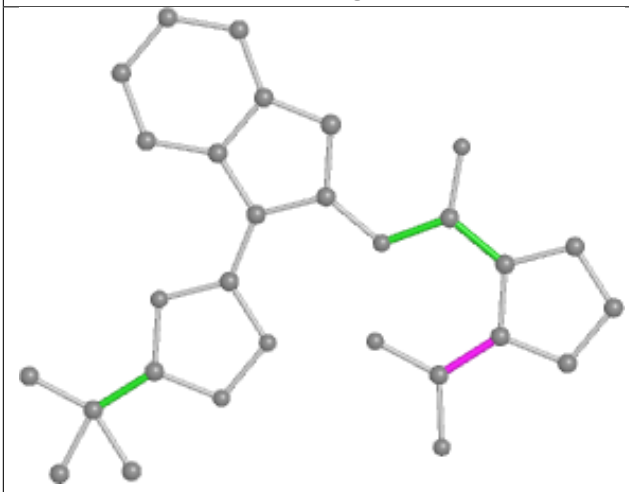
Ligand WII E 500



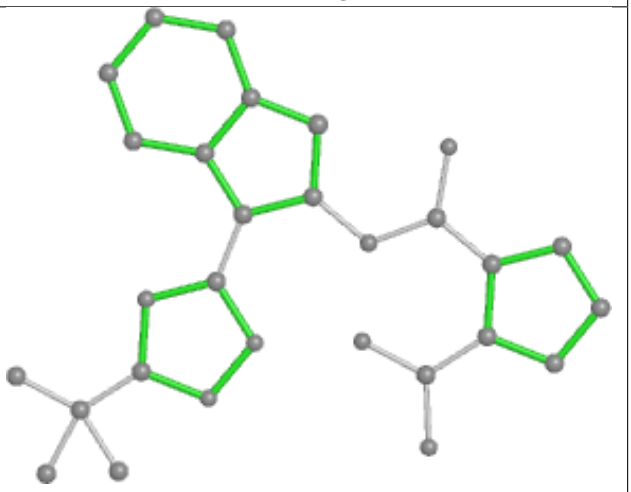
Bond lengths



Bond angles

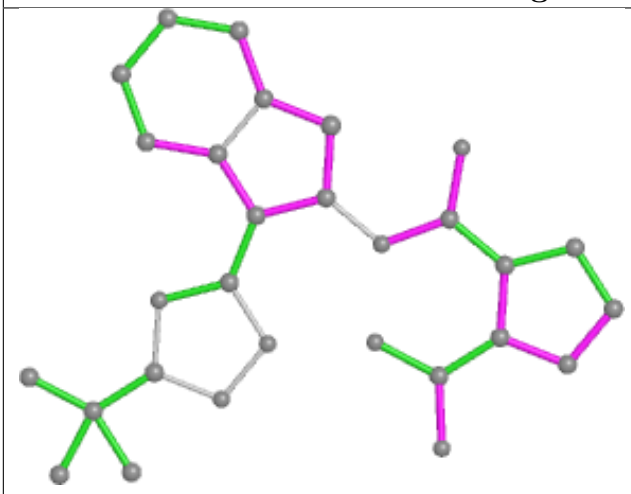


Torsions

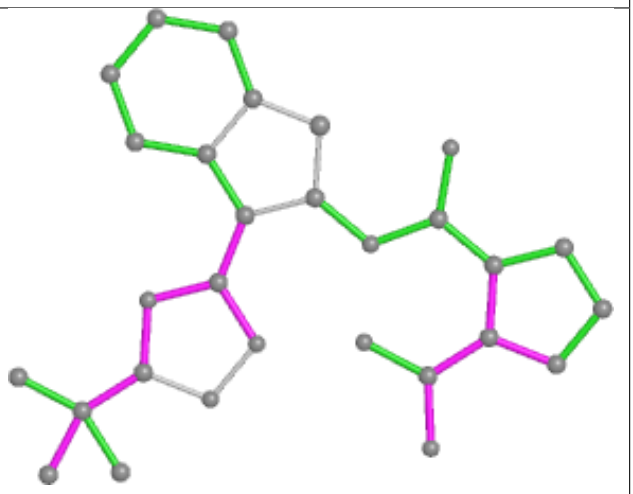


Rings

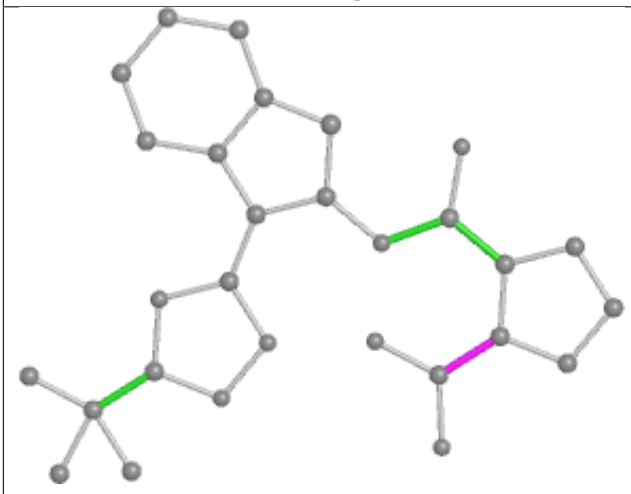
Ligand WII F 502



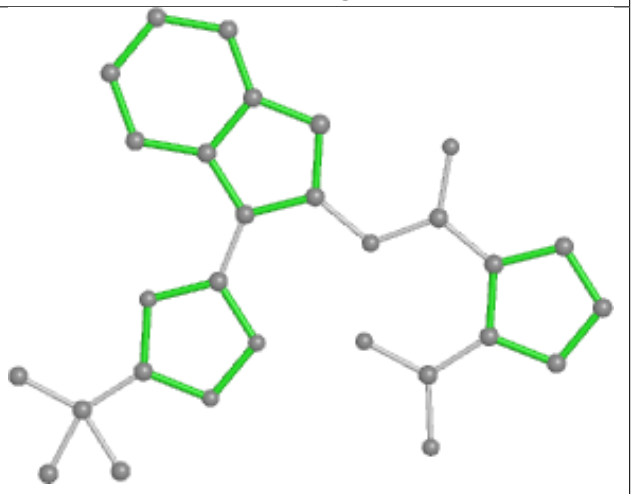
Bond lengths



Bond angles

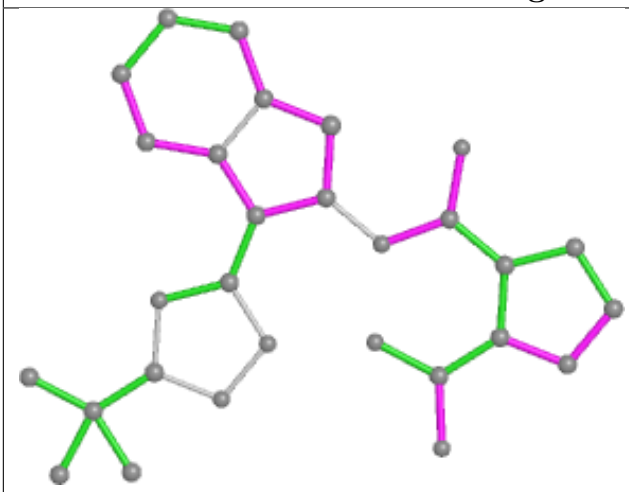


Torsions

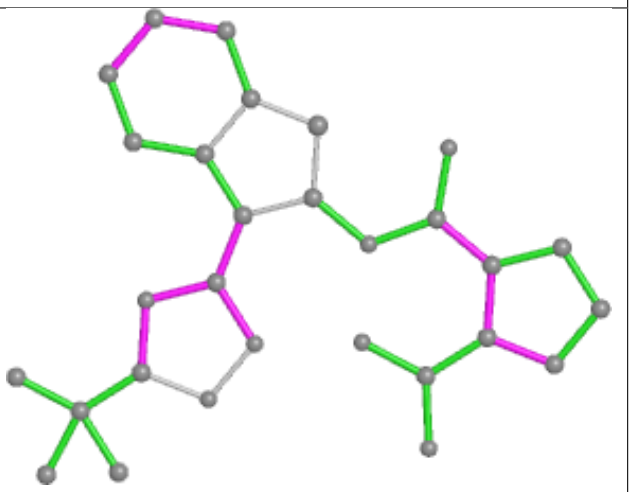


Rings

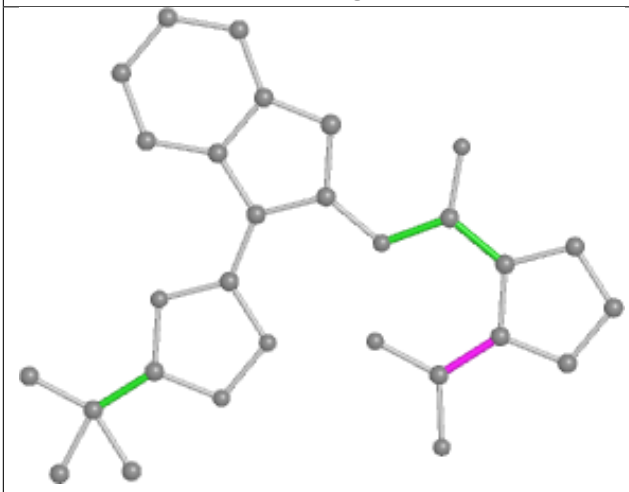
Ligand WII H 500



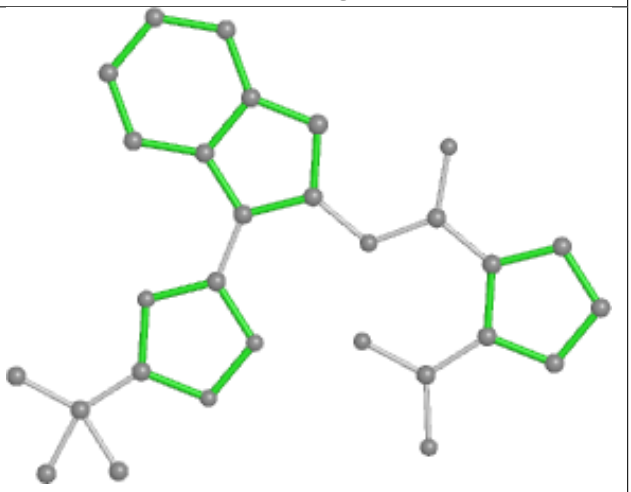
Bond lengths



Bond angles

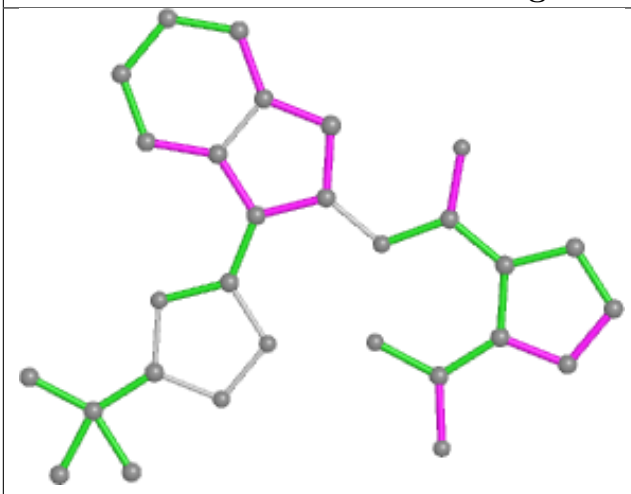


Torsions

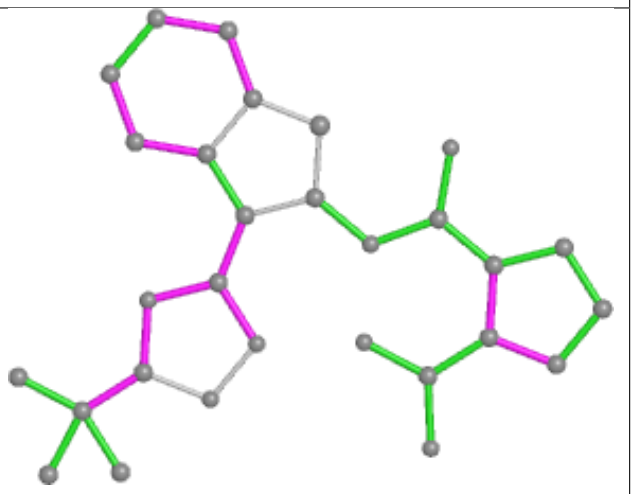


Rings

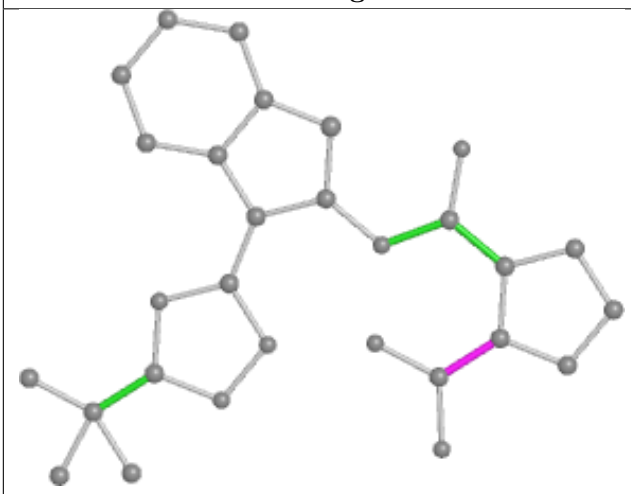
Ligand WII A 500



Bond lengths



Bond angles



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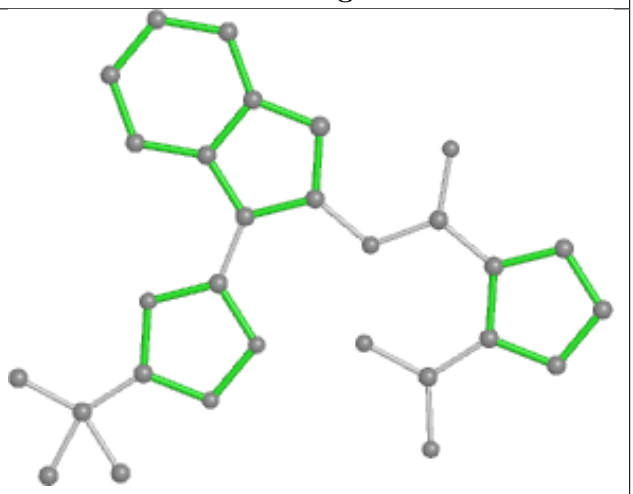
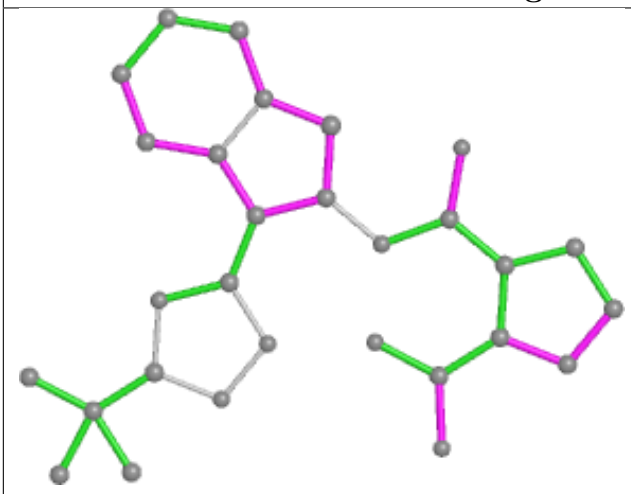
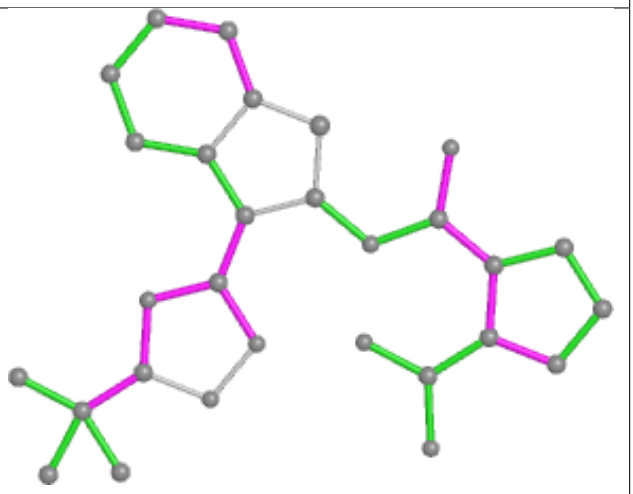


Rings

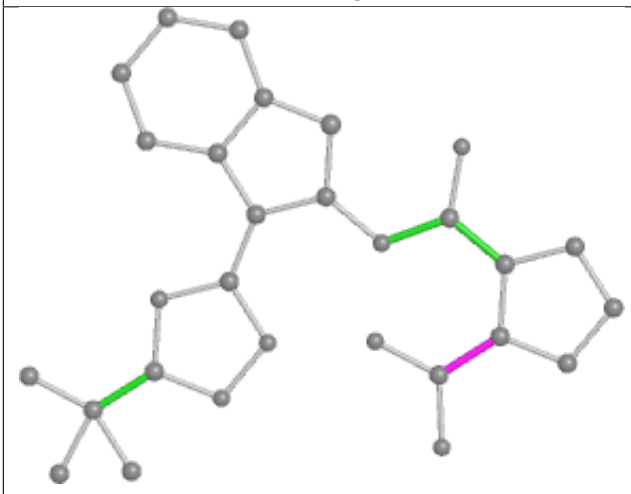
Ligand WII M 500



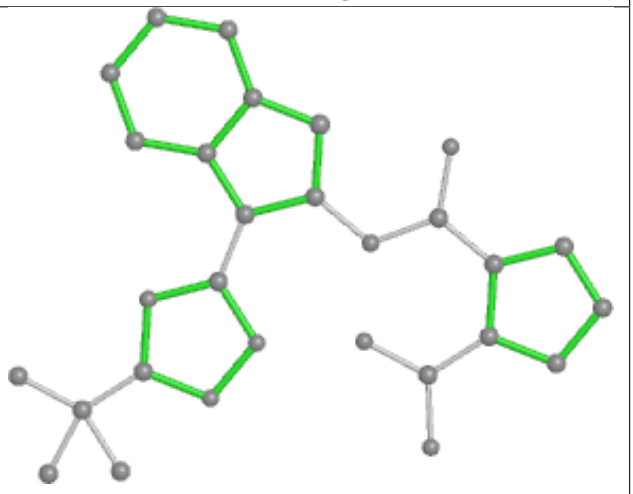
Bond lengths



Bond angles

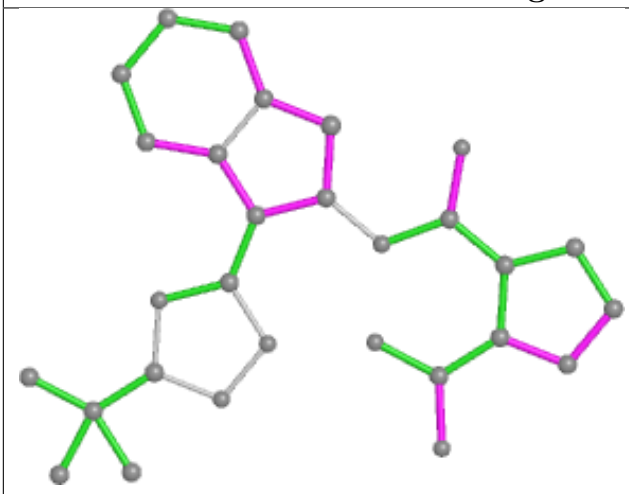


Torsions

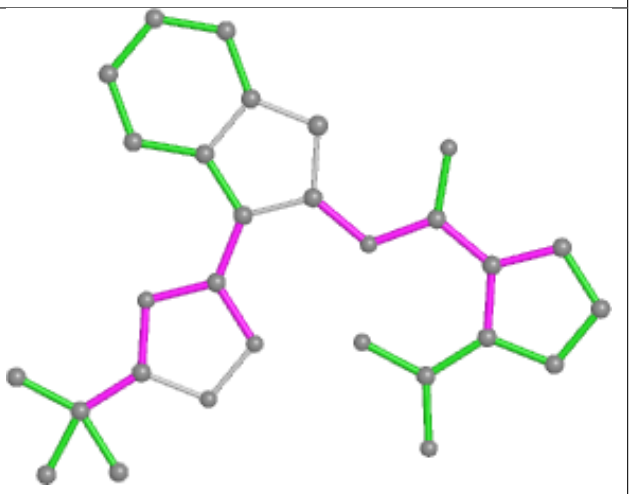


Rings

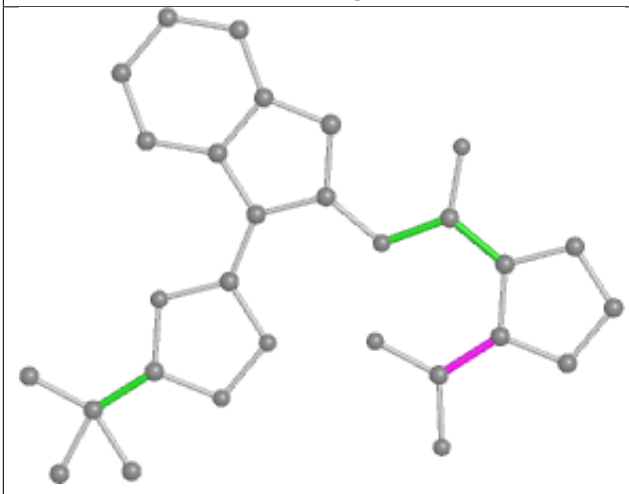
Ligand WII K 500



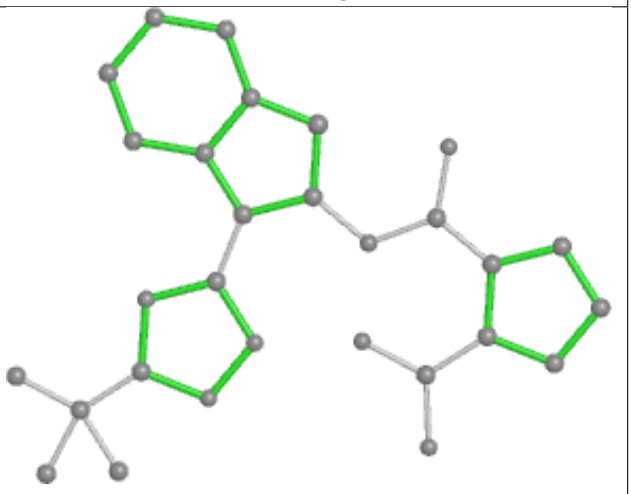
Bond lengths



Bond angles

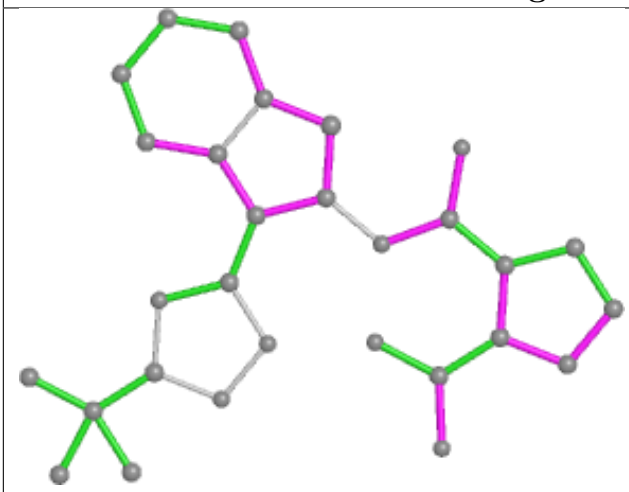


Torsions

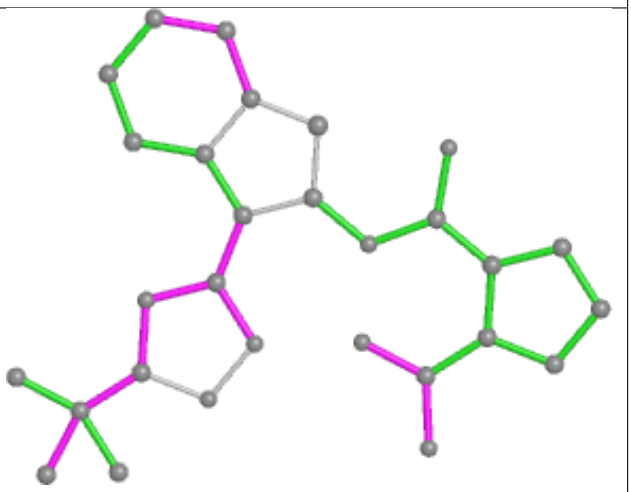


Rings

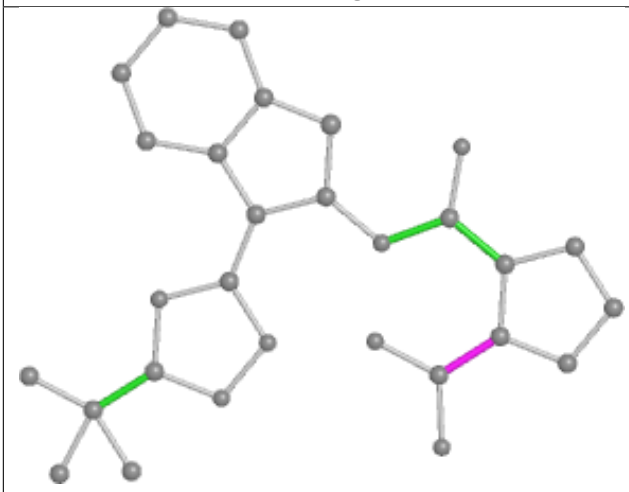
Ligand WII O 500



Bond lengths



Bond angles



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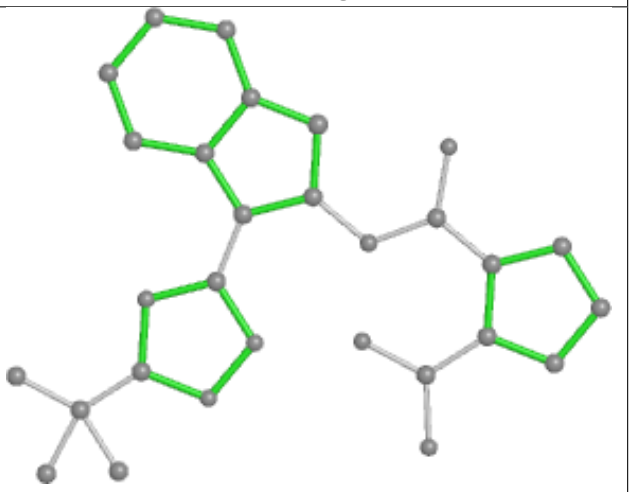
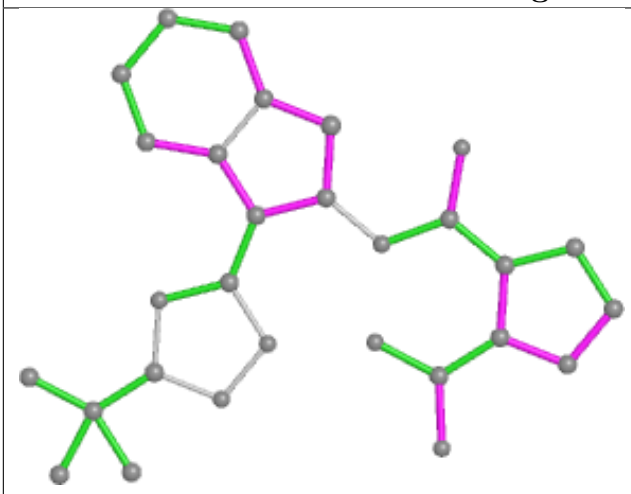
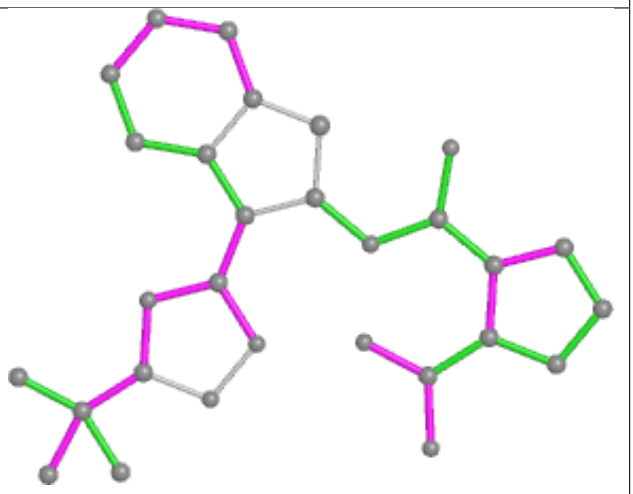


Rings

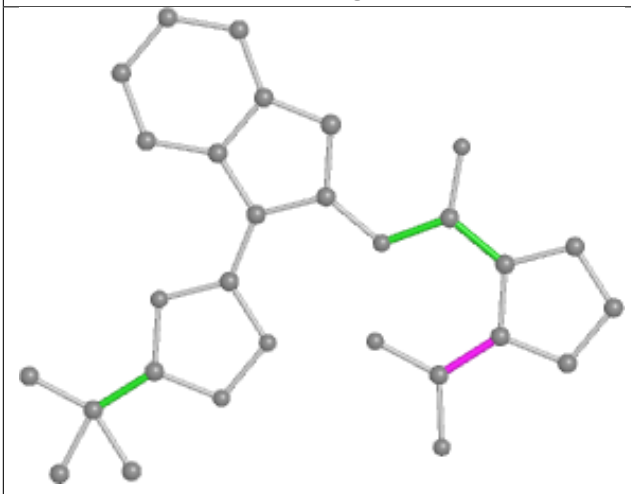
Ligand WII L 500



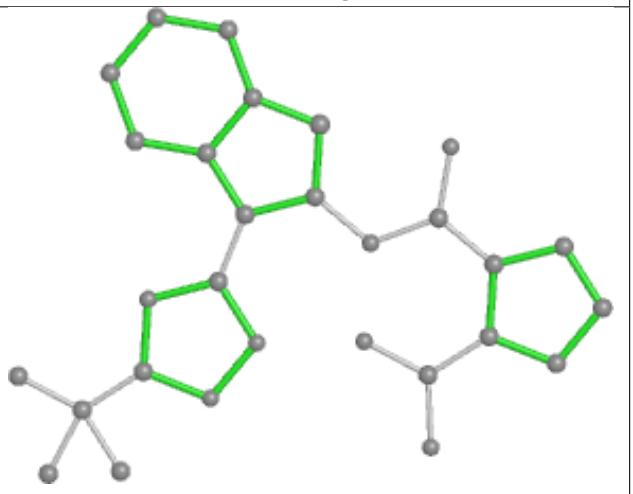
Bond lengths



Bond angles

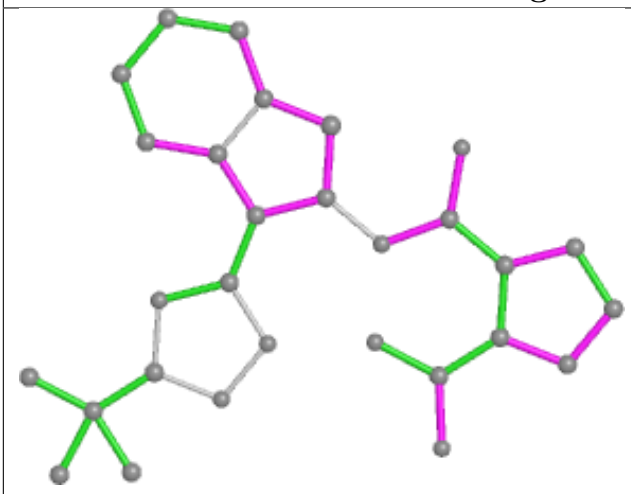


Torsions

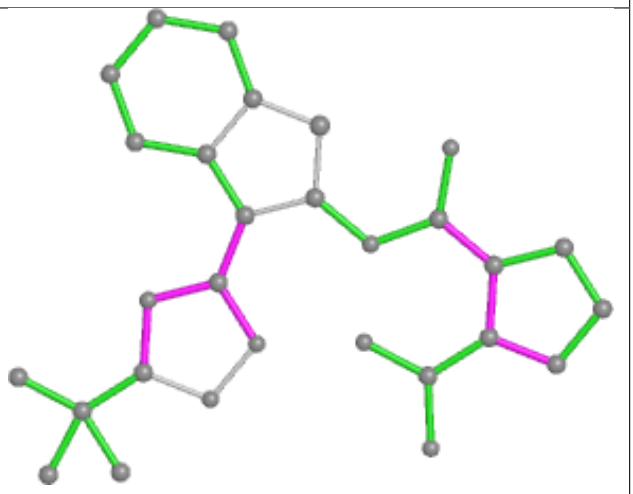


Rings

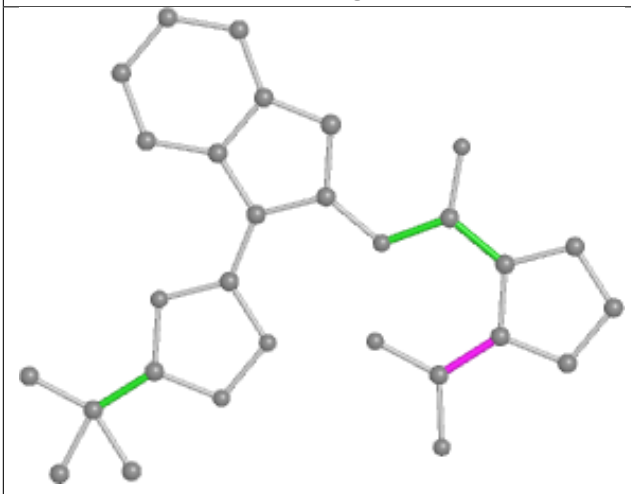
Ligand WII P 500



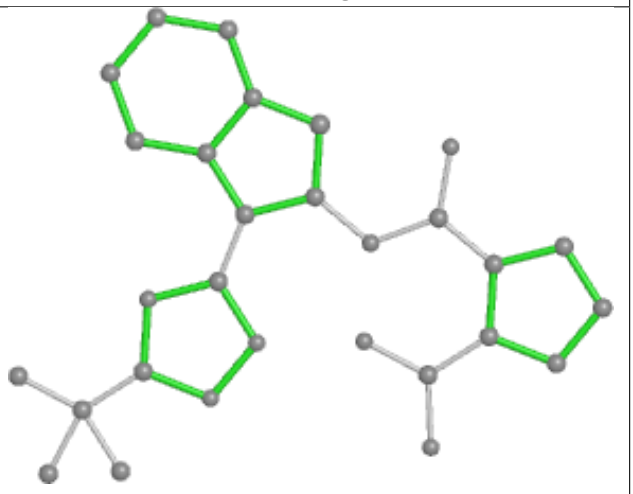
Bond lengths



Bond angles

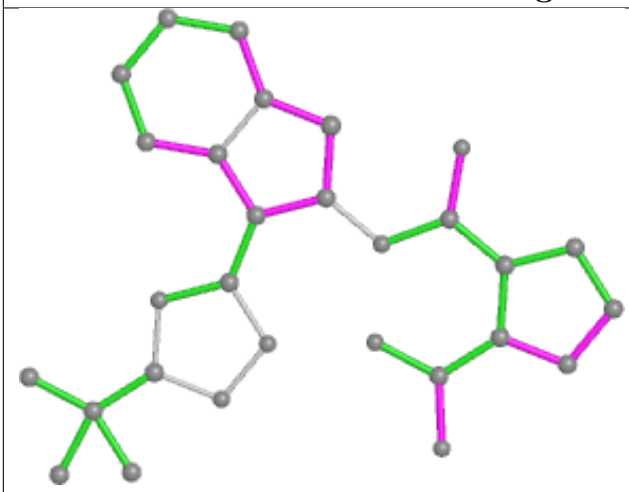


Torsions

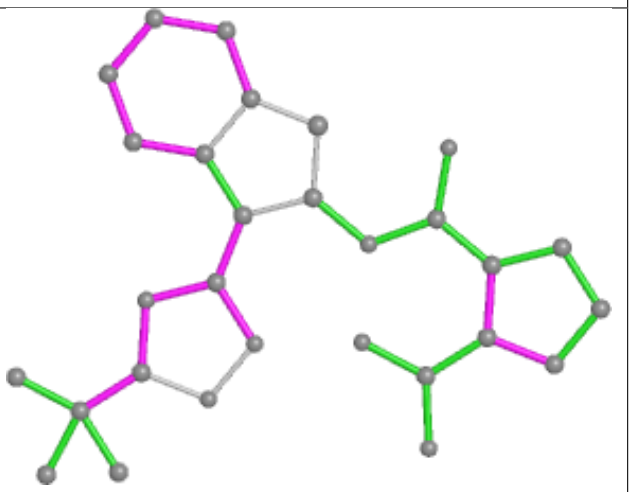


Rings

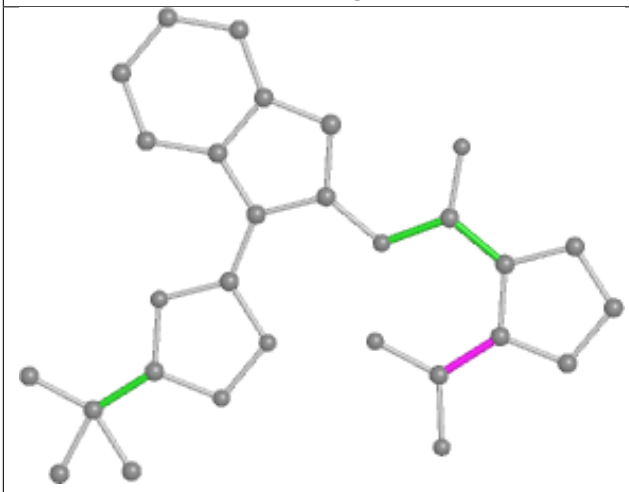
Ligand WII I 500



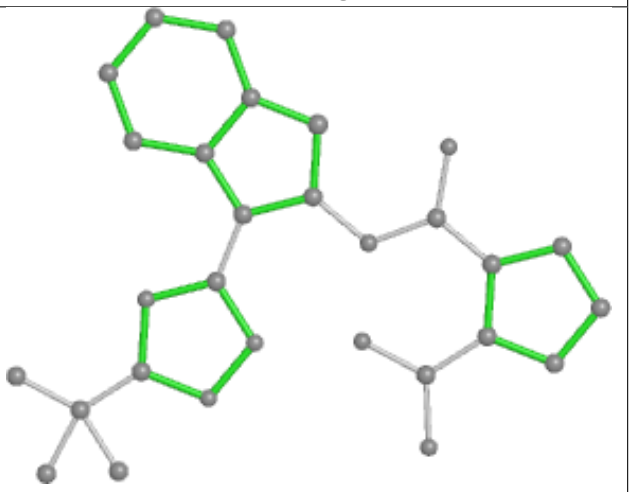
Bond lengths



Bond angles

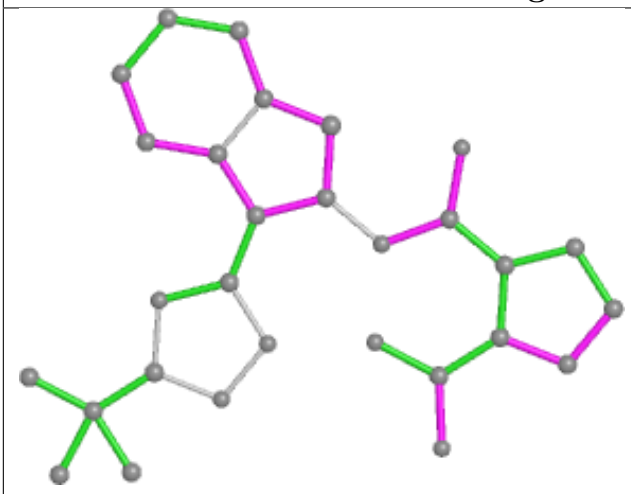


Torsions

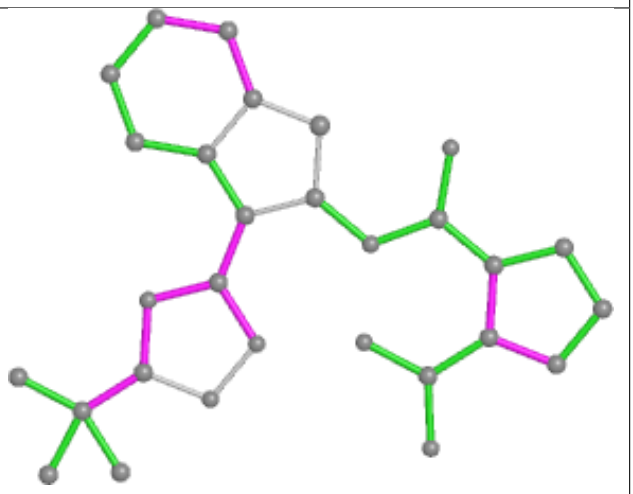


Rings

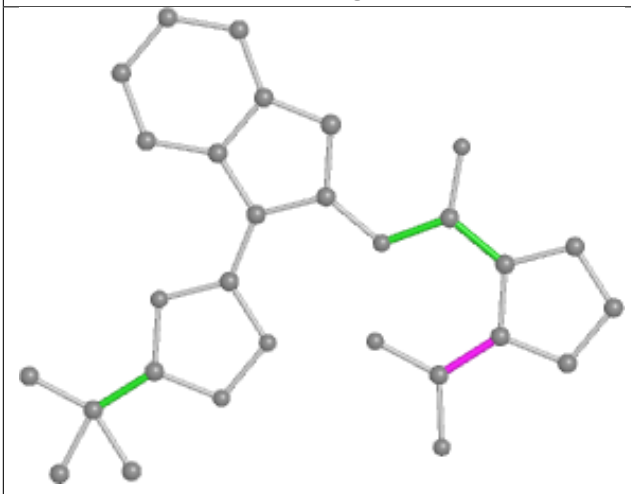
Ligand WII N 502



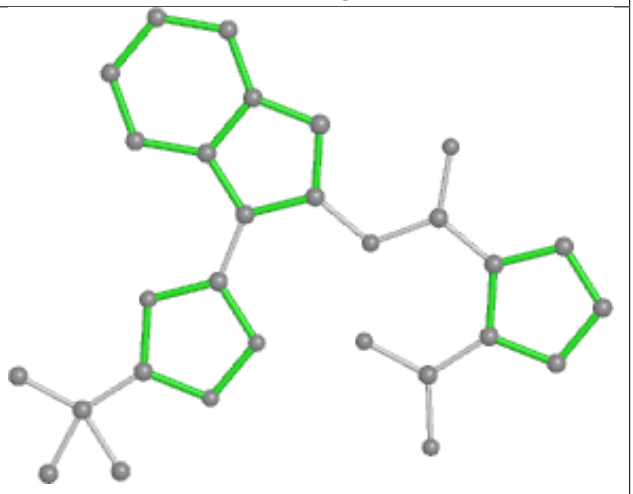
Bond lengths



Bond angles

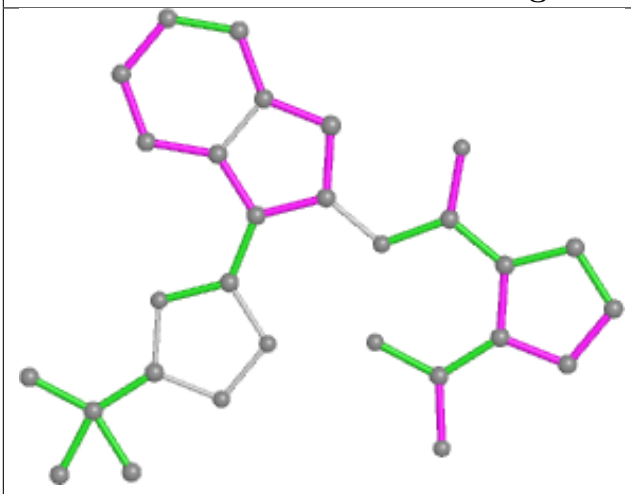


Torsions

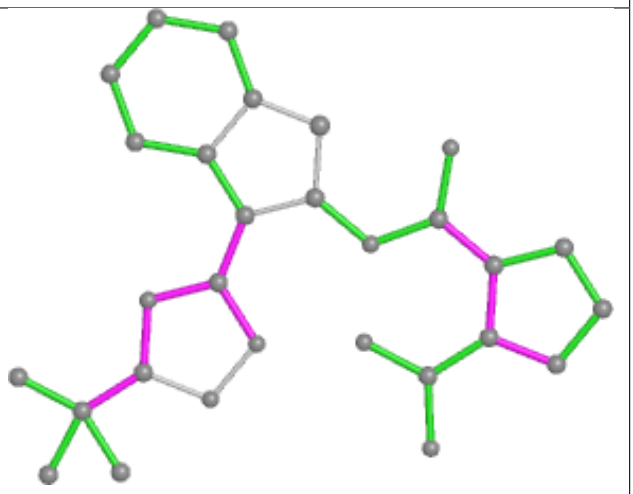


Rings

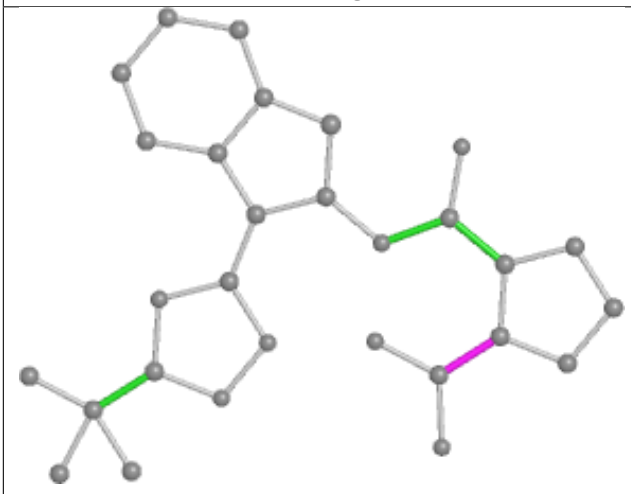
Ligand WII B 201



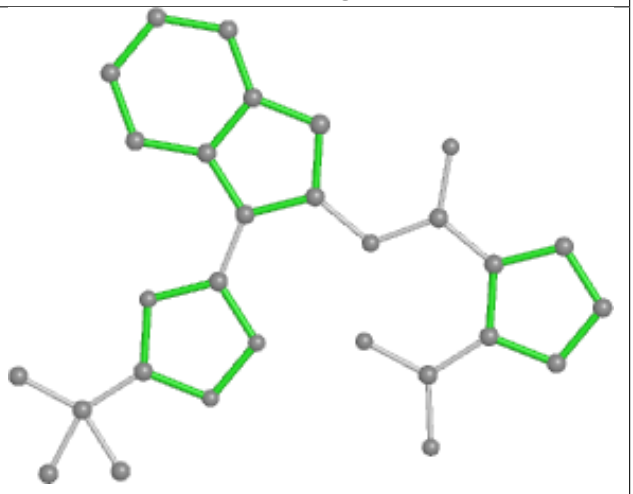
Bond lengths



Bond angles

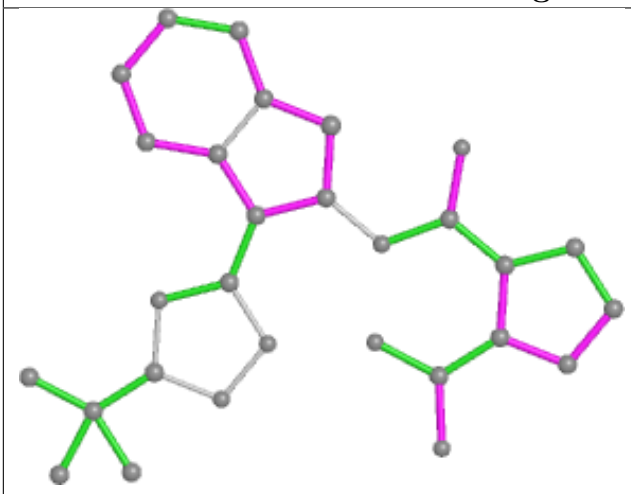


Torsions

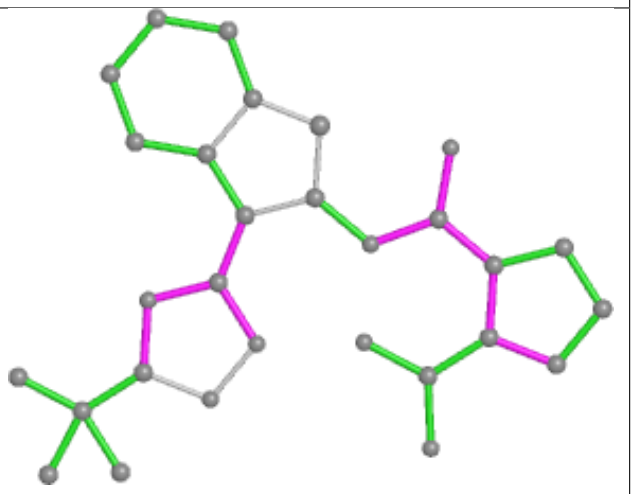


Rings

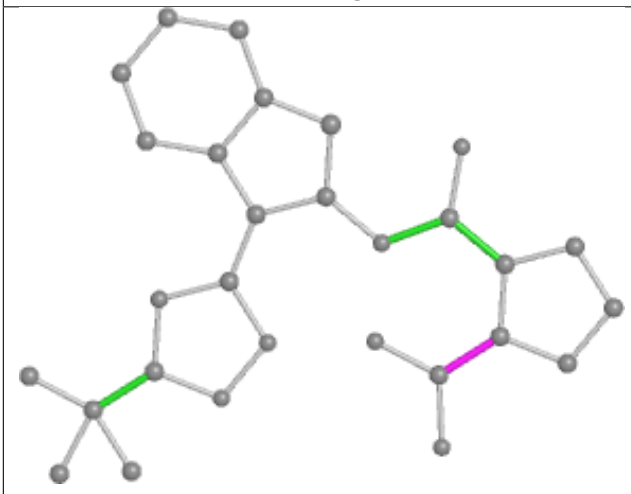
Ligand WII J 201



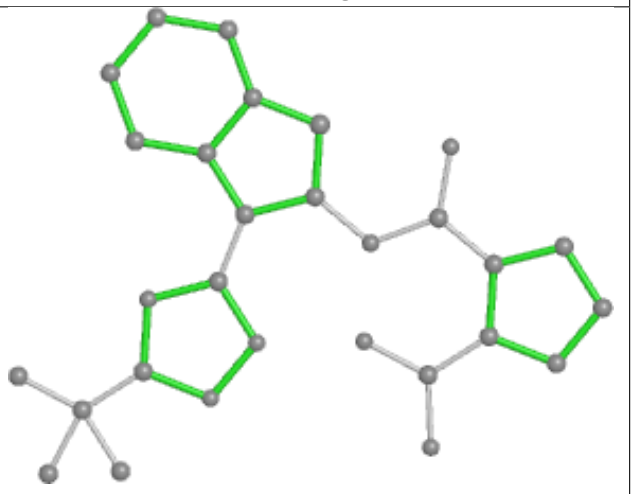
Bond lengths



Bond angles

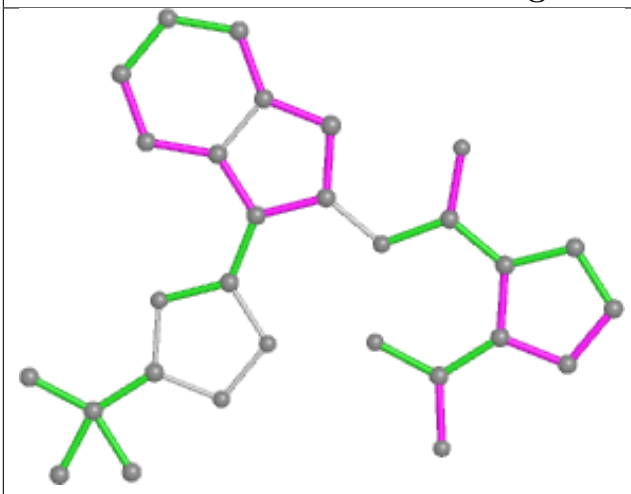


Torsions

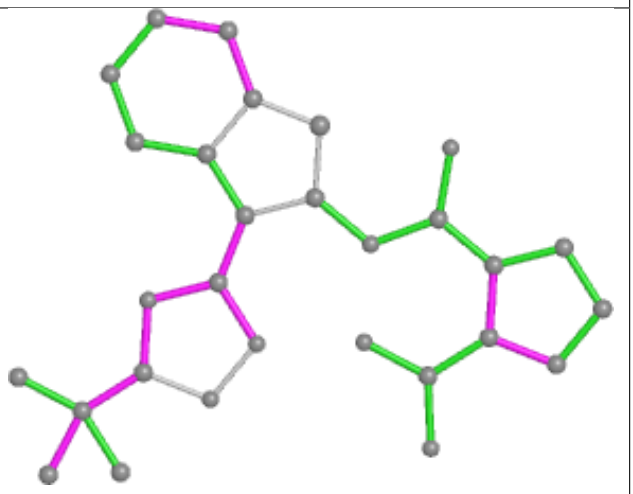


Rings

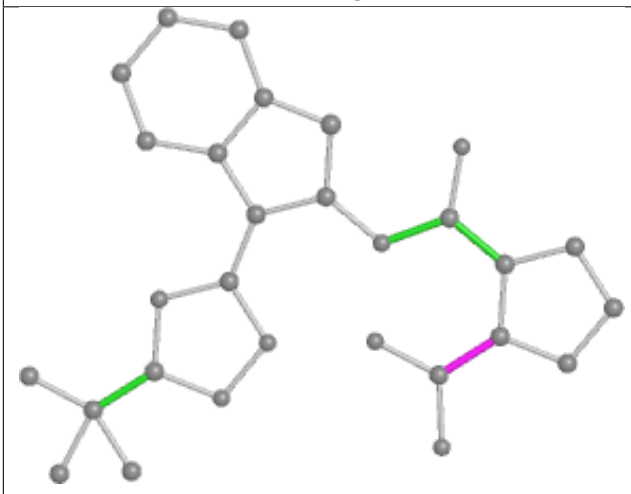
Ligand WII D 500



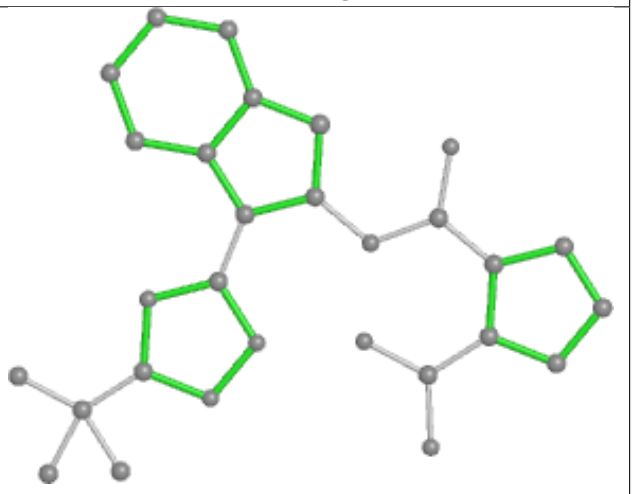
Bond lengths



Bond angles

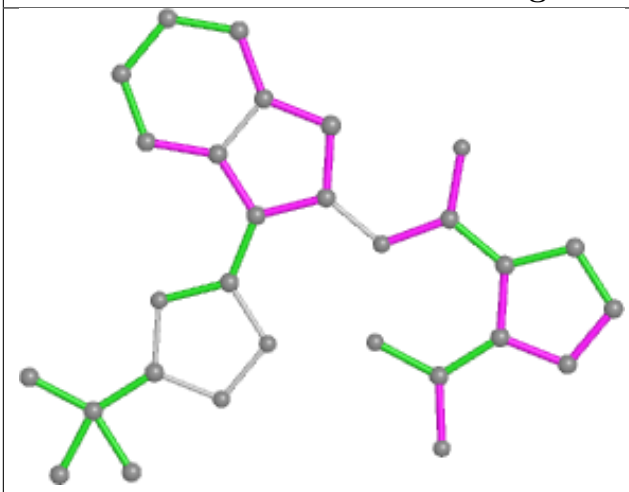


Torsions

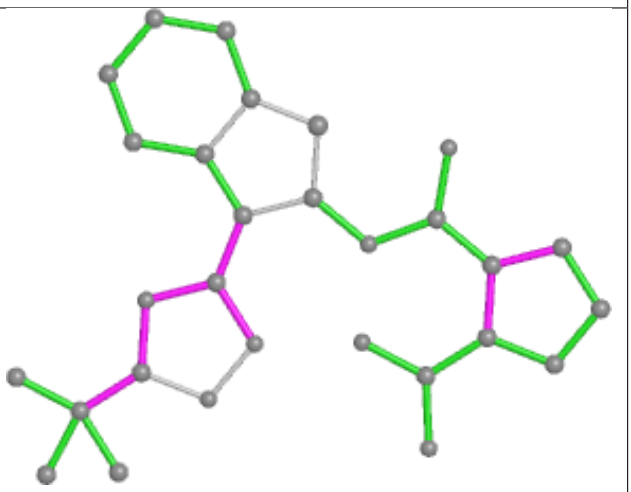


Rings

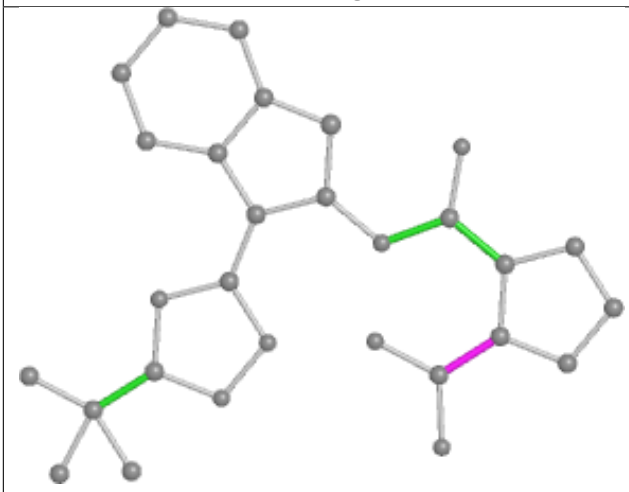
Ligand WII C 500



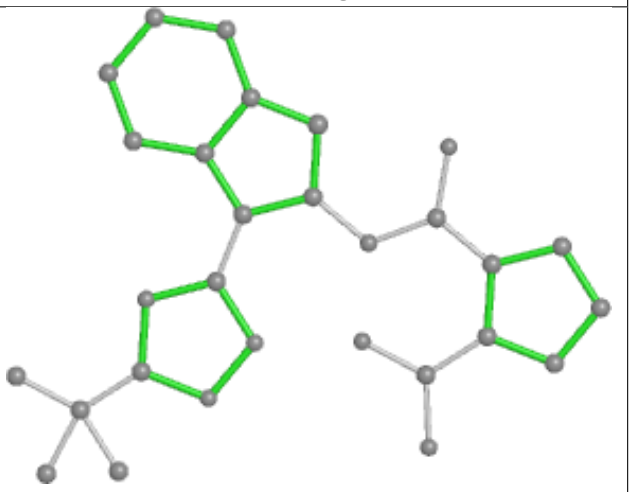
Bond lengths



Bond angles

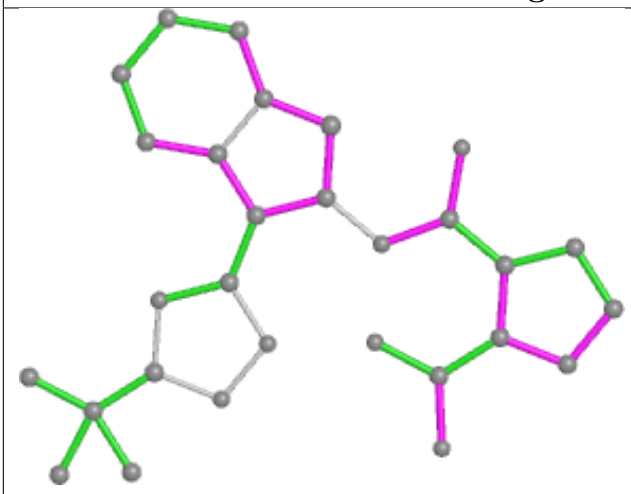


Torsions

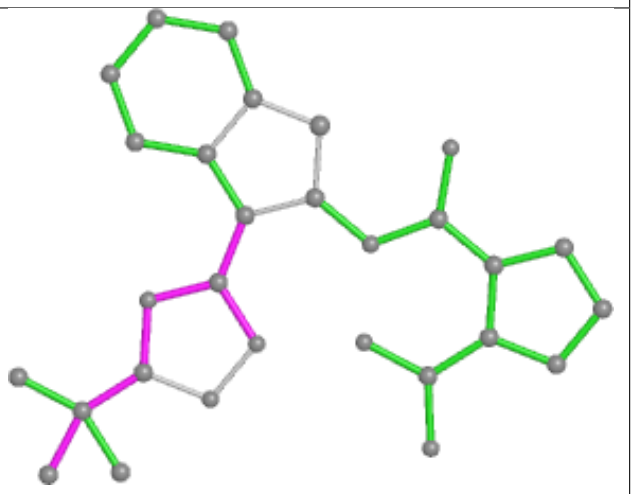


Rings

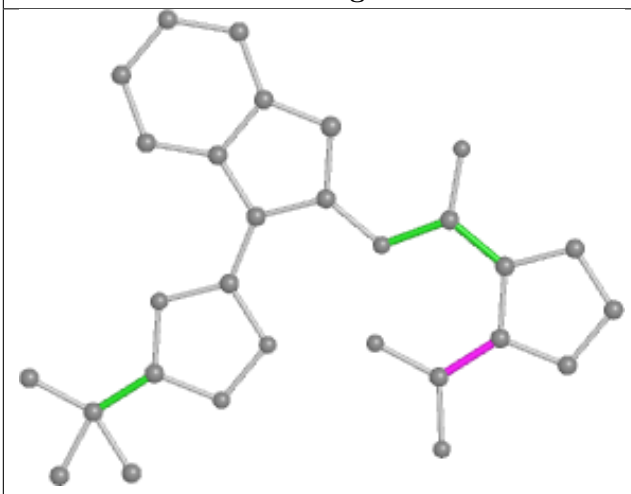
Ligand WII G 500



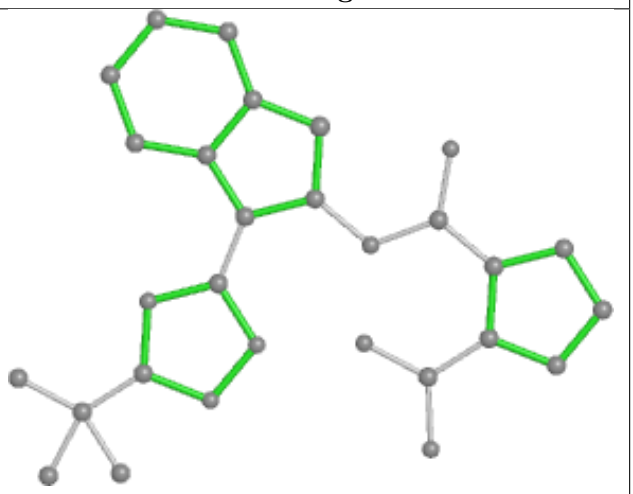
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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^2)	Q<0.9
1	A	127/130 (97%)	-0.45	0 100 100	38, 48, 71, 96	0
1	B	127/130 (97%)	-0.50	0 100 100	39, 50, 72, 95	0
1	C	127/130 (97%)	-0.51	0 100 100	40, 49, 68, 91	0
1	D	127/130 (97%)	-0.38	1 (0%) 86 84	42, 52, 72, 100	0
1	E	129/130 (99%)	-0.41	0 100 100	40, 53, 77, 102	0
1	F	128/130 (98%)	-0.48	0 100 100	39, 49, 72, 110	0
1	G	127/130 (97%)	-0.41	0 100 100	41, 51, 71, 104	0
1	H	130/130 (100%)	-0.38	0 100 100	37, 52, 76, 106	0
1	I	127/130 (97%)	-0.42	0 100 100	39, 49, 71, 94	0
1	J	127/130 (97%)	-0.47	0 100 100	39, 49, 72, 94	0
1	K	127/130 (97%)	-0.50	0 100 100	40, 49, 71, 96	0
1	L	127/130 (97%)	-0.41	1 (0%) 86 84	41, 52, 72, 97	0
1	M	129/130 (99%)	-0.43	0 100 100	40, 52, 76, 99	0
1	N	128/130 (98%)	-0.45	1 (0%) 86 84	37, 49, 72, 116	0
1	O	127/130 (97%)	-0.40	1 (0%) 86 84	40, 51, 72, 94	0
1	P	129/130 (99%)	-0.38	0 100 100	39, 52, 77, 97	0
All	All	2043/2080 (98%)	-0.44	4 (0%) 95 95	37, 51, 74, 116	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	76	GLY	3.2
1	N	0	HIS	2.6
1	O	76	GLY	2.5
1	D	76	GLY	2.4

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 (i)

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^{th} 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^2)	Q<0.9
3	SCN	E	501	3/3	0.77	0.53	72,72,92,103	0
3	SCN	M	501	3/3	0.80	0.59	74,74,98,112	0
3	SCN	O	501	3/3	0.84	0.22	50,50,51,75	0
3	SCN	D	501	3/3	0.89	0.26	60,60,70,71	0
3	SCN	P	501	3/3	0.90	0.59	71,71,80,93	0
3	SCN	H	501	3/3	0.92	0.35	66,66,88,98	0
3	SCN	L	501	3/3	0.93	0.16	55,55,64,73	0
3	SCN	G	501	3/3	0.93	0.22	44,44,53,75	0
2	WII	N	502	29/29	0.95	0.18	29,53,77,79	0
2	WII	F	502	29/29	0.95	0.19	35,53,70,89	0
2	WII	G	500	29/29	0.95	0.19	50,66,82,86	0
3	SCN	B	202	3/3	0.96	0.13	43,43,49,52	0
2	WII	C	500	29/29	0.96	0.18	35,51,67,87	0
2	WII	D	500	29/29	0.96	0.15	46,62,79,92	0
2	WII	H	500	29/29	0.96	0.15	28,47,63,71	0
2	WII	J	201	29/29	0.96	0.22	32,47,63,81	0
2	WII	K	500	29/29	0.96	0.15	42,52,77,91	0
2	WII	L	500	29/29	0.96	0.19	46,60,73,83	0
2	WII	E	500	29/29	0.96	0.16	32,48,66,73	0
2	WII	O	500	29/29	0.96	0.21	45,62,80,86	0
3	SCN	A	501	3/3	0.97	0.18	52,52,52,67	0
2	WII	M	500	29/29	0.97	0.14	29,48,67,73	0
2	WII	B	201	29/29	0.97	0.17	34,47,64,72	0
2	WII	A	500	29/29	0.97	0.16	31,46,61,68	0
2	WII	P	500	29/29	0.97	0.14	25,48,58,73	0
3	SCN	J	203	3/3	0.98	0.14	53,53,53,54	0
2	WII	I	500	29/29	0.98	0.19	30,48,67,79	0

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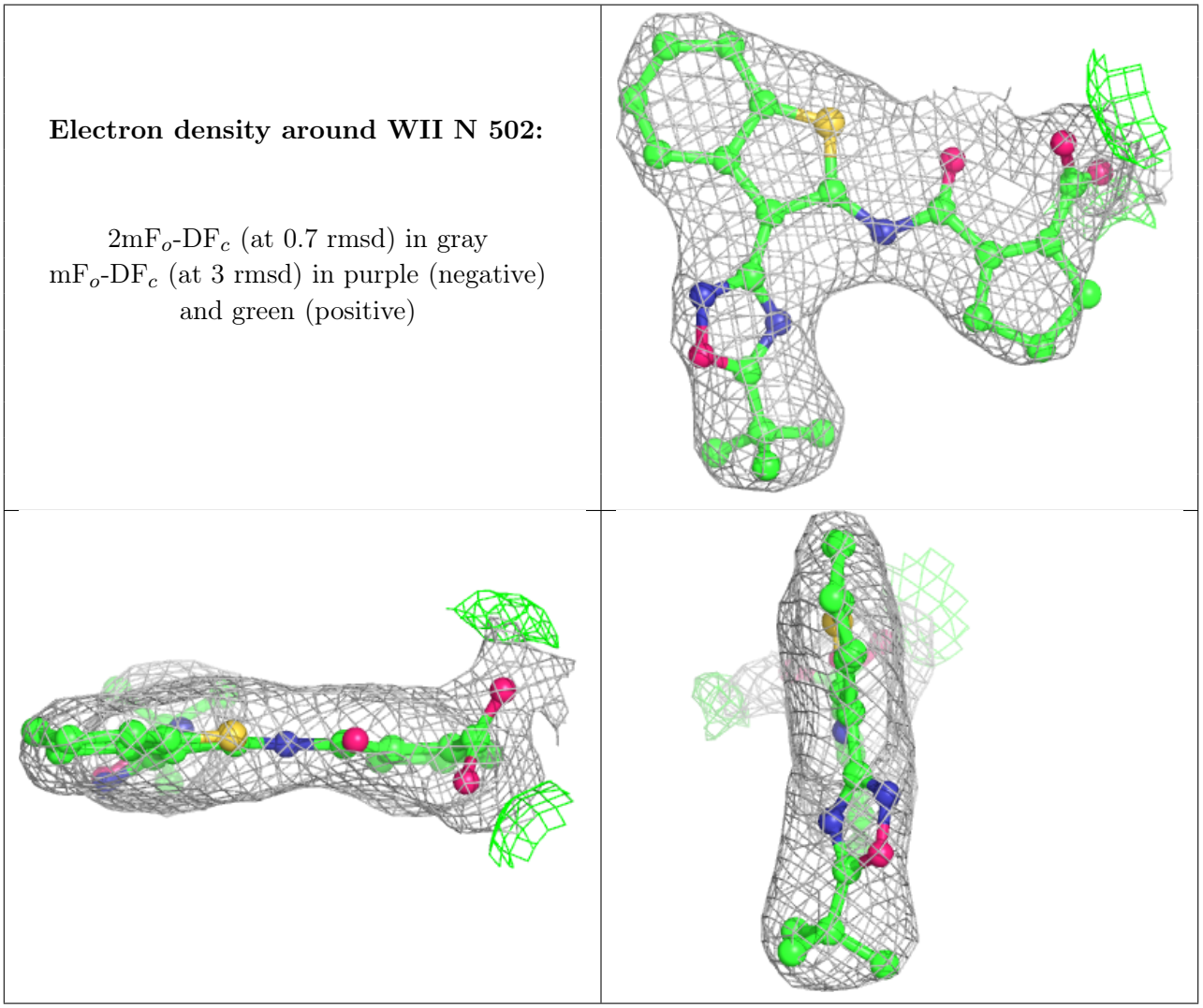
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SCN	F	501	3/3	0.98	0.10	43,43,54,74	0
3	SCN	N	501	3/3	0.98	0.16	55,55,57,63	0
3	SCN	I	501	3/3	0.98	0.15	48,48,57,59	0
3	SCN	J	202	3/3	0.98	0.22	52,52,55,66	0
3	SCN	B	203	3/3	0.99	0.19	53,53,64,77	0

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.

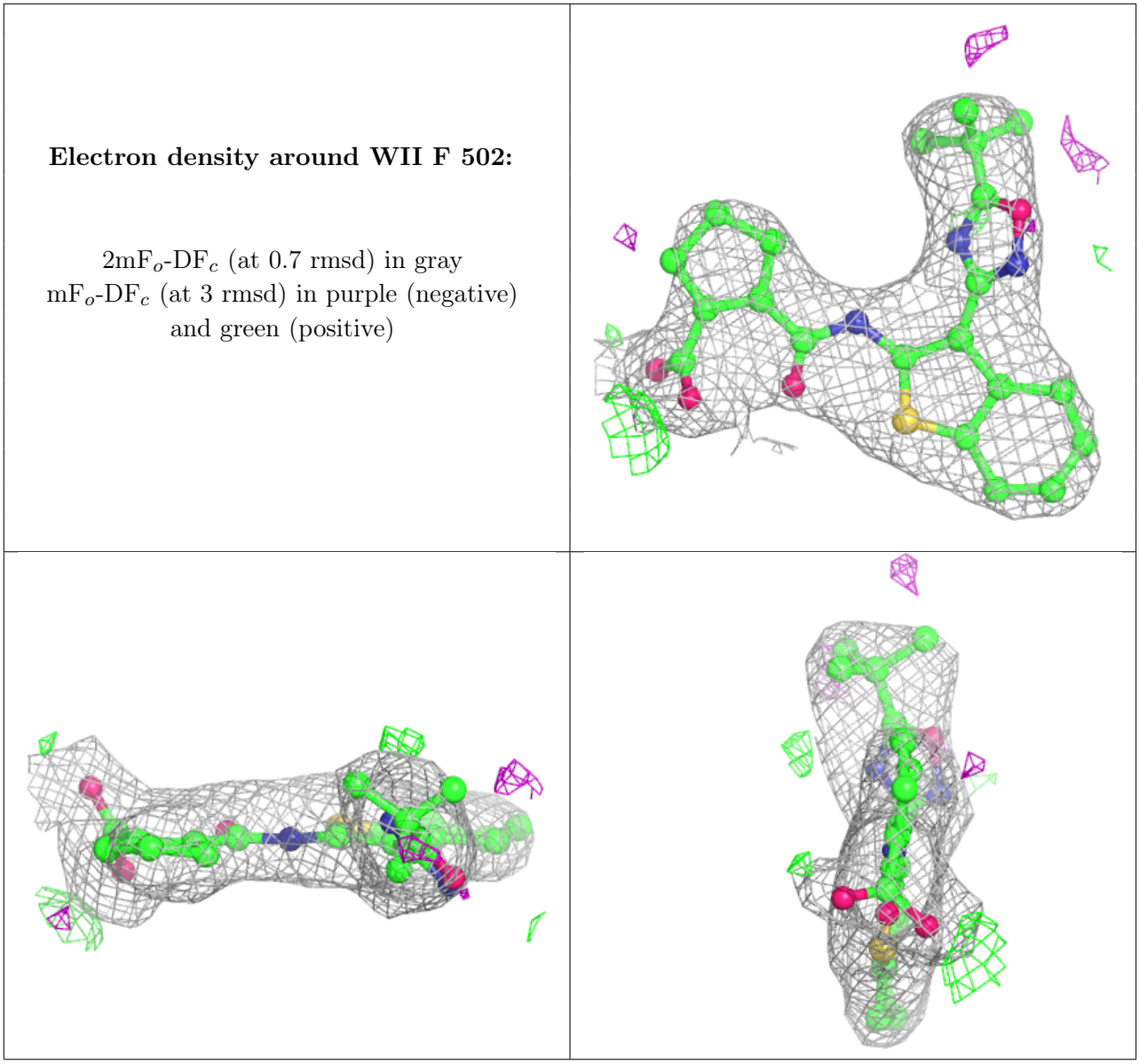
Electron density around WII N 502:

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



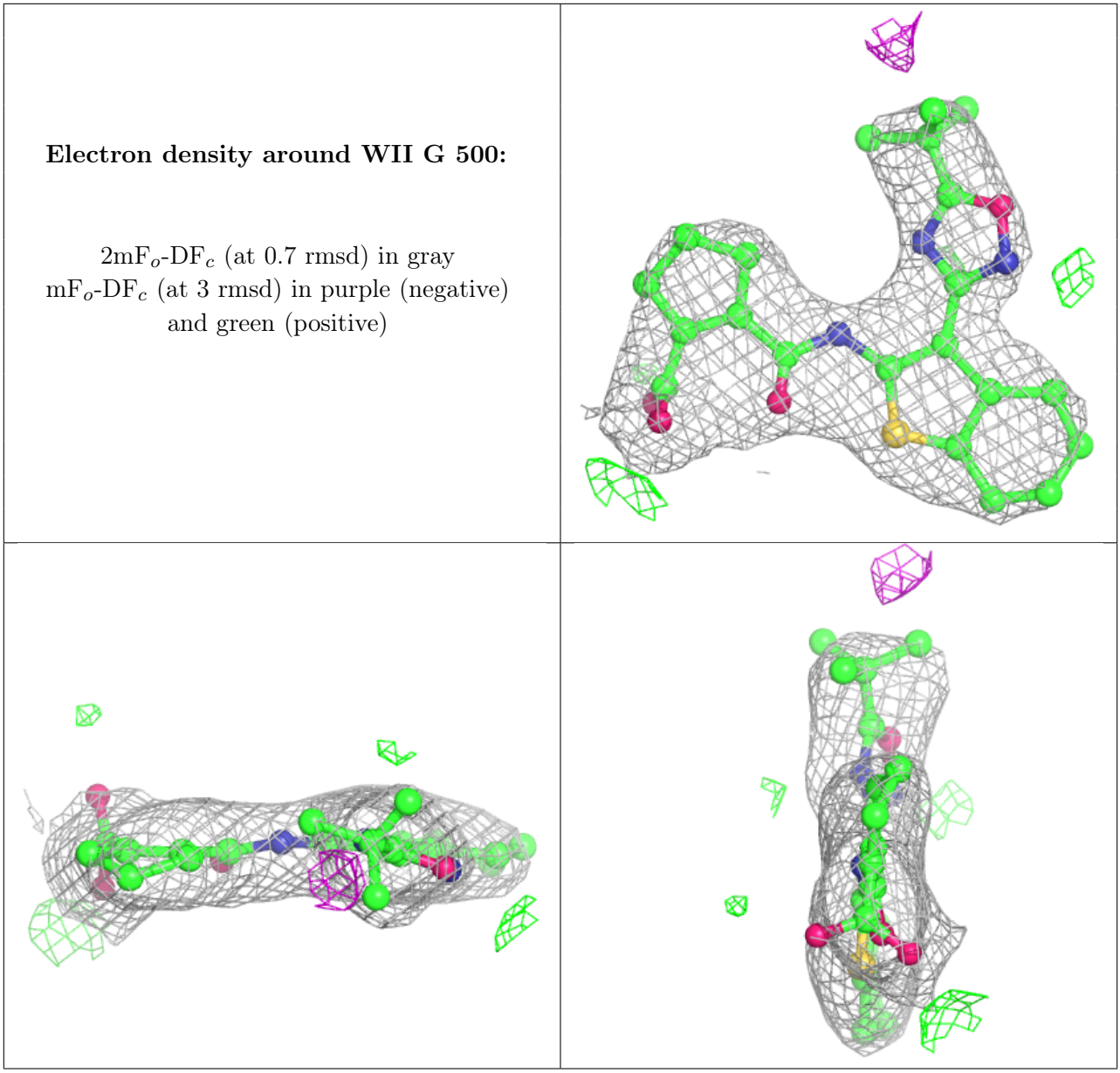
Electron density around WII F 502:

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



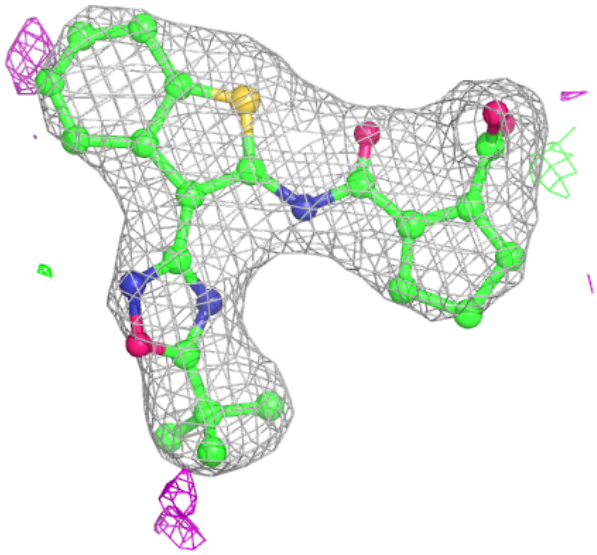
Electron density around WII G 500:

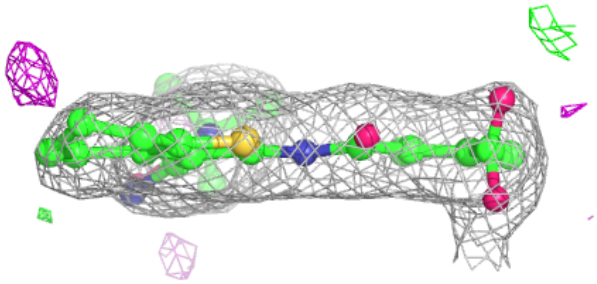
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

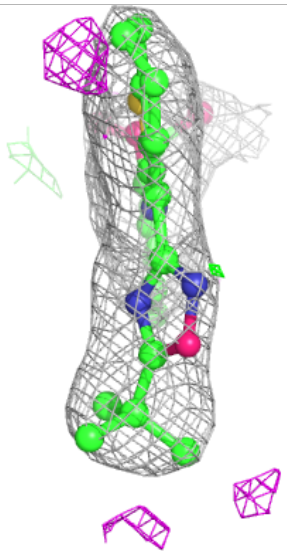


Electron density around WII C 500:

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

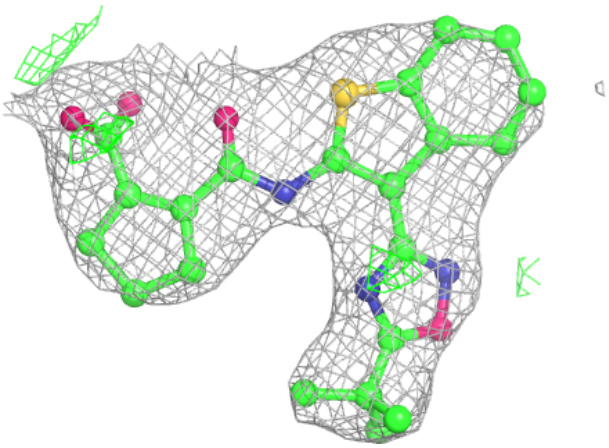


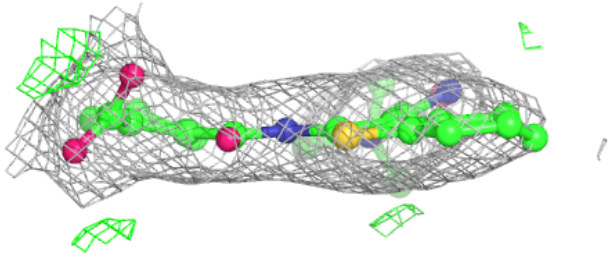


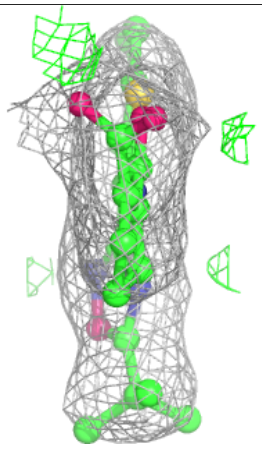


Electron density around WII D 500:

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

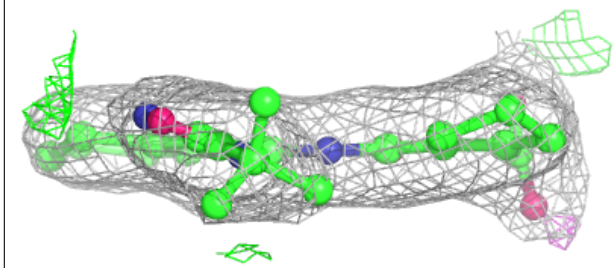


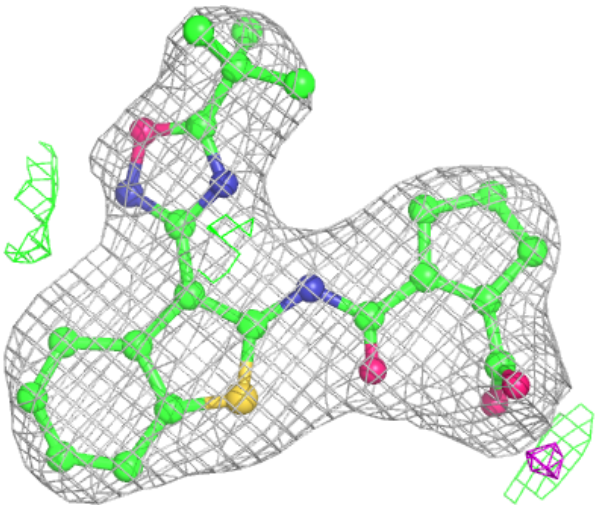




Electron density around WII H 500:

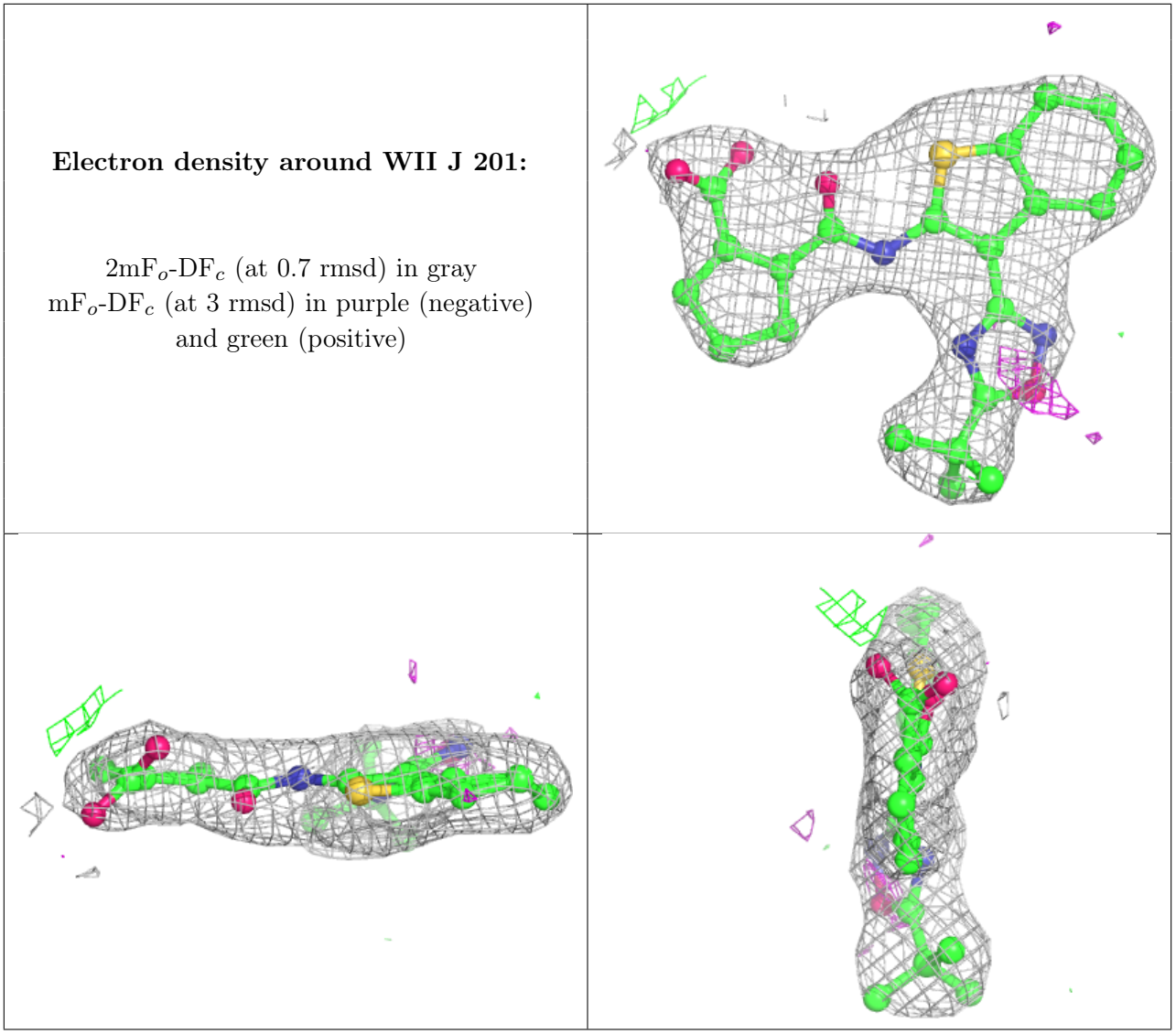
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





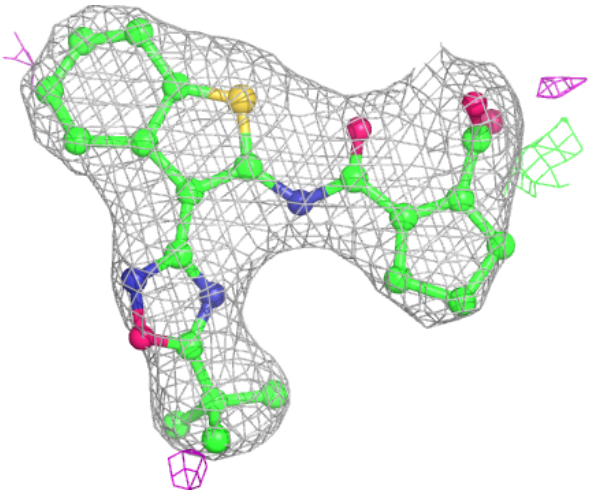
Electron density around WII J 201:

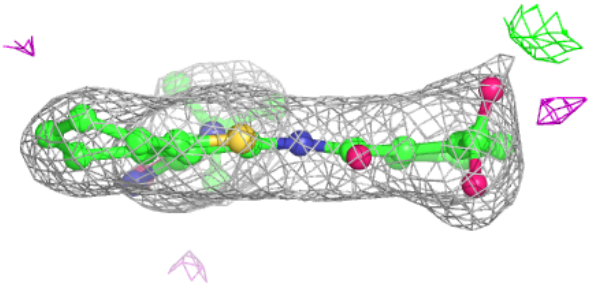
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

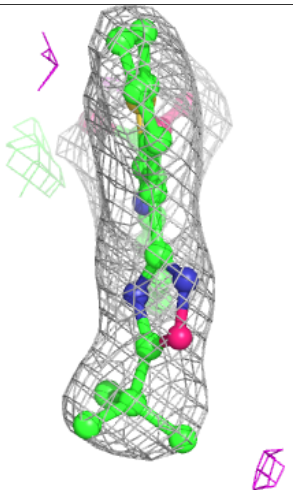


Electron density around WII K 500:

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

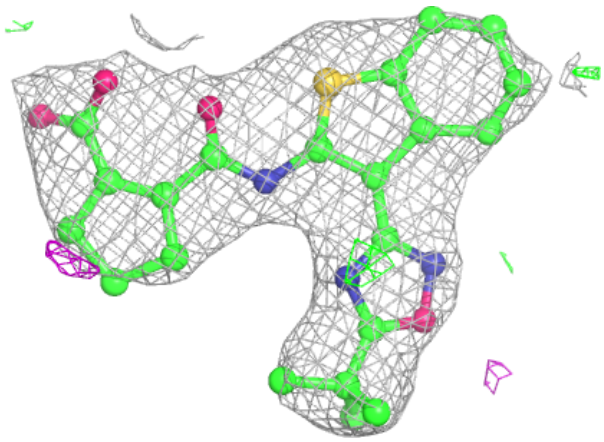


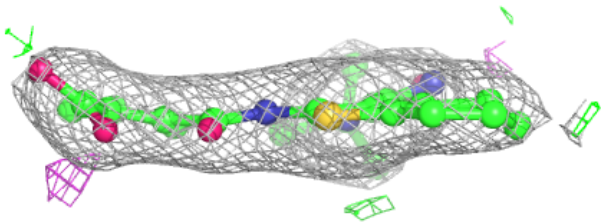


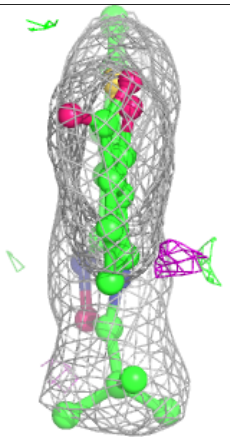


Electron density around WII L 500:

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

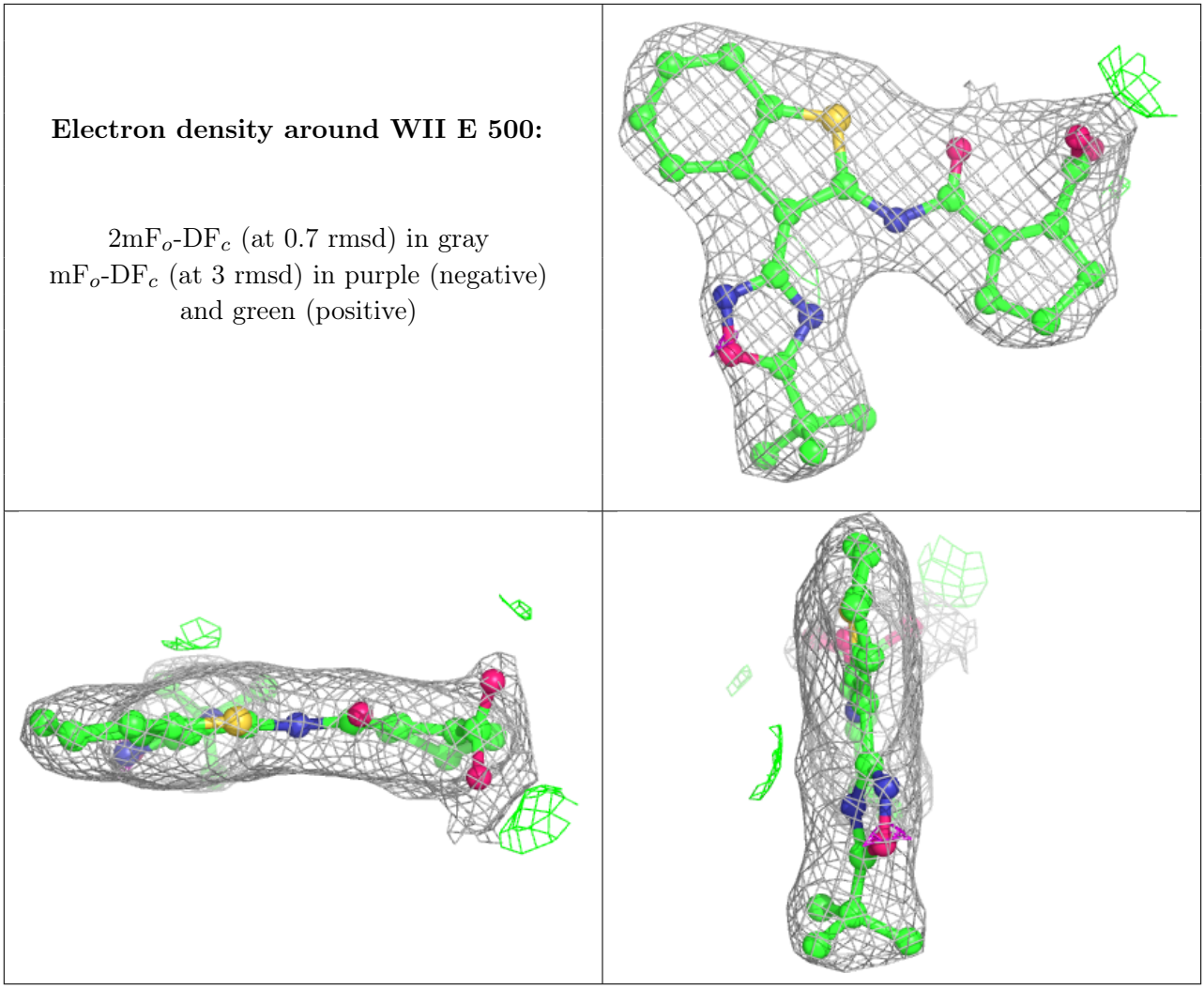






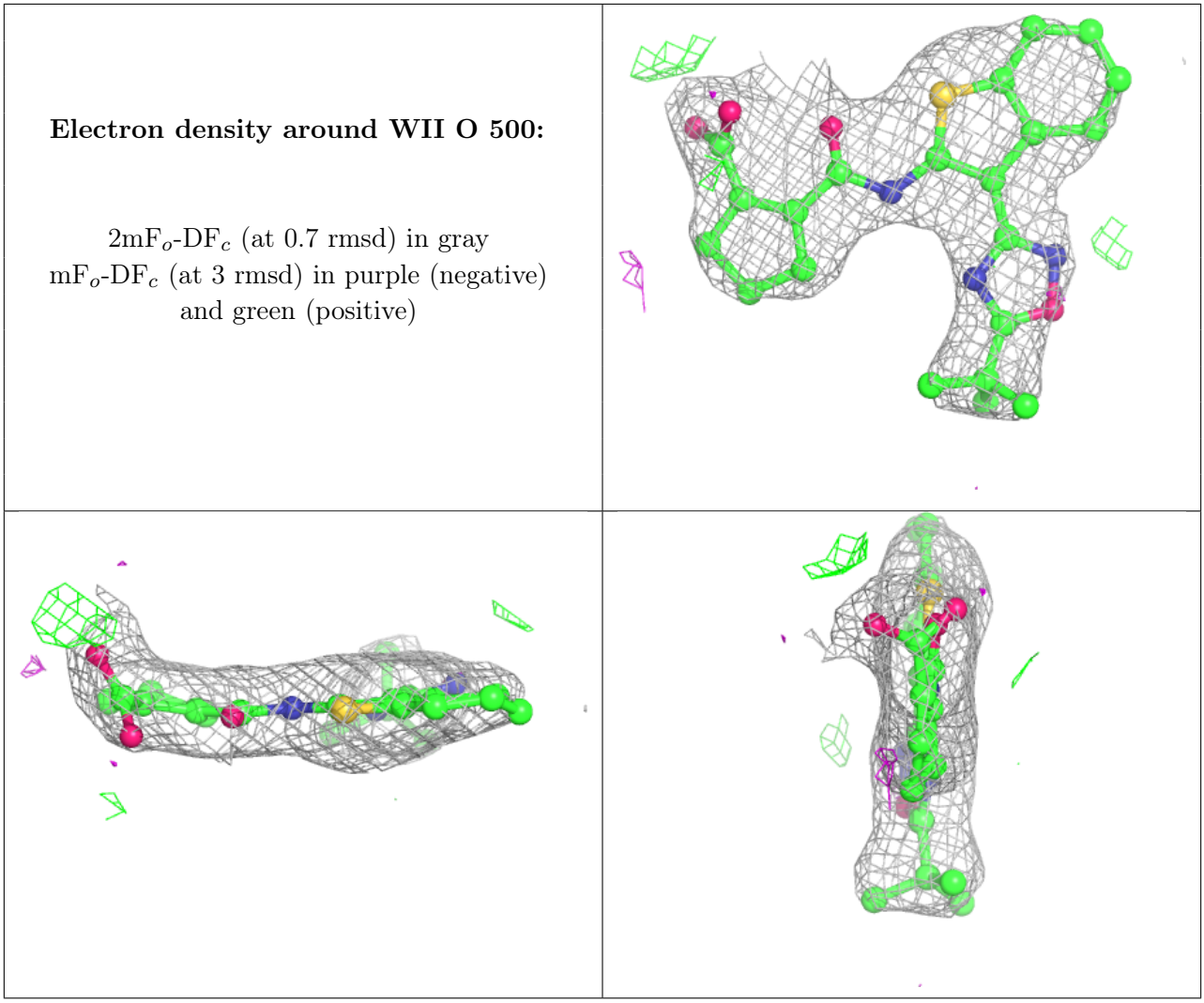
Electron density around WII E 500:

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



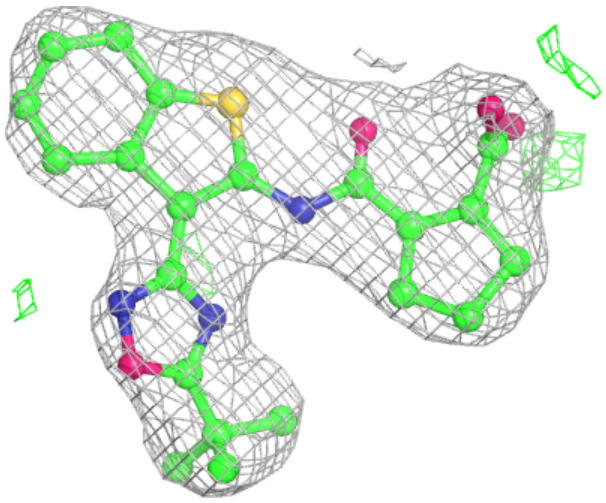
Electron density around WII O 500:

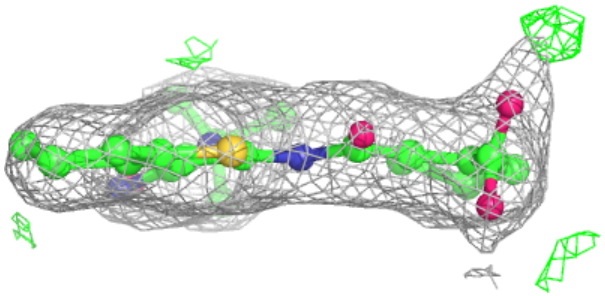
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

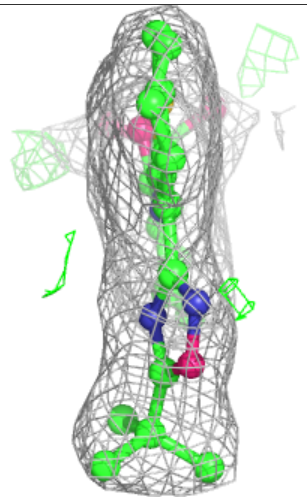


Electron density around WII M 500:

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

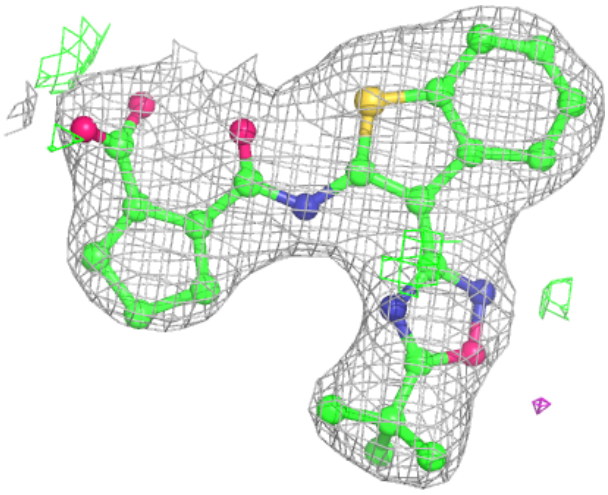


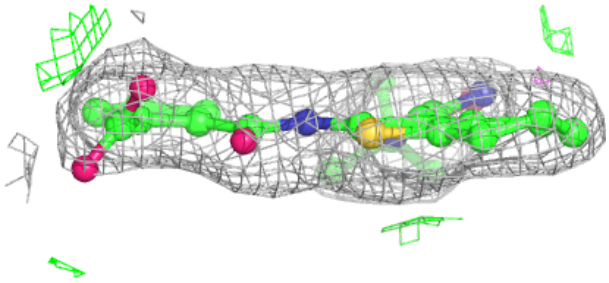


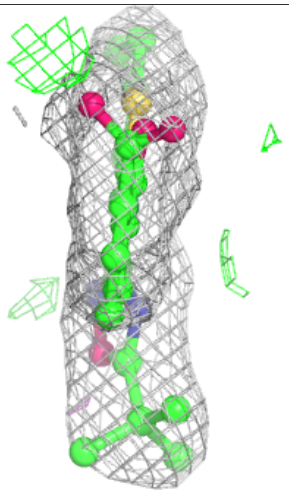


Electron density around WII B 201:

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

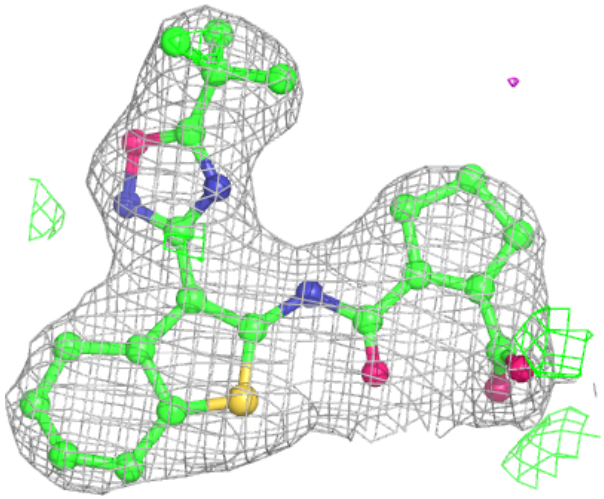


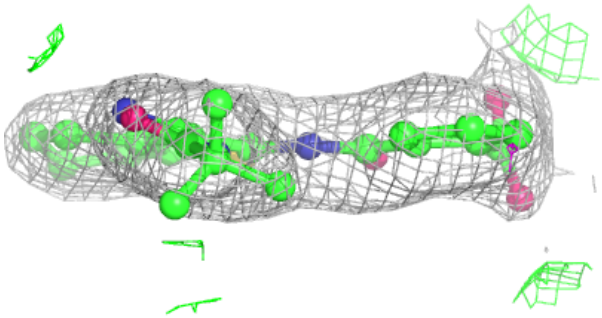


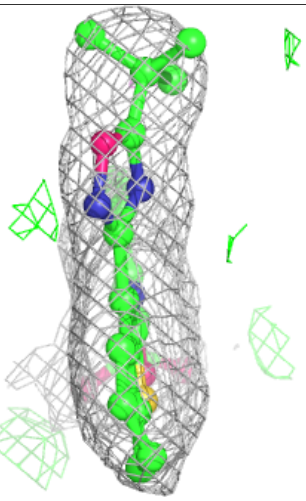


Electron density around WII A 500:

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

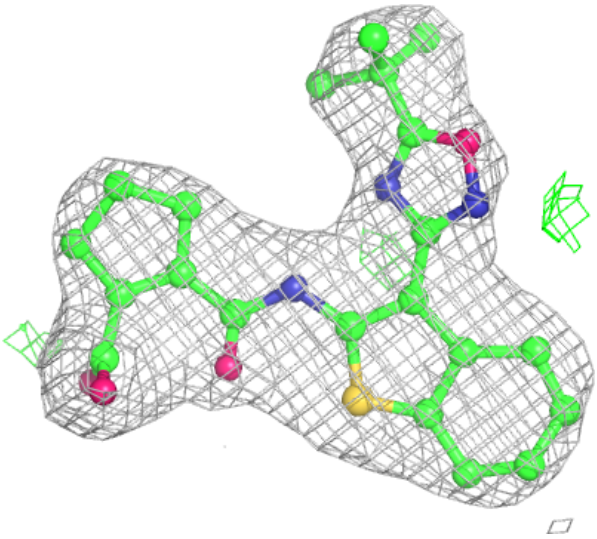


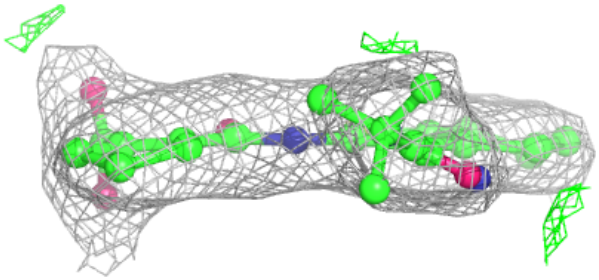


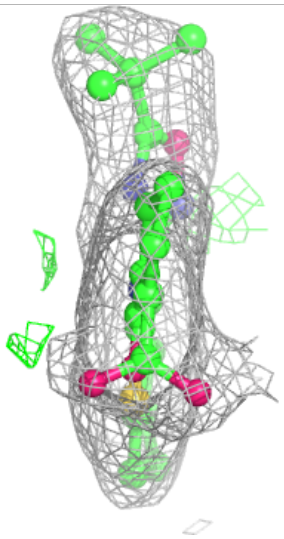


Electron density around WII P 500:

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

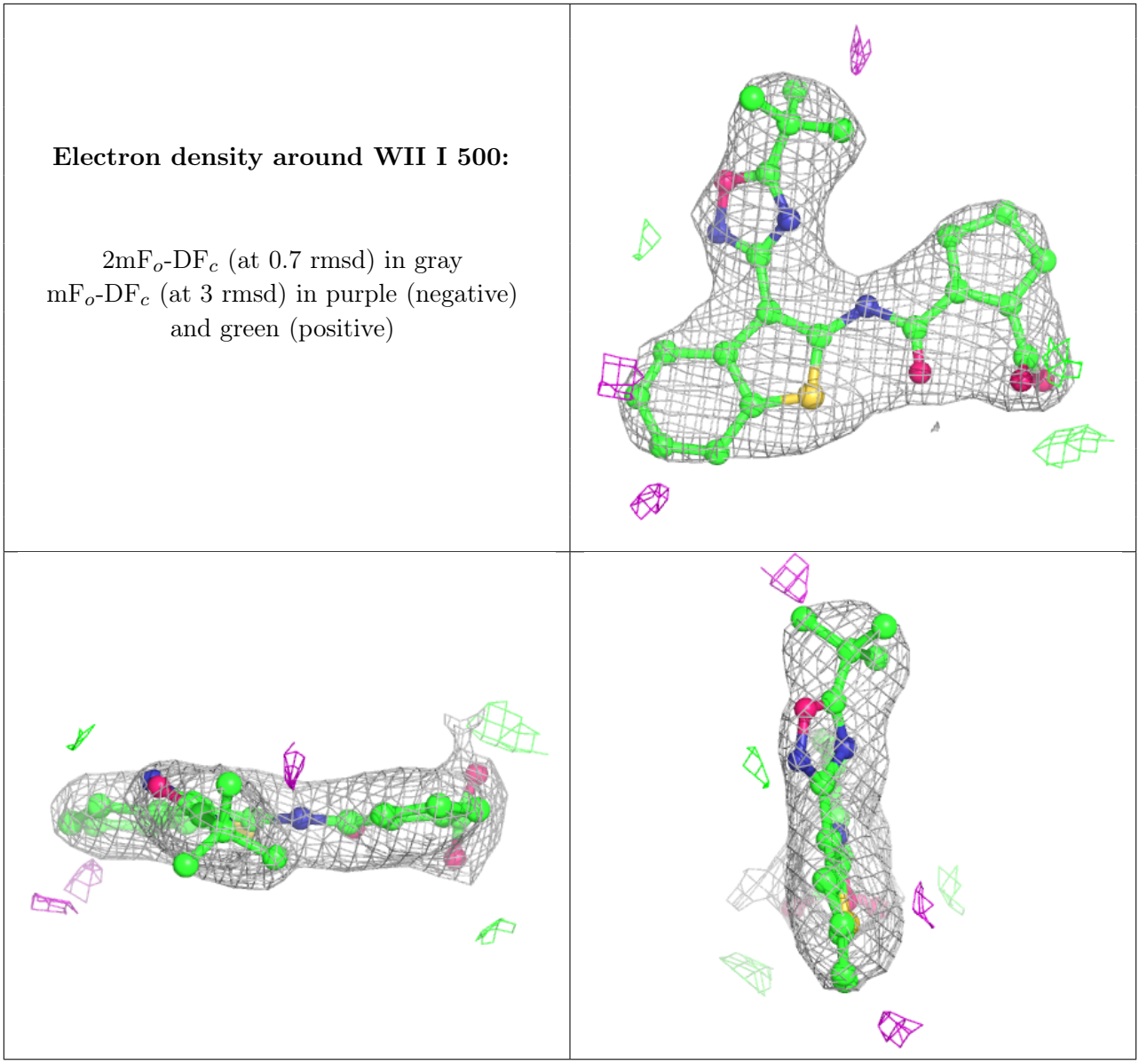






Electron density around WII I 500:

$2mF_o$-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

There are no such residues in this entry.