wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2023 – 01:46 AM EDT

PDB ID	:	6Q2A
Title	:	Trypanosoma brucei CLK1 kinase domain in complex with a covalent aminobenzimidazole inhibitor AB1
Authors	:	Ma, X.; Ornelas, E.
Deposited on	:	2019-08-07
Resolution	:	2.60 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

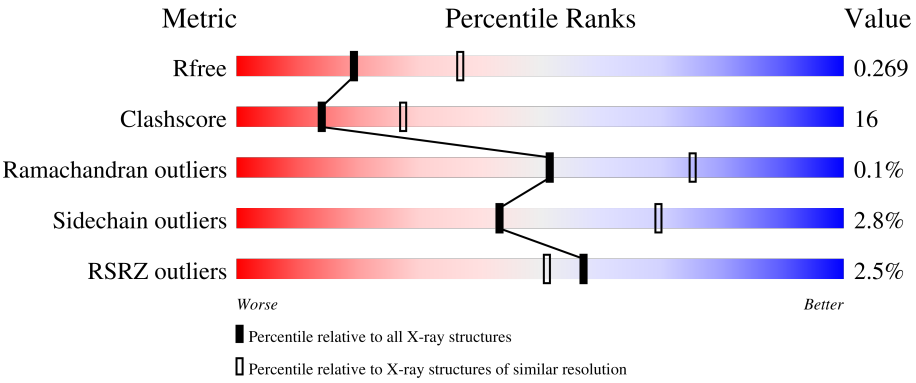
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.60 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	354	2% 63% 28%
1	B	354	% 69% 23%
1	C	354	3% 66% 26%
1	D	354	4% 71% 23%
1	E	354	% 73% 20%

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Mol	Chain	Length	Quality of chain
1	F	354	3% 68% 25%
1	G	354	2% 61% 30%
1	H	354	6% 60% 30% 5%
1	I	354	2% 68% 24%
1	J	354	% 71% 21%
1	K	354	% 72% 21%
1	L	354	% 73% 21%
1	M	354	2% 65% 27%
1	N	354	5% 63% 30%
1	O	354	4% 63% 27% 5%
1	P	354	2% 60% 32%

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
2	SO4	E	501	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 45588 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 Protein kinase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	B	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	C	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	D	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	E	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	F	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	G	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	H	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	I	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	J	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	K	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	L	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	M	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	N	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	O	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			
1	P	339	Total	C	N	O	S	0	0	0
			2772	1755	508	483	26			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	112	GLY	-	expression tag	UNP Q382U0
A	113	PRO	-	expression tag	UNP Q382U0
A	114	SER	-	expression tag	UNP Q382U0
A	115	MET	-	expression tag	UNP Q382U0
A	116	HIS	-	expression tag	UNP Q382U0
B	112	GLY	-	expression tag	UNP Q382U0
B	113	PRO	-	expression tag	UNP Q382U0
B	114	SER	-	expression tag	UNP Q382U0
B	115	MET	-	expression tag	UNP Q382U0
B	116	HIS	-	expression tag	UNP Q382U0
C	112	GLY	-	expression tag	UNP Q382U0
C	113	PRO	-	expression tag	UNP Q382U0
C	114	SER	-	expression tag	UNP Q382U0
C	115	MET	-	expression tag	UNP Q382U0
C	116	HIS	-	expression tag	UNP Q382U0
D	112	GLY	-	expression tag	UNP Q382U0
D	113	PRO	-	expression tag	UNP Q382U0
D	114	SER	-	expression tag	UNP Q382U0
D	115	MET	-	expression tag	UNP Q382U0
D	116	HIS	-	expression tag	UNP Q382U0
E	112	GLY	-	expression tag	UNP Q382U0
E	113	PRO	-	expression tag	UNP Q382U0
E	114	SER	-	expression tag	UNP Q382U0
E	115	MET	-	expression tag	UNP Q382U0
E	116	HIS	-	expression tag	UNP Q382U0
F	112	GLY	-	expression tag	UNP Q382U0
F	113	PRO	-	expression tag	UNP Q382U0
F	114	SER	-	expression tag	UNP Q382U0
F	115	MET	-	expression tag	UNP Q382U0
F	116	HIS	-	expression tag	UNP Q382U0
G	112	GLY	-	expression tag	UNP Q382U0
G	113	PRO	-	expression tag	UNP Q382U0
G	114	SER	-	expression tag	UNP Q382U0
G	115	MET	-	expression tag	UNP Q382U0
G	116	HIS	-	expression tag	UNP Q382U0
H	112	GLY	-	expression tag	UNP Q382U0
H	113	PRO	-	expression tag	UNP Q382U0
H	114	SER	-	expression tag	UNP Q382U0
H	115	MET	-	expression tag	UNP Q382U0
H	116	HIS	-	expression tag	UNP Q382U0
I	112	GLY	-	expression tag	UNP Q382U0
I	113	PRO	-	expression tag	UNP Q382U0

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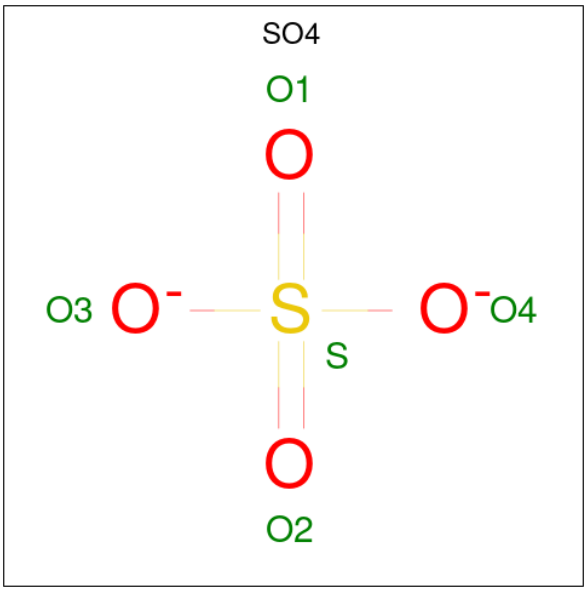
Chain	Residue	Modelled	Actual	Comment	Reference
I	114	SER	-	expression tag	UNP Q382U0
I	115	MET	-	expression tag	UNP Q382U0
I	116	HIS	-	expression tag	UNP Q382U0
J	112	GLY	-	expression tag	UNP Q382U0
J	113	PRO	-	expression tag	UNP Q382U0
J	114	SER	-	expression tag	UNP Q382U0
J	115	MET	-	expression tag	UNP Q382U0
J	116	HIS	-	expression tag	UNP Q382U0
K	112	GLY	-	expression tag	UNP Q382U0
K	113	PRO	-	expression tag	UNP Q382U0
K	114	SER	-	expression tag	UNP Q382U0
K	115	MET	-	expression tag	UNP Q382U0
K	116	HIS	-	expression tag	UNP Q382U0
L	112	GLY	-	expression tag	UNP Q382U0
L	113	PRO	-	expression tag	UNP Q382U0
L	114	SER	-	expression tag	UNP Q382U0
L	115	MET	-	expression tag	UNP Q382U0
L	116	HIS	-	expression tag	UNP Q382U0
M	112	GLY	-	expression tag	UNP Q382U0
M	113	PRO	-	expression tag	UNP Q382U0
M	114	SER	-	expression tag	UNP Q382U0
M	115	MET	-	expression tag	UNP Q382U0
M	116	HIS	-	expression tag	UNP Q382U0
N	112	GLY	-	expression tag	UNP Q382U0
N	113	PRO	-	expression tag	UNP Q382U0
N	114	SER	-	expression tag	UNP Q382U0
N	115	MET	-	expression tag	UNP Q382U0
N	116	HIS	-	expression tag	UNP Q382U0
O	112	GLY	-	expression tag	UNP Q382U0
O	113	PRO	-	expression tag	UNP Q382U0
O	114	SER	-	expression tag	UNP Q382U0
O	115	MET	-	expression tag	UNP Q382U0
O	116	HIS	-	expression tag	UNP Q382U0
P	112	GLY	-	expression tag	UNP Q382U0
P	113	PRO	-	expression tag	UNP Q382U0
P	114	SER	-	expression tag	UNP Q382U0
P	115	MET	-	expression tag	UNP Q382U0
P	116	HIS	-	expression tag	UNP Q382U0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

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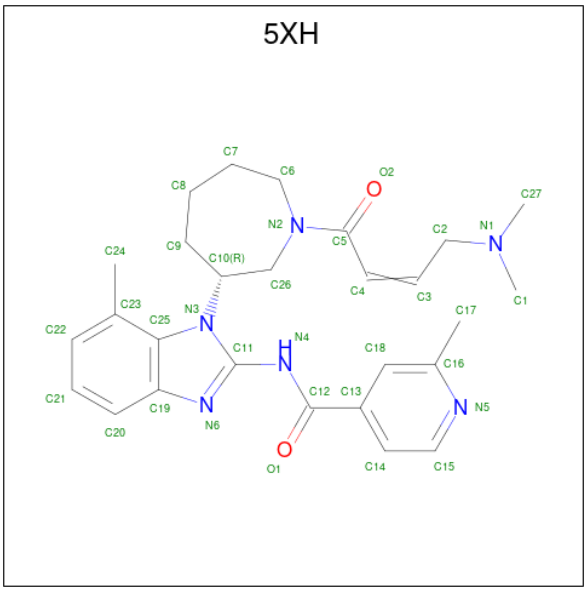
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total O S 5 4 1	0	0
2	H	1	Total O S 5 4 1	0	0
2	H	1	Total O S 5 4 1	0	0
2	I	1	Total O S 5 4 1	0	0
2	I	1	Total O S 5 4 1	0	0
2	I	1	Total O S 5 4 1	0	0
2	J	1	Total O S 5 4 1	0	0
2	J	1	Total O S 5 4 1	0	0
2	J	1	Total O S 5 4 1	0	0
2	K	1	Total O S 5 4 1	0	0
2	K	1	Total O S 5 4 1	0	0
2	L	1	Total O S 5 4 1	0	0
2	L	1	Total O S 5 4 1	0	0
2	M	1	Total O S 5 4 1	0	0
2	N	1	Total O S 5 4 1	0	0
2	O	1	Total O S 5 4 1	0	0
2	O	1	Total O S 5 4 1	0	0
2	P	1	Total O S 5 4 1	0	0
2	P	1	Total O S 5 4 1	0	0

- Molecule 3 is {N}-[1-[(3 {R})-1-[4-(dimethylamino)but-2-enoyl]azepan-3-yl]-7-methyl-benzimidazol-2-yl]-2-methyl-pyridine-4-carboxamide (three-letter code: 5XH) (formula: $C_{27}H_{34}N_6O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	35	27	6	2	0	0
3	B	1	35	27	6	2	0	0
3	C	1	35	27	6	2	0	0
3	D	1	35	27	6	2	0	0
3	E	1	35	27	6	2	0	0
3	F	1	35	27	6	2	0	0
3	G	1	35	27	6	2	0	0
3	H	1	35	27	6	2	0	0
3	I	1	35	27	6	2	0	0
3	J	1	35	27	6	2	0	0
3	K	1	35	27	6	2	0	0
3	L	1	35	27	6	2	0	0
3	M	1	35	27	6	2	0	0
3	N	1	35	27	6	2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	O	1	Total C N O 35 27 6 2	0	0
3	P	1	Total C N O 35 27 6 2	0	0

- Molecule 4 is water.

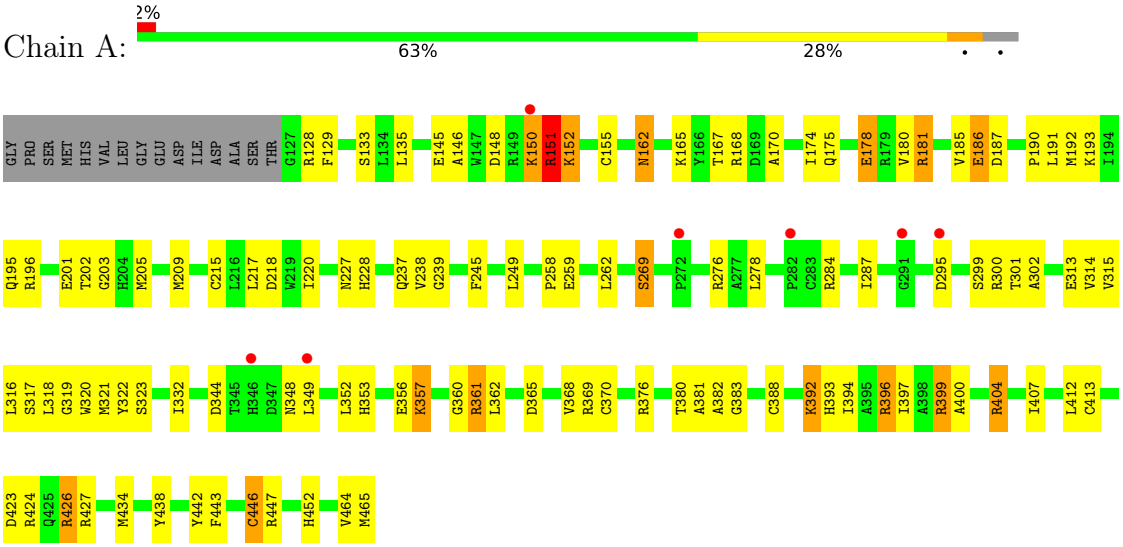
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	33	Total O 33 33	0	0
4	B	27	Total O 27 27	0	0
4	C	37	Total O 37 37	0	0
4	D	32	Total O 32 32	0	0
4	E	39	Total O 39 39	0	0
4	F	37	Total O 37 37	0	0
4	G	31	Total O 31 31	0	0
4	H	22	Total O 22 22	0	0
4	I	34	Total O 34 34	0	0
4	J	29	Total O 29 29	0	0
4	K	29	Total O 29 29	0	0
4	L	34	Total O 34 34	0	0
4	M	43	Total O 43 43	0	0
4	N	26	Total O 26 26	0	0
4	O	28	Total O 28 28	0	0
4	P	30	Total O 30 30	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

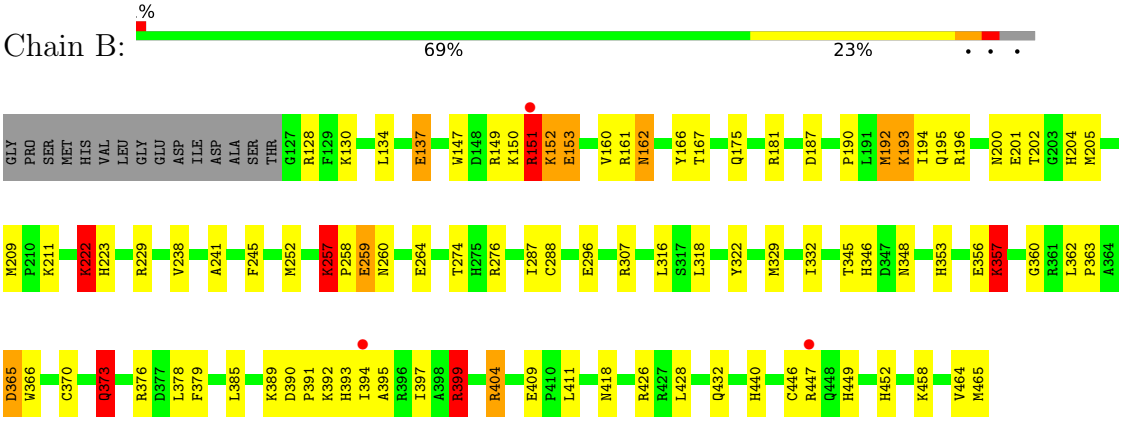
• Molecule 1: Protein kinase, putative

Chain A:



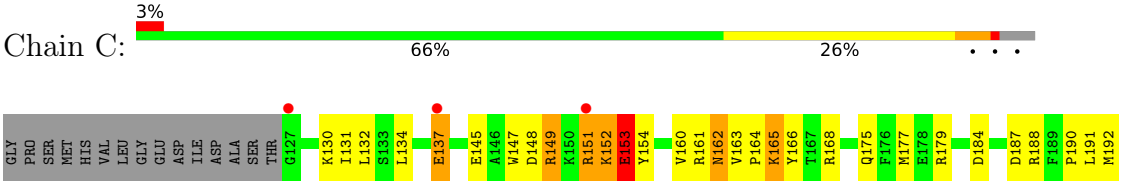
• Molecule 1: Protein kinase, putative

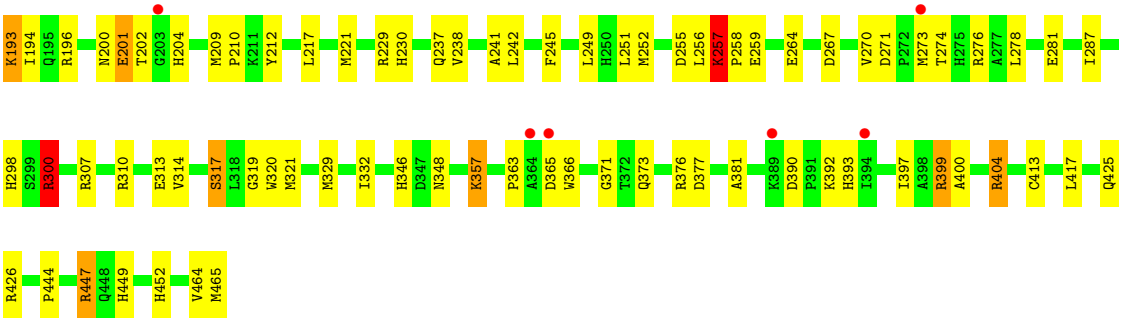
Chain B:



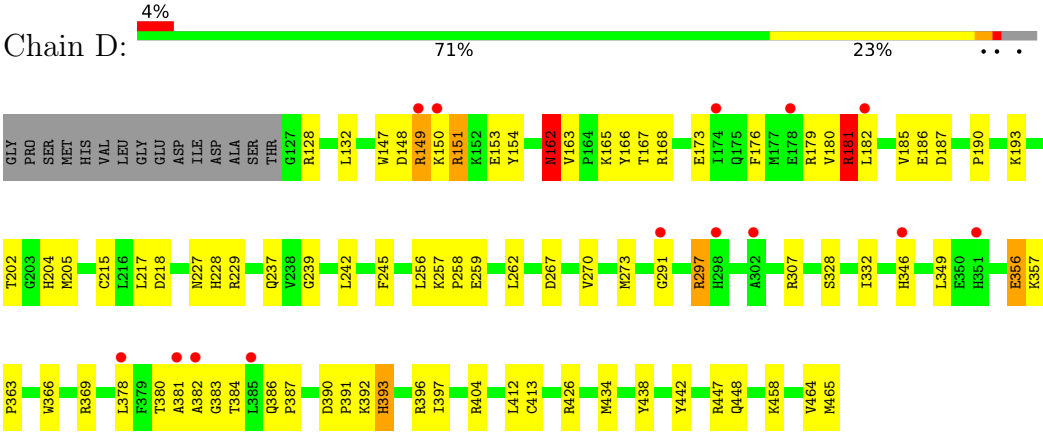
• Molecule 1: Protein kinase, putative

Chain C:

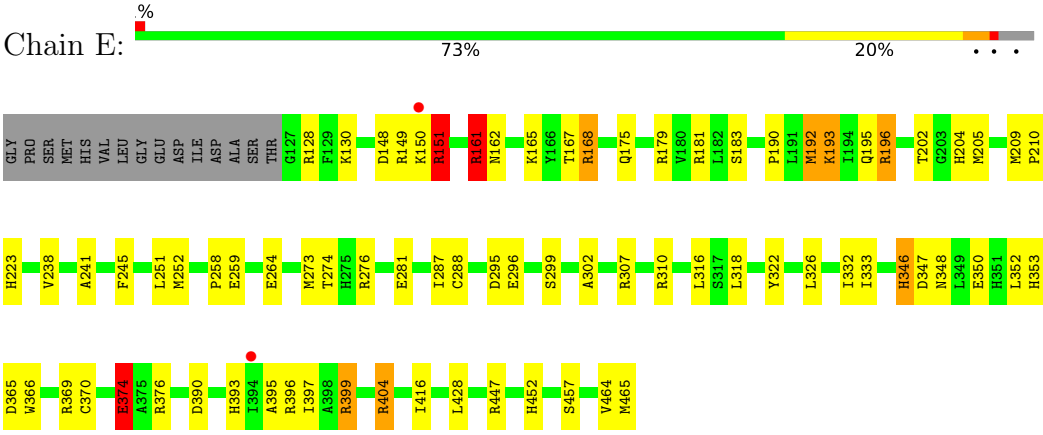




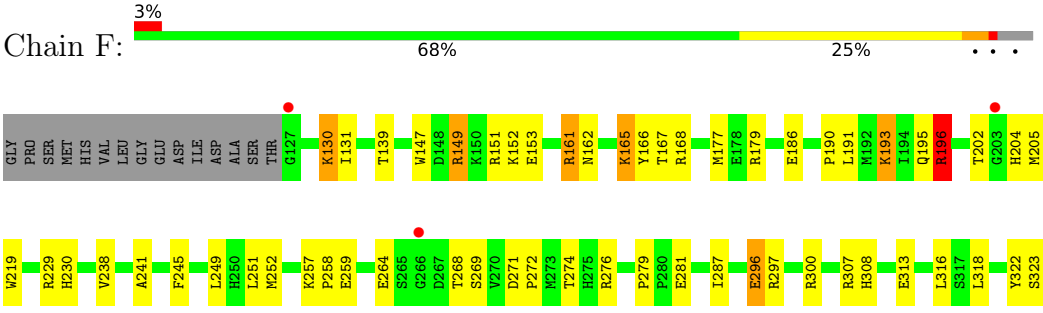
• Molecule 1: Protein kinase, putative

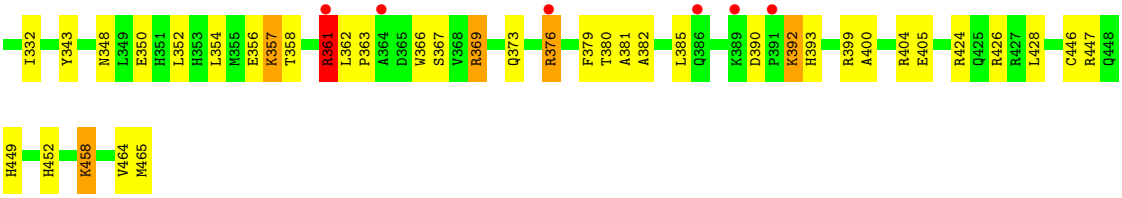


• Molecule 1: Protein kinase, putative



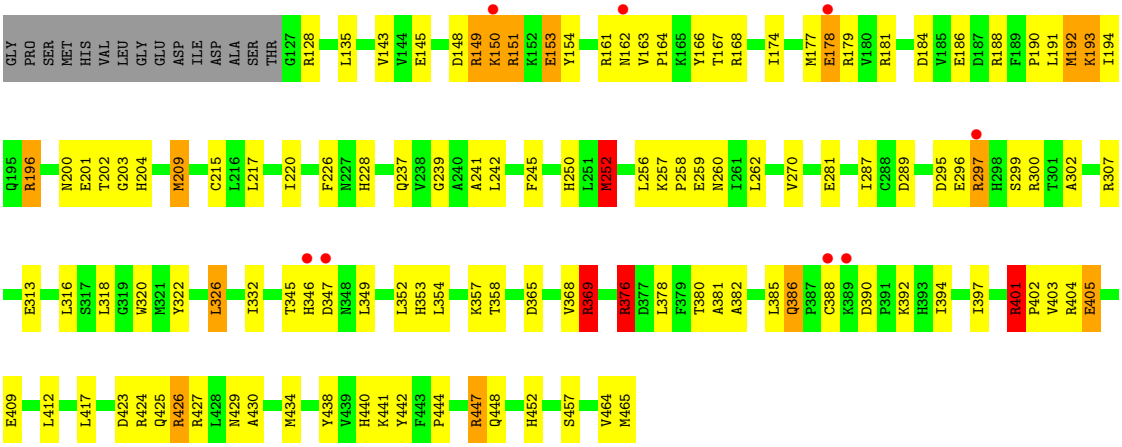
• Molecule 1: Protein kinase, putative





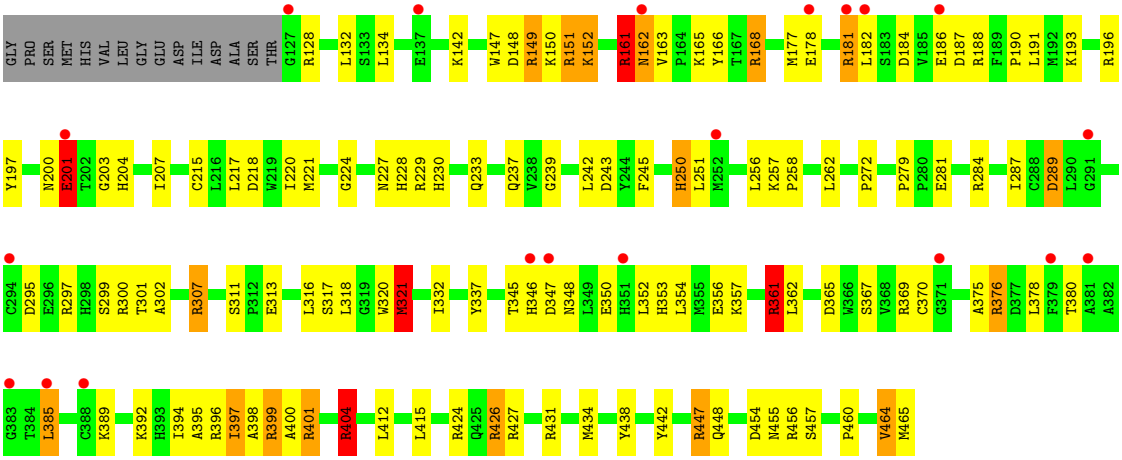
• Molecule 1: Protein kinase, putative

Chain G:



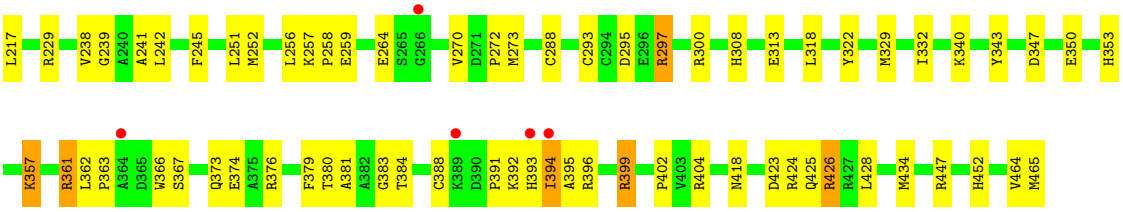
• Molecule 1: Protein kinase, putative

Chain H:



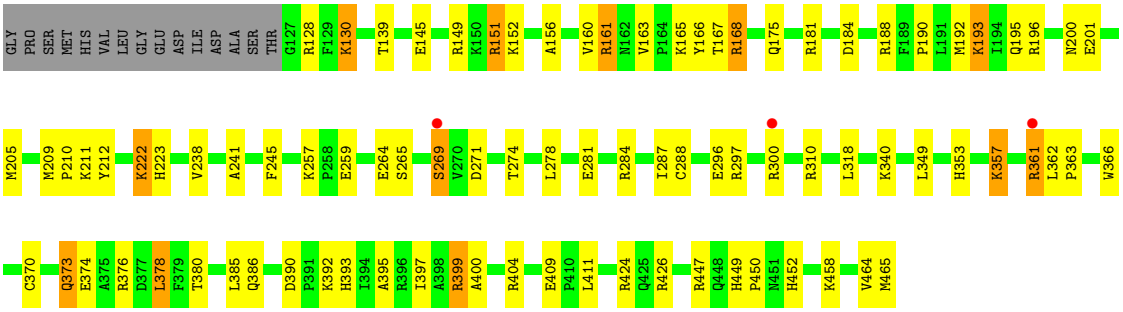
• Molecule 1: Protein kinase, putative

Chain I:



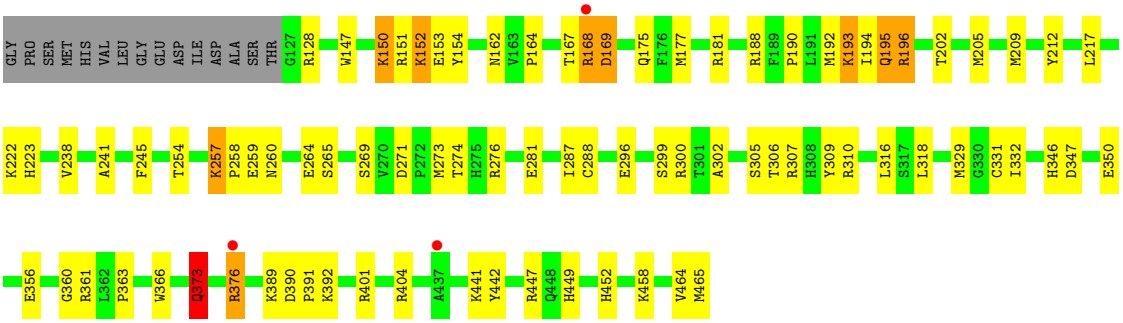
• Molecule 1: Protein kinase, putative

Chain J:



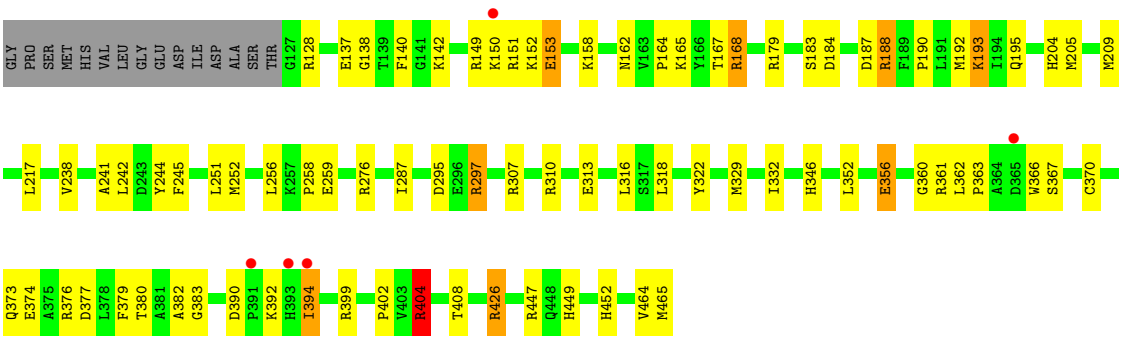
• Molecule 1: Protein kinase, putative

Chain K:



• Molecule 1: Protein kinase, putative

Chain L:

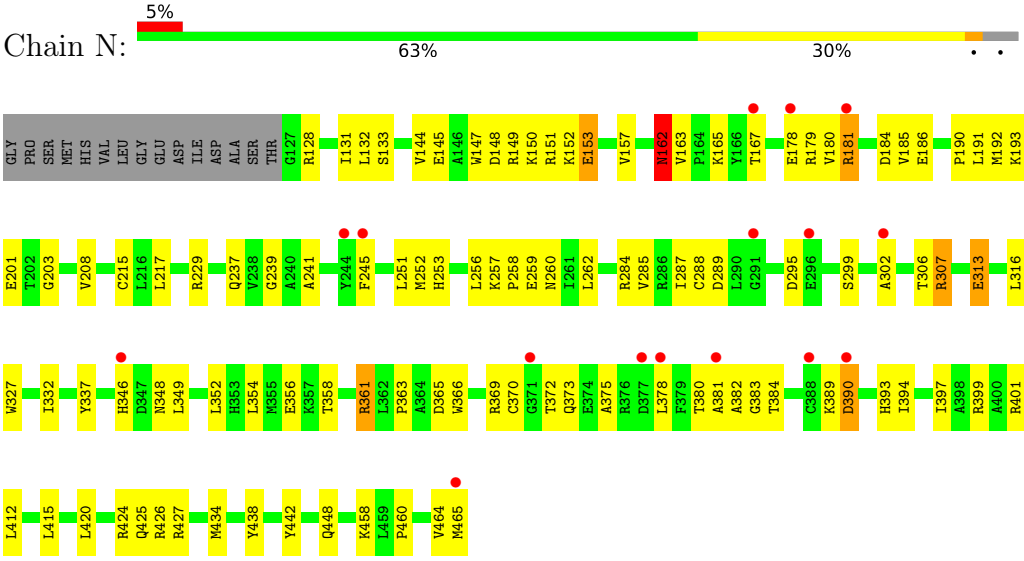


• Molecule 1: Protein kinase, putative

Chain M:

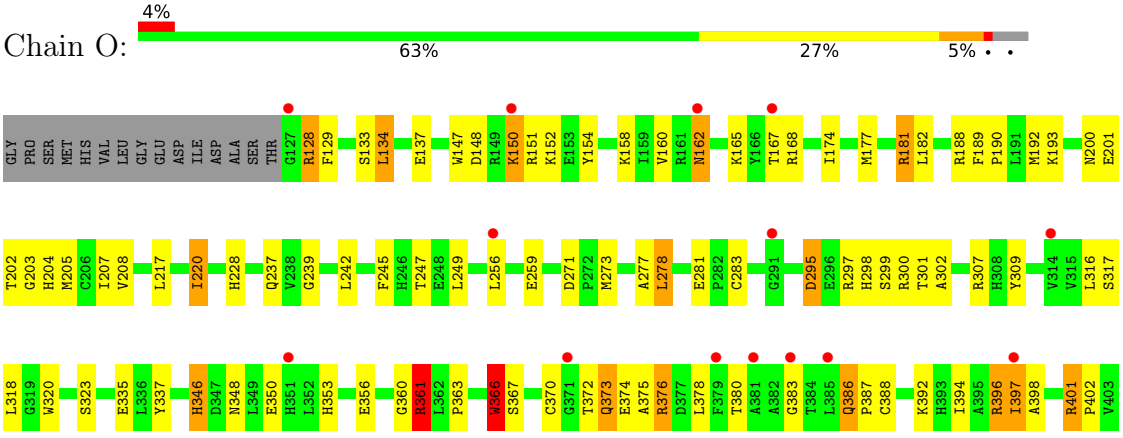
• Molecule 1: Protein kinase, putative

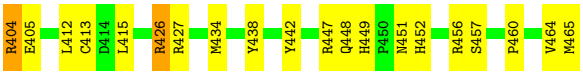
Chain N:



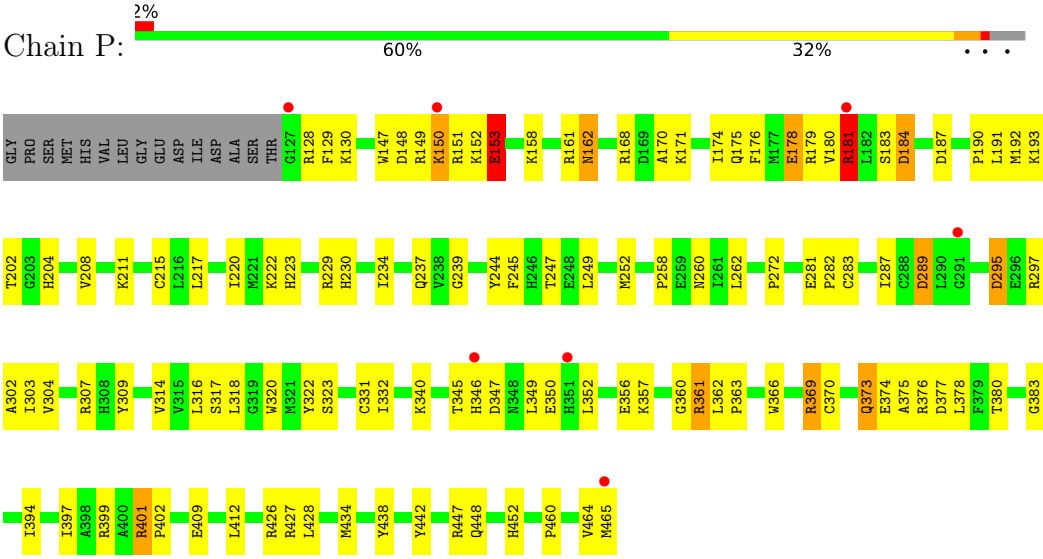
• Molecule 1: Protein kinase, putative

Chain O:





• Molecule 1: Protein kinase, putative



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	147.15Å 147.15Å 264.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.39 – 2.60 47.39 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.39-2.60) 98.7 (47.39-2.60)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.70 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.266 , 0.313 0.266 , 0.269	Depositor DCC
R_{free} test set	9696 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	38.2	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 22.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.448 for -h,-k,l 0.449 for h,-h-k,-l 0.449 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	45588	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 31.39 % 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 1.1155e-03. 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 5XH, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.50	2/2844 (0.1%)	0.99	33/3847 (0.9%)
1	B	0.55	7/2844 (0.2%)	0.88	19/3847 (0.5%)
1	C	0.62	7/2844 (0.2%)	1.19	38/3847 (1.0%)
1	D	0.44	1/2844 (0.0%)	0.77	16/3847 (0.4%)
1	E	0.44	2/2844 (0.1%)	0.82	20/3847 (0.5%)
1	F	0.48	3/2844 (0.1%)	1.02	32/3847 (0.8%)
1	G	0.56	2/2844 (0.1%)	1.07	36/3847 (0.9%)
1	H	0.56	1/2844 (0.0%)	1.17	45/3847 (1.2%)
1	I	0.46	2/2844 (0.1%)	0.83	22/3847 (0.6%)
1	J	0.57	5/2844 (0.2%)	1.06	34/3847 (0.9%)
1	K	0.50	4/2844 (0.1%)	0.81	16/3847 (0.4%)
1	L	0.50	2/2844 (0.1%)	0.94	21/3847 (0.5%)
1	M	0.52	5/2844 (0.2%)	0.89	22/3847 (0.6%)
1	N	0.53	2/2844 (0.1%)	0.92	21/3847 (0.5%)
1	O	0.60	5/2844 (0.2%)	0.93	19/3847 (0.5%)
1	P	0.51	2/2844 (0.1%)	0.89	17/3847 (0.4%)
All	All	0.52	52/45504 (0.1%)	0.96	411/61552 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	1
1	D	0	1
1	E	0	2
1	F	0	1
1	G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	3
1	I	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	2
1	P	0	3
All	All	0	23

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	150	LYS	CD-CE	-10.51	1.25	1.51
1	J	404	ARG	CB-CG	-8.83	1.28	1.52
1	J	361	ARG	CB-CG	-8.67	1.29	1.52
1	N	402	PRO	N-CD	-8.03	1.36	1.47
1	B	259	GLU	CD-OE1	7.92	1.34	1.25

The worst 5 of 411 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	404	ARG	NE-CZ-NH2	-24.96	107.82	120.30
1	C	300	ARG	NE-CZ-NH1	24.11	132.36	120.30
1	F	196	ARG	NE-CZ-NH2	-21.71	109.45	120.30
1	B	399	ARG	NE-CZ-NH2	-19.63	110.49	120.30
1	C	300	ARG	CG-CD-NE	-19.26	71.36	111.80

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	151	ARG	Peptide
1	A	162	ASN	Sidechain
1	B	373	GLN	Sidechain
1	B	399	ARG	Sidechain
1	C	300	ARG	Sidechain

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	2772	0	2765	101	4
1	B	2772	0	2767	74	0
1	C	2772	0	2767	102	4
1	D	2772	0	2767	67	0
1	E	2772	0	2767	65	0
1	F	2772	0	2767	83	0
1	G	2772	0	2767	95	0
1	H	2772	0	2767	118	0
1	I	2772	0	2767	91	0
1	J	2772	0	2766	67	3
1	K	2772	0	2767	87	1
1	L	2772	0	2767	67	0
1	M	2772	0	2767	89	1
1	N	2772	0	2765	110	0
1	O	2772	0	2767	120	3
1	P	2772	0	2767	134	0
2	A	5	0	0	0	0
2	B	15	0	0	1	0
2	C	15	0	0	1	0
2	D	5	0	0	0	0
2	E	15	0	0	3	0
2	F	15	0	0	1	0
2	G	5	0	0	1	0
2	H	10	0	0	2	0
2	I	15	0	0	0	0
2	J	15	0	0	0	0
2	K	10	0	0	1	0
2	L	10	0	0	1	0
2	M	5	0	0	1	0
2	N	5	0	0	0	0
2	O	10	0	0	1	0
2	P	10	0	0	0	0
3	A	35	0	0	2	0
3	B	35	0	0	0	0
3	C	35	0	0	0	0
3	D	35	0	0	1	0
3	E	35	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	35	0	0	0	0
3	G	35	0	0	0	0
3	H	35	0	0	1	0
3	I	35	0	0	0	0
3	J	35	0	0	0	0
3	K	35	0	0	0	0
3	L	35	0	0	0	0
3	M	35	0	0	0	0
3	N	35	0	0	0	0
3	O	35	0	0	0	0
3	P	35	0	0	0	0
4	A	33	0	0	7	0
4	B	27	0	0	0	0
4	C	37	0	0	7	0
4	D	32	0	0	2	0
4	E	39	0	0	5	0
4	F	37	0	0	5	0
4	G	31	0	0	2	0
4	H	22	0	0	6	0
4	I	34	0	0	6	0
4	J	29	0	0	3	0
4	K	29	0	0	3	0
4	L	34	0	0	8	0
4	M	43	0	0	8	0
4	N	26	0	0	3	0
4	O	28	0	0	4	0
4	P	30	0	0	11	0
All	All	45588	0	44267	1403	8

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 16.

The worst 5 of 1403 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:193:LYS:CE	1:L:193:LYS:NZ	1.68	1.52
1:N:307:ARG:NH2	1:N:346:HIS:CD2	2.08	1.22
1:B:151:ARG:HG2	1:B:153:GLU:OE1	1.40	1.21
1:K:151:ARG:HB2	1:K:153:GLU:OE2	1.43	1.18
1:N:402:PRO:HD2	1:N:405:GLU:CD	1.65	1.17

The worst 5 of 8 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:361:ARG:NH1	1:O:361:ARG:NH1[1_455]	1.32	0.88
1:A:404:ARG:NH1	1:C:404:ARG:NE[1_445]	1.80	0.40
1:A:404:ARG:NE	1:C:404:ARG:NH2[1_445]	1.98	0.22
1:A:404:ARG:NH1	1:C:404:ARG:NH2[1_445]	2.05	0.15
1:K:168:ARG:NH2	1:M:377:ASP:OD2[2_445]	2.06	0.14

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	337/354 (95%)	330 (98%)	7 (2%)	0	100	100
1	B	337/354 (95%)	326 (97%)	11 (3%)	0	100	100
1	C	337/354 (95%)	326 (97%)	10 (3%)	1 (0%)	41	64
1	D	337/354 (95%)	328 (97%)	9 (3%)	0	100	100
1	E	337/354 (95%)	325 (96%)	12 (4%)	0	100	100
1	F	337/354 (95%)	328 (97%)	9 (3%)	0	100	100
1	G	337/354 (95%)	324 (96%)	12 (4%)	1 (0%)	41	64
1	H	337/354 (95%)	324 (96%)	11 (3%)	2 (1%)	25	47
1	I	337/354 (95%)	328 (97%)	9 (3%)	0	100	100
1	J	337/354 (95%)	326 (97%)	11 (3%)	0	100	100
1	K	337/354 (95%)	327 (97%)	10 (3%)	0	100	100
1	L	337/354 (95%)	326 (97%)	11 (3%)	0	100	100
1	M	337/354 (95%)	328 (97%)	9 (3%)	0	100	100
1	N	337/354 (95%)	326 (97%)	11 (3%)	0	100	100
1	O	337/354 (95%)	326 (97%)	11 (3%)	0	100	100
1	P	337/354 (95%)	325 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	5392/5664 (95%)	5223 (97%)	165 (3%)	4 (0%)	51 75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	457	SER
1	C	153	GLU
1	H	457	SER
1	H	321	MET

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	305/317 (96%)	297 (97%)	8 (3%)	46 72
1	B	305/317 (96%)	293 (96%)	12 (4%)	32 58
1	C	305/317 (96%)	299 (98%)	6 (2%)	55 78
1	D	305/317 (96%)	296 (97%)	9 (3%)	41 67
1	E	305/317 (96%)	293 (96%)	12 (4%)	32 58
1	F	305/317 (96%)	297 (97%)	8 (3%)	46 72
1	G	305/317 (96%)	294 (96%)	11 (4%)	35 61
1	H	305/317 (96%)	298 (98%)	7 (2%)	50 75
1	I	305/317 (96%)	301 (99%)	4 (1%)	69 86
1	J	305/317 (96%)	300 (98%)	5 (2%)	62 82
1	K	305/317 (96%)	296 (97%)	9 (3%)	41 67
1	L	305/317 (96%)	300 (98%)	5 (2%)	62 82
1	M	305/317 (96%)	294 (96%)	11 (4%)	35 61
1	N	305/317 (96%)	298 (98%)	7 (2%)	50 75
1	O	305/317 (96%)	294 (96%)	11 (4%)	35 61
1	P	305/317 (96%)	295 (97%)	10 (3%)	38 64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4880/5072 (96%)	4745 (97%)	135 (3%)	43 69

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	168	ARG
1	O	361	ARG
1	P	297	ARG
1	F	245	PHE
1	F	193	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	455	ASN
1	P	373	GLN
1	M	195	GLN
1	N	237	GLN
1	F	393	HIS

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)

49 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	5XH	F	504	1	31,38,38	1.55	2 (6%)	35,53,53	1.40	1 (2%)
2	SO4	P	501	-	4,4,4	0.40	0	6,6,6	0.24	0
3	5XH	A	501	1	31,38,38	1.55	2 (6%)	35,53,53	1.39	1 (2%)
3	5XH	I	504	1	31,38,38	1.56	2 (6%)	35,53,53	1.40	1 (2%)
2	SO4	P	502	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	F	502	-	4,4,4	0.15	0	6,6,6	0.17	0
2	SO4	E	503	-	4,4,4	0.14	0	6,6,6	0.06	0
3	5XH	C	504	1	31,38,38	1.54	2 (6%)	35,53,53	1.67	1 (2%)
3	5XH	K	503	1	31,38,38	1.54	2 (6%)	35,53,53	1.41	1 (2%)
2	SO4	F	501	-	4,4,4	0.15	0	6,6,6	0.14	0
2	SO4	A	500	-	4,4,4	0.13	0	6,6,6	0.08	0
2	SO4	G	500	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	D	500	-	4,4,4	0.13	0	6,6,6	0.09	0
2	SO4	I	501	-	4,4,4	0.15	0	6,6,6	0.04	0
2	SO4	K	502	-	4,4,4	0.17	0	6,6,6	0.08	0
2	SO4	L	502	-	4,4,4	0.16	0	6,6,6	0.06	0
2	SO4	K	501	-	4,4,4	0.14	0	6,6,6	0.12	0
2	SO4	J	503	-	4,4,4	0.16	0	6,6,6	0.09	0
2	SO4	C	501	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	I	502	-	4,4,4	0.14	0	6,6,6	0.09	0
2	SO4	L	501	-	4,4,4	0.13	0	6,6,6	0.10	0
3	5XH	B	504	1	31,38,38	1.55	2 (6%)	35,53,53	1.39	1 (2%)
3	5XH	N	501	1	31,38,38	1.55	2 (6%)	35,53,53	1.38	1 (2%)
3	5XH	P	503	1	31,38,38	1.55	2 (6%)	35,53,53	1.41	1 (2%)
3	5XH	J	504	1	31,38,38	1.56	2 (6%)	35,53,53	1.40	1 (2%)
2	SO4	B	502	-	4,4,4	0.15	0	6,6,6	0.16	0
2	SO4	C	502	-	4,4,4	0.15	0	6,6,6	0.16	0
3	5XH	G	501	1	31,38,38	1.55	2 (6%)	35,53,53	1.42	1 (2%)
2	SO4	O	502	-	4,4,4	0.15	0	6,6,6	0.06	0
3	5XH	L	503	1	31,38,38	1.53	2 (6%)	35,53,53	1.36	1 (2%)
2	SO4	H	502	-	4,4,4	0.15	0	6,6,6	0.06	0
2	SO4	B	503	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	B	501	-	4,4,4	0.13	0	6,6,6	0.07	0
2	SO4	E	501	-	4,4,4	0.23	0	6,6,6	0.37	0
2	SO4	H	501	-	4,4,4	0.30	0	6,6,6	1.50	1 (16%)
2	SO4	N	500	-	4,4,4	0.14	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	5XH	M	501	1	31,38,38	1.55	2 (6%)	35,53,53	1.39	1 (2%)
2	SO4	E	502	-	4,4,4	0.14	0	6,6,6	0.20	0
2	SO4	M	500	-	4,4,4	0.14	0	6,6,6	0.06	0
2	SO4	F	503	-	4,4,4	0.13	0	6,6,6	0.07	0
2	SO4	J	501	-	4,4,4	0.15	0	6,6,6	0.08	0
3	5XH	O	503	1	31,38,38	1.55	2 (6%)	35,53,53	1.38	1 (2%)
3	5XH	D	501	1	31,38,38	1.55	2 (6%)	35,53,53	1.38	1 (2%)
2	SO4	O	501	-	4,4,4	0.15	0	6,6,6	0.11	0
2	SO4	J	502	-	4,4,4	0.15	0	6,6,6	0.06	0
3	5XH	H	503	1	31,38,38	1.54	2 (6%)	35,53,53	1.39	1 (2%)
3	5XH	E	504	1	31,38,38	1.56	2 (6%)	35,53,53	1.39	1 (2%)
2	SO4	C	503	-	4,4,4	0.12	0	6,6,6	0.09	0
2	SO4	I	503	-	4,4,4	0.16	0	6,6,6	0.06	0

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	5XH	J	504	1	-	1/14/33/33	0/4/4/4
3	5XH	D	501	1	-	1/14/33/33	0/4/4/4
3	5XH	F	504	1	-	1/14/33/33	0/4/4/4
3	5XH	G	501	1	-	1/14/33/33	0/4/4/4
3	5XH	L	503	1	-	1/14/33/33	0/4/4/4
3	5XH	A	501	1	-	1/14/33/33	0/4/4/4
3	5XH	I	504	1	-	1/14/33/33	0/4/4/4
3	5XH	K	503	1	-	1/14/33/33	0/4/4/4
3	5XH	M	501	1	-	1/14/33/33	0/4/4/4
3	5XH	H	503	1	-	1/14/33/33	0/4/4/4
3	5XH	B	504	1	-	1/14/33/33	0/4/4/4
3	5XH	E	504	1	-	1/14/33/33	0/4/4/4
3	5XH	C	504	1	-	1/14/33/33	0/4/4/4
3	5XH	N	501	1	-	1/14/33/33	0/4/4/4
3	5XH	P	503	1	-	1/14/33/33	0/4/4/4
3	5XH	O	503	1	-	1/14/33/33	0/4/4/4

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	504	5XH	C4-C3	8.01	1.52	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	504	5XH	C4-C3	7.99	1.52	1.32
3	P	503	5XH	C4-C3	7.97	1.52	1.32
3	I	504	5XH	C4-C3	7.96	1.52	1.32
3	A	501	5XH	C4-C3	7.96	1.52	1.32

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	504	5XH	C2-C3-C4	-9.15	109.94	124.67
3	G	501	5XH	C2-C3-C4	-7.70	112.28	124.67
3	I	504	5XH	C2-C3-C4	-7.60	112.43	124.67
3	K	503	5XH	C2-C3-C4	-7.60	112.44	124.67
3	J	504	5XH	C2-C3-C4	-7.59	112.45	124.67

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	5XH	C2-C3-C4-C5
3	B	504	5XH	C2-C3-C4-C5
3	C	504	5XH	C2-C3-C4-C5
3	D	501	5XH	C2-C3-C4-C5
3	E	504	5XH	C2-C3-C4-C5

There are no ring outliers.

14 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	5XH	2	0
2	F	502	SO4	1	0
2	G	500	SO4	1	0
2	K	501	SO4	1	0
2	L	501	SO4	1	0
2	B	502	SO4	1	0
2	C	502	SO4	1	0
2	O	502	SO4	1	0
2	H	502	SO4	1	0
2	E	501	SO4	3	0
2	H	501	SO4	1	0
2	M	500	SO4	1	0
3	D	501	5XH	1	0

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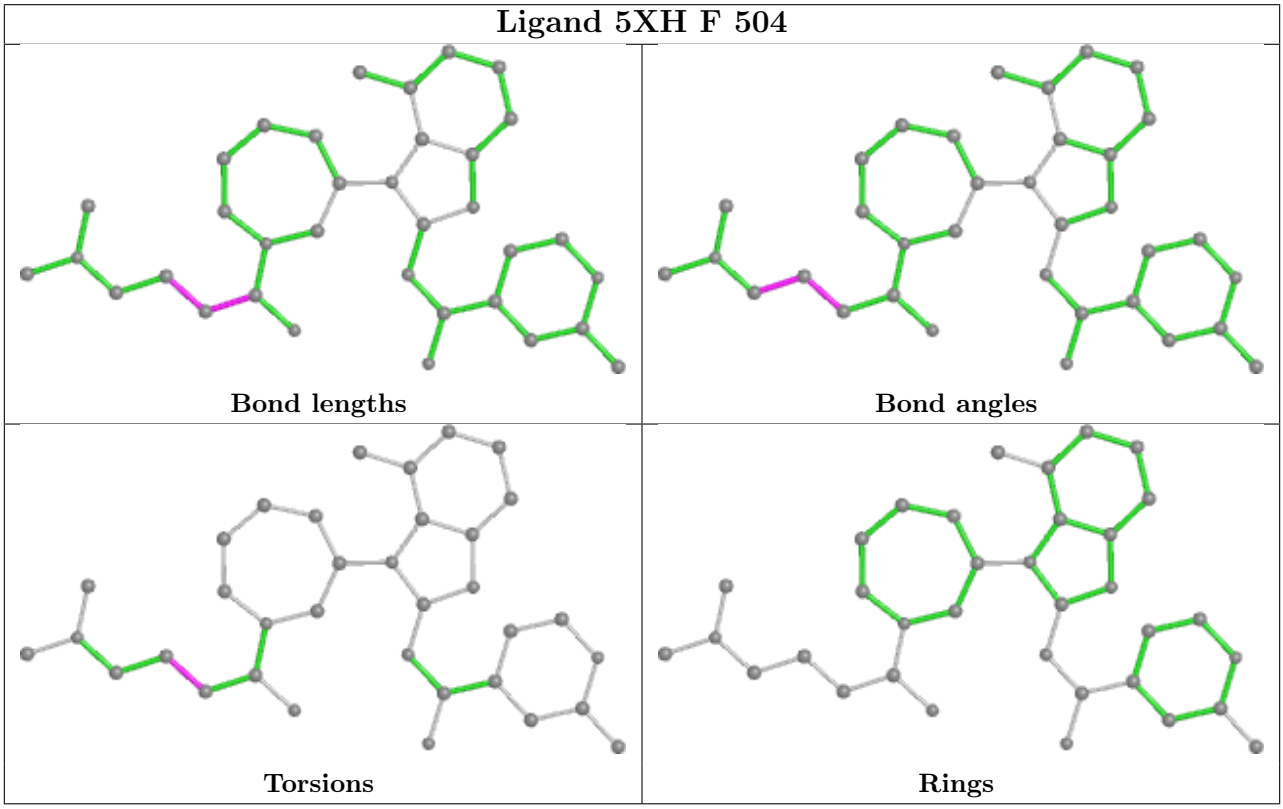
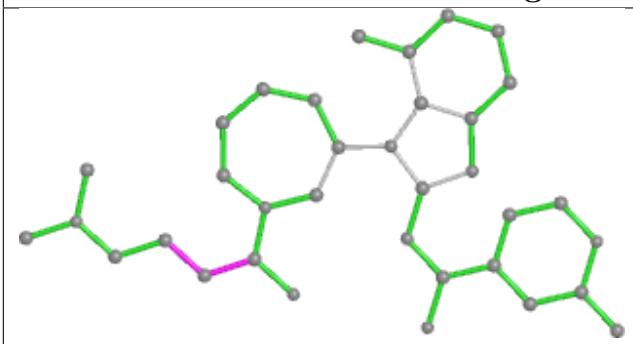
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	503	5XH	1	0

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 5XH A 501



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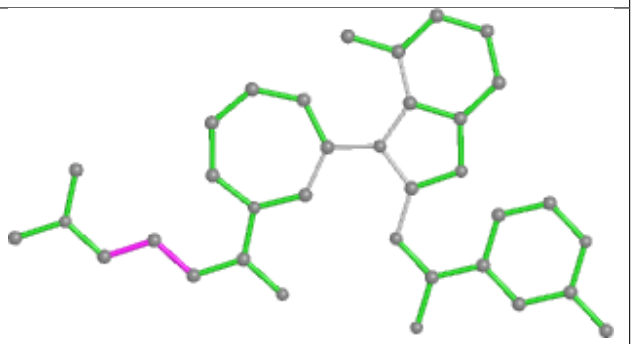
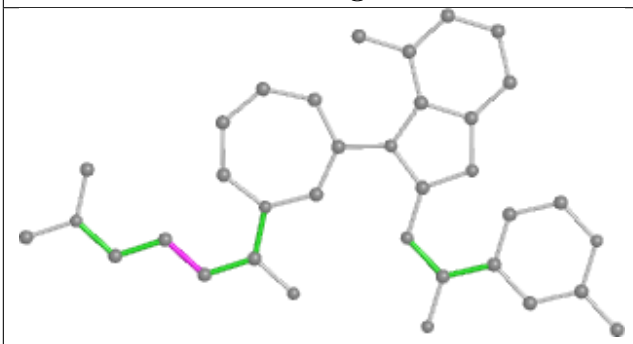
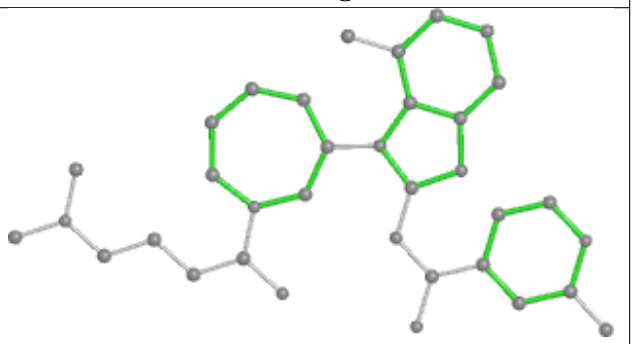


Bond angles

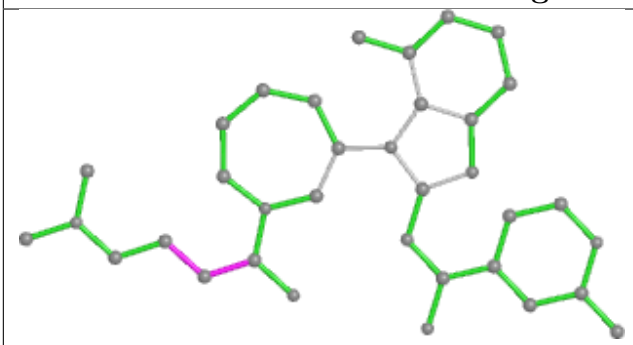


Torsions



Rings

Ligand 5XH I 504



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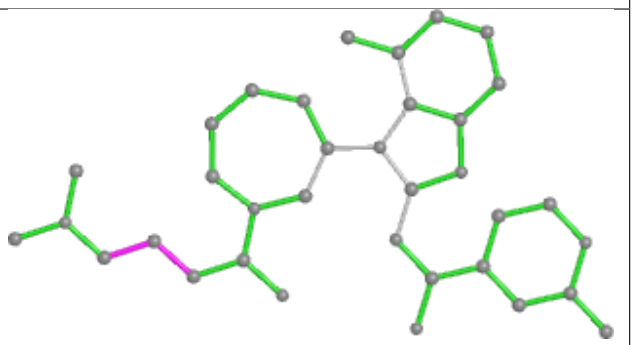

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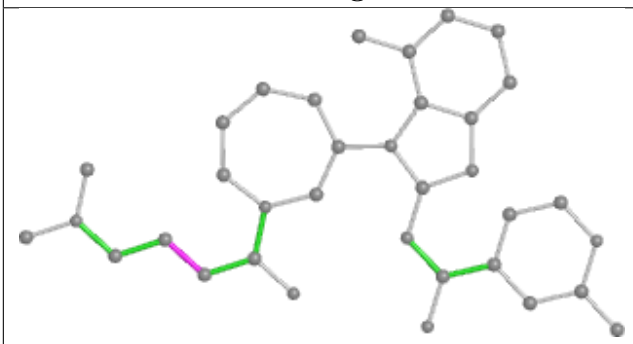

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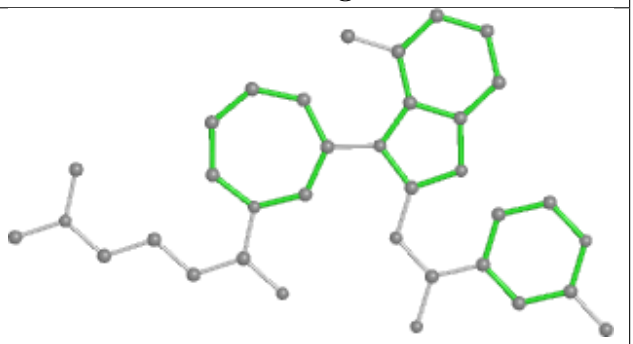
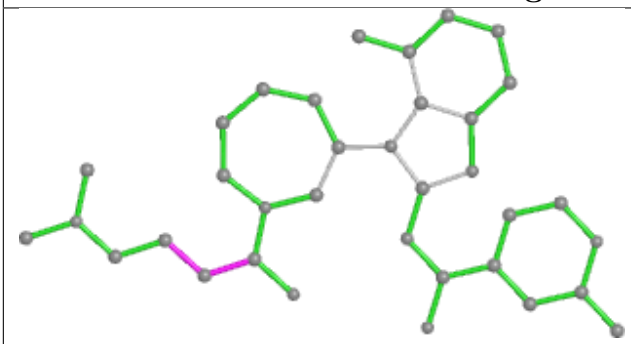


Rings

Ligand 5XH C 504



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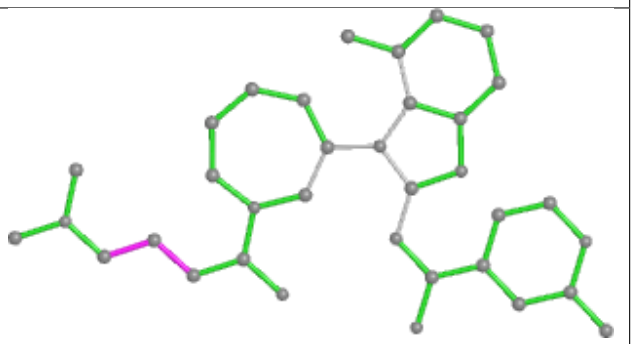
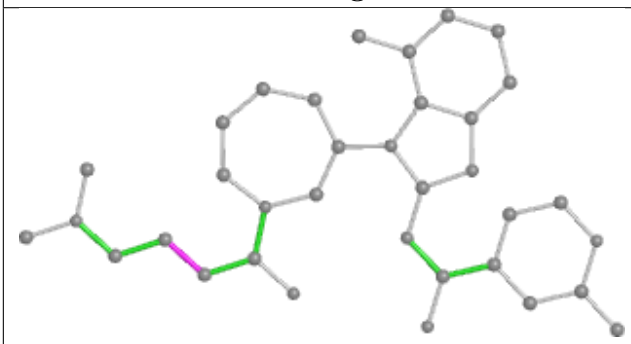


Bond angles



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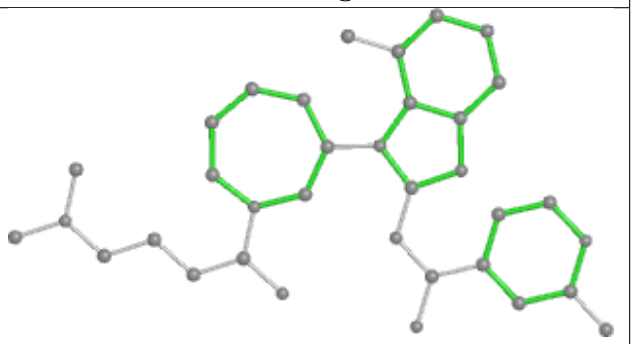
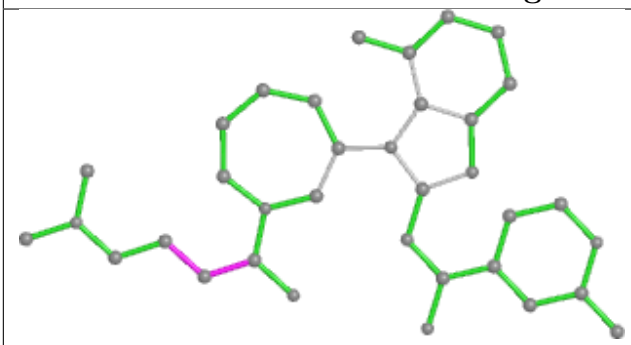


Rings

Ligand 5XH K 503



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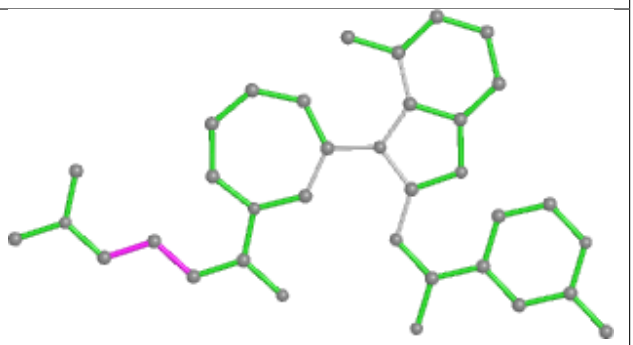
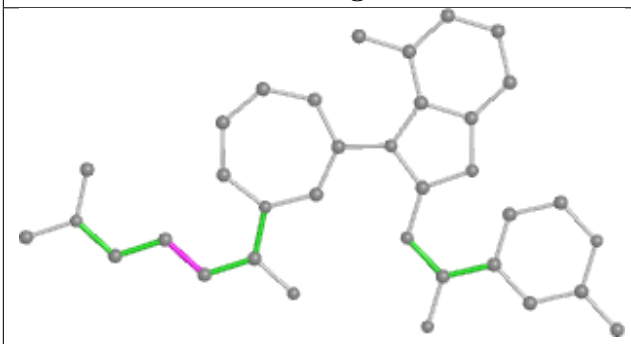


Bond angles



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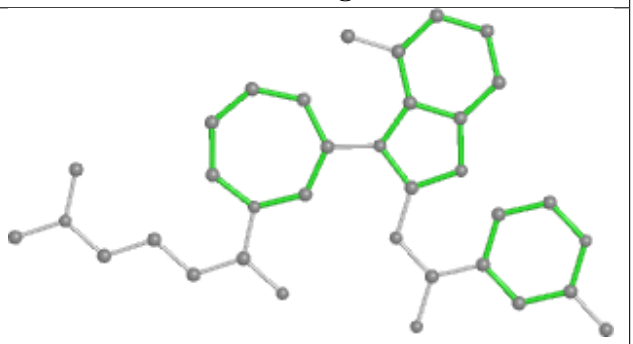
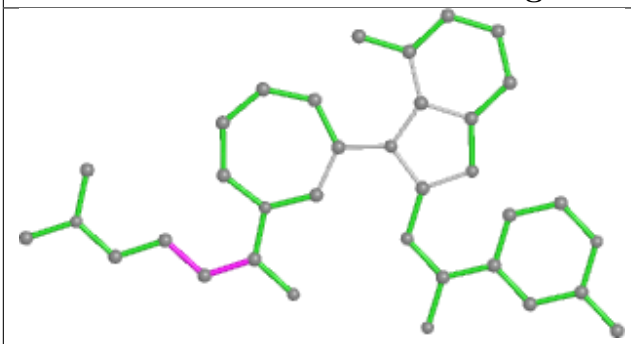


Rings

Ligand 5XH B 504



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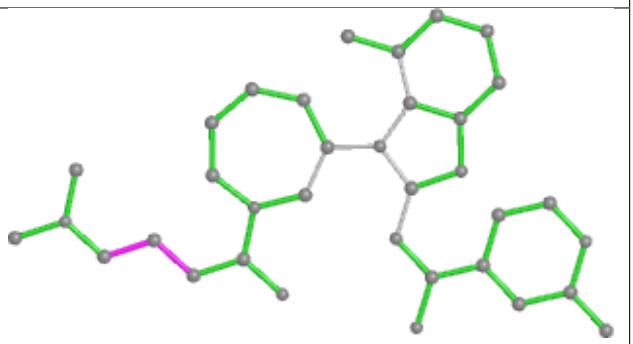

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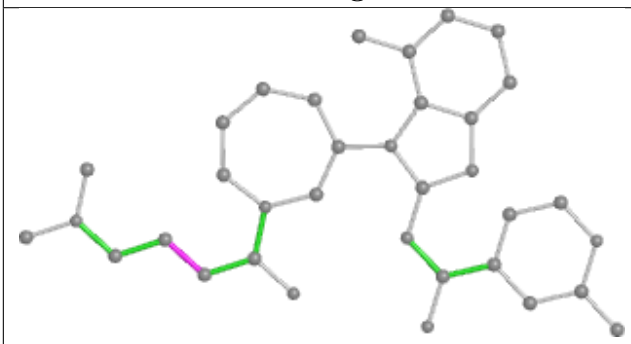

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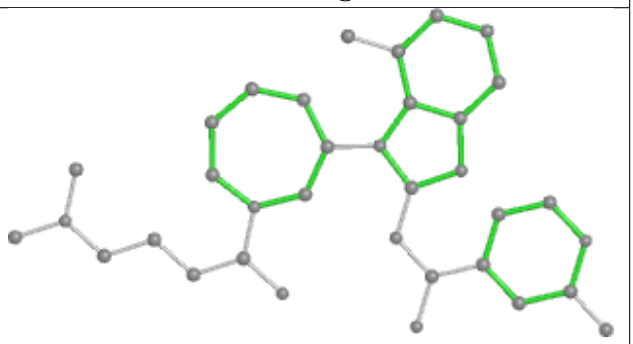
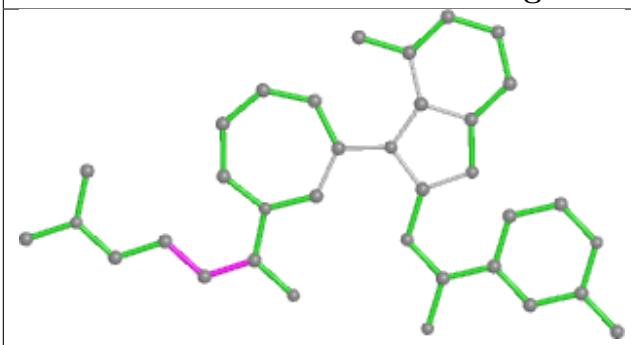


Rings

Ligand 5XH N 501



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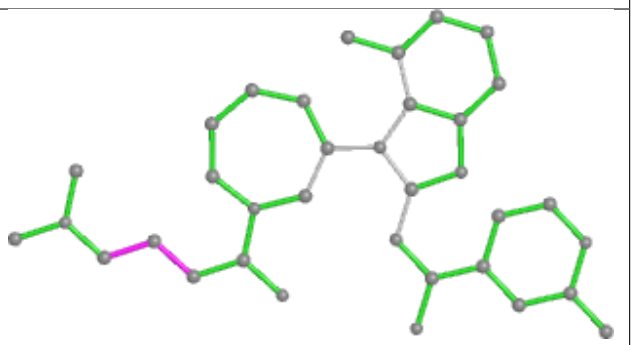

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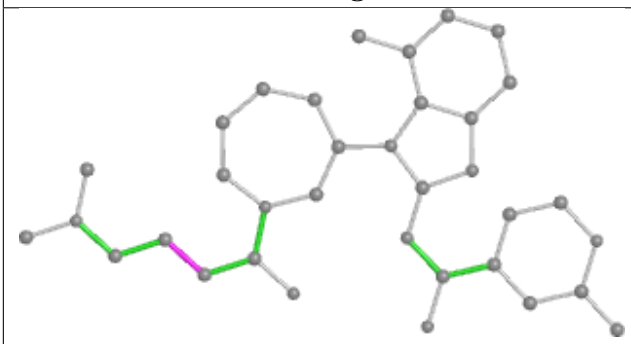

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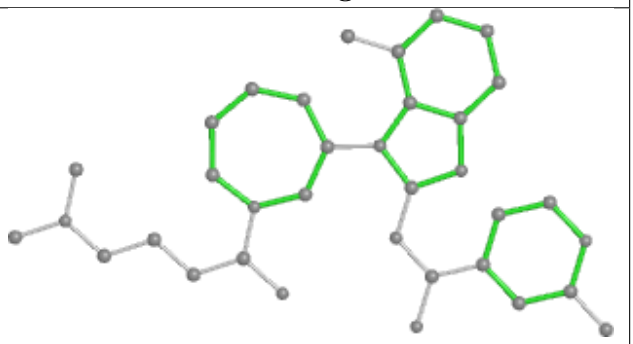
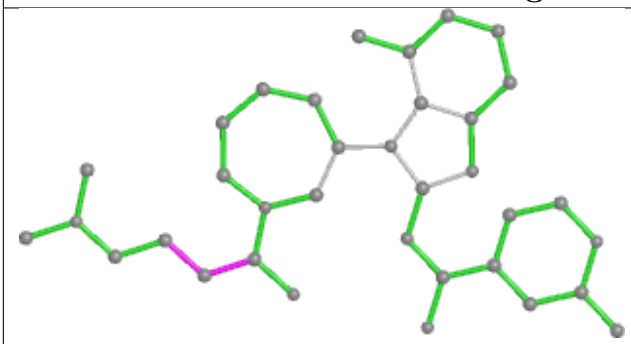


Rings

Ligand 5XH P 503



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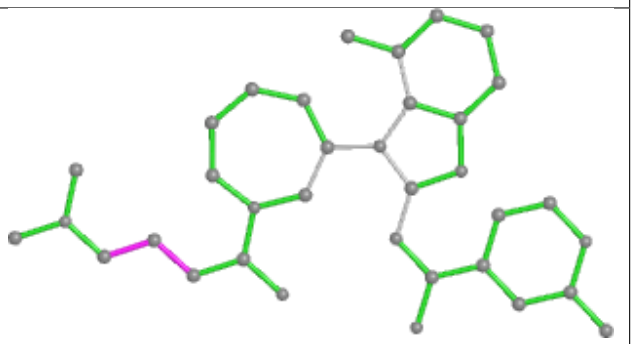

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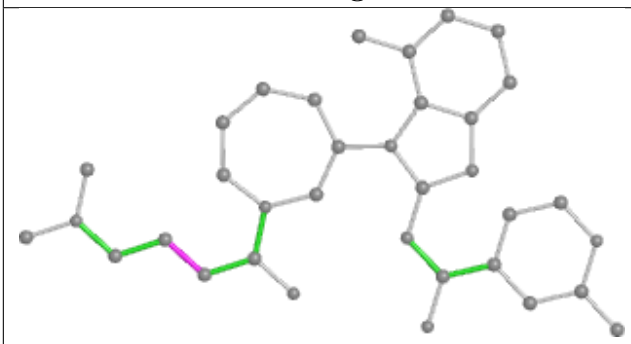

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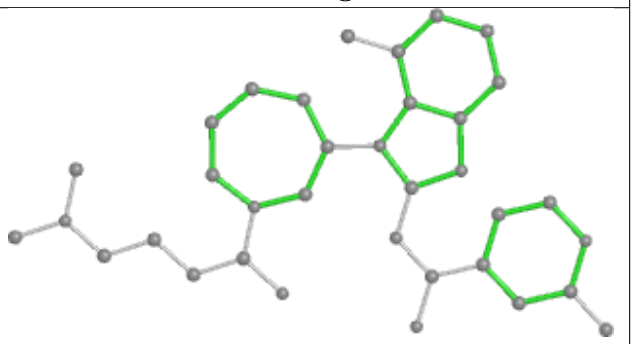
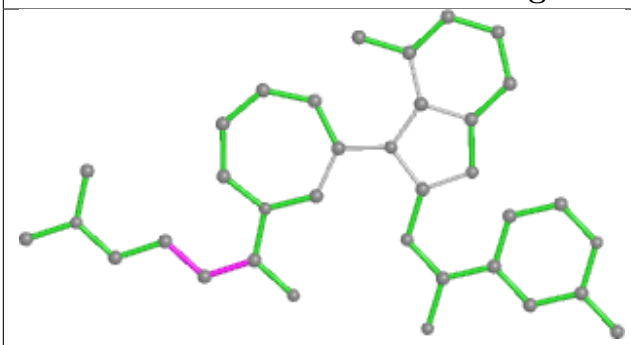


Rings

Ligand 5XH J 504



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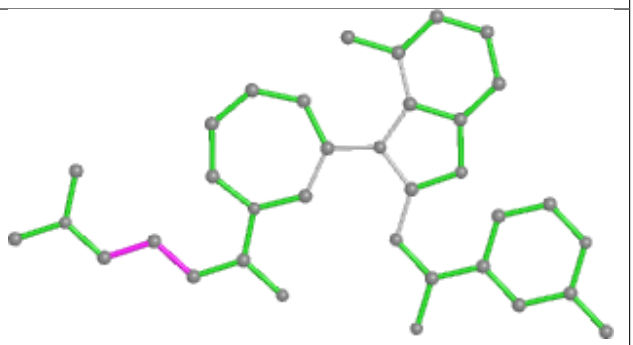

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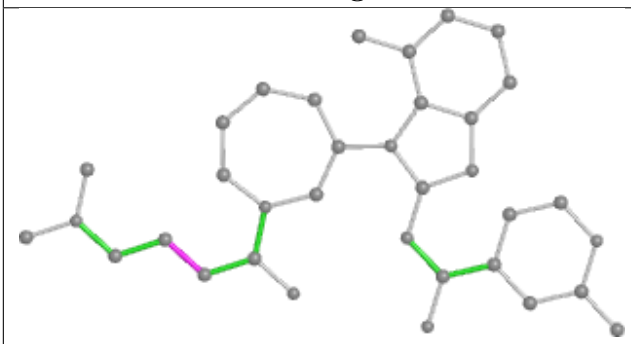

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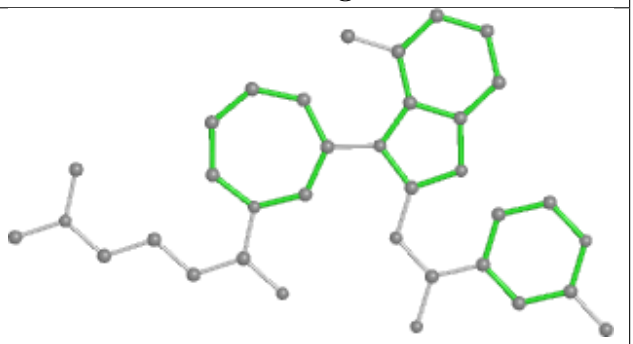
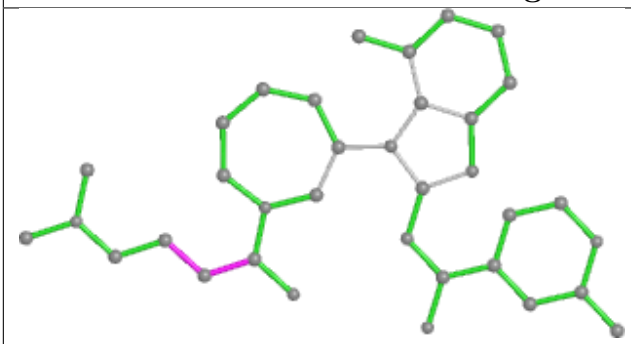


Rings

Ligand 5XH G 501



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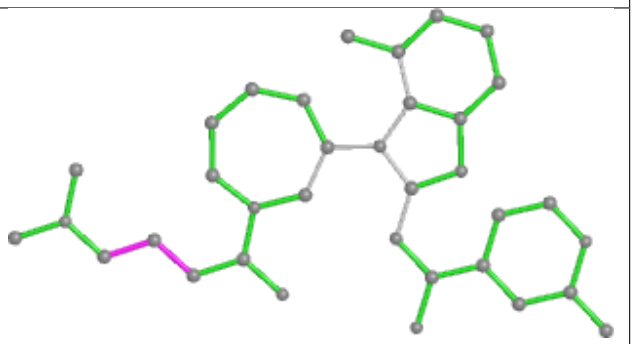

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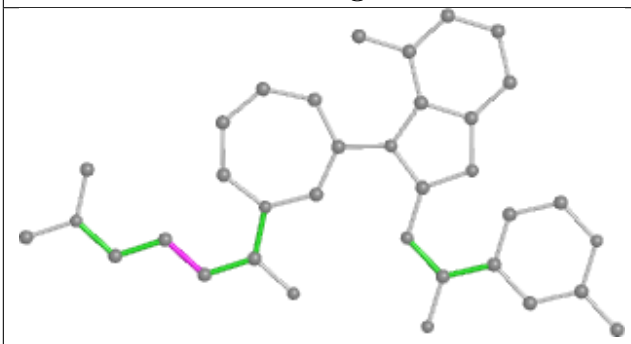

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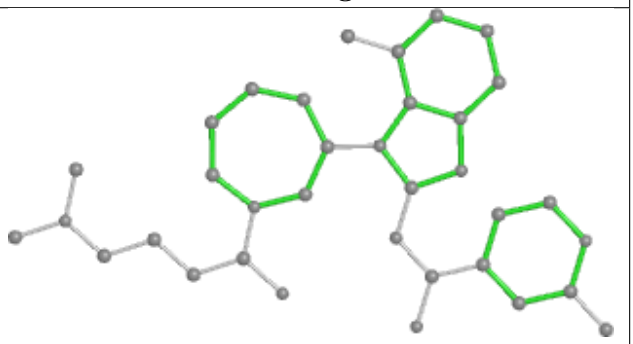
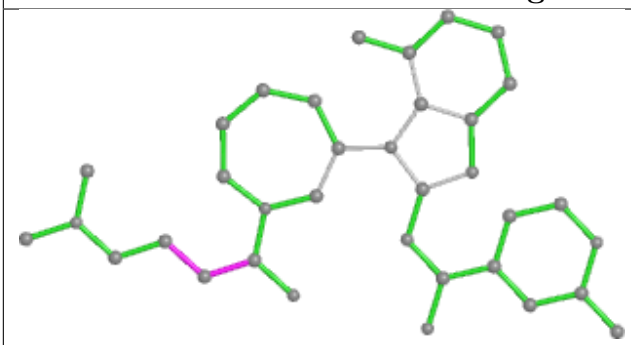


Rings

Ligand 5XH L 503



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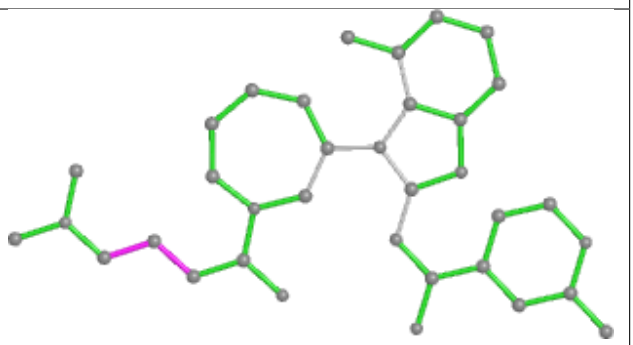
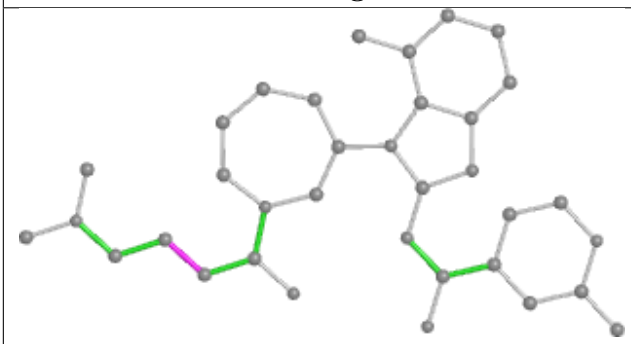


Bond angles



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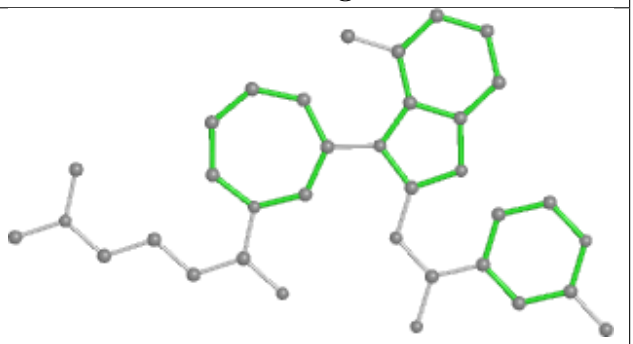
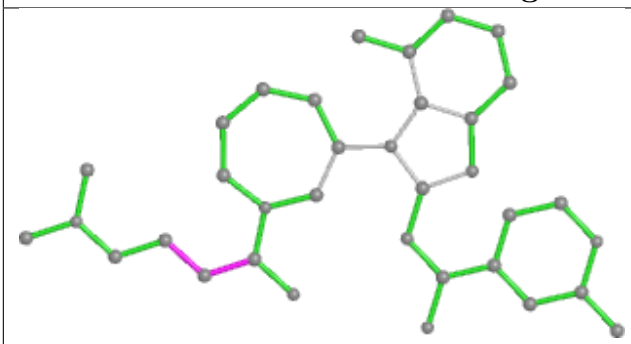


Rings

Ligand 5XH M 501



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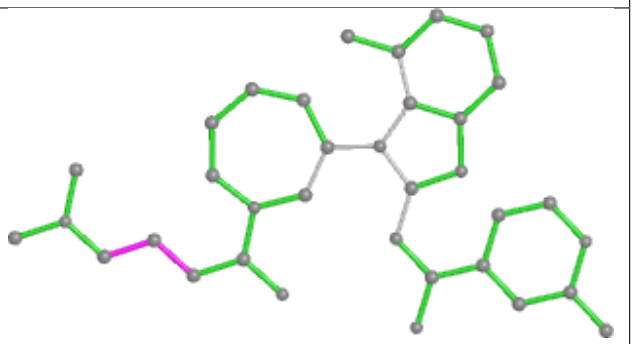
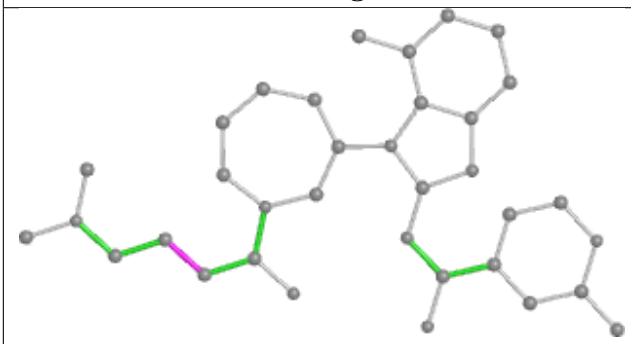
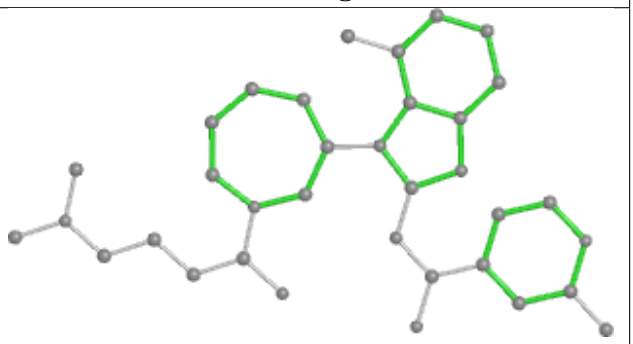


Bond angles

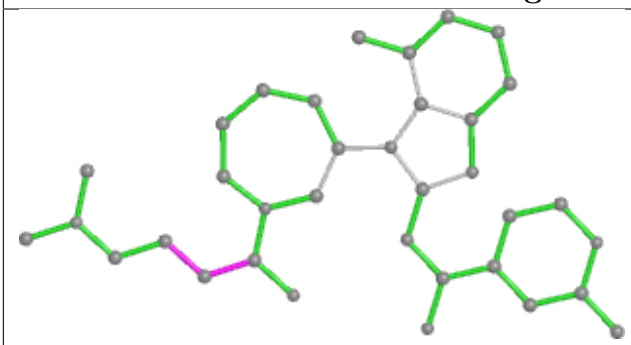


Torsions

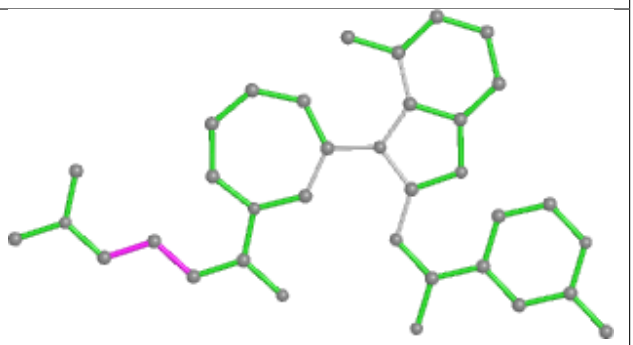


Rings

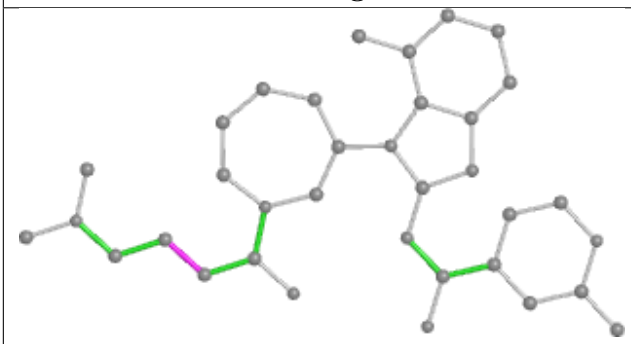
Ligand 5XH O 503



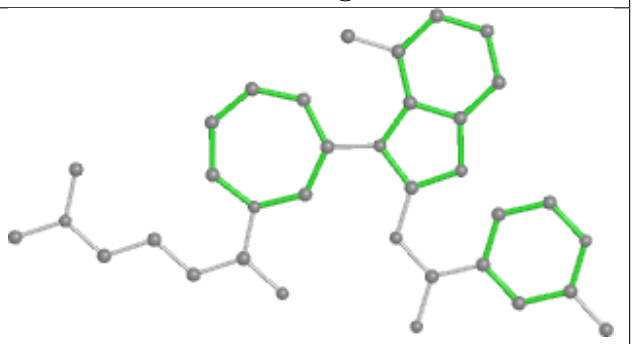
Bond lengths



Bond angles

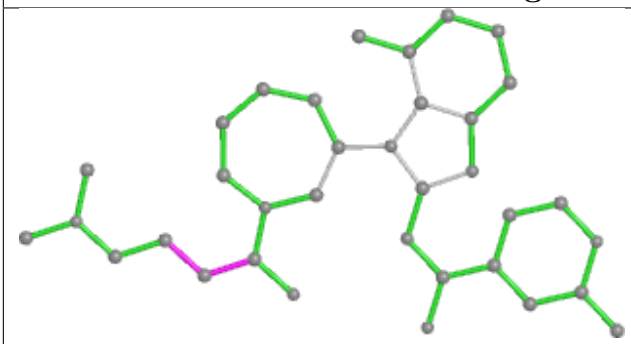


Torsions

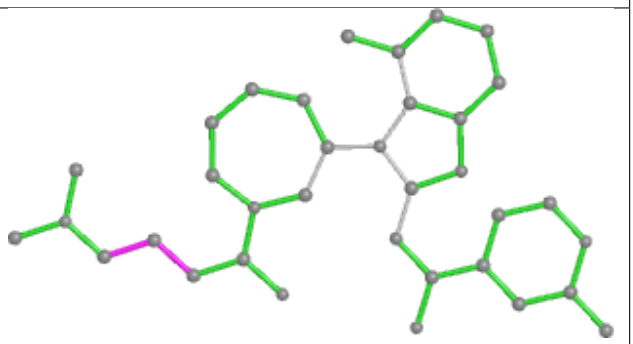


Rings

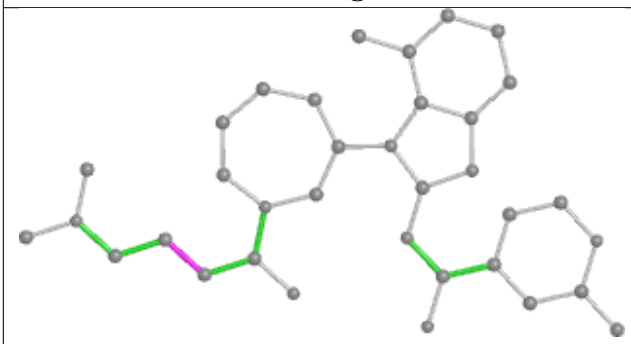
Ligand 5XH D 501



Bond lengths



Bond angles



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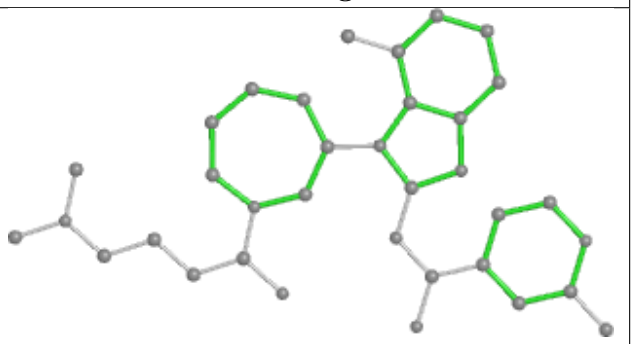
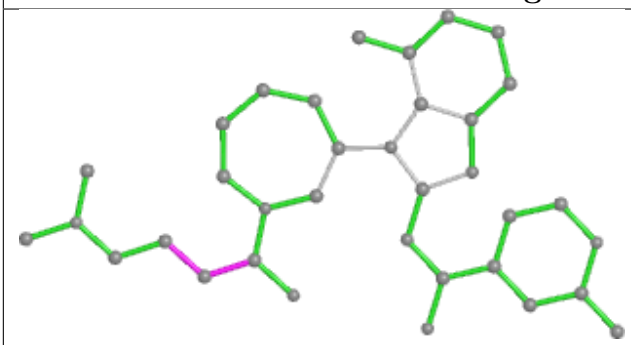
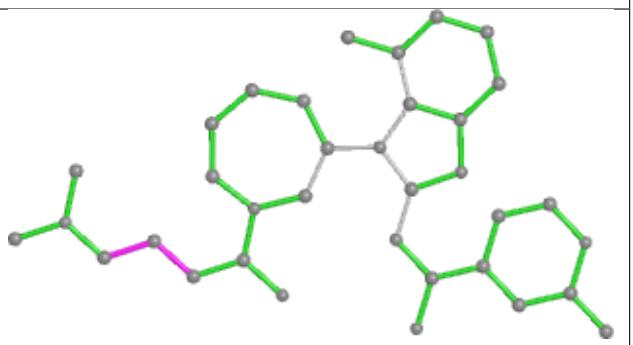


Rings

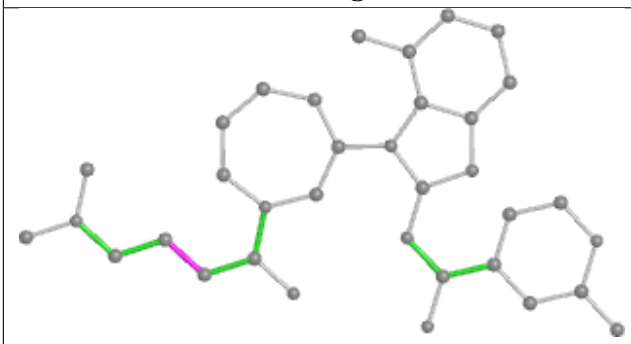
Ligand 5XH H 503



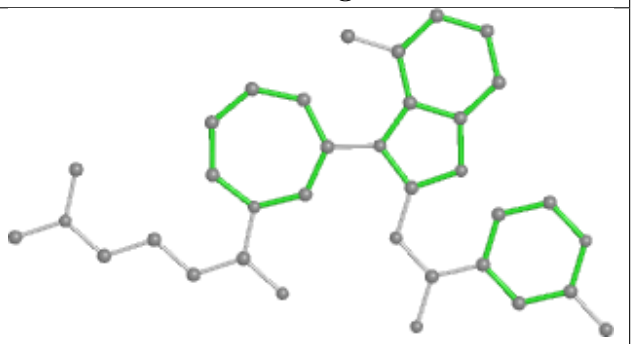
Bond lengths



Bond angles

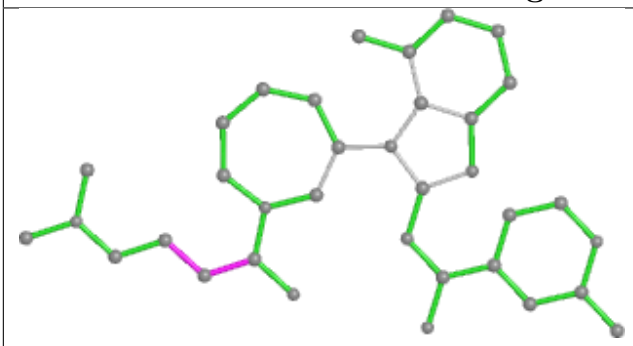


Torsions

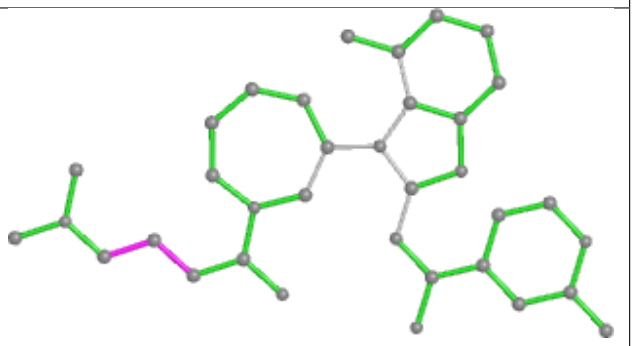


Rings

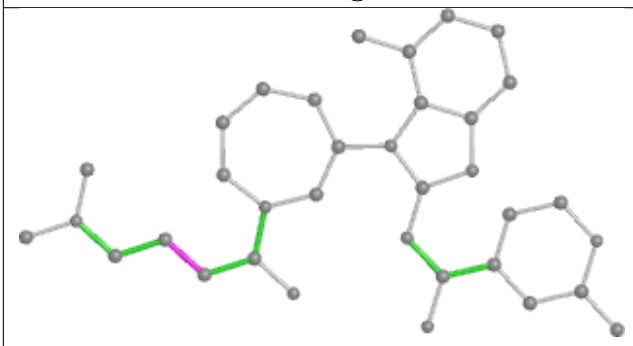
Ligand 5XH E 504



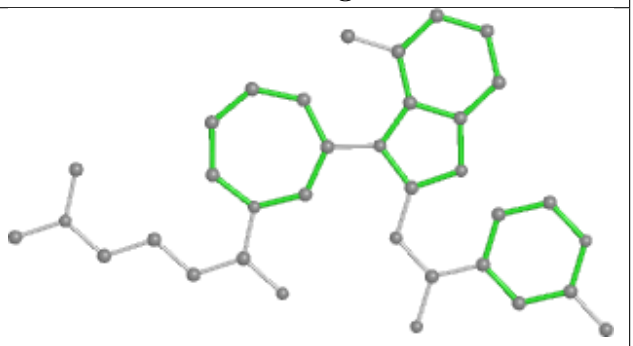
Bond lengths



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^{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	339/354 (95%)	0.19	7 (2%)	63	58	26, 53, 92, 116	0
1	B	339/354 (95%)	0.00	3 (0%)	84	82	26, 45, 82, 114	0
1	C	339/354 (95%)	0.14	9 (2%)	54	48	25, 46, 89, 118	0
1	D	339/354 (95%)	0.28	14 (4%)	37	30	25, 55, 97, 117	0
1	E	339/354 (95%)	0.01	3 (0%)	84	82	25, 45, 82, 106	0
1	F	339/354 (95%)	0.10	9 (2%)	54	48	25, 46, 87, 107	0
1	G	339/354 (95%)	0.20	8 (2%)	59	53	26, 52, 93, 115	0
1	H	339/354 (95%)	0.41	20 (5%)	22	17	29, 55, 102, 128	0
1	I	339/354 (95%)	0.03	6 (1%)	68	64	23, 45, 84, 111	0
1	J	339/354 (95%)	-0.00	3 (0%)	84	82	27, 46, 81, 103	0
1	K	339/354 (95%)	-0.01	3 (0%)	84	82	26, 45, 78, 101	0
1	L	339/354 (95%)	0.05	5 (1%)	73	70	23, 45, 84, 111	0
1	M	339/354 (95%)	0.21	8 (2%)	59	53	28, 53, 93, 109	0
1	N	339/354 (95%)	0.32	16 (4%)	31	25	29, 55, 96, 121	0
1	O	339/354 (95%)	0.35	14 (4%)	37	30	30, 54, 96, 142	0
1	P	339/354 (95%)	0.20	7 (2%)	63	58	27, 52, 90, 116	0
All	All	5424/5664 (95%)	0.15	135 (2%)	57	51	23, 49, 91, 142	0

The worst 5 of 135 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	127	GLY	9.2
1	O	383	GLY	5.7
1	H	181	ARG	4.4
1	D	291	GLY	4.3
1	H	346	HIS	4.3

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
2	SO4	K	501	5/5	0.65	0.30	100,102,103,104	0
2	SO4	L	501	5/5	0.84	0.22	99,100,101,101	0
2	SO4	C	502	5/5	0.87	0.24	92,94,95,96	0
2	SO4	P	501	5/5	0.87	0.29	98,102,105,106	0
2	SO4	B	502	5/5	0.88	0.22	95,97,99,100	0
2	SO4	O	501	5/5	0.89	0.25	95,98,102,103	0
2	SO4	H	501	5/5	0.91	0.17	92,97,102,104	0
2	SO4	J	502	5/5	0.91	0.13	85,87,89,89	0
2	SO4	F	502	5/5	0.91	0.30	96,98,99,100	0
3	5XH	N	501	35/35	0.91	0.21	18,35,50,53	0
2	SO4	E	503	5/5	0.92	0.15	70,71,72,79	0
2	SO4	E	501	5/5	0.92	0.20	91,94,97,101	0
3	5XH	M	501	35/35	0.92	0.20	21,36,51,54	0
2	SO4	E	502	5/5	0.92	0.21	93,96,99,100	0
3	5XH	P	503	35/35	0.92	0.20	22,30,52,59	0
3	5XH	G	501	35/35	0.93	0.19	21,34,56,58	0
3	5XH	L	503	35/35	0.93	0.19	22,35,51,53	0
2	SO4	C	503	5/5	0.93	0.17	78,81,83,84	0
2	SO4	F	503	5/5	0.93	0.15	76,78,79,83	0
3	5XH	O	503	35/35	0.93	0.19	25,36,55,60	0
3	5XH	D	501	35/35	0.93	0.19	24,37,51,53	0
3	5XH	H	503	35/35	0.94	0.18	26,35,51,57	0
3	5XH	I	504	35/35	0.94	0.17	18,35,61,62	0
3	5XH	J	504	35/35	0.94	0.17	17,35,52,62	0
3	5XH	K	503	35/35	0.94	0.17	18,33,49,53	0
2	SO4	H	502	5/5	0.94	0.18	77,77,78,84	0
3	5XH	A	501	35/35	0.94	0.20	22,33,57,58	0

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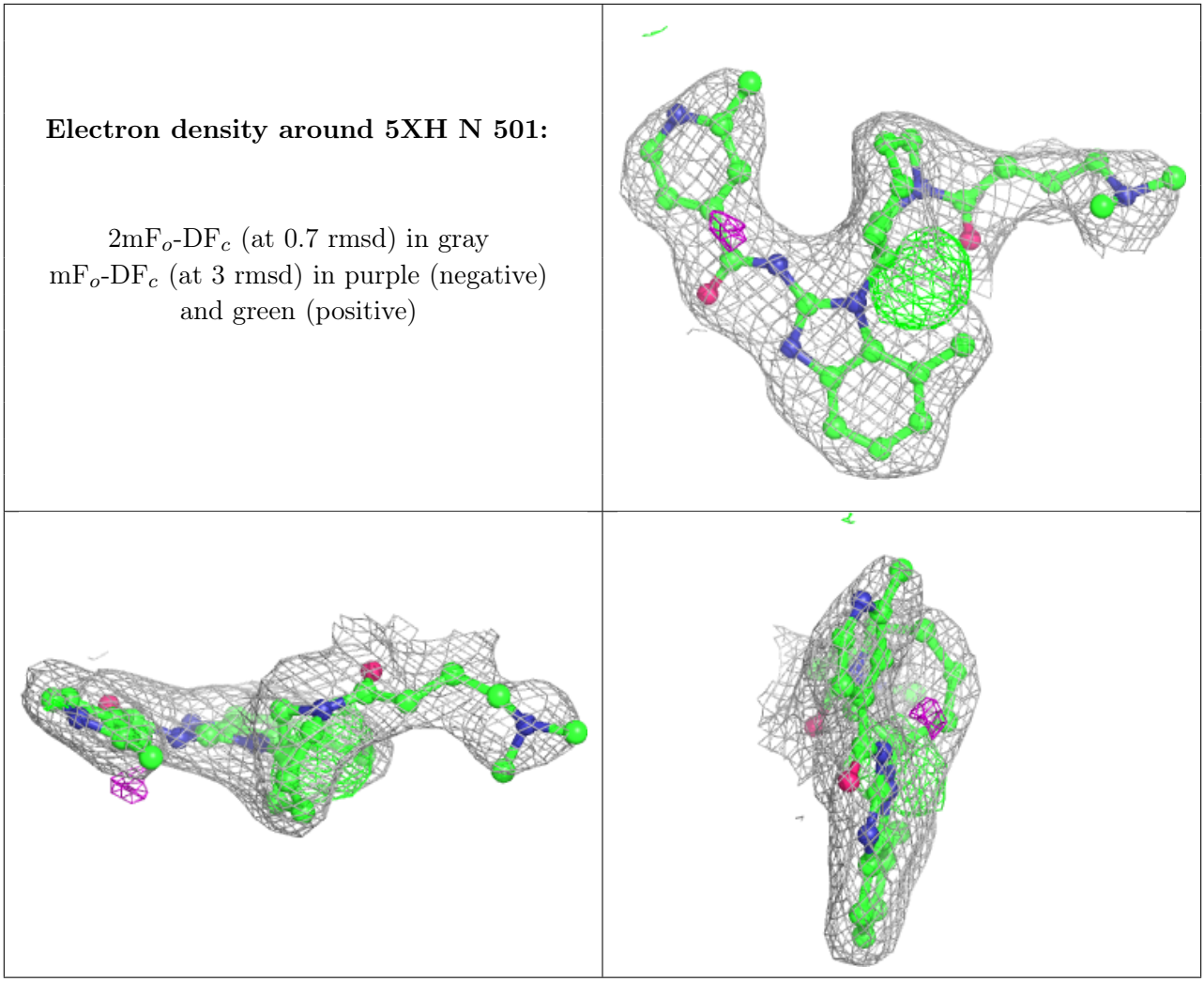
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	I	502	5/5	0.94	0.17	85,86,88,88	0
3	5XH	F	504	35/35	0.94	0.18	17,30,56,57	0
2	SO4	O	502	5/5	0.94	0.14	79,82,84,85	0
3	5XH	E	504	35/35	0.95	0.17	20,31,54,57	0
2	SO4	K	502	5/5	0.95	0.16	71,71,77,78	0
2	SO4	A	500	5/5	0.95	0.22	81,82,86,87	0
2	SO4	L	502	5/5	0.95	0.16	75,77,82,86	0
2	SO4	D	500	5/5	0.95	0.17	79,83,86,86	0
2	SO4	J	501	5/5	0.95	0.14	91,92,93,96	0
2	SO4	B	503	5/5	0.95	0.15	68,71,75,78	0
2	SO4	P	502	5/5	0.95	0.20	76,78,83,83	0
2	SO4	J	503	5/5	0.95	0.15	72,74,78,79	0
3	5XH	B	504	35/35	0.95	0.15	11,27,49,50	0
3	5XH	C	504	35/35	0.95	0.17	14,31,53,53	0
2	SO4	B	501	5/5	0.95	0.14	74,77,81,84	0
2	SO4	I	503	5/5	0.96	0.17	73,74,75,79	0
2	SO4	G	500	5/5	0.96	0.19	76,76,80,81	0
2	SO4	M	500	5/5	0.96	0.16	72,73,73,77	0
2	SO4	N	500	5/5	0.96	0.16	80,81,87,87	0
2	SO4	I	501	5/5	0.97	0.09	81,82,86,89	0
2	SO4	C	501	5/5	0.97	0.12	75,76,76,77	0
2	SO4	F	501	5/5	0.98	0.12	75,76,80,84	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.

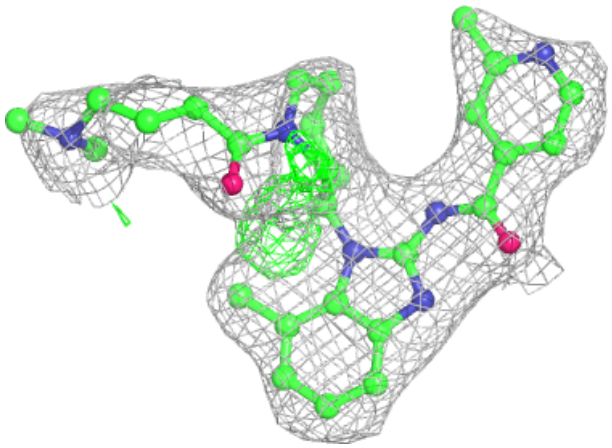
Electron density around 5XH N 501:

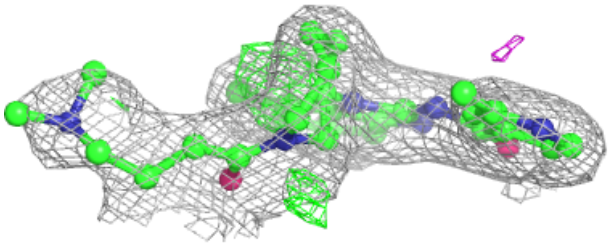
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

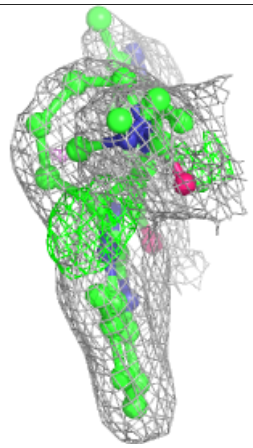


Electron density around 5XH M 501:

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

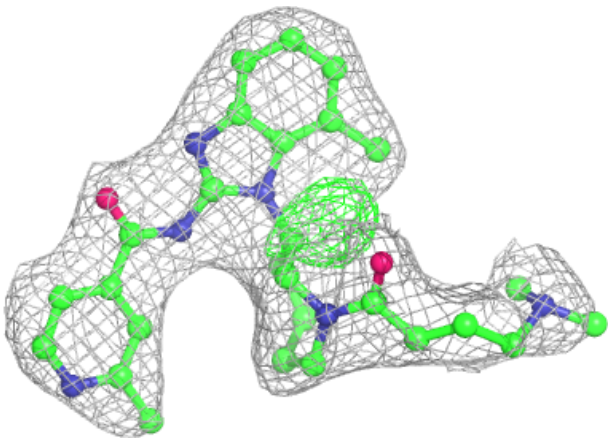


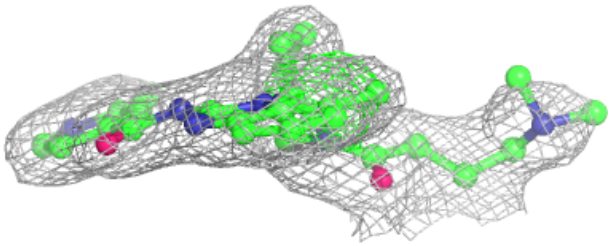


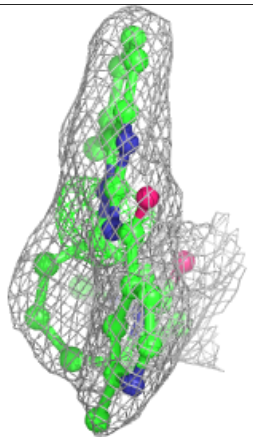


Electron density around 5XH P 503:

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

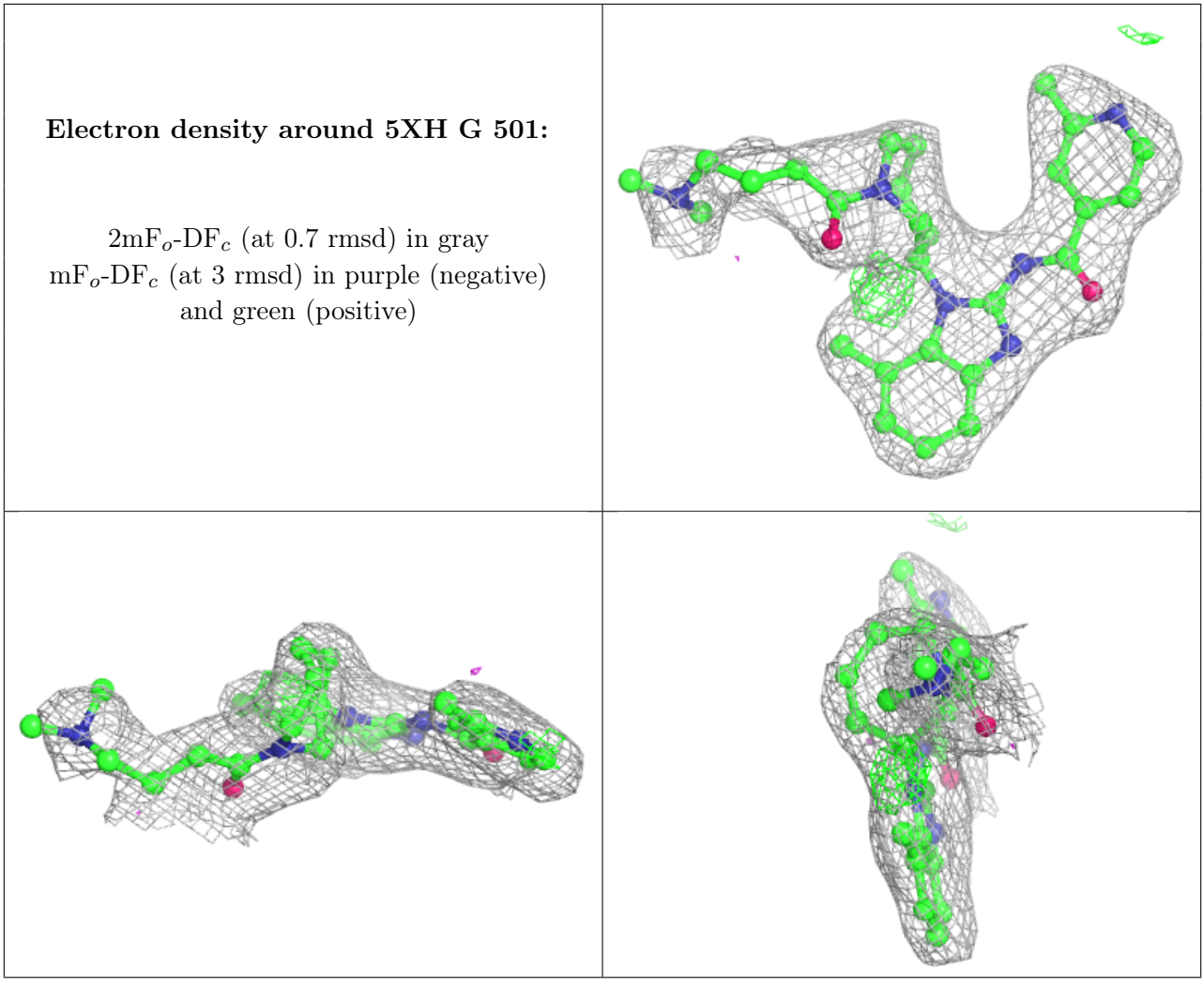






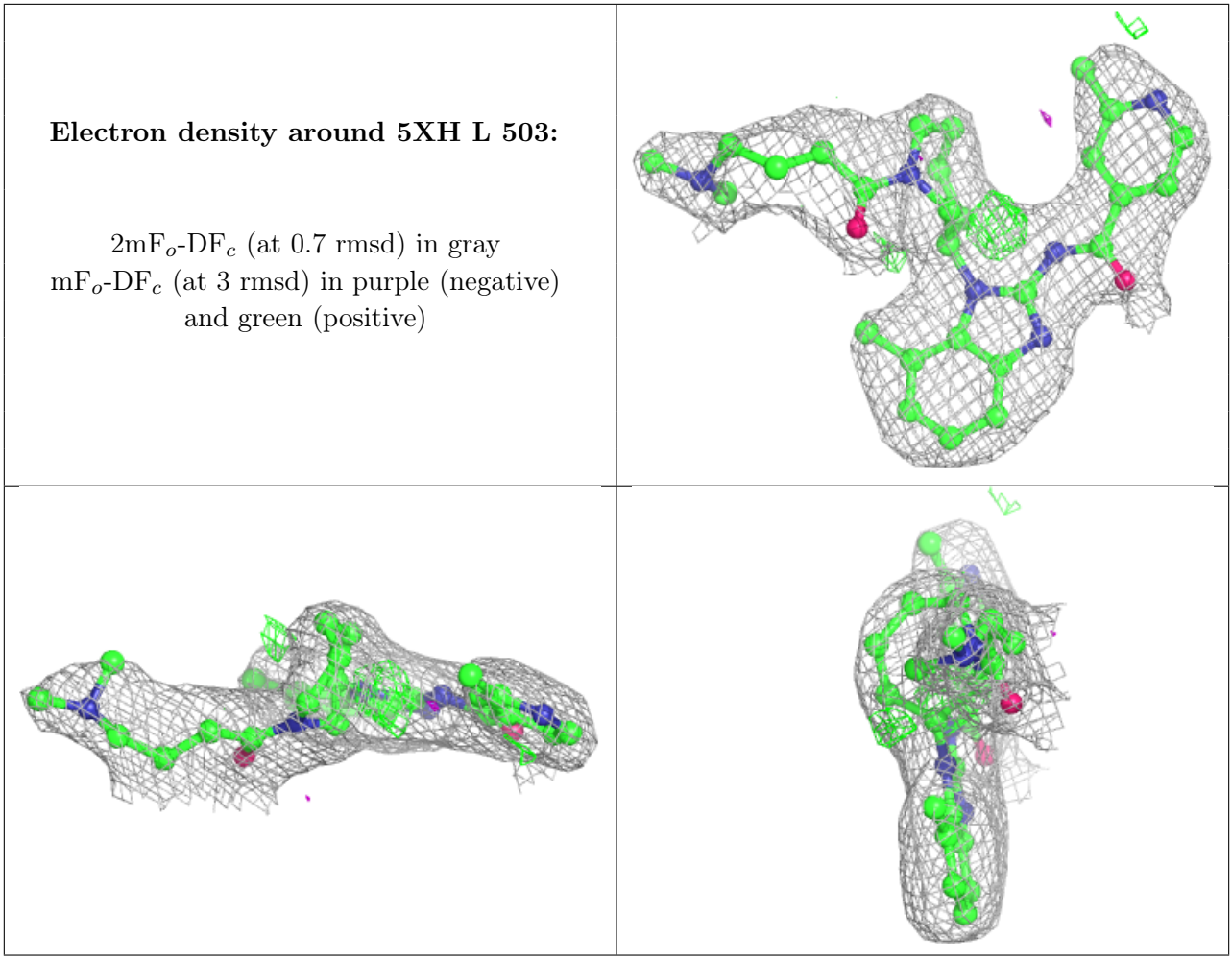
Electron density around 5XH G 501:

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



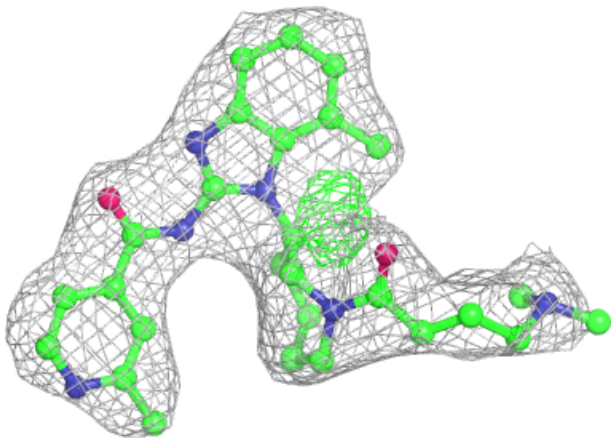
Electron density around 5XH L 503:

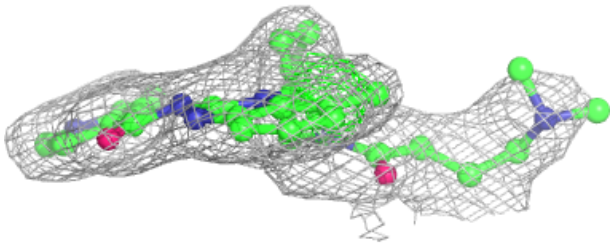
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

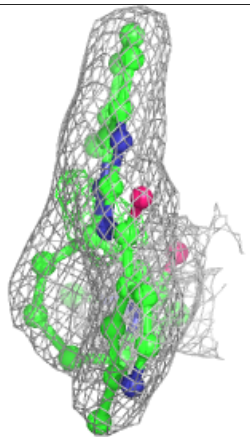


Electron density around 5XH O 503:

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

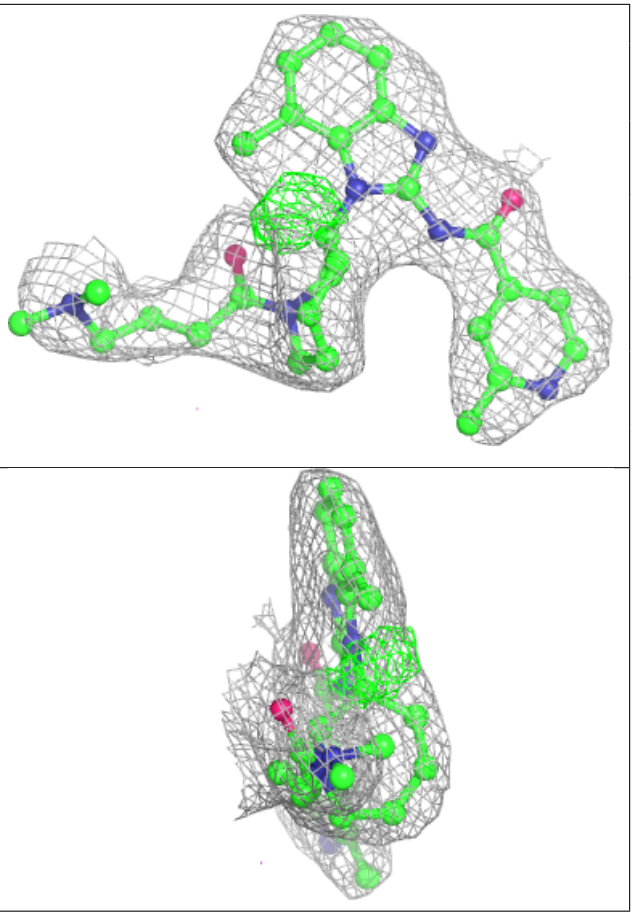


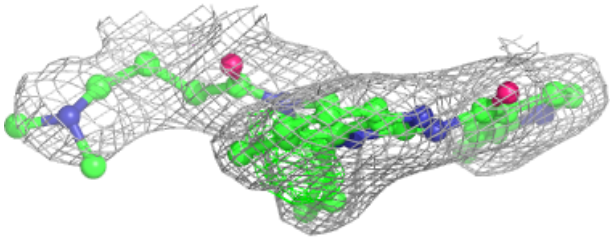




Electron density around 5XH D 501:

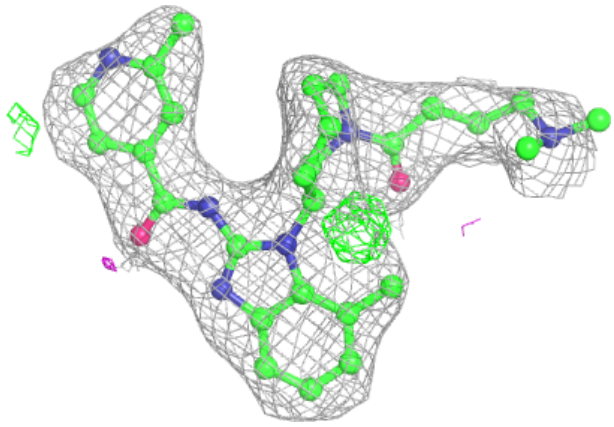
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

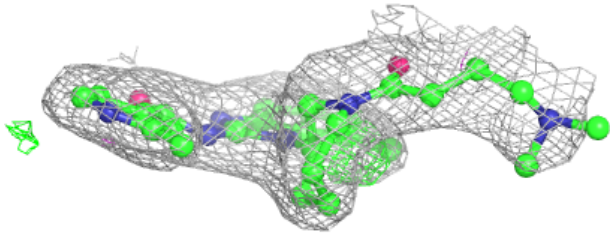


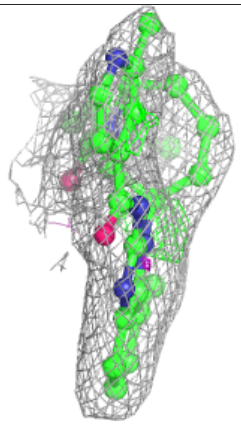


Electron density around 5XH H 503:

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

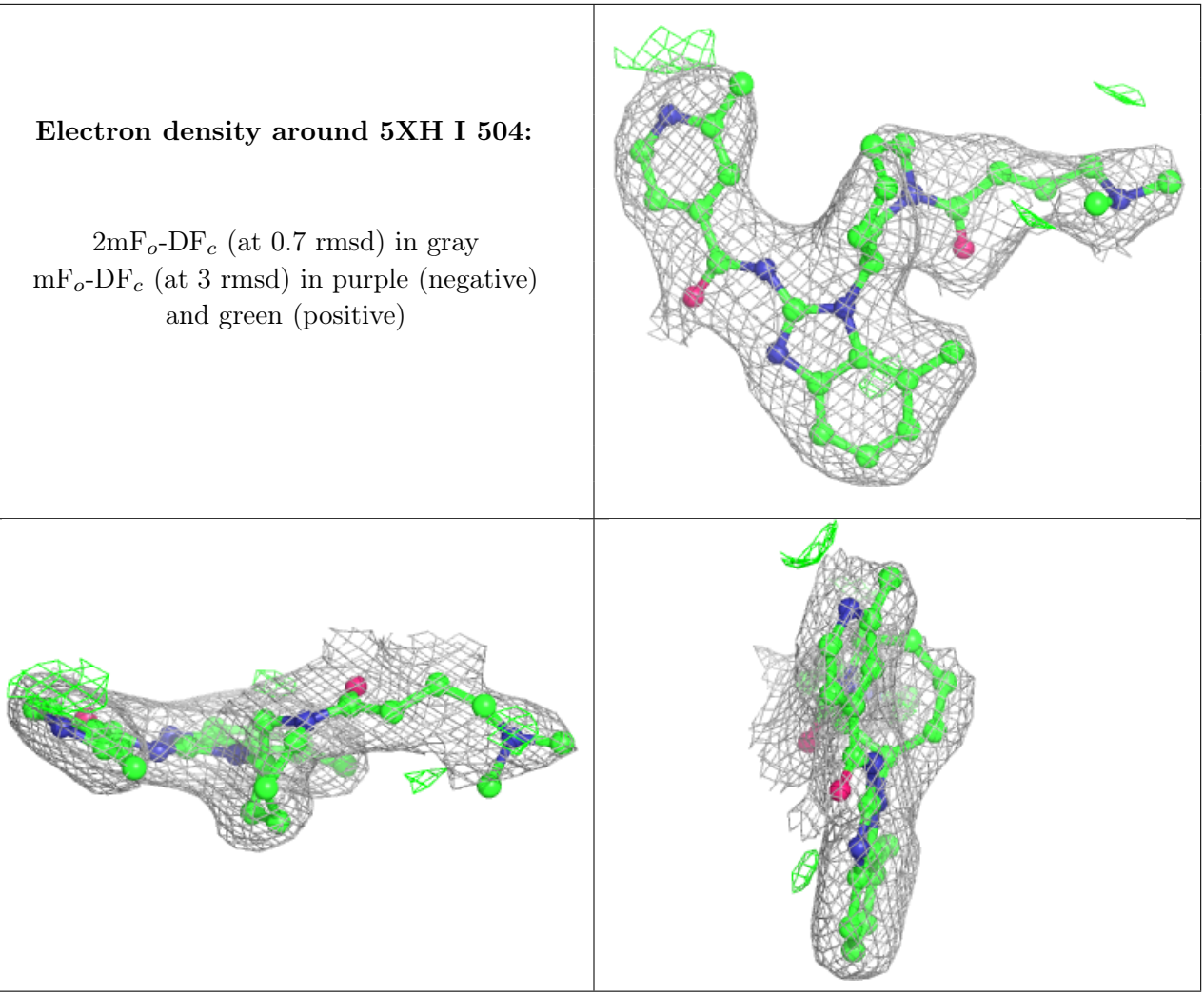






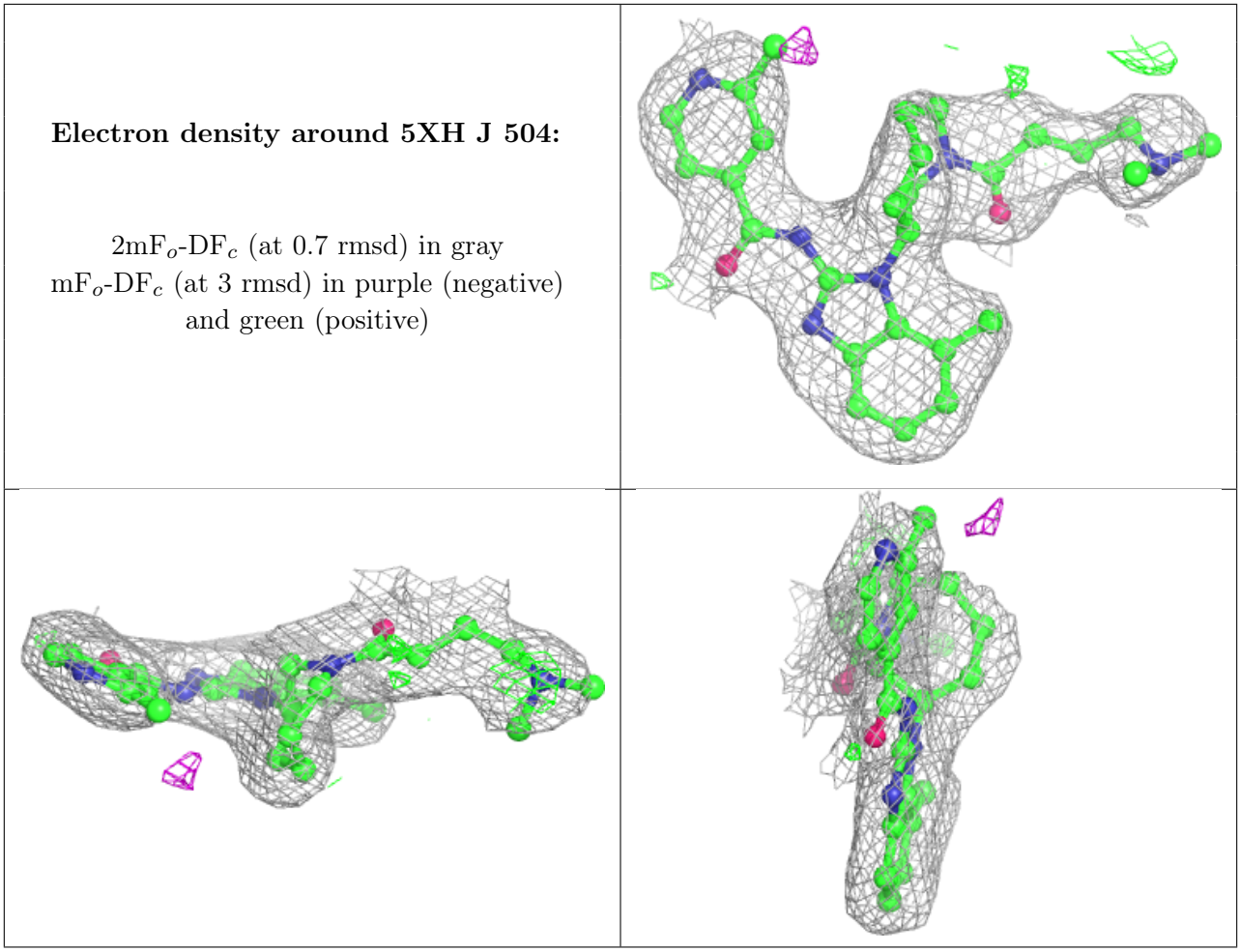
Electron density around 5XH I 504:

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



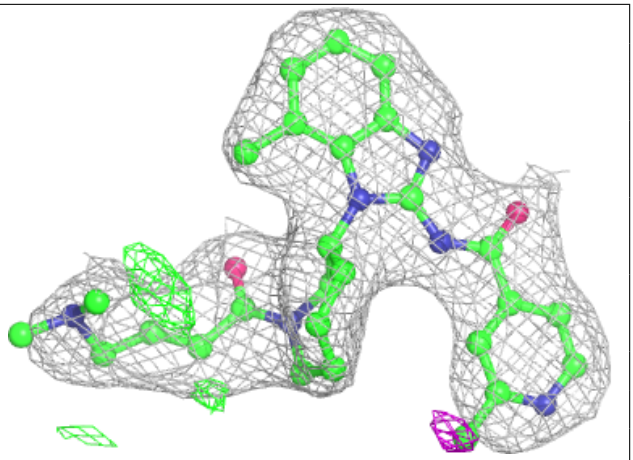
Electron density around 5XH J 504:

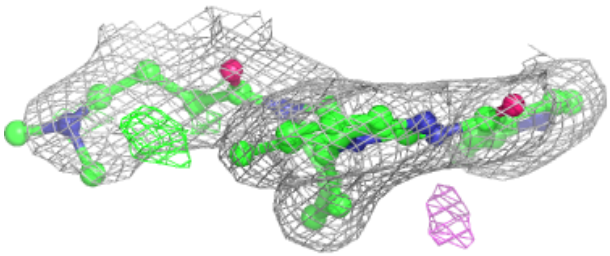
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

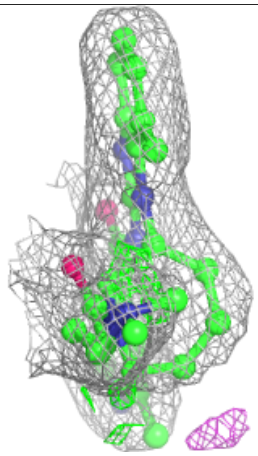


Electron density around 5XH K 503:

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

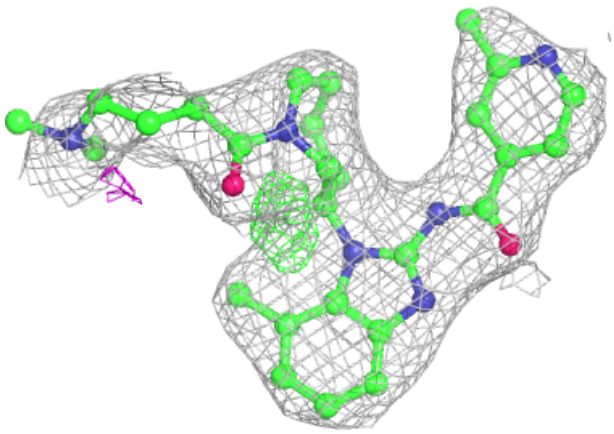


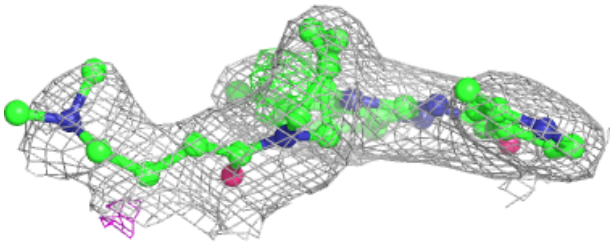


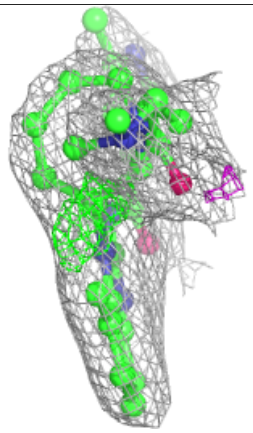


Electron density around 5XH A 501:

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

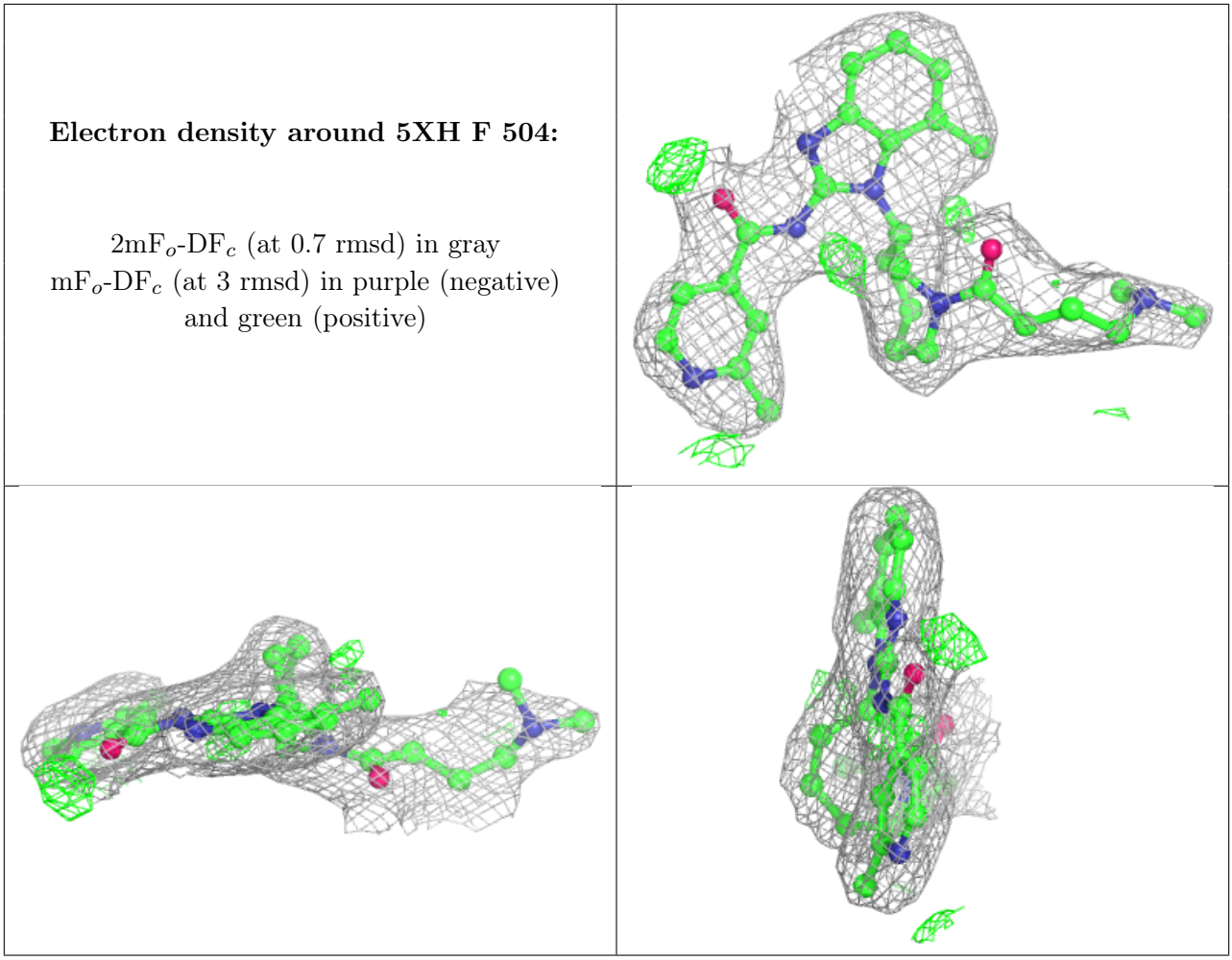






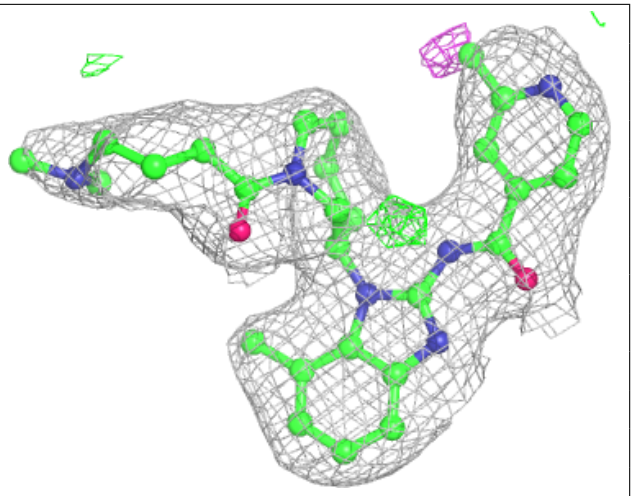
Electron density around 5XH F 504:

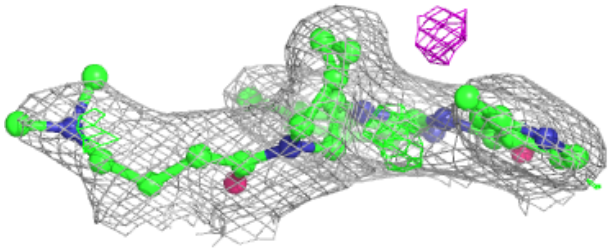
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

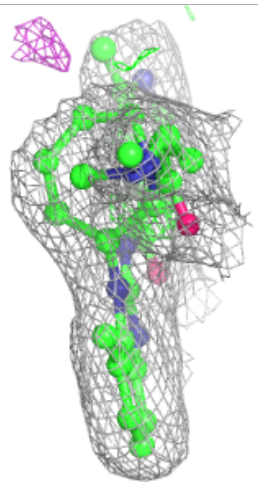


Electron density around 5XH E 504:

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

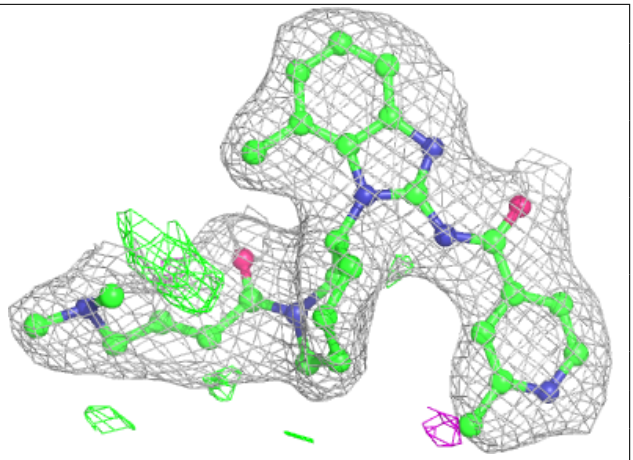


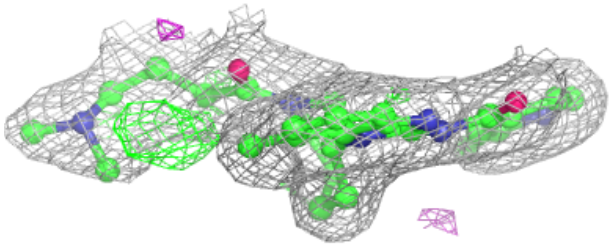


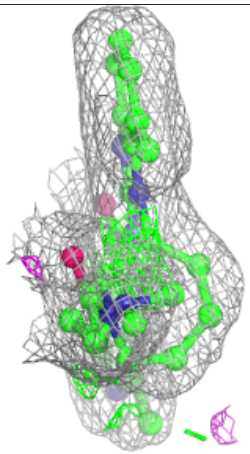


Electron density around 5XH B 504:

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

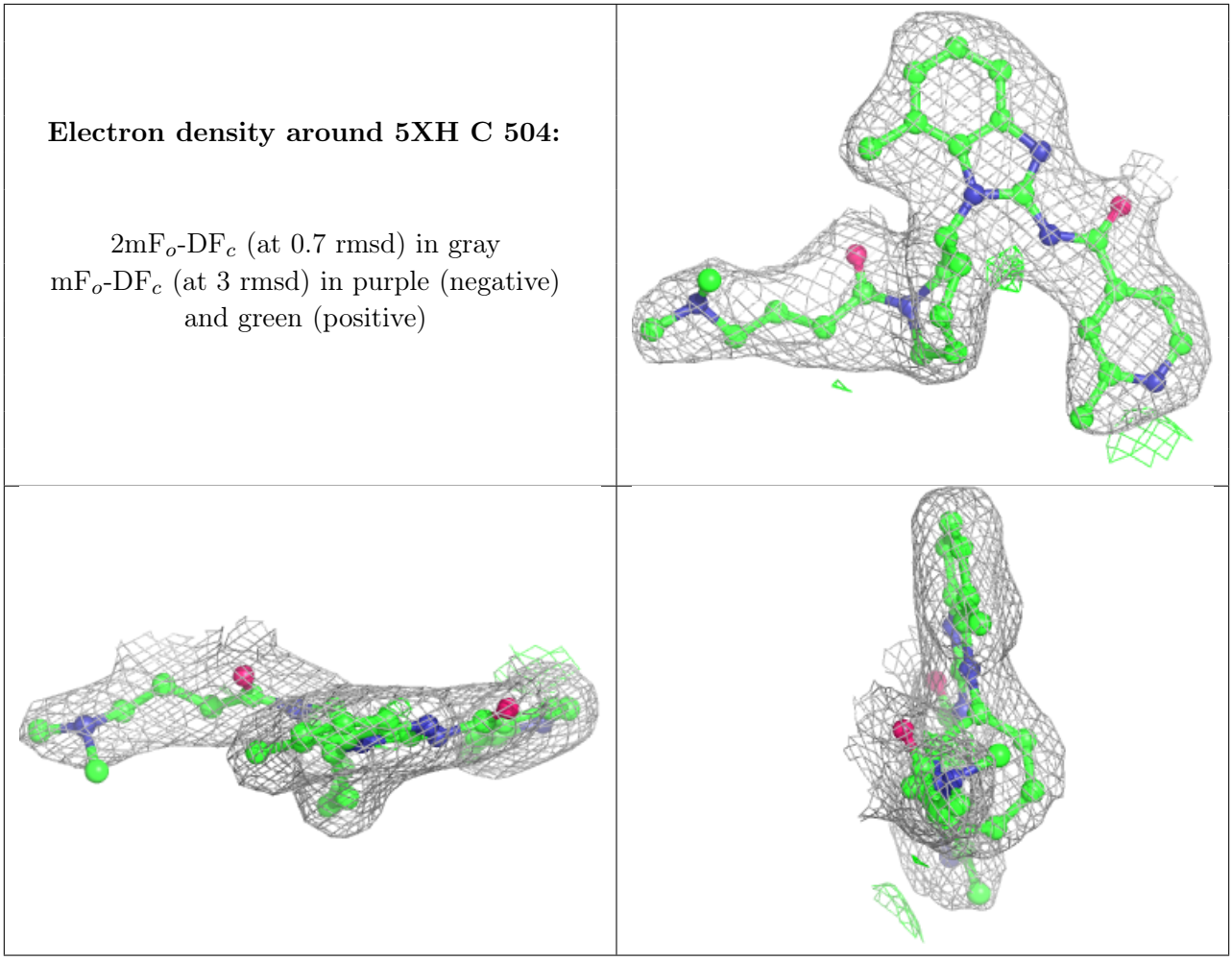






Electron density around 5XH C 504:

$2mF_o$-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.