



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:27 PM UTC

PDB ID : 4KIU / pdb_00004kiu
Title : Design and structural analysis of aromatic inhibitors of type II dehydroquinase dehydratase from Mycobacterium tuberculosis - compound 49d [5-[(3-nitrobenzyl)oxy]benzene-1,3-dicarboxylic acid]
Authors : Dias, M.V.B.; Howard, N.G.; Blundell, T.L.; Abell, C.
Deposited on : 2013-05-02
Resolution : 2.40 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

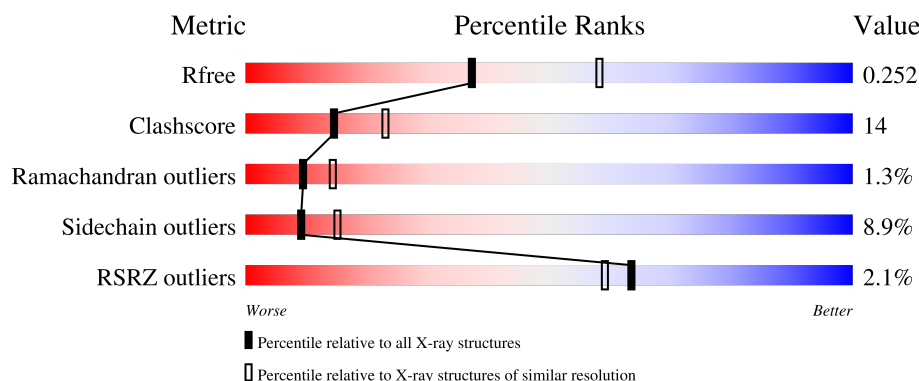
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	153	5% 63% 26% • 8%
1	B	153	% 71% 18% •• 8%
1	C	153	% 72% 17% •• 8%
1	D	153	% 70% 21% • 7%

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Mol	Chain	Length	Quality of chain
1	E	153	
1	F	153	
1	G	153	
1	H	153	
1	I	153	
1	J	153	
1	K	153	
1	L	153	
1	M	153	
1	N	153	
1	O	153	
1	P	153	
1	Q	153	
1	R	153	
1	S	153	
1	T	153	
1	U	153	
1	V	153	
1	W	153	
1	X	153	

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	KIU	B	201	-	X	-	-
2	KIU	I	201	-	-	X	-
2	KIU	K	201	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	KIU	P	201	-	X	X	-
2	KIU	V	201	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 26970 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 3-dehydroquinate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	B	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	C	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	D	143	Total	C	N	O	S	0	0	0
			1082	681	198	202	1			
1	E	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	F	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	G	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	H	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	I	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	J	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	K	141	Total	C	N	O	S	0	0	0
			1065	671	193	200	1			
1	L	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	M	135	Total	C	N	O	S	0	0	0
			1021	644	184	192	1			
1	N	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	O	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	P	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	R	141	Total	C	N	O	S	0	0	0
			1065	671	193	200	1			
1	S	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	T	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	U	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	V	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	W	141	Total	C	N	O	S	0	0	0
			1071	674	196	200	1			
1	X	147	Total	C	N	O	S	0	0	0
			1121	707	202	210	2			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP P0A4Z6
A	-5	TYR	-	expression tag	UNP P0A4Z6
A	-4	PHE	-	expression tag	UNP P0A4Z6
A	-3	GLN	-	expression tag	UNP P0A4Z6
A	-2	SER	-	expression tag	UNP P0A4Z6
A	-1	HIS	-	expression tag	UNP P0A4Z6
B	-6	LEU	-	expression tag	UNP P0A4Z6
B	-5	TYR	-	expression tag	UNP P0A4Z6
B	-4	PHE	-	expression tag	UNP P0A4Z6
B	-3	GLN	-	expression tag	UNP P0A4Z6
B	-2	SER	-	expression tag	UNP P0A4Z6
B	-1	HIS	-	expression tag	UNP P0A4Z6
C	-6	LEU	-	expression tag	UNP P0A4Z6
C	-5	TYR	-	expression tag	UNP P0A4Z6
C	-4	PHE	-	expression tag	UNP P0A4Z6
C	-3	GLN	-	expression tag	UNP P0A4Z6
C	-2	SER	-	expression tag	UNP P0A4Z6
C	-1	HIS	-	expression tag	UNP P0A4Z6
D	-6	LEU	-	expression tag	UNP P0A4Z6
D	-5	TYR	-	expression tag	UNP P0A4Z6
D	-4	PHE	-	expression tag	UNP P0A4Z6
D	-3	GLN	-	expression tag	UNP P0A4Z6
D	-2	SER	-	expression tag	UNP P0A4Z6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	HIS	-	expression tag	UNP P0A4Z6
E	-6	LEU	-	expression tag	UNP P0A4Z6
E	-5	TYR	-	expression tag	UNP P0A4Z6
E	-4	PHE	-	expression tag	UNP P0A4Z6
E	-3	GLN	-	expression tag	UNP P0A4Z6
E	-2	SER	-	expression tag	UNP P0A4Z6
E	-1	HIS	-	expression tag	UNP P0A4Z6
F	-6	LEU	-	expression tag	UNP P0A4Z6
F	-5	TYR	-	expression tag	UNP P0A4Z6
F	-4	PHE	-	expression tag	UNP P0A4Z6
F	-3	GLN	-	expression tag	UNP P0A4Z6
F	-2	SER	-	expression tag	UNP P0A4Z6
F	-1	HIS	-	expression tag	UNP P0A4Z6
G	-6	LEU	-	expression tag	UNP P0A4Z6
G	-5	TYR	-	expression tag	UNP P0A4Z6
G	-4	PHE	-	expression tag	UNP P0A4Z6
G	-3	GLN	-	expression tag	UNP P0A4Z6
G	-2	SER	-	expression tag	UNP P0A4Z6
G	-1	HIS	-	expression tag	UNP P0A4Z6
H	-6	LEU	-	expression tag	UNP P0A4Z6
H	-5	TYR	-	expression tag	UNP P0A4Z6
H	-4	PHE	-	expression tag	UNP P0A4Z6
H	-3	GLN	-	expression tag	UNP P0A4Z6
H	-2	SER	-	expression tag	UNP P0A4Z6
H	-1	HIS	-	expression tag	UNP P0A4Z6
I	-6	LEU	-	expression tag	UNP P0A4Z6
I	-5	TYR	-	expression tag	UNP P0A4Z6
I	-4	PHE	-	expression tag	UNP P0A4Z6
I	-3	GLN	-	expression tag	UNP P0A4Z6
I	-2	SER	-	expression tag	UNP P0A4Z6
I	-1	HIS	-	expression tag	UNP P0A4Z6
J	-6	LEU	-	expression tag	UNP P0A4Z6
J	-5	TYR	-	expression tag	UNP P0A4Z6
J	-4	PHE	-	expression tag	UNP P0A4Z6
J	-3	GLN	-	expression tag	UNP P0A4Z6
J	-2	SER	-	expression tag	UNP P0A4Z6
J	-1	HIS	-	expression tag	UNP P0A4Z6
K	-6	LEU	-	expression tag	UNP P0A4Z6
K	-5	TYR	-	expression tag	UNP P0A4Z6
K	-4	PHE	-	expression tag	UNP P0A4Z6
K	-3	GLN	-	expression tag	UNP P0A4Z6
K	-2	SER	-	expression tag	UNP P0A4Z6

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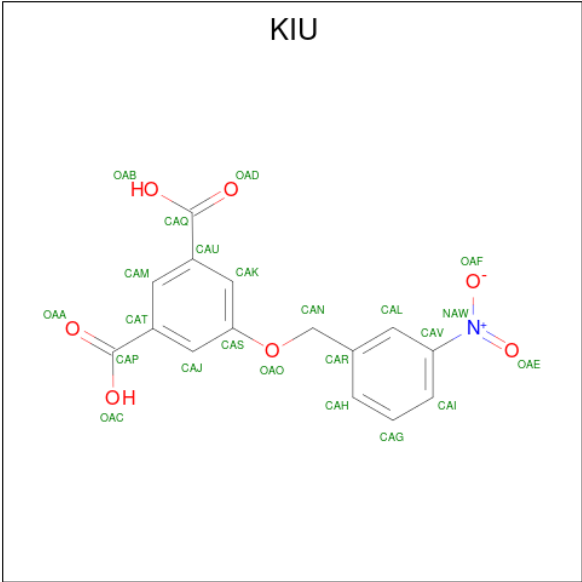
Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	HIS	-	expression tag	UNP P0A4Z6
L	-6	LEU	-	expression tag	UNP P0A4Z6
L	-5	TYR	-	expression tag	UNP P0A4Z6
L	-4	PHE	-	expression tag	UNP P0A4Z6
L	-3	GLN	-	expression tag	UNP P0A4Z6
L	-2	SER	-	expression tag	UNP P0A4Z6
L	-1	HIS	-	expression tag	UNP P0A4Z6
M	-6	LEU	-	expression tag	UNP P0A4Z6
M	-5	TYR	-	expression tag	UNP P0A4Z6
M	-4	PHE	-	expression tag	UNP P0A4Z6
M	-3	GLN	-	expression tag	UNP P0A4Z6
M	-2	SER	-	expression tag	UNP P0A4Z6
M	-1	HIS	-	expression tag	UNP P0A4Z6
N	-6	LEU	-	expression tag	UNP P0A4Z6
N	-5	TYR	-	expression tag	UNP P0A4Z6
N	-4	PHE	-	expression tag	UNP P0A4Z6
N	-3	GLN	-	expression tag	UNP P0A4Z6
N	-2	SER	-	expression tag	UNP P0A4Z6
N	-1	HIS	-	expression tag	UNP P0A4Z6
O	-6	LEU	-	expression tag	UNP P0A4Z6
O	-5	TYR	-	expression tag	UNP P0A4Z6
O	-4	PHE	-	expression tag	UNP P0A4Z6
O	-3	GLN	-	expression tag	UNP P0A4Z6
O	-2	SER	-	expression tag	UNP P0A4Z6
O	-1	HIS	-	expression tag	UNP P0A4Z6
P	-6	LEU	-	expression tag	UNP P0A4Z6
P	-5	TYR	-	expression tag	UNP P0A4Z6
P	-4	PHE	-	expression tag	UNP P0A4Z6
P	-3	GLN	-	expression tag	UNP P0A4Z6
P	-2	SER	-	expression tag	UNP P0A4Z6
P	-1	HIS	-	expression tag	UNP P0A4Z6
Q	-6	LEU	-	expression tag	UNP P0A4Z6
Q	-5	TYR	-	expression tag	UNP P0A4Z6
Q	-4	PHE	-	expression tag	UNP P0A4Z6
Q	-3	GLN	-	expression tag	UNP P0A4Z6
Q	-2	SER	-	expression tag	UNP P0A4Z6
Q	-1	HIS	-	expression tag	UNP P0A4Z6
R	-6	LEU	-	expression tag	UNP P0A4Z6
R	-5	TYR	-	expression tag	UNP P0A4Z6
R	-4	PHE	-	expression tag	UNP P0A4Z6
R	-3	GLN	-	expression tag	UNP P0A4Z6
R	-2	SER	-	expression tag	UNP P0A4Z6

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-1	HIS	-	expression tag	UNP P0A4Z6
S	-6	LEU	-	expression tag	UNP P0A4Z6
S	-5	TYR	-	expression tag	UNP P0A4Z6
S	-4	PHE	-	expression tag	UNP P0A4Z6
S	-3	GLN	-	expression tag	UNP P0A4Z6
S	-2	SER	-	expression tag	UNP P0A4Z6
S	-1	HIS	-	expression tag	UNP P0A4Z6
T	-6	LEU	-	expression tag	UNP P0A4Z6
T	-5	TYR	-	expression tag	UNP P0A4Z6
T	-4	PHE	-	expression tag	UNP P0A4Z6
T	-3	GLN	-	expression tag	UNP P0A4Z6
T	-2	SER	-	expression tag	UNP P0A4Z6
T	-1	HIS	-	expression tag	UNP P0A4Z6
U	-6	LEU	-	expression tag	UNP P0A4Z6
U	-5	TYR	-	expression tag	UNP P0A4Z6
U	-4	PHE	-	expression tag	UNP P0A4Z6
U	-3	GLN	-	expression tag	UNP P0A4Z6
U	-2	SER	-	expression tag	UNP P0A4Z6
U	-1	HIS	-	expression tag	UNP P0A4Z6
V	-6	LEU	-	expression tag	UNP P0A4Z6
V	-5	TYR	-	expression tag	UNP P0A4Z6
V	-4	PHE	-	expression tag	UNP P0A4Z6
V	-3	GLN	-	expression tag	UNP P0A4Z6
V	-2	SER	-	expression tag	UNP P0A4Z6
V	-1	HIS	-	expression tag	UNP P0A4Z6
W	-6	LEU	-	expression tag	UNP P0A4Z6
W	-5	TYR	-	expression tag	UNP P0A4Z6
W	-4	PHE	-	expression tag	UNP P0A4Z6
W	-3	GLN	-	expression tag	UNP P0A4Z6
W	-2	SER	-	expression tag	UNP P0A4Z6
W	-1	HIS	-	expression tag	UNP P0A4Z6
X	-6	LEU	-	expression tag	UNP P0A4Z6
X	-5	TYR	-	expression tag	UNP P0A4Z6
X	-4	PHE	-	expression tag	UNP P0A4Z6
X	-3	GLN	-	expression tag	UNP P0A4Z6
X	-2	SER	-	expression tag	UNP P0A4Z6
X	-1	HIS	-	expression tag	UNP P0A4Z6

- Molecule 2 is 5-[(3-nitrobenzyl)oxy]benzene-1,3-dicarboxylic acid (CCD ID: KIU) (formula: C₁₅H₁₁NO₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	15	1	7		
2	B	1	Total	C	N	O	0	0
			23	15	1	7		
2	C	1	Total	C	N	O	0	0
			23	15	1	7		
2	D	1	Total	C	N	O	0	0
			23	15	1	7		
2	E	1	Total	C	N	O	0	0
			23	15	1	7		
2	F	1	Total	C	N	O	0	0
			23	15	1	7		
2	G	1	Total	C	N	O	0	0
			23	15	1	7		
2	H	1	Total	C	N	O	0	0
			23	15	1	7		
2	I	1	Total	C	N	O	0	0
			23	15	1	7		
2	J	1	Total	C	N	O	0	0
			23	15	1	7		
2	K	1	Total	C	N	O	0	0
			23	15	1	7		
2	L	1	Total	C	N	O	0	0
			23	15	1	7		
2	N	1	Total	C	N	O	0	0
			23	15	1	7		
2	O	1	Total	C	N	O	0	0
			23	15	1	7		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	P	1	Total	C	N	O	0	0
			23	15	1	7		
2	Q	1	Total	C	N	O	0	0
			23	15	1	7		
2	R	1	Total	C	N	O	0	0
			23	15	1	7		
2	T	1	Total	C	N	O	0	0
			23	15	1	7		
2	U	1	Total	C	N	O	0	0
			23	15	1	7		
2	V	1	Total	C	N	O	0	0
			23	15	1	7		
2	W	1	Total	C	N	O	0	0
			23	15	1	7		
2	X	1	Total	C	N	O	0	0
			23	15	1	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	29	Total	O	0	0
			29	29		
3	B	34	Total	O	0	0
			34	34		
3	C	44	Total	O	0	0
			44	44		
3	D	40	Total	O	0	0
			40	40		
3	E	38	Total	O	0	0
			38	38		
3	F	48	Total	O	0	0
			48	48		
3	G	33	Total	O	0	0
			33	33		
3	H	34	Total	O	0	0
			34	34		
3	I	41	Total	O	0	0
			41	41		
3	J	41	Total	O	0	0
			41	41		
3	K	28	Total	O	0	0
			28	28		

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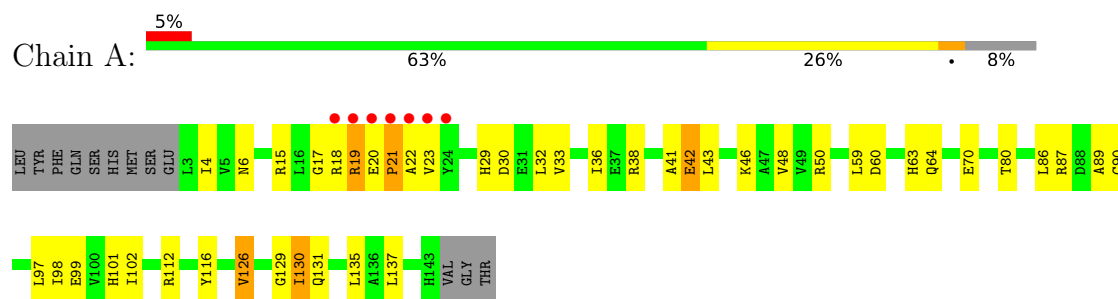
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	27	Total 27	O 27	0	0
3	M	29	Total 29	O 29	0	0
3	N	19	Total 19	O 19	0	0
3	O	36	Total 36	O 36	0	0
3	P	26	Total 26	O 26	0	0
3	Q	19	Total 19	O 19	0	0
3	R	26	Total 26	O 26	0	0
3	S	28	Total 28	O 28	0	0
3	T	37	Total 37	O 37	0	0
3	U	33	Total 33	O 33	0	0
3	V	24	Total 24	O 24	0	0
3	W	16	Total 16	O 16	0	0
3	X	31	Total 31	O 31	0	0

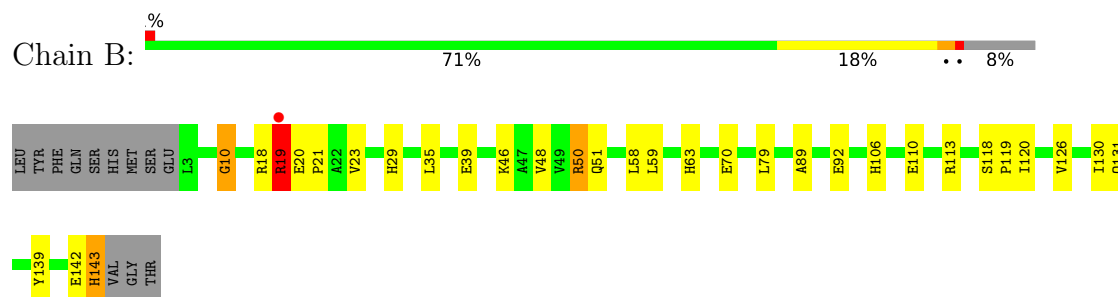
3 Residue-property plots [i](#)

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.

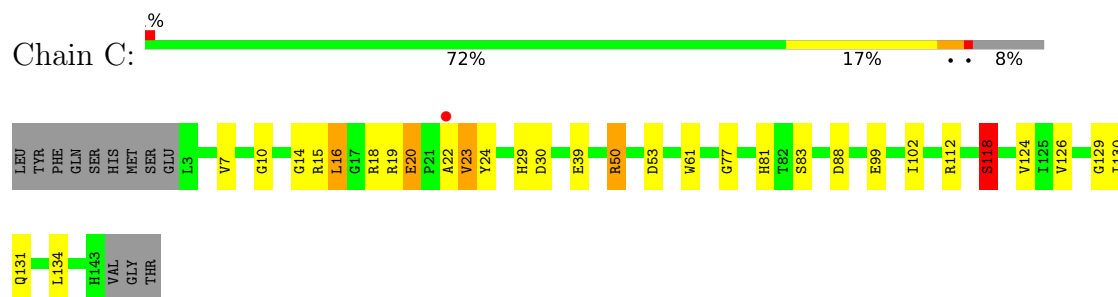
- Molecule 1: 3-dehydroquinase dehydratase



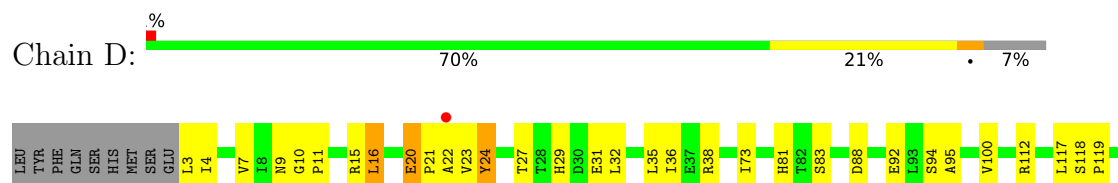
- Molecule 1: 3-dehydroquinase dehydratase

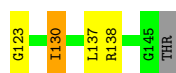


- Molecule 1: 3-dehydroquinase dehydratase



- Molecule 1: 3-dehydroquinase dehydratase





- Molecule 1: 3-dehydroquinate dehydratase



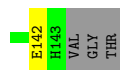
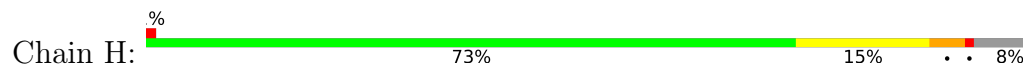
- Molecule 1: 3-dehydroquinate dehydratase



- Molecule 1: 3-dehydroquinate dehydratase



- Molecule 1: 3-dehydroquinate dehydratase

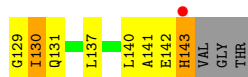


- Molecule 1: 3-dehydroquinate dehydratase





Chain J: 66% 21% 8%



Chain K: %



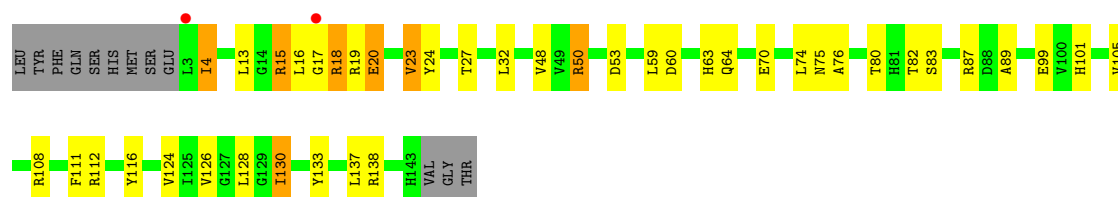
Chain L: %



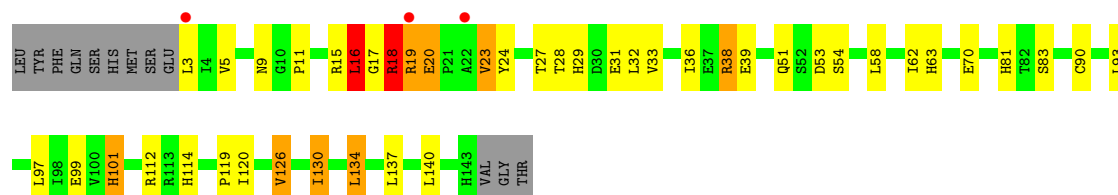
Chain M:



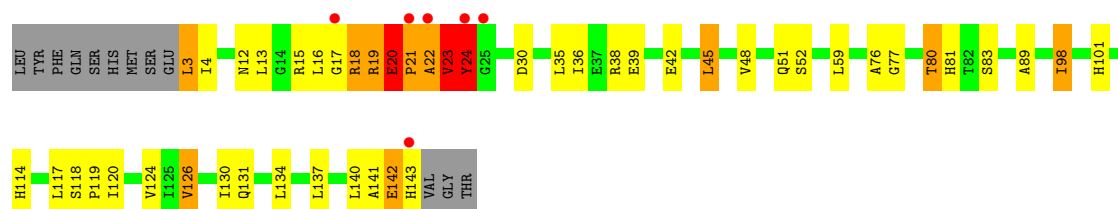
- Molecule 1: 3-dehydroquinate dehydratase



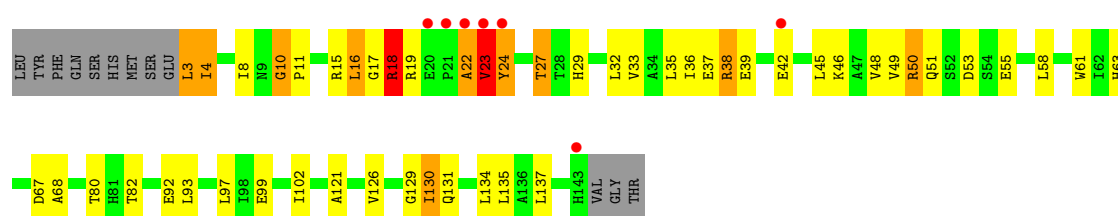
- Molecule 1: 3-dehydroquinate dehydratase



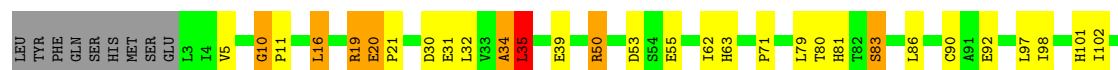
- Molecule 1: 3-dehydroquinate dehydratase



- Molecule 1: 3-dehydroquinate dehydratase

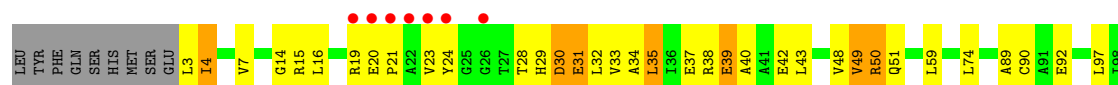


- Molecule 1: 3-dehydroquinate dehydratase





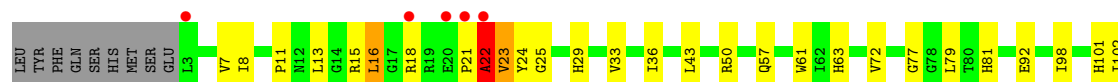
- Molecule 1: 3-dehydroquininate dehydratase



- Molecule 1: 3-dehydroquininate dehydratase



- Molecule 1: 3-dehydroquininate dehydratase

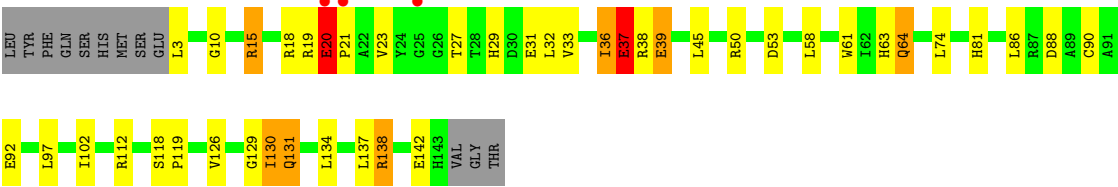


- Molecule 1: 3-dehydroquininate dehydratase

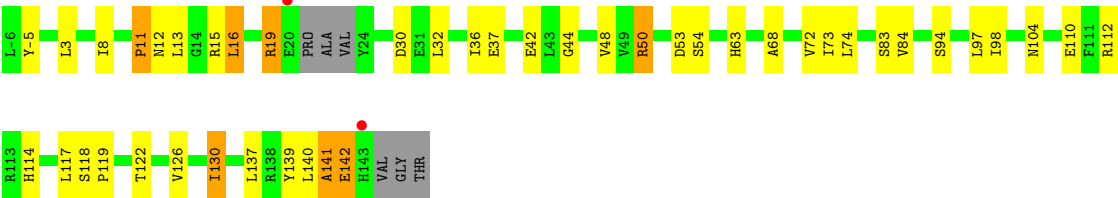


- Molecule 1: 3-dehydroquininate dehydratase





● Molecule 1: 3-dehydroquinate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.41Å 139.15Å 143.29Å 90.00° 96.60° 90.00°	Depositor
Resolution (Å)	45.28 – 2.40 45.28 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.0 (45.28-2.40) 95.0 (45.28-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.190 , 0.265 (Not available) , 0.252	Depositor DCC
R_{free} test set	6962 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	26970	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KIU

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	1.08	0/1089	1.13	2/1483 (0.1%)
1	B	1.11	1/1089 (0.1%)	1.14	4/1483 (0.3%)
1	C	1.12	2/1089 (0.2%)	1.15	7/1483 (0.5%)
1	D	1.16	0/1100	1.26	8/1498 (0.5%)
1	E	1.11	0/1089	1.16	4/1483 (0.3%)
1	F	1.06	0/1089	1.14	6/1483 (0.4%)
1	G	1.09	0/1089	1.18	2/1483 (0.1%)
1	H	1.13	0/1089	1.11	0/1483
1	I	1.12	2/1089 (0.2%)	1.16	4/1483 (0.3%)
1	J	1.12	1/1089 (0.1%)	1.23	4/1483 (0.3%)
1	K	1.07	2/1083 (0.2%)	1.13	1/1476 (0.1%)
1	L	1.14	0/1089	1.27	6/1483 (0.4%)
1	M	1.04	0/1037	1.17	7/1411 (0.5%)
1	N	0.97	0/1089	1.08	1/1483 (0.1%)
1	O	1.10	2/1089 (0.2%)	1.19	6/1483 (0.4%)
1	P	1.02	2/1089 (0.2%)	1.19	3/1483 (0.2%)
1	Q	0.97	0/1089	1.17	7/1483 (0.5%)
1	R	0.99	0/1083	1.12	4/1476 (0.3%)
1	S	1.03	1/1089 (0.1%)	1.10	2/1483 (0.1%)
1	T	1.08	0/1089	1.16	4/1483 (0.3%)
1	U	1.02	0/1089	1.11	3/1483 (0.2%)
1	V	1.08	3/1089 (0.3%)	1.18	3/1483 (0.2%)
1	W	0.94	0/1089	1.08	2/1483 (0.1%)
1	X	1.05	1/1140 (0.1%)	1.12	4/1549 (0.3%)
All	All	1.07	17/26134 (0.1%)	1.16	94/35587 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2
1	E	0	1
1	I	0	1
1	O	0	1
1	P	0	2
1	Q	0	1
1	U	0	1
1	W	0	1
All	All	0	10

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	58	LEU	C-O	-5.79	1.17	1.24
1	V	4	ILE	N-CA	5.77	1.53	1.46
1	J	114	HIS	CG-CD2	5.67	1.42	1.35
1	B	143	HIS	CG-CD2	5.49	1.41	1.35
1	O	101	HIS	CG-CD2	5.45	1.41	1.35

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	20	GLU	CA-C-N	-11.41	105.58	119.84
1	L	20	GLU	C-N-CA	-11.41	105.58	119.84
1	I	24	TYR	N-CA-C	10.91	127.90	113.72
1	P	24	TYR	N-CA-C	10.26	125.96	113.23
1	Q	23	VAL	N-CA-C	10.20	126.73	112.35

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	22	ALA	Peptide
1	D	24	TYR	Peptide
1	E	20	GLU	Peptide
1	I	24	TYR	Peptide
1	O	16	LEU	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1071	0	1079	39	0
1	B	1071	0	1079	18	0
1	C	1071	0	1079	23	0
1	D	1082	0	1091	27	0
1	E	1071	0	1079	24	0
1	F	1071	0	1079	25	0
1	G	1071	0	1079	28	0
1	H	1071	0	1079	25	0
1	I	1071	0	1079	36	0
1	J	1071	0	1079	33	0
1	K	1065	0	1068	29	0
1	L	1071	0	1079	27	0
1	M	1021	0	1025	33	0
1	N	1071	0	1079	39	0
1	O	1071	0	1079	39	0
1	P	1071	0	1079	40	0
1	Q	1071	0	1079	34	0
1	R	1065	0	1068	34	0
1	S	1071	0	1079	25	0
1	T	1071	0	1079	33	0
1	U	1071	0	1079	28	0
1	V	1071	0	1079	63	0
1	W	1071	0	1079	46	0
1	X	1121	0	1114	32	0
2	A	23	0	9	2	0
2	B	23	0	9	2	0
2	C	23	0	9	6	0
2	D	23	0	9	3	0
2	E	23	0	9	2	0
2	F	23	0	9	6	0
2	G	23	0	9	2	0
2	H	23	0	9	4	0
2	I	23	0	9	7	0
2	J	23	0	9	6	0
2	K	23	0	9	8	0
2	L	23	0	9	4	0
2	N	23	0	9	5	0
2	O	23	0	9	3	0
2	P	23	0	9	7	0
2	Q	23	0	9	1	0
2	R	23	0	9	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	T	23	0	9	6	0
2	U	23	0	9	4	0
2	V	23	0	9	16	0
2	W	23	0	9	5	0
2	X	23	0	9	5	0
3	A	29	0	0	0	0
3	B	34	0	0	0	0
3	C	44	0	0	0	0
3	D	40	0	0	0	0
3	E	38	0	0	1	0
3	F	48	0	0	1	0
3	G	33	0	0	2	0
3	H	34	0	0	0	0
3	I	41	0	0	1	0
3	J	41	0	0	0	0
3	K	28	0	0	0	0
3	L	27	0	0	2	0
3	M	29	0	0	0	0
3	N	19	0	0	0	0
3	O	36	0	0	0	0
3	P	26	0	0	1	0
3	Q	19	0	0	1	0
3	R	26	0	0	0	0
3	S	28	0	0	1	0
3	T	37	0	0	0	0
3	U	33	0	0	1	0
3	V	24	0	0	0	0
3	W	16	0	0	0	0
3	X	31	0	0	0	0
All	All	26970	0	26065	729	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 14.

The worst 5 of 729 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)
2:I:201:KIU:NAW	2:I:201:KIU:OAF	1.56	1.37
2:I:201:KIU:NAW	2:I:201:KIU:OAE	1.60	1.35
2:T:201:KIU:NAW	2:T:201:KIU:OAE	1.61	1.33
2:J:201:KIU:NAW	2:J:201:KIU:OAF	1.61	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:201:KIU:NAW	2:B:201:KIU:OAF	1.62	1.31

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	139/153 (91%)	126 (91%)	10 (7%)	3 (2%)	5	6
1	B	139/153 (91%)	129 (93%)	7 (5%)	3 (2%)	5	6
1	C	139/153 (91%)	134 (96%)	4 (3%)	1 (1%)	18	28
1	D	141/153 (92%)	133 (94%)	8 (6%)	0	100	100
1	E	139/153 (91%)	134 (96%)	4 (3%)	1 (1%)	18	28
1	F	139/153 (91%)	131 (94%)	8 (6%)	0	100	100
1	G	139/153 (91%)	133 (96%)	6 (4%)	0	100	100
1	H	139/153 (91%)	129 (93%)	7 (5%)	3 (2%)	5	6
1	I	139/153 (91%)	129 (93%)	9 (6%)	1 (1%)	18	28
1	J	139/153 (91%)	130 (94%)	4 (3%)	5 (4%)	2	2
1	K	139/153 (91%)	131 (94%)	7 (5%)	1 (1%)	18	28
1	L	139/153 (91%)	131 (94%)	5 (4%)	3 (2%)	5	6
1	M	131/153 (86%)	122 (93%)	9 (7%)	0	100	100
1	N	139/153 (91%)	129 (93%)	9 (6%)	1 (1%)	18	28
1	O	139/153 (91%)	131 (94%)	7 (5%)	1 (1%)	18	28
1	P	139/153 (91%)	125 (90%)	8 (6%)	6 (4%)	2	1
1	Q	139/153 (91%)	131 (94%)	6 (4%)	2 (1%)	9	13
1	R	139/153 (91%)	129 (93%)	7 (5%)	3 (2%)	5	6
1	S	139/153 (91%)	126 (91%)	11 (8%)	2 (1%)	9	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	139/153 (91%)	134 (96%)	5 (4%)	0	100	100
1	U	139/153 (91%)	127 (91%)	11 (8%)	1 (1%)	18	28
1	V	139/153 (91%)	126 (91%)	12 (9%)	1 (1%)	18	28
1	W	139/153 (91%)	126 (91%)	9 (6%)	4 (3%)	3	3
1	X	143/153 (94%)	133 (93%)	9 (6%)	1 (1%)	18	28
All	All	3334/3672 (91%)	3109 (93%)	182 (6%)	43 (1%)	9	14

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	PRO
1	B	19	ARG
1	C	23	VAL
1	H	21	PRO
1	I	19	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	110/121 (91%)	101 (92%)	9 (8%)	10	18
1	B	110/121 (91%)	100 (91%)	10 (9%)	9	14
1	C	110/121 (91%)	103 (94%)	7 (6%)	16	28
1	D	111/121 (92%)	105 (95%)	6 (5%)	20	35
1	E	110/121 (91%)	102 (93%)	8 (7%)	13	22
1	F	110/121 (91%)	100 (91%)	10 (9%)	9	14
1	G	110/121 (91%)	100 (91%)	10 (9%)	9	14
1	H	110/121 (91%)	103 (94%)	7 (6%)	16	28
1	I	110/121 (91%)	101 (92%)	9 (8%)	10	18
1	J	110/121 (91%)	99 (90%)	11 (10%)	7	11
1	K	109/121 (90%)	100 (92%)	9 (8%)	10	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	110/121 (91%)	104 (94%)	6 (6%)	19	34
1	M	105/121 (87%)	97 (92%)	8 (8%)	12	21
1	N	110/121 (91%)	101 (92%)	9 (8%)	10	18
1	O	110/121 (91%)	100 (91%)	10 (9%)	9	14
1	P	110/121 (91%)	94 (86%)	16 (14%)	3	4
1	Q	110/121 (91%)	95 (86%)	15 (14%)	3	5
1	R	109/121 (90%)	102 (94%)	7 (6%)	16	28
1	S	110/121 (91%)	96 (87%)	14 (13%)	4	6
1	T	110/121 (91%)	99 (90%)	11 (10%)	7	11
1	U	110/121 (91%)	104 (94%)	6 (6%)	19	34
1	V	110/121 (91%)	95 (86%)	15 (14%)	3	5
1	W	110/121 (91%)	99 (90%)	11 (10%)	7	11
1	X	115/121 (95%)	105 (91%)	10 (9%)	9	16
All	All	2639/2904 (91%)	2405 (91%)	234 (9%)	9	15

5 of 234 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	27	THR
1	W	131	GLN
1	P	131	GLN
1	W	126	VAL
1	V	4	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	51	GLN
1	V	131	GLN
1	P	57	GLN
1	S	143	HIS
1	W	64	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

22 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	KIU	H	201	-	24,24,24	6.45	6 (25%)	31,33,33	1.97	12 (38%)
2	KIU	J	201	-	24,24,24	7.03	7 (29%)	31,33,33	2.30	8 (25%)
2	KIU	U	201	-	24,24,24	4.45	5 (20%)	31,33,33	1.30	3 (9%)
2	KIU	K	201	-	24,24,24	2.51	6 (25%)	31,33,33	1.98	10 (32%)
2	KIU	I	201	-	24,24,24	5.04	9 (37%)	31,33,33	1.63	7 (22%)
2	KIU	G	201	-	24,24,24	7.07	8 (33%)	31,33,33	1.73	8 (25%)
2	KIU	V	201	-	24,24,24	2.43	6 (25%)	31,33,33	1.90	10 (32%)
2	KIU	W	201	-	24,24,24	2.87	6 (25%)	31,33,33	1.65	5 (16%)
2	KIU	R	201	-	24,24,24	3.59	5 (20%)	31,33,33	1.26	2 (6%)
2	KIU	P	201	-	24,24,24	5.03	8 (33%)	31,33,33	3.79	15 (48%)
2	KIU	E	201	-	24,24,24	3.54	7 (29%)	31,33,33	1.62	5 (16%)
2	KIU	O	201	-	24,24,24	3.26	6 (25%)	31,33,33	1.88	9 (29%)
2	KIU	C	201	-	24,24,24	3.29	7 (29%)	31,33,33	1.34	4 (12%)
2	KIU	B	201	-	24,24,24	5.78	7 (29%)	31,33,33	2.48	15 (48%)
2	KIU	N	201	-	24,24,24	3.61	6 (25%)	31,33,33	2.14	8 (25%)
2	KIU	Q	201	-	24,24,24	5.28	8 (33%)	31,33,33	1.77	7 (22%)
2	KIU	D	201	-	24,24,24	3.52	7 (29%)	31,33,33	2.25	8 (25%)
2	KIU	T	201	-	24,24,24	5.16	8 (33%)	31,33,33	3.72	13 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	KIU	A	201	-	24,24,24	2.49	5 (20%)	31,33,33	1.41	5 (16%)
2	KIU	F	201	-	24,24,24	4.14	6 (25%)	31,33,33	2.02	8 (25%)
2	KIU	L	201	-	24,24,24	2.83	8 (33%)	31,33,33	2.07	8 (25%)
2	KIU	X	201	-	24,24,24	3.83	7 (29%)	31,33,33	1.52	6 (19%)

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	KIU	H	201	-	-	5/15/17/17	0/2/2/2
2	KIU	J	201	-	-	7/15/17/17	0/2/2/2
2	KIU	U	201	-	-	10/15/17/17	0/2/2/2
2	KIU	K	201	-	-	11/15/17/17	0/2/2/2
2	KIU	I	201	-	-	5/15/17/17	0/2/2/2
2	KIU	G	201	-	-	7/15/17/17	0/2/2/2
2	KIU	V	201	-	-	10/15/17/17	0/2/2/2
2	KIU	W	201	-	-	9/15/17/17	0/2/2/2
2	KIU	R	201	-	-	3/15/17/17	0/2/2/2
2	KIU	P	201	-	-	11/15/17/17	0/2/2/2
2	KIU	E	201	-	-	5/15/17/17	0/2/2/2
2	KIU	O	201	-	-	8/15/17/17	0/2/2/2
2	KIU	C	201	-	-	9/15/17/17	0/2/2/2
2	KIU	B	201	-	-	9/15/17/17	0/2/2/2
2	KIU	N	201	-	-	8/15/17/17	0/2/2/2
2	KIU	Q	201	-	-	3/15/17/17	0/2/2/2
2	KIU	D	201	-	-	10/15/17/17	0/2/2/2
2	KIU	T	201	-	-	8/15/17/17	0/2/2/2
2	KIU	A	201	-	-	7/15/17/17	0/2/2/2
2	KIU	F	201	-	-	6/15/17/17	0/2/2/2
2	KIU	L	201	-	-	5/15/17/17	0/2/2/2
2	KIU	X	201	-	-	5/15/17/17	0/2/2/2

The worst 5 of 148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	201	KIU	OAE-NAW	32.92	1.79	1.22
2	G	201	KIU	OAE-NAW	32.40	1.78	1.22
2	H	201	KIU	OAE-NAW	29.62	1.73	1.22
2	B	201	KIU	OAE-NAW	26.34	1.68	1.22
2	Q	201	KIU	OAE-NAW	23.42	1.63	1.22

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	201	KIU	CAL-CAV-NAW	13.39	130.28	118.74
2	P	201	KIU	CAL-CAV-NAW	11.76	128.87	118.74
2	P	201	KIU	CAI-CAV-NAW	-10.56	110.11	119.34
2	T	201	KIU	CAI-CAV-NAW	-9.17	111.33	119.34
2	D	201	KIU	CAI-CAV-NAW	7.59	125.97	119.34

There are no chirality outliers.

5 of 161 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	KIU	CAL-CAV-NAW-OAE
2	A	201	KIU	CAI-CAV-NAW-OAE
2	F	201	KIU	CAL-CAV-NAW-OAE
2	F	201	KIU	CAI-CAV-NAW-OAE
2	K	201	KIU	CAL-CAV-NAW-OAE

There are no ring outliers.

22 monomers are involved in 108 short contacts:

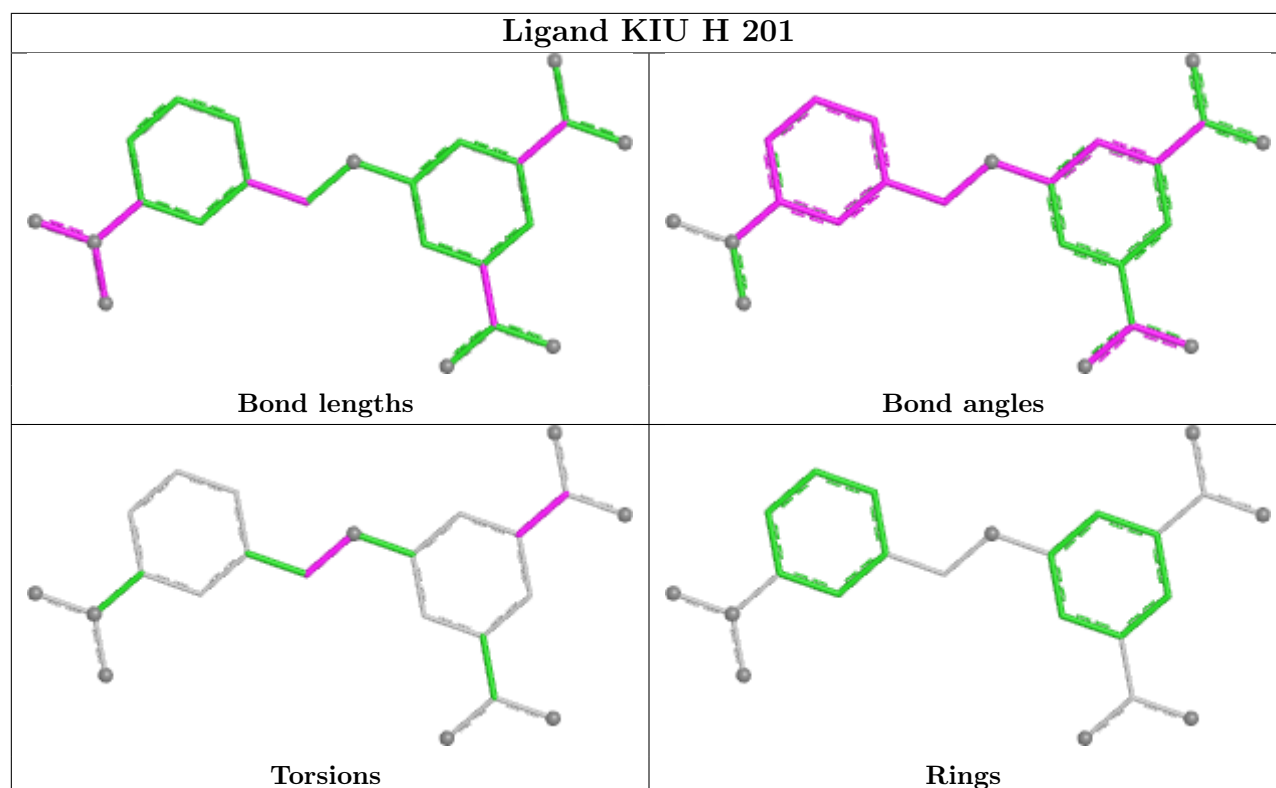
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	201	KIU	4	0
2	J	201	KIU	6	0
2	U	201	KIU	4	0
2	K	201	KIU	8	0
2	I	201	KIU	7	0
2	G	201	KIU	2	0
2	V	201	KIU	16	0
2	W	201	KIU	5	0
2	R	201	KIU	4	0
2	P	201	KIU	7	0
2	E	201	KIU	2	0
2	O	201	KIU	3	0
2	C	201	KIU	6	0

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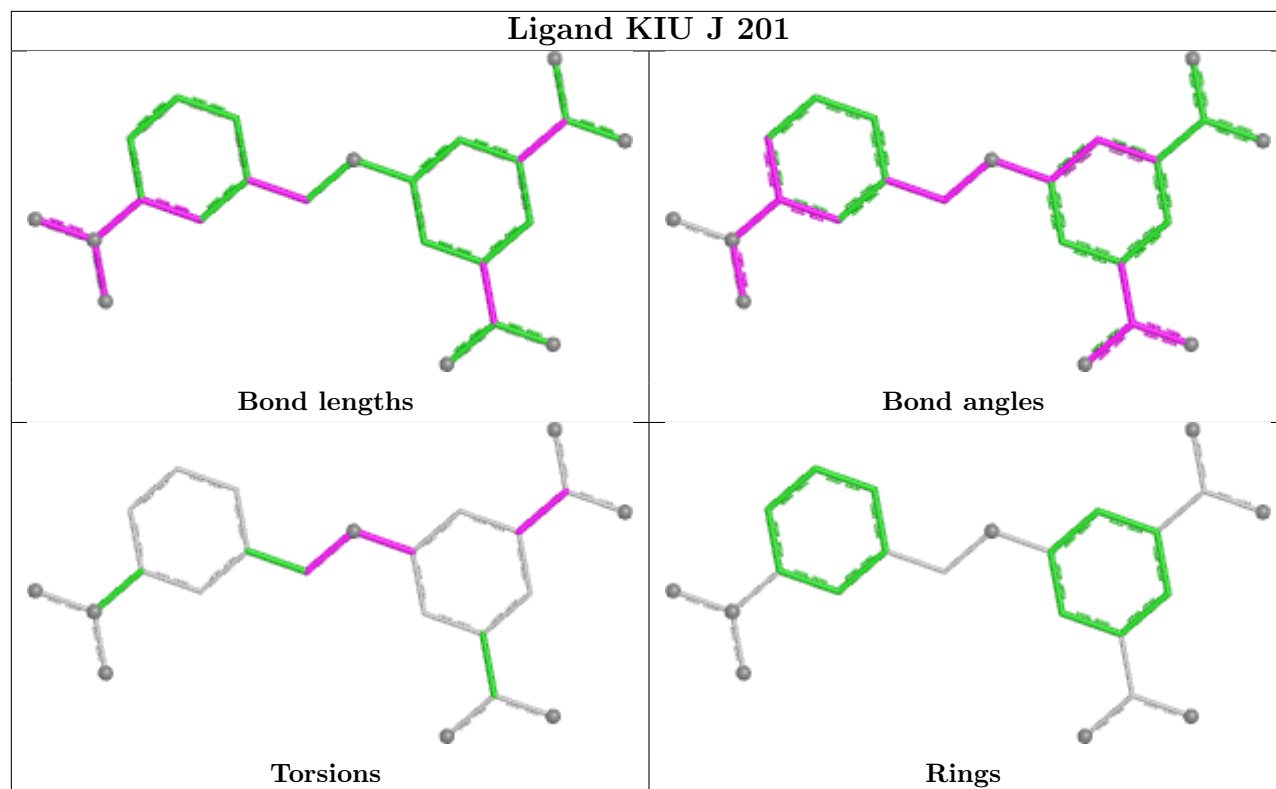
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	KIU	2	0
2	N	201	KIU	5	0
2	Q	201	KIU	1	0
2	D	201	KIU	3	0
2	T	201	KIU	6	0
2	A	201	KIU	2	0
2	F	201	KIU	6	0
2	L	201	KIU	4	0
2	X	201	KIU	5	0

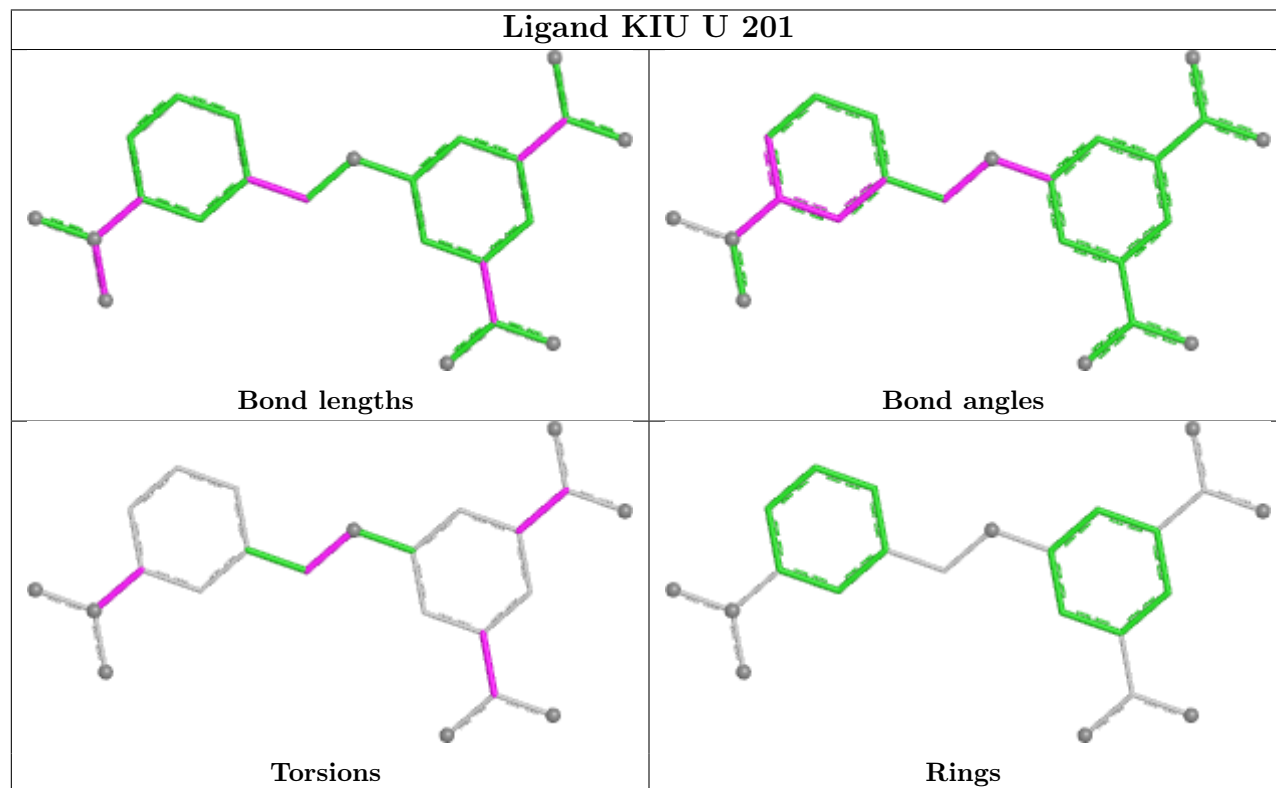
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



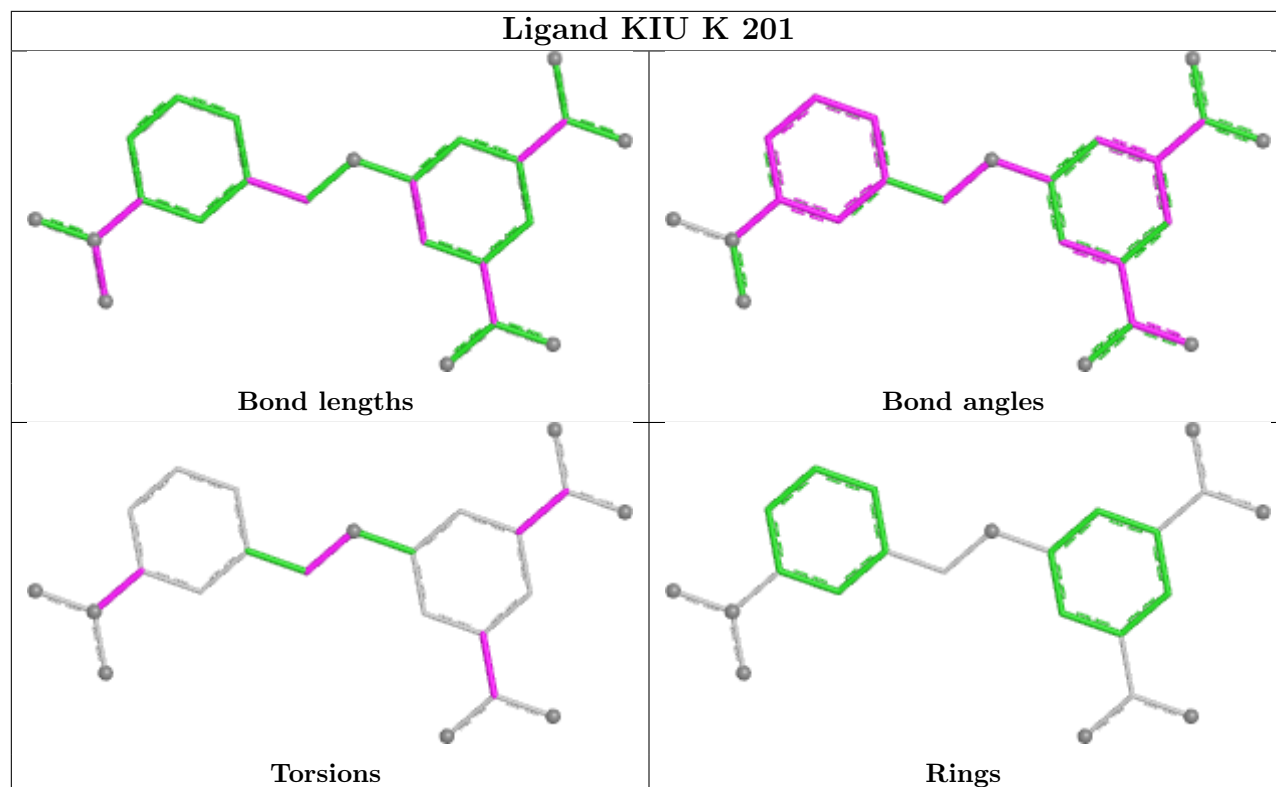
Ligand KIU J 201



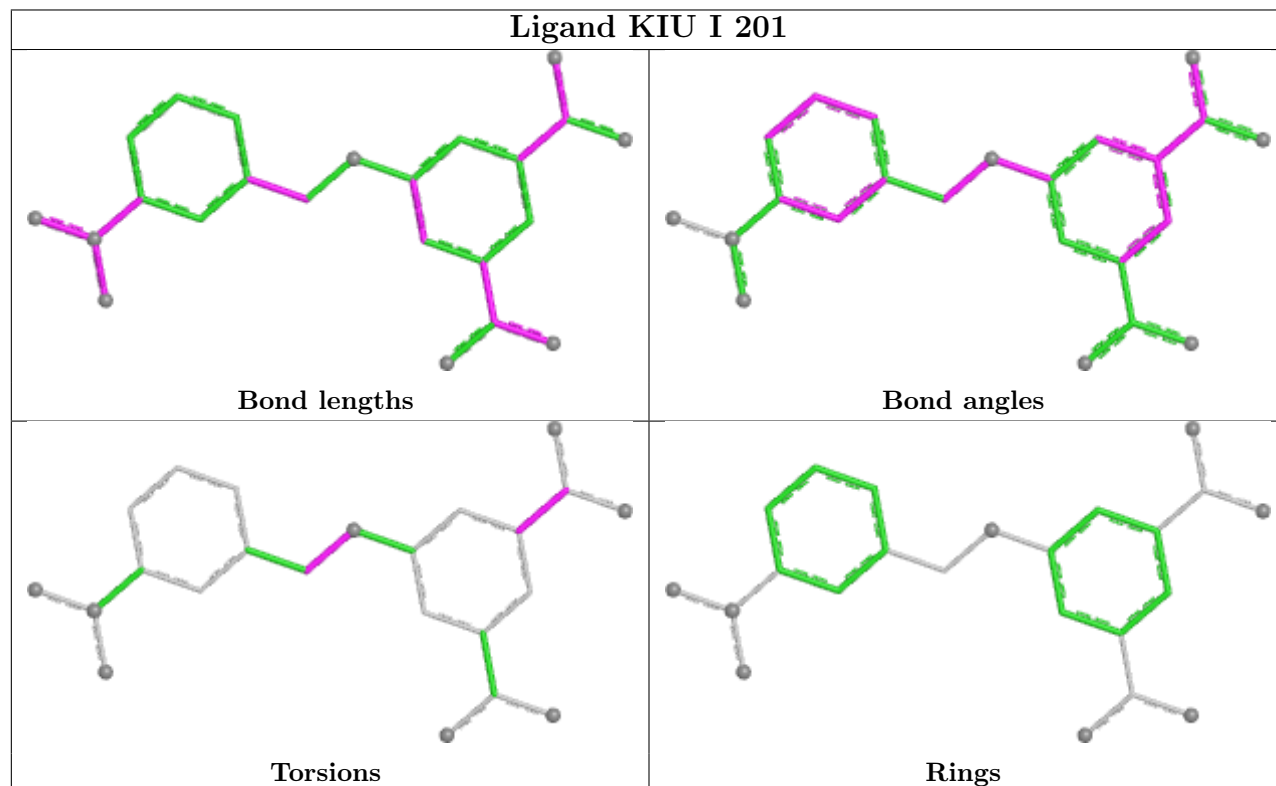
Ligand KIU U 201



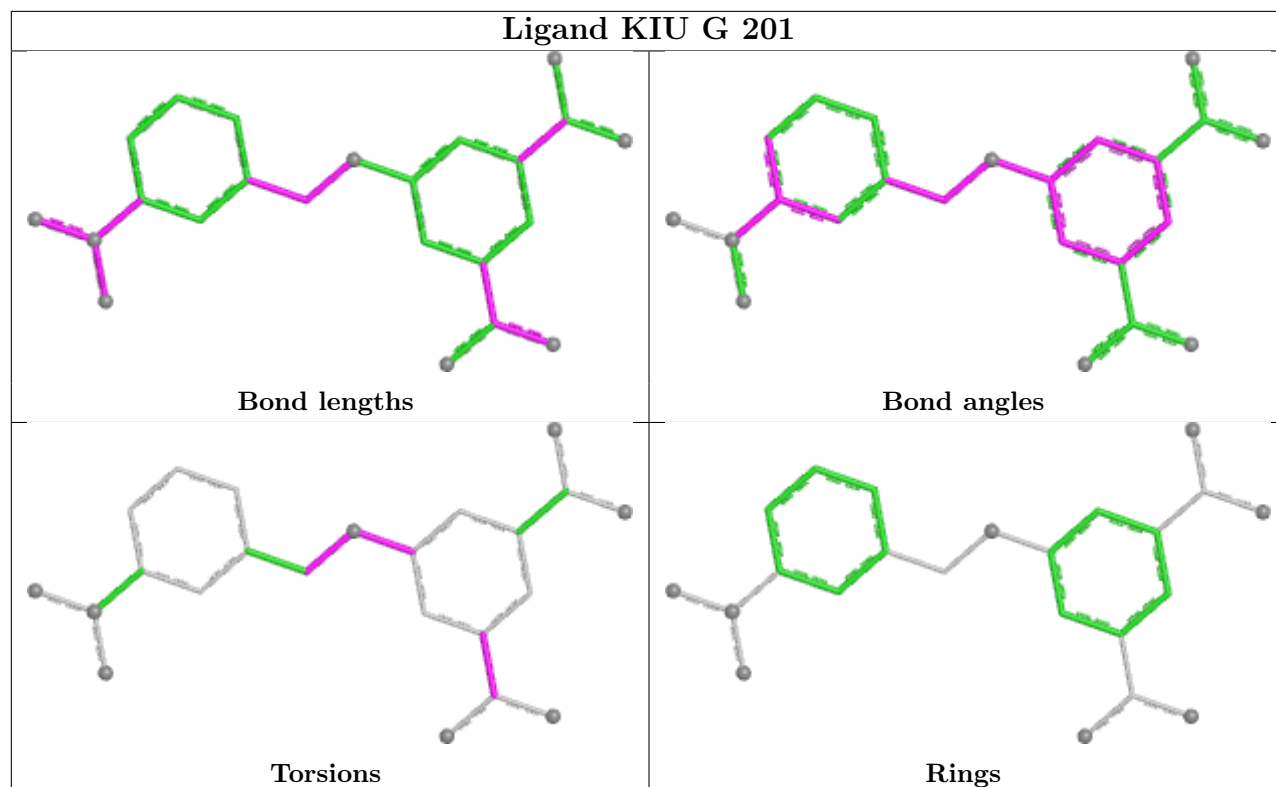
Ligand KIU K 201



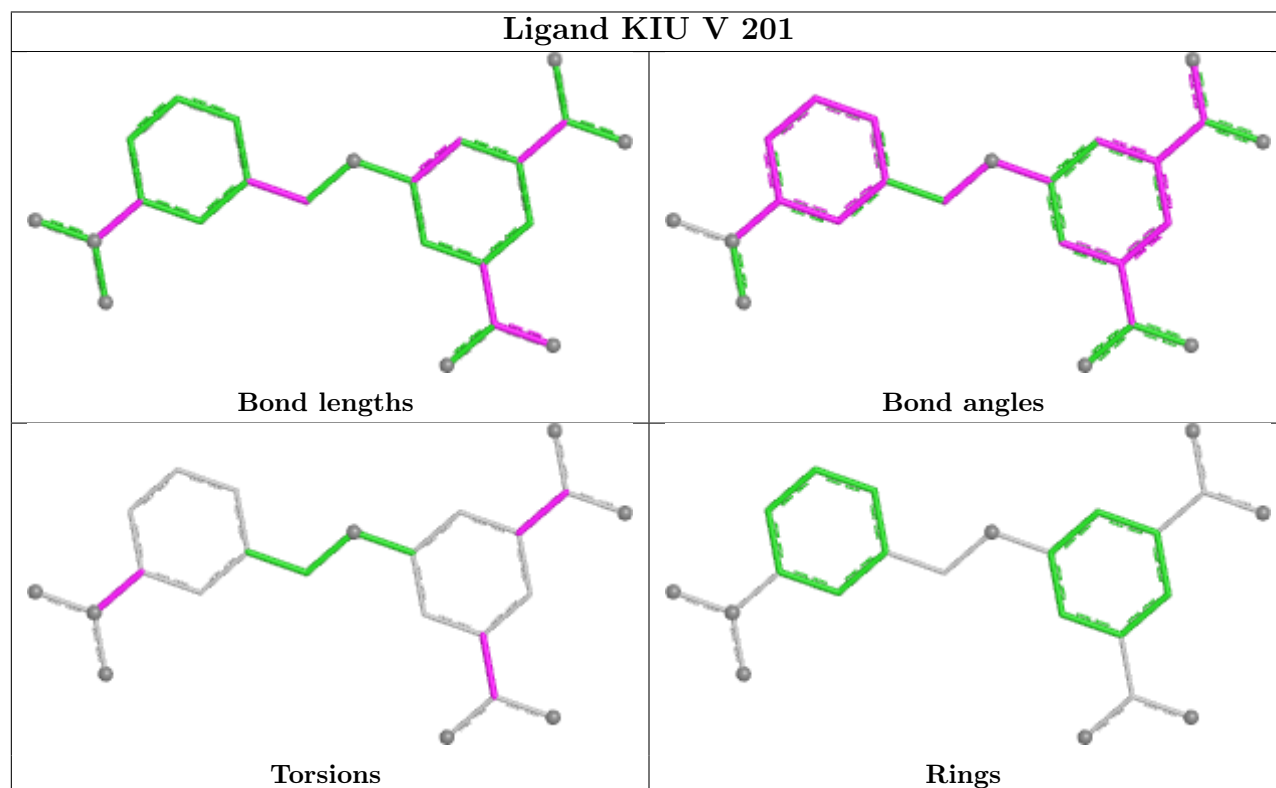
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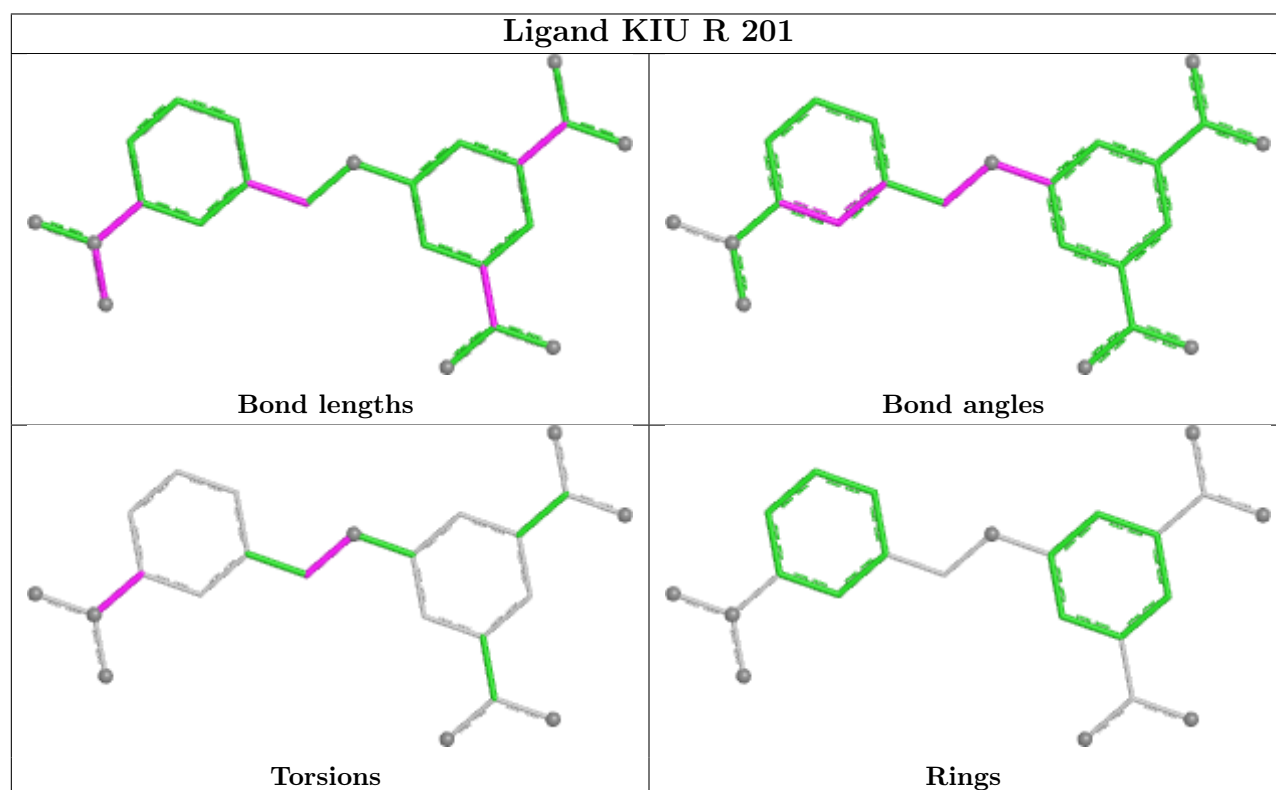
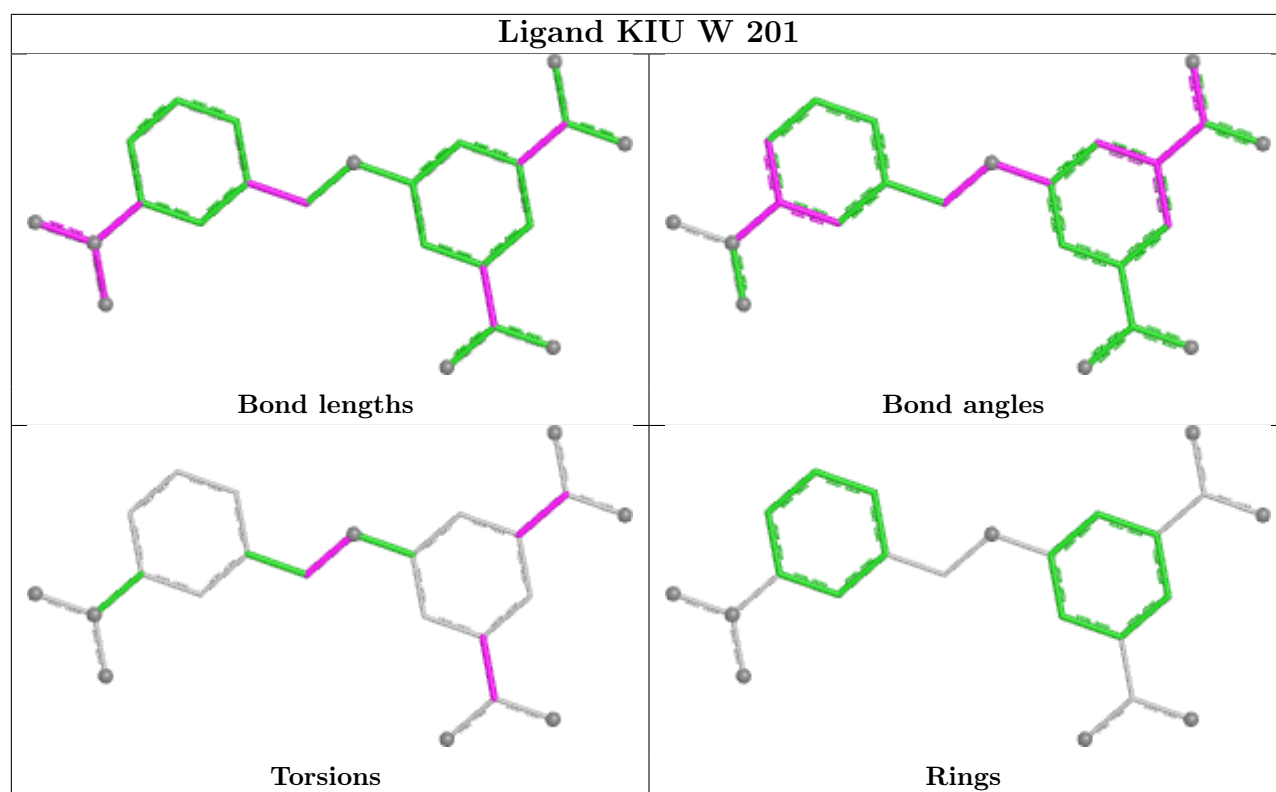


Ligand KIU G 201

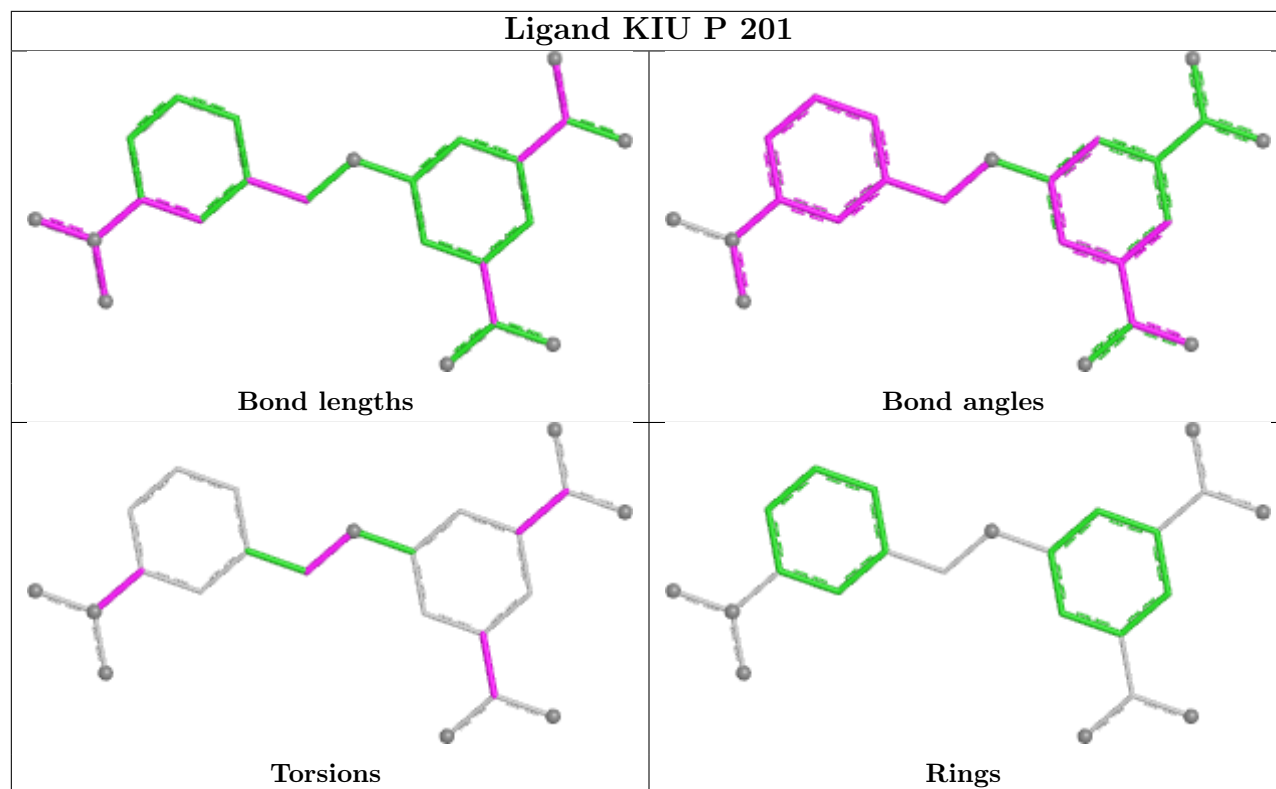


Ligand KIU V 201

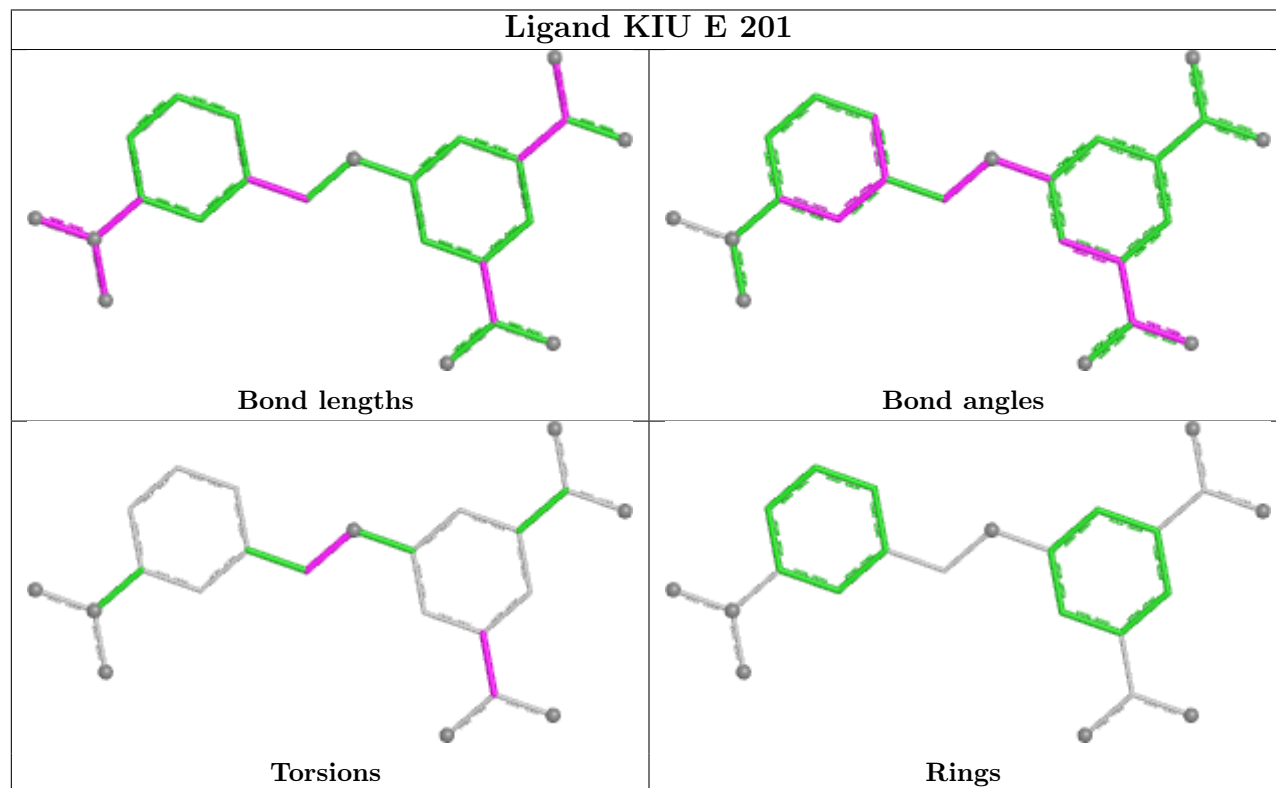




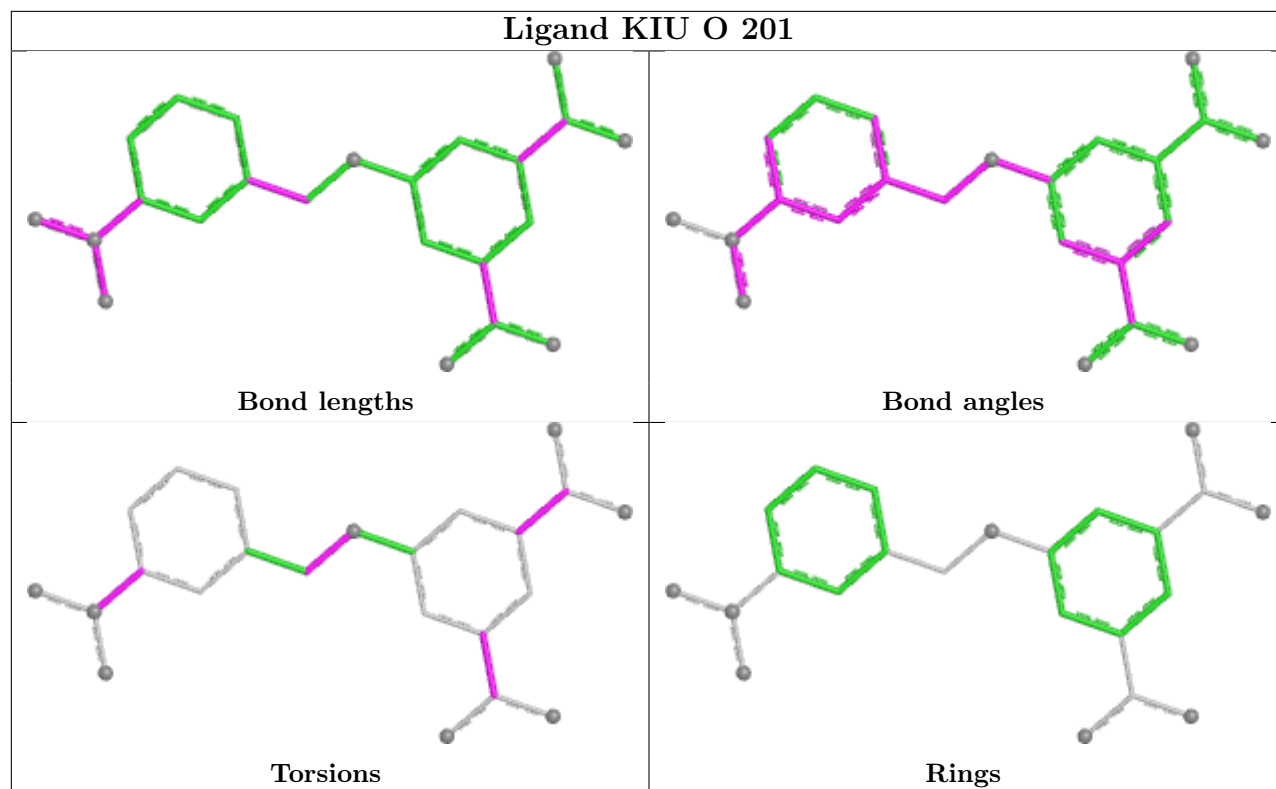
Ligand KIU P 201



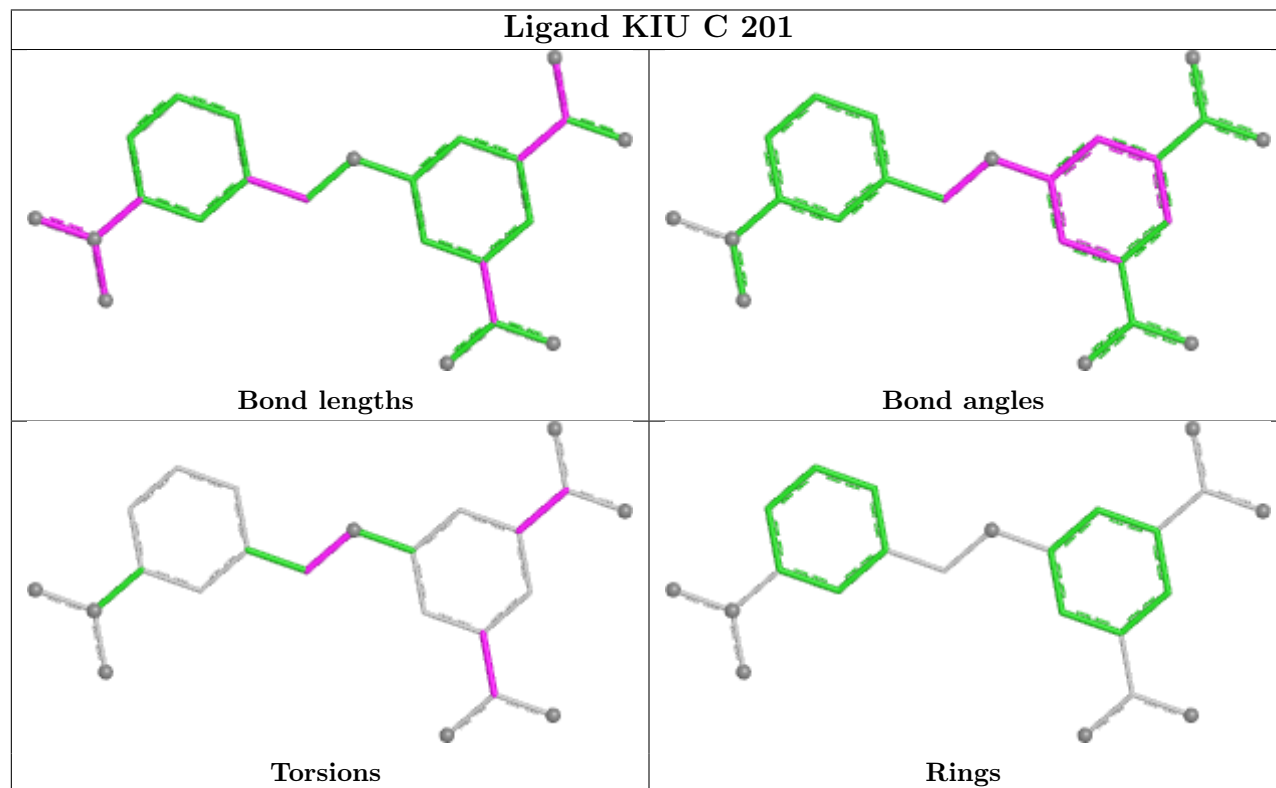
Ligand KIU E 201



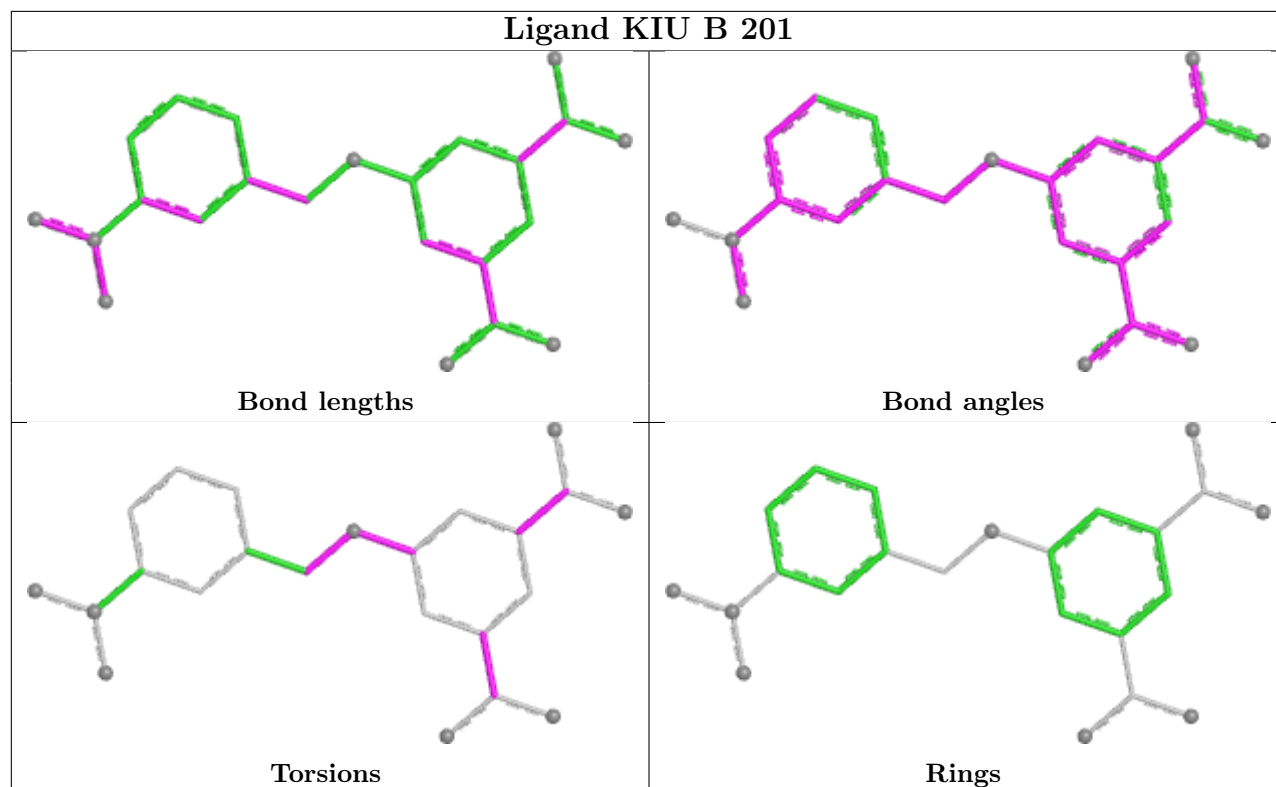
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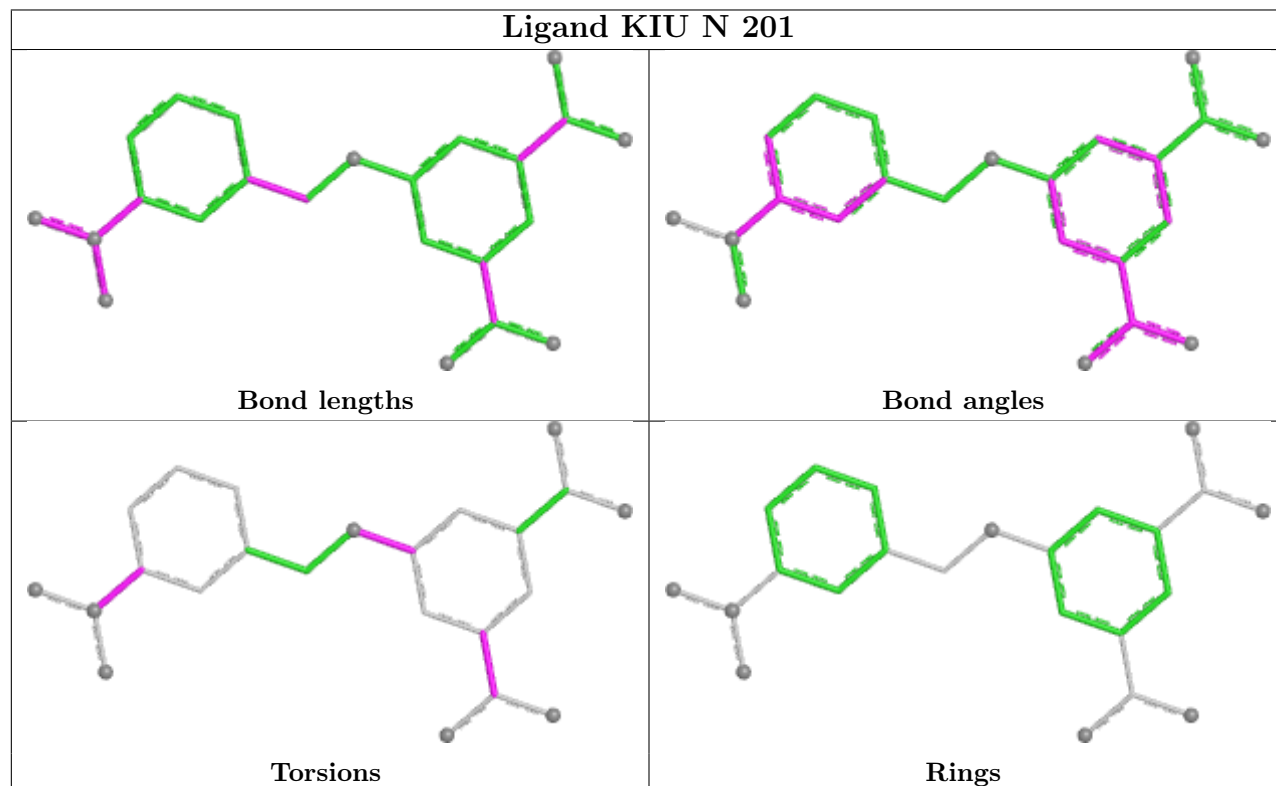
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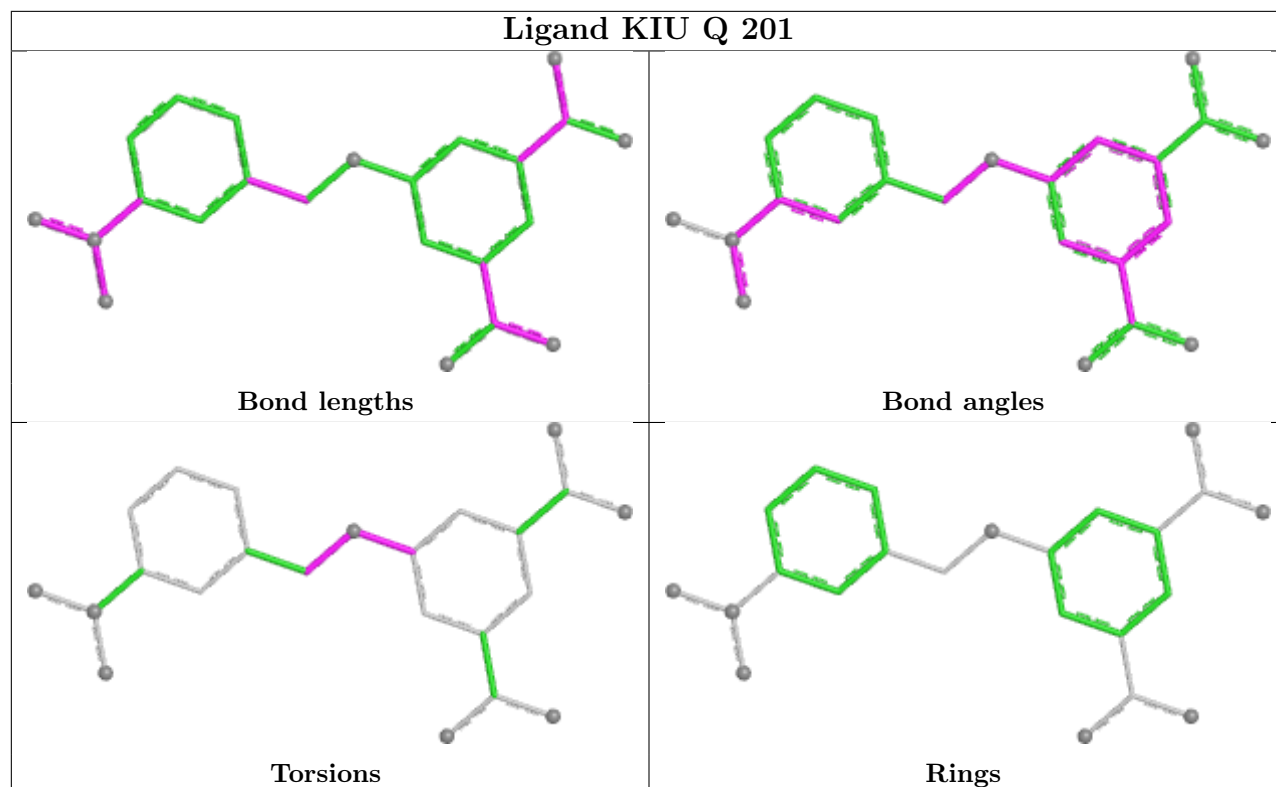
Ligand KIU B 201



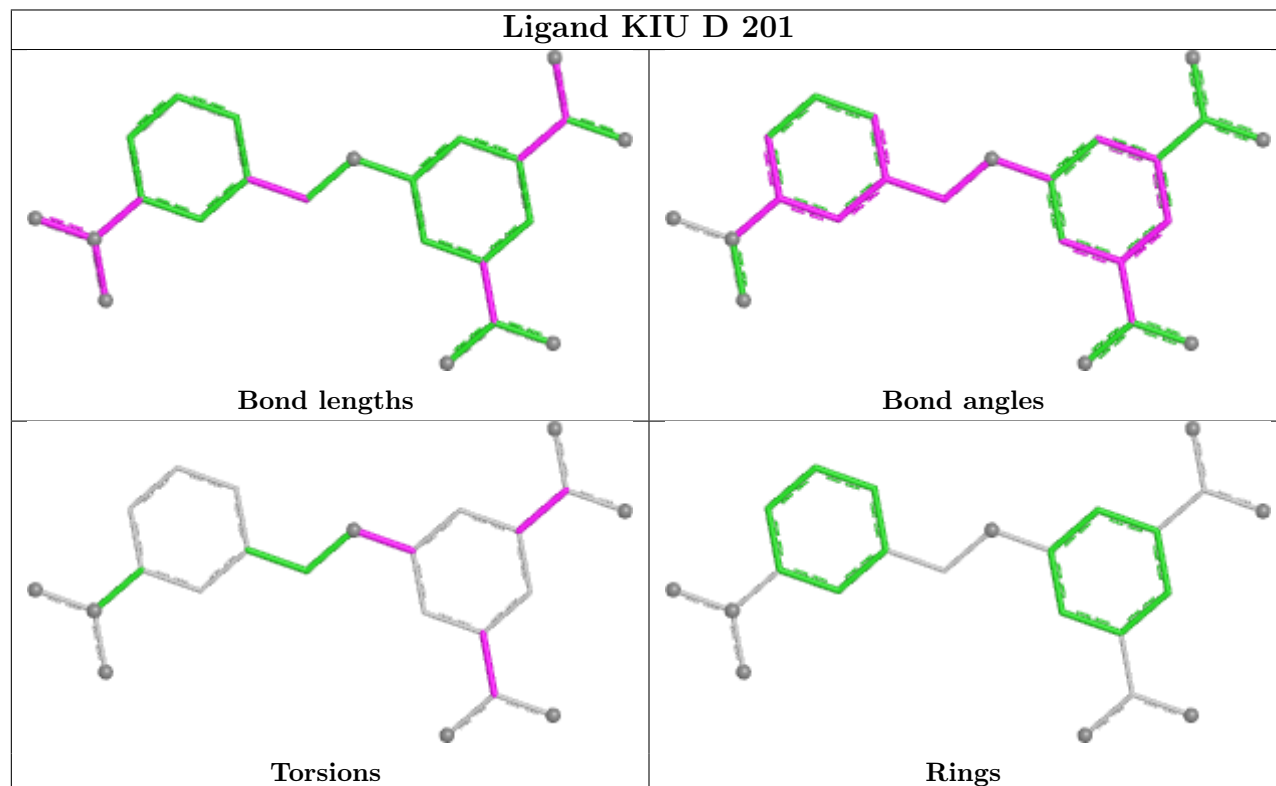
Ligand KIU N 201



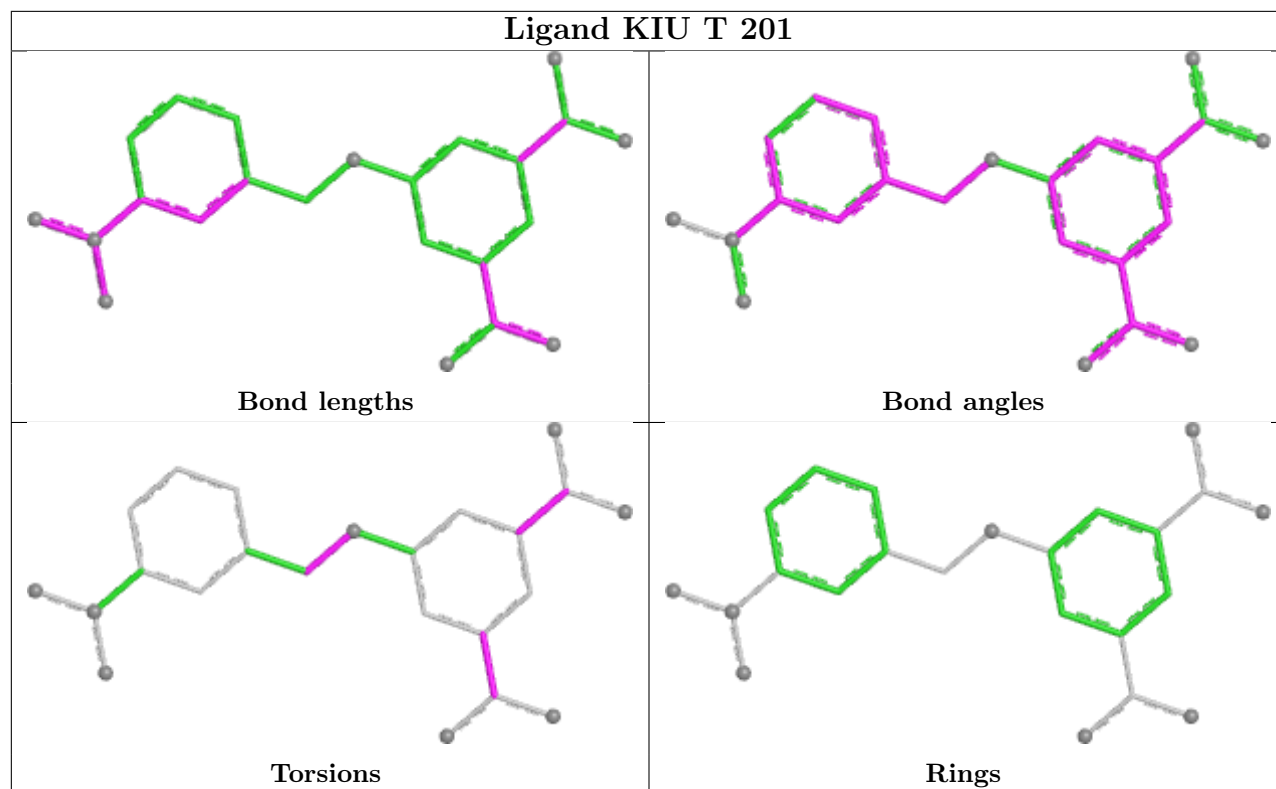
Ligand KIU Q 201



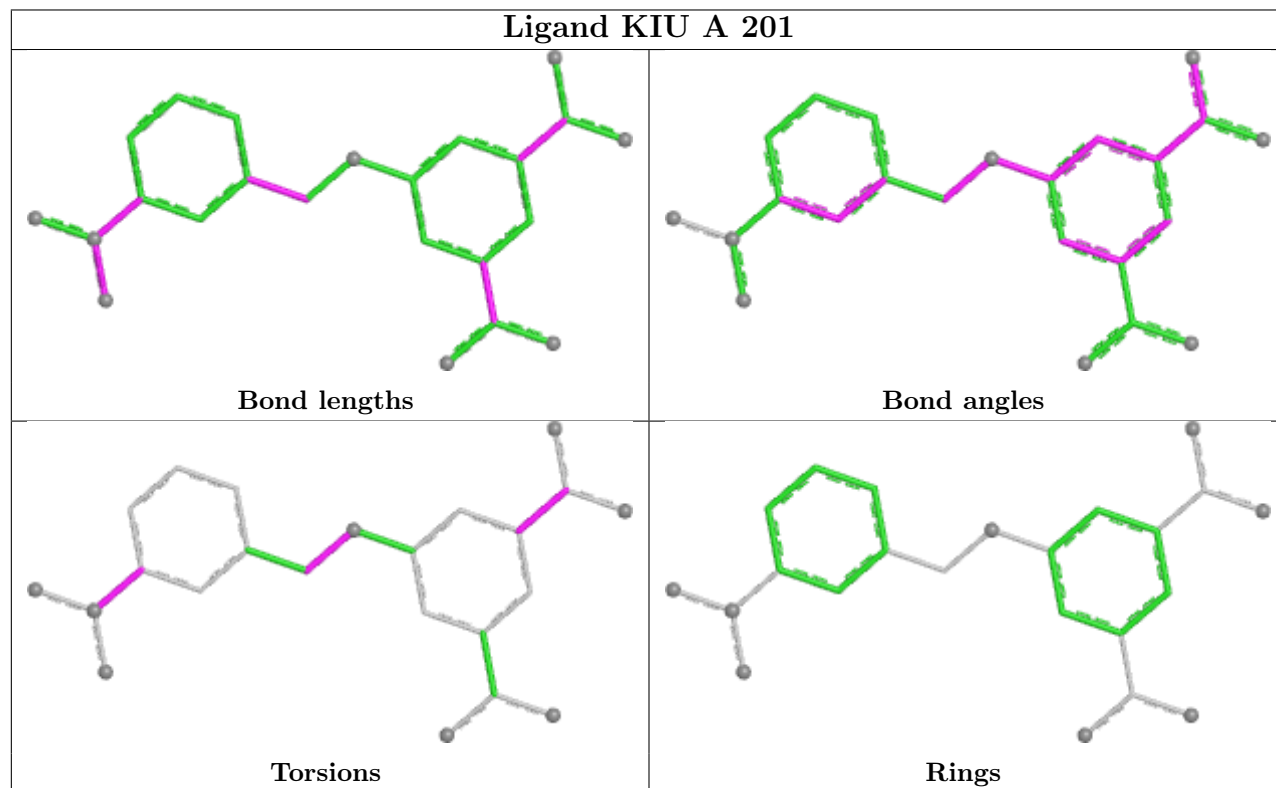
Ligand KIU D 201



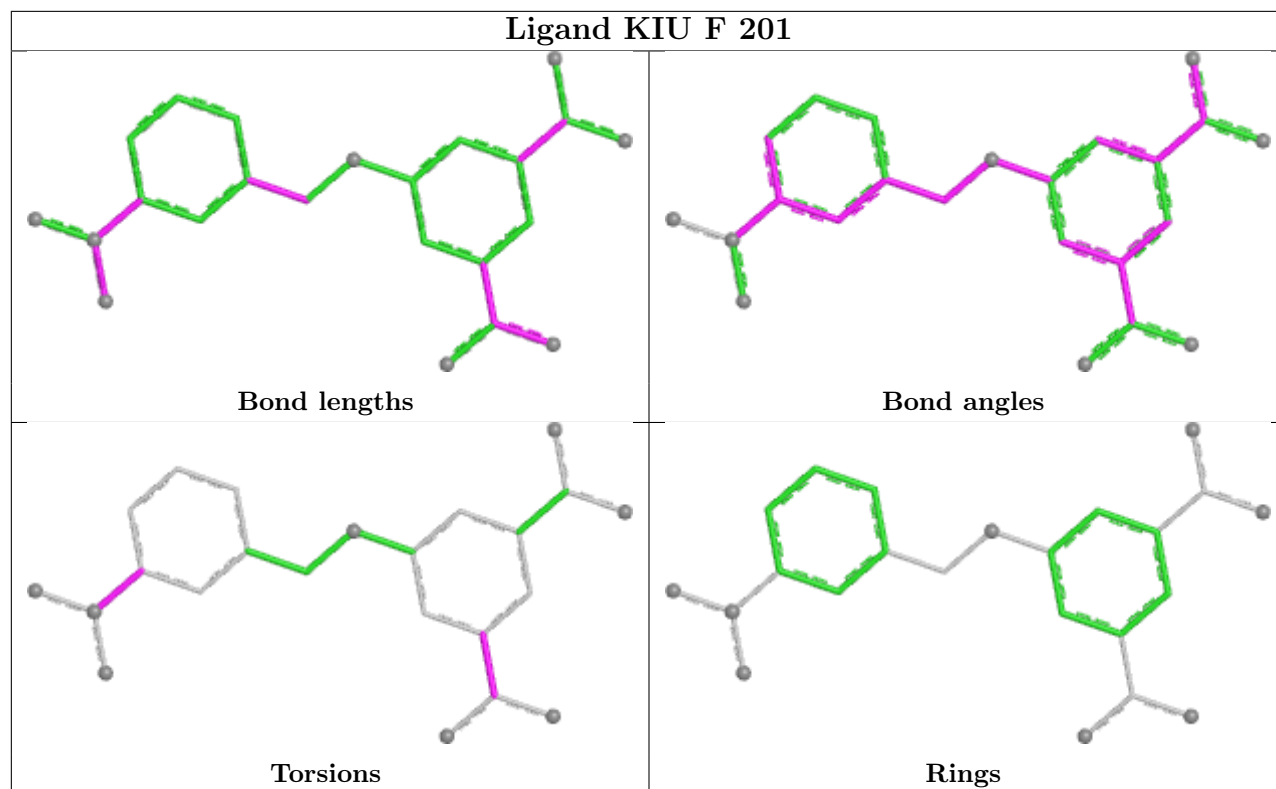
Ligand KIU T 201



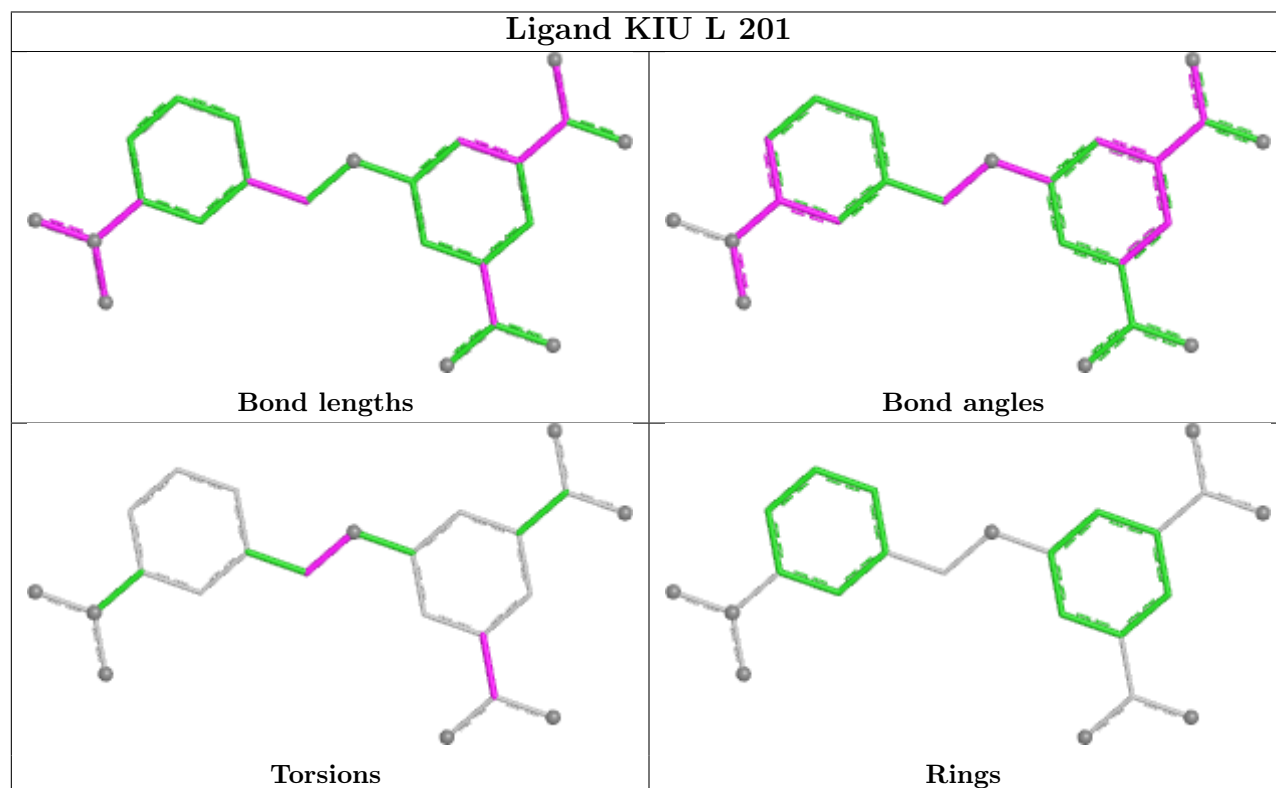
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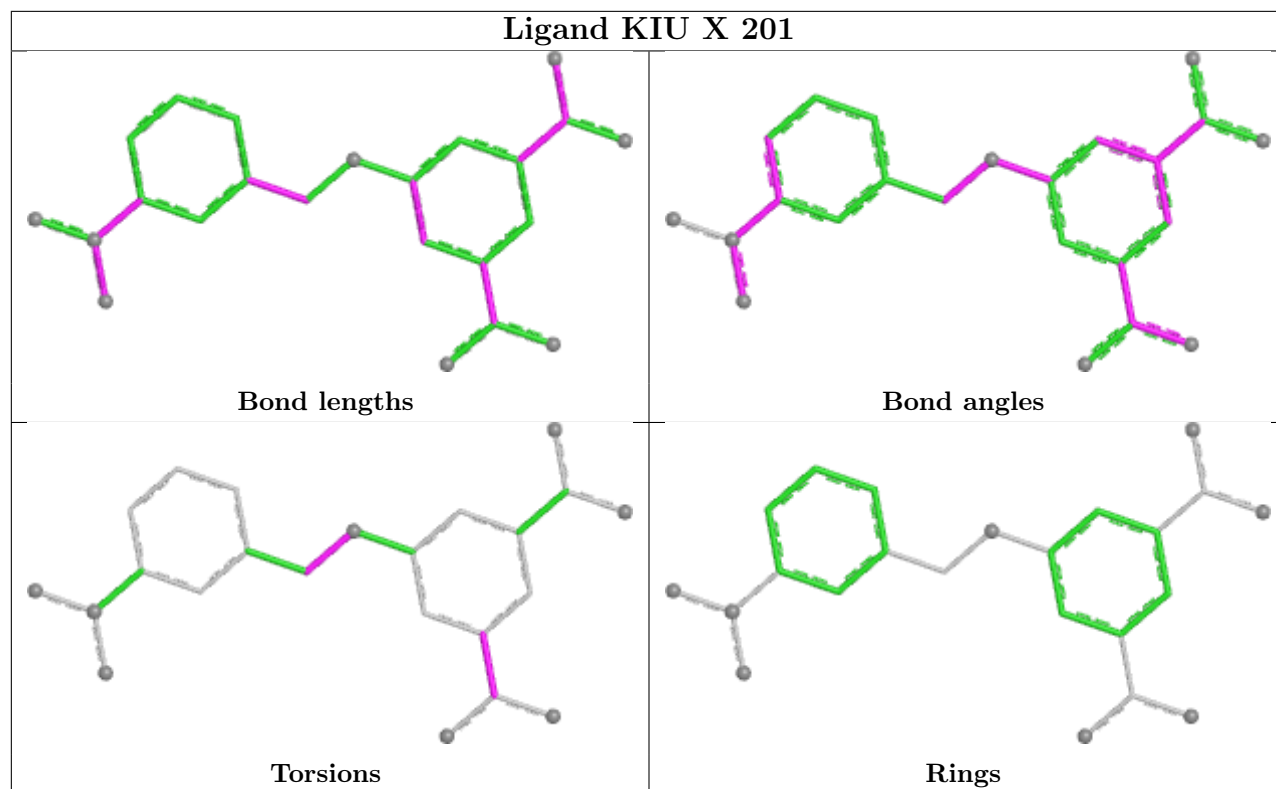


Ligand KIU F 201



Ligand KIU L 201





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, 95th 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	141/153 (92%)	-0.32	7 (4%) 34 30	15, 23, 59, 109	0
1	B	141/153 (92%)	-0.59	1 (0%) 84 81	12, 20, 41, 76	0
1	C	141/153 (92%)	-0.55	1 (0%) 84 81	11, 21, 48, 76	0
1	D	143/153 (93%)	-0.57	1 (0%) 84 81	12, 19, 40, 59	0
1	E	141/153 (92%)	-0.43	3 (2%) 63 59	15, 24, 59, 78	0
1	F	141/153 (92%)	-0.51	2 (1%) 73 69	14, 21, 48, 71	0
1	G	141/153 (92%)	-0.52	1 (0%) 84 81	12, 20, 43, 66	1 (0%)
1	H	141/153 (92%)	-0.52	2 (1%) 73 69	13, 21, 48, 84	0
1	I	141/153 (92%)	-0.49	1 (0%) 84 81	11, 21, 49, 63	0
1	J	141/153 (92%)	-0.59	2 (1%) 73 69	12, 19, 44, 75	0
1	K	141/153 (92%)	-0.45	1 (0%) 84 81	13, 23, 49, 68	0
1	L	141/153 (92%)	-0.54	1 (0%) 84 81	13, 21, 42, 54	0
1	M	135/153 (88%)	-0.19	4 (2%) 52 48	18, 30, 54, 98	0
1	N	141/153 (92%)	-0.09	2 (1%) 73 69	21, 31, 66, 85	0
1	O	141/153 (92%)	-0.43	3 (2%) 63 59	15, 23, 43, 77	0
1	P	141/153 (92%)	-0.21	6 (4%) 40 36	18, 31, 65, 103	0
1	Q	141/153 (92%)	0.04	7 (4%) 34 30	22, 36, 67, 108	0
1	R	141/153 (92%)	-0.23	1 (0%) 84 81	21, 30, 64, 79	0
1	S	141/153 (92%)	-0.10	8 (5%) 29 25	19, 29, 69, 111	1 (0%)
1	T	141/153 (92%)	-0.52	3 (2%) 63 59	13, 22, 50, 83	0
1	U	141/153 (92%)	-0.27	6 (4%) 40 36	16, 28, 57, 92	0
1	V	141/153 (92%)	-0.32	2 (1%) 73 69	17, 25, 59, 76	0
1	W	141/153 (92%)	0.01	3 (2%) 63 59	25, 35, 66, 99	0
1	X	147/153 (96%)	-0.40	2 (1%) 73 69	17, 26, 49, 65	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3386/3672 (92%)	-0.37	70 (2%) 63 59	11, 26, 58, 111	2 (0%)

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	23	VAL	5.0
1	U	21	PRO	4.8
1	A	21	PRO	4.7
1	S	21	PRO	4.7
1	S	24	TYR	4.4

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th 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	KIU	Q	201	23/23	0.77	0.31	41,50,57,59	23
2	KIU	P	201	23/23	0.82	0.18	48,66,74,80	0
2	KIU	B	201	23/23	0.84	0.16	35,45,53,55	0
2	KIU	T	201	23/23	0.84	0.14	44,53,57,58	0
2	KIU	G	201	23/23	0.86	0.13	26,40,54,57	0
2	KIU	N	201	23/23	0.87	0.15	52,63,88,96	0
2	KIU	U	201	23/23	0.87	0.13	40,56,60,70	0
2	KIU	J	201	23/23	0.88	0.12	34,41,53,55	0
2	KIU	E	201	23/23	0.88	0.13	42,53,63,66	0
2	KIU	H	201	23/23	0.88	0.14	34,51,70,79	0
2	KIU	W	201	23/23	0.88	0.16	20,28,37,39	23
2	KIU	R	201	23/23	0.89	0.14	51,56,73,77	0
2	KIU	V	201	23/23	0.90	0.13	49,62,66,67	0

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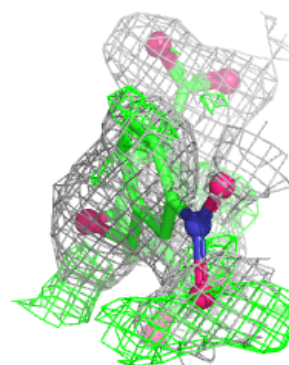
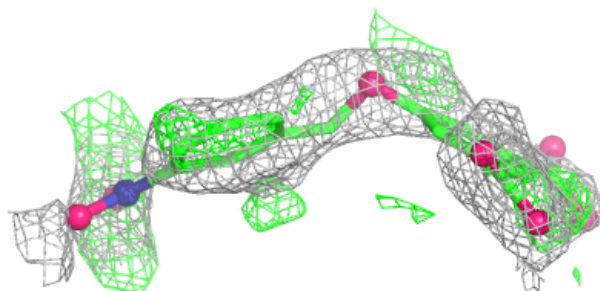
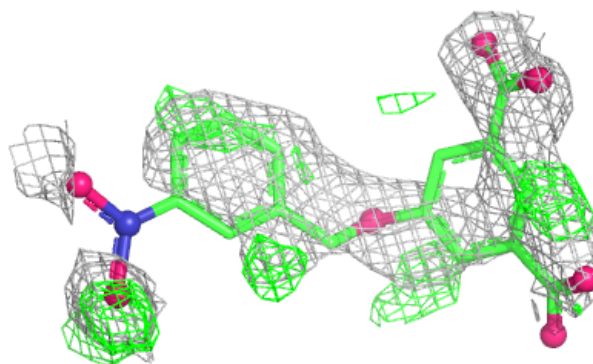
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	KIU	A	201	23/23	0.90	0.12	45,60,64,67	0
2	KIU	X	201	23/23	0.90	0.13	47,57,65,73	0
2	KIU	O	201	23/23	0.92	0.10	36,45,50,52	0
2	KIU	K	201	23/23	0.92	0.10	32,45,55,58	0
2	KIU	C	201	23/23	0.92	0.10	31,42,50,58	0
2	KIU	F	201	23/23	0.93	0.09	32,40,50,56	0
2	KIU	L	201	23/23	0.93	0.09	30,34,42,43	0
2	KIU	I	201	23/23	0.94	0.09	19,31,53,66	0
2	KIU	D	201	23/23	0.95	0.08	25,39,48,56	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.

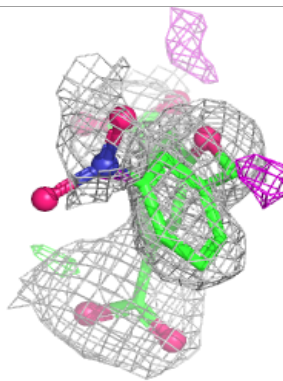
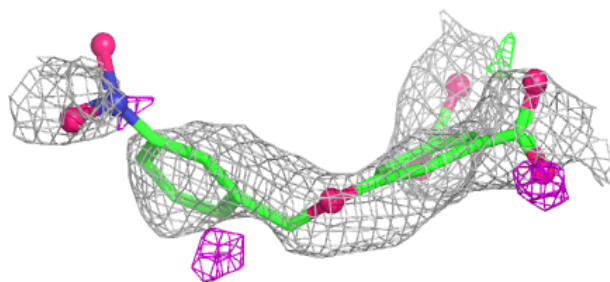
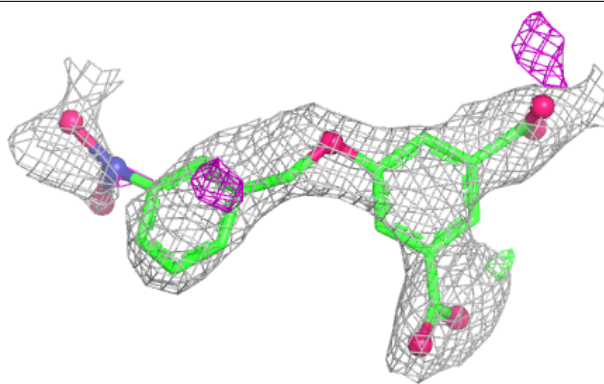
Electron density around KIU Q 201:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

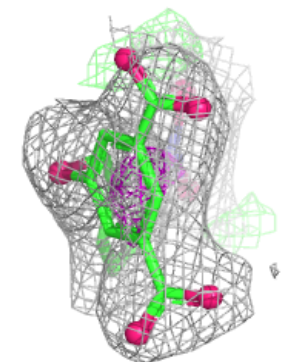
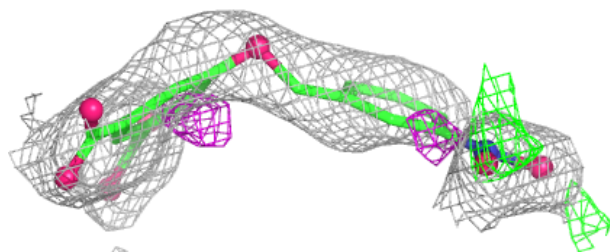
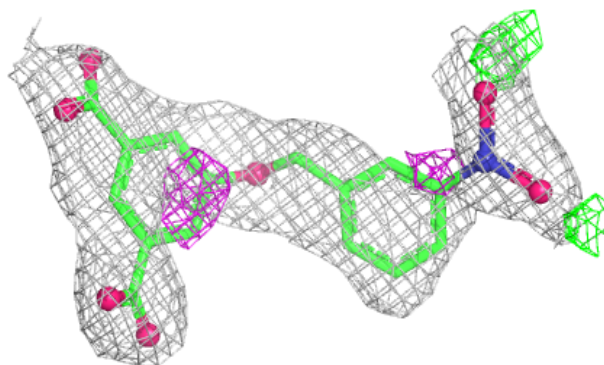


Electron density around KIU P 201:

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and green (positive)

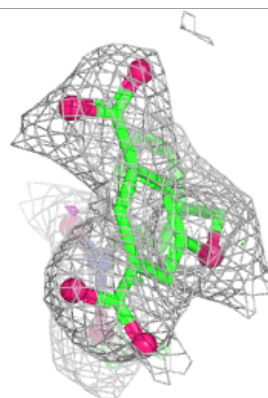
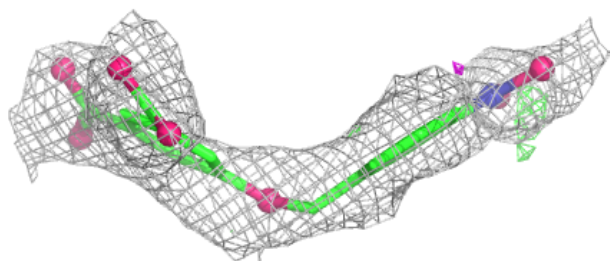
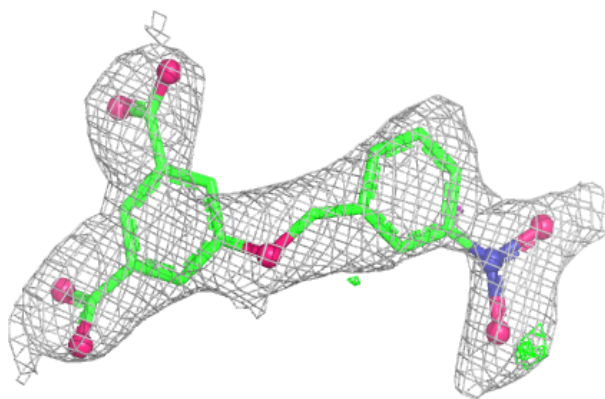
**Electron density around KIU B 201:**

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and green (positive)

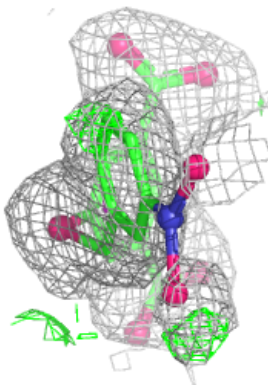
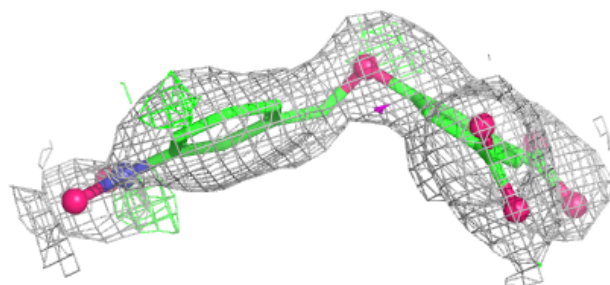
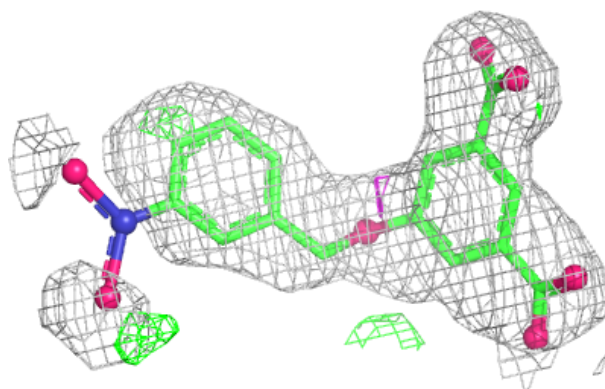


Electron density around KIU T 201:

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and green (positive)

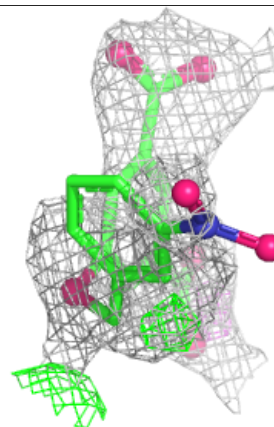
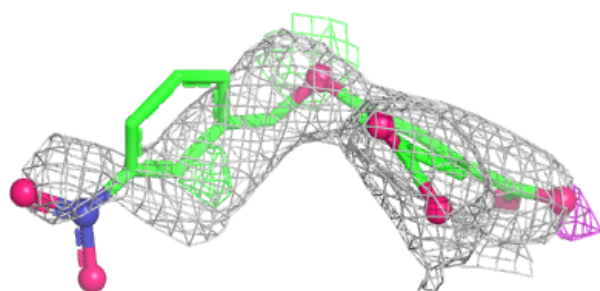
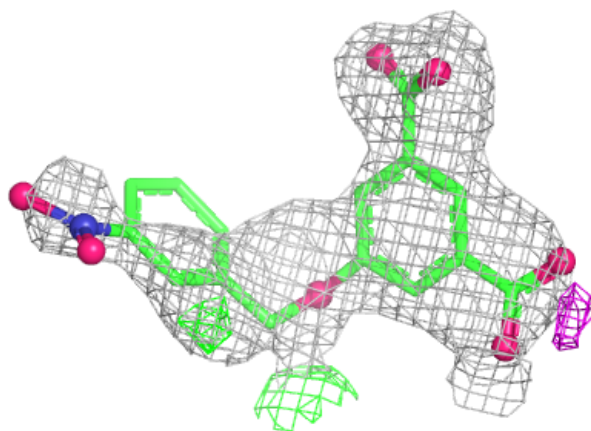
**Electron density around KIU G 201:**

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

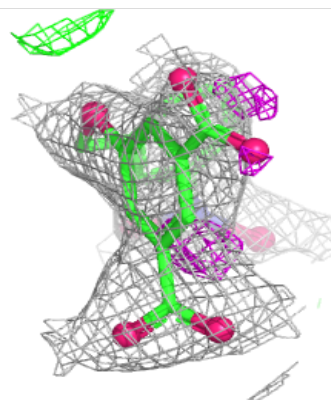
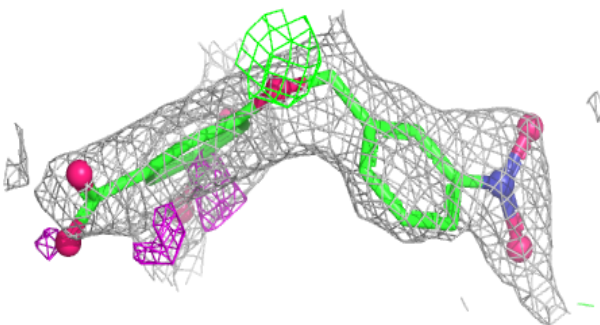
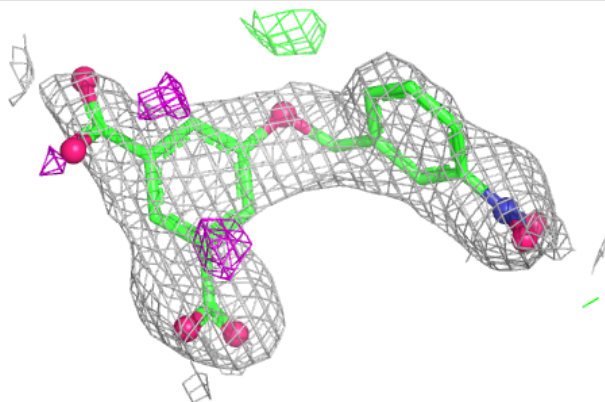


Electron density around KIU N 201:

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

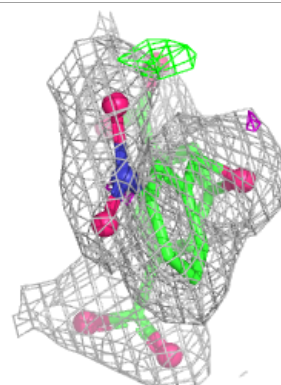
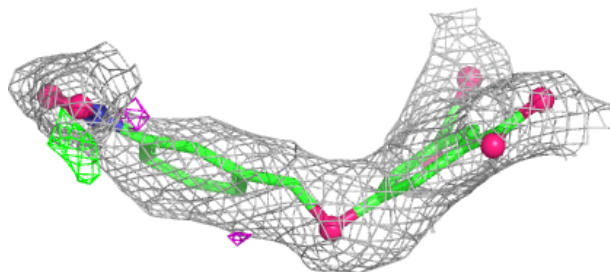
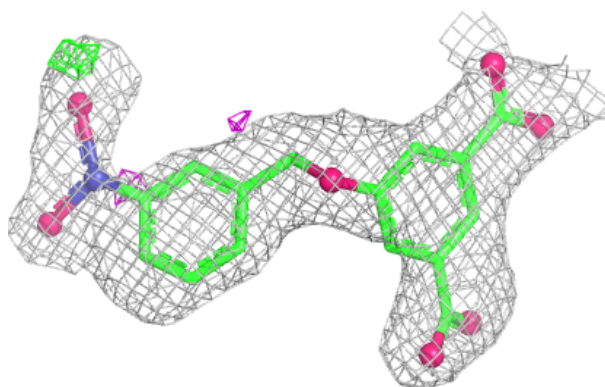
**Electron density around KIU U 201:**

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

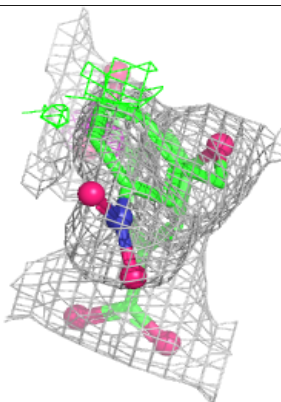
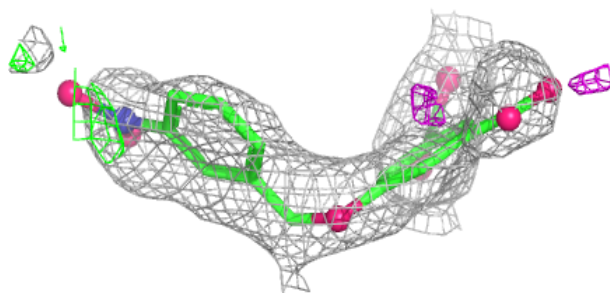
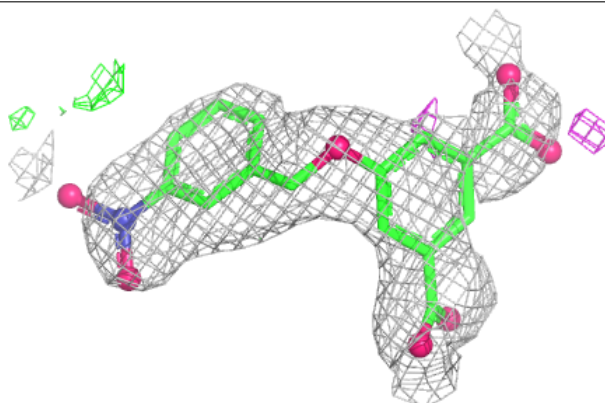


Electron density around KIU J 201:

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

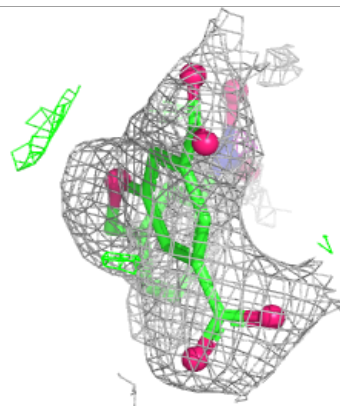
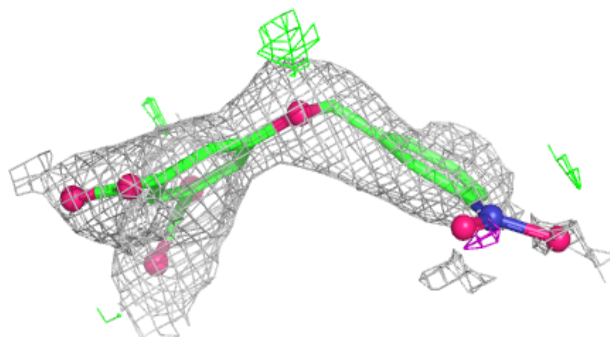
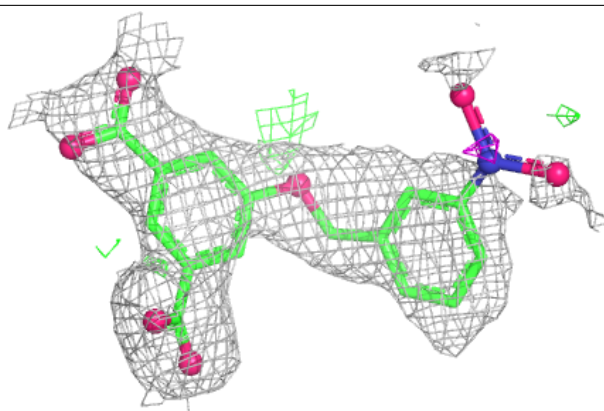
**Electron density around KIU E 201:**

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

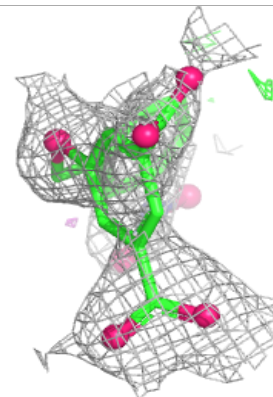
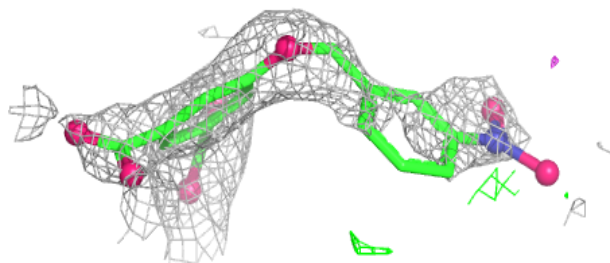
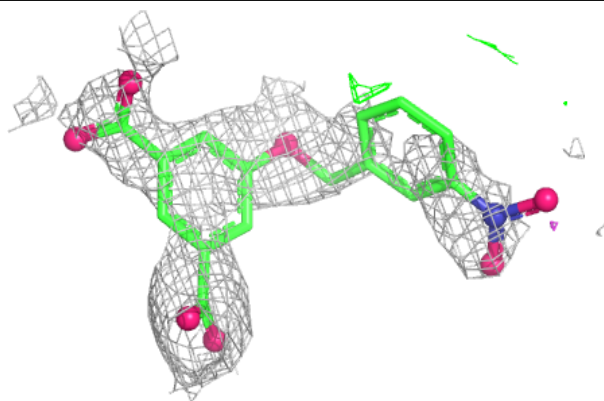


Electron density around KIU H 201:

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

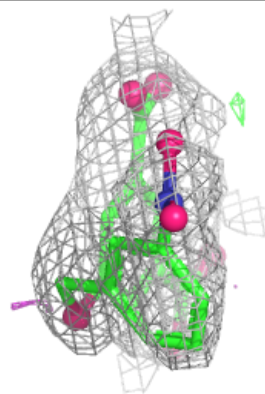
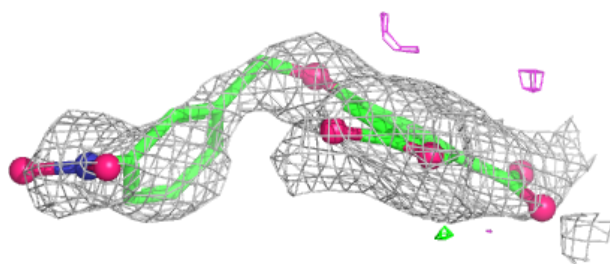
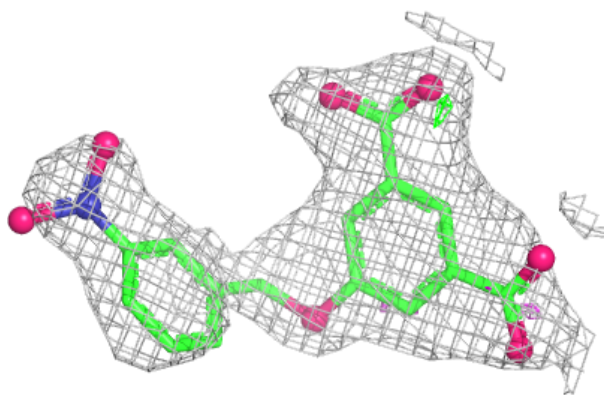
**Electron density around KIU W 201:**

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

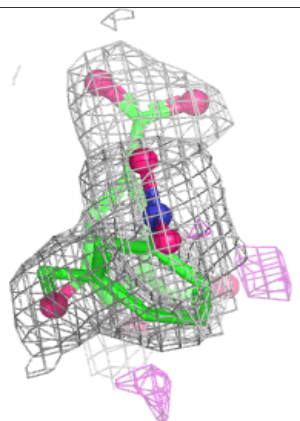
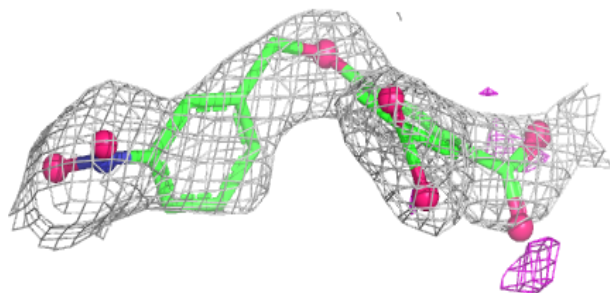
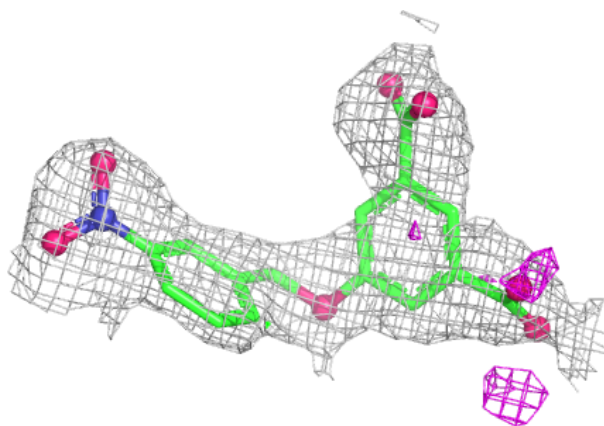


Electron density around KIU R 201:

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

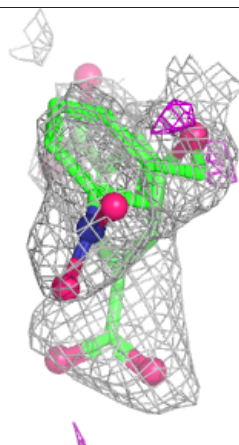
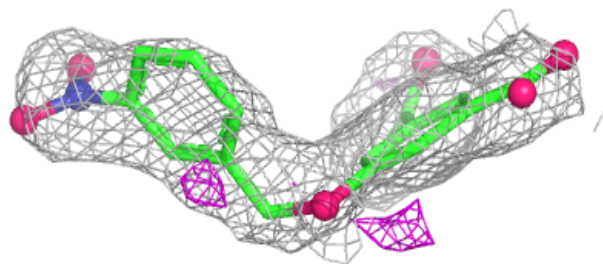
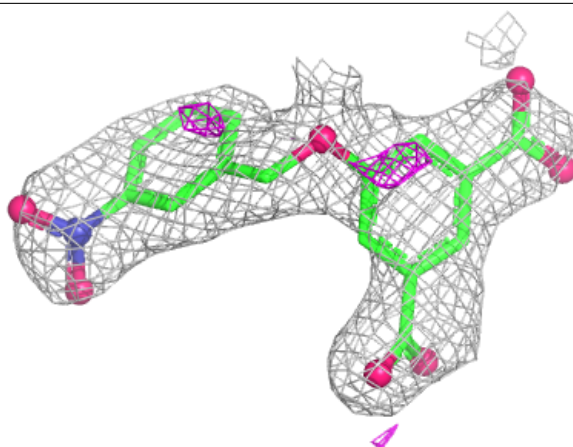
**Electron density around KIU V 201:**

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

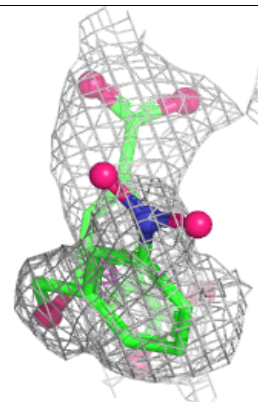
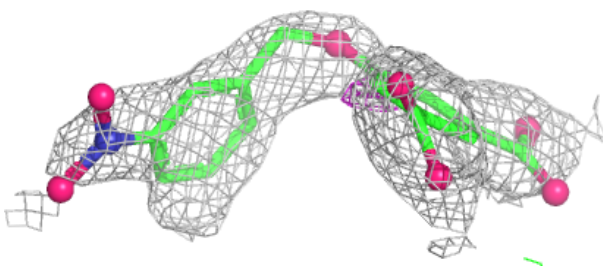
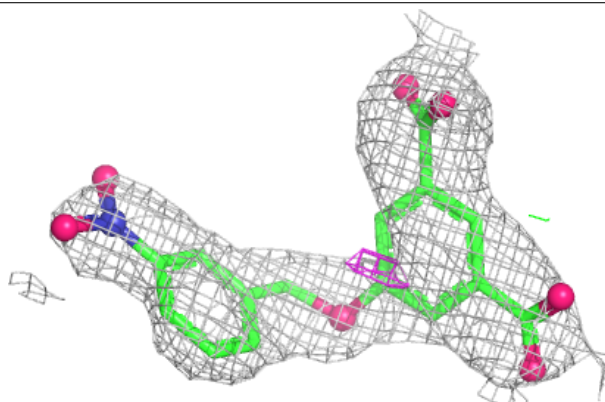


Electron density around KIU A 201:

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

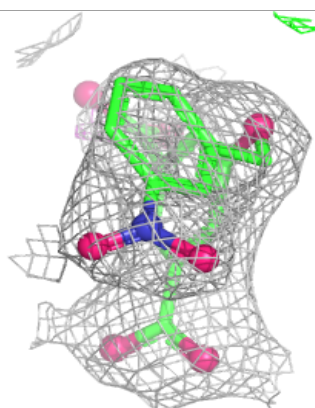
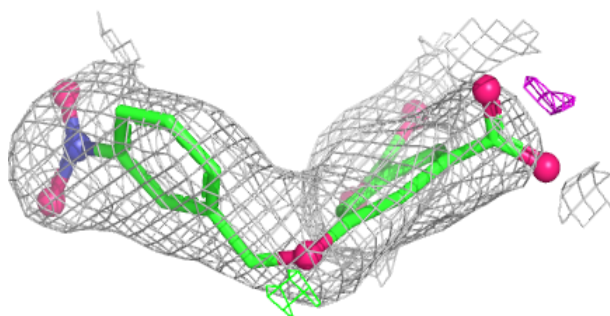
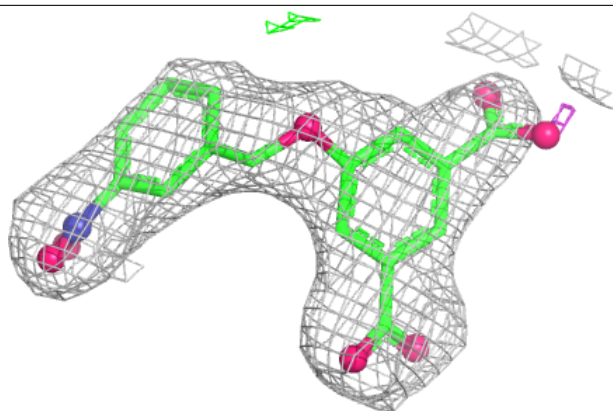
**Electron density around KIU X 201:**

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

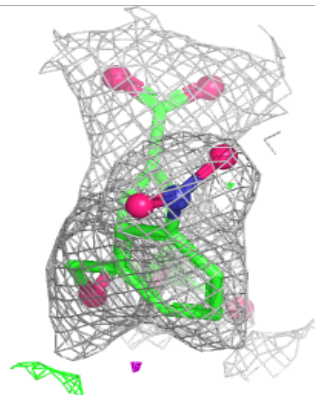
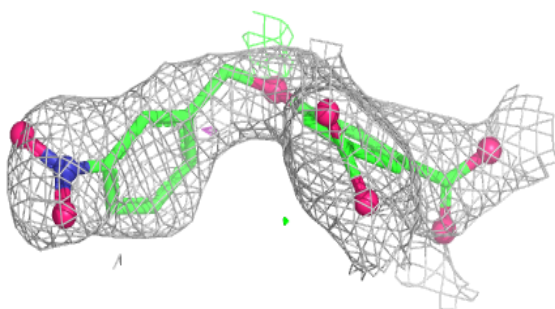
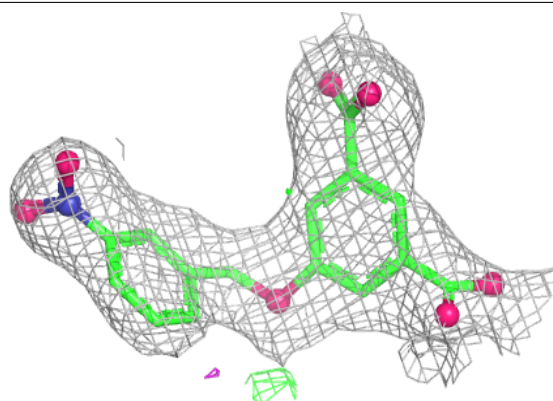


Electron density around KIU O 201:

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

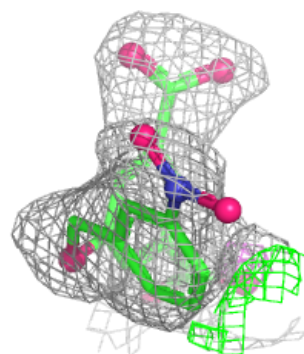
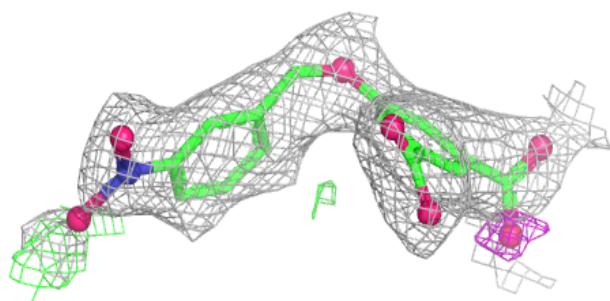
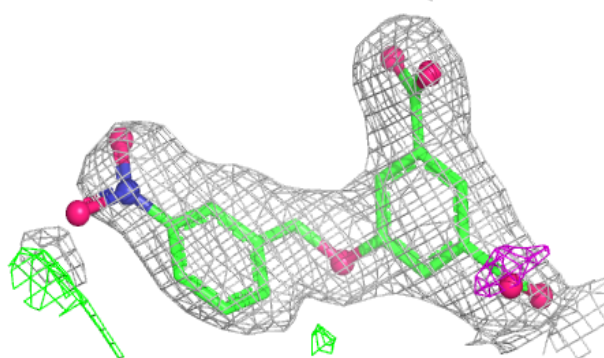
**Electron density around KIU K 201:**

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

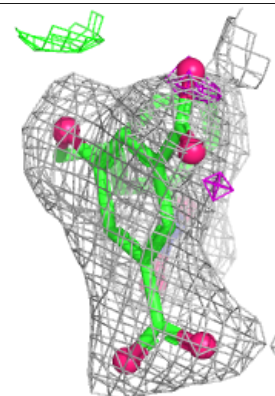
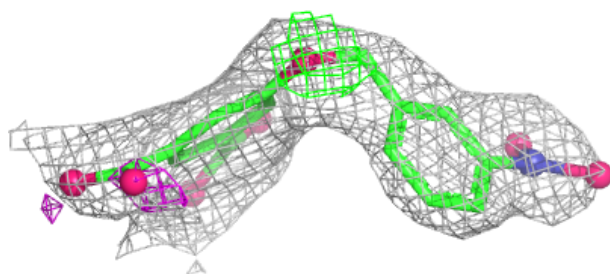
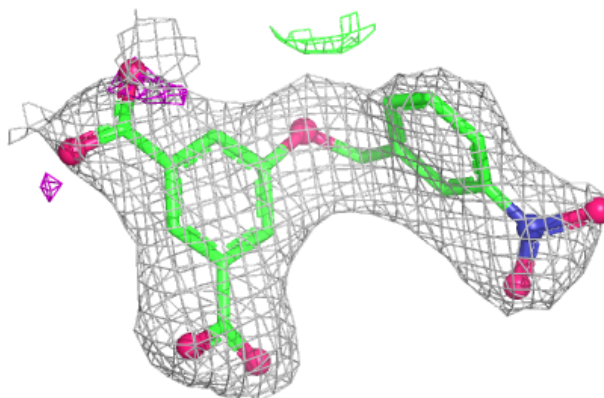


Electron density around KIU C 201:

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

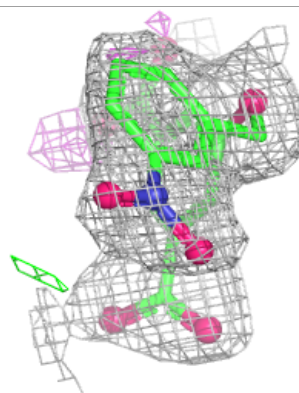
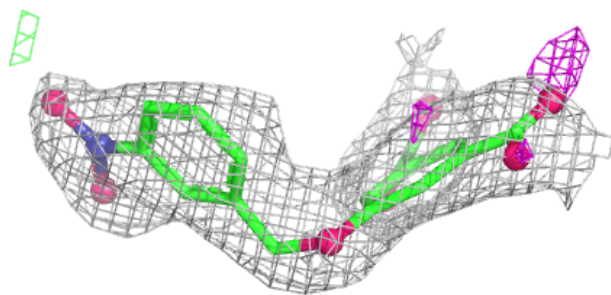
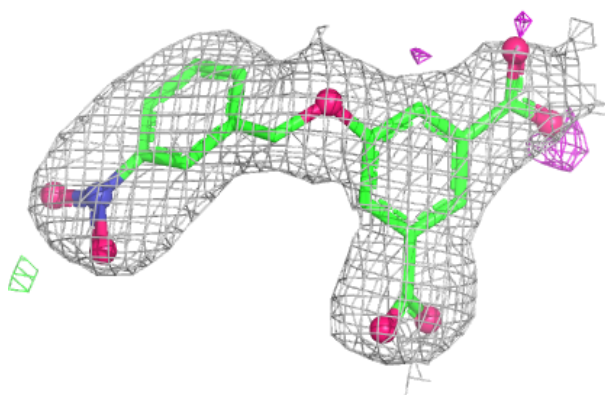
**Electron density around KIU F 201:**

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

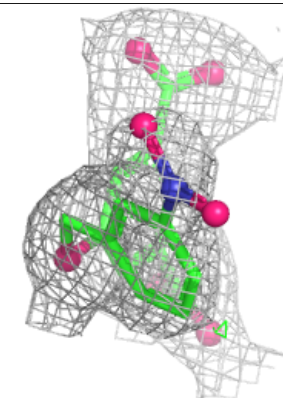
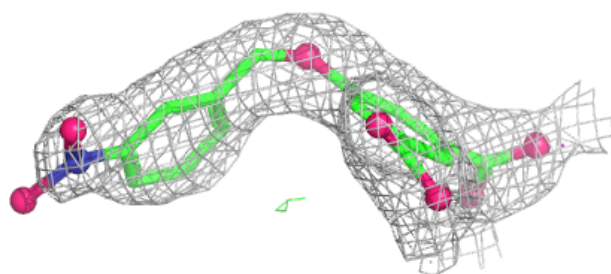
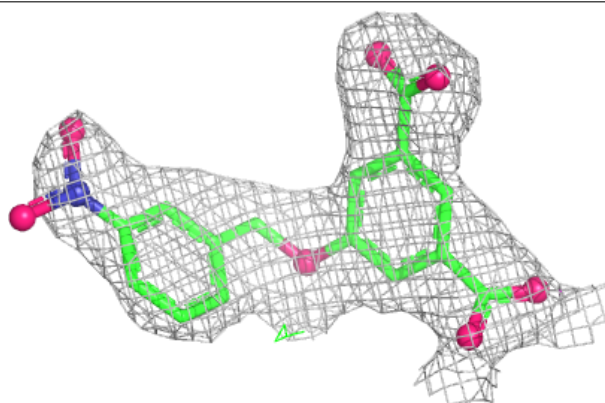


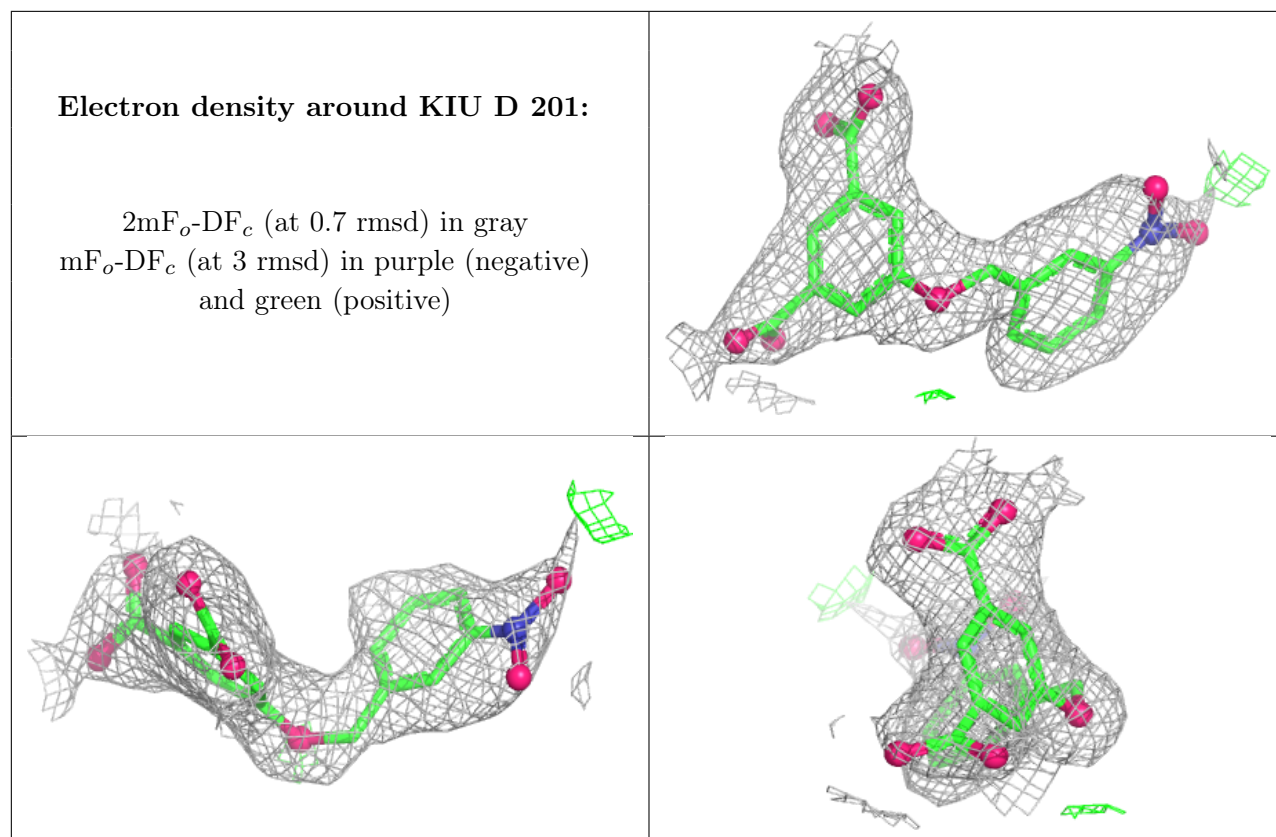
Electron density around KIU L 201:

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

**Electron density around KIU I 201:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.