



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 06:23 AM UTC

PDB ID : 5MU8 / pdb_00005mu8
Title : HUMAN TNF-ALPHA IN COMPLEX WITH JNJ525
Authors : Blevitt, J.M.; Hack, M.D.; Herman, K.L.; Jackson, P.F.; Krawczuk, P.J.; Lebsack, A.D.; Liu, A.X.; Mirzadegan, T.; Nelen, M.I.; Patrick, A.P.; Steinbacher, S.; Milla, M.E.; Lumb, K.J.
Deposited on : 2017-01-12
Resolution : 3.00 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

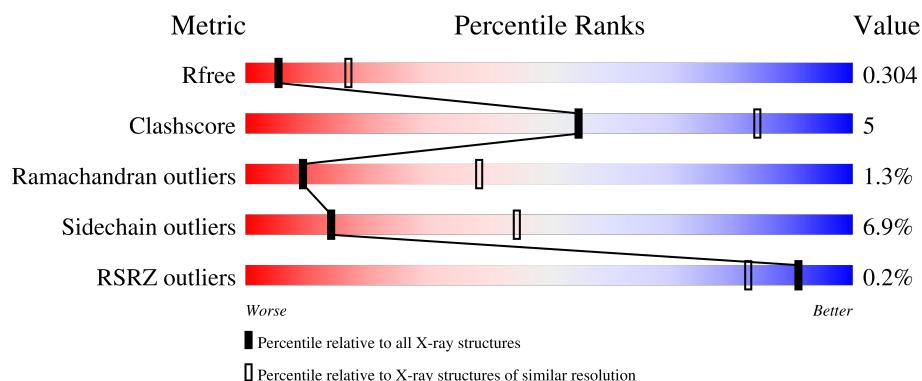
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	159	
1	B	159	
1	C	159	
1	D	159	

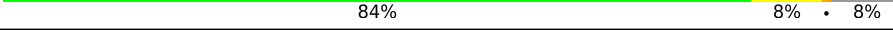
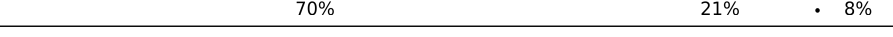
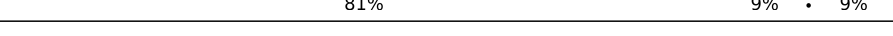
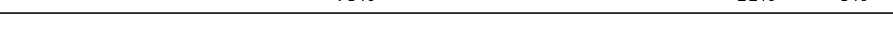
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Mol	Chain	Length	Quality of chain
1	F	159	
1	G	159	
1	H	159	
1	I	159	
1	J	159	
1	K	159	
1	L	159	
1	M	159	
1	N	159	
1	O	159	
1	P	159	
1	Q	159	
1	R	159	
1	S	159	
1	T	159	
1	U	159	
1	V	159	
1	W	159	
1	X	159	
1	Y	159	
1	Z	159	
1	a	159	
1	b	159	
1	c	159	
1	d	159	

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Mol	Chain	Length	Quality of chain
1	e	159	 70%20%••6%
1	f	159	 80%10%10%
1	g	159	 75%15%•9%
1	h	159	 75%10%•14%
1	i	159	 73%17%•9%
1	j	159	 83%11%•6%
1	k	159	 76%13%11%
1	l	159	 70%19%•10%
1	m	159	 84%8%•8%
1	n	159	 84%9%8%
1	o	159	 70%21%•8%
1	p	159	 76%11%13%
1	q	159	 80%13%•6%
1	r	159	 81%9%•9%
1	s	159	 77%16%•6%
1	t	159	 76%13%•10%
1	u	159	 75%16%•9%
1	v	159	 86%5%9%
1	w	159	 79%11%•9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 56305 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 Tumor necrosis factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1105	709	186	208	2			
1	B	145	Total	C	N	O	S	0	0	0
			1139	728	197	212	2			
1	C	146	Total	C	N	O	S	0	0	0
			1145	733	198	212	2			
1	D	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	F	140	Total	C	N	O	S	0	0	0
			1099	707	184	206	2			
1	G	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	H	150	Total	C	N	O	S	0	0	0
			1172	748	202	220	2			
1	I	141	Total	C	N	O	S	0	0	0
			1104	708	190	204	2			
1	J	138	Total	C	N	O	S	0	0	0
			1085	699	182	202	2			
1	K	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	L	142	Total	C	N	O	S	0	0	0
			1111	713	191	205	2			
1	M	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	N	143	Total	C	N	O	S	0	0	0
			1117	717	187	211	2			
1	O	145	Total	C	N	O	S	0	0	0
			1140	728	197	213	2			
1	P	145	Total	C	N	O	S	0	0	0
			1140	729	196	213	2			
1	Q	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	138	Total	C	N	O	S	0	0	0
			1083	697	182	202	2			
1	S	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	T	146	Total	C	N	O	S	0	0	0
			1145	733	198	212	2			
1	U	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	V	138	Total	C	N	O	S	0	0	0
			1085	699	182	202	2			
1	W	143	Total	C	N	O	S	0	0	0
			1126	720	195	209	2			
1	X	150	Total	C	N	O	S	0	0	0
			1172	748	202	220	2			
1	Y	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	Z	143	Total	C	N	O	S	0	0	0
			1117	717	187	211	2			
1	a	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	b	144	Total	C	N	O	S	0	0	0
			1133	725	196	210	2			
1	c	145	Total	C	N	O	S	0	0	0
			1140	728	197	213	2			
1	d	138	Total	C	N	O	S	0	0	0
			1085	699	182	202	2			
1	e	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	f	143	Total	C	N	O	S	0	0	0
			1124	719	194	209	2			
1	g	145	Total	C	N	O	S	0	0	0
			1138	728	197	211	2			
1	h	137	Total	C	N	O	S	0	0	0
			1078	694	181	201	2			
1	i	145	Total	C	N	O	S	0	0	0
			1138	728	197	211	2			
1	j	150	Total	C	N	O	S	0	0	0
			1172	748	202	220	2			
1	k	142	Total	C	N	O	S	0	0	0
			1119	716	194	207	2			
1	l	143	Total	C	N	O	S	0	0	0
			1117	717	187	211	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	m	147	Total	C	N	O	S	0	0	0
			1152	736	199	215	2			
1	n	147	Total	C	N	O	S	0	0	0
			1154	738	199	215	2			
1	o	147	Total	C	N	O	S	0	0	0
			1151	735	199	215	2			
1	p	139	Total	C	N	O	S	0	0	0
			1090	702	183	203	2			
1	q	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	r	144	Total	C	N	O	S	0	0	0
			1131	724	195	210	2			
1	s	149	Total	C	N	O	S	0	0	0
			1165	743	201	219	2			
1	t	143	Total	C	N	O	S	0	0	0
			1117	717	187	211	2			
1	u	145	Total	C	N	O	S	0	0	0
			1138	728	197	211	2			
1	v	144	Total	C	N	O	S	0	0	0
			1131	724	195	210	2			
1	w	145	Total	C	N	O	S	0	0	0
			1138	728	197	211	2			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	expression tag	UNP P01375
A	0	MET	-	expression tag	UNP P01375
B	-1	ALA	-	expression tag	UNP P01375
B	0	MET	-	expression tag	UNP P01375
C	-1	ALA	-	expression tag	UNP P01375
C	0	MET	-	expression tag	UNP P01375
D	-1	ALA	-	expression tag	UNP P01375
D	0	MET	-	expression tag	UNP P01375
F	-1	ALA	-	expression tag	UNP P01375
F	0	MET	-	expression tag	UNP P01375
G	-1	ALA	-	expression tag	UNP P01375
G	0	MET	-	expression tag	UNP P01375
H	-1	ALA	-	expression tag	UNP P01375
H	0	MET	-	expression tag	UNP P01375
I	-1	ALA	-	expression tag	UNP P01375
I	0	MET	-	expression tag	UNP P01375
J	-1	ALA	-	expression tag	UNP P01375

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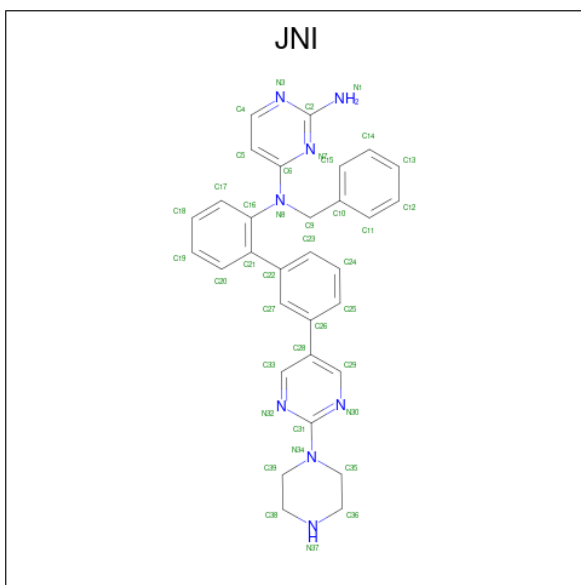
Chain	Residue	Modelled	Actual	Comment	Reference
J	0	MET	-	expression tag	UNP P01375
K	-1	ALA	-	expression tag	UNP P01375
K	0	MET	-	expression tag	UNP P01375
L	-1	ALA	-	expression tag	UNP P01375
L	0	MET	-	expression tag	UNP P01375
M	-1	ALA	-	expression tag	UNP P01375
M	0	MET	-	expression tag	UNP P01375
N	-1	ALA	-	expression tag	UNP P01375
N	0	MET	-	expression tag	UNP P01375
O	-1	ALA	-	expression tag	UNP P01375
O	0	MET	-	expression tag	UNP P01375
P	-1	ALA	-	expression tag	UNP P01375
P	0	MET	-	expression tag	UNP P01375
Q	-1	ALA	-	expression tag	UNP P01375
Q	0	MET	-	expression tag	UNP P01375
R	-1	ALA	-	expression tag	UNP P01375
R	0	MET	-	expression tag	UNP P01375
S	-1	ALA	-	expression tag	UNP P01375
S	0	MET	-	expression tag	UNP P01375
T	-1	ALA	-	expression tag	UNP P01375
T	0	MET	-	expression tag	UNP P01375
U	-1	ALA	-	expression tag	UNP P01375
U	0	MET	-	expression tag	UNP P01375
V	-1	ALA	-	expression tag	UNP P01375
V	0	MET	-	expression tag	UNP P01375
W	-1	ALA	-	expression tag	UNP P01375
W	0	MET	-	expression tag	UNP P01375
X	-1	ALA	-	expression tag	UNP P01375
X	0	MET	-	expression tag	UNP P01375
Y	-1	ALA	-	expression tag	UNP P01375
Y	0	MET	-	expression tag	UNP P01375
Z	-1	ALA	-	expression tag	UNP P01375
Z	0	MET	-	expression tag	UNP P01375
a	-1	ALA	-	expression tag	UNP P01375
a	0	MET	-	expression tag	UNP P01375
b	-1	ALA	-	expression tag	UNP P01375
b	0	MET	-	expression tag	UNP P01375
c	-1	ALA	-	expression tag	UNP P01375
c	0	MET	-	expression tag	UNP P01375
d	-1	ALA	-	expression tag	UNP P01375
d	0	MET	-	expression tag	UNP P01375
e	-1	ALA	-	expression tag	UNP P01375

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Chain	Residue	Modelled	Actual	Comment	Reference
e	0	MET	-	expression tag	UNP P01375
f	-1	ALA	-	expression tag	UNP P01375
f	0	MET	-	expression tag	UNP P01375
g	-1	ALA	-	expression tag	UNP P01375
g	0	MET	-	expression tag	UNP P01375
h	-1	ALA	-	expression tag	UNP P01375
h	0	MET	-	expression tag	UNP P01375
i	-1	ALA	-	expression tag	UNP P01375
i	0	MET	-	expression tag	UNP P01375
j	-1	ALA	-	expression tag	UNP P01375
j	0	MET	-	expression tag	UNP P01375
k	-1	ALA	-	expression tag	UNP P01375
k	0	MET	-	expression tag	UNP P01375
l	-1	ALA	-	expression tag	UNP P01375
l	0	MET	-	expression tag	UNP P01375
m	-1	ALA	-	expression tag	UNP P01375
m	0	MET	-	expression tag	UNP P01375
n	-1	ALA	-	expression tag	UNP P01375
n	0	MET	-	expression tag	UNP P01375
o	-1	ALA	-	expression tag	UNP P01375
o	0	MET	-	expression tag	UNP P01375
p	-1	ALA	-	expression tag	UNP P01375
p	0	MET	-	expression tag	UNP P01375
q	-1	ALA	-	expression tag	UNP P01375
q	0	MET	-	expression tag	UNP P01375
r	-1	ALA	-	expression tag	UNP P01375
r	0	MET	-	expression tag	UNP P01375
s	-1	ALA	-	expression tag	UNP P01375
s	0	MET	-	expression tag	UNP P01375
t	-1	ALA	-	expression tag	UNP P01375
t	0	MET	-	expression tag	UNP P01375
u	-1	ALA	-	expression tag	UNP P01375
u	0	MET	-	expression tag	UNP P01375
v	-1	ALA	-	expression tag	UNP P01375
v	0	MET	-	expression tag	UNP P01375
w	-1	ALA	-	expression tag	UNP P01375
w	0	MET	-	expression tag	UNP P01375

- Molecule 2 is {N}4-(phenylmethyl)- {N}4-[2-[3-(2-piperazin-1-ylpyrimidin-5-yl)phenyl]phenyl]pyrimidine-2,4-diamine (CCD ID: JN1) (formula: C₃₁H₃₀N₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 39	C 31	N 8	0	0
2	A	1	Total 39	C 31	N 8	0	0
2	C	1	Total 39	C 31	N 8	0	0
2	C	1	Total 39	C 31	N 8	0	0
2	D	1	Total 39	C 31	N 8	0	0
2	F	1	Total 39	C 31	N 8	0	0
2	F	1	Total 39	C 31	N 8	0	0
2	H	1	Total 39	C 31	N 8	0	0
2	H	1	Total 39	C 31	N 8	0	0
2	J	1	Total 39	C 31	N 8	0	0
2	J	1	Total 39	C 31	N 8	0	0
2	L	1	Total 39	C 31	N 8	0	0
2	M	1	Total 39	C 31	N 8	0	0
2	N	1	Total 39	C 31	N 8	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	P	1	Total	C	N	0	0
			39	31	8		
2	P	1	Total	C	N	0	0
			39	31	8		
2	Q	1	Total	C	N	0	0
			39	31	8		
2	R	1	Total	C	N	0	0
			39	31	8		
2	U	1	Total	C	N	0	0
			39	31	8		
2	V	1	Total	C	N	0	0
			39	31	8		
2	V	1	Total	C	N	0	0
			39	31	8		
2	X	1	Total	C	N	0	0
			39	31	8		
2	X	1	Total	C	N	0	0
			39	31	8		
2	Z	1	Total	C	N	0	0
			39	31	8		
2	Z	1	Total	C	N	0	0
			39	31	8		
2	b	1	Total	C	N	0	0
			39	31	8		
2	b	1	Total	C	N	0	0
			39	31	8		
2	d	1	Total	C	N	0	0
			39	31	8		
2	f	1	Total	C	N	0	0
			39	31	8		
2	f	1	Total	C	N	0	0
			39	31	8		
2	h	1	Total	C	N	0	0
			39	31	8		
2	h	1	Total	C	N	0	0
			39	31	8		
2	j	1	Total	C	N	0	0
			39	31	8		
2	j	1	Total	C	N	0	0
			39	31	8		
2	l	1	Total	C	N	0	0
			39	31	8		

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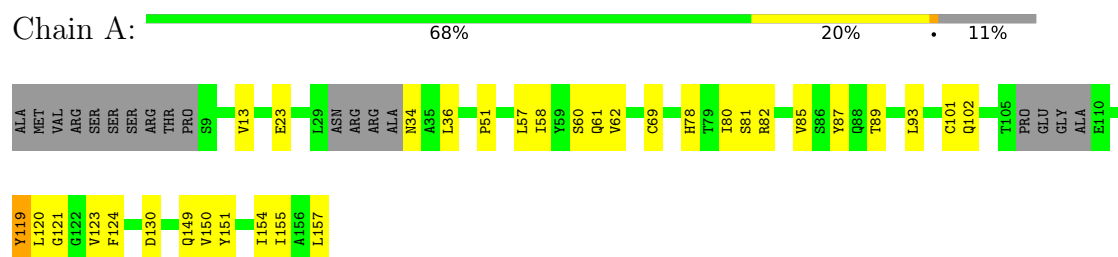
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	n	1	Total	C	N	0	0
			39	31	8		
2	n	1	Total	C	N	0	0
			39	31	8		
2	o	1	Total	C	N	0	0
			39	31	8		
2	p	1	Total	C	N	0	0
			39	31	8		
2	p	1	Total	C	N	0	0
			39	31	8		
2	r	1	Total	C	N	0	0
			39	31	8		
2	r	1	Total	C	N	0	0
			39	31	8		
2	t	1	Total	C	N	0	0
			39	31	8		
2	t	1	Total	C	N	0	0
			39	31	8		
2	v	1	Total	C	N	0	0
			39	31	8		
2	v	1	Total	C	N	0	0
			39	31	8		

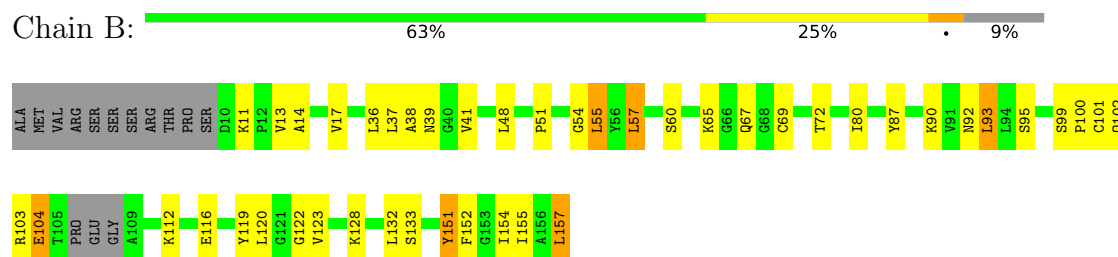
3 Residue-property plots

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.

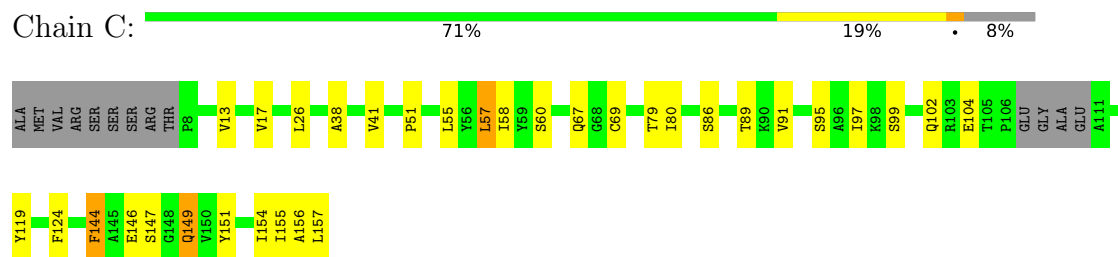
- Molecule 1: Tumor necrosis factor



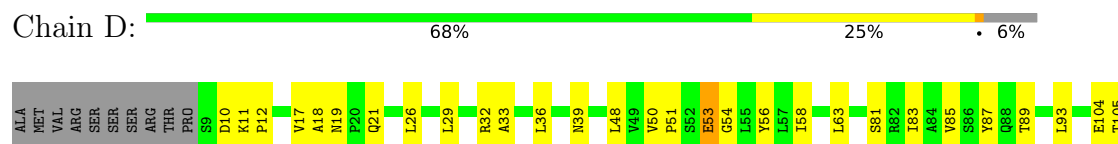
- Molecule 1: Tumor necrosis factor



- Molecule 1: Tumor necrosis factor



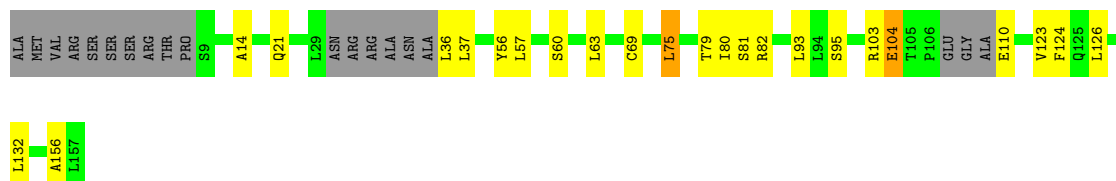
- Molecule 1: Tumor necrosis factor





- Molecule 1: Tumor necrosis factor

Chain F: 73% 14% 12%



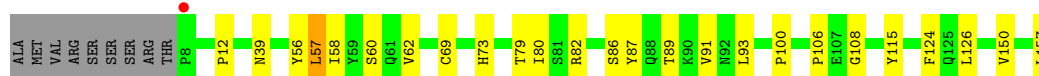
- Molecule 1: Tumor necrosis factor

Chain G: 79% 13% 6%



- Molecule 1: Tumor necrosis factor

Chain H: 79% 15% 6%



- Molecule 1: Tumor necrosis factor

Chain I: 79% 9% 11%



- Molecule 1: Tumor necrosis factor

Chain J: 73% 14% 13%



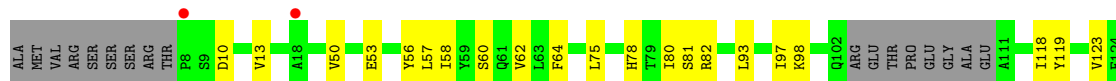
- Molecule 1: Tumor necrosis factor

Chain K: 74% 19% 6%

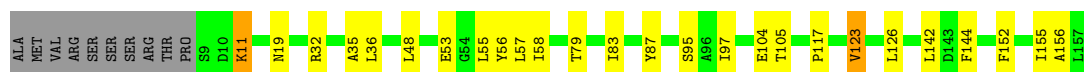
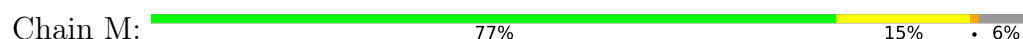




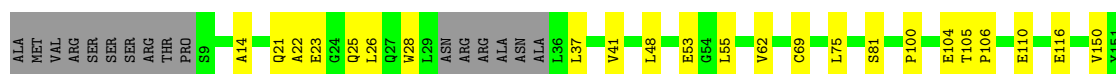
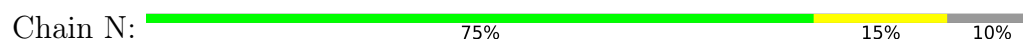
- Molecule 1: Tumor necrosis factor



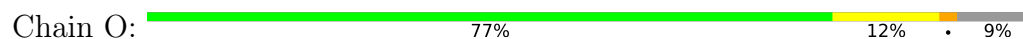
- Molecule 1: Tumor necrosis factor



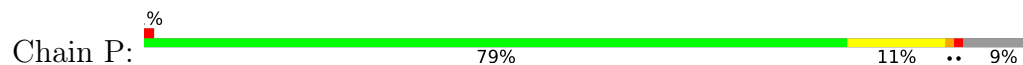
- Molecule 1: Tumor necrosis factor



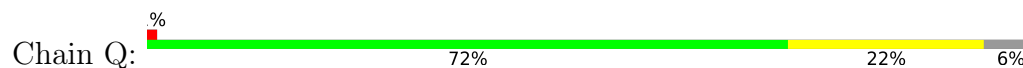
- Molecule 1: Tumor necrosis factor

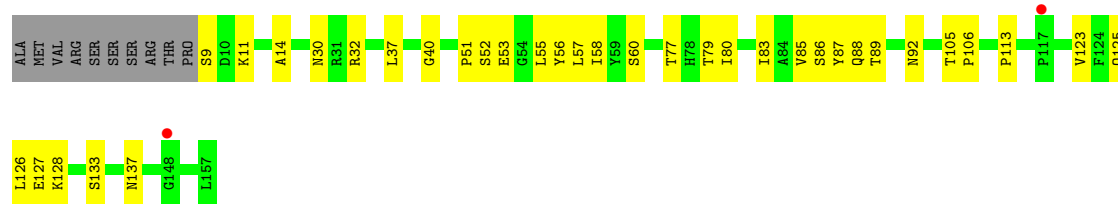


- Molecule 1: Tumor necrosis factor



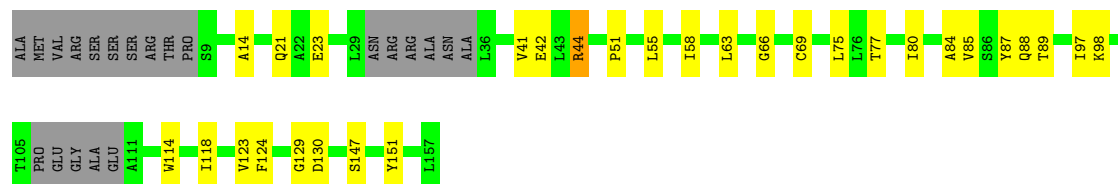
- Molecule 1: Tumor necrosis factor





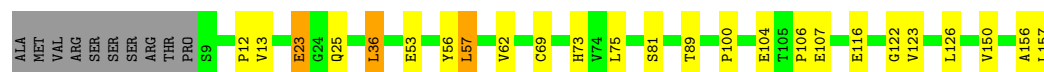
- Molecule 1: Tumor necrosis factor

Chain R: 68% 18% 13%



- Molecule 1: Tumor necrosis factor

Chain S: 78% 14% 6%



- Molecule 1: Tumor necrosis factor

Chain T: 83% 9% 8%



- Molecule 1: Tumor necrosis factor

Chain U: 86% 6% 6%



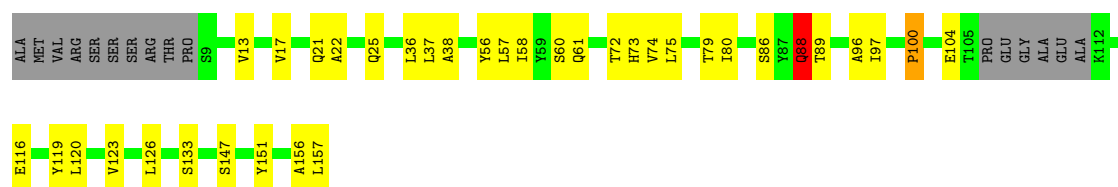
- Molecule 1: Tumor necrosis factor

Chain V: 79% 7% 13%



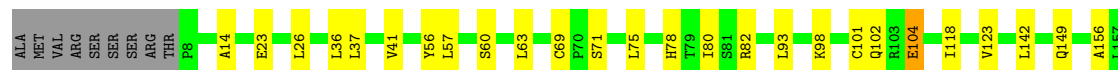
- Molecule 1: Tumor necrosis factor

Chain W: 67% 21% 10%



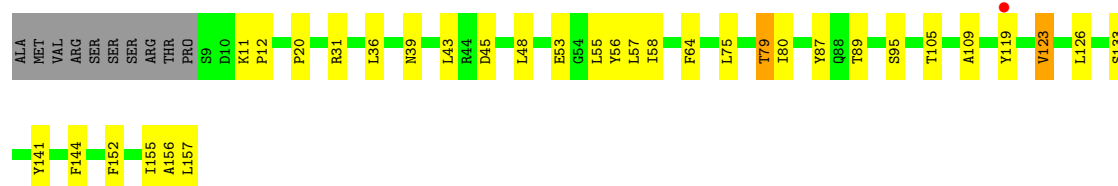
- Molecule 1: Tumor necrosis factor

Chain X: 78% 16% 6%



- Molecule 1: Tumor necrosis factor

Chain Y: 73% 19% 6%



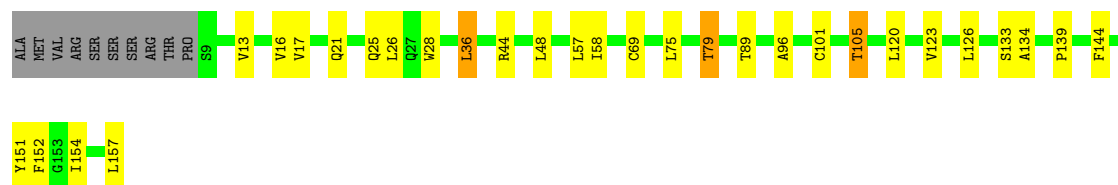
- Molecule 1: Tumor necrosis factor

Chain Z: 77% 13% 10%



- Molecule 1: Tumor necrosis factor

Chain a: 75% 17% 6%



- Molecule 1: Tumor necrosis factor

Chain b: 79% 11% 9%



- Molecule 1: Tumor necrosis factor

Chain c:  74% 16% 9%



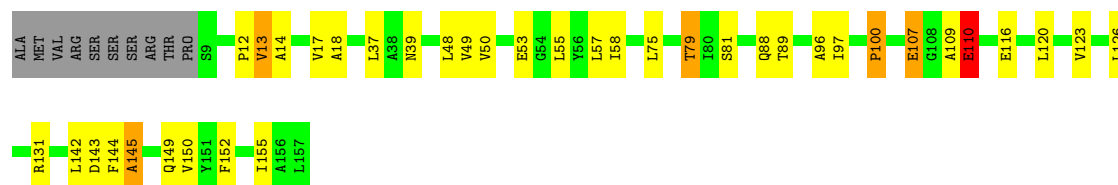
• Molecule 1: Tumor necrosis factor

Chain d:  77% 9% 13%



• Molecule 1: Tumor necrosis factor

Chain e:  70% 20% 6%



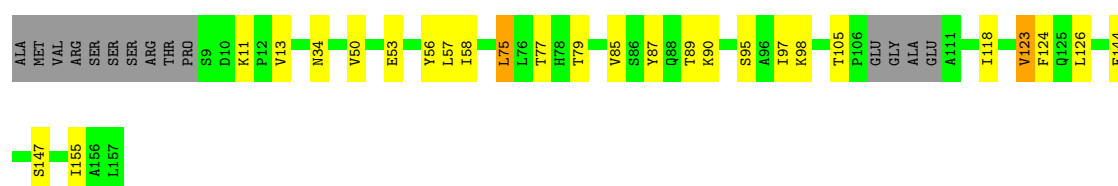
• Molecule 1: Tumor necrosis factor

Chain f:  80% 10% 10%



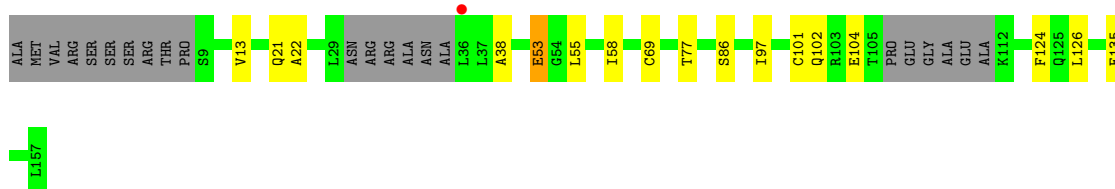
• Molecule 1: Tumor necrosis factor

Chain g:  75% 15% 9%



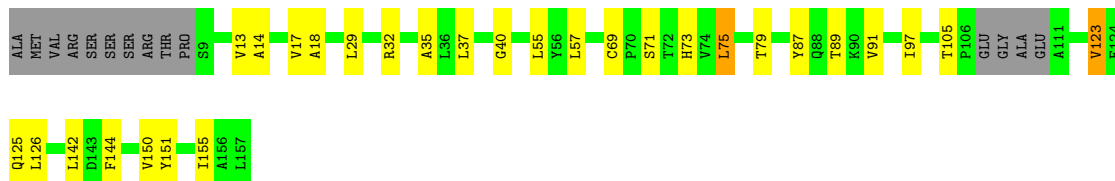
• Molecule 1: Tumor necrosis factor

Chain h:  75% 10% 14%



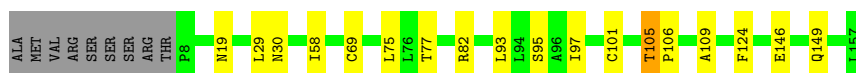
- Molecule 1: Tumor necrosis factor

Chain i: 73% 17% 9%



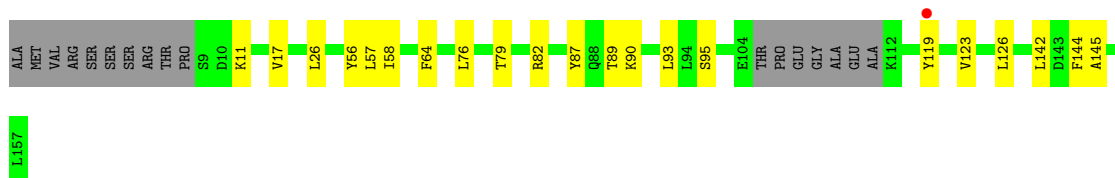
- Molecule 1: Tumor necrosis factor

Chain j: 83% 11% 6%



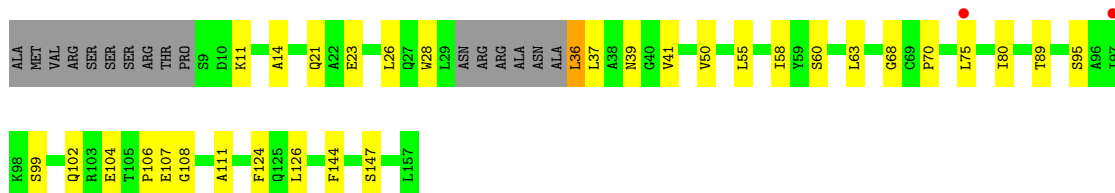
- Molecule 1: Tumor necrosis factor

Chain k: 76% 13% 11%



- Molecule 1: Tumor necrosis factor

Chain l: 70% 19% 10%



- Molecule 1: Tumor necrosis factor

Chain m: 84% 8% 8%



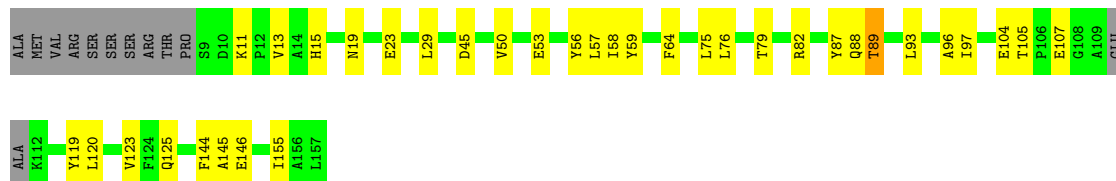
- Molecule 1: Tumor necrosis factor

Chain n:  84% 9% 8%



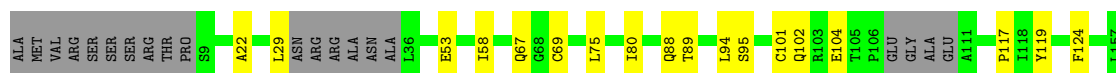
- Molecule 1: Tumor necrosis factor

Chain o:  70% 21% 8%



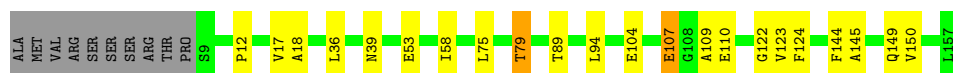
- Molecule 1: Tumor necrosis factor

Chain p:  76% 11% 13%



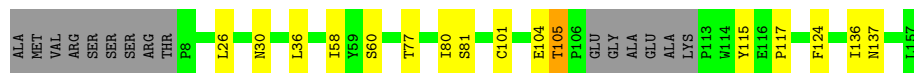
- Molecule 1: Tumor necrosis factor

Chain q:  80% 13% 6%



- Molecule 1: Tumor necrosis factor

Chain r:  81% 9% 9%



- Molecule 1: Tumor necrosis factor

Chain s:  77% 16% 6%

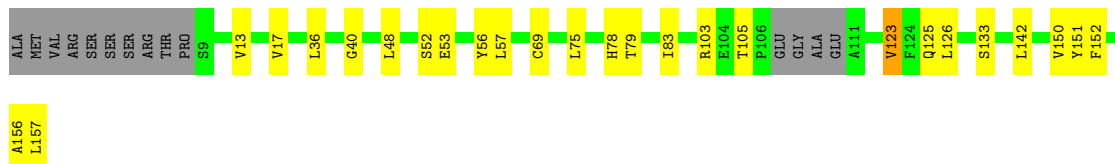


- Molecule 1: Tumor necrosis factor

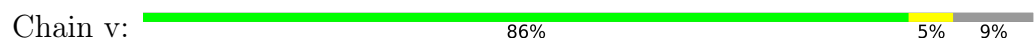
Chain t:  76% 13% 10%



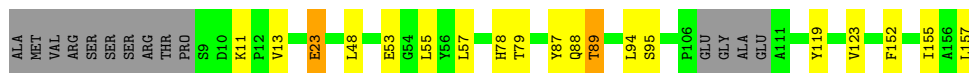
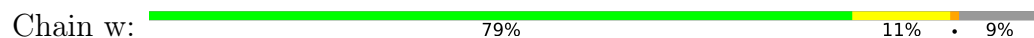
- Molecule 1: Tumor necrosis factor



- Molecule 1: Tumor necrosis factor



- Molecule 1: Tumor necrosis factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	104.89Å 118.35Å 186.75Å 97.57° 94.31° 98.75°	Depositor
Resolution (Å)	184.24 – 3.00 184.24 – 3.00	Depositor EDS
% Data completeness (in resolution range)	90.6 (184.24-3.00) 90.6 (184.24-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.211 , 0.300 0.213 , 0.304	Depositor DCC
R_{free} test set	445 reflections (0.25%)	wwPDB-VP
Wilson B-factor (Å ²)	93.9	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 80.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	56305	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.62% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: JN1

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	0.65	0/1128	0.89	1/1532 (0.1%)
1	B	0.70	1/1163 (0.1%)	0.96	3/1580 (0.2%)
1	C	0.61	0/1171	0.82	0/1592
1	D	0.68	0/1191	0.96	2/1620 (0.1%)
1	F	0.60	0/1123	0.84	0/1526
1	G	0.61	0/1191	0.90	3/1620 (0.2%)
1	H	0.58	0/1199	0.77	0/1631
1	I	0.61	0/1128	0.83	0/1533
1	J	0.62	0/1109	0.80	0/1507
1	K	0.65	0/1191	0.85	0/1620
1	L	0.59	0/1136	0.79	0/1544
1	M	0.65	0/1191	0.84	0/1620
1	N	0.64	0/1142	0.85	0/1553
1	O	0.62	0/1164	0.85	0/1581
1	P	0.60	0/1166	0.85	1/1585 (0.1%)
1	Q	0.58	0/1191	0.84	0/1620
1	R	0.58	0/1106	0.79	0/1502
1	S	0.68	0/1191	0.92	1/1620 (0.1%)
1	T	0.65	0/1171	0.85	0/1592
1	U	0.64	0/1191	0.86	0/1620
1	V	0.58	0/1109	0.75	0/1507
1	W	0.66	0/1150	0.88	2/1562 (0.1%)
1	X	0.60	0/1199	0.83	0/1631
1	Y	0.73	0/1191	0.89	0/1620
1	Z	0.61	0/1142	0.79	0/1553
1	a	0.67	0/1191	0.89	1/1620 (0.1%)
1	b	0.65	0/1158	0.85	2/1573 (0.1%)
1	c	0.64	0/1164	0.85	0/1581
1	d	0.61	0/1109	0.81	1/1507 (0.1%)
1	e	0.66	0/1191	0.86	1/1620 (0.1%)
1	f	0.64	0/1149	0.79	0/1561
1	g	0.68	0/1163	0.87	0/1581

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	h	0.65	0/1101	0.85	0/1495
1	i	0.65	0/1163	0.88	0/1581
1	j	0.67	0/1199	0.85	0/1631
1	k	0.61	0/1143	0.82	0/1552
1	l	0.61	0/1142	0.84	1/1553 (0.1%)
1	m	0.62	0/1177	0.84	1/1600 (0.1%)
1	n	0.64	0/1180	0.85	0/1604
1	o	0.63	0/1176	0.82	1/1598 (0.1%)
1	p	0.65	0/1114	0.86	0/1514
1	q	0.63	0/1191	0.84	1/1620 (0.1%)
1	r	0.62	0/1157	0.78	0/1573
1	s	0.68	0/1191	0.86	0/1620
1	t	0.63	0/1142	0.80	1/1553 (0.1%)
1	u	0.64	0/1163	0.85	1/1581 (0.1%)
1	v	0.67	0/1157	0.82	0/1573
1	w	0.60	0/1163	0.79	1/1581 (0.1%)
All	All	0.64	1/55718 (0.0%)	0.84	25/75743 (0.0%)

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	W	0	1
1	e	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	99	SER	C-N	5.89	1.38	1.33

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	36	LEU	N-CA-C	7.64	121.07	109.23
1	A	102	GLN	N-CA-C	-7.07	103.53	112.93
1	D	36	LEU	N-CA-C	6.94	119.79	108.55
1	q	36	LEU	N-CA-C	6.15	118.48	108.76
1	G	101	CYS	N-CA-C	6.03	119.08	107.44

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	W	100	PRO	Peptide
1	e	100	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1105	0	1098	27	0
1	B	1139	0	1136	56	0
1	C	1145	0	1145	18	0
1	D	1165	0	1158	41	3
1	F	1099	0	1094	12	0
1	G	1165	0	1158	8	0
1	H	1172	0	1166	9	0
1	I	1104	0	1104	13	0
1	J	1085	0	1083	7	0
1	K	1165	0	1158	13	0
1	L	1111	0	1112	14	0
1	M	1165	0	1158	12	0
1	N	1117	0	1109	7	0
1	O	1140	0	1136	11	0
1	P	1140	0	1134	14	0
1	Q	1165	0	1158	19	0
1	R	1083	0	1081	17	0
1	S	1165	0	1158	17	0
1	T	1145	0	1145	3	0
1	U	1165	0	1158	5	0
1	V	1085	0	1083	4	0
1	W	1126	0	1125	18	0
1	X	1172	0	1166	11	0
1	Y	1165	0	1158	15	0
1	Z	1117	0	1109	5	0
1	a	1165	0	1158	10	0
1	b	1133	0	1133	8	0
1	c	1140	0	1136	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	1085	0	1083	4	0
1	e	1165	0	1158	22	0
1	f	1124	0	1121	7	0
1	g	1138	0	1137	10	0
1	h	1078	0	1076	5	0
1	i	1138	0	1137	15	0
1	j	1172	0	1166	4	0
1	k	1119	0	1118	11	0
1	l	1117	0	1109	11	0
1	m	1152	0	1148	5	0
1	n	1154	0	1151	3	0
1	o	1151	0	1146	13	0
1	p	1090	0	1088	4	0
1	q	1165	0	1158	9	0
1	r	1131	0	1128	5	0
1	s	1165	0	1158	7	3
1	t	1117	0	1109	8	0
1	u	1138	0	1137	9	0
1	v	1131	0	1128	0	0
1	w	1138	0	1137	6	0
2	A	78	0	0	5	0
2	C	78	0	0	22	0
2	D	39	0	0	0	0
2	F	78	0	0	0	0
2	H	78	0	0	0	0
2	J	78	0	0	0	0
2	L	39	0	0	2	0
2	M	39	0	0	0	0
2	N	39	0	0	0	0
2	P	78	0	0	8	0
2	Q	39	0	0	0	0
2	R	39	0	0	1	0
2	U	39	0	0	1	0
2	V	78	0	0	0	0
2	X	78	0	0	0	0
2	Z	78	0	0	0	0
2	b	78	0	0	1	0
2	d	39	0	0	0	0
2	f	78	0	0	0	0
2	h	78	0	0	0	0
2	j	78	0	0	0	0
2	l	39	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	n	78	0	0	0	0
2	o	39	0	0	0	0
2	p	78	0	0	0	0
2	r	78	0	0	0	0
2	t	78	0	0	0	0
2	v	78	0	0	0	0
All	All	56305	0	54310	526	3

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 5.

The worst 5 of 526 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:B:92:ASN:ND2	1:W:86:SER:O	1.87	1.06
2:C:202:JNI:C5	2:C:202:JNI:C27	2.38	0.99
1:S:56:TYR:CD1	1:S:126:LEU:HD12	1.99	0.97
2:C:202:JNI:C5	2:C:202:JNI:C22	2.50	0.90
1:D:10:ASP:HB2	1:D:39:ASN:HB3	1.51	0.90

All (3) 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:D:32:ARG:NH2	1:s:23:GLU:OE1[1_545]	1.43	0.77
1:D:32:ARG:CZ	1:s:23:GLU:OE1[1_545]	1.78	0.42
1:D:32:ARG:NH1	1:s:23:GLU:OE1[1_545]	2.15	0.05

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	135/159 (85%)	118 (87%)	15 (11%)	2 (2%)	8	35
1	B	141/159 (89%)	126 (89%)	14 (10%)	1 (1%)	18	53
1	C	142/159 (89%)	130 (92%)	10 (7%)	2 (1%)	9	36
1	D	147/159 (92%)	122 (83%)	21 (14%)	4 (3%)	4	22
1	F	134/159 (84%)	116 (87%)	18 (13%)	0	100	100
1	G	147/159 (92%)	136 (92%)	9 (6%)	2 (1%)	9	36
1	H	148/159 (93%)	136 (92%)	9 (6%)	3 (2%)	6	28
1	I	137/159 (86%)	126 (92%)	10 (7%)	1 (1%)	18	53
1	J	132/159 (83%)	121 (92%)	9 (7%)	2 (2%)	8	35
1	K	147/159 (92%)	128 (87%)	17 (12%)	2 (1%)	9	36
1	L	138/159 (87%)	131 (95%)	7 (5%)	0	100	100
1	M	147/159 (92%)	134 (91%)	10 (7%)	3 (2%)	6	28
1	N	139/159 (87%)	121 (87%)	16 (12%)	2 (1%)	9	36
1	O	141/159 (89%)	132 (94%)	9 (6%)	0	100	100
1	P	141/159 (89%)	129 (92%)	12 (8%)	0	100	100
1	Q	147/159 (92%)	131 (89%)	11 (8%)	5 (3%)	3	17
1	R	132/159 (83%)	123 (93%)	6 (4%)	3 (2%)	5	25
1	S	147/159 (92%)	137 (93%)	9 (6%)	1 (1%)	18	53
1	T	142/159 (89%)	135 (95%)	7 (5%)	0	100	100
1	U	147/159 (92%)	134 (91%)	12 (8%)	1 (1%)	18	53
1	V	132/159 (83%)	117 (89%)	15 (11%)	0	100	100
1	W	139/159 (87%)	133 (96%)	5 (4%)	1 (1%)	18	53
1	X	148/159 (93%)	140 (95%)	8 (5%)	0	100	100
1	Y	147/159 (92%)	131 (89%)	12 (8%)	4 (3%)	4	22
1	Z	139/159 (87%)	124 (89%)	12 (9%)	3 (2%)	5	26
1	a	147/159 (92%)	134 (91%)	13 (9%)	0	100	100
1	b	140/159 (88%)	129 (92%)	11 (8%)	0	100	100
1	c	141/159 (89%)	125 (89%)	13 (9%)	3 (2%)	5	27
1	d	132/159 (83%)	122 (92%)	9 (7%)	1 (1%)	16	50
1	e	147/159 (92%)	132 (90%)	12 (8%)	3 (2%)	6	28
1	f	139/159 (87%)	129 (93%)	10 (7%)	0	100	100
1	g	141/159 (89%)	132 (94%)	6 (4%)	3 (2%)	5	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	h	131/159 (82%)	121 (92%)	8 (6%)	2 (2%)	8	35
1	i	141/159 (89%)	130 (92%)	11 (8%)	0	100	100
1	j	148/159 (93%)	134 (90%)	11 (7%)	3 (2%)	6	28
1	k	138/159 (87%)	127 (92%)	9 (6%)	2 (1%)	9	36
1	l	139/159 (87%)	122 (88%)	12 (9%)	5 (4%)	2	16
1	m	143/159 (90%)	134 (94%)	8 (6%)	1 (1%)	18	53
1	n	143/159 (90%)	133 (93%)	9 (6%)	1 (1%)	18	53
1	o	143/159 (90%)	131 (92%)	8 (6%)	4 (3%)	4	21
1	p	133/159 (84%)	113 (85%)	18 (14%)	2 (2%)	8	35
1	q	147/159 (92%)	134 (91%)	10 (7%)	3 (2%)	6	28
1	r	140/159 (88%)	124 (89%)	14 (10%)	2 (1%)	9	36
1	s	147/159 (92%)	132 (90%)	9 (6%)	6 (4%)	2	13
1	t	139/159 (87%)	125 (90%)	12 (9%)	2 (1%)	9	36
1	u	141/159 (89%)	126 (89%)	15 (11%)	0	100	100
1	v	140/159 (88%)	126 (90%)	12 (9%)	2 (1%)	9	36
1	w	141/159 (89%)	124 (88%)	15 (11%)	2 (1%)	9	36
All	All	6777/7632 (89%)	6150 (91%)	538 (8%)	89 (1%)	9	38

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	110	GLU
1	M	105	THR
1	Q	105	THR
1	R	23	GLU
1	R	88	GLN

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	120/134 (90%)	113 (94%)	7 (6%)	18	51
1	B	122/134 (91%)	115 (94%)	7 (6%)	18	52
1	C	124/134 (92%)	110 (89%)	14 (11%)	5	24
1	D	125/134 (93%)	122 (98%)	3 (2%)	43	73
1	F	120/134 (90%)	112 (93%)	8 (7%)	15	46
1	G	125/134 (93%)	112 (90%)	13 (10%)	7	28
1	H	126/134 (94%)	119 (94%)	7 (6%)	19	52
1	I	119/134 (89%)	113 (95%)	6 (5%)	22	56
1	J	119/134 (89%)	111 (93%)	8 (7%)	15	46
1	K	125/134 (93%)	109 (87%)	16 (13%)	4	19
1	L	120/134 (90%)	113 (94%)	7 (6%)	18	51
1	M	125/134 (93%)	115 (92%)	10 (8%)	11	38
1	N	121/134 (90%)	112 (93%)	9 (7%)	13	42
1	O	123/134 (92%)	112 (91%)	11 (9%)	9	34
1	P	124/134 (92%)	117 (94%)	7 (6%)	19	52
1	Q	125/134 (93%)	121 (97%)	4 (3%)	34	67
1	R	118/134 (88%)	112 (95%)	6 (5%)	21	55
1	S	125/134 (93%)	117 (94%)	8 (6%)	16	48
1	T	124/134 (92%)	115 (93%)	9 (7%)	13	42
1	U	125/134 (93%)	119 (95%)	6 (5%)	23	57
1	V	119/134 (89%)	110 (92%)	9 (8%)	12	41
1	W	122/134 (91%)	111 (91%)	11 (9%)	9	34
1	X	126/134 (94%)	117 (93%)	9 (7%)	13	43
1	Y	125/134 (93%)	116 (93%)	9 (7%)	13	43
1	Z	121/134 (90%)	112 (93%)	9 (7%)	13	42
1	a	125/134 (93%)	111 (89%)	14 (11%)	6	24
1	b	123/134 (92%)	120 (98%)	3 (2%)	43	73
1	c	123/134 (92%)	112 (91%)	11 (9%)	9	34
1	d	119/134 (89%)	112 (94%)	7 (6%)	18	50
1	e	125/134 (93%)	117 (94%)	8 (6%)	16	48
1	f	122/134 (91%)	118 (97%)	4 (3%)	33	67
1	g	123/134 (92%)	114 (93%)	9 (7%)	13	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	h	118/134 (88%)	110 (93%)	8 (7%)	14	45
1	i	123/134 (92%)	113 (92%)	10 (8%)	11	38
1	j	126/134 (94%)	118 (94%)	8 (6%)	16	48
1	k	121/134 (90%)	116 (96%)	5 (4%)	27	61
1	l	121/134 (90%)	109 (90%)	12 (10%)	7	30
1	m	124/134 (92%)	115 (93%)	9 (7%)	13	42
1	n	125/134 (93%)	118 (94%)	7 (6%)	19	52
1	o	124/134 (92%)	116 (94%)	8 (6%)	15	47
1	p	119/134 (89%)	108 (91%)	11 (9%)	8	33
1	q	125/134 (93%)	118 (94%)	7 (6%)	19	52
1	r	123/134 (92%)	116 (94%)	7 (6%)	18	52
1	s	125/134 (93%)	113 (90%)	12 (10%)	8	31
1	t	121/134 (90%)	115 (95%)	6 (5%)	22	56
1	u	123/134 (92%)	111 (90%)	12 (10%)	7	30
1	v	123/134 (92%)	117 (95%)	6 (5%)	22	56
1	w	123/134 (92%)	113 (92%)	10 (8%)	11	38
All	All	5892/6432 (92%)	5485 (93%)	407 (7%)	14	45

5 of 407 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	c	21	GLN
1	i	144	PHE
1	w	55	LEU
1	c	133	SER
1	g	53	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
1	f	102	GLN
1	n	67	GLN
1	j	30	ASN
1	k	73	HIS
1	q	19	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

46 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	JNI	L	201	-	44,44,44	1.39	9 (20%)	59,60,60	3.32	28 (47%)
2	JNI	J	202	-	44,44,44	0.84	2 (4%)	59,60,60	2.35	16 (27%)
2	JNI	A	202	-	44,44,44	0.86	3 (6%)	59,60,60	2.42	20 (33%)
2	JNI	j	201	-	44,44,44	1.07	3 (6%)	59,60,60	2.96	23 (38%)
2	JNI	v	202	-	44,44,44	1.13	3 (6%)	59,60,60	2.80	22 (37%)
2	JNI	v	201	-	44,44,44	0.90	2 (4%)	59,60,60	2.64	21 (35%)
2	JNI	Z	202	-	44,44,44	0.93	2 (4%)	59,60,60	2.49	22 (37%)
2	JNI	P	201	-	44,44,44	0.81	2 (4%)	59,60,60	2.32	18 (30%)
2	JNI	X	202	-	44,44,44	1.23	4 (9%)	59,60,60	2.93	27 (45%)
2	JNI	d	201	-	44,44,44	0.93	1 (2%)	59,60,60	2.61	21 (35%)
2	JNI	p	201	-	44,44,44	0.91	2 (4%)	59,60,60	2.42	17 (28%)
2	JNI	p	202	-	44,44,44	0.90	2 (4%)	59,60,60	2.56	26 (44%)
2	JNI	R	201	-	44,44,44	1.13	3 (6%)	59,60,60	2.75	22 (37%)
2	JNI	C	202	-	44,44,44	0.78	2 (4%)	59,60,60	2.59	20 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	JNI	t	201	-	44,44,44	0.97	2 (4%)	59,60,60	2.56	21 (35%)
2	JNI	f	202	-	44,44,44	0.90	2 (4%)	59,60,60	2.35	17 (28%)
2	JNI	J	201	-	44,44,44	0.88	2 (4%)	59,60,60	2.39	17 (28%)
2	JNI	C	201	-	44,44,44	0.84	2 (4%)	59,60,60	2.62	25 (42%)
2	JNI	n	202	-	44,44,44	1.09	4 (9%)	59,60,60	2.81	28 (47%)
2	JNI	M	201	-	44,44,44	0.89	2 (4%)	59,60,60	2.70	19 (32%)
2	JNI	j	202	-	44,44,44	1.13	2 (4%)	59,60,60	2.91	30 (50%)
2	JNI	D	201	-	44,44,44	0.83	2 (4%)	59,60,60	2.46	17 (28%)
2	JNI	n	201	-	44,44,44	1.01	3 (6%)	59,60,60	2.68	23 (38%)
2	JNI	r	201	-	44,44,44	0.89	2 (4%)	59,60,60	2.48	21 (35%)
2	JNI	H	201	-	44,44,44	0.93	2 (4%)	59,60,60	2.53	16 (27%)
2	JNI	o	201	-	44,44,44	0.89	2 (4%)	59,60,60	2.70	20 (33%)
2	JNI	l	201	-	44,44,44	1.08	4 (9%)	59,60,60	2.59	23 (38%)
2	JNI	F	201	-	44,44,44	0.96	0	59,60,60	2.40	17 (28%)
2	JNI	t	202	-	44,44,44	0.95	2 (4%)	59,60,60	2.63	23 (38%)
2	JNI	Q	201	-	44,44,44	0.84	2 (4%)	59,60,60	2.52	17 (28%)
2	JNI	r	202	-	44,44,44	1.25	5 (11%)	59,60,60	2.85	28 (47%)
2	JNI	f	201	-	44,44,44	1.01	4 (9%)	59,60,60	2.85	23 (38%)
2	JNI	A	201	-	44,44,44	0.85	3 (6%)	59,60,60	2.34	18 (30%)
2	JNI	b	202	-	44,44,44	1.41	8 (18%)	59,60,60	2.88	27 (45%)
2	JNI	b	201	-	44,44,44	1.08	5 (11%)	59,60,60	2.86	23 (38%)
2	JNI	V	202	-	44,44,44	0.97	2 (4%)	59,60,60	2.73	18 (30%)
2	JNI	Z	201	-	44,44,44	0.91	1 (2%)	59,60,60	2.43	18 (30%)
2	JNI	H	202	-	44,44,44	1.34	6 (13%)	59,60,60	3.21	27 (45%)
2	JNI	F	202	-	44,44,44	0.83	2 (4%)	59,60,60	2.35	19 (32%)
2	JNI	U	201	-	44,44,44	1.12	5 (11%)	59,60,60	2.86	22 (37%)
2	JNI	P	202	-	44,44,44	0.79	2 (4%)	59,60,60	2.24	16 (27%)
2	JNI	h	202	-	44,44,44	1.08	3 (6%)	59,60,60	2.67	20 (33%)
2	JNI	N	201	-	44,44,44	0.78	2 (4%)	59,60,60	2.23	18 (30%)
2	JNI	V	201	-	44,44,44	0.98	2 (4%)	59,60,60	2.37	18 (30%)
2	JNI	h	201	-	44,44,44	1.12	5 (11%)	59,60,60	2.83	23 (38%)
2	JNI	X	201	-	44,44,44	0.99	4 (9%)	59,60,60	2.86	23 (38%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
 '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	JNI	L	201	-	-	4/24/32/32	0/6/6/6
2	JNI	J	202	-	-	11/24/32/32	0/6/6/6
2	JNI	A	202	-	-	10/24/32/32	0/6/6/6
2	JNI	j	201	-	-	3/24/32/32	0/6/6/6
2	JNI	v	202	-	-	9/24/32/32	1/6/6/6
2	JNI	v	201	-	-	8/24/32/32	0/6/6/6
2	JNI	Z	202	-	-	8/24/32/32	0/6/6/6
2	JNI	P	201	-	-	6/24/32/32	0/6/6/6
2	JNI	X	202	-	-	10/24/32/32	0/6/6/6
2	JNI	d	201	-	-	4/24/32/32	0/6/6/6
2	JNI	p	201	-	-	4/24/32/32	0/6/6/6
2	JNI	p	202	-	-	13/24/32/32	0/6/6/6
2	JNI	R	201	-	-	2/24/32/32	0/6/6/6
2	JNI	C	202	-	-	9/24/32/32	0/6/6/6
2	JNI	t	201	-	-	2/24/32/32	0/6/6/6
2	JNI	f	202	-	-	8/24/32/32	0/6/6/6
2	JNI	J	201	-	-	2/24/32/32	0/6/6/6
2	JNI	C	201	-	-	11/24/32/32	0/6/6/6
2	JNI	n	202	-	-	14/24/32/32	0/6/6/6
2	JNI	M	201	-	-	5/24/32/32	0/6/6/6
2	JNI	j	202	-	-	16/24/32/32	0/6/6/6
2	JNI	D	201	-	-	2/24/32/32	0/6/6/6
2	JNI	n	201	-	-	10/24/32/32	0/6/6/6
2	JNI	r	201	-	-	8/24/32/32	0/6/6/6
2	JNI	H	201	-	-	6/24/32/32	0/6/6/6
2	JNI	o	201	-	-	8/24/32/32	0/6/6/6
2	JNI	l	201	-	-	4/24/32/32	0/6/6/6
2	JNI	F	201	-	-	4/24/32/32	0/6/6/6
2	JNI	t	202	-	-	8/24/32/32	0/6/6/6
2	JNI	Q	201	-	-	5/24/32/32	0/6/6/6
2	JNI	r	202	-	-	11/24/32/32	0/6/6/6
2	JNI	f	201	-	-	6/24/32/32	0/6/6/6
2	JNI	A	201	-	-	2/24/32/32	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	JNI	b	202	-	-	11/24/32/32	0/6/6/6
2	JNI	b	201	-	-	4/24/32/32	0/6/6/6
2	JNI	V	202	-	-	10/24/32/32	0/6/6/6
2	JNI	Z	201	-	-	2/24/32/32	0/6/6/6
2	JNI	H	202	-	-	3/24/32/32	0/6/6/6
2	JNI	F	202	-	-	11/24/32/32	0/6/6/6
2	JNI	U	201	-	-	6/24/32/32	0/6/6/6
2	JNI	P	202	-	-	13/24/32/32	0/6/6/6
2	JNI	h	202	-	-	8/24/32/32	0/6/6/6
2	JNI	N	201	-	-	1/24/32/32	0/6/6/6
2	JNI	V	201	-	-	7/24/32/32	0/6/6/6
2	JNI	h	201	-	-	2/24/32/32	0/6/6/6
2	JNI	X	201	-	-	6/24/32/32	0/6/6/6

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	201	JNI	C31-N34	3.63	1.43	1.35
2	j	202	JNI	C2-N1	3.59	1.41	1.33
2	r	202	JNI	C2-N1	3.33	1.40	1.33
2	b	202	JNI	C21-C16	3.26	1.45	1.41
2	j	202	JNI	C21-C16	3.21	1.45	1.41

The worst 5 of 978 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	201	JNI	C33-N32-C31	9.74	124.30	115.68
2	M	201	JNI	C2-N7-C6	9.35	124.05	116.61
2	U	201	JNI	C2-N7-C6	9.32	124.02	116.61
2	j	201	JNI	C2-N7-C6	9.31	124.01	116.61
2	X	201	JNI	C2-N7-C6	8.91	123.70	116.61

There are no chirality outliers.

5 of 317 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	202	JNI	C21-C16-N8-C9
2	C	202	JNI	C5-C6-N8-C16
2	C	202	JNI	N7-C6-N8-C16

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Mol	Chain	Res	Type	Atoms
2	C	202	JNI	N32-C31-N34-C39
2	D	201	JNI	N32-C31-N34-C39

All (1) ring outliers are listed below:

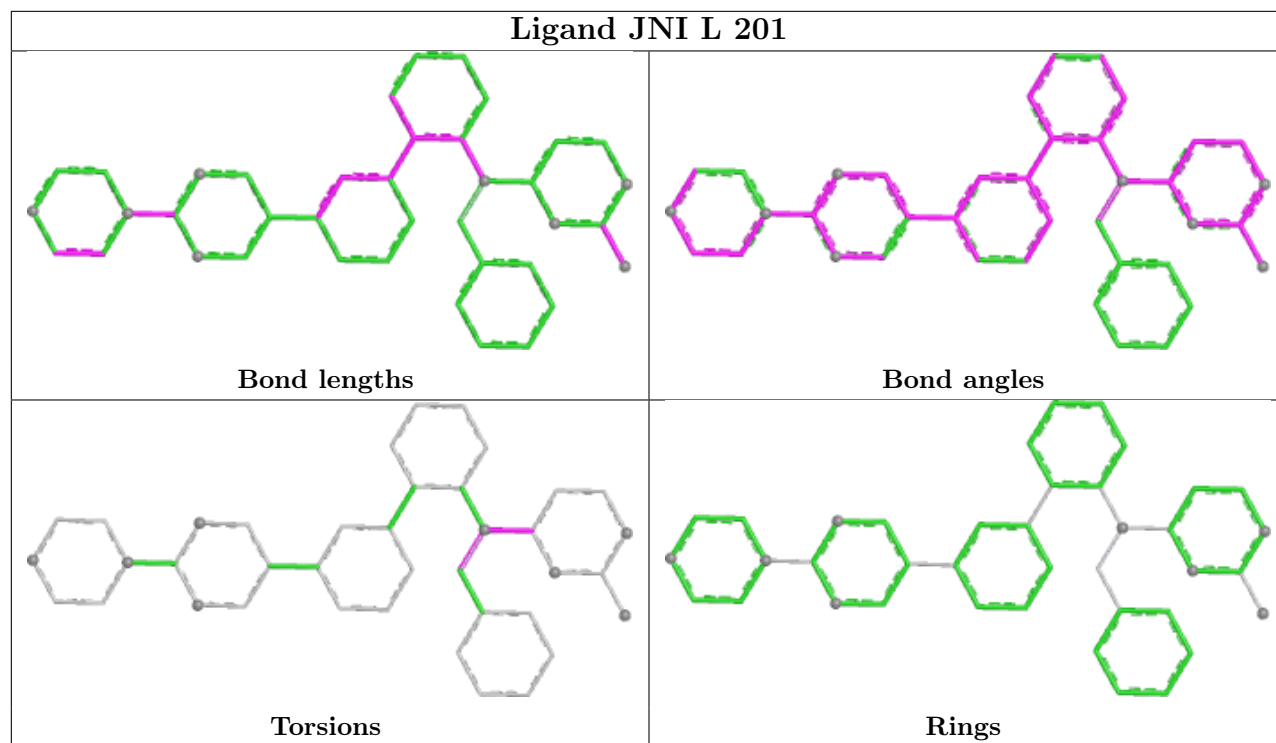
Mol	Chain	Res	Type	Atoms
2	v	202	JNI	C35-C36-C38-C39-N34-N37

9 monomers are involved in 40 short contacts:

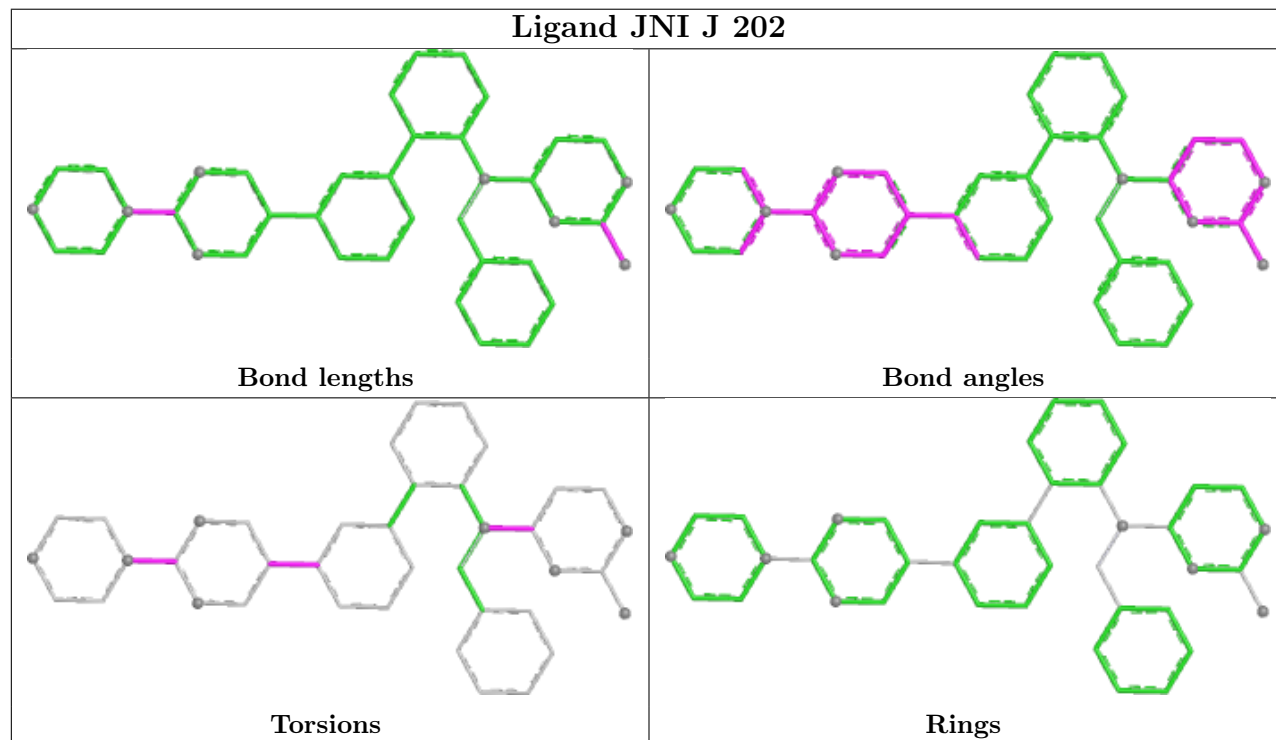
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	201	JNI	2	0
2	A	202	JNI	1	0
2	R	201	JNI	1	0
2	C	202	JNI	14	0
2	C	201	JNI	8	0
2	A	201	JNI	4	0
2	b	201	JNI	1	0
2	U	201	JNI	1	0
2	P	202	JNI	8	0

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.

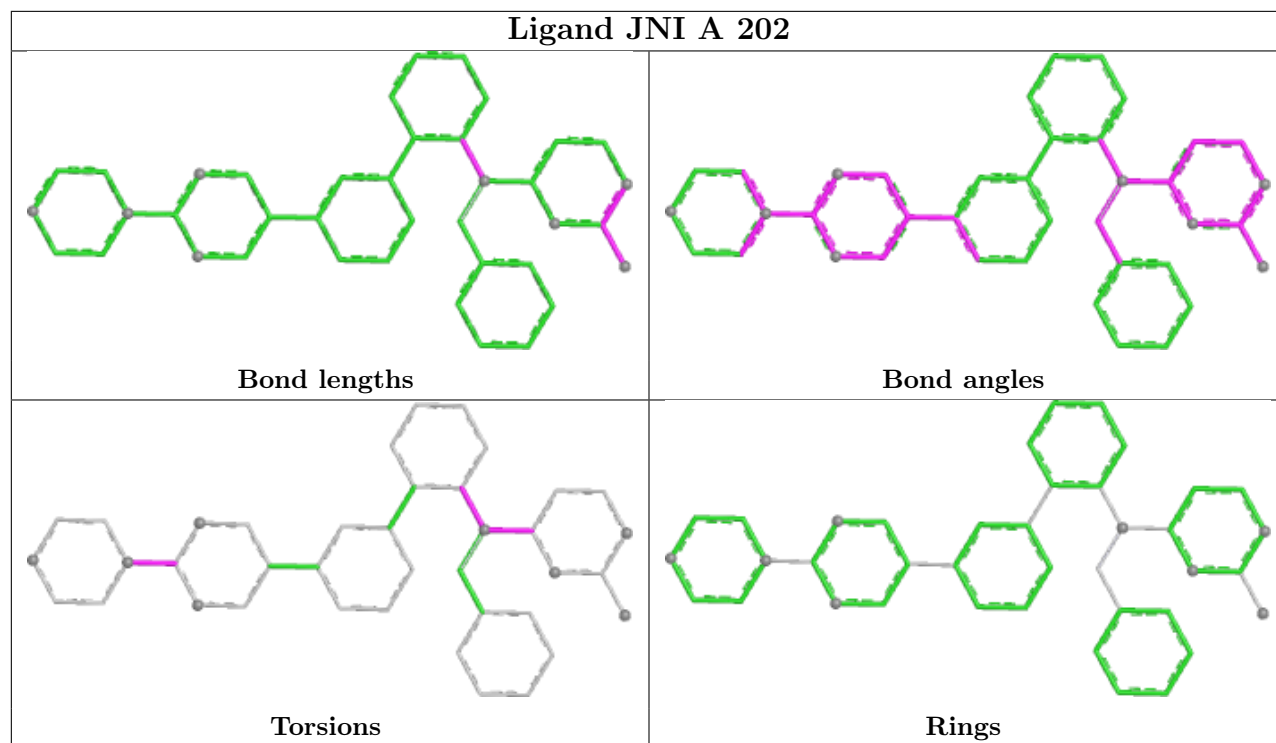
Ligand JNI L 201



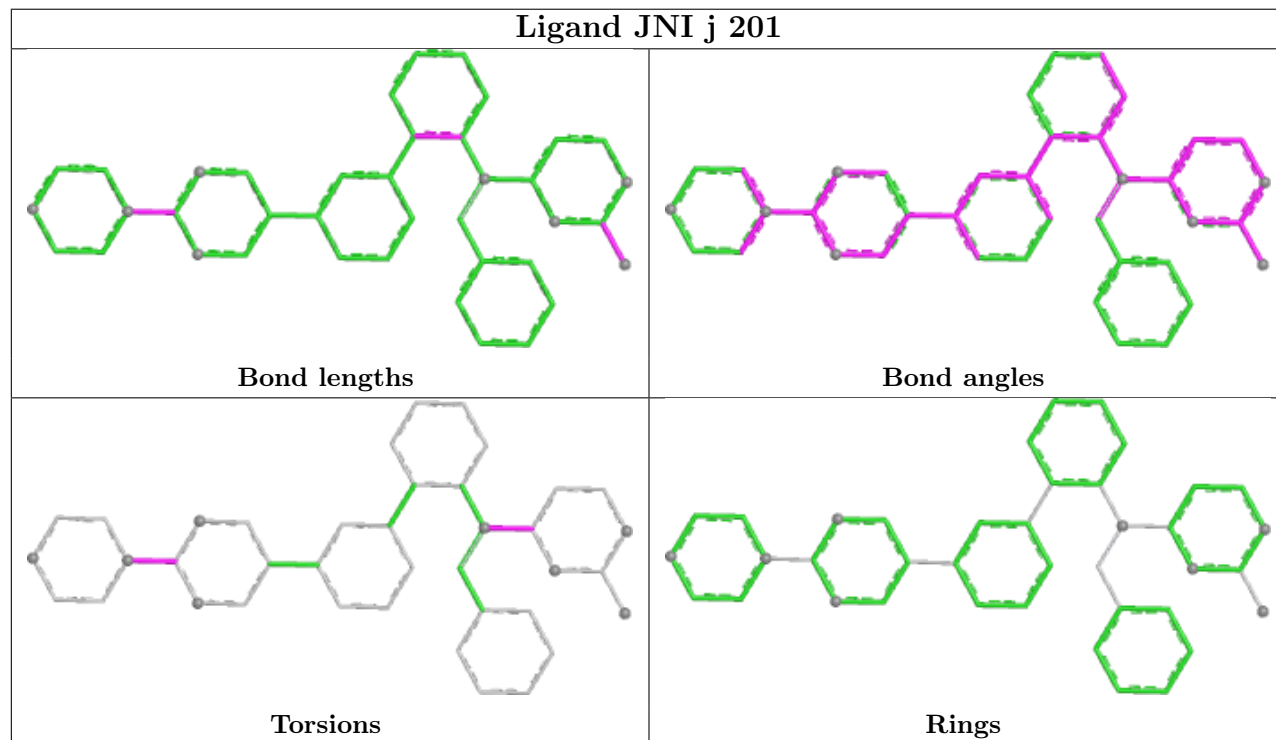
Ligand JNI J 202

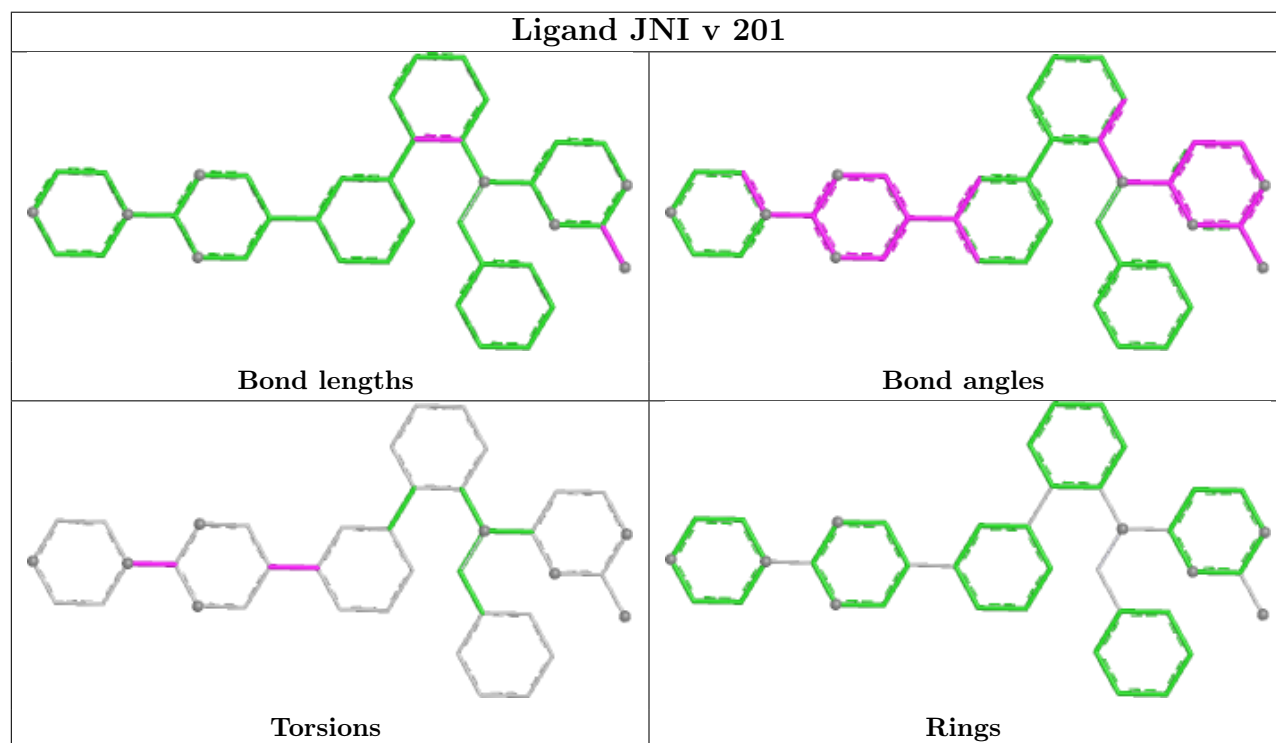
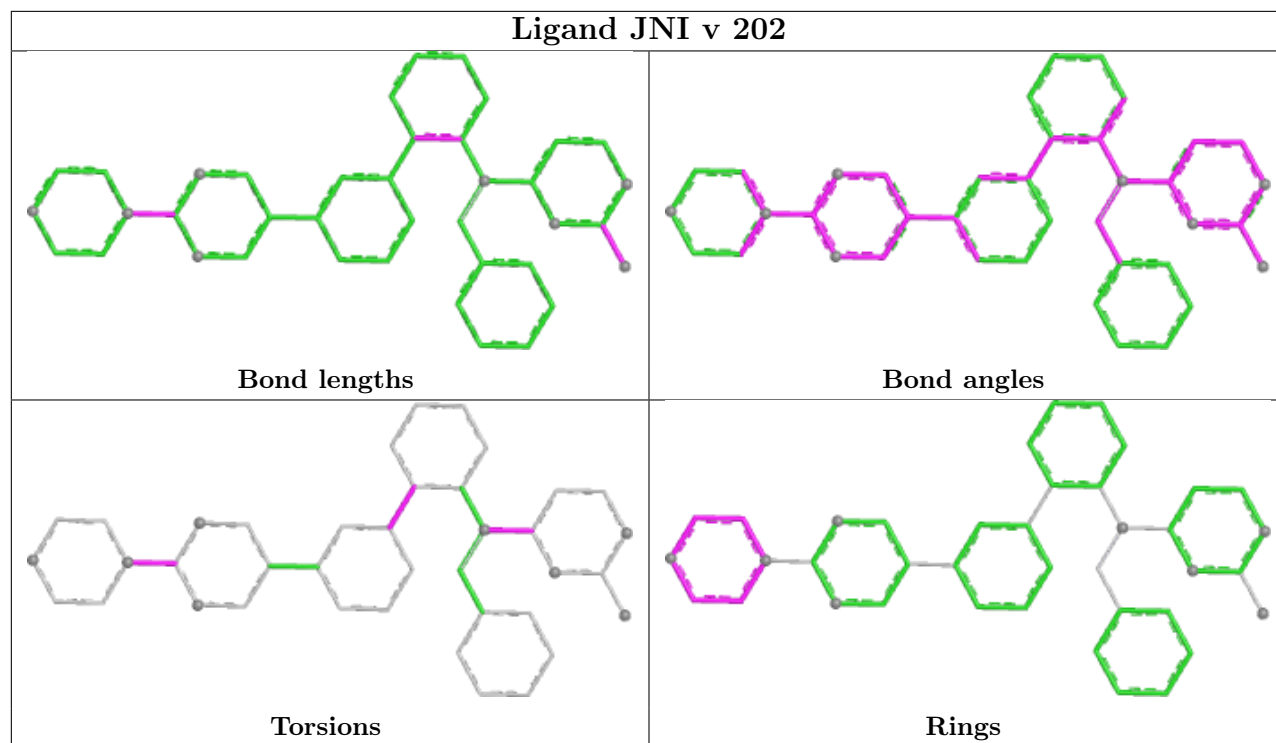


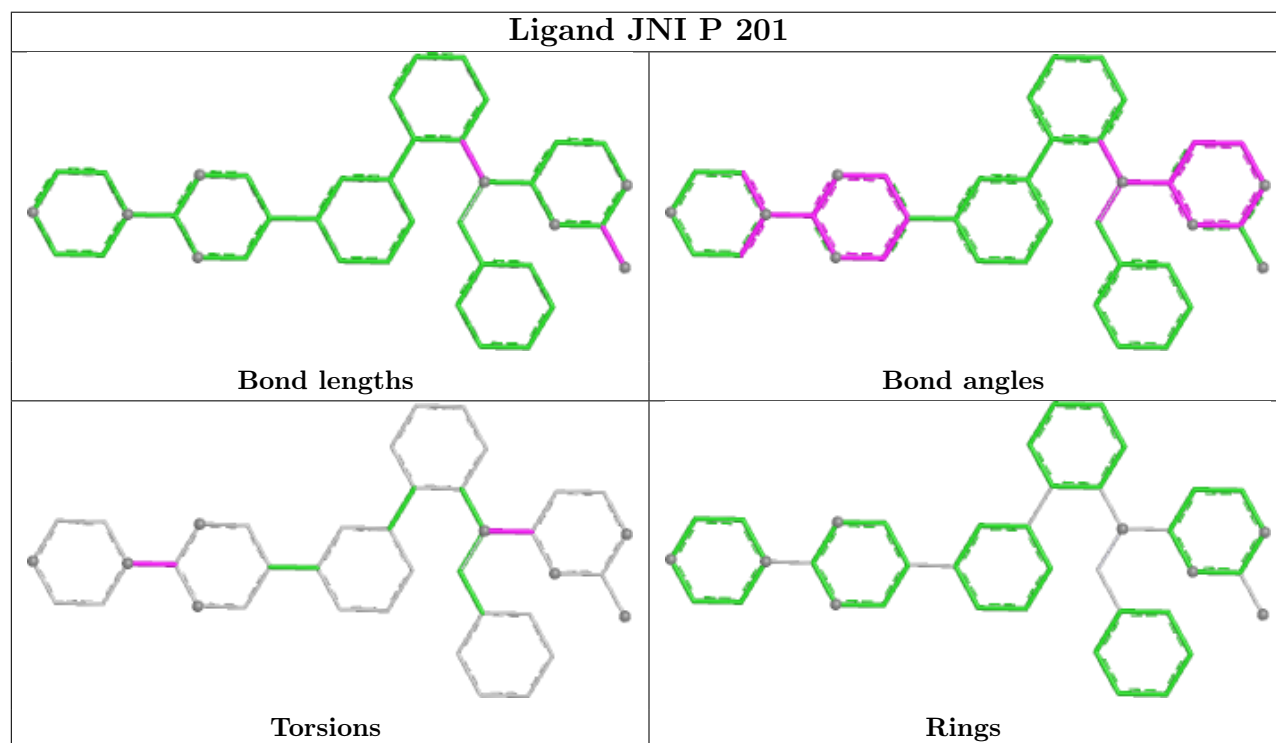
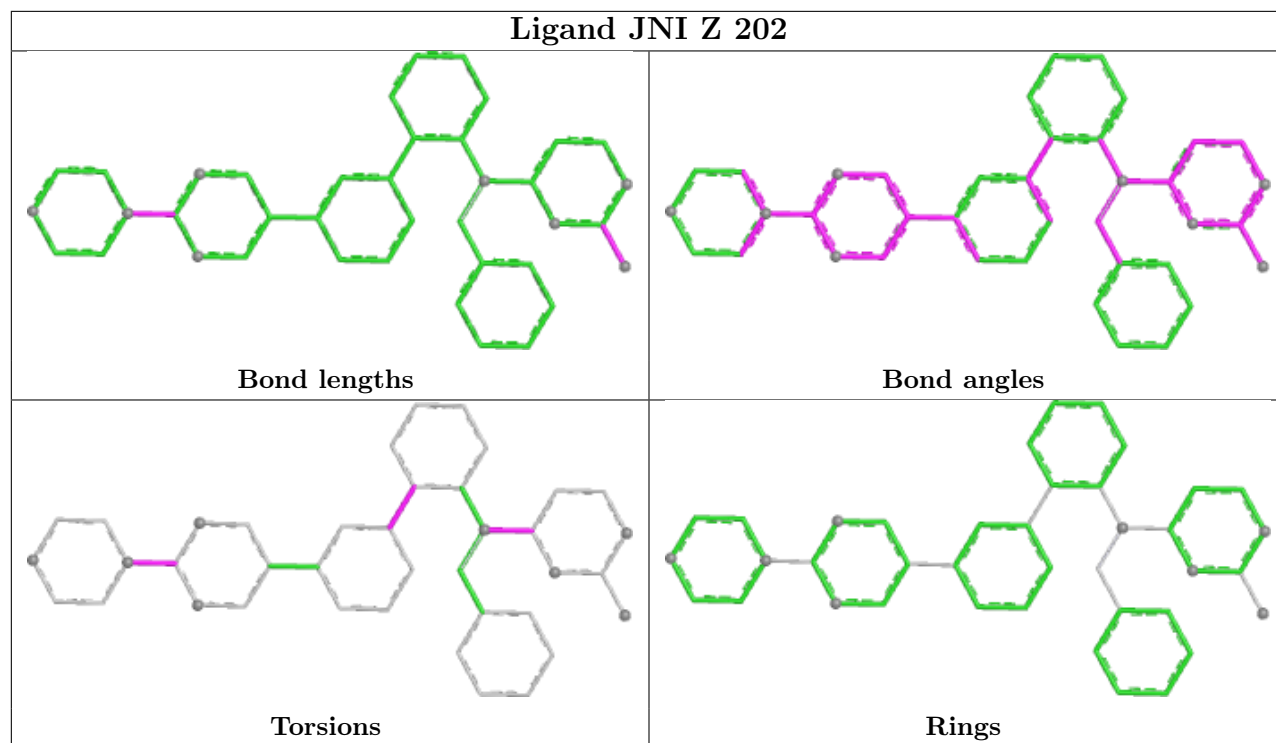
Ligand JNI A 202



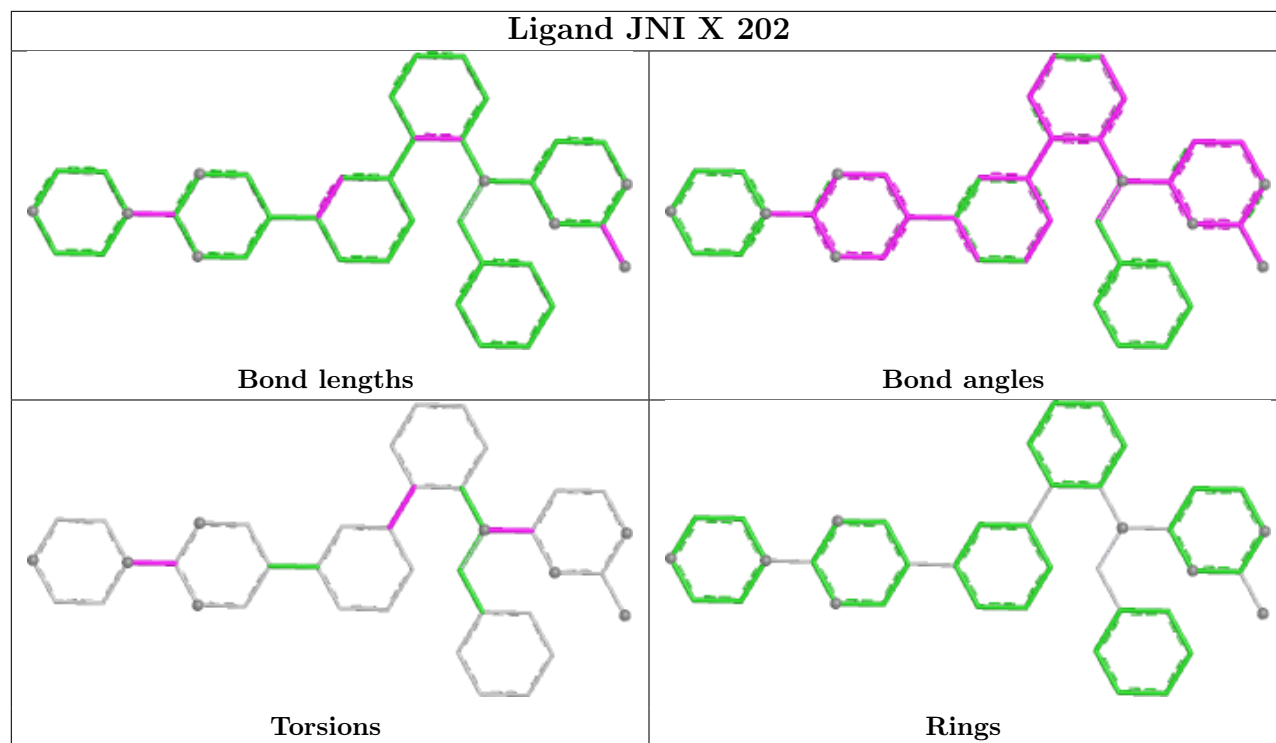
Ligand JNI j 201



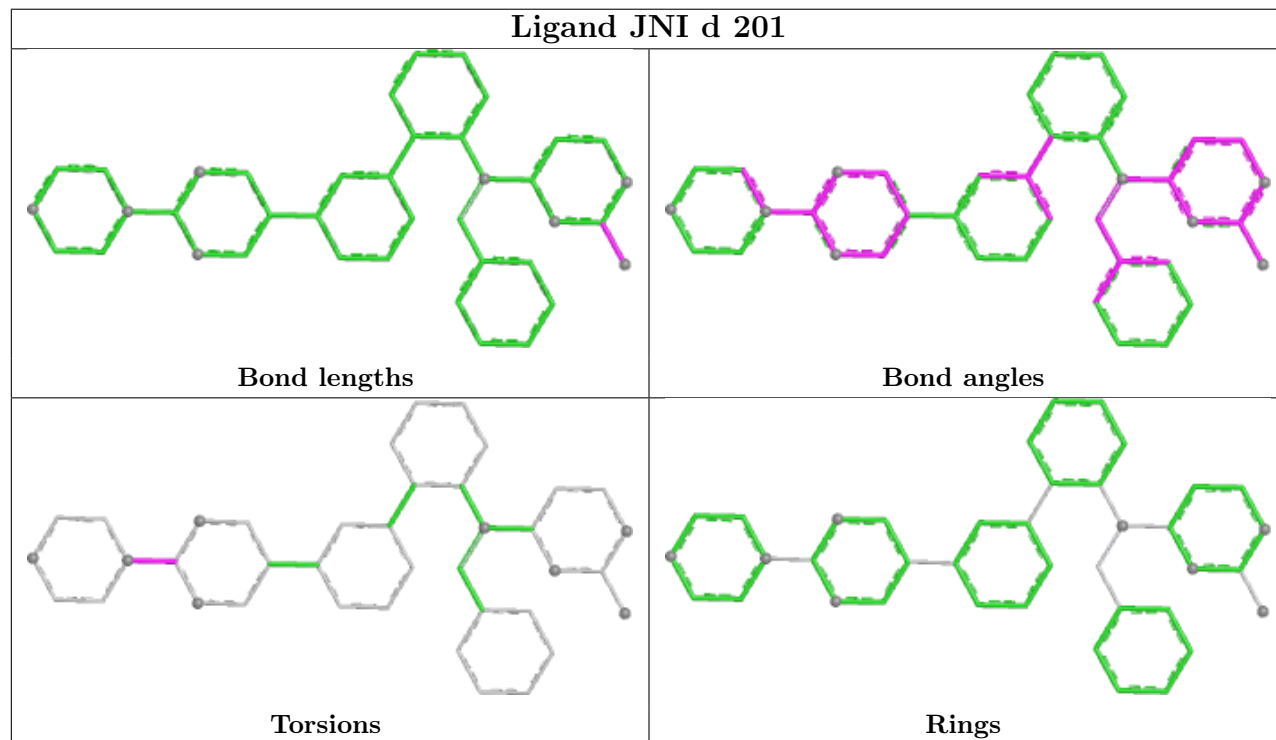


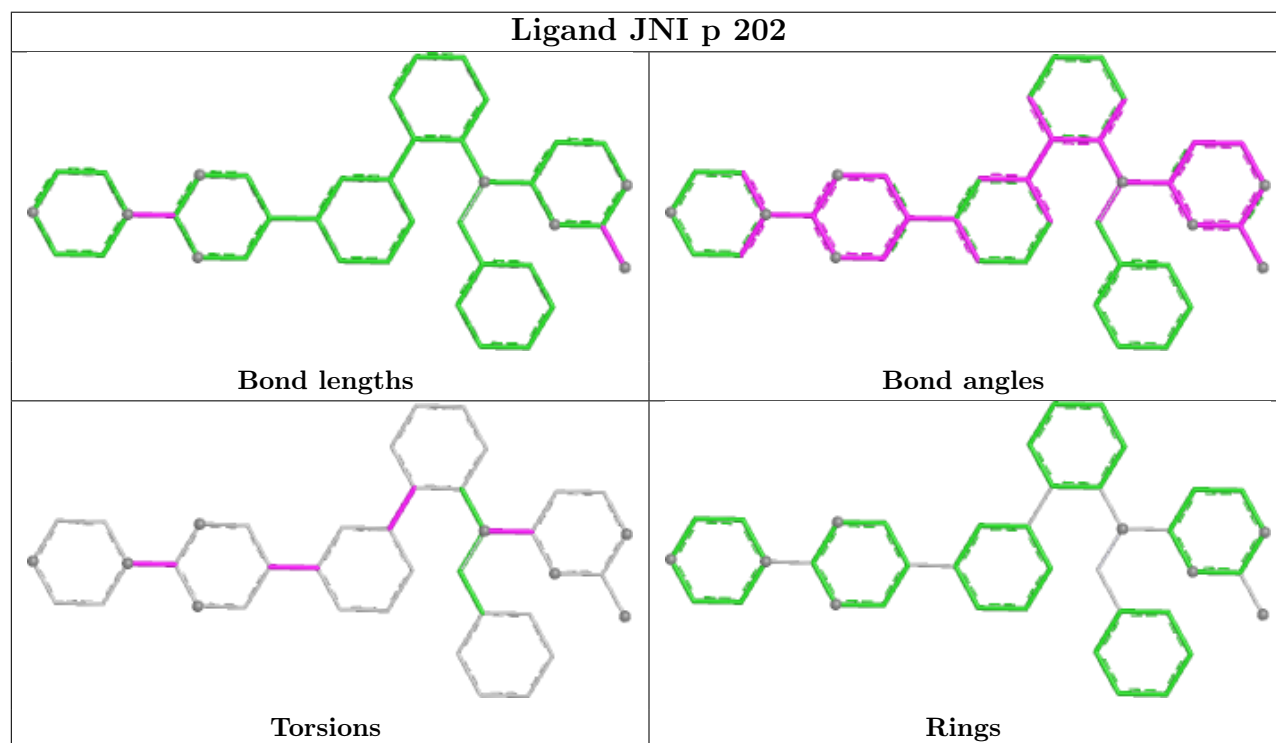
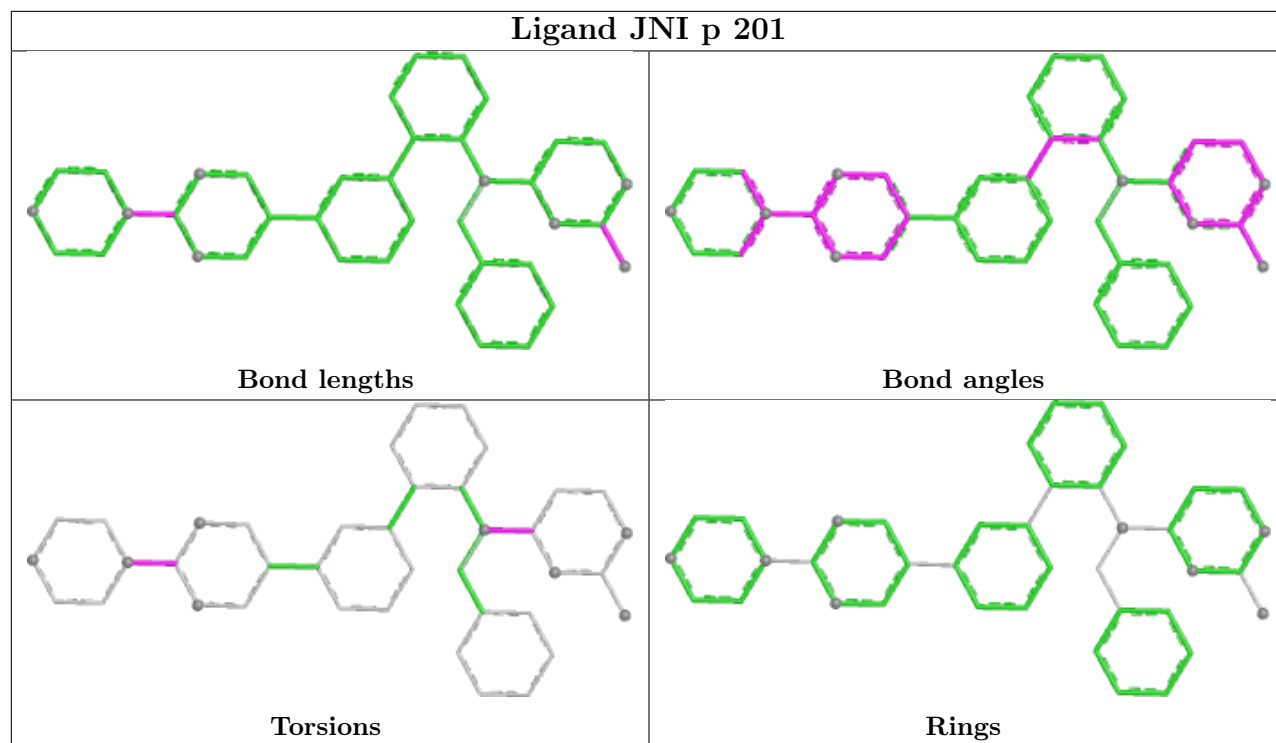


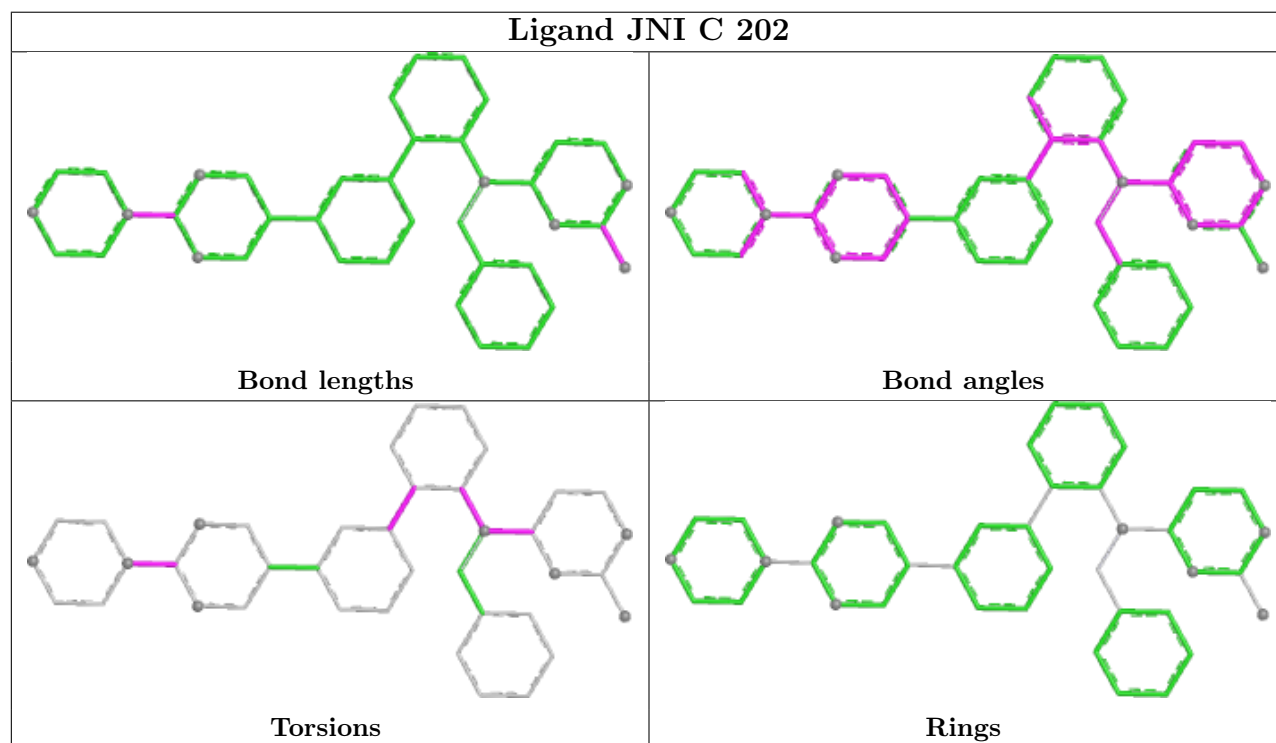
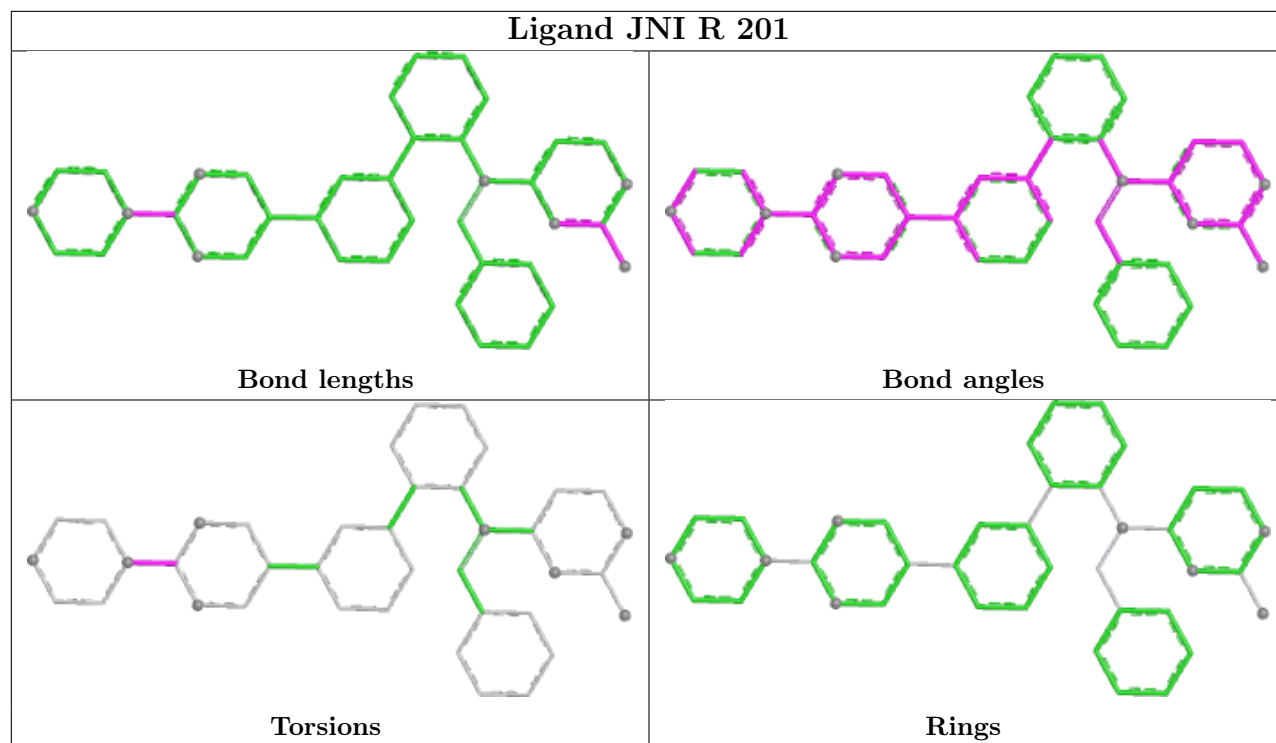
Ligand JNI X 202

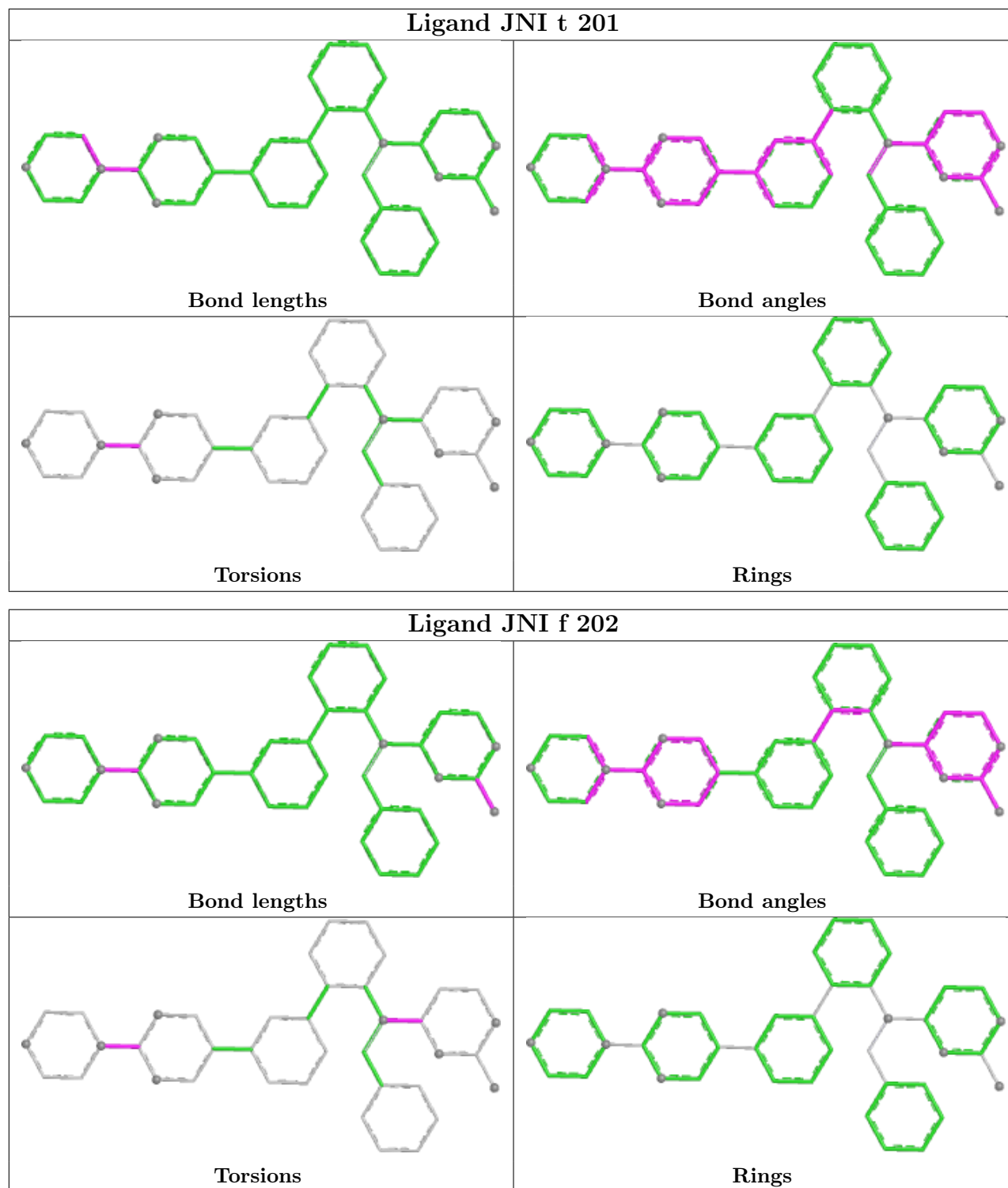


Ligand JNI d 201

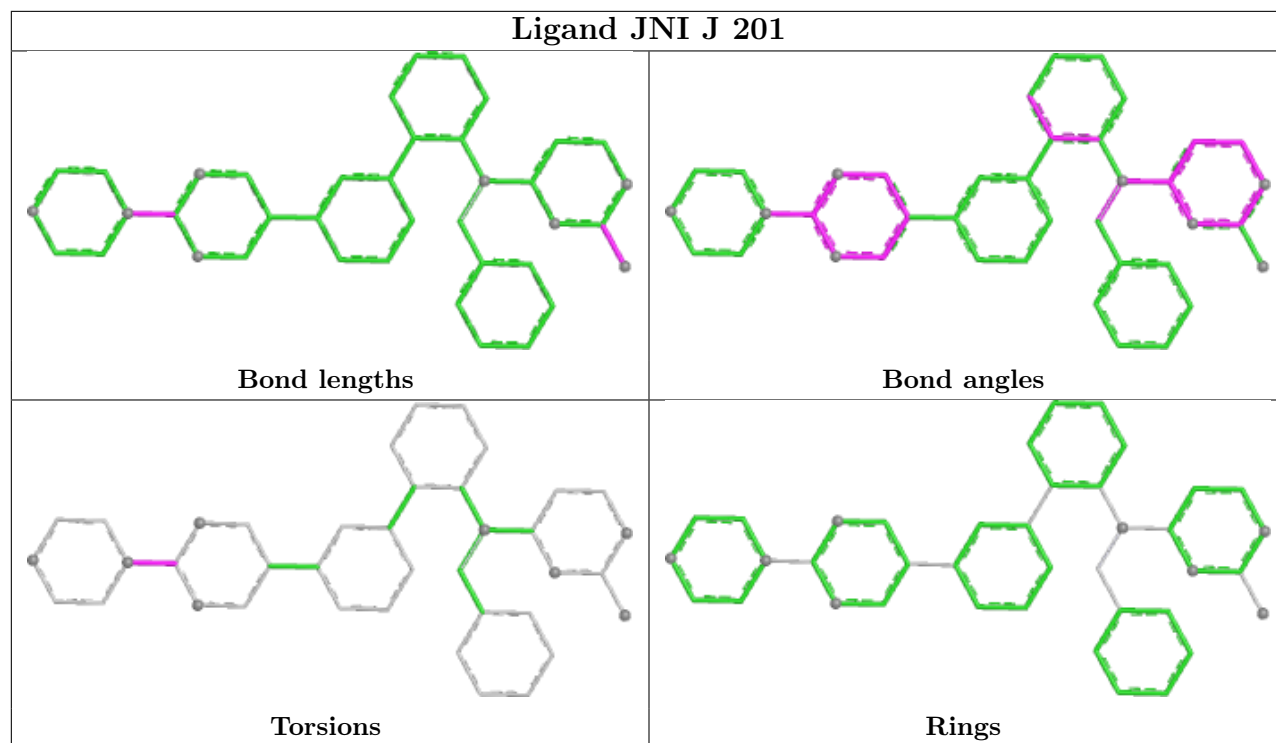




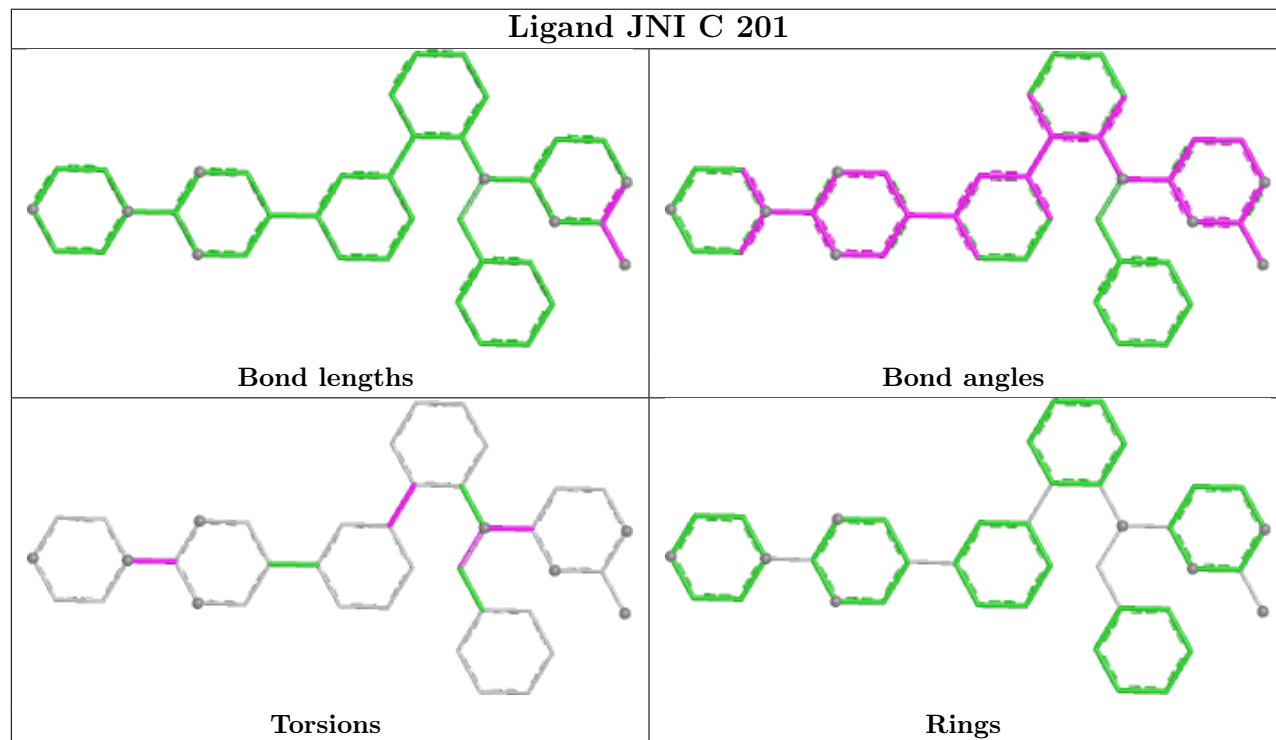


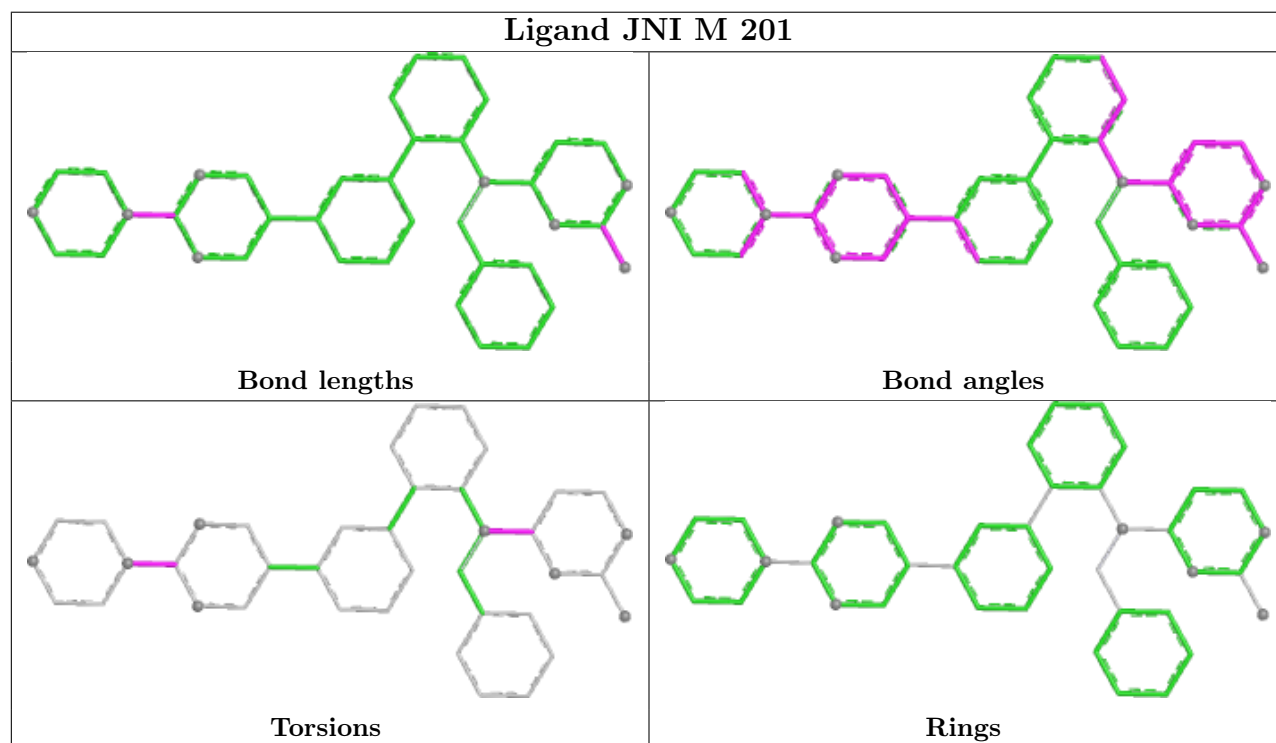
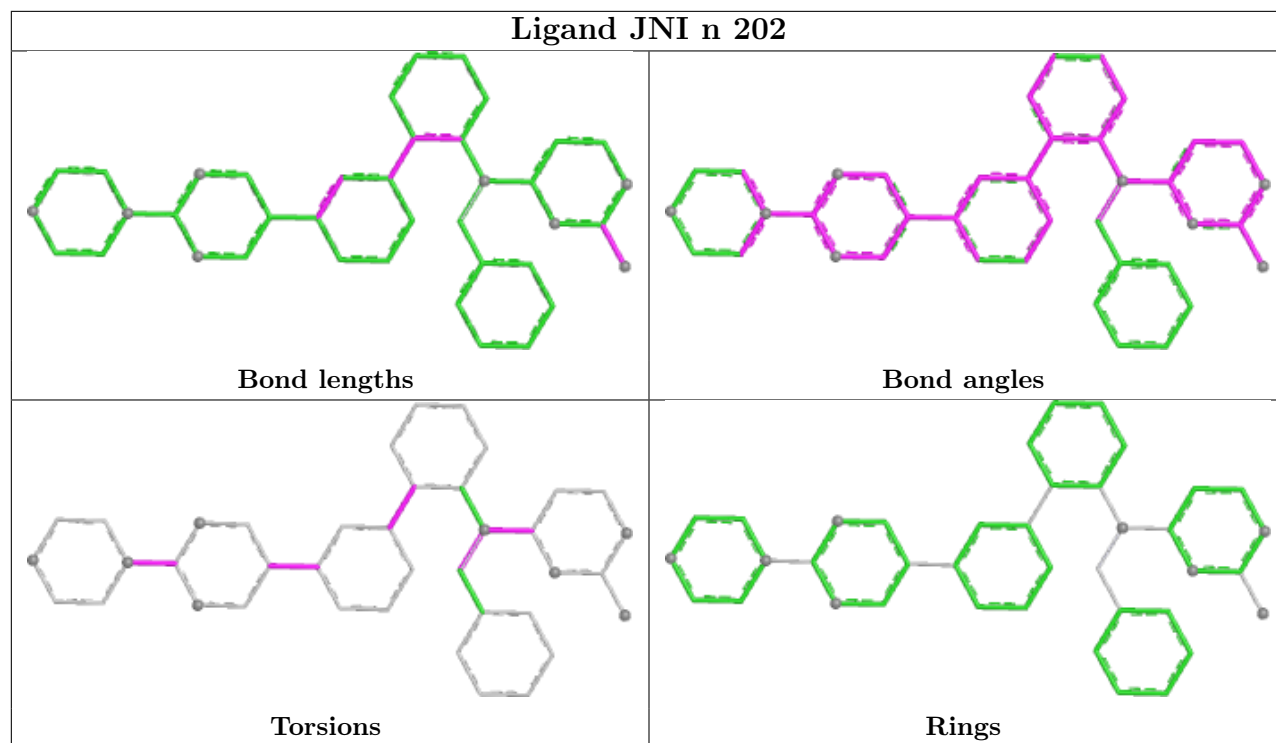


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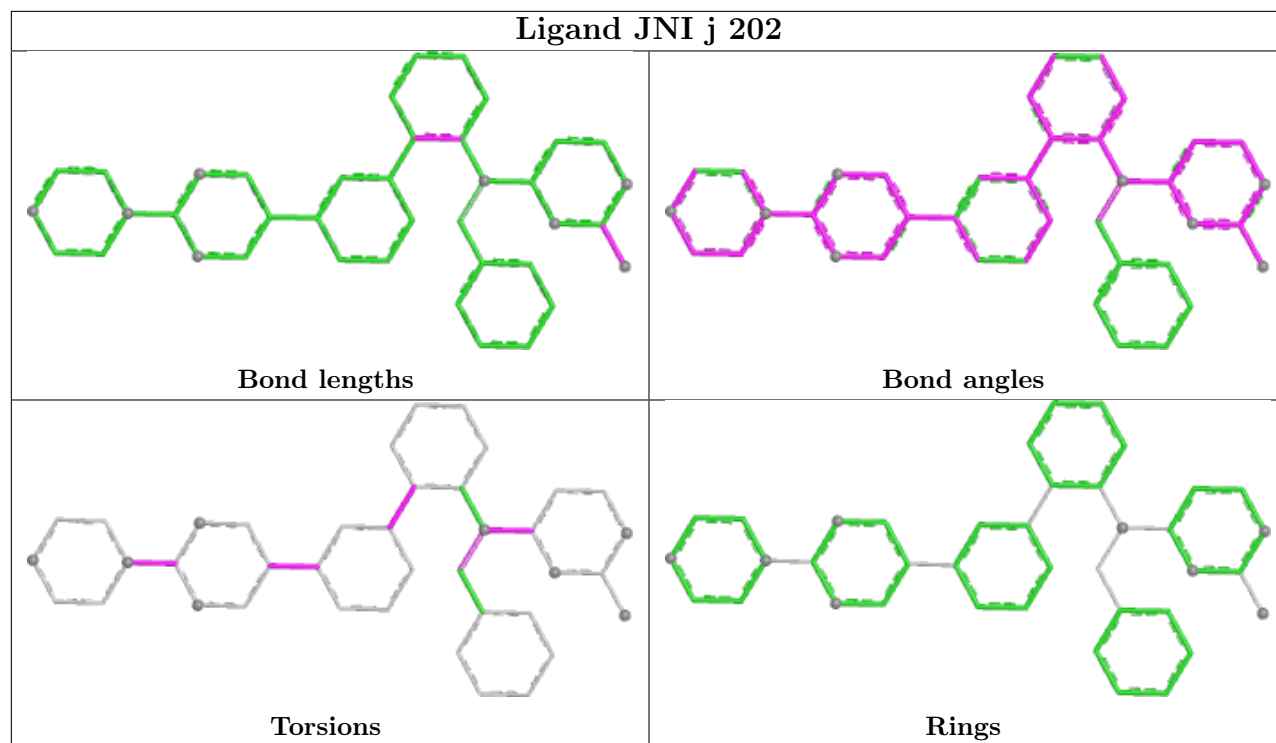


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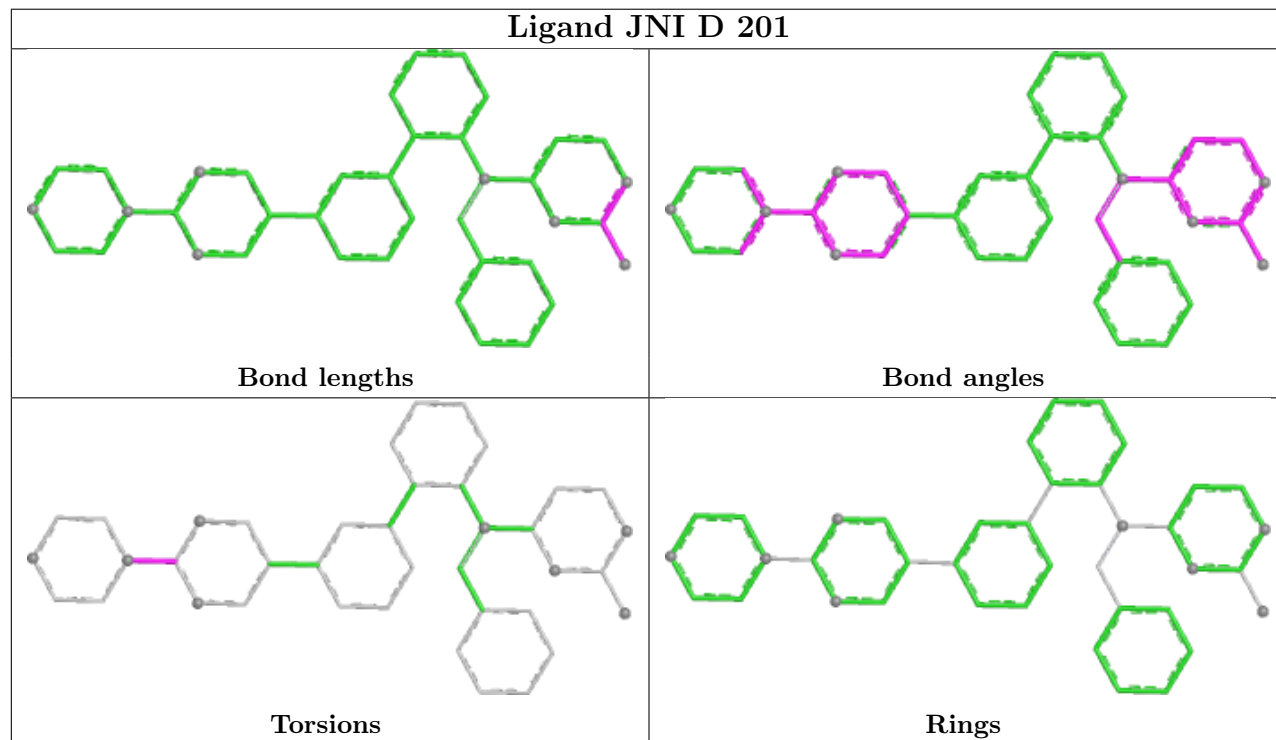


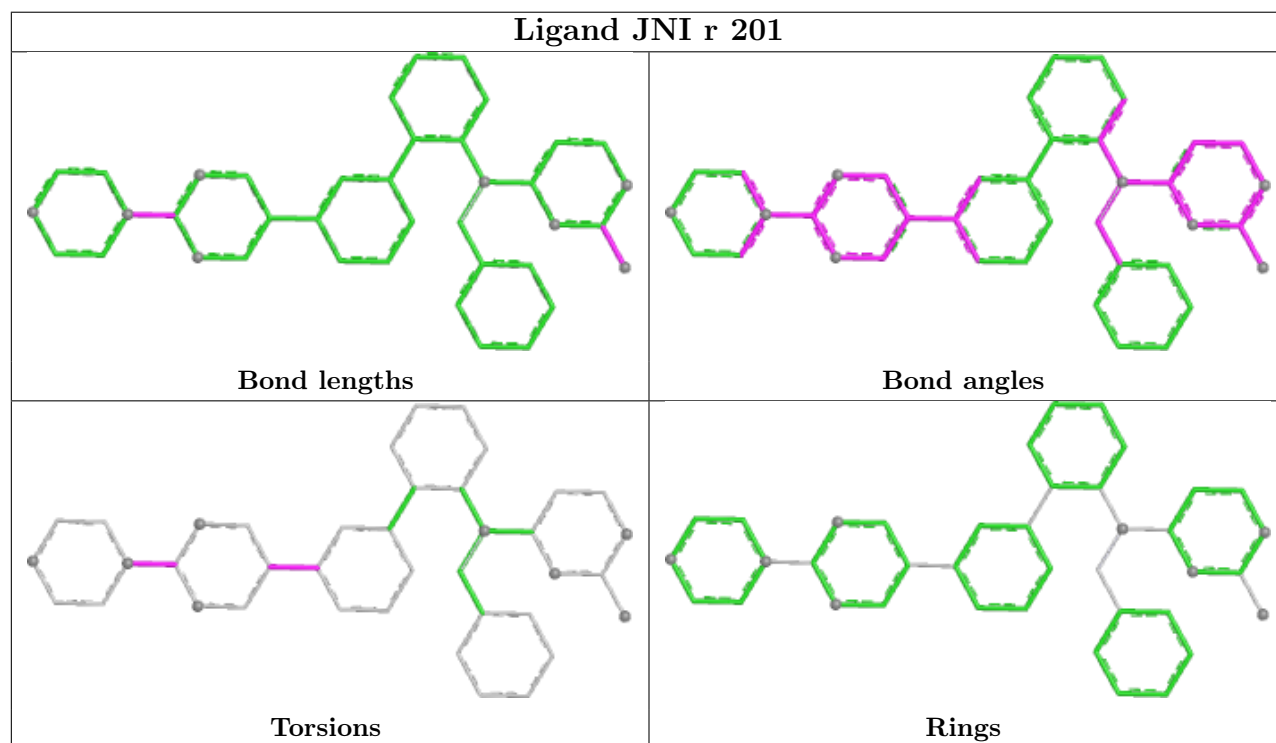
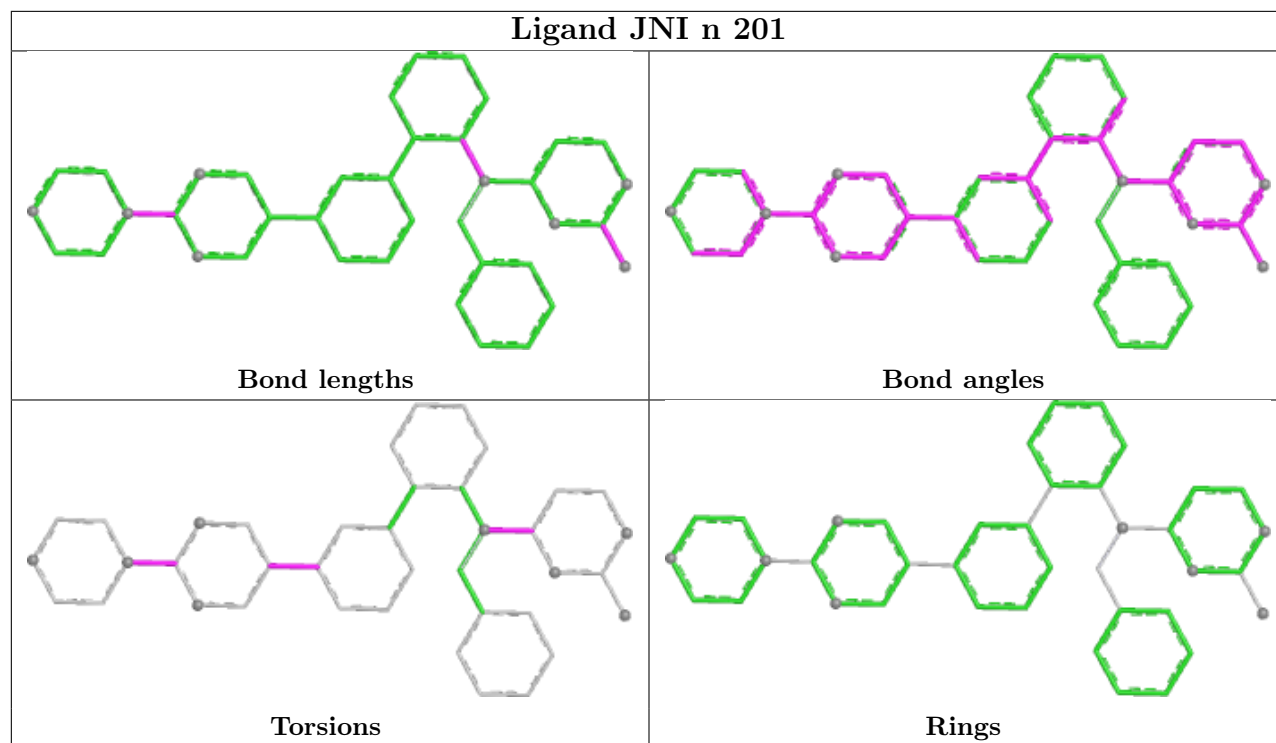


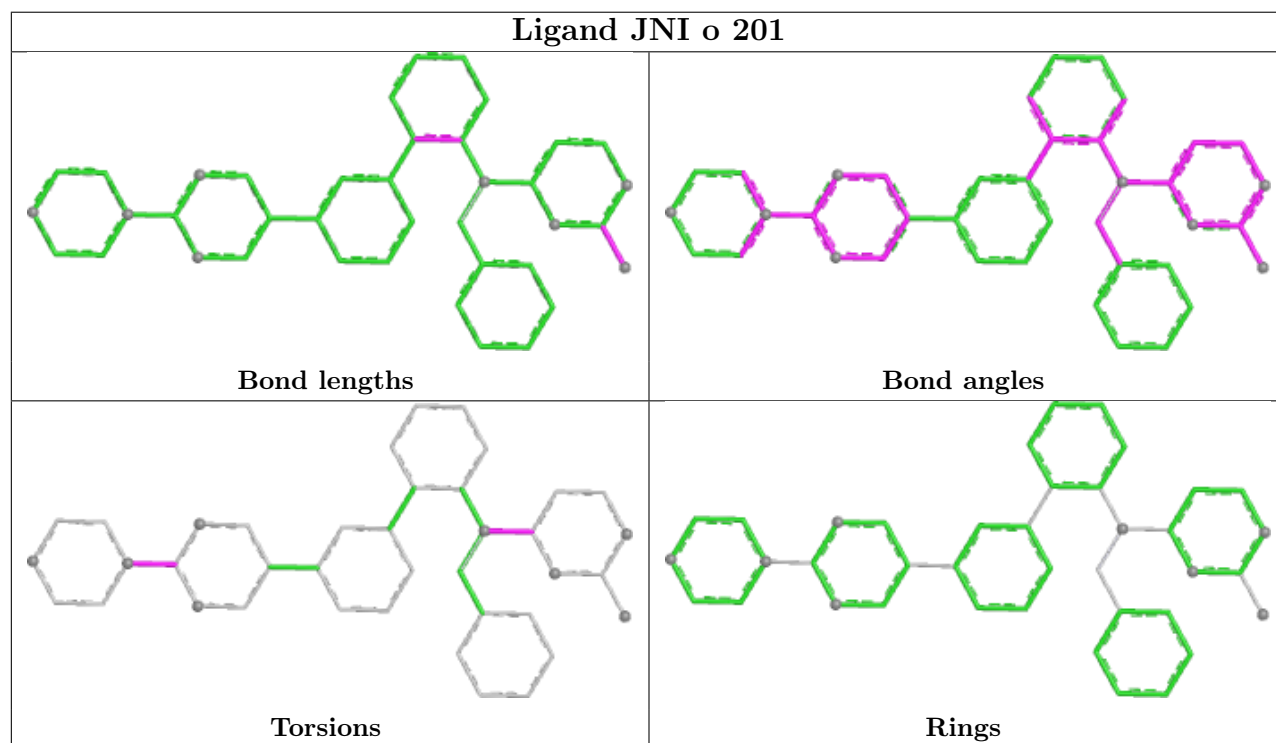
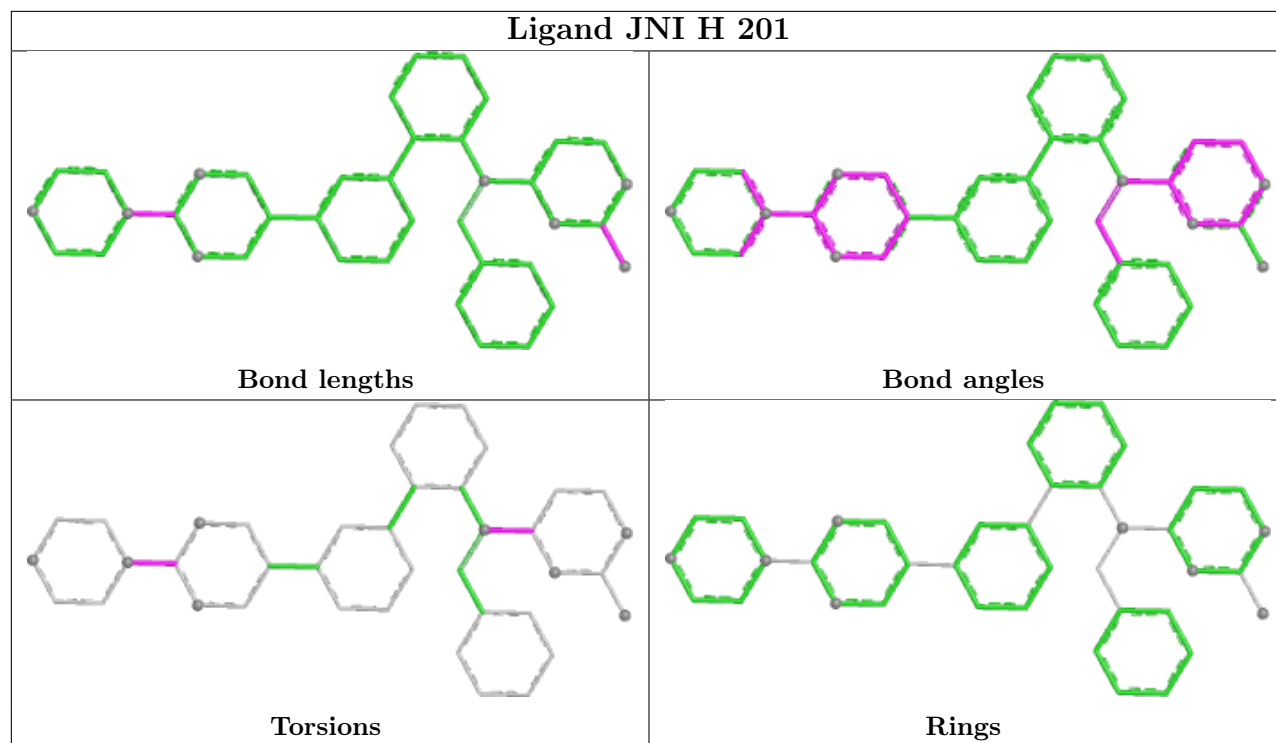
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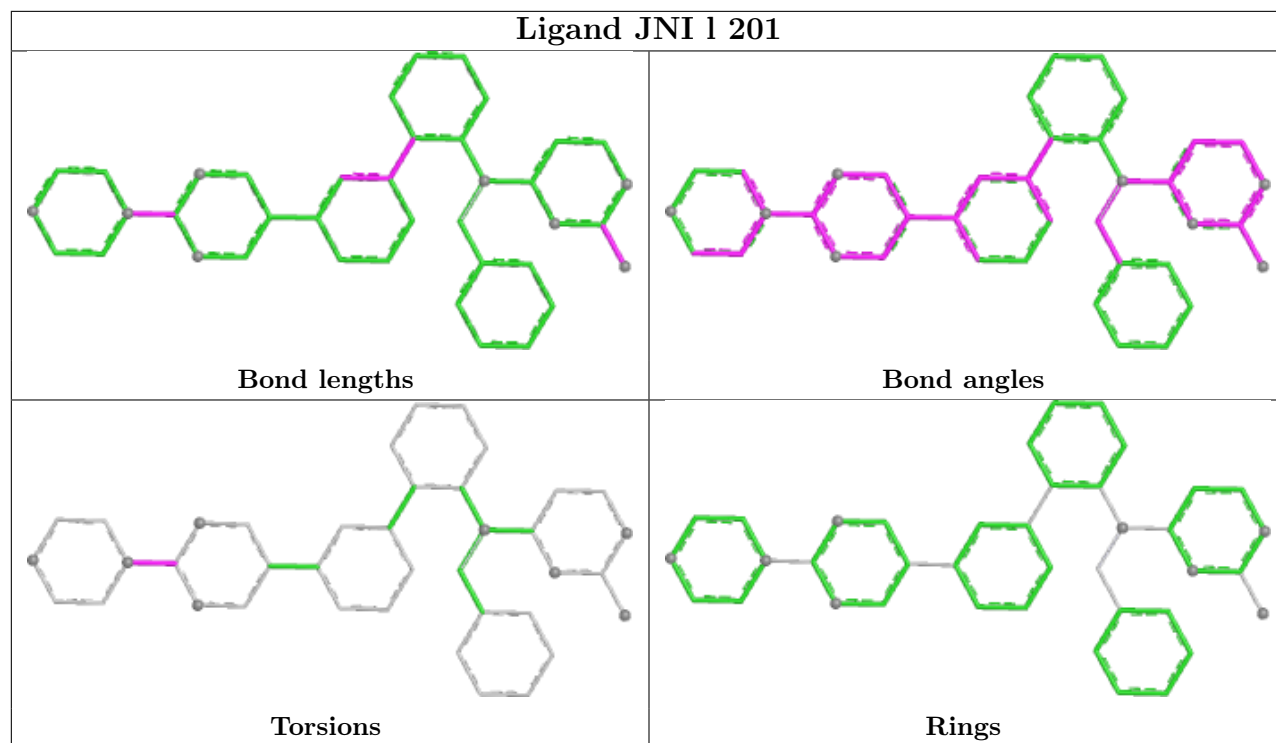
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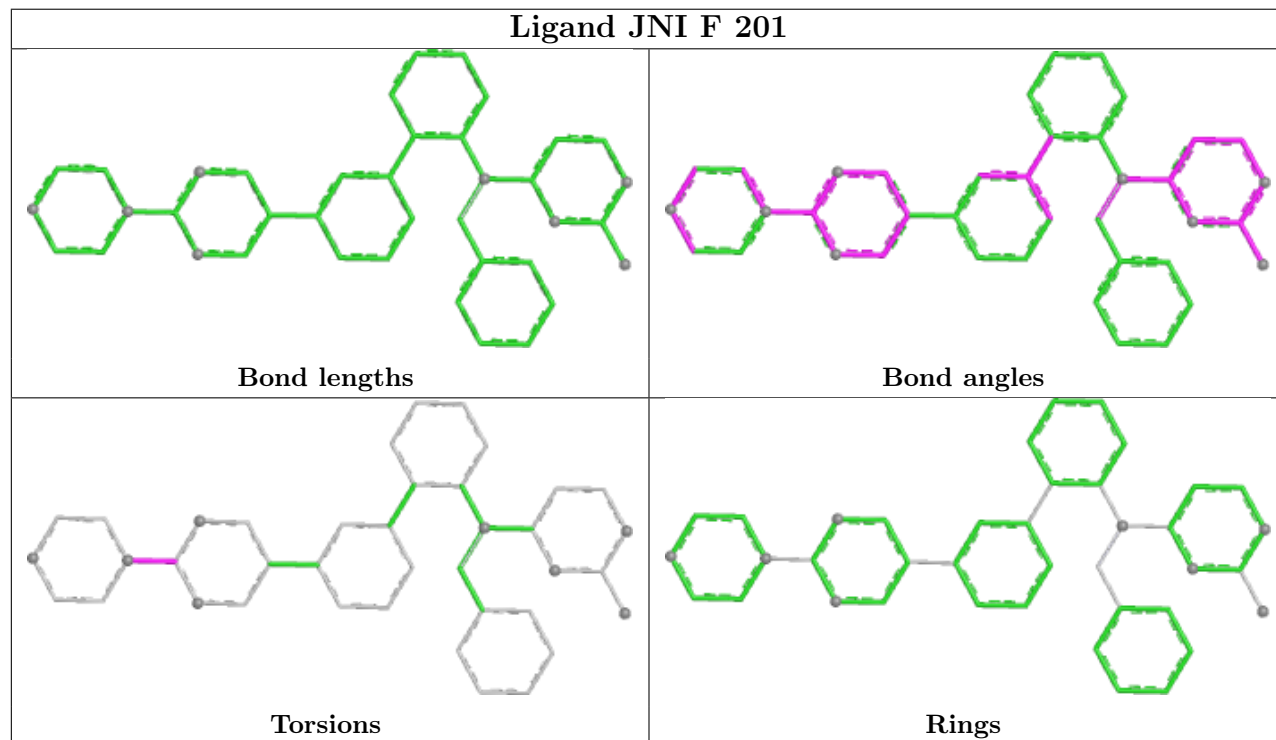




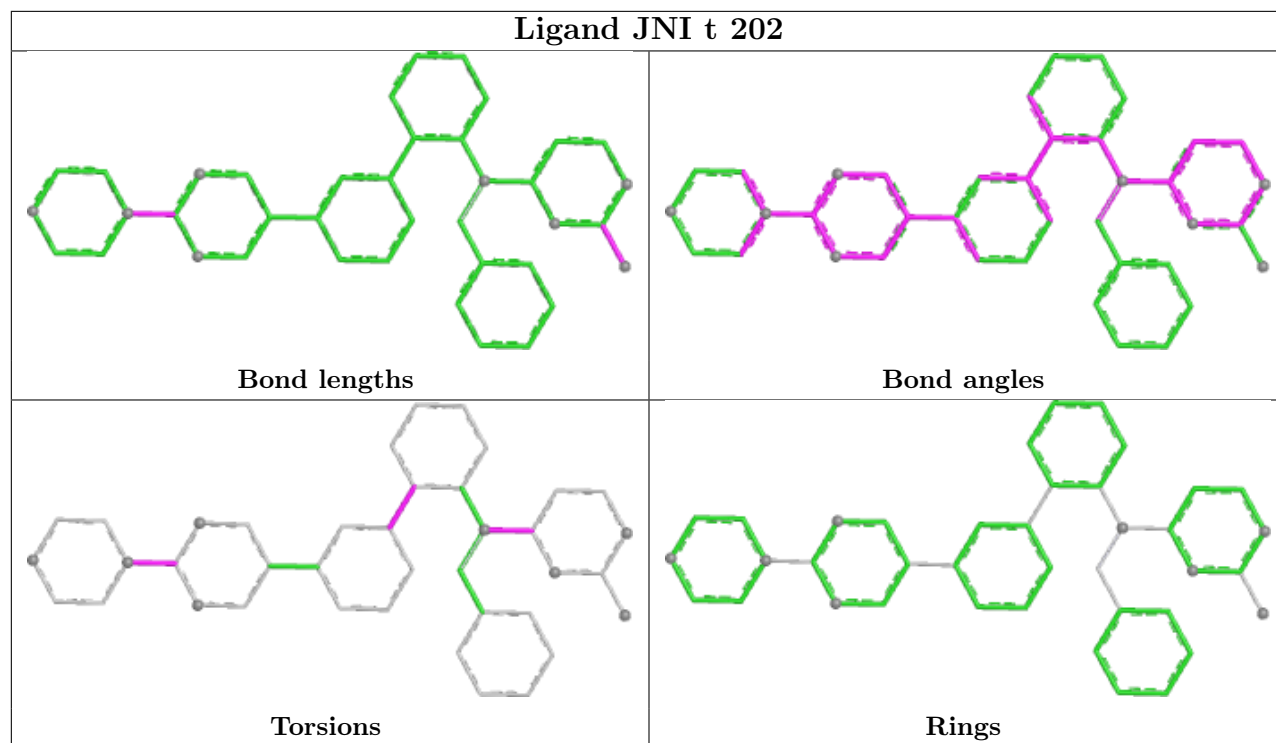
Ligand JNI 1 201



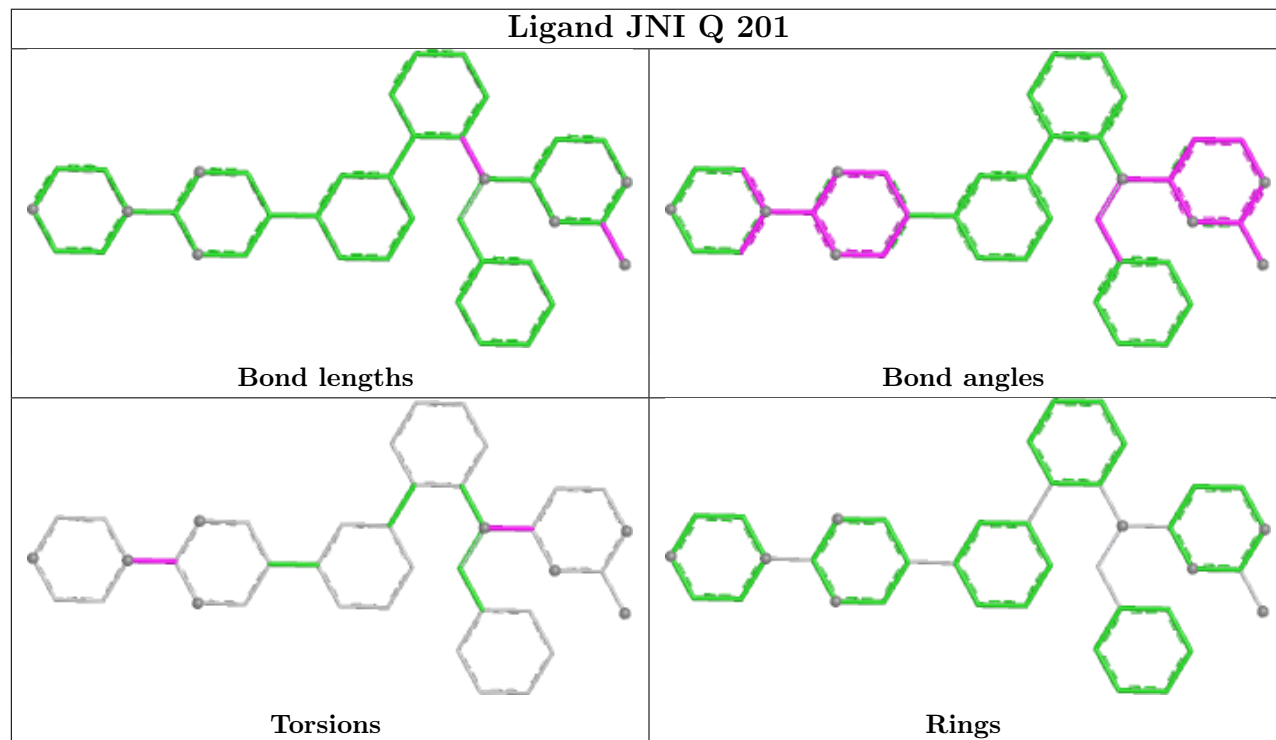
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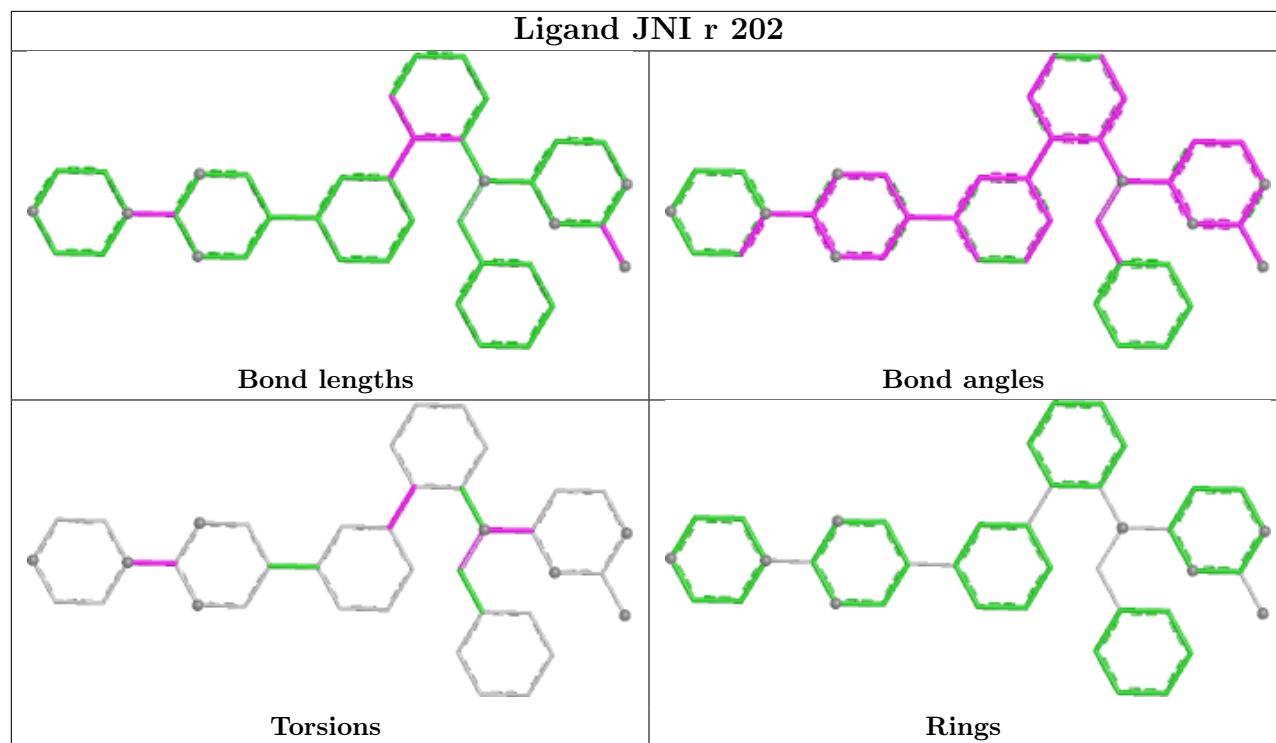
Ligand JNI t 202



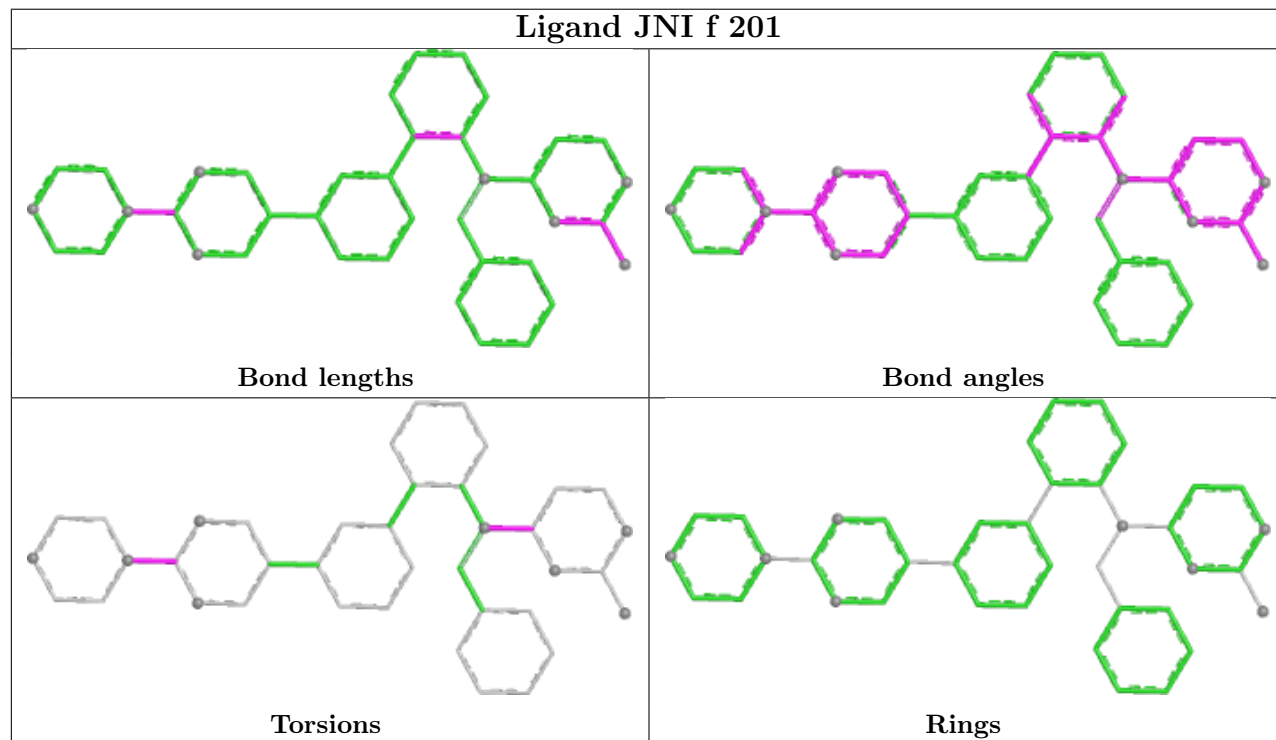
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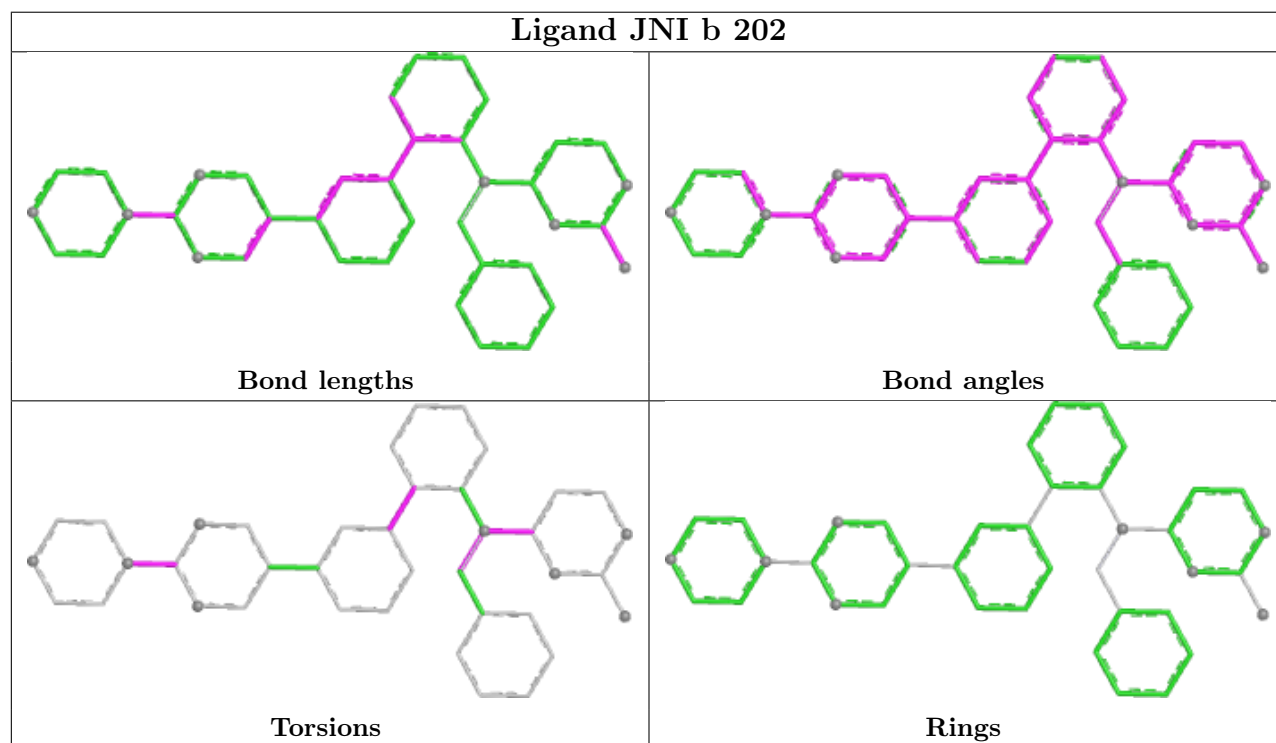
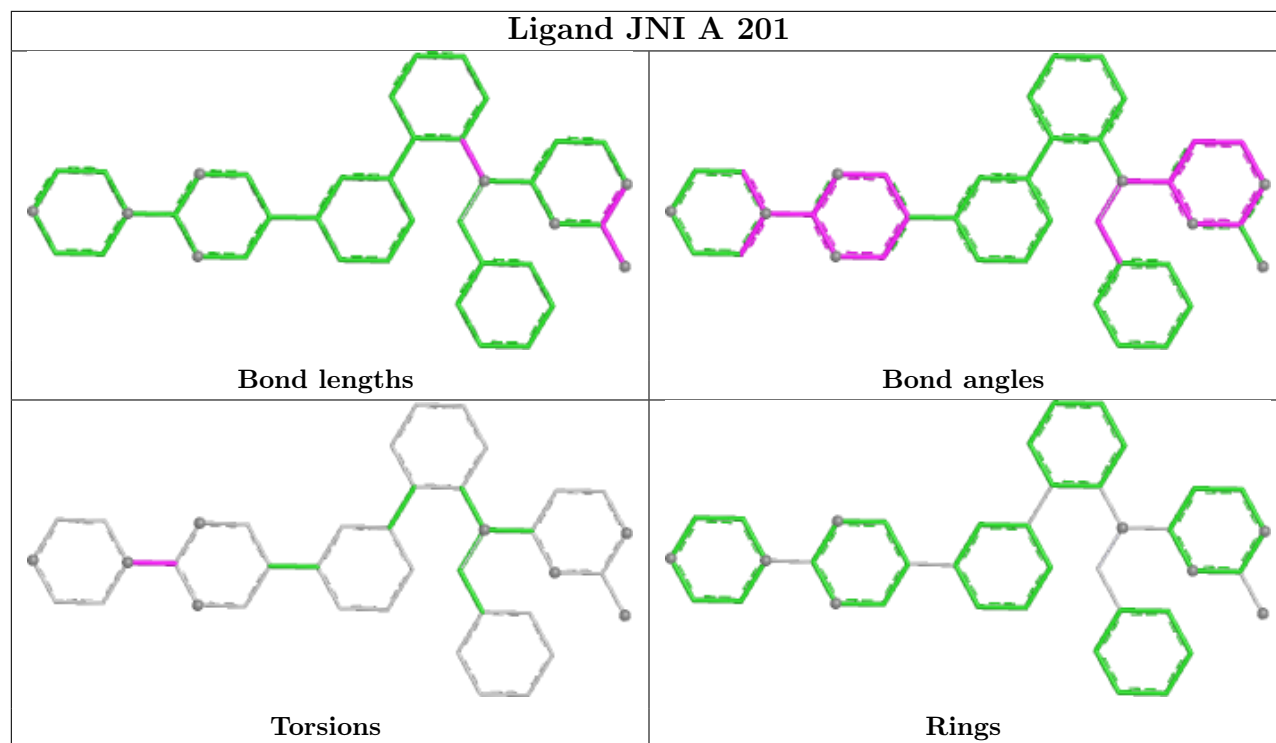


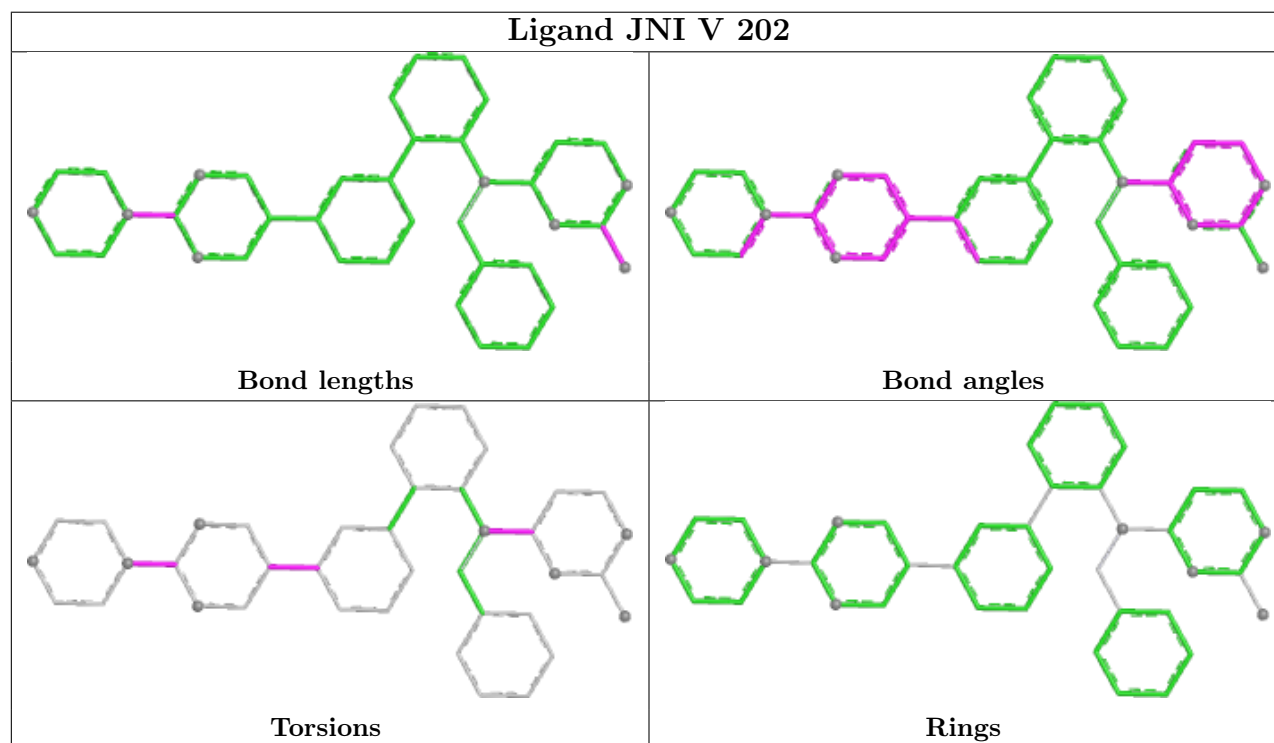
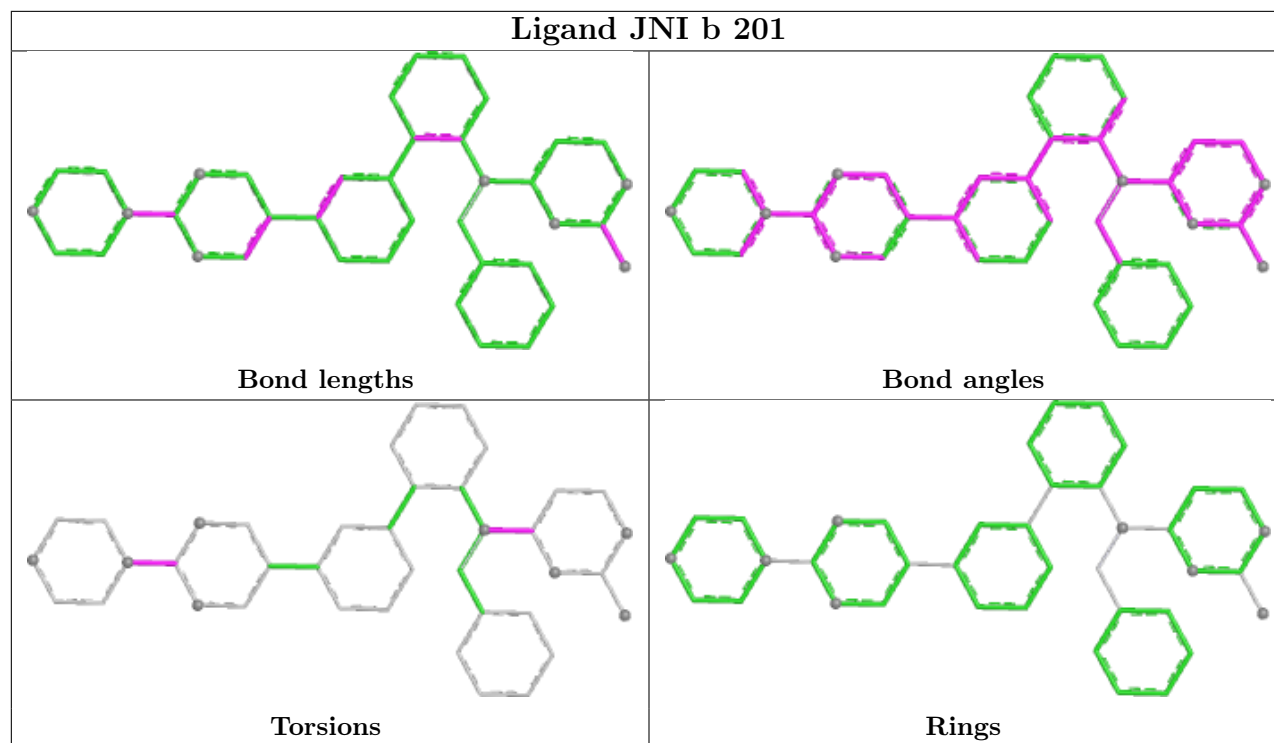
Ligand JNI r 202

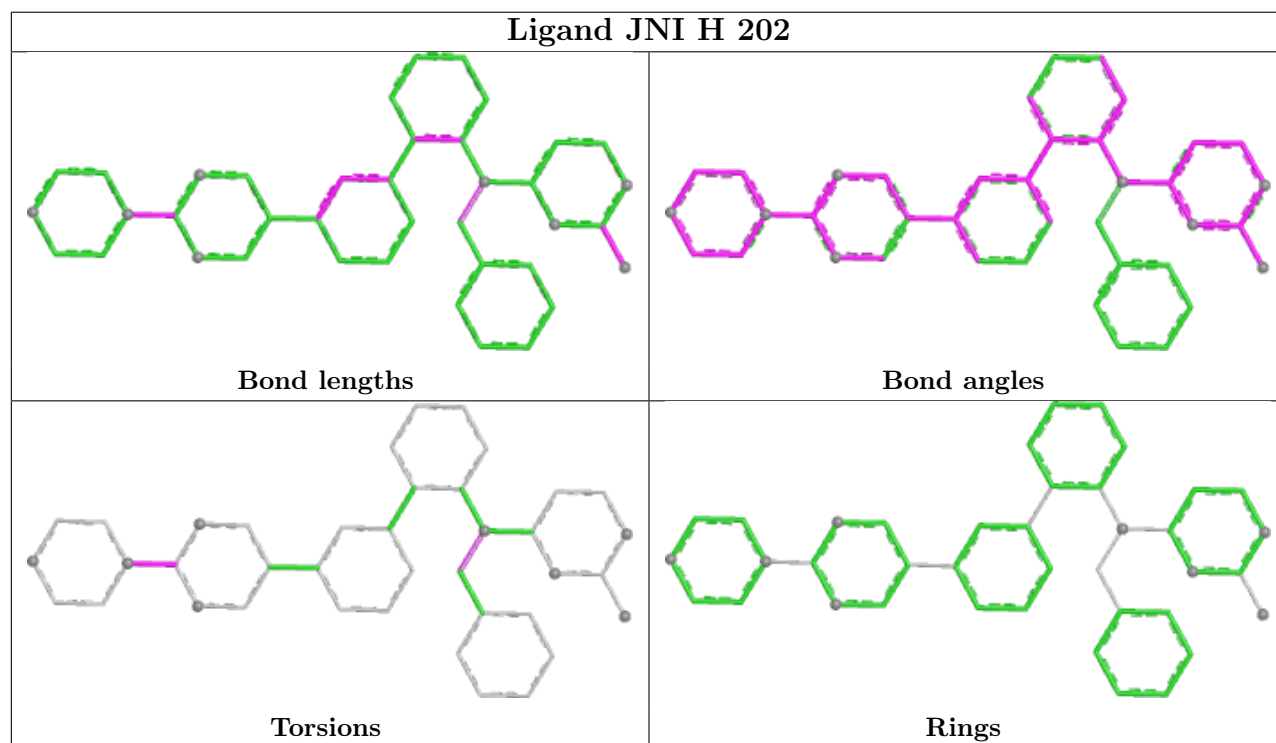
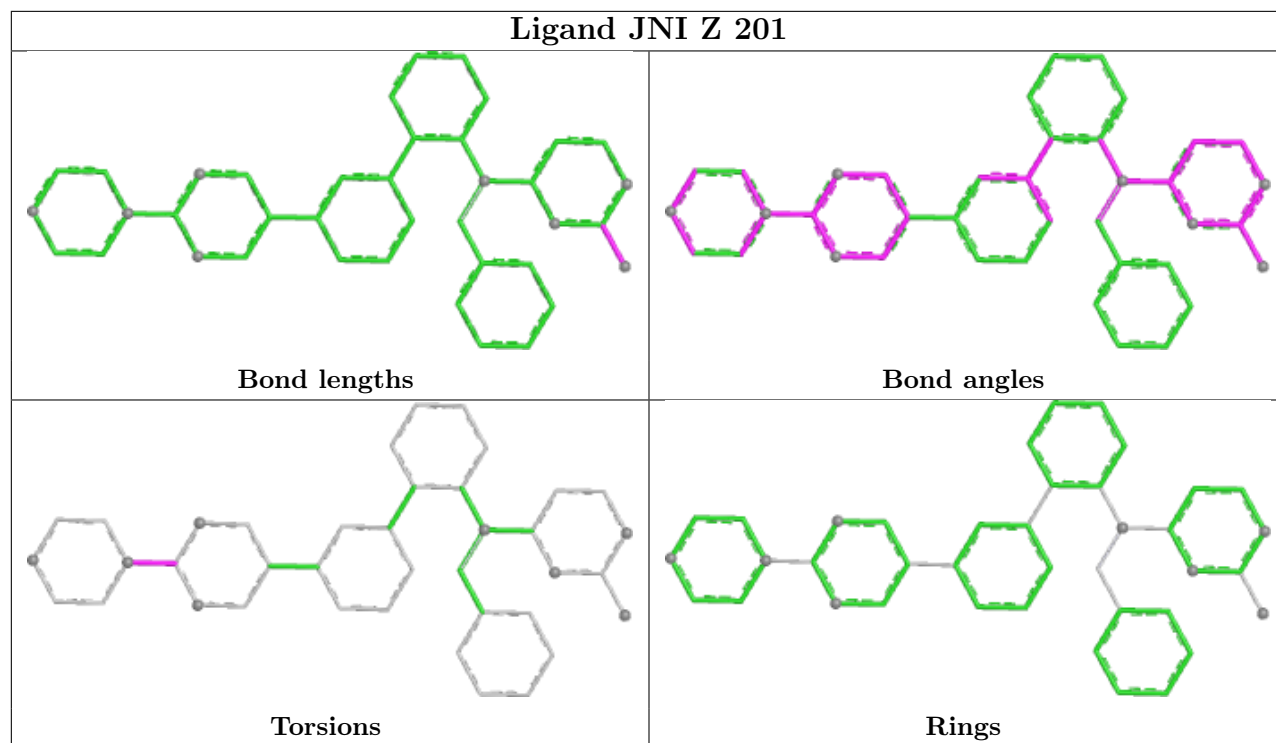


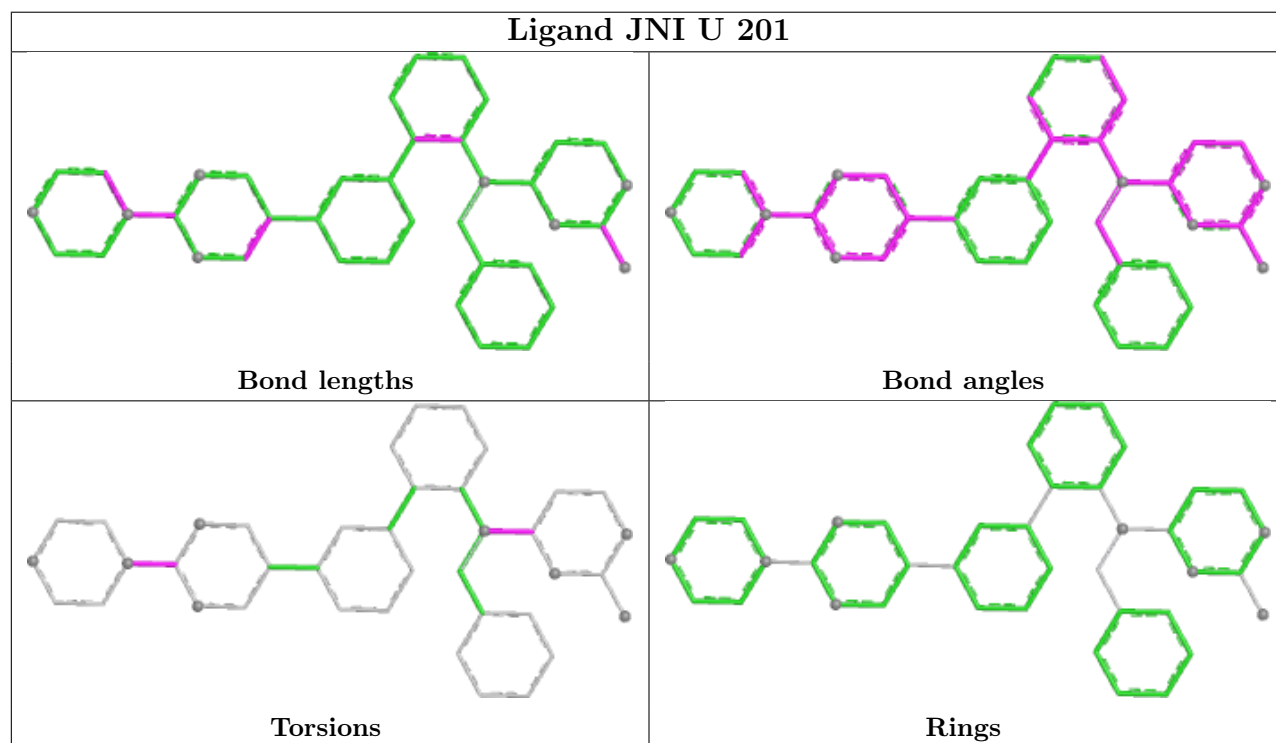
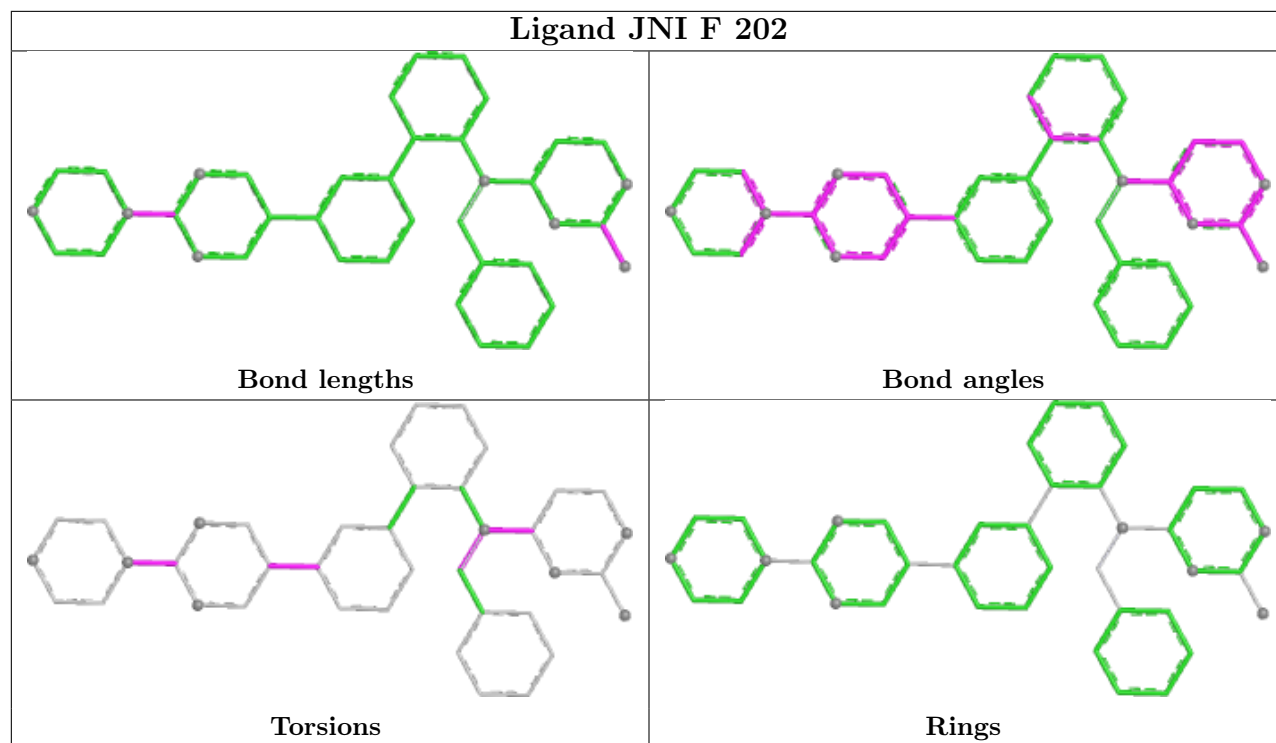
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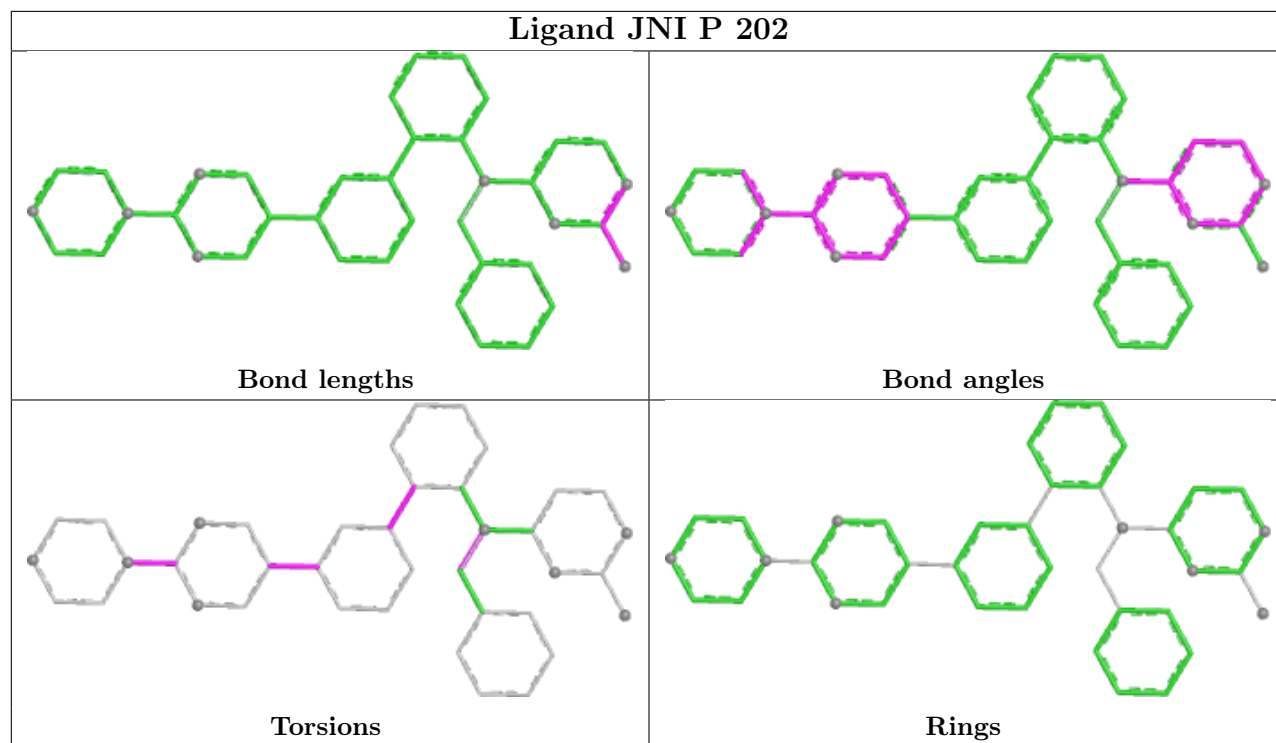




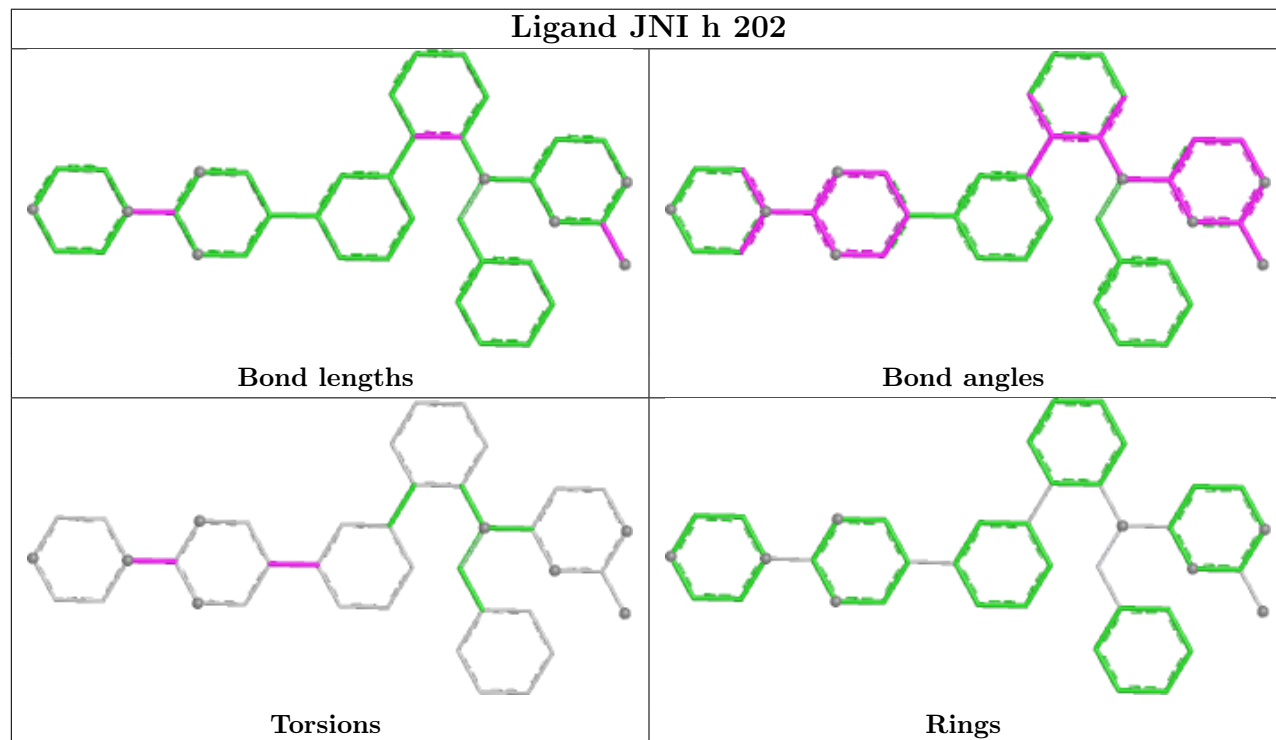




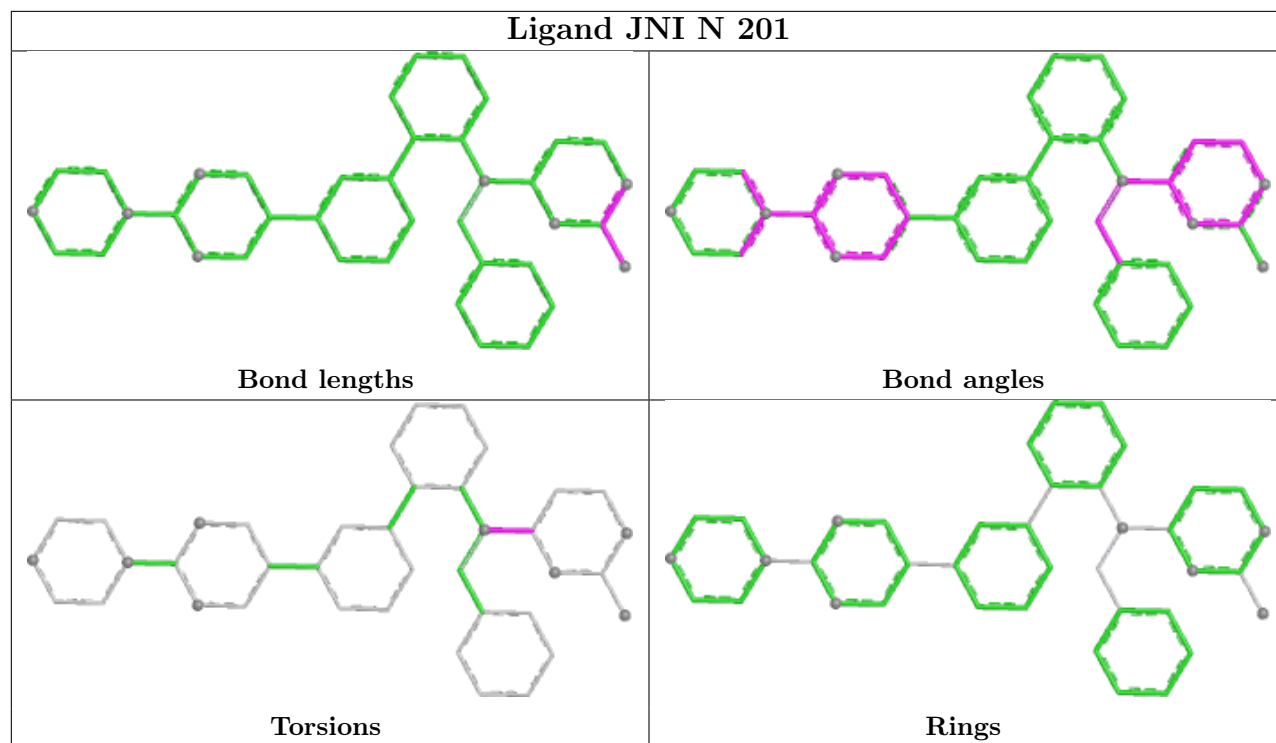
Ligand JNI P 202



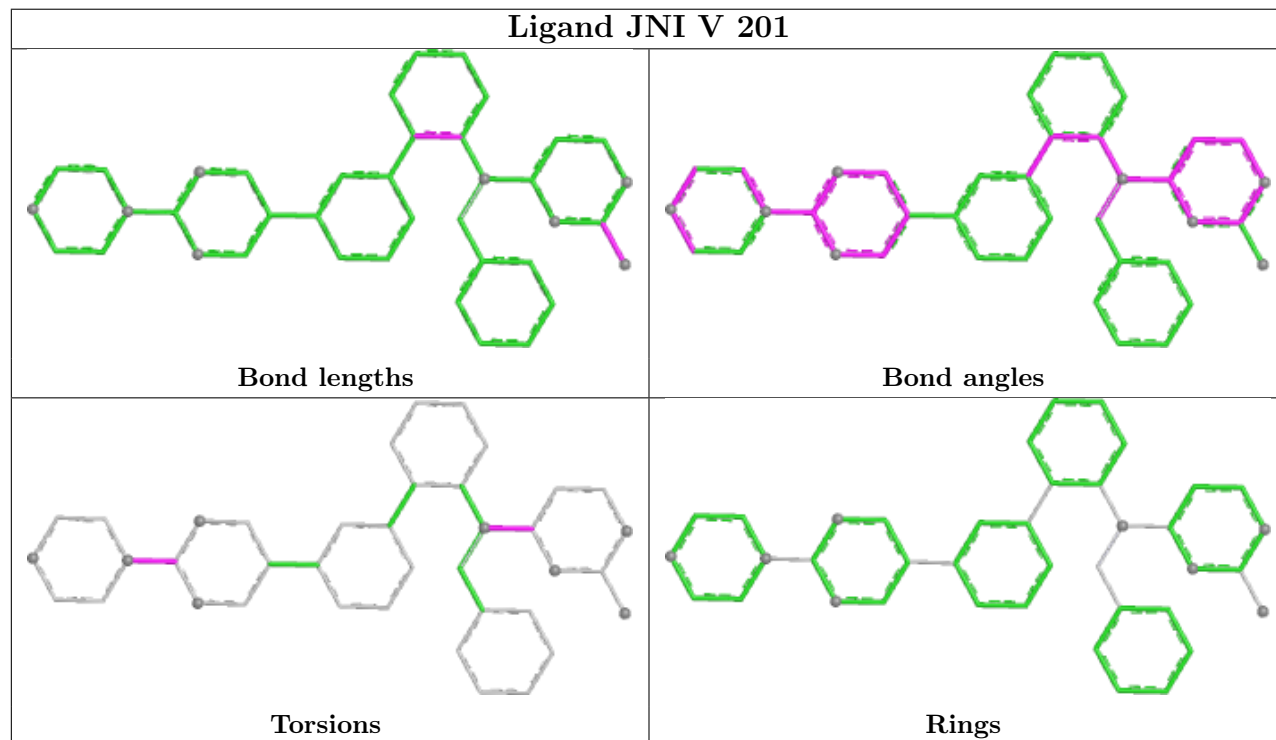
Ligand JNI h 202

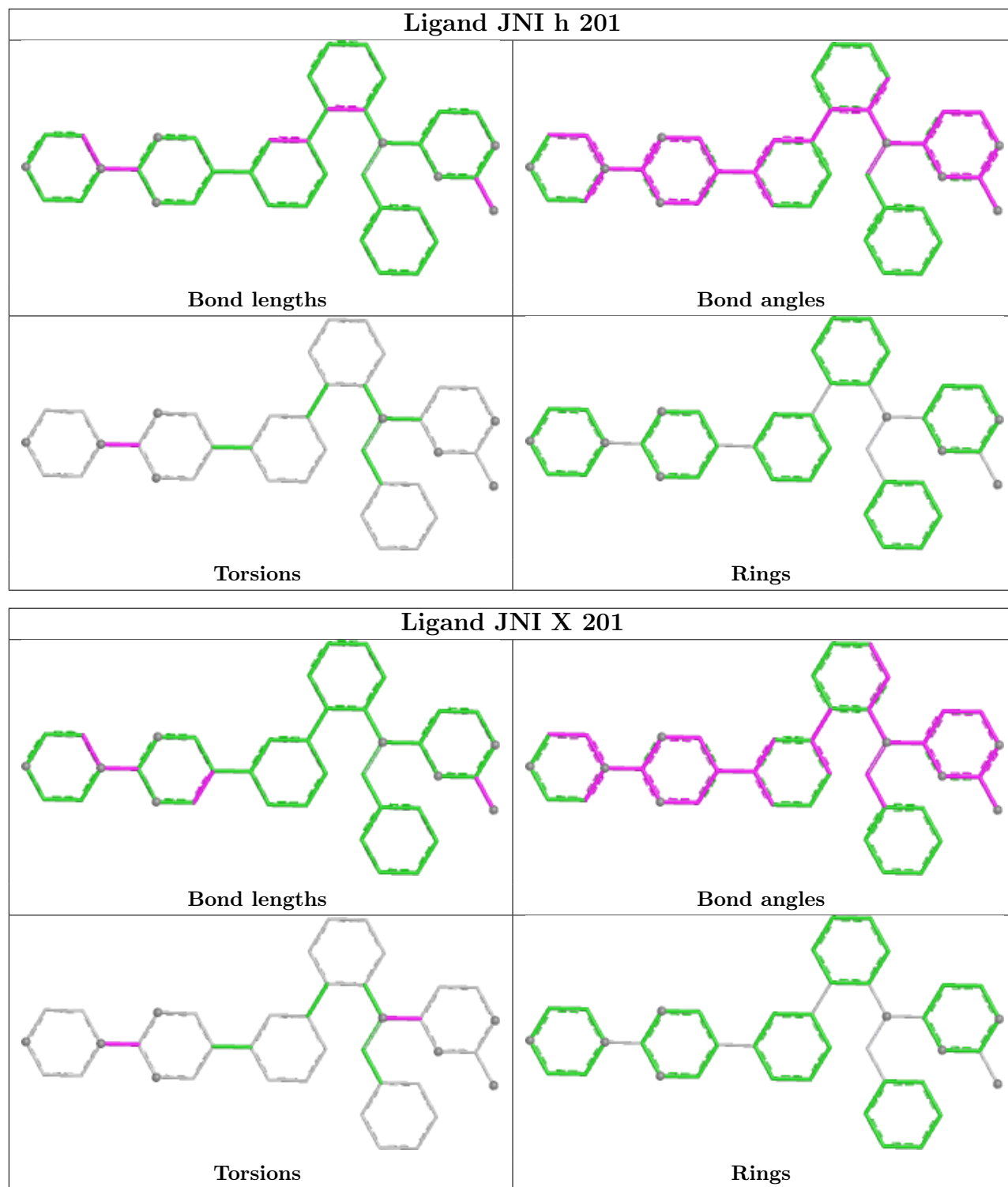


Ligand JNI N 201



Ligand JNI V 201





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	141/159 (88%)	-0.34	0 100 100	76, 112, 164, 196	0
1	B	145/159 (91%)	-0.57	0 100 100	59, 84, 133, 165	0
1	C	146/159 (91%)	-0.40	0 100 100	82, 128, 177, 195	0
1	D	149/159 (93%)	-0.48	0 100 100	66, 83, 151, 180	0
1	F	140/159 (88%)	-0.45	0 100 100	64, 95, 175, 222	0
1	G	149/159 (93%)	-0.53	0 100 100	56, 84, 154, 189	0
1	H	150/159 (94%)	-0.50	1 (0%) 84 66	84, 127, 182, 217	0
1	I	141/159 (88%)	-0.56	0 100 100	66, 91, 139, 160	0
1	J	138/159 (86%)	-0.36	0 100 100	81, 133, 183, 195	0
1	K	149/159 (93%)	-0.52	0 100 100	59, 87, 161, 207	0
1	L	142/159 (89%)	-0.32	2 (1%) 73 51	95, 142, 198, 234	0
1	M	149/159 (93%)	-0.56	0 100 100	64, 89, 157, 194	0
1	N	143/159 (89%)	-0.37	0 100 100	74, 100, 167, 211	0
1	O	145/159 (91%)	-0.56	0 100 100	66, 90, 136, 161	0
1	P	145/159 (91%)	-0.34	1 (0%) 84 66	86, 131, 178, 217	0
1	Q	149/159 (93%)	-0.40	2 (1%) 75 53	68, 94, 154, 193	0
1	R	138/159 (86%)	-0.46	0 100 100	70, 104, 162, 214	0
1	S	149/159 (93%)	-0.48	0 100 100	62, 84, 150, 198	0
1	T	146/159 (91%)	-0.28	0 100 100	66, 104, 169, 206	0
1	U	149/159 (93%)	-0.33	0 100 100	61, 95, 162, 207	0
1	V	138/159 (86%)	-0.41	0 100 100	79, 123, 187, 207	0
1	W	143/159 (89%)	-0.55	0 100 100	61, 82, 133, 160	0
1	X	150/159 (94%)	-0.32	0 100 100	68, 99, 183, 212	0
1	Y	149/159 (93%)	-0.36	1 (0%) 84 66	63, 83, 160, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Z	143/159 (89%)	-0.48	0 100 100	80, 119, 185, 219	0
1	a	149/159 (93%)	-0.54	0 100 100	69, 91, 165, 235	0
1	b	144/159 (90%)	-0.47	1 (0%) 84 66	80, 116, 171, 190	0
1	c	145/159 (91%)	-0.61	0 100 100	63, 86, 146, 165	0
1	d	138/159 (86%)	-0.35	0 100 100	78, 116, 174, 211	0
1	e	149/159 (93%)	-0.38	0 100 100	60, 85, 131, 189	0
1	f	143/159 (89%)	-0.29	0 100 100	93, 142, 190, 206	0
1	g	145/159 (91%)	-0.44	0 100 100	70, 98, 148, 170	0
1	h	137/159 (86%)	-0.35	1 (0%) 84 66	84, 120, 185, 204	0
1	i	145/159 (91%)	-0.55	0 100 100	66, 89, 158, 186	0
1	j	150/159 (94%)	-0.23	0 100 100	80, 136, 197, 221	0
1	k	142/159 (89%)	-0.44	1 (0%) 84 66	63, 90, 139, 171	0
1	l	143/159 (89%)	-0.30	2 (1%) 73 51	77, 106, 171, 240	0
1	m	147/159 (92%)	-0.47	0 100 100	72, 94, 145, 186	0
1	n	147/159 (92%)	-0.32	0 100 100	107, 149, 188, 213	0
1	o	147/159 (92%)	-0.35	0 100 100	79, 110, 158, 189	0
1	p	139/159 (87%)	-0.16	0 100 100	101, 148, 198, 214	0
1	q	149/159 (93%)	-0.46	0 100 100	75, 99, 141, 168	0
1	r	144/159 (90%)	-0.37	0 100 100	94, 146, 187, 215	0
1	s	149/159 (93%)	-0.49	0 100 100	71, 93, 145, 177	0
1	t	143/159 (89%)	-0.30	0 100 100	92, 131, 178, 200	0
1	u	145/159 (91%)	-0.41	0 100 100	77, 100, 144, 170	0
1	v	144/159 (90%)	-0.22	0 100 100	121, 154, 199, 233	0
1	w	145/159 (91%)	-0.31	0 100 100	76, 111, 164, 186	0
All	All	6955/7632 (91%)	-0.41	12 (0%) 91 83	56, 106, 177, 240	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	k	119	TYR	2.9
1	Y	119	TYR	2.7
1	l	97	ILE	2.7
1	P	95	SER	2.5
1	Q	117	PRO	2.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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, 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($\text{\AA}^2$)	Q<0.9
2	JNI	P	202	39/39	0.75	0.15	80,129,210,215	0
2	JNI	p	202	39/39	0.78	0.13	103,140,220,241	0
2	JNI	f	201	39/39	0.79	0.14	92,130,170,171	0
2	JNI	X	202	39/39	0.80	0.17	65,112,179,192	0
2	JNI	v	202	39/39	0.80	0.15	97,150,214,219	0
2	JNI	j	202	39/39	0.81	0.19	93,148,193,200	0
2	JNI	n	202	39/39	0.81	0.15	88,133,183,186	0
2	JNI	d	201	39/39	0.82	0.13	91,123,170,180	0
2	JNI	C	202	39/39	0.82	0.13	85,167,208,219	0
2	JNI	r	202	39/39	0.82	0.16	88,144,228,245	0
2	JNI	H	202	39/39	0.82	0.20	59,128,217,244	0
2	JNI	h	202	39/39	0.83	0.15	61,132,171,220	0
2	JNI	t	202	39/39	0.83	0.13	87,160,187,203	0
2	JNI	f	202	39/39	0.83	0.13	117,175,241,261	0
2	JNI	V	202	39/39	0.84	0.16	85,121,189,247	0
2	JNI	L	201	39/39	0.84	0.14	73,119,190,221	0
2	JNI	b	202	39/39	0.84	0.17	58,126,198,209	0
2	JNI	C	201	39/39	0.84	0.17	59,121,184,199	0
2	JNI	R	201	39/39	0.84	0.15	55,91,170,183	0
2	JNI	U	201	39/39	0.84	0.15	59,93,151,157	0
2	JNI	h	201	39/39	0.84	0.13	72,111,141,166	0
2	JNI	n	201	39/39	0.85	0.15	67,125,200,203	0
2	JNI	j	201	39/39	0.85	0.17	82,121,168,184	0
2	JNI	l	201	39/39	0.86	0.15	69,103,136,147	0
2	JNI	o	201	39/39	0.87	0.15	89,119,195,210	0
2	JNI	Z	202	39/39	0.87	0.16	79,130,160,183	0
2	JNI	F	201	39/39	0.87	0.15	57,94,163,186	0

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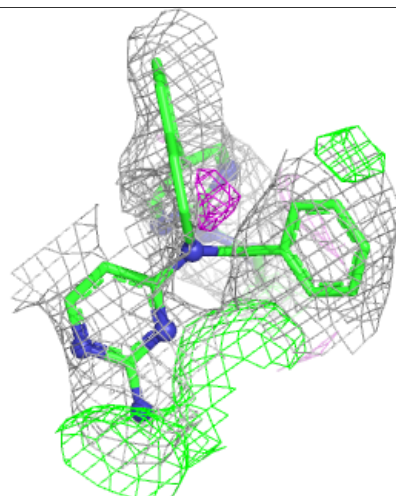
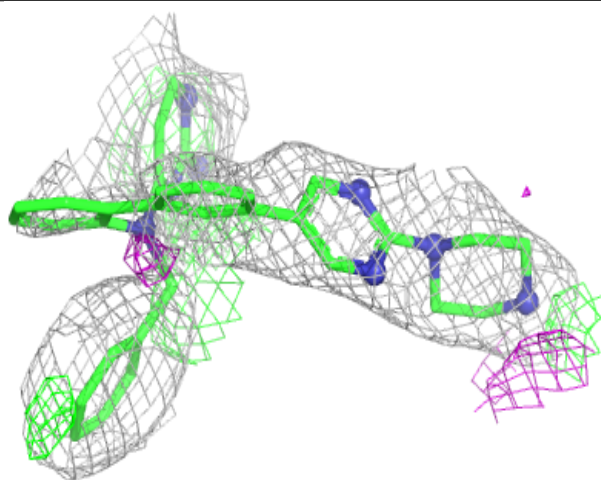
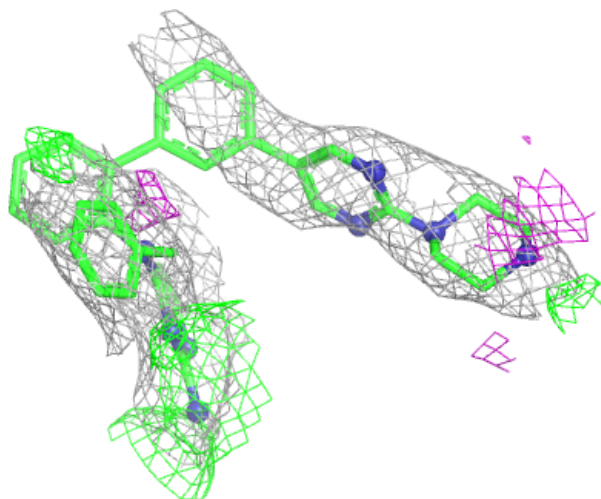
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	JNI	X	201	39/39	0.87	0.13	67,96,126,165	0
2	JNI	J	202	39/39	0.87	0.17	101,150,181,185	0
2	JNI	r	201	39/39	0.88	0.16	100,172,215,232	0
2	JNI	V	201	39/39	0.88	0.12	63,89,147,155	0
2	JNI	F	202	39/39	0.89	0.14	86,118,162,186	0
2	JNI	J	201	39/39	0.89	0.13	54,115,146,157	0
2	JNI	t	201	39/39	0.89	0.11	75,102,125,129	0
2	JNI	p	201	39/39	0.89	0.11	64,114,170,175	0
2	JNI	v	201	39/39	0.89	0.13	106,139,183,205	0
2	JNI	M	201	39/39	0.89	0.12	67,108,136,144	0
2	JNI	Q	201	39/39	0.90	0.12	67,88,141,169	0
2	JNI	A	202	39/39	0.90	0.11	76,96,124,128	0
2	JNI	N	201	39/39	0.90	0.12	47,74,95,99	0
2	JNI	H	201	39/39	0.90	0.11	69,91,142,182	0
2	JNI	b	201	39/39	0.90	0.13	62,94,136,141	0
2	JNI	Z	201	39/39	0.91	0.13	68,96,133,138	0
2	JNI	A	201	39/39	0.92	0.11	33,84,117,140	0
2	JNI	P	201	39/39	0.92	0.10	62,102,142,154	0
2	JNI	D	201	39/39	0.92	0.09	56,71,112,141	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.

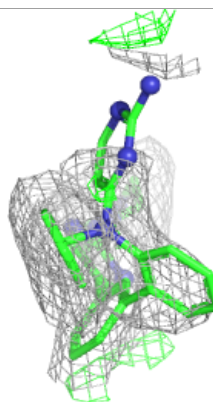
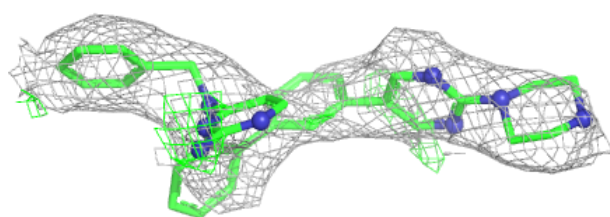
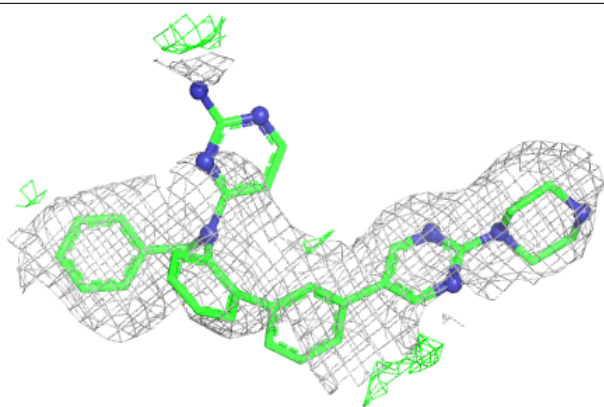
Electron density around JNI P 202:

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

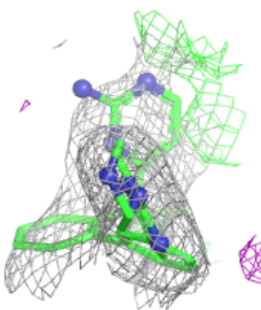
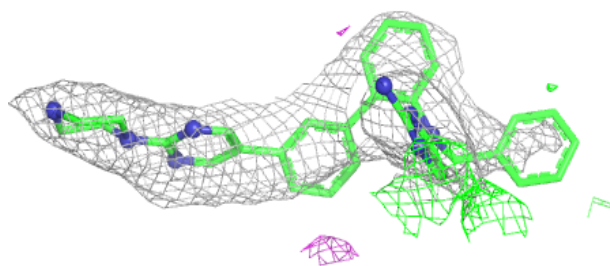
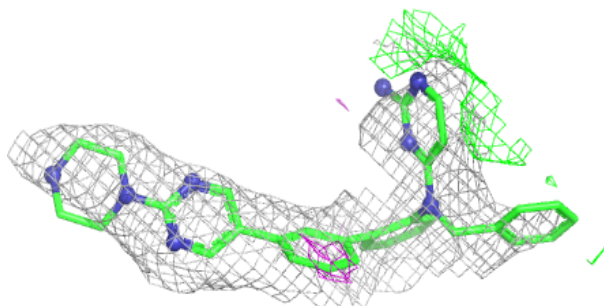


Electron density around JNI p 202:

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

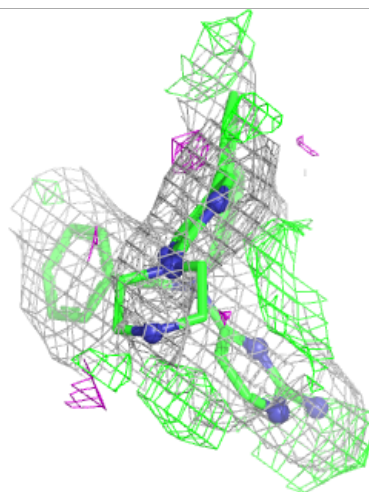
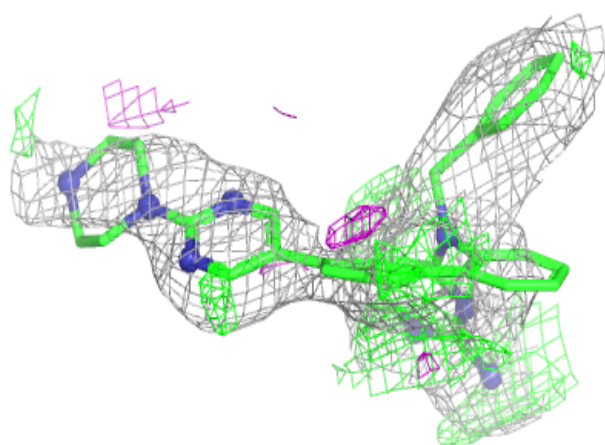
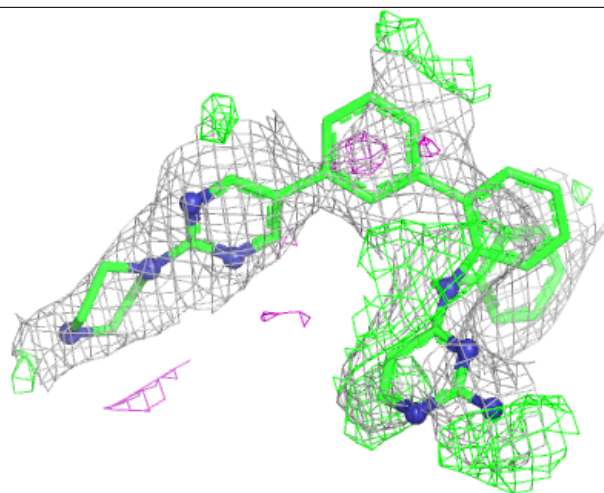
**Electron density around JNI f 201:**

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



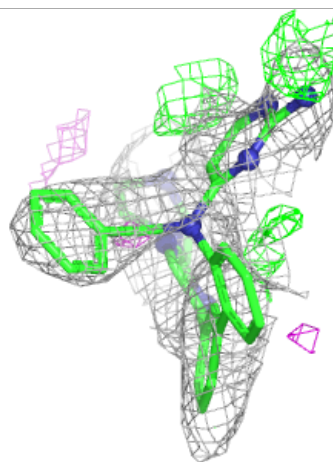
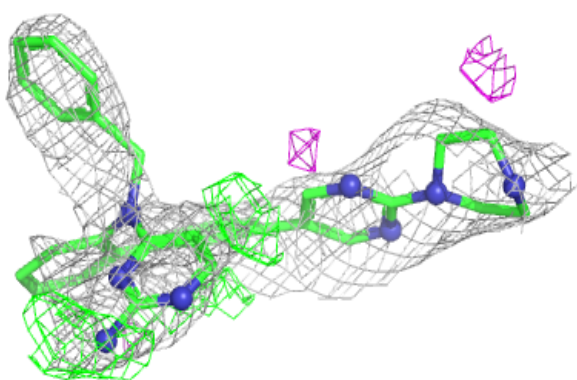
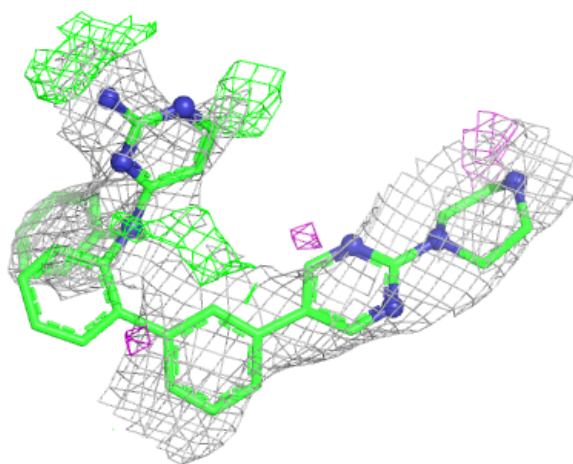
Electron density around JNI X 202:

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



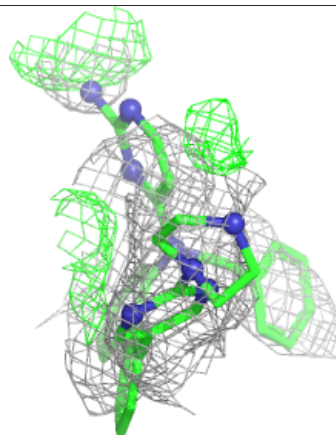
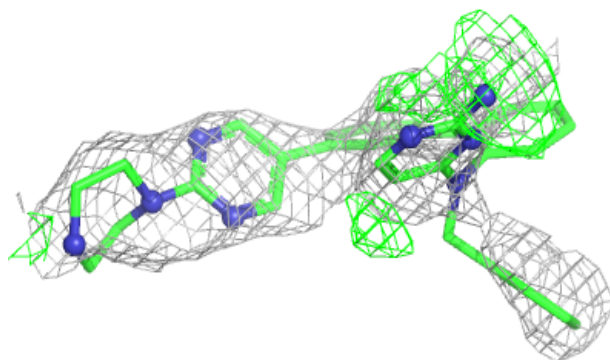
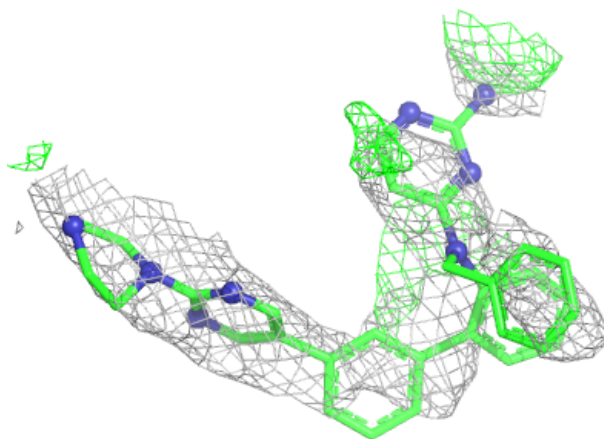
Electron density around JNI v 202:

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



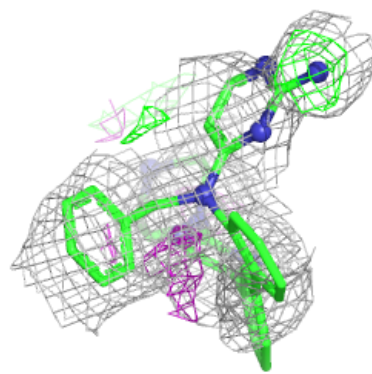
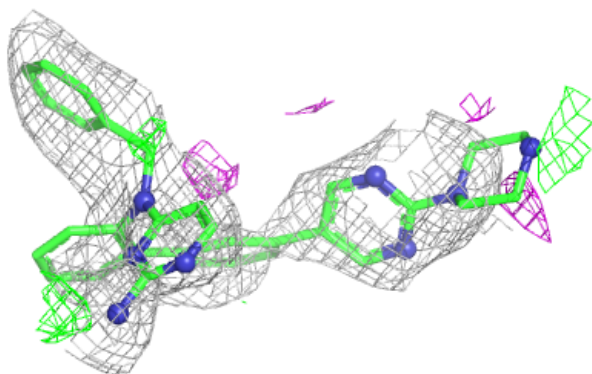
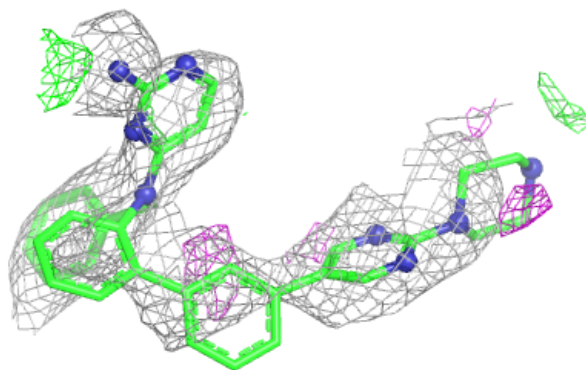
Electron density around JNI j 202:

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

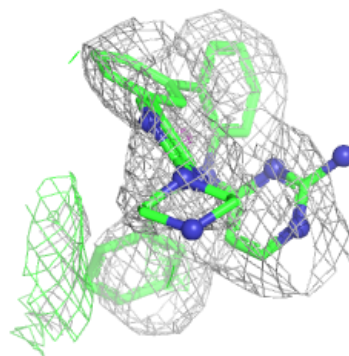
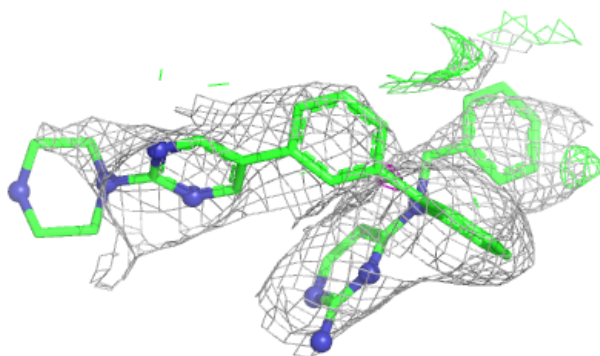
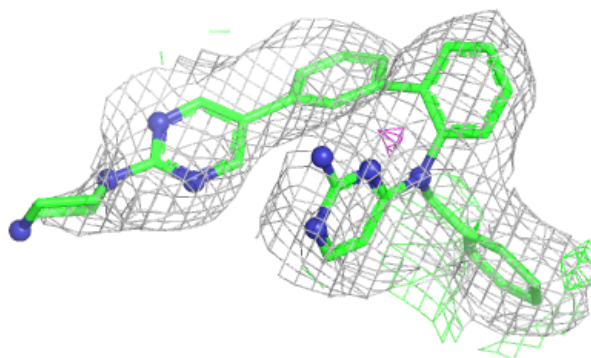


Electron density around JNI n 202:

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

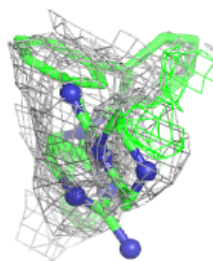
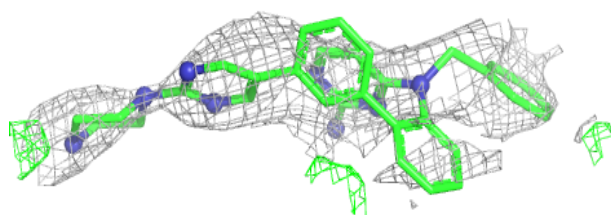
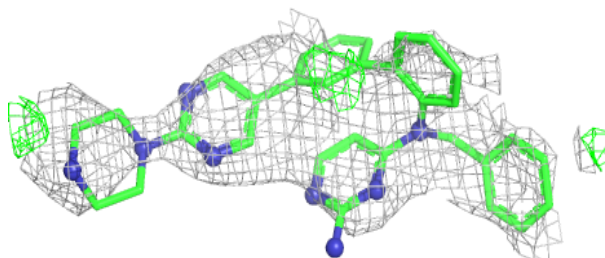
**Electron density around JNI d 201:**

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



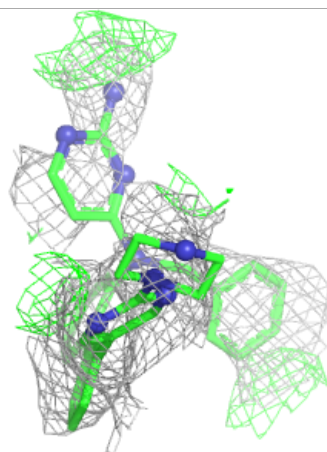
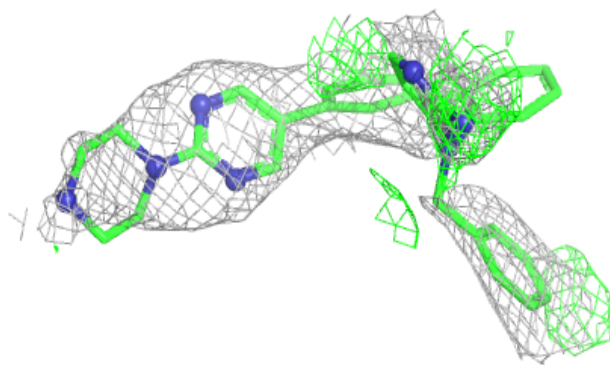
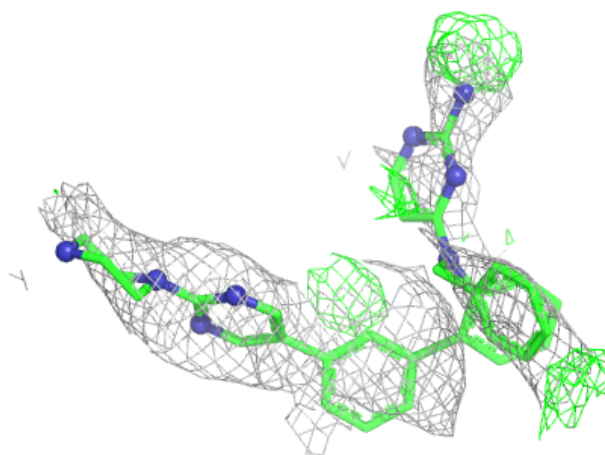
Electron density around JNI C 202:

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



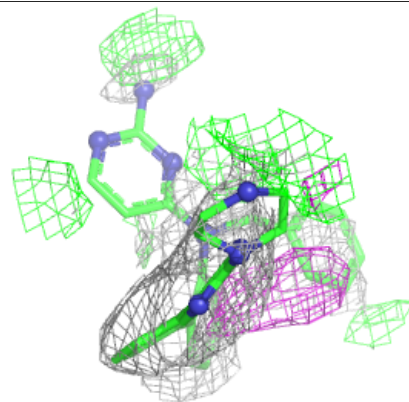
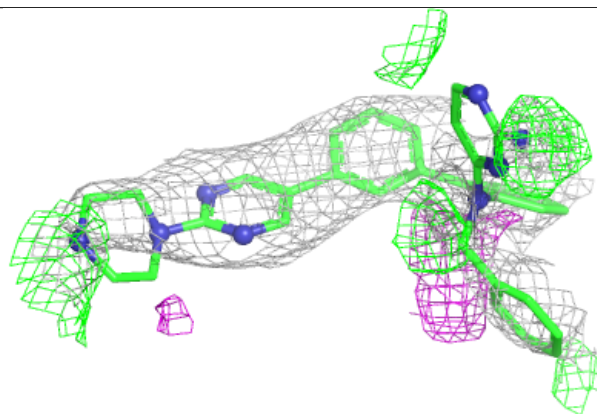
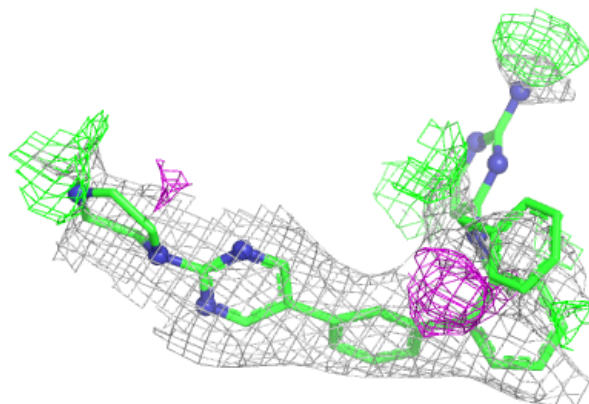
Electron density around JN1 r 202:

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

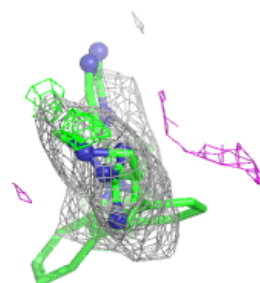
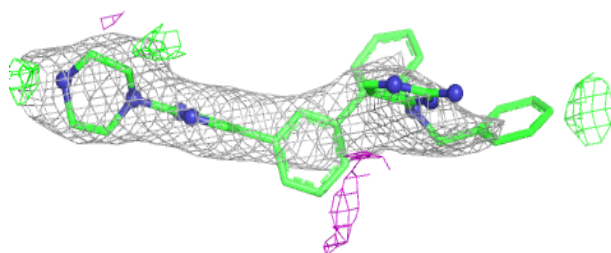
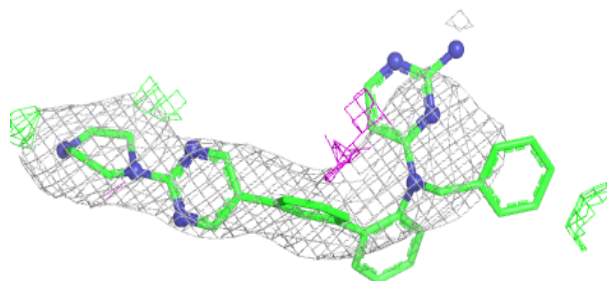


Electron density around JNI H 202:

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

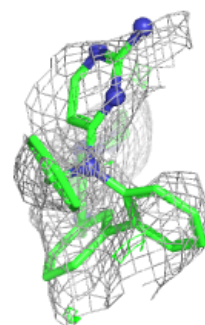
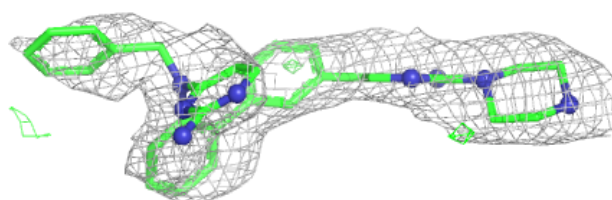
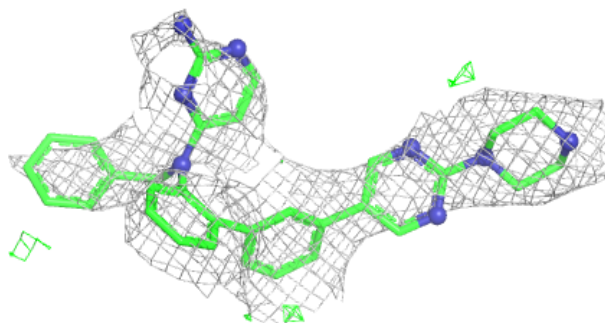
**Electron density around JNI h 202:**

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

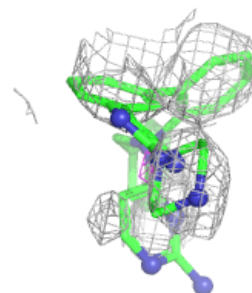
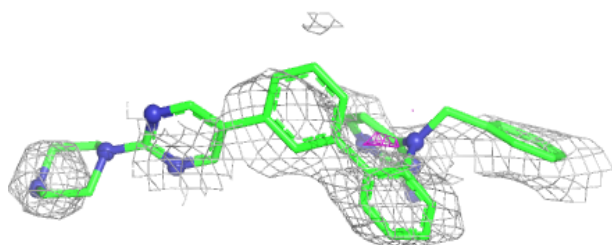
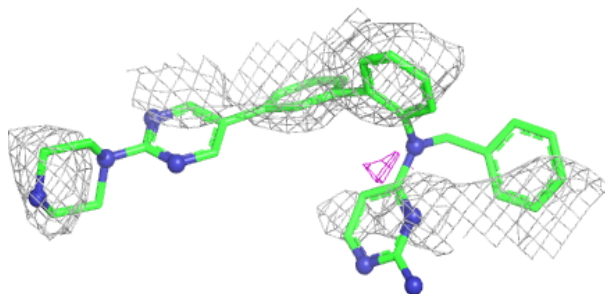


Electron density around JNI t 202:

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

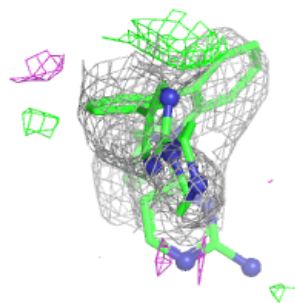
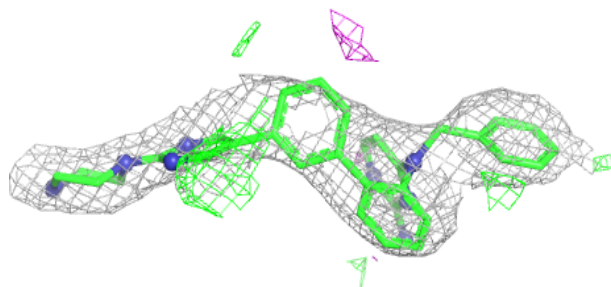
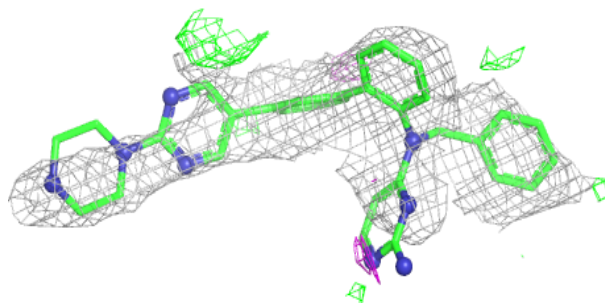
**Electron density around JNI f 202:**

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

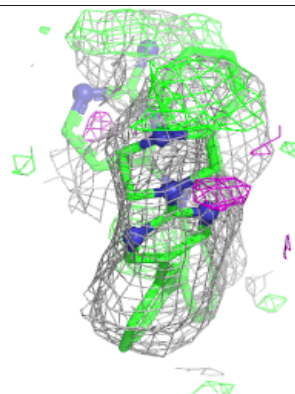
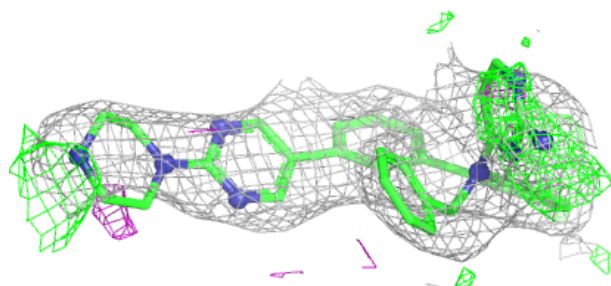
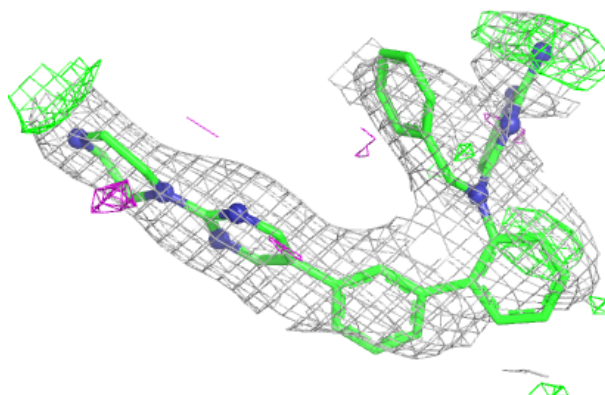


Electron density around JNI V 202:

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

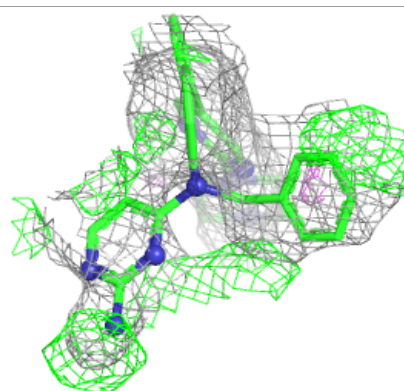
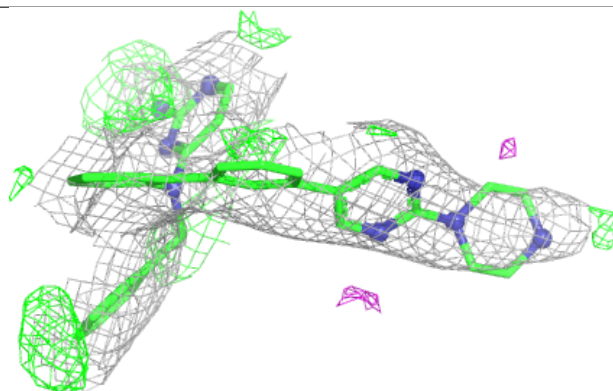
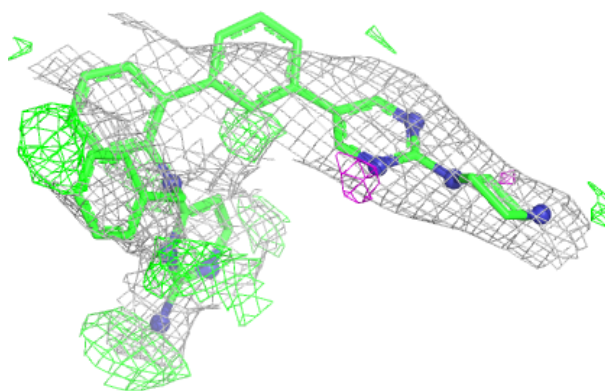
**Electron density around JNI L 201:**

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

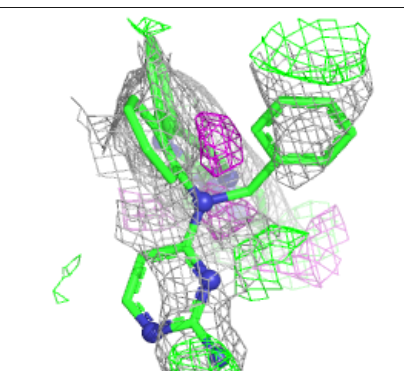
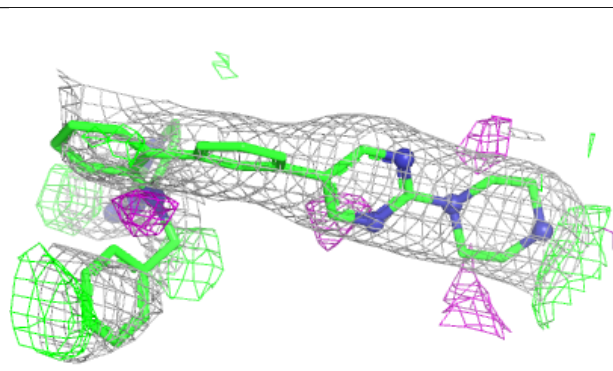
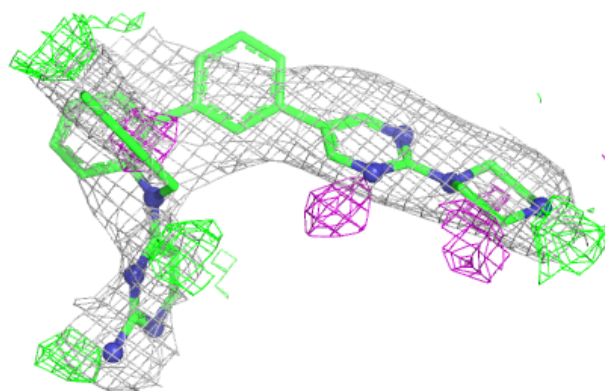


Electron density around JNI b 202:

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

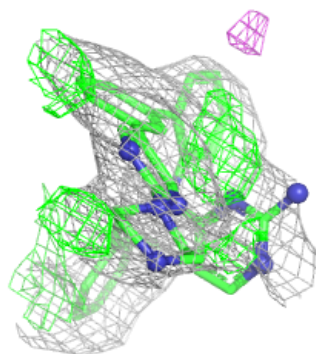
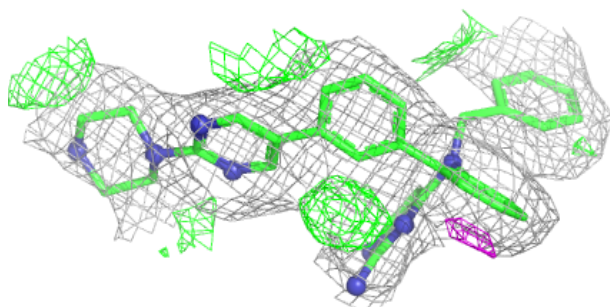
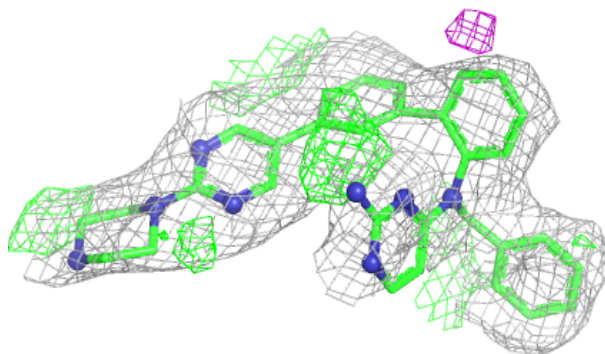
**Electron density around JNI C 201:**

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

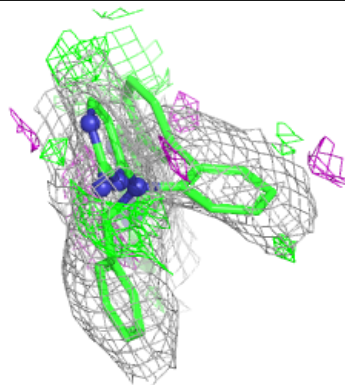
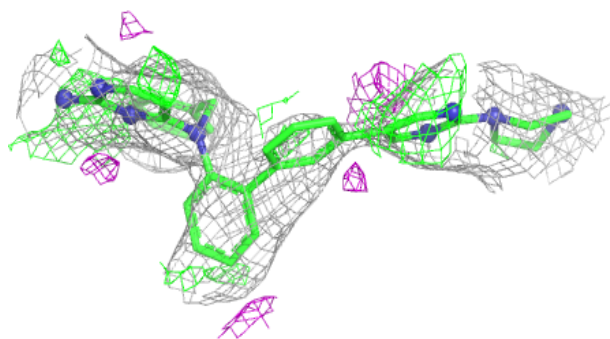
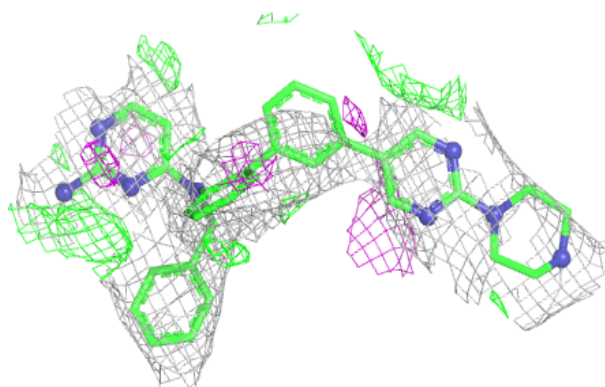


Electron density around JNI R 201:

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

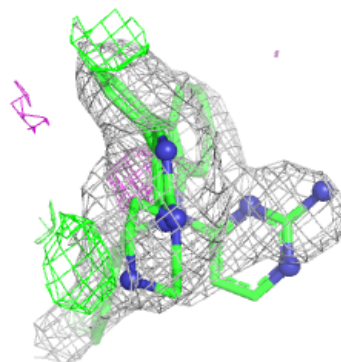
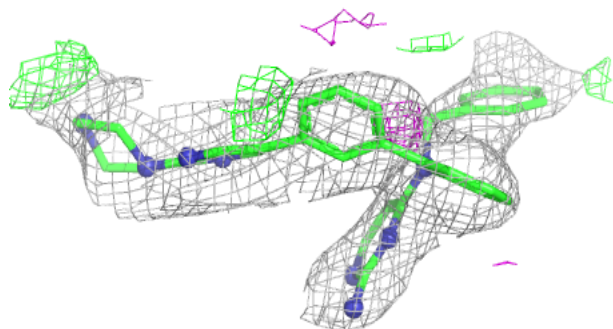
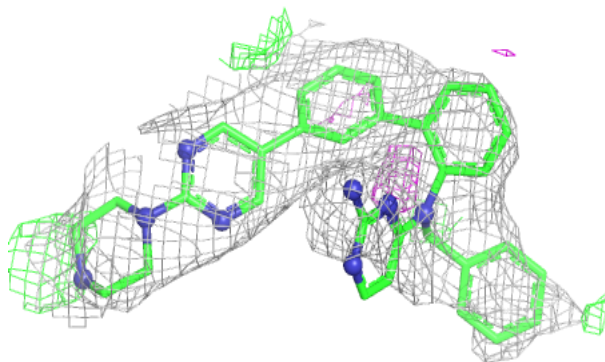
**Electron density around JNI U 201:**

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

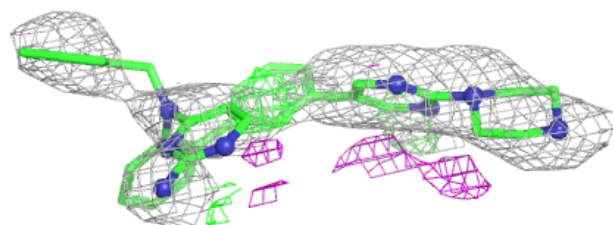
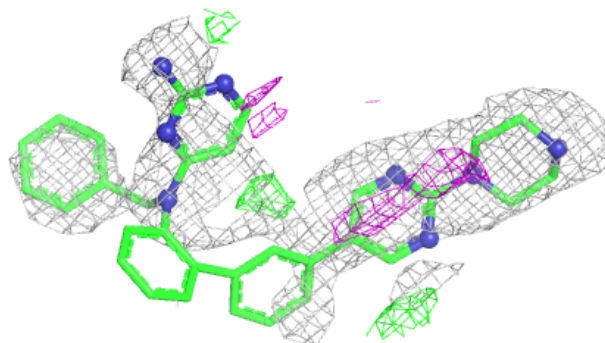


Electron density around JNI h 201:

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

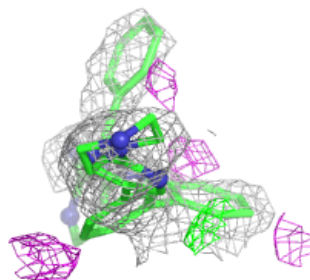
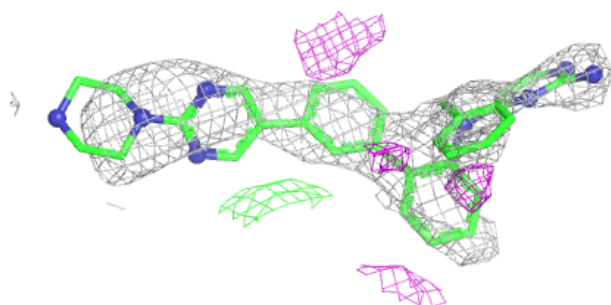
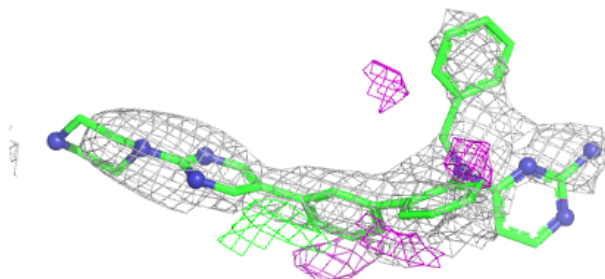
**Electron density around JNI n 201:**

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

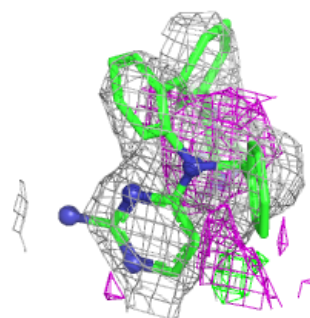
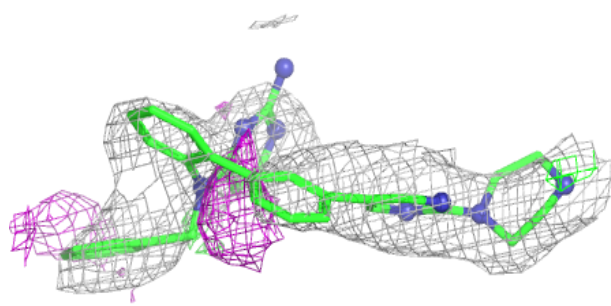
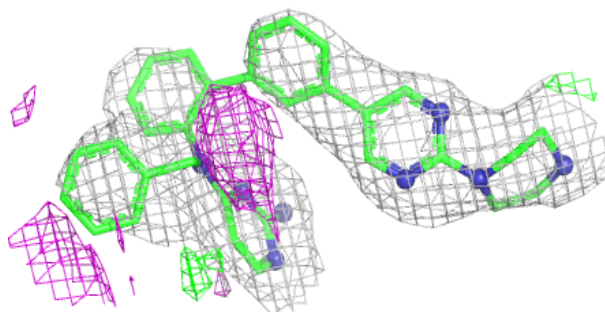


Electron density around JNI j 201:

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

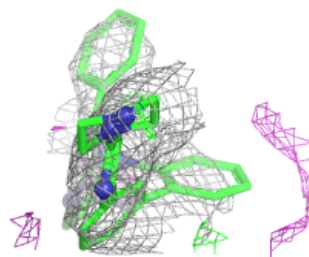
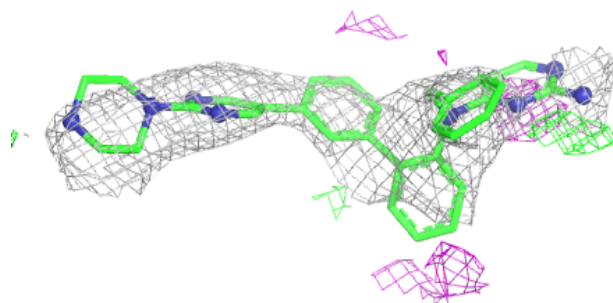
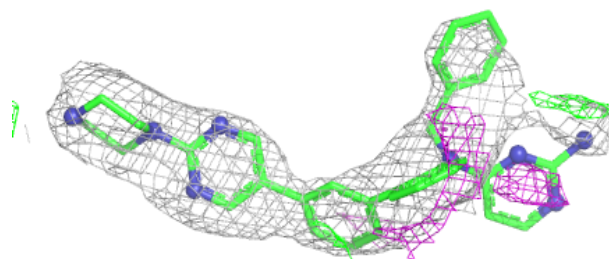
**Electron density around JNI l 201:**

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

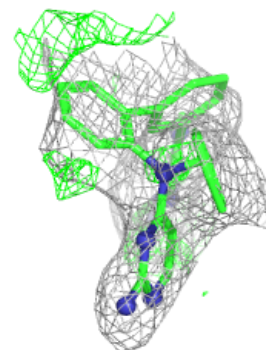
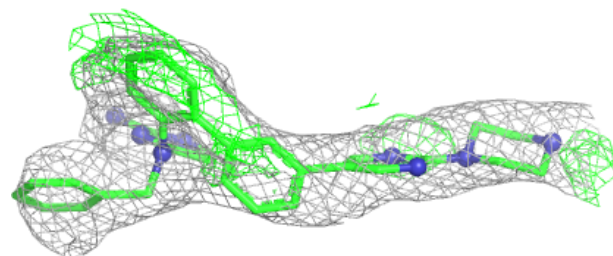
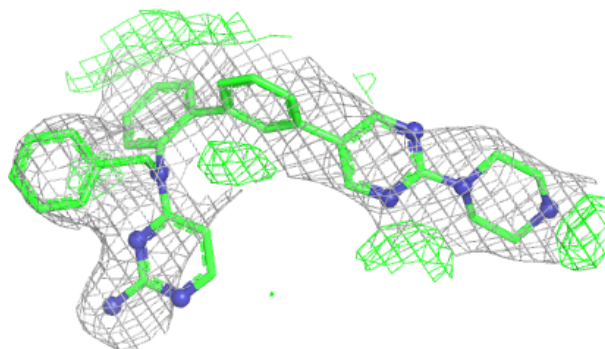


Electron density around JNI o 201:

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

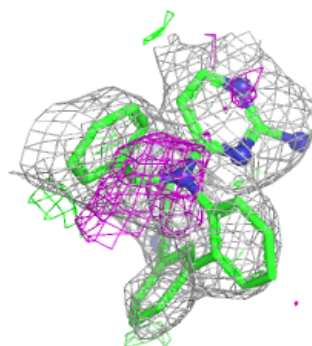
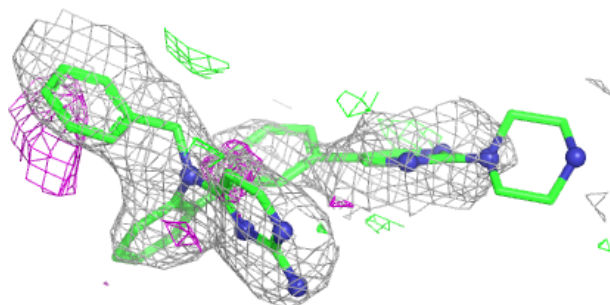
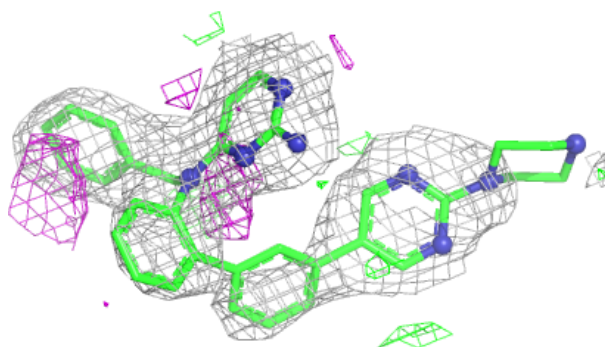
**Electron density around JNI Z 202:**

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

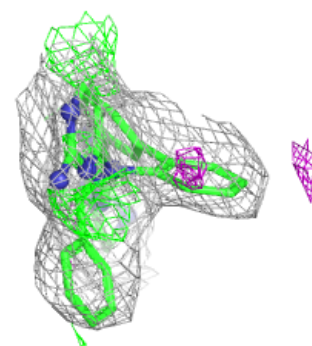
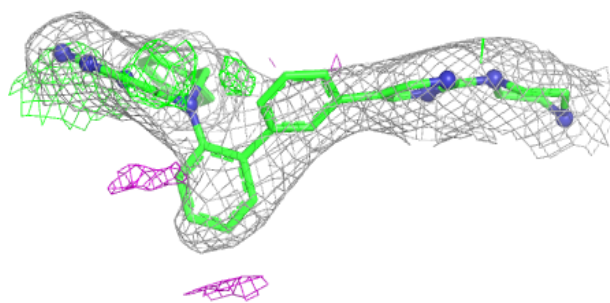
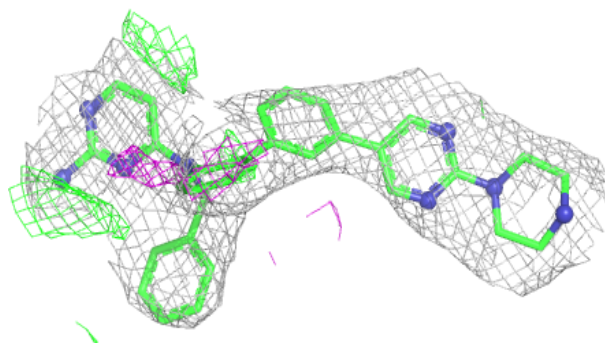


Electron density around JNI F 201:

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

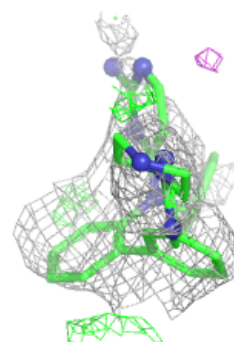
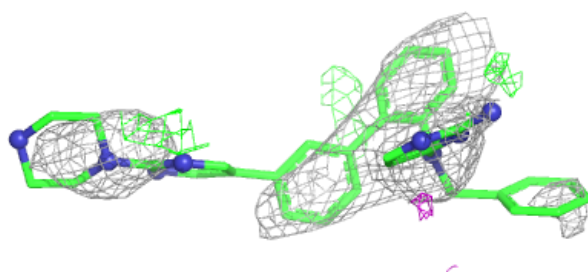
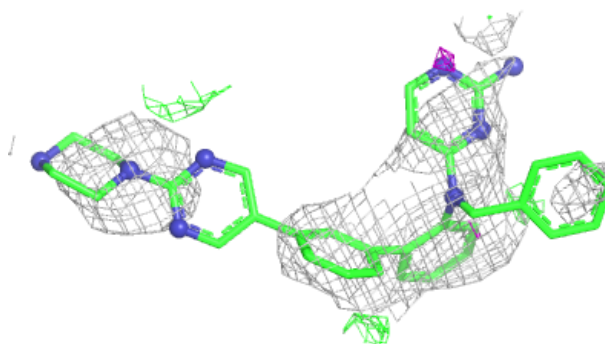
**Electron density around JNI X 201:**

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

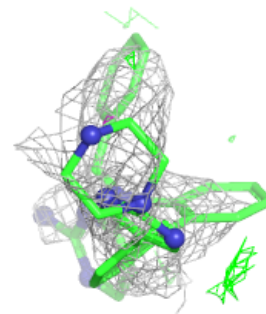
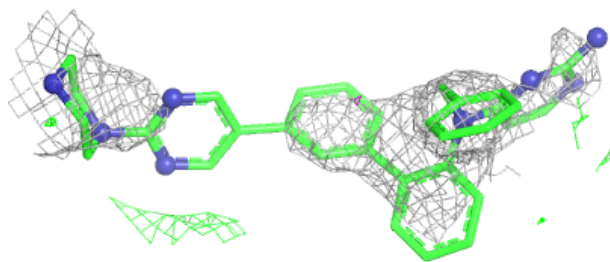
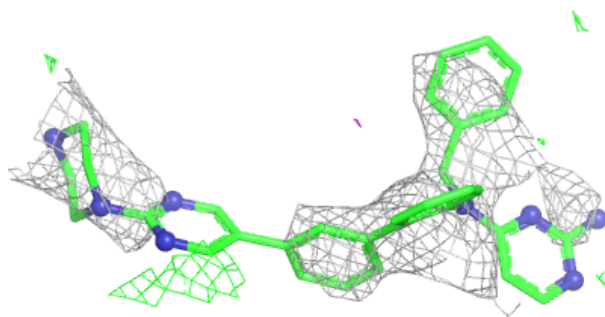


Electron density around JNI J 202:

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

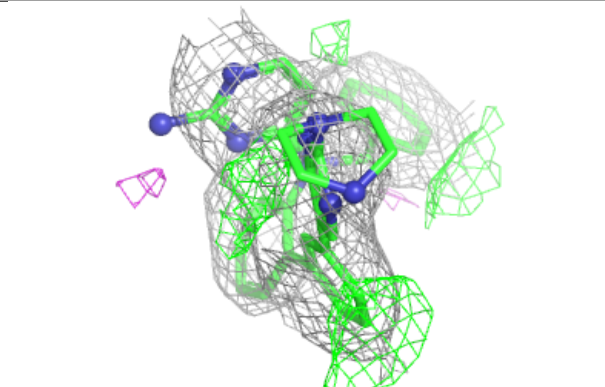
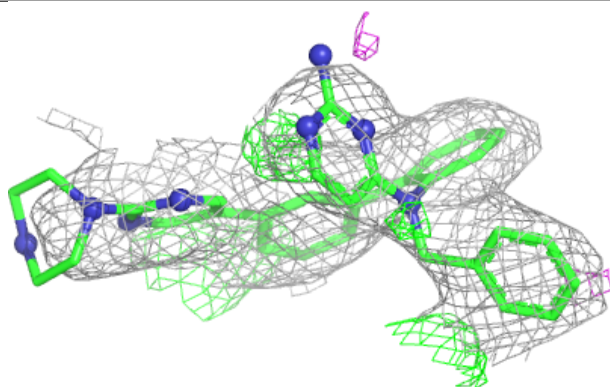
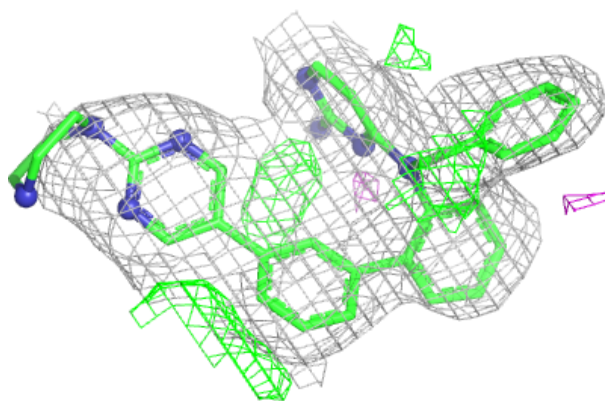
**Electron density around JNI r 201:**

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

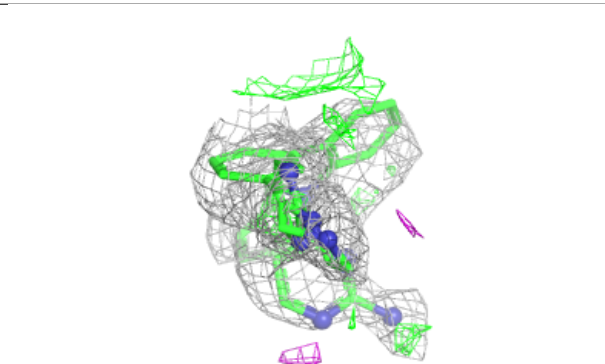
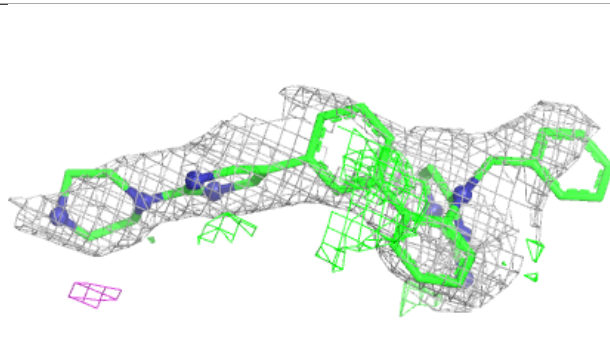
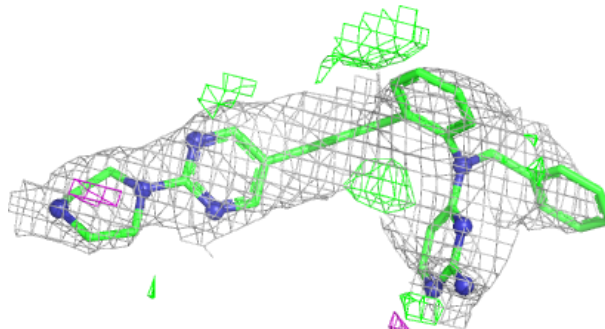


Electron density around JNI V 201:

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

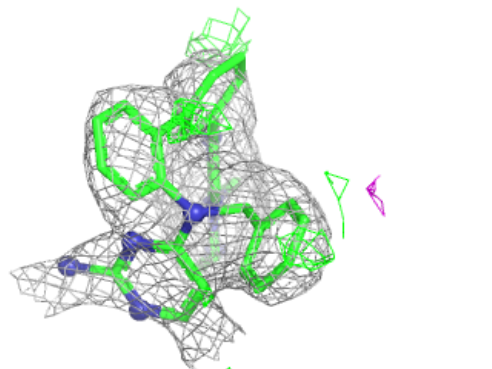
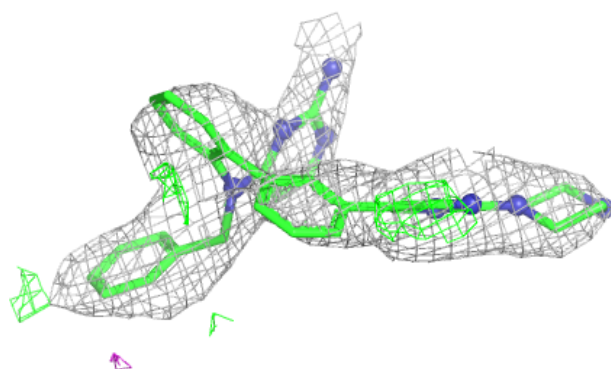
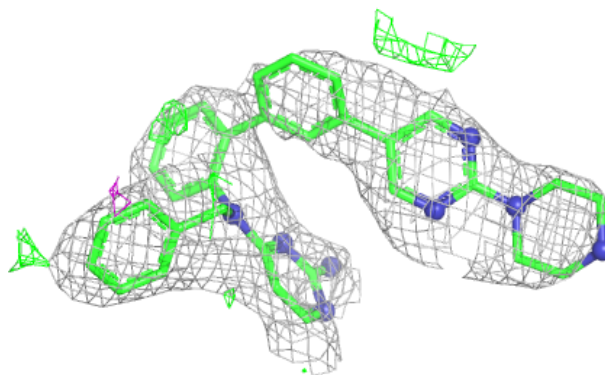
**Electron density around JNI F 202:**

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

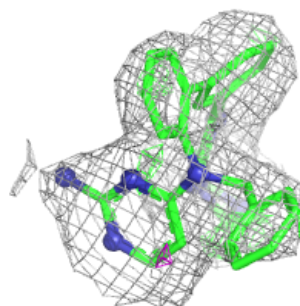
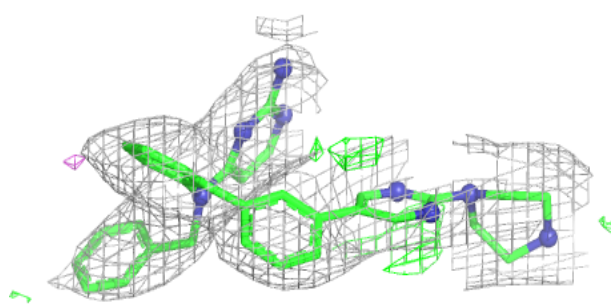
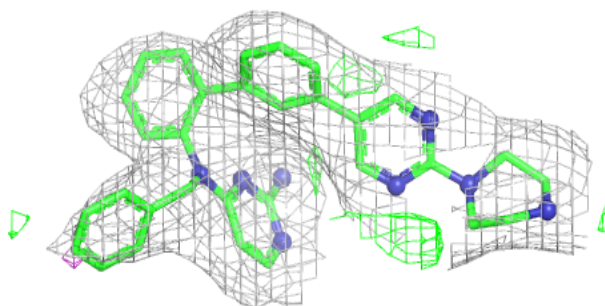


Electron density around JNI J 201:

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

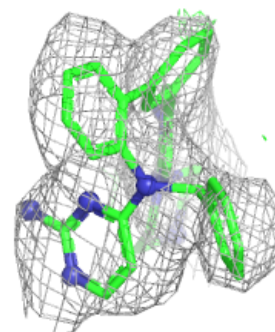
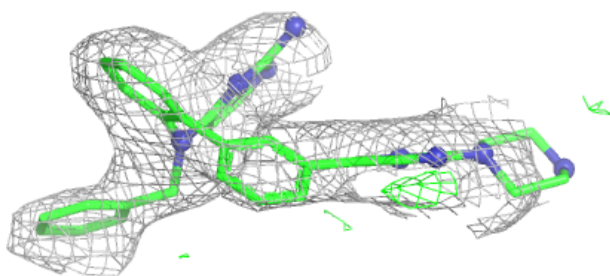
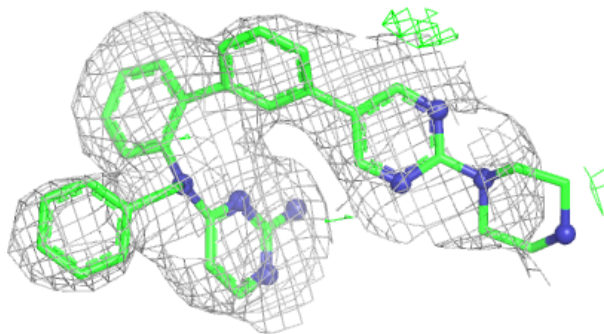
**Electron density around JNI t 201:**

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

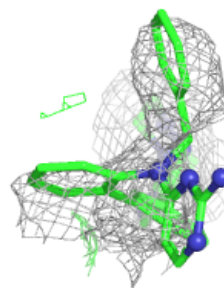
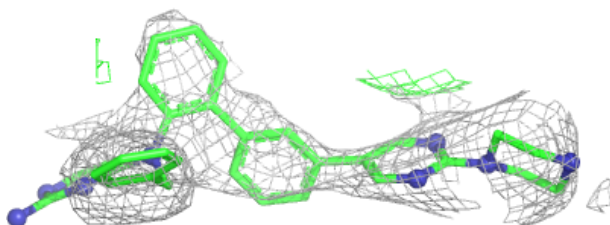
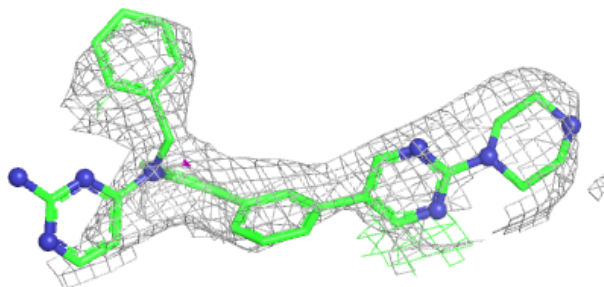


Electron density around JNI p 201:

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

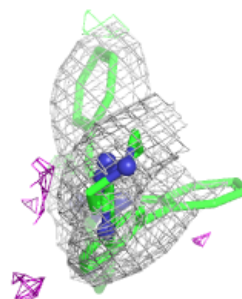
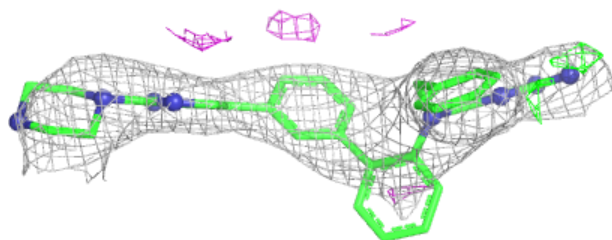
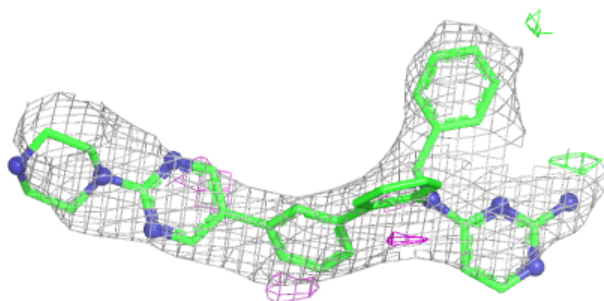
**Electron density around JNI v 201:**

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

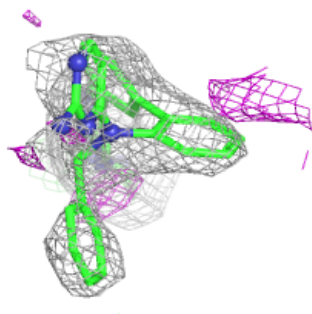
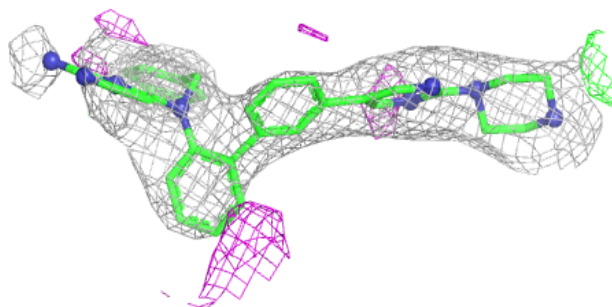
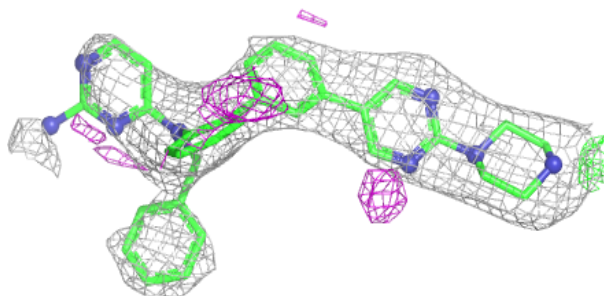


Electron density around JNI M 201:

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

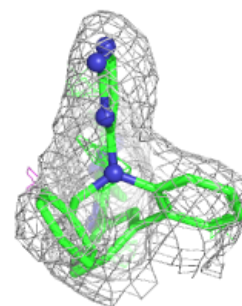
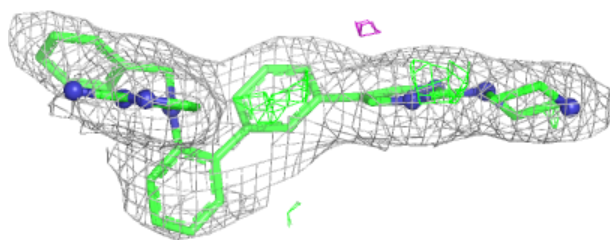
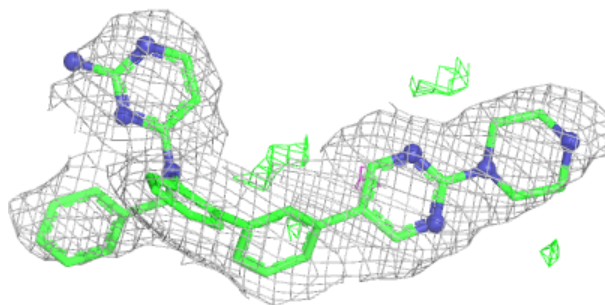
**Electron density around JNI Q 201:**

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

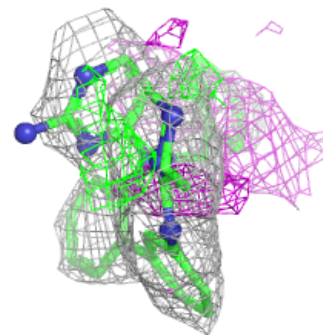
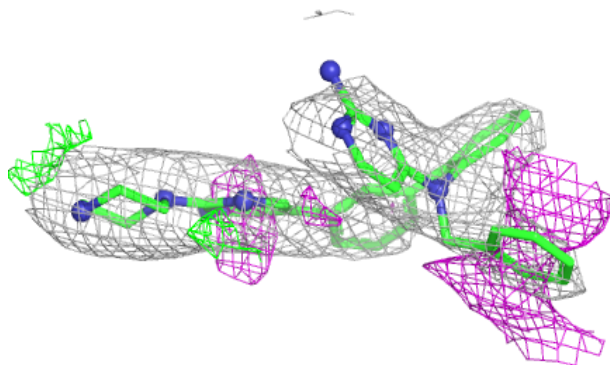
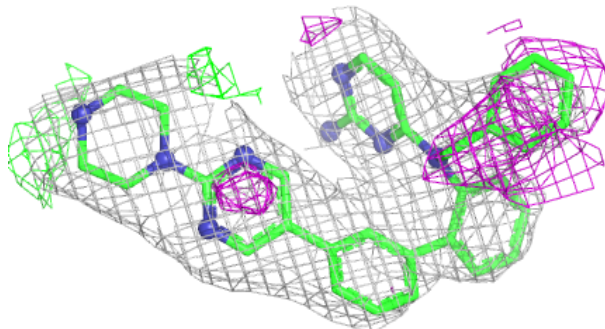


Electron density around JNI A 202:

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

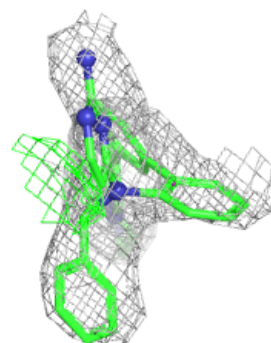
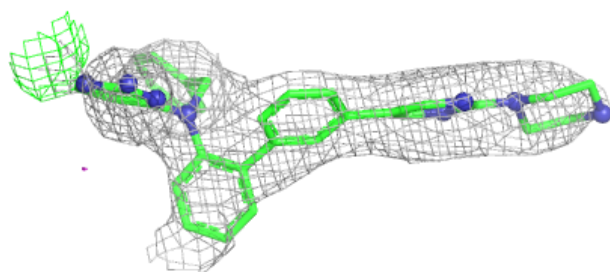
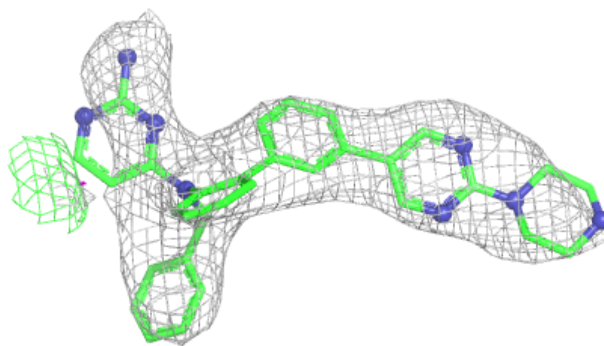
**Electron density around JNI N 201:**

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

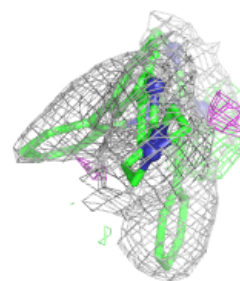
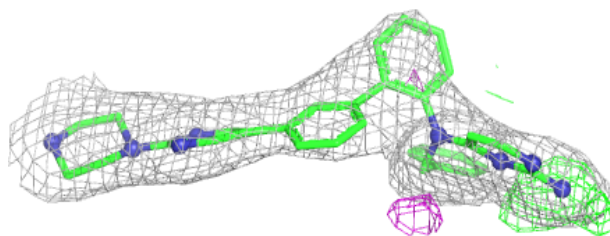
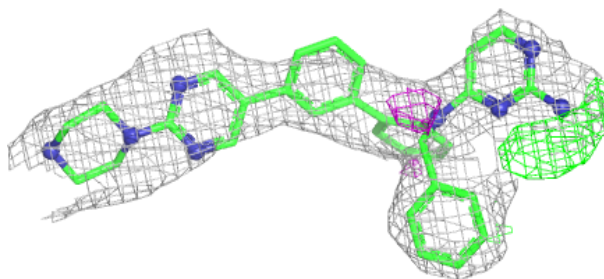


Electron density around JNI H 201:

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

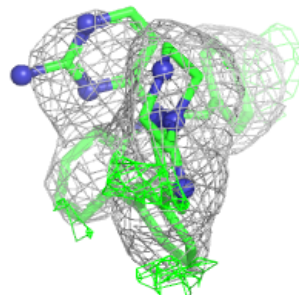
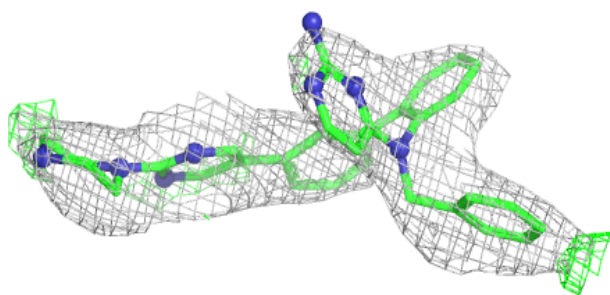
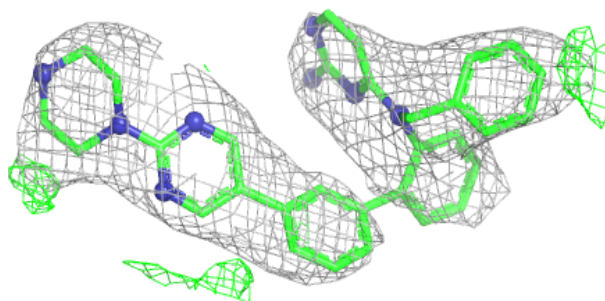
**Electron density around JNI b 201:**

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

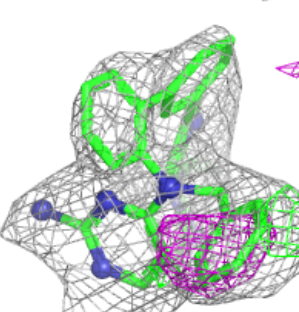
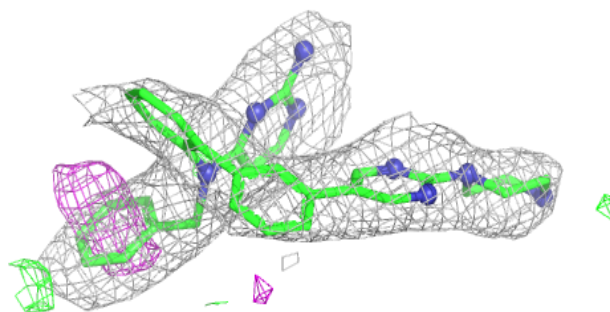
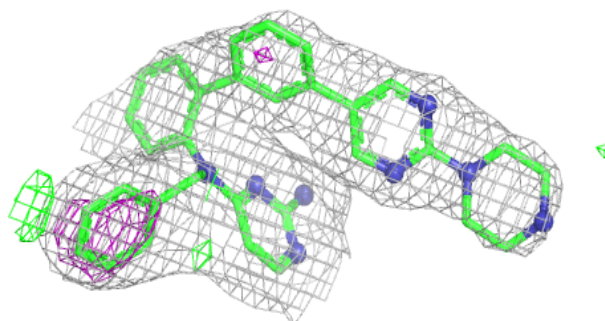


Electron density around JNI Z 201:

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

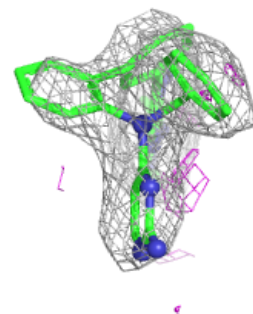
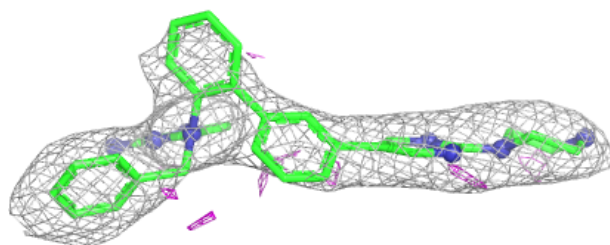
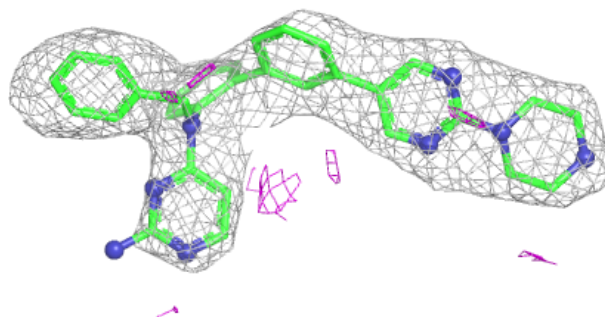
**Electron density around JNI A 201:**

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

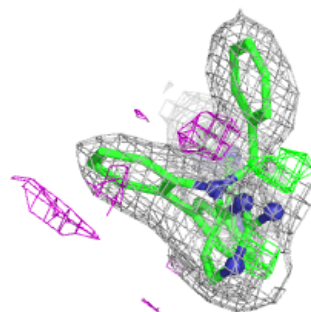
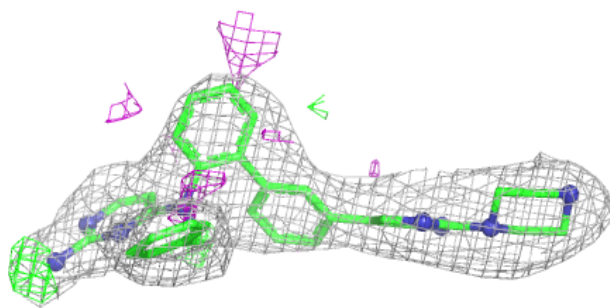
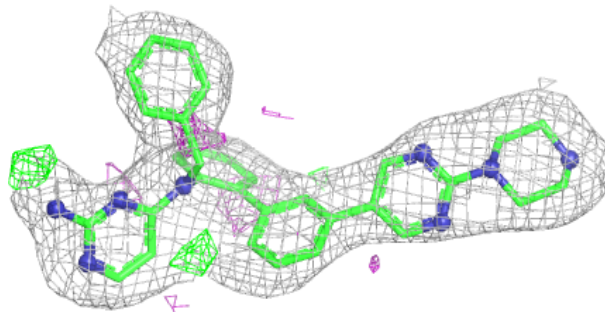


Electron density around JNI P 201:

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

**Electron density around JNI D 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.