wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 3, 2020 – 09:33 am GMT

PDB ID	:	6Z86
Title	:	human GTP cyclohydrolase I in complex with 7-deaza-GTP
Authors	:	Ebenhoch, R.; Nar, H.
Deposited on	:	2020-06-02
Resolution	:	2.21 Å(reported)

The following versions of software and data (see references ①) were used in the production of this report:

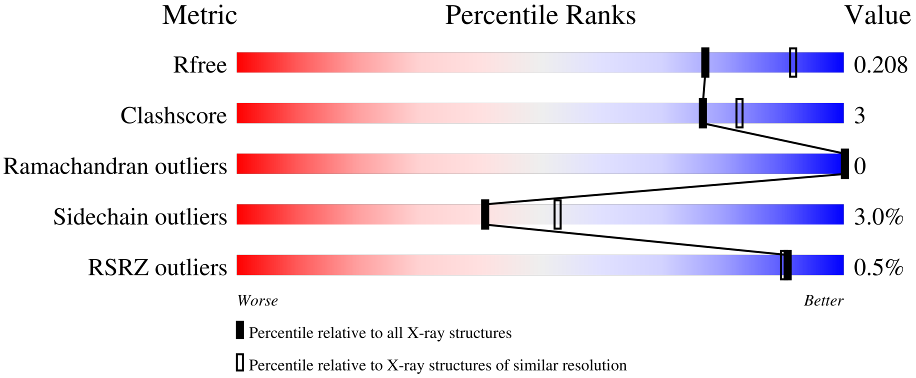
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 2.21 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	224	
1	B	224	
1	C	224	
1	D	224	
1	E	224	

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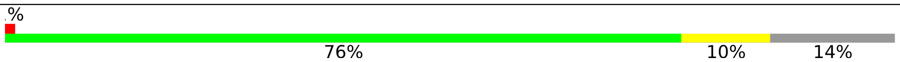
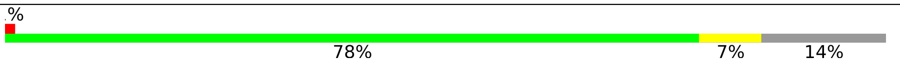
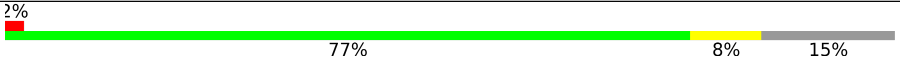
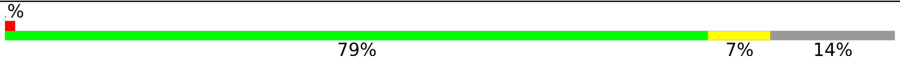
Mol	Chain	Length	Quality of chain
1	F	224	
1	G	224	
1	H	224	
1	I	224	
1	J	224	
1	K	224	
1	L	224	
1	M	224	
1	N	224	
1	O	224	
1	P	224	
1	Q	224	
1	R	224	
1	S	224	
1	T	224	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 31346 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 GTP cyclohydrolase 1.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	192	Total C N O S 1515 956 265 283 11	0	0	0
1	B	190	Total C N O S 1497 945 260 281 11	0	0	0
1	C	191	Total C N O S 1504 950 261 282 11	0	0	0
1	D	191	Total C N O S 1508 951 264 282 11	0	0	0
1	E	190	Total C N O S 1497 945 260 281 11	0	0	0
1	F	190	Total C N O S 1497 945 260 281 11	0	0	0
1	G	193	Total C N O S 1521 959 266 285 11	0	0	0
1	H	192	Total C N O S 1525 960 269 285 11	0	1	0
1	I	192	Total C N O S 1515 956 265 283 11	0	0	0
1	J	190	Total C N O S 1497 945 260 281 11	0	0	0
1	K	192	Total C N O S 1514 954 265 284 11	0	0	0
1	L	191	Total C N O S 1504 950 261 282 11	0	0	0
1	M	191	Total C N O S 1504 950 261 282 11	0	0	0
1	N	193	Total C N O S 1521 959 266 285 11	0	0	0
1	O	191	Total C N O S 1503 948 261 283 11	0	0	0
1	P	189	Total C N O S 1486 939 256 280 11	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	190	Total 1497	C 945	N 260	O 281	S 11	0	0	0
1	R	191	Total 1503	C 948	N 261	O 283	S 11	0	0	0
1	S	188	Total 1477	C 933	N 255	O 278	S 11	0	0	0
1	T	186	Total 1465	C 928	N 256	O 270	S 11	0	0	0

There are 280 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	initiating methionine	UNP P30793
A	28	HIS	-	expression tag	UNP P30793
A	29	HIS	-	expression tag	UNP P30793
A	30	HIS	-	expression tag	UNP P30793
A	31	HIS	-	expression tag	UNP P30793
A	32	HIS	-	expression tag	UNP P30793
A	33	HIS	-	expression tag	UNP P30793
A	34	GLY	-	expression tag	UNP P30793
A	35	SER	-	expression tag	UNP P30793
A	36	ASP	-	expression tag	UNP P30793
A	37	ASP	-	expression tag	UNP P30793
A	38	ASP	-	expression tag	UNP P30793
A	39	ASP	-	expression tag	UNP P30793
A	40	LYS	-	expression tag	UNP P30793
B	27	MET	-	initiating methionine	UNP P30793
B	28	HIS	-	expression tag	UNP P30793
B	29	HIS	-	expression tag	UNP P30793
B	30	HIS	-	expression tag	UNP P30793
B	31	HIS	-	expression tag	UNP P30793
B	32	HIS	-	expression tag	UNP P30793
B	33	HIS	-	expression tag	UNP P30793
B	34	GLY	-	expression tag	UNP P30793
B	35	SER	-	expression tag	UNP P30793
B	36	ASP	-	expression tag	UNP P30793
B	37	ASP	-	expression tag	UNP P30793
B	38	ASP	-	expression tag	UNP P30793
B	39	ASP	-	expression tag	UNP P30793
B	40	LYS	-	expression tag	UNP P30793
C	27	MET	-	initiating methionine	UNP P30793
C	28	HIS	-	expression tag	UNP P30793
C	29	HIS	-	expression tag	UNP P30793

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Chain	Residue	Modelled	Actual	Comment	Reference
C	30	HIS	-	expression tag	UNP P30793
C	31	HIS	-	expression tag	UNP P30793
C	32	HIS	-	expression tag	UNP P30793
C	33	HIS	-	expression tag	UNP P30793
C	34	GLY	-	expression tag	UNP P30793
C	35	SER	-	expression tag	UNP P30793
C	36	ASP	-	expression tag	UNP P30793
C	37	ASP	-	expression tag	UNP P30793
C	38	ASP	-	expression tag	UNP P30793
C	39	ASP	-	expression tag	UNP P30793
C	40	LYS	-	expression tag	UNP P30793
D	27	MET	-	initiating methionine	UNP P30793
D	28	HIS	-	expression tag	UNP P30793
D	29	HIS	-	expression tag	UNP P30793
D	30	HIS	-	expression tag	UNP P30793
D	31	HIS	-	expression tag	UNP P30793
D	32	HIS	-	expression tag	UNP P30793
D	33	HIS	-	expression tag	UNP P30793
D	34	GLY	-	expression tag	UNP P30793
D	35	SER	-	expression tag	UNP P30793
D	36	ASP	-	expression tag	UNP P30793
D	37	ASP	-	expression tag	UNP P30793
D	38	ASP	-	expression tag	UNP P30793
D	39	ASP	-	expression tag	UNP P30793
D	40	LYS	-	expression tag	UNP P30793
E	27	MET	-	initiating methionine	UNP P30793
E	28	HIS	-	expression tag	UNP P30793
E	29	HIS	-	expression tag	UNP P30793
E	30	HIS	-	expression tag	UNP P30793
E	31	HIS	-	expression tag	UNP P30793
E	32	HIS	-	expression tag	UNP P30793
E	33	HIS	-	expression tag	UNP P30793
E	34	GLY	-	expression tag	UNP P30793
E	35	SER	-	expression tag	UNP P30793
E	36	ASP	-	expression tag	UNP P30793
E	37	ASP	-	expression tag	UNP P30793
E	38	ASP	-	expression tag	UNP P30793
E	39	ASP	-	expression tag	UNP P30793
E	40	LYS	-	expression tag	UNP P30793
F	27	MET	-	initiating methionine	UNP P30793
F	28	HIS	-	expression tag	UNP P30793
F	29	HIS	-	expression tag	UNP P30793

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Chain	Residue	Modelled	Actual	Comment	Reference
F	30	HIS	-	expression tag	UNP P30793
F	31	HIS	-	expression tag	UNP P30793
F	32	HIS	-	expression tag	UNP P30793
F	33	HIS	-	expression tag	UNP P30793
F	34	GLY	-	expression tag	UNP P30793
F	35	SER	-	expression tag	UNP P30793
F	36	ASP	-	expression tag	UNP P30793
F	37	ASP	-	expression tag	UNP P30793
F	38	ASP	-	expression tag	UNP P30793
F	39	ASP	-	expression tag	UNP P30793
F	40	LYS	-	expression tag	UNP P30793
G	27	MET	-	initiating methionine	UNP P30793
G	28	HIS	-	expression tag	UNP P30793
G	29	HIS	-	expression tag	UNP P30793
G	30	HIS	-	expression tag	UNP P30793
G	31	HIS	-	expression tag	UNP P30793
G	32	HIS	-	expression tag	UNP P30793
G	33	HIS	-	expression tag	UNP P30793
G	34	GLY	-	expression tag	UNP P30793
G	35	SER	-	expression tag	UNP P30793
G	36	ASP	-	expression tag	UNP P30793
G	37	ASP	-	expression tag	UNP P30793
G	38	ASP	-	expression tag	UNP P30793
G	39	ASP	-	expression tag	UNP P30793
G	40	LYS	-	expression tag	UNP P30793
H	27	MET	-	initiating methionine	UNP P30793
H	28	HIS	-	expression tag	UNP P30793
H	29	HIS	-	expression tag	UNP P30793
H	30	HIS	-	expression tag	UNP P30793
H	31	HIS	-	expression tag	UNP P30793
H	32	HIS	-	expression tag	UNP P30793
H	33	HIS	-	expression tag	UNP P30793
H	34	GLY	-	expression tag	UNP P30793
H	35	SER	-	expression tag	UNP P30793
H	36	ASP	-	expression tag	UNP P30793
H	37	ASP	-	expression tag	UNP P30793
H	38	ASP	-	expression tag	UNP P30793
H	39	ASP	-	expression tag	UNP P30793
H	40	LYS	-	expression tag	UNP P30793
I	27	MET	-	initiating methionine	UNP P30793
I	28	HIS	-	expression tag	UNP P30793
I	29	HIS	-	expression tag	UNP P30793

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Chain	Residue	Modelled	Actual	Comment	Reference
I	30	HIS	-	expression tag	UNP P30793
I	31	HIS	-	expression tag	UNP P30793
I	32	HIS	-	expression tag	UNP P30793
I	33	HIS	-	expression tag	UNP P30793
I	34	GLY	-	expression tag	UNP P30793
I	35	SER	-	expression tag	UNP P30793
I	36	ASP	-	expression tag	UNP P30793
I	37	ASP	-	expression tag	UNP P30793
I	38	ASP	-	expression tag	UNP P30793
I	39	ASP	-	expression tag	UNP P30793
I	40	LYS	-	expression tag	UNP P30793
J	27	MET	-	initiating methionine	UNP P30793
J	28	HIS	-	expression tag	UNP P30793
J	29	HIS	-	expression tag	UNP P30793
J	30	HIS	-	expression tag	UNP P30793
J	31	HIS	-	expression tag	UNP P30793
J	32	HIS	-	expression tag	UNP P30793
J	33	HIS	-	expression tag	UNP P30793
J	34	GLY	-	expression tag	UNP P30793
J	35	SER	-	expression tag	UNP P30793
J	36	ASP	-	expression tag	UNP P30793
J	37	ASP	-	expression tag	UNP P30793
J	38	ASP	-	expression tag	UNP P30793
J	39	ASP	-	expression tag	UNP P30793
J	40	LYS	-	expression tag	UNP P30793
K	27	MET	-	initiating methionine	UNP P30793
K	28	HIS	-	expression tag	UNP P30793
K	29	HIS	-	expression tag	UNP P30793
K	30	HIS	-	expression tag	UNP P30793
K	31	HIS	-	expression tag	UNP P30793
K	32	HIS	-	expression tag	UNP P30793
K	33	HIS	-	expression tag	UNP P30793
K	34	GLY	-	expression tag	UNP P30793
K	35	SER	-	expression tag	UNP P30793
K	36	ASP	-	expression tag	UNP P30793
K	37	ASP	-	expression tag	UNP P30793
K	38	ASP	-	expression tag	UNP P30793
K	39	ASP	-	expression tag	UNP P30793
K	40	LYS	-	expression tag	UNP P30793
L	27	MET	-	initiating methionine	UNP P30793
L	28	HIS	-	expression tag	UNP P30793
L	29	HIS	-	expression tag	UNP P30793

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Chain	Residue	Modelled	Actual	Comment	Reference
L	30	HIS	-	expression tag	UNP P30793
L	31	HIS	-	expression tag	UNP P30793
L	32	HIS	-	expression tag	UNP P30793
L	33	HIS	-	expression tag	UNP P30793
L	34	GLY	-	expression tag	UNP P30793
L	35	SER	-	expression tag	UNP P30793
L	36	ASP	-	expression tag	UNP P30793
L	37	ASP	-	expression tag	UNP P30793
L	38	ASP	-	expression tag	UNP P30793
L	39	ASP	-	expression tag	UNP P30793
L	40	LYS	-	expression tag	UNP P30793
M	27	MET	-	initiating methionine	UNP P30793
M	28	HIS	-	expression tag	UNP P30793
M	29	HIS	-	expression tag	UNP P30793
M	30	HIS	-	expression tag	UNP P30793
M	31	HIS	-	expression tag	UNP P30793
M	32	HIS	-	expression tag	UNP P30793
M	33	HIS	-	expression tag	UNP P30793
M	34	GLY	-	expression tag	UNP P30793
M	35	SER	-	expression tag	UNP P30793
M	36	ASP	-	expression tag	UNP P30793
M	37	ASP	-	expression tag	UNP P30793
M	38	ASP	-	expression tag	UNP P30793
M	39	ASP	-	expression tag	UNP P30793
M	40	LYS	-	expression tag	UNP P30793
N	27	MET	-	initiating methionine	UNP P30793
N	28	HIS	-	expression tag	UNP P30793
N	29	HIS	-	expression tag	UNP P30793
N	30	HIS	-	expression tag	UNP P30793
N	31	HIS	-	expression tag	UNP P30793
N	32	HIS	-	expression tag	UNP P30793
N	33	HIS	-	expression tag	UNP P30793
N	34	GLY	-	expression tag	UNP P30793
N	35	SER	-	expression tag	UNP P30793
N	36	ASP	-	expression tag	UNP P30793
N	37	ASP	-	expression tag	UNP P30793
N	38	ASP	-	expression tag	UNP P30793
N	39	ASP	-	expression tag	UNP P30793
N	40	LYS	-	expression tag	UNP P30793
O	27	MET	-	initiating methionine	UNP P30793
O	28	HIS	-	expression tag	UNP P30793
O	29	HIS	-	expression tag	UNP P30793

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Chain	Residue	Modelled	Actual	Comment	Reference
O	30	HIS	-	expression tag	UNP P30793
O	31	HIS	-	expression tag	UNP P30793
O	32	HIS	-	expression tag	UNP P30793
O	33	HIS	-	expression tag	UNP P30793
O	34	GLY	-	expression tag	UNP P30793
O	35	SER	-	expression tag	UNP P30793
O	36	ASP	-	expression tag	UNP P30793
O	37	ASP	-	expression tag	UNP P30793
O	38	ASP	-	expression tag	UNP P30793
O	39	ASP	-	expression tag	UNP P30793
O	40	LYS	-	expression tag	UNP P30793
P	27	MET	-	initiating methionine	UNP P30793
P	28	HIS	-	expression tag	UNP P30793
P	29	HIS	-	expression tag	UNP P30793
P	30	HIS	-	expression tag	UNP P30793
P	31	HIS	-	expression tag	UNP P30793
P	32	HIS	-	expression tag	UNP P30793
P	33	HIS	-	expression tag	UNP P30793
P	34	GLY	-	expression tag	UNP P30793
P	35	SER	-	expression tag	UNP P30793
P	36	ASP	-	expression tag	UNP P30793
P	37	ASP	-	expression tag	UNP P30793
P	38	ASP	-	expression tag	UNP P30793
P	39	ASP	-	expression tag	UNP P30793
P	40	LYS	-	expression tag	UNP P30793
Q	27	MET	-	initiating methionine	UNP P30793
Q	28	HIS	-	expression tag	UNP P30793
Q	29	HIS	-	expression tag	UNP P30793
Q	30	HIS	-	expression tag	UNP P30793
Q	31	HIS	-	expression tag	UNP P30793
Q	32	HIS	-	expression tag	UNP P30793
Q	33	HIS	-	expression tag	UNP P30793
Q	34	GLY	-	expression tag	UNP P30793
Q	35	SER	-	expression tag	UNP P30793
Q	36	ASP	-	expression tag	UNP P30793
Q	37	ASP	-	expression tag	UNP P30793
Q	38	ASP	-	expression tag	UNP P30793
Q	39	ASP	-	expression tag	UNP P30793
Q	40	LYS	-	expression tag	UNP P30793
R	27	MET	-	initiating methionine	UNP P30793
R	28	HIS	-	expression tag	UNP P30793
R	29	HIS	-	expression tag	UNP P30793

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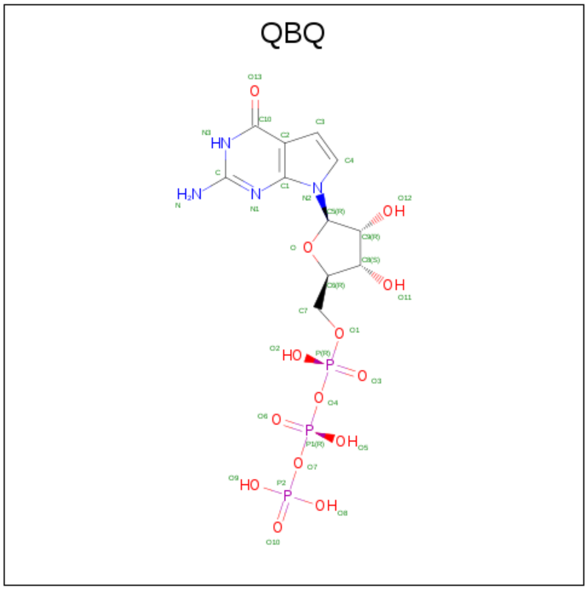
Chain	Residue	Modelled	Actual	Comment	Reference
R	30	HIS	-	expression tag	UNP P30793
R	31	HIS	-	expression tag	UNP P30793
R	32	HIS	-	expression tag	UNP P30793
R	33	HIS	-	expression tag	UNP P30793
R	34	GLY	-	expression tag	UNP P30793
R	35	SER	-	expression tag	UNP P30793
R	36	ASP	-	expression tag	UNP P30793
R	37	ASP	-	expression tag	UNP P30793
R	38	ASP	-	expression tag	UNP P30793
R	39	ASP	-	expression tag	UNP P30793
R	40	LYS	-	expression tag	UNP P30793
S	27	MET	-	initiating methionine	UNP P30793
S	28	HIS	-	expression tag	UNP P30793
S	29	HIS	-	expression tag	UNP P30793
S	30	HIS	-	expression tag	UNP P30793
S	31	HIS	-	expression tag	UNP P30793
S	32	HIS	-	expression tag	UNP P30793
S	33	HIS	-	expression tag	UNP P30793
S	34	GLY	-	expression tag	UNP P30793
S	35	SER	-	expression tag	UNP P30793
S	36	ASP	-	expression tag	UNP P30793
S	37	ASP	-	expression tag	UNP P30793
S	38	ASP	-	expression tag	UNP P30793
S	39	ASP	-	expression tag	UNP P30793
S	40	LYS	-	expression tag	UNP P30793
T	27	MET	-	initiating methionine	UNP P30793
T	28	HIS	-	expression tag	UNP P30793
T	29	HIS	-	expression tag	UNP P30793
T	30	HIS	-	expression tag	UNP P30793
T	31	HIS	-	expression tag	UNP P30793
T	32	HIS	-	expression tag	UNP P30793
T	33	HIS	-	expression tag	UNP P30793
T	34	GLY	-	expression tag	UNP P30793
T	35	SER	-	expression tag	UNP P30793
T	36	ASP	-	expression tag	UNP P30793
T	37	ASP	-	expression tag	UNP P30793
T	38	ASP	-	expression tag	UNP P30793
T	39	ASP	-	expression tag	UNP P30793
T	40	LYS	-	expression tag	UNP P30793

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	P	1	Total Zn 1 1	0	0
2	G	1	Total Zn 1 1	0	0
2	J	1	Total Zn 1 1	0	0
2	Q	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	K	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	T	1	Total Zn 1 1	0	0
2	N	1	Total Zn 1 1	0	0
2	O	1	Total Zn 1 1	0	0
2	R	1	Total Zn 1 1	0	0
2	L	1	Total Zn 1 1	0	0
2	S	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0
2	M	1	Total Zn 1 1	0	0

- Molecule 3 is 7-deaza-GTP (three-letter code: QBQ) (formula: $C_{11}H_{17}N_4O_{14}P_3$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 32 11 4 14 3	0	0
3	B	1	Total C N O P 32 11 4 14 3	0	0
3	C	1	Total C N O P 32 11 4 14 3	0	0
3	D	1	Total C N O P 32 11 4 14 3	0	0
3	E	1	Total C N O P 32 11 4 14 3	0	0
3	F	1	Total C N O P 32 11 4 14 3	0	0
3	G	1	Total C N O P 32 11 4 14 3	0	0
3	H	1	Total C N O P 32 11 4 14 3	0	0
3	I	1	Total C N O P 32 11 4 14 3	0	0
3	J	1	Total C N O P 32 11 4 14 3	0	0
3	K	1	Total C N O P 32 11 4 14 3	0	0
3	L	1	Total C N O P 32 11 4 14 3	0	0
3	M	1	Total C N O P 32 11 4 14 3	0	0
3	N	1	Total C N O P 32 11 4 14 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	O	1	Total C N O P 32 11 4 14 3	0	0
3	P	1	Total C N O P 32 11 4 14 3	0	0
3	Q	1	Total C N O P 32 11 4 14 3	0	0
3	R	1	Total C N O P 32 11 4 14 3	0	0
3	S	1	Total C N O P 32 11 4 14 3	0	0
3	T	1	Total C N O P 32 11 4 14 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	34	Total O 34 34	0	0
4	B	46	Total O 46 46	0	0
4	C	30	Total O 30 30	0	0
4	D	32	Total O 32 32	0	0
4	E	35	Total O 35 35	0	0
4	F	38	Total O 38 38	0	0
4	G	33	Total O 33 33	0	0
4	H	29	Total O 29 29	0	0
4	I	34	Total O 34 34	0	0
4	J	33	Total O 33 33	0	0
4	K	34	Total O 34 34	0	0
4	L	24	Total O 24 24	0	0
4	M	31	Total O 31 31	0	0

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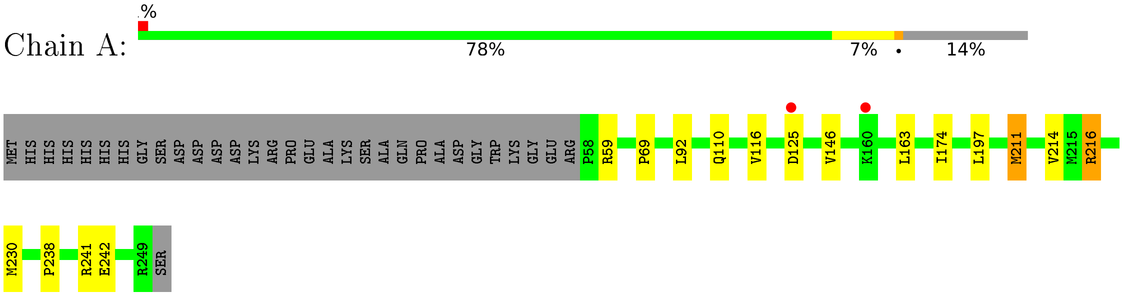
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	N	34	Total O 34 34	0	0
4	O	30	Total O 30 30	0	0
4	P	19	Total O 19 19	0	0
4	Q	33	Total O 33 33	0	0
4	R	32	Total O 32 32	0	0
4	S	24	Total O 24 24	0	0
4	T	31	Total O 31 31	0	0

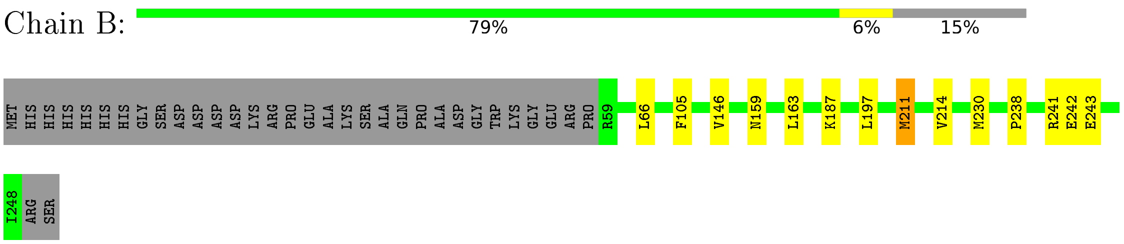
3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

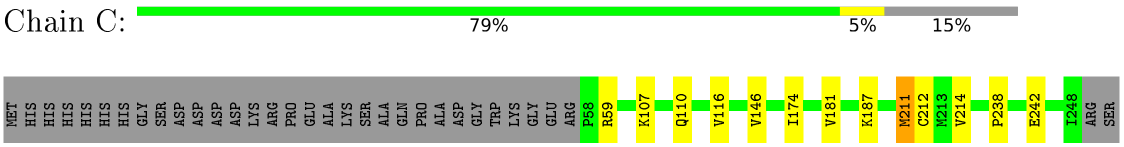
- Molecule 1: GTP cyclohydrolase 1



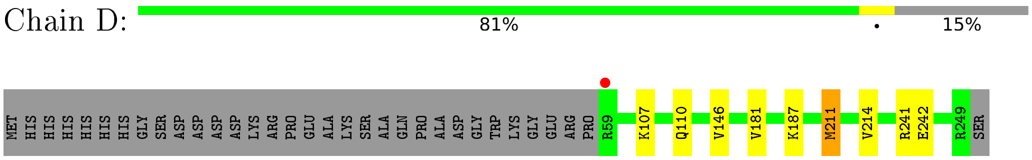
- Molecule 1: GTP cyclohydrolase 1



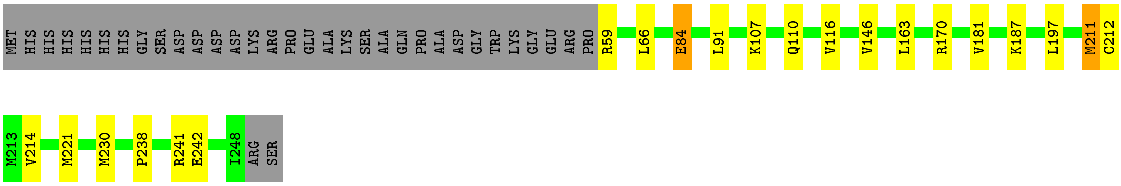
- Molecule 1: GTP cyclohydrolase 1



- Molecule 1: GTP cyclohydrolase 1

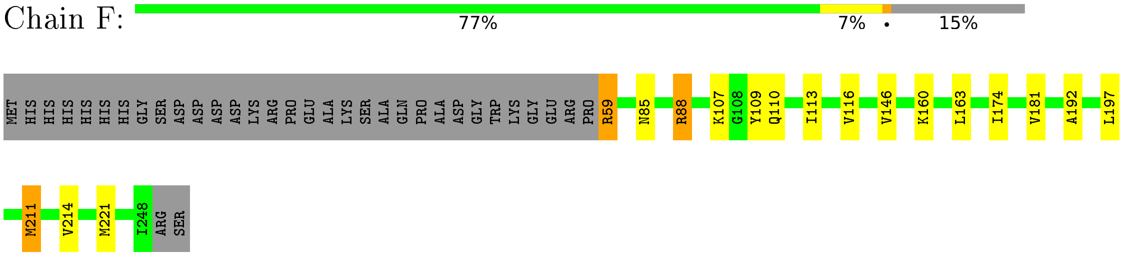


- Molecule 1: GTP cyclohydrolase 1



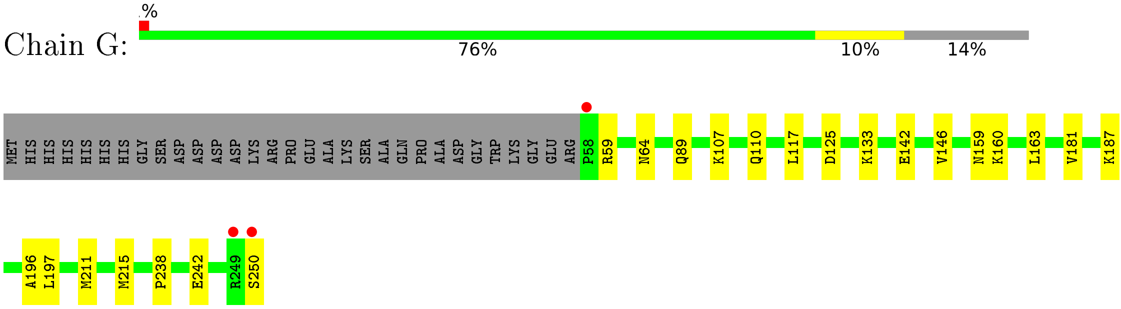
- Molecule 1: GTP cyclohydrolase 1

Chain F:



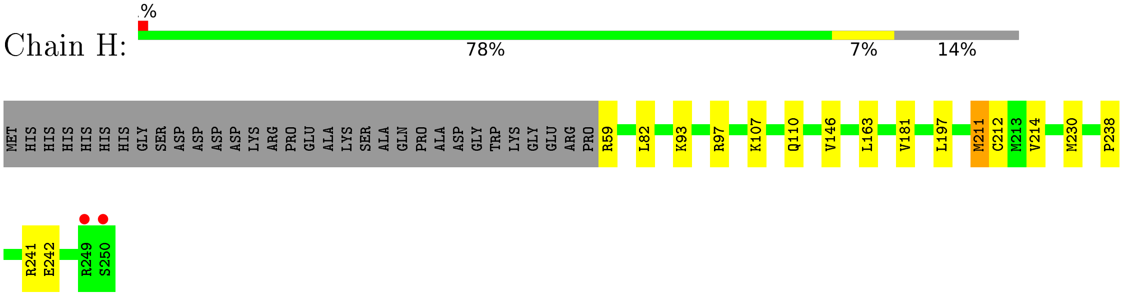
- Molecule 1: GTP cyclohydrolase 1

Chain G:



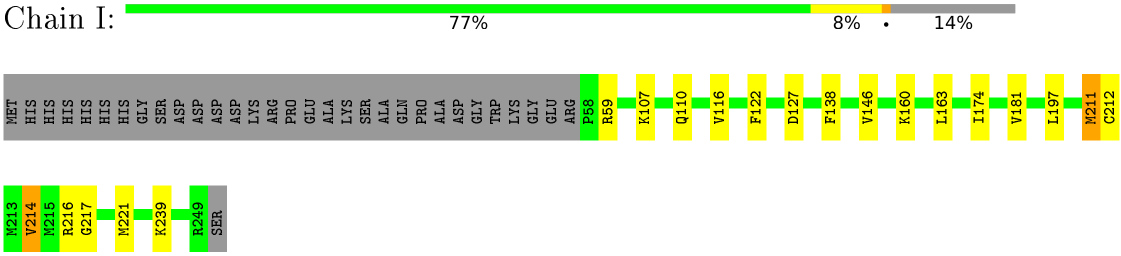
- Molecule 1: GTP cyclohydrolase 1

Chain H:

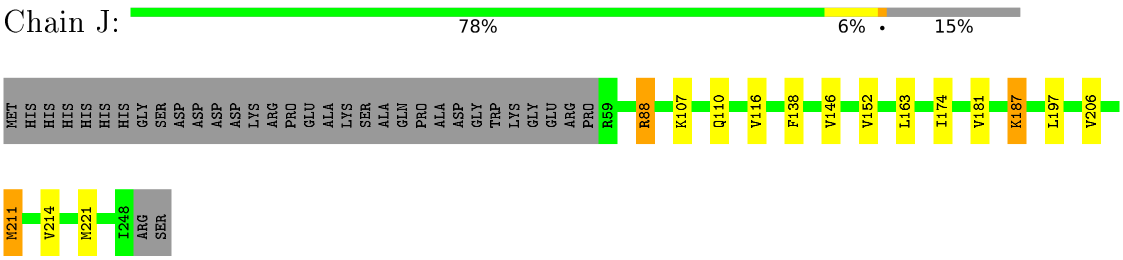


- Molecule 1: GTP cyclohydrolase 1

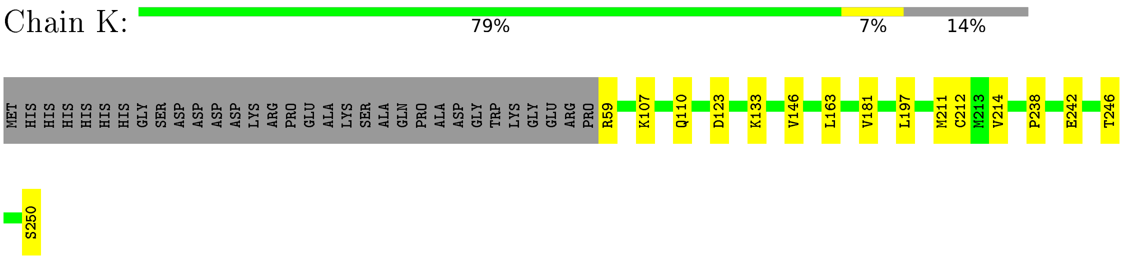
Chain I:



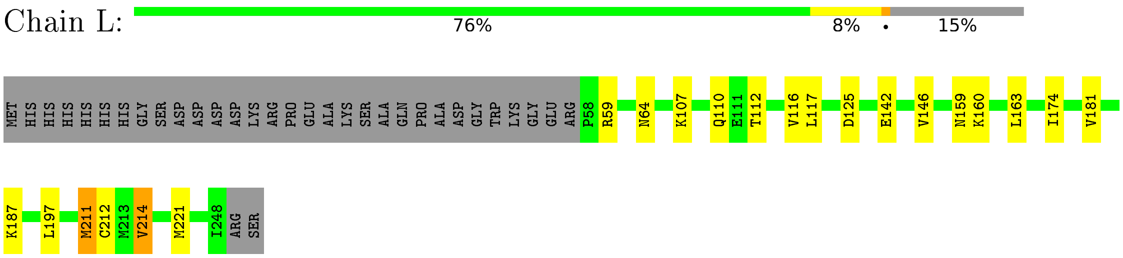
- Molecule 1: GTP cyclohydrolase 1



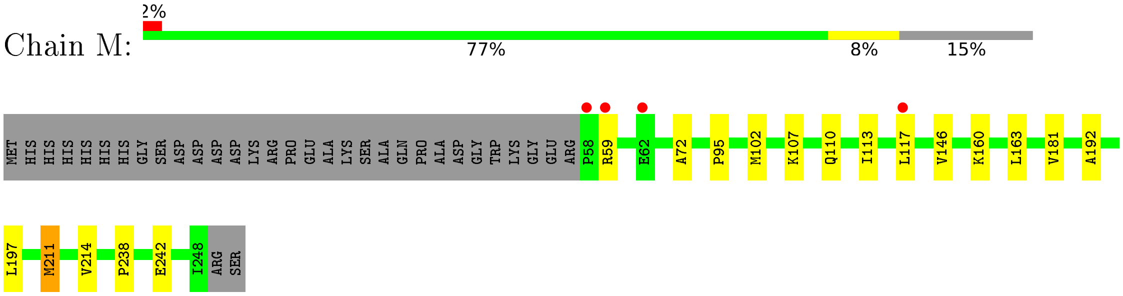
- Molecule 1: GTP cyclohydrolase 1



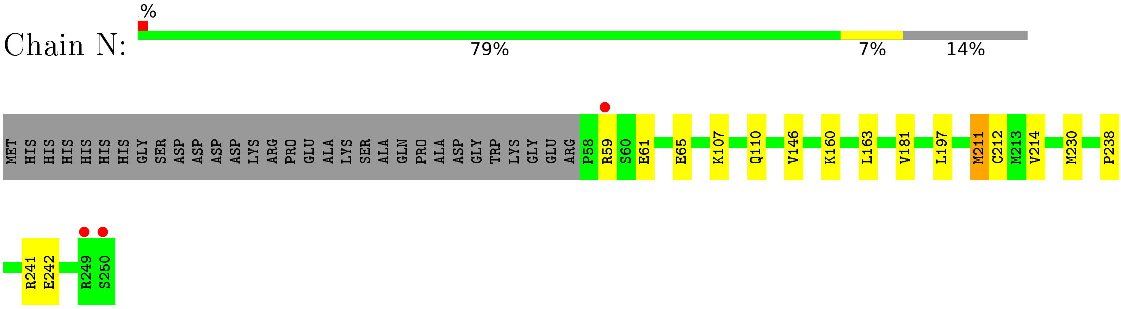
- Molecule 1: GTP cyclohydrolase 1



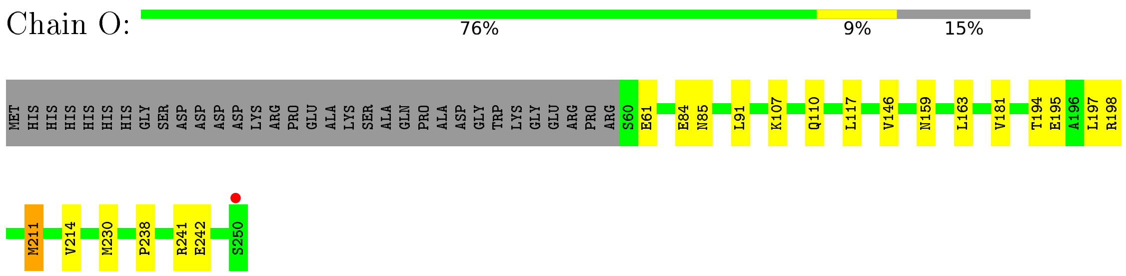
- Molecule 1: GTP cyclohydrolase 1



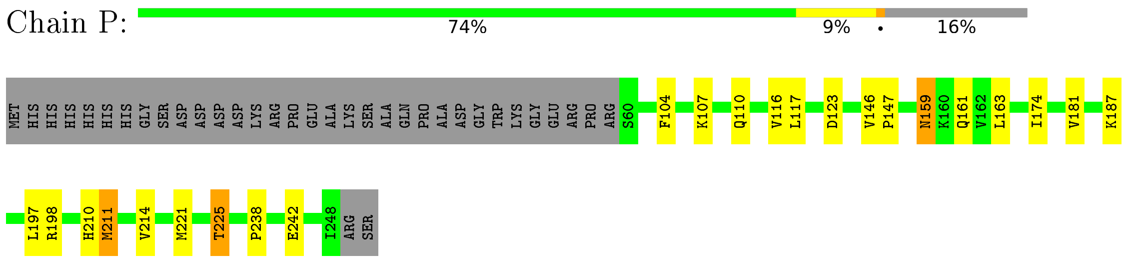
- Molecule 1: GTP cyclohydrolase 1



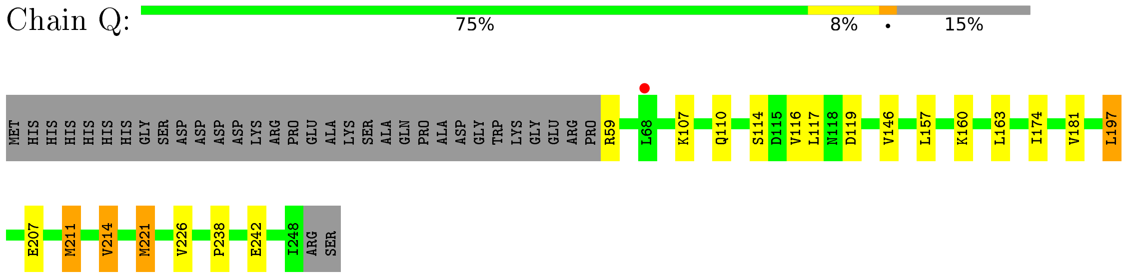
- Molecule 1: GTP cyclohydrolase 1



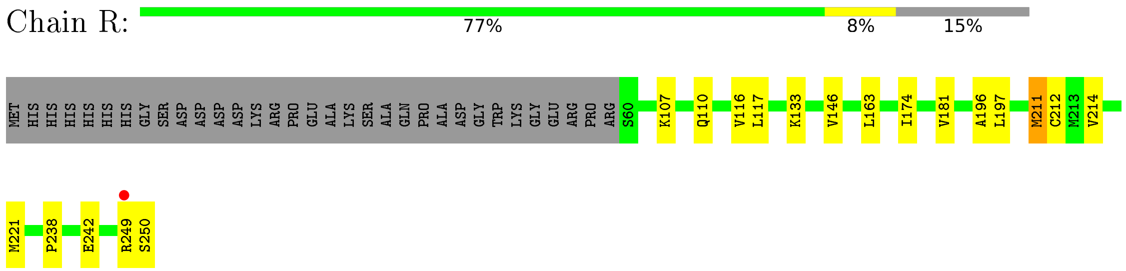
- Molecule 1: GTP cyclohydrolase 1



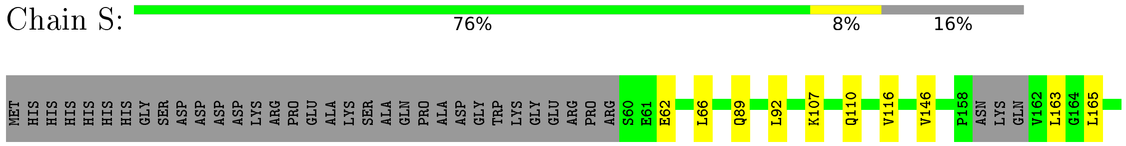
- Molecule 1: GTP cyclohydrolase 1

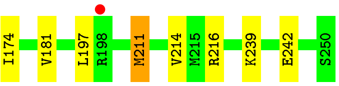


- Molecule 1: GTP cyclohydrolase 1

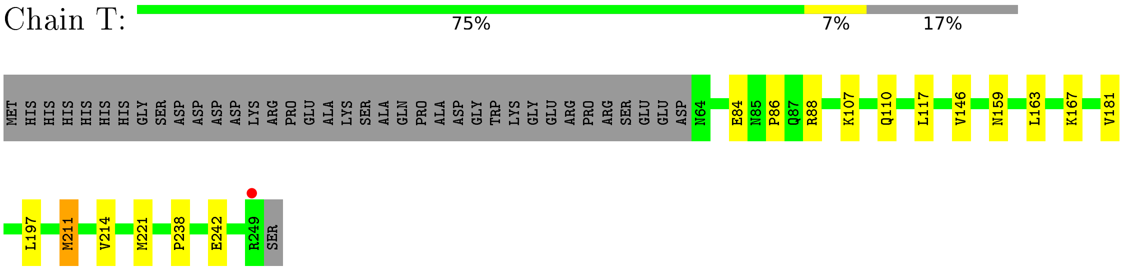


- Molecule 1: GTP cyclohydrolase 1





- Molecule 1: GTP cyclohydrolase 1



4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	87.86Å 88.59Å 163.57Å 85.22° 88.91° 83.55°	Depositor
Resolution (Å)	162.99 – 2.21 162.99 – 2.21	Depositor EDS
% Data completeness (in resolution range)	57.9 (162.99-2.21) 58.0 (162.99-2.21)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	1.29 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.183 , 0.208 0.185 , 0.208	Depositor DCC
R_{free} test set	2913 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å^2)	42.4	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 36.3	EDS
L-test for twinning[2]	$< \|L\| >$ = 0.51, $< L^2 >$ = 0.34	Xtriage
Estimated twinning fraction	0.003 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	31346	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.43	0/1540	0.64	0/2079
1	B	0.44	0/1521	0.65	0/2054
1	C	0.42	0/1529	0.62	0/2065
1	D	0.42	0/1532	0.62	0/2068
1	E	0.44	0/1521	0.63	0/2054
1	F	0.47	0/1521	0.63	0/2054
1	G	0.43	0/1546	0.63	0/2087
1	H	0.42	0/1549	0.63	0/2090
1	I	0.43	0/1540	0.64	0/2079
1	J	0.42	0/1521	0.64	0/2054
1	K	0.43	0/1538	0.62	0/2076
1	L	0.40	0/1529	0.61	0/2065
1	M	0.43	0/1529	0.65	0/2065
1	N	0.42	0/1546	0.64	0/2087
1	O	0.41	0/1527	0.64	0/2062
1	P	0.39	0/1510	0.64	0/2040
1	Q	0.39	0/1521	0.62	1/2054 (0.0%)
1	R	0.41	0/1527	0.62	0/2062
1	S	0.43	0/1500	0.65	0/2025
1	T	0.41	0/1489	0.63	0/2011
All	All	0.42	0/30536	0.63	1/41231 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	Q	221	MET	CB-CG-SD	-5.28	96.57	112.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1515	0	1539	9	0
1	B	1497	0	1518	6	0
1	C	1504	0	1526	7	0
1	D	1508	0	1531	3	0
1	E	1497	0	1518	14	0
1	F	1497	0	1518	10	0
1	G	1521	0	1544	12	0
1	H	1525	0	1548	12	0
1	I	1515	0	1539	11	0
1	J	1497	0	1518	9	0
1	K	1514	0	1536	12	0
1	L	1504	0	1526	12	0
1	M	1504	0	1526	11	0
1	N	1521	0	1544	8	0
1	O	1503	0	1523	11	0
1	P	1486	0	1505	13	0
1	Q	1497	0	1518	10	0
1	R	1503	0	1523	10	0
1	S	1477	0	1495	8	0
1	T	1465	0	1497	8	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
3	A	32	0	0	0	0
3	B	32	0	0	0	0
3	C	32	0	0	1	0
3	D	32	0	0	0	0
3	E	32	0	0	0	0
3	F	32	0	0	0	0
3	G	32	0	0	0	0
3	H	32	0	0	0	0
3	I	32	0	0	0	0
3	J	32	0	0	0	0
3	K	32	0	0	0	0
3	L	32	0	0	0	0
3	M	32	0	0	0	0
3	N	32	0	0	0	0
3	O	32	0	0	0	0
3	P	32	0	0	0	0
3	Q	32	0	0	1	0
3	R	32	0	0	0	0
3	S	32	0	0	0	0
3	T	32	0	0	0	0
4	A	34	0	0	1	0
4	B	46	0	0	0	0
4	C	30	0	0	0	0
4	D	32	0	0	0	0
4	E	35	0	0	1	0
4	F	38	0	0	0	0
4	G	33	0	0	1	0
4	H	29	0	0	0	0
4	I	34	0	0	2	0
4	J	33	0	0	1	0
4	K	34	0	0	0	0
4	L	24	0	0	1	0
4	M	31	0	0	1	0
4	N	34	0	0	2	0
4	O	30	0	0	0	0
4	P	19	0	0	1	0
4	Q	33	0	0	0	0
4	R	32	0	0	0	0
4	S	24	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	T	31	0	0	1	0
All	All	31346	0	30492	186	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 186 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:R:133:LYS:NZ	1:R:250:SER:HB3	1.84	0.92
1:E:84:GLU:HG3	1:E:91:LEU:HD11	1.58	0.85
1:R:133:LYS:HZ2	1:R:250:SER:HB3	1.41	0.84
1:O:238:PRO:O	1:O:242:GLU:HG2	1.86	0.76
1:E:163:LEU:HB2	1:E:197:LEU:HD11	1.66	0.75

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	190/224 (85%)	185 (97%)	5 (3%)	0	100	100
1	B	188/224 (84%)	186 (99%)	2 (1%)	0	100	100
1	C	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	D	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	E	188/224 (84%)	186 (99%)	2 (1%)	0	100	100
1	F	188/224 (84%)	186 (99%)	2 (1%)	0	100	100
1	G	191/224 (85%)	189 (99%)	2 (1%)	0	100	100
1	H	191/224 (85%)	189 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	190/224 (85%)	188 (99%)	2 (1%)	0	100	100
1	J	188/224 (84%)	186 (99%)	2 (1%)	0	100	100
1	K	190/224 (85%)	187 (98%)	3 (2%)	0	100	100
1	L	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	M	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	N	191/224 (85%)	189 (99%)	2 (1%)	0	100	100
1	O	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	P	187/224 (84%)	185 (99%)	2 (1%)	0	100	100
1	Q	188/224 (84%)	186 (99%)	2 (1%)	0	100	100
1	R	189/224 (84%)	187 (99%)	2 (1%)	0	100	100
1	S	184/224 (82%)	184 (100%)	0	0	100	100
1	T	184/224 (82%)	181 (98%)	3 (2%)	0	100	100
All	All	3772/4480 (84%)	3729 (99%)	43 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	169/195 (87%)	164 (97%)	5 (3%)	41	53
1	B	167/195 (86%)	162 (97%)	5 (3%)	41	53
1	C	168/195 (86%)	164 (98%)	4 (2%)	49	62
1	D	168/195 (86%)	163 (97%)	5 (3%)	41	53
1	E	167/195 (86%)	162 (97%)	5 (3%)	41	53
1	F	167/195 (86%)	161 (96%)	6 (4%)	35	45
1	G	170/195 (87%)	165 (97%)	5 (3%)	42	54
1	H	170/195 (87%)	167 (98%)	3 (2%)	59	72
1	I	169/195 (87%)	164 (97%)	5 (3%)	41	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	167/195 (86%)	162 (97%)	5 (3%)	41	53
1	K	169/195 (87%)	167 (99%)	2 (1%)	71	83
1	L	168/195 (86%)	161 (96%)	7 (4%)	30	38
1	M	168/195 (86%)	165 (98%)	3 (2%)	59	72
1	N	170/195 (87%)	166 (98%)	4 (2%)	49	62
1	O	168/195 (86%)	162 (96%)	6 (4%)	35	45
1	P	166/195 (85%)	158 (95%)	8 (5%)	25	32
1	Q	167/195 (86%)	161 (96%)	6 (4%)	35	45
1	R	168/195 (86%)	163 (97%)	5 (3%)	41	53
1	S	165/195 (85%)	160 (97%)	5 (3%)	41	53
1	T	163/195 (84%)	157 (96%)	6 (4%)	34	43
All	All	3354/3900 (86%)	3254 (97%)	100 (3%)	41	53

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	187	LYS
1	L	211	MET
1	S	211	MET
1	J	211	MET
1	L	112	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	222	ASN
1	M	70	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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 40 ligands modelled in this entry, 20 are monoatomic - leaving 20 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	QBQ	R	302	-	26,34,34	0.95	1 (3%)	34,54,54	3.04	5 (14%)
3	QBQ	A	302	-	26,34,34	0.83	1 (3%)	34,54,54	2.98	3 (8%)
3	QBQ	T	302	-	26,34,34	0.91	1 (3%)	34,54,54	3.03	3 (8%)
3	QBQ	C	302	-	26,34,34	0.90	1 (3%)	34,54,54	2.98	3 (8%)
3	QBQ	E	302	-	26,34,34	0.92	1 (3%)	34,54,54	3.04	6 (17%)
3	QBQ	H	302	-	26,34,34	0.93	1 (3%)	34,54,54	3.02	3 (8%)
3	QBQ	G	302	-	26,34,34	0.86	1 (3%)	34,54,54	3.05	5 (14%)
3	QBQ	J	302	-	26,34,34	0.86	1 (3%)	34,54,54	2.99	3 (8%)
3	QBQ	L	302	-	26,34,34	0.87	1 (3%)	34,54,54	2.97	3 (8%)
3	QBQ	N	302	-	26,34,34	0.86	1 (3%)	34,54,54	3.00	6 (17%)
3	QBQ	B	302	-	26,34,34	0.97	2 (7%)	34,54,54	2.98	4 (11%)
3	QBQ	Q	302	-	26,34,34	0.87	1 (3%)	34,54,54	3.05	3 (8%)
3	QBQ	D	302	-	26,34,34	0.83	1 (3%)	34,54,54	3.01	3 (8%)
3	QBQ	S	302	-	26,34,34	0.92	1 (3%)	34,54,54	2.99	3 (8%)
3	QBQ	F	302	-	26,34,34	0.86	1 (3%)	34,54,54	3.00	4 (11%)
3	QBQ	I	302	-	26,34,34	0.93	1 (3%)	34,54,54	3.00	4 (11%)
3	QBQ	K	302	-	26,34,34	0.82	1 (3%)	34,54,54	3.01	4 (11%)
3	QBQ	M	302	-	26,34,34	0.82	1 (3%)	34,54,54	3.00	3 (8%)
3	QBQ	P	302	-	26,34,34	0.92	1 (3%)	34,54,54	3.02	3 (8%)
3	QBQ	O	302	-	26,34,34	0.91	1 (3%)	34,54,54	2.96	3 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	QBQ	R	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	A	302	-	-	6/18/38/38	0/3/3/3
3	QBQ	T	302	-	-	4/18/38/38	0/3/3/3
3	QBQ	C	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	E	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	H	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	G	302	-	-	4/18/38/38	0/3/3/3
3	QBQ	J	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	L	302	-	-	3/18/38/38	0/3/3/3
3	QBQ	N	302	-	-	4/18/38/38	0/3/3/3
3	QBQ	B	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	Q	302	-	-	4/18/38/38	0/3/3/3
3	QBQ	D	302	-	-	8/18/38/38	0/3/3/3
3	QBQ	S	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	F	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	I	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	K	302	-	-	3/18/38/38	0/3/3/3
3	QBQ	M	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	P	302	-	-	5/18/38/38	0/3/3/3
3	QBQ	O	302	-	-	5/18/38/38	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	302	QBQ	C10-N3	3.42	1.39	1.33
3	H	302	QBQ	C10-N3	3.41	1.39	1.33
3	R	302	QBQ	C10-N3	3.38	1.38	1.33
3	P	302	QBQ	C10-N3	3.36	1.38	1.33
3	T	302	QBQ	C10-N3	3.34	1.38	1.33

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	Q	302	QBQ	C2-C10-N3	-15.77	113.40	124.40
3	H	302	QBQ	C2-C10-N3	-15.67	113.47	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	302	QBQ	C2-C10-N3	-15.64	113.50	124.40
3	R	302	QBQ	C2-C10-N3	-15.59	113.53	124.40
3	G	302	QBQ	C2-C10-N3	-15.57	113.54	124.40

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	302	QBQ	P1-O7-P2-O9
3	B	302	QBQ	P1-O7-P2-O9
3	S	302	QBQ	P1-O7-P2-O9
3	A	302	QBQ	P1-O7-P2-O9
3	H	302	QBQ	P1-O7-P2-O9

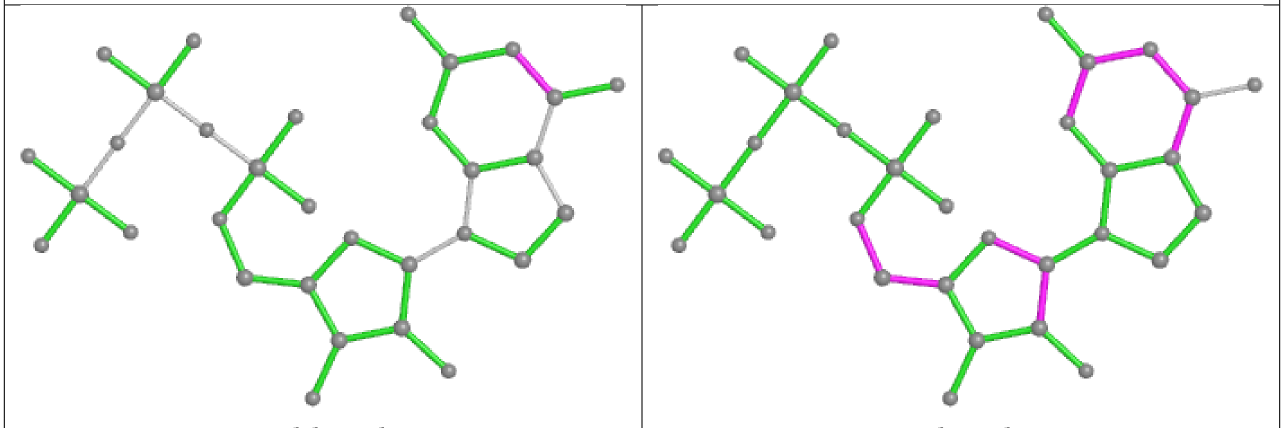
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	302	QBQ	1	0
3	Q	302	QBQ	1	0

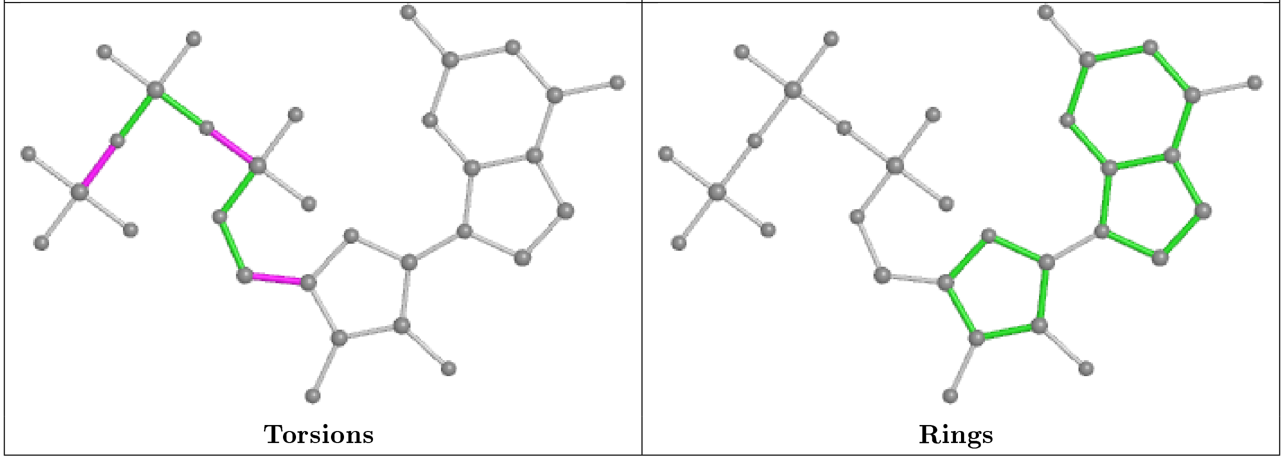
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand QBQ R 302



Bond lengths

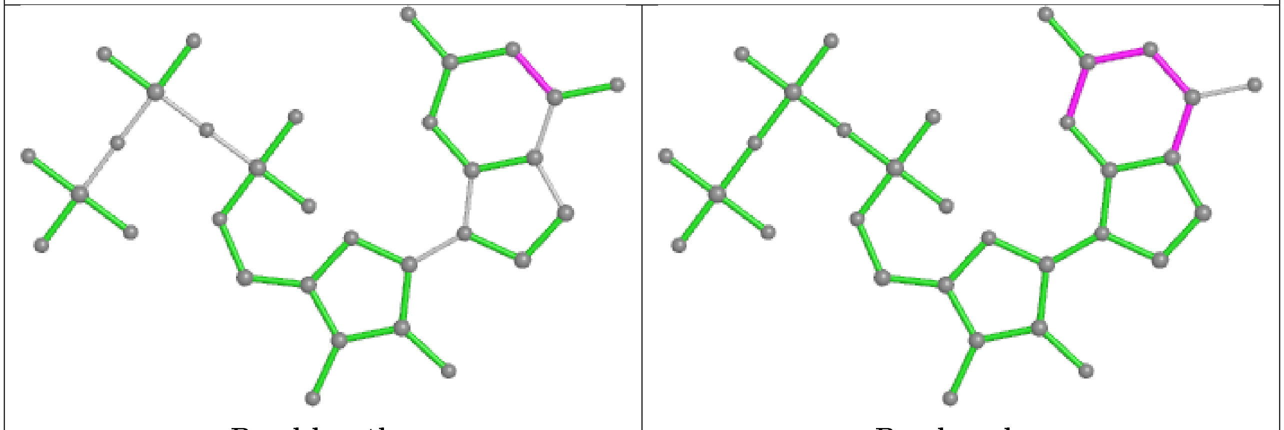
Bond angles



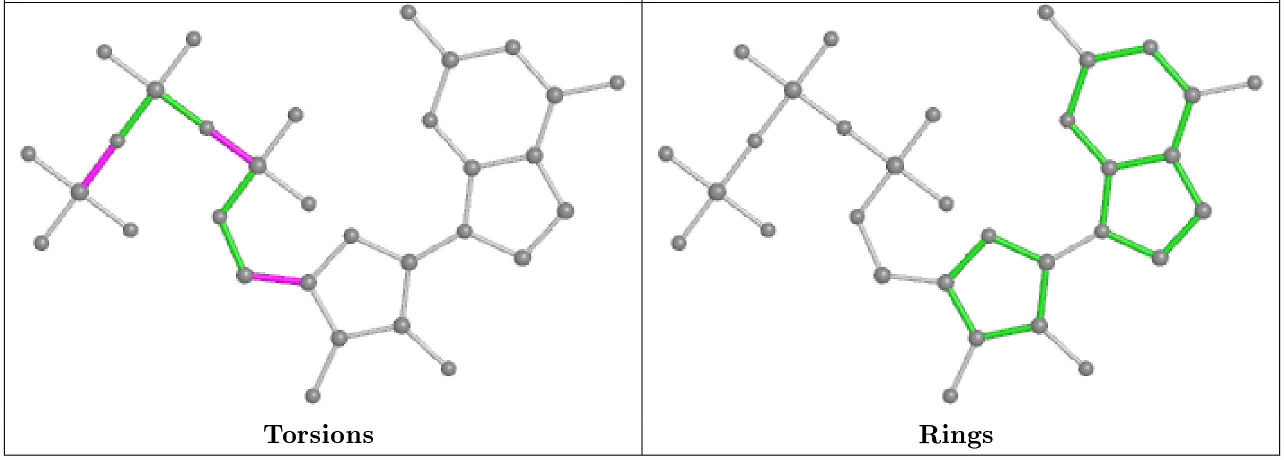
Torsions

Rings

Ligand QBQ A 302

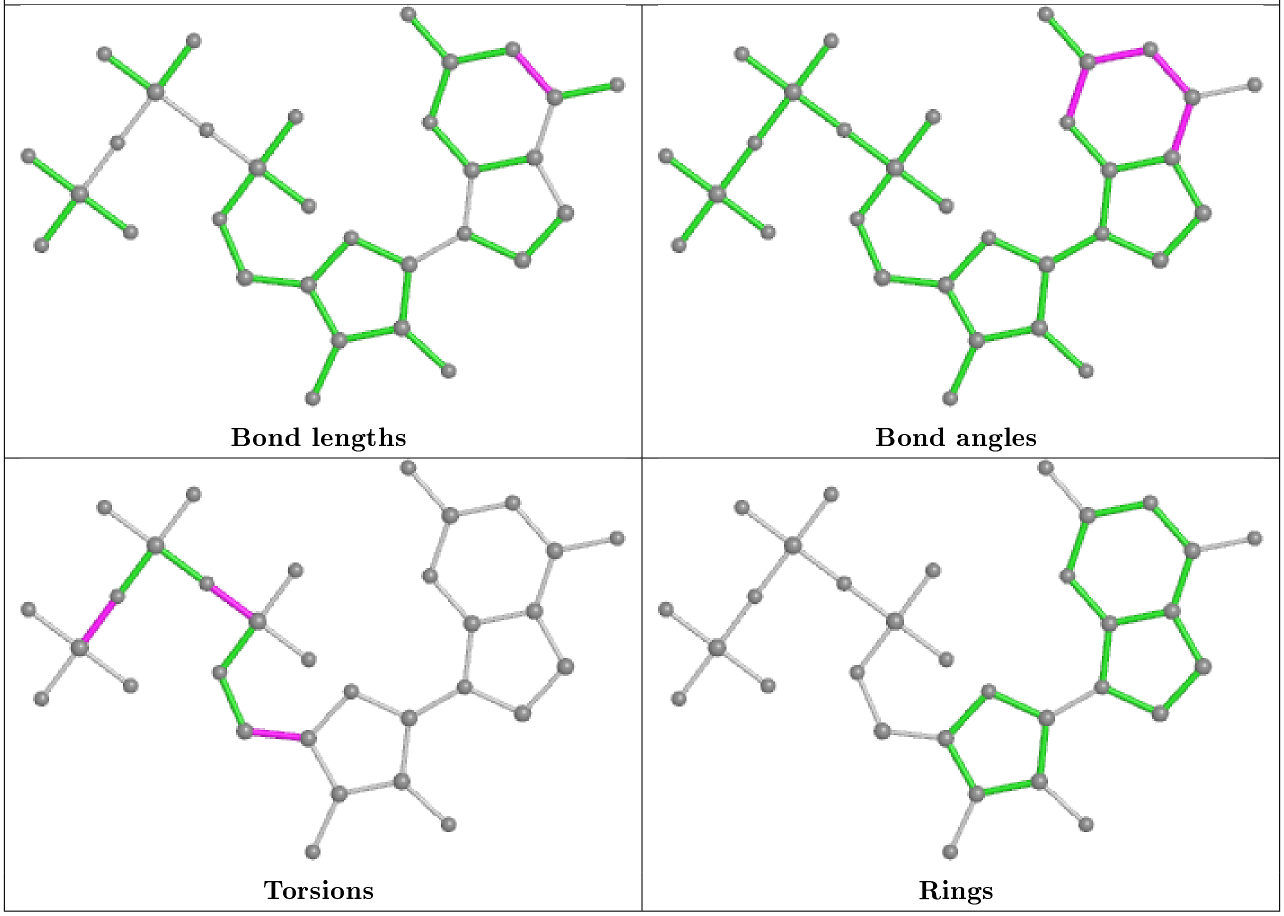


Bond lengths **Bond angles**



Torsions **Rings**

Ligand QBQ T 302



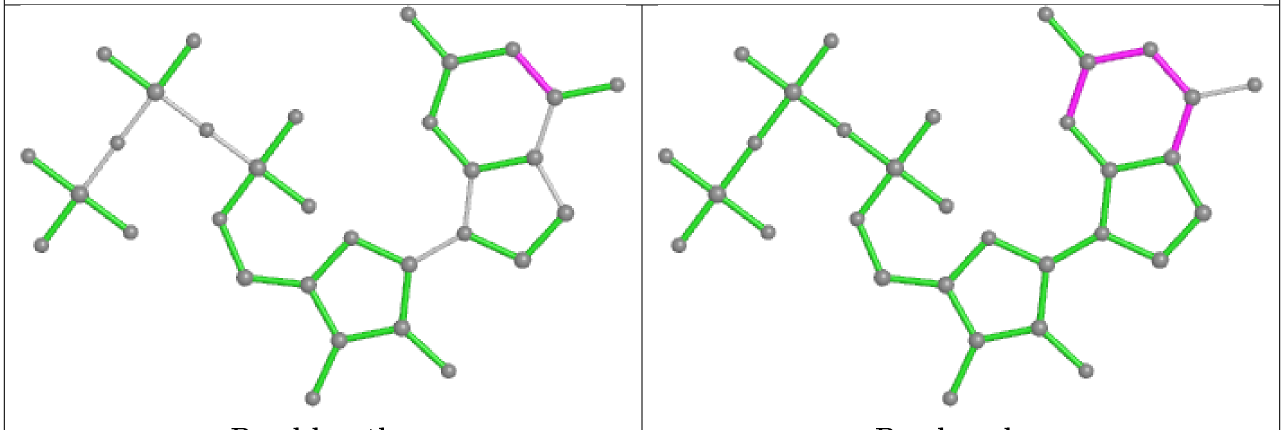
Bond lengths

Bond angles

Torsions

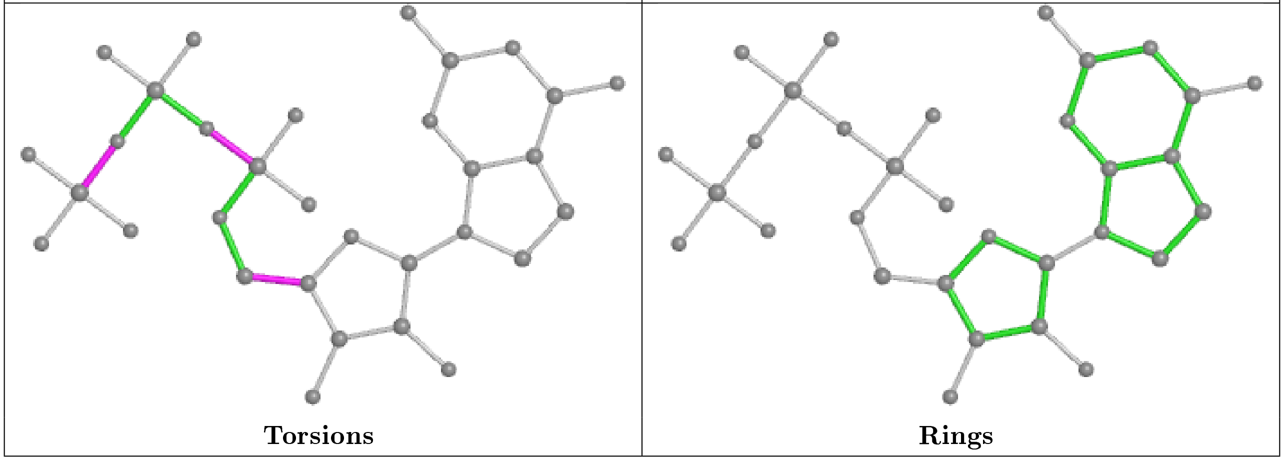
Rings

Ligand QBQ C 302



Bond lengths

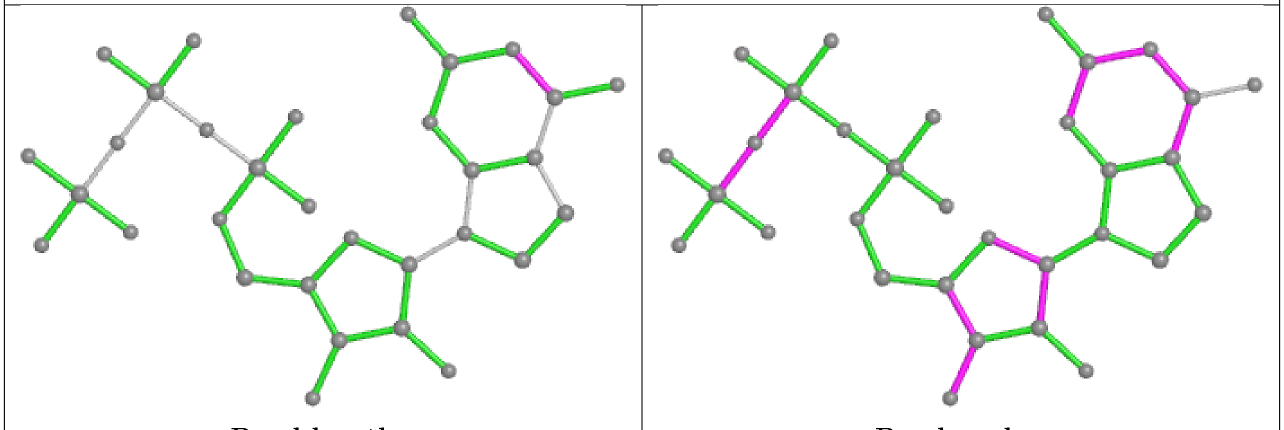
Bond angles



Torsions

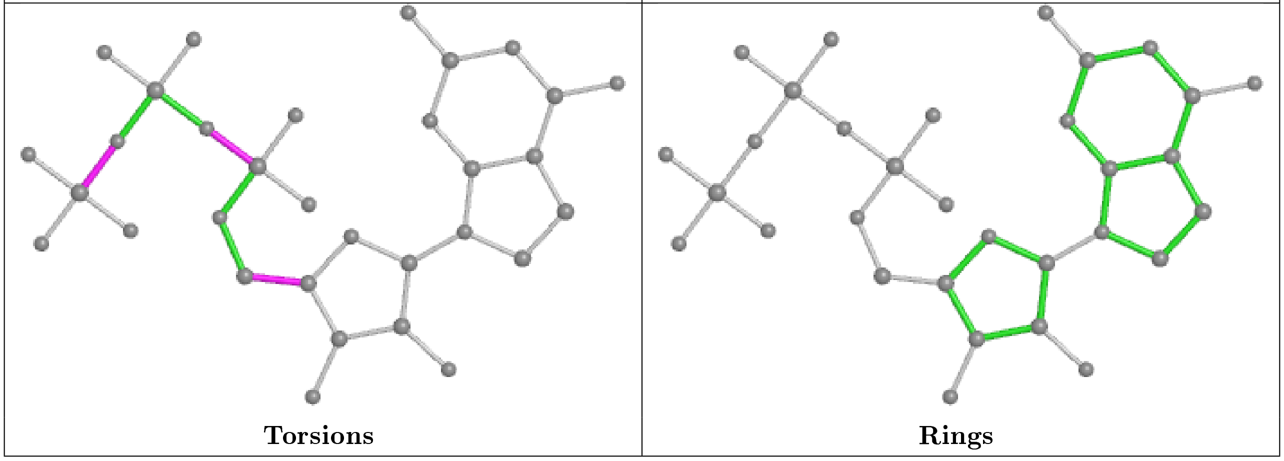
Rings

Ligand QBQ E 302



Bond lengths

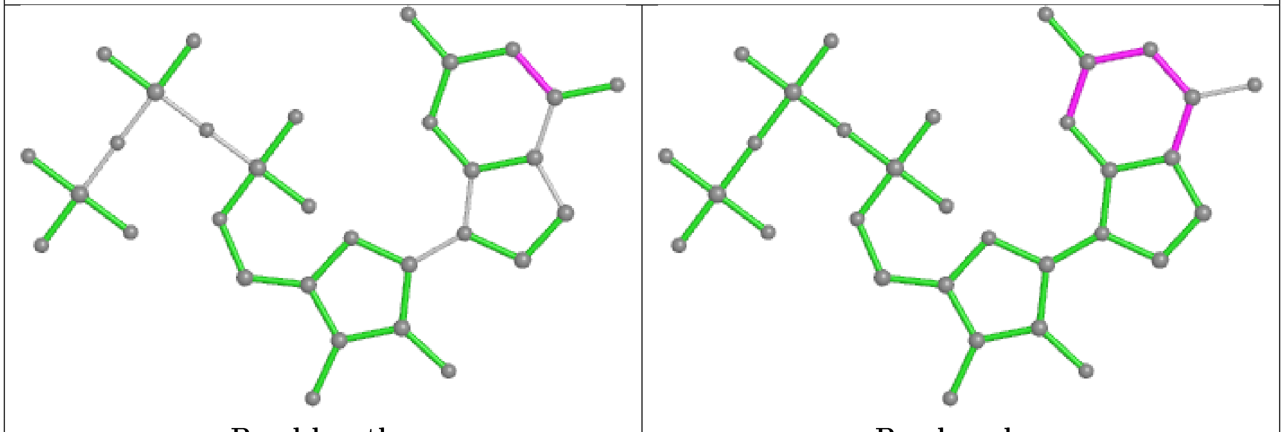
Bond angles



Torsions

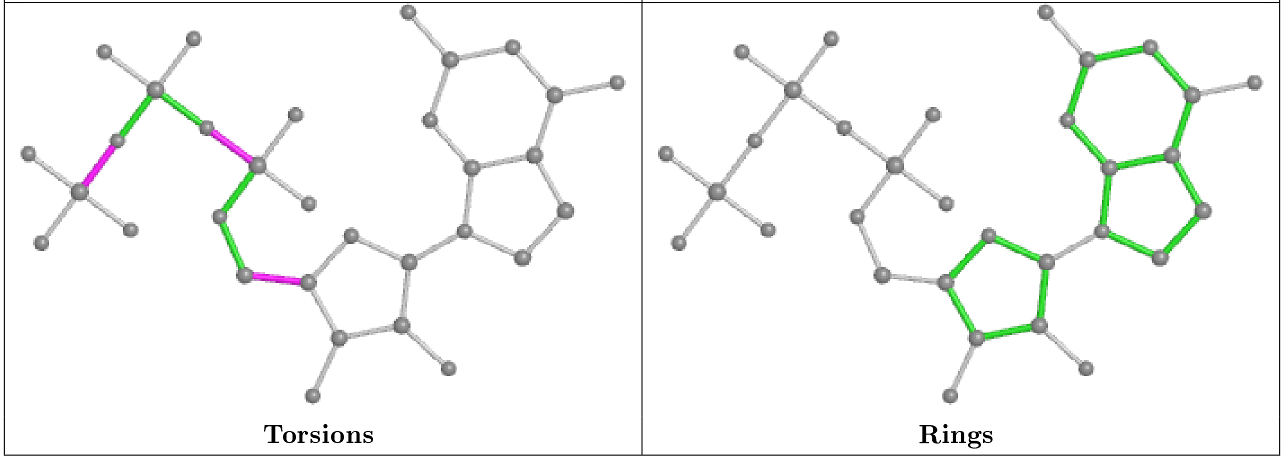
Rings

Ligand QBQ H 302



Bond lengths

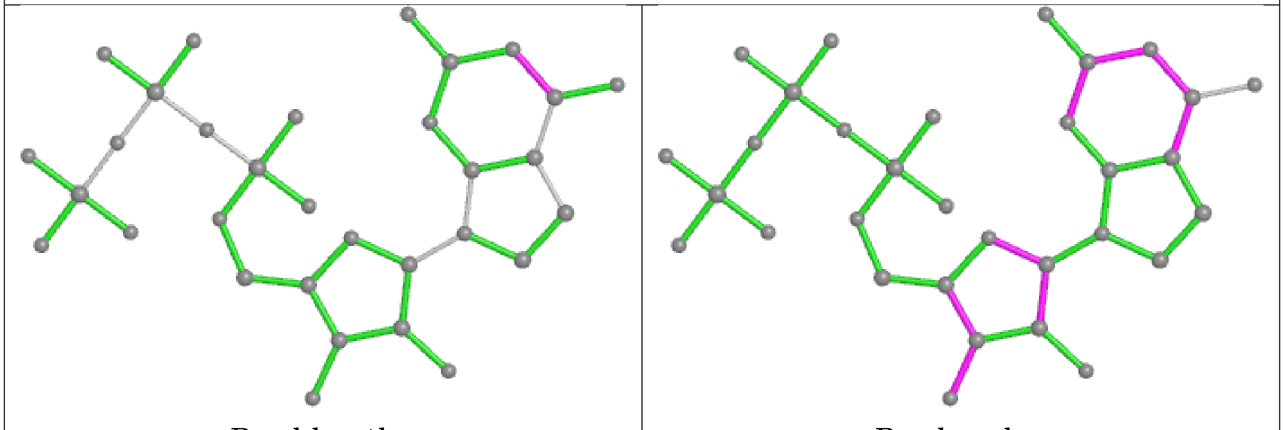
Bond angles



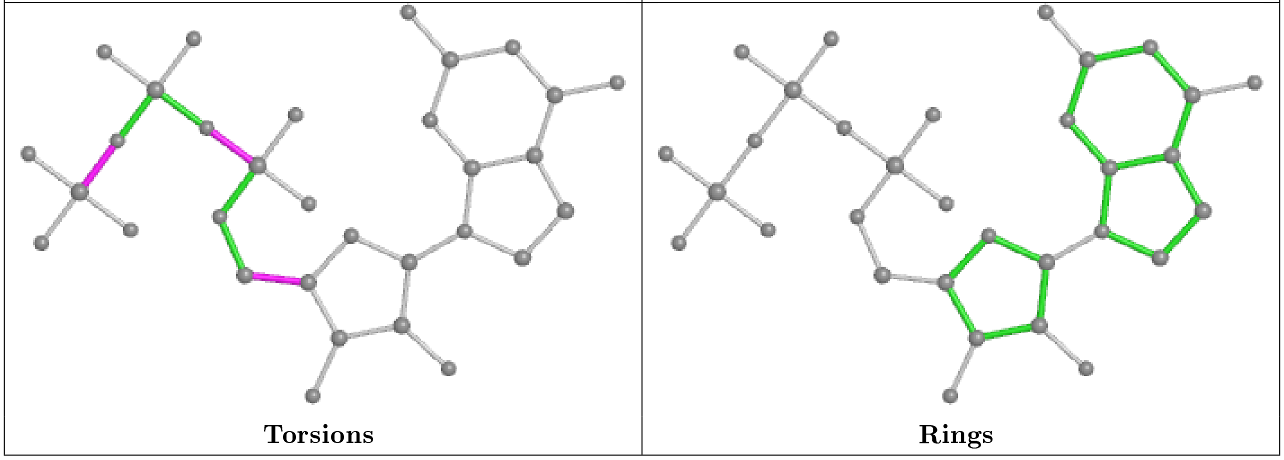
Torsions

Rings

Ligand QBQ G 302

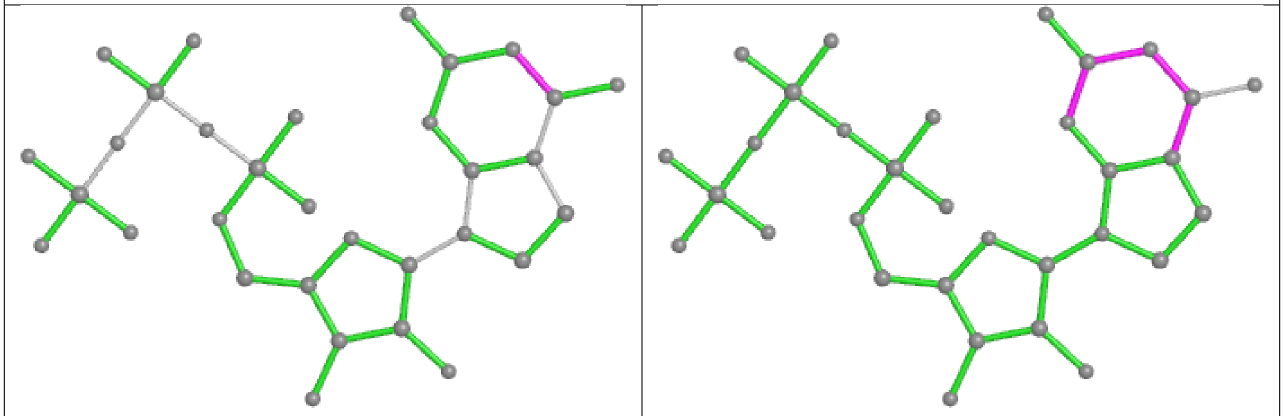


Bond lengths **Bond angles**

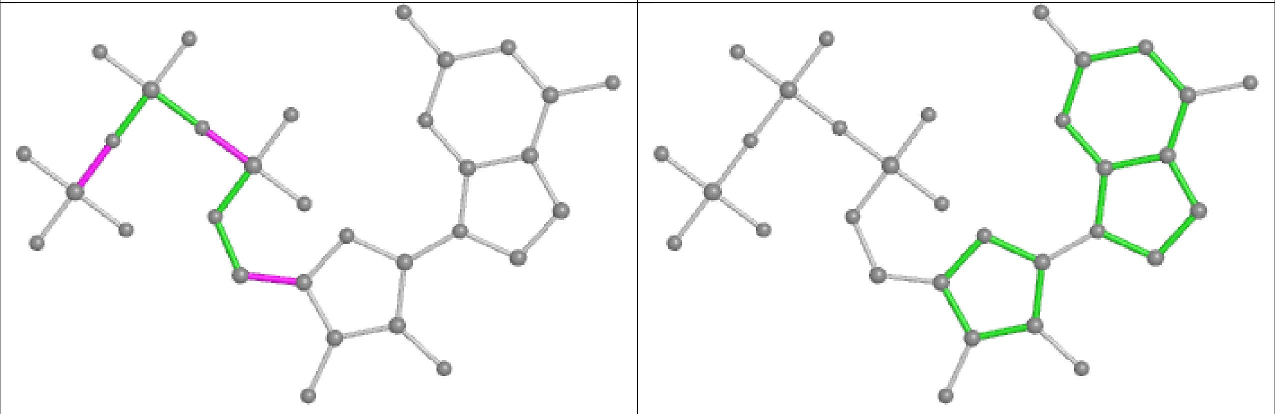


Torsions **Rings**

Ligand QBQ J 302

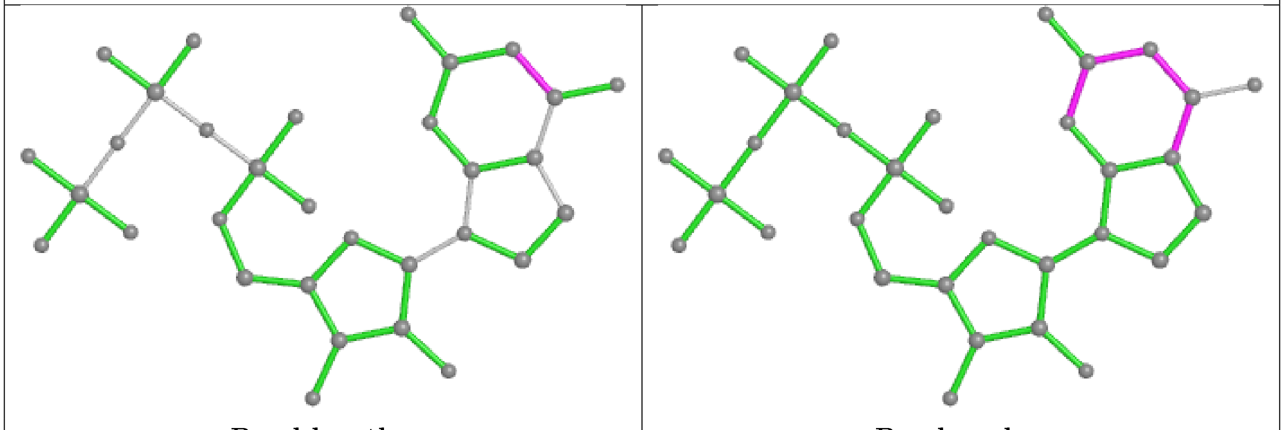


Bond lengths Bond angles

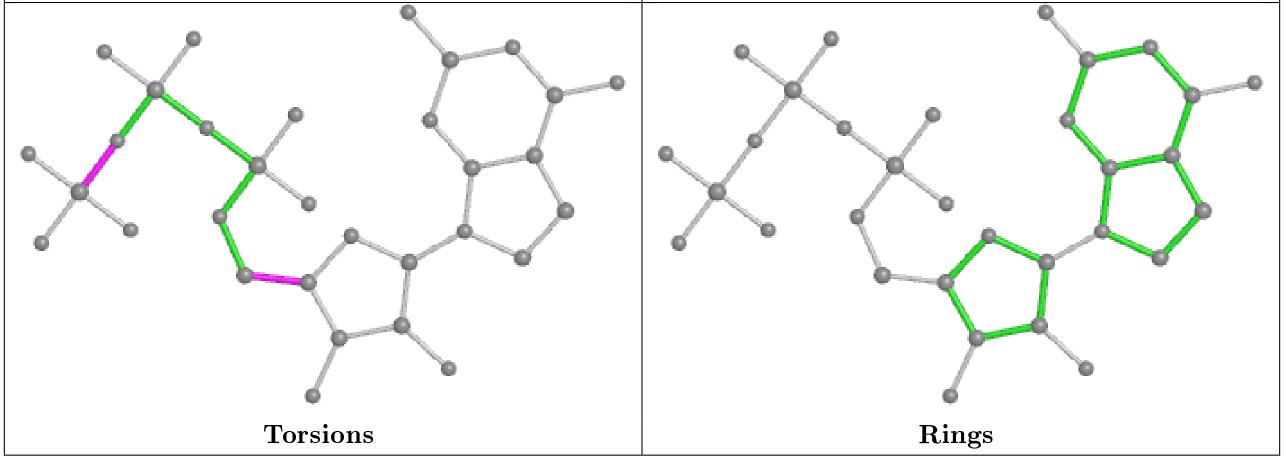


Torsions Rings

Ligand QBQ L 302

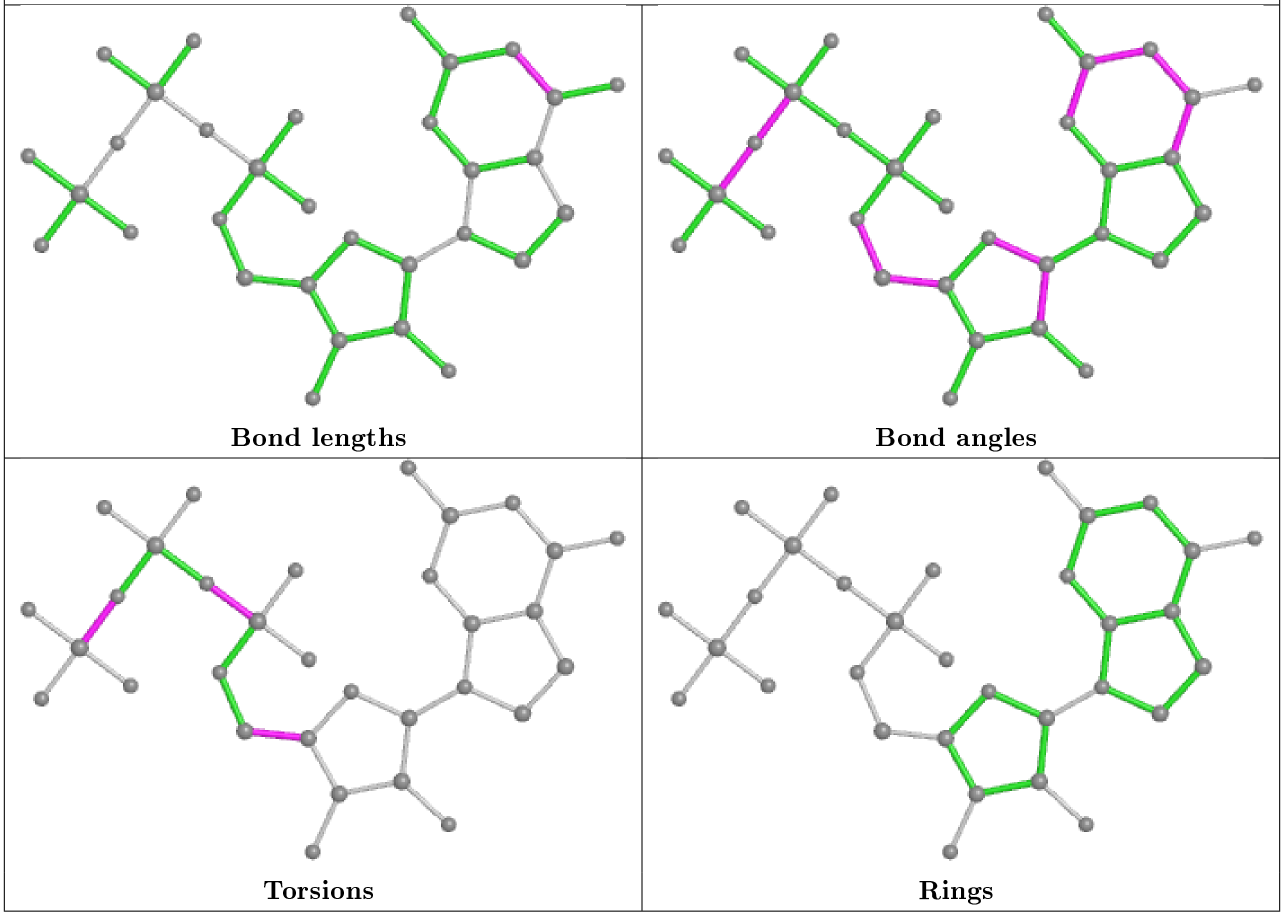


Bond lengths **Bond angles**



Torsions **Rings**

Ligand QBQ N 302



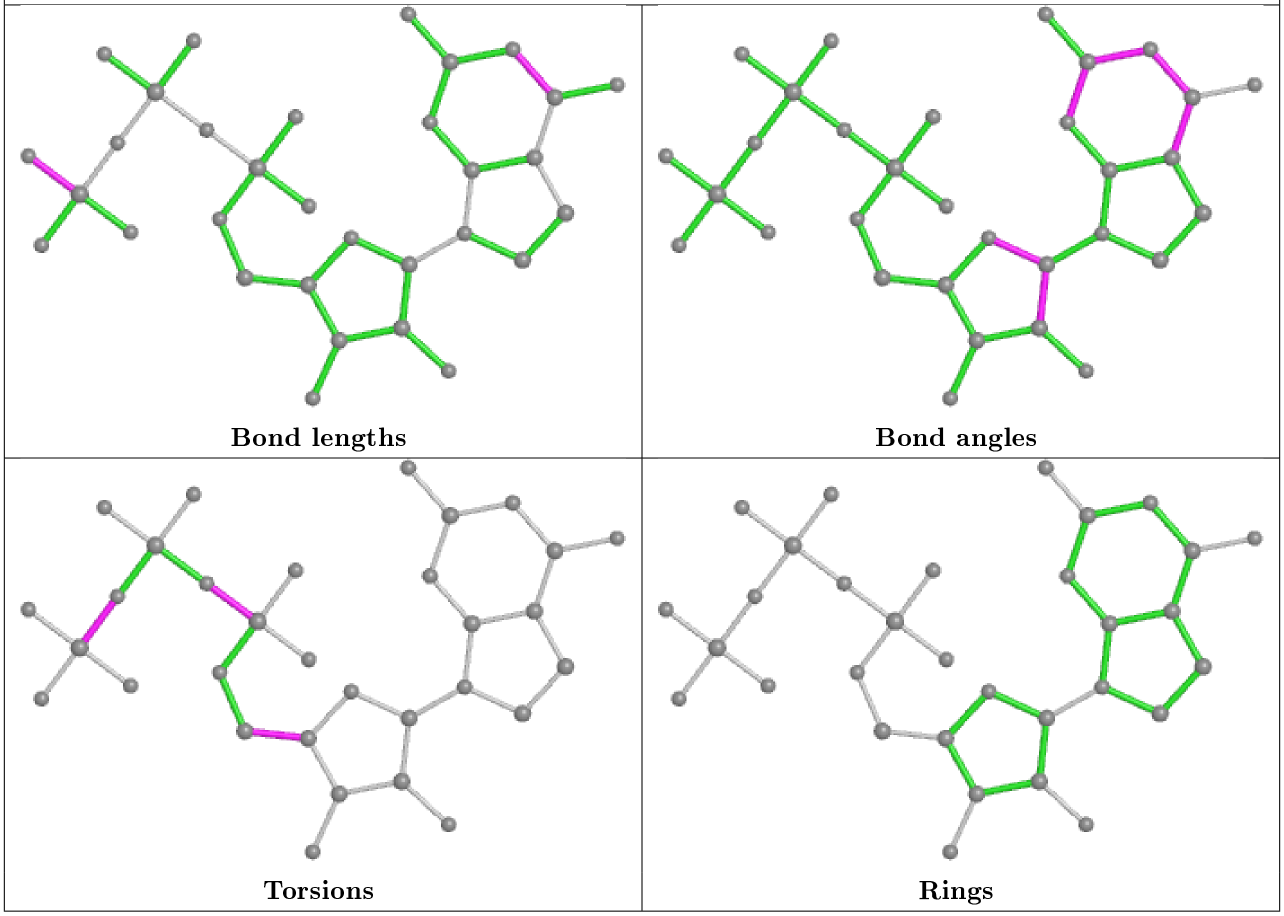
Bond lengths

Bond angles

Torsions

Rings

Ligand QBQ B 302



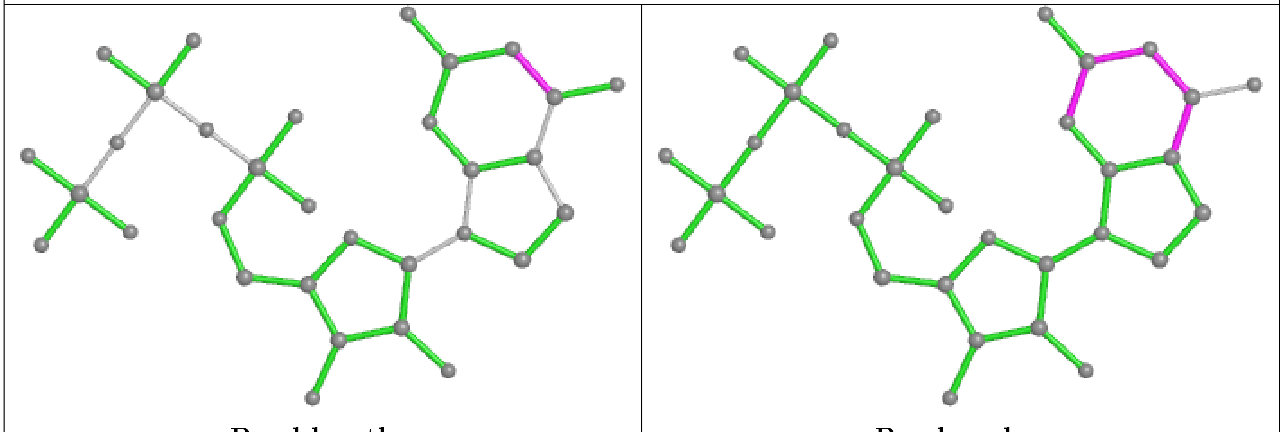
Bond lengths

Bond angles

Torsions

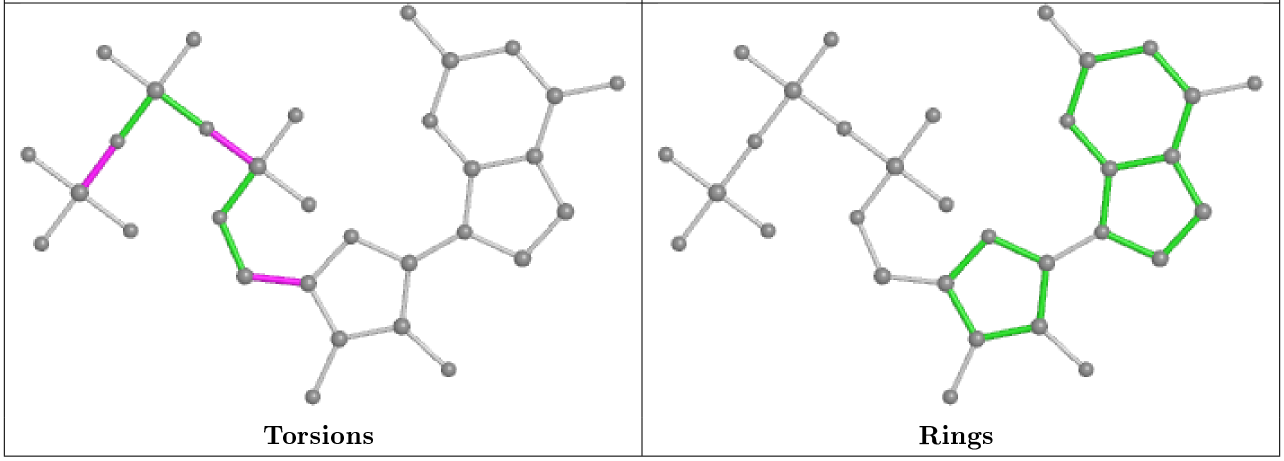
Rings

Ligand QBQ Q 302



Bond lengths

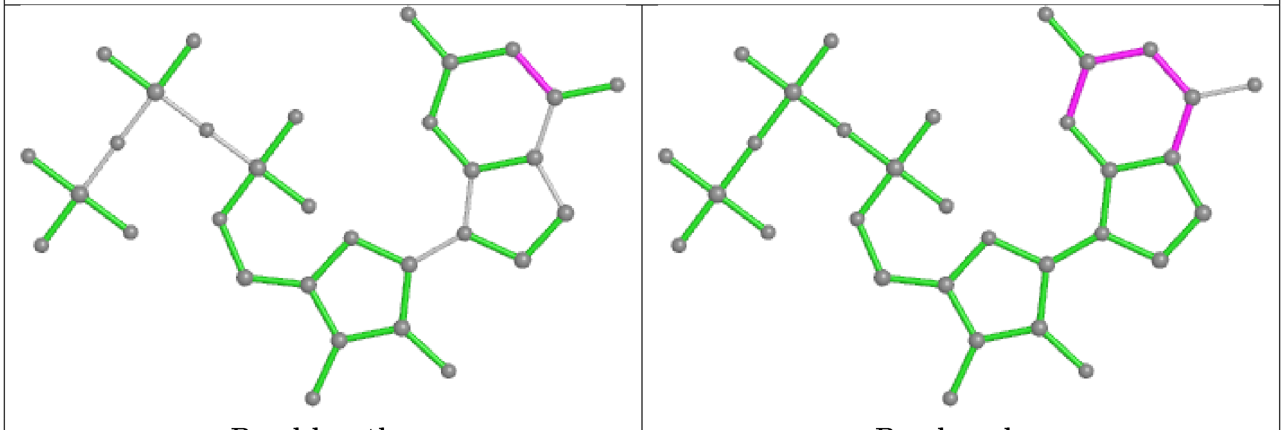
Bond angles



Torsions

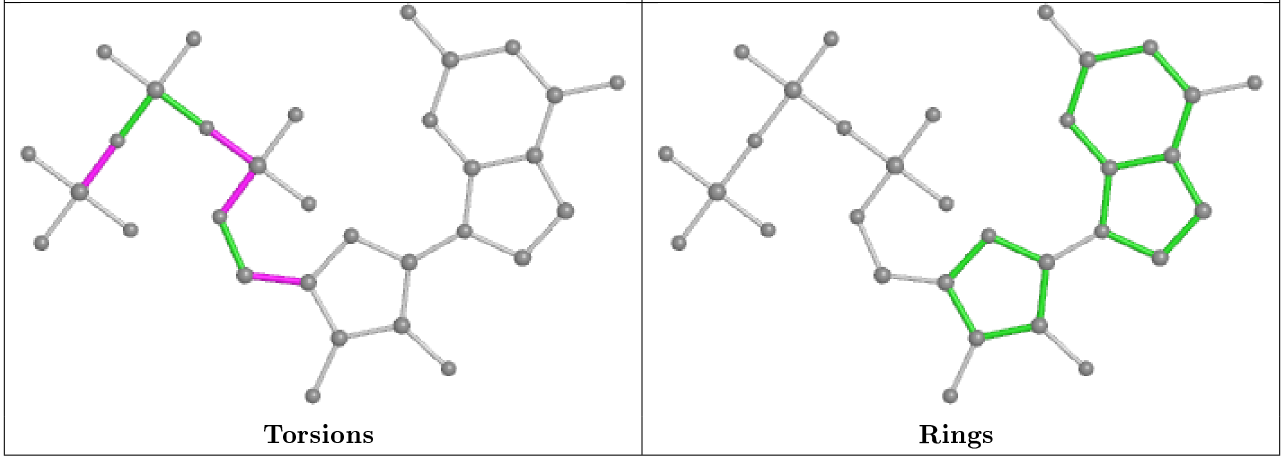
Rings

Ligand QBQ D 302



Bond lengths

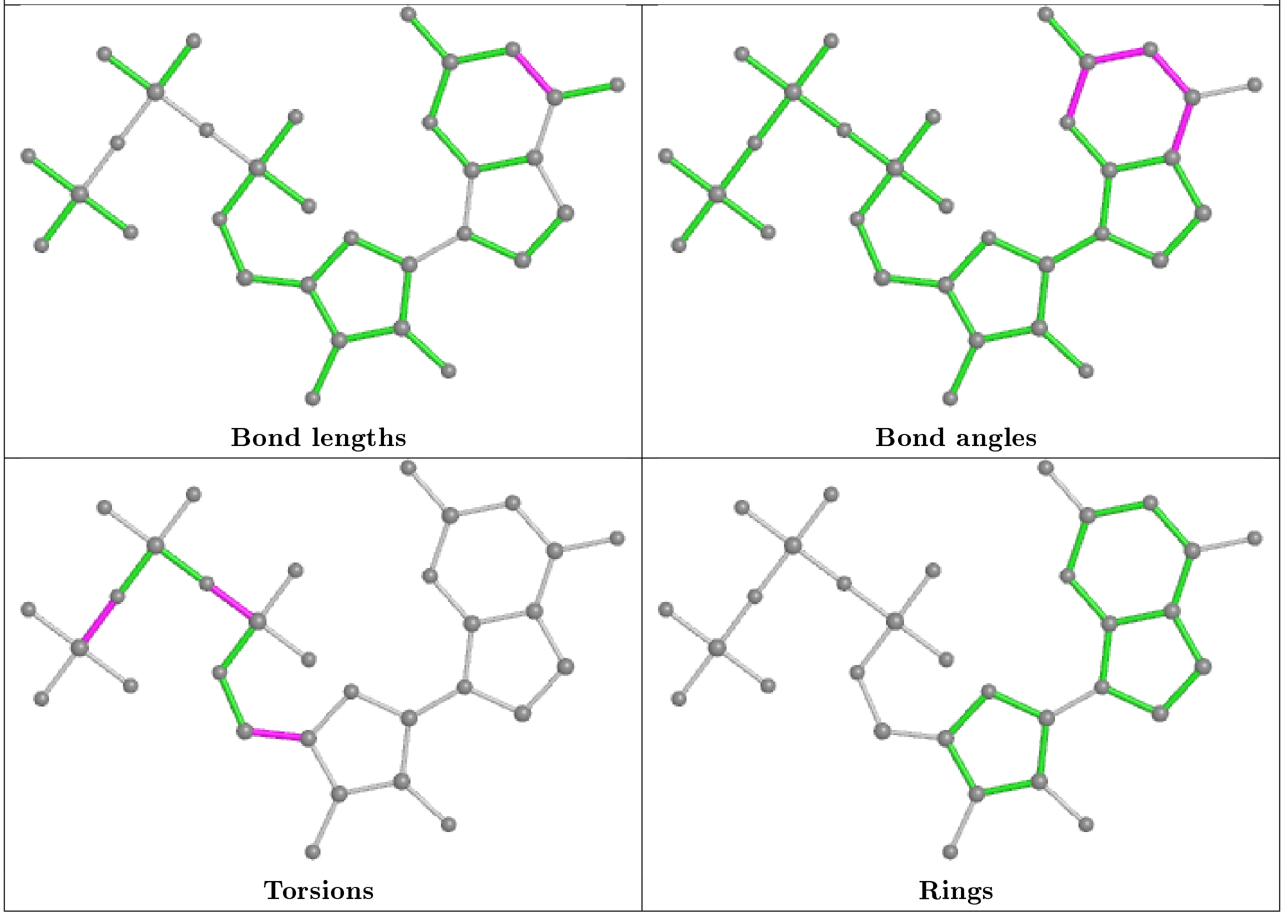
Bond angles



Torsions

Rings

Ligand QBQ S 302



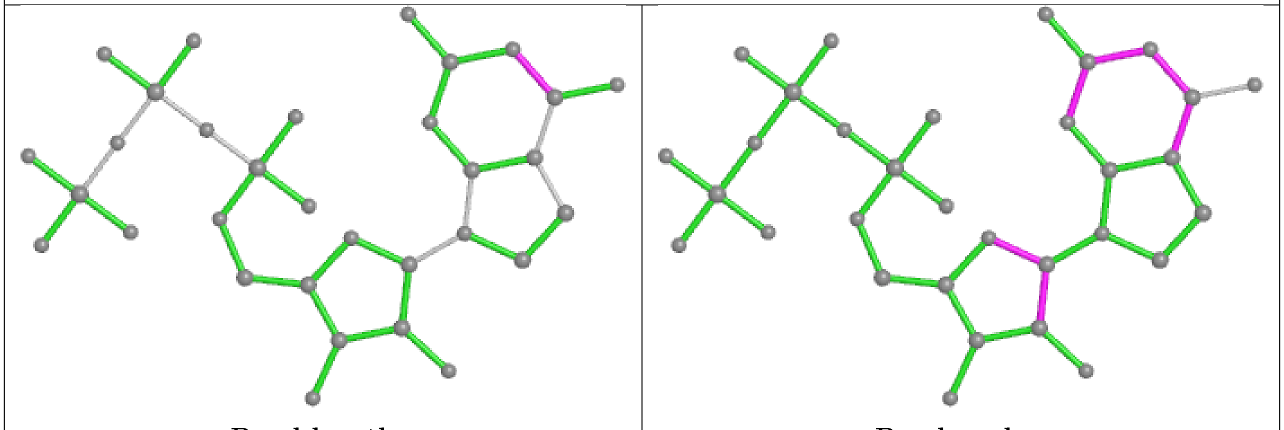
Bond lengths

Bond angles

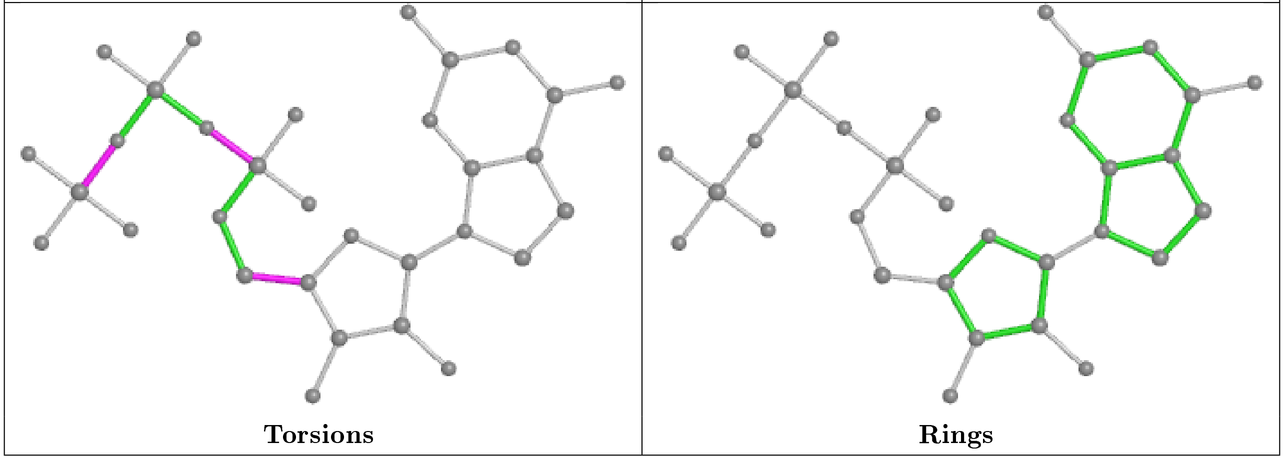
Torsions

Rings

Ligand QBQ F 302

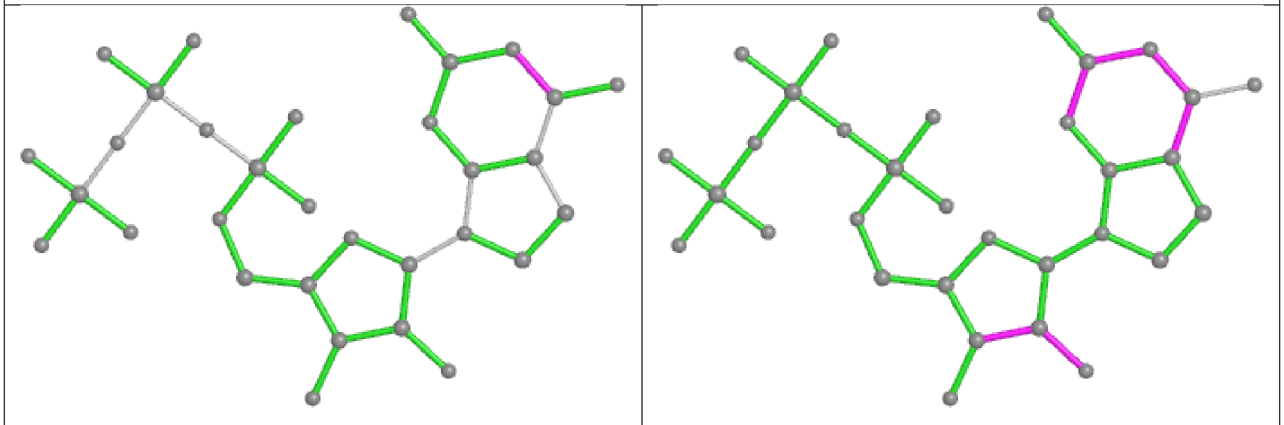


Bond lengths **Bond angles**

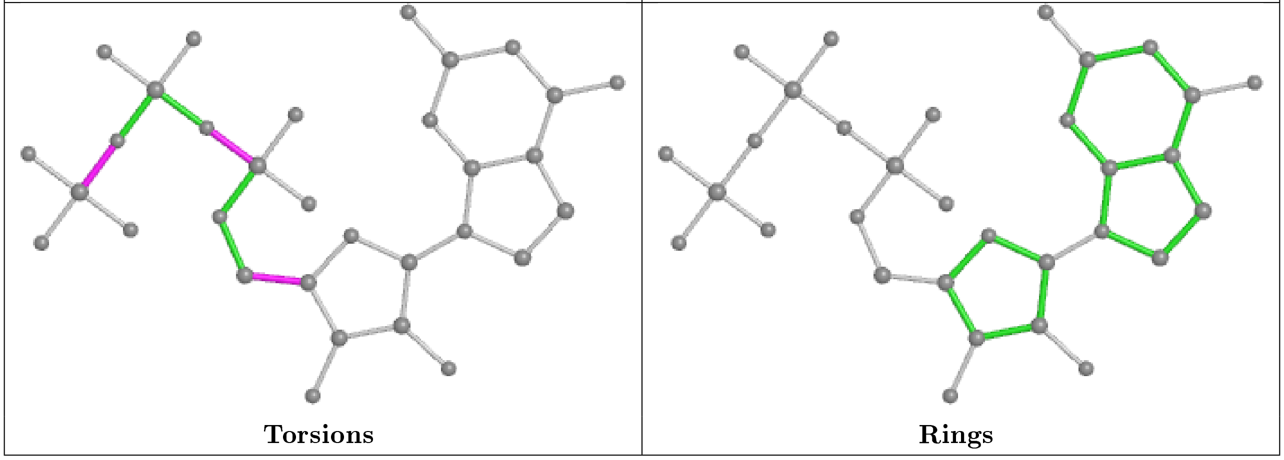


Torsions **Rings**

Ligand QBQ I 302

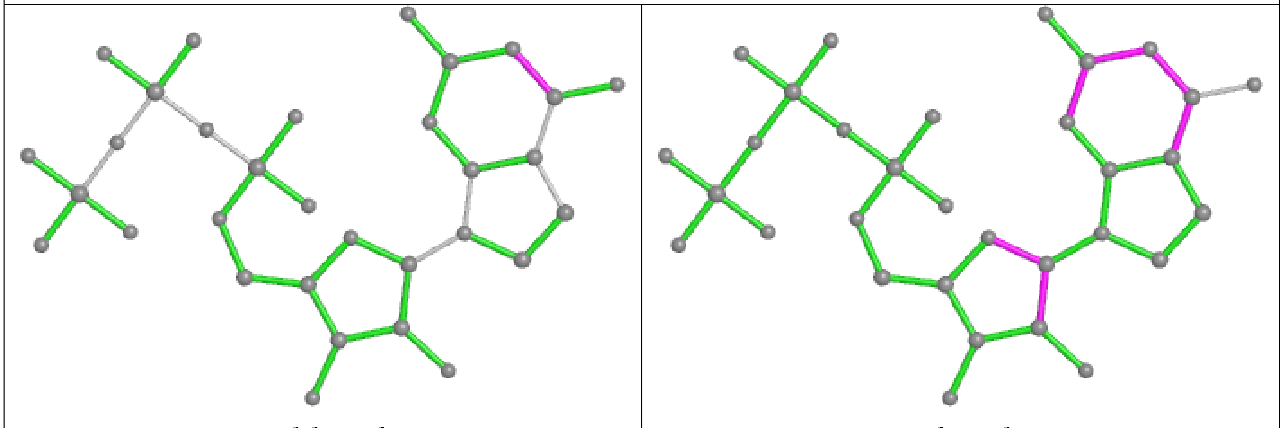


Bond lengths **Bond angles**

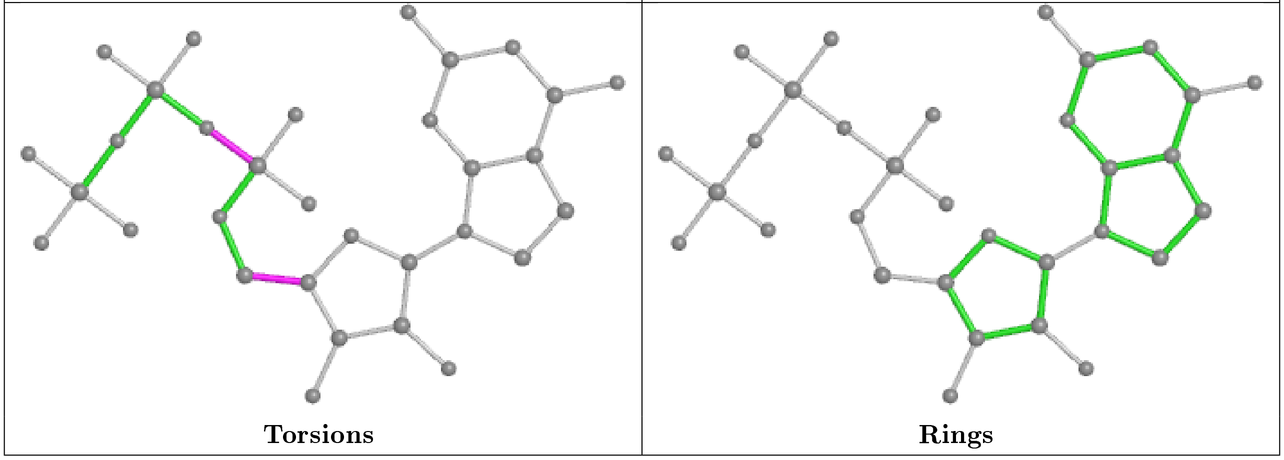


Torsions **Rings**

Ligand QBQ K 302

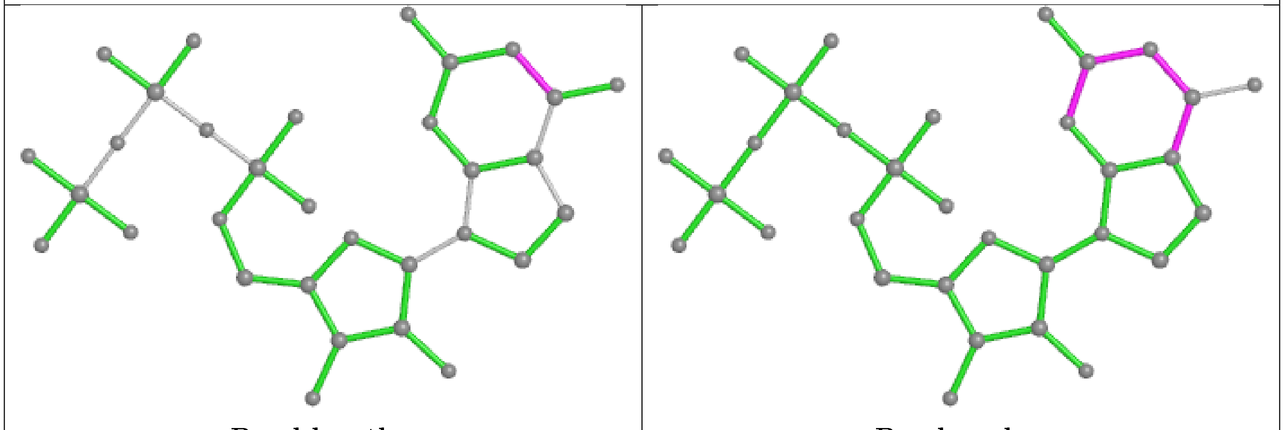


Bond lengths **Bond angles**

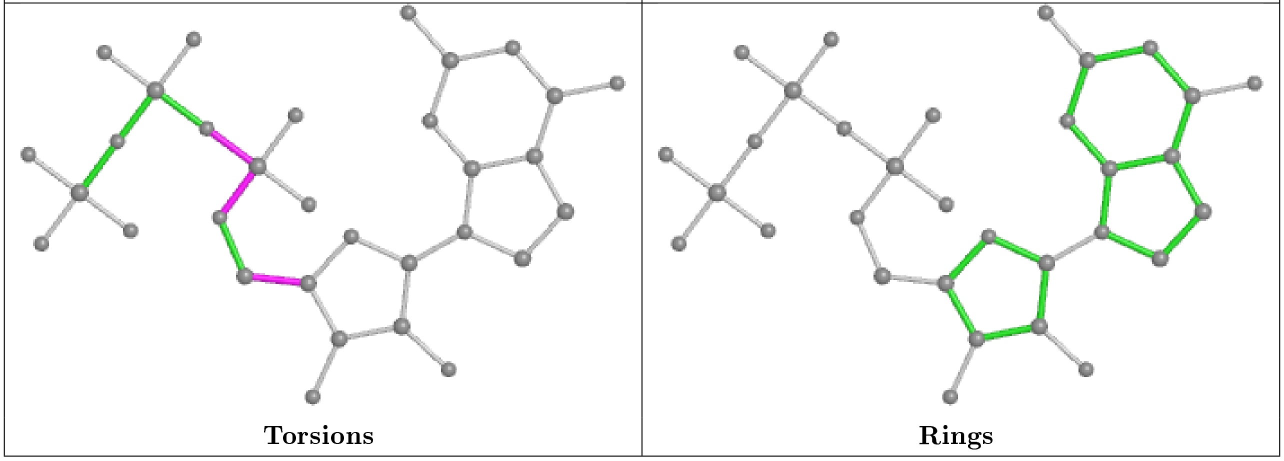


Torsions **Rings**

Ligand QBQ M 302

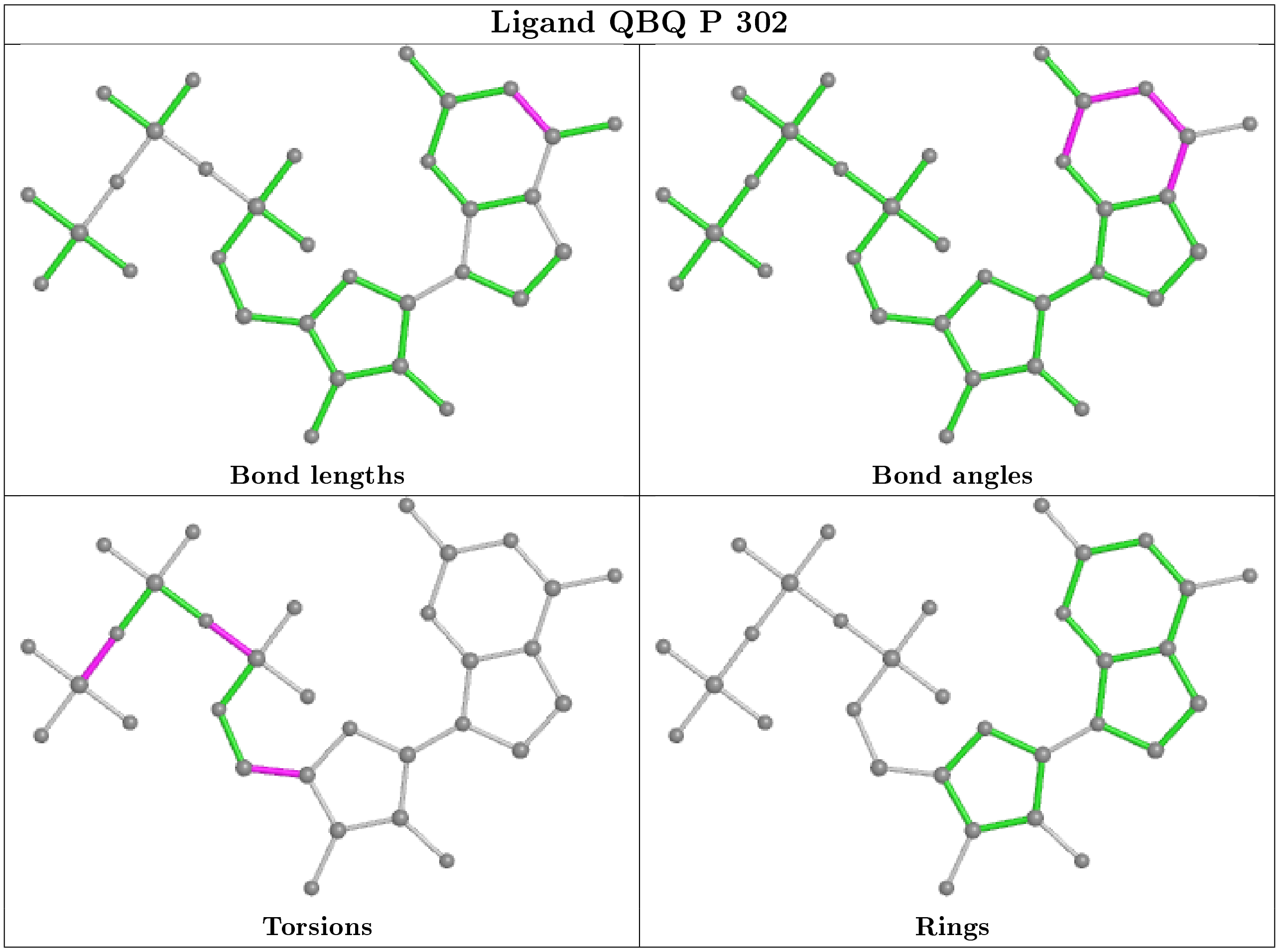


Bond lengths **Bond angles**



Torsions **Rings**

Ligand QBQ P 302



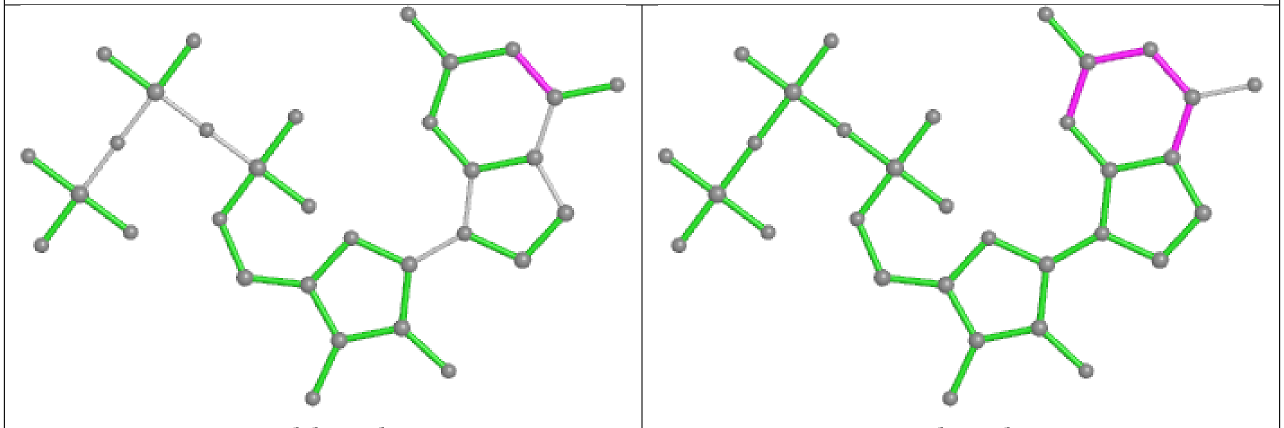
Bond lengths

Bond angles

Torsions

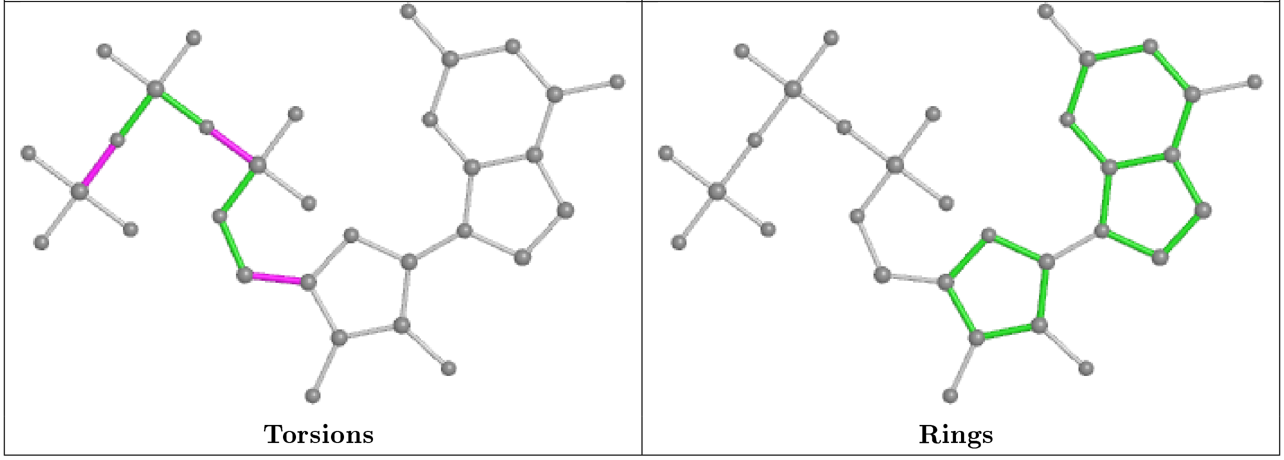
Rings

Ligand QBQ O 302



Bond lengths

Bond angles



Torsions

Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	192/224 (85%)	-0.27	2 (1%)	82	81	28, 40, 72, 90	0
1	B	190/224 (84%)	-0.31	0	100	100	24, 39, 64, 82	0
1	C	191/224 (85%)	-0.29	0	100	100	28, 43, 70, 89	0
1	D	191/224 (85%)	-0.28	1 (0%)	91	90	23, 43, 69, 98	0
1	E	190/224 (84%)	-0.26	0	100	100	26, 40, 62, 86	0
1	F	190/224 (84%)	-0.32	0	100	100	26, 38, 66, 86	0
1	G	193/224 (86%)	-0.22	3 (1%)	72	70	27, 40, 74, 97	0
1	H	192/224 (85%)	-0.23	2 (1%)	82	81	25, 41, 71, 88	0
1	I	192/224 (85%)	-0.28	0	100	100	33, 45, 72, 85	0
1	J	190/224 (84%)	-0.19	0	100	100	27, 42, 75, 102	0
1	K	192/224 (85%)	-0.29	0	100	100	27, 45, 78, 108	0
1	L	191/224 (85%)	-0.31	0	100	100	33, 49, 78, 99	0
1	M	191/224 (85%)	-0.15	4 (2%)	63	61	27, 42, 74, 98	0
1	N	193/224 (86%)	-0.17	3 (1%)	72	70	29, 49, 79, 109	0
1	O	191/224 (85%)	-0.24	1 (0%)	91	90	28, 48, 80, 110	0
1	P	189/224 (84%)	-0.27	0	100	100	29, 53, 79, 110	0
1	Q	190/224 (84%)	-0.36	1 (0%)	91	90	33, 52, 79, 103	0
1	R	191/224 (85%)	-0.12	1 (0%)	91	90	28, 44, 72, 98	0
1	S	188/224 (83%)	-0.23	1 (0%)	91	90	32, 46, 78, 93	0
1	T	186/224 (83%)	-0.17	1 (0%)	91	90	28, 47, 81, 93	0
All	All	3813/4480 (85%)	-0.25	20 (0%)	91	90	23, 45, 76, 110	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	250	SER	4.7
1	O	250	SER	4.4
1	T	249	ARG	4.0
1	G	250	SER	3.9
1	G	58	PRO	3.3

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	ZN	L	301	1/1	0.97	0.12	67,67,67,67	0
2	ZN	P	301	1/1	0.97	0.12	69,69,69,69	0
2	ZN	K	301	1/1	0.97	0.11	62,62,62,62	0
3	QBQ	I	302	32/32	0.98	0.10	44,47,50,52	0
3	QBQ	A	302	32/32	0.98	0.10	44,48,52,54	0
2	ZN	E	301	1/1	0.98	0.11	53,53,53,53	0
3	QBQ	D	302	32/32	0.98	0.11	37,43,50,51	0
2	ZN	C	301	1/1	0.98	0.10	55,55,55,55	0
3	QBQ	M	302	32/32	0.98	0.10	47,49,49,49	0
3	QBQ	B	302	32/32	0.98	0.11	33,37,39,39	0
2	ZN	G	301	1/1	0.98	0.12	52,52,52,52	0
2	ZN	Q	301	1/1	0.98	0.13	61,61,61,61	0
3	QBQ	R	302	32/32	0.98	0.10	43,45,49,50	0
3	QBQ	E	302	32/32	0.98	0.12	32,38,41,42	0
3	QBQ	G	302	32/32	0.98	0.11	43,46,49,49	0
3	QBQ	P	302	32/32	0.98	0.10	40,44,48,49	0
2	ZN	D	301	1/1	0.98	0.11	51,51,51,51	0
3	QBQ	S	302	32/32	0.98	0.10	51,53,56,56	0
3	QBQ	L	302	32/32	0.98	0.12	43,47,51,51	0

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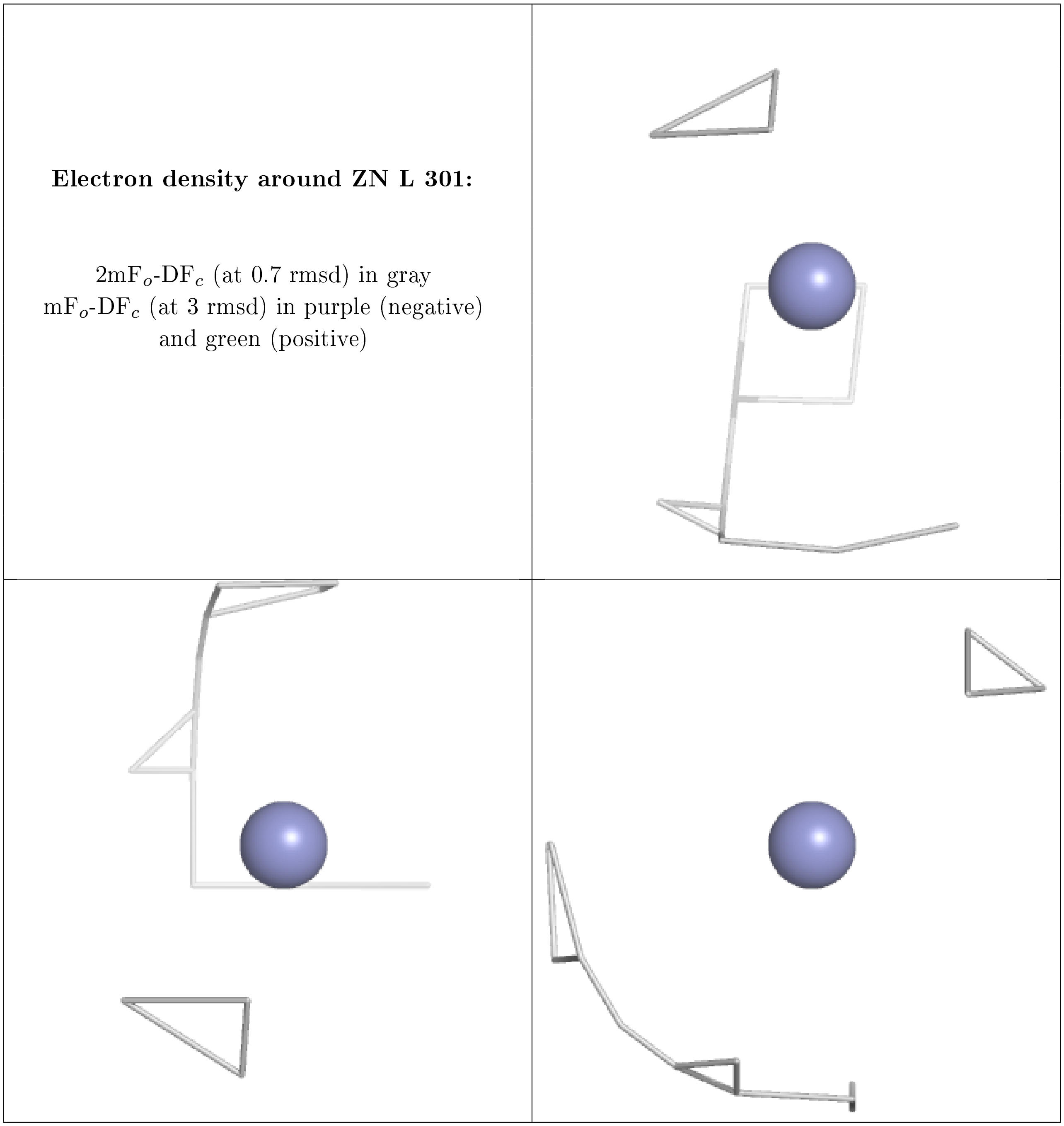
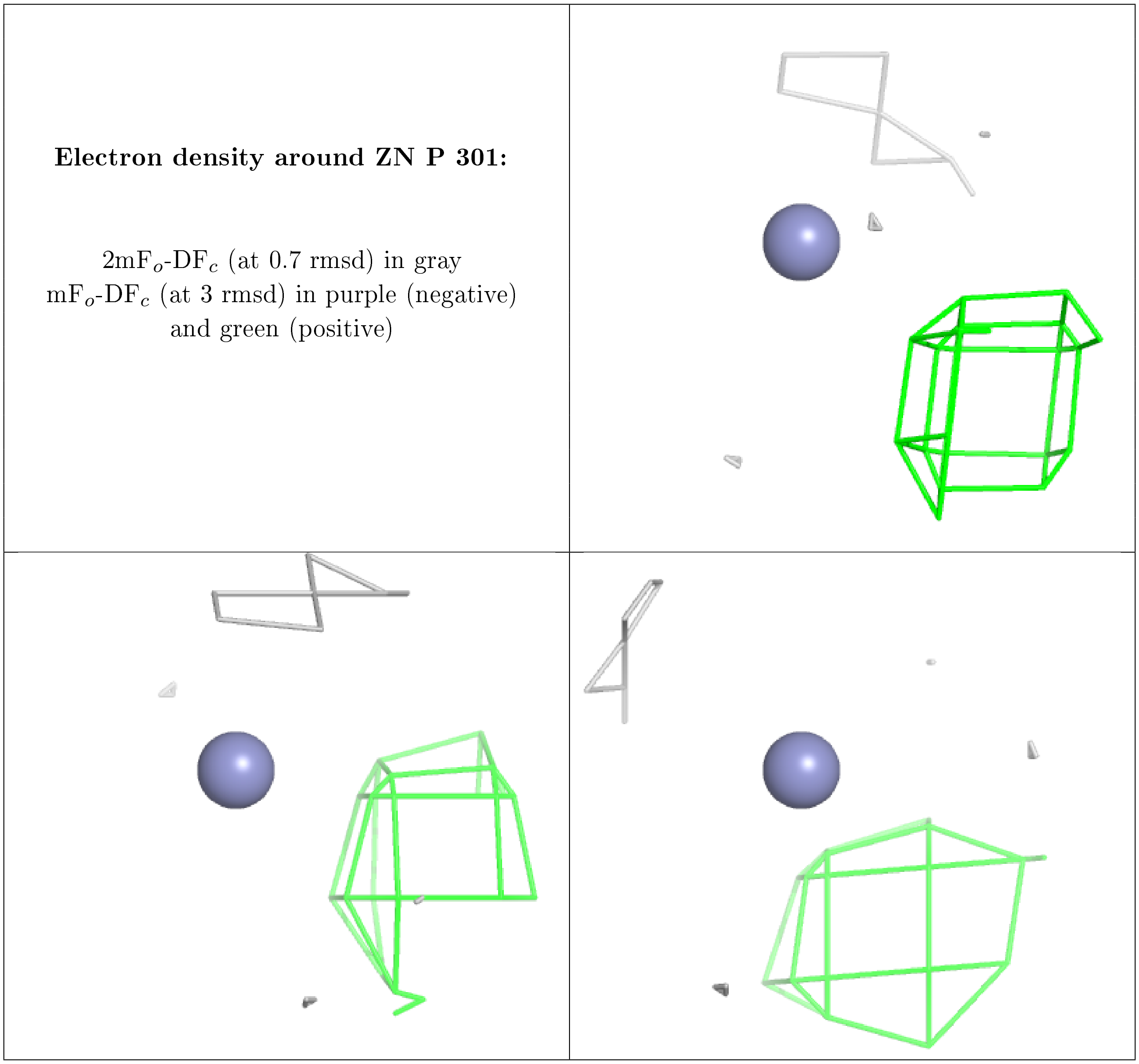
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	QBQ	C	302	32/32	0.99	0.12	36,40,45,46	0
2	ZN	J	301	1/1	0.99	0.10	54,54,54,54	0
3	QBQ	N	302	32/32	0.99	0.12	40,42,44,44	0
2	ZN	H	301	1/1	0.99	0.09	56,56,56,56	0
3	QBQ	H	302	32/32	0.99	0.10	33,36,38,39	0
3	QBQ	O	302	32/32	0.99	0.11	38,39,43,44	0
3	QBQ	J	302	32/32	0.99	0.10	32,37,40,41	0
2	ZN	T	301	1/1	0.99	0.09	64,64,64,64	0
2	ZN	M	301	1/1	0.99	0.14	55,55,55,55	0
2	ZN	N	301	1/1	0.99	0.10	64,64,64,64	0
3	QBQ	Q	302	32/32	0.99	0.10	39,42,46,47	0
2	ZN	F	301	1/1	0.99	0.11	45,45,45,45	0
3	QBQ	F	302	32/32	0.99	0.11	30,36,41,41	0
2	ZN	O	301	1/1	0.99	0.11	62,62,62,62	0
3	QBQ	K	302	32/32	0.99	0.12	28,34,38,40	0
3	QBQ	T	302	32/32	0.99	0.11	40,42,44,46	0
2	ZN	R	301	1/1	0.99	0.12	52,52,52,52	0
2	ZN	A	301	1/1	0.99	0.10	51,51,51,51	0
2	ZN	B	301	1/1	1.00	0.10	54,54,54,54	0
2	ZN	I	301	1/1	1.00	0.12	53,53,53,53	0
2	ZN	S	301	1/1	1.00	0.11	58,58,58,58	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 ZN L 301:

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 ZN P 301:

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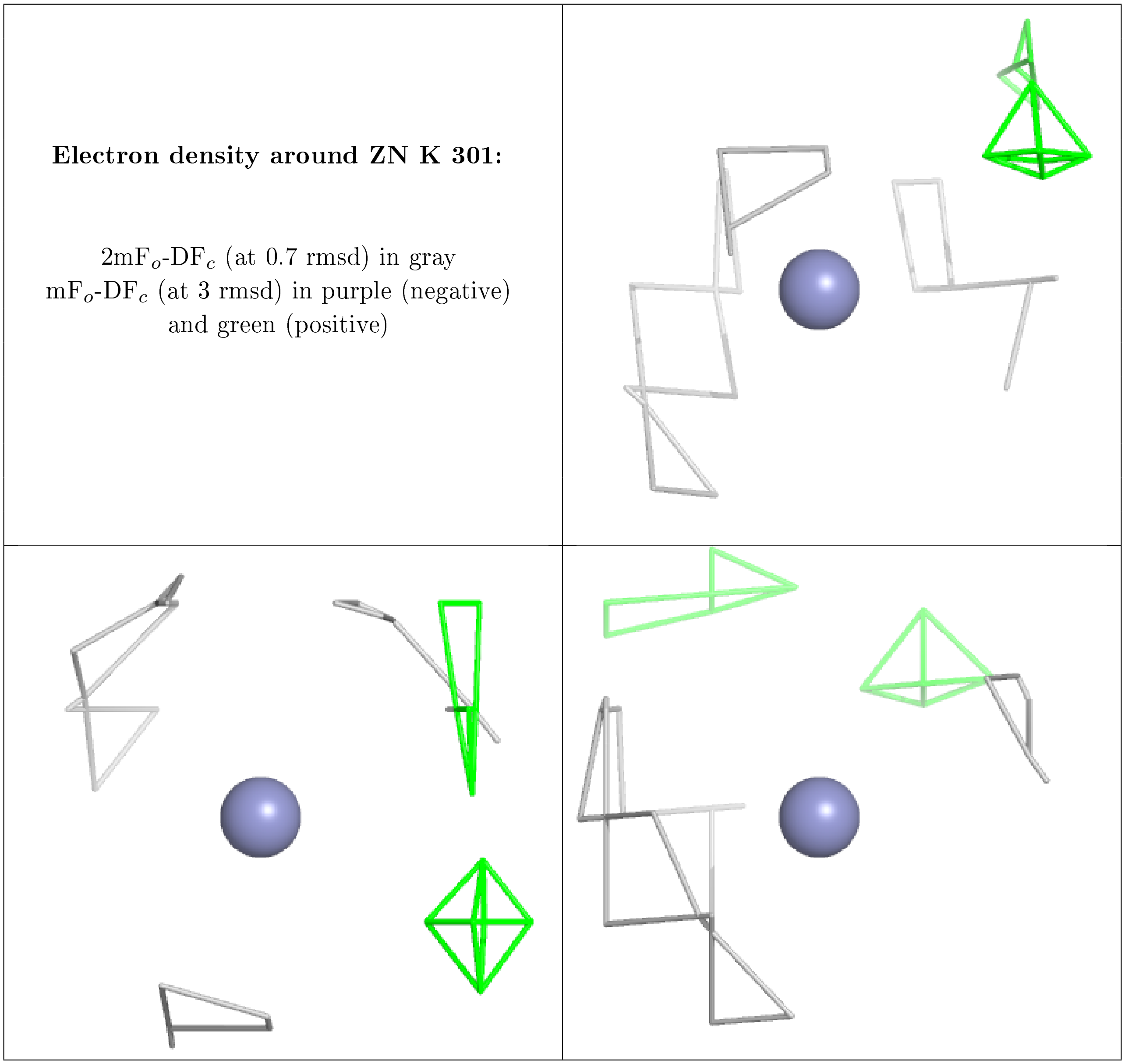
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

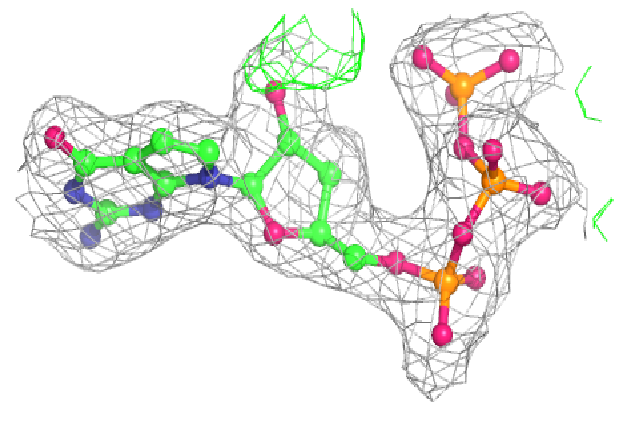


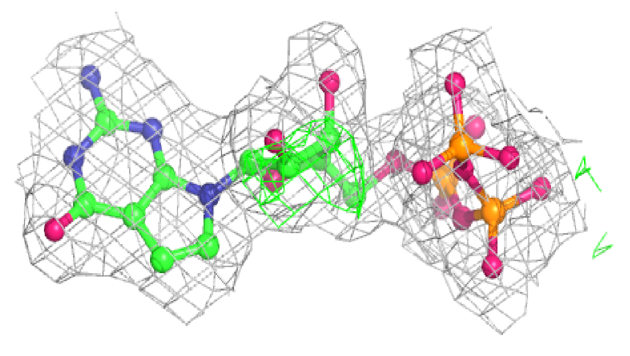
Electron density around ZN K 301:

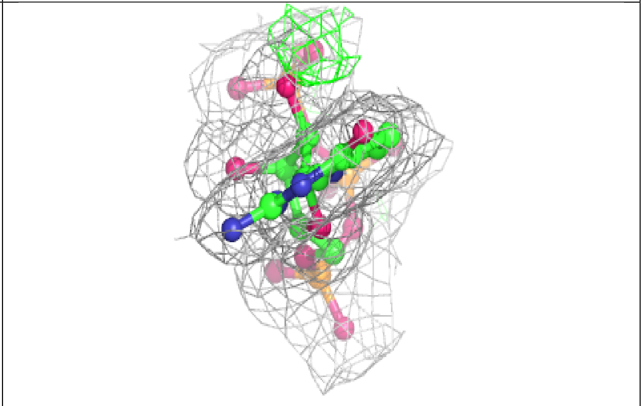
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around QBQ I 302:

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







Electron density around QBQ A 302:

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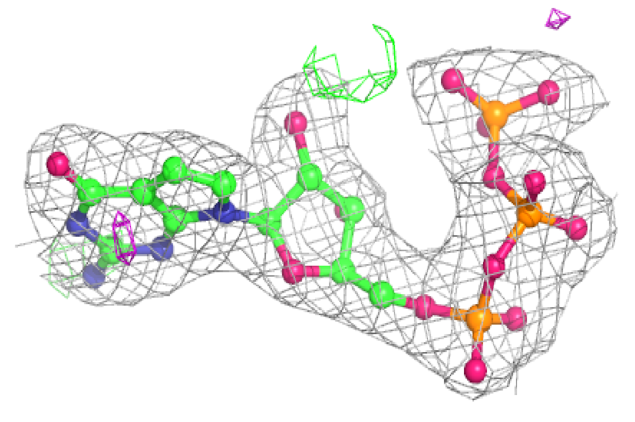
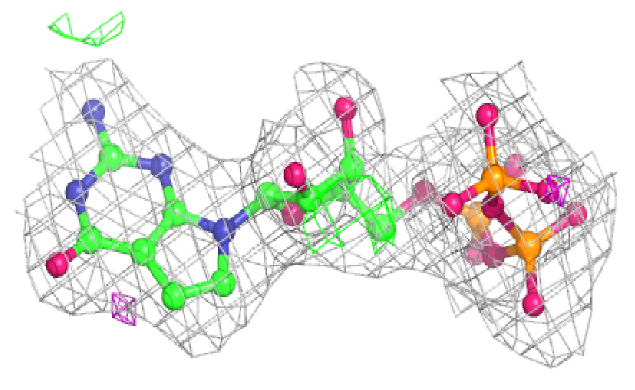
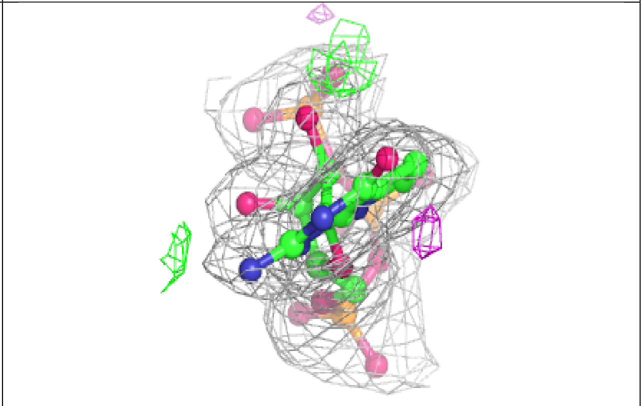
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around ZN E 301:

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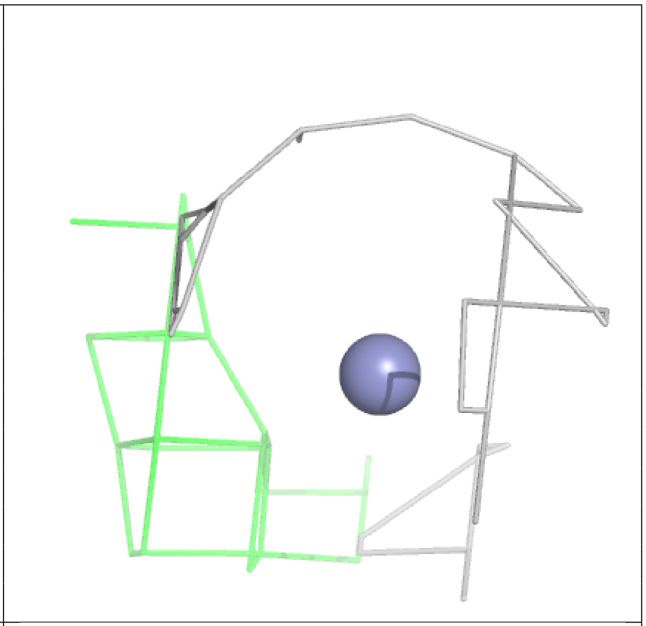
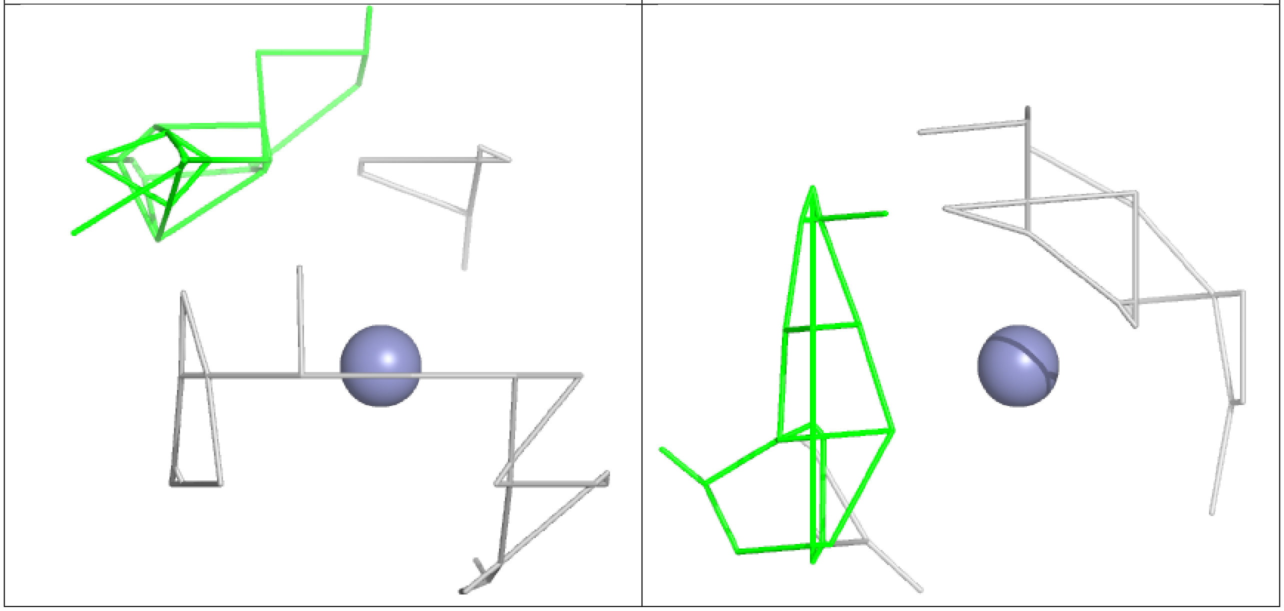
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around QBQ D 302:

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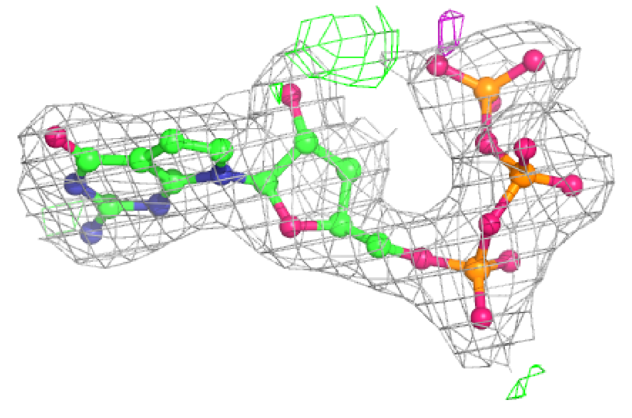
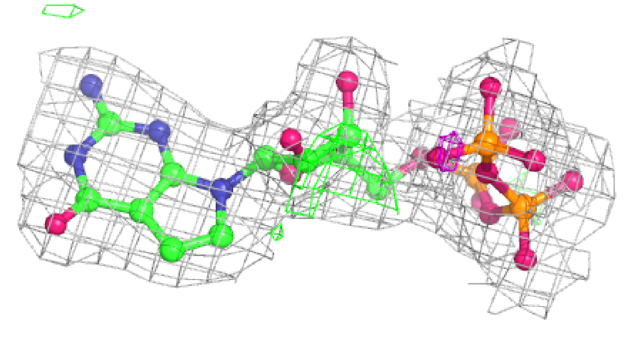
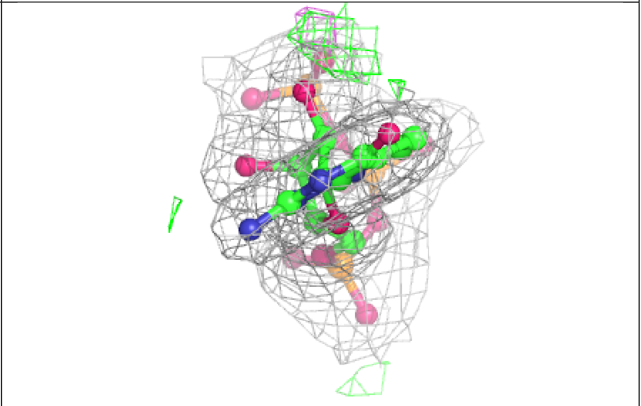
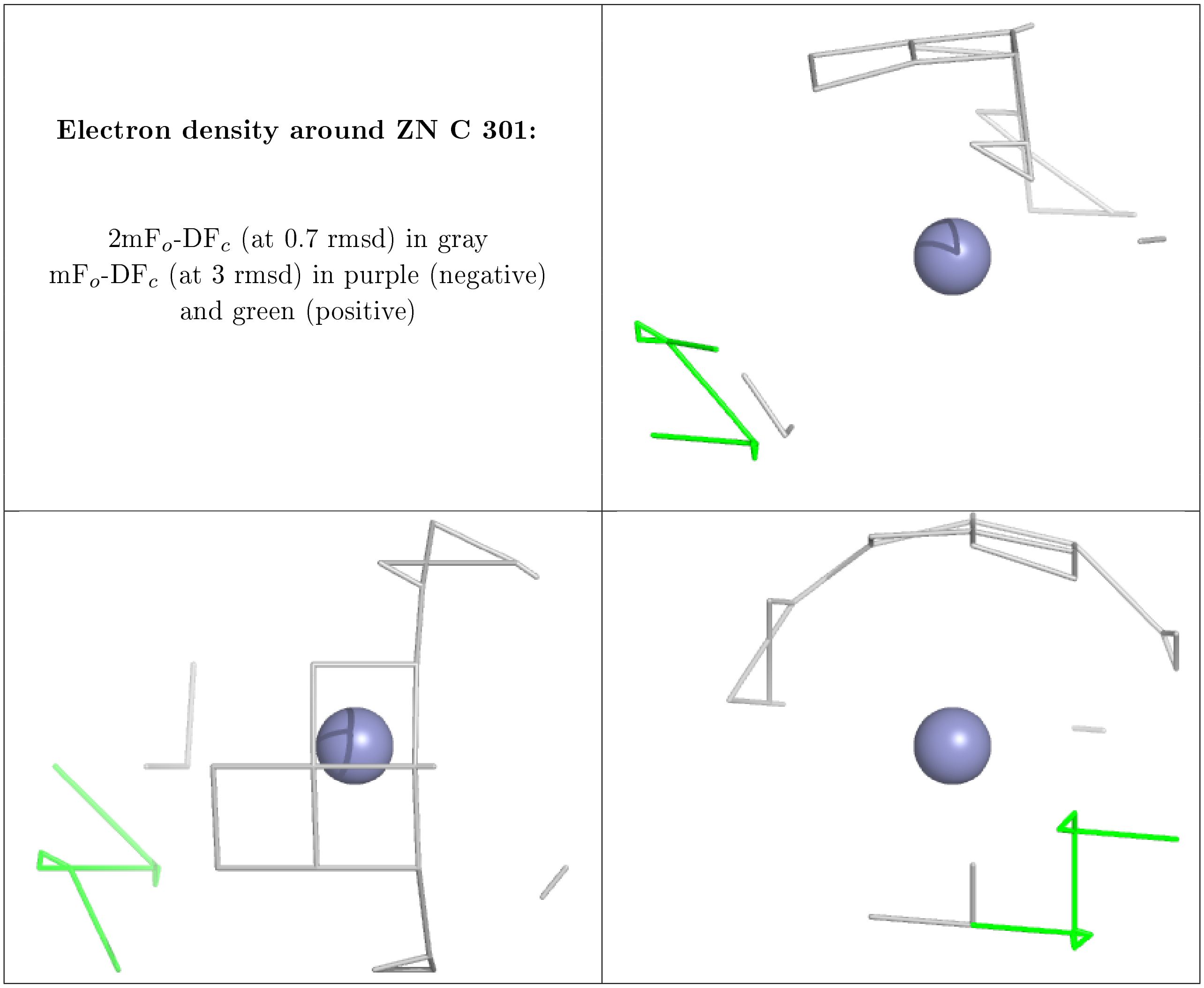
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







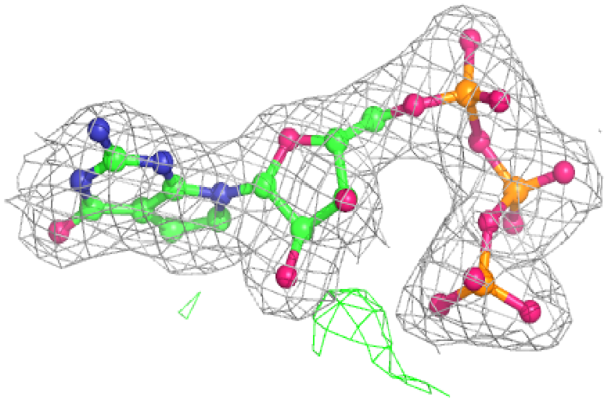


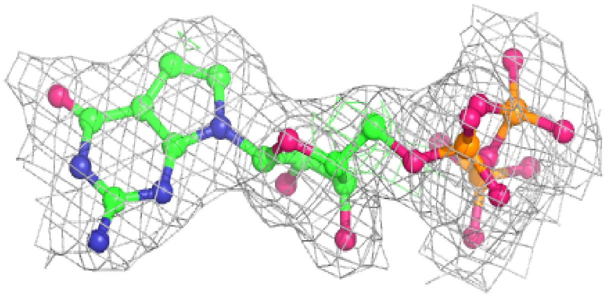
Electron density around ZN C 301:

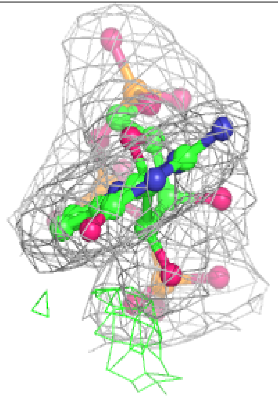
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around QBQ M 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

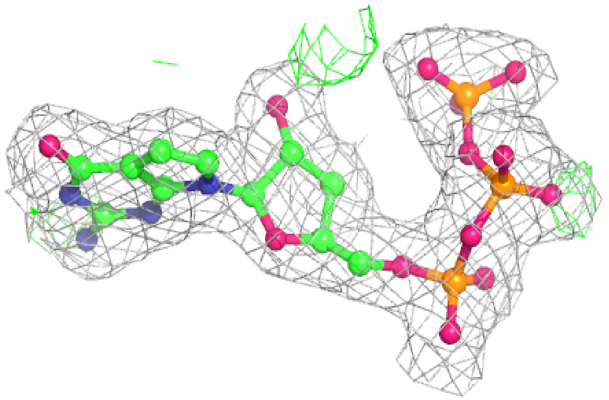


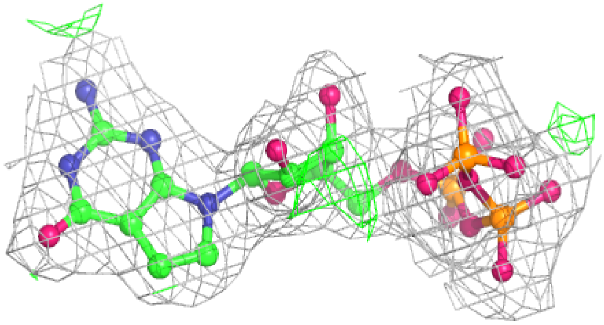




Electron density around QBQ B 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around ZN G 301:

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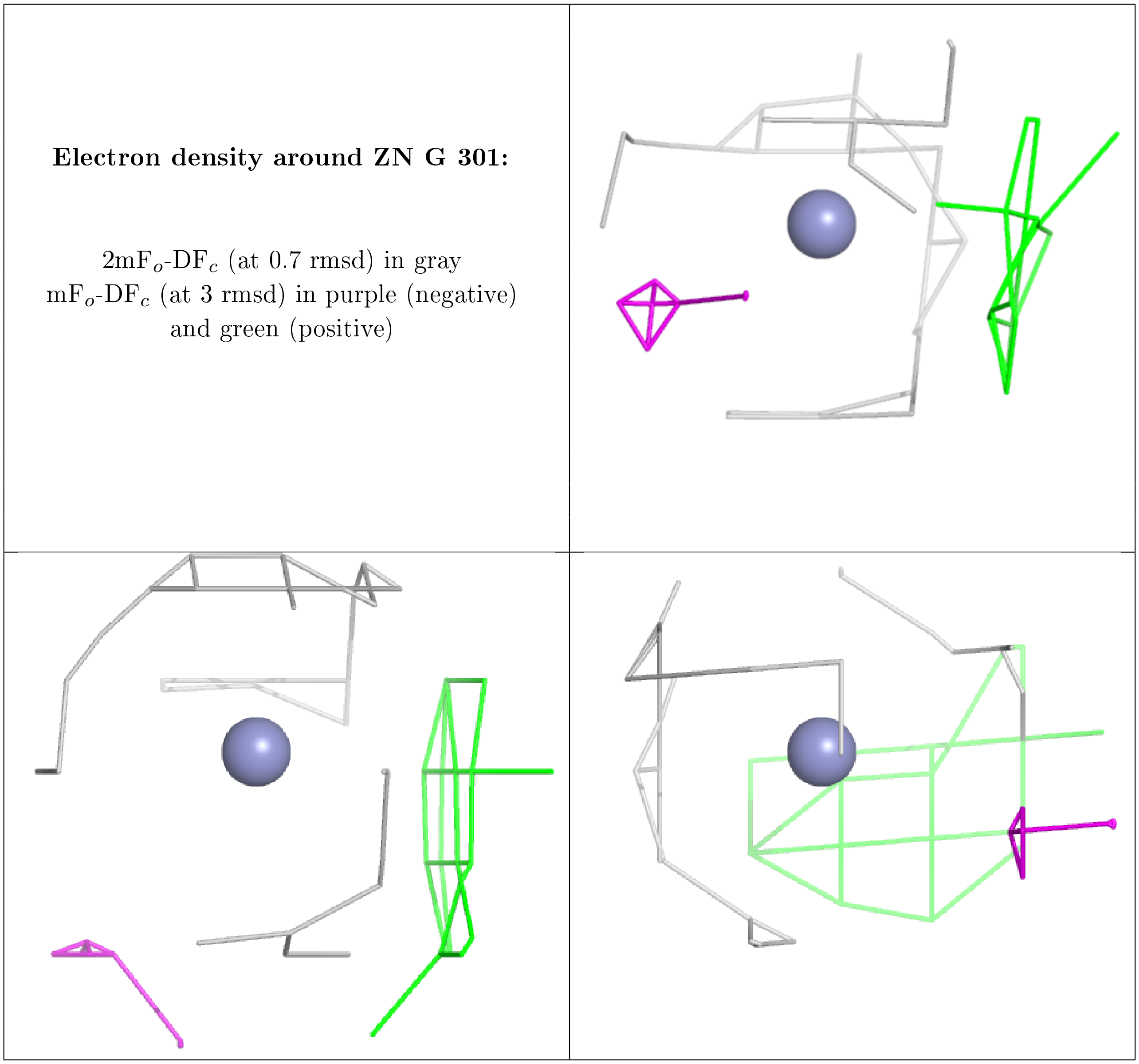
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN Q 301:

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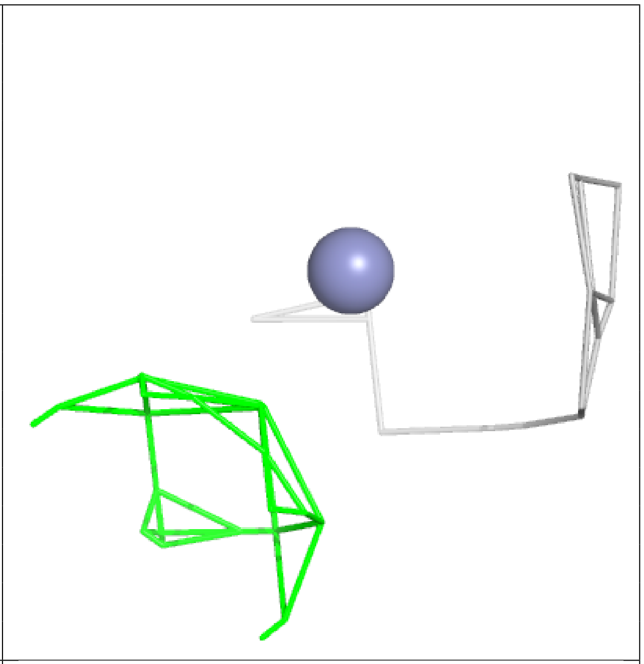
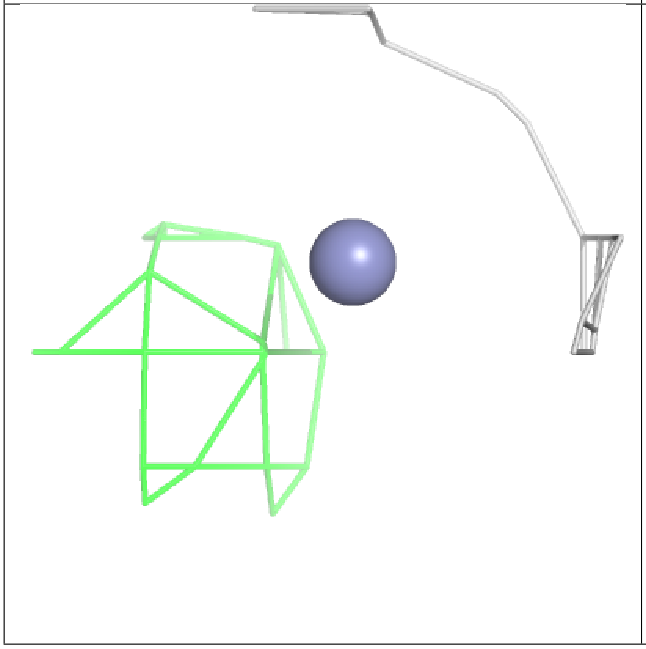
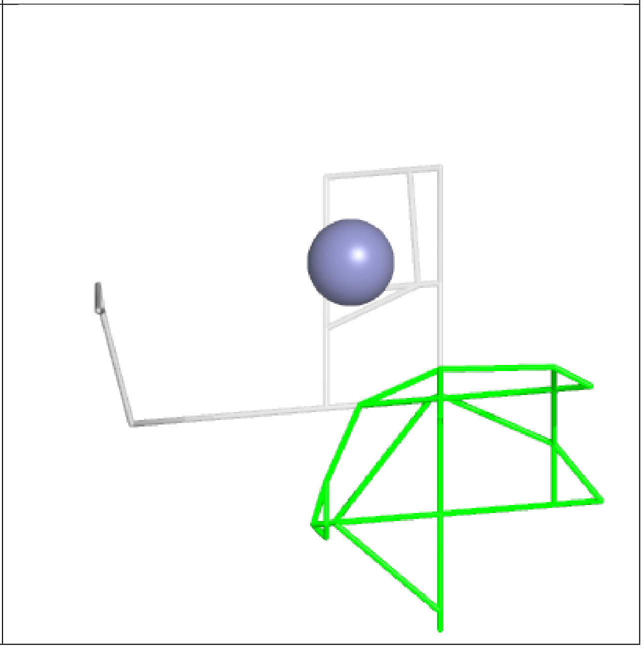
and green (positive)







Electron density around QBQ R 302:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
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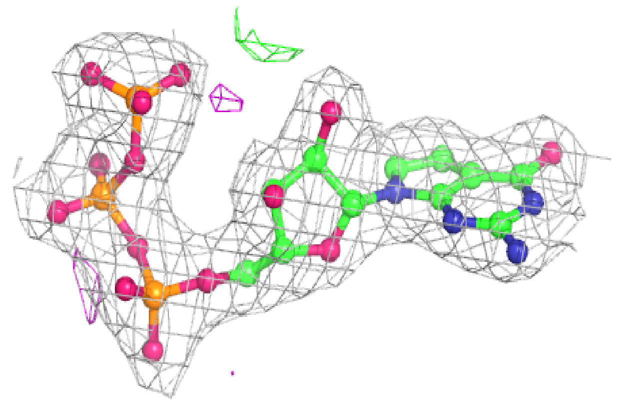

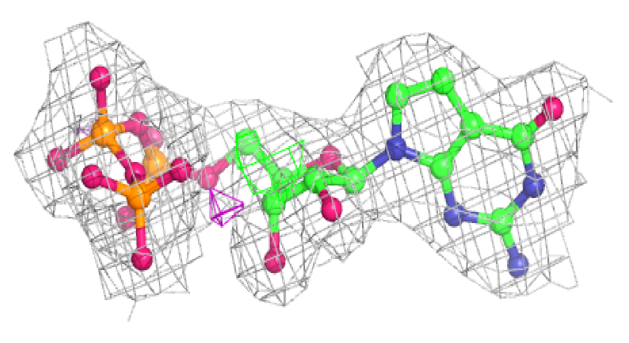

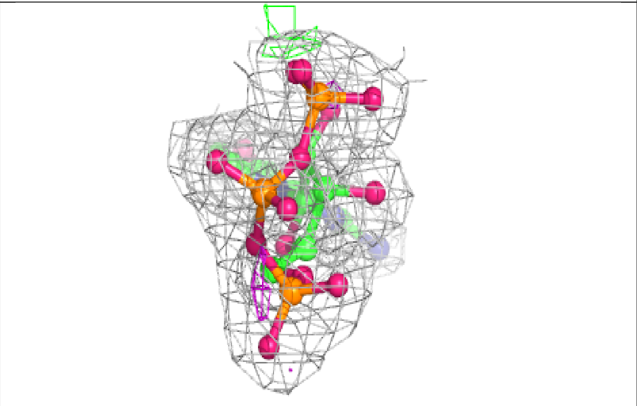

Electron density around QBQ E 302:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
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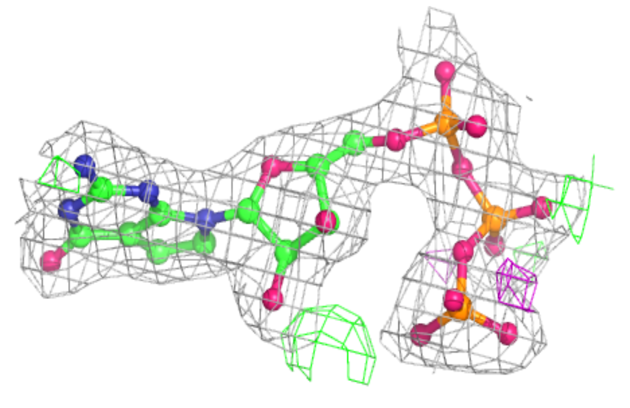

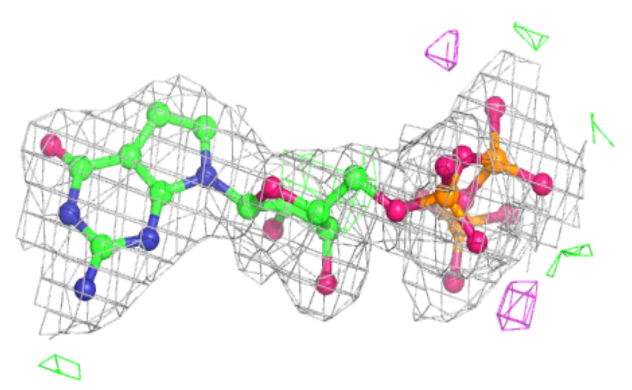

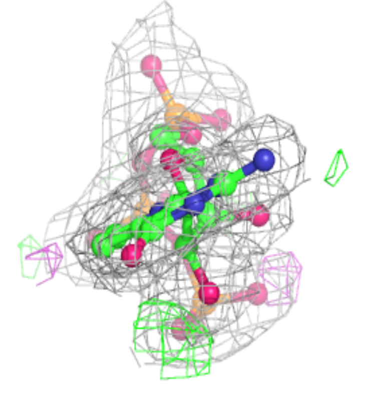

Electron density around QBQ G 302:

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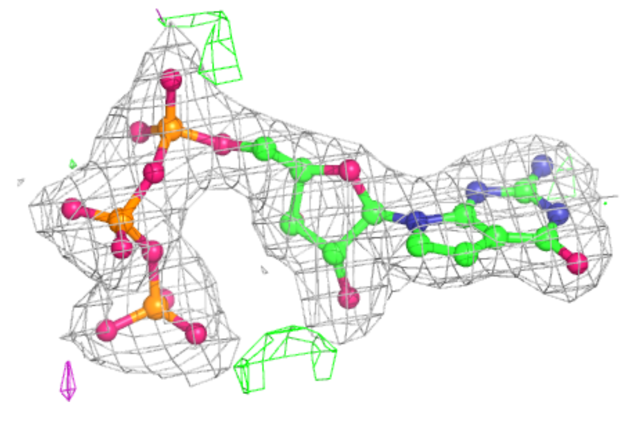
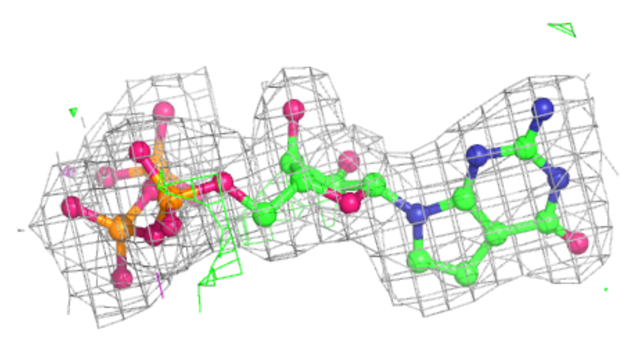
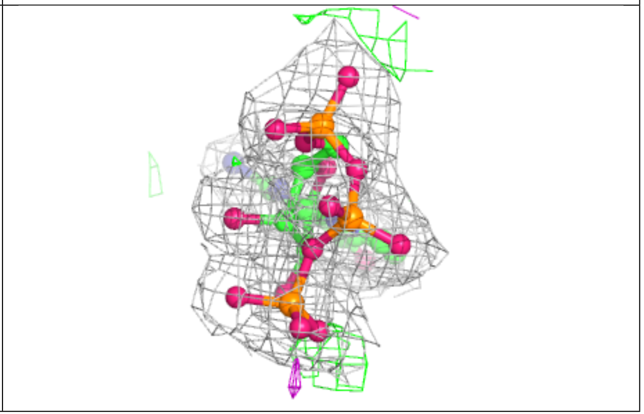
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around QBQ P 302:

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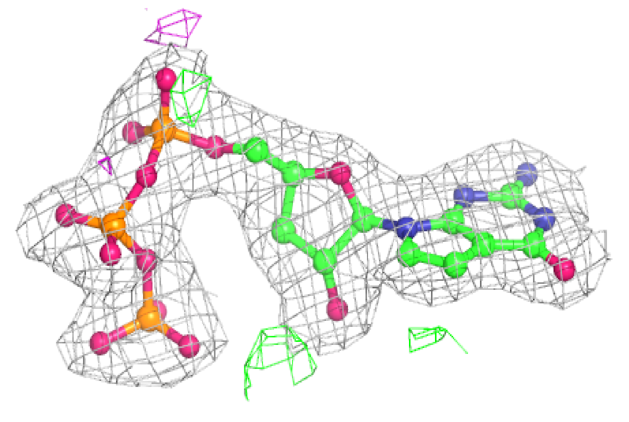
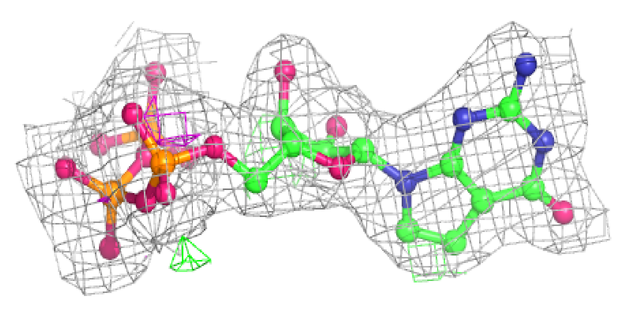
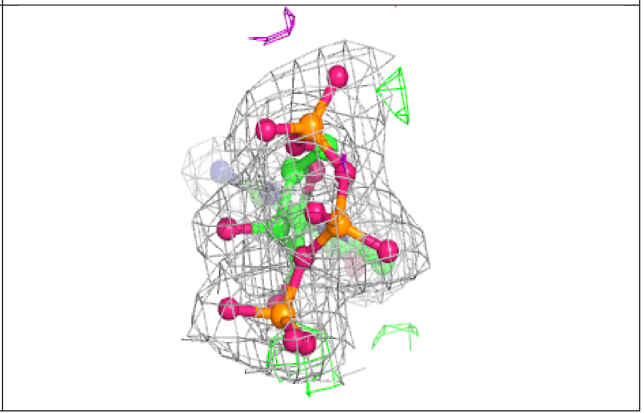
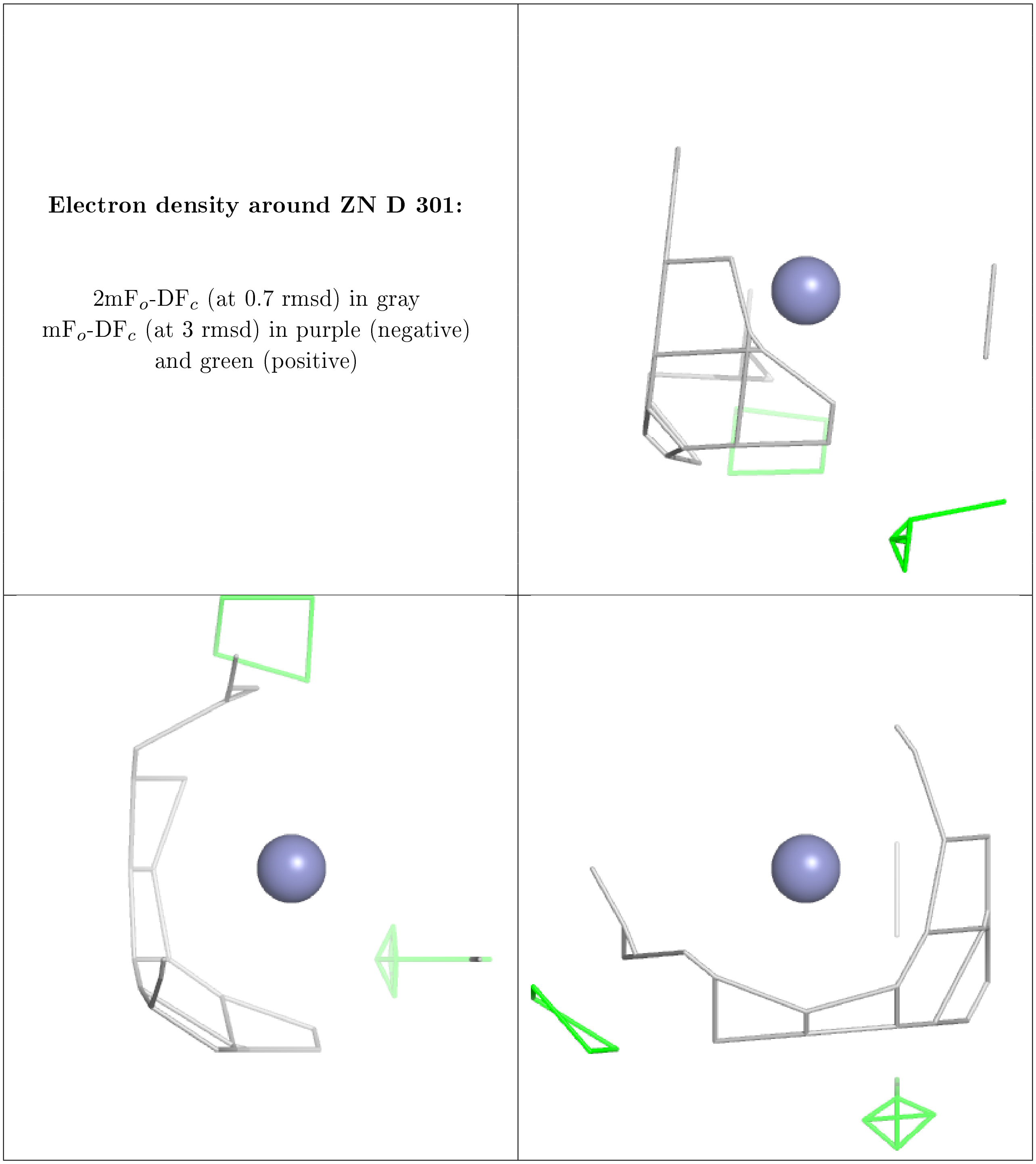
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)









Electron density around ZN D 301:

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

Electron density around QBQ S 302:

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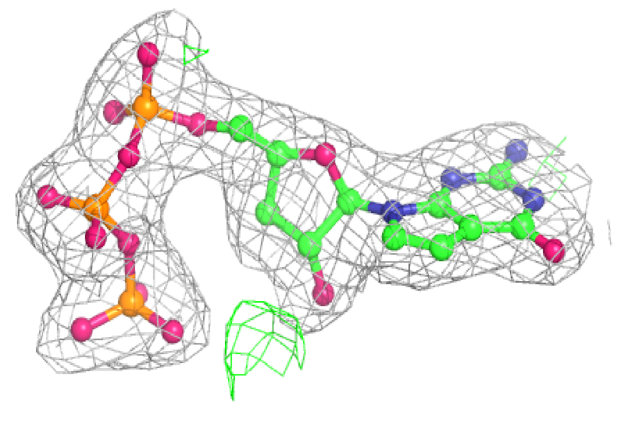
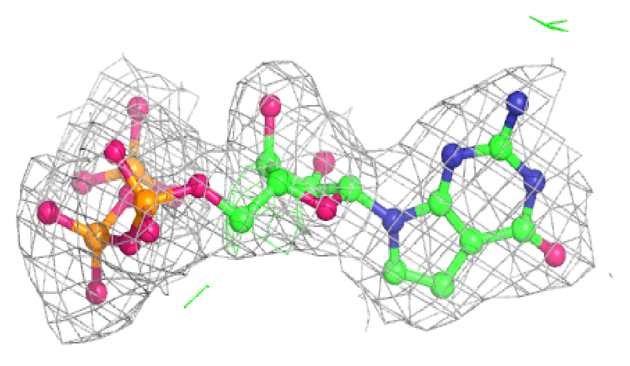
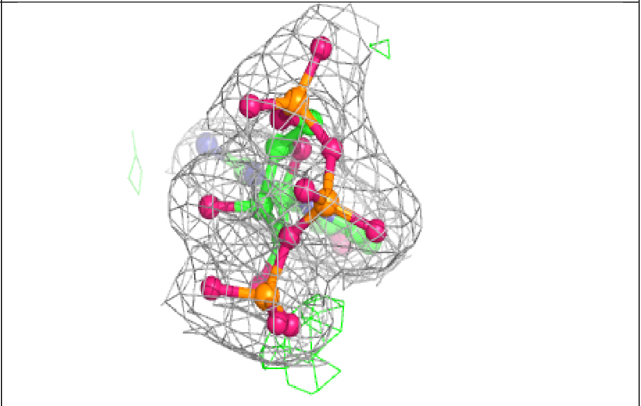
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around QBQ L 302:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
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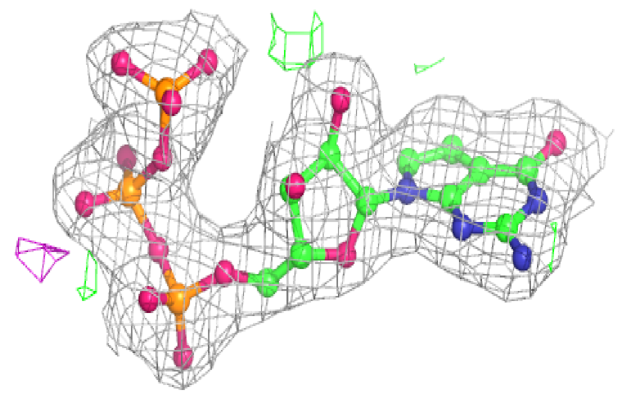

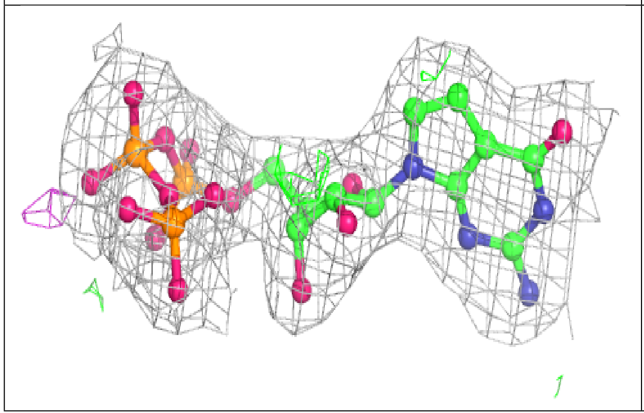

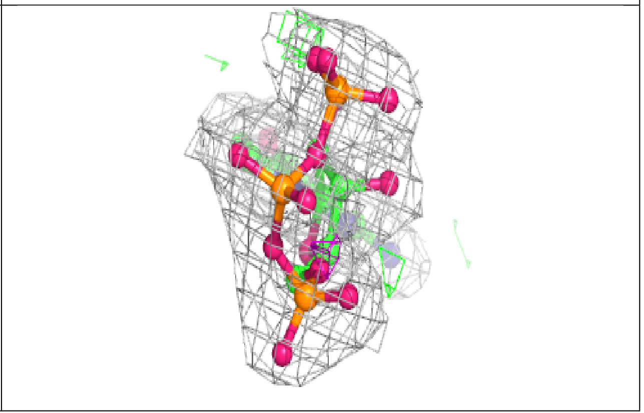

Electron density around QBQ C 302:

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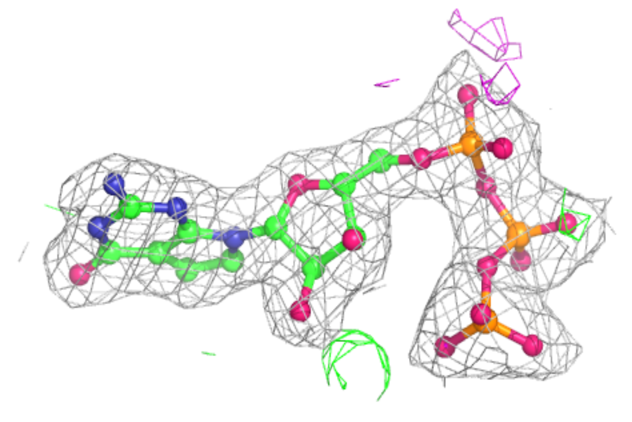
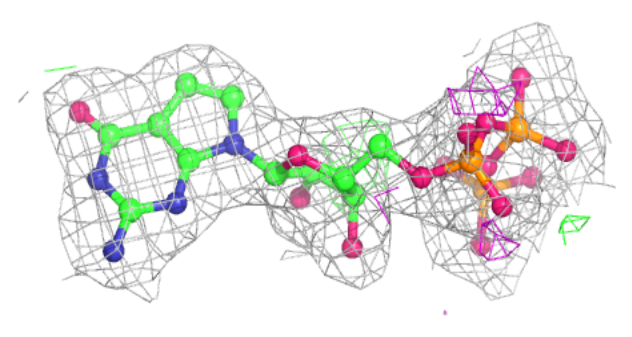
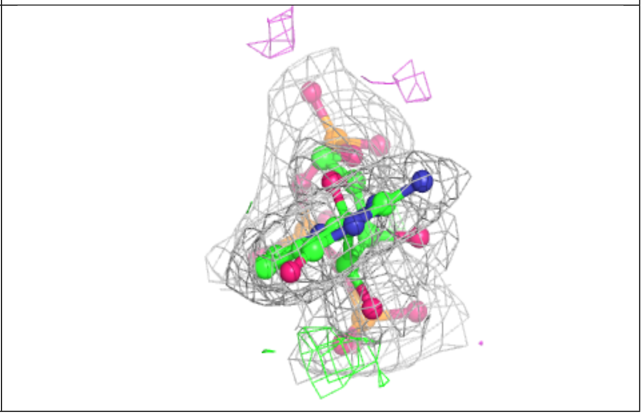
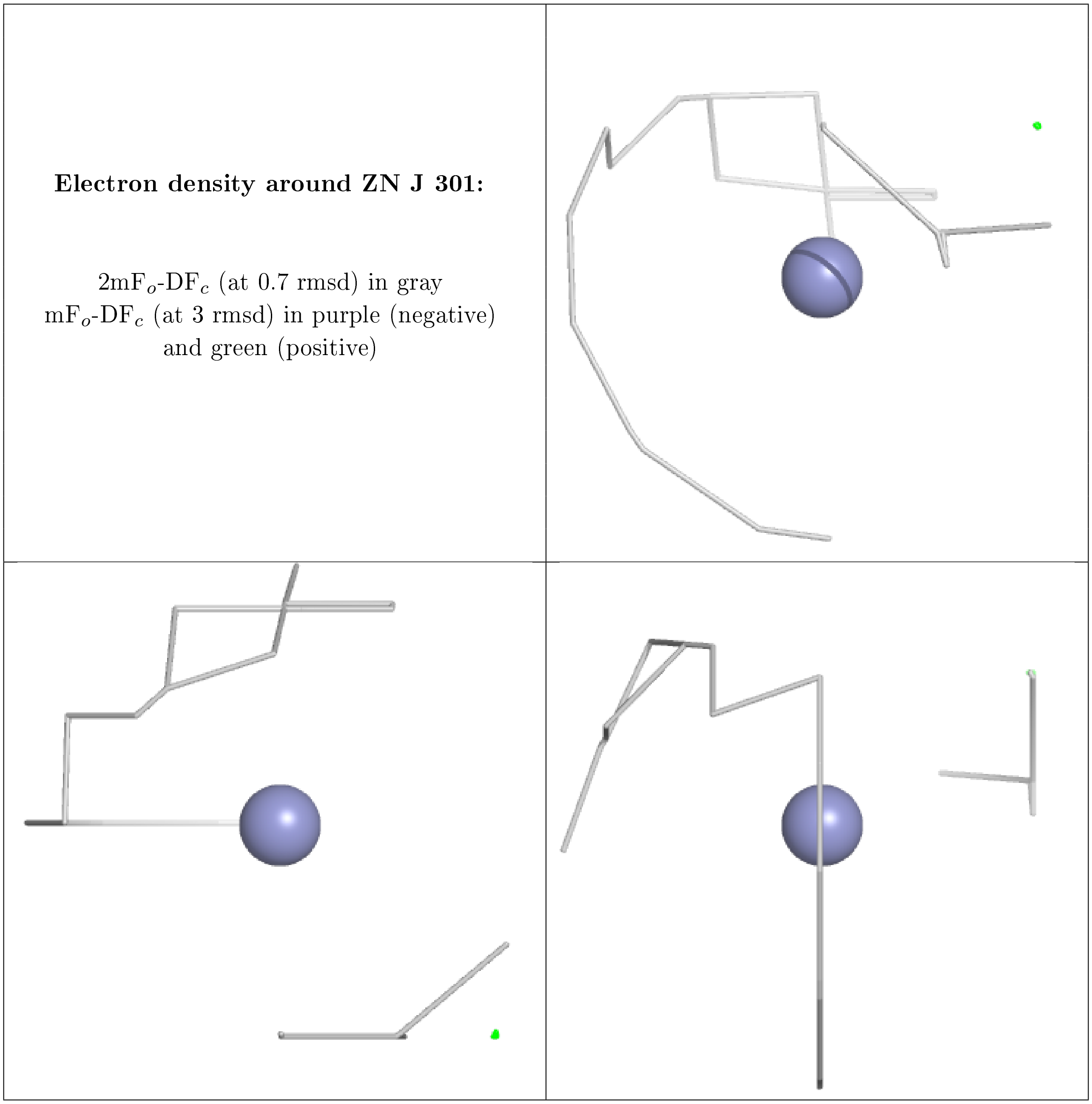






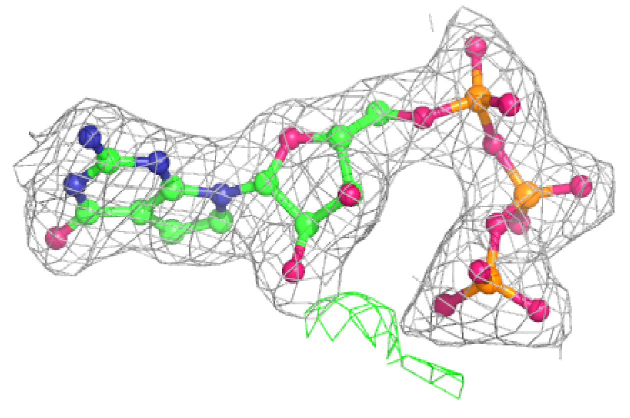


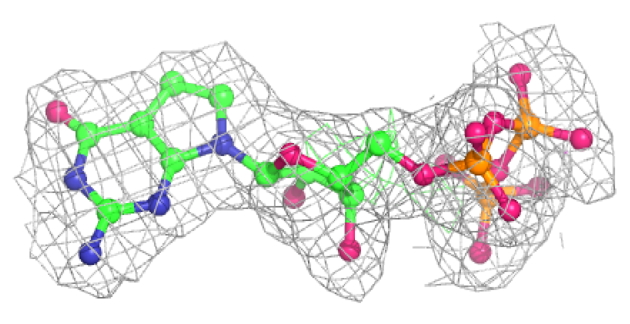
Electron density around ZN J 301:

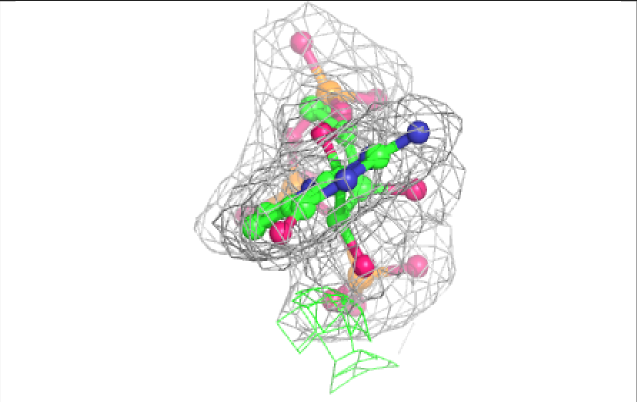
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

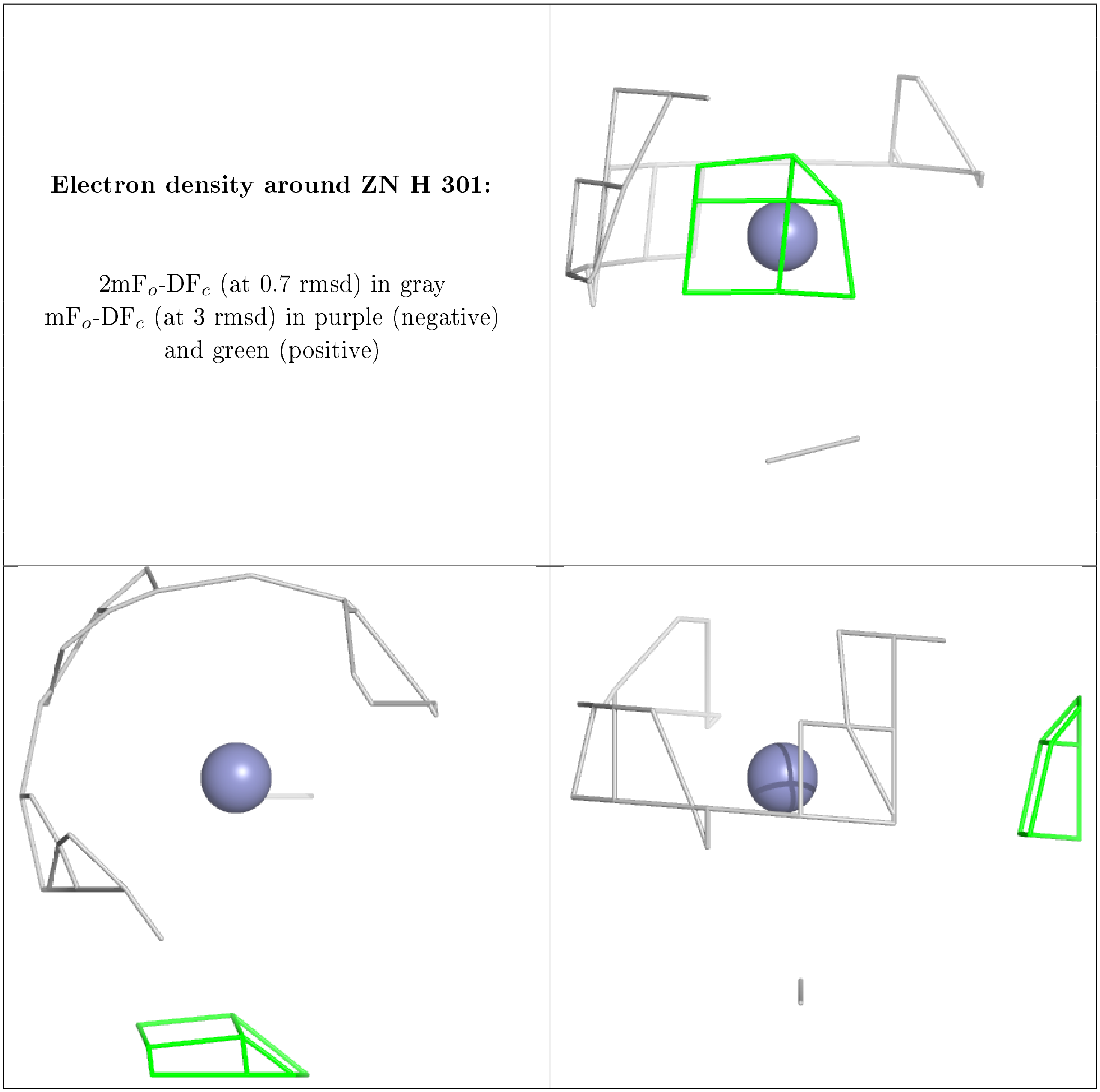
Electron density around QBQ N 302:

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







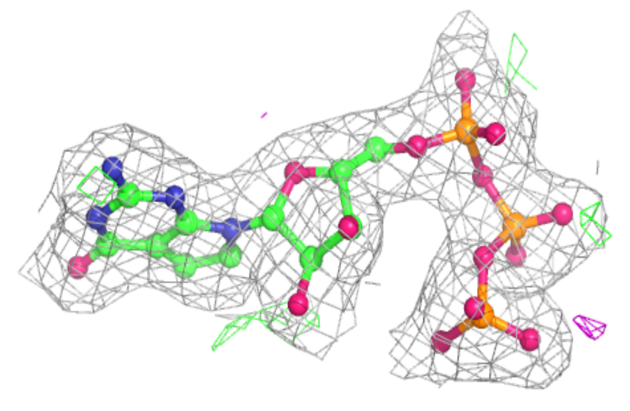


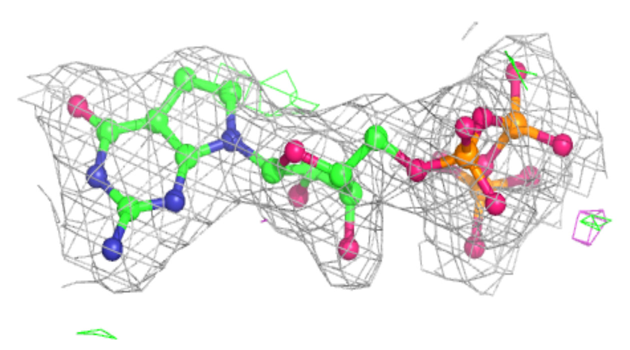
Electron density around ZN H 301:

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 QBQ H 302:

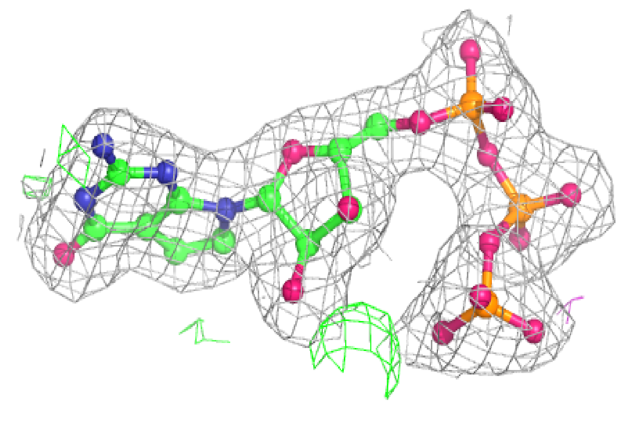
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

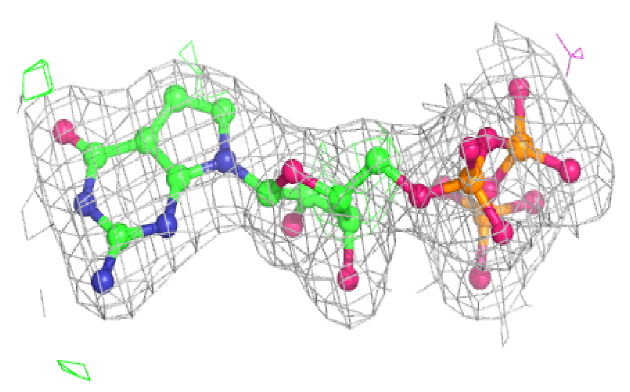


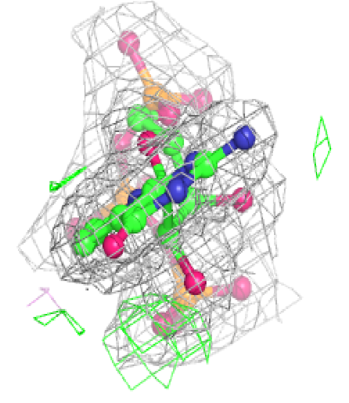


Electron density around QBQ O 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

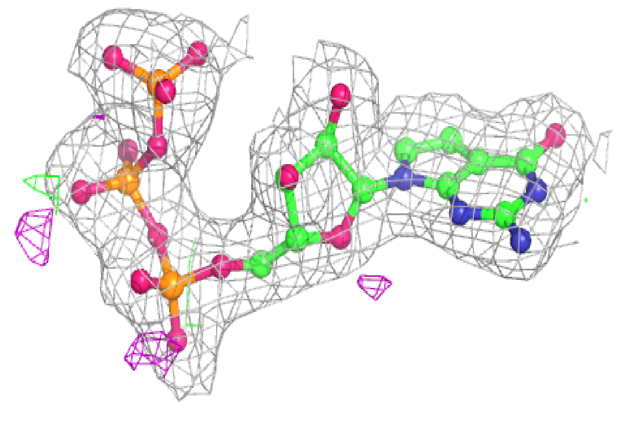


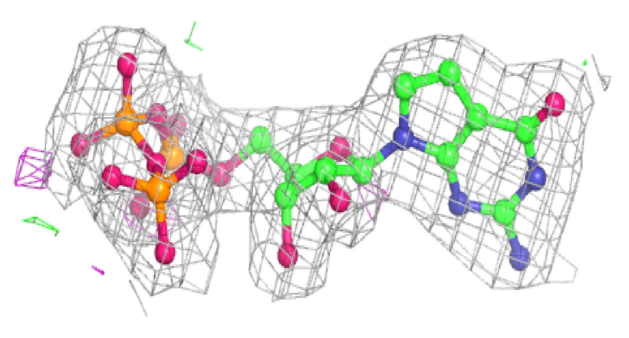


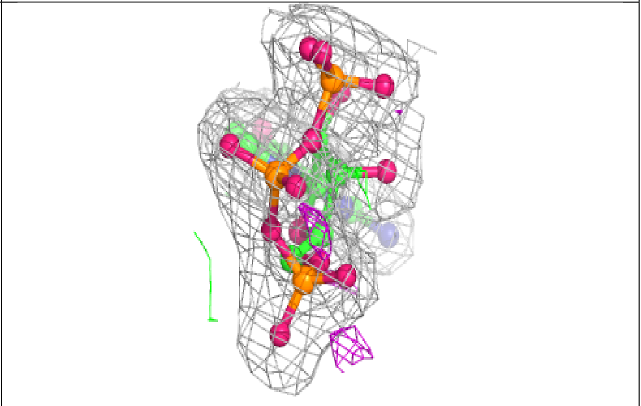


Electron density around QBQ J 302:

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

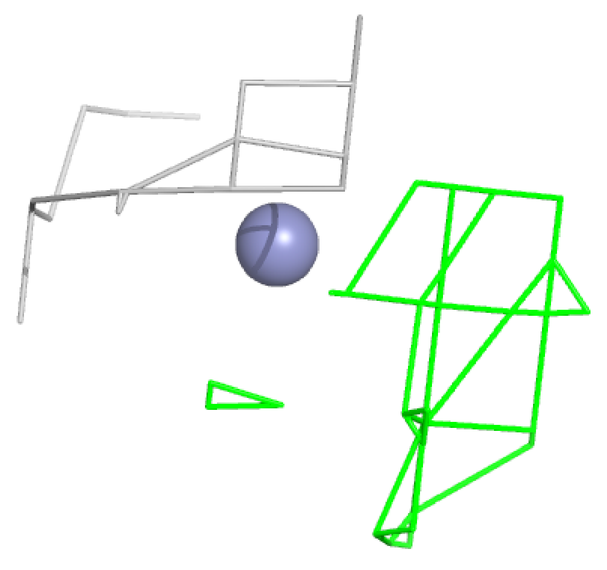


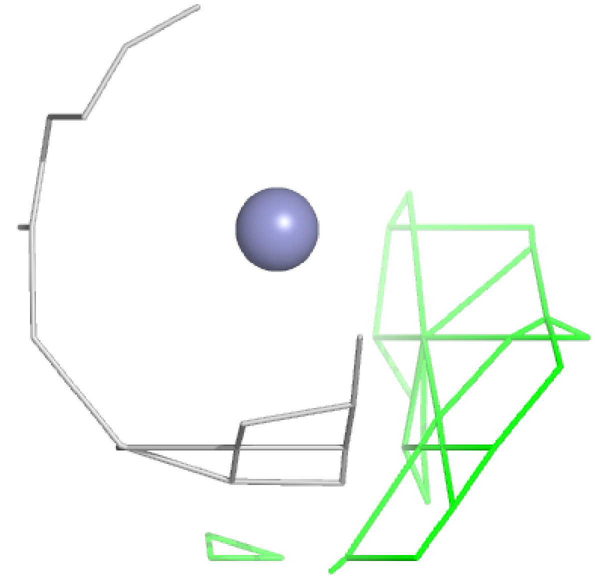


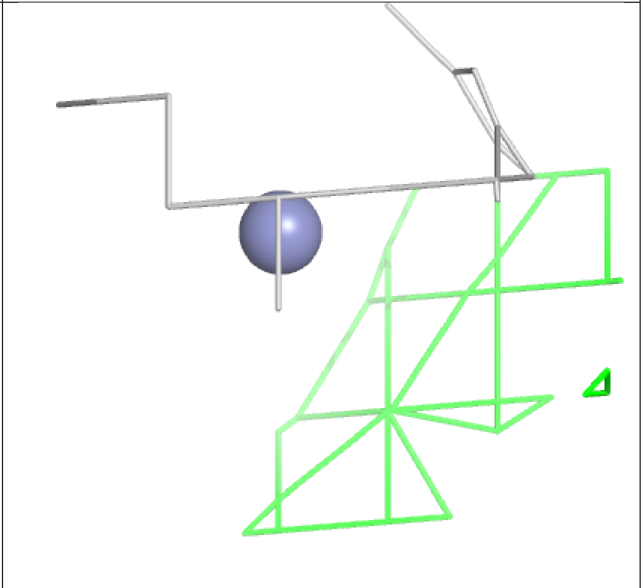


Electron density around ZN T 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

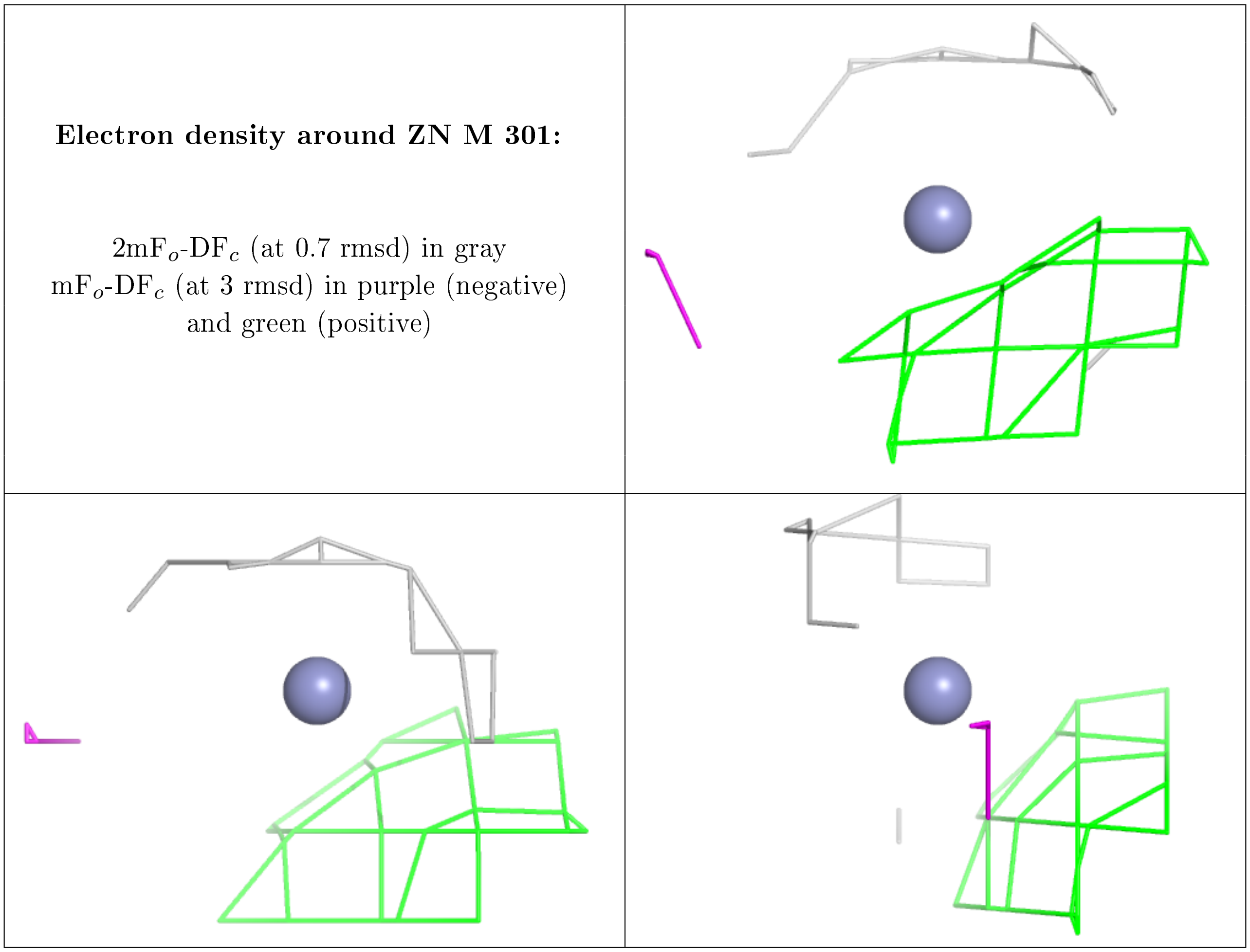


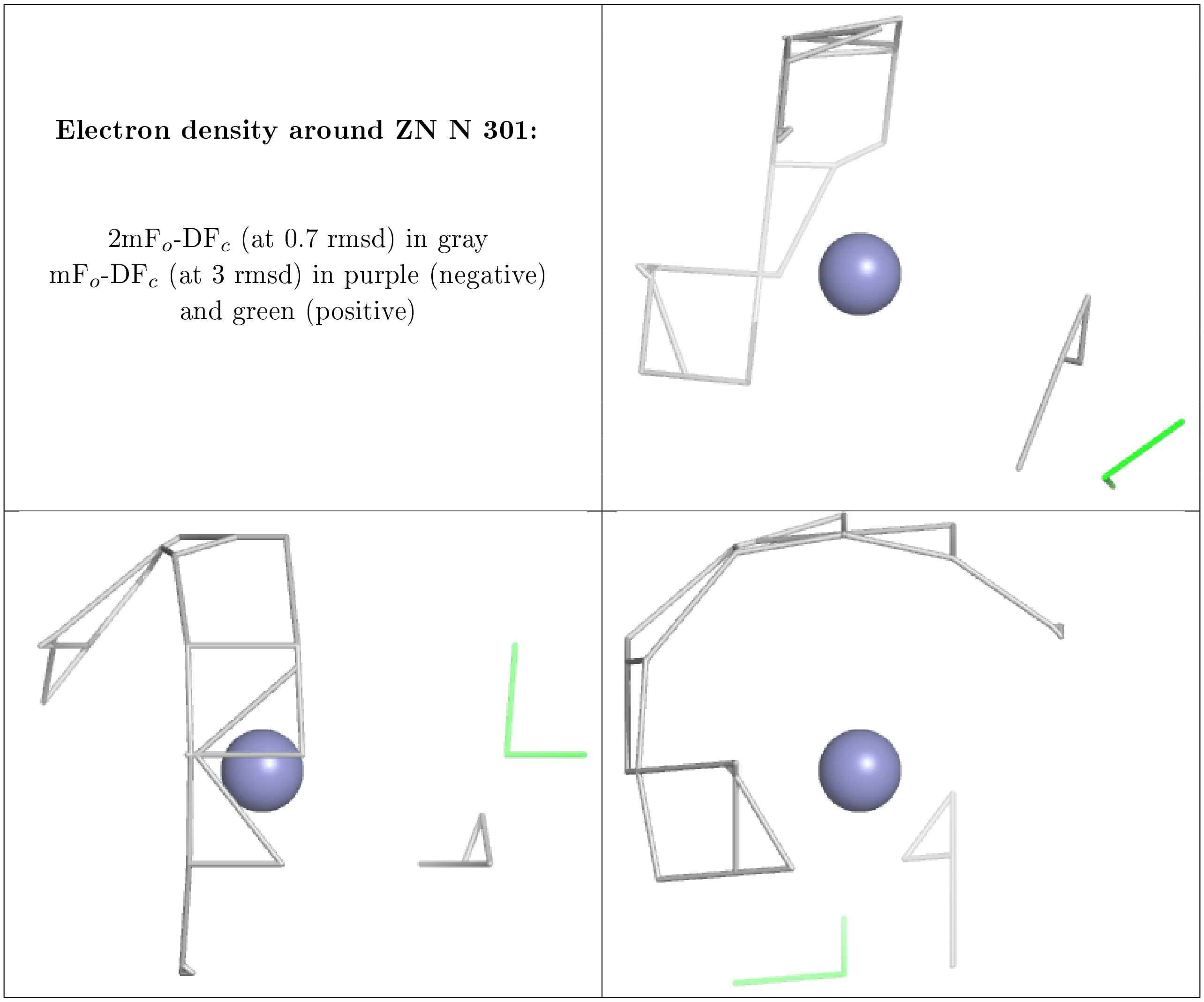




Electron density around ZN M 301:

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



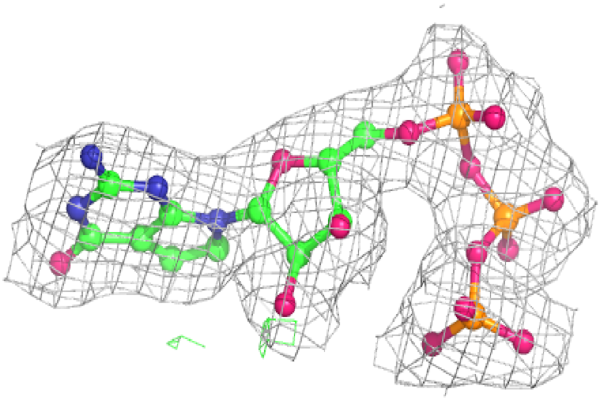


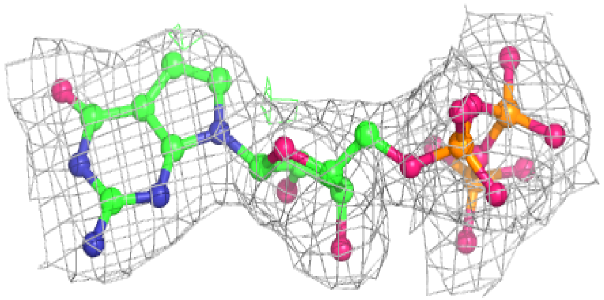
Electron density around ZN N 301:

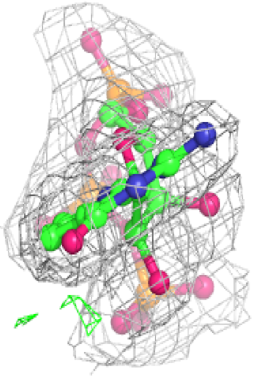
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around QBQ Q 302:

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

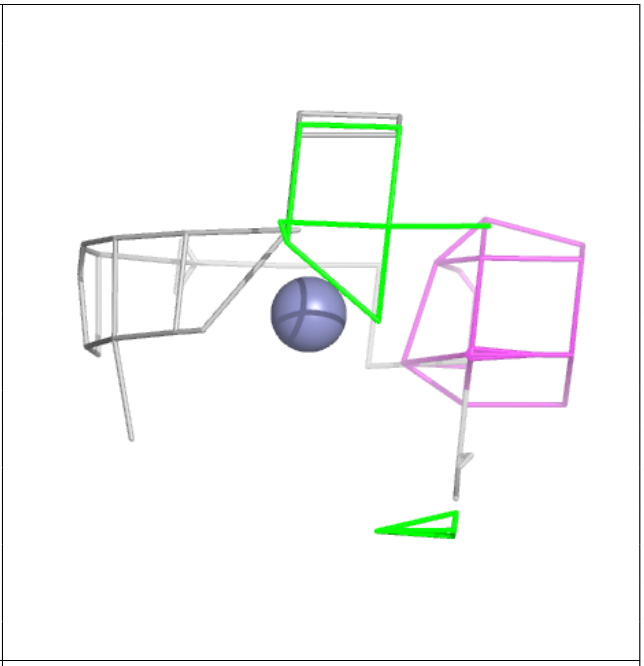


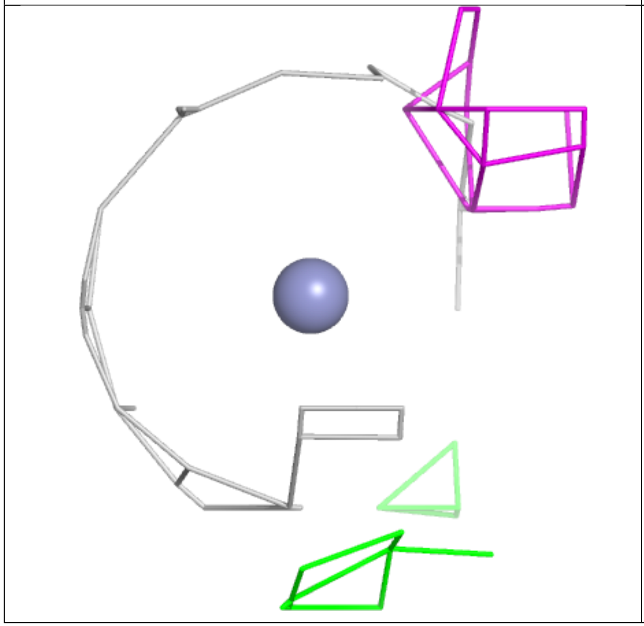


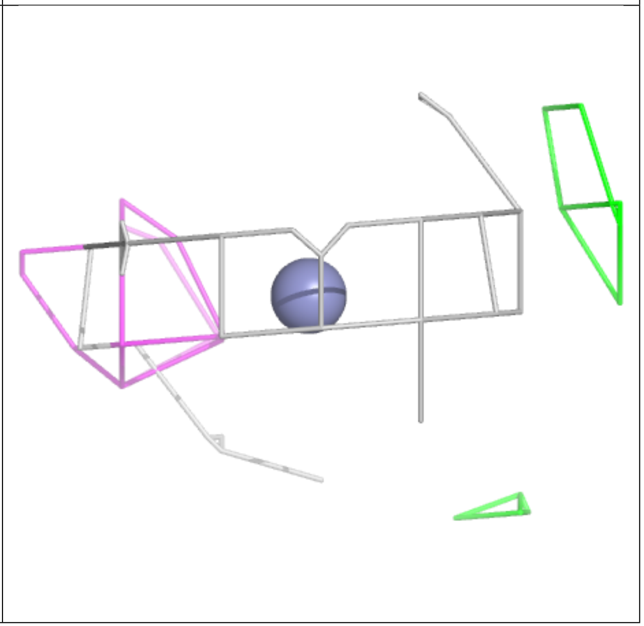


Electron density around ZN F 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

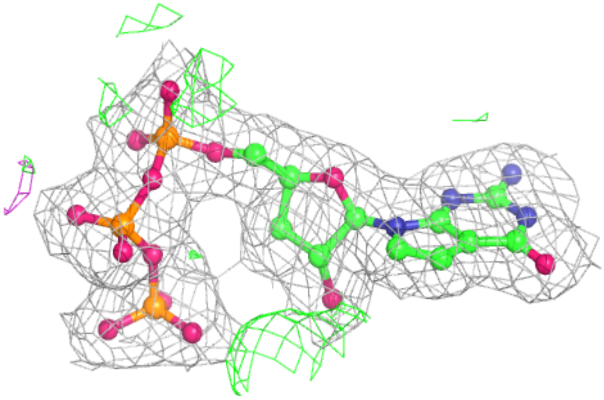


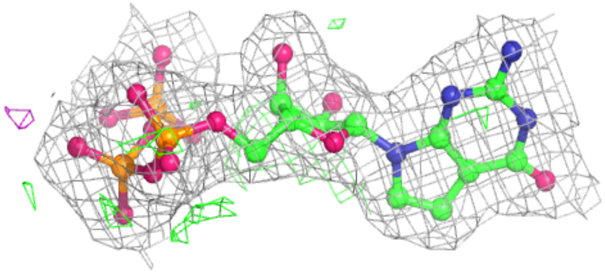


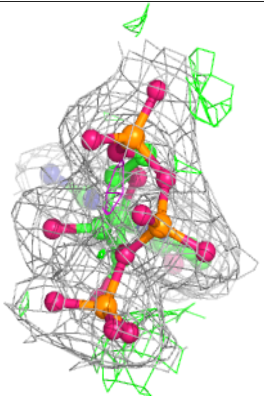


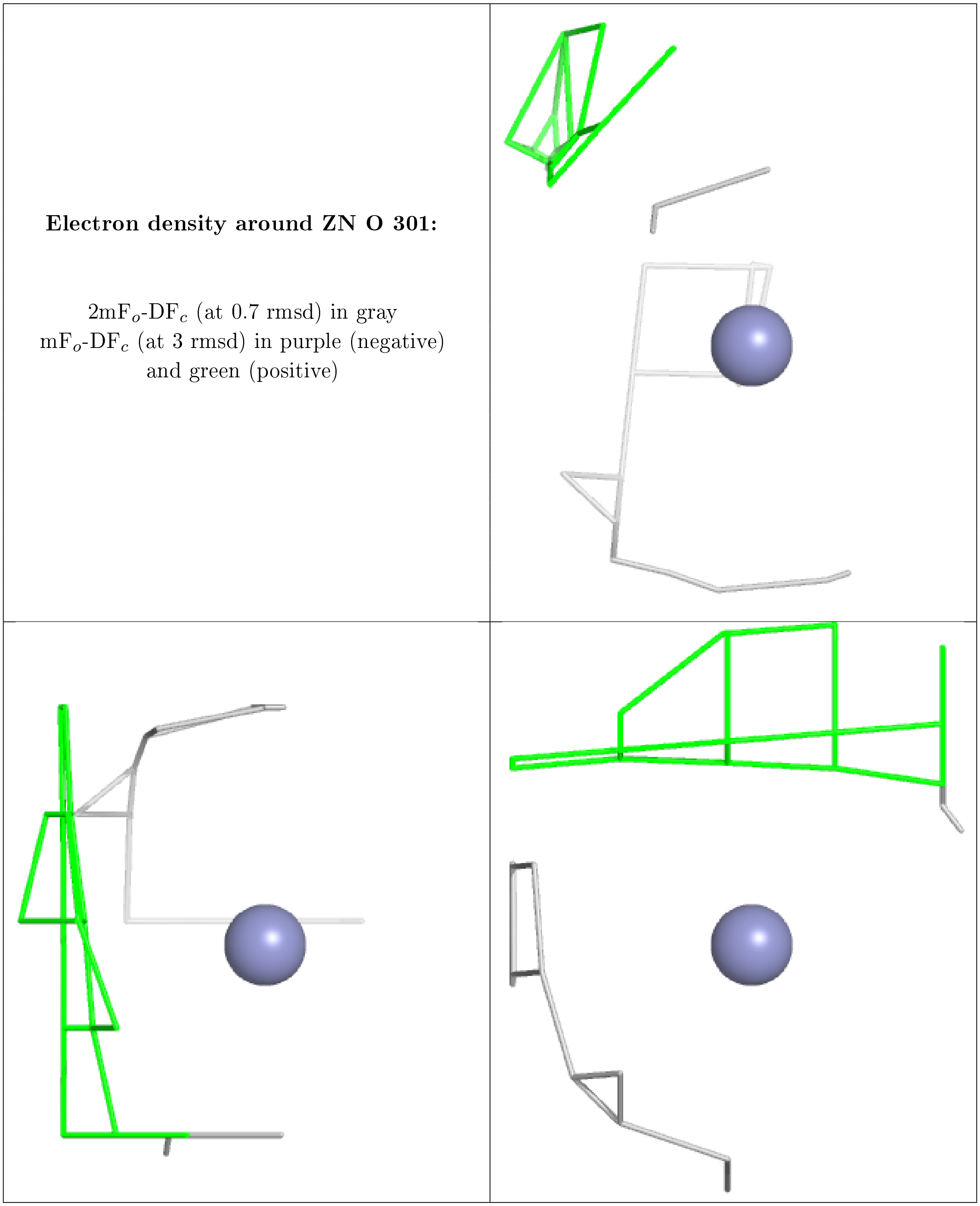
Electron density around QBQ F 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)







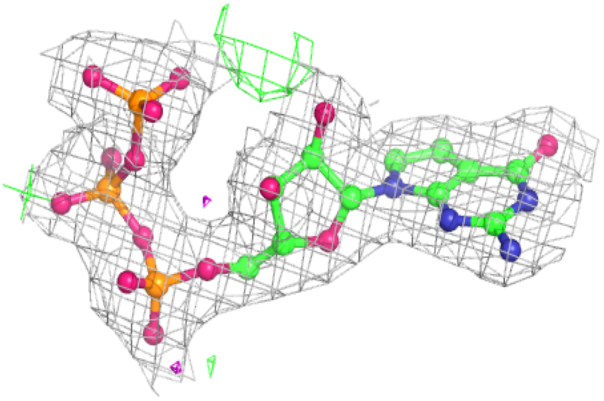


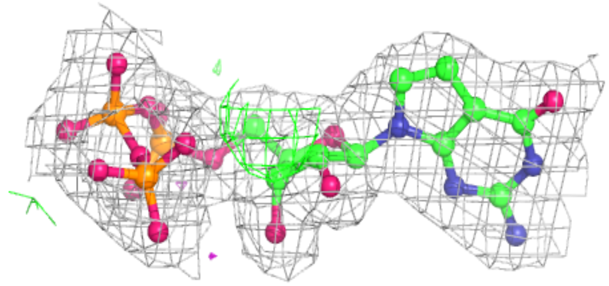
Electron density around ZN O 301:

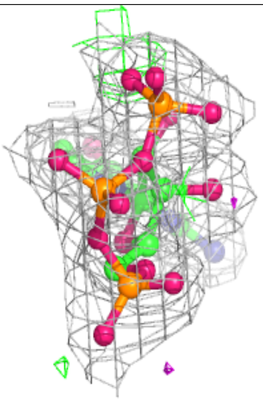
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around QBQ K 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

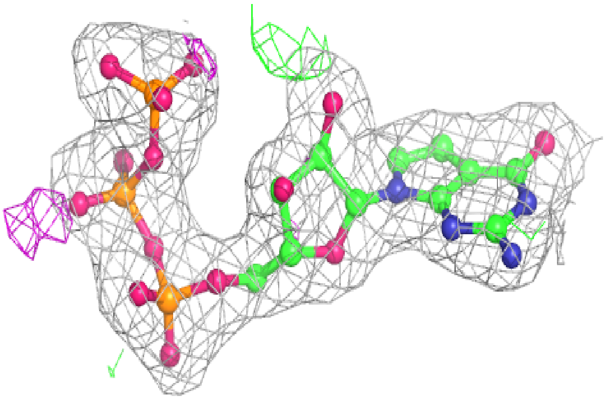


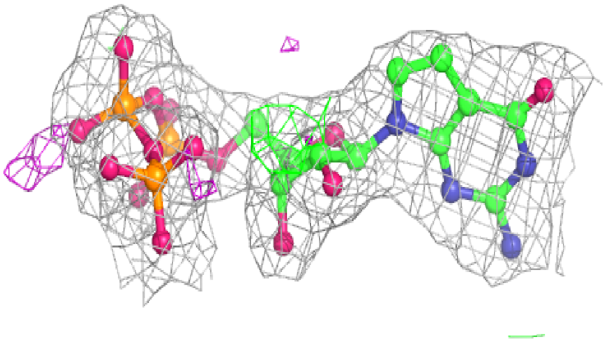


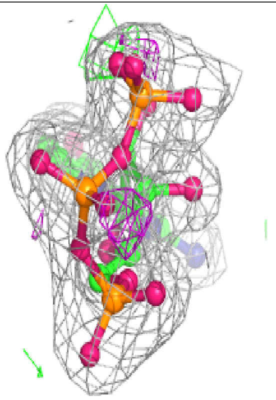


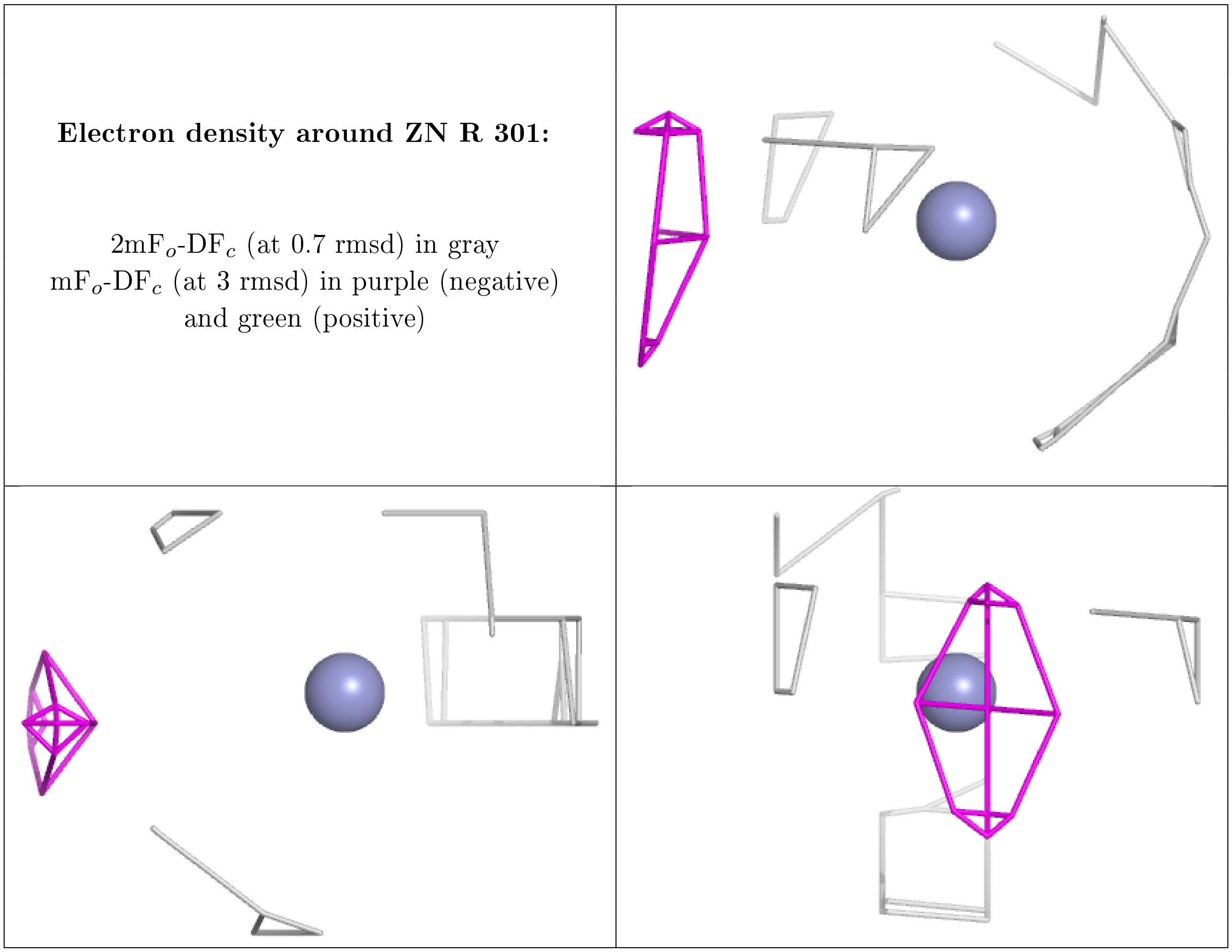
Electron density around QBQ T 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)



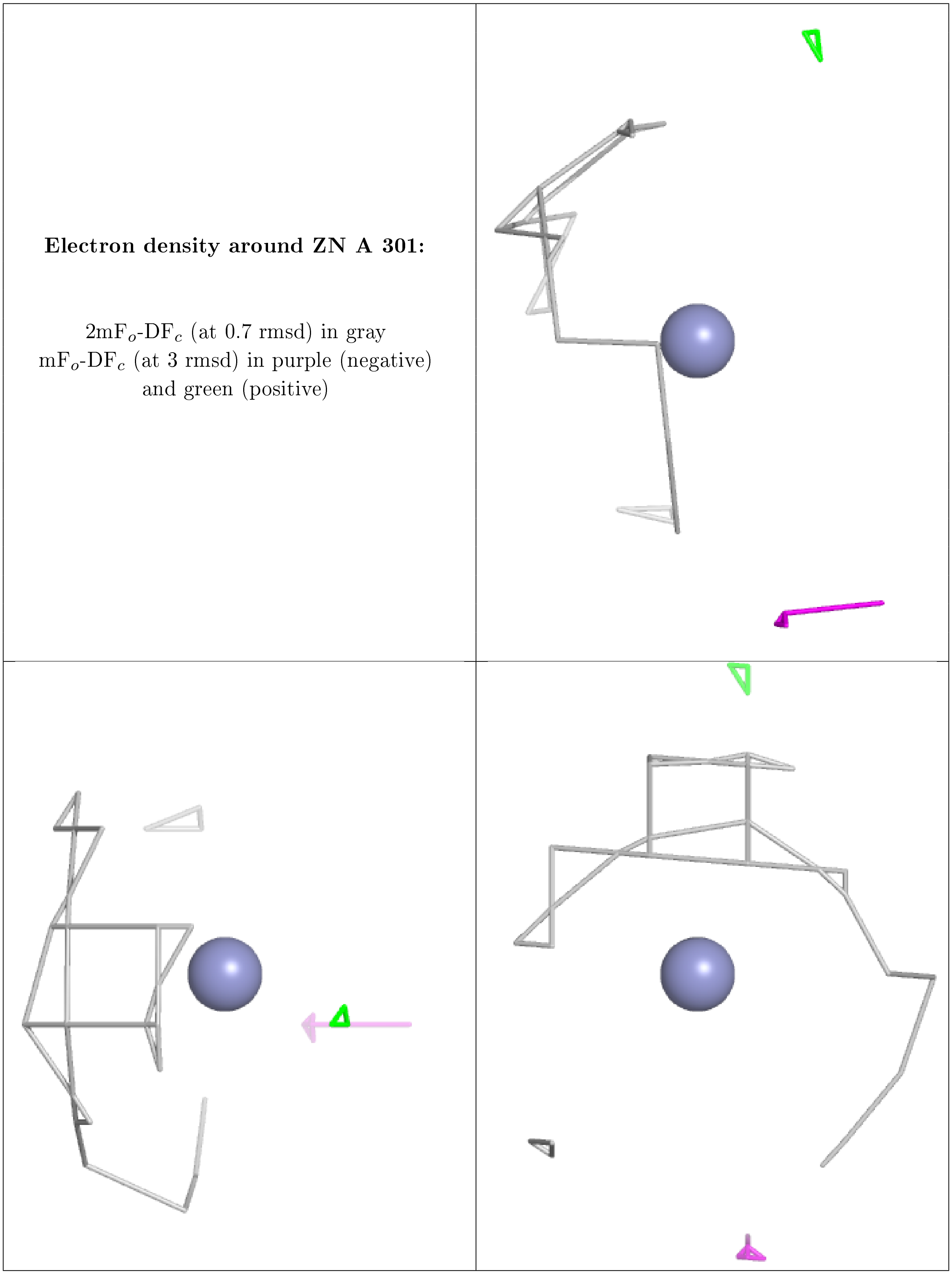






Electron density around ZN R 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

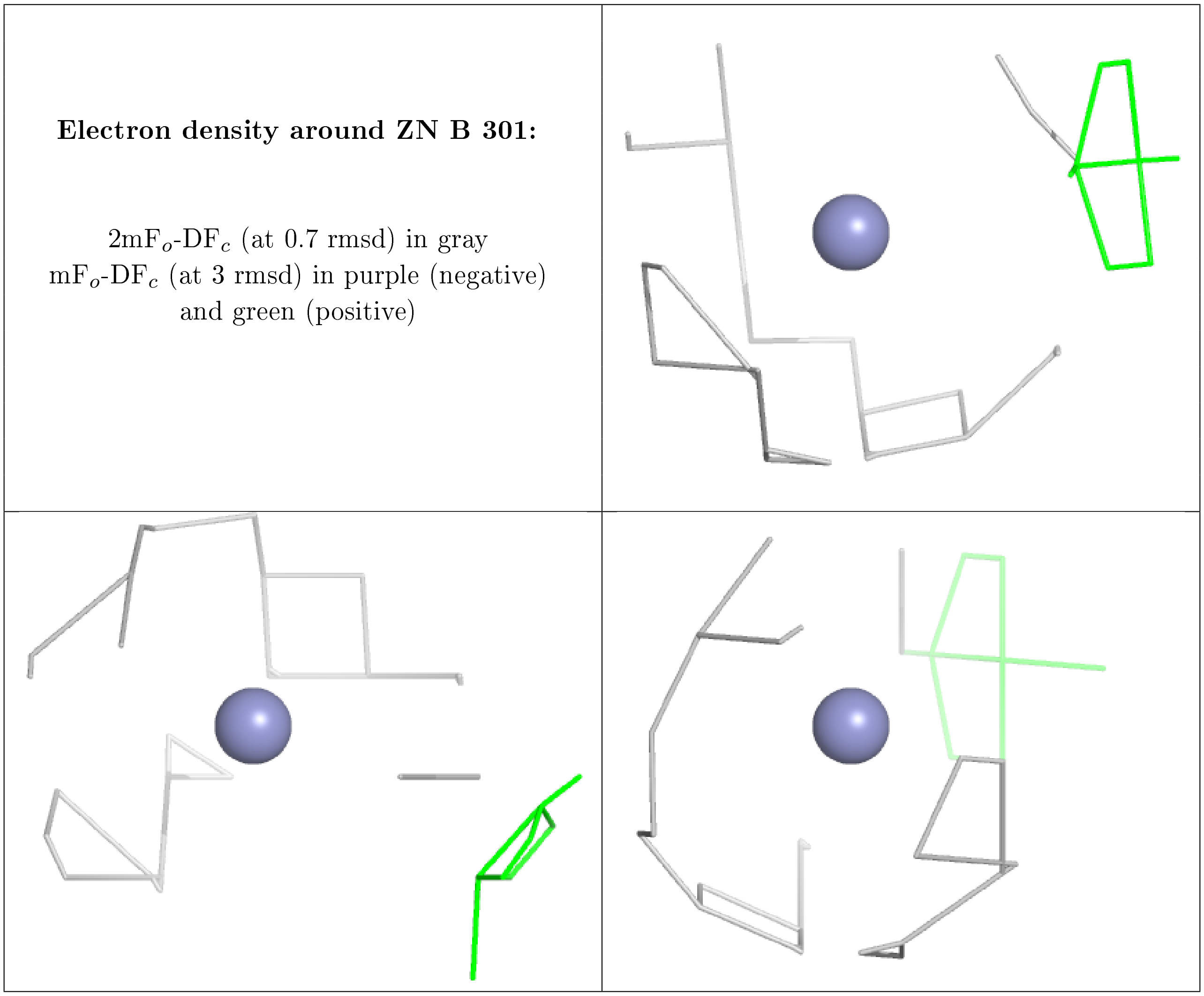


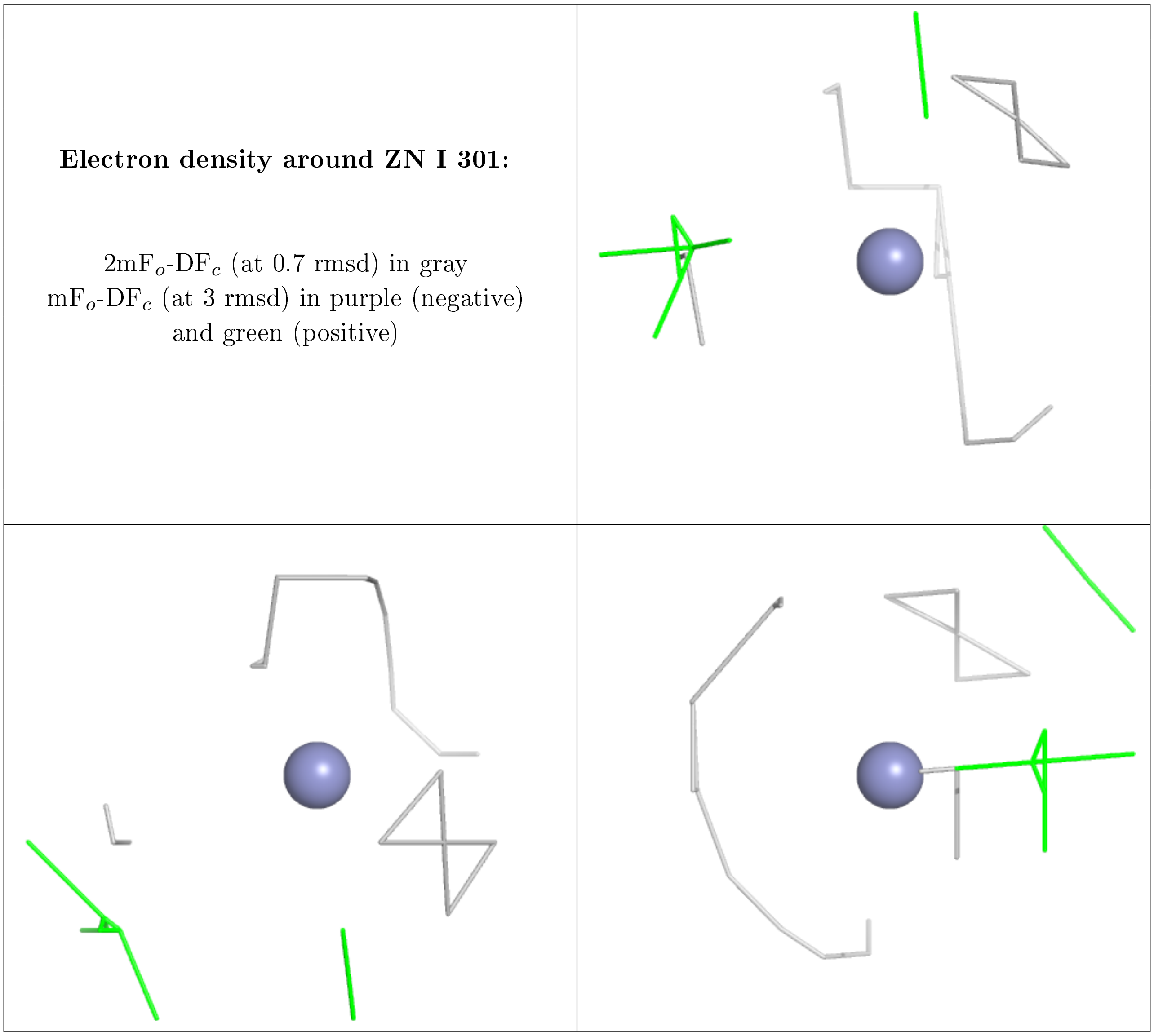
Electron density around ZN A 301:

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 ZN B 301:

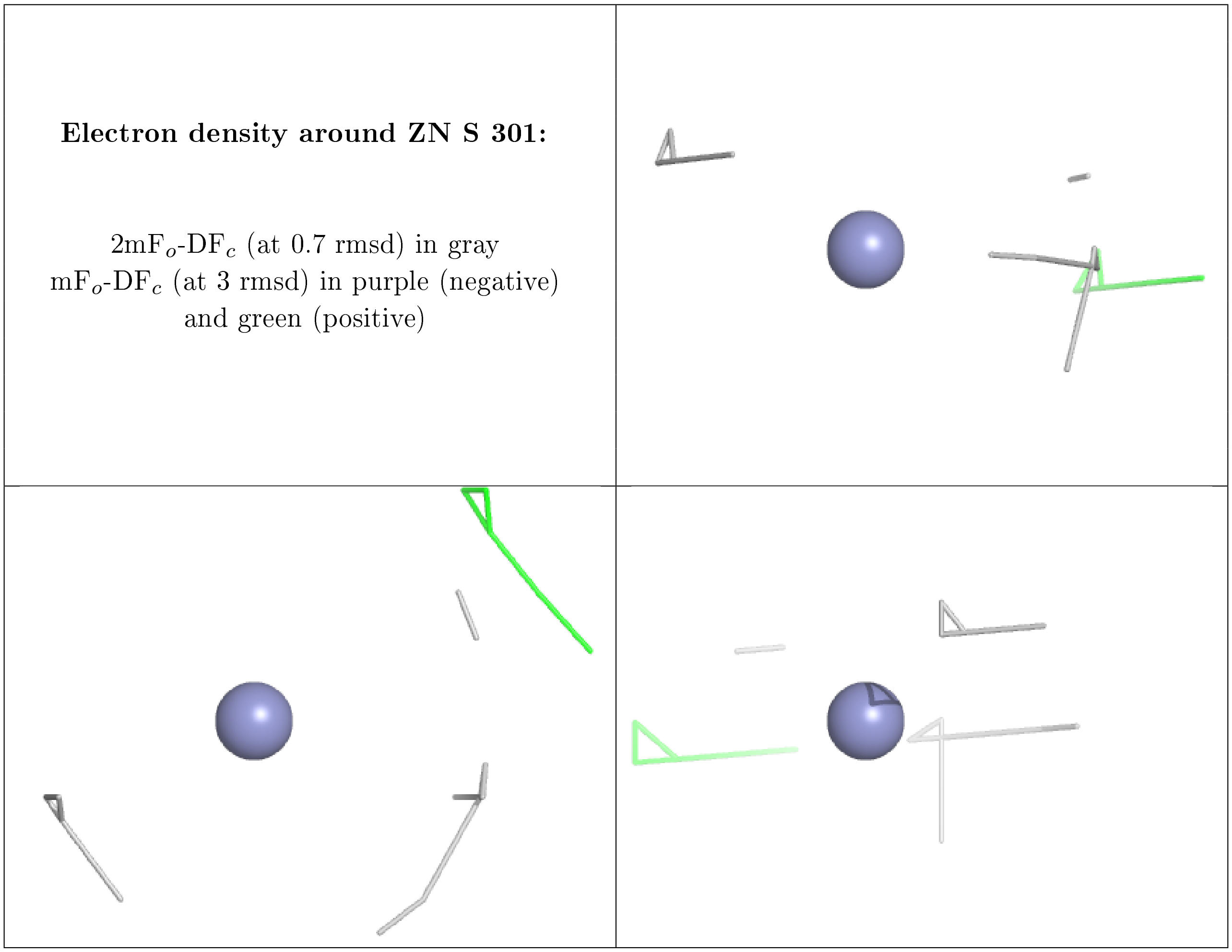
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around ZN I 301:

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



Electron density around ZN S 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers ⓘ

There are no such residues in this entry.