



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2024 – 12:54 pm BST

PDB ID : 5K09
Title : Crystal Structure of COMT in complex with a thiazole ligand
Authors : Ehler, A.; Rodriguez-Sarmiento, R.M.; Rudolph, M.G.
Deposited on : 2016-05-17
Resolution : 2.70 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	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
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)	:	2.36.2

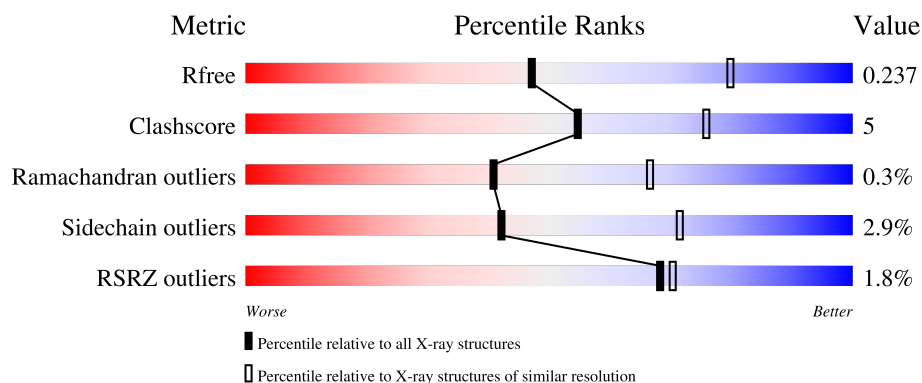
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.







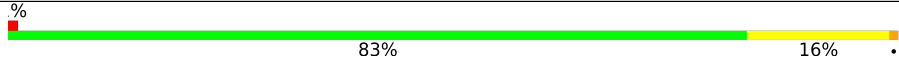
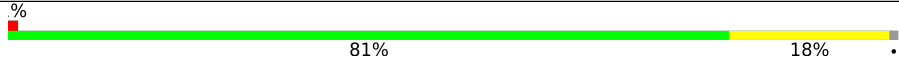
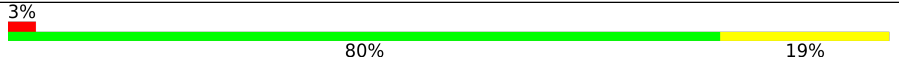
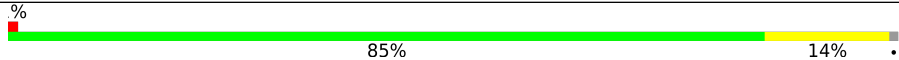
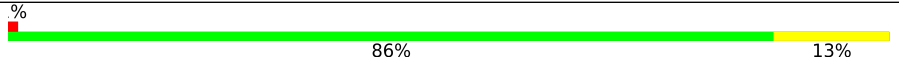
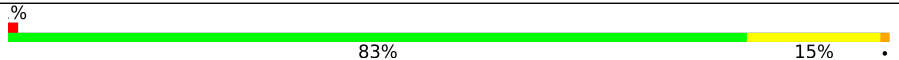
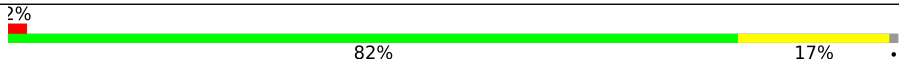
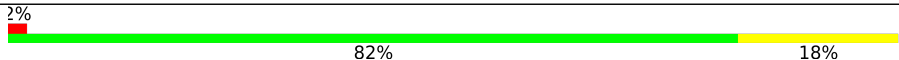


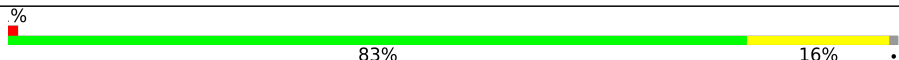
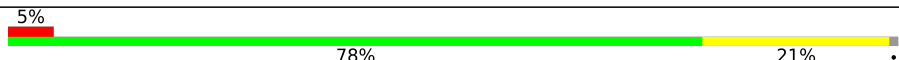
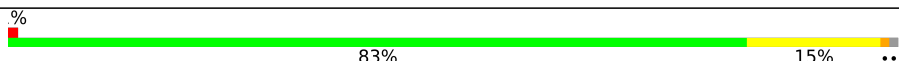
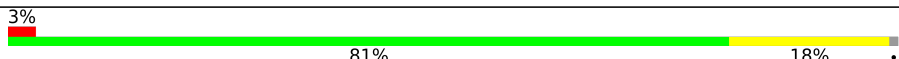
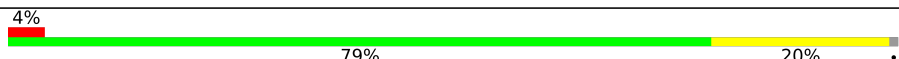
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	217	<div> <div>88%</div> <div>12%</div> </div>
1	B	217	<div> <div>89%</div> <div>10%</div> </div>
1	C	217	<div> <div>2%</div> <div>82%</div> <div>16%</div> </div>
1	D	217	<div> <div>84%</div> <div>14%</div> </div>
1	E	217	<div> <div>5%</div> <div>84%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain	
1	F	217		.
1	G	217		.
1	H	217		.
1	I	217		.
1	J	217		.
1	K	217		.
1	L	217		.
1	M	217		.
1	N	217		.
1	O	217		.
1	P	217		.
1	Q	217		.
1	R	217		.
1	S	217		..
1	T	217		.
1	U	217		.
1	V	217		..
1	W	217		.
1	X	217		.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PO4	I	304	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 41639 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 Catechol O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1697	1075	281	329	12			
1	B	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	C	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	D	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	E	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	F	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	G	217	Total	C	N	O	S	0	0	0
			1697	1075	281	329	12			
1	H	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	I	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	J	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	K	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	L	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	M	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	N	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	O	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	P	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	216	Total	C	N	O	S	0	0	0
			1689	1071	280	326	12			
1	R	217	Total	C	N	O	S	0	0	0
			1697	1075	281	329	12			
1	S	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	T	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	U	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	V	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	W	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			
1	X	215	Total	C	N	O	S	0	0	0
			1683	1068	279	324	12			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	91	ILE	MET	engineered mutation	UNP P22734
A	95	CYS	TYR	engineered mutation	UNP P22734
A	156	GLU	LYS	engineered mutation	UNP P22734
A	218	ASP	-	expression tag	UNP P22734
B	91	ILE	MET	engineered mutation	UNP P22734
B	95	CYS	TYR	engineered mutation	UNP P22734
B	156	GLU	LYS	engineered mutation	UNP P22734
B	218	ASP	-	expression tag	UNP P22734
C	91	ILE	MET	engineered mutation	UNP P22734
C	95	CYS	TYR	engineered mutation	UNP P22734
C	156	GLU	LYS	engineered mutation	UNP P22734
C	218	ASP	-	expression tag	UNP P22734
D	91	ILE	MET	engineered mutation	UNP P22734
D	95	CYS	TYR	engineered mutation	UNP P22734
D	156	GLU	LYS	engineered mutation	UNP P22734
D	218	ASP	-	expression tag	UNP P22734
E	91	ILE	MET	engineered mutation	UNP P22734
E	95	CYS	TYR	engineered mutation	UNP P22734
E	156	GLU	LYS	engineered mutation	UNP P22734
E	218	ASP	-	expression tag	UNP P22734
F	91	ILE	MET	engineered mutation	UNP P22734
F	95	CYS	TYR	engineered mutation	UNP P22734
F	156	GLU	LYS	engineered mutation	UNP P22734

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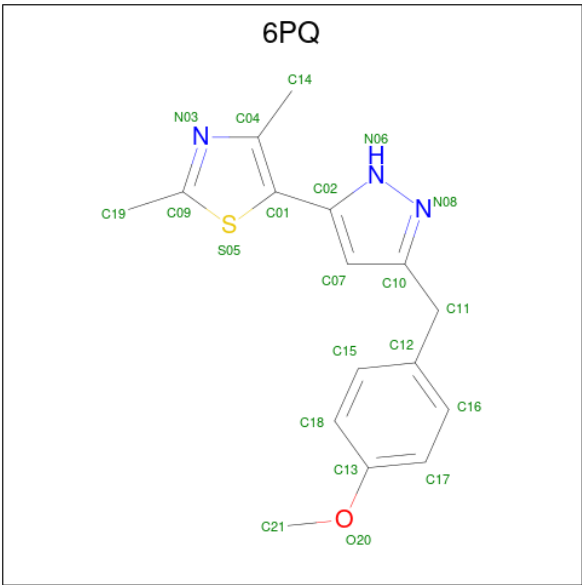
Chain	Residue	Modelled	Actual	Comment	Reference
F	218	ASP	-	expression tag	UNP P22734
G	91	ILE	MET	engineered mutation	UNP P22734
G	95	CYS	TYR	engineered mutation	UNP P22734
G	156	GLU	LYS	engineered mutation	UNP P22734
G	218	ASP	-	expression tag	UNP P22734
H	91	ILE	MET	engineered mutation	UNP P22734
H	95	CYS	TYR	engineered mutation	UNP P22734
H	156	GLU	LYS	engineered mutation	UNP P22734
H	218	ASP	-	expression tag	UNP P22734
I	91	ILE	MET	engineered mutation	UNP P22734
I	95	CYS	TYR	engineered mutation	UNP P22734
I	156	GLU	LYS	engineered mutation	UNP P22734
I	218	ASP	-	expression tag	UNP P22734
J	91	ILE	MET	engineered mutation	UNP P22734
J	95	CYS	TYR	engineered mutation	UNP P22734
J	156	GLU	LYS	engineered mutation	UNP P22734
J	218	ASP	-	expression tag	UNP P22734
K	91	ILE	MET	engineered mutation	UNP P22734
K	95	CYS	TYR	engineered mutation	UNP P22734
K	156	GLU	LYS	engineered mutation	UNP P22734
K	218	ASP	-	expression tag	UNP P22734
L	91	ILE	MET	engineered mutation	UNP P22734
L	95	CYS	TYR	engineered mutation	UNP P22734
L	156	GLU	LYS	engineered mutation	UNP P22734
L	218	ASP	-	expression tag	UNP P22734
M	91	ILE	MET	engineered mutation	UNP P22734
M	95	CYS	TYR	engineered mutation	UNP P22734
M	156	GLU	LYS	engineered mutation	UNP P22734
M	218	ASP	-	expression tag	UNP P22734
N	91	ILE	MET	engineered mutation	UNP P22734
N	95	CYS	TYR	engineered mutation	UNP P22734
N	156	GLU	LYS	engineered mutation	UNP P22734
N	218	ASP	-	expression tag	UNP P22734
O	91	ILE	MET	engineered mutation	UNP P22734
O	95	CYS	TYR	engineered mutation	UNP P22734
O	156	GLU	LYS	engineered mutation	UNP P22734
O	218	ASP	-	expression tag	UNP P22734
P	91	ILE	MET	engineered mutation	UNP P22734
P	95	CYS	TYR	engineered mutation	UNP P22734
P	156	GLU	LYS	engineered mutation	UNP P22734
P	218	ASP	-	expression tag	UNP P22734
Q	91	ILE	MET	engineered mutation	UNP P22734

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	95	CYS	TYR	engineered mutation	UNP P22734
Q	156	GLU	LYS	engineered mutation	UNP P22734
Q	218	ASP	-	expression tag	UNP P22734
R	91	ILE	MET	engineered mutation	UNP P22734
R	95	CYS	TYR	engineered mutation	UNP P22734
R	156	GLU	LYS	engineered mutation	UNP P22734
R	218	ASP	-	expression tag	UNP P22734
S	91	ILE	MET	engineered mutation	UNP P22734
S	95	CYS	TYR	engineered mutation	UNP P22734
S	156	GLU	LYS	engineered mutation	UNP P22734
S	218	ASP	-	expression tag	UNP P22734
T	91	ILE	MET	engineered mutation	UNP P22734
T	95	CYS	TYR	engineered mutation	UNP P22734
T	156	GLU	LYS	engineered mutation	UNP P22734
T	218	ASP	-	expression tag	UNP P22734
U	91	ILE	MET	engineered mutation	UNP P22734
U	95	CYS	TYR	engineered mutation	UNP P22734
U	156	GLU	LYS	engineered mutation	UNP P22734
U	218	ASP	-	expression tag	UNP P22734
V	91	ILE	MET	engineered mutation	UNP P22734
V	95	CYS	TYR	engineered mutation	UNP P22734
V	156	GLU	LYS	engineered mutation	UNP P22734
V	218	ASP	-	expression tag	UNP P22734
W	91	ILE	MET	engineered mutation	UNP P22734
W	95	CYS	TYR	engineered mutation	UNP P22734
W	156	GLU	LYS	engineered mutation	UNP P22734
W	218	ASP	-	expression tag	UNP P22734
X	91	ILE	MET	engineered mutation	UNP P22734
X	95	CYS	TYR	engineered mutation	UNP P22734
X	156	GLU	LYS	engineered mutation	UNP P22734
X	218	ASP	-	expression tag	UNP P22734

- Molecule 2 is 5-{3-[(4-methoxyphenyl)methyl]-1H-pyrazol-5-yl}-2,4-dimethyl-1,3-thiazole (three-letter code: 6PQ) (formula: C₁₆H₁₇N₃OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	B	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	C	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	D	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	E	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	F	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	G	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	H	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	I	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	J	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	K	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	L	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	M	1	Total	C	N	O	S	0	0
			21	16	3	1	1		
2	N	1	Total	C	N	O	S	0	0
			21	16	3	1	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	O	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	P	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	Q	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	R	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	S	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	T	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	U	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	V	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	W	1	Total 21	C 16	N 3	O 1	S 1	0	0
2	X	1	Total 21	C 16	N 3	O 1	S 1	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

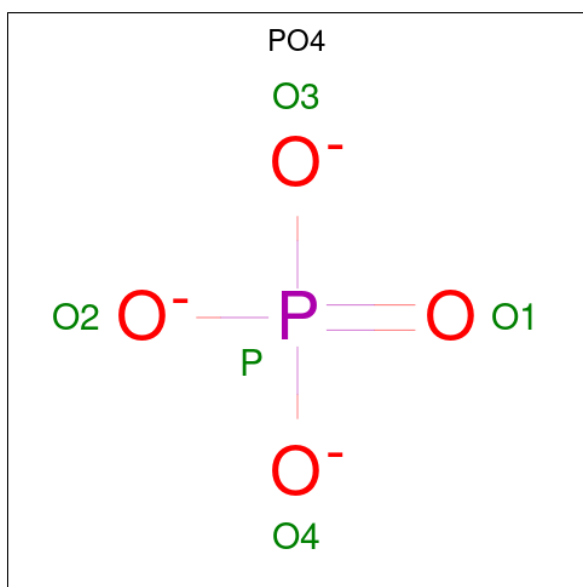
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total 3	K 3	0	0
3	B	2	Total 2	K 2	0	0
3	C	2	Total 2	K 2	0	0
3	D	2	Total 2	K 2	0	0
3	E	2	Total 2	K 2	0	0
3	F	2	Total 2	K 2	0	0
3	G	3	Total 3	K 3	0	0
3	H	2	Total 2	K 2	0	0
3	I	2	Total 2	K 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	3	Total 3	K 3	0	0
3	K	3	Total 3	K 3	0	0
3	L	3	Total 3	K 3	0	0
3	M	3	Total 3	K 3	0	0
3	N	3	Total 3	K 3	0	0
3	O	3	Total 3	K 3	0	0
3	P	2	Total 2	K 2	0	0
3	Q	2	Total 2	K 2	0	0
3	R	3	Total 3	K 3	0	0
3	S	3	Total 3	K 3	0	0
3	T	2	Total 2	K 2	0	0
3	U	2	Total 2	K 2	0	0
3	V	2	Total 2	K 2	0	0
3	W	2	Total 2	K 2	0	0
3	X	2	Total 2	K 2	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		
4	H	1	Total	O	P	0	0
			5	4	1		
4	I	1	Total	O	P	0	0
			5	4	1		
4	K	1	Total	O	P	0	0
			5	4	1		
4	M	1	Total	O	P	0	0
			5	4	1		
4	N	1	Total	O	P	0	0
			5	4	1		
4	Q	1	Total	O	P	0	0
			5	4	1		
4	S	1	Total	O	P	0	0
			5	4	1		
4	T	1	Total	O	P	0	0
			5	4	1		
4	V	1	Total	O	P	0	0
			5	4	1		
4	W	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	23	Total O 23 23	0	0
5	B	33	Total O 33 33	0	0
5	C	23	Total O 23 23	0	0
5	D	20	Total O 20 20	0	0
5	E	17	Total O 17 17	0	0
5	F	24	Total O 24 24	0	0
5	G	16	Total O 16 16	0	0
5	H	31	Total O 31 31	0	0
5	I	21	Total O 21 21	0	0
5	J	27	Total O 27 27	0	0
5	K	30	Total O 30 30	0	0
5	L	24	Total O 24 24	0	0
5	M	23	Total O 23 23	0	0
5	N	43	Total O 43 43	0	0
5	O	26	Total O 26 26	0	0
5	P	12	Total O 12 12	0	0
5	Q	24	Total O 24 24	0	0
5	R	27	Total O 27 27	0	0
5	S	22	Total O 22 22	0	0
5	T	23	Total O 23 23	0	0
5	U	10	Total O 10 10	0	0
5	V	15	Total O 15 15	0	0

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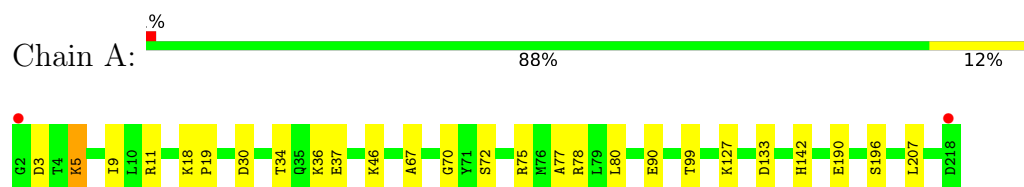
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	W	13	Total 13	O 13	0	0
5	X	8	Total 8	O 8	0	0

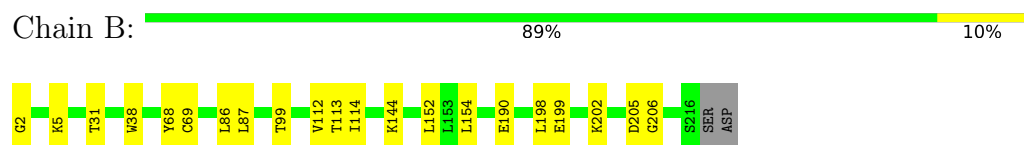
3 Residue-property plots [i](#)

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

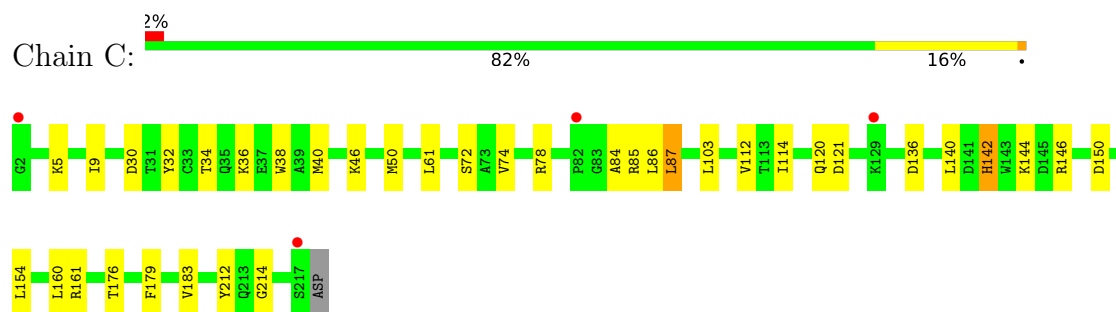
- Molecule 1: Catechol O-methyltransferase



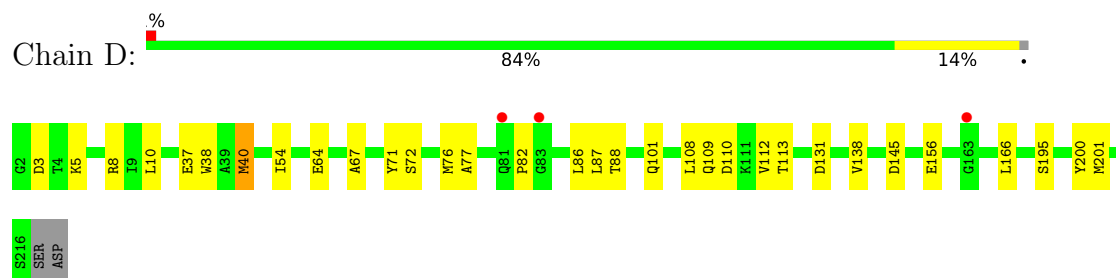
- Molecule 1: Catechol O-methyltransferase



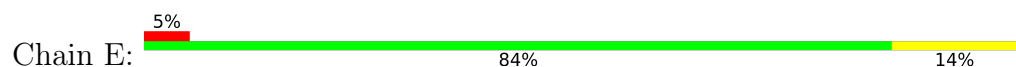
- Molecule 1: Catechol O-methyltransferase

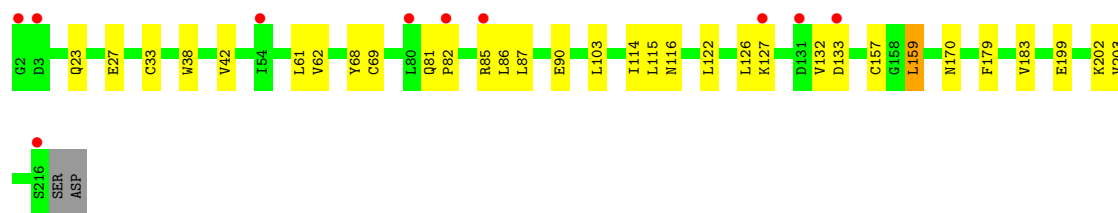


- Molecule 1: Catechol O-methyltransferase

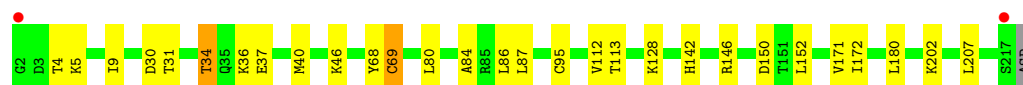
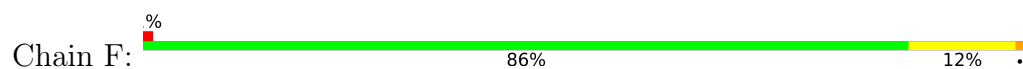


- Molecule 1: Catechol O-methyltransferase

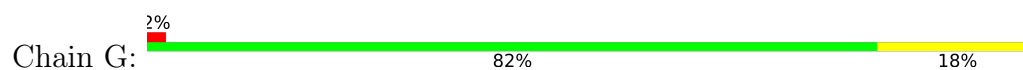




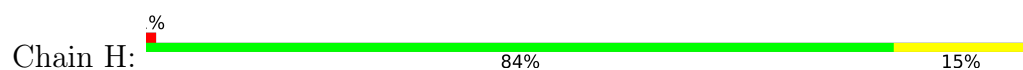
- Molecule 1: Catechol O-methyltransferase



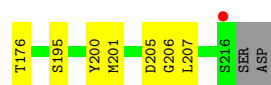
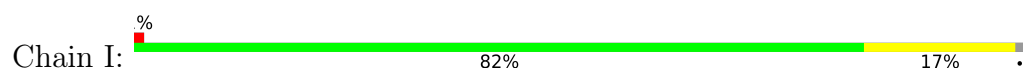
- Molecule 1: Catechol O-methyltransferase



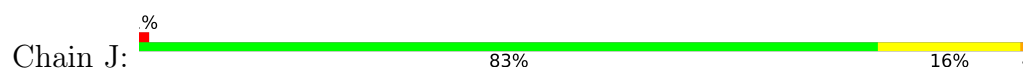
- Molecule 1: Catechol O-methyltransferase



- Molecule 1: Catechol O-methyltransferase

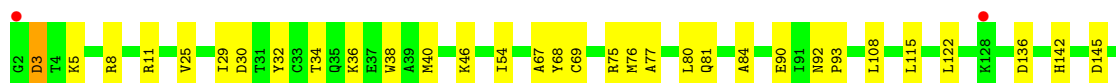
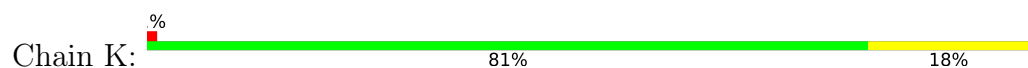


- Molecule 1: Catechol O-methyltransferase

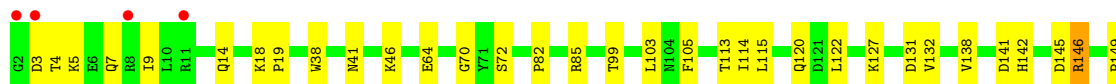
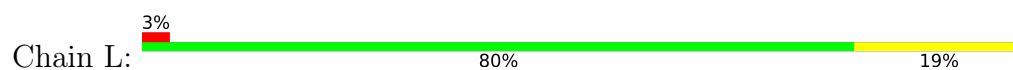




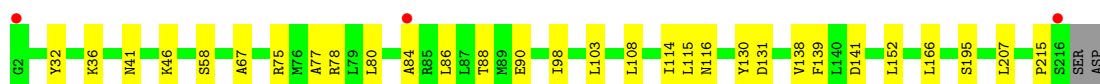
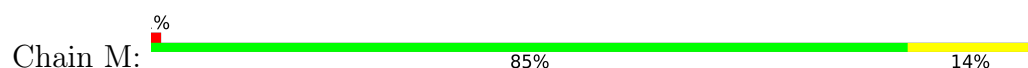
- Molecule 1: Catechol O-methyltransferase



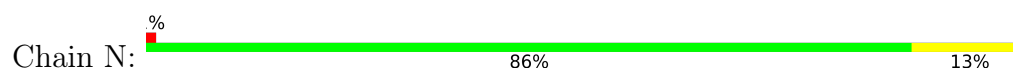
- Molecule 1: Catechol O-methyltransferase



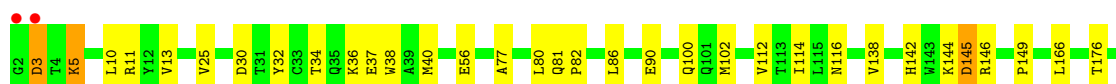
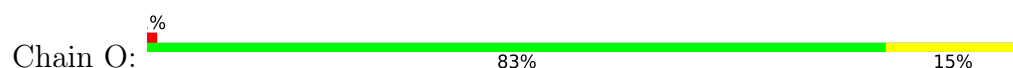
- Molecule 1: Catechol O-methyltransferase



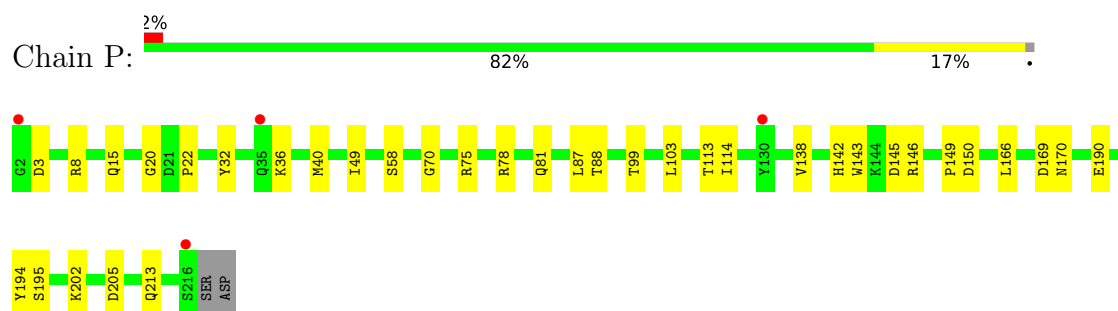
- Molecule 1: Catechol O-methyltransferase



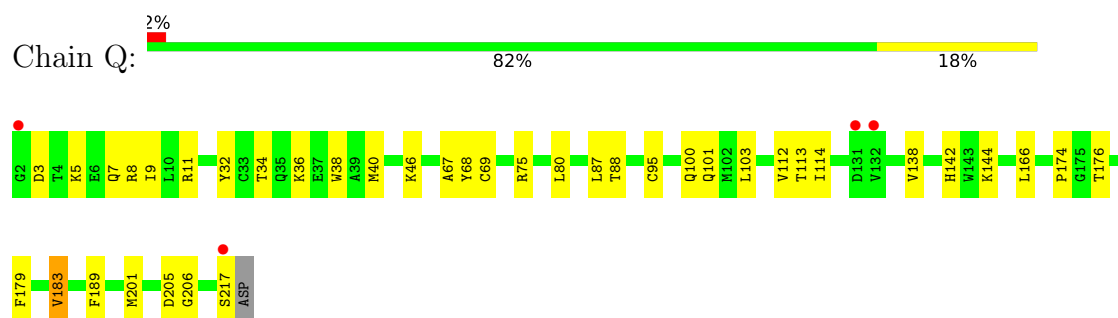
- Molecule 1: Catechol O-methyltransferase



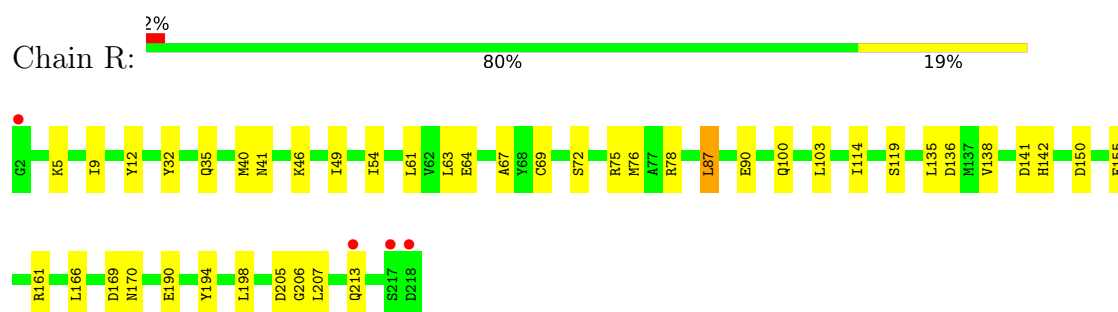
- Molecule 1: Catechol O-methyltransferase



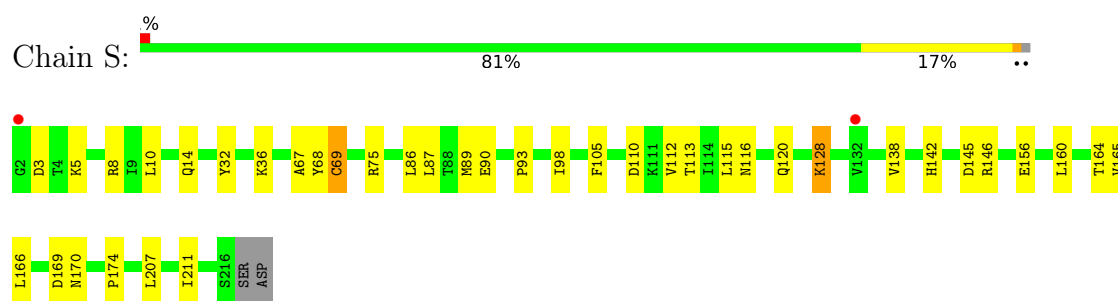
- Molecule 1: Catechol O-methyltransferase



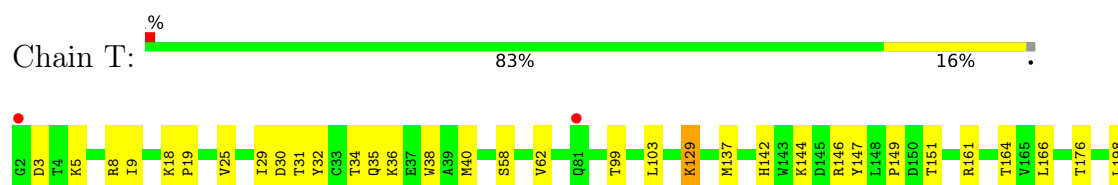
- Molecule 1: Catechol O-methyltransferase

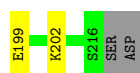


- Molecule 1: Catechol O-methyltransferase

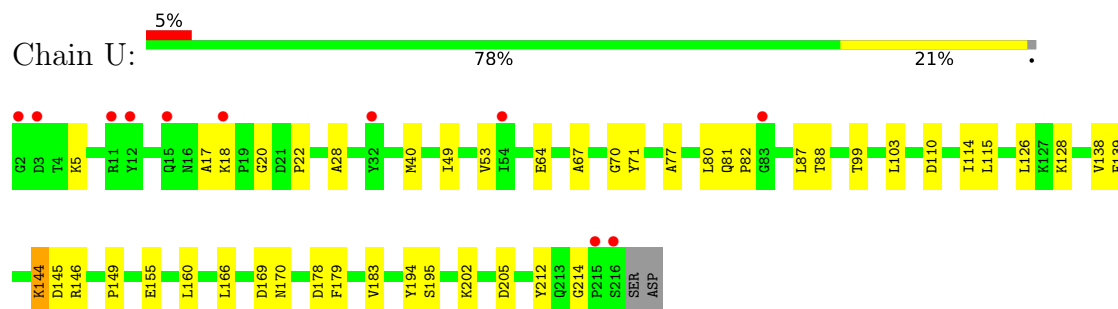


- Molecule 1: Catechol O-methyltransferase

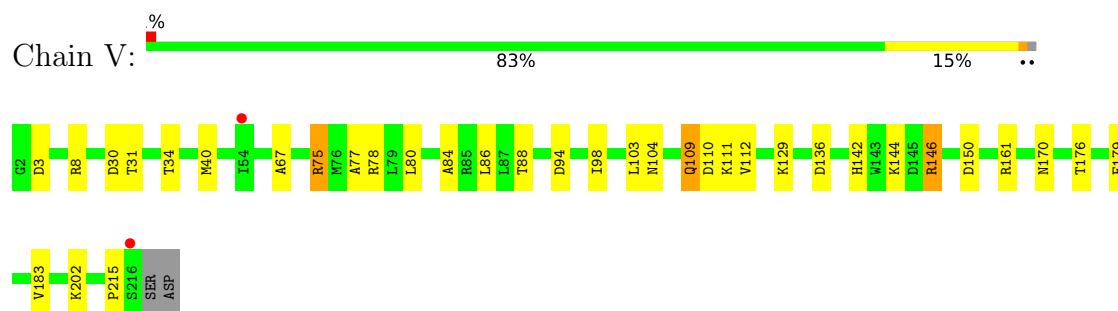




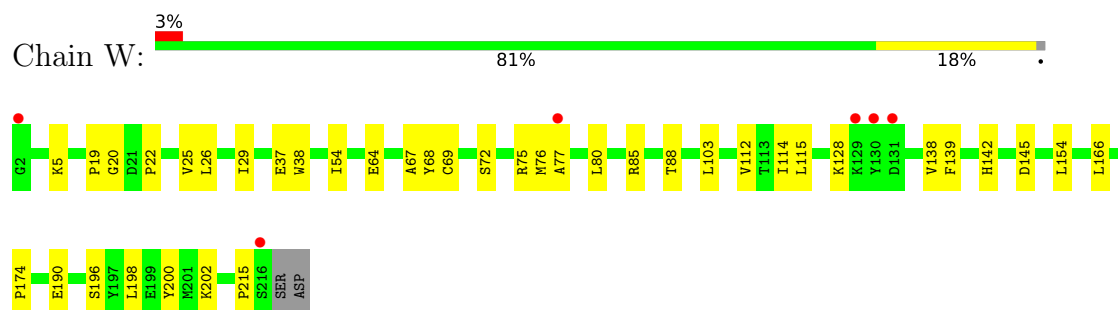
- Molecule 1: Catechol O-methyltransferase



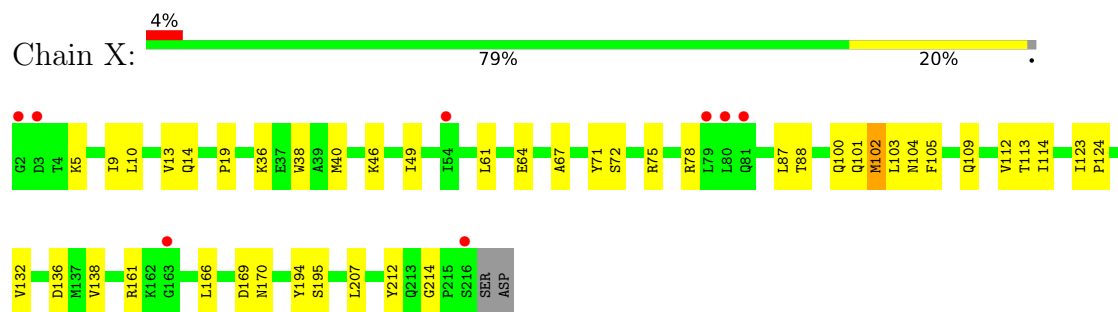
- Molecule 1: Catechol O-methyltransferase



- Molecule 1: Catechol O-methyltransferase



- Molecule 1: Catechol O-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	84.03Å 138.42Å 158.50Å 91.48° 97.19° 90.16°	Depositor
Resolution (Å)	48.84 – 2.70 48.83 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.8 (48.84-2.70) 87.3 (48.83-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.165 , 0.236 0.168 , 0.237	Depositor DCC
R_{free} test set	9582 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.042 for -h,k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	41639	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.11% 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: 6PQ, K, PO4

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	0.40	0/1728	0.54	0/2343
1	B	0.43	0/1714	0.58	0/2324
1	C	0.40	0/1720	0.55	0/2332
1	D	0.40	0/1714	0.54	0/2324
1	E	0.36	0/1714	0.51	0/2324
1	F	0.44	1/1720 (0.1%)	0.57	0/2332
1	G	0.40	0/1728	0.55	0/2343
1	H	0.44	0/1720	0.58	0/2332
1	I	0.39	0/1714	0.55	0/2324
1	J	0.42	0/1720	0.57	0/2332
1	K	0.45	0/1714	0.59	1/2324 (0.0%)
1	L	0.42	0/1720	0.57	0/2332
1	M	0.41	0/1714	0.58	0/2324
1	N	0.44	1/1720 (0.1%)	0.57	0/2332
1	O	0.42	0/1720	0.59	0/2332
1	P	0.38	0/1714	0.54	0/2324
1	Q	0.42	0/1720	0.57	0/2332
1	R	0.40	0/1728	0.53	0/2343
1	S	0.39	0/1714	0.54	0/2324
1	T	0.41	0/1714	0.58	0/2324
1	U	0.36	0/1714	0.52	0/2324
1	V	0.39	0/1714	0.53	0/2324
1	W	0.36	0/1714	0.51	0/2324
1	X	0.36	0/1714	0.51	0/2324
All	All	0.40	2/41226 (0.0%)	0.55	1/55897 (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	N	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	69	CYS	CB-SG	-6.30	1.71	1.82
1	F	69	CYS	CB-SG	-5.21	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	152	LEU	CA-CB-CG	-6.05	101.38	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	40	MET	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1697	0	1689	13	0
1	B	1683	0	1681	10	0
1	C	1689	0	1686	21	0
1	D	1683	0	1681	14	0
1	E	1683	0	1681	20	0
1	F	1689	0	1686	14	0
1	G	1697	0	1690	19	0
1	H	1689	0	1686	19	0
1	I	1683	0	1681	18	0
1	J	1689	0	1685	19	0
1	K	1683	0	1680	20	0
1	L	1689	0	1685	20	0
1	M	1683	0	1681	12	0
1	N	1689	0	1685	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	1689	0	1685	18	0
1	P	1683	0	1681	20	0
1	Q	1689	0	1686	21	0
1	R	1697	0	1690	22	0
1	S	1683	0	1680	18	0
1	T	1683	0	1681	19	0
1	U	1683	0	1681	25	0
1	V	1683	0	1681	18	0
1	W	1683	0	1681	19	0
1	X	1683	0	1681	25	0
2	A	21	0	0	0	0
2	B	21	0	0	0	0
2	C	21	0	0	0	0
2	D	21	0	0	0	0
2	E	21	0	0	0	0
2	F	21	0	0	1	0
2	G	21	0	0	0	0
2	H	21	0	0	0	0
2	I	21	0	0	0	0
2	J	21	0	0	0	0
2	K	21	0	0	0	0
2	L	21	0	0	0	0
2	M	21	0	0	0	0
2	N	21	0	0	0	0
2	O	21	0	0	0	0
2	P	21	0	0	0	0
2	Q	21	0	0	0	0
2	R	21	0	0	0	0
2	S	21	0	0	0	0
2	T	21	0	0	0	0
2	U	21	0	0	0	0
2	V	21	0	0	0	0
2	W	21	0	0	0	0
2	X	21	0	0	0	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	3	0	0	0	0
3	H	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	2	0	0	0	0
3	J	3	0	0	1	0
3	K	3	0	0	0	0
3	L	3	0	0	0	0
3	M	3	0	0	0	0
3	N	3	0	0	0	0
3	O	3	0	0	0	0
3	P	2	0	0	0	0
3	Q	2	0	0	0	0
3	R	3	0	0	0	0
3	S	3	0	0	0	0
3	T	2	0	0	0	0
3	U	2	0	0	0	0
3	V	2	0	0	0	0
3	W	2	0	0	0	0
3	X	2	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
4	H	5	0	0	0	0
4	I	5	0	0	2	0
4	K	5	0	0	0	0
4	M	5	0	0	0	0
4	N	5	0	0	0	0
4	Q	5	0	0	0	0
4	S	5	0	0	0	0
4	T	5	0	0	0	0
4	V	5	0	0	0	0
4	W	5	0	0	1	0
5	A	23	0	0	0	0
5	B	33	0	0	0	0
5	C	23	0	0	0	0
5	D	20	0	0	0	0
5	E	17	0	0	0	0
5	F	24	0	0	0	0
5	G	16	0	0	0	0
5	H	31	0	0	1	0
5	I	21	0	0	0	0
5	J	27	0	0	2	0
5	K	30	0	0	0	0
5	L	24	0	0	0	0
5	M	23	0	0	0	0
5	N	43	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	O	26	0	0	0	0
5	P	12	0	0	0	0
5	Q	24	0	0	0	0
5	R	27	0	0	1	0
5	S	22	0	0	0	0
5	T	23	0	0	0	0
5	U	10	0	0	0	0
5	V	15	0	0	1	0
5	W	13	0	0	0	0
5	X	8	0	0	0	0
All	All	41639	0	40404	421	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 5.

The worst 5 of 421 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:E:127:LYS:HE3	1:E:159:LEU:HD22	1.48	0.94
3:J:302:K:K	5:J:419:HOH:O	1.85	0.88
1:O:3:ASP:OD2	1:O:11:ARG:NH2	2.11	0.81
1:R:103:LEU:HD12	1:R:114:ILE:HD11	1.65	0.77
1:L:41:ASN:ND2	1:L:141:ASP:OD2	2.23	0.71

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	215/217 (99%)	207 (96%)	7 (3%)	1 (0%)	29 54
1	B	213/217 (98%)	204 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	214/217 (99%)	203 (95%)	11 (5%)	0	100	100
1	D	213/217 (98%)	199 (93%)	12 (6%)	2 (1%)	17	40
1	E	213/217 (98%)	198 (93%)	15 (7%)	0	100	100
1	F	214/217 (99%)	201 (94%)	13 (6%)	0	100	100
1	G	215/217 (99%)	201 (94%)	14 (6%)	0	100	100
1	H	214/217 (99%)	200 (94%)	14 (6%)	0	100	100
1	I	213/217 (98%)	199 (93%)	14 (7%)	0	100	100
1	J	214/217 (99%)	206 (96%)	7 (3%)	1 (0%)	29	54
1	K	213/217 (98%)	199 (93%)	13 (6%)	1 (0%)	29	54
1	L	214/217 (99%)	194 (91%)	19 (9%)	1 (0%)	29	54
1	M	213/217 (98%)	200 (94%)	11 (5%)	2 (1%)	17	40
1	N	214/217 (99%)	202 (94%)	11 (5%)	1 (0%)	29	54
1	O	214/217 (99%)	200 (94%)	13 (6%)	1 (0%)	29	54
1	P	213/217 (98%)	201 (94%)	12 (6%)	0	100	100
1	Q	214/217 (99%)	203 (95%)	10 (5%)	1 (0%)	29	54
1	R	215/217 (99%)	201 (94%)	14 (6%)	0	100	100
1	S	213/217 (98%)	200 (94%)	13 (6%)	0	100	100
1	T	213/217 (98%)	201 (94%)	12 (6%)	0	100	100
1	U	213/217 (98%)	196 (92%)	17 (8%)	0	100	100
1	V	213/217 (98%)	203 (95%)	9 (4%)	1 (0%)	29	54
1	W	213/217 (98%)	197 (92%)	13 (6%)	3 (1%)	11	28
1	X	213/217 (98%)	200 (94%)	13 (6%)	0	100	100
All	All	5126/5208 (98%)	4815 (94%)	296 (6%)	15 (0%)	41	66

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	41	ASN
1	N	41	ASN
1	W	215	PRO
1	A	37	GLU
1	L	82	PRO

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	186/186 (100%)	180 (97%)	6 (3%)	39	68
1	B	184/186 (99%)	179 (97%)	5 (3%)	44	74
1	C	185/186 (100%)	181 (98%)	4 (2%)	52	79
1	D	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	E	184/186 (99%)	182 (99%)	2 (1%)	73	90
1	F	185/186 (100%)	180 (97%)	5 (3%)	44	74
1	G	186/186 (100%)	183 (98%)	3 (2%)	62	85
1	H	185/186 (100%)	181 (98%)	4 (2%)	52	79
1	I	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	J	185/186 (100%)	183 (99%)	2 (1%)	73	90
1	K	184/186 (99%)	174 (95%)	10 (5%)	22	47
1	L	185/186 (100%)	180 (97%)	5 (3%)	44	74
1	M	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	N	185/186 (100%)	180 (97%)	5 (3%)	44	74
1	O	185/186 (100%)	178 (96%)	7 (4%)	33	62
1	P	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	Q	185/186 (100%)	180 (97%)	5 (3%)	44	74
1	R	186/186 (100%)	182 (98%)	4 (2%)	52	79
1	S	184/186 (99%)	176 (96%)	8 (4%)	29	57
1	T	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	U	184/186 (99%)	179 (97%)	5 (3%)	44	74
1	V	184/186 (99%)	177 (96%)	7 (4%)	33	62
1	W	184/186 (99%)	178 (97%)	6 (3%)	38	67
1	X	184/186 (99%)	180 (98%)	4 (2%)	52	79
All	All	4430/4464 (99%)	4303 (97%)	127 (3%)	42	71

5 of 127 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	146	ARG
1	V	31	THR
1	O	40	MET
1	U	195	SER
1	W	142	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	41	ASN
1	Q	100	GLN
1	S	116	ASN
1	W	81	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 94 ligands modelled in this entry, 58 are monoatomic - leaving 36 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	$\# Z > 2$
2	6PQ	S	301	-	19,23,23	1.19	1 (5%)	17,32,32	1.68	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	N	305	-	4,4,4	0.84	0	6,6,6	0.83	0
2	6PQ	K	301	-	19,23,23	1.18	1 (5%)	17,32,32	1.84	3 (17%)
2	6PQ	N	301	-	19,23,23	1.13	1 (5%)	17,32,32	1.75	3 (17%)
4	PO4	Q	304	-	4,4,4	0.90	0	6,6,6	0.48	0
2	6PQ	D	301	-	19,23,23	1.23	1 (5%)	17,32,32	1.67	3 (17%)
2	6PQ	G	301	-	19,23,23	1.23	1 (5%)	17,32,32	1.66	3 (17%)
4	PO4	T	304	-	4,4,4	0.88	0	6,6,6	0.41	0
4	PO4	V	304	-	4,4,4	0.90	0	6,6,6	0.35	0
4	PO4	W	304	-	4,4,4	0.91	0	6,6,6	0.38	0
4	PO4	H	304	-	4,4,4	0.87	0	6,6,6	0.41	0
2	6PQ	T	301	-	19,23,23	1.24	1 (5%)	17,32,32	1.60	3 (17%)
2	6PQ	X	301	-	19,23,23	1.24	2 (10%)	17,32,32	1.50	3 (17%)
2	6PQ	V	301	-	19,23,23	1.16	1 (5%)	17,32,32	1.67	3 (17%)
2	6PQ	A	301	-	19,23,23	1.12	1 (5%)	17,32,32	1.80	3 (17%)
2	6PQ	I	301	-	19,23,23	1.20	1 (5%)	17,32,32	1.66	3 (17%)
4	PO4	I	304	-	4,4,4	0.86	0	6,6,6	0.58	0
2	6PQ	Q	301	-	19,23,23	1.19	1 (5%)	17,32,32	1.70	3 (17%)
4	PO4	C	304	-	4,4,4	0.92	0	6,6,6	0.42	0
2	6PQ	M	301	-	19,23,23	1.20	2 (10%)	17,32,32	1.76	3 (17%)
4	PO4	D	304	-	4,4,4	0.92	0	6,6,6	0.44	0
2	6PQ	B	301	-	19,23,23	1.20	1 (5%)	17,32,32	1.83	3 (17%)
4	PO4	S	305	-	4,4,4	0.91	0	6,6,6	0.53	0
2	6PQ	C	301	-	19,23,23	1.21	1 (5%)	17,32,32	1.62	3 (17%)
2	6PQ	O	301	-	19,23,23	1.27	1 (5%)	17,32,32	1.53	3 (17%)
2	6PQ	U	301	-	19,23,23	1.22	1 (5%)	17,32,32	1.65	3 (17%)
2	6PQ	P	301	-	19,23,23	1.25	1 (5%)	17,32,32	1.77	4 (23%)
2	6PQ	W	301	-	19,23,23	1.23	1 (5%)	17,32,32	1.69	2 (11%)
4	PO4	K	305	-	4,4,4	0.83	0	6,6,6	0.53	0
2	6PQ	H	301	-	19,23,23	1.24	2 (10%)	17,32,32	1.67	3 (17%)
2	6PQ	J	301	-	19,23,23	1.25	2 (10%)	17,32,32	1.68	3 (17%)
2	6PQ	L	301	-	19,23,23	1.22	1 (5%)	17,32,32	1.75	3 (17%)
2	6PQ	F	301	-	19,23,23	1.28	2 (10%)	17,32,32	1.71	4 (23%)
2	6PQ	R	301	-	19,23,23	1.15	1 (5%)	17,32,32	1.71	3 (17%)
2	6PQ	E	301	-	19,23,23	1.21	2 (10%)	17,32,32	1.71	3 (17%)
4	PO4	M	305	-	4,4,4	0.83	0	6,6,6	0.36	0

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

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6PQ	S	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	K	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	N	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	D	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	G	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	T	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	X	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	V	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	A	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	I	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	Q	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	M	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	B	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	C	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	O	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	U	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	P	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	W	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	H	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	J	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	L	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	F	301	-	-	2/6/10/10	0/3/3/3
2	6PQ	R	301	-	-	0/6/10/10	0/3/3/3
2	6PQ	E	301	-	-	2/6/10/10	0/3/3/3

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	6PQ	N08-N06	-3.84	1.30	1.37
2	U	301	6PQ	N08-N06	-3.70	1.30	1.37
2	H	301	6PQ	N08-N06	-3.64	1.30	1.37
2	T	301	6PQ	N08-N06	-3.64	1.30	1.37
2	S	301	6PQ	N08-N06	-3.62	1.30	1.37

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	301	6PQ	C19-C09-S05	5.60	127.65	120.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	301	6PQ	C19-C09-S05	5.26	127.19	120.12
2	B	301	6PQ	C19-C09-S05	5.24	127.16	120.12
2	A	301	6PQ	C19-C09-S05	5.14	127.03	120.12
2	K	301	6PQ	C19-C09-S05	5.08	126.95	120.12

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

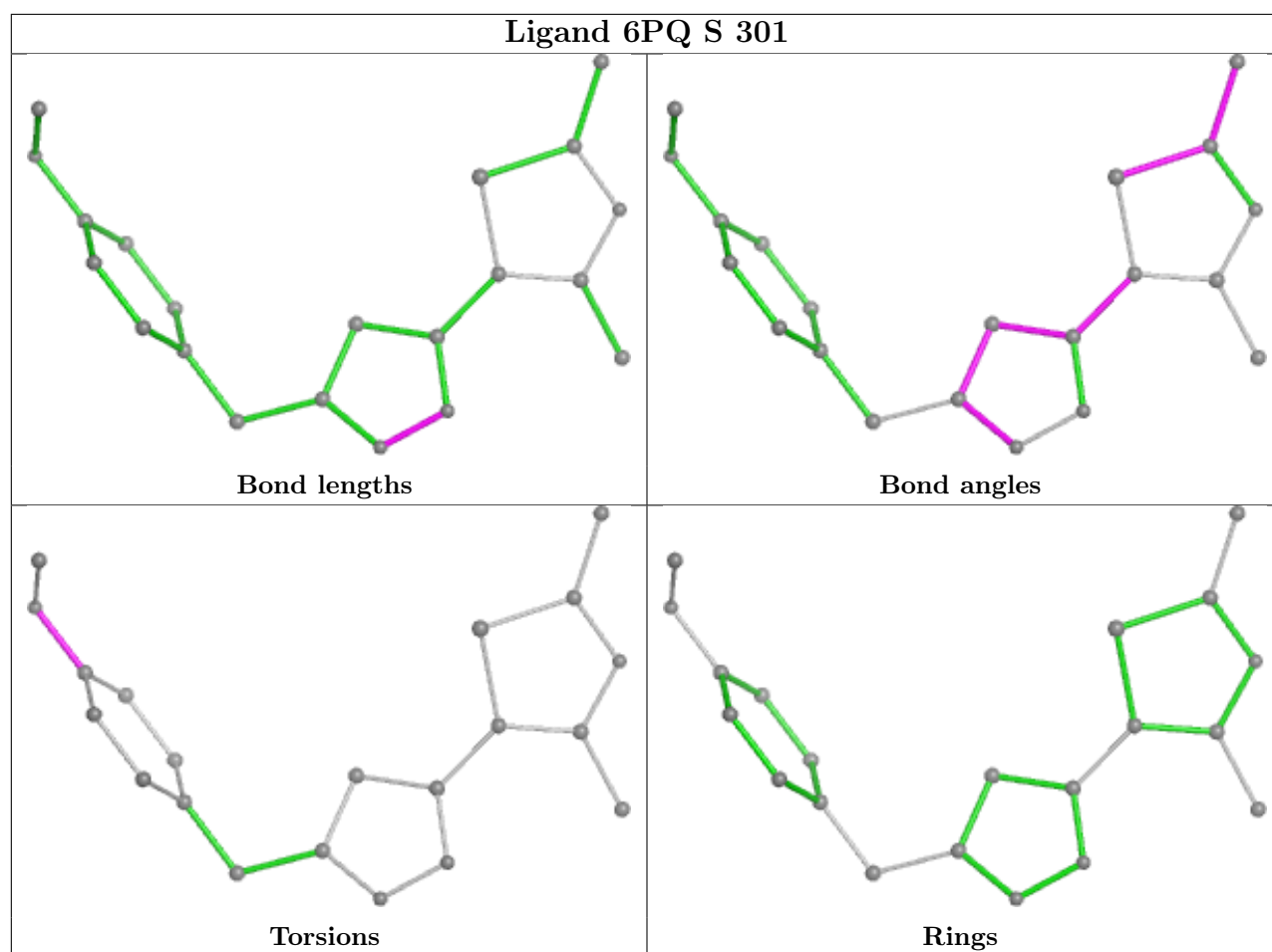
Mol	Chain	Res	Type	Atoms
2	I	301	6PQ	C17-C13-O20-C21
2	I	301	6PQ	C18-C13-O20-C21
2	P	301	6PQ	C18-C13-O20-C21
2	P	301	6PQ	C17-C13-O20-C21
2	N	301	6PQ	C17-C13-O20-C21

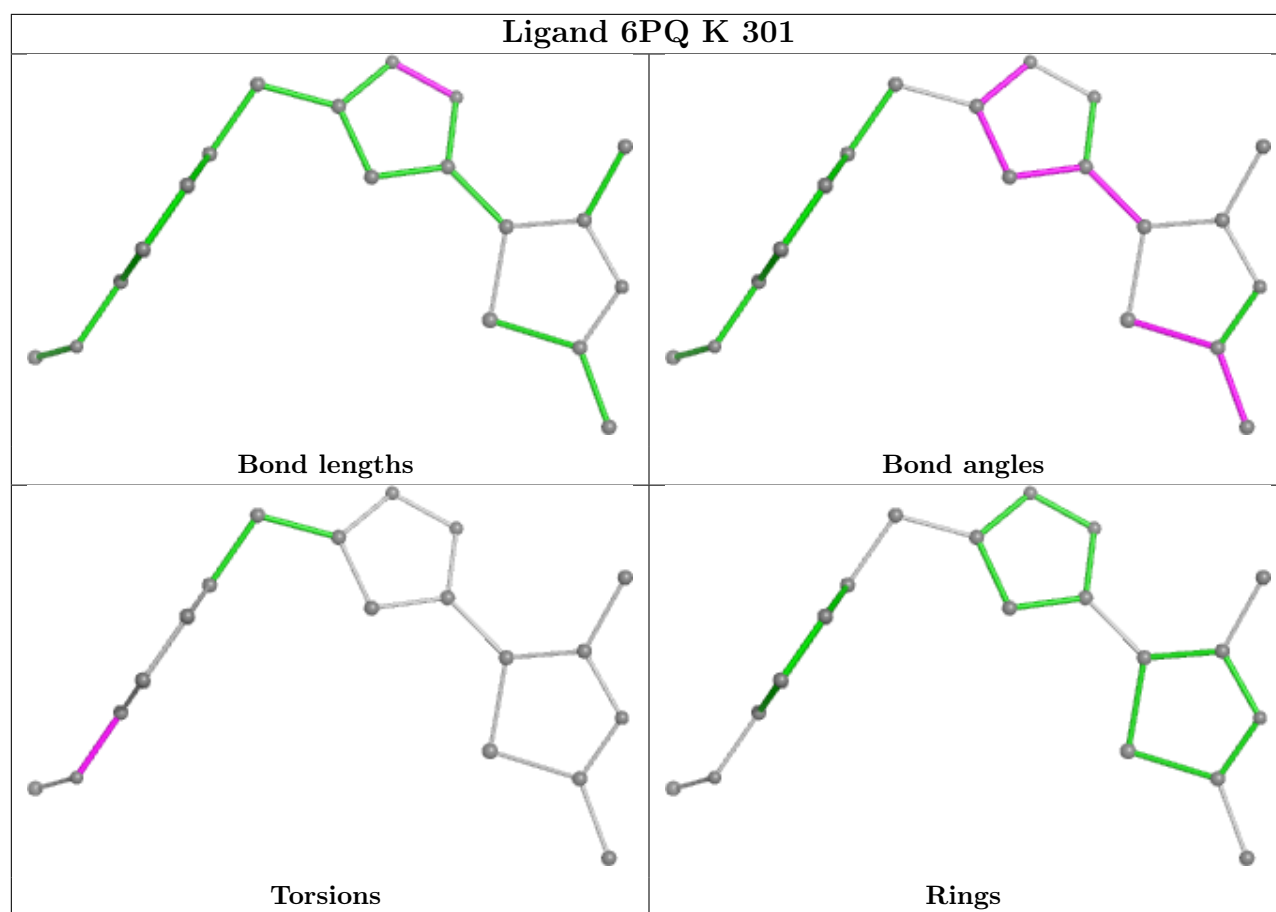
There are no ring outliers.

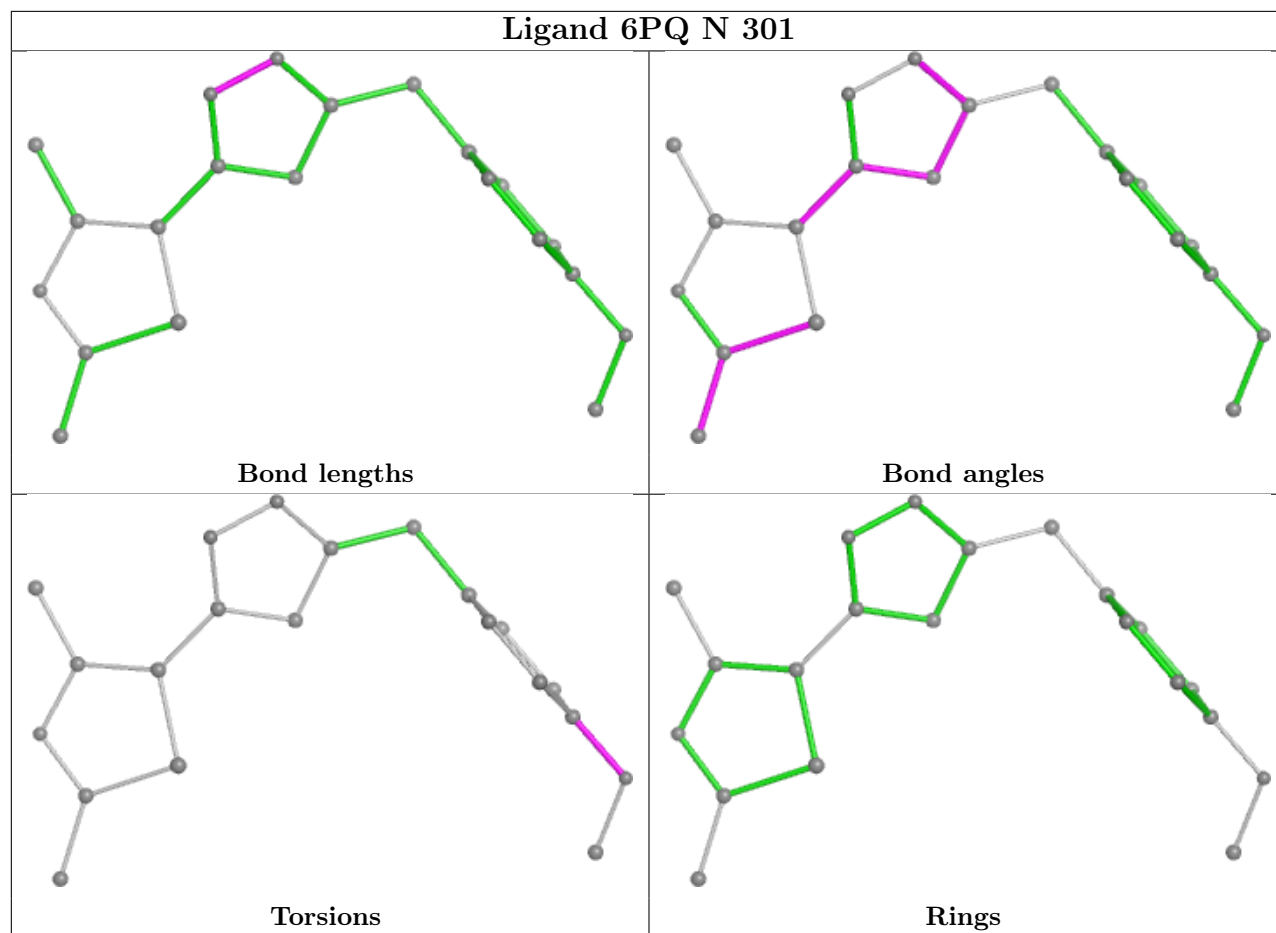
3 monomers are involved in 4 short contacts:

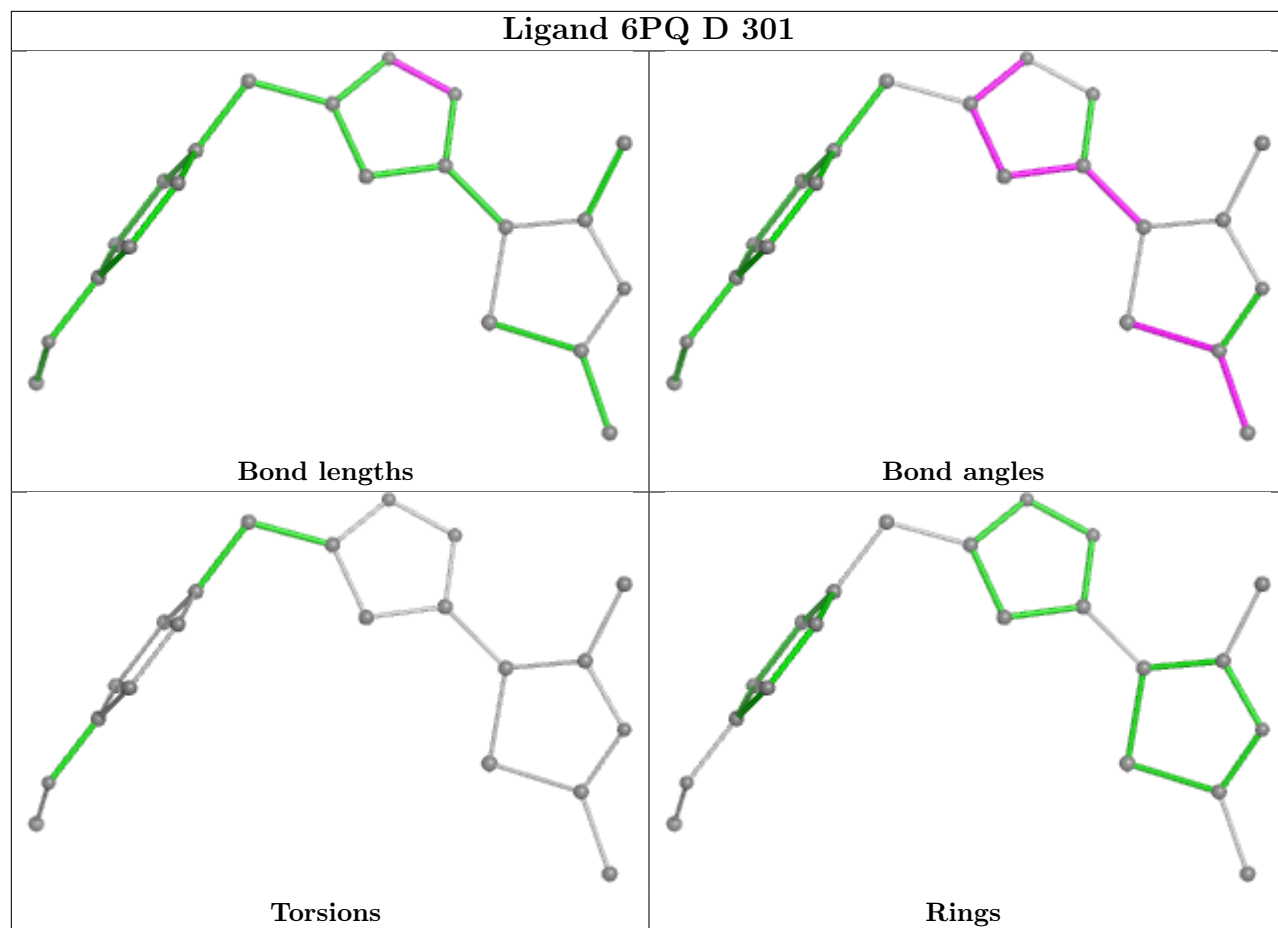
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	W	304	PO4	1	0
4	I	304	PO4	2	0
2	F	301	6PQ	1	0

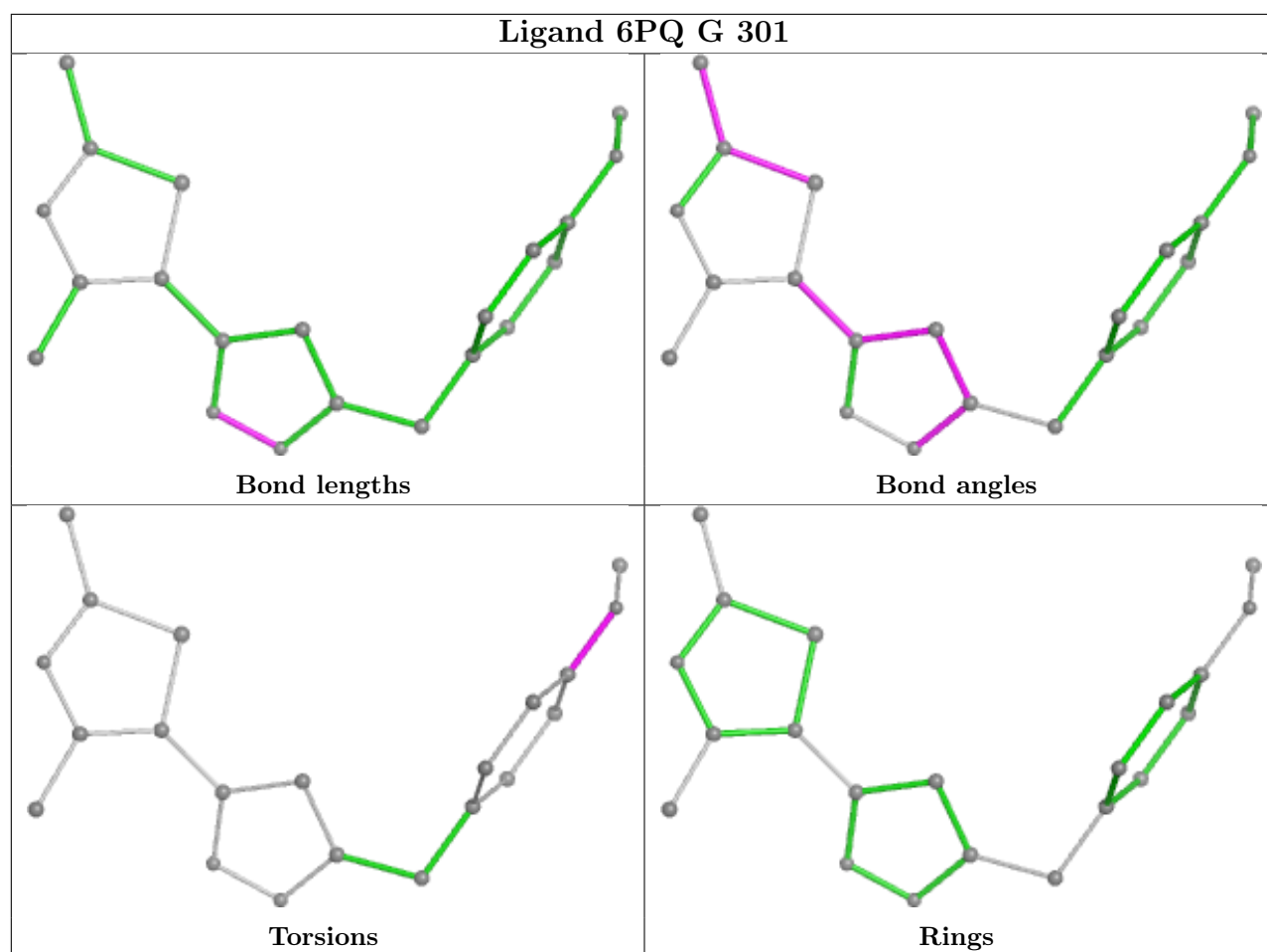
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

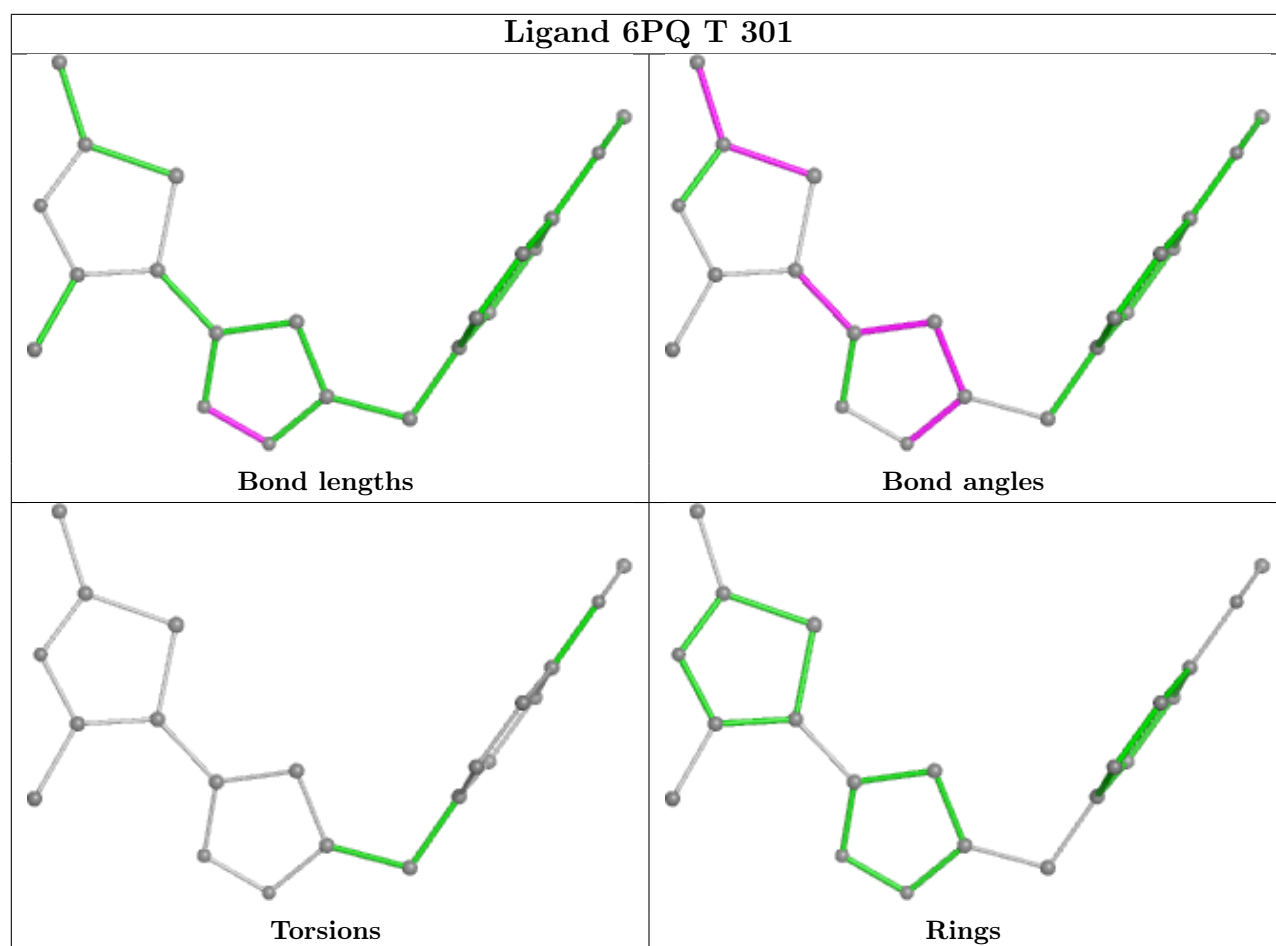


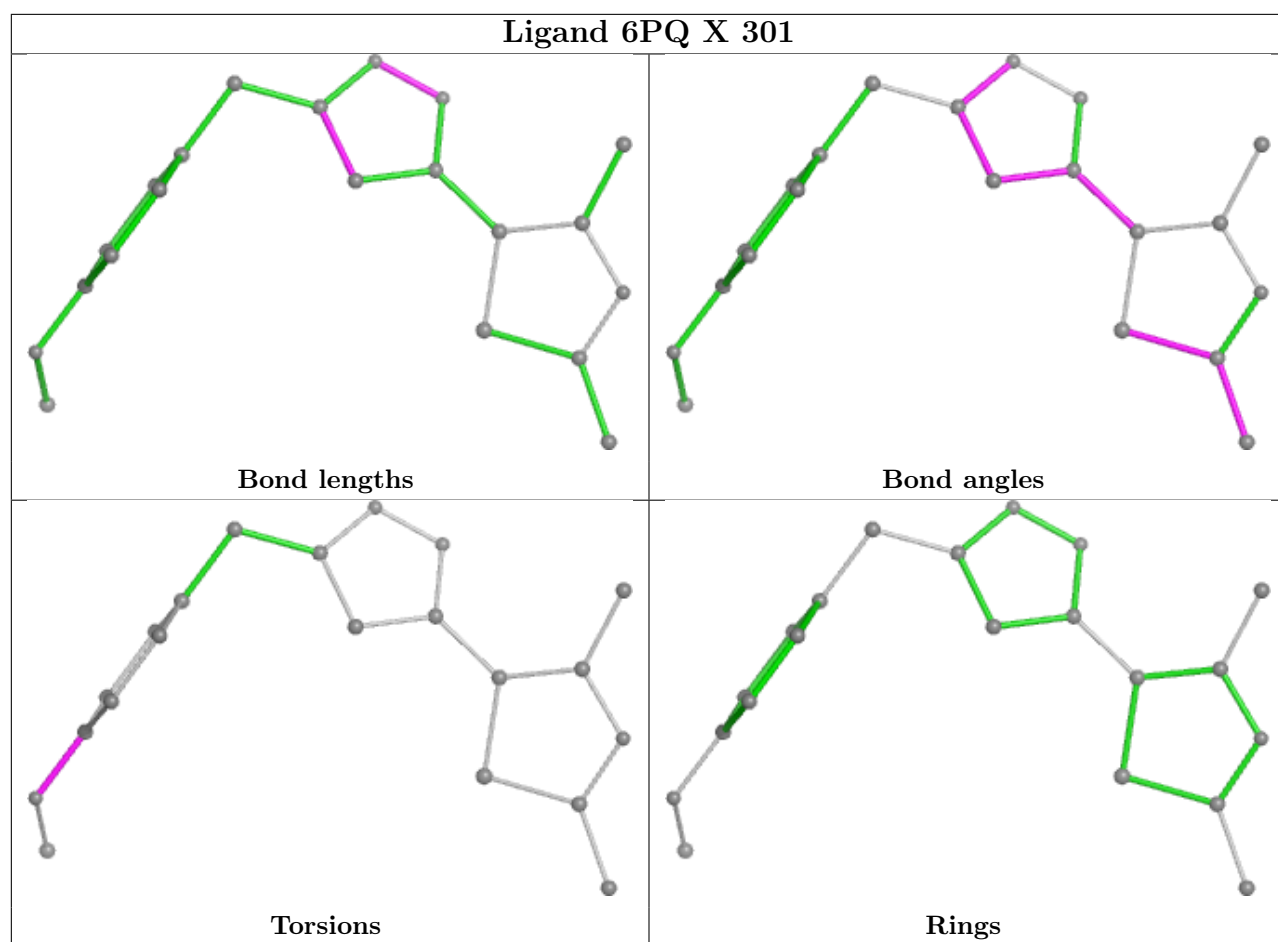


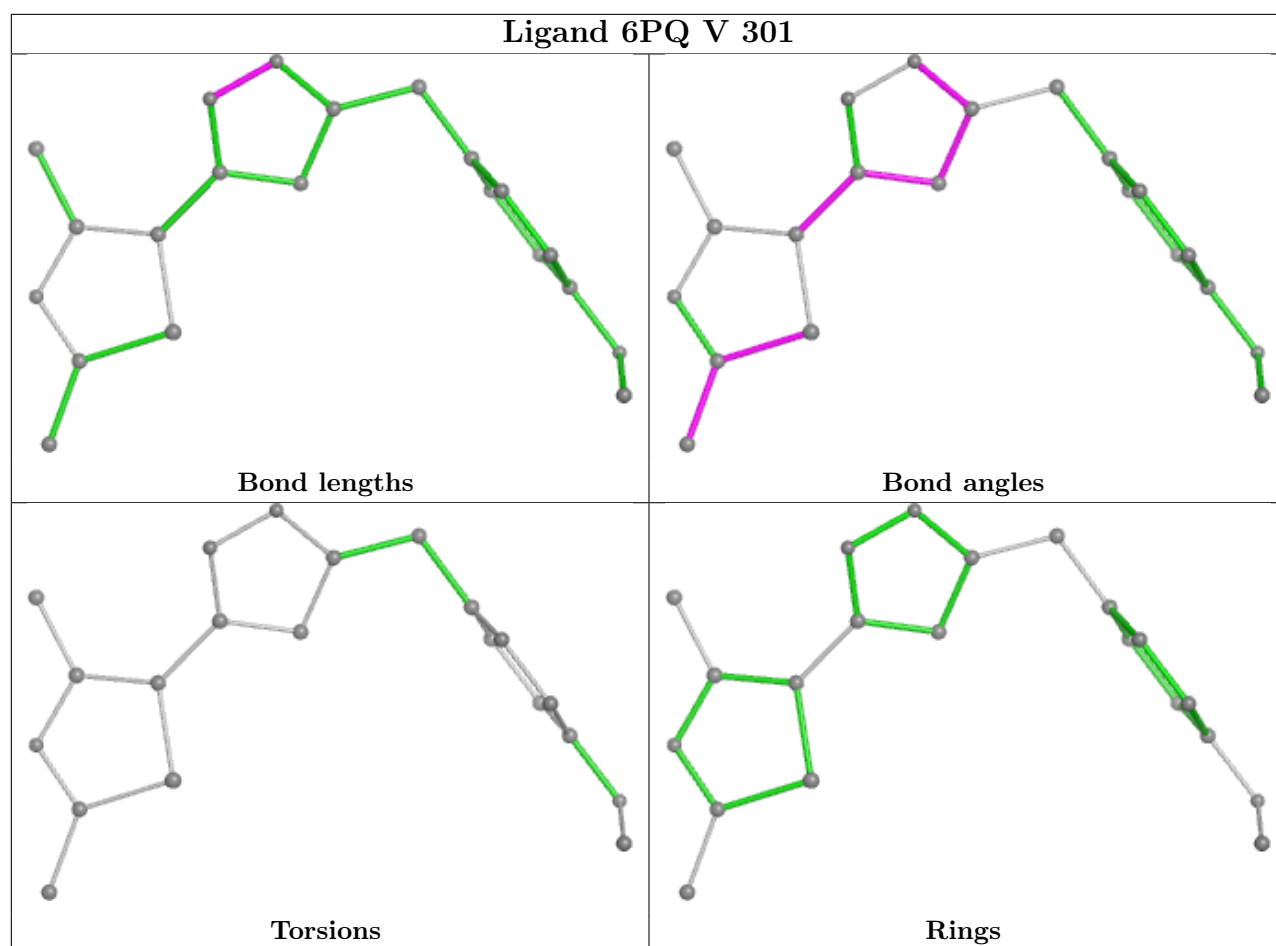




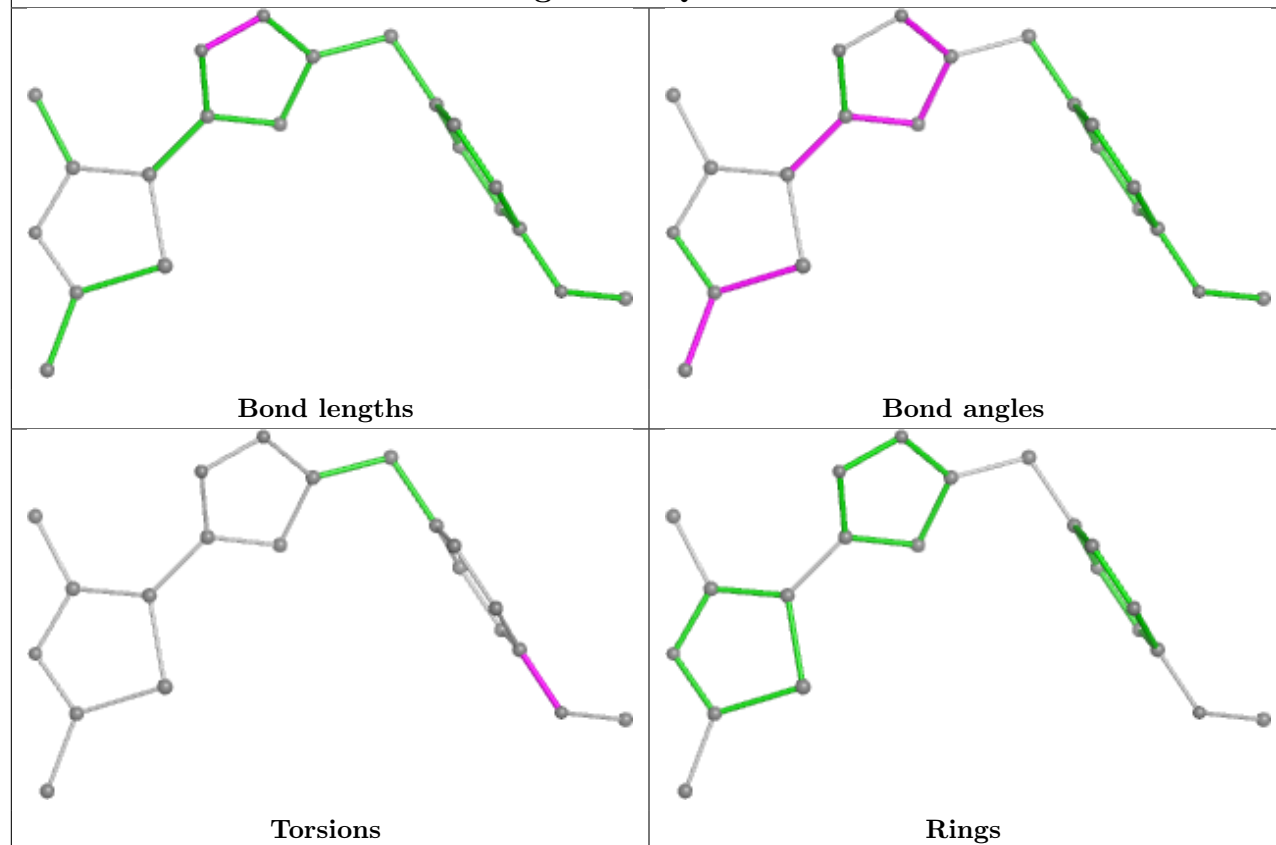




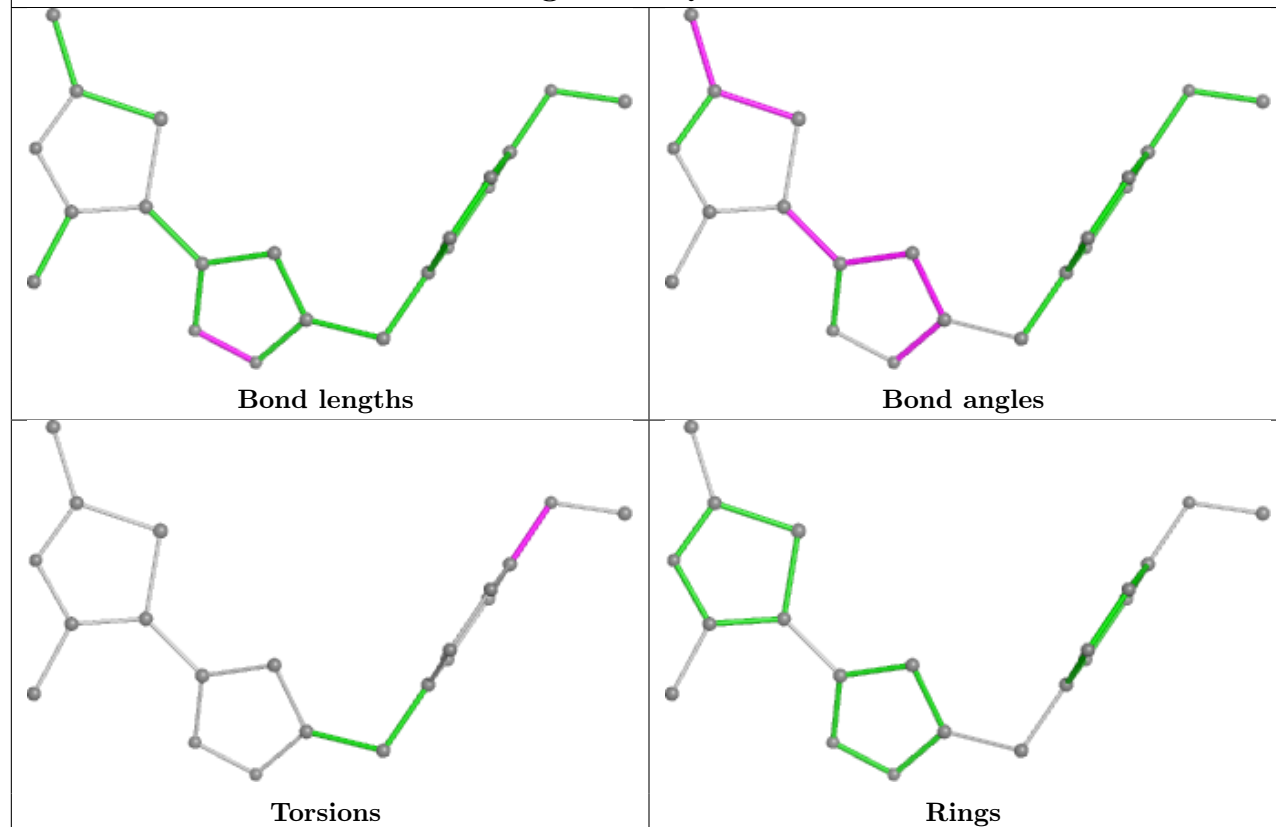


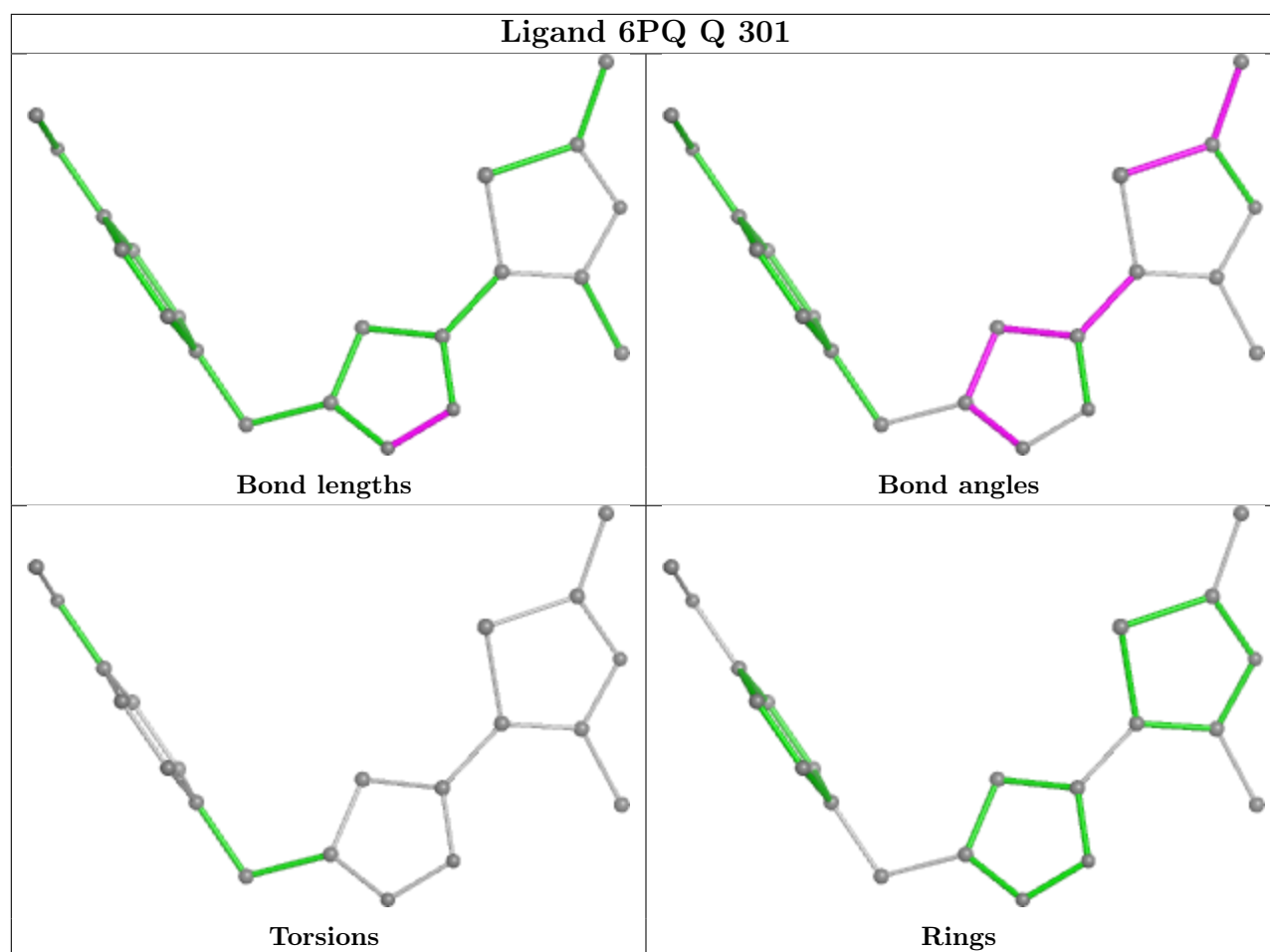


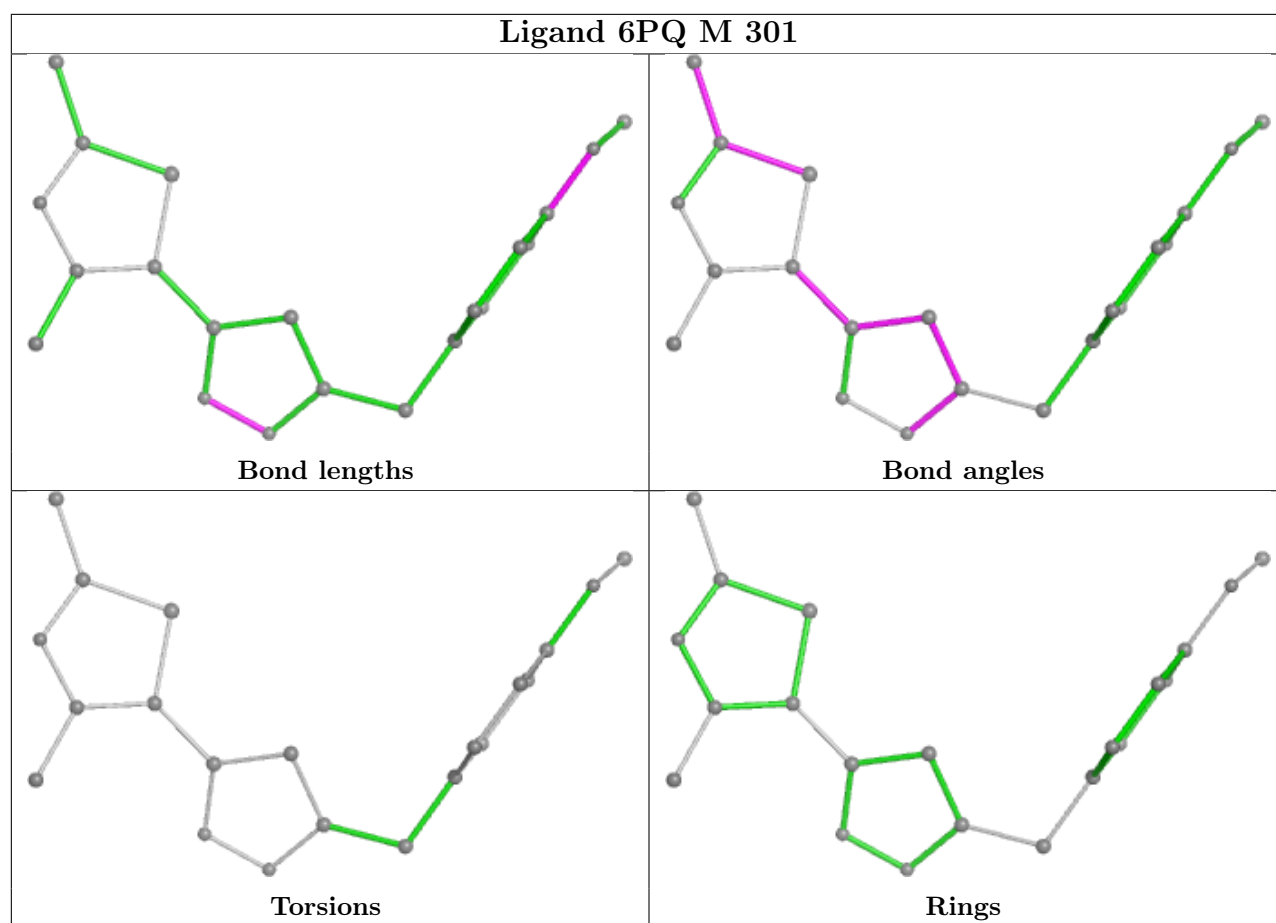
Ligand 6PQ A 301

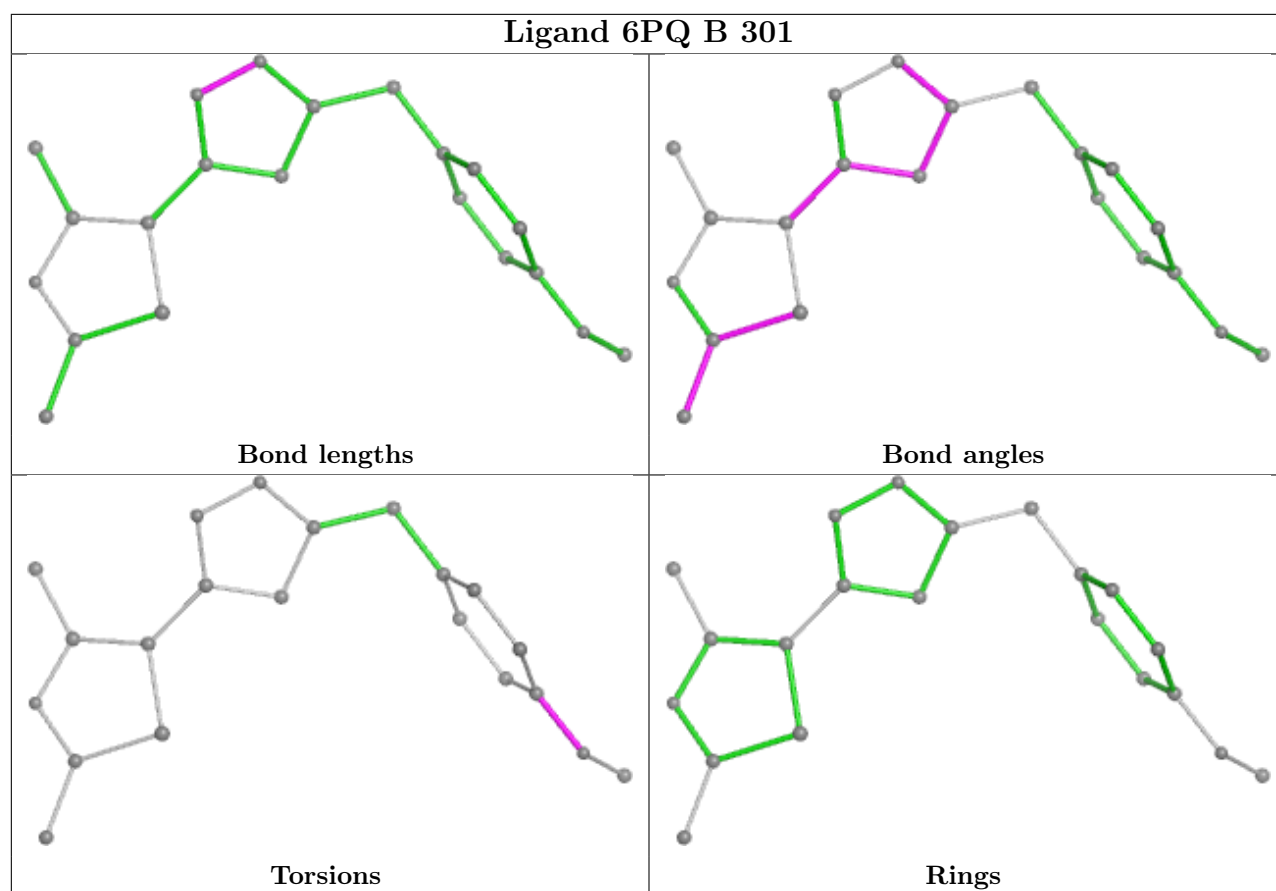


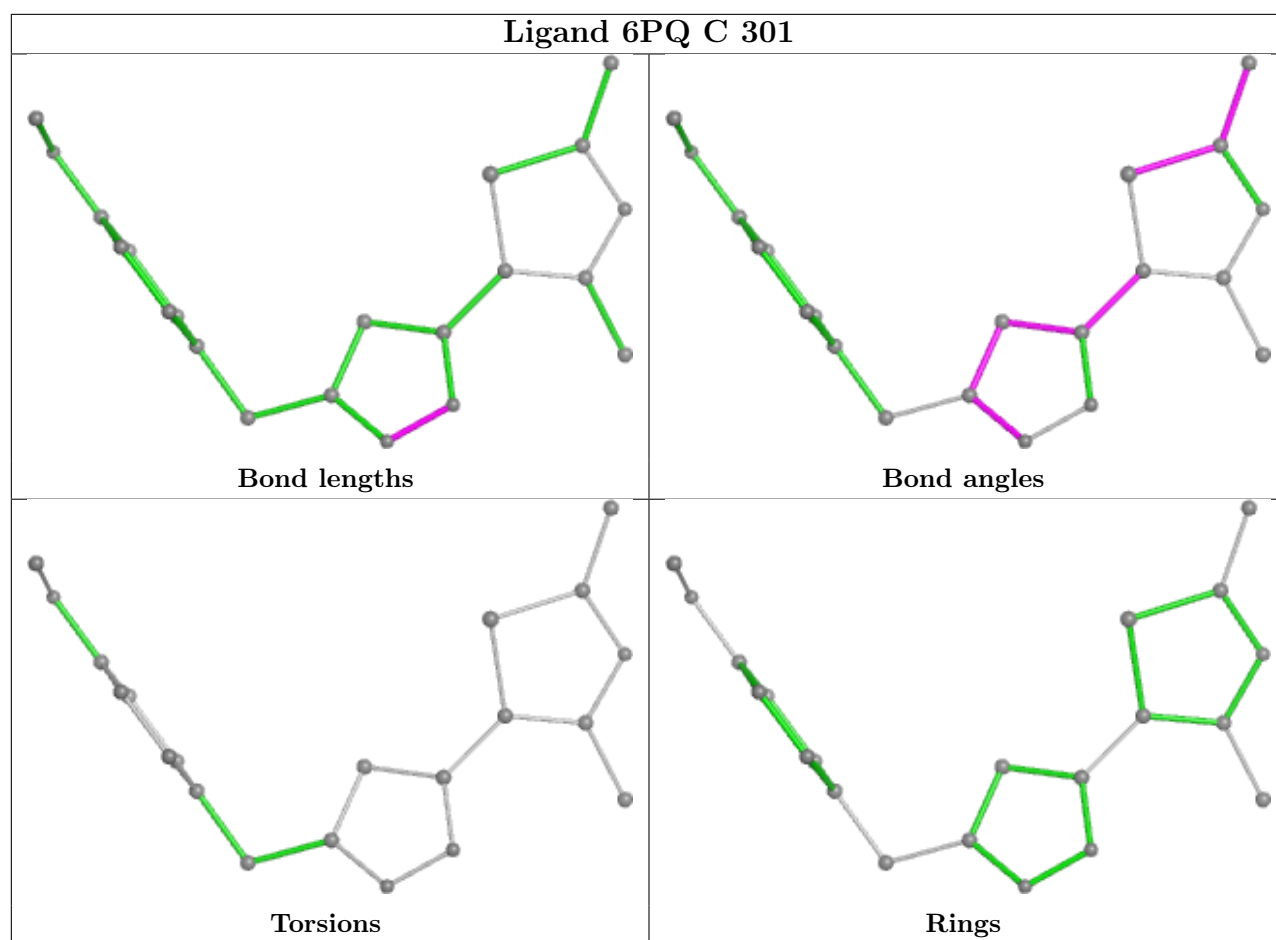
Ligand 6PQ I 301

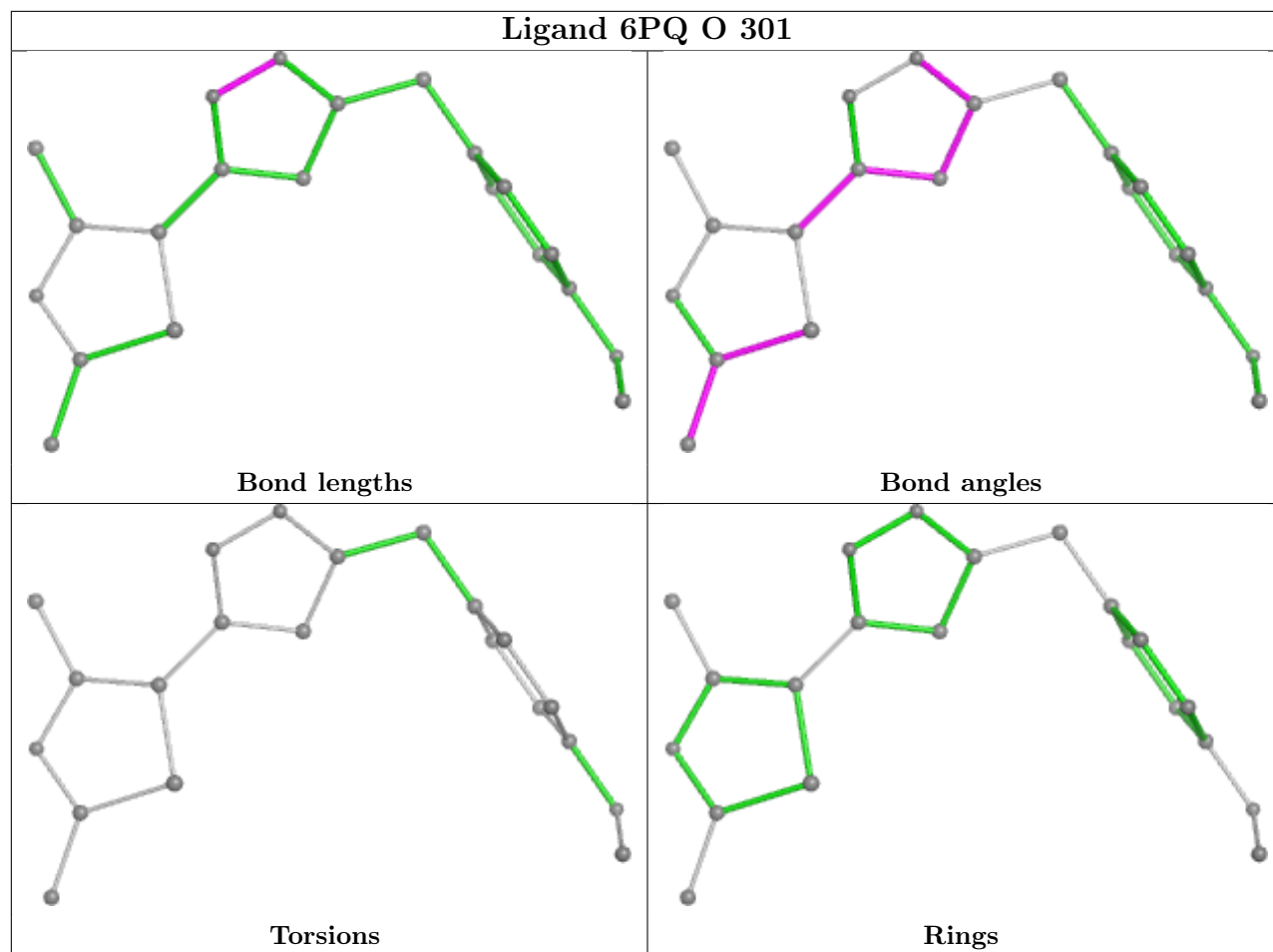


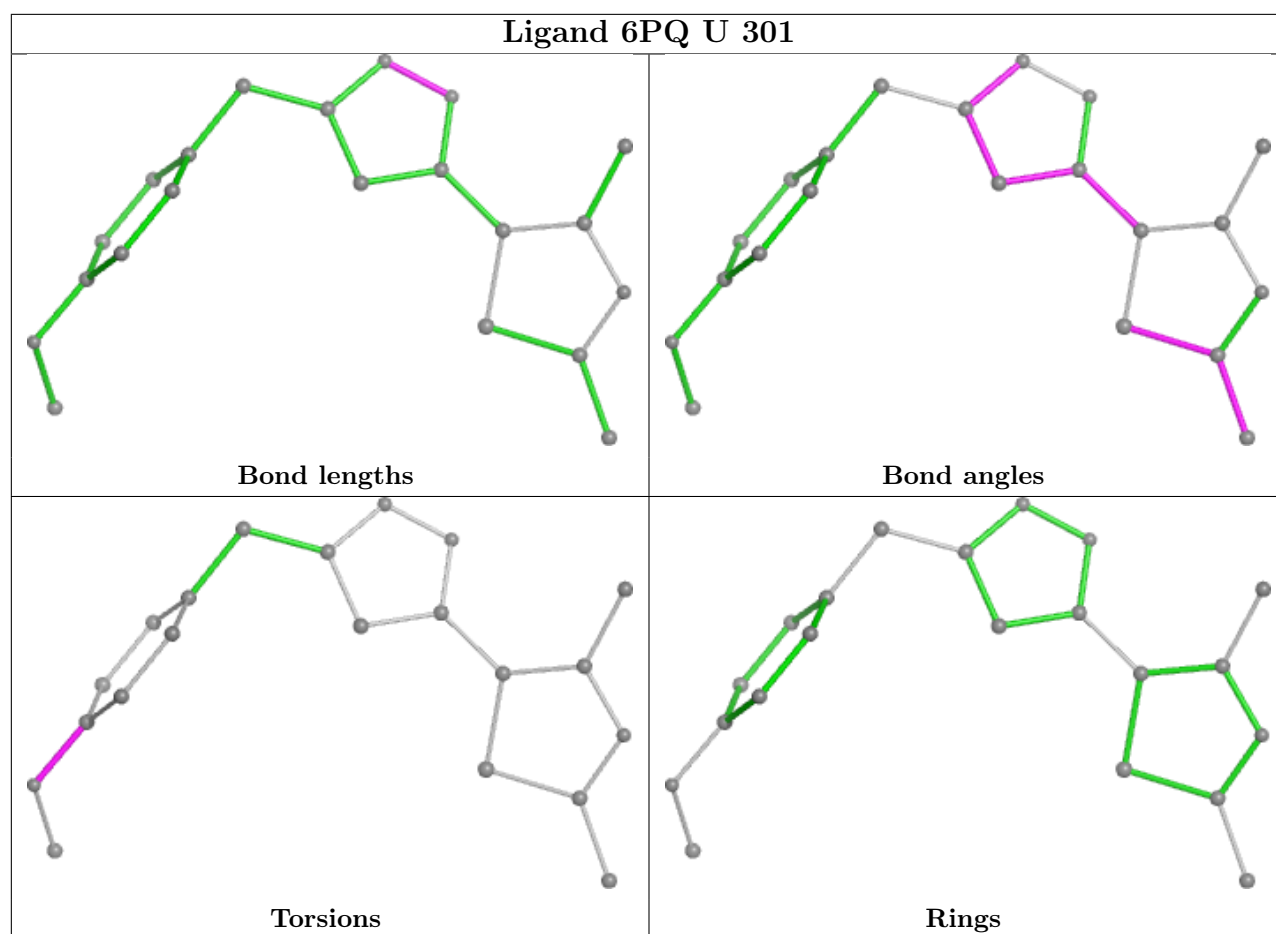


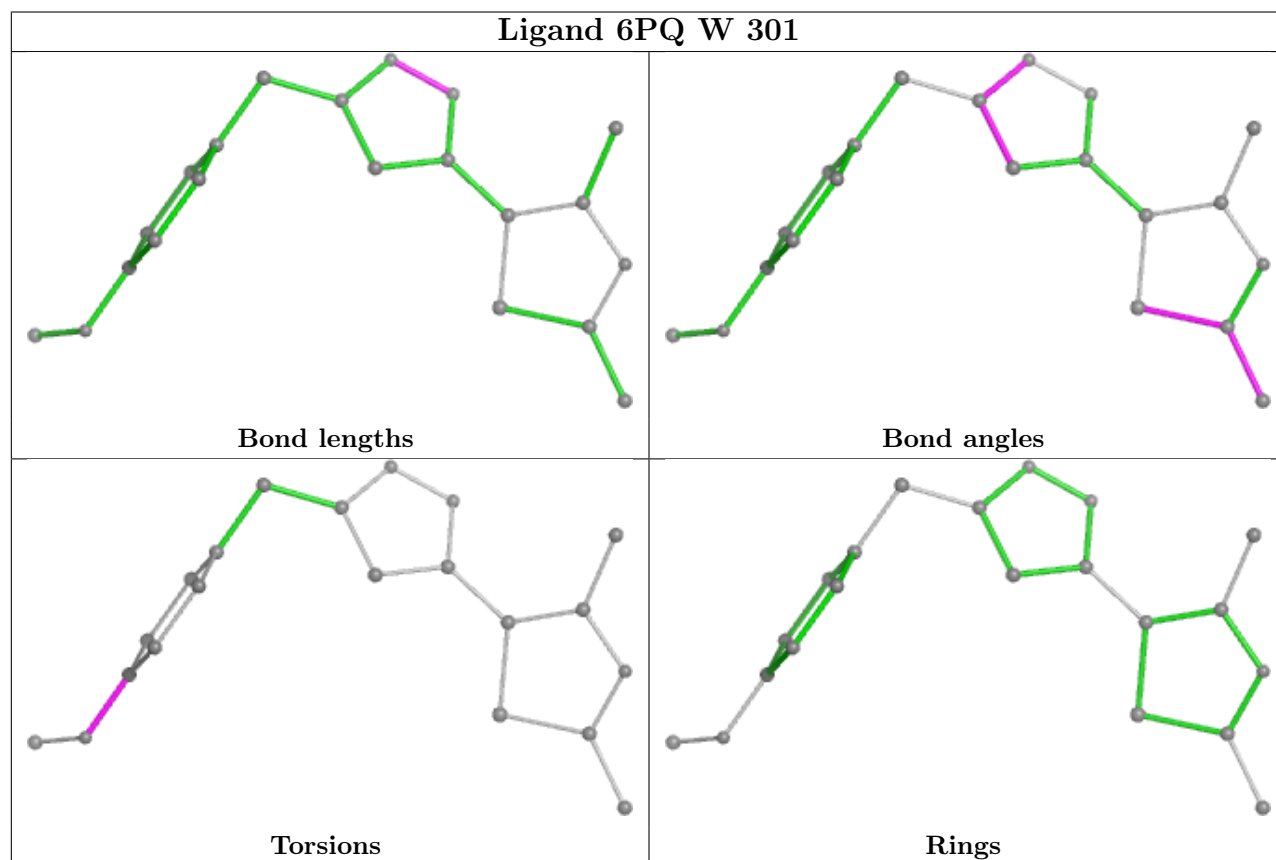
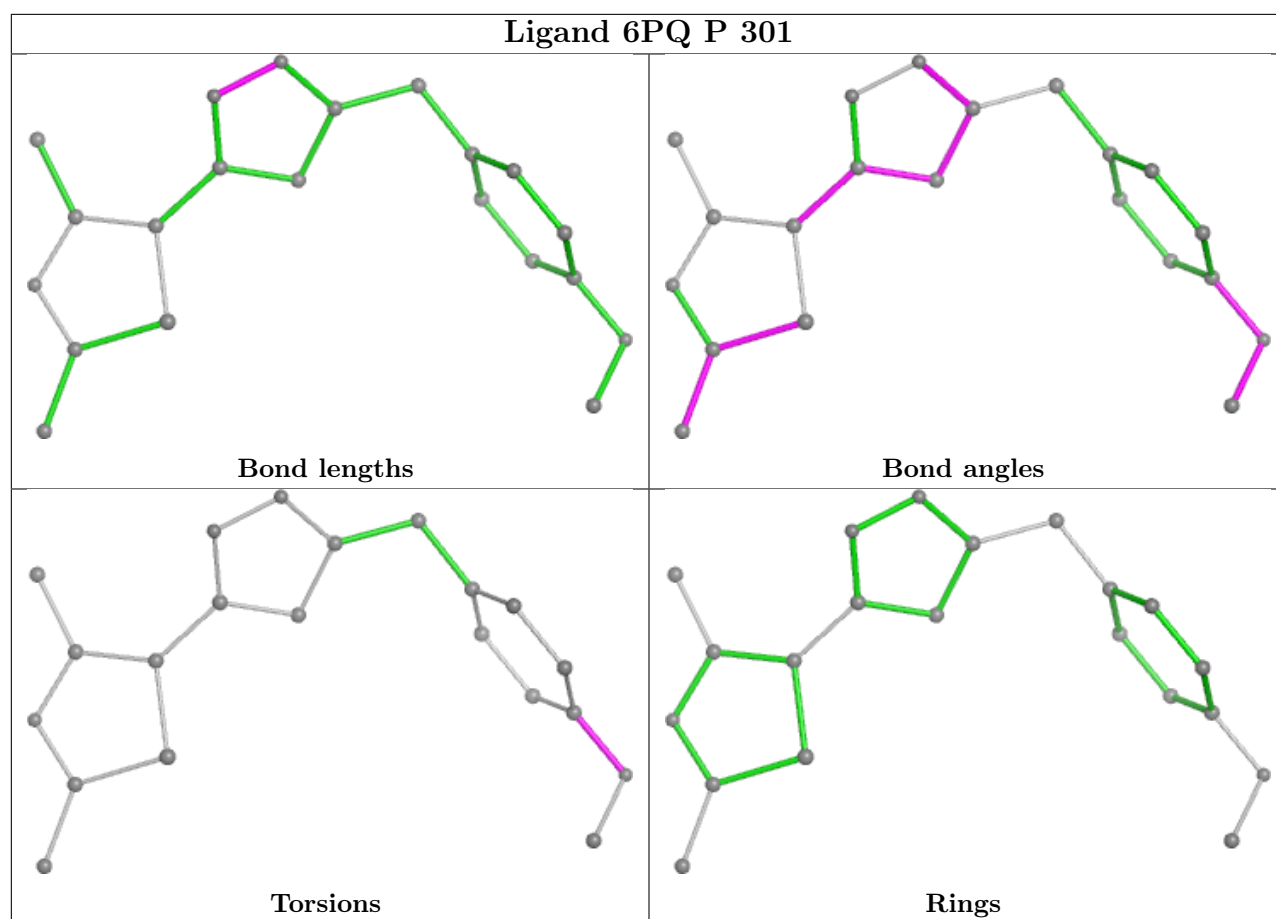


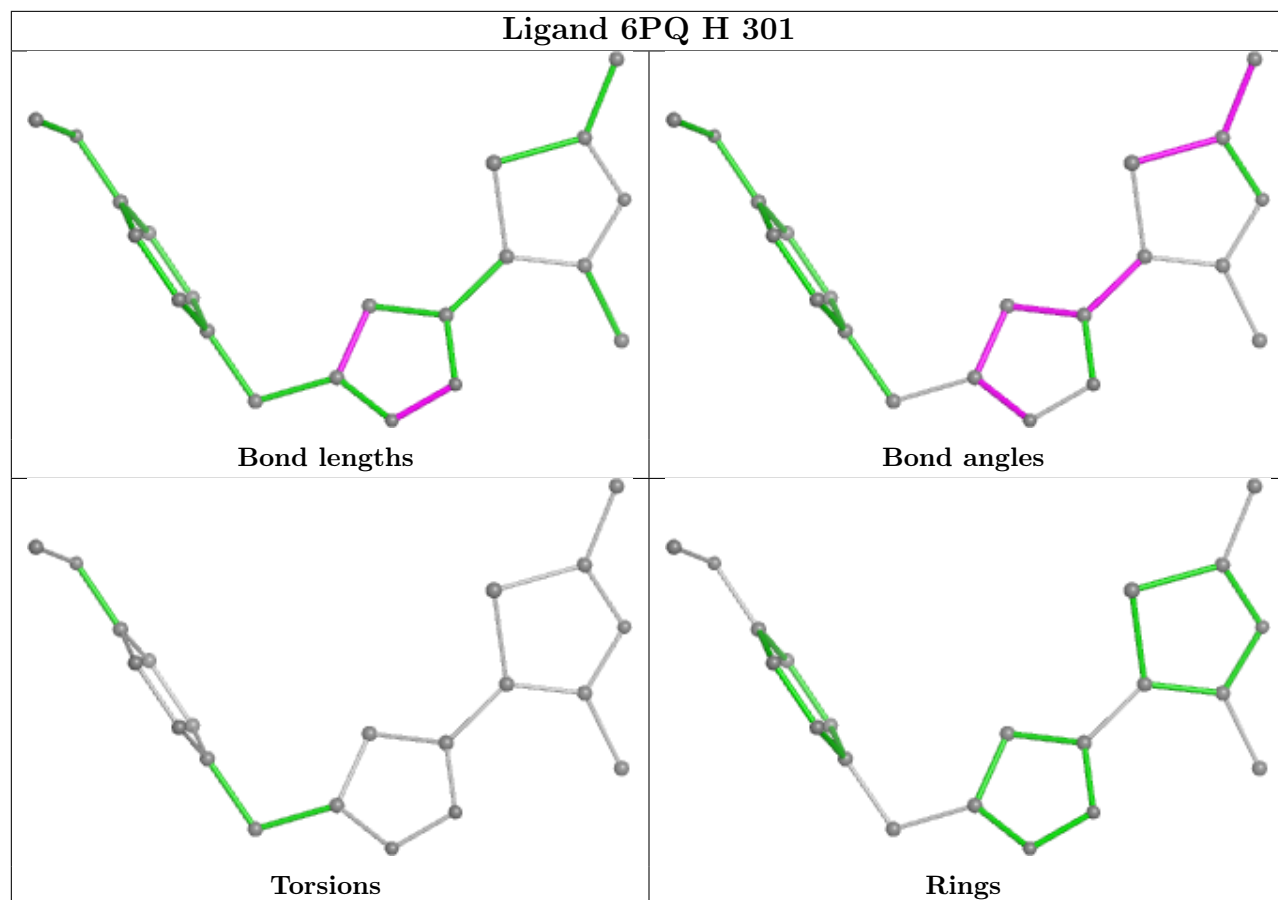


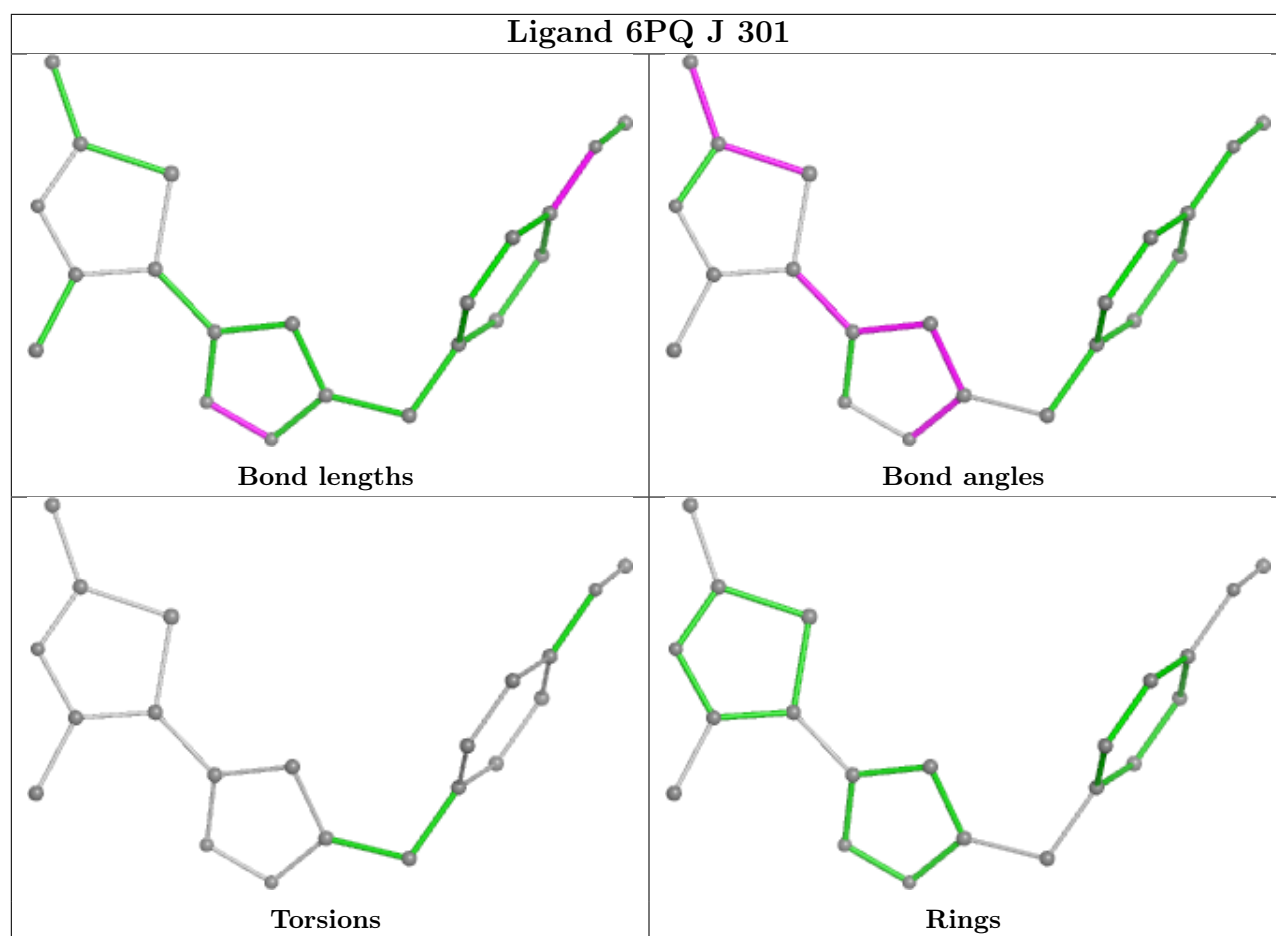


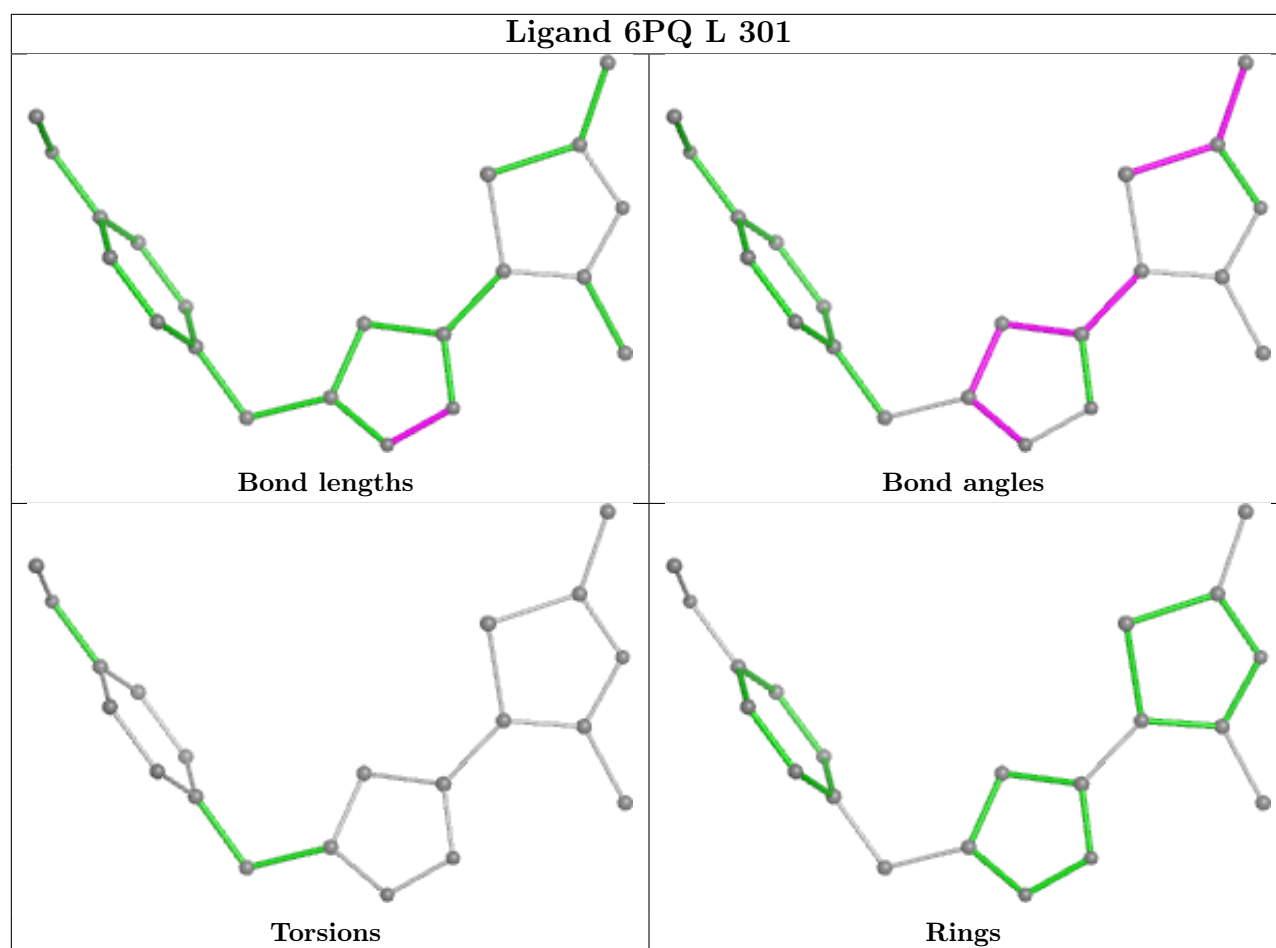


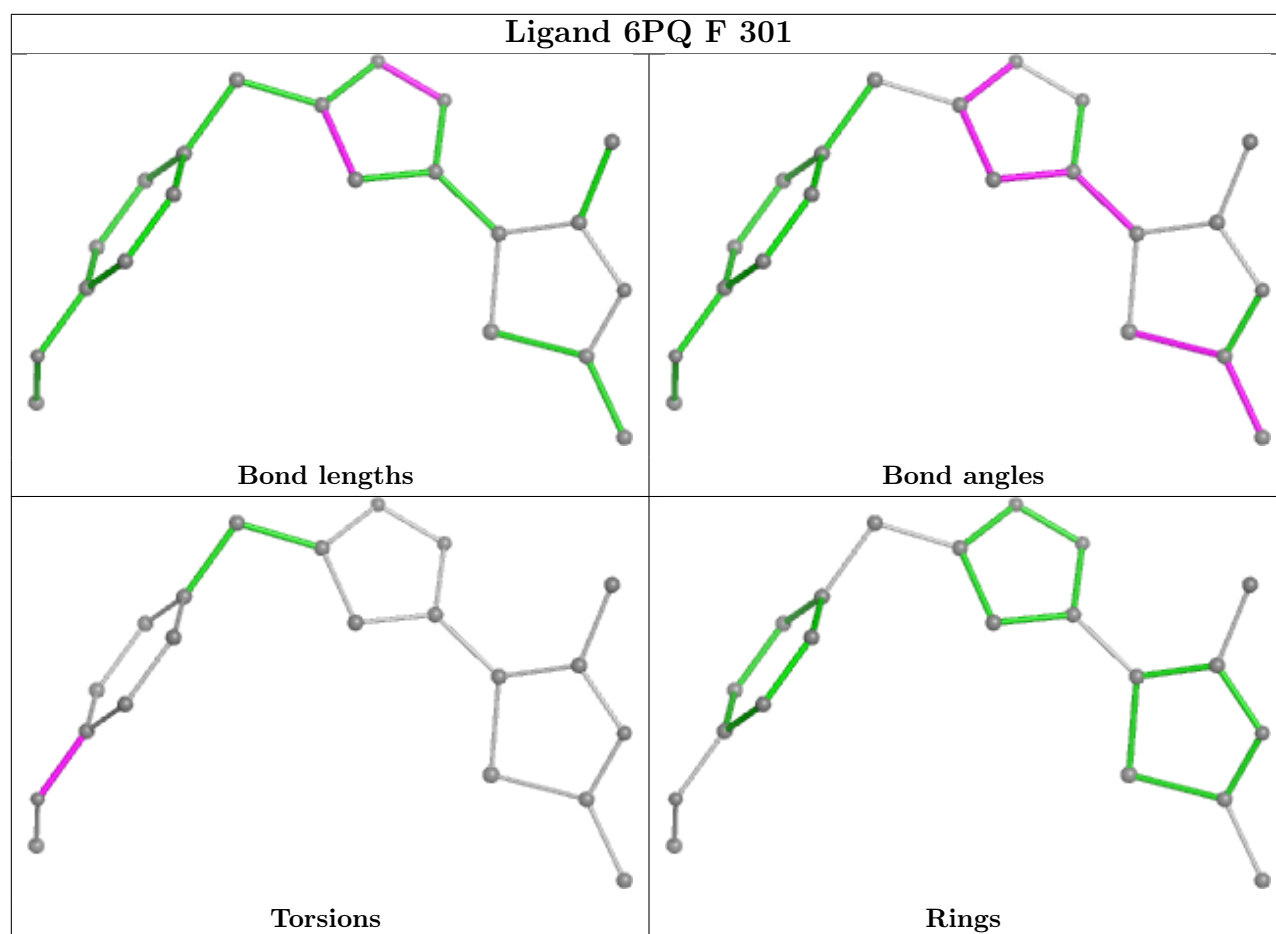


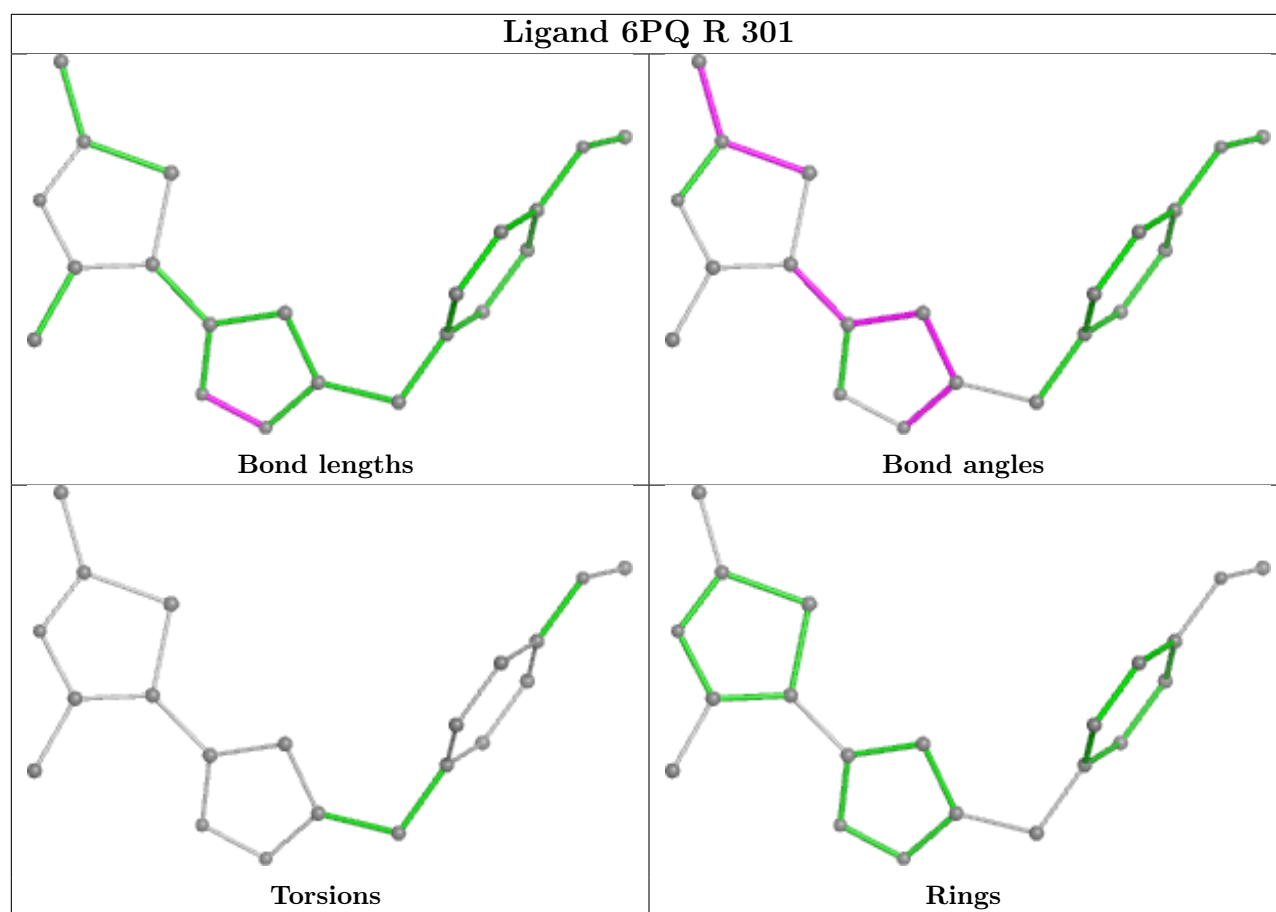


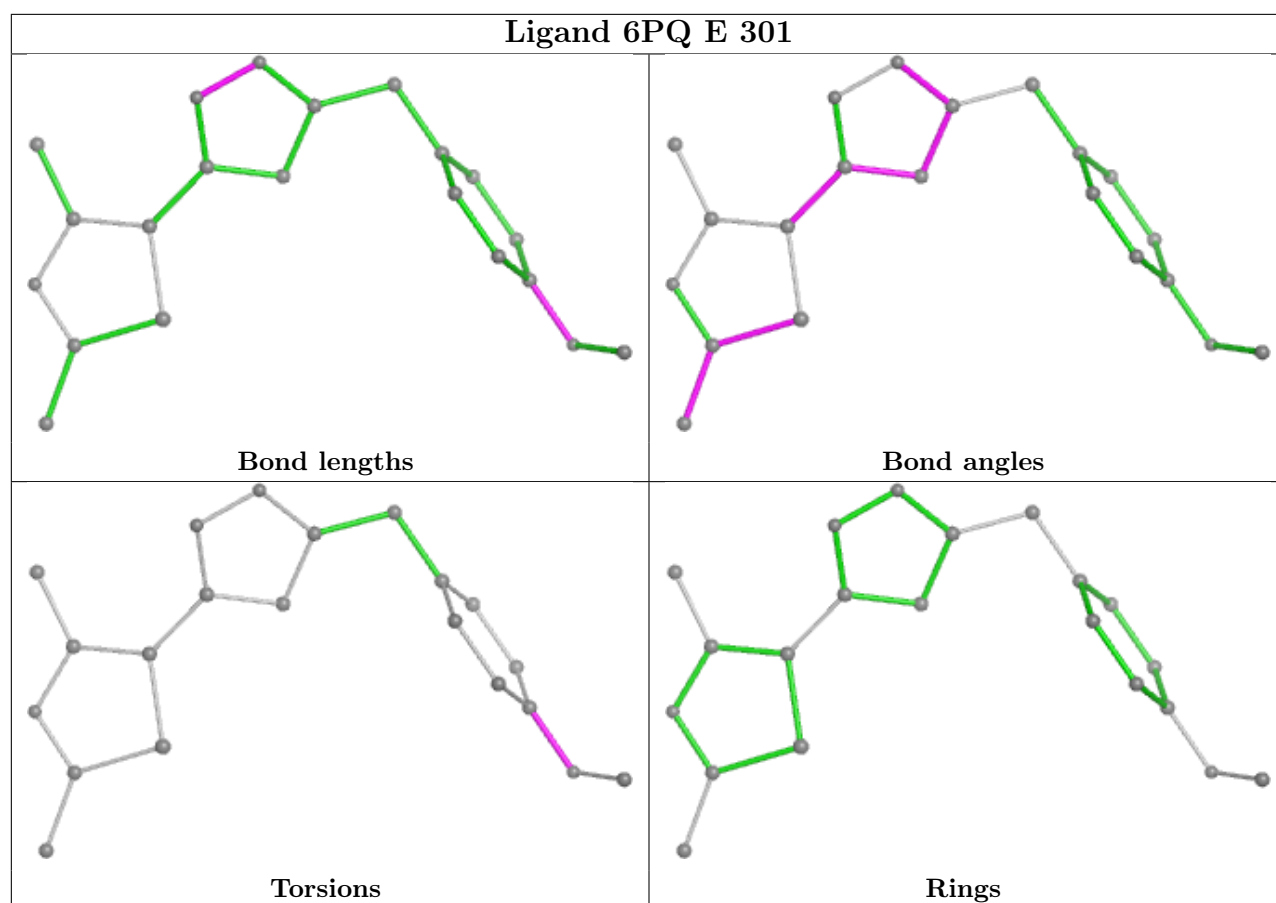












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	217/217 (100%)	-0.23	2 (0%) 84 85	32, 46, 72, 141	0
1	B	215/217 (99%)	-0.32	0 100 100	28, 40, 74, 114	0
1	C	216/217 (99%)	0.01	4 (1%) 66 69	31, 50, 73, 126	0
1	D	215/217 (99%)	0.07	3 (1%) 75 77	31, 49, 75, 114	0
1	E	215/217 (99%)	0.22	10 (4%) 31 30	42, 69, 104, 148	0
1	F	216/217 (99%)	-0.24	2 (0%) 84 85	29, 43, 72, 114	0
1	G	217/217 (100%)	-0.09	4 (1%) 68 70	31, 48, 79, 151	0
1	H	216/217 (99%)	-0.07	3 (1%) 75 77	31, 44, 69, 143	0
1	I	215/217 (99%)	0.06	3 (1%) 75 77	32, 51, 78, 121	0
1	J	216/217 (99%)	-0.22	2 (0%) 84 85	33, 46, 73, 116	0
1	K	215/217 (99%)	-0.25	3 (1%) 75 77	29, 39, 66, 120	0
1	L	216/217 (99%)	-0.10	6 (2%) 53 54	35, 47, 79, 107	0
1	M	215/217 (99%)	-0.02	3 (1%) 75 77	33, 49, 77, 131	0
1	N	216/217 (99%)	-0.17	3 (1%) 75 77	32, 46, 77, 126	0
1	O	216/217 (99%)	-0.18	2 (0%) 84 85	34, 48, 74, 124	0
1	P	215/217 (99%)	0.21	4 (1%) 66 69	36, 62, 96, 125	0
1	Q	216/217 (99%)	-0.12	4 (1%) 66 69	32, 47, 76, 110	0
1	R	217/217 (100%)	0.07	4 (1%) 68 70	33, 60, 90, 136	0
1	S	215/217 (99%)	0.09	2 (0%) 84 85	34, 57, 92, 124	0
1	T	215/217 (99%)	0.03	2 (0%) 84 85	31, 49, 78, 111	0
1	U	215/217 (99%)	0.43	11 (5%) 28 26	34, 69, 107, 124	0
1	V	215/217 (99%)	0.05	2 (0%) 84 85	37, 56, 83, 134	0
1	W	215/217 (99%)	0.20	6 (2%) 53 54	37, 62, 97, 118	0
1	X	215/217 (99%)	0.31	8 (3%) 41 41	37, 76, 111, 139	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	5174/5208 (99%)	-0.01	93 (1%) 68 70	28, 51, 91, 151	0

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	218	ASP	5.6
1	H	216	SER	5.2
1	V	216	SER	5.0
1	N	216	SER	4.9
1	O	2	GLY	4.9

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
3	K	K	304	1/1	0.55	0.22	110,110,110,110	0
3	K	A	304	1/1	0.71	0.11	96,96,96,96	0
3	K	S	303	1/1	0.73	0.10	115,115,115,115	0
3	K	M	304	1/1	0.74	0.16	101,101,101,101	0
4	PO4	W	304	5/5	0.76	0.30	135,136,139,143	0
3	K	Q	303	1/1	0.80	0.12	82,82,82,82	0
3	K	R	303	1/1	0.80	0.17	105,105,105,105	0
4	PO4	V	304	5/5	0.88	0.15	109,109,112,113	0
3	K	L	304	1/1	0.88	0.08	76,76,76,76	0
3	K	G	302	1/1	0.89	0.16	100,100,100,100	0
4	PO4	K	305	5/5	0.91	0.31	119,120,122,125	0
3	K	S	304	1/1	0.91	0.08	70,70,70,70	0
4	PO4	H	304	5/5	0.91	0.22	99,100,101,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	K	N	304	1/1	0.92	0.06	85,85,85,85	0
4	PO4	I	304	5/5	0.92	0.31	102,102,105,111	0
3	K	P	303	1/1	0.92	0.14	62,62,62,62	0
4	PO4	S	305	5/5	0.92	0.12	96,98,102,105	0
3	K	E	303	1/1	0.92	0.09	68,68,68,68	0
4	PO4	D	304	5/5	0.92	0.20	88,88,95,107	0
4	PO4	M	305	5/5	0.93	0.22	90,91,99,100	0
3	K	J	302	1/1	0.93	0.29	64,64,64,64	0
3	K	F	303	1/1	0.94	0.08	69,69,69,69	0
3	K	F	302	1/1	0.94	0.26	41,41,41,41	0
3	K	J	304	1/1	0.95	0.07	81,81,81,81	0
3	K	M	303	1/1	0.95	0.09	56,56,56,56	0
3	K	Q	302	1/1	0.95	0.13	37,37,37,37	0
3	K	U	303	1/1	0.95	0.06	65,65,65,65	0
4	PO4	Q	304	5/5	0.95	0.11	86,88,91,92	0
3	K	V	303	1/1	0.95	0.11	54,54,54,54	0
4	PO4	T	304	5/5	0.95	0.19	90,90,92,99	0
4	PO4	C	304	5/5	0.95	0.15	94,96,99,103	0
3	K	I	303	1/1	0.95	0.07	49,49,49,49	0
3	K	W	303	1/1	0.96	0.08	58,58,58,58	0
2	6PQ	N	301	21/21	0.96	0.17	26,36,56,63	0
2	6PQ	R	301	21/21	0.96	0.15	33,50,59,62	0
2	6PQ	L	301	21/21	0.96	0.14	29,41,48,51	0
3	K	R	302	1/1	0.96	0.17	42,42,42,42	0
3	K	C	302	1/1	0.96	0.20	38,38,38,38	0
3	K	D	302	1/1	0.96	0.14	43,43,43,43	0
3	K	N	303	1/1	0.96	0.07	52,52,52,52	0
3	K	D	303	1/1	0.96	0.08	45,45,45,45	0
3	K	V	302	1/1	0.96	0.21	45,45,45,45	0
3	K	O	304	1/1	0.96	0.15	72,72,72,72	0
3	K	W	302	1/1	0.96	0.16	45,45,45,45	0
2	6PQ	W	301	21/21	0.97	0.15	35,40,49,51	0
3	K	U	302	1/1	0.97	0.13	39,39,39,39	0
3	K	A	303	1/1	0.97	0.09	64,64,64,64	0
2	6PQ	F	301	21/21	0.97	0.17	29,39,50,53	0
3	K	B	303	1/1	0.97	0.12	48,48,48,48	0
2	6PQ	I	301	21/21	0.97	0.13	29,44,56,57	0
2	6PQ	J	301	21/21	0.97	0.16	36,43,51,53	0
3	K	X	303	1/1	0.97	0.10	64,64,64,64	0
2	6PQ	B	301	21/21	0.97	0.17	28,37,45,49	0
3	K	O	302	1/1	0.97	0.16	39,39,39,39	0
3	K	O	303	1/1	0.97	0.06	46,46,46,46	0

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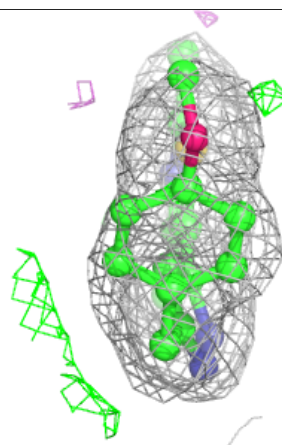
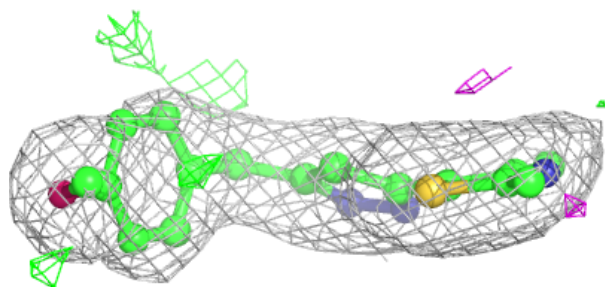
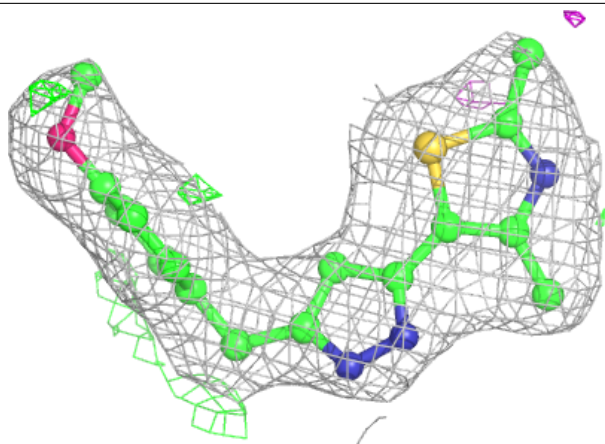
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	K	E	302	1/1	0.97	0.17	53,53,53,53	0
2	6PQ	M	301	21/21	0.97	0.14	29,38,46,50	0
2	6PQ	D	301	21/21	0.97	0.16	35,42,49,52	0
4	PO4	N	305	5/5	0.97	0.12	46,55,59,66	0
2	6PQ	O	301	21/21	0.97	0.13	32,45,53,54	0
2	6PQ	P	301	21/21	0.97	0.18	32,52,57,61	0
2	6PQ	E	301	21/21	0.97	0.18	43,52,58,60	0
3	K	R	304	1/1	0.97	0.07	60,60,60,60	0
2	6PQ	S	301	21/21	0.97	0.15	44,55,62,63	0
3	K	K	302	1/1	0.98	0.25	43,43,43,43	0
3	K	K	303	1/1	0.98	0.08	45,45,45,45	0
3	K	T	303	1/1	0.98	0.09	43,43,43,43	0
2	6PQ	G	301	21/21	0.98	0.13	25,41,49,50	0
3	K	L	303	1/1	0.98	0.09	64,64,64,64	0
3	K	C	303	1/1	0.98	0.12	46,46,46,46	0
3	K	M	302	1/1	0.98	0.22	38,38,38,38	0
2	6PQ	H	301	21/21	0.98	0.15	28,40,49,52	0
2	6PQ	T	301	21/21	0.98	0.15	20,36,47,55	0
3	K	N	302	1/1	0.98	0.19	42,42,42,42	0
2	6PQ	U	301	21/21	0.98	0.14	35,43,55,64	0
2	6PQ	V	301	21/21	0.98	0.13	32,41,53,56	0
2	6PQ	C	301	21/21	0.98	0.14	22,43,51,55	0
2	6PQ	X	301	21/21	0.98	0.15	45,53,66,69	0
3	K	A	302	1/1	0.98	0.24	37,37,37,37	0
3	K	G	303	1/1	0.98	0.04	56,56,56,56	0
3	K	G	304	1/1	0.98	0.22	36,36,36,36	0
2	6PQ	A	301	21/21	0.98	0.15	35,41,48,56	0
2	6PQ	K	301	21/21	0.98	0.16	11,28,36,44	0
3	K	J	303	1/1	0.98	0.09	48,48,48,48	0
2	6PQ	Q	301	21/21	0.98	0.14	28,35,46,51	0
3	K	S	302	1/1	0.98	0.16	39,39,39,39	0
3	K	H	303	1/1	0.99	0.08	46,46,46,46	0
3	K	T	302	1/1	0.99	0.21	38,38,38,38	0
3	K	X	302	1/1	0.99	0.19	51,51,51,51	0
3	K	L	302	1/1	0.99	0.16	29,29,29,29	0
3	K	I	302	1/1	0.99	0.12	32,32,32,32	0
3	K	P	302	1/1	0.99	0.16	47,47,47,47	0
3	K	B	302	1/1	0.99	0.17	25,25,25,25	0
3	K	H	302	1/1	0.99	0.22	38,38,38,38	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.

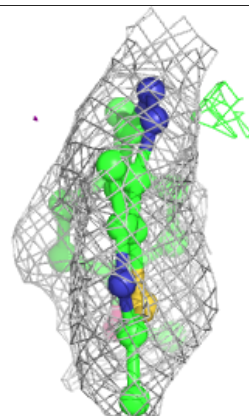
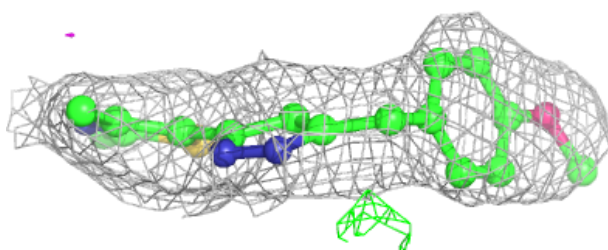
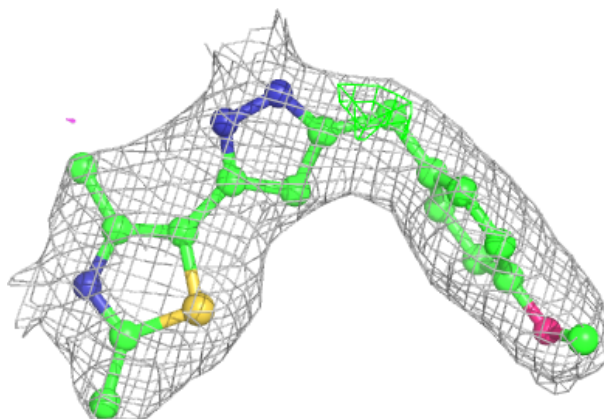
Electron density around 6PQ N 301:

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

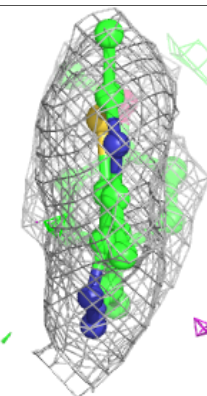
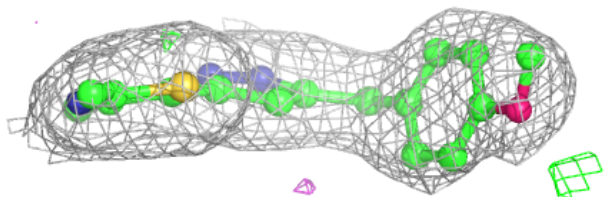
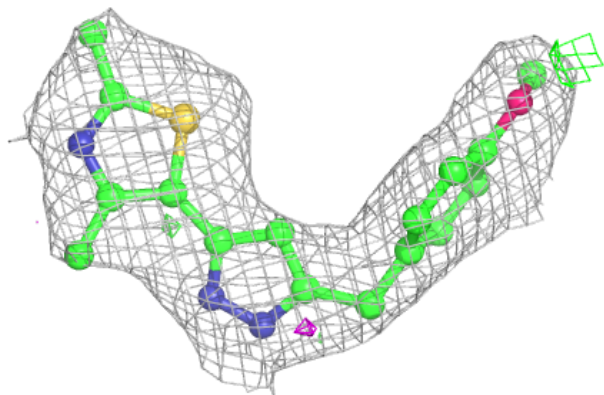


Electron density around 6PQ R 301:

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

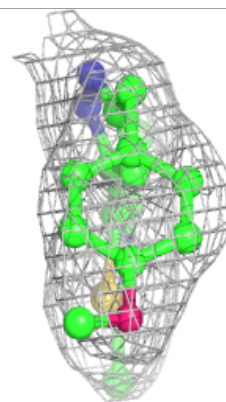
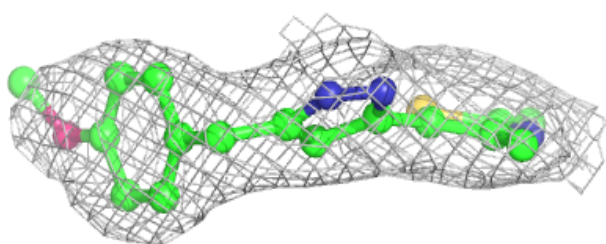
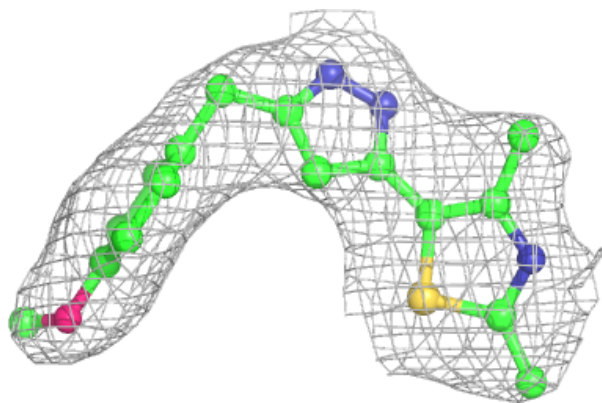
**Electron density around 6PQ L 301:**

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

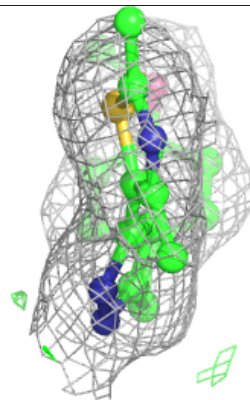
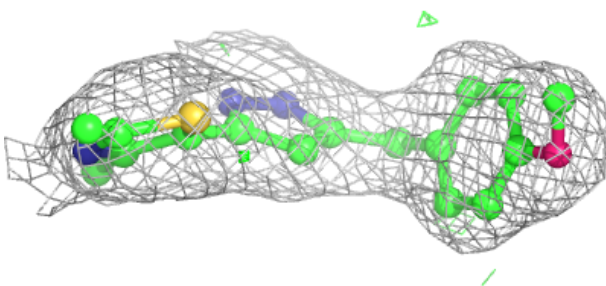
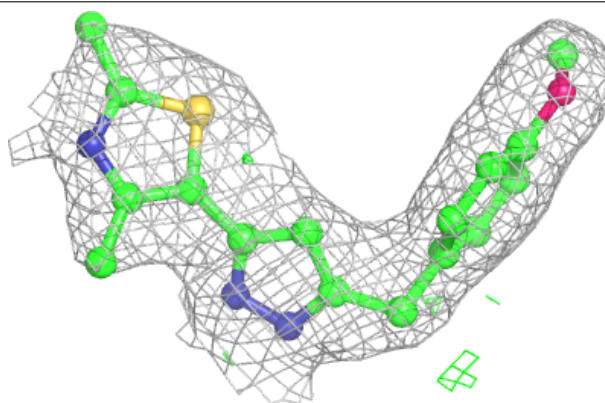


Electron density around 6PQ W 301:

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

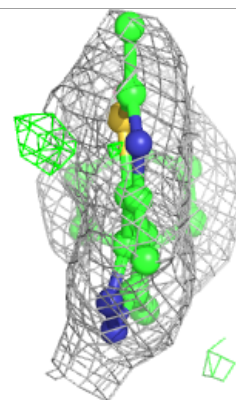
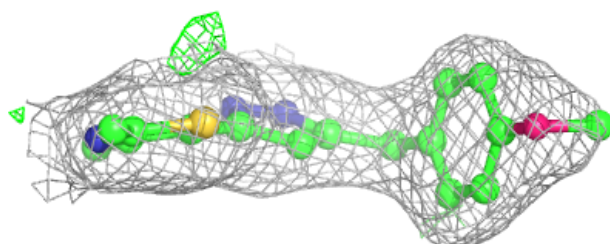
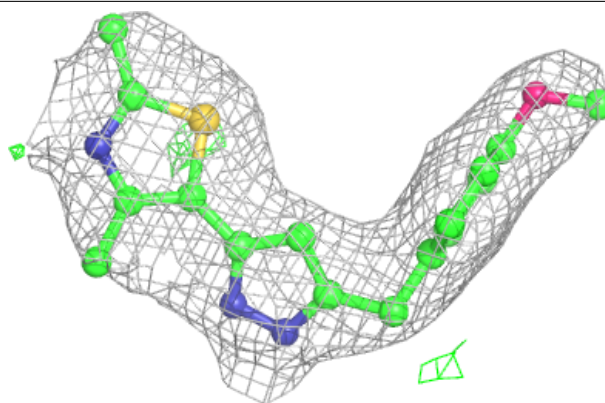
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

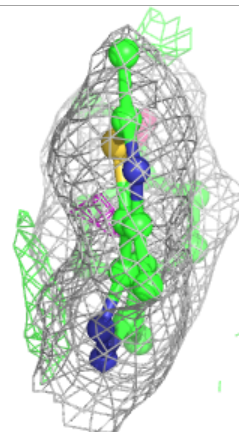
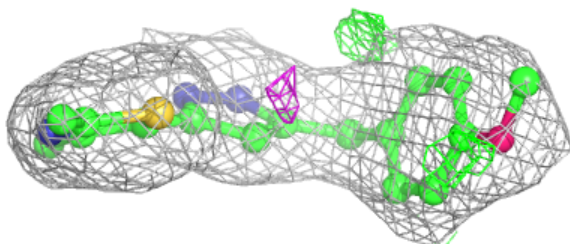
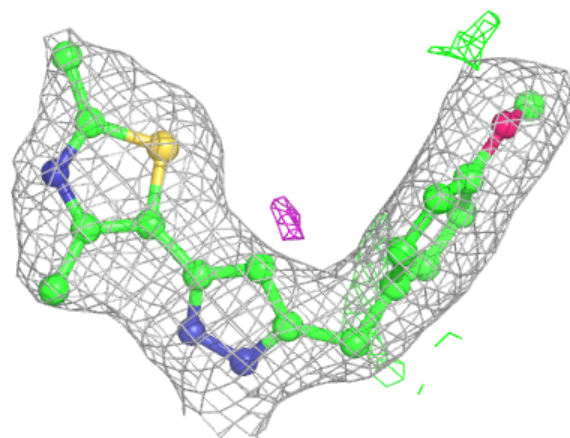


Electron density around 6PQ I 301:

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

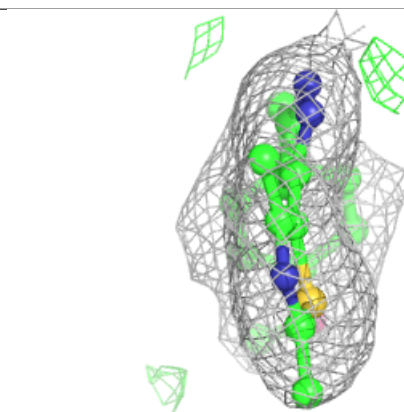
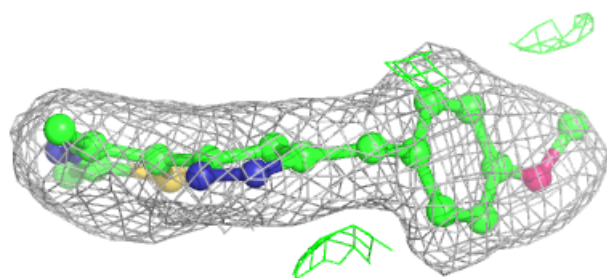
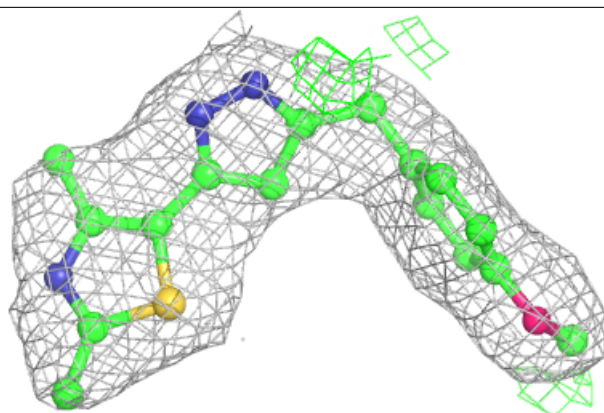
**Electron density around 6PQ J 301:**

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

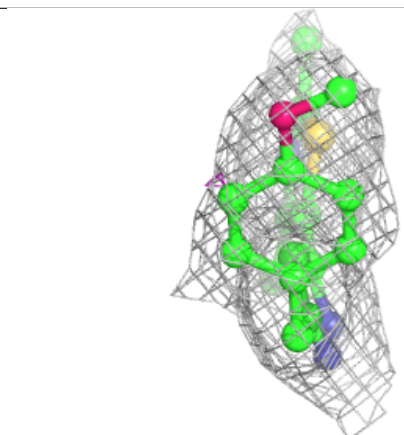
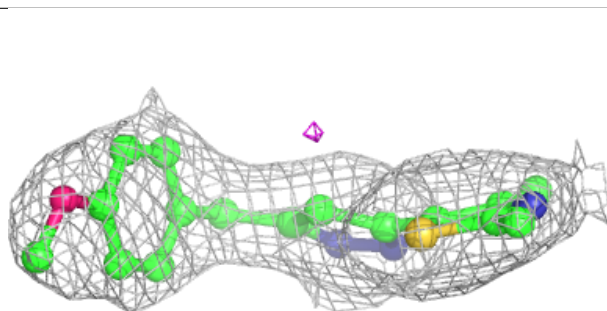
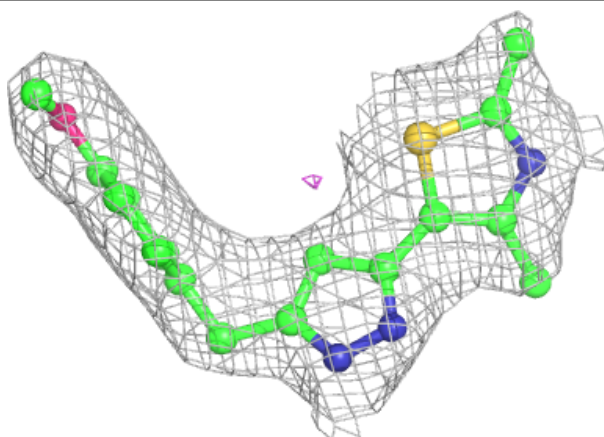


Electron density around 6PQ B 301:

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

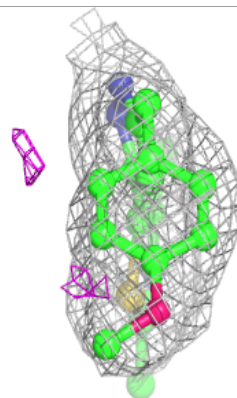
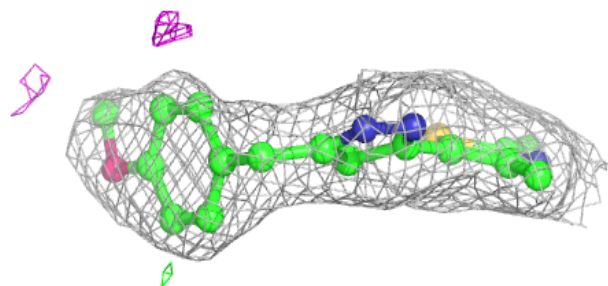
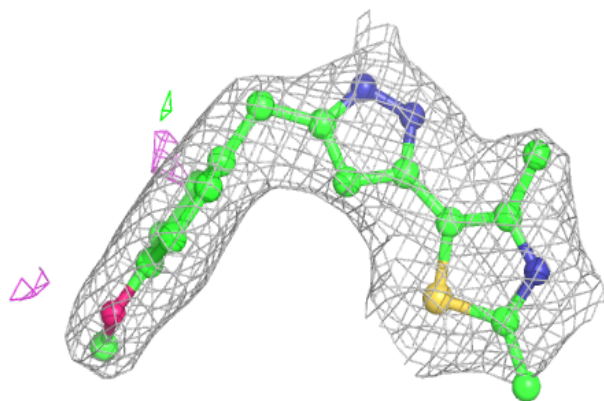
**Electron density around 6PQ M 301:**

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

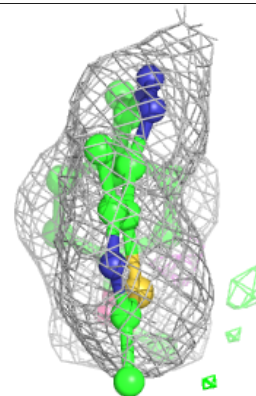
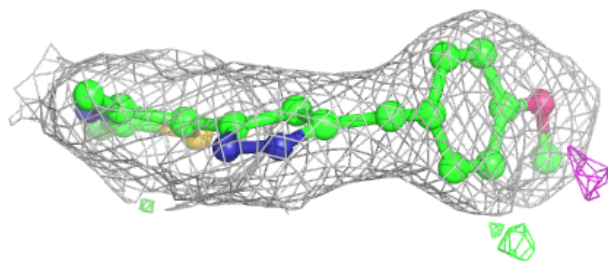
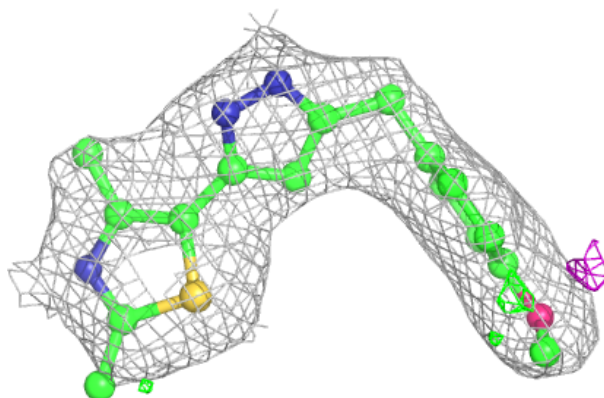


Electron density around 6PQ D 301:

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and green (positive)

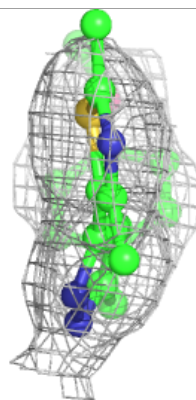
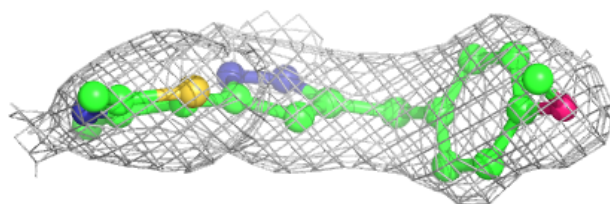
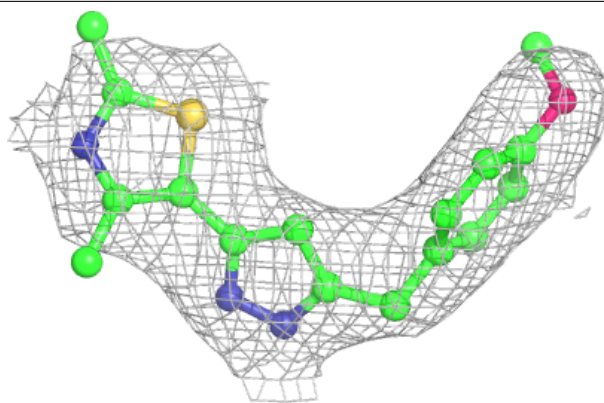
**Electron density around 6PQ O 301:**

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and green (positive)

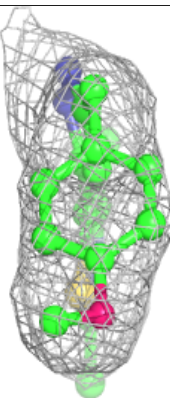
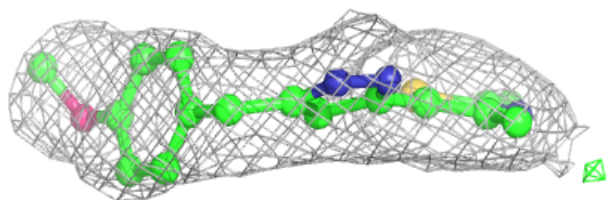
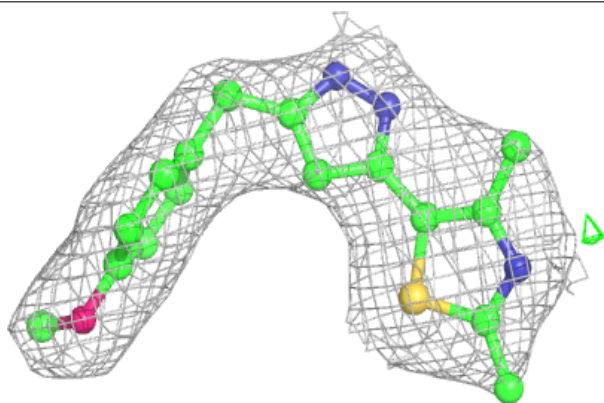


Electron density around 6PQ P 301:

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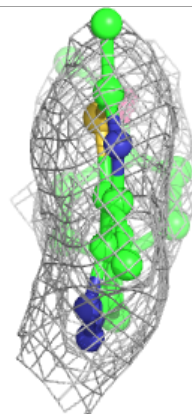
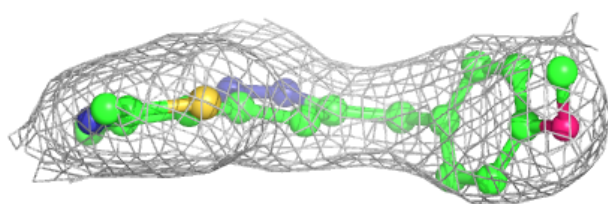
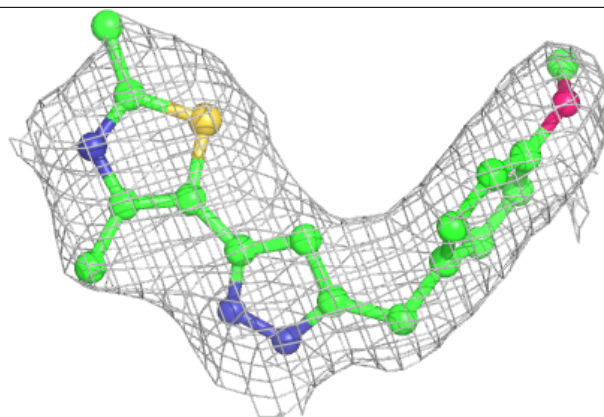
**Electron density around 6PQ E 301:**

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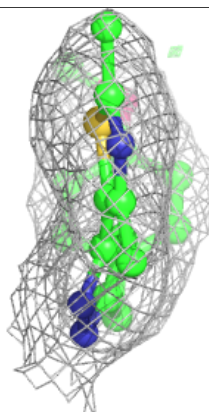
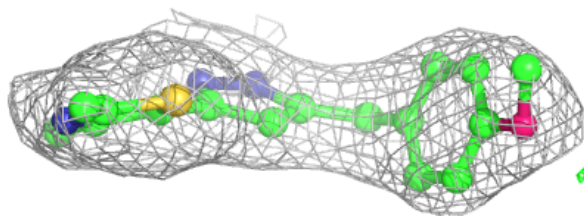
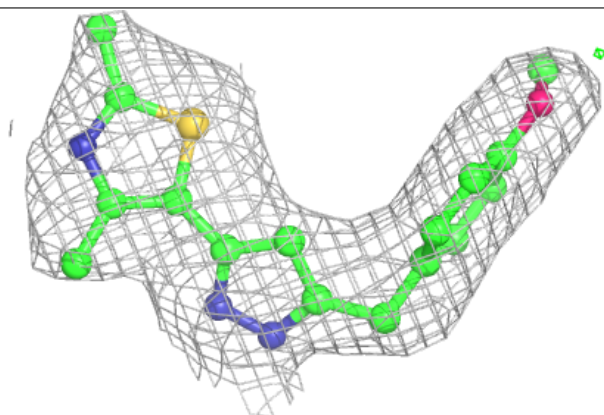


Electron density around 6PQ S 301:

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and green (positive)

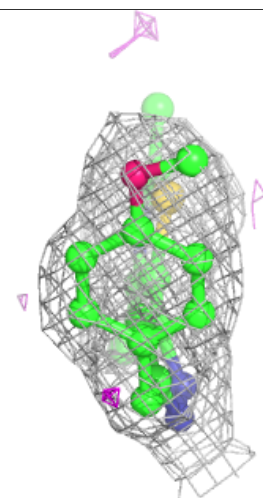
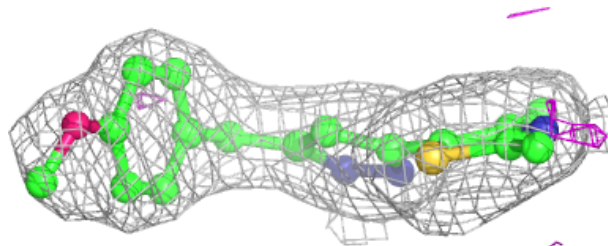
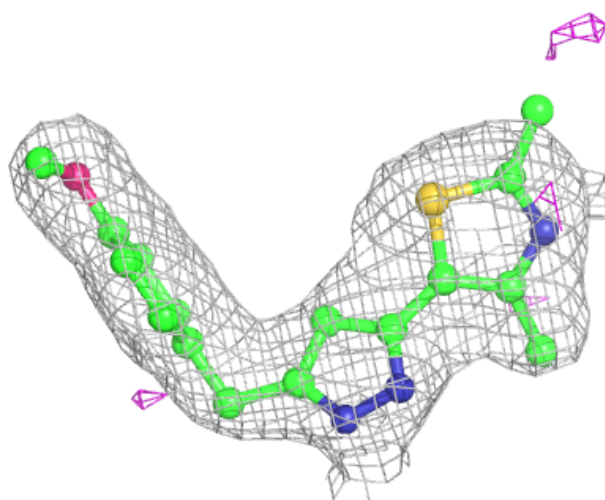
**Electron density around 6PQ G 301:**

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



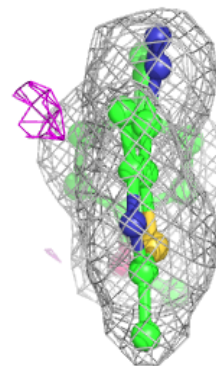
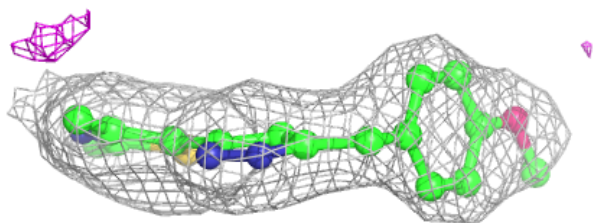
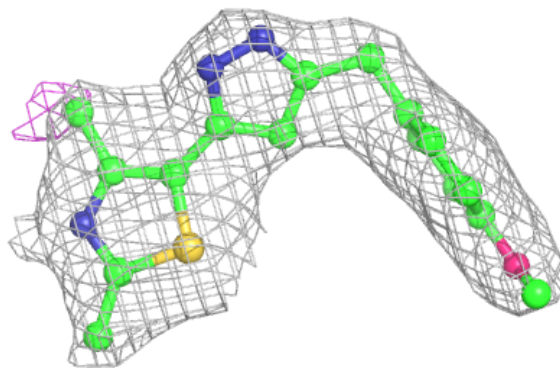
Electron density around 6PQ H 301:

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and green (positive)



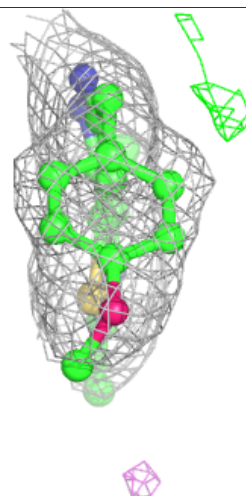
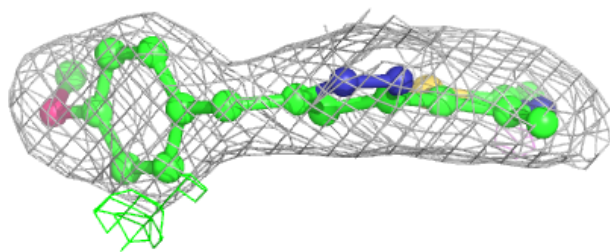
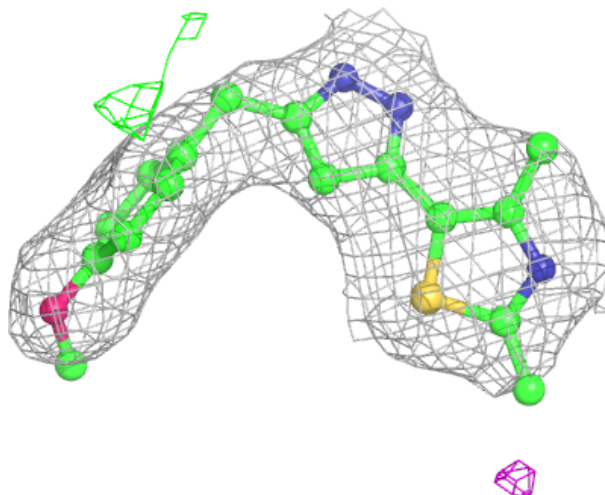
Electron density around 6PQ T 301:

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and green (positive)



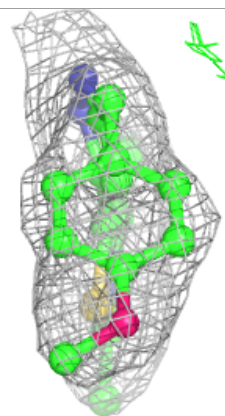
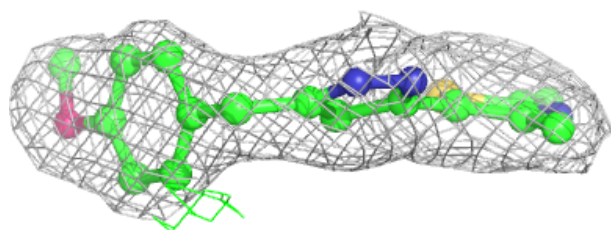
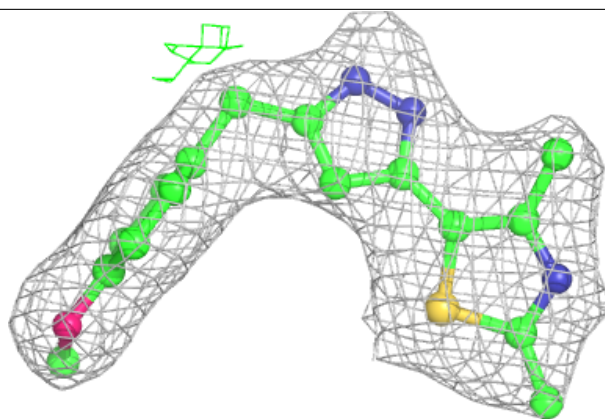
Electron density around 6PQ U 301:

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

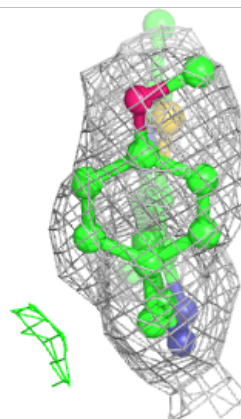
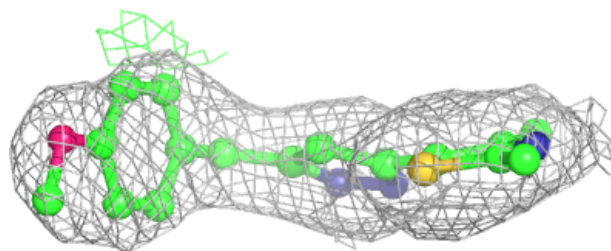
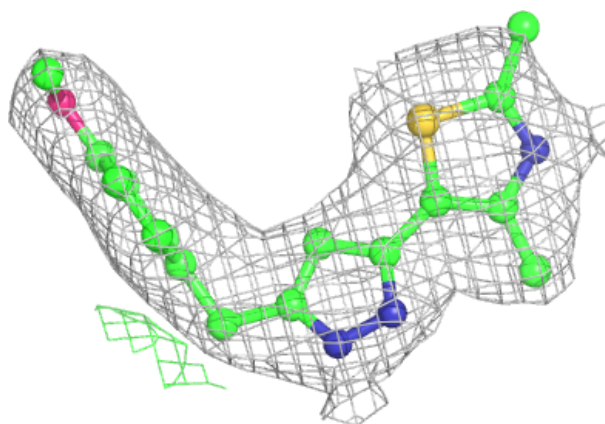


Electron density around 6PQ V 301:

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

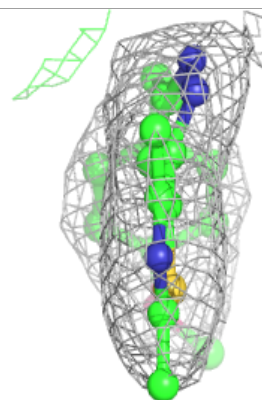
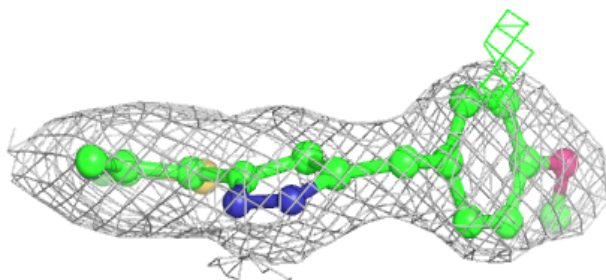
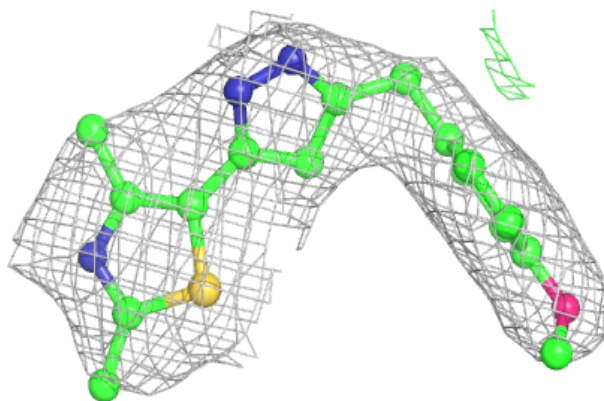
**Electron density around 6PQ C 301:**

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

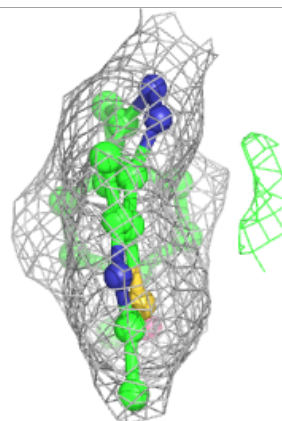
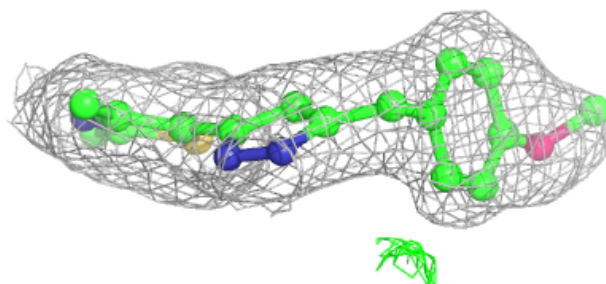
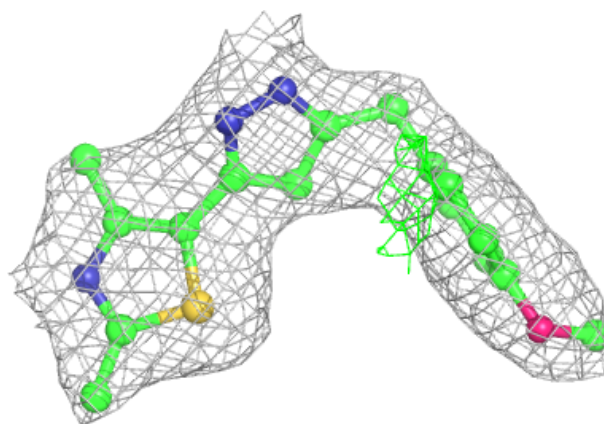


Electron density around 6PQ X 301:

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

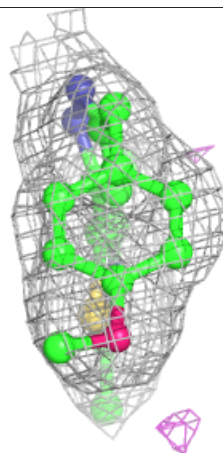
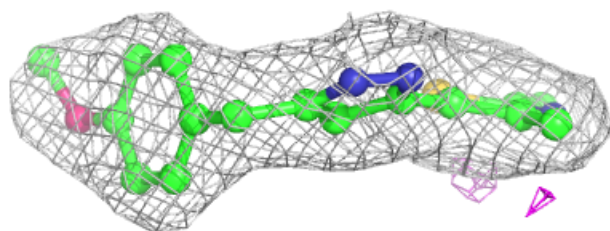
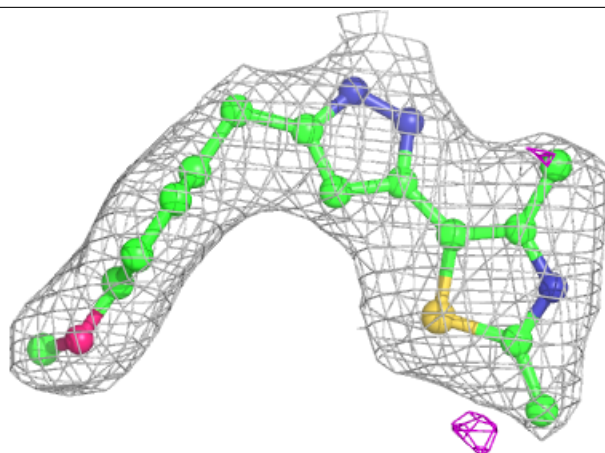
**Electron density around 6PQ A 301:**

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

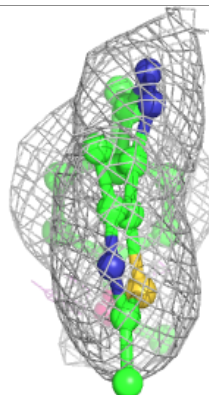
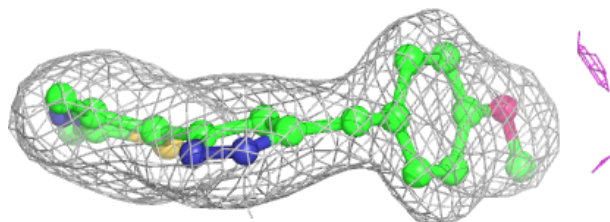
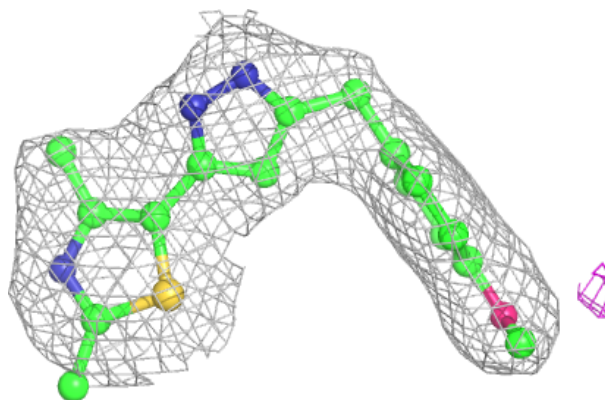


Electron density around 6PQ K 301:

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

**Electron density around 6PQ Q 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 [i](#)

There are no such residues in this entry.