



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:27 PM UTC

PDB ID : 3GH8 / pdb_00003gh8
Title : Crystal structure of Mus musculus iodotyrosine deiodinase (IYD) bound to FMN and di-iodotyrosine (DIT)
Authors : Thomas, S.R.; McTamney, P.M.; Adler, J.M.; LaRonde-LeBlanc, N.; Rokita, S.E.
Deposited on : 2009-03-03
Resolution : 2.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

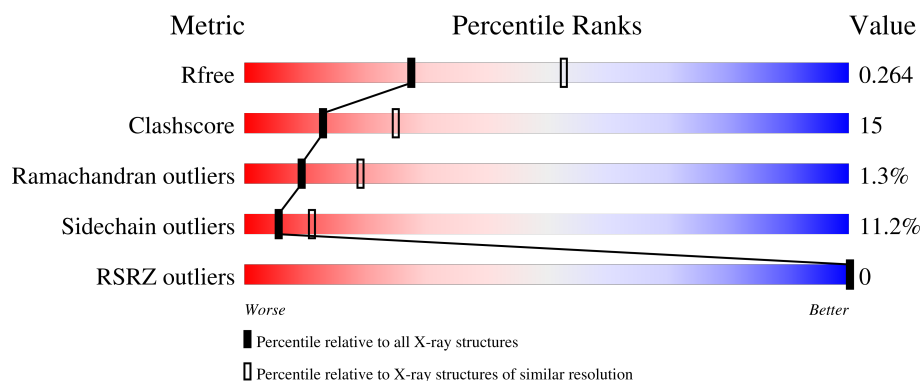
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	259	
1	B	259	
1	C	259	
1	D	259	

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Mol	Chain	Length	Quality of chain
1	E	259	 53% 29% • 15%
1	F	259	 57% 23% 5% 15%
1	G	259	 54% 26% • • 15%
1	H	259	 53% 29% • 15%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14910 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 Iodotyrosine dehalogenase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	B	220	Total	C	N	O	S	0	0	0
			1773	1136	314	314	9			
1	C	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	D	220	Total	C	N	O	S	0	0	0
			1777	1139	316	313	9			
1	E	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	F	220	Total	C	N	O	S	0	0	0
			1773	1136	314	314	9			
1	G	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	H	220	Total	C	N	O	S	0	0	0
			1777	1139	316	313	9			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MET	-	expression tag	UNP Q9DCX8
A	286	HIS	-	expression tag	UNP Q9DCX8
A	287	HIS	-	expression tag	UNP Q9DCX8
A	288	HIS	-	expression tag	UNP Q9DCX8
A	289	HIS	-	expression tag	UNP Q9DCX8
A	290	HIS	-	expression tag	UNP Q9DCX8
A	291	HIS	-	expression tag	UNP Q9DCX8
B	33	MET	-	expression tag	UNP Q9DCX8
B	286	HIS	-	expression tag	UNP Q9DCX8
B	287	HIS	-	expression tag	UNP Q9DCX8
B	288	HIS	-	expression tag	UNP Q9DCX8
B	289	HIS	-	expression tag	UNP Q9DCX8
B	290	HIS	-	expression tag	UNP Q9DCX8

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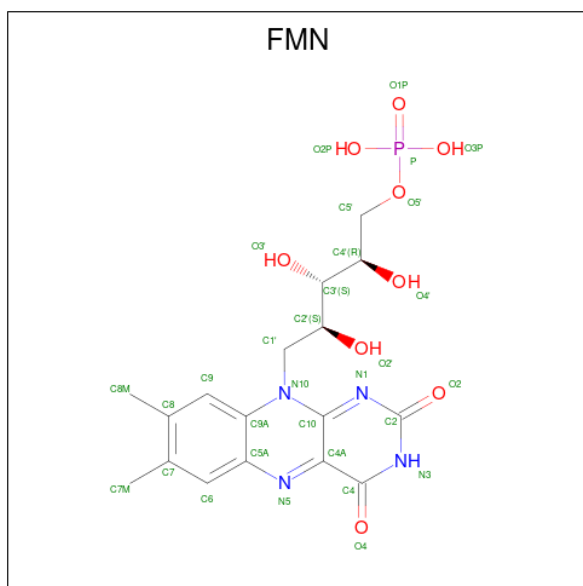
Chain	Residue	Modelled	Actual	Comment	Reference
B	291	HIS	-	expression tag	UNP Q9DCX8
C	33	MET	-	expression tag	UNP Q9DCX8
C	286	HIS	-	expression tag	UNP Q9DCX8
C	287	HIS	-	expression tag	UNP Q9DCX8
C	288	HIS	-	expression tag	UNP Q9DCX8
C	289	HIS	-	expression tag	UNP Q9DCX8
C	290	HIS	-	expression tag	UNP Q9DCX8
C	291	HIS	-	expression tag	UNP Q9DCX8
D	33	MET	-	expression tag	UNP Q9DCX8
D	286	HIS	-	expression tag	UNP Q9DCX8
D	287	HIS	-	expression tag	UNP Q9DCX8
D	288	HIS	-	expression tag	UNP Q9DCX8
D	289	HIS	-	expression tag	UNP Q9DCX8
D	290	HIS	-	expression tag	UNP Q9DCX8
D	291	HIS	-	expression tag	UNP Q9DCX8
E	33	MET	-	expression tag	UNP Q9DCX8
E	286	HIS	-	expression tag	UNP Q9DCX8
E	287	HIS	-	expression tag	UNP Q9DCX8
E	288	HIS	-	expression tag	UNP Q9DCX8
E	289	HIS	-	expression tag	UNP Q9DCX8
E	290	HIS	-	expression tag	UNP Q9DCX8
E	291	HIS	-	expression tag	UNP Q9DCX8
F	33	MET	-	expression tag	UNP Q9DCX8
F	286	HIS	-	expression tag	UNP Q9DCX8
F	287	HIS	-	expression tag	UNP Q9DCX8
F	288	HIS	-	expression tag	UNP Q9DCX8
F	289	HIS	-	expression tag	UNP Q9DCX8
F	290	HIS	-	expression tag	UNP Q9DCX8
F	291	HIS	-	expression tag	UNP Q9DCX8
G	33	MET	-	expression tag	UNP Q9DCX8
G	286	HIS	-	expression tag	UNP Q9DCX8
G	287	HIS	-	expression tag	UNP Q9DCX8
G	288	HIS	-	expression tag	UNP Q9DCX8
G	289	HIS	-	expression tag	UNP Q9DCX8
G	290	HIS	-	expression tag	UNP Q9DCX8
G	291	HIS	-	expression tag	UNP Q9DCX8
H	33	MET	-	expression tag	UNP Q9DCX8
H	286	HIS	-	expression tag	UNP Q9DCX8
H	287	HIS	-	expression tag	UNP Q9DCX8
H	288	HIS	-	expression tag	UNP Q9DCX8
H	289	HIS	-	expression tag	UNP Q9DCX8
H	290	HIS	-	expression tag	UNP Q9DCX8

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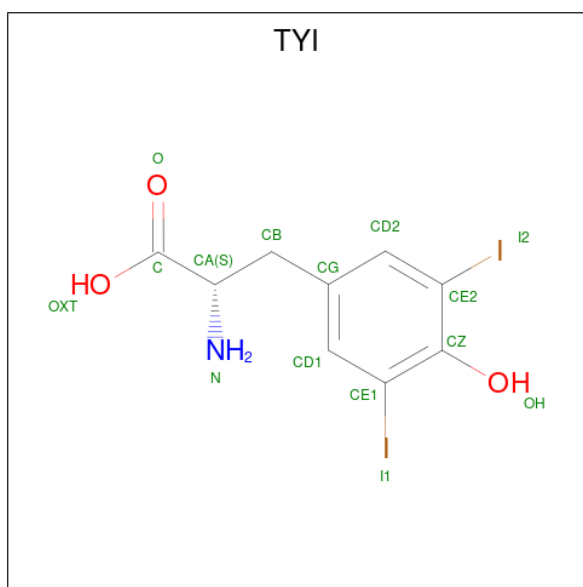
Chain	Residue	Modelled	Actual	Comment	Reference
H	291	HIS	-	expression tag	UNP Q9DCX8

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	C	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	E	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	F	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	G	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	H	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is 3,5-DIODOTYROSINE (CCD ID: TYI) (formula: $C_9H_9I_2NO_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	B	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	C	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	D	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	E	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	F	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	G	1	Total 15	C 9	I 2	N 1	O 3	0	0
3	H	1	Total 15	C 9	I 2	N 1	O 3	0	0

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		

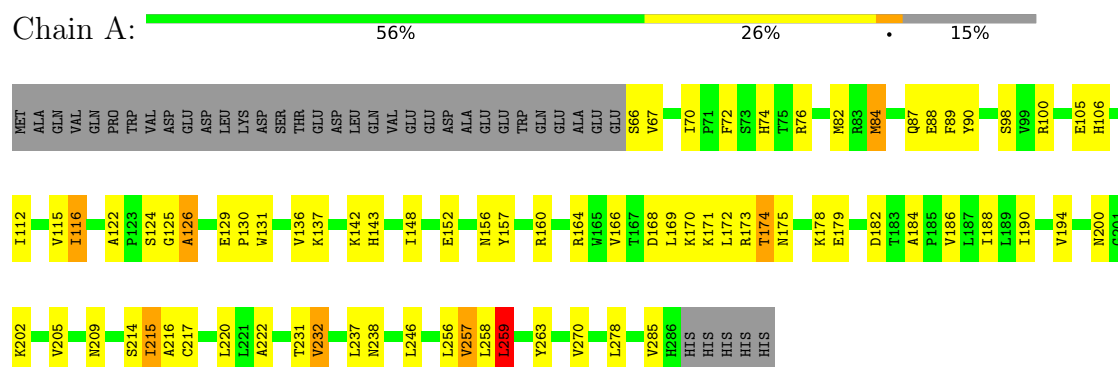
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		
5	B	38	Total	O	0	0
			38	38		
5	C	39	Total	O	0	0
			39	39		
5	D	23	Total	O	0	0
			23	23		
5	E	48	Total	O	0	0
			48	48		
5	F	40	Total	O	0	0
			40	40		
5	G	38	Total	O	0	0
			38	38		
5	H	38	Total	O	0	0
			38	38		

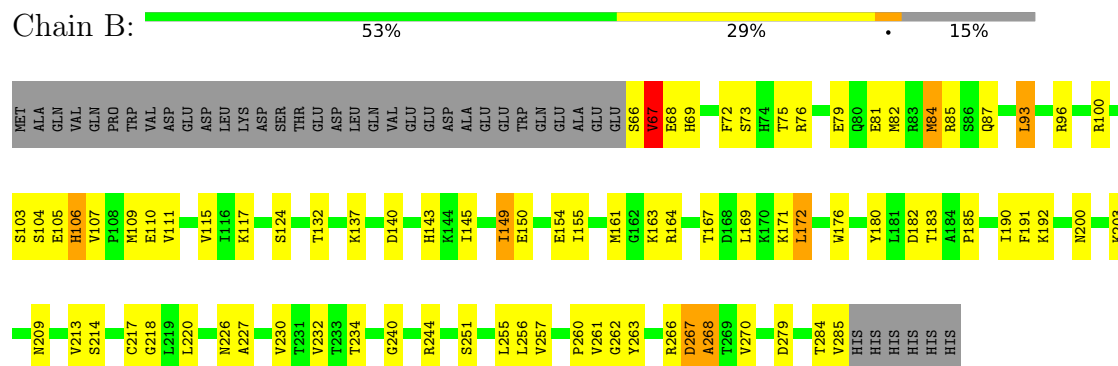
3 Residue-property plots [i](#)

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.

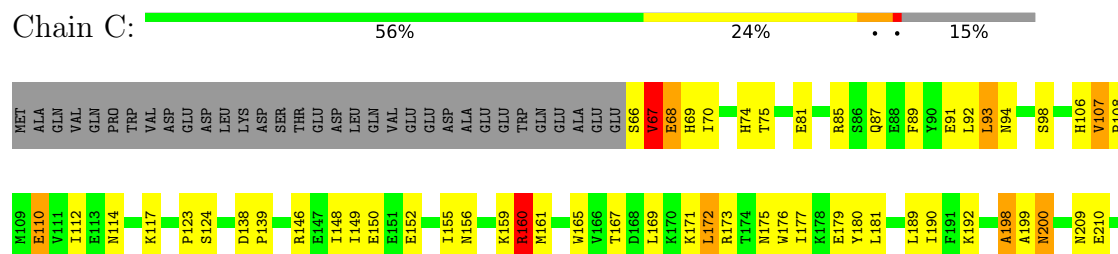
• Molecule 1: Iodotyrosine dehalogenase 1



• Molecule 1: Iodotyrosine dehalogenase 1



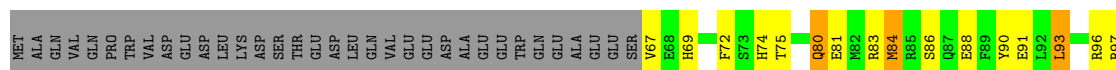
• Molecule 1: Iodotyrosine dehalogenase 1





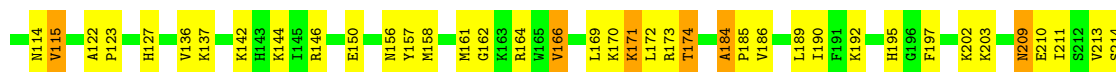
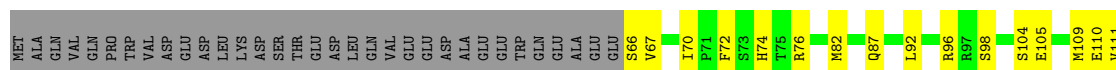
• Molecule 1: Iodotyrosine dehalogenase 1

Chain D: 54% 25% 5% 15%



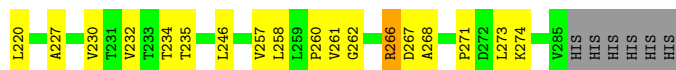
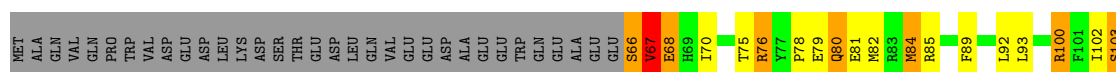
• Molecule 1: Iodotyrosine dehalogenase 1

Chain E: 53% 29% 15% 5%



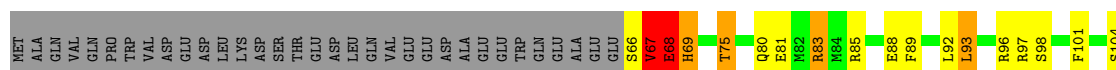
• Molecule 1: Iodotyrosine dehalogenase 1

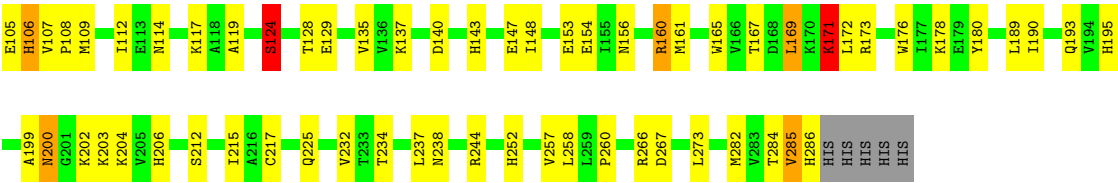
Chain F: 57% 23% 5% 15%



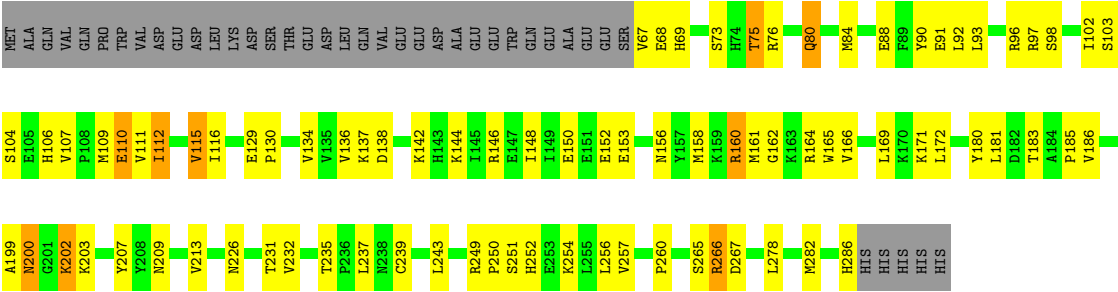
• Molecule 1: Iodotyrosine dehalogenase 1

Chain G: 54% 26% 15% 5%





• Molecule 1: Iodotyrosine dehalogenase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.61Å 112.57Å 189.25Å 90.00° 89.92° 90.00°	Depositor
Resolution (Å)	30.00 – 2.61 30.00 – 2.61	Depositor EDS
% Data completeness (in resolution range)	96.8 (30.00-2.61) 96.8 (30.00-2.61)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.181 , 0.264 0.182 , 0.264	Depositor DCC
R_{free} test set	3203 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.986	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 12.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.457 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14910	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, PO4, TYI

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.12	3/1823 (0.2%)	1.26	6/2468 (0.2%)
1	B	1.10	1/1812 (0.1%)	1.27	10/2453 (0.4%)
1	C	1.07	2/1823 (0.1%)	1.25	11/2468 (0.4%)
1	D	1.08	0/1817	1.25	6/2460 (0.2%)
1	E	1.12	0/1823	1.27	11/2468 (0.4%)
1	F	1.12	3/1812 (0.2%)	1.25	5/2453 (0.2%)
1	G	1.09	3/1823 (0.2%)	1.26	12/2468 (0.5%)
1	H	1.11	3/1817 (0.2%)	1.21	7/2460 (0.3%)
All	All	1.10	15/14550 (0.1%)	1.25	68/19698 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	F	1	1
1	G	0	1
All	All	1	3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	LEU	CA-C	-7.63	1.46	1.52
1	C	149	ILE	CA-CB	6.93	1.62	1.54
1	A	222	ALA	CA-CB	-6.69	1.42	1.53
1	H	129	GLU	C-O	-6.63	1.20	1.23
1	F	129	GLU	CA-C	6.44	1.57	1.53
1	B	155	ILE	CA-CB	6.11	1.61	1.54
1	A	129	GLU	CA-C	5.83	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	217	CYS	N-CA	-5.67	1.39	1.46
1	G	129	GLU	C-O	-5.65	1.21	1.23
1	H	75	THR	CA-CB	5.43	1.60	1.53
1	H	130	PRO	CA-C	-5.34	1.48	1.53
1	G	217	CYS	N-CA	-5.30	1.39	1.46
1	G	285	VAL	CA-CB	5.21	1.61	1.54
1	C	217	CYS	N-CA	-5.16	1.40	1.46
1	F	111	VAL	CA-CB	5.16	1.60	1.54

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	160	ARG	N-CA-C	9.61	121.83	111.36
1	A	70	ILE	CA-C-N	-9.06	111.06	120.03
1	A	70	ILE	C-N-CA	-9.06	111.06	120.03
1	E	70	ILE	CA-C-N	-8.32	112.16	120.31
1	E	70	ILE	C-N-CA	-8.32	112.16	120.31
1	C	160	ARG	N-CA-C	8.28	122.66	112.23
1	A	168	ASP	N-CA-C	-8.06	102.90	112.89
1	C	107	VAL	CA-C-N	7.98	128.45	119.83
1	C	107	VAL	C-N-CA	7.98	128.45	119.83
1	G	69	HIS	N-CA-C	7.92	122.15	108.76
1	F	67	VAL	N-CA-C	7.85	125.67	109.34
1	E	281	ILE	N-CA-C	-7.69	105.64	113.10
1	H	186	VAL	N-CA-C	7.43	118.15	108.35
1	F	100	ARG	NE-CZ-NH1	-6.98	114.52	121.50
1	D	160	ARG	N-CA-C	6.90	118.80	111.28
1	G	124	SER	N-CA-C	-6.70	98.17	108.76
1	D	138	ASP	CA-C-N	6.67	126.18	119.24
1	D	138	ASP	C-N-CA	6.67	126.18	119.24
1	B	263	TYR	CA-C-N	-6.65	113.13	119.85
1	B	263	TYR	C-N-CA	-6.65	113.13	119.85
1	E	184	ALA	CA-C-N	6.65	126.34	119.56
1	E	184	ALA	C-N-CA	6.65	126.34	119.56
1	B	240	GLY	CA-C-N	6.64	126.15	119.24
1	B	240	GLY	C-N-CA	6.64	126.15	119.24
1	G	128	THR	N-CA-C	-6.59	105.77	113.88
1	C	138	ASP	CA-C-N	6.48	126.71	119.32
1	C	138	ASP	C-N-CA	6.48	126.71	119.32
1	C	124	SER	N-CA-C	-6.42	98.62	108.76
1	F	114	ASN	N-CA-C	6.20	118.84	111.71
1	E	195	HIS	N-CA-C	-6.11	100.31	108.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	270	VAL	CA-C-N	-6.05	113.55	119.78
1	B	270	VAL	C-N-CA	-6.05	113.55	119.78
1	B	67	VAL	N-CA-C	5.98	121.78	109.34
1	C	74	HIS	N-CA-C	5.87	119.09	108.69
1	G	129	GLU	CA-C-N	5.85	127.15	119.84
1	G	129	GLU	C-N-CA	5.85	127.15	119.84
1	E	173	ARG	CB-CA-C	-5.66	104.28	111.86
1	C	217	CYS	N-CA-C	-5.66	105.19	111.36
1	E	261	VAL	N-CA-C	5.65	116.02	108.11
1	G	119	ALA	N-CA-C	-5.53	105.41	111.82
1	A	184	ALA	CA-C-N	5.51	125.34	119.28
1	A	184	ALA	C-N-CA	5.51	125.34	119.28
1	G	106	HIS	N-CA-C	5.51	118.06	110.35
1	F	268	ALA	N-CA-C	5.50	118.29	110.10
1	B	93	LEU	N-CA-C	-5.49	105.70	112.90
1	D	215	ILE	CB-CA-C	-5.47	104.97	111.97
1	E	285	VAL	N-CA-C	5.42	115.89	107.28
1	C	110	GLU	N-CA-C	-5.39	105.31	111.07
1	H	160	ARG	CB-CG-CD	-5.39	98.91	111.30
1	H	129	GLU	CB-CA-C	-5.37	107.39	111.20
1	E	114	ASN	N-CA-C	5.36	118.62	111.75
1	D	201	GLY	N-CA-C	5.35	123.01	115.30
1	B	279	ASP	N-CA-C	-5.33	106.75	113.20
1	D	143	HIS	N-CA-C	5.27	117.03	111.28
1	G	129	GLU	CB-CA-C	-5.24	106.44	111.00
1	G	285	VAL	N-CA-C	5.24	116.04	107.24
1	C	148	ILE	CB-CA-C	-5.24	105.00	111.70
1	B	268	ALA	N-CA-C	5.22	121.92	110.80
1	H	138	ASP	CA-C-N	5.21	125.26	119.32
1	H	138	ASP	C-N-CA	5.21	125.26	119.32
1	G	104	SER	CB-CA-C	5.14	118.68	110.09
1	F	100	ARG	NE-CZ-NH2	5.13	123.82	119.20
1	G	282	MET	N-CA-C	5.13	117.26	108.90
1	E	211	ILE	N-CA-C	-5.10	105.53	110.42
1	H	251	SER	N-CA-C	5.09	118.59	112.38
1	A	285	VAL	N-CA-C	5.07	115.14	107.75
1	C	69	HIS	N-CA-C	5.02	117.15	109.07
1	G	114	ASN	N-CA-C	5.00	116.73	111.28

All (1) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
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Mol	Chain	Res	Type	Atom
1	F	67	VAL	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	285	VAL	Peptide
1	F	66	SER	Peptide
1	G	285	VAL	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	1783	0	1839	48	0
1	B	1773	0	1832	65	0
1	C	1783	0	1839	69	0
1	D	1777	0	1834	70	0
1	E	1783	0	1839	40	0
1	F	1773	0	1832	62	0
1	G	1783	0	1839	56	0
1	H	1777	0	1834	72	0
2	A	31	0	19	3	0
2	B	31	0	19	4	0
2	C	31	0	19	2	0
2	D	31	0	19	0	0
2	E	31	0	19	1	0
2	F	31	0	19	1	0
2	G	31	0	19	0	0
2	H	31	0	19	0	0
3	A	15	0	8	3	0
3	B	15	0	8	5	0
3	C	15	0	8	2	0
3	D	15	0	7	2	0
3	E	15	0	8	0	0
3	F	15	0	8	3	0
3	G	15	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	15	0	7	3	0
4	C	5	0	0	0	0
4	G	5	0	0	0	0
5	A	36	0	0	7	0
5	B	38	0	0	13	0
5	C	39	0	0	10	0
5	D	23	0	0	7	0
5	E	48	0	0	9	0
5	F	40	0	0	13	0
5	G	38	0	0	11	0
5	H	38	0	0	19	0
All	All	14910	0	14902	444	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 15.

All (444) 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:164:ARG:HD3	5:E:305:HOH:O	1.38	1.21
1:B:191:PHE:HB2	5:B:294:HOH:O	1.43	1.14
1:D:266:ARG:CB	1:D:266:ARG:HH11	1.61	1.13
1:B:132:THR:HB	5:B:294:HOH:O	1.51	1.08
1:E:110:GLU:HA	5:E:403:HOH:O	1.53	1.07
1:D:266:ARG:HH11	1:D:266:ARG:HB3	1.16	1.06
1:G:156:ASN:HD22	1:G:160:ARG:HD3	1.08	1.06
1:G:156:ASN:ND2	1:G:160:ARG:HD3	1.69	1.06
1:F:84:MET:HG3	5:F:297:HOH:O	1.57	1.03
5:G:470:HOH:O	1:H:109:MET:HE2	1.63	0.98
1:A:164:ARG:HG3	5:A:461:HOH:O	1.63	0.98
1:B:67:VAL:HG12	1:B:68:GLU:N	1.77	0.97
1:B:106:HIS:HB2	5:B:311:HOH:O	1.64	0.96
1:G:67:VAL:HG13	1:H:171:LYS:HA	1.44	0.96
1:D:164:ARG:HG3	1:D:164:ARG:HH11	1.30	0.95
1:F:67:VAL:O	1:F:68:GLU:CB	2.16	0.94
1:C:200:ASN:HD22	1:C:200:ASN:H	1.14	0.93
1:G:67:VAL:O	1:G:68:GLU:HB3	1.65	0.93
1:G:200:ASN:HD22	1:G:200:ASN:H	1.12	0.92
1:F:76:ARG:HG2	1:F:76:ARG:HH11	1.37	0.89
1:B:67:VAL:HG12	1:B:68:GLU:H	1.35	0.88
1:C:173:ARG:HG3	1:D:69:HIS:CE1	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:67:VAL:O	1:F:68:GLU:HB3	1.73	0.86
1:B:172:LEU:HD13	3:B:302:TYI:I1	2.47	0.85
1:D:156:ASN:HA	1:D:160:ARG:HB2	1.58	0.85
1:D:266:ARG:HB3	1:D:266:ARG:NH1	1.92	0.84
1:E:171:LYS:HD2	5:E:432:HOH:O	1.77	0.83
1:D:156:ASN:ND2	1:D:160:ARG:NH1	2.25	0.82
1:G:200:ASN:H	1:G:200:ASN:ND2	1.73	0.82
5:A:409:HOH:O	1:B:82:MET:HE3	1.79	0.82
1:G:106:HIS:HD2	5:H:414:HOH:O	1.63	0.82
1:C:286:HIS:HB3	5:C:296:HOH:O	1.78	0.81
1:B:284:THR:HG22	5:B:493:HOH:O	1.80	0.81
1:A:171:LYS:HA	1:B:67:VAL:HG22	1.63	0.80
1:F:202:LYS:HE2	1:F:202:LYS:HA	1.63	0.80
1:A:157:TYR:OH	1:A:174:THR:HG23	1.82	0.80
1:E:164:ARG:HG2	5:E:294:HOH:O	1.83	0.78
1:C:156:ASN:HD22	1:C:160:ARG:HD2	1.48	0.77
1:C:198:ALA:CB	1:C:200:ASN:HD21	1.95	0.77
1:C:67:VAL:O	1:C:68:GLU:CB	2.32	0.77
1:E:157:TYR:OH	1:E:174:THR:HG23	1.86	0.75
5:A:409:HOH:O	1:B:82:MET:CE	2.33	0.75
1:D:164:ARG:HG3	1:D:164:ARG:NH1	1.97	0.74
1:C:156:ASN:ND2	1:C:160:ARG:HD2	2.03	0.74
1:D:266:ARG:CB	1:D:266:ARG:NH1	2.45	0.74
1:E:98:SER:HB3	1:E:232:VAL:HG23	1.70	0.74
1:F:172:LEU:HD13	3:F:302:TYI:I1	2.57	0.74
1:D:266:ARG:HH11	1:D:266:ARG:HB2	1.54	0.73
1:G:156:ASN:HD22	1:G:160:ARG:CD	1.95	0.73
1:A:72:PHE:CE2	1:A:74:HIS:HB2	2.23	0.73
1:H:181:LEU:HB3	5:H:297:HOH:O	1.87	0.72
1:C:198:ALA:CB	1:C:200:ASN:ND2	2.53	0.72
1:D:200:ASN:C	1:D:200:ASN:HD22	1.97	0.72
2:F:301:FMN:O1P	5:F:423:HOH:O	2.06	0.72
1:H:146:ARG:CA	5:H:297:HOH:O	2.38	0.71
1:C:114:ASN:HB2	1:D:86:SER:HB2	1.72	0.71
1:C:198:ALA:HB3	1:C:200:ASN:ND2	2.06	0.71
1:D:172:LEU:HD13	3:D:302:TYI:I1	2.60	0.71
1:C:67:VAL:O	1:C:68:GLU:HB3	1.89	0.71
1:H:146:ARG:N	5:H:297:HOH:O	2.22	0.71
1:H:111:VAL:O	1:H:115:VAL:HG13	1.90	0.70
1:H:200:ASN:HD22	1:H:202:LYS:H	1.38	0.70
1:F:81:GLU:O	1:F:85:ARG:HG3	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:THR:HA	1:C:259:LEU:HD23	1.71	0.70
2:A:301:FMN:HM82	1:B:124:SER:HA	1.73	0.70
1:C:200:ASN:HD22	1:C:200:ASN:N	1.88	0.70
1:D:286:HIS:CE1	5:D:358:HOH:O	2.44	0.69
1:C:190:ILE:HD12	1:C:257:VAL:HG23	1.73	0.69
1:F:200:ASN:ND2	5:F:415:HOH:O	2.26	0.69
1:H:286:HIS:O	5:H:481:HOH:O	2.10	0.69
1:E:111:VAL:O	1:E:115:VAL:HG13	1.93	0.69
1:B:143:HIS:HD2	1:B:182:ASP:OD2	1.76	0.68
1:E:162:GLY:O	1:E:166:VAL:HG12	1.93	0.68
1:B:140:ASP:HB3	5:B:364:HOH:O	1.92	0.68
1:B:81:GLU:O	1:B:85:ARG:HG3	1.94	0.67
1:C:173:ARG:HD2	5:C:305:HOH:O	1.93	0.67
1:A:76:ARG:NH2	1:B:105:GLU:OE2	2.28	0.67
1:D:277:ALA:N	1:D:280:GLN:OE1	2.22	0.66
1:G:173:ARG:HD2	1:H:69:HIS:CE1	2.31	0.66
1:A:257:VAL:HG23	1:A:259:LEU:HD23	1.77	0.66
1:F:103:SER:OG	1:F:105:GLU:HG3	1.96	0.66
1:G:83:ARG:HG2	1:H:110:GLU:HG2	1.77	0.66
1:H:156:ASN:ND2	1:H:160:ARG:HH11	1.93	0.66
1:B:244:ARG:HG2	1:B:244:ARG:HH11	1.61	0.66
1:A:112:ILE:O	1:A:116:ILE:HG13	1.96	0.66
5:C:340:HOH:O	1:D:69:HIS:HD2	1.78	0.66
1:F:76:ARG:HH11	1:F:76:ARG:CG	2.07	0.65
1:F:142:LYS:HE3	1:F:184:ALA:O	1.96	0.65
1:F:266:ARG:HG3	5:F:300:HOH:O	1.97	0.65
1:F:104:SER:HB2	5:F:449:HOH:O	1.96	0.65
1:H:106:HIS:CE1	5:H:296:HOH:O	2.49	0.65
1:E:192:LYS:NZ	1:E:210:GLU:OE1	2.31	0.64
1:A:257:VAL:HG23	1:A:259:LEU:CD2	2.26	0.64
1:D:67:VAL:N	5:D:322:HOH:O	2.30	0.64
1:B:150:GLU:HG2	1:B:176:TRP:O	1.96	0.64
1:C:200:ASN:H	1:C:200:ASN:ND2	1.90	0.64
1:D:161:MET:HE2	1:D:165:TRP:CE2	2.31	0.64
1:F:198:ALA:HB3	5:F:415:HOH:O	1.97	0.64
1:C:81:GLU:O	1:C:85:ARG:HG3	1.97	0.64
1:G:117:LYS:HB3	1:H:90:TYR:CD1	2.33	0.64
1:D:109:MET:O	1:D:113:GLU:HG3	1.97	0.63
1:E:66:SER:N	5:E:452:HOH:O	2.30	0.63
1:A:202:LYS:HG2	5:A:384:HOH:O	1.98	0.63
1:C:156:ASN:ND2	1:C:160:ARG:HH11	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:HD13	3:A:302:TYI:I1	2.69	0.62
1:A:137:LYS:HE2	5:A:294:HOH:O	1.99	0.62
1:C:198:ALA:HB1	1:C:200:ASN:HD21	1.62	0.62
1:G:81:GLU:O	1:G:85:ARG:HG3	1.98	0.62
5:E:432:HOH:O	1:F:67:VAL:HG21	1.98	0.62
1:B:87:GLN:HA	5:B:297:HOH:O	1.99	0.62
1:G:178:LYS:HD2	1:G:180:TYR:OH	1.98	0.62
1:F:266:ARG:HH11	1:F:266:ARG:CG	2.13	0.62
1:F:274:LYS:HE2	5:F:451:HOH:O	1.99	0.62
1:H:156:ASN:HD22	1:H:160:ARG:HD2	1.63	0.62
1:C:173:ARG:CD	5:C:305:HOH:O	2.47	0.61
1:C:233:THR:HA	1:C:259:LEU:CD2	2.29	0.61
1:D:136:VAL:HG13	1:D:187:LEU:HB2	1.81	0.61
1:F:67:VAL:O	1:F:68:GLU:HB2	2.00	0.61
1:C:232:VAL:O	1:C:234:THR:HG23	2.01	0.61
1:A:263:TYR:CE1	1:B:82:MET:HE1	2.35	0.61
1:H:200:ASN:ND2	1:H:202:LYS:H	1.98	0.61
1:C:67:VAL:HG13	5:C:433:HOH:O	1.99	0.60
1:D:156:ASN:ND2	1:D:160:ARG:HH11	1.97	0.60
1:H:172:LEU:HD13	3:H:302:TYI:I1	2.71	0.60
1:B:161:MET:HE1	3:B:302:TYI:HB2	1.82	0.60
1:D:155:ILE:HG22	1:D:160:ARG:HD3	1.83	0.60
1:B:67:VAL:CG1	1:B:68:GLU:N	2.51	0.60
1:B:232:VAL:O	1:B:234:THR:HG23	2.01	0.60
1:D:214:SER:O	1:D:217:CYS:HB3	2.02	0.60
1:F:104:SER:CB	5:F:370:HOH:O	2.49	0.60
1:H:278:LEU:HD11	1:H:282:MET:SD	2.42	0.60
1:E:127:HIS:CG	1:E:127:HIS:O	2.55	0.59
1:F:266:ARG:HG3	1:F:266:ARG:HH11	1.67	0.59
1:C:172:LEU:HD13	3:C:302:TYI:I1	2.72	0.59
1:C:139:PRO:HG2	1:H:73:SER:HB3	1.85	0.59
1:H:80:GLN:HA	1:H:80:GLN:NE2	2.17	0.59
1:C:110:GLU:HG3	5:C:294:HOH:O	2.02	0.59
1:G:135:VAL:HG21	1:H:282:MET:HE3	1.83	0.59
1:G:232:VAL:O	1:G:234:THR:HG23	2.03	0.59
1:H:137:LYS:NZ	5:H:400:HOH:O	2.34	0.59
1:G:83:ARG:HD2	5:G:327:HOH:O	2.04	0.58
1:A:148:ILE:O	1:A:152:GLU:HG2	2.02	0.58
1:E:267:ASP:OD1	1:E:267:ASP:N	2.34	0.58
1:A:82:MET:HG2	1:B:227:ALA:O	2.02	0.58
1:A:263:TYR:HE1	1:B:82:MET:HE1	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:ARG:HH22	1:F:105:GLU:CD	2.11	0.58
1:G:83:ARG:CG	1:H:110:GLU:HG2	2.34	0.58
1:G:171:LYS:HB2	5:G:482:HOH:O	2.04	0.58
1:D:136:VAL:CG1	1:D:187:LEU:HB2	2.34	0.58
1:A:205:VAL:H	1:B:164:ARG:NH2	2.02	0.57
2:B:301:FMN:O1P	5:B:300:HOH:O	2.17	0.57
1:H:266:ARG:NH1	1:H:266:ARG:HB3	2.20	0.57
1:H:161:MET:HE2	1:H:165:TRP:CE2	2.38	0.57
1:E:258:LEU:HD23	1:E:259:LEU:N	2.20	0.57
1:B:180:TYR:CD2	1:B:260:PRO:HG3	2.40	0.57
1:D:104:SER:HA	1:D:183:THR:O	2.04	0.57
1:F:66:SER:HB2	1:F:67:VAL:HG23	1.87	0.57
1:A:100:ARG:NH2	3:A:302:TYI:I1	3.08	0.56
5:G:498:HOH:O	1:H:69:HIS:HD2	1.88	0.56
1:G:200:ASN:ND2	1:G:200:ASN:N	2.49	0.56
1:H:146:ARG:HG3	1:H:181:LEU:HB2	1.87	0.56
1:B:109:MET:HE2	5:B:438:HOH:O	2.05	0.56
1:B:180:TYR:CE2	1:B:260:PRO:HG3	2.40	0.56
1:D:146:ARG:HG3	1:D:181:LEU:HB2	1.88	0.56
1:D:198:ALA:HB3	1:D:200:ASN:ND2	2.21	0.56
1:C:156:ASN:HD21	1:C:238:ASN:HD22	1.53	0.55
1:G:109:MET:SD	1:G:137:LYS:HD3	2.47	0.55
1:A:175:ASN:HB2	5:A:408:HOH:O	2.05	0.55
1:C:198:ALA:HB1	1:C:200:ASN:ND2	2.19	0.55
1:H:80:GLN:HB2	5:H:359:HOH:O	2.06	0.55
1:G:258:LEU:C	1:G:258:LEU:HD23	2.32	0.55
1:H:98:SER:HB3	1:H:232:VAL:HG23	1.88	0.55
1:F:140:ASP:O	1:F:144:LYS:HG3	2.07	0.55
1:F:180:TYR:CD2	1:F:260:PRO:HG3	2.41	0.55
1:E:190:ILE:HD12	1:E:257:VAL:HG23	1.87	0.55
1:D:106:HIS:HD2	5:D:313:HOH:O	1.89	0.55
1:C:159:LYS:HG3	1:C:160:ARG:N	2.22	0.55
1:F:106:HIS:HB2	5:F:21:HOH:O	2.06	0.54
1:A:178:LYS:NZ	3:A:302:TYI:OXT	2.38	0.54
1:C:107:VAL:HG23	1:C:112:ILE:HD13	1.88	0.54
1:C:198:ALA:HB3	1:C:200:ASN:HD21	1.68	0.54
1:E:156:ASN:HB3	1:E:161:MET:HE2	1.90	0.54
1:G:204:LYS:NZ	5:G:361:HOH:O	2.40	0.54
1:C:107:VAL:HG21	1:C:112:ILE:HD11	1.90	0.54
1:G:284:THR:HG21	5:G:470:HOH:O	2.07	0.54
1:G:101:PHE:HB3	5:G:490:HOH:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:72:PHE:CE2	1:D:74:HIS:HB2	2.43	0.54
1:G:68:GLU:OE1	1:G:69:HIS:N	2.41	0.53
1:G:143:HIS:HB3	5:G:456:HOH:O	2.08	0.53
1:E:171:LYS:CD	5:E:432:HOH:O	2.44	0.53
1:D:107:VAL:HG21	1:D:112:ILE:HD11	1.90	0.53
1:H:161:MET:HE1	3:H:302:TYI:HB2	1.89	0.53
1:D:156:ASN:HD21	1:D:160:ARG:NH1	2.05	0.53
1:D:194:VAL:HG22	1:D:252:HIS:O	2.08	0.53
1:A:190:ILE:HD13	1:A:257:VAL:HG22	1.89	0.53
1:D:198:ALA:HB3	1:D:200:ASN:HD21	1.73	0.53
1:D:286:HIS:HE1	5:D:358:HOH:O	1.87	0.53
1:G:66:SER:O	1:H:171:LYS:HB3	2.09	0.53
1:B:145:ILE:O	1:B:149:ILE:HG13	2.09	0.52
1:F:185:PRO:HD2	1:F:261:VAL:O	2.09	0.52
1:H:209:ASN:O	1:H:213:VAL:HG23	2.09	0.52
1:A:257:VAL:CG2	1:A:259:LEU:HD21	2.39	0.52
1:D:202:LYS:HD2	1:D:203:LYS:H	1.74	0.52
1:E:189:LEU:HG	1:E:258:LEU:HG	1.91	0.52
1:A:98:SER:OG	2:A:301:FMN:O2P	2.25	0.52
1:B:109:MET:CE	5:B:438:HOH:O	2.57	0.52
1:C:171:LYS:HG2	1:D:67:VAL:HG12	1.90	0.52
2:A:301:FMN:H4'	1:B:124:SER:O	2.09	0.52
1:B:105:GLU:O	1:B:185:PRO:HG3	2.10	0.52
1:F:100:ARG:NH2	3:F:302:TYI:I1	3.13	0.52
1:B:244:ARG:HG2	1:B:244:ARG:NH1	2.24	0.52
1:B:285:VAL:C	5:B:493:HOH:O	2.53	0.51
1:C:67:VAL:HG13	1:D:171:LYS:HA	1.91	0.51
1:C:150:GLU:HG2	1:C:176:TRP:O	2.10	0.51
1:C:98:SER:HB3	1:C:232:VAL:HG23	1.92	0.51
1:H:96:ARG:O	1:H:97:ARG:HD2	2.09	0.51
1:H:202:LYS:HD2	1:H:203:LYS:H	1.74	0.51
1:A:122:ALA:HB2	1:A:216:ALA:HA	1.92	0.51
1:D:110:GLU:HB3	5:D:295:HOH:O	2.11	0.51
2:B:301:FMN:O4	3:B:302:TYI:N	2.43	0.51
1:H:156:ASN:HA	1:H:160:ARG:HB2	1.91	0.51
1:D:276:LYS:HB3	1:D:280:GLN:HB2	1.92	0.51
1:B:161:MET:HE1	3:B:302:TYI:CB	2.40	0.51
1:C:98:SER:OG	2:C:301:FMN:O2P	2.27	0.51
1:C:175:ASN:HD21	1:C:177:ILE:HD12	1.76	0.51
1:E:282:MET:HE2	5:E:298:HOH:O	2.09	0.51
1:H:171:LYS:HD3	5:H:314:HOH:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:185:PRO:HB2	5:H:400:HOH:O	2.10	0.50
1:C:161:MET:HG2	1:C:165:TRP:CD2	2.46	0.50
1:C:152:GLU:HB2	1:C:239:CYS:SG	2.52	0.50
1:D:200:ASN:ND2	1:D:202:LYS:H	2.10	0.50
1:G:190:ILE:HD12	1:G:257:VAL:HG23	1.92	0.50
1:D:96:ARG:O	1:D:97:ARG:HD2	2.11	0.50
1:F:156:ASN:HA	1:F:160:ARG:HB2	1.93	0.50
1:G:68:GLU:OE1	1:G:68:GLU:C	2.54	0.50
1:B:96:ARG:NH1	5:B:303:HOH:O	2.39	0.50
1:G:225:GLN:HA	5:G:506:HOH:O	2.11	0.50
1:H:162:GLY:O	1:H:166:VAL:HG23	2.12	0.50
1:H:266:ARG:HB3	1:H:266:ARG:HH11	1.75	0.50
1:F:89:PHE:HA	5:F:410:HOH:O	2.12	0.49
1:F:154:GLU:O	1:F:158:MET:HG3	2.12	0.49
1:E:214:SER:O	1:E:217:CYS:HB3	2.12	0.49
1:F:81:GLU:HA	1:F:84:MET:HE2	1.94	0.49
1:F:154:GLU:HG3	1:F:176:TRP:CE2	2.48	0.49
1:C:117:LYS:HB3	1:D:90:TYR:CD1	2.47	0.49
1:A:173:ARG:NE	1:B:67:VAL:HG11	2.28	0.49
1:D:165:TRP:HD1	1:D:165:TRP:O	1.95	0.49
5:G:406:HOH:O	1:H:235:THR:HB	2.13	0.49
1:A:156:ASN:HA	1:A:160:ARG:HB3	1.94	0.49
1:G:153:GLU:HA	1:G:156:ASN:HB2	1.95	0.49
1:F:111:VAL:O	1:F:115:VAL:HG13	2.13	0.48
1:H:146:ARG:CB	5:H:297:HOH:O	2.58	0.48
1:B:214:SER:O	1:B:217:CYS:HB3	2.13	0.48
1:F:258:LEU:C	1:F:258:LEU:HD23	2.38	0.48
1:H:156:ASN:ND2	1:H:160:ARG:HD2	2.28	0.48
1:B:209:ASN:O	1:B:213:VAL:HG23	2.13	0.48
1:H:180:TYR:CD2	1:H:260:PRO:HG3	2.47	0.48
1:C:180:TYR:CD2	1:C:260:PRO:HG3	2.48	0.48
1:D:130:PRO:HG3	5:D:17:HOH:O	2.12	0.48
1:E:273:LEU:HD13	1:F:127:HIS:CG	2.49	0.48
1:B:190:ILE:O	1:B:255:LEU:HD12	2.14	0.48
1:D:81:GLU:HA	1:D:84:MET:SD	2.53	0.47
1:H:112:ILE:O	1:H:116:ILE:HG12	2.14	0.47
1:A:278:LEU:HD13	1:B:117:LYS:HG2	1.96	0.47
1:E:98:SER:OG	2:E:301:FMN:O2P	2.33	0.47
1:C:89:PHE:HB2	1:D:226:ASN:ND2	2.29	0.47
1:D:286:HIS:C	5:D:10:HOH:O	2.58	0.47
1:G:172:LEU:HD13	3:G:302:TYI:I1	2.84	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:VAL:O	1:C:68:GLU:HB2	2.12	0.47
1:H:144:LYS:O	1:H:148:ILE:HG13	2.15	0.47
1:D:163:LYS:HD3	1:D:163:LYS:N	2.30	0.47
1:F:180:TYR:HA	1:F:183:THR:OG1	2.15	0.47
1:C:106:HIS:CE1	5:C:405:HOH:O	2.68	0.47
1:C:171:LYS:O	1:D:69:HIS:HE1	1.98	0.47
1:A:215:ILE:HG23	1:B:218:GLY:HA2	1.95	0.47
2:C:301:FMN:O4	3:C:302:TYI:N	2.48	0.47
1:A:143:HIS:HD2	1:A:182:ASP:OD2	1.97	0.46
1:D:99:VAL:HG12	1:D:101:PHE:H	1.80	0.46
1:A:258:LEU:C	1:A:259:LEU:HD23	2.41	0.46
1:D:146:ARG:O	1:D:150:GLU:HG3	2.15	0.46
1:F:127:HIS:CG	1:F:127:HIS:O	2.67	0.46
1:D:161:MET:HE1	3:D:302:TYI:HB2	1.97	0.46
1:E:146:ARG:HE	1:E:150:GLU:CD	2.23	0.46
1:A:90:TYR:CE1	1:B:117:LYS:HB3	2.51	0.46
1:B:192:LYS:CB	1:B:213:VAL:HG21	2.46	0.46
1:C:66:SER:HB3	5:C:297:HOH:O	2.16	0.46
1:E:72:PHE:CE2	1:E:74:HIS:HB2	2.50	0.46
1:E:96:ARG:O	1:E:275:ARG:NH2	2.47	0.46
1:H:96:ARG:HD2	5:H:321:HOH:O	2.15	0.46
1:E:263:TYR:CE1	1:F:82:MET:HE1	2.51	0.46
1:G:106:HIS:CD2	5:H:414:HOH:O	2.51	0.46
1:H:266:ARG:NH1	1:H:266:ARG:CB	2.79	0.46
1:D:164:ARG:HH11	1:D:164:ARG:CG	2.14	0.46
1:F:232:VAL:O	1:F:234:THR:HG23	2.16	0.46
1:H:165:TRP:HB2	5:H:356:HOH:O	2.16	0.46
1:A:171:LYS:HA	1:B:67:VAL:CG2	2.42	0.45
1:B:96:ARG:HG2	1:B:96:ARG:HH11	1.80	0.45
1:F:161:MET:HE1	3:F:302:TYI:HB2	1.97	0.45
1:H:146:ARG:HB2	5:H:297:HOH:O	2.14	0.45
1:H:180:TYR:CE2	1:H:260:PRO:HG3	2.51	0.45
1:A:171:LYS:HG2	5:A:296:HOH:O	2.16	0.45
1:H:169:LEU:HD22	3:H:302:TYI:CE1	2.46	0.45
1:B:66:SER:C	1:B:67:VAL:HG23	2.41	0.45
5:E:419:HOH:O	1:F:82:MET:CE	2.64	0.45
1:F:246:LEU:O	1:F:246:LEU:HG	2.16	0.45
1:A:84:MET:O	1:A:88:GLU:HG3	2.16	0.45
1:B:96:ARG:NH1	1:B:96:ARG:HG2	2.31	0.45
1:D:111:VAL:O	1:D:115:VAL:HG13	2.16	0.45
1:B:104:SER:HB3	5:B:295:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:ASN:O	1:D:161:MET:HG3	2.16	0.45
1:E:171:LYS:O	1:F:67:VAL:HG12	2.17	0.45
1:E:209:ASN:O	1:E:213:VAL:HG23	2.16	0.45
1:G:161:MET:HG2	1:G:165:TRP:CE3	2.51	0.45
1:A:256:LEU:O	1:A:257:VAL:HG12	2.17	0.45
1:F:150:GLU:HG2	1:F:176:TRP:O	2.17	0.45
1:G:96:ARG:HG2	1:G:97:ARG:N	2.32	0.45
1:G:195:HIS:CE1	1:G:252:HIS:HB3	2.52	0.45
1:E:82:MET:HG2	1:F:227:ALA:O	2.18	0.44
1:E:239:CYS:O	1:E:240:GLY:C	2.60	0.44
1:F:112:ILE:O	1:F:115:VAL:HG22	2.16	0.44
1:H:165:TRP:O	1:H:165:TRP:HD1	2.00	0.44
1:C:189:LEU:N	1:C:189:LEU:HD12	2.32	0.44
1:D:93:LEU:HD12	1:D:93:LEU:HA	1.78	0.44
1:H:200:ASN:HD22	1:H:200:ASN:C	2.25	0.44
1:B:167:THR:C	1:B:169:LEU:H	2.26	0.44
1:E:263:TYR:HE1	1:F:82:MET:HE1	1.83	0.44
1:D:236:PRO:HB2	1:D:239:CYS:HB2	2.00	0.44
1:C:87:GLN:HG3	1:C:91:GLU:OE2	2.17	0.44
1:C:146:ARG:HA	1:C:181:LEU:HD13	2.00	0.44
1:H:164:ARG:HD2	5:H:295:HOH:O	2.17	0.44
1:A:231:THR:OG1	1:A:232:VAL:N	2.51	0.44
1:B:100:ARG:NH2	3:B:302:TYI:I1	3.21	0.44
1:B:267:ASP:HA	5:B:436:HOH:O	2.17	0.44
5:C:405:HOH:O	1:G:267:ASP:HB2	2.18	0.44
1:F:171:LYS:H	1:F:171:LYS:HG2	1.55	0.44
2:B:301:FMN:C9	2:B:301:FMN:H2'	2.48	0.43
1:C:267:ASP:OD1	1:C:267:ASP:N	2.51	0.43
1:E:162:GLY:O	1:E:166:VAL:CG1	2.64	0.43
1:G:140:ASP:HA	5:G:456:HOH:O	2.18	0.43
1:G:156:ASN:OD1	1:G:237:LEU:HB3	2.18	0.43
1:F:146:ARG:NH2	1:F:179:GLU:HA	2.33	0.43
1:G:171:LYS:HG2	1:H:67:VAL:HG12	2.00	0.43
1:C:161:MET:HG2	1:C:165:TRP:CE3	2.53	0.43
1:D:80:GLN:NE2	1:D:83:ARG:HH21	2.17	0.43
1:E:197:PHE:HA	1:E:202:LYS:O	2.19	0.43
1:F:266:ARG:HD3	5:F:298:HOH:O	2.17	0.43
1:G:180:TYR:CD2	1:G:260:PRO:HG3	2.53	0.43
1:B:180:TYR:HA	1:B:183:THR:OG1	2.19	0.43
1:C:94:ASN:ND2	1:C:275:ARG:HH11	2.17	0.43
1:C:114:ASN:CB	1:D:86:SER:HB2	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:ASN:ND2	1:C:200:ASN:N	2.58	0.43
1:F:76:ARG:CG	1:F:76:ARG:NH1	2.77	0.43
1:G:112:ILE:HD13	1:G:112:ILE:HA	1.78	0.43
1:D:274:LYS:HD3	1:D:274:LYS:HA	1.67	0.43
1:F:230:VAL:HG22	1:F:262:GLY:O	2.18	0.43
1:H:104:SER:HA	1:H:183:THR:O	2.19	0.43
1:H:266:ARG:HH11	1:H:266:ARG:CG	2.31	0.43
1:E:122:ALA:HB1	1:E:123:PRO:HD2	2.01	0.43
1:C:272:ASP:O	1:D:67:VAL:HG21	2.18	0.43
1:D:148:ILE:O	1:D:152:GLU:HG2	2.19	0.43
1:G:98:SER:HB3	1:G:232:VAL:HG23	2.00	0.43
1:C:123:PRO:HD3	1:D:96:ARG:CZ	2.49	0.43
1:G:80:GLN:OE1	1:G:80:GLN:HA	2.19	0.43
1:C:107:VAL:CG2	1:C:112:ILE:CD1	2.97	0.42
1:D:156:ASN:HD22	1:D:160:ARG:HH11	1.65	0.42
1:G:105:GLU:CD	1:H:76:ARG:HH22	2.27	0.42
1:H:156:ASN:HD22	1:H:160:ARG:CD	2.30	0.42
1:A:76:ARG:HH22	1:B:105:GLU:CD	2.27	0.42
1:A:270:VAL:HG13	1:B:72:PHE:HB2	2.00	0.42
1:B:84:MET:HE2	1:B:84:MET:HB2	1.95	0.42
1:C:209:ASN:O	1:C:213:VAL:HG23	2.19	0.42
1:A:156:ASN:ND2	1:A:237:LEU:HB3	2.35	0.42
1:C:146:ARG:NE	1:C:150:GLU:OE2	2.50	0.42
1:G:156:ASN:HD21	1:G:238:ASN:HD22	1.67	0.42
1:H:231:THR:OG1	1:H:232:VAL:N	2.53	0.42
1:H:266:ARG:HH11	1:H:266:ARG:CB	2.32	0.42
1:A:89:PHE:HB2	1:B:226:ASN:ND2	2.35	0.42
1:A:124:SER:O	1:A:125:GLY:C	2.60	0.42
1:B:143:HIS:CD2	1:B:182:ASP:OD2	2.65	0.42
1:D:273:LEU:O	1:D:274:LYS:HD3	2.20	0.42
1:E:235:THR:HG22	1:E:257:VAL:HG12	2.02	0.42
1:G:244:ARG:HG2	1:G:244:ARG:HH11	1.85	0.42
1:H:239:CYS:HB3	1:H:243:LEU:CD1	2.49	0.42
1:A:178:LYS:O	1:A:179:GLU:C	2.60	0.42
1:B:66:SER:O	1:B:67:VAL:HB	2.20	0.42
1:C:266:ARG:HD3	1:C:266:ARG:HA	1.88	0.42
1:D:229:LEU:HD23	1:D:229:LEU:HA	1.83	0.42
1:E:215:ILE:O	1:E:216:ALA:C	2.62	0.42
1:A:125:GLY:O	1:A:126:ALA:C	2.62	0.42
1:A:257:VAL:HG21	1:A:259:LEU:HD21	2.01	0.42
1:B:256:LEU:HD12	1:B:256:LEU:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:LYS:HB2	5:C:348:HOH:O	2.20	0.42
1:B:67:VAL:CG1	1:B:69:HIS:HD2	2.32	0.42
1:C:68:GLU:HA	1:C:68:GLU:OE1	2.20	0.42
1:D:200:ASN:HD22	1:D:202:LYS:H	1.67	0.42
1:H:107:VAL:HG21	1:H:112:ILE:HD11	2.01	0.42
1:H:256:LEU:HG	1:H:257:VAL:HG23	2.02	0.42
1:F:198:ALA:O	1:F:199:ALA:C	2.63	0.41
1:G:154:GLU:HG3	1:G:176:TRP:CE2	2.54	0.41
1:E:278:LEU:HD13	1:F:117:LYS:HG2	2.02	0.41
1:G:193:GLN:HE21	1:G:206:HIS:HE1	1.67	0.41
1:C:192:LYS:NZ	1:C:210:GLU:OE1	2.52	0.41
1:G:124:SER:HA	1:G:212:SER:HB3	2.02	0.41
1:A:156:ASN:OD1	1:A:160:ARG:NE	2.48	0.41
1:A:214:SER:O	1:A:217:CYS:HB3	2.19	0.41
1:B:185:PRO:HD2	1:B:261:VAL:O	2.20	0.41
1:D:138:ASP:HA	1:D:139:PRO:HD3	1.81	0.41
1:H:250:PRO:HB2	1:H:252:HIS:CE1	2.56	0.41
1:G:189:LEU:HD12	1:G:189:LEU:N	2.36	0.41
1:G:89:PHE:HB2	1:H:226:ASN:ND2	2.36	0.41
1:H:207:TYR:HA	5:H:7:HOH:O	2.20	0.41
1:A:215:ILE:O	1:A:216:ALA:C	2.64	0.41
1:D:146:ARG:HA	1:D:181:LEU:HD13	2.02	0.41
1:F:189:LEU:N	1:F:189:LEU:HD12	2.36	0.41
1:F:266:ARG:HH11	1:F:266:ARG:CB	2.34	0.41
1:C:107:VAL:HG23	1:C:112:ILE:CD1	2.51	0.41
1:E:184:ALA:HA	1:E:185:PRO:HD2	1.90	0.41
1:F:104:SER:HB2	5:F:370:HOH:O	2.19	0.41
1:G:107:VAL:HA	1:G:108:PRO:HD3	1.89	0.41
1:G:165:TRP:CD1	1:G:169:LEU:HD22	2.56	0.41
1:H:265:SER:HB3	1:H:267:ASP:OD1	2.21	0.41
1:B:111:VAL:O	1:B:115:VAL:HG13	2.21	0.41
1:B:230:VAL:HG22	1:B:262:GLY:O	2.20	0.41
1:C:93:LEU:HD12	1:C:93:LEU:HA	1.74	0.41
1:C:217:CYS:SG	1:C:257:VAL:HG21	2.61	0.41
1:F:104:SER:HB3	5:F:370:HOH:O	2.18	0.41
1:F:266:ARG:CB	1:F:266:ARG:NH1	2.84	0.41
1:A:173:ARG:HE	1:B:67:VAL:HG11	1.85	0.40
1:E:243:LEU:O	1:E:247:LEU:HD12	2.21	0.40
1:H:134:VAL:HG21	1:H:249:ARG:HD3	2.02	0.40
1:E:127:HIS:CG	1:F:273:LEU:HD13	2.57	0.40
1:H:106:HIS:HE1	5:H:296:HOH:O	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:PRO:HD2	1:A:131:TRP:CE3	2.57	0.40
2:B:301:FMN:H2'	2:B:301:FMN:H9	2.03	0.40
1:C:70:ILE:O	1:C:70:ILE:HG13	2.21	0.40
1:H:152:GLU:HB2	1:H:239:CYS:SG	2.61	0.40
1:H:146:ARG:HE	1:H:150:GLU:CD	2.29	0.40
1:C:107:VAL:HA	1:C:108:PRO:HD3	1.82	0.40
1:D:163:LYS:N	1:D:163:LYS:CD	2.85	0.40
1:F:78:PRO:O	1:F:80:GLN:N	2.55	0.40
1:F:271:PRO:HB2	1:F:273:LEU:HG	2.04	0.40
1:G:93:LEU:HD12	1:G:93:LEU:HA	1.69	0.40
1:G:266:ARG:HA	1:G:266:ARG:HD3	1.72	0.40
1:H:106:HIS:HA	5:H:400:HOH:O	2.21	0.40

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	219/259 (85%)	201 (92%)	16 (7%)	2 (1%)	14	28
1	B	218/259 (84%)	199 (91%)	16 (7%)	3 (1%)	9	17
1	C	219/259 (85%)	202 (92%)	13 (6%)	4 (2%)	6	13
1	D	218/259 (84%)	204 (94%)	13 (6%)	1 (0%)	24	44
1	E	219/259 (85%)	206 (94%)	10 (5%)	3 (1%)	9	17
1	F	218/259 (84%)	201 (92%)	13 (6%)	4 (2%)	6	13
1	G	219/259 (85%)	200 (91%)	14 (6%)	5 (2%)	5	8
1	H	218/259 (84%)	203 (93%)	14 (6%)	1 (0%)	24	44
All	All	1748/2072 (84%)	1616 (92%)	109 (6%)	23 (1%)	9	19

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	VAL
1	A	126	ALA
1	B	67	VAL
1	B	79	GLU
1	C	68	GLU
1	C	198	ALA
1	E	67	VAL
1	F	67	VAL
1	F	68	GLU
1	F	79	GLU
1	G	68	GLU
1	C	199	ALA
1	F	199	ALA
1	G	171	LYS
1	G	199	ALA
1	D	272	ASP
1	G	75	THR
1	C	67	VAL
1	B	268	ALA
1	E	236	PRO
1	H	199	ALA
1	G	67	VAL
1	E	240	GLY

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	198/233 (85%)	173 (87%)	25 (13%)	4	8
1	B	197/233 (84%)	175 (89%)	22 (11%)	6	11
1	C	198/233 (85%)	181 (91%)	17 (9%)	10	20
1	D	197/233 (84%)	171 (87%)	26 (13%)	4	7
1	E	198/233 (85%)	172 (87%)	26 (13%)	4	7
1	F	197/233 (84%)	178 (90%)	19 (10%)	8	16
1	G	198/233 (85%)	178 (90%)	20 (10%)	7	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	197/233 (84%)	175 (89%)	22 (11%)	6	11
All	All	1580/1864 (85%)	1403 (89%)	177 (11%)	6	11

All (177) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	84	MET
1	A	87	GLN
1	A	105	GLU
1	A	106	HIS
1	A	115	VAL
1	A	116	ILE
1	A	136	VAL
1	A	142	LYS
1	A	166	VAL
1	A	169	LEU
1	A	170	LYS
1	A	174	THR
1	A	186	VAL
1	A	188	ILE
1	A	194	VAL
1	A	200	ASN
1	A	209	ASN
1	A	215	ILE
1	A	220	LEU
1	A	232	VAL
1	A	238	ASN
1	A	246	LEU
1	A	257	VAL
1	A	259	LEU
1	B	73	SER
1	B	75	THR
1	B	76	ARG
1	B	84	MET
1	B	93	LEU
1	B	103	SER
1	B	106	HIS
1	B	107	VAL
1	B	110	GLU
1	B	137	LYS
1	B	149	ILE

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Mol	Chain	Res	Type
1	B	154	GLU
1	B	163	LYS
1	B	171	LYS
1	B	172	LEU
1	B	200	ASN
1	B	203	LYS
1	B	220	LEU
1	B	251	SER
1	B	257	VAL
1	B	266	ARG
1	B	267	ASP
1	C	67	VAL
1	C	75	THR
1	C	92	LEU
1	C	93	LEU
1	C	155	ILE
1	C	160	ARG
1	C	167	THR
1	C	169	LEU
1	C	172	LEU
1	C	179	GLU
1	C	200	ASN
1	C	215	ILE
1	C	219	LEU
1	C	265	SER
1	C	267	ASP
1	C	285	VAL
1	C	286	HIS
1	D	75	THR
1	D	80	GLN
1	D	84	MET
1	D	88	GLU
1	D	91	GLU
1	D	93	LEU
1	D	103	SER
1	D	112	ILE
1	D	136	VAL
1	D	142	LYS
1	D	158	MET
1	D	159	LYS
1	D	160	ARG
1	D	163	LYS

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Mol	Chain	Res	Type
1	D	164	ARG
1	D	171	LYS
1	D	200	ASN
1	D	202	LYS
1	D	203	LYS
1	D	220	LEU
1	D	232	VAL
1	D	237	LEU
1	D	257	VAL
1	D	266	ARG
1	D	267	ASP
1	D	274	LYS
1	E	87	GLN
1	E	92	LEU
1	E	104	SER
1	E	105	GLU
1	E	109	MET
1	E	115	VAL
1	E	136	VAL
1	E	137	LYS
1	E	142	LYS
1	E	144	LYS
1	E	158	MET
1	E	166	VAL
1	E	169	LEU
1	E	170	LYS
1	E	171	LYS
1	E	172	LEU
1	E	174	THR
1	E	186	VAL
1	E	203	LYS
1	E	209	ASN
1	E	220	LEU
1	E	238	ASN
1	E	246	LEU
1	E	265	SER
1	E	266	ARG
1	E	286	HIS
1	F	67	VAL
1	F	70	ILE
1	F	75	THR
1	F	76	ARG

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Mol	Chain	Res	Type
1	F	80	GLN
1	F	84	MET
1	F	92	LEU
1	F	93	LEU
1	F	102	ILE
1	F	103	SER
1	F	106	HIS
1	F	163	LYS
1	F	164	ARG
1	F	171	LYS
1	F	220	LEU
1	F	235	THR
1	F	257	VAL
1	F	266	ARG
1	F	267	ASP
1	G	67	VAL
1	G	68	GLU
1	G	75	THR
1	G	83	ARG
1	G	88	GLU
1	G	92	LEU
1	G	93	LEU
1	G	124	SER
1	G	147	GLU
1	G	148	ILE
1	G	160	ARG
1	G	167	THR
1	G	169	LEU
1	G	171	LYS
1	G	200	ASN
1	G	202	LYS
1	G	203	LYS
1	G	215	ILE
1	G	273	LEU
1	G	286	HIS
1	H	68	GLU
1	H	75	THR
1	H	80	GLN
1	H	84	MET
1	H	88	GLU
1	H	91	GLU
1	H	92	LEU

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Mol	Chain	Res	Type
1	H	93	LEU
1	H	102	ILE
1	H	103	SER
1	H	110	GLU
1	H	112	ILE
1	H	115	VAL
1	H	136	VAL
1	H	142	LYS
1	H	153	GLU
1	H	158	MET
1	H	200	ASN
1	H	202	LYS
1	H	237	LEU
1	H	254	LYS
1	H	266	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	143	HIS
1	B	69	HIS
1	B	80	GLN
1	B	143	HIS
1	B	200	ASN
1	B	226	ASN
1	B	238	ASN
1	C	87	GLN
1	C	94	ASN
1	C	106	HIS
1	C	143	HIS
1	C	156	ASN
1	C	175	ASN
1	C	193	GLN
1	C	200	ASN
1	D	69	HIS
1	D	80	GLN
1	D	143	HIS
1	D	156	ASN
1	D	193	GLN
1	D	200	ASN
1	D	209	ASN

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Mol	Chain	Res	Type
1	D	238	ASN
1	E	143	HIS
1	E	209	ASN
1	E	238	ASN
1	E	280	GLN
1	F	80	GLN
1	F	114	ASN
1	F	143	HIS
1	F	200	ASN
1	G	74	HIS
1	G	94	ASN
1	G	156	ASN
1	G	193	GLN
1	H	69	HIS
1	H	80	GLN
1	H	143	HIS
1	H	156	ASN
1	H	195	HIS
1	H	200	ASN
1	H	238	ASN
1	H	286	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

18 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TYI	E	302	-	14,15,15	1.62	3 (21%)	17,21,21	1.84	6 (35%)
2	FMN	F	301	-	33,33,33	1.29	4 (12%)	48,50,50	1.40	9 (18%)
3	TYI	H	302	-	14,15,15	1.03	0	17,21,21	1.80	5 (29%)
2	FMN	E	301	-	33,33,33	1.01	1 (3%)	48,50,50	1.67	12 (25%)
2	FMN	C	301	-	33,33,33	1.20	2 (6%)	48,50,50	1.50	10 (20%)
3	TYI	B	302	-	14,15,15	1.91	3 (21%)	17,21,21	2.17	5 (29%)
3	TYI	F	302	-	14,15,15	1.73	2 (14%)	17,21,21	1.89	6 (35%)
2	FMN	A	301	-	33,33,33	1.12	3 (9%)	48,50,50	1.66	12 (25%)
2	FMN	B	301	-	33,33,33	1.24	3 (9%)	48,50,50	1.94	18 (37%)
2	FMN	D	301	-	33,33,33	1.20	4 (12%)	48,50,50	1.63	12 (25%)
2	FMN	H	301	-	33,33,33	1.03	1 (3%)	48,50,50	1.56	10 (20%)
3	TYI	A	302	-	14,15,15	1.39	2 (14%)	17,21,21	1.98	4 (23%)
3	TYI	C	302	-	14,15,15	1.73	3 (21%)	17,21,21	2.31	6 (35%)
4	PO4	C	1	-	4,4,4	0.87	0	6,6,6	0.90	0
3	TYI	D	302	-	14,15,15	1.32	3 (21%)	17,21,21	2.41	6 (35%)
2	FMN	G	301	-	33,33,33	1.43	5 (15%)	48,50,50	1.77	14 (29%)
4	PO4	G	2	-	4,4,4	0.90	0	6,6,6	0.72	0
3	TYI	G	302	-	14,15,15	1.54	3 (21%)	17,21,21	2.31	5 (29%)

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	TYI	E	302	-	-	0/8/8/8	0/1/1/1
2	FMN	F	301	-	-	2/18/18/18	0/3/3/3
3	TYI	H	302	-	-	0/8/8/8	0/1/1/1
2	FMN	E	301	-	-	2/18/18/18	0/3/3/3
2	FMN	C	301	-	-	2/18/18/18	0/3/3/3
3	TYI	B	302	-	-	0/8/8/8	0/1/1/1
3	TYI	F	302	-	-	0/8/8/8	0/1/1/1
2	FMN	A	301	-	-	0/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	B	301	-	-	5/18/18/18	0/3/3/3
2	FMN	D	301	-	-	0/18/18/18	0/3/3/3
2	FMN	H	301	-	-	0/18/18/18	0/3/3/3
3	TYI	A	302	-	-	0/8/8/8	0/1/1/1
3	TYI	C	302	-	-	0/8/8/8	0/1/1/1
3	TYI	D	302	-	-	0/8/8/8	0/1/1/1
2	FMN	G	301	-	-	6/18/18/18	0/3/3/3
3	TYI	G	302	-	-	0/8/8/8	0/1/1/1

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	302	TYI	CZ-CE1	4.50	1.49	1.40
2	G	301	FMN	C4A-N5	4.23	1.39	1.30
3	G	302	TYI	CZ-CE2	4.14	1.49	1.40
3	C	302	TYI	CZ-CE2	3.99	1.48	1.40
3	F	302	TYI	CZ-CE1	3.98	1.48	1.40
3	F	302	TYI	CZ-CE2	3.90	1.48	1.40
3	A	302	TYI	CZ-CE1	3.83	1.48	1.40
3	B	302	TYI	CZ-CE2	3.63	1.47	1.40
2	H	301	FMN	C4A-N5	3.57	1.38	1.30
3	E	302	TYI	CZ-CE1	3.57	1.47	1.40
3	C	302	TYI	CZ-CE1	3.56	1.47	1.40
2	D	301	FMN	C4A-N5	3.37	1.38	1.30
2	F	301	FMN	C4A-N5	3.29	1.37	1.30
2	C	301	FMN	C4A-N5	3.26	1.37	1.30
2	C	301	FMN	C10-N1	3.16	1.39	1.33
2	A	301	FMN	C4A-N5	3.00	1.37	1.30
2	B	301	FMN	C4A-N5	2.96	1.37	1.30
2	G	301	FMN	C4'-C3'	-2.90	1.48	1.53
3	E	302	TYI	CZ-CE2	2.85	1.46	1.40
3	D	302	TYI	CZ-CE2	2.84	1.46	1.40
2	G	301	FMN	C10-N1	2.83	1.38	1.33
3	D	302	TYI	CZ-CE1	2.72	1.45	1.40
3	C	302	TYI	OXT-C	-2.62	1.22	1.30
2	F	301	FMN	C10-N1	2.62	1.38	1.33
2	E	301	FMN	C4A-N5	2.61	1.36	1.30
3	B	302	TYI	CE1-I1	-2.61	2.04	2.10
2	B	301	FMN	C5'-C4'	2.54	1.55	1.51
2	G	301	FMN	C2'-C3'	-2.52	1.49	1.53
3	E	302	TYI	OXT-C	-2.48	1.22	1.30
3	G	302	TYI	CZ-CE1	2.43	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	FMN	C4A-C10	-2.30	1.37	1.44
2	A	301	FMN	C10-N1	2.28	1.37	1.33
2	D	301	FMN	P-O1P	2.25	1.57	1.50
2	D	301	FMN	C1'-N10	2.22	1.53	1.47
3	G	302	TYI	OXT-C	-2.17	1.23	1.30
3	A	302	TYI	CZ-CE2	2.17	1.44	1.40
2	A	301	FMN	C1'-N10	2.15	1.53	1.47
2	F	301	FMN	C4A-C10	-2.14	1.37	1.44
3	D	302	TYI	OXT-C	-2.11	1.23	1.30
2	F	301	FMN	O3'-C3'	-2.10	1.37	1.43
2	D	301	FMN	C2'-C3'	-2.09	1.49	1.53
2	G	301	FMN	O4'-C4'	-2.03	1.39	1.43

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	302	TYI	CZ-CE1-I1	-5.71	111.06	119.35
3	B	302	TYI	CZ-CE1-I1	-5.68	111.09	119.35
3	C	302	TYI	CZ-CE1-I1	-5.47	111.40	119.35
2	B	301	FMN	C4A-C10-N10	5.43	124.26	116.48
3	G	302	TYI	CD1-CE1-I1	5.18	128.19	118.46
3	D	302	TYI	CD1-CE1-I1	4.87	127.59	118.46
3	D	302	TYI	CG-CB-CA	4.66	123.67	114.13
3	A	302	TYI	CZ-CE2-I2	-4.62	112.63	119.35
3	D	302	TYI	CZ-CE1-I1	-4.28	113.13	119.35
3	A	302	TYI	CD2-CE2-I2	4.20	126.35	118.46
3	C	302	TYI	CD1-CE1-I1	4.17	126.28	118.46
2	D	301	FMN	O4-C4-C4A	-4.17	115.53	126.53
2	A	301	FMN	C7M-C7-C6	-4.03	112.47	119.57
2	A	301	FMN	O4-C4-C4A	-3.95	116.10	126.53
2	A	301	FMN	C4A-C10-N10	3.87	122.02	116.48
3	F	302	TYI	CD1-CE1-I1	3.84	125.67	118.46
2	H	301	FMN	C5A-C9A-N10	3.73	121.34	117.97
2	D	301	FMN	O5'-P-O1P	3.69	116.41	106.44
2	G	301	FMN	C5'-C4'-C3'	-3.68	105.27	112.22
3	D	302	TYI	CB-CG-CD2	-3.66	114.14	120.43
2	H	301	FMN	O5'-P-O1P	3.63	116.25	106.44
2	B	301	FMN	O3P-P-O5'	3.61	116.07	106.67
3	C	302	TYI	OXT-C-O	-3.57	115.97	124.08
3	F	302	TYI	CZ-CE1-I1	-3.57	114.16	119.35
3	E	302	TYI	CZ-CE2-I2	-3.57	114.17	119.35
2	E	301	FMN	C4A-C10-N10	3.54	121.54	116.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	302	TYI	OXT-C-O	-3.49	116.17	124.08
2	H	301	FMN	O4-C4-C4A	-3.48	117.34	126.53
2	B	301	FMN	C4-N3-C2	-3.48	119.47	125.64
3	B	302	TYI	CB-CG-CD2	-3.45	114.51	120.43
2	G	301	FMN	C4-N3-C2	-3.39	119.62	125.64
2	E	301	FMN	O5'-P-O1P	3.36	115.53	106.44
3	H	302	TYI	CZ-CE2-I2	-3.32	114.53	119.35
2	G	301	FMN	C4-C4A-N5	3.32	122.79	118.21
2	G	301	FMN	C4A-C4-N3	3.25	121.51	113.25
2	E	301	FMN	C5A-C9A-N10	3.19	120.85	117.97
2	F	301	FMN	O4-C4-C4A	-3.19	118.12	126.53
2	G	301	FMN	C7M-C7-C8	-3.16	114.30	120.76
2	C	301	FMN	C4-N3-C2	-3.15	120.04	125.64
3	H	302	TYI	OXT-C-O	-3.13	116.97	124.08
2	G	301	FMN	C1'-C2'-C3'	-3.10	101.25	109.66
3	B	302	TYI	CD1-CE1-I1	3.07	124.23	118.46
2	H	301	FMN	C4-N3-C2	-3.06	120.20	125.64
2	D	301	FMN	O3'-C3'-C2'	-3.05	102.01	108.93
2	B	301	FMN	O2-C2-N1	-3.04	116.75	121.80
2	G	301	FMN	O4-C4-C4A	-3.02	118.57	126.53
2	E	301	FMN	C4-C4A-C10	3.00	122.08	116.93
3	E	302	TYI	OH-CZ-CE1	2.99	128.03	120.30
3	C	302	TYI	CB-CG-CD2	-2.99	115.30	120.43
2	F	301	FMN	C4A-C10-N10	2.97	120.74	116.48
2	B	301	FMN	C9A-N10-C10	-2.96	116.23	120.75
2	G	301	FMN	C4A-C10-N10	2.95	120.71	116.48
2	E	301	FMN	C9A-N10-C10	-2.95	116.26	120.75
2	D	301	FMN	C5A-C9A-N10	2.92	120.61	117.97
3	H	302	TYI	CG-CB-CA	2.92	120.11	114.13
2	A	301	FMN	O2-C2-N3	2.91	124.17	118.58
3	F	302	TYI	CD2-CE2-I2	2.91	123.92	118.46
3	H	302	TYI	CD2-CE2-I2	2.88	123.87	118.46
3	F	302	TYI	OXT-C-O	-2.88	117.54	124.08
2	D	301	FMN	C4A-C10-N10	2.86	120.58	116.48
2	C	301	FMN	C4A-C10-N10	2.86	120.58	116.48
2	F	301	FMN	C7M-C7-C6	-2.85	114.55	119.57
3	C	302	TYI	CD2-CE2-I2	2.85	123.81	118.46
3	E	302	TYI	CG-CB-CA	2.81	119.89	114.13
2	A	301	FMN	C5A-C9A-N10	2.78	120.48	117.97
2	C	301	FMN	C4A-C10-N1	-2.77	117.81	124.59
2	H	301	FMN	O3P-P-O2P	2.76	118.15	107.80
2	G	301	FMN	C10-C4A-N5	-2.73	119.23	124.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	FMN	C10-C4A-N5	-2.73	119.23	124.81
2	B	301	FMN	O2-C2-N3	2.71	123.78	118.58
2	E	301	FMN	C4-N3-C2	-2.70	120.84	125.64
2	F	301	FMN	C4-N3-C2	-2.69	120.86	125.64
3	D	302	TYI	CB-CG-CD1	2.67	125.02	120.43
2	B	301	FMN	C1'-N10-C9A	2.67	125.82	120.63
3	E	302	TYI	OXT-C-O	-2.65	118.07	124.08
2	A	301	FMN	C9A-N10-C10	-2.64	116.73	120.75
2	B	301	FMN	O4-C4-C4A	-2.64	119.57	126.53
2	E	301	FMN	C1'-C2'-C3'	2.63	116.80	109.66
2	H	301	FMN	C9A-C5A-N5	-2.62	119.67	122.45
2	B	301	FMN	O4'-C4'-C5'	2.62	115.75	109.99
2	E	301	FMN	O4-C4-C4A	-2.61	119.64	126.53
2	C	301	FMN	C4-C4A-C10	2.61	121.40	116.93
2	D	301	FMN	C8M-C8-C9	-2.59	115.00	119.57
2	C	301	FMN	C4A-C4-N3	2.59	119.84	113.25
2	G	301	FMN	O4-C4-N3	-2.59	115.25	120.11
2	G	301	FMN	C9A-C5A-N5	-2.53	119.77	122.45
2	F	301	FMN	C4A-C4-N3	2.50	119.62	113.25
2	G	301	FMN	O3'-C3'-C4'	-2.47	103.31	108.93
2	G	301	FMN	C8M-C8-C7	-2.46	115.74	120.76
2	H	301	FMN	C8M-C8-C9	-2.45	115.25	119.57
2	B	301	FMN	C10-C4A-N5	-2.43	119.84	124.81
2	D	301	FMN	O2P-P-O5'	-2.38	100.46	106.67
2	F	301	FMN	O2P-P-O5'	2.38	112.86	106.67
2	B	301	FMN	C5A-C9A-N10	2.37	120.11	117.97
3	E	302	TYI	CB-CG-CD2	-2.37	116.35	120.43
3	F	302	TYI	CB-CG-CD2	-2.36	116.37	120.43
2	E	301	FMN	C4A-C10-N1	-2.36	118.81	124.59
2	C	301	FMN	O2P-P-O5'	2.34	112.77	106.67
2	A	301	FMN	O3'-C3'-C2'	-2.34	103.61	108.93
2	C	301	FMN	O3P-P-O5'	2.31	112.70	106.67
2	A	301	FMN	O2-C2-N1	-2.28	118.01	121.80
3	B	302	TYI	CB-CG-CD1	2.28	124.34	120.43
2	C	301	FMN	O4-C4-C4A	-2.27	120.55	126.53
2	B	301	FMN	C4A-C4-N3	2.25	118.99	113.25
2	A	301	FMN	O5'-P-O1P	2.25	112.51	106.44
3	A	302	TYI	OH-CZ-CE1	2.23	126.06	120.30
2	D	301	FMN	O4'-C4'-C5'	-2.22	105.08	109.99
3	C	302	TYI	CD2-CG-CD1	2.22	122.03	119.01
3	H	302	TYI	CD1-CE1-I1	2.22	122.63	118.46
3	A	302	TYI	OXT-C-O	-2.21	119.07	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	FMN	C4-C4A-C10	2.21	120.72	116.93
2	E	301	FMN	O3'-C3'-C2'	2.19	113.92	108.93
3	D	302	TYI	CD2-CE2-I2	2.19	122.57	118.46
2	G	301	FMN	C6-C5A-N5	2.18	122.07	118.44
3	E	302	TYI	CB-CG-CD1	2.17	124.15	120.43
2	E	301	FMN	C8M-C8-C9	-2.17	115.75	119.57
2	B	301	FMN	C1'-C2'-C3'	2.16	115.53	109.66
3	B	302	TYI	OXT-C-O	-2.16	119.19	124.08
2	A	301	FMN	C4A-C4-N3	2.15	118.73	113.25
2	A	301	FMN	C4-N3-C2	-2.13	121.86	125.64
2	B	301	FMN	C6-C5A-C9A	2.13	121.97	119.05
2	D	301	FMN	O3P-P-O5'	2.10	112.15	106.67
3	G	302	TYI	CD2-CE2-I2	2.10	122.40	118.46
2	F	301	FMN	C4A-C10-N1	-2.10	119.45	124.59
2	D	301	FMN	C10-C4A-N5	-2.09	120.53	124.81
2	B	301	FMN	C7M-C7-C8	-2.09	116.49	120.76
2	F	301	FMN	O3'-C3'-C4'	-2.08	104.20	108.93
2	B	301	FMN	C4-C4A-C10	2.08	120.50	116.93
2	B	301	FMN	C10-N1-C2	2.08	121.34	116.85
2	E	301	FMN	C5'-C4'-C3'	-2.08	108.30	112.22
2	H	301	FMN	C4-C4A-C10	2.06	120.47	116.93
2	B	301	FMN	O5'-C5'-C4'	-2.06	103.87	109.36
2	H	301	FMN	C4A-C4-N3	2.05	118.47	113.25
2	D	301	FMN	C4-N3-C2	-2.04	122.01	125.64
2	H	301	FMN	C9A-C9-C8	2.04	123.31	119.22
2	C	301	FMN	C4'-C3'-C2'	-2.04	110.18	113.57
2	F	301	FMN	C4-C4A-C10	2.03	120.42	116.93
3	F	302	TYI	CD2-CG-CD1	2.03	121.77	119.01
3	G	302	TYI	CB-CG-CD2	-2.02	116.95	120.43
2	A	301	FMN	C1'-N10-C9A	2.01	124.53	120.63

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	FMN	C3'-C4'-C5'-O5'
2	B	301	FMN	C5'-O5'-P-O1P
2	B	301	FMN	C5'-O5'-P-O2P
2	B	301	FMN	C5'-O5'-P-O3P
2	G	301	FMN	C2'-C3'-C4'-O4'
2	G	301	FMN	O3'-C3'-C4'-O4'
2	G	301	FMN	C3'-C4'-C5'-O5'

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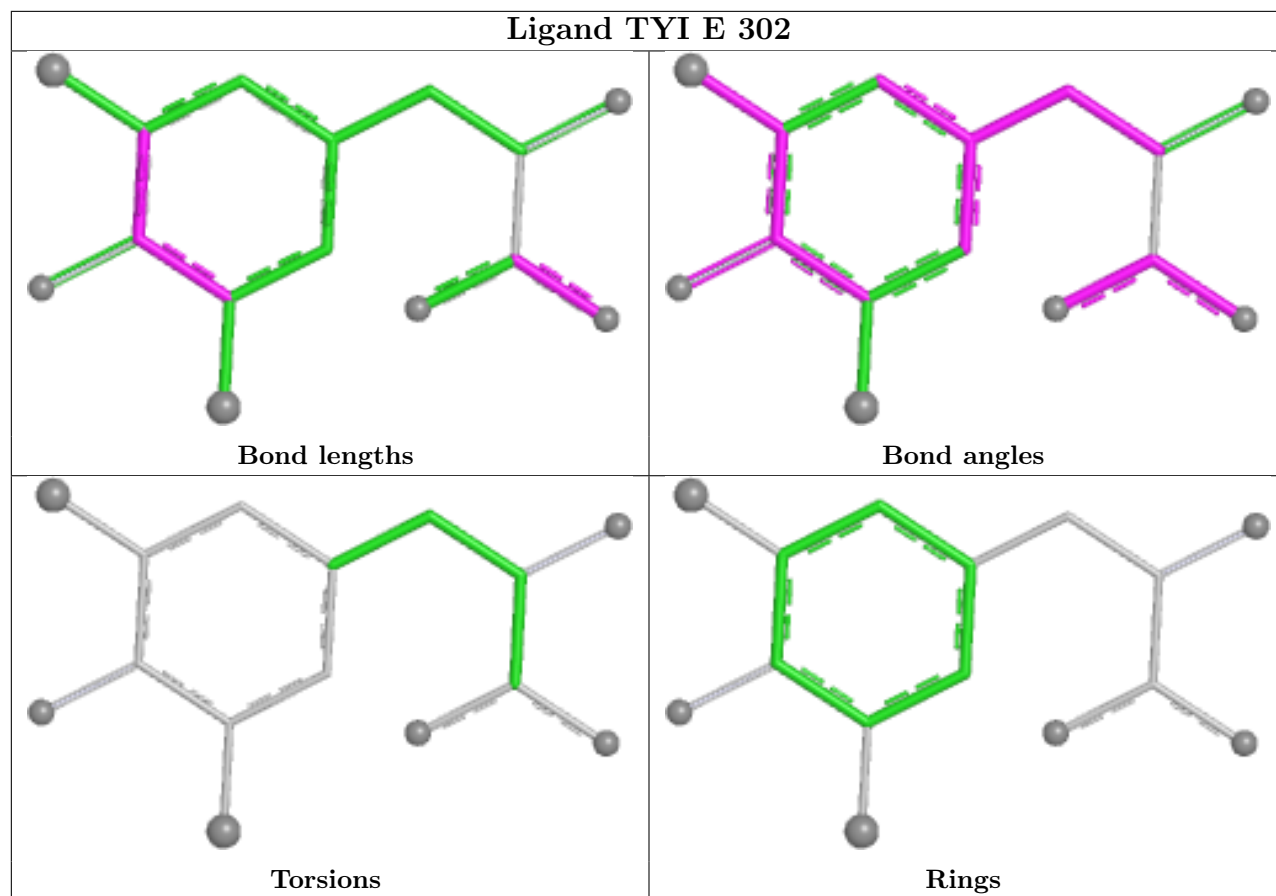
Mol	Chain	Res	Type	Atoms
2	G	301	FMN	O4'-C4'-C5'-O5'
2	G	301	FMN	C2'-C3'-C4'-C5'
2	B	301	FMN	O4'-C4'-C5'-O5'
2	G	301	FMN	O3'-C3'-C4'-C5'
2	C	301	FMN	C2'-C3'-C4'-O4'
2	E	301	FMN	C5'-O5'-P-O1P
2	F	301	FMN	C2'-C3'-C4'-O4'
2	E	301	FMN	C5'-O5'-P-O3P
2	C	301	FMN	C2'-C3'-C4'-C5'
2	F	301	FMN	O3'-C3'-C4'-O4'

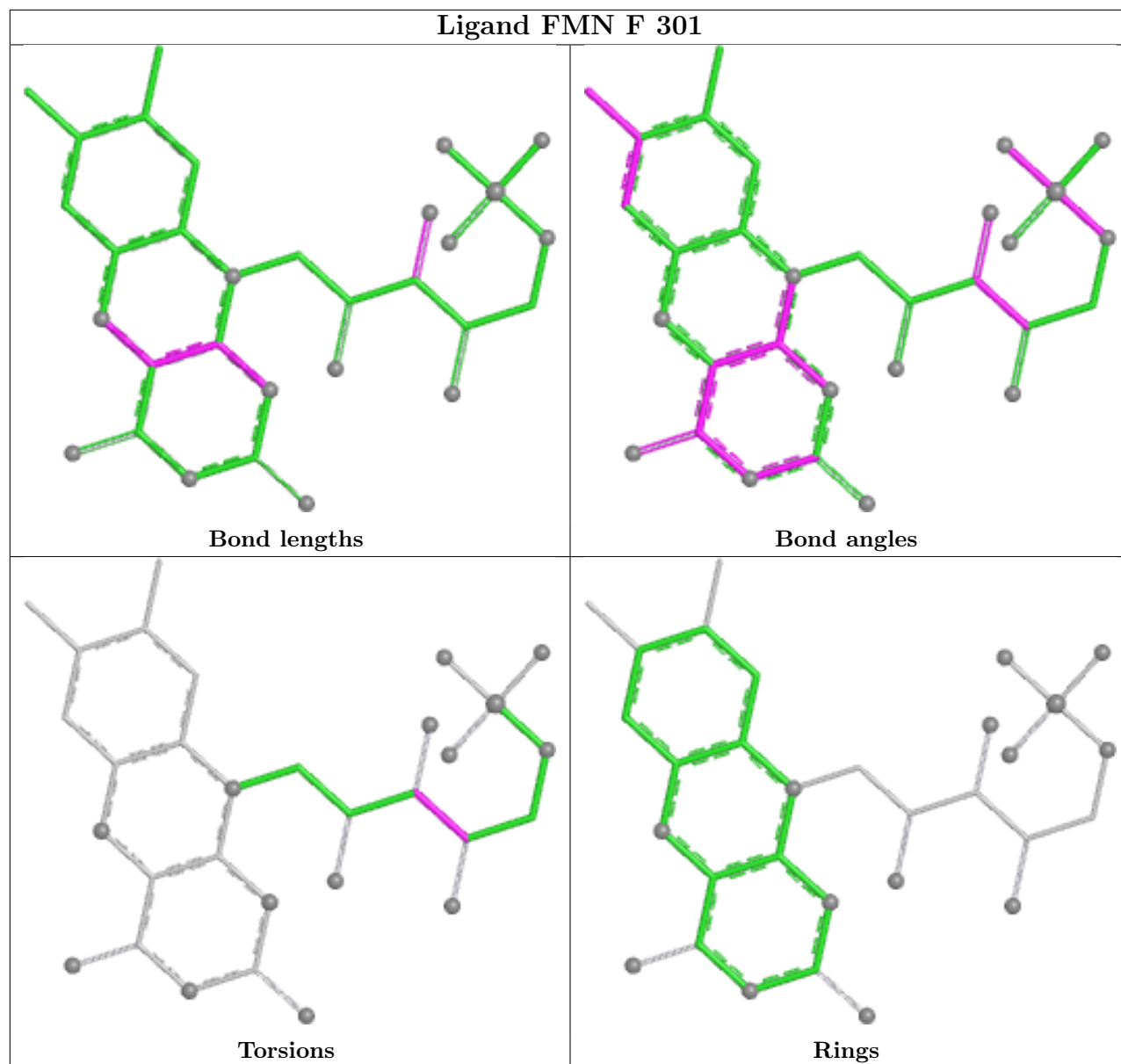
There are no ring outliers.

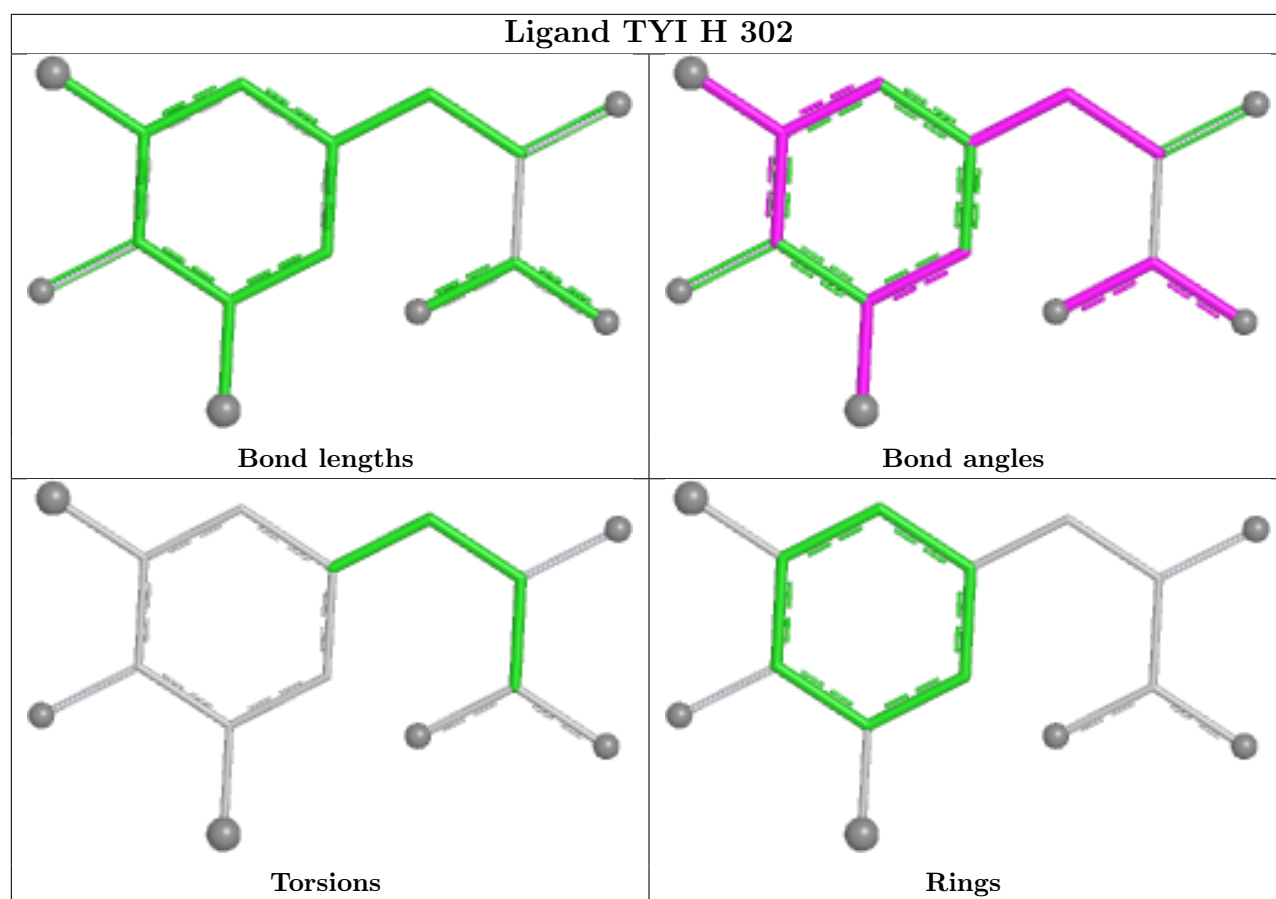
12 monomers are involved in 28 short contacts:

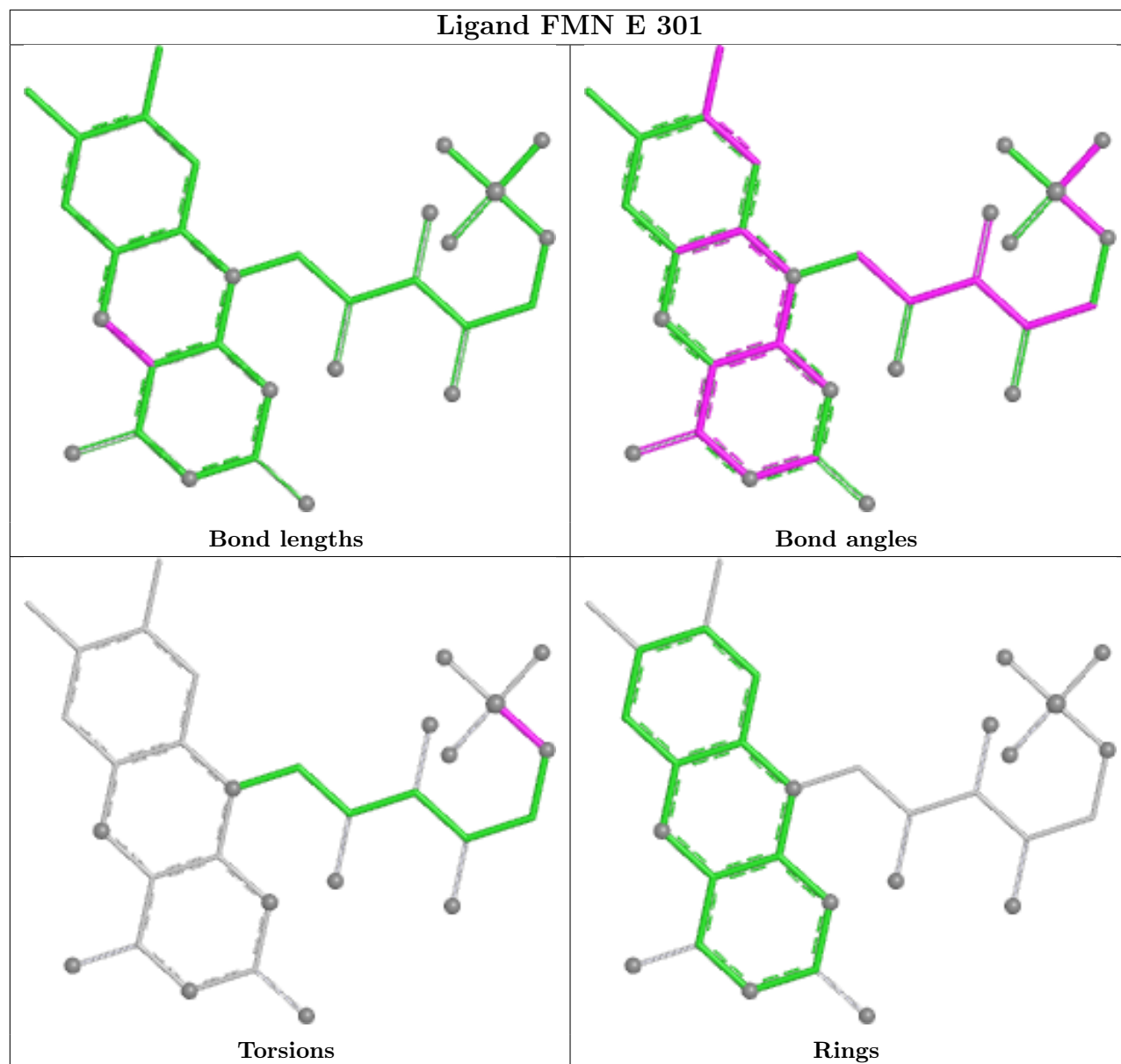
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	FMN	1	0
3	H	302	TYI	3	0
2	E	301	FMN	1	0
2	C	301	FMN	2	0
3	B	302	TYI	5	0
3	F	302	TYI	3	0
2	A	301	FMN	3	0
2	B	301	FMN	4	0
3	A	302	TYI	3	0
3	C	302	TYI	2	0
3	D	302	TYI	2	0
3	G	302	TYI	1	0

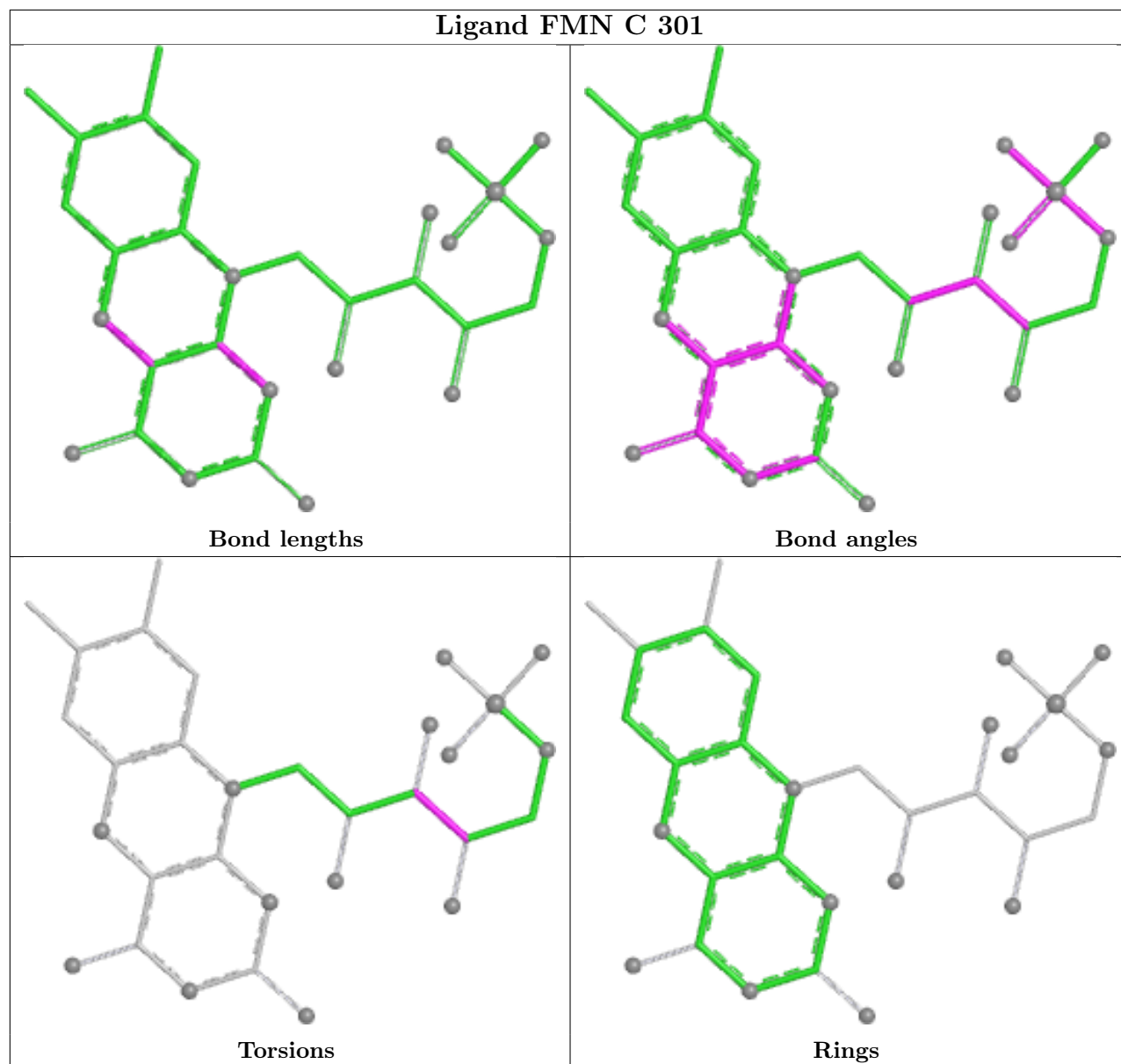
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



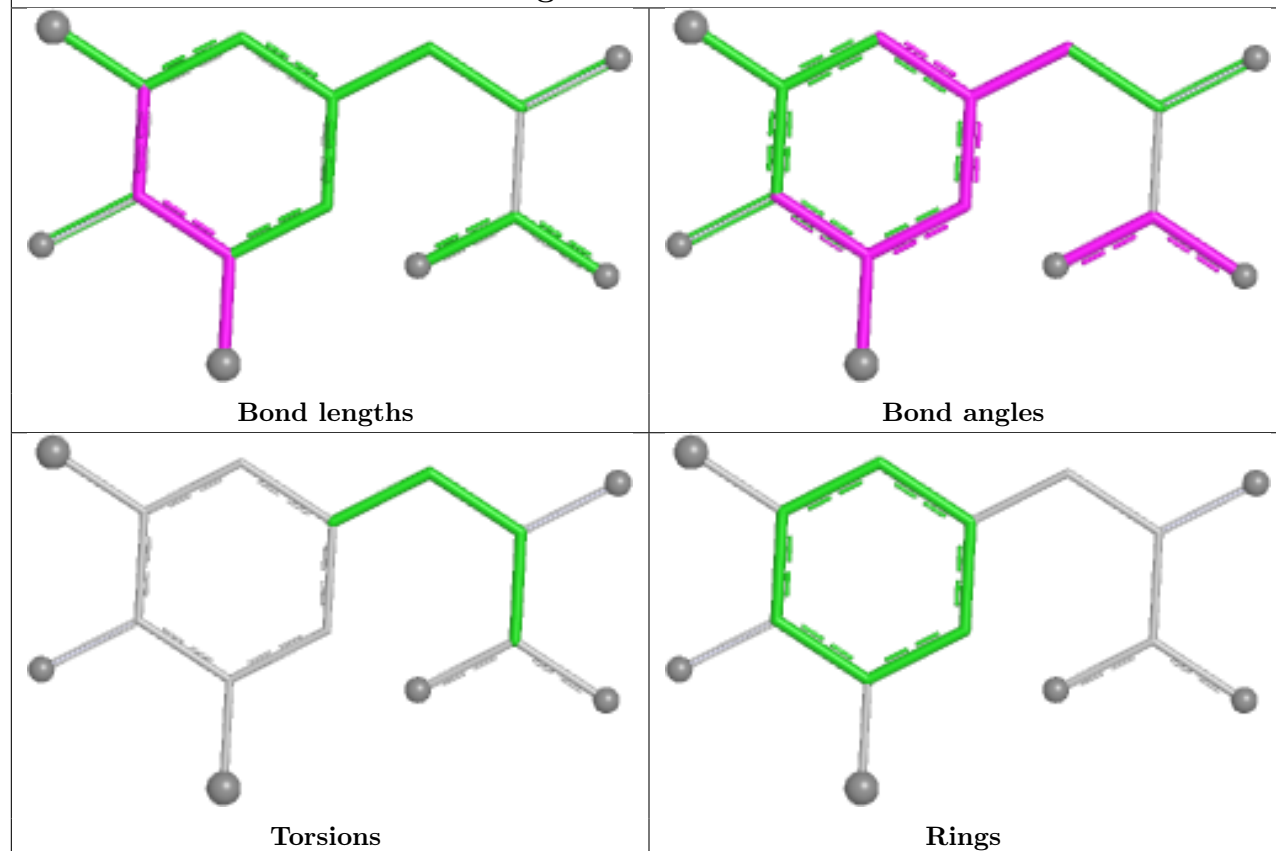




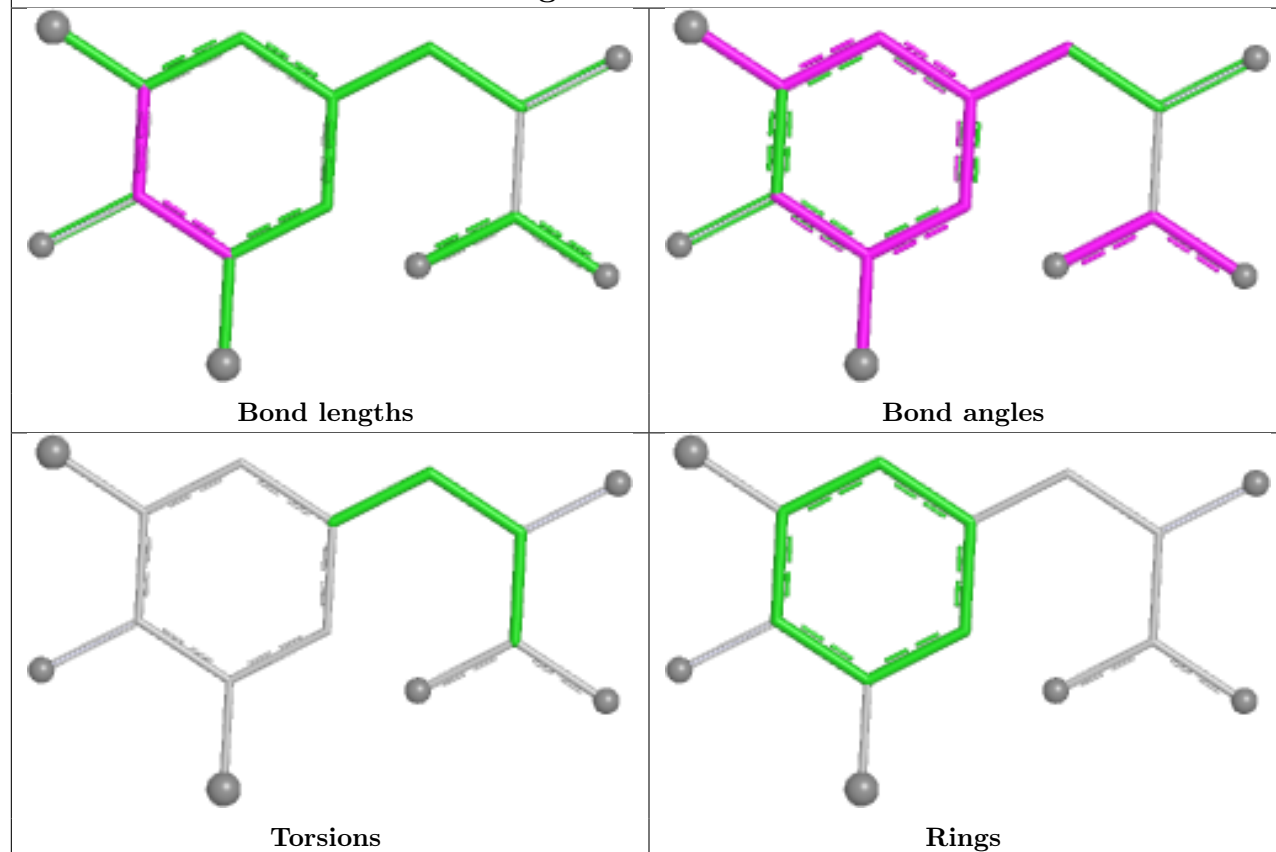


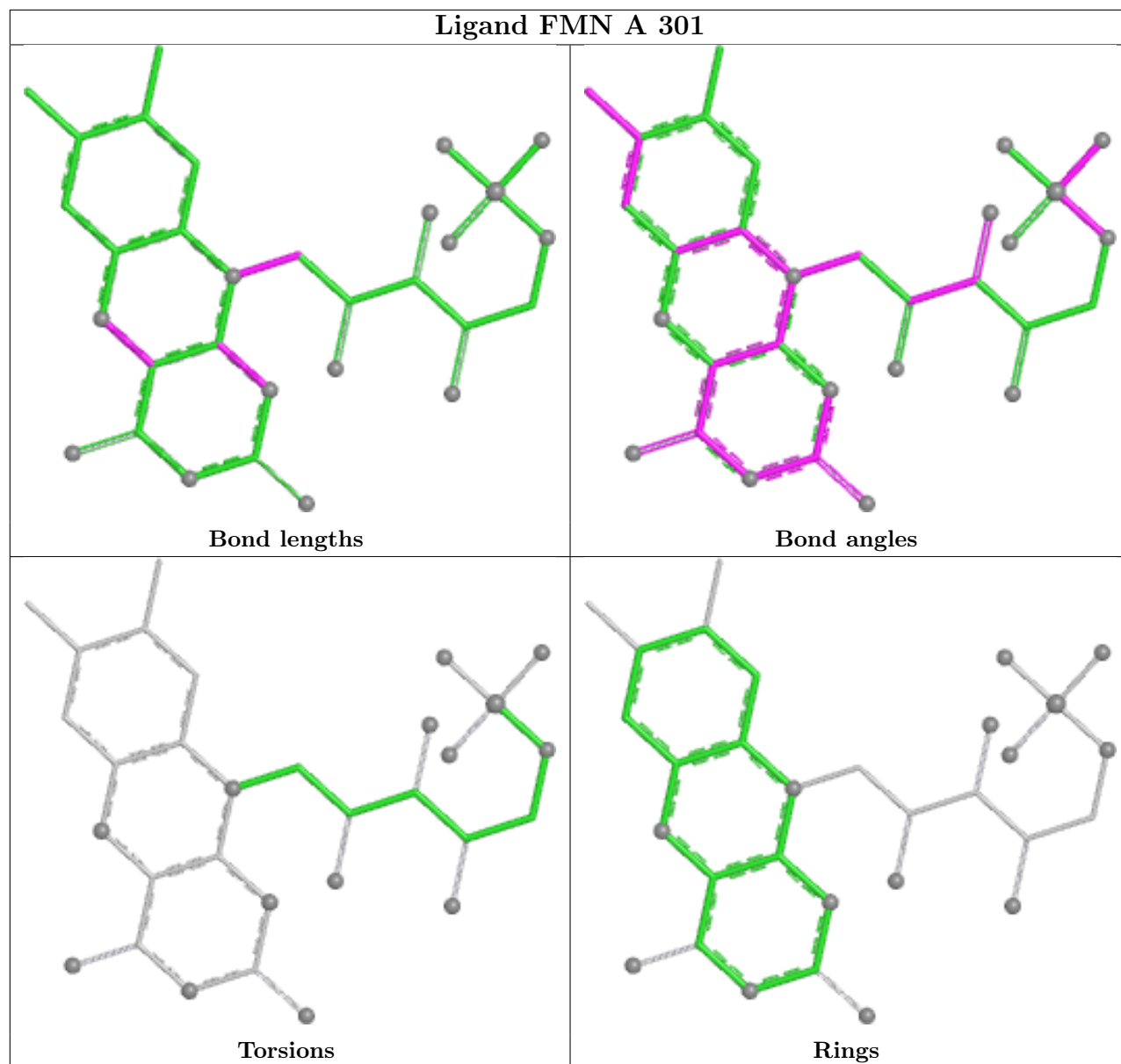


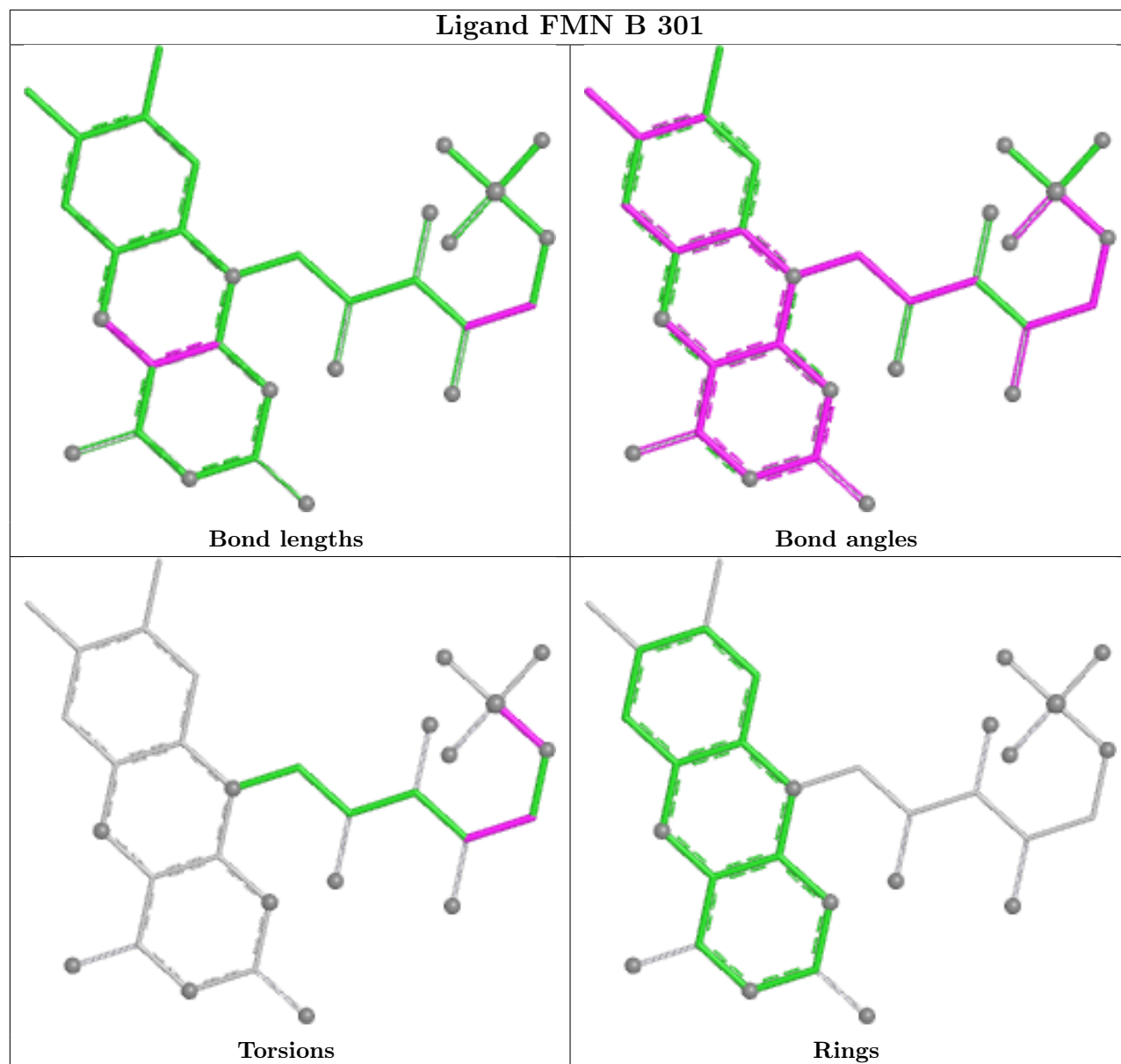
Ligand TYI B 302

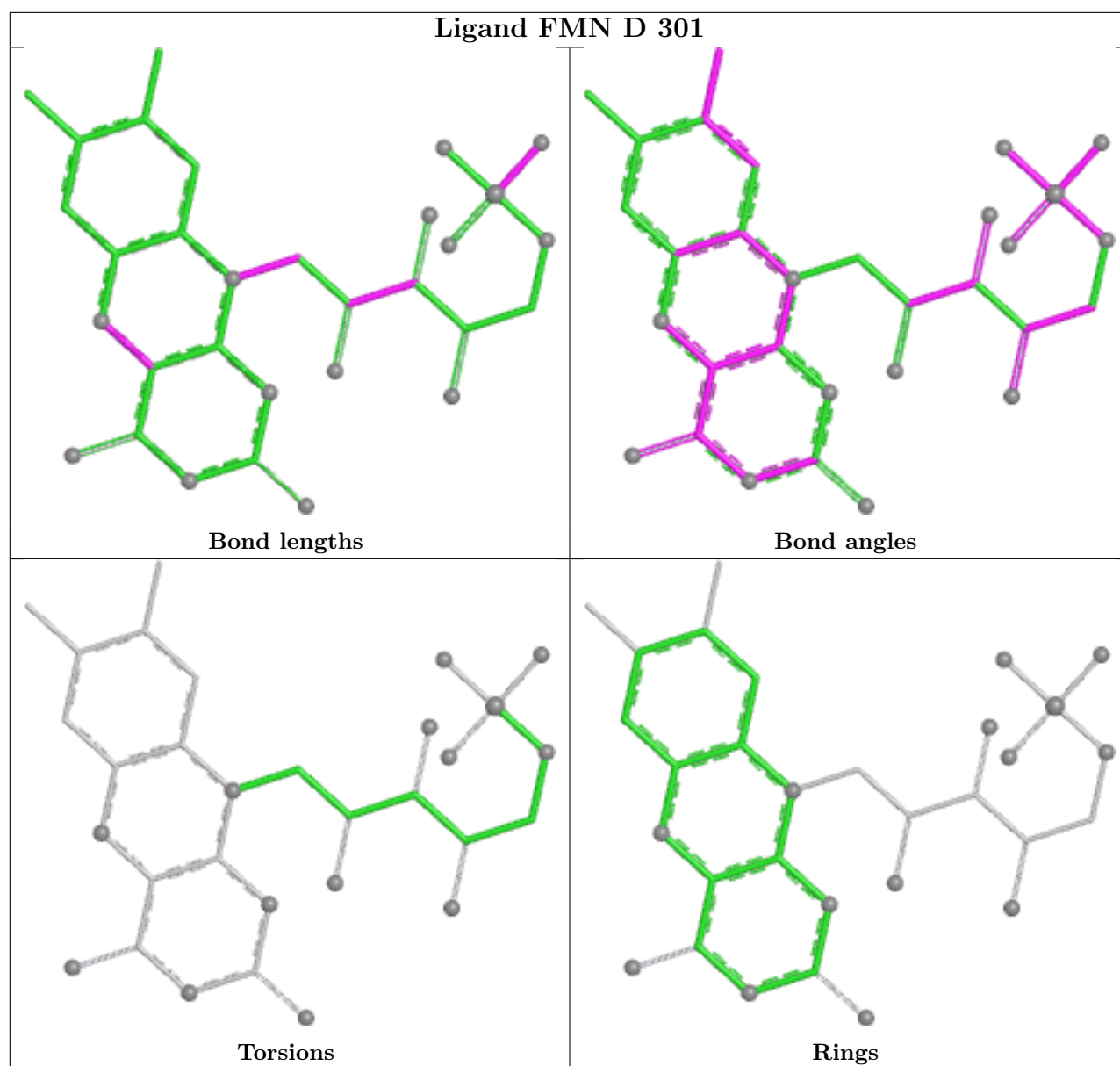


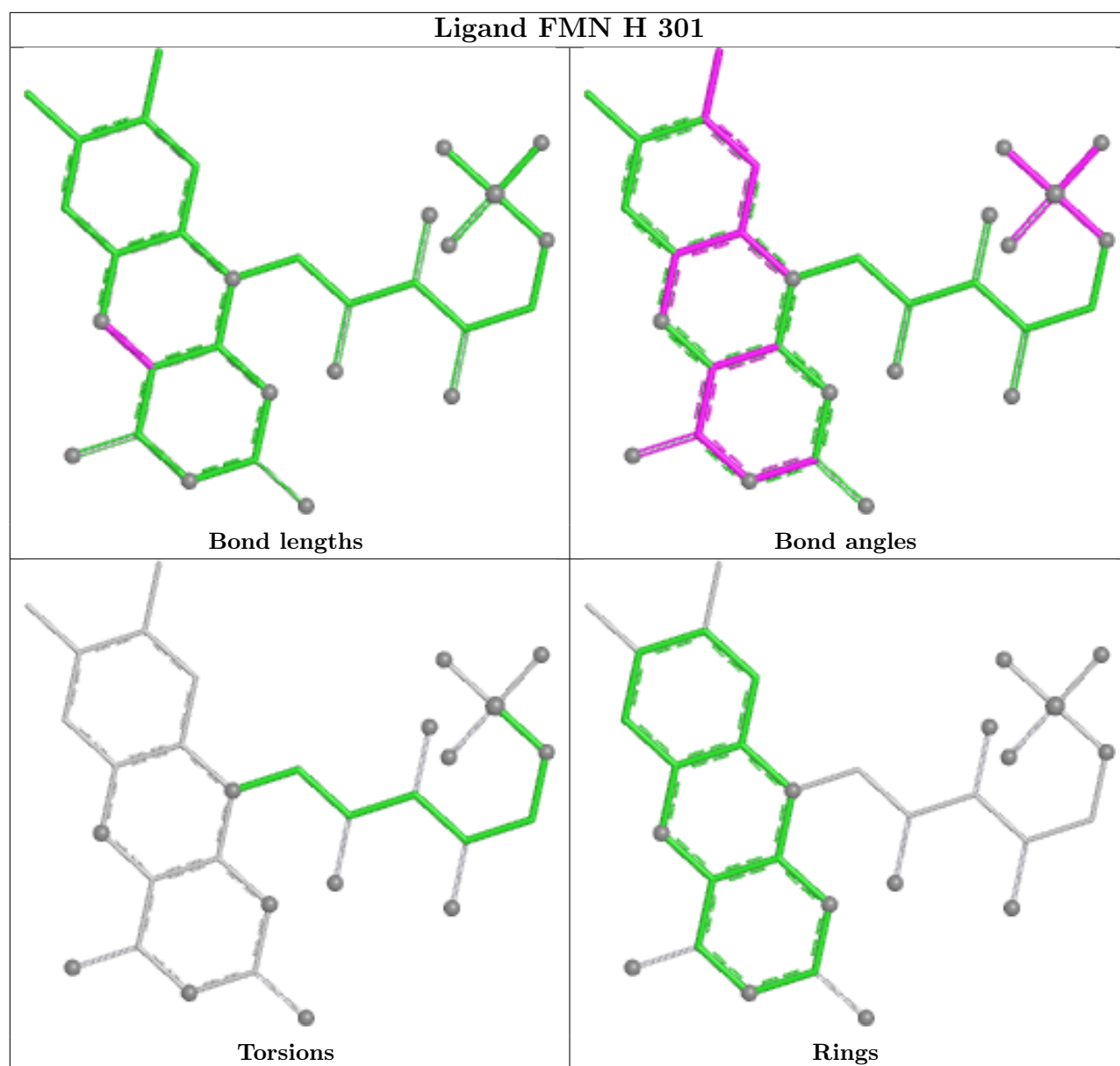
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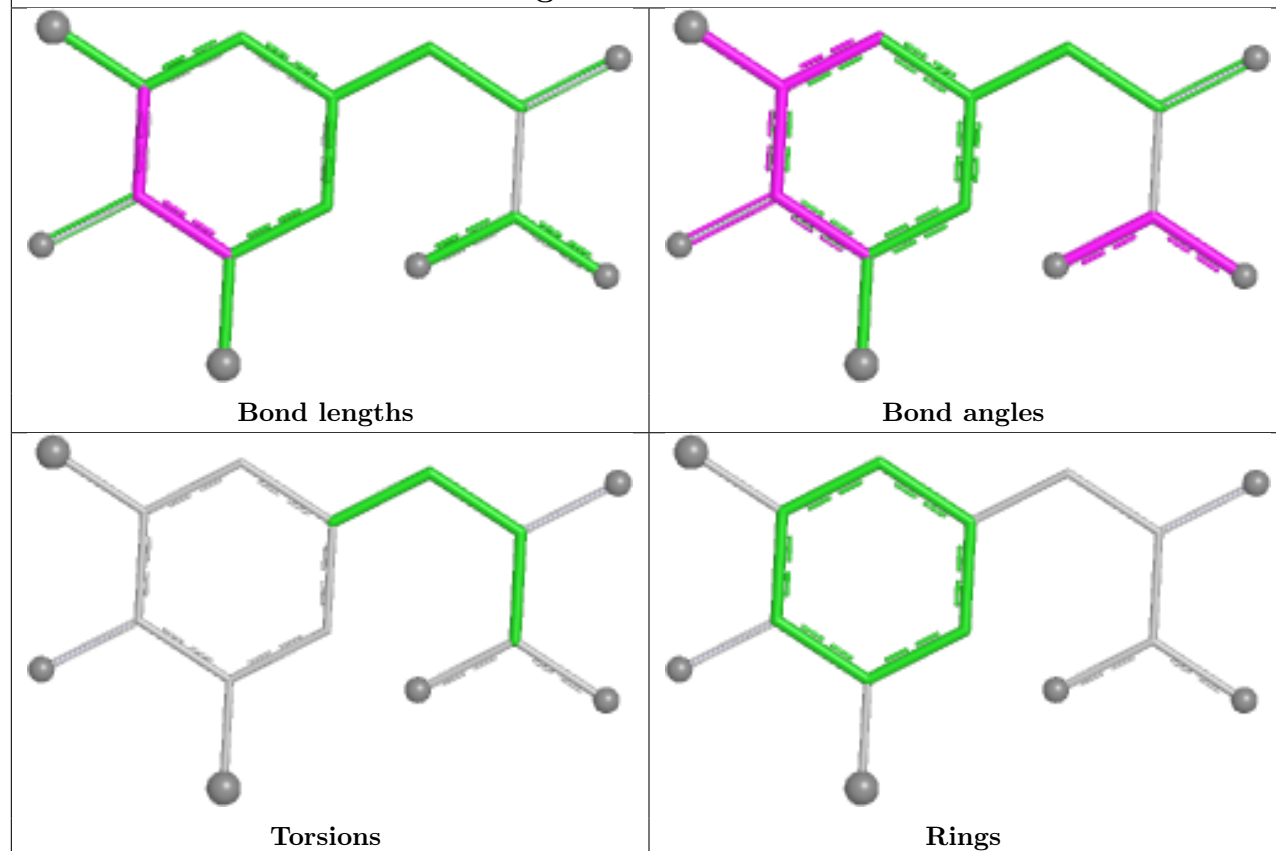




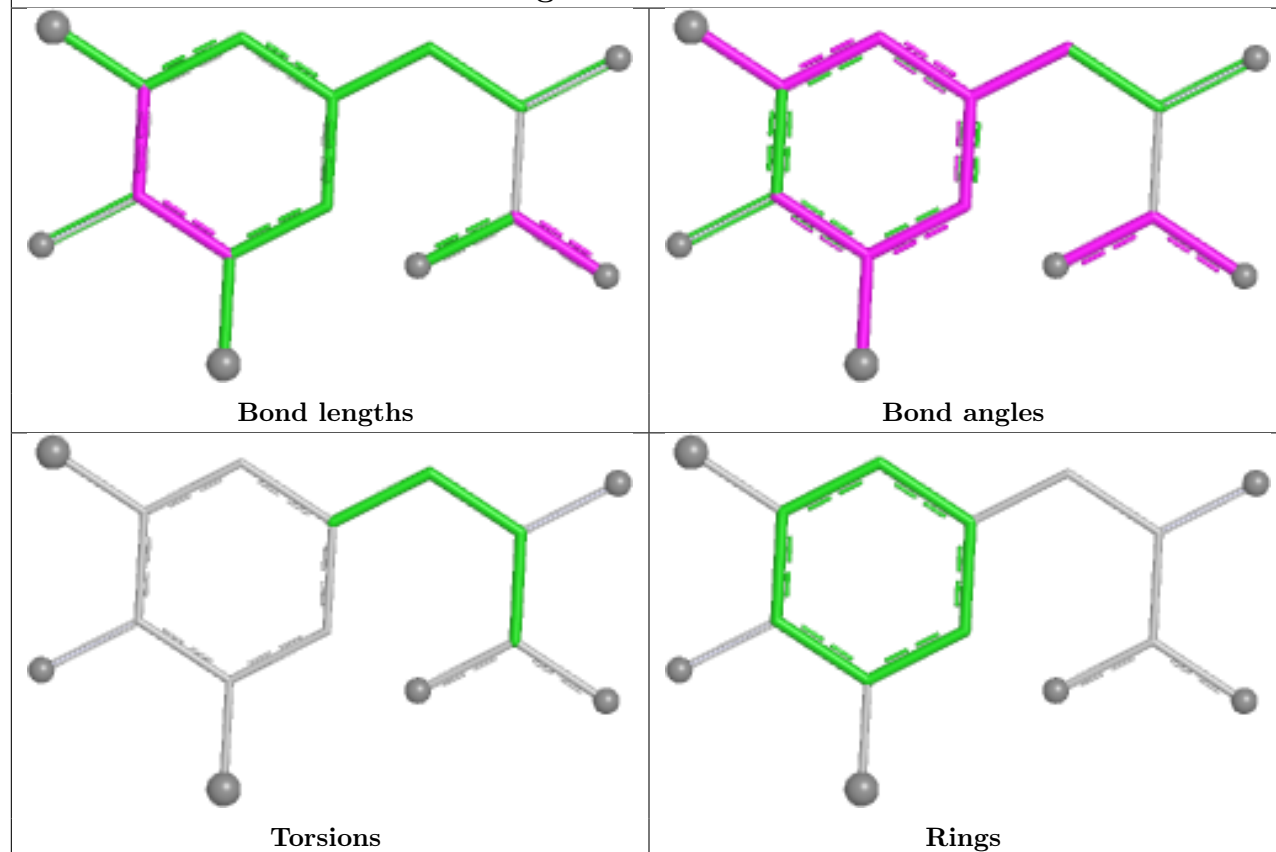


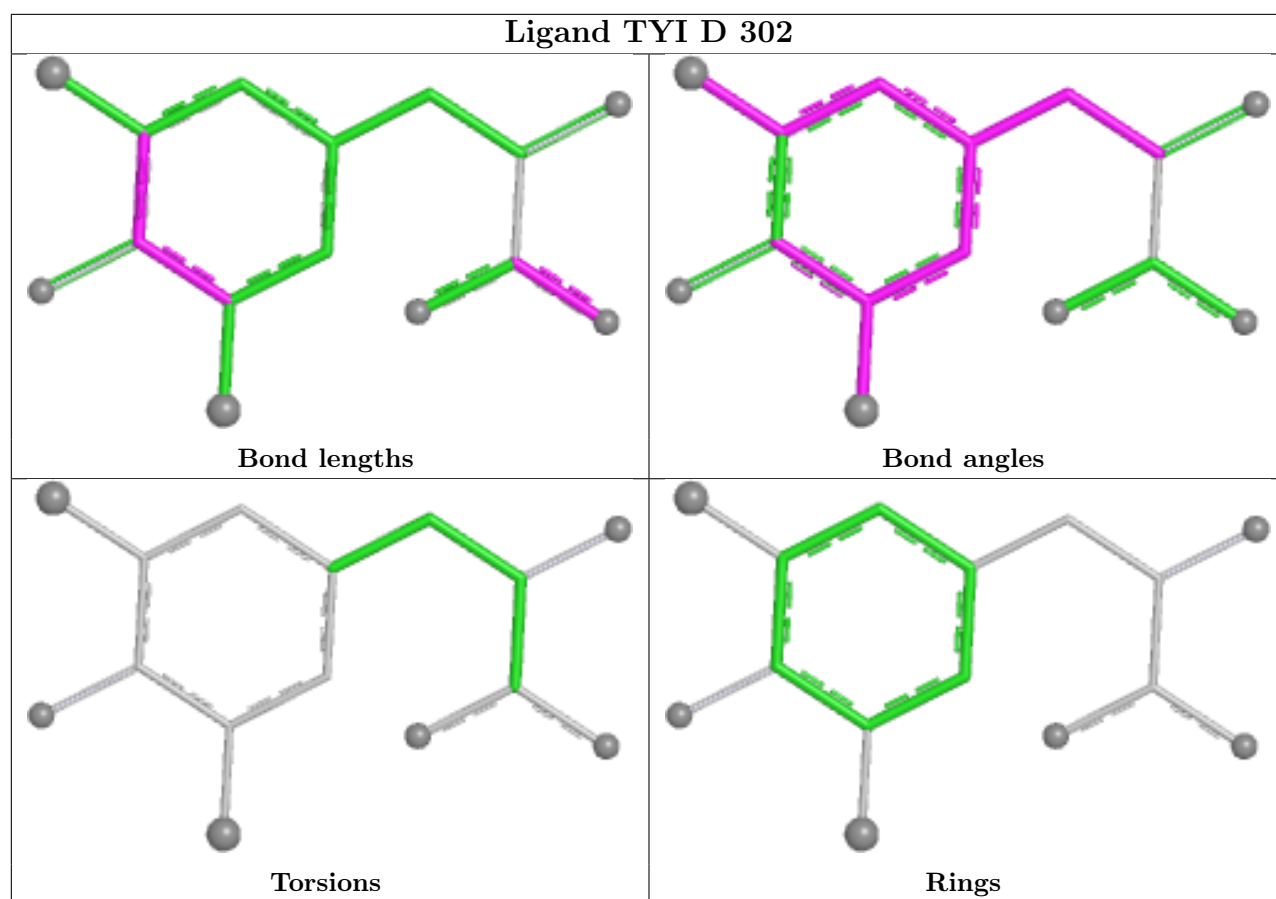


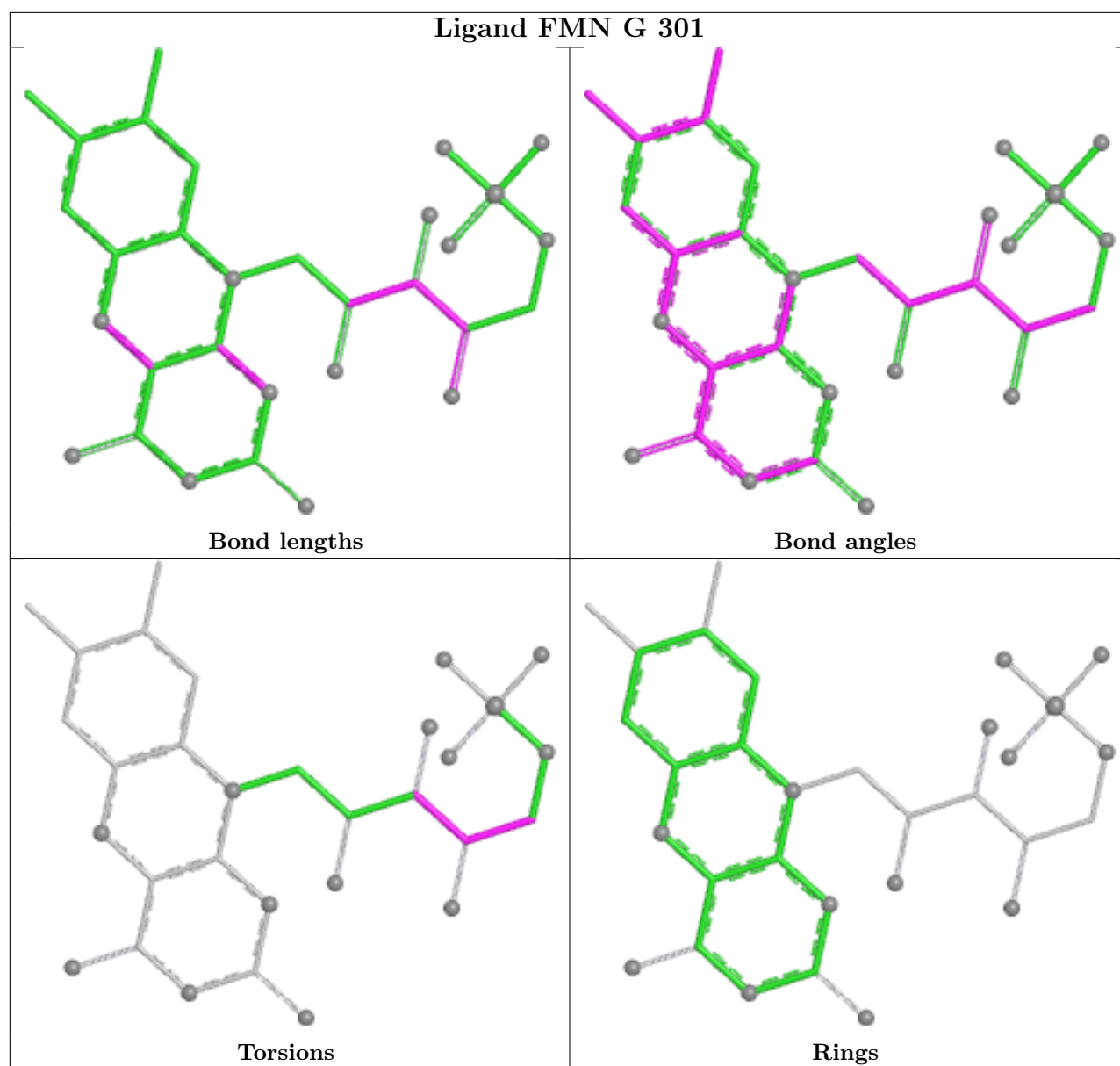
Ligand TYI A 302

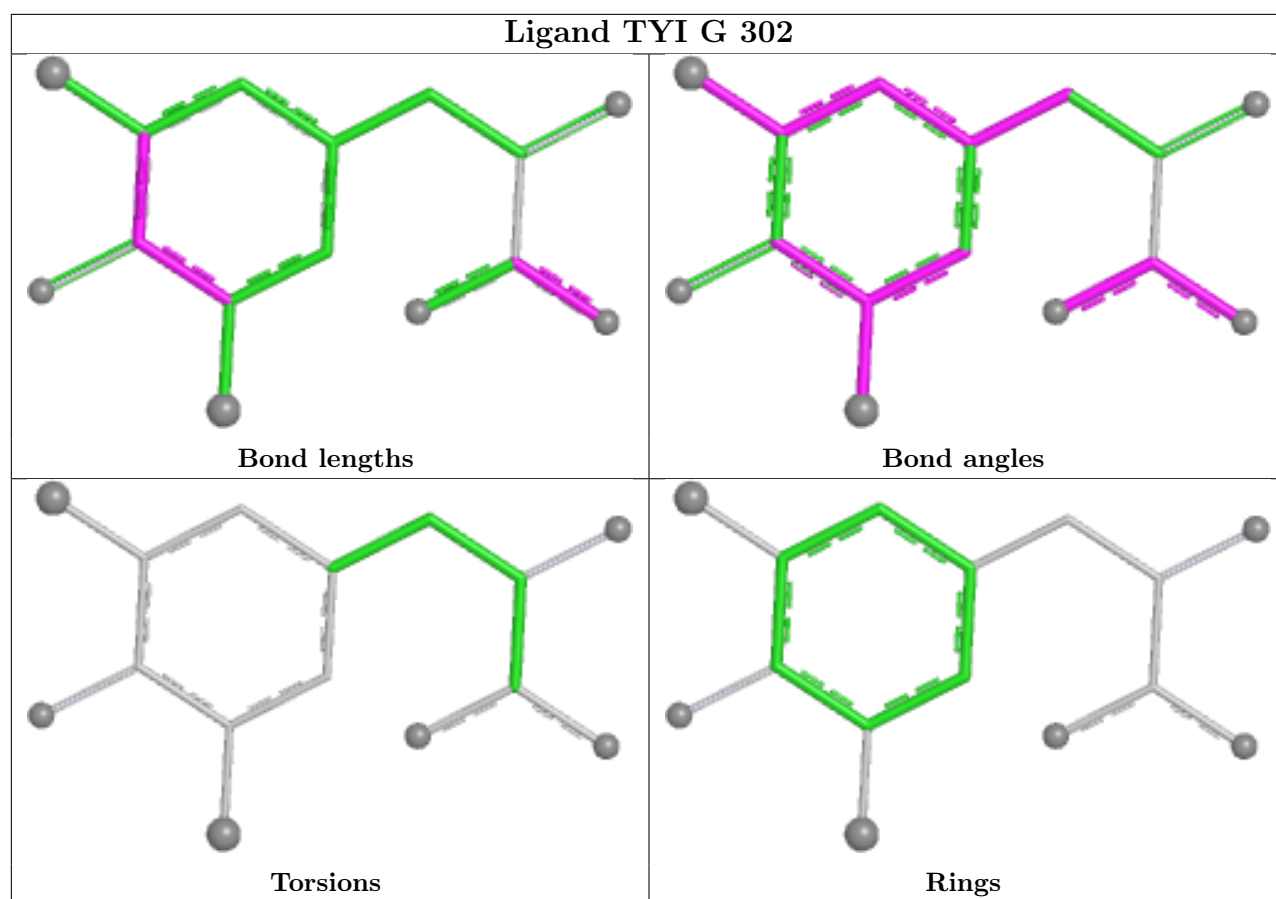


Ligand TYI C 302









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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	221/259 (85%)	-1.63	0 100 100	15, 33, 45, 56	2 (0%)
1	B	220/259 (84%)	-1.62	0 100 100	16, 31, 47, 55	1 (0%)
1	C	221/259 (85%)	-1.60	0 100 100	24, 34, 46, 68	0
1	D	220/259 (84%)	-1.62	0 100 100	25, 35, 45, 58	0
1	E	221/259 (85%)	-1.63	0 100 100	16, 35, 51, 63	2 (0%)
1	F	220/259 (84%)	-1.62	0 100 100	17, 33, 52, 61	1 (0%)
1	G	221/259 (85%)	-1.59	0 100 100	20, 37, 53, 67	0
1	H	220/259 (84%)	-1.63	0 100 100	22, 36, 51, 56	0
All	All	1764/2072 (85%)	-1.62	0 100 100	15, 34, 50, 68	6 (0%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

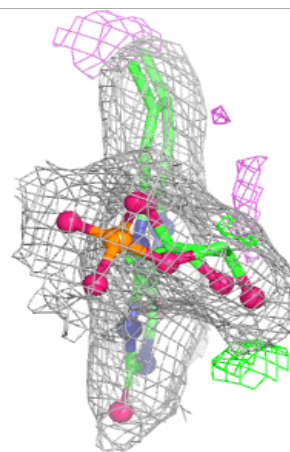
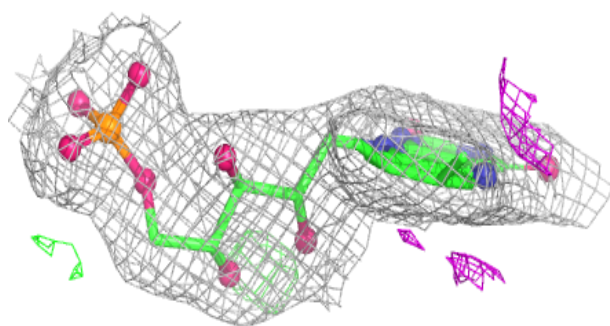
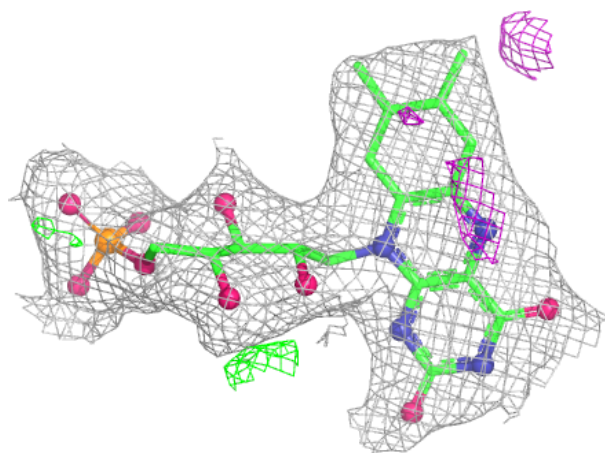
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PO4	G	2	5/5	0.98	0.05	78,80,82,82	0
2	FMN	B	301	31/31	0.99	0.03	15,24,26,30	0
2	FMN	D	301	31/31	0.99	0.03	24,28,29,31	0
2	FMN	E	301	31/31	0.99	0.03	18,25,28,29	0
2	FMN	F	301	31/31	0.99	0.03	11,21,23,26	0
2	FMN	G	301	31/31	0.99	0.03	14,24,27,27	0
2	FMN	H	301	31/31	0.99	0.03	23,27,30,32	0
4	PO4	C	1	5/5	0.99	0.06	76,79,80,80	0
2	FMN	A	301	31/31	0.99	0.03	16,27,29,30	0
3	TYI	B	302	15/15	1.00	0.03	35,38,40,46	1
3	TYI	C	302	15/15	1.00	0.04	39,40,45,49	1
3	TYI	D	302	15/15	1.00	0.04	39,41,44,50	1
3	TYI	E	302	15/15	1.00	0.03	35,38,41,43	2
3	TYI	F	302	15/15	1.00	0.02	38,42,43,50	1
3	TYI	G	302	15/15	1.00	0.03	42,44,48,49	1
3	TYI	H	302	15/15	1.00	0.03	33,35,40,47	1
2	FMN	C	301	31/31	1.00	0.03	17,24,26,26	0
3	TYI	A	302	15/15	1.00	0.03	37,39,41,42	2

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.

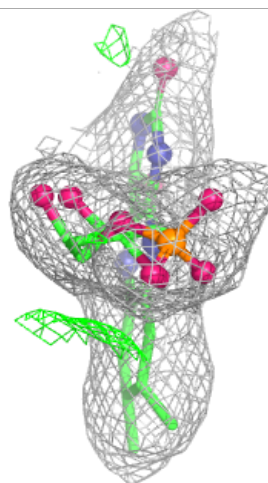
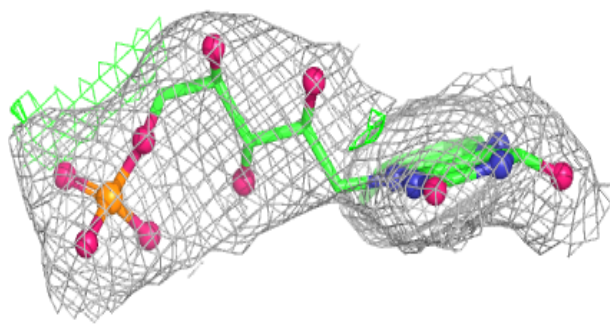
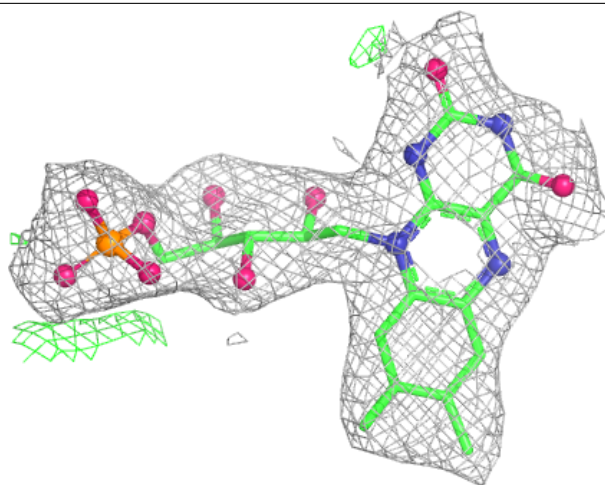
Electron density around FMN B 301:

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



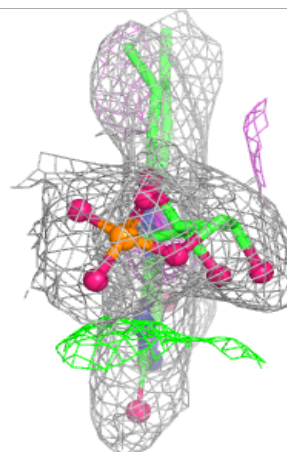
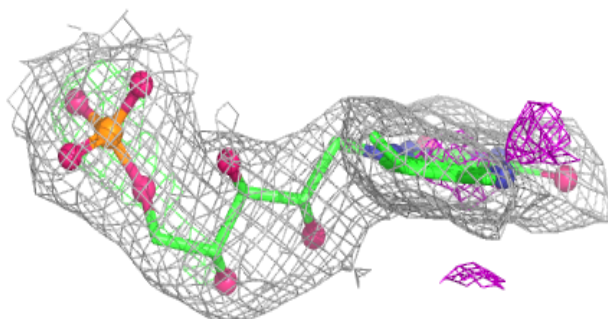
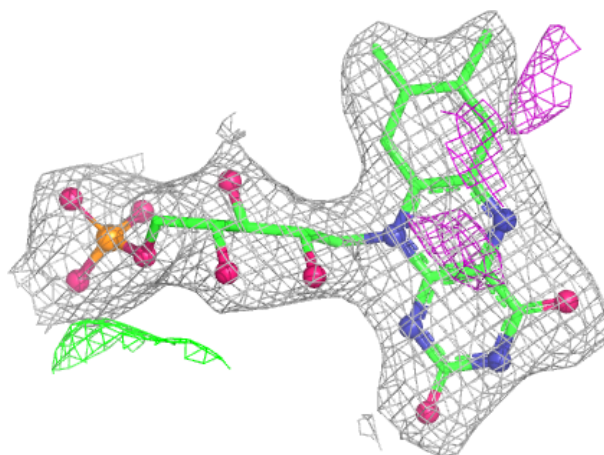
Electron density around FMN D 301:

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



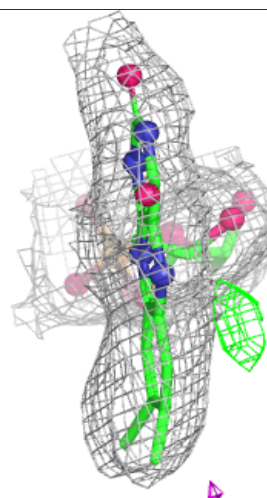
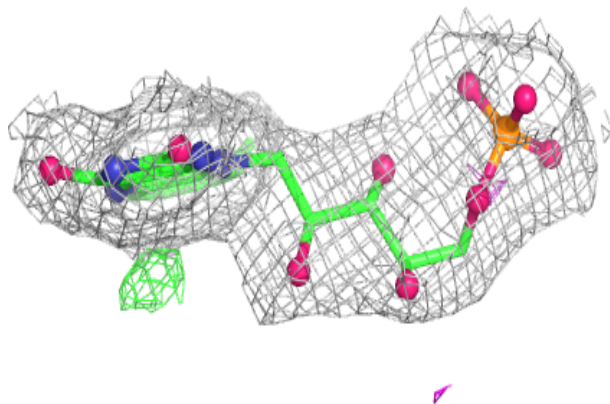
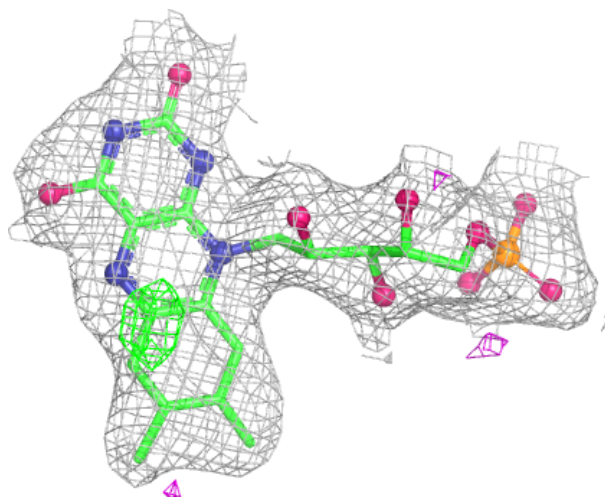
Electron density around FMN E 301:

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and green (positive)



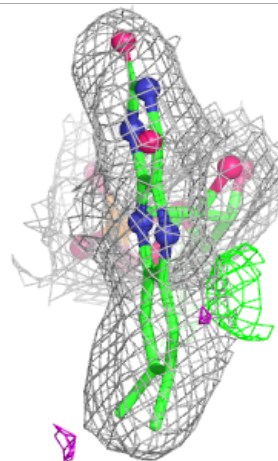
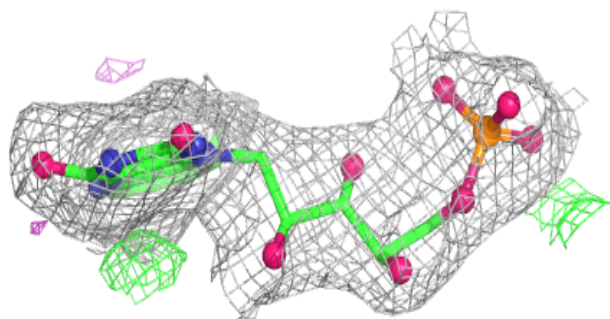
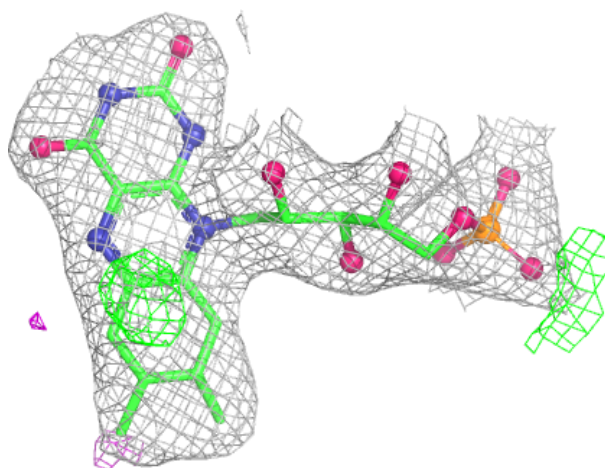
Electron density around FMN F 301:

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



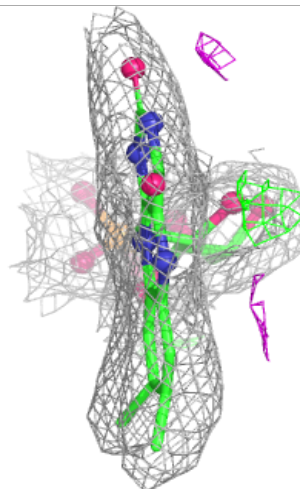
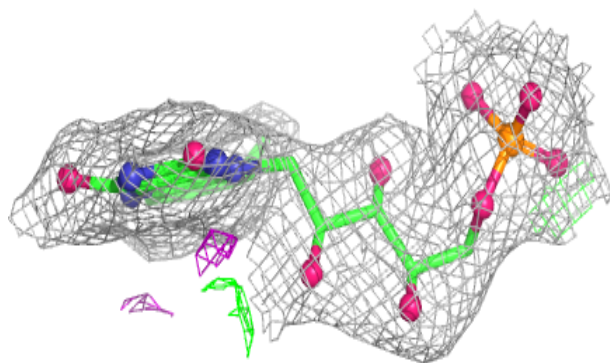
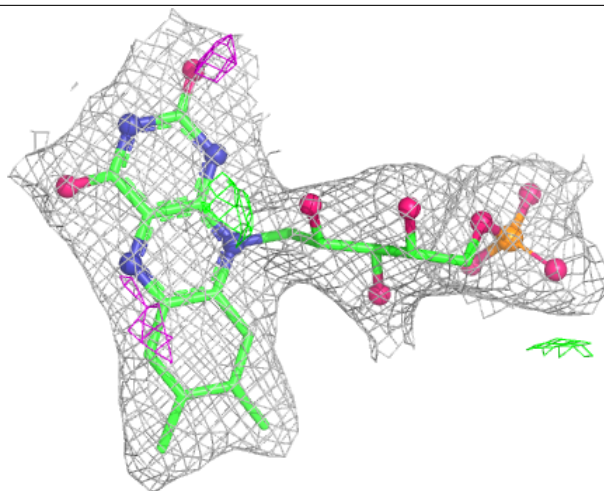
Electron density around FMN G 301:

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



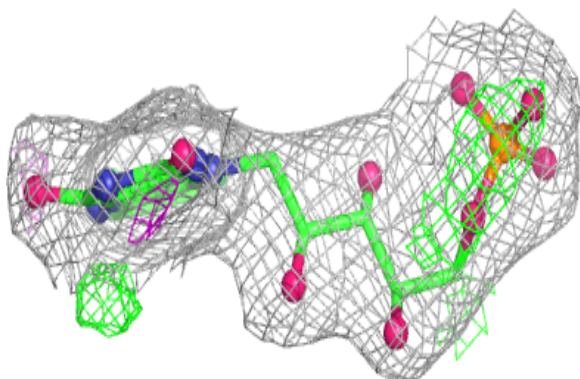
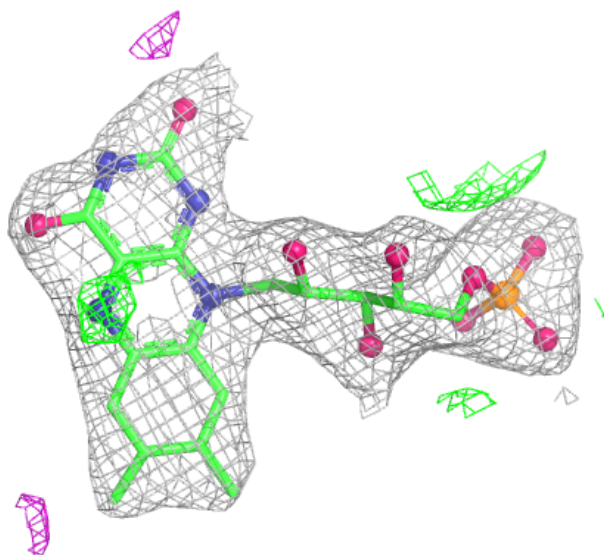
Electron density around FMN H 301:

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



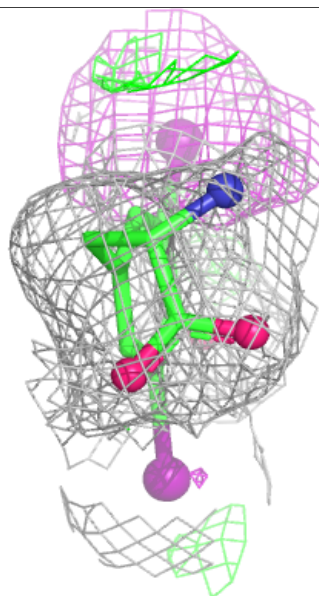
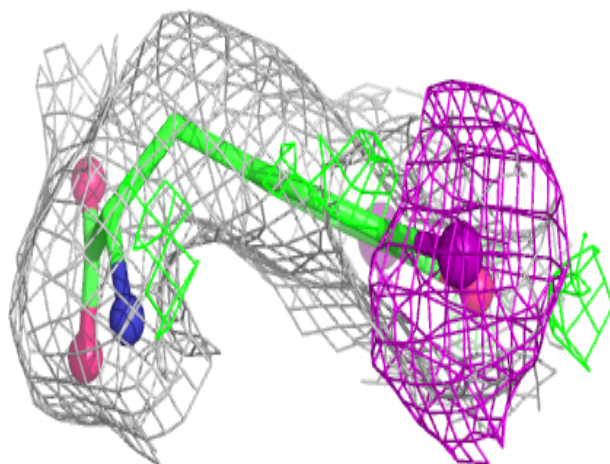
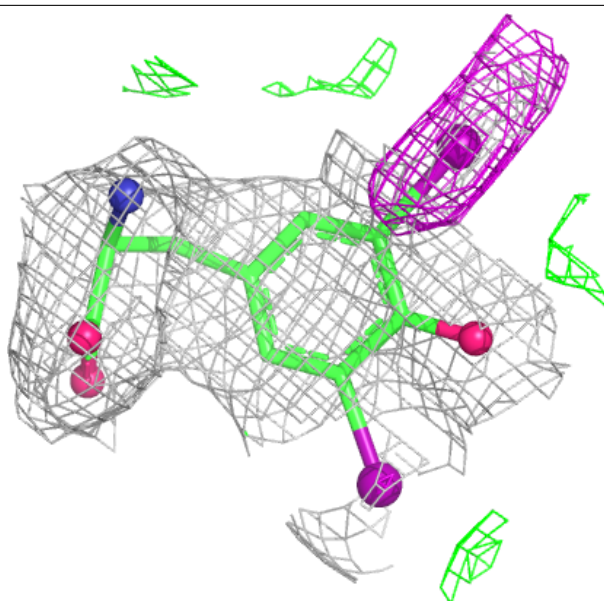
Electron density around FMN A 301:

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



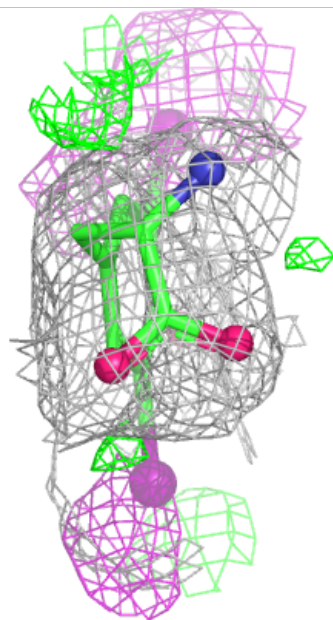
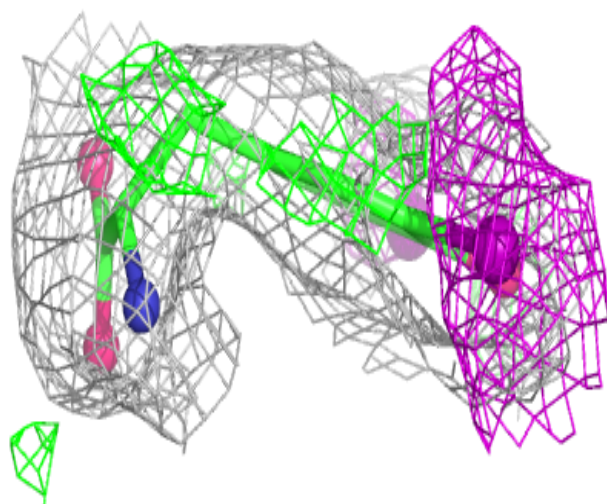
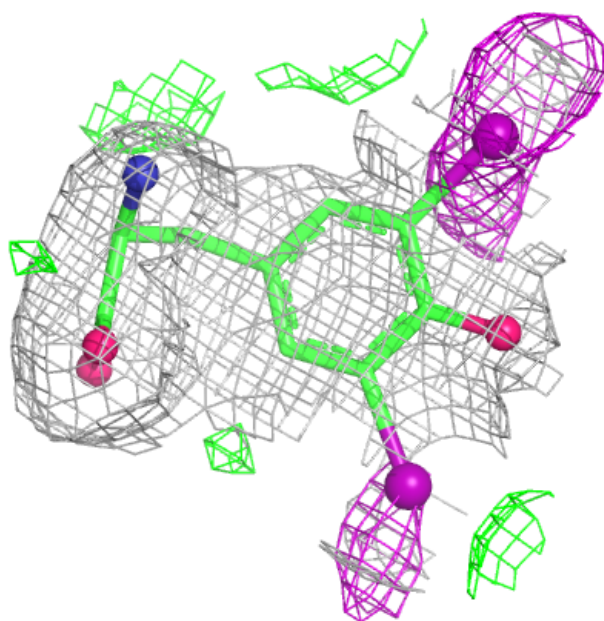
Electron density around TYI B 302:

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



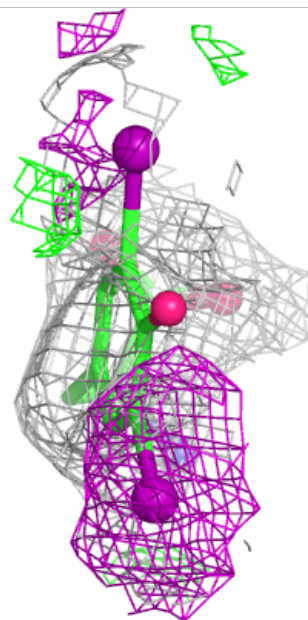
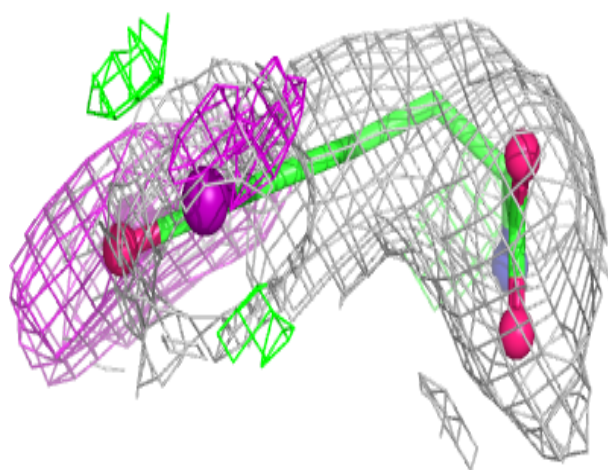
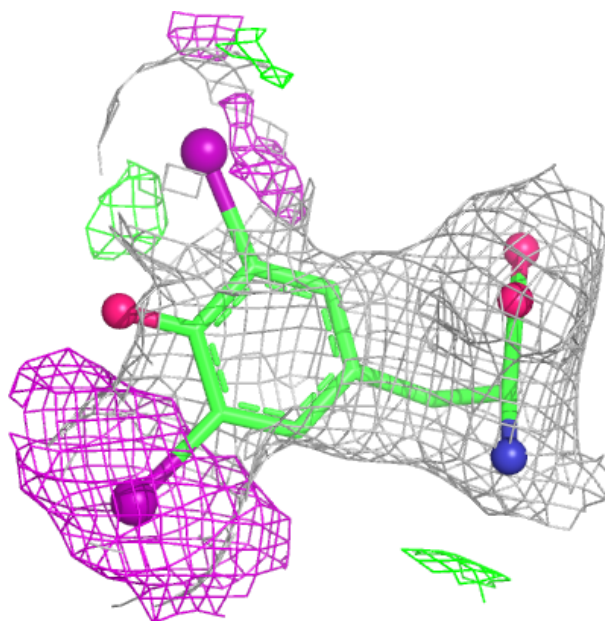
Electron density around TYI C 302:

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



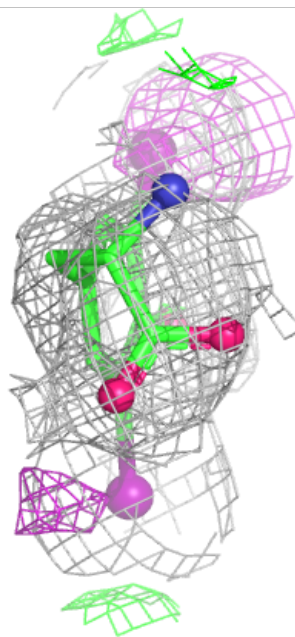
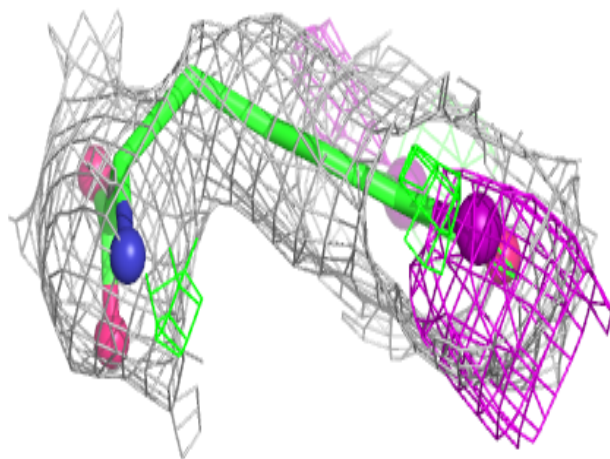
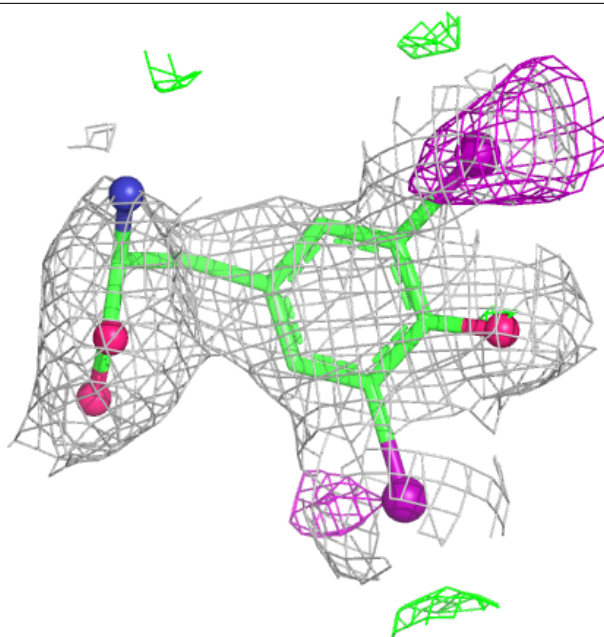
Electron density around TYI D 302:

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



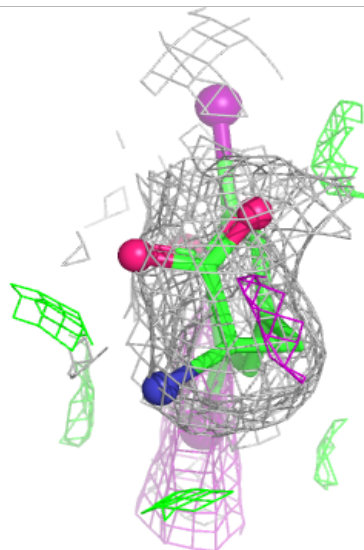
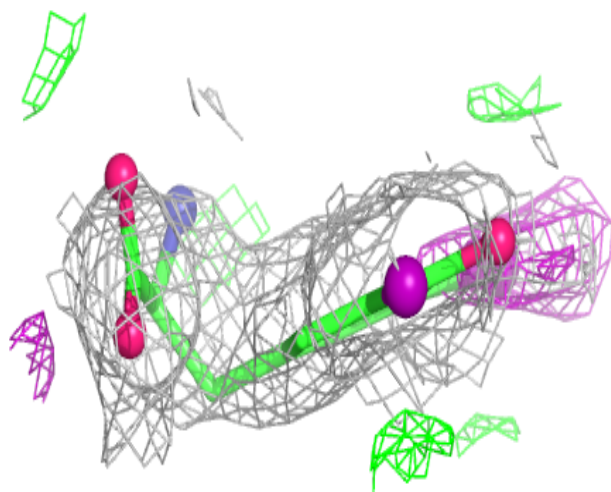
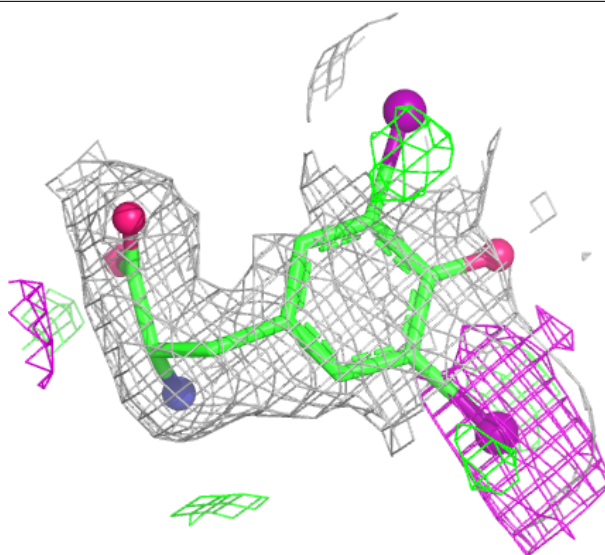
Electron density around TYI E 302:

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



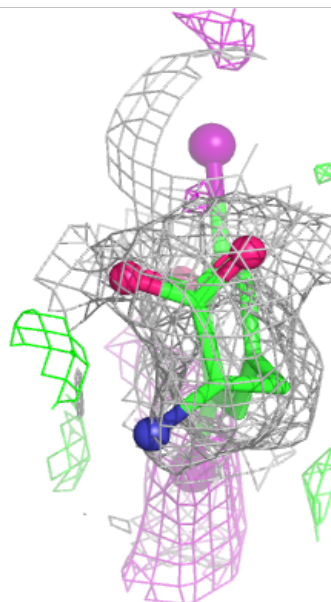
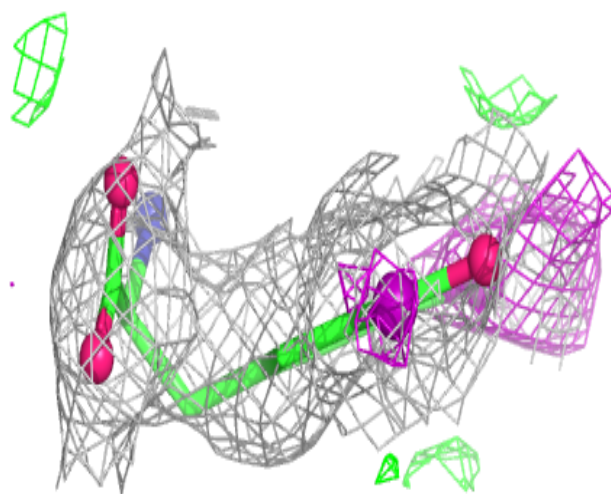
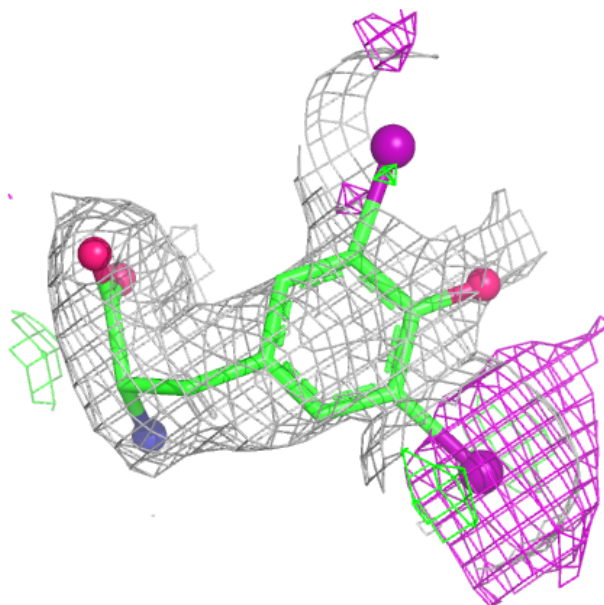
Electron density around TYI F 302:

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



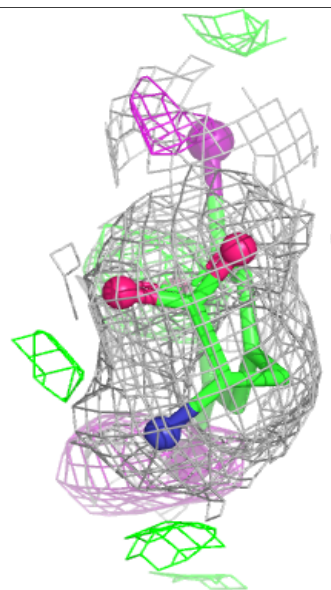
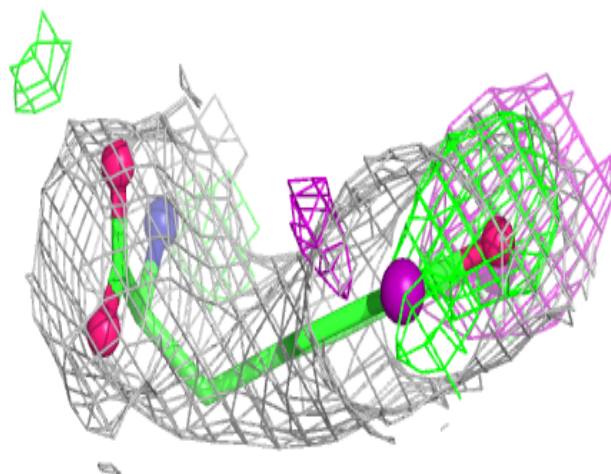
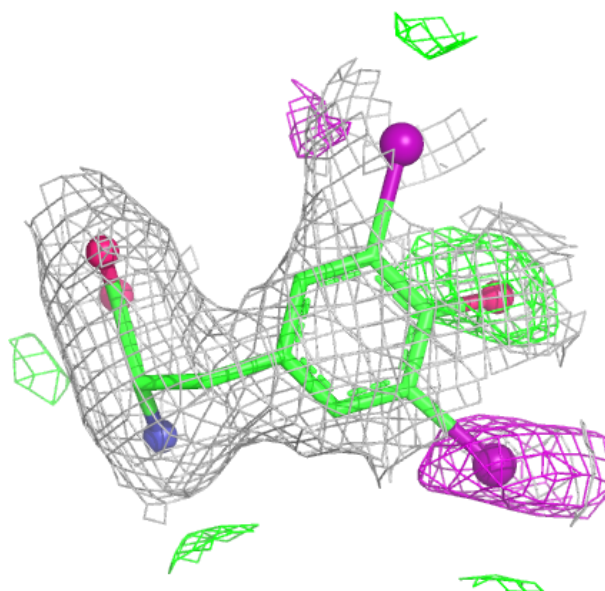
Electron density around TYI G 302:

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



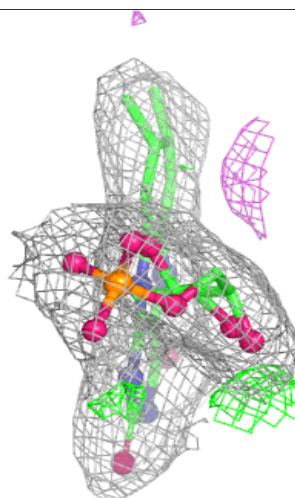
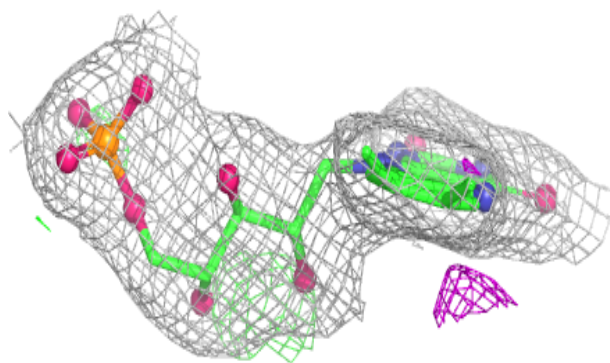
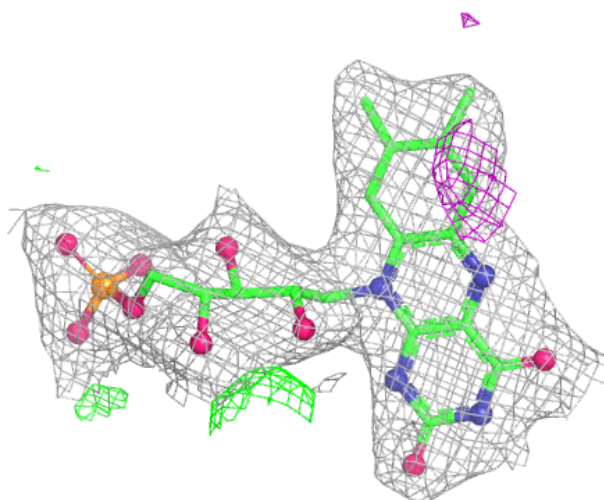
Electron density around TYI H 302:

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



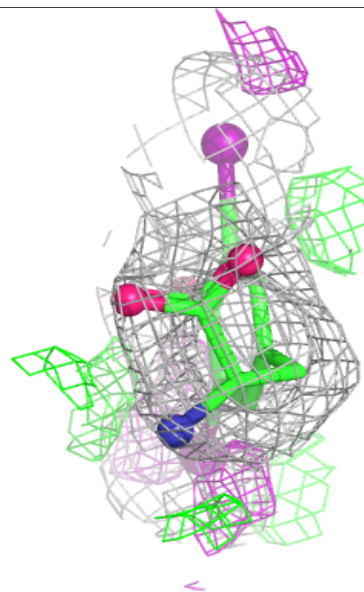
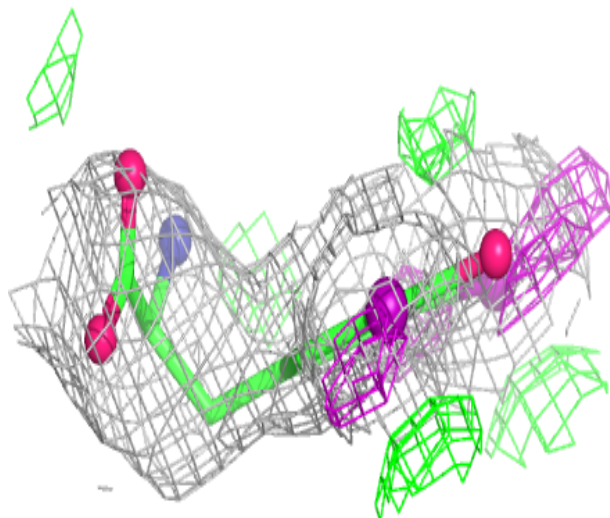
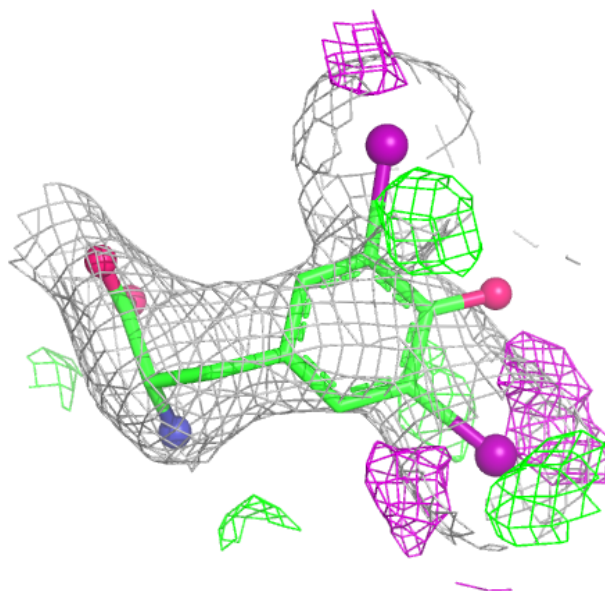
Electron density around FMN C 301:

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



Electron density around TYI A 302:

$2mF_o-DF_c$ (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.