



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 27, 2024 – 04:10 PM EDT

PDB ID : 1TEZ
Title : COMPLEX BETWEEN DNA AND THE DNA PHOTOLYASE FROM ANA-CYSTIS NIDULANS
Authors : Essen, L.-O.; Carell, T.; Mees, A.; Klar, T.
Deposited on : 2004-05-26
Resolution : 1.80 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

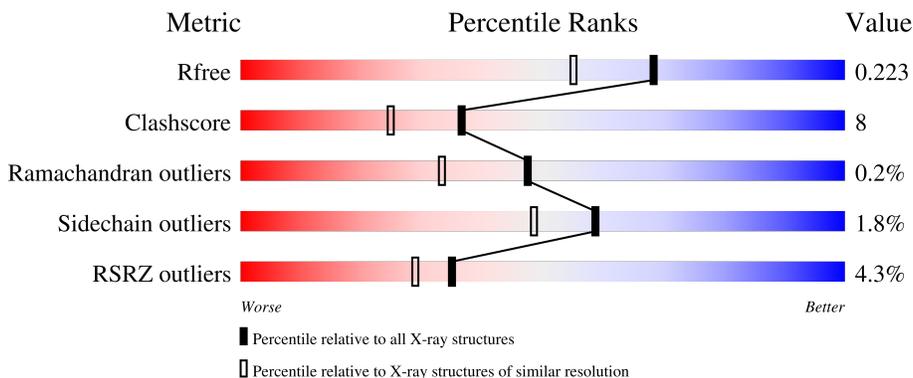
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	I	11	18% (Poor fit) 64% (0 outliers) 36% (1 outlier)
1	K	11	27% (Poor fit) 64% (0 outliers) 36% (1 outlier)
2	J	9	22% (Poor fit) 56% (0 outliers) 44% (1 outlier)
2	L	9	33% (Poor fit) 44% (0 outliers) 56% (1 outlier)
3	M	4	100% (0 outliers)

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Mol	Chain	Length	Quality of chain
3	O	4	
4	N	5	
4	P	5	
5	A	474	
5	B	474	
5	C	474	
5	D	474	

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
8	HDF	A	5486	X	-	-	-
8	HDF	B	6486	X	-	-	-
8	HDF	C	7486	X	-	-	-
8	HDF	D	8486	X	-	-	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 18206 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 DNA chain called 5'-D(*AP*TP*CP*GP*GP*CP*T*(TCP)P*CP*GP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	I	11	Total 218	C 107	N 38	O 64	P 9	0	0	0
1	K	11	Total 218	C 107	N 38	O 64	P 9	0	0	0

- Molecule 2 is a DNA chain called 5'-D(P*CP*GP*AP*AP*GP*CP*CP*GP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	J	9	Total 186	C 87	N 39	O 51	P 9	0	0	0
2	L	9	Total 186	C 87	N 39	O 51	P 9	0	0	0

- Molecule 3 is a DNA chain called 5'-D(*TP*CP*GP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	M	4	Total 77	C 38	N 13	O 23	P 3	1	0	0
3	O	4	Total 77	C 38	N 13	O 23	P 3	0	0	0

- Molecule 4 is a DNA chain called 5'-D(P*GP*CP*CP*GP*A)-3'.

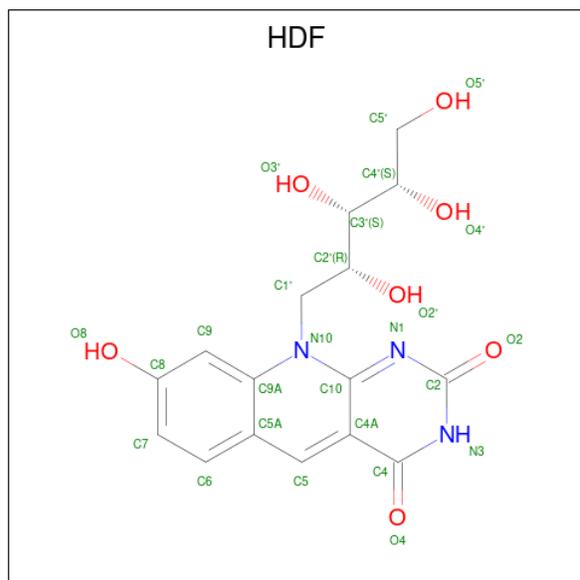
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	N	5	Total 103	C 48	N 21	O 29	P 5	0	0	0
4	P	5	Total 103	C 48	N 21	O 29	P 5	0	0	0

- Molecule 5 is a protein called Deoxyribodipyrimidine photo-lyase type I.

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
7	D	1	53	27	9	15	2	0	0

- Molecule 8 is 8-HYDROXY-10-(D-RIBO-2,3,4,5-TETRAHYDROXYPENTYL)-5-DEAZAI SOALLOXAZINE (three-letter code: HDF) (formula: C₁₆H₁₇N₃O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
8	A	1	26	16	3	7	0	0
8	B	1	26	16	3	7	0	0
8	C	1	26	16	3	7	0	0
8	D	1	26	16	3	7	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	I	10	10	10	0	0
9	J	11	11	11	0	0
9	K	8	8	8	0	0
9	L	9	9	9	0	0

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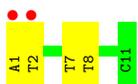
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	14	Total 14	O 14	0	0
9	N	10	Total 10	O 10	0	0
9	P	5	Total 5	O 5	0	0
9	A	409	Total 409	O 409	0	0
9	B	404	Total 404	O 404	0	0
9	C	374	Total 374	O 374	0	0
9	D	360	Total 360	O 360	0	0

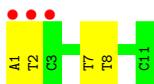
3 Residue-property plots [i](#)

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.

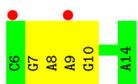
- Molecule 1: 5'-D(*AP*TP*CP*GP*GP*CP*T*(TCP)P*CP*GP*C)-3'



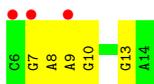
- Molecule 1: 5'-D(*AP*TP*CP*GP*GP*CP*T*(TCP)P*CP*GP*C)-3'



- Molecule 2: 5'-D(P*CP*GP*AP*AP*GP*CP*CP*GP*A)-3'



- Molecule 2: 5'-D(P*CP*GP*AP*AP*GP*CP*CP*GP*A)-3'



- Molecule 3: 5'-D(*TP*CP*GP*C)-3'



There are no outlier residues recorded for this chain.

- Molecule 3: 5'-D(*TP*CP*GP*C)-3'





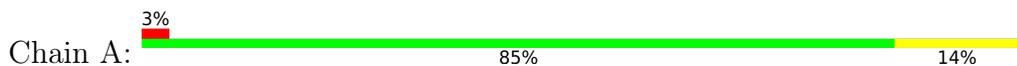
- Molecule 4: 5'-D(P*GP*CP*CP*GP*A)-3'



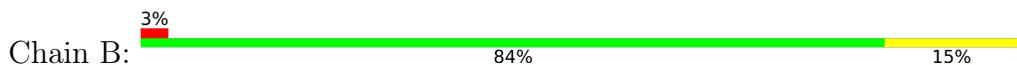
- Molecule 4: 5'-D(P*GP*CP*CP*GP*A)-3'



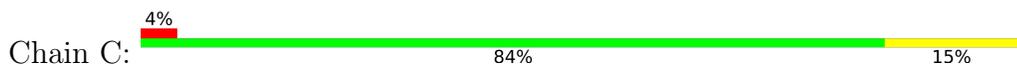
- Molecule 5: Deoxyribodipyrimidine photo-lyase type I

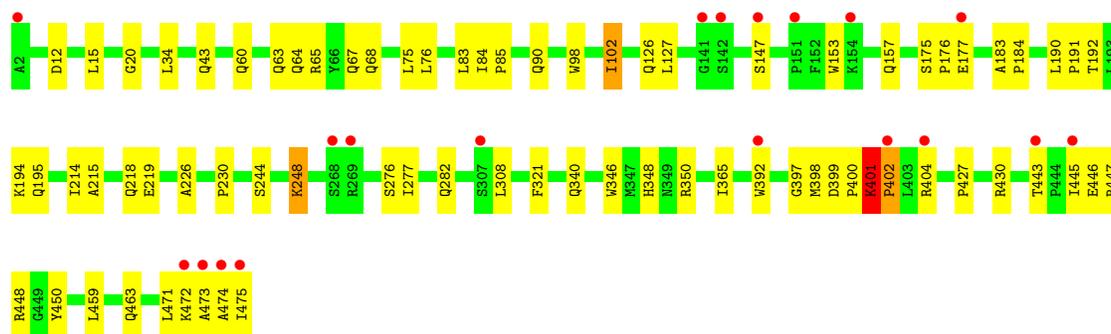


- Molecule 5: Deoxyribodipyrimidine photo-lyase type I

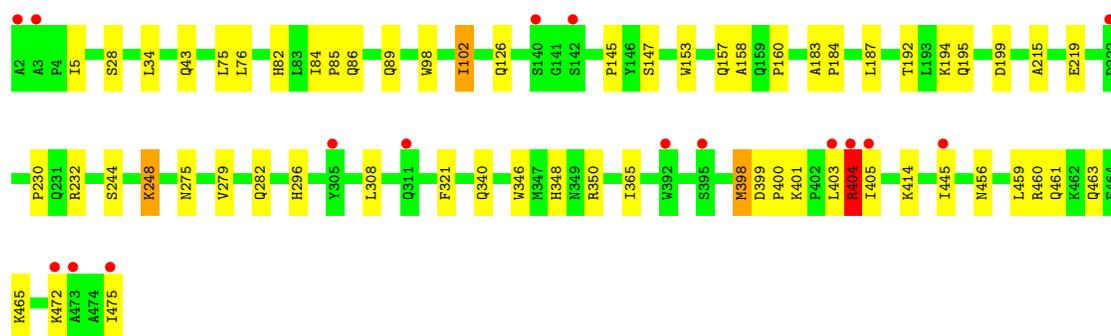
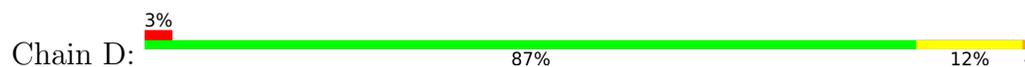


- Molecule 5: Deoxyribodipyrimidine photo-lyase type I





• Molecule 5: Deoxyribodipyrimidine photo-lyase type I



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	173.81Å 88.50Å 161.62Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	29.92 – 1.80 29.92 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.1 (29.92-1.80) 95.8 (29.92-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.80Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.205 , 0.226 0.203 , 0.223	Depositor DCC
R_{free} test set	7425 reflections (3.40%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtrriage
Anisotropy	0.348	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.417 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18206	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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: FAD, TCP, HDF, MG

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	I	0.27	0/222	0.67	0/338
1	K	0.28	0/222	0.68	0/338
2	J	0.42	0/209	0.72	0/320
2	L	0.43	0/209	0.72	0/320
3	M	0.38	0/85	0.85	0/129
3	O	0.34	0/85	0.82	0/129
4	N	0.54	0/115	0.76	0/175
4	P	0.52	0/115	0.76	0/175
5	A	0.32	0/3883	0.54	0/5292
5	B	0.32	0/3891	0.55	0/5302
5	C	0.32	0/3882	0.55	0/5292
5	D	0.32	0/3886	0.56	0/5296
All	All	0.32	0/16804	0.57	0/23106

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	I	218	0	128	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	218	0	128	10	0
2	J	186	0	100	5	0
2	L	186	0	100	5	0
3	M	77	0	47	0	0
3	O	77	0	47	1	0
4	N	103	0	56	0	0
4	P	103	0	56	1	0
5	A	3774	0	3681	60	0
5	B	3782	0	3694	61	0
5	C	3773	0	3674	66	0
5	D	3777	0	3685	56	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	53	0	31	0	0
7	B	53	0	31	1	0
7	C	53	0	31	1	0
7	D	53	0	31	1	0
8	A	26	0	15	0	0
8	B	26	0	16	0	0
8	C	26	0	15	0	0
8	D	26	0	15	0	0
9	A	409	0	0	5	0
9	B	404	0	0	7	0
9	C	374	0	0	8	0
9	D	360	0	0	10	0
9	I	10	0	0	0	0
9	J	11	0	0	0	0
9	K	8	0	0	0	0
9	L	9	0	0	0	0
9	M	14	0	0	0	0
9	N	10	0	0	0	0
9	P	5	0	0	0	0
All	All	18206	0	15581	255	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 8.

The worst 5 of 255 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)
5:C:401:LYS:HB2	5:C:402:PRO:HD2	1.33	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:401:LYS:HG2	5:C:404:ARG:HH21	1.29	0.98
5:C:401:LYS:HG2	5:C:404:ARG:NH2	1.88	0.88
5:D:199:ASP:HB2	9:D:8744:HOH:O	1.75	0.85
5:C:226:ALA:HA	9:C:7764:HOH:O	1.78	0.84

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	
5	A	472/474 (100%)	457 (97%)	15 (3%)	0	100	100
5	B	472/474 (100%)	458 (97%)	14 (3%)	0	100	100
5	C	472/474 (100%)	454 (96%)	15 (3%)	3 (1%)	25	12
5	D	472/474 (100%)	453 (96%)	18 (4%)	1 (0%)	47	33
All	All	1888/1896 (100%)	1822 (96%)	62 (3%)	4 (0%)	47	33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	D	404	ARG
5	C	474	ALA
5	C	402	PRO
5	C	401	LYS

5.3.2 Protein sidechains [i](#)

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	
5	A	383/385 (100%)	377 (98%)	6 (2%)	62	54
5	B	385/385 (100%)	377 (98%)	8 (2%)	53	42
5	C	383/385 (100%)	376 (98%)	7 (2%)	59	48
5	D	384/385 (100%)	378 (98%)	6 (2%)	62	54
All	All	1535/1540 (100%)	1508 (98%)	27 (2%)	59	48

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	C	90	GLN
5	C	230	PRO
5	D	248	LYS
5	C	157	GLN
5	C	248	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
5	C	63	GLN
5	C	372	GLN
5	D	463	GLN
5	C	77	GLN
5	C	126	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](#)

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TCP	I	8	1	19,19,19	0.24	0	27,27,27	0.61	0
1	TCP	K	8	1	19,19,19	0.27	0	27,27,27	0.63	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
1	TCP	I	8	1	-	4/7/19/19	0/2/2/2
1	TCP	K	8	1	-	4/7/19/19	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	I	8	TCP	C2'-C1'-N1-C6
1	K	8	TCP	C2'-C1'-N1-C6
1	I	8	TCP	O4'-C1'-N1-C6
1	K	8	TCP	O4'-C1'-N1-C6
1	I	8	TCP	C2'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	I	8	TCP	6	0
1	K	8	TCP	6	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
7	FAD	C	7485	-	53,58,58	1.22	5 (9%)	68,89,89	1.08	5 (7%)
8	HDF	D	8486	-	25,28,28	2.67	4 (16%)	29,41,41	4.40	9 (31%)
7	FAD	A	5485	-	53,58,58	1.23	6 (11%)	68,89,89	1.04	5 (7%)
7	FAD	B	6485	-	53,58,58	1.28	5 (9%)	68,89,89	1.06	5 (7%)
8	HDF	A	5486	-	25,28,28	2.61	4 (16%)	29,41,41	4.46	10 (34%)
8	HDF	C	7486	-	25,28,28	2.56	4 (16%)	29,41,41	4.41	10 (34%)
8	HDF	B	6486	-	25,28,28	2.48	4 (16%)	29,41,41	4.42	9 (31%)
7	FAD	D	8485	-	53,58,58	1.28	6 (11%)	68,89,89	1.06	5 (7%)

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
7	FAD	C	7485	-	-	5/30/50/50	0/6/6/6
8	HDF	D	8486	-	2/2/3/3	5/14/14/14	0/3/3/3
7	FAD	A	5485	-	-	5/30/50/50	0/6/6/6
7	FAD	B	6485	-	-	5/30/50/50	0/6/6/6
8	HDF	C	7486	-	2/2/3/3	6/14/14/14	0/3/3/3
8	HDF	A	5486	-	2/2/3/3	5/14/14/14	0/3/3/3
8	HDF	B	6486	-	2/2/3/3	5/14/14/14	0/3/3/3
7	FAD	D	8485	-	-	5/30/50/50	0/6/6/6

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	8486	HDF	C1'-N10	-10.40	1.37	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	5486	HDF	C1'-N10	-10.22	1.37	1.48
8	C	7486	HDF	C1'-N10	-9.69	1.38	1.48
8	B	6486	HDF	C1'-N10	-9.38	1.38	1.48
8	D	8486	HDF	C10-N1	5.25	1.40	1.33

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	7486	HDF	C4A-C4-N3	-15.45	113.63	124.40
8	A	5486	HDF	C4A-C4-N3	-15.36	113.69	124.40
8	B	6486	HDF	C4A-C4-N3	-15.34	113.70	124.40
8	D	8486	HDF	C4A-C4-N3	-15.12	113.86	124.40
8	A	5486	HDF	C2-N3-C4	13.27	126.35	115.14

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	A	5486	HDF	C4'
8	A	5486	HDF	C2'
8	B	6486	HDF	C4'
8	B	6486	HDF	C2'
8	C	7486	HDF	C4'

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	5485	FAD	C5B-O5B-PA-O1A
7	B	6485	FAD	C5B-O5B-PA-O1A
8	A	5486	HDF	N10-C1'-C2'-O2'
8	A	5486	HDF	N10-C1'-C2'-C3'
8	A	5486	HDF	O2'-C2'-C3'-O3'

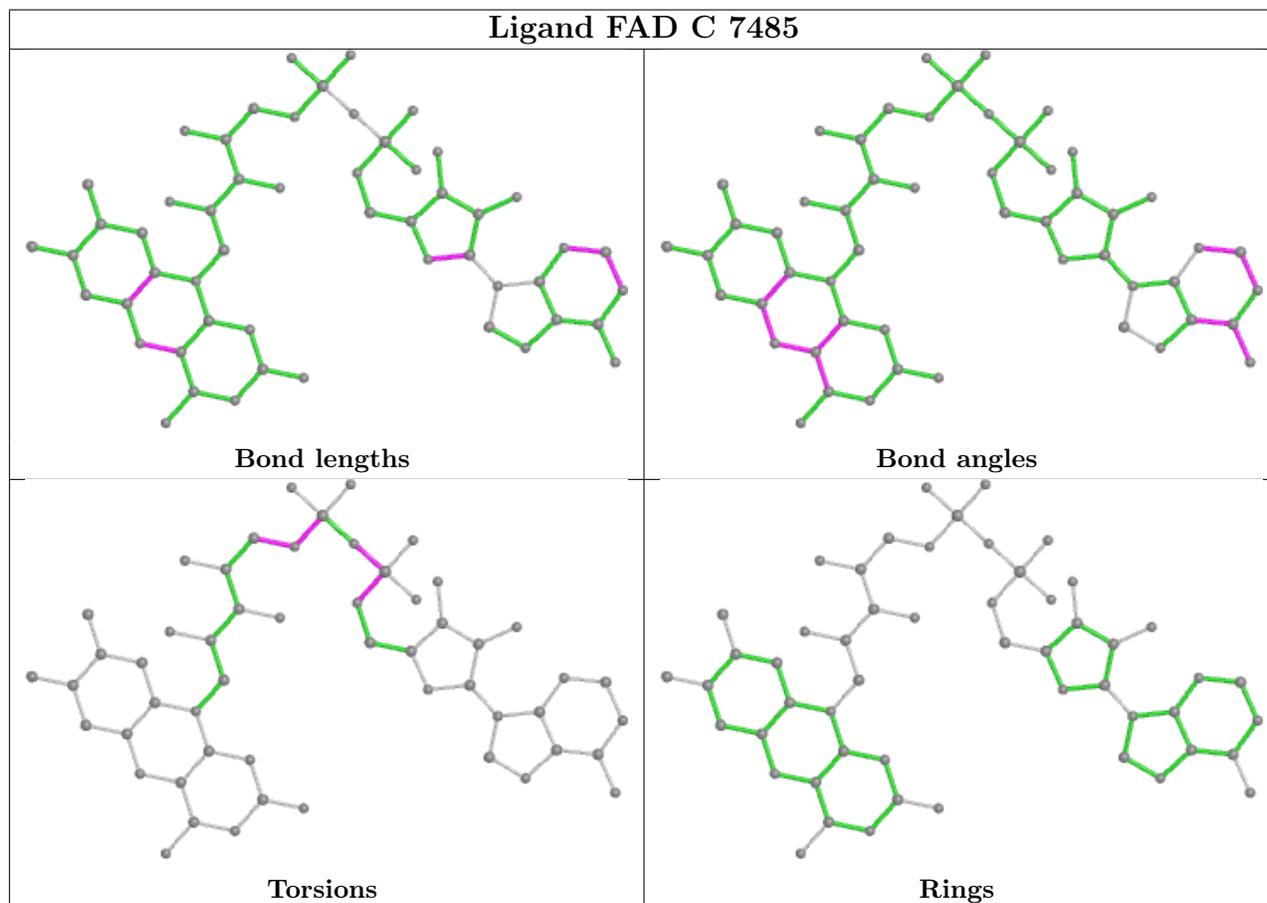
There are no ring outliers.

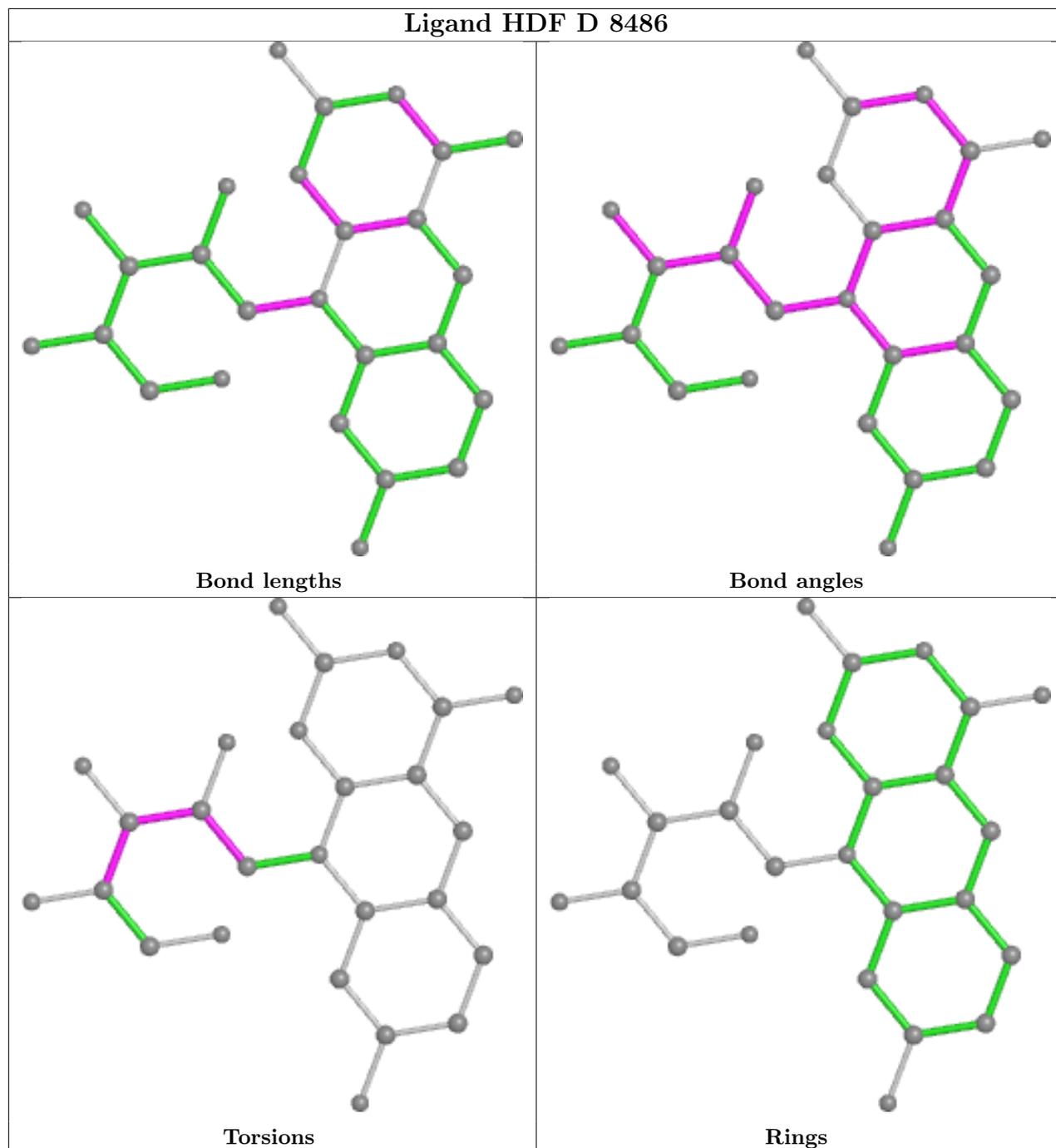
3 monomers are involved in 3 short contacts:

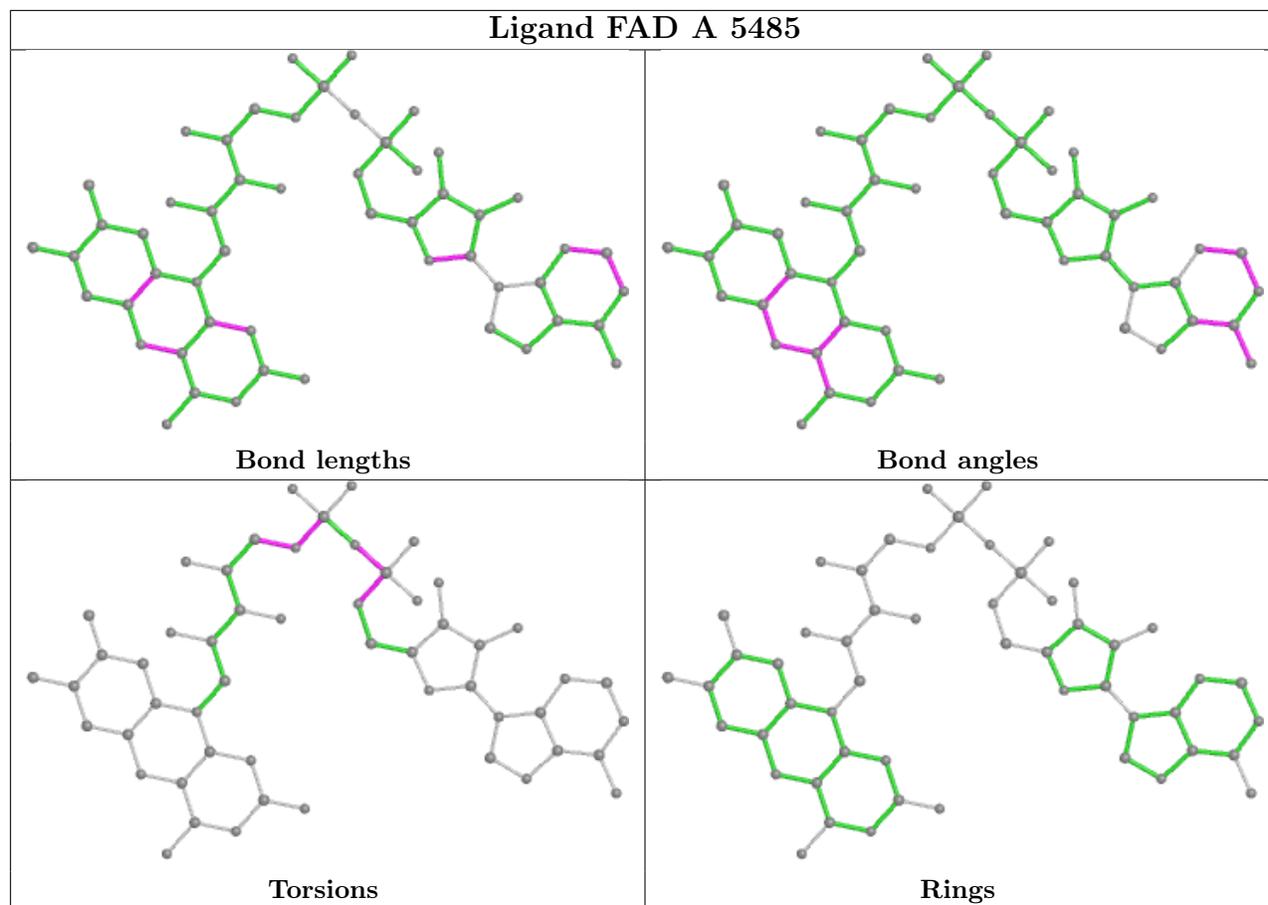
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	7485	FAD	1	0
7	B	6485	FAD	1	0
7	D	8485	FAD	1	0

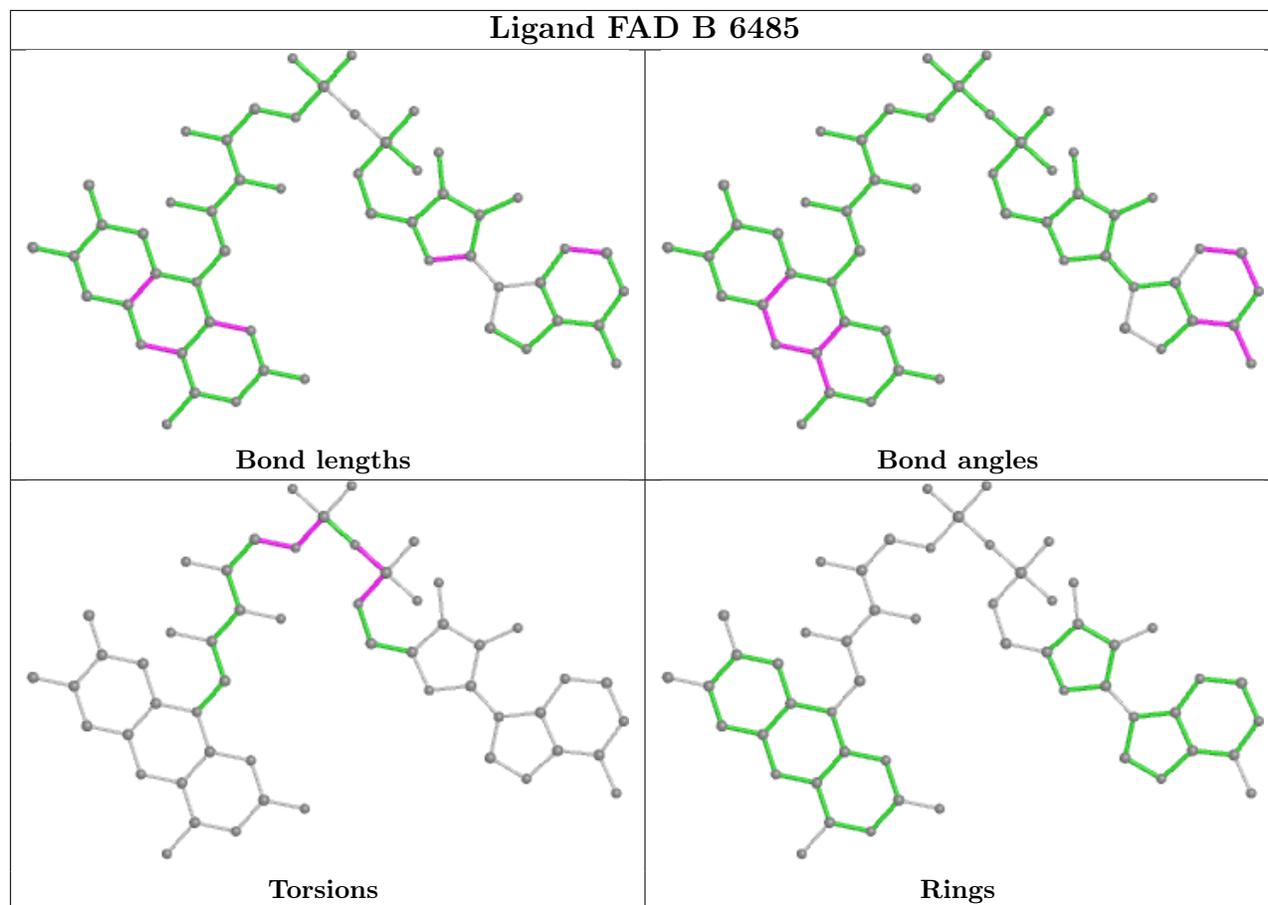
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

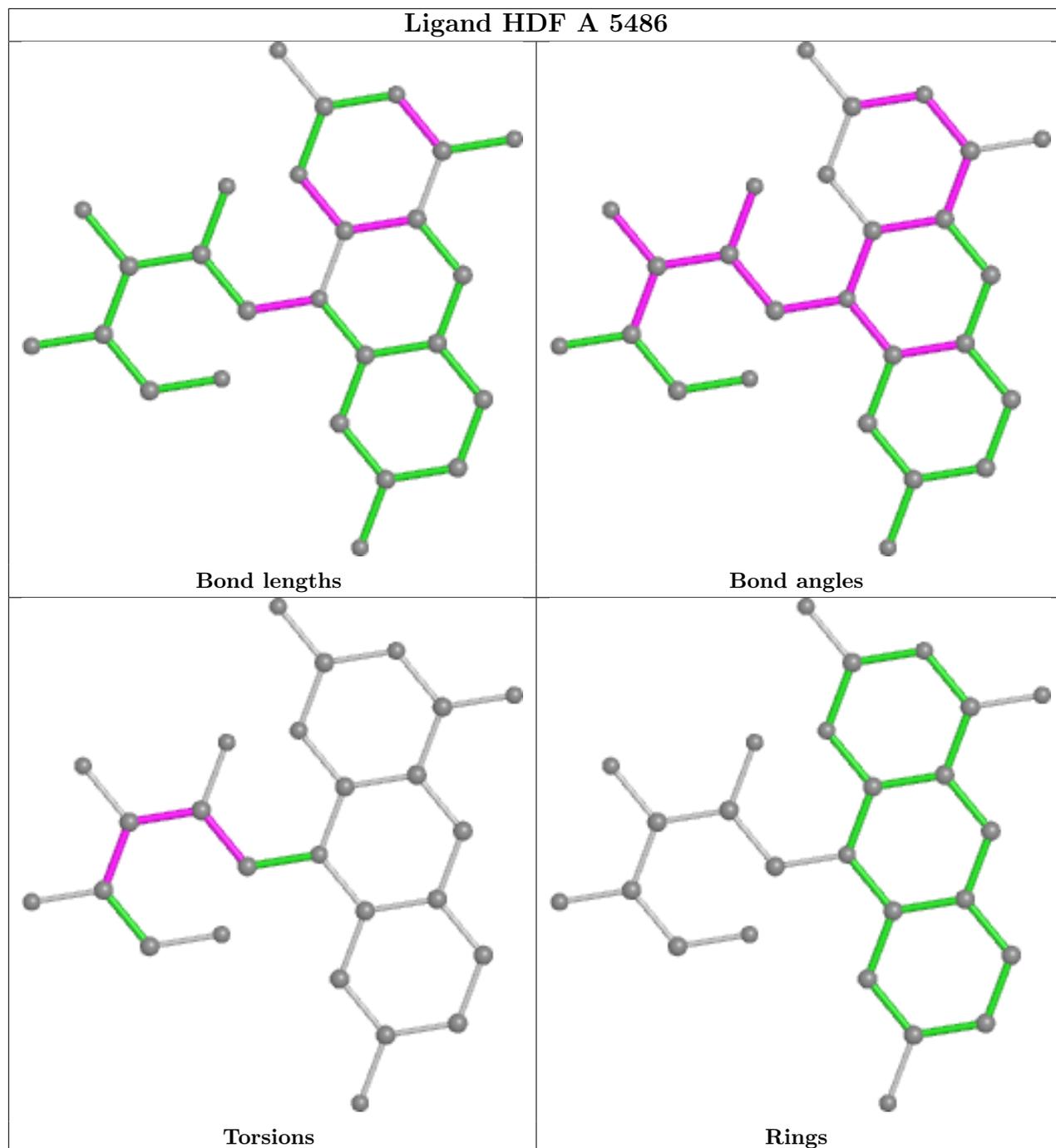
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.

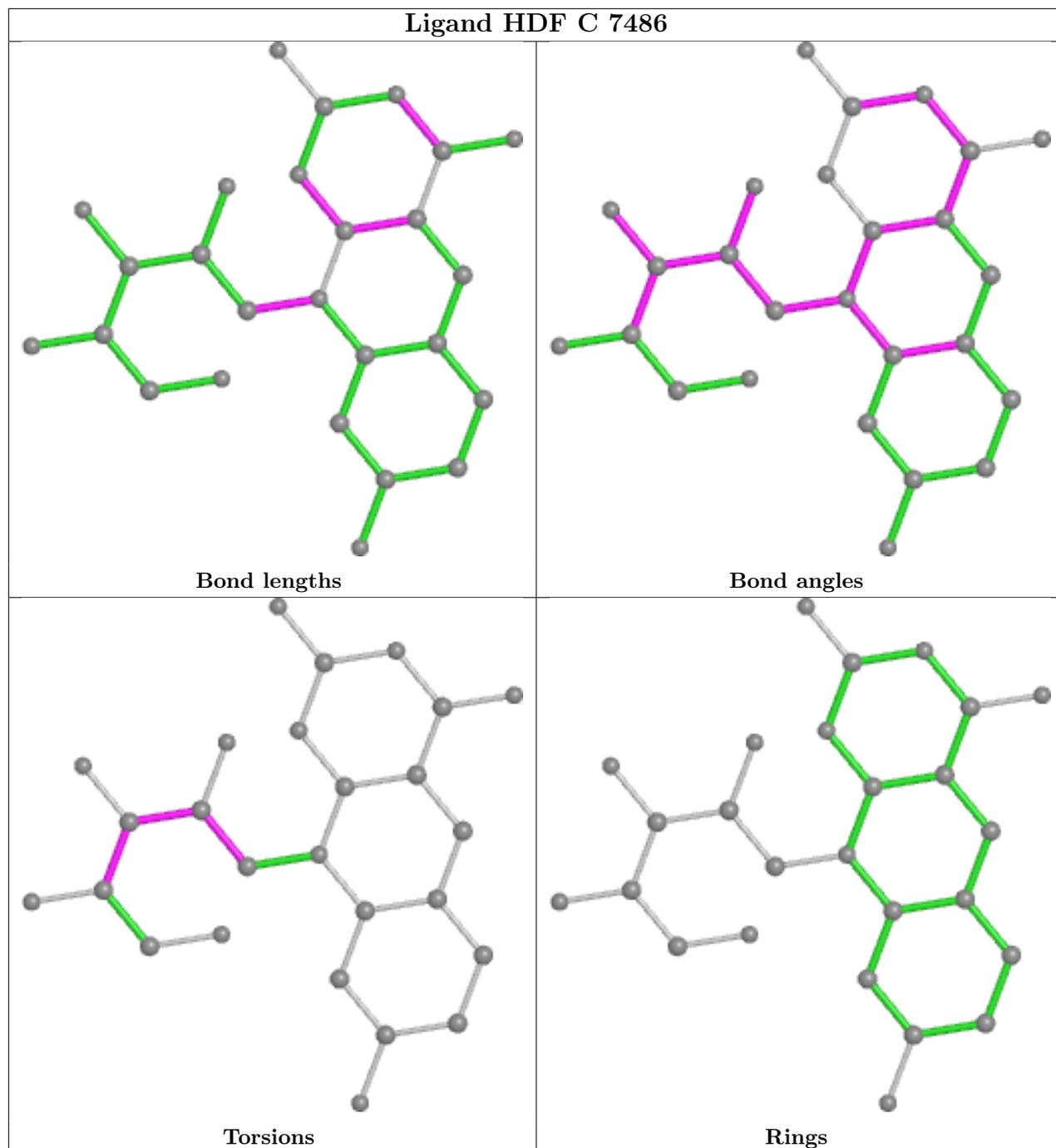


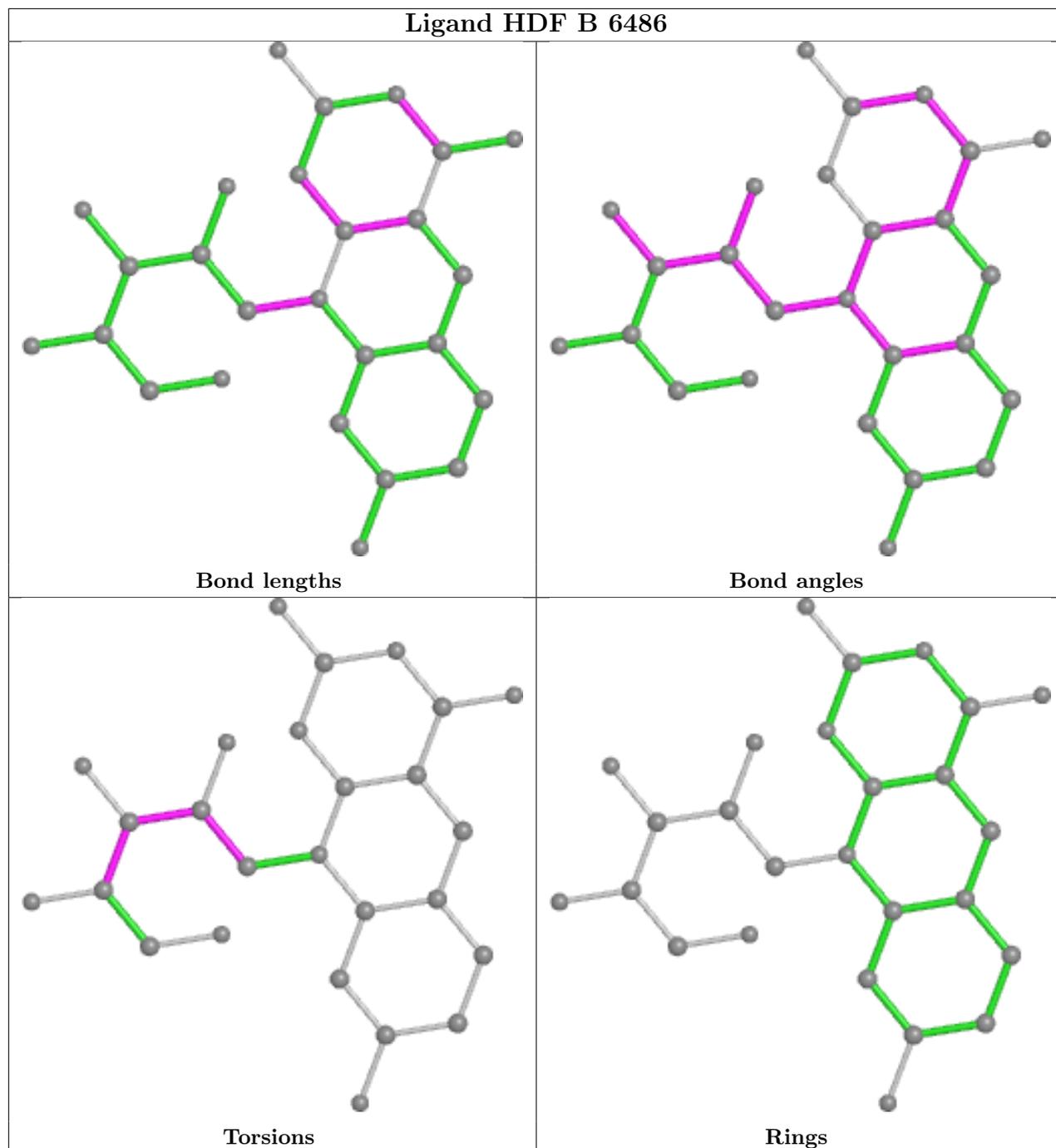


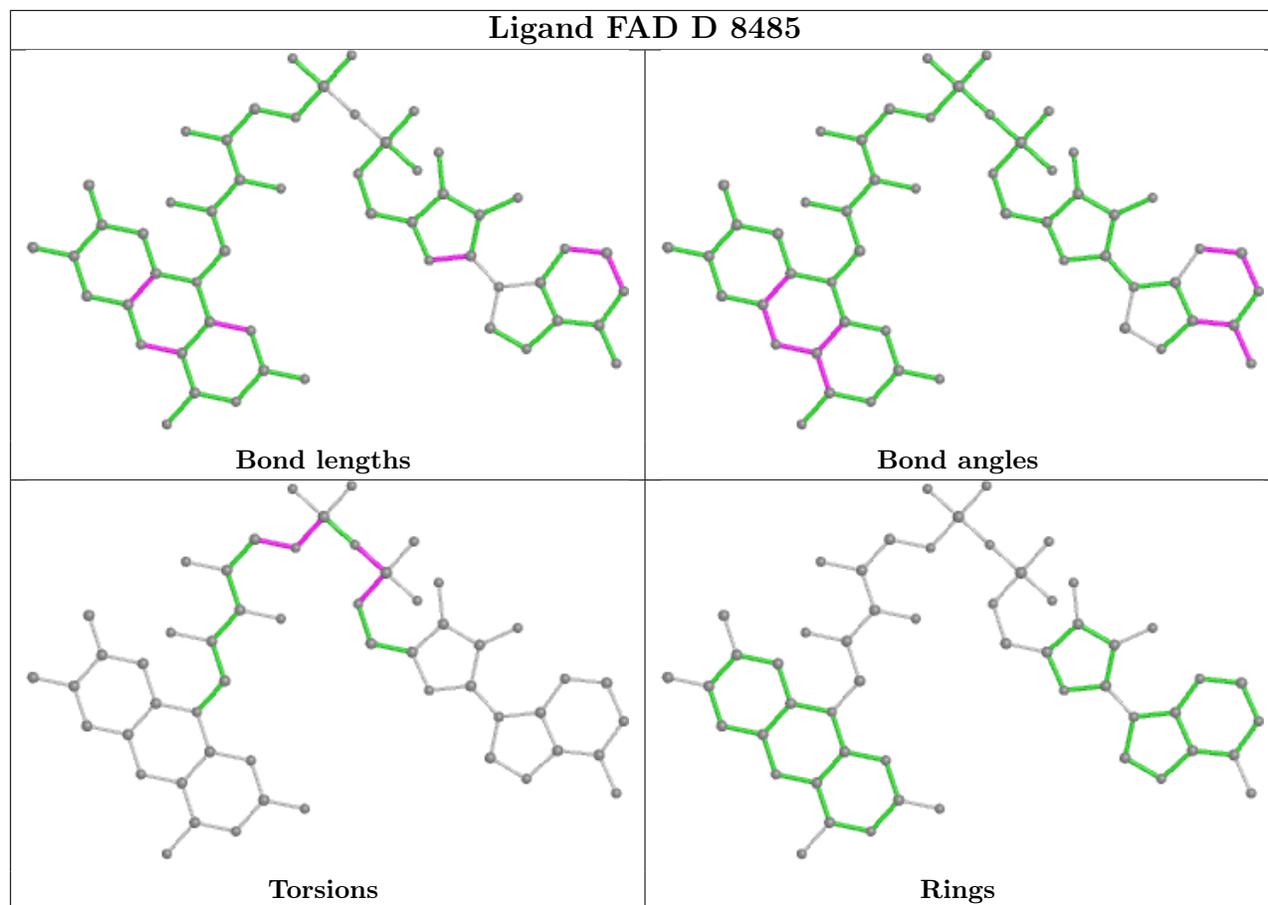












5.7 Other polymers [i](#)

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	I	10/11 (90%)	1.12	2 (20%) 1 0	41, 49, 58, 60	10 (100%)
1	K	10/11 (90%)	1.52	3 (30%) 0 0	42, 48, 60, 60	10 (100%)
2	J	9/9 (100%)	1.36	2 (22%) 0 0	37, 48, 62, 63	9 (100%)
2	L	9/9 (100%)	1.38	3 (33%) 0 0	42, 50, 62, 64	9 (100%)
3	M	4/4 (100%)	0.99	0 100 100	39, 47, 48, 51	4 (100%)
3	O	4/4 (100%)	2.30	2 (50%) 0 0	47, 52, 55, 56	4 (100%)
4	N	5/5 (100%)	5.22	5 (100%) 0 0	51, 53, 56, 59	5 (100%)
4	P	5/5 (100%)	3.23	2 (40%) 0 0	43, 47, 55, 60	5 (100%)
5	A	474/474 (100%)	0.07	16 (3%) 45 39	15, 27, 48, 63	1 (0%)
5	B	474/474 (100%)	-0.04	14 (2%) 50 44	14, 26, 47, 65	2 (0%)
5	C	474/474 (100%)	0.06	19 (4%) 38 32	14, 25, 48, 65	0
5	D	474/474 (100%)	0.07	16 (3%) 45 39	16, 27, 48, 63	2 (0%)
All	All	1952/1954 (99%)	0.09	84 (4%) 35 29	14, 27, 50, 65	61 (3%)

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	A	2	ALA	8.0
5	C	2	ALA	7.9
4	N	10	DG	7.4
4	P	10	DG	6.5
4	N	11	DC	5.9

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	TCP	K	8	18/18	0.85	0.17	33,35,39,42	18
1	TCP	I	8	18/18	0.92	0.14	32,34,37,40	18

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

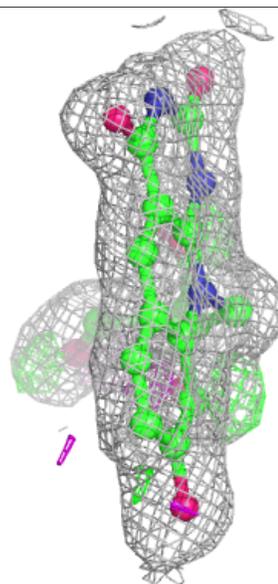
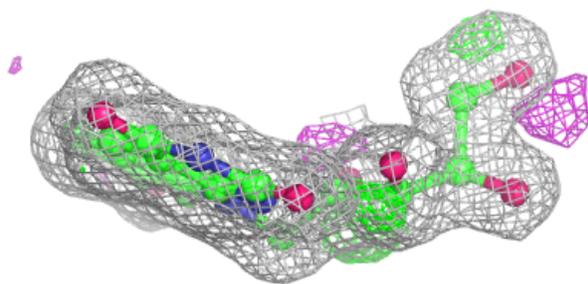
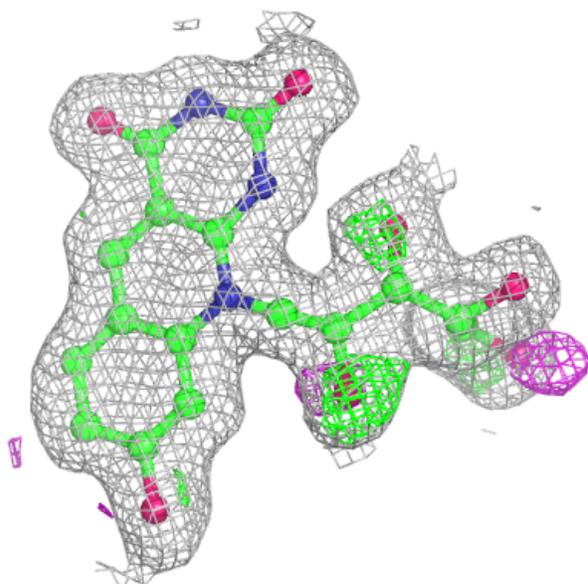
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	HDF	A	5486	26/26	0.92	0.10	13,18,25,29	0
8	HDF	D	8486	26/26	0.92	0.11	14,18,24,30	0
8	HDF	C	7486	26/26	0.93	0.10	12,16,19,23	0
8	HDF	B	6486	26/26	0.94	0.10	12,16,19,25	0
6	MG	B	9001	1/1	0.94	0.06	51,51,51,51	0
6	MG	A	9002	1/1	0.94	0.04	50,50,50,50	0
7	FAD	A	5485	53/53	0.97	0.09	13,16,18,19	0
7	FAD	B	6485	53/53	0.97	0.09	11,16,19,20	0
7	FAD	C	7485	53/53	0.97	0.09	12,16,19,19	0
7	FAD	D	8485	53/53	0.97	0.09	12,16,19,21	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.

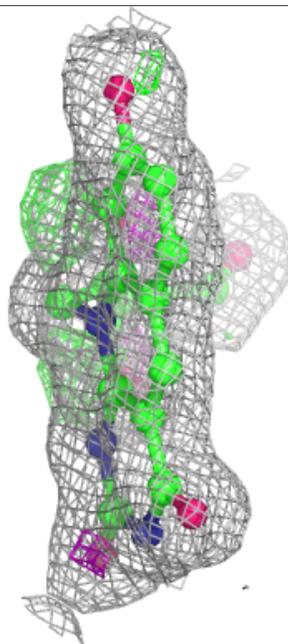
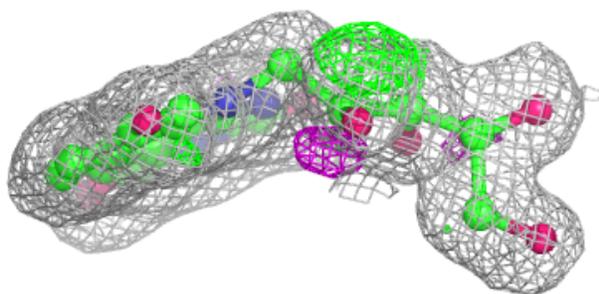
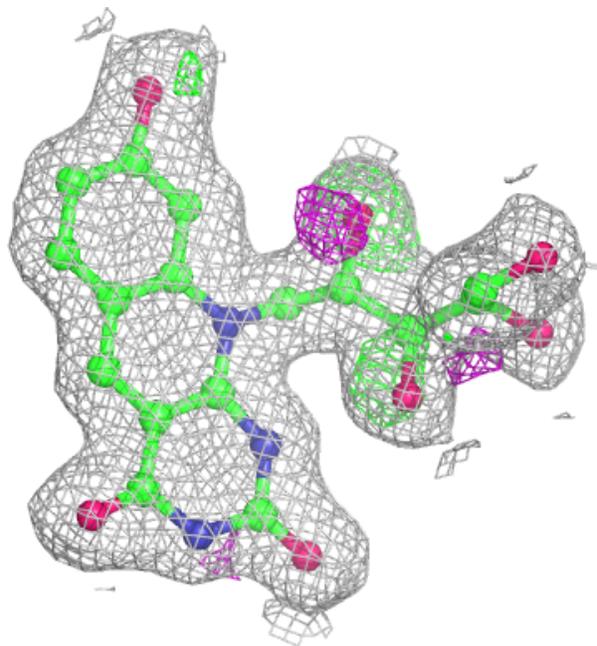
Electron density around HDF A 5486:

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



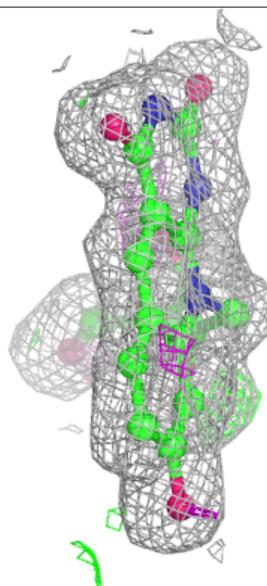
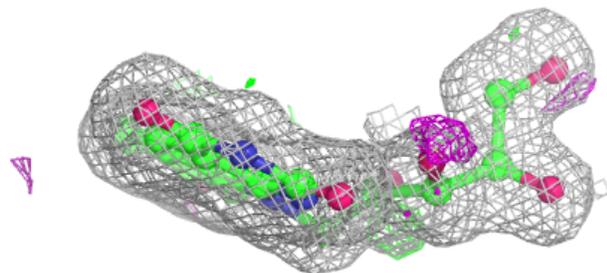
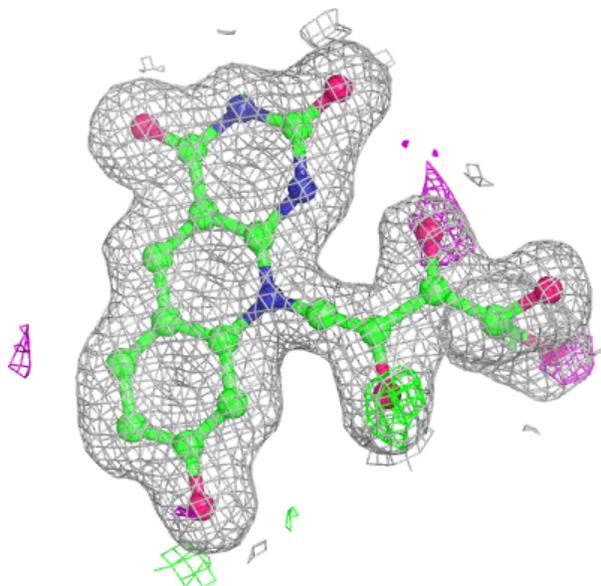
Electron density around HDF D 8486:

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



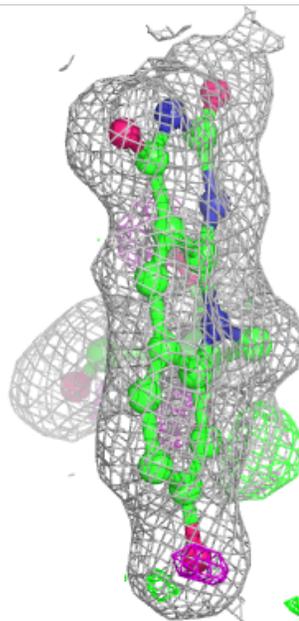
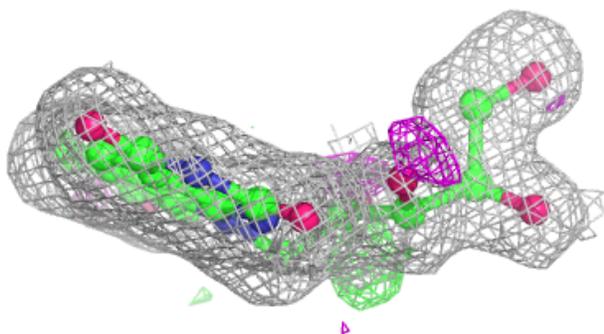
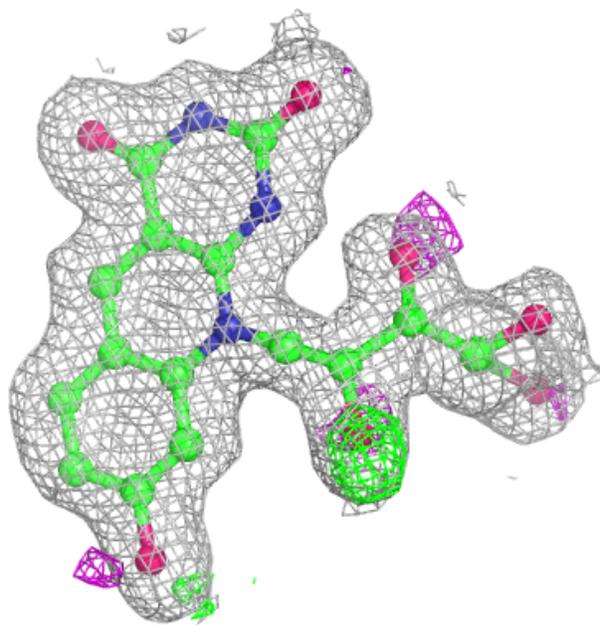
Electron density around HDF C 7486:

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



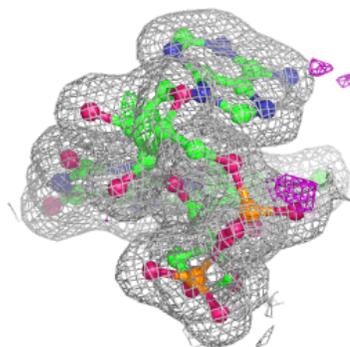
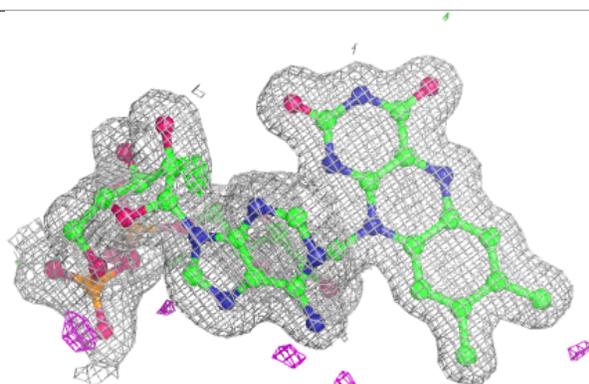
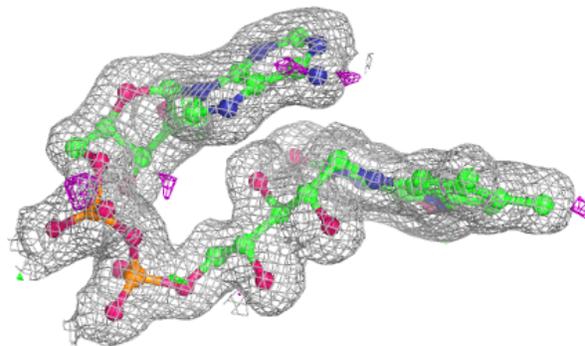
Electron density around HDF B 6486:

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

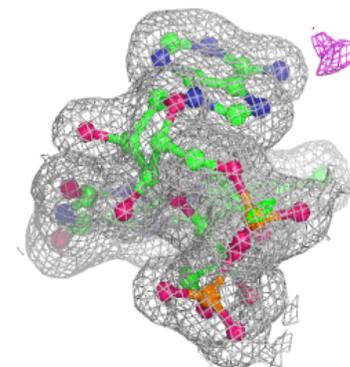
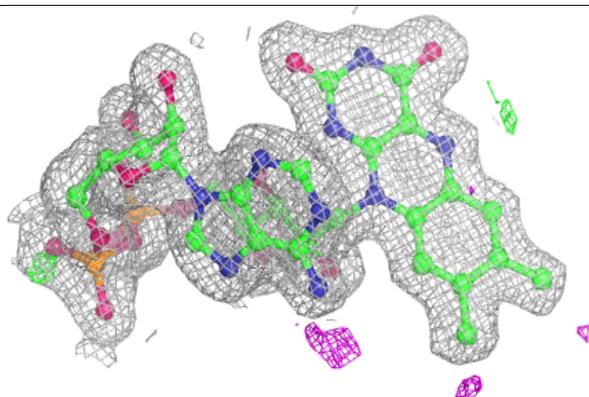
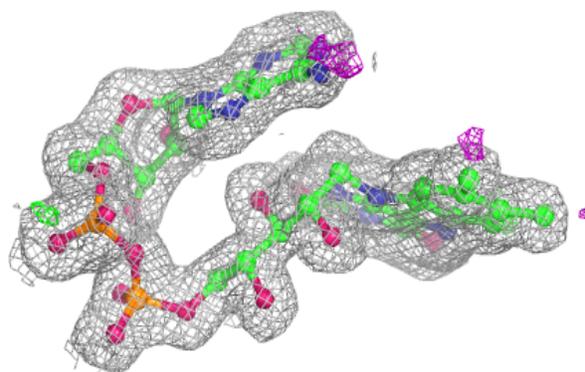


Electron density around FAD A 5485:

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

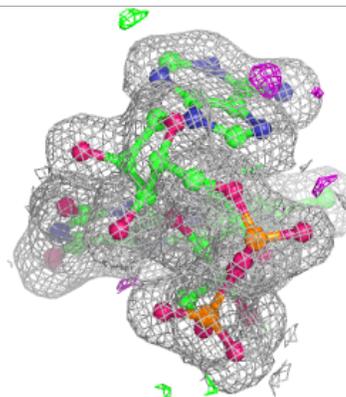
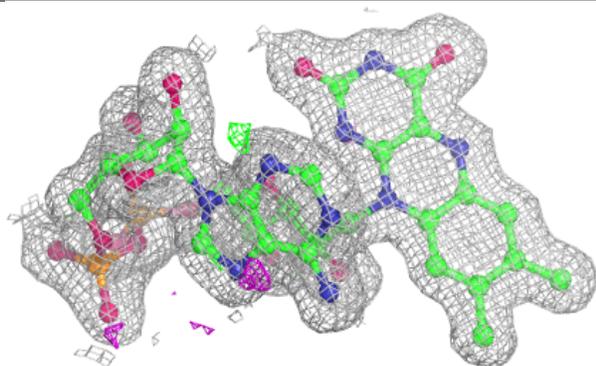
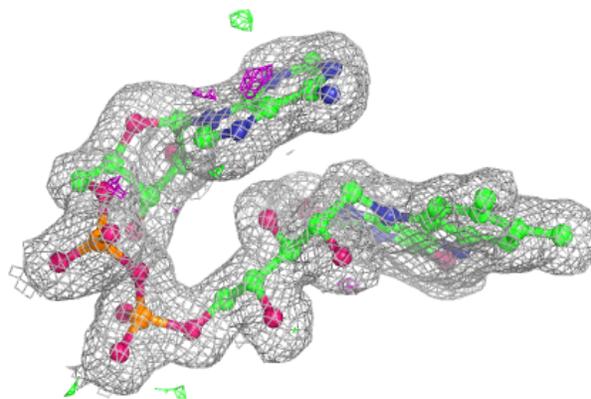
**Electron density around FAD B 6485:**

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and green (positive)

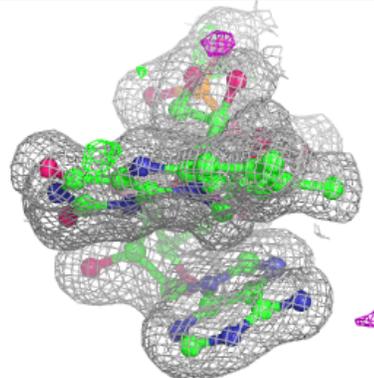
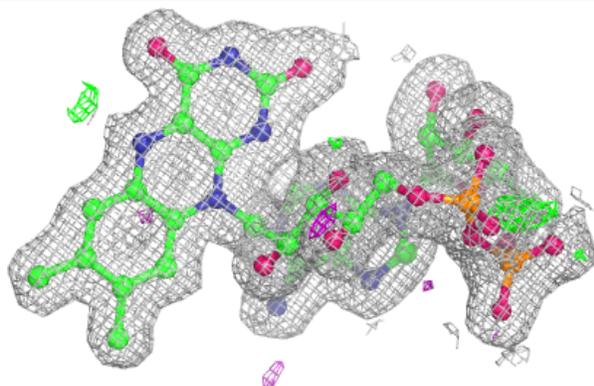
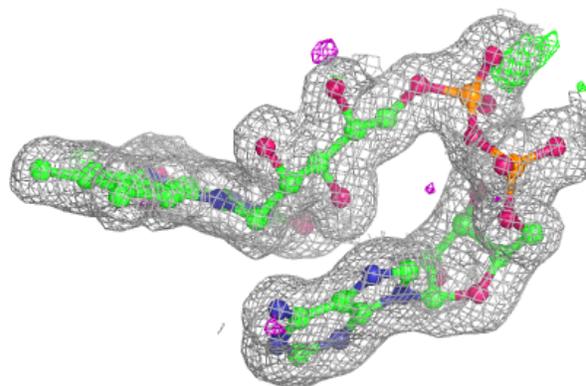


Electron density around FAD C 7485:

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

**Electron density around FAD D 8485:**

$2mF_o-DF_c$ (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.