



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 01:13 PM UTC

PDB ID : 1J9Z / pdb_00001j9z
Title : CYPOR-W677G
Authors : Hubbard, P.A.; Shen, A.L.; Paschke, R.; Kasper, C.B.; Kim, J.J.
Deposited on : 2001-05-29
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 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

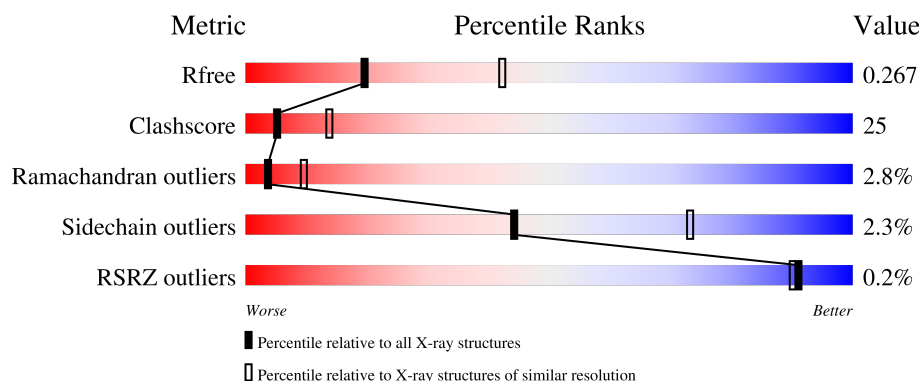
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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

Mol	Chain	Length	Quality of chain
1	A	622	 54% 42% ..
1	B	622	 52% 42% ..

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10265 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.

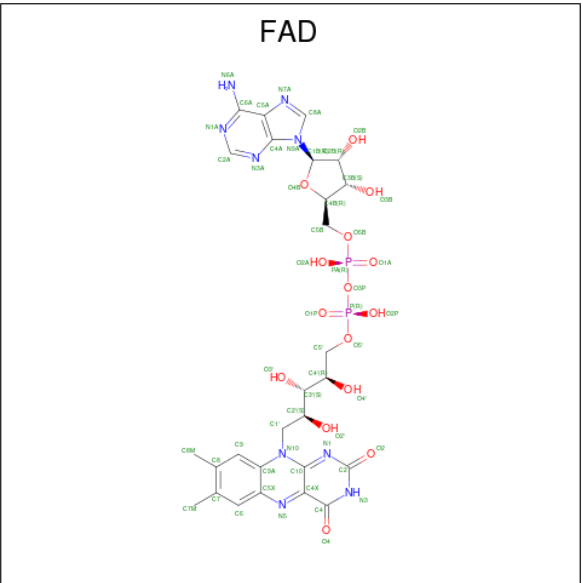
- Molecule 1 is a protein called NADPH-Cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	0	0
			4901	3099	844	935	23			
1	B	611	Total	C	N	O	S	0	0	0
			4890	3092	842	933	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	677	GLY	TRP	engineered mutation	UNP P00388
B	677	GLY	TRP	engineered mutation	UNP P00388

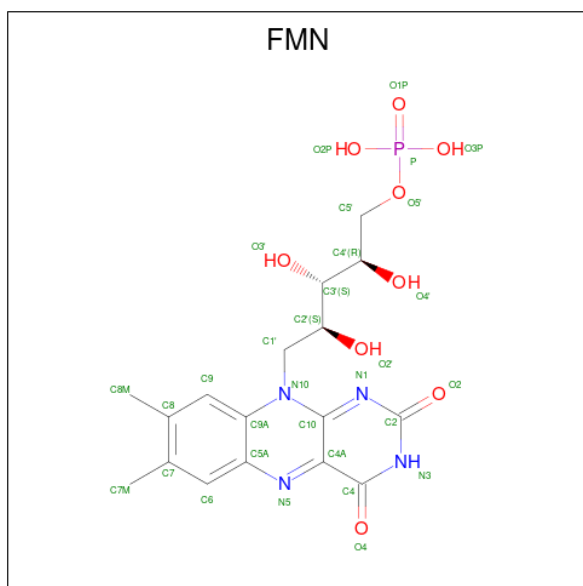
- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Continued from previous page...

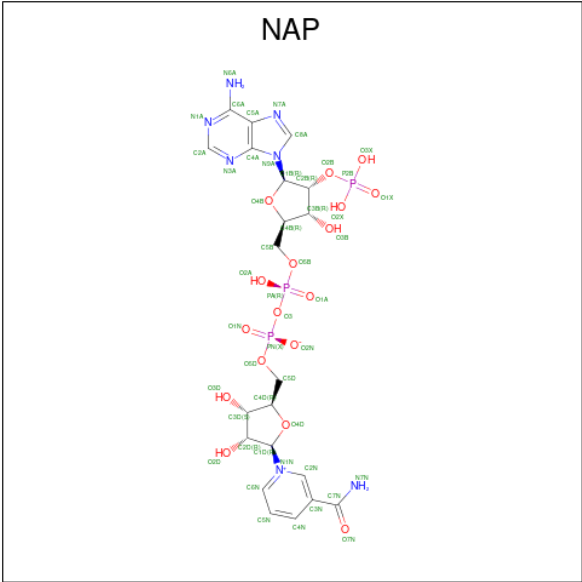
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

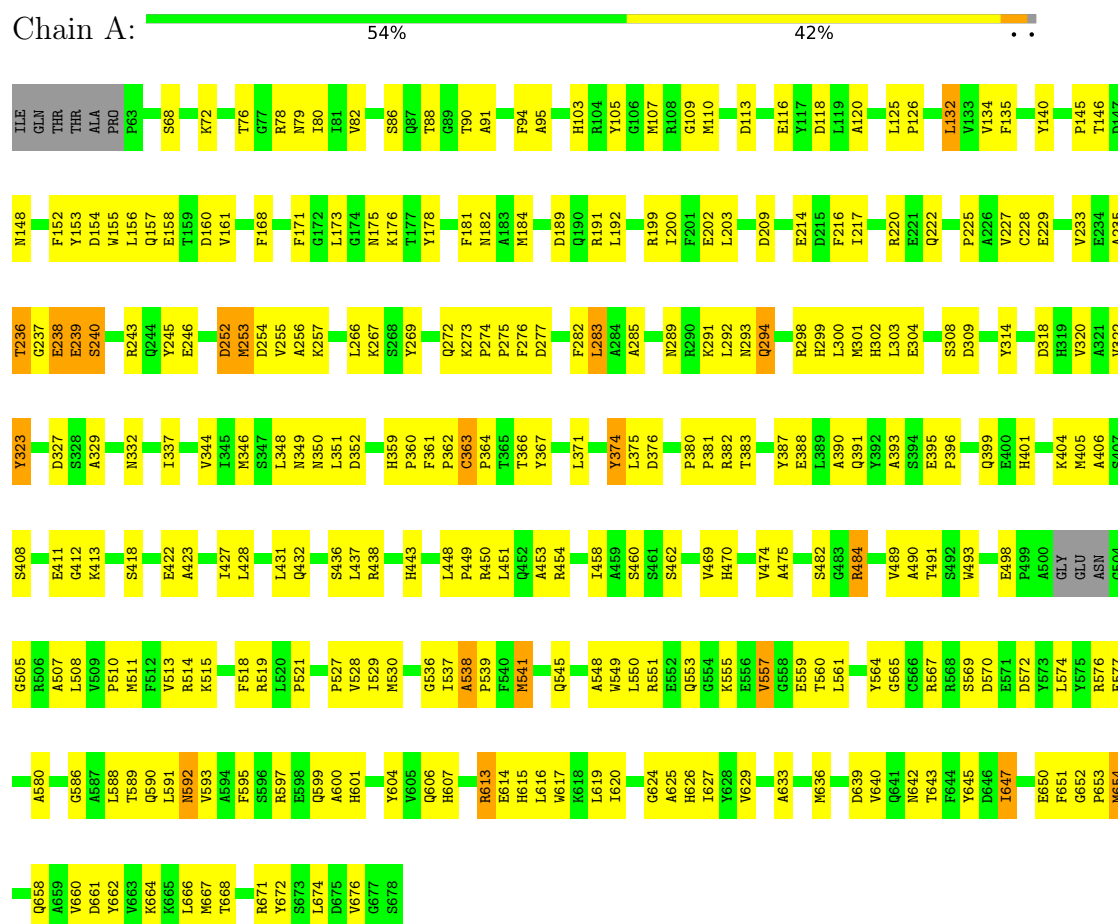
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	109	Total	O	0	0
			109	109		
5	B	101	Total	O	0	0
			101	101		

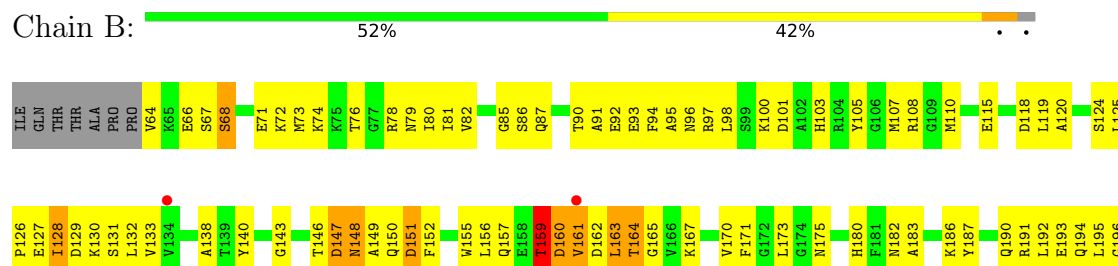
3 Residue-property plots

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

• Molecule 1: NADPH-Cytochrome P450 reductase



• Molecule 1: NADPH-Cytochrome P450 reductase



V648	A649	E650	F651	G652	P653	M654	E655	H656	A659	V660	K664	K665	K669	G670	R671	L674	D675	V676	G677	S678																														
G554	K555	E556	E559	L562	Y563	Y564	R568	S569	D570	E571	L574	Y575	Q590	L591	N592	V593	Q599	A600	Y604	V605	Q606	R613	B614	H615	L616	W617	K618	L619	I620	G624	A625	H626	V629	G630	G631	D632	A633	R634	M635	M636	A637	K638								
S460	H470	I471	C472	A473	V474	A475	E479	A480	K481	S482	G483	R484	G488	T491	S492	W493	A500	GLY	GLU	ASN	GLY	G505	R506	A507	L508	F512	V513	R514	F518	R519	S524	T525	T526	P527	V528	P533	A538	W541	E546	R547	A548	W549	L550	R551	E552	Q553				
Y374	L375	D376	N379	N384	V385	L386	Y387	E388	L389	A390	Q391	Y392	A393	S394	E395	E398	Q399	E400	H401	W405	A406	S409	K413	Y416	L417	S418	W419	W420	W421	E422	A423	L428	L431	Q432	S436	I437	R438	P439	P440	I441	D442	P449	A453	R454	Y455	Y456				
P274	P275	F276	F282	N289	R290	K291	L292	N293	N294	E297	R298	H299	M301	H302	L303	E304	S310	K311	I312	R313	A321	V322	Y323	P324	A329	N332	Q333	I334	I337	L338	D341	V344	I345	M346	N349	N350	L351	D352	E353	H359	P360	F361	P362	C363	P364	T365				
I200	F201	E202	L203	G204	L205	G206	D207	D208	D209	G210	N211	L212	E213	E214	I217	Q222	P225	F230	F231	G232	V233	E234	A235	T236	G237	E238	E239	S240	S241	I242	Y245	E246	L247	V248	V249	H250	E251	D252	M253	D254	V255	A256	K257	V258	Y259	T260	G261	E262	K267	E270

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	101.63Å 116.06Å 118.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 30.00 – 2.71	Depositor EDS
% Data completeness (in resolution range)	79.6 (30.00-2.70) 79.5 (30.00-2.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.72Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.188 , 0.270 0.187 , 0.267	Depositor DCC
R_{free} test set	1535 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.034 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10265	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.35% 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, FAD, NAP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/5016	0.92	15/6784 (0.2%)
1	B	0.43	0/5004	0.92	15/6768 (0.2%)
All	All	0.45	0/10020	0.92	30/13552 (0.2%)

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	B	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	163	LEU	N-CA-C	7.08	117.59	108.24
1	B	479	GLU	N-CA-C	-7.08	99.34	109.96
1	B	297	GLU	N-CA-C	-7.05	102.79	111.33
1	B	553	GLN	N-CA-C	-6.52	105.31	113.20
1	A	363	CYS	N-CA-C	6.25	113.85	108.22

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	456	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4901	0	4748	238	0
1	B	4890	0	4737	247	0
2	A	53	0	31	0	0
2	B	53	0	31	1	0
3	A	31	0	19	4	0
3	B	31	0	19	1	0
4	A	48	0	25	0	0
4	B	48	0	25	3	0
5	A	109	0	0	6	0
5	B	101	0	0	2	0
All	All	10265	0	9635	483	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 25.

The worst 5 of 483 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:SER:HB2	1:B:91:ALA:HB3	1.30	1.14
1:B:527:PRO:HB2	1:B:625:ALA:HB2	1.33	1.09
1:B:78:ARG:HH22	1:B:352:ASP:HB2	1.26	1.00
1:B:107:MET:HE2	1:B:233:VAL:HG11	1.46	0.97
1:B:163:LEU:HB2	1:B:196:GLY:HA3	1.44	0.96

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	609/622 (98%)	536 (88%)	61 (10%)	12 (2%)	6	16
1	B	607/622 (98%)	516 (85%)	69 (11%)	22 (4%)	2	6
All	All	1216/1244 (98%)	1052 (86%)	130 (11%)	34 (3%)	4	9

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	GLU
1	B	159	THR
1	B	160	ASP
1	B	202	GLU
1	B	234	GLU

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	523/530 (99%)	510 (98%)	13 (2%)	42	71
1	B	522/530 (98%)	511 (98%)	11 (2%)	47	75
All	All	1045/1060 (99%)	1021 (98%)	24 (2%)	44	73

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	128	ILE
1	B	260	THR
1	B	242	ILE
1	B	262	GLU
1	A	283	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	182	ASN
1	B	349	ASN
1	B	271	ASN
1	B	302	HIS
1	B	467	ASN

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](#)

6 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	FMN	A	751	-	33,33,33	2.21	12 (36%)	48,50,50	1.53	8 (16%)
2	FAD	B	850	-	58,58,58	2.65	21 (36%)	85,89,89	1.37	12 (14%)
3	FMN	B	851	-	33,33,33	2.45	12 (36%)	48,50,50	1.69	10 (20%)
4	NAP	A	752	-	50,52,52	4.16	21 (42%)	71,80,80	1.47	12 (16%)
4	NAP	B	852	-	50,52,52	4.15	18 (36%)	71,80,80	1.47	12 (16%)
2	FAD	A	750	-	58,58,58	2.64	23 (39%)	85,89,89	1.36	12 (14%)

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	FMN	A	751	-	-	0/18/18/18	0/3/3/3
2	FAD	B	850	-	-	2/34/50/50	0/6/6/6
3	FMN	B	851	-	-	0/18/18/18	0/3/3/3
4	NAP	A	752	-	-	5/35/67/67	0/5/5/5
4	NAP	B	852	-	-	9/35/67/67	0/5/5/5
2	FAD	A	750	-	-	3/34/50/50	0/6/6/6

The worst 5 of 107 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	752	NAP	C2N-N1N	15.61	1.52	1.35
4	B	852	NAP	C2N-N1N	15.38	1.51	1.35
4	B	852	NAP	C4N-C3N	11.94	1.57	1.39
4	A	752	NAP	C4N-C3N	11.35	1.56	1.39
4	B	852	NAP	PN-O3	-9.10	1.49	1.59

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	851	FMN	C9A-C5A-N5	4.39	127.11	122.45
2	A	750	FAD	C4'-C3'-C2'	4.38	120.85	113.57
2	B	850	FAD	C5X-C9A-N10	-3.94	114.41	117.97
3	A	751	FMN	C9A-C5A-N5	3.82	126.51	122.45
3	B	851	FMN	C4'-C3'-C2'	-3.80	107.25	113.57

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

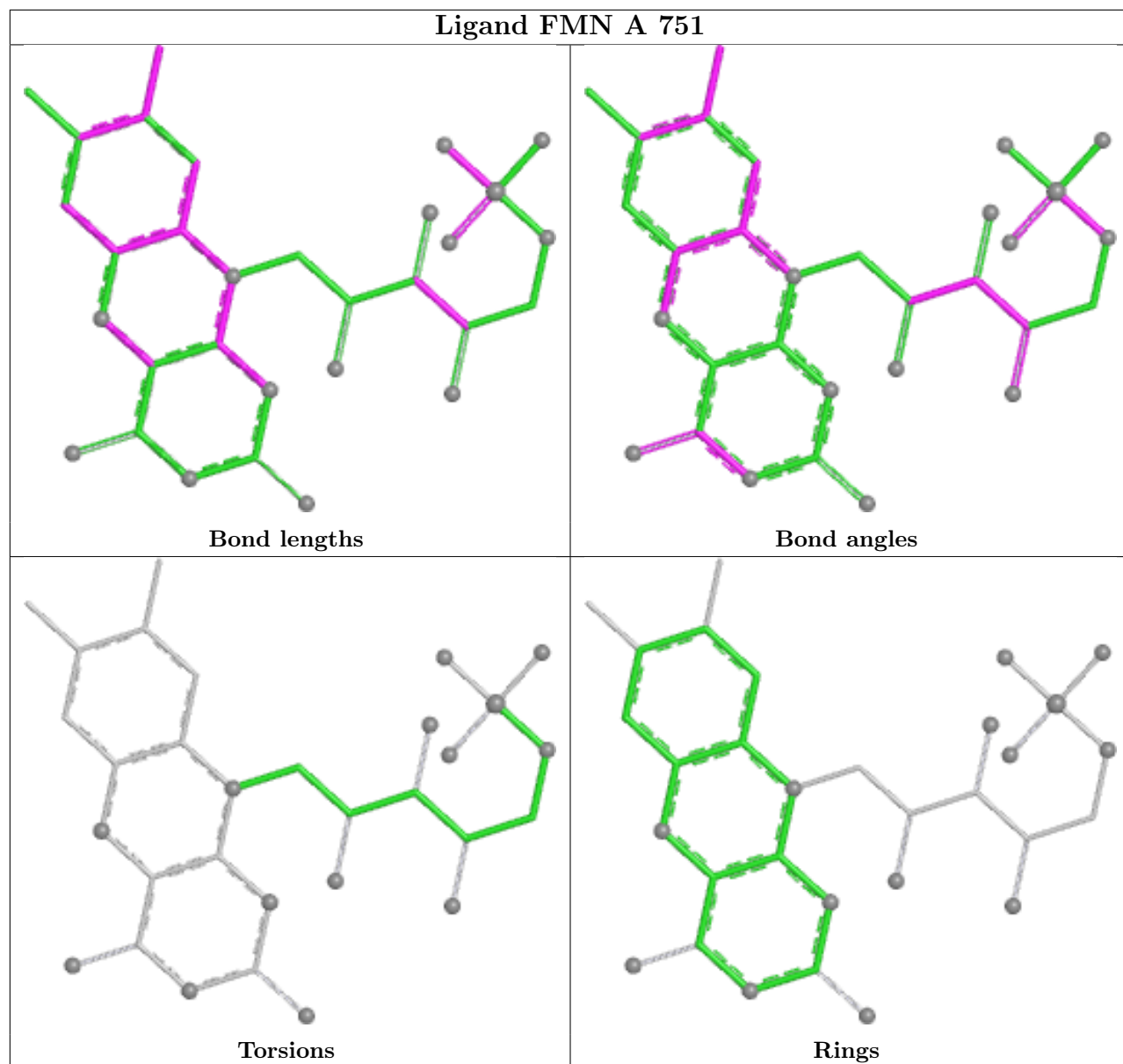
Mol	Chain	Res	Type	Atoms
4	B	852	NAP	O4D-C1D-N1N-C6N
4	A	752	NAP	O4D-C4D-C5D-O5D
4	B	852	NAP	C2B-C1B-N9A-C8A
4	B	852	NAP	O4D-C4D-C5D-O5D
4	A	752	NAP	C3D-C4D-C5D-O5D

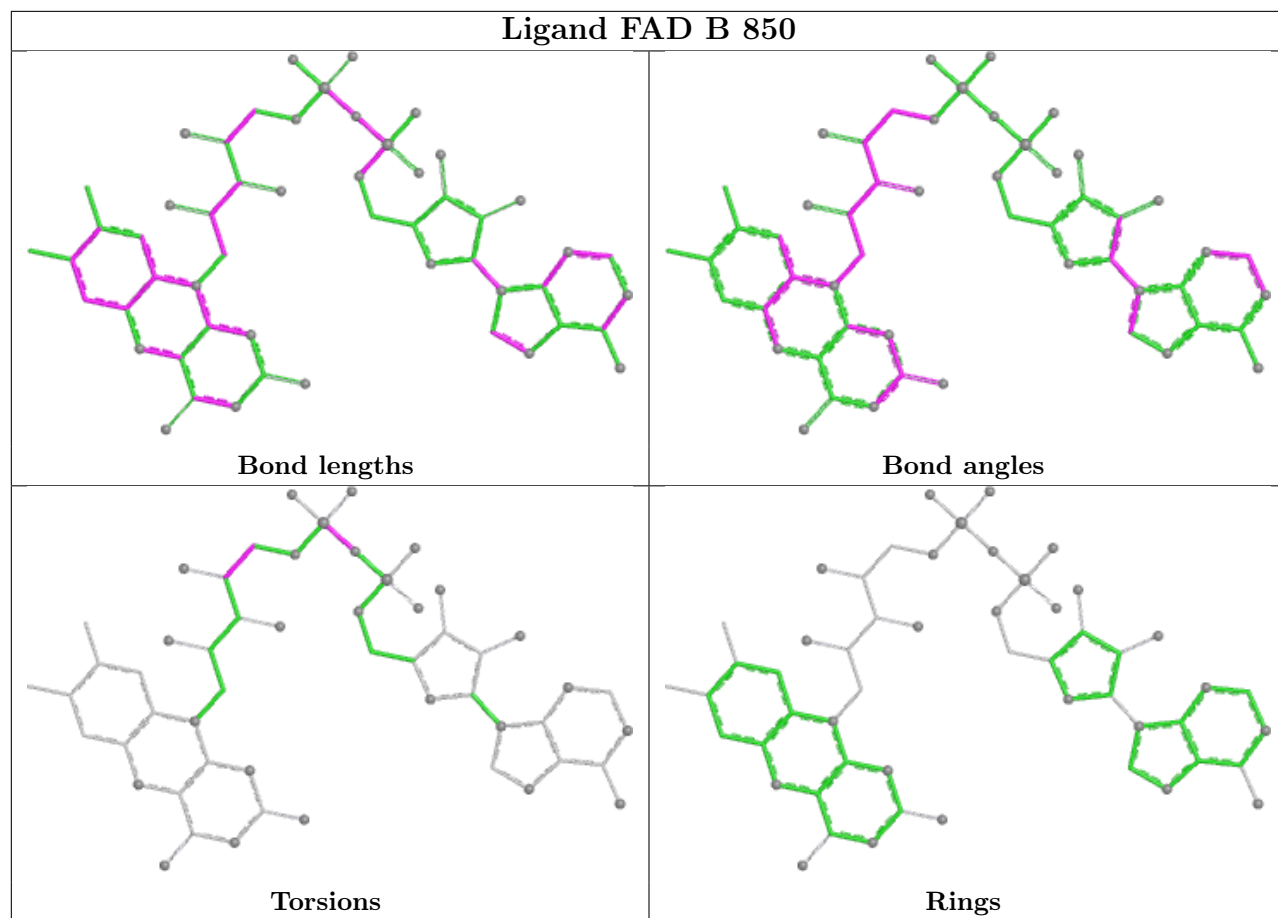
There are no ring outliers.

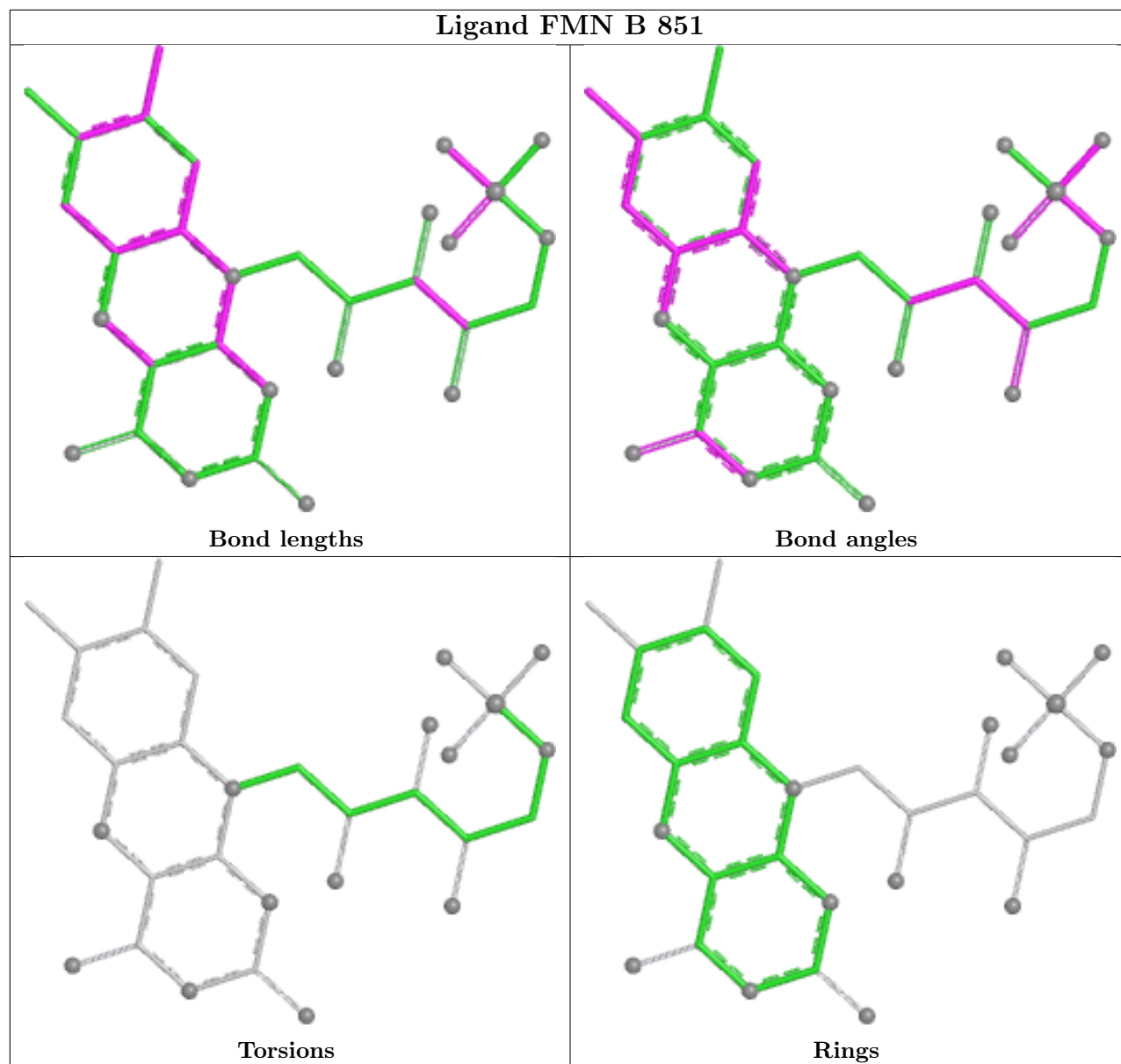
4 monomers are involved in 9 short contacts:

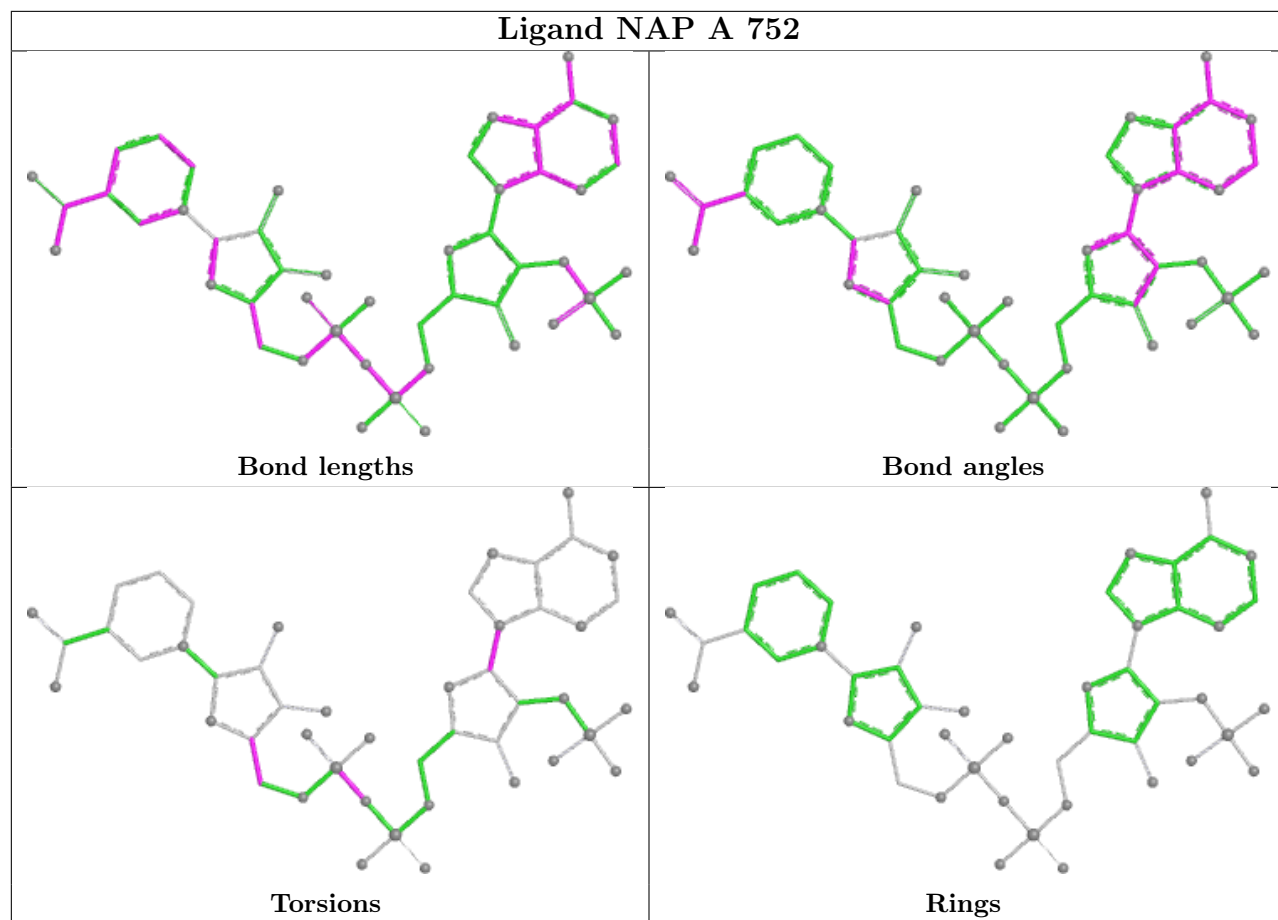
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	751	FMN	4	0
2	B	850	FAD	1	0
3	B	851	FMN	1	0
4	B	852	NAP	3	0

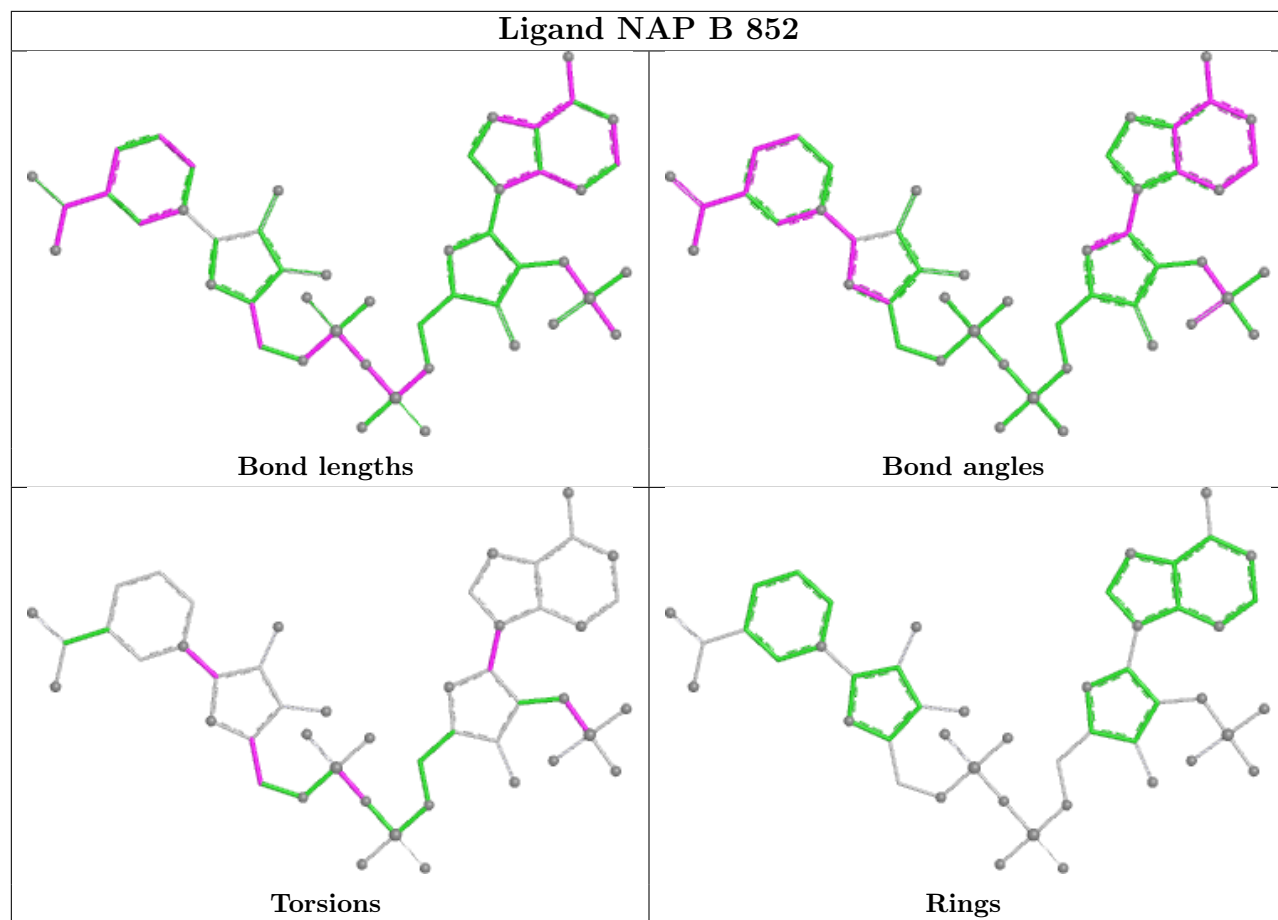
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

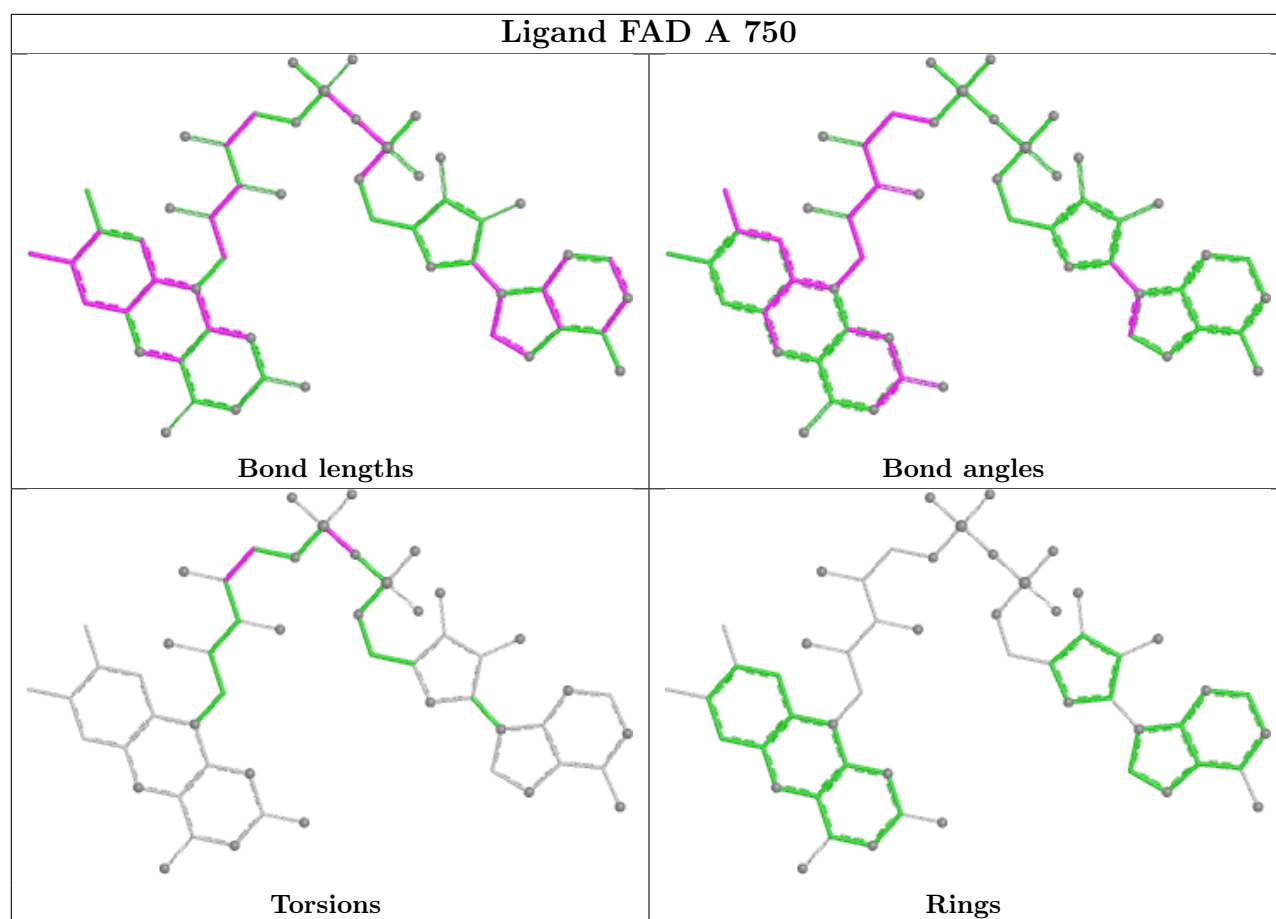












5.7 Other polymers [i](#)

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	A	613/622 (98%)	-0.66	0	100 100	16, 36, 57, 87	0
1	B	611/622 (98%)	-0.34	2 (0%)	90 89	16, 44, 92, 107	0
All	All	1224/1244 (98%)	-0.50	2 (0%)	91 90	16, 38, 85, 107	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	134	VAL	2.3
1	B	161	VAL	2.0

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(Å ²)	Q < 0.9
3	FMN	B	851	31/31	0.90	0.10	75,91,94,94	0
3	FMN	A	751	31/31	0.95	0.07	37,55,58,58	0
4	NAP	A	752	48/48	0.96	0.08	26,40,70,74	0

Continued on next page...

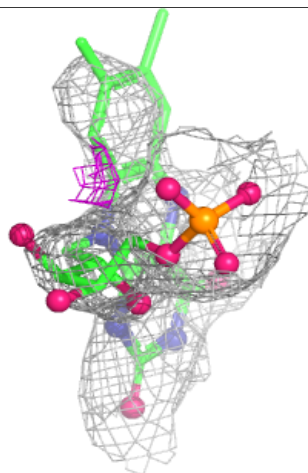
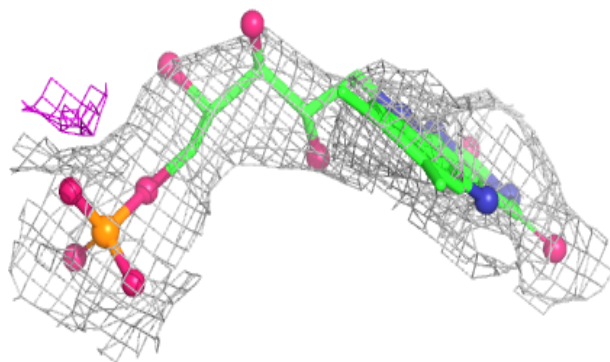
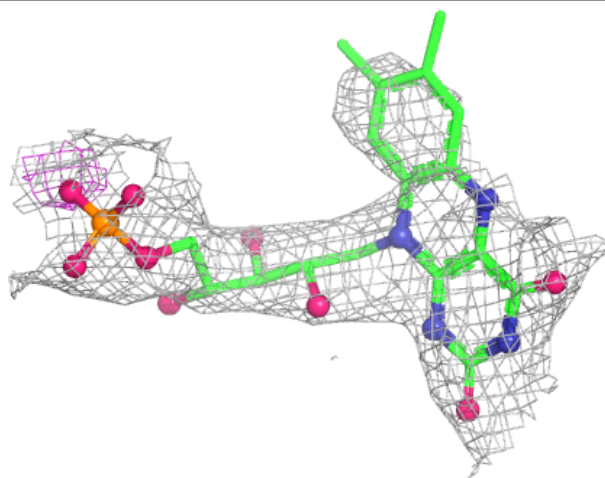
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAP	B	852	48/48	0.96	0.08	26,34,72,74	0
2	FAD	A	750	53/53	0.97	0.06	24,30,35,35	0
2	FAD	B	850	53/53	0.97	0.07	16,21,24,27	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.

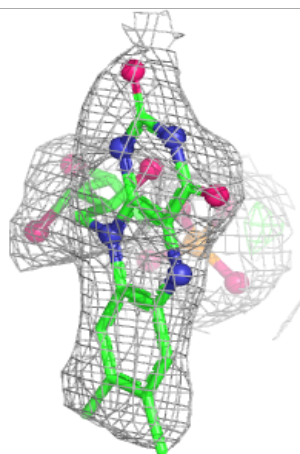
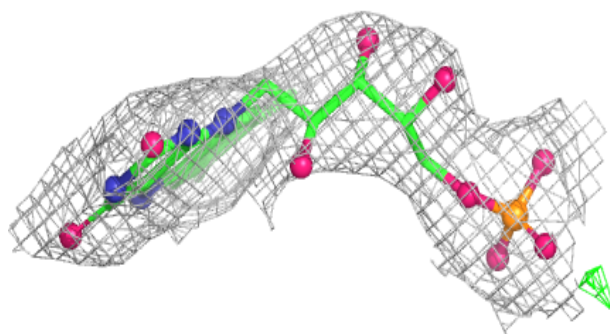
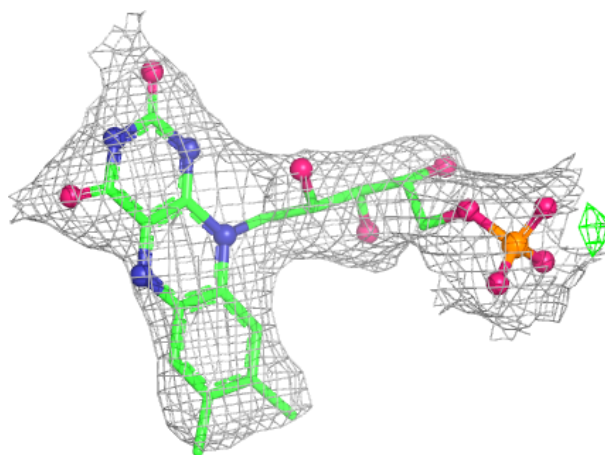
Electron density around FMN B 851:

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



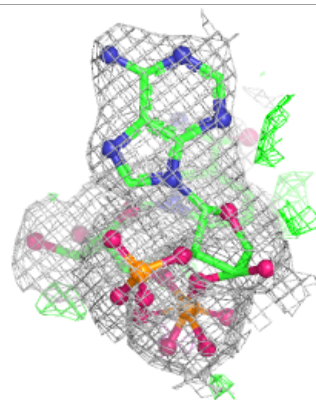
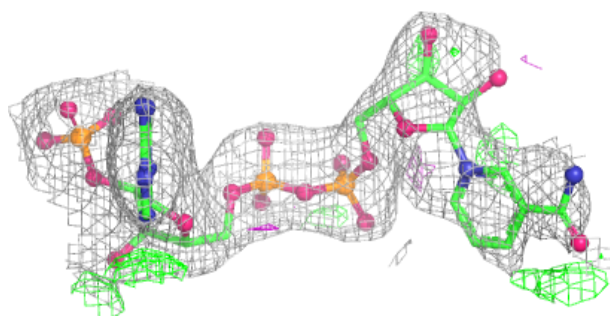
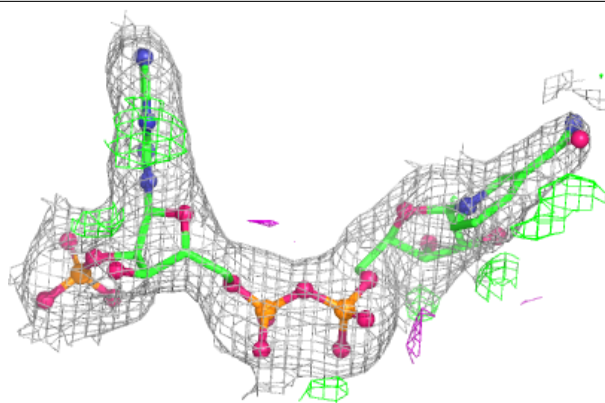
Electron density around FMN A 751:

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

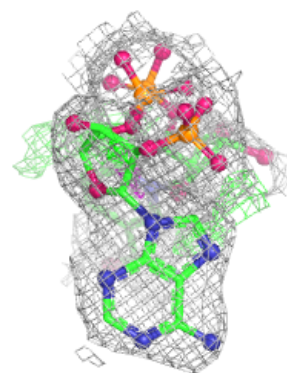
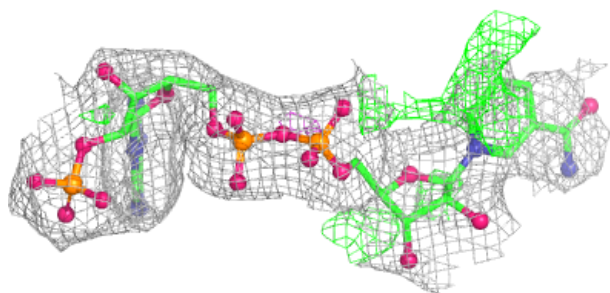
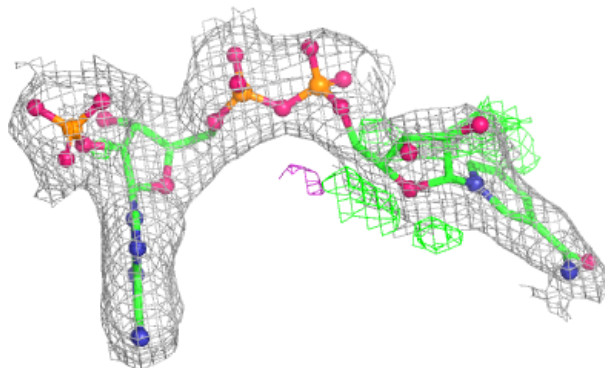


Electron density around NAP A 752:

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

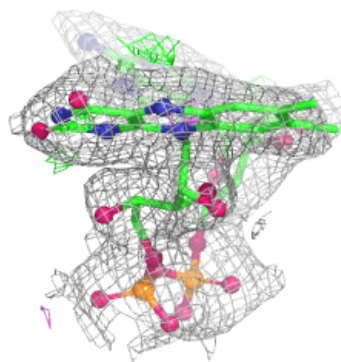
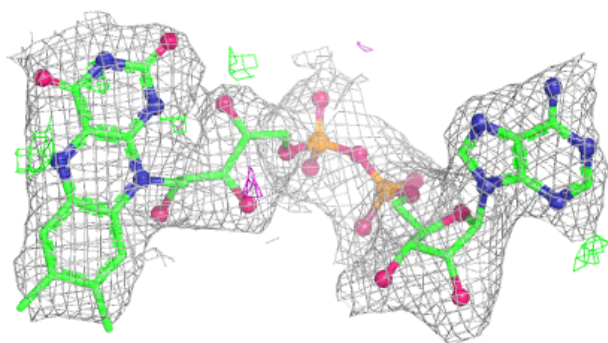
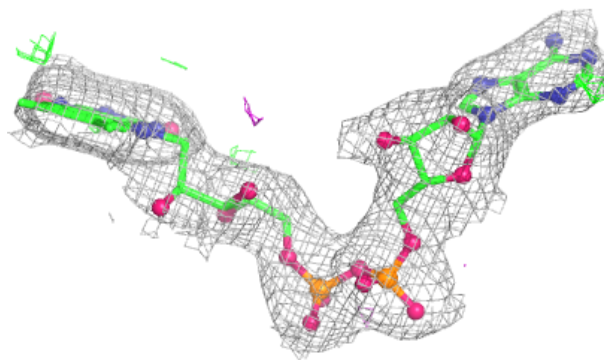
**Electron density around NAP B 852:**

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

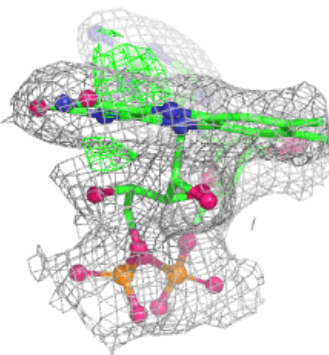
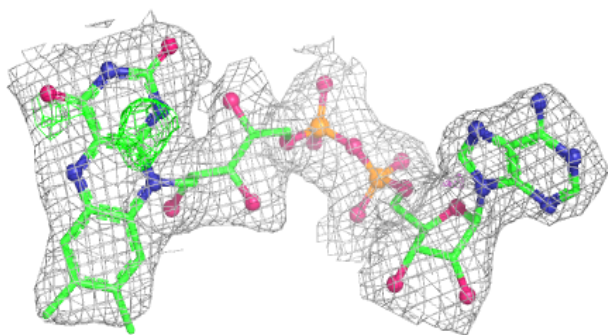
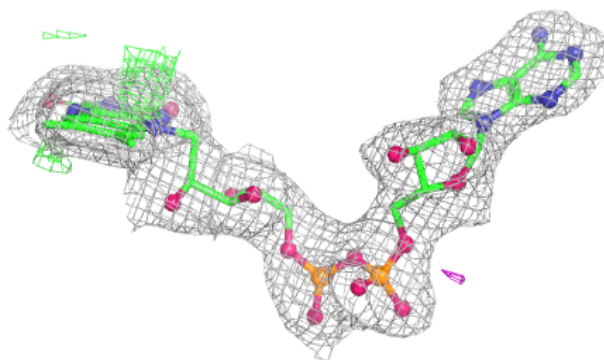


Electron density around FAD A 750:

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

**Electron density around FAD B 850:**

$2mF_o-DF_c$ (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.