



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 09:33 AM BST

PDB ID : 6QKX  
Title : 2-Naphthoyl-CoA Reductase-DiHydroNaphthoyl-CoA complex(NCR-DHNCOA co-crystallized complex)  
Authors : Kayastha, K.; Ermler, U.  
Deposited on : 2019-01-30  
Resolution : 2.40 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](mailto: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.

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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)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

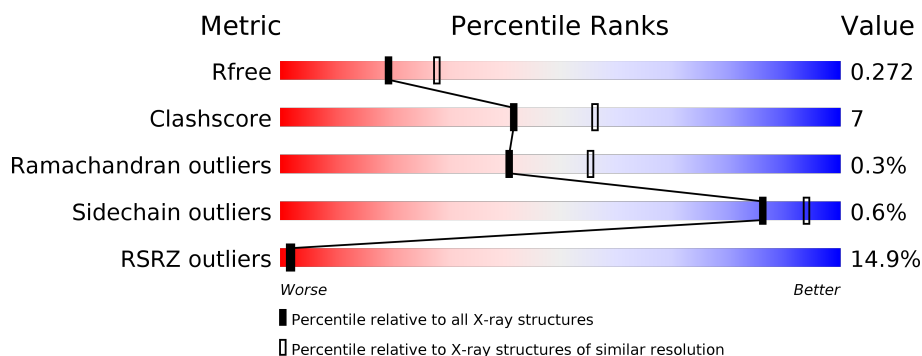
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	714	<div> <div>14%</div> <div>77%</div> <div>15%</div> <div>8%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5243 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 NCR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	660	Total	C	N	O	S	5	0	0
			5064	3198	878	951	37			

There are 44 discrepancies between the modelled and reference sequences:

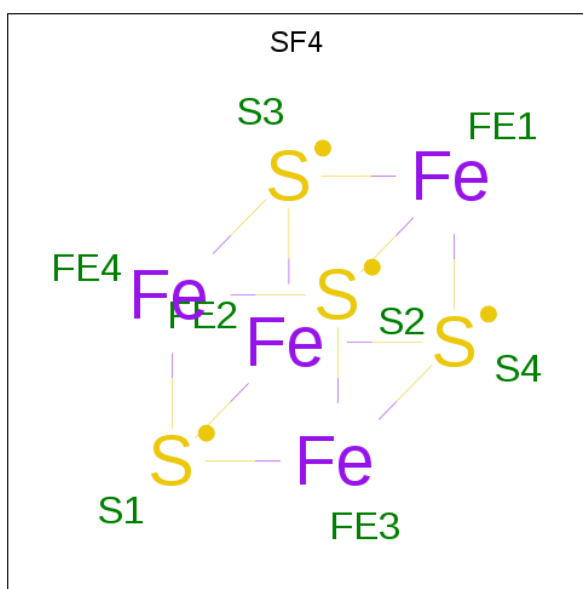
Chain	Residue	Modelled	Actual	Comment	Reference
A	671	ARG	-	expression tag	UNP E1YD54
A	672	GLY	-	expression tag	UNP E1YD54
A	673	SER	-	expression tag	UNP E1YD54
A	674	LEU	-	expression tag	UNP E1YD54
A	675	GLU	-	expression tag	UNP E1YD54
A	676	VAL	-	expression tag	UNP E1YD54
A	677	ASP	-	expression tag	UNP E1YD54
A	678	LEU	-	expression tag	UNP E1YD54
A	679	GLN	-	expression tag	UNP E1YD54
A	680	GLY	-	expression tag	UNP E1YD54
A	681	ASP	-	expression tag	UNP E1YD54
A	682	HIS	-	expression tag	UNP E1YD54
A	683	GLY	-	expression tag	UNP E1YD54
A	684	LEU	-	expression tag	UNP E1YD54
A	685	SER	-	expression tag	UNP E1YD54
A	686	ALA	-	expression tag	UNP E1YD54
A	687	TRP	-	expression tag	UNP E1YD54
A	688	SER	-	expression tag	UNP E1YD54
A	689	HIS	-	expression tag	UNP E1YD54
A	690	PRO	-	expression tag	UNP E1YD54
A	691	GLN	-	expression tag	UNP E1YD54
A	692	PHE	-	expression tag	UNP E1YD54
A	693	GLU	-	expression tag	UNP E1YD54
A	694	LYS	-	expression tag	UNP E1YD54
A	695	GLY	-	expression tag	UNP E1YD54
A	696	GLY	-	expression tag	UNP E1YD54
A	697	GLY	-	expression tag	UNP E1YD54

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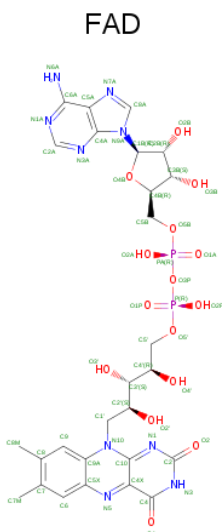
Chain	Residue	Modelled	Actual	Comment	Reference
A	698	SER	-	expression tag	UNP E1YD54
A	699	GLY	-	expression tag	UNP E1YD54
A	700	GLY	-	expression tag	UNP E1YD54
A	701	GLY	-	expression tag	UNP E1YD54
A	702	SER	-	expression tag	UNP E1YD54
A	703	GLY	-	expression tag	UNP E1YD54
A	704	GLY	-	expression tag	UNP E1YD54
A	705	GLY	-	expression tag	UNP E1YD54
A	706	SER	-	expression tag	UNP E1YD54
A	707	TRP	-	expression tag	UNP E1YD54
A	708	SER	-	expression tag	UNP E1YD54
A	709	HIS	-	expression tag	UNP E1YD54
A	710	PRO	-	expression tag	UNP E1YD54
A	711	GLN	-	expression tag	UNP E1YD54
A	712	PHE	-	expression tag	UNP E1YD54
A	713	GLU	-	expression tag	UNP E1YD54
A	714	LYS	-	expression tag	UNP E1YD54

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



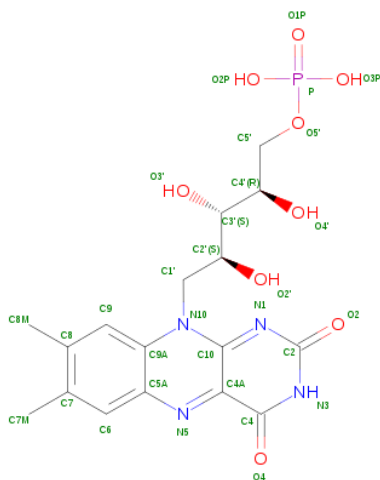
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



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

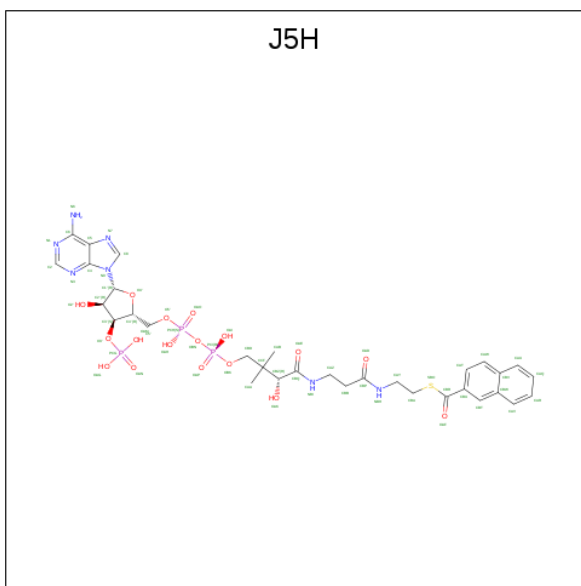
- Molecule 4 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula:  $C_{17}H_{21}N_4O_9P$ ).



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

- Molecule 5 is {S}-[2-[3-[(2 {R})-4-[[[(2 {R}),3 {S}),4 {R}),5 {R}]-5-(6-aminopurin-9-yl)-4-oxidany-3-phosphonoxy-oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-oxidanyl-phosphoryl]oxy-3,3-dimethyl-2-oxidanyl-butanoyl]amino]propanoylamino]ethyl] naphthalene-2-carbothi

oate (three-letter code: J5H) (formula: C<sub>32</sub>H<sub>42</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			60	32	7	17	3	1		

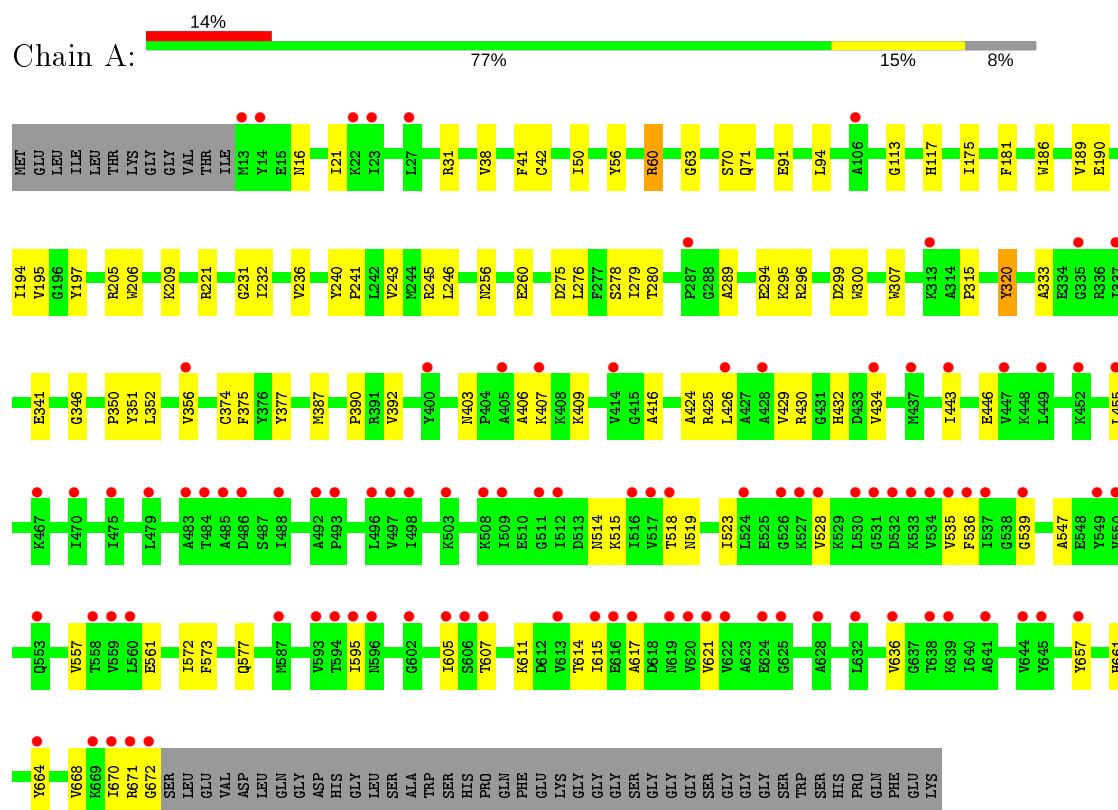
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	27	Total	O	0	0
			27	27		

### 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: NCR



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	176.86Å 176.86Å 49.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.42 – 2.40 47.42 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (47.42-2.40) 99.1 (47.42-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, $R_{free}$	0.229 , 0.274 0.234 , 0.272	Depositor DCC
$R_{free}$ test set	1451 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.8	Xtriage
Anisotropy	0.778	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 62.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.016 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5243	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: FMN, SF4, J5H, FAD

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	0.31	0/5156	0.56	1/6961 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	194	ILE	C-N-CA	5.60	135.69	121.70

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	A	5064	0	5101	72	0
2	A	8	0	0	0	0
3	A	53	0	31	1	0
4	A	31	0	19	2	0
5	A	60	0	0	0	0
6	A	27	0	0	0	0
All	All	5243	0	5151	72	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 7.

All (72) 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:A:60:ARG:NH1	1:A:346:GLY:O	2.08	0.86
1:A:523:ILE:HD13	1:A:528:VAL:HG11	1.64	0.79
1:A:221:ARG:NH1	1:A:256:ASN:OD1	2.23	0.72
1:A:409:LYS:HE3	1:A:672:GLY:HA3	1.73	0.70
1:A:205:ARG:NH2	1:A:260:GLU:OE2	2.30	0.64
1:A:670:ILE:HG22	1:A:670:ILE:O	2.01	0.61
1:A:426:LEU:HD22	1:A:664:TYR:CD1	2.38	0.58
1:A:387:MET:HA	1:A:657:TYR:HD1	1.68	0.58
1:A:377:TYR:HH	1:A:657:TYR:HE2	1.52	0.58
1:A:539:GLY:N	1:A:561:GLU:OE1	2.31	0.58
1:A:175:ILE:HD11	1:A:231:GLY:HA3	1.85	0.57
1:A:387:MET:HA	1:A:657:TYR:CD1	2.40	0.56
1:A:38:VAL:HG23	1:A:71:GLN:OE1	2.06	0.55
1:A:42:CYS:SG	1:A:71:GLN:NE2	2.80	0.55
1:A:636:VAL:HG23	1:A:636:VAL:O	2.07	0.55
1:A:374:CYS:SG	1:A:375:PHE:N	2.81	0.54
1:A:407:LYS:HG2	1:A:409:LYS:HE2	1.92	0.52
1:A:245:ARG:NH1	1:A:341:GLU:OE2	2.42	0.52
1:A:403:ASN:O	1:A:430:ARG:HD2	2.08	0.52
1:A:432:HIS:CE1	1:A:670:ILE:HG22	2.45	0.52
1:A:425:ARG:NH2	1:A:426:LEU:HD11	2.24	0.51
1:A:432:HIS:NE2	1:A:670:ILE:HG22	2.24	0.51
1:A:425:ARG:O	1:A:429:VAL:HG23	2.10	0.51
1:A:424:ALA:HB1	1:A:434:VAL:HG11	1.92	0.51
1:A:296:ARG:N	1:A:299:ASP:OD2	2.42	0.51
1:A:189:VAL:HG23	1:A:240:TYR:HE2	1.76	0.51
1:A:320:TYR:CD1	1:A:320:TYR:N	2.79	0.51
1:A:60:ARG:NH1	1:A:350:PRO:HB3	2.25	0.51
1:A:536:PHE:CE1	1:A:621:VAL:HG21	2.48	0.49
1:A:455:LEU:HD13	1:A:577:GLN:NE2	2.28	0.49
1:A:320:TYR:HD1	1:A:320:TYR:N	2.11	0.48
1:A:91:GLU:HG3	1:A:94:LEU:HD12	1.96	0.47
1:A:232:ILE:O	1:A:236:VAL:HG22	2.15	0.46
1:A:245:ARG:HG2	1:A:278:SER:HB3	1.97	0.46
1:A:60:ARG:NH2	1:A:392:VAL:HG22	2.30	0.46
1:A:514:ASN:OD1	1:A:515:LYS:N	2.48	0.46
1:A:276:LEU:HD12	1:A:315:PRO:O	2.15	0.46
1:A:595:ILE:HD13	1:A:605:ILE:HG22	1.96	0.46
1:A:426:LEU:CD2	1:A:664:TYR:CD1	2.99	0.46
1:A:38:VAL:HG12	4:A:803:FMN:N5	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:LEU:O	1:A:356:VAL:HG23	2.16	0.45
1:A:113:GLY:HA3	1:A:181:PHE:CE1	2.52	0.45
1:A:416:ALA:CB	1:A:443:ILE:HG22	2.47	0.44
1:A:572:ILE:HG13	1:A:573:PHE:HD1	1.81	0.44
1:A:390:PRO:HA	1:A:661:HIS:CE1	2.53	0.44
1:A:614:THR:HG22	1:A:615:ILE:N	2.33	0.43
1:A:21:ILE:HB	1:A:31:ARG:NE	2.34	0.43
1:A:280:THR:HB	1:A:320:TYR:OH	2.18	0.43
1:A:70:SER:HB3	1:A:186:TRP:CH2	2.53	0.43
1:A:117:HIS:O	1:A:197:TYR:HB3	2.18	0.43
1:A:190:GLU:HG3	1:A:243:VAL:HG23	2.01	0.43
1:A:246:LEU:HD23	1:A:307:TRP:HH2	1.84	0.43
1:A:664:TYR:HE1	1:A:668:VAL:HG11	1.83	0.43
1:A:246:LEU:O	1:A:279:ILE:HA	2.17	0.43
1:A:16:ASN:ND2	1:A:333:ALA:HB2	2.34	0.42
1:A:547:ALA:HB1	1:A:557:VAL:HG11	2.02	0.42
1:A:56:TYR:O	1:A:60:ARG:HD3	2.19	0.42
1:A:206:TRP:O	1:A:209:LYS:HE2	2.20	0.41
1:A:518:THR:HG21	1:A:523:ILE:HD11	2.03	0.41
1:A:535:VAL:HG23	1:A:617:ALA:HB2	2.02	0.41
1:A:519:ASN:O	1:A:523:ILE:HG12	2.20	0.41
1:A:56:TYR:HE1	1:A:60:ARG:HH21	1.69	0.41
1:A:607:THR:OG1	1:A:611:LYS:HB2	2.21	0.41
1:A:446:GLU:OE1	3:A:802:FAD:H3'	2.21	0.41
1:A:289:ALA:HB2	1:A:294:GLU:OE1	2.21	0.41
1:A:295:LYS:HE2	1:A:300:TRP:CZ2	2.55	0.40
1:A:664:TYR:HE1	1:A:668:VAL:CG1	2.34	0.40
1:A:320:TYR:CD1	4:A:803:FMN:H5'1	2.56	0.40
1:A:241:PRO:HA	1:A:275:ASP:OD2	2.21	0.40
1:A:424:ALA:CB	1:A:434:VAL:HG11	2.52	0.40
1:A:41:PHE:O	1:A:50:ILE:HD11	2.21	0.40
1:A:63:GLY:HA2	1:A:351:TYR:CD1	2.57	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	658/714 (92%)	625 (95%)	31 (5%)	2 (0%)	41 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	VAL
1	A	406	ALA

### 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	532/572 (93%)	529 (99%)	3 (1%)	86 94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ARG
1	A	320	TYR
1	A	671	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 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	$\# Z  > 2$
4	FMN	A	803	-	31,33,33	1.25	4 (12%)	40,50,50	1.69	7 (17%)
3	FAD	A	802	-	51,58,58	1.22	6 (11%)	60,89,89	2.20	8 (13%)
5	J5H	A	804	-	56,64,64	3.27	26 (46%)	72,95,95	1.86	13 (18%)
2	SF4	A	801	1	0,12,12	0.00	-	-		

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
4	FMN	A	803	-	-	3/18/18/18	0/3/3/3
3	FAD	A	802	-	-	3/30/50/50	0/6/6/6
5	J5H	A	804	-	-	14/51/71/71	0/5/5/5
2	SF4	A	801	1	-	-	0/6/5/5

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	804	J5H	CAQ-CAU	8.65	1.56	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	804	J5H	CAT-CBU	7.83	1.52	1.39
5	A	804	J5H	O4'-C1'	7.56	1.51	1.41
5	A	804	J5H	CAR-CAV	7.51	1.53	1.36
5	A	804	J5H	CAU-CBV	6.46	1.57	1.41
5	A	804	J5H	CAQ-CAR	6.17	1.54	1.38
3	A	802	FAD	C4X-C10	5.49	1.44	1.38
5	A	804	J5H	CBP-NBH	5.47	1.45	1.33
5	A	804	J5H	CBQ-NBI	5.45	1.45	1.33
5	A	804	J5H	CBT-CBW	4.74	1.52	1.42
5	A	804	J5H	CAV-CBW	4.51	1.52	1.41
5	A	804	J5H	CAW-CBV	4.47	1.52	1.41
5	A	804	J5H	C5-N7	3.82	1.53	1.39
4	A	803	FMN	C10-N1	3.63	1.37	1.33
5	A	804	J5H	CBT-CBU	-3.34	1.31	1.37
5	A	804	J5H	PCG-O3'	3.29	1.65	1.59
5	A	804	J5H	C2'-C1'	-3.18	1.48	1.53
5	A	804	J5H	C6-N6	3.11	1.45	1.34
5	A	804	J5H	C4-N3	-3.10	1.31	1.35
3	A	802	FAD	C4-N3	2.93	1.38	1.33
5	A	804	J5H	C2'-C3'	-2.83	1.46	1.52
4	A	803	FMN	C4-N3	2.79	1.37	1.33
4	A	803	FMN	C4A-N5	2.73	1.37	1.33
5	A	804	J5H	CBR-SBO	2.71	1.82	1.76
5	A	804	J5H	O4'-C4'	2.35	1.50	1.45
3	A	802	FAD	C4-C4X	2.34	1.45	1.41
3	A	802	FAD	C5X-N5	2.33	1.39	1.35
5	A	804	J5H	CAW-CAT	-2.23	1.31	1.36
5	A	804	J5H	PCG-OAM	-2.17	1.46	1.54
3	A	802	FAD	C9A-N10	2.13	1.41	1.38
5	A	804	J5H	PCG-OAG	-2.07	1.46	1.54
4	A	803	FMN	C1'-N10	2.05	1.50	1.48
5	A	804	J5H	OAD-CBP	-2.04	1.19	1.23
5	A	804	J5H	CBV-CBW	-2.02	1.37	1.42
5	A	804	J5H	OAE-CBQ	-2.02	1.19	1.23
3	A	802	FAD	C4X-N5	-2.00	1.30	1.33

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	FAD	C4-N3-C2	12.69	125.86	115.14
5	A	804	J5H	CBA-SBO-CBR	7.82	109.63	99.80
3	A	802	FAD	C4X-C4-N3	-6.95	113.92	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	803	FMN	C4-N3-C2	5.64	119.91	115.14
5	A	804	J5H	C4-C5-N7	-5.22	103.96	109.40
5	A	804	J5H	C1'-N9-C4	-5.11	117.67	126.64
3	A	802	FAD	C10-C4X-N5	4.73	124.53	121.26
5	A	804	J5H	N3-C2-N1	-4.43	121.75	128.68
4	A	803	FMN	C4A-N5-C5A	4.36	121.13	116.77
5	A	804	J5H	CAR-CAQ-CAU	-4.19	114.57	120.44
3	A	802	FAD	C4-C4X-C10	-3.80	117.44	119.95
3	A	802	FAD	C4X-C10-N10	-3.41	116.80	120.30
4	A	803	FMN	C1'-N10-C9A	3.27	120.87	118.29
4	A	803	FMN	C10-C4A-N5	-3.21	119.04	121.26
3	A	802	FAD	C1'-N10-C9A	3.16	120.78	118.29
4	A	803	FMN	C4A-C4-N3	-3.06	119.25	123.43
5	A	804	J5H	PCH-OBN-PCI	-2.49	124.29	132.83
3	A	802	FAD	C5A-C6A-N6A	2.36	123.94	120.35
5	A	804	J5H	C3'-C2'-C1'	2.33	105.05	99.89
3	A	802	FAD	P-O3P-PA	-2.27	125.04	132.83
4	A	803	FMN	C5A-C9A-N10	2.26	119.36	117.72
5	A	804	J5H	OAH-PCH-OAO	-2.25	101.14	112.24
5	A	804	J5H	OAI-PCI-OAP	-2.24	101.19	112.24
5	A	804	J5H	CAB-CCF-CBD	2.21	111.84	108.23
5	A	804	J5H	CBB-CBP-NBH	2.13	120.01	116.42
5	A	804	J5H	CBB-CAZ-NBI	-2.13	107.59	111.90
4	A	803	FMN	O3P-P-O5'	2.10	112.31	106.73
5	A	804	J5H	CBA-CAY-NBH	-2.03	108.16	112.42

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	803	FMN	C3'-C4'-C5'-O5'
4	A	803	FMN	O4'-C4'-C5'-O5'
5	A	804	J5H	CBU-CBR-SBO-CBA
5	A	804	J5H	OAF-CBR-SBO-CBA
5	A	804	J5H	NBI-CAZ-CBB-CBP
5	A	804	J5H	OBK-CBD-CCF-CBZ
5	A	804	J5H	OBK-CBD-CCF-CAA
5	A	804	J5H	OBK-CBD-CCF-CAB
5	A	804	J5H	CBD-OBK-PCI-OBN
5	A	804	J5H	C5'-O5'-PCH-OBN
3	A	802	FAD	O4B-C4B-C5B-O5B
3	A	802	FAD	C3B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
5	A	804	J5H	O4'-C4'-C5'-O5'
3	A	802	FAD	PA-O3P-P-O5'
5	A	804	J5H	CBD-OBK-PCI-OAP
5	A	804	J5H	CBD-OBK-PCI-OAI
5	A	804	J5H	C5'-O5'-PCH-OAH
5	A	804	J5H	C3'-C4'-C5'-O5'
5	A	804	J5H	C4'-C3'-O3'-PCG
4	A	803	FMN	C4'-C5'-O5'-P

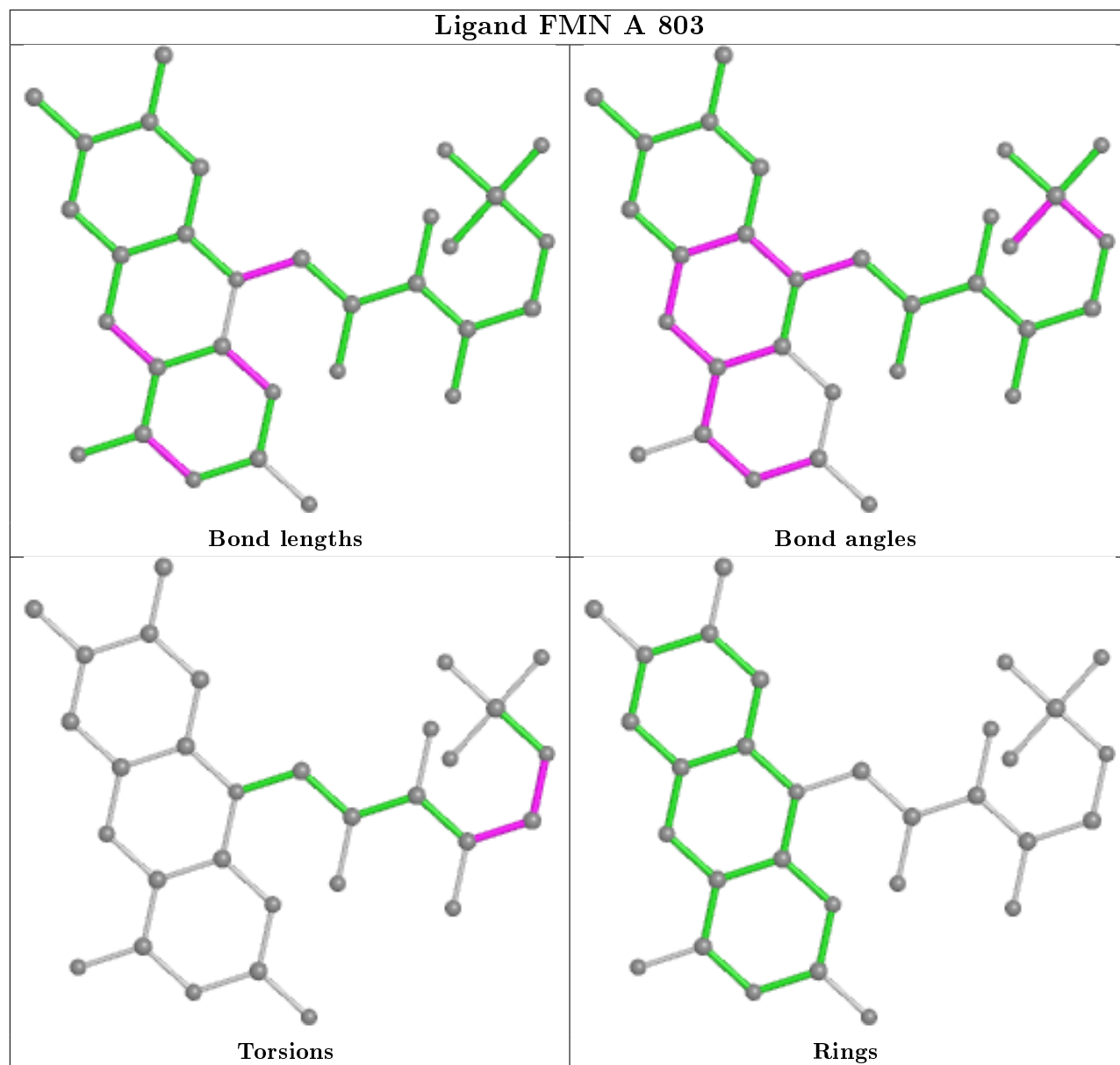
There are no ring outliers.

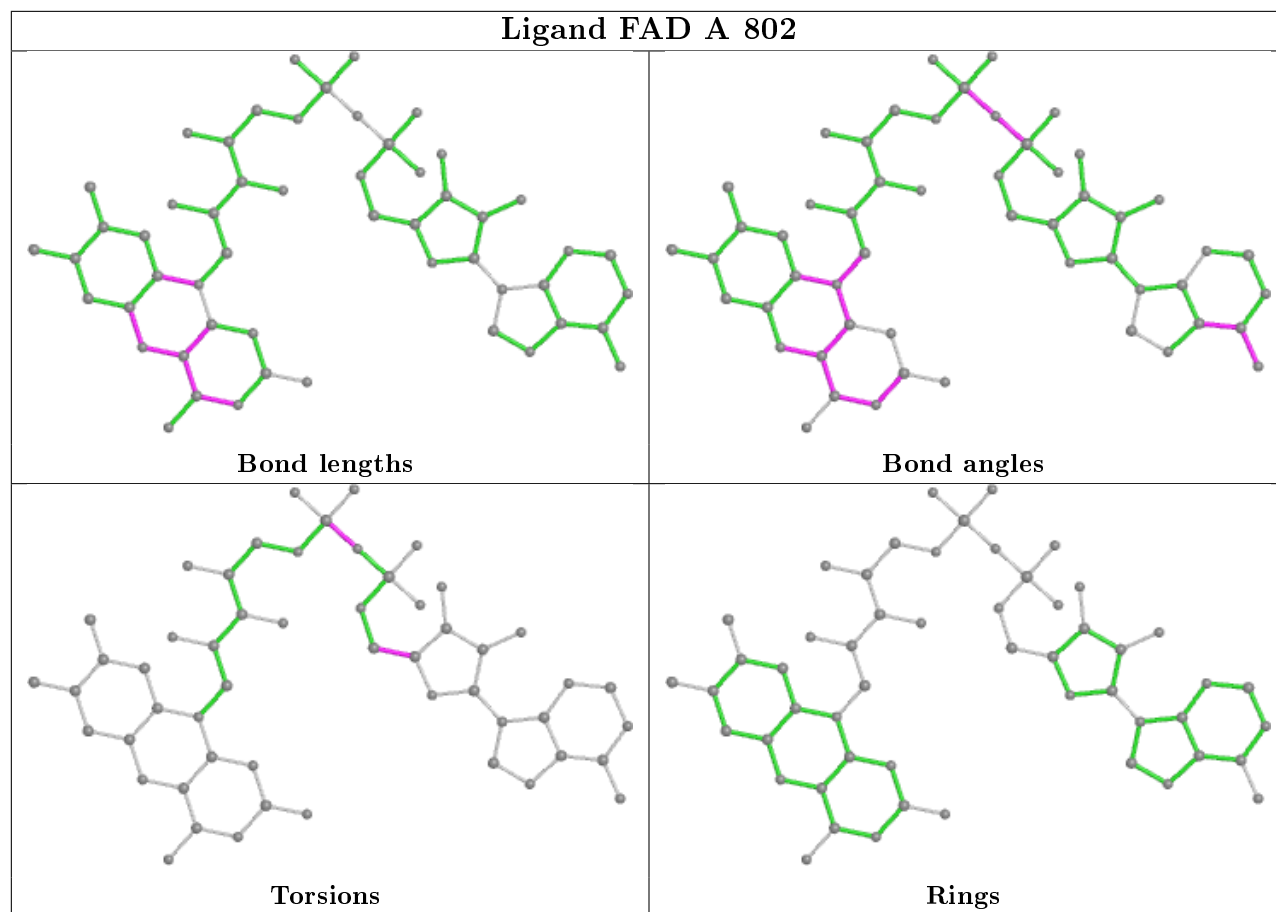
2 monomers are involved in 3 short contacts:

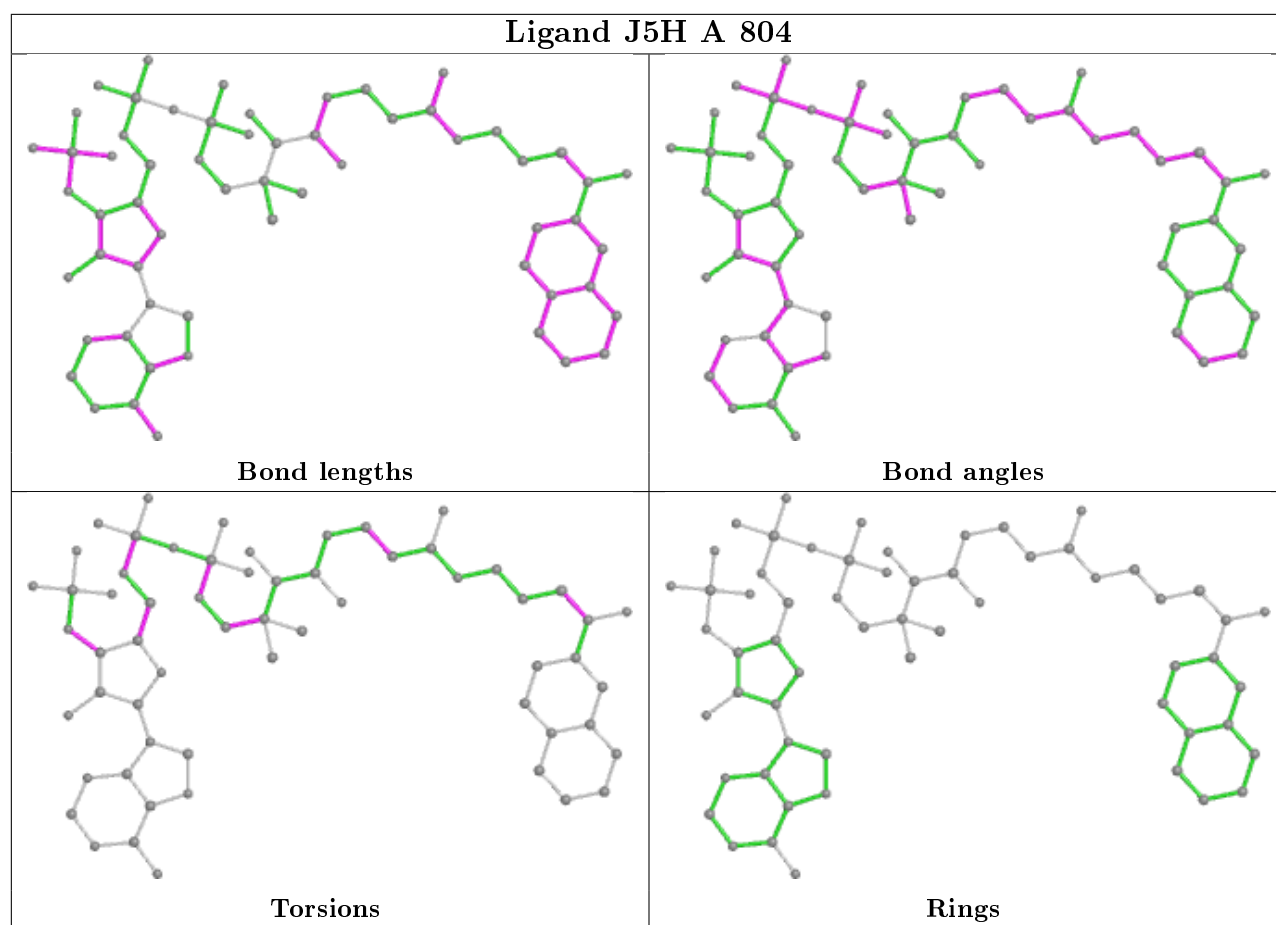
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	803	FMN	2	0
3	A	802	FAD	1	0

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	659/714 (92%)	0.88	98 (14%) 2 2	51, 85, 153, 200	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	620	VAL	8.0
1	A	516	ILE	6.0
1	A	488	ILE	5.8
1	A	414	VAL	5.5
1	A	530	LEU	5.5
1	A	641	ALA	5.1
1	A	595	ILE	5.0
1	A	524	LEU	4.8
1	A	517	VAL	4.6
1	A	508	LYS	4.6
1	A	671	ARG	4.5
1	A	535	VAL	4.5
1	A	621	VAL	4.5
1	A	664	TYR	4.4
1	A	449	LEU	4.2
1	A	437	MET	4.1
1	A	615	ILE	4.0
1	A	644	VAL	3.9
1	A	496	LEU	3.7
1	A	509	ILE	3.7
1	A	639	LYS	3.6
1	A	434	VAL	3.6
1	A	13	MET	3.5
1	A	485	ALA	3.4
1	A	511	GLY	3.3
1	A	558	THR	3.3
1	A	636	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	405	ALA	3.3
1	A	498	ILE	3.3
1	A	27	LEU	3.2
1	A	512	ILE	3.2
1	A	624	GLU	3.2
1	A	106	ALA	3.2
1	A	539	GLY	3.1
1	A	593	VAL	3.1
1	A	455	LEU	3.1
1	A	531	GLY	3.0
1	A	428	ALA	3.0
1	A	475	ILE	3.0
1	A	407	LYS	3.0
1	A	560	LEU	3.0
1	A	497	VAL	3.0
1	A	657	TYR	3.0
1	A	533	LYS	3.0
1	A	493	PRO	2.9
1	A	594	THR	2.9
1	A	527	LYS	2.8
1	A	492	ALA	2.8
1	A	356	VAL	2.7
1	A	447	VAL	2.7
1	A	452	LYS	2.7
1	A	537	ILE	2.7
1	A	605	ILE	2.7
1	A	616	GLU	2.7
1	A	22	LYS	2.6
1	A	619	ASN	2.6
1	A	672	GLY	2.6
1	A	467	LYS	2.5
1	A	528	VAL	2.5
1	A	628	ALA	2.5
1	A	645	TYR	2.5
1	A	536	PHE	2.5
1	A	486	ASP	2.5
1	A	553	GLN	2.5
1	A	470	ILE	2.5
1	A	313	LYS	2.4
1	A	587	MET	2.4
1	A	479	LEU	2.4
1	A	534	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	625	GLY	2.4
1	A	526	GLY	2.4
1	A	559	VAL	2.4
1	A	617	ALA	2.4
1	A	613	VAL	2.3
1	A	549	TYR	2.3
1	A	550	VAL	2.3
1	A	483	ALA	2.3
1	A	14	TYR	2.3
1	A	337	ILE	2.2
1	A	632	LEU	2.2
1	A	606	SER	2.2
1	A	518	THR	2.2
1	A	607	THR	2.2
1	A	400	TYR	2.2
1	A	669	LYS	2.2
1	A	443	ILE	2.2
1	A	670	ILE	2.2
1	A	622	VAL	2.1
1	A	602	GLY	2.1
1	A	503	LYS	2.1
1	A	23	ILE	2.1
1	A	335	GLY	2.1
1	A	596	ASN	2.1
1	A	484	THR	2.1
1	A	638	THR	2.1
1	A	426	LEU	2.0
1	A	532	ASP	2.0
1	A	287	PRO	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

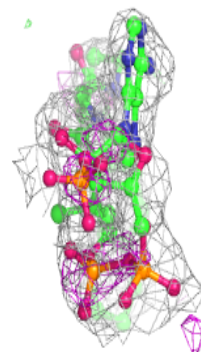
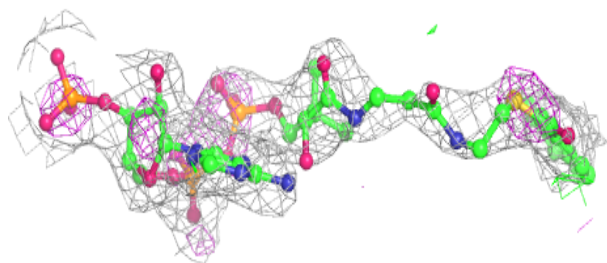
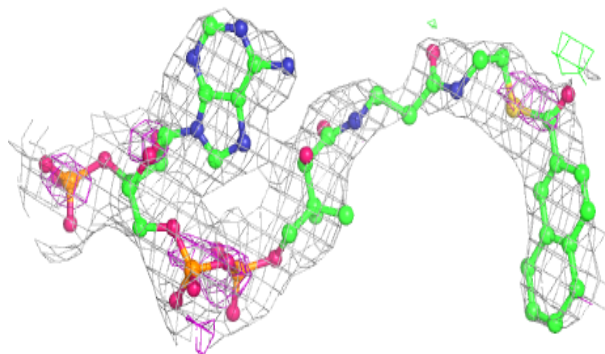
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	J5H	A	804	60/60	0.91	0.20	74,90,110,112	9
3	FAD	A	802	53/53	0.92	0.17	89,100,118,120	0
4	FMN	A	803	31/31	0.94	0.18	54,63,69,71	1
2	SF4	A	801	8/8	0.96	0.25	65,67,77,77	4

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.

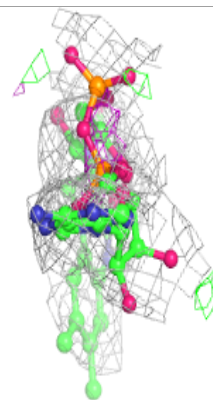
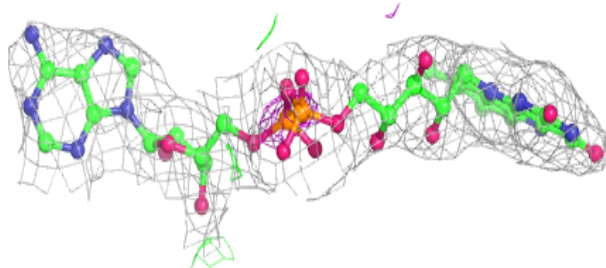
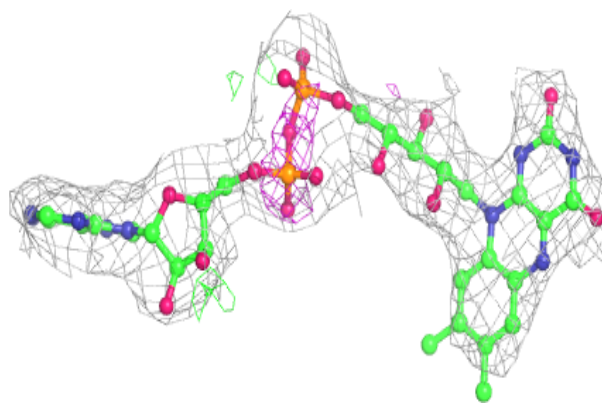
### Electron density around J5H A 804:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

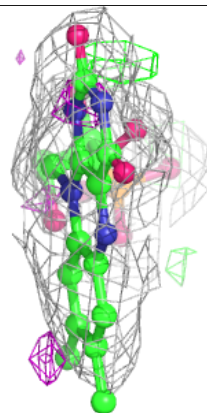
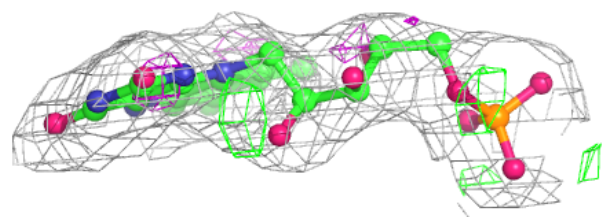
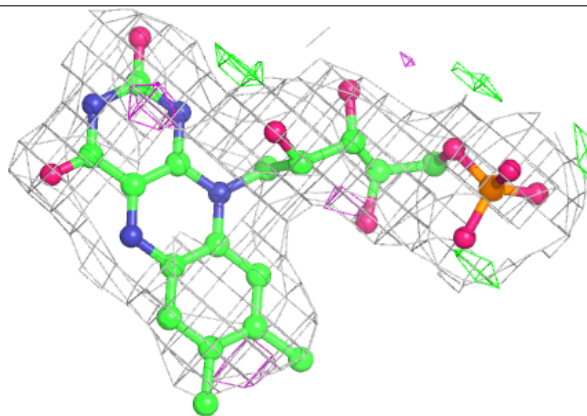


**Electron density around FAD A 802:**

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

**Electron density around FMN A 803:**

$2mF_o-DF_c$  (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.