



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 05:15 PM UTC

PDB ID : 3NHL / pdb_00003nhl
Title : X-ray Crystallographic Structure Activity Relationship (SAR) of Casimiroin and its Analogs Bound to Human Quinone Reductase 2
Authors : Sturdy, M.
Deposited on : 2010-06-14
Resolution : 1.57 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

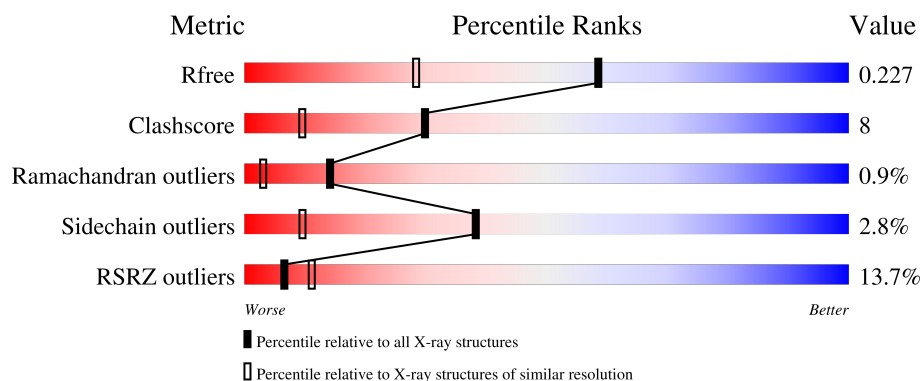
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.57 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	230	20% 70% 26% ..
1	B	230	8% 82% 17% .

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	YTR	A	233	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4174 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.

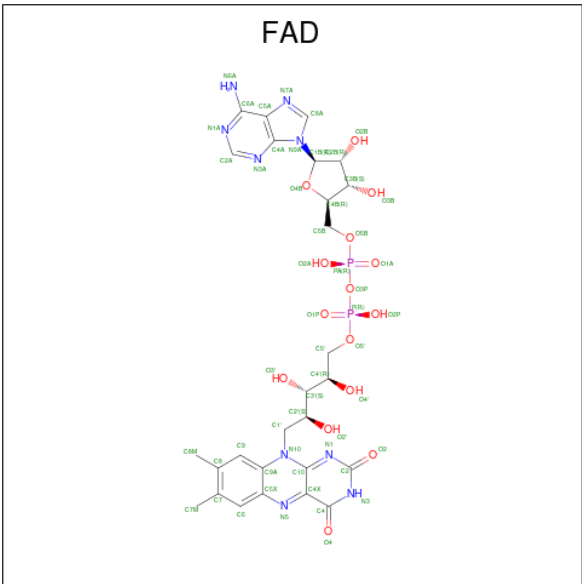
- Molecule 1 is a protein called Ribosyldihydronicotinamide dehydrogenase [quinone].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1824	1174	304	338	8			
1	B	230	Total	C	N	O	S	0	0	0
			1824	1174	304	338	8			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

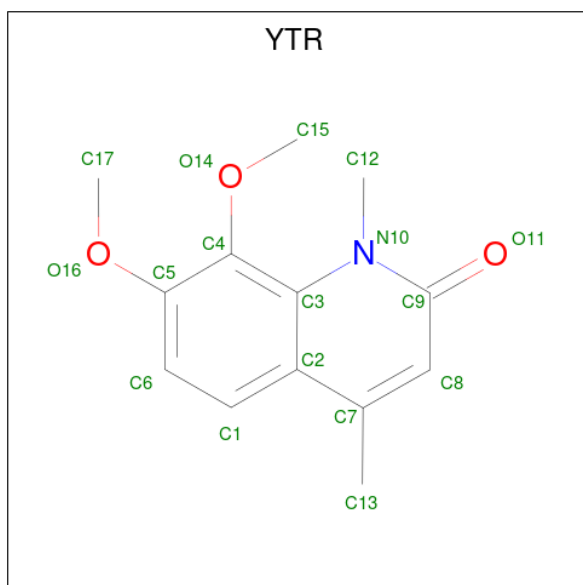
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 4 is 7,8-dimethoxy-1,4-dimethylquinolin-2(1H)-one (CCD ID: YTR) (formula: $C_{13}H_{15}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	13	1	3		
4	B	1	Total	C	N	O	0	0
			17	13	1	3		

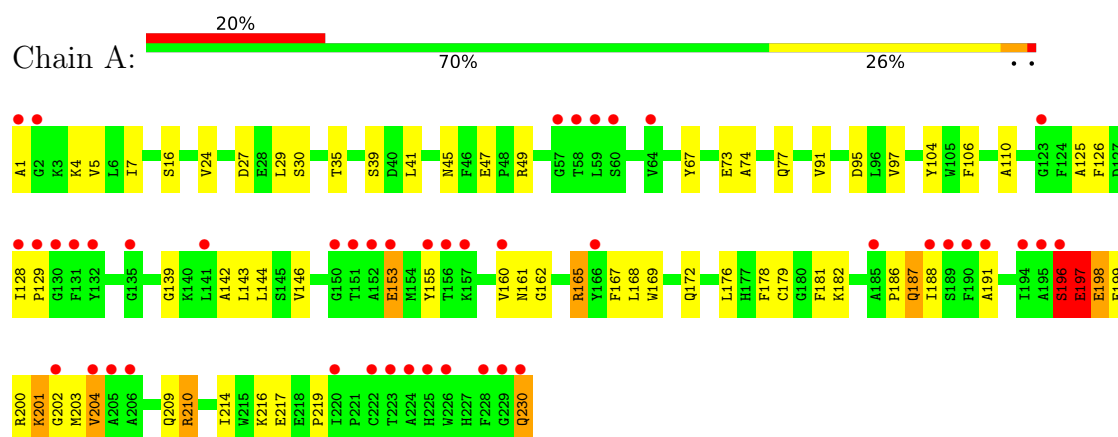
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	164	Total	O	0	0
			164	164		
5	B	220	Total	O	0	0
			220	220		

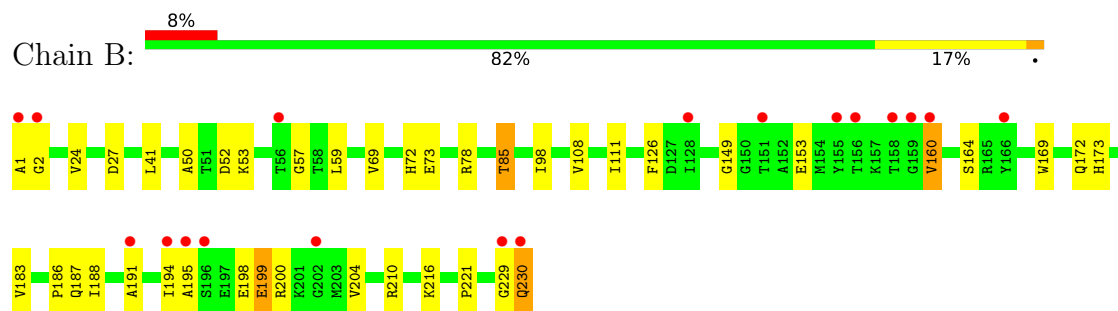
3 Residue-property plots

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: Ribosyldihyronicotinamide dehydrogenase [quinone]



- Molecule 1: Ribosyldihyronicotinamide dehydrogenase [quinone]



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.10Å 83.16Å 106.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.57 50.00 – 1.57	Depositor EDS
% Data completeness (in resolution range)	96.6 (50.00-1.57) 96.6 (50.00-1.57)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.37 (at 1.58Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.191 , 0.231 0.189 , 0.227	Depositor DCC
R_{free} test set	3424 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.723	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4174	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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: YTR, FAD, ZN

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	1.74	24/1874 (1.3%)	1.49	16/2542 (0.6%)
1	B	1.68	16/1874 (0.9%)	1.44	10/2542 (0.4%)
All	All	1.71	40/3748 (1.1%)	1.47	26/5084 (0.5%)

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	A	0	2

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	191	ALA	C-O	9.42	1.28	1.23
1	A	191	ALA	CA-CB	9.40	1.61	1.52
1	A	178	PHE	N-CA	-8.20	1.36	1.46
1	B	27	ASP	N-CA	7.96	1.55	1.46
1	A	7	ILE	CA-CB	-7.59	1.45	1.54
1	A	188	ILE	C-O	7.31	1.32	1.24
1	A	176	LEU	N-CA	7.17	1.54	1.46
1	A	143	LEU	N-CA	-7.07	1.38	1.46
1	A	217	GLU	CB-CG	-6.84	1.31	1.52
1	A	214	ILE	CA-CB	6.68	1.64	1.54
1	B	216	LYS	N-CA	6.67	1.54	1.46
1	B	221	PRO	N-CA	-6.44	1.41	1.47
1	A	187	GLN	N-CA	-6.31	1.38	1.46
1	B	191	ALA	CA-CB	6.30	1.58	1.52
1	A	97	VAL	C-O	6.05	1.30	1.24
1	B	173	HIS	N-CA	-6.05	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	57	GLY	N-CA	5.82	1.51	1.45
1	A	216	LYS	N-CA	5.74	1.53	1.46
1	B	98	ILE	CA-CB	5.64	1.61	1.54
1	A	210	ARG	CA-CB	5.63	1.62	1.53
1	A	144	LEU	CA-C	-5.62	1.45	1.52
1	B	169	TRP	C-O	-5.61	1.19	1.24
1	A	95	ASP	N-CA	5.61	1.53	1.46
1	B	221	PRO	C-O	-5.60	1.19	1.24
1	A	5	VAL	CA-CB	-5.56	1.47	1.54
1	A	165	ARG	N-CA	-5.45	1.39	1.46
1	A	39	SER	N-CA	5.45	1.53	1.46
1	A	74	ALA	CA-CB	5.29	1.61	1.53
1	B	108	VAL	CA-C	5.28	1.58	1.52
1	B	50	ALA	CA-CB	5.27	1.59	1.52
1	A	106	PHE	C-N	5.20	1.39	1.33
1	A	169	TRP	CA-CB	5.20	1.60	1.53
1	B	111	ILE	N-CA	5.17	1.52	1.46
1	A	27	ASP	N-CA	5.16	1.52	1.46
1	B	59	LEU	C-O	5.16	1.30	1.23
1	A	30	SER	N-CA	5.13	1.52	1.46
1	A	67	TYR	CA-CB	5.08	1.61	1.53
1	B	183	VAL	N-CA	-5.08	1.40	1.46
1	B	188	ILE	C-O	5.07	1.29	1.24
1	A	49	ARG	CA-C	-5.01	1.46	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	ARG	NE-CZ-NH1	-6.65	114.85	121.50
1	B	160	VAL	CB-CA-C	-6.35	103.56	112.14
1	A	16	SER	N-CA-C	6.29	118.84	110.53
1	B	72	HIS	O-C-N	6.24	128.50	122.07
1	A	196	SER	N-CA-C	-5.88	102.35	110.35
1	B	149	GLY	CA-C-N	5.77	125.83	120.34
1	B	149	GLY	C-N-CA	5.77	125.83	120.34
1	A	161	ASN	N-CA-C	5.74	120.12	113.18
1	B	78	ARG	NE-CZ-NH2	-5.71	114.06	119.20
1	A	41	LEU	CA-C-O	-5.64	114.44	120.42
1	A	196	SER	CA-C-N	5.57	132.18	121.54
1	A	196	SER	C-N-CA	5.57	132.18	121.54
1	B	41	LEU	CA-C-O	-5.57	114.51	120.42
1	A	91	VAL	O-C-N	5.48	127.47	121.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ALA	N-CA-C	5.44	117.91	111.33
1	A	95	ASP	N-CA-C	-5.40	106.82	113.41
1	B	78	ARG	NE-CZ-NH1	5.37	126.87	121.50
1	A	146	VAL	CB-CA-C	-5.27	102.77	110.62
1	A	139	GLY	N-CA-C	-5.22	108.47	114.69
1	A	47	GLU	CA-C-N	-5.20	113.34	119.84
1	A	47	GLU	C-N-CA	-5.20	113.34	119.84
1	A	204	VAL	N-CA-C	-5.19	105.48	110.72
1	A	29	LEU	N-CA-C	-5.16	105.74	111.36
1	B	85	THR	OG1-CB-CG2	-5.15	99.00	109.30
1	B	69	VAL	N-CA-C	-5.03	105.81	110.53
1	B	164	SER	O-C-N	-5.02	116.48	122.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	SER	Peptide
1	A	197	GLU	Peptide

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	1824	0	1779	38	0
1	B	1824	0	1779	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	53	0	31	8	0
3	B	53	0	31	1	0
4	A	17	0	15	7	0
4	B	17	0	15	5	0
5	A	164	0	0	3	1
5	B	220	0	0	5	2
All	All	4174	0	3650	63	2

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.

All (63) 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:45:ASN:ND2	5:A:277:HOH:O	1.69	1.19
1:A:126:PHE:CZ	4:A:233:YTR:H17A	2.05	0.91
1:A:198:GLU:O	1:A:200:ARG:N	2.21	0.73
1:B:53:LYS:HA	1:B:53:LYS:HE2	1.73	0.71
1:A:126:PHE:HZ	4:A:233:YTR:H17A	1.51	0.71
4:B:233:YTR:H12B	4:B:233:YTR:O14	1.93	0.69
1:A:200:ARG:HB3	3:A:232:FAD:C2A	2.22	0.69
1:B:230:GLN:HE21	1:B:230:GLN:HA	1.58	0.68
1:A:126:PHE:HZ	4:A:233:YTR:C17	2.08	0.66
1:B:73:GLU:OE1	5:B:417:HOH:O	2.14	0.66
4:A:233:YTR:H12B	4:A:233:YTR:O14	1.99	0.62
1:A:126:PHE:CZ	4:A:233:YTR:C17	2.79	0.62
1:A:200:ARG:HD2	3:A:232:FAD:N3A	2.15	0.61
1:B:52:ASP:OD1	1:B:53:LYS:HE3	2.00	0.61
1:A:200:ARG:HB3	3:A:232:FAD:H2A	1.84	0.60
1:A:172:GLN:HE22	1:A:186:PRO:HD3	1.67	0.59
1:A:196:SER:O	1:A:198:GLU:O	2.20	0.59
1:B:1:ALA:N	5:B:378:HOH:O	2.35	0.59
1:B:187:GLN:HE21	1:B:210:ARG:HH11	1.51	0.58
1:B:53:LYS:HA	1:B:53:LYS:CE	2.33	0.58
1:A:165:ARG:HA	1:A:168:LEU:HD12	1.88	0.56
1:B:230:GLN:HE21	1:B:230:GLN:CA	2.17	0.55
1:A:187:GLN:HE21	1:A:210:ARG:HH11	1.53	0.55
1:B:24:VAL:HG11	1:B:204:VAL:CG1	2.37	0.54
1:A:200:ARG:NH1	3:A:232:FAD:N3A	2.54	0.54
1:A:126:PHE:CE1	4:A:233:YTR:H17A	2.45	0.52
1:A:142:ALA:HB2	1:A:181:PHE:CD1	2.47	0.50
1:A:24:VAL:HG11	1:A:204:VAL:CG1	2.41	0.50
4:B:233:YTR:O14	4:B:233:YTR:C12	2.59	0.50
1:A:230:GLN:HA	1:A:230:GLN:OE1	2.12	0.49
1:A:4:LYS:HG2	1:A:35:THR:HB	1.94	0.49
1:B:172:GLN:HE22	1:B:186:PRO:HD3	1.78	0.48
1:A:73:GLU:O	1:A:77:GLN:HG3	2.14	0.48
1:B:194:ILE:HG13	5:B:265:HOH:O	2.14	0.47
1:A:187:GLN:NE2	1:A:210:ARG:HH11	2.11	0.47
1:A:182:LYS:HB3	1:A:219:PRO:HB3	1.97	0.47
1:B:195:ALA:HB1	1:B:199:GLU:HB3	1.97	0.47
1:A:104:TYR:HA	3:A:232:FAD:C5X	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:GLU:HG3	5:A:348:HOH:O	2.15	0.45
1:A:104:TYR:HA	3:A:232:FAD:C6	2.47	0.45
3:A:232:FAD:C6	4:B:233:YTR:H17B	2.48	0.44
1:B:187:GLN:NE2	1:B:210:ARG:HH11	2.16	0.44
1:A:201:LYS:HD2	1:A:201:LYS:HA	1.79	0.44
1:A:1:ALA:N	5:A:335:HOH:O	2.36	0.44
1:B:53:LYS:HE2	5:B:304:HOH:O	2.18	0.43
1:B:53:LYS:CE	1:B:53:LYS:CA	2.96	0.43
1:A:128:ILE:HA	1:A:129:PRO:HA	1.82	0.42
1:B:126:PHE:CE1	4:B:233:YTR:H17A	2.54	0.42
1:A:196:SER:HA	1:A:197:GLU:HB2	2.02	0.42
4:A:233:YTR:O14	4:A:233:YTR:C12	2.66	0.42
1:A:155:TYR:HA	1:A:162:GLY:O	2.20	0.42
1:A:182:LYS:HB3	1:A:219:PRO:CB	2.50	0.42
1:A:182:LYS:HB3	1:A:219:PRO:CG	2.50	0.41
1:B:85:THR:HG21	5:B:397:HOH:O	2.20	0.41
1:B:200:ARG:HD2	3:B:231:FAD:O4B	2.20	0.41
1:A:203:MET:HB2	1:A:203:MET:HE3	1.83	0.41
1:A:196:SER:C	1:A:198:GLU:O	2.63	0.41
1:A:200:ARG:HH11	3:A:232:FAD:C2A	2.33	0.41
1:B:229:GLY:O	1:B:230:GLN:CB	2.68	0.41
4:B:233:YTR:H1	4:B:233:YTR:H13B	1.85	0.40
1:A:125:ALA:HB1	1:A:179:CYS:SG	2.62	0.40
1:A:200:ARG:C	1:A:202:GLY:N	2.78	0.40
1:A:167:PHE:CD1	1:A:167:PHE:C	3.00	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:397:HOH:O	5:B:451:HOH:O[2_555]	1.18	1.02
5:B:427:HOH:O	5:B:436:HOH:O[3_554]	2.17	0.03

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/230 (99%)	220 (96%)	5 (2%)	3 (1%)	9	1
1	B	228/230 (99%)	221 (97%)	6 (3%)	1 (0%)	30	12
All	All	456/460 (99%)	441 (97%)	11 (2%)	4 (1%)	14	3

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	GLU
1	A	197	GLU
1	A	198	GLU
1	B	2	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	194/194 (100%)	188 (97%)	6 (3%)	35	7
1	B	194/194 (100%)	189 (97%)	5 (3%)	40	11
All	All	388/388 (100%)	377 (97%)	11 (3%)	38	9

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	GLU
1	A	160	VAL
1	A	196	SER
1	A	201	LYS
1	A	209	GLN
1	A	230	GLN
1	B	153	GLU
1	B	160	VAL
1	B	198	GLU

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Mol	Chain	Res	Type
1	B	199	GLU
1	B	230	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	HIS
1	A	100	GLN
1	A	172	GLN
1	A	187	GLN
1	A	212	GLN
1	A	225	HIS
1	B	100	GLN
1	B	138	GLN
1	B	172	GLN
1	B	187	GLN
1	B	230	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z > 2$
3	FAD	B	231	-	58,58,58	1.75	13 (22%)	85,89,89	2.24	28 (32%)
4	YTR	B	233	-	17,18,18	2.55	4 (23%)	19,26,26	2.71	8 (42%)
4	YTR	A	233	-	17,18,18	2.79	6 (35%)	19,26,26	2.41	7 (36%)
3	FAD	A	232	-	58,58,58	2.29	15 (25%)	85,89,89	2.56	28 (32%)

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	FAD	B	231	-	-	8/34/50/50	0/6/6/6
4	YTR	B	233	-	-	2/4/4/4	0/2/2/2
4	YTR	A	233	-	-	0/4/4/4	0/2/2/2
3	FAD	A	232	-	-	4/34/50/50	0/6/6/6

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	232	FAD	C6-C7	-7.86	1.28	1.39
3	A	232	FAD	C4X-N5	6.94	1.45	1.30
4	A	233	YTR	C8-C7	6.78	1.44	1.35
4	A	233	YTR	C2-C3	6.15	1.49	1.40
4	B	233	YTR	C8-C7	5.90	1.42	1.35
3	A	232	FAD	C1'-C2'	5.63	1.60	1.52
4	B	233	YTR	C2-C3	5.44	1.48	1.40
3	B	231	FAD	C4X-N5	4.84	1.41	1.30
3	A	232	FAD	C5X-N5	-4.65	1.30	1.39
4	B	233	YTR	C3-C4	4.60	1.48	1.40
3	B	231	FAD	P-O3P	4.52	1.64	1.59
3	B	231	FAD	C1'-C2'	4.48	1.58	1.52
3	A	232	FAD	C10-N1	4.29	1.41	1.33
3	A	232	FAD	PA-O3P	4.17	1.64	1.59
4	A	233	YTR	C5-C4	3.82	1.49	1.41
3	A	232	FAD	P-O3P	3.80	1.63	1.59
3	B	231	FAD	PA-O3P	3.47	1.63	1.59
4	A	233	YTR	C3-C4	3.38	1.46	1.40
3	B	231	FAD	C6-C7	-3.33	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	231	FAD	C10-N1	3.30	1.39	1.33
3	B	231	FAD	C10-N10	3.11	1.44	1.37
4	B	233	YTR	C5-C4	3.07	1.47	1.41
3	A	232	FAD	C2A-N3A	2.97	1.39	1.33
3	B	231	FAD	O4'-C4'	-2.90	1.37	1.43
3	A	232	FAD	O2'-C2'	-2.87	1.37	1.43
4	A	233	YTR	C2-C7	2.83	1.49	1.45
3	B	231	FAD	C2A-N3A	2.71	1.38	1.33
3	A	232	FAD	P-O1P	2.64	1.60	1.50
3	B	231	FAD	P-O1P	-2.56	1.41	1.50
3	A	232	FAD	C2A-N1A	2.55	1.38	1.33
4	A	233	YTR	O11-C9	2.49	1.28	1.23
3	A	232	FAD	O4'-C4'	-2.49	1.38	1.43
3	B	231	FAD	C2A-N1A	2.42	1.38	1.33
3	B	231	FAD	C4-N3	2.42	1.43	1.38
3	B	231	FAD	C5X-N5	-2.39	1.35	1.39
3	A	232	FAD	O4-C4	-2.38	1.19	1.23
3	A	232	FAD	C4'-C3'	2.04	1.57	1.53
3	A	232	FAD	C1'-N10	2.01	1.52	1.47

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	232	FAD	C7M-C7-C6	-10.96	100.26	119.57
4	B	233	YTR	C8-C9-N10	7.56	122.83	115.44
3	B	231	FAD	C7M-C7-C6	-6.75	107.67	119.57
4	A	233	YTR	C8-C9-N10	6.29	121.58	115.44
3	B	231	FAD	N3A-C2A-N1A	-6.22	119.16	128.58
3	A	232	FAD	C5A-C4A-N3A	-5.89	118.60	126.72
4	B	233	YTR	C15-O14-C4	5.64	130.04	114.74
3	A	232	FAD	N3A-C2A-N1A	-5.59	120.12	128.58
4	A	233	YTR	C17-O16-C5	5.55	125.65	117.51
3	A	232	FAD	C7M-C7-C8	5.50	131.99	120.76
3	A	232	FAD	C6-C7-C8	5.46	127.70	119.69
3	B	231	FAD	N9A-C8A-N7A	-5.22	106.53	113.94
3	A	232	FAD	C6-C5X-N5	-5.01	110.14	118.44
3	A	232	FAD	C9A-C5X-N5	4.99	127.75	122.45
3	B	231	FAD	C5A-N7A-C8A	4.79	110.98	103.45
3	B	231	FAD	C8M-C8-C7	4.52	130.00	120.76
3	B	231	FAD	C4X-C10-N10	4.41	122.79	116.48
3	A	232	FAD	C4X-C10-N10	4.25	122.57	116.48
3	B	231	FAD	C4-N3-C2	-4.19	118.19	125.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	232	FAD	C2A-N3A-C4A	4.18	122.04	111.83
3	A	232	FAD	C5A-N7A-C8A	4.15	109.97	103.45
3	B	231	FAD	C6-C7-C8	3.80	125.27	119.69
3	B	231	FAD	C4A-C5A-N7A	-3.78	106.26	110.58
3	B	231	FAD	C5A-C4A-N3A	-3.71	121.60	126.72
3	B	231	FAD	C9A-C5X-N5	3.70	126.38	122.45
3	A	232	FAD	C4A-C5A-N7A	-3.68	106.38	110.58
3	B	231	FAD	C9-C8-C7	-3.59	114.41	119.69
3	A	232	FAD	N9A-C8A-N7A	-3.57	108.87	113.94
3	A	232	FAD	C8M-C8-C7	3.57	128.04	120.76
3	A	232	FAD	N3A-C4A-N9A	3.55	133.20	127.17
3	B	231	FAD	O4'-C4'-C3'	-3.48	101.11	109.25
3	B	231	FAD	C4A-N9A-C8A	3.38	109.29	105.74
3	A	232	FAD	C4-C4X-N5	3.28	122.74	118.21
3	B	231	FAD	C2A-N3A-C4A	3.17	119.58	111.83
4	A	233	YTR	C2-C3-C4	-3.09	116.84	120.32
3	B	231	FAD	C7M-C7-C8	3.09	127.06	120.76
3	A	232	FAD	C10-C4X-N5	-2.99	118.71	124.81
3	A	232	FAD	C8M-C8-C9	-2.98	114.33	119.57
3	B	231	FAD	C9A-N10-C10	-2.97	116.22	120.75
3	A	232	FAD	C5X-C6-C7	-2.89	115.47	120.83
3	A	232	FAD	O2B-C2B-C1B	2.88	120.02	110.10
4	B	233	YTR	O11-C9-C8	-2.85	118.58	125.61
3	A	232	FAD	C2B-C1B-N9A	2.81	120.29	113.30
4	B	233	YTR	C1-C2-C7	-2.75	120.60	124.30
4	B	233	YTR	C13-C7-C8	2.71	124.22	120.98
4	A	233	YTR	C15-O14-C4	2.61	121.84	114.74
3	B	231	FAD	C10-C4X-N5	-2.58	119.53	124.81
3	B	231	FAD	O4'-C4'-C5'	-2.57	104.32	109.99
3	B	231	FAD	N3A-C4A-N9A	2.54	131.48	127.17
3	A	232	FAD	C4X-C4-N3	2.53	119.69	113.25
4	B	233	YTR	C13-C7-C2	-2.53	117.08	119.94
3	A	232	FAD	C4-N3-C2	-2.52	121.17	125.64
3	B	231	FAD	C4X-C10-N1	-2.48	118.50	124.59
4	B	233	YTR	C9-C8-C7	-2.45	120.42	123.48
3	B	231	FAD	C4X-C4-N3	2.31	119.13	113.25
3	B	231	FAD	C2A-N1A-C6A	2.30	122.52	118.73
3	B	231	FAD	C8M-C8-C9	-2.27	115.57	119.57
4	A	233	YTR	C13-C7-C2	-2.26	117.38	119.94
3	A	232	FAD	O2P-P-O5'	2.26	117.80	107.57
3	A	232	FAD	O2A-PA-O3P	2.26	113.37	107.27
3	B	231	FAD	O4-C4-N3	-2.21	115.95	120.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	232	FAD	C6-C5X-C9A	2.21	122.08	119.05
4	A	233	YTR	C1-C2-C7	-2.19	121.35	124.30
3	A	232	FAD	C5A-C4A-N9A	2.19	108.20	105.81
3	B	231	FAD	C10-N1-C2	2.15	121.51	116.85
3	A	232	FAD	O3P-PA-O1A	-2.13	104.30	110.70
3	A	232	FAD	O4'-C4'-C3'	-2.11	104.31	109.25
3	B	231	FAD	C4A-N9A-C1B	-2.09	121.75	126.63
4	A	233	YTR	C13-C7-C8	2.08	123.48	120.98
3	B	231	FAD	O4B-C1B-N9A	2.03	111.98	108.09
4	B	233	YTR	C2-C3-C4	-2.01	118.06	120.32

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	232	FAD	C2B-C1B-N9A-C8A
3	B	231	FAD	C5B-O5B-PA-O1A
3	B	231	FAD	C5B-O5B-PA-O2A
3	B	231	FAD	C5B-O5B-PA-O3P
4	B	233	YTR	C5-C4-O14-C15
3	A	232	FAD	C2B-C1B-N9A-C4A
4	B	233	YTR	C3-C4-O14-C15
3	B	231	FAD	C2B-C1B-N9A-C8A
3	A	232	FAD	P-O3P-PA-O2A
3	A	232	FAD	C4'-C5'-O5'-P
3	B	231	FAD	C4'-C5'-O5'-P
3	B	231	FAD	O4'-C4'-C5'-O5'
3	B	231	FAD	C4B-C5B-O5B-PA
3	B	231	FAD	O4B-C1B-N9A-C8A

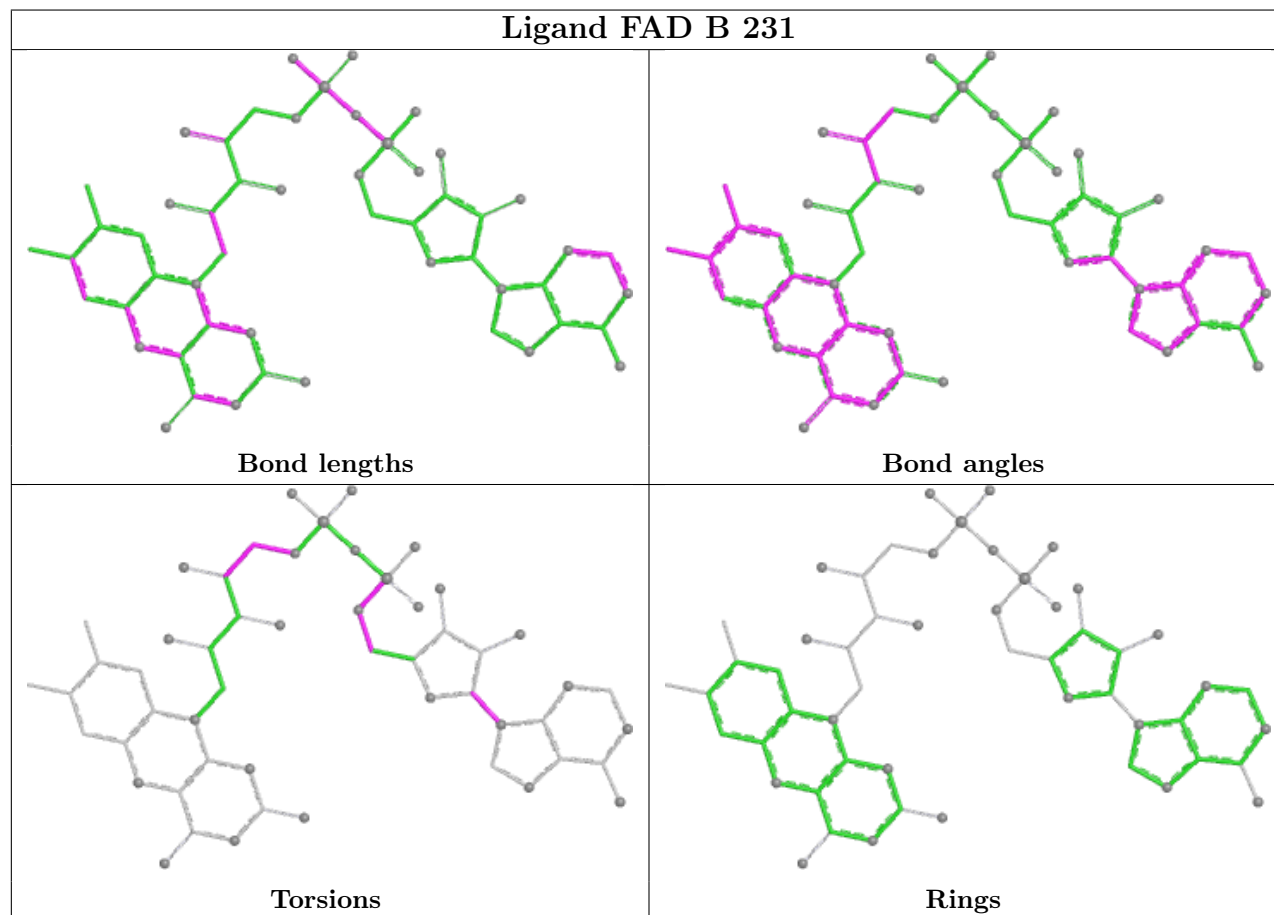
There are no ring outliers.

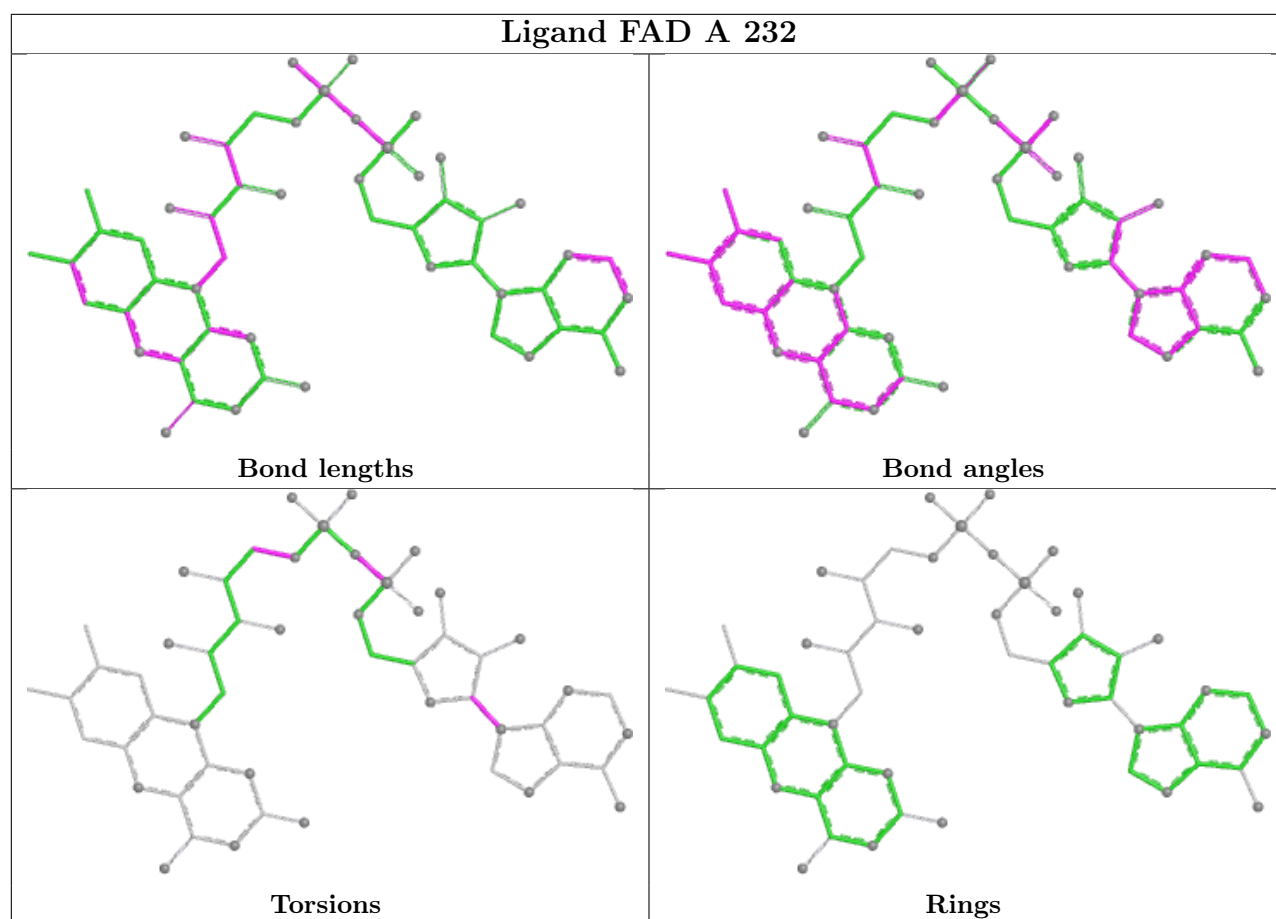
4 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	231	FAD	1	0
4	B	233	YTR	5	0
4	A	233	YTR	7	0
3	A	232	FAD	8	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, 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	230/230 (100%)	1.02	45 (19%) 3 5	11, 26, 49, 63	0
1	B	230/230 (100%)	0.39	18 (7%) 19 28	10, 19, 43, 56	0
All	All	460/460 (100%)	0.71	63 (13%) 6 11	10, 21, 48, 63	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	ALA	7.7
1	A	1	ALA	7.5
1	A	128	ILE	6.7
1	B	2	GLY	6.4
1	B	194	ILE	4.3
1	A	130	GLY	4.0
1	A	229	GLY	4.0
1	B	229	GLY	3.9
1	B	230	GLN	3.9
1	A	129	PRO	3.9
1	B	151	THR	3.7
1	A	202	GLY	3.5
1	A	150	GLY	3.4
1	A	228	PHE	3.3
1	A	205	ALA	3.3
1	A	151	THR	3.2
1	A	226	TRP	3.2
1	A	160	VAL	3.2
1	A	194	ILE	3.1
1	B	195	ALA	3.1
1	A	155	TYR	3.1
1	A	156	THR	3.1
1	B	128	ILE	3.1
1	A	58	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	195	ALA	3.0
1	A	196	SER	3.0
1	A	190	PHE	3.0
1	A	123	GLY	2.9
1	A	132	TYR	2.9
1	A	152	ALA	2.9
1	A	2	GLY	2.9
1	A	185	ALA	2.8
1	A	64	VAL	2.8
1	A	222	CYS	2.8
1	A	191	ALA	2.7
1	A	57	GLY	2.6
1	B	155	TYR	2.6
1	A	135	GLY	2.6
1	A	60	SER	2.6
1	B	160	VAL	2.5
1	B	196	SER	2.5
1	A	157	LYS	2.5
1	A	204	VAL	2.5
1	A	131	PHE	2.5
1	B	159	GLY	2.4
1	B	156	THR	2.4
1	B	158	THR	2.4
1	A	188	ILE	2.4
1	A	166	TYR	2.4
1	B	191	ALA	2.3
1	B	56	THR	2.3
1	B	166	TYR	2.3
1	A	230	GLN	2.3
1	A	223	THR	2.3
1	B	202	GLY	2.3
1	A	225	HIS	2.2
1	A	206	ALA	2.2
1	A	141	LEU	2.2
1	A	220	ILE	2.2
1	A	189	SER	2.2
1	A	153	GLU	2.1
1	A	59	LEU	2.1
1	A	224	ALA	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](#)

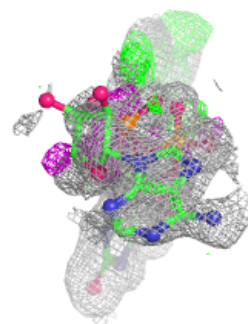
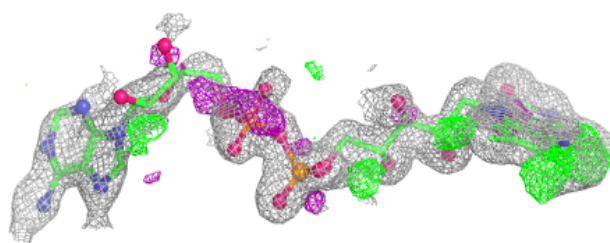
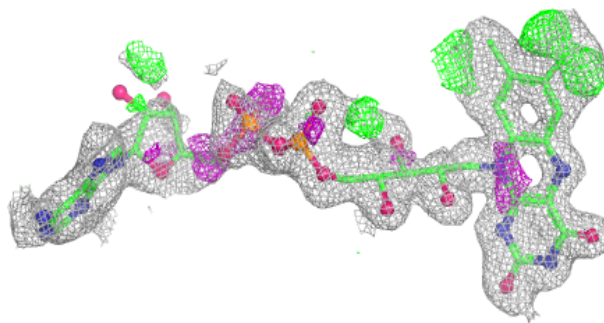
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	YTR	A	233	17/17	0.80	0.16	32,36,44,46	0
4	YTR	B	233	17/17	0.82	0.13	28,33,39,43	0
3	FAD	B	231	53/53	0.89	0.12	18,27,54,60	0
3	FAD	A	232	53/53	0.90	0.13	15,29,61,62	0
2	ZN	A	231	1/1	0.94	0.14	30,30,30,30	0
2	ZN	B	232	1/1	0.98	0.05	21,21,21,21	0

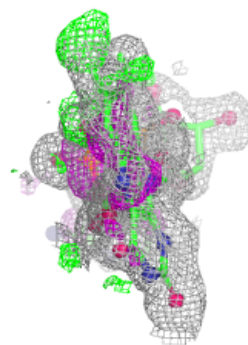
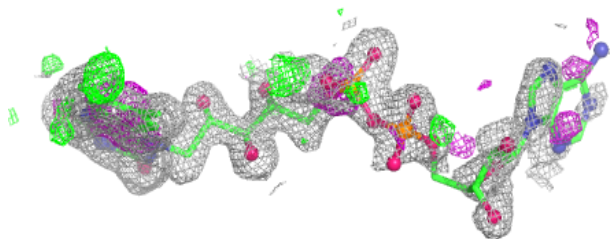
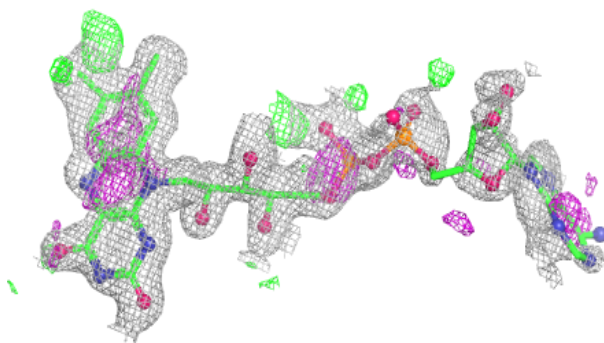
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FAD B 231:

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

**Electron density around FAD A 232:**

$2mF_o-DF_c$ (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.