



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:37 AM UTC

PDB ID : 7A76 / pdb_00007a76
Title : Bacillithiol Disulfide Reductase Bdr (YpdA) from Bacillus cereus
Authors : Hammerstad, M.; Gudim, I.; Hersleth, H.-P.
Deposited on : 2020-08-27
Resolution : 1.65 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

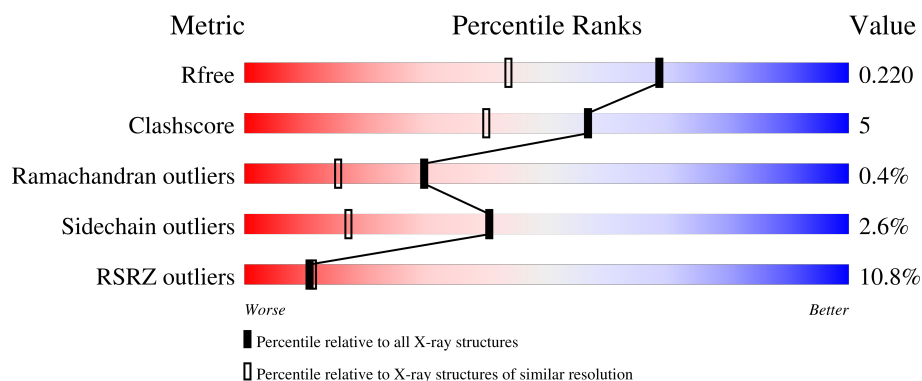
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	326	4% 93% 6%
1	B	326	7% 88% 11%
1	C	326	11% 88% 12%
1	D	326	21% 84% 13%

2 Entry composition ⓘ

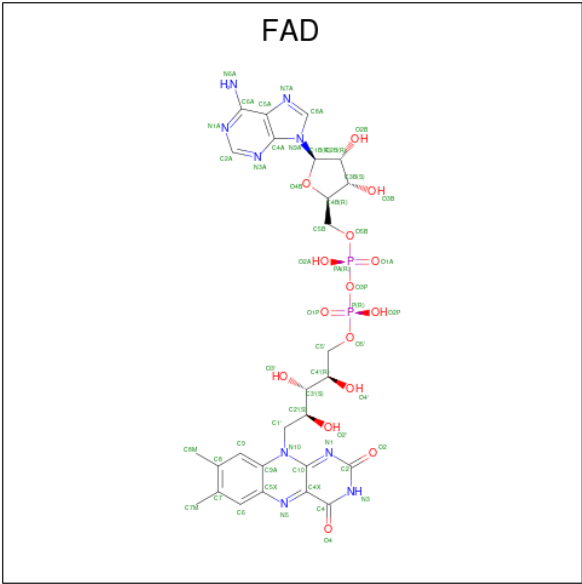
There are 4 unique types of molecules in this entry. The entry contains 11737 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 THIOREDOXIN REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	9	0
			2658	1687	460	503	8			
1	B	326	Total	C	N	O	S	0	13	0
			2695	1717	465	506	7			
1	C	325	Total	C	N	O	S	0	11	0
			2657	1688	456	505	8			
1	D	324	Total	C	N	O	S	0	11	0
			2654	1688	455	504	7			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	B	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	283	Total	O	0	7
			283	283		
4	B	251	Total	O	0	7
			251	251		
4	C	182	Total	O	0	4
			182	182		
4	D	141	Total	O	0	2
			141	141		

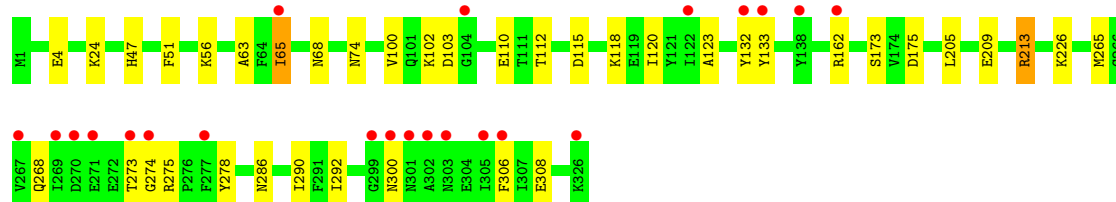
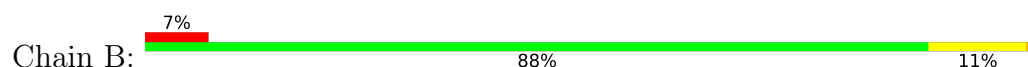
3 Residue-property plots [i](#)

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.

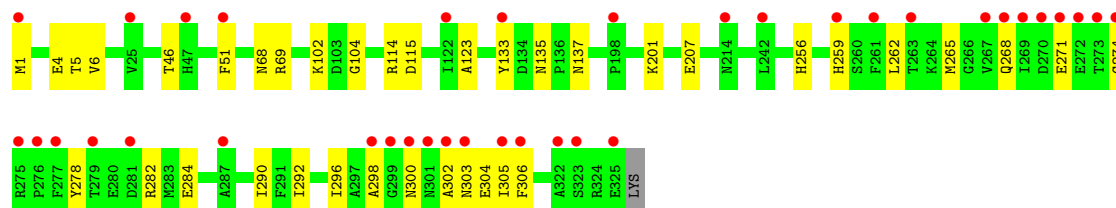
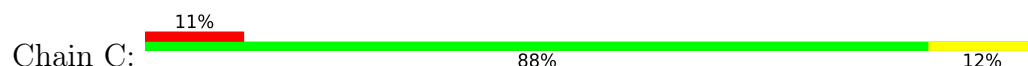
• Molecule 1: THIOREDOXIN REDUCTASE



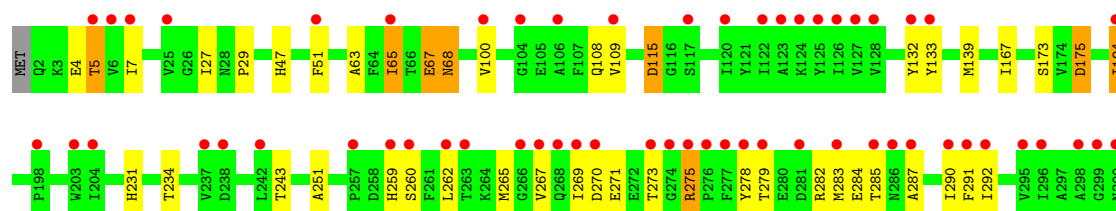
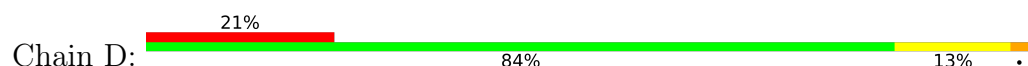
• Molecule 1: THIOREDOXIN REDUCTASE



• Molecule 1: THIOREDOXIN REDUCTASE



• Molecule 1: THIOREDOXIN REDUCTASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.73Å 114.90Å 146.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.23 – 1.65 45.23 – 1.65	Depositor EDS
% Data completeness (in resolution range)	97.5 (45.23-1.65) 97.5 (45.23-1.65)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 1.65Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, REFMAC 5.8.0253	Depositor
R, R_{free}	0.190 , 0.218 0.192 , 0.220	Depositor DCC
R_{free} test set	8791 reflections (4.45%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.401	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11737	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% 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: NA, 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	0.29	0/2713	0.50	0/3666
1	B	0.30	0/2753	0.52	0/3725
1	C	0.26	0/2713	0.46	0/3671
1	D	0.24	0/2709	0.46	0/3667
All	All	0.27	0/10888	0.49	0/14729

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	A	2658	0	2618	15	0
1	B	2695	0	2652	28	0
1	C	2657	0	2607	25	0
1	D	2654	0	2604	36	0
2	A	53	0	31	0	0
2	B	53	0	31	3	0
2	C	53	0	31	2	0
2	D	53	0	31	3	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	283	0	0	1	1
4	B	251	0	0	6	1
4	C	182	0	0	5	1
4	D	141	0	0	2	1
All	All	11737	0	10605	100	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 5.

All (100) 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:D:285:THR:HG23	1:D:287:ALA:H	1.53	0.74
1:A:273:THR:HG23	1:A:275:ARG:H	1.54	0.73
1:A:47:HIS:CE1	1:B:74[B]:ASN:HD21	2.08	0.72
1:A:99:LYS:NZ	1:A:101:GLN:OE1	2.25	0.69
1:A:124:LYS:HE3	1:A:326:LYS:HG2	1.78	0.66
1:D:282:ARG:NH1	1:D:284:GLU:OE1	2.30	0.64
1:D:51:PHE:N	2:D:401:FAD:O4	2.31	0.63
1:D:47:HIS:HD2	4:D:539:HOH:O	1.83	0.62
1:B:47:HIS:HD2	4:B:547:HOH:O	1.83	0.60
1:C:265[B]:MET:HE2	1:C:290:ILE:HD13	1.83	0.59
1:D:100:VAL:HG22	1:D:109:VAL:HG12	1.84	0.59
1:B:133[A]:TYR:OH	2:B:401:FAD:H9	2.03	0.59
1:B:273:THR:O	1:B:275:ARG:N	2.33	0.59
1:B:112:THR:OG1	1:B:118:LYS:NZ	2.30	0.58
1:D:313:HIS:O	1:D:317:ILE:HG12	2.04	0.58
1:B:24:LYS:NZ	4:B:502:HOH:O	2.33	0.58
1:D:283:MET:HB2	1:D:317:ILE:HD11	1.85	0.58
1:B:226:LYS:NZ	4:B:504:HOH:O	2.36	0.57
1:D:265:MET:HE2	1:D:290:ILE:HD13	1.86	0.57
1:B:47:HIS:HE1	1:B:175:ASP:OD1	1.87	0.57
1:B:51:PHE:N	2:B:401:FAD:O4	2.35	0.56
1:C:133[A]:TYR:OH	2:C:401:FAD:H9	2.07	0.55
1:D:115[A]:ASP:OD1	1:D:115[A]:ASP:N	2.31	0.55
1:D:285:THR:HG22	1:D:290:ILE:O	2.07	0.54
1:B:68:ASN:HB2	4:B:597:HOH:O	2.08	0.54
1:C:274:GLY:HA3	1:C:300:ASN:ND2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:PHE:N	2:C:401:FAD:O4	2.40	0.53
1:D:47:HIS:HE1	1:D:175[B]:ASP:OD1	1.92	0.53
1:C:115:ASP:OD2	1:D:231:HIS:HE1	1.90	0.53
1:D:234:THR:HG23	4:D:540:HOH:O	2.07	0.53
1:D:267:VAL:HG22	1:D:285:THR:HG21	1.92	0.51
1:D:283:MET:HB2	1:D:317:ILE:CD1	2.40	0.51
1:D:234:THR:HG22	1:D:243:THR:OG1	2.10	0.51
1:D:259:HIS:HB3	1:D:269:ILE:HD13	1.91	0.51
1:C:304:GLU:HG3	1:C:305:ILE:HG13	1.93	0.50
1:B:100:VAL:HB	1:B:265:MET:HG3	1.93	0.50
1:C:298:ALA:HB1	1:C:302:ALA:HA	1.92	0.50
1:D:4:GLU:HG3	1:D:7[B]:ILE:HD11	1.92	0.50
1:A:47:HIS:CE1	1:B:74[B]:ASN:ND2	2.78	0.50
1:C:137:ASN:OD1	1:C:256:HIS:HD2	1.95	0.50
1:C:259:HIS:CE1	1:C:300:ASN:HD21	2.30	0.50
1:D:139[B]:MET:HE3	1:D:251:ALA:HB1	1.94	0.50
1:D:4:GLU:O	1:D:5:THR:OG1	2.20	0.49
1:B:226:LYS:NZ	4:B:507:HOH:O	2.45	0.49
1:D:285:THR:HG23	1:D:287:ALA:N	2.26	0.49
1:A:231:HIS:HE1	1:B:115:ASP:OD2	1.96	0.49
1:C:5:THR:HG22	1:C:6:VAL:HG23	1.95	0.49
1:A:69[B]:ARG:NE	1:C:207:GLU:OE2	2.46	0.49
1:D:47:HIS:HE1	1:D:175[A]:ASP:OD2	1.95	0.49
1:D:194:ILE:HD13	1:D:194:ILE:H	1.77	0.48
1:D:27:ILE:O	1:D:29:PRO:HD3	2.14	0.48
1:C:114:ARG:NH2	4:C:504:HOH:O	2.26	0.48
1:D:278:TYR:CD1	1:D:292:ILE:HD11	2.48	0.47
1:C:278:TYR:CD2	1:C:292:ILE:HD11	2.49	0.47
1:D:262:LEU:O	1:D:265:MET:HG2	2.14	0.47
1:C:68:ASN:HB2	4:C:554:HOH:O	2.14	0.47
1:A:256:HIS:HE1	4:A:742:HOH:O	1.99	0.46
1:B:132:TYR:HE1	1:B:133[A]:TYR:CE1	2.33	0.46
1:B:56:LYS:HB3	1:B:308:GLU:HG2	1.98	0.45
1:A:1:MET:HG3	1:A:122:ILE:HG12	1.99	0.45
1:B:268:GLN:HG3	1:B:286:ASN:ND2	2.32	0.45
1:A:219[B]:MET:HG2	1:A:221:PHE:CE2	2.52	0.45
1:A:271:GLU:O	1:A:272:GLU:HB3	2.16	0.45
1:C:69:ARG:O	4:C:502:HOH:O	2.21	0.45
1:A:270:ASP:HB3	1:A:273:THR:HG22	1.99	0.45
1:D:291:PHE:HB3	1:D:317:ILE:HD12	1.98	0.44
1:C:51:PHE:HB3	1:C:201:LYS:HE2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282:ARG:NH1	1:C:284:GLU:OE1	2.50	0.44
1:B:4:GLU:O	1:B:123:ALA:HA	2.18	0.43
1:D:63:ALA:HB1	1:D:65:ILE:HD13	2.00	0.43
1:D:275:ARG:O	1:D:275:ARG:HG2	2.18	0.43
1:C:300:ASN:N	1:C:300:ASN:HD22	2.16	0.43
1:C:262:LEU:HD11	1:C:296:ILE:HD11	2.01	0.43
1:C:135:ASN:HB2	1:C:256:HIS:O	2.19	0.43
1:B:213:ARG:HE	1:B:213:ARG:HB3	1.59	0.43
1:D:291:PHE:CE2	1:D:321:ILE:HD11	2.54	0.43
1:C:46:THR:O	4:C:503:HOH:O	2.22	0.42
1:B:65[B]:ILE:HG23	4:C:570:HOH:O	2.17	0.42
1:D:273:THR:HG23	1:D:275:ARG:H	1.83	0.42
1:B:133[A]:TYR:OH	2:B:401:FAD:H1'1	2.20	0.42
1:B:278:TYR:CD1	1:B:292:ILE:HD11	2.53	0.42
1:A:108:GLN:HG2	1:A:122:ILE:HD13	2.02	0.42
1:B:162[A]:ARG:NH2	4:B:511:HOH:O	2.51	0.41
1:B:265:MET:HG2	1:B:290:ILE:HD13	2.02	0.41
1:C:102:LYS:HD2	1:C:104:GLY:O	2.21	0.41
1:C:262:LEU:O	1:C:265[B]:MET:HG2	2.20	0.41
1:B:63:ALA:HB1	1:B:65[A]:ILE:HD13	2.03	0.41
1:A:137:ASN:OD1	1:A:256:HIS:HD2	2.04	0.41
1:B:205:LEU:HG	1:B:209:GLU:HG3	2.03	0.41
1:C:4:GLU:O	1:C:123:ALA:HA	2.20	0.41
1:D:139[B]:MET:HE1	1:D:167:ILE:CD1	2.51	0.41
1:D:270:ASP:OD2	1:D:275:ARG:NH2	2.54	0.41
2:D:401:FAD:HM83	2:D:401:FAD:HM71	1.91	0.41
1:C:298:ALA:CB	1:C:302:ALA:HA	2.49	0.41
1:D:133[A]:TYR:OH	2:D:401:FAD:H9	2.20	0.41
1:B:65[B]:ILE:O	1:B:65[B]:ILE:HG13	2.22	0.40
1:A:194:ILE:H	1:A:194:ILE:HG13	1.77	0.40
1:B:110:GLU:HG2	1:B:120:ILE:HG12	2.03	0.40
1:D:67[A]:GLU:HG3	1:D:68:ASN:N	2.36	0.40
1:D:273:THR:HG21	1:D:275:ARG:CZ	2.51	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)
4:C:654:HOH:O	4:D:629:HOH:O[4_754]	2.15	0.05
4:A:737:HOH:O	4:B:524:HOH:O[2_555]	2.17	0.03

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	333/326 (102%)	324 (97%)	8 (2%)	1 (0%)	36	21
1	B	337/326 (103%)	325 (96%)	10 (3%)	2 (1%)	21	8
1	C	334/326 (102%)	327 (98%)	7 (2%)	0	100	100
1	D	333/326 (102%)	320 (96%)	11 (3%)	2 (1%)	21	8
All	All	1337/1304 (102%)	1296 (97%)	36 (3%)	5 (0%)	30	15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	ASN
1	D	5	THR
1	B	274	GLY
1	D	271	GLU
1	A	325	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	282/273 (103%)	276 (98%)	6 (2%)	47	24
1	B	286/273 (105%)	279 (98%)	7 (2%)	43	20
1	C	283/273 (104%)	278 (98%)	5 (2%)	51	30
1	D	282/273 (103%)	267 (95%)	15 (5%)	20	4
All	All	1133/1092 (104%)	1100 (97%)	33 (3%)	40	14

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	LYS
1	A	132	TYR
1	A	219[A]	MET
1	A	219[B]	MET
1	A	260	SER
1	A	325	GLU
1	B	65[A]	ILE
1	B	65[B]	ILE
1	B	102	LYS
1	B	103	ASP
1	B	173	SER
1	B	213	ARG
1	B	306	PHE
1	C	1	MET
1	C	268	GLN
1	C	271	GLU
1	C	303	ASN
1	C	306	PHE
1	D	65	ILE
1	D	67[A]	GLU
1	D	67[B]	GLU
1	D	68	ASN
1	D	108	GLN
1	D	115[A]	ASP
1	D	115[B]	ASP
1	D	132	TYR
1	D	173	SER
1	D	175[A]	ASP
1	D	175[B]	ASP
1	D	194	ILE
1	D	260	SER
1	D	275	ARG
1	D	279	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	231	HIS
1	A	256	HIS
1	B	47	HIS

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Mol	Chain	Res	Type
1	C	23	GLN
1	C	47	HIS
1	C	48	GLN
1	C	101	GLN
1	C	256	HIS
1	C	300	ASN
1	C	319	GLN
1	D	2	GLN
1	D	43	ASN
1	D	47	HIS
1	D	224	HIS
1	D	231	HIS
1	D	256	HIS
1	D	259	HIS
1	D	300	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 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
2	FAD	B	401	-	58,58,58	0.61	1 (1%)	85,89,89	0.44	0
2	FAD	C	401	-	58,58,58	0.63	1 (1%)	85,89,89	0.41	0
2	FAD	A	401	-	58,58,58	0.40	0	85,89,89	0.52	1 (1%)
2	FAD	D	401	-	58,58,58	0.45	0	85,89,89	0.44	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
2	FAD	B	401	-	-	0/34/50/50	0/6/6/6
2	FAD	C	401	-	-	0/34/50/50	0/6/6/6
2	FAD	A	401	-	-	1/34/50/50	0/6/6/6
2	FAD	D	401	-	-	1/34/50/50	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	FAD	P-O3P	-3.99	1.55	1.59
2	B	401	FAD	P-O3P	3.27	1.63	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	FAD	O2A-PA-O1A	2.18	122.59	112.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	FAD	PA-O3P-P-O5'
2	D	401	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

3 monomers are involved in 8 short contacts:

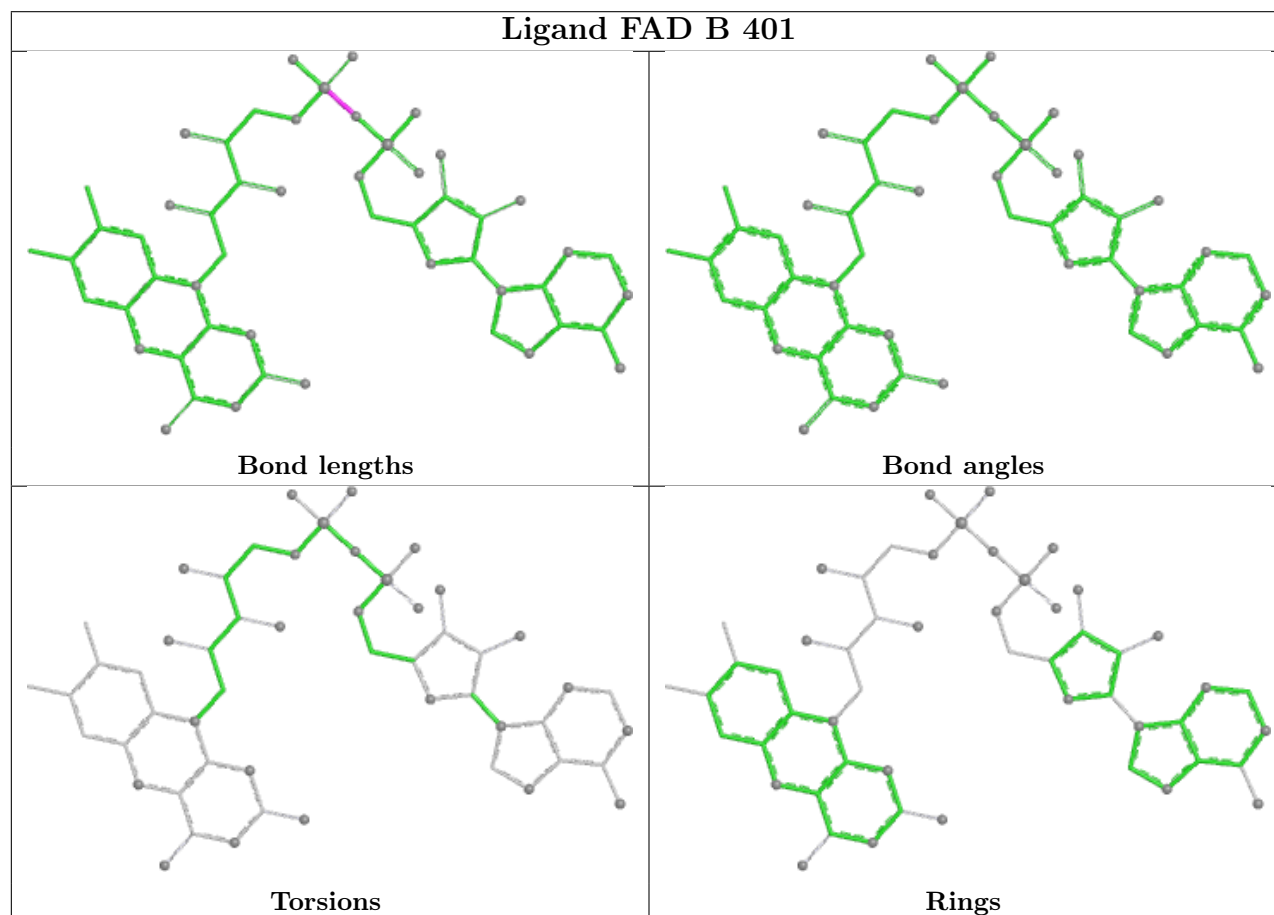
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	FAD	3	0
2	C	401	FAD	2	0

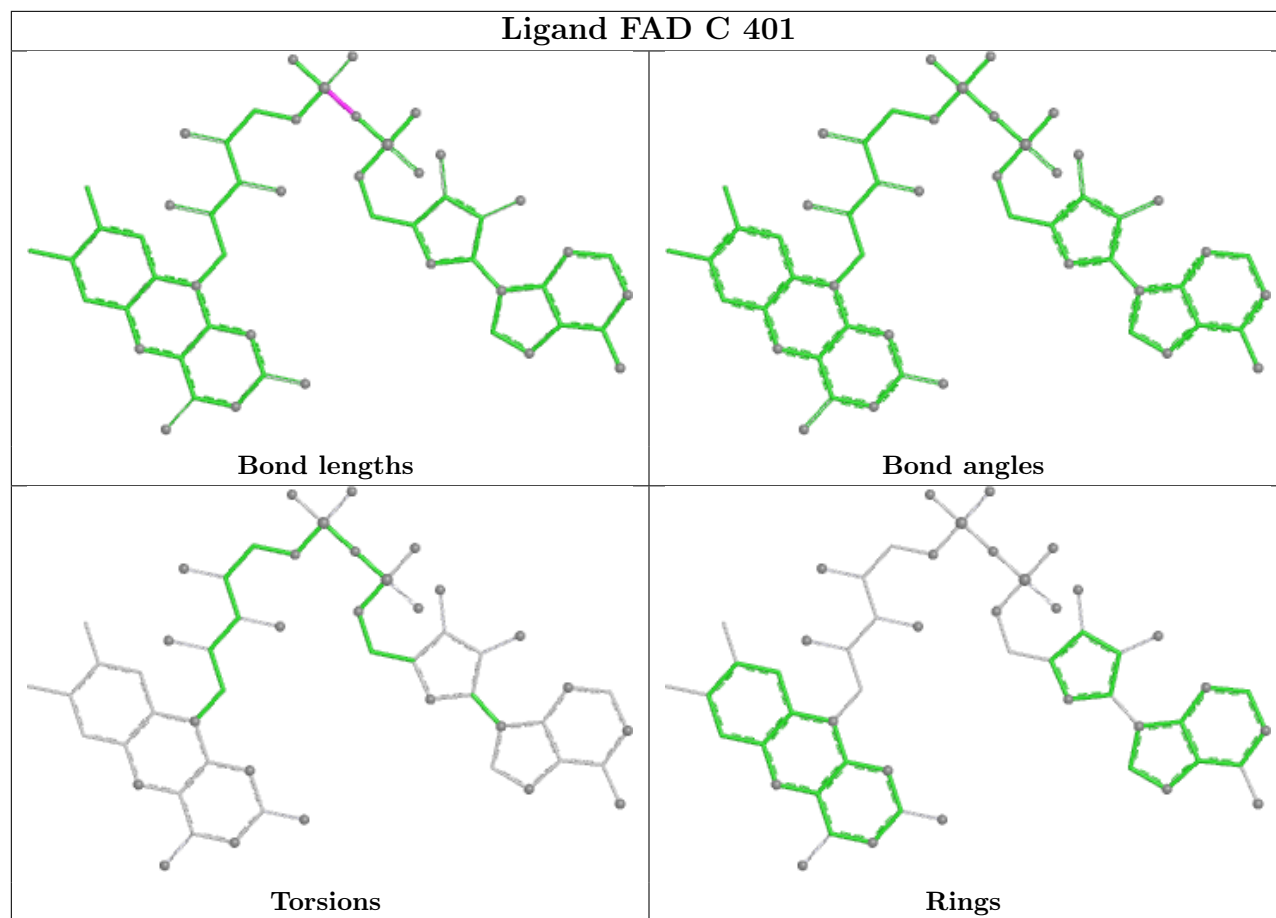
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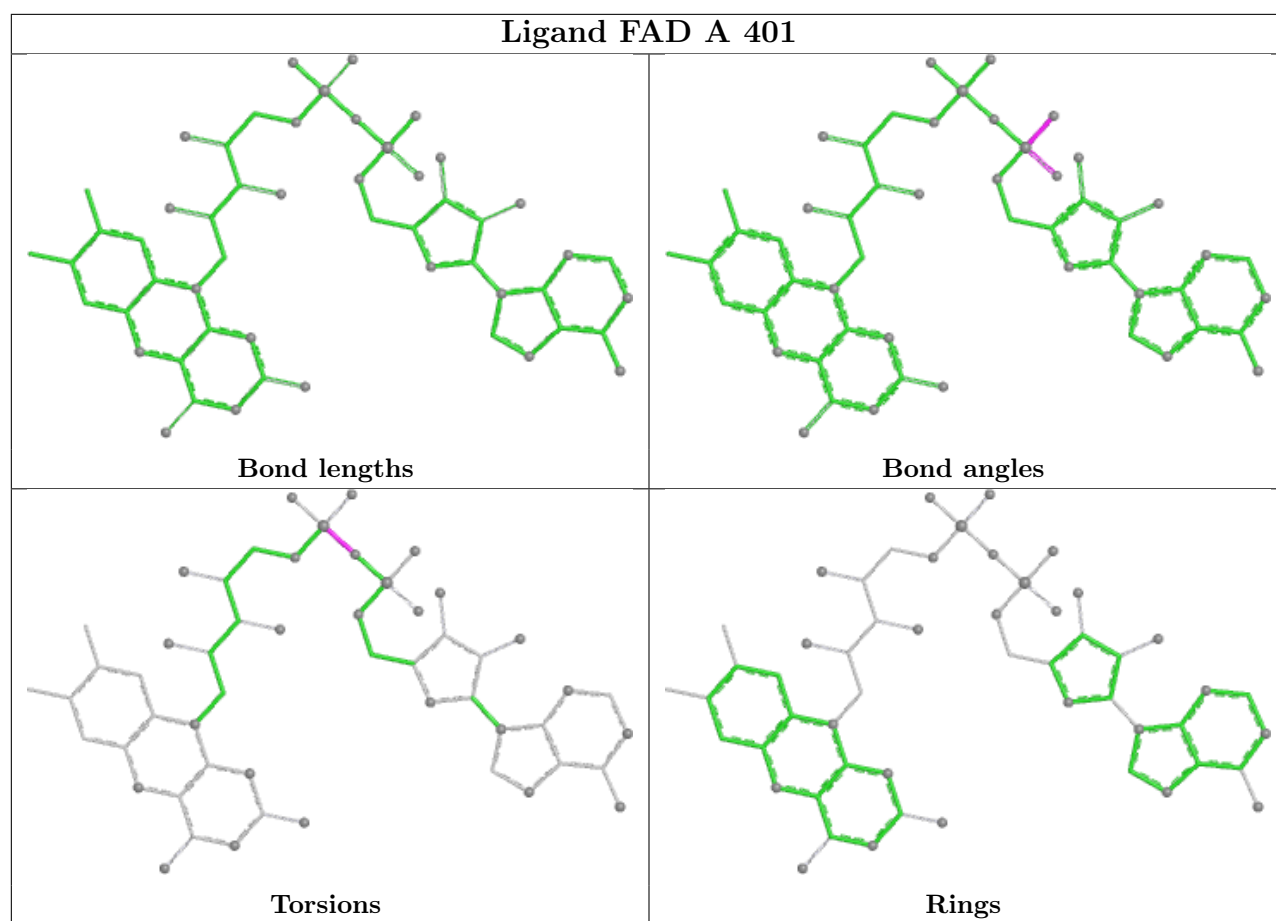
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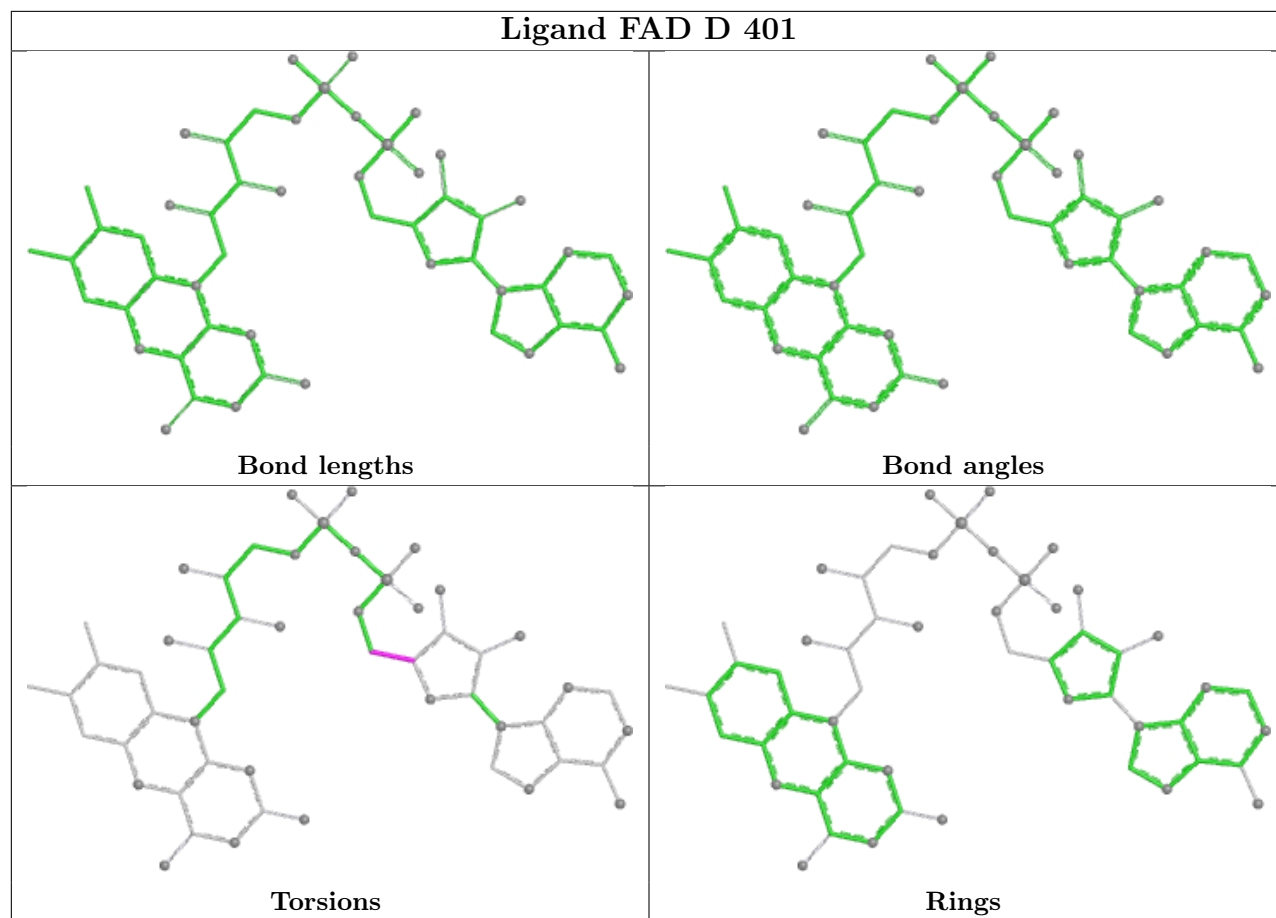
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	FAD	3	0

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

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	326/326 (100%)	0.23	13 (3%)	42	46	11, 33, 56, 82	9 (2%)
1	B	326/326 (100%)	0.30	22 (6%)	24	27	11, 31, 62, 92	13 (3%)
1	C	325/326 (99%)	0.68	37 (11%)	10	10	12, 40, 77, 94	11 (3%)
1	D	324/326 (99%)	1.05	69 (21%)	2	3	12, 48, 92, 132	11 (3%)
All	All	1301/1304 (99%)	0.56	141 (10%)	11	11	11, 37, 78, 132	44 (3%)

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277[A]	PHE	6.1
1	C	269	ILE	5.7
1	D	269	ILE	5.7
1	D	277	PHE	5.3
1	D	274	GLY	5.3
1	C	302	ALA	5.3
1	C	214[A]	ASN	5.1
1	B	273	THR	5.0
1	A	326	LYS	5.0
1	C	277	PHE	4.9
1	C	273	THR	4.7
1	B	133[A]	TYR	4.6
1	D	133[A]	TYR	4.5
1	D	267	VAL	4.4
1	D	276	PRO	4.3
1	D	323	SER	4.3
1	D	306	PHE	4.3
1	D	295	VAL	4.1
1	D	298	ALA	4.0
1	D	300	ASN	3.9
1	D	299	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	302	ALA	3.7
1	D	259	HIS	3.6
1	A	302	ALA	3.5
1	C	1	MET	3.5
1	C	275	ARG	3.5
1	C	51	PHE	3.5
1	C	323	SER	3.5
1	D	320	THR	3.5
1	D	65	ILE	3.4
1	C	267	VAL	3.4
1	C	274	GLY	3.4
1	D	285	THR	3.3
1	B	301	ASN	3.3
1	B	302	ALA	3.3
1	B	274	GLY	3.3
1	D	321	ILE	3.3
1	C	270	ASP	3.2
1	D	322	ALA	3.2
1	C	303	ASN	3.2
1	D	268	GLN	3.2
1	C	301	ASN	3.1
1	C	268	GLN	3.1
1	D	270	ASP	3.1
1	D	305	ILE	3.1
1	C	263	THR	3.1
1	B	306	PHE	3.0
1	A	305	ILE	3.0
1	D	273	THR	3.0
1	C	259	HIS	3.0
1	D	275	ARG	3.0
1	A	69[A]	ARG	3.0
1	D	301	ASN	3.0
1	D	303	ASN	3.0
1	C	281[A]	ASP	2.9
1	A	273	THR	2.9
1	D	51	PHE	2.9
1	D	296	ILE	2.9
1	B	305	ILE	2.9
1	D	126	ILE	2.9
1	D	291	PHE	2.8
1	C	305	ILE	2.8
1	D	122	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	271	GLU	2.8
1	D	5	THR	2.8
1	D	198	PRO	2.7
1	D	242	LEU	2.7
1	C	306	PHE	2.7
1	D	238	ASP	2.7
1	B	269	ILE	2.7
1	C	271	GLU	2.6
1	C	299	GLY	2.6
1	D	104	GLY	2.6
1	D	278	TYR	2.6
1	D	120	ILE	2.6
1	D	106	ALA	2.6
1	D	279	THR	2.6
1	D	262	LEU	2.6
1	B	138[A]	TYR	2.6
1	B	267	VAL	2.6
1	D	127	VAL	2.6
1	D	132	TYR	2.6
1	D	7[A]	ILE	2.6
1	D	203	TRP	2.6
1	C	300	ASN	2.6
1	C	242[A]	LEU	2.6
1	A	300	ASN	2.6
1	A	301	ASN	2.6
1	D	237	VAL	2.5
1	B	122	ILE	2.5
1	C	122	ILE	2.5
1	D	290	ILE	2.5
1	C	276	PRO	2.5
1	B	303	ASN	2.4
1	C	198	PRO	2.4
1	C	287	ALA	2.4
1	A	267	VAL	2.4
1	D	109	VAL	2.4
1	D	307	ILE	2.4
1	A	281	ASP	2.4
1	A	274	GLY	2.4
1	D	117	SER	2.4
1	A	132	TYR	2.4
1	B	299	GLY	2.4
1	D	257	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	287	ALA	2.4
1	D	263	THR	2.4
1	B	162[A]	ARG	2.4
1	D	6	VAL	2.4
1	D	304	GLU	2.3
1	D	124	LYS	2.3
1	B	132	TYR	2.3
1	B	104	GLY	2.3
1	C	279	THR	2.3
1	D	125	TYR	2.3
1	D	194	ILE	2.3
1	C	261	PHE	2.2
1	D	204	ILE	2.2
1	D	25	VAL	2.2
1	D	100	VAL	2.2
1	D	286	ASN	2.2
1	C	298	ALA	2.2
1	D	283	MET	2.2
1	C	47	HIS	2.2
1	C	133[A]	TYR	2.2
1	B	300	ASN	2.2
1	D	266	GLY	2.2
1	D	281	ASP	2.1
1	A	47	HIS	2.1
1	B	270	ASP	2.1
1	C	325	GLU	2.1
1	C	25	VAL	2.1
1	D	123	ALA	2.1
1	D	128	VAL	2.1
1	B	326	LYS	2.1
1	D	260	SER	2.1
1	B	65[A]	ILE	2.1
1	C	322	ALA	2.1
1	C	272	GLU	2.1
1	A	68	ASN	2.0
1	D	292	ILE	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

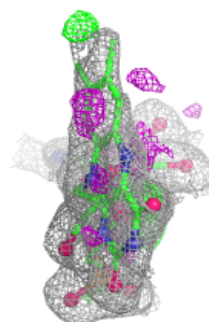
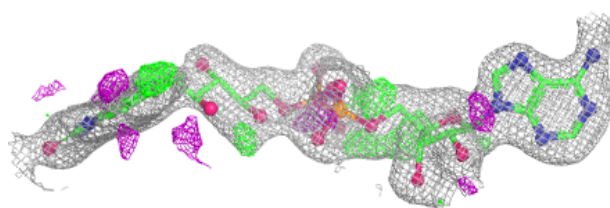
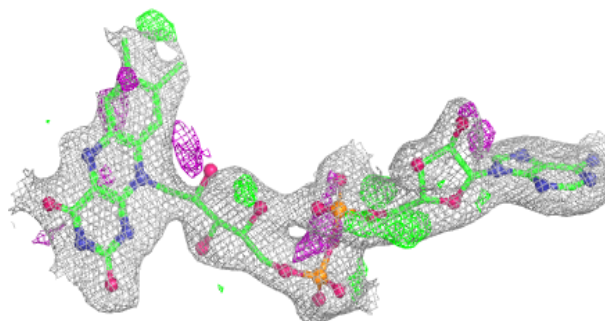
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	NA	D	402	1/1	0.89	0.10	29,29,29,29	0
2	FAD	D	401	53/53	0.93	0.12	26,44,74,79	0
2	FAD	C	401	53/53	0.95	0.09	22,30,39,44	0
2	FAD	B	401	53/53	0.97	0.07	17,26,48,50	0
3	NA	C	402	1/1	0.97	0.05	26,26,26,26	0
2	FAD	A	401	53/53	0.97	0.07	21,27,33,39	0
3	NA	A	402	1/1	0.98	0.10	25,25,25,25	0
3	NA	B	402	1/1	0.99	0.07	22,22,22,22	0

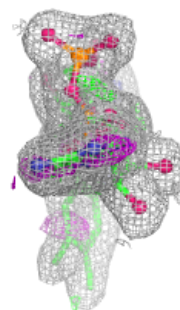
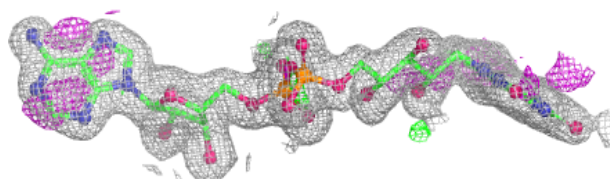
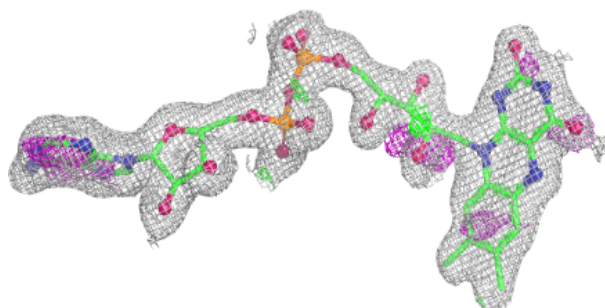
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD D 401:

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

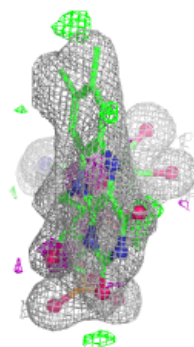
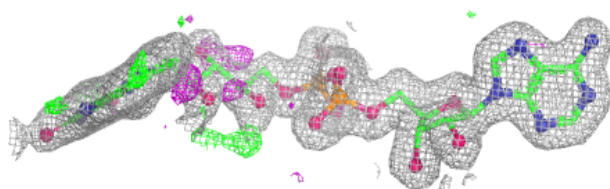
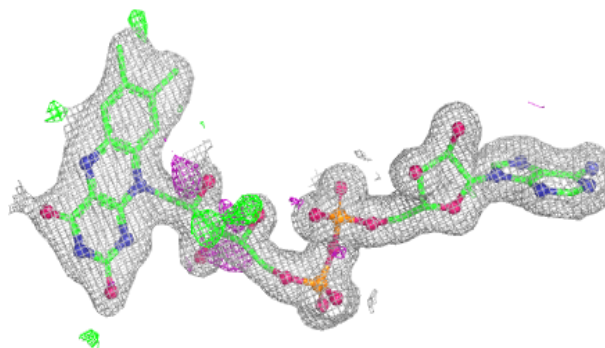
**Electron density around FAD C 401:**

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

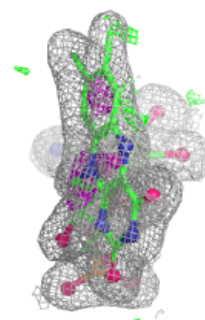
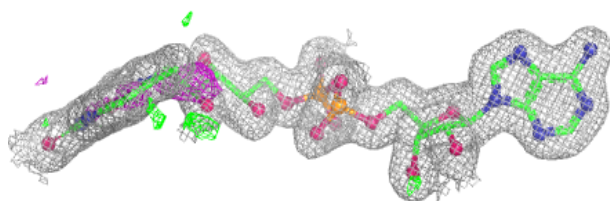
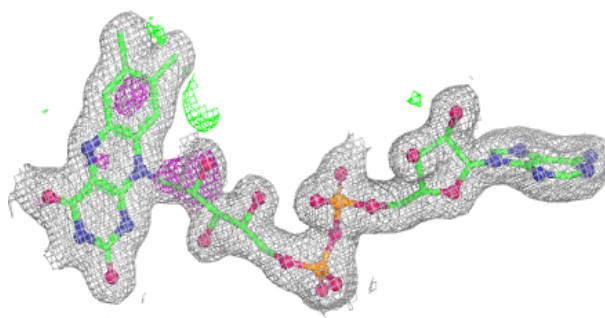


Electron density around FAD B 401:

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

**Electron density around FAD A 401:**

$2mF_o-DF_c$ (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.