



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:02 PM UTC

PDB ID : 6HF3 / pdb_00006hf3
Title : M tuberculosis DprE1 in complex with a covalently bound nitrobenzothiazine
Authors : Futterer, K.; Batt, S.M.; Besra, G.S.
Deposited on : 2018-08-21
Resolution : 2.20 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

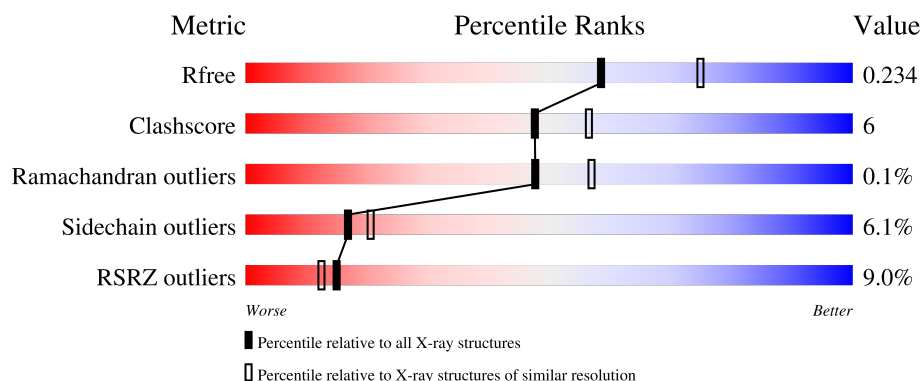
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	481	7% 77% 10% • 11%
1	B	481	9% 70% 15% • 14%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6560 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 Decaprenylphosphoryl-beta-D-ribose oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3214	2039	569	596	10			
1	B	414	Total	C	N	O	S	0	0	0
			3141	1992	556	583	10			

There are 40 discrepancies between the modelled and reference sequences:

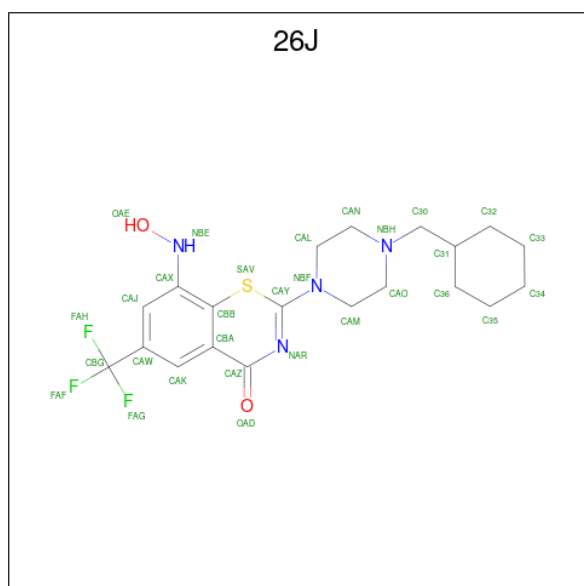
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P9WJF1
A	-18	GLY	-	expression tag	UNP P9WJF1
A	-17	SER	-	expression tag	UNP P9WJF1
A	-16	SER	-	expression tag	UNP P9WJF1
A	-15	HIS	-	expression tag	UNP P9WJF1
A	-14	HIS	-	expression tag	UNP P9WJF1
A	-13	HIS	-	expression tag	UNP P9WJF1
A	-12	HIS	-	expression tag	UNP P9WJF1
A	-11	HIS	-	expression tag	UNP P9WJF1
A	-10	HIS	-	expression tag	UNP P9WJF1
A	-9	SER	-	expression tag	UNP P9WJF1
A	-8	SER	-	expression tag	UNP P9WJF1
A	-7	GLY	-	expression tag	UNP P9WJF1
A	-6	LEU	-	expression tag	UNP P9WJF1
A	-5	VAL	-	expression tag	UNP P9WJF1
A	-4	PRO	-	expression tag	UNP P9WJF1
A	-3	ARG	-	expression tag	UNP P9WJF1
A	-2	GLY	-	expression tag	UNP P9WJF1
A	-1	SER	-	expression tag	UNP P9WJF1
A	0	HIS	-	expression tag	UNP P9WJF1
B	-19	MET	-	initiating methionine	UNP P9WJF1
B	-18	GLY	-	expression tag	UNP P9WJF1
B	-17	SER	-	expression tag	UNP P9WJF1
B	-16	SER	-	expression tag	UNP P9WJF1
B	-15	HIS	-	expression tag	UNP P9WJF1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP P9WJF1
B	-13	HIS	-	expression tag	UNP P9WJF1
B	-12	HIS	-	expression tag	UNP P9WJF1
B	-11	HIS	-	expression tag	UNP P9WJF1
B	-10	HIS	-	expression tag	UNP P9WJF1
B	-9	SER	-	expression tag	UNP P9WJF1
B	-8	SER	-	expression tag	UNP P9WJF1
B	-7	GLY	-	expression tag	UNP P9WJF1
B	-6	LEU	-	expression tag	UNP P9WJF1
B	-5	VAL	-	expression tag	UNP P9WJF1
B	-4	PRO	-	expression tag	UNP P9WJF1
B	-3	ARG	-	expression tag	UNP P9WJF1
B	-2	GLY	-	expression tag	UNP P9WJF1
B	-1	SER	-	expression tag	UNP P9WJF1
B	0	HIS	-	expression tag	UNP P9WJF1

- Molecule 2 is 2-(4-(cyclohexylmethyl)piperazin-1-yl)-8-nitro-6-(trifluoromethyl)-4H-benzo[e][1,3]thiazin-4-one, bound form (CCD ID: 26J) (formula: C₂₀H₂₅F₃N₄O₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			20	11	3	3	2	1		
2	B	1	Total	C	F	N	O	S	0	0
			18	9	3	3	2	1		

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



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	33	Total O 33 33	0	0
4	B	28	Total O 28 28	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.23Å 84.11Å 80.77Å 90.00° 103.36° 90.00°	Depositor
Resolution (Å)	76.11 – 2.20 76.11 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.5 (76.11-2.20) 98.5 (76.11-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, R_{free}	0.206 , 0.238 0.203 , 0.234	Depositor DCC
R_{free} test set	2591 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6560	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, 26J

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	0.56	0/3283	0.87	2/4462 (0.0%)
1	B	0.51	1/3210 (0.0%)	0.86	0/4362
All	All	0.53	1/6493 (0.0%)	0.87	2/8824 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	96	VAL	CA-CB	5.40	1.60	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	329	PRO	N-CA-CB	6.83	110.51	103.00
1	A	316	PRO	N-CA-CB	6.57	110.15	103.25

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	3214	0	3141	27	0
1	B	3141	0	3063	44	0
2	A	20	0	3	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	18	0	3	0	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0
4	A	33	0	0	2	0
4	B	28	0	0	1	0
All	All	6560	0	6272	71	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 6.

All (71) 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:347:PHE:HE1	1:B:386:ILE:HD11	1.23	1.00
1:B:347:PHE:CE1	1:B:386:ILE:HD11	2.07	0.89
1:B:159:ARG:HG2	1:B:159:ARG:HH11	1.46	0.79
1:B:83:ILE:HG12	1:B:90:VAL:HG22	1.70	0.73
1:B:99:ASP:OD2	1:B:119:ARG:NH1	2.22	0.73
1:B:240:LEU:HD22	1:B:355:GLN:HG2	1.71	0.72
1:A:345:ASP:OD1	1:A:345:ASP:N	2.29	0.66
1:B:12:ARG:HH21	1:B:21:PRO:HG3	1.62	0.65
1:A:83:ILE:HG12	1:A:90:VAL:HG22	1.81	0.62
1:A:28:ARG:NH1	1:A:73:ASP:OD2	2.35	0.60
1:A:386:ILE:HD12	1:A:386:ILE:N	2.17	0.60
1:A:337:PHE:CZ	1:A:386:ILE:HD13	2.37	0.60
1:B:375:ALA:HB3	1:B:378:SER:HB2	1.84	0.59
1:A:119:ARG:HB2	1:A:119:ARG:HH11	1.69	0.58
1:B:159:ARG:HG2	1:B:159:ARG:NH1	2.14	0.58
1:A:257:PRO:HG2	1:A:260:LEU:HD22	1.86	0.58
1:B:155:ASP:OD1	1:B:155:ASP:N	2.38	0.56
1:B:347:PHE:HE1	1:B:386:ILE:CD1	2.06	0.56
1:B:209:LEU:HB2	1:B:241:GLY:HA3	1.88	0.56
1:A:375:ALA:HB3	1:A:378:SER:HB2	1.87	0.56
1:A:40:ALA:O	1:A:44:GLU:HG2	2.06	0.55
1:B:116:PRO:HG2	1:B:118:THR:O	2.07	0.54
1:A:263:GLU:N	1:A:263:GLU:OE1	2.41	0.54
1:B:414:LEU:HD12	1:B:422:THR:HG21	1.90	0.53
1:B:205:VAL:HG11	1:B:298:ARG:HA	1.91	0.52
1:B:159:ARG:HH11	1:B:159:ARG:CG	2.19	0.52
1:A:418:LYS:NZ	2:A:501:26J:OAE	2.43	0.51
1:A:315:HIS:O	1:A:317:LEU:N	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:PHE:O	1:A:307:VAL:HA	2.12	0.50
1:B:93:ASP:O	1:B:96:VAL:HG13	2.12	0.49
1:A:63:ASN:HB3	1:A:454:MET:SD	2.52	0.49
1:B:386:ILE:HD12	1:B:386:ILE:N	2.28	0.49
1:A:231:PHE:HB3	1:A:364:ASN:HB2	1.94	0.48
1:B:346:GLU:HG2	1:B:410:PHE:CD1	2.49	0.48
1:A:347:PHE:HE1	1:A:386:ILE:HD11	1.78	0.47
1:B:18:ARG:HH21	1:B:331:GLY:HA2	1.79	0.47
1:B:18:ARG:HH22	1:B:332:PHE:H	1.62	0.47
1:B:18:ARG:NH2	1:B:332:PHE:H	2.13	0.47
1:B:371:PRO:HA	1:B:382:PRO:HG3	1.96	0.47
1:B:205:VAL:CG1	1:B:298:ARG:HA	2.45	0.47
1:B:25:ASN:O	1:B:70:LEU:HD12	2.16	0.46
1:A:77:LEU:O	1:A:93:ASP:HB3	2.15	0.46
1:B:404:ASP:OD2	1:B:421:ARG:NH2	2.48	0.46
1:B:29:THR:HG21	1:B:34:MET:HB2	1.98	0.46
1:B:335:TYR:HB3	1:B:388:VAL:HG23	1.98	0.46
1:A:25:ASN:O	1:A:70:LEU:HD12	2.16	0.46
1:A:334:GLN:H	1:A:334:GLN:CD	2.22	0.45
1:B:344:VAL:O	1:B:347:PHE:HB3	2.17	0.45
1:A:134:LYS:HD3	4:A:604:HOH:O	2.17	0.44
1:B:372:ARG:NH2	1:B:375:ALA:O	2.50	0.44
1:A:221:GLU:HG2	4:A:618:HOH:O	2.17	0.44
1:A:349:LYS:HE3	1:A:406:ARG:NH2	2.33	0.44
1:A:77:LEU:HD23	1:A:93:ASP:CG	2.43	0.43
1:A:90:VAL:HG13	1:A:92:ILE:HG23	1.99	0.43
1:B:416:THR:HB	1:B:454:MET:HE1	2.01	0.43
1:B:440:VAL:HA	1:B:443:LYS:HE3	2.01	0.43
1:B:74:MET:HE1	1:B:77:LEU:HD22	2.01	0.42
1:A:285:ASN:OD1	1:A:288:THR:OG1	2.32	0.42
1:B:103:LYS:HG2	4:B:606:HOH:O	2.19	0.42
1:B:60:TYR:CD2	1:B:418:LYS:HD3	2.55	0.42
1:B:63:ASN:OD1	1:B:63:ASN:N	2.52	0.42
1:A:116:PRO:HG2	1:A:118:THR:O	2.19	0.41
1:B:216:HIS:CE1	1:B:366:PHE:HE1	2.38	0.41
1:B:345:ASP:OD1	1:B:345:ASP:N	2.53	0.41
1:B:112:VAL:HG22	1:B:191:MET:HE1	2.03	0.41
1:B:403:LEU:HA	1:B:403:LEU:HD23	1.79	0.40
1:B:31:ASP:OD1	1:B:33:GLU:HG2	2.22	0.40
1:B:367:LYS:HG3	1:B:368:LEU:N	2.36	0.40
1:A:401:SER:O	1:A:404:ASP:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:GLU:OE2	1:B:298:ARG:NH1	2.51	0.40
1:B:245:VAL:HG12	1:B:247:ARG:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	419/481 (87%)	409 (98%)	9 (2%)	1 (0%)	43	51
1	B	406/481 (84%)	396 (98%)	10 (2%)	0	100	100
All	All	825/962 (86%)	805 (98%)	19 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	ALA

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	324/385 (84%)	302 (93%)	22 (7%)	14	17
1	B	318/385 (83%)	301 (95%)	17 (5%)	20	26
All	All	642/770 (83%)	603 (94%)	39 (6%)	17	20

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ARG
1	A	23	VAL
1	A	34	MET
1	A	77	LEU
1	A	88	LYS
1	A	90	VAL
1	A	92	ILE
1	A	119	ARG
1	A	121	VAL
1	A	159	ARG
1	A	200	ILE
1	A	253	VAL
1	A	256	LEU
1	A	260	LEU
1	A	307	VAL
1	A	345	ASP
1	A	355	GLN
1	A	386	ILE
1	A	396	LEU
1	A	406	ARG
1	A	421	ARG
1	A	422	THR
1	B	9	THR
1	B	18	ARG
1	B	19	THR
1	B	23	VAL
1	B	27	LEU
1	B	92	ILE
1	B	96	VAL
1	B	155	ASP
1	B	159	ARG
1	B	253	VAL
1	B	260	LEU
1	B	314	TYR
1	B	350	ILE
1	B	389	ASP
1	B	396	LEU
1	B	413	ARG
1	B	447	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	65	GLN
1	B	428	HIS

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](#)

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	$\# Z > 2$
3	FAD	B	502	-	58,58,58	1.81	8 (13%)	85,89,89	1.62	17 (20%)
3	FAD	A	502	-	58,58,58	1.69	8 (13%)	85,89,89	1.63	16 (18%)
2	26J	A	501	1	20,21,33	1.98	4 (20%)	24,32,48	2.21	5 (20%)
2	26J	B	501	1	17,19,33	2.02	4 (23%)	21,29,48	1.44	4 (19%)

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	502	-	-	2/34/50/50	0/6/6/6
3	FAD	A	502	-	-	2/34/50/50	0/6/6/6
2	26J	A	501	1	-	3/11/12/34	0/2/2/4
2	26J	B	501	1	-	1/7/8/34	0/2/2/4

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	FAD	O4-C4	6.77	1.36	1.23
3	A	502	FAD	O4-C4	6.28	1.35	1.23
3	B	502	FAD	O2-C2	5.88	1.36	1.24
2	B	501	26J	OAE-NBE	-5.82	1.23	1.39
2	A	501	26J	OAE-NBE	-5.68	1.23	1.39
3	A	502	FAD	O2-C2	5.67	1.35	1.24
3	B	502	FAD	C9A-C5X	5.42	1.49	1.41
3	A	502	FAD	C9A-C5X	4.96	1.49	1.41
3	B	502	FAD	PA-O3P	4.56	1.64	1.59
2	A	501	26J	CAY-NBF	4.25	1.42	1.35
3	B	502	FAD	C8-C7	3.59	1.49	1.40
2	B	501	26J	CBB-SAV	-3.59	1.69	1.75
2	B	501	26J	CAY-NBF	3.45	1.41	1.34
2	A	501	26J	CBB-SAV	-3.38	1.70	1.75
3	A	502	FAD	C8-C7	3.30	1.48	1.40
3	A	502	FAD	C4X-N5	2.76	1.36	1.30
2	A	501	26J	CAY-SAV	-2.75	1.70	1.76
3	B	502	FAD	C4X-N5	2.47	1.36	1.30
2	B	501	26J	CAY-NAR	2.32	1.35	1.31
3	A	502	FAD	PA-O3P	2.29	1.62	1.59
3	A	502	FAD	C4-N3	-2.16	1.34	1.38
3	B	502	FAD	C5A-N7A	-2.15	1.35	1.39
3	B	502	FAD	C8A-N7A	2.11	1.35	1.31
3	A	502	FAD	C2-N3	-2.00	1.34	1.39

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	26J	CAM-NBF-CAY	-6.33	109.51	121.36
3	B	502	FAD	C5A-C4A-N3A	-5.38	119.31	126.72
2	A	501	26J	CAL-NBF-CAY	-5.10	111.81	121.36
3	B	502	FAD	N3A-C2A-N1A	-5.10	120.86	128.58
3	A	502	FAD	N3A-C2A-N1A	-4.98	121.04	128.58
3	A	502	FAD	C5A-C4A-N3A	-4.90	119.97	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	FAD	N9A-C8A-N7A	-3.80	108.54	113.94
3	B	502	FAD	C2A-N3A-C4A	3.56	120.53	111.83
3	B	502	FAD	N3A-C4A-N9A	3.56	133.22	127.17
3	A	502	FAD	N3A-C4A-N9A	3.41	132.97	127.17
3	A	502	FAD	C2A-N3A-C4A	3.40	120.13	111.83
3	A	502	FAD	C4A-N9A-C8A	3.28	109.18	105.74
3	B	502	FAD	N9A-C8A-N7A	-3.23	109.35	113.94
3	A	502	FAD	C4-N3-C2	-3.12	120.09	125.64
2	A	501	26J	CBA-CBB-SAV	-3.09	117.84	122.11
3	A	502	FAD	C9A-C5X-N5	-2.97	119.30	122.45
3	A	502	FAD	C4X-C10-N10	2.94	120.69	116.48
3	B	502	FAD	C9A-C5X-N5	-2.88	119.40	122.45
3	A	502	FAD	O4-C4-C4X	-2.85	119.00	126.53
3	B	502	FAD	C4-N3-C2	-2.84	120.59	125.64
3	B	502	FAD	C4A-C5A-N7A	-2.77	107.41	110.58
3	A	502	FAD	C5A-N7A-C8A	2.77	107.80	103.45
3	A	502	FAD	C4A-C5A-N7A	-2.77	107.42	110.58
3	B	502	FAD	O4-C4-C4X	-2.76	119.25	126.53
2	B	501	26J	CBA-CAZ-NAR	2.75	123.42	118.33
3	B	502	FAD	C5A-N7A-C8A	2.75	107.77	103.45
3	B	502	FAD	C4X-C10-N10	2.65	120.27	116.48
2	A	501	26J	CBA-CAZ-NAR	2.64	123.22	118.33
3	A	502	FAD	C4X-C4-N3	2.62	119.92	113.25
2	B	501	26J	SAV-CAY-NAR	-2.59	121.07	125.83
3	A	502	FAD	C10-N1-C2	2.45	122.15	116.85
2	B	501	26J	OAD-CAZ-CBA	-2.45	117.39	121.33
2	B	501	26J	CBA-CBB-SAV	-2.39	118.81	122.11
2	A	501	26J	CAL-NBF-CAM	-2.24	108.72	115.87
3	B	502	FAD	C10-N1-C2	2.23	121.69	116.85
3	A	502	FAD	O2P-P-O3P	2.20	113.22	107.27
3	A	502	FAD	O3P-P-O1P	-2.18	104.14	110.70
3	B	502	FAD	C4A-N9A-C8A	2.16	108.01	105.74
3	B	502	FAD	O2A-PA-O1A	2.11	122.28	112.44
3	B	502	FAD	O2P-P-O3P	2.10	112.95	107.27
3	B	502	FAD	C4X-C4-N3	2.09	118.58	113.25
3	B	502	FAD	O3P-P-O1P	-2.01	104.67	110.70

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	26J	CAJ-CAX-NBE-OAE

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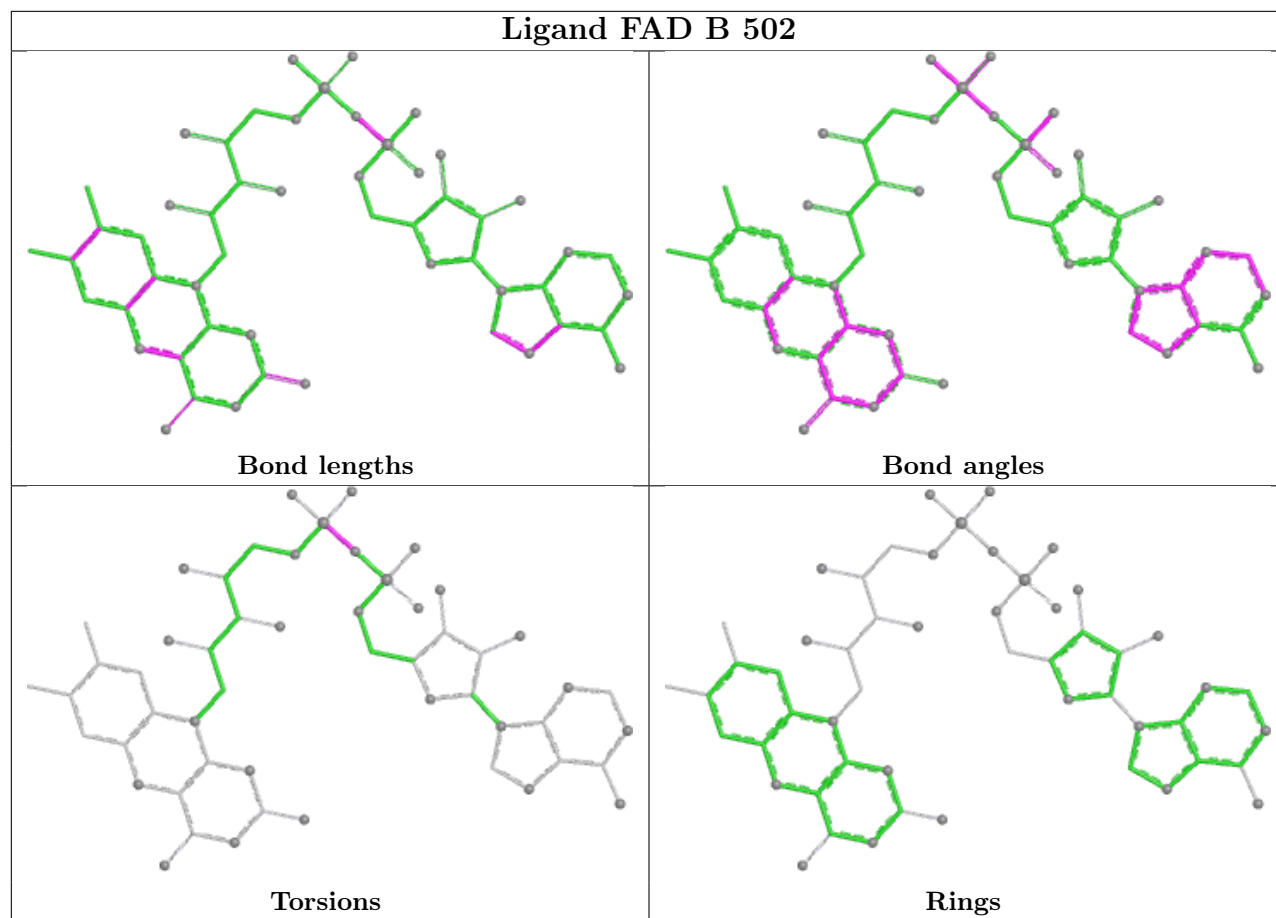
Mol	Chain	Res	Type	Atoms
2	A	501	26J	SAV-CAY-NBF-CAM
2	A	501	26J	NAR-CAY-NBF-CAM
2	B	501	26J	CAJ-CAX-NBE-OAE
3	A	502	FAD	PA-O3P-P-O2P
3	B	502	FAD	PA-O3P-P-O2P
3	A	502	FAD	PA-O3P-P-O1P
3	B	502	FAD	PA-O3P-P-O1P

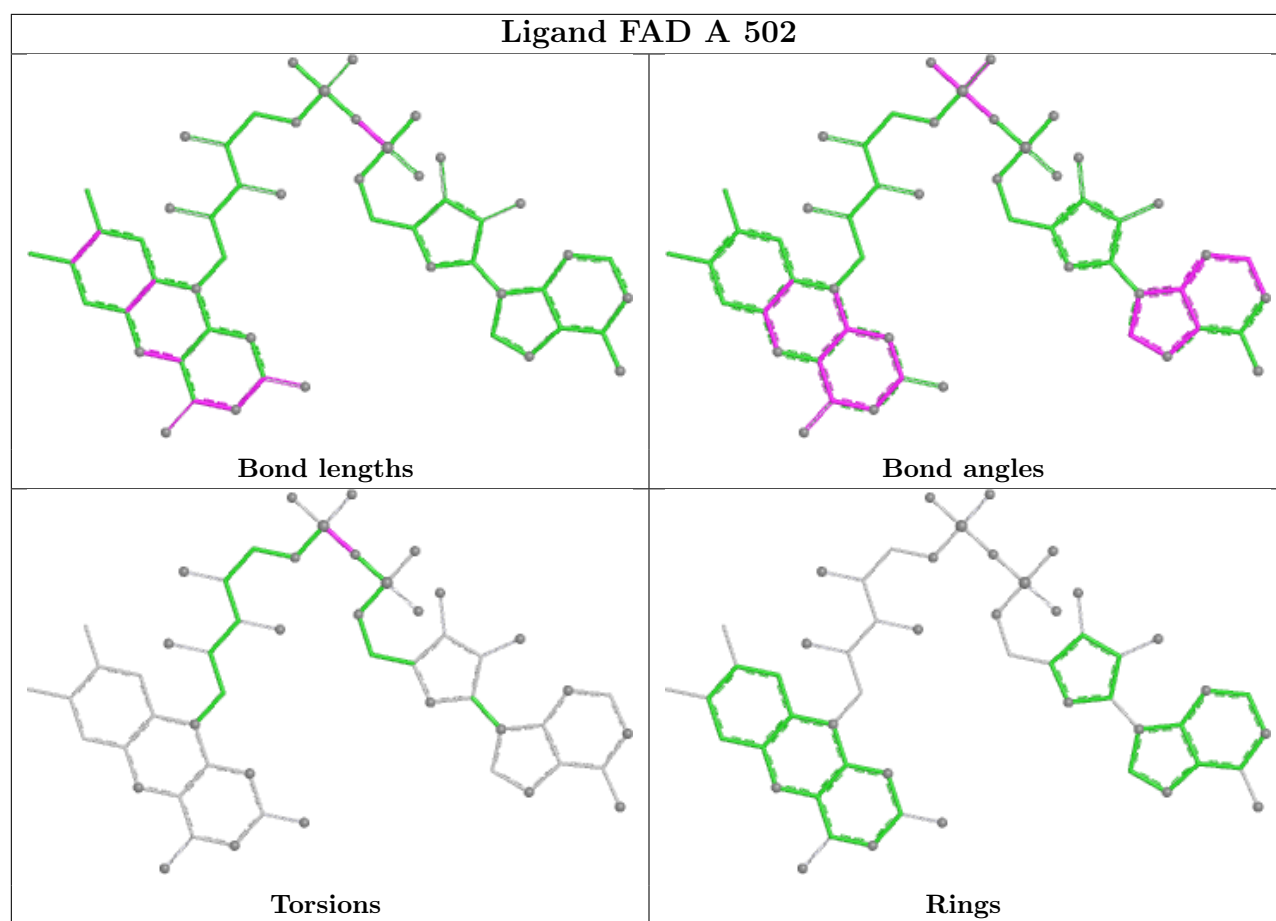
There are no ring outliers.

1 monomer is involved in 1 short contact:

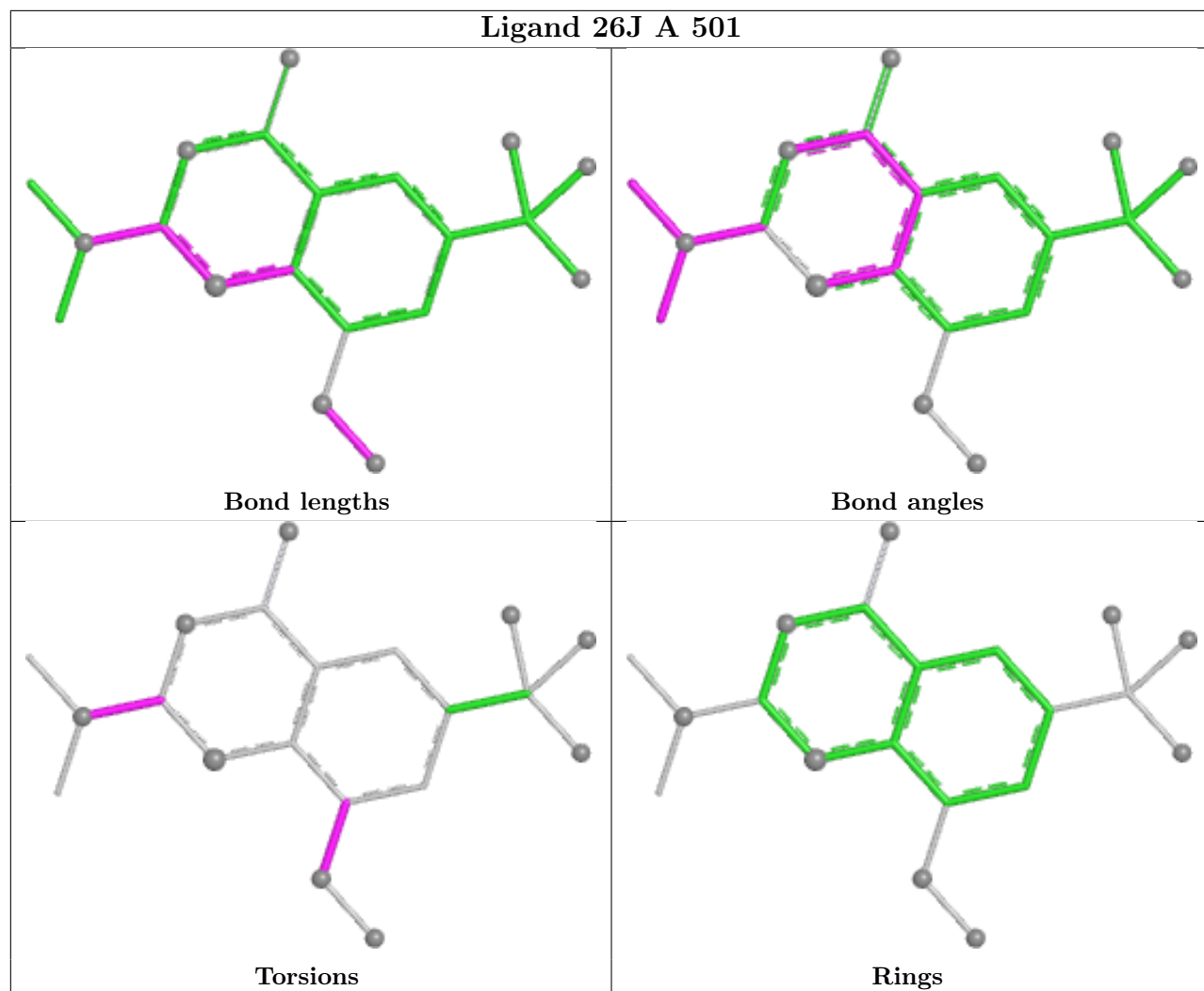
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	26J	1	0

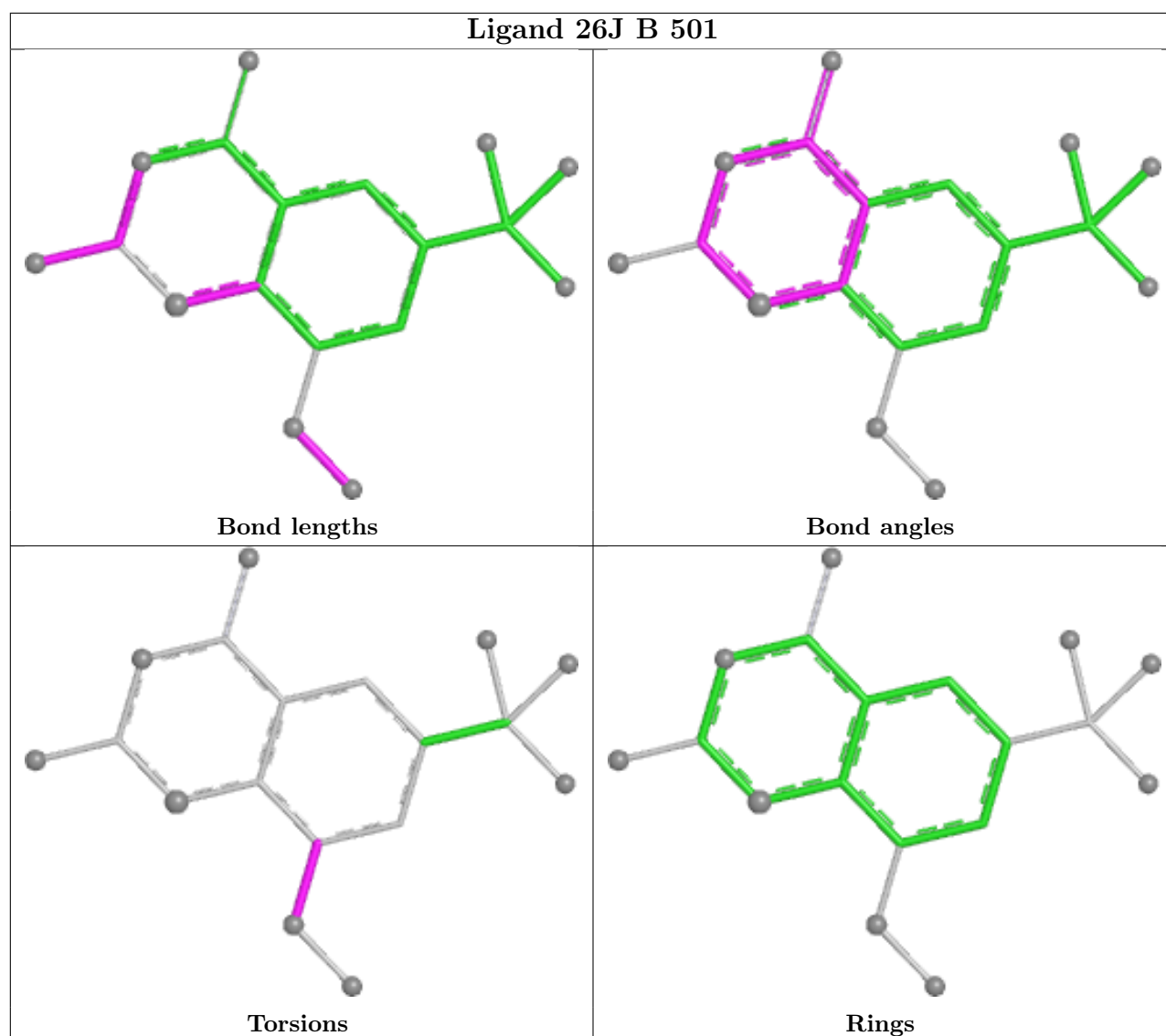
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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





Ligand 26J A 501





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	427/481 (88%)	0.43	32 (7%) 20 17	33, 54, 96, 140	0
1	B	414/481 (86%)	0.64	44 (10%) 11 8	32, 63, 105, 154	0
All	All	841/962 (87%)	0.54	76 (9%) 15 12	32, 58, 103, 154	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	268	ASP	7.0
1	A	267	PHE	4.6
1	B	7	THR	4.4
1	A	330	ALA	4.4
1	A	268	ASP	4.2
1	B	23	VAL	4.2
1	A	387	CYS	4.2
1	B	315	HIS	4.2
1	A	48	GLY	4.0
1	A	329	PRO	4.0
1	B	334	GLN	3.7
1	A	7	THR	3.7
1	A	166	GLU	3.7
1	A	316	PRO	3.7
1	B	293	GLY	3.6
1	B	447	LEU	3.6
1	B	19	THR	3.5
1	B	16	TRP	3.5
1	B	13	LEU	3.5
1	B	296	TRP	3.4
1	B	362	PHE	3.3
1	A	317	LEU	3.3
1	A	289	PHE	3.3
1	B	20	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	295	LEU	3.2
1	B	230	TRP	3.2
1	A	414	LEU	3.2
1	B	389	ASP	3.2
1	A	238	PRO	3.1
1	B	387	CYS	3.1
1	B	119	ARG	3.0
1	B	345	ASP	2.9
1	A	20	ALA	2.9
1	A	165	GLY	2.8
1	B	60	TYR	2.8
1	B	165	GLY	2.8
1	B	8	THR	2.6
1	B	331	GLY	2.6
1	A	45	SER	2.6
1	B	48	GLY	2.6
1	B	164	THR	2.6
1	A	334	GLN	2.6
1	B	200	ILE	2.5
1	A	44	GLU	2.5
1	B	41	ARG	2.5
1	A	284	ALA	2.5
1	A	19	THR	2.5
1	B	267	PHE	2.4
1	B	11	THR	2.4
1	B	360	TYR	2.4
1	A	360	TYR	2.3
1	A	292	ILE	2.3
1	B	117	GLY	2.2
1	A	9	THR	2.2
1	A	230	TRP	2.2
1	A	386	ILE	2.2
1	B	460	LEU	2.2
1	A	362	PHE	2.2
1	A	454	MET	2.2
1	B	33	GLU	2.2
1	B	363	LEU	2.2
1	A	41	ARG	2.2
1	B	393	LYS	2.2
1	B	398	LYS	2.2
1	B	9	THR	2.2
1	B	223	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	231	PHE	2.2
1	A	13	LEU	2.1
1	A	461	LEU	2.1
1	B	386	ILE	2.1
1	A	34	MET	2.1
1	A	293	GLY	2.1
1	B	18	ARG	2.1
1	B	10	ALA	2.0
1	B	461	LEU	2.0
1	B	45	SER	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](#)

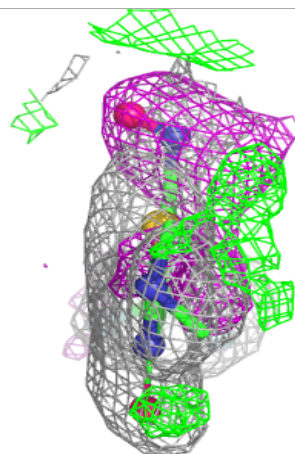
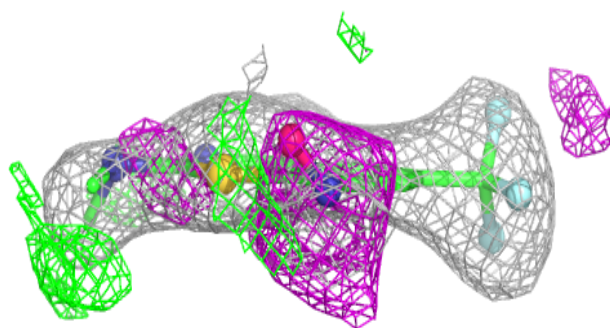
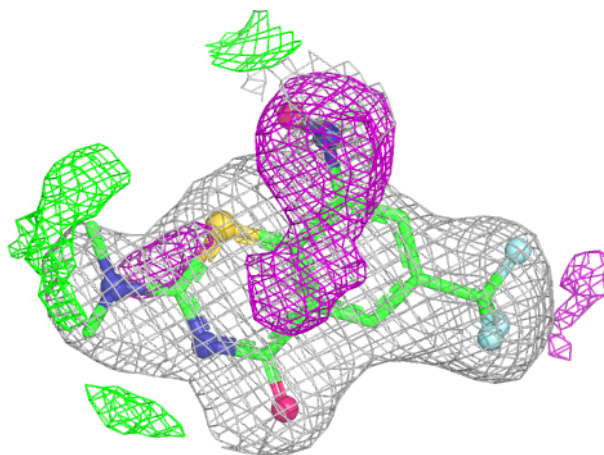
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	26J	A	501	20/30	0.70	0.20	75,77,80,80	0
2	26J	B	501	18/30	0.82	0.17	98,101,104,105	0
3	FAD	A	502	53/53	0.97	0.07	38,38,38,38	0
3	FAD	B	502	53/53	0.97	0.07	45,45,45,45	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.

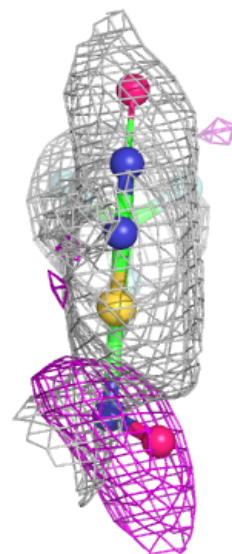
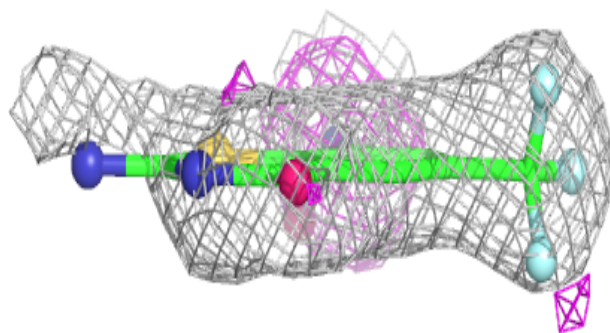
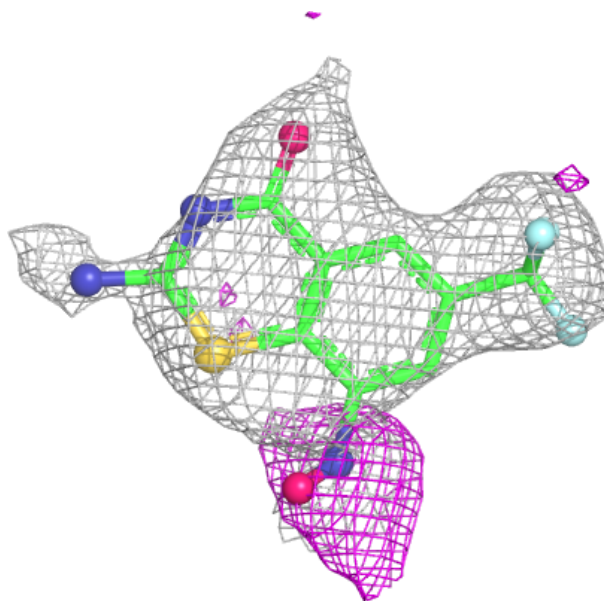
Electron density around 26J A 501:

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



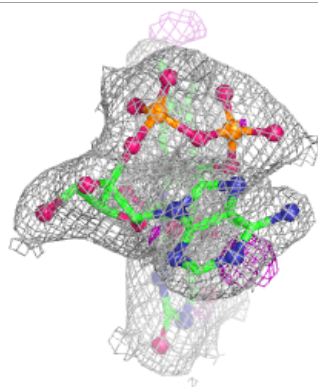
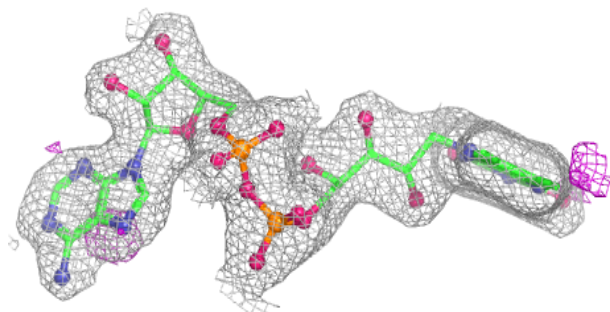
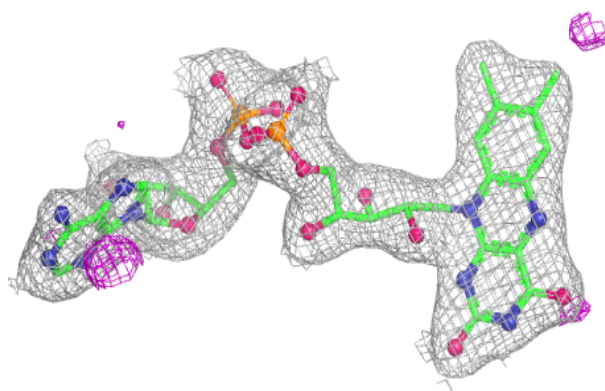
Electron density around 26J B 501:

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

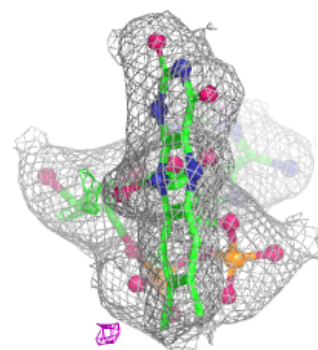
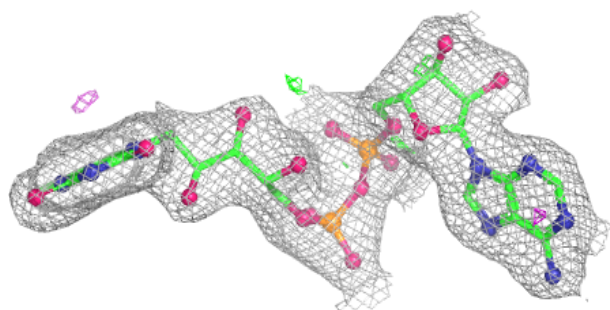
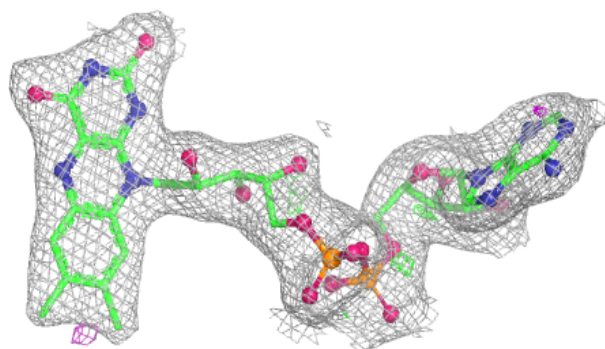


Electron density around FAD A 502:

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

**Electron density around FAD B 502:**

$2mF_o - DF_c$ (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.