



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 01:53 am BST

PDB ID : 4P8M
Title : Crystal structure of M. tuberculosis DprE1 in complex with the non-covalent inhibitor QN114
Authors : Neres, J.; Pojer, F.; Cole, S.T.
Deposited on : 2014-03-31
Resolution : 2.09 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 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 : 2.11
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) : 2.11

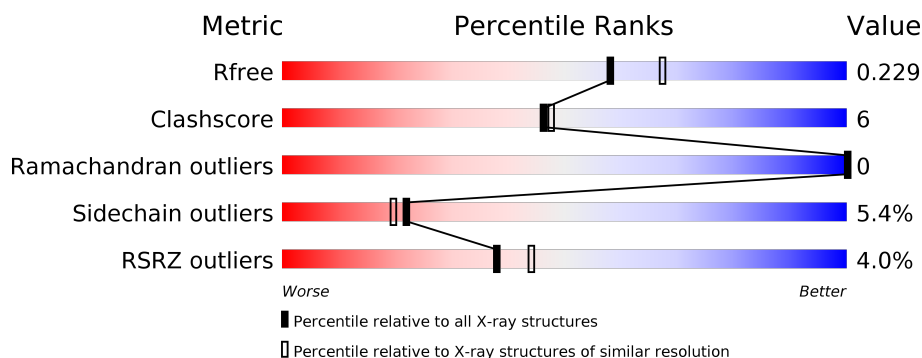
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 ≥ 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	480	<div> <div>5%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>11%</div> </div> </div>
1	B	480	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>8%</div> <div>15%</div> </div> </div>

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
3	R58	A	502	-	-	X	-
3	R58	B	502	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6792 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 Probable decaprenylphosphoryl-beta-D-ribose oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	4	0
			3298	2097	584	606	11			
1	B	406	Total	C	N	O	S	0	2	0
			3115	1975	552	577	11			

There are 38 discrepancies between the modelled and reference sequences:

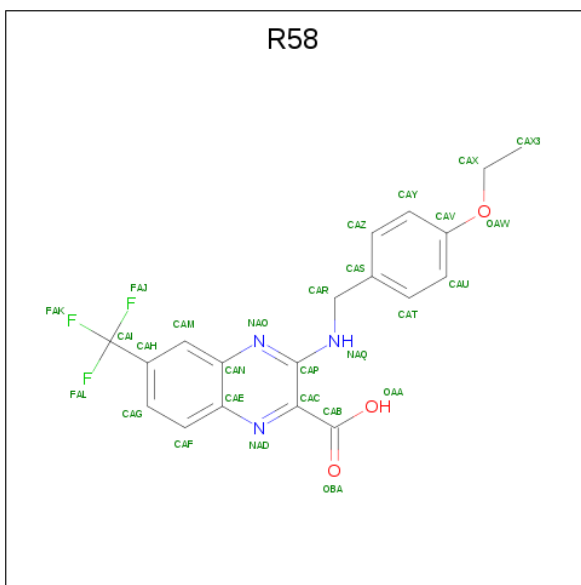
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP P72056
A	-17	SER	-	expression tag	UNP P72056
A	-16	SER	-	expression tag	UNP P72056
A	-15	HIS	-	expression tag	UNP P72056
A	-14	HIS	-	expression tag	UNP P72056
A	-13	HIS	-	expression tag	UNP P72056
A	-12	HIS	-	expression tag	UNP P72056
A	-11	HIS	-	expression tag	UNP P72056
A	-10	HIS	-	expression tag	UNP P72056
A	-9	SER	-	expression tag	UNP P72056
A	-8	SER	-	expression tag	UNP P72056
A	-7	GLY	-	expression tag	UNP P72056
A	-6	LEU	-	expression tag	UNP P72056
A	-5	VAL	-	expression tag	UNP P72056
A	-4	PRO	-	expression tag	UNP P72056
A	-3	ARG	-	expression tag	UNP P72056
A	-2	GLY	-	expression tag	UNP P72056
A	-1	SER	-	expression tag	UNP P72056
A	0	HIS	-	expression tag	UNP P72056
B	-18	GLY	-	expression tag	UNP P72056
B	-17	SER	-	expression tag	UNP P72056
B	-16	SER	-	expression tag	UNP P72056
B	-15	HIS	-	expression tag	UNP P72056
B	-14	HIS	-	expression tag	UNP P72056
B	-13	HIS	-	expression tag	UNP P72056

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP P72056
B	-11	HIS	-	expression tag	UNP P72056
B	-10	HIS	-	expression tag	UNP P72056
B	-9	SER	-	expression tag	UNP P72056
B	-8	SER	-	expression tag	UNP P72056
B	-7	GLY	-	expression tag	UNP P72056
B	-6	LEU	-	expression tag	UNP P72056
B	-5	VAL	-	expression tag	UNP P72056
B	-4	PRO	-	expression tag	UNP P72056
B	-3	ARG	-	expression tag	UNP P72056
B	-2	GLY	-	expression tag	UNP P72056
B	-1	SER	-	expression tag	UNP P72056
B	0	HIS	-	expression tag	UNP P72056

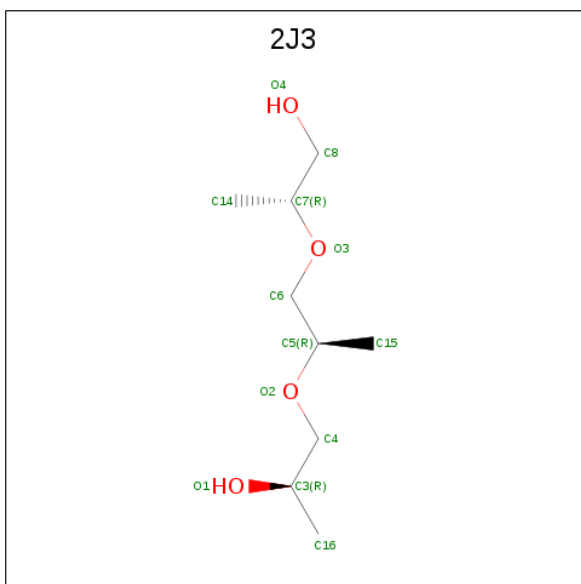
- # FAD

- Molecule 3 is 3-[(4-ethoxybenzyl)amino]-6-(trifluoromethyl)quinoxaline-2-carboxylic acid (three-letter code: R58) (formula: $C_{19}H_{16}F_3N_3O_3$).



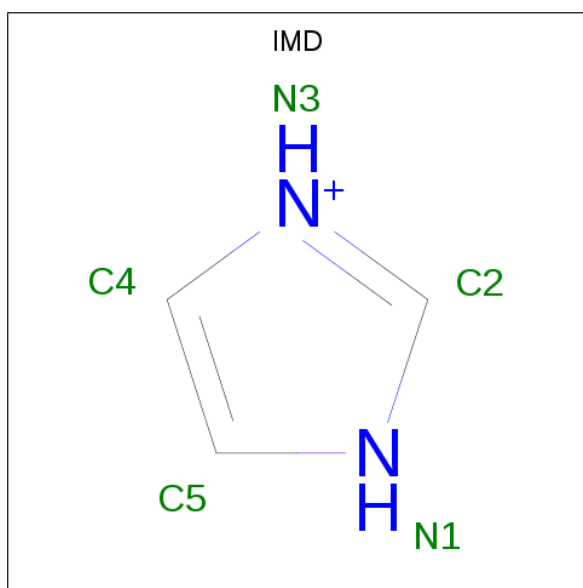
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			28	19	3	3	3		
3	B	1	Total	C	F	N	O	0	0
			28	19	3	3	3		

- Molecule 4 is (2R)-2-([(2R)-2-([(2R)-2-hydroxypropyl]oxy)propyl]oxy)propan-1-ol (three-letter code: 2J3) (formula: C₉H₂₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	9	4		

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			5	3	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	101	Total	O	0	0
			101	101		
6	B	98	Total	O	0	0
			98	98		

These plots are drawn for all protein, RNA and DNA 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 ($\text{RSRZ} > 2$). 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.

- Chain A:
-
- Sequence logo for Chain A. The y-axis represents information content in bits. The x-axis shows positions 1 to 100. A color scale at the top indicates conservation levels: 5% (red), 78% (green), 11% (yellow), and 11% (grey).
- Key residues (positions and amino acids) are highlighted in the sequence logo:
- Position 1: Y314
 - Position 2: R315
 - Position 3: R316
 - Position 4: L317
 - Position 5: ASP
 - Position 6: MET
 - Position 7: PHE
 - Position 8: GLY
 - Position 9: GLY
 - Position 10: GLU
 - Position 11: TRP
 - Position 12: ASN
 - Position 13: ARG
 - Position 14: A326
 - Position 15: G327
 - Position 16: G328
 - Position 17: P329
 - Position 18: A330
 - Position 19: E346
 - Position 20: Q355
 - Position 21: M364
 - Position 22: R365
 - Position 23: P366
 - Position 24: K367
 - Position 25: R372
 - Position 26: A375
 - Position 27: S378
 - Position 28: I381
 - Position 29: I386
 - Position 30: C387
 - Position 31: L396
 - Position 32: R406
 - Position 33: F410
 - Position 34: R413
 - Position 35: K418
 - Position 36: D419
 - Position 37: S420
 - Position 38: R456
 - Position 39: L461

- Chain B:
-
- 29% 75% 8% 15%
- GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRQ ARG GLY SER HIS HIS VAL VAL GLY ALA T7 R12 R18 G46 G47 G48 R49 G50 A51 Y60 L70 I92 P116 G117 T118 E157 I158 R159 H160 L161 D167 I200 F230 F231
- L240 A251 T252 V253 E254 Q255 L256 L260 L261 K266 F267 ASP ALA PRQ GLN LEU LEU THR PRQ ASP VAL PHE ASN GLY LEU ALA ASN LYS TVR THR PHE GLY PRQ ILE GLU LEU TRP ARG LYS SER G303 L310 Q311 Q312 F313 TYR HIS PRQ LEU ASP NPT
- PHE GLY GLU TRP ASN ARG ALA TYR GLY PRQ A330 Q334 E342 F347 I351 Q355 F362 L363 M364 A375 S378 I386 C387 L396 R413 K418 R421 W437 K443 R448 L461

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.24Å 83.98Å 90.05Å 90.00° 100.53° 90.00°	Depositor
Resolution (Å)	47.90 – 2.09 47.86 – 2.09	Depositor EDS
% Data completeness (in resolution range)	97.7 (47.90-2.09) 97.7 (47.86-2.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.190 , 0.229 0.189 , 0.229	Depositor DCC
R_{free} test set	2557 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.7	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	0.95	EDS
Total number of atoms	6792	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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: R58, 2J3, IMD, 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	0.51	2/3388 (0.1%)	0.59	0/4600
1	B	0.50	1/3189 (0.0%)	0.58	0/4327
All	All	0.50	3/6577 (0.0%)	0.58	0/8927

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	437	TRP	CD2-CE2	5.32	1.47	1.41
1	A	172	TRP	CD2-CE2	5.31	1.47	1.41
1	A	296	TRP	CD2-CE2	5.04	1.47	1.41

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	3298	0	3281	36	0
1	B	3115	0	3104	28	0
2	A	53	0	31	0	0
2	B	53	0	31	0	0
3	A	28	0	15	9	0
3	B	28	0	15	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	13	0	20	6	0
5	A	5	0	5	0	0
6	A	101	0	0	1	0
6	B	98	0	0	2	0
All	All	6792	0	6502	83	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 (83) 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:159:ARG:HG2	1:A:159:ARG:HH11	1.06	1.13
3:B:502:R58:CAX3	3:B:502:R58:H14	0.97	1.12
3:A:502:R58:CAX3	3:A:502:R58:H15	0.97	1.11
3:B:502:R58:H15	3:B:502:R58:CAX3	0.97	1.10
3:A:502:R58:H16	3:A:502:R58:CAX3	0.97	1.08
3:A:502:R58:CAX3	3:A:502:R58:H14	0.97	1.07
3:B:502:R58:H16	3:B:502:R58:CAX3	0.97	1.07
1:A:372:ARG:HG2	4:A:503:2J3:H2	1.38	1.04
1:B:261:ARG:HH11	1:B:261:ARG:HG3	1.29	0.95
1:B:261:ARG:HH11	1:B:261:ARG:CG	1.87	0.86
3:A:502:R58:H16	3:A:502:R58:CAX	2.06	0.86
3:B:502:R58:H15	3:B:502:R58:CAX	2.06	0.86
1:A:159:ARG:NH1	1:A:159:ARG:HG2	1.80	0.85
3:B:502:R58:H14	3:B:502:R58:CAX	2.06	0.85
3:B:502:R58:H16	3:B:502:R58:H14	1.58	0.85
3:B:502:R58:H16	3:B:502:R58:CAX	2.06	0.85
3:A:502:R58:CAX	3:A:502:R58:H14	2.06	0.85
3:B:502:R58:H16	3:B:502:R58:H15	1.58	0.84
3:A:502:R58:H16	3:A:502:R58:H15	1.58	0.84
3:A:502:R58:CAX	3:A:502:R58:H15	2.06	0.84
3:B:502:R58:H15	3:B:502:R58:H14	1.58	0.83
3:A:502:R58:H14	3:A:502:R58:H15	1.58	0.83
3:A:502:R58:H16	3:A:502:R58:H14	1.58	0.83
1:A:159:ARG:CG	1:A:159:ARG:HH11	1.91	0.81
1:B:261:ARG:NH1	1:B:261:ARG:HG3	1.97	0.77
1:A:298:ARG:HH11	1:A:298:ARG:HG2	1.50	0.76
1:B:200:ILE:HD12	1:B:251:ALA:HA	1.71	0.71
1:B:159:ARG:HH11	1:B:159:ARG:HG2	1.58	0.69
1:A:308:GLN:HB3	1:A:312:GLN:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:ARG:CG	1:B:159:ARG:HH11	2.12	0.63
1:B:347:PHE:CE1	1:B:386:ILE:HD12	2.32	0.63
1:A:366:PHE:HD2	1:A:386:ILE:HD11	1.63	0.63
1:B:240:LEU:HD22	1:B:355:GLN:HG2	1.80	0.63
1:A:240:LEU:HD22	1:A:355:GLN:HG2	1.81	0.63
1:A:99:ASP:OD1	1:A:119:ARG:NH1	2.33	0.61
1:B:60:TYR:CE2	1:B:334:GLN:HG3	2.35	0.61
1:B:159:ARG:NH1	1:B:159:ARG:HG2	2.18	0.57
1:A:231:PHE:CE1	1:A:364:ASN:HB3	2.40	0.56
1:B:116:PRO:HG2	1:B:118:THR:O	2.05	0.56
1:A:205:VAL:HG11	1:A:298:ARG:HG3	1.88	0.56
1:A:311:THR:HG22	1:A:315:HIS:O	2.06	0.55
1:B:342:GLU:HG2	6:B:695:HOH:O	2.05	0.55
1:A:372:ARG:NH1	4:A:503:2J3:H17	2.22	0.55
1:B:261:ARG:NH1	1:B:261:ARG:CG	2.57	0.54
1:A:93:ASP:O	1:A:96:VAL:HG13	2.08	0.54
1:A:42:VAL:O	1:A:46:GLY:HA3	2.08	0.54
1:B:387[A]:CYS:SG	1:B:418:LYS:NZ	2.81	0.54
1:B:347:PHE:CZ	1:B:386:ILE:HD12	2.42	0.54
1:A:372:ARG:NH2	1:A:375:ALA:O	2.42	0.52
1:B:375:ALA:HB3	1:B:378:SER:HB2	1.92	0.52
1:A:372:ARG:HD2	4:A:503:2J3:H17	1.91	0.51
1:A:375:ALA:HB3	1:A:378:SER:HB2	1.92	0.51
1:A:102:MET:SD	1:A:310:LEU:HD22	2.51	0.51
1:A:249[A]:ARG:NH1	6:A:699:HOH:O	2.44	0.51
1:B:347:PHE:HE1	1:B:386:ILE:HD12	1.76	0.50
1:A:372:ARG:HD2	4:A:503:2J3:H13	1.94	0.49
1:A:346:GLU:HB3	1:A:410:PHE:CD2	2.48	0.49
1:A:381:ILE:HG21	4:A:503:2J3:H15	1.95	0.48
1:A:366:PHE:HD2	1:A:386:ILE:CD1	2.26	0.47
1:A:258:ALA:HA	1:A:261:ARG:HE	1.80	0.47
1:A:387[A]:CYS:SG	1:A:418:LYS:NZ	2.88	0.47
1:B:231:PHE:CE1	1:B:364:ASN:HB3	2.51	0.46
1:A:372:ARG:CD	4:A:503:2J3:H13	2.45	0.46
1:A:257:PRO:HG2	1:A:260:LEU:HD22	1.98	0.46
1:A:298:ARG:HG2	1:A:298:ARG:NH1	2.25	0.46
1:B:200:ILE:HD13	1:B:255:GLN:CD	2.37	0.45
1:B:342:GLU:CG	6:B:695:HOH:O	2.65	0.44
1:B:267:PHE:HE1	1:B:310:LEU:HB3	1.82	0.44
1:A:346:GLU:HG2	1:A:410:PHE:CD1	2.53	0.44
1:B:159:ARG:CG	1:B:159:ARG:NH1	2.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ILE:HG12	1:A:90:VAL:HG12	2.00	0.43
1:B:200:ILE:HD13	1:B:255:GLN:NE2	2.33	0.43
1:B:51:ALA:HA	1:B:70:LEU:O	2.19	0.43
1:A:42:VAL:O	1:A:46:GLY:CA	2.67	0.43
1:A:298:ARG:HH11	1:A:298:ARG:CG	2.26	0.41
1:B:443:LYS:HB2	1:B:443:LYS:HE3	1.92	0.41
3:B:502:R58:OAA	3:B:502:R58:NAQ	2.45	0.41
1:A:456:ARG:HG2	1:A:461:LEU:HD22	2.02	0.41
1:B:351:ILE:HD11	1:B:386:ILE:HD13	2.03	0.41
1:B:231:PHE:CE1	1:B:386:ILE:HG12	2.56	0.41
1:A:119:ARG:HE	1:A:315:HIS:CD2	2.39	0.41
1:A:61:GLY:HA2	1:A:420:SER:HB3	2.01	0.41
1:B:161:LEU:HD22	1:B:167:ASP:HB3	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	425/480 (88%)	415 (98%)	10 (2%)	0	100	100
1	B	402/480 (84%)	395 (98%)	7 (2%)	0	100	100
All	All	827/960 (86%)	810 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	343/384 (89%)	326 (95%)	17 (5%)	24	23
1	B	325/384 (85%)	306 (94%)	19 (6%)	20	17
All	All	668/768 (87%)	632 (95%)	36 (5%)	22	20

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LYS
1	A	92	ILE
1	A	103	LYS
1	A	121	VAL
1	A	159	ARG
1	A	167	ASP
1	A	256	LEU
1	A	298	ARG
1	A	311	THR
1	A	314	TYR
1	A	317	LEU
1	A	355	GLN
1	A	367	LYS
1	A	396	LEU
1	A	406	ARG
1	A	413	ARG
1	A	421	ARG
1	B	7	THR
1	B	12	ARG
1	B	18	ARG
1	B	49	ARG
1	B	92	ILE
1	B	157	GLU
1	B	159	ARG
1	B	253	VAL
1	B	254	GLU
1	B	256	LEU
1	B	261	ARG
1	B	266	LYS
1	B	311	THR
1	B	355	GLN
1	B	386	ILE
1	B	396	LEU

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Mol	Chain	Res	Type
1	B	413	ARG
1	B	421	ARG
1	B	448	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	315	HIS
1	B	25	ASN
1	B	355	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	2J3	A	503	-	9,12,12	0.56	0	10,14,14	1.06	0
2	FAD	A	501	-	51,58,58	1.81	9 (17%)	60,89,89	1.97	9 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FAD	B	501	-	51,58,58	2.03	9 (17%)	60,89,89	2.08	10 (16%)
3	R58	A	502	-	27,30,30	1.10	2 (7%)	36,43,43	1.02	3 (8%)
3	R58	B	502	-	27,30,30	1.16	2 (7%)	36,43,43	1.07	1 (2%)
5	IMD	A	504	-	3,5,5	0.37	0	4,5,5	0.66	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
4	2J3	A	503	-	-	7/12/12/12	-
2	FAD	A	501	-	-	2/30/50/50	0/6/6/6
2	FAD	B	501	-	-	1/30/50/50	0/6/6/6
3	R58	A	502	-	-	3/14/18/18	0/3/3/3
3	R58	B	502	-	-	2/14/18/18	0/3/3/3
5	IMD	A	504	-	-	-	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FAD	C4X-C10	10.15	1.49	1.38
2	A	501	FAD	C4X-C10	8.42	1.47	1.38
2	B	501	FAD	C4-C4X	4.87	1.49	1.41
2	A	501	FAD	C4-C4X	4.16	1.48	1.41
3	B	502	R58	CAP-NAO	3.96	1.36	1.31
2	A	501	FAD	C9A-C5X	3.85	1.50	1.42
2	B	501	FAD	C9A-C5X	3.73	1.50	1.42
2	B	501	FAD	C8-C7	3.44	1.49	1.40
3	A	502	R58	CAP-NAO	3.35	1.35	1.31
2	A	501	FAD	C8-C7	3.35	1.49	1.40
2	B	501	FAD	C9A-N10	3.15	1.42	1.38
2	A	501	FAD	C9A-N10	2.63	1.42	1.38
2	B	501	FAD	C4X-N5	2.58	1.37	1.33
2	B	501	FAD	C5A-C4A	2.51	1.47	1.40
3	A	502	R58	CAC-NAD	2.50	1.36	1.32
2	A	501	FAD	C5A-C4A	2.44	1.47	1.40
3	B	502	R58	CAC-NAD	2.24	1.35	1.32
2	B	501	FAD	C10-N1	2.21	1.36	1.33
2	A	501	FAD	C10-N1	2.20	1.36	1.33
2	B	501	FAD	C2A-N3A	2.02	1.35	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FAD	C1'-N10	-2.02	1.46	1.48
2	A	501	FAD	O4B-C1B	2.01	1.43	1.41

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	FAD	C4-N3-C2	8.96	122.70	115.14
2	A	501	FAD	C4-N3-C2	8.03	121.92	115.14
2	A	501	FAD	C4-C4X-C10	-7.04	115.29	119.95
2	B	501	FAD	C4-C4X-C10	-6.85	115.42	119.95
2	A	501	FAD	C1'-N10-C9A	4.98	122.22	118.29
2	B	501	FAD	C1'-N10-C9A	4.53	121.86	118.29
2	B	501	FAD	C4-C4X-N5	4.43	123.66	118.60
2	B	501	FAD	C4X-N5-C5X	4.19	120.95	116.77
2	B	501	FAD	N3A-C2A-N1A	-4.08	122.30	128.68
2	A	501	FAD	C4X-N5-C5X	4.01	120.78	116.77
2	A	501	FAD	C4-C4X-N5	3.88	123.03	118.60
2	A	501	FAD	N3A-C2A-N1A	-3.77	122.79	128.68
2	B	501	FAD	C4X-C4-N3	-3.39	118.79	123.43
2	B	501	FAD	C2A-N1A-C6A	2.69	123.36	118.75
2	A	501	FAD	C4X-C4-N3	-2.53	119.97	123.43
2	B	501	FAD	C4A-C5A-N7A	-2.51	106.78	109.40
3	B	502	R58	CAC-CAP-NAQ	-2.45	117.57	121.69
2	B	501	FAD	C9A-N10-C10	-2.27	118.93	121.91
2	A	501	FAD	C2A-N1A-C6A	2.26	122.62	118.75
3	A	502	R58	CAC-CAP-NAO	-2.16	119.58	121.65
3	A	502	R58	CAP-NAO-CAN	2.16	120.72	116.56
2	A	501	FAD	C4A-C5A-N7A	-2.13	107.17	109.40
3	A	502	R58	CAS-CAR-NAQ	-2.08	108.37	113.77

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	2J3	O2-C5-C6-O3
4	A	503	2J3	C15-C5-C6-O3
4	A	503	2J3	O3-C7-C8-O4
3	A	502	R58	CAU-CAV-OAW-CAX
3	A	502	R58	CAY-CAV-OAW-CAX
3	A	502	R58	CAX3-CAX-OAW-CAV
4	A	503	2J3	C3-C4-O2-C5
3	B	502	R58	CAY-CAV-OAW-CAX

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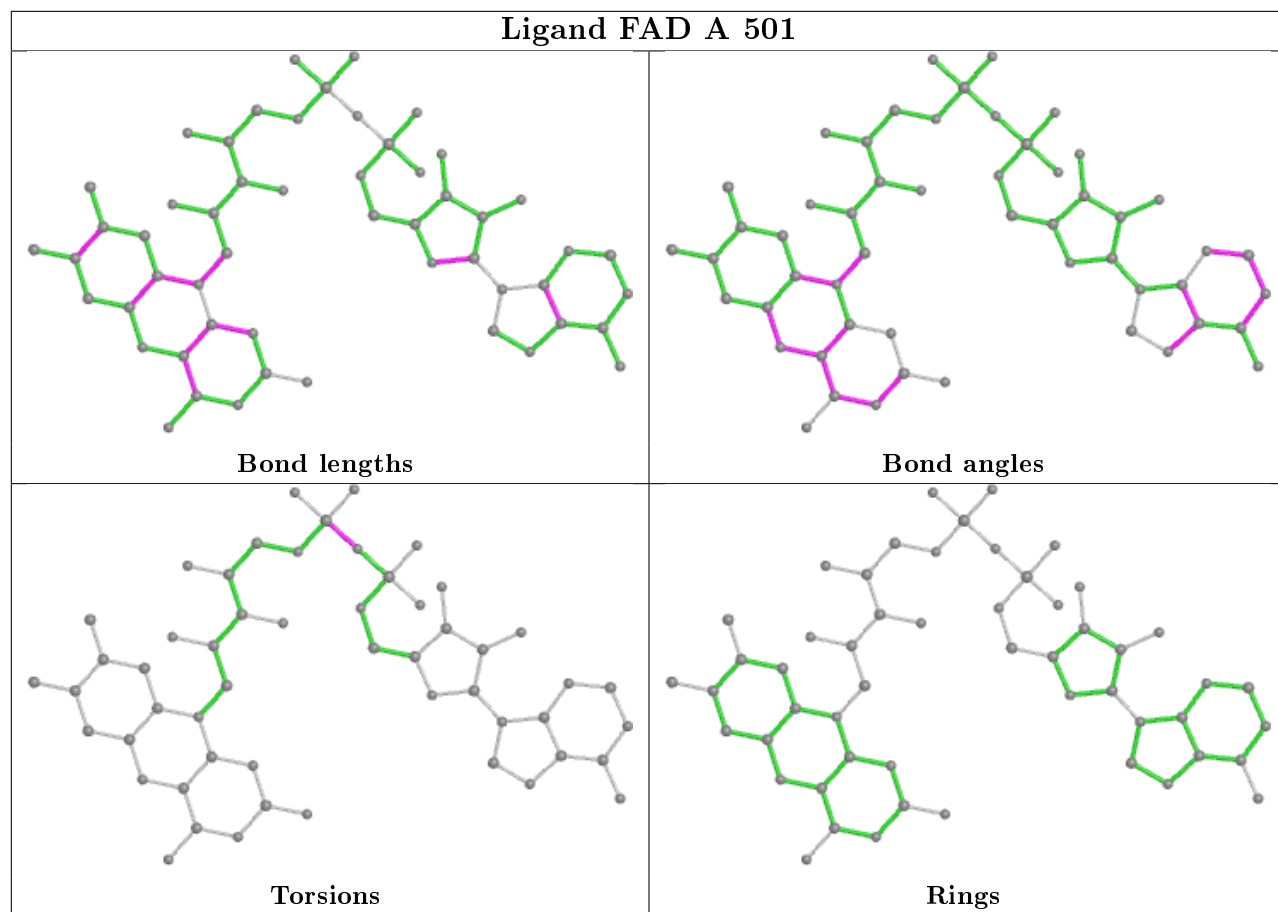
Mol	Chain	Res	Type	Atoms
3	B	502	R58	CAU-CAV-OAW-CAX
4	A	503	2J3	C14-C7-C8-O4
2	A	501	FAD	PA-O3P-P-O2P
4	A	503	2J3	C15-C5-O2-C4
4	A	503	2J3	C5-C6-O3-C7
2	A	501	FAD	PA-O3P-P-O1P
2	B	501	FAD	PA-O3P-P-O2P

There are no ring outliers.

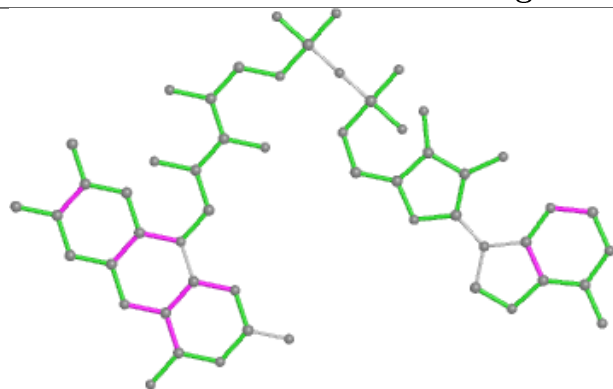
3 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	2J3	6	0
3	A	502	R58	9	0
3	B	502	R58	10	0

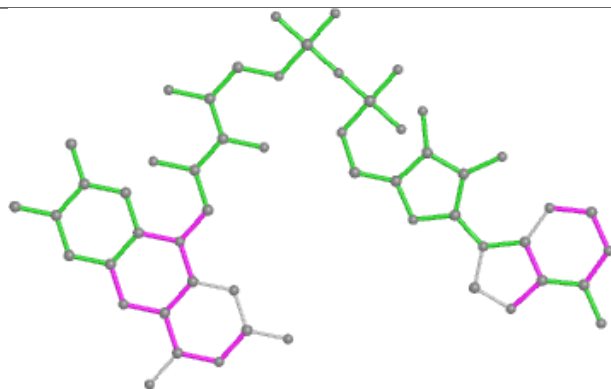
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



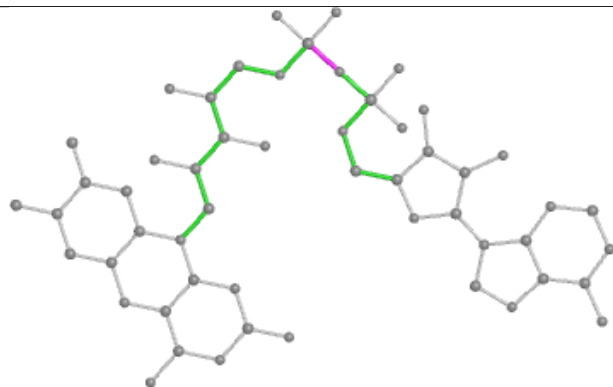
Ligand FAD B 501



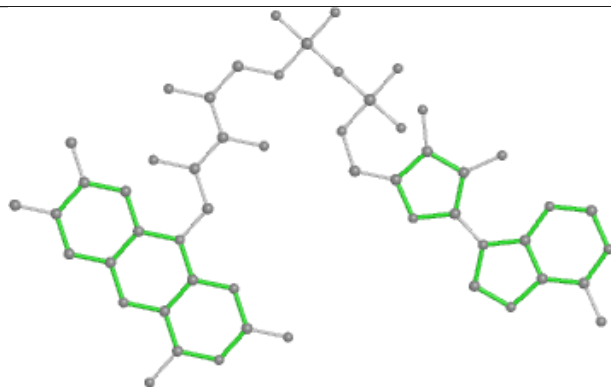
Bond lengths



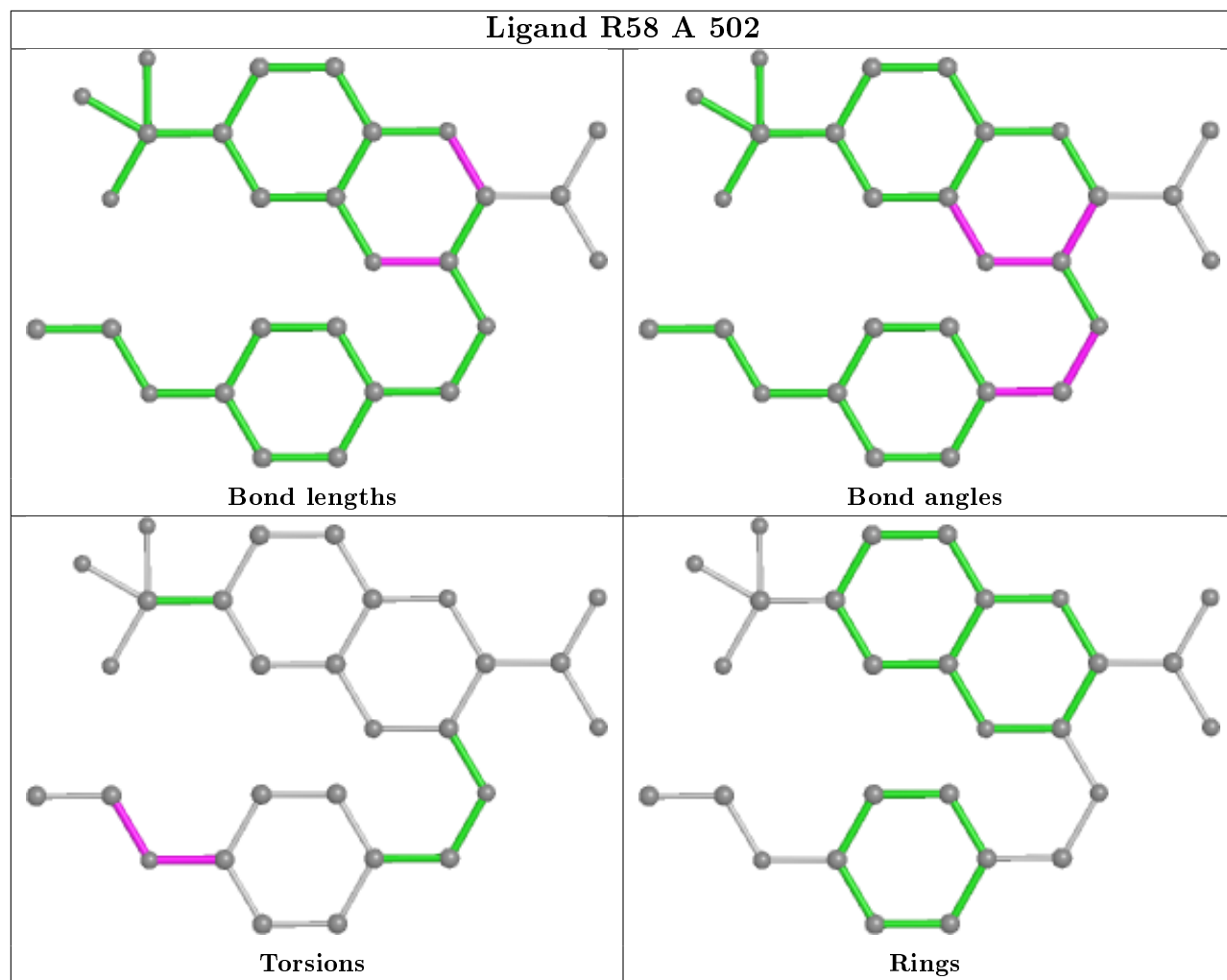
Bond angles

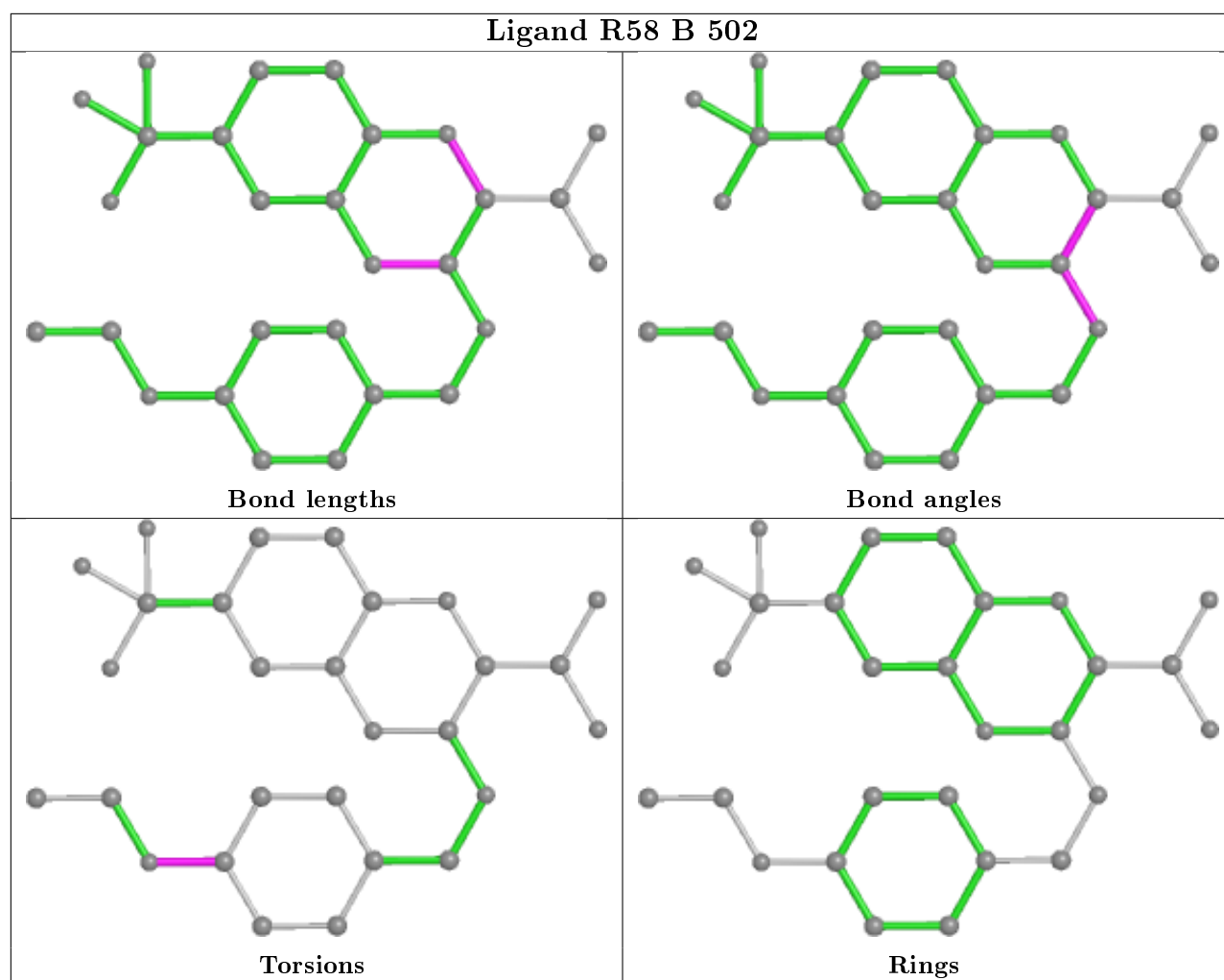


Torsions



Rings





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	427/480 (88%)	0.09	25 (5%) 22 27	17, 29, 68, 87	0
1	B	406/480 (84%)	-0.10	8 (1%) 65 69	18, 30, 52, 69	0
All	All	833/960 (86%)	-0.01	33 (3%) 38 44	17, 29, 58, 87	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	46	GLY	6.9
1	A	270	PRO	5.0
1	A	296	TRP	4.6
1	B	362	PHE	4.2
1	A	316	PRO	4.1
1	A	269	ALA	3.8
1	A	297	TYR	3.7
1	B	46	GLY	3.6
1	B	230[A]	TRP	3.5
1	A	292	ILE	3.5
1	B	330	ALA	3.4
1	A	330	ALA	3.4
1	A	327	TYR	3.2
1	A	47	GLY	3.1
1	A	315	HIS	3.1
1	A	461	LEU	3.0
1	B	47	GLY	2.9
1	B	461	LEU	2.9
1	B	260	LEU	2.9
1	A	326	ALA	2.9
1	A	329	PRO	2.7
1	A	8	THR	2.7
1	A	317	LEU	2.6
1	A	328	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	13	LEU	2.4
1	A	19	THR	2.3
1	A	230[A]	TRP	2.2
1	B	7	THR	2.2
1	A	290	GLY	2.1
1	A	268	ASP	2.1
1	A	299	LYS	2.1
1	A	18	ARG	2.1
1	A	12	ARG	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 carbohydrates in this entry.

6.4 Ligands [i](#)

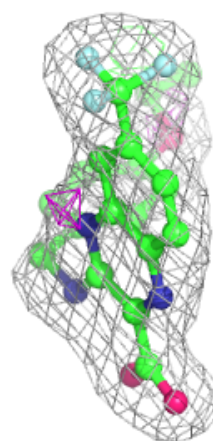
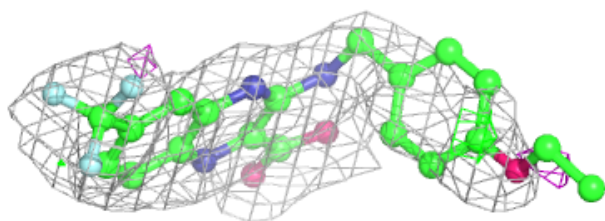
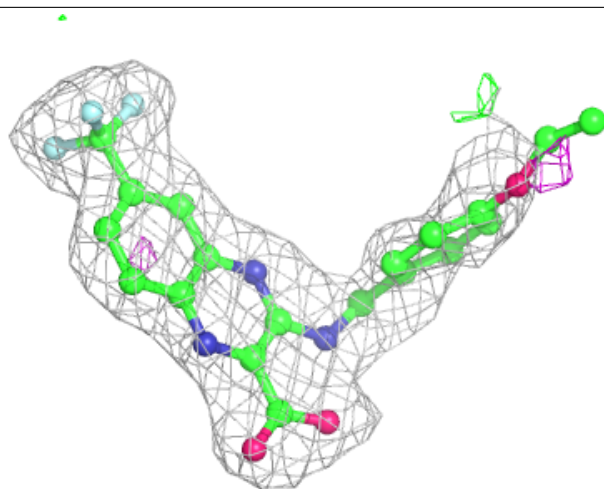
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	2J3	A	503	13/13	0.80	0.28	40,43,46,48	0
3	R58	B	502	28/28	0.92	0.18	34,38,58,59	0
3	R58	A	502	28/28	0.94	0.14	30,35,56,58	0
5	IMD	A	504	5/5	0.97	0.12	34,35,36,36	0
2	FAD	B	501	53/53	0.98	0.10	19,21,23,24	0
2	FAD	A	501	53/53	0.98	0.10	19,21,23,24	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.

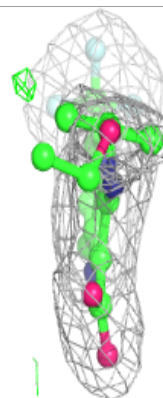
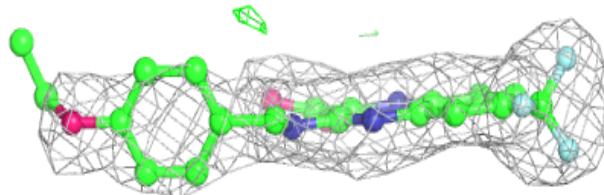
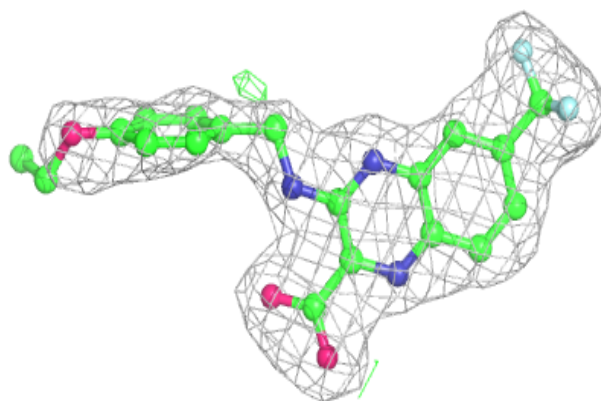
Electron density around R58 B 502:

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

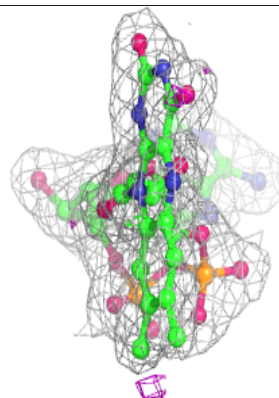
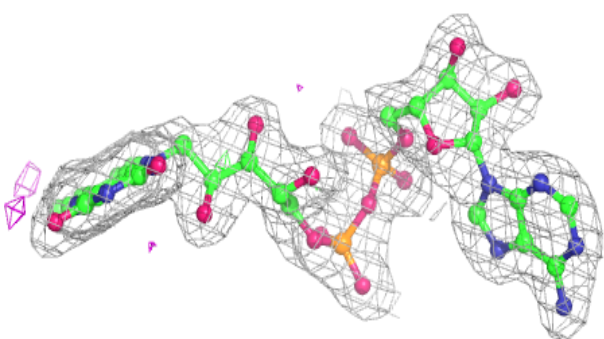
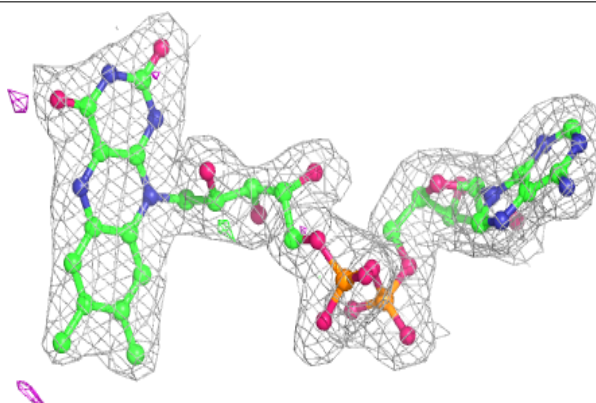


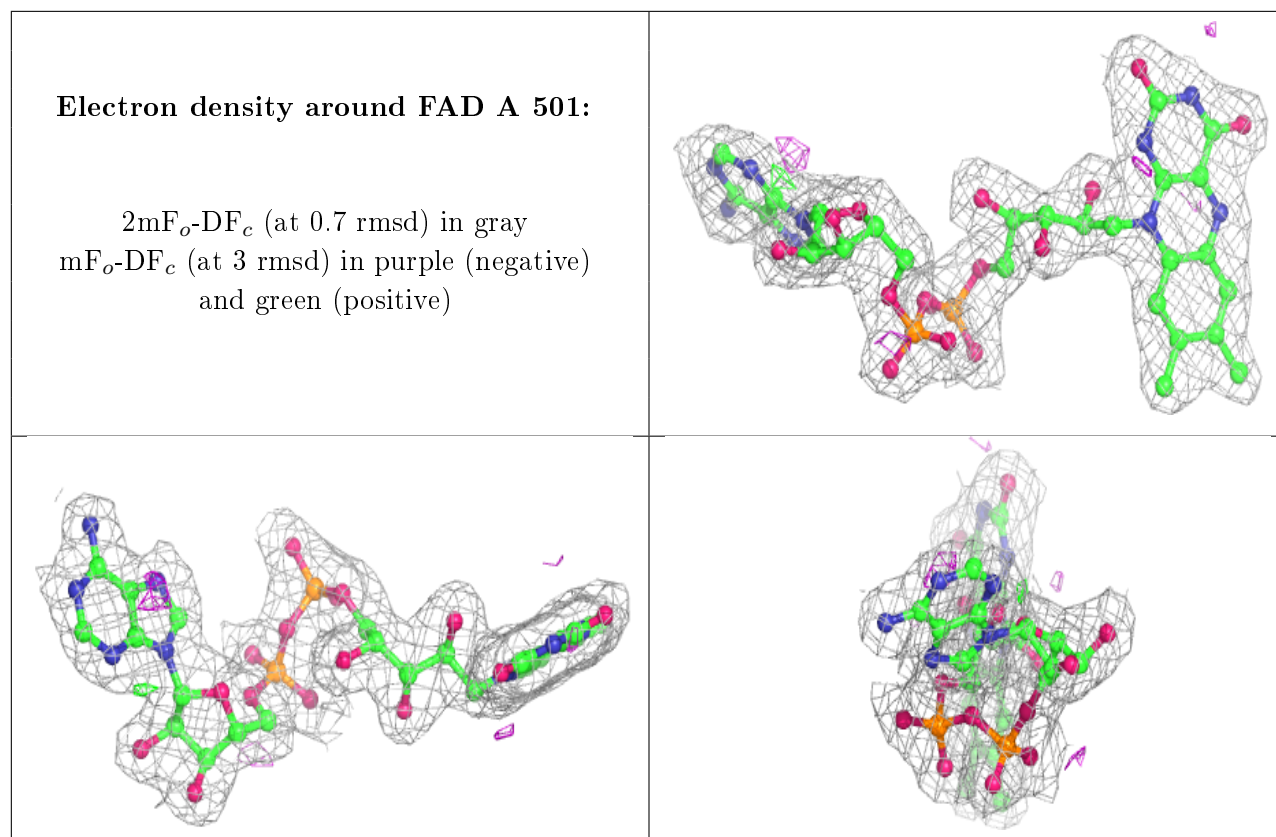
Electron density around R58 A 502:

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

**Electron density around FAD B 501:**

$2mF_o-DF_c$ (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.