



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2021 – 04:03 PM EST

PDB ID : 6WTB
Title : Sort-Tagged Drosophila Cryptochrome
Authors : Schneps, C.M.; Crane, B.R.
Deposited on : 2020-05-02
Resolution : 2.58 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 : 2.23.2
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) : 2.23.2

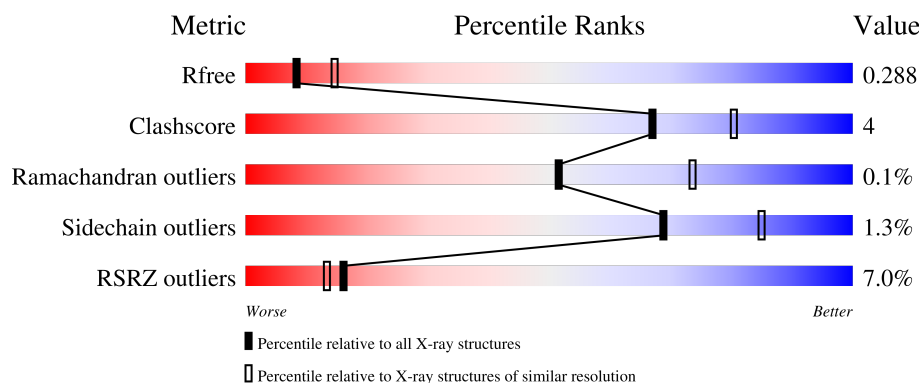
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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	593	<div> <div>7%</div> <div>80%</div> <div>10%</div> <div>9%</div> </div>
1	B	593	<div> <div>6%</div> <div>82%</div> <div>10%</div> <div>8%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9008 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 Cryptochrome-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	537	Total	C	N	O	S	0	1	0
			4375	2793	774	782	26			
1	B	547	Total	C	N	O	S	0	1	0
			4429	2824	784	794	27			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-44	MET	-	initiating methionine	UNP O77059
A	-43	GLY	-	expression tag	UNP O77059
A	-42	SER	-	expression tag	UNP O77059
A	-41	SER	-	expression tag	UNP O77059
A	-40	TRP	-	expression tag	UNP O77059
A	-39	SER	-	expression tag	UNP O77059
A	-38	HIS	-	expression tag	UNP O77059
A	-37	PRO	-	expression tag	UNP O77059
A	-36	GLN	-	expression tag	UNP O77059
A	-35	PHE	-	expression tag	UNP O77059
A	-34	GLU	-	expression tag	UNP O77059
A	-33	LYS	-	expression tag	UNP O77059
A	-32	GLY	-	expression tag	UNP O77059
A	-31	GLY	-	expression tag	UNP O77059
A	-30	GLY	-	expression tag	UNP O77059
A	-29	SER	-	expression tag	UNP O77059
A	-28	GLY	-	expression tag	UNP O77059
A	-27	GLY	-	expression tag	UNP O77059
A	-26	GLY	-	expression tag	UNP O77059
A	-25	SER	-	expression tag	UNP O77059
A	-24	GLY	-	expression tag	UNP O77059
A	-23	GLY	-	expression tag	UNP O77059
A	-22	SER	-	expression tag	UNP O77059
A	-21	ALA	-	expression tag	UNP O77059
A	-20	TRP	-	expression tag	UNP O77059

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	SER	-	expression tag	UNP O77059
A	-18	HIS	-	expression tag	UNP O77059
A	-17	PRO	-	expression tag	UNP O77059
A	-16	GLN	-	expression tag	UNP O77059
A	-15	PHE	-	expression tag	UNP O77059
A	-14	GLU	-	expression tag	UNP O77059
A	-13	LYS	-	expression tag	UNP O77059
A	-12	GLY	-	expression tag	UNP O77059
A	-11	GLY	-	expression tag	UNP O77059
A	-10	GLU	-	expression tag	UNP O77059
A	-9	ASN	-	expression tag	UNP O77059
A	-8	LEU	-	expression tag	UNP O77059
A	-7	TYR	-	expression tag	UNP O77059
A	-6	PHE	-	expression tag	UNP O77059
A	-5	GLN	-	expression tag	UNP O77059
A	-4	SER	-	expression tag	UNP O77059
A	-3	GLY	-	expression tag	UNP O77059
A	-2	GLY	-	expression tag	UNP O77059
A	-1	HIS	-	expression tag	UNP O77059
A	0	MET	-	expression tag	UNP O77059
A	540	LEU	-	expression tag	UNP O77059
A	541	PRO	-	expression tag	UNP O77059
A	542	GLY	-	expression tag	UNP O77059
A	543	THR	-	expression tag	UNP O77059
A	544	GLY	-	expression tag	UNP O77059
A	545	GLY	-	expression tag	UNP O77059
A	546	GLY	-	expression tag	UNP O77059
A	547	GLY	-	expression tag	UNP O77059
A	548	CYS	-	expression tag	UNP O77059
B	-44	MET	-	initiating methionine	UNP O77059
B	-43	GLY	-	expression tag	UNP O77059
B	-42	SER	-	expression tag	UNP O77059
B	-41	SER	-	expression tag	UNP O77059
B	-40	TRP	-	expression tag	UNP O77059
B	-39	SER	-	expression tag	UNP O77059
B	-38	HIS	-	expression tag	UNP O77059
B	-37	PRO	-	expression tag	UNP O77059
B	-36	GLN	-	expression tag	UNP O77059
B	-35	PHE	-	expression tag	UNP O77059
B	-34	GLU	-	expression tag	UNP O77059
B	-33	LYS	-	expression tag	UNP O77059
B	-32	GLY	-	expression tag	UNP O77059

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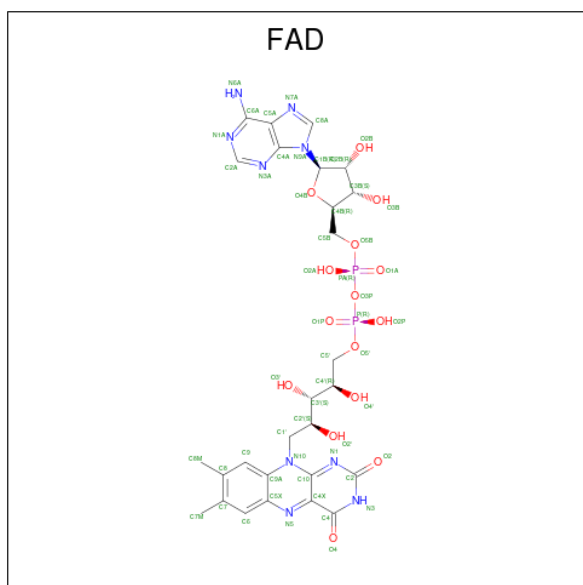
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-31	GLY	-	expression tag	UNP O77059
B	-30	GLY	-	expression tag	UNP O77059
B	-29	SER	-	expression tag	UNP O77059
B	-28	GLY	-	expression tag	UNP O77059
B	-27	GLY	-	expression tag	UNP O77059
B	-26	GLY	-	expression tag	UNP O77059
B	-25	SER	-	expression tag	UNP O77059
B	-24	GLY	-	expression tag	UNP O77059
B	-23	GLY	-	expression tag	UNP O77059
B	-22	SER	-	expression tag	UNP O77059
B	-21	ALA	-	expression tag	UNP O77059
B	-20	TRP	-	expression tag	UNP O77059
B	-19	SER	-	expression tag	UNP O77059
B	-18	HIS	-	expression tag	UNP O77059
B	-17	PRO	-	expression tag	UNP O77059
B	-16	GLN	-	expression tag	UNP O77059
B	-15	PHE	-	expression tag	UNP O77059
B	-14	GLU	-	expression tag	UNP O77059
B	-13	LYS	-	expression tag	UNP O77059
B	-12	GLY	-	expression tag	UNP O77059
B	-11	GLY	-	expression tag	UNP O77059
B	-10	GLU	-	expression tag	UNP O77059
B	-9	ASN	-	expression tag	UNP O77059
B	-8	LEU	-	expression tag	UNP O77059
B	-7	TYR	-	expression tag	UNP O77059
B	-6	PHE	-	expression tag	UNP O77059
B	-5	GLN	-	expression tag	UNP O77059
B	-4	SER	-	expression tag	UNP O77059
B	-3	GLY	-	expression tag	UNP O77059
B	-2	GLY	-	expression tag	UNP O77059
B	-1	HIS	-	expression tag	UNP O77059
B	0	MET	-	expression tag	UNP O77059
B	540	LEU	-	expression tag	UNP O77059
B	541	PRO	-	expression tag	UNP O77059
B	542	GLY	-	expression tag	UNP O77059
B	543	THR	-	expression tag	UNP O77059
B	544	GLY	-	expression tag	UNP O77059
B	545	GLY	-	expression tag	UNP O77059
B	546	GLY	-	expression tag	UNP O77059
B	547	GLY	-	expression tag	UNP O77059
B	548	CYS	-	expression tag	UNP O77059

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).



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	46	Total O 46 46	0	0
4	B	49	Total O 49 49	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	72.98Å 122.19Å 81.95Å 90.00° 115.48° 90.00°	Depositor
Resolution (Å)	39.00 – 2.58 39.03 – 2.58	Depositor EDS
% Data completeness (in resolution range)	96.6 (39.00-2.58) 96.6 (39.03-2.58)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.17.1	Depositor
R, R_{free}	0.234 , 0.287 0.234 , 0.288	Depositor DCC
R_{free} test set	1837 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9008	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.04% 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: FAD, MG

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	0.23	0/4498	0.38	0/6111
1	B	0.23	0/4553	0.39	0/6184
All	All	0.23	0/9051	0.38	0/12295

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

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	4375	0	4275	34	0
1	B	4429	0	4325	34	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0
4	A	46	0	0	3	0
4	B	49	0	0	1	0
All	All	9008	0	8662	68	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 4.

All (68) 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:218:LEU:H	1:B:372:ALA:HB1	1.59	0.67
1:B:221:ILE:HG23	1:B:263:PRO:HD3	1.77	0.65
1:A:412:ASP:HB2	1:A:415:VAL:HB	1.78	0.65
1:B:412:ASP:HB2	1:B:415:VAL:HB	1.79	0.64
1:A:487:ILE:HD11	1:A:493:GLU:HG3	1.81	0.61
1:A:455:LYS:HB3	1:A:462:MET:HG3	1.83	0.60
1:B:230:ALA:HB1	1:B:275:LEU:HB2	1.86	0.58
1:A:10:TRP:HB3	1:A:106:ILE:HG22	1.85	0.57
1:A:122:ARG:NH1	4:A:705:HOH:O	2.37	0.57
1:B:433:ASP:HB3	1:B:506:MET:HG2	1.88	0.55
1:A:88:PRO:HB2	1:A:121:ILE:HD11	1.88	0.55
1:A:358:THR:HG23	1:A:360:PHE:H	1.71	0.55
1:B:429:GLU:HG3	1:B:525:PRO:HD2	1.89	0.54
1:B:532:ARG:HG2	1:B:541:PRO:HB2	1.90	0.54
1:B:10:TRP:HB3	1:B:106:ILE:HG22	1.92	0.52
1:B:91:ILE:HG23	1:B:196:LEU:HD23	1.91	0.52
1:B:14:GLY:HA2	1:B:273:GLY:HA3	1.92	0.51
1:B:539:ASP:HB3	1:B:540:LEU:HD22	1.92	0.51
1:A:80:ARG:NH1	4:A:703:HOH:O	2.37	0.49
1:A:14:GLY:HA2	1:A:273:GLY:HA3	1.94	0.49
1:B:109:ASP:HB3	1:B:114:TRP:CD1	2.47	0.49
1:B:262:SER:HB2	1:B:263:PRO:HD2	1.95	0.49
1:B:27:LEU:HD21	1:B:36:LEU:HD22	1.94	0.48
1:B:234:LEU:HD22	1:B:275:LEU:HD11	1.95	0.48
1:A:111:GLU:HB2	1:A:114:TRP:CD1	2.49	0.48
1:A:358:THR:HG22	1:A:364:ASP:OD1	2.15	0.47
1:A:245:PHE:HZ	1:A:291:VAL:HG21	1.79	0.47
1:B:394:TRP:HH2	1:B:509:MET:HG2	1.80	0.47
1:A:122:ARG:HA	1:A:126:ARG:HH21	1.80	0.46
1:A:242:GLN:HA	1:A:245:PHE:HB3	1.96	0.46
1:A:377:HIS:ND1	1:A:379:THR:HG22	2.30	0.46
1:B:437:VAL:HG13	1:B:438:THR:HG23	1.98	0.46
1:A:532:ARG:HG3	1:A:537:LEU:HD12	1.98	0.46
1:A:349:LEU:HD23	1:A:495:ILE:HD12	1.98	0.45
1:A:476:SER:OG	1:A:477:ALA:N	2.49	0.45
1:B:111:GLU:HB2	1:B:114:TRP:CD1	2.50	0.45
1:A:126:ARG:HH22	1:A:132:PHE:HB2	1.82	0.45
1:A:37:ILE:HG22	1:A:39:VAL:HG23	1.99	0.45
1:B:96:HIS:CE1	1:B:101:LEU:H	2.34	0.45
1:B:9:ILE:HG23	1:B:38:PRO:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:LEU:HD23	1:B:188:LEU:HA	1.86	0.44
1:A:107:GLU:OE1	1:A:137:SER:OG	2.28	0.44
1:B:63:SER:HA	1:B:226:GLY:HA2	2.00	0.44
1:B:284:VAL:HG11	1:B:308:ILE:HB	2.00	0.44
1:A:262:SER:O	1:A:264:LYS:HD3	2.17	0.43
1:A:19:ASP:OD2	1:A:276:SER:OG	2.24	0.43
1:A:173:ARG:HG2	1:A:282:TRP:CE2	2.53	0.43
1:B:235:ASP:O	1:B:239:LYS:HG2	2.17	0.43
1:A:125:CYS:HB2	1:A:126:ARG:NH2	2.32	0.43
1:B:347:GLU:HA	1:B:350:LEU:HB2	2.01	0.43
1:B:404:PHE:O	1:B:408:LEU:HB2	2.19	0.43
1:B:143:PRO:HB3	1:B:320:THR:HG23	2.00	0.43
1:B:189:ASP:HB3	1:B:192:PHE:HB3	1.99	0.43
1:B:220:LYS:HD3	1:B:221:ILE:HG12	2.01	0.43
1:B:408:LEU:HB3	1:B:411:ALA:HB2	2.00	0.42
1:A:202:LEU:HD12	1:A:203:PRO:HD2	2.00	0.42
1:A:87:GLU:OE1	1:A:90:TYR:N	2.52	0.42
1:B:125:CYS:HB3	1:B:130:ILE:O	2.19	0.42
1:A:51:ASN:O	1:A:56:ARG:NH2	2.50	0.42
1:A:189:ASP:OD2	1:A:192:PHE:N	2.52	0.41
1:B:31:ASP:OD1	1:B:31:ASP:N	2.44	0.41
1:A:532:ARG:HB3	1:A:539:ASP:HB2	2.01	0.41
1:A:330:ARG:NH2	4:A:712:HOH:O	2.52	0.41
1:A:426:SER:HB2	1:A:432:LEU:HD12	2.02	0.41
1:A:493:GLU:HG2	1:A:494:ARG:N	2.36	0.41
1:B:406:LYS:NZ	4:B:709:HOH:O	2.47	0.40
1:A:528:GLU:HG2	1:A:532:ARG:HH11	1.87	0.40
1:B:540:LEU:HB3	1:B:546:GLY:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	536/593 (90%)	507 (95%)	29 (5%)	0	100	100
1	B	546/593 (92%)	522 (96%)	23 (4%)	1 (0%)	47	69
All	All	1082/1186 (91%)	1029 (95%)	52 (5%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	541	PRO

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	472/507 (93%)	464 (98%)	8 (2%)	60	79
1	B	476/507 (94%)	472 (99%)	4 (1%)	81	92
All	All	948/1014 (94%)	936 (99%)	12 (1%)	69	85

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ARG
1	A	100	ARG
1	A	126	ARG
1	A	260	HIS
1	A	264	LYS
1	A	271	ARG
1	A	410	ASP
1	A	429	GLU
1	B	12	ARG
1	B	217	PHE
1	B	271	ARG
1	B	280	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	A	602	2	51,58,58	1.20	5 (9%)	60,89,89	2.22	8 (13%)
3	FAD	B	603	2	51,58,58	1.21	6 (11%)	60,89,89	2.23	8 (13%)

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	A	602	2	-	5/30/50/50	0/6/6/6
3	FAD	B	603	2	-	5/30/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	603	FAD	C4X-C10	5.55	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	FAD	C4X-C10	5.48	1.44	1.38
3	A	602	FAD	C4-N3	3.02	1.38	1.33
3	B	603	FAD	C4-N3	2.97	1.38	1.33
3	A	602	FAD	C9A-N10	2.35	1.41	1.38
3	B	603	FAD	C9A-N10	2.31	1.41	1.38
3	B	603	FAD	C4-C4X	2.31	1.45	1.41
3	A	602	FAD	C4-C4X	2.28	1.45	1.41
3	A	602	FAD	C5X-N5	2.17	1.38	1.35
3	B	603	FAD	C5X-N5	2.09	1.38	1.35
3	B	603	FAD	C4X-N5	-2.04	1.30	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	603	FAD	C4-N3-C2	12.96	126.09	115.14
3	A	602	FAD	C4-N3-C2	12.93	126.06	115.14
3	A	602	FAD	C4X-C4-N3	-6.97	113.90	123.43
3	B	603	FAD	C4X-C4-N3	-6.94	113.94	123.43
3	B	603	FAD	C10-C4X-N5	4.84	124.60	121.26
3	A	602	FAD	C10-C4X-N5	4.77	124.56	121.26
3	B	603	FAD	C4-C4X-C10	-3.80	117.43	119.95
3	A	602	FAD	C4-C4X-C10	-3.71	117.49	119.95
3	B	603	FAD	C4X-C10-N10	-3.43	116.77	120.30
3	A	602	FAD	C4X-C10-N10	-3.39	116.81	120.30
3	B	603	FAD	C1'-N10-C9A	3.34	120.92	118.29
3	A	602	FAD	C1'-N10-C9A	3.30	120.89	118.29
3	B	603	FAD	P-O3P-PA	-2.72	123.50	132.83
3	A	602	FAD	P-O3P-PA	-2.69	123.58	132.83
3	A	602	FAD	C5A-C6A-N6A	2.31	123.86	120.35
3	B	603	FAD	C5A-C6A-N6A	2.28	123.81	120.35

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	FAD	C5B-O5B-PA-O2A
3	A	602	FAD	C5B-O5B-PA-O3P
3	A	602	FAD	N10-C1'-C2'-O2'
3	B	603	FAD	C5B-O5B-PA-O2A
3	B	603	FAD	C5B-O5B-PA-O3P
3	B	603	FAD	C5B-O5B-PA-O1A
3	B	603	FAD	N10-C1'-C2'-O2'

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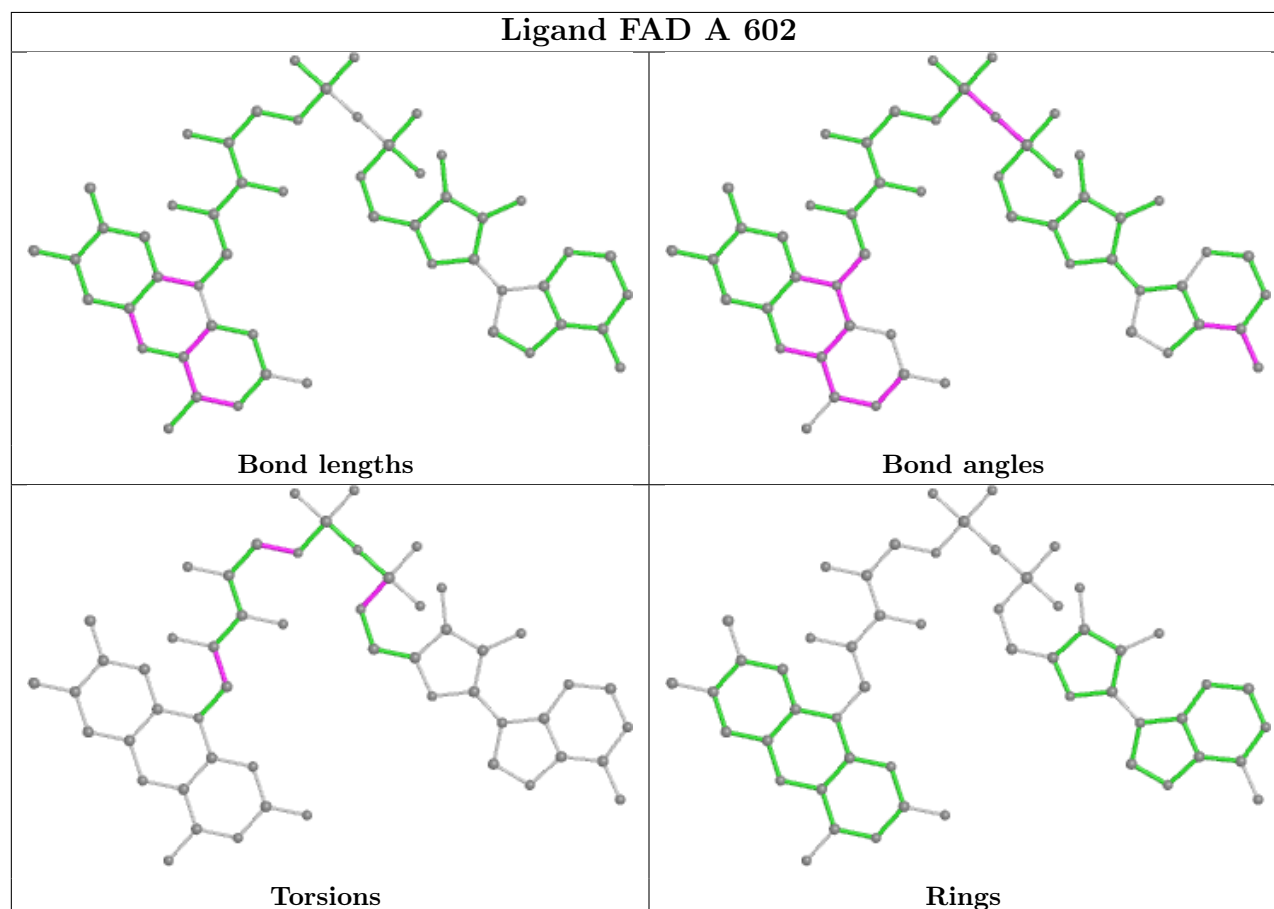
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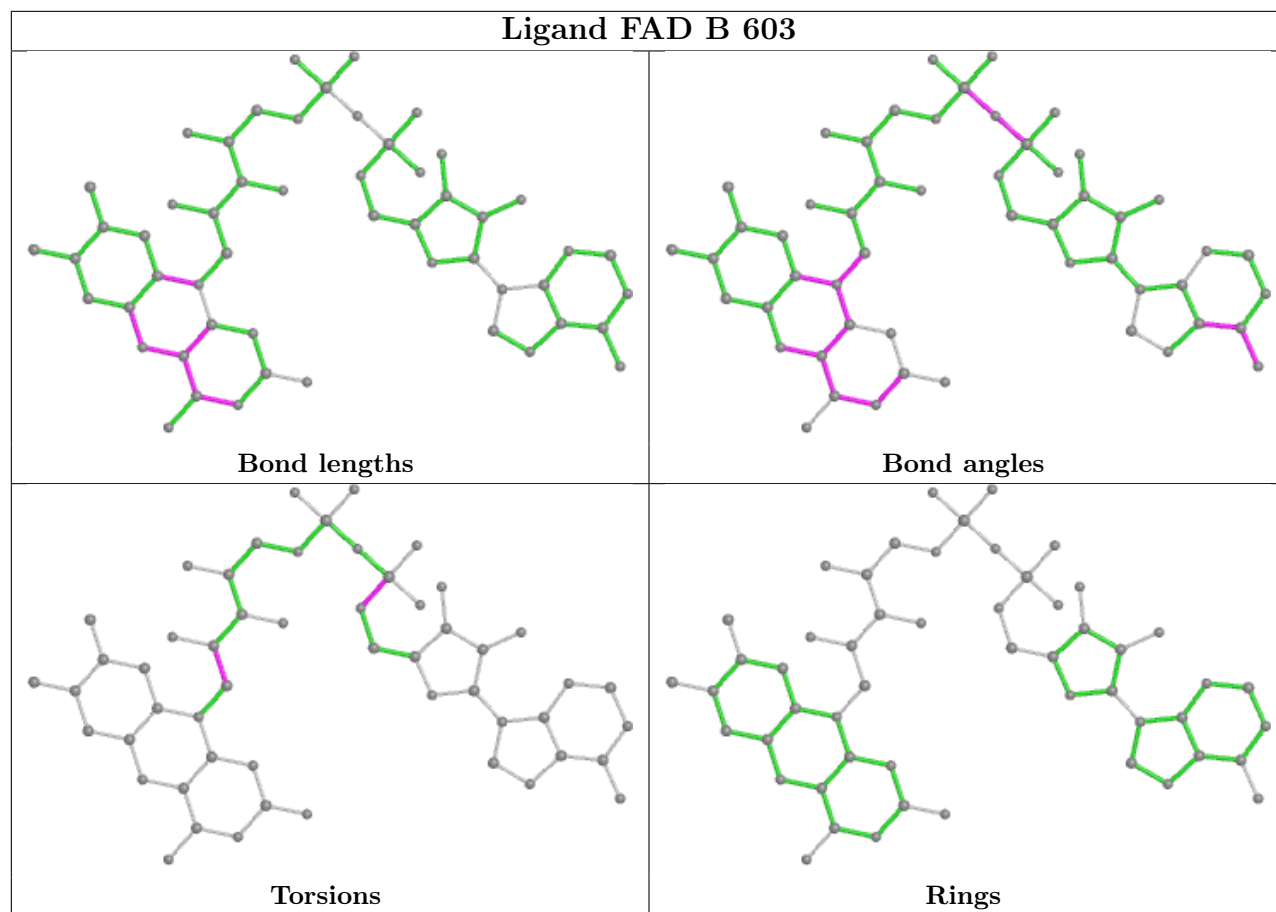
Mol	Chain	Res	Type	Atoms
3	A	602	FAD	N10-C1'-C2'-C3'
3	B	603	FAD	N10-C1'-C2'-C3'
3	A	602	FAD	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

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	537/593 (90%)	0.60	42 (7%)	13 10	34, 55, 83, 108	0
1	B	547/593 (92%)	0.63	34 (6%)	20 17	36, 56, 83, 125	0
All	All	1084/1186 (91%)	0.62	76 (7%)	16 13	34, 55, 83, 125	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	PHE	9.5
1	B	546	GLY	8.7
1	A	219	ALA	7.8
1	A	221	ILE	7.3
1	A	539	ASP	6.6
1	B	545	GLY	6.2
1	B	541	PRO	5.8
1	B	548	CYS	5.6
1	A	218	LEU	5.6
1	B	218	LEU	5.4
1	B	221	ILE	4.9
1	B	544	GLY	4.9
1	B	262	SER	4.4
1	A	476	SER	4.3
1	B	542	GLY	4.1
1	B	547	GLY	4.1
1	A	478	GLU	4.0
1	B	484	GLU	3.8
1	B	2	ALA	3.8
1	B	516	LEU	3.6
1	B	543	THR	3.6
1	A	487	ILE	3.5
1	A	517	ILE	3.4
1	B	219	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	289	LYS	3.3
1	B	220	LYS	3.3
1	A	289	LYS	3.3
1	B	188	LEU	3.2
1	A	163	HIS	3.1
1	A	180	LEU	3.0
1	B	248	GLY	2.8
1	A	516	LEU	2.7
1	B	213	ASP	2.6
1	A	514	ASN	2.6
1	B	211	TYR	2.6
1	A	296[A]	CYS	2.5
1	B	490	HIS	2.5
1	B	538	ALA	2.5
1	B	180	LEU	2.5
1	A	461	LEU	2.4
1	B	423	VAL	2.4
1	A	261	ASP	2.4
1	B	222	ASN	2.3
1	B	419	ASN	2.3
1	A	486	LEU	2.3
1	A	167	ILE	2.3
1	A	484	GLU	2.3
1	A	475	MET	2.3
1	A	503	LYS	2.3
1	A	185	PHE	2.3
1	A	455	LYS	2.2
1	A	485	CYS	2.2
1	A	126	ARG	2.2
1	A	420	TRP	2.2
1	B	253	ASN	2.2
1	A	87	GLU	2.2
1	A	294	ARG	2.2
1	A	76	ASP	2.1
1	A	349	LEU	2.1
1	A	4	ARG	2.1
1	A	181	GLU	2.1
1	A	538	ALA	2.1
1	A	489	VAL	2.1
1	A	423	VAL	2.1
1	A	440	PRO	2.1
1	B	438	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	489	VAL	2.1
1	A	69	ASP	2.1
1	B	163	HIS	2.1
1	A	355	LEU	2.1
1	A	474	ARG	2.0
1	B	217	PHE	2.0
1	A	223	TRP	2.0
1	B	417	ALA	2.0
1	A	415	VAL	2.0
1	B	245	PHE	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 monosaccharides in this entry.

6.4 Ligands [i](#)

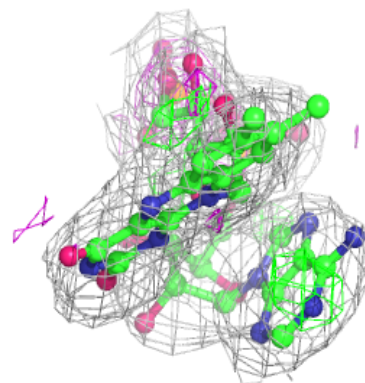
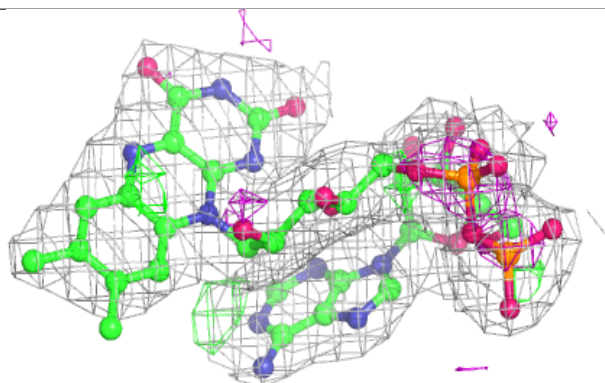
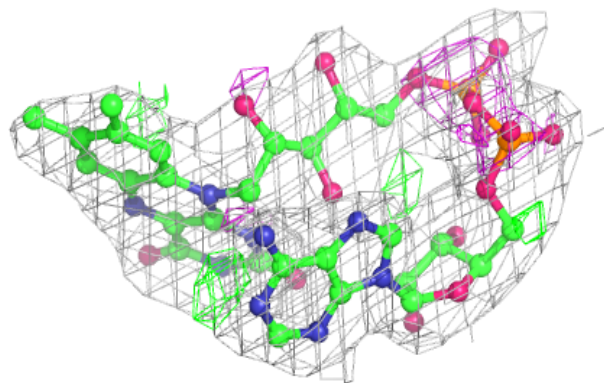
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	B	602	1/1	0.76	0.23	45,45,45,45	0
2	MG	B	601	1/1	0.80	0.21	65,65,65,65	0
3	FAD	B	603	53/53	0.92	0.19	32,41,46,48	0
3	FAD	A	602	53/53	0.95	0.20	33,42,48,52	0
2	MG	A	601	1/1	0.95	0.59	48,48,48,48	0

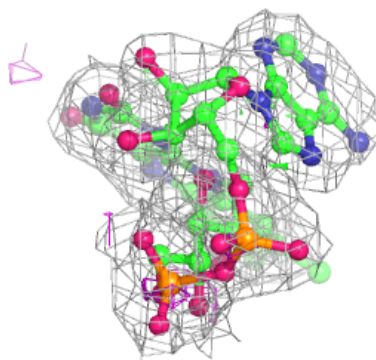
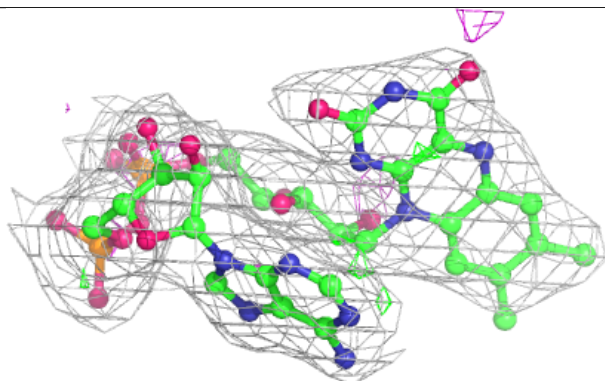
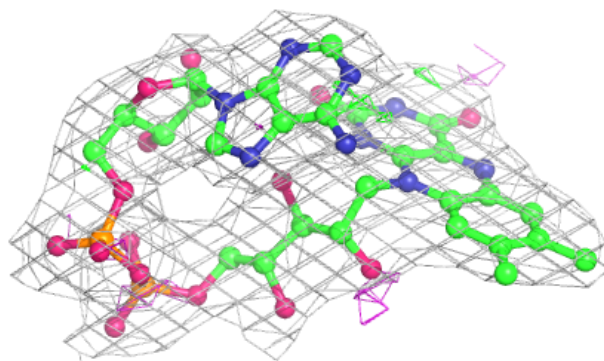
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 603:

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

**Electron density around FAD A 602:**

$2mF_o-DF_c$ (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.