



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:46 PM UTC

PDB ID : 6WTB / pdb_00006wtb
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 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

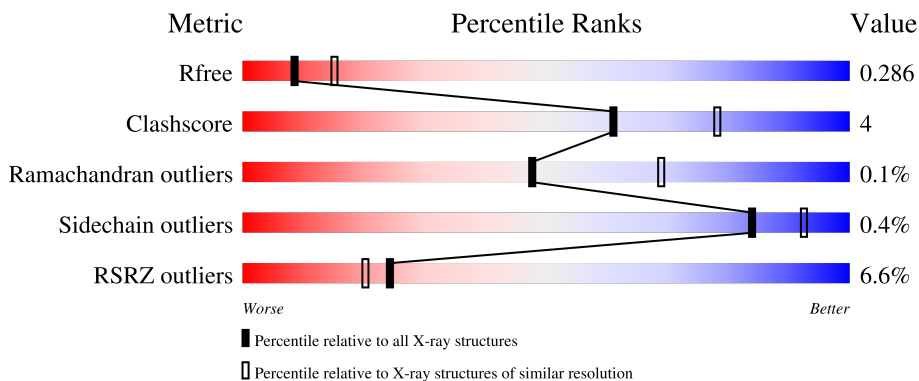
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (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	
1	B	593	

2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	537	4375	2793	774	782	26	0	1	0
1	B	547	4429	2824	784	794	27	0	1	0

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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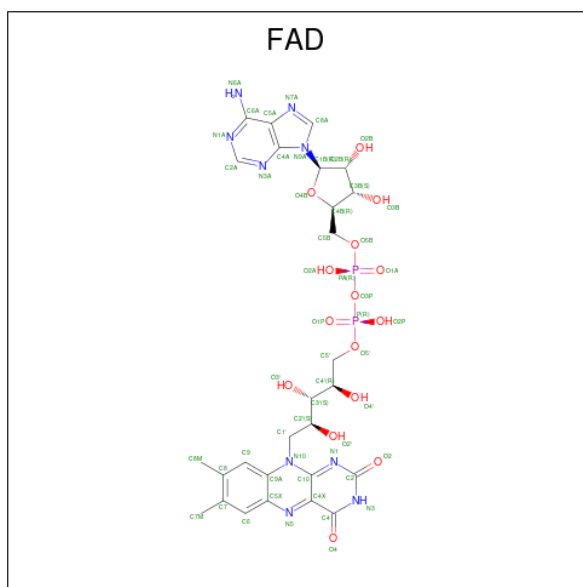
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-31	GLY	-	expression tag	UNP O77059
B	-30	GLY	-	expression tag	UNP O77059
B	-29	SER	-	expression tag	UNP O77059
B	-28	GLY	-	expression tag	UNP O77059
B	-27	GLY	-	expression tag	UNP O77059
B	-26	GLY	-	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 (CCD ID: 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 (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



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

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 39.00 – 2.58	Depositor EDS
% Data completeness (in resolution range)	96.6 (39.00-2.58) 96.6 (39.00-2.58)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.58Å)	Xtrriage
Refinement program	PHENIX 1.17.1	Depositor
R, R_{free}	0.234 , 0.287 0.234 , 0.286	Depositor DCC
R_{free} test set	2003 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtrriage
Anisotropy	0.608	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtrriage
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

Xtrriage'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: MG, 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	0.08	0/4498	0.26	0/6111
1	B	0.08	0/4553	0.27	0/6184
All	All	0.08	0/9051	0.27	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	37	0
1	B	4429	0	4325	36	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	73	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 (73) 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:B:52:VAL:HG11	1:B:57:MET:HE2	1.97	0.45
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:ASP:OD2	1:A:491:TYR:OH	2.32	0.45
1:B:9:ILE:HG23	1:B:38:PRO:HA	1.99	0.44
1:B:427:ALA:HA	1:B:509:MET:HE1	1.99	0.44
1:A:497:ASP:HB3	1:A:500:MET:HE3	1.99	0.44
1:A:17:LEU:H	1:A:227:GLU:CD	2.25	0.44
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 [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	536/593 (90%)	507 (95%)	29 (5%)	0	100	100
1	B	546/593 (92%)	522 (96%)	23 (4%)	1 (0%)	43	63
All	All	1082/1186 (91%)	1029 (95%)	52 (5%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	541	PRO

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	472/507 (93%)	468 (99%)	4 (1%)	73	87
1	B	476/507 (94%)	476 (100%)	0	100	100
All	All	948/1014 (94%)	944 (100%)	4 (0%)	84	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	ASN
1	A	260	HIS
1	A	410	ASP
1	A	517	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	GLN
1	A	108	GLN
1	A	163	HIS
1	A	301	GLN
1	B	51	ASN
1	B	108	GLN
1	B	269	HIS
1	B	378	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](#)

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	58,58,58	0.29	0	85,89,89	0.28	0
3	FAD	B	603	2	58,58,58	0.30	0	85,89,89	0.28	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
3	FAD	A	602	2	-	5/34/50/50	0/6/6/6
3	FAD	B	603	2	-	5/34/50/50	0/6/6/6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

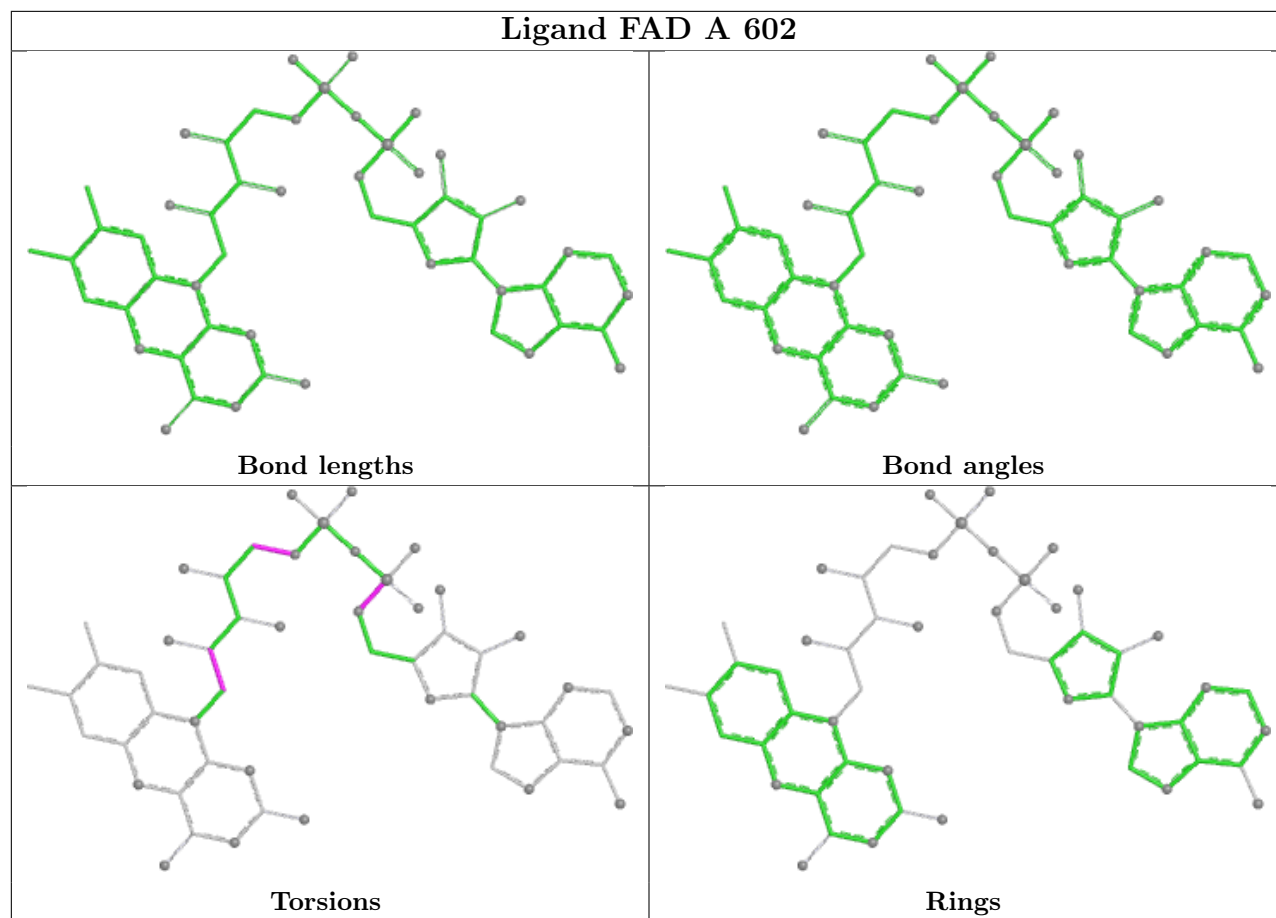
All (10) torsion outliers are listed below:

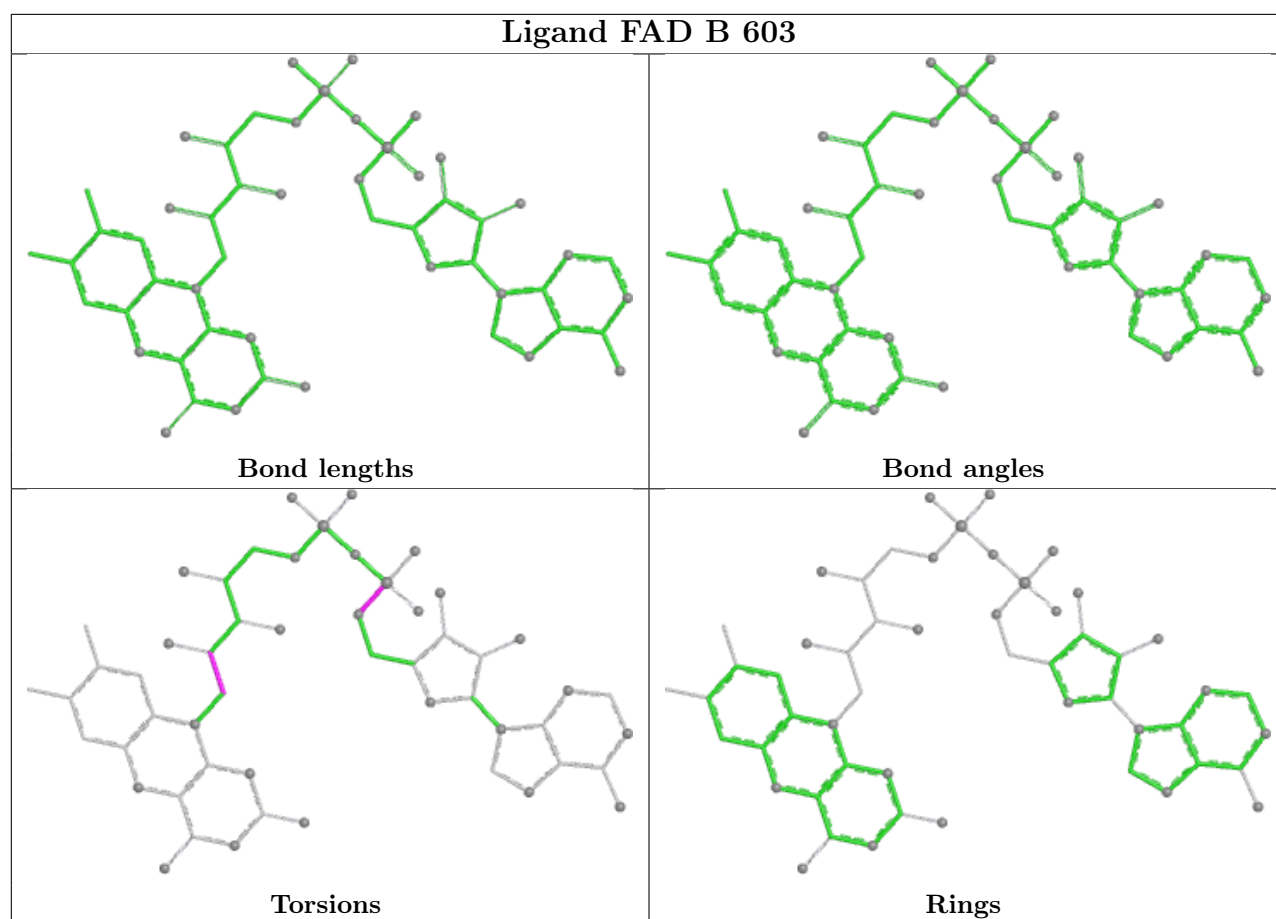
Mol	Chain	Res	Type	Atoms
3	A	602	FAD	C5B-O5B-PA-O2A
3	A	602	FAD	C5B-O5B-PA-O3P
3	A	602	FAD	N10-C1'-C2'-O2'
3	A	602	FAD	N10-C1'-C2'-C3'
3	B	603	FAD	C5B-O5B-PA-O1A
3	B	603	FAD	C5B-O5B-PA-O2A
3	B	603	FAD	C5B-O5B-PA-O3P
3	B	603	FAD	N10-C1'-C2'-C3'
3	B	603	FAD	N10-C1'-C2'-O2'
3	A	602	FAD	C4'-C5'-O5'-P

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	32 (5%) 27 23	34, 55, 83, 108	1 (0%)
1	B	547/593 (92%)	0.68	40 (7%) 21 17	36, 56, 83, 125	1 (0%)
All	All	1084/1186 (91%)	0.64	72 (6%) 24 20	34, 55, 83, 125	2 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	219	ALA	6.2
1	A	221	ILE	5.9
1	B	221	ILE	4.6
1	B	248	GLY	4.4
1	B	262	SER	4.1
1	B	219	ALA	3.9
1	A	217	PHE	3.7
1	A	216	GLY	3.6
1	A	461	LEU	3.5
1	A	440	PRO	3.4
1	B	212	GLY	3.3
1	B	541	PRO	3.3
1	A	212	GLY	3.2
1	B	213	ASP	3.2
1	A	218	LEU	3.1
1	A	436	LEU	3.1
1	A	180	LEU	3.0
1	B	218	LEU	2.8
1	A	262	SER	2.8
1	B	440	PRO	2.8
1	A	214	ASN	2.8
1	B	516	LEU	2.8
1	A	539	ASP	2.7
1	B	31	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	547	GLY	2.7
1	A	517	ILE	2.6
1	A	295	ALA	2.6
1	A	487	ILE	2.6
1	B	543	THR	2.6
1	B	545	GLY	2.6
1	B	546	GLY	2.6
1	B	437	VAL	2.6
1	B	436	LEU	2.5
1	B	540	LEU	2.5
1	A	213	ASP	2.5
1	B	261	ASP	2.5
1	B	331	MET	2.4
1	A	519	PRO	2.4
1	B	498	LEU	2.4
1	A	425	SER	2.3
1	B	518	THR	2.3
1	B	66	ASP	2.3
1	A	110	CYS	2.3
1	A	240	VAL	2.3
1	A	437	VAL	2.3
1	B	291	VAL	2.3
1	A	297	VAL	2.3
1	B	544	GLY	2.2
1	B	438	THR	2.2
1	A	87	GLU	2.2
1	A	360	PHE	2.2
1	B	519	PRO	2.2
1	A	469	VAL	2.2
1	A	223	TRP	2.2
1	B	240	VAL	2.1
1	B	469	VAL	2.1
1	B	217	PHE	2.1
1	B	490	HIS	2.1
1	A	538	ALA	2.1
1	B	216	GLY	2.1
1	B	496	ILE	2.1
1	B	484	GLU	2.1
1	A	261	ASP	2.1
1	A	280	PHE	2.1
1	A	486	LEU	2.1
1	B	3	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	425	SER	2.1
1	B	520	PRO	2.1
1	B	188	LEU	2.0
1	A	228	THR	2.0
1	B	2	ALA	2.0
1	B	295	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

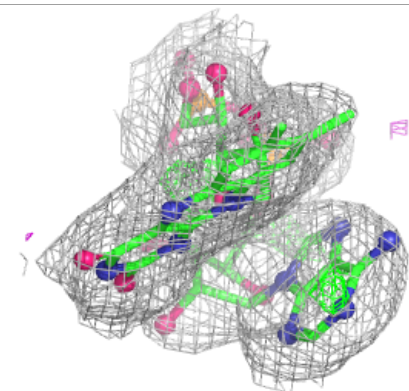
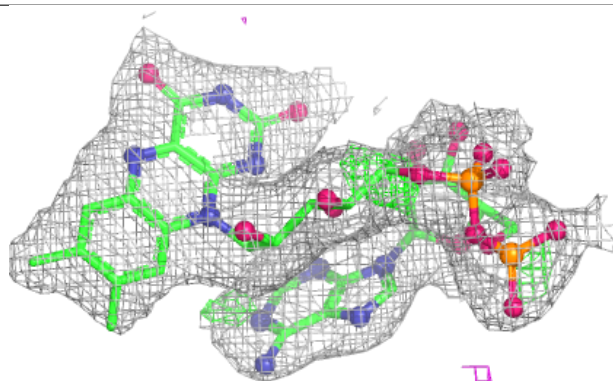
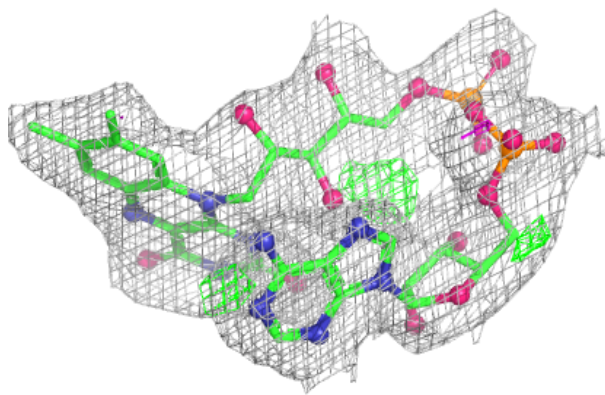
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	B	602	1/1	0.87	0.13	45,45,45,45	0
2	MG	A	601	1/1	0.90	0.22	48,48,48,48	0
3	FAD	B	603	53/53	0.91	0.10	32,41,46,48	0
3	FAD	A	602	53/53	0.94	0.08	33,42,48,52	0
2	MG	B	601	1/1	0.96	0.12	65,65,65,65	0

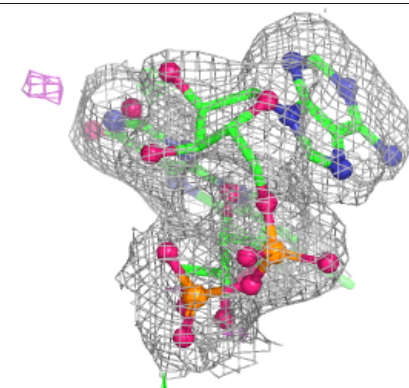
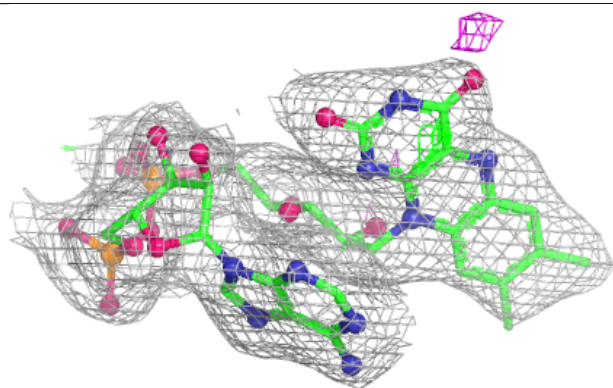
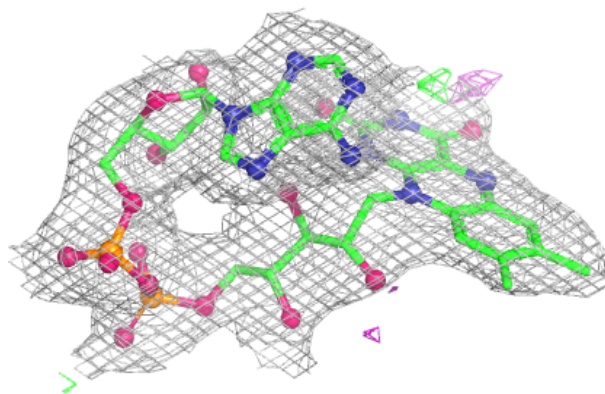
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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