



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:40 PM UTC

PDB ID : 4EIP / pdb_00004eip
Title : Native and K252c bound RebC-10x
Authors : Goldman, P.J.; Ryan, K.S.; Howard-Jones, A.R.; Hamill, M.J.; Elliott, S.J.;
Walsh, C.T.; Drennan, C.L.
Deposited on : 2012-04-05
Resolution : 2.33 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)
Xtrriage (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

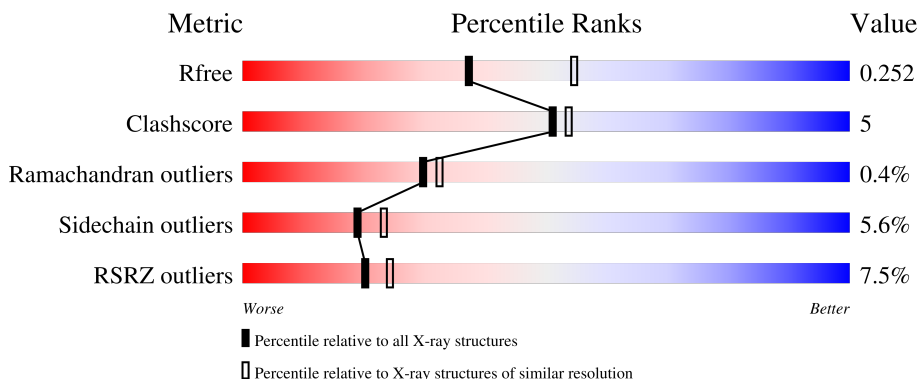
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.33 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	549	 7% 80% 13% • 5%
1	B	549	 7% 81% 11% • 7%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 8306 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 Putative FAD-monoxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	521	3997	2504	757	726	10	1	1	0
1	B	510	3875	2434	723	709	9	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q8KI25
A	-18	GLY	-	expression tag	UNP Q8KI25
A	-17	SER	-	expression tag	UNP Q8KI25
A	-16	SER	-	expression tag	UNP Q8KI25
A	-15	HIS	-	expression tag	UNP Q8KI25
A	-14	HIS	-	expression tag	UNP Q8KI25
A	-13	HIS	-	expression tag	UNP Q8KI25
A	-12	HIS	-	expression tag	UNP Q8KI25
A	-11	HIS	-	expression tag	UNP Q8KI25
A	-10	HIS	-	expression tag	UNP Q8KI25
A	-9	SER	-	expression tag	UNP Q8KI25
A	-8	SER	-	expression tag	UNP Q8KI25
A	-7	GLY	-	expression tag	UNP Q8KI25
A	-6	LEU	-	expression tag	UNP Q8KI25
A	-5	VAL	-	expression tag	UNP Q8KI25
A	-4	PRO	-	expression tag	UNP Q8KI25
A	-3	ARG	-	expression tag	UNP Q8KI25
A	-2	GLY	-	expression tag	UNP Q8KI25
A	-1	SER	-	expression tag	UNP Q8KI25
A	0	HIS	-	expression tag	UNP Q8KI25
A	36	ASP	GLU	engineered mutation	UNP Q8KI25
A	37	ALA	GLN	engineered mutation	UNP Q8KI25
A	38	GLY	THR	engineered mutation	UNP Q8KI25
A	46	LYS	ARG	engineered mutation	UNP Q8KI25
A	48	SER	GLY	engineered mutation	UNP Q8KI25

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Chain	Residue	Modelled	Actual	Comment	Reference
A	117	ALA	GLN	engineered mutation	UNP Q8KI25
A	216	VAL	PHE	engineered mutation	UNP Q8KI25
A	231	SER	ALA	engineered mutation	UNP Q8KI25
A	239	ASN	ARG	engineered mutation	UNP Q8KI25
A	241	VAL	THR	engineered mutation	UNP Q8KI25
B	-19	MET	-	initiating methionine	UNP Q8KI25
B	-18	GLY	-	expression tag	UNP Q8KI25
B	-17	SER	-	expression tag	UNP Q8KI25
B	-16	SER	-	expression tag	UNP Q8KI25
B	-15	HIS	-	expression tag	UNP Q8KI25
B	-14	HIS	-	expression tag	UNP Q8KI25
B	-13	HIS	-	expression tag	UNP Q8KI25
B	-12	HIS	-	expression tag	UNP Q8KI25
B	-11	HIS	-	expression tag	UNP Q8KI25
B	-10	HIS	-	expression tag	UNP Q8KI25
B	-9	SER	-	expression tag	UNP Q8KI25
B	-8	SER	-	expression tag	UNP Q8KI25
B	-7	GLY	-	expression tag	UNP Q8KI25
B	-6	LEU	-	expression tag	UNP Q8KI25
B	-5	VAL	-	expression tag	UNP Q8KI25
B	-4	PRO	-	expression tag	UNP Q8KI25
B	-3	ARG	-	expression tag	UNP Q8KI25
B	-2	GLY	-	expression tag	UNP Q8KI25
B	-1	SER	-	expression tag	UNP Q8KI25
B	0	HIS	-	expression tag	UNP Q8KI25
B	36	ASP	GLU	engineered mutation	UNP Q8KI25
B	37	ALA	GLN	engineered mutation	UNP Q8KI25
B	38	GLY	THR	engineered mutation	UNP Q8KI25
B	46	LYS	ARG	engineered mutation	UNP Q8KI25
B	48	SER	GLY	engineered mutation	UNP Q8KI25
B	117	ALA	GLN	engineered mutation	UNP Q8KI25
B	216	VAL	PHE	engineered mutation	UNP Q8KI25
B	231	SER	ALA	engineered mutation	UNP Q8KI25
B	239	ASN	ARG	engineered mutation	UNP Q8KI25
B	241	VAL	THR	engineered mutation	UNP Q8KI25

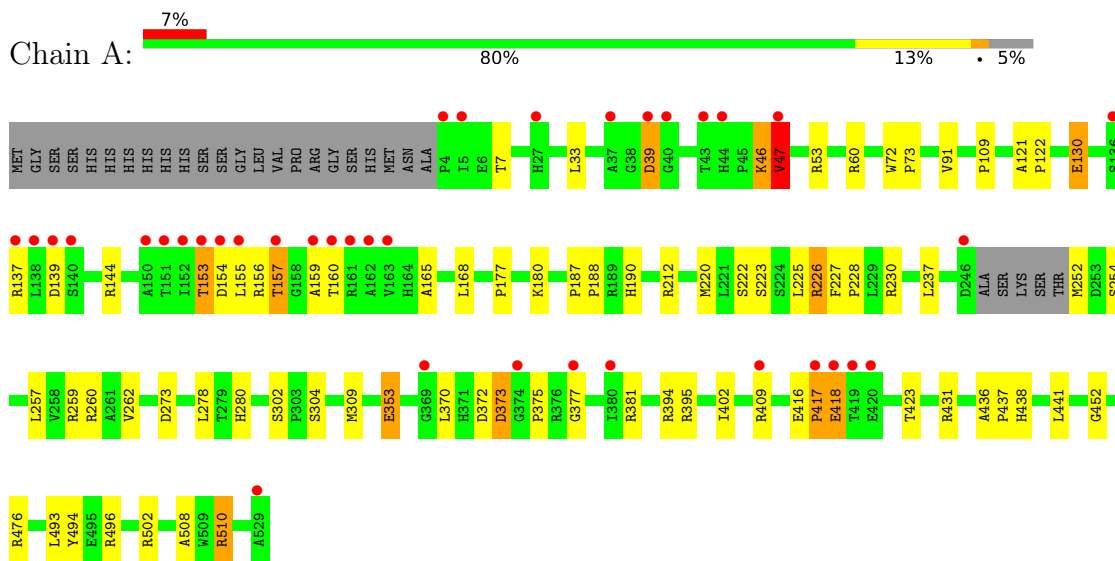
- Molecule 2 is 6,7,12,13-tetrahydro-5H-indolo[2,3-a]pyrrolo[3,4-c]carbazol-5-one (CCD ID: K2C) (formula: C₂₀H₁₃N₃O).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	170	Total 170	O 170	0	0
4	B	134	Total 134	O 134	0	0

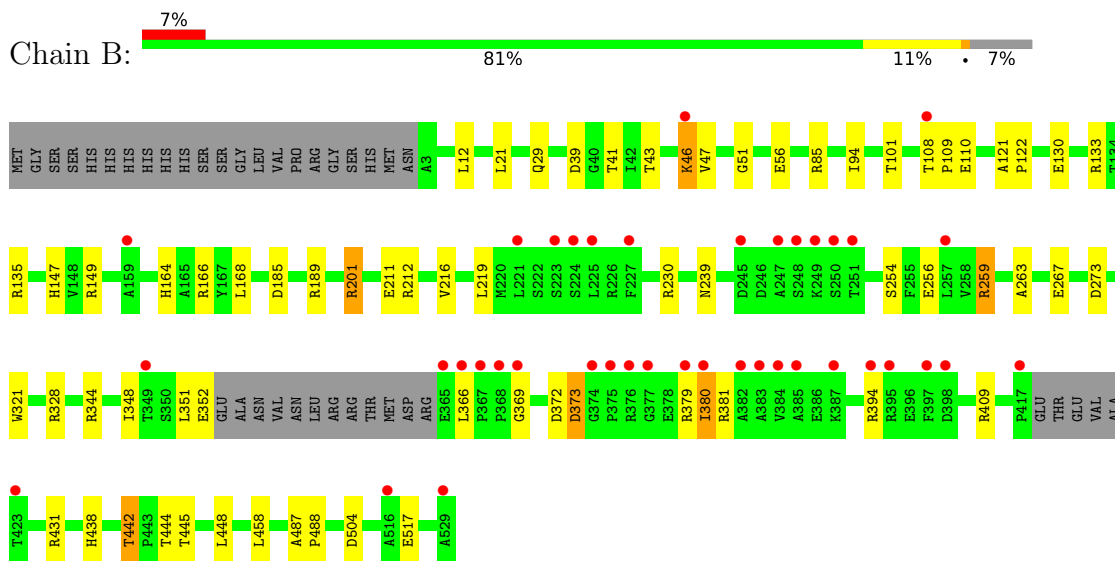
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Putative FAD-monooxygenase



- Molecule 1: Putative FAD-monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.31Å 78.59Å 125.72Å 90.00° 99.87° 90.00°	Depositor
Resolution (Å)	41.37 – 2.33 41.37 – 2.33	Depositor EDS
% Data completeness (in resolution range)	97.7 (41.37-2.33) 97.7 (41.37-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.77 (at 2.34Å)	Xtrriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, R_{free}	0.213 , 0.260 0.207 , 0.252	Depositor DCC
R_{free} test set	2616 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtrriage
Anisotropy	0.048	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8306	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: K2C, 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	0.37	0/4096	0.79	1/5574 (0.0%)
1	B	0.34	0/3972	0.78	4/5410 (0.1%)
All	All	0.35	0/8068	0.79	5/10984 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	VAL	CB-CA-C	-7.60	101.14	111.63
1	B	366	LEU	CA-C-N	6.83	124.58	119.66
1	B	366	LEU	C-N-CA	6.83	124.58	119.66
1	B	51	GLY	CA-C-N	5.88	125.57	119.05
1	B	51	GLY	C-N-CA	5.88	125.57	119.05

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	3997	0	3936	47	0
1	B	3875	0	3795	32	0
2	A	24	0	13	1	0
3	A	53	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	53	0	31	2	0
4	A	170	0	0	5	0
4	B	134	0	0	3	0
All	All	8306	0	7806	82	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 5.

All (82) 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:416:GLU:HB3	1:A:417:PRO:HD2	1.41	1.00
1:B:46:LYS:HG3	1:B:47:VAL:HG23	1.48	0.95
1:B:108:THR:HG22	1:B:110:GLU:H	1.39	0.86
1:B:46:LYS:HE3	4:B:791:HOH:O	1.77	0.83
1:A:417:PRO:O	1:A:418:GLU:O	2.04	0.76
1:A:157:THR:HG22	1:A:159:ALA:H	1.51	0.75
1:A:252:MET:HE1	1:A:260:ARG:HD2	1.71	0.72
1:B:130:GLU:O	1:B:133:ARG:NH1	2.22	0.72
1:A:278:LEU:HD11	1:A:302:SER:HA	1.72	0.72
1:B:39:ASP:HB3	1:B:135:ARG:HD3	1.73	0.70
1:B:372:ASP:O	1:B:381:ARG:NH2	2.25	0.69
1:B:46:LYS:CG	1:B:47:VAL:HG23	2.21	0.69
1:B:442:THR:HG23	1:B:444:THR:H	1.57	0.69
1:B:189:ARG:HG3	1:B:351:LEU:HD13	1.74	0.68
1:A:259:ARG:NH1	1:A:262:VAL:O	2.27	0.68
1:A:372:ASP:O	1:A:381:ARG:NH2	2.27	0.66
1:A:91:VAL:HG21	1:A:220:MET:HE2	1.78	0.65
1:A:416:GLU:HB3	1:A:417:PRO:CD	2.22	0.63
1:B:85:ARG:HD3	1:B:263:ALA:HB2	1.81	0.62
1:A:39:ASP:OD1	1:A:39:ASP:N	2.34	0.60
1:A:373:ASP:HA	1:A:381:ARG:HH22	1.67	0.59
1:A:395:ARG:NH1	4:A:757:HOH:O	2.38	0.57
1:B:373:ASP:OD2	1:B:373:ASP:N	2.39	0.54
1:A:46:LYS:HD3	1:A:47:VAL:HG13	1.90	0.54
1:A:252:MET:HE2	1:A:257:LEU:HD23	1.91	0.53
1:A:496:ARG:HD3	1:A:510:ARG:HD3	1.91	0.53
1:A:220:MET:HE3	1:A:370:LEU:HD21	1.92	0.52
1:B:216:VAL:HG13	1:B:230:ARG:HG2	1.92	0.51
1:A:254:SER:OG	1:A:273:ASP:OD2	2.28	0.51
1:B:256:GLU:OE1	1:B:259:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:PHE:HB3	1:A:228:PRO:HD2	1.93	0.51
1:A:437:PRO:HB2	1:A:493:LEU:HD21	1.92	0.50
3:B:600:FAD:O5'	3:B:600:FAD:O1A	2.30	0.50
1:A:137:ARG:HD3	1:A:155:LEU:HD21	1.95	0.48
1:B:94:ILE:HD13	1:B:394:ARG:HB3	1.95	0.48
1:A:153:THR:HA	1:A:160:THR:HA	1.96	0.48
1:A:437:PRO:HD2	1:A:494:TYR:CZ	2.50	0.47
1:A:130:GLU:H	1:A:130:GLU:CD	2.21	0.47
1:A:137:ARG:O	4:A:860:HOH:O	2.20	0.47
1:A:416:GLU:OE2	1:A:510:ARG:HD2	2.15	0.47
1:A:222:SER:O	1:A:226:ARG:HG2	2.16	0.46
1:B:56:GLU:OE2	1:B:108:THR:HG23	2.16	0.46
1:A:187:PRO:HA	1:A:188:PRO:HD3	1.80	0.46
1:A:154:ASP:OD1	1:A:156:ARG:HG2	2.15	0.46
1:A:72:TRP:HA	1:A:73:PRO:HD3	1.86	0.45
1:A:60:ARG:HD2	1:A:452:GLY:HA3	1.99	0.45
1:B:149:ARG:HG2	1:B:164:HIS:CE1	2.52	0.45
1:A:137:ARG:N	4:A:860:HOH:O	2.50	0.44
1:B:239:ASN:ND2	4:B:753:HOH:O	2.49	0.44
1:B:442:THR:HG22	1:B:445:THR:H	1.83	0.44
1:A:372:ASP:O	1:A:377:GLY:HA3	2.18	0.44
1:B:321:TRP:CD1	1:B:504:ASP:HB3	2.53	0.44
1:A:436:ALA:HA	1:A:437:PRO:HD3	1.75	0.43
1:B:121:ALA:HB3	1:B:122:PRO:HD3	2.00	0.43
1:B:201:ARG:NH1	1:B:267:GLU:OE2	2.51	0.43
1:A:476:ARG:NH2	4:A:855:HOH:O	2.52	0.43
1:B:254:SER:HB3	1:B:273:ASP:OD2	2.18	0.43
1:B:487:ALA:HA	1:B:488:PRO:HD3	1.88	0.43
1:A:190:HIS:HB2	1:A:280:HIS:CD2	2.54	0.42
1:B:212:ARG:HD2	4:B:834:HOH:O	2.19	0.42
2:A:601:K2C:O24	2:A:601:K2C:H4	2.18	0.42
1:A:137:ARG:NH1	1:A:139:ASP:OD2	2.52	0.42
1:B:46:LYS:HG2	1:B:47:VAL:N	2.33	0.42
1:B:109:PRO:HD3	1:B:438:HIS:CG	2.55	0.42
3:B:600:FAD:H1'1	3:B:600:FAD:H9	1.80	0.42
1:A:502:ARG:HG3	1:A:508:ALA:HB2	2.03	0.41
1:A:109:PRO:HD3	1:A:438:HIS:CG	2.55	0.41
1:B:380:ILE:H	1:B:380:ILE:HG12	1.40	0.41
1:B:369:GLY:HA2	1:B:372:ASP:CG	2.46	0.41
1:A:223:SER:O	1:A:226:ARG:HD2	2.21	0.41
1:B:442:THR:CG2	1:B:444:THR:H	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ALA:HB3	1:A:122:PRO:HD3	2.01	0.41
1:A:416:GLU:CB	1:A:417:PRO:CD	2.94	0.41
1:B:41:THR:HG22	1:B:43:THR:HG23	2.03	0.41
1:B:344:ARG:CZ	1:B:348:ILE:HD11	2.51	0.41
1:A:353:GLU:HG3	1:A:402:ILE:HD11	2.02	0.41
1:A:431:ARG:NH1	4:A:841:HOH:O	2.54	0.40
1:B:147:HIS:NE2	1:B:149:ARG:HD2	2.36	0.40
1:A:47:VAL:O	1:A:47:VAL:CG2	2.66	0.40
1:A:177:PRO:HA	1:A:180:LYS:HE3	2.02	0.40
1:A:309:MET:HE2	1:A:309:MET:HB3	2.01	0.40
1:A:7:THR:O	1:A:165:ALA:HA	2.21	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	518/549 (94%)	499 (96%)	15 (3%)	4 (1%)	16	16
1	B	504/549 (92%)	486 (96%)	18 (4%)	0	100	100
All	All	1022/1098 (93%)	985 (96%)	33 (3%)	4 (0%)	30	32

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	417	PRO
1	A	418	GLU
1	A	375	PRO
1	A	304	SER

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	407/432 (94%)	385 (95%)	22 (5%)	20	24
1	B	392/432 (91%)	369 (94%)	23 (6%)	18	21
All	All	799/864 (92%)	754 (94%)	45 (6%)	19	23

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	39	ASP
1	A	46	LYS
1	A	47	VAL
1	A	53	ARG
1	A	130	GLU
1	A	144	ARG
1	A	153	THR
1	A	157	THR
1	A	168	LEU
1	A	212	ARG
1	A	225	LEU
1	A	226	ARG
1	A	230	ARG
1	A	237	LEU
1	A	353	GLU
1	A	373	ASP
1	A	394	ARG
1	A	409	ARG
1	A	423	THR
1	A	441	LEU
1	A	510	ARG
1	B	12	LEU
1	B	21	LEU
1	B	29	GLN
1	B	46	LYS
1	B	101	THR

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Mol	Chain	Res	Type
1	B	166	ARG
1	B	168	LEU
1	B	185	ASP
1	B	201	ARG
1	B	211	GLU
1	B	219	LEU
1	B	259	ARG
1	B	328	ARG
1	B	352	GLU
1	B	373	ASP
1	B	379	ARG
1	B	380	ILE
1	B	409	ARG
1	B	431	ARG
1	B	442	THR
1	B	448	LEU
1	B	458	LEU
1	B	517	GLU

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

Mol	Chain	Res	Type
1	A	355	ASN
1	B	89	HIS
1	B	477	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

3 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	A	602	-	58,58,58	1.47	9 (15%)	85,89,89	1.56	16 (18%)
3	FAD	B	600	-	58,58,58	1.46	9 (15%)	85,89,89	1.53	15 (17%)
2	K2C	A	601	-	29,29,29	1.84	7 (24%)	44,45,45	2.76	21 (47%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	K2C	A	601	-	-	-	0/6/6/6
3	FAD	A	602	-	-	14/34/50/50	0/6/6/6
3	FAD	B	600	-	-	9/34/50/50	0/6/6/6

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	FAD	C9A-C5X	5.22	1.49	1.41
3	B	600	FAD	C9A-C5X	5.18	1.49	1.41
2	A	601	K2C	C7-C22	-4.76	1.46	1.50
3	A	602	FAD	C5A-C4A	4.63	1.47	1.39
3	B	600	FAD	C5A-C4A	4.58	1.47	1.39
2	A	601	K2C	C20-C21	-4.09	1.37	1.46
2	A	601	K2C	C15-C16	-3.90	1.37	1.46
3	B	600	FAD	C8-C7	3.39	1.49	1.40
3	A	602	FAD	C8-C7	3.35	1.49	1.40
2	A	601	K2C	C7-N6	2.94	1.48	1.45
3	A	602	FAD	C5A-C6A	2.73	1.48	1.41
2	A	601	K2C	C16-C17	-2.73	1.36	1.41
3	B	600	FAD	C5A-C6A	2.71	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	K2C	O24-C5	2.57	1.29	1.23
3	B	600	FAD	C4-N3	-2.51	1.34	1.38
3	A	602	FAD	C4-N3	-2.49	1.34	1.38
2	A	601	K2C	C21-C18	-2.49	1.37	1.41
3	B	600	FAD	C8A-N7A	2.32	1.36	1.31
3	A	602	FAD	C8A-N7A	2.31	1.36	1.31
3	A	602	FAD	C5A-N7A	-2.29	1.34	1.39
3	B	600	FAD	C5A-N7A	-2.25	1.35	1.39
3	A	602	FAD	C4X-N5	2.21	1.35	1.30
3	B	600	FAD	C4X-N5	2.20	1.35	1.30
3	B	600	FAD	C5X-N5	-2.11	1.35	1.39
3	A	602	FAD	C5X-N5	-2.01	1.35	1.39

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	K2C	C7-N6-C5	-6.83	107.63	113.86
2	A	601	K2C	C21-C22-C23	-5.94	117.34	121.25
3	A	602	FAD	C5A-C4A-N3A	-5.83	118.69	126.72
3	B	600	FAD	C5A-C4A-N3A	-5.70	118.87	126.72
2	A	601	K2C	C16-C23-C22	5.68	124.72	120.76
2	A	601	K2C	C23-C5-N6	5.52	111.64	106.38
2	A	601	K2C	C7-C22-C23	5.49	111.90	109.88
3	A	602	FAD	N3A-C4A-N9A	4.59	134.97	127.17
2	A	601	K2C	C22-C23-C5	-4.48	104.34	108.09
3	B	600	FAD	N3A-C4A-N9A	4.47	134.77	127.17
3	A	602	FAD	C2A-N3A-C4A	3.73	120.93	111.83
3	B	600	FAD	C2A-N3A-C4A	3.68	120.81	111.83
2	A	601	K2C	C8-C20-C19	3.59	123.03	119.07
3	B	600	FAD	C4A-C5A-N7A	-3.57	106.50	110.58
3	A	602	FAD	C4A-C5A-N7A	-3.49	106.59	110.58
2	A	601	K2C	C1-C14-N13	3.28	133.74	129.07
2	A	601	K2C	C11-C19-N12	3.27	133.74	129.07
3	B	600	FAD	N3A-C2A-N1A	-3.24	123.68	128.58
3	A	602	FAD	N3A-C2A-N1A	-3.24	123.68	128.58
2	A	601	K2C	C4-C15-C14	3.23	122.63	119.07
3	A	602	FAD	C4-C4X-N5	2.92	122.25	118.21
2	A	601	K2C	C1-C14-C15	-2.91	118.65	121.68
2	A	601	K2C	C11-C19-C20	-2.82	118.75	121.68
2	A	601	K2C	C22-C7-N6	2.80	104.48	101.75
3	B	600	FAD	C4-C4X-N5	2.76	122.02	118.21
3	B	600	FAD	C4A-N9A-C8A	2.71	108.58	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	K2C	C7-C22-C21	2.68	130.76	128.73
3	B	600	FAD	C5A-N7A-C8A	2.61	107.56	103.45
3	A	602	FAD	C4A-N9A-C8A	2.60	108.47	105.74
3	A	602	FAD	C5A-N7A-C8A	2.58	107.51	103.45
3	B	600	FAD	C4X-C10-N1	-2.45	118.59	124.59
3	A	602	FAD	C4X-C10-N1	-2.44	118.61	124.59
2	A	601	K2C	C21-C20-C19	2.43	108.57	106.21
3	A	602	FAD	C3B-C2B-C1B	2.25	105.73	101.46
3	B	600	FAD	O4-C4-C4X	-2.24	120.61	126.53
3	B	600	FAD	C6A-C5A-N7A	2.22	136.37	132.09
2	A	601	K2C	O24-C5-N6	-2.18	122.92	125.35
3	A	602	FAD	O4-C4-C4X	-2.16	120.83	126.53
2	A	601	K2C	C8-C20-C21	-2.14	128.40	133.49
2	A	601	K2C	C17-C18-N12	-2.14	127.47	130.50
3	A	602	FAD	C10-N1-C2	2.12	121.43	116.85
3	A	602	FAD	C6A-C5A-N7A	2.10	136.14	132.09
2	A	601	K2C	C16-C15-C14	2.10	108.25	106.21
2	A	601	K2C	O24-C5-C23	-2.10	125.43	128.47
3	B	600	FAD	C10-N1-C2	2.08	121.36	116.85
3	A	602	FAD	C4X-C4-N3	2.07	118.53	113.25
3	B	600	FAD	N9A-C8A-N7A	-2.07	111.00	113.94
3	A	602	FAD	C4X-C10-N10	2.06	119.43	116.48
3	B	600	FAD	C4X-C10-N10	2.06	119.42	116.48
3	B	600	FAD	C4X-C4-N3	2.05	118.47	113.25
2	A	601	K2C	C16-C17-N13	2.02	111.02	108.89
3	A	602	FAD	N9A-C8A-N7A	-2.00	111.09	113.94

There are no chirality outliers.

All (23) 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	C3'-C4'-C5'-O5'
3	A	602	FAD	O4'-C4'-C5'-O5'
3	A	602	FAD	C5'-O5'-P-O1P
3	A	602	FAD	C5'-O5'-P-O2P
3	A	602	FAD	C5'-O5'-P-O3P
3	B	600	FAD	C3'-C4'-C5'-O5'
3	B	600	FAD	O4'-C4'-C5'-O5'
3	B	600	FAD	C5'-O5'-P-O1P
3	B	600	FAD	C5'-O5'-P-O2P

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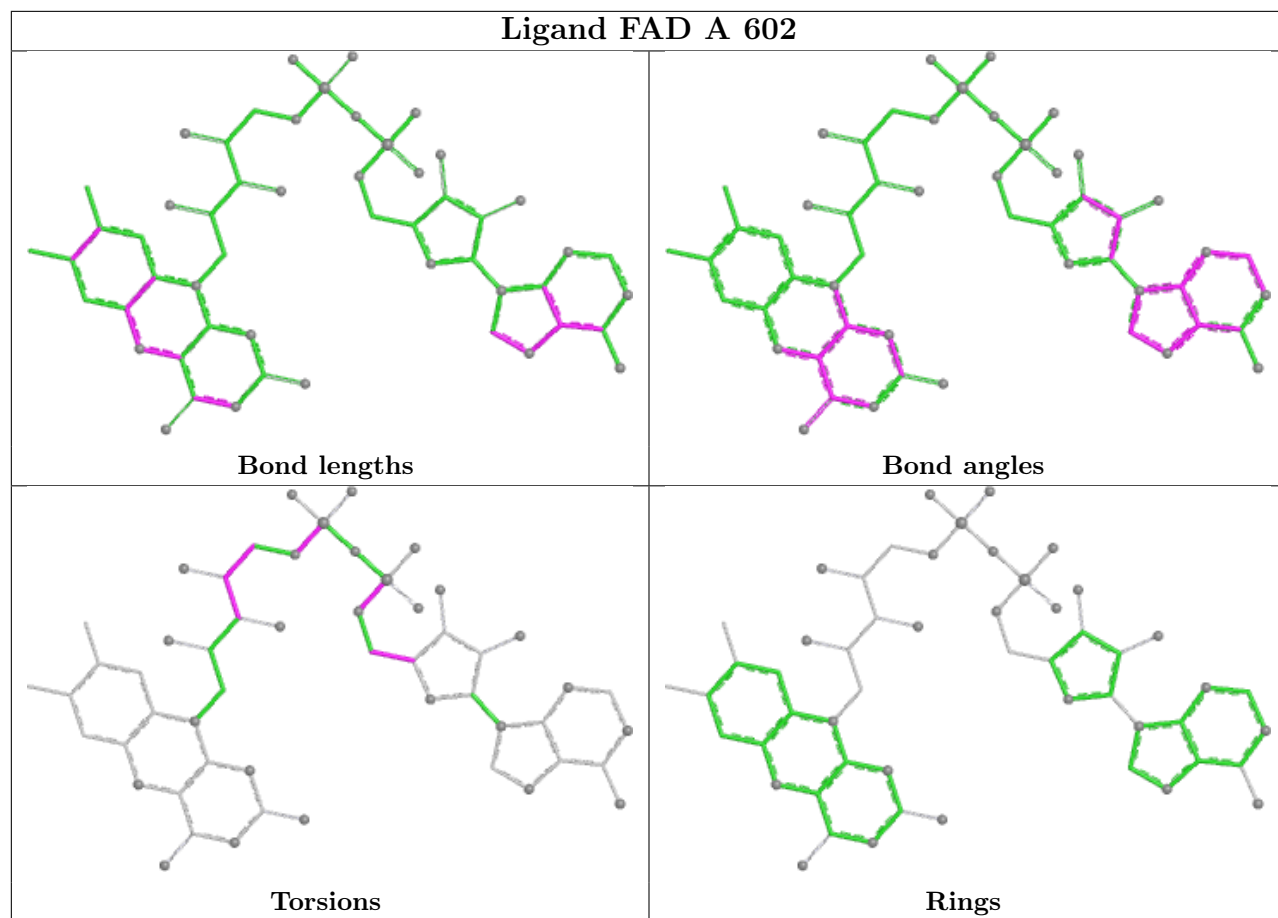
Mol	Chain	Res	Type	Atoms
3	B	600	FAD	C5'-O5'-P-O3P
3	A	602	FAD	O4B-C4B-C5B-O5B
3	A	602	FAD	C3B-C4B-C5B-O5B
3	B	600	FAD	PA-O3P-P-O5'
3	A	602	FAD	C2'-C3'-C4'-O4'
3	A	602	FAD	C5B-O5B-PA-O1A
3	A	602	FAD	O3'-C3'-C4'-C5'
3	B	600	FAD	O4B-C4B-C5B-O5B
3	A	602	FAD	O3'-C3'-C4'-O4'
3	B	600	FAD	P-O3P-PA-O1A
3	A	602	FAD	C2'-C3'-C4'-C5'
3	B	600	FAD	P-O3P-PA-O2A

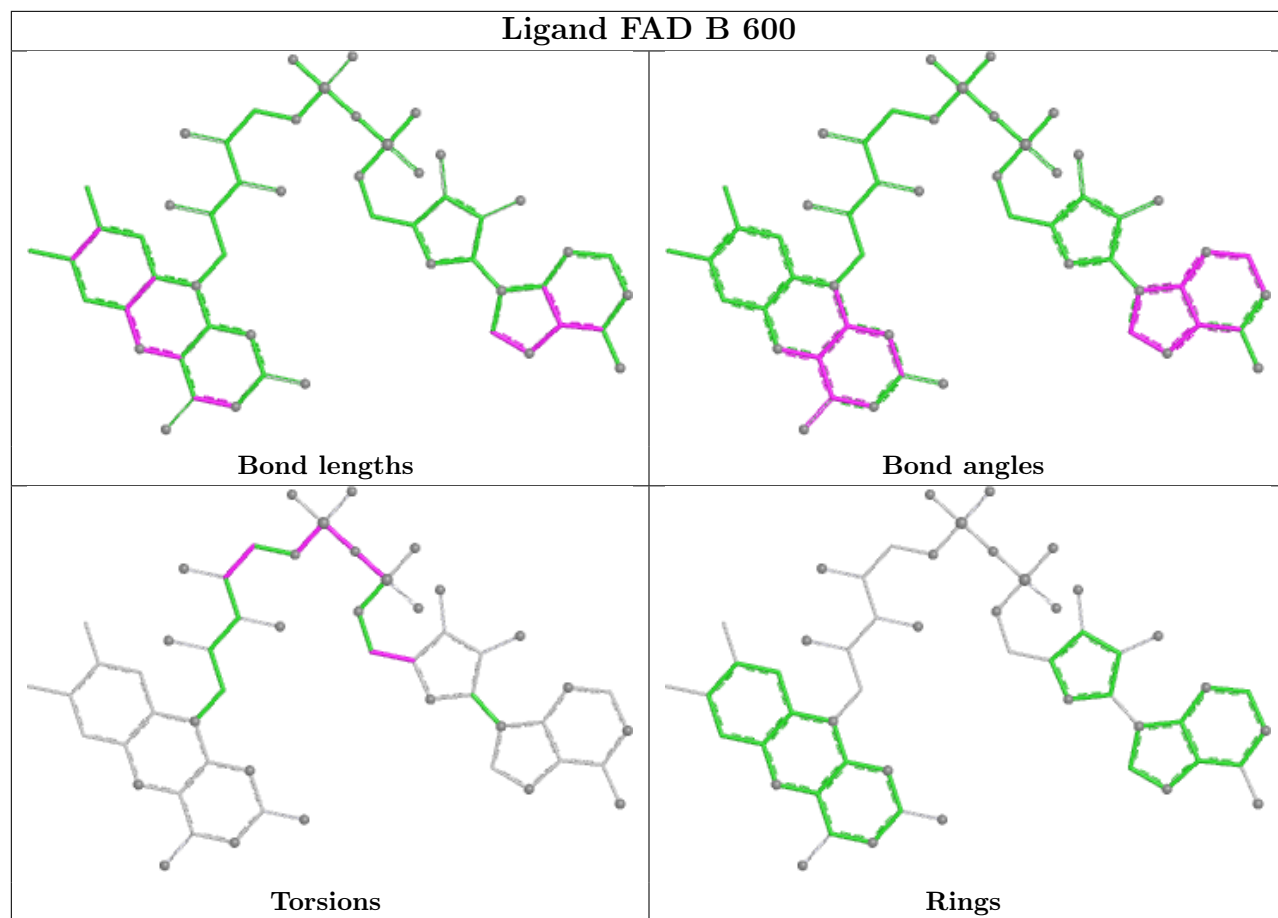
There are no ring outliers.

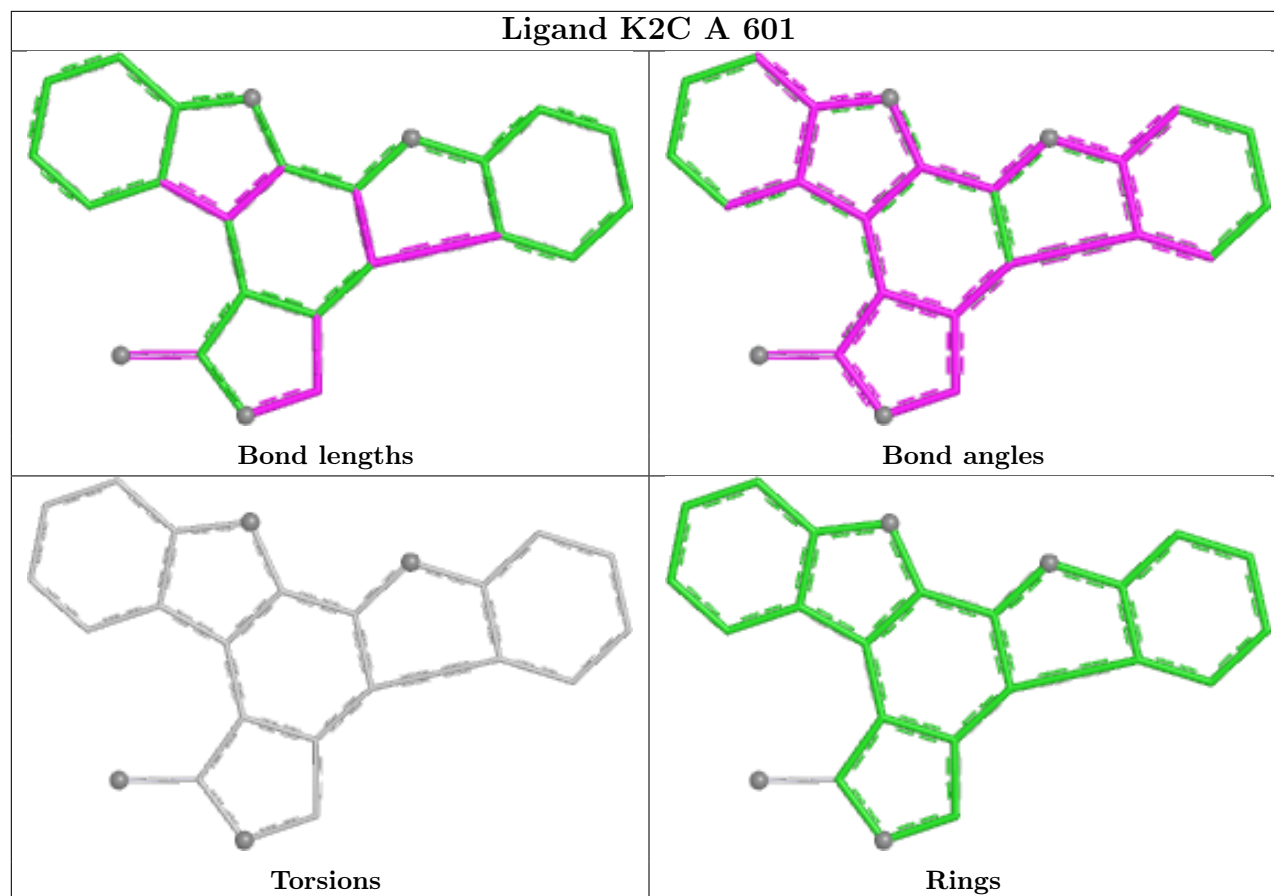
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	600	FAD	2	0
2	A	601	K2C	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.







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	521/549 (94%)	0.27	37 (7%) 22 26	13, 31, 56, 68	1 (0%)
1	B	510/549 (92%)	0.58	40 (7%) 19 23	24, 40, 71, 92	0
All	All	1031/1098 (93%)	0.42	77 (7%) 20 24	13, 35, 64, 92	1 (0%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	155	LEU	4.5
1	A	160	THR	4.0
1	A	27[A]	HIS	3.9
1	B	369	GLY	3.8
1	A	418	GLU	3.7
1	A	4	PRO	3.7
1	B	221	LEU	3.6
1	B	247	ALA	3.6
1	B	250	SER	3.5
1	A	137	ARG	3.5
1	A	417	PRO	3.5
1	A	246	ASP	3.5
1	B	368	PRO	3.3
1	B	423	THR	3.3
1	A	151	THR	3.2
1	A	5	ILE	3.1
1	B	377	GLY	3.1
1	A	43	THR	3.1
1	A	47	VAL	3.0
1	A	369	GLY	3.0
1	A	529	ALA	2.9
1	B	516	ALA	2.9
1	B	349	THR	2.9
1	A	139	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	152	ILE	2.9
1	A	162	ALA	2.8
1	A	157	THR	2.8
1	B	46	LYS	2.8
1	B	251	THR	2.8
1	A	40	GLY	2.8
1	B	223	SER	2.8
1	A	150	ALA	2.8
1	B	380	ILE	2.7
1	B	225	LEU	2.7
1	A	153	THR	2.7
1	B	367	PRO	2.7
1	B	249	LYS	2.6
1	B	245	ASP	2.6
1	A	380	ILE	2.6
1	B	383	ALA	2.6
1	B	248	SER	2.6
1	B	529	ALA	2.5
1	B	384	VAL	2.5
1	A	44	HIS	2.5
1	B	365	GLU	2.5
1	A	409	ARG	2.4
1	B	398	ASP	2.4
1	B	366	LEU	2.4
1	B	397	PHE	2.4
1	B	108	THR	2.3
1	B	257	LEU	2.3
1	B	375	PRO	2.3
1	B	387	LYS	2.3
1	B	382	ALA	2.3
1	A	419	THR	2.3
1	B	376	ARG	2.3
1	A	377	GLY	2.3
1	A	163	VAL	2.2
1	A	39	ASP	2.2
1	B	417	PRO	2.2
1	B	385	ALA	2.2
1	A	420	GLU	2.2
1	A	374	GLY	2.2
1	B	159	ALA	2.2
1	A	159	ALA	2.1
1	B	224	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	227	PHE	2.1
1	B	379	ARG	2.1
1	B	395	ARG	2.1
1	A	136	SER	2.1
1	A	140	SER	2.1
1	A	161	ARG	2.1
1	A	138	LEU	2.1
1	B	394	ARG	2.1
1	A	37	ALA	2.0
1	B	374	GLY	2.0
1	A	154	ASP	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](#)

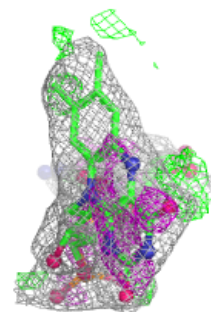
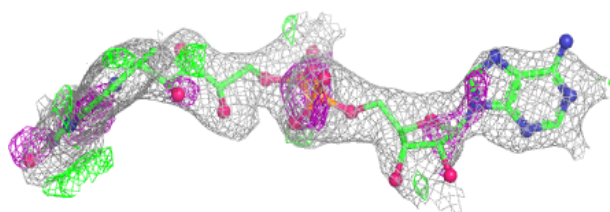
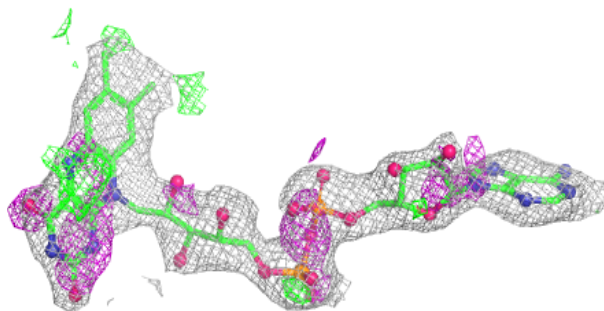
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FAD	A	602	53/53	0.82	0.14	34,42,54,56	0
2	K2C	A	601	24/24	0.89	0.10	29,30,34,35	0
3	FAD	B	600	53/53	0.93	0.09	28,34,43,47	0

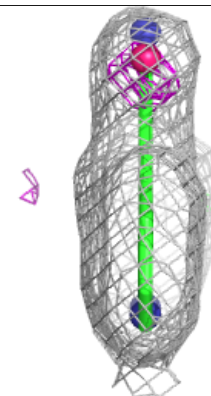
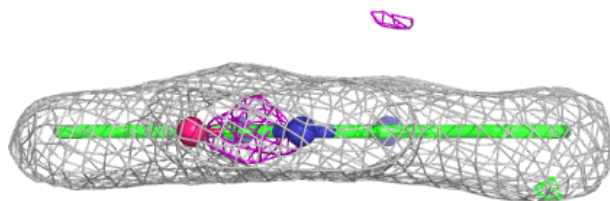
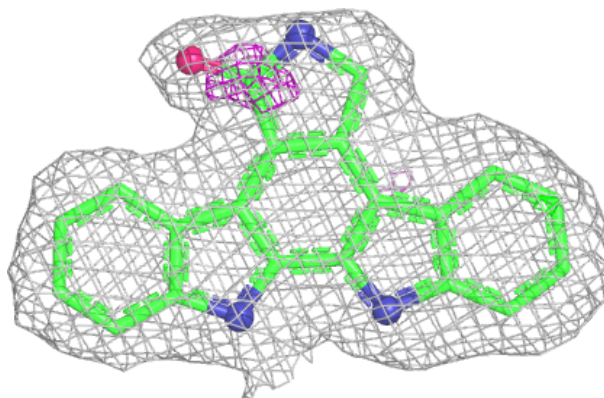
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

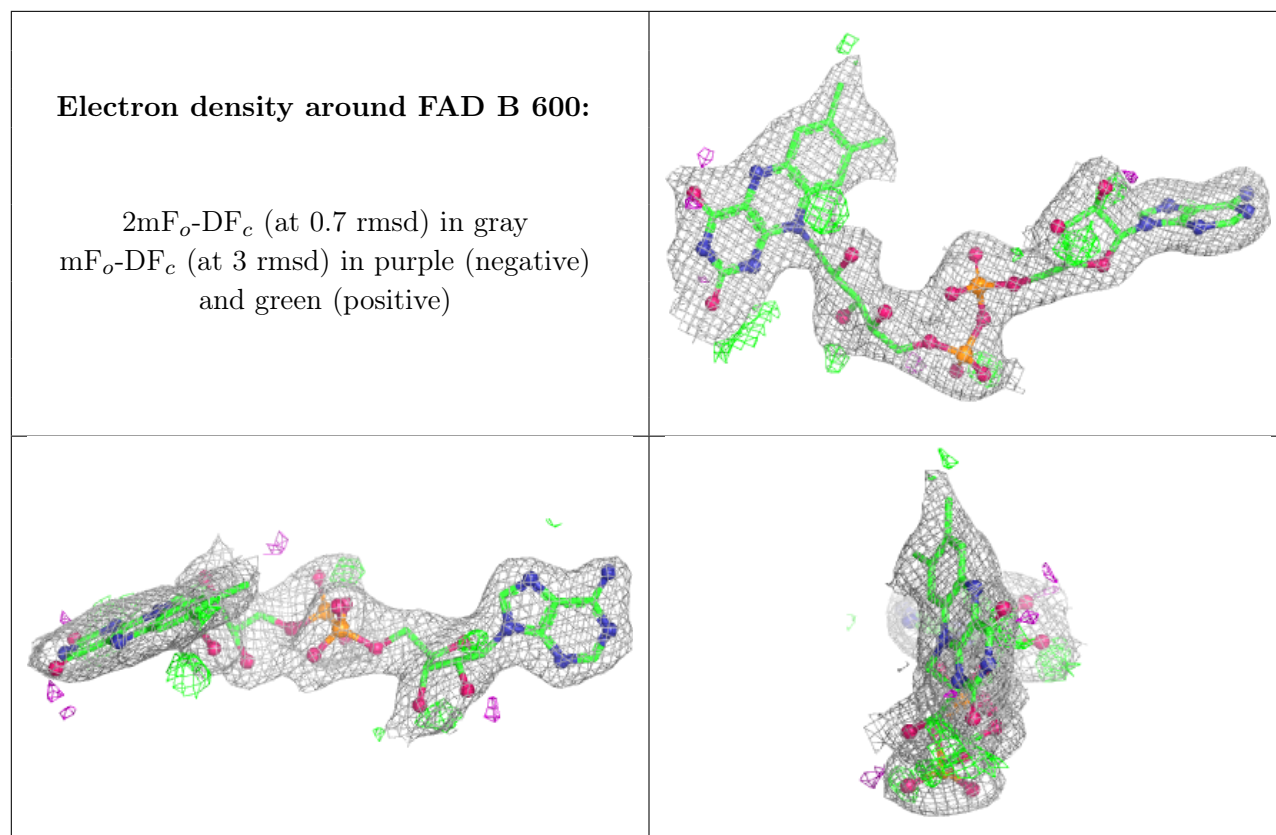
Electron density around FAD A 602:

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

**Electron density around K2C A 601:**

$2mF_o-DF_c$ (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.