



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:45 PM UTC

PDB ID : 3W8X / pdb_00003w8x
Title : The complex structure of EncM with trifluorotriketide
Authors : Teufel, R.; Miyanaga, A.; Stull, F.; Michaudel, Q.; Louie, G.; Noel, J.P.;
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Deposited on : 2013-03-22
Resolution : 1.82 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

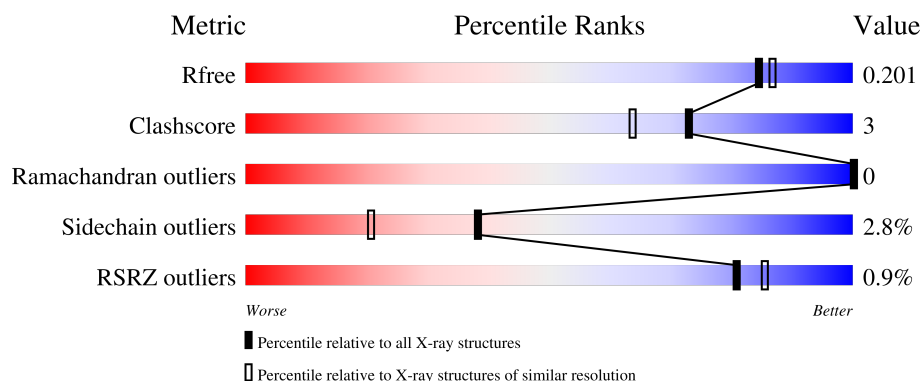
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	468	89% 8% ..
1	B	468	89% 9% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7813 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.

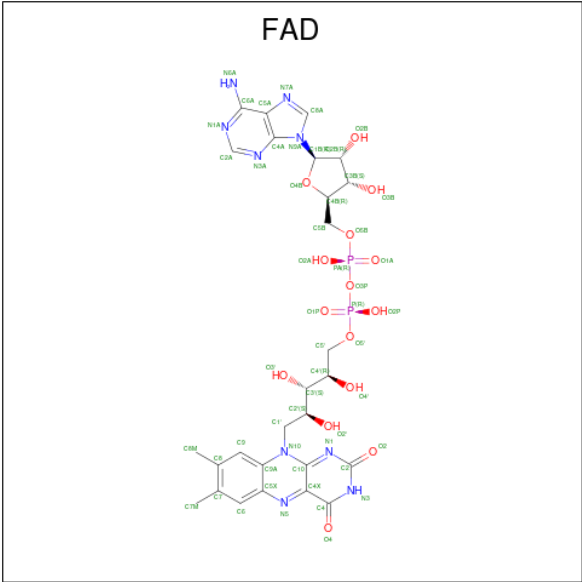
- Molecule 1 is a protein called Putative FAD-dependent oxygenase EncM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	0	0
			3507	2216	626	652	13			
1	B	461	Total	C	N	O	S	0	0	0
			3507	2216	626	652	13			

There are 8 discrepancies between the modelled and reference sequences:

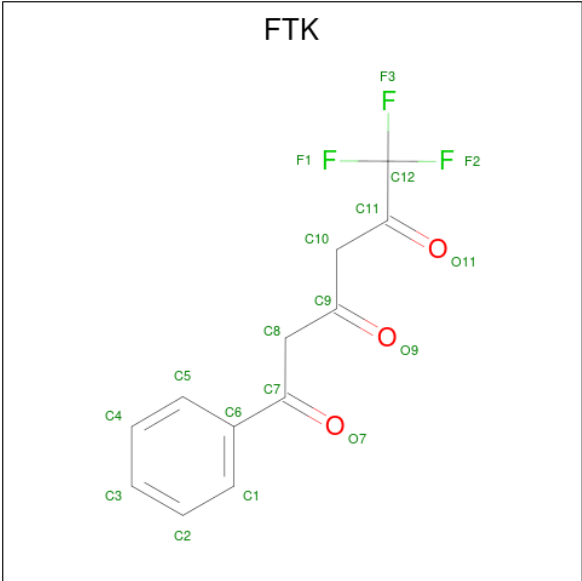
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q9KHK2
A	-2	SER	-	expression tag	UNP Q9KHK2
A	-1	HIS	-	expression tag	UNP Q9KHK2
A	0	GLY	-	expression tag	UNP Q9KHK2
B	-3	GLY	-	expression tag	UNP Q9KHK2
B	-2	SER	-	expression tag	UNP Q9KHK2
B	-1	HIS	-	expression tag	UNP Q9KHK2
B	0	GLY	-	expression tag	UNP Q9KHK2

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 3 is 6,6,6-trifluoro-1-phenylhexane-1,3,5-trione (CCD ID: FTK) (formula: C₁₂H₉F₃O₃).



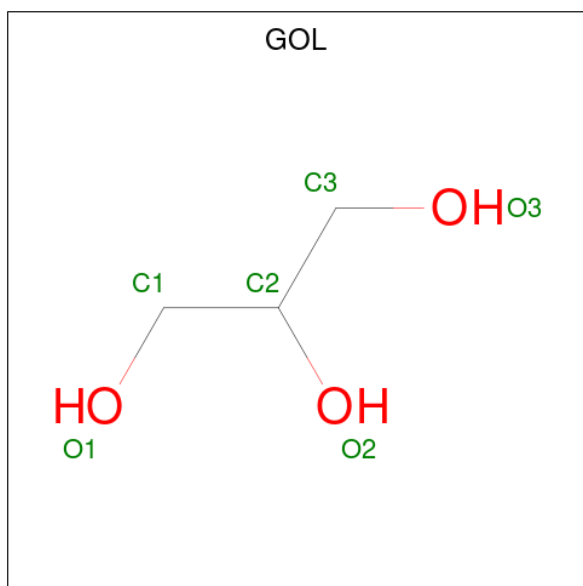
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	O	0	0
			18	12	3	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	F	O	0	0
			18	12	3	3		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

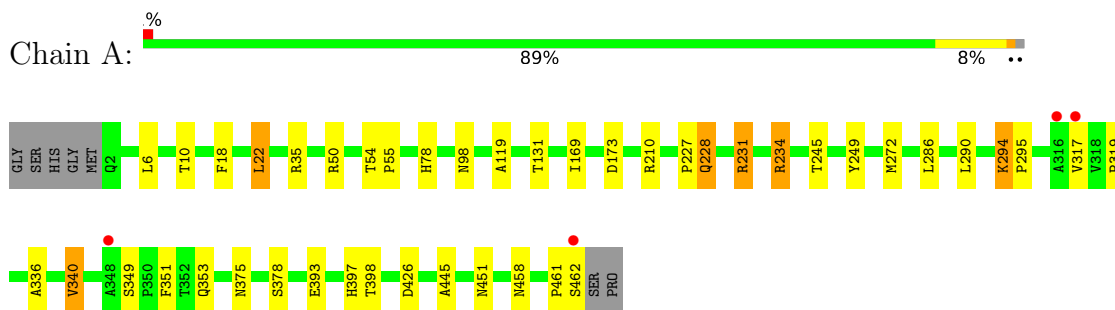
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	323	Total	O	0	0
			323	323		
5	B	328	Total	O	0	0
			328	328		

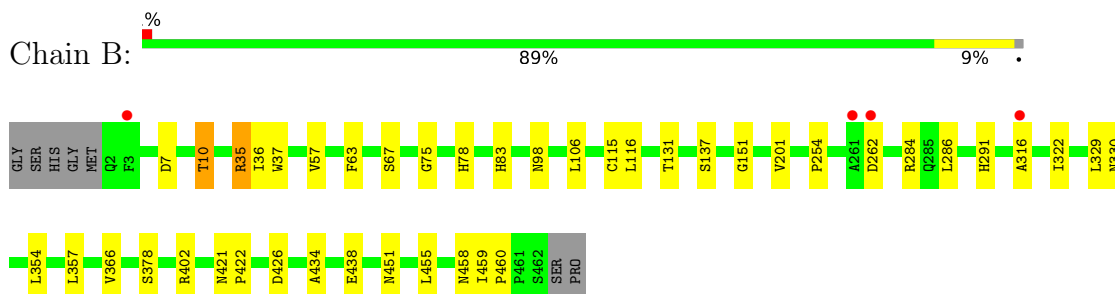
3 Residue-property plots [i](#)

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-dependent oxygenase EncM



- Molecule 1: Putative FAD-dependent oxygenase EncM



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.25Å 85.17Å 79.36Å 90.00° 99.47° 90.00°	Depositor
Resolution (Å)	48.52 – 1.82 48.52 – 1.82	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.52-1.82) 99.6 (48.52-1.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.153 , 0.192 0.163 , 0.201	Depositor DCC
R_{free} test set	4148 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7813	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.45% 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: FTK, FAD, GOL

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	1.35	9/3598 (0.3%)	1.14	4/4904 (0.1%)
1	B	1.27	8/3598 (0.2%)	1.17	11/4904 (0.2%)
All	All	1.31	17/7196 (0.2%)	1.16	15/9808 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	75	GLY	CA-C	7.47	1.56	1.51
1	A	349	SER	CA-C	7.33	1.60	1.53
1	B	460	PRO	C-O	-6.75	1.19	1.24
1	B	402	ARG	CD-NE	-6.69	1.36	1.46
1	A	169	ILE	N-CA	-6.58	1.38	1.46
1	B	330	ASN	C-O	-6.36	1.15	1.24
1	A	375	ASN	CG-OD1	6.04	1.35	1.23
1	A	398	THR	CB-CG2	-5.95	1.32	1.52
1	A	234	ARG	C-O	-5.89	1.17	1.24
1	A	119	ALA	CA-C	5.73	1.60	1.52
1	B	291	HIS	C-O	-5.54	1.16	1.24
1	B	201	VAL	C-O	5.42	1.29	1.24
1	A	98	ASN	N-CA	5.33	1.52	1.46
1	B	137	SER	C-O	-5.19	1.18	1.24
1	A	319	PRO	C-O	-5.13	1.18	1.23
1	B	378	SER	C-N	-5.02	1.27	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	10	THR	N-CA	5.01	1.52	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	366	VAL	CA-C-N	-7.45	112.11	119.78
1	B	366	VAL	C-N-CA	-7.45	112.11	119.78
1	A	378	SER	CA-C-N	-6.88	111.24	119.84
1	A	378	SER	C-N-CA	-6.88	111.24	119.84
1	B	459	ILE	CA-C-N	-6.69	114.84	119.66
1	B	459	ILE	C-N-CA	-6.69	114.84	119.66
1	B	378	SER	CA-C-N	-5.96	113.62	119.64
1	B	378	SER	C-N-CA	-5.96	113.62	119.64
1	B	434	ALA	N-CA-C	5.87	117.67	111.28
1	B	83	HIS	N-CA-C	5.46	119.20	112.54
1	B	57	VAL	N-CA-C	-5.44	105.22	110.72
1	A	234	ARG	CG-CD-NE	-5.30	100.35	112.00
1	A	231	ARG	CB-CG-CD	5.21	123.28	111.30
1	B	254	PRO	O-C-N	5.17	123.58	121.15
1	B	35	ARG	NE-CZ-NH2	5.07	123.76	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	461	PRO	Peptide

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	3507	0	3418	27	0
1	B	3507	0	3418	18	0
2	A	53	0	31	5	0
2	B	53	0	31	6	0
3	A	18	0	9	1	0
3	B	18	0	9	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
5	A	323	0	0	4	0
5	B	328	0	0	0	0
All	All	7813	0	6924	45	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 3.

All (45) 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:78:HIS:ND1	2:A:600:FAD:HM82	1.14	1.45
1:B:78:HIS:ND1	2:B:600:FAD:HM82	1.14	1.43
1:A:78:HIS:ND1	2:A:600:FAD:C8M	2.04	1.21
1:B:78:HIS:ND1	2:B:600:FAD:C8M	2.04	1.18
1:B:451:ASN:HD21	1:B:458:ASN:HD21	1.25	0.82
1:A:228:GLN:HE21	1:A:228:GLN:H	1.25	0.81
1:A:78:HIS:CG	2:A:600:FAD:HM82	2.13	0.80
1:A:445:ALA:HB2	1:A:462:SER:HA	1.64	0.77
1:A:227:PRO:O	1:A:231:ARG:HD3	1.85	0.76
1:B:78:HIS:CE1	2:B:600:FAD:HM82	2.18	0.74
1:A:451:ASN:HD21	1:A:458:ASN:HD21	1.35	0.72
1:A:78:HIS:CE1	2:A:600:FAD:HM82	2.19	0.69
1:B:78:HIS:CG	2:B:600:FAD:HM82	2.20	0.67
1:A:173:ASP:OD2	5:A:1004:HOH:O	2.14	0.65
1:B:7:ASP:OD2	1:B:10:THR:HG23	1.98	0.63
1:A:210:ARG:NH2	1:B:316:ALA:O	2.33	0.60
1:A:249:TYR:CE2	1:A:272:MET:HE2	2.38	0.58
1:B:78:HIS:ND1	2:B:600:FAD:C8	2.66	0.57
1:A:78:HIS:ND1	2:A:600:FAD:C8	2.65	0.57
1:B:421:ASN:HB2	1:B:422:PRO:CD	2.35	0.57
1:B:357:LEU:HD11	3:B:601:FTK:H7	1.87	0.57
1:A:317:VAL:CG2	1:A:351:PHE:CZ	2.92	0.53
1:A:245:THR:HG21	3:A:601:FTK:H3	1.91	0.51
1:A:18:PHE:CE2	1:A:22:LEU:HD13	2.45	0.51
1:A:336:ALA:O	1:A:340:VAL:HG13	2.12	0.50
1:B:37:TRP:CH2	2:B:600:FAD:HM81	2.45	0.50
1:B:322:ILE:C	1:B:322:ILE:HD12	2.37	0.49
1:A:228:GLN:HE21	1:A:228:GLN:N	2.02	0.48
1:A:317:VAL:HG21	1:A:351:PHE:CZ	2.48	0.48
3:B:601:FTK:O9	3:B:601:FTK:H1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ARG:HD2	5:A:707:HOH:O	2.15	0.45
1:A:294:LYS:HD2	1:A:295:PRO:HD2	1.98	0.45
1:A:294:LYS:HD2	1:A:294:LYS:C	2.43	0.44
1:B:63:PHE:O	1:B:67:SER:HB3	2.19	0.43
1:B:35:ARG:NH2	1:B:36:ILE:O	2.52	0.42
1:A:393:GLU:HB3	1:A:397:HIS:CD2	2.54	0.42
1:B:421:ASN:HB2	1:B:422:PRO:HD2	2.02	0.42
1:A:35:ARG:NH2	5:A:1008:HOH:O	2.53	0.41
1:B:151:GLY:HA2	3:B:601:FTK:C5	2.49	0.41
1:A:54:THR:N	1:A:55:PRO:CD	2.82	0.41
1:A:286:LEU:O	1:A:290:LEU:HG	2.21	0.41
1:B:329:LEU:HD12	1:B:329:LEU:N	2.35	0.40
1:A:50:ARG:HD2	5:A:710:HOH:O	2.20	0.40
1:B:98:ASN:OD1	1:B:115:CYS:HA	2.22	0.40
1:A:317:VAL:CG2	1:A:351:PHE:CE1	3.04	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	459/468 (98%)	451 (98%)	8 (2%)	0	100	100
1	B	459/468 (98%)	452 (98%)	7 (2%)	0	100	100
All	All	918/936 (98%)	903 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	356/361 (99%)	347 (98%)	9 (2%)	42	25
1	B	356/361 (99%)	345 (97%)	11 (3%)	35	17
All	All	712/722 (99%)	692 (97%)	20 (3%)	38	21

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	22	LEU
1	A	131	THR
1	A	228	GLN
1	A	234	ARG
1	A	294	LYS
1	A	340	VAL
1	A	353	GLN
1	A	426	ASP
1	B	10	THR
1	B	106	LEU
1	B	116	LEU
1	B	131	THR
1	B	262	ASP
1	B	284	ARG
1	B	286	LEU
1	B	354	LEU
1	B	426	ASP
1	B	438	GLU
1	B	455	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	GLN
1	A	138	HIS
1	A	228	GLN
1	A	236	HIS
1	A	264	HIS
1	A	330	ASN

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Mol	Chain	Res	Type
1	A	353	GLN
1	A	375	ASN
1	A	418	ASN
1	A	458	ASN
1	B	125	GLN
1	B	138	HIS
1	B	163	ASN
1	B	228	GLN
1	B	330	ASN
1	B	458	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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	GOL	B	602	-	5,5,5	0.40	0	5,5,5	1.30	1 (20%)
2	FAD	B	600	-	58,58,58	1.81	13 (22%)	85,89,89	1.40	13 (15%)
3	FTK	A	601	-	18,18,18	1.56	3 (16%)	23,25,25	2.44	13 (56%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FTK	B	601	-	18,18,18	1.75	2 (11%)	23,25,25	4.08	9 (39%)
2	FAD	A	600	-	58,58,58	1.65	9 (15%)	85,89,89	1.45	14 (16%)

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	GOL	B	602	-	-	0/4/4/4	-
2	FAD	B	600	-	-	4/34/50/50	0/6/6/6
3	FTK	A	601	-	-	4/18/18/18	0/1/1/1
3	FTK	B	601	-	-	5/18/18/18	0/1/1/1
2	FAD	A	600	-	-	6/34/50/50	0/6/6/6

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	FAD	PA-O3P	7.49	1.67	1.59
2	B	600	FAD	PA-O3P	6.62	1.66	1.59
3	B	601	FTK	O11-C11	6.37	1.31	1.21
2	A	600	FAD	P-O3P	4.23	1.64	1.59
3	A	601	FTK	O11-C11	4.23	1.28	1.21
2	B	600	FAD	C4X-N5	4.14	1.39	1.30
2	A	600	FAD	C4X-N5	3.96	1.39	1.30
2	B	600	FAD	C4-N3	-3.57	1.32	1.38
3	A	601	FTK	O9-C9	3.31	1.27	1.21
2	B	600	FAD	C8A-N7A	3.03	1.37	1.31
2	B	600	FAD	C2-N3	-3.01	1.32	1.39
2	B	600	FAD	C2'-C3'	-2.93	1.48	1.53
2	B	600	FAD	P-O3P	2.75	1.62	1.59
2	A	600	FAD	C8A-N7A	2.72	1.36	1.31
2	A	600	FAD	C2A-N1A	-2.63	1.29	1.33
2	B	600	FAD	C8M-C8	2.61	1.55	1.51
2	B	600	FAD	C4A-N9A	-2.57	1.32	1.37
2	A	600	FAD	C4-N3	-2.51	1.34	1.38
2	B	600	FAD	O2B-C2B	2.49	1.49	1.43
2	A	600	FAD	O4'-C4'	2.40	1.48	1.43
2	B	600	FAD	C5'-C4'	-2.34	1.48	1.51
3	A	601	FTK	O7-C7	2.30	1.26	1.22
3	B	601	FTK	O9-C9	2.22	1.25	1.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	FAD	C10-N10	2.14	1.42	1.37
2	B	600	FAD	O4-C4	2.05	1.27	1.23
2	A	600	FAD	O4B-C1B	2.04	1.46	1.42
2	A	600	FAD	C4X-C10	2.01	1.50	1.44

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	FTK	O7-C7-C8	-11.18	107.23	120.58
3	B	601	FTK	C8-C7-C6	10.31	138.55	118.99
3	B	601	FTK	O9-C9-C8	-7.68	109.34	121.20
3	B	601	FTK	O7-C7-C6	-4.98	114.07	120.73
3	A	601	FTK	F3-C12-F2	-4.54	86.62	106.20
3	A	601	FTK	O11-C11-C12	4.37	127.38	116.37
3	A	601	FTK	O7-C7-C8	4.18	125.57	120.58
2	B	600	FAD	C5A-C4A-N3A	-4.11	121.06	126.72
3	B	601	FTK	C10-C9-C8	3.95	127.86	118.58
2	A	600	FAD	C5A-C4A-N3A	-3.78	121.51	126.72
3	B	601	FTK	F3-C12-F1	-3.47	91.22	106.20
3	A	601	FTK	C5-C6-C1	3.30	122.76	118.57
2	A	600	FAD	C3B-C2B-C1B	3.25	107.61	101.46
3	A	601	FTK	O9-C9-C8	-3.22	116.23	121.20
3	A	601	FTK	F1-C12-C11	3.20	128.64	112.62
2	A	600	FAD	O2-C2-N1	-3.13	116.61	121.80
3	B	601	FTK	F1-C12-C11	3.07	128.01	112.62
3	B	601	FTK	F3-C12-F2	-2.93	93.57	106.20
3	A	601	FTK	F2-C12-F1	-2.85	93.93	106.20
2	A	600	FAD	O3P-PA-O1A	-2.72	102.51	110.70
4	B	602	GOL	C3-C2-C1	-2.65	102.09	111.80
2	B	600	FAD	C5A-C4A-N9A	2.62	108.67	105.81
2	B	600	FAD	N3A-C2A-N1A	-2.62	124.62	128.58
2	A	600	FAD	O4-C4-C4X	-2.59	119.70	126.53
2	A	600	FAD	N3A-C2A-N1A	-2.53	124.75	128.58
2	A	600	FAD	O2A-PA-O3P	2.53	114.10	107.27
2	B	600	FAD	C8M-C8-C9	-2.52	115.14	119.57
2	B	600	FAD	C2B-C1B-N9A	2.48	119.47	113.30
2	B	600	FAD	C5A-C6A-N6A	-2.47	117.17	123.29
2	B	600	FAD	O4B-C1B-N9A	-2.46	103.36	108.09
3	A	601	FTK	C8-C7-C6	-2.44	114.35	118.99
2	A	600	FAD	C7M-C7-C6	-2.43	115.29	119.57
2	B	600	FAD	O3P-PA-O1A	-2.36	103.59	110.70
3	A	601	FTK	C5-C6-C7	-2.35	115.33	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	FTK	F3-C12-F1	-2.34	96.10	106.20
3	B	601	FTK	F2-C12-F1	-2.32	96.19	106.20
2	A	600	FAD	C2A-N3A-C4A	2.31	117.47	111.83
2	A	600	FAD	C2B-C1B-N9A	2.30	119.03	113.30
2	B	600	FAD	C4-C4X-N5	2.26	121.32	118.21
3	A	601	FTK	O11-C11-C10	-2.25	111.17	122.97
3	A	601	FTK	F3-C12-C11	2.23	123.80	112.62
2	B	600	FAD	O4-C4-C4X	-2.22	120.68	126.53
2	B	600	FAD	C2A-N3A-C4A	2.20	117.21	111.83
2	A	600	FAD	C4X-C10-N1	-2.19	119.21	124.59
2	B	600	FAD	C4'-C3'-C2'	-2.15	110.00	113.57
2	A	600	FAD	C5A-C4A-N9A	2.14	108.14	105.81
2	A	600	FAD	O2P-P-O3P	-2.13	101.52	107.27
2	A	600	FAD	C10-C4X-N5	-2.10	120.53	124.81
2	B	600	FAD	C9A-C5X-N5	-2.07	120.26	122.45
3	A	601	FTK	C2-C1-C6	-2.02	118.38	120.36

There are no chirality outliers.

All (19) torsion outliers are listed below:

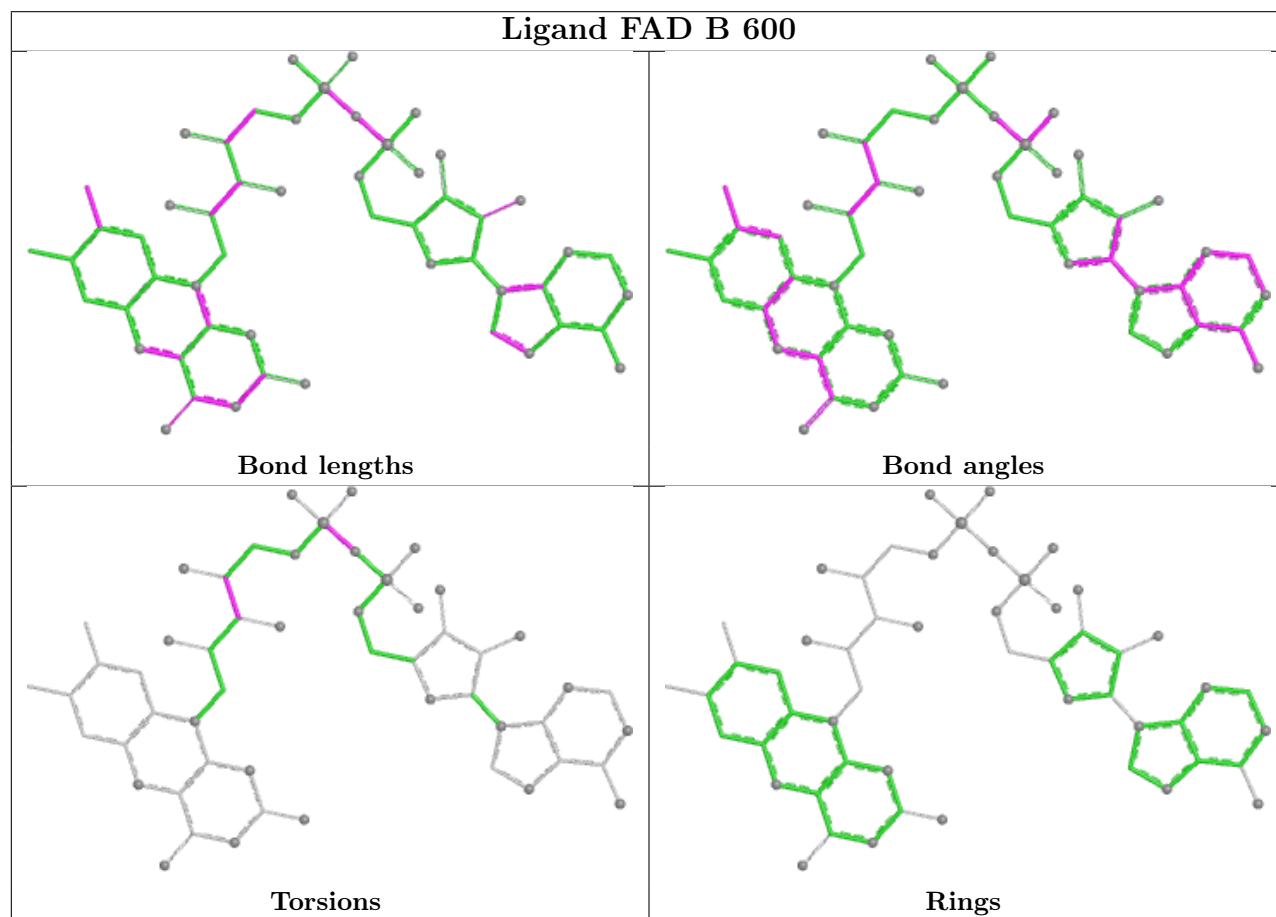
Mol	Chain	Res	Type	Atoms
3	B	601	FTK	C6-C7-C8-C9
2	A	600	FAD	O3'-C3'-C4'-O4'
2	A	600	FAD	C2'-C3'-C4'-O4'
2	A	600	FAD	C2'-C3'-C4'-C5'
3	A	601	FTK	C9-C10-C11-O11
2	B	600	FAD	O3'-C3'-C4'-O4'
2	A	600	FAD	N10-C1'-C2'-C3'
2	B	600	FAD	C2'-C3'-C4'-O4'
2	A	600	FAD	O3'-C3'-C4'-C5'
3	B	601	FTK	C9-C10-C11-O11
3	B	601	FTK	C10-C11-C12-F1
3	A	601	FTK	C11-C10-C9-C8
3	B	601	FTK	C7-C8-C9-C10
3	A	601	FTK	O11-C11-C12-F3
2	A	600	FAD	PA-O3P-P-O2P
2	B	600	FAD	O3'-C3'-C4'-C5'
3	A	601	FTK	C11-C10-C9-O9
3	B	601	FTK	C7-C8-C9-O9
2	B	600	FAD	PA-O3P-P-O2P

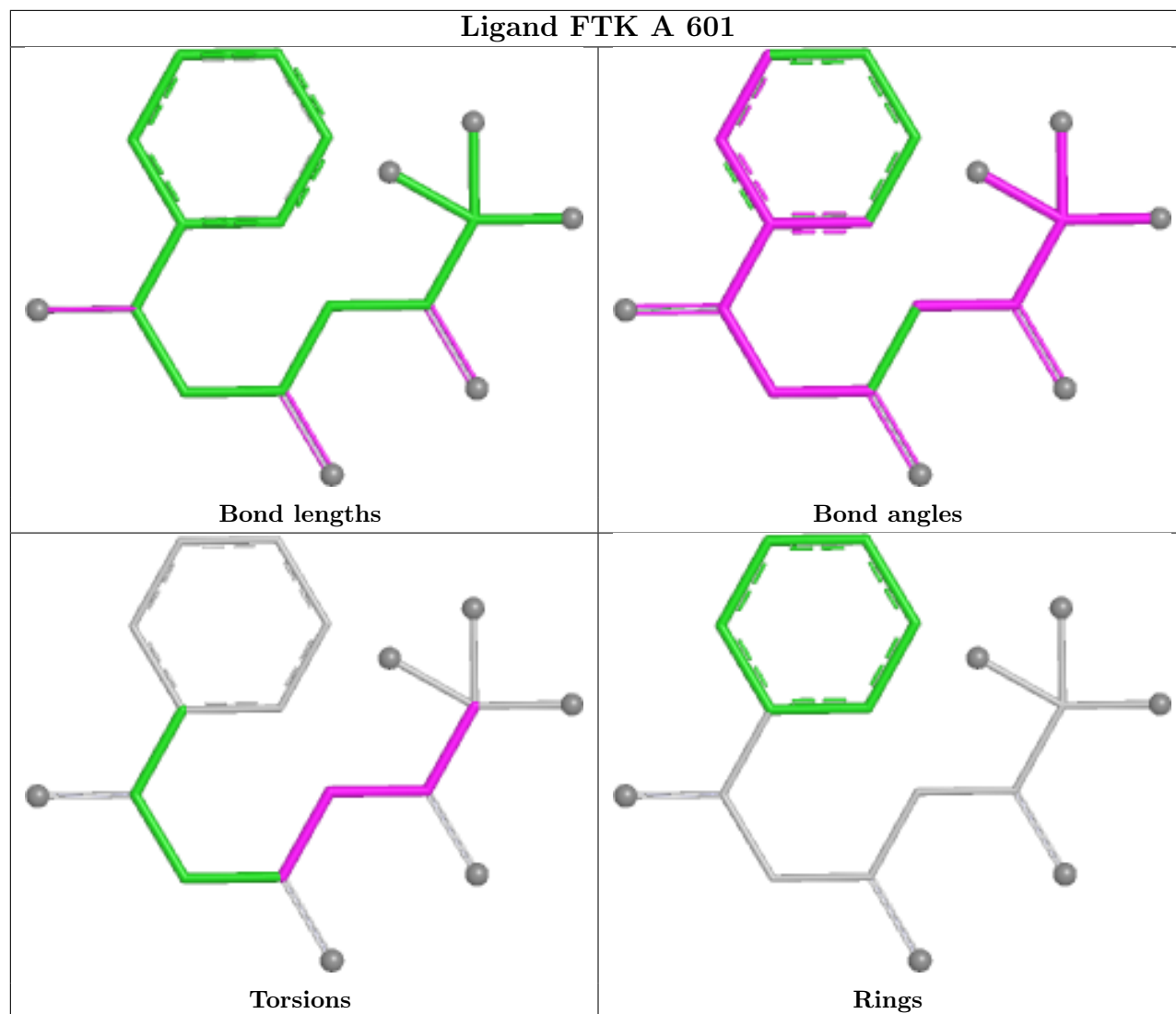
There are no ring outliers.

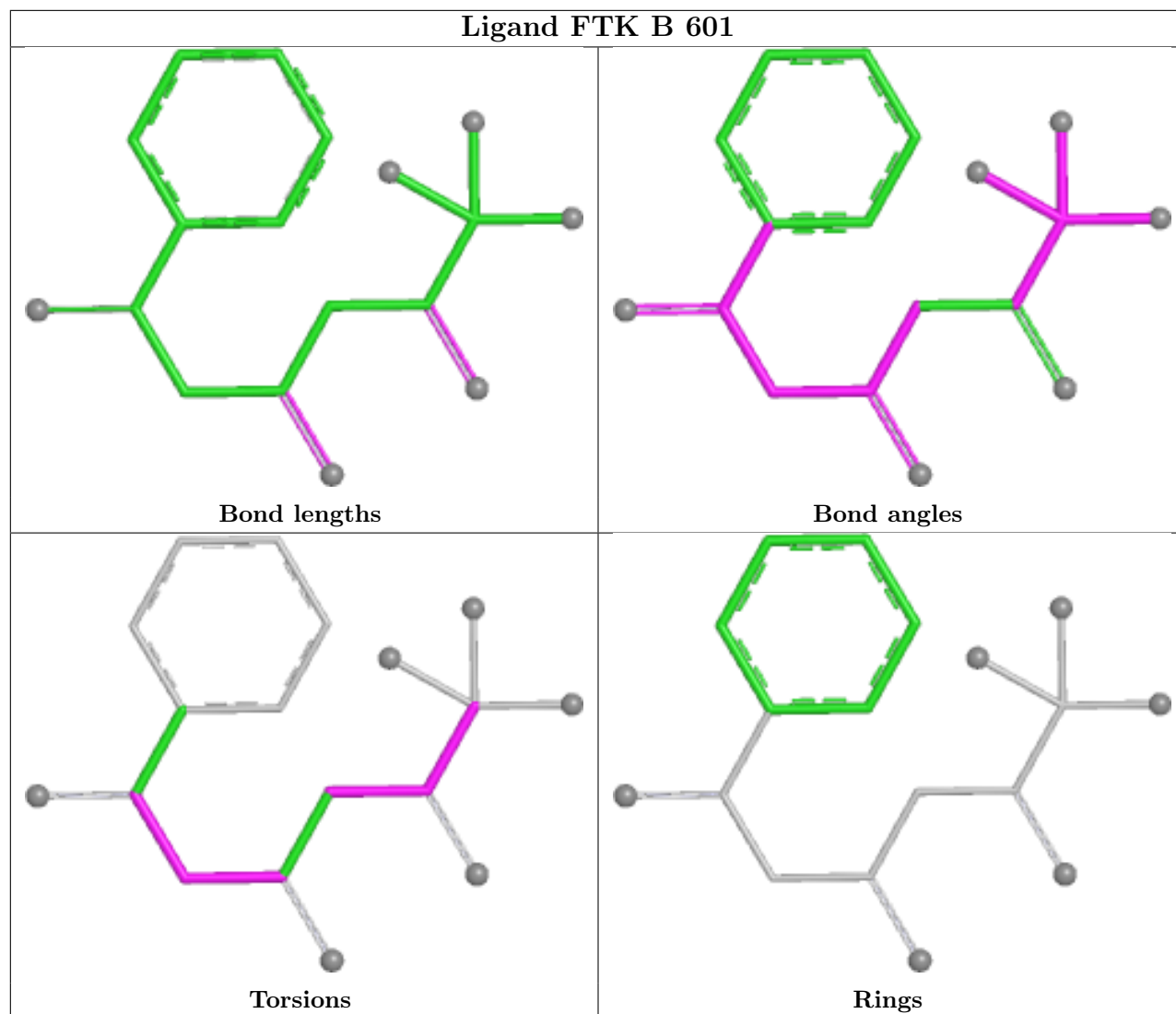
4 monomers are involved in 15 short contacts:

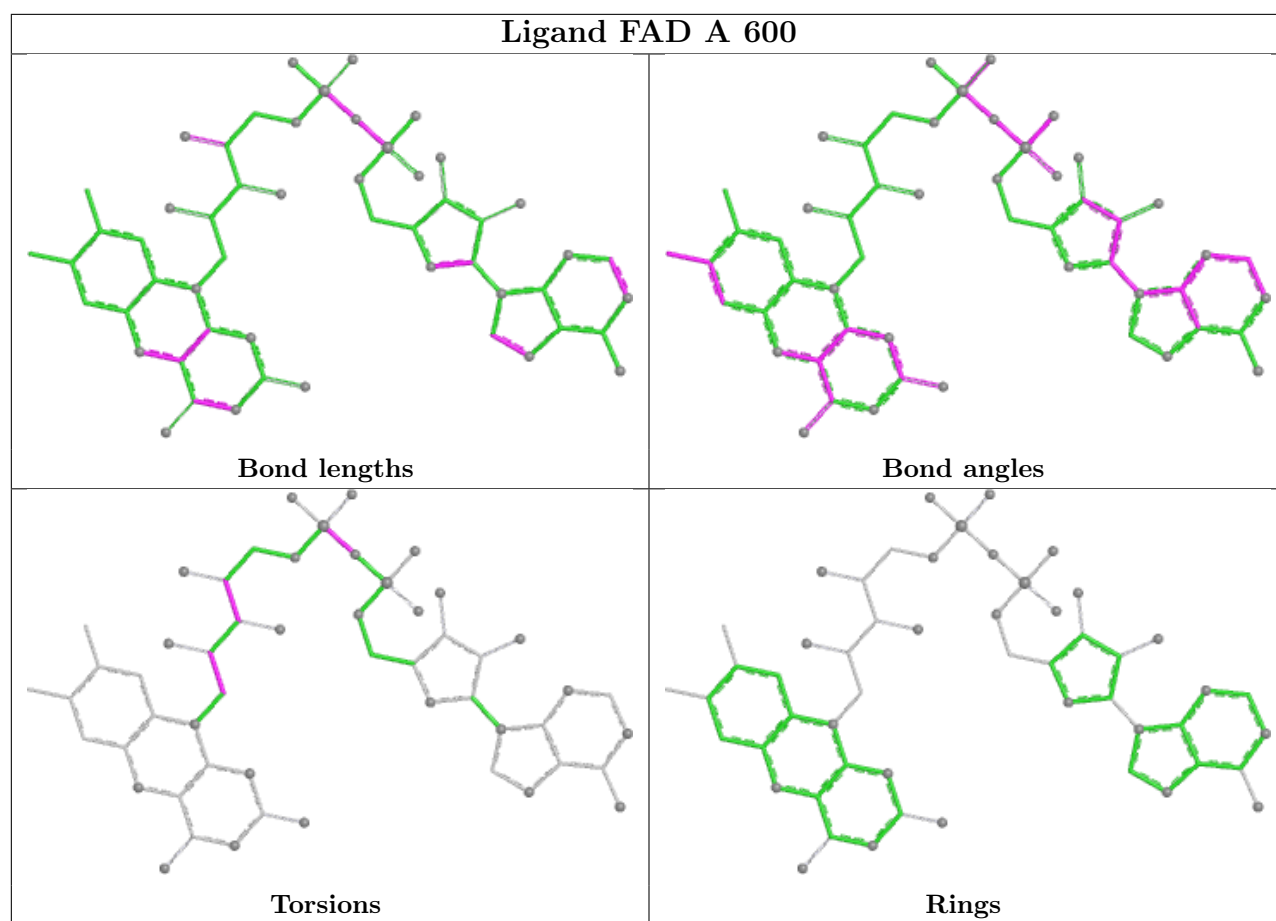
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	600	FAD	6	0
3	A	601	FTK	1	0
3	B	601	FTK	3	0
2	A	600	FAD	5	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	461/468 (98%)	-0.30	4 (0%) 81 85	10, 17, 31, 43	0
1	B	461/468 (98%)	-0.22	4 (0%) 81 85	10, 18, 35, 49	0
All	All	922/936 (98%)	-0.26	8 (0%) 81 85	10, 18, 33, 49	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	462	SER	2.9
1	B	316	ALA	2.7
1	A	316	ALA	2.5
1	A	348	ALA	2.5
1	B	3	PHE	2.4
1	A	317	VAL	2.3
1	B	262	ASP	2.2
1	B	261	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.

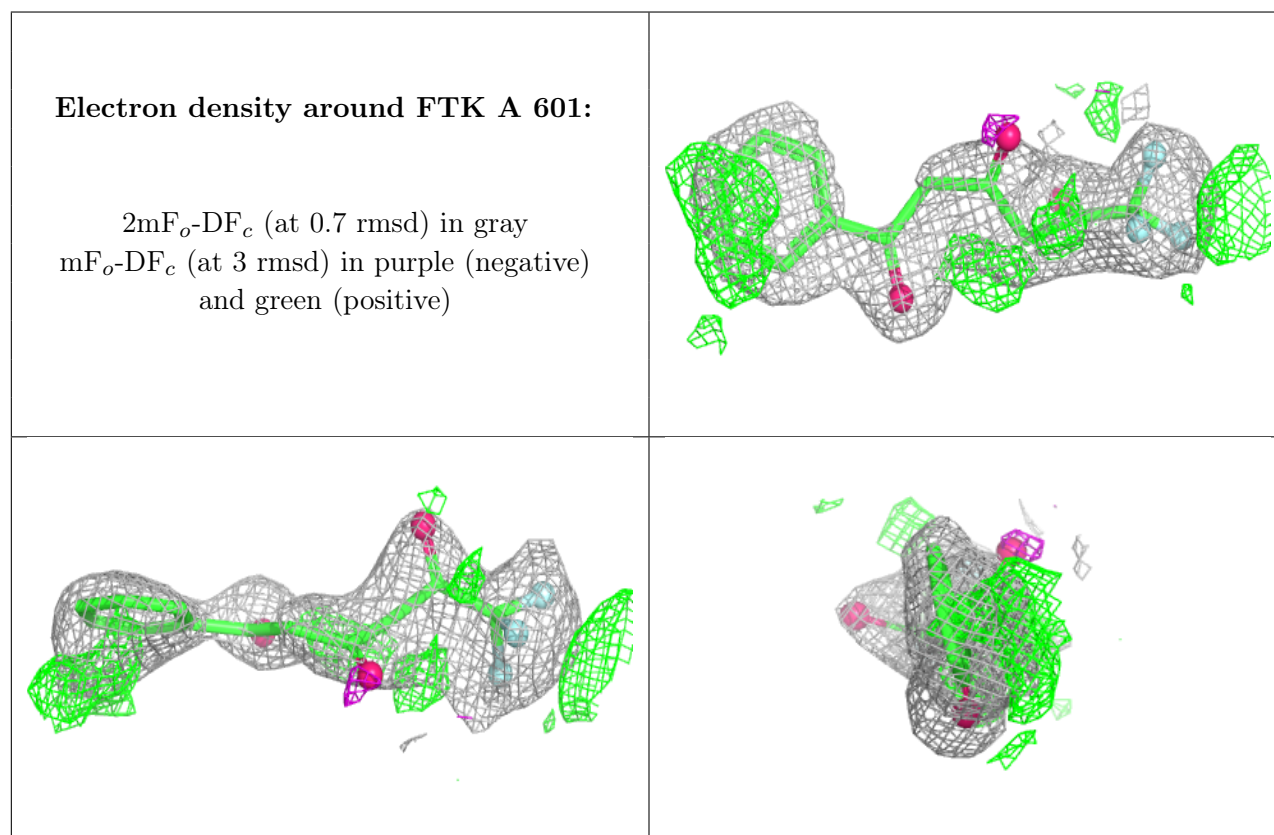
6.4 Ligands [i](#)

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.

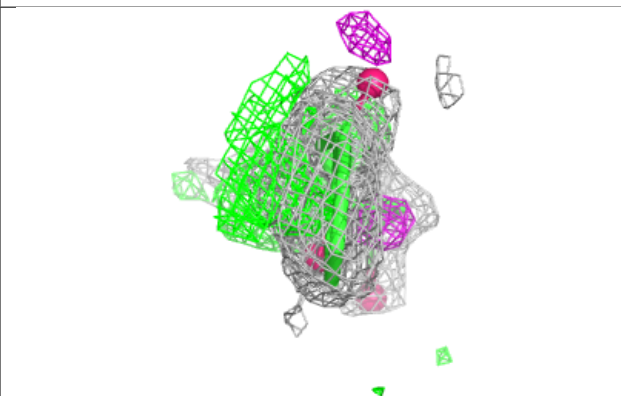
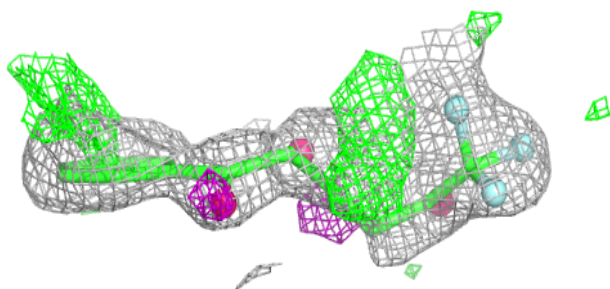
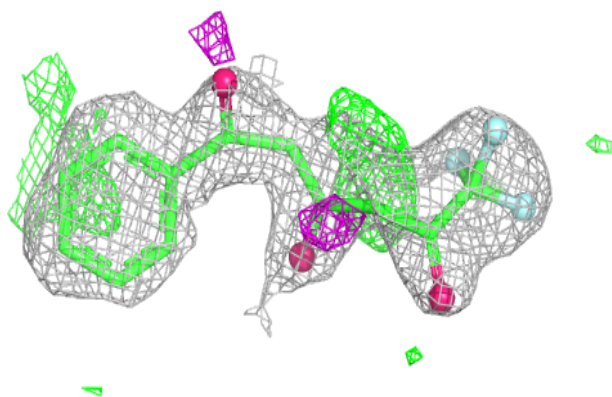
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FTK	A	601	18/18	0.72	0.17	20,23,34,39	18
3	FTK	B	601	18/18	0.77	0.16	17,24,35,36	18
4	GOL	B	602	6/6	0.95	0.08	17,21,29,36	0
2	FAD	B	600	53/53	0.98	0.05	9,11,14,18	0
2	FAD	A	600	53/53	0.98	0.05	9,10,14,16	0

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.

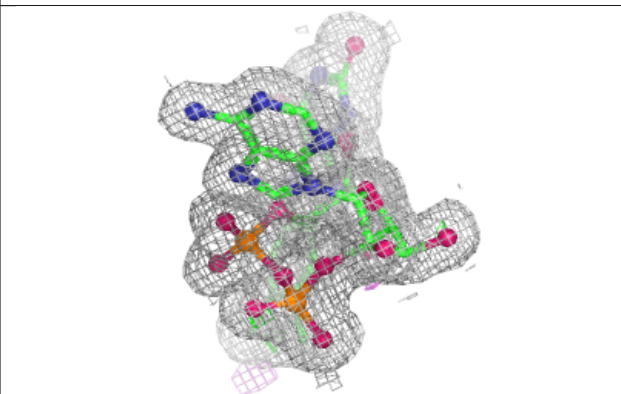
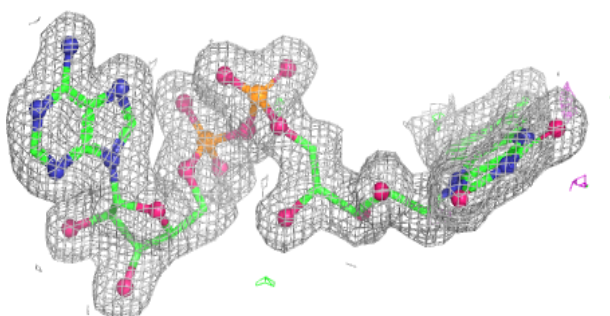
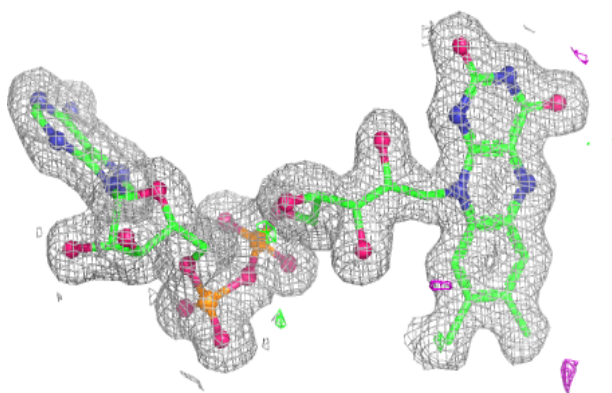


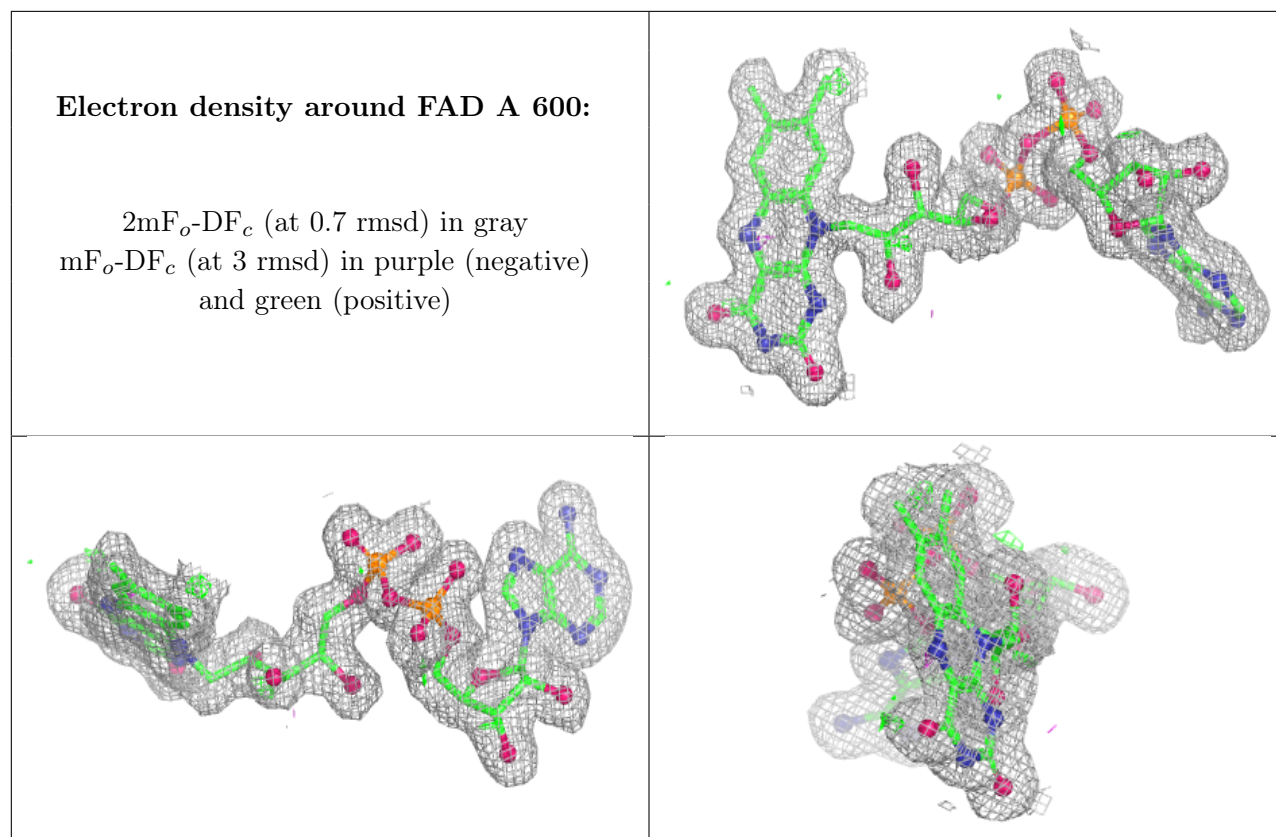
Electron density around FTK B 601:

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

**Electron density around FAD B 600:**

$2mF_o-DF_c$ (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.