



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2021 – 08:53 PM JST

PDB ID : 7E8Q
Title : Crystal structure of a Flavin-dependent Monooxygenase HadA F441V mutant complexed with reduced FAD and 4-nitrophenol
Authors : Pimviriyakul, P.; Jaruwat, A.; Chitnumsub, P.; Chaiyen, P.
Deposited on : 2021-03-02
Resolution : 2.30 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	:	2.23.1
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)	:	2.23.1

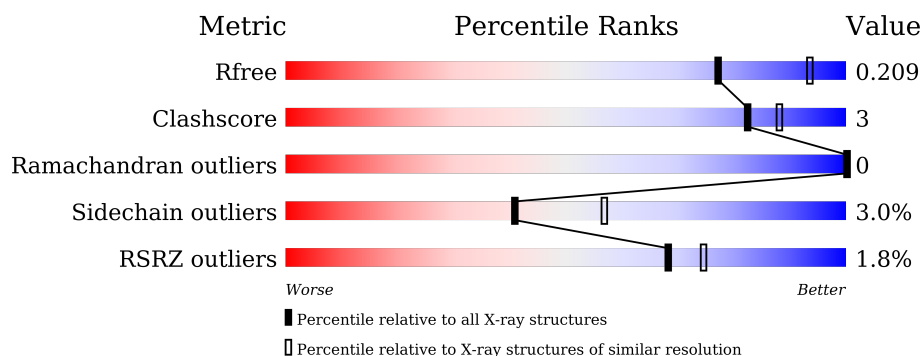
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	517	<div> <div>2%</div> <div>84% 8% • 7%</div> </div>
1	B	517	<div> <div>2%</div> <div>85% 8% 7%</div> </div>
1	C	517	<div> <div>2%</div> <div>86% 7% • 7%</div> </div>
1	D	517	<div> <div>%</div> <div>87% 5% • 7%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16665 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.

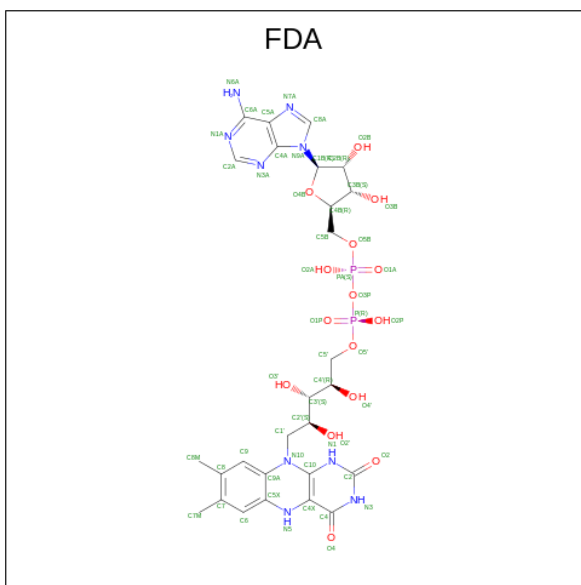
- Molecule 1 is a protein called Chlorophenol monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	480	Total	C	N	O	S	0	0	0
			3851	2442	699	694	16			
1	B	480	Total	C	N	O	S	0	0	0
			3851	2442	699	694	16			
1	C	480	Total	C	N	O	S	0	0	0
			3851	2442	699	694	16			
1	D	482	Total	C	N	O	S	0	0	0
			3865	2449	701	699	16			

There are 4 discrepancies between the modelled and reference sequences:

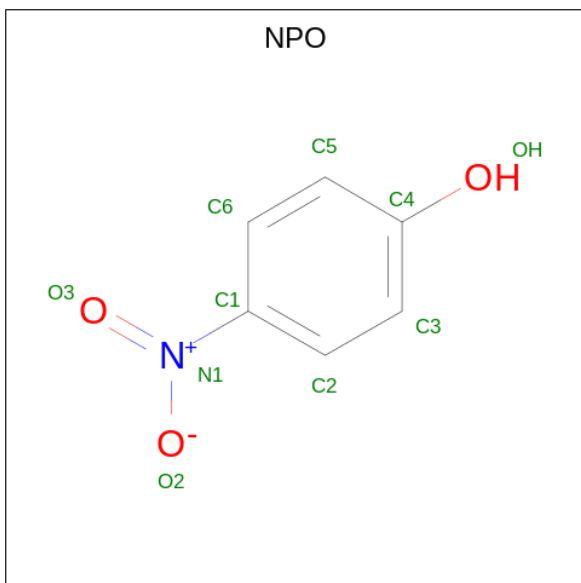
Chain	Residue	Modelled	Actual	Comment	Reference
A	441	VAL	PHE	engineered mutation	UNP Q53008
B	441	VAL	PHE	engineered mutation	UNP Q53008
C	441	VAL	PHE	engineered mutation	UNP Q53008
D	441	VAL	PHE	engineered mutation	UNP Q53008

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula: C₂₇H₃₅N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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
2	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	D	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is P-NITROPHENOL (three-letter code: NPO) (formula: $\text{C}_6\text{H}_5\text{NO}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	B	1	Total	C	N	O	0	0
			10	6	1	3		
3	C	1	Total	C	N	O	0	0
			10	6	1	3		
3	C	1	Total	C	N	O	0	0
			10	6	1	3		
3	D	1	Total	C	N	O	0	0
			10	6	1	3		

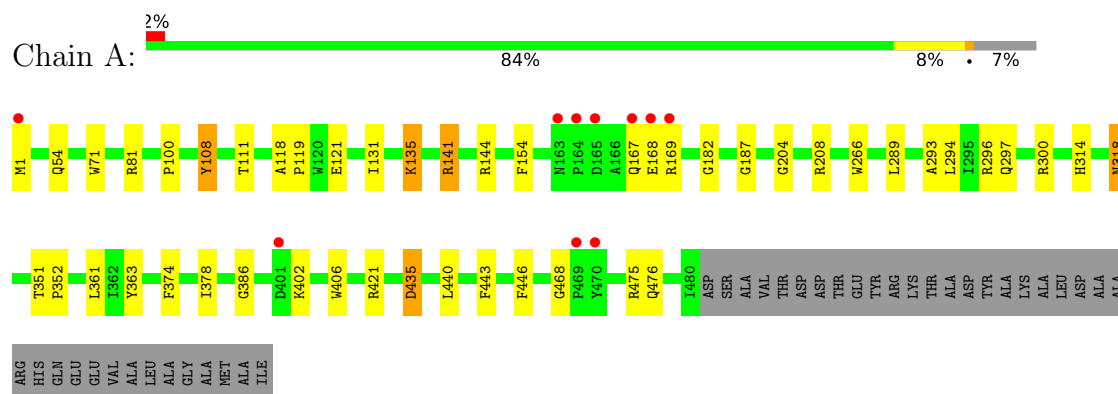
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	247	Total	O	0	0
			247	247		
4	B	219	Total	O	0	0
			219	219		
4	C	262	Total	O	0	0
			262	262		
4	D	247	Total	O	0	0
			247	247		

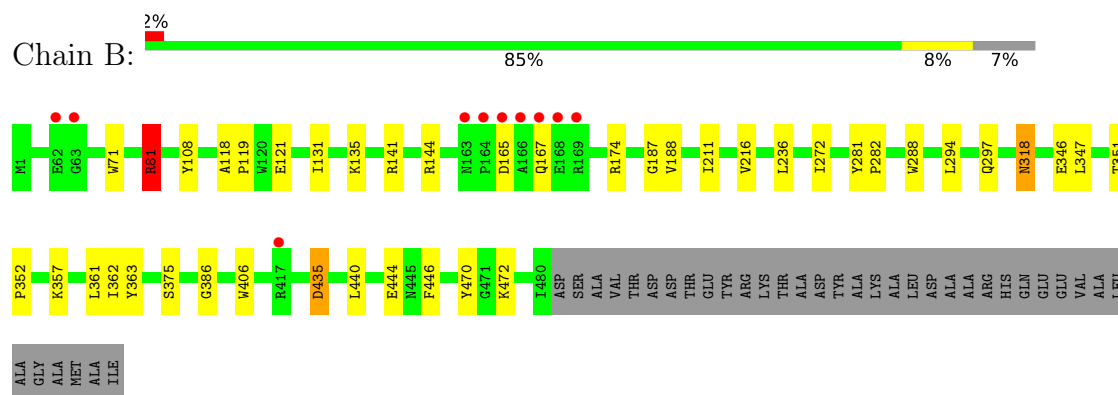
3 Residue-property plots [i](#)

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.

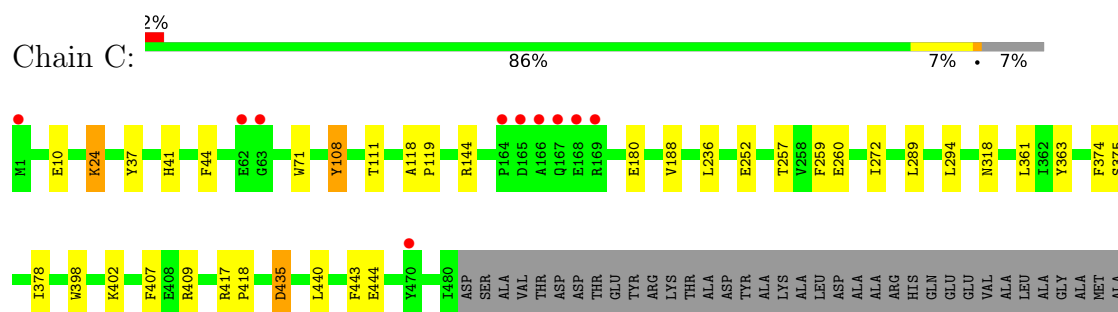
• Molecule 1: Chlorophenol monooxygenase



• Molecule 1: Chlorophenol monooxygenase

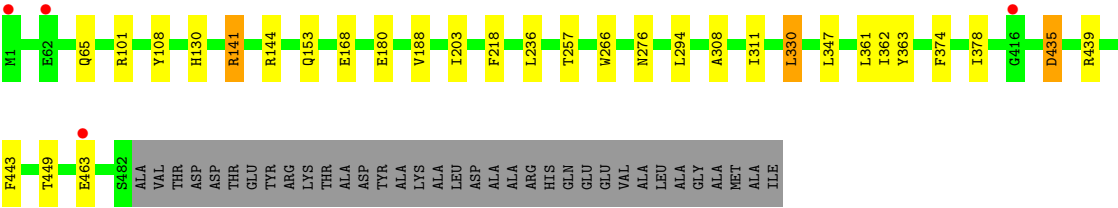
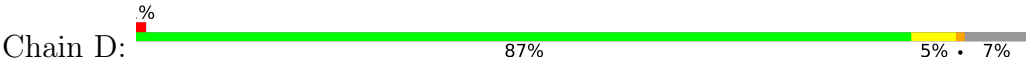


• Molecule 1: Chlorophenol monooxygenase



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● Molecule 1: Chlorophenol monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.84Å 161.65Å 168.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.10 – 2.30 21.10 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.4 (21.10-2.30) 99.6 (21.10-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.60 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.166 , 0.209 0.169 , 0.209	Depositor DCC
R_{free} test set	5847 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16665	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: FDA, NPO

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	0.72	0/3952	0.85	0/5360
1	B	0.71	0/3952	0.85	1/5360 (0.0%)
1	C	0.73	2/3952 (0.1%)	0.86	2/5360 (0.0%)
1	D	0.73	0/3966	0.88	1/5379 (0.0%)
All	All	0.72	2/15822 (0.0%)	0.86	4/21459 (0.0%)

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	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	444	GLU	CD-OE2	-6.28	1.18	1.25
1	C	260	GLU	CD-OE2	5.78	1.32	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	409	ARG	NE-CZ-NH1	7.21	123.91	120.30
1	B	81	ARG	NE-CZ-NH2	-6.51	117.04	120.30
1	C	409	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	D	101	ARG	NE-CZ-NH2	-5.12	117.74	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	272	ILE	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	3851	0	3756	28	0
1	B	3851	0	3756	21	0
1	C	3851	0	3756	16	0
1	D	3865	0	3765	17	0
2	A	53	0	33	1	0
2	B	53	0	33	0	0
2	C	53	0	33	1	0
2	D	53	0	33	1	0
3	A	20	0	9	0	0
3	B	10	0	5	0	0
3	C	20	0	9	0	0
3	D	10	0	4	0	0
4	A	247	0	0	2	0
4	B	219	0	0	0	0
4	C	262	0	0	3	0
4	D	247	0	0	0	0
All	All	16665	0	15192	78	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 (78) 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:D:374:PHE:CE2	1:D:378:ILE:HD11	2.20	0.77
1:C:435:ASP:HB2	4:C:855:HOH:O	1.97	0.65
1:B:294:LEU:HD12	1:B:297:GLN:NE2	2.15	0.61
1:A:374:PHE:CE2	1:A:378:ILE:HD11	2.36	0.61
1:B:121:GLU:HG3	1:B:131:ILE:O	2.01	0.61
1:C:440:LEU:HB2	4:C:945:HOH:O	2.04	0.58
1:C:443:PHE:HA	2:C:600:FDA:HM73	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:LEU:HD13	1:B:435:ASP:HB2	1.86	0.57
1:B:294:LEU:HD22	1:B:363:TYR:CB	2.35	0.56
1:B:294:LEU:HD22	1:B:363:TYR:HB2	1.87	0.56
1:A:208:ARG:NH2	4:A:701:HOH:O	2.32	0.55
1:B:118:ALA:HB3	1:B:119:PRO:HD3	1.88	0.55
1:C:71:TRP:CG	1:C:144:ARG:HG3	2.43	0.54
1:D:374:PHE:CD2	1:D:378:ILE:HD11	2.44	0.53
1:C:118:ALA:HB3	1:C:119:PRO:HD3	1.91	0.53
1:D:294:LEU:HD22	1:D:363:TYR:CB	2.39	0.53
1:A:406:TRP:CH2	1:B:187:GLY:HA2	2.45	0.52
1:A:108:TYR:O	1:A:111:THR:HG23	2.11	0.51
1:C:417:ARG:N	1:C:418:PRO:HD3	2.25	0.51
1:C:374:PHE:CE2	1:C:378:ILE:HD11	2.46	0.51
1:C:294:LEU:HD22	1:C:363:TYR:HA	1.93	0.50
1:A:187:GLY:HA2	1:B:406:TRP:CH2	2.47	0.49
1:D:347:LEU:HD12	1:D:362:ILE:CD1	2.43	0.49
1:D:308:ALA:HB2	1:D:330:LEU:HD23	1.93	0.49
1:A:435:ASP:HB2	4:A:738:HOH:O	2.12	0.49
1:A:300:ARG:NH1	1:A:440:LEU:HD23	2.27	0.49
1:A:118:ALA:HB3	1:A:119:PRO:HD3	1.95	0.49
1:A:167:GLN:HE21	1:A:208:ARG:HB3	1.78	0.48
1:A:318:ASN:HD22	1:A:318:ASN:H	1.62	0.47
1:A:443:PHE:HA	2:A:600:FDA:HM73	1.96	0.47
1:A:141:ARG:N	1:A:141:ARG:HD2	2.28	0.47
1:B:167:GLN:HE22	1:B:211:ILE:HB	1.79	0.47
1:B:351:THR:HB	1:B:352:PRO:HD2	1.96	0.47
1:C:318:ASN:ND2	4:C:710:HOH:O	2.47	0.47
1:D:236:LEU:HD13	1:D:435:ASP:HB2	1.95	0.47
1:D:294:LEU:HD22	1:D:363:TYR:HA	1.96	0.47
1:D:443:PHE:HA	2:D:601:FDA:HM73	1.96	0.47
1:A:182:GLY:HA2	1:A:266:TRP:CD1	2.50	0.47
1:A:351:THR:HB	1:A:352:PRO:HD2	1.97	0.47
1:B:318:ASN:HD22	1:B:318:ASN:H	1.63	0.47
1:A:468:GLY:O	1:A:475:ARG:NH2	2.48	0.46
1:A:167:GLN:HE21	1:A:208:ARG:CB	2.29	0.46
1:C:37:TYR:CZ	1:C:252:GLU:HG3	2.51	0.46
1:C:398:TRP:CZ3	1:C:407:PHE:HB3	2.50	0.46
1:A:293:ALA:O	1:A:297:GLN:HG3	2.16	0.46
1:A:167:GLN:NE2	1:A:208:ARG:HB2	2.31	0.45
1:A:71:TRP:CG	1:A:144:ARG:HG3	2.52	0.45
1:B:347:LEU:HD12	1:B:362:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:TYR:O	1:C:111:THR:HG23	2.17	0.44
1:B:216:VAL:O	1:B:272:ILE:HA	2.18	0.44
1:D:294:LEU:HD22	1:D:363:TYR:HB2	1.99	0.44
1:A:121:GLU:HG3	1:A:131:ILE:O	2.18	0.44
1:C:24:LYS:HA	1:C:24:LYS:HD2	1.84	0.44
1:D:130:HIS:HB3	1:D:266:TRP:CG	2.52	0.44
1:D:308:ALA:CB	1:D:330:LEU:HD23	2.48	0.44
1:A:386:GLY:HA2	1:B:446:PHE:CE1	2.53	0.44
1:A:446:PHE:CE1	1:B:386:GLY:HA2	2.53	0.44
1:D:153:GLN:HE22	1:D:257:THR:CB	2.30	0.44
1:A:100:PRO:HB3	1:A:296:ARG:NE	2.33	0.43
1:A:135:LYS:HA	1:A:135:LYS:HD2	1.64	0.43
1:B:281:TYR:N	1:B:282:PRO:CD	2.81	0.43
1:B:440:LEU:O	1:B:444:GLU:HG3	2.19	0.42
1:C:236:LEU:HD22	1:C:435:ASP:HB3	2.01	0.42
1:D:141:ARG:HG3	1:D:144:ARG:NH2	2.34	0.42
1:A:154:PHE:HA	1:A:204:GLY:O	2.18	0.42
1:B:347:LEU:HD12	1:B:362:ILE:HD11	2.01	0.42
1:B:81:ARG:NH2	1:B:346:GLU:OE2	2.47	0.42
1:B:288:TRP:CH2	1:B:357:LYS:HG3	2.55	0.41
1:D:180:GLU:H	1:D:180:GLU:CD	2.23	0.41
1:A:71:TRP:CE2	1:A:144:ARG:HA	2.55	0.41
1:B:71:TRP:CE2	1:B:144:ARG:HA	2.55	0.41
1:D:439:ARG:HD3	1:D:439:ARG:C	2.41	0.41
1:A:314:HIS:CE1	1:A:421:ARG:HB2	2.56	0.41
1:A:294:LEU:HD22	1:A:363:TYR:CB	2.51	0.41
1:C:257:THR:HG22	1:C:259:PHE:CE1	2.55	0.41
1:D:311:ILE:HD12	1:D:311:ILE:HA	1.94	0.41
1:C:41:HIS:O	1:C:44:PHE:HB3	2.22	0.40
1:D:203:ILE:O	1:D:218:PHE:HA	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	478/517 (92%)	466 (98%)	12 (2%)	0	100	100
1	B	478/517 (92%)	462 (97%)	16 (3%)	0	100	100
1	C	478/517 (92%)	470 (98%)	8 (2%)	0	100	100
1	D	480/517 (93%)	467 (97%)	13 (3%)	0	100	100
All	All	1914/2068 (93%)	1865 (97%)	49 (3%)	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	406/432 (94%)	392 (97%)	14 (3%)	37	51
1	B	406/432 (94%)	393 (97%)	13 (3%)	39	54
1	C	406/432 (94%)	396 (98%)	10 (2%)	47	65
1	D	408/432 (94%)	397 (97%)	11 (3%)	44	61
All	All	1626/1728 (94%)	1578 (97%)	48 (3%)	41	57

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	54	GLN
1	A	81	ARG
1	A	108	TYR
1	A	135	LYS
1	A	141	ARG
1	A	168	GLU
1	A	169	ARG
1	A	289	LEU
1	A	318	ASN

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Mol	Chain	Res	Type
1	A	361	LEU
1	A	402	LYS
1	A	435	ASP
1	A	476	GLN
1	B	81	ARG
1	B	108	TYR
1	B	135	LYS
1	B	141	ARG
1	B	165	ASP
1	B	174	ARG
1	B	188	VAL
1	B	318	ASN
1	B	361	LEU
1	B	375	SER
1	B	435	ASP
1	B	470	TYR
1	B	472	LYS
1	C	10	GLU
1	C	24	LYS
1	C	108	TYR
1	C	180	GLU
1	C	188	VAL
1	C	289	LEU
1	C	361	LEU
1	C	375	SER
1	C	402	LYS
1	C	435	ASP
1	D	65	GLN
1	D	108	TYR
1	D	141	ARG
1	D	168	GLU
1	D	188	VAL
1	D	276	ASN
1	D	330	LEU
1	D	361	LEU
1	D	435	ASP
1	D	449	THR
1	D	463	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	153	GLN
1	A	167	GLN
1	A	318	ASN
1	A	376	GLN
1	B	54	GLN
1	B	153	GLN
1	B	167	GLN
1	B	318	ASN
1	C	65	GLN
1	C	123	GLN
1	C	153	GLN
1	C	318	ASN
1	C	376	GLN
1	C	452	GLN
1	D	39	GLN
1	D	153	GLN
1	D	167	GLN
1	D	318	ASN
1	D	376	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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	NPO	A	601	-	9,10,10	0.99	0	11,13,13	0.56	0
3	NPO	A	602	-	9,10,10	0.36	0	11,13,13	0.66	0
3	NPO	C	602	-	9,10,10	0.36	0	11,13,13	0.92	0
3	NPO	D	602	-	9,10,10	0.34	0	11,13,13	0.60	0
2	FDA	A	600	-	51,58,58	0.74	0	60,89,89	0.77	0
2	FDA	B	601	-	51,58,58	0.68	0	60,89,89	0.78	1 (1%)
3	NPO	C	601	-	9,10,10	0.74	0	11,13,13	0.73	0
3	NPO	B	602	-	9,10,10	0.47	0	11,13,13	0.71	0
2	FDA	D	601	-	51,58,58	0.70	0	60,89,89	0.63	0
2	FDA	C	600	-	51,58,58	0.80	0	60,89,89	0.87	2 (3%)

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	NPO	A	601	-	-	0/2/4/4	0/1/1/1
3	NPO	A	602	-	-	0/2/4/4	0/1/1/1
3	NPO	C	602	-	-	0/2/4/4	0/1/1/1
3	NPO	D	602	-	-	0/2/4/4	0/1/1/1
2	FDA	A	600	-	-	2/30/50/50	0/6/6/6
2	FDA	B	601	-	-	0/30/50/50	0/6/6/6
3	NPO	C	601	-	-	0/2/4/4	0/1/1/1
3	NPO	B	602	-	-	0/2/4/4	0/1/1/1
2	FDA	D	601	-	-	1/30/50/50	0/6/6/6
2	FDA	C	600	-	-	3/30/50/50	0/6/6/6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	600	FDA	O2'-C2'-C1'	3.24	117.40	109.59
2	C	600	FDA	C10-C4X-N5	2.23	122.80	121.26
2	B	601	FDA	O2'-C2'-C1'	2.12	114.69	109.59

There are no chirality outliers.

All (6) torsion outliers are listed below:

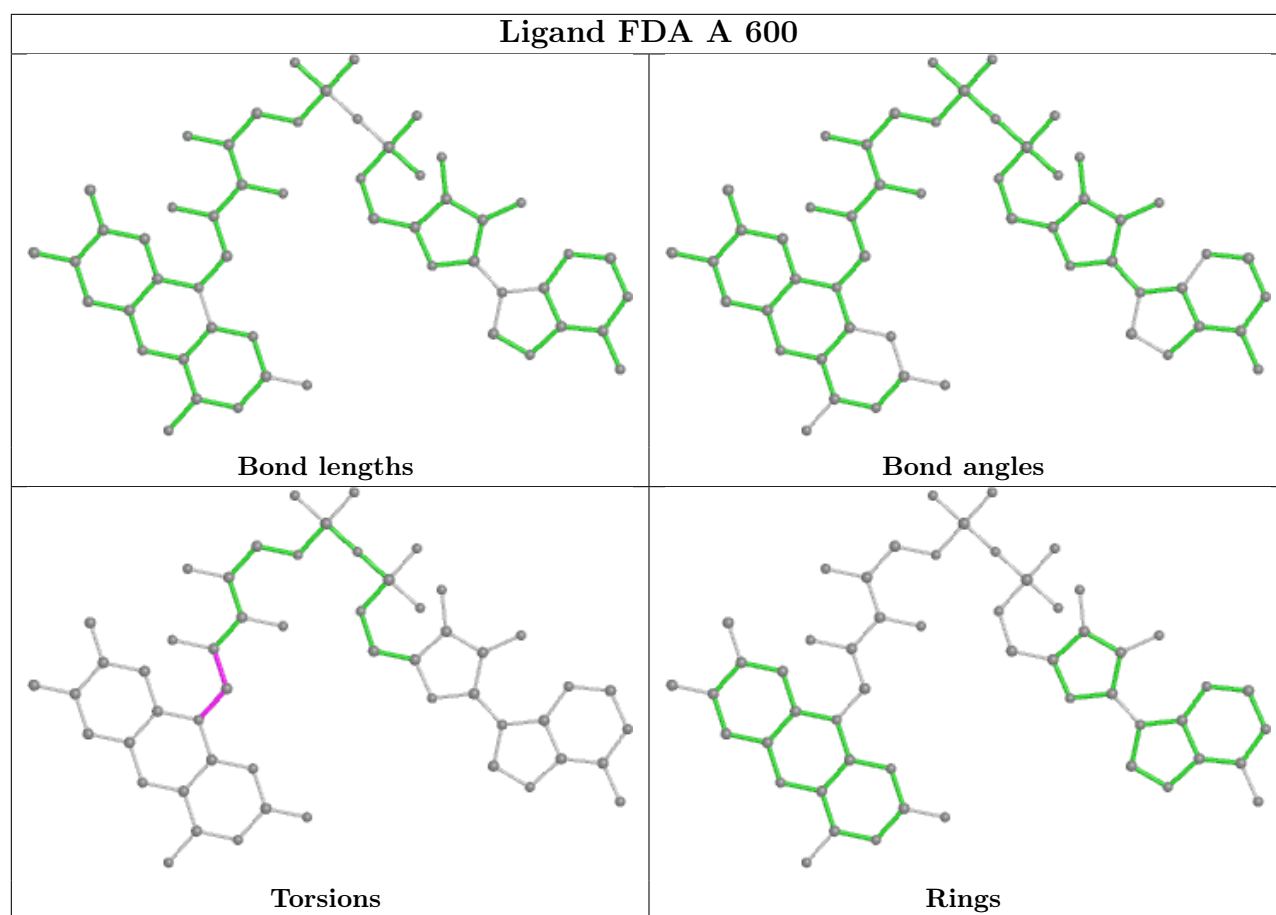
Mol	Chain	Res	Type	Atoms
2	A	600	FDA	C2'-C1'-N10-C10
2	C	600	FDA	C2'-C1'-N10-C10
2	D	601	FDA	C2'-C1'-N10-C10
2	C	600	FDA	O2'-C2'-C3'-C4'
2	A	600	FDA	N10-C1'-C2'-O2'
2	C	600	FDA	N10-C1'-C2'-O2'

There are no ring outliers.

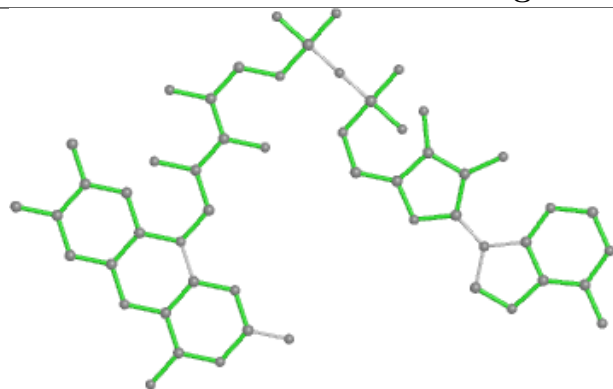
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FDA	1	0
2	D	601	FDA	1	0
2	C	600	FDA	1	0

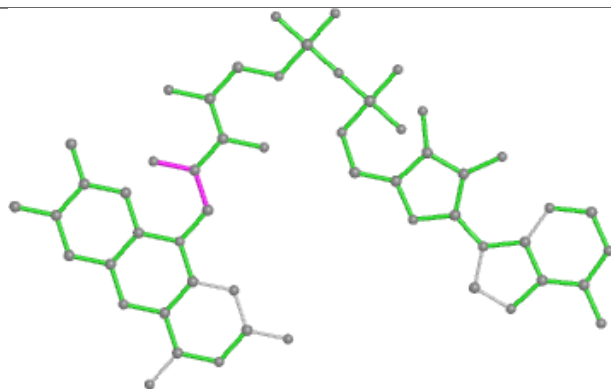
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



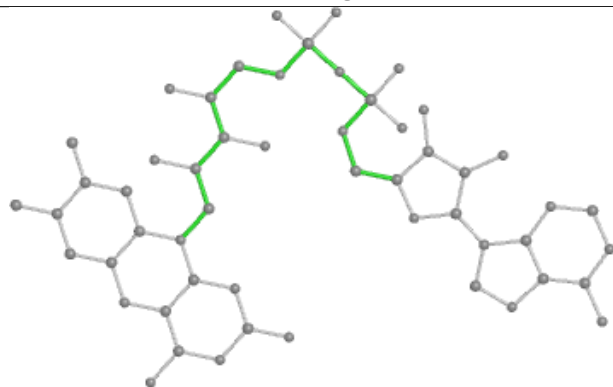
Ligand FDA B 601



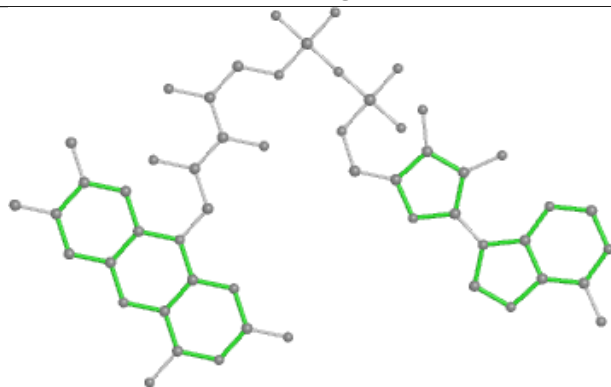
Bond lengths



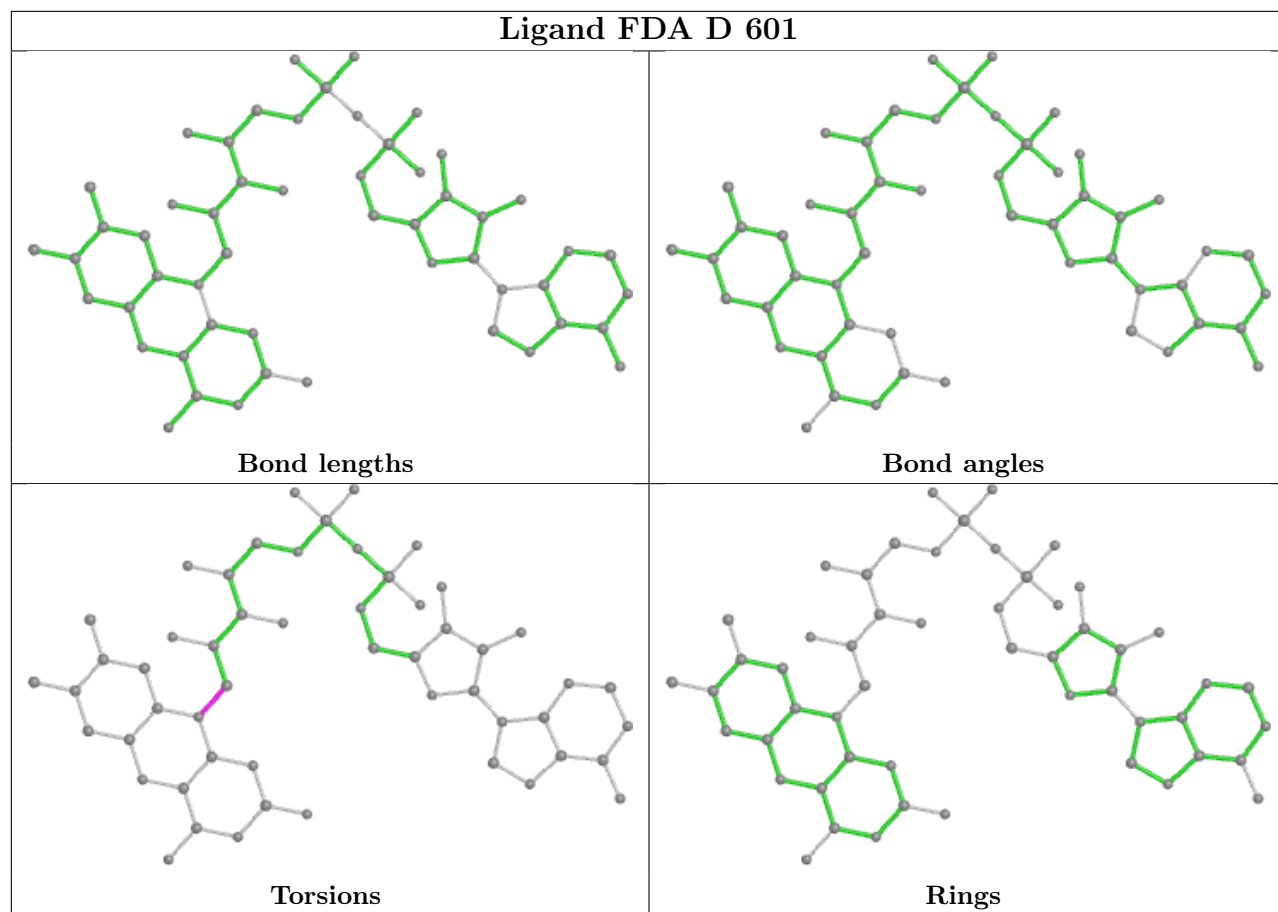
Bond angles

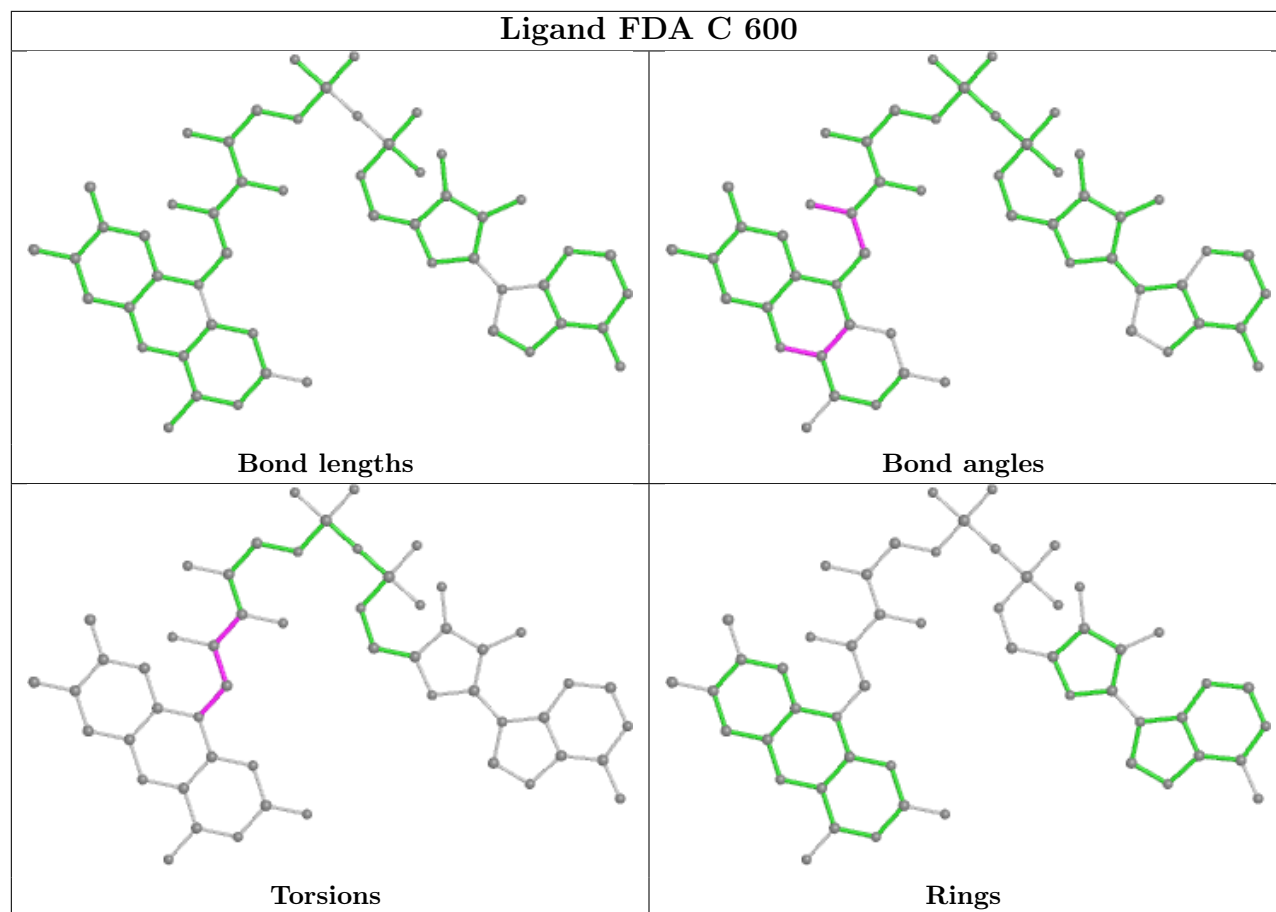


Torsions



Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	480/517 (92%)	-0.59	10 (2%) 63 70	5, 11, 32, 91	0
1	B	480/517 (92%)	-0.42	10 (2%) 63 70	6, 16, 43, 117	0
1	C	480/517 (92%)	-0.52	10 (2%) 63 70	5, 12, 33, 112	0
1	D	482/517 (93%)	-0.61	4 (0%) 86 89	5, 11, 30, 58	0
All	All	1922/2068 (92%)	-0.53	34 (1%) 68 74	5, 13, 35, 117	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	166	ALA	4.9
1	B	165	ASP	4.5
1	C	167	GLN	4.4
1	C	165	ASP	4.2
1	B	168	GLU	4.0
1	C	168	GLU	4.0
1	A	165	ASP	4.0
1	B	169	ARG	3.9
1	B	62	GLU	3.8
1	B	164	PRO	3.7
1	B	166	ALA	3.3
1	A	164	PRO	3.2
1	C	1	MET	3.1
1	C	164	PRO	3.0
1	A	163	ASN	3.0
1	A	167	GLN	2.8
1	B	163	ASN	2.8
1	A	1	MET	2.7
1	A	470	TYR	2.7
1	C	470	TYR	2.7
1	B	63	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	169	ARG	2.7
1	A	168	GLU	2.6
1	C	62	GLU	2.4
1	B	167	GLN	2.4
1	D	62	GLU	2.4
1	C	63	GLY	2.3
1	D	416	GLY	2.3
1	A	469	PRO	2.3
1	B	417	ARG	2.2
1	A	169	ARG	2.1
1	D	1	MET	2.1
1	D	463	GLU	2.0
1	A	401	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](#)

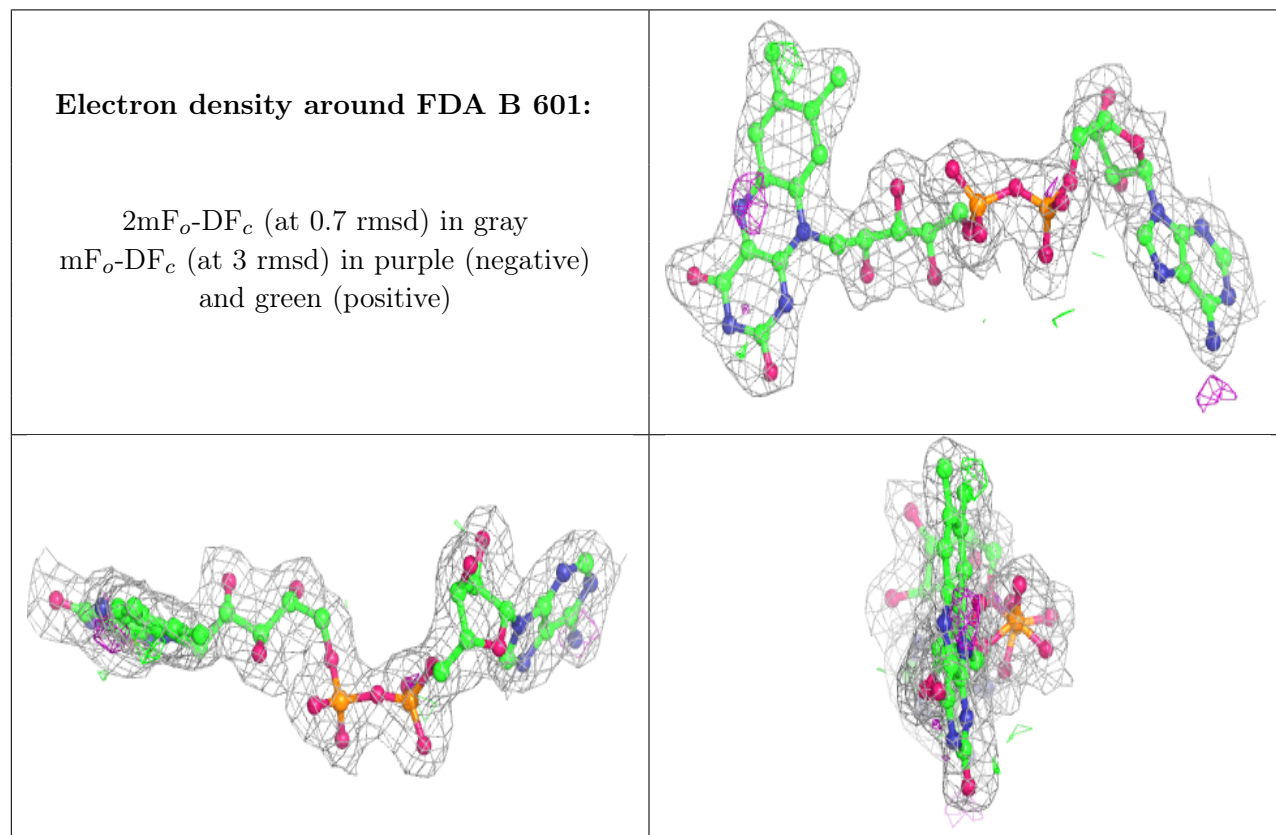
There are no monosaccharides in this entry.

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.

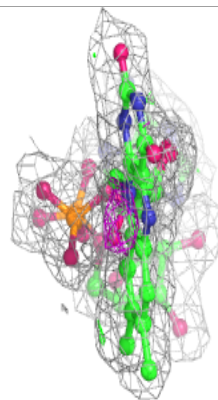
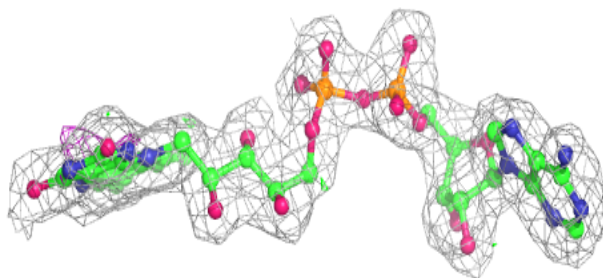
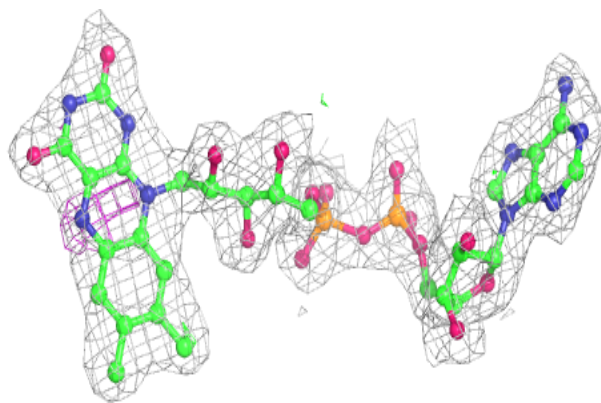
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NPO	C	601	10/10	0.68	0.28	37,43,52,52	0
3	NPO	A	601	10/10	0.70	0.31	26,39,53,53	0
3	NPO	A	602	10/10	0.92	0.13	30,32,34,38	0
3	NPO	C	602	10/10	0.92	0.12	27,28,32,36	0
3	NPO	D	602	10/10	0.93	0.14	23,25,27,28	0
3	NPO	B	602	10/10	0.94	0.14	28,31,33,36	0
2	FDA	B	601	53/53	0.95	0.11	10,14,16,18	0
2	FDA	C	600	53/53	0.96	0.09	7,10,11,12	0
2	FDA	A	600	53/53	0.97	0.08	4,6,7,8	0
2	FDA	D	601	53/53	0.97	0.08	5,6,8,8	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.

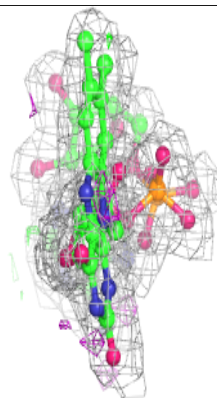
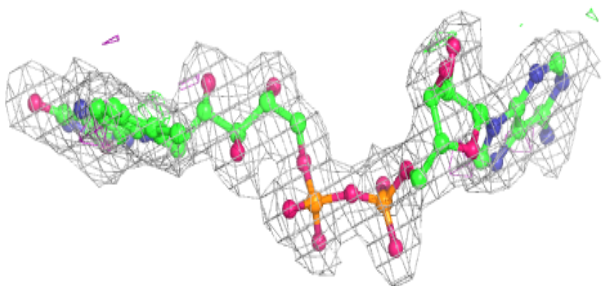
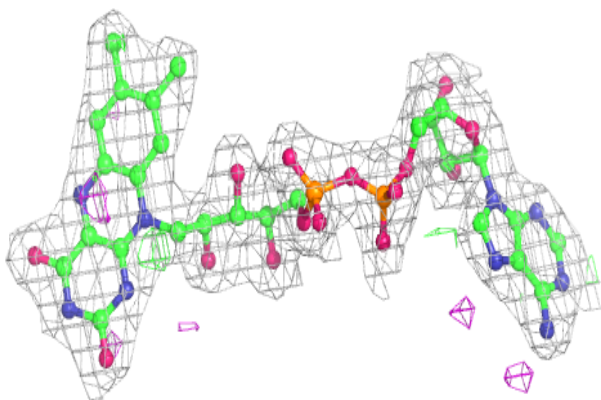


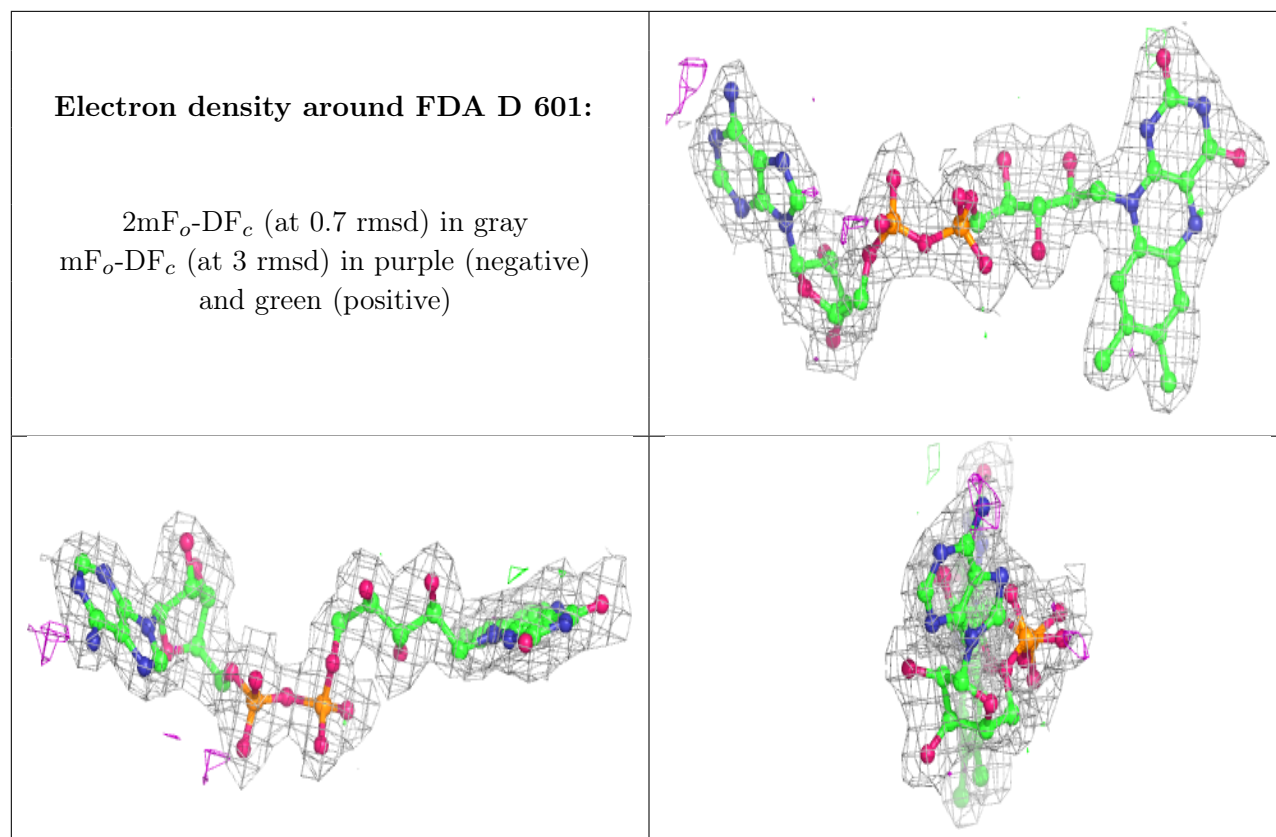
Electron density around FDA C 600:

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

**Electron density around FDA A 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.