



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:04 PM UTC

PDB ID : 4MOF / pdb_00004mof
Title : Pyranose 2-oxidase H450G mutant with 2-fluorinated glucose
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Deposited on : 2013-09-12
Resolution : 1.85 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

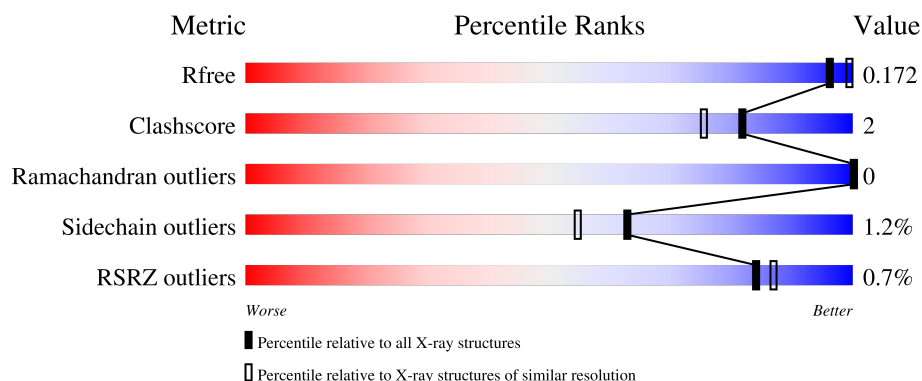
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	633	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5199 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.

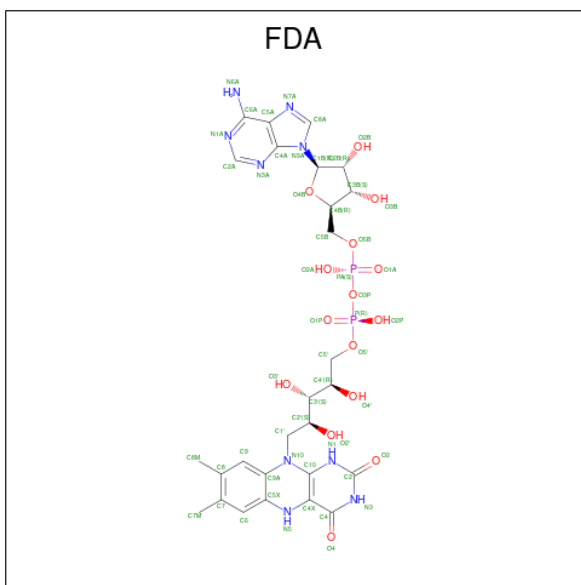
- Molecule 1 is a protein called Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	0	0	0
			4512	2849	772	867	24			

There are 13 discrepancies between the modelled and reference sequences:

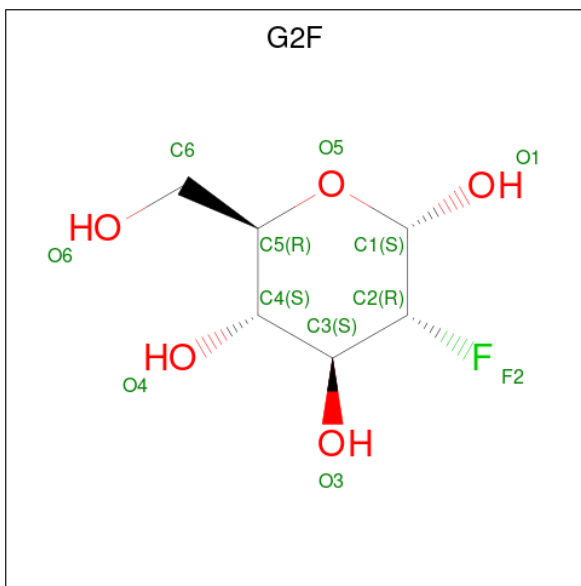
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	SER	SEE REMARK 999	UNP Q7ZA32
A	450	GLY	HIS	engineered mutation	UNP Q7ZA32
A	623	ALA	-	expression tag	UNP Q7ZA32
A	624	ALA	-	expression tag	UNP Q7ZA32
A	625	ALA	-	expression tag	UNP Q7ZA32
A	626	LEU	-	expression tag	UNP Q7ZA32
A	627	GLU	-	expression tag	UNP Q7ZA32
A	628	HIS	-	expression tag	UNP Q7ZA32
A	629	HIS	-	expression tag	UNP Q7ZA32
A	630	HIS	-	expression tag	UNP Q7ZA32
A	631	HIS	-	expression tag	UNP Q7ZA32
A	632	HIS	-	expression tag	UNP Q7ZA32
A	633	HIS	-	expression tag	UNP Q7ZA32

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



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

- Molecule 3 is 2-deoxy-2-fluoro-alpha-D-glucopyranose (CCD ID: G2F) (formula: $\text{C}_6\text{H}_{11}\text{FO}_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	O	0	0
			12	6	1	5		

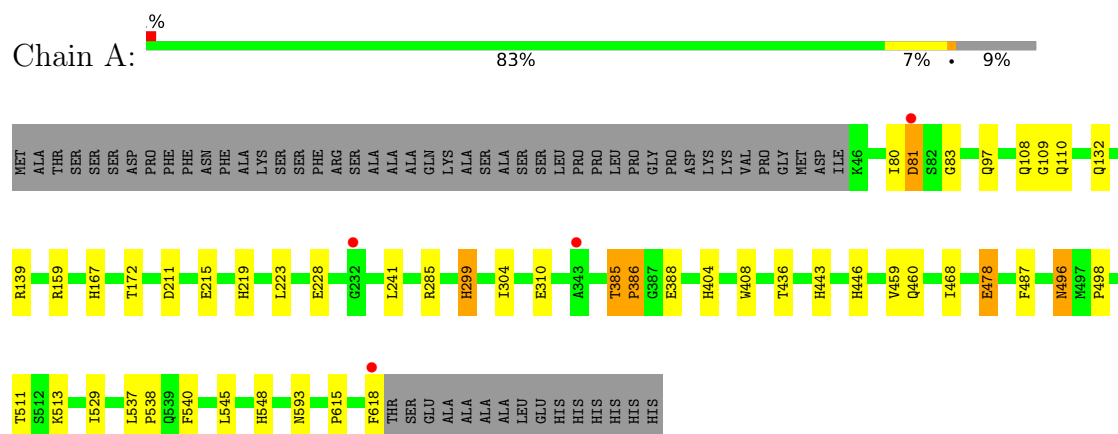
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	622	Total 622	O 622	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: Pyranose 2-oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.34Å 102.34Å 128.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.85 50.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-1.85) 99.4 (50.00-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.158 , 0.194 (Not available) , 0.172	Depositor DCC
R_{free} test set	1796 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5199	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 3.19% 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: G2F, FDA

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	1.39	19/4627 (0.4%)	1.12	11/6291 (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 (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	ASP	CG-OD1	8.48	1.41	1.25
1	A	81	ASP	CB-CG	-7.48	1.33	1.52
1	A	299	HIS	CG-CD2	7.29	1.43	1.35
1	A	80	ILE	C-O	-6.65	1.17	1.24
1	A	548	HIS	ND1-CE1	6.19	1.38	1.32
1	A	446	HIS	CG-CD2	6.03	1.42	1.35
1	A	299	HIS	ND1-CE1	6.01	1.38	1.32
1	A	219	HIS	CG-CD2	5.83	1.42	1.35
1	A	109	GLY	C-O	-5.78	1.17	1.24
1	A	139	ARG	CD-NE	-5.44	1.38	1.46
1	A	386	PRO	CA-C	-5.41	1.46	1.52
1	A	408	TRP	C-O	5.30	1.30	1.24
1	A	241	LEU	C-O	5.16	1.29	1.24
1	A	540	PHE	C-O	5.16	1.30	1.23
1	A	132	GLN	C-O	5.10	1.30	1.23
1	A	83	GLY	C-O	-5.10	1.17	1.23
1	A	529	ILE	C-O	-5.05	1.18	1.23
1	A	172	THR	CA-CB	5.04	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	478	GLU	CD-OE2	5.01	1.34	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ARG	NE-CZ-NH2	-9.30	110.83	119.20
1	A	81	ASP	CB-CA-C	-7.17	97.58	110.35
1	A	81	ASP	N-CA-C	6.46	123.40	113.19
1	A	615	PRO	CB-CA-C	-6.22	102.83	110.98
1	A	139	ARG	CD-NE-CZ	5.90	132.66	124.40
1	A	139	ARG	CG-CD-NE	-5.66	99.55	112.00
1	A	139	ARG	NE-CZ-NH1	5.46	126.96	121.50
1	A	285	ARG	CB-CA-C	-5.32	100.43	110.16
1	A	459	VAL	N-CA-CB	5.25	116.25	110.53
1	A	211	ASP	CB-CG-OD1	5.16	130.26	118.40
1	A	97	GLN	CA-CB-CG	-5.02	104.05	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	THR	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	4512	0	4360	22	0
2	A	53	0	31	1	0
3	A	12	0	11	0	0
4	A	622	0	0	11	0
All	All	5199	0	4402	22	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 2.

All (22) 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:110:GLN:HE21	1:A:167:HIS:HD1	1.26	0.81
1:A:513:LYS:NZ	4:A:1422:HOH:O	2.26	0.67
1:A:443:HIS:HD2	4:A:997:HOH:O	1.77	0.66
1:A:545:LEU:HD12	4:A:1316:HOH:O	1.98	0.64
1:A:385:THR:HG23	1:A:388:GLU:OE1	1.98	0.63
1:A:443:HIS:HE1	4:A:1100:HOH:O	1.82	0.63
1:A:404:HIS:HE1	4:A:1197:HOH:O	1.86	0.58
1:A:618:PHE:C	1:A:618:PHE:CD1	2.84	0.55
1:A:496:ASN:ND2	4:A:1460:HOH:O	2.39	0.55
1:A:618:PHE:C	1:A:618:PHE:HD1	2.14	0.54
1:A:478:GLU:HG3	1:A:511:THR:OG1	2.10	0.51
1:A:215:GLU:HG3	4:A:1341:HOH:O	2.11	0.50
1:A:460:GLN:NE2	1:A:468:ILE:HD11	2.33	0.44
1:A:223:LEU:CD2	4:A:1339:HOH:O	2.65	0.44
1:A:108:GLN:HG2	4:A:1409:HOH:O	2.19	0.43
1:A:537:LEU:HB3	1:A:538:PRO:HD2	2.01	0.42
1:A:487:PHE:HB3	1:A:498:PRO:HB2	2.01	0.42
1:A:404:HIS:CE1	4:A:1197:HOH:O	2.68	0.42
1:A:215:GLU:CG	4:A:1341:HOH:O	2.68	0.41
1:A:385:THR:HA	1:A:386:PRO:HD3	1.95	0.41
1:A:299:HIS:CD2	1:A:310:GLU:HG2	2.56	0.41
1:A:159:ARG:HA	2:A:801:FDA:O2B	2.20	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	571/633 (90%)	555 (97%)	16 (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	500/547 (91%)	494 (99%)	6 (1%)	63 55

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	ASP
1	A	228	GLU
1	A	304	ILE
1	A	385	THR
1	A	496	ASN
1	A	593	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	GLN
1	A	233	GLN
1	A	257	ASN
1	A	263	GLN
1	A	341	ASN
1	A	344	ASN
1	A	365	GLN
1	A	419	HIS
1	A	443	HIS
1	A	496	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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$
2	FDA	A	801	1	57,58,58	1.60	14 (24%)	78,89,89	1.98	22 (28%)
3	G2F	A	802	-	12,12,12	1.50	3 (25%)	16,17,17	3.20	9 (56%)

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	FDA	A	801	1	-	2/34/50/50	0/6/6/6
3	G2F	A	802	-	-	2/2/22/22	0/1/1/1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FDA	C4-N3	-4.01	1.31	1.38
2	A	801	FDA	P-O3P	3.38	1.63	1.59
3	A	802	G2F	O1-C1	3.17	1.49	1.39
2	A	801	FDA	C5X-C9A	-3.12	1.37	1.40
2	A	801	FDA	C2B-C3B	-3.10	1.45	1.53
2	A	801	FDA	C5'-C4'	3.02	1.55	1.51
2	A	801	FDA	C8A-N9A	-2.75	1.32	1.37
2	A	801	FDA	C2-N1	-2.70	1.33	1.37
3	A	802	G2F	C2-C1	-2.49	1.50	1.52
2	A	801	FDA	C1'-N10	2.49	1.53	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FDA	O4B-C4B	-2.48	1.39	1.45
3	A	802	G2F	C2-C3	-2.45	1.50	1.52
2	A	801	FDA	PA-O3P	2.28	1.62	1.59
2	A	801	FDA	C7M-C7	2.24	1.55	1.51
2	A	801	FDA	C9-C8	2.10	1.42	1.39
2	A	801	FDA	PA-O2A	-2.07	1.45	1.55
2	A	801	FDA	C8-C7	2.03	1.45	1.40

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	G2F	O5-C1-C2	6.87	118.62	109.75
3	A	802	G2F	F2-C2-C1	5.75	114.25	107.81
2	A	801	FDA	N3A-C2A-N1A	-5.66	120.02	128.58
2	A	801	FDA	C4A-N9A-C8A	5.09	111.08	105.74
3	A	802	G2F	O1-C1-O5	-4.56	96.86	110.41
3	A	802	G2F	O5-C5-C4	4.48	117.77	109.70
2	A	801	FDA	N9A-C8A-N7A	-4.42	107.67	113.94
2	A	801	FDA	C1B-N9A-C8A	-4.27	117.62	127.09
2	A	801	FDA	O4B-C1B-N9A	3.98	115.73	108.09
2	A	801	FDA	O3B-C3B-C4B	3.84	122.10	111.08
2	A	801	FDA	N3A-C4A-N9A	3.60	133.30	127.17
2	A	801	FDA	C2B-C1B-N9A	3.56	122.16	113.30
3	A	802	G2F	C1-O5-C5	3.48	120.39	113.65
2	A	801	FDA	O2A-PA-O3P	3.36	116.35	107.27
2	A	801	FDA	O4B-C4B-C5B	3.15	119.42	109.33
2	A	801	FDA	C2A-N3A-C4A	3.10	119.39	111.83
2	A	801	FDA	C7M-C7-C6	-3.05	114.20	119.57
2	A	801	FDA	C5A-C4A-N3A	-3.05	122.52	126.72
3	A	802	G2F	O3-C3-C4	2.88	117.16	110.38
2	A	801	FDA	N3-C2-N1	2.87	120.26	115.74
2	A	801	FDA	C7M-C7-C8	2.65	126.16	120.76
2	A	801	FDA	O3P-PA-O1A	-2.61	102.85	110.70
3	A	802	G2F	F2-C2-C3	2.47	110.96	108.81
2	A	801	FDA	O4B-C1B-C2B	2.31	111.56	106.62
3	A	802	G2F	O4-C4-C5	2.27	114.93	109.32
3	A	802	G2F	C1-C2-C3	2.17	113.92	110.69
2	A	801	FDA	O4-C4-N3	2.15	124.16	120.11
2	A	801	FDA	O4-C4-C4X	-2.13	122.12	127.26
2	A	801	FDA	C5A-N7A-C8A	2.12	106.78	103.45
2	A	801	FDA	C5B-C4B-C3B	2.07	122.66	115.21
2	A	801	FDA	O4'-C4'-C3'	2.03	114.00	109.25

There are no chirality outliers.

All (4) torsion outliers are listed below:

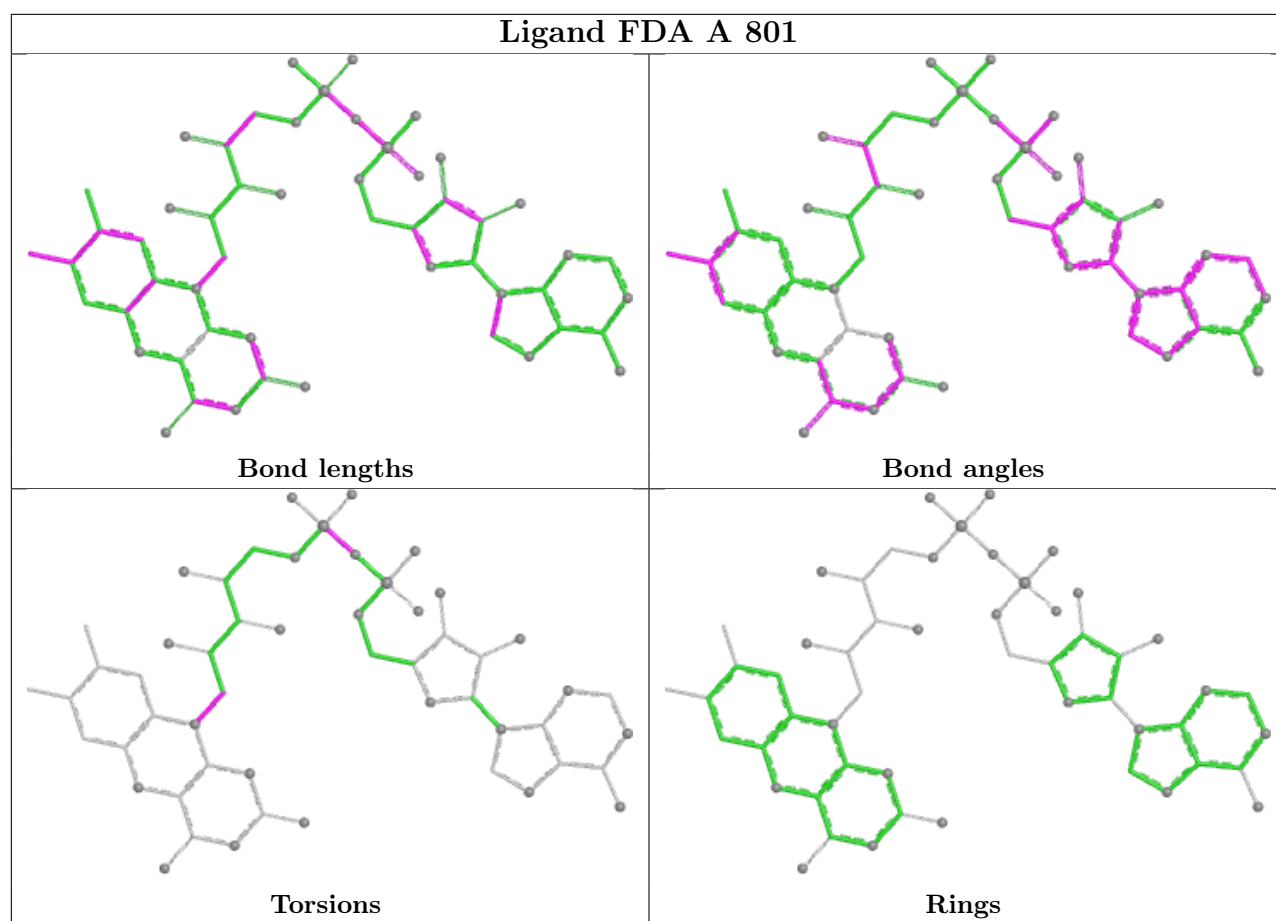
Mol	Chain	Res	Type	Atoms
3	A	802	G2F	C4-C5-C6-O6
3	A	802	G2F	O5-C5-C6-O6
2	A	801	FDA	PA-O3P-P-O5'
2	A	801	FDA	C2'-C1'-N10-C10

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	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.



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	573/633 (90%)	-0.37	4 (0%) 84 87	11, 17, 36, 55	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	618	PHE	3.8
1	A	81	ASP	2.9
1	A	232	GLY	2.4
1	A	343	ALA	2.2

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.

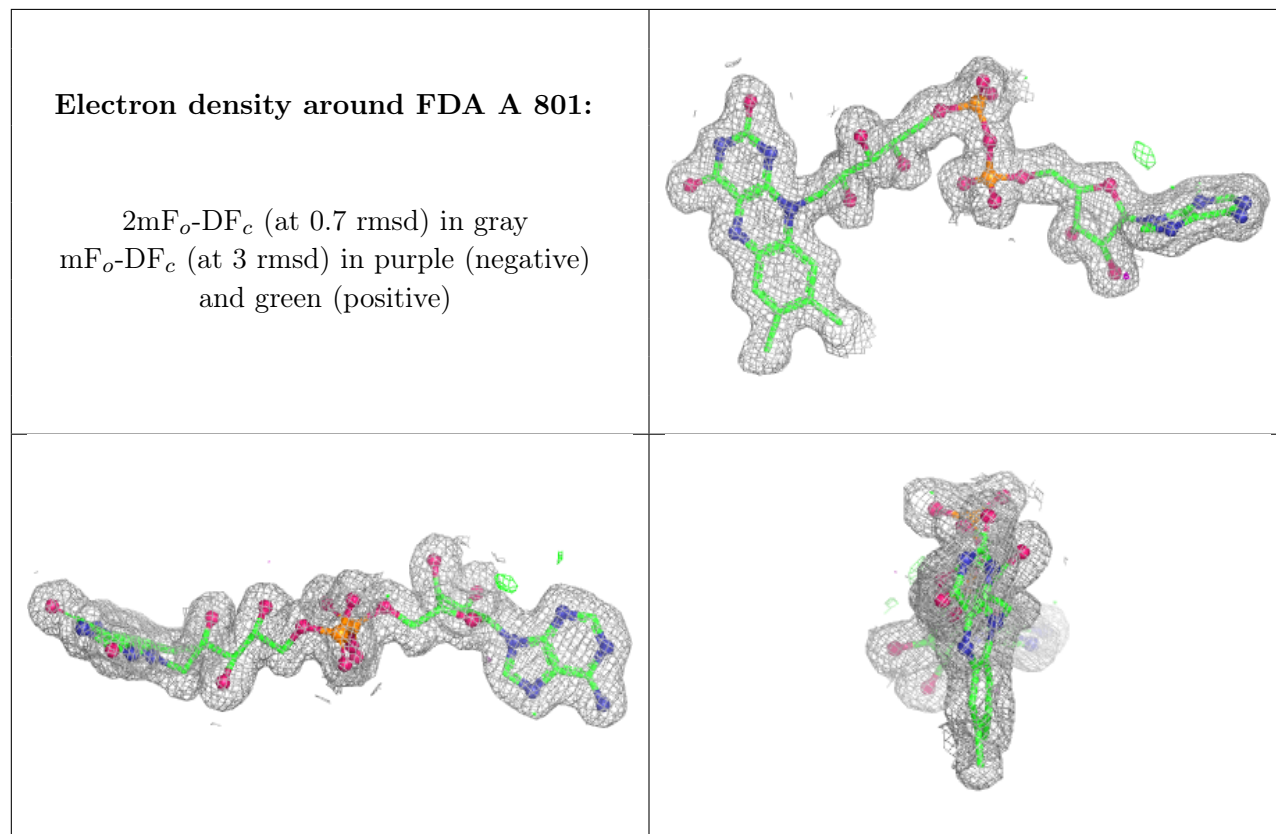
6.4 Ligands [i](#)

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	G2F	A	802	12/12	0.97	0.05	14,15,17,17	0
2	FDA	A	801	53/53	0.98	0.04	10,13,14,15	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.