



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 10, 2023 – 02:28 PM EDT

PDB ID : 4K2X
Title : OxyS anhydrotetracycline hydroxylase from *Streptomyces rimosus*
Authors : Wang, P.; Sawaya, M.R.; Tang, Y.
Deposited on : 2013-04-09
Resolution : 2.55 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

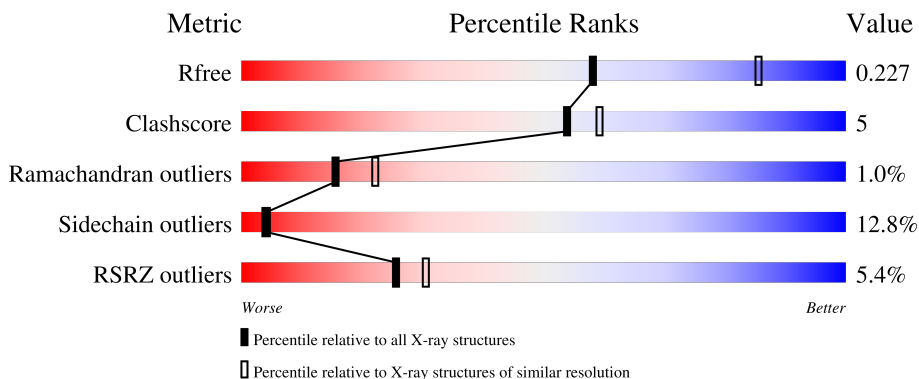
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	523	
1	B	523	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 7588 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 Polyketide oxygenase/hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	488	3712	2344	658	696	14	0	0	0
1	B	490	3722	2350	660	698	14	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

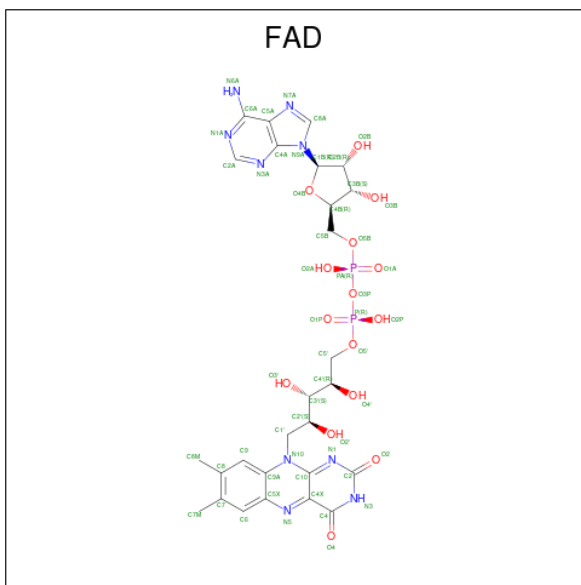
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP L8EUQ6
A	-18	GLY	-	expression tag	UNP L8EUQ6
A	-17	SER	-	expression tag	UNP L8EUQ6
A	-16	SER	-	expression tag	UNP L8EUQ6
A	-15	HIS	-	expression tag	UNP L8EUQ6
A	-14	HIS	-	expression tag	UNP L8EUQ6
A	-13	HIS	-	expression tag	UNP L8EUQ6
A	-12	HIS	-	expression tag	UNP L8EUQ6
A	-11	HIS	-	expression tag	UNP L8EUQ6
A	-10	HIS	-	expression tag	UNP L8EUQ6
A	-9	SER	-	expression tag	UNP L8EUQ6
A	-8	SER	-	expression tag	UNP L8EUQ6
A	-7	GLY	-	expression tag	UNP L8EUQ6
A	-6	LEU	-	expression tag	UNP L8EUQ6
A	-5	VAL	-	expression tag	UNP L8EUQ6
A	-4	PRO	-	expression tag	UNP L8EUQ6
A	-3	ARG	-	expression tag	UNP L8EUQ6
A	-2	GLY	-	expression tag	UNP L8EUQ6
A	-1	SER	-	expression tag	UNP L8EUQ6
A	0	HIS	-	expression tag	UNP L8EUQ6
B	-19	MET	-	expression tag	UNP L8EUQ6
B	-18	GLY	-	expression tag	UNP L8EUQ6
B	-17	SER	-	expression tag	UNP L8EUQ6
B	-16	SER	-	expression tag	UNP L8EUQ6
B	-15	HIS	-	expression tag	UNP L8EUQ6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP L8EUQ6
B	-13	HIS	-	expression tag	UNP L8EUQ6
B	-12	HIS	-	expression tag	UNP L8EUQ6
B	-11	HIS	-	expression tag	UNP L8EUQ6
B	-10	HIS	-	expression tag	UNP L8EUQ6
B	-9	SER	-	expression tag	UNP L8EUQ6
B	-8	SER	-	expression tag	UNP L8EUQ6
B	-7	GLY	-	expression tag	UNP L8EUQ6
B	-6	LEU	-	expression tag	UNP L8EUQ6
B	-5	VAL	-	expression tag	UNP L8EUQ6
B	-4	PRO	-	expression tag	UNP L8EUQ6
B	-3	ARG	-	expression tag	UNP L8EUQ6
B	-2	GLY	-	expression tag	UNP L8EUQ6
B	-1	SER	-	expression tag	UNP L8EUQ6
B	0	HIS	-	expression tag	UNP L8EUQ6

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



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

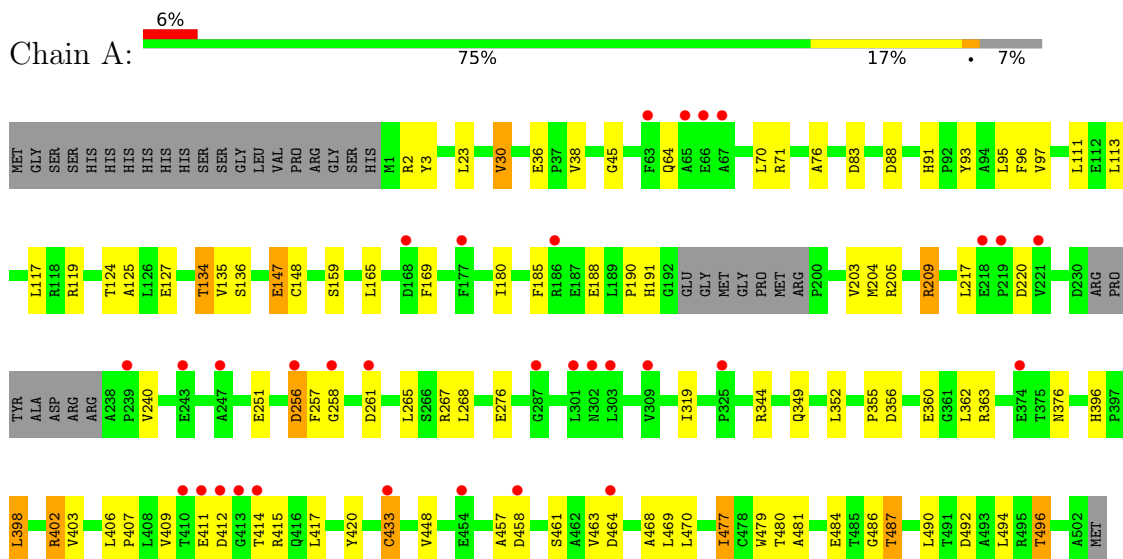
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total 23	O 23	0	0
3	B	25	Total 25	O 25	0	0

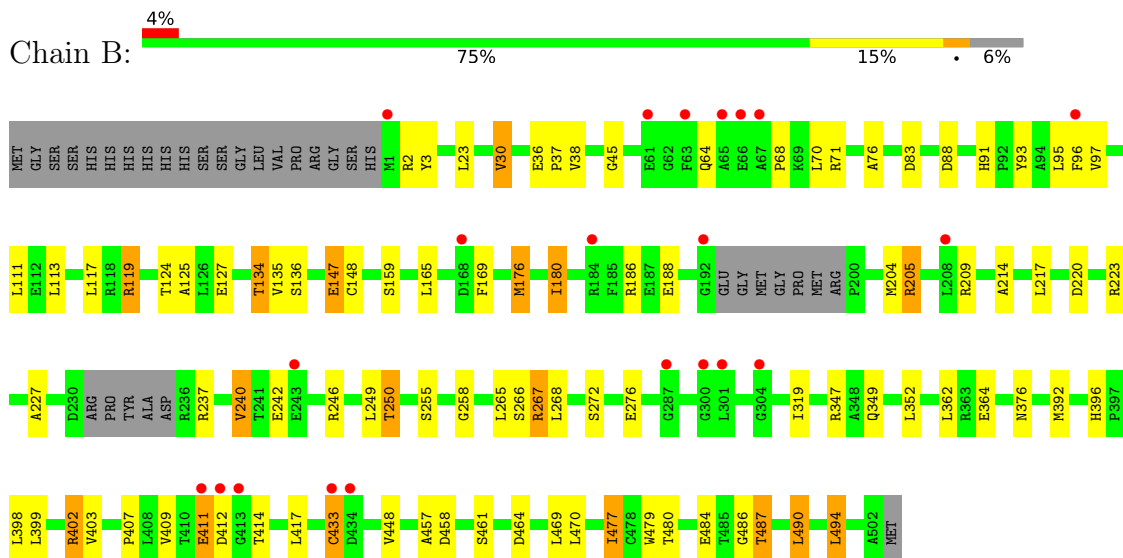
3 Residue-property plots [i](#)

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: Polyketide oxygenase/hydroxylase



- Molecule 1: Polyketide oxygenase/hydroxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.06Å 115.13Å 121.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.05 – 2.55 34.05 – 2.55	Depositor EDS
% Data completeness (in resolution range)	89.0 (34.05-2.55) 89.0 (34.05-2.55)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 2.54Å)	Xtrriage
Refinement program	BUSTER-TNT, BUSTER 2.10.0	Depositor
R, R_{free}	0.187 , 0.229 0.186 , 0.227	Depositor DCC
R_{free} test set	1573 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtrriage
Anisotropy	0.258	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.006 for -h,l,k	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7588	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.40 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.7090e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 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	0.51	0/3795	0.78	0/5169
1	B	0.53	0/3805	0.78	1/5183 (0.0%)
All	All	0.52	0/7600	0.78	1/10352 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	38	VAL	N-CA-CB	-5.01	100.47	111.50

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	3712	0	3651	39	0
1	B	3722	0	3655	41	0
2	A	53	0	31	0	0
2	B	53	0	31	1	0
3	A	23	0	0	0	0
3	B	25	0	0	0	0
All	All	7588	0	7368	79	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 (79) 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:492:ASP:O	1:A:496:THR:HG22	1.80	0.81
1:A:362:LEU:HD21	1:B:362:LEU:HD21	1.63	0.78
1:A:477:ILE:HD11	1:A:480:THR:HG23	1.66	0.76
1:B:83:ASP:H	1:B:376:ASN:HD21	1.34	0.76
1:B:477:ILE:HD11	1:B:480:THR:HG23	1.66	0.76
1:A:83:ASP:H	1:A:376:ASN:HD21	1.35	0.74
1:A:76:ALA:H	1:A:349:GLN:HE21	1.41	0.66
1:B:242:GLU:OE2	1:B:246:ARG:NH1	2.29	0.65
1:B:490:LEU:HD22	1:B:494:LEU:HD22	1.77	0.65
1:A:256:ASP:OD1	1:A:258:GLY:N	2.30	0.64
1:B:30:VAL:HG22	1:B:117:LEU:HD13	1.80	0.64
1:A:256:ASP:OD1	1:A:256:ASP:C	2.36	0.63
1:A:469:LEU:HD23	1:A:480:THR:HG22	1.82	0.62
1:A:30:VAL:HG22	1:A:117:LEU:HD13	1.81	0.62
1:A:88:ASP:O	1:A:402:ARG:NH2	2.34	0.61
1:A:134:THR:CG2	1:A:147:GLU:HG3	2.32	0.59
1:A:76:ALA:HB2	1:A:349:GLN:HG2	1.83	0.59
1:B:469:LEU:HD23	1:B:480:THR:HG22	1.83	0.59
1:B:134:THR:CG2	1:B:147:GLU:HG3	2.32	0.59
1:B:88:ASP:O	1:B:402:ARG:NH2	2.36	0.57
1:A:256:ASP:O	1:A:257:PHE:HB2	2.04	0.56
1:A:45:GLY:HA2	1:A:97:VAL:H	1.71	0.54
1:B:45:GLY:HA2	1:B:97:VAL:H	1.72	0.54
1:A:76:ALA:H	1:A:349:GLN:NE2	2.06	0.54
1:A:180:ILE:HD11	1:A:268:LEU:HB2	1.89	0.53
1:A:468:ALA:HB3	1:A:481:ALA:HB3	1.92	0.52
1:B:134:THR:HG22	1:B:147:GLU:HG3	1.90	0.52
1:A:406:LEU:HD11	1:A:463:VAL:HG21	1.91	0.52
1:A:479:TRP:CH2	1:A:481:ALA:HB2	2.46	0.50
1:A:190:PRO:HD3	1:A:257:PHE:CZ	2.46	0.50
1:A:134:THR:HG22	1:A:147:GLU:HG3	1.93	0.50
1:B:407:PRO:HB2	1:B:457:ALA:HB3	1.93	0.50
1:A:415:ARG:HG2	1:A:420:TYR:CE2	2.48	0.49
1:B:237:ARG:HA	1:B:267:ARG:NH2	2.28	0.49
1:A:209:ARG:HD3	1:A:356:ASP:HB2	1.95	0.48
1:A:134:THR:HG23	1:A:147:GLU:HG3	1.96	0.48
1:B:477:ILE:HD11	1:B:480:THR:CG2	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:GLU:OE1	1:A:363:ARG:NH1	2.47	0.47
1:B:76:ALA:H	1:B:349:GLN:HE21	1.61	0.47
1:A:470:LEU:HB3	1:A:479:TRP:HB3	1.96	0.47
1:A:407:PRO:HB2	1:A:457:ALA:HB3	1.96	0.47
1:B:214:ALA:HA	1:B:223:ARG:O	2.15	0.47
1:B:396:HIS:HB2	1:B:399:LEU:HD13	1.97	0.47
1:A:477:ILE:HD11	1:A:480:THR:CG2	2.42	0.46
1:B:470:LEU:HB3	1:B:479:TRP:HB3	1.97	0.46
1:B:237:ARG:HA	1:B:267:ARG:HH22	1.81	0.46
1:B:246:ARG:O	1:B:250:THR:HB	2.16	0.46
1:B:91:HIS:HD2	1:B:93:TYR:OH	1.99	0.46
1:A:396:HIS:CE1	1:A:398:LEU:HB2	2.51	0.46
1:B:180:ILE:HD12	1:B:266:SER:HB3	1.98	0.46
1:B:240:VAL:HG21	1:B:266:SER:CA	2.45	0.46
1:B:180:ILE:HD11	1:B:268:LEU:HB2	1.98	0.46
1:B:134:THR:HG23	1:B:147:GLU:HG3	1.98	0.45
1:A:344:ARG:HE	1:B:364:GLU:HB3	1.81	0.45
1:A:70:LEU:HD11	1:A:96:PHE:HB2	1.98	0.45
1:A:91:HIS:HD2	1:A:93:TYR:OH	1.98	0.45
1:B:70:LEU:HD11	1:B:96:PHE:HB2	1.99	0.45
1:B:204:MET:O	1:B:205:ARG:HG2	2.17	0.45
1:B:2:ARG:HD2	1:B:147:GLU:HB3	1.99	0.44
1:A:2:ARG:HD2	1:A:147:GLU:HB3	1.99	0.44
1:A:125:ALA:HB3	1:A:136:SER:HB2	2.00	0.44
1:B:64:GLN:HG2	1:B:95:LEU:HD21	1.98	0.44
1:B:272:SER:HB3	1:B:347:ARG:HE	1.83	0.44
1:B:176:MET:HE2	1:B:227:ALA:HB1	1.99	0.44
1:A:185:PHE:HD2	1:A:257:PHE:HB3	1.83	0.43
1:B:125:ALA:HB3	1:B:136:SER:HB2	2.01	0.43
1:B:272:SER:CB	1:B:347:ARG:HE	2.32	0.43
1:B:186:ARG:HB2	1:B:258:GLY:HA3	2.01	0.42
1:B:37:PRO:HG3	1:B:119:ARG:NH2	2.35	0.42
1:A:64:GLN:HG2	1:A:95:LEU:HD21	2.00	0.42
1:B:477:ILE:CD1	1:B:480:THR:HG23	2.44	0.41
1:A:477:ILE:CD1	1:A:480:THR:HG23	2.43	0.41
1:B:68:PRO:HG2	1:B:96:PHE:HB3	2.03	0.41
1:B:95:LEU:HB3	1:B:97:VAL:HG23	2.02	0.41
1:B:411:GLU:O	1:B:412:ASP:HB2	2.21	0.41
2:B:601:FAD:H9	2:B:601:FAD:H1'1	1.87	0.41
1:B:3:TYR:O	1:B:148:CYS:HA	2.21	0.40
1:A:204:MET:SD	1:A:355:PRO:HB3	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:TYR:O	1:A:148:CYS: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	482/523 (92%)	462 (96%)	15 (3%)	5 (1%)	15	22
1	B	484/523 (92%)	465 (96%)	14 (3%)	5 (1%)	15	22
All	All	966/1046 (92%)	927 (96%)	29 (3%)	10 (1%)	15	22

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	461	SER
1	B	461	SER
1	A	486	GLY
1	A	487	THR
1	B	486	GLY
1	B	487	THR
1	A	159	SER
1	B	159	SER
1	A	433	CYS
1	B	433	CYS

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	376/405 (93%)	327 (87%)	49 (13%)	4	3
1	B	376/405 (93%)	329 (88%)	47 (12%)	4	4
All	All	752/810 (93%)	656 (87%)	96 (13%)	4	4

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	30	VAL
1	A	36	GLU
1	A	38	VAL
1	A	71	ARG
1	A	111	LEU
1	A	113	LEU
1	A	119	ARG
1	A	124	THR
1	A	127	GLU
1	A	134	THR
1	A	135	VAL
1	A	147	GLU
1	A	165	LEU
1	A	169	PHE
1	A	188	GLU
1	A	191	HIS
1	A	203	VAL
1	A	205	ARG
1	A	209	ARG
1	A	217	LEU
1	A	220	ASP
1	A	240	VAL
1	A	251	GLU
1	A	256	ASP
1	A	261	ASP
1	A	265	LEU
1	A	267	ARG
1	A	276	GLU
1	A	319	ILE
1	A	352	LEU
1	A	398	LEU
1	A	402	ARG

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Mol	Chain	Res	Type
1	A	403	VAL
1	A	409	VAL
1	A	411	GLU
1	A	412	ASP
1	A	414	THR
1	A	417	LEU
1	A	433	CYS
1	A	448	VAL
1	A	458	ASP
1	A	464	ASP
1	A	477	ILE
1	A	484	GLU
1	A	487	THR
1	A	490	LEU
1	A	494	LEU
1	A	496	THR
1	B	23	LEU
1	B	30	VAL
1	B	36	GLU
1	B	71	ARG
1	B	111	LEU
1	B	113	LEU
1	B	119	ARG
1	B	124	THR
1	B	127	GLU
1	B	134	THR
1	B	135	VAL
1	B	147	GLU
1	B	165	LEU
1	B	169	PHE
1	B	176	MET
1	B	180	ILE
1	B	188	GLU
1	B	205	ARG
1	B	209	ARG
1	B	217	LEU
1	B	220	ASP
1	B	240	VAL
1	B	249	LEU
1	B	250	THR
1	B	255	SER
1	B	265	LEU

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Mol	Chain	Res	Type
1	B	267	ARG
1	B	276	GLU
1	B	319	ILE
1	B	352	LEU
1	B	392	MET
1	B	398	LEU
1	B	402	ARG
1	B	403	VAL
1	B	409	VAL
1	B	411	GLU
1	B	414	THR
1	B	417	LEU
1	B	433	CYS
1	B	448	VAL
1	B	458	ASP
1	B	464	ASP
1	B	477	ILE
1	B	484	GLU
1	B	487	THR
1	B	490	LEU
1	B	494	LEU

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

Mol	Chain	Res	Type
1	A	91	HIS
1	A	349	GLN
1	A	376	ASN
1	B	91	HIS
1	B	206	HIS
1	B	349	GLN
1	B	376	ASN
1	B	422	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 monosaccharides 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	FAD	A	601	-	53,58,58	0.51	0	68,89,89	0.79	2 (2%)
2	FAD	B	601	-	53,58,58	0.54	0	68,89,89	0.79	2 (2%)

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	FAD	A	601	-	-	1/30/50/50	0/6/6/6
2	FAD	B	601	-	-	1/30/50/50	0/6/6/6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FAD	P-O3P-PA	-2.37	124.68	132.83
2	B	601	FAD	P-O3P-PA	-2.22	125.22	132.83
2	A	601	FAD	C5A-C6A-N6A	2.18	123.67	120.35
2	B	601	FAD	O3B-C3B-C4B	-2.08	105.03	111.05

There are no chirality outliers.

All (2) torsion outliers are listed below:

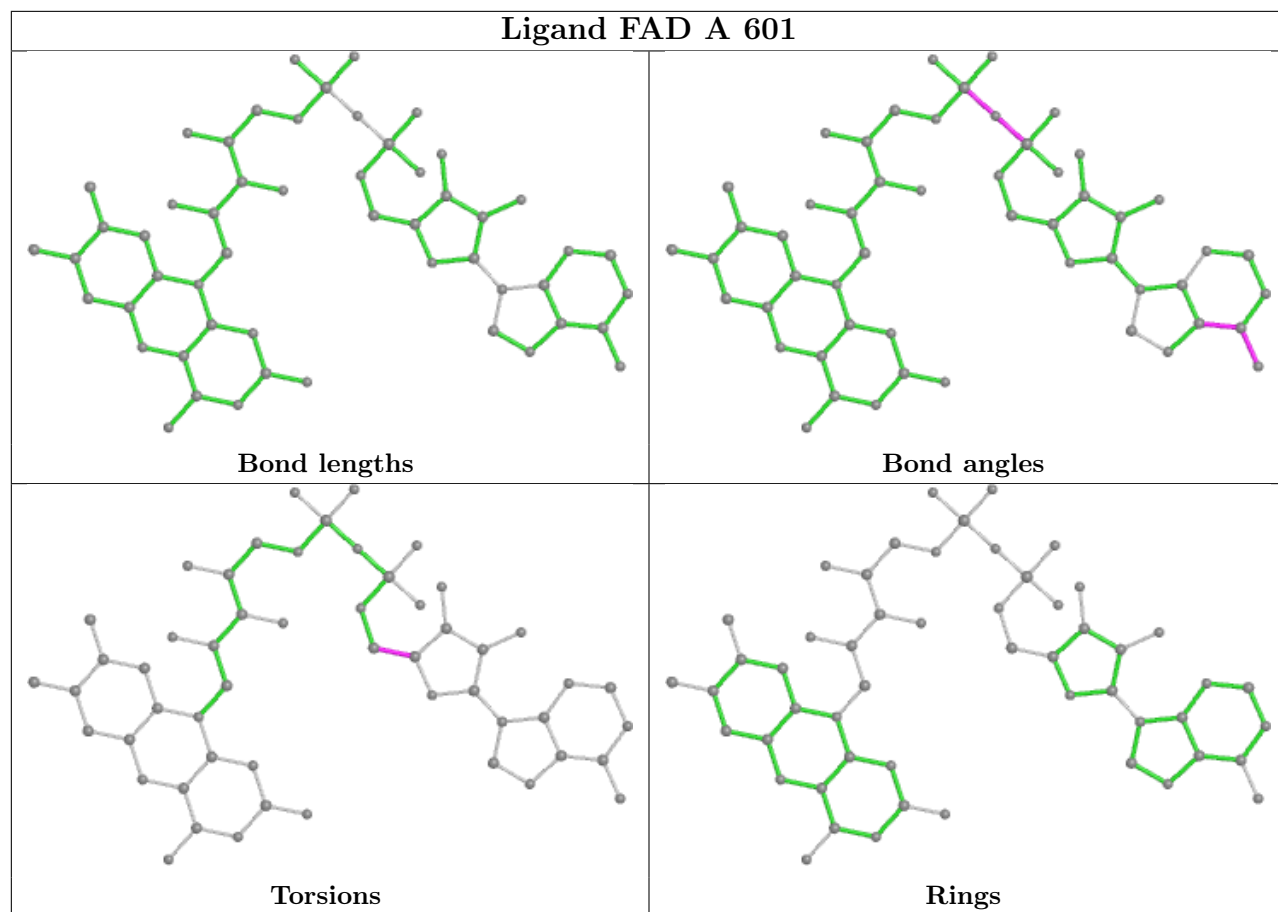
Mol	Chain	Res	Type	Atoms
2	A	601	FAD	O4B-C4B-C5B-O5B
2	B	601	FAD	O4B-C4B-C5B-O5B

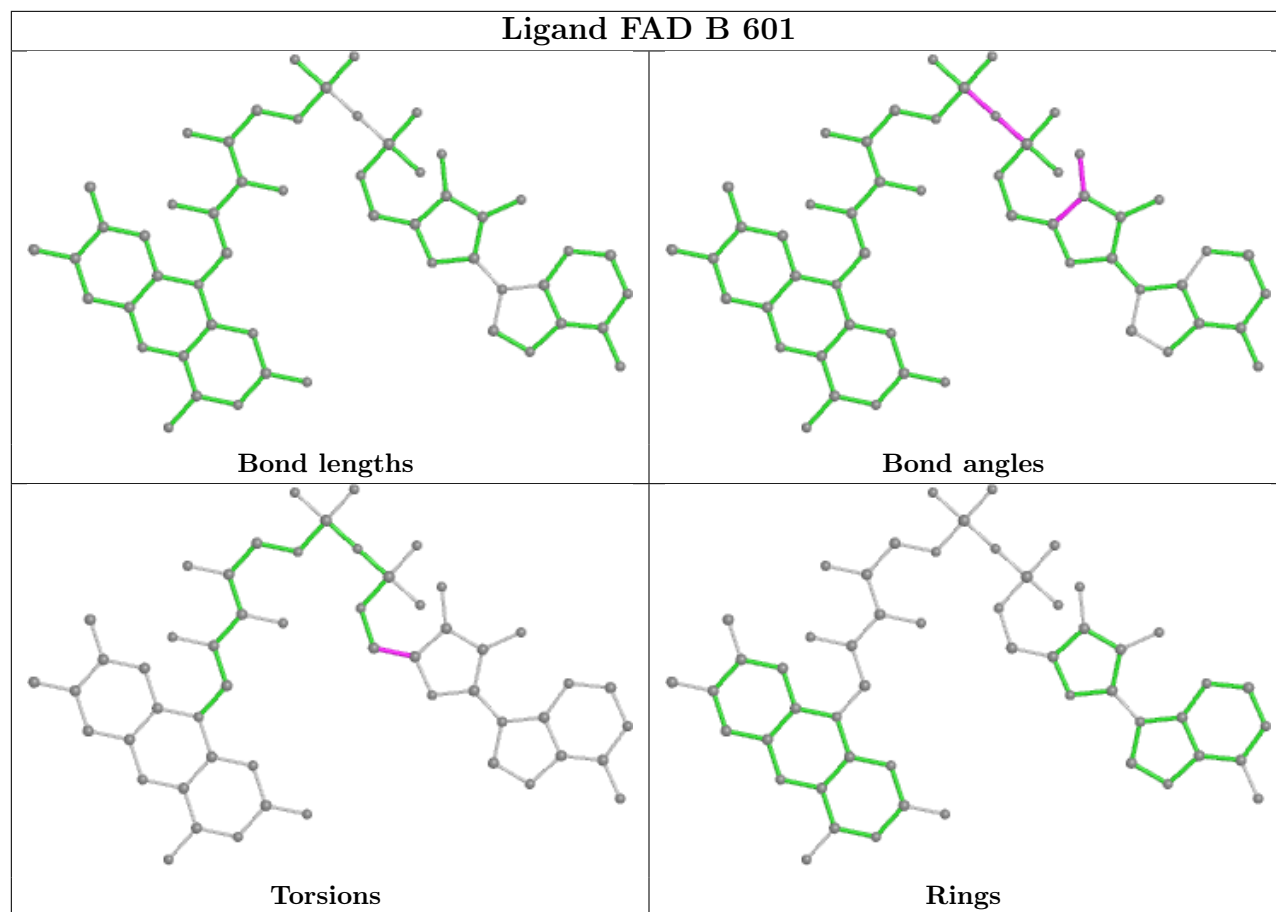
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	FAD	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	488/523 (93%)	0.38	32 (6%) 18 21	28, 46, 79, 107	0
1	B	490/523 (93%)	0.26	21 (4%) 35 42	27, 42, 75, 104	0
All	All	978/1046 (93%)	0.32	53 (5%) 25 30	27, 44, 78, 107	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	433	CYS	8.0
1	A	412	ASP	7.6
1	B	192	GLY	7.5
1	B	412	ASP	6.8
1	A	66	GLU	6.0
1	A	433	CYS	5.7
1	B	66	GLU	5.0
1	A	413	GLY	4.7
1	A	67	ALA	4.5
1	A	410	THR	4.0
1	A	258	GLY	3.8
1	A	65	ALA	3.7
1	A	411	GLU	3.7
1	B	411	GLU	3.5
1	A	63	PHE	3.5
1	B	65	ALA	3.4
1	A	458	ASP	3.3
1	B	168	ASP	3.2
1	B	63	PHE	2.8
1	B	301	LEU	2.8
1	B	67	ALA	2.8
1	A	287	GLY	2.7
1	A	218	GLU	2.7
1	B	208	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	219	PRO	2.7
1	A	186	ARG	2.7
1	A	414	THR	2.6
1	B	61	GLU	2.6
1	A	302	ASN	2.6
1	A	464	ASP	2.6
1	B	413	GLY	2.5
1	B	434	ASP	2.5
1	A	303	LEU	2.5
1	B	300	GLY	2.5
1	B	1	MET	2.4
1	A	168	ASP	2.4
1	B	304	GLY	2.3
1	A	177	PHE	2.3
1	A	247	ALA	2.2
1	B	287	GLY	2.2
1	A	239	PRO	2.2
1	A	454	GLU	2.2
1	A	301	LEU	2.2
1	B	184	ARG	2.2
1	B	243	GLU	2.2
1	A	309	VAL	2.1
1	A	243	GLU	2.1
1	A	221	VAL	2.1
1	A	374	GLU	2.1
1	A	256	ASP	2.1
1	A	325	PRO	2.0
1	B	96	PHE	2.0
1	A	261	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](#)

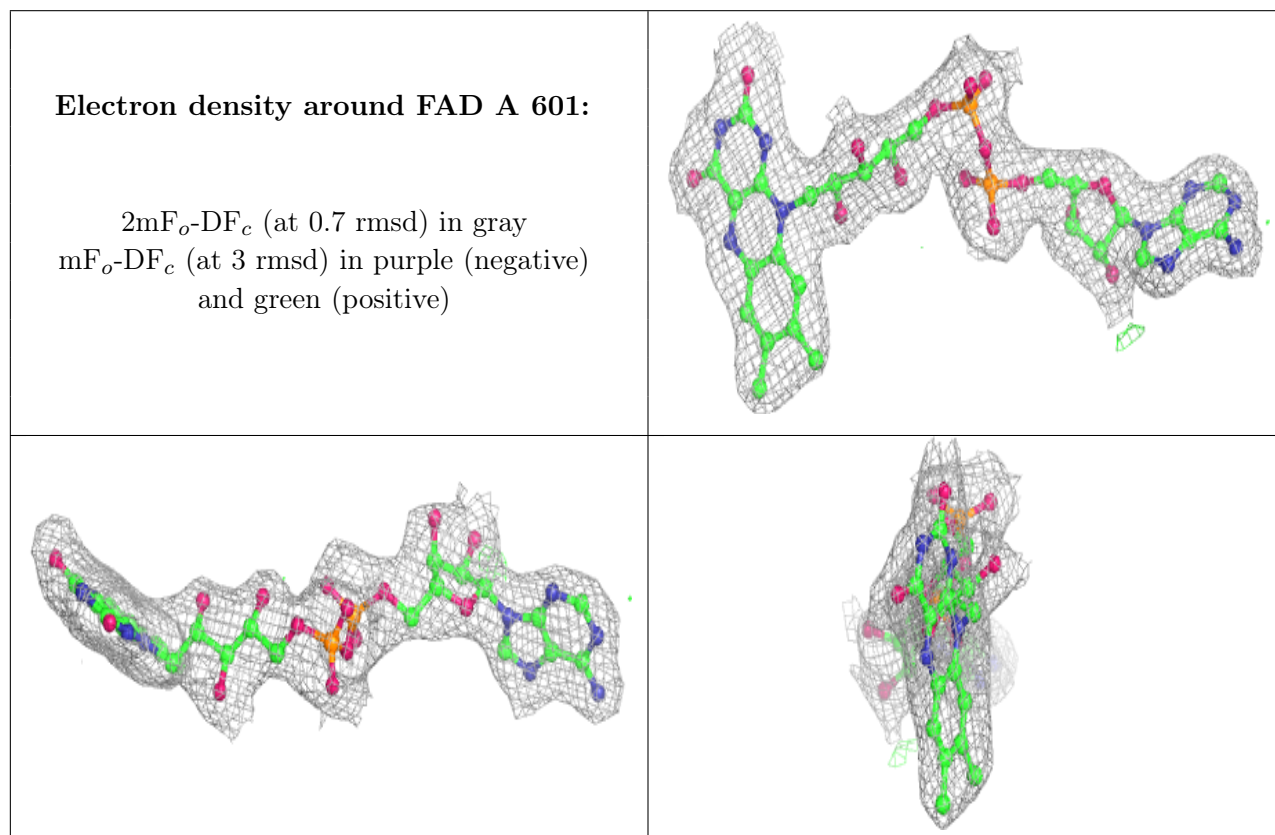
There are no monosaccharides in this entry.

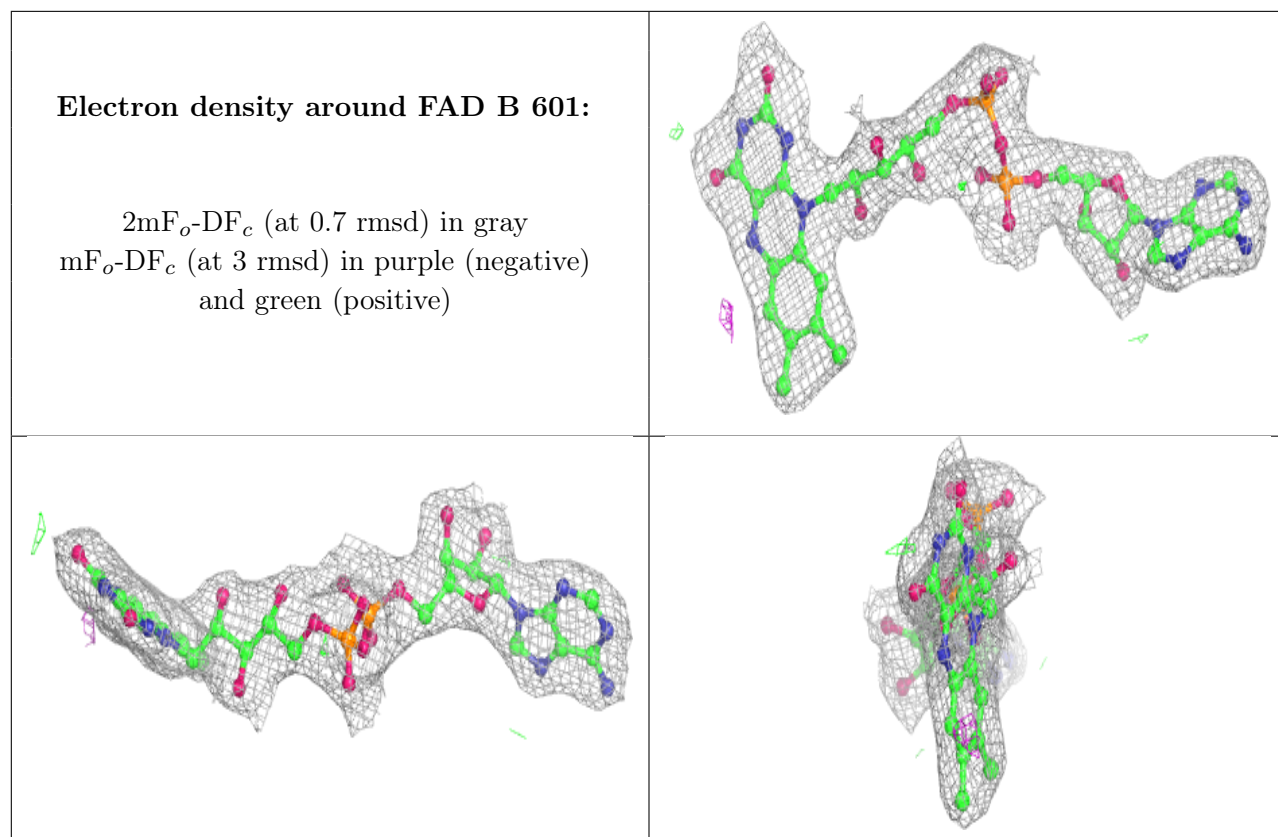
6.4 Ligands [i](#)

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(Å ²)	Q<0.9
2	FAD	A	601	53/53	0.97	0.20	22,34,41,46	0
2	FAD	B	601	53/53	0.98	0.20	23,33,38,44	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.