



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:07 PM UTC

PDB ID : 4AP1 / pdb_00004ap1
Title : Oxidized steroid monooxygenase bound to NADP
Authors : Franceschini, S.; van Beek, H.L.; Martinoli, C.; Pennetta, A.; Fraaije, M.W.;
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Deposited on : 2012-03-30
Resolution : 2.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

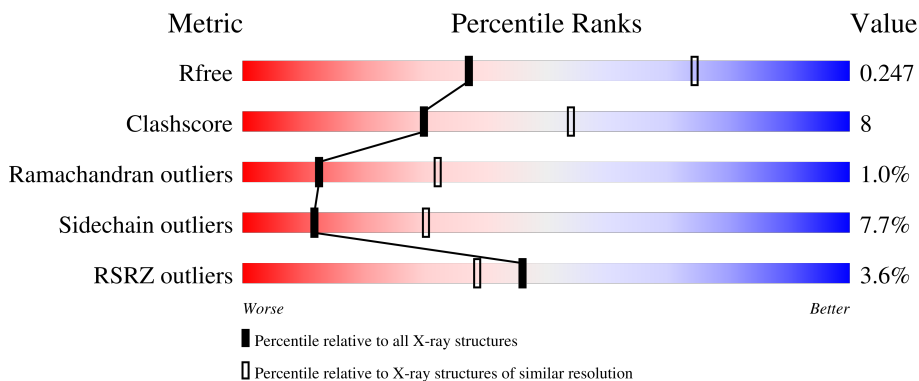
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	549	 3% 75% 18% • 5%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4106 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.

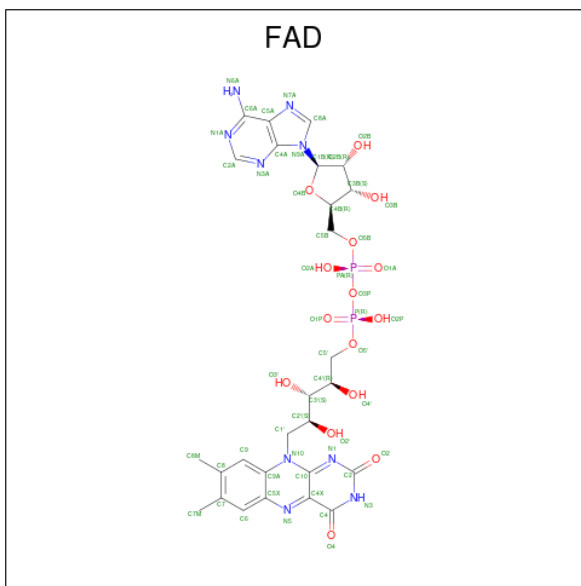
- Molecule 1 is a protein called STEROID MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	523	3982	2525	694	756	7	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	295	ALA	LYS	conflict	UNP O50641

- 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
			Total	C	N	O	P		
3	A	1	48	21	7	17	3	0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O S		
4	A	1	5	4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total	O	0	0
			18	18		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.17Å 82.17Å 228.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.10 – 2.95 58.10 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (58.10-2.95) 99.9 (58.10-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.96Å)	Xtrriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.200 , 0.249 0.198 , 0.247	Depositor DCC
R_{free} test set	890 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4106	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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: SO4, NAP, 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	0.76	0/4082	0.99	5/5563 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	476	GLY	N-CA-C	5.93	120.41	110.56
1	A	498	SER	N-CA-C	5.59	118.13	110.24
1	A	480	THR	CA-C-N	5.23	126.38	119.84
1	A	480	THR	C-N-CA	5.23	126.38	119.84
1	A	43	GLN	N-CA-C	-5.02	106.85	113.17

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	3982	0	3776	67	0
2	A	53	0	31	1	0
3	A	48	0	25	0	0
4	A	5	0	0	1	0
5	A	18	0	0	0	0
All	All	4106	0	3832	67	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 8.

All (67) 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:412:ARG:HH11	1:A:412:ARG:HG3	1.12	1.09
1:A:189:PHE:H	1:A:213:GLN:NE2	1.64	0.93
1:A:413:THR:HB	1:A:416:GLU:HG3	1.49	0.92
1:A:100:GLU:HA	1:A:100:GLU:OE1	1.69	0.90
1:A:472:ARG:HH11	1:A:472:ARG:HG2	1.40	0.86
1:A:189:PHE:H	1:A:213:GLN:HE21	1.21	0.85
1:A:412:ARG:HH11	1:A:412:ARG:CG	1.90	0.84
1:A:222:ARG:HG3	1:A:364:ARG:HH21	1.45	0.81
1:A:412:ARG:HG3	1:A:412:ARG:NH1	1.85	0.79
1:A:532:ILE:O	1:A:536:VAL:HG23	1.92	0.69
1:A:228:ILE:HD13	1:A:343:ILE:HG21	1.76	0.66
1:A:307:ASN:HD21	1:A:338:ILE:H	1.43	0.66
1:A:110:ASP:OD1	1:A:115:ARG:NH2	2.29	0.65
1:A:102:LEU:O	1:A:106:GLU:HG3	1.99	0.62
1:A:159:SER:OG	1:A:395:ASP:HB3	1.99	0.61
1:A:471:ALA:O	1:A:473:GLY:N	2.35	0.59
1:A:472:ARG:HG2	1:A:472:ARG:NH1	2.17	0.59
1:A:116:ARG:HB3	4:A:1551:SO4:O4	2.06	0.56
1:A:228:ILE:CD1	1:A:343:ILE:HG21	2.36	0.56
1:A:86:GLU:HG2	1:A:247:TYR:CE2	2.40	0.56
1:A:63:ASN:ND2	1:A:65:TYR:HE2	2.04	0.56
1:A:402:ASP:O	1:A:415:LYS:NZ	2.40	0.55
1:A:189:PHE:N	1:A:213:GLN:NE2	2.46	0.54
1:A:398:THR:OG1	1:A:399:GLY:N	2.41	0.54
1:A:68:ALA:HA	1:A:205:GLN:NE2	2.24	0.53
1:A:142:ARG:HH11	1:A:142:ARG:HG3	1.74	0.53
1:A:189:PHE:N	1:A:213:GLN:HE21	2.01	0.53
1:A:278:ARG:HG3	1:A:297:PHE:CE2	2.45	0.52
1:A:395:ASP:O	1:A:506:TRP:HZ2	1.94	0.51
1:A:183:PRO:HG2	1:A:187:VAL:CG2	2.40	0.51
1:A:189:PHE:HB2	1:A:213:GLN:HG3	1.92	0.51
1:A:95:TYR:OH	1:A:288:LEU:O	2.30	0.50
1:A:220:PHE:HB3	1:A:363:LEU:HD21	1.94	0.50
1:A:86:GLU:HG2	1:A:247:TYR:CD2	2.48	0.49
1:A:222:ARG:CG	1:A:364:ARG:HH21	2.21	0.49
1:A:412:ARG:CG	1:A:412:ARG:NH1	2.59	0.49
1:A:66:PRO:HD3	1:A:182:TRP:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:TRP:CH2	1:A:318:ILE:HG12	2.48	0.49
1:A:75:ILE:HD11	1:A:250:ARG:CZ	2.43	0.48
1:A:196:VAL:HG22	1:A:389:VAL:HB	1.96	0.48
1:A:58:GLY:HA2	2:A:1001:FAD:O3B	2.14	0.47
1:A:100:GLU:OE1	1:A:100:GLU:CA	2.47	0.47
1:A:439:LEU:O	1:A:458:HIS:ND1	2.46	0.47
1:A:72:VAL:HG12	1:A:77:TYR:HB2	1.96	0.46
1:A:426:LEU:HD13	1:A:533:ILE:HG22	1.96	0.46
1:A:72:VAL:CG1	1:A:77:TYR:HB2	2.45	0.45
1:A:375:GLY:HA3	1:A:383:TYR:O	2.16	0.45
1:A:472:ARG:HH11	1:A:472:ARG:CG	2.20	0.45
1:A:424:THR:HG22	1:A:430:ILE:HG12	1.99	0.44
1:A:472:ARG:HG2	1:A:472:ARG:H	1.55	0.44
1:A:519:PHE:CE2	1:A:521:PRO:HD2	2.53	0.44
1:A:355:ARG:HB2	1:A:358:VAL:HG13	1.99	0.43
1:A:387:MET:HE3	1:A:387:MET:HB2	1.90	0.43
1:A:409:ARG:HG3	1:A:432:GLY:HA2	2.00	0.43
1:A:192:LYS:HD3	1:A:387:MET:HE3	2.00	0.43
1:A:78:SER:C	1:A:452:VAL:HG11	2.44	0.42
1:A:418:TRP:CG	1:A:422:PRO:HA	2.54	0.42
1:A:349:TYR:O	1:A:352:THR:HB	2.19	0.42
1:A:141:ASP:OD1	1:A:141:ASP:C	2.63	0.42
1:A:439:LEU:HD23	1:A:439:LEU:HA	1.86	0.41
1:A:270:ALA:HA	1:A:297:PHE:CD1	2.55	0.41
1:A:367:PRO:O	1:A:378:THR:HA	2.21	0.41
1:A:58:GLY:O	1:A:59:VAL:C	2.64	0.41
1:A:84:GLU:O	1:A:85:LEU:C	2.64	0.41
1:A:95:TYR:H	1:A:232:ASN:HD21	1.69	0.41
1:A:64:ARG:HD2	1:A:184:HIS:CE1	2.56	0.40
1:A:222:ARG:HA	1:A:363:LEU:HB2	2.04	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	520/549 (95%)	493 (95%)	22 (4%)	5 (1%)	12	32

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	471	ALA
1	A	472	ARG
1	A	290	GLY
1	A	399	GLY
1	A	267	PRO

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	392/435 (90%)	362 (92%)	30 (8%)	12	30

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	42	SER
1	A	59	VAL
1	A	92	SER
1	A	100	GLU
1	A	212	GLU
1	A	222	ARG
1	A	228	ILE
1	A	239	THR
1	A	240	ARG
1	A	247	TYR
1	A	264	ARG
1	A	271	LEU
1	A	294	SER

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Mol	Chain	Res	Type
1	A	335	ASP
1	A	341	LYS
1	A	358	VAL
1	A	364	ARG
1	A	365	SER
1	A	392	THR
1	A	404	LEU
1	A	412	ARG
1	A	413	THR
1	A	415	LYS
1	A	472	ARG
1	A	484	VAL
1	A	489	GLU
1	A	498	SER
1	A	523	LEU
1	A	548	GLU

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	63	ASN
1	A	87	GLN
1	A	98	GLN
1	A	160	ASN
1	A	178	HIS
1	A	205	GLN
1	A	213	GLN
1	A	225	ASN
1	A	232	ASN
1	A	307	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FAD	A	1001	-	58,58,58	1.55	10 (17%)	85,89,89	1.54	15 (17%)
3	NAP	A	1002	-	50,52,52	1.45	6 (12%)	71,80,80	1.64	14 (19%)
4	SO4	A	1551	-	4,4,4	0.54	0	6,6,6	0.35	0

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	1001	-	-	7/34/50/50	0/6/6/6
3	NAP	A	1002	-	-	9/35/67/67	0/5/5/5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	FAD	C9A-C5X	5.78	1.50	1.41
3	A	1002	NAP	C5A-C4A	5.27	1.48	1.39
2	A	1001	FAD	C5A-C4A	4.83	1.47	1.39
2	A	1001	FAD	C8-C7	3.98	1.50	1.40
3	A	1002	NAP	PA-O3	3.35	1.63	1.59
3	A	1002	NAP	PN-O3	3.26	1.63	1.59
3	A	1002	NAP	C5A-C6A	3.25	1.50	1.41
3	A	1002	NAP	O4D-C1D	2.81	1.44	1.40
3	A	1002	NAP	C8A-N7A	2.52	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	FAD	C5X-N5	-2.36	1.35	1.39
2	A	1001	FAD	C4A-N9A	-2.34	1.32	1.37
2	A	1001	FAD	C8A-N7A	2.33	1.36	1.31
2	A	1001	FAD	C5A-C6A	2.19	1.47	1.41
2	A	1001	FAD	C4-N3	-2.14	1.34	1.38
2	A	1001	FAD	C10-N10	2.08	1.41	1.37
2	A	1001	FAD	C5A-N7A	-2.02	1.35	1.39

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1002	NAP	C5A-C4A-N3A	-5.38	119.31	126.72
3	A	1002	NAP	N3A-C4A-N9A	4.46	134.76	127.17
2	A	1001	FAD	C5A-C4A-N3A	-4.16	120.99	126.72
2	A	1001	FAD	N3A-C4A-N9A	3.86	133.74	127.17
2	A	1001	FAD	C4A-N9A-C8A	3.81	109.74	105.74
3	A	1002	NAP	C4A-C5A-N7A	-3.75	106.30	110.58
3	A	1002	NAP	C2A-N3A-C4A	3.56	120.53	111.83
3	A	1002	NAP	C4A-N9A-C8A	3.42	109.33	105.74
2	A	1001	FAD	N3A-C2A-N1A	-3.20	123.74	128.58
3	A	1002	NAP	N3A-C2A-N1A	-3.15	123.81	128.58
3	A	1002	NAP	C4D-O4D-C1D	2.98	112.66	109.92
3	A	1002	NAP	O4B-C1B-N9A	2.97	113.79	108.09
2	A	1001	FAD	C2A-N3A-C4A	2.95	119.04	111.83
3	A	1002	NAP	C5A-N7A-C8A	2.86	107.94	103.45
2	A	1001	FAD	O4-C4-C4X	-2.78	119.19	126.53
2	A	1001	FAD	O2B-C2B-C1B	-2.73	100.72	110.10
2	A	1001	FAD	N9A-C8A-N7A	-2.65	110.17	113.94
2	A	1001	FAD	O4B-C1B-N9A	2.61	113.10	108.09
2	A	1001	FAD	C4X-C10-N1	-2.59	118.24	124.59
3	A	1002	NAP	C6A-C5A-N7A	2.56	137.02	132.09
2	A	1001	FAD	C4A-C5A-N7A	-2.48	107.75	110.58
3	A	1002	NAP	C6N-N1N-C2N	-2.43	119.81	121.88
3	A	1002	NAP	N9A-C8A-N7A	-2.42	110.50	113.94
3	A	1002	NAP	O7N-C7N-N7N	-2.37	119.20	122.62
2	A	1001	FAD	C10-N1-C2	2.33	121.88	116.85
2	A	1001	FAD	C5A-N7A-C8A	2.31	107.08	103.45
2	A	1001	FAD	C6A-C5A-N7A	2.11	136.16	132.09
2	A	1001	FAD	C4X-C4-N3	2.09	118.58	113.25
3	A	1002	NAP	C2D-C3D-C4D	2.06	106.58	102.61

There are no chirality outliers.

All (16) torsion outliers are listed below:

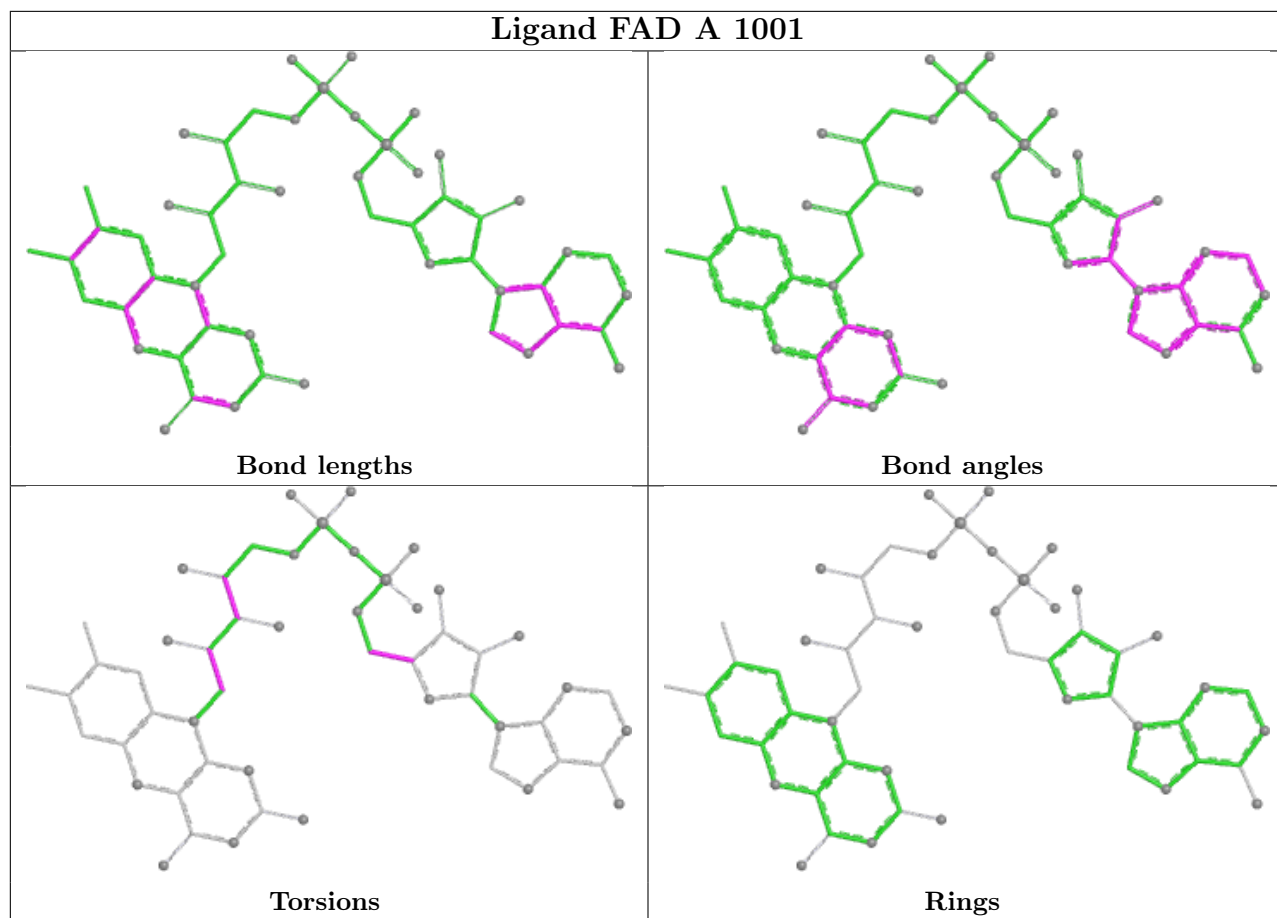
Mol	Chain	Res	Type	Atoms
2	A	1001	FAD	N10-C1'-C2'-O2'
2	A	1001	FAD	N10-C1'-C2'-C3'
2	A	1001	FAD	C2'-C3'-C4'-C5'
2	A	1001	FAD	O3'-C3'-C4'-C5'
3	A	1002	NAP	C5B-O5B-PA-O2A
3	A	1002	NAP	C5B-O5B-PA-O3
3	A	1002	NAP	C5D-O5D-PN-O3
3	A	1002	NAP	C5D-O5D-PN-O1N
3	A	1002	NAP	C5D-O5D-PN-O2N
2	A	1001	FAD	O3'-C3'-C4'-O4'
2	A	1001	FAD	C2'-C3'-C4'-O4'
3	A	1002	NAP	C5B-O5B-PA-O1A
3	A	1002	NAP	O4B-C4B-C5B-O5B
3	A	1002	NAP	PA-O3-PN-O1N
2	A	1001	FAD	O4B-C4B-C5B-O5B
3	A	1002	NAP	PA-O3-PN-O2N

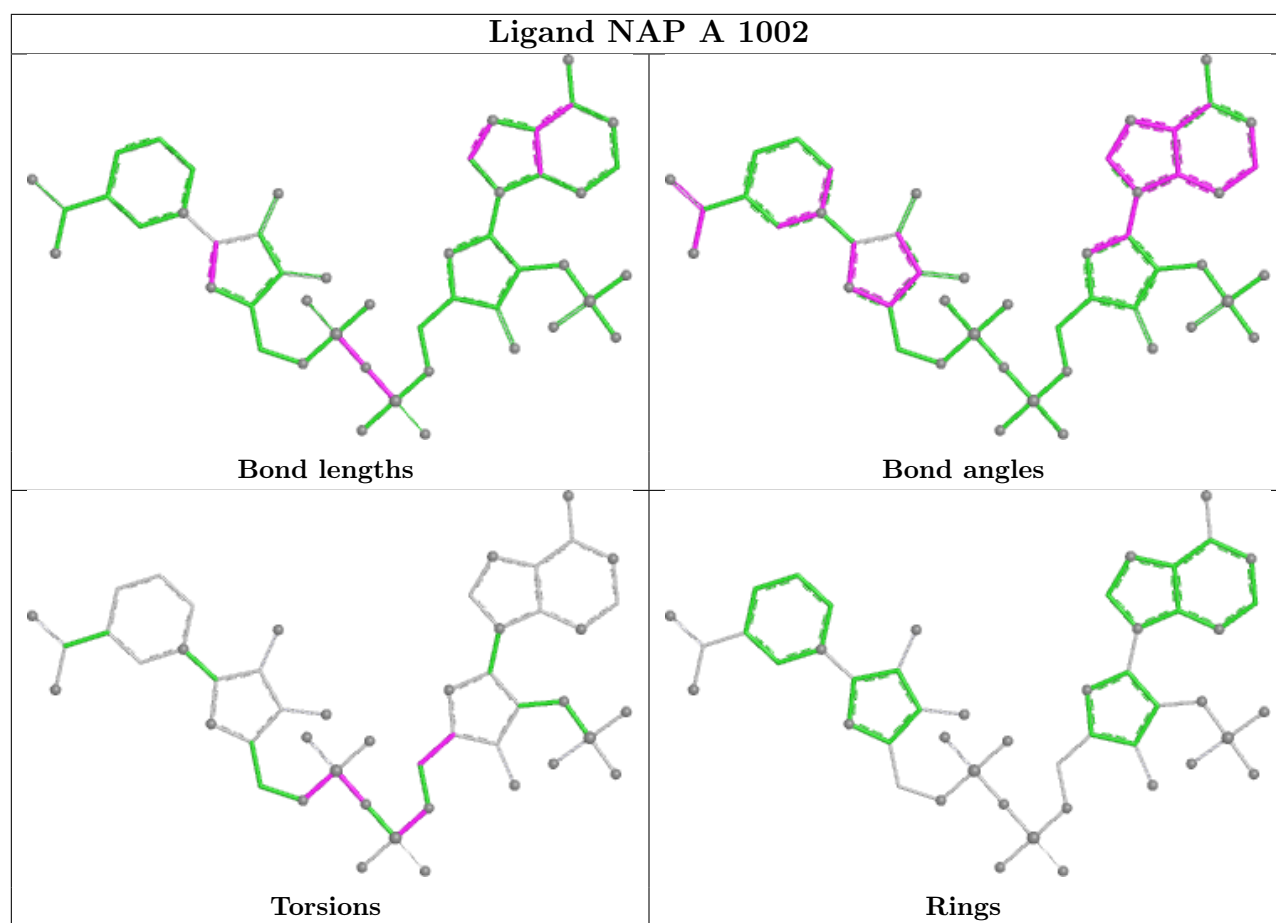
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	FAD	1	0
4	A	1551	SO4	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	523/549 (95%)	-0.05	19 (3%) 46 38	30, 55, 117, 170	1 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	233	VAL	6.1
1	A	510	ALA	4.5
1	A	268	LYS	4.0
1	A	504	ASN	3.2
1	A	271	LEU	3.2
1	A	276	GLU	3.1
1	A	396	ALA	3.0
1	A	234	PRO	3.0
1	A	273	VAL	3.0
1	A	100	GLU	2.7
1	A	272	GLU	2.5
1	A	395	ASP	2.4
1	A	292	LEU	2.3
1	A	242	GLU	2.2
1	A	503	ALA	2.2
1	A	232	ASN	2.2
1	A	274	SER	2.1
1	A	316	GLU	2.1
1	A	398	THR	2.1

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](#)

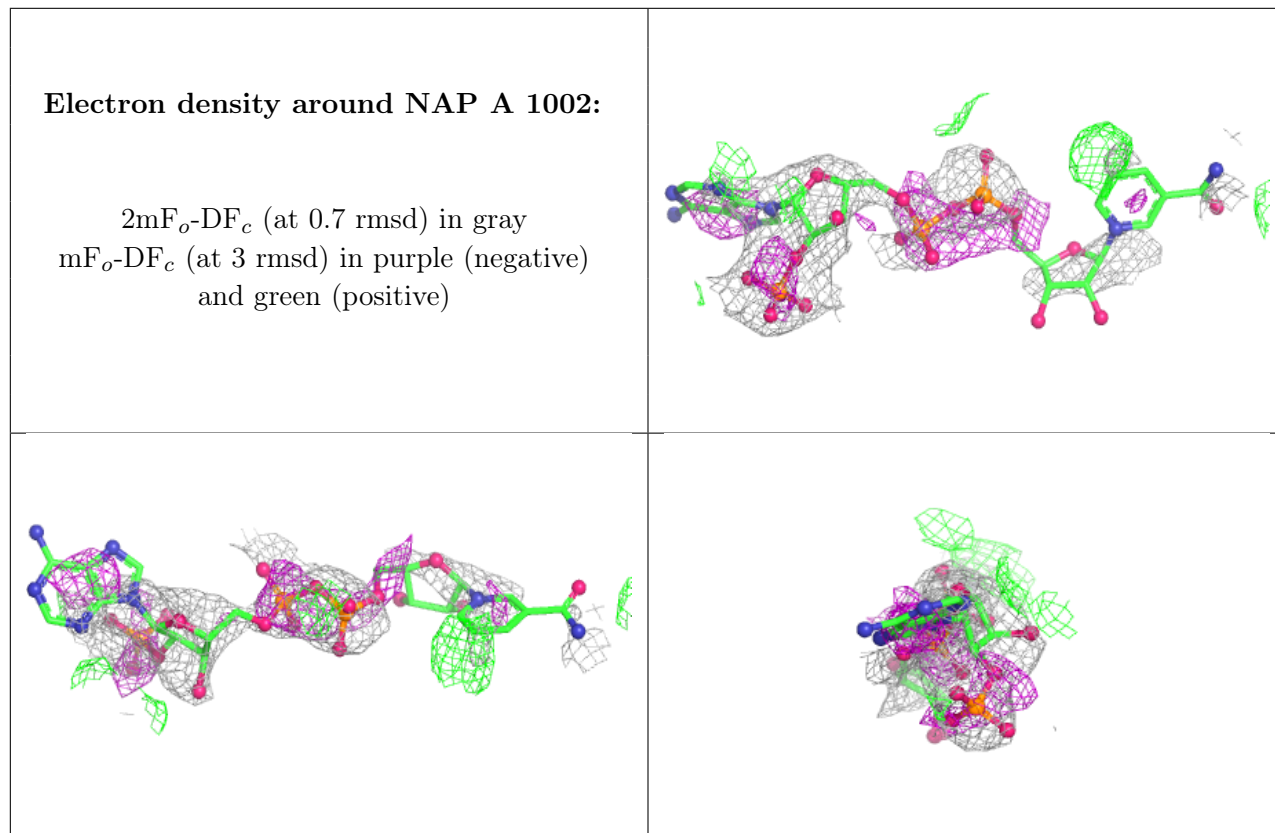
There are no oligosaccharides in this entry.

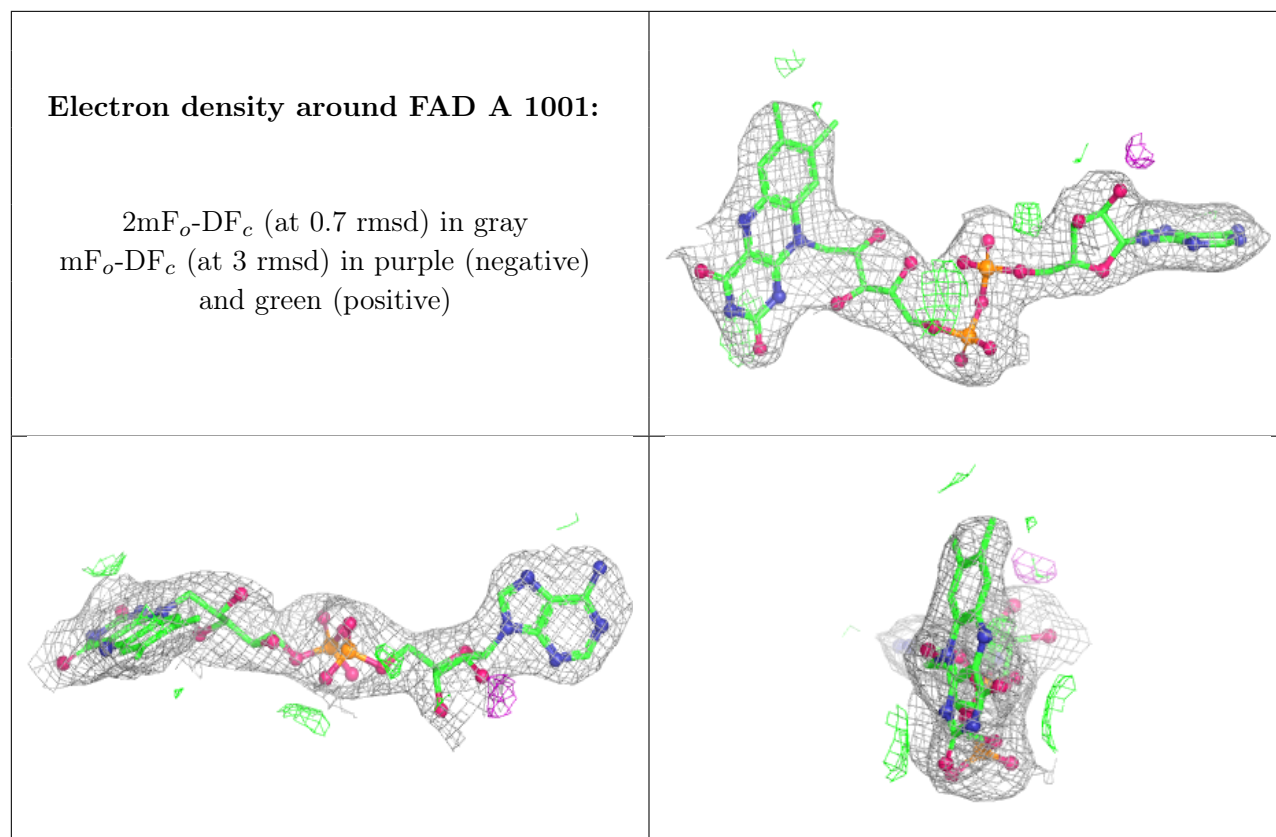
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	NAP	A	1002	48/48	0.68	0.23	91,125,154,157	0
4	SO4	A	1551	5/5	0.96	0.12	56,59,60,65	0
2	FAD	A	1001	53/53	0.98	0.06	26,33,50,52	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.