



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 02:40 pm BST

PDB ID : 3GWD
Title : Closed crystal structure of cyclohexanone monooxygenase
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Deposited on : 2009-03-31
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 : 2.11
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) : 2.11

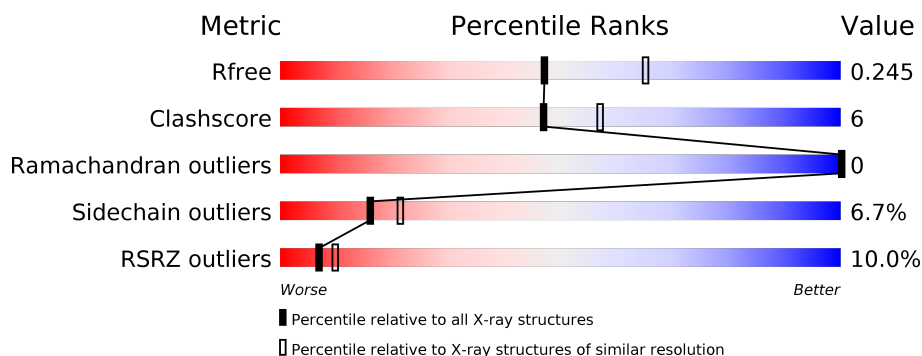
1 Overall quality at a glance

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 on 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	540	<div> <div>10%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4454 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.

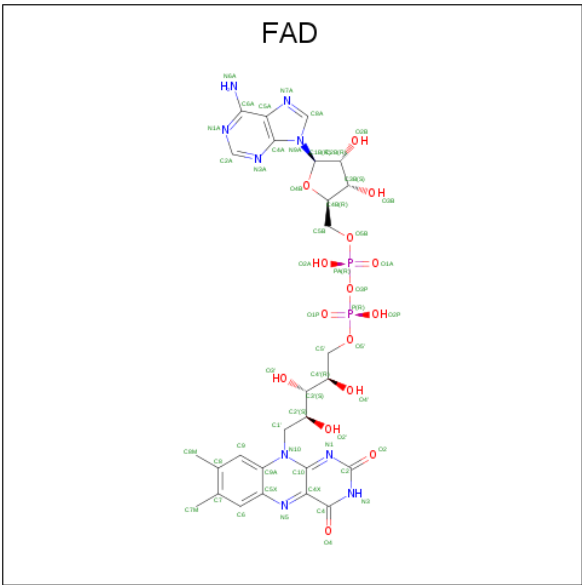
- Molecule 1 is a protein called Cyclohexanone monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	531	4178	2660	709	801	8	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

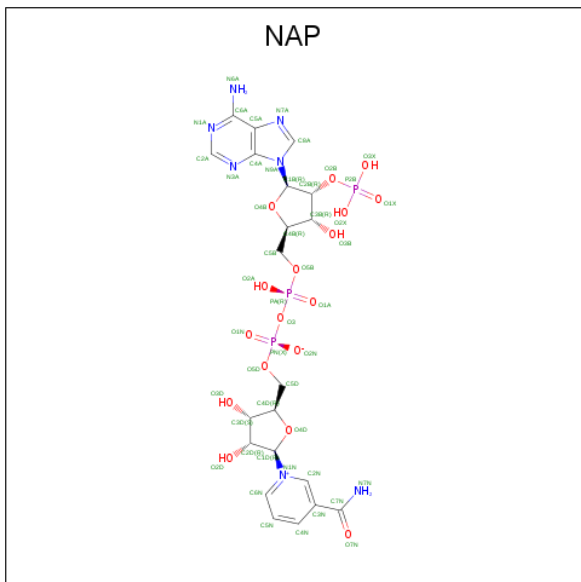
Chain	Residue	Modelled	Actual	Comment	Reference
A	6	THR	ILE	CONFLICT	UNP Q6RXW1
A	81	THR	SER	CONFLICT	UNP Q6RXW1
A	223	ASN	THR	CONFLICT	UNP Q6RXW1
A	323	LYS	THR	CONFLICT	UNP Q6RXW1

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	A	1	Total 26	C 11	N 2	O 11	P 2	0	0

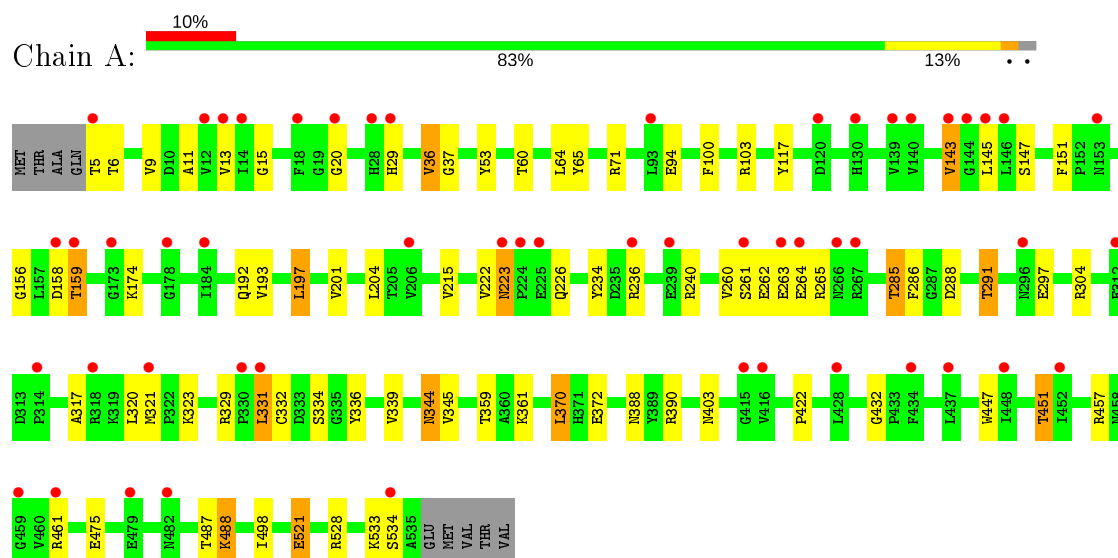
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	149	Total O 149 149	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Cyclohexanone monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.48 Å 90.99 Å 100.41 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.53 – 2.30 26.53 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.9 (26.53-2.30) 99.6 (26.53-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 2.29 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.183 , 0.245 0.182 , 0.245	Depositor DCC
R_{free} test set	2644 reflections (10.07%)	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4454	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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: 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	0.71	4/4292 (0.1%)	0.68	0/5848

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	263	GLU	CD-OE2	16.64	1.44	1.25
1	A	264	GLU	CD-OE1	10.06	1.36	1.25
1	A	264	GLU	CD-OE2	9.11	1.35	1.25
1	A	264	GLU	CG-CD	8.01	1.64	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	4178	0	4000	51	0
2	A	53	0	31	3	0
3	A	74	0	39	3	0
4	A	149	0	0	2	0
All	All	4454	0	4070	52	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 6.

All (52) 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:147:SER:HB2	3:A:543:NAP:N7N	1.97	0.79
1:A:475:GLU:HG3	4:A:693:HOH:O	1.82	0.77
1:A:297:GLU:OE2	1:A:304:ARG:NH2	2.23	0.70
1:A:344:ASN:ND2	1:A:345:VAL:HG23	2.07	0.69
1:A:336:TYR:O	1:A:339:VAL:HG22	1.92	0.69
1:A:94:GLU:OE1	1:A:103:ARG:NH2	2.26	0.68
1:A:156:GLY:O	1:A:159:THR:HB	1.97	0.64
1:A:236:ARG:HE	1:A:240:ARG:HH12	1.45	0.63
1:A:260:VAL:HG22	1:A:261:SER:H	1.65	0.62
1:A:53:TYR:OH	1:A:192:GLN:NE2	2.34	0.60
1:A:344:ASN:HD22	1:A:344:ASN:C	2.05	0.59
1:A:223:ASN:ND2	1:A:226:GLN:H	2.00	0.59
1:A:215:VAL:O	1:A:332:CYS:HA	2.02	0.59
1:A:223:ASN:HD22	1:A:226:GLN:H	1.52	0.58
1:A:390:ARG:HH11	1:A:403:ASN:HD22	1.52	0.57
1:A:236:ARG:NE	1:A:240:ARG:HH12	2.02	0.57
2:A:541:FAD:HM73	3:A:542:NAP:C5N	2.35	0.56
1:A:223:ASN:HD22	1:A:223:ASN:C	2.11	0.54
1:A:447:TRP:CZ3	1:A:451:THR:HG21	2.42	0.54
1:A:329:ARG:O	1:A:331:LEU:HD13	2.08	0.52
1:A:390:ARG:HH11	1:A:403:ASN:ND2	2.07	0.52
1:A:222:VAL:HG13	1:A:226:GLN:HB3	1.92	0.51
1:A:147:SER:OG	1:A:388:ASN:ND2	2.45	0.50
1:A:262:GLU:OE1	1:A:265:ARG:NH1	2.45	0.49
1:A:9:VAL:HG11	1:A:36:VAL:HG23	1.95	0.49
1:A:432:GLY:HA3	4:A:593:HOH:O	2.13	0.48
1:A:288:ASP:HB2	1:A:291:THR:HG22	1.96	0.47
1:A:317:ALA:O	1:A:321[A]:MET:HG2	2.13	0.47
1:A:461:ARG:NH1	1:A:534:SER:O	2.47	0.47
1:A:60:THR:HB	1:A:65:TYR:HB2	1.97	0.46
1:A:143:VAL:HG22	2:A:541:FAD:C8A	2.46	0.46
1:A:15:GLY:O	1:A:20:GLY:HA3	2.15	0.46
1:A:521:GLU:OE2	1:A:528:ARG:NH1	2.41	0.46
1:A:204:LEU:HB3	1:A:345:VAL:HG22	1.98	0.45
1:A:447:TRP:O	1:A:451:THR:CG2	2.65	0.44
1:A:461:ARG:NH2	1:A:533:LYS:HE2	2.32	0.44
1:A:370:LEU:HD13	1:A:372:GLU:HG2	1.99	0.44
1:A:344:ASN:HD21	1:A:345:VAL:HG23	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:HIS:HE1	1:A:100:PHE:O	2.01	0.43
1:A:147:SER:HB2	3:A:543:NAP:H72N	1.77	0.43
1:A:344:ASN:ND2	1:A:344:ASN:C	2.71	0.43
1:A:143:VAL:HG22	2:A:541:FAD:N7A	2.34	0.43
1:A:285:THR:CG2	1:A:286:PHE:N	2.83	0.42
1:A:117:TYR:CZ	1:A:422:PRO:HG2	2.55	0.42
1:A:13:VAL:O	1:A:37:GLY:HA2	2.21	0.41
1:A:260:VAL:HG22	1:A:261:SER:N	2.34	0.41
1:A:288:ASP:HA	1:A:291:THR:HG22	2.02	0.41
1:A:193:VAL:HG22	1:A:197:LEU:HD22	2.01	0.41
1:A:9:VAL:HG12	1:A:11:ALA:H	1.86	0.41
1:A:390:ARG:CG	1:A:403:ASN:HD21	2.33	0.41
1:A:487:THR:HG23	1:A:488:LYS:HG2	2.02	0.40
1:A:159:THR:HG22	1:A:359:THR:C	2.42	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	530/540 (98%)	514 (97%)	16 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	435/442 (98%)	406 (93%)	29 (7%)	16	21

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	6	THR
1	A	36	VAL
1	A	64	LEU
1	A	71	ARG
1	A	143	VAL
1	A	145	LEU
1	A	151	PHE
1	A	158	ASP
1	A	159	THR
1	A	174	LYS
1	A	197	LEU
1	A	201	VAL
1	A	223	ASN
1	A	234	TYR
1	A	285	THR
1	A	291	THR
1	A	320	LEU
1	A	323	LYS
1	A	331	LEU
1	A	334	SER
1	A	344	ASN
1	A	361	LYS
1	A	370	LEU
1	A	451	THR
1	A	457	ARG
1	A	488	LYS
1	A	498	ILE
1	A	521	GLU

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

Mol	Chain	Res	Type
1	A	51	ASN
1	A	141	ASN
1	A	192	GLN
1	A	223	ASN

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Mol	Chain	Res	Type
1	A	353	ASN
1	A	388	ASN
1	A	403	ASN
1	A	431	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 carbohydrates 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	541	-	51,58,58	1.42	6 (11%)	60,89,89	1.48	7 (11%)
3	NAP	A	543	-	24,27,52	2.02	1 (4%)	34,41,80	0.98	2 (5%)
3	NAP	A	542	-	45,52,52	1.65	4 (8%)	56,80,80	1.21	5 (8%)

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	541	-	-	6/30/50/50	0/6/6/6
3	NAP	A	543	-	-	0/20/36/67	0/2/2/5
3	NAP	A	542	-	-	1/31/67/67	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	543	NAP	O7N-C7N	8.91	1.41	1.24
3	A	542	NAP	O7N-C7N	8.43	1.40	1.24
2	A	541	FAD	C4X-N5	5.24	1.40	1.33
2	A	541	FAD	C10-N1	4.17	1.38	1.33
3	A	542	NAP	C2A-N3A	3.67	1.38	1.32
2	A	541	FAD	C4-N3	3.36	1.38	1.33
2	A	541	FAD	C2A-N3A	3.09	1.37	1.32
3	A	542	NAP	C2N-N1N	2.75	1.38	1.35
2	A	541	FAD	C2A-N1A	2.44	1.38	1.33
2	A	541	FAD	C1'-N10	2.32	1.50	1.48
3	A	542	NAP	C2A-N1A	2.03	1.37	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	541	FAD	N3A-C2A-N1A	-5.89	119.48	128.68
3	A	542	NAP	N3A-C2A-N1A	-5.20	120.54	128.68
2	A	541	FAD	C4-N3-C2	4.34	118.81	115.14
3	A	542	NAP	C3N-C7N-N7N	4.05	122.61	117.75
2	A	541	FAD	C5X-C9A-N10	3.48	120.24	117.72
2	A	541	FAD	C4X-N5-C5X	3.17	119.94	116.77
3	A	543	NAP	PN-O3-PA	-2.74	123.41	132.83
3	A	542	NAP	O7N-C7N-C3N	-2.38	116.78	119.63
3	A	542	NAP	PN-O3-PA	-2.36	124.72	132.83
3	A	543	NAP	O2A-PA-O3	2.35	112.53	104.64
3	A	542	NAP	O3X-P2B-O2B	2.24	116.01	105.99
2	A	541	FAD	C4-C4X-N5	2.15	121.06	118.60
2	A	541	FAD	P-O3P-PA	-2.11	125.59	132.83
2	A	541	FAD	C1'-N10-C10	2.06	120.25	118.41

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	541	FAD	N10-C1'-C2'-O2'

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Mol	Chain	Res	Type	Atoms
2	A	541	FAD	N10-C1'-C2'-C3'
2	A	541	FAD	O4B-C4B-C5B-O5B
2	A	541	FAD	O3'-C3'-C4'-C5'
2	A	541	FAD	C3B-C4B-C5B-O5B
2	A	541	FAD	O3'-C3'-C4'-O4'
3	A	542	NAP	O4B-C4B-C5B-O5B

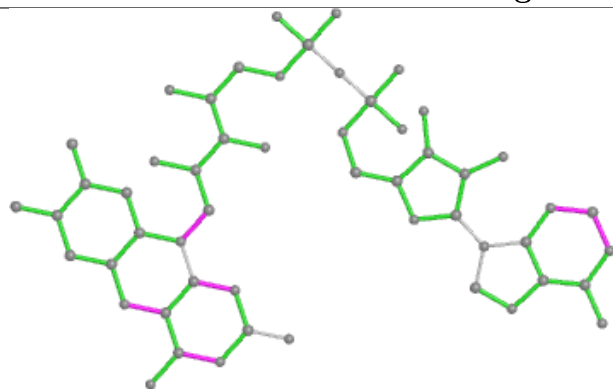
There are no ring outliers.

3 monomers are involved in 5 short contacts:

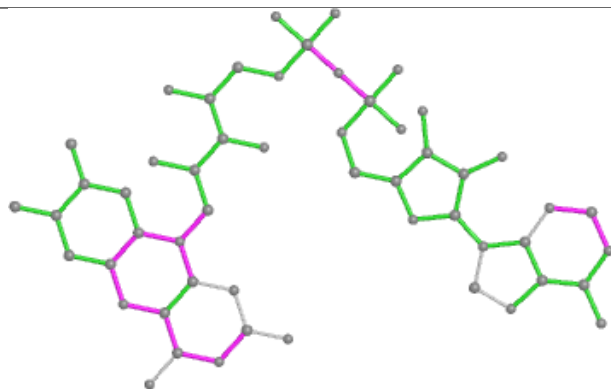
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	541	FAD	3	0
3	A	543	NAP	2	0
3	A	542	NAP	1	0

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.

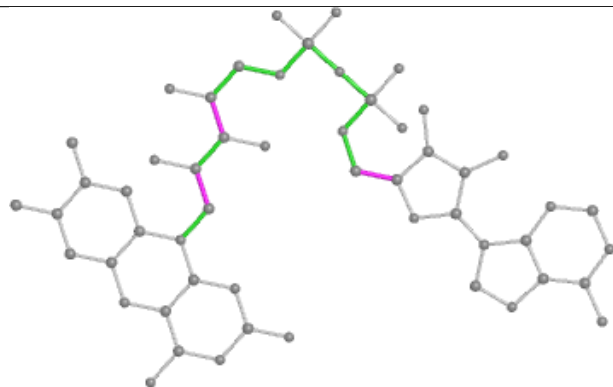
Ligand FAD A 541



Bond lengths



Bond angles

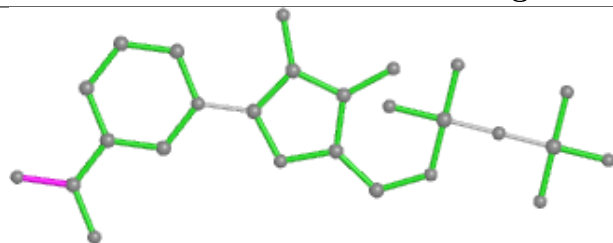


Torsions

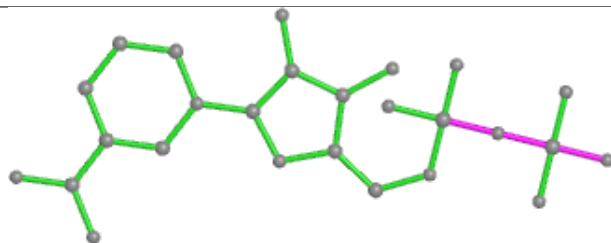


Rings

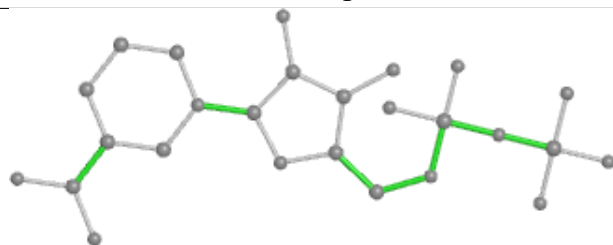
Ligand NAP A 543



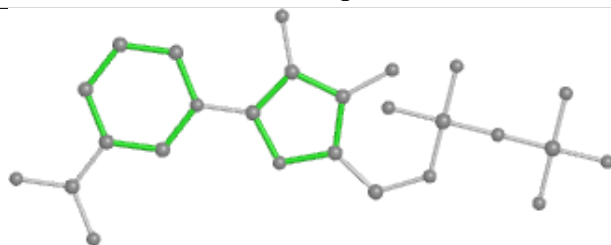
Bond lengths



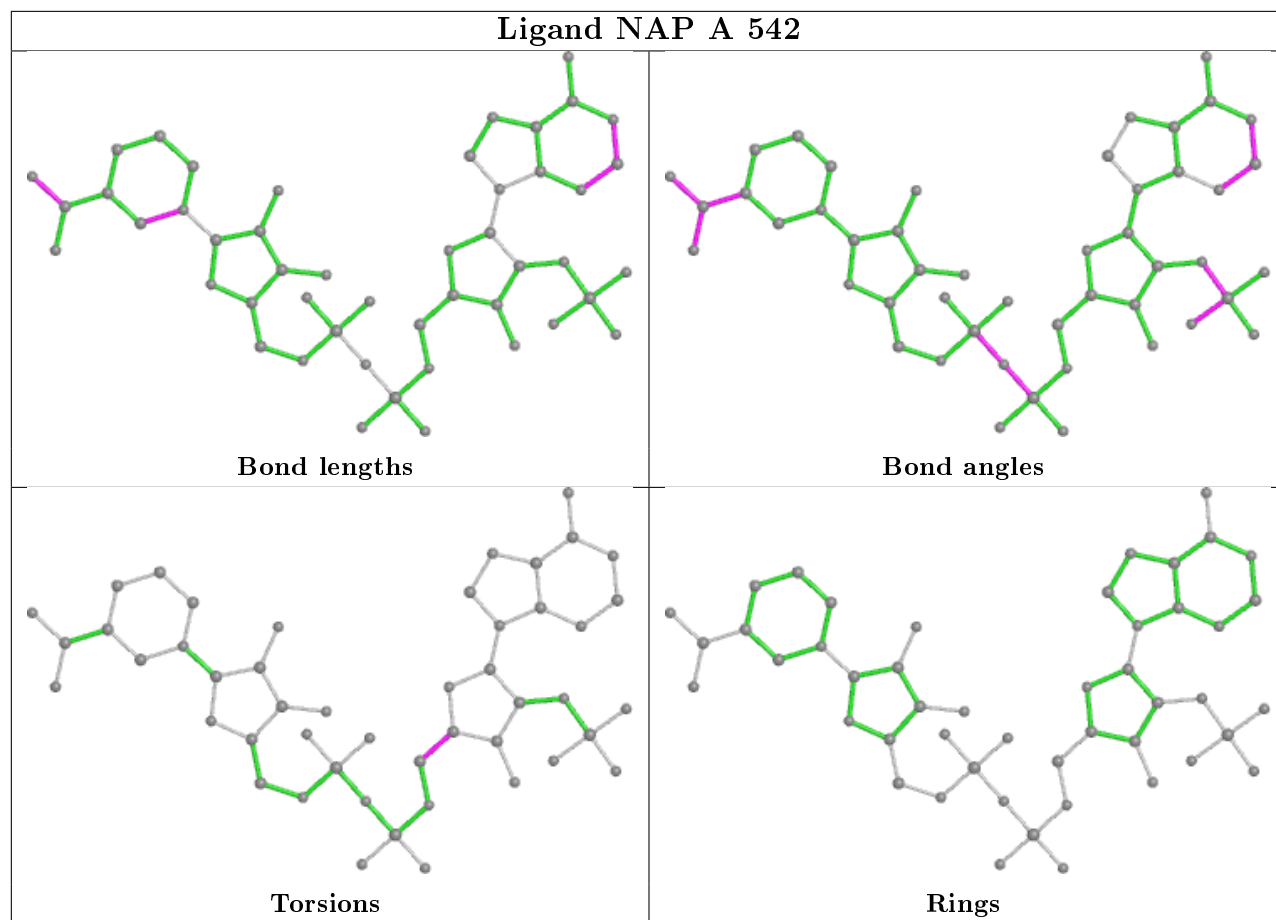
Bond angles



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	531/540 (98%)	0.56	53 (9%) 7 10	34, 44, 52, 61	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	158	ASP	5.0
1	A	263	GLU	4.9
1	A	143	VAL	4.8
1	A	261	SER	4.3
1	A	13	VAL	3.9
1	A	140	VAL	3.9
1	A	139	VAL	3.9
1	A	12	VAL	3.8
1	A	145	LEU	3.8
1	A	224	PRO	3.7
1	A	130	HIS	3.7
1	A	144	GLY	3.5
1	A	437	LEU	3.3
1	A	18	PHE	3.3
1	A	225	GLU	3.2
1	A	5	THR	3.2
1	A	312	GLU	3.2
1	A	236	ARG	3.1
1	A	461	ARG	3.0
1	A	29	HIS	2.9
1	A	479	GLU	2.9
1	A	14	ILE	2.9
1	A	318	ARG	2.9
1	A	452	ILE	2.8
1	A	314	PRO	2.7
1	A	428	LEU	2.7
1	A	223	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	146	LEU	2.7
1	A	159	THR	2.7
1	A	331	LEU	2.6
1	A	321[A]	MET	2.6
1	A	173	GLY	2.5
1	A	434	PHE	2.5
1	A	266	ASN	2.4
1	A	153	ASN	2.4
1	A	448	ILE	2.3
1	A	459	GLY	2.3
1	A	534	SER	2.3
1	A	296	ASN	2.3
1	A	482	ASN	2.3
1	A	264	GLU	2.3
1	A	239	GLU	2.3
1	A	416	VAL	2.3
1	A	415	GLY	2.2
1	A	267	ARG	2.1
1	A	184	ILE	2.1
1	A	93	LEU	2.1
1	A	330	PRO	2.1
1	A	120	ASP	2.1
1	A	178	GLY	2.1
1	A	28	HIS	2.0
1	A	206	VAL	2.0
1	A	20	GLY	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 [\(i\)](#)

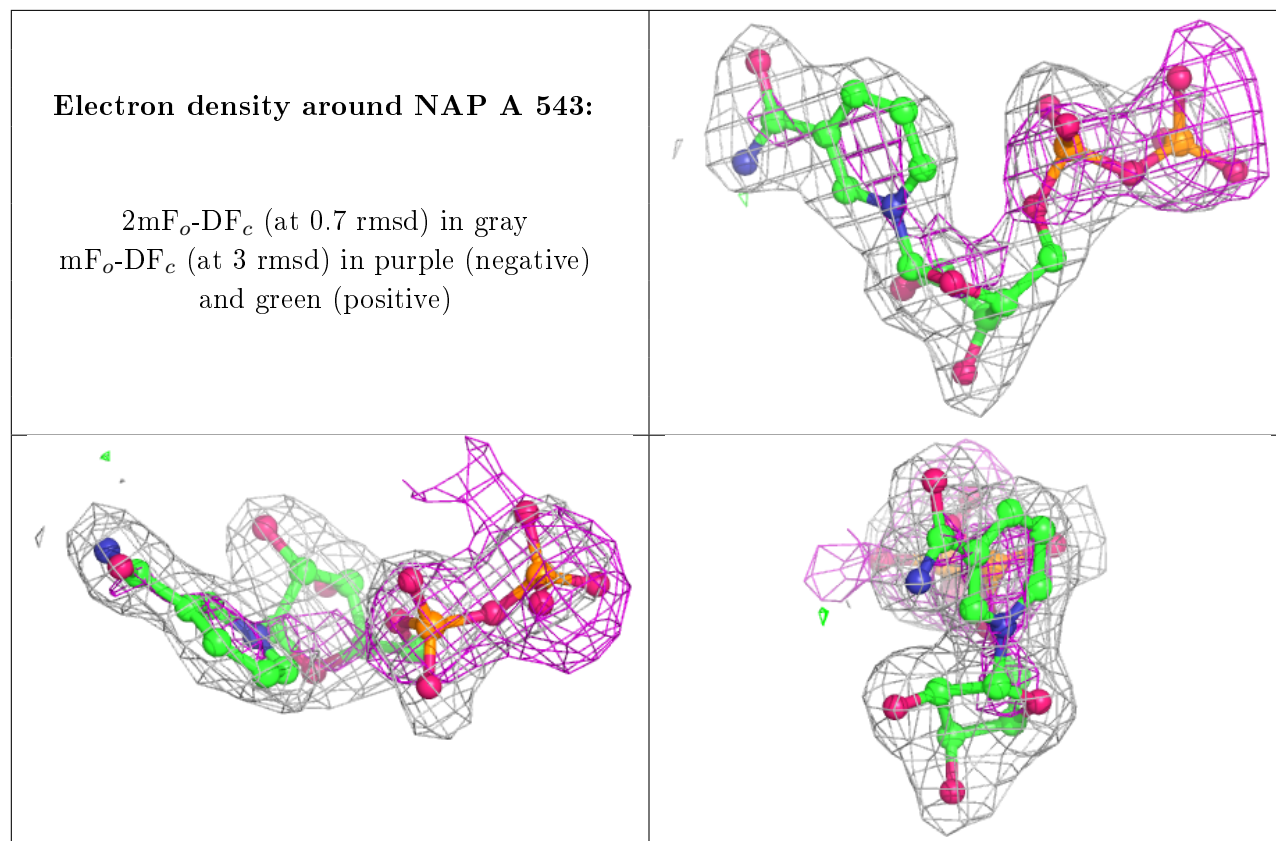
There are no carbohydrates in this entry.

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.

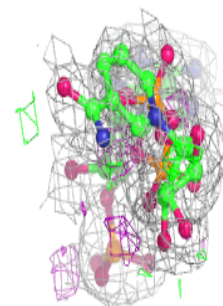
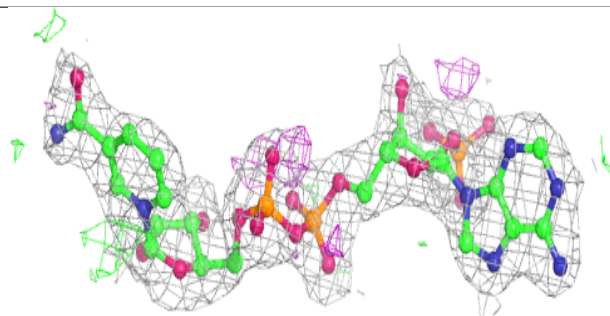
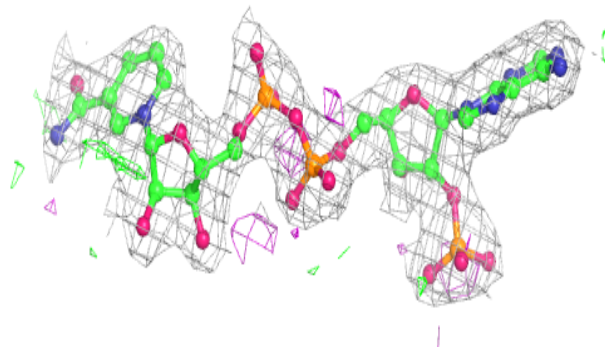
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAP	A	543	26/48	0.87	0.28	33,42,63,65	0
3	NAP	A	542	48/48	0.92	0.21	17,26,29,30	0
2	FAD	A	541	53/53	0.95	0.18	22,28,29,31	0

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.

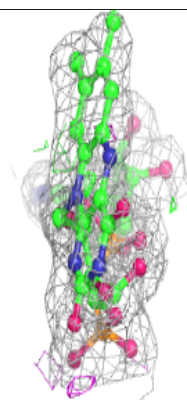
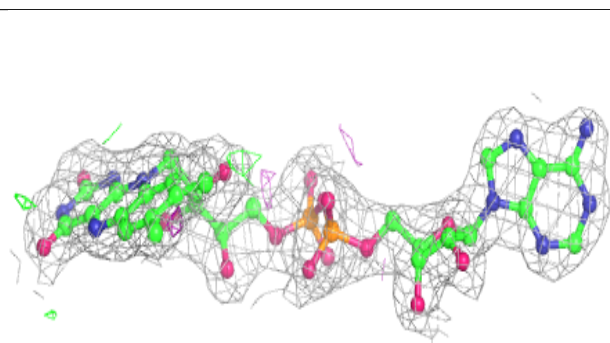
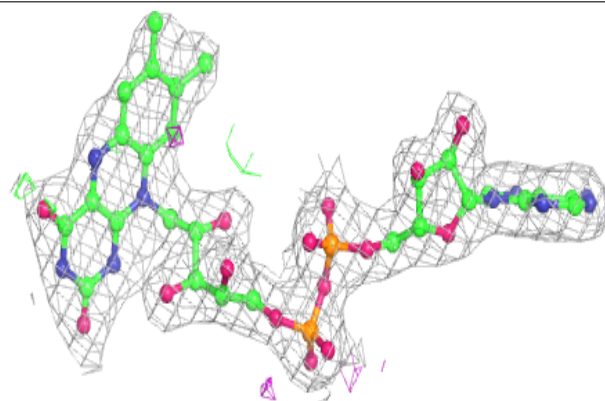


Electron density around NAP A 542:

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

**Electron density around FAD A 541:**

$2mF_o-DF_c$ (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.