



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 12:23 am BST

PDB ID : 3CGC
Title : Pyridine Nucleotide Complexes with Bacillus anthracis Coenzyme A-Disulfide Reductase: A Structural Analysis of Dual NAD(P)H Specificity
Authors : Wallen, J.R.
Deposited on : 2008-03-05
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

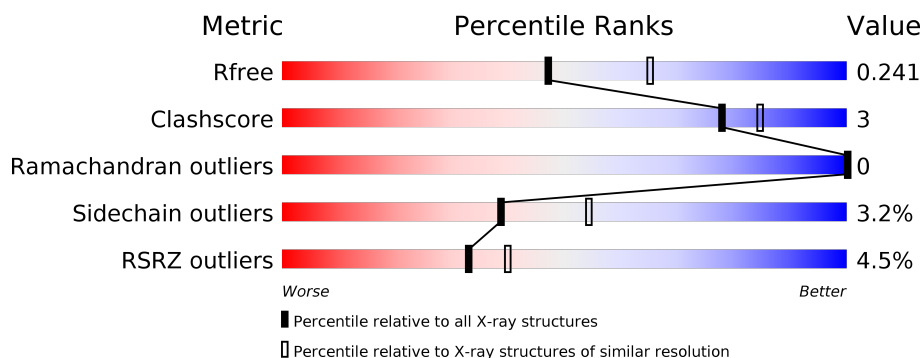
1 Overall quality at a glance

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	480	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>8%</div> <div>8%</div> </div> </div>
1	B	480	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>6%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7640 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 Pyridine nucleotide-disulfide oxidoreductase, class I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	2	0
			3490	2204	603	668	15			
1	B	444	Total	C	N	O	S	0	1	0
			3484	2200	602	667	15			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-34	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-33	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-32	SER	-	EXPRESSION TAG	UNP Q81TK8
A	-31	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-30	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-29	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-28	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-27	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-26	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-25	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-24	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-23	ALA	-	EXPRESSION TAG	UNP Q81TK8
A	-22	SER	-	EXPRESSION TAG	UNP Q81TK8
A	-21	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-20	THR	-	EXPRESSION TAG	UNP Q81TK8
A	-19	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-18	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-17	GLN	-	EXPRESSION TAG	UNP Q81TK8
A	-16	GLN	-	EXPRESSION TAG	UNP Q81TK8
A	-15	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-14	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-13	ARG	-	EXPRESSION TAG	UNP Q81TK8
A	-12	THR	-	EXPRESSION TAG	UNP Q81TK8
A	-11	LEU	-	EXPRESSION TAG	UNP Q81TK8

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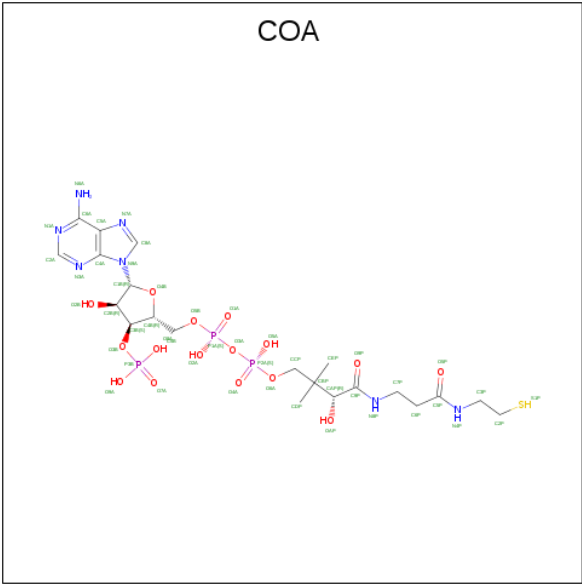
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	TYR	-	EXPRESSION TAG	UNP Q81TK8
A	-9	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-8	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-7	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-6	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-5	LYS	-	EXPRESSION TAG	UNP Q81TK8
A	-4	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-3	ARG	-	EXPRESSION TAG	UNP Q81TK8
A	-2	TRP	-	EXPRESSION TAG	UNP Q81TK8
A	-1	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	0	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-35	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-34	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-33	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-32	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-31	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-30	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-29	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-28	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-27	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-26	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-25	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-24	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-23	ALA	-	EXPRESSION TAG	UNP Q81TK8
B	-22	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-21	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-20	THR	-	EXPRESSION TAG	UNP Q81TK8
B	-19	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-18	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-17	GLN	-	EXPRESSION TAG	UNP Q81TK8
B	-16	GLN	-	EXPRESSION TAG	UNP Q81TK8
B	-15	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-14	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-13	ARG	-	EXPRESSION TAG	UNP Q81TK8
B	-12	THR	-	EXPRESSION TAG	UNP Q81TK8
B	-11	LEU	-	EXPRESSION TAG	UNP Q81TK8
B	-10	TYR	-	EXPRESSION TAG	UNP Q81TK8
B	-9	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-8	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-7	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-6	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-5	LYS	-	EXPRESSION TAG	UNP Q81TK8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-3	ARG	-	EXPRESSION TAG	UNP Q81TK8
B	-2	TRP	-	EXPRESSION TAG	UNP Q81TK8
B	-1	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	0	SER	-	EXPRESSION TAG	UNP Q81TK8

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	1
			59	23	7	23	5	1		
2	B	1	Total	C	N	O	P	S	0	1
			59	23	7	23	5	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

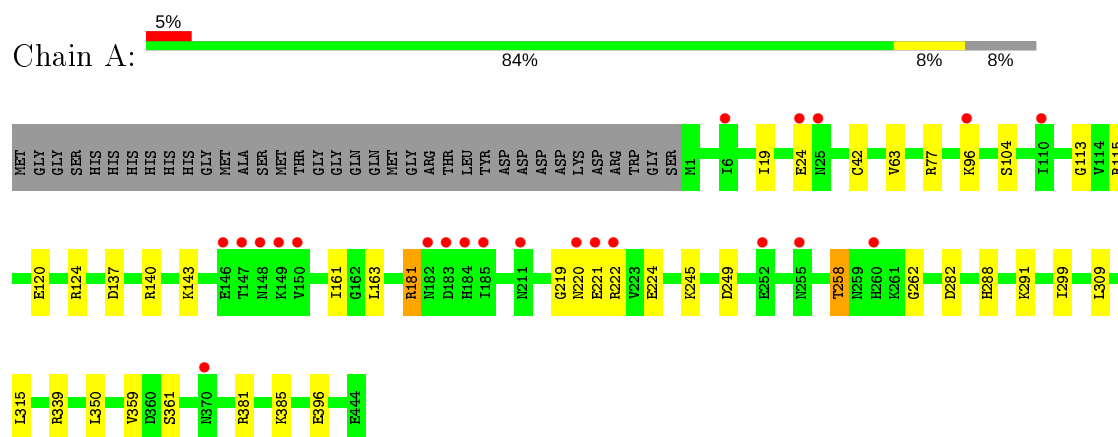
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	214	Total	O	0	0
			214	214		
4	B	228	Total	O	0	0
			228	228		

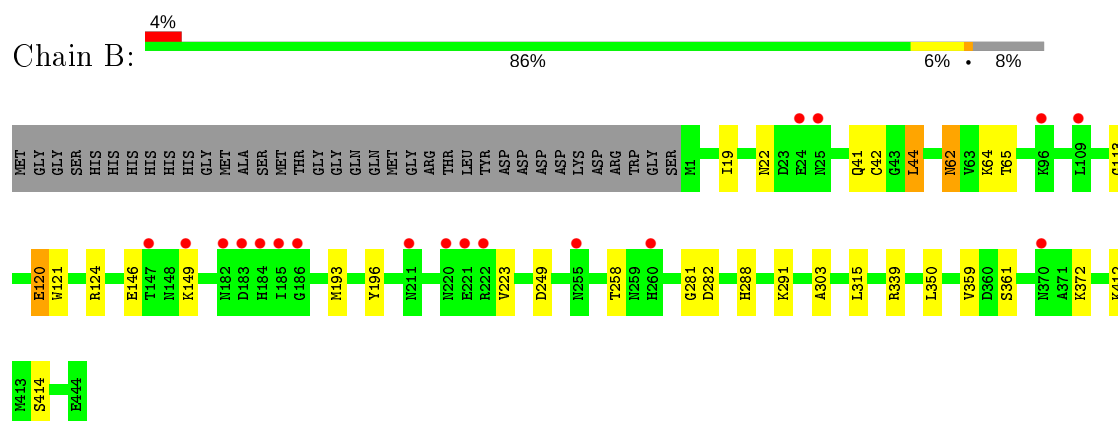
3 Residue-property plots [i](#)

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: Pyridine nucleotide-disulfide oxidoreductase, class I



- Molecule 1: Pyridine nucleotide-disulfide oxidoreductase, class I



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.53Å 81.74Å 98.37Å 90.00° 103.97° 90.00°	Depositor
Resolution (Å)	25.11 – 2.30 25.11 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.11-2.30) 99.9 (25.11-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.54 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.192 , 0.237 0.194 , 0.241	Depositor DCC
R_{free} test set	2949 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7640	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: COA, 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	0.40	0/3554	0.54	0/4800
1	B	0.40	0/3545	0.55	0/4788
All	All	0.40	0/7099	0.54	0/9588

There are no bond length outliers.

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	3490	0	3521	23	0
1	B	3484	0	3512	17	0
2	A	59	0	22	0	0
2	B	59	0	22	0	0
3	A	53	0	31	4	0
3	B	53	0	31	2	0
4	A	214	0	0	1	0
4	B	228	0	0	0	0
All	All	7640	0	7139	40	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 (40) 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:181:ARG:H	1:A:181:ARG:HE	1.07	1.01
1:A:181:ARG:H	1:A:181:ARG:NE	1.84	0.75
1:B:193:MET:HE2	1:B:193:MET:HA	1.68	0.74
1:A:258:THR:HG23	1:A:262:GLY:HA2	1.77	0.66
1:B:120:GLU:HA	1:B:124:ARG:HD2	1.79	0.64
1:B:121:TRP:O	1:B:124:ARG:HG3	1.99	0.63
1:A:258:THR:CG2	1:A:262:GLY:HA2	2.31	0.59
1:A:120:GLU:HA	1:A:124:ARG:HD2	1.84	0.59
1:A:288:HIS:HB3	1:A:291:LYS:HB2	1.85	0.59
1:A:42:CYS:SG	3:A:446:FAD:C4X	2.91	0.58
1:B:291:LYS:HG2	1:B:350:LEU:HD11	1.83	0.58
1:B:42:CYS:SG	3:B:446:FAD:C4X	2.92	0.58
1:A:299:ILE:HG12	3:A:446:FAD:O2	2.05	0.57
1:B:42:CYS:SG	3:B:446:FAD:C10	2.93	0.57
1:A:359:VAL:HG12	1:A:361:SER:HB2	1.88	0.55
1:A:42:CYS:SG	3:A:446:FAD:C10	2.95	0.55
1:B:359:VAL:HG12	1:B:361:SER:HB2	1.88	0.55
1:A:63:VAL:HG12	4:A:659:HOH:O	2.09	0.53
1:A:181:ARG:N	1:A:181:ARG:HE	1.91	0.52
1:A:19:ILE:HA	1:A:315:LEU:HD11	1.92	0.51
1:A:115:ARG:NH2	1:A:245:LYS:HD3	2.28	0.48
1:B:19:ILE:HA	1:B:315:LEU:HD11	1.96	0.47
1:B:113:GLY:HA2	1:B:282:ASP:HB2	1.97	0.46
1:B:62:ASN:HD22	1:B:65:THR:H	1.64	0.46
1:B:22:ASN:HB2	1:B:315:LEU:HD13	1.97	0.46
1:A:220:ASN:CG	1:A:221:GLU:H	2.18	0.46
1:A:291:LYS:HG2	1:A:350:LEU:HD11	1.98	0.45
1:B:193:MET:CE	1:B:196:TYR:HE1	2.29	0.45
1:B:288:HIS:HB3	1:B:291:LYS:HB2	1.99	0.45
1:B:41:GLN:HA	1:B:44:LEU:HD22	1.99	0.44
1:A:161:ILE:HG12	3:A:446:FAD:HM73	1.99	0.44
1:A:113:GLY:HA2	1:A:282:ASP:HB2	2.00	0.43
1:B:281:GLY:HA2	1:B:303:ALA:HA	1.99	0.43
1:A:381:ARG:O	1:A:385:LYS:HA	2.19	0.42
1:B:62:ASN:ND2	1:B:65:THR:H	2.17	0.42
1:A:77:ARG:HD3	1:A:96:LYS:HG2	2.02	0.41
1:B:359:VAL:CG1	1:B:361:SER:HB2	2.50	0.41
1:A:219:GLY:HA2	1:A:224:GLU:HG2	2.01	0.41
1:A:137:ASP:OD1	1:A:140:ARG:NH2	2.55	0.40
1:A:220:ASN:H	1:A:220:ASN:ND2	2.19	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	444/480 (92%)	430 (97%)	14 (3%)	0	100	100
1	B	443/480 (92%)	430 (97%)	13 (3%)	0	100	100
All	All	887/960 (92%)	860 (97%)	27 (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	372/398 (94%)	360 (97%)	12 (3%)	39	54
1	B	371/398 (93%)	357 (96%)	14 (4%)	33	47
All	All	743/796 (93%)	717 (96%)	26 (4%)	39	50

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	104	SER
1	A	143	LYS
1	A	163	LEU
1	A	181	ARG

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Mol	Chain	Res	Type
1	A	222	ARG
1	A	249[A]	ASP
1	A	249[B]	ASP
1	A	258	THR
1	A	309	LEU
1	A	339	ARG
1	A	396	GLU
1	B	44	LEU
1	B	62	ASN
1	B	64	LYS
1	B	120	GLU
1	B	146	GLU
1	B	149	LYS
1	B	223	VAL
1	B	249[A]	ASP
1	B	249[B]	ASP
1	B	258	THR
1	B	339	ARG
1	B	372	LYS
1	B	412	LYS
1	B	414	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	275	GLN
1	A	304	ASN
1	B	25	ASN
1	B	62	ASN
1	B	148	ASN
1	B	334	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	COA	A	445[B]	-	41,50,50	0.71	1 (2%)	52,75,75	1.49	9 (17%)
2	COA	A	445[A]	-	41,50,50	0.71	1 (2%)	52,75,75	1.30	6 (11%)
2	COA	B	445[A]	-	41,50,50	0.71	0	52,75,75	1.31	4 (7%)
3	FAD	B	446	-	51,58,58	0.98	2 (3%)	60,89,89	1.84	10 (16%)
2	COA	B	445[B]	-	41,50,50	0.71	0	52,75,75	1.38	5 (9%)
3	FAD	A	446	-	51,58,58	0.97	3 (5%)	60,89,89	1.78	8 (13%)

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	COA	A	445[B]	-	-	4/44/64/64	0/3/3/3
2	COA	A	445[A]	-	-	7/44/64/64	0/3/3/3
2	COA	B	445[A]	-	-	9/44/64/64	0/3/3/3
3	FAD	B	446	-	-	1/30/50/50	0/6/6/6
2	COA	B	445[B]	-	-	6/44/64/64	0/3/3/3
3	FAD	A	446	-	-	1/30/50/50	0/6/6/6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	446	FAD	C9A-N10	3.05	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	446	FAD	C9A-N10	2.99	1.42	1.38
3	A	446	FAD	C4X-N5	2.39	1.36	1.33
3	B	446	FAD	C4X-N5	2.36	1.36	1.33
2	A	445[B]	COA	C2A-N3A	2.11	1.35	1.32
2	A	445[A]	COA	C2A-N3A	2.11	1.35	1.32
3	A	446	FAD	C10-N1	2.07	1.35	1.33

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	446	FAD	C4-N3-C2	7.23	121.25	115.14
3	A	446	FAD	C4-N3-C2	6.82	120.90	115.14
3	A	446	FAD	C4X-N5-C5X	5.57	122.33	116.77
3	B	446	FAD	C4X-N5-C5X	5.40	122.17	116.77
3	A	446	FAD	N3A-C2A-N1A	-5.04	120.80	128.68
3	B	446	FAD	C1'-N10-C9A	5.02	122.24	118.29
2	B	445[A]	COA	N3A-C2A-N1A	-4.84	121.11	128.68
2	B	445[B]	COA	N3A-C2A-N1A	-4.84	121.11	128.68
3	B	446	FAD	N3A-C2A-N1A	-4.74	121.27	128.68
2	A	445[B]	COA	N3A-C2A-N1A	-4.56	121.55	128.68
2	A	445[A]	COA	N3A-C2A-N1A	-4.56	121.55	128.68
2	A	445[B]	COA	C2P-C3P-N4P	-4.26	102.57	112.31
2	A	445[A]	COA	C2P-C3P-N4P	-4.26	102.57	112.31
3	A	446	FAD	C1'-N10-C9A	4.20	121.60	118.29
2	B	445[A]	COA	C2P-C3P-N4P	-4.15	102.83	112.31
2	B	445[B]	COA	C2P-C3P-N4P	-4.15	102.83	112.31
2	A	445[B]	COA	O6A-CCP-CBP	3.64	116.40	110.55
2	B	445[B]	COA	O6A-CCP-CBP	3.04	115.43	110.55
3	B	446	FAD	C4X-C4-N3	-3.02	119.30	123.43
3	B	446	FAD	C4-C4X-N5	2.93	121.95	118.60
3	A	446	FAD	C4-C4X-N5	2.88	121.89	118.60
2	A	445[B]	COA	CDP-CBP-CCP	-2.87	103.56	108.23
3	A	446	FAD	C4X-C4-N3	-2.75	119.67	123.43
2	B	445[B]	COA	P2A-O3A-P1A	-2.63	123.81	132.83
2	A	445[B]	COA	CEP-CBP-CCP	2.62	112.51	108.23
2	B	445[A]	COA	P2A-O3A-P1A	-2.58	123.97	132.83
3	B	446	FAD	C4-C4X-C10	-2.56	118.25	119.95
2	A	445[B]	COA	P2A-O3A-P1A	-2.56	124.04	132.83
3	A	446	FAD	C4-C4X-C10	-2.53	118.27	119.95
3	B	446	FAD	C9A-N10-C10	-2.43	118.72	121.91
2	A	445[A]	COA	P2A-O3A-P1A	-2.33	124.82	132.83
2	A	445[B]	COA	C6P-C7P-N8P	-2.31	107.24	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	445[A]	COA	C6P-C7P-N8P	-2.31	107.24	111.90
2	B	445[A]	COA	C4A-C5A-N7A	-2.22	107.09	109.40
2	B	445[B]	COA	C4A-C5A-N7A	-2.22	107.09	109.40
2	A	445[B]	COA	C4A-C5A-N7A	-2.21	107.10	109.40
2	A	445[A]	COA	C4A-C5A-N7A	-2.21	107.10	109.40
3	B	446	FAD	C4A-C5A-N7A	-2.14	107.17	109.40
3	B	446	FAD	C10-C4X-N5	-2.11	119.80	121.26
3	A	446	FAD	C10-C4X-N5	-2.06	119.83	121.26
2	A	445[B]	COA	C3B-C2B-C1B	2.01	104.34	99.89
2	A	445[A]	COA	C3B-C2B-C1B	2.01	104.34	99.89

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	445[B]	COA	CCP-O6A-P2A-O3A
2	A	445[B]	COA	CCP-O6A-P2A-O4A
2	A	445[A]	COA	CCP-O6A-P2A-O4A
2	A	445[A]	COA	CDP-CBP-CCP-O6A
2	A	445[A]	COA	CAP-CBP-CCP-O6A
2	B	445[A]	COA	P2A-O3A-P1A-O5B
2	B	445[A]	COA	CCP-O6A-P2A-O3A
2	B	445[A]	COA	CCP-O6A-P2A-O4A
2	B	445[A]	COA	CDP-CBP-CCP-O6A
2	B	445[A]	COA	CEP-CBP-CCP-O6A
2	B	445[A]	COA	CAP-CBP-CCP-O6A
2	B	445[B]	COA	C5B-O5B-P1A-O1A
2	B	445[B]	COA	C5B-O5B-P1A-O3A
2	A	445[A]	COA	CEP-CBP-CCP-O6A
2	A	445[A]	COA	P2A-O3A-P1A-O5B
2	A	445[A]	COA	CCP-O6A-P2A-O3A
2	B	445[A]	COA	CCP-O6A-P2A-O5A
2	A	445[B]	COA	C3B-C4B-C5B-O5B
2	B	445[B]	COA	CEP-CBP-CCP-O6A
2	A	445[A]	COA	P1A-O3A-P2A-O5A
2	B	445[A]	COA	C3B-C4B-C5B-O5B
2	B	445[B]	COA	CDP-CBP-CCP-O6A
3	B	446	FAD	O4B-C4B-C5B-O5B
2	B	445[A]	COA	P1A-O3A-P2A-O5A
2	A	445[B]	COA	C5B-O5B-P1A-O1A
2	B	445[B]	COA	C5B-O5B-P1A-O2A
2	B	445[B]	COA	CCP-O6A-P2A-O4A

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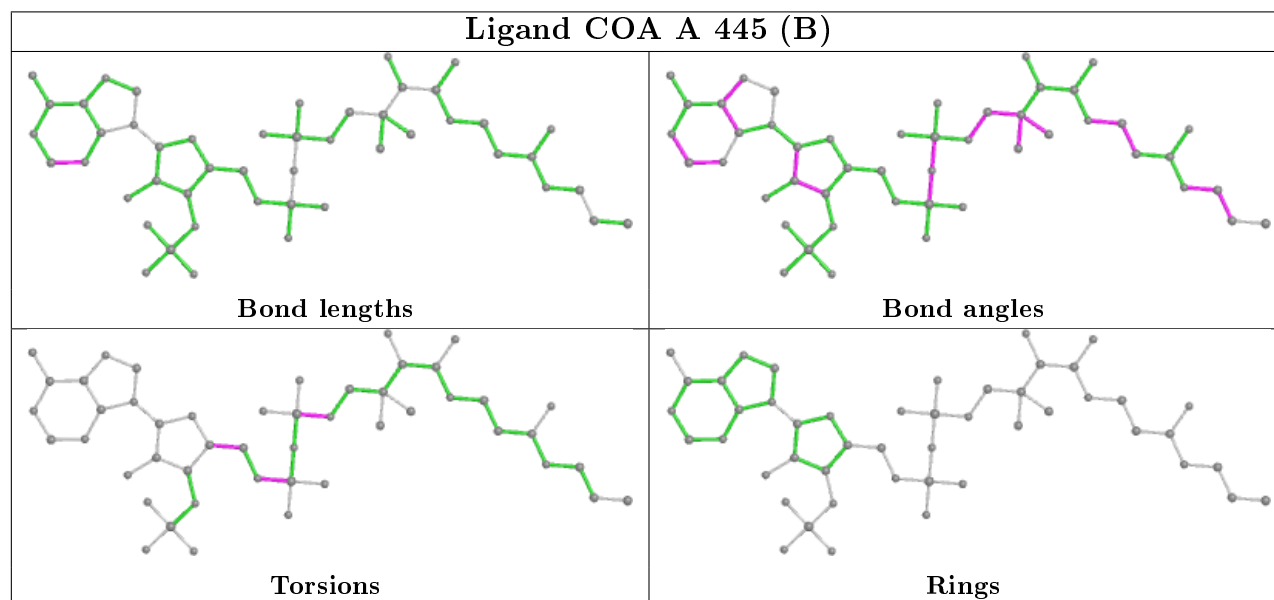
Mol	Chain	Res	Type	Atoms
3	A	446	FAD	O4B-C4B-C5B-O5B

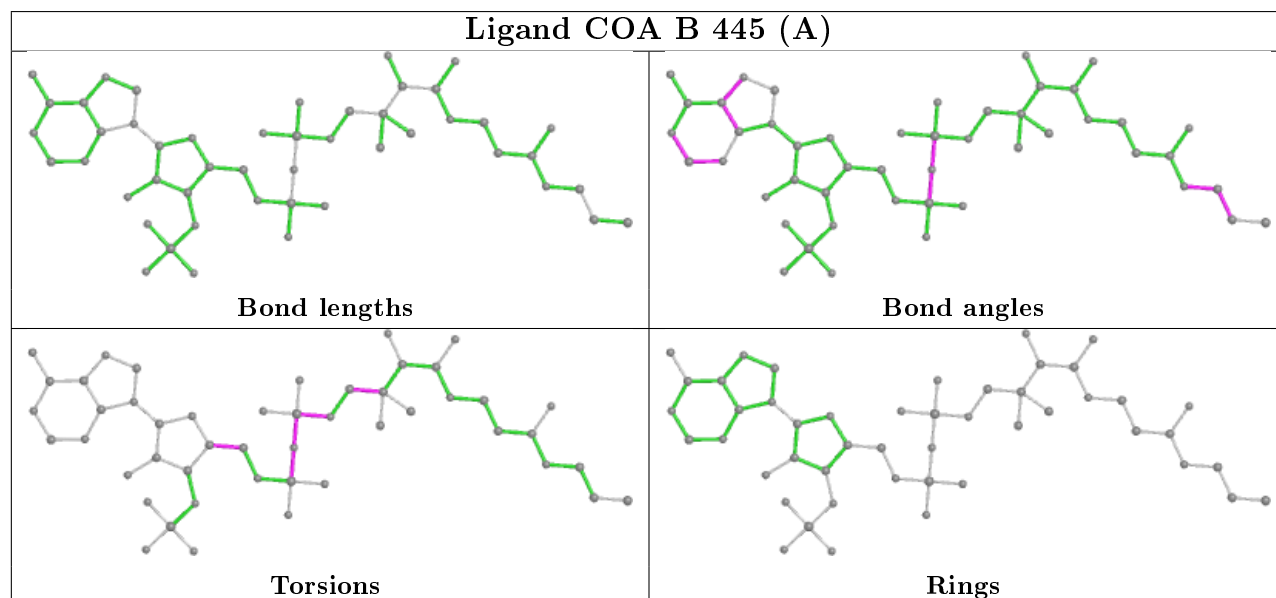
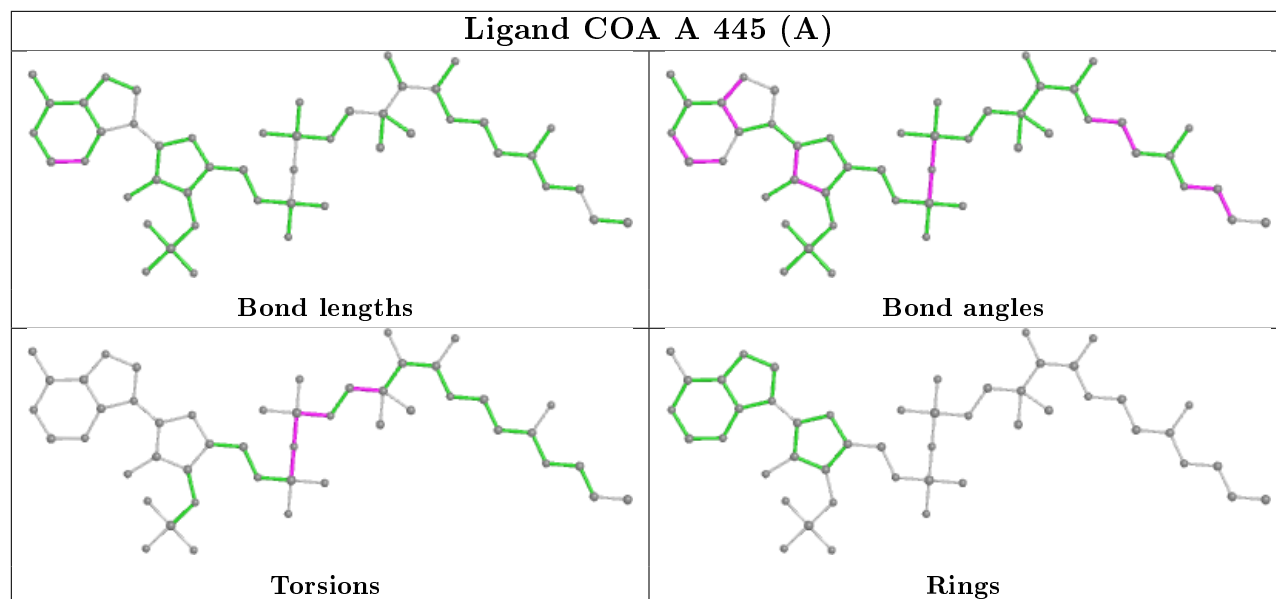
There are no ring outliers.

2 monomers are involved in 6 short contacts:

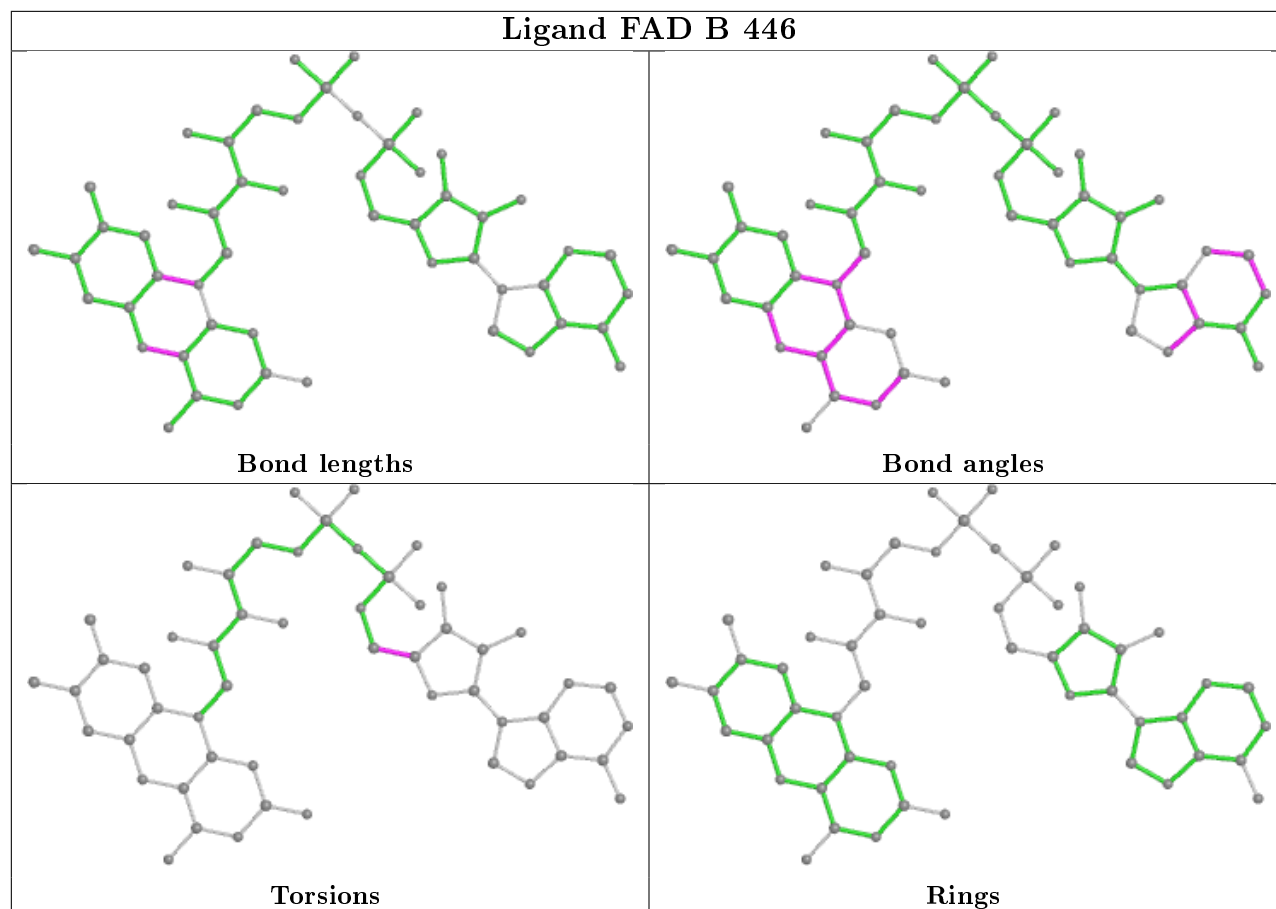
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	446	FAD	2	0
3	A	446	FAD	4	0

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.

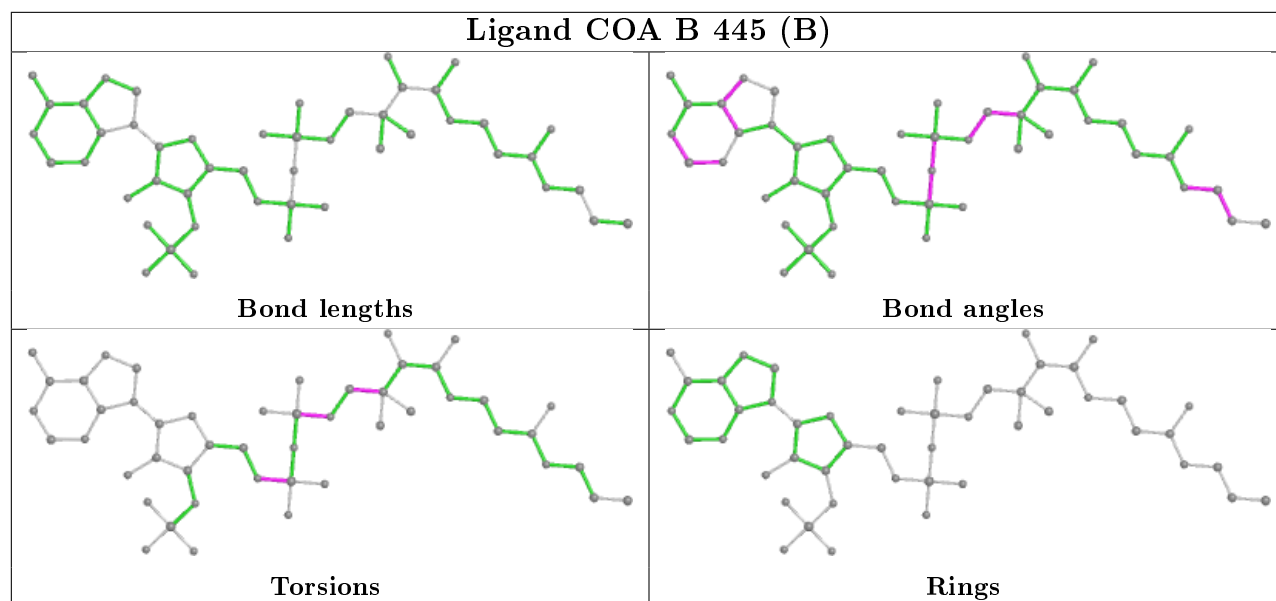


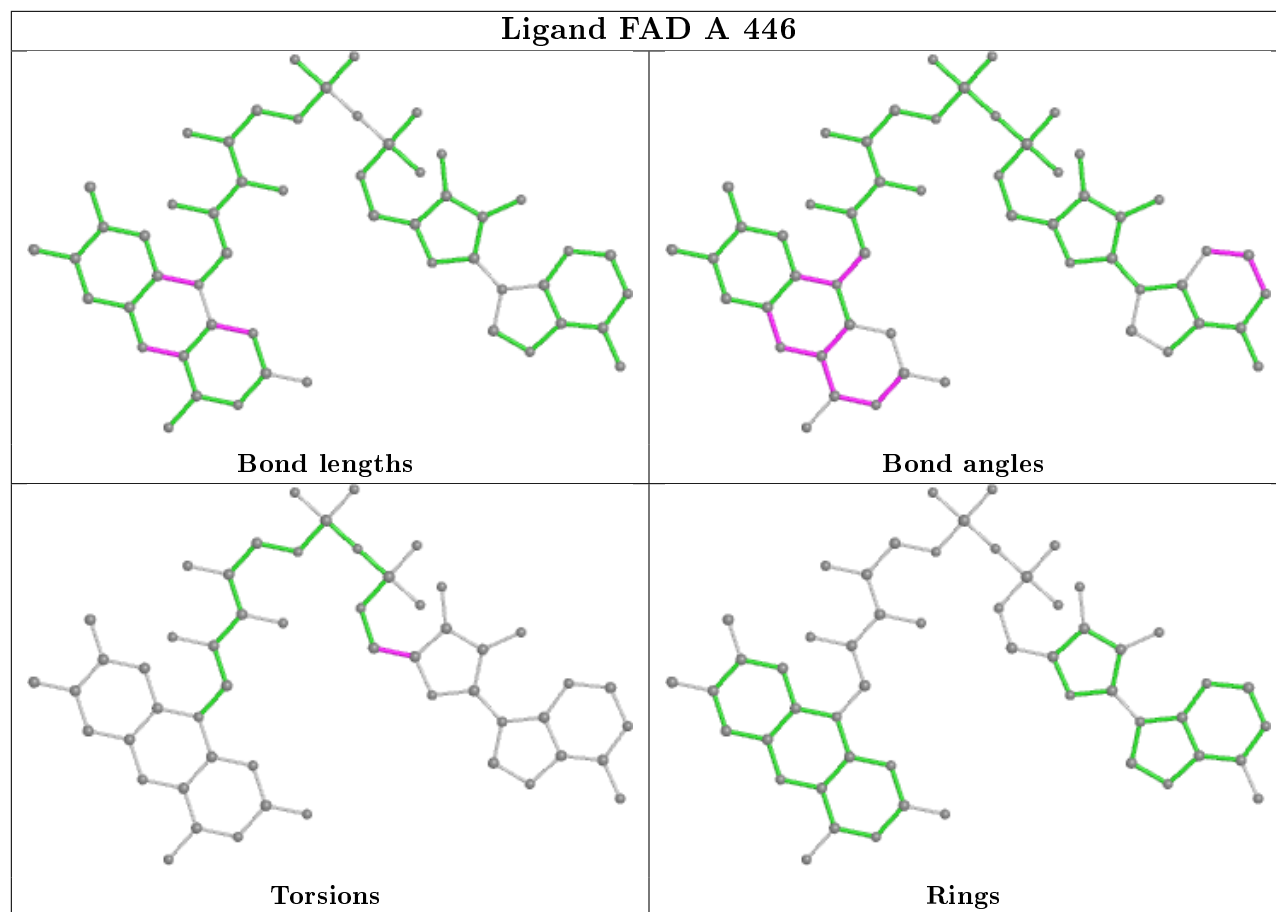


Ligand FAD B 446



Ligand COA B 445 (B)





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	444/480 (92%)	0.09	22 (4%) 28 35	11, 22, 38, 50	0
1	B	444/480 (92%)	0.07	18 (4%) 37 44	10, 22, 39, 48	0
All	All	888/960 (92%)	0.08	40 (4%) 33 40	10, 22, 39, 50	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	184	HIS	6.0
1	B	184	HIS	5.5
1	A	183	ASP	5.5
1	B	221	GLU	5.2
1	A	185	ILE	5.1
1	A	370	ASN	4.7
1	A	182	ASN	4.7
1	A	221	GLU	4.6
1	B	147	THR	4.5
1	A	24	GLU	4.4
1	B	220	ASN	4.2
1	B	183	ASP	4.2
1	B	185	ILE	4.1
1	A	220	ASN	4.0
1	A	25	ASN	4.0
1	B	24	GLU	4.0
1	A	260	HIS	3.9
1	B	222	ARG	3.7
1	B	260	HIS	3.6
1	B	370	ASN	3.6
1	B	186	GLY	3.0
1	B	25	ASN	3.0
1	B	211	ASN	2.9
1	A	148	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	147	THR	2.8
1	A	255	ASN	2.7
1	B	149	LYS	2.7
1	B	96	LYS	2.6
1	A	222	ARG	2.6
1	B	182	ASN	2.6
1	A	252	GLU	2.5
1	A	110	ILE	2.5
1	A	96	LYS	2.4
1	A	6	ILE	2.4
1	A	150	VAL	2.4
1	B	109	LEU	2.3
1	A	211	ASN	2.3
1	A	149	LYS	2.2
1	A	146	GLU	2.1
1	B	255	ASN	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](#)

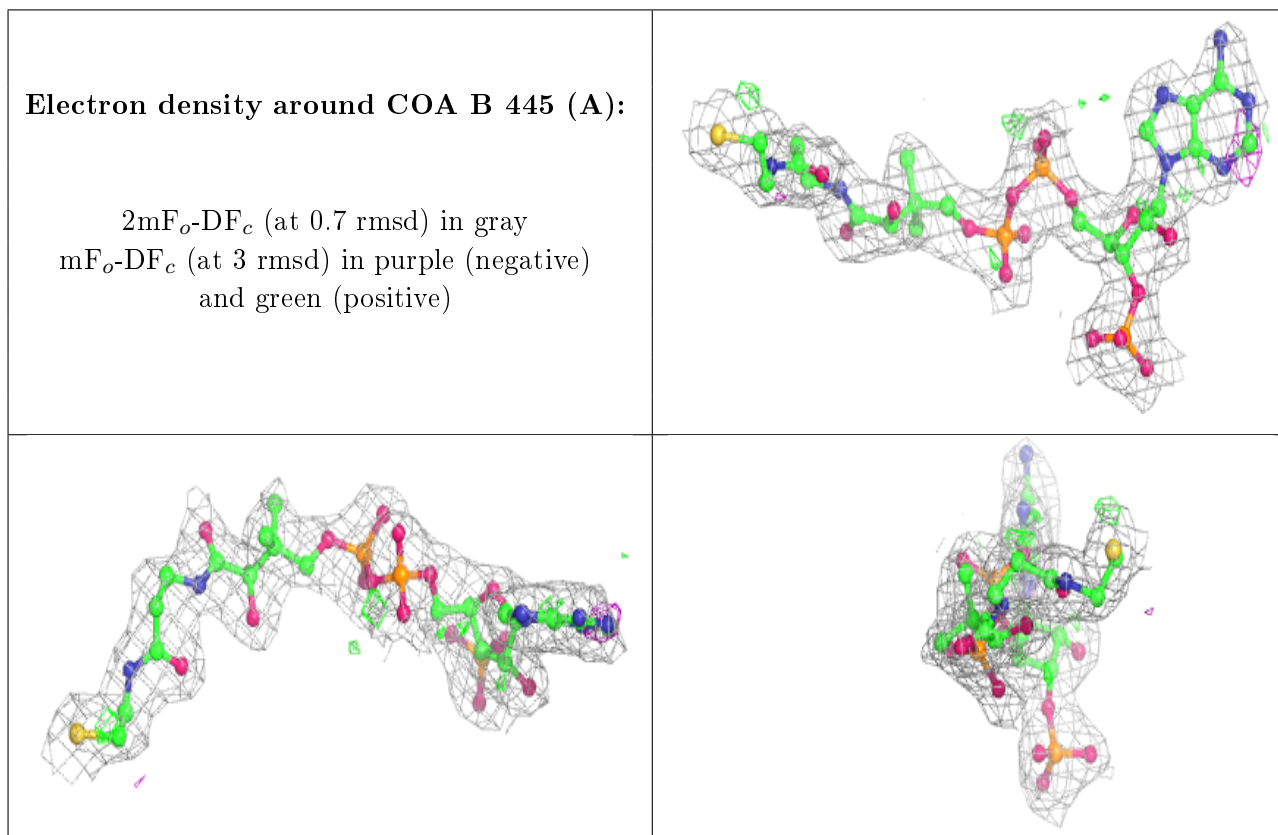
There are no carbohydrates in this entry.

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.

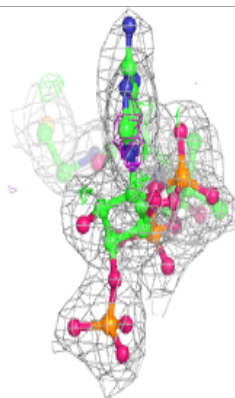
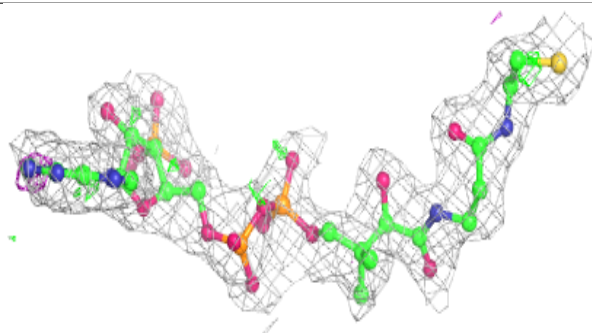
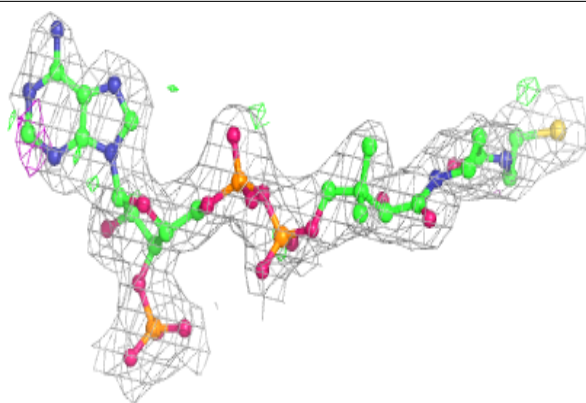
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	COA	B	445[A]	48/48	0.92	0.15	19,23,33,34	11
2	COA	B	445[B]	48/48	0.92	0.15	19,24,33,34	11
2	COA	A	445[B]	48/48	0.93	0.15	20,23,33,34	11
2	COA	A	445[A]	48/48	0.93	0.15	19,22,33,34	11
3	FAD	A	446	53/53	0.97	0.10	12,15,17,17	0
3	FAD	B	446	53/53	0.98	0.10	10,14,17,17	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.

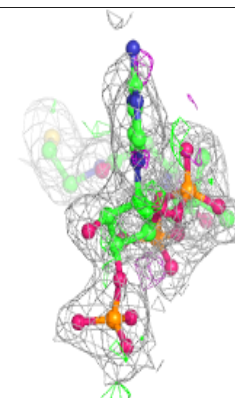
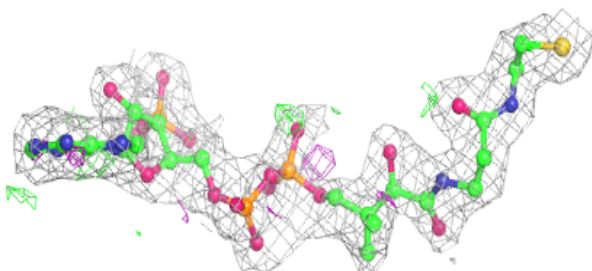
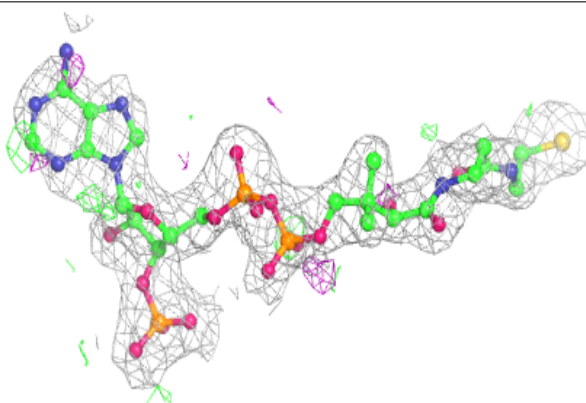


Electron density around COA B 445 (B):

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

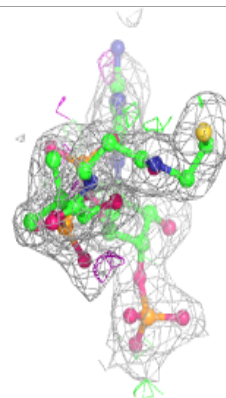
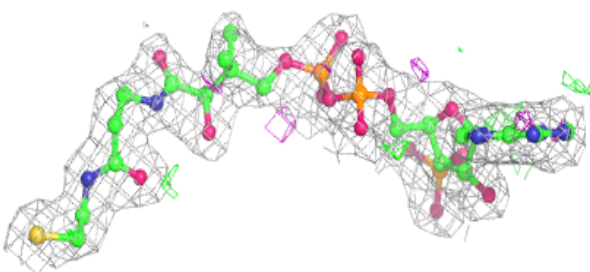
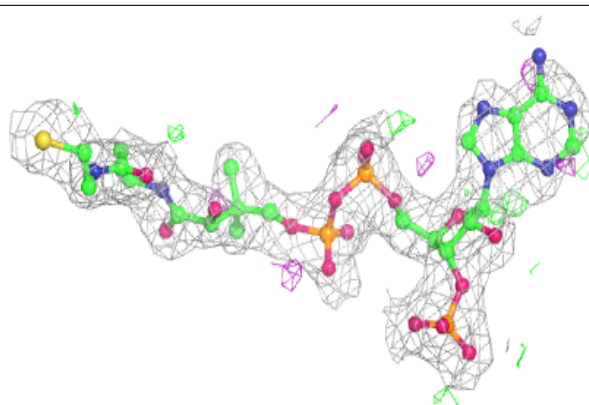
**Electron density around COA A 445 (B):**

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

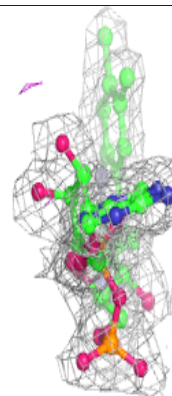
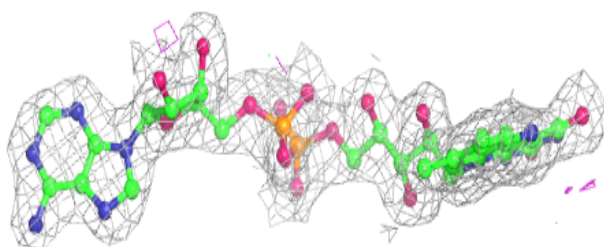
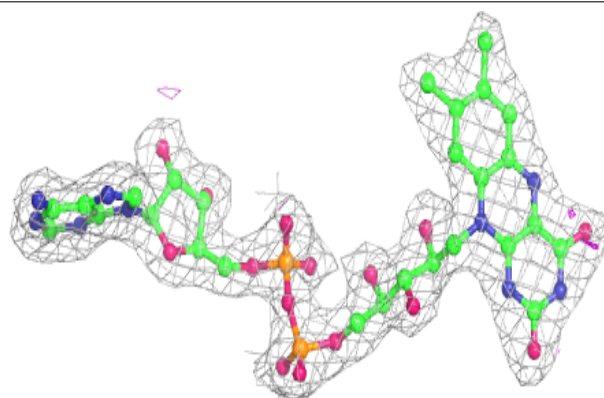


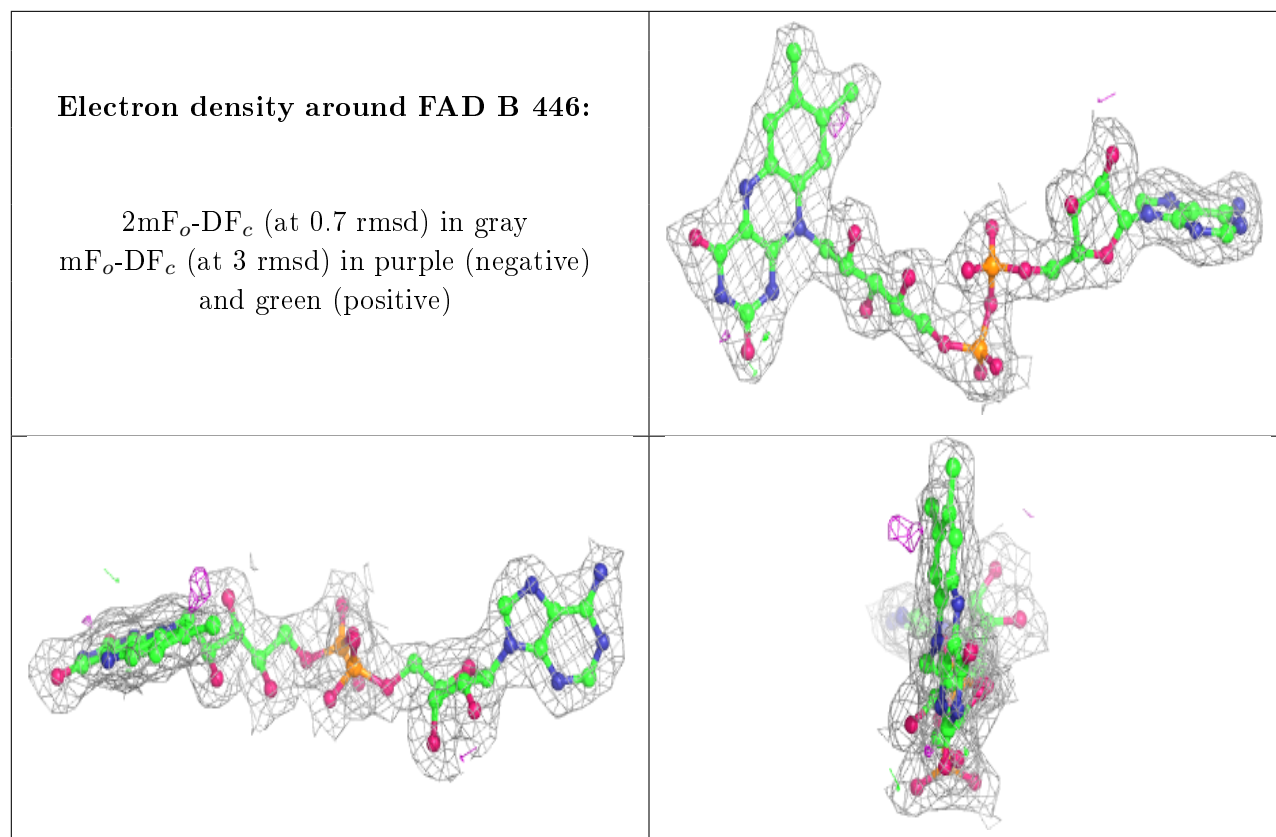
Electron density around COA A 445 (A):

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

**Electron density around FAD A 446:**

$2mF_o-DF_c$ (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.