wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 04:05 PM EDT

PDB ID	:	1YCF / pdb_00001ycf
Title	:	Oxidized (di-ferric) FprA from Moorella thermoacetica
Authors	:	Silaghi-Dumitrescu, R.; Kurtz, D.M.; Lanzilotta, W.N.
Deposited on	:	2004-12-22
Resolution	:	3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

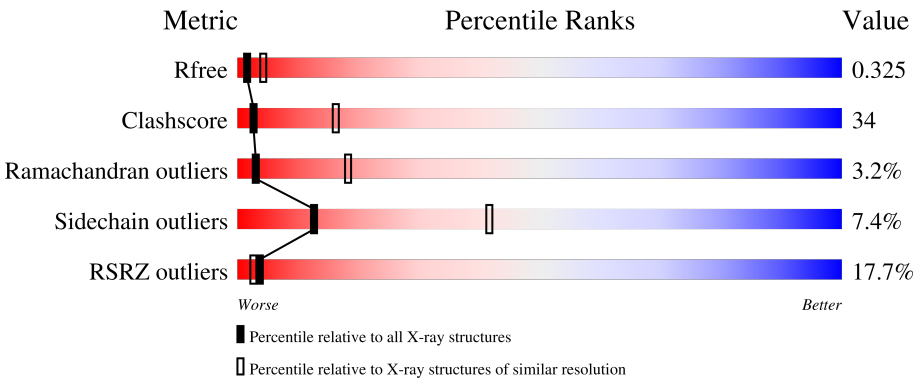
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 <=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	398	23% 47% 46% 6% •
1	B	398	13% 44% 47% 8% •
1	C	398	23% 55% 38% 7% •
1	D	398	12% 46% 45% 8% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	OXY	C	521	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 12668 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.

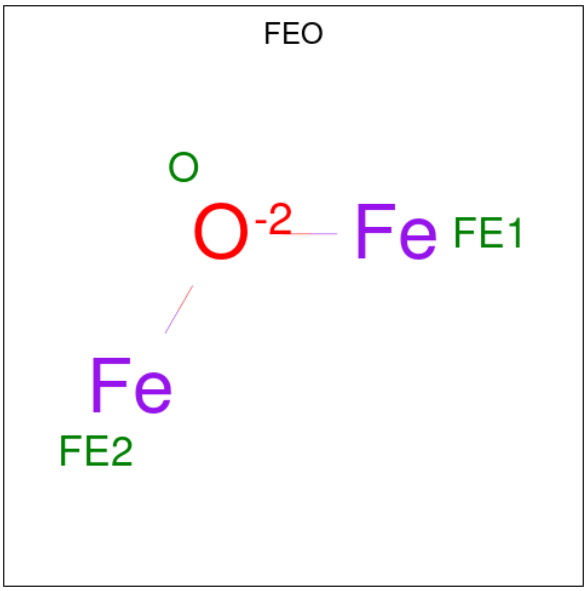
- Molecule 1 is a protein called Nitric oxide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	398	3115	2006	525	572	12	0	0	0
1	B	398	3115	2006	525	572	12	0	0	0
1	C	398	3115	2006	525	572	12	0	0	0
1	D	398	3115	2006	525	572	12	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

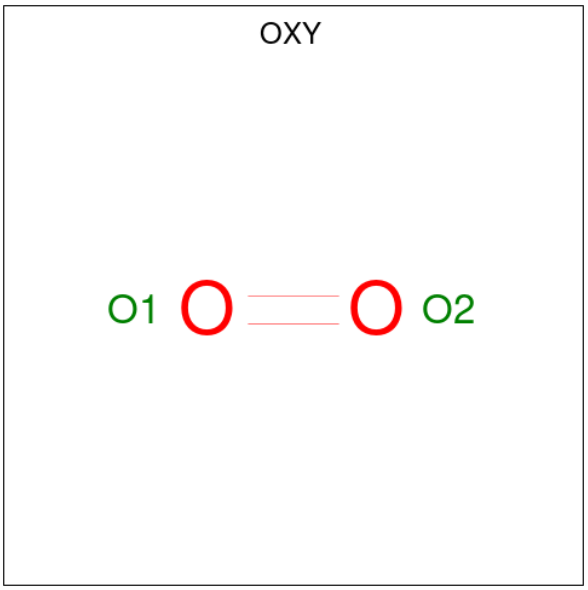
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	2	2	2	0	0
2	B	1	1	1	0	0

- Molecule 3 is MU-OXO-DIIRON (CCD ID: FEO) (formula: Fe_2O).



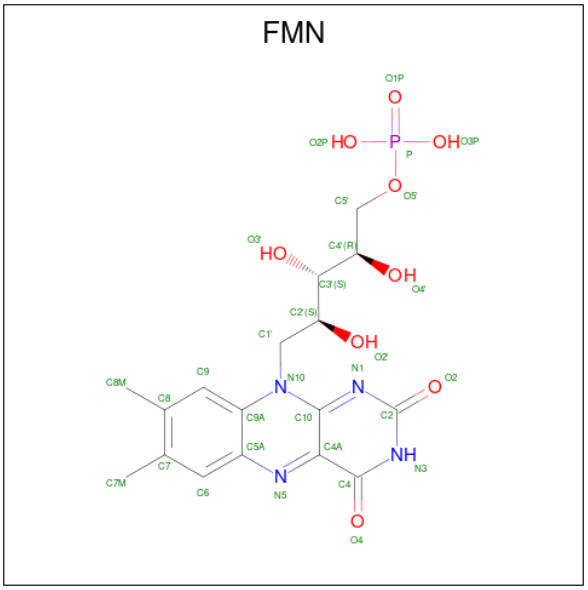
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	O		
3	A	1	3	2	1	0	0
3	B	1	3	2	1	0	0
3	C	1	3	2	1	0	0
3	D	1	3	2	1	0	0

- Molecule 4 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 2 2	0	0
4	B	1	Total O 2 2	0	0
4	C	1	Total O 2 2	0	0
4	D	1	Total O 2 2	0	0

- Molecule 5 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 31 17 4 9 1	0	0
5	B	1	Total C N O P 31 17 4 9 1	0	0
5	C	1	Total C N O P 31 17 4 9 1	0	0
5	D	1	Total C N O P 31 17 4 9 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	15	Total O 15 15	0	0
6	B	14	Total O 14 14	0	0

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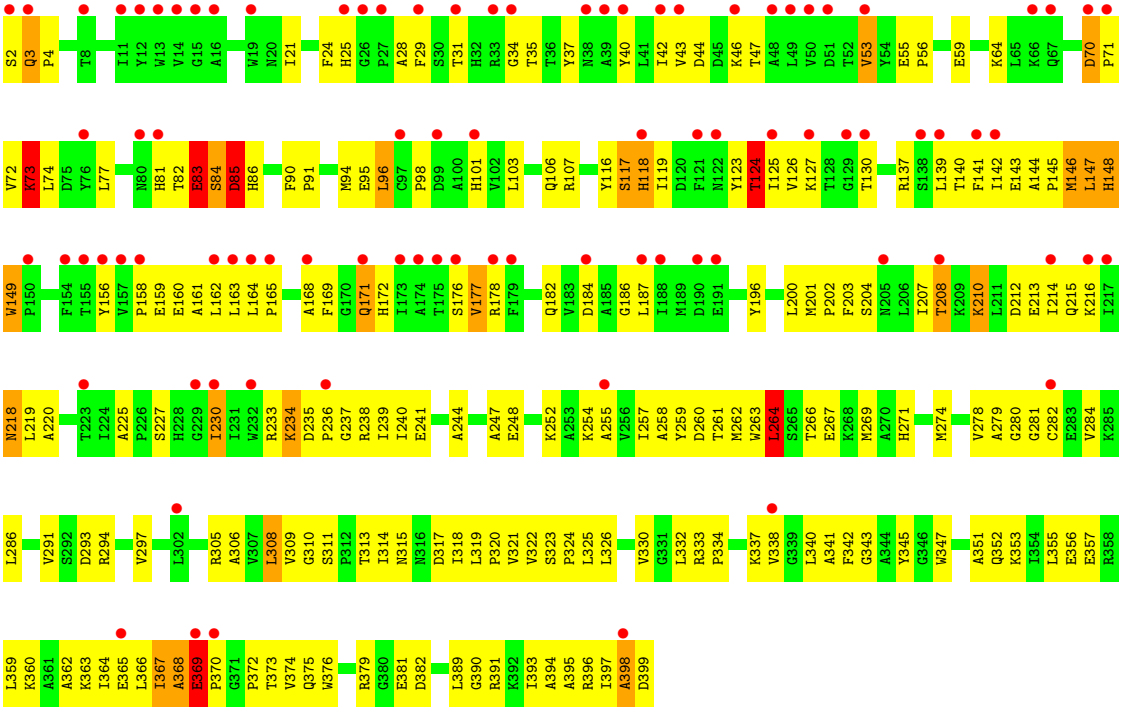
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	C	16	16	16	0	0
			Total	O		
6	D	16	16	16	0	0

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.

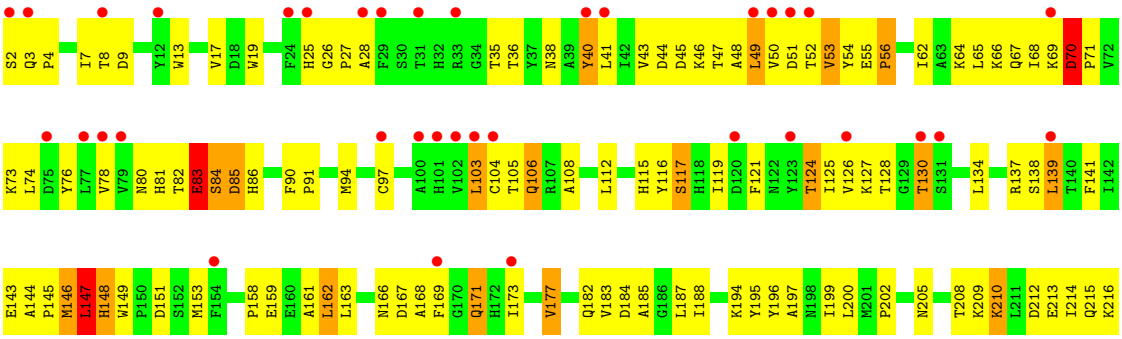
- Molecule 1: Nitric oxide reductase

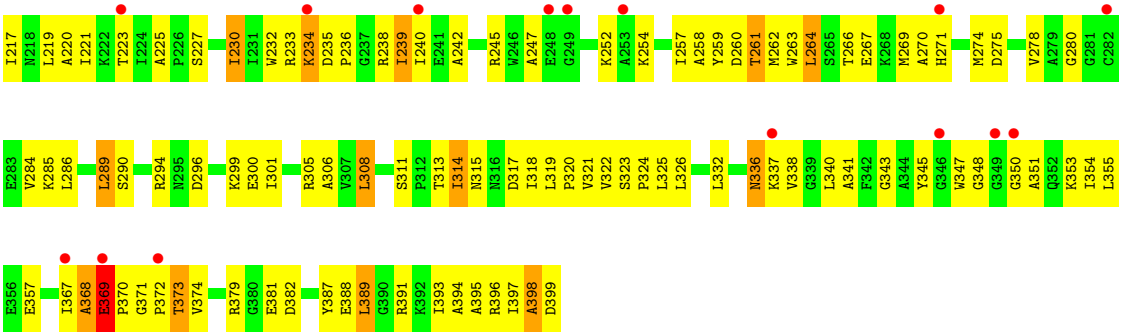
Chain A:



- Molecule 1: Nitric oxide reductase

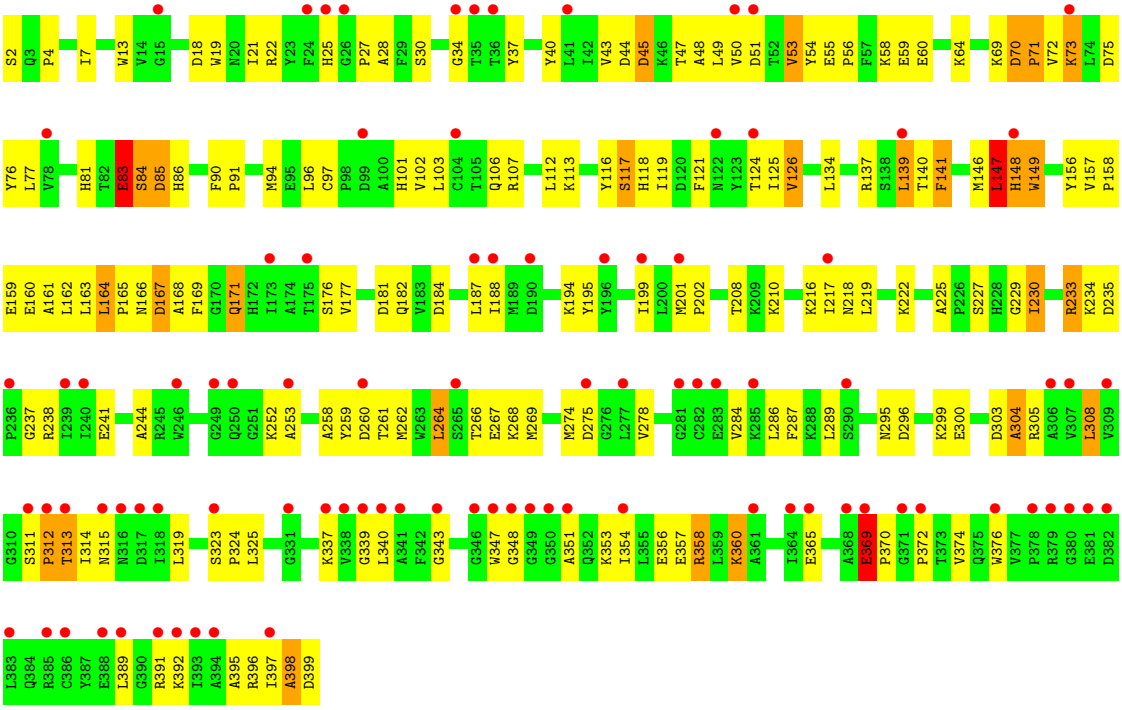
Chain B:





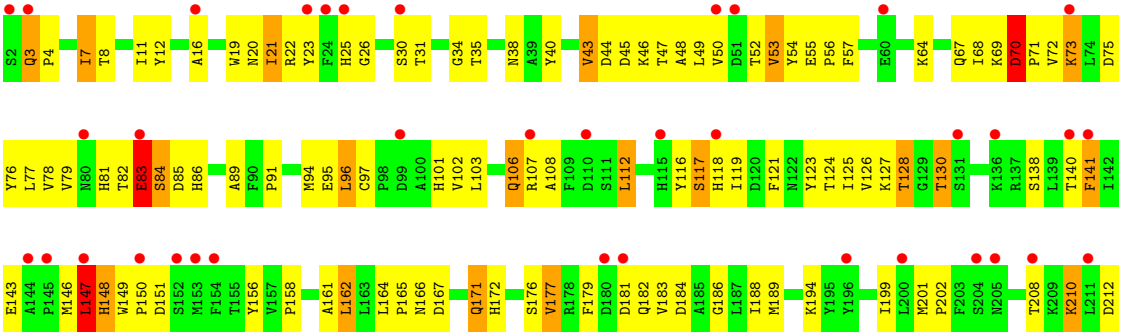
- Molecule 1: Nitric oxide reductase

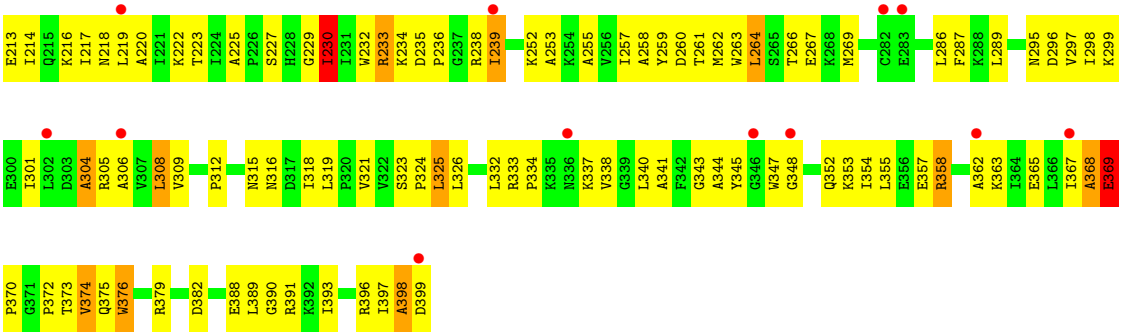
Chain C:



- Molecule 1: Nitric oxide reductase

Chain D:




E213 I214 Q215 K216 I217 N218 L219 A220 I221 K222 T223 I224 A225 P226 S227 H228 G229 I230 I231 W232 R233 K234 D235 P236 G237 R238 I239
K252 A253 K254 A255 V256 I257 A258 Y259 D260 T261 M262 W263 L264 S265 T266 E267 K268 M269
C282 E283
L286 F287 K288 L289
N295 D296 V297 I298 K299
E300 I301 L302 D303 A304 R305 A306 V307 L308 V309
P312
N315 N316 D317 I318 L319 P320 V321 V322 S323 P324 L325 L326
L332 R333 P334 K335 M336 K337 V338 G339 L340 A341 F342 G343 A344 Y345 G346 W347 G348
Q352 K353 I354 L355 E356 E357 R358
A362 K363 I364 E365 L366 I367 A368 E369
P370 G371 P372 T373 V374 Q375 W376
R379
D382
E388 L389 G390 R391 K392 I393
R396 I397 A398 D399

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	159.67Å 159.67Å 276.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.71 – 3.00 49.71 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.71-3.00) 99.2 (49.71-3.01)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 2.99Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.217 , 0.260 0.307 , 0.325	Depositor DCC
R_{free} test set	3604 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	81.2	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 59.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	12668	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: FEO, ZN, OXY, FMN

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	0.43	0/3189	0.97	11/4335 (0.3%)
1	B	0.42	0/3189	0.99	17/4335 (0.4%)
1	C	0.44	0/3189	1.04	26/4335 (0.6%)
1	D	0.46	0/3189	1.07	25/4335 (0.6%)
All	All	0.44	0/12756	1.02	79/17340 (0.5%)

There are no bond length outliers.

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	3	GLN	N-CA-C	11.14	126.34	110.40
1	C	147	LEU	N-CA-C	-9.02	96.09	109.62
1	C	83	GLU	N-CA-C	8.71	121.56	111.11
1	C	199	ILE	N-CA-C	8.39	119.17	112.12
1	D	85	ASP	N-CA-C	-7.78	103.79	113.20

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	3115	0	3130	231	1
1	B	3115	0	3131	239	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3115	0	3131	169	1
1	D	3115	0	3131	233	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	1	0
3	C	3	0	0	0	0
3	D	3	0	0	1	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0
4	C	2	0	0	0	0
4	D	2	0	0	1	0
5	A	31	0	19	1	0
5	B	31	0	19	1	0
5	C	31	0	19	0	0
5	D	31	0	19	1	0
6	A	15	0	0	0	0
6	B	14	0	0	3	1
6	C	16	0	0	2	0
6	D	16	0	0	3	1
All	All	12668	0	12599	850	2

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 34.

The worst 5 of 850 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:D:306:ALA:HB2	1:D:397:ILE:HD11	1.23	1.16
1:B:314:ILE:HD11	1:B:319:LEU:HA	1.15	1.09
1:D:261:THR:HG22	1:D:266:THR:HB	1.38	1.03
1:D:70:ASP:HB3	1:D:71:PRO:HD3	1.39	1.00
1:A:305:ARG:HH12	1:A:399:ASP:HB2	1.25	0.98

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:SER:OG	1:C:275:ASP:OD2[5_653]	1.73	0.47
6:B:628:HOH:O	6:D:675:HOH:O[5_653]	1.92	0.28

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	396/398 (100%)	347 (88%)	36 (9%)	13 (3%)	3	17
1	B	396/398 (100%)	337 (85%)	44 (11%)	15 (4%)	2	15
1	C	396/398 (100%)	348 (88%)	36 (9%)	12 (3%)	3	19
1	D	396/398 (100%)	350 (88%)	36 (9%)	10 (2%)	4	23
All	All	1584/1592 (100%)	1382 (87%)	152 (10%)	50 (3%)	3	18

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ALA
1	A	118	HIS
1	A	124	THR
1	A	148	HIS
1	A	369	GLU

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	329/329 (100%)	303 (92%)	26 (8%)	11	39
1	B	329/329 (100%)	304 (92%)	25 (8%)	12	41
1	C	329/329 (100%)	306 (93%)	23 (7%)	14	44
1	D	329/329 (100%)	305 (93%)	24 (7%)	13	42
All	All	1316/1316 (100%)	1218 (93%)	98 (7%)	13	42

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	126	VAL
1	C	358	ARG
1	C	147	LEU
1	C	230	ILE
1	D	49	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	218	ASN
1	D	106	GLN
1	C	295	ASN
1	C	384	GLN
1	D	166	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)

Of 15 ligands modelled in this entry, 3 are monoatomic - leaving 12 for Mogul analysis.

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	$\#\|Z\| > 2$
3	FEO	B	510	1,4	0,2,2	-	-	-		
4	OXY	D	531	3	1,1,1	0.20	0	-		
3	FEO	A	500	1	0,2,2	-	-	-		
4	OXY	A	501	-	1,1,1	0.27	0	-		
5	FMN	A	701	-	33,33,33	3.00	12 (36%)	48,50,50	2.47	17 (35%)
5	FMN	B	702	-	33,33,33	3.09	11 (33%)	48,50,50	2.45	16 (33%)
3	FEO	D	530	1,4	0,2,2	-	-	-		
4	OXY	C	521	-	1,1,1	0.29	0	-		
3	FEO	C	520	1	0,2,2	-	-	-		
5	FMN	D	704	-	33,33,33	3.01	12 (36%)	48,50,50	2.45	18 (37%)
5	FMN	C	703	-	33,33,33	3.00	11 (33%)	48,50,50	2.43	17 (35%)
4	OXY	B	511	3	1,1,1	0.28	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
5	FMN	C	703	-	-	0/18/18/18	0/3/3/3
5	FMN	A	701	-	-	2/18/18/18	0/3/3/3
5	FMN	B	702	-	-	0/18/18/18	0/3/3/3
5	FMN	D	704	-	-	0/18/18/18	0/3/3/3

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	702	FMN	C9A-C5A	7.82	1.53	1.41
5	C	703	FMN	C9-C9A	7.73	1.52	1.39
5	B	702	FMN	C9-C9A	7.68	1.52	1.39
5	A	701	FMN	C9-C9A	7.59	1.51	1.39
5	C	703	FMN	C9A-C5A	7.50	1.53	1.41

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	704	FMN	C5A-C9A-N10	7.07	124.36	117.97
5	B	702	FMN	C5A-C9A-N10	6.84	124.15	117.97
5	A	701	FMN	C5A-C9A-N10	6.80	124.12	117.97
5	C	703	FMN	C5A-C9A-N10	6.55	123.89	117.97
5	C	703	FMN	C7M-C7-C6	-6.28	108.52	119.57

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	701	FMN	O4'-C4'-C5'-O5'
5	A	701	FMN	C3'-C4'-C5'-O5'

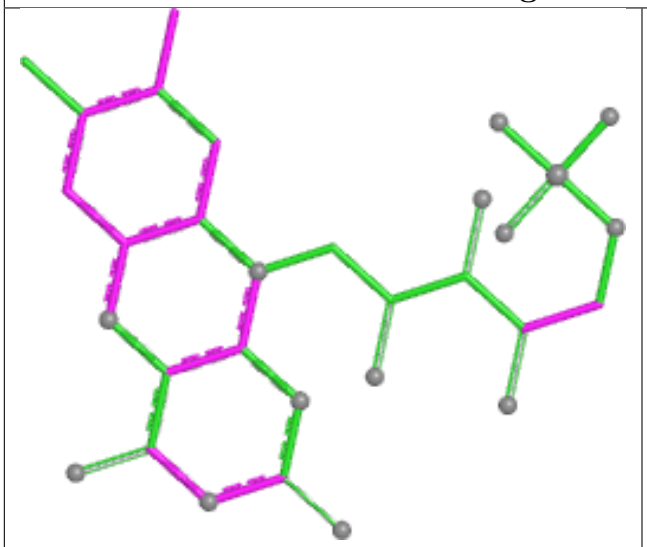
There are no ring outliers.

7 monomers are involved in 5 short contacts:

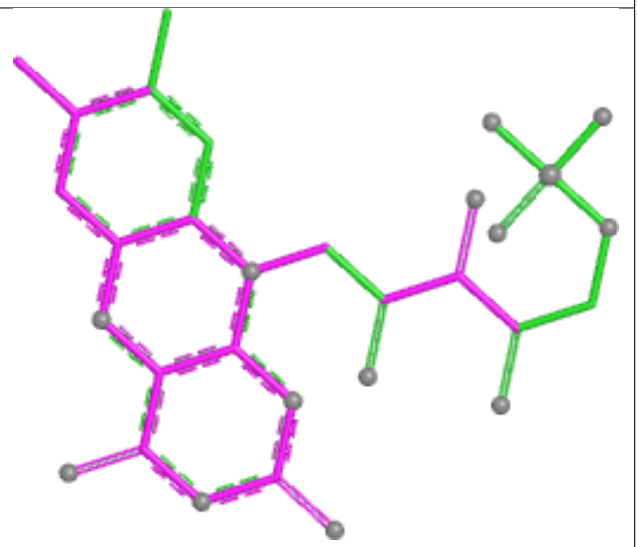
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	510	FEO	1	0
4	D	531	OXY	1	0
5	A	701	FMN	1	0
5	B	702	FMN	1	0
3	D	530	FEO	1	0
5	D	704	FMN	1	0
4	B	511	OXY	1	0

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 then 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.

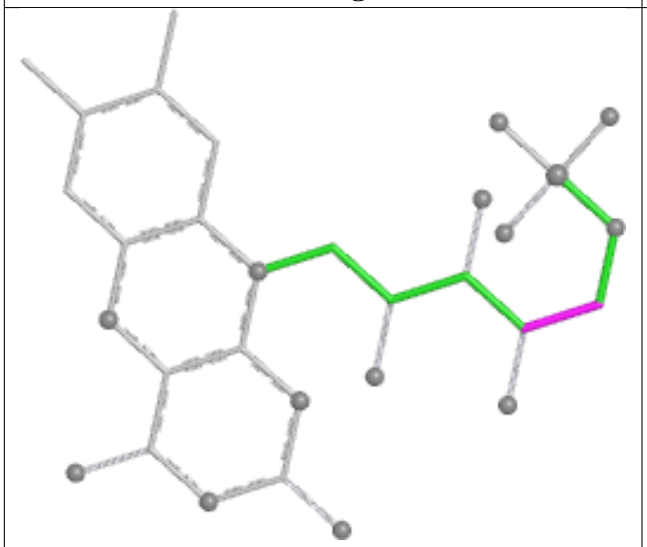
Ligand FMN A 701



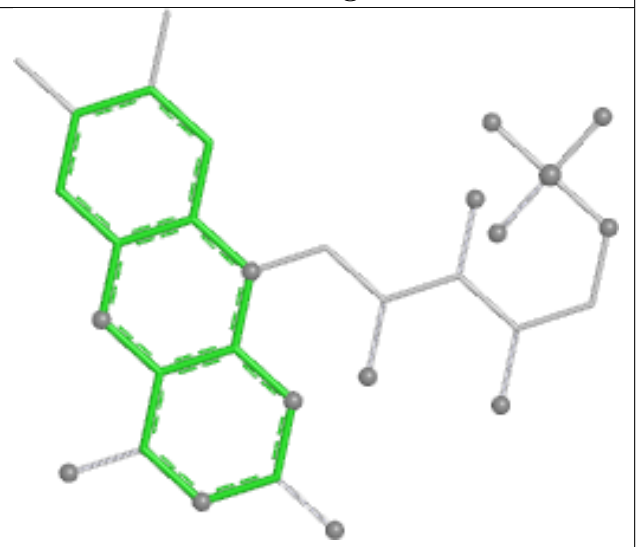
Bond lengths



Bond angles

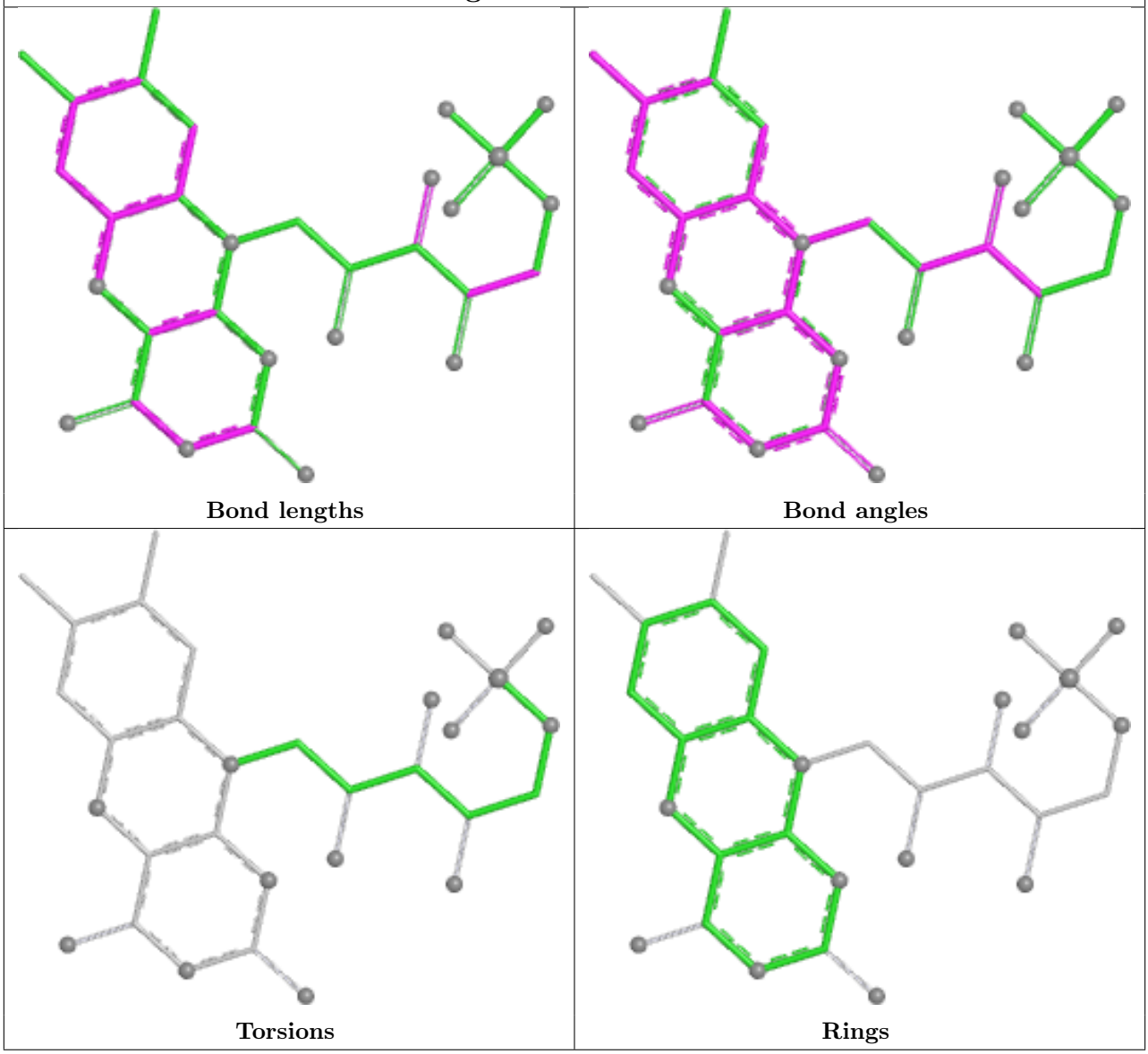


Torsions

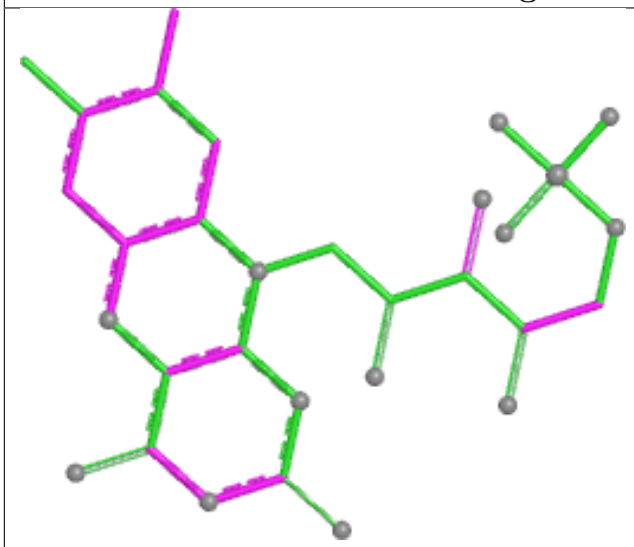


Rings

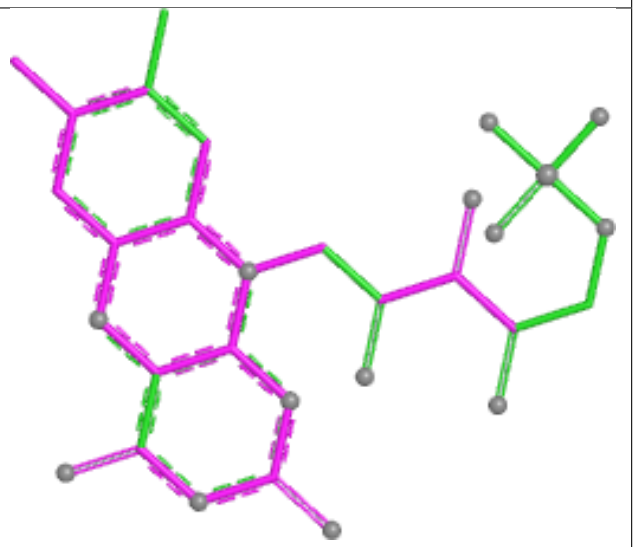
Ligand FMN B 702



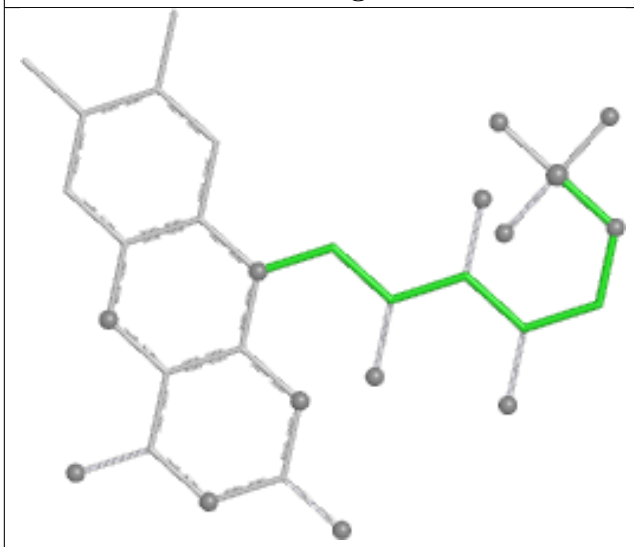
Ligand FMN D 704



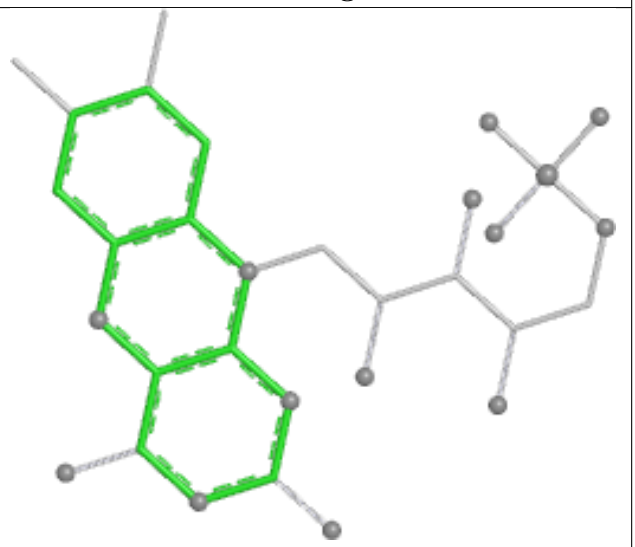
Bond lengths



Bond angles

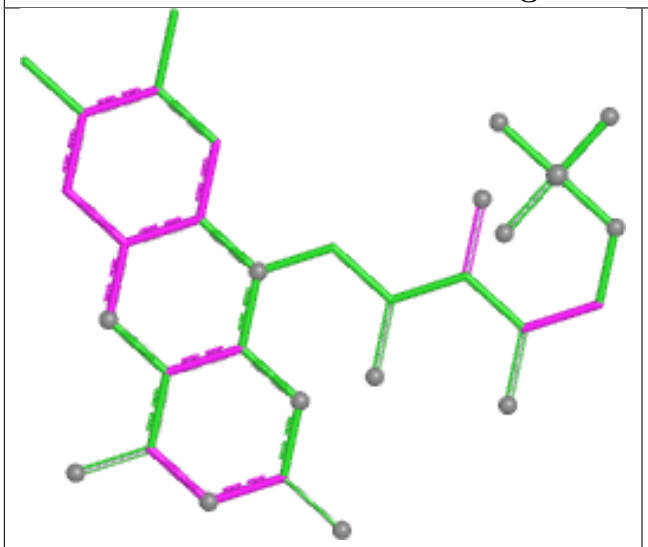


Torsions

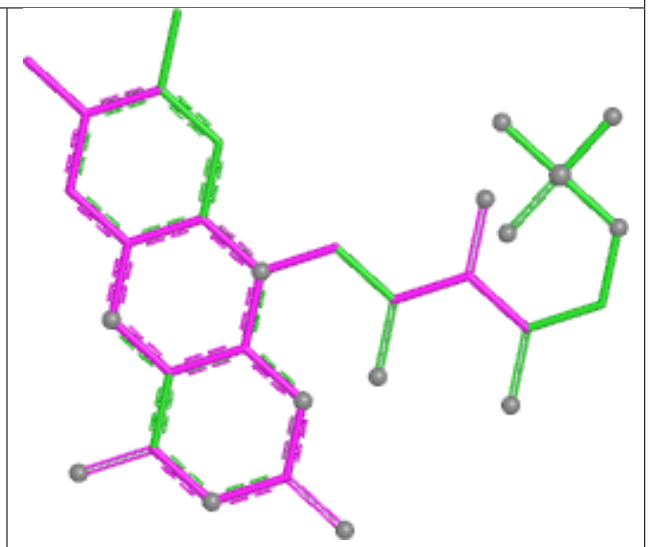


Rings

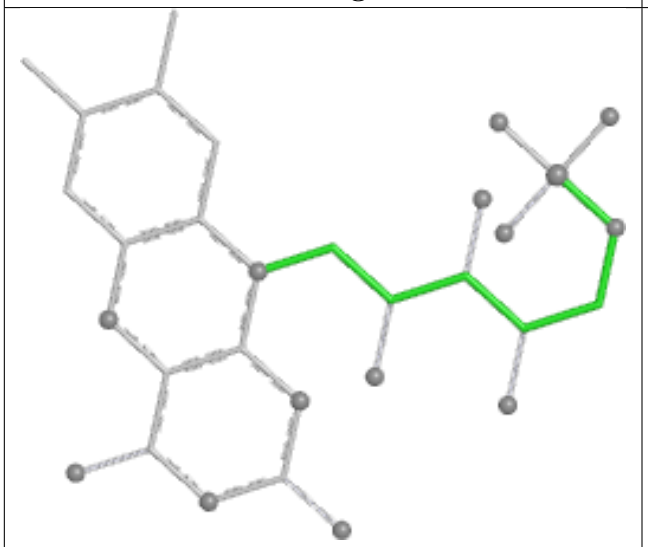
Ligand FMN C 703



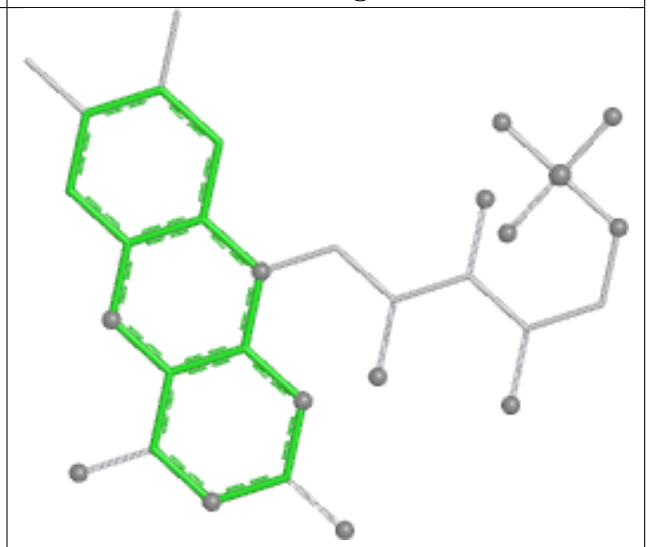
Bond lengths



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 (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	398/398 (100%)	1.25	90 (22%)	2	1	20, 56, 82, 102	2 (0%)
1	B	398/398 (100%)	1.05	51 (12%)	7	5	24, 59, 93, 117	2 (0%)
1	C	398/398 (100%)	1.45	91 (22%)	2	1	9, 49, 74, 102	2 (0%)
1	D	398/398 (100%)	1.01	49 (12%)	8	5	11, 47, 76, 99	2 (0%)
All	All	1592/1592 (100%)	1.19	281 (17%)	4	2	9, 52, 84, 117	8 (0%)

The worst 5 of 281 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	51	ASP	14.4
1	D	51	ASP	12.4
1	C	51	ASP	12.2
1	A	51	ASP	10.1
1	C	50	VAL	10.0

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 oligosaccharides in this entry.

6.4 Ligands (i)

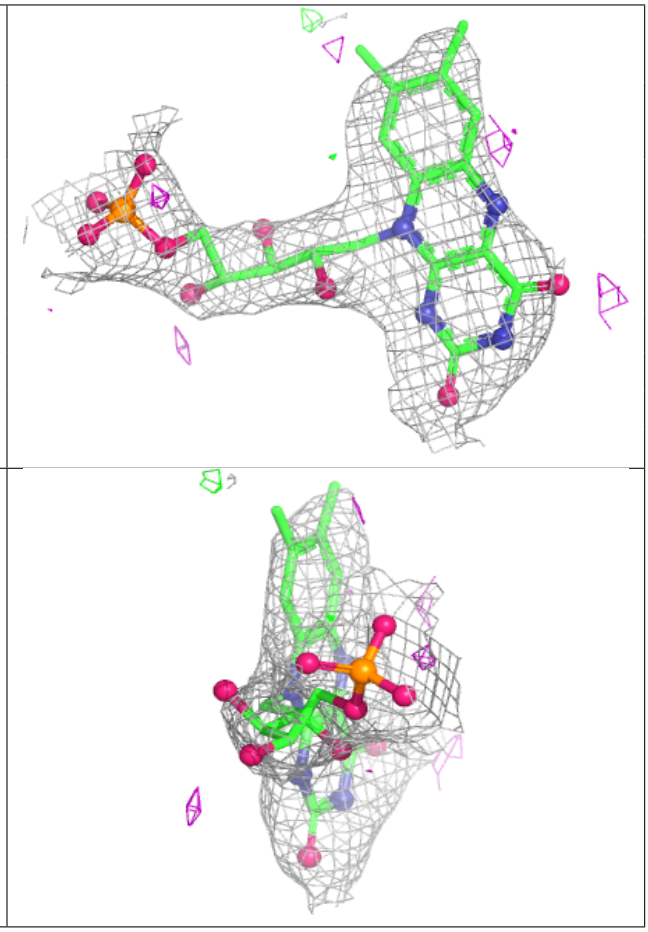
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	OXY	D	531	2/2	0.64	0.24	38,38,38,38	0
2	ZN	A	502	1/1	0.70	0.12	70,70,70,70	0
4	OXY	C	521	2/2	0.72	0.43	42,42,42,56	0
4	OXY	B	511	2/2	0.85	0.37	73,73,73,76	0
2	ZN	B	512	1/1	0.86	0.16	132,132,132,132	0
4	OXY	A	501	2/2	0.87	0.35	51,51,51,56	0
5	FMN	C	703	31/31	0.87	0.15	26,44,57,63	0
5	FMN	D	704	31/31	0.87	0.15	30,53,61,68	0
5	FMN	A	701	31/31	0.90	0.15	39,76,89,98	0
2	ZN	A	503	1/1	0.92	0.15	71,71,71,71	0
5	FMN	B	702	31/31	0.92	0.14	40,72,81,90	0
3	FEO	D	530	3/3	0.96	0.06	38,38,44,46	0
3	FEO	A	500	3/3	0.97	0.06	45,45,51,54	0
3	FEO	C	520	3/3	0.98	0.06	34,34,39,40	0
3	FEO	B	510	3/3	0.98	0.04	51,51,52,56	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.

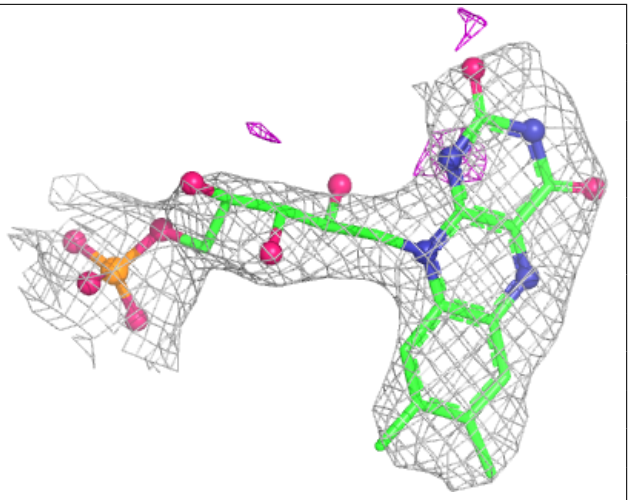
Electron density around FMN C 703:

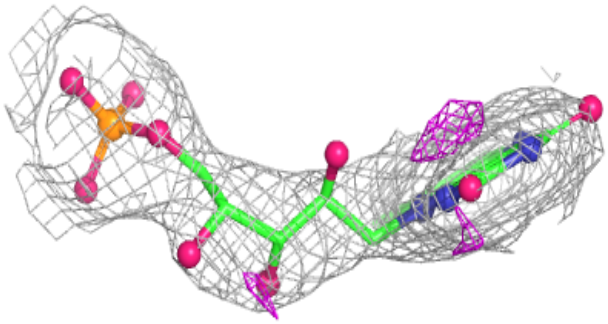
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

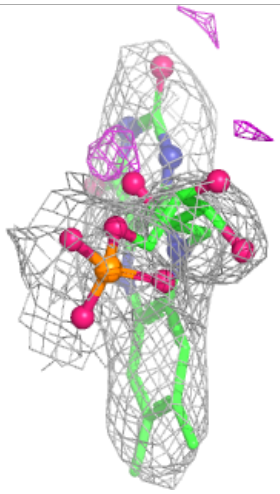


Electron density around FMN D 704:

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

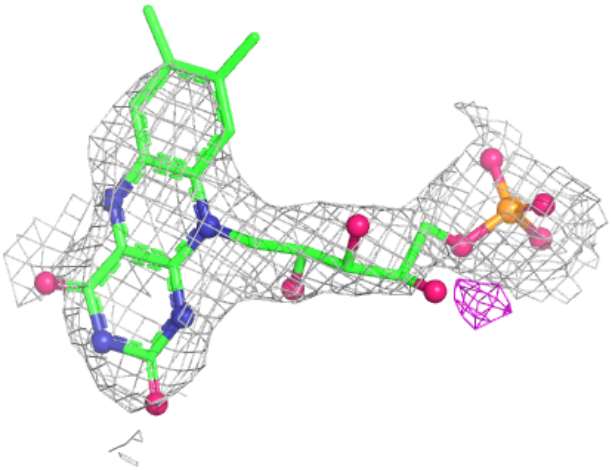


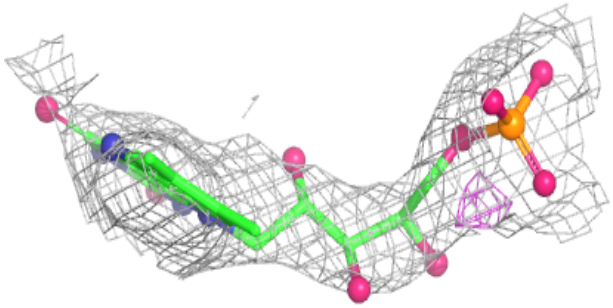


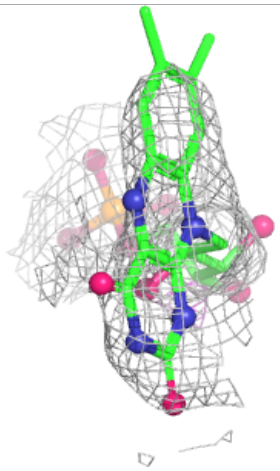


Electron density around FMN A 701:

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

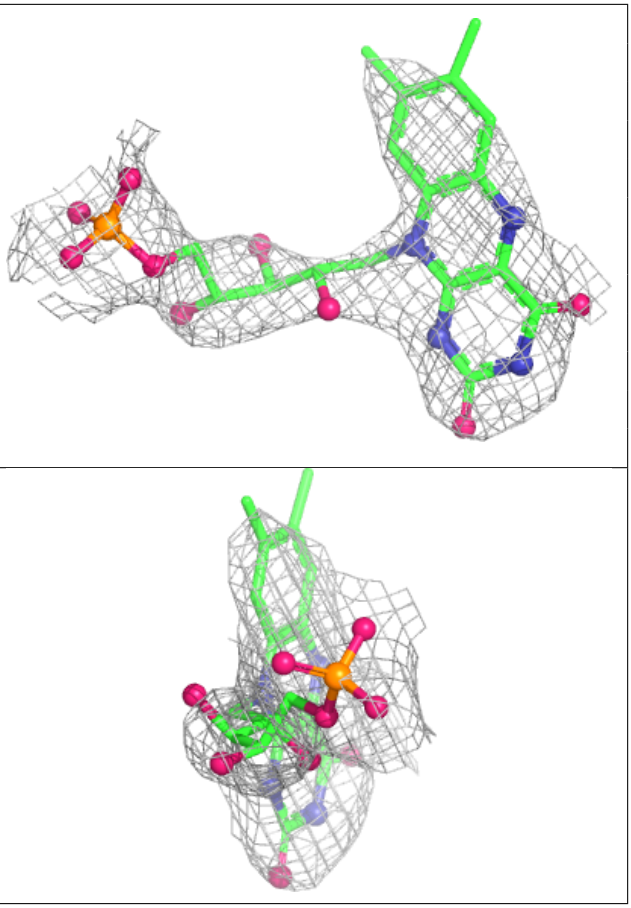






Electron density around FMN B 702:

$2mF_o$-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.