

wwPDB X-ray Structure Validation Summary Report (i)

Jul 25, 2023 – 10:24 am BST

PDB ID : 8PUN

Title: Old Yellow Enzyme from the thermophilic Ferrovum sp. JA12

Authors: Polidori, N.; Gruber, K.

Deposited on : 2023-07-17

Resolution : 2.30 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.34

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)

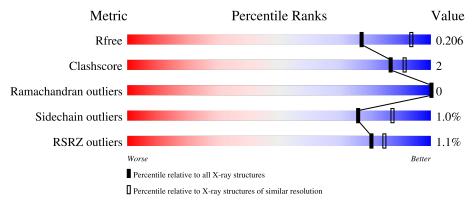
Validation Pipeline (wwPDB-VP) : 2.34

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 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
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 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	373	89%	6%	5%
1	В	373	90%	6%	5%
1	С	373	91%	5%	5%
1	D	373	90%	5%	5%

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
3	PEG	A	402	-	-	-	X
8	PGE	В	403	-	-	-	X



2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 11933 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 NADPH dehydrogenase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	356	Total	С	N	О	S	0	4	0
1	A	990	2775	1758	497	507	13	0	4	0
1	В	356	Total	С	N	О	S	0	2	0
1	Б	350	2757	1746	493	505	13	U		0
1	С	356	Total	С	N	О	S	0	4	0
1		0 300	2773	1755	493	512	13	0	4	0
1	D	256	Total	С	N	О	S	0	1	0
	356	2772	1756	493	510	13		4	U	

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP A0A0R0LNE8
A	-17	GLY	-	expression tag	UNP A0A0R0LNE8
A	-16	SER	-	expression tag	UNP A0A0R0LNE8
A	-15	SER	-	expression tag	UNP A0A0R0LNE8
A	-14	HIS	-	expression tag	UNP A0A0R0LNE8
A	-13	HIS	-	expression tag	UNP A0A0R0LNE8
A	-12	HIS	-	expression tag	UNP A0A0R0LNE8
A	-11	HIS	-	expression tag	UNP A0A0R0LNE8
A	-10	HIS	-	expression tag	UNP A0A0R0LNE8
A	-9	HIS	-	expression tag	UNP A0A0R0LNE8
A	-8	SER	-	expression tag	UNP A0A0R0LNE8
A	-7	SER	-	expression tag	UNP A0A0R0LNE8
A	-6	GLY	-	expression tag	UNP A0A0R0LNE8
A	-5	LEU	-	expression tag	UNP A0A0R0LNE8
A	-4	VAL	-	expression tag	UNP A0A0R0LNE8
A	-3	PRO	-	expression tag	UNP A0A0R0LNE8
A	-2	ARG	-	expression tag	UNP A0A0R0LNE8
A	-1	GLY	-	expression tag	UNP A0A0R0LNE8
A	0	SER	-	expression tag	UNP A0A0R0LNE8
В	-18	MET	-	initiating methionine	UNP A0A0R0LNE8
В	-17	GLY	-	expression tag	UNP A0A0R0LNE8

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Chain	Residue	Modelled	Actual	Comment	Reference
В	-16	SER	-	expression tag	UNP A0A0R0LNE8
В	-15	SER	-	expression tag	UNP A0A0R0LNE8
В	-14	HIS	-	expression tag	UNP A0A0R0LNE8
В	-13	HIS	-	expression tag	UNP A0A0R0LNE8
В	-12	HIS	-	expression tag	UNP A0A0R0LNE8
В	-11	HIS	-	expression tag	UNP A0A0R0LNE8
В	-10	HIS	-	expression tag	UNP A0A0R0LNE8
В	-9	HIS	-	expression tag	UNP A0A0R0LNE8
В	-8	SER	-	expression tag	UNP A0A0R0LNE8
В	-7	SER	-	expression tag	UNP A0A0R0LNE8
В	-6	GLY	-	expression tag	UNP A0A0R0LNE8
В	-5	LEU	-	expression tag	UNP A0A0R0LNE8
В	-4	VAL	-	expression tag	UNP A0A0R0LNE8
В	-3	PRO	-	expression tag	UNP A0A0R0LNE8
В	-2	ARG	-	expression tag	UNP A0A0R0LNE8
В	-1	GLY	-	expression tag	UNP A0A0R0LNE8
В	0	SER	-	expression tag	UNP A0A0R0LNE8
С	-18	MET	-	initiating methionine	UNP A0A0R0LNE8
С	-17	GLY	-	expression tag	UNP A0A0R0LNE8
С	-16	SER	-	expression tag	UNP A0A0R0LNE8
С	-15	SER	-	expression tag	UNP A0A0R0LNE8
С	-14	HIS	-	expression tag	UNP A0A0R0LNE8
С	-13	HIS	_	expression tag	UNP A0A0R0LNE8
С	-12	HIS	-	expression tag	UNP A0A0R0LNE8
С	-11	HIS	-	expression tag	UNP A0A0R0LNE8
С	-10	HIS	-	expression tag	UNP A0A0R0LNE8
С	-9	HIS	_	expression tag	UNP A0A0R0LNE8
С	-8	SER	-	expression tag	UNP A0A0R0LNE8
С	-7	SER	-	expression tag	UNP A0A0R0LNE8
С	-6	GLY	-	expression tag	UNP A0A0R0LNE8
С	-5	LEU	-	expression tag	UNP A0A0R0LNE8
С	-4	VAL	-	expression tag	UNP A0A0R0LNE8
С	-3	PRO	-	expression tag	UNP A0A0R0LNE8
С	-2	ARG	-	expression tag	UNP A0A0R0LNE8
С	-1	GLY	-	expression tag	UNP A0A0R0LNE8
С	0	SER	-	expression tag	UNP A0A0R0LNE8
D	-18	MET	-	initiating methionine	UNP A0A0R0LNE8
D	-17	GLY	-	expression tag	UNP A0A0R0LNE8
D	-16	SER	-	expression tag	UNP A0A0R0LNE8
D	-15	SER	-	expression tag	UNP A0A0R0LNE8
D	-14	HIS	-	expression tag	UNP A0A0R0LNE8
D	-13	HIS	-	expression tag	tinued on next rage

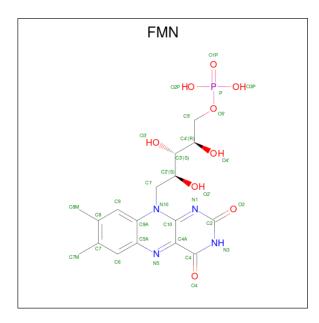
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	HIS	-	expression tag	UNP A0A0R0LNE8
D	-11	HIS	-	expression tag	UNP A0A0R0LNE8
D	-10	HIS	-	expression tag	UNP A0A0R0LNE8
D	-9	HIS	-	expression tag	UNP A0A0R0LNE8
D	-8	SER	-	expression tag	UNP A0A0R0LNE8
D	-7	SER	-	expression tag	UNP A0A0R0LNE8
D	-6	GLY	-	expression tag	UNP A0A0R0LNE8
D	-5	LEU	-	expression tag	UNP A0A0R0LNE8
D	-4	VAL	-	expression tag	UNP A0A0R0LNE8
D	-3	PRO	-	expression tag	UNP A0A0R0LNE8
D	-2	ARG	-	expression tag	UNP A0A0R0LNE8
D	-1	GLY	-	expression tag	UNP A0A0R0LNE8
D	0	SER	-	expression tag	UNP A0A0R0LNE8

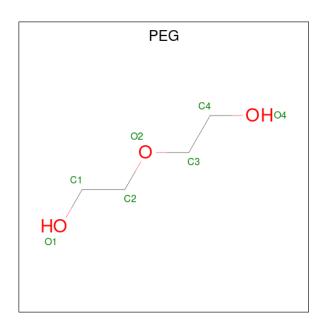
 $\bullet \ \ Molecule\ 2 \ is\ FLAVIN\ MONONUCLEOTIDE\ (three-letter\ code:\ FMN)\ (formula:\ C_{17}H_{21}N_4O_9P).$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	Λ	1	Total	С	N	О	Р	0	0	
	Λ	1	31	17	4	9	1	0		
2	R	1	Total	С	N	О	Р	0	0	
	2 D	1	31	17	4	9	1			
2	С	1	Total	С	N	О	Р	0	0	
		1	31	17	4	9	1	U		
2	D	1	Total	С	N	О	Р	0	0	
	ש	1	31	17	4	9	1	U	U	

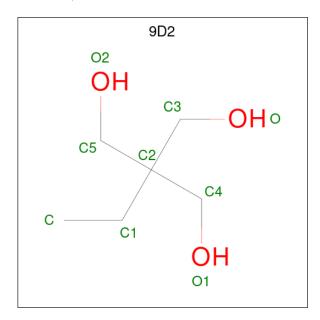
 $\bullet \ \, \text{Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$)}. \\$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	С	1	Total C O 7 4 3	0	0

• Molecule 4 is 2-ethyl-2-(hydroxymethyl) propane-1,3-diol (three-letter code: 9D2) (formula: $C_6H_{14}O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 9 6 3	0	0
4	В	1	Total C O 9 6 3	0	0

• Molecule 5 is YTTRIUM (III) ION (three-letter code: YT3) (formula: Y).

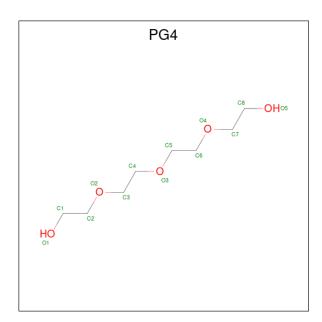
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Y 2 2	0	0
5	В	2	Total Y 2 2	0	0
5	С	1	Total Y 1 1	0	0
5	D	2	$\begin{array}{cc} \text{Total} & Y \\ 2 & 2 \end{array}$	0	0

• Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0
6	В	1	Total Cl 1 1	0	0
6	С	1	Total Cl 1 1	0	0
6	D	2	Total Cl 2 2	0	0

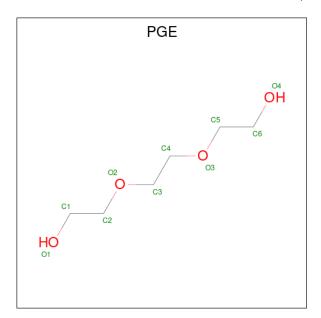
 \bullet Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $\mathrm{C_8H_{18}O_5}).$





Mol	Chain	Residues	Ato	ms		ZeroOcc	AltConf
7	В	1	Total 13	C 8	O 5	0	0

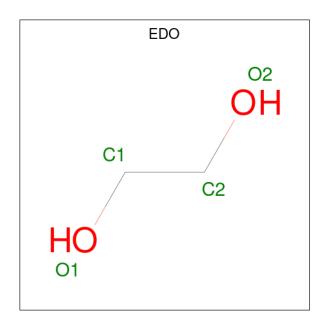
 \bullet Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $\mathrm{C_6H_{14}O_4}).$



\mathbf{Mol}	Chain	Residues	Ato	oms		ZeroOcc	AltConf
8	В	1	Total 10	C 6	O 4	0	0

 \bullet Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	С	1	Total C O 4 2 2	0	0
9	С	1	Total C O 4 2 2	0	0
9	D	1	Total C O 4 2 2	0	0
9	D	1	Total C O 4 2 2	0	0

• Molecule 10 is water.

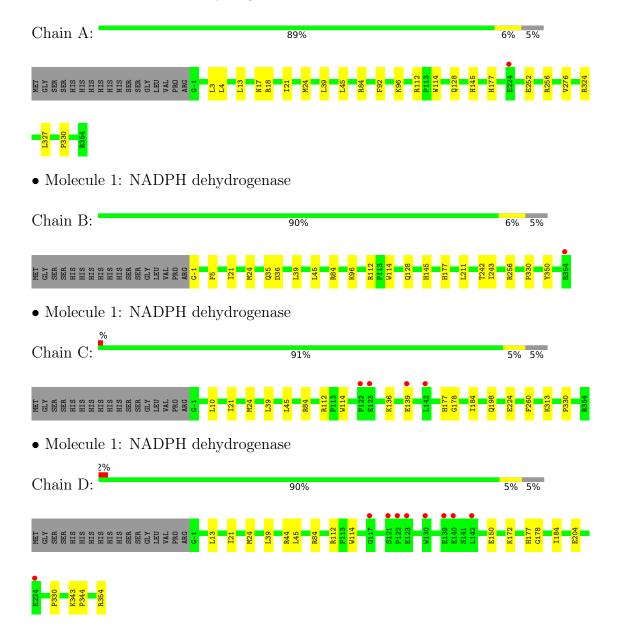
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	152	Total O 152 152	0	0
10	В	175	Total O 175 175	0	0
10	С	155	Total O 155 155	0	0
10	D	160	Total O 160 160	0	0



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: NADPH dehydrogenase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants	187.71Å 187.71Å 129.32Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.30 - 2.30	Depositor
rtesolution (A)	48.30 - 2.30	EDS
% Data completeness	99.5 (48.30-2.30)	Depositor
(in resolution range)	99.7 (48.30-2.30)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.80 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D.D.	0.180 , 0.205	Depositor
R, R_{free}	0.181 , 0.206	DCC
R_{free} test set	5145 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 37.6	EDS
L-test for twinning ²	$ < L >=0.58, < L^2>=0.43$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11933	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 48.66 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.3355e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: YT3, 9D2, PGE, CL, PG4, EDO, PEG, 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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.26	0/2845	0.45	0/3864	
1	В	0.26	0/2826	0.44	0/3837	
1	С	0.26	0/2842	0.45	0/3859	
1	D	0.26	0/2841	0.44	0/3858	
All	All	0.26	0/11354	0.45	0/15418	

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 (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	2775	0	2739	15	0
1	В	2757	0	2722	15	0
1	С	2773	0	2727	10	0
1	D	2772	0	2732	11	0
2	A	31	0	19	1	0
2	В	31	0	19	1	0
2	С	31	0	19	1	0
2	D	31	0	19	1	0
3	A	14	0	20	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	С	7	0	10	1	0
4	A	9	0	0	0	0
4	В	9	0	0	0	0
5	A	2	0	0	0	0
5	В	2	0	0	0	0
5	С	1	0	0	0	0
5	D	2	0	0	0	0
6	A	1	0	0	0	0
6	В	1	0	0	0	0
6	С	1	0	0	0	0
6	D	2	0	0	0	0
7	В	13	0	18	5	0
8	В	10	0	14	2	0
9	С	8	0	12	1	0
9	D	8	0	12	1	0
10	A	152	0	0	0	0
10	В	175	0	0	0	0
10	С	155	0	0	0	0
10	D	160	0	0	1	0
All	All	11933	0	11082	47	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 2.

The worst 5 of 47 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:C:39:LEU:HD12	1:D:39:LEU:HD12	1.67	0.76
1:B:36:ASP:HB2	7:B:401:PG4:H52	1.78	0.65
1:A:39:LEU:HD23	1:B:39:LEU:HD23	1.79	0.65
1:C:330:PRO:HG2	1:D:330:PRO:HG2	1.83	0.59
1:B:128:GLN:OE1	1:B:145:HIS:NE2	2.36	0.59

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	Percer	ntiles
1	A	358/373 (96%)	350 (98%)	8 (2%)	0	100	100
1	В	356/373~(95%)	347 (98%)	9 (2%)	0	100	100
1	С	358/373 (96%)	350 (98%)	8 (2%)	0	100	100
1	D	358/373 (96%)	350 (98%)	8 (2%)	0	100	100
All	All	1430/1492 (96%)	1397 (98%)	33 (2%)	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	Perce	ntiles
1	A	285/296~(96%)	283 (99%)	2 (1%)	84	92
1	В	283/296 (96%)	280 (99%)	3 (1%)	73	86
1	С	285/296 (96%)	282 (99%)	3 (1%)	73	86
1	D	285/296 (96%)	281 (99%)	4 (1%)	67	81
All	All	1138/1184 (96%)	1126 (99%)	12 (1%)	76	86

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	224	GLU
1	D	84	ARG
1	D	343	LYS

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Mol	Chain	Res	Type
1	D	150	GLU
1	В	84[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 27 ligands modelled in this entry, 12 are monoatomic - leaving 15 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	Mol Type Chain		Res	Link	Вс	Bond lengths			Bond angles		
MIOI	wor Type Chain	Chain	ries	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
9	EDO	D	402	-	3,3,3	0.51	0	2,2,2	0.17	0	
2	FMN	D	401	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	7 (14%)	
3	PEG	A	402	-	6,6,6	0.49	0	5,5,5	0.29	0	
2	FMN	A	401	-	33,33,33	1.06	2 (6%)	48,50,50	1.24	7 (14%)	
3	PEG	С	404	-	6,6,6	0.47	0	5,5,5	0.30	0	
7	PG4	В	401	-	12,12,12	0.52	0	11,11,11	0.28	0	
2	FMN	В	402	-	33,33,33	1.07	2 (6%)	48,50,50	1.25	7 (14%)	
2	FMN	С	401	-	33,33,33	1.07	2 (6%)	48,50,50	1.25	7 (14%)	



Mol	Mol Type Chain		Res	Res Link	Во	ond leng	$ ag{ths}$	Bond angles		
MIOI	of Type Chain	Counts			RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
8	PGE	В	403	-	9,9,9	0.51	0	8,8,8	0.21	0
3	PEG	A	406	5	6,6,6	0.49	0	5,5,5	0.22	0
9	EDO	С	405	-	3,3,3	0.47	0	2,2,2	0.37	0
9	EDO	D	404	-	3,3,3	0.50	0	2,2,2	0.21	0
4	9D2	В	404	-	8,8,8	0.54	0	10,10,10	0.91	1 (10%)
9	EDO	С	402	-	3,3,3	0.50	0	2,2,2	0.27	0
4	9D2	A	403	-	8,8,8	0.48	0	10,10,10	0.76	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
9	EDO	D	402	-	-	0/1/1/1	-
2	FMN	D	401	-	-	1/18/18/18	0/3/3/3
3	PEG	A	402	-	-	4/4/4/4	-
2	FMN	A	401	-	-	1/18/18/18	0/3/3/3
3	PEG	С	404	-	-	1/4/4/4	-
7	PG4	В	401	-	-	8/10/10/10	-
2	FMN	В	402	-	-	1/18/18/18	0/3/3/3
2	FMN	С	401	-	-	1/18/18/18	0/3/3/3
8	PGE	В	403	-	-	4/7/7/7	-
3	PEG	A	406	5	-	1/4/4/4	-
9	EDO	С	405	-	-	0/1/1/1	-
9	EDO	D	404	-	-	0/1/1/1	-
4	9D2	В	404	-	-	0/12/12/12	-
9	EDO	С	402	-	-	0/1/1/1	-
4	9D2	A	403	-	-	9/12/12/12	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
2	С	401	FMN	C4A-N5	4.05	1.38	1.30
2	D	401	FMN	C4A-N5	4.00	1.38	1.30
2	В	402	FMN	C4A-N5	3.89	1.38	1.30
2	A	401	FMN	C4A-N5	3.87	1.38	1.30
2	С	401	FMN	C10-N1	2.54	1.38	1.33

The worst 5 of 29 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
2	D	401	FMN	C4-N3-C2	-3.28	119.58	125.64
2	В	402	FMN	C4-N3-C2	-3.20	119.73	125.64
2	С	401	FMN	C4-N3-C2	-3.15	119.81	125.64
2	A	401	FMN	C4-N3-C2	-3.15	119.82	125.64
2	D	401	FMN	C4A-C4-N3	2.87	120.47	113.19

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	9D2	C1-C2-C5-O2
4	A	403	9D2	C-C1-C2-C4
4	A	403	9D2	C-C1-C2-C5
4	A	403	9D2	C-C1-C2-C3
3	A	402	PEG	O1-C1-C2-O2

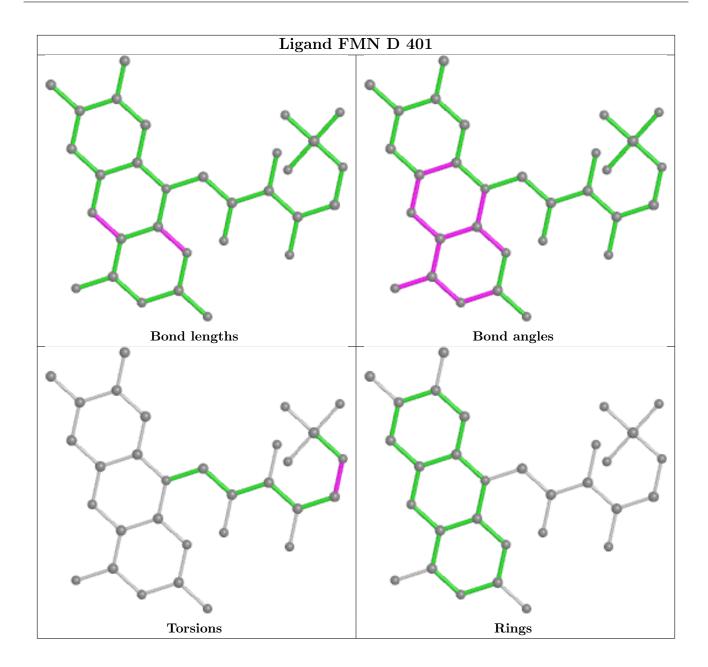
There are no ring outliers.

10 monomers are involved in 17 short contacts:

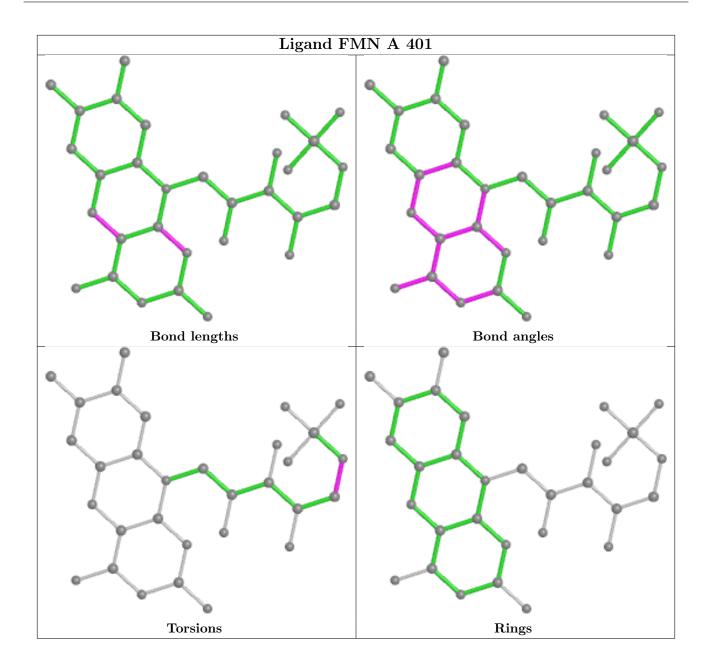
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	FMN	1	0
3	A	402	PEG	3	0
2	A	401	FMN	1	0
3	С	404	PEG	1	0
7	В	401	PG4	5	0
2	В	402	FMN	1	0
2	С	401	FMN	1	0
8	В	403	PGE	2	0
9	D	404	EDO	1	0
9	C	402	EDO	1	0

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.

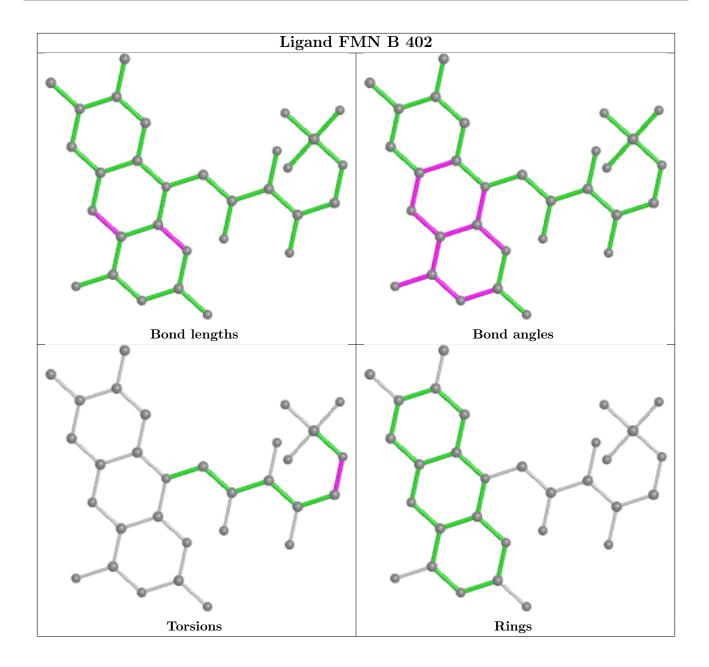




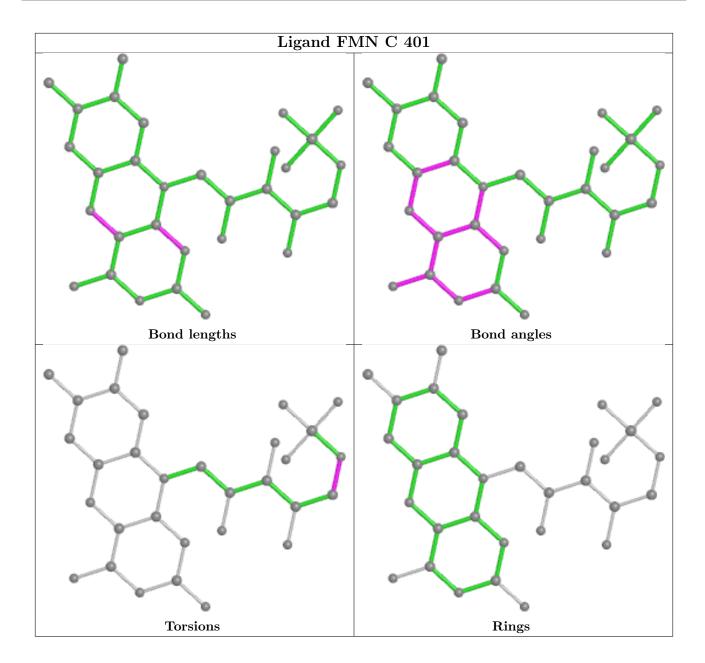












5.7 Other polymers (i)

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, 95^{th} 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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	356/373~(95%)	-0.34	1 (0%) 94 96	28, 36, 54, 74	0
1	В	356/373~(95%)	-0.40	1 (0%) 94 96	27, 36, 54, 70	0
1	С	356/373~(95%)	-0.31	4 (1%) 80 85	28, 37, 59, 81	0
1	D	356/373~(95%)	-0.25	9 (2%) 57 64	28, 37, 63, 80	0
All	All	1424/1492 (95%)	-0.33	15 (1%) 80 85	27, 36, 57, 81	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	123	GLU	4.4
1	С	123	GLU	3.7
1	D	117	GLY	3.1
1	D	140	GLU	3.0
1	D	122	PRO	3.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

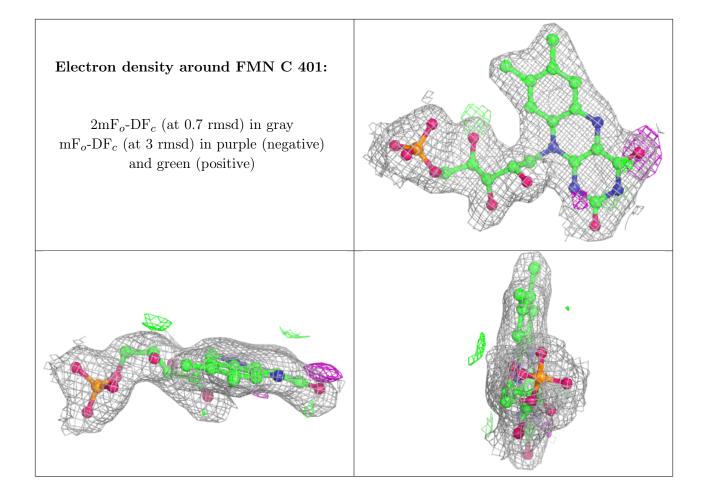
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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



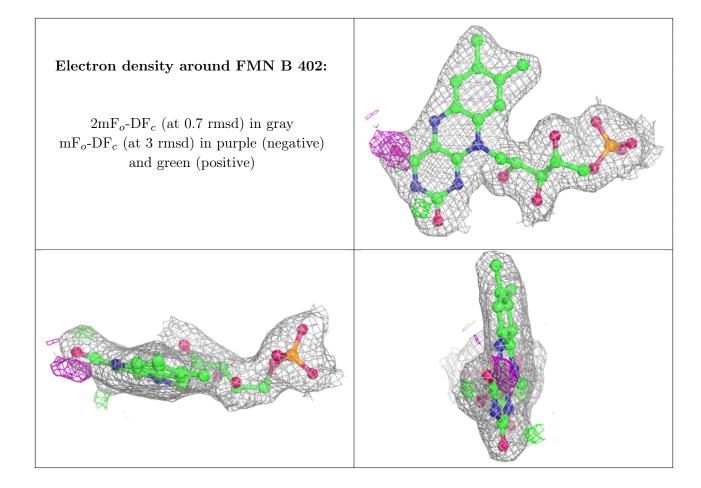
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	PEG	A	406	7/7	0.60	0.39	49,67,75,80	0
9	EDO	D	402	4/4	0.62	0.34	43,45,51,56	4
7	PG4	В	401	13/13	0.65	0.39	42,55,71,72	0
8	PGE	В	403	10/10	0.68	0.49	48,55,61,62	10
9	EDO	D	404	4/4	0.72	0.35	38,43,50,55	4
3	PEG	A	402	7/7	0.78	0.51	46,55,64,74	0
9	EDO	С	402	4/4	0.78	0.24	40,51,55,58	0
3	PEG	С	404	7/7	0.81	0.24	60,71,77,79	0
6	CL	С	406	1/1	0.82	0.23	71,71,71,71	0
9	EDO	С	405	4/4	0.84	0.17	54,55,69,71	0
5	YT3	A	404	1/1	0.88	0.13	93,93,93,93	0
4	9D2	A	403	9/9	0.88	0.21	34,50,57,60	0
5	YT3	В	406	1/1	0.89	0.11	88,88,88,88	0
6	CL	A	407	1/1	0.91	0.14	59,59,59,59	0
6	CL	В	407	1/1	0.91	0.15	52,52,52,52	0
5	YT3	С	403	1/1	0.91	0.06	84,84,84,84	0
6	CL	D	406	1/1	0.91	0.16	66,66,66,66	0
5	YT3	D	405	1/1	0.91	0.09	84,84,84,84	0
4	9D2	В	404	9/9	0.92	0.15	34,44,49,57	0
6	CL	D	407	1/1	0.92	0.05	78,78,78,78	0
5	YT3	D	403	1/1	0.93	0.03	120,120,120,120	0
2	FMN	С	401	31/31	0.97	0.13	26,32,39,42	0
5	YT3	A	405	1/1	0.98	0.20	39,39,39,39	0
2	FMN	В	402	31/31	0.98	0.13	22,29,36,37	0
2	FMN	A	401	31/31	0.98	0.11	23,31,37,40	0
2	FMN	D	401	31/31	0.98	0.11	26,32,38,41	0
5	YT3	В	405	1/1	0.99	0.20	37,37,37,37	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.

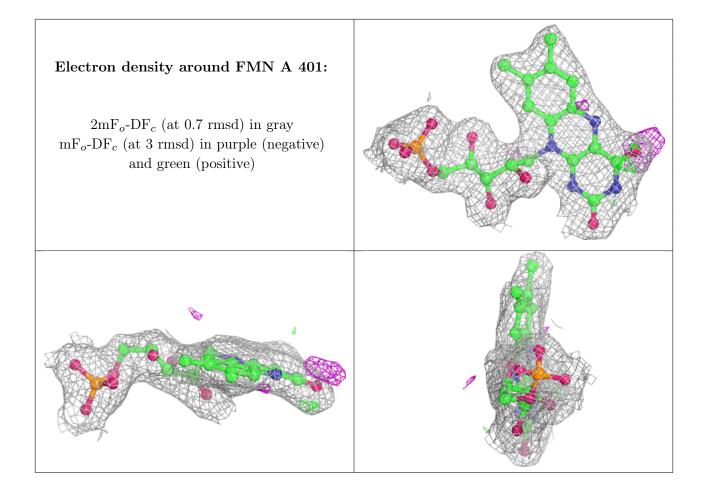




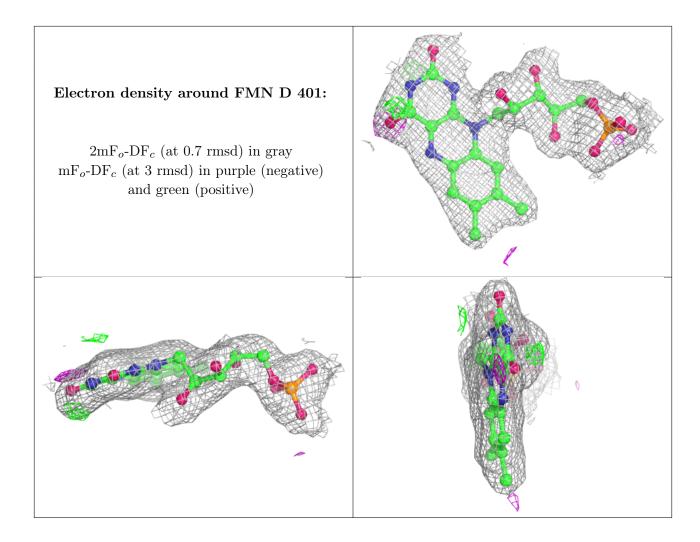












6.5 Other polymers (i)

There are no such residues in this entry.

