



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 05:05 PM UTC

PDB ID : 2Q3O / pdb_00002q3o
Title : Ensemble refinement of the protein crystal structure of 12-oxo-phytodienoate reductase isoform 3
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2007-05-30
Resolution : 2.00 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 ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

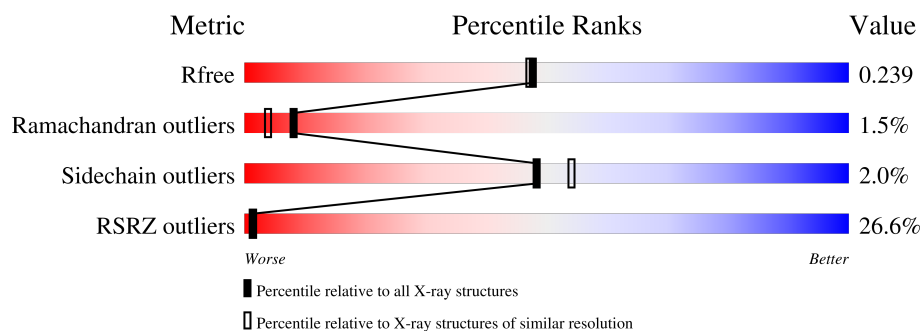
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	1-A	391	
1	1-B	391	
1	10-A	391	
1	10-B	391	
1	11-A	391	
1	11-B	391	

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Mol	Chain	Length	Quality of chain
1	12-A	391	 90% • 7%
1	12-B	391	 91% • 6%
1	13-A	391	 91% • 7%
1	13-B	391	 90% • 6%
1	14-A	391	 91% • 7%
1	14-B	391	 90% • 6%
1	15-A	391	 91% • 7%
1	15-B	391	 90% • 6%
1	16-A	391	 91% • 7%
1	16-B	391	 91% • 6%
1	2-A	391	 90% • 7%
1	2-B	391	 91% • 6%
1	3-A	391	 92% • 7%
1	3-B	391	 90% • 6%
1	4-A	391	 91% • 7%
1	4-B	391	 91% • 6%
1	5-A	391	 92% • 7%
1	5-B	391	 91% • 6%
1	6-A	391	 92% • 7%
1	6-B	391	 92% • 6%
1	7-A	391	 91% • 7%
1	7-B	391	 90% • 6%
1	8-A	391	 91% • 7%
1	8-B	391	 91% • 6%
1	9-A	391	 90% • 7%

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Mol	Chain	Length	Quality of chain
1	9-B	391	 91% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 97936 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 12-oxophytodienoate reductase 3.

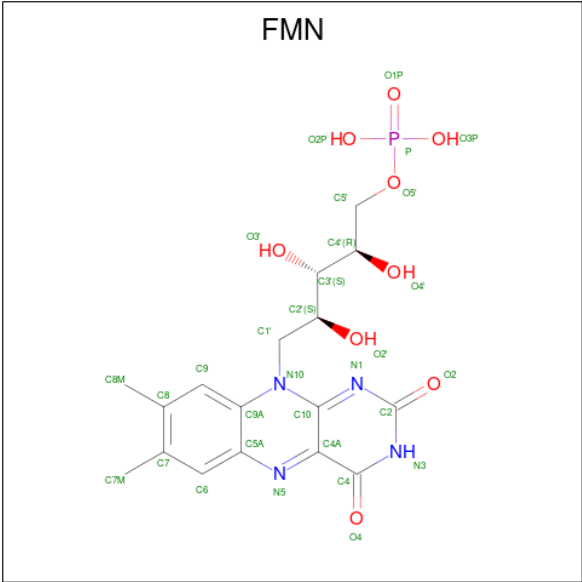
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	2-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	3-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	4-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	5-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	6-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	7-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	8-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	9-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	10-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	11-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	12-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	13-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	14-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	15-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			
1	16-A	365	Total	C	N	O	S	0	0	0
			2810	1779	495	524	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	2-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	3-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	4-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	5-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	6-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	7-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	8-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	9-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	10-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	11-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	12-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	13-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	14-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	15-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			
1	16-B	367	Total	C	N	O	S	0	0	0
			2839	1799	499	529	12			

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	1-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	2-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	3-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	4-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	5-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	6-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	7-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	8-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	9-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	10-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	11-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	12-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	13-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	14-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	15-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	16-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	1-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	2-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	3-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	4-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	5-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	6-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	7-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	8-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	9-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	10-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	11-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	12-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	13-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	14-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	15-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	16-B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1-A	202	Total	O	0	0
			202	202		

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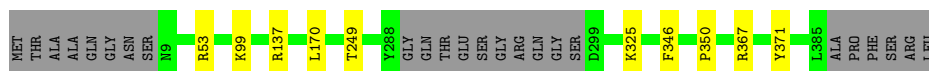
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	2-A	202	Total O 202 202	0	0
3	3-A	202	Total O 202 202	0	0
3	4-A	203	Total O 203 203	0	0
3	5-A	205	Total O 205 205	0	0
3	6-A	203	Total O 203 203	0	0
3	7-A	203	Total O 203 203	0	0
3	8-A	201	Total O 201 201	0	0
3	9-A	205	Total O 205 205	0	0
3	10-A	200	Total O 200 200	0	0
3	11-A	203	Total O 203 203	0	0
3	12-A	206	Total O 206 206	0	0
3	13-A	206	Total O 206 206	0	0
3	14-A	202	Total O 202 202	0	0
3	15-A	200	Total O 200 200	0	0
3	16-A	204	Total O 204 204	0	0
3	1-B	208	Total O 208 208	0	0
3	2-B	208	Total O 208 208	0	0
3	3-B	208	Total O 208 208	0	0
3	4-B	207	Total O 207 207	0	0
3	5-B	205	Total O 205 205	0	0
3	6-B	207	Total O 207 207	0	0

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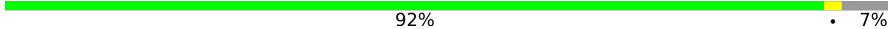
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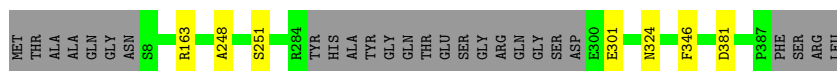
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	7-B	207	Total 207	O 207	0	0
3	8-B	209	Total 209	O 209	0	0
3	9-B	205	Total 205	O 205	0	0
3	10-B	210	Total 210	O 210	0	0
3	11-B	207	Total 207	O 207	0	0
3	12-B	204	Total 204	O 204	0	0
3	13-B	204	Total 204	O 204	0	0
3	14-B	208	Total 208	O 208	0	0
3	15-B	210	Total 210	O 210	0	0
3	16-B	206	Total 206	O 206	0	0

Chain 2-B:  91% • 6%



- Molecule 1: 12-oxophytodienoate reductase 3

Chain 3-A:  92% • 7%



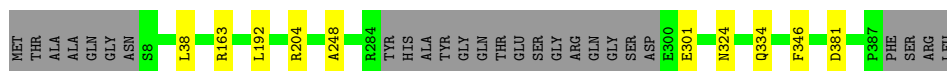
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 3-B:  90% • 6%



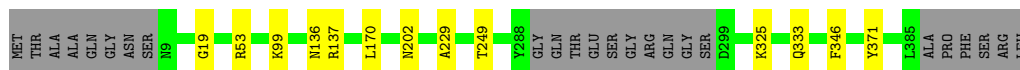
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 4-A:  91% • 7%



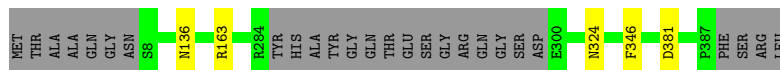
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 4-B:  91% • 6%



- Molecule 1: 12-oxophytodienoate reductase 3

Chain 5-A:  92% • 7%

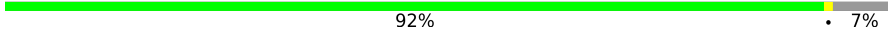


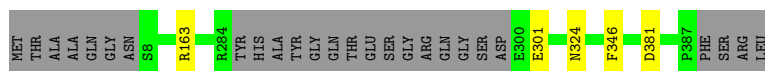
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 5-B:  91% • 6%



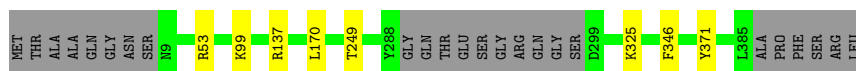
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 6-A:  92% • 7%



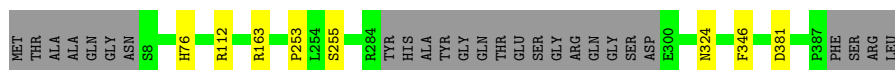
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 6-B:  92% • 6%



- Molecule 1: 12-oxophytodienoate reductase 3

Chain 7-A:  91% • 7%



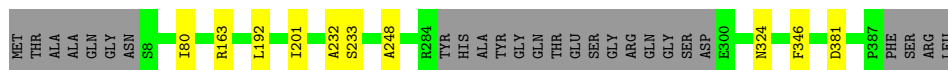
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 7-B:  90% • 6%



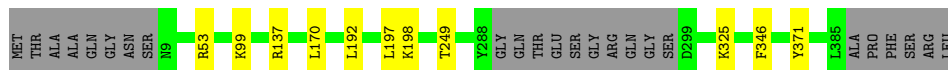
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 8-A:  91% • 7%



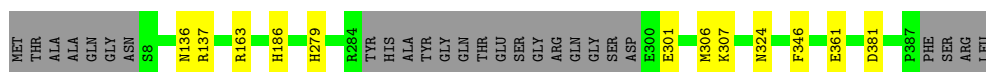
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 8-B:  91% • 6%



- Molecule 1: 12-oxophytodienoate reductase 3

Chain 9-A:  90% • 7%



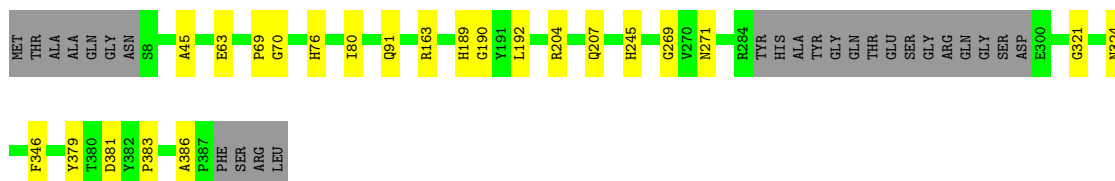
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 9-B:  91% 6%



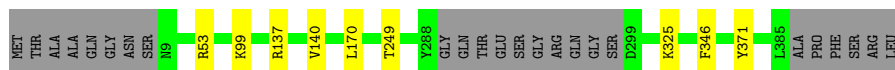
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 10-A:  87% 6% 7%



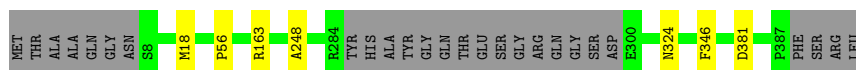
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 10-B:  92% 6%



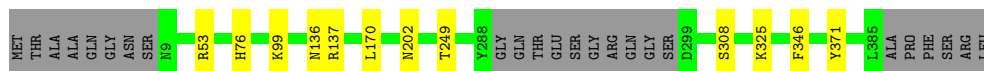
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 11-A:  92% 7%



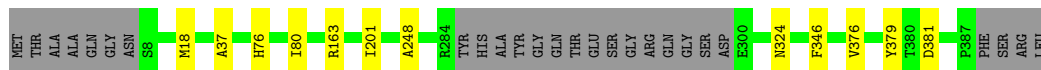
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 11-B:  91% 6%



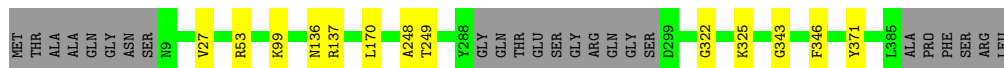
- Molecule 1: 12-oxophytodienoate reductase 3

Chain 12-A:  90% 7%

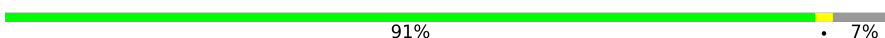
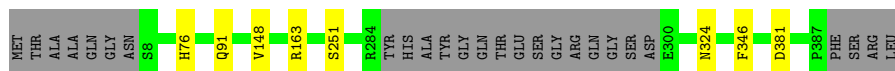


- Molecule 1: 12-oxophytodienoate reductase 3

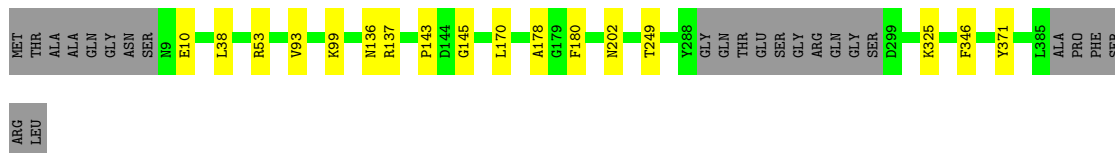
Chain 12-B:  91% 6%



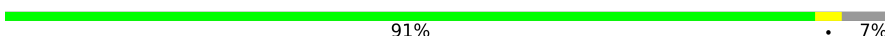
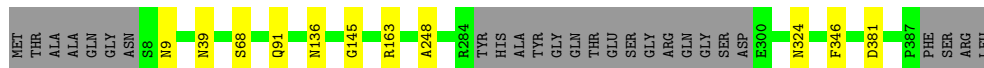
● Molecule 1: 12-oxophytodienoate reductase 3

Chain 13-A:  91% 7%

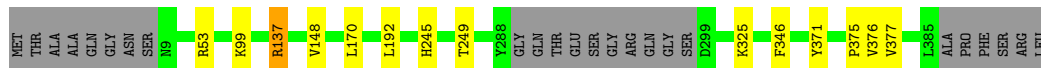
● Molecule 1: 12-oxophytodienoate reductase 3

Chain 13-B:  90% 6%

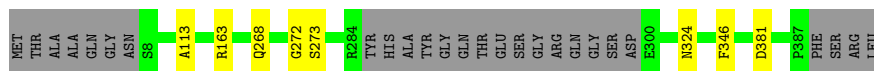
● Molecule 1: 12-oxophytodienoate reductase 3

Chain 14-A:  91% 7%

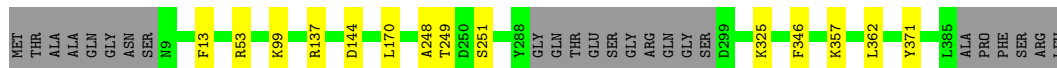
● Molecule 1: 12-oxophytodienoate reductase 3

Chain 14-B:  90% 6%

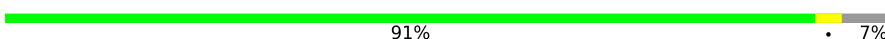
● Molecule 1: 12-oxophytodienoate reductase 3

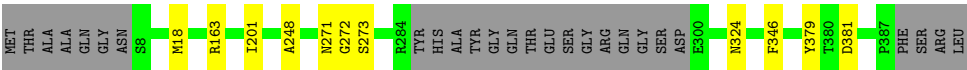
Chain 15-A:  91% 7%

● Molecule 1: 12-oxophytodienoate reductase 3

Chain 15-B:  90% 6%

● Molecule 1: 12-oxophytodienoate reductase 3

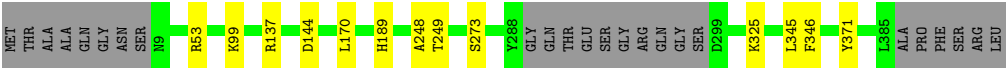
Chain 16-A:  91% 7%



● Molecule 1: 12-oxophytodienoate reductase 3

Chain 16-B:

91%6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.11Å 85.07Å 121.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.90 – 2.00 24.90 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.1 (24.90-2.00) 91.2 (24.90-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 1.99Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.180 , 0.235 0.186 , 0.239	Depositor DCC
R_{free} test set	2572 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.02 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	97936	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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: 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	1-A	0.21	0/2875	0.42	0/3895
1	1-B	0.23	0/2906	0.44	0/3937
1	2-A	0.21	0/2875	0.42	0/3895
1	2-B	0.23	0/2906	0.44	0/3937
1	3-A	0.21	0/2875	0.42	0/3895
1	3-B	0.23	0/2906	0.44	0/3937
1	4-A	0.21	0/2875	0.42	0/3895
1	4-B	0.23	0/2906	0.44	0/3937
1	5-A	0.21	0/2875	0.42	0/3895
1	5-B	0.23	0/2906	0.44	0/3937
1	6-A	0.21	0/2875	0.42	0/3895
1	6-B	0.23	0/2906	0.44	0/3937
1	7-A	0.21	0/2875	0.42	0/3895
1	7-B	0.23	0/2906	0.44	0/3937
1	8-A	0.21	0/2875	0.42	0/3895
1	8-B	0.23	0/2906	0.44	0/3937
1	9-A	0.21	0/2875	0.42	0/3895
1	9-B	0.23	0/2906	0.44	0/3937
1	10-A	0.21	0/2875	0.42	0/3895
1	10-B	0.23	0/2906	0.44	0/3937
1	11-A	0.21	0/2875	0.42	0/3895
1	11-B	0.23	0/2906	0.44	0/3937
1	12-A	0.21	0/2875	0.42	0/3895
1	12-B	0.23	0/2906	0.44	0/3937
1	13-A	0.21	0/2875	0.42	0/3895
1	13-B	0.23	0/2906	0.44	0/3937
1	14-A	0.21	0/2875	0.42	0/3895
1	14-B	0.23	0/2906	0.44	0/3937
1	15-A	0.21	0/2875	0.42	0/3895
1	15-B	0.23	0/2906	0.44	0/3937
1	16-A	0.21	0/2875	0.42	0/3895
1	16-B	0.23	0/2906	0.44	0/3937

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.22	0/92496	0.43	0/125312

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	1-A	2810	0	2766	0	0
1	1-B	2839	0	2783	0	0
1	2-A	2810	0	2766	0	0
1	2-B	2839	0	2783	0	0
1	3-A	2810	0	2766	0	0
1	3-B	2839	0	2783	0	0
1	4-A	2810	0	2766	0	0
1	4-B	2839	0	2783	0	0
1	5-A	2810	0	2766	0	0
1	5-B	2839	0	2783	0	0
1	6-A	2810	0	2766	0	0
1	6-B	2839	0	2783	0	0
1	7-A	2810	0	2766	0	0
1	7-B	2839	0	2783	0	0
1	8-A	2810	0	2766	0	0
1	8-B	2839	0	2783	0	0
1	9-A	2810	0	2766	0	0
1	9-B	2839	0	2783	0	0
1	10-A	2810	0	2766	0	0
1	10-B	2839	0	2783	0	0
1	11-A	2810	0	2766	0	0
1	11-B	2839	0	2783	0	0
1	12-A	2810	0	2766	0	0
1	12-B	2839	0	2783	0	0
1	13-A	2810	0	2766	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	13-B	2839	0	2783	0	0
1	14-A	2810	0	2766	0	0
1	14-B	2839	0	2783	0	0
1	15-A	2810	0	2766	0	0
1	15-B	2839	0	2783	0	0
1	16-A	2810	0	2766	0	0
1	16-B	2839	0	2783	0	0
2	1-A	31	0	19	0	0
2	1-B	31	0	19	0	0
2	2-A	31	0	19	0	0
2	2-B	31	0	19	0	0
2	3-A	31	0	19	0	0
2	3-B	31	0	19	0	0
2	4-A	31	0	19	0	0
2	4-B	31	0	19	0	0
2	5-A	31	0	19	0	0
2	5-B	31	0	19	0	0
2	6-A	31	0	19	0	0
2	6-B	31	0	19	0	0
2	7-A	31	0	19	0	0
2	7-B	31	0	19	0	0
2	8-A	31	0	19	0	0
2	8-B	31	0	19	0	0
2	9-A	31	0	19	0	0
2	9-B	31	0	19	0	0
2	10-A	31	0	19	0	0
2	10-B	31	0	19	0	0
2	11-A	31	0	19	0	0
2	11-B	31	0	19	0	0
2	12-A	31	0	19	0	0
2	12-B	31	0	19	0	0
2	13-A	31	0	18	0	0
2	13-B	31	0	19	0	0
2	14-A	31	0	19	0	0
2	14-B	31	0	18	0	0
2	15-A	31	0	19	0	0
2	15-B	31	0	19	0	0
2	16-A	31	0	18	0	0
2	16-B	31	0	19	0	0
3	1-A	202	0	0	0	0
3	1-B	208	0	0	0	0
3	2-A	202	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	2-B	208	0	0	0	0
3	3-A	202	0	0	0	0
3	3-B	208	0	0	0	0
3	4-A	203	0	0	0	0
3	4-B	207	0	0	0	0
3	5-A	205	0	0	0	0
3	5-B	205	0	0	0	0
3	6-A	203	0	0	0	0
3	6-B	207	0	0	0	0
3	7-A	203	0	0	0	0
3	7-B	207	0	0	0	0
3	8-A	201	0	0	0	0
3	8-B	209	0	0	0	0
3	9-A	205	0	0	0	0
3	9-B	205	0	0	0	0
3	10-A	200	0	0	0	0
3	10-B	210	0	0	0	0
3	11-A	203	0	0	0	0
3	11-B	207	0	0	0	0
3	12-A	206	0	0	0	0
3	12-B	204	0	0	0	0
3	13-A	206	0	0	0	0
3	13-B	204	0	0	0	0
3	14-A	202	0	0	0	0
3	14-B	208	0	0	0	0
3	15-A	200	0	0	0	0
3	15-B	210	0	0	0	0
3	16-A	204	0	0	0	0
3	16-B	206	0	0	0	0
All	All	97936	0	89389	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1-A	361/391 (92%)	317 (88%)	35 (10%)	9 (2%)	4	1
1	1-B	363/391 (93%)	333 (92%)	25 (7%)	5 (1%)	9	4
1	2-A	361/391 (92%)	300 (83%)	51 (14%)	10 (3%)	4	1
1	2-B	363/391 (93%)	337 (93%)	24 (7%)	2 (1%)	21	17
1	3-A	361/391 (92%)	336 (93%)	22 (6%)	3 (1%)	16	11
1	3-B	363/391 (93%)	339 (93%)	18 (5%)	6 (2%)	7	3
1	4-A	361/391 (92%)	322 (89%)	33 (9%)	6 (2%)	7	3
1	4-B	363/391 (93%)	338 (93%)	20 (6%)	5 (1%)	9	4
1	5-A	361/391 (92%)	331 (92%)	29 (8%)	1 (0%)	36	35
1	5-B	363/391 (93%)	341 (94%)	20 (6%)	2 (1%)	21	17
1	6-A	361/391 (92%)	338 (94%)	22 (6%)	1 (0%)	36	35
1	6-B	363/391 (93%)	341 (94%)	22 (6%)	0	100	100
1	7-A	361/391 (92%)	333 (92%)	24 (7%)	4 (1%)	11	7
1	7-B	363/391 (93%)	334 (92%)	23 (6%)	6 (2%)	7	3
1	8-A	361/391 (92%)	324 (90%)	31 (9%)	6 (2%)	7	3
1	8-B	363/391 (93%)	332 (92%)	28 (8%)	3 (1%)	16	11
1	9-A	361/391 (92%)	330 (91%)	23 (6%)	8 (2%)	5	2
1	9-B	363/391 (93%)	335 (92%)	26 (7%)	2 (1%)	21	17
1	10-A	361/391 (92%)	309 (86%)	33 (9%)	19 (5%)	1	0
1	10-B	363/391 (93%)	338 (93%)	24 (7%)	1 (0%)	36	35
1	11-A	361/391 (92%)	336 (93%)	22 (6%)	3 (1%)	16	11
1	11-B	363/391 (93%)	337 (93%)	22 (6%)	4 (1%)	11	7
1	12-A	361/391 (92%)	328 (91%)	25 (7%)	8 (2%)	5	2
1	12-B	363/391 (93%)	326 (90%)	32 (9%)	5 (1%)	9	4
1	13-A	361/391 (92%)	322 (89%)	35 (10%)	4 (1%)	11	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	13-B	363/391 (93%)	327 (90%)	27 (7%)	9 (2%)	4	1
1	14-A	361/391 (92%)	312 (86%)	42 (12%)	7 (2%)	6	3
1	14-B	363/391 (93%)	311 (86%)	45 (12%)	7 (2%)	6	3
1	15-A	361/391 (92%)	324 (90%)	33 (9%)	4 (1%)	11	7
1	15-B	363/391 (93%)	326 (90%)	31 (8%)	6 (2%)	7	3
1	16-A	361/391 (92%)	324 (90%)	30 (8%)	7 (2%)	6	3
1	16-B	363/391 (93%)	332 (92%)	26 (7%)	5 (1%)	9	4
All	All	11584/12512 (93%)	10513 (91%)	903 (8%)	168 (2%)	8	4

5 of 168 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	233	SER
1	1-A	303	ALA
1	2-A	13	PHE
1	2-A	15	SER
1	2-A	76	HIS

5.3.2 Protein sidechains ⓘ

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	1-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	1-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	2-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	2-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	3-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	3-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	4-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	4-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	5-A	298/317 (94%)	294 (99%)	4 (1%)	61	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	5-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	6-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	6-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	7-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	7-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	8-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	8-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	9-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	9-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	10-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	10-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	11-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	11-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	12-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	12-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	13-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	13-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	14-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	14-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	15-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	15-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
1	16-A	298/317 (94%)	294 (99%)	4 (1%)	61	68
1	16-B	300/317 (95%)	292 (97%)	8 (3%)	39	42
All	All	9568/10144 (94%)	9376 (98%)	192 (2%)	48	54

5 of 192 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	10-B	170	LEU
1	12-B	371	TYR
1	10-B	371	TYR
1	11-B	346	PHE
1	13-B	137	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 356 such sidechains are listed below:

Mol	Chain	Res	Type
1	11-A	333	GLN
1	14-A	221	GLN
1	11-B	268	GLN
1	12-B	268	GLN
1	14-B	268	GLN

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](#)

32 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	FMN	16-A	7401	-	33,33,33	2.25	10 (30%)	48,50,50	3.35	19 (39%)
2	FMN	13-B	9401	-	33,33,33	2.63	13 (39%)	48,50,50	3.86	23 (47%)
2	FMN	9-B	9401	-	33,33,33	2.07	11 (33%)	48,50,50	3.53	13 (27%)
2	FMN	12-B	9401	-	33,33,33	2.01	12 (36%)	48,50,50	3.27	15 (31%)
2	FMN	10-B	9401	-	33,33,33	2.00	9 (27%)	48,50,50	3.46	14 (29%)
2	FMN	4-B	9401	-	33,33,33	1.59	7 (21%)	48,50,50	3.22	13 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FMN	12-A	7401	-	33,33,33	1.64	8 (24%)	48,50,50	2.69	16 (33%)
2	FMN	3-A	7401	-	33,33,33	2.05	9 (27%)	48,50,50	3.01	15 (31%)
2	FMN	8-A	7401	-	33,33,33	1.96	11 (33%)	48,50,50	2.78	16 (33%)
2	FMN	5-B	9401	-	33,33,33	1.93	7 (21%)	48,50,50	3.44	18 (37%)
2	FMN	14-A	7401	-	33,33,33	2.22	14 (42%)	48,50,50	3.11	20 (41%)
2	FMN	8-B	9401	-	33,33,33	1.69	7 (21%)	48,50,50	3.44	19 (39%)
2	FMN	16-B	9401	-	33,33,33	1.98	10 (30%)	48,50,50	3.68	21 (43%)
2	FMN	9-A	7401	-	33,33,33	1.82	10 (30%)	48,50,50	2.81	15 (31%)
2	FMN	14-B	9401	-	33,33,33	2.08	10 (30%)	48,50,50	3.50	16 (33%)
2	FMN	6-A	7401	-	33,33,33	2.15	6 (18%)	48,50,50	2.89	16 (33%)
2	FMN	1-B	9401	-	33,33,33	1.97	6 (18%)	48,50,50	3.39	13 (27%)
2	FMN	2-A	7401	-	33,33,33	1.65	8 (24%)	48,50,50	2.56	13 (27%)
2	FMN	7-B	9401	-	33,33,33	2.38	9 (27%)	48,50,50	3.73	21 (43%)
2	FMN	2-B	9401	-	33,33,33	2.20	13 (39%)	48,50,50	3.88	20 (41%)
2	FMN	4-A	7401	-	33,33,33	1.88	5 (15%)	48,50,50	2.88	14 (29%)
2	FMN	3-B	9401	-	33,33,33	1.99	8 (24%)	48,50,50	3.70	19 (39%)
2	FMN	11-B	9401	-	33,33,33	2.09	5 (15%)	48,50,50	3.44	11 (22%)
2	FMN	15-B	9401	-	33,33,33	2.64	12 (36%)	48,50,50	3.88	24 (50%)
2	FMN	10-A	7401	-	33,33,33	1.53	7 (21%)	48,50,50	2.65	18 (37%)
2	FMN	7-A	7401	-	33,33,33	2.34	8 (24%)	48,50,50	3.34	23 (47%)
2	FMN	6-B	9401	-	33,33,33	2.14	13 (39%)	48,50,50	3.83	19 (39%)
2	FMN	5-A	7401	-	33,33,33	1.98	7 (21%)	48,50,50	2.88	15 (31%)
2	FMN	11-A	7401	-	33,33,33	1.96	5 (15%)	48,50,50	2.86	14 (29%)
2	FMN	13-A	7401	-	33,33,33	2.28	11 (33%)	48,50,50	3.37	20 (41%)
2	FMN	15-A	7401	-	33,33,33	1.94	9 (27%)	48,50,50	2.89	15 (31%)
2	FMN	1-A	7401	-	33,33,33	2.04	7 (21%)	48,50,50	2.85	13 (27%)

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	FMN	16-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	13-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	9-B	9401	-	-	2/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	12-B	9401	-	-	3/18/18/18	0/3/3/3
2	FMN	10-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	4-B	9401	-	-	2/18/18/18	0/3/3/3
2	FMN	12-A	7401	-	-	1/18/18/18	0/3/3/3
2	FMN	3-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	8-A	7401	-	-	3/18/18/18	0/3/3/3
2	FMN	5-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	14-A	7401	-	-	1/18/18/18	0/3/3/3
2	FMN	8-B	9401	-	-	2/18/18/18	0/3/3/3
2	FMN	16-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	9-A	7401	-	-	3/18/18/18	0/3/3/3
2	FMN	14-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	6-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	1-B	9401	-	-	2/18/18/18	0/3/3/3
2	FMN	2-A	7401	-	-	3/18/18/18	0/3/3/3
2	FMN	7-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	2-B	9401	-	-	3/18/18/18	0/3/3/3
2	FMN	4-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	3-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	11-B	9401	-	-	2/18/18/18	0/3/3/3
2	FMN	15-B	9401	-	-	4/18/18/18	0/3/3/3
2	FMN	10-A	7401	-	-	3/18/18/18	0/3/3/3
2	FMN	7-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	6-B	9401	-	-	2/18/18/18	0/3/3/3
2	FMN	5-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	11-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	13-A	7401	-	-	4/18/18/18	0/3/3/3
2	FMN	15-A	7401	-	-	2/18/18/18	0/3/3/3
2	FMN	1-A	7401	-	-	4/18/18/18	0/3/3/3

The worst 5 of 287 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7-A	7401	FMN	C1'-C2'	-9.03	1.40	1.52
2	11-B	9401	FMN	C5'-C4'	-8.35	1.40	1.51
2	1-B	9401	FMN	C5'-C4'	-7.97	1.41	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7-B	9401	FMN	C1'-C2'	-7.56	1.42	1.52
2	6-A	7401	FMN	C5'-C4'	-7.54	1.41	1.51

The worst 5 of 541 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-B	9401	FMN	C4'-C3'-C2'	-11.95	93.68	113.57
2	11-B	9401	FMN	O3P-P-O5'	-11.73	76.08	106.67
2	4-A	7401	FMN	O3P-P-O5'	-11.55	76.56	106.67
2	6-B	9401	FMN	C4'-C3'-C2'	-11.42	94.56	113.57
2	1-B	9401	FMN	O3P-P-O5'	-11.28	77.27	106.67

There are no chirality outliers.

5 of 102 torsion outliers are listed below:

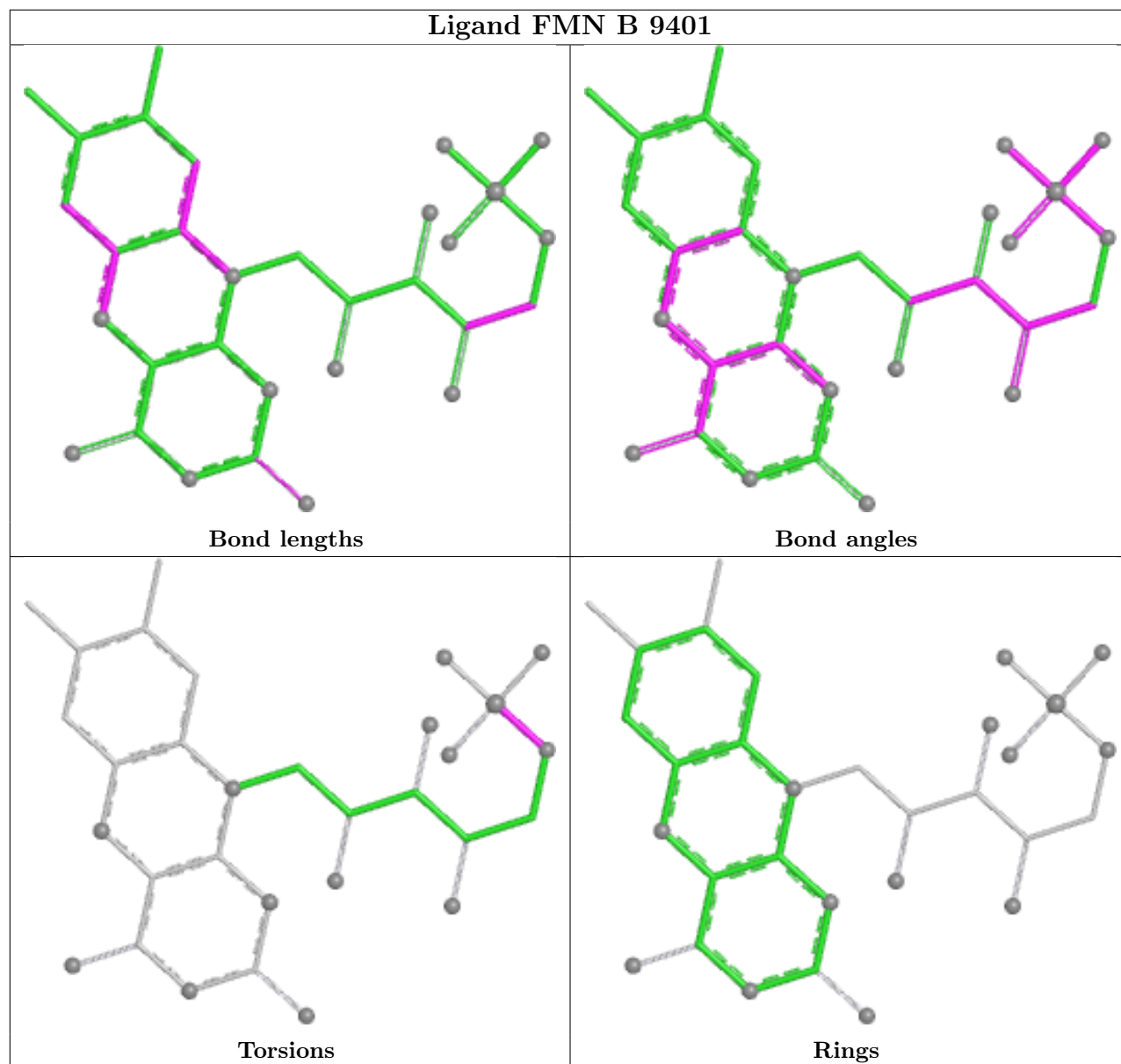
Mol	Chain	Res	Type	Atoms
2	1-A	7401	FMN	C2'-C1'-N10-C10
2	1-A	7401	FMN	C5'-O5'-P-O3P
2	2-A	7401	FMN	C2'-C1'-N10-C10
2	2-A	7401	FMN	C5'-O5'-P-O3P
2	3-A	7401	FMN	C2'-C1'-N10-C10

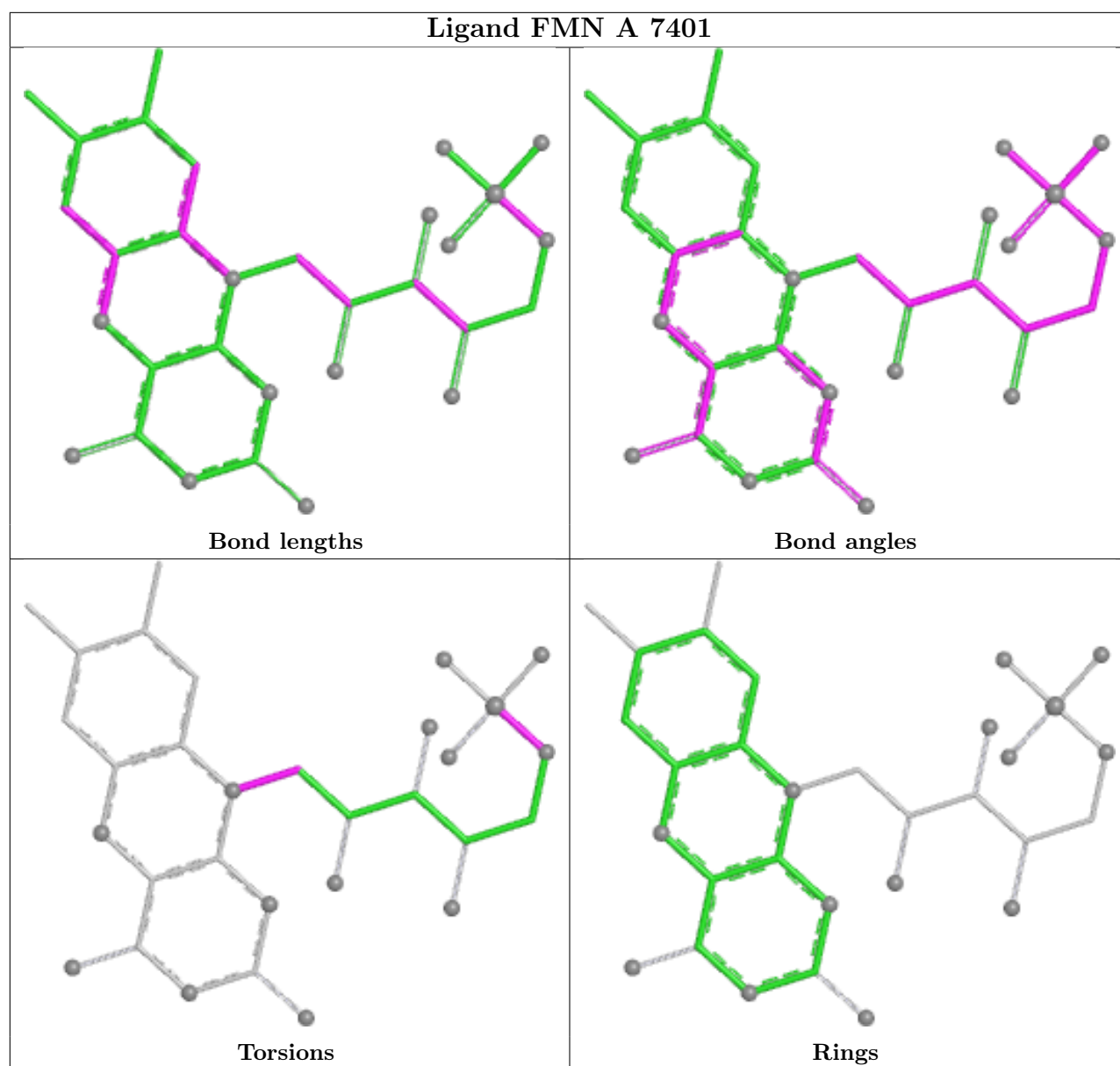
There are no ring outliers.

No monomer is involved in short contacts.

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 FMN B 9401





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	1-A	365/391 (93%)	1.69	100 (27%) ⓘ ⓘ	1, 1, 2, 3	365 (100%)
1	1-B	367/391 (93%)	1.47	95 (25%) ⓘ ⓘ	1, 1, 2, 3	367 (100%)
1	2-A	0/391	-	-	-	-
1	2-B	0/391	-	-	-	-
1	3-A	0/391	-	-	-	-
1	3-B	0/391	-	-	-	-
1	4-A	0/391	-	-	-	-
1	4-B	0/391	-	-	-	-
1	5-A	0/391	-	-	-	-
1	5-B	0/391	-	-	-	-
1	6-A	0/391	-	-	-	-
1	6-B	0/391	-	-	-	-
1	7-A	0/391	-	-	-	-
1	7-B	0/391	-	-	-	-
1	8-A	0/391	-	-	-	-
1	8-B	0/391	-	-	-	-
1	9-A	0/391	-	-	-	-
1	9-B	0/391	-	-	-	-
1	10-A	0/391	-	-	-	-
1	10-B	0/391	-	-	-	-
1	11-A	0/391	-	-	-	-
1	11-B	0/391	-	-	-	-
1	12-A	0/391	-	-	-	-
1	12-B	0/391	-	-	-	-
1	13-A	0/391	-	-	-	-
1	13-B	0/391	-	-	-	-
1	14-A	0/391	-	-	-	-
1	14-B	0/391	-	-	-	-
1	15-A	0/391	-	-	-	-
1	15-B	0/391	-	-	-	-
1	16-A	0/391	-	-	-	-
1	16-B	0/391	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	732/12512 (5%)	1.58	195 (26%) 1 1	1, 1, 2, 3	732 (100%)

The worst 5 of 195 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	303	ALA	11.2
1	1-B	371	TYR	10.6
1	1-B	9	ASN	9.8
1	1-A	107	LEU	9.3
1	1-B	57	GLY	7.7

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
2	FMN	1-B	9401	31/31	0.70	0.20	1,12,18,23	31
2	FMN	2-A	7401	31/31	-	-	1,8,20,22	31
2	FMN	3-A	7401	31/31	-	-	1,6,18,24	31
2	FMN	4-A	7401	31/31	-	-	1,8,19,24	31
2	FMN	5-A	7401	31/31	-	-	1,8,18,24	31
2	FMN	6-A	7401	31/31	-	-	1,7,17,19	31
2	FMN	7-A	7401	31/31	-	-	1,5,14,20	31
2	FMN	8-A	7401	31/31	-	-	1,5,21,25	31
2	FMN	9-A	7401	31/31	-	-	1,4,21,25	31
2	FMN	10-A	7401	31/31	-	-	1,4,8,15	31
2	FMN	11-A	7401	31/31	-	-	1,8,18,23	31
2	FMN	12-A	7401	31/31	-	-	1,9,17,18	31
2	FMN	13-A	7401	31/31	-	-	1,2,14,16	31

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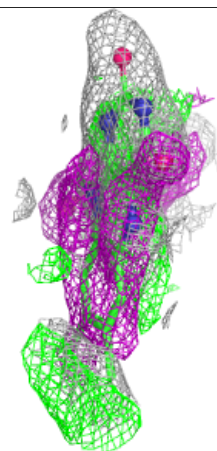
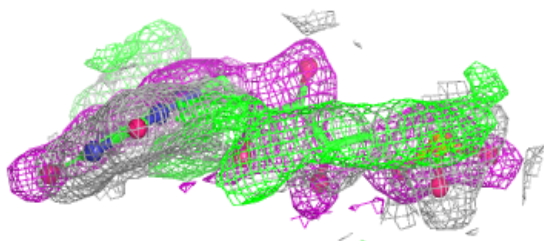
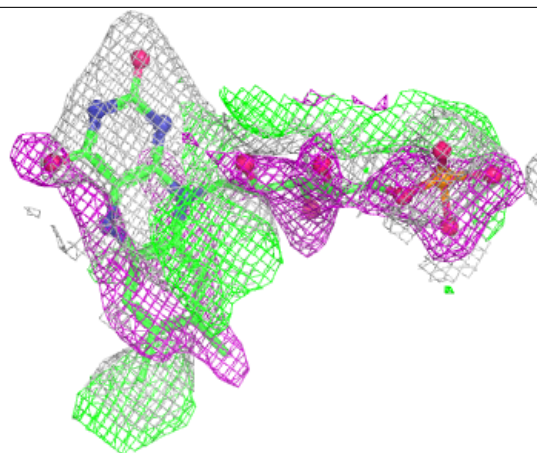
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FMN	14-A	7401	31/31	-	-	1,7,10,14	31
2	FMN	15-A	7401	31/31	-	-	1,6,14,18	31
2	FMN	16-A	7401	31/31	-	-	1,2,12,16	31
2	FMN	1-A	7401	31/31	0.77	0.15	1,8,19,24	31
2	FMN	2-B	9401	31/31	-	-	1,8,14,19	31
2	FMN	3-B	9401	31/31	-	-	1,8,18,19	31
2	FMN	4-B	9401	31/31	-	-	1,8,14,15	31
2	FMN	5-B	9401	31/31	-	-	1,8,15,16	31
2	FMN	6-B	9401	31/31	-	-	1,8,15,19	31
2	FMN	7-B	9401	31/31	-	-	1,7,12,14	31
2	FMN	8-B	9401	31/31	-	-	1,6,17,20	31
2	FMN	9-B	9401	31/31	-	-	1,9,16,18	31
2	FMN	10-B	9401	31/31	-	-	4,10,14,16	31
2	FMN	11-B	9401	31/31	-	-	1,11,18,21	31
2	FMN	12-B	9401	31/31	-	-	1,8,16,17	31
2	FMN	13-B	9401	31/31	-	-	1,8,16,20	31
2	FMN	14-B	9401	31/31	-	-	1,8,14,15	31
2	FMN	15-B	9401	31/31	-	-	1,8,15,20	31
2	FMN	16-B	9401	31/31	-	-	1,9,15,18	31

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.

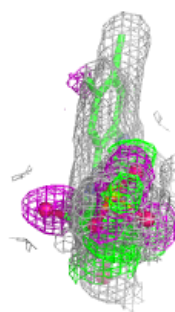
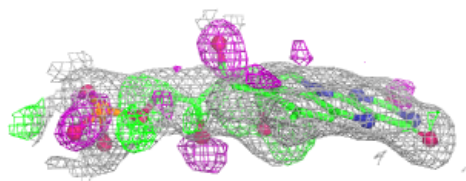
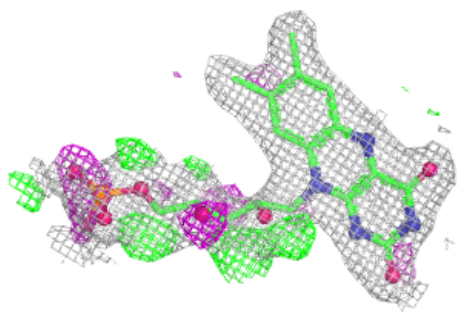
Electron density around FMN B 9401:

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



Electron density around FMN A 7401:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.