



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 14, 2025 – 07:21 PM EDT

PDB ID : 2Q3R / pdb_00002q3r
Title : Ensemble refinement of the protein crystal structure of At1g76680 from *Arabidopsis thaliana*
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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

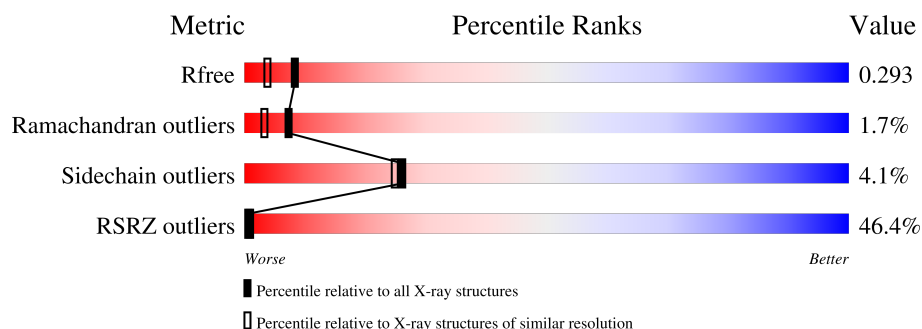
1 Overall quality at a glance

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}	164625	9409 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (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	372	
1	10-A	372	
1	11-A	372	
1	12-A	372	
1	13-A	372	
1	14-A	372	

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Mol	Chain	Length	Quality of chain
1	15-A	372	 90% • 6%
1	16-A	372	 87% 7% 6%
1	2-A	372	 90% • • 6%
1	3-A	372	 90% • 6%
1	4-A	372	 90% • 6%
1	5-A	372	 91% • 6%
1	6-A	372	 88% 6% 6%
1	7-A	372	 91% • 6%
1	8-A	372	 90% • 6%
1	9-A	372	 90% 5% 6%

2 Entry composition

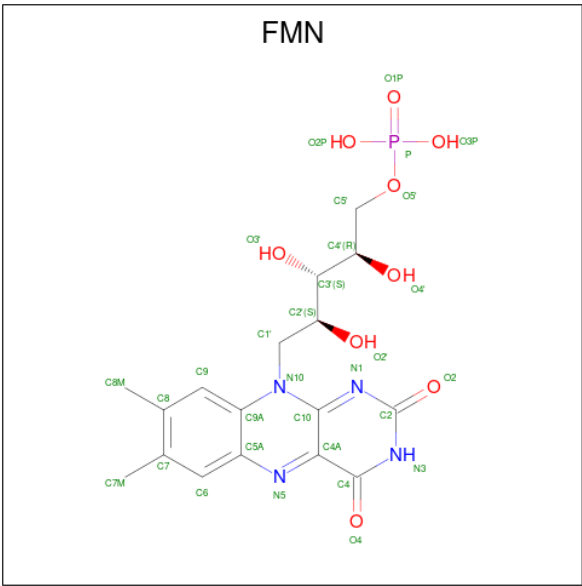
There are 3 unique types of molecules in this entry. The entry contains 46176 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	2-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	3-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	4-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	5-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	6-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	7-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	8-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	9-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	10-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	11-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	12-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	13-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	14-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	15-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			
1	16-A	351	Total	C	N	O	S	0	0	0
			2748	1749	478	508	13			

- 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		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	14-A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
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		

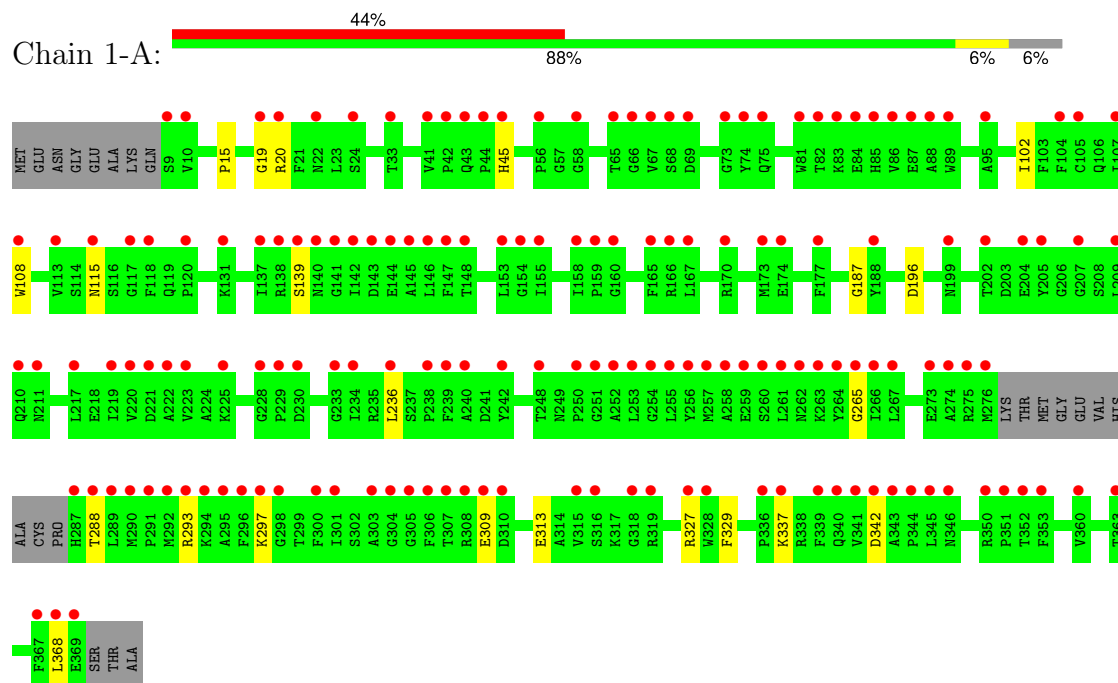
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1-A	107	Total	O	0	0
			107	107		
3	2-A	107	Total	O	0	0
			107	107		
3	3-A	107	Total	O	0	0
			107	107		
3	4-A	107	Total	O	0	0
			107	107		
3	5-A	107	Total	O	0	0
			107	107		
3	6-A	107	Total	O	0	0
			107	107		
3	7-A	107	Total	O	0	0
			107	107		
3	8-A	107	Total	O	0	0
			107	107		
3	9-A	107	Total	O	0	0
			107	107		
3	10-A	107	Total	O	0	0
			107	107		
3	11-A	107	Total	O	0	0
			107	107		
3	12-A	107	Total	O	0	0
			107	107		
3	13-A	107	Total	O	0	0
			107	107		
3	14-A	107	Total	O	0	0
			107	107		
3	15-A	107	Total	O	0	0
			107	107		
3	16-A	107	Total	O	0	0
			107	107		

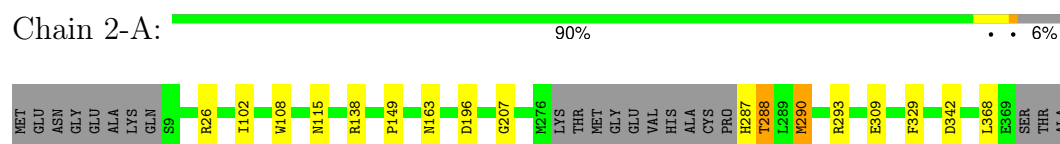
3 Residue-property plots [i](#)

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.

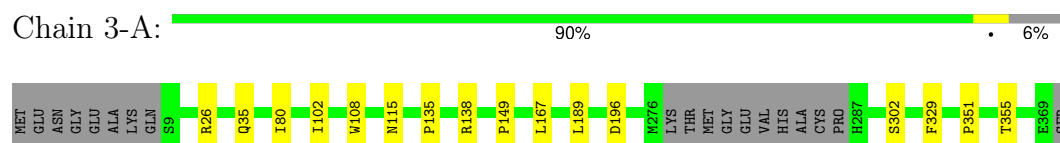
• Molecule 1: 12-oxophytodienoate reductase 1



• Molecule 1: 12-oxophytodienoate reductase 1



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• Molecule 1: 12-oxophytodienoate reductase 1





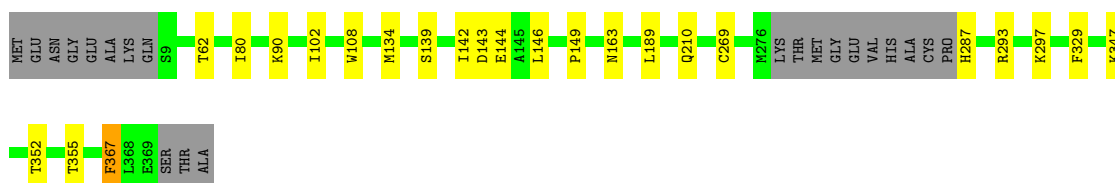
- Molecule 1: 12-oxophytodienoate reductase 1

Chain 5-A: 91% 6%



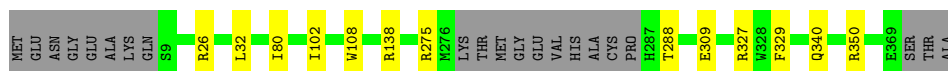
- Molecule 1: 12-oxophytodienoate reductase 1

Chain 6-A: 88% 6% 6%



- Molecule 1: 12-oxophytodienoate reductase 1

Chain 7-A: 91% 6%



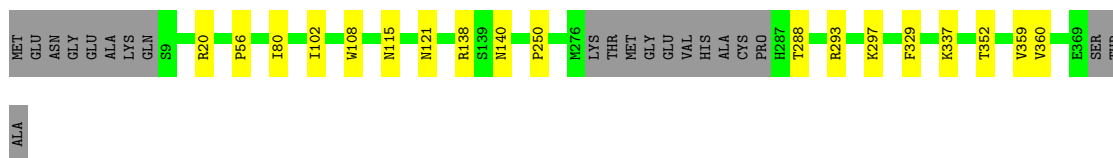
- Molecule 1: 12-oxophytodienoate reductase 1

Chain 8-A: 90% 6%



- Molecule 1: 12-oxophytodienoate reductase 1

Chain 9-A: 90% 5% 6%



- Molecule 1: 12-oxophytodienoate reductase 1

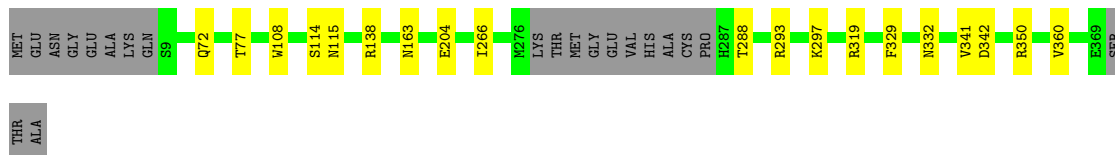
Chain 10-A: 90% 6%



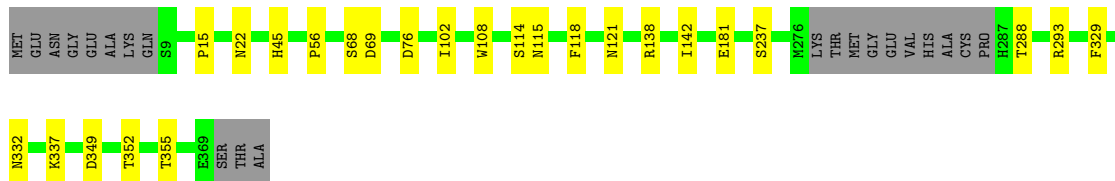
● Molecule 1: 12-oxophytodienoate reductase 1

Chain 11-A:  91% 6%

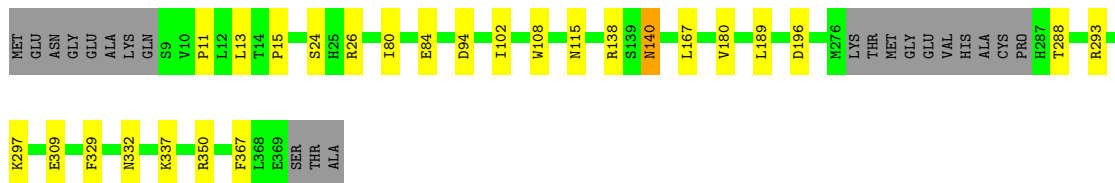
● Molecule 1: 12-oxophytodienoate reductase 1

Chain 12-A:  89% 5% 6%

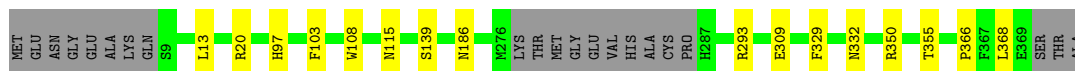
● Molecule 1: 12-oxophytodienoate reductase 1

Chain 13-A:  88% 7% 6%

● Molecule 1: 12-oxophytodienoate reductase 1

Chain 14-A:  87% 7% 6%

● Molecule 1: 12-oxophytodienoate reductase 1

Chain 15-A:  90% 6%

● Molecule 1: 12-oxophytodienoate reductase 1

Chain 16-A:  87% 7% 6%

F306	F313	F329	Q340	R350	P351	T352	E369	SER	THR	ALA
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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	46.69Å 88.07Å 149.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.24 – 2.00 42.24 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.9 (42.24-2.00) 98.1 (42.24-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.195 , 0.282 0.209 , 0.293	Depositor DCC
R_{free} test set	1071 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.02 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	46176	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% 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	0.48	0/2822	0.70	1/3831 (0.0%)
1	2-A	0.48	0/2822	0.69	1/3831 (0.0%)
1	3-A	0.50	0/2822	0.69	1/3831 (0.0%)
1	4-A	0.49	0/2822	0.69	1/3831 (0.0%)
1	5-A	0.49	0/2822	0.69	1/3831 (0.0%)
1	6-A	0.49	0/2822	0.69	1/3831 (0.0%)
1	7-A	0.48	0/2822	0.68	1/3831 (0.0%)
1	8-A	0.48	0/2822	0.69	1/3831 (0.0%)
1	9-A	0.49	0/2822	0.69	1/3831 (0.0%)
1	10-A	0.49	0/2822	0.68	0/3831
1	11-A	0.49	0/2822	0.68	1/3831 (0.0%)
1	12-A	0.48	0/2822	0.69	0/3831
1	13-A	0.57	0/2822	0.75	0/3831
1	14-A	0.55	0/2822	0.75	1/3831 (0.0%)
1	15-A	0.54	0/2822	0.75	0/3831
1	16-A	0.55	0/2822	0.75	1/3831 (0.0%)
All	All	0.50	0/45152	0.71	12/61296 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	14-A	102	ILE	N-CA-C	-5.80	95.35	111.00
1	16-A	102	ILE	N-CA-C	-5.73	95.54	111.00
1	1-A	102	ILE	N-CA-C	-5.63	95.79	111.00
1	8-A	102	ILE	N-CA-C	-5.19	96.99	111.00
1	7-A	102	ILE	N-CA-C	-5.16	97.07	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	2748	0	2676	0	0
1	2-A	2748	0	2676	0	0
1	3-A	2748	0	2676	0	0
1	4-A	2748	0	2676	0	0
1	5-A	2748	0	2676	0	0
1	6-A	2748	0	2676	0	0
1	7-A	2748	0	2676	0	0
1	8-A	2748	0	2676	0	0
1	9-A	2748	0	2676	0	0
1	10-A	2748	0	2676	0	0
1	11-A	2748	0	2676	0	0
1	12-A	2748	0	2676	0	0
1	13-A	2748	0	2676	0	0
1	14-A	2748	0	2676	0	0
1	15-A	2748	0	2676	0	0
1	16-A	2748	0	2676	0	0
2	1-A	31	0	19	0	0
2	2-A	31	0	19	0	0
2	3-A	31	0	19	0	0
2	4-A	31	0	19	0	0
2	5-A	31	0	19	0	0
2	6-A	31	0	19	0	0
2	7-A	31	0	19	0	0
2	8-A	31	0	19	0	0
2	9-A	31	0	19	0	0
2	10-A	31	0	19	0	0
2	11-A	31	0	19	0	0
2	12-A	31	0	19	0	0
2	13-A	31	0	19	0	0
2	14-A	31	0	19	0	0
2	15-A	31	0	18	0	0
2	16-A	31	0	18	0	0
3	1-A	107	0	0	0	0
3	2-A	107	0	0	0	0
3	3-A	107	0	0	0	0
3	4-A	107	0	0	0	0
3	5-A	107	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	6-A	107	0	0	0	0
3	7-A	107	0	0	0	0
3	8-A	107	0	0	0	0
3	9-A	107	0	0	0	0
3	10-A	107	0	0	0	0
3	11-A	107	0	0	0	0
3	12-A	107	0	0	0	0
3	13-A	107	0	0	0	0
3	14-A	107	0	0	0	0
3	15-A	107	0	0	0	0
3	16-A	107	0	0	0	0
All	All	46176	0	43118	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 [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	1-A	347/372 (93%)	300 (86%)	40 (12%)	7 (2%)	6	2
1	2-A	347/372 (93%)	307 (88%)	34 (10%)	6 (2%)	7	3
1	3-A	347/372 (93%)	313 (90%)	28 (8%)	6 (2%)	7	3
1	4-A	347/372 (93%)	298 (86%)	41 (12%)	8 (2%)	5	2
1	5-A	347/372 (93%)	315 (91%)	29 (8%)	3 (1%)	14	10
1	6-A	347/372 (93%)	304 (88%)	35 (10%)	8 (2%)	5	2
1	7-A	347/372 (93%)	315 (91%)	27 (8%)	5 (1%)	9	4
1	8-A	347/372 (93%)	318 (92%)	24 (7%)	5 (1%)	9	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	9-A	347/372 (93%)	311 (90%)	28 (8%)	8 (2%)	5	2
1	10-A	347/372 (93%)	315 (91%)	25 (7%)	7 (2%)	6	2
1	11-A	347/372 (93%)	321 (92%)	24 (7%)	2 (1%)	22	17
1	12-A	347/372 (93%)	301 (87%)	39 (11%)	7 (2%)	6	2
1	13-A	347/372 (93%)	312 (90%)	27 (8%)	8 (2%)	5	2
1	14-A	347/372 (93%)	312 (90%)	30 (9%)	5 (1%)	9	4
1	15-A	347/372 (93%)	312 (90%)	33 (10%)	2 (1%)	22	17
1	16-A	347/372 (93%)	292 (84%)	47 (14%)	8 (2%)	5	2
All	All	5552/5952 (93%)	4946 (89%)	511 (9%)	95 (2%)	7	3

5 of 95 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	139	SER
1	1-A	368	LEU
1	4-A	140	ASN
1	4-A	189	LEU
1	4-A	308	ARG

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	290/306 (95%)	276 (95%)	14 (5%)	21	19
1	2-A	290/306 (95%)	278 (96%)	12 (4%)	26	25
1	3-A	290/306 (95%)	281 (97%)	9 (3%)	35	36
1	4-A	290/306 (95%)	284 (98%)	6 (2%)	48	53
1	5-A	290/306 (95%)	281 (97%)	9 (3%)	35	36
1	6-A	290/306 (95%)	274 (94%)	16 (6%)	18	15
1	7-A	290/306 (95%)	283 (98%)	7 (2%)	44	47
1	8-A	290/306 (95%)	280 (97%)	10 (3%)	32	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	9-A	290/306 (95%)	281 (97%)	9 (3%)	35	36
1	10-A	290/306 (95%)	282 (97%)	8 (3%)	38	40
1	11-A	290/306 (95%)	282 (97%)	8 (3%)	38	40
1	12-A	290/306 (95%)	278 (96%)	12 (4%)	26	25
1	13-A	290/306 (95%)	273 (94%)	17 (6%)	16	13
1	14-A	290/306 (95%)	269 (93%)	21 (7%)	12	8
1	15-A	290/306 (95%)	276 (95%)	14 (5%)	21	19
1	16-A	290/306 (95%)	273 (94%)	17 (6%)	16	13
All	All	4640/4896 (95%)	4451 (96%)	189 (4%)	26	25

5 of 189 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	12-A	293	ARG
1	14-A	108	TRP
1	12-A	350	ARG
1	13-A	293	ARG
1	14-A	293	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
1	11-A	97	HIS
1	13-A	115	ASN
1	11-A	171	ASN
1	12-A	97	HIS
1	14-A	35	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

16 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	14-A	373	-	33,33,33	2.38	11 (33%)	48,50,50	3.23	15 (31%)
2	FMN	12-A	373	-	33,33,33	1.76	8 (24%)	48,50,50	2.95	17 (35%)
2	FMN	9-A	373	-	33,33,33	1.48	5 (15%)	48,50,50	2.84	12 (25%)
2	FMN	5-A	373	-	33,33,33	1.92	11 (33%)	48,50,50	2.87	14 (29%)
2	FMN	3-A	373	-	33,33,33	2.07	9 (27%)	48,50,50	2.71	15 (31%)
2	FMN	13-A	373	-	33,33,33	2.43	14 (42%)	48,50,50	3.59	19 (39%)
2	FMN	7-A	373	-	33,33,33	2.58	11 (33%)	48,50,50	2.73	15 (31%)
2	FMN	10-A	373	-	33,33,33	1.86	7 (21%)	48,50,50	2.98	19 (39%)
2	FMN	1-A	373	-	33,33,33	1.70	9 (27%)	48,50,50	3.08	20 (41%)
2	FMN	2-A	373	-	33,33,33	1.86	8 (24%)	48,50,50	2.98	19 (39%)
2	FMN	15-A	373	-	33,33,33	2.52	16 (48%)	48,50,50	3.64	19 (39%)
2	FMN	6-A	373	-	33,33,33	1.99	8 (24%)	48,50,50	2.77	18 (37%)
2	FMN	8-A	373	-	33,33,33	1.90	9 (27%)	48,50,50	2.92	18 (37%)
2	FMN	16-A	373	-	33,33,33	2.29	13 (39%)	48,50,50	3.63	18 (37%)
2	FMN	4-A	373	-	33,33,33	1.74	8 (24%)	48,50,50	2.94	18 (37%)
2	FMN	11-A	373	-	33,33,33	1.90	9 (27%)	48,50,50	2.92	17 (35%)

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	14-A	373	-	-	3/18/18/18	0/3/3/3
2	FMN	12-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	9-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	5-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	3-A	373	-	-	3/18/18/18	0/3/3/3
2	FMN	13-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	7-A	373	-	-	1/18/18/18	0/3/3/3
2	FMN	10-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	1-A	373	-	-	1/18/18/18	0/3/3/3
2	FMN	2-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	15-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	6-A	373	-	-	2/18/18/18	0/3/3/3
2	FMN	8-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	16-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	4-A	373	-	-	4/18/18/18	0/3/3/3
2	FMN	11-A	373	-	-	4/18/18/18	0/3/3/3

The worst 5 of 156 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7-A	373	FMN	O2-C2	-9.72	1.05	1.24
2	3-A	373	FMN	C5'-C4'	-7.66	1.41	1.51
2	6-A	373	FMN	C5'-C4'	-6.64	1.42	1.51
2	15-A	373	FMN	C1'-C2'	-6.42	1.43	1.52
2	13-A	373	FMN	C1'-C2'	-5.55	1.44	1.52

The worst 5 of 273 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	9-A	373	FMN	O3P-P-O5'	-12.66	73.66	106.67
2	12-A	373	FMN	O3P-P-O5'	-11.59	76.45	106.67
2	4-A	373	FMN	O3P-P-O5'	-11.50	76.69	106.67
2	16-A	373	FMN	O5'-C5'-C4'	-11.16	79.58	109.36
2	15-A	373	FMN	O5'-C5'-C4'	-11.11	79.69	109.36

There are no chirality outliers.

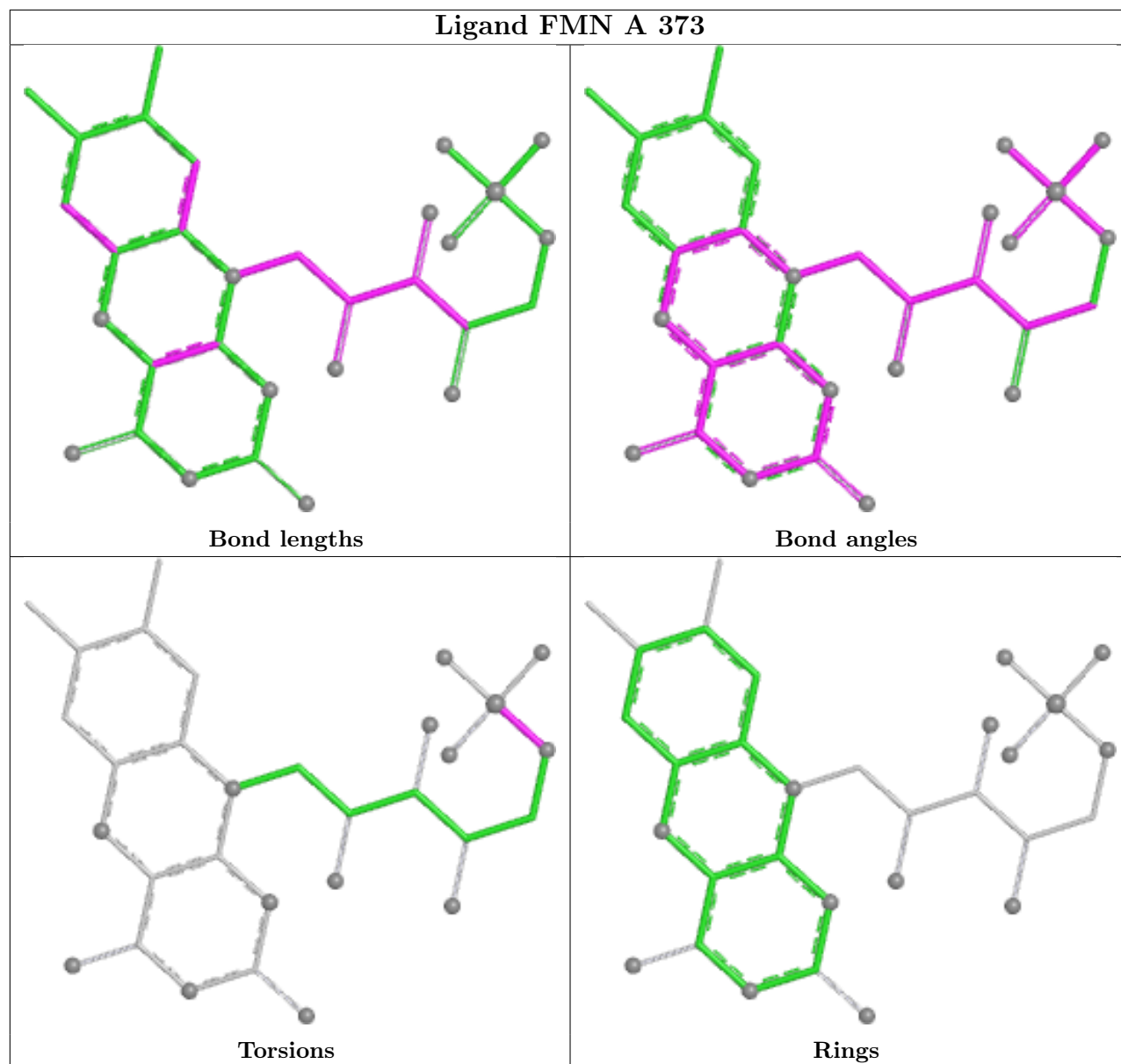
5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	1-A	373	FMN	C5'-O5'-P-O3P
2	2-A	373	FMN	C2'-C1'-N10-C10
2	2-A	373	FMN	C5'-O5'-P-O3P
2	3-A	373	FMN	C5'-O5'-P-O3P
2	4-A	373	FMN	C2'-C1'-N10-C9A

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.



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	1-A	351/372 (94%)	2.13	163 (46%) 0 1	1, 2, 3, 4	351 (100%)
1	2-A	0/372	-	-	-	-
1	3-A	0/372	-	-	-	-
1	4-A	0/372	-	-	-	-
1	5-A	0/372	-	-	-	-
1	6-A	0/372	-	-	-	-
1	7-A	0/372	-	-	-	-
1	8-A	0/372	-	-	-	-
1	9-A	0/372	-	-	-	-
1	10-A	0/372	-	-	-	-
1	11-A	0/372	-	-	-	-
1	12-A	0/372	-	-	-	-
1	13-A	0/372	-	-	-	-
1	14-A	0/372	-	-	-	-
1	15-A	0/372	-	-	-	-
1	16-A	0/372	-	-	-	-
All	All	351/5952 (5%)	2.13	163 (46%) 0 1	1, 2, 3, 4	351 (100%)

The worst 5 of 163 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	254	GLY	10.6
1	1-A	255	LEU	10.3
1	1-A	258	ALA	9.1
1	1-A	319	ARG	5.8
1	1-A	139	SER	5.7

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](#)

LIGAND-RSR INFOmissingINFO

6.5 Other polymers [i](#)

There are no such residues in this entry.