

Full wwPDB X-ray Structure Validation Report (i)

Sep 13, 2020 – 05:11 PM BST

PDB ID : 4M2M

Title : Crystal structure of PLP-dependent cyclase OrfR in complex with PLP-L-Arg

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Deposited on : 2013-08-05

Resolution : 1.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp

with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.14.4.dev1

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)

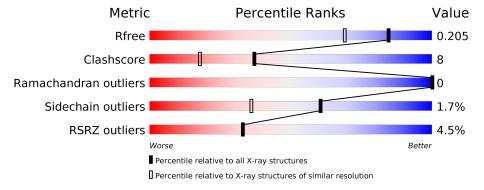
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

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 1.58 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$		
R_{free}	130704	5534 (1.60-1.56)		
Clashscore	141614	5861 (1.60-1.56)		
Ramachandran outliers	138981	5708 (1.60-1.56)		
Sidechain outliers	138945	5703 (1.60-1.56)		
RSRZ outliers	127900	5431 (1.60-1.56)		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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		
			4%		
1	A	406	83%	10%	• 6%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3435 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 Aminotransferase.

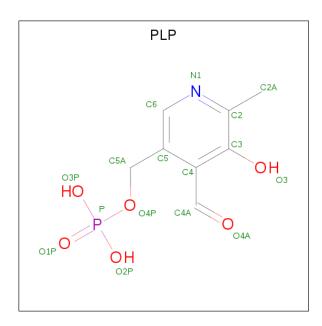
\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	$\mathbf{AltConf}$	Trace	
1	A	380	Total 2878	C 1805	N 536	O 531	S 6	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP G9MBV4
A	-18	GLY	-	EXPRESSION TAG	UNP G9MBV4
A	-17	SER	_	EXPRESSION TAG	UNP G9MBV4
A	-16	SER	-	EXPRESSION TAG	UNP G9MBV4
A	-15	HIS	-	EXPRESSION TAG	UNP G9MBV4
A	-14	HIS	_	EXPRESSION TAG	UNP G9MBV4
A	-13	HIS	-	EXPRESSION TAG	UNP G9MBV4
A	-12	HIS	_	EXPRESSION TAG	UNP G9MBV4
A	-11	HIS	-	EXPRESSION TAG	UNP G9MBV4
A	-10	HIS	-	EXPRESSION TAG	UNP G9MBV4
A	-9	SER	_	EXPRESSION TAG	UNP G9MBV4
A	-8	SER	_	EXPRESSION TAG	UNP G9MBV4
A	-7	GLY	_	EXPRESSION TAG	UNP G9MBV4
A	-6	LEU	-	EXPRESSION TAG	UNP G9MBV4
A	-5	VAL	_	EXPRESSION TAG	UNP G9MBV4
A	-4	PRO	_	EXPRESSION TAG	UNP G9MBV4
A	-3	ARG	-	EXPRESSION TAG	UNP G9MBV4
A	-2	GLY	-	EXPRESSION TAG	UNP G9MBV4
A	-1	SER		EXPRESSION TAG	UNP G9MBV4
A	0	HIS	_	EXPRESSION TAG	UNP G9MBV4

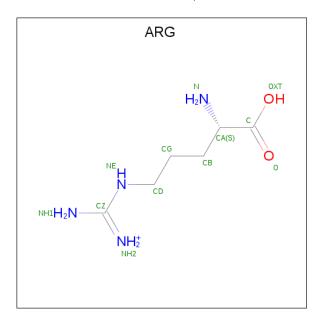
• Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	A	1	Total	С	N	Ο	Р	0	0
_		_	15	8	1	5	1		

 \bullet Molecule 3 is ARGININE (three-letter code: ARG) (formula: $\rm C_6H_{15}N_4O_2).$



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 12	C 6	N 4	O 2	0	0

• Molecule 4 is water.



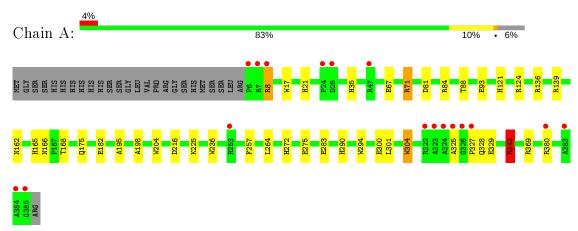
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	530	Total O 530 530	0	0



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: Aminotransferase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	138.46Å 138.46Å 48.96Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 - 1.58	Depositor
Resolution (A)	27.69 - 1.58	EDS
% Data completeness	88.9 (30.00-1.58)	Depositor
(in resolution range)	88.9 (27.69-1.58)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.78 (at 1.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
D D.	0.180 , 0.205	Depositor
R, R_{free}	0.179 , 0.205	DCC
R_{free} test set	2973 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	13.3	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 36.9	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3435	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.63% of the height of the origin peak. No significant pseudotranslation is detected.

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: PLP

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	Boı	nd lengths	Bond angles		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.74	$5/2946 \ (0.2\%)$	0.79	3/4016 (0.1%)	

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	A	17	TRP	CD2-CE2	5.53	1.48	1.41
1	A	236	TRP	CD2-CE2	5.45	1.47	1.41
1	A	204	TRP	CD2-CE2	5.20	1.47	1.41
1	A	304	TRP	CD2-CE2	5.15	1.47	1.41
1	A	294	TRP	CD2-CE2	5.14	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathbf{Ideal}(^o)$
1	A	71	ARG	NE-CZ-NH2	9.87	125.23	120.30
1	A	71	ARG	NE-CZ-NH1	-8.35	116.12	120.30
1	A	342	ARG	NE-CZ-NH1	-6.30	117.15	120.30

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	2878	0	2834	43	1
2	A	15	0	6	0	0
3	A	12	0	12	4	0
4	A	530	0	0	30	1
All	All	3435	0	2852	45	1

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 8.

All (45) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:81:ASP:HB2	4:A:835:HOH:O	1.41	1.20
1:A:327:PRO:HB2	4:A:1023:HOH:O	1.45	1.16
1:A:175:GLN:HG3	4:A:682:HOH:O	1.48	1.14
1:A:327:PRO:CB	4:A:1023:HOH:O	1.95	1.14
1:A:380:ARG:HG2	4:A:1030:HOH:O	1.56	1.06
1:A:216:ASP:O	4:A:1005:HOH:O	1.91	0.88
1:A:325:ALA:HB2	4:A:887:HOH:O	1.80	0.81
1:A:380:ARG:CG	4:A:1030:HOH:O	2.23	0.74
1:A:136:ARG:HD2	4:A:998:HOH:O	1.86	0.73
1:A:182:GLU:HG2	4:A:909:HOH:O	1.89	0.72
1:A:84:ARG:NH2	4:A:990:HOH:O	2.11	0.71
1:A:328:GLN:HB2	4:A:881:HOH:O	1.90	0.70
1:A:35:HIS:HD2	4:A:567:HOH:O	1.74	0.69
1:A:21:HIS:HD2	4:A:935:HOH:O	1.75	0.68
1:A:225:LYS:NZ	3:A:402:ARG:HA	2.08	0.68
1:A:275:GLU:HG3	4:A:1015:HOH:O	1.94	0.66
1:A:21:HIS:HE1	4:A:938:HOH:O	1.81	0.64
1:A:327:PRO:HB3	4:A:1023:HOH:O	1.82	0.62
1:A:369:ARG:NE	4:A:1027:HOH:O	1.96	0.61
1:A:35:HIS:HE1	1:A:283:GLU:OE1	1.84	0.61
1:A:290:HIS:HD2	4:A:932:HOH:O	1.86	0.58
1:A:300:GLU:HG2	1:A:301:LEU:HG	1.85	0.58
1:A:225:LYS:HZ1	3:A:402:ARG:HA	1.69	0.57
1:A:67:GLU:HG2	1:A:71:ARG:HD2	1.87	0.57
1:A:290:HIS:HE1	4:A:725:HOH:O	1.89	0.56
3:A:402:ARG:HG2	3:A:402:ARG:OXT	2.06	0.56
1:A:182:GLU:CG	4:A:909:HOH:O	2.49	0.56
1:A:121:HIS:HD2	4:A:954:HOH:O	1.91	0.53
1:A:165:HIS:HD2	1:A:168:THR:OG1	1.91	0.52
1:A:380:ARG:NH2	4:A:1029:HOH:O	2.43	0.51

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}({ m \AA})$	overlap (Å)
1:A:162:ASN:ND2	1:A:166:ASN:H	2.08	0.50
1:A:195:ALA:HB1	1:A:198:ALA:HB2	1.92	0.50
1:A:175:GLN:CG	4:A:682:HOH:O	2.30	0.50
1:A:124:ARG:HG3	4:A:645:HOH:O	2.10	0.49
1:A:136:ARG:HG3	4:A:557:HOH:O	2.14	0.48
1:A:121:HIS:HE1	4:A:996:HOH:O	1.97	0.47
1:A:264:LEU:C	1:A:264:LEU:HD23	2.36	0.46
1:A:272:HIS:HD2	1:A:275:GLU:OE1	1.99	0.44
1:A:369:ARG:CD	4:A:1027:HOH:O	2.58	0.44
3:A:402:ARG:CG	3:A:402:ARG:OXT	2.67	0.42
1:A:342:ARG:HA	1:A:342:ARG:NE	2.34	0.42
1:A:88:THR:HB	1:A:93:GLU:HB3	2.02	0.42
1:A:84:ARG:NE	4:A:631:HOH:O	2.51	0.42
1:A:216:ASP:HB2	4:A:1005:HOH:O	2.19	0.42
1:A:8:ARG:H	1:A:8:ARG:HG2	1.72	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{\AA}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:329:GLU:OE1	4:A:909:HOH:O[1_556]	2.17	0.03

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	378/406 (93%)	368 (97%)	10 (3%)	0	100 100

There are no Ramachandran outliers to report.



5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Analysed Rotameric O		Percentiles
1	A	289/312 (93%)	284 (98%)	5 (2%)	60 36

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	139	ARG
1	A	257	PHE
1	A	304	TRP
1	A	342	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	HIS
1	A	35	HIS
1	A	89	HIS
1	A	121	HIS
1	A	162	ASN
1	A	165	HIS
1	A	272	HIS
1	A	290	HIS

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)

2 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	Tuna	Chain	Res	Link	Bo	nd leng	${ m ths}$	В	ond ang	les
MIGI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ARG	A	402	2	7,11,11	1.23	0	6,13,13	0.26	0
2	PLP	A	401	3	15,15,16	2.65	8 (53%)	20,22,23	1.13	1 (5%)

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
3	ARG	A	402	2	_	1/7/11/11	-
2	PLP	A	401	3	-	0/6/6/8	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	A	401	PLP	C2A-C2	-5.35	1.41	1.50
2	A	401	PLP	C4A-C4	-4.31	1.42	1.51
2	A	401	PLP	C3-C2	-3.61	1.37	1.40
2	A	401	PLP	P-O3P	-3.25	1.42	1.54
2	A	401	PLP	P-O2P	-3.12	1.42	1.54
2	A	401	PLP	C5-C4	-2.90	1.37	1.40
2	A	401	PLP	C5A-C5	-2.37	1.44	1.50
2	A	401	PLP	O4P-C5A	-2.32	1.36	1.45

All (1) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	401	PLP	O4P-C5A-C5	3.88	116.75	109.35

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	ARG	CG-CD-NE-CZ

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	ARG	4	0

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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	380/406 (93%)	-0.00	17 (4%) 33 33	6, 12, 27, 55	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	385	GLY	9.2
1	A	324	ALA	8.5
1	A	325	ALA	7.2
1	A	327	PRO	5.7
1	A	8	ARG	5.6
1	A	322	ARG	5.1
1	A	7	ARG	5.0
1	A	6	PRO	5.0
1	A	253	ARG	4.5
1	A	326	GLY	4.2
1	A	384	ALA	4.1
1	A	383	ALA	3.9
1	A	47	ARG	2.9
1	A	24	PRO	2.9
1	A	25	ASP	2.9
1	A	323	ALA	2.6
1	A	380	ARG	2.4

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	ARG	A	402	12/12	0.91	0.15	12,18,25,25	0
2	PLP	A	401	15/16	0.99	0.07	8,8,10,11	0

6.5 Other polymers (i)

There are no such residues in this entry.

