



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2017 – 01:30 AM EDT

PDB ID : 5MSS  
Title : Structure of the A-PCP didomain of carboxylic acid reductase (CAR) from  
Segniliparus rugosus in complex with AMP  
Authors : Gahloth, D.; Leys, D.  
Deposited on : unknown  
Resolution : 1.96 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

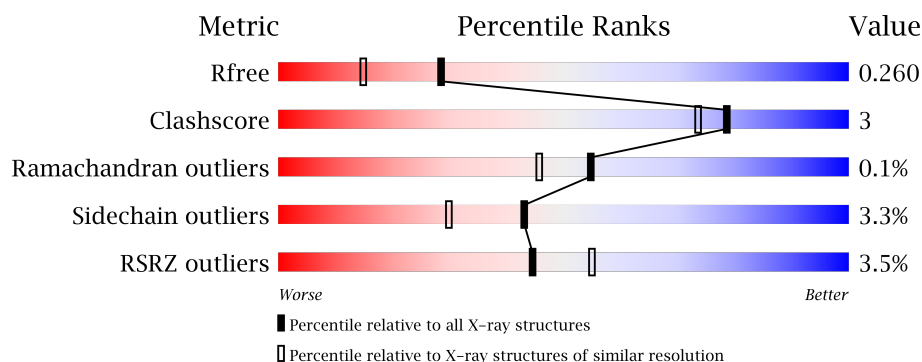
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.96 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))
$R_{free}$	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	A	1188	<div> <div>2%</div> <div>54%</div> <div>6%</div> <div>40%</div> </div>

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	NA	A	1202	-	-	-	X

## 2 Entry composition [i](#)

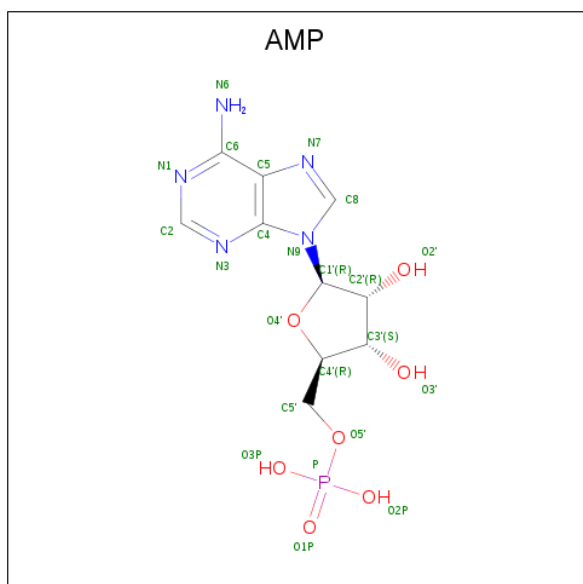
There are 4 unique types of molecules in this entry. The entry contains 5900 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Thioester reductase domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	717	5450	3451	935	1057	7	0	0	0

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	23	10	5	7	1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	426	Total 426	O 426	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.72Å 127.69Å 212.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	106.12 – 1.96 106.12 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.0 (106.12-1.96) 99.0 (106.12-1.96)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.204 , 0.254 0.212 , 0.260	Depositor DCC
$R_{free}$ test set	2911 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.7	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5900	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, AMP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.96	0/5554	1.00	15/7550 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	522	ARG	NE-CZ-NH1	16.23	128.41	120.30
1	A	522	ARG	NE-CZ-NH2	-15.76	112.42	120.30
1	A	351	ARG	NE-CZ-NH2	-9.92	115.34	120.30
1	A	523	ARG	NE-CZ-NH2	-8.61	116.00	120.30
1	A	393	ARG	NE-CZ-NH1	7.93	124.27	120.30
1	A	105	ARG	NE-CZ-NH1	7.32	123.96	120.30
1	A	523	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	A	393	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	351	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	360	ARG	NE-CZ-NH2	-6.01	117.30	120.30
1	A	360	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	A	141	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	A	457	ASP	CB-CG-OD1	5.18	122.96	118.30
1	A	245	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	A	472	ARG	NE-CZ-NH1	5.09	122.84	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	5450	0	5439	36	0
2	A	23	0	12	0	0
3	A	1	0	0	0	0
4	A	426	0	0	4	0
All	All	5900	0	5451	36	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 3.

All (36) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:663:VAL:C	1:A:666:GLY:N	2.36	0.78
1:A:522:ARG:HD3	1:A:526:VAL:O	1.97	0.65
1:A:141:ASP:OD2	4:A:1301:HOH:O	2.15	0.64
1:A:618:THR:HG23	1:A:621:ASN:H	1.64	0.62
1:A:662:ARG:O	1:A:663:VAL:HG23	2.01	0.60
1:A:671:ILE:HG13	1:A:675:GLN:HE21	1.68	0.58
1:A:117:ALA:O	4:A:1302:HOH:O	2.17	0.57
1:A:321:GLY:O	1:A:325:THR:HG23	2.05	0.57
1:A:695:PHE:HA	1:A:698:LEU:HD12	1.88	0.55
1:A:478:LYS:HE3	1:A:502:PHE:CE1	2.42	0.55
1:A:689:VAL:HG22	1:A:690:ASP:H	1.71	0.55
1:A:522:ARG:CD	1:A:526:VAL:O	2.55	0.54
1:A:663:VAL:HG13	1:A:667:GLU:H	1.72	0.53
1:A:653:THR:O	1:A:655:ALA:N	2.43	0.52
1:A:85:ARG:NH2	1:A:212:GLU:OE1	2.43	0.51
1:A:339:ASP:O	1:A:340:LEU:HB2	2.09	0.50
1:A:663:VAL:HG12	1:A:663:VAL:O	2.10	0.50
1:A:615:ASP:OD1	4:A:1303:HOH:O	2.20	0.48
1:A:663:VAL:HG13	1:A:667:GLU:N	2.30	0.47
1:A:69:ALA:HB2	1:A:99:TYR:CD1	2.49	0.47
1:A:649:GLN:O	1:A:653:THR:HB	2.15	0.46
1:A:618:THR:HG22	1:A:621:ASN:ND2	2.30	0.46
1:A:284:GLN:HA	1:A:288:GLY:HA3	1.97	0.46
1:A:513:ALA:O	1:A:514:PRO:C	2.54	0.46
1:A:80:ASP:OD1	1:A:83:THR:HG22	2.16	0.45
1:A:520:VAL:HG12	1:A:521:ASP:HB2	1.98	0.45
1:A:369:TYR:CZ	1:A:373:LEU:HD21	2.52	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:TYR:O	1:A:373:LEU:HD23	2.18	0.43
1:A:544:TYR:CD1	1:A:592:LEU:HG	2.54	0.43
1:A:243:LEU:HB3	1:A:244:PRO:HD2	2.00	0.42
1:A:101:GLU:O	1:A:105:ARG:HG3	2.19	0.42
1:A:19:LEU:HD22	4:A:1705:HOH:O	2.19	0.42
1:A:663:VAL:HG11	1:A:668:ARG:CZ	2.50	0.42
1:A:183:ASP:OD1	1:A:220:ARG:NH1	2.51	0.42
1:A:407:GLY:O	1:A:408:SER:HB2	2.20	0.41
1:A:722:VAL:O	1:A:726:VAL:HG22	2.22	0.40

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	A	709/1188 (60%)	692 (98%)	16 (2%)	1 (0%)	55 46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	654	GLN

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	571/947 (60%)	552 (97%)	19 (3%)	43	30

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ARG
1	A	72	GLN
1	A	89	THR
1	A	137	TYR
1	A	265	THR
1	A	289	ILE
1	A	291	HIS
1	A	323	MET
1	A	335	ILE
1	A	338	SER
1	A	371	SER
1	A	383	PRO
1	A	384	GLN
1	A	440	TRP
1	A	468	SER
1	A	629	LYS
1	A	653	THR
1	A	658	LEU
1	A	718	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	675	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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	AMP	A	1201	-	22,25,25	1.14	2 (9%)	24,38,38	2.00	6 (25%)

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	AMP	A	1201	-	-	0/6/26/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	AMP	C5-N7	-2.41	1.31	1.39
2	A	1201	AMP	C5-C4	3.12	1.47	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	AMP	N3-C2-N1	-6.16	123.49	128.86
2	A	1201	AMP	C4'-O4'-C1'	-2.61	106.99	109.77
2	A	1201	AMP	C2-N1-C6	2.05	122.35	118.77
2	A	1201	AMP	O3'-C3'-C4'	2.39	118.06	111.09
2	A	1201	AMP	N6-C6-N1	2.75	124.22	118.77
2	A	1201	AMP	O3P-P-O2P	4.34	125.12	107.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	717/1188 (60%)	0.19	25 (3%) 44 55	13, 27, 59, 88	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	684	ALA	6.6
1	A	293	ALA	4.1
1	A	294	PHE	4.0
1	A	726	VAL	3.7
1	A	731	ASN	3.5
1	A	692	GLU	3.3
1	A	719	GLU	3.2
1	A	729	ALA	3.2
1	A	728	ALA	3.2
1	A	733	ARG	2.9
1	A	291	HIS	2.8
1	A	658	LEU	2.7
1	A	695	PHE	2.6
1	A	663	VAL	2.5
1	A	744	SER	2.5
1	A	689	VAL	2.4
1	A	667	GLU	2.3
1	A	590	ASP	2.3
1	A	681	LEU	2.2
1	A	655	ALA	2.2
1	A	652	GLU	2.1
1	A	743	ARG	2.1
1	A	683	GLY	2.1
1	A	662	ARG	2.0
1	A	730	ASN	2.0

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NA	A	1202	1/1	0.97	0.16	2.94	36,36,36,36	0
2	AMP	A	1201	23/23	0.98	0.09	-0.97	14,18,26,28	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.