

### Strain identifier

**BacDive ID:** 534                      **DOI:** 10.13145/bacdive534.20190402.4  
**Type strain:** yes                      **Designation:** CW5  
**Culture col. no.:** DSM 21987, JCM 14755, KCTC 12893

### Sections

[Name and taxonomic classification](#)  
[Morphology and physiology](#)  
[Culture and growth conditions](#)  
[Isolation, sampling and environmental information](#)  
[Application and interaction](#)  
[Molecular biology](#)  
[Strain availability](#)  
[References](#)

### Name and taxonomic classification

Ref.: 16080	<b>Domain</b>	Bacteria
Ref.: 16080	<b>Phylum</b>	Proteobacteria
Ref.: 16080	<b>Class</b>	Alphaproteobacteria
Ref.: 16080	<b>Order</b>	Rhizobiales
Ref.: 16080	<b>Family</b>	Aurantimonadaceae
Ref.: 16080	<b>Genus</b>	Aureimonas
Ref.: 16080	<b>Species</b>	Aureimonas frigidaquae
Ref.: 16080	<b>Full Scientific Name</b>	Aureimonas frigidaquae (Kim et al. 2008) Rathsack et al. 2011
Ref.: 16080	<b>Designation:</b>	CW5
Ref.: 16080	<b>Type strain:</b>	yes

#### **Prokaryotic Nomenclature Up-to-date (PNU)**

Ref.: 20215	<b>Domain</b>	Bacteria
Ref.: 20215	<b>Phylum</b>	Proteobacteria
Ref.: 20215	<b>Class</b>	Alphaproteobacteria
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 56:1
Ref.: 20215	<b>Family</b>	Aurantimonadaceae
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 52:685
Ref.: 20215	<b>Genus</b>	Aureimonas

Ref.: 20215	Taxonomical status	gen. nov. (VP)
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 61:2722*
Ref.: 20215	<b>Species</b>	Aureimonas frigidaquae
Ref.: 20215	Taxonomical status	comb. nov. (VP)
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 61:2722*
Ref.: 20215	<b>Full Scientific Name</b>	Aureimonas frigidaquae (Kim et al. 2008) Rath sack et al. 2011
Ref.: 20215	<b>Synonym</b>	Aurantimonas frigidaquae

**Morphology and physiology**

Ref.: 23136	<b>Gram stain</b>	negative
Ref.: 23136	<b>Cell length</b>	0.8-1.2 µm
Ref.: 23136	<b>Cell width</b>	0.6-0.8 µm
Ref.: 23136	<b>Cell shape</b>	rod-shaped
Ref.: 23136	<b>Motility</b>	yes
Ref.: 23136	<b>Cultivation medium used</b>	TSA
Ref.: 23136	<b>Colony size</b>	3.0 mm
Ref.: 23136	<b>Colony shape</b>	circular
Ref.: 23136	<b>Incubation period</b>	5 days

Enzymes	Enzyme	Enzyme activity	EC number
Ref.: 23136	acid phosphatase	+	3.1.3.2
Ref.: 23136	alpha-chymotrypsin	-	3.4.21.1
Ref.: 23136	alpha-fucosidase	-	3.2.1.51
Ref.: 23136	alpha-glucosidase	-	3.2.1.20
Ref.: 23136	alpha-mannosidase	-	3.2.1.24
Ref.: 23136	beta-glucuronidase	-	3.2.1.31
Ref.: 23136	catalase	+	1.11.1.6
Ref.: 23136	cystine arylamidase	-	3.4.11.3
Ref.: 23136	cytochrome oxidase	+	1.9.3.1
Ref.: 23136	esterase (C 4)	+	
Ref.: 23136	esterase lipase (C 8)	+	
Ref.: 23136	leucine arylamidase	+	3.4.11.1
Ref.: 23136	lipase (C 14)	-	
Ref.: 23136	lysine decarboxylase	-	4.1.1.18
Ref.: 23136	N-acetyl-beta-glucosaminidase	-	3.2.1.52

Ref.: 23136

ornithine decarboxylase	-	4.1.1.17
valine arylamidase	-	

Ref.: 23136

**Halophily**

Ref.: 23136

Ref.: 23136

Salt	Tested relation	Salt conc.
NaCl	maximum	<7 %(w/v)
NaCl	optimum	0 %(w/v)

**Antibiotica**

Ref.: 23136

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Chebi ID	Metabolite	Antib. sensitivity	Conc.	Antib. resistance	Conc.
28971	Ampicillin	yes	10 µg (disc)		
28669	Bacitracin			yes	10 µg (disc)
17698	Chloramphenicol	yes	30 µg (disc)		
48923	Erythromycin	yes	15 µg (disc)		
17833	Gentamicin	yes	10 µg (disc)		
6104	Kanamycin	yes	30 µg (disc)		
100147	Nalidixic acid	yes	30 µg (disc)		
17334	Penicillin			yes	10 Unit
8309	Polymyxin B	yes	300 Unit		
17076	Streptomycin	yes	10 µg (disc)		
27902	Tetracycline	yes	30 µg (disc)		
28001	Vancomycin			yes	30 µg (disc)

**Metabolite production**

Ref.: 23136

Chebi ID	Metabolite	Production
15688	Acetoin	no

**Physiological tests**

Ref.: 23136

Ref.: 23136

Chebi ID	Metabolite	Voges-Proskauer-test	Methylred-test
15688	Acetoin	-	
17234	Glucose		-

	<b>Metabolite utilization</b>	<b>Chebi ID</b>	<b>Metabolite</b>	<b>Utilization activity</b>	<b>Kind of utilization tested</b>
Ref.: 23357		17521	(-)-Quinic acid	-	carbon source
Ref.: 23136		16808	2-Dehydro-D-glucuronate	-	builds acid from
Ref.: 23357		1148	2-Hydroxybutyric acid	-	carbon source
Ref.: 23357		30831	2-Oxobutanoic acid	-	carbon source
Ref.: 23357		33033	2-Oxovaleric acid	-	carbon source
Ref.: 23357		20067	3-Hydroxybutyric acid	-	carbon source
Ref.: 23357		16865	4-Aminobutyric acid	-	carbon source
Ref.: 23357		30830	4-Hydroxybutyric acid	-	carbon source
Ref.: 23136		17426	5-Dehydro-D-glucuronate	-	builds acid from
Ref.: 23357		15366	Acetic acid	-	carbon source
Ref.: 23357		15963	Adonitol	-	carbon source
Ref.: 23136		15963	Adonitol	+	builds acid from
Ref.: 23357		40585	alpha-Cyclodextrin	-	carbon source
Ref.: 23357		17716	alpha-D-Lactose	-	carbon source
Ref.: 23136		27613	Amygdalin	+	builds acid from
Ref.: 23136		18305	Arbutin	+	builds acid from
Ref.: 23357		73712	Bromosuccinic acid	-	carbon source
Ref.: 23136			Casein	-	hydrolysis
Ref.: 23357		17057	Cellobiose	-	carbon source
Ref.: 23136		17057	Cellobiose	+	builds acid from
Ref.: 23357		15570	D-Alanine	-	carbon source
Ref.: 23357		18333	D-Arabitol	-	carbon source
Ref.: 23136		18333	D-Arabitol	+	builds acid from
Ref.: 23357		15824	D-Fructose	-	carbon source
Ref.: 23136		28847	D-Fucose	+	builds acid from
Ref.: 23357		15895	D-Galactonic acid lactone	-	carbon source
Ref.: 23357		12936	D-Galactose	-	carbon source
Ref.: 23357		16002	D-Gluconic acid	-	carbon source
Ref.: 23357		33198	D-Gluconic acid	-	carbon source
Ref.: 23357		17784	D-Glucosaminic acid	-	carbon source
Ref.: 23357		16899	D-Mannitol	-	carbon source



Ref.: 23357	16024	D-Mannose	-	carbon source
Ref.: 23357	17924	D-Sorbitol	-	carbon source
Ref.: 23136	16443	D-Tagatose	-	builds acid from
Ref.: 23357	23652	Dextrin	+	carbon source
Ref.: 23357	17126	DL-Carnitine	-	carbon source
Ref.: 23136	16991	DNA	-	hydrolysis
Ref.: 23357	17113	Erythritol	-	carbon source
Ref.: 23136	17113	Erythritol	+	carbon source
Ref.: 23136	4853	Esculin	+	builds acid from
Ref.: 23136	4853	Esculin	+	hydrolysis
Ref.: 23357	30751	Formic acid	+	carbon source
Ref.: 23136	28757	Fructose	+	builds acid from
Ref.: 23136	16813	Galactitol	-	builds acid from
Ref.: 23136	5291	Gelatin	-	hydrolysis
Ref.: 23357	28066	Gentiobiose	-	carbon source
Ref.: 23136	28066	Gentiobiose	+/-	carbon source
Ref.: 23136	24265	Gluconate	-	builds acid from
Ref.: 23136	24265	Gluconate	+/-	carbon source
Ref.: 23136	17234	Glucose	-	fermentation
Ref.: 23136	17234	Glucose	+	builds acid from
Ref.: 23357	32323	Glucuronamide	-	carbon source
Ref.: 23136	17754	Glycerol	-	builds acid from
Ref.: 23357	17754	Glycerol	-	carbon source
Ref.: 23357	15978	Glycerol 3-phosphate	-	carbon source
Ref.: 23136	28087	Glycogen	-	builds acid from
Ref.: 23357	28087	Glycogen	-	carbon source
Ref.: 23357	73804	Glycyl L-Aspartic acid	-	carbon source
Ref.: 23136	16136	Hydrogen sulfide	-	other
Ref.: 23357	24741	Hydroxyproline	-	carbon source
Ref.: 23357	17268	Inositol	-	carbon source
Ref.: 23136	17268	Inositol	+	builds acid from
Ref.: 23136	15443	Inulin	-	builds acid from
Ref.: 23357	30838	Itaconic acid	-	carbon source
Ref.: 23357	21217	L-Alaninamide	-	carbon source
Ref.: 23357	16977	L-Alanine	-	carbon source
Ref.: 23357	73786	L-Alanylglycine	-	carbon source



Ref.: 23357	30849	L-Arabinose	-	carbon source
Ref.: 23136	30849	L-Arabinose	-	carbon source
Ref.: 23136	18403	L-Arabitol	+	builds acid from
Ref.: 23357	17196	L-Asparagine	-	carbon source
Ref.: 23357	17053	L-Aspartic acid	-	carbon source
Ref.: 23357	18287	L-Fucose	-	carbon source
Ref.: 23136	18287	L-Fucose	+	carbon source
Ref.: 23357	16015	L-Glutamic acid	-	carbon source
Ref.: 23357	15971	L-Histidine	-	carbon source
Ref.: 23357	15603	L-Leucine	-	carbon source
Ref.: 23357	15729	L-Ornithine	-	carbon source
Ref.: 23357	17203	L-Proline	-	carbon source
Ref.: 23357	18183	L-Pyroglutamic acid	-	carbon source
Ref.: 23357	62345	L-Rhamnose	-	carbon source
Ref.: 23357	17115	L-Serine	-	carbon source
Ref.: 23357	16857	L-Threonine	-	carbon source
Ref.: 23136	65328	L-Xylose	-	carbon source
Ref.: 23357	78320	Lactic acid	-	carbon source
Ref.: 23136	17716	Lactose	-	builds acid from
Ref.: 23136	17306	Maltose	-	builds acid from
Ref.: 23357	17306	Maltose	-	carbon source
Ref.: 23136	17306	Maltose	-	carbon source
Ref.: 23136	29864	Mannitol	+	builds acid from
Ref.: 23136	29864	Mannitol	+	carbon source
Ref.: 23136	6731	Melezitose	-	builds acid from
Ref.: 23357	28053	Melibiose	-	carbon source
Ref.: 23357	320061	Methyl alpha-D-glu copyranoside	-	carbon source
Ref.: 23136	43943	Methyl alpha-D-mannoside	-	builds acid from
Ref.: 23136	320055	methyl beta-D-glucopyranoside	-	builds acid from
Ref.: 23136	74863	Methyl beta-D-xylopyranoside	-	builds acid from
Ref.: 23357	75146	Monomethyl succinate	-	carbon source
Ref.: 23357	28037	N-Acetylgalactosamine	-	carbon source
Ref.: 23136	506227	N-Acetylglucosamine	+	builds acid from



Ref.: 23136	506227	N-Acetylglucosamine	+	carbon source
Ref.: 23357	73801	N-Glycyl-L-glutamic acid	-	carbon source
Ref.: 23357	30768	Propionic acid	-	carbon source
Ref.: 23357	33951	Psicose	-	carbon source
Ref.: 23357	17148	Putrescine	-	carbon source
Ref.: 23357	32816	Pyruvic acid	-	carbon source
Ref.: 23357	16634	Raffinose	-	carbon source
Ref.: 23136	16634	Raffinose	+	builds acid from
Ref.: 23136	26546	Rhamnose	-	carbon source
Ref.: 23136	33942	Ribose	+/-	carbon source
Ref.: 23136	17814	Salicin	+	builds acid from
Ref.: 23136	28017	Starch	-	builds acid from
Ref.: 23136	28017	Starch	-	hydrolysis
Ref.: 23357	50398	Succinamic acid	-	carbon source
Ref.: 23357	15741	Succinic acid	-	carbon source
Ref.: 23357	17992	Sucrose	-	carbon source
Ref.: 23136	17992	Sucrose	+	builds acid from
Ref.: 23357	17748	Thymidine	-	carbon source
Ref.: 23357	32528	Turanose	-	carbon source
Ref.: 23357	53423	Tween 40	-	carbon source
Ref.: 23136	53426	Tween 80	-	hydrolysis
Ref.: 23136	18186	Tyrosine	-	hydrolysis
Ref.: 23357	16704	Uridine	-	carbon source
Ref.: 23357	27248	Urocanic acid	-	carbon source
Ref.: 23357	17151	Xylitol	-	carbon source

Ref.: 23136      **Oxygen tolerance**      facultative anaerobe

Ref.: 23136      **Pigmentation color**      yellow

**Culture and growth conditions**

Ref.: 16080      **Culture medium**      TRYPTICASE SOY BROTH AGAR (DSMZ Medium 535), 28°C

Ref.: 16080      **Culture medium growth**      yes

Ref.: 16080      **Culture medium link**      [https://www.dsmz.de/microorganisms/medium/pdf/DSMZ\\_Medium535.pdf](https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium535.pdf)

Ref.: 16080	<b>Culture medium</b>	TRYPTONE SOYA BROTH (TSB) (DSMZ Medium 545), 28°C
Ref.: 16080	<b>Culture medium growth</b>	yes
Ref.: 16080	<b>Culture medium link</b>	<a href="https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium545.pdf">https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium545.pdf</a>
Ref.: 16080	<b>Culture medium</b>	BACTO MARINE BROTH (DIFCO 2216) (DSMZ Medium 514), 28°C
Ref.: 16080	<b>Culture medium growth</b>	yes
Ref.: 16080	<b>Culture medium link</b>	<a href="https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium514.pdf">https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium514.pdf</a>
Ref.: 23136	<b>Culture medium</b>	PCA, TSA, NA, R2A, MA and MacConkey agar
Ref.: 23136	<b>Culture medium growth</b>	yes
Ref.: 23136	<b>Culture medium</b>	TSA
Ref.: 23136	<b>Culture medium growth</b>	yes

**Temperatures**

Ref.: 16080  
Ref.: 23136  
Ref.: 23136  
Ref.: 23136

Kind of temperature	Temperature
growth	28 °C
maximum	37 °C
minimum	15 °C
optimum	25 °C

Ref.: 16080	<b>Temperature range</b>	mesophilic
Ref.: 23136	<b>Temperature range</b>	mesophilic
Ref.: 23136	<b>Temperature range</b>	psychrophilic
Ref.: 23136	<b>Temperature range</b>	mesophilic

**pH**

Ref.: 23136  
Ref.: 23136  
Ref.: 23136

Kind of pH	pH
minimum	5.0
maximum	11.0
optimum	7.0

**Isolation, sampling and environmental information**

Ref.: 16080	<b>Sample type/isolated from</b>	water-cooling system
Ref.: 16080	<b>Geographic location (country and/or sea, region)</b>	Gwangyang
Ref.: 16080	<b>Country</b>	Republic of Korea





Ref.: 16080      **Continent**      Asia

Ref.: 23136      **Sample type/isolated from**      cooled water sample from an oxygen-producing plant

Ref.: 23136      **Enrichment culture**      2005-02

Isolation sources categories	Cat1	Cat2	Cat3
	#Engineered	#Industrial	#Plant (Factory)
	#Environmental	#Aquatic	#Freshwater
	#Condition	#Psychrophilic (<10°C)	-
	#Engineered	#Industrial	#Engineered product

**Application and interaction**

Ref.: 16080      **Biosafety level**      1 Risk group (German classification)

**Molecular biology**

Ref.: 16080      **GC-content**      63.9 mol% thermal denaturation, midpoint method (Tm)

Ref.: 23136      **GC-content**      63.9 mol% Thermal denaturation, fluorometry

	Sequence database	Sequence accession description	Sequence accession number	Sequence length(bp)	Associated NCBI tax ID
Ref.: 16080	GenBank Direct submission	Aurantimonas frigidaquae strain CW5 16S ribosomal RNA gene, partial sequence	EF373540	1378	424757

**Strain availability**

Ref.: 16080      **Culture collection no.**      DSM 21987, JCM 14755, KCTC 12893

Ref.: 16080      **Strain history**      <- JCM/RIKEN <- C. N. Seong, Suncheon Natl. Univ., Korea; CW5

**Associated Passport(s) in StrainInfo**

Ref.: 20218      867603 - <http://www.straininfo.net/strains/867603>

Ref.: 20218      822591 - <http://www.straininfo.net/strains/822591>

Ref.: 20218      822592 - <http://www.straininfo.net/strains/822592>

**References**



- Ref.: 16080      Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; Curators of the DSMZ; DSM 21987
- Ref.: 20215      D.Gleim, M.Kracht, N.Weiss et. al.: Prokaryotic Nomenclature Up-to-date - compilation of all names of Bacteria and Archaea, validly published according to the Bacteriological Code since 1. Jan. 1980, and validly published nomenclatural changes since.
- Ref.: 20218      Verslyppe, B., De Smet, W., De Baets, B., De Vos, P., Dawyndt P. StrainInfo introduces electronic passports for microorganisms.. Syst Appl Microbiol. 37: 42-50 2014 (10.1016/j.syapm.2013.11.002, 24321274)
- Ref.: 23136      Mi Sun Kim, Kieu Thi Quynh Hoa, Keun Sik Baik, Seong Chan Park, Chi Nam Seong Aurantimonas frigidaquae sp. nov., isolated from a water-cooling system. IJSEM 58: 1142-1146 2008 (10.1099/ijs.0.65421-0, None)
- Ref.: 23357      K. Rathsack, J. Reitner, E. Stackebrandt, B. J. Tindall Reclassification of Aurantimonas altamirensis (Jurado et al. 2006), Aurantimonas ureilytica (Weon et al. 2007) and Aurantimonas frigidaquae (Kim et al. 2008) as members of a new genus, Aureimonas gen. nov., as Aureimonas altamirensis gen. nov., comb. nov., Aureimonas ureilytica comb. nov. and Aureimonas frigidaquae comb. nov., and emended descriptions of the genera Aurantimonas and Fulvimarina. IJSEM 61: 2722-2728 2011 (10.1099/ijs.0.027029-0, None)

**\* These References are textmined**

[back to top](#)