

Strain identifier

BacDive ID: 355 **DOI:** 10.13145/bacdive355.20190402.4
Type strain: yes **Designation:** CDC 7603 MC213
Culture col. no.: DSM 7531, ATCC 17960, CCUG 13463, LMG 5303

Sections

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Name and taxonomic classification

Ref.: 3204	Domain	Bacteria
Ref.: 3204	Phylum	Proteobacteria
Ref.: 3204	Class	Betaproteobacteria
Ref.: 3204	Order	Burkholderiales
Ref.: 3204	Family	Alcaligenaceae
Ref.: 3204	Genus	Oligella
Ref.: 3204	Species	Oligella urethralis
Ref.: 3204	Full Scientific Name	Oligella urethralis (Lautrop et al. 1970) Rossau et al. 1987
Ref.: 3204	Designation:	CDC 7603 MC213
Ref.: 3204	Type strain:	yes

Prokaryotic Nomenclature Up-to-date (PNU)

Ref.: 20215	Domain	Bacteria
Ref.: 20215	Phylum	Proteobacteria
Ref.: 20215	Class	Betaproteobacteria
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 56:1
Ref.: 20215	Family	Alcaligenaceae
Ref.: 20215	Genus	Oligella
Ref.: 20215	Taxonomical status	gen. nov. (VP)



Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 37:198*
Ref.: 20215	Species	Oligella urethralis
Ref.: 20215	Taxonomical status	comb. nov. (VP)
Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 37:198*
Ref.: 20215	Full Scientific Name	Oligella urethralis (Lautrop et al. 1970) Rossau et al. 1987
Ref.: 20215	Synonym	Moraxella urethralis

Morphology and physiology

Ref.: 23272	Gram stain	negative
Ref.: 23272	Cell length	1 µm
Ref.: 23272	Cell shape	rod-shaped
Ref.: 23272	Motility	no
Ref.: 23272	Type of hemolysis	gamma

Enzymes	Enzyme	Enzyme activity	EC number
Ref.: 23272	Acid phosphatase	-	3.1.3.2
Ref.: 23272	Alkaline phosphatase	-	3.1.3.1
Ref.: 23272	alpha-chymotrypsin	-	3.4.21.1
Ref.: 23272	alpha-fucosidase	-	3.2.1.51
Ref.: 23272	alpha-galactosidase	-	3.2.1.22
Ref.: 23272	alpha-glucosidase	-	3.2.1.20
Ref.: 23272	alpha-mannosidase	-	3.2.1.24
Ref.: 23272	arginine dihydrolase	-	3.5.3.6
Ref.: 23272	beta-galactosidase	-	3.2.1.23
Ref.: 23272	beta-glucuronidase	-	3.2.1.31
Ref.: 23272	beta-glucosidase	-	3.2.1.21
Ref.: 23272	cystine arylamidase	-	3.4.11.3
Ref.: 23272	cytochrome oxidase	+	1.9.3.1
Ref.: 23272	esterase (C 4)	+	
Ref.: 23272	esterase lipase (C 8)	+	
Ref.: 23272	leucine arylamidase	+	3.4.11.1
Ref.: 23272	lipase (C 14)	-	
Ref.: 23272	lysine decarboxylase	-	4.1.1.18
Ref.: 23272	N-acetyl-beta-glucosaminidase	-	3.2.1.52
Ref.: 23272	naphthol-AS-BI-phosphohydrolase	-	



Ref.: 23272

ornithine decarboxylase	-	4.1.1.17
trypsin	-	3.4.21.4
urease	-	3.5.1.5
valine arylamidase	-	

Ref.: 23272

Ref.: 23272

Ref.: 23272

Halophily

Salt	Tested relation	Salt conc.
NaCl	maximum	3 %

Ref.: 23272

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API NH

API ID	970
PEN	-
GLU	-
FRU	-
MAL	-
SAC	-
ODC	-
URE	-
LIP	-
PAL	-
betaGAL	-
ProA	+
GGT	+
IND	-

Antibiotica

Chebi ID	Metabolite	Antib. sensitivity
17334	Penicillin	yes

Ref.: 23272

Metabolite production

Chebi ID	Metabolite	Production
16136	Hydrogen sulfide	no
35581	Indole	no

Ref.: 23272

Ref.: 23272

Metabolite utilization

Chebi ID	Metabolite	Utilization activity	Kind of utilization tested
17656	(R)-Mandelic acid	-	carbon source
30797	(S)-Malic acid	+	carbon source
32800	(S)-Mandelic acid	-	growth
16567	2-Aminobenzoate	-	carbon source
28340	2-Aminobutyrate	-	growth

Ref.: 23272

Ref.: 23272

Ref.: 23272

Ref.: 23272

Ref.: 23272



Ref.: 23272	19475	2-Aminopentanoic acid	-	growth
Ref.: 23272	16808	2-Dehydro-D-glucuronate	-	carbon source
Ref.: 23272	30915	2-Oxoglutaric acid	+	carbon source
Ref.: 23272	30761	3-Aminobenzoate	-	carbon source
Ref.: 23272	87997	3-Aminobutyrate	-	carbon source
Ref.: 23272	30764	3-Hydroxybenzoic acid	-	growth
Ref.: 23272	20067	3-Hydroxybutyric acid	+	carbon source
Ref.: 23272	17836	4-Aminobenzoate	-	carbon source
Ref.: 23272	16865	4-Aminobutyric acid	-	growth
Ref.: 23272	30763	4-Hydroxybenzoic acid	-	growth
Ref.: 23272	45630	4-Oxopentanoic acid	-	carbon source
Ref.: 23272	15887	5-Aminovaleric acid	+	growth
Ref.: 23272	17426	5-Dehydro-D-glucuronate	-	carbon source
Ref.: 23272	27856	Acetamide	-	carbon source
Ref.: 23272	27856	Acetamide	-	hydrolysis
Ref.: 23272	15366	Acetic acid	+	carbon source
Ref.: 23272	22210	Aconitate	-	carbon source
Ref.: 23272	30832	Adipic acid	-	carbon source
Ref.: 23272	15963	Adonitol	-	builds acid from
Ref.: 23272	15963	Adonitol	-	carbon source
Ref.: 23272	27613	Amygdalin	-	carbon source
Ref.: 23272	18305	Arbutin	-	carbon source
Ref.: 23272	48131	Azelaic acid	-	carbon source
Ref.: 23272	16150	Benzoate	+	carbon source
Ref.: 23272	40538	Benzylamine	-	carbon source
Ref.: 23272	16958	beta-Alanine	-	carbon source
Ref.: 23272		Betaine	-	carbon source
Ref.: 23272	43799	Butan-1-amine	-	carbon source
Ref.: 23272	30772	Caprate	-	carbon source
Ref.: 23272	25646	Caprylate	-	carbon source
Ref.: 23272	17057	Cellobiose	-	carbon source
Ref.: 23272	3565	Cetrimide	-	growth
Ref.: 23272	17626	Citraconic acid	-	carbon source



Ref.: 23272	30769	Citric acid	+	growth
Ref.: 23272	16919	Creatine	-	carbon source
Ref.: 23272	15570	D-Alanine	+	growth
Ref.: 23272	17108	D-Arabinose	-	carbon source
Ref.: 23272	18333	D-Arabitol	-	carbon source
Ref.: 23272	15824	D-Fructose	-	builds acid from
Ref.: 23272	15824	D-Fructose	-	carbon source
Ref.: 23272	28847	D-Fucose	-	carbon source
Ref.: 23272	12936	D-Galactose	-	carbon source
Ref.: 23272	33198	D-Gluconic acid	-	carbon source
Ref.: 23272	17315	D-Glucosamine	-	carbon source
Ref.: 23272	17634	D-Glucose	-	builds acid from
Ref.: 23272	17634	D-Glucose	-	carbon source
Ref.: 23272	62318	D-Lyxose	-	carbon source
Ref.: 23272	15588	D-Malate	+	growth
Ref.: 23272	16899	D-Mannitol	-	carbon source
Ref.: 23272	16024	D-Mannose	-	carbon source
Ref.: 23272	16988	D-Ribose	-	carbon source
Ref.: 23272	16443	D-Tagatose	-	carbon source
Ref.: 23272	30927	D-Tartrate	-	carbon source
Ref.: 23272	16296	D-Tryptophan	-	carbon source
Ref.: 23272	65327	D-Xylose	-	builds acid from
Ref.: 23272	65327	D-Xylose	-	carbon source
Ref.: 23272	33871	DL-Glycerate	-	carbon source
Ref.: 23272	16991	DNA	-	hydrolysis
Ref.: 23272	17113	Erythritol	-	carbon source
Ref.: 23272	4853	Esculin	-	carbon source
Ref.: 23272	4853	Esculin	-	hydrolysis
Ref.: 23272	16000	Ethanolamine	-	carbon source
Ref.: 23272	15862	Ethylamine	-	carbon source
Ref.: 23272	18012	Fumaric acid	+	carbon source
Ref.: 23272	16813	Galactitol	-	carbon source
Ref.: 23272	5291	Gelatin	-	hydrolysis
Ref.: 23272	28066	Gentiobiose	-	carbon source
Ref.: 23272	17859	Glutaric acid	+	growth
Ref.: 23272	15428	Glycine	-	carbon source
Ref.: 23272	28087	Glycogen	-	carbon source
Ref.: 23272	17497	Glycolate	-	carbon source



Ref.: 23272	32362	Heptanoate	-	carbon source
Ref.: 23272	18295	Histamine	-	carbon source
Ref.: 23272	15443	Inulin	-	carbon source
Ref.: 23272	48944	Isobutyrate	+	growth
Ref.: 23272	30802	Isophthalic acid	-	carbon source
Ref.: 23272	28484	Isovalerate	+	growth
Ref.: 23272	30838	Itaconic acid	+	growth
Ref.: 23272	28683	Kynurenine	-	carbon source
Ref.: 23272	16977	L-Alanine	+	growth
Ref.: 23272	30849	L-Arabinose	-	carbon source
Ref.: 23272	18403	L-Arabitol	-	carbon source
Ref.: 23272	16467	L-Arginine	-	carbon source
Ref.: 23272	17053	L-Aspartic acid	-	growth
Ref.: 23272	16349	L-Citrulline	-	carbon source
Ref.: 23272	17561	L-Cysteine	-	carbon source
Ref.: 23272	18287	L-Fucose	-	carbon source
Ref.: 23272	16015	L-Glutamic acid	+	carbon source
Ref.: 23272	15971	L-Histidine	-	carbon source
Ref.: 23272	17191	L-Isoleucine	+	growth
Ref.: 23272	15603	L-Leucine	+	growth
Ref.: 23272	18019	L-Lysine	-	carbon source
Ref.: 23272	16643	L-Methionine	-	carbon source
Ref.: 23272	18347	L-Norleucine	+	growth
Ref.: 23272	15729	L-Ornithine	-	carbon source
Ref.: 23272	17295	L-Phenylalanine	-	carbon source
Ref.: 23272	17203	L-Proline	+	growth
Ref.: 23272	62345	L-Rhamnose	-	carbon source
Ref.: 23272	17115	L-Serine	-	carbon source
Ref.: 23272	17266	L-Sorbose	-	carbon source
Ref.: 23272	30924	L-Tartrate	-	growth
Ref.: 23272	16857	L-Threonine	-	carbon source
Ref.: 23272	16828	L-Tryptophan	-	carbon source
Ref.: 23272	17895	L-Tyrosine	-	carbon source
Ref.: 23272	16414	L-Valine	+	growth
Ref.: 23272	65328	L-Xylose	-	carbon source
Ref.: 23272	78320	Lactic acid	+	carbon source
Ref.: 23272	17716	Lactose	-	carbon source
Ref.: 23272	18300	Maleic acid	-	carbon source



Ref.: 23272	30794	Malonic acid	-	carbon source
Ref.: 23272	17306	Maltose	-	builds acid from
Ref.: 23272	17306	Maltose	-	carbon source
Ref.: 23272	6731	Melezitose	-	carbon source
Ref.: 23272	28053	Melibiose	-	carbon source
Ref.: 23272	36986	Mesaconate	-	growth
Ref.: 23272	30928	meso-Tartrate	-	carbon source
Ref.: 23272	320061	Methyl alpha-D-glu copyranoside	-	carbon source
Ref.: 23272	43943	Methyl alpha-D-mannoside	-	carbon source
Ref.: 23272	74863	Methyl beta-D-xylo pyranoside	-	carbon source
Ref.: 23272	506227	N-Acetylglucosamin e	-	carbon source
Ref.: 23272	17632	Nitrate	-	reduction
Ref.: 23272	16301	Nitrite	+	reduction
Ref.: 23272	29019	Nonanoic acid	-	carbon source
Ref.: 23272	16995	Oxalic acid	-	carbon source
Ref.: 23272	74848	Pentan-1-amine	-	carbon source
Ref.: 23272	30745	Phenylacetic acid	-	growth
Ref.: 23272	29069	Phthalic acid	-	carbon source
Ref.: 23272	30531	Pimelic acid	-	carbon source
Ref.: 23272	30768	Propionic acid	+	growth
Ref.: 23272	17148	Putrescine	-	carbon source
Ref.: 23272	32816	Pyruvic acid	+	carbon source
Ref.: 23272	16634	Raffinose	-	carbon source
Ref.: 23272	17814	Salicin	-	carbon source
Ref.: 23272	15611	Sarcosine	-	carbon source
Ref.: 23272	41865	Sebacic acid	-	carbon source
Ref.: 23272	30911	Sorbitol	-	carbon source
Ref.: 23272	15746	Spermine	-	carbon source
Ref.: 23272	28017	Starch	-	carbon source
Ref.: 23272	28017	Starch	-	hydrolysis
Ref.: 23272	9300	Suberic acid	-	carbon source
Ref.: 23272	15741	Succinic acid	+	carbon source
Ref.: 23272	17992	Sucrose	-	carbon source
Ref.: 23272	15702	Terephthalic acid	-	carbon source
Ref.: 23272	27082	Trehalose	-	carbon source

Ref.: 23272	18123	Trigonelline	-	growth
Ref.: 23272	16765	Tryptamine	-	carbon source
Ref.: 23272	32528	Turanose	-	carbon source
Ref.: 23272	53426	Tween 80	-	hydrolysis
Ref.: 23272	16199	Urea	-	carbon source
Ref.: 23272	17418	Valeric acid	+	growth
Ref.: 23272	17151	Xylitol	-	carbon source

Ref.: 23272 **Nutrition type** chemoorganotroph

Ref.: 23272 **Oxygen tolerance** aerobe

Ref.: 23272 **Ability of spore formation** no

Culture and growth conditions

Ref.: 3204 **Culture medium** BHI MEDIUM (DSMZ Medium 215), 37°C

Ref.: 3204 **Culture medium growth** yes

Ref.: 3204 **Culture medium link** https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium215.pdf

Ref.: 23272 **Culture medium** nutrient agar

Ref.: 23272 **Culture medium growth** yes

Ref.: 38118 **Culture medium** MEDIUM 3 - Columbia agar

Ref.: 38118 **Culture medium growth** yes

Ref.: 38118 **Culture medium composition** Columbia agar (39.000 g);distilled water (1000.000 ml)

Temperatures

	Kind of temperature	Temperature
Ref.: 3204	growth	37 °C
Ref.: 23272	growth	42 °C
Ref.: 23272	growth	30-37 °C
Ref.: 38118	growth	30 °C

Ref.: 3204 **Temperature range** mesophilic

Ref.: 23272 **Temperature range** mesophilic

Ref.: 38118 **Temperature range** mesophilic

Isolation, sampling and environmental information

Ref.: 3204 **Sample type/isolated from** human ear

Isolation sources categories

Cat1	Cat2	Cat3
#Host	#Human	-
#Host Body-Site	#Organ	#Ear

Application and interaction

Ref.: 3204 **Pathogenicity (human)** yes

Ref.: 3204 **Pathogenicity (animal)** yes

Ref.: 3204 **Biosafety level** 1 Risk group (German classification)

Molecular biology

Ref.: 3204 **GC-content** 47.5 mol%

Ref.: 3204 **GC-content** 47.7 mol%

Ref.: 23272 **GC-content** 46-47.5 mol% thermal denaturation, midpoint method (Tm)

	Sequence database	Sequence accession description	Sequence accession number	Sequence length(bp)	Associated NCBI tax ID	
Ref.: 20218	Marker Gene (GenBank Direct submission)	Oligella urethralis 16S ribosomal RNA gene, partial sequence	AF227163	1458	90245	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Oligella urethralis strain ATCC 17960 Cpn60 (cpn60) gene, partial cds	AY123665	555	90245	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Oligella urethralis strain CIP 103116 16S ribosomal RNA gene, partial sequence	AF133538	1486	90245	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Oligella urethralis strain DSM 7531 23S ribosomal RNA gene, partial sequence	AF124622	199	90245	*
Ref.: 20218	Marker Gene (EMBL Direct submission)	Oligella urethralis 16S rRNA gene, partial	AJ247262	457	90245	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_0.1_C, whole genome shotgun sequence	AQVB01000001	335121	1122620	*



Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_1.2_C, whole genome shotgun sequence	AQVB01000002	206573	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_2.3_C, whole genome shotgun sequence	AQVB01000003	167699	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_3.4_C, whole genome shotgun sequence	AQVB01000004	152622	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_4.5_C, whole genome shotgun sequence	AQVB01000005	150210	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_5.6_C, whole genome shotgun sequence	AQVB01000006	137917	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_6.7_C, whole genome shotgun sequence	AQVB01000007	116883	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_7.8_C, whole genome shotgun sequence	AQVB01000008	91286	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_8.9_C, whole genome shotgun sequence	AQVB01000009	90846	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_9.10_C, whole genome shotgun sequence	AQVB01000010	84536	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_10.11_C, whole genome shotgun sequence	AQVB01000011	76314	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_11.12_C, whole genome shotgun sequence	AQVB01000012	74507	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_12.13_C, whole genome shotgun sequence	AQVB01000013	69696	1122620	*



Oligella urethralis

Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_13.14_C, whole genome shotgun sequence	AQVB01000014	68848	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_14.15_C, whole genome shotgun sequence	AQVB01000015	63155	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_15.16_C, whole genome shotgun sequence	AQVB01000016	47118	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_16.17_C, whole genome shotgun sequence	AQVB01000017	44090	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_17.18_C, whole genome shotgun sequence	AQVB01000018	38158	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_18.19_C, whole genome shotgun sequence	AQVB01000019	37988	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_19.20_C, whole genome shotgun sequence	AQVB01000020	28136	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_20.21_C, whole genome shotgun sequence	AQVB01000021	19921	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_21.22_C, whole genome shotgun sequence	AQVB01000022	18925	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_22.23_C, whole genome shotgun sequence	AQVB01000023	18361	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_23.24_C, whole genome shotgun sequence	AQVB01000024	16990	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_24.25_C, whole genome shotgun sequence	AQVB01000025	15727	1122620	*



Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_25.26_C, whole genome shotgun sequence	AQVB01000026	15496	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_26.27_C, whole genome shotgun sequence	AQVB01000027	13515	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_27.28_C, whole genome shotgun sequence	AQVB01000028	13461	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_28.29_C, whole genome shotgun sequence	AQVB01000029	12717	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_29.30_C, whole genome shotgun sequence	AQVB01000030	11818	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_30.31_C, whole genome shotgun sequence	AQVB01000031	10819	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_31.32_C, whole genome shotgun sequence	AQVB01000032	10237	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_32.33_C, whole genome shotgun sequence	AQVB01000033	8030	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_33.34_C, whole genome shotgun sequence	AQVB01000034	7754	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_34.35_C, whole genome shotgun sequence	AQVB01000035	7353	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_35.36_C, whole genome shotgun sequence	AQVB01000036	6224	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_36.37_C, whole genome shotgun sequence	AQVB01000037	5270	1122620	*



Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_37.38_C, whole genome shotgun sequence	AQVB01000038	3328	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_38.39_C, whole genome shotgun sequence	AQVB01000039	2706	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_39.40_C, whole genome shotgun sequence	AQVB01000040	2366	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_40.41_C, whole genome shotgun sequence	AQVB01000041	2150	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_41.42_C, whole genome shotgun sequence	AQVB01000042	1579	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_42.43_C, whole genome shotgun sequence	AQVB01000043	1519	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_43.44_C, whole genome shotgun sequence	AQVB01000044	1241	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_44.45_C, whole genome shotgun sequence	AQVB01000045	1235	1122620	*
Ref.: 20218	Whole Genome Shotgun (WGS) Sequence INSDC	Oligella urethralis DSM 7531 A3GADRAFT_scaffold_45.46_C, whole genome shotgun sequence	AQVB01000046	1165	1122620	*
Ref.: 20218	Marker Gene (EMBL Direct submission)	Oligella urethralis 16S rRNA gene, strain LMG 1015	AJ251911	1489	90245	*
Ref.: 3204	INSDC (WGS)		AQVB00000000			

Strain availability

Ref.: 3204 **Culture collection no.** DSM 7531, ATCC 17960, CCUG 13463, LMG 5303

Ref.: 3204 **Strain history** <- ATCC <- CDC, 7603 <- Washington State Board of Health, MC213

Associated Passport(s) in StrainInfo

Ref.: 20218	160903 - http://www.straininfo.net/strains/160903
Ref.: 20218	15815 - http://www.straininfo.net/strains/15815
Ref.: 20218	15816 - http://www.straininfo.net/strains/15816
Ref.: 20218	15818 - http://www.straininfo.net/strains/15818

References

Ref.: 3204	Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; Curators of the DSMZ; DSM 7531
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.: 23272	R. Rossau, K. Kersters, E. Falsen, E. Jantzen, P. Segers, A. Union, L. Nehls, J. De Ley Oligella, a New Genus Including Oligella urethralis comb. nov. (Formerly Moraxella urethralis) and Oligella ureolytica sp. nov. (Formerly CDC Group IVe): Relationship to Taylorella equigenitalis and Related Taxa. IJSEM 37: 198-210 1987 (10.1099/00207713-37-3-198, None)
Ref.: 38118	None; Curators of the CIP; None

*** These References are textmined**

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