

Strain identifier

BacDive ID: 4358 **DOI:** 10.13145/bacdive4358.20191129.4.1
Type strain: yes **Designation:** CDC 819-56
Culture col. no.: NCDC 819-56, IFO 13534, DSM 30053, ATCC 13048, CCUG 1429, CECT 684, CIP 60.86, DSM 26516, JCM 1235, KCTC 2190, LMG 2094, NBRC 13534, NCTC 10006, WDCM 00175

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Name and taxonomic classification

| | | |
|----------------------------|-----------------------------|---|
| Ref.: 9102 | Domain | Bacteria |
| Ref.: 9102 | Phylum | Proteobacteria |
| Ref.: 9102 | Class | Gammaproteobacteria |
| Ref.: 9102 | Order | Enterobacteriales, not validated |
| Ref.: 9102 | Family | Enterobacteriaceae |
| Ref.: 9102 | Genus | Klebsiella |
| Ref.: 9102 | Species | Klebsiella aerogenes |
| Ref.: 9102 | Full Scientific Name | Enterobacter aerogenes Hormaeche and Edwards 1960 |
| Ref.: 9102 | Designation: | CDC 819-56 |
| Ref.: 9102 | Type strain: | yes |

Prokaryotic Nomenclature Up-to-date (PNU)

| | | |
|-----------------------------|----------------------|--|
| Ref.: 20215 | Domain | Bacteria |
| Ref.: 20215 | Phylum | Proteobacteria |
| Ref.: 20215 | Class | Gammaproteobacteria |
| Ref.: 20215 | Literature reference | Int. J. Syst. Evol. Microbiol. 55:2235 |
| Ref.: 20215 | Family | Enterobacteriaceae |
| Ref.: 20215 | Literature reference | Int. J. Syst. Bacteriol. 30:225 |
| Ref.: 20215 | Genus | Klebsiella |

| | | |
|-------------|-----------------------------|---|
| Ref.: 20215 | Taxonomical status | genus (AL) |
| Ref.: 20215 | Literature reference | Int. J. Syst. Bacteriol. 30:225 |
| Ref.: 20215 | Species | Klebsiella aerogenes |
| Ref.: 20215 | Taxonomical status | comb. nov. (VP) |
| Ref.: 20215 | Literature reference | Int. J. Syst. Evol. Microbiol. 67:502* |
| Ref.: 20215 | Full Scientific Name | Klebsiella aerogenes (Hormaeche and Edwards 1960) Tindall et al. 2017 |
| Ref.: 20215 | Synonym | Enterobacter aerogenes |
| Ref.: 20215 | Synonym | Klebsiella mobilis |

Morphology and physiology

Fatty acid profile

| | | |
|-----------------------------|-----------------------------|------------|
| Type of FA analysis | whole cell analysis | |
| Incubation medium | | |
| Agar/liquid | | |
| Incubation temperature (°C) | | |
| Incubation time (d) | | |
| Incubation pH | | |
| Incubation oxygen condition | | |
| Treatment/condition | | |
| Software version | | |
| Library/peak naming table | | |
| FA_system | | |
| FA_instrument | | |
| Method/protocol | CCUG | |
| Cutoff value | | |
| Reference | Ref.: 44375 | |
| Fatty acid | Percentage | ECL |
| 12:0 | 2.4 | 12.0 |
| 13:0 | 0.3 | 13.0 |
| 14:0 | 9.3 | 14.0 |
| 15:0 | 3.0 | 15.0 |
| 16:0 | 28.4 | 16.0 |
| 17:0 | 1.1 | 17.0 |
| 18:0 | 0.4 | 18.0 |
| 13:0 3OH/15:1 i l/H | 0.2 | 14.469 |
| 14:0 3OH/16:1 ISO I | 6.9 | 15.485 |



| | | |
|----------------------|------|--------|
| 16:1 ω7c | 13.7 | 15.819 |
| 16:1 ω9c | 0.1 | 15.774 |
| 17:0 CYCLO | 11.6 | 16.888 |
| 17:1 ω8c | 0.3 | 16.792 |
| 18:1 ω7c /12t/9t | 17.5 | 17.824 |
| 18:1 ω9c | 0.6 | 17.769 |
| 18:2 ω6,9c/18:0 ANTE | 0.5 | 17.724 |
| 19:0 CYCLO ω8c | 1.3 | 18.9 |
| Unidentified | 0.6 | 9.136 |
| Unidentified | 0.5 | 10.908 |
| Unidentified | 0.3 | 13.934 |
| Unidentified | 0.4 | 15.174 |
| unknown 14.503 | 0.8 | 14.503 |

Ref.: 9102

API 20E

| API ID | 7572 | 7447 | 6647 | 6483 | 6371 |
|-----------|------|------|------|------|------|
| ONPG | + | + | + | + | + |
| ADH (Arg) | - | - | + | - | - |
| LDC (Lys) | + | + | + | + | + |
| ODC | + | + | + | + | + |
| CIT | + | + | + | + | + |
| H2S | - | - | - | - | - |
| URE | - | - | - | - | - |
| TDA (Trp) | - | - | - | - | - |
| IND | - | - | - | - | - |
| VP | + | + | + | + | + |
| GEL | - | - | - | - | - |
| GLU | + | + | + | + | + |
| MAN | + | + | + | + | + |
| INO | + | + | + | + | + |
| Sor | + | + | + | + | + |
| RHA | + | + | + | + | + |
| SAC | + | + | + | + | + |
| MEL | + | + | + | + | + |
| AMY | + | + | + | + | + |
| ARA | + | + | + | + | + |
| OX | - | - | - | - | - |
| NO2 | n.d. | n.d. | n.d. | n.d. | n.d. |



| | | | | | |
|------|------|------|------|------|------|
| N2 | n.d. | n.d. | n.d. | n.d. | n.d. |
| MOB | n.d. | n.d. | n.d. | n.d. | n.d. |
| MAC | n.d. | n.d. | n.d. | n.d. | n.d. |
| OF-O | n.d. | n.d. | n.d. | n.d. | n.d. |
| OF-F | n.d. | n.d. | n.d. | n.d. | n.d. |

Antibiotic susceptibility testing

| | Test 1 | Test 2 | Test 3 |
|------------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Reference | Ref.: 9102 | Ref.: 9102 | Ref.: 9102 |
| Medium | Mueller-Hinton Agar | Mueller-Hinton Agar | Mueller-Hinton Agar |
| Incubation temperature [°C] | 30 | 30 | 30 |
| Incubation time [d] | 1 | | |
| Oxygen condition | aerob | aerob | aerob |
| Manual Annotation | yes | yes | yes |
| | Inhibition zone diameter in mm | Inhibition zone diameter in mm | Inhibition zone diameter in mm |
| Penicillin G | 0 | 0 | 0 |
| Oxacillin | 0 | 0 | 0 |
| Ampicillin | 0 | 0 | 0 |
| Ticarcillin | 28 | 26-28 | 28 |
| Mezlocillin | 20 | 22 | 20 |
| Cefalotin | 12 | 12-14 | 12 |
| Cefazolin | 20 | 20 | 20 |
| Cefotaxime | 34-36 | 36 | 34 |
| Aztreonam | 34-36 | 32-34 | 32-34 |
| Imipenem | 30 | 28-30 | 30 |
| Tetracycline | 26 | 26 | 26 |
| Chloramphenicol | 24 | 26-28 | 28 |
| Gentamycin | 20 | 24 | 22 |
| Amikacin | 22 | 24 | 22-24 |
| Vancomycin | 0 | 0 | 0 |
| Erythromycin | 8 | 10-12 | 10 |
| Lincomycin | 0 | 0 | 0 |
| Ofloxacin | 34 | 34 | 30-32 |
| Norfloxacin | 40 | 40 | 38 |
| Colistin | 12-14 | 14 | 14 |
| Pipemidic acid | 30 | 30 | 30 |



| | | | |
|---------------------------|-------|-------|-------|
| Nitrofurantoin | 16 | 14-16 | 16 |
| Bacitracin | 0 | 0 | 0 |
| Polymyxin B | 14-16 | 16 | 16 |
| Kanamycin | 20-22 | 24 | 22 |
| Neomycin | 18 | 20 | 18-20 |
| Doxycycline | 20 | 18-20 | 20 |
| Ceftriaxone | 32 | 32-34 | 32-34 |
| Clindamycin | 0 | 0 | 0 |
| Fosfomycin | 22 | 20 | 22 |
| Moxifloxacin | 32 | 32 | 30 |
| Linezolid | 0 | 0 | 0 |
| Nystatin | 0 | 0 | 0 |
| Quinupristin/Dalfopristin | 0 | 0 | 0 |
| Teicoplanin | 0 | 0 | 0 |
| Piperacillin/Tazobactam | 24 | 22-24 | 22 |

| | Test 4 | Test 5 |
|-----------------------------|--------------------------------|--------------------------------|
| Reference | Ref.: 9102 | Ref.: 9102 |
| Medium | Mueller-Hinton Agar | Mueller-Hinton Agar |
| Incubation temperature [°C] | | |
| Incubation time [d] | | |
| Oxygen condition | | |
| Manual Annotation | yes | yes |
| | Inhibition zone diameter in mm | Inhibition zone diameter in mm |
| Penicillin G | 0 | 0 |
| Oxacillin | 0 | 0 |
| Ampicillin | 0 | 0 |
| Ticarcillin | 30 | 32 |
| Mezlocillin | 22 | 22 |
| Cefalotin | 12 | 14-16 |
| Cefazolin | 20 | 20 |
| Cefotaxime | 38 | 38 |
| Aztreonam | 36 | 40 |
| Imipenem | 30 | 32 |
| Tetracycline | 26 | 26 |

| | | |
|---------------------------|-------|-------|
| Chloramphenicol | 24-26 | 28-30 |
| Gentamycin | 22 | 22 |
| Amikacin | 24 | 24 |
| Vancomycin | 0 | 0 |
| Erythromycin | 10 | 8-10 |
| Lincomycin | 0 | 0 |
| Ofloxacin | 34 | 32-34 |
| Norfloxacin | 34 | 34 |
| Colistin | 14 | 14-16 |
| Pipemidic acid | 30 | 30 |
| Nitrofurantoin | 14-16 | 14 |
| Bacitracin | 0 | 0 |
| Polymyxin B | 14 | 16 |
| Kanamycin | 24 | 34-36 |
| Neomycin | 20 | 20 |
| Doxycycline | 20 | 20 |
| Ceftriaxone | 34 | 34 |
| Clindamycin | 0 | 0 |
| Fosfomycin | 22 | 24-26 |
| Moxifloxacin | 30 | 30 |
| Linezolid | 0 | 0 |
| Nystatin | 0 | 0 |
| Quinupristin/Dalfopristin | 0 | 0 |
| Teicoplanin | 0 | 0 |
| Piperacillin/Tazobactam | 24 | 24 |

Culture and growth conditions

| | | |
|------------|------------------------------|---|
| Ref.: 9102 | Culture medium | COLUMBIA BLOOD MEDIUM (DSMZ Medium 693), 30°C |
| Ref.: 9102 | Culture medium growth | yes |
| Ref.: 9102 | Culture medium link | https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium693.pdf |
| Ref.: 9102 | Culture medium | NUTRIENT AGAR (DSMZ Medium 1), 30°C |
| Ref.: 9102 | Culture medium growth | yes |
| Ref.: 9102 | Culture medium link | https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium1.pdf |



Ref.: 42267 **Culture medium** MEDIUM 72- for trypto casein soja agar

Ref.: 42267 **Culture medium growth** yes

Ref.: 42267 **Culture medium composition** Distilled water make up to (1000.000 ml);Tryptocasein soy agar (40.000 g)

| Ref.: 9102 | Temperatures | Kind of temperature | Temperature |
|-------------|--------------|---------------------|-------------|
| | | growth | 30 °C |
| Ref.: 42267 | | growth | 30 °C |

Ref.: 9102 **Temperature range** mesophilic

Ref.: 42267 **Temperature range** mesophilic

Isolation, sampling and environmental information

Ref.: 9102 **Sample type/isolated from** sputum

Ref.: 44375 **Sample type/isolated from** Human sputum

| Isolation sources categories | Cat1 | Cat2 | Cat3 |
|------------------------------|--------------------|---------|---------|
| | #Host Body Product | #Fluids | #Sputum |

Application and interaction

Ref.: 9102 **Pathogenicity (human)** yes

Ref.: 9102 **Pathogenicity (animal)** yes

Ref.: 9102 **Biosafety level** 2 Risk group (German classification)

Molecular biology

| | Sequence database | Sequence accession description | Sequence accession number | Sequence length(bp) | Associated NCBI tax ID |
|------------|---|--|---------------------------|---------------------|------------------------|
| Ref.: 9102 | 16S rRNA gene, Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes gene for 16S ribosomal RNA, partial sequence | AB004750 | 1438 | 548 |
| Ref.: 9102 | 16S rRNA gene, Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes gene for 16S rRNA, partial sequence, strain: NBRC 13534 | AB680425 | 1465 | 548 |

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|-------------|--|---|----------|---------|---------|---|
| Ref.: 9102 | complete genome, GenBank Genome project data | Enterobacter aerogenes KCTC 2190, complete genome | CP002824 | 5280350 | 1028307 | |
| Ref.: 20218 | Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes genes for ORF, L-2,4-diaminobutyrate decarboxylase, partial and complete cds | AB032468 | 1800 | 548 | * |
| Ref.: 20218 | Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes gyrB gene for gyrase B, partial cds, strain:ATCC13048 | AB084010 | 1171 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes DNA gyrase A (gyrA) gene, partial cds | AF052255 | 589 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes osmoporin Omp36 (omp36) gene, complete cds | AF335467 | 1164 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes partial gyrB gene for DNA gyrase B subunit strain CIP 60.86T, ATCC 13048T | AJ300554 | 972 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes marA gene, marC gene (partial), marR gene and marB gene (partial) | AJ404624 | 1280 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes ramA gene and ORF | AJ404625 | 1050 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes soxR gene for redox-sensitive transcriptional activator SOXR | AJ419596 | 594 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Sequence 1671 from Patent WO0123604 | AX110938 | 772 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes DNA topoisomerase IV subunit C (parC) gene, partial cds | AY049061 | 564 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 internal transcribed spacer 1, complete sequence | AY116917 | 346 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 23S ribosomal RNA gene, partial sequence | AY116918 | 2458 | 548 | * |



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|-------------|---|---|----------|------|-----|---|
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 outer membrane porin protein (omp35) gene, complete cds | AY487903 | 1077 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 tmRNA gene, partial sequence | AY491435 | 318 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ICMP 15660 ATP synthase beta subunit (atpD) gene, partial cds | DQ859778 | 1264 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ICMP 15660 carbamoylphosphate synthetase small subunit (carA) gene, partial cds | DQ859844 | 966 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 thymidine phosphorylase (deoA) gene, complete cds | EU275208 | 1323 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 purine nucleoside phosphorylase (deoD) gene, complete cds | EU419851 | 720 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 uridine phosphorylase (udp) gene, complete cds | EU443096 | 735 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 histidine decarboxylase (hdc) gene, partial cds | FJ469567 | 709 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 16S ribosomal RNA gene, partial sequence | FJ971882 | 795 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 elongation factor tu (tuf) gene, partial cds | JX397942 | 515 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 23S ribosomal RNA gene, partial sequence | JX869176 | 720 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 DNA gyrase subunit B (gyrB) gene, partial cds | JX983652 | 994 | 548 | * |



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|-------------|---|--|----------|------|-----|---|
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 16S ribosomal RNA gene, partial sequence | KC429778 | 1376 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 23S ribosomal RNA gene, partial sequence | KC768828 | 672 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 23S ribosomal RNA gene, partial sequence | KC768836 | 611 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 16S ribosomal RNA gene, partial sequence | KF516237 | 1347 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 elongation factor EF-G (fusA) gene, partial cds | KF516286 | 633 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 gyrase B subunit (gyrB) gene, partial cds | KF516335 | 417 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 leucine tRNA synthetase (leuS) gene, partial cds | KF516384 | 642 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain ATCC 13048 RNA polymerase beta subunit (rpoB) gene, partial cds | KF516433 | 501 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | E.aerogenes tonB gene | X68477 | 1381 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | E.aerogenes (ATCC13048) tsx gene for outer membrane protein Tsx | Z26655 | 1833 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes ampR gene for transcriptional activator protein AmpR and partial ampC gene for beta-lactamase precursor | AJ487977 | 1316 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain CIP 60.86 elongation factor EF-G (fusA) gene, partial cds | EU010017 | 633 | 548 | * |



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|-------------|---|--|----------|------|---------|---|
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain CIP 60.86 leucine tRNA synthetase (leuS) gene, partial cds | EU010044 | 642 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain CIP 60.86 CTP synthetase (pyrG) gene, partial cds | EU010071 | 306 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain CIP 60.86 RNA polymerase beta subunit (rpoB) gene, partial cds | EU010098 | 501 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain DSM 30053 origin of replication oriC, complete sequence | DQ227466 | 290 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain DSM 30053 ThdF (thdF) gene, partial cds | EU569333 | 1320 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain DSM 30053 RecN (recN) gene, partial cds | EU569426 | 1633 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain DSM 30053 RpoA (rpoA) gene, partial cds | EU569536 | 926 | 548 | * |
| Ref.: 20218 | Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes gene for GroES protein homologue, GroEL protein homologue, partial cds | AB008141 | 1927 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | TPA: Enterobacter aerogenes KCTC 2190 transfer-messenger mRNA Enter_aerog_13048, single chain mature transcript | HG784760 | 363 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST1 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512359 | 864 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST2 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512360 | 335 | 1028307 | * |



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|-------------|----------------|--|----------|-----|---------|---|
| Ref.: 20218 | INSDC Sequence | CIFRI EST3 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512361 | 190 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST4 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512362 | 309 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST5 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512363 | 779 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST6 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512364 | 939 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST7 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512365 | 207 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST8 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512366 | 153 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST9 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512367 | 290 | 1028307 | * |



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|-------------|----------------|---|----------|------|---------|---|
| Ref.: 20218 | INSDC Sequence | CIFRI EST10 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512368 | 494 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST11 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512369 | 245 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST12 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512370 | 439 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST13 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512371 | 1159 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST14 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512372 | 118 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST15 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512373 | 254 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST16 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512374 | 160 | 1028307 | * |



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|-------------|---|---|----------|------|---------|---|
| Ref.: 20218 | INSDC Sequence | CIFRI EST17 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512375 | 281 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST18 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512376 | 294 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST19 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512377 | 223 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST20 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512378 | 467 | 1028307 | * |
| Ref.: 20218 | INSDC Sequence | CIFRI EST21 Enterobacter aerogenes KCTC 2190 salt tolerant library Enterobacter aerogenes KCTC 2190 cDNA similar to Bacterial Salt Tolerant Gene, mRNA sequence | JK512379 | 302 | 1028307 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain LMG 2094 RpoB (rpoB) gene, partial cds | DQ836222 | 1011 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain LMG 2094 ATP synthase beta subunit (atpD) gene, partial cds | JX424969 | 642 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain LMG 2094 DNA gyrase (gyrB) gene, partial cds | JX425098 | 742 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain LMG 2094 initiation translation factor 2 (infB) gene, partial cds | JX425228 | 615 | 548 | * |



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|-------------|---|---|----------|------|-----|---|
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes strain LMG 2094 RNA polymerase beta subunit (rpoB) gene, partial cds | JX425354 | 637 | 548 | * |
| Ref.: 20218 | Marker Gene (DDBJ Direct submission) | Enterobacter aerogenes groEL gene for GroEL, complete cds, strain: NBRC 13534 | AB375469 | 1647 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes 16S ribosomal RNA, partial 5' end, strain NCTC 10006 T | AJ001237 | 509 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes 16S ribosomal RNA, partial 3' end, NCTC 10006 T | AJ001238 | 509 | 548 | * |
| Ref.: 20218 | Marker Gene (EMBL Direct submission) | Enterobacter aerogenes partial 16S rRNA gene, strain NCTC10006T | AJ251468 | 1511 | 548 | * |
| Ref.: 20218 | Marker Gene (GenBank Direct submission) | Enterobacter aerogenes major cold-shock protein (cspA) gene, partial cds | U60034 | 139 | 548 | * |

Strain availability

Ref.: 9102 **Culture collection no.** NCDC 819-56, IFO 13534, DSM 30053, ATCC 13048, CCUG 1429, CECT 684, CIP 60.86, DSM 26516, JCM 1235, KCTC 2190, LMG 2094, NBRC 13534, NCTC 10006, WDCM 00175

Ref.: 9102 **Strain history** <- ATCC <- CDC, 819-56

Associated Passport(s) in StrainInfo

- Ref.: 20218 8979 - <http://www.straininfo.net/strains/8979>
- Ref.: 20218 8973 - <http://www.straininfo.net/strains/8973>
- Ref.: 20218 8975 - <http://www.straininfo.net/strains/8975>
- Ref.: 20218 289919 - <http://www.straininfo.net/strains/289919>
- Ref.: 20218 233844 - <http://www.straininfo.net/strains/233844>
- Ref.: 20218 8983 - <http://www.straininfo.net/strains/8983>
- Ref.: 20218 321557 - <http://www.straininfo.net/strains/321557>
- Ref.: 20218 8972 - <http://www.straininfo.net/strains/8972>
- Ref.: 20218 332558 - <http://www.straininfo.net/strains/332558>
- Ref.: 20218 8987 - <http://www.straininfo.net/strains/8987>
- Ref.: 20218 866247 - <http://www.straininfo.net/strains/866247>

References

- [Ref.: 9102](#) Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; Curators of the DSMZ; DSM 30053
- [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.: 42267](#) None; Curators of the CIP; None
- [Ref.: 44375](#) Culture Collection University of Gothenburg (CCUG); Curators of the CCUG; CCUG 1429

*** These References are textmined**

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