

## Genome sequences of *Bacteria* and *Archaea* published outside of *Standards in Genomic Sciences*, June – September 2011

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The purpose of this table is to provide the community with a citable record of publications of ongoing genome sequencing projects that have led to a publication in the scientific literature. While our goal is to make the list complete, there is no guarantee that we may have omitted one or more publications appearing in this time frame. Readers and authors who wish to have publications added to this subsequent versions of this list are invited to provide the bibliometric data for such references to the SIGS editorial office.

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### Phylum *Crenarchaeota*

#### Phylum *Euryarchaeota*

*Pyrococcus yayanosii* CH1, sequence accession CP002779 [1]

*Methanocella paludicola*, sequence accession AP011532 [2]

*Halorhabdus tiamatea*, sequence accession AFNT00000000 [3]

*Thermococcus* sp. Strain 4557, sequence accession CP002920 [4]

### Phylum *Chloroflexi*

#### Phylum *Proteobacteria*

*Ralstonia solanacearum* strain Po82, sequence accession CP002819 (chromosome) and CP002820 (megaplasmid) [5]

*Desulfovibrio alaskensis* G20, sequence accession CP000112 [6]

*Methylophaga aminisulfidivorans* MP<sup>T</sup>, sequence accession AFIG00000000 [7]

*Acinetobacter* sp. P8-3-8, sequence accession AFIE00000000 [8]

*Sphingomonas* strain KC8, sequence accession AFMP01000000 [9]

*Brucella pinnipedialis* B2/94, sequence accession CP002078 and CP002079 [10]

*Salmonella enterica* Serovar Typhimurium UK-1, sequence accession CP002614 (chromosome), CP002615 (plasmid) [11]

*Bordetella pertussis* CS, sequence accession CP002695 [12]

*Alteromonas* sp. Strain SN2, sequence accession CP002339 [13]

*Escherichia coli* O104:H4, sequence accession AFOB00000000 (LB226692) and AFPS00000000 (01-09591) [14]

*Acidithiobacillus caldus*, sequence accession CP002573 (Chromosome), CP002574 (pLAtcm), CP002575 (pLAtc1), CP002576 (pLAtc2), CP002577 (pLAtc3) [15]

- Cupriavidus necator* N-1, sequence accession CP002877 (chromosome 1), CP002878 (chromosome 2), CP002879 (pBB1), and CP002880 (pBB2) [16]
- Oligotropha carboxidovorans* OM4, sequence accession CP002821 (OM4 chromosome), CP002822 (pHCG3b), CP002823 (pOC167B) [17]
- Oligotropha carboxidovorans* OM5, sequence accession CP002826 (OM5 chromosome), CP002827 (pHCG3), and CP002828 (pOC167) [17]
- Pantoea ananatis* LMG20103, sequence accession CP001875 [18]
- Helicobacter bizzozeronii* strain CIII-1, sequence accession FR871757 (chromosome) and FR871758 (HBZ-1) [19]
- Vibrio anguillarum* 775, sequence accession CP002284 to CP002285 [20]
- Zymomonas mobilis* subsp. pomaceae, sequence accession CP002865 (chromosome), CP002866 (p29192\_1), CP002867 (p29192\_2) [21]
- Agrobacterium* sp. strain ATCC 31749, sequence accession AECL01000000 [22]
- Xanthomonas* spp. strain Xrc, sequence accesssion CP002789 [23]
- Xanthomonas* spp. strain Xoc, sequence accesssion AAQN00000000 [23]
- Glaciecola* sp. Strain 4H-3-7+YE-5, sequence accession CP002526 (chromosome) and CP002527 (plasmid) [24]
- Escherichia coli* Strain HM605, sequence accession CADZ01000001 through CADZ01000154 [25]
- Salinisphaera shabanensis*, sequence accession AFNV00000000 [26]
- Methyloversatilis universalis* FAM5<sup>T</sup>, sequence accession AFHG00000000 [27]
- Alicyclophilus denitrificans* Strain BC, sequence accession CP002449 (chromosome), CP002450 (megaplasmid), CP002451 (plasmid) [28].
- Alicyclophilus denitrificans* K601<sup>T</sup>, sequence accession CP002657 (chromosome) and CP002658 (plasmid) [28]
- Oligotropha carboxidovorans* Strain OM4, sequence accession CP002821 (chromosome), CP002822 (pHCG3b), CP002823 (pOC167B) [29]
- Oligotropha carboxidovorans* Strain OM5, sequence accession CP002826 (chromosome), CP002827 (pHCG3), and CP002828 (pOC167) [29]
- Bradyrhizobiaceae* strain SG-6C, sequence accession AFOF01000000 [30]
- Hyphomicrobium* sp. Strain MC1, sequence accession FQ859181 [31]
- Shewanella* sp. Strain HN-41, sequence accession AFOZ01000000 [32]
- Myxococcus fulvus* HW-1, sequence accession CP002830 [33]
- Nitrosomonas* sp. Strain AL212, sequence accession NC\_015222 (chromosome), NC\_015223 (pNAL21201), NC\_015221 (pNAL21202) [34]
- Ruegeria* sp. Strain KLH11, sequence accession ACCW00000000 [35]
- Acidovorax avenae* subsp. *avenae* RS-1, sequence accession AFPT01000000 [36]
- Escherichia coli* (ExPEC), sequence accession AFAT00000000 [37]

- Vibrio mimicus* SX-4, sequence accession ADOO01000000 [38]  
*Agrobacterium tumefaciens* Strain F2, sequence accession AFSD00000000 [39]  
*Pasteurella multocida* subsp. gallicida AFRR01000001 to AFRR01000489 [40]  
*Pseudomonas aeruginosa* 138244, sequence accession AEVV00000000 [41]  
*Pseudomonas aeruginosa* 152504, sequence accession AEVW00000000 [41]  
*Campylobacter jejuni* strain 305, sequence accession ADHL00000000 [42]  
*Campylobacter jejuni* strain DFVF1099, sequence accession ADHK00000000 [42]  
*Xanthomonas campestris* pv. *raphani* strain 756C, sequence accession CP002789 [43]  
*Xanthomonas campestris* pv. *raphani* strain BLS256, sequence accession AAQN01000001 [43]  
*Rickettsia heilongjiangensis*, sequence accession CP002912 [44]  
*Acidiphilium* sp. Strain PM (DSM 24941), sequence accession AFPR00000000 [45]  
*Pseudomonas putida* Strain S16, sequence accession CP002870 [46]  
*Acinetobacter lwoffii*, sequence accession AFQY01000000 [47]

#### **Phylum Firmicutes**

- Caldalkalibacillus thermarum* strain TA2.A1, sequence accession AFCE00000000 [48]  
*Listeria monocytogenes* Scott A, sequence accession AFGI00000000 [49]  
*Lactococcus garvieae* 8831, sequence accession AFCD00000000 [50]  
*Natranaerobius thermophilus* JW/NM-WN-LF, sequence accession CP001034 (chromosome), CP001035 (plasmid) [51]  
*Melissococcus plutonius* ATCC 35311, sequence accession AP012200 (chromosome) and AP012201 (plasmid) [52]  
*Lactobacillus buchneri* NRRL B-30929, sequence accession CP002652 (chromosome), CP002653 (plasmid pLBU01), CP002654 (plasmid pLBU02), and CP002655 (plasmid pLBU03) [53]  
*Lactobacillus kefiranofaciens* ZW3, sequence accession CP002764 (chromosome), CP002765 (plasmid), and CP002766 (plasmid) [54]  
*Bacillus megaterium* strain QM B1551, sequence accession CP001983 (chromosome), CP001984 to CP001990 (plasmids pBM100 through pBM700) [55]  
*Bacillus megaterium* strain DSM319, sequence accession CP001982 (chromosome) [55]  
*Listeria monocytogenes* serovar 4a strain M7, sequence accession CP002816 [56]  
*Bacillus coagulans* 2-6, sequence accession CP002472 [57]  
*Streptococcus salivarius* strain CCHSS3, sequence accession FR873481 [58]  
*Paenibacillus elgii* B69, sequence accession AFHW01000000 [59]  
*Lactobacillus pentosus* MP-10, sequence accession FR871759 through FR871848 [60]

- Leuconostoc pseudomesenteroides* KCTC 3652, sequence accession AEOQ00000001 through AEOQ00001160 [61]
- Lactobacillus mali* KCTC 3596, sequence accession BACP01000001 through BACP01000122 [62]
- Paenibacillus polymyxa* Type Strain ATCC 842<sup>T</sup>, sequence accession AFOX01000000 [63]
- Streptococcus salivarius* strain JIM8777, sequence accession FR873482 [64]
- Lactobacillus cypricasei* KCTC 13900, sequence accession BACS01000001 to BACS01000487 [65]
- Lactobacillus zeae* KCTC 3804, sequence accession BACQ01000001 to BACQ101000113 [66]
- Listeria monocytogenes* Serovar 4a Strain M7, sequence accession CP002816 [67]
- Lactobacillus salivarius* GJ-24, sequence accession AFOI00000000 [68]
- Lactobacillus johnsonii* PF01, sequence accession AFQJ01000000 [69]
- Clostridium acetobutylicum* DSM 1731, sequence accession CP002660 through CP002662 [70]
- Lactobacillus suebicus* KCTC 3549, sequence accession BAC001000000 [71]
- Brevibacillus laterosporus* LMG 15441, sequence accession AFRV00000000 [72]
- Lactobacillus salivarius* NIAS840, sequence accession AFMN00000000 [73]
- Bifidobacterium animalis* subsp. lactis CNCM I-2494, sequence accession CP002915 [74]
- Megasphaera elsdenii*, sequence accession HE576794 [75]
- Lactobacillus versmoldensis* KCTC 3814, sequence accession BACR01000001 to BACR01000102 [76]
- Lactobacillus pentosus* IG1, sequence accession FR874848 to FR874860 [77]
- Alicyclobacillus acidocaldarius* Strain Tc-4-1, sequence accession CP002902 [78]
- Streptococcus thermophilus* Strain JIM8232, sequence accession FR875178 [79]
- Streptococcus equi* subsp. zooepidemicus Strain ATCC 35246, sequence accession CP002904 [80]
- Bacillus amyloliquefaciens* XH7, sequence accession CP002927 [81]
- Leuconostoc kimchii* Strain C2, sequence accession CP002898 [82]
- Lactobacillus malefermentans* KCTC 3548, sequence accession BACN01000001 to BACN01000172 [83]
- Weissella koreensis* KACC 15510, sequence accession CP002900 [84]

### **Phylum Tenericutes**

- Mycoplasma bovis* Strain Hubei-1, sequence accession CP002513 [85]
- Mycoplasma fermentans* Strain M64, sequence accession NC\_014921 [86]

*Haloplasma contractile*, sequence accession AFNU00000000 [87]

*Mycoplasma ovipneumoniae* Strain SC01, sequence accession AFH001000000 [88]

### **Phylum Actinobacteria**

*Kocuria rhizophila* P7-4, sequence accession AFID00000000 [89]

*Streptomyces* S4, sequence accession CADY01000000 [90]

*Corynebacterium nuruki* S6-4<sup>T</sup>, sequence accession AFIZ00000000 [91]

*Propionibacterium humerusii*, sequence accession AFAM00000000.1 [92]

Strain JDM601, sequence accession CP002329 [93]

*Streptomyces* sp. strain Tü6071, sequence accession AFHJ01000000 [94]

*Bifidobacterium breve* UCC2003, sequence accession CP000303 [95]

*Propionibacterium acnes*, sequence accession CP002815 [96]

*Amycolicococcus subflavus* DQS3-9A1<sup>T</sup>, sequence accession CP002786 (chromosome), CP002787 (plasmid pAS9A-1), and CP002788 (plasmid pAS9A-2). [97]

*Gordonia neofelifaecis* NRRL B-59395, sequence accession AEUD01000000 [98]

*Pseudonocardia dioxanivorans* strain CB1190, sequence accession NC\_015312-4 and CP002595-7 [99]

*Bifidobacterium longum* subsp. *longum* KACC 91563, sequence accession CP002794 to CP002796 [100]

*Streptomyces cattleya* NRRL 8057, sequence accession FQ859185 (chromosome) and FQ859184 (megaplasmid) [101]

*Rhodococcus* sp. Strain R04, sequence accession AFAQ01000000 [102]

*Mycobacterium bovis* BCG Moreau, sequence accession [103]

*Saccharopolyspora spinosa* NRRL 18395, sequence accession [104]

*Mycobacterium tuberculosis* CCDC5079, sequence accession [105]

*Mycobacterium tuberculosis* CCDC5180, sequence accession [105]

*Amycolatopsis mediterranei* S699, sequence accession CP002896 [106]

*Nesterenkonia* sp. Strain F, sequence accession AFRW01000000 [107]

*Streptomyces xinghaiensis* NRRL B24674<sup>T</sup>, sequence accession AFRP01000000 [108]

### **Phylum Chlamydiae**

*Chlamydophila abortus* variant strain LLG, sequence accession AFHM01000000 [109]

*Chlamydia psittaci* 6BC, sequence accession CP002586 (chromosome), CP002587 (plasmid) [110]

*Chlamydia psittaci* Cal10, sequence accession AEZD00000000 (draft chromosome and plasmid) [110]

*Chlamydia trachomatis*, sequence accession CP002024 [111]

### **Phylum Spirochaetes**

*Spirochaeta thermophila* DSM 6192, sequence accession CP001698 [112]

*Brachyspira intermedia*, sequence accession CP002874 (chromosome) and CP002875 (plasmid) [113]

### **Phylum *Fibrobacteres***

### **Phylum *Bacteroidetes***

*Porphyromonas gingivalis* TDC60, sequence accession AP012203 [114]

*Krokinobacter* sp. strain 4H-3-7-5, sequence accession CP002528 [115]

*Lacinutrix* sp. strain 5H-3-7-4, sequence accession CP002825 [115]

*Bacterium* HQM9, sequence accession AFPB00000000 [116]

*Anaerophaga* sp. Strain HS1, sequence accession AFSL00000000 [117]

*Capnocytophaga canimorsus* Strain 5, sequence accession CP002113 [118]

*Mesoflavibacter zeaxanthinifaciens* strain S86, sequence accession AFOE00000000 [119]

### **Phylum *Verrucomicrobia***

### **Phylum *Lentisphaerae***

### **Phylum *Thermotogae***

*Kosmotoga olearia* Strain TBF 19.5.1, sequence accession CP001634 [120]

### **Domain *Archaea***

"*Candidatus Nitrosoarchaeum koreensis*" MY1, sequence accession AFPU00000000 [121]

### **Non-Bacterial genomes**

*Cucumis sativus* L., North-European Cucumber, sequence accession FI132140–FI136208, GS765762–GS766880, GS815969–GS874855 [122]

*Ricinus communis* Castor bean organelle genome, sequence accession JF937588(chloroplast), HQ874649 (mitochondria) [123]

Stretch Lagoon Orbivirus *Umatilla*, sequence accession HQ842619 through HQ842628 [124]

*Gadus morhua* Atlantic cod, sequence accession CAEA01000001 through CAEA01554869 [125]

*Solanum tuberosum* L. Potato, sequence accession GS025503 through GS026177 [126]

ΦCA82, sequence accession HQ264138 [127]

*Paramecium caudatum* reveals mitochondria, sequence accession NC001324 [128]

bacteriophage IME08, sequence accession NC\_014260 [129]

virus (ILTV), sequence accession HQ\_630064 [130]

*Macropus eugenii* Australian kangaroo, sequence accession ABQ000000000 [131]

Aichi virus, sequence accession FJ890523 [132]

"*Candidatus Tremblaya princeps*" Strain PCVAL, sequence accession CP002918 [133]



## References

1. Jun X, Lupeng L, Minjuan X, Oger P, Fengping W, Jebbar M, Xiang X. Complete Genome Sequence of the Obligate Piezophilic Hyperthermophilic Archaeon *Pyrococcus yanosii* CH1. *J Bacteriol* 2011; **193**:4297-4298. [PubMed doi:10.1128/JB.05345-11](#)
2. Sakai S, Takaki Y, Shimamura S, Sekine M, Tajima T, Kosugi H, Ichikawa N, Tasumi E, Hiraki A, Shimizu A, et al. Genome Sequence of a Mesophilic Hydrogenotrophic Methanogen *Methanocella paludicola*, the First Cultivated Representative of the Order *Methanocellales*. [date unknown]. *PLoS ONE* 2011; **6**:e22898. [PubMed doi:10.1371/journal.pone.0022898](#)
3. Antunes A, Alam I, Bajic VB, Stingl U. Genome Sequence of Halorhabdus tiamatea, the First Archaeon Isolated from a Deep-Sea Anoxic Brine Lake. *J Bacteriol* 2011; **193**:4553-4554. [PubMed doi:10.1128/JB.05462-11](#)
4. Wang X, Gao Z, Xu X, Ruan L. Complete Genome Sequence of *Thermococcus* sp. Strain 4557, a Hyperthermophilic Archaeon Isolated from a Deep-Sea Hydrothermal Vent Area. *J Bacteriol* 2011; **193**:5544-5545. [PubMed doi:10.1128/JB.05851-11](#)
5. Xu J, Zheng HJ, Liu L, Pan ZC, Prior P, Tang B, Xu JS, Zhang H, Tian Q, Zhang LQ, et al. The complete genome sequence of plant pathogen *Ralstonia solanacearum* strain Po82. *J Bacteriol* 2011; **193**:4261-4262. [PubMed doi:10.1128/JB.05384-11](#)
6. Hauser LJ, Land ML, Brown SD, Larimer F, Keller KL, Rapp-Giles BJ, Price MN, Lin M, Bruce DC, Detter JC, et al. The Complete Genome Sequence and Updated Annotation of *Desulfovibrio alaskensis* G20. *J Bacteriol* 2011; **193**:193. [PubMed doi:10.1128/JB.05400-11](#)
7. Han GH, Kim W, Chun J, Kim SW. Draft genome sequence of *Methylophaga aminisulfidivorans* MPT. *J Bacteriol* 2011;
8. Kim YO, Kim WJ, Choi SH, Kim DS, Kim DW, Lee JS, Kong HJ, Nam BH, Kim BS, Lee SJ, et al. Genome Sequence of *Acinetobacter* sp. P8-3-8, isolated from *Fistularia commersonii* in Vietnam. *J Bacteriol* 2011;
9. Hu A, He J, Chu KH, Yu CP. Genome Sequence of a 17-Estradiol-Utilizing Bacterium *Sphingomonas* strain KC8. *J Bacteriol* 2011;
10. Audic S, Lescot M, Claverie JM, Cloeckaert A, Zygmunt M. The genome sequence of *Brucella pinnipedialis* B2/94 sheds light on the evolutionary history of the genus *Brucella*. *BMC Evol Biol* 2011; **11**:200. [PubMed doi:10.1186/1471-2148-11-200](#)
11. Luo Y, Kong Q, Yang J, Golden G, Wanda SY, Jensen RV, Ernst PB, Curtiss R. Complete Genome Sequence of the Universal Killer *Salmonella enterica* Serovar *Typhimurium* UK-1 (ATCC 68169). *J Bacteriol* 2011; **193**:4035-4036. [PubMed doi:10.1128/JB.05224-11](#)
12. Zhang S, Xu Y, Zhou Z, Wang S, Yang R, Wang J, Wang L. Complete Genome Sequence of *Bordetella pertussis* CS, a Chinese Pertussis Vaccine Strain. *J Bacteriol* 2011; **193**:4017-4018. [PubMed doi:10.1128/JB.05184-11](#)
13. Jin HM, Jeong H, Moon EJ, Math RK, Lee K, Kim HJ, Jeon CO, Oh TK, Kim JF. Complete Genome Sequence of the Polycyclic Aromatic Hydrocarbon-Degrading Bacterium *Alteromonas* sp. Strain SN2. *J Bacteriol* 2011; **193**:4292-4293. [PubMed doi:10.1128/JB.05252-11](#)
14. Mellmann A, Harmsen D, Cummings C, Zentz E, Leopold S, Rico A, Prior K, Szczepanowski R, Ji Y, Zhang W, et al. Prospective Genomic Characterization of the German Enterohemorrhagic *Escherichia coli* O104:H4 Outbreak by Rapid Next Generation Sequencing Technology. *PLoS ONE* 2011; **6**:e22751. [PubMed doi:10.1371/journal.pone.0022751](#)
15. You XY, Guo X, Zheng HJ, Zhang MJ, Liu LJ, Zhu YQ, Zhu B, Wang SY, Zhao GP, Poetsch A, et al. Unraveling the *Acidithiobacillus caldus* complete genome and its central metabolisms for carbon assimilation. *J Genet Genomics* 2011; **38**:243-252. [PubMed doi:10.1016/j.jgg.2011.04.006](#)
16. Poehlein A, Kusian B, Friedrich B, Daniel R, Bowen B. Complete genome sequence of the type strain *Cupriavidus necator* N-1. *J Bacteriol* 2011;
17. Volland S, Rachinger M, Strittmatter A, Daniel R, Gottschalk G, Meyer O. Complete genome sequences of the chemolithoautotrophic strains *Oligotropha carboxidovorans* OM4 and OM5. *J Bacteriol* 2011;
18. De Maayer P, Chan WY, Venter SN, Toth IK, Birch PRJ, Joubert F, Coutinho TA. Genome Sequence of *Pantoea ananatis* LMG20103, the Causative Agent of Eucalyptus Blight and Dieback. *J Bacteriol* 2010; **192**:2936-2937. [PubMed doi:10.1128/JB.00060-10](#)
19. Schott T, Rossi M, Hanninen ML. Genome sequence of *Helicobacter bizzozeronii* strain CIII-1,

- an isolate from human gastric mucosa . *J Bacteriol* 2011;
20. Naka H, Dias GM, Thompson CC, Dubay C, Thompson FL, Crosa JH. Complete Genome Sequence of the Marine Fish Pathogen *Vibrio anguillarum* Harboring the pJM1 Virulence Plasmid and Genomic Comparison with Other Virulent Strains of *V. anguillarum* and *V. ordalii*. *Infect Immun* 2011; **79**:2889-2900. [PubMed doi:10.1128/IAI.05138-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/IAI.05138-11)
  21. Kouvelis VN, Davenport KW, Brettin TS, Bruce D, Detter C, Han C, Nolan M, Tapia R, Damoulaki A, Kyrpides NC, et al. Genome sequence of the ethanol-producing *Zymomonas mobilis* subsp. pomaceae lectotype ATCC 29192 . *J Bacteriol* 2011;
  22. Ruffing AM, Castro-Melchor M, Hu WS, Chen RR. Genome Sequence of the Curdlan-Producing *Agrobacterium* sp. Strain ATCC 31749. *J Bacteriol* 2011; **193**:4294-4295. [PubMed doi:10.1128/JB.05302-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05302-11)
  23. Bogdanove AJ, Koebnik R, Lu H, Furutani A, Angiuoli SV, Patil PB, Van Sluys MA, Ryan RP, Meyer DF, Han SW, et al. Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas* spp. . *J Bacteriol* 2011;
  24. Klippel B, Lochner A, Bruce DC, Walston Davenport K, Detter C, Goodwin LA, Han J, Han S, Land ML, Mikhailova N, et al. Complete Genome Sequence of the Marine Cellulose- and Xylan-Degrading Bacterium *Glaciicola* sp. Strain 4H-3-7+YE-5. *J Bacteriol* 2011; **193**:4547-4548. [PubMed doi:10.1128/JB.05468-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05468-11)
  25. Clarke DJ, Chaudhuri RR, Martin HM, Campbell BJ, Rhodes JM, Constantinidou C, Pallen MJ, Loman NJ, Cunningham AF, Browning DF, et al. Complete Genome Sequence of the Crohn's Disease-Associated Adherent-Invasive *Escherichia coli* Strain HM605. *J Bacteriol* 2011; **193**:4540. [PubMed doi:10.1128/JB.05374-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05374-11)
  26. Antunes A, Alam I, Bajic VB, Stingl U. Genome Sequence of *Salinisphaera shabanensis*, a Gammaproteobacterium from the Harsh, Variable Environment of the Brine-Seawater Interface of the Shaban Deep in the Red Sea. *J Bacteriol* 2011; **193**:4555-4556. [PubMed doi:10.1128/JB.05459-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05459-11)
  27. Kittichotirat W, Good NM, Hall R, Bringel F, Lajus A, Medigue C, Smalley NE, Beck D, Bumgarner R, Vuilleumier S, et al. Genome Sequence of *Methyloversatilis universalis* FAM5T, a Methy-
  - lotrophic Representative of the Order *Rhodocyclales*. *J Bacteriol* 2011; **193**:4541-4542. [PubMed doi:10.1128/JB.05331-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05331-11)
  28. Oosterkamp MJ, Veuskens T, Plugge CM, Langenhoff AAM, Gerritse J, van Berkel WJH, Pieper DH, Junca H, Goodwin LA, Daligault HE, et al. Genome Sequences of *Alicyclophilus denitrificans* Strains BC and K601<sup>T</sup>. *J Bacteriol* 2011; **193**:5028-5029. [PubMed doi:10.1128/JB.00365-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.00365-11)
  29. Volland S, Rachinger M, Strittmatter A, Daniel R, Gottschalk G, Meyer O. Complete Genome Sequences of the Chemolithoautotrophic *Oligotropha carboxidovorans* Strains OM4 and OM5. *J Bacteriol* 2011; **193**:5043. [PubMed doi:10.1128/JB.05619-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05619-11)
  30. Pearce SL, Pandey R, Dorrian SJ, Russell RJ, Oakeshott JG, Pandey G. Genome Sequence of the Newly Isolated Chemolithoautotrophic *Bradyrhizobiaceae* Strain SG-6C. *J Bacteriol* 2011; **193**:5057. [PubMed doi:10.1128/JB.05647-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05647-11)
  31. Vuilleumier S, Nadalig T, Farhan Ul Haque M, Magdelenat G, Lajus A, Roselli S, Muller EEL, Gruffaz C, Barbe V, Medigue C, et al. Complete Genome Sequence of the Chloromethane-Degrading *Hyphomicrobium* sp. Strain MC1. *J Bacteriol* 2011; **193**:5035-5036. [PubMed doi:10.1128/JB.05627-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05627-11)
  32. Kim DH, Jiang S, Lee JH, Cho YJ, Chun J, Choi SH, Park HS, Hur HG. Draft Genome Sequence of *Shewanella* sp. Strain HN-41, Which Produces Arsenic-Sulfide Nanotubes. *J Bacteriol* 2011; **193**:5039-5040. [PubMed doi:10.1128/JB.05578-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05578-11)
  33. Li ZF, Li X, Liu H, Liu X, Han K, Wu ZH, Hu W. Li F-fei, Li Y-Z: Genome Sequence of the Halotolerant Marine Bacterium *Myxococcus fulvus* HW-1. *J Bacteriol* 2011; **193**:5015-5016. [PubMed doi:10.1128/JB.05516-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05516-11)
  34. Yuichi S, Norton JM, Bollmann A, Klotz MG, Stein LY, Laanbroek HJ, Arp DJ, Goodwin LA, Chertkov O, Held B, et al. Genome Sequence of *Nitrosomonas* sp. Strain AL212, an Ammonia-Oxidizing Bacterium Sensitive to High Levels of Ammonia. *J Bacteriol* 2011; **193**:5047-5048. [PubMed doi:10.1128/JB.05521-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05521-11)
  35. Zan J, Fricke WF, Fuqua C, Ravel J, Hill RT. Genome Sequence of *Ruegeria* sp. Strain KLH11, an N-Acylhomoserine Lactone-Producing Bacterium Isolated from the Marine Sponge *Mycale laxissima*. *J Bacteriol* 2011; **193**:5011-5012. [PubMed doi:10.1128/JB.05556-11](https://pubmed.ncbi.nlm.nih.gov/doi/10.1128/JB.05556-11)



36. Xie GL, Zhang GQ, Liu H, Lou MM, Tian WX, Li B, Zhou XP, Zhu B, Jin GL. Genome Sequence of the Rice-Pathogenic Bacterium *Acidovorax avenae* subsp. *avenae* RS-1. *J Bacteriol* 2011; **193**:5013-5014. [PubMed doi:10.1128/JB.05594-11](#)
37. Tan C, Xu Z, Zheng H, Liu W, Tang X, Shou J, Wu B, Wang S, Zhao GP, Chen H. Genome Sequence of a Porcine Extraintestinal Pathogenic *Escherichia coli* Strain. *J Bacteriol* 2011; **193**:5038. [PubMed doi:10.1128/JB.05551-11](#)
38. Wang D, Wang H, Zhou Y, Zhang Q, Zhang F, Du P, Wang S, Chen C, Kan B. Genome Sequencing Reveals Unique Mutations in Characteristic Metabolic Pathways and the Transfer of Virulence Genes between *V. mimicus* and *V. cholerae*. *PLoS ONE* 2011; **6**:e21299. [PubMed doi:10.1371/journal.pone.0021299](#)
39. Li A, Geng J, Cui D, Shu C, Zhang S, Yang J, Xing J, Wang J, Ma F, Hu S. Genome Sequence of *Agrobacterium tumefaciens* Strain F2, a Biofloculant-Producing Bacterium. *J Bacteriol* 2011; **193**:5531. [PubMed doi:10.1128/JB.05690-11](#)
40. Ahir VB, Roy A, Jhala MK, Bhandari BB, Mathakiya RA, Bhatt VD, Padiya KB, Jakhesara SJ, Koringa PG, Joshi CG. Genome Sequence of *Pasteurella multocida* subsp. *gallicida* Anand1\_poultry. *J Bacteriol* 2011; **193**:5604. [PubMed doi:10.1128/JB.05706-11](#)
41. Soares-Castro P, Marques D, Demyanchuk S, Faustino A, Santos PM. Draft Genome Sequences of Two *Pseudomonas aeruginosa* Clinical Isolates with Different Antibiotic Susceptibilities. *J Bacteriol* 2011; **193**:5573. [PubMed doi:10.1128/JB.05446-11](#)
42. Takamiya M, Ozen A, Rasmussen M, Alter T, Gilbert T, Ussery DW, Knochel S. Genome Sequences of Two Stress-Tolerant *Campylobacter jejuni* Poultry Strains, 305 and DFVF1099. *J Bacteriol* 2011; **193**:5546-5547. [PubMed doi:10.1128/JB.05753-11](#)
43. Bogdanove AJ, Koebnik R, Lu H, Furutani A, Angiuoli SV, Patil PB, Van Sluys MA, Ryan RP, Meyer DF, Han SW, et al. Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic *Xanthomonas* spp. *J Bacteriol* 2011; **193**:5450-5464. [PubMed doi:10.1128/JB.05262-11](#)
44. Duan C, Tong Y, Huang Y, Wang X, Xiong X, Wen B. Complete Genome Sequence of *Rickettsia heilongjiangensis*, an Emerging Tick-Transmitted Human Pathogen. *J Bacteriol* 2011; **193**:5564-5565. [PubMed doi:10.1128/JB.05852-11](#)
45. San Martin-Uriz P, Gomez MJ, Arcas A, Bargiela R, Amils R. Draft Genome Sequence of the Electrogenic *Acidiphilium* sp. Strain PM (DSM 24941). *J Bacteriol* 2011; **193**:5585-5586. [PubMed doi:10.1128/JB.05386-11](#)
46. Yu H, Tang H, Wang L, Yao Y, Wu G, Xu P. Complete Genome Sequence of the Nicotine-Degrading *Pseudomonas putida* Strain S16. *J Bacteriol* 2011; **193**:5541-5542. [PubMed doi:10.1128/JB.05663-11](#)
47. Hu Y, Zhang W, Liang H, Liu L, Peng G, Pan Y, Yang X, Zheng B, Gao GF, Zhu B, et al. Whole-Genome Sequence of a Multidrug-Resistant Clinical Isolate of *Acinetobacter lwoffii*. *J Bacteriol* 2011; **193**:5549-5550. [PubMed doi:10.1128/JB.05617-11](#)
48. Kalamorz F, Keis S, McMillan DGG, Olsson K, Stanton J-A, Stockwell P, Black MA, Klingeman DM, Land ML, Han CS, et al.: Draft Genome Sequence of Thermoalkaliphilic *Caldalkalibacillus thermarum* strain TA2.A1. *J. Bacteriol.* 2011,
49. Briers Y, Klumpp J, Schuppler M, Loessner MJ. Genome sequence of *Listeria monocytogenes* Scott A, a clinical isolate from a foodborne listeriosis outbreak. *J Bacteriol* 2011;
50. Aguado-Urda M, Lopez-Campos GH, Gibello A, Cutuli MT, Lopez-Alonso V, Fernandez-Garayzabal JF, Blanco MM. Genome sequence of *Lactococcus garvieae* 8831, isolated from rainbow trout lactococcosis outbreaks in Spain. *J Bacteriol* 2011;
51. Zhao B, Mesbah NM, Dalin E, Goodwin L, Nolan M, Pitluck S, Chertkov O, Brettin TS, Han J, Larimer FW, et al. Complete Genome Sequence of the Anaerobic, Halophilic Alkalithermophile *Natronaerobius thermophilus* JW/NM-WN-LF. *J Bacteriol* 2011; **193**:4023-4024. [PubMed doi:10.1128/JB.05157-11](#)
52. Okumura K, Arai R, Okura M, Kirikae T, Takamatsu D, Osaki M, Miyoshi-Akiyama T. Complete Genome Sequence of *Melissococcus plutonius* ATCC 35311. *J Bacteriol* 2011; **193**:4029-4030. [PubMed doi:10.1128/JB.05151-11](#)
53. Liu S, Leathers TD, Copeland A, Chertkov O, Goodwin L, Mills DA. Complete Genome Sequence of *Lactobacillus buchneri* NRRL B-30929, a Novel Strain from a Commercial Ethanol Plant. *J Bacteriol* 2011; **193**:4019-4020. [PubMed doi:10.1128/JB.05180-11](#)

54. Wang Y, Wang J, Ahmed Z, Bai X, Wang J. Complete Genome Sequence of *Lactobacillus kefirano-faciens* ZW3. *J Bacteriol* 2011; **193**:4280-4281. [PubMed doi:10.1128/JB.05306-11](#)
55. Eppinger M, Bunk B, Johns MA, Edirisinghe JN, Kutumbaka KK, Koenig SSK, Huot Creasy H, Rosovitz MJ, Riley DR, Daugherty S, et al. Genome Sequences of the Biotechnologically Important *Bacillus megaterium* Strains QM B1551 and DSM319. *J Bacteriol* 2011; **193**:4199-4213. [PubMed doi:10.1128/JB.00449-11](#)
56. Chen J, Xia Y, Cheng C, Fang C, Shan Y, Jin G, Fang W. Genome sequence of a non-pathogenic *Listeria monocytogenes* serovar 4a strain M7. *J Bacteriol* 2011;
57. Su F, Yu B, Sun J, Ou HY, Zhao B, Wang L, Qin J, Tang H, Tao F, Jarek M, et al. Genome Sequence of Thermophilic Strain *Bacillus coagulans* 2-6, an Efficient Producer of High Optical Purity L-Lactic Acid. *J Bacteriol* 2011;
58. Delorme C, Guedon E, Pons N, Cruaud C, Couloux A, Loux V, Chiapello H, Poyart C, Gautier C, Sanchez N, et al. Complete Genome Sequence of the clinical *Streptococcus salivarius* strain CCHSS3. *J Bacteriol* 2011; 10.1128/JB.05416-11.
59. Ding R, Li Y, Qian C, Wu X. Draft Genome Sequence of *Paenibacillus elgii* B69, a Strain with Broad Antimicrobial Activity. *J Bacteriol* 2011; **193**:4537. [PubMed doi:10.1128/JB.00406-11](#)
60. Abriouel H, Benomar N, Perez Pulido R, Canamero MM, Galvez A. Annotated Genome Sequence of *Lactobacillus pentosus* MP-10, Which Has Probiotic Potential, from Naturally Fermented Aloreña Green Table Olives. *J Bacteriol* 2011; **193**:4559-4560. [PubMed doi:10.1128/JB.05171-11](#)
61. Kim DW, Choi SH, Kang A, Nam SH, Kim RN, Kim A, Kim DS, Park HS. Genome Sequence of *Leuconostoc pseudomesenteroides* KCTC 3652. *J Bacteriol* 2011; **193**:4299. [PubMed doi:10.1128/JB.05433-11](#)
62. Kim DW, Choi SH, Kang A, Nam SH, Kim DS, Kim RN, Kim A, Park HS. Draft Genome Sequence of *Lactobacillus mali* KCTC 3596. *J Bacteriol* 2011; **193**:5037. [PubMed doi:10.1128/JB.05686-11](#)
63. Jeong H, Park SY, Chung WH, Kim SH, Kim N, Park SH, Kim JF. Draft Genome Sequence of the *Paenibacillus polymyxa* Type Strain (ATCC 842T), a Plant Growth-Promoting Bacterium. *J Bacteriol* 2011; **193**:5026-5027. [PubMed doi:10.1128/JB.05447-11](#)
64. Guédon E, Delorme C, Pons N, Cruaud C, Loux V, Couloux A, Gautier C, Sanchez N, Layec S, Gal-leron N, et al. Complete Genome Sequence of the Commensal *Streptococcus salivarius* Strain JIM8777. *J Bacteriol* 2011; **193**:5024-5025. [PubMed doi:10.1128/JB.05390-11](#)
65. Kim DS, Choi SH, Kim DW, Kim RN, Nam SH, Kang A, Kim A, Park HS. Genome Sequence of *Lactobacillus cypricasei* KCTC 13900. *J Bacteriol* 2011; **193**:5053-5054. [PubMed doi:10.1128/JB.05659-11](#)
66. Kim DW, Choi SH, Kang A, Nam SH, Kim DS, Kim RN, Kim A, Park HS. Draft Genome Sequence of *Lactobacillus zeae* KCTC 3804. *J Bacteriol* 2011; **193**:5023. [PubMed doi:10.1128/JB.05602-11](#)
67. Chen J, Xia Y, Cheng C, Fang C, Shan Y, Jin G, Fang W. Genome Sequence of the Nonpathogenic *Listeria monocytogenes* Serovar 4a Strain M7. *J Bacteriol* 2011; **193**:5019-5020. [PubMed doi:10.1128/JB.05501-11](#)
68. Cho YJ, Choi JK, Kim JH, Lim YS, Ham JS, Kang DK, Chun J, Paik HD, Kim GB. Genome Sequence of *Lactobacillus salivarius* GJ-24, a Probiotic Strain Isolated from Healthy Adult Intestine. *J Bacteriol* 2011; **193**:5021-5022. [PubMed doi:10.1128/JB.05616-11](#)
69. Lee JH, Chae JP, Lee JY, Lim JS, Kim GB, Ham JS, Chun J, Kang DK. Genome Sequence of *Lactobacillus johnsonii* PF01, Isolated from Piglet Feces. *J Bacteriol* 2011; **193**:5030-5031. [PubMed doi:10.1128/JB.05640-11](#)
70. Bao G, Wang R, Zhu Y, Dong H, Mao S, Zhang Y, Chen Z, Li Y, Ma Y. Complete Genome Sequence of *Clostridium acetobutylicum* DSM 1731, a Solvent-Producing Strain with Multireplicon Genome Architecture. *J Bacteriol* 2011; **193**:5007-5008. [PubMed doi:10.1128/JB.05596-11](#)
71. Nam SH, Choi SH, Kang A, Kim DW, Kim RN, Kim DS, Kim A, Park HS. Genome Sequence of *Lactobacillus suebicus* KCTC 3549. *J Bacteriol* 2011; **193**:5532-5533. [PubMed doi:10.1128/JB.05814-11](#)
72. Djukic M, Poehlein A, Thurmer A, Daniel R. Genome Sequence of *Brevibacillus laterosporus* LMG 15441, a Pathogen of Invertebrates. *J Bacteriol* 2011; **193**:5535-5536. [PubMed doi:10.1128/JB.05696-11](#)
73. Ham JS, Kim HW, Seol KH, Jang A, Jeong SG, Oh MH, Kim DH, Kang DK, Kim GB, Cha CJ. Genome Sequence of *Lactobacillus salivarius* NIAS840, Isolated from Chicken Intestine. *J Bac-*

- teriol* 2011; **193**:5551-5552.  
[PubMed doi:10.1128/JB.05688-11](#)
74. Chervaux C, Grimaldi C, Bolotin A, Quinquis B, Legrain-Raspaud S, van Hylckama Vlieg JET, Denariáz G, Smokvina T. Genome Sequence of the Probiotic Strain *Bifidobacterium animalis* subsp. *lactis* CNCM I-2494. *J Bacteriol* 2011; **193**:5560-5561. [PubMed doi:10.1128/JB.05716-11](#)
  75. Marx H, Graf AB, Tatto NE, Thallinger GG, Matanovich D, Sauer M. Genome Sequence of the Ruminant Bacterium *Megasphaera elsdenii*. *J Bacteriol* 2011; **193**:5578-5579. [PubMed doi:10.1128/JB.05861-11](#)
  76. Kim DS, Choi SH, Kim DW, Kim RN, Nam SH, Kang A, Kim A, Park HS. Genome Sequence of *Lactobacillus versmoldensis* KCTC 3814. *J Bacteriol* 2011; **193**:5589-5590. [PubMed doi:10.1128/JB.05708-11](#)
  77. Maldonado-Barragán A, Caballero-Guerrero B, Lucena-Padros H, Ruiz-Barba JL. Genome Sequence of *Lactobacillus pentosus* IG1, a Strain Isolated from Spanish-Style Green Olive Fermentations. *J Bacteriol* 2011; **193**:5605. [PubMed doi:10.1128/JB.05736-11](#)
  78. Chen Y, He Y, Zhang B, Yang J, Li W, Dong Z, Hu S. Complete Genome Sequence of *Alicyclobacillus acidocaldarius* Strain Tc-4-1. *J Bacteriol* 2011; **193**:5602-5603. [PubMed doi:10.1128/JB.05709-11](#)
  79. Delorme C, Bartholini C, Luraschi M, Pons N, Loux V, Almeida M, Guedon E, Gibrat JF, Renault P. Complete Genome Sequence of the Pigmented *Streptococcus thermophilus* Strain JIM8232. *J Bacteriol* 2011; **193**:5581-5582. [PubMed doi:10.1128/JB.05404-11](#)
  80. Ma Z, Geng J, Zhang H, Yu H, Yi L, Lei M. Lu C-ping, Fan H-jie, Hu S: Complete Genome Sequence of *Streptococcus equi* subsp. *zooepidemicus* Strain ATCC 35246. *J Bacteriol* 2011; **193**:5583-5584. [PubMed doi:10.1128/JB.05700-11](#)
  81. Yang H, Liao Y, Wang B, Lin Y, Pan L. Complete Genome Sequence of *Bacillus amyloliquefaciens* XH7, Which Exhibits Production of Purine Nucleosides. *J Bacteriol* 2011; **193**:5593-5594. [PubMed doi:10.1128/JB.05880-11](#)
  82. Lee SH, Jung JY, Lee SH, Jeon CO. Complete Genome Sequence of *Leuconostoc kimchii* Strain C2, Isolated from Kimchi. *J Bacteriol* 2011; **193**:5548. [PubMed doi:10.1128/JB.05707-11](#)
  83. Kim DW, Choi SH, Kang A, Nam SH, Kim DS, Kim RN, Kim A, Park HS. Draft Genome Sequence of *Lactobacillus malefermentans* KCTC 3548. *J Bacteriol* 2011; **193**:5537. [PubMed doi:10.1128/JB.05710-11](#)
  84. Lee SH, Jung JY, Lee SH, Jeon CO. Complete Genome Sequence of *Weissella koreensis* KACC 15510, Isolated from Kimchi. *J Bacteriol* 2011; **193**:5534. [PubMed doi:10.1128/JB.05704-11](#)
  85. Li Y, Zheng H, Liu Y, Jiang Y. Jiuqing Xi, Chen W, Song Z: The Complete Genome Sequence of *Mycoplasma bovis* Strain Hubei-1. *PLoS ONE* 2011; **6**:e20999. [PubMed doi:10.1371/journal.pone.0020999](#)
  86. Shu HW, Liu TT, Chan HI, Liu YM, Wu KM, Shu HY, Tsai SF, Hsiao KJ, Hu WS, Ng WV. Genome Sequence of the Repetitive-Sequence-Rich *Mycoplasma fermentans* Strain M64. *J Bacteriol* 2011; **193**:4302-4303. [PubMed doi:10.1128/JB.05228-11](#)
  87. Antunes A, Alam I, El Dorry H, Siam R, Robertson A, Bajic VB, Stingl U. Genome Sequence of *Halo-plasma contractile*, an Unusual Contractile Bacterium from a Deep-Sea Anoxic Brine Lake. *J Bacteriol* 2011; **193**:4551-4552. [PubMed doi:10.1128/JB.05461-11](#)
  88. Yang F, Tang C, Wang Y, Zhang H, Yue H. Genome Sequence of *Mycoplasma ovipneumoniae* Strain SC01. *J Bacteriol* 2011; **193**:5018. [PubMed doi:10.1128/JB.05363-11](#)
  89. Kim WJ, Kim YO, Kim DS, Choi SH, Kim DW, Lee JS, Kong HJ, Nam BH, Kim BS, Lee SJ, et al. Draft Genome Sequence of *Kocuria rhizophila* P7-4. *J Bacteriol* 2011;
  90. Seipke RF, Crossman L, Drou N, Heavens D, Bibb MJ, Caccamo M, Hutchings MI. Draft Genome Sequence of *Streptomyces* S4, a symbiont of the leafcutter ant *Acromyrmex octospinosus*. *J Bacteriol* 2011;
  91. Shin NR, Whon TW, Roh SW, Kim MS, Jung MJ, Lee J, Bae JW. Genome Sequence of *Corynebacterium nuruki* S6-4T, Isolated from Alcohol Fermentation Starter. *J Bacteriol* 2011;
  92. Butler-Wu SM, Sengupta DJ, Kittichotirat W, Matzen FA, Bumgarner RE. Genome Sequence of a Novel Species, *Propionibacterium humerusii*. *J Bacteriol* 2011; **193**:3678. [PubMed doi:10.1128/JB.05036-11](#)
  93. Zhang ZY, Sun ZQ, Wang ZL, Wen ZL, Sun QW, Zhu ZQ, Song YZ, Zhao JW, Wang HH, Zhang SL, et al. Complete Genome Sequence of a Novel

- Clinical Isolate, the Nontuberculous *Mycobacterium* Strain JDM601. *J Bacteriol* 2011; **193**:4300-4301. [PubMed doi:10.1128/JB.05291-11](#)
94. Erxleben A, Wunsch-Palasis J, Gruning BA, Luzhetska M, Bechthold A, Gunther S. Genome Sequence of *Streptomyces* sp. Strain Tu6071. *J Bacteriol* 2011; **193**:4278-4279. [PubMed doi:10.1128/JB.00377-11](#)
  95. O'Connell Motherway M, Zomer A, Leahy SC, Reunanen J, Bottacini F, Claesson MJ, O'Brien F, Flynn K, Casey PG, Moreno Munoz JA, et al. Functional genome analysis of *Bifidobacterium breve* UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. *Proc Natl Acad Sci USA* 2011; **108**:11217-11222. [PubMed doi:10.1073/pnas.1105380108](#)
  96. Hunyadkurti J, Feltoti Z, Horvath B, Nagymihaly M, Voros A, McDowell A, Patrick S, Urban E, Nagy I. Complete Genome Sequence of *Propionibacterium acnes* Type IB strain 6609. *J Bacteriol* 2011; **193**: [doi:10.1128/JB.05372-11](#)
  97. Cai M, Chen WM, Nie Y, Chi CQ, Wang YN, Tang YQ, Li GY, Wu XL. Complete Genome Sequence of *Amycolicococcus subflavus* DQS3-9A1T, an Actinomycete Isolated from Crude Oil-Polluted Soil. *J Bacteriol* 2011; **193**:4538-4539. [PubMed doi:10.1128/JB.05388-11](#)
  98. Ge F, Li W, Chen G, Liu Y, Zhang G, Yong B, Wang Q, Wang N, Huang Z, Li W, et al. Draft Genome Sequence of *Gordonia neofelifaecis* NRRL B-59395, a Cholesterol-Degrading Actinomycete. *J Bacteriol* 2011; **193**:5045-5046. [PubMed doi:10.1128/JB.05531-11](#)
  99. Sales CM, Mahendra S, Grostern A, Parales RE, Goodwin LA, Woyke T, Nolan M, Lapidus A, Chertkov O, Ovchinnikova G, et al. Genome Sequence of the 1,4-Dioxane-Degrading *Pseudonocardia dioxanivorans* Strain CB1190. *J Bacteriol* 2011; **193**:4549-4550. [PubMed doi:10.1128/JB.00415-11](#)
  100. Ham JS, Lee T, Byun MJ, Lee KT, Kim MK, Han GS, Jeong SG, Oh MH, Kim DH, Kim H. Complete Genome Sequence of *Bifidobacterium longum* subsp. *longum* KACC 91563. *J Bacteriol* 2011; **193**:5044. [PubMed doi:10.1128/JB.05620-11](#)
  101. Barbe V, Bouzon M, Mangenot S, Badet B, Poulain J, Segurens B, Vallenet D, Marliere P, Weissenbach J. Complete Genome Sequence of *Streptomyces cattleya* NRRL 8057, a Producer of Antibiotics and Fluorometabolites. *J Bacteriol* 2011; **193**:5055-5056. [PubMed doi:10.1128/JB.05583-11](#)
  102. Yang X, Xue R, Shen C, Li S, Gao C, Wang Q, Zhao X. Genome Sequence of *Rhodococcus* sp. Strain R04, a Polychlorinated-Biphenyl Biodegrader. *J Bacteriol* 2011; **193**:5032-5033. [PubMed doi:10.1128/JB.05635-11](#)
  103. Gomes LHF, Otto TD, Vasconcellos EA, Ferrao PM, Maia RM, Moreira AS, Ferreira MA, Castello-Branco LRR, Degraive WM, Mendonca-Lima L. Genome Sequence of *Mycobacterium bovis* BCG Moreau, the Brazilian Vaccine Strain against Tuberculosis. *J Bacteriol* 2011; **193**:5600-5601. [PubMed doi:10.1128/JB.05827-11](#)
  104. Pan Y, Yang X, Li J, Zhang R, Hu Y, Zhou Y, Wang J, Zhu B. Genome Sequence of the Spinosyns-Producing Bacterium *Saccharopolyspora spinosa* NRRL 18395. *J Bacteriol* 2011; **193**:3150-3151. [PubMed doi:10.1128/JB.00344-11](#)
  105. Zhang Y, Chen C, Liu J, Deng H, Pan A, Zhang L, Zhao X, Huang M, Lu B, Dong H, et al. Complete Genome Sequences of *Mycobacterium tuberculosis* Strains CCDC5079 and CCDC5080, Which Belong to the Beijing Family. *J Bacteriol* 2011; **193**:5591-5592. [PubMed doi:10.1128/JB.05452-11](#)
  106. Verma M, Kaur J, Kumar M, Kumari K, Saxena A, Anand S, Nigam A, Ravi V, Raghuvanshi S, Khurana P, et al. Whole Genome Sequence of the Rifamycin B-Producing Strain *Amycolatopsis mediterranei* S699. *J Bacteriol* 2011; **193**:5562-5563. [PubMed doi:10.1128/JB.05819-11](#)
  107. Sarikhan S, Azarbajjani R, Yeganeh LP, Fazeli AS, Amoozegar MA, Salekdeh GH. Draft Genome Sequence of *Nesterenkonia* sp. Strain F, Isolated From Aran-Bidgol Salt Lake in Iran. *J Bacteriol* 2011; **193**:5580. [PubMed doi:10.1128/JB.05808-11](#)
  108. Zhao X, Yang T. Draft Genome Sequence of the Marine Sediment-Derived Actinomycete *Streptomyces xinghaiensis* NRRL B24674T. *J Bacteriol* 2011; **193**:5543. [PubMed doi:10.1128/JB.05689-11](#)
  109. Sait M, Clark EM, Wheelhouse N, Livingstone M, Spalding L, Siarkou VI, Vretou E, Smith DGE, Lainson FA, Longbottom D. Genome sequence of the *Chlamydophila abortus* variant strain LLG. *J Bacteriol* 2011; **193**:4276-4277. [PubMed doi:10.1128/JB.05290-11](#)
  110. Grinblat-Huse V, Drabek EF, Creasy HH, Daugherty SC, Jones KM, Santana-Cruz I, Tallon LJ, Read TD, Hatch TP, Bavoil P, et al. Genome Se-



- quences of the Zoonotic Pathogens *Chlamydia psittaci* 6BC and Cal10. *J Bacteriol* 2011; **193**:4039-4040. [PubMed doi:10.1128/JB.05277-11](#)
111. Somboonna N, Wan R, Ojcius DM, Pettengill MA, Joseph SJ, Chang A, Hsu R, Read TD, Dean D: Hypervirulent *Chlamydia trachomatis* Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L2) and D Lineages. *mBio* May, 2.
  112. Angelov A, Loderer C, Pompei S, Liebl W. A novel family of carbohydrate-binding modules revealed by the genome sequence of *Spirochaeta thermophila* DSM 6192. *Appl Environ Microbiol* 2011; **77**:5483-5489. [PubMed doi:10.1128/AEM.00523-11](#)
  113. Håfström T, Jansson D, Segerman B. Complete Genome Sequence of *Brachyspira intermedia* Reveals Unique Genomic Features in *Brachyspira* Species and Phage-mediated Horizontal Gene Transfer. *BMC Genomics* 2011; **12**:395. [PubMed doi:10.1186/1471-2164-12-395](#)
  114. Watanabe T, Maruyama F, Nozawa T, Aoki A, Okano S, Shibata Y, Oshima K, Kurokawa K, Hattori M, Nakagawa I, *et al.* Complete Genome Sequence of the Bacterium *Porphyromonas gingivalis* TDC60, Which Causes Periodontal Disease. *J Bacteriol* 2011; **193**:4259-4260. [PubMed doi:10.1128/JB.05269-11](#)
  115. Klippel B, Lochner A, Bruce DC, Walston Davenport K, Detter C, Goodwin LA, Han J, Han S, Hauser L, Land ML, *et al.* Complete Genome Sequences of *Krokinobacter* sp. Strain 4H-3-7-5 and *Lacinutrix* sp. Strain 5H-3-7-4, Polysaccharide-Degrading Members of the Family *Flavobacteriaceae*. *J Bacteriol* 2011; **193**:4545-4546. [PubMed doi:10.1128/JB.05518-11](#)
  116. Du Z, Zhang Z, Miao T, Wu J, Lu G, Yu J, Xiao J, Chen G. Draft Genome Sequence of the Novel Agar-Digesting Marine Bacterium HQM9. *J Bacteriol* 2011; **193**:4557-4558. [PubMed doi:10.1128/JB.05513-11](#)
  117. Gao Z, Liu X, Ruan L. Genome Sequence of *Anaerophaga* sp. Strain HS1, a Novel, Moderately Thermophilic, Strictly Anaerobic Bacterium Isolated from Hot Spring Sediment. *J Bacteriol* 2011; **193**:5572. [PubMed doi:10.1128/JB.05719-11](#)
  118. Manfredi P, Pagni M, Cornelis GR. Complete Genome Sequence of the Dog Commensal and Human Pathogen *Capnocytophaga canimorsus* Strain 5. *J Bacteriol* 2011; **193**:5558-5559. [PubMed doi:10.1128/JB.05853-11](#)
  119. Oh C, Heo SJ, De Zoysa M, Affan A, Jung WK, Park HS, Lee Y, Lee J, Yoon KT, Kang DH. Whole-Genome Sequence of the Xylanase-Producing *Mesoflavibacter zeaxanthinifaciens* Strain S86. *J Bacteriol* 2011; **193**:5557. [PubMed doi:10.1128/JB.05793-11](#)
  120. Swithers KS, DiPippo JL, Bruce DC, Detter C, Tapia R, Han S, Goodwin LA, Han J, Woyke T, Pitluck S, *et al.* Genome Sequence of *Kosmotoga olearia* Strain TBF 19.5.1, a Thermophilic Bacterium with a Wide Growth Temperature Range, Isolated from the Troll B Oil Platform in the North Sea. *J Bacteriol* 2011; **193**:5566-5567. [PubMed doi:10.1128/JB.05828-11](#)
  121. Kim BK, Jung MY, Yu DS, Park SJ, Oh TK, Rhee SK, Kim JF. Genome Sequence of an Ammonia-Oxidizing Soil Archaeon, “*Candidatus Nitrosoarchaeum koreensis*” MY1. *J Bacteriol* 2011; **193**:5539-5540. [PubMed doi:10.1128/JB.05717-11](#)
  122. Wóycicki R, Witkowicz J, Gawroński P, Dąbrowska J, Lomsadze A, Pawełkowicz M, Siedlecka E, Yagi K, Pląder W, Seroczyńska A, *et al.* The Genome Sequence of the North-European Cucumber (*Cucumis sativus* L.) Unravels Evolutionary Adaptation Mechanisms in Plants. *PLoS ONE* 2011; **6**:e22728. [PubMed doi:10.1371/journal.pone.0022728](#)
  123. Rivarola M, Foster JT, Chan AP, Williams AL, Rice DW, Liu X, Melake-Berhan A, Huot Creasy H, Puiu D, Rosovitz MJ, *et al.* Castor Bean Organellar Genome Sequencing and Worldwide Genetic Diversity Analysis. *PLoS ONE* 2011; **6**:e21743. [PubMed doi:10.1371/journal.pone.0021743](#)
  124. Belaganahalli MN, Maan S, Maan NS, Tesh R, Attoui H, Mertens PPC. Umatilla Virus Genome Sequencing and Phylogenetic Analysis: Identification of Stretch Lagoon Orbivirus as a New Member of the Umatilla virus Species. *PLoS ONE* 2011; **6**:e23605. [PubMed doi:10.1371/journal.pone.0023605](#)
  125. Star B, Nederbragt AJ, Jentoft S, Grimholt U, Malmstrom M, Gregers TF, Rounge TB, Paulsen J, Solbakken MH, Sharma A, *et al.*: The genome sequence of Atlantic cod reveals a unique immune system. *Nature* 2011, advance online publication.
  126. Genome sequence and analysis of the tuber crop potato. *Nature* 2011; **475**:189-195. [PubMed doi:10.1038/nature10158](#)
  127. Zsak L, Day J, Oakley B, Seal B: The complete genome sequence and genetic analysis of ΦCA82

- a novel uncultured microphage from the turkey gastrointestinal system. [date unknown], 8:331.
128. Barth D, Berendonk T. The mitochondrial genome sequence of the ciliate *Paramecium caudatum* reveals a shift in nucleotide composition and codon usage within the genus *Paramecium*. *BMC Genomics* 2011; **12**:272. [PubMed doi:10.1186/1471-2164-12-272](https://doi.org/10.1186/1471-2164-12-272)
129. Jiang X, Jiang H, Li C, Wang S, Mi Z, An X, Chen J, Tong Y: Sequence characteristics of T4-like bacteriophage IME08 genome termini revealed by high throughput sequencing. [date unknown], 8:194.
130. Lee SW, Markham P, Markham J, Petermann I, Noormohammadi A, Browning G, Ficorilli N, Hartley C, Devlin J. First complete genome sequence of infectious laryngotracheitis virus. *BMC Genomics* 2011; **12**:197. [PubMed doi:10.1186/1471-2164-12-197](https://doi.org/10.1186/1471-2164-12-197)
131. Renfree MB, Papenfuss AT, Deakin JE, Lindsay J, Heider T, Belov K, Rens W, Waters PD, Pharo EA, Shaw G, *et al.* Genome sequence of an Australian kangaroo, *Macropus eugenii*, provides insight into the evolution of mammalian reproduction and development. *Genome Biol* 2011; **12**:R81. [PubMed doi:10.1186/gb-2011-12-8-r81](https://doi.org/10.1186/gb-2011-12-8-r81)
132. Han X, Zhang W, Xue Y, Shao S. Sequence analysis reveals mosaic genome of Aichi virus. *Virology* 2011; **8**:390. [PubMed doi:10.1186/1743-422X-8-390](https://doi.org/10.1186/1743-422X-8-390)
133. López-Madrugal S, Latorre A, Porcar M, Moya A, Gil R. Complete Genome Sequence of “*Candidatus Tremblaya princeps*” Strain PCVAL, an Intriguing Translational Machine below the Living-Cell Status. *J Bacteriol* 2011; **193**:5587-5588. [PubMed doi:10.1128/JB.05749-11](https://doi.org/10.1128/JB.05749-11)