

## Genome sequences published outside of *Standards in Genomic Sciences*, December 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 subsequent versions of this list are invited to provide the bibliographic data for such references to the SIGS editorial office.

### Phylum *Euryarchaeota*

*Halobiforma lacisalsi* AJ5, sequence accession AGFZ01000000 [1]

*Thermococcus* sp. strain AM4, sequence accession CP002952 [2]

### Phylum *Proteobacteria*

*Acidithiobacillus thiooxidans* ATCC 19377, sequence accession AFOH01000000 [3]

*Acinetobacter* sp. strain D499, sequence accession AGFH01000000 [4]

*Azospirillum brasilense* Sp245, sequence accession HE577327 (chromosome), HE577328 (p1), HE577329 (p2), HE577330 (p3), HE577331 (p4), HE577332 (p5), HE577333 (p6) [5]

*Azospirillum lipoferum* strain 4B, sequence accession FQ311868 (chromosome), FQ311869 (p1), FQ311870 (p2), FQ311871 (p3), FQ311872 (p4), FQ311873 (p5), FQ311874 (p6) [5]

*Escherichia coli* F18, sequence accession AGTD01000000 [6]

*Escherichia coli* K88, sequence accession CP002729 (chromosome), CP002730 (pUMNK88\_K88), CP002731 (pUMNK88\_Incl1), CP002732 (pUMNK88\_Ent), CP002733 (pUMNK88\_Hly), and HQ023862 (pUMNK88) [6]

*Escherichia coli* Strain CE10, sequence accession CP003034 to CP003038 [7]

*Gluconacetobacter xylinus*, NBRC 3288, sequence accession AP012159 through AP012166 [8]

*Halomonas* sp. Strain HAL1, sequence accession AGIB00000000 [9]

*Methylomonas methanica* MC09, sequence accession CP002738 [10]

*Novosphingobium nitrogenifigens* Y88, sequence accession [11]

*Pelagibacterium halotolerans* B2, sequence accession CP003075 (chromosome), CP003076 (plasmid) [12]

*Pseudomonas aeruginosa* PAO1, sequence accession GSE34141 [13]

*Pseudomonas putida* Idaho, sequence accession AGFJ01000000 [14]

*Sphingomonas elodea* ATCC 31461, sequence accession AGFU01000000 [15]

### Phylum *Firmicutes*

*Acidaminococcus intestini* RYC-MR95, sequence accession CP003058 [16]

*Lactobacillus rhamnosus* strain CASL, sequence accession AFYD00000000 [17]

*Pseudomonas aeruginosa* NCGM2.S1, sequence accession AP012280 [18]

### Phylum *Actinobacteria*

*Candidatus Frankia datiscae*, sequence accession NC\_015656 [19]

*Corynebacterium pseudotuberculosis* Strain CIP 52.97, sequence accession CP003061 [20]

*Propionibacterium acnes* Type II Strain ATCC 11828, sequence accession CP003084 [21]

*Streptomyces chartreusis* NRRL 12338, sequence accession AGDE00000000 [22]

*Streptomyces chartreusis* NRRL 3882, sequence accession AGDD00000000 [22]

*Streptomyces lysosuperificus* ATCC 31396, accession number AGDC00000000 [22]

*Streptomyces* sp. Strain Wigar10, sequence accession AGDF01000000 [23]

## Phylum Spirochaetes

*Borrelia afzelii* PKo, sequence accession CP002933 (Chromosome), CP002942 (Ip17), CP002943 (Ip28-2), CP002944 (Ip28-3), CP002945 (Ip28-4), CP002946 (Ip28-7), CP002947 (IP28-8), CP002949 (Ip38), CP002950 (Ip54), CP002934 (cp26), CP002937 (cp32-1), CP002938 (cp32-3), CP002939 (cp32-5), CP002940 (cp32-7), CP002940 (cp32-9), CP002948 (cp32-10), CP002935 (cp32-11), CP002936 (cp32-12) [24]

*Borrelia afzelii* ACA-1, sequence accession AB-CU02000001-2 (Chromosome), CP001239 (Ip17), CP001238 (Ip28-1), CP001244 (Ip28-2), CP001241 (Ip28-3), CP001249 (Ip28-4), CP001242 (Ip-7), CP001246 (Ip38), CP001247 (Ip54), CP001250 (cp26), CP001243 (cp32-1), CP001237 (cp32-3), CP001240 (cp32-4), CP001248 (cp32-5), CP001245 (cp32-10) [24]

*Borrelia garinii* PBr, sequence accession ABJV02000001-5 (Chromosome), CP001309 (Ip17), CP001301 (Ip25), CP001310 (Ip28-1), CP001307 (Ip28-3), CP001304 (Ip28-4), CP001311 (Ip28-7), CP001302 (Ip36), CP001308 (Ip54), CP001305 (Ip26), CP001303 (Ip32-5), CP001306 (Ip32-10) [24]

*Borrelia garinii* Far 04, sequence accession ABPZ02000001-33 (Chromosome), CP001315 (Ip17), CP001317 (Ip25), CP001316 (Ip28-1), CP001314 (Ip36), CP001318 (Ip54), CP001319 (Ip26), CP001320 (Ip32-10) [24]

## References

- Jiang X, Wang S, Cheng H, Huo Y, Zhang X, Zhu X, Han X, Ni P, Wu M. Genome sequence of *Halobiforma lacisalsi* AJ5, an extremely halophilic archaeon which harbors a bop Gene. *J Bacteriol* 2011; **193**:7023-7024. [PubMed](http://dx.doi.org/10.1128/JB.06282-11) <http://dx.doi.org/10.1128/JB.06282-11>
- Oger P, Sokolova TG, Kozhevnikova DA, Chernyh NA, Bartlett DH, Bonch-Osmolovskaya EA,

## Non-Bacterial genomes

B1 Human Adenovirus HAdV-16 strain E26, sequence accession JN860680 [25]

B1 Human Adenovirus HAdV-3/16, sequence accession JN860678 [25]

B1 Human Adenovirus HAdV-3+7, sequence accession JN860679 [25]

B1 Human Adenovirus HAdV-7d2, sequence accession JN860677 [25]

B1 Human Adenovirus HAdV-7h, sequence accession JN860676 [25]

*Bacillus cereus* bacteriophage BCP78, sequence accession JN797797 [26]

Circoviridae member (not yet validated), sequence accession JF803741 [27]

Coccolithovirus *Emiliania huxleyi* Virus 203, sequence accession JF974291 [28]

*Cryptococcus gattii* BC, sequence accession SRP006436 [29]

*Erwinia amylovora* plasmid pEI70, sequence accession CP002951 [30]

*Mortierella alpina*, sequence accession ADAG00000000 [31]

Parvovirus Aj-BtPV-1, sequence accession JN860679 [32]

Parvovirus Eh-BtPV-1, sequence accession JN860679 [32]

*Penicillium marneffeii* PM1, sequence accession AGCC00000000 [33]

*Pseudomonas fluorescens* phage OBP, sequence accession JN627160 [34]

*Salmonella* bacteriophage SPN3US, sequence accession JN641803 [35]

Tailam virus, sequence accession JN689227 [36]

Lebedinsky AV. Complete genome sequence of the hyperthermophilic archaeon *Thermococcus* sp. strain AM4, capable of organotrophic growth and growth at the expense of hydrogenogenic or sulfidogenic oxidation of carbon monoxide. *J Bacteriol* 2011; **193**:7019-7020. [PubMed](http://dx.doi.org/10.1128/JB.06259-11) <http://dx.doi.org/10.1128/JB.06259-11>

3. Valdes J, Ossandon F, Quatrini R, Dopson M, Holmes DS. Draft genome sequence of the extremely acidophilic biomining bacterium *Acidithiobacillus thiooxidans* ATCC 19377 provides insights into the evolution of the *Acidithiobacillus* genus. *J Bacteriol* 2011; **193**:7003-7004. [PubMed](#) <http://dx.doi.org/10.1128/JB.06281-11>
4. Chen Y, Cui Y, Pu F, Jiang G, Zhao X, Yuan Y, Zhao W, Li D, Liu H, Li Y, et al. Draft genome sequence of an *Acinetobacter* genomic species 3 Strain harboring a blaNDM-1 Gene. *J Bacteriol* 2012; **194**:204-205. [PubMed](#) <http://dx.doi.org/10.1128/JB.06202-11>
5. Wisniewski-Dyé F, Borziak K, Khalsa-Moyers G, Alexandre G, Sukharnikov LO, Wuichet K, Hurst GB, McDonald WH, Robertson JS, Barbe V, et al. *Azospirillum* genomes reveal transition of bacteria from aquatic to terrestrial environments. *PLoS Genet* 2011; **7**:e1002430. <http://dx.doi.org/10.1371/journal.pgen.1002430>
6. Shepard SM, Danzeisen JL, Isaacson RE, Seemann T, Achtman M, Johnson TJ. Genome sequences and phylogenetic analysis of K88- and F18-positive porcine enterotoxigenic *Escherichia coli*. *J Bacteriol* 2011. [PubMed](#)
7. Lu S, Zhang X, Zhu Y, Kim KS, Yang J, Jin Q. Complete genome sequence of the neonatal-meningitis-associated *Escherichia coli* Strain CE10. *J Bacteriol* 2011; **193**:7005. [PubMed](#) <http://dx.doi.org/10.1128/JB.06284-11>
8. Ogino H, Azuma Y, Hosoyama A, Nakazawa H, Matsutani M, Hasegawa A, Otsuyama K, Matsushita K, Fujita N, Shirai M. Complete genome sequence of NBRC 3288, a unique cellulose-nonproducing strain of *Gluconacetobacter xylinus* isolated from vinegar. *J Bacteriol* 2011; **193**:6997-6998. [PubMed](#) <http://dx.doi.org/10.1128/JB.06158-11>
9. Lin Y, Fan H, Hao X, Johnstone L, Hu Y, Wei G, Alwathnani HA, Wang G, Rensing C. Draft genome sequence of *Halomonas* sp. Strain HAL1, a moderately halophilic arsenite-oxidizing bacterium isolated from gold-mine soil. *J Bacteriol* 2012; **194**:199-200. [PubMed](#) <http://dx.doi.org/10.1128/JB.06359-11>
10. Boden R, Cunliffe M, Scanlan J, Moussard H, Kits KD, Klotz MG, Jetten MSM, Vuilleumier S, Han J, Peters L, et al. Complete genome sequence of the aerobic marine methanotroph *Methylomonas methanica* MC09. *J Bacteriol* 2011; **193**:7001-7002. [PubMed](#) <http://dx.doi.org/10.1128/JB.06267-11>
11. Strabala TJ, Macdonald L, Liu V, Smit AM. Draft genome sequence of *Novosphingobium nitrogenifigens* Y88<sup>T</sup>. *J Bacteriol* 2012; **194**:201. [PubMed](#) <http://dx.doi.org/10.1128/JB.06381-11>
12. Huo YY, Cheng H, Han XF, Jiang XW, Sun C, Zhang XQ, Zhu XF, Liu YF, Li PF, Ni PX, et al. Complete genome sequence of *Pelagibacterium halotolerans* B2<sup>T</sup>. *J Bacteriol* 2012; **194**:197-198. [PubMed](#) <http://dx.doi.org/10.1128/JB.06343-11>
13. Wei Q, Tarighi S, Dötsch A, Häussler S, Müsken M, Wright VJ, Cámara M, Williams P, Haenen S, Boerjan B, et al. Phenotypic and genome-wide analysis of an antibiotic-resistant small colony variant (SCV) of *Pseudomonas aeruginosa*. *PLoS ONE* 2011; **6**:e29276. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0029276>
14. Tao F, Tang H, Gai Z, Su F, Wang X, He X, Xu P. Genome sequence of *Pseudomonas putida* Idaho, a unique organic solvent-tolerant bacterium. *J Bacteriol* 2011; **193**:7011-7012. [PubMed](#) <http://dx.doi.org/10.1128/JB.06200-11>
15. Gai Z, Wang X, Zhang X, Su F, Wang X, Tang H, Tai C, Tao F, Ma C, Xu P. Genome sequence of *Sphingomonas elodea* ATCC 31461, a highly productive industrial strain of gellan gum. *J Bacteriol* 2011; **193**:7015-7016. [PubMed](#) <http://dx.doi.org/10.1128/JB.06307-11>
16. D'Auria G, Galán JC, Rodríguez-Alcayna M, Moya A, Baquero F, Latorre A. Complete genome sequence of *Acidaminococcus intestini* RYC-MR95, a Gram-negative bacterium from the phylum *Firmicutes*. *J Bacteriol* 2011; **193**:7008-7009. [PubMed](#) <http://dx.doi.org/10.1128/JB.06301-11>
17. Yu B, Su F, Wang L, Zhao B, Qin J, Ma C, Xu P, Ma Y. Genome sequence of *Lactobacillus rhamnosus* strain CASL, an efficient l-lactic acid producer from cheap substrate cassava. *J Bacteriol* 2011; **193**:7013-7014. [PubMed](#) <http://dx.doi.org/10.1128/JB.06285-11>
18. Miyoshi-Akiyama T, Matsumura K, Kobayashi N, Maeda S, Kirikae T. Genome sequence of clinical isolate *Mycobacterium tuberculosis* NCGM2209. *J Bacteriol* 2011; **193**:6792. [PubMed](#) <http://dx.doi.org/10.1128/JB.06233-11>
19. Persson T, Benson DR, Normand P, Vanden Heuvel B, Pujic P, Chertkov O, Teshima H, Bruce DC, Detter C, Tapia R, et al. Genome sequence of "Candidatus Frankia datisciae" Dg1, the uncultured microsymbiont from nitrogen-fixing root nodules of the dicot *Datisca glomerata*. *J Bacteriol* 2011; **193**:7017-7018. [PubMed](#) <http://dx.doi.org/10.1128/JB.06208-11>

20. Cerdeira LT, Schneider MPC, Pinto AC, de Almeida SS, dos Santos AR, Barbosa EGV, Ali A, Aburjaile FF, de Abreu VAC, Guimarães LC, *et al.* Complete genome sequence of *Corynebacterium pseudotuberculosis* strain CIP 52.97, isolated from a horse in Kenya. *J Bacteriol* 2011; **193**:7025-7026. [PubMed](#) <http://dx.doi.org/10.1128/JB.06293-11>
21. Horváth B, Hunyadkürti J, Vörös A, Fekete C, Urbán E, Kemény L, Nagy I. Genome Sequence of *Propionibacterium acnes* Type II Strain ATCC 11828. *J Bacteriol* 2012; **194**:202-203. [PubMed](#) <http://dx.doi.org/10.1128/JB.06388-11>
22. Doroghazi JR, Ju KS, Brown DW, Labeda DP, Deng Z, Metcalf WW, Chen W, Price NPJ. Genome sequences of three tunicamycin-producing *Streptomyces* strains, *S. chartreusis* NRRL 12338, *S. chartreusis* NRRL 3882, and *S. lysosuperificus* ATCC 31396. *J Bacteriol* 2011; **193**:7021-7022. [PubMed](#) <http://dx.doi.org/10.1128/JB.06262-11>
23. Klassen JL, Adams SM, Bramhacharya S, Giles SS, Goodwin LA, Woyke T, Currie CR. Draft genome sequence of *Streptomyces* sp. strain Wigar10, isolated from a surface-sterilized garlic bulb. *J Bacteriol* 2011; **193**:6999-7000. [PubMed](#) <http://dx.doi.org/10.1128/JB.06257-11>
24. Casjens SR, Mongodin EF, Qiu WG, Dunn JJ, Luft BJ, Fraser-Liggett CM, Schutzer SE. Whole-Genome Sequences of two *Borrelia afzelii* and two *Borrelia garinii* Lyme disease agent isolates. *J Bacteriol* 2011; **193**:6995-6996. [PubMed](#) <http://dx.doi.org/10.1128/JB.05951-11>
25. Dehghan S, Liu EB, Seto J, Torres SF, Hudson NR, Kajon AE, Metzgar D, Dyer DW, Chodosh J, Jones MS, *et al.* Five genome sequences of subspecies B1 human adenoviruses associated with acute respiratory disease. *J Virol* 2012; **86**:635-636. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06593-11>
26. Lee JH, Shin H, Son B, Ryu S. Complete genome sequence of *Bacillus cereus* bacteriophage BCP78. *J Virol* 2012; **86**:637-638. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06520-11>
27. Wen L, He K, Yu Z, Mao A, Ni Y, Zhang X, Guo R, Li B, Wang X, Zhou J, *et al.* Complete Genome sequence of a novel porcine Circovirus-like agent. *J Virol* 2012; **86**:639. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06469-11>
28. Nissimov JI, Worthy CA, Rooks P, Napier JA, Kimmance SA, Henn MR, Ogata H, Allen MJ. Draft genome sequence of the Coccolithovirus *Emiliania huxleyi* virus 203. *J Virol* 2011; **85**:13468-13469. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06440-11>
29. Gillette JD, Schupp JM, Balajee SA, Harris J, Pearson T, Yan Y, Keim P, DeBess E, Marsden-Haug N, Wohrle R, *et al.* Whole genome sequence analysis of *Cryptococcus gattii* from the Pacific Northwest reveals unexpected diversity. *PLoS ONE* 2011; **6**:e28550. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0028550>
30. Llop P, Cabrefiga J, Smits THM, Dreö T, Barbé S, Pulawska J, Bultreys A, Blom J, Duffy B, Montesinos E, *et al.* *Erwinia amylovora* novel plasmid pEI70: Complete sequence, biogeography, and role in aggressiveness in the fire blight phytopathogen. *PLoS ONE* 2011; **6**:e28651. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0028651>
31. Wang L, Chen W, Feng Y, Ren Y, Gu Z, Chen H, Wang H, Thomas MJ, Zhang B, Berquin IM, *et al.* Genome characterization of the oleaginous fungus *Mortierella alpina*. *PLoS ONE* 2011; **6**:e28319. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0028319>
32. Canuti M, Eis-Huebinger AM, Deijs M, de Vries M, Drexler JF, Oppong SK, Müller MA, Klose SM, Wellinghausen N, Cottontail VM, *et al.* Two novel parvoviruses in frugivorous new and old world bats. *PLoS ONE* 2011; **6**:e29140. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0029140>
33. Woo PCY, Lau SKP, Liu B, Cai JJ, Chong KTK, Tse H, Kao RYT, Chan CM, Chow WN, Yuen KY. Draft genome sequence of *Penicillium marneffeii* strain PM1. *Eukaryot Cell* 2011; **10**:1740-1741. [PubMed](#) <http://dx.doi.org/10.1128/EC.05255-11>
34. Cornelissen A, Hardies SC, Shaburova OV, Krylov VN, Mattheus W, Kropinski AM, Lavigne R. Complete genome sequence of the giant virus OBP and comparative genome analysis of the diverse  $\phi$ KZ-related phages. *J Virol* 2011. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06330-11>
35. Lee JH, Shin H, Kim H, Ryu S. Complete genome sequence of *Salmonella* bacteriophage SPN3US. *J Virol* 2011; **85**:13470-13471. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06344-11>
36. Woo PCY, Lau SKP, Wong BHL, Wong AYP, Poon RWS, Yuen KY. Complete genome sequence of a novel *Paramyxovirus*, Tailam virus, discovered in Sikkim rats. *J Virol* 2011; **85**:13473-13474. [PubMed](#) <http://dx.doi.org/10.1128/JVI.06356-11>