

## Genome sequences published outside of Standards in Genomic Sciences, March-April 2012

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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*

*Halococcus* hamelinensis, sequence accession PRJNA80845 [1]

“*Methanocella* conradii” HZ254, sequence accession CP003243 [2]

*Thermococcus* litoralis NS-C, sequence accession AHVB00000000 [3]

### Phylum *Crenarchaeota*

Candidatus Nitrosopumilus salaria” BD31, sequence accession AEXL00000000 [4]

Candidatus Nitrosoarchaeum limnia, sequence accession AHJG00000000 [5]

### Phylum *Deinococcus-Thermus*

*Deinococcus* gobiensis, sequence accession CP002536 [6]

### Phylum *Proteobacteria*

*Aggregatibacter actinomycetemcomitans* strain ANH9381, sequence accession CP003099 [7]

*Alishewanella jeotgali*, sequence accession AHTH00000000 [8]

*Enterobacter aerogenes* KCTC 2190, sequence accession CP002824 [9]

*Escherichia coli* O104:H4, sequence accession AFOB02000092 [10]

*Helicobacter pylori* strains 17874, sequence accession PRJNA76569 [11]

*Helicobacter pylori* strains P79, sequence accession PRJNA76567 [11]

*Janthinobacterium* sp. Strain PAMC 25724, sequence accession AHHB00000000 [12]

*Klebsiella oxytoca* KCTC 1686, sequence accession CP003218 [13]

*Klebsiella pneumoniae* subsp. *pneumoniae* HS11286, sequence accession CP003200 (chromosome), CP003223 (plasmid pKPHS1), CP003224 (plasmid pKPHS2), CP003225 (plasmid pKPHS3), CP003226 (plasmid pKPHS4), CP003227 (plasmid pKPHS5), CP003228 (plasmid pKPHS6) [14]

*Oceanimonas* sp. GK1, sequence accession CP003171 [15]

“*Pseudogulbenkiania ferrooxidans*” Strain 2002, sequence accession NZ\_ACIS01000000 [16]

*Pseudomonas extremaustralis* 14-3b, sequence accession AHIP00000000 [17]

*Pseudomonas* sp. Strain PAMC 25886, sequence accession AHHC00000000 [18]

*Psychrobacter*, sequence accession AHVZ00000000 [19]

*Rahnella* sp. Strain Y9602, sequence accession CP002505 [20]

*Rhizobium* sp. Strain PDO1-076, sequence accession AHZC00000000 [21]

*Rhodospirillum photometricum* DSM122, sequence accession HE663493 [22]

“*Rickettsia sibirica sibirica*”, sequence accession AHIZ00000000 [23]

*Rickettsia sibirica* subsp. *mongolitimonae* strain HA-91, sequence accession AHZB00000000 [24]

*Salmonella enterica* subsp. *enterica* Serotype Enteritidis Strain LA5, sequence accession [25]

*Salmonella enterica* subsp. *enterica* Serotype Senftenberg Strain SS209, sequence accession CAGQ00000000 [26]

*Salmonella enterica subsp. enterica* Serovar Typhi P-stx-12, sequence accession CP003278 (chromosome) and CP003279 (plasmid) [27]

*Sphingomonas echinoides* ATCC 14820, sequence accession AHIR00000000 [28]

Strain HIMB55, sequence accession AGIF00000000 [29]

*Vibrio harveyi* CAIM 1792, sequence accession AHHQ00000000 [30]

*Wolbachia* Strain wAlbB, sequence accession CAGB01000001 to CAGB01000165 [31]

*Xanthomonas axonopodis* pv. *punicae* Strain LMG 859, sequence accession CAGJ01000001 to CAGJ01000217 [32]

### Phylum *Tenericutes*

*Mycoplasma hyorhinitidis* Strain GDL-1, sequence accession CP003231 [33]

### Phylum *Firmicutes*

*Bacillus subtilis*, sequence accession BGSCID 3A27 through BGSCID 28A4 [34]

*Clostridium difficile* Strain CD37, sequence accession AHJJ00000000 [35]

*Clostridium perfringens*, sequence accession AFES00000000 [36]

*Lactobacillus fructivorans* KCTC 3543, sequence accession AEQY00000000 [37]

*Lactococcus lactis* IO-1, sequence accession AP012281 [38]

*Lactobacillus plantarum* strain NC8, sequence accession AGR100000000 [39]

*Paenibacillus dendritiformis* C454, sequence accession AHKH00000000 [40]

*Paenibacillus* sp. Strain Aloe-11, sequence accession AGFI00000000 [41]

"*Peptoniphilus rhinitidis*" 1-13<sup>T</sup>, sequence accession BAEW01000001 to BAEW01000056 [42]

*Streptococcus macedonicus* ACA-DC 198, sequence accession HE613569 and HE613570 [43]

*Staphylococcus aureus* VC40, sequence accession CP003033 [44]

*Streptococcus infantarius subsp. infantarius* Strain CJ18, sequence accession CP003295 (chromosome), CP003296 (plasmid) [45]

*Streptococcus macedonicus* ACA-DC 198, sequence accession HE613569 (chromosome), HE613570 (plasmid pSMA198) [46]

### Phylum *Actinobacteria*

*Actinoplanes* sp. SE50/110, sequence accession CP003170 [47]

*Amycolatopsis* sp. Strain ATCC 39116, sequence accession [48]

*Nocardia cyriacigeorgica* GUH-2, sequence accession FO082843 [49]

*Salinibacterium* sp., sequence accession AHWA00000000 [50]

*Streptomyces acidiscabies* 84-104, sequence accession AHBFB00000000 [51]

### Non-Bacterial genomes

Bluetongue Virus Serotype 2, sequence accession AJ783905 (Seg-6) and JQ681257 (Seg-1), JQ681257 (Seg-1), JQ681258 (Seg-2), JQ681259 (Seg-3), JQ681260 (Seg-4), JQ681261 (Seg-5), JQ681262 (Seg-7), JQ6812563 (Seg-8), JQ6812564 (Seg-9), to JQ681265 (Seg-10) [52]

Virus Serotype 1, sequence accession AJ585111 (Seg-2), AJ586659 (Seg-6), JQ282770 (Seg-1), JQ282771 (Seg-3), JQ282772 (Seg-4), JQ282773 (Seg-5), JQ282774 (Seg-7), JQ282775 (Seg-8), JQ282776 (Seg-9), and JQ282777 (Seg-10) [52]

Chloroplast genome of *Erycina pusilla*, sequence accession JF\_746994 [53]

*Danio rerio*, sequence accession JQ434101 [54]

Enterococcal Bacteriophage SAP6, sequence accession JF731128 [55]

*Eubenangee* virus, sequence accession JQ070376 through JQ070385 [56]

Fujian/411-like viruses, sequence accession CY087969 to CY088568 [57]

Hantavirus Variant of Rio Mamoré Virus, Maripa Virus, sequence accession JQ611712 (segment S), JQ611713 (segment M), and JQ611714 (segment L) [58]

*Pata* virus, sequence accession JQ070386 through JQ070395 [59]

Porcine Circovirus 2, sequence accession JQ413808 [60]

Porcine Reproductive and Respiratory Syndrome Virus, sequence accession JQ326271 [61]

*Streptococcus mutans* Phage M102AD, sequence accession DQ386162 [62]

*Tilligery* virus, sequence accession JQ070366 through JQ070375 [63]

## References

1. Burns BP, Gudhka RK, Neilan BA. Genome Sequence of the Halophilic Archaeon *Halococcus hamelinensis*. *J Bacteriol* 2012; **194**:2100-2101. [PubMed](http://dx.doi.org/10.1128/JB.06599-11) <http://dx.doi.org/10.1128/JB.06599-11>
2. Lü Z, Lu Y. Complete Genome Sequence of a Thermophilic Methanogen, *Methanocella conradii* HZ254, Isolated from Chinese Rice Field Soil. *J Bacteriol* 2012; **194**:2398-2399. [PubMed](http://dx.doi.org/10.1128/JB.00207-12) <http://dx.doi.org/10.1128/JB.00207-12>
3. Gardner AF, Kumar S, Perler FB. Genome Sequence of the Model Hyperthermophilic Archaeon *Thermococcus litoralis* NS-C. *J Bacteriol* 2012; **194**:2375-2376. [PubMed](http://dx.doi.org/10.1128/JB.00123-12) <http://dx.doi.org/10.1128/JB.00123-12>
4. Mosier AC, Allen EE, Kim M, Ferriera S, Francis CA. Genome Sequence of "Candidatus Nitrosopumilus salaria" BD31, an Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. *J Bacteriol* 2012; **194**:2121-2122. [PubMed](http://dx.doi.org/10.1128/JB.00013-12) <http://dx.doi.org/10.1128/JB.00013-12>
5. Mosier AC, Allen EE, Kim M, Ferriera S, Francis CA. Genome Sequence of "Candidatus Nitrosoarchaeum limnia" BG20, a Low-Salinity Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. *J Bacteriol* 2012; **194**:2119-2120. [PubMed](http://dx.doi.org/10.1128/JB.00007-12) <http://dx.doi.org/10.1128/JB.00007-12>
6. Yuan M, Chen M, Zhang W, Lu W, Wang J, Yang M, Zhao P, Tang R, Li X, Hao Y, et al. Genome Sequence and Transcriptome Analysis of the Radioresistant Bacterium *Deinococcus gobiensis*. Insights into the Extreme Environmental Adaptations. *PLoS ONE* 2012; **7**:e34458. [PubMed](http://dx.doi.org/10.1371/journal.pone.0034458) <http://dx.doi.org/10.1371/journal.pone.0034458>
7. Chen C, Kittichotirat W, Chen W, Downey JS, Bumgarner R. Genome Sequence of a Serotype B Non-JP2 *Aggregatibacter actinomycetemcomitans* Strain, ANH9381, from a Periodontally Healthy Individual. *J Bacteriol* 2012; **194**:1837. [PubMed](http://dx.doi.org/10.1128/JB.06770-11) <http://dx.doi.org/10.1128/JB.06770-11>
8. Jung J, Chun J, Park W. Genome Sequence of Extracellular-Protease-Producing *Alishewanella jeotgali* Isolated from Traditional Korean Fermented Seafood. *J Bacteriol* 2012; **194**:2097. [PubMed](http://dx.doi.org/10.1128/JB.00153-12) <http://dx.doi.org/10.1128/JB.00153-12>
9. Shin SH, Kim S, Kim JY, Lee S, Um Y, Oh MK, Kim YR, Lee J, Yang KS. Complete Genome Sequence of *Enterobacter aerogenes* KCTC 2190. *J Bacteriol* 2012; **194**:2373-2374. [PubMed](http://dx.doi.org/10.1128/JB.00028-12) <http://dx.doi.org/10.1128/JB.00028-12>
10. Scholl D, Gebhart D, Williams SR, Bates A, Mandrell R. Genome Sequence of *E. coli* O104:H4 Leads to Rapid Development of a Targeted Antimicrobial Agent against This Emerging Pathogen. *PLoS ONE* 2012; **7**:e33637. [PubMed](http://dx.doi.org/10.1371/journal.pone.0033637) <http://dx.doi.org/10.1371/journal.pone.0033637>
11. Clancy CD, Forde BM, Moore SA, O'Toole PW. Draft Genome Sequences of *Helicobacter pylori* Strains 17874 and P79. *J Bacteriol* 2012; **194**:2402. [PubMed](http://dx.doi.org/10.1128/JB.00230-12) <http://dx.doi.org/10.1128/JB.00230-12>
12. Kim SJ, Shin SC, Hong SG, Lee YM, Lee H, Lee J, Choi IG, Park H. Genome Sequence of *Janthinobacterium* sp. Strain PAMC 25724, Isolated from Alpine Glacier Cryoconite. *J Bacteriol* 2012; **194**:2096. [PubMed](http://dx.doi.org/10.1128/JB.00096-12) <http://dx.doi.org/10.1128/JB.00096-12>
13. Shin SH, Kim S, Kim JY, Lee S, Um Y, Oh MK, Kim YR, Lee J, Yang KS. Complete Genome Sequence of *Klebsiella oxytoca* KCTC 1686, Used in Production of 2,3-Butanediol. *J Bacteriol* 2012; **194**:2371-2372. [PubMed](http://dx.doi.org/10.1128/JB.00026-12) <http://dx.doi.org/10.1128/JB.00026-12>
14. Liu P, Li P, Jiang X, Bi D, Xie Y, Tai C, Deng Z, Rajakumar K, Ou HY. Complete Genome Sequence of *Klebsiella pneumoniae* Subsp. *pneumoniae* HS11286, a Multidrug-Resistant Strain Isolated from Human Sputum. *J Bacteriol* 2012; **194**:1841-1842. [PubMed](http://dx.doi.org/10.1128/JB.00043-12) <http://dx.doi.org/10.1128/JB.00043-12>
15. Parsa Yeganeh L, Azarbaijani R, Sarikhan S, Mousavi H, Ramezani M, Amoozegar MA, Shahzadeh Fazeli A, Hosseini Salekdeh G. Complete Genome Sequence of *Oceanimonas* sp. GK1, a Halotolerant Bacterium from Gavkhouni Wetland in Iran. *J Bacteriol* 2012; **194**:2123-2124. [PubMed](http://dx.doi.org/10.1128/JB.00023-12) <http://dx.doi.org/10.1128/JB.00023-12>
16. Byrne-Bailey KG, Weber KA, Coates JD. Draft Genome Sequence of the Anaerobic, Nitrate-Dependent, Fe(II)-Oxidizing Bacterium *Pseudogulbenkiania ferrooxidans* Strain 2002. *J Bacteriol* 2012; **194**:2400-2401. [PubMed](http://dx.doi.org/10.1128/JB.00214-12) <http://dx.doi.org/10.1128/JB.00214-12>
17. Tribelli PM, Raiger lustman LJ, Catone MV, Di Martino C, Revale S, Méndez BS, López NI. Genome Sequence of the Polyhydroxybutyrate Producer *Pseudomonas extremaustralis*, a Highly Stress-Resistant Antarctic Bacterium. *J Bacteriol* 2012; **194**:2381-2382. [PubMed](http://dx.doi.org/10.1128/JB.00172-12) <http://dx.doi.org/10.1128/JB.00172-12>

18. Shin SC, Kim SJ, Hong SG, Ahn DH, Lee YM, Lee H, Lee J, Park H. Genome Sequence of *Pseudomonas* sp. Strain PAMC 25886, Isolated from Alpine Glacial Cryoconite. *J Bacteriol* 2012; **194**:1844. [PubMed](#) <http://dx.doi.org/10.1128/JB.00057-12>
19. Kim SJ, Shin SC, Hong SG, Lee YM, Choi IG, Park H. Genome Sequence of a Novel Member of the Genus *Psychrobacter* Isolated from Antarctic Soil. *J Bacteriol* 2012; **194**:2403. [PubMed](#) <http://dx.doi.org/10.1128/JB.00234-12>
20. Martinez RJ, Bruce D, Detter C, Goodwin LA, Han J, Han CS, Held B, Land ML, Mikhailova N, Nolan M, et al. Complete Genome Sequence of *Rahnella* sp. Strain Y9602, a Gammaproteobacterium Isolate from Metal- and Radionuclide-Contaminated Soil. *J Bacteriol* 2012; **194**:2113-2114. [PubMed](#) <http://dx.doi.org/10.1128/JB.00095-12>
21. Brown SD, Klingeman DM, Lu TYS, Johnson CM, Utturkar SM, Land ML, Schadt CW, Doktycz MJ, Pelletier DA. Draft Genome Sequence of *Rhizobium* sp. Strain PDO1-076, a Bacterium Isolated from *Populus Deltoides*. *J Bacteriol* 2012; **194**:2383-2384. [PubMed](#) <http://dx.doi.org/10.1128/JB.00198-12>
22. Duquesne K, Sturgis JN. Shotgun Genome Sequence of the Large Purple Photosynthetic Bacterium *Rhodospirillum photometricum* DSM122. *J Bacteriol* 2012; **194**:2380. [PubMed](#) <http://dx.doi.org/10.1128/JB.00168-12>
23. Sentausa E, El Karkouri K, Robert C, Raoult D, Fournier PE. Sequence and Annotation of *Rickettsia sibirica sibirica* Genome. *J Bacteriol* 2012; **194**:2377. [PubMed](#) <http://dx.doi.org/10.1128/JB.00150-12>
24. Sentausa E, El Karkouri K, Robert C, Raoult D, Fournier PE. Genome Sequence of "*Rickettsia sibirica* subsp. mongolitimonaе.". *J Bacteriol* 2012; **194**:2389-2390. [PubMed](#) <http://dx.doi.org/10.1128/JB.00239-12>
25. Grépinet O, Rossignol A, Loux V, Chiapello H, Gendrault A, Gibrat JF, Velge P, Virlogeux-Payant I. Genome Sequence of the Invasive *Salmonella enterica* subsp. *enterica* Serotype Enteritidis Strain LA5. *J Bacteriol* 2012; **194**:2387-2388. [PubMed](#) <http://dx.doi.org/10.1128/JB.00256-12>
26. Grépinet O, Boumart Z, Virlogeux-Payant I, Loux V, Chiapello H, Gendrault A, Gibrat JF, Chemaly M, Velge P. Genome Sequence of the Persistent *Salmonella enterica* Subsp. *Enterica* Serotype Senftenberg Strain SS209. *J Bacteriol* 2012; **194**:2385-2386. [PubMed](#) <http://dx.doi.org/10.1128/JB.00255-12>
27. Ong SY, Pratap CB, Wan X, Hou S, Abdul Rahman AY, Saito JA, Nath G, Alam M. Complete Genome Sequence of *Salmonella enterica* subsp. *Enterica* Serovar Typhi P-Stx-12. *J Bacteriol* 2012; **194**:2115-2116. [PubMed](#) <http://dx.doi.org/10.1128/JB.00121-12>
28. Shin SC, Kim SJ, Ahn DH, Lee JK, Park H. Draft genome sequence of *Sphingomonas echinoides* ATCC 14820. *J Bacteriol* 2012; **194**:1843. [PubMed](#) <http://dx.doi.org/10.1128/JB.00046-12>
29. Huggett MJ, Rappé MS. Genome sequence of strain HIMB55, a novel marine Gammaproteobacterium of the OM60/NOR5 Clade. *J Bacteriol* 2012; **194**:2393-2394. [PubMed](#) <http://dx.doi.org/10.1128/JB.00171-12>
30. Espinoza-Valles I, Soto-Rodríguez S, Edwards RA, Wang Z, Vora GJ, Gómez-Gil B. Draft genome sequence of the shrimp pathogen *Vibrio harveyi* CAIM 1792. *J Bacteriol* 2012; **194**:2104. [PubMed](#) <http://dx.doi.org/10.1128/JB.00079-12>
31. Mavingui P, Valiente Moro C, Tran-Van V, Wisniewski-Dyé F, Raquin V, Minard G, Tran FH, Voronin D, Rouy Z, Bustos P, et al. Whole-Genome sequence of *Wolbachia* strain wAlbB, an endosymbiont of Tiger mosquito vector *Aedes albopictus*. *J Bacteriol* 2012; **194**:1840. [PubMed](#) <http://dx.doi.org/10.1128/JB.00036-12>
32. Sharma V, Midha S, Ranjan M, Pinnaka AK, Patil PB. Genome Sequence of *Xanthomonas axonopodis* Pv. *Punicae* Strain LMG 859. *J Bacteriol* 2012; **194**:2395. [PubMed](#) <http://dx.doi.org/10.1128/JB.00181-12>
33. Calcutt MJ, Foecking MF, Rosales RS, Ellis RJ, Nicholas RAJ. Genome sequence of *Mycoplasma hyorhinis* Strain GDL-1. *J Bacteriol* 2012; **194**:1848. [PubMed](#) <http://dx.doi.org/10.1128/JB.00033-12>
34. Earl AM, Eppinger M, Fricke WF, Rosovitz MJ, Rasko DA, Daugherty S, Losick R, Kolter R, Ravel J. Whole-Genome sequences of *Bacillus subtilis* and close relatives. *J Bacteriol* 2012; **194**:2378-2379. [PubMed](#) <http://dx.doi.org/10.1128/JB.05675-11>
35. Brouwer MSM, Allan E, Mullany P, Roberts AP. Draft genome sequence of the Nontoxigenic *Clostridium difficile* Strain CD37. *J Bacteriol* 2012; **194**:2125-2126. [PubMed](#) <http://dx.doi.org/10.1128/JB.00122-12>

36. Nowell VJ, Kropinski AM, Songer JG, MacInnes JI, Parreira VR, Prescott JF. Genome sequencing and analysis of a Type A *Clostridium perfringens* isolate from a case of bovine clostridial abomasitis. *PLoS ONE* 2012; **7**:e32271. [PubMed](#) <http://dx.doi.org/10.1371/journal.pone.0032271>
37. Nam SH, Choi SH, Kang A, Lee KS, Kim DW, Kim RN, Kim DS, Park HS. Genome sequence of *Lactobacillus fructivorans* KCTC 3543. *J Bacteriol* 2012; **194**:2111. [PubMed](#) <http://dx.doi.org/10.1128/JB.00075-12>
38. Kato H, Shiwa Y, Oshima K, Machii M, Araya-Kojima T, Zendo T, Shimizu-Kadota M, Hattori M, Sonomoto K, Yoshikawa H. Complete genome sequence of *Lactococcus lactis* IO-1, a lactic acid bacterium that utilizes xylose and produces high levels of L-Lactic acid. *J Bacteriol* 2012; **194**:2102-2103. [PubMed](#) <http://dx.doi.org/10.1128/JB.00074-12>
39. Axelsson L, Rud I, Naterstad K, Blom H, Renckens B, Boekhorst J, Kleerebezem M, Van Hijum S, Siezen RJ. Genome sequence of the naturally plasmid-free *Lactobacillus plantarum* strain NC8 (CCUG 61730). *J Bacteriol* 2012; **194**:2391-2392. [PubMed](#) <http://dx.doi.org/10.1128/JB.00141-12>
40. Sirota-Madi A, Olender T, Helman Y, Brainis I, Finkelshtein A, Roth D, Hagai E, Leshkowitz D, Brodsky L, Galatenko V, et al. Genome sequence of the pattern-forming social bacterium *Paenibacillus dendritiformis* C454 chiral morphotype. *J Bacteriol* 2012; **194**:2127-2128. [PubMed](#) <http://dx.doi.org/10.1128/JB.00158-12>
41. Li NZ, Xia T, Xu YL, Qiu RR, Xiang H, He D, Peng YY. Genome sequence of *Paenibacillus* sp. strain aloe-11, an endophytic bacterium with broad antimicrobial activity and intestinal colonization ability. *J Bacteriol* 2012; **194**:2117-2118. [PubMed](#) <http://dx.doi.org/10.1128/JB.00087-12>
42. Kim DS, Jung MY, Kang A, Cho J, Sin Y, Paek J, Kim DW, Kim RN, Nam SH, Kim A, et al. Genome sequence of *Peptoniphilus rhinitidis* 1-13<sup>T</sup>, an anaerobic coccus strain isolated from clinical specimens. *J Bacteriol* 2012; **194**:2405-2406. [PubMed](#) <http://dx.doi.org/10.1128/JB.00192-12>
43. Papadimitriou K, Ferreira S, Papandreou NC, Mavrogonatou E, Supply P, Pot B, Tsakalidou E. Complete genome sequence of the dairy isolate *Streptococcus macedonicus* ACA-DC 198. *J Bacteriol* 2012; **194**:1838-1839. [PubMed](#) <http://dx.doi.org/10.1128/JB.06804-11>
44. Sass P, Berscheid A, Jansen A, Oedenkoven M, Szekat C, Strittmatter A, Gottschalk G, Bierbaum G. Genome sequence of *Staphylococcus aureus* VC40, a vancomycin- and daptomycin-resistant strain, to study the genetics of development of resistance to currently applied last-resort antibiotics. *J Bacteriol* 2012; **194**:2107-2108. [PubMed](#) <http://dx.doi.org/10.1128/JB.06631-11>
45. Jans C, Follador R, Lacroix C, Meile L, Stevens MJA. Complete genome sequence of the african dairy isolate *Streptococcus infantarius subsp. infantarius* Strain CJ18. *J Bacteriol* 2012; **194**:2105-2106. [PubMed](#) <http://dx.doi.org/10.1128/JB.00160-12>
46. Papadimitriou K, Ferreira S, Papandreou NC, Mavrogonatou E, Supply P, Pot B, Tsakalidou E. Complete genome sequence of the dairy isolate *Streptococcus macedonicus* ACA-DC 198. *J Bacteriol* 2012; **194**:1838-1839. [PubMed](#) <http://dx.doi.org/10.1128/JB.06804-11>
47. Schwientek P, Szczepanowski R, Ruckert C, Kalinowski J, Klein A, Selber K, Wehmeier UF, Stoye J, Puhler A. The complete genome sequence of the acarbose producer *Actinoplanes* sp. SE50/110. *BMC Genomics* 2012; **13**:112. [PubMed](#) <http://dx.doi.org/10.1186/1471-2164-13-112>
48. Davis JR, Goodwin LA, Woyke T, Teshima H, Bruce D, Detter C, Tapia R, Han S, Han J, Pitluck S, et al. Genome sequence of *Amycolatopsis* Sp. Strain ATCC 39116, a plant biomass-degrading actinomycete. *J Bacteriol* 2012; **194**:2396-2397. [PubMed](#) <http://dx.doi.org/10.1128/JB.00186-12>
49. Zoropogui A, Pujic P, Normand P, Barbe V, Beaman B, Beaman L, Boiron P, Colinon C, Deredjian A, Graindorge A, et al. Genome sequence of the human- and animal-pathogenic strain *Nocardia cyriacigeorgica* GUH-2. *J Bacteriol* 2012; **194**:2098-2099. [PubMed](#) <http://dx.doi.org/10.1128/JB.00161-12>
50. Shin SC, Kim SJ, Ahn DH, Lee JK, Lee H, Lee J, Hong SG, Lee YM, Park H. Genome sequence of a *Salinibacterium* sp. isolated from antarctic soil. *J Bacteriol* 2012; **194**:2404. [PubMed](#) <http://dx.doi.org/10.1128/JB.00235-12>
51. Huguet-Tapia JC, Loria R. Draft genome sequence of *Streptomyces acidiscabies* 84-104, an emergent plant pathogen. *J Bacteriol* 2012; **194**:1847. [PubMed](#) <http://dx.doi.org/10.1128/JB.06767-11>
52. Maan NS, Maan S, Guimera M, Pullinger G, Singh KP, Nomikou K, Belaganahalli MN, Mertens PPC. Complete genome sequence of an isolate of Bluetongue Virus Serotype 2, demonstrating circulation of a western topotype in

- southern India. *J Virol* 2012; **86**:5404-5405. [PubMed http://dx.doi.org/10.1128/JVI.00420-12](http://dx.doi.org/10.1128/JVI.00420-12)
53. Pan IC, Liao DC, Wu FH, Daniell H, Singh ND, Chang C, Shih MC, Chan MT, Lin CS. Complete chloroplast genome sequence of an orchid model plant candidate. *Erycina pusilla* apply in tropical Oncidium breeding. *PLoS ONE* 2012; **7**:e34738. [PubMed http://dx.doi.org/10.1371/journal.pone.0034738](http://dx.doi.org/10.1371/journal.pone.0034738)
54. Voz ML, Coppieeters W, Manfroid I, Baudhuin A, Von Berg V, Charlier C, Meyer D, Driever W, Martial JA, Peers B. Fast homozygosity mapping and identification of a zebrafish ENU-induced mutation by whole-genome sequencing. *PLoS ONE* 2012; **7**:e34671. [PubMed http://dx.doi.org/10.1371/journal.pone.0034671](http://dx.doi.org/10.1371/journal.pone.0034671)
55. Lee YD, Park JH. Complete genome sequence of enterococcal bacteriophage SAP6. *J Virol* 2012; **86**:5402-5403. [PubMed http://dx.doi.org/10.1128/JVI.00321-12](http://dx.doi.org/10.1128/JVI.00321-12)
56. Belaganahalli MN, Maan S, Maan NS, Nomikou K, Pritchard I, Lunt R, Kirkland PD, Attoui H, Brownlie J, Mertens PPC. Full genome sequencing and genetic characterization of Eubenangee viruses identify pata virus as a distinct species within the genus Orbivirus. *PLoS ONE* 2012; **7**:e31911. [PubMed http://dx.doi.org/10.1371/journal.pone.0031911](http://dx.doi.org/10.1371/journal.pone.0031911)
57. Galiano M, Johnson BF, Myers R, Ellis J, Daniels R, Zambon M. Fatal cases of influenza A(H3N2) in children. Insights from whole genome sequence analysis. *PLoS ONE* 2012; **7**:e33166. [PubMed http://dx.doi.org/10.1371/journal.pone.0033166](http://dx.doi.org/10.1371/journal.pone.0033166)
58. Matheus S, Lavergne A, De Thoisy B, Dussart P, Lacoste V. Complete genome sequence of a novel Hantavirus variant of Rio Mamoré virus, Maripa virus, from French Guiana. *J Virol* 2012; **86**:5399. [PubMed http://dx.doi.org/10.1128/JVI.00337-12](http://dx.doi.org/10.1128/JVI.00337-12)
59. Belaganahalli MN, Maan S, Maan NS, Nomikou K, Pritchard I, Lunt R, Kirkland PD, Attoui H, Brownlie J, Mertens PPC. Full genome sequencing and genetic characterization of Eubenangee viruses identify pata virus as a distinct species within the genus Orbivirus. *PLoS ONE* 2012; **7**:e31911. [PubMed http://dx.doi.org/10.1371/journal.pone.0031911](http://dx.doi.org/10.1371/journal.pone.0031911)
60. Li B, Ma J, Liu Y, Wen L, Yu Z, Ni Y, Zhang X, Zhou J, Guo R, Wang X, et al. Complete genome sequence of a highly prevalent Porcine Circovirus 2 isolated from piglet stool samples in China. *J Virol* 2012; **86**:4716. [PubMed http://dx.doi.org/10.1128/JVI.00268-12](http://dx.doi.org/10.1128/JVI.00268-12)
61. Song T, Fang L, Zeng S, Li B, Chen H, Xiao S. Complete genome sequence of porcine reproductive and respiratory syndrome virus isolated from piglet stool samples. *J Virol* 2012; **86**:4040-4041. [PubMed http://dx.doi.org/10.1128/JVI.00055-12](http://dx.doi.org/10.1128/JVI.00055-12)
62. Delisle AL, Guo M, Chalmers NI, Barcak GJ, Rousseau GM, Moineau S. Biology and genome sequence of *Streptococcus mutans* phage M102AD. *Appl Environ Microbiol* 2012; **78**:2264-2271. [PubMed http://dx.doi.org/10.1128/AEM.07726-11](http://dx.doi.org/10.1128/AEM.07726-11)
63. Belaganahalli MN, Maan S, Maan NS, Nomikou K, Pritchard I, Lunt R, Kirkland PD, Attoui H, Brownlie J, Mertens PPC. Full genome sequencing and genetic characterization of Eubenangee viruses identify Pata virus as a distinct species within the genus Orbivirus. *PLoS ONE* 2012; **7**:e31911. [PubMed http://dx.doi.org/10.1371/journal.pone.0031911](http://dx.doi.org/10.1371/journal.pone.0031911)