

## SYSTEMS

1. Markowitz VM, Korzeniewski F, Palaniappan K, Szeto E, Ivanova N, Kyrpides NC. (2005) The Integrated Microbial Genomes (IMG) System, A Case Study in Biological Data Management, Proc. of 31st *Int. Conf. on Very Large Data Bases*.
2. Markowitz VM, Korzeniewski F, Palaniappan K, Szeto E, Werner G, Padki A, Zhao X, Dubchak I, Hugenholtz P, Anderson I, Mavromatis K, Ivanova N, Kyrpides NC. (2006) The Integrated Microbial Genomes (IMG) system. *Nucleic Acids Research*, 34: D344-D348.
3. Markowitz, V.M. and Kyrpides, N. (2007) Comparative Genome Analysis in the Integrated Microbial Genomes (IMG) System, book chapter in *Comparative Genomics*, Vol. 1, Bergman (ed.), Humana Press Inc.
4. Markowitz VM, Szeto E, Palaniappan K, Grechkin Y, Chu K, Chen I-M, Dubchak I, Anderson I, Lykidis A, Mavromatis K, Ivanova N, Kyrpides NC. (2008) The Integrated Microbial Genomes (IMG) system in 2007: data content and analysis tool extensions. *Nucleic Acids Research*, 38.
5. Angiuoli, S.V., Gusmman, A., Klimke, W., Cochrane, G., Field, D., Garrity, G., Kodira, C.D., Kyrpides, N.C., Madupu, R., Markowitz, V.M., Tatusova, T., Thomson, N., White, O. (2008) Toward an Online Repository of Standard Operating Procedures (SOPs) for (Meta)genomic Annotation, OMICS **12** (2).
6. Hirschman, L., Clark, C., Cohen, B., Mardis, S., Luciano, J., Kottmann, R., Cole, J., Markowitz, V.M., Kyrpides, N.C., Field, D. (2008) Habitat-Lite: A GSC Case Study Based on Free Text Terms for Environmental Metadata, OMICS **12** (2).

## BIOLOGY

### 2005

1. Feil H, Feil WS, Chain P, Larimer F, DiBartolo G, et al. (2005) Comparison of the complete genome sequences of *Pseudomonas syringae* pv. *syringae* B728a and pv. *tomato* DC3000. *PNAS*, 102(31): 11064-11069.
2. Selmer T, Pierik AJ, Heider J. (2005) New glycyl radical enzymes catalysing key metabolic steps in anaerobic bacteria. *Biol Chem.* 386(10):981-8.
3. Ren J, Kotaka M, Lockyer M, Lamb HK, Hawkins AR, Stammers DK. (2005) GTP cyclohydrolase II structure and mechanism. *J Biol Chem.* 280(44):36912-9
4. Groh JL, Luo Q, Ballard JD, Krumholz LR. (2005) A method adapting microarray technology for signature-tagged mutagenesis of *Desulfovibrio desulfuricans* G20 and *Shewanella oneidensis* MR-1 in anaerobic sediment survival experiments. *Appl Environ Microbiol.* 71(11):7064-74.

5. Lupa, B., Lyon, D., Gibbs, M.D., Reeves, R.A., Wiegel, J. (2005) Distribution of genes encoding the microbial non-oxidative reversible hydroxyarylic acid decarboxylases/phenol carboxylases, *Genomics* **86**(3), 342-351.

## 2006

1. Starkenburg SR, Chain PSG, Sayavedra-Soto LA, Hauser L, Land ML, et al. (2006) Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium Nitrobacter winogradskyi Nb-255. *Applied and Environmental Microbiology*, 72 (3): 2050-2063.
2. Mavromatis K, Kuyler DC, Lykidis A, Ivanova N, Francino P, et al. (2006) The genome of obligately intracellular Ehrlichia canis reveals themes of complex membrane structure and immune evasion strategies. *Journal of Bacteriology* 189:4015-4023.
3. Klotz MG, Arp DJ, Chain PS, El-Sheikh AF, Hauser LJ, et al. (2006) Free in PMC Complete genome sequence of the marine, chemolithoautotrophic, ammonia-oxidizing bacterium Nitrosococcus oceani ATCC 19707. *Appl Environ Microbiol.* 72(9):6299-315.
4. Scott KM, Sievert SM, Abril FN, Ball LA, Barrett CJ, et al. (2006) Free in PMC The genome of deep-sea vent chemolithoautotroph Thiomicrospira crunogena XCL-2. *PLoS Biol.* 4(12):e383.
5. Beller HR, Chain PS, Letain TE, Chakicherla A, Larimer FW, Richardson PM, Coleman MA, Wood AP, Kelly DP. (2006) The genome sequence of the obligately chemolithoautotrophic, facultatively anaerobic bacterium Thiobacillus denitrificans. *J Bacteriol.* 188(4):1473-88.
6. Scott KM, Sievert SM, Abril FN, et al. (2006) The genome of deep-sea vent chemolithoautotroph Thiomicrospira crunogena XCL-2. *PLoS Biol.* 4 (12): 2196-2212
7. Ashby MK. (2006) Distribution, structure and diversity of "bacterial" genes encoding two-component proteins in the Euryarchaeota. *Archaea.* 2(1):11-30
8. Ashby MK, Houmard J. (2006) Cyanobacterial two-component proteins: structure, diversity, distribution, and evolution. *Microbiol Mol Biol Rev.* 70(2):472-509
9. Nichols CE, Sainsbury S, Berrow NS, Alderton D, Saunders NJ, Stammers DK, Owens RJ. (2006) Structure of the PII signal transduction protein of Neisseria meningitidis at 1.85 Å resolution. *Acta Crystallograph Sect F Struct Biol Cryst Commun.* 62(Pt 6):494-7
10. Liang C, Zhao F, Wei W, Wen Z, Qin S. (2006) Carotenoid biosynthesis in cyanobacteria: structural and evolutionary scenarios based on comparative genomics. *Int J Biol Sci.* 2(4):197-207.

11. Sun S, Gan JH, Paynter JJ, Tucker SJ. (2006) Cloning and functional characterization of a superfamily of microbial inwardly rectifying potassium channels. *Physiol Genomics*. 26(1):1-7.
12. Lau WW, Armbrust EV. (2006) Detection of glycolate oxidase gene glcD diversity among cultured and environmental marine bacteria. *Environ Microbiol*. 8(10):1688-702
13. Liang Y, Gardner DR, Miller CD, Chen D, Anderson AJ, Weimer BC, Sims RC. (2006) Study of biochemical pathways and enzymes involved in pyrene degradation by *Mycobacterium* sp. strain KMS. *Appl Environ Microbiol*. 72(12):7821-8
14. Argueta C, Yuksek K, Patel R, Summers ML. (2006) Identification of *Nostoc punctiforme* akinete-expressed genes using differential display. *Mol Microbiol*. 61(3):748-57
15. Hensen D, Sperling D, Truper HG, Brune DC, Dahl C. (2006) Thiosulphate oxidation in the phototrophic sulphur bacterium *Allochromatium vinosum*. *Mol Microbiol*. 62(3):794-810.
16. Friedrich U, Lenke J. (2006) Improved enumeration of lactic acid bacteria in mesophilic dairy starter cultures by using multiplex quantitative real-time PCR and flow cytometry-fluorescence in situ hybridization. *Appl Environ Microbiol*. 72(6):4163-71.
17. Worden AZ, Cuvelier ML & DH Bartlett (2006). In-depth marine microbial community genomics. *TRENDS in Microbiology*. Vol. 14:331-336.
18. Dyhrman, S.T., Chappell, P.D., Haley, S.T., Moffett, J.W., Orchard, E.D., Waterbury, J.B, Webb, E.A. (2006) Phosphonate utilization by the globally important marine diazotroph *Trichodesmium*, *Nature* **439**.
19. Lu, Y.J., Zhang, Y.M., Grimes, K.D., Qi, J., Lee, R.E., Rock, C.O. (2006) Acyl-Phosphates Initiate Membrane Phospholipid Synthesis in Gram-Positive Pathogens, *Molecular Cell* **23**, 765-772.
20. Chain, P., Denef, V.J., et al. (2006) *Burkholderia xenovorans* LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility, *PNAS* **103**(42), 15280-15287.
21. Halam, S.J., Konstantinidis, K.T., Putnam, N., Schleper, C. et al. (2006) Genomic analysis of the uncultivated marine crenarchaeote *Cenarchaeum symbiosum*, *PNAS* **103**(48), 18296-18301.
22. Culley, D.E., Kovacik, W.P., Brockman, F.J., Zhang, W. (2006) Optimization of RNA isolation from the archaebacterium *Methanosaarcina barkeri* and validation for oligonucleotide microarray analysis, *Journal of Microbiological Methods* **67**(1), 36-43.
23. Bryant, D.A., Frigaard, N.U. (2006) Prokaryotic photosynthesis and phototrophy illuminated, *Trends in Microbiology* **14**(11), 488-496.

24. Chew, A.G.M. and Bryant, D.A. (2006) Characterization of Plant-Like Protochlorophyllide A Divinyl Reductase in Green Sulfur Bacteria, *Journal of Biological Chemistry*.
25. Gralnick, J.A., Vali, H., Lies, D.P., Newman, D.K. (2006) Extracellular respiration of dimethyl sulfoxide by *Shewanella oneidensis* strain MR-1, *PNAS* **103**(12), 4669-4674.
26. Wu, Q., Pei, J., Turse, C., Ficht, T.A. (2006) Mariner mutagenesis of *Brucella melitensis* reveals genes with previously uncharacterized roles in virulence and survival, *BMC Microbiology* **6**:102.

## 2007

1. Maeder DL, Anderson A, Brettin TS, Bruce DC, Gilna P, et al. (2007) The Methanosaerica barkeri Genome: Comparative Analysis with Methanosaerica acetivorans and Methanosaerica mazei Reveals Extensive Rearrangement within Methanosaericinal Genomes. *Journal of Bacteriology* 188(22): 7922-7931.
2. Morth, J.P., Gosmann, S., Nowak, E., and Tucker, P.A. (2007) A novel two-component system found in *Mycobacterium tuberculosis* Federation of European Biochemical Societies (FEBS) Letters 579 (19), 4145-4148.
3. Lykidis A, Mavromatis K, Ivanova N, Anderson I, Land M, et al. (2007) Genome sequence and analysis of soil cellulolytic actinomycete *Tthermobifida fusca* YX. *Journal of Bacteriology*, 189(6): 2477-2486.
4. Normand P, Lapierre P, Tisa LS, Gogarten JP, Alloisio N, et al. (2007) Genome characteristics of facultatively symbiotic Frankia sp. strains reflect host range and host plant biogeography. *Genome Res.* 17(1):7-15.
5. Kerfeld CA, Simons RW (2007) The undergraduate genomics research initiative. *PLoS Biol.* (5): 980-983 .
6. Normand P, Lapierre P, Tisa LS, et al. (2007) Genome characteristics of facultatively symbiotic Frankia sp strains reflect host range and host plant biogeography. *Genome Res.* 17 (1): 7-15.
7. Zhao F, Qin S. (2007) Comparative molecular population genetics of phycoerythrin locus in Prochlorococcus. *Genetica*. 129(3):291-9
8. Kim SJ, Kweon O, Jones RC, Freeman JP, Edmondson RD, Cerniglia CE. (2007) Complete and integrated pyrene degradation pathway in *Mycobacterium vanbaalenii* PYR-1 based on systems biology. *J Bacteriol.* 189(2):464-72.
9. Rodrigues DF, Tiedje JM. (2007) Multi-locus real-time PCR for quantitation of bacteria in the environment reveals *Exiguobacterium* to be prevalent in permafrost. *FEMS Microbiol Ecol.* 59(2):489-99
10. Chew AG, Bryant DA. (2007) Characterization of a plant-like protochlorophyllide a divinyl reductase in green sulfur bacteria. *J Biol Chem.* 282(5):2967-75

11. Kim HJ, Nam HS, Anderson AJ, Yang KY, Cho BH, Kim YC. (2007) Mutation in the edd gene encoding the 6-phosphogluconate dehydratase of *Pseudomonas chlororaphis* O6 impairs root colonization and is correlated with reduced induction of systemic resistance. *Lett Appl Microbiol.* 44(1):56-61.
12. Chen F, Wang K, Stewart J, Belas R. (2007) Free in PMC Induction of multiple prophages from a marine bacterium: a genomic approach. *Appl Environ Microbiol.* 72(7):4995-5001.
13. Xu Y, Labedan B, Glansdorff N. (2007) Surprising arginine biosynthesis: a reappraisal of the enzymology and evolution of the pathway in microorganisms. *Microbiol Mol Biol Rev.* 71(1):36-47.
14. Fischer WW, Pearson A. (2007) Hypotheses for the origin and early evolution of triterpenoid cyclases. *Geobiology* 5(1):19-34.
15. Xie G, Bruce DC, Challacombe JF, Chertkov O, et al. (2007) Genome sequence of the cellulolytic gliding bacterium *Cytophaga hutchinsonii*. *Applied and Environmental Microbiology* 73 (11):3536-46.
16. Fuhrer, T., Chen, L., Sauer, U., Vitkup, D. (2007) Computational Prediction and Experimental Verification of the Gene Encoding the NAD+/NADP+-Dependent Succinate Semialdehyde Dehydrogenase in *Escherichia coli*, *Journal of Bacteriology* 189(22), 8073-8078.
17. Yu, M., Faan, Y.W., Chung, W.Y.C., Tsang, J.S.H. (2007) Isolation and Characterization of a Novel Haloacid Permease from *Burkholderia cepacia* MBA4, *Applied and Environmental Microbiology*, Vol. 73, No. 15, p. 4874-4880.
18. Passel, M.W.J., Smillie, C.S., Ochman, H. (2007) Gene decay in archaea. *Archaea* 2, 137-143.
19. Achour, A.R., Billard, P.B. (2007) Diversity of arsenite transporter genes from arsenic-resistant soil bacteria. *Research in Microbiology* 158(2), 128-137.
20. Kehrer D, Ahmed H, Brinkmann H, Siebers B. (2007) Glycerate kinase of the hyperthermophilic archaeon *Thermoproteus tenax*: new insights into the phylogenetic distribution and physiological role of members of the three different glycerate kinase classes. *BMC Genomics.* 8:301.
21. Simmons SL, Bazylinski DA, Edwards KJ. (2007) Population dynamics of marine magnetotactic bacteria in a meromictic salt pond described with qPCR. *Environmental Microbiology* 9(9):2162-74.
22. Gendlina I, Held KG, Bartra SS, Gallis BM, Doneanu CE, Goodlett DR, Plano GV, Collins CM. (2007) Identification and type III-dependent secretion of the *Yersinia pestis* insecticidal-like proteins. *Mol Microbiol.* 64(5):1214-27.
23. Frigaard, N.U., and Bryant, D.A. (2007) Genomic and Evolutionary Perspectives on Sulfur Metabolism in Green Sulfur Bacteria. In *Microbial Sulfur Metabolism*, Springer, 60-76.

24. Galindo, E., Pena, C., Nunez, C., Segura, D., Espin, G. (2007) Molecular and bioengineering strategies to improve alginate and polyhydroxyalkanoate production by *Azotobacter vinelandii*, *Microbial Cell Factories* **6**: 7.
25. Udwary, D.W., Zeigler, L., Asolkar, R.N., Singan, V. et al. (2007) Genome sequencing reveals complex secondary metabolome in the marine actinomycete *Salinispora tropica*, *PNAS* **104**(25), 10376-10381.
26. Schell, M.A., Ulrich, R.L., Ribot, W.J., et al. (2007) Type VI secretion is a major virulence determinant in *Burkholderia mallei*, *Molecular Microbiology* **64** (6) , 1466–1485.
27. Grabov A. (2007) Plant KT/KUP/HAK Potassium Transporters: Single Family – Multiple Functions, *Annals of Botany* **99**(6):1035-1041.
28. N. Vermeulen, M.G. Gänzle, R.F. Vogel (2007) Glutamine deamidation by cereal-associated lactic acid bacteria, *Journal of Applied Microbiology* **103** (4) , 1197–1205.
29. Guan, X., Qin, S., Zhao, F., Zhang, X., Tang, X. (2007) Phycobilisomes linker family in cyanobacterial genomes: divergence and evolution, *Int J Biol Sci.* **3**(7): 434–445.
30. Normand, P., Queiroux, C., Tisa, L.S., et al. (2007) Exploring the genomes of *Frankia*, *Physiologia Plantarum* **130** (3) , 331–343.
31. N. Vermeulen, M.G. Gänzle, R.F. Vogel (2007) Glutamine deamidation by cereal-associated lactic acid bacteria, *Journal of Applied Microbiology* **103** (4) , 1197–1205.
32. Flanagan, J.U., Huber, T. (2007), Structural Evolution of the ABC Transporter Subfamily B, *Evolutionary Bioinformatics* **3**, 309-316.
33. Makarova, K.S., Omelchenko, M.V., Gaidamakova, E.K. et al. (2007) *Deinococcus geothermalis*: The Pool of Extreme Radiation Resistance Genes Shrinks, *PLoS ONE* **2**(9).
34. Arp, D.J., Chain, P.S.G., Klotz, M.G. (2007) The Impact of Genome Analyses on Our Understanding of Ammonia-Oxidizing Bacteria, *Annual Review of Microbiology* **61**, 503-528.
35. Lau, W.W.Y., Keil, R.G., Armbrust, E.V. (2007) Succession and Diel Transcriptional Response of the Glycolate-Utilizing Component of the Bacterial Community during a Spring Phytoplankton Bloom, *Applied and Environmental Microbiology* **73** (8), 2440-2450.
36. Woodger, F.J., Bryant, D.A., Price, G.D. (2007) Transcriptional Regulation of the CO<sub>2</sub>-Concentrating Mechanism in a Euryhaline, Coastal Marine Cyanobacterium, *Synechococcus* sp. Strain PCC 7002: Role of NdhR/CcmR, *Journal of Bacteriology* **189**(9), 3335-3347.
37. Pearson, A., Flood Page, S.R., Jorgenson, T.L., Fischer, W.W., Higgins, M.B. (2007) Novel hopanoid cyclases from the environment *Environmental Microbiology* **9** (9) , 2175–2188.

38. Meyer, B., Imhoff, J.F., Kuever J. (2007) Molecular analysis of the distribution and phylogeny of the *soxB* gene among sulfur-oxidizing bacteria - evolution of the Sox sulfur oxidation enzyme system, *Environmental Microbiology* **9** (12), 2957–2977.
39. Cherif-Zahar, B., Durand, A., Schmidt, I. et al. (2007) Evolution and Functional Characterization of the *RH50* Gene from the Ammonia-Oxidizing Bacterium *Nitrosomonas europaea*, *Journal of Bacteriology* **189** (24), 9090-9100.
40. Zhang, X., Zhao, F., Guan, X., Yang, Y., Liang, C., Qin, S. (2007) Genome-wide survey of putative Serine/Threonine protein kinases in cyanobacteria, *BMC Genomics* **8**: 395.
41. Fischer, W. W. and Pearson, A. (2007) Hypotheses for the origin and early evolution of triterpenoid cyclases, *Geobiology* **5** (1), 19–34.
42. Suen, G, Goldman, B.S., Welch, R.D. (2007) Predicting Prokaryotic Ecological Niches Using Genome Sequence Analysis, *PLoS ONE* **2**(8).
43. Tabita, F.R., Hanson, T.E., Li, H. et al. (2007) Function, Structure, and Evolution of the RubisCO-Like Proteins and Their RubisCO Homologs, *Microbiology and Molecular Biology Reviews*, **71** (4), 576-599.
44. Granja, A.T., Popescu, A., Marques, A.R., Sa-Correia, I., Fialho, A.M. (2007) Biochemical characterization and phylogenetic analysis of UDP-glucose dehydrogenase from the gellan gum producer *Sphingomonas elodea* ATCC 31461, *Applied Microbiology and Biotechnology* **76**(6), 1319-1327.
45. Sen, G., Sur, S., Bose, D. et al. (2007) Analysis of Codon Usage Patterns and Predicted Highly Expressed Genes for Six Phytopathogenic *Xanthomonas* Genomes Shows a High Degree of Conservation, *In Silico Biology* **7**(4-5), 547-558.
46. Stephens, C. Christen, B., et al. (2007) Regulation of D-Xylose Metabolism in *Caulobacter crescentus* by a LacI-Type Repressor, *Journal of Bacteriology*, **189**(24), 8828-8834.
47. Kirkland, P.A., Reuter, C.J., and Maupin-Furlow, J.A. (2007) Effect of proteasome inhibitor *clasto-lactacystin-β-lactone* on the proteome of the haloarchaeon *Haloferax volcanii*, *Microbiology* **153**, 2271-2280.
48. T. de Vrije, A. E. Mars, M. A. W. Budde, M. H. Lai, C. Dijkema, P. de Waard and P. A. M. Claassen (2007) Glycolytic pathway and hydrogen yield studies of the extreme thermophile *Caldicellulosiruptor saccharolyticus*, *Applied Microbiology and Biotechnology* **74**(6), 1358-1367.
49. Meyer, B., and Kuever, J. (2007) Phylogeny of the alpha and beta subunits of the dissimilatory adenosine-5'-phosphosulfate (APS) reductase from sulfate-reducing prokaryotes – origin and evolution of the dissimilatory sulfate-reduction pathway, *Microbiology* **153**, 2026-2044.

50. Meyer, B., and Kuever, J. (2007) Molecular analysis of the distribution and phylogeny of dissimilatory adenosine-5'-phosphosulfate reductase-encoding genes (*aprBA*) among sulfur-oxidizing prokaryotes, *Microbiology* **153**, 3478-3498.
51. Vigneuz, F., Zumbihl, R., Jubelin, G. et al. (2007) The *xaxAB* Genes Encoding a New Apoptotic Toxin from the Insect Pathogen *Xenorhabdus nematophila* Are Present in Plant and Human Pathogens, *J. Biol. Chem.* **282** (13), 9571-9580.
52. Beck, L.L., Smith, T.G., Hoover, T.R. (2007) Look, no hands! Unconventional transcriptional activators in bacteria, *Trends in Microbiology* **15**(12), 530-537.
53. Paz-Yepes, J., Herrero, A., and Flores, E. (2007) The NtcA-Regulated *amtB* Gene Is Necessary for Full Methylammonium Uptake Activity in the Cyanobacterium *Synechococcus elongatus*, *Journal of Bacteriology*, **189**(21) , 7791-7798.
54. Campbell, E.L., Summers, M.L., Christman, H., Martin, M.E., Meeks, J.C. (2007) Global Gene Expression Patterns of *Nostoc punctiforme* in Steady-State Dinitrogen-Grown Heterocyst-Containing Cultures and at Single Time Points during the Differentiation of Akinetes and Hormogonia, *Journal of Bacteriology* **189**(14), 5247-5256.
55. Mikucki, J.A., and Priscu, J.C. (2007) Bacterial Diversity Associated with Blood Falls, a Subglacial Outflow from the Taylor Glacier, Antarctica, *Applied and Environmental Microbiology* **73**(12), 4029-4039.
56. Hau, H.H., and Gralnick, J.A. (2007) Ecology and Biotechnology of the Genus *Shewanella*, *Annual Review of Microbiology* **61**, 237-258.
57. Kapteyn, J., Qualley, A.V., Xie, Z., Fridman, E., Dudareva, N., and Gang, D.R. (2007) Evolution of Cinnamate/*p*-Coumarate Carboxyl Methyltransferases and Their Role in the Biosynthesis of Methylcinnamate, *The Plant Cell* **19**, 3212-3229.
58. Mavrodi, D.V., Paulsen, I.T., Ren, Q., Loper, J.E. (2007) Genomics of *Pseudomonas fluorescens* Pf-5, in *Pseudomonas*, Springer, 3-30.
59. Yang Y, Qin S, et al. (2007) Comparison of envelope-related genes in unicellular and filamentous cyanobacteria. *Comp Funct Genomics* **2007**: 25751.
60. Jin H, Retallack DM, et al. (2007) Characterization of the SOS response of *Pseudomonas fluorescens* strain DC206 using whole-genome transcript analysis. *FEMS Microbiol Lett* **269**(2): 256-264.

## 2008

1. Badger, M.R. and Bek, E.J. (2008) Multiple Rubisco forms in proteobacteria: their functional significance in relation to CO<sub>2</sub> acquisition by the CBB cycle, *Journal of Experimental Botany*.
2. Brinkhoff, T. Giebel, H.A., and Simon, M. (2008) Diversity, ecology, and genomics of the *Roseobacter* clade: a short overview. *Archives of Microbiology* **189**(6), 531-539.

3. Chen, D.E., Podell, S., Sauer, J.D., Swanson, M.S., and Saier, M.H. (2008) The phagosomal nutrient transporter (Pht) family, *Microbiology* **154**, 42-53.
4. Suarez, G., Sierra, J.C., Sha, J. et al. (2008) Molecular characterization of a functional type VI secretion system from a clinical isolate of *Aeromonas hydrophila*. *Microbial Pathogenesis* **44**(4), 344-361.
5. Mastronunzio, J.E., Tisa, L.S., Normand, P., and Benson, D.R. (2008) Comparative secretome analysis suggests low plant cell wall degrading capacity in *Frankia* symbionts, *BMC Genomics* **9**: 47.
6. Norton, J.M., Klotz, M.G., Stein, L.Y., et al. (2008) Complete genome sequence of *Nitrosospira multiformis*, an ammonia-oxidizing bacterium from the soil environment, *Appl. Environ. Microbiol.*
7. El Sheikh, A., Poret-Peterson, A.T., and Klotz, M.G. (2008) Characterization of Two New Genes, *amoR* and *amoD*, in the *amo* Operon of the Marine Ammonia Oxidizer *Nitrosococcus oceani* ATCC 19707, *Applied and Environmental Microbiology*, **74**(1), 312-318.
8. Elizaquível, P., Chenoll, E., Aznar, R. (2008) A TaqMan-based real-time PCR assay for the specific detection and quantification of *Leuconostoc mesenteroides* in meat products, *FEMS Microbiology Letters* **278** (1), 62–71
9. Shen, G., Schluchter, W.M., Bryant, D.A. (2008) Biogenesis of Phycobiliproteins. I. *cpcS-I* and *cpcU* Mutants of the Cyanobacterium *Synechococcus* SP. PCC 7002 Define a Heterodimeric Phycocyanobilin Lyase Specific for β-Phycocyanin and Allophycocyanin Subunits. *Journal of Biological Chemistry* **238**(12), 7503-7512.
10. Lapidus, A., Goltsman, E. Auger, S. et al. (2008) Extending the *Bacillus cereus* group genomics to putative food-borne pathogens of different toxicity, *Chemico-Biological Interactions* **171**(2), 236-249.
11. Kilian, O., Steunou, A.S., Grossman, A.R., and Bhaya D. (2008) A Novel Two Domain-Fusion Protein in Cyanobacteria with Similarity to the CAB/ELIP/HLIP Superfamily: Evolutionary Implications and Regulation, *Molecular Plant* **1**(1):155-166.
12. Pinchuk, G.E., Ammons, C., Culley, D.E. et al. (2008) Utilization of DNA as a Sole Source of Phosphorus, Carbon, and Energy by *Shewanella* spp.: Ecological and Physiological Implications for Dissimilatory Metal Reduction, *Applied and Environmental Microbiology*, **74**(4), 1198-1208.
13. Naponelli, V., Noiri, A., Ziemak, M.J. et al. (2008) Phylogenomic and Functional Analysis of Pterin-4a-Carbinolamine Dehydratase Family (COG2154) Proteins in Plants and Microorganisms, *Plant Physiology* **146**:1515-1527.
14. Sen, A., Sur, S. Bothra, A.K. et al. (2008) The implication of life style on codon usage patterns and predicted highly expressed genes for three *Frankia* genomes, *Antonie van Leeuwenhoek* **93**(4), 335-346.

15. Shell, M.A., Lipscomb, L., and DeShazer, D. (2008) Comparative Genomics and an Insect Model Rapidly Identify Novel Virulence Genes of *Burkholderia mallei*, Jurnal of Bacteriology, **190**(7), 2306-2313.
16. Sutcliffe, I.C., Black, G.W., and Harrington, D.J. (2008) Bioinformatic insights into the biosynthesis of the Group B carbohydrate in *Streptococcus agalactiae*, Microbiology **154** (2008), 1354-1363.
17. Crabbé, A., De Boever, P., Van Houdt, R., Moors, H., Mergeay, M., Cornelis, P. (2008) Use of the rotating wall vessel technology to study the effect of shear stress on growth behaviour of *Pseudomonas aeruginosa* PA01, Environmental Microbiology.
18. Vinatzer, B., Yan, S. (2008) Mining the genomes of plant pathogenic bacteria: how not to drown in gigabases of sequence, Molecular Plant Pathology **9**(1) , 105–118.
19. Gao, H., Wang, X., Yang, Z.K., Palzkill, T., and Zhou, J. (2008) Probing regulon of ArcA in *Shewanella oneidensis* MR-1 by integrated genomic analyses, BMC Genomics **9**:42.
20. Chan, L.K., Weber, T.S., Morgan-Kiss, R.M., Hanson, T.E. (2008) A genomic region required for phototrophic thiosulfate oxidation in the green sulfur bacterium *Chlorobium tepidum* (syn. *Chlorobaculum tepidum*), Microbiology **154**, 818-829.
21. Haverkamp, T., Acinas, S.G., Doeelman, M., Stomp, M., Huisman, J., Stal L.J. (2008) Diversity and phylogeny of Baltic Sea picocyanobacteria inferred from their ITS and phycobiliprotein operons, Environmental Microbiology **10** (1) , 174–188.
22. Ettema, T.J.G., Ahmed, H., Geerling, A.C.M., der Oost, J., Siebers, B. (2008) The non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GAPN) of *Sulfolobus solfataricus* : a key-enzyme of the semi-phosphorylative branch of the Entner–Doudoroff pathway, Extremophiles **12**(1), 75-88.
23. Caffrey, S.M., Park, H.S., Been, J., Gordon, P., Sensen, C.W., Voordouw, G. (2008). Gene Expression by the Sulfate-Reducing Bacterium *Desulfovibrio vulgaris* Hildenborough Grown on an Iron Electrode under Cathodic Protection Conditions, Applied and Environmental Microbiology, **74**(8), 2404-2413.
24. Zhao, J.S., Manno, D., and Hawari, J. (2008) Regulation of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) metabolism in *Shewanella halifaxensis* HAW-EB4 by terminal electron acceptor and involvement of c-type cytochrome, Microbiology **154**, 1026-1037.
25. Talbot, G., Topp, E., Palin, M.F., Masse, D.I. (2008) Evaluation of molecular methods used for establishing the interactions and functions of microorganisms in
26. Elkins, G.J., Podar, M. et al (2008) A korarchaeal genome reveals insights into the evolution of the Archaea. Proc PNAS **105**(23):8102-7.

27. Grzymski, J.J., Murray, A.E. et al. (2008) Metagenome analysis of an extreme microbial symbiosis reveals eurythermal adaptation and metabolic flexibility, *PNAS* **105** (45):17516-17521.
28. Podar, M., Anderson, I., Makarova, K.S., Elkins, J.G. et al. (2008) A genomic analysis of the archaeal system Ignicoccus hospitalis: Nanoarchaeum equitans. *Genome Biology* **9**(11).
29. Thomas T, Evans FF, et al. (2008) Analysis of the Pseudoalteromonas tunicata genome reveals properties of a surface-associated life style in the marine environment. *PLoS ONE* **3**(9): e3252.
30. van de Werken HJ, Verhaart MR, et al. (2008) Hydrogenomics of the extremely thermophilic bacterium Caldicellulosiruptor saccharolyticus. *Appl Environ Microbiol* **74**(21): 6720-6729.
31. Chen DE, Podell S, et al. (2008) The phagosomal nutrient transporter (Pht) family. *Microbiology* **154**: 42-53.
32. Anderson MT and Armstrong SK. (2008) Norepinephrine mediates acquisition of transferrin-iron in *Bordetella bronchiseptica*. *J Bacteriol.* **190** (11):3940-3947.
33. Reysenbach AL and Flores GE. (2008) Electron microscopy encounters with unusual thermophiles helps direct genomic analysis of Aciduliprofundum boonei. *Geobiology* **6**(3): 331-336.
34. Chan LK, Weber TS et al. (2008) A genomic region required for phototrophic thiosulfate oxidation in the green sulfur bacterium *Chlorobium tepidum* (syn. *Chlorobaculum tepidum*). *Microbiology* **154**: 818-829.
35. Tamura M and D'haeseleer P. (2008) Microbial genotype-phenotype mapping by class association rule mining. *Bioinformatics* **24**(13): 1523-1529.
36. Matz C, Webb JS, Schupp PJ, et al. (2008) Marine Biofilm Bacteria Evade Eukaryotic Predation by Targeted Chemical Defense , *PLoS ONE* **3**(7): e2744.
37. Rodrigues DF, Ivanova N, He A, Huebner M, et al. (2008) Architecture of thermal adaptation in an *Exiguobacterium sibiricum* strain isolated from 3 million year old permafrost: A genome and transcriptome approach. *BMC Genomics* **9**(1):547.