

Dr. Robert A. Edwards, B. Sc. D. Phil.

Professor of Computer Science and Biology

Department of Computer Science

GMCS411

5500 Campanile Drive

San Diego, CA 92182-7720

Tel: 619 594 1672

Fax: 619 594 6746

Email: redwards@mail.sdsu.edu

Web Site: <http://edwards.sdsu.edu/research>

Google Scholar: <http://scholar.google.com/citations?user=e7fvl1kAAAAJ>

Curriculo Lattes: <http://buscatextual.cnpq.br/buscatextual/visualizacv.do?id=K4327547Y9>

Positions and affiliations

Professor, Department of Computer Science, San Diego State University

Professor, Department of Biology, San Diego State University

Education, Positions, And Employment Experience

Year	Position
2015-	Professor, Department of Computer Science, San Diego State University
2015-	Professor, Department of Biology, San Diego State University
2015	Visiting Scientist, University of Queensland Diamantina Institute
2011-2015	Associate Professor, Department of Computer Science, San Diego State University
2011-2015	Associate Professor, Department of Biology, San Diego State University
2010-2015	Visiting Scholar, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil
2007-2011	Assistant Professor, Department of Computer Science, San Diego State University
2007-2011	Assistant Professor, Department of Biology, San Diego State University
2007-2015	Visiting Scientist, Argonne National Laboratory, Argonne, IL
2004-	Fellow, Fellowship for Interpretation of Genomes
2004-2007	Adjunct Assistant Professor, Department of Biology, San Diego State University
2005-2007	Adjunct Assistant Professor, Computational Sciences Research Center, San Diego State University, San Diego, CA
2004-2008	Adjunct Assistant Professor, The Burnham Institute for Medical Research, San Diego, CA
2003-2004	Assistant Facility Manager, University of Tennessee BSL3 Laboratory
2001-2004	Director Bioinformatics, University of Tennessee Medical Resource Center
2001-	Fellow, Center for Microbial Sciences, San Diego, CA
2000-2004	Assistant Professor of Microbiology, Department of Molecular Sciences, University of Tennessee Health Sciences Center, Memphis, TN.
1999-2002	Consultant, Integrated Genomics, Inc, Chicago, IL
1997-2000	Postdoctoral Researcher at the University of Illinois. Genetic and pathogenic studies on

- 1994-1997 Salmonella enterica serovar Enteritidis
Postdoctoral Researcher at the University of Pennsylvania, Philadelphia. Molecular genetic studies on the 987P fimbriae of enterotoxigenic E. coli.
- 1991-1994 D. Phil. Microbial Genetics. University of Sussex, Brighton, England.
- 1987-1991 B. Sc. Science and the Environment, De Montfort University, Leicester, England

Professional Activities

Extramural Grants:

- 2013 NSF CNS 1305112: Computational Metagenomics (PI). \$560,934 direct costs.
- 2013 NSF DEB 1321737. US/Indonesia Workshop on Biodiversity (PI). \$62,402 direct costs.
- 2013 NSF MCB 1330800. Connecting Genotype and Phenotype (PI). \$900,000 direct costs.
- 2013 NSF – TUES Type II: STEMM: Sequencing Technology Education Using Microbial Metagenomes (Co-PI) \$600,000 direct costs.
- 2011 USGS – Development of an interface of Prosilica GigE Cameras. \$40,000 direct costs.
- 2010 Dept. Education – FIPSE-CAPES San Diego-Brazil Consortium on Marine Sciences (PI) \$250,000 direct costs.
- 2010 NSF – TUES Type I: Microbes, Metagenomes and Marine Mammals: Enabling the Next Generation of Scientists to Enter the Genomic Era (Co-PI) \$200,000 direct costs.
- 2010 NSF DEB 1046413 – Dimensions: Shedding Light on Viral Dark Matter - Genetic, Taxonomic, and Functional Diversity of Coral Reef Viromes (Co-PI) \$2,999,783 direct costs.
- 2008 NSF DBI 0850356 – Collaborative Research: PHANTOME: PHage ANnotation TOols and Methods (PI) \$873,111 direct costs.
- 2004 NSF – GE:GenEn: Solar Saltern Extremophage: Genomics and Population Modeling (Co-PI) \$1,652,581 direct costs.

REU Supplements: (support undergraduate research in my lab):

- 2014 Supplement to NSF MCB 1330800
- 2013 Supplement to NSF DEB 1046413
- 2011 Supplement to NSF DBI 0850356
- 2010 Supplement to NSF DBI 0850356

National Awards:

- 2011 Kavli Frontiers Fellow, National Academy of Sciences

Institutional Awards:

- 2015 San Diego Chapter Sigma Xi Award for Distinguished Achievement
- 2015 SDSU Outstanding International Scholar
- 2012 SDSU Most Influential Faculty Member
- 2009 SDSU Most Influential Faculty Member
- 2008 SDSU Teacher/Scholar Award
- 2004 UTHSC Award for Outstanding Teacher in the Graduate Health Sciences Program

Meeting and Workshop Organizer:

- 2015 Genomics, Metagenomics, and Viromics, Flinders University, Adelaide, Australia
- 2015 Genomics, Metagenomics, and Viromics, San Diego State University
- 2015 High performance computing workshop, San Diego State University
- 2013 Scientific Chair, LIPI-NSF, Workshop on Dimensions of Biodiversity, Cibinong, Indonesia 2/2013
- 2002 Microbes: Invisible Invader...Amazing Allies. Public Exhibition. Pink Palace Museum, Memphis
- 2002 UT Bioinformatics Retreat
- 2000 Salmonella Genome Annotation Meeting, University of Illinois
- 1999 Advanced Bacterial Genetics Conference for Young Investigators. With Dr. Mike Laird, Genentech

Invited Advisor:

- 2013 ASM Viruses
- 2012 Gordon and Betty Moore Foundation Marine Microbial Initiative Review
- 2009 USDA Panel on Metagenomics, Maryland
- 2007 US/EU Workshop on Marine Genomics. Washington, DC.
- 2005 US/EU Workshop on Marine Genomics. Bremen, Germany
- 2005 National Academy of Sciences Panel on Metagenomics, Washington, DC.
- 2004 NIH review and update of the BMBL Handbook. NIH, Bethesda, Maryland
- 2003 American Society of Microbiology, Washington, DC

Peer Reviewer (2000-present):

Journals/Books:

AAAS	Genomics	Nucleic Acids Research
AEM	Infection and Immunity	PeerJ
ASM Press	Int. J. of Mol. Sci.	PLoS Biology
Bioinformatics	ISME J	PLoS Genetics
BioTechniques	J. Bacteriology	PLOS Genetics
BMC Bioinformatics	Microbial Ecology	PLoS One
BMC Genomics	Mol. Biol. Evol.	PNAS
BMC Research Notes	Molecular Microbiology	Res. Microbiology
Drug Discovery	Nature	TIM
Env. Microbiology	Nature Methods	Trends in Microbiology
Genome Research	Nucl. Acids Rev.	

Grant Reviews:

Am. Assoc. Advancement of Science	National Science Foundation
American Cancer Society	US Dept. of Agriculture
National Institutes of Health	Dept. of Energy

Member, Professional Societies:

American Society for Microbiology

International Society for Computational Biology
International Committee on the Taxonomy of Viruses, Bacteria and Archaeal Viruses Subcommittee
Society for General Microbiology (UK)
American Association for the Advancement of Science
Sigma Xi
Association of Computing Machinery
Institute of Electrical and Electronic Engineers

Outreach:

2014 Interviewed on *Science Friday* (broadcast on NPR) about our identification of a novel virus
2013 Participant in the Line Islands Expedition, Rediscovering the Coral Reefs.
2011 ASM Branch Enhancement Activity Workshop Presenter
2010 Public Lecture on the Line Islands, San Diego Council of Divers
2007 Participant in the Line Islands Expedition, Rediscovering the Coral Reefs.
2005 Participant in the Line Islands Expedition, Rediscovering the Coral Reefs
2003 Registered with the FBI and CDC to ship, receive, and handle Select Agents and other pathogens
2003 Certified to work in BSL-3 laboratory conditions.
2000 Interviewed on NPR about Salmonella infections.

Peer-Reviewed Publications

Citation metrics

As of January 1st, 2016. Updated citation metrics can be found at <http://scholar.google.com/citations?user=e7fvl1kAAAAJ>

	<i>All</i>	<i>Last 5 years</i>
Citations	18,358	13,260
h-index	52	47
i10-index	93	88

Journal Manuscripts:

1. Knowles B, Silveira CB, Bailey BA, Barott K, Cantu A, Cobián-Güemes AG, Coutinho FH, Dinsdale E, Felts B, Furby KA, George EE, Green KT, Gregoracci GB, Haas AF, Haggerty JM, Hester ER, Hisakawa NG, Kelly LW, Lim YW, Little M, Luque A, McDole-Somera T, McNair K, de Oliveira LS5, Quistad SD, Robinett NL, Sala E, Salamon P, Sanchez SE, Sandin S, Silva GGZ, Smith J, Sullivan C, Thompson C, Vermeij MJA, Youle M, Young C, Zgliczynski B, Brainard R, **Edwards RA**, Nulton J, Thompson F, Rohwer F. Lytic to Temperate Switching of Viral Communities. *Nature*. March 16th 2016.
2. Lopes FAC, Catão ECP, Santana RH, Cabral A de S, Paranhos R, Rangel TP, Rezende CE de,

- Edwards RA**, Thompson CC, Thompson FL, Kruger RH. 2016. Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. *PLoS ONE* 11:e0148296.
3. **Edwards RA**, McNair K, Faust K, Raes J, Dutilh BE. 2016. Computational approaches to predict bacteriophage–host relationships. *FEMS Microbiology Reviews* fuv048. *Editors choice for 2016. Top three most downloaded articles in FEMS Micro. Rev.*
 4. Yue M, Han X, Masi LD, Zhu C, Ma X, Zhang J, Wu R, Schmieder R, Kaushik RS, Fraser GP, Zhao S, McDermott PF, Weill F-X, Mainil JG, Arze C, Fricke WF, **Edwards RA**, Brisson D, Zhang NR, Rankin SC, Schifferli DM. 2015. Allelic variation contributes to bacterial host specificity. *Nat Commun* 6:8754.
 5. Kryshatfovych A, Moulton J, Baslé A, Burgin A, Craig TK, **Edwards RA**, Fass D, Hartmann MD, Korycinski M, Lewis RJ, Lorimer D, Lupas AN, Newman J, Peat TS, Piepenbrink KH, Prahlad J, van Raaij MJ, Rohwer F, Segall AM, Seguritan V, Sundberg EJ, Singh AK, Wilson MA, Schwede T. 2015. Some of the most interesting CASP11 targets through the eyes of their authors. *Proteins*.
 6. Silva GGZ, Green KT, Dutilh BE, **Edwards RA**. 2015. SUPER-FOCUS: A tool for agile functional analysis of shotgun metagenomic data. *Bioinformatics* btv584.
 7. McNair K, **Edwards RA**. 2015. GenomePeek—an online tool for prokaryotic genome and metagenome analysis. *PeerJ* 3:e1025. *Chosen as one of the top 10 genomics papers in PeerJ 2013-2015.*
 8. Meirelles PM, Amado-Filho GM, Pereira-Filho GH, Pinheiro HT, de Moura RL, Joyeux J-C, Mazzei EF, Bastos AC, **Edwards RA**, Dinsdale E, Paranhos R, Santos EO, Iida T, Gotoh K, Nakamura S, Sawabe T, Rezende CE, Gadelha LMR Jr, Francini-Filho RB, Thompson C, Thompson FL. 2015. Baseline Assessment of Mesophotic Reefs of the Vitória-Trindade Seamount Chain Based on Water Quality, Microbial Diversity, Benthic Cover and Fish Biomass Data. *PLoS ONE* 10:e0130084.
 9. Navarrete AA, Diniz TR, Braga LPP, Silva GGZ, Franchini JC, Rossetto R, **Edwards RA**, Tsai SM. 2015. Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. *PLoS ONE* 10:e0129765.
 10. Sanchez SE, Cuevas DA, Rostron JE, Liang TY, Pivaroff CG, Haynes MR, Nulton J, Felts B, Bailey BA, Salamon P, **Edwards RA**, Burgin AB, Segall AM, Rohwer F. 2015. Phage Phenomics: Physiological Approaches to Characterize Novel Viral Proteins. *Journal of Visualized Experiments*.
 11. Matthews TD, Schmieder R, Silva GGZ, Busch J, Cassman N, Dutilh BE, Green D, Matlock B, Heffernan B, Olsen GJ, Farris Hanna L, Schifferli DM, Maloy S, Dinsdale EA, **Edwards RA**. 2015. Genomic Comparison of the Closely-Related *Salmonella enterica* Serovars Enteritidis, Dublin and Gallinarum. *PLoS ONE* 10:e0126883.
 12. Adriaenssens EM, **Edwards R**, Nash JHE, Mahadevan P, Seto D, Ackermann H-W, Lavigne R, Kropinski AM. 2015. Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. *Virology* 477:144–154.
 13. Aziz, R.K., Dwivedi, B., Akhter, S., Breitbart, M., and **R.A. Edwards** 2015. Multidimensional metrics for estimating phage abundance, distribution, gene density, and sequence coverage in metagenomes. *Front. Microbiol.* doi: 10.3389/fmicb.2015.00381.
 14. Brettin, T., J.J. Davis, T. Disz, **R.A. Edwards**, S. Gerdes, G.J. Olsen, R. Olson, R., Overbeek, B. Parrello, G.D. Pusch, S. Maulik, J.A. Thomason, R. Stevens, V. Vonstein, A.R. Wattam,

- and F. Xia 2015. RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Nature Sci. Rep.* 5. doi: 10.1038/srep08365
15. Thompson, C.C., Amaral, G.R., Campeão, M., Edwards, R.A., Polz, M.F., Dutilh, B.E., Ussery, D.W., Sawabe, T., Swings, J., and Thompson, F.L. 2015. Microbial taxonomy in the post-genomic era: Rebuilding from scratch? *Arch Microbiol* 1–12.
 16. G.G.Z. Silva[§], B E. Dutilh, **R.A. Edwards**. 2014. FORMAL: A model to identify organisms present in metagenomes using Monte Carlo Simulation. *bioRxiv*. doi: <http://dx.doi.org/10.1101/010801>
 17. Dutilh BE, Cassman N[§], McNair K, Sanchez S[§], Silva GGZ[§], Boling L^u, Barr JJ^p, Speth DR, Seguritan V[§], Aziz RK, Felts B, Dinsdale EA, Mokili JL, **Edwards RA**. 2014. A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. *Nature Communications* 5:4498. <http://dx.doi.org/10.1038/ncomms5498> 2014 journal impact factor 10.742. Cited by 1
 18. Cuevas, D.[§], Garza, D., Sanchez, S.[§], Rostron, J., Henry, C., Vonstein, V., Overbeek, R., Segall, A., Rohwer, F., Dinsdale, EA., **Edwards RA**. 2014. Elucidating genomic gaps using phenotypic profiles. *F1000Research*. <http://dx.doi.org/10.12688/f1000research.5140.1> (No impact factor yet.)
 19. Lim YW[§], Haas A^p, Cuevas D[§], Silva GGZ[§], Dinsdale E, Lee C, Harkins TT, Rohwer F, **Edwards RA**. Sequencing At Sea: Challenges and Experiences in Ion Torrent Sequencing during the 2013 Southern Line Islands Research Expedition. *PeerJ* 2:e520 <http://dx.doi.org/10.7717/peerj.520> (No impact factor yet.) ***This article was picked as one of the PeerJ Top 20 articles for 2014.***
 20. Dutilh BE, Tompson C, Vicente AC, Marin MA, Lee CF, Silva GGZ[§], Schmieder R, Andrade BGN, Chimetto L, Cuevas D, Garza DR, Okeke IN, Aboderin O, Spangler J, Ross T, Dinsdale EA, Thompson FL, Harkins TT, **Edwards RA**. 2014 Comparative genomics of 274 *Vibrio cholerae* genomes reveals mobile functions structuring three niche dimensions. *BMC Genomics* 15:654 <http://dx.doi.org/10.1186/1471-2164-15-654> 2014 journal impact factor 4.041
 21. Kelly LW[§], Williams GJ^p, Barott KL^p, Carlson CA, Dinsdale EA, **Edwards RA**, Haas AF^p, Haynes M, Lim YW[§], McDole T[§], Nelson CE[§], Sala E, Sandin SA, Smith JE, Vermeij MJA, Youle M, Rohwer F. 2014. Local genomic adaptation of coral reef-associated microbiomes to gradients of natural variability and anthropogenic stressors. *Proc. Natl. Acad. Sci.* 111:10227-10232 <http://dx.doi.org/10.1073/pnas.1403319111> 2014 journal impact factor 9.809. Cited by 1
 22. Silva GGZ[§], Cuevas DA[§], Dutilh BE, **Edwards RA**. 2014. FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. *PeerJ* 2:e425. (No impact factor yet.). <http://dx.doi.org/10.7717/peerj.425> Cited by 1
 23. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, **Edwards RA**, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res.* 42:D206-14. <http://dx.doi.org/10.1093/nar/gkt1226> 2014 journal impact factor 8.808. Cited by 28
 24. Lim, Y.W., Schmieder, R., Haynes, M., Furlan, M., Matthews, T.D., Whiteson, K., Poole, S.J., Hayes, C.S., Low, D.A., Maughan, H., **Edwards, R.A.**, Conrad, D., and F. Rohwer. 2013.

Mechanistic model of *Rothia mucilaginosa* adaptation toward persistence in the CF lung, based on a genome reconstructed from metagenomic data. PLoS One 8:e64285.

<http://dx.doi.org/10.1371/journal.pone.0064285> 2014 journal impact factor 3.534. Cited by 6

25. Lim, YW.[§], Evangelista, J., Schmieder, R.[§], Bailey, B., Haynes, M., Furlan, M., Maughan, H., **Edwards, R.**, Rohwer, F., and D. Conrad. 2014. Clinical Insights from Metagenomic Analysis of Cystic Fibrosis Sputum. *J. Clin. Microbiol.* 52:425-437. <http://dx.doi.org/10.1128/JCM.02204-13> 2014 journal impact factor 4.232. Cited by 5
26. **Edwards RA**, Haggerty JM[§], Cassman N[§], Busch JC[§], Aguinaldo K[§], Chinta S[§], Vaughn MH, Morey R, Harkins TT, Teiling C, Fredrikson K, Dinsdale EA. 2013. Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. *BMC Genomics* 14:600. <http://dx.doi.org/10.1186/1471-2164-14-600> 2014 journal impact factor 4.041. Cited by 1
27. Silva, G.G.[§], Dutilh, B.E., Matthews, T.D.^p, Elkins, K.^u, Schmieder, R., Dinsdale E.A., and **R.A. Edwards**. 2013. Combining de novo and reference-guided assembly with scaffold_builder. *Source Code for Biology and Medicine* 2013, 8:23. <http://dx.doi.org/10.1186/1751-0473-8-23> (No impact factor yet). Cited by 2
28. Thompson, C.C., Chimetto, L.[§], **Edwards, R.A.**, Swings, J., Stackebrandt E., and FL Thompson. 2013. Microbial genomic taxonomy. *BMC Genomics* 2013, 14:913 <http://dx.doi.org/10.1186/1471-2164-14-913> 2014 journal impact factor 4.041. Cited by 6
29. Thompson, C.C., Silva, G.G.Z., Vieira, N.M., **Edwards, R.**, Vicente, A.C.P., and Thompson, F.L. Genomic Taxonomy of the Genus *Prochlorococcus*. *Microbial Ecology* 1–11. <http://dx.doi.org/10.1007/s00248-013-0270-8> 2014 journal impact factor 3.118. Cited by 6
30. Dinsdale EA, **Edwards RA**, Bailey B, Tuba I, Akhter S[§], McNair K, Schmieder R[§], Apkarian N^u, Creek M^u, Guan E^u, Hernandez M^u, Isaacs K^u, Peterson C^u, Regh T^u, Ponomarenko V. 2013. Multivariate analysis of functional metagenomes. *Front. Genet.* 4:41. <http://dx.doi.org/10.3389/fgene.2013.00041> (No impact factor yet). Cited by 8
31. Dutilh, B.E., Backus, L., **Edwards, R.A.**, Wels, M., Bayjanov, J.R., and S.A.F.T. van Hijum 2013. Explaining microbial phenotypes on a genomic scale: GWAS for microbes. *Brief Funct Genomics.* 2013 Jul;12(4):366-80. <http://dx.doi.org/10.1093/bfgp/elt008> 2014 journal impact factor 3.427. Cited by 2
32. Dwivedi, B., Xue, B., Lundin, D., **Edwards R.A.**, and Breitbart, M. 2013. A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. *BMC Evolutionary Biology.* <http://dx.doi.org/10.1186/1471-2148-13-33> 2014 journal impact factor 3.407. Cited by 13
33. Garcia GD, Gregoracci GB, de O Santos E, Meirelles PM, Silva GG, **Edwards R.A.**, Sawabe T, Gotoh K, Nakamura S, Iida T, de Moura RL, Thompson FL. 2013. Metagenomic Analysis of Healthy and White Plague-Affected *Mussismilia braziliensis* Corals. *Microb Ecol.* 65:1076-1086 <http://dx.doi.org/10.1007/s00248-012-0161-4> 2014 journal impact factor 3.118. Cited by 13
34. Frank JA, Lorimer D, Youle M, Witte P, Craig T, Abendroth J, Rohwer F, **Edwards R.A.**, Segall AM, Burgin AB Jr. 2013. Structure and function of a cyanophage-encoded peptide deformylase. *ISME J.* <http://dx.doi.org/10.1038/ismej.2013.4> 2014 journal impact factor 9.267. Cited by 3
35. Akhter S[§], Bailey BA, Salamon P, Aziz RK, **Edwards RA**. 2013. Applying Shannon's

- information theory to bacterial and phage genomes and metagenomes. Nature Scientific Reports. 3:1033 <http://dx.doi.org/10.1038/srep01033>. 2014 journal impact factor 5.078. Cited by 4
36. Lim YW[§], Schmieder R[§], Haynes M, Willner D, Furlan M[§], Youle M, Abbott K, **Edwards R**, Evangelista J, Conrad D, Rohwer F. 2012. Metagenomics and metatranscriptomics: Windows on CF-associated viral and microbial communities. Journal of Cystic Fibrosis. <http://dx.doi.org/10.1016/j.jcf.2012.07.009>. 2014 journal impact factor 3.82. Cited by 19
 37. Dutilh, B. E., Schmieder, R.[§], Nulton, J., Felts, B., Salamon, P., **Edwards R. A.** and J. L. Mokili. 2012. Reference-independent comparative metagenomics using cross-assembly: crAss. Bioinformatics. <http://dx.doi.org/10.1093/bioinformatics/bts613> 2014 journal impact factor 4.621. Cited by 9.
 38. **Edwards, R.A.** Olson, R., Disz, T., Pusch, G.D., Vonstein, V., Stevens, R., and R. Overbeek. 2012. Real Time Metagenomics: Using k-mers to annotate meta-genomes. Bioinformatics <http://dx.doi.org/10.1093/bioinformatics/bts599> 2014 journal impact factor 4.621. Cited by 14.
 39. Aziz, R.A., Devoid, S., Disz, T., **Edwards, R.A.**, Henry, C.S., Olsen, G.J., Olson, R., Overbeek, R., Parrello, B., Pusch, G.D., Stevens, R.L., Vonstein, V., and F. Xia. 2012. SEED Servers: high-performance access to the SEED genomes, annotations, and metabolic models. PLoS One 7:e48053. <http://dx.doi.org/10.1371/journal.pone.0048053> 2014 journal impact factor 3.534. Cited by 27.
 40. Yue, M., Schmieder, R.[§], **Edwards, R.A.**, Rankin, S.C., and D.M. Schifferli. 2012 Microfluidic PCR combined with pyrosequencing identify allelic variants with phenotypic associations in targeted *Salmonella* genes. Appl. Env. Microbiol. 78:7480-7482 <http://dx.doi.org/10.1128/AEM.01703-12> 2014 journal impact factor 3.952. Cited by 3.
 41. Bruce T., Meirelles P.M., Garcia G., Paranhos R., Rezende C.E., de Moura, R.L., Filho, R-F., Coni, E.O.C., Vasconcelos, A.T., Filho, G.A., Hatay, M., Schmieder, R., **Edwards, R.A.**, Dinsdale, E.A., and F.L. Thompson 2012. Abrolhos Bank Reef Health Evaluated by Means of Water Quality, Microbial Diversity, Benthic Cover, and Fish Biomass Data. PLoS ONE 7:e36687. <http://dx.doi.org/10.1371/journal.pone.0036687> 2014 journal impact factor 3.534. Cited by 28.
 42. Garza DR, Thompson CC, Loureiro ECB, Dutilh BE, Inada DT, Sousa, E.C. Jr., Cardoso, J.F., Nunes, M.R.T., Silva de Lima, C.P., Duarte Silvestre, R.V., Barbosa Nunes, K.N., Santos, E.C.O., **Edwards, R.A.**, Vicente, A.C.P., and L.L. Canto de Sá Morais. 2012. Genome-Wide Study of the Defective Sucrose Fermenter Strain of *Vibrio cholerae* from the Latin American Cholera Epidemic. PLoS ONE 7: e37283. <http://dx.doi.org/10.1371/journal.pone.0037283> 2014 journal impact factor 3.534. Cited by 7.
 43. Lynch, E.A.[§], Langille, M.G.I., Darling, A., Wilbanks, E.G., Haltiner, C., Shao, K.S.Y., Starr, M.O., Teiling, C., Harkins, T.T., **Edwards, R.A.** Eisen, J.A., and M.T Facciotti. 2012. Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS One. 7:e41389. <http://dx.doi.org/10.1371/journal.pone.0041389> 2014 journal impact factor 3.534. Cited by 10.
 44. Yue, M., Rankin, S.C., Blanchet, R.T.[¶], Nulton, J.D., **Edwards, R.A.** and D.M. Schifferli. 2012. Diversification of the *Salmonella* Fimbriae: A Model of Macro-and Microevolution. PLoS One. 7:e38596. <http://dx.doi.org/10.1371/journal.pone.0038596> 2014 journal impact factor

- 3.534. Cited by 12.
45. Trindade-Silva A.E.[§], Rua C.[§], Silva G.G.Z.^u, Dutilh B.E., Moreira A.P.B., **Edwards, R.A.**, Hajdu, E., Lobo-Hajdu, G., Vasconcelos, A.T., Berlinck, R.G.S., and F.L. Thompson. 2012. Taxonomic and Functional Microbial Signatures of the Endemic Marine Sponge *Arenosclera brasiliensis*. PLoS ONE 7: e39905. <http://dx.doi.org/10.1371/journal.pone.0039905> 2014 journal impact factor 3.534. Cited by 13.
 46. Luckwu de Lucena, B.T.[§], Silva, G.G.^u, Manoel Dos Santos, B., Dias, G.M., Amaral, G.R.[§], Moreira, A.P., de Moraes Júnior, M.A., Dutilh, B.E., **Edwards, R.A.**, Balbino, V., Thompson, C.C., and Thompson, F.L. 2012. Genome Sequences of the Ethanol-Tolerant *Lactobacillus vini* Strains LMG 23202T and JP7.8.9. J. Bacteriol. 194:3018. <http://dx.doi.org/10.1128/JB.00446-12> 2014 journal impact factor 2.688. Cited by 5.
 47. Amaral G.R.[§], Silva B.S.[§], Santos, E.O., Dias, G.M., Lopes, R.M., **Edwards, R.A.**, Thompson, C.C., and Thompson, F.L.. 2012. Genome sequence of the bacterioplanktonic mixotrophic *Vibrio campbellii* PEL22A isolated in the Abrolhos Bank. J Bacteriol. 194:2759-60. <http://dx.doi.org/10.1128/JB.00377-12> 2014 journal impact factor 2.688. Cited by 6.
 48. Espinoza-Valles, I.[§], Soto-Rodríguez, S., **Edwards, R.A.**, Wang, Z., Vora, G., and B. Gomez-Gil. 2012. Draft Genome Sequence of the Shrimp Pathogen *Vibrio harveyi* CAIM 1792. J. Bacteriol. 194:2104. <http://dx.doi.org/10.1128/JB.00079-12> 2014 journal impact factor 2.688. Cited by 5.
 49. Akhter, S.[§], Aziz, R., and **Edwards, R.A.** 2012. PhiSpy: a novel algorithm for finding prophages in bacterial genomes that combines similarity- and composition-based strategies. Nucleic Acids Res. <http://dx.doi.org/10.1093/nar/gks406> 2014 journal impact factor 8.808. Cited by 27.
 50. Farris-Hanna, L.[§], Matthews, T.D., Dinsdale, E.A., Hasty, D., and **Edwards, R.A.** 2012 Characterization of the ELPhiS Prophage from Salmonella enterica serovar Enteritidis strain LK5. Appl. Environ. Microbiol. <http://dx.doi.org/10.1128/AEM.07241-11> 2014 journal impact factor 3.952. Cited by 7.
 51. McNair, K.[§], Bailey, B., and **Edwards, R.A.** 2012. PHACTS, a computational approach to classifying the lifestyle of phages. Bioinformatics. 28:614-8. <http://dx.doi.org/10.1093/bioinformatics/bts014> 2014 journal impact factor 4.621. Cited by 18.
 52. Miller, M.E.[§], Yeoman, C.J., Chia, N., Tringe, S.G., Angly, F.E., **Edwards, R.A.**, Flint, H.J., Lamed, R., Bayer, E.A., and B.A. White. 2012. Phage-Bacteria Relationships and CRISPR Elements Revealed by a Metagenomic Survey of the Rumen Microbiome. Environmental Microbiology. 14:207–227. <http://dx.doi.org/10.1111/j.1462-2920.2011.02593.x> 2014 journal impact factor 6.24. Cited by 34.
 53. Bolser, D.M., Chibon, P.Y., Palopoli, N., Gong, S., Jacob, D., Del Angel, V.D., Swan, D., Bassi, S., González, V., Suravajhala, P., Hwang, S., Romano, P., **Edwards, R.A.**, Bishop, B., Eargle, J., Shtatland, T., Provart, N.J., Clements, D., Renfro, D.P., Bhak, D., and Bhak J. 2012 MetaBase: A community database of biological databases. Nucleic Acids Res. 40(Database issue):D1250-4. <http://dx.doi.org/10.1093/nar/gkr1099> 2014 journal impact factor 8.808. Cited by 17.
 54. Dwivedi, B., Schmieder, R., Goldsmith, D.B.[§], **Edwards, R.A.**, and Breitbart, M. 2012. PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for

- examining phage diversity. BMC Bioinformatics. BMC Bioinformatics 13:37
<http://dx.doi.org/10.1186/1471-2105-13-37> 2014 journal impact factor 4.621. Cited by 9.
55. Schmieder, R,[§] Lim Y.W.[§] and **Edwards, R.A.** 2011. Identification and removal of ribosomal RNA sequences from metatranscriptomes. Bioinformatics 2011;
<http://dx.doi.org/10.1093/bioinformatics/btr669> 2014 journal impact factor 4.621. Cited by 20.
56. Schmieder, R.[§], and **Edwards, R.A.** 2011. Insights into antibiotic resistance through metagenomic approaches. Future Microbiology. 7:73-89
<http://dx.doi.org/10.2217/fmb.11.135> 2014 journal impact factor 3.819 2014 journal impact factor 3.819. Cited by 51. Ranked as one of the top 50 highest read pieces in 2015 across all the Future Medicine journal titles.
57. Thompson, C.C., Marin, M.A., Dias, G.M., Dutilh, B.E., **Edwards, R.A.**, Iida, T. Thompson, F.L. and Vicente, A.C.P. 2011. Genome sequence of the human pathogen *Vibrio cholerae* Amazonia. J. Bacteriol. 193:5877-5878 <http://dx.doi.org/10.1128/JB.05643-11> 2014 journal impact factor 2.688. Cited by 4.
58. Schmieder, R,[§] and **Edwards, R.A.** 2011. Fast identification and removal of sequence contamination from genomic and metagenomic datasets. PLoS One. 6:e17288.
<http://dx.doi.org/10.1371/journal.pone.0017288>. 2014 journal impact factor 3.534. Cited by 66.
59. Schmieder, R,[§] and **Edwards, R.A.** 2011. Quality control and preprocessing of metagenomic datasets. Bioinformatics. 27:863-864. <http://dx.doi.org/10.1093/bioinformatics/btr026> 2014 journal impact factor 4.621. Cited by 203.
60. Henry, C.S., Overbeek, R.A., Xia, F., Best, A.A., Glass, E. Gilbert, J.A., Larsen, P.E., **Edwards, R.A.**, Disz, T., Meyer, F., Vonstein, V., DeJongh, M., Bartels, D., Desai, M., D'Souza, M., Devoid, S., Keegan, K.P., Olson, R., Wilke, A., Wilkening, J., Stevens, R.L. 2011. Connecting Genotype to Phenotype in the Era of High-throughput Sequencing. Biochem. Biophys. Acta. <http://dx.doi.org/10.1016/j.bbagen.2011.03.010> 2014 journal impact factor 3.829. Cited by 19.
61. Desnues, C.G.^p, Rodriguez-Brito, B.[§], Rayhawk, S.[§], Kelley, S., Tran, T.[§], Haynes, M., Liu, H., Hall, D.[§], Angly, F.E.[§], **Edwards, R.A.**, Vega, R.^p, Breitbart, M., Siefert, J., Souza, V., Reid, P., Rohwer, F. 2011. Biodiversity and biogeography of phages in modern stromatolites and thrombolites. Pages 37-44. Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats. Wiley-Blackwell, Hoboken, NJ. ISBN 978-0-470-64719-6.
62. F.L. Thompson, Rodrigues, T.B., Gonzalez, A., Cardoso, A. Clementino, M., Costagliola, M., Hozbor, C., Otero, E., Paranhos, R., Piccini, C., Peressutti, S., *Schmieder, R.[§]*, **Edwards, R.**, Smith, M., Takiyama, L.R., Vieira, R., Artigas, L.F. 2011. Coastal bacterioplankton community diversity along a latitudinal gradient in Latin America by means of V6-tag pyrosequencing. 2010. Arch. Microbiol. <http://dx.doi.org/10.1007/s00203-010-0644-y> 2014 journal impact factor 1.861. Cited by 10.
63. T. D. Matthews, **R. Edwards**, and S. Maloy. 2010. Chromosomal Rearrangements Formed by *rrn* Recombination Do Not Improve Replichore Balance in Host-specific Salmonella enterica Serovars. PLoS One. <http://dx.doi.org/10.1371/journal.pone.0013503>. 2014 journal impact factor 3.534. Cited by 5.
64. Schmieder R.[§], Lim Y.W.[§], Rohwer F., **Edwards R.** 2010. TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. BMC Bioinformatics

- 11:341-355. <http://dx.doi.org/10.1186/1471-2105-11-341> 2014 journal impact factor: 2.672. Cited by 45.
65. Disz, T., Akhter, S.[§], Cuevas, D.^u, Olson, R., Overbeek, R., Vonstein, V., Stevens, R., and **R.A. Edwards**. 2010. Accessing the SEED genome databases via Web services API: Tools for Programmers. BMC Bioinformatics 11:319-330. <http://dx.doi.org/10.1186/1471-2105-11-319> 2014 journal impact factor: 2.672. Cited by 45.
66. Aziz, R.^p, Breitbart, M., and **Edwards, R.** 2010. Transposases are the most abundant, most ubiquitous genes in nature. Nucl. Acids Research 38:4207-4217 <http://dx.doi.org/10.1093/nar/gkq140> 2014 journal impact factor 8.808. Cited by 98.
67. Rodriguez-Brito, B.[§], Li, L.[§], Wegley, L.[§], Furlan, M.[§], Angly, F.[§], Brietbart, M, Buchanan, J., Desnues, C.^p, Dinsdale, E., **Edwards, R.A.**, Felts, B., Wilner, D.[§], Haynes, M., Liu, H., Lipson, D., Mahaffy, J., Martin-Cuadrado, A.B., Mira, A., Nulton, J., Pasic, L., Rayhawk, S.[§], Rodriguez-Mueller, J., Rodriguez-Valera, F., Salamon, P., Srinagesh, S.[§], Thingstad, T., Tran, T.[§], Vega Thurber, R.^p, Youle, M., Rohwer, F. 2010 Viral and microbial community dynamics in four aquatic environments. ISME J. 1-13. <http://dx.doi.org/10.1038/ismej.2010.1> 2014 journal impact factor 9.267. Cited by 135.
68. Mobberley, J.[§], Authement, R.N.[§], Segall, A.M., **Edwards, R.A.**, Slepecky, R.A., and Paul, J.H. 2010. Lysogeny and Sporulation in *Bacillus* Isolates from the Gulf of Mexico. Appl. Env. Microbiol. 76:829-842. <http://dx.doi.org/10.1128/AEM.01710-09> 2014 journal impact factor: 3.952. Cited by 3.
69. Vega Thurber R.[§], Willner-Hall D.[§], Rodriguez-Mueller B.[§], Desnues C.^p, **Edwards RA**, Angly F.[§], Dinsdale E., Kelly L.[§], Rohwer F 2009. Metagenomic analysis of stressed coral holobionts. Environ Microbiol. 1:2148-63. <http://dx.doi.org/10.1111/j.1462-2920.2009.01935.x> 2014 journal impact factor: 6.24. Cited by 147.
70. Wagner, C.^u, Salamon, A.[§], **Edwards, R.A.**, Rohwer, F., and P. Salamon. 2009. Deviations from Ultrametricity in Phage Protein Distances. Open Systems & Information Dynamics 16:75–84 . <http://dx.doi.org/10.1142/S1230161209000062> 2014 journal impact factor: 0.808
71. Angly FE.[§], Willner D.[§], Prieto-Davó A.^p, **Edwards RA**, Schmieder R.[§], Vega-Thurber R.[§], Antonopoulos DA, Barott K.[§], Cottrell MT, Desnues C.^p, Dinsdale EA, Furlan M.[§], Haynes M, Henn MR, Hu Y, Kirchman DL, McDole T.[§], McPherson JD, Meyer F, Miller RM, Mundt E, Naviaux RK, Rodriguez-Mueller B.[§], Stevens R, Wegley L, Zhang L, Zhu B, Rohwer F. 2009. The GAAS metagenomic tool and its estimations of viral and microbial average genome size in four major biomes. PLoS Comput. Biol 5:e1000593. <http://dx.doi.org/10.1371/journal.pcbi.1000593> 2014 journal impact factor: 4.829. Cited by 100.
72. Brulc, J.M.[§], Antonopoulos, D.A.^p, Berg Miller, M.E., Wilson, M.K., Yannarell, A.C., Dinsdale, E.A., **Edwards, R.A.** Frank, E.D., Emerson, J.B., Wacklin, P., Coutinho, P.M., Henrissat, B., Nelson, K.E., and White, B.A.. 2009 Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. Proc Natl Acad Sci USA. 106:1948 –1953. <http://dx.doi.org/10.1073/pnas.0806191105> 2014 journal impact factor: 9.809. Cited by 276.
73. Edwards, R.A. 2009. Gaining New Insights into Microbial Communities. SciDac Review 13:43
74. Breitbart, M., Hoare, A., Nitti, A., Siefert, J., Haynes, M., Dinsdale, E., **Edwards, R.**, Souza, V., Rohwer, F., and Hollander, D. 2009. Metagenomic and Stable Isotopic Analyses of Modern Freshwater Microbialites in Cuatro Ciénegas, Mexico. Env. Microbiol.11:16-34.

- <http://dx.doi.org/10.1111/j.1462-2920.2008.01725.x> 2014 journal impact factor: 6.24. Cited by 78.
75. Dinsdale, E.A., **Edwards, R.A.**, Hall, D.[§], Angly, F.[§], Breitbart, M., Brulc, J.[§], Chau, B.[§], Furlan, M.[§], Desnues, C.G.^p, Haynes, M., Li, L.[§], McDaniel, L., Moran, M.A., Nelson, K.E., Nilsson, C., Olson, R., Paul, J., Rodriguez-Brito, B.[§], Swan, B.[§], Stevens, R., Valentine, D., Vega-Thurber, R.^p, Wegley, L.[§], White, B., and F. Rohwer. 2008. Functional Metagenomic Profiling of Nine Biomes. *Nature* 452:629-632. <http://dx.doi.org/10.1038/nature06810> 2014 journal impact factor 42.351. Cited by 531.
76. Dinsdale, E. A., Pantos O.^p, Smriga, S.[§], **Edwards, R.A.**, Angly, F.[§], Wegley, L.[§], Hatay, M., Hall, D.[§], Brown, E.[§], Haynes, M., Krause, L.[§], Sala, E., Sandin, S.A., Thurber, R. V., Willis, B.L., Azam, F., Knowlton, N., and Rohwer, F. 2008. Microbial ecology of four coral atolls in the northern line islands. *PLoS ONE* 3:e1584. <http://dx.doi.org/10.1371/journal.pone.0001584> 2014 journal impact factor 3.534. Cited by 197.
77. Desnues, C.G.^p, Rodriguez-Brito, B.[§], Rayhawk, S.[§], Kelley, S., Tran, T.[§], Haynes, M., Liu, H., Hall, D.[§], Angly, F.E.[§], **Edwards, R.A.**, Vega, R.^p, Breitbart, M., Siefert, J., Souza, V., Reid, P., Rohwer, F. 2008. Biodiversity and biogeography of phages in modern stromatolites and thrombolites. *Nature* 452:340-343. <http://dx.doi.org/10.1038/nature06735> 2014 journal impact factor: 42.351. Cited by 148.
78. Mou, X.^p, Sun, S., **Edwards, R.**, Hodson, R., and Moran, M.A. 2008. Bacterial Carbon Processing by Generalist Species in the Coastal Ocean. *Nature*. 451:709-711. <http://dx.doi.org/10.1038/nature06513> 2014 journal impact factor: 42.351. Cited by 158.
79. Meyer, F. Paarmann, D., D'Souza, M., Olson, R.D., Glass, E.M., Kubal, M., Paczian, T., Rodriguez, A., Stevens, R., Wilke, A., Wilkening, J. and **R.A. Edwards**. 2008. The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. *BMC Bioinformatics* 9:386. <http://dx.doi.org/10.1186/1471-2105-9-386> 2014 journal impact factor: 2.672. Cited by 837.
80. Breitbart M, Haynes M, Kelley S, Angly F[§], **Edwards RA**, Felts B, Mahaffy JM, Mueller J, Nulton J, Rayhawk S[§], Rodriguez-Brito B[§], Salamon P, Rohwer F. 2008. Viral diversity and dynamics in an infant gut. *Res. Microbiol* 159:367-373. <http://dx.doi.org/10.1016/j.resmic.2008.04.006> 2014 journal impact factor: 2.826. Cited by 111.
81. Gilbert, J.A., Field, D., Huang, Y., **Edwards, R.**, Li, W., Gilna, P., and I. Joint. 2008. Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. *PLoS ONE* 3(8): e3042. <http://dx.doi.org/10.1371/journal.pone.0003042> 2014 journal impact factor 3.534. Cited by 217.
82. Vega Thurber RL, Barott KL, Hall D, Liu H, Rodriguez-Mueller B, Desnues C, **Edwards RA**, Haynes M, Angly FE, Wegley L, Rohwer FL. 2008. Metagenomic analysis indicates that stressors induce production of herpes-like viruses in the coral *Porites compressa*. *Proc. Natl. Acad. Sci. USA* 105:18413–18418. <http://dx.doi.org/10.1073/pnas.0808985105> 2014 journal impact factor: 9.809. Cited by 84.
83. Qu, A.[§], Brulc, J. M.[§], Wilson, M.K., Law, B.F., Theoret, J.R., Joens, L.A., Konkel, M.A., Angly, F.[§], Dinsdale, E.A., **Edwards, R.A.**, Nelson, K.E., and White, B.A. 2008. Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene

- Transfer Elements in the Chicken Cecum Microbiome. PLoS One, 3(8):e2945. <http://dx.doi.org/10.1371/journal.pone.0002945> 2014 journal impact factor 3.534. Cited by 101.
84. Marhaver, K.L.[§], **Edwards, R.A.**, and F. Rohwer. Viral communities associated with healthy and bleaching corals. 2008. *Env Microbiol.* 10:2277-2286. <http://dx.doi.org/10.1111/j.1462-2920.2008.01652.x> 2014 journal impact factor: 3.264. Cited by 58.
85. Krause, L.[§], Diaz, N. N., **Edwards, R.A.**, Gartemann, K-H., Krömeke, H., Neuweger, H., Pühler, A., Runte, K., Schlüter, A., Stoye, J., Szczepanowski, R., Tauch, A., and Goesmann, A. 2008. Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. *J. Biotechnology*, 136:91-101. <http://dx.doi.org/10.1016/j.jbiotec.2008.06.003> 2014 journal impact factor: 2.884. Cited by 96.
86. Krause L,[§] Diaz NN,[§] Goesmann A, Kelley S, Nattkemper TW, Rohwer F, **Edwards RA**, and Stoye J. 2008. Phylogenetic classification of short environmental DNA fragments. *Nucleic Acids Res.* 36:2230-9. <http://dx.doi.org/10.1093/nar/gkn038> 2014 journal impact factor 8.808. Cited by 189.
87. Field, D., Garrity, G., Gray, T., Morrison, N., Selengut, J., Sterk, P., Tatusova, T., Thomson, N., Allen, M.J., Ashburner, M., Baldauf, S., Ballard, S., Boore, J., Cochrane, G., Cole, J., dePamphilis, C., **Edwards, R.**, Faruque, N., Feldman, R., Glockner, F-O., Haft, D., Hancock, D., Hermjakob, H., Hertz-Fowler, C., Hugenholtz, P., Joint, I., Kane, M., Kennedy, J., Kowalchuk, G., Kottmann, R., Kolker, E., Kyrpides, N., Leebens-Mack, J., Lewis, S.E., Liste, A., Lord, P., Maltsev, N., Markowitz, V., Martiny, J., Methe, B., Moxon, R., Nelson, K., Parkhill, J., Sansone, S-A., Spiers, A., Stevens, R., Swift, P., Taylor, C., Tateno, Y., Tett, A., Turner, S., Ussery, D., Vaughan, B., Ward, N., Whetzl, T., Wilson, G., and Wipat, A., 2008. The minimum information about a genome sequence (MIGS) specification. *Nature Biotechnol.* 26:541–547. <http://dx.doi.org/10.1038/nbt1360> 2014 journal impact factor: 39.08. Cited by 563.
88. Aziz. R. K.^p, Bartels. D., Best. A. A., DeJongh. M., Disz. T., **Edwards. R. A.**, Formsma. K., Gerdes. S., Glass. E. M., Kubal. M., Meyer. F., Olsen. G. J., Olson. R., Osterman. A. L., Overbeek. R. A., McNeil. L. K., Paarmann. D., Paczian. T., Parrello. B., Pusch. G. D., Reich. C., Stevens. R., Vassieva. O., Vonstein. V., Wilke. A., Zagnitko. O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75> 2014 journal impact factor 4.041. Cited by 1812.
89. Gupta, N., Tanner, S., Jaitly, N., Adkins, J., Lipton, M., **Edwards, R.**, Romine, M., Osterman, A., Bafna, V., Smith, R.D., and Pevzner P. 2007. Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. *Genome Research.* 17:1362-1377. <http://dx.doi.org/10.1101/gr.6427907> 2014 journal impact factor: 13.852. Cited by 131.
90. **Edwards, R.A.** and Dinsdale, E.A. 2007. Marine Environmental Genomics: Unlocking the Ocean's Secrets. *Oceanography.* 20:56-61. <http://dx.doi.org/10.5670/oceanog.2007.48> 2014 journal impact factor: 3.285. Cited by 6.
91. Fierer N, Breitbart M, Nulton J, Salamon P, Lozupone P, Jones R, Robeson M, **Edwards RA**, Felts B, Rayhawk S, Knight R, Rohwer F, Jackson RB. 2007. Metagenomic and small-subunit RNA surveys reveal the high genetic diversity of bacteria, archaea, fungi, and viruses in soil. *Appl. Env. Microbiol.* 73:7059–7066. <http://dx.doi.org/10.1128/AEM.00358->

- [07](#) 2014 journal impact factor 3.952. Cited by 248.
92. Wegley, L.[§], **Edwards, R.A.**, Rodriguez-Brito, B.[§], Liu, H.[§], and Rohwer, F. 2007. Metagenomic analysis of the microbial community associated with the coral *Porites astreoides*. *Env. Microbiol.* 9:2707-2719. <http://dx.doi.org/10.1111/j.1462-2920.2007.01383.x> 2014 journal impact factor: 3.264. Cited by 198.
93. McNeil, L., Reich, C., Aziz, R.^p, Disz, T., Cohoon, M., **Edwards, R.**, Gerdes, S., Hwang, K., Kubal, M., Margaryan, G., Olsen, G., Olson, R., Osterman, A., Parrello, B., Vassieva, O., Vonstein, V., Xia, F., Zagnitko, O., Overbeek, R., and Stevens, R. 2007. The National Microbial Pathogen Database Resource (NMPDR): A genomics platform based on subsystem annotation. *Nucl. Acids Research* 35:D347-353. <http://dx.doi.org/10.1093/nar/gkl947> 2014 journal impact factor 8.808. Cited by 81.
94. Joyce, A.R.[§], Reed, J.L.[§], White, A., **Edwards, R.**, Osterman, A., Baba, T., Mori, H., Lesely, S.A., Palsson, B.O., Agarwalla, S. 2006. Experimental and computational assessment of conditionally essential genes in *E. coli*. *J Bacteriol.* 188:8259-8271. <http://dx.doi.org/10.1128/JB.00740-06> 2014 journal impact factor 2.688. Cited by 415.
95. Angly, F.E.[§], Felts, B., Breitbart, M., Salamon, P., **Edwards, R.A.**, Carlson, C., Chan, A.M., Haynes, M., Kelley, S., Liu, H., Mahaffy, J.M., Mueller, J.E., Nulton, J., Olson, R., Parsons, R., Rayhawk, S.[§], Suttle, C.A., and Rohwer, F. 2006. The Marine Viromes of Four Oceanic Regions. *PLoS Biology*. 4:e368. <http://dx.doi.org/10.1371/journal.pbio.0040368> 2014 journal impact factor: 11.771. Cited by 552.
96. Gerdes, S, **Edwards, R.A.**, Kubal, M. Fonstein, M., Stevens, R., and Osterman, A. 2006. Essential genes on metabolic maps. *Curr. Opinion Biotech.* 17:448-456. <http://dx.doi.org/10.1016/j.copbio.2006.08.006> 2014 journal impact factor: 8.035. Cited by 76.
97. Krause, L., [§] Diaz, N.N., Bartels, D., **Edwards, R.A.**, Pühler, A., Rohwer, F., Meyer, F., and Stoye, J. 2006. Finding Novel Genes in Bacterial Communities Isolated from the Environment. *Bioinformatics.* 22:e281-9. <http://dx.doi.org/10.1093/bioinformatics/btl247> 2014 journal impact factor 4.621. Cited by 70.
98. Smith, J.E., **Edwards, R.A.**, Obura, D., Pantos, O.^p, Sala, E., Sandin, S.A., Shaw, M., Smriga, S.[§], and Rohwer, F. 2006. Indirect effects of algae on coral: algae-mediated, microbe-induced coral mortality. *Ecol. Letts.* 9: 835. <http://dx.doi.org/10.1111/j.1461-0248.2006.00937.x> 2014 journal impact factor: 13.042. Cited by 184.
99. **Edwards, R.A.**, Rodriguez-Brito, B.[§], Wegley, L.[§], Haynes, M., Breitbart, M., Peterson, D.M., Saar, M.O., Alexander, S., Alexander Jr., E.C., and Rohwer, F. 2006. Using pyrosequencing to shed light on deep mine microbial ecology under extreme hydrogeological conditions. *BMC Genomics*, 7:57. <http://dx.doi.org/10.1186/1471-2164-7-57> 2014 journal impact factor 4.041. Cited by 377. Cited by 377.
100. Madsen, M. L.[§], Nettleton, D., Thacker, E.L., **Edwards, R.**, and Minion, F.C. 2006. Transcriptional profiling of *Mycoplasma hyopneumoniae* during heat shock using microarrays. *Infect Immun* 74: 160-6. <http://dx.doi.org/10.1128/IAI.74.1.160-166.2006> 2014 journal impact factor: 4.156. Cited by 42.
101. Rodriguez-Brito, B.[§], Rohwer, R., and **Edwards, R.A.** 2006. An application of statistics to comparative metagenomics. *BMC Bioinformatics* 7:162. <http://dx.doi.org/10.1186/1471-2105-7-162> 2014 journal impact factor: 2.672. Cited by 123.
102. DeLong, E. F., C. M. Preston, T. Mincer, V. Rich, S. J. Hallam, N. U. Frigaard, A. Martinez, M.

- B. Sullivan, **R. Edwards**, B. R. Brito[§], S. W. Chisholm and D. M. Karl. 2006. Community genomics among stratified microbial assemblages in the ocean's interior. *Science* 311: 496-503. <http://dx.doi.org/10.1126/science.1120250> 2014 journal impact factor: 31.477. Cited by 787.
103. Trotter, M., McAuliffe, O. Callanan, M. **Edwards**, R. Fitzgerald, G. F. Coffey, A. and Ross, R. P. 2006. Genome analysis of the obligately lytic bacteriophage 4268 of *Lactococcus lactis* provides insight into its adaptable nature. *Gene*. 366:189-199. <http://dx.doi.org/10.1016/j.gene.2005.09.022> 2014 journal impact factor: 2.082. Cited by 18.
104. Overbeek, R., T. Begley, R. M. Butler, J. V. Choudhuri, H. Y. Chuang, M. Cohoon, V. de Crecy-Lagard, N. Diaz, T. Disz, **R. Edwards**, M. Fonstein, E. D. Frank, S. Gerdes, E. M. Glass, A. Goesmann, A. Hanson, D. Iwata-Reuyl, R. Jensen, N. Jamshidi, L. Krause, M. Kubal, N. Larsen, B. Linke, A. C. McHardy, F. Meyer, H. Neuweger, G. Olsen, R. Olson, A. Osterman, V. Portnoy, G. D. Pusch, D. A. Rodionov, C. Ruckert, J. Steiner, R. Stevens, I. Thiele, O. Vassieva, Y. Ye, O. Zagnitko and V. Vonstein 2005. The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Res.* 33: 5691-702. <http://dx.doi.org/10.1093/nar/gki866> 2014 journal impact factor 8.808. Cited by 814.
105. Musumeci, L., C. Bongiorni, L. Tautz, **R. A. Edwards**, A. Osterman, M. Perego, T. Mustelin and N. Bottini (2005). Low-Molecular-Weight Protein Tyrosine Phosphatases of *Bacillus subtilis*. *J Bacteriol* 187: 4945-56. <http://dx.doi.org/10.1128/JB.187.14.4945-4956.2005> 2014 journal impact factor 2.688. Cited by 31.
106. **Edwards, R.A.** and Rohwer, F. 2005. Viral Metagenomics. *Nature Rev. Microbiol.* 3:504-511. <http://dx.doi.org/10.1038/nrmicro1163> 2014 journal impact factor: 23.317. Cited by 412.
107. Aziz, R.K.[§], **Edwards, R.A.**, Taylor, W.W., Low, D.E., McGeer, A., and Kotb. M. 2005. Mosaic Prophages with Horizontally Acquired Genes Account for the Emergence and Diversification of the Globally Disseminated M1T1 Clone of *Streptococcus pyogenes*. *J. Bacteriol.* 187: 3311-3318. 2014 journal impact factor 2.688. Cited by 82.
108. Mijakovic, I., Musumeci, L., Tautz, L., Petranovic, D., **Edwards, R.A.**, Jensen, P.R., Mustelin, T., Deutscher, J., and Bottini, N.. *In Vitro* Characterization of the *Bacillus subtilis* Protein Tyrosine Phosphatase YwqE. *J. Bacteriol.* 187: 3384-3390. <http://dx.doi.org/10.1128/JB.187.10.3384-3390.2005> 2014 journal impact factor 2.688. Cited by 35.
109. Purdy A., Rohwer F., **Edwards R.**, Azam F., and Bartlett DH. 2005. A Glimpse into the Expanded Genome Content of *Vibrio cholerae* through Identification of Genes Present in Environmental Strains. *J Bacteriol.* 187:2992-3001. <http://dx.doi.org/10.1128/JB.187.9.2992-3001.2005> 2014 journal impact factor 2.688. Cited by 46.
110. **Edwards R.A.**, Breitbart M.[§], and Rohwer F.L. 2004. Hidden messages within the genetic code. *ASM news.* July.
111. O'Flaherty S., Ross R.P., **Edwards R.**, Meaney W., Fitzgerald G.F., and Coffey A. 2004. Genome of Staphylococcal Phage K: a New Lineage of Myoviridae Infecting Gram-Positive Bacteria with a Low G+C Content. *J. Bacteriol.* 186:2862-2871. <http://dx.doi.org/10.1128/JB.186.9.2862-2871.2004> 2014 journal impact factor 2.688. Cited by 114.

112. Bhattacharyya A, Stilwagen S, Reznik G, Feil H, Feil WS, Anderson I, Bernal A, D'Souza M, Ivanova N, Kapatral V, Larsen N, Los T, Lykidis A, Selkov E Jr, Walunas TL, Purcell A, **Edwards RA**, Hawkins T, Haselkorn, R, Overbeek R, Kyrpidis NC, and Predki PF. 2002 Draft Sequencing and Comparative Genomics of *Xylella fastidiosa* Strains Reveal Novel Biological Insights. *Genome Res.* 12:1556-63. <http://dx.doi.org/10.1101/gr.370702> 2014 journal impact factor: 13.852. Cited by 68.
113. Rohwer, F.L. and **Edwards, R.A.** 2002. The Phage Proteomic Tree: A Genome-Based Taxonomy for Phage *J. Bacteriol.* 184:4529-35. <http://dx.doi.org/10.1128/JB.184.16.4529-4535.2002> 2014 journal impact factor 2.688. Cited by 339.
114. **Edwards, R.A.**, G.J. Olsen, and S.R. Maloy. 2002. The importance of complete genome sequences. *Trends Microbiol.* 10:220. [http://dx.doi.org/10.1016/S0966-842X\(02\)02354-5](http://dx.doi.org/10.1016/S0966-842X(02)02354-5) 2014 journal impact factor: 9.808
115. **Edwards, R.A.**, G.J. Olsen, and S.R. Maloy. 2002. Comparative genomics of closely related salmonellae. *Trends Microbiol.* 10:94-99. 10.1016/S0966-842X(01)02293-4 2014 journal impact factor: 9.808. Cited by 184.
116. Townsend, S.M., Kramer, N.E. **Edwards, R.A.**, Baker, S., Hamlin, N., Simmonds, M., Stevens, K., Maloy, S.R., Parkhill, J. And Bäumlner, A. J. 2001. *Salmonella enterica* serotype Typhi possesses a unique repertoire of fimbrial genes. *Infect Immun* 69:2894-901. <http://dx.doi.org/10.1128/IAI.69.5.2894-2901.2001> 2014 journal impact factor: 4.156. Cited by 137.
117. **Edwards, R.A.** 2001. Microbial Genome Sequencing. *ASM News.* 67:121.
118. **Edwards, R.A.**, Matlock, B.C., Heffernan, B.J., and Maloy, S.R. 2001. Genomic Analysis and Growth Phase Dependent Regulation Of The SEF14 Fimbriae of *Salmonella enterica* Serovar Enteritidis. *Microbiology.* 147:2705-2715. 2014 journal impact factor: 2.835. Cited by 19.
119. **Edwards, R.A.** and S.R. Maloy. 2001. Inside or Outside: Determining the location of intracellular pathogens. *BioTechniques* 30:304-311. 2014 journal impact factor: 2.754. Cited by 4.
120. **Edwards, R.A.**, D.M. Schifferli, and S.R. Maloy. 2000. A role for *Salmonella fimbriae* in intraperitoneal infections. *Proc. Natl. Acad. Sci USA.* 97:1258-1262. <http://dx.doi.org/10.1073/pnas.97.3.1258> Reviewed in *Trends Microbiol.* 8:211. 2014 journal impact factor: 9.809. Cited by 83.
121. **Edwards, R.A.**, R.A. Helm and S.R. Maloy. 1999. Increasing DNA transfer efficiency by temporary inactivation of host restriction. *BioTechniques* 26: 892-900. 2014 journal impact factor: 2.754. Cited by 32.
122. **Edwards, R.A.**, and J.L. Puente. 1998. Fimbrial expression in enteric bacteria: A critical step in intestinal pathogenesis. *Trends Microbiol.* 6: 282-287. [http://dx.doi.org/10.1016/S0966-842X\(98\)01288-8](http://dx.doi.org/10.1016/S0966-842X(98)01288-8) 2014 journal impact factor: 9.809. Cited by 63.
123. **Edwards, R.A.**, L.H. Keller, and D.M. Schifferli. 1998. Improved allelic exchange vectors and their use to analyze 987P fimbria gene expression. *Gene* 207: 149-157. [http://dx.doi.org/10.1016/S0378-1119\(97\)00619-7](http://dx.doi.org/10.1016/S0378-1119(97)00619-7) 2014 journal impact factor: 2.082. Cited by 276.
124. **Edwards, R.A.**, and D.M. Schifferli. 1997. Differential regulation of *fasA* and *fasH* expression of *Escherichia coli* 987P fimbriae by environmental cues. *Mol. Microbiol.* 25: 797-809. <http://dx.doi.org/10.1046/j.1365-2958.1997.5161875.x> 2014 journal impact factor: 5.026.

Cited by 38.

125. **Edwards, R.A.**, J. Cao, and D.M. Schifferli. 1996. Identification of major and minor chaperone proteins involved in the export of 987P fimbriae. *J. Bacteriol.* 178: 3426-3433. 2014 journal impact factor 2.688. Cited by 25.
126. Merrick, M.J., and **R.A. Edwards**. 1995. Nitrogen control in bacteria. *Microbiol. Mol. Biol. Rev.* 59:604-622. 2014 journal impact factor: 15.255. Cited by 564.
127. **Edwards, R.A.**, and M.J. Merrick. 1995. The role of uridylyltransferase in the control of *Klebsiella pneumoniae nif* gene regulation. *Mol. Gen. Genet.* 247: 189-198. 2014 journal impact factor: 2.831. Cited by 43.

^pDenotes postdoctoral researcher

^gDenotes graduate student.

^uDenotes undergraduate student

Citations from Google Scholar as of September 1st, 2014.

Journal impact factors from <http://www.citefactor.org/> as of September 1st, 2014.

Genome Announcements (not peer reviewed):

1. Lorenzi AS, Silva GGZ, Lopes FAC, Chia MA, **Edwards RA**, Bittencourt-Oliveira MC. 2016. Draft Genome Sequence of *Cylindrospermopsis raciborskii* (Cyanobacteria) Strain ITEP-A1 Isolated from a Brazilian Semiarid Freshwater Body: Evidence of Saxitoxin and Cylindrospermopsin Synthetase Genes. *Genome Announc* 4:e00228–16.
2. Calva E, Silva C, Zaidi MB, Sanchez-Flores A, Estrada K, Silva GGZ, Soto-Jiménez LM, Wiesner M, Fernández-Mora M, **Edwards RA**, Vinuesa P. 2015. Complete Genome Sequencing of a Multidrug-Resistant and Human-Invasive *Salmonella enterica* Serovar Typhimurium Strain of the Emerging Sequence Type 213 Genotype. *Genome Announc* 3:e00663–15.
3. Eppinger Mg , McNair K, Zogaj X, Dinsdale EA, Edwards RA, Klose KE. 2013. Draft Genome Sequence of the Fish Pathogen *Piscirickettsia salmonis*. *Genome Announc.* 1. <http://dx.doi.org/10.1128/genomeA.00926-13> (No impact factor). Cited by 1

Published Meeting Abstracts:

1. R.K. Aziz, Dwivedi, B., Breitbart, M., and **Edwards, R.A.** 2011 Phage Eco-Locator: a web tool for visualization and analysis of phage genomes in metagenomic data sets *BMC Bioinformatics* 12:A9doi:10.1186/1471-2105-12-S7-A9
2. Wu, W., **Edwards, R.A.**, Judson, I. R., Papka, M. E., Thomas, M., and Stevens, R. 2008. TeraGrid Open Life Science Gateway. Proceedings of the 3rd annual TeraGrid Conference, TeraGrid '08.
3. **RA Edwards**. 2008. The smallest cells pose the biggest problems: high-performance computing and the analysis of metagenome sequence data. *J. Phys.: Conf. Ser.* 125 012050. <http://dx.doi.org/10.1088/1742-6596/125/1/012050> Cited by 1.

Published Meeting And Book Reviews:

1. Farris, L.A. and R.A. Edwards. 2001. An old dog learns new tricks. *Trends. Microbiol.* 95:243
2. Edwards, R.A., and S.R. Maloy. 2000. Microbial genomics and evolution. *Trends Genet* 16:115.
3. Edwards, R.A. 2000. Big bugs need little bugs to help them bite. *Trends. Microbiol* 8:384-385
4. Maloy, S.R., and R.A. Edwards. 1999. Eye of newt and toe of frog. *Trends Genet* 15:250.
5. Edwards, R.A., and S.R. Maloy. 1998. Examining *E. coli*. *Bioscience* 48:323-324.

World Wide Web Sites:

1. The Salmonella Source: <http://www.salmonella.org/>. Reviewed in *Science* 2001 293(5532):1019
2. SCUMS: <http://scums.sdsu.edu/> The San Diego Center for Universal Microbial Sequencing.
3. Edwards Lab: <http://edwards.sdsu.edu/research>
4. PhAnToMe: <http://www.phantome.org/>
5. The Phage SEED: <http://www.phantome.org/PhageSeed/>
6. Viral Dark Matter: <http://vdm.sdsu.edu/>

Major contributions:

1. RAST <http://rast.nmpdr.org/>
2. MG-RAST <http://metagenomics.anl.gov/>
3. SEED <http://www.theseed.org/>
4. NMPDR <http://www.nmpdr.org/>

Invited Presentations (Since 2000):

1. Computational Sciences Research Center, SDSU, 1/2016
2. Translational Research Institute, Brisbane, Australia, 11/2015
3. Federal University of Rio de Janeiro, Brazil 11/2015
4. Univeristy of Queensland, Australia 11/2015
5. Flinders University, Australia 9/2015
6. University of Illinois at Urbana Champaign, 9/2015
7. University of Iowa Medical School, 4/2015
8. Asociacion Mexicana de Microbiología Querétaro, Mexico (two talks) 3/2015
9. JAMS-TOAST, Australian Museum, 2/2015
10. University of New South Wales, 2/2015
11. Sydney Institute of Marine Sciences, 2/2015
12. Flinders University, Adelaide, Australia, 1/2015
13. University of Sao Paulo, Sao Paulo, Brazil, 11/2014
14. University of Sao Paulo, Piracicaba, Brazil, 11/2014
15. Radboud University Medical Center Nijmegen, The Netherlands, 7/2014
16. Viruses of Microbes Meeting, Zurich, Switzerland 7/2014
17. Diponegoro University, Semarang, Indonesia 5/2014
18. Hasanuddin University, Makassar, Indonesia 5/2014
19. Federal University of Rio de Janeiro (UFRJ), Rio de Janeiro, Brazil. 4/2014
20. Computational Sciences Research Center, San Diego 11/2013
21. Lawrence Berkley National Laboratory, 7/2103

22. American Society of Microbiology, Biology of Viruses, San Francisco 7/2013
23. Autonomous University of Mexico, Cuernavaca 4/2013
24. Federal University of Rio de Janeiro (UFRJ), Rio de Janeiro, Brazil. 3/2013
25. Case Western Reserve University Graduate Student invited speaker. Cleveland, OH 3/2013
26. Biolog SRI Conference on Predicting Cell Metabolism and Phenotypes, Menlo Park, CA 3/2013
27. University of California, San Diego. San Diego, CA. 2/2013
28. University of Southern California, Los Angeles, CA. 2/2013
29. LIPI-NSF, Workshop on Dimensions of Biodiversity, Cibinong, Indonesia 2/2013
30. National Science Foundation, Washington DC. 1/2013
31. Southern California Systems Biology Conference, Irvine, CA. 1/2013
32. Congresso Brasileiro de Oceanografia - CBO 2012, Rio de Janeiro, Brazil 11/2012
33. 7th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil 11/2012
34. Bigelow Laboratory, ME 10/2012
35. Bertinoro Computational Biology Meeting, Bertinoro, Italy, 10/2012
36. International Conference of the IEEE Engineering in Medicine and Biology Society, San Diego, CA 8/2012
37. American Society Microbiology General Meeting, San Francisco, CA 6/2012
38. Roche/454 User Group Meeting, Indianapolis, IN 5/2012
39. International Workshop on Bioinformatics. Cuernavaca, Mexco. 1/2012
40. Instituto de Biotecnología. Cuernavaca, Mexco. 1/2012
41. 6th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil 10/2011
42. Kavli Foundation Frontiers in Science, National Academy of Sciences, 11/2011
43. Metagenomics Workshop. Florida Branch ASM, 10/2011
44. San Diego State University Research Foundation Inaugural PI Presentation, San Diego 9/2011
45. Ecology and Genomics of Cystic Fibrosis, CO 7/2011
46. Microbial Genomics and Modelling, Park City, UT 7/2011.
47. Life Technologies, 5/2011
48. Computational and Comparative Genomics, Cold Spring Harbor, NY 11/2010
49. Computational Genomics, Cuernavaca, Mexico, 10/2010
50. FIPSE-CAPES directors meeting, Florianopolis, Brazil, 9/2010
51. Molecular Genetics of Bacteria and Phages, Cold Spring Harbor Laboratory, NY, 8/2010
52. 5th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil 8/2010
53. Advanced Bacterial Genetics Course, Cold Spring Harbor, NY 6/2010
54. American Society for Microbiology, San Diego, CA 5/2010
55. Roche Asia User Group Meeting, Hong Kong, 5/2010
56. Scripps Institution of Oceanography, San Diego, CA 4/2010
57. University of California, Santa Barbara, CA, 4/2010
58. Centro de Investigación Científica y de Educación Superior de Ensenada, BC, Mexico 4/2010
59. First Mexican Congress on Microbiology and Biochemistry, Pachuca, Mexico, 3/2010
60. Bioinformatics Two Day Course, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, Mexico 1/2010
61. Rocky 2009, Snowmass, CO, 12/2009

62. Mexican National Congress of Virology, Merida, Mexico, 11/2009
63. University of Florida, Gainesville, FL 10/2009
64. Florida Branch of the American Society for Microbiology, Key West, FL 10/2009
65. Computational Sciences Research Center, San Diego, 9/2009
66. San Diego Consortium for Systems Biology, Salk Institute, San Diego, 8/2009
67. DOE Computing in the Extreme, Chicago IL 8/2009
68. Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil 8/2009
69. 4th Workshop on Comparative Microbial Genomics and Taxonomy, Petropolis, Brazil 8/2009
70. C-MORES Workshop on Marine Microbiology, Honolulu, Hawai'i, 5/2009
71. American Society of Microbiology, Philadelphia, PA 5/2009
72. Autonomous University of Mexico, Cuernavaca 03/2009
73. CHI New Genomics Workshop, San Diego, CA 03/2009
74. Collabrx, Palo Alto, CA 03/2009
75. United States Department of Agriculture, Washington DC 02/2009
76. University of California, Santa Barbara 02/2009
77. University of California, Los Angeles 01/2009
78. Rocky Mountain Bioinformatics Meeting, Snowmass, CO 12/2008
79. Roche 454, New Haven, CT 9/2008
80. Scientific Discoveries Through Advanced Computing, Seattle, WA 7/2008
81. International Coral Reef Society Meeting, Fort Lauderdale, FL 7/2008
82. Advanced Bacterial Genetics Course, Cold Spring Harbor, NY 6/2008
83. American Society of Microbiology (ASM), Boston, MA 06/2008
84. Rocky Mountain Bioinformatics Meeting, Snowmass, CO 12/2007
85. US/EU Conference on CyberInfrastructure, Washington, DC 10/2007
86. American Society of Microbiology (ASM), Toronto, Canada 06/2007
87. CHI New Genomics Workshop, San Diego, CA 05/2007
88. Argonne National Labs, Argonne, IL. 03/2007
89. Metagenomics 2006, San Diego, CA 10/2006
90. Joint Genome Institute, Walnut Creek, CA. 09/2006
91. Genome Standard Consortium, Cambridge, England. 09/2006
92. California Metagenomics Workshop, Berkeley, CA. 09/2006
93. ASM/NCBI Genome Annotation Workshop, NIH Bethesda, MD. 08/2006
94. Scientific Committee on Oceanographic Research (SCOR), Vancouver, Canada. 06/2006
95. Scripps Institute of Oceanography 06/2006
96. The Sanger Center, Cambridge, England. 05/2006
97. Society for General Microbiology, Warwick, England. 05/2006
98. San Diego State University Computational Sciences Research Center. 03/2006
99. American Society of Limnology and Oceanography (ASLO), Session Organizer and Chair, HI 02/2006
100. Argonne National Labs, Argonne, IL. 01/2006
101. Analytical Genetics, San Diego, CA. 10/2005
102. Barcode of Life Meeting, Panama. 09/2006
103. American Society of Microbiology (ASM), Session Organizer and Chair. 06/2005
104. San Diego Microbiology Group, San Diego, CA. 05/2005
105. US/EU Conference on Marine Genomics, Bremen, Germany. 05/2005

106. The Burnham Institute for Medical Research, San Deigo, CA. 07/2004
107. The New Phage Meeting, Key Biscayne, FL. 06/2004
108. American Society of Microbiology (ASM), 05/2004
109. The University of Memphis, Memphis, TN 11/2003
110. The VA Hospital, Memphis, TN 07/2003
111. University of Oxford, England, 02/2003
112. University of Missouri, Columbia, MO 01/2003
113. San Diego State University, San Diego, CA 11/2002
114. South East Regional Bioterrorism Workshop, Memphis TN 07/2003
115. Centre National de la Recherche Scientifique, Gif-sur-Yvette, France,10/2002
116. Analytical Genetics, Santorini, Greece 10/2002
117. The University of Sheffield, England 9/2002
118. American Society of Microbiology (ASM) (session chair), 05/2002
119. Southern Illinois University, Carbondale, IL 04/2002
120. Institute of Biotechnology, Cuernavaca, MX 01/2002
121. Furman College, Greenville, SC 11/2001
122. Oak Ridge National Laboratory, 10/2001
123. Molecular Genetics of Bacteria and Phage, Cold Spring Harbor, 09/2001.
124. Iowa State University, Ames, IA. 04/2001
125. The Center for Ecology and Hydrology, Oxford University, England, 03/2001
126. Veterinary School, Autonomous University of Mexico, Mexico, MX 01/2001
127. Institute of Biotechnology, Cuernavaca, MX 01/2001
128. Midwest Pathogenesis Meeting, Columbus, OH 10/2000
129. Molecular Genetics of Bacteria and Phage, Madison, WI, 09/2000.
130. The VA Hospital, Memphis, TN 07/2000
131. Salmonella Genomics Meeting, St. Louis MO 04/2000
132. Midwest Prokaryotic Molecular Biology Meeting, Chicago IL 01/2000

Teaching:

San Diego State University:

Primary instructor

2014	Fall	Programming Problems in Bioinformatics, CS696
2014	Fall	Computational Genomics, CS609
2014	Spring	Topics in Comptuational Science, COMP800
2014	Spring	Topics in Global Climate Change, COS696
2014	Spring	Web scripting languages, CS547
2014	Spring	Data Structures, CS310
2013	Fall	Scientific Data Base Techniques, CS503
2013	Spring	Data Structures, CS310
2013	Spring	Web scripting languages, CS547
2012	Fall	CS Advanced Topics: Computational Genomics, CS596
2012	Fall	Scientific Data Base Techniques, CS503

Dr. Robert Edwards. Biosketch

2012	Spring	Data Structures, CS310
2011	Fall	CS Advanced Topics: Computational Genomics, CS596
2011	Spring	Data Structures, CS310
2010	Fall	CS Advanced Topics: Computational Genomics, CS596. This class is being taught in collaboration with Dr. Rosy Guterrez at the Autonomous University of Mexico, Cuernavaca, Mexico, using the SDSU distance learning technology (video conferencing).
2010	Fall	Computational Sciences Interdisciplinary Approaches, COMP 800
2010	Spring	Data Structures, CS310
2009	Fall	Scientific Data Base Techniques, CS503
2009	Spring	CS Advanced Topics: Genome Annotation and Analysis, CS696
2009	Spring	Data Structures, CS310
2008	Fall	Scientific Data Base Techniques, CS503
2008	Spring	Data Structures, CS310

Guest instructor

2014	Summer	Bridges to the Baccalaueate Program
2014	Spring	SDSU/UCSD Integrated Microbiology
2014	Spring	Ecological metagenomics, BIO 562
2013	Summer	Bridges to the Baccalaueate Program
2013	Spring	SDSU/UCSD Integrated Microbiology
2013	Spring	Ecological metagenomics, BIO 562
2012	Spring	Ecological metagenomics, BIO 562
2012	Summer	Howard Hughes Program, SDSU
2012	Summer	Bridges to the Baccalaueate Program
2011	Fall	S-STEM
2011	Summer	Bridges to the Baccalaueate Program
2011	Spring	Microbial genetics and physiology BIOL 549
2011	Spring	Methods in Bioinformatics CS600
2011	Spring	Ecological metagenomics, BIO 562
2010	Summer	Bridges to the Baccalaueate Program
2010	Spring	Microbial genetics and physiology BIOL 549
2010	Spring	Ecological metagenomics, BIO 562
2010	Spring	Advanced topics in molecular biology, MBIO610
2009	Summer	Bridges to the Baccalaueate Program
2009	Summer	Research Experience for Undergraduates
2009	Spring	Advanced topics in computational science COMP 670
2009	Spring	Microbial genetics and physiology BIOL 549
2008	Summer	Bridges to the Baccalaueate Program
2008	Spring	Microbial genetics and physiology BIOL 549
2007	Summer	Bridges to the Baccalaueate Program
2007	Spring	Microbial genetics and physiology BIOL 549

University of Tennessee Health Sciences Center:

- 2004 Molecular Biology, MSCI816
- 2004 Bioinformatics, MSCI814, course director
- 2003 Molecular Biology, MSCI816
- 2002 Bacterial Pathogenesis, MSCI700, course designer and director
- 2002 Bioinformatics, MSCI814, course director
- 2002 Molecular Biology, MSCI816
- 2002 Bioinformatics, MSCI815
- 2001 Molecular Techniques, MSCI929

Workshops:

Instructor

- 2015 Genomics, Metagenomics, and Viromics, Flinders, Australia (organizer and instructor)
- 2015 Genomics, Metagenomics, and Viromics, San Diego, CA (organizer and instructor)
- 2015 High performance computing workshop, San Diego, CA (organizer and instructor)
- 2015 STEMM: Sequencing Technology Education Using Microbial Metagenomes, San Diego, CA
- 2015 Tutorial on Omics Analysis and Tools, Sydney, Australia
- 2015 SIMS Summer Course on Marine Microbial Ecology, Sydney, Australia
- 2014 2nd Workshop on analysis of microbial genome sequences and metagenomics, Ensenada, Mexico
- 2014 STEMM: Sequencing Technology Education Using Microbial Metagenomes, San Diego, CA
- 2013 Workshop on analysis of microbial genome sequences and metagenomics, La Paz, Mexico
- 2012 7th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil
- 2012 International Workshop on Bioinformatics, Cuernavaca, Mexico.
- 2011 6th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil
- 2010 5th Workshop on Comparative Microbial Genomics and Taxonomy, Rio de Janeiro, Brazil
- 2010 CICESE Two-day course in Bioinformatics and Computational Biology.
- 2010 Computational Genomics, Cold Spring Harbor Laboratory, NY
- 2010 Advanced Bacterial Genetics, Cold Spring Harbor Laboratory, NY
- 2010 UCSB Special Workshop on metagenomics. A two day workshop for 15 students and faculty members of the bioinformatics of metagenomics data.
- 2010 Microbial genomics and metagenomics workshop, Rio de Janeiro, Brazil. An invited lecturer in a week long workshop on microbial genomics, metagenomics, and taxonomy.
- 2009 Metagenomics Workshop, Argonne National Laboratory, Argonne IL,
- 2009 Microbial genomics and metagenomics workshop, Petropolis, Brazil. An invited lecturer in a week long workshop on microbial genomics, metagenomics, and taxonomy.
- 2009 C-MORES Workshop on Marine Biology. An invited lecturer in this week-long workshop to teach metagenomics and bioinformatics.
- 2008 Metagenomics Workshop, Argonne National Laboratory, Argonne IL,
- 2008 Advanced Bacterial Genetics, Cold Spring Harbor Laboratory, NY
- 2007 Metagenomics Workshop, Argonne National Laboratory, Argonne IL,
- 2005 Second International Minicourse on Genetics, Genomics, and Epidemiology of Salmonella, Nanning, China. November
- 2004 First International Minicourse on Genetics, Genomics, and Epidemiology of Salmonella,

Cuernavaca, Mexico. November

Participant

- 1999 NSF/DOE sponsored participant in the 7th Conference on Small Genomes, Arlington VA
- 1995 Participant in the Advanced Bacterial Genetics Course, Cold Spring Harbor Laboratory
06/1995

Trainees:

Visting scholars

- Cazares, Adrian (Visiting scholar from CINVESTAV, Mexico City, Mexico)
- Dutilh, Bas (Visiting scholar from Radboud University Medical Centre, the Netherlands)
- Fernandes, Lohengrin (Visiting scholar from the Brazilian navy)
- Paterson, James (Flinders University, Adelaide, Australia)
- Smith, Renee (Flinders University, Adelaide, Australia)
- Thompson, Cristiane (Visiting scholar from FIOCRUZ, Brazil)
- Thompson, Fabiano (Visiting scholar from the Federal University of Rio de Janeiro, Brazil)

Postdoctoral Researchers

- Aziz, Ramy (currently an Assistant Professor, University of Cairo)
- Frank, Jeremy (currently a Postdoctoral Researcher at Norwegian University of Life Sciences)
- Matthews, Dave (currently a Head of Technology at Phyllom, Inc)

Ph.D. Graduates

- Schmieder, Robert (currently at Illumina, San Diego)
- Akhter, Sajia (currently at Stanford University)

Ph.D. Students

- Cantu, Adrian
- Cuevas, Daniel
- Silva, Genivaldo
- Bose, Promita
- Farris, Leigh
- Seguritan, Victor

M.Sc. Students

- Baer, Adam
- Cheng, Carny
- Feupe, Stephanie Feudjio
- Fuyu, David
- Grant, Matthew
- Hamel, Kristina

Hisakawa, Nao
Hull, Brad
Kang, Han Suh
Liang, Tiff Yujing
Levi, Kyle
McNair, Kate
Naoman, Amna
O'Connell, Taylor
Park, Songduk
Raheema, Julian
Robinson, Blaire
Sadural, Jeffrey
Sanchez, Savannah
Smith, Iris
Soury, Rima
Turner, Nick
Williams, Steve
Wright, Sheridan

Undergraduate Students

Beacher, Jon
Belon, Patrick
Benavides, Georgina
Blanco, Andres
Celms, Nick
Comeau, Joey
Cuevas, Daniel
Dempsey, Michael
Garrido, Haydee
Goodwin, Josh
Hagen, Matthew
Hoffman, Josh
Hudson, Brian
Kamikisidian, Vasken
Kassen, Ted
Lentz, Palla
Li, Jimmy
Lin, Joseph
Lui, Heqiao
Matonis, Ryan
Pham, Huy
Robinson, Blaire
Sadural, Jeffrey
Sanchez, Savannah
Seitz, Matt

Dr. Robert Edwards. Biosketch

Smith, Dwaine
Steinman, Tracy
Tadesse, Ruth
Tam, Evan
Tosti, Salvatore
Turner, Nick
Turner, Tyler
Vega, Alejandro
Wellington-Oguri, Michiyo
Westerhoff, David
Wright, Sheridan
Zhou, Meng

Visting Brazilian Students (Students in my lab only. The exchange welcomed 35 scholars to SDSU)

Ballester, Marcela
Correia, Guilherme
Dias da Silva, Tharles
Gambarini, Victor
Garza, Daniel
Machado, Augustoa
Martins, Karen
Meirelles, Pedro
Monteirocosta, Leonardo
Navarrete, Acacio
Silva, Jose Aldo
Trinidad, Amanda

High School Students

Baxi, Ankita, AP Biology Research Intern
Klimkowsky, Miron High School Summer Studentt
St. Bernard, Nashan. McNair Summer Student
Davis, Shanita McNair Summer Student
Holmes, Stacy McNair Summer Student

SDSU Committees:

Special Review Panel of the College of Sciences Policy and Planning Committee, 2015
Association of Computing Machinery Faculty Advisor, 2011-
Bioinformatics and Medical Informatics Curriculum Committee, 2008-
Biotechnology Students Association Faculty Advisor, 2011-
Computational Sciences Research Center Advisory Committee, 2007-

Computer Science Faculty Search Committee, 2014

Dean Maloy five year review. 2013

Diving Safety Committee, 2008-

International Committee, 2010-

Viromics Institute BioMath position Faculty Search Committee, 2014

Viromics Institute Structural Biology position Faculty Search Committee, 2014

Thesis Committee Meetings:

<i>Student</i>	<i>Program</i>	<i>Role</i>	<i>Degree</i>	<i>Date</i>
Robert Schmieder	CSRC	Chair	PhD	11/30/2012
Sajia Akhter	CSRC	Chair	PhD	08/30/2013
Amna Naoman	CS	Chair	Msc	11/23/2009
Songduk Park	CS	Chair	Msc	11/30/2009
Matthew Grant	CS	Chair	Msc	12/08/2009
Stephanie Feudjio	BMI	Chair	Msc	05/01/2011
Kate McNair	CSRC	Chair	Msc	07/22/2011
Jimmie Dixon	CS	Chair	Msc	08/31/2011
Sheridan Wright	CS	Chair	Msc	11/05/2012
Steven Williams	CS	Chair	Msc	11/21/2012
Andrew Luxner	CS	Chair	Msc	04/18/2013
Tiff Liang	BMI	Chair	Msc	06/25/2014
Matthew Shaw	CS	Chair	Msc	12/02/2014
Adriel Carolina	BMI		Msc	03/26/2013
Angela DiDomenico	Biology		Msc	05/08/2014
Beltran Rodriguez Brito	CSRC		PhD	06/09/2009
Ben Knowles	Biology		PhD	06/20/2014
Burak Cebecioglu	Math		Msc	05/13/2010
Burak Cebecioglu	Math		Msc	05/13/2010
Byant Fulk	Geology		Msc	05/07/2010
Dave Carlson	Biology		Msc	11/21/2013
Dave Carlson	Biology		Msc	06/15/2015
Florent Angly	CSRC		PhD	06/04/2009
Gauree Bhole	CS		Msc	05/14/2010
Hoda Sayyadinejad	CS		Msc	08/28/2014
Jake Minich	BMI		Msc	05/30/2014
Jordan Satler	Biology		Msc	05/10/2011
Ketake Raste	CS		Msc	04/14/2014
Lauryn Keeler	BMI		Msc	10/04/2013
Lee Ripma	Biology		Msc	12/02/2013
Lena van der Stapp	CSRC		Msc	10/14/2011
Mackenzie Mabry	Biology		Msc	11/26/2013
Martis Cowles	Biology*		PhD	03/13/2013
Martis Cowles	Biology		PhD	02/20/2014
Matt Munoz	Biology		Msc	01/06/2012

Nori Cassman	BMI		Msc	12/16/2013
Paul Fryling	BMI		Msc	05/08/2013
Pedro Tores	BMI		Msc	09/10/2013
Pratyusha Uddaraju	CS	Chair	Msc	10/29/2015
Savannah Sanchez	Biology		Msc	02/21/2014
Seena Farzaneh	BMI		Msc	04/08/2013
Shashank Sathe	BMI		Msc	11/26/2013
Shashank Sathe	BMI		Msc	07/10/2015
Sowmya Vijay	BMI		Msc	04/16/2014
Srinidhi Balaram	CS		Msc	04/09/2015
Steve Quistad	Biology*		PhD	01/31/2013
Steve Quistad	Biology		PhD	05/01/2015
Veronica Casas	Biology		PhD	04/22/2011
Wei Wang	CS*		PhD	03/13/2014
Wei Wang	CS		PhD	03/26/2015
Yan Wei Lim	Biology		PhD	02/15/2012
Yan Wei Lim	Biology*		PhD	02/14/2014
Yan Wei Lim	Biology*		Msc	05/09/2011

* Proposal meeting

Student Research Projects (since 2011):

<i>Semester</i>	<i>Name</i>	<i>Class</i>	<i>Project</i>
Spring 2014	Genivaldo Silva	Comp 894	Genivaldo wrote and implemented the FOCUS tool for analysis of metagenomes
Spring 2014	Daniel Cuevas	Comp 897	Daniel worked on the Viral Dark Matter project, analyzing and modeling the growth of bacteria
Spring 2014	David Westerhoff	CS 499	David designed an API for the Viral Dark Matter database to allow computational access of the data
Spring 2014	Ryan Matonis	CS 499	Ryan worked on the analysis of Shannon's theory as it applies to DNA sequence analysis
Spring 2014	Salvatore Tosti	CS 499	Salvatore implemented a complete Python version of the image detection and classification problem for coral reef images
Spring 2014	Ted Kassen	CS 499	Ted built a website for analysis of Viral Dark Matter data
Spring 2014	Andrew Miller	CS 797	Andrew is writing a suffix trie to store genomic data
Spring 2013	Sajia Akhter	Comp 899	Sajia worked on her PhD thesis
Spring 2013	Patrick Belon	CS 497	Patrick built an autonomous heart rate measuring device
Spring 2013	Heqiao Liu	CS 498	HQ designed and implemented the database and website for the Viral Dark Matter project.
Spring 2013	Blaire Robinson	CS 499	Blaire designed and implemented a microbial database that is used to capture information about how microbes grow
Spring 2013	Dwaine Smith	CS 499	Dwaine was responsible for adding all the microbe data to the database designed by Blaire.

Spring 2013	Haydee Garrido	CS 499	Haydee worked on data mining for the Viral Dark Matter Project, implementing different algorithms to explore the raw data.
Spring 2013	Jeff Sadural	CS 499	Jeff has converted PrinSeq, written by PhD student Rob Schmieder, into C++ code
Spring 2013	Tyler Turner	CS 499	Tyler wrote and implemented the Prosilica interface for the ATRIS project.
Spring 2012	Robert Schmieder	Comp 897	Rob worked on his PhD thesis
Spring 2012	Sajia Akhter	Comp 897	Sajia worked on her PhD thesis
Spring 2012	Brian Hudson	CS 497	Brian designed and implemented the prosilica interface for the ATRIS software
Spring 2012	Heqiao Liu	CS 499	HQ designed and implemented the database and website for the Viral Dark Matter project.
Spring 2012	Jimmy Li	CS 499	Jimmy created a website for automated image analysis, allowing users to upload a set of images and have them analyzed
Spring 2012	Michiyo Wellington-Oguri	CS 499	Michiyo wrote novel data mining algorithms to identify the host of different kinds of virus
Spring 2011	Katelyn McNair	Comp 798	Katelyn wrote PHACTS for the comparison of phage genomes
Spring 2011	Robert Schmieder	Comp 897	Rob worked on his PhD thesis
Spring 2011	Sajia Akhter	Comp 897	Sajia worked on her PhD thesis
Spring 2011	Alf Scotland	CS 499	Alf wrote image analysis software to detect the movement of objects in a series of images
Spring 2011	Brian Hudson	CS 499	Brian designed and implemented the prosilica interface for the ATRIS software
Spring 2011	Daniel Cuevas	CS 499	Daniel worked on the Viral Dark Matter project, analyzing and modeling the growth of bacteria
Fall 2013	Blaire Robinson	Bio 499	Blaire designed and implemented a microbial database that is used to capture information about how microbes grow
Fall 2013	Daniel Cuevas	Comp 897	Daniel worked on the Viral Dark Matter project, analyzing and modeling the growth of bacteria
Fall 2013	David Westerhoff	CS 499	David designed an API for the Viral Dark Matter database to allow computational access of the data
Fall 2013	Patrick Belon	CS 499	Patrick built an autonomous heart rate measuring device
Fall 2013	Ryan Matonis	CS 499	Ryan worked on the analysis of Shannon's theory as it applies to DNA sequence analysis
Fall 2013	Ted Kassen	CS 499	Ted built a website for analysis of Viral Dark Matter data
Fall 2012	Vernon Wages	Comp 797	Vernon wrote an image stitching algorithm that can handle thousands of images simultaneously.
Fall 2012	Sajia Akhter	Comp 897	Sajia worked on her PhD thesis
Fall 2012	Robert Schmieder	Comp 899	Rob worked on his PhD thesis
Fall 2012	Dwaine Smith	CS 497	Dwaine was responsible for adding all the microbe data to the database designed by Blaire.

Dr. Robert Edwards. Biosketch

Fall 2012	Haydee Garrido	CS 497	Haydee worked on data mining for the Viral Dark Matter Project, implementing different algorithms to explore the raw data.
Fall 2012	Jeff Sadural	CS 497	Jeff has converted PrinSeq, written by PhD student Rob Schmieder, into C++ code
Fall 2012	Michael Dempsey	CS 497	Mike wrote image analysis code in Python using OpenCV to detect movement in images
Fall 2012	Tyler Turner	CS 497	Tyler wrote and implemented the Prosilica interface for the ATRIS project.
Fall 2012	Blaire Robinson	CS 499	Blaire designed and implemented a microbial database that is used to capture information about how microbes grow
Fall 2012	Daniel Cuevas	CS 797	Daniel worked on the Viral Dark Matter project, analyzing and modeling the growth of bacteria
Fall 2011	Robert Schmieder	Comp 897	Rob worked on his PhD thesis
Fall 2011	Sajia Akhter	Comp 897	Sajia worked on her PhD thesis
Fall 2011	Brian Hudson	CS 499	Brian designed and implemented the prosilica interface for the ATRIS software
Fall 2011	Jimmy Li	CS 499	Jimmy created a website for automated image analysis, allowing users to upload a set of images and have them analyzed
Fall 2011	Michiyo Wellington-Oguri	CS 499	Michiyo wrote novel data mining algorithms to identify the host of different kinds of virus
Fall 2011	Nicholas Turner	CS 499	Nick helped design the database for the viral dark matter project