

# Kim RUTHERFORD

*Software Development and Bioinformatics*

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## Profile

I am a software developer and bioinformatician. For the last 18 years I have been helping biologists to analyse and interpret genomic data.

## Education

Bachelor of Science with Honours in Computer Science and Mathematics. Victoria University, Wellington, New Zealand

## Skills and Experience

- Software development: web, desktop and server
- Database administration and maintenance
- Genome annotation and analysis
- Processing, management and analysis of next generation sequencing data
- Systems administration including software and database installation and configuration

## Work experience

Sept 2012 – Present **Scientific Officer** *Gemmell lab*  
Department of Anatomy, University of Otago  
*Tasks* bioinformatics support for the group  
genome and transcriptome assembly and analysis  
mentoring / training of group members in bioinformatics  
[🌐 tuatara](#) [🌐 genome project](#)

June 2010 – Present **Programmer** *S. pombe genome database (PomBase)*  
Department of Biochemistry, University of Cambridge  
*Tasks* web and database programming  
system administration for [curation.pombase.org](http://curation.pombase.org)  
*Main project* [🌐 Canto](#) - a community curation tool

Feb 2009 – June 2010 **Computer Associate** *Baulcombe Group*  
Department of Plant Sciences, University of Cambridge  
*Tasks* bioinformatics support  
creation of a short read analysis pipeline

Sept 2007 – Feb 2009 **Programmer** *modENCODE Data Coordination Center*  
Cambridge Systems Biology Centre  
*Tasks* helped create the data warehouse for the data from modENCODE:  
[🌐 modMine](#)

Feb 2004 – Sept 2007 **Programmer** *FlyMine/InterMine group*  
Department of Genetics, University of Cambridge  
*Tasks* Java programming for the [🌐 InterMine](#) project

Sept 1998 – Feb 2004 **Principal Computer Programmer** *Pathogen Sequencing Unit*  
The Sanger Institute  
*Tasks* programming and bioinformatics support  
*Major projects* [🌐 Artemis](#) - a genome analysis and annotation tool  
[🌐 ACT](#) - a genome comparison viewer

## Publications

- Feb 2000 **The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.**  
J. Parkhill et al.  
*Nature*. 2000 Feb 10;403(6770):665-8.
- Mar 2000 **Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.**  
J. Parkhill et al.  
*Nature*. 2000 Mar 30;404(6777):502-6.
- Oct 2000 **Artemis: sequence visualisation and annotation.**  
K. Rutherford, J. Parkhill, J. Crook, T. Horsnell, P. Rice, M-A. Rajandream and B. Barrell  
*Bioinformatics*. 2000 Oct;16(10):944-5.
- Feb 2001 **Massive gene decay in the leprosy bacillus.**  
S. Cole et al.  
*Nature*. 2001 Feb 22;409(6823):1007-11.
- June 2001 **A Re-annotation of the *Saccharomyces cerevisiae* Genome.**  
V. Wood, K. M. Rutherford, A. Ivens, M-A Rajandream and B. Barrell  
*Comp Funct Genomics*. 2001 June; 2(3): 143-154.
- Oct 2001 **Genome sequence of *Yersinia pestis*, the causative agent of plague.**  
J. Parkhill et al.  
*Nature*. 2001 Oct 4;413(6855):523-7.
- Oct 2001 **Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.**  
J. Parkhill et al.  
*Nature*. 2001 Oct 25;413(6858):848-52.
- Feb 2002 **The genome sequence of *Schizosaccharomyces pombe*.**  
V. Wood et al.  
*Nature*. 2002 Feb 21;415(6874):871-80.
- May 2002 **Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).**  
S. Bentley et al.  
*Nature*. 2002 May 9;417(6885):141-7.
- Oct 2002 **Sequence of *Plasmodium falciparum* chromosomes 1, 3-9 and 13.**  
N. Hall et al.  
*Nature*. 2002 Oct 3;419(6906):527-31.
- Oct 2002 **Genome sequence of the human malaria parasite *Plasmodium falciparum*.**  
J. Malcolm et al.  
*Nature*. 2002 Oct 3;419(6906):498-511.
- June 2003 **Viewing and annotating sequence data with Artemis.**  
M. Berriman and K. Rutherford  
*Brief Bioinform*. 2003 Jun;4(2):124-32.
- Aug 2003 **The DNA sequence of chromosome I of an African trypanosome: Gene content, chromosome organisation, recombination and polymorphism**  
N. Hall et al.  
*Nucl. Acids Res*. (2003) 31 (16): 4864-4873.
- Nov 2003 **The complete genome sequence and analysis of *Corynebacterium diphtheriae* NCTC13129.**  
A. Cerdeño-Tárraga et al.  
*Nucleic Acids Res*. 2003 Nov 15;31(22):6516-23.
- Jan 2004

- GeneDB: a resource for prokaryotic and eukaryotic organisms.**  
Hertz-Fowler C et al.  
*Nucleic Acids Res.* 2004 Jan 1;32(Database issue):D339-43.
- June 2004 **Complete genomes of two clinical *Staphylococcus aureus* strains: Evidence for the rapid evolution of virulence and drug resistance.**  
M. Holden et al.  
*Proc Natl Acad Sci U S A.* 2004 Jun 29;101(26):9786-91a
- Sep 2004 **Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*.**  
M. Holden et al.  
*Proc Natl Acad Sci U S A.* 2004 Sep 28;101(39):14240-5.
- Jan 2005 **A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses**  
N. Hall  
*Science* 07 Jan 2005: Vol. 307, Issue 5706, pp. 82-86
- June 2005 **A Human-Curated Annotation of the *Candida albicans* Genome**  
Braun et al.  
*PLoS Genet.* 2005 Jul;1(1):36-57. Epub 2005 Jun 17
- Aug 2005 **ACT: the Artemis comparison tool.**  
T. Carver, K. Rutherford, M. Berriman, M-A. Rajandream, B.. Barrell and J. Parkhill  
*Bioinformatics.* 2005 Aug 15;21(16):3422-3
- Sep 2005 **WebACT - An online companion for the Artemis Comparison Tool**  
J. Abbott, D. Aanensen, K. Rutherford, S. Butcher and B. Spratt  
*Bioinformatics.* 2005 Sep 15;21(18):3665-6. Epub 2005 Aug 2
- July 2007 **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**  
R. Lyne et al.  
*Genome Biol.* 2007;8(7):R129.
- Dec 2010 **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**  
The modENCODE Consortium  
*Science.* 2010 Dec 24;330(6012):1775-87.
- Dec 2010 **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**  
The modENCODE Consortium  
*Science.* 2010 Dec 24;330(6012):1787-97.
- Nov 2011 **The Gene Ontology: enhancements for 2011.**  
Gene Ontology Consortium. *Nucleic Acids Res.* 2012 Jan;40(Database issue):D559-64. Epub 2011 Nov 18.
- Jan 2012 **PomBase: a comprehensive online resource for fission yeast.**  
Wood V et al.  
*Nucleic Acids Res.* 2012 Jan;40(Database issue):D695-9.
- Jan 2012 **modMine: flexible access to modENCODE data.**  
S. Contrino et al.  
*Nucleic Acids Res.* 2012 Jan;40(Database issue):D1082-8.
- Sep 2012 **InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data** R. Smith et al.  
*Bioinformatics.* (2012) 28 (23):3163-3165.
- Jan 2013

**Gene ontology annotations and resources.**

Gene Ontology Consortium

*Nucleic Acids Res.* 2013 Jan;41(Database issue):D530-5. doi: 10.1093/nar/gks1050

- Feb 2014 **Canto: An online tool for community literature curation**  
K. Rutherford, M. A. Harris, A. Lock, S. G. Oliver and V. Wood  
*Bioinformatics* (2014) doi: 10.1093/bioinformatics/btu103
- June 2014 **Improving functional annotation for industrial microbes: A case study with *Pichia pastoris***  
D. Dikicioglu, V. Wood, K. Rutherford, M. McDowall, S. Oliver  
*Trends in Biotechnology* (2014) 10.1016/j.tibtech.2014.05.003
- Oct 2014 **PomBase 2015: updates to the fission yeast database**  
M. McDowall, M. Harris, A. Lock, K. Rutherford, D. Staines, J. Bähler, P. Kersey, S. Oliver and V. Wood  
*Nucl. Acids Res.* (2014) doi: 10.1093/nar/gku1040
- Dec 2014 **Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia**  
D. E. Janes et al.  
*Biol Lett.* 2014 Dec; 10(12): 20140809.
- Jan 2015 **Gene Ontology Consortium: going forward**  
The Gene Ontology Consortium  
*Nucl. Acids Res.* (28 January 2015) 43 (D1): D1049-D1056.
- Nov 2015 **Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish**  
H. Liu, M. Lamm, K. Rutherford, M. Black, J. Godwin and N. Gemmell  
*Biology of Sex Differences* (2015) 6:26
- Feb 2016 **Uncovering the pathways underlying whole body regeneration in a chordate model, *Botrylloides leachi* using de novo transcriptome analysis**  
L. Zondag, K. Rutherford, N. Gemmell and M. Wilson  
*BMC Genomics*, in press