

Kim RUTHERFORD

Software Development and Bioinformatics

+64 212508293
✉ kmr@bioinformatics.nz
🌐 <http://kmr.bioinformatics.nz>
Dunedin, New Zealand

Profile

I am a software developer and bioinformatician. For the last 17 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
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

● [🌐 Scopus profile](#) ● [🌐 Google Scholar](#) ● [🌐 ORCID](#)

- 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 (2016) 17:114 DOI 10.1186/s12864-016-2435-6

● [kim_rutherford](#) ● [kimrutherford](#) ● [kmr.bioinformatics.nz](#) ● [keybase.io/kmr](#) ● Skype: kim_rutherford