Kim RUTHERFORD

Software Development and Bioinformatics

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Profile

I am a software developer and bioinformatician. For the last 20 years I have been helping biologists to capture, analyse and interpret genomic data.

Skills and Experience

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

Work experience

June 2010 – Present	**Programmer** *S. pombe genome database (PomBase)* Department of Biochemistry, University of Cambridge

Tasks	web and database programming system administration
Major projects	Canto - a community curation tool PomBase v2
Secondments	FlyBase - 3 months customising Canto for drosophila phenotypes PHI-base - 6 months adapting Canto for pathogen-host interaction phenotype curation

Sept 2012 – Dec 2016	**Scientific Officer** (part time) *Gemmell Group* 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

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 modENCODE project: modMine

Feb 2004 – Sept 2007	**Programmer** *FlyMine/InterMine group* Department of Genetics, University of Cambridge

Tasks	Java programming for the InterMine project

Oct 2001 – 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

Apr 1999 – Oct 2001	**Senior Computer Programmer** *Pathogen Sequencing Unit* The Sanger Institute

Sept 1998 – Apr 1999	**Computer Programmer** *Pathogen Sequencing Unit* The Sanger Institute

Publications

● Google Scholar ● ORCID ● Europe PMC ● ResearcherID ● Scopus profile

Feb 2021	**A genome-wide investigation of adaptive signatures in protein-coding genes related to tool behaviour in New Caledonian and Hawaiian crows** N. Dussex *et al.* *Molecular Ecology.* *DOI: 10.1111/mec.15775*

Jan 2021	**The Gene Ontology resource: enriching a GOld mine** The Gene Ontology Consortium *Nucleic Acids Research.* *DOI: 10.1093/nar/gkaa1113*

Nov 2020	

Dense sampling of bird diversity increases power of comparative genomics
S. Feng *et al.*
Nature. ⬈ *DOI10.1038/s41586-020-2873-9*

Sep 2020 **Term Matrix: A novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns**
V. Wood *at al.*
Open Biology. ⬈ *DOI10.1098/rsob.200149*

Aug 2020 **The tuatara genome reveals ancient features of amniote evolution**
N. Gemmell, K. Rutherford, S. Prost, M. Tollis, D.J. Winter, J.R.Macey, D.L. Adelson, A. Suh, T. Bertozzi, J. Grau, C. Organ, P. Gardner, *et al.*
Nature. ⬈ *DOI10.1038/s41586-020-2561-9*

July 2020 **DNA from mollusc shell: a valuable and underutilised substrate for genetic analyses**
S. Ferreira, R. Ashby, G-J. Jeunen, K. Rutherford, C. Collins, E.V. Todd, N.J. Gemmell
PeerJ. ⬈ *DOI10.7717/peerj.9420*

Apr 2020 **Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications**
A. Lock, M. Harris, K. Rutherford, J. Hayles, V. Wood
Database. ⬈ *DOI10.1093/database/baaa028*

Jan 2020 **PHI-base: the pathogen–host interactions database**
M. Urban, A. Cuzick, J. Seager, V. Wood, K. Rutherford, S. Yagwakote Venkatesh, N. De Silva, M. Carbajo Martinez, H. Pedro, A.D. Yates, K. Hassani-Pak, K.E. Hammond-Kosack
Nucleic Acids Research. ⬈ *10.1093/nar/gkz904*

Mar 2019 **Molecular structure of sauropsid β-keratins from tuatara (*Sphenodon punctatus*)**
D. Parry, R. Fraser, L. Alibardi, K. Rutherford, N. Gemmell
Journal of Structural Biology. ⬈ *10.1016/j.jsb.2019.04.008*

Jan 2019 **PomBase 2018: user-driven reimplementation of the fission yeast database provides rapid and intuitive access to diverse, interconnected information**
A. Lock, K. Rutherford, M.A. Harris, J Hayles, S.G. Oliver, J. Bähler, V. Wood
Nucleic Acids Research. ⬈ *10.1093/nar/gky961*

Dec 2018 **Stress, novel sex genes and epigenetic reprogramming orchestrate socially-controlled sex change**
E.V. Todd, O. Ortega-Recalde, H. Liu, M.S. Lamm, K.M. Rutherford, H. Cross, M.A. Black, O. Kardailsky, J.A. Graves, T.A. Hore, J.R. Godwin, N.J. Gemmell
Science Advances. ⬈ *10.1126/sciadv.aaw7006*

Nov 2018 **Hidden in plain sight: What remains to be discovered in the eukaryotic proteome?**
V. Wood, A. Lock, M. Harris, K. Rutherford, J. Bahler, S Oliver
Open Biology. ⬈ *10.1098/rsob.180241*

Oct 2018 **RNAcentral: a hub of information for non-coding RNA sequences**
The RNAcentral Constortium
Nucleic Acids Research. ⬈ *10.1093/nar/gky1034*

Oct 2018 **The Gene Ontology Resource: 20 years and still GOing strong**
The Gene Ontology Consortium
Nucleic Acids Research. ⬈ *10.1093/nar/gky1055*

Aug 2018 **Evolutionary history of the podoplanin gene**
J. Renart, D. San Mauro, A. Agorreta, K. Rutherford, N. J. Gemmell, M Quintanill
Gene Reports. ⬈ *10.1016/j.genrep.2018.08.005*

Aug 2018 **Reduced representation sequencing detects only subtle regional structure in a heavily exploited and rapidly recolonizing marine mammal species**
N. Dussex, H.R. Taylor, W.R. Stovall, K. Rutherford, K.G. Dodds, S.M. Clarke, N.J. Gemmell
Ecology and Evolution. ⬈ *10.1002/ece3.4411*

Apr 2018 **Adipose Transcriptome Analysis Provides Novel Insights into Molecular Regulation of Prolonged Fasting in Northern Elephant Seal Pups**
B. Martinez, J. Khudyakov, K. Rutherford, D. Crocker, N. Gemmell, R. Ortiz
Physiological Genomics. ⬈ *10.1152/physiolgenomics.00002.2018*

Apr 2018 **De novo draft assembly of the *Botrylloides leachii* genome provides further insight into tunicate evolution**
S. Blanchoud, K. Rutherford, L. Zondag, N. Gemmell, M Wilson
Scientific Reports. ⬈ *10.1038/s41598-018-23749-w.*

Feb 2018 **Genetic sex assignment in wild populations using GBS data: a statistical threshold approach**
W. Stovall, H.R. Taylor, M. Black, S. Grosser, K. Rutherford, N.J. Gemmell
Molecular Ecology Resources. ⬈ *10.1111/1755-0998.12767*

Dec 2017 **Analysis of the genome of the New Zealand giant collembolan (*Holacanthella duospinosa*) sheds light on hexapod evolution**
C. Wu, M.D. Jordan, R.D. Newcomb, N.J. Gemmell, S. Bank, K. Meusemann, P.K. Dearden, E.J. Duncan, S. Grosser, K. Rutherford, P.P. Gardner, R.N. Crowhurst, B. Steinwender, L.K. Tooman, M.I. Stevens, T.R. Buckley
BMC Genomics. ⬈ *10.1186/s12864-017-4197-1.*

Dec 2017

Identification of sex differences in zebrafish (*Danio rerio*) brains during early sexual differentiation and masculinisation using 17α-methyltestoterone
S.L.J. Lee, J.A. Horsfield, M.A. Black, K.M. Rutherford, N.J. Gemmell
Biology of Reproduction. ☐ *10.1093/biolre/iox175*

Nov 2017   **Female mimicry by sneaker males has a transcriptomic signature in both the brain and gonad in a sex changing fish**
E.V. Todd, H. Liu, M.S. Lamm, J.T. Thomas, K. Rutherford, K.C. Thompson, J.R. Godwin, N.J. Gemmell
Molecular Biology and Evolution. ☐ *10.1093/molbev/msx293*

July 2017   **Male-female relatedness at specific SNP-linkage groups influences cryptic female choice in Chinook salmon (*Oncorhynchus tshawytscha*)**
C. Gessner, S.L. Johnson, P. Fisher, S. Clarke, K. Rutherford, J. Symonds, N.J. Gemmell
Proc. R. Soc. B. ☐ *10.1098/rspb.2017.0853.*

July 2017   **Histological and transcriptomic effects of 17α-methyltestosterone on zebrafish gonad development**
S.L.J. Lee, J.A. Horsfield, M.A. Black, K. Rutherford, A. Fisher, N.J. Gemmell
BMC Genomics. ☐ *10.1186/s12864-017-3915-z*

June 2017   **PomBase – the scientific resource for fission yeast**
V. Wood, A. Lock, K. Rutherford, M.A. Harris
Methods in Molecular Biology. ☐ *10.17863/CAM.12124*

Jan 2017   **PHI-base: A new interface and further additions for the multi-species pathogen-host interactions database.**
Urban, M., Alayne Cuzick, A., Rutherford, K., Irvine, A., Pedro, H., Pant, R., Sadanadan, V., Khamari, L., Billal, S., Mohanty S., and. Hammond-Kosack, K.E.
Nucleic Acids Research. ☐ *10.1093/nar/gkw1089*

Nov 2016   **The Gene Ontology Consortium; Expansion of the Gene Ontology knowledgebase and resources.**
The Gene Ontology Consortium
Nucleic Acids Research. ☐ *10.1093/nar/gkw1108*

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. ☐ *10.1186/s12864-016-2435-6*

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. ☐ *10.1186/s13293-015-0044-8*

Jan 2015   **Gene Ontology Consortium: going forward**
The Gene Ontology Consortium
Nucleic Acids Research. ☐ *10.1093/nar/gku1179*

Dec 2014   **Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia**
D. E. Janes *et al.*
Biology Letters. ☐ *10.1098/rsbl.2014.0809*

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
Nucleic Acids Research. ☐ *DOI10.1093/nar/gku1040*

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. ☐ *DOI10.1016/j.tibtech.2014.05.003*

Feb 2014   **Canto: An online tool for community literature curation**
K. Rutherford, M. A. Harris, A. Lock, S. G. Oliver and V. Wood
Bioinformatics. ☐ *DOI10.1093/bioinformatics/btu103*

Jan 2013   **Gene ontology annotations and resources.**
Gene Ontology Consortium
Nucleic Acids Research. ☐ *10.1093/nar/gks1050*

Sep 2012   **InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data**
R.N. Smith, J. Aleksic, D. Butano, A. Carr, S. Contrino, F. Hu, M. Lyne, R. Lyne, A. Kalderimis, K. Rutherford, R. Stepan, J. Sullivan, M. Wakeling, X. Watkins, G. Micklem
Bioinformatics. ☐ *10.1093/bioinformatics/bts577*

Jan 2012   **modMine: flexible access to modENCODE data.**
S. Contrino, R.N. Smith, D. Butano, A. Carr, F. Hu, R. Lyne, K. Rutherford, A. Kalderimis, J. Sullivan, S. Carbon, E.T. Kephart, P. Lloyd, E.O. Stinson, N.L. Washington, M.D. Perry, P. Ruzanov, Z. Zha, S.E. Lewis, L.D. Stein, G. Micklem
Nucleic Acids Research. ☐ *10.1093/nar/gkr921*

Jan 2012   **PomBase: a comprehensive online resource for fission yeast.**
V. Wood, M.A. Harris, M.D. McDowall, K. Rutherford, B.W. Vaughan, D.M. Staines, M. Aslett, A. Lock, J. Bähler, P.J. Kersey, S.G. Oliver
Nucleic Acids Research. ☐ *10.1093/nar/gkr853*

Nov 2011   **The Gene Ontology: enhancements for 2011.**
Gene Ontology Consortium.
Nucleic Acids Research. ☐ *10.1093/nar/gkr1028*

Dec 2010   **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**
The modENCODE Consortium
Science. ⤢ *10.1126/science.1198374*

Dec 2010   **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**
The modENCODE Consortium
Science. ⤢ *10.1126/science.1196914*

July 2007   **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**
R. Lyne *et al.*
Genome Biology. ⤢ *10.1186/gb-2007-8-7-r129*

Sep 2005   **WebACT - An online companion for the Artemis Comparison Tool**
J. Abbott, D. Aanensen, K. Rutherford, S. Butcher and B. Spratt
Bioinformatics. ⤢ *10.1093/bioinformatics/bti601*

Aug 2005   **ACT: the Artemis comparison tool.**
T. Carver, K. Rutherford, M. Berriman, M-A. Rajandream, B.. Barrell and J. Parkhill
Bioinformatics. ⤢ *10.1093/bioinformatics/bti553*

June 2005   **A Human-Curated Annotation of the *Candida albicans* Genome**
B.R. Braun *et al.*
PLoS Genetics. ⤢ *10.1371/journal.pgen.0010001*

Jan 2005   **A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses**
N. Hall *et al.*
Science. ⤢ *10.1126/science.1103717*

Sep 2004   **Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*.**
M. Holden *et al.*
Proc Natl Acad Sci. ⤢ *10.1073/pnas.0403302101*

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. ⤢ *10.1073/pnas.0402521101*

Jan 2004   **GeneDB: a resource for prokaryotic and eukaryotic organisms.**
Hertz-Fowler C *et al.*
Nucleic Acids Research. ⤢ *10.1093/nar/gkh007*

Nov 2003   **The complete genome sequence and analysis of *Corynebacterium diphtheriae* NCTC13129.**
A. Cerdeño-Tárraga *et al.*
Nucleic Acids Research. ⤢ *10.1093/nar/gkg874*

Aug 2003   **The DNA sequence of chromosome I of an African trypanosome: Gene content, chromosome organisation, recombination and polymorphism**
N. Hall *et al.*
Nucleic Acids Research. ⤢ *10.1093/nar/gkg674*

June 2003   **Viewing and annotating sequence data with Artemis.**
M. Berriman and K. Rutherford
Briefing in Bioinformatics. ⤢ *10.1093/bib/4.2.124*

Oct 2002   **Genome sequence of the human malaria parasite *Plasmodium falciparum*.**
J. Malcolm *et al.*
Nature. ⤢ *10.1038/nature01097*

Oct 2002   **Sequence of *Plasmodium falciparum* chromosomes 1, 3–9 and 13.**
N. Hall *et al.*
Nature. ⤢ *10.1038/nature01095*

May 2002   **Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).**
S. Bentley *et al.*
Nature. ⤢ *10.1038/417141a*

Feb 2002   **The genome sequence of *Schizosaccharomyces pombe*.**
V. Wood *et al.*
Nature. ⤢ *10.1038/nature724*

Oct 2001   **Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.**
J. Parkhill *et al.*
Nature. ⤢ *10.1038/35101607*

Oct 2001   **Genome sequence of *Yersinia pestis*, the causative agent of plague.**
J. Parkhill *et al.*
Nature. ⤢ *10.1038/35097083*

June 2001   **A Re-annotation of the *Saccharomyces cerevisiae* Genome.**
V. Wood, K. M. Rutherford, A. Ivens, M-A Rajandream and B. Barrell
Comparative and Functional Genomics. ⤢ *10.1002/cfg.86*

Feb 2001 **Massive gene decay in the leprosy bacillus.**
S. Cole *et al.*
Nature. ⎋ *10.1038/35059006*

Oct 2000 **Artemis: sequence visualisation and annotation.**
K. Rutherford, J. Parkhill, J. Crook, T. Horsnell, P. Rice, M-A. Rajandream and B. Barrell
Bioinformatics. ⎋ *10.1093/bioinformatics/16.10.944*

Sep 2000 **Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal to *his5*.**
Z. Xiang *et al.*
Yeast. ⎋ *PMID:11054821*

Mar 2000 **Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.**
J. Parkhill *et al.*
Nature. ⎋ *10.1038/35006655*

Feb 2000 **The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.**
J. Parkhill *et al.*
Nature. ⎋ *10.1038/35001088*

Book Chapters

Apr 2018 **PomBase: The Scientific Resource for Fission Yeast**
"Eukaryotic Genomic Databases : Methods and Protocols"
A Lock, K Rutherford, M.A. Harris, V. Wood
Methods in Molecular Biology. ⎋ *10.1007/978-1-4939-7737-6_4*

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