

• [kimrutherford](#) • [ORCID](#) • [Google Scholar](#)

Profile

I am a software developer and bioinformatician. For the last 25 years I have been helping biologists to capture, analyse and interpret genomic data.

Skills and Experience

- Software development
- 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

- › full stack development
- › bioinformatics support
- › system administration

Major projects

- › [PomBase](#)
- › [JaponicusDB](#)
- › [Canto](#) - a community curation tool

Secondments

- › PHI-base - 6 months adapting Canto for pathogen-host interaction phenotype curation
- › FlyBase - 3 months customising [Canto](#) for *Drosophila* phenotypes

Sept 2012 – Dec 2016 Scientific Officer (part time) *Gemmell Group*
Department of Anatomy, University of Otago

Tasks

- › bioinformatics support
- › genome and transcriptome assembly and analysis
- › bioinformatics mentoring and training
- › [tuatara](#) [genome project](#)

Feb 2009 – June 2010

Publications

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:
[↗ NAR publication](#)

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

Tasks

- › Software engineering for the InterMine data warehouse project:
[↗ Bioinformatics publication](#)

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

• [↗ Google Scholar](#) • [↗ ORCID](#) • [↗ Europe PMC](#) • [↗ ResearcherID](#) • [↗ Scopus profile](#)

Oct 2025 RNAcentral in 2026: Genes and literature integration
A.F. Green *et al.*
preprint [↗ DOI: 10.1101/2025.09.19.677274](#)

Feb 2025 A compendium of human gene functions derived from evolutionary modelling
The Gene Ontology Consortium
Nature (2025) [↗ DOI: 10.1038/s41586-025-08592-0](#)

Feb 2024 PomBase: a Global Core Biodata Resource — growth, collaboration, and sustainability
K.M. Rutherford, M. Lera-Ramírez, V. Wood
Genetics, *iyae007* [↗ DOI: 10.1093/genetics/iyae007](#)

Oct 2023 Revised fission yeast gene and allele nomenclature guidelines for machine readability
M. Lera-Ramírez, J. Bähler, J. Mata, K. Rutherford, C.S. Hoffman, S. Lambert, S. Oliferenko, S.G. Martin, K.L. Gould, L-L. Du, S.A. Sabatinos, S.L. Forsburg, O. Nielsen, P. Nurse, V. Wood

Genetics, iyad143 [DOI: 10.1093/genetics/iyad143](https://doi.org/10.1093/genetics/iyad143)

- July 2023 A framework for community curation of interspecies interactions literature
A. Cuzick, J. Seager, V. Wood, M. Urban, K. Rutherford, K.E. Hammond-Kosack
eLife. [DOI: 10.7554/eLife.84658](https://doi.org/10.7554/eLife.84658)
- March 2023 The Gene Ontology knowledgebase in 2023
The Gene Ontology Consortium
Genetics. [DOI: 10.1093/genetics/iyad031](https://doi.org/10.1093/genetics/iyad031)
- Dec 2021 JaponicusDB: Rapid deployment of a model organism database for an emerging model species
K. Rutherford, M. Harris, S. Oliferenko, V. Wood
Genetics. [DOI: 10.1093/genetics/iyab223](https://doi.org/10.1093/genetics/iyab223)
- Dec 2021 Fission stories: Using PomBase to understand *Schizosaccharomyces pombe* biology
M. Harris, K. Rutherford, J. Hayles, A. Lock, J. Bähler, S. Oliver, J. Mata, V. Wood
Genetics. [DOI: 10.1093/genetics/iyab222](https://doi.org/10.1093/genetics/iyab222)
- Nov 2021 PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions
M. Urban *et al.*
NAR [DOI: 10.1093/nar/gkab1037](https://doi.org/10.1093/nar/gkab1037)
- Dec 2020 The Gene Ontology resource: enriching a GOLD mine
The Gene Ontology Consortium
Nucleic Acids Research. [DOI: 10.1093/nar/gkaa1113](https://doi.org/10.1093/nar/gkaa1113)
- Dec 2020 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](https://doi.org/10.1111/mec.15775)
- Nov 2020 Dense sampling of bird diversity increases power of comparative genomics
S. Feng *et al.*
Nature. [DOI: 10.1038/s41586-020-2873-9](https://doi.org/10.1038/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 *et al.*
Open Biology. [DOI: 10.1098/rsob.200149](https://doi.org/10.1098/rsob.200149)
- Aug 2020 The tuatara genome reveals ancient features of amniote evolution
N. Gemmell, K. Rutherford, *et al.*
Nature. [DOI: 10.1038/s41586-020-2561-9](https://doi.org/10.1038/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. [DOI: 10.7717/peerj.9420](https://doi.org/10.7717/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. [DOI: 10.1093/database/baaa028](https://doi.org/10.1093/database/baaa028)
- Nov 2019 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. [DOI: 10.1093/nar/gkz904](https://doi.org/10.1093/nar/gkz904)
- July 2019 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. [DOI: 10.1126/sciadv.aaw7006](https://doi.org/10.1126/sciadv.aaw7006)
- July 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. [DOI: 10.1016/j.jsb.2019.04.008](https://doi.org/10.1016/j.jsb.2019.04.008)
- Feb 2019 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. [DOI: 10.1098/rsob.180241](https://doi.org/10.1098/rsob.180241)
- Nov 2018 RNAcentral: a hub of information for non-coding RNA sequences
The RNAcentral Consortium
Nucleic Acids Research. [DOI: 10.1093/nar/gky1034](https://doi.org/10.1093/nar/gky1034)
- Oct 2018 PomBase 2018: user-driven reimplementations 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. [DOI: 10.1093/nar/gky961](https://doi.org/10.1093/nar/gky961)
- Oct 2018 The Gene Ontology Resource: 20 years and still GOing strong
The Gene Ontology Consortium
Nucleic Acids Research. [DOI: 10.1093/nar/gky1055](https://doi.org/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. Quintanilla
Gene Reports. [DOI: 10.1016/j.genrep.2018.08.005](https://doi.org/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. [DOI: 10.1002/ece3.4411](https://doi.org/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. [DOI: 10.1152/physiolgenomics.00002.2018](https://doi.org/10.1152/physiolgenomics.00002.2018)
- Apr 2018 *De novo* draft assembly of the *Botryllodes leachii* genome provides further insight into tunicate evolution
S. Blanchoud, K. Rutherford, L. Zondag, N. Gemmell, M Wilson
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Molecular Ecology Resources. [DOI: 10.1111/1755-0998.12767](https://doi.org/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
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- Dec 2017 Identification of sex differences in zebrafish (*Danio rerio*) brains during early sexual differentiation and masculinisation using 17 α -methyltestosterone
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- Nov 2017 Female mimicry by sneaker males has a transcriptomic signature in both the brain and gonad in a sex changing fish
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Molecular Biology and Evolution. [DOI: 10.1093/molbev/msx293](https://doi.org/10.1093/molbev/msx293)
- July 2017 Male-female relatedness at specific SNP-linkage groups influences cryptic female choice in Chinook salmon (*Oncorhynchus tshawytscha*)
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Proc. R. Soc. B. [DOI: 10.1098/rspb.2017.0853](https://doi.org/10.1098/rspb.2017.0853).
- July 2017 Histological and transcriptomic effects of 17 α -methyltestosterone on zebrafish gonad development
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- Nov 2016 The Gene Ontology Consortium; Expansion of the Gene Ontology knowledgebase and resources.
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- 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
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 H. Liu, M. Lamm, K. Rutherford, M. Black, J. Godwin and N. Gemmell
Biology of Sex Differences. [DOI: 10.1186/s13293-015-0044-8](#)
- Jan 2015 Gene Ontology Consortium: going forward
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- Dec 2014 Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia
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- Oct 2014 PomBase 2015: updates to the fission yeast database
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Nucleic Acids Research. [DOI: 10.1093/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
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- Feb 2014 Canto: An online tool for community literature curation
 K. Rutherford, M. A. Harris, A. Lock, S. G. Oliver and V. Wood
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- Jan 2013 Gene ontology annotations and resources.
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Nucleic Acids Research. [DOI: 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
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- 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
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 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
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- Dec 2010 Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.
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- Dec 2010 Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.
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Science. [DOI: 10.1126/science.1196914](#)
- July 2007 FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.
 R. Lyne *et al.*
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- Oct 2002 Sequence of *Plasmodium falciparum* chromosomes 1, 3–9 and 13.
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Mar 2000 Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

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Feb 2000 The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.

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Book Chapters

May 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. [DOI: 10.1007/978-1-4939-7737-6_4](#)