

SAM BUCKBERRY

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The University of Western Australia • M316, 35 Stirling Highway, Crawley 6009

Current position (2015 - present)

Postdoctoral Research Fellow - Genome Bioinformatics

Lister Lab (epigenetics and genomics)

Harry Perkins Institute of Medical Research

The School of Molecular Sciences

The University of Western Australia

Education

Doctor of Philosophy (2012-2015)

The University of Adelaide

Robinson Research Institute

Thesis: An integrative analysis of the human placental transcriptome

Awarded the Dean's commendation for doctoral thesis excellence

Bachelor of Health Science - First Class Honours (2011)

The University of Adelaide

Robinson Research Institute

Awarded the Petrucco Honours Scholarship

Bachelor of Science (2008-2010)

Flinders University

Extended Major in Biological Sciences

Chancellor's Commendation 2009 and 2010

Research funding

Google Cloud Research Grant (2021): Solving the problem of epigenetic memory in reprogrammed human cells. **CIA Buckberry \$6,796**

WA Department of Health Merit Award (2020): Repairing abnormal genomic imprinting in induced pluripotent stem cells with naive reprogramming and targeted epigenome engineering. **CIA Buckberry \$95,000**

NHMRC-ARC Dementia Research Development Fellowship Grant (2016-2019): The Role of the neuronal methylome in natural brain ageing and the progression of Alzheimer's Disease (APP1111206).

CIA Buckberry \$584,644

NHMRC Peter Doherty Biomedical Early Career Fellowship Award (2016-2019): The role of atypical DNA methylation in neuronal genome regulation and neurodevelopmental disorders (APP1110063).

CIA Buckberry \$314,644. *This fellowship was relinquished to accept the grant above.*

Robinson Research Institute Seed Funding (2015-2016): A multi-faceted approach to understanding the consequences of diabetes in early pregnancy. Brown HM, Nottle M, Gatford K, Dunning K, Breen J & **Buckberry S. \$25,000**

Robinson Research Institute Seed Funding (2014-2015): Investigating new mechanisms regulating transcription in the pre-implantation embryo. Brown HM, Bent SJ, **Buckberry S**, Thompson JG. **\$25,000**

Awards, scholarships & fellowships

- Finalist - Woodside Early Career Scientist of the Year (2020) - WA Premier's Science Awards.
- Raine Research Prize - Raine Medical Research Foundation (2019). *Awarded for the best biomedical research paper by an early career researcher in Western Australia*
- Ana Africh Stem Cell Research Travel Scholarship (2019)
- Best Oral Presentation by Early Career Researcher at Australasian Genomic Technologies Association (AGTA) conference (2016)
- NHMRC-ARC Dementia Research Fellowship (2016-2019)
- NHMRC Peter Doherty Biomedical Early Career Fellowship (2016-2019) *relinquished*
- Y.W Loke New Investigator Travel Award, IFPA Conference (2015)
- Dean's Commendation for Doctoral Thesis Excellence (2015)
- Promega PhD Student Award, Lorne Genome Conference (2014)
- ANZPRA New Investigator Award Finalist (2013)
- Healthy Development Adelaide & Channel 7 Children's Research Foundation PhD Scholarship (2012-2015)
- NHMRC grant-funded PhD top-up scholarship (2012-2015)
- ANZPRA New Investigator Award Finalist (2012)
- The Robinson Research Institute Petrucco Honours Scholarship (2011)
- AR Riddle Honours Grant, The University of Adelaide (2011)
- Flinders University Chancellors Commendation (2011)
- Flinders University Chancellors commendation (2010)
- Flinders University Summer Research Scholarship (2010)

Service and community engagement

- Current director on the Australasian Genomics Technology Association (AGTA) executive committee. Key contributions include establishing the AGTA PhD scholarship
- Human Research Ethics Committee Member - WA Department of Health
- Speaker - Pint of Science Festival 2018, a forum for communicating contemporary scientific developments to the public
- STEM mentor through The School of Indigenous Studies, The University of Western Australia (2018)
- Placental epigenetics workshop organiser - 2015 International Federation of Placental Associations (IFPA) conference
- Conference organising committee for the 2014 Australian and New Zealand Placental Research Association (ANZPRA) conference

Professional societies

- Australasian Genomic Technologies Association (AGTA) - Executive committee since 2017
- Australian Bioinformatics and Computational Biology Society (ABACBS) - Member
- International Society for Stem Cell Research (ISSCR) - Member
- Stem Cells Australia - Member

Peer review

- NHMRC project grant reviewer (2017, 2018)
- Internal project grant reviewer - University of Western Australia (2016 - 2020)
- Peer reviewer for journals including *Genome Research*, *Clinical Epigenetics*, *BMC Genomics*, *Scientific Reports*, *Placenta*, *F1000 Research* and *PLoS ONE*.

Training

- Data Science Specialisation – Johns Hopkins University & Coursera (2014-2015)
- Advanced bioinformatics workshop, Australian Centre for Ancient DNA (2014)
- Software carpentry Boot Camp for Bioinformaticians, Adelaide (2013)
- Advanced bioinformatics workshop, Australian Centre for Ancient DNA (2013)
- EMBL-EBI bioinformatics workshop, Adelaide (2012)
- Advanced bioinformatics workshop, Australian Centre for Ancient DNA (2012)
- Beyond Words - public speaking coaching (2012)
- Australian Science Communicators media training (2010)

Higher degree by research supervision & mentoring

- Dawid Maksoa, PhD candidate – Forrest Research Foundation Scholar, The University of Western Australia and the Harry Perkins Institute of Medical Research. Project entitled '*Epigenetics of ageing*'
- Mitchell Bestry, PhD candidate, The University of Western Australia and Telethon Kids Institute. Project entitled '*The epigenetic origin of fetal alcohol-induced disorders: A cross-species study*'
- Karthik Mandoran, MSc candidate (2020-2021). The University of Western Australia and the Harry Perkins Institute of Medical Research.
- Thomas Frazer, BSc (Biotechnology) Honours (2019), The University of Western Australia. *Awarded first class honours*
- Benjamin Mayne - PhD student 2014-2017 who I mentored and trained in bioinformatics at The University of Adelaide. Currently postdoctoral fellow in bioinformatics at the CSIRO.
- Fleur Spronk - 2014 BHLthSc First Class Honours student who I mentored and trained at The University of Adelaide. Currently a postgraduate medical student.

Teaching

- Lecturer for the Masters unit *Collecting, Analysing and Interpreting Big Data in Biology* (2018-2020). School of Molecular Sciences, The University of Western Australia.
- Lecturer for the Masters unit *The Objectives and Applications of Genomics* (2017). School of Molecular Sciences, The University of Western Australia.
- Teaching for RNA-Seq analysis workshops at BioInfoSummer Conference - Australian Mathematical Sciences Institute and the University of Adelaide (2013).
- Teaching of postgraduate bioinformatics workshops at The University of Adelaide (2013).
- Coordinator and tutor for undergraduate biology Peer Assisted Study Sessions (PASS), Flinders University (2010-2011). In this role, I was mentored by Prof. Karen Burke da Silva (2016 University Teacher of the Year).

Selected presentations

Overcoming the epigenetic barriers to cellular reprogramming. *South Australia Health and Medical Research Institute (SAHMRI) 2019. Adelaide, Australia. Invited presentation*

Profiling the shifting epigenetic landscape during human reprogramming. *Epigenetics Consortium of South Australia (EpiCSA) Annual Research Meeting 2019. Adelaide Australia. Invited presentation and received the People's Choice Award*

Using big data to understand the human brain - Pint of Science Festival 2018 *Sold-out audience*

Characterising epigenome dynamics during the reprogramming of somatic cells to iPS cells. *Lorne Genome Conference 2017. Lorne, Australia.*

Characterising epigenome dynamics during the reprogramming of somatic cells to iPS cells. **Best ECR oral presentation**, *Australasian Genomic Technologies Association (AGTA) Conference 2016. Auckland, New Zealand.*

Moving towards integrative epigenomic analyses. *International Federation of Placenta Associations (IFPA) Conference 2015. Brisbane, Australia.* **Invited presentation.**

Integrative analysis of placental transcriptome organization reveals highly conserved regulatory programs and points toward a preeclampsia gene cluster. **New investigator award session.** *International Federation of Placenta Associations (IFPA) Conference 2015. Brisbane, Australia.*

Integrative transcriptome meta-analysis reveals widespread sex-biased gene expression patterns in human extra-embryonic tissue. **Promega PhD Student Award**, *Lorne Genome Conference 2014. Lorne Victoria, Australia.*

What can big data tell us about big tummies? *Robinson Research Institute Symposium 2014. Adelaide, Australia.* **Invited presentation.**

Using RNA sequencing to comprehensively profile the transcriptomes of reproductive tissues. *Society for Reproductive Biology Conference 2014. Melbourne, Australia.* **Invited presentation.**

Sexual inequality begins *in utero* with genome-wide differences in the human placental transcriptome. **ANZPRA new investigator award session**, *Society for Reproductive Biology Conference 2013. Sydney, Australia.*

Using RNA sequencing to quantify placental transcriptomes. *Methods in Reproductive Biology Symposium 2013. Mercy Hospital for Women, Melbourne, Australia.* **Invited presentation.**

Publications

Pre-print manuscripts

Grubman A, Choo XY, Chew G, Ouyang JF, Sun G, Croft NP, Rossello FJ, Simmons R, **Buckberry S**, Landin DV, Pflueger J, Vandekolk TH, Abay Z, Liu X, Haynes JM, McLean C, Williams S, Chai SY, Wilson T, Lister R, Pouton CW, Purcell AW, Rackham OJ, Petretto E, and Polo JM (2019). Mouse and human microglial phenotypes in Alzheimer's disease are controlled by amyloid plaque phagocytosis through Hif1a. *bioRxiv*

Peer-reviewed articles

de Mendoza A, Poppe D, **Buckberry S**, Pflueger J, Albertin AB, Daish T, Bertrand S, de la Calle-Mustienes E, Gómez-Skarmeta JL, Nery JR, Ecker JR, Baer B, Ragsdale CW, Grützner F, Escrivá H, Venkatesh B, Bogdanovic O and Lister R (2021) The emergence of the brain non-CpG methylation system in vertebrates. *Nature Ecology and Evolution*

Liu X, Ouyang JF, Rossello FJ, Tan JP, Davidson KC, Valdes DS, Schröder J, Sun YBY, Chen J, Knaupp AS, Sun G, Chy HS, Huang Z, Pflueger J, Firas J, Tano V, **Buckberry S**, Paynter JM, Larcombe MR, Choo XY, O'Brien CM, Pastor WA, Chen D, Leichter AL, Naeem H, Tripathi P, Das PP, Grubman A, Powell DR, Laslett AL, David L, Nilsson SK, Clark AT, Lister R, Nefzger CM, Martelotto LG, Rackham OJL and Polo JM (2020). Extra and intra-embryonic programs are established during human reprogramming allowing the derivation of induced trophoblast stem cells. *Nature* 586:101-107

Grubman A, Chew G, Ouyang JF, Sun G, Choo XY, McLean C, Simmons R, **Buckberry S**, Landin DV, Poppe D, Pflueger J, Lister R, Rackham OJ, Petretto E and Polo JM (2020). A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. *Nature Neuroscience* 22:2087–2097

- de Mendoza A, Hatleberg WL, Pang K, Leininger S, Bogdanovic O, Pflueger J, **Buckberry S**, Technau U, Hejnol A, Adamska M, Degnan BM, Degnan SM and Lister R (2019). Convergent evolution of a vertebrate-like methylome in a marine sponge. *Nature Ecology and Evolution* 3;10:1464-1473
- de Mendoza A, Bonnet A, Vargas-Landin DB, Ji N, Hong F, Yang F, Li L, Hori K, Pflueger J, **Buckberry S**, Ohta H, Rosic N, Lesage P, Lin S and Lister R (2018). Recurrent acquisition of cytosine methyltransferases into eukaryotic retrotransposons. *Nature Communications* 9;1:1341
- Mayne BT, Leemaqz SY, **Buckberry S**, Rodriguez Lopez CM, Roberts CT, Bianco-Miotto T and Breen J (2018). msgbsR: An R package for analysing methylation-sensitive restriction enzyme sequencing data. *Scientific Reports* 8;1:2190
- Knaupp AS¹, **Buckberry S**¹, Pflueger J, Lim SM, Ford E, Larcombe MR, Rossello FJ, de Mendoza A, Alaei S, Firas J, Holmes ML, Nair SS, Clark SJ, Nefzger CM, Lister R and Polo JM (2017). Transient and permanent reconfiguration of chromatin and transcription factor occupancy drive reprogramming. *Cell Stem Cell* 21, 1-12 ¹ **Equal first author**
- Nefzger CM, Rossello FJ, Chen J, Liu X, Knaupp AS, Firas J, Paynter J, Pflueger J, **Buckberry S**, Lim SM, Williams B, Alaei S, Keshav Faye-Chauhan K, Nilsson SK, Lister R, Ramialison M, Powel DR, Rackham OJL and Polo JM (2017). Cell type of origin dictates the route to pluripotency. *Cell Reports* 21:10.
- Wilson RL, Leemaqz SY, Goh Z, McAninch D, Jankovic-Karasoulos T, Leghi GE, Phillips JA, Colafella KM, Tran C, O’Leary S, **Buckberry S**, Pederson S, Robertson SA, Bianco-Miotto T, Roberts CT (2017). Zinc is a critical regulator of placental morphogenesis and maternal hemodynamics during pregnancy in mice. *Scientific Reports* 7(1):15137.
- Valensisi C, Andrus C, **Buckberry S**, Doni Jayavelu N, Lund RJ, Lister R and Hawkins RD (2017). Epigenomic Landscapes of hESC-Derived Neural Rosettes: Modeling Neural Tube Formation and Diseases. *Cell Reports* 8:20.
- Lumb R, **Buckberry S**, Secker G, Lawrence D and Schwarz Q (2017). Transcriptome profiling reveals expression signatures of cranial neural crest cells arising from different axial levels. *BMC Developmental Biology* 17:5.
- Buckberry S**, Bianco-Miotto T, Bent SJ, Clifton V, Shoubridge C, Shankar K and Roberts CT (2017). Placental transcriptome co-expression analysis reveals conserved regulatory programs across gestation. *BMC Genomics* 18:10.
- Mayne B, Bianco-Miotto T, **Buckberry S**, Breen J, Clifton V, Shoubridge C, Roberts CT (2016). Large scale gene expression meta-analysis reveals tissue-specific, sex-biased gene expression in humans. *Frontiers in Genetics* 7:183
- Hight AR, **Buckberry S**, Mayne BT, Khoda SM, Bianco-Miotto T, Roberts CT (2016). First trimester trophoblasts forming endothelial-like tubes in vitro emulate a ‘blood vessel development’ gene expression profile. *Gene Expression Patterns* 21(2):103-10
- Bianco-Miotto T, Mayne B, **Buckberry S**, Breen J, Rodriguez Lopez C, Roberts CT (2016). Recent progress towards understanding the role of DNA methylation in human placental development. *Reproduction* 152(1): R23–R30.
- Hight HR, Khoda SM, **Buckberry S**, Leemaqz S, Bianco-Miotto T, Harrington E, Ricciardelli C & Roberts CT (2015). Hypoxia induced HIF-1/HIF-2 activity alters trophoblast transcriptional regulation and promotes invasion. *European Journal of Cell Biology* 94(12):589-602.
- Wilson RL ¹, **Buckberry S**¹, Spronk F¹, Laurence JA, Leemaqz S, O’Leary S, Bianco-Miotto T, Du J, Anderson PH & Roberts CT (2015). Vitamin D Receptor Gene Ablation in the Conceptus Has Limited Effects on Placental Morphology, Function and Pregnancy Outcome. *PLoS ONE* 10(6):e0131287. ¹ **Equal first author**
- Buckberry S**, Bianco-Miotto T, Bent SJ, Dekker GA & Roberts CT (2014). Integrative transcriptome meta-analysis reveals widespread sex-biased gene expression at the human fetal–maternal interface. *Molecular Human Reproduction* 20(8):810-9.

Buckberry S, Bent SJ, Bianco-Miotto T & Roberts CT (2014). MassiR: a method for predicting the sex of samples in gene expression microarray datasets. *Bioinformatics* 30(14):2084-5.

Buckberry S, Bianco-Miotto T & Roberts CT (2014). Imprinted and X-linked non-coding RNAs as potential regulators of human placental function, *Epigenetics* 9(1):81-9.

Gatford KL, Heinemann GK, Thompson SD, Zhang JV, **Buckberry S**, Owens J, Dekker GA & Roberts CT (2014). Circulating IGF1 and IGF2 and SNP genotypes in pregnant and non-pregnant women and men. *Endocrine Connections* 3(3):138-149.

Buckberry S, Bianco-Miotto T, Hiendleder S & Roberts CT (2012). Quantitative Allele-Specific Expression and DNA Methylation Analysis of H19, IGF2 and IGF2R in the Human Placenta across Gestation Reveals H19 Imprinting Plasticity. *PLoS ONE* 7(12):e51210.

Buckberry S & Burke da Silva K (2012). Evolution: improving the understanding of undergraduate students with an active pedagogical approach. *Evolution, Education & Outreach* 5(2):266-273.

Book chapters

Stuart T, **Buckberry S**, Lister R (2018). Approaches for the Analysis and Interpretation of Whole Genome Bisulfite Sequencing Data. *Methods in Molecular Biology* 1767:299-310.

Workshop reports

Bianco-Miotto T, Blundell C, **Buckberry S**, Chamley L, Chong S, Cottrell E, Dawson P, Hanna C, Holland O, Lewis RM, Moritz K, Myatt L, Perkins AV, Powell T, Saffery R, Sferruzzi-Perri A, Sibley C, Simmons D & O'Tierney-Ginn PF (2016). IFPA meeting 2015 workshop report I: placental mitochondrial function, transport systems and epigenetics. *Placenta* 48(S3-36).

Datasets

Buckberry S, Spronk F, Wilson RL, Laurence JA, Bianco-Miotto T, Leemaqz S, O'Leary S, Anderson PH & Roberts CT (2015). The effect of Vdr gene ablation on global gene expression in the mouse placenta. *Genomics Data* 6:72-73.

Feature articles

Buckberry S & Roberts CT (2014). Why are males more at risk in the womb? *Australasian Science*, November 2014.