

# Curriculum Vitae

## Sam Buckberry

The University of Western Australia  
Faculty of Science  
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## Current position

### NHMRC-ARC Dementia Research Fellow

Lister Lab (epigenetics and genomics)  
Harry Perkins Institute of Medical Research  
The University of Western Australia

## Education

### Doctor of Philosophy - Medicine

The University of Adelaide (2012-2015)  
*Thesis: An integrative analysis of the human placental transcriptome.*  
*Submitted April 2015 and accepted without change July 2015.*  
*Awarded the Dean's commendation for doctoral thesis excellence.*

### Bachelor of Health Science - First Class Honours

The University of Adelaide (2011)  
*This honours research revealed epigenetic imprinting plasticity of a long non-coding RNA in the human placenta during early development.*

### Bachelor of Science

Flinders University (2008-2010)  
Extended Major in Biological Sciences  
*Graduated among the top 10% of students and received the Chancellor's Commendation in two consecutive years.*

## Research funding

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). **Buckberry S (CIA) \$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). **Buckberry S (CIA) \$314,644.** *This research 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**

## Teaching

Lecturer for the Masters level topic *The Objectives and Applications of Genomics 2017* (SCIE4001). School of Chemistry and Biochemistry, The University of Western Australia.

Teaching Assistant for RNA-Seq analysis workshops at BioInfoSummer Conference 2013, Australian Mathematical Sciences Institute and the University of Adelaide.

Teaching Assistant for the Bioinformatics Workshops 2013, the University of Adelaide.

Tutor and Coordinator for undergraduate biology Peer Assisted Study Sessions (PASS), Flinders University (2010–2011).

## Awards, scholarships & fellowships

- 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 Young Investigator 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)
- Commonwealth of Australia Education Scholarship (2008-2010)

## Training

- Data Science Specialization – 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)
- University of Adelaide bioinformatics and scripting workshop (2010)
- Australian Science Communicators media training (2010)

## Memberships and affiliations

- Executive committee member - Australian Genomic Technologies Association (AGTA)
- Australian Bioinformatics and Computational Biology Society (ABACBS)
- Founding member - Epigenetics Consortium of South Australia (EpiCSA)

## Conference presentations

### Oral presentations

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.**

Sex-biased gene expression at the human fetal-maternal interface. *Australian Society for Medical Research Annual Meeting 2013. Adelaide, Australia.*

Quantitative allele-specific expression analysis reveals imprinting plasticity of the H19 lincRNA. **ANZPRA new investigator award session**, *Society for Reproductive Biology Conference 2012. Gold Coast, Australia.*

Allele-specific expression of H19 and IGF2 in the human placenta across gestation. **Honours award session**, *Australian Society for Medical Research Annual Meeting 2012. Adelaide, Australia.*

### Poster presentations

Placental transcriptome co-expression analysis reveals conserved regulatory programs and points toward a preeclampsia gene cluster. *Australian Society for Medical Research Annual Meeting 2015. Adelaide, Australia*

Quantitative analysis of imprinted genes in the human placenta reveals developmental stage-specific imprinting plasticity. *Lorne Genome Conference 2013. Lorne, Australia.*

Allele-specific expression of H19, IGF2 and IGF2R in the human placenta through gestation. *Epigenetics Alliance Conference 2012. Adelaide, Australia.*

## Publications

### Peer-reviewed articles

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 AS<sup>1</sup>, **Buckberry S**<sup>1</sup>, 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 <sup>1</sup> *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 <sup>1</sup>, **Buckberry S**<sup>1</sup>, Spronk F<sup>1</sup>, 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. <sup>1</sup> *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

## Feature articles

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

## 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.