

Post ARC-BTP Service Publications:

- de Castro, Minique & de Klerk, Daniel & Pienaar, Ronel & Jasper G Rees, D & Mans, Ben. (2017). Sialotranscriptomics of *Rhipicephalus zambeziensis* reveals intricate expression profiles of secretory proteins and suggests tight temporal transcriptional regulation during blood-feeding. *Parasites & Vectors*. 10. 384. 10.1186/s13071-017-2312-4.
- Mans, Ben & de Klerk, Daniel & Pienaar, Ronel & de Castro, Minique & Latif, Abdalla. (2015). Next-generation sequencing as means to retrieve tick systematic markers, with the focus on *Nuttalliella namaqua* (Ixodoidea: Nuttalliellidae). *Ticks and Tick-borne Diseases*. 20. 10.1016/j.ttbdis.2015.03.013.
- de Castro, Minique & de Klerk, Daniel & Pienaar, Ronel & Latif, Abdalla & Jasper G. Rees, D & Mans, Ben. (2016). De novo assembly and annotation of the salivary gland transcriptome of *Rhipicephalus appendiculatus* male and female ticks during blood feeding. *Ticks and Tick-borne Diseases*. 7. . 10.1016/j.ttbdis.2016.01.014.
- Mans BJ, de Klerk D, Pienaar R, de Castro MH, Latif AA (2013) Correction: The Mitochondrial Genomes of *Nuttalliella namaqua* (Ixodoidea: Nuttalliellidae) and *Argas africanus* (Ixodidae: Argasidae): Estimation of Divergence Dates for the Major Tick Lineages and Reconstruction of Ancestral Blood-Feeding Characters. *PLOS ONE* 8(7): 10.1371/annotation/19fe1c45-57c3-4008-9733-ebdf39202075
- Arnold T. Kanengoni, Michael Chimonyo, Taurai Tasara, Paul Cormican, Aspinas Chapwanya, Bongani K. Ndimba, Kennedy Dzama; A comparison of faecal microbial populations of South African Windsnyer-type indigenous pigs (SAWIPs) and Large White × Landrace (LW × LR) crosses fed diets containing ensiled maize cobs, *FEMS Microbiology Letters*, Volume 362, Issue 13, 1 July 2015, fnv100, <https://doi.org/10.1093/femsle/fnv100>
- Ibaba, Jacques & Laing, Mark & Gubba, Augustine. (2016). Pepo aphid-borne yellows virus: a new species in the genus Polerovirus. *Virus Genes*. 53. 134-136. 10.1007/s11262-016-1390-2.
- Ibaba, Jacques & Laing, Mark & Gubba, Augustine. (2016). Zucchini shoestring virus: a distinct potyvirus in the papaya ringspot virus cluster. *Archives of Virology*. 161. 2321-2323. 10.1007/s00705-016-2899-3.

- Ibaba, Jacques & Laing, Mark & Gubba, Augustine. (2016). Genome sequence analysis of two South African isolates of Moroccan watermelon mosaic virus infecting cucurbits. *Virus Genes*. 52. 896-899. [10.1007/s11262-016-1372-4](https://doi.org/10.1007/s11262-016-1372-4).
- Kidanemariam Gelaw, A., Bihon, W., Faranani, R., Mafofo, J., Rees, J., & Madoroba, E. (2015). Complete Genome Sequence of *Mannheimia haemolytica* Strain Mh10517, Isolated from Sheep in South Africa. *Genome Announcements*, 3(2), e00129–15. <http://doi.org/10.1128/genomeA.00129-15>
- Schabort DTWP, Letebele PK, Steyn L, Kilian SG, du Preez JC (2016) Differential RNA-seq, Multi-Network Analysis and Metabolic Regulation Analysis of *Kluyveromyces marxianus* Reveals a Compartmentalised Response to Xylose. *PLOS ONE* 11(6): e0156242. <https://doi.org/10.1371/journal.pone.0156242>
- Zablocki, O. & Pietersen, G. *Arch Virol* (2014). Characterization of a novel citrus tristeza virus genotype within three cross-protecting source GFMS12 sub-isolates in South Africa by means of Illumina sequencing. 159: 2133. <https://doi.org/10.1007/s00705-014-2041-3>
- Makina, S. O., Muchadeyi, F. C., van Marle-Köster, E., Taylor, J. F., Makgahlela, M. L., & Maiwashe, A. (2015). Genome-wide scan for selection signatures in six cattle breeds in South Africa. *Genetics, Selection, Evolution : GSE*, 47, 92. <http://doi.org/10.1186/s12711-015-0173-x>
- Maree HJ, Pirie MD, Oosthuizen K, Bester R, Rees DJG, et al. (2015) Phylogenomic Analysis Reveals Deep Divergence and Recombination in an Economically Important Grapevine Virus. *PLOS ONE* 10(5): e0126819. <https://doi.org/10.1371/journal.pone.0126819>
- Dodd, A., Swanevelder, D., Featherston, J., & Rumbold, K. (2013). Draft Genome Sequence of *Streptomyces albulus* Strain CCRC 11814, an ϵ -Poly-L-Lysine-Producing Actinomycete. *Genome Announcements*, 1(5), e00696–13. <http://doi.org/10.1128/genomeA.00696-13>
- Khanyile, Khulekani & Dzomba, Edgar & Muchadeyi, Farai. (2015). Population genetic structure, linkage disequilibrium and effective population size of conserved and

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- Soobramoney, L.-A. O., Featherston, J., & Gray, V. M. (2015). Draft Whole-Genome Sequence of *Xenorhabdus* sp. Strain GDC328, Isolated from the Indigenous South African Nematode Host *Steinernema khoisanae*. *Genome Announcements*, 3(5), e01239–15. <http://doi.org/10.1128/genomeA.01239-15>
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- Mothupi, B., Featherston, J., & Gray, V. (2015). Draft Whole-Genome Sequence and Annotation of *Xenorhabdus griffinae* Strain BMMCB Associated with the South African Entomopathogenic Nematode *Steinernema khoisanae* Strain BMMCB. *Genome Announcements*, 3(4), e00785–15. <http://doi.org/10.1128/genomeA.00785-15>