

Curriculum Vitae

Phillip Armand Bester

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Personal details	
Surname	Bester
Names	Phillip <u>Armand</u>
Identity no	8112235032088
Gender	Male
Nationality	South African
Criminal record	None
Languages	English and Afrikaans

Health Professions Council of South Africa registration

Date Obtained: 01/12/2014

Category: Virology

Number: MS 0001511

Education

- **2007 M.Sc** Distinction UFS. Department of Biotechnology

- **2004 B.Sc.** Honours UFS. Biochemistry
- **2003 B.Sc** UFS. Biochemistry

Experience

Timeline

- **2004 - 2010** Practical Assistant for Undergraduate practicals (UFS)
- **2005** Part-time Lecturer (Central University of Technology)
- **2007 - 2010** Research Assistant for the National Earthquake Laboratory of South African Mines
- **2011- 2015** Assistant Researcher. Development and application of a HIV resistance genotyping assay. Data analysis and management of collected genotypes and clinical information.
- **2015 - current** Medical scientist. Virology, NHLS Universitas, Bloemfontein

Teaching experience at NHLS/UFS

- Main and co- supervision for Honours and M. students
 - Main supervisor for Honours student developing an HIV integrase drug resistance assay.
 - Equally shared supervisor for two Honours students on: A simple and rapid approach to prepare Sindbis and West Nile viral RNA controls for differentiation between positive samples and laboratory contamination as shown in the publication list.
 - Co-supervisor for M. Med student looking at the influence of volumes on dry blood spot samples for infant HIV diagnostics.
 - Co-supervision of M. Med student looking at HBV drug resistance and viral loads
- Marking of Honours and M. students dissertations
 - Marking of M. Sc thesis for Prof Gert van Zyl, Stellenbosch University
- Lecturing Honours students and medical registrars in bioinformatics (<http://vdeb.hpc.ufs.ac.za/>)
- University of the Free State Medical Faculty Scientific committee member

Academic background

M.Sc in biochemistry with experience in molecular biology, including nucleic acid extraction, polymerase chain reaction and designing of PCR primers, recombinant DNA techniques, cloning, site directed mutagenesis, DNA sequencing, recombinant protein expression and enzyme kinetics.

Working experience

In my time working in Virology I have developed an HIV protease and reverse transcriptase drug resistance assay which I also validated in terms of sensitivity, specificity, accuracy and precision. I am also a member of the national NHLS HIV drug resistance subcommittee where we meet once a quarter to discuss operational, QA/QC, clinical and research related to HIV drug resistance. This allowed me to be part of this assay's costing analysis. We are subscribed to the QCMD EQA program for HIV drug resistance where we always scored above 98% and 99.4% in 2020. I was also involved in getting this assay SANAS accredited and maintaining accreditation with proper GLP. I am the author of our inhouse HIV drug resistance SOP and do training and competency evaluations on staff.

As our HIV sequence database grew, the need for more sophisticated phylogenetics arose. With the help of collaborators, I developed a phylogenetic pipeline which we published in PLOS ONE (PhyloPi: An affordable, purpose built phylogenetic pipeline for the HIV drug resistance testing facility). This also allowed us to reach out to the public in the form of a four-part blog post. This is available online on RStudio's blog, rviews (<https://rviews.rstudio.com/2019/04/30/analysing-hiv-pandemic-part-1/>). PhyloPi is now an integrated part of QA/QC in the Universitas and Charlotte Maxeke drug resistance testing facilities with plans to roll out to the remainder of the NHLS facilities as well early this year. Not only does this provide valuable spot checks, but has identified numerous sample swaps originating from health care facilities that otherwise would not have been noticed.

The ongoing pandemic is having devastating consequences around the world. However, it has challenged the discipline's workforce to levels previously not tested. I was entrusted with the SARS-CoV-2 diagnostics in the verification of the various assays, operations, QC/QA, procurement and workflows. This also includes training of staff and competency evaluation. I have also trained staff at NHLS in Kimberley.

Our laboratory has verified and implemented the following SARS-CoV-2 assays:

- NucliSense extraction with Seegene Allplex 2019-nCoV assay
- MagMAX Viral and Pathogen Nucleic Acid Isolation Kit extraction with TaqPath covid-19 kit
- Seegene Numbis extraction with Seegene Allplex 2019-nCoV assay
- Bosphore EX-Tract extraction with Seegene Allplex 2019-nCoV assay
- MagMAX Viral and Pathogen Nucleic Acid Isolation Kit extraction with BGI RT-PCR
- Roche COBAS 8800*
- Abbott M2000*
- BioFire FilmArray*

Assays tested but not implemented:

- Thermal extraction with Seegene Allplex 2019-nCoV assay
- GeneChecker

(**Only involved with evaluation reports*)

In any laboratory things can go wrong and especially in diagnostic facilities, this can have profound implications if it goes unnoticed. In the time working at Virology I have plenty of experience in noticing problems, troubleshooting and root cause analysis.

My python and R experience helped in the analysis and creation of assay evaluation reports. I have created a script that accepts data in a spreadsheet and calculates various metrics of agreement and other statistics. The well-cited python package, statsmodels, was used to do the statistical calculations for serology and molecular assay validations. I have created numerous reports for pathologists to sign off.

Ongoing and recent academic projects (2020-2021)

I am involved in various projects where I co-manage research projects with one or more of our pathologists. In many of the projects and research outputs listed below, I was heavily involved in data analysis and/or bio-informatics.

HBV

We are in collaboration with an Oxford group (Wellcome Trust funding under Oxford PI Prof Philippa Matthews) with a few Hepatitis B virus projects. One of our projects was a systematic review of HBV seroepidemiology in Africa. Here I was involved in visualizations one of which is available at <https://hbv-geo.shinyapps.io/oxafricahbv/>.

We are analysing retrospective data from the NHLS Central Data Warehouse with the main focus on HBV infection stratified by other factors such as HIV status, gender, age and health outcomes.

Together with structural biologists, we are looking at HBV reverse transcriptase expression of domains with the aim of crystallising and structure determination.

Co-supervision of an M. Med student looking at HBV, viral loads, tenofovir resistance and the correlation with HIV status and viral loads (NHLS RTG funded).

HIV

Co-supervision M. Med with the aim of determining the effect of volume on dry blood spot cards used for infant HIV diagnosis. (M. Med awarded)

Co-supervision of HIV drug resistance mutations K65R and M184V to determine if these mutations can reside on the same virus by using a cloning strategy. This was part of an HPCSA portfolio for an intern.

Consultant on PhD project looking at mother to child HIV transmission and drug resistance profiles (PhD awarded).

Successfully raised publication fees for our PhyloPi paper published in PLoS ONE as listed under publications.

SARS-COV2

Next generation sequencing and surveillance of SARS-COV2 genomes where I am involved in sample selection, bio-informatics and genome consensus generation and quality control (MRC funding as a member of the Network for Genomic Surveillance in South Africa).

Seroepidemiology from HIV viral load samples using repeated cross-sectional sampling of approximately 5000 samples.

Diabetes type 2

Co-supervisor for genetics M. Sc student looking at epigenetics involvement and type 2 Diabetes. (M.Sc awarded)

Readiness in a world of data

Proficient in the R statistical programming language, python programming language and bash scripting. Proficient with data cleaning and wrangling using both R or python pandas as well as data representation in both R and python.

Next generation sequencing data analysis including *de novo* assembly as well as mapping applications such as SNP discovery.

<https://github.com/ArmandBester/>

I constantly try to better my coding ability and statistical knowledge with the focus on problem solving in the real world. I enrol frequently in online training courses like Udemy and freeCodeCamp.

Since 2023, I have been involved with the Grid Related Research Group (GRRG) at the University of the Free State and the Interdisciplinary Center for Digital Futures (ICDF), also at the University of the Free State. One of the goals of the GRRG is to understand the power demand on it's campuses and the optimized incorporation of renewable energy. In the midst of South Africa's energy crisis it is important to monitor, analyse and understand the electrical grid dynamics in order to act appropriately. One of the outcomes of my involvement was the establishment of an open source pipeline for the real time accusation fo the measurements on both Bloemfontein and QwaQwa campus (a dashbourd of that is available at <https://s.ern.ufs.ac.za/grrg>). I have also been invited to present at a collocium and a workshop for the groups focusing on data mining and time series analysis. In this capacity I have been invited to co-supervise a M.Sc student at the Norwegian University of Life Sciences (NMBU) which will conclude in 2024.

Academic

Peer reviewed publications

- J. Maritz, L. R. Gorjão, **P. A. Bester**, N. Esterhuysen, S. Erasmus, S. Riekert, R. Immelman, T. Geldenhuys, A. Viljoen, C. Bodenstein. "Data-Driven Modeling of Frequency Dynamics Observed in Operating Microgrids: A South African University Campus Case Study," in IEEE Access, vol. 12, pp. 14466-14473, 2024, doi: 10.1109/ACCESS.2024.3357945.
- Nicole Kennedy, Dominique Goedhals, Sabeehah Vawda, **Philip Armand Bester**, Felicity Burt. Sindbis Virus Antibody Seroprevalence in Central Plateau Populations, South Africa. 2022. Emerging Infectious Diseases 28(10):2137-2139. Advancing HIV Drug Resistance Technologies and Strategies: Insights from South Africa's Experience and Future Directions for Resource-Limited Settings. 2023. Diagnostics 13(13)
- Kim Steegen, Gert U. van Zyl, Mathilda Claassen, Aabida Khan, Melendhran Pillay, Subitha Govender **Phillip A. Bester**, Johanna M. van Straaten, Vibha Kana, Ewaldé Cutler, Monalisa N. Kalimashe, Ramokone L. Lebelo, Mokopi B. H. Moloi and Lucia Hans. Advancing HIV Drug Resistance Technologies and Strategies: Insights from South Africa's Experience and Future Directions for Resource-Limited Settings. Diagnostics 2023, 13, 2209
- Mwangi Peter, Okendo Javan, Mogotsi Milton, Ogunbayo Ayodeji, Adelabu Olusesan, Sondlane Hlengiwe, Maotoana Makgotso, Mahomed Lutfiyya, Morobadi Molefi Daniel, Vawda Sabeehah, von Gottberg Anne, Bhiman Jinal, Tegally Houriiyah, Wilkinson Eduan, Giandhari Jennifer, Pillay Sureshnee, Naidoo Yeshnee, Ramphal Upasana, de Oliveira Tulio, **Bester Armand**, Goedhals Dominique, Nyaga Martin. SARS-CoV-2 variants from COVID-19 positive cases in the Free State province, South Africa from July 2020 to December 2021. 2022. Frontiers in Virology
- Peter Mwangi, Milton Mogotsi, Ayodeji Ogunbayo, Teboho Mooko, Wairimu Maringa, Hlengiwe Sondlane, Kelebogile Nkwadipo, Olusesan Adelabu, **Philip Armand Bester**, Dominique Goedhals, Martin Nyaga. A decontamination strategy for resolving SARS-CoV-2 amplicon contamination in a next-generation sequencing laboratory. 2022. Archives of Virology. 10.1007/s00705-022-05411-z
- Tegally Houriiyah, Moir Monika, Everatt Josie, Giovanetti Marta, Scheepers Cathrine, Wilkinson Eduan, Subramoney Kathleen, Makatini Zinhle, Moyo Sikhulile, Amoako Daniel G., Baxter Cheryl, Althaus Christian L., Anyaneji Ugochukwu J., Kekana Dikeledi, Viana Raquel, Giandhari Jennifer, Lessells Richard J., Maponga Tongai, Maruapula Dorcas, Choga Wonderful, Matshaba Mogomotsi, Mbulawa Mpaphi B., Msomi Nokukhanya, **Bester Armand Phillip**, Claassen Mathilda, Doolabh Deelan, Mudau Innocent, Mbhele Nokuzola, Engelbrecht Susan, Goedhals Dominique, Hardie Diana, Hsiao Nei-Yuan, Iranzadeh Arash, Ismail Arshad, Joseph Rageema, Maharaj Arisha, Mahlangu Boitshoko, Mahlakwane Kamela, Davis Ashlyn, Marais Gert, Mlisana Koleka, Mnguni Anele, Mohale Thabo, Motsatsi Gerald, Mwangi Peter, Ntuli Noxolo, Nyaga Martin, Olubayo Luicer, Radibe Botshelo, Ramphal Yajna, Ramphal Upasana, Strasheim Wilhelmina, Tebeila Naume, van Wyk Stephanie, Wilson Shannon, Lucaci Alexander G., Weaver Steven, Maharaj Akhil, Pillay Yusasha, Davids Michaela, Mendes Adriano, Mayaphi Simnikiwe, Naidoo Yeshnee, Pillay Sureshnee, Sanko Tomasz Janusz, San James E., Scott Lesley, Singh Lavanya, Magini Nonkululeko A., Smith-Lawrence Pamela,

Stevens Wendy, Dor Graeme, Tshiabuila Derek, Wolter Nicole, Preiser Wolfgang, Treurnicht Florette K., Venter Marietjie, Chiloane Georginah, McIntyre Caitlyn, O'Toole Aine, Ruis Christopher, Peacock Thomas P., Roemer Cornelius, Kosakovsky Pond Sergei L., Williamson Carolyn, Pybus Oliver G., Bhiman Jinal N., Glass Allison, Martin Darren P., Jackson Ben, Rambaut Andrew, Laguda-Akingba Oluwakemi, Gaseitsiwe Simani, von Gottberg Anne, de Oliveira Tulio Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. *Nat Med* 28, 1785–1790 (2022).

<https://doi.org/10.1038/s41591-022-01911-2>

- Raquel Viana, Sikhulile Moyo, Daniel G. Amoako, Houriiyah Tegally, Cathrine Scheepers, Christian L. Althaus, Ugochukwu J. Anyaneji, **Phillip A. Bester**, Maciej F. Boni, Mohammed Chand, Wonderful T. Choga, Rachel Colquhoun, Michaela Davids, Koen Deforche, Deelan Doolabh, Louis du Plessis, Susan Engelbrecht, Josie Everatt, Jennifer Giandhari, Marta Giovanetti, Diana Hardie, Verity Hill, Nei-Yuan Hsiao, Arash Iranzadeh, Arshad Ismail, Charity Joseph, Rageema Joseph, Legodile Koopile, Sergei L. Kosakovsky Pond, Moritz U. G. Kraemer, Lesego Kuate-Lere, Oluwakemi Laguda-Akingba, Onalethatha Lesetedi-Mafoko, Richard J. Lessells, Shahin Lockman, Alexander G. Lucaci, Arisha Maharaj, Boitshoko Mahlangu, Tongai Maponga, Kamela Mahlakwane, Zinhle Makatini, Gert Marais, Dorcas Maruapula, Kereng Masupu, Mogomotsi Matshaba, Simnikiwe Mayaphi, Nokuzola Mbhele, Mpaphi B. Mbulawa, Adriano Mendes, Koleka Mlisana, Anele Mnguni, Thabo Mohale, Monika Moir, Kgomotso Moruisi, Mosepele Mosepele, Gerald Motsatsi, Modisa S. Motswaledi, Thongbotho Mphoyakgosi, Nokukhanya Msomi, Peter N. Mwangi, Yeshnee Naidoo, Noxolo Ntuli, Martin Nyaga, Lucier Olubayo, Sureshnee Pillay, Botshelo Radibe, Yajna Ramphal, Upasana Ramphal, James E. San, Lesley Scott, Roger Shapiro, Lavanya Singh, Pamela Smith-Lawrence, Wendy Stevens, Amy Strydom, Kathleen Subramoney, Naume Tebeila, Derek Tshiabuila, Joseph Tsui, Stephanie van Wyk, Steven Weaver, Constantinos K. Wibmer, Eduan Wilkinson, Nicole Wolter, Alexander E. Zarebski, Boitumelo Zuze, Dominique Goedhals, Wolfgang Preiser, Florette Treurnicht, Marietje Venter, Carolyn Williamson, Oliver G. Pybus, Jinal Bhiman, Allison Glass, Darren P. Martin, Andrew Rambaut, Simani Gaseitsiwe, Anne von Gottberg & Tulio de Oliveira. Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. 2022. *Nature*. 10.1038/s41586-022-04411-y
- Yuri Munsamy, Riaz Y. Seedat, Tumelo R. Sekee, **Phillip A. Bester**, Danelle van Jaarsveldt, Felicity J. Burt. Whole-Genome Sequence and Comparative Analysis of Human Papillomavirus Type 18 Isolated from a Nasopharyngeal Carcinoma from South Africa. 2021. *Microbiology Resource Announcements*. <https://doi.org/10.1128/MRA.00630-21>
- Yuri Munsamy, Riaz Y. Seedat, Tumelo R. Sekee, **Phillip A. Bester**, Felicity J. Burt. Complete genome sequence of a HPV31 isolate from laryngeal squamous cell carcinoma and biological consequences for p97 promoter activity. 2021. *PLOS ONE*. <https://doi.org/10.1371/journal.pone.0252524>
- Oosthuizen Jaco, Kotze Maritha J, Van Der Merwe Nicole, Myburgh Ettienne J, **Bester Phillip**, van der Merwe Nerina C. Rare BRCA2 Variants With Founder Haplotypes in the South African Population: Implications for Point-of-Care Testing Based on a Single-Institution BRCA1/2 Next-Generation Sequencing Study. 2021. *Frontiers in Oncology*. 10(3403)
<https://www.frontiersin.org/article/10.3389/fonc.2020.619469>
- Zhongning Zhao , Neil Heideman, **Phillip Bester**, Adriaan Jordaan and Margaretha D. Hofmeyr. Climatic and topographic changes since the Miocene influenced the diversification and biogeography of the tent tortoise (*Psammobates tentorius*) species complex in Southern Africa.

- Milton T. Mogotsi, Peter N. Mwangi, **Phillip A. Bester**, M. Jeffrey Mphahlele, Mapaseka L. Seheri, Hester G. O'Neill and Martin M. Nyaga. Metagenomic Analysis of the Enteric RNA Virome of Infants from the Oukase Clinic, North West Province, South Africa, Reveals Diverse Eukaryotic Viruses. 2020. Viruses 12(11), 1260. <https://doi.org/10.3390/v12111260>
- S. Vawda, **P.A. Bester**, D. Morobadi, P. Matthews, J. Mokaya, D. Goedhals. Characteristics of individuals with hepatitis B virus infection in the Free State and Northern Cape provinces of South Africa. 2020. International Journal of Infectious Diseases. DOI:<https://doi.org/10.1016/j.ijid.2020.09.1363>
- Leholonolo Mathengtheng, Dominique Goedhals, **Phillip A. Bester**, Jacqueline Goedhals, Felicity J. Burt. Persistence of Crimean- Congo Hemorrhagic Fever Virus RNA. 2020. Emerging Infectious Diseases, 26(2), 385-387. <https://dx.doi.org/10.3201/eid2602.191460>.
- Micah Dimaculangan, Siewert C. Wiid, Phillip A. Bester, Tumelo R. Sekee, Felicity J. Burt. A simple and rapid approach to prepare Sindbis and West Nile viral RNA controls for differentiation between positive samples and laboratory contamination. 2020. Journal of Virological Methods (278). <https://doi.org/10.1016/j.jviromet.2020.113822>.
- Zhao, Z, Heideman, N, Grobler, P, Jordaan, **A, Bester**, P, Hofmeyr, MD. Unraveling the diversification and systematic puzzle of the highly polymorphic *Psammobates tentorius* (Bell, 1828) complex (Reptilia: Testudinidae) through phylogenetic analyses and species delimitation approaches. *J Zool Syst Evol Res*. 2020; 58: 308– 326. <https://doi.org/10.1111/jzs.12338>
- McNaughton AL, Lourenço J, **Bester PA**, Mokaya J, Lumley SF, Obolski U, Forde D, Maponga TG, Katumba KR, Goedhals D, Gupta S, Seeley J, Newton R, Ocamo P, Matthews PC. Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis. PLoS Med. 2020 Apr 21;17(4):e1003068. doi: 10.1371/journal.pmed.1003068. PMID: 32315297; PMCID: PMC7173646.
- **Phillip Armand Bester**, Andrie De Vries, Stephanus Riekert, Kim Steegen, Gert van Zyl, Dominique Goedhals. PhyloPi: An affordable, purpose built phylogenetic pipeline for the HIV drug resistance testing facility. 2019. PloS ONE. <https://doi.org/10.1371/journal.pone.0213241>
- Sabeehah Vawda, Dominique Goedhals, **Phillip Armand Bester**, Felicity Burt. Seroepidemiologic Survey of Crimean-Congo Hemorrhagic Fever Virus in Selected Risk Groups, South Africa. July 2018. Emerging Infectious Diseases 24(7):1360-1363. 10.3201/eid2407.172096
- Riaz Seedat, C. E. Combrink, **Phillip Armand Bester**, Felicity Burt. Determination of the complete genome and functional analysis of HPV6 isolate VBD19/10 from a patient with aggressive recurrent respiratory papillomatosis. March 201. Epidemiology and Infection -1(10):1-8. DOI: 10.1017/S0950268816000388
- Gregson J, Tang M, Ndambi N, Hamers RL, Rhee SY, Marconi VC, Diero L, Brooks K, Theys, K, Rinke de Wit TF, Arruda M, Garcia F, Monge S, Günthard, HF, Hoffmann, CJ, Kanki PJ, Kumarasamy, N, Kerschberger B, Mor O, Charpentier C, Todesco E, Rokx C, Gras L, Halvas EK, Sunpath H, Di Carlo D, Antinori A, Andreoni M, Latini A, Mussini C, Aghokeng A, Sonnerborg A, Ujjwal Neogi U, Fessel WJ, Agolory S, Yang C, Blanco JL, Juma JM, Smit, E, Schmidt, D, Watera C, Asio J, Kirungi W, Tostevin A, El- Hay T, Clumeck N, Goedhals D; van Vuuren C, **Bester PA**, Sabin C, Mukui I, Santoro MM, Perno CF, Hunt G, Morris L, Camacho R, de Oliveira T, Pillay D, Schuster E, Akio Murakami- Ogasawara A, Reyes- Terán G, Romero K, Avila- Rios S, Sirivichayakul, S, Ruxrungtham K, Mekprasan S, Dunn, D, Kaleebu, P, Raizes E, Kantor R, Shafer RW, Gupta RK on behalf of the TenoRes study group. (2016). *Global epidemiology of drug resistance following failure of WHO recommended first line regimens*

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- Goedhals D, **Bester PA**, Paweska JT, Swanepoel R, Burt FJ. Comparative analysis of the L, M, and S RNA segments of Crimean-Congo haemorrhagic fever virus isolates from southern Africa. Journal of medical virology. 2015 Feb Vol 85, Issue 5 p717-724. DOI: 10.1002/jmv.24079
- Goedhals D, **Bester PA**, Paweska JT, Swanepoel R, Burt FJ. Next-generation sequencing of southern African Crimean-Congo haemorrhagic fever virus isolates reveals a high frequency of M segment reassortment. Epidemiology and Infection. 2014 May 1:1-11. [Epub ahead of print] PubMed PMID: 24786748.
- Manasa J, Lessells R, Rossouw T, Naidu K, Van Vuuren C, Goedhals D, van Zyl G, **Bester A**, Skingsley A, Stott K, Danaviah S, Chetty T, Singh L, Moodley P, Iwuji C, McGrath N, Seebregts CJ, de Oliveira T. Southern African Treatment Resistance Network (SATuRN) RegaDB HIV drug resistance and clinical management database: supporting patient management, surveillance and research in southern Africa. Database (Oxford). 2014 Feb 6; 2014:bat082. doi: 10.1093/database/bat082. Print 2014. PubMed PMID: 24504151
- Johanna Lippmann-Pipke, Jörg Erzinger, Martin Zimmer, Christian Kujawa; Margaret Boettcher, Esta van Heerden, **Armand Bester**; Hannes Moller; Nicole A Stroncik, Zeev Reches. Direct observation of geogas transport through an inactive fault system at 3.54 km depth, TauTona gold mine, South Africa. Applied Geochemistry, 26, 12, 2134-2146
- Borgonie, G., García-Moyano, A., Litthauer, D., Bert, W., **Bester, P.A.**, van Heerden, E and Onstott, T.C. (2011). Worms from hell: Nematoda from the terrestrial deep subsurface of South Africa. Nature 2009-12-15946E, volume 474, issue 7349 from 02 June 2011.
- **Bester, P.A.**, Litthauer, D., Piater, L.A., and van Heerden, E. (2010). A thioredoxin reductase-like protein from the thermophile, *Thermus scotoductus* SA-01, displaying iron reductase activity. FEMS Microbiology Letters 302, 182 -188.
- Van Heerden, E, Opperman, D.J., **Bester, P.A.**, Van Marwijk, J., Cason, E.D., Litthauer, D., Piater, L.A. and Onstott, T.C. (2008). Metabolic promiscuity from the deep subsurface: a story of Survival or Superiority. Instruments, Methods, and Missions for Astrobiology XI. Edited by Hoover, Richard B.; Levin, Gilbert V.; Rozanov, Alexei Y.; Davies, Paul C. Proceedings of the SPIE, Volume 7097, pp. 70970S-70970S-12.

Talks (International)

- **PA Bester**, A De Vries, SJPK Riekert, K Steegen, G van Zyl, D. Goedhals. PhyloPi: an affordable, purpose built phylogenetic pipeline for the HIV drug resistance testing facility. 27th International Workshop on HIV Drug Resistance and Treatment Strategies. 22-23 October 2018.
- Lippman-Pipke, J., Erzinger, J., Zimmer, M., Kujawa, C., Boettcher, M.S., Van Aswegen, G., Moller, H., Van Heerden, E., **Bester, A.**, Reches, Z. Long-term, on-site borehole monitoring of gases released from an active fault system at 3.6km depth, TauTona Gold Mine, South Africa. 2009 AGU Fall Meeting, 14-18 December, San Francisco, California.
- van Heerden, E., **Bester, P.A.**, Gounder, K., Litthauer, D., and Opperman, D.J. Mechanisms and Multitasking of “reductases” from *Thermus scotoductus* SA01. Thermophiles 2009. August 16-21. Beijing China.
- Onstott, T.C., E. Chan, Van Heerden, E. , Litthauer, D., **Bester, A.**, Reches, Z., Van Aswegen, G., Moller, H., and Lippman-Pipke, J.,. An *in situ* bioseismicity experiment 3.6 km beneath the surface at

NELSAM. AGU Fall Meeting 2008: Special Section H66, 15 – 19 December 2008, San Francisco, California, USA.

- Lippman-Pipke, J., Erzinger, J., Zimmer, M., Kujawa, C., Van Heerden, E., **Bester, A.**, Moller, H., Boettcher, M. and Reches, Z. Direct observation of blasting triggered geogas transport through an inactive fault system at 3.6km depth, Tautona gold mine, SA National meeting on ICDP/IODP-projects in Hannover, Germany (March, 12-14th, 2008).
- G. Lacrampe-Couloume, Van Heerden, E., Piater, L.A., Opperman, D.J., **Bester, A.**, Lippman-Pipke, J., Slater, G.F., Ontstott, T.C., and B. Sherwood Lollar. Microbial methanogenesis in ancient groundwaters in Witwatersrand Basin: The timing of deep subsurface life. ABSCICON 2008. The 5th Astrobiology Science Conference April 14 - 17, 2008. Santa Clara Convention Center Santa Clara, California, USA

Posters (International)

- **PA Bester**, A De Vries, SJPK Riekert, K Steegen, G van Zyl, D. Goedhals. PhyloPi: an affordable, purpose built phylogenetic pipeline for the HIV drug resistance testing facility. 27th International Workshop on HIV Drug Resistance and Treatment Strategies. 22-23 October 2018.
- D. Goedhals, **P. A. Bester**, J. T. Paweska, R. Swanepoel, F. J. Burt. Next generation sequencing of southern African Crimean-Congo haemorrhagic fever virus isolates. 16th ICID, Cape Town, South Africa, 2-5 April 2014.
- Lacrampe-Couloume, G., Van Heerden, E., Piater, L.A., Opperman, D.J., **Bester, A.**, Lippman-Pipke, J., Slater, G.F., Ontstott, T.C., and B. Sherwood Lollar. Microbial methanogenesis in ancient groundwaters in Witwatersrand Basin: The timing of deep subsurface life. Poster presentation. ABSCICON 2008. The 5th Astrobiology Science Conference, 14 – 17 April, 2008, Santa Clara Convention Center Santa Clara, California, USA
- Lippman-Pipke, J., Erzinger, J., Zimmer, M., Kujawa, C., Van Heerden, E., **Bester, A.** Moller, H., Boettcher, M., and Reches, E. Direct observation of blasting triggered geogas transport through an inactive fault system at 3.6 km depth, TauTona gold mine. Poster presentation. SA National meeting on ICDP/IODP-projects, 12 – 14 March 2008, Hannover, Germany.
- Van Heerden, E., Opperman, D.J., **Bester, A.**, Möller, C., Litthauer, D., and Parro, V. Metal reductases from the South African Deep Subsurface. International conference - Thermophiles 2007. September 24-27, Bergen. Norway

Talks (National)

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