DUT
DURBAN UNIVERSITY OF TECHNOLOGY
INYUVESI YASETHEKWINI YEZOBUCHWEPHESHE

FACULTY OF APPLIED SCIENCES

DEPARTMENT OF BIOTECHNOLOGY & FOOD SCIENCE

CSBRG
COMPUTATIONAL & SYSTEMS BIOLOGY RESEARCH GROUP

Computational and Systems Biology Conference 2024

"Bridging the gap between theoretical and experimental biological sciences through computational systems biology"

KEYNOTE SPEAKER PROFILES & BOOK OF ABSTRACTS

24th - 26th June 2024

DURBAN UNIVERSITY OF TECHNOLOGY (DUT)

COMPUTATIONAL AND SYSTEMS BIOLOGY CONFERENCE (CSBC) 2024

INTRODUCTION

In the era of ravaging global disease trends, computational and systems biology (CSB)-based research and platforms have proved to be formidable in responding and tackling health-related global challenges. Hence, the acquisition of relevant skills within this research field is crucial to ensuring accuracy and precision in data mining and processing workflows. It is essential to produce dependable and reproducible science-backed conclusions from CSB data in order to influence and guide pertinent health policies and actions that might be developed in the future.

The event is envisaged to bring together researchers and practitioners interested in both theoretical advances and applications of artificial intelligence and other computational tools in knowledge areas related to biology and medicine.

WORKSHOP AND CONFERENCE THEME

Bridging the gap between theoretical and experimental biological sciences through computational systems biology.

AIM

To give participants a foundational appreciation of CSB workflows and subfields, while availing them the opportunity to interact, network, forge new collaborations, present and discuss their various CSB-based research findings. Since the gathering involves the acquisition of practical skills and theoretical knowledge, it will enhance the capacity of participants to efficiently navigate CSB workflows and associated downstream data analysis.

CONFERENCE INFORMATION

Intended and targeted audience

- Postgraduate students currently conducting research in relevant CSB fields.
- Researchers and practitioners, including biotechnologists, medicinal chemists, microbiologists, biochemists, health professionals and informatics/computer scientists.
- Other interested parties who plan to work in related CSB fields in future.
- Experts and industries in CSB research fields.

Participants will be introduced to:

- Metabolomics workflows and platforms
- Molecular fingerprinting and modelling showcasing docking workflow
- Construction of new chemical entity scaffolds
- 16S/ITS metagenomics data analysis

Host

DUT's Computational and Systems Biology Research Group (CSBRG)

Research Group Lead: Prof. S. Sabiu

Contact: sabius@dut.ac.za

KEYNOTE SPEAKERS

1. Prof. K. Bisetty (Professor and Lead, Computational Modelling and Bioanalytical Chemistry Research Group, Chemistry Department, Durban University of Technology, South Africa)

2. Prof. L. O. Olasunkanmi (Associate Professor of Physical Chemistry; Vice-Dean, Student Affairs, Obafemi Awolowo University, Nigeria; and Senior Research Associate, University of Johannesburg, South Africa)

3. Prof. M. Trindade (Director, Institute for Microbial Biotechnology and Metagenomics, University of the Western Cape, South Africa)

4. Prof. M. Nyaga (Associate Professor, Next Generation Sequencing Unit, Office of the Dean and Division of Virology, Faculty of Health Sciences, University of Free State, South Africa; and Director, WHO Collaborating Centre for Vaccine Preventable Diseases (VPD) Surveillance and Pathogen Genomics, Bloemfontein, South Africa)

5. Prof. S. Singh (Senior Vice President, Computational Science & Structural Biology, Matchpoint Therapeutics, USA)

6. Prof. K. Syed (Professor of Biochemistry and Lead, Cytochrome P450 monooxygenases Research Group, University of Zululand, South Africa)

7. Prof. K. Rajshekhar (Lead, Synthetic Medical Chemistry Research Group, University of Kwazulu-Natal, South Africa)

LOCAL ORGANIZING COMMITTEE (LOC)

Coordinator of the sub-committees: Prof. S. Sabiu

Planning, content and technical sub-committee: Dr. B.O. Yusuf, Dr. C.E. Aruwa, J.O. Aribisala, & Prof. V. Mohanlall

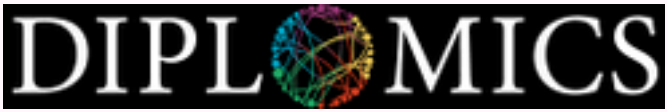
Logistics sub-committee: Dr. C. Pillay, P. Phillips, R.A. Abdulsalam, O.M. Ayodele, S. Mthembu, J. Uhomoibhi, & A. Akoonjee

Publicity sub-committee: H.Y. Lukman, C. Peter, A.A. Lanrewaju, Y. Dweba, V. Nwokorogu, B.O. Ajibade, & N.W. S'thebe

IT Support: N. Nkululeko

FUNDING ORGANISATIONS

SPONSORS



CONTENTS

Programme Outline

Day 1: Workshop (Computer Laboratory S6 L0, Steve Biko Campus, DUT)

Monday, 24 June 2024

07h00 – 07h50	**Registration and welcome tea**
07h50 – 08h00	**Welcome message** Prof. F. M. Swalaha (Head of Department: Biotechnology and Food Science, DUT)
08h00 – 08h10	**Opening of the workshop** Prof. S. Singh (Executive Dean: Faculty of Applied Sciences, DUT)
08h10 – 11h00	**Opening of the workshop** ▪**An overview of metabolomics workflow & data processing/analysis via MetaboAnalyst** ▪**LCMS spectral data – metabolite annotation (overview)** ▪**Computational tools/methods for spectral data (metabolite) annotation and visualization** Dr F. Tugizimana, K. Othibeng, and A. Myoli (UJ)
11h00 – 11h30	**Construction of new chemical entity scaffolds** Dr. E.O. Akintemi (UNISA)
11h30 – 13h00	**Molecular docking workflows and molecular fingerprinting** A.A. Lanrewaju & C. Peter (DUT)
13h00 – 13h45	**Lunch break**
13h45 – 14h45	**Molecular docking workflows and molecular fingerprinting** A.A. Lanrewaju & C. Peter (DUT)
14h45 – 17h30	**16S/ITS metagenomics data analysis** Prof. E. Cason (UFS), Dr. K. Moloantoa (UKZN) and R.A. Abdulsalam (DUT)
17h30 – 17h40	**Closing** Prof. S. Sabiu

Day 2: Conference Day 1 (Coastlands Hotel, Musgrave, Durban)

Tuesday, 25 June 2024

08h00 – 09h00	**Registration and welcome tea**
09h00 – 09h10	**Welcome address** Prof. S. Singh (Executive Dean: Faculty of Applied Sciences, DUT)
09h10 – 09h20	**Opening of the conference** Prof. F. Nemavhola (Deputy Vice-Chancellor: Research Innovation and Engagement)
	SESSION 1 **Chairpersons: Prof. K. Syed (UNIZULU) & Prof. S. Pillai (DUT)**
	KEYNOTE ADDRESSES
09h20 – 09h50	**Synergy unleashed: Sensor innovation with experimental and computational chemistry** Prof. K. Bisetty (DUT)
09h50 – 10h20	**The nexus between computational chemical biology and drug discovery** Prof. L. O. Olasunkanmi (OAU)
10h20 – 10h50	**Tea break/Poster presentation**
	PRESENTATIONS
10h50 – 11h05	**A new horizon in antimalaria drug design: Peptide-based inhibitors targeting *Plasmodium falciparum* Grp94** W. Mthembu, M. Rautenbach, & T. Zininga (SU)
11h05 – 11h20	**Modeling covalent enzyme inhibition** Jerônimo Lameira (FUP, Brazil)
11h20 – 11h35	**Evaluating the active compounds of *Momordica charantia* seed crude extracts for antimalaria drug design using *in silico* molinspiration and molecular docking screening** E. O. Akintemi, O. P. Akoniyon, & H. S. Clayton (UNISA)
11h35 – 11h50	**A new class of linezolid-based molecules as potential antimicrobial and antitubercular agents: A rational approach** S. Nadigar, B. Kushwaha, & R. Karpoormath (UKZN)
11h50 – 12h05	**Molecular characterization of tomatoes spoilage bacteria and bioprospection of essential oils against their key druggable targets** R.A. Abdulsalam, O.A. Ijabadeniyi, & S. Sabiu (DUT)
12h05 – 12h20	**Molecular epidemiology of antibiotic-resistant *Escherichia coli* from companion animals attending veterinary practices in Durban, KwaZulu-Natal, South Africa** N. L. Ntuli, A.L.K. Abia, J. Mbanga, S.Y. Essack (UKZN)
12h20 – 12h30	**Voting Session: People's Choice for Best Presenter**
12h30 – 12h50	**Molecular and analytical companies' presentations** QIAGEN Apex Scientific Shalom Laboratory Supplies
12h50 – 13h40	**Lunch break**

	SESSION 2 **Chairpersons: Prof. J. Mellem (DUT) & Prof. L. O. Olasunkanmi (OAU)**
	KEYNOTE ADDRESSES
13h40 – 14h00	**Unravelling six decades of the mystery of the evolution of living protein fossil iron-sulfur cluster proteins** Prof. K. Syed (UNIZULU)
14h00 – 14h20	**Deciphering the epidemiology, dynamics, and detection of enteric and respiratory viral pathogens using next generation sequencing: Prospects and advances** Prof. M. Nyaga (UFS)
	PRESENTATIONS
14h20 – 14h35	**Assessment of antibiotic resistance and efflux pump gene expression in Neisseria gonorrhoeae isolates from South Africa by quantitative real-time PCR and regression analysis** N. Mitchev, R. Singh, V. Ramsuran, A. Ismail, M. Allam, S. Kwenda, F. Mnyameni, N. Garrett, K.S. Swe-Han, A.J. Niehaus and K.P (UKZN)
14h35 – 14h50	**Charting the Cannabis plant chemical space with computational metabolomics** A. Myoli, M. Choene, A. P. Kappo, E. N. Madala, J.J. van der Hooft, & F. Tugizimana (UJ)
14h50 – 15h05	**Computational and bioinformatics strategies in mining and interpreting metabolomics data: the case of biostimulants-maize interactions** K. Othibeng, F. Tugizimana, D. Petras, & K. B. Kang (UJ)
15h05 – 15h20	**Metabolites profiling and bacterial diversity of traditionally produced Amasi- a South African fermented product** B.O. Ajibade, T. A. Ajayeoba, S. Sabiu, K. V. Moiseenko, T.V. Fedorova, & O.A. Ijabadeniyi (DUT)
15h20 – 15h35	**Cheminformatics identification of LasR modulators of *Pseudomonas aeruginosa* from selected South African essential oils** Y. Dweba, C.E. Aruwa, & S. Sabiu (DUT)
15h35 – 15h40	**Voting Session: People's Choice for Best Presenter**
15h40 – 17h00	**Durban Tour/Beach Visit**

Day 3: Conference Day 2 (Coastland Hotels, Musgrave, Durban)

Wednesday, 26 June 2024

08h30 – 09h30	**Registration and welcome tea**
	SESSION 1 **Chairpersons: Prof. E.O. Amonsou (DUT) & Prof. T.O. Uthman (NUN)**
	KEYNOTE ADDRESSES
09h30 – 10h00	**Exploring innovative approaches in target-based drug design** Prof. R. Karpoormath (UKZN)
10h00 – 10h30	**Genome-guided discovery to deliver biotechnological solutions** Prof. M. Trindade (UWC)
10h30 – 11h00	**Tea break/Poster presentation**
	PRESENTATIONS
11h00 – 11h15	***Aspergillus fumigatus* secretes a protease(s) that displays *in silico* binding affinity towards the SARS-CoV-2 spike protein and mediates SARS-CoV-2 pseudovirion entry into HEK 293T cells** N. Mjokane, S. Sabiu, O. M. N. Gcilitshana, J. Albertyn, C. H. Pohl, & O. M. Sebolai (UFS)
11h15 – 11h30	**Computational bioprospection of selected plant secondary metabolites against VP7 (capsid protein) of rotavirus A** A. A Lanrewaju, A. M. Enitan-Folami, S. Sabiu, and F. M. Swalaha (DUT)
11h30 – 11h45	**An *in silico* genome mining approach to discover potential antimicrobial peptides from bacteria** N. Kumar, P. Bhagwat, S. Singh, & P. S. Pillai (DUT)
11h45 – 12h00	**Structural-based investigation of novel pyrazole-thiazole hybrids as dual CDK-1 and CDK-2 inhibitors for cancer chemotherapy** V. A. Obakachi, I. Kehinde, N. D. Kushwaha, O. I. Akinpelu, B. Kushwaha, S. R. Merugu, F. Kayamba, H.M. Kumalo, & R. Karpoormath (UKZN)
12h00 – 12h15	**Therapeutic path to triple knockout: Investigating the pan-inhibitory mechanisms Of AKT, CDK9, and TNKS2 by a novel 2-phenylquinazolinone derivative in cancer therapy- An *in-Silico* investigation** X.Q. Peters, G. Elamin, A. Aljoundi, M.I. Alahmdi, E.N. Abo-Dya, P.A. Sidhom, A.M. Tawfeek, M.A.A. Ibrahim, O. Soremekun, & M.E.S. Soliman (UKZN)
12h15 – 12h30	**Longitudinal investigation of the faecal RNA viral structural dynamics of commercially bred asymptomatic chickens from Durban, KwaZulu-Natal province, South Africa** V.C. Nwokorogu, S. Pillai, J.E. San, C. Pillay, M.M. Nyaga, S. Sabiu (DUT)
12h30 – 12h45	**Voting Session: People's Choice for Best Presenter**
12h45 – 13h45	**Lunch break**

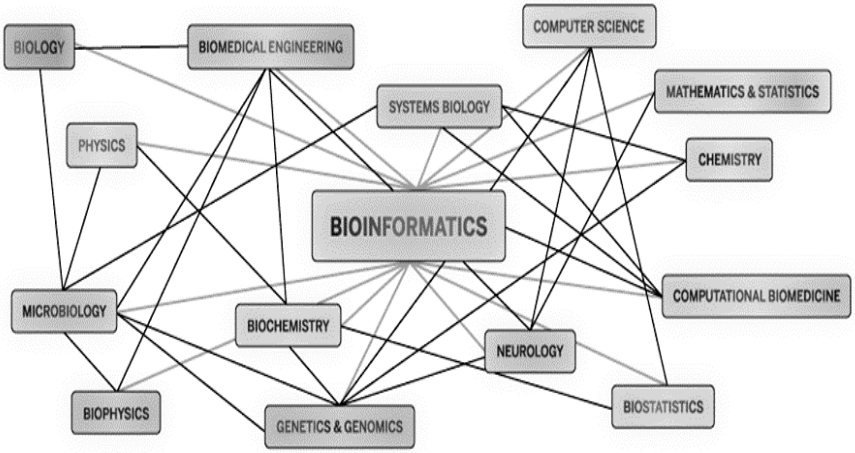
SESSION 2 Chairpersons: Prof. V. Mohanlall (DUT) & Prof. R. Karpoormath (UKZN)	
	KEYNOTE ADDRESS
13h45 – 14h15	**Computational design in drug discovery** Prof. S. Singh (Matchpoint, USA)
	PRESENTATIONS
14h15 – 14h30	**Integrating artificial intelligence with molecular docking in profiling new active pharmaceutical ingredients** Karishma Singh (MUT)
14h30 – 14h45	**Unveiling the mechanism of action of corn silk in type 2 diabetes intervention through integrated network pharmacology and down regulation of *ADORA1* and *GABBR1*** A. Akoonjee, T. Ghazi, A. Chuturgoon, & S. Sabiu (DUT)
14h45 – 15h00	**Synthesis and antidiabetic potential of quinoline–pyrazolopyrimidine hybrids and quinoline-4-arylamines** S. Mishra, Nosipho, P. Singh, & Md. S. Islam (UKZN)
15h00 – 15h15	**Exploring *Helianthus annuus* L. (sunflower) seeds as potential antidiabetics through network pharmacology, molecular dynamic simulations and *in vitro* validation in HepG2 cells** A. Rampadarath, S. Sabiu, T. Ghazi, & A. Chuturgoon (DUT)
15h15 – 15h30	**Structure-function analysis of the essential *Mycobacterium tuberculosis* P450 drug target, CYP121A1** T. Padayachee, D. Lamb, D. R. Nelson, & K. Syed (UNIZULU)
15h30 – 15h45	***Synadenium Cupulare* regulates cellular protein synthesis in triple negative breast cancer *in vitro*** J. C. Nwabuife, O. Gcaba, R. Lefojane, V. Fasiku, A. Adegoke, & M. P. Sekhoacha (UFS)
15h45 – 16h00	**Deciphering the neuro-modulatory effect of *Cannabis sativa* using network pharmacology and molecular dynamics simulation apparoaches** H.Y. Lukman, C. Peter, N.W. S'thebe, U.A. Sanni, & S. Sabiu (DUT)
16h00 – 16h20	**Tea break/Poster presentation**
16h20 – 16h30	**Voting Session: People's Choice for Best Presenter**
16h30	**Closing** Prof S. Sabiu
16h30 – 18h00	**Free time to explore Durban**
18h00 – 18h30	**Presentation of Awards and Prizes** Coastlands Hotel, 315-319 Peter Mokaba Ridge, Musgrave, Durban (Prof. S. Singh, Prof. T. Kudanga and Prof. F. M. Swalaha)
18h30 – 22h00	**Dinner**

Poster Presentations

P1	**Novel thiomorpholine tethered isatin hydrazones as potential inhibitors of resistant *Mycobacterium tuberculosis*** B. B. Shaik, S. Karunanidhi, B. Chandrasekaran, R. Karpoormath, H. M. Patel, F. Kayamba, S. R. Merugu, V. Kumar, S. Dhawan, B. Kushwaha, & M. C. Mahlalela (UKZN)
P2	**Metagenome of dairy wastewater reveals potential steroid degraders** P. Parab, M. A. Malla, P. Bhagwat, S. Kumari, & P. S. Pillai (DUT)
P3	**An unprecedented number of cytochrome P450s are involved in secondary metabolism in *Salinispora* species** N. A. Malinga, N. Nzuza, T. Padayachee, P. R. Syed, R. Karpoormath, D. Gront, D. R. Nelson, K. Syed (UNIZULU)
P4	**Detection, prevalence and molecular characterization of Rotavirus G and F from South African chickens** V. C. Nwokorogu, S. Pillai, J. E. San, C. Pillay, M. M. Nyaga, S. Sabiu (DUT)
P5	**Novel binary glutamine-based deep eutectic solvents: physicochemical and thermal characterization** G. Abel, A. Amobonye, B. Prashant, K. Permaul, S. Pillai (DUT)
P6	**Ultrasonic energy promoted synthesis of bisthioglycolic acid derivatives in deep eutectic solvents-A greener approach** G. Kumar, R. Kumar, & P. Singh, (UKZN)
P7	**Synthesis, antibacterial screening, and computational studies of quinazoline-4 (3H)-one-triazole conjugates** A. N. Manhas & Parvesh Singh (UKZN)
P8	**Screening traditional African fermented milk beverages for probiotic potential** B. Pillay, P. Bhagwat, & P. S. Pillai (DUT)
P9	**Design and synthesis of quinoline-pyrimidine inspired hybrids as potential plasmodial inhibitors** S. B. Mohite, F. Kayamba, S. B. Baba, & R. Karpoormath (UKZN)

COMPUTATIONAL &
SYSTEMS BIOLOGY
RESEARCH GROUP

KEYNOTE SPEAKER PROFILES



Prof. Krishna Bisetty, *FRSC*
Department of Chemistry, Durban University of Technology, South Africa
bisettyk@dut.ac.za

Prof Krishna Bisetty has been in the field of higher education for over 30 years, and he is an NRF C1-Rated Scientist. He currently leads the "Computational Modelling and Bioanalytical Chemistry" research focus group in the Department of Chemistry at the Durban University of Technology (DUT). He was admitted as a Fellow of the Royal Society of Chemistry (FRSC) in 2022. His research work focuses on the design of novel smart functional nanomaterials for next-generation electroanalytical sensors supplemented with computational modelling. His work has impact on the attainment of the UN SDG 3 on health and well-being for all and the UN SDG 7 on the accessibility and sustainability of energy. He was instrumental in setting up the research labs focusing on computational modelling and electrochemistry at DUT. He has supervised and trained 8 postdoctoral fellows, 13 doctoral students and 18 masters students at DUT. In addition to training and mentoring young black academics in chemistry, he co-authored over 140 published papers in peer-reviewed journals, with over 3000 citations and an H-index of 29 (Scopus). The impact of his research is also attributed to the 10 international and 5 national collaborative linkages sustained over the years. In addition, he delivered several keynotes and invited talks, both locally and internationally. He is a reviewer for 25 journals and a Guest Editor for Nanomaterials.

Prof. Lukman O. Olasunkanmi
Department of Chemistry, Obafemi Awolowo University (OAU), Ile-Ife, Nigeria
loolasunkanmi@oauife.edu.ng; lolasunkanmi@uj.ac.za

Lukman O. Olasunkanmi is an Associate Professor of Physical Chemistry in the Department of Chemistry, Obafemi Awolowo University (OAU), Ile-Ife, Nigeria. He obtained his PhD (Chemistry) from the North-West University (NWU), South Africa in 2016, MSc. (Chemistry) and BSc. (Hons) (Chemistry) with a First Class in 2012 and 2007, respectively from Obafemi Awolowo University, Ile-Ife, Nigeria. He had utilized Postdoctoral Fellowships at North-West University and University of Johannesburg. His research interests cover kinetics and thermodynamics of metals/alloys corrosion, corrosion inhibition, as well as quantum chemical calculations of molecular and electronic structures. He has made significant contributions to research in corrosion science and inhibition, as well as theoretical investigation of molecular and electronic properties of organic molecules and metal complexes, leading to the design of materials with fascinating physical and chemical/ biochemical properties. He has used computational quantum chemical calculations to derive structure-activity relationships for important chemical and biochemical systems. His works have also featured in-silico calculations for ligand-protein interactions. He has authored/co-authored over a hundred publications in reputable peer-reviewed journals and presented his research works at various conferences. He is a reviewer to many scientific journals. He is a sectional editor of "Computational Chemistry", a section of the journal, Computation (a MDPI Journal). He has supervised/co-supervised several postgraduate students (M.Sc. and PhD). He has won several academic excellence awards, including the Global Excellence and Stature Postdoctoral Fellowship Award of the University of Johannesburg (2020 – 2021), Dapo Afolabi Most Productive Science Scholar Award of the Faculty of Science, OAU, Nigeria (2017), and Kayode Adebowale National Young Scientist Prize in Chemical Sciences (awarded by the Nigerian Young Academy) (2017). He is a Fellow of the Africa Science Leadership Programme (ASLP), a Fellow of the Nigerian Young Academy (NYA), a member of Chemical Society of Nigeria and an affiliate member of African Academy of Science (AAS). Professor Olasunkanmi currently holds a Senior Research Associateship position at the Department of Chemical Sciences, Faculty of Science, University of Johannesburg (UJ). He has served as a speaker/facilitator/resource person at numerous career enriching workshops and seminars. He has also delivered keynote address and plenary at conferences and workshops. He is currently the Vice-Dean, Division of Student Affairs, Obafemi Awolowo University, Ile-Ife,

Prof. Khajaamohiddin Syed
Department of Biochemistry and Microbiology, University of Zululand, South Africa
syedk@unizulu.ac.za

Professor Khajaamohiddin Syed completed his Master's degree in Biochemistry in 2000, earning a gold medal. He obtained his Ph.D. from Sri Krishnadevaraya University in Andhra Pradesh, India in 2006. Following this, he served as a postdoctoral research associate at the University of the Free State in Bloemfontein, South Africa from 2006 to 2009. He then held the position of visiting scholar at the University of Cincinnati in Ohio, USA from 2009 to 2013. Subsequently, he served as a Lecturer and then as an Associate Professor at the Central University of Technology in South Africa from 2013 to 2017. From 2018 to 2021, he held the position of Associate Professor and became a full Professor at the University of Zululand in South Africa in 2022. He is currently a C1-rated researcher with the National Research Foundation (NRF) in South Africa. Professor Syed's research group focuses on cytochrome P450 monooxygenases (CYPs/P450s), enzymes that are well-known for their role in drug metabolism and toxicity. They specifically study the annotation, structure-function analysis, evolution, and applications of these enzymes using bioinformatics (in silico) methods. The group also conducts research on ferredoxins, which are proteins involved in electron transfer to P450s. Collaborating with renowned researchers worldwide, including Prof. David R. Nelson from the University of Tennessee, USA, who is an expert in P450 phylogenetics, Professor Syed's group has become a leading research group in the annotation and evolutionary analysis of P450s in microorganisms. Through collaborative efforts with national and international researchers, Professor Syed's research group has achieved significant milestones. They have made groundbreaking discoveries, including the identification of a novel P450 fusion protein and the development of P450 family-specific signature sequence patterns. They have also proposed a subtype classification for ferredoxins and identified new classes of glutathione transferases. Moreover, their research has led to the understanding that Archaeal P450s originate from bacteria and that the original Archaea does not possess P450s. They have put forth a widely accepted hypothesis that P450s play a crucial role in organism adaptation, influencing the P450 content in their genome. Additionally, they have developed mathematical formulas for comparing key features of P450s in different organisms.

Professor Syed's research has been recognized and published in esteemed scientific journals such as Science, PLOS Genetics, PNAS USA, and Current Biology, among others. As of May 10, 2024, his Google Scholar index includes 5476 citations, with an h-index of 24 and an i10-index of 41. This recognition has resulted in numerous invitations to speak at national and international conferences and to train local and international researchers. He has also been honoured with a visiting professorship at the University of Warsaw in Poland.

Prof. Martin M. Nyaga
Next Generation Sequencing Unit, University of Free State, South Africa
nyagamm@ufs.ac.za

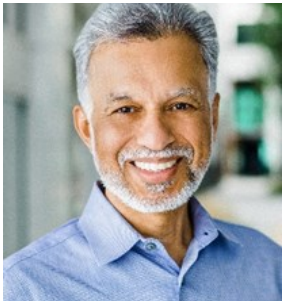
Martin Nyaga is an Associate Professor and the Head of the University of the Free State-Next Generation Sequencing (UFS-NGS) Unit and the unit's Initiatives Principal Investigator (PI). The UFS-NGS Unit is the WHO collaborating Center for Vaccine-Preventable Diseases (VPD) Surveillance and Pathogen Genomics, which Prof. Nyaga serves as the Director. His academic affiliation is the Division of Medical Virology within the Faculty of Health Sciences. Prof Nyaga's research interests utilise genomics surveillance on VPD, particularly pre- and post-vaccination of enteric viruses surveillance at whole genome level for the WHO African Rotavirus Surveillance Network (ARSN) and the Africa CDC Pathogen Genomics Initiative (PGI) VPD focus group, with the aim of providing technical guidance and support to develop a continental VPD road map and implementation strategy for enhancing priority genomics surveillance in Africa. He is currently the PI in two Bill and Melinda Gates Foundation funded studies investigating the long-term effects of the introduction of the monovalent Rotarix vaccine and the Sequencing of the Antigenic Cartography of Enteric Viruses (SACEV) in five African countries (Cameroon, Ghana, Malawi, Kenya, and South Africa) through the African Enteric Viruses Genome Initiative (AEVGI). One of the key goals of the AEVGI is to leverage a genomics and bioinformatics approach to complement the routine work done by the ARSN. He is the team lead for studies on metagenomics of gut and respiratory virome in the UFS-NGS Unit. These studies aim to establish the role played by the gut and respiratory virome in young children over time to effect normal and metabolic disorders that may influence a child's healthy growth or impact medical conditions such as obesity later in life. Prof Nyaga is an NRF-rated researcher. His research initiatives are funded by both third-stream and national funding streams. He has disseminated over 150 peer-reviewed articles in international journals and scientific conferences, deposited over 50,000 full-length and partial genome sequences at the NCBI GenBank and supervised over 30 postgraduate students. Some of his research profile can be accessed through the following link https://orcid.org/0000-0002-5017-5584

Prof Rajshekhar Karpoormath
University of KwaZulu-Natal (UKZN)
karpoormath@ukzn.ac.za

Prof Karpoormath has had an illustrious career in independent research since 2014, having established the Synthetic and Medicinal Chemistry Research Group (SMCRG) at UKZN. His unwavering commitment to securing institutional, national and international grants has led to establishing a well-equipped Drug Discovery Laboratory at UKZN. Through this, he has hosted numerous international postgraduates, academics, and researchers from Africa and Asia under various exchange programmes, making the laboratory a centre of excellence in drug discovery research. Further, he has successfully established research collaborations globally with researchers from institutes/Universities of high repute. His research has focused on target-based drug design and synthesis, methodology development, and nanomaterial-based electrochemical biosensors. His research group in less than 10 years (Since 2014) has published over 160 peer-reviewed articles in international journals, (https://scholar.google.co.za/
citationshl=en&user=Z3lDBMkAAAAJ&view_op=list_works&sortby=pubdate),
six book chapters, one book, and two patents, which is a testament to his dedication. He has supervised 44 postgraduate students (23 PhD's and 19 Masters) and 18 postdoctoral research scholars since 2014. His SMCRG team comprises eight Masters, 15 PhDs, and two postdoctoral research scholars. Prof Karpoormath has been recognized as one of the top researchers and appeared in UKZN's top 30 researchers list in 2017, 2021, and 2022. His national ranking of 27th for scholarly outputs in Applied Chemistry from 2018 to 2021, according to Scopus (https://www.scival.com/overview/authors?uri=Country/710), is a testament to his contributions to Medicinal Chemistry. His research, especially on Anti-TB drug discovery, has resulted in five leads currently in pre-clinical investigations. Professor Karpoormath has been invited speaker at several national and international conferences and workshops. He is a National Research Foundation (NRF), South Africa C2-rated scientist since 2021. and is currently a Health Science panel member of NRF-SA. He has also served as an expert reviewer on several national and international grants such as the Water Research Commission- South Africa, United Kingdom, Medical Research Council (UK-MRC), South African Health Products Regulatory Authority (SAHPRA), RMIT University Australia, National Research, Development, and Innovation Office (NKFIH), Government of Hungary etc.

Professor Marla Trindade
Institute for Microbial Biotechnology and Metagenomics, University of Western Cape
South Africa
ituffin@uwc.ac.za

Marla Trindade is the Director of the Institute for Microbial Biotechnology and Metagenomics and holds the DSI/NRF SARChI Research Chair in Microbial Genomics at the University of the Western Cape, South Africa. She has played a significant role in building capacity for genomics in South Africa, establishing next generation sequencing and single cell genomics service platforms at UWC. Her laboratory has a strong international reputation as a go-to facility for omics and genetic engineering training. She has established a microbial biodiscovery pipeline that develops and commercialises innovative products and services through the sustainable exploitation of indigenous biodiversity using genomics approaches. Her multidisciplinary and highly collaborative research has led to the identification and functional characterisation of novel bacterial and phage species, biosynthetic pathways, enzymes, and compounds for application in the human health, agriculture, environmental and industrial sectors. The products/services being developed address national and global socio-economic priorities listed in the UN SDGs.

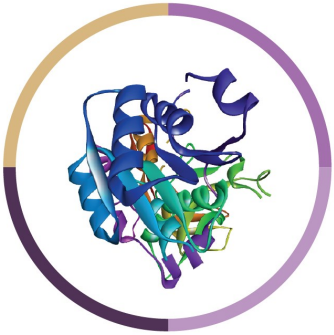


Prof. Suresh Singh

Senior Vice President, Computational Sciences of Matchpoint Therapeutics, USA

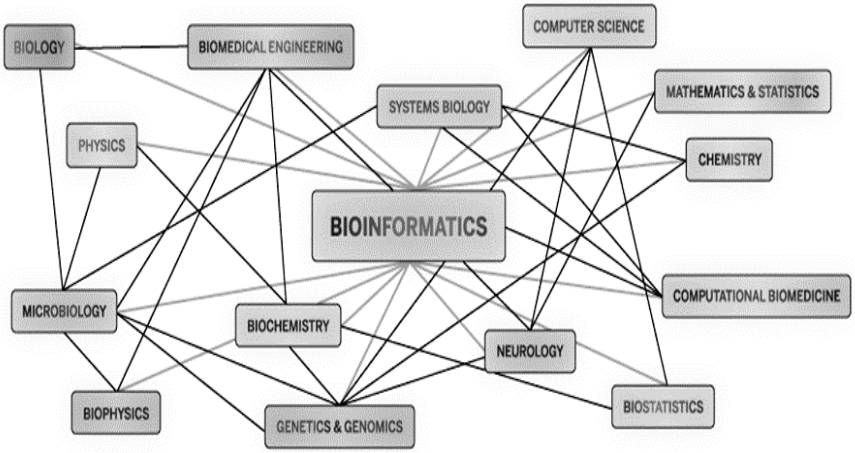
Suresh Singh, PhD, is Senior Vice President of Computational Sciences of Matchpoint Therapeutics where he oversees computational chemistry and structural biology across the portfolio as well as the development and implementation of machine learning solutions. Prior to Matchpoint, Suresh served as Vice President of Computational Sciences at HotSpot Therapeutics. In that role, he was instrumental in establishing the platform enabling the discovery and targeting of protein pockets that have regulatory function. He was previously at Vitae Pharmaceuticals, where he established the computational design group and was part of the team that progressed 8 compounds into the clinic for cardiovascular, inflammation, diabetes, and cancer indications. Earlier, at Merck, Suresh was part of the team that discovered JANUVIA® and MARIZEV®. He is an inventor on more than 50 issued U.S. patents and a co-author of more than 50 peer-reviewed publications. Suresh earned his PhD in Computational Chemistry at New York University and completed his post-doc fellowship at University of California at San Francisco. He also holds a master's in biochemistry from Boston University.

.



COMPUTATIONAL & SYSTEMS BIOLOGY
RESEARCH GROUP

ABSTRACTS



Synergy unleashed: Sensor innovation with experimental and computational chemistry

Krishna Bisetty
Professor and Lead, Computational Modelling and Bioanalytical Chemistry Research Group, Chemistry Department, Faculty of applied Sciences, Durban University of Technology South Africa.
Email: bisettyk@dut.ac.za

The integration of nanomaterials could lead to new miniaturized biosensors with high sensitivity and ultrafast response. This technology has already evolved to a highly advanced level, but a combined strategy could be highly beneficial and bring forth fresh perspectives in the era of artificial intelligence. Thus, the goal of this talk is to introduce new methodologies that can be used in an integrated fashion in the design of electrochemical nano bio/chemical sensors. In this context, the synergies between the experimental and computational approaches in addressing the design and mechanism of electrochemical sensors for applications in the food, health and environmental sectors will be demonstrated. Further, the role of machine learning in improving electrochemical analyses will be introduced. In summary, the integration of nanomaterials into biosensors holds great promise for advancing healthcare and environmental monitoring.

Keywords: Sensors, Nanomaterials, Computational and Machine Learning

The nexus between computational chemical biology and drug discovery

Lukman O. Olasunkanmi
Associate Professor, Department of Chemistry, Faculty of Science, Obafemi Awolowo University, Ile-Ife, Nigeria
Senior Research Associate, University of Johannesburg, South Africa
Email: loolasunkanmi@oauife.edu.ng; lolasunkanmi@uj.ac.za

Chemical biology as a research field entails the study of chemical techniques and reactions as well as the interactions of chemical species with biological systems. The development of new drugs to tackle diseases requires proper understanding of the concerned biological systems at molecular level and being able to synthesize compounds that can manipulate the biological processes. Understanding the metabolic processes that are associated with a disease is critical to designing a drug to tackle the disease. Unfortunately, there are often numerous biological mechanisms associated with a disease and very many potential drug candidates that could be explored. Interestingly, advancements in computer science and technology have greatly improved the intelligence of predictive models across all fields, including chemistry and biology. By leveraging on the achievements in computer science and technology, physical and life scientists are now able to predict favourable conditions for laboratory experiments, eliminate several least promising experimental factorials and concentrate on the few with auspicious outcome. Computational chemical biology offers the opportunity of using models and simulations to cut down timeline and costs that would hitherto be incurred on screening, designing, synthesizing, and testing new drugs. By reducing the number of experimental trials, computational studies in the field of chemical biology also reduce experimental bye-products and discharge to the environment, thereby supporting the advocacy for "green science" and sustainable environment. Numerous theoretical and computational approaches, such as molecular modelling, quantum chemical calculations, molecular docking, molecular dynamics and Monte Carlo simulations are combined in the popular computer-aided drug design/ discovery (CADD) methods. Translational research efforts have greatly improved our skills of finding the relationship between chemical structure and biological activity. From the QSAR approach to machine learning, large chemical libraries can now be screened efficiently within a very short period to identify promising drug candidates for a biological problem. In this presentation, the importance of computational studies in drug discovery will be x-rayed with reference to recent relevant research outputs.

Keywords: quantum chemistry, structure-property-relationship, cheminformatics, binding energy, drug-protein interactions.

A new horizon in antimalaria drug design: Peptide-based inhibitors targeting *Plasmodium falciparum* Grp94

Wendy Mthembu, Marina Rautenbach and Tawanda Zininga*
Department of Biochemistry, Stellenbosch University, Stellenbosch, 7600, South Africa
*correspondence: tzininga@sun.ac.za

Plasmodium falciparum parasites remain the main cause of malaria in sub-Saharan Africa. The parasite leads a complicated life cycle that involves the vector mosquito and the human host. For survival in different physiological environments, the parasite remodels the host for nutrient uptake and evades the immune system. Moreover, the parasite exports almost 10% of its proteome to the host cell. However, these extensive remodeling events require robust protein folding efficient endoplasmic reticulum (ER) processing before secretion. The main players in protein quality control in the ER are the glucose-regulated proteins of sizes 94 kDa (PfGrp94). Furthermore, PfGrp94 is an essential protein implicated in the ER-associated antimalarial drug resistance to the first line of small molecule treatment options available. In this study we sought to evaluate the peptide based antimalarials. Antimicrobial peptides have gained interest as therapeutic agents due to their specificity and selectivity. The 3D structures of PfGrp94 obtained from AlphaFold were modeled on Schrodinger Maestro Suite to determine their active sites on SiteMap. Using sitemap scores a receptor grid was generated to define the position for ligands to bind. The Glide program was used to dock all the ligands of TrcA in either PfGrp94 grid receptor to determine the non-covalent interactions and binding affinities. These interactions were confirmed using molecular dynamic simulations. The predicted interaction of Tyrocidine A (TrcA) with PfGrp94 on the substrate binding domains suggests that TrcA is a promising inhibitor of ER protein chaperones and can serve as a promising antimalarial drug.

Keywords: Antimalarial drug resistance; PfGrp94; ER-protein folding; Peptide inhibitors

Design and synthesis of quinoline-pyrimidine inspired hybrids as potential plasmodial inhibitors

Sachin Balaso Mohite, Francis Kayamba, Shaik Baji Baba, Karpoormath Rajshekhar*

Department of Pharmaceutical Chemistry, College of Health Sciences, University of KwaZulu-Natal, Durban, 4000, South Africa.
*Correspondence: sachins1252@gmail.com

Artemisinin-based combination therapy is the first-line therapy of *Plasmodium falciparum* malaria. Proteases that are expressed during the erythocytic stage of *Plasmodium falciparum* are newly explored drug targets for the treatment of malaria. Research on antimalarial pharmacophores revealed that, in addition to other vast medicinal properties, the pyrimidine moiety displayed admirable antimalarial properties. Objective: Design and synthesis of novel quinoline-pyrimidine hybrids and evaluation of their inhibitory activity against the NF54 chloroquine-susceptible strain as a promising class of antimalarial compounds. Method: The promising antiplasmodial activity of the synthesized analogues were designed using molecular hybridization approach, synthesized by new chemical routes and performed in vitro antiplasmodial activity. Conclusion: The anti-plasmodial screening revealed that most analogues showed promising to potent activity with half-maximal inhibitory concentration IC50:0.32µM-4.30µM. Compound with 1,4-diamine butyl linker and 4-hydroxyl phenyl on fourth and sixth position of pyrimidine found the most prominent activity with an IC50 of 0.32±0.06 µM, with a favourable safety profile of 9.79 to human kidney epithelial (HEK293) cells.

Evaluating the active compounds of *Momordica charantia* seed crude extracts for antimalaria drug design using *in silico* molinspiration and molecular docking screening

Eric O. Akintemi[1], Oluwasegun P. Akoniyon[2] and Hadley S. Clayton[1]
[1]Department of Chemistry, University of South Africa, Florida Science Campus Johannesburg, 1709, South Africa.
[2]Department of Genetics, School of Life Sciences, University of KwaZulu-Natal, Westville Campus, Durban 4041, South Africa.
*Correspondence: fisayo.eric@gmail.com

Antimalarial drugs have been one of the most effective strategies in malaria control throughout history. However, the evolution and spread of parasite strains resistant to several antimalarial drugs constitute a major obstacle to malaria treatment. Here in, 26 bioactive compounds from the crude extracts of *Momordica charantia* seed have been identified and evaluated through virtual screening for antimalaria drug design using certain tools of in silico studies. CD36 protein structure, which is a scavenger receptor and the most common target of the PfEMP1 proteins of the malaria parasite was considered as the receptor for inhibition. Four of FDA approved antimalaria drugs, amodiaquine (amo), artemether (art), artesunate (ats) and lumefantrine (lum) were used as standard drugs and their antimalaria activities compared with those of the 26 bioactive compounds, as shown in the binding scores (ΔG) against the receptor. Compound 25, being Curcumin, with ΔG = -5.5 kcal/mol showed the highest inhibition among the bioactive compounds. It has higher inhibition potential than three standard drugs namely amo, art and lum with same ΔG of -5.3 kcal/mol, but lower inhibition potential than standard drug ats with ΔG of -6.0 kcal/mol. Compound 25 and four other bioactive compounds 15, 26, 21 and 22 with relatively high ΔG values -4.9, -4.8, -4.7 and -4.7 kcal/mol, respectively; are the top 5 compounds among the 25 active compounds of Momordica charantia seed with potential antimalaria activities.

Keywords: *Momordica charantia*, *Plasmodium falciparum*, antimalarial activity, curcumin, in silico.

A new class of linezolid-based molecules as potential antimicrobial and antitubercular agents: A rational approach.

Siddaram Nadigar, Babita Kushwaha, and Rajshekhar Karpoormath.
*Correspondence: msnadigh198@gmail.com

A total of 19 linezolid-based novel molecules were synthesized by utilizing a simple and convenient synthetic method. Structures of all the novel derivatives were established by ^{1}H, ^{13}C NMR, FT-IR and mass spectroscopic methods. In addition, structural elucidation of some representative compounds by 19F, 2DNMR and single crystal X-ray experiment's (6d and 8b) further confirmed the structures of the desired compounds. All the final compounds were evaluated for their in vitro antitubercular (*Mycobacterium tuberculosis* H37RV strain), antibacterial (*S. aureus, B. subtilis*, *E. coli* and *P. aeruginosa*) and antifungal (*C. neoformans*, *C. albicans* and *A. niger*) activities. The docking study of most active compounds were also performed towards 50S ribosomal unit of *Haloarcula marismortui*. The Lipinski's rule of five and significant ADME pharmacokinetic parameters were also analysed indicating potential to develop good oral antimicrobial and antitubercular drug candidates.

Molecular characterization of tomatoes spoilage bacteria and bioprospection of essential oils against their key druggable targets

Rukayat Abiola Abdulsalam, Oluwatosin Ademola Ijabadeniyi, and Saheed Sabiu*
Department of Biotechnology and Food Science, Faculty of Applied Sciences, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa
*correspondence: sabius@dut.ac.za

The need for an alternative biological measure to control microbial spoilage in tomatoes as against the currently used synthetic chemicals is imperative to reduce postharvest losses. This study involved the molecular characterization of spoilage bacteria isolated from Jam and Round tomato cultivars and evaluates the antibacterial properties of two indigenous essential oils from South Africa: buchu oil (BO) and sweet orange oil (SOO). BO exhibited the most potent antibacterial effect, with MIC/MBC ranges of 1.59-3.18 mg/ml and 6.35-12.71 mg/ml, respectively. Gas chromatography-mass spectrometry (GC-MS) identified key constituents of BO, which were further analyzed using computational techniques targeting bacterial topoisomerase 2A subunits. Following a 200-nanosecond, molecular dynamics (MD) simulation indicates that myrtenyl acetate (-21.44 ± 3.73 kcal/mol), pseudodiosphenol (−30.95 ± 2.81 kcal/mol), trans-carvyl acetate (-11.83 ± 6.65 kcal/mol), and methyl eugenol (-29.99 ± 2.59 kcal/mol) had the best affinity and structural compactness towards GyrA, GyrB, ParC and ParE, respectively, suggesting their potential as modulators of topoisomerase 2A with root mean square deviation values of 0.93 Å, 1.74 Å, 2.23 Å, and 3.43 Å, respectively. These findings provide scientific insight into the inhibitory mechanism of BO key constituents against spoilage bacteria in tomatoes and suggest potential applications in developing a potent, natural, and biodegradable edible coating for tomato preservation. Thus, it indicates promising prospects for biodegradable preservatives in agricultural practices.

Keywords: Buchu oil, Sweet orange oil, Molecular Dynamic simulation, Antibacterial activity, Microbial spoilage

Molecular epidemiology of antibiotic-resistant *Escherichia coli* from companion animals attending veterinary practices in Durban, KwaZulu-Natal, South Africa

N.L. Ntuli[1], A.L.K. Abia[1,2], J. Mbanga[1,3], S.Y. Essack[1]*

[1]Antimicrobial Research Unit, College of Health Sciences, University of KwaZulu-Natal Durban, South Africa.

[2] Environmental Research Foundation, Westville, 2630, South Africa.

[3]Department of Applied Biology and Biochemistry, National University of Science and Technology, P.O Box AC 939 Ascot, Bulawayo, 00263, Zimbabwe.

*Correspondence: essacks@ukzn.ac.za

Companion animals are globally documented to harbour antibiotic-resistant *E. coli*. This study investigated the prevalence and phylotyping of antibiotic-resistant *E. coli* from companion animals presenting at veterinary practices in Durban. Rectal-swab samples were collected from dogs (44) and cats (21) from the selected veterinary practices. *E. coli* was isolated and confirmed using real-time polymerase chain reaction (PCR) of the *uidA* gene and 330 *E. coli* (234 dog and 96 cat) were obtained. Susceptibility testing against 20 antibiotics revealed that dog isolates were most resistant to tetracycline (25.2%) and least to amikacin (0.4%) and piperacillin-tazobactam (0.4%). In cats, the highest resistance was against tetracycline (22.4%) and the lowest against piperacillin-tazobactam (1.0%) and ceftazidime (1.0%). Moreover, twenty-two different phenotypic patterns were displayed by 10.6% of multidrug-resistant *E. coli*. The presence of selected antibiotic-resistance genes (ARGs), conferring third-generation cephalosporins (bla_{TEM}, bla_{SHV}, and bla_{CTX-M}), tetracycline (*tet*A, and *tet*B), and tigecycline (*tet*X/X2, *tet*X3, and *tet*X4) resistance, were detected using conventional PCR and amplicon sequencing. The $bla_{CTX-M-15}$ (8%) and *tet*A (24%) were the most prevalent resistance genes and no $bla_{SHV,}$ *tet*X/X2, *tet*X3, and *tet*X4 genes were detected. Clonality evaluated using Enterobacterial Repetitive Intergenic Consensus PCR revealed, forty-eight clusters using a 75% similarity cut-off, suggesting a high diversity of *E. coli* in Durban. No evidence of antibiotic-resistant *E. coli* transmission in Durban was observed. Resistance of *E. coli* from companion animals to medically important antimicrobials for humans is of particular concern, requiring measures to control the spread of antibiotic-resistant bacteria and ARGs between companion animals and humans.

Keywords: antibiotic-resistance; antibiotic-resistance genes; *E. coli*; companion animals; veterinary practice; South Africa

Unravelling six decades of the mystery of the evolution of living protein fossil iron -sulfur cluster proteins

Khajamohiddin Syed
Professor, Department of Biochemistry and Microbiology, Faculty of Sciences and Agriculture, University of Zululand, KwaDlangezwa, KwaZulu-Natal, South Africa
Email: syedk@unizulu.ac.za

Ferredoxins, iron-sulfur (Fe-S) cluster proteins, play a crucial role in oxidoreduction reactions. Previous evolutionary analyses of these proteins have mainly focused on the abundance of different Fe-S cluster types (2Fe-2S, 3Fe-4S, 4Fe-4S, 7Fe-8S, and 2 [4Fe-4S]), without considering the diversity of ferredoxins within these clusters. To address this gap, we propose a classification and naming system for ferredoxins based on the spacing between the cysteine amino acids of the Fe-S binding motif as a signature of the subtype. To test this idea, we conducted a comparative analysis of ferredoxins in various bacterial groups, including *Alphaproteobacteria*, *Bacteroidetes*, and *Firmicutes*, as well as ferredoxins from species across different domains of life. Our analysis revealed a high diversity of ferredoxin subtypes, with many alphaproteobacterial species sharing subtypes with *Bacteroidetes* and *Firmicutes* species. Additionally, we observed common ferredoxin subtypes across species of Bacteria, Archaea, and Eukarya, suggesting a shared ancestral origin of ferredoxins between Archaea and Bacteria and lateral gene transfer of ferredoxins from prokaryotes (Archaea/Bacteria) to eukaryotes. This study has opened up new avenues for further exploration of ferredoxin diversity in living organisms.

Keywords: Archaea; Bacteria; Eukarya; evolution; ferredoxins; lateral gene transfer

Deciphering the epidemiology, dynamics, and detection of enteric and respiratory viral pathogens using Next-generation sequencing: Prospects and advances.

Martin Nyaga

Associate Professor, Next Generation Sequencing Unit, Office of the Dean and Division of Virology, Faculty of Health Sciences, University of Free State, South Africa; and Director, WHO Collaborating Centre for Vaccine Preventable Diseases (VPD) Surveillance and Pathogen Genomics, Bloemfontein, South Africa

*Email: nyagamm@ufs.ac.za

Historically, epidemiological monitoring of infectious diseases relied on case counts from clinical diagnosis and sought to turn data about the infected populations into inferences about where and how the infectious disease spread. Advances in diagnostic tools have led to a more refined understanding of the dynamics of many infectious diseases. Respiratory and enteric diseases are notable cases of interest. Respiratory and enteric system diseases are responsible for a significant morbidity and mortality in all population annually. The most comprehensive analyses fail to identify and etiologic agent in 35% of respiratory tract infections and in 30% of enteric infections. In addition, the emergence of new infectious agents, many of which manifest the clinical symptoms characteristic of these diseases, necessitates the critical need to define the complete spectrum and phylogeny of viruses capable of causing these diseases. More so, over the years, concerns regarding the threat of human viral infectious diseases of animal origin have grown. Many of these diseases are of pandemic potential and are efficiently transmitted between humans via faecal to oral route and aerosol/respiratory droplets. Currently, next-generation sequencing of viral pathogen genomes, together with date, location, clinical manifestation, and other relevant data on sample origins, can contribute to describing nearly every aspect of detection, transmission dynamics, including local transmission and global spread. The analyses of these data have implications for all levels of research, clinical and public health practice, from institutional infection control to policies for surveillance, prevention, and treatment. While these genome sequences are being used to augment diagnostic, epidemiological inquiry and generate inferences about the spread and evolution of pathogens, regional dearth of information persists. This talk aims to detail on years of genomics study performed at the UFS-NGS Unit in exploring the diagnosis, epidemiology, and phylogeny of clinically significant enteric and respiratory viral pathogens in South Africa.

Assessment of antibiotic resistance and efflux pump gene expression in *Neisseria gonorrhoeae* isolates from South Africa by quantitative real-time PCR and regression analysis

Nireshni Mitchev[1], Ravesh Singh[1,2], Veron Ramsuran[1], Arshad Ismail[3,4], Mushal Allam[3,5], Stanford Kwenda[3], Florah Mnyameni[3], Nigel Garrett[6,7], Khine Swe Swe-Han[1,2], Abraham J Niehaus[1] and Koleka P Mlisana[1,6,8]

[1]School of Laboratory Medicine and Medical Sciences, University of KwaZulu Natal (UKZN), Durban, South Africa; [2]National Health Laboratory Service, Durban, South Africa; [3]Sequencing Core Facility, National Institute for Communicable Diseases, National Health Laboratory Service, Johannesburg, South Africa; [4]Department of Biochemistry and Microbiology, Faculty of Science, Engineering and Agriculture, University of Venda, Thohoyandou, South Africa; [5]Department of Genetics and Genomics, United Arab Emirates University, Al Ain, United Arab Emirates; [6]Centre for the AIDS Programme of Research in South Africa, Durban, South Africa; [7]School of Nursing and Public Health, UKZN, Durban, South Africa; [8]National Health Laboratory Service, Johannesburg, South Africa

Treatment of gonorrhoea infection is limited by the increasing prevalence of multi-drug-resistant strains. Cost-effective molecular diagnostic tests can guide effective antimicrobial stewardship. This study correlated mRNA expression levels in *Neisseria gonorrhoeae* antibiotic target genes and efflux pump genes to antibiotic resistance in the study population. The expression profile of antibiotic resistance-associated genes (*penA*, *ponA*, *pilQ*, *mtrR*, *mtrA*, *mtrF*, *gyrA*, *parC*, *parE*, *rpsJ*, *16S rRNA*, *23S rRNA*) and efflux pump genes (*macAB*, *norM* and *mtrCDE*), was investigated by qPCR, in clinical isolates from KwaZulu-Natal, South Africa. Whole-genome sequencing was used to determine the presence or absence of mutations. *N. gonorrhoeae* isolates, from patients presenting for care at clinics, were analysed. As determined by binomial regression and ROC analysis, the most significant (p=<0.05) markers for resistance prediction in this population, and their cutoff values, were determined to be *mtrC* (p=0.024; cutoff <0.089), *gyrA* (p=0.027; cutoff <0.0518), *parE* (p=0.036; cutoff <0.0033), *rpsJ* (p=0.047; cutoff <0.0012) and 23S rRNA (p=0.042; cutoff >7.754). Antimicrobial stewardship includes exploring options to conserve currently available drugs for gonorrhoea treatment. There is the potential to predict an isolate as either susceptible or non-susceptible based on the mRNA expression level of specific candidate markers, to inform patient management. This qPCR approach, with few targets, can be further investigated for use as a potentially cost-effective diagnostic tool to detect resistance.

Charting the cannabis plant chemical space with computational metabolomics

Akhona Myoli[1], Mpho Choene[1], Abidemi Paul Kappo[1], Edwin N. Madala[2], Justin J.J. van der Hooft[1,3], Fidele Tugizimana[1,4]

[1] Department of Biochemistry, University of Johannesburg, Auckland Park, Johannesburg, South Africa

[2]Department of Biochemistry and Microbiology, University of Venda, Thohoyandou South Africa

[3]Bioinformatics Group, Wageningen University, 6708 PB Wageningen, the Netherlands

[4]International Research and Development Division, Omnia Group, Ltd., Bryanston Johannesburg 2021, South Africa

The chemical classification of Cannabis is typically confined to the cannabinoid content, whilst Cannabis encompasses diverse chemical classes that vary in abundance among all its varieties. Neglecting other chemical classes within Cannabis strains results in a restricted and biased comprehension of elements that may contribute to chemical intricacy and the resultant medicinal qualities of the plant. Thus, reported herein is a computational metabolomics study to elucidate the Cannabis metabolic map beyond the cannabinoids. Mass spectrometry-based computational tools such as feature-based molecular networking, MS2LDA and MolNetEnhancer were used to mine and evaluate the methanolic leaf and flower extracts of two Cannabis cultivars (Amnesia haze, AMNH and Royal dutch cheese, RDC). Additionally, the anti-cancer properties of the studied cultivars were evaluated through bioassays and molecular docking studies. The results revealed the presence of different chemical compound classes including cannabinoids, but extending it to flavonoids, polyketides, and phospholipids at varying distributions across the cultivar plant tissues. Therefore, the two cultivars were differentiated based on the overall chemical content of their plant tissues where AMNH was observed to be more dominant in the flavonoid content while RDC was more dominant in the lipid-like molecules. Additionally, *in silico* molecular docking studies in combination with biological assays indicated the potentially differing anti-cancer properties of the two cultivars resulting from the elucidated chemical profiles. These findings highlight distinctive chemical profiles beyond cannabinoids in Cannabis strains. Mapping these profiles provides insights into plant biochemistry and justifies selecting certain varieties for medicinal use. Such comprehensive and precise deconvolution of the chemical space of the plant contributes to ongoing efforts in cannabis research and applications; also, towards the realization of UN SDG #3, good health, and well-being.

Keywords: Cannabis, Medicinal, LC-MS/MS, Computational tools, Metabolic map, Chemovars, GNPS

Computational and bioinformatics strategies in mining and interpreting metabolomics data: The case of biostimulants-maize interactions

Kgalaletso Othibeng[1], Fidele Tugizimana[1], Daniel Petras[2], Prof. Kyo Bin Kang[3]
[1]Department of Biochemistry, University of Johannesburg, Auckland Park, Johannesburg, South Africa
[2]University of Tubingen, Germany
[3]Sookmyung Women's University, South Korea

Metabolomics, a systems biology discipline representing analysis of metabolome, provides a functional readout of the cellular state and an indispensable approach to interrogate cellular biochemistry. The application of this 4IR-driven multidisciplinary *omics* science spans a wide range of research fields from basic biology to applied disciplines such as medicine, environment, and agriculture. Despite the maturity of metabolomics over the last two decades, metabolite annotation and identification remain one of the bottlenecks in untargeted metabolomics. Most of the information collected by untargeted metabolomics studies is "dark matter", chemical signals that are not characterized. Computational solutions have been proposed as the only way to overcome this challenge. Thus, reported herein are metabolomics studies exploring the use of emerging computational metabolome mining strategies to investigate the effects of biostimulants on crop plants. Biostimulants have emerged as sustainable strategies for improved crop productivity; however, the underlying biostimulant-induced changes at molecular and cellular levels for plant growth promotion and stress resilience remain enigmatic. Computational metabolomics, reported herein, allowed the characterization of metabolic landscape of maize plants treated with biostimulants, under normal and stress conditions. Molecular networking strategies aided in the putative annotation of the maize metabolome, which comprised different classes of metabolites including amino acids, hormones, HCA, and flavonoid derivatives. Metabolic pathway analysis revealed key impacted biological pathways which were found to be involved in growth promotion, priming and stress tolerance. Thus, the results revealed that (both microbial and non-microbial) biostimulants induced a remodelling of metabolic networks in maize (involving both primary and secondary metabolism), subsequently readjusting the plant physiology towards growth promotion and stress alleviation. Such fundamental knowledge is necessary for development of the biostimulant industry, for sustainable food security.

Metabolite profiling and bacterial diversity of traditionally produced Amasi- a South African fermented product

Ajibade Betty Olusola[1], Ajayeoba Titilayo Adenike[1], Sabiu Saheed[1], Konstantin V. Moiseenko[2], Tatyana V. Fedorova[2,] and Ijabadeniyi Oluwatosin Ademola[1]

[1]Biotechnology and Food Technology, Faculty of Applied Sciences, Durban University of Technology, Durban 4001, KwaZulu-Natal Province, South Africa

[2]A.N. Bach Institute of Biochemistry, Research Center of Biotechnology, Russian Academy of Sciences, 119071 Moscow, Russia

Correspondence: bettyajibade@gmail.com

Amasi, a traditional fermented milk produced in Southern Africa, is associated with several health benefits, such as probiotic activities, immune system modulation, antimicrobial, antitumor and antioxidant activity. This study investigated the microbial diversity in amasi (produced from cow and goat milk) through targeted metagenomic bacterial 16S rRNA sequencing and profiled their amino acids constituents using liquid chromatographic-mass spectrophotometry (LC-MS). The results obtained revealed Firmicutes, Bacteroidetes and Proteobacteria as the prevalent bacterial phyla, with *Lactococcus* and *Lactobacillus* being the most prevalent genus. Comparatively, CMA showed more microbial diversity than GMA, though there were relative similarities in their microbiome composition. Functional prediction of drug and disease metabolism pathways revealed significant metabolites in the two amasi samples, with amino acids validation revealing glutamine and asparagine as the most significant ($p< 0.05$) for cow milk Amasi (CMA) and goat milk Amasi (GMA), respectively. Overall, data from this study showed heterogeneity in diversity, abundance distributions, metabolites, and nutritional balance between raw cow/goat milk Amasi samples.

Keywords: Amasi, Probiotics, Microbial diversity, Illumina Miseq, 16S rRNA, Metagenomics.

Cheminformatics identification of *LasR* modulators of *Pseudomonas aeruginosa* from selected South African essential oils

Dweba Yamkela*, Christiana E. Aruwa, and Saheed Sabiu

Department of Biotechnology and Food Science, Faculty of Applied Sciences,

Durban University of Technology, Durban 4001, South Africa

*Pseudomonas aeruginos*a is the common cause of life-threatening nosocomial infections that have become increasingly difficult to treat due to biofilm formation. Biofilm formation in *P. aeruginosa* is majorly associated with the LasR-LasI quorum sensing regulation system. As such, there is an urgent need for the discovery and development of LasR modulators. In this study, the anti-LasR activity of bioactives from essential oils (buchu, wormwood, rose geranium, verbena, and lemongrass) were evaluated using computational techniques. The thermodynamic refinements and stability, feasible synthetic score, and pharmacokinetics properties of the top five essential oil components with the highest negative docking scores against LasR were determined over a 200 ns MD simulation period. The results revealed that the lead compounds had higher binding free energies relative to the two standards [cinnamaldehyde (-16.06 kcal/mol), erythromycin (-30.75 kcal/mol)] and N-3-oxo-dodecanoyl-homoserinelactone native ligand (-25.26 kcal/mol), with geranyl linalool (-53.41 kcal/mol) having the highest score. The top five lead molecules complexed with LasR showed thermodynamic stability, with geranyl tiglate (1.45 Å) exhibiting the best stability. The lead compounds' quantum features assessed using DFT/B3LYP revealed that geranyl linalool had the highest ionization energy and electron affinity, suggesting its better potential to interact with the LasR active site relative to other investigated compounds. While these observations lent credence to geranyl linalool as the most promising LasR modulator, further confirmatory efforts via *in vitro* and *in vivo* studies are ongoing.

Genome-guided discovery to deliver biotechnological solutions

M. Trindade, L Van Zyl, A Burger
Professor and Director, Institute for Microbial Biotechnology and Metagenomics, University of Western Cape, South Africa
E-mail: ituffin@uwc.ac.za

Over the course of 10 years we have screened microbial collections from several environments towards the discovery of novel drugs and products for numerous biotechnological applications. These collections exhibit potent activities against pathogenic and multidrug resistant microbial strains, as well as anti-inflammation, anti-cancer and neuroprotective activities, amongst others. The small molecule discovery process is time-consuming and hampered by major hurdles associated with compound supply, dereplication and structure elucidation. To alleviate these obstacles we have employed complimentary top-down and bottom-up approaches to focus our efforts on the most novel pathways/compounds/activities. Through metagenomic screening, bioactivity/chemistry-guided fractionation, genome-guided dereplication, heterologous expression and proteomics we have isolated novel carotenoids, siderophores, non-ribosomal peptides, butyrolactones, lanthipeptides, biosurfactants and quorum sensing molecules. Application in wastewater treatment strategies, as agricultural adjuvants, in cosmetic formulations and as possible sedatives represent some of the avenues that we are pursuing to valorise these compounds. In the presentation I will detail our small molecule discovery journey and highlight key examples that demonstrate the benefit of taking a multi-angled and collaborative approach.

Aspergillus fumigatus secretes a protease(s) that displays _in silico_ binding affinity towards the SARS-CoV-2 spike protein and mediates SARS-CoV-2 pseudovirion entry into HEK 293T cells

Nozethu Mjokane[1], Saheed Sabiu[2], Onele M. N. Gcilitshana[1], Jacobus Albertyn[1], Carolina H. Pohl[1], Olihile M. Sebolai[1]

[1] Department of Microbiology and Biochemistry, University of the Free State, 205 Nelson Mandela Drive, Park West, Bloemfontein, 9301, South Africa.

[2] Department of Biotechnology and Food Science, Faculty of Applied Science, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa

*Correspondence: sebolaiom@ufs.ac.za

The novel coronavirus disease of 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). Data from the COVID-19 clinical control case studies showed that this disease could also manifest in patients with underlying microbial infections such as aspergillosis. The current study aimed to determine if the *Aspergillus* (A.) *fumigatus* culture media (i.e., supernatant) possessed protease activity that was sufficient to activate the SARS-CoV-2 spike protein. The supernatant was first analysed for protease activity. Thereafter, it was assessed to determine if it possessed proteolytic activity to cleave a fluorogenic mimetic peptide of the SARS-CoV-2 spike protein that contained the S1/S2 site and a full-length spike protein contained in a SARS-CoV-2 pseudovirion. To complement this, a computer-based tool, HADDOCK, was used to predict if *A. fumigatus* alkaline protease 1 could bind to the SARS-CoV-2 spike. We show that the supernatant possessed proteolytic activity, and analyses of the molecular docking parameters revealed that *A. fumigatus* alkaline protease 1 could bind to the spike protein. To confirm the *in silico* data, it was imperative to provide experimental evidence for enzymatic activity. Here, it was noted that the *A. fumigatus* supernatant cleaved the mimetic peptide as well as transduced the HEK-293T cells with SARS-CoV-2 pseudovirions. These results suggest that *A. fumigatus* secretes a protease(s) that activates the SARS-CoV-2 spike protein. Importantly, should these two infectious agents co-occur, there is the potential for *A. fumigatus* to activate the SARS-CoV-2 spike protein, thus aggravating COVID-19 development.

Keywords: *Aspergillus (A) fumigatus, A. fumigatus* alkaline protease 1, HADDOCK, HEK-293T cells, SARS-CoV-2 spike protein, Supernatant.

Computational bioprospection of selected plant secondary metabolites against VP7 (capsid protein) of rotavirus A

Adedayo Ayodeji Lanrewaju, Abimbola Motunrayo Enitan-Folami, Saheed Sabiu* and Feroz Mahomed Swalaha

Department of Biotechnology and Food Science, Faculty of Applied Science, Durban University of Technology, P. O. Box 1334, Durban 4000, South Africa

*Correspondence: fswalaha@dut.ac.za

Despite the global implementation of prequalified oral vaccines by the World Health Organization (WHO) in numerous countries, rotavirus A (RVA) have continued to be the principal cause of acute dehydrating diarrhoea in children under five years of age. Unfortunately, no medication is approved by the Food and Drug Administration (FDA) especially for rotavirus A-induced diarrhoea. Hence, it is crucial to prioritize the development of specialized therapeutics to combat rotaviral infections. *Spondias mombin*, *Macaranga barteri* and *Dicerocaryum eriocarpum* metabolites were thus screened using computational techniques to identify potential novel modulators with broad-spectrum activity against VP7 epitopes (capsid protein) of RVA. Compounds with poor pharmacokinetics and drug-likeness were screened out from the initial top 20 metabolites identified using molecular docking. Thereafter, molecular dynamics (MD) simulation was used to assess the ability of the resulting compounds to modulate the selected VP7 epitopes. Remarkably, all the lead compounds had higher negative binding free energy than tizoxanide across the three epitopes of VP7, with apigenin-4'-glucoside having the highest affinity for VP7A (-24.13 kcal/mol) and VP7C (-43.67 kcal/mol) while the highest affinity for VP7D was observed in 2SG (-36.08 kcal/mol). Interestingly, 2SG (-18.24 kcal/mol, -31.21 kcal/mol, -36.08 kcal/mol), apigenin-4'-glucoside (-24.13 kcal/mol, -43.67 kcal/mol, -33.52 kcal/mol) and gnetin L (-21.21 kcal/mol, -27.56 kcal/mol, -32.48 kcal/mol) had better broad-spectrum affinities for VP7A, C and D relative to tizoxanide (-10.36 kcal/mol, -18.32 kcal/mol, -12.98 kcal/mol) respectively. While this study unearths the lead compounds' promising ability to modulate the investigated VP7 epitopes, further confirmatory *in vitro* and *in vivo* studies are recommended.

Keywords: VP7 epitopes, capsid protein, binding free energy, thermodynamic stability, molecular dynamics simulation

An *in silico* genome mining approach to discover potential antimicrobial peptides from bacteria

Naveen Kumar[1], Prashant Bhagwat[1], Suren Singh[1], Santhosh Pillai[1]*
[1]Department of Biotechnology and Food Science, Faculty of Applied Sciences, Durban University of Technology, PO Box 1334, Durban, 4000, South Africa
*Correspondence: santhoshk@dut.ac.za

Antimicrobial resistance (AMR) is a global concern and remains a great threat to global health. Whenever new antibiotics are introduced, antibiotic resistance also emerges. Therefore, it is imperative to find alternative antimicrobial agents to traditional antibiotics. In response to the World Health Organisation's (WHO) global call for action, other alternatives have been explored for novel and safe antimicrobial candidates. Antimicrobial peptides (AMPs) have shown considerable promise in this regard, as microbes develop little or no resistance against them. This study employed an *in silico* approach to identify potential antimicrobial peptides from the genus *Actinobacillus*. All the available genomes of *Actinobacillus* were analysed from the BactPepDB database and 1006 potential AMP sequences were extracted. Subsequently, the probability of the sequences being AMP or non-AMP was tested by the $CAMP_{R3}$ database. The putative 198 AMP sequences were analysed for their physicochemical properties such as charge, hydrophobicity, toxicity, Boman index, and molecular weight. Following this rigorous analysis, seven sequences with varying lengths of 14 to 75 amino acids were finalised as possible potent AMPs. Molecular docking analyses were conducted to predict the potential interactions between the AMP sequences and the bacterial target proteins. UCSF Chimera was used to build the 3D structures of the AMPs and the PyRx tool was used for molecular docking analysis. Docking results showed that the AMP with sequence 'SFTRNAKWRKPQASGVFGRLGG' has the highest protein binding affinity of -16.4 Kcal/mol, against carbapenam synthetase protein target. Similarly, other AMP sequences showed comparable binding affinities against the other protein targets and predicted the strong probability of comprising antimicrobial activity. However, further in vitro studies such as synthesising peptides and evaluating their antimicrobial activity and biofilm inhibition assays could corroborate the in silico results, thus confirming their potential to be antimicrobial drug candidates.

Keywords: *Actinobacillus*, Antimicrobial peptides, antimicrobial resistance, genome mining, *in silico*, molecular docking

Structural-based investigation of novel pyrazole-thiazole hybrids as dual CDK-1 and CDK-2 inhibitors for cancer chemotherapy

Vincent A. Obakachi, Idowu Kehinde, Narva Deshwar Kushwaha, Olayinka I. Akinpelu, Babita Kushwaha, Srinivas Reddy Merugu, Francis Kayamba, Hezekiel M. Kumalo and Rajshekhar Karpoormath*

Department of Pharmaceutical Chemistry, College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa

*Correspondence: Karpoormath@ukzn.ac.za

CDK-1 and CDK-2 represent promising targets for cancer treatment as they are vital in tumour development, proliferation, and apoptosis during the cell cycle process. In treating cancers, CDK inhibitors (small molecules) are used to prevent the overproliferation of cancer cells. Consequently, inhibiting CDKs is a promising treatment strategy in the field of oncology. The limitations imposed by current CDK-1 and CDK-2 inhibitors in neurotoxicity and the development of resistance have prompted our group to use the novel synthesized pyrazole-thiazole hybrid analogues to investigate their possible potency against CDK-1 and CDK-2. The research study employed detailed computational techniques to predict the inhibitory potentials of synthesized pyrazole-thiazole hybrid analogues against CDK -1 and CDK-2. The *in-silico* binding free energy analysis revealed that four (7g, 8a, 8b, and 8h) of the tested molecules against CDK-1 demonstrated higher and better binding affinity than the conventional drugs roscovitine (RVT). Similarly, in the case of CDK-2, only four (7b, 8a, 8b, and 8f) of the tested compounds show higher binding energy than (RVT). Furthermore, structural examination of the two proteins after binding to the inhibitors revealed that the compounds form stable complexes with the targets and significantly reduced the structural flexibility of the proteins. Therefore, this study suggests the novel pyrazole-thiazole hybrid analogues as potential CDK-1 and CDK-2 inhibitors against cancer development and management.

Keywords: Cancer; CDK-1; CDK-2; pyrazole-thiazole; molecular dynamics simulation

Therapeutic path to triple knockout: Investigating the pan-inhibitory mechanisms of AKT, CDK9, and TNKS2 by a novel 2-phenylquinazolinone derivative in cancer therapy- An in-silico investigation

Peters, Xylia Q.; Elamin, Ghazi; Aljoundi, Aimen; Alahmdi, Mohamed I.; Abo-Dya, Nader E.; Sidhom, Peter A.; Tawfeek, Ahmed M.; Ibrahim, Mahmoud A. A.; Soremekun, Opeyemi; Soliman, Mahmoud E. S.

Blocking the oncogenic Wnt//β-catenin pathway has lately been investigated as a viable therapeutic approach in the treatment of cancer. This involves the multi-targeting of members of the tankyrase-kinase family, which propagate the oncogenic Wnt/β-catenin signaling pathway. During a recent investigation, the pharmacological activity of 2-(4-aminophenyl)-7-chloro-3H-quinazolin-4-one was repurposed to serve as a 'triple-target' inhibitor of TNKS2, AKT, and CDK9. Yet, the molecular mechanism that surrounds its multi-targeting activity remains unanswered. As such, this study aims to explore the pan-inhibitory mechanism of 2-(4-aminophenyl)-7-chloro-3H-quinazolin-4-one towards AKT, CDK9, and TNKS2, using *in-silico* techniques. Results revealed favorable binding affinities for 2-(4-aminophenyl)-7-chloro-3H-quinazolin-4-one towards TNKS2, CDK9, and AKT, respectively. Pan-inhibitory binding of 2-(4-aminophenyl)-7-chloro-3H-quinazolin-4-one is illustrated by close interaction with specific residues on tankyrase-kinase. Structurally, 2-(4-aminophenyl)-7-chloro-3H-quinazolin-4-one had an impact on the flexibility, solvent-accessible surface area, and stability of all three proteins, which was illustrated by numerous modifications observed in the unbound as well as the bound states of the structures, which evidenced the disruption of their biological function. Determining the criticality of the interactions that exist between the pyrimidine ring and catalytic residues could offer insight into the structure-based design of innovative tankyrase-kinase inhibitors with enhanced therapeutic effects.

Longitudinal investigation of the faecal RNA viral structural dynamics of commercially bred asymptomatic chickens from Durban, KwaZulu-Natal province, South Africa

Vivian C. Nwokorogu [1], Santhosh Pillai [1], James E. San [3], Charlene Pillay [1], Martin M. Nyaga [2], Saheed Sabiu [1]*.

[1] Department of Biotechnology and Food Science, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa

[2] Next Generation Sequencing Unit and Division of Virology, Faculty of Health Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.

[3] KwaZulu-Natal Research Innovation and Sequencing platform unit, Nelson Mandela School of Medicine, University of KwaZulu-Natal. 719 Umbilo Road, Durban 4001, South Africa.

*Corresponding: sabius@dut.ac.za

Virome studies on birds including chickens are relatively scarce, particularly from the African continent and the information on RNA virome composition is even scantier despite the continuous evolution of RNA viruses, and severe losses recorded in poultry resulting from seasonal viral outbreaks. Also, information on factors modulating the occurrence of some viruses in birds are limited particularly for domesticated birds. Viral metagenomics through advancements in sequencing technologies, has enabled the characterization of virome of diverse host species. The complex RNA viral constituents present in 27 faecal samples of asymptomatic chickens from South African farm collected at 3-time points from 2 independent season were determined using viral metagenomics and the impact of chicken's age and collection season on viral abundance and diversity were investigated. The results obtained revealed a total of 48 viral species spanning across 11 orders, 15 families and 21 genera. Viral RNA families such as *Coronaviridae, Picornaviridae, Reoviridae, Astroviridae, Caliciviridae, Picorbirnaviridae* and *Retroviridae* were abundant, among which picornaviruses, demonstrated a 100% prevalence across the three age groups (2, 4 and 7 weeks) and two seasons (summer and winter). Variation between the different chicken groups investigated indicated that viral diversity and abundance was significantly influenced by age ($P = 0.01099$) and season ($P = 0.00099$) between chicken groups, while there was no effect within samples in a group (alpha diversity) for age ($P = 0.146$) and season ($P = 0.242$). The presence of an exceedingly varied chicken RNA viruses, encompassing avian, mammalian, fungal, and dietary-associated viruses, underscores the complexities inherent in comprehending the causation, dynamics, and interspecies transmission of RNA viruses within the investigated chicken population. Hence, chickens, even in the absence of discernible symptoms, can harbour viruses that may exhibit opportunistic, commensal, or pathogenic characteristics.

Keywords**:** Viral metagenomics, Faecal virome, RNA viruses, Next-generation sequencing, Chicken, Viral diversity.

Integrating artificial intelligence with molecular docking in profiling new active pharmaceutical ingredients

Karishma Singh
Department of Nature Conservation, Faculty of Natural Sciences, Mangosuthu University of Technology, P.O. Box 12363, Jacobs, 4026, Durban, KwaZulu- Natal, South Africa
Correspondence: singh.karishma@mut.ac.za

The combination of artificial intelligence (AI) and molecular docking represents a paradigm shift in computational biology and drug discovery. This synergy uses AI's predictive power to improve the accuracy, efficiency, and scope of molecular docking studies. AI algorithms, particularly machine learning and deep learning models, can identify complex patterns and relationships in large datasets, allowing for unprecedented precision in predicting protein-ligand interactions. This integration addresses several traditional docking challenges, including improving scoring functions, optimizing binding pose predictions, and reducing computational time. Furthermore, AI-driven approaches make it easier to screen large compound libraries, identify novel drug candidates, and discover new therapeutic targets. This review examines the current state of AI-enhanced molecular docking, highlighting major accomplishments, methodological advances, and practical applications. It also discusses future prospects and potential obstacles, emphasizing the importance of ongoing interdisciplinary collaboration. By leveraging AI capabilities, the field of molecular docking has the potential to accelerate drug discovery, opening new avenues for the development of innovative treatments and personalized medicine.

Keywords: Artificial intelligence, molecular docking, drug discovery, computational biology, algorithms.

Unveiling the mechanism of action of corn silk in type 2 diabetes intervention through integrated network pharmacology and down regulation of *ADORA1* and *GABBR1*

Ayesha Akoonjee[1], Terisha Ghazi[2] and Anil Chuturgoon[2], Saheed Sabiu[1]*
[1]Department of Biotechnology and Food Science, Durban University of Technology, Durban, South Africa.
[2]Department of Medical Biochemistry, University of KwaZulu-Natal, Durban, South Africa.
*Correspondence: sabius@dut.ac.za

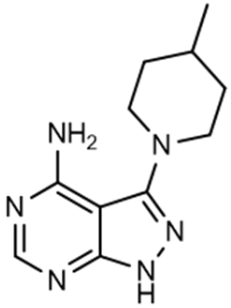
Type 2 diabetes mellitus (T2DM) is a chronic metabolic disease which is characterised by defective insulin production and/or resistance to insulin. Although, the antidiabetic action of corn silk (CS) has been established, the underlying mechanism of action (MoA) remains unclear. This study elucidated the MoA of both the mature and premature samples of CS as therapeutics to manage T2DM using computational and *in vitro* approaches. Ultra-performance liquid chromatography-mass spectrometry analysis was employed to chemically profile CS, while network pharmacology complemented with molecular dynamics (MD) simulation was used to determine the relationship between the CS constituents and target genes implicated in the pathogenesis of T2DM. Further validation *in vitro* was performed using HepG2 cells through complementary assays including 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) cell viability, glucose uptake and real-time polymerase chain reaction (RT-qPCR). Network pharmacology analysis identified the cAMP pathway as the hub signaling pathway, in which adenosine receptor A1 (*ADORA1*), gamma-aminobutyric acid type B subunit 1 (*GABBR1*) and hydroxycarboxylic acid receptor 2 (*HCAR2)* were identified as the key targets associated with gallicynoic acid (- 48.74 kcal/mol), dodecanedioc acid (-34.53 kcal/mol), and tetradecanedioc acid (-36.80 kcal/mol), respectively, which were thermodynamically stable, suggesting their putative role as potential drug candidates against T2DM. Discovery into the modulatory role of CS on the expression of the profiled genes *in vitro* revealed that, relative to metformin and insulin, the premature CS down regulated the expression of *ADORA1* and *GABBR1* in insulin resistant HepG2 cells. The downregulation of *ADORA1* and *GABBR1* following CS treatment could be associated with increased glucose uptake in HepG2 cells, which is indicative of its antidiabetic potential.

Keywords: *ADORA1*, Corn silk, *GABBR1*, HepG2 cells, Network pharmacology, Molecular dynamics simulation

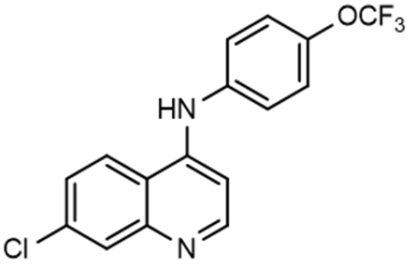
Synthesis and antidiabetic potential of quinoline–pyrazolopyrimidine hybrids and quinoline-4-arylamines.

Sahil Mishra[a], Nosipho,[a] Parvesh Singh*[a] Md. Shahidul Islam[b]
*School of Chemistry and Physics, University of KwaZulu-Natal, P/Bag X54001, Westville, Durban, South Africa.
[b] Department of Biochemistry, School of Life Sciences, University of Kwazulu-Natal, Westville, Durban, South Africa
Correspondence: singhp4@ukzn.ac.za, parveshdurban@gmail.com

A novel series of 1-(7-chloroquinolin-4-yl)-1H-pyrazolo[3,4–d]pyrimidin-4-amine and Quinoline-4-Arylamines were synthesized and evaluated for their anti-diabetic potential targeting α-glucosidase and α-amylase. Biological studies showed the compounds to be more effective against α-glucosidase than α-amylase. As per the SAR analysis compounds bearing electron-withdrawing groups specifically fluorinated, were more effective than electron-donating groups. Compounds with 4 -methyl piperidine and para-trifluoromethoxy groups, respectively, showed the most promising α-glucosidase inhibition activity with IC_{50} = 46.70 and 40.84 μM, compared to the reference inhibitor, acarbose (IC_{50} = 51.73 μM). Further, modifications are required for activity against α-amylase.



IC_{50} = 46.70 micro molar



IC_{50} = 40.84 micro molar

Exploring *Helianthus annuus* L. seeds as potential antidiabetics through computational and *in vitro* validation in HepG2 cells

Athika Rampadarath[1], Saheed Sabiu[1*], Terisha Ghazi[2] and Anil Chuturgoon[2]
[1]Department of Biotechnology and Food Science, Durban University of Technology, Durban, South Africa.
[2]Department of Medical Biochemistry, University of KwaZulu-Natal, Durban, South Africa.
*Correspondence: sabius@dut.ac.za

Helianthus annuus (sunflower) seeds, a popular oilseed crop may harbour promising therapeutic potential against type 2 diabetes (T2DM). However, the exact mechanism of antidiabetic action remains unclear. This study employed network pharmacology (NP), molecular dynamic (MD) simulations, and *in vitro* validation in insulin resistant HepG2 cells to explore the molecular basis of sunflower seed's antidiabetic activity in T2DM. Six sunflower seed cultivars were profiled using LC-MS and GC-MS techniques. NP analysis identified signalling pathways and their target genes through which metabolites of sunflower seeds may aid in the amelioration of T2DM. MD simulations identified potential lead metabolites targeting key genes in the PPAR pathway. *In vitro* validation was performed in HepG2 cells to evaluate the antidiabetic activity of the cultivars through glucose consumption assays and gene expression analysis. All six cultivars saw the presence of the same metabolites with slight variations. MD simulations identified three metabolites CFG, GPA and CGA (-45.36 to -41.62 kcal/mol) with stronger binding to MMP1 and, HGM and AZA to PPARA (-33.83 and -31.60 kcal/mol) than controls (ROS, MET) within the PPAR pathway. These metabolites also showed good stability and flexibility. Glucose consumption assay saw cultivars AGSUN 5103 CLP, 8251, and 5101 CLP (13.25 -14.85 mmol/L) show the most significant reduction in glucose levels relative than controls (metformin, insulin) and untreated (17 mmol/L) HepG2 cells. All three cultivars also upregulated the expression of MMP1 and PPARA genes more effectively than controls. AGSUN 5101 CLP had the greatest fold increase against MMP1 ($2^{-\Delta\Delta Ct}$ =1.88) and PPARA ($2^{-\Delta\Delta Ct}$ = 4.59). The findings of this study conclude that amongst the sunflower seeds, AGSUN 5101 CLP exhibits potential for T2DM management via PPAR pathway upregulation of MMP1 and PPARA. MD simulations were able to provide suggestive metabolites present in cultivar 5: CGA, GPA, CFG (MMP1) and HGM, AZA (PPARA) that may act as agonists for their respective genes, potentially exerting antidiabetic effects.

Keywords: Type-2 diabetes, sunflower seed, network pharmacology, molecular dynamic simulations, HepG2 cells

Structure-function analysis of the essential *Mycobacterium tuberculosis* P450 drug target, CYP121A1

Tiara Padayachee[1], David Lamb[2], David R Nelson[3] and Khajamohiddin Syed[1]*
[1]Department of Biochemistry and Microbiology, Faculty of Science, Agriculture and Engineering, University of Zululand, KwaDlangezwa 3886, South Africa
[2]Faculty of Medicine, Health and Life Sciences, Swansea University, Swansea SA2 8PP, UK.
3. Department of Microbiology, Immunology and Biochemistry, University of Tennessee Health Science Center, Memphis, TN 38163, USA
* Correspondence: khajamohiddinsyed@gmail.com

Cytochrome P450 CYP121A1 is a well-known drug target against *Mycobacterium tuberculosis*, the human pathogen that causes the deadly disease tuberculosis (TB). CYP121A1 is a unique P450 enzyme because it uses classical and non-classical P450 catalytic processes and has distinct structural features among P450s. However, a detailed investigation of CYP121A1 protein structures in terms of active site cavity dynamics and key amino acids interacting with bound ligands has yet to be undertaken. To address this research knowledge gap 53 CYP121A1 crystal structures were investigated in this study. Critical amino acids required for CYP121A1's overall activity were identified and highlighted this enzyme's rigid architecture and substrate selectivity. The CYP121A1-fluconazole crystal structure revealed a novel azole drug-P450 binding mode in which azole heme coordination was facilitated by a water molecule. Fragment-based inhibitor approaches revealed that CYP121A1 can be inhibited by molecules that block the substrate channel or by directly interacting with the P450 heme. This study serves as a reference for the precise understanding of CYP121A1 interactions with different ligands and the structure-function analysis of P450 enzymes in general. Our findings provide critical information for the synthesis of more specific CYP121A1 inhibitors and their development as novel anti-TB drugs.

Keywords: Cytochrome P450; *Mycobacterium tuberculosis*; CYP121A1; cYY; active site; crystal structure

Synadenium cupulare* regulates cellular protein synthesis in triple negative breast cancer *in vitro

Joshua C. Nwabuife, Othembele Gcaba, Relebohile Lefojane, Victoria Fasiku, Ayodeji Adegoke, Mamello P. Sekhoacha*
Department of Pharmacology, Faculty of Health Sciences, University of The Free State, Bloemfontein, 9300, South Africa.

Triple-negative breast cancer (TNBC) a subtype of breast cancer is known to lack the expression of estrogen, progesterone and human epidermal growth factor receptors. Treatment options for TNBC includes chemotherapy, surgery therapy and radiation, which unfortunately have drawbacks of resistance, and non-specific targeting. Medicinal plants as an alternative source of TNBC treatment are recently gaining popularity. *Synadenium cupulare* has been shown to inhibit TNBC cell growth. However, the regulation of cellular protein synthesis as a mechanism of action against TNBC is still not known. Hence, the current study investigated the mechanism of regulating cellular protein synthesis as a possible mode of action of *S. cupulare* against TNBC cells. Plant leaf extractions were conducted using cold solvent extraction method and cytotoxicity against TNBC cell line (MDAMB-231) and normal cell line (Vero) was evaluated using SRB assay. Bicinchoninic Acid (BCA) protein quantification assay was performed, and the protein expression and suppression were investigated using simple qualitative western blot. An extraction yield of 21.13% was obtained and cytotoxicity results revealed high growth inhibition by extract in TNBC cells (IC50: 32.81 µg/ml) compared to positive control which never attained an IC50 (doxorubicin) at the same concentrations, and no toxicity recorded to normal cells (indicating possible selectivity), while positive control showed IC50 of 10. 41 µg/ml against normal cells. The protein quantity in treated TNBC cell line was reduced from approximately 60.64 ± 7.27% (Untreated) to 47.00 ± 4.81% (extract) and 42.00 ± 0.58% (doxorubicin) at the highest concentration (100 µg/ml). Simple qualitative western blot results confirmed the regulation of cellular protein synthesis as seen in the intensity of some protein bands. Conclusively, the leaf extract of *S. cupulare* was observed to inhibit TNBC cell growth by regulating the process of cellular protein synthesis, which suggests it could be one of its mechanisms of action.

Keywords: Triple Negative Breast Cancer, MDA-MB-231, Cellular Protein Synthesis and *Synadenium Cupulare*.

Deciphering the neuro-modulatory effect of *Cannabis sativa* using network pharmacology and molecular dynamics simulations

Halimat Yusuf Lukman[1], Christina Peter[1], Nosipho Wendy S'thebe[1], Usman Abiola Sanni[2,3], Saheed Sabiu[1]*

[1]Department of Biotechnology and Food Science, Faculty of Applied Sciences, Durban University of Technology, Durban, South Africa; [2]Federal University Teaching Hospital, Birnin Kebbi, Nigeria; [3]Partners in Health, Sierra Leone

*Correspondence: sabius@dut.ac.za

Although, studies have reported the use of cannabis as a temporary antidepressant and implicated its chronic use in neurological diseases, the exact mechanisms through these happen remain elusive. This study employed network pharmacology and molecular dynamics simulation to discern the mechanism of cannabis as a temporary antidepressant and potential agent implicated in neurological disorders in relation to its modulatory effect on neurotransmitters. A total of 156 metabolites retrieved from *Cannabis sativa* metabolites were pharmacokinetically screened. 22 overlapping genes were identified between the screened metabolites genes and the genes of the central nervous system (CNS) neurotransmitters. The gene ontology presented the glutamate receptor activity, an excitatory neurotransmitter receptor, as the most enriched biological process while the Kyoto encyclopaedia of genes and genome analysis revealed 16 signalling pathways with the neuroactive ligand receptor activity (NALR) as the most significant pathway and followed by glutamatergic synapse. The CNR1 and GRM2, previously implicated in brain functioning were identified as key targets in the NALR pathway. A probe into the structural stability of top-ranked metabolites identified only CNR1-cholesterol (-73.88 kcal/mol) with the highest negative free binding energy than reference antidepressant drug (anandamide) (-58.78 kcal/mol). Except for delta-8-tetrahydrocannabinolic acid-CNR1 and isolinolenic acid-GRM2 complexes with RMSD values of 3.27±0.85 and 2.52±0.60 Å, respectively, other top-ranked metabolites had remarkable stability and compactness with the apo-genes. Data from this study shows that the profiled cannabis metabolites displayed modulatory effects on key neurotransmitters of the CNS and their receptors as well as stable binding interaction with genes implicated in brain functioning. These findings are suggestive of the mechanism of action of cannabis on brain activity during depression and the predisposition of chronic users to neurological disorders.

Keywords: *Cannabis sativa,* Cannabinoid receptors, Network pharmacology, Depression, Neurological diseases, Neurotransmitters.

Novel thiomorpholine tethered isatin hydrazones as potential inhibitors of resistant *Mycobacterium tuberculosis*

Baji Baba Shaik, Sivanandhan Karunanidhi, Balakumar Chandrasekaran, Rajshekhar Karpoormath, Harun M Patel, Francis Kayamba, Srinivas Reddy Merugu, Vishal Kumar, Sanjeev Dhawan, Babita Kushwaha, Mavela Cleopus Mahlalela
Department of Pharmaceutical Chemistry, Discipline of Pharmaceutical Sciences, College of Health Sciences, University of KwaZulu-Natal (Westville), Durban 4000, South Africa.

Tuberculosis (TB) is an airborne infectious disease caused by organisms of the *Mycobacterium tuberculosis* complex Novel chemotherapeutic agents against multidrug resistant-tuberculosis (MDR-TB) are urgently needed at this juncture to save the life of TB-infected patients. We have synthesized and characterized novel isatin hydrazones 4(a-o) and their thiomorpholine tethered analogues 5(a-o) using NMR, IR and HRMS analysis. All the synthesized compounds were initially screened for their anti-mycobacterial activity against the $H_{37}Rv$ strain of MTB under level-I testing. In level-II testing, potent compounds were evaluated against five drug-resistant isolates namely INH-R1, INH-R2, RIF-R1, RIF-R2, and FQ-R1 of MTB under aerobic conditions. Remarkably, five compounds 4f, 4h, 4n, 5f and 5m (IC_{50} = 1.9 µM to 9.8 µM) were found to be most active, with 4f (IC_{50} = 1.9 µM) indicating highest inhibition of $H_{37}Rv$. These compounds were further evaluated at level-II testing against the five drug-resistant strains. Interestingly, 4f and 5f emerged as the most potent compounds with IC_{50} of 3.6 µM and 1.9 µM against RIF-R1 MTB strain, followed by INH-R1 MTB strain with IC_{50} of 3.5 µM and 3.4 µM, respectively. Against FQ-R1 MTB strain, the lead compounds 4f and 5f displayed excellent inhibition at IC_{50} 5.9 µM and 4.9 µM, respectively indicating broad-spectrum of activity. In summary, isatin hydrazones 4(a-o) and 5(a-o) were synthesized, characterized and screened at level-I against MTB H37Rv for their anti-mycobacterial activity. Compounds 4f and 5f emerged as the most potent compounds exhibiting highest inhibition against both the normal (H37Rv) and drug-resistant MTB strains.

Metagenome of dairy wastewater reveals potential steroid degraders

Prasiddhi Parab[1], Muneer Ahmad Malla[2], Prashant Bhagwat[1], Sheena Kumari[2] Santhosh Pillai[1]

[1]Department of Biotechnology and Food Science, Faculty of Applied Sciences, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa.

[2]Institute of Water and Wastewater Technology, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa

*Correspondence: santhoshk@dut.ac.za

The extensive use of reproductive drugs in livestock farming has led to the gradual build-up of synthetic estrogen hormones in the aquatic environment through wastewater discharge. This poses a significant threat to global health due to their endocrine-disrupting activities, urging the need for their removal from the ecosystem. Thus, this study focuses on identifying potential steroid-degrading microbial communities in dairy wastewater. Through successive enrichment strategies, a microbial consortium utilising estradiol as the sole carbon source was obtained. To characterise the microbial composition, total genomic DNA was extracted from raw wastewater (control) and enriched samples and sequenced using Illumina's NextSeq platform. Downstream processing of the obtained raw reads was performed using the Squeeze Meta pipeline with default parameters. All the statistical analysis was performed in R. The comparative metagenome between non-enriched and enriched samples demonstrated that estradiol had a significant effect on microbial shift ($p=0.007$) and composition (PERMANOVA $F =89.6$; $R 2 = 0.97p < 0.001$). Specifically, the relative abundance of bacterial species such as *Acidocella, Mycobacterium* and *Lactobacillus* sp., along with fungal species including *Pichia*, *Cyberlindnera,* and *Aspergillus*, were significantly higher in enriched samples. Among these, *Acidocella* (40%) and *Pichia* (85%) were predominant in enriched samples, highlighting the significance of this study in identifying and characterising previously unknown microbial communities capable of the degradation of steroid hormones. This insight could be pivotal in developing effective biological treatment methods, thereby strengthening robust bioremediation strategies for mitigating steroid hormones in contaminated environments.

Keywords: Bioremediation; EDCs; Metagenomics; Microbial degradation; Steroid hormones

An unprecedented number of cytochrome P450s are involved In secondary metabolism In *Salinispora* species

N A Malinga, N Nzuza, T Padayachee, P R Syed, R Karpoormath, D Gront, D R. Nelson, K Syed

[1]Department of Biochemistry and Microbiology, Faculty of Science and Agriculture University of Zululand, KwaDlangezwa 3886, South Africa.

[2]Department of Pharmaceutical Chemistry, College of Health Sciences, University of KwaZulu-Natal, Durban 4000, South Africa

[3]Faculty of Chemistry, Biological and Chemical Research Center, University of Warsaw Pasteura 1, 02-093 Warsaw, Poland

[4] Department of Microbiology, Immunology and Biochemistry, University of Tennessee Health Science Center, Memphis

Correspondence: drnelson1@gmail.com (D.N.R.); and khajamohiddinsyed@gmail.com

Cytochrome P450 monooxygenases (CYPs/P450s) are heme thiolate proteins present in species across the biological kingdoms. By virtue of their broad substrate promiscuity and regio- and stereo-selectivity, these enzymes enhance or attribute diversity to the secondary metabolites. Actinomycetes species are well-known producers of secondary metabolites, especially Salinispora species. Despite the importance of P450s, a comprehensive comparative analysis of P450s and their role in secondary metabolism in Salinispora species is not reported. We, therefore, analyzed P450s in 126 strains from three different species Salinispora *arenicola, S. pacifica,* and *S. tropica.* The study revealed the presence of 2643 P450s that can be grouped into 45 families and 103 subfamilies. CYP107 and CYP125 families are conserved, and CYP105 and CYP107 families are bloomed (a P450 family with many members) across Salinispora species. Analysis of P450s that are part of secondary metabolite biosynthetic gene clusters (smBGCs) revealed Salinispora species have an unprecedented number of P450s (1236 P450s-47%) part of smBGCs compared to other bacterial species belonging to the genera Streptomyces (23%) and Mycobacterium (11%), phyla Cyanobacteria (8%) and Firmicutes (18%) and the classes Alphaproteobacteria (2%) and Gammaproteobacteria (18%). A peculiar characteristic of up to six P450s in smBGCs was observed in Salinispora species. Future characterization Salinispora species P450s and their smBGCs have the potential for discovering novel secondary metabolites.

Keywords: Natural products; Secondary metabolites; Actinomycete; Marine; Salinispora arenicola; Cytochrome P450; Biosynthetic gene clusters; Genome-data mining; Diversity; Streptomyces; Mycobacterium.

Detection, prevalence and molecular characterization of rotavirus G and F from South African chickens

Vivian C. Nwokorogu [1], Santhosh Pillai [1], James E. San [3], Martin M. Nyaga [2], Saheed Sabiu *[1]

[1] Department of Biotechnology and Food Science, Durban University of Technology, P.O. Box 1334, Durban 4000, South Africa

[2] Next Generation Sequencing Unit and Division of Virology, Faculty of Health Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.

[3] KwaZulu-Natal Research Innovation and Sequencing platform unit, Nelson Mandela School of Medicine, University of KwaZulu-Natal. 719 Umbilo Road, Durban 4001, South Africa.

* Correspondence: sabius@dut.ac.za

Avian rotaviruses (RVs) are implicated as significant etiologic agents of gastroenteritis in birds. Currently, avian RVs are understudied globally, consequently, this paucity of information regarding these viruses and their true diversities needs to be unravelled. As a result, characterizing these viral species is critical since more detailed information on genomic, epidemiologic, and evolutionary characteristics can delineate the significance of these infections and advise efficient preventative and control approaches. In this study, we present partial and full genome characterizations of the two avian RV species, RVF and RVG, identified from 27 faecal samples of asymptomatic South African chickens using viral metagenomics. Complete or partial sequences of the 11 genomic segments encoding VP1, VP2, VP3, VP4, VP6, VP7, NSP1, NSP2, NSP3, NSP4 and NSP of 2 RVG and 5 RVF strains were recovered, revealing that different variants of both RVF and RVG circulate among South African chickens. Among the two RV species, RVG was predominantly more abundant than RVF with relative abundance of 66.8% and 33.2% respectively. Similarly, RVG and RVF demonstrated 88.9% and 33.3% prevalence across the 27 samples. In addition, significant information regarding the genomic features, genetic diversity and evolutionary relatedness of RVF and RVG strains are demonstrated. Hence, the data generated in this study contributes to a better understanding of the genomics and ecology of these viruses. Nevertheless, the absence of larger number of RVs genome sequences for comparison remains a challenge, and more sequences are needed to advance our knowledge of the evolution and cross-species spillovers of avian RVs.

Keywords: Viral metagenomics, Faecal virome, Rotaviruses, Poultry, Chicken, and Viral diversity.

Novel binary glutamine-based deep eutectic solvents: Physicochemical and thermal characterisation

Grace Abel, Ayodeji Amobonye, Bhagwat Prashant, Kugen Permaul, Santhosh Pillai
Department of Biotechnology and Food Science, Faculty of Applied Sciences,
Durban University of Technology, P O Box 1334, Durban, 4000, South Africa

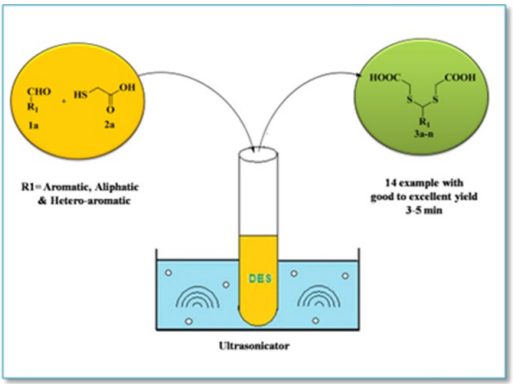
Amino acid based deep eutectic solvents (AADESs) being subclass of natural deep eutectic solvents (NADES) have been gaining research attention with prospective applications especially in the energy and pharmaceutical industries. Herein this study, novel binary glutamine-lactic acid based DESs were synthesised by the heating and stirring method with glutamine as hydrogen bond acceptor (HBA) and lactic acid as hydrogen bond donor (HBD) at different ratios (1:2 to 1:6). Thereafter, the solvents were evaluated for selected physicochemical and thermal properties according to standard protocol. Based on the results, the physicochemical properties of glutamine lactic acid (GL) DESs showed that the densities and viscosities decreased as the molar ratio increased with the highest in GL1:2. Conductivity increased as water content increased with increasing molar ratio of the DESs. The thermogravimetric profile of the DESs revealed similar T_{onset} value for all the DESs with the operative temperature at < 373.15 K while the T_{peak} values were in the range 483.15 to 553.15 K in the following order: 1:2 > 1:3 > 1:4 > 1:5 > 1:6. In conclusion, the novel GL DESs which remained liquid at room temperature showed physicochemical properties that were greatly influenced by the HBD lactic acid. This implies that DESs with any property of interest can be synthesised by altering the ratio of HBD to HBA. GL 1:2 showed the highest stability with a T_{peak} of 553.15 K. Overall, the GL DESs can be suitable for application in chemical processes such as biomass transformation and extraction of compounds.

Keywords: amino acid, biomass pretreatment, glutamine, green solvents, natural deep eutectic solvents

Ultrasonic energy promoted synthesis of bisthioglycolic acid derivatives in deep eutectic solvents-A greener approach

Gobind Kumar,[a] Rupesh Kumar,*[b] Parvesh Singh,*[a]
[a]School of Chemistry and Physics, University of KwaZulu Natal, P/Bag X54001, Westville Durban 4000, South Africa
[b]Department of chemical sciences, I. K. Gujral Punjab Technical University Kapurthala Punjab-144603, India
*correspondence: singhp4@ukzn.ac.za

Carbon–Sulfur bond formation strategies are significant due to the importance of linkages in the sulfur-containing scaffolds which are found in biologically active compounds. Sulfones, and sulfonamides are common sulfur-containing scaffolds that are found in medicinal drug. For instance, 1,3-oxathiolan-5-one has shown antiviral activity, and PLA2 inhibitory activity. Moreover, bisthioglycolic acid and its derivatives have been reported to play a significant role as a precursor in the formation of many sulfur-containing heterocyclic compounds. The present methodology explored the effectiveness and versatility of deep eutectic solvent with ultrasonic energy as an eco-friendly protocol for the synthesis of bisthioglycolic acid derivatives. Bisthioglycolic moiety holds its role as a potent scaffold in sulfur- containing drugs. The presented strategy offers significant advantages such as green catalyst as well as solvent, excellent yield, short reaction time, and simple reaction workup. This methodology shows a wide range of substrate scope that contain both electron-donating as well as electron-withdrawing groups.

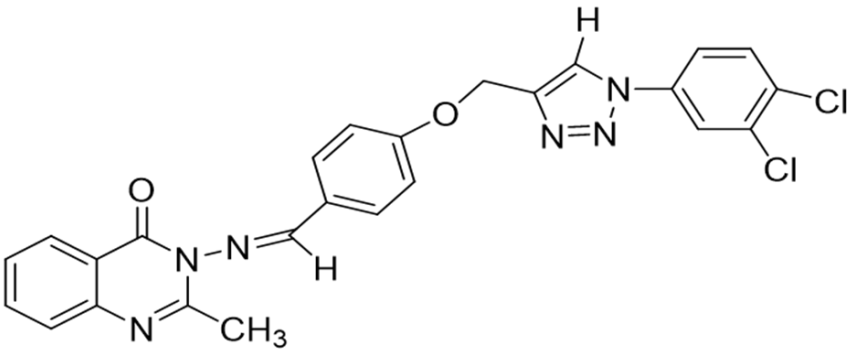


Keywords: Viral metagenomics, Faecal virome, Rotaviruses, Poultry, Chicken, and Viral diversity.

Synthesis, antibacterial screening, and computational studies of quinazoline-4 (3H)-one-triazole conjugates

Ankit, Neha Manhas, Parvesh Singh*
School of Chemistry and Physics, University of KwaZulu-Natal,
Private Bag X54001, Durban, 4000, South Africa
*Correspondence: Singhp4@ukzn.ac.za

A novel series of quinazoline-4 (3H)-one-tagged triazole conjugates were created. Using the copper(I)-catalyzed azide-alkyne cycloaddition (CuAAC) technique. The structures of all produced compounds were clarified using further spectrum evidence and 2D-NMR (HMBC, HSQC, and COSY) techniques. These substances' in vitro antibacterial properties were assessed and contrasted with those of the prescription medications levofloxacin, ampicillin, and ciprofloxacin. Strong activity and selectivity were demonstrated by four compounds (4a, 4d, 4g, and 4i) in the series against the gram-negative bacterial strains. Out of all of these, 4i proved to be the most effective conjugation, showing nearly a 12-fold increase in activity over ampicillin against gram-negative *Klebsiella pneumoniae*, which is one of the most difficult multidrug-resistant bacteria in the world. Additionally, a structure-activity relationship (SAR) investigation showed that quinazoline's antibacterial activity was significantly enhanced by the addition of a triazole ring.



Screening traditional African fermented milk beverages for probiotic potential

Brynita Pillay, Prashant Bhagwat, Santhosh Pillai
Department of Biotechnology and Food Science, Faculty of Applied Sciences, Durban University of Technology, P. O. Box 1334, Durban, 4000, South Africa.

Traditionally fermented African milk products have gained attraction as functional foods with health-promoting properties due to their diverse probiotic bacterial and yeast communities. The current study focuses on the probiotic properties of indigenously fermented milk products, Amasi and Madila, using *in vitro* approaches and metagenomic profiling to unravel its microbiome post-fermentation. The biochemical screening of the milk products led to a total of 52 isolates. Further screening for survival tolerance within gastrointestinal conditions resulted in 28 isolates, with isolate AV2-9 exhibiting the highest tolerance to bile fluid (96.5% ± 1.01) and gastric fluids (95.4% ± 1.7). Thereafter, all isolates demonstrated positive auto-aggregation properties (≥65%), with the isolate AV1-3 displaying the highest auto-aggregation (91.7% ± 0.06). The cell surface hydrophobicity tests identified the highest hydrophobicity levels with xylene for AV2-9 (61.4% ± 0.04), hexane for AV3-9 (70% ± 0.05) and chloroform for MV3-4 (61.4% ± 0.14). The isolates were further assessed for their co-aggregation properties, and the highest co-aggregation was observed for AV2-9 against *Bacillus cereus* at 4 h (37.39% ± 0.06) and 24 h (64.51% ± 0.01). The antibacterial activity testing of the isolates' cell-free supernatants showed the zones of inhibition against *Staphylococcus aureus* (14.5 ± 0.71 mm)*, Escherichia coli* (16.5 ± 0.71 mm)*, Salmonella typhimurium* (17.5 ± 0.71 mm) and *Listeria monocytogenes* (16.0 ± 1.41 mm). The current findings highlight the promising probiotic potential of the fermented milk isolates, showcasing gastric tolerance, cell adhesion, hydrophobicity and antimicrobial properties. The metagenomic analysis of the fermented milk products is in progress.

Keywords: Fermented milk; Probiotics; Metagenomics; Microbiome

Exploring innovative approaches in target-based drug design

Prof Rajshekhar Karpoormath
Synthetic and Medicinal Chemistry Research Group (SMCRG)
Department of Pharmaceutical Chemistry
University of KwaZulu-Natal (UKZN)

The quest for more effective and selective therapeutic agents has driven significant drug discovery and development advancements. We at the Synthetic and Medicinal Chemistry Research Group (SMCRG), Department of Pharmaceutical Chemistry, University of KwaZulu-Natal (UKZN) explore innovative approaches in target-based drug design, emphasizing the critical integration of chemistry, synthesis, and pharmacological evaluations. We have developed a series of novel compounds through rational drug design strategies by identifying and validating specific molecular targets associated with both infectious and non-infectious diseases. These compounds were synthesized using novel chemical methodologies, ensuring high purity and yield. Subsequent pharmacological evaluations, a crucial step in our research, were conducted to assess these newly synthesized molecules' efficacy, potency, and safety. This multidisciplinary approach, which we value, facilitates the discovery of promising drug candidates and enhances our understanding of the underlying biological processes and molecular interactions. SMCRG has developed several novel lead compounds over the years, which have the potential to be optimized further as drug candidates.

Modeling Covalent Enzyme Inhibition

Jerônimo Lameira, PhD

Institute of Biological Sciences. Federal University of Para, 66075-110, Belem, Para, Brazil

Covalent Inhibitor are of interest for therapeutic intervention in the treatment of a number of human diseases, including Covid-19, where the main coronavirus protease (SARS-CoV-2 Mpro) is an important target for drug development. Enzymatic Covalent Inhibitors affords a unique set of advantages and it is a common strategy in cancer therapy. Covalent inhibitor can be also used for Leishmanioses and Chagas Disease. In general, one can rely on an integrated approach where the three pillars of drug development (computational chemistry, organic synthesis and biological studies) are explored for developing discovery new Covalent Inhibitors. Besides, the detailed understanding of the protein-ligand interactions is fundamental for discovery of novel drug that can treat important illness. The development and application of computer-assisted tools to predict the biological activity of small molecules integrated with synthesis and biological assay is key for drug discovery. The complete drug discovery pipeline includes high-throughput screening of molecular libraries and the optimization of lead compounds. In this context, this talk will highlight several challenging aspects of the molecular modeling of covalent enzyme inhibition.

NOTES

NOTES

ENVISION2030

STATEMENT OF INTENT

By 2030

Our people will be creative, innovative, entrepreneurial and adaptive to changes in the world;
Our people will participate productively in the development of our region, country and the world;
Our state-of-the-art infrastructure and systems will enhance an ecosystem created to achieve this vision.

DUT
DURBAN UNIVERSITY OF TECHNOLOGY
INYUVESI YASETHEKWINI YEZOBUCHWEPHESHE
Creative. Distinctive. Impactful.

...and thus contribute to **Improving Lives and Livelihoods**

EFFECTING AND ENABLING — INFLUENCING AND IMPACTING

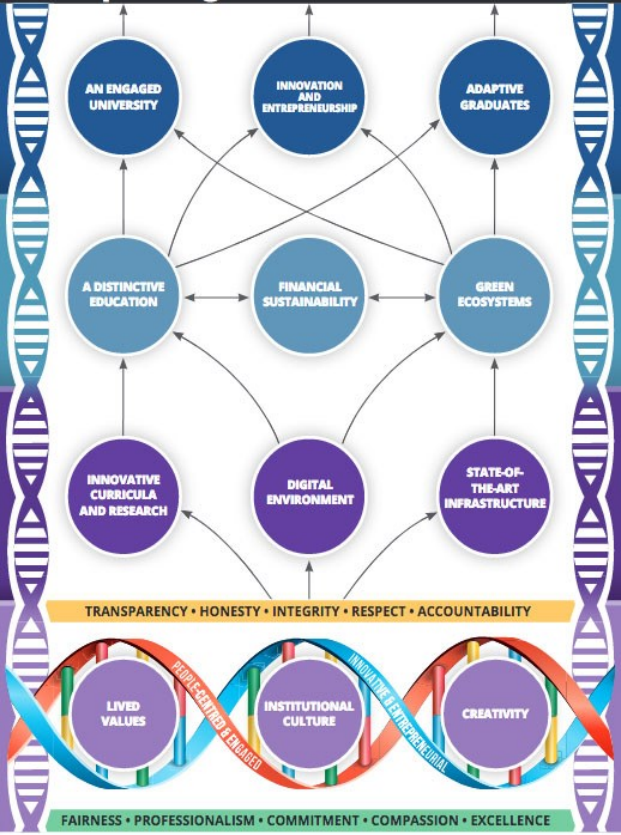
SOCIETY
...that leads to mutually beneficial collaborations, the practical application of knowledge and future-ready graduates...

SUSTAINABILITY
...resulting in the delivery of a distinctively DUT experience, within an environmentally responsible and financially sustainable framework...

SYSTEMS & PROCESSES
...we will build an enabling environment that supports dynamic curricula that inspire innovation and entrepreneurship...

STEWARDSHIP
By living our values and principles within a culture of shared responsibility and accountability, and embracing creativity...

START



AN ENGAGED UNIVERSITY
Be engaged and productive glocal citizens that establish mutually beneficial partnerships

INNOVATION AND ENTREPRENEURSHIP
Leverage new knowledge and solutions for societal impact

ADAPTIVE GRADUATES
Develop graduates with the acumen to initiate and/or respond to change

A DISTINCTIVE EDUCATION
Create a compelling and future-oriented living and learning environment

FINANCIAL SUSTAINABILITY
Engender a sustainable and efficient business model

GREEN ECOSYSTEMS
Make environmental sustainability core to all university activities

INNOVATIVE CURRICULA AND RESEARCH
Provide curricula that stimulate creativity and innovation to generate new knowledge and solutions

DIGITAL ENVIRONMENT
Adopt integrated digital systems and processes that enable our people to deliver optimally

STATE-OF-THE-ART INFRASTRUCTURE
Provide contemporary work, learning and living spaces

LIVED VALUES
Nurture a people-centred culture that embodies our values and principles

INSTITUTIONAL CULTURE
Foster a culture of accountability and shared responsibility in achieving the DUT way

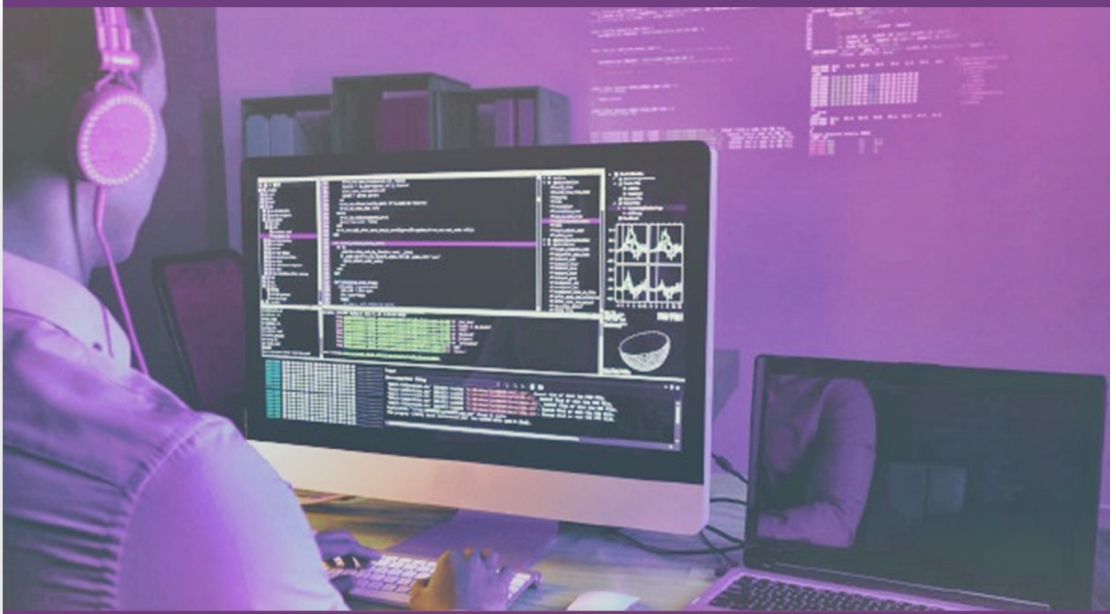
CREATIVITY
Inspire innovation and entrepreneurship

DUT
DURBAN UNIVERSITY OF TECHNOLOGY
INYUVESI YASETHEKWINI YEZOBUCHWEPHESHE

FACULTY OF APPLIED SCIENCES

DEPARTMENT OF BIOTECHNOLOGY &FOOD SCIENCE

COMPUTATIONAL AND SYSTEMS BIOLOGY CONFERENCE 2024



ENVISION2030 transparency • honesty • integrity • respect • accountability
fairness • professionalism commitment • compassion excellence

CREATIVE. DISTINCTIVE. IMPACTFUL.