BIOINFORMATION
Discovery at the interface of physical and biological sciences

OPEN ACCESS GOLD

BIOMEDICAL INFORMATICS

www.bioinformation.net
Volume 17(1)

Editorial

From Anna University to America and to Agriculture

Pandjassarame Kangueane*

Biomedical Informatics (P) Ltd, Irulan Sandy Annex, Pondicherry 607 402, India; *Corresponding author; Pandjassarame Kangueane - E-mail ID: kangueane@gmail.com

Received November 6, 2020; Accepted November 6, 2020; Published January 31, 2021

DOI: 10.6026/97320630017029

Abstract:
Anna University (AU) is an awesome *alma mater* for attracting the attention of the invincible through awareness from education. It is a place with a plan for preparing a palace in a person's life. It is an avenue for America through adequate cGPA and Advanced GRE (AGRE) with good TOEFL score. The views, visions, modes and models of several faculty members shaped many technocrats, teachers, entrepreneurs, journalists, editors and even farmers. Technology is engineering with science. The foundation and facilities at AU is priceless. AU created the framework for Industrial Biotechnology, a truly inter disciplinary curriculum with an optimal blend of Engineering and Science (Biology especially Agriculture and Healthcare through Organic chemistry) in 1992 almost 28 years back. The place was positioned just perfect in the world for wonders to come true. The Raman auditorium (in reverence to the Nobel Laureate Sir CV Raman) reassured rational research with reasonable respect in many minds at the ACTECH (Alagappa College of Technology) under the administration of AU. The admiration, acknowledgement and accountability for the *alma mater*, the AU will always remain precious.

Keyword: Science, Engineering, Technology, Biotechnology

Industrial Biotechnology at Anna University, India

My excitement to move to Chennai (formally a British colony) from Pondicherry (formally a French colony) was high, as soon as a call letter was received from Anna University for admission in Bachelor of Technology (B. Tech) in Industrial Biotechnology. Literally, my mind was prepared to see the DNA with my own eyes in 1993. Kunthala Jayaraman (KJ) is the mother of Industrial Biotechnology Education in the world who created the syllabus for it with a perfect mix of Science, Engineering and Technology at Anna University (**Figure 1**) **[1]**. She was extremely active, forceful; women of wonders, and an awesome dealmaker during post Independence India. She appointed several faculty members who returned from USA after their doctoral/postdoctoral training. The subject was truly inter-disciplinary. She appointed people from various backgrounds in science and engineering, especially from Organic chemistry to Chemical Engineering so as to create a beautiful blend for Industrial Biotechnology (**Figure 2**). She created "*corpus funds*" to support faculty members. The curriculum had fluid mechanics on one side and molecular biology on the other side. Thus, Industrial Biotechnology Education was novel to the world in 1992. My enthusiasm to join the programme in 1993 was tremendous. The class of 1997 (batch 1993-1997) was a small group with 20 members (**Figure 3**). We were interacting very well with one another discussing different aspects of Industrial Biotechnology amidst confusion, exaggeration, infatuation and love. A

BIOINFORMATION
Discovery at the interface of physical and biological sciences

Bachelor of Technology (B. Tech) degree in Industrial Biotechnology was confirmed on us from the Centre for Biotechnology, Alagappa College of Technology (ACTECH), ANNA UNIVERSITY in 1997 (**Figure 4**). Most of us went to the USA either for higher education (Master of Science) in Biology through research or for work through the Information Technology sector. Many of us settled in the USA with a happy family life. Biotechnology was new to the industries in India in the 90's and the job market was weak. However, Anna University provided the foundation to explore several aspects of Industrial Biotechnology from 1993 to 1998 in our life.

Figure 1: Kunthala Jayaraman (fondly referred as KJ) is the mother of Industrial Biotechnology Education in the world who created it with a perfect mix of Science, Engineering and Technology at Anna University. She is a Biochemistry alumnus at the Indian Institute of Science, Bangalore. She could collaborate with both Engineers and Technocrats with an entrepreneurial spirit. She is a truly sensational scientist for the Indian society with a young democracy. Her birthday falls on the first of January every year and the New Year celebrations catalyzed creativity at her birthday parties.

Research on *Cry toxin* from *Bacillus thuriengis* at Anna University

We (P. Kangueane, G. Kalaiselvi and R. Sachidanandam) were trying to estimate the individual population dynamics of *B.t.a* (*Bacillus thuriengis subspecies*aizawai) and *B.t.k (Bacillus thuriengis subspecies* kurstaki*)* in a co-culture system to develop a combined formulation for better pesticide activity. Similar morphology between *B.t.a and B.t.k* gave us hard time, determining the individual species dynamics in a co-culture system. Nonetheless, G Kalaiselvi and R Sachidanandam managed to develop a bioprocess system for the maintenance of *Bacillus sphaericus* 1593M in Bioreactors **[3]**. Kalaiselvi was cool, calm and courageous to create literature in Biotechnology during her early 20's. This is not easy.

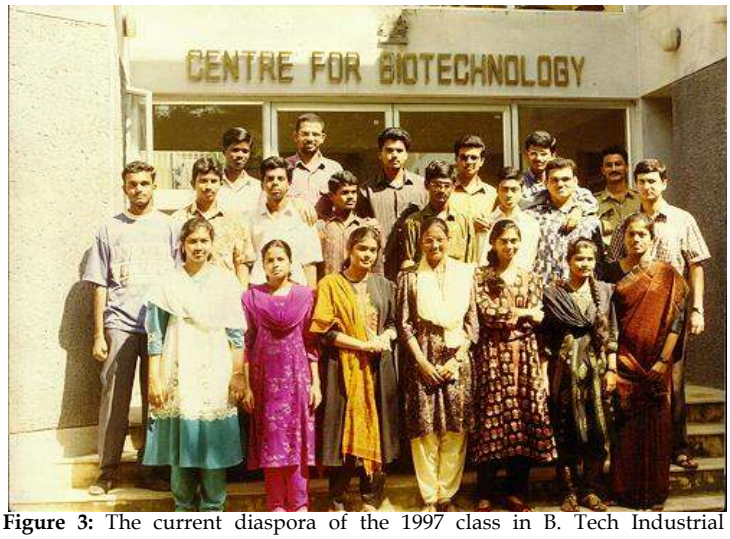
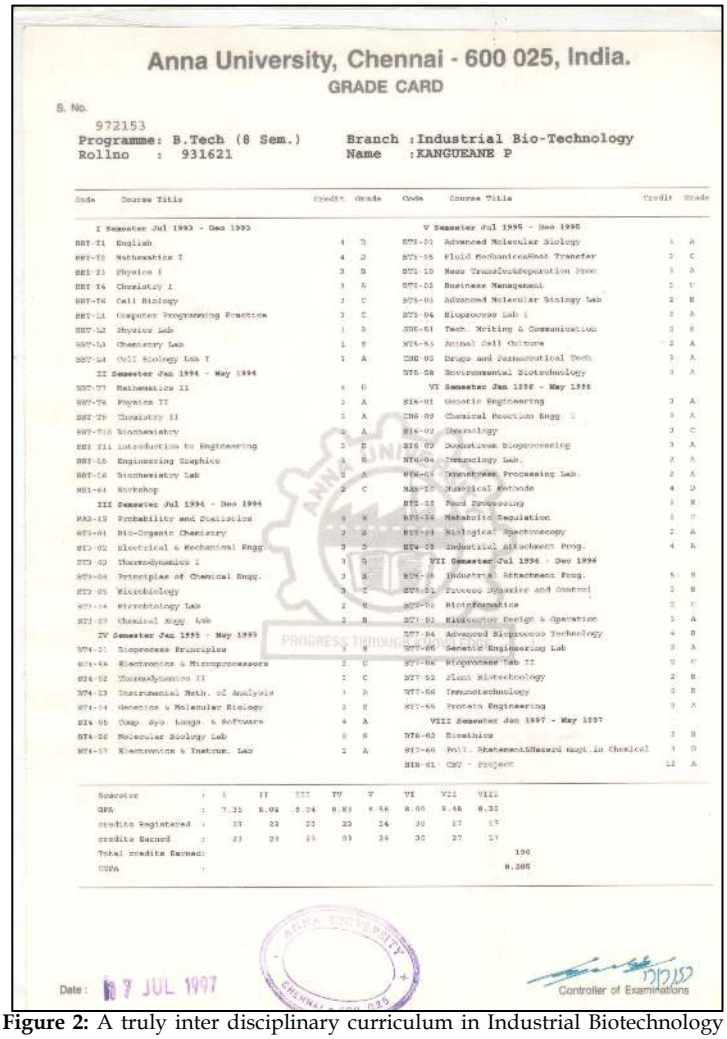


Figure 3: The current diaspora of the 1997 class in B. Tech Industrial Biotechnology with a global presence. Top row: S Sakthivelu (USA), Arvind Babu Ginjupali (USA), Gopalan Vivek (Medgenome Ltd, Bangalore, India, Singapore, US return), C Naveen (USA), Vamsi Kiran Badugu (India, US return); Middle row: J Karthikeyan (USA), G Bansidhar (GenenTech, USA), S Manikavasagam (India), S Prem Kumar (USA), P. Kangueane (Chief Editor, Bioinformation, India, Singapore, Malaysia, US return), M. Madhu Kumar (India), S Rajesh (India), Kedar Gokalae (Director, Bombay Chemicals, India), Bottom row: K Usha (GenenTech, USA), G Kalaiselvi (Maths Teacher, India, US return), D Joythi (Veeva Systems, USA), R Preethi (Managing Director, Accenture, USA), Madhavi Krishnan (Oxford University, UK, US return), K Radha (USA) and B Subhashini (Pacific Cheese, USA).

Research on lipase at Anna University

It was a pleasure to interact with P Gautam and BS Lakshmi on several aspects of lipase engineering. We (BS Lakshmi, P Kangueane, B Abraham & P Gautam) optimized lipase production using *Candida rugosa* with vegetable oils (coconut, sesame, castor, palm and sunflower) as substrates in 1999 **[4]**. Seasame increased lipase secretion by *Candida rugosa*. The lipase enzyme was known for its stereo-specificity. We (BS Lakshmi, P. Kangueane, Y Gao, YZ. Chen & P Gautam) showed the stereo-specificity of S(+) ibuprofen to *Candida rugosa* lipase in 2000 **[5]**. We (BS Lakshmi, P Kangueane, M Krishnan) also developed a simple, fast, sensitive assay method for *Candida rugosa* lipase using a bi-phasic reaction system **[6]**. We (J James, BS Lakshmi, P Gautam, P Kangueane) further showed the flap movement in different pH conditions using molecular dynamics simulation **[7].** It was fun to feel the joy for working on lipase engineering with BS Lakshmi and P Gautam. P Gautam views everything with a vision for everyone. BS Lakshmi is a scientist with substance and smile.

BIOINFORMATION
Discovery at the interface of physical and biological sciences



Anna University, Chennai - 600 025, India.

GRADE CARD

S. No. 972153

Programme: B.Tech (8 Sem.) Branch :Industrial Bio-Technology

Rollno : 931621 Name :KANGUEANE P

Code	Course Title	Credit	Grade	Code	Course Title	Credit	Grade
I Semester Jul 1992 - Dec 1992				V Semester Jul 1995 - Dec 1995			
BBT-T1	English	4	D	BTE-05	Advanced Molecular Biology	3	A
BBT-T2	Mathematics I	4	B	BTE-06	Fluid MoMonicsHeat Transfer	3	C
BBI-T3	Physics I	3	B	BTE-10	Mass TransEvaSeparation Proc	3	A
BBT-T4	Chemistry I	3	A	BTE-02	Business Management	3	C
BBT-T5	Cell Biology	3	C	BTE-03	Advanced Molecular Biology Lab	2	B
BBT-L1	Computer Programming Practice	3	C	BTE-04	Bioprocess Lab I	2	A
BBT-L2	Physics Lab	1	B	BBE-E1	Tech. Writing & Communication	3	B
BBT-L3	Chemistry Lab	1	B	BTE-E5	Animal Cell Culture	2	A
BBT-L4	Cell Biology Lab I	1	A	CHE-E2	Drugs and Pharmaceutical Tech	3	A
II Semester Jan 1994 - May 1994				BTE-E8	Environmental Biotechnology	3	A
BBT-T7	Mathematics II	4	C	VI Semester Jan 1996 - May 1996			
BBT-T8	Physics II	3	A	BIE-E1	Genetic Engineering	3	A
BBT-T9	Chemistry II	3	A	CHE-E9	Chemical Reaction Engg. I	3	A
BBT-T10	Biochemistry	3	A	BIE-E7	Immunology	3	C
BBI III	Introduction to Engineering	3	B	BIE-E9	Downstream Bioprocessing	3	A
BBT-L5	Engineering Graphics	3	B	BTE-04	Immunology Lab.	2	A
BBT-L6	Biochemistry Lab	2	A	BTE-E5	Downstream Processing Lab.	2	A
MBI-E1	Workshop	2	C	MAE-E5	Numerical Methods	4	D
III Semester Jul 1994 - Dec 1994				BTE-E6	Food Processing	3	B
MAE-E5	Probability and Statistics	4	A	BTE-E4	Metabolic Regulation	3	C
BTE-E1	Bio-Organic Chemistry	3	B	BTE-E3	Biological Spectroscopy	2	A
BTE-02	Electrical & Mechanical Engg.	3	B	BTE-E2	Industrial Attachment Prog.	4	A
BTE-03	Thermodynamics I	3	B	VII Semester Jul 1996 - Dec 1996			
BBE-E4	Principles of Chemical Engg.	3	B	BTE-E8	Industrial Attachment Prog.	5	B
BTE-05	Microbiology	3	C	BTE-E1	Process Dynamics and Control	3	B
BTE-04	Microbiology Lab	2	B	BTE-E6	Bioinformatics	3	C
BTE-E7	Chemical Engg. Lab	2	B	BTE-E3	Bioreactor Design & Operation	3	A
IV Semester Jan 1995 - May 1995				BTE-E4	Advanced Bioprocess Technology	4	B
BTE-01	Bioprocess Principles	3	B	BTE-E7	Genetic Engineering Lab	3	A
BTE-E6	Electronics & Microprocessors	3	C	BTE-E8	Bioprocess Lab II	3	C
BTE-02	Thermodynamics II	3	C	BTE-E2	Plant Biotechnology	3	B
BTE-E3	Instrumental Meth. of Analysis	3	A	BTE-E6	Immunotechnology	3	B
BTE-E4	Genetics & Molecular Biology	3	B	BTE-E5	Protein Engineering	3	A
BTE-05	Comp. Sys. Langs. & Software	4	A	VIII Semester Jan 1997 - May 1997			
BTE-06	Molecular Biology Lab	3	B	BTE-E2	Bioethics	3	B
BTE-E7	Electronics & Instrum. Lab	2	A	BTE-E0	Poll. Abatement&Hazard mgt.in Chemical	3	D
				BIE-E1	CEP - Project	12	A

Semester	I	II	III	IV	V	VI	VII	VIII
GPA	7.25	6.04	8.24	8.83	8.56	8.00	8.48	8.32
Credits Registered	23	23	23	23	24	30	27	19
Credits Earned	23	23	23	23	24	30	27	19

Total credits Earned: 190

CGPA : 8.205

Date : 7 JUL 1997

Controller of Examinations

Figure 2: A truly inter disciplinary curriculum in Industrial Biotechnology created by Kunthala Jayaraman in 1992

Bioinformatics at the National University of Singapore, Singapore (NUS)

National University of Singapore **[2]** was my destination in 2008 to pursue a doctoral degree in Bioinformatics (**Figure 6**) with specific interest in MHC Informatics for the development of Vaccine Science and Technology. Tan Tinwee (**Figure 5**) was the founding Director for the Bioinformatics Centre, NUS. His passion for Molecular Biology, Internet, networking, GRID technology and international multi-lingual Domain Name Server (iDNS) was exceptional. He was the architect of Bioinformatics in Singapore with the help of S Subbiah. The role played by Limsoon Wong, Betty Cheng and Prasanna R Kolatkar (PK) is highly remarkable. S Subbiah solved side chain packing for homology modelling with the Nobel Laureate Micheal Levitt at the Stanford University in the early 90s. He also cracked multiple sequence alignment with Steve Harrison at Harvard University in the late 80s. These methods are magical for creating miracles in modern molecular medicine. Prasanna R Kolatkar (PK) was a pleasant protein crystallographer. PK is an *alumnus* of the University of Texas, Austin and he worked with Micheal Rossmann (the Rossmann protein fold) at Purdue University, USA. Limsoon Wong was the master in biological data mining using Standard Mark-up Language (SML).

Anna University

The Syndicate of the Anna University hereby makes known that

KANGUEANE .P.

has been admitted to the Degree of Bachelor of Technology in INDUSTRIAL BIOTECHNOLOGY, *he having satisfactorily completed the prescribed course of study at the Alagappa College of Technology and having been certified by duly appointed Examiners to be qualified to receive the same and having been placed by them in the First Class with Distinction at the Examination held in the month of* MAY *in the year* 1997.

Given under the Seal of the University

ANNA UNIVERSITY MADRAS

University Buildings, Madras-600 025

Dated -4 SEP 1997

Registrar *Vice - Chancellor*

Figure 4: Graduation certificate in Bachelor of Technology in Industrial Biotechnology

BIOINFORMATION
Discovery at the interface of physical and biological sciences

Figure 5: Tan Tinwee (1999) at the Bioinformatics Centre, National University of Singapore. The centre was hosted at the National University Hospital. He was the architect of Bioinformatics infrastructure in Singapore with the help of S Subbiah. Tan Tinwee was a born leader with patriotism. His birthday falls on the first of January every year along with the New Year celebrations. Simplicity is the speciality of this Singaporean. Singapore is a business centre in Asia with high dynamics in economics through changing commerce. Tan Tinwee managed to secure funds from the Economic Development Board (EBD) and National Science and Technology Board (NSTB) of Singapore. The e-library at the National University of Singapore was the best in the world with access to data from both the western and eastern world. Thus, NUS was a perfect place for Bioinformatics (librarian science in the words of Sydney Brenner) related data mining.

Research on MHC Informatics for Short peptide vaccine design at NUS

Short antigen peptides capable of binding to host HLA molecules (**Figure 7**) can be used to design peptide vaccines by exploiting the T-cell immunity. The design of such a cocktail vaccine is often linked to the antigen peptide diversity from viral/bacterial proteome and the host HLA allele polymorphism **[8-24].** We (P Kangueane, MK Sakharkar, EC Ren and PR Kolatkar) developed a method to predict peptides binding to HLA molecules using side chain packing molecular modeling techniques developed by S. Subbiah (Kangueane *et al.* 2000). It should be noted that S Subbiah made several generous contributions towards this study. We (EC Ren, P Kangueane and PR Kolatkar) also studied the binding of mHag (minor histo-compatibility antigen involved in graft versus host disease) peptides to HLA A alleles (Ren *et al.* 2000). Betty Cheng gave her ORIGIN SGI machine to perform the modeling calculation. Her generosity is generally gentle. We (P Kangueane, MK Sakharkar, EC. Ren and P.R. Kolatkar) studied the structural principles of HLA-peptide binding using a dataset of HLA-peptide crystal structures (Kangueane *et al.* 2001). Adrian Png helped to study the type of inter-atomic interactions at the interfaces of HLA-peptide structures using a dataset (Adrian *et al.* 2002). We did develop the MIDB (MHC-peptide interaction database) to provide gleaned information (Govindarajan *et al.* 2003). Bing Zhao helped to develop a method to compress functional diversity among HLA alleles (Zhao *et al.* 2003a) and this was fundamental for creating a novel model to predict HLA-peptide binding (Zhao *et al.* 2003b). This later helped us to subtype HLA super-types (functional overlap among alleles) in 2005 (Kangueane *et al.* 2005). We then demonstrated the utility of this technology in the design of a gp120 peptide vaccine cocktail vaccine for NeuroAIDS in a book chapter edited by Karl Goodkin (Kangueane *et al.* 2008). Mohana Priya completed class 2 HLA-peptide binding prediction using structural principles (Mohanapriya, 2009; 2010).

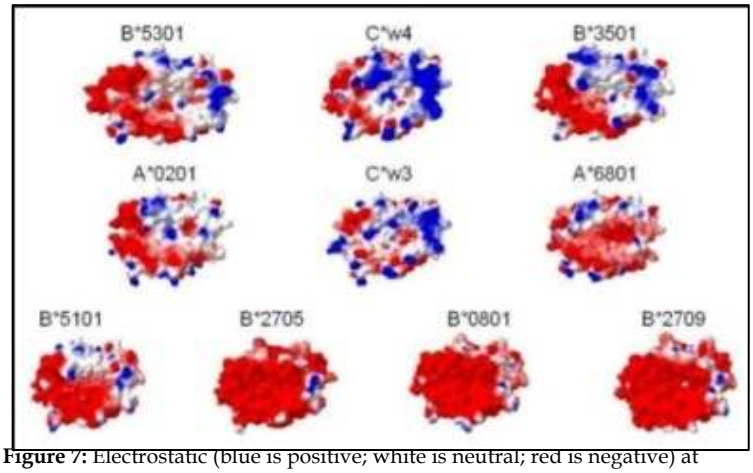


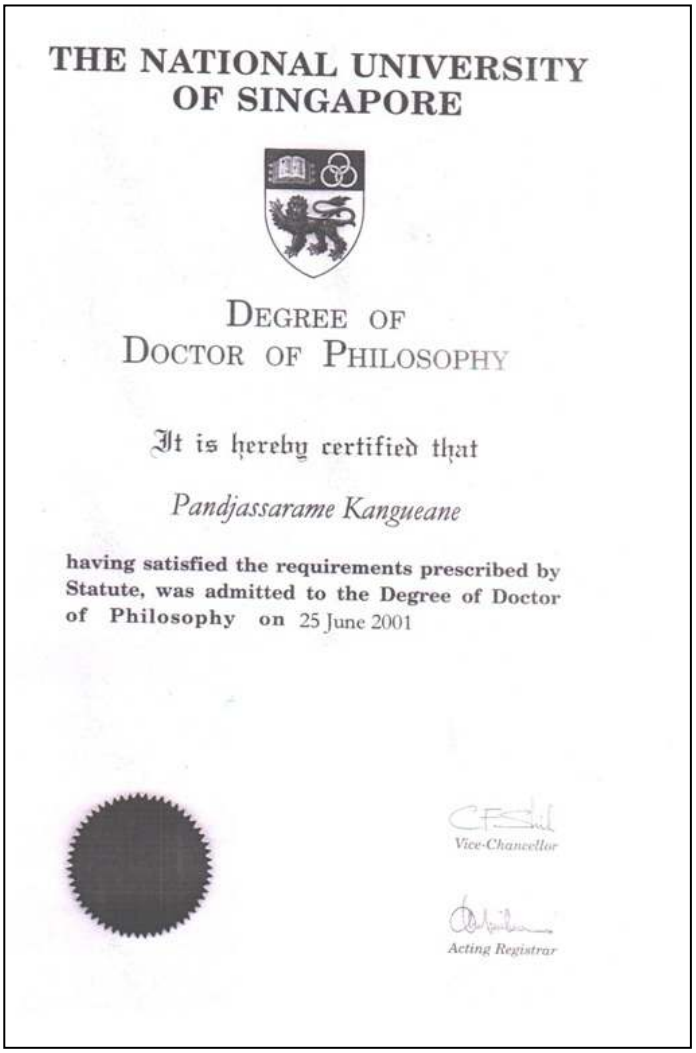
Figure 7: Electrostatic (blue is positive; white is neutral; red is negative) at the peptide binding groove of Human Leukocyte Antigen (HLA) is shown. This varies for different ethnic groups (Caucasoid, black, Hispanic, oriental, pacific islander and Australian aboriginal). HLA typing helps in the selection of donor and recipients in organ transplantation. It is also relevant in the study of disease susceptibility for combat and care **[8-24]**.

Research on Protein-protein interaction (PPI) at IISc, NTU, VITU and AIMST

An opportunity to work on the principles of protein-protein interaction (PPI) (**Figure 8**) at the labs of P Balaram and C Ramakrishnan using a dataset of protein structural complexes during the summer of 1995 was bliss. The work with K Gunasekaran to understand principles of PPI at the Molecular Biophysics Unit, Indian Institute of Science was inspiring. Graduate students at the NANYANG Technological University, Li Lei and Cui Zhanhua showed interest to study protein-protein interaction during 2000 and 2006. Li Lei helped to explore LIGAND effect at the homo-dimer interface (Li *et al.* 2005) and homo-dimer folding (Li *et al.* 2005). Cui Zhanhua helped to identify critical interaction parameters at the hetero-dimer interface (Zhanhua *et al.* 2005) and differentiated hetero-dimer from homo-dimer interfaces (Zhanhua *et al.* 2005). Sajitha Lulu, a graduate student at VITU, India looked at the principles of homo-dimer folding and binding using structural data (Lulu *et al.* 2009; 2007-2008). The contribution

BIOINFORMATION
Discovery at the interface of physical and biological sciences

from V Karthikraja (2009); A Suresh (2009-2010); G Sowmya (2009-2010), G Shamini (2009-2010) and Christina Nilofer (2017) in the understanding of PPI [25-38] is admirable.



THE NATIONAL UNIVERSITY OF SINGAPORE

DEGREE OF DOCTOR OF PHILOSOPHY

It is hereby certified that

Pandjassarame Kangueane

having satisfied the requirements prescribed by Statute, was admitted to the Degree of Doctor of Philosophy on 25 June 2001

Vice-Chancellor

Acting Registrar

Figure 6: Graduation certificate in Doctor of Philosophy in Bioinformatics (Bioinformatics Centre and Department of Microbiology), Faculty of Medicine, National University of Singapore.

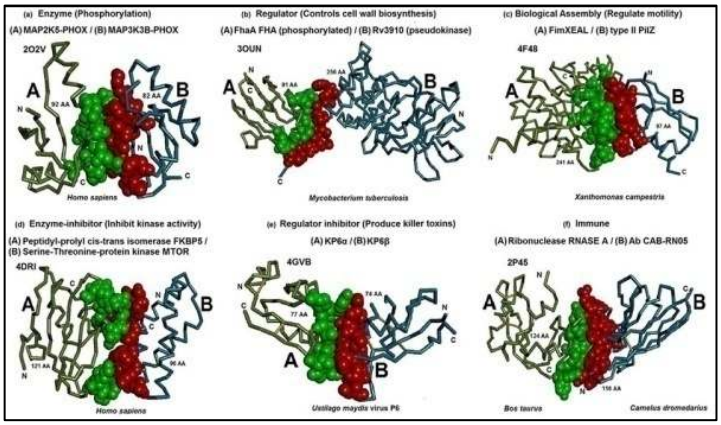


Figure 8: Protein-protein interactions (PPI) are illustrated [**25-38**]. The molecular principles of PPI are key for understanding normal cell division to help differentiate abnormal cell division, referred as cancer in clinical science.

Intron research at NUS and NTU

Meena Kishore Sakharkar collaborated with Sandro J De Souza (currently in Brazil) on intron evolution right from her days at the lab of the noble laureate Walter Gilbert. It was a great pleasure to work with Meena Kishore Sakharkar during 1998-2000 on the development of IEKB (Intron-Exon knowledge base) using ExInt and GenBank (Sakharkar *et al.* 2000). We continued to work on SEGE (single exon genes in eukaryotes) during 2001-2002 (Sakharkar *et al.* 2002). Later, we developed Genome SEGE and examined their features (Sakharkar *et al.* 2004a; Sakharkar *et al.* 2004b; Sakharkar *et al.* 2005). Nidhi Dhandona, Iti Chadurvedi and Kingshuk Gosh made contributions among many others towards these developments. Lee Pern Chern, Xue Hao and Bhagavati Perumal did look into many other issues of introns in eukaryotes. This let to the continued maintenance of ExInt (Sakharkar *et al.* 2005d), development of human alternative splicing database (Sakharkar *et al.* 2004), a study on introns in tubulins (Bhagavati et al. 2005) and gene patterns by exon-intron combinations in the human genome (Sakharkar *et al.* 2005a). We did find that the total length in introns and intergenic DNA on each chromosome is significantly correlated to the chromosome size in both human and mouse genomes (Sakharkar *et al.* 2004; Sakharkar *et al.* 2005). These findings have implications for chromosome design and evolution in eukaryotes. We also further developed the U-genome database containing information on exon-intron-exon in unicellular eukaryotic genomes (Sakharkar *et al.* 2005). Meena Kishore Sakharkar was a true leader in science with passion for data mining using association rules with computer-aided tools [**43-55**].

Research on Gene fusion at NTU:

Meena Kishore Sakharkar was fascinated by gene fusion [**39-41**] in evolution through the work of Manyuan Long at the University of Chicago. Her networking skill is exceptional and she collaborated with Manyuan Long since her friendship days at the labs of Walter Gilbert (Harvard University). Gene fusion is found to mimic operons and protein-protein interfaces in

BIOINFORMATION
Discovery at the interface of physical and biological sciences

prokaryotes. They are also found to exhibit multiple functions and alternative splicing. We provided a comprehensive list of fusion proteins of prokaryotic origin in the human genome (Yu *et al.* 2004). We also suggested that fusion gene products and their evolution have a key role in the selection of complex multifaceted networks (Sakharkar *et al.* 2005). The evolutionary force for gene fusion is illustrated using molecular dynamics simulation of IGPS (Yiting *et al.* 2006).

Figure 9: Jaime Escabedo, Chief Scientific officer (Biology) at Chiron Corporation, Emeryville, California, USA in 2001 during a period when "The Human Genome Project" was completed. He was a true scientist with passion and love for Biology. Moreover, he was open to truth in business. This is not usual in business. There was a heated negotiation to purchase the genome data from Celera Genomics just weeks before the NIH public data was released for free. Celera went broke promptly. Thus, the private to public pressure is pleasant with pain in pleasing the people of this planet.

Figure 10: Precision farming (2012) is perfect for people of present period. Green chillies and Dwarf – Tall (D&T) coconut plants. These D&T are offspring's of cross-pollination of flowers from a tall plant with the dwarf mother plant (rare species).

Service to the society, research, teaching, farming and business

Serving as a Bioinformatics Technology Scientist (Cancer Gene Discovery), **Chiron Corporation** (in deputation from **S*BIO Pte Ltd, Singapore**), Emeryville, Bay Area, California, USA during 2001 was sensible. S*BIO Pte Ltd, Singapore is an (Economic Development Board) EDB funded company founded by Lily Chan, Singapore. S*BIO Pte Ltd acquired technology from Chiron Corporation on its cancer technology platform. This concept was enriching to the minds of many in Singapore. Jaime Escabedo, Chief Scientific Officer (Biology) at Chiron Corporation, Emeryville, California, USA in 2001 during a period when "The Human Genome Project" was completed (**Figure 9**). There was a heated negotiation to purchase the genome data from Celera Genomics just weeks before the NIH public data was released for free. Celera went broke promptly. Thus, the private to public pressure is pleasant with pain in pleasing the people of this planet. Subsequently, my service at **NANYANG Technological University as Assistant Professor** (2002-2006) both teaching and developing cutting edge technologies in the field of Bioinformatics were productive. We founded **Biomedical Informatics (P) Ltd** in 2001. We made considerable progress providing service in the filed. Responsibility as a P**rofessor (Visiting)** at the Vellore Institute of Technology University, India (2007-2009) and **Professor** (Asian Institute for Medical Science and Technology, Malaysia (2009-2011) was engaging. Teaching students was fun at the organizations such as NTU, VIT and AIMST (**Table 1**).

Collaborations with Paul Shapshak (University of Miami, Florida) on several data mining aspects of HIV-1/AIDS related research was always filled with positive vibrations **[56-59].** My association as Associate Editor, BMC Bioinformatics (a UK based Biomed Central publication since 2005) was judicious. Serving as advisors to several students leading to the award of the PhD degree by Research in the field is often sensitive **[60-62]**. My research contributions in Biotechnology and Bioinformatics include that of lipase engineering, vaccine science, genome design, protein-protein interactions and interfaces cholera toxins is a lifetime experience with enthusiasm. These find application in drug discovery and vaccine developments of industrial utility for social benefits. I managed to author several books (**Figure 11**) published by **Springer, USA** (2008; 2009; 2018); **NOVA USA** (2011) and **LAP, Germany** (2011) **[63-69]**. My excitement for farming several crops including sugarcane, peanut, black gram, coconut, lemon, rice and chrysanthemum (Chamomile) since 1990 is often special (**Figure 10**).

Open access to literature:

Access to available literature for advancement through the application of science for the society is secretly sensitive. The quote from BOAI "the promise was that removing access barriers would allow the world to "accelerate research, enrich education, share the learning of the rich with the poor and the poor with the rich … and lay the foundation for uniting humanity in a common intellectual conversation and quest for knowledge" explains everything. Thus, the formation of Bioinformation (**Figure 12**), an open access (free to read) journal in Biology is engaging, entertaining and enterprising **[42].**

BIOINFORMATION
Discovery at the interface of physical and biological sciences

Table 1: Teaching Experience: Computational Biology (M.S students, B.S students – NTU, VITU, AIMST); Bioprocess and Biotechnology (B.S students - NTU); Computing (B.S students - NTU); Molecular Modeling and Drug Design (B.S students – VITU, AIMST); Comparative Genomics (B.S students – VITU, AIMST); Bioinformatics (M. S students, B. S students, VIT, NTU, AIMST)

University	Code	Degree	Course	Year	Semester	Subject	Lecture Hrs	Students #
NTU 02-06	M6545	M. Sc	Biomedical Eng.	Y2 PE	1	Clin. & Comp. Biology	09	50
NTU 02-06	FE1008	B. Eng	Common Eng.	Year 1	1 & 2	Computing (C++)	100	40
NTU 02-06	M489	B. Eng	Mechanical Eng.	Y4 PE	2	Biochem. & Bioprocess.	19	100
VITU 07-08	MPH508	M. Tech	Pharma. Chem.	Year 1	2	Bioinformatics	60	30
VITU 08	5BBTE07	B. Tech	Biotech & Bioinf.	Y4 PE	1	Mol. Mod. & Drug Design	30	95
VITU 08-09	05BIFE04	B. Tech	Bioinformatics	Y3 PE	2	Comparative Genomics	30	36
AIMST 9-11	32108	B.S	Biotechnology	Y2	2	Bioinformatics	48	60
AIMST 9-11	32107	B.S	Biotechnology	Year 3	2	Genomics & Prospective	10	80
AIMST 9-11	33111	B.S	Biotechnology	Year 3	1	Molecular Modeling	40	80
AIMST 9-11	00000	B.S	Biotechnology	Year 3	2	Comparative Genomics	40	30

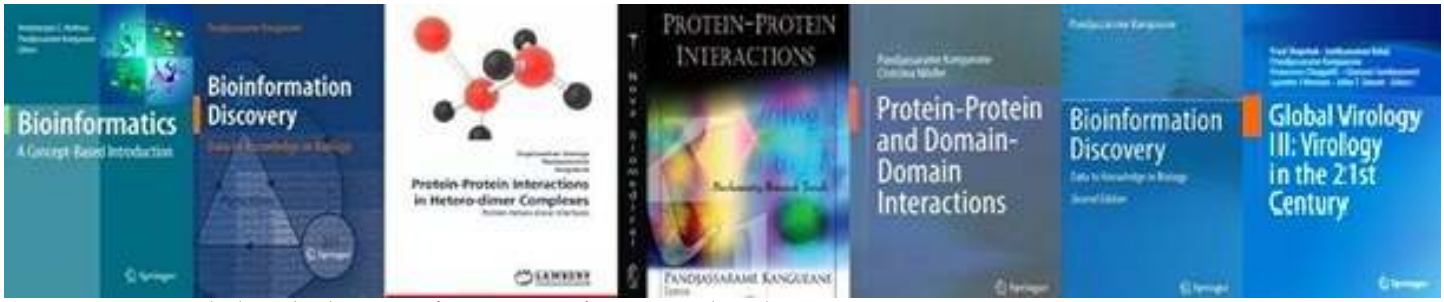


Figure 11: Writing and editing books on Bioinformatics, Bioinformation and Virology

BIOINFORMATION
Discovery at the interface of physical and biological sciences

Figure 12: An open access journal in Biology

Conclusion:

This journey as a scientist, an author of scholarly materials, teacher of higher education, professor, educationalist, editor, journalist, entrepreneur, philanthropist within "possible limits", social reformer, and a farmer over the last 3 decades has been wonderful. The constant hope to bring smile in the face of the under privileged has been both challenging and awesome.

References:

1) https://www.annauniv.edu/
2) https://www.nus.edu.sg/
3) R. Sachidanandham, G. Kalaiselvi, Maintenance requirements in Bacillus sphaericus 1593M under dual substrate limitations estimated at zero growth rate in a total cell retention culture, Bioprocess Engineering 19 (1998) 243-245
4) Lakshmi BS, Kangueane P, Guo Y, Chen YZ, Gautam P. Molecular basis for the stereo-specificity of Candida rugosa lipase (CRL) towards ibuprofen. BIO-CATALYSIS AND BIOTRANSFORMATION. 17: 475 - 486, Jan 2000.
5) Lakshmi BS, Kangueane P, Madhavi K, Mukut K, Gautam P. Solvent hydrophobicity in the interfacial activation of Candida rugosa lipase. JOURNAL OF BIOCHEMISTRY, MOLECULAR BIOLOGY AND BIOPHYSICS. 4: 293-298, Feb 2000.
6) Lakshmi BS, Kangueane P, Abraham B, Pennathur G. Effect of vegetable oils in the secretion of lipase from Candida rugosa (DSM 2031). LETTERS IN APPLIED MICROBIOLOGY. 29: 66-70, Sep 1999.
7) James JJ, Lakshmi BS, Raviprasad V, Ananth MJ, Kangueane P, Gautam P, Insights from molecular dynamics simulations into pH dependent enantio-selective hydrolysis of Ibuprofen esters by Candida rugosa lipase, PROTEIN ENGINEERING, 16(12), 1017-1024, Dec 2003.
8) Ren EC, Kangueane P, Kolatkar P, Lin MT, Tseng LH, Hansen JA. Molecular modeling of the minor histocompatibility antigen HA-1 peptides binding to HLA-A alleles. TISSUE ANTIGENS. 55(1): 24-30, Jan 2000.
9) Kangueane P, Sakharkar MK, Kolatkar PR, Ren EC. Towards the MHC-peptide combinatorics. HUMAN IMMUNOLOGY. 62(5): 539-56, May 2001.
10) Kangueane P, Sakharkar MK, Lim KS, Hao H, Lin K, Ren EC, Kolatkar PR. Knowledge-based grouping of modeled HLA peptide complexes. HUMAN IMMUNOLOGY. 61(5): 460-6, May 2000.
11) P. Kangueane, Designing Short Peptides as Viral Vaccines, (2009) J Proteomics Bioinform S3:6 ISSN: 0974-276X JPB.
12) Mohanapriya A, Lulu S, Kayathri R, Kangueane P, Class II HLA-peptide binding prediction using structural principles, (2009) HUMAN IMMUNOLOGY, 70:159-169.
13) Kangueane P, Sakharkar MK HLA-peptide binding prediction using structural and modeling principles., METHODS IN MOLECULAR BIOLOGY (Clifton, N.J.), 409: 293-299 (2007)
14) Kangueane P, Sakharkar MK, Grouping of class I HLA alleles using electrostatic distribution maps of the peptide binding grooves., METHODS IN MOLECULAR BIOLOGY (Clifton, N.J.), 409: 175-181 (2007).
15) Kangueane P, Sakharkar MK, Structural basis for HLA-A2 supertypes., METHODS IN MOLECULAR BIOLOGY (Clifton, N.J.), 409: 155-162 (2007)
16) Zhao B, Mathura VS, Rajaseger G, Moochhala S, Sakharkar MK, Kangueane P. A novel MHCp binding prediction model. HUMAN IMMUNOLOGY. 64(12): 1123-1143, Dec 2003.
17) Adrian PEH, Rajaseger G, Mathura V, Sakharkar MK, Kangueane P. Types of inter-atomic interactions at the MHC-peptide interface - Identifying commonality from accumulated data. BMC STRUCTURAL BIOLOGY. 2: 1-14, May 2002.
18) Zhao B, Png AE, Ren EC, Kolatkar PR, Mathura VS, Sakharkar MK, Kangueane P. Compression of functional space in HLA-A sequence diversity. HUMAN IMMUNOLOGY. 64(7): 718-28, Jul 2003.
19) Govindarajan KR, Kangueane P, Tan TW, Ranganathan S. MPID: MHC-Peptide Interaction Database for sequence-structure-function information on peptides binding to MHC molecules. BIOINFORMATICS (oxford, England). 19(2): 309-10, Jan 2003.
20) Sowmya G, Vaishnai A, Kangueane P, Structure modeling based computer aided T-cell epitope design (2008) Bio-Algorithms and Med-Systems, 4(8): 5-13 (Invited opening paper)
21) Mohanapriya A, Nandagond S, Shapshak P, Kangueane U., Kangueane P, A HLA-DRB supertype chart with potential overlapping peptide binding function (2010) BIOINFORMATION 4 (7): 300-309.
22) Kangueane P & Sakharkar M.K, T-Epitope Designer: A HLA-peptide binding prediction server. BIOINFORMATION 1(1): 21-24 (2005)

BIOINFORMATION
Discovery at the interface of physical and biological sciences

23) Kangueane P., Sakharkar M.K., Rajaseger G., Bolisetty S., Sivasekari B., Zhao B., Ravichandran M., Shapshak P, Subbiah S. A framework to sub-type HLA supertypes. FRONTIERS IN BIOSCIENCE, 10: 879-886, Jan, 2005.
24) Zhao B, Sakharkar KR, Lim CS, Kangueane P, Sakharkar MK, MHC-peptide binding prediction for epitope based vaccine design, IJIB 1(2):127-140 (2007)
25) C. Nilofer, S. Anshul, A. Mohanapriya, P Kangueane, Protein-protein interfaces are vdW dominant with selective H-bonds and (or) electrostatics towards broad functional specificity Bioinformation 2017, 13(6) 164-173
26) Nilofer C, Sukhwal A, Mohanapriya A, Sakharkar MK, Kangueane P. Small protein-protein interfaces rich in electrostatic are often linked to regulatory function. J Biomol Struct Dyn. 2020 Jul;38(11):3260-3279. doi: 10.1080/07391102.2019.1657040. Epub 2019 Sep 9. PMID: 31495333.
27) Sowmya G, Anita S, Kangueane P. Insights from the structural analysis of protein heterodimer interfaces. Bioinformation. 2011 May 7;6(4):137-43. PubMed PMID: 21572879; PubMed Central PMCID: PMC3092946.
28) Sowmya G, Shamini G, Anita S, Sakharkar M, Mathura V, Rodriguez H, Levine AJ, Singer E, Commins D, Somboonwit C, Sinnott JT, Sidhu HS, Rajaseger G, Pushparaj PN, Kangueane P, Shapshak P. HIV-1 envelope accessible surface and polarity: clade, blood, and brain. Bioinformation. 2011 Mar 22;6(2):48-56. PubMed PMID: 21544164; PubMed Central PMCID: PMC3082861.
29) Shamini G, Ravichandran M, Sinnott JT, Somboonwit C, Sidhu HS, Shapshak P, Kangueane P. Structural inferences for Cholera toxin mutations in Vibrio cholerae. Bioinformation. 2011 Mar 2;6(1):1-9. PubMed PMID: 21464837; PubMed Central PMCID: PMC3064844.
30) Li L, Gunasekaran K, Gan GK, Zhanhua C, Shapshak P, Sakharkar MK, Kangueane P. Structural features differentiate the mechanisms between 2S (2 state) and 3S (3 state) folding homodimers. BIOINFORMATION 1(2): 42-49 (2005)
31) Zhanhua C, Li L, Gan GK, Sakharkar MK, Kangueane P. Protein subunit interfaces: Homo-dimers versus Heterodimers. BIOINFORMATION 1(2): 28-39 (2005)
32) Zhanhua C., Gan GKJ, Lei L, Mathura VS, Sakharkar MK, Kangueane P. Identification of critical heterodimer protein interface parameters by multi-dimensional scaling in Euclidian space. FRONTIERS IN BIOSCIENCE, 10: 844-852, Jan, 2005.
33) Li L., Gan GK., Cui Z., Sakharkar MK., Kangueane P. Generation of a dataset for studying ligand effect on homodimer interface, FRONTIERS IN BIOSCIENCE 10, 1977-1984 May 1, 2005
34) Suresh A, Lalitha P, Kangueane P (2010) CART Assignment of Folding Mechanisms to Homodimers with Known Structures. J Proteomics Bioinform 3: 279-285. doi:10.4172/jpb.1000152
35) Vaishnai A, Sowmya G, Kalaivanii J, Ilakya S, Kangueane U, Kangueane P, Interaction modes at protein hetero-dimer interfaces (2010), BIOINFORMATION 4 (7): 310-319.
36) Suresh A, Karthikraja V, Lulu S, Kangueane U, Kangueane P, A decision tree model for the prediction of homodimer folding mechanism, (2009), BIOINFORMATION 4 (5): 197-205.
37) Karthikraja V, Suresh A, Lulu S, Kangueane U, Kangueane P., Types of interfaces for homodimer folding and binding (2009) BIOINFORMATION, 4:101-111.
38) Lulu S, Karthikraja V, Suresh A. Mohanapriya A, Kayathri R, Kangueane P, Structural features for homodimer folding mechanism (2009) J. Mol. Graphics. Modeling, 28: 88-94.
39) Sakharkar MK, Kangueane P, Sakharkar KR and Zhong Z, Huge proteins in the human proteome and their participation in hereditary diseases, IN SILICO BIOLOGY 6(4): 275-279 (2006)
40) Li L, Zhao B., Zhanhua. C., Gan GK., Sakharkar MK., Kangueane P. Identification of hot spot residues at protein-protein interface. BIOINFORMATION 1(4): 121-126 (2006)
41) Yiting Y, Li L., Sakharkar MK, Kangueane P. Insight into gene fusion from molecular dynamics simulation of fused and un-fused IGPS (Imidazole Glycerol Phosphate Synthetase) BIOINFORMATION 1(3): 99-104 (2006)
42) Kangueane P, Welcome to "Bioinformation" a data journal, BIOINFORMATION, 1(1): 1. (2005).
43) Sakharkar KR, Chaturvedi I, Chow VTK, Kwoh CK, Kangueane P. and MK Sakharkar u-Genome: A database on genome design in unicellular genomes, IN SILICO BIOLOGY 5(5-6), 611-615 (2005)
44) Sakharkar MK, Perumal BS, Sakharkar KR, Kangueane P., An analysis on gene architecture in human and mouse genomes. IN SILICO BIOLOGY 5(4), 347-365 2005.
45) Sakharkar MK, Kangueane P, Perumal BS, Chow VTK, Sorscher E., Sakharkar KR, Hill A., Human genome – from pieces to patterns. FRONTIERS IN BIOSCIENCE 10, 2576-2584, Sep 1, 2005.
46) Perumal BS, Sakharkar KR, Chow VTK, Kangueane P, Sakharkar MK., Intron position conservation across eukaryotic lineages in tubulin genes. FRONTIERS IN BIOSCIENCE 10, 2412-2419, Sep 1, 2005.
47) Sakharkar MK. Chow VTK., Ghosh K., Chaturvedi I., Lee PC., Bagavathi SP., Shapshak P., Subbiah S., Kangueane P. Computational prediction of SEG (Single Exon Gene) function in humans FRONTIERS IN BIOSCIENCE 10, 1382-1395 May 1, 2005
48) Sakharkar MK., Yiting Y, Chow VTK, Kangueane P. Insights to metabolic network evolution by fusion proteins FRONTIERS IN BIOSCIENCE 10: 1070-1078, May, 2005
49) Sakharkar MK, Perumal BS, Lim YP, Lee PC, Yiting Y, Kangueane P. Alternatively spliced human genes by exon skipping - A database (ASHESdb), IN SILICO BIOLOGY, 5(3): 221 – 225, Web:0021, Dec 2004.
50) Sakharkar MK, Chow VTK, Chaturvedi I, Mathura VS, Shapshak P, Kangueane P, A report on single exon genes (SEG) in eukaryotes. FRONTIERS IN BIOSCIENCE, 9: 3262-3267, Sep 2004.
51) Sakharkar MK, Chow VTK, Kangueane P, Distributions of exons and introns in the human genome. IN SILICO BIOLOGY, 4(4), 387-393. WEB: 0032, Jun 2004.
52) Sakharkar MK, Kangueane P, Genome SEGE: A database for 'intronless' genes in eukaryotic genomes BMC BIOINFORMATICS, 5(1): 67, Jun 2004.
53) Sakharkar MK, Kangueane P, Woon TW, Tan TW, Kolatkar PR, Long M, de Souza SJ. IE-Kb: intron exon Knowledge Base. BIOINFORMATICS (oxford, England). 16(12): 1151-2, Dec 2000.
54) Yiting Y, Chaturvedi I, Liew KM, Kangueane P, Sakharkar MK., Can Ends Justify the Means? Digging deep for human fusion genes of prokaryotic origin. FRONTIERS IN BIOSCIENCE, 9: 2964-2971, Sep 2004.
55) Sakharkar MK, Kangueane P, Petrov DA, Kolaskar AS, Subbiah S. SEGE: A database on 'intron less/single exonic' genes from eukaryotes. BIOINFORMATICS (oxford, England). 18(9): 1266-7, Sep 2002.
56) Shapshak P, Duncan R, Turchan J, Nath A, Minagar A, Kangueane P, Davis W, Chiappelli F, Elkomy F., Seth R, and Kazic T. Bioinformatics models in drug abuse and Neuro-AIDS: Using and developing databases. BIOINFORMATION 1(3): 86-88 (2006)
57) Shapshak P, Duncan R, Turchan J, Nath A, Minagar A, Kangueane P, Davis W, Chiappelli F, Elkomy F., Seth R, and Kazic T. Bioinformatics models in drug abuse and Neuro-AIDS: Using and developing databases. BIOINFORMATION 1(3): 86-88 (2006)
58) Shapshak P, Duncan R, Kangueane P, Somboonwit C, Sinnott J, Commins D, Singer E, Levine A. HIV associated dementia and HIV encephalitis II: Genes on chromosome 22 expressed in individually microdissected Globus pallidus neurons (Preliminary analysis). Bioinformation. 2011;6(5):183-6. Epub 2011 May 26. PubMed PMID: 21738310; PubMed Central PMCID: PMC3124795.
59) Shapshak P, Duncan R, Nath A, Turchan J , Kangueane P, Shapshak SAM, Rodriguez H, Duran EM, Ziegler F, Amaro E, Lewis A, Rodriguez A, Minagar A, Davis W, Seth R, Chiappelli F, and Kazic T. Gene Chromosomal Organization and Expression in Cultured Human Neurons Exposed to Cocaine and HIV-1 proteins gp120 and tat: Drug Abuse and NeuroAIDS. FRONTIERS IN BIOSCIENCE 11, 1774-1793 (2006)
60) Jayanthi M., Udaya Prakash, N.A, Kangueane P, Sekar K. Effect of Disulfide Bonds in Antifungal Peptide from Petunia Hybrida: A Molecular Dynamics Study (2009) OPEN STRUCTURAL BIOLOGY JOURNAL, 3:84-93.
61) Udaya Prakash NA, Jayanthi M, Sabarinathan R, Kangueane P, Mathew L, Sekar K. Evolution, homology conservation, and identification of unique sequence signatures in GH19 family chitinases. J Mol Evol. 2010 May;70(5):466-78. doi:10.1007/s00239-010-9345-z. Epub 2010 May 18. PubMed PMID: 20480157.
62) Jayanthi M., Kangueane P., Udaya Prakash N.A., Sekar K. Influence of disulfide bonds on the conformation of the antifungal protein from Eucommia ulmoides oliver (2009) OPEN STRUCTURAL BIOLOGY JOURNAL, 3:94-103.
63) Mathura V.S., Kangueane P. (ed.). Bioinformatics: A Concept-Based Introduction, Pages 1-200, ISBN: 978-0-387-84869-3 e-ISBN: 978-0-387-84870-9, 23 illus., Hardcover, SPRINGER New York, USA, 2008, US$ $69.95
64) Kangueane P., (Single author) Bioinformation Discovery: From data to knowledge in Biology, Pages 1-250, ISBN: 978-1-4419-0518-5, ~180 pages 82 illus., Hardcover, SPRINGER, New York, USA, 2009, approx. US $159.00
65) Kangueane P., (Editor) Protein-protein Interactions, Hardcover, NOVA publisher, USA, 2010, ISBN: 978-1-61761-548-1, ~200 pages with 140 illus., approx. US $140.50
66) Kangueane P & Nilofer C, Protein-Protein & Domain-Domain Interactions, 2018, Springer Nature, USA ISBN: 978-981-10-7347-2 [180 pages with 200 illustrations in colour]
67) Kangueane P., (Single author) Bioinformation Discovery: From data to knowledge in Biology, Pages 1-300, ISBN: 978-3-319-95327-4 2nd Edition. Hardcover, SPRINGER NATURE, New York, USA, 2018
68) Gopichandran Sowmya, Pandjassarame Kangueane, Protein-Protein Interactions in Hetero-dimer Complexes: Protein Hetero-dimer Interfaces, LAP Lambert Academic Publishing (2011-06-02) ISBN-13: 978-3-8443-8546-5; ISBN-10: 3844385460; EAN: 9783844385465; € 49.00
69) Shapshak, P., Balaji, S., Kangueane, P., Chiappelli, F., Somboonwit, C., Menezes, L.J., Sinnott, J.T. (Eds.) Global Virology III: Virology in the 21st Century Springer International Publishing, 2019 eBook ISBN 978-3-030-29022-1 DOI 10.1007/978-3-030-29022-1 Hardcover ISBN 978-3-030-29021-4 SPRINGER Nature, Switzerland

Citation: Kangueane, Bioinformation 17(1): 29-36 (2021)