Shoba Ranganathan

Professor & Chair of Bioinformatics

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***NATIONALITY**: AUSTRALIAN*

ACADEMIC BACKGROUND

1983-84	**Post-Doctoral Research** – Institut de Biologie Physico-Chimique, Fondation Edmond de Rothschild, Laboratoire de Biochimie quantique associé au CNRS, Paris, France with *Prof. B. Pullman and Mme. Pullman A* – Computational Biology
1978-83	**PhD** Chemistry – Indian Institute of Technology Delhi, India – "Quantum Chemical Studies of quadratic potential functions using CNDO/Force method and compliance constant formalism" supervisors: *Prof. Murthy ASN*
1976-78	**MSc** Chemistry – Indian Institute of Technology Madras, Chennai, India – "Elucidation of New Atomic Screening Constants" – supervisor: *Prof. M.S. Gopinathan*
1973-76	**BSc** Chemistry – University of Madras, Chennai, India

SCHOLARSHIPS AND AWARDS

2006-08	UNESCO Chair of Biodiversity Informatics
1993-95	HB & FM Gritton Research Fellowship of the University of Sydney
1990-92	Biophysics Fellow, International Centre for Theoretical Physics, Trieste, Italy
1983-84	French Government Scholarship for Post-Doctoral Research
1973-83	National Science Talent Scholarship of the Government of India for BSc/MSc/PhD education in Basic Science

PROFESSIONAL EXPERIENCE

2004-present	Chair Professor of Bioinformatics, Macquarie University, Australia
2012-present	Member, NH&MRC Expert Panel on Bioinformatics and Biostatistics
2004-2013	Adjunct Professor, National University of Singapore, Singapore
2006-2007	Visiting Scientist, Institute for Infocomm Research (I2R), Singapore
2006-2008	UNESCO Chair of Biodiversity Informatics, Macquarie University, Australia
2001-2003	Associate Professor – Dept. of Biochemistry (Faculty of Medicine) & Dept. of Biological Sciences (Faculty of Science), National University of Singapore
2000-2001	Research Associate Professor – Bioinformatics Centre, National University of Singapore, Singapore
1999-2000	Consultant: Molecular Modelling - eBioinformatics Pty. Ltd., Australia
1998-2000	Research Fellow - Australian Genomic Information Centre, University of Sydney, Australia
1995-1998	Research Fellow - Division of Biochemistry & Molecular Biology, John Curtin School of Medical Research, Australian National University, Australia
1993-1995	HB & FM Gritton Research Fellow - Department of Biochemistry, University of Sydney, Australia
1991-93	Information Scientist - Bioinformatics Centre, Jawaharlal Nehru University (JNU), New Delhi, India (secondment from University of Delhi)

1985-93	Senior Lecturer and Head, Chemistry Department (1990-91) - Maitreyi College, University of Delhi, India
1985	Lecturer - Gargi College, University of Delhi, India
1985	Research Associate with Prof. Peter Politzer, at the Department of Chemistry, University of New Orleans, USA

CURRENT RESPONSIBILITIES

- Graduate Research Program in Bioinformatics
- Master of Science: focussing on Science Leadership, Entrepreneurship and Innovation
- Provide education, training and consultancy in Bioinformatics

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PROFESSIONAL APPOINTMENTS (LAST 5 YEARS)

- **Director (2016-)** – ***Asia-Pacific Bioinformatics Network Pty. Ltd.,*** Singapore
- **Editor-in-Chief – *Encyclopedia of Bioinformatics and Systems Biology*** (http://mrw.elsevier.com/BICB/index.html)
- **Section Editor: Bioinformatics – *Encyclopedia of Life Sciences*** (http://mrw.elsevier.com/LIFE/index.html)
- **Life Member & Past Director** (2003-5) – ***International Society for Computational Biology*** (ISCB; www.iscb.org) and Chair (2005) of Education Committee; Member: ISCB Conference & Education Committees
- **President (2005-2016)** – ***Asia-Pacific Bioinformatics Network*** (APBioNet; www.apbionet.org)
- **External Examiner** (2009-2012) - University of Malaya Bioinformatics Degree program
- **Editorial Board Member –** PLoS ONE, BMC Bioinformatics, BMC Proceedings, BMC Research Notes, Immunome Research, Frontiers in T Cell Biology.
- **Associate Editor** - BMC Bioinformatics.
- **Journal Referee** – Trends in Immunology, PLoS One, PLoS Computational Biology, PLoS Genetics, PLoS NTDs, Genome Biology, Genome Research,Heredity, Biochemistry, Bioinformatics, BMC Genomics, BMC Pharmacology, Biodata Mining, Journal of Proteome Research, Nucleic Acids Research, Protein Science, Protein Engineering, Design and Selection, Proteins, Molecular Genetics and Genomics, *In silico* Biology, Viral Immunology
- **Conference Chair –** International Conference in Bioinformatics (InCoB) 2014
- **Chair – Program Committee**, InCoB, 2006-17.
- **Grant Reviewer** – Australian Research Council; National Health and Medical Research Council, Australia; Medical Research Council, UK; Wellcome Trust, UK; Biomedical Research Council, Singapore; UGC, Hong Kong; FBBVA, Spain, National Science Foundation, USA.
- **Tenure/Promotion Reviewer** – University of Chicago at Illinois, USA; University of Arkansas at Little Rock, USA; MD Anderson Cancer Center, Houston, USA; Nanyang Technological University, Singapore; Academia Sinica, Taiwan; Khalifa University of Science and Technology, UAE.
- **Member** – Human Proteome Organization (HUPO) & co-Chair, CompMS

AREAS OF EXPERTISE

Bioinformatics and Computational Biology

SPECIAL INTERESTS

- Genome, Transcriptome and Proteome analysis
- Protein interactions and networks
- Structural Immunoinformatics
- Biodiversity Informatics
- Chemoinformatics

RESEARCH EXPERIENCE

- Genome annotation and comparative geneome analysis
- Transcriptomics: EST analysis and alternative splicing
- Protein Structure, Function and Evolution
- Immunoinformatics: candidate peptide vaccine prediction and complement activation
- Systems Biology: protein-protein Interactions, pathways and networks.

COMPUTER SKILLS

- Parallel and grid computing
- Artificial intelligence and machine learning approaches
- Semi-empirical/*ab initio* quantum and hybrid quantum/molecular mechanical methods
- Secondary and tertiary structure prediction and comparative protein modelling

TEACHING EXPERIENCE

- Graduate level Bioinformatics modules: **MSc** Bioinformatics, NUS
- Bioinformatics lectures: **BSc** and **M** Biotechnology, Macquarie University, Sydney
- Biochemistry: **BSc/MSc/PG Dip**, Macquarie University, Sydney
- Sequence Analysis: **PhD** Biotechnology, JNU, India
- Physical, Analytical & Environmental Chemistry – **BSc**, University of Delhi, India
- Physical Chemistry: **UG**, University of New Orleans, USA

SUPERVISION OF STUDENTS/RESEARCHERS

- **Macquarie University:**
    - Post-doctoral Fellow: A. Cootes, J.M. Khan, G. Garg, A. Mohamedali.
    - Ph.D.: 2007: D. Bollina, 2008: S.H. Nagaraj, 2011: J. Gaikwad, J.M. Khan, V. Khanna, 2012: G. Kumar, R. Menon, 2013: G. Garg, 2016: S. Gopichandran, 2017: M.T. Islam, A. Hardianto.
    - Ph.D.: A. Jabeen, Z. Noor, D. Southwood.
    - M. Phil. : M.T. Islam (2010)
    - MSc. Biotechnology: K. Patil (2006), J. Khan (2006), T. Hyunh (2011), DL Hyunh (2013), I Nawar (2014), C. Fernandes (2015), A.A.A. Alnakli
    - Hons.: J. Lenffer (2005), C. Ng (2005, UNSW), C. Wang (2006, UNSW)
- **National University of Singapore Graduate Program in Bioinformatics:**
    - M.Sc. by research: K.R. Govindarajan (2002), Anita Suresh (2003)
    - Ph.D.: 2006: B.T.K. Lee, G. Vivek, P.J.T. Tan, K. Lesheng, J.C. Tong (winner of 2008 TR35 Young Innovators award from MIT, USA and 2009 Singapore Youth Award), 2009: L.J.K. Wee, K.H. Choo
    - Hons.: L. Ming (2002), J.C.T. Wah (2003), L.J.K. Wee (2003)
    - UROPS: S. Liang (2004)
- **University of Sydney**
    - PDF: J. Flanagan, AGIC, Australia (1999)

GRANTS (LAST 10 YEARS - FROM 2007)

- **Co-PI - Australian Research Council Discovery Project grant, 2018-20:** Searching for near-exact protein models, A$438K
- **Co-PI - Australian Research Council LIEF grant, 2015:** A multi-omics platform for molecular evolution and developmental biology, A$540K
- **Co-PI - National Health & Medical Research Council Project Project grant, 2012-14:** Analysis and manipulation of the genome-wide integration signatures of gamma-retroviral and lentiviral vectors in human haematopoietic stem cells, A$590K
- **Co-PI - National Health & Medical Research Council Project grant APP 1028092, 2012-14:** Investigation of Australian and Papua New Guinean Traditional Medicines for Drug Discovery and Cultural Preservation, A$361K

- **PI - Atlas of Living Australia/CSIRO, 2011-12:** Customary Medicinal Knowledgebase (CMKb) Data Integration, A$50K
- **Co-PI – Australian Research Council LIEF grant, 2009**: A high performance computing cluster and storage for the INTERSECT Consortium of NSW, A$500K
- **Co-PI – Australian Research Council Centre of Excellence in Bioinformatics extension, 2008-2010:** A$3.3M
- **Co-PI – National Health & Medical Research Council Project Complementary and Alternate Medicine, 2008-2010:** Alternative Medicines from Medicinal Plants of Aboriginal People of Northern New South Wales, A$150K

PRESENTATIONS (LAST 5 YEARS; *INVITED)

2017* *Accelerating the Search for Human Proteome's "Missing Proteins"* – Indian Institutte of Technology Madras, Chennai, India, Feb. 2017

2016* *Accelerating the Search for Human Proteome's "Missing Proteins"* – 12th International Conference of the Brazilian Association of Bioinformatics and Computational Biology (AB^{3}C) (X-meeting 2016), Belo Horizonte, Brazil, Nov. 2016

2016* *Careers in Bioinformatics* – 1st Brazilian Student Council Symposium, ISCB Regional Student Group, Belo Horizonte, Brazil, Nov. 2016

2016* *Zooming in on protein-protein interaction sites from structural modelling and docking* – Flinders Medical Centre, Adelaide, Oct. 2016.

2016* *Acceletarting the Search for Human Proteome's "Missing Proteins"* – 15th International Conference On BioInformatics (InCOB 2016), Singapore, Sept. 2016

2016* *A systems approach to biomarker discovery* - 2nd Hunter Systems Meeting, Lovedale, April 2016

2015* *Biomarker discovery in ovarian cancer - a systems approach* – BioInfoSummer 2015, Sydney, Dec. 2015

2015* *Biomarker discovery in ovarian cancer – a Systems approach* – 16th International Conference on Systems Biology, Singapore, Nov. 2015

2015* *Integrin αvβ6- uPAR interaction site from modelling as a potential therapeutic target in cancer*, International Molecular Graphics and Modelling Symposium, Singapore, Nov. 2015

2015* *Structural Features of Protein Interfaces* – 2015 International Workshop and Summer School on Biological Big Bytes, Nanning, China, Sept. 2015

2015* *Biomarkers for ovarian cancer using an integrated approach in a Boolean framework* – 2015 Genome Rearrangements Symposium, Sydney, Apr. 2015

2015* *Structural Immunoinformatics: towards rational design of MHC epitopes for T cell activation* - 5th Annual Symposium of the Cluster of Excellence "Inflammation at Interfaces," Kiel, Germany, Feb. 2015

2014* *Big Data to Knowledge: Using Bioinformatics to develop personalized health care using -omics data*, Perdana University - Centre for Bioinformatics (PU-CBi) Asia-Pacific Bioinformatics Network Joint Inaugural Lecture, Serdang, Malaysia, Nov. 2014

2014 *Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the "Missing" Human Proteome,* Madrid, Spain, Oct. 2014

2014* *Bioinformatics strategies for Chr 7-HPP* - HUPO HPP (Human Proteome Project) Workshop, Segovia, Spain, Oct. 2014

2014* *Unlocking the Puzzling Biology of the Black Périgord Truffle Tuber melanosporum* – 19th Lorne Proteomics Symposium, Lorne, Feb. 2014

2014* *Unlocking the Puzzling Biology of the Black Périgord Truffle Tuber melanosporum* – Australian Truffle Growers Association 2014 Conference, Launceston, Sept. 2014

2013* *Integrated Proteome Analysis Facility - an eResearch approach* - CSIRO Computational and Simulation Sciences and eResearch Annual Conference, Melbourne, Australia, Mar. 2013.

PUBLICATIONS (IN REVERSE CHRONOLOGICAL ORDER)

BOOKS

1. Roitberg BD, Cotter PD, Dixon B, Giordano A, O'Neill SD, Pentimalli F, **Ranganathan S**, Sharfstein ST, Vitale I, Wilson K, Yelon D, Zarafoza O, Zhou HX (Eds) (2016) Reference Module in Life Sciences, Elsevier, ISBN: 978-0-12-809633-8
2. Tong JC, **Ranganathan S** (2013) Computer-aided vaccine design, Woodhead Publishing Series in Biomedicine No. 23, Woodhead, Cambridge, UK, pp 1-164.
3. Indigenous Bioresources Research Group (Packer J, Gaikwad J, Harrington D, **Ranganathan S**, Vemulpad S, Jamie J) and Yaegl Aboriginal Elders (2011): Yaegl Medicinal and Plant Resources Handbook 2011, Edition 1, Macquarie University, Sydney, 978-1-74138-361-4, pp.1-72.
4. Davies MN, **Ranganathan S,** Flower DR (eds.) (2010) Bioinformatics for Immunomics, Springer, New York.
5. Schönbach C, **Ranganathan S,** Brusic V (eds.) (2008) Immunoinformatics, Immunomics Reviews (vol. 1), Springer.

BOOK SECTIONS

1. **Ranganathan S**. (2017) Bioinformatics. In: Roitberg BD, Cotter PD, Dixon B, Giordano A, O'Neill SD, Pentimalli F, Ranganathan S, Sharfstein ST, Vitale I, Wilson K, Yelon D, Zarafoza O, Zhou HX (Eds) Reference Module in Life Sciences, Elsevier, ISBN: 978-0-12-809633-8
2. Islam MT, Mohamedali A, Ahn SB, Nawar I, Baker MS, **Ranganathan S** (2017) A systematic bioinformatics approach to identify high quality MS data and functionally annotate proteins and proteomes. In: Methods in Molecular Biology, 1549, 163-176. doi: 10.1007/978-1-4939-6740-7_13.
3. Islam MT, Mohamedali A, Fernandes CF, Baker MS, **Ranganathan S** (2017) *De novo* peptide sequencing: deep mining of high-resolution mass spectrometry data. In: Methods in Molecular Biology, 1549, 119-134. doi: 10.1007/978-1-4939-6740-7_10.
4. **Ranganathan S** (2014) Advanced *in silico* analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance. In: Noor, NM (ed.) Bioinformatics in Systems Biology & Cryopreservation in Agrobiodiversity. Penerbit University Kebangsan Malaysia, Selangor, Malaysia, ISBN: 978-967-412-247-8, pp. 35-57.
5. Khanna V, **Ranganathan S** (2015) Chemogenomics approach to computer-aided drug discovery. In: Sakharkar K, Sakharkar MK, Chandra R (Eds.) Post-Genomic Approaches in Drug and Vaccine Development, River Publishers, ISBN: 9788793102842*,* pp. 91-111.
6. **Ranganathan S** (2013) Adaptive Immune System. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306219.html
7. **Ranganathan S** (2013) T cell Signaling. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306227.html
8. **Ranganathan S** (2013) T Cell Activation. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306225.html
9. **Ranganathan S** (2013) Structural Immunoinformatics. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306224.html

10. **Ranganathan S** (2013) Reverse Vaccinology. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306223.html
11. **Ranganathan S** (2013) T Cell Epitopes. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306226.html
12. **Ranganathan S** (2013) TR Germline Bias. In: Dubitzky W., Wolkenhauer O., Cho K., Yokota H. (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg, 2013. URL: http://www.springerreference.com/docs/html/chapterdbid/306229.html
13. **Ranganathan S** (2013) pMHC epitope. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. URL: http://www.springerreference.com/docs/html/chapterdbid/306228.html
14. Khan J, **Ranganathan S** (2013) TR recognition of MHC-peptide complexes. In: Dubitzky W, Wolkenhauer O, Cho K, Yokota H (Ed.) Encyclopedia of Systems Biology: SpringerReference (www.springerreference.com). Springer-Verlag Berlin Heidelberg. DOI: 10.1007/SpringerReference_306267
15. Garg G, **Ranganathan S** (2013) High-throughput functional annotation and data mining of fungal genomes to identify therapeutic targets. In: Eds. Gupta VK, Tuohy M, Ayyachamy M, Turner KM, O'Donovan A. Laboratory protocols in fungal biology: current methods in fungal biology. Springer, New York, USA. ISBN 978-1-4614-2355-3, Invited book chapter, pp.559-564.
16. Kumar G, **Ranganathan S** (2013) Biological data integration using network models. In: Elloumi M, Zomaya AY (Eds). Biological Knowledge Discovery Handbook: Prepossessing, Mining and Postprocessing of Biological Data, Wiley Series in Bioinformatics. John Wiley & Sons, New Jersey. ISBN: 978-1-1181-3273-9, pp.155-173, *invited chapter.*
17. Packer J, Gaikwad J, Harrington D, **Ranganathan S**, Vemulpad S, Jamie J (2012): Medicinal Plants of New South Wales: In: Singh RJ (Ed.) Genetic Resources, Chromosome Engineering and Crop Improvement Series: Medicinal Crops, CRC Press, Taylor & Francis Group, USA. 259-296.
18. Chacko E, **Ranganathan S** (2011): Graphs in Bioinformatics, in Algorithms. In: Elloumi M, Zomaya AY (Eds.) Computational Molecular Biology: Techniques, Approaches and Applications, Wiley, pp.193-219.
19. Kumar G, **Ranganathan S** (2011): Untangling Biological Networks Using Bioinformatics. In: Elloumi M, Zomaya AY (Eds.) Algorithms in Computational Molecular Biology: Techniques, Approaches and Applications, Wiley, pp.867-892.
20. Khanna V, **Ranganathan S** (2011): *In Silico* Methods for the Analysis of Metabolites and Drug Molecules. In: Elloumi M, Zomaya AY (Eds.), Algorithms in Computational Molecular Biology: Techniques, Approaches and Applications, Wiley, pp.363-383.
21. Gaikwad J, Wilson K, Kohen J, Vemulpad S, Jamie J, **Ranganathan S** (2011): Combining Ethnobotany and Informatics to Discover Knowledge from Data. In: Rai M, Acharya D, Rios JL (Eds.), Ethnomedicinal Plants: Revitalization of Traditional Knowledge of Herbs, Science Publishers, USA, pp.444-457.
22. Khan JM, Tong JC, **Ranganathan S** (2010) Structural Immunoinformatics: understanding MHC-Peptide-TR binding. In: Davies N, Ranganathan S, Flower DR (Eds.), Bioinformatics for Immunomics, Springer, New York, pp.77-93.

23. **Ranganathan S**, Tong JC (2007) A Practical Guide to Structure-based Prediction of MHC Binding Peptides. In: Flower DR (Ed.), Immunoinformatics: predicting Immunogenicity *in silico,* Humana Press, Methods in Molecular Biology, vol. 409, pp.297-305.
24. **Ranganathan S** (2003) Molecular Modeling on the web, Biocomputing. In: Brown SM (Ed.) Computer Tools for Biologists, Biotechniques Press, Eaton Publishing, Westborough, USA, chap. 49, pp. 411-417.
25. Gready JE, **Ranganathan S,** Cummins PL (1998) Reaction Mechanisms in Enzyme Active Sites using a "Divide and Conquer" Approach: Hybrid Quantum and Molecular Mechanics (QM/MM). In: Michalewicz MT, Witten M (Eds) Proceedings of the 2nd CSIRO Symposium on Computational Challenges in Life Sciences, CSIRO, Melbourne, pp. 201-212.

JOURNALS

1. Hardianto A, Yusuf M, Liu F, **Ranganathan S** (2017) Exploration of charge states of balanol analogues acting as ATP-competitive inhibitors in kinases. *BMC Bioinformatics*. 18(Suppl 16):572
2. Mohamedali A, Ahn SB, Sreenivasan VKA, **Ranganathan S**, Baker MS (2017) Human Prestin: A Candidate PE1 Protein Lacking Stringent Mass Spectrometric Evidence? *J Proteome Res.* 16, 4531-4535.
3. Jiao X, **Ranganathan S** (2017) Prediction of interface residue based on the features of residue interaction network. *J Theor Biol*. 432:49-54.
4. Baker MS, Ahn SB, Mohamedali A, Islam MT, Cantor D, Verhaert PD, Fanayan S, Sharma S, Nice EC, Connor M, **Ranganathan S** (2017) Accelerating the search for the missing proteins in the human proteome. *Nat Commun.* 8, 14271.
5. Patel AR, Hardianto A, Ranganathan S, Liu F (2017) Divergent response of homologous ATP sites to stereospecific ligand fluorination for selectivity enhancement. *Org Biomol Chem.* 15, 1570-1574.
6. Schönbach C, Verma C, Bond PJ, **Ranganathan S** (2016) Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). *BMC Bioinformatics*. 17 Suppl 19, 524.
7. Schönbach C, Verma C, Wee LJ, Bond PJ, **Ranganathan S** (2016) 2016 update on APBioNet's annual international conference on bioinformatics (InCoB). *BMC Genomics*. 17 Suppl 13,1036.
8. Liu F, Koval M, **Ranganathan S**, Fanayan S, Hancock WS, Lundberg EK, Beavis RC, Lane L, Duek P, McQuade L, Kelleher NL, Baker MS (2016) Systems Proteomics View of the Endogenous Human Claudin Protein Family. *J Proteome Res.* 15, 339-59.
9. Schönbach C, Horton P, Yiu SM, Tan TW, **Ranganathan S** (2015) GIW and InCoB, two premier bioinformatics conferences in Asia with a combined 40 years of history. *BMC Genomics*. 16 Suppl 12, I1.
10. Schönbach C, Horton P, Yiu SM, Tan TW, **Ranganathan S** (2015) GIW and InCoB are advancing bioinformatics in the Asia-Pacific. *BMC Bioinformatics*. 16 Suppl 18, I1.
11. Sowmya G, **Ranganathan S** (2015) Discrete structural features among interface residue-level classes. *BMC Bioinformatics*. 16 Suppl 18, S8.
12. Horton P, Schönbach C, **Ranganathan S**, Yiu SM (2015) Introduction to selected papers from GIW/InCoB 2015. *J Bioinform Comput Biol.* 13,1502003.
13. Sowmya G, Breen EJ, **Ranganathan S** (2015) Linking structural features of protein complexes and biological function. *Protein Sci.* 24, 1486-94.
14. Horvatovich P, Lundberg EK, Chen YJ, Sung TY, He F, Nice EC, Goode RJ, Yu S, **Ranganathan S**, Baker MS, Domont GB, Velasquez E, Li D, Liu S, Wang Q, He QY, Menon R, Guan Y, Corrales FJ, Segura V, Casal JI, Pascual-Montano A, Albar JP, Fuentes M, Gonzalez-Gonzalez M, Diez P, Ibarrola N, Degano RM, Mohammed Y,

Borchers CH, Urbani A, Soggiu A, Yamamoto T, Salekdeh GH, Archakov A, Ponomarenko E, Lisitsa A, Lichti CF, Mostovenko E, Kroes RA, Rezeli M, Végvári Á, Fehniger TE, Bischoff R, Vizcaíno JA, Deutsch EW, Lane L, Nilsson CL, Marko-Varga G, Omenn GS, Jeong SK, Lim JS, Paik YK, Hancock WS (2015) Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. *J Proteome Res*. 14, 3415-31.

15. Sadia M, Ahn SB, Cheruku HR, Cantor D, Rennel E, Fredriksson S, Edfeldt G, Breen EJ, Khan A, Mohamedali A, Muktadir MG, **Ranganathan S**, Tan SH, Nice E, Baker MS (2015) A novel multiplexed immunoassay identifies CEA, IL-8 and prolactin as prospective markers for Dukes' stages A-D colorectal cancers. *Clinical Proteomics*, 12, 10.
16. Atwood TK, Bongcam-Rudloff E, Brazas ME, Corpas M, Gaudet P, Lewitter F, Mulder N, Palagi PM, Schneider MV, van Gelder CW, GOBLET Consortium (including **Ranganathan S**) (2015) GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. *PLoS Comput Biol.* 11, e1004143.
17. Alexander I, Hallwirth C, Garg G, Peters T, Kramer B, Malani N, Hyman J, Ruan X, Ginn S, Hetherington N, Veeravalli L, Shahab A, **Ranganathan S**, Wei CL, Liddle C, Thrasher A, Bushman F, Buckley M (2015) Coherence analysis discriminates between retroviral integration patterns in CD34+ cells transduced under differing clinical trial conditions. *Molecular Therapy - Methods and Clinical Development*, **2**, 15015.
18. Tang YT, Gao X, Rosa BA, Abubucker S, Hallsworth-Pepin K, Martin J, Tyagi R, Heizer E, Zhang X, Bhonagiri-Palsikar V, Minx P, Warren WC, Zhan B, Hotez PJ, Sternberg PW, Dougall A, Gaze ST, Bethony J, Mulvenna J, **Ranganathan S**, Rabelo EM, Wilson RW, Felgner PL, Hawdon JM, Gasser RB, Loukas A, Mitreva M (2014) Genome of the human hookworm *Necator americanus*. *Nature Genetics*, 46, 261–269.
19. **Ranganathan S**, Tan T, Schönbach C. (2014) InCoB2014: Systems Biology update from the Asia-Pacific. *BMC Syst Biol.* 8 Suppl 4, I1.
20. Schönbach C, Tan T, **Ranganathan S**. (2014) InCoB2014: mining biological data from genomics for transforming industry and health. *BMC Genomics*. 15 Suppl 9, I1.
21. **Ranganathan S**, Tan T, Schönbach C. (2014) InCoB2014: bioinformatics to tackle the data to knowledge challenge. *BMC Bioinformatics*. 15 Suppl 16, I1.
22. Ahn SB, Mohamedali A, Anand S, Cheruku HR, Birch D, Sowmya G, Cantor D, **Ranganathan S**, Inglis DW, Frank R, Agrez M, Nice EC, Baker MS. Characterization of the interaction between heterodimeric αvβ6 integrin and urokinase plasminogen activator receptor (uPAR) using functional proteomics. *J Proteome Res.* 13, 5956-5964.
23. Sowmya G, Khan JM, Anand S, Ahn SB, Baker MS, **Ranganathan S** (2014) A site for direct integrin αvβ6•uPAR interaction from structural modelling and docking. *J Struct Biol,* 185, 327-335.
24. Krajaejun T, Lerksuthirat T, Garg G, Lowhnoo T, Yingyong W, Khositnithikul R, Tangphatsornruang S, Suriyaphol P, **Ranganathan S**, Sullivan TD (2014) Transcriptome Analysis Reveals Pathogenicity and Evolutionary History of the Pathogenic Oomycete *Pythium insidiosum*. *Fungal Biol*, 118, 640-653.
25. Islam MT, Garg G, Hancock WS, Risk BA, Baker MS, **Ranganathan S** (2014) Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the "Missing" Human Proteome. *J Proteome Res*. 13, 76-83.
26. Sowmya G, **Ranganathan S** (2014) Protein-protein interactions and prediction: a comprehensive overview. *Peptide & Protein Letters*, 21, 779-789. *(invited)*
27. Islam MT, Mohamedali A, Garg G, Khan JM, Gorse AD, Parsons J, Marshall P, **Ranganathan S***, Baker MS* (2013) Unlocking the Puzzling Biology of the Black Périgord Truffle *Tuber melanosporum. J Proteome Res.* 12, 5349-56. (joint corresponding authors)
28. Khan AM, Tan TW, Schönbach C, **Ranganathan S** (2013) APBioNet – transforming bioinformatics in the Asia-Pacific Region. *PLoS Comput Biol*, *invited editorial,* 9, e1003317.

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