

Steven G. Rozen, Ph.D.

Curriculum Vitae

Associate Dean of Research Informatics
Professor, Cancer and Stem Cell Biology Program
Director, Duke-NUS Centre for Computational Biology
Duke-NUS Medical School



Background

Education

- Ph.D.** Courant Institute of Mathematical Sciences at New York University, Computer Science (advisor: Dennis Shasha). Dissertation topic: automatic physical database design
- M.S.** Courant Institute at New York University, Computer Science
- B.A.** cum laude, University of California at Riverside

Academic and Research Positions

- 2016-present Associate Dean of Research Informatics, Duke-NUS Medical School, Singapore
- 2015-present Professor with tenure, Duke-NUS Medical School, Singapore
- 2012-present Director, Duke-NUS Centre for Computational Biology
- 2015-present Interim Chief Information Officer, PRISM (PReclSion Medicine Institute of SingHealth and Duke-NUS)
- 2010-present Associate Professor Track V, Department of Psychiatry and Behavioral Sciences, Duke University Medical Center
- 2015-present Research Scientist, National Heart Research Institute Singapore
- 2009-present Faculty Member, National University of Singapore Graduate School for Integrative Sciences and Engineering
- 2014-2015 Visiting Scientist, National Heart Research Institute Singapore
- 2008-2015 Associate Professor with tenure, Duke-NUS Medical School Singapore
- 1993-2008 Research Scientist (1994-2008) Whitehead Institute, Cambridge MA
- 1996-2008 Bioinformatics Consultant (part-time)
- 1999-2001 Director of yearly, intensive course, *Bioinformatics: Writing Software for Genome* Research, Cold Spring Harbor Laboratory, New York
- 1989-1993 Research Software Engineer (full-time) Software Options, Inc. (research funded by the Defense Advanced Research Projects Agency), Cambridge, MA
- 1988-1989 Graduate Assistant/Instructor, Department of Computer Science, Courant Institute at New York University, New York

Teaching and Mentoring

- 2016-present Chair of Executive Committee of the Duke-NUS PhD Programme in Integrated Biostatistics and Bioinformatics (IBB, <http://tinyurl.com/DNUS-IBB>)
- 2011-present Duke-NUS Medical School, Singapore Ph.D. Program; students: Mini Huang (graduated 2017), Yuka Suzuki
- 2009-present Faculty of the NUS Graduate School for Integrative Sciences and Engineering, National University of Singapore; Ph.D. students: Thomas Thurnherr (co-supervised with Caroline Lee, graduated 2015), Alvin Ng
- 2008-2014 Faculty of the Singapore-MIT Alliance, Programme in Computation and Systems Biology; Ph.D. students: Alice Yingting Wu (graduated 2013), Yujing Liu (graduated, 2014; co-supervised with Patrick Tan)
- 2009-present Postdoctoral fellow Yew Chung Tang
- 2010-2017 Postdoctoral fellow John McPherson (now at Ab Initio software)
- 2009-2013 Postdoctoral fellow Zhengdeng Lei; current position: Bioinformatics Specialist at the University of Chicago
- 2001-2001 Co-supervisor of PhD student Sjoerd Repping; current position: Professor and Head of the Center for Reproductive Medicine, University of Amsterdam
- 2009-present Faculty of the 1st year medical course “Molecules to Cells” at Duke-NUS Medical School
- 2010-2013 Faculty of the 1st year Ph.D. student core course “Molecules to Medicines” at Duke-NUS Medical School
- 1999, 2000, 2001 Cold Spring Harbor Laboratory, New York, organized and directed course *Bioinformatics: Writing Software for Genome Research*, a course to train researchers in the creation and integration of software for genomics, genetics, and molecular biology; this two-week, intensive (all day and evening) course covered use of the Unix/Linux operating system, Perl programming, database design, creation of dynamic Web pages, and analysis of DNA sequence and gene expression microarray data; it was aimed at the needs of biologists with little or no prior hands-on experience in these areas
- 1992 International Conference on Very Large Data Bases, *Database Tuning Tutorial* (with D. Shasha)
- 1989 New York University, Courant Institute, Department of Computer Science taught graduate course *Special Topics: Parallel Algorithms, Architectures, and Applications* (with D. Shasha)
- 1988 New York University, Courant Institute, Department of Computer Science, taught undergraduate *Introduction to Database Systems*

Other professional experience

- 1995-1997 Database consultant (part-time) Marble Associates Inc., Boston MA
- 1986-1988 Database architect and software engineer, Prudential-Bache Securities, New York
- 1983-1986 Information technology specialist and programmer, Chemical Bank, New York

Current Grants (as Principal Investigator)

Grant Title	Funding Source	Amount Singapore \$ US\$	Amount Includes Indirect?	Dates
Discovery and validation of oncogenic splice variants as drug targets in gastrointestinal cancers, NMRC/CIRG/1393/2014	Singapore National Medical Research Council (CS-IRG)	1,370,845 US\$ ~1,090,000	direct only	July 2014 to June 2018
Systems for assessing mutation signatures in-vitro and discovering mutagenic exposures in tumors, NMRC/CIRG/1422/2015	Singapore National Medical Research Council (CS-IRG)	1,746,600 US\$ ~1,245,000	direct and indirect	July 2015 to July 2018
Molecular atlas of hepatocarcinogenesis - longitudinal study to analyse the mutational and transcriptional changes during the development of hepatocellular carcinoma, SingHealth/Duke-NUS/RCG/2015/0002	SingHealth Foundation (SingHealth PI, Kanaga Sabapathy)	300,000 US\$ ~210,903	direct	Oct 2015 to Sept 2017
Integrating miRNA expression into a clinically testable predictor for early stage colorectal cancer likely to metastasize, SingHealth/Duke-NUS/RCG/2015/0005	SingHealth Foundation (SingHealth PI, CHEAH Peh Yean)	300,000 US\$ ~210,903	direct	Oct 2015 to Sept 2018

Current Grants (as Co-Investigator)

Grant Title	Funding Source	Amount Singapore \$ US\$	Amount Includes Indirect?	Dates
National Lymphoma Translational Research Program: From Genomics to Therapeutics, TCR/010-NCC/2013	Singapore National Medical Research Council	8,999,280 US\$ ~7,200,000	direct and indirect	Feb 2014 to Jan 2019
Customizable circulating tumor nucleic acid assays to monitor disease burden, detect known drug resistance mutations and identify novel drug resistance mutations in patients with metastatic gastrointestinal cancers, Clinician Scientist Award NMRC/CSA-INV/0001/2014	Singapore National Medical Research Council	~1,530,000 US\$ ~1,145,931	direct and indirect	Nov 2014 to Nov 2017
The role of physiologic hypoxia in the pathogenesis of chronic myeloid leukaemia, NMRC/CIRG/1404/2014	Singapore National Medical Research Council	1,490,000 US\$ ~1,185,000	direct only	Jan 2015 to Dec 2017
Alternative splicing networks in gastric cancer, CBRG15may016	Singapore National Medical Research Council	1,012,000 US\$ ~738,845	direct only	Mar 2016 to Mar 2019
Epigenomic Profiling of Altered Chromatin States in Gastrointestinal Cancer NMRC/STaR/0026/2015	Singapore National Medical Research Council	5,000,000 US\$ ~3,715,065	direct only	Apr 2016 to Mar 2021

Previous Grants

Grant Title	Role	Funding Source	Amount Singapore \$ US\$	Amount Includes Indirect?	Dates
Identifying genes associated with breast cancer susceptibility in an Asian population, NMRC/CBRG/0034/2013	Co-I	Singapore National Medical Research Council	966,517 US\$ ~770,000	direct only	Aug 2013 to Aug 2016
Multimodal connectome analysis for differentiating subtypes within early-stage dementia and mild cognitive impairment, TCRP 13/1/96/19/687	Co-I	Singapore Biomedical Research Council, Duke-NUS SingHealth Academic Clinical Programme	1,495,080 US\$ ~1,200,000	direct and indirect	Apr 2013 to Mar 2016
Identification of drugs for targeted treatment of PTEN-deficient tumors, NMRC/GMS/CIRG/1324/2012	PI	Singapore National Medical Research Council	1,389,000 US\$ ~1,110,000	direct only	June 2012 to June 2016
Developing a clinically testable biomarker-based predictor for early stage colorectal cancer likely to metastasize, BMRC 13/1/96/191684	PI	Singapore Biomedical Research Council, Duke-NUS SingHealth Academic Clinical Programme	1,500,000 US\$ ~1,200,000	direct only	Apr 2013 to Mar 2016
miRNAs and small RNAs as potential biomarkers for the identification of cirrhosis and hepatocellular carcinoma, BMRC 13/1/96/191684	PI	Singapore Biomedical Research Council, Duke-NUS SingHealth Academic Clinical Programme	1,151,510 US\$ ~921,000	direct only	Apr 2013 to Mar 2016

A striatal synaptic dysfunction hypothesis for repetitive behaviors in autism evaluated by re-sequencing of candidate genes, NMRC/GMS/1248/2010	PI	Singapore National Medical Research Council	1,250,000 US\$ ~1,000,000	direct only	Sept 2010 to July 2014
Lineage-specific survival oncogenes in gastric cancer: Functional characterization, genomic dissection, and integration with classical genetic circuits, project number 1012419665	Co-I	Singapore Biomedical Research Council	1,131,500 US\$ ~900,000	direct only	Aug 2011 to July 2014
Metabolomic signatures and biomarkers for schizophrenia, R01 MH084941	Collaborator	US National Institutes of Health	1,016,953 US\$ 760,353	direct and indirect	Aug 2010 to May 2012
Metabolic Signatures for Alzheimer's Disease. Cerebrospinal fluid metabolomics in patients with pathologically confirmed diagnosis, R01 NS054008	Collaborator	US National Institutes of Health	1,231,840 US\$ 921,022	direct and indirect	Sept 2007 to Aug 2010
Genomic studies of sex chromosomes, R01 HG00275	Co-PI	US National Institutes of Health	4,651,440 US\$ 3,477,821	directs and indirects	Apr 2006 to Mar 2009
Genomic studies of sex chromosomes, R01 HG00275	Co-PI	US National Institutes of Health	3,794,928 US\$ 2,837,650	direct and indirect	Mar 2003 to Mar 2006
Genetic studies of spermatogenic failure in humans, R01 HD32907	Co-PI	US National Institutes of Health	2,752,320 US\$ 2,058,848	direct and indirect	May 2000 to Apr 2006
Genomic studies of the Y chromosome, R01 HG00257	Co-PI	US National Institutes of Health	3,007,596 US\$ 2,249,801	direct and indirect	Jan 2000 to Feb 2003
Mapping and sequencing the Y chromosome, R01 HG00257-07	Co-PI	US National Institutes of Health	3,583,450 US\$ 2,680,749	direct and indirect	Jan 1997 to Dec 1999
Freely sharable DBMS for genome informatics systems, DE-FG02-95ER62101	Co-PI	US Department of Energy	Not available	Not applicable	Sept 1995 to Sept 1998

Workflow-management software
for genome-laboratory
informatics, R01 HG0367-01

Co-I

US National
Institutes of
Health

~388,597
US\$ ~291,000

direct only

May 1996
to Apr
1999

Awards

2015 Singapore *President's Science Award*, team award to Professors Patrick Tan, Bin Tean Teh, and Steven Rozen, for outstanding integrative and translational research in Asian cancer genomics

2006 *Faculty of 1000 Medicine, Must Read* for Repping et al., 2006, listed below in Publications

2003 *Faculty of 1000 Biology, Recommended Paper* for Rozen, et al., 2003, listed below in Publications

2003 *A Breakthrough of the Year by the News and Editorial Staffs of Science*, for sequencing the human Y chromosome, reported in Rozen et al., 2003 and Skaletsky et al., 2003, listed below in Publications

2003 *Faculty of 1000 Biology, Exceptional Paper* for Repping, et al., 2003, listed below in Publications.

2003 *Cotterman Award from the American Society of Human Genetics* for Repping et al., 2002, listed below in Publications

Publications

(IF indicates journal impact factor for year closest to publication year.)

Published

Y. Suzuki, S.B. Ng, C. Chua, W.Q. Leow, J. Chng, S.Y. Liu, K. Ramnarayanan, A. Gan, D.L. Ho, R. Ten, Y. Su, A. Lezhava, J. H. Lai, D. Koh, K.H. Lim, P. Tan, **S.G. Rozen***, I.B. Tan* "Multiregion ultra-deep sequencing reveals early intermixing and variable levels of intratumoral heterogeneity in colorectal cancer" *Mol Oncol* doi:10.1002/1878-0261.12012 (2016) (* = corresponding author) IF 5.37

W.F. Ooi, M. Xing, C. Xu, X. Yao, M.K. Ramlee, M.C. Lim, F. Cao, K. Lim, D. Babu, L.-F. Poon, J.L. Suling, A. Qamra, A. Irwanto, J.Q. Zhengzhong, T. Nandi, A.P. Lee-Lim, Y.S. Chan, S.T. Tay, M.H. Lee, J.O.J. Davies, W.K. Wong, K.C. Soo, W.H. Chan, H.S. Ong, P. Chow, C.Y. Wong, S.Y. Rha, J. Liu, A.M. Hillmer, J.R. Hughes, **S. Rozen**, B.T. Teh, M.J. Fullwood, S. Li, P. Tan "Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity" *Nature Commun* 7: 12983 (2016) IF 11.32

B. Madan, Z. Ke, Z.D. Lei, F.A. Oliver, M. Oshima, M.A. Lee, **S. Rozen**, D.M. Virshup. "NOTUM is a potential pharmacodynamic biomarker of Wnt pathway inhibition" *Oncotarget* 7:12386 (2016) IF 6.35

T. Thurnherr, W.-C. Mah, Z. Lei, Y. Jin, **S.G. Rozen**, C.G. Lee. "Differentially expressed miRNAs in hepatocellular carcinoma target genes in the genetic information processing and metabolism pathways" *Sci Rep* 6:20065 (2016) IF 5.57

T.H.M. Chan, A. Qamra, K.T. Tan, J. Guo, H. Yang, L. Qi, J.S. Lin, V.H.E. Ng, Y. Song, H. Hong, S.T. Tay, Y. Liu, J. Lee, S.Y. Rha, Z. Feng, J.B.Y. So, B.T. Teh, Y.K. Guan, **S.**

- Rozen**, D.G. Tenen, P. Tan, L. Chen "ADAR-mediated RNA editing predicts progression and prognosis of gastric cancer" *Gastroenterol* 151:637-650 (2016) IF 16.71
- C. Wang, J.R. McPherson, L.-H. Zhang, **S. Rozen**, K. Sabapathy "Transcription-associated mutation of *lasR* in *Pseudomonas aeruginosa*" *DNA repair* 46:6-19 (2016) IF 3.92
- C.C. Liu, D.L. Ma, T.-D. Yan, X. Fan, Z. Poon, L.-F. Poon, S.-A. Goh, **S.G. Rozen**, W.Y.K. Hwang, V. Tergaonkar, P. Tan, S. Ghosh, D.M. Virshup, E.L.K. Goh, S. Li. "Distinct responses of stem cells to telomere uncapping—a potential strategy to improve the safety of cell therapy" *Stem Cells* advance online pub June (2016) IF 5.90
- T. Souma, S.W. Tompson, B.R. Thomson, O.M. Siggs, K. Kizhatil, S. Yamaguchi, L. Feng, V. Limviphuvadh, K.N. Whisenhunt, S. Maurer-Stroh, T.L. Yanovitch, L. Kalaydjieva, D.N. Azmanov, S. Finzi, L. Mauri, S. Javadiyan, E. Souzeau, T. Zhou, A.W. Hewitt, B. Kloss, K.P. Burdon, D.A. Mackey, K.F. Allen, J. B. Ruddle, S.-H. Lim, **S. Rozen**, K.-N. Tran-Viet, X. Liu, S. John, J.L. Wiggs, F. Pasutto, J.E. Craig, J. Jin, S.E. Quaggin, T.L. Young. "Angiopoietin receptor TEK mutations underlie primary congenital glaucoma with variable expressivity" *J Clin Invest.* 126:7 (2016) IF 13.26
- C. Chan, T. Thurnherr, J. Wang, X. Gallart-Palau, S.K. Sze, **S. Rozen**, C.G. Lee. "Global rewiring of p53 transcription regulation by the hepatitis B virus X protein" *Mol Oncol* advance online pub June (2016) IF 5.33
- W. Zhang, P.J. Kim, Z. Chen, H. Lokman, L. Qiu, K. Zhang, **S.G. Rozen**, E.K. Tan, H.S. Je, L. Zeng. "MiRNA-128 regulates the proliferation and neurogenesis of neural precursors by targeting PCM1 in the developing cortex" *eLife* 5: e11324 (2016) IF 9.32
- M.L. Nairismägi, J. Tan, J.Q. Lim, S. Nagarajan, C.C.Y. Ng, V. Rajasegaran, D. Huang, W.K. Lim, Y. Laurensia, G.C. Wijaya, Z.M. Li, I. Cutcutache, W.L. Pang, S. Thangaraju, J. Ha, L.P. Khoo, S.T. Chin, S. Dey, G. Poore, L.H.C. Tan, H.K.M. Koh, K. Sabai, H.L. Rao, K.L. Chuah, Y.H. Ho, S.B. Ng, S.S. Chuang, F. Zhang, Y.H. Liu, T. Pongpruttipan, Y.H. Ko, P.L. Cheah, N. Karim, W.J. Chng, T. Tang, M. Tao, K. Tay, M. Farid, R. Quek, **S.G. Rozen**, P. Tan, B.T. Teh, S.T. Lim, S.Y. Tan, C.K. Ong. "JAK-STAT and G-protein-coupled receptor signaling pathways are frequently altered in epitheliotropic intestinal T-cell lymphoma" *Leukemia* advance online pub Mar (2016) IF 10.43
- K. Das, X.B. Chan, D. Epstein, B.T. Teh, K.-M. Kim, S.T. Kim, S.H. Park, W.K. Kang, **S. Rozen**, J. Lee, P. Tan. "NanoString expression profiling identifies candidate biomarkers of RAD001 response in metastatic gastric cancer" *ESMO Open* 1:e000009 (2016) new journal, no IF
- J. Tan, C.K. Ong, W.K. Lim, C.C.Y. Ng, A.A. Thike, L.M. Ng, V. Rajasegaran, S.S. Myint, S. Nagarajan, S. Thangaraju, S. Dey, N.D. Md Nasir, G.C. Wijaya, J.Q. Lim, D. Huang, Z. Li, B.H. Wong, J.Y.S. Chan, J.R. McPherson, I. Cutcutache, G. Poore, S.T. Tay, W.J. T. Tan, C. Putti, B.S. Ahmad, P. Iau, C.W. Chan, A.P.T. Tang, W.S. Yong, P. Madhukumar, G.H. Ho, V.K.M. Tan, C.Y. Wong, M. Hartman, K.W. Ong, B.K.T. Tan, **S.G. Rozen***, P. Tan*, P.H. Tan*, B.T. Teh*. "Genomic landscapes of breast fibroepithelial tumors" *Nat Genet* 47:1341–1345 (2015) (* = corresponding author) IF 29.35
- K.K. Huang, K.W. Jang, S. Kim, H.S. Kim, S.-M. Kim, H.J. Kwon, H.R. Kim, H.J. Yun, M.J. Ahn, K.U. Park, K. Ramnarayanan, J.R. McPherson, S. Zhang, J.-K. Rhee, A.L. Vettore, K. Das, T. Ishimoto, J.H. Kim, Y.W. Koh, S.H. Kim, E.C. Choi, B.T. Teh,

- S.G. Rozen**, T.-M. Kim, P. Tan, B.C. Cho. "Exome sequencing reveals recurrent REV3L mutations in cisplatin-resistant squamous cell carcinoma of head and neck" *Sci Rep* 6:19552 (2016) IF 5.57
- E.S.Y. Wong, S. Shekar, M. Met-Domestici, C. Chan, M. Sze, Y.S. Yap, **S.G. Rozen**, M.-H. Tan, P. Ang, J. Ngeow, A.S.G. Lee. "Inherited breast cancer predisposition in Asians: multigene panel testing outcomes from Singapore" *npj Genomic Medicine* 1:15003 (2016) new journal, no IF
- M.N. Huang, J.R. McPherson, I. Cutcutache, B.T. Teh, P. Tan, **S.G. Rozen**. "MSIseq: Software for assessing microsatellite instability from catalogs of somatic mutations" *Sci. Rep.* 5:13321 (2015) IF 5.58
- I. Cutcutache, A.Y. Wu, Y. Suzuki, J.R. McPherson, Z. Lei, N. Deng, S. Zhang, W.K. Wong, K.C. Soo, W.H. Chan, L.L. Ooi, R. Welsch, P. Tan, **S.G. Rozen**. "Abundant copy-number loss of CYCLOPS and STOP genes in gastric adenocarcinoma" *Gastric Cancer* 1-13 (2015) IF 3.71
- I. Cutcutache, Y. Suzuki, I. B. Tan, S. Ramgopal, S. Zhang, K. Ramnarayana, A. Gan, H.H. Lee, S.T. Tay, A. Ooi, C.K. Ong, J.T. Bolthouse, B.R. Lane, J.G. Anema, R.J. Kahnoski, P. Tan*, B.T. Teh*, **S.G. Rozen***. "Exome-wide sequencing shows low mutation rates and identifies novel mutated genes in seminomas" *Eur. Urol.* 68(1):77-83 (2015) (* = corresponding author). Designated "Platinum Priority" and highlighted in a journal editorial. IF 13.93
- S.L. Poon, M.N. Huang, Y. Choo, J.R. McPherson, W. Yu, H.L. Heng, A. Gan, S.S. Myint, E.Y. Siew, L.D. Ler, L.G. Ng, W.-H. Weng, C.-K. Chuang, J.S.P Yuen, S.-T. Pang*, P. Tan*, B.T. Teh*, **S.G. Rozen***. "Mutation signatures implicate aristolochic acid in bladder cancer development" *Genome Med.* 7:38 (2015) (* = corresponding author) IF 5.81
- A.L. Vettore, K. Ramnarayanan, G. Poore, K. Lim, C.K. Ong, K.K. Huang, H.S. Leong, F.T. Chong, T.K.-H. Lim, W.K. Lim, I. Cutcutache, J.R. Mcpherson, Y. Suzuki1, S. Zhang, T. Skanthakumar, W. Wang, D.S.W. Tan, B.C. Cho, B.T. Teh*, **S. Rozen***, P. Tan*, N.G. Iyer*. "Mutational landscapes of tongue carcinoma" *Genome Med.* 7:98 (2015) (* = corresponding author) IF 5.81
- M.T. Voso, E. Fabiani, Z. Zang, L. Fianchi, G. Falconi, A. Padella, M. Martini, S.L. Zhang, R. Santangelo, L.M. Larocca, M. Criscuolo, A. La Brocca, I. Cutcutache, **S. Rozen**, G. Simonetti, M. Manfrini, G. Martinelli, S. Hohaus, G. Leone, P. Tan, D.G. Tenen. "Fanconi anemia gene variants in therapy-related myeloid neoplasms" *Blood Cancer. J.* 5:7 (2015) IF 3.46
- F. Yang, S. Silber, N.A. Leu, R.D. Oates, J.D. Marszalek, H. Skaletsky, L.G. Brown, **S. Rozen**, D.C. Page, P.J. Wang. "TEX11 is mutated in infertile men with azoospermia and regulates genome-wide recombination rates in mouse" *EMBO Mol. Med.* 7:1198-1210 (2015) IF 8.66
- I. Tan, S. Malik, K. Ramnarayanan, J. McPherson, D. Ho, Y. Suzuki, S. Ng, S. Yan, K. Lim, D. Koh, C. Hoe, C. Chan, R. Ten, B. Goh, A. Chung, J. Tan, C. Chan, S. Tay, L. Alexander, N. Nagarajan, A. Hillmer, C. Tang, C. Chua, B. Teh, **S. Rozen**, P. Tan. "High-depth sequencing of over 750 genes supports linear progression of primary tumors and metastases in most patients with liver-limited metastatic colorectal cancer" *Genome Biol.* 16:32 (2015) IF 10.47
- S. Kongpetch, A. Jusakul, C.K. Ong, W.K. Lim, **S.G. Rozen**, P. Tan, B.T. Teh. "Pathogenesis of cholangiocarcinoma: from genetics to signaling pathways" *Best Pract. Res. Clin. Gastroenterol.* 29:233-244 (2015) IF 3.28

- M.K. Keck, Z. Zuo, A. Khattri, T.P. Stricker, C. Brown, M. Imanguli, D. Rieke, K. Endhardt, P. Fang, J. Bragelmann, R. DeBoer, M. El Dinali, S. Aktolga, Z. Lei, P. Tan, **S.G. Rozen**, R. Salgia, R.R. Weichselbaum, M.W. Lingen, M.D. Story, K.K. Ang, E.E. Cohen, K.P. White, E.E. Vokes, T.Y. Seiwert. "Integrative analysis of head and neck cancer identifies two biologically distinct HPV and three non-HPV subtypes" *Clin. Cancer Res.* 21:870-881 (2015) IF 8.19
- W.K. Lim, C.K. Ong, J. Tan, A.A. Thike, C.C. Ng, V. Rajasegaran, S.S. Myint, S. Nagarajan, N.D. Nasir, J.R. McPherson, I. Cutcutache, G. Poore, S.T. Tay, W.S. Ooi, V.K. Tan, M. Hartman, K.W. Ong, B.K. Tan, **S.G. Rozen***, P.H. Tan*, P. Tan*, B.T. Teh*. "Exome sequencing identifies highly recurrent *MED12* somatic mutations in breast fibroadenoma" *Nat. Genet.* 46:877-880 (2014) (* = corresponding author) IF 29.6
- Y. Itahana, R. Han, S. Barbier, Z. Lei, **S. Rozen**, K. Itahana. "The uric acid transporter SLC2A9 is a direct target gene of the tumor suppressor p53 contributing to antioxidant defense" *Oncogene* 34:1799-1810 (2015) IF 8.6
- K.K. Huang, J.R. McPherson, S.T. Tay, K. Das, I.B. Tan, C.C.Y. Ng, N.-Y. Chia, S.L. Zhang, S.S. Myint, L. Hu, V. Rajasegaran, D. Huang, J.L. Loh, A. Gan, A.N.H. Sairi, X.X. Sam, L.T. Dominguez, M. Lee, K.C. Soo, L.L.P.J. Ooi, H.S. Ong, A. Chung, P.K.-H. Chow, W.K. Wong, S. Selvarajan, C.K. Ong, K.H. Lim, T. Nandi, **S. Rozen**, B.T. Teh, R. Quek, P. Tan. "SETD2 histone modifier loss in aggressive GI stromal tumours" *Gut*, gutjnl-2015-309482 (2015) IF 14.66
- J.R. McPherson, C.-K. Ong, C.C.-Y. Ng, V. Rajasegaran, H.-L. Heng, W.S.-S. Yu, B.K.-T. Tan, P. Madhukumar, M.C.-C. Teo, J. Ngeow, A.-A. Thike, **S.G. Rozen**, P.-H. Tan, A.S.-G. Lee, B.-T. Teh, Y.-S. Yap. "Whole-exome sequencing of breast cancer, malignant peripheral nerve sheath tumor and neurofibroma from a patient with neurofibromatosis type 1" *Cancer Med.* (advance online publication, 2015) IF 2.50
- N.Y. Chia, N. Deng, K. Das, D. Huang, L. Hu, Y. Zhu, K.H. Lim, M.H. Lee, J. Wu, X.X. Sam, G.S. Tan, W.K. Wan, W. Yu, A. Gan, A.L. Tan, S.T. Tay, K.C. Soo, W.K. Wong, L.T. Dominguez, H.H. Ng, **S. Rozen**, L.K. Goh, B.T. Teh, P. Tan. "Regulatory crosstalk between lineage-survival oncogenes *KLF5*, *GATA4* and *GATA6* cooperatively promotes gastric cancer development" *Gut* 64:707-719 (2015) IF13.3
- L.B. Tanner, C. Chng, X.L. Guan, Z. Lei, **S.G. Rozen**, M.R. Wenk. "Lipidomics identifies a requirement for peroxisomal function during influenza virus replication" *J. Lipid Res.* 55:1357-1365 (2014) IF 4.7
- Z.X. Yeo, J.C. Wong, **S.G. Rozen***, A.S. Lee*. "Evaluation and optimisation of indel detection workflows for ion torrent sequencing of the BRCA1 and BRCA2 genes" *BMC Genomics* 15:516 (2014) (* = corresponding author) IF 4.0
- W. Yu, J.R. McPherson, M. Stevenson, R. van Eijk, H. Lee Heng, P. Newey, A. Gan, D. Ruano, D. Huang, S. Ling Poon, C.K. Ong, T. van Wezel, B. Cavaco, **S.G. Rozen**, P. Tan, B.T. Teh, R.V. Thakker, H. Morreau. "Whole-exome sequencing studies of parathyroid carcinomas reveal novel PRUNE2 mutations, distinctive mutational spectra related to APOBEC-catalyzed DNA mutagenesis and mutational enrichment in kinases associated with cell migration and invasion" *J. Clin. Endocrinol. Metab.* 100:E360–E364 (2014) IF 6.4
- Y.S. Yap, J.R. McPherson, C.K. Ong, **S.G. Rozen**, B.T. Teh, A.S. Lee, D.F. Callen. "The NF1 gene revisited - from bench to bedside" *Oncotarget* 5:5873–5892 (2014) IF 6.6
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- S. Rozen**, L. Stein, N. Goodman. "LabBase: A database to manage laboratory data in a large-scale genome-mapping project" *IEEE Engineering in Medicine and Biology*. 14:702-709 (1995)
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- S. Rozen**, L. Stein, N. Goodman. "Constructing a domain-specific DBMS using a persistent object system" *Sixth International Workshop on Persistent Object Systems*. (1994) acceptance ratio 27/56
- L. Stein, A. Marquis, E. Dredge, M.P. Reeve, M. Daly, **S. Rozen**, N. Goodman. "Splicing UNIX into a genome mapping laboratory" *USENIX Summer 1994 Technical Conference*. pages 221-229 (1994)
- S. Rozen**. "Automating Physical Database Design: An Extensible Approach" Ph.D. thesis, Courant Institute of Mathematical Sciences, New York University (Mar 1993), 124 pages
- S. Rozen**, D. Shasha. "A framework for automating physical database design" *Proceedings of the 17th International Conference on Very Large Data Bases*. pages 401-411 (1991) acceptance ratio 59/323
- S. Rozen**, D. Shasha. "Rationale and design of BULK" *Proceedings of the Third International Workshop on Database Programming Languages*. pages 71-85 (1991)
- S. Rozen**, D. Shasha. "Using a relational system on Wall Street: The good, the bad, the ugly, and the ideal" *Communications of the ACM*. 32:8 988-994 (1989)

Software, technical reports, proposals, etc.

- S. Rozen**, W.C. Warren, G. Weinstock, S.J. O'Brien, R.A. Gibbs, R.K. Wilson, D.C. Page. "Sequencing and Annotating New Mammalian Y Chromosomes, A White Paper Proposal, July, 2006" A proposal to the National Human Genome Research Institute, NIH
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- N. Goodman, **S. Rozen**, L. Stein. "Database-and Workflow-Management Challenges Posed by the Human Genome Project" Technical Report (1995) 31 pages
- N. Goodman, **S. Rozen**. "A Freely Sharable Database Management System Designed for Use in Component-Based, Modular Genome Informatics Systems" From a proposal to the Department of Energy (1994) 22 pages
- S. Rozen**, M.J. Daly, M.-P. Reeve, N. Goodman. "GENOME-MAP: Real-World Test Data and Queries for Logic Databases" Technical Report (1993) 7 pages
- S. Rozen**, D. Shasha. "Automating physical database design: A general approach and its evaluation" Technical Report (1993) 51 pages
- M. Karr, W.G. Morris, **S. Rozen**. "Global optimization for a coagulating code generator: Final technical report" Software Options, Inc., Technical Report (1991) 7 pages
- W.G. Morris, **S. Rozen**. "Interim report on E-L/CCG benchmarks" Technical Report SOI-01-90, Software Options, Inc. (1991) 40 pages

Other Activities

2000 to present, Editorial Board for *Information Systems*

2005 to 2010, Member of Scientific Board, *Metabolomics Society*
(<http://www.metabolomicssociety.org>)

2006 Issue editor for *Current Opinion in Genetics and Development*, vol. 16, issue 16, "Genetics of disease, The sex chromosomes and human disease" with A. Ballabio and D. Nelson

2013 to 2015, Academic Editor for *PLOS ONE*

2013 to present, Principal Investigator, *International Cancer Genome Consortium*
(Singapore, Biliary Duct Cancer)

2014 to present, Editorial Board for *Genome Medicine*

2014 to present, Principal Investigator, *International Cancer Genome Consortium*
(Singapore, T-Cell and NK-Cell Lymphomas)

2014 to present, co-leader of the International Cancer Genome Consortium's Pan Cancer Analysis Working on Mutation Signatures

Reviewer for

American Journal of Human Genetics
Annals, Academy of Medicine, Singapore
Annals of Human Genetics
Bioinformatics
BMC Medical Genomics
Gene
Genome Biology
Genome Research
Human Molecular Genetics
Human Reproduction
Information Systems
International Journal of Andrology
Journal of Clinical Investigation
Metabolomics
Nature
Nature Genetics
New England Journal of Medicine
Nucleic Acids Research
Oncogene
PLOS Genetics
PLOS ONE
Science Translational Medicine

Study sections and funding application reviews

2015 UK Medical Research Council, Career Development Award
2013 A*STAR (Singapore) JCO Project Grant
2011 National Medical Research Council, Singapore
2007 NIH Clinical Special Emphasis Panel in Digestive Sciences
2006 GenomeCanada
2005 National Cancer Institute/NIH, Metabolomics for Early Cancer Detection

Patents

Grouping for Classifying Gastric Cancer. US Patent 20150254400, published 2015/9/10

Grouping for Classifying Gastric Cancer and Methods of Using the Same. (EPTL ref. BRC/P/07175/00/SG) Singapore filing 201206943-1 (2012)

Markers of Alterations in the Y Chromosome and Uses Therefor. EP Patent 1,794,321 (2007); US Patent App. 11/195,344 (2005); US Patent App. 12/251,270 (2008)

Coding Sequence Polymorphisms in Vascular Pathology Genes. US Patent 6,692,909 (2004); EP Patent 1,068,353 (2001); WO Patent 1,999,050,454 (1999)

International Invited Lectures

2016 Keynote Speaker at the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (IEEE CIBCB 2016) Chiang Mai, Thailand, Oct 5, 2016, *Big Genome Data Sheds Light on Cancer Causes*

2016 EMGS 47th Annual Meeting, From Environment to (Epi)Genome and Back Again, Kansas City, MO, USA, Sep 25, *Genome-Wide Aflatoxin B1 Mutational Signature in*

Cells, Mice, and Human Tumors: Implications for Molecular Epidemiology; also served as session chair

- 2016 International Cancer Genome Consortium 12th Scientific Workshop, Boston, MA, USA, Sep 19, *ICGC Pan Cancer Mutational Signatures Preliminary Results*
- 2016 NIEHS, Durham, NC, USA, Sep 13, *Detection and experimental elucidation of mutation signatures and their value for understanding cancer development and epidemiology*
- 2016 International Agency for Research on Cancer (IARC) Conference, Global Cancer Occurrence, Causes, and Avenues to Prevention, Lyon, France, June 10, *Genome-wide AFB1-induced mutational signature in cells, mice and human tumors – implications for molecular epidemiology*
- 2015 Keynote Speaker at the 6th International Conference on Computational Systems-Biology and Bioinformatics, Bangkok, Thailand, Nov. 23, *Genome bioinformatics' successes, challenges, and opportunities in the era of low-cost sequencing*
- 2015 Genome Informatics Workshop / International Conference on Bioinformatics (GIW/InCoB), Tokyo, Japan, Sept. 11, *Mutation signatures implicate aristolochic acid in bladder cancer development*
- 2015 NGS Data Congress, London, UK, June 15, *Genome-wide somatic mutation signatures reveal environmental causes of cancer* (also acted as session chair for "NGS Data Management")
- 2015 The Francis Crick Institute, London, UK, June 17, *Genome-wide somatic mutation signatures reveal environmental causes of cancer*
- 2015 World Health Organization, International Agency for Research on Cancer, Lyon, France, Feb. 19, *Physical mutation signatures for safety testing and cancer epidemiology: review and update*
- 2014 Korean Society for Bioinformatics and Systems Biology, 2014 Conference on Bioinformatics, Seoul, Korea, Nov. 14, *Keynote talk: Genome bioinformatics past, present, and future*
- 2014 World Health Organization, International Agency for Research on Cancer, Lyon, France, Sept. 10, *High-throughput physical mutation signatures for safety testing and cancer epidemiology*
- 2014 The First International Workshop of Biomarkers for Human Diseases –Cancer, Shenzhen, April 18, *Mutational fingerprints of an incredibly genotoxic herbal remedy*
- 2013 8th International Conference on Genomics, Shenzhen, Nov. 1, *Making sense of cancer genomes*
- 2013 3rd Annual Next Generation Sequencing Asia Congress, Singapore, October 8, *Making sense of cancer genomes*
- 2013 Controversies in Personalized Oncology, Barcelona, March 9, *Molecular subtypes of gastric cancer show systematic differences in response to PI3K inhibitors and fluorouracil*
- 2013 Human Genome Meeting and International Conference on Genetics (HGM ICG 2013), Singapore, April 18, *Bioinformatics for genetics and genomics: what should we be teaching?*
- 2013 Illumina Asia-Pacific Scientific Summit, Phuket, Thailand, April 23, *Next generation sequencing identifies new driver genes in Asian cancers*

- 2013 Quantitative Medicine Forum, Duke-NUS, Singapore, Feb 13, *Cancer genomics: Finding therapeutically promising subtypes of gastric cancer*
- 2012 Frontiers in Cancer Science, Singapore, Nov. 7, *Molecular subtypes of gastric cancer show systematic differences in genomic and epigenetic characteristics and in drug response*
- 2012 Duke-NUS Medical School, Singapore, talk for parents of children with ASD, Sept 22, *Finding genetic causes of autism spectrum disorders*
- 2012 Agilent Human Genetics Summit, Singapore, July 2-3, *Exome sequencing identifies new driver genes in Asian cancers*
- 2011 Pathlight School, Singapore, talk for parents of children with ASD, Oct 29, *Finding genetic causes of autism spectrum disorders*
- 2011 Federation of Asian and Oceanian Biochemists and Molecular Biologists (FAOBMB) Conference, Singapore, Oct. 5-7, *Analyzing NGS data: From sequence to function in tumor resequencing*
- 2008, Department of Biological Sciences, National University of Singapore, Sept. 26, *Human Y chromosome mutation and sperm production*
- 2008, Department of Veterinary Anatomy & Public Health, Texas A&M, Texas, April 3, *Y Chromosomes — Collateral damage in the war between the sexes*
- 2008, University of Georgia, March 31, *Y Chromosomes — Collateral damage in the war between the sexes*
- 2008, University of Kansas, March 26, *Y Chromosomes — Collateral damage in the war between the sexes*
- 2008, Mayo Clinic, Rochester Minnesota, March 7, *Generating, analyzing, interpreting metabolomic data*
- 2006, Kato Ladies Clinic, Tokyo, Japan, March 31, *Human Y chromosome: Evolution and sequence*
- 2006, DNA Structure, Genomic Rearrangements and Human Disease, Institute of Biosciences and Technology, Houston, Texas, March 12-14, *Large Scale variation among human y chromosomes*
- 2005, Pacific Grove, California, Y Chromosome and Male Germ Cell Biology in Health and Disease in the Post Genomic Era, Sept. 21-23, *The Human Y chromosome: Structure and genes*
- 2005, University of Pennsylvania, Center for Research on Reproduction and Women's Health, Nov 30, *The human Y chromosome and spermatogenesis*
- 2003, Center for Reproductive Medicine University of Amsterdam, The Netherlands, Oct., *How testis genes survive on the Y chromosome*
- 2003, Department of Growth and Reproduction, Rigshospitalet, Copenhagen, Denmark, Oct., *How testis genes survive on the Y chromosome*
- 2002, Germ Cells, Cold Spring Harbor Laboratory, New York, Oct. 9-13, *Rethinking the rotting Y: Palindromes, gene conversion, and germ-cell genes*
- 2000, Boston University, Boston, Massachusetts, April 10, *The Y chromosome exposed: sequence, genes, phenotypes, and functional variation*
- 2000, Clontech Laboratories, Palo Alto, California, June 15, *Sequence of the human Y chromosome genes, phenotypes, and functional variation*

- 2000, Great Apes: Phenotypes and Genotypes, Banbury Center, Cold Spring Harbor Laboratory, March 19-22, *Sequence of the human Y chromosome: genes, gene families, and phenotypes*
- 1997, Third International HUGO Single Chromosome Workshop on the Y Chromosome, University of Heidelberg, Germany, April 13-16, *Mapping and sequencing the human Y chromosome*
- 1994, Conference on Computers in Medicine, Austin, Texas, *managing laboratory workflow with LabBase*
- 1994, 20th International Conference on Very Large Data Bases, Santiago, Chile, *Building a laboratory information system around a C++-based object-oriented DBMS*
- 1994, Sixth International Workshop on Persistent Object Systems, Tarascon, France *Constructing a domain-specific DBMS using a persistent object system*
- 1991, 17th International Conference on Very Large Data Bases, Barcelona, Spain, *A framework for automating physical database design*
- 1991, Third International Workshop on Database Programming Languages, Nafplion, Greece, *rationale and design of BULK*

Local Invited Lectures

- 2017 Autism Spectrum Disorder – New Advances in Autism Research Symposium (Duke-NUS), Jan 17, *Genomics Linked to In-Depth Functional Studies to Identify Genetic Causes of Autism*
- 2016 The Centre for Big Data and Integrative Genomics (c-BIG), 10 Nov, *PRISM: Big Data, Genomics, and Precision Healthcare in Singapore*
- 2016 Roundtable leader for *NGS: from genomic data to personalized healthcare: creating the foundation for translational science* at Proventa International Bioinformatics Strategy Meeting, Oct 19
- 2016 Keynote Speaker for Raffles Science Symposium, 27 Jan, *Data driven biomedicine*
- 2015 Duke-NUS CSCB & NCC RIP/JC Conference, Sep 14, *Mutation signatures implicate aristolochic acid in bladder cancer development*
- 2014 Signature Seminar Series, Duke-NUS Graduate School Singapore, Oct 28, *Genome bioinformatics past, present, and future*
- 2014 Workshop on Predictive Models, Alternative Methods and Tissue Engineering sponsored by A*STAR and L'Oreal, May 20, *Assessing mutagenicity with massively parallel sequencing*
- 2012 Principles of Pharmacogenetics for Drug Regulators, for the Health Services Authority, Singapore, Feb. 9, *Basic principles of human genetics*
- 2011 Singapore Institute of Mental Health, Child Guidance Centre, talk for parents of children with ASD, May 21, *Finding genetic causes of autism spectrum disorders*
- 2011 Singapore Institute of Mental Health, Child Guidance Centre, talk for parents of children with ASD, April 9, *Finding genetic causes of autism spectrum disorders*
- 2010, Pharmacogenomics Workshop for the Health Services Authority, Singapore, Jan 25, *Basic principles of human genetics*

- 2009, Joint BII-DBS Workshop – Modern Approaches to Biological Problems, National University of Singapore, Sept. 3-4, *Can exon arrays help us understand cancer development?*
- 2009, Singapore MIT Alliance, Programme in Computation and Systems Biology Research Symposium, Singapore, July 28, *Cancer genomics, bioinformatics, and high-throughput systems biology*
- 2004, Mammalian Genetics, Genomics and Development, Whitehead Institute, Jan. 12, *How lively is the human Y chromosome? A survey of large scale rearrangements*
- 2004, Massachusetts Institute of Technology, course 18.417, “Introduction to Computational Molecular Biology,” Nov. 2, lecture *Microarrays and analysis of gene expression data from microarrays*
- 2003, Whitehead Institute, Whitehead Forum, Nov. 20, *How have testis genes survived on the human Y chromosome?*
- 2001, Boston IVF, Waltham, Massachusetts, January 25, 2001, *Recent advances in understanding the sequence of the Y chromosome*
- 2000, Whitehead Institute, Lecture Series for High School Teachers, April 28, *The human X and Y: A 300 million year history*
- 1998, Massachusetts Institute of Technology, Independent Activities Period (IAP) lecture, Jan., *Common variants project, finding common alleles responsible for common phenotypes*

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