# Raunak Shrestha, PhD

*Curriculum Vitae* [Last Updated: July 15, 2020]

Helen Diller Family Comprehensive Cancer Center,
University of California, San Francisco,
1450 3rd St, San Francisco, CA 94158, USA

**Email:** raunakman . shrestha @ ucsf . edu
**Email:** shrestha . raunak @ naamii . org . np
**Web:** http://raunakms.github.io/
**Publications:** [Google Scholar]

## Employment

| | |
|---|---|
| Oct 2019 - Current | Post-doctoral Research Fellow, **Helen Diller Family Comprehensive Cancer Center**, **University of California, San Francisco (UCSF)**, San Francisco, CA, USA <br> Advisor: Dr. Felix Y. Feng |
| June 2020 - Current | Adjunct Research Scientist (Faculty), <br> **Nepal Applied Mathematics & Informatics Institute (NAAMII)**, Kathmandu, Nepal |
| Sept 2018 - Aug 2019 | Post-doctoral Research Fellow, <br> **University of British Columbia**, Vancouver, BC, Canada <br> **Vancouver Prostate Centre**, Vancouver, BC, Canada <br> Advisor: Dr. Colin C. Collins |
| July 2009 - July 2011 | Research Associate, **Center for Molecular Dynamics Nepal**, Kathmandu, Nepal |

## Post-Secondary Education

| | |
|---|---|
| Sept 2012 - Aug 2018 | Doctor of Philosophy in Bioinformatics, **University of British Columbia**, Canada <br> **Vancouver Prostate Centre**, Vancouver, BC, Canada <br> under CIHR Bioinformatics Training Program <br> Advisors: Dr. Colin C. Collins and Dr. S. Cenk Sahinalp <br> Thesis Title: "*Computational Prioritization of Cancer Driver Genes for Precision Oncology*" |
| Sept 2011 - Aug 2012 | Master of Science in Bioinformatics, **Simon Fraser University**, Canada <br> under CIHR Bioinformatics Training Program <br> (Transferred to PhD program) |
| 2005 - 2009 | Bachelors of Technology (B.Tech.) in Biotechnology, **Kathmandu University**, Nepal |

## Selected Publications

[1] **R. Shrestha**, M. L. Fernandez, A. Dawson, J. Hoenisch, S. Volik, Y.-Y. Lin, S. Anderson, H. Kim, A. Haegert, S. Colborne, B. McConeghy, R. H. Bell, S. Brahmbhatt, G. E. DiMattia, S. Le Bihan, G. B. Morin, C. C. Collins, and M. S. Carey. *Multiomics Characterization of Potential Therapeutic Vulnerabilities in Low-grade Serous Ovarian Carcinoma*. *bioRxiv preprint*, 2020a. doi: 10.1101/2020.06.18.13506. URL https://doi.org/10.1101/2020.06.18.135061. (*Submitted*)

[2] **R. Shrestha**, N. Nabavi, Y.-Y. Lin, F. Mo, S. Anderson, S. Volik, H. H. Adomat, D. Lin, H. Xue, X. Dong, R. Shukin, R. H. Bell, B. McConeghy, A. Haegert, S. Brahmbhatt, E. Li, H. Z. Oo, A. Hurtado-Coll, L. Fazli, J. Zhou, Y. McConnell, A. McCart, A. Lowy, G. B. Morin, T. Chen, M. Daugaard, S. C. Sahinalp, F. Hach, S. Le Bihan, M. E. Gleave, Y. Wang, A. Churg, and C. C. Collins. *BAP1 Haploinsufficiency Predicts a Distinct Immunogenic Class of Malignant Peritoneal Mesothelioma*. **Genome Medicine**, 2019. doi: 10.1186/s13073-019-0620-3. URL https://pubmed.ncbi.nlm.nih.gov/30777124

[3] **R. Shrestha**, E. Hodzic, T. Sauerwald, P. Dao, K. Wang, J. Yeung, S. Anderson, F. Vandin, G. Haffari, C. C. Collins, and S. C. Sahinalp. *HIT'nDRIVE: patient-specific multidriver gene prioritization for precision oncology*. **Genome Research**, 27(9):1573–1588, sep 2017. ISSN 1549-5469. doi: 10.1101/gr.221218.117. URL https://pubmed.ncbi.nlm.nih.gov/28768687

[4] **R. Shrestha**, E. Hodzic, J. Yeung, K. Wang, T. Sauerwald, P. Dao, S. Anderson, H. Beltran, M. A. Rubin, C. C. Collins, G. Haffari, and S. C. Sahinalp. *HIT'nDRIVE: Multi-driver Gene Prioritization Based on Hitting Time*. *Research in Computational Molecular Biology: 18th Annual International Conference*, **RECOMB 2014**, *Pittsburgh, PA, USA, April 2-5, 2014, Proceedings*, pages 293–306, 2014. doi: 10.1007/978-3-319-05269-4_23. URL http://dx.doi.org/10.1007/978-3-319-05269-4_23

[5] E. Hodzic, **R. Shrestha***, K. Zhu, K. Cheng, C. C. Collins, and S. C. Sahinalp. Combinatorial detection of conserved alteration patterns for identifying cancer subnetworks. **GigaScience**, 8(4), 04 2019. ISSN 2047-217X. doi: 10.1093/gigascience/giz024. URL https://pubmed.ncbi.nlm.nih.gov/30978274. *As joint first author

[6] **R. Shrestha**, N. Nabavi, , S. Volik, S. Anderson, A. Haegert, B. McConeghy, F. Sar, S. Brahmbhatt, R. H. Bell, S. Le Bihan, Y. Wang, C. C. Collins, and A. Churg. *Well-Differentiated Papillary Mesothelioma of the Peritoneum is Genetically Distinct from Malignant Mesothelioma*. **Cancers**, 12(6), 06 2020b. doi: 10.3390/cancers12061568. URL https://pubmed.ncbi.nlm.nih.gov/32545767

## Relevant Publications

[7] W. S. Chen, W. A. Haynes, R. Waitz, K. Kamath, A. Vega-Crespo, **R. Shrestha**, M. Zhang, A. Foye, I. B. Carretero, I. G. Perez, M. Zhang, S. G. Zhao, M. Sjöström, D. A. Quigley, J. Chou, T. M. Beer, M. Rettig, M. Gleave, C. P. Evans, P. Lara, K. N. Chi, R. E. Reiter, J. J. Alumkal, R. Aggarwal, E. J. Small, P. S. Daugherty, A. Ribas, D. Y. Oh, J. C. Shon, and F. Y. Feng. Autoantibody landscape of advanced prostate cancer. *bioRxiv preprint*, 2020. doi: 10.1101/2020.05.02.074575. URL https://doi.org/10.1101/2020.05.02.074575. (*Submitted*)

[8] N. Rydzewski, J. M. Lang, M. Yu, M. Sjöström, S. L. Chang, W. Chen, **R. Shrestha**, M. Zhang, D. A. Quigley, R. Aggarwal, E. Small, D. R. Wahl, F. Y. Feng, and S. G. Zhao. Predicting cancer drug targets - treatment response glmnet signatures. *(In Submission)*, 2020

[9] R. Das, M. Sjostrom, **R. Shrestha**, C. Yogodzinski, E. A. Egusa, L. Chesner, W. S. Chen, J. Chou, D. K. Dang, A. Ge, S. Kabir, D. A. Quigley, A. Ashworth, F. Y. Feng, and L. A. Gilbert. An integrated functional and clinical genomics approach reveal genesdriving aggressive metastatic prostate cancer. *(In Submission)*, 2020

[10] ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. Pan-cancer analysis of whole genomes. **Nature**, 578(7793):82–93, feb 2020. ISSN 1476-4687. doi: 10.1038/s41586-020-1969-6. URL https://pubmed.ncbi.nlm.nih.gov/32025007

[11] M. A. Reyna, D. Haan, M. Paczkowska, L. P. C. Verbeke, M. Vazquez, A. Kahraman, S. Pulido-Tamayo, J. Barenboim, L. Wadi, P. Dhingra, **R. Shrestha**, G. Getz, M. S. Lawrence, J. S. Pedersen, M. A. Rubin, D. A. Wheeler, S. Brunak, J. M. G. Izarzugaza, E. Khurana, K. Marchal, C. von Mering, S. C. Sahinalp, A. Valencia, PCAWG Drivers and Functional Interpretation Working Group, J. Reimand, J. M. Stuart, B. J. Raphael, and PCAWG Consortium. Pathway and network analysis of more than 2500 whole cancer genomes. **Nature communications**, 11(1):729, feb 2020. ISSN 2041-1723. doi: 10.1038/s41467-020-14367-0. URL https://pubmed.ncbi.nlm.nih.gov/32024854

[12] E. Hodzic, **R. Shrestha**, S. Malikic, C. C. Collins, K. Litchfield, S. Turajlic, and C. Sahinalp. Identification of conserved evolutionary trajectories in tumors. **Bioinformatics**, 36(Supplement1):i427–i435, 07 2020. ISSN 1367-4803. doi: 10.1093/bioinformatics/btaa453. URL https://pubmed.ncbi.nlm.nih.gov/32657374. (*ISMB 2020*)

[13] N. M. D'Costa, D. Cina, **R. Shrestha**, R. H. Bell, Y.-y. Lin, H. Asghari, C. U. Monjaras-Avila, C. Kollmannsberger, F. Hach, C. I. Chavez-Munoz, and A. I. So. Identification of gene signature for treatment response to guide precision oncology in clear-cell renal cell carcinoma. **Scientific Reports**, 10(1):2026, feb 2020a. ISSN 2045-2322. doi: 10.1038/s41598-020-58804-y. URL https://pubmed.ncbi.nlm.nih.gov/32029828

[14] N. M. D'Costa, M. R. Lowerison, P. A. Raven, Z. Tan, M. E. Roberts, **R. Shrestha**, M. W. Urban, C. U. Monjaras-Avila, H. Z. Oo, A. Hurtado-Coll, C. Chavez-Munoz, and A. I. So. Y-box binding protein-1 is crucial in acquired drug resistance development in metastatic clear-cell renal cell carcinoma. **Journal of experimental & clinical cancer research: CR**, 39(1):33, feb 2020b. ISSN 1756-9966. doi: 10.1186/s13046-020-1527-y. URL https://pubmed.ncbi.nlm.nih.gov/32041631

[15] R. K. Shrestha and **R. Shrestha**\*. *Nudging households towards clean cooking: the role of group segmentation based on diversity in fuel choice. arXiv preprint*, 2020. URL https://arxiv.org/abs/2005.09616. \*As joint first author

[16] H. Sharifi-Noghabi, Y. Liu, N. Erho, **R. Shrestha**, M. Alshalalfa, E. Davicioni, C. C. Collins, and M. Ester. *Deep Genomic Signature for early metastasis prediction in prostate cancer. bioRxiv preprint*, 2018. doi: 10.1101/276055. URL https://doi.org/10.1101/276055. (*Submitted*)

[17] M. Yamada, J. Tang, J. Lugo-Martinez, E. Hodzic, **R. Shrestha**, H. Ouyang, P. Radivojac, C. Sahinalp, F. Menczer, Y. Chang, A. Saha, H. Mamitsuka, and D. Yin. *Ultra High-Dimensional Nonlinear Feature Selection for Big Biological Data*. **IEEE Transactions on Knowledge and Data Engineering**, 30(7):1352–1365, 2018. ISSN 1041-4347. doi: 10.1109/TKDE.2018.2789451. URL https://doi.org/10.1109/TKDE.2018.2789451

[18] E. E. Gill, L. S. Chan, G. L. Winsor, N. Dobson, R. Lo, S. J. Ho Sui, B. K. Dhillon, P. K. Taylor, **R. Shrestha**, C. Spencer, R. E. W. Hancock, P. J. Unrau, and F. S. L. Brinkman. *High-throughput detection of RNA processing in bacteria*. **BMC Genomics**, 19(1):223, 2018. ISSN 1471-2164. doi: 10.1186/s12864-018-4538-8. URL https://pubmed.ncbi.nlm.nih.gov/29587634

[19] I. S. U. Luk, **R. Shrestha**, H. Xue, Y. Wang, F. Zhang, D. Lin, A. Haegert, R. Wu, X. Dong, C. C. Collins, A. Zoubeidi, M. E. Gleave, P. W. Gout, and Y. Wang. *BIRC6 Targeting as Potential Therapy for Advanced, Enzalutamide-Resistant Prostate Cancer*. **Clinical Cancer Research**, 23(6):1542–1551, mar 2017. ISSN 1078-0432. doi: 10.1158/1078-0432.CCR-16-0718. URL https://pubmed.ncbi.nlm.nih.gov/27663589

[20] A. W. Wyatt, F. Mo, K. Wang, B. McConeghy, S. Brahmbhatt, L. Jong, D. M. Mitchell, R. L. Johnston, A. Haegert, E. Li, J. Liew, J. Yeung, **R. Shrestha**, A. V. Lapuk, A. McPherson, R. Shukin, R. H. Bell, S. Anderson, J. Bishop, A. Hurtado-Coll, H. Xiao, A. M. Chinnaiyan, R. Mehra, D. Lin, Y. Wang, L. Fazli, M. E. Gleave, S. V. Volik, and C. C. Collins. *Heterogeneity in the inter-tumor transcriptome of high risk prostate cancer*. **Genome Biology**, 15(8):426, Aug 2014. ISSN 1474-760X. doi: 10.1186/s13059-014-0426-y. URL https://pubmed.ncbi.nlm.nih.gov/25155515

[21] K. Wang, **R. Shrestha**, A. W. Wyatt, A. Reddy, J. Lehár, Y. Wang, A. Lapuk, and C. C. Collins. *A meta-analysis approach for characterizing pan-cancer mechanisms of drug sensitivity in cell lines*. **PloS One**, 9(7): e103050, 2014. ISSN 1932-6203. doi: 10.1371/journal.pone.0103050. URL https://pubmed.ncbi.nlm.nih.gov/25036042

[22] **R. Shrestha**, R. N. Joshi, K. Joshi, B. H. Poudel, and B. G. Shrestha. *Analysis of KatG Ser315Thr Mutation in Multidrug Resistant Mycobacterium tuberculosis and SLC11A1 Polymorphism in Multidrug Resistance Tuberculosis in Central Development Region of Nepal Using PCR-RFLP Technique: A Pilot Study*. **Nepal Journal of Biotechnology**, 1(1):14–21, 2011

## Thesis

- **R. Shrestha**. *Computational Prioritization of Cancer Driver Genes for Precision Oncology*. PhD thesis, The University of British Columbia, 2018. URL https://open.library.ubc.ca/cIRcle/collections/24/items/1.0370936. Advisors: Dr. Colin C. Collins & Dr. S. Cenk Sahinalp

## PRESENTATIONS

### Selected Oral Talks

- *Inactivation of BAP1 Predicts a Distinct Immunogenic Class of Malignant Peritoneal Mesothelioma.* **Terry Fox Seminar, Vancouver Prostate Centre**. September 28, 2018, Vancouver General Hospital, Vancouver, Canada.

- *BAP1 Loss Predicts Therapeutic Vulnerability in Malignant Peritoneal Mesothelioma.* **14th International Conference of the International Mesothelioma Interest Group (iMig2018)**. May 2-5, 2018, Ottawa, Canada

- *HIT'nDRIVE: Patient-Specific Multi-Driver Gene Prioritization for Precision Oncology.* **8th Annual Scientific Meeting, Terry Fox Research Institute**. November 4, 2017, Vancouver, Canada

- *Translating Big-Data to Precision Oncology.* **Terry Fox Seminar, Vancouver Prostate Centre**. February 17, 2017, Vancouver General Hospital, Vancouver, Canada.

- *HIT'nDRIVE: Patient-Specific Multi-Driver Gene Prioritization for Precision Oncology.* **Vancouver Bioinformatics User Group (VanBUG)**. November 3, 2016, Vancouver, Canada

- *HIT'nDRIVE: Patient-Specific Multi-Driver Gene Prioritization for Precision Oncology.* **10th Annual Lorne D. Sullivan Lectureship & Research Day**. June 21, 2016, Vancouver General Hospital, Vancouver, Canada.

- *HIT'nDRIVE: Patient-Specific Multi-Driver Gene Prioritization to Guide Precision Cancer Medicine.* **Workshop on Network Biology (Algorithmic Challenges in Genomics)**. April 11-15, 2016, Simons Institute for the Theory of Computing, University of California Berkeley, Berkeley, CA, USA.
  https://simons.berkeley.edu/talks/raunak-shrestha-04-12-16

- *Computational Detection and Prioritization of Driver Alterations in Cancer.* **Terry Fox Seminar, Vancouver Prostate Centre**. November 3, 2014, Vancouver General Hospital, Vancouver, Canada.

- *HIT'nDRIVE: Multi-Driver Gene Prioritization based on Hitting Time.* **18th Annual International Conference on Research in Computational Molecular Biology (RECOMB)**. April 2-5, 2014, Pittsburgh, PA, USA.


### Invited Talks

- *Computational Prioritization of Cancer Driver Genes for Precision Oncology.* **University of California San Francisco**. April 8, 2019, San Francisco, CA, USA.

- *Computational Prioritization of Cancer Driver Genes for Precision Oncology.* **National Cancer Institute**. December 10, 2018, Bethesda, MD, USA.

- *Computational Prioritization of Cancer Driver Genes for Precision Oncology.* **University of California San Diego**. November 13, 2018, San Diego, CA, USA.

- *Computational Prioritization of Cancer Driver Genes for Precision Oncology.* **University of California Santa Cruz**. November 9, 2018, Santa Cruz, CA, USA.

## Awards and Honors

| | |
|---|---|
| 2018 | UBC Translational Cancer Genomics Travel Award (iMig2018). |
| 2016-2018 | Mitacs Accelerate PhD Fellowship. |
| 2015-2016 | Prostate Cancer Foundation - British Columbia (PCF-BC) Research Awards - 2015. |
| 2014-2016 | Faculty of Science Graduate Award, University of British Columbia. |
| 2014 | International Society for Computational Biology (ISCB) Travel Fellowship (RECOMB-2014). |
| 2011-2013 | CIHR Bioinformatics Training Program for Health Research. |

## Research Interest

| | | | |
|---|---|---|---|
| Cancer Genomics | Prostate Cancer | Immuno-Oncogenomics | Sequencing |
| Single-cell Genomics | Epigenomics | Precision Oncology | Network Medicine |
| Infectious Disease Genomics | Machine Learning | Data Science | |

## Technical Skills

| | |
|---|---|
| Programming Languages | R, perl, python, C, C++ |
| Web Development | php, HTML/5, CSS, JavaScript, R-shiny |
| Databases & Query Languages | MySQL |
| Others | CPLEX, GitHub |
| Molecular Biology | Experienced in routine genomics & proteomics laboratory works |

## Software Packages & Data Analytics

- **HIT'nDRIVE** (https://github.com/sfu-compbio/hitndrive)

- **cd-CAP** (https://github.com/ehodzic/cd-CAP)

- **Group Segmentation and Diversity** *Nudging households towards clean cooking: the role of group segmentation based on diversity in fuel choice* (`https://github.com/raunakms/diversity_cooking_fuel`)

## Students Mentored

| | | |
|---|---|---|
| 2020- | Aroj Hada | Research Intern, Bioinformatics, NAAMII, Nepal |
| 2020- | Rajesh Timilsina | Research Intern, Machine Learning, NAAMII, Nepal |
| 2017-2019 | Hossein Sharifi-Noghabi | Ph.D. Student, Computer Science. Simon Fraser University, Canada |

## Academic Papers Peer Reviewed

(number of reviews parenthesized)

| | |
|---|---|
| Nature | (1) |
| Science | (3) |
| Nature Communications | (3) |
| Bioinformatics | (3) |
| Cancer Research | (1) |
| Genome Medicine | (1) |
| European Urology | (1) |
| BMC Genomics | (1) |
| BMC Bioinformatics | (1) |
| Neoplasia | (1) |
| Research in Computational Molecular Biology (RECOMB) | (3) |
| International Conference on Intelligent Systems for Molecular Biology (ISMB) | (1) |
| The Asia Pacific Bioinformatics Conference (APBC) | (1) |
| Workshop on Algorithms in Bioinformatics (WABI) | (1) |
| International Conference on Computational Advances in Bio and medical Sciences (ICCABS) | (1) |
| Nepal Journal of Biotechnology | (8) |

# References

References can be made available upon request