PICHAI RAMAN, PHD

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PROFESSIONAL SUMMARY

Computational biology leader with 20+ years of experience across pharma, biotech, and academia, specializing in oncology informatics and driving biological insight across the R&D pipeline from target identification and validation through translational biomarker discovery, patient stratification, and clinical data integration. Deep expertise integrating public and proprietary multi-omics, functional genomics, single-cell and clinical genomics, and real-world evidence (RWE) using advanced statistical modeling and AI/ML to generate actionable insights that inform oncology program and portfolio decisions. Proven collaborative leader, building and mentoring high-performing teams and partnering closely with discovery, translational, and clinical groups to advance oncology and complex disease programs from early discovery through clinical stages.

CAREER HIGHLIGHTS

- Led target discovery efforts in a multi-institutional collaboration (Pediatric Cancer Dream Team / Stand Up to Cancer), identifying GPC2 as a key neuroblastoma target that advanced to clinical trials (NCI-2023-06712)
- Integrated DepMap data with proteomics, transcriptomics, and epigenomics to prioritize DLK1 as a novel immunotherapeutic target in neuroblastoma, leading to a Phase 1 clinical trial (NCT06041516)
- PedcBioPortal: Headed effort to collaborate with MSKCC, DFCI, and Princess Margaret and build a pediatric-focused cBioPortal for use by the pediatric cancer community (pedcbioportal.org) comprising both NGS and EHR data.
- Identified FXYD5 as a driver of metastasis and poor prognosis marker in ovarian cancer, foundational work validated by subsequent studies confirming its role in chemotherapy resistance and epithelial-to-mesenchymal transition
- Identified enrichment of targetable mutations in Foundation Medicine sequencing data from 151 neuroblastoma samples at relapse, revealing therapeutic opportunities in chemotherapy-resistant pediatric cancer.
- Played a key role in the original Cancer Cell Line Encyclopedia (CCLE) project and leveraged the data to identify the target and MOA of Englerin A.
- Contributed to groundbreaking research on mechanisms of resistance to CD19-targeted CAR T-cell therapy, identifying alternative splicing and acquired mutations in CD19 as key factors enabling immune evasion in leukemia.
- Senior author on the development of a robust transcriptome-based classifier for medulloblastoma subtyping, achieving over 97% accuracy across independent datasets and enabling reliable patient stratification based on retrospective and prospective RNA-based data.

SKILLS

- Target Identification & Prioritization
- Translational Biomarker Discovery
- Oncology Informatics
- Patient Stratification modeling
- NGS Data Analysis & Scalable Genomics Workflows
- Mechanism of Action (MoA) Resistance Analysis
- Clinical Genomics
- Predictive Modeling
- Survival Analysis
- Real-World Evidence (RWE) & Clinical Data Integration
- Multimodal Data Integration
- Pathway, Network & Systems Biology Modeling
- Team Building & mentorship
- Knowledge Graph– and Literature-Driven Discovery
- Data Visualization & Decision-Support Analytics
- Cross-Functional Leadership (Discovery–Translational–Clinical)
- Strategic Road mapping for Computational Biology & AI

WORK EXPERIENCE

CADENT Philadelphia, PA — 10/2025 – Present

Senior Director, Data Science

Led the Data Science function delivering large-scale identity and audience intelligence solutions, translating complex data into actionable insights for clients and customers.

- Directed teams processing 200+ billion data points daily using Google Cloud Platform and BigQuery to power real-time analytics and decisioning
- Oversaw development and productionization of dozens of machine learning models, optimizing tradeoffs between predictive accuracy and audience reach to meet diverse business and customer objectives

SPARK THERAPEUTICS (ROCHE GROUP), Philadelphia, PA 04/2021 – 5/2025

Director of Computational Biology and Machine Learning

Responsible for leading the computational biology and machine learning team in support of research projects and technical development projects.

- Contributed to barcode enrichment-based single-nucleus RNA sequencing analysis to profile AAV capsid tropism across neuronal subtypes in non-human primates, identifying MNM021 as a lead therapeutic candidate for Parkinson's disease
- Collaborated with translational and clinical teams to identify cytokine, chemokine, and immune biomarkers associated with cytotoxic T-lymphocyte (CTL) events in clinical cell therapy programs using visual analytics to support therapeutic optimization
- Developed a machine learning-based target identification engine integrating Open Targets and multi-omics datasets to systematically prioritize and validate novel therapeutic targets for complex disease programs

GLAXOSMITHKLINE, Collegeville, PA 11/2019 – 04/2021

Oncology Data Strategy and Design Director

Defined the data strategy and developed workflows and end points to support oncology research and clinical activities and projects while leading a matrixed team across functions to ensure alignment and execution. Led data science initiatives to build data products and product analytics tools, ensuring data quality and driving data-driven decisions.

- Oncology Workflows: Spearheaded the development of scalable workflows and tools for translational oncology team to enhance biomarker analytics. Championed strategic AI and ML initiatives to streamline oncology drug discovery, integrating cheminformatics and predictive analytics.
- Data Frameworks: Led strategic initiatives to optimize data solutions and design frameworks, significantly improving the efficiency of oncology research.

CHILDREN'S HOSPITAL OF PHILADELPHIA, Philadelphia, PA 02/2013 – 11/2019

Bioinformatics Supervisor and Director of Scientific and Analytic Services (09/2016 – 11/2019)

Bioinformatics Scientist III (02/2013 – 09/2016)

Developed and led an interdisciplinary team of bioinformatic analysts, data scientists, and engineers to deliver strategic informatics solutions and support scientific programs and projects in the pediatric cancer space.

- Cavatica: Worked with Seven Bridges Genomics to develop a cloud platform for genomic analysis and collaboration (cavatica.org).
- Kids First: Helped to design and create the Kids First genomic application that houses pediatric cancer and birth defect genomic and phenotypic data (kidsfirstdrc.org/portal).
- Mechanisms of Compound Sensitivity: Collaborated with various pharmaceutical companies to determine mechanisms of sensitivity to certain cancer therapeutics.
- Target Discovery in Pediatric Cancer: Led target discovery aim in a multi-institution effort (Pediatric Cancer Dream Team / Stand Up to Cancer) dedicated to cancer immunotherapy by building scalable bioinformatics workflows.

NOVARTIS, Cambridge, MA 09/2005 – 02/2013

Scientific Technical Leader I (02/2012 – 02/2013)

Scientist II (04/2010 – 02/2012)

Scientist I (04/2008 – 04/2010)

Scientific Associate II (09/2005 – 05/2008)

Led computational biology initiatives to support early discovery and translational research through the integration of high-dimensional data, development of analysis platforms, and collaborative pipeline building. Focused on accelerating target identification, pathway analysis, and compound profiling across diverse therapeutic areas.

- DiseasExpress: Worked with cross-departmental team to develop expression warehouse for Novartis with over 60K samples.
- GSEA Project: Developed application in Java (J2EE) to store, manage, and share gene sets. In addition, implemented GSEA to use sets in analysis of microarray and other high-throughput data.
- Compound Set Enrichment: Implemented set enrichment type approach (Pipeline Pilot) to aid in reducing FP rate of high-throughput screens. Worked with other internal groups to determine best methods for clustering and grouping of compound data for use with this approach.
- Cancer Cell Line Encyclopedia: Worked as part of a collaborative team (Broad / NIBR) to develop a pipeline (R) to determine

markers (genetic lesion / expression) of sensitivity to compounds across a set of cell lines.
- Expression Signature Project: Spearheaded initiative to create gene expression signatures (R/Bioconductor) to determine pathway activity for use in patient stratification and compound MoA determination.
- mTORC1 Project: Worked with Manning Lab (HMS) to determine specific set of TSC regulated genes from microarray data and associated processes (Metacore). Analysis used to help elucidate biology around mTOR Complex 1.
- Early Target Discovery: Integrated various data types, including copy number data, shRNA / siRNA data, expression data, and mutation data from both tissue and cell line data and developed analysis file in Spotfire DXP for early target discovery purposes. Data sources included internal and public repositories such as the TCGA, GEO, and ArrayExpress. Metacore and IPA used additionally to determine relevant disease pathway links and connections to known oncogenes or disease markers.
- Proteomics: Worked with iTRAQ data across cell lines and compared to mRNA for target / model nomination. Analysis displayed and reported out to interested parties in Spotfire DXP.
- Education: Developed program alongside education office and quantitative biology unit to educate wet bench biologists on analysis of certain common types of data as well as use of Spotfire DXP.

EDUCATION

Doctor of Philosophy (PhD), Biomedical Engineering, Science and Health Systems, DREXEL UNIVERSITY, Philadelphia, PA (2016)

Master of Science (MS), Bioinformatics, OHIO STATE UNIVERSITY, Columbus, OH (2005)

Bachelor of Science (BS), Cell and Molecular Biology, UNIVERSITY OF MICHIGAN, Ann Arbor, MI

PUBLICATIONS

53 Total Publications | 5 First Author | 4 Second Author | 1 Last Author

Selected Publications Listed Below – Full list available at https://pichairaman.github.io/

1. Nabbi A, Beck P, Delaidelli A, Oldridge DA, Sudhaman S, Zhu K, Yang SYC, Mulder DT, Bruce JP, Paulson JN, **Raman P**, Zhu Y, Resnick AC, Sorensen PH, Sill M, Brabetz S, Lambo S, Malkin D, Johann PD, Kool M, Jones DTW, Pfister SM, Jäger N, Pugh TJ. Transcriptional immunogenomic analysis reveals distinct immunological clusters in paediatric nervous system tumours. *Genome Medicine*, 15(1). doi:10.1186/s13073-023-01219-x (2023). PMID: 37679810

2. Shapiro JA, Gaonkar KS, Spielman SJ, Savonen CL, Bethell CJ, Jin R, Rathi KS, Zhu Y, Egolf LE, Farrow BK, Miller DP, Yang Y, Koganti T, Noureen N, Koptyra MP, Duong N, Santi M, Kim J, Robins S, Storm PB, Mack SC, Lilly JV, Xie HM, Jain P, **Raman P**, Rood BR, Lulla RR, Nazarian J, Kraya AA, Vaksman Z, Heath AP, Kline C, Scolaro L, Viaene AN, Huang X, Way GP, Foltz SM, Zhang B, Poetsch AR, Mueller S, Ennis BM, Prados M, Diskin SJ, Zheng S, Guo Y, Kannan S, Waanders AJ, Margol AS, Kim MC, Hanson D, Van Kuren N, Wong J, Kaufman RS, Coleman N, Blackden C, Cole KA, Mason JL, Madsen PJ, Koschmann CJ, Stewart DR, Wafula E, Brown MA, Resnick AC, Greene CS, Rokita JL, Taroni JN; Children's Brain Tumor Network; Pacific Pediatric Neuro-Oncology Consortium. OpenPBTA: The Open Pediatric Brain Tumor Atlas. *Cell Genomics*, 3(7):100340. doi: 10.1016/j.xgen.2023.100340. eCollection (2023). PMID: 37492101

3. Dang MT, Gonzalez MV, Gaonkar KS, Rathi KS, Young P, Arif S, Zhai L, Alam Z, Devalaraja S, To TKJ, Folkert IW, **Raman P**, Rokita JL, Martinez D, Taroni JN, Shapiro JA, Greene CS, Savonen C, Mafra F, Hakonarson H, Curran T, Haldar M. Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. *Cell Reports*, 42(6):112600. doi: 10.1016/j.celrep.2023.112600. Epub (2023). PMID: 37235472

4. Maddipati R, Norgard RJ, Baslan T, Rathi KS, Zhang A, Saeid A, Higashihara T, Wu F, Kumar A, Annamalai V, Bhattacharya S, **Raman P**, Adkisson CA, Pitarresi JR, Wengyn MD, Yamazoe T, Li J, Balli D, LaRiviere MJ, Ngo TC, Folkert IW, Millstein ID, Bermeo, J, Carpenter EL, McAuliffe JC, Oktay MH, Brekken RA, Lowe SW, Iacobuzio-Donahue CA, Notta F, Stanger BZ. MYC Levels Regulate Metastatic Heterogeneity in Pancreatic Adenocarcinoma. *Cancer Discovery*, 12(2):542-561. doi: 10.1158/2159-8290.CD-20-1826. Epub (2021). PMID: 34551968

5. Tong CCL, Koptyra M, **Raman P**, Rathi KS, Choudhari N, Lin X, Seckar T, Wei Z, Kohanski MA, O'Malley BW, Cohen NA, Kennedy DW, Adappa ND, Robertson ES, Baranov E, Kuan EC, Papagiannopoulos P, Jalaly JB, Feldman MD, Storm PB, Resnick AC, Palmer JN. Targeted gene expression profiling of inverted papilloma and squamous cell carcinoma. *Int Forum Allergy Rhinol*, 12(2), 200-209. doi: 10.1002/alr.22882. Epub (2021). PMID: 34510780

6. Dang MT, Gonzalez MV, Gaonkar KS, Rathi KS, Young P, Arif S, Zhai L, Alam Z, Devalaraja S, To TKJ, Folkert IW, **Raman P**, Rokita JL, Martinez D, Taroni JN, Shapiro JA, Greene CS, Savonen C, Mafra F, Hakonarson H, Curran T, Haldar M.

Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. *Cell Rep*, 34(13), 108917. doi: 10.1016/j.celrep (2021). PMID: 33789113

7. Kundra R, Zhang H, Sheridan R, Sirintrapun S, Wang A, Ochoa A, Wilson M, Gross B, Sun Y, Madupuri R, Satravada B, Reales D, Vakiani E, Al-Ahmadie H, Dogan A, Arcila M, Zehir A, Maron S, Berger M, Viaplana C, Janeway K, Ducar M, Sholl L, Dogan S, Bedard P, Surrey L, Sanchez I, Syed A, Rema A, Chakravarty D, Suehnholz S, Nissan M, Iyer G, Murali R, Bouvier N, Soslow R, Hyman D, Younes A, Intlekofer A, Harding J, Carvajal R, Sabbatini P, Abou-Alfa G, Morris L, Janjigian Y, Gallagher M, Soumerai T, Mellinghoff I, Hakimi A, Fury M, Huse J, Bagrodia A, Hameed M, Thomas S, Gardos S, Cerami E, Mazor T, Kumari P, **Raman P**, Shivdasani P, MacFarland S, Newman S, Waanders A, Gao J, Solit DSchultz N. OncoTree: A Cancer Classification System for Precision Oncology. *JCO Clinical Cancer Informatics* 221-230 doi:10.1200/cci.20.0010 (2021). PMID: 33625877

8. Petralia F, Tignor N, Reva B, Koptyra M, Chowdhury S, Rykunov D, Krek A, Ma W, Zhu Y, Ji J, Calinawan A, Whiteaker J, Colaprico A, Stathias V, Omelchenko T, Song X, **Raman P**, Guo Y, Brown M, Ivey R, Szpyt J, Guha Thakurta S, Gritsenko M, Weitz K, Lopez G, Kalayci S, Gümüş Z, Yoo S, da Veiga Leprevost F, Chang H, Krug K, Katsnelson L, Wang Y, Kennedy J, Voytovich U, Zhao L, Gaonkar K, Ennis B, Zhang B, Baubet V, Tauhid L, Lilly J, Mason J, Farrow B, Young N, Leary S, Moon J, Petyuk V, Nazarian J, Adappa N, Palmer J, Lober R, Rivero-Hinojosa S, Wang L, Wang J, Broberg M, Chu R, Moore R, Monroe M, Zhao R, Smith R, Zhu J, Robles A, Mesri M, Boja E, Hiltke T, Rodriguez H, Zhang B, Schadt E, Mani D, Ding L, Iavarone A, Wiznerowicz M, Schürer S, Chen X, Heath A, Rokita J, Nesvizhskii A, Fenyö D, Rodland K, Liu T, Gygi S, Paulovich A, Resnick A, Storm P, Rood B, Wang P, Francis A, Morgan A, Waanders A, Viaene A, Buccoliero A, Chinnaiyan A, Leonard C, Kline C, Caporalini C, Kinsinger C, Li C, Kram D, Hanson D, Appert E, Kawaler E, Raabe E, Jackson E, Greenfield J, Stone G, Getz G, Grant G, Teo G, Pollack I, Cain J, Foster J, Phillips J, Palma J, Ketchum K, Ruggles K, Blumenberg L, Cornwell M, Sarmady M, Domagalski M, Cieślik M, Santi M, Li M, Ellis M, Wyczalkowski M, Connors M, Scagnet M, Gupta N, Edwards N, Vitanza N, Vaske O, Becher O, McGarvey P, Firestein R, Mueller S, Winebrake S, Dhanasekaran S, Cai S, Partap S, Patton T, Le T, Lorentzen T, Liu WBocik W. Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. *Cell* 183: 1962-1985.e31 doi:10.1016/j.cell.2020.10.044 (2020**).** PMID: 33242424

9. Gaonkar K, Marini F, Rathi K, Jain P, Zhu Y, Chimicles N, Brown M, Naqvi A, Zhang B, Storm P, Maris J, **Raman P**, Resnick A, Strauch K, Taroni JRokita J. annoFuse: an R Package to annotate, prioritize, and interactively explore putative oncogenic RNA fusions. *BMC Bioinformatics* 21: doi:10.1186/s12859-020-03922-7 (2020). PMID: 33317447

10. Rathi K, Arif S, Koptyra M, Naqvi A, Taylor D, Storm P, Resnick A, Rokita J, **Raman P** (2020) A transcriptome-based classifier to determine molecular subtypes in medulloblastoma. *PLOS Computational Biology* 16: e1008263 doi:10.1371/journal.pcbi.1008263 (2020). PMID: 33119584

11. Tetri L, Kolla V, Golden R, Iyer R, Croucher J, Choi J, Macfarland S, Naraparaju K, Guan P, Nguyen F, Gaonkar K, **Raman P**, Brodeur G. RET receptor expression and interaction with TRK receptors in neuroblastomas. *Oncology Reports* doi:10.3892/or.2020.7583 (2020). PMID: 32319659

12. Rentas S, Rathi K, Kaur M, **Raman P**, Krantz I, Sarmady MTayoun A. Diagnosing Cornelia de Lange syndrome and related neurodevelopmental disorders using RNA sequencing. *Genetics in Medicine* 22: 927-936 doi:10.1038/s41436-019-0741-5 (2020). PMID: 31911672

13. Martin C, Datta A, Littlefield C, Kalra A, Chapron C, Wawersik S, Dagbay K, Brueckner C, Nikiforov A, Danehy F, Streich F, Boston C, Simpson A, Jackson J, Lin S, Danek N, Faucette R, **Raman P**, Capili A, Buckler A, Carven G, Schürpf T. Selective inhibition of TGFβ1 activation overcomes primary resistance to checkpoint blockade therapy by altering tumor immune landscape. *Science Translational Medicine* 12: eaay8456 doi:10.1126/scitranslmed.aay8456 (2020). PMID: 32213632

14. Sussman R, Rokita J, Huang K, **Raman P**, Rathi K, Martinez D, Bosse K, Lane M, Hart L, Bhatti T, Pawel B, Maris J. CAMKV Is a Candidate Immunotherapeutic Target in MYCN Amplified Neuroblastoma. *Frontiers in Oncology* 10: doi:10.3389/fonc.2020.00302 (2020). PMID: 32211329

15. Ijaz H, Koptyra M, Gaonkar K, Rokita J, Baubet V, Tauhid L, Zhu Y, Brown M, Lopez G, Zhang B, Diskin S, Vaksman Z, Mason J, Appert E, Lilly J, Lulla R, De Raedt T, Heath A, Felmeister A, **Raman P**, Nazarian J, Santi M, Storm P, Resnick A, Waanders A, Cole K. Pediatric high-grade glioma resources from the Children's Brain Tumor Tissue Consortium. *Neuro-Oncology* 22: 163-165 doi:10.1093/neuonc/noz192 (2019). PMID: 32256484

16. MacFarland S, Zelley K, Surrey L, Gallo D, Luo M, **Raman P**, Wertheim G, Hunger S, Li MBrodeur G. Pediatric Somatic Tumor Sequencing Identifies Underlying Cancer Predisposition. *JCO Precision Oncology* 1-26 doi:10.1200/po.19.00062 (2019). PMID: 32783018

17. Rokita J, Rathi K, Cardenas M, Upton K, Jayaseelan J, Cross K, Pfeil J, Egolf L, Way G, Farrel A, Kendsersky N, Patel K, Gaonkar K, Modi A, Berko E, Lopez G, Vaksman Z, Mayoh C, Nance J, McCoy K, Haber M, Evans K, McCalmont H, Bendak K, Böhm J,

Marshall G, Tyrrell V, Kalletla K, Braun F, Qi L, Du Y, Zhang H, Lindsay H, Zhao S, Shu J, Baxter P, Morton C, Kurmashev D, Zheng S, Chen Y, Bowen J, Bryan A, Leraas K, Coppens S, Doddapaneni H, Momin Z, Zhang W, Sacks G, Hart L, Krytska K, Mosse Y, Gatto G, Sanchez Y, Greene C, Diskin S, Vaske O, Haussler D, Gastier-Foster J, Kolb E, Gorlick R, Li X, Reynolds C, Kurmasheva R, Houghton P, Smith M, Lock R, **Raman P**, Wheeler DMaris J. Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. *Cell Reports* 29: 1675-1689.e9 doi:10.1016/j.celrep.2019.09.071 (2019). PMID: 31693904

18. **Raman P**, Zimmerman S, Rathi K, de Torrenté L, Sarmady M, Wu C, Leipzig J, Taylor D, Tozeren A, Mar J. A comparison of survival analysis methods for cancer gene expression RNA-Sequencing data. *Cancer Genet.* 2019;235-236:1-12. doi:10.1016/j.cancergen.2019.04.004 (2019). Science Direct: S2210776218304897

19. **Raman P**, Maddipati R, Lim K, Tozeren A. Pancreatic cancer survival analysis defines a signature that predicts outcome. *PLOS ONE*, 13(8):e0201751 (2018). PMID: 30092011

20. Campbell B, Light N, Fabrizio D, Zatzman M, Fuligni F, de Borja R, Davidson S, Edwards M, Elvin J, Hodel K, Zahurancik W, Suo Z, Lipman T, Wimmer K, Kratz C, Bowers D, Laetsch T, Dunn G, Johanns T, Grimmer M, Smirnov I, Larouche V, Samuel D, Bronsema A, Osborn M, Stearns D, **Raman P**, Cole K, Storm P, Yalon M, Opocher E, Mason G, Thomas G, Sabel M, George B, Ziegler D, Lindhorst S, Issai V, Constantini S, Toledano H, Elhasid R, Farah R, Dvir R, Dirks P, Huang A, Galati M, Chung J, Ramaswamy V, Irwin M, Aronson M, Durno C, Taylor M, Rechavi G, Maris J, Bouffet E, Hawkins C, Costello J, Meyn M, Pursell Z, Malkin D, Tabori U, Shlien A. Comprehensive Analysis of Hypermutation in Human Cancer. *Cell*,171(5):1042-1056.e10 (2017). PMID: 29056344

21. Mackay A, Burford A, Carvalho D, Izquierdo E, Fazal-Salom J, Taylor K, Bjerke L, Clarke M, Vinci M, Nandhabalan M, Temelso S, Popov S, Molinari V, **Raman P**, Waanders A, Han H, Gupta S, Marshall L, Zacharoulis S, Vaidya S, Mandeville H, Bridges L, Martin A, Al-Sarraj S, Chandler C, Ng H, Li X, Mu K, Trabelsi S, Brahim D, Kisljakov A, Konovalov D, Moore A, Carcaboso A, Sunol M, de Torres C, Cruz O, Mora J, Shats L, Stavale J, Bidinotto L, Reis R, Entz-Werle N, Farrell M, Cryan J, Crimmins D, Caird J, Pears J, Monje M, Debily M, Castel D, Grill J, Hawkins C, Nikbakht H, Jabado N, Baker S, Pfister S, Jones D, Fouladi M, von Bueren A, Baudis M, Resnick A, Jones C. Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma. *Cancer Cell*, 32(4):520-537.e5 (2017). PMID: 28966033

22. Bosse K, **Raman P**, Zhu Z, Lane M, Martinez D, Heitzeneder S, Rathi K, Kendsersky N, Randall M, Donovan L, Morrissy S, Sussman R, Zhelev D, Feng Y, Wang Y, Hwang J, Lopez G, Harenza J, Wei J, Pawel B, Bhatti T, Santi M, Ganguly A, Khan J, Marra M, Taylor M, Dimitrov, D, Mackall C. and Maris, J. "Identification of GPC2 as an Oncoprotein and Candidate Immunotherapeutic Target in High-Risk Neuroblastoma". *Cancer Cell*, 32(3), pp.295-309.e12 (2017). PMID: 28898695

23. Padovan-Merhar O, **Raman P** (co-first author), Ostrovnaya I, Kalletla K, Rubnitz K, Sanford E, Ali S, Miller V, Mossé Y, Granger M, Weiss B, Maris J, Modak S. "Enrichment of Targetable Mutations in the Relapsed Neuroblastoma Genome." *PLOS Genetics*, 12(12), p.e1006501 (2016). PMID: 27997549

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26. Carson C, **Raman P**, Tullai J, Xu L, Henault M, Thomas E, Yeola S, Lao J, McPate M, Verkuyl J, Marsh G, Sarber J, Amaral A, Bailey S, Lubicka D, Pham H, Miranda N, Ding J, Tang H, Ju H, Tranter P, Ji N, Krastel P, Jain R, Schumacher A, Loureiro J, George E, Berellini G, Ross N, Bushell S, Erdemli G, Solomon, J. "Englerin A Agonizes the TRPC4/C5 Cation Channels to Inhibit Tumor Cell Line Proliferation." *PLOS ONE*, 10(6), p.e0127498 (2015). PMID: 26098886

27. Barretina J, Caponigro G, Stransky N, Venkatesan K, Margolin AA, Kim S, Wilson CJ, Lehár J, Kryukov GV, Sonkin D, Reddy A, Liu M, Murray L, Berger MF, Monahan JE, Morais P, Meltzer J, Korejwa A, Jané-Valbuena J, Mapa FA, Thibault J, Bric-Furlong E, **Raman P**, Shipway A, Engels IH, Cheng J, Yu GK, Yu J, Aspesi P Jr, de Silva M, Jagtap K, Jones MD, Wang L, Hatton C, Palescandolo E, Gupta S, Mahan S, Sougnez C, Onofrio RC, Liefeld T, MacConaill L, Winckler W, Reich M, Li N, Mesirov JP, Gabriel SB, Getz G, Ardlie K, Chan V, Myer VE, Weber BL, Porter J, Warmuth M, Finan P, Harris JL, Meyerson M, Golub TR, Morrissey MP, Sellers WR, Schlegel R, Garraway LA. "The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity." *Nature*, 483(7391):603-7 (2012). PMID: 22460905

28. Düvel K, Yecies JL, Menon S, **Raman P** (co-second author), Lipovsky AI, Souza AL, Triantafellow E, Ma Q, Gorski R, Cleaver S, Vander Heiden MG, MacKeigan JP, Finan PM, Clish CB, Murphy LO, Manning BD. "Activation of a metabolic gene regulatory network downstream of mTOR complex 1." *Mol Cell*, 39(2):171-83 (2010). PMID: 20670887

29. Asur S, **Raman P**, Otey ME, Parthasarathy S. "A model-based approach for mining membrane protein crystallization trials." *Bioinformatics*, 22(14):e40-8 (2006) PMID: 16873499

30. **Raman P**, Cherezov V, Caffrey M. "The Membrane Protein Data Bank." *Cell Mol Life Sci*, 63(1):36-51 (2006). PMID: 16314922