

Stanford



Akash Kumar

Adjunct Clinical Instructor, Pediatrics - Medical Genetics

CLINICAL OFFICES

- **Pediatric Genetics**

300 Pasteur Dr Rm H315

Stanford, CA 94305

Tel (650) 723-6858 **Fax** (650) 498-4555

- **Stanford Children's Health Specialty Services Sunnyvale**

1195 W Fremont Ave

Sunnyvale, CA 94087

Tel (408) 426-5590 **Fax** (669) 233-2878

Bio

CLINICAL FOCUS

- Genetics
- Medical Genetics

PROFESSIONAL EDUCATION

- Board Certification: Pediatrics, American Board of Pediatrics (2020)
- Residency: Stanford University Division of Medical Genetics (2020) CA
- Medical Education: University of Washington School of Medicine (2016) WA

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Akash is passionate about taking advances in genomics and applying them for patient care. After training in Chemical and Bioengineering at the University of Minnesota and Stanford University he started the Medical Scientist Training Program (MSTP) at the University of Washington and obtained a PhD in Genome Sciences. With his thesis advisor, Jay Shendure, Akash used next generation sequencing technologies to characterize the development and evolution of prostate cancer and glioblastoma. He also designed and implemented new methods using next-generation sequencing with applications for cancer genetics and prenatal genetic testing. He has published six first-author publications in journals including Nature Medicine, PNAS and Genome Medicine and is a co-inventor on one licensed patent. As a medical geneticist, Akash believes that the best approach to improve outcomes for children with complex congenital medical conditions stems from earlier diagnosis and intervention. To that effect, his current research goals are 1) to develop new genomic methods that identify children at risk for complex congenital diseases earlier, 2) to understand the molecular mechanisms of neurodevelopmental disease in children that may serve as potential avenues for treatment and 3) to improve access and implementation of genomics more broadly in the clinic.

Publications

PUBLICATIONS

- **Whole-genome risk prediction of common diseases in human preimplantation embryos** *NATURE MEDICINE*
Kumar, A., Im, K., Banjevic, M., Ng, P. C., Tunstall, T., Garcia, G., Galhardo, L., Sun, J., Schaedel, O. N., Levy, B., Hongo, D., Kijacic, D., Kiehl, et al
2022; 28 (3): 513-+
- **Extracutaneous manifestations in phacomatosis cesioflammea and cesiomarmorata: Case series and literature review** *AMERICAN JOURNAL OF MEDICAL GENETICS PART A*
Kumar, A., Zastrow, D. B., Kravets, E. J., Belefond, D., Ruzhnikov, M. Z., Grove, M. E., Dries, A. M., Kohler, J. N., Waggott, D. M., Yang, Y., Huang, Y., Mackenzie, K. M., Eng, et al
2019; 179 (6): 966-77
- **Extracutaneous manifestations in phacomatosis cesioflammea and cesiomarmorata: Case series and literature review.** *American journal of medical genetics. Part A*
Kumar, A., Zastrow, D. B., Kravets, E. J., Belefond, D., Ruzhnikov, M. R., Grove, M. E., Dries, A. M., Kohler, J. N., Waggott, D. M., Yang, Y., Huang, Y., Undiagnosed Diseases Network, Mackenzie, K. M., et al
2019
- **The Rhododendron genome and chromosomal organization provide insight into shared whole genome duplications across the heath family (Ericaceae).** *Genome biology and evolution*
Soza, V. L., Lindsley, D. n., Waalkes, A. n., Ramage, E. n., Patwardhan, R. P., Burton, J. N., Adey, A. n., Kumar, A. n., Qiu, R. n., Shendure, J. n., Hall, B. n.
2019
- **Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer** *NATURE MEDICINE*
Kumar, A., Coleman, I., Morrissey, C., Zhang, X., True, L. D., Gulati, R., Etzioni, R., Bolouri, H., Montgomery, B., White, T., Lucas, J. M., Brown, L. G., Dumpit, et al
2016; 22 (4): 369-?
- **Recurrent Somatic Loss of TNFRSF14 in Classical Hodgkin Lymphoma** *GENES CHROMOSOMES & CANCER*
Salipante, S. J., Adey, A., Thomas, A., Lee, C., Liu, Y. J., Kumar, A., Lewis, A. P., Wu, D., Fromm, J. R., Shendure, J.
2016; 55 (3): 278-287
- **Whole genome prediction for preimplantation genetic diagnosis** *GENOME MEDICINE*
Kumar, A., Ryan, A., Kitzman, J. O., Wemmer, N., Snyder, M. W., Sigurjonsson, S., Lee, C., Banjevic, M., Zarutskie, P. W., Lewis, A. P., Shendure, J., Rabinowitz, M.
2015; 7
- **In vitro, long-range sequence information for de novo genome assembly via transposase contiguity.** *Genome research*
Adey, A., Kitzman, J. O., Burton, J. N., Daza, R., Kumar, A., Christiansen, L., Ronaghi, M., Amini, S., Gunderson, K. L., Steemers, F. J., Shendure, J.
2014; 24 (12): 2041-9
- **MIPgen: optimized modeling and design of molecular inversion probes for targeted resequencing** *BIOINFORMATICS*
Boyle, E. A., O'Roak, B. J., Martin, B. K., Kumar, A., Shendure, J.
2014; 30 (18): 2670-2672
- **Genome Sequencing of Idiopathic Pulmonary Fibrosis in Conjunction with a Medical School Human Anatomy Course** *PLOS ONE*
Kumar, A., Dougherty, M., Findlay, G. M., Geisheker, M., Klein, J., Lazar, J., Machkovech, H., Resnick, J., Resnick, R., Salter, A. I., Talebi-Liasi, F., Arakawa, C., Baudin, et al
2014; 9 (9)
- **Complex MSH2 and MSH6 mutations in hypermutated microsatellite unstable advanced prostate cancer** *NATURE COMMUNICATIONS*
Pritchard, C. C., Morrissey, C., Kumar, A., Zhang, X., Smith, C., Coleman, I., Salipante, S. J., Milbank, J., Yu, M., Grady, W. M., Tait, J. F., Corey, E., Vessella, et al
2014; 5
- **Deep sequencing of multiple regions of glial tumors reveals spatial heterogeneity for mutations in clinically relevant genes** *GENOME BIOLOGY*
Kumar, A., Boyle, E. A., Tokita, M., Mikheev, A. M., Sanger, M. C., Girard, E., Silber, J. R., Gonzalez-Cuyar, L. F., Hiatt, J. B., Adey, A., Lee, C., Kitzman, J. O., Born, et al

2014; 15 (12)

- **Germline Missense Variants in the BTNL2 Gene Are Associated with Prostate Cancer Susceptibility.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
FitzGerald, L. M., Kumar, A., Boyle, E. A., Zhang, Y., McIntosh, L. M., Kolb, S., Stott-Miller, M., Smith, T., Karyadi, D. M., Ostrander, E. A., Hsu, L., Shendure, J., Stanford, et al
2013; 22 (9): 1520-1528

- **Multiplex Targeted Sequencing Identifies Recurrently Mutated Genes in Autism Spectrum Disorders** *SCIENCE*
O'Roak, B. J., Vives, L., Fu, W., Egerton, J. D., Stanaway, I. B., Phelps, I. G., Carvill, G., Kumar, A., Lee, C., Ankenman, K., Munson, J., Hiatt, J. B., Turner, et al
2012; 338 (6114): 1619-1622

- **Exome sequencing identifies a spectrum of mutation frequencies in advanced and lethal prostate cancers** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kumar, A., White, T. A., MacKenzie, A. P., Clegg, N., Lee, C., Dumpit, R. F., Coleman, I., Ng, S. B., Salipante, S. J., Rieder, M. J., Nickerson, D. A., Corey, E., Lange, et al
2011; 108 (41): 17087-17092

- **Target-enrichment strategies for next-generation sequencing** *NATURE METHODS*
Mamanova, L., Coffey, A. J., Scott, C. E., Kozarewa, I., Turner, E. H., Kumar, A., Howard, E., Shendure, J., Turner, D. J.
2010; 7 (2): 111-118