

# Petar Stojanov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11906081/publications.pdf>

Version: 2024-02-01

30  
papers

30,314  
citations

201575

27  
h-index

454834

30  
g-index

30  
all docs

30  
docs citations

30  
times ranked

46899  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Data-Driven Approach to Multiple-Source Domain Adaptation. Proceedings of Machine Learning Research, 2019, 89, 3487-3496.  | 0.3  | 1         |
| 2  | Low-Dimensional Density Ratio Estimation for Covariate Shift Correction. Proceedings of Machine Learning Research, 2019, 89, 3449-3458.  | 0.3  | 2         |
| 3  | Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.  | 13.7 | 269       |
| 4  | Reconstructing cancer drug response networks using multitask learning. BMC Systems Biology, 2017, 11, 96.  | 3.0  | 5         |
| 5  | Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.  | 13.5 | 363       |
| 6  | Paired exome analysis of Barrett's esophagus and adenocarcinoma. Nature Genetics, 2015, 47, 1047-1055.   | 9.4  | 310       |
| 7  | Integrative and Comparative Genomic Analysis of HPV-Positive and HPV-Negative Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2015, 21, 632-641.                 | 3.2  | 525       |
| 8  | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.  | 13.5 | 2,318     |
| 9  | The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.  | 7.7  | 415       |
| 10 | Somatic Mutations Predict Poor Outcome in Patients With Myelodysplastic Syndrome After Hematopoietic Stem-Cell Transplantation. Journal of Clinical Oncology, 2014, 32, 2691-2698. | 0.8  | 359       |
| 11 | Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.  | 7.7  | 847       |
| 12 | Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.      | 15.2 | 508       |
| 13 | Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. Nature Biotechnology, 2014, 32, 71-75.   | 9.4  | 120       |
| 14 | Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.  | 13.7 | 2,586     |
| 15 | Integrative and Comparative Genomic Analysis of Lung Squamous Cell Carcinomas in East Asian Patients. Journal of Clinical Oncology, 2014, 32, 121-128.                             | 0.8  | 176       |
| 16 | Somatic mutation as a mechanism of Wnt/ $\beta$ -catenin pathway activation in CLL. Blood, 2014, 124, 1089-1098.   | 0.6  | 65        |
| 17 | Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. Science, 2014, 345, 216-220.  | 6.0  | 808       |
| 18 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.   | 7.7  | 665       |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 19 | An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. <i>Nature Genetics</i> , 2013, 45, 970-976.   | 9.4  | 1,023     |
| 20 | The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.   | 13.5 | 3,979     |
| 21 | Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2013, 152, 714-726.   | 13.5 | 1,202     |
| 22 | Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.   | 9.4  | 671       |
| 23 | Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.   | 13.7 | 4,761     |
| 24 | Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3879-3884. | 3.3  | 853       |
| 25 | Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. <i>Cell</i> , 2012, 150, 1107-1120.   | 13.5 | 1,591     |
| 26 | Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <i>Nature</i> , 2012, 488, 106-110.  | 13.7 | 675       |
| 27 | Melanoma genome sequencing reveals frequent PREX2 mutations. <i>Nature</i> , 2012, 485, 502-506.   | 13.7 | 671       |
| 28 | Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. <i>Nature Genetics</i> , 2012, 44, 685-689.  | 9.4  | 1,300     |
| 29 | <i>CDKN2A</i> and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. <i>New England Journal of Medicine</i> , 2011, 365, 2497-2506.   | 13.9 | 1,021     |
| 30 | The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. <i>Science</i> , 2011, 333, 1157-1160.  | 6.0  | 2,225     |