Petar Stojanov

List of Publications by Year
in descending order

30 papers	30,314 citations

201575

27 h-index	30 g-index

454834

30 all docs	30 docs citations	30 times ranked	46899 citing authors

#	Article	IF	Citations
1	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
2	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
3	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	13.7	2,586
4	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
5	The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. Science, 2011, 333, 1157-1160.	6.0	2,225
6	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
7	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
8	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	13.5	1,202
9	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. Nature Genetics, 2013, 45, 970-976.	9.4	1,023
10	*SF3B1* and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. New England Journal of Medicine, 2011, 365, 2497-2506.	13.9	1,021
11	Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3879-3884.	3.3	853
12	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	7.7	847
13	Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. Science, 2014, 345, 216-220.	6.0	808
14	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110.	13.7	675
15	Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506.	13.7	671
16	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	9.4	671
17	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	7.7	415
21	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	13.5	363
22	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
23	Paired exome analysis of Barrett's esophagus and adenocarcinoma. Nature Genetics, 2015, 47, 1047-1055.	9.4	310
24	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	13.7	269
25	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
26	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. Nature Biotechnology, 2014, 32, 71-75.	9.4	120
27	Somatic mutation as a mechanism of Wnt/Î²-catenin pathway activation in CLL. Blood, 2014, 124, 1089-1098.	0.6	65
28	Reconstructing cancer drug response networks using multitask learning. BMC Systems Biology, 2017, 11, 96.	3.0	5
29	Low-Dimensional Density Ratio Estimation for Covariate Shift Correction. Proceedings of Machine Learning Research, 2019, 89, 3449-3458.	0.3	2
30	Data-Driven Approach to Multiple-Source Domain Adaptation. Proceedings of Machine Learning Research, 2019, 89, 3487-3496.	0.3	1