Boris A Reva

List of Publications by Year
in descending order

68 papers	72,225 citations
76326 40 h-index	123424 61 g-index
73 all docs	73 docs citations
73 times ranked	84038 citing authors

#	Article	IF	Citations
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	9.4	12,801
2	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
3	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
4	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	27.8	6,879
5	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
6	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
7	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
8	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
9	Integrative Genomic Profiling of Human Prostate Cancer. Cancer Cell, 2010, 18, 11-22.	16.8	3,151
10	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
11	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
12	Predicting the functional impact of protein mutations: application to cancer genomics. Nucleic Acids Research, 2011, 39, e118-e118.	14.5	1,622
13	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721.	21.4	642
14	The nuclear deubiquitinase BAP1 is commonly inactivated by somatic mutations and 3p21.1 losses in malignant pleural mesothelioma. Nature Genetics, 2011, 43, 668-672.	21.4	617
15	p53 Regulates Hematopoietic Stem Cell Quiescence. Cell Stem Cell, 2009, 4, 37-48.	11.1	485
16	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
17	A Specificity Map for the PDZ Domain Family. PLoS Biology, 2008, 6, e239.	5.6	410
18	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410

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19	*EGFR* Exon 20 Insertion Mutations in Lung Adenocarcinomas: Prevalence, Molecular Heterogeneity, and Clinicopathologic Characteristics. Molecular Cancer Therapeutics, 2013, 12, 220-229.	4.1	367
20	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
21	Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators *BAP1* and *SETD2*: A Report by MSKCC and the KIRC TCGA Research Network. Clinical Cancer Research, 2013, 19, 3259-3267.	7.0	301
22	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
23	Determinants of protein function revealed by combinatorial entropy optimization. Genome Biology, 2007, 8, R232.	9.6	262
24	Direct in Vivo RNAi Screen Unveils Myosin IIa as a Tumor Suppressor of Squamous Cell Carcinomas. Science, 2014, 343, 309-313.	12.6	234
25	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
26	What is the probability of a chance prediction of a protein structure with an rmsd of 6 Ã¥?. Folding & Design, 1998, 3, 141-147.	4.5	185
27	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
28	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
29	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
30	A search for the most stable folds of protein chains. Nature, 1991, 351, 497-499.	27.8	140
31	*MAP2K1* (*MEK1*) Mutations Define a Distinct Subset of Lung Adenocarcinoma Associated with Smoking. Clinical Cancer Research, 2015, 21, 1935-1943.	7.0	124
32	The molecular diversity of Luminal A breast tumors. Breast Cancer Research and Treatment, 2013, 141, 409-420.	2.5	120
33	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. Nature Communications, 2013, 4, 2730.	12.8	104
34	Genomic Analysis of Uterine Lavage Fluid Detects Early Endometrial Cancers and Reveals a Prevalent Landscape of Driver Mutations in Women without Histopathologic Evidence of Cancer: A Prospective Cross-Sectional Study. PLoS Medicine, 2016, 13, e1002206.	8.4	83
35	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
36	Necdin, a p53 target gene, regulates the quiescence and response to genotoxic stress of hematopoietic stem/progenitor cells. Blood, 2012, 120, 1601-1612.	1.4	69

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37	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. Nature Communications, 2017, 8, 767.	12.8	67
38	Strand-specific in vivo screen of cancer-associated miRNAs unveils a role for miR-21â^— in SCC progression. Nature Cell Biology, 2016, 18, 111-121.	10.3	53
39	Matrix Metalloproteinase-9 (MMP-9) polymorphisms in patients with cutaneous malignant melanoma. BMC Medical Genetics, 2007, 8, 10.	2.1	44
40	Mutation Screening of Candidate Genes in Patients with Nonsyndromic Sagittal Craniosynostosis. Plastic and Reconstructive Surgery, 2016, 137, 952-961.	1.4	27
41	Averaging interaction energies over homologs improves protein fold recognition in gapless threading. Proteins: Structure, Function and Bioinformatics, 1999, 35, 353-359.	2.6	23
42	Accurate general method for lattice approximation of three-dimensional structure of a chain molecule. Proteins: Structure, Function and Bioinformatics, 1995, 22, 100-109.	2.6	22
43	Clinical and in vivo Evidence that EGFR S768I Mutant Lung Adenocarcinomas Are Sensitive to Erlotinib. Journal of Thoracic Oncology, 2014, 9, e73-e74.	1.1	22
44	Search for the most stable folds of protein chains: I. Application of a self-consistent molecular field theory to a problem of protein three-dimensional structure prediction. Protein Engineering, Design and Selection, 1996, 9, 387-397.	2.1	19
45	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	6.2	19
46	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	2.5	19
47	Search for the most stable folds of protein chains: II. Computation of stable architectures of Î²-proteins using a self-consistent molecular field theory. Protein Engineering, Design and Selection, 1996, 9, 399-411.	2.1	18
48	Threading with chemostructural restrictions method for predicting fold and functionally significant residues: Application to dipeptidylpeptidase IV (DPP-IV). Proteins: Structure, Function and Bioinformatics, 2002, 47, 180-193.	2.6	17
49	A new molecular signature method for prediction of driver cancer pathways from transcriptional data. Nucleic Acids Research, 2016, 44, e110-e110.	14.5	15
50	Nonsyndromic craniosynostosis: novel coding variants. Pediatric Research, 2019, 85, 463-468.	2.3	14
51	Constructing Lattice Models of Protein Chains with Side Groups. Journal of Computational Biology, 1995, 2, 527-535.	1.6	13
52	Optimization of Protein Structure on Lattices Using a Self-Consistent Field Approach. Journal of Computational Biology, 1998, 5, 531-538.	1.6	12
53	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. Journal of Physical Education and Sports Management, 2018, 4, a003269.	1.2	11
54	ProTrack: An Interactive Multiâ€Omics Data Browser for Proteogenomic Studies. Proteomics, 2020, 20, e1900359.	2.2	11

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55	Building self-avoiding lattice models of proteins using a self-consistent field optimization. , 1996, 26, 1-8.		9
56	Identification and Functional Characterization of *EGFR* V769M, a Novel Germline Variant Associated With Multiple Lung Adenocarcinomas. JCO Precision Oncology, 2017, 1, 1-10.	3.0	9
57	Adjusting potential energy functions for lattice models of chain molecules. , 1996, 25, 379-388.		8
58	Immune Escape in Prostate Cancer. Urologic Clinics of North America, 2020, 47, e9-e16.	1.8	7
59	Unsuspected Collision of Synchronous Lung Adenocarcinomas: A Potential Cause of Aberrant Driver Mutation Profiles. Journal of Thoracic Oncology, 2014, 9, e1-e3.	1.1	6
60	Lattice modeling: Accuracy of energy calculations. Journal of Computational Chemistry, 1996, 17, 1025-1032.	3.3	5
61	Post-anticoagulant D-dimer is a highly prognostic biomarker of COVID-19 mortality. ERJ Open Research, 2021, 7, 00018-2021.	2.6	5
62	Association between Incidental Pelvic Inflammation and Aggressive Prostate Cancer. Cancers, 2022, 14, 2734.	3.7	5
63	1068 ADVERSE OUTCOMES IN CLEAR CELL RENAL CELL CARCINOMA WITH MUTATIONS OF EPIGENETIC REGULATORS BAP1 AND SETD2. Journal of Urology, 2013, 189, .	0.4	0
64	Abstract 5061: Genomic and functional analysis of Myxofibrosarcoma identifies novel prognostic markers and promising therapeutic targets. , 2012, , .		0
65	Title is missing!. Journal of Computational Chemistry, 1996, 17, 1025.	3.3	0
66	Abstract LB-318: A directin vivoRNAi screen unveils a myosin as potent tumor suppressor in head & neck squamous cell carcinomas. , 2014, , .		0
67	Abstract 2729: Development of a targeted liquid biopsy for early gynecologic cancer detection leads to discovery of a highly prevalent genomic landscape of cancer driver gene mutations in uterine tissue from women without cancer. , 2019, , .		0
68	Abstract 1313: Genomic and transcriptomic profiles of primary prostate cancer identify unique targets for therapeutic intervention. , 2020, , .		0