

Boris A Reva

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

72,225
citations

87401

40
h-index

139680

61
g-index

73
all docs

73
docs citations

73
times ranked

91067
citing authors

#	ARTICLE	IF	CITATIONS
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
2	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
3	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
4	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	13.7	6,879
5	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	13.7	6,541
6	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
7	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
8	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
9	Integrative Genomic Profiling of Human Prostate Cancer. <i>Cancer Cell</i> , 2010, 18, 11-22.	7.7	3,151
10	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
11	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
12	Predicting the functional impact of protein mutations: application to cancer genomics. <i>Nucleic Acids Research</i> , 2011, 39, e118-e118.	6.5	1,622
13	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , 2010, 42, 715-721.	9.4	642
14	The nuclear deubiquitinase BAP1 is commonly inactivated by somatic mutations and 3p21.1 losses in malignant pleural mesothelioma. <i>Nature Genetics</i> , 2011, 43, 668-672.	9.4	617
15	p53 Regulates Hematopoietic Stem Cell Quiescence. <i>Cell Stem Cell</i> , 2009, 4, 37-48.	5.2	485
16	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
17	A Specificity Map for the PDZ Domain Family. <i>PLoS Biology</i> , 2008, 6, e239.	2.6	410
18	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410

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19	<i>EGFR</i> Exon 20 Insertion Mutations in Lung Adenocarcinomas: Prevalence, Molecular Heterogeneity, and Clinicopathologic Characteristics. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 220-229.	1.9	367
20	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
21	Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators <i>BAP1</i> and <i>SETD2</i> : A Report by MSKCC and the KIRC TCGA Research Network. <i>Clinical Cancer Research</i> , 2013, 19, 3259-3267.	3.2	301
22	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
23	Determinants of protein function revealed by combinatorial entropy optimization. <i>Genome Biology</i> , 2007, 8, R232.	13.9	262
24	Direct in Vivo RNAi Screen Unveils Myosin IIa as a Tumor Suppressor of Squamous Cell Carcinomas. <i>Science</i> , 2014, 343, 309-313.	6.0	234
25	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	7.7	189
26	What is the probability of a chance prediction of a protein structure with an rmsd of 6 Å? <i>Folding & Design</i> , 1998, 3, 141-147.	4.5	185
27	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
28	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
29	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	9.0	161
30	A search for the most stable folds of protein chains. <i>Nature</i> , 1991, 351, 497-499.	13.7	140
31	<i>MAP2K1</i> (<i>MEK1</i>) Mutations Define a Distinct Subset of Lung Adenocarcinoma Associated with Smoking. <i>Clinical Cancer Research</i> , 2015, 21, 1935-1943.	3.2	124
32	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
33	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. <i>Nature Communications</i> , 2013, 4, 2730.	5.8	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. <i>PLoS Medicine</i> , 2016, 13, e1002206.	3.9	83
35	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	3.6	71
36	Necdin, a p53 target gene, regulates the quiescence and response to genotoxic stress of hematopoietic stem/progenitor cells. <i>Blood</i> , 2012, 120, 1601-1612.	0.6	69

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37	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. <i>Nature Communications</i> , 2017, 8, 767.	5.8	67
38	Strand-specific in vivo screen of cancer-associated miRNAs unveils a role for miR-21 in SCC progression. <i>Nature Cell Biology</i> , 2016, 18, 111-121.	4.6	53
39	Matrix Metalloproteinase-9 (MMP-9) polymorphisms in patients with cutaneous malignant melanoma. <i>BMC Medical Genetics</i> , 2007, 8, 10.	2.1	44
40	Mutation Screening of Candidate Genes in Patients with Nonsyndromic Sagittal Craniosynostosis. <i>Plastic and Reconstructive Surgery</i> , 2016, 137, 952-961.	0.7	27
41	Averaging interaction energies over homologs improves protein fold recognition in gapless threading. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 353-359.	1.5	23
42	Accurate general method for lattice approximation of three-dimensional structure of a chain molecule. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 100-109.	1.5	22
43	Clinical and in vivo Evidence that EGFR S768I Mutant Lung Adenocarcinomas Are Sensitive to Erlotinib. <i>Journal of Thoracic Oncology</i> , 2014, 9, e73-e74.	0.5	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. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 387-397.	1.0	19
45	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	2.9	19
46	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. <i>PLoS ONE</i> , 2014, 9, e101685.	1.1	19
47	Search for the most stable folds of protein chains: II. Computation of stable architectures of β^2 -proteins using a self-consistent molecular field theory. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 399-411.	1.0	18
48	Threading with chemostructural restrictions method for predicting fold and functionally significant residues: Application to dipeptidylpeptidase IV (DPP-IV). <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 180-193.	1.5	17
49	A new molecular signature method for prediction of driver cancer pathways from transcriptional data. <i>Nucleic Acids Research</i> , 2016, 44, e110-e110.	6.5	15
50	Nonsyndromic craniosynostosis: novel coding variants. <i>Pediatric Research</i> , 2019, 85, 463-468.	1.1	14
51	Constructing Lattice Models of Protein Chains with Side Groups. <i>Journal of Computational Biology</i> , 1995, 2, 527-535.	0.8	13
52	Optimization of Protein Structure on Lattices Using a Self-Consistent Field Approach. <i>Journal of Computational Biology</i> , 1998, 5, 531-538.	0.8	12
53	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003269.	0.5	11
54	ProTrack: An Interactive Multi-Omics Data Browser for Proteogenomic Studies. <i>Proteomics</i> , 2020, 20, e1900359.	1.3	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 <i>EGFR</i> V769M, a Novel Germline Variant Associated With Multiple Lung Adenocarcinomas. JCO Precision Oncology, 2017, 1, 1-10.	1.5	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.	0.8	7
59	Unsuspected Collision of Synchronous Lung Adenocarcinomas: A Potential Cause of Aberrant Driver Mutation Profiles. Journal of Thoracic Oncology, 2014, 9, e1-e3.	0.5	6
60	Lattice modeling: Accuracy of energy calculations. Journal of Computational Chemistry, 1996, 17, 1025-1032.	1.5	5
61	Post-anticoagulant D-dimer is a highly prognostic biomarker of COVID-19 mortality. ERJ Open Research, 2021, 7, 00018-2021.	1.1	5
62	Association between Incidental Pelvic Inflammation and Aggressive Prostate Cancer. Cancers, 2022, 14, 2734.	1.7	5
63	1068 ADVERSE OUTCOMES IN CLEAR CELL RENAL CELL CARCINOMA WITH MUTATIONS OF EPIGENETIC REGULATORS BAP1 AND SETD2. Journal of Urology, 2013, 189, .	0.2	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.	1.5	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