Boris A Reva

List of Publications by Year
in descending order

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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	Association between Incidental Pelvic Inflammation and Aggressive Prostate Cancer. Cancers, 2022, 14, 2734.	3.7	5
2	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
3	Post-anticoagulant D-dimer is a highly prognostic biomarker of COVID-19 mortality. ERJ Open Research, 2021, 7, 00018-2021.	2.6	5
4	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
5	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
6	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
7	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
8	Immune Escape in Prostate Cancer. Urologic Clinics of North America, 2020, 47, e9-e16.	1.8	7
9	ProTrack: An Interactive Multiâ€Omics Data Browser for Proteogenomic Studies. Proteomics, 2020, 20, e1900359.	2.2	11
10	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410
11	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
12	Abstract 1313: Genomic and transcriptomic profiles of primary prostate cancer identify unique targets for therapeutic intervention. , 2020, , .		0
13	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
14	Nonsyndromic craniosynostosis: novel coding variants. Pediatric Research, 2019, 85, 463-468.	2.3	14
15	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
16	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. Journal of Physical Education and Sports Management, 2018, 4, a003269.	1.2	11
17	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. Nature Communications, 2017, 8, 767.	12.8	67
18	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.	3.0	9

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19	A new molecular signature method for prediction of driver cancer pathways from transcriptional data. Nucleic Acids Research, 2016, 44, e110-e110.	14.5	15
20	Mutation Screening of Candidate Genes in Patients with Nonsyndromic Sagittal Craniosynostosis. Plastic and Reconstructive Surgery, 2016, 137, 952-961.	1.4	27
21	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
22	Strand-specific in vivo screen of cancer-associated miRNAs unveils a role for miR-21âˆ— in SCC progression. Nature Cell Biology, 2016, 18, 111-121.	10.3	53
23	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
24	<i>MAP2K1</i> (<i>MEK1</i>) Mutations Define a Distinct Subset of Lung Adenocarcinoma Associated with Smoking. Clinical Cancer Research, 2015, 21, 1935-1943.	7.0	124
25	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
26	Direct in Vivo RNAi Screen Unveils Myosin IIa as a Tumor Suppressor of Squamous Cell Carcinomas. Science, 2014, 343, 309-313.	12.6	234
27	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
28	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
29	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	2.5	19
30	Abstract LB-318: A directin vivoRNAi screen unveils a myosin as potent tumor suppressor in head & neck squamous cell carcinomas. , 2014, , .		0
31	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
32	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
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	The molecular diversity of Luminal A breast tumors. Breast Cancer Research and Treatment, 2013, 141, 409-420.	2.5	120
35	<i>EGFR</i> Exon 20 Insertion Mutations in Lung Adenocarcinomas: Prevalence, Molecular Heterogeneity, and Clinicopathologic Characteristics. Molecular Cancer Therapeutics, 2013, 12, 220-229.	4.1	367
36	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

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37	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
38	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
39	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. Clinical Cancer Research, 2013, 19, 3259-3267.	7.0	301
40	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
41	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	9.4	12,801
42	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
43	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
44	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
45	Abstract 5061: Genomic and functional analysis of Myxofibrosarcoma identifies novel prognostic markers and promising therapeutic targets. , 2012, , .		0
46	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
47	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
48	Predicting the functional impact of protein mutations: application to cancer genomics. Nucleic Acids Research, 2011, 39, e118-e118.	14.5	1,622
49	Integrative Genomic Profiling of Human Prostate Cancer. Cancer Cell, 2010, 18, 11-22.	16.8	3,151
50	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721.	21.4	642
51	p53 Regulates Hematopoietic Stem Cell Quiescence. Cell Stem Cell, 2009, 4, 37-48.	11.1	485
52	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	27.8	6,879
53	A Specificity Map for the PDZ Domain Family. PLoS Biology, 2008, 6, e239.	5.6	410
54	Determinants of protein function revealed by combinatorial entropy optimization. Genome Biology, 2007, 8, R232.	9.6	262

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55	Matrix Metalloproteinase-9 (MMP-9) polymorphisms in patients with cutaneous malignant melanoma. BMC Medical Genetics, 2007, 8, 10.	2.1	44
56	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
57	Averaging interaction energies over homologs improves protein fold recognition in gapless threading. Proteins: Structure, Function and Bioinformatics, 1999, 35, 353-359.	2.6	23
58	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
59	Optimization of Protein Structure on Lattices Using a Self-Consistent Field Approach. Journal of Computational Biology, 1998, 5, 531-538.	1.6	12
60	Lattice modeling: Accuracy of energy calculations. Journal of Computational Chemistry, 1996, 17, 1025-1032.	3.3	5
61	Adjusting potential energy functions for lattice models of chain molecules. , 1996, 25, 379-388.		8
62	Building self-avoiding lattice models of proteins using a self-consistent field optimization. , 1996, 26, 1-8.		9
63	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
64	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
65	Title is missing!. Journal of Computational Chemistry, 1996, 17, 1025.	3.3	0
66	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
67	Constructing Lattice Models of Protein Chains with Side Groups. Journal of Computational Biology, 1995, 2, 527-535.	1.6	13
68	A search for the most stable folds of protein chains. Nature, 1991, 351, 497-499.	27.8	140