Rajarshi Guha

List of Publications by Year
in descending order

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102	7,077	66343	60623
papers	citations	42 h-index	81 g-index

112	112	112	11658
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The synergy of BET inhibitors with aurora A kinase inhibitors in MYCN-amplified neuroblastoma is heightened with functional TP53. Neoplasia, 2021, 23, 624-633.	5.3	8
2	Moving targets in drug discovery. Scientific Reports, 2020, 10, 20213.	3.3	23
3	Matrix Drug Screen Identifies Synergistic Drug Combinations to Augment SMAC Mimetic Activity in Ovarian Cancer. Cancers, 2020, 12, 3784.	3.7	3
4	Drugs Targeting Tumor-Initiating Cells Prolong Survival in a Post-Surgery, Post-Chemotherapy Ovarian Cancer Relapse Model. Cancers, 2020, 12, 1645.	3.7	25
5	High-throughput screening identifies candidate drugs for the treatment of recurrent respiratory papillomatosis. Papillomavirus Research (Amsterdam, Netherlands), 2019, 8, 100181.	4.5	18
6	Mutation Profiles in Glioblastoma 3D Oncospheres Modulate Drug Efficacy. SLAS Technology, 2019, 24, 28-40.	1.9	14
7	High-Throughput Screening for Drug Combinations. Methods in Molecular Biology, 2019, 1939, 11-35.	0.9	10
8	High-throughput Chemical Screening Identifies Focal Adhesion Kinase and Aurora Kinase B Inhibition as a Synergistic Treatment Combination in Ewing Sarcoma. Clinical Cancer Research, 2019, 25, 4552-4566.	7.0	30
9	Target Deconvolution of a Multikinase Inhibitor with Antimetastatic Properties Identifies TAOK3 as a Key Contributor to a Cancer Stem Cellâ€“Like Phenotype. Molecular Cancer Therapeutics, 2019, 18, 2097-2110.	4.1	16
10	A High-Throughput Screen of a Library of Therapeutics Identifies Cytotoxic Substrates of P-glycoprotein. Molecular Pharmacology, 2019, 96, 629-640.	2.3	22
11	Therapeutic strategies for diffuse midline glioma from high-throughput combination drug screening. Science Translational Medicine, 2019, 11, .	12.4	129
12	A Combination CDK4/6 and IGF1R Inhibitor Strategy for Ewing Sarcoma. Clinical Cancer Research, 2019, 25, 1343-1357.	7.0	69
13	Glypicanâ€3â€Specific Antibody Drug Conjugates Targeting Hepatocellular Carcinoma. Hepatology, 2019, 70, 563-576.	7.3	65
14	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	46.4	263
15	Characterization of clinically used oral antiseptics as quadruplex-binding ligands. Nucleic Acids Research, 2018, 46, 2722-2732.	14.5	27
16	High-throughput screens identify HSP90 inhibitors as potent therapeutics that target inter-related growth and survival pathways in advanced prostate cancer. Scientific Reports, 2018, 8, 17239.	3.3	29
17	Canvass: A Crowd-Sourced, Natural-Product Screening Library for Exploring Biological Space. ACS Central Science, 2018, 4, 1727-1741.	11.3	32
18	Resistance to Epigenetic-Targeted Therapy Engenders Tumor Cell Vulnerabilities Associated with Enhancer Remodeling. Cancer Cell, 2018, 34, 922-938.e7.	16.8	63

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19	Using Machine Learning to Predict Synergistic Antimalarial Compound Combinations With Novel Structures. Frontiers in Pharmacology, 2018, 9, 1096.	3.5	27
20	A single nucleotide polymorphism in the Plasmodium falciparum atg18 gene associates with artemisinin resistance and confers enhanced parasite survival under nutrient deprivation. Malaria Journal, 2018, 17, 391.	2.3	30
21	Identification of Combinations of Approved Drugs With Synergistic Activity Against Ebola Virus in Cell Cultures. Journal of Infectious Diseases, 2018, 218, S672-S678.	4.0	49
22	A systematic and prospectively validated approach for identifying synergistic drug combinations against malaria. Malaria Journal, 2018, 17, 160.	2.3	19
23	Pharmacological and genomic profiling of neurofibromatosis type 1 plexiform neurofibroma-derived schwann cells. Scientific Data, 2018, 5, 180106.	5.3	20
24	Pharos: Collating protein information to shed light on the druggable genome. Nucleic Acids Research, 2017, 45, D995-D1002.	14.5	271
25	A High-Throughput Screening Model of the Tumor Microenvironment for Ovarian Cancer Cell Growth. SLAS Discovery, 2017, 22, 494-506.	2.7	26
26	Chemotaxis of Molecular Dyes in Polymer Gradients in Solution. Journal of the American Chemical Society, 2017, 139, 15588-15591.	13.7	28
27	Matrix Screen Identifies Synergistic Combination of PARP Inhibitors and Nicotinamide Phosphoribosyltransferase (NAMPT) Inhibitors in Ewing Sarcoma. Clinical Cancer Research, 2017, 23, 7301-7311.	7.0	44
28	The Chemistry Development Kit (CDK) v2.0: atom typing, depiction, molecular formulas, and substructure searching. Journal of Cheminformatics, 2017, 9, 33.	6.1	275
29	The phosphatidylinositol-3-phosphate 5-kinase inhibitor apilimod blocks filoviral entry and infection. PLoS Neglected Tropical Diseases, 2017, 11, e0005540.	3.0	97
30	Drug target ontology to classify and integrate drug discovery data. Journal of Biomedical Semantics, 2017, 8, 50.	1.6	63
31	Evaluation of the Activity of Lamivudine and Zidovudine against Ebola Virus. PLoS ONE, 2016, 11, e0166318.	2.5	28
32	Large-scale pharmacological profiling of 3D tumor models of cancer cells. Cell Death and Disease, 2016, 7, e2492-e2492.	6.3	26
33	Modelling of compound combination effects and applications to efficacy and toxicity: state-of-the-art, challenges and perspectives. Drug Discovery Today, 2016, 21, 225-238.	6.4	162
34	Ranking Differential Drug Activities from Dose-Response Synthetic Lethality Screens. Journal of Biomolecular Screening, 2016, 21, 942-955.	2.6	4
35	A Druggable TCF4- and BRD4-Dependent Transcriptional Network Sustains Malignancy in Blastic Plasmacytoid Dendritic Cell Neoplasm. Cancer Cell, 2016, 30, 764-778.	16.8	116
36	mQC: A Heuristic Quality-Control Metric for High-Throughput Drug Combination Screening. Scientific Reports, 2016, 6, 37741.	3.3	8

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37	Augmented efficacy of brentuximab vedotin combined with ruxolitinib and/or Navitoclax in a murine model of human Hodgkinâ€™s lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1624-1629.	7.1	38
38	Chemical Screens Identify Drugs that Enhance or Mitigate Cellular Responses to Antibody-Toxin Fusion Proteins. PLoS ONE, 2016, 11, e0161415.	2.5	8
39	High-throughput matrix screening identifies synergistic and antagonistic antimalarial drug combinations. Scientific Reports, 2015, 5, 13891.	3.3	92
40	Selective targeting of JAK/STAT signaling is potentiated by Bcl-xL blockade in IL-2-dependent adult T-cell leukemia. Retrovirology, 2015, 12, .	2.0	3
41	Novel Phenotypic Outcomes Identified for a Public Collection of Approved Drugs from a Publicly Accessible Panel of Assays. PLoS ONE, 2015, 10, e0130796.	2.5	18
42	Synergy Maps: exploring compound combinations using network-based visualization. Journal of Cheminformatics, 2015, 7, 36.	6.1	32
43	Chemogenomic Profiling of Endogenous PARK2 Expression Using a Genome-Edited Coincidence Reporter. ACS Chemical Biology, 2015, 10, 1188-1197.	3.4	52
44	Whole-genome RNAi screen highlights components of the endoplasmic reticulum/Golgi as a source of resistance to immunotoxin-mediated cytotoxicity. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1135-42.	7.1	22
45	Selective targeting of JAK/STAT signaling is potentiated by Bcl-xL blockade in IL-2â€“dependent adult T-cell leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12480-12485.	7.1	81
46	Actinoramide A Identified as a Potent Antimalarial from Titration-Based Screening of Marine Natural Product Extracts. Journal of Natural Products, 2015, 78, 2411-2422.	3.0	30
47	Aurora B kinase is a potent and selective target in MYCN-driven neuroblastoma. Oncotarget, 2015, 6, 35247-35262.	1.8	52
48	Genome Editing-Enabled HTS Assays Expand Drug Target Pathways for Charcotâ€“Marieâ€“Tooth Disease. ACS Chemical Biology, 2014, 9, 2594-2602.	3.4	31
49	High-throughput combinatorial screening identifies drugs that cooperate with ibrutinib to kill activated B-cellâ€“like diffuse large B-cell lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2349-2354.	7.1	355
50	Blockade of oncogenic ÎºB kinase activity in diffuse large B-cell lymphoma by bromodomain and extraterminal domain protein inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11365-11370.	7.1	166
51	On the validity versus utility of activity landscapes: are all activity cliffs statistically significant?. Journal of Cheminformatics, 2014, 6, 11.	6.1	9
52	A High-Throughput Assay for Small Molecule Destabilizers of the KRAS Oncoprotein. PLoS ONE, 2014, 9, e103836.	2.5	18
53	High-content genome-wide RNAi screens identify regulators of parkin upstream of mitophagy. Nature, 2013, 504, 291-295.	27.8	301
54	Large-scale screening identifies a novel microRNA, miR-15a-3p, which induces apoptosis in human cancer cell lines. RNA Biology, 2013, 10, 287-300.	3.1	41

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55	Profile of the GSK Published Protein Kinase Inhibitor Set Across ATP-Dependent and-Independent Luciferases: Implications for Reporter-Gene Assays. PLoS ONE, 2013, 8, e57888.	2.5	65
56	On Exploring Structureâ€“Activity Relationships. Methods in Molecular Biology, 2013, 993, 81-94.	0.9	102
57	A Survey of Quantitative Descriptions of Molecular Structure. Current Topics in Medicinal Chemistry, 2013, 12, 1946-1956.	2.1	6
58	A 1536-Well Quantitative High-Throughput Screen to Identify Compounds Targeting Cancer Stem Cells. Journal of Biomolecular Screening, 2012, 17, 1231-1242.	2.6	35
59	A Survey of Quantitative Descriptions of Molecular Structure. Current Topics in Medicinal Chemistry, 2012, 12, 1946-1956.	2.1	48
60	Exploring Uncharted Territories: Predicting Activity Cliï¬€s in Structureâ€“Activity Landscapes. Journal of Chemical Information and Modeling, 2012, 52, 2181-2191.	5.4	33
61	High-throughput screening for genes that prevent excess DNA replication in human cells and for molecules that inhibit them. Methods, 2012, 57, 234-248.	3.8	11
62	A furoxanâ€“amodiaquine hybrid as a potential therapeutic for three parasitic diseases. MedChemComm, 2012, 3, 1505.	3.4	21
63	Exploring structureâ€“activity data using the landscape paradigm. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2012, 2, 829-841.	14.6	34
64	Exploiting Synthetic Lethality for the Therapy of ABC Diffuse Large B Cell Lymphoma. Cancer Cell, 2012, 21, 723-737.	16.8	460
65	Chemical Genomic Profiling for Antimalarial Therapies, Response Signatures, and Molecular Targets. Science, 2011, 333, 724-729.	12.6	130
66	Using a neural network for mining interpretable relationships of West Nile risk factors. Social Science and Medicine, 2011, 72, 418-429.	3.8	13
67	Exploratory analysis of kinetic solubility measurements of a small molecule library. Bioorganic and Medicinal Chemistry, 2011, 19, 4127-4134.	3.0	27
68	Open Data, Open Source and Open Standards in chemistry: The Blue Obelisk five years on. Journal of Cheminformatics, 2011, 3, 37.	6.1	63
69	KNIME Workflow to Assess PAINS Filters in SMARTS Format. Comparison of RDKit and Indigo Cheminformatics Libraries. Molecular Informatics, 2011, 30, 847-850.	2.5	118
70	Discovery of new antimalarial chemotypes through chemical methodology and library development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6775-6780.	7.1	42
71	The Ups and Downs of Structureâ€“Activity Landscapes. Methods in Molecular Biology, 2010, 672, 101-117.	0.9	28
72	Use of genetic algorithm and neural network approaches for risk factor selection: A case study of West Nile virus dynamics in an urban environment. Computers, Environment and Urban Systems, 2010, 34, 189-203.	7.1	14

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73	Towards interoperable and reproducible QSAR analyses: Exchange of datasets. Journal of Cheminformatics, 2010, 2, 5.	6.1	39
74	Advances in Cheminformatics Methodologies and Infrastructure to Support the Data Mining of Large, Heterogeneous Chemical Datasets. Current Computer-Aided Drug Design, 2010, 6, 50-67.	1.2	28
75	A Risk Factor Analysis of West Nile Virus: Extraction of Relationships from a Neural-Network Model. Lecture Notes in Computer Science, 2010, , 208-217.	1.3	1
76	Navigating structureâ€“activity landscapes. Drug Discovery Today, 2009, 14, 698-705.	6.4	161
77	Chemoinformatic Analysis of Combinatorial Libraries, Drugs, Natural Products, and Molecular Libraries Small Molecule Repository. Journal of Chemical Information and Modeling, 2009, 49, 1010-1024.	5.4	138
78	Utilizing high throughput screening data for predictive toxicology models: protocols and application to MLSCN assays. Journal of Computer-Aided Molecular Design, 2008, 22, 367-384.	2.9	43
79	On the interpretation and interpretability of quantitative structureâ€“activity relationship models. Journal of Computer-Aided Molecular Design, 2008, 22, 857-871.	2.9	70
80	Structureâ^'Activity Landscape Index:â€‰ Identifying and Quantifying Activity Cliffs. Journal of Chemical Information and Modeling, 2008, 48, 646-658.	5.4	281
81	Flexible Web Service Infrastructure for the Development and Deployment of Predictive Models. Journal of Chemical Information and Modeling, 2008, 48, 456-464.	5.4	22
82	Assessing How Well a Modeling Protocol Captures a Structureâ^'Activity Landscape. Journal of Chemical Information and Modeling, 2008, 48, 1716-1728.	5.4	84
83	Chemical Data Mining of the NCI Human Tumor Cell Line Database. Journal of Chemical Information and Modeling, 2007, 47, 2063-2076.	5.4	30
84	Ensemble Feature Selection:â€‰ Consistent Descriptor Subsets for Multiple QSAR Models. Journal of Chemical Information and Modeling, 2007, 47, 989-997.	5.4	51
85	Counting Clusters Using R-NN Curves. Journal of Chemical Information and Modeling, 2007, 47, 1308-1318.	5.4	3
86	Web Service Infrastructure for Chemoinformatics. Journal of Chemical Information and Modeling, 2007, 47, 1303-1307.	5.4	41
87	Userscripts for the Life Sciences. BMC Bioinformatics, 2007, 8, 487.	2.6	14
88	Local Lazy Regression:Â Making Use of the Neighborhood to Improve QSAR Predictions. Journal of Chemical Information and Modeling, 2006, 46, 1836-1847.	5.4	65
89	The Blue Obeliskâ€”Interoperability in Chemical Informatics. Journal of Chemical Information and Modeling, 2006, 46, 991-998.	5.4	366
90	Scalable Partitioning and Exploration of Chemical Spaces Using Geometric Hashing. Journal of Chemical Information and Modeling, 2006, 46, 321-333.	5.4	22

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91	R-NN Curves:Â An Intuitive Approach to Outlier Detection Using a Distance Based Method. Journal of Chemical Information and Modeling, 2006, 46, 1713-1722.	5.4	20
92	Recent Developments of the Chemistry Development Kit (CDK) - An Open-Source Java Library for Chemo- and Bioinformatics. Current Pharmaceutical Design, 2006, 12, 2111-2120.	1.9	418
93	Development of Linear, Ensemble, and Nonlinear Models for the Prediction and Interpretation of the Biological Activity of a Set of PDGFR Inhibitors.. ChemInform, 2005, 36, no.	0.0	0
94	Determining the Validity of a QSAR Model ? A Classification Approach.. ChemInform, 2005, 36, no.	0.0	0
95	Interpreting Computational Neural Network Quantitative Structureâ€”Activity Relationship Models: A Detailed Interpretation of the Weights and Biases.. ChemInform, 2005, 36, no.	0.0	0
96	Interpreting Computational Neural Network Quantitative Structureâ˜Activity Relationship Models:Â A Detailed Interpretation of the Weights and Biases. Journal of Chemical Information and Modeling, 2005, 45, 1109-1121.	5.4	63
97	Determining the Validity of a QSAR Model â˜ A Classification Approach. Journal of Chemical Information and Modeling, 2005, 45, 65-73.	5.4	88
98	Interpreting Computational Neural Network QSAR Models:Â A Measure of Descriptor Importance. Journal of Chemical Information and Modeling, 2005, 45, 800-806.	5.4	94
99	Development of QSAR Models to Predict and Interpret the Biological Activity of Artemisinin Analogues.. ChemInform, 2004, 35, no.	0.0	0
100	Generation of QSAR sets with a self-organizing map. Journal of Molecular Graphics and Modelling, 2004, 23, 1-14.	2.4	52
101	Development of Linear, Ensemble, and Nonlinear Models for the Prediction and Interpretation of the Biological Activity of a Set of PDGFR Inhibitors. Journal of Chemical Information and Computer Sciences, 2004, 44, 2179-2189.	2.8	78
102	Development of QSAR Models To Predict and Interpret the Biological Activity of Artemisinin Analogues. Journal of Chemical Information and Computer Sciences, 2004, 44, 1440-1449.	2.8	60