Shruti Rao

List of Publications by Year
in descending order

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48	578	687363 13	677142 22
papers	citations	h-index	g-index

55	55	55	1221
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC). Genetics in Medicine, 2022, 24, 986-998.	2.4	55
2	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
3	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
4	Abstract 1193: Enhancing pediatric cancer variant curation and representation through standardized classification and automation. Cancer Research, 2022, 82, 1193-1193.	0.9	1
5	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
6	30. Curation of genetic variants in childhood cancers within the Clinical Genome Resource (ClinGen). Cancer Genetics, 2020, 244, 11-12.	0.4	0
7	46. ClinGen somatic cancer working group: Enhancing standardized interpretation of cancer genetic data for clinical use. Cancer Genetics, 2020, 244, 17-18.	0.4	0
8	Evidence-Based Network Approach to Recommending Targeted Cancer Therapies. JCO Clinical Cancer Informatics, 2020, 4, 71-88.	2.1	8
9	Prioritizing targeted therapies in an evidence-based manner, integrating biological context and functional precision medicine.. Journal of Clinical Oncology, 2020, 38, e14065-e14065.	1.6	1
10	Abstract 3222: The Virtual Molecular Tumor Board of the Variant Interpretation for Cancer Consortium: A systematic gateway connecting cancer genome interpretation and progress in genomic knowledgebases in cancer. , 2020, , .		0
11	Abstract 3211: Evolution of the CIViC knowledgebase for community driven curation of clinical variants in cancer. , 2020, , .		0
12	Abstract 1096: Harmonization standards from the Variant Interpretation for Cancer Consortium. , 2020, , .		0
13	Abstract 3215: ClinGen somatic cancer working group: Disseminating standardized cancer molecular diagnostic data and evidence through global collaboration and expert curation. , 2020, , .		0
14	Abstract A58: Curation of pediatric cancer variants within the Clinical Genome Resource (ClinGen). , 2020, , .		0
15	Expert Variant Curation Combined with in-Silico analysis for Clinical Interpretation of BCL2 variants in Resistance to BCL2 Inhibitors in Chronic Lymphocytic Leukemia/ Small Lymphocytic Lymphoma. Blood, 2020, 136, 42-43.	1.4	0
16	Expert Curation of Somatic Variants in Hematological Malignancies By the Clingen Somatic Hematological Cancer Taskforce (ClinGen HCT). Blood, 2020, 136, 23-23.	1.4	0
17	34. Curation of variants associated with pediatric tumors within the Clinical Genome Resource (ClinGen). Cancer Genetics, 2019, 233-234, S14.	0.4	0
18	Dynamic Regulation of Caveolin-1 Phosphorylation and Caveolae Formation by Mammalian Target of Rapamycin Complex 2 in Bladder Cancer Cells. American Journal of Pathology, 2019, 189, 1846-1862.	3.8	13

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19	A virtual molecular tumor board to improve efficiency and scalability of delivering precision oncology to physicians and their patients. JAMIA Open, 2019, 2, 505-515.	2.0	56
20	A case for expert curation: an overview of cancer curation in the Clinical Genome Resource (ClinGen). Journal of Physical Education and Sports Management, 2019, 5, a004739.	1.2	14
21	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
22	ClinGen Cancer Somatic Working Group â€“ standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. , 2018, , .		12
23	Acquired Resistance to a MET Antibody In Vivo Can Be Overcome by the MET Antibody Mixture Sym015. Molecular Cancer Therapeutics, 2018, 17, 1259-1270.	4.1	8
24	Future of Evidence Synthesis in Precision Oncology: Between Systematic Reviews and Biocuration. JCO Precision Oncology, 2018, 2, 1.	3.0	5
25	iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	22
26	Eye-Tracking Study to Enhance Usability of Molecular Diagnostics Reports in Cancer Precision Medicine. JCO Precision Oncology, 2018, 2, 1-11.	3.0	6
27	Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data communityâ€driven standards. Human Mutation, 2018, 39, 1721-1732.	2.5	15
28	21. Cancer curation in the clinical genome resource (on behalf of the ClinGen Somatic Working) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	0.4	0
29	29. Integrating ClinGen somatic cancer variant description standards into crowdsourced curation technology via CIViC database for ClinVar submission. Cancer Genetics, 2018, 226-227, 47.	0.4	0
30	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 247-258.	0.7	13
31	Standardizing And Democratizing Access To Cancer Molecular Diagnostic Test Data From Patients To Drive Translational Research. AMIA Summits on Translational Science Proceedings, 2018, 2017, 152-159.	0.4	0
32	eGARD: Extracting associations between genomic anomalies and drug responses from text. PLoS ONE, 2017, 12, e0189663.	2.5	14
33	Quantification and expert evaluation of evidence for chemopredictive biomarkers to personalize cancer treatment. Oncotarget, 2017, 8, 37923-37934.	1.8	23
34	Abstract 2604: The Georgetown Database of Cancer (G-DOC): A web-based data sharing platform for precision medicine. , 2017, , .		2
35	Abstract 3158:In vivoacquired resistance to an emibetuzumab analogue inMET-amplified gastric xenografts can be overcome by a MET-targeting antibody mixture or PIK3CA/AKT/mTOR inhibition. , 2017, , .		0
36	Discovery of Metabolic Biomarkers for Duchenne Muscular Dystrophy within a Natural History Study. PLoS ONE, 2016, 11, e0153461.	2.5	26

#	Article	IF	Citations
37	Somatic cancer variant curation and harmonization through consensus minimum variant level data. Genome Medicine, 2016, 8, 117.	8.2	61
38	MET network in PubMed: a text-mined network visualization and curation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw090.	3.0	6
39	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
40	Molecular profiling of TOPO1: A way to evaluate irinotecan treatment in colorectal cancer?. Journal of Clinical Oncology, 2016, 34, 546-546.	1.6	1
41	In silico Analysis of Vaccination Adverse Events. Journal of Allergy and Clinical Immunology, 2015, 135, AB104.	2.9	0
42	SNP2Structure: A Public and Versatile Resource for Mapping and Three-Dimensional Modeling of Missense SNPs on Human Protein Structures. Computational and Structural Biotechnology Journal, 2015, 13, 514-519.	4.1	16
43	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. BMC Immunology, 2014, 15, 61.	2.2	21
44	Extracting predictor variables for late effects of childhood cancer treatments from clinical notes.. Journal of Clinical Oncology, 2014, 32, 10085-10085.	1.6	0
45	Structural and functional studies of S-adenosyl-L-methionine binding proteins: a ligand-centric approach. BMC Structural Biology, 2013, 13, 6.	2.3	50
46	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. , 2013, , .		0
47	SNP2Structure. , 2013, , .		0
48	Genomic Profiling Reveals the Potential Role of TCL1A and MDR1 Deficiency in Chemotherapy-Induced Cardiotoxicity. International Journal of Biological Sciences, 2013, 9, 350-360.	6.4	31