Kumardeep Chaudhary

List of Publications by Year
in descending order

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72 papers	7,414 citations	134610 34 h-index	100535 70 g-index
87 all docs	87 docs citations	87 times ranked	12466 citing authors

#	Article	IF	Citations
1	Population-Based Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 350.	3.8	34
2	Coronary Risk Estimation Based on Clinical Data in Electronic Health Records. Journal of the American College of Cardiology, 2022, 79, 1155-1166.	1.2	14
3	Editorial: Systems Biology and Omics Approaches for Understanding Complex Disease Biology. Frontiers in Genetics, 2022, 13, 896818.	1.1	4
4	Genome-First Recall of Healthy Individuals by Polygenic Risk Score Reveals Differences in Coronary Artery Calcium. American Heart Journal, 2022, 250, 29-29.	1.2	1
5	A machine learning-based approach to determine infection status in recipients of BBV152 (Covaxin) whole-virion inactivated SARS-CoV-2 vaccine for serological surveys. Computers in Biology and Medicine, 2022, 146, 105419.	3.9	8
6	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e003092.	1.6	25
7	Prediction of Incident Heart Failure in TTR Val122Ile Carriers One Year Ahead of Diagnosis in a Multiethnic Biobank. American Journal of Cardiology, 2021, 142, 151-153.	0.7	1
8	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	3.0	500
9	Kidney disease genetic risk variants alter lysosomal beta-mannosidase (MANBA) expression and disease severity. Science Translational Medicine, 2021, 13, .	5.8	30
10	Exome-wide evaluation of rare coding variants using electronic health records identifies new geneâ€“phenotype associations. Nature Medicine, 2021, 27, 66-72.	15.2	44
11	Comparison of Approaches for Prediction of Renal Replacement Therapy-Free Survival in Patients with Acute Kidney Injury. Blood Purification, 2021, 50, 621-627.	0.9	14
12	Association of SARS-CoV-2 viral load at admission with in-hospital acute kidney injury: A retrospective cohort study. PLoS ONE, 2021, 16, e0247366.	1.1	5
13	Genome-wide polygenic risk score for retinopathy of type 2 diabetes. Human Molecular Genetics, 2021, 30, 952-960.	1.4	14
14	Genetic pleiotropy of ERCC6 lossâ€ofâ€function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. Human Mutation, 2021, 42, 969-977.	1.1	3
15	Predictive Approaches for Acute Dialysis Requirement and Death in COVID-19. Clinical Journal of the American Society of Nephrology: CJASN, 2021, 16, 1158-1168.	2.2	15
16	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
17	DeepProg: an ensemble of deep-learning and machine-learning models for prognosis prediction using multi-omics data. Genome Medicine, 2021, 13, 112.	3.6	90
18	Derivation and Validation of Genomeâ€Wide Polygenic Score for Ischemic Heart Failure. Journal of the American Heart Association, 2021, 10, e021916.	1.6	3

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19	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. American Journal of Human Genetics, 2021, 108, 2301-2318.	2.6	21
20	Natural language processing of electronic health records is superior to billing codes to identify symptom burden in hemodialysis patients. Kidney International, 2020, 97, 383-392.	2.6	27
21	Exome sequencing reveals a high prevalence of BRCA1 and BRCA2 founder variants in a diverse population-based biobank. Genome Medicine, 2020, 12, 2.	3.6	68
22	Utilization of Deep Learning for Subphenotype Identification in Sepsis-Associated Acute Kidney Injury. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 1557-1565.	2.2	59
23	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	2.9	19
24	The association of standard Kt/V and surface areaâ€normalized standard Kt/V with clinical outcomes in hemodialysis patients. Hemodialysis International, 2020, 24, 495-505.	0.4	3
25	Association of APOL1 Risk Genotype and Air Pollution for Kidney Disease. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 401-403.	2.2	14
26	Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. Journal of the American College of Cardiology, 2020, 75, 2769-2780.	1.2	88
27	Derivation and validation of genome-wide polygenic score for urinary tract stone diagnosis. Kidney International, 2020, 98, 1323-1330.	2.6	12
28	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. Leukemia, 2020, 34, 1866-1874.	3.3	36
29	PD04-08â€ƒPOLYGENIC RISK SCORE ASSOCIATES WITH URINARY TRACT STONE DIAGNOSIS IN MULTIETHNIC COHORT. Journal of Urology, 2020, 203, .	0.2	0
30	Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. Clinical Cancer Research, 2019, 25, 463-472.	3.2	41
31	Machine Learning in Glomerular Diseases: Promise for Precision Medicine. American Journal of Kidney Diseases, 2019, 74, 290-292.	2.1	7
32	Rate of Correction of Hypernatremia and Health Outcomes in Critically Ill Patients. Clinical Journal of the American Society of Nephrology: CJASN, 2019, 14, 656-663.	2.2	60
33	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 2191.	3.8	93
34	Deep Learning Accurately Predicts Estrogen Receptor Status in Breast Cancer Metabolomics Data. Journal of Proteome Research, 2018, 17, 337-347.	1.8	176
35	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418.	5.8	14
36	Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants. Journal of Translational Medicine, 2018, 16, 181.	1.8	60

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37	In Silico Approach for Prediction of Antifungal Peptides. Frontiers in Microbiology, 2018, 9, 323.	1.5	113
38	Deep Learningâ€“Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer. Clinical Cancer Research, 2018, 24, 1248-1259.	3.2	670
39	Deep Learning data integration for better risk stratification models of bladder cancer. AMIA Summits on Translational Science Proceedings, 2018, 2017, 197-206.	0.4	18
40	Assessing therapeutic potential of molecules: molecular property diagnostic suite for tuberculosis $$(mathbf{MPDS}^{mathbf{TB}})$$ (MPDS TB). Journal of Chemical Sciences, 2017, 129, 515-531.	0.7	20
41	Gene expression-based biomarkers for discriminating early and late stage of clear cell renal cancer. Scientific Reports, 2017, 7, 44997.	1.6	92
42	More Is Better: Recent Progress in Multi-Omics Data Integration Methods. Frontiers in Genetics, 2017, 8, 84.	1.1	517
43	Computational Prediction of the Immunomodulatory Potential of RNA Sequences. Methods in Molecular Biology, 2017, 1632, 75-90.	0.4	12
44	Prioritization of anticancer drugs against a cancer using genomic features of cancer cells: A step towards personalized medicine. Scientific Reports, 2016, 6, 23857.	1.6	54
45	Prediction of anticancer molecules using hybrid model developed on molecules screened against NCI-60 cancer cell lines. BMC Cancer, 2016, 16, 77.	1.1	39
46	Prediction of Immunomodulatory potential of an RNA sequence for designing non-toxic siRNAs and RNA-based vaccine adjuvants. Scientific Reports, 2016, 6, 20678.	1.6	18
47	A Web Server and Mobile App for Computing Hemolytic Potency of Peptides. Scientific Reports, 2016, 6, 22843.	1.6	135
48	A web-based resource for designing therapeutics against Ebola Virus. Scientific Reports, 2016, 6, 24782.	1.6	14
49	CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides. Nucleic Acids Research, 2016, 44, D1098-D1103.	6.5	241
50	SATPdb: a database of structurally annotated therapeutic peptides. Nucleic Acids Research, 2016, 44, D1119-D1126.	6.5	131
51	Managing Drug Resistance in Cancer: Role of Cancer Informatics. Methods in Molecular Biology, 2016, 1395, 299-312.	0.4	12
52	A Platform for Designing Genome-Based Personalized Immunotherapy or Vaccine against Cancer. PLoS ONE, 2016, 11, e0166372.	1.1	14
53	An in silico platform for predicting, screening and designing of antihypertensive peptides. Scientific Reports, 2015, 5, 12512.	1.6	123
54	VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants. Scientific Reports, 2015, 5, 12478.	1.6	34

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55	AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides. Nucleic Acids Research, 2015, 43, D956-D962.	6.5	143
56	PEPstrMOD: structure prediction of peptides containing natural, non-natural and modified residues. Biology Direct, 2015, 10, 73.	1.9	164
57	Identification and characterization of novel protein-derived arginine-rich cell-penetrating peptides. European Journal of Pharmaceutics and Biopharmaceutics, 2015, 89, 93-106.	2.0	35
58	Peptide Toxicity Prediction. Methods in Molecular Biology, 2015, 1268, 143-157.	0.4	105
59	Computer-Aided Virtual Screening and Designing of Cell-Penetrating Peptides. Methods in Molecular Biology, 2015, 1324, 59-69.	0.4	56
60	ParaPep: a web resource for experimentally validated antiparasitic peptide sequences and their structures. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau051-bau051.	1.4	60
61	Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides. Nucleic Acids Research, 2014, 42, D444-D449.	6.5	105
62	PCMdb: Pancreatic Cancer Methylation Database. Scientific Reports, 2014, 4, 4197.	1.6	28
63	Designing of promiscuous inhibitors against pancreatic cancer cell lines. Scientific Reports, 2014, 4, 4668.	1.6	19
64	Tumor Homing Peptides as Molecular Probes for Cancer Therapeutics, Diagnostics and Theranostics. Current Medicinal Chemistry, 2014, 21, 2367-2391.	1.2	80
65	In silico approaches for designing highly effective cell penetrating peptides. Journal of Translational Medicine, 2013, 11, 74.	1.8	242
66	Computational approach for designing tumor homing peptides. Scientific Reports, 2013, 3, 1607.	1.6	69
67	CancerDR: Cancer Drug Resistance Database. Scientific Reports, 2013, 3, 1445.	1.6	102
68	In Silico Models for Designing and Discovering Novel Anticancer Peptides. Scientific Reports, 2013, 3, 2984.	1.6	226
69	In Silico Approach for Predicting Toxicity of Peptides and Proteins. PLoS ONE, 2013, 8, e73957.	1.1	1,120
70	CPPsite: a curated database of cell penetrating peptides. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas015-bas015.	1.4	161
71	TumorHoPe: A Database of Tumor Homing Peptides. PLoS ONE, 2012, 7, e35187.	1.1	118
72	Indiaâ€™s top science awards heavily gender skewed. Nature India, 0, , .	0.0	0