Panagiostis Katsonis

List of Publications by Year
in descending order

60	3,656	304743	138484
papers	citations	22 h-index	58 g-index

65	65	65	7679
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
2	Evolutionary Action Score of TP53 Identifies High-Risk Mutations Associated with Decreased Survival and Increased Distant Metastases in Head and Neck Cancer. Cancer Research, 2015, 75, 1527-1536.	0.9	139
3	A formal perturbation equation between genotype and phenotype determines the Evolutionary Action of protein-coding variations on fitness. Genome Research, 2014, 24, 2050-2058.	5.5	122
4	Deleterious Effect of RAS and Evolutionary High-risk TP53 Double Mutation in Colorectal Liver Metastases. Annals of Surgery, 2019, 269, 917-923.	4.2	121
5	Metastable Liquid Clusters in Super- and Undersaturated Protein Solutions. Journal of Physical Chemistry B, 2007, 111, 3106-3114.	2.6	112
6	Mitochondrial Neurogastrointestinal Encephalopathy Due to Mutations in RRM2B. Archives of Neurology, 2009, 66, 1028-32.	4.5	103
7	Wee-1 Kinase Inhibition Overcomes Cisplatin Resistance Associated with High-RiskTP53Mutations in Head and Neck Cancer through Mitotic Arrest Followed by Senescence. Molecular Cancer Therapeutics, 2015, 14, 608-619.	4.1	97
8	Single nucleotide variations: Biological impact and theoretical interpretation. Protein Science, 2014, 23, 1650-1666.	7.6	94
9	Evolutionary Action Score of TP53 Coding Variants Is Predictive of Platinum Response in Head and Neck Cancer Patients. Cancer Research, 2015, 75, 1205-1215.	0.9	78
10	Separation of Recombination and SOS Response in Escherichia coli RecA Suggests LexA Interaction Sites. PLoS Genetics, 2011, 7, e1002244.	3.5	71
11	Molecular defects in human carbamoy phosphate synthetase I: mutational spectrum, diagnostic and protein structure considerations. Human Mutation, 2011, 32, 579-589.	2.5	67
12	Desmosterolosisâ€"phenotypic and molecular characterization of a third case and review of the literature. American Journal of Medical Genetics, Part A, 2011, 155, 1597-1604.	1.2	52
13	Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. Nature Medicine, 2018, 24, 505-511.	30.7	47
14	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. Progress in Biophysics and Molecular Biology, 2021, 163, 87-108.	2.9	45
15	Comprehensive Genomic Characterization of Parathyroid Cancer Identifies Novel Candidate Driver Mutations and Core Pathways. Journal of the Endocrine Society, 2019, 3, 544-559.	0.2	40
16	Targeting SARS-CoV-2 Nsp3 macrodomain structure with insights from human poly(ADP-ribose) glycohydrolase (PARG) structures with inhibitors. Progress in Biophysics and Molecular Biology, 2021, 163, 171-186.	2.9	39
17	Specific TP53 Mutants Overrepresented in Ovarian Cancer Impact CNV, TP53 Activity, Responses to Nutlin-3a, and Cell Survival. Neoplasia, 2015, 17, 789-803.	5.3	37
18	Predicting phenotype from genotype: Improving accuracy through more robust experimental and computational modeling. Human Mutation, 2017, 38, 569-580.	2.5	36

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19	Mutational Landscape of the BAP1 Locus Reveals an Intrinsic Control to Regulate the miRNA Network and the Binding of Protein Complexes in Uveal Melanoma. Cancers, 2019, 11, 1600.	3.7	30
20	Protein stabilization improves STAT3 function in autosomal dominant hyper-IgE syndrome. Blood, 2016, 128, 3061-3072.	1.4	28
21	FARS2 deficiency; new cases, review of clinical, biochemical, and molecular spectra, and variants interpretation based on structural, functional, and evolutionary significance. Molecular Genetics and Metabolism, 2018, 125, 281-291.	1.1	28
22	Cdkn2asuppresses metastasis in squamous cell carcinomas induced by the gain-of-function mutantp53R172H. Journal of Pathology, 2016, 240, 224-234.	4.5	27
23	Objective assessment of the evolutionary action equation for the fitness effect of missense mutations across CAGIâ€blinded contests. Human Mutation, 2017, 38, 1072-1084.	2.5	26
24	CAGI5: Objective performance assessments of predictions based on the Evolutionary Action equation. Human Mutation, 2019, 40, 1436-1454.	2.5	26
25	Genome interpretation using in silico predictors of variant impact. Human Genetics, 2022, 141, 1549-1577.	3.8	26
26	Prediction and redesign of proteinâ€“protein interactions. Progress in Biophysics and Molecular Biology, 2014, 116, 194-202.	2.9	25
27	Gnathodiaphyseal dysplasia: Severe atypical presentation with novel heterozygous mutation of the anoctamin gene (ANO5). Bone, 2018, 107, 161-171.	2.9	23
28	Corresponding-States Laws for Protein Solutions. Journal of Physical Chemistry B, 2006, 110, 17638-17644.	2.6	21
29	Negative Feedback in Genetic Circuits Confers Evolutionary Resilience and Capacitance. Cell Reports, 2014, 7, 1789-1795.	6.4	20
30	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. Human Mutation, 2019, 40, 1546-1556.	2.5	19
31	A method to delineate de novo missense variants across pathways prioritizes genes linked to autism. Science Translational Medicine, 2021, 13, .	12.4	19
32	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	2.5	17
33	Protein Kinase A and Phosphodiesterase-4D3 Binding to Coding Polymorphisms of Cardiac Muscle Anchoring Protein (mAKAP). Journal of Molecular Biology, 2013, 425, 3277-3288.	4.2	16
34	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	2.5	16
35	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
36	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13

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37	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 207-18.	0.7	13
38	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	2.5	11
39	Evolutionary action of mutations reveals antimicrobial resistance genes in Escherichia coli. Nature Communications, 2022, 13, .	12.8	11
40	Human muscle-specific A-kinase anchoring protein polymorphisms modulate the susceptibility to cardiovascular diseases by altering cAMP/PKA signaling. American Journal of Physiology - Heart and Circulatory Physiology, 2018, 315, H109-H121.	3.2	10
41	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	2.5	10
42	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
43	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
44	Variants in PRKAR1B cause a neurodevelopmental disorder with autism spectrum disorder, apraxia, and insensitivity to pain. Genetics in Medicine, 2021, 23, 1465-1473.	2.4	10
45	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. , 2016, , .		10
46	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
47	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	2.5	8
48	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. Human Mutation, 2019, 40, 1612-1622.	2.5	8
49	A general calculus of fitness landscapes finds genes under selection in cancers. Genome Research, 2022, , gr.275811.121.	5.5	7
50	Structure and evolutionary trace-assisted screening of a residue swapping the substrate ambiguity and chiral specificity in an esterase. Computational and Structural Biotechnology Journal, 2021, 19, 2307-2317.	4.1	6
51	Identification of evolutionarily stable functional and immunogenic sites across the SARS-CoV-2 proteome and greater coronavirus family. Bioinformatics, 2021, 37, 4033-4040.	4.1	6
52	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
53	Evolutionary action score identifies a subset of TP53 mutated myelodysplastic syndrome with favorable prognosis. Blood Cancer Journal, 2021, 11, 52.	6.2	5
54	Codon-level co-occurrences of germline variants and somatic mutations in cancer are rare but often lead to incorrect variant annotation and underestimated impact prediction. PLoS ONE, 2017, 12, e0174766.	2.5	4

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55	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. Methods in Enzymology, 2021, 661, 407-431.	1.0	4
56	Decoding Cancer Variants of Unknown Significance for Helicaseâ€“Nucleaseâ€“RPA Complexes Orchestrating DNA Repair During Transcription and Replication. Frontiers in Molecular Biosciences, 2021, 8, 791792.	3.5	4
57	PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPARÎ³â€“DNMT1 Interactions in the Genome. Cancers, 2021, 13, 3993.	3.7	2
58	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. Methods in Enzymology, 2021, 661, 407-431.	1.0	2
59	Abstract 24010: Muscle-specific A-Kinase Anchoring Protein Polymorphisms Pre-dispose Humans to Cardiovascular Diseases by Affecting cyclic AMP/PKA Signaling. Circulation, 2017, 136, .	1.6	1
60	Evolutionary Action Score Identifies a Subset of TP53 Mutated Myelodysplastic Syndrome with Favorable Prognosis. Blood, 2020, 136, 4-5.	1.4	0