Panagiostis Katsonis

List of Publications by Year
in descending order

60 papers	3,656 citations	304743 22 h-index	138484 58 g-index
65 all docs	65 docs citations	65 times ranked	7679 citing authors

#	Article	IF	Citations
1	A general calculus of fitness landscapes finds genes under selection in cancers. Genome Research, 2022, , gr.275811.121.	5.5	7
2	Genome interpretation using in silico predictors of variant impact. Human Genetics, 2022, 141, 1549-1577.	3.8	26
3	Evolutionary action of mutations reveals antimicrobial resistance genes in Escherichia coli. Nature Communications, 2022, 13, .	12.8	11
4	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
5	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
6	Evolutionary action score identifies a subset of TP53 mutated myelodysplastic syndrome with favorable prognosis. Blood Cancer Journal, 2021, 11, 52.	6.2	5
7	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
8	A method to delineate de novo missense variants across pathways prioritizes genes linked to autism. Science Translational Medicine, 2021, 13, .	12.4	19
9	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
10	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
11	PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPARÎ³â€"DNMT1 Interactions in the Genome. Cancers, 2021, 13, 3993.	3.7	2
12	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
13	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
14	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
15	Evolutionary Action Score Identifies a Subset of TP53 Mutated Myelodysplastic Syndrome with Favorable Prognosis. Blood, 2020, 136, 4-5.	1.4	0
16	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
17	CAGI5: Objective performance assessments of predictions based on the Evolutionary Action equation. Human Mutation, 2019, 40, 1436-1454.	2.5	26
18	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

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19	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. Human Mutation, 2019, 40, 1546-1556.	2.5	19
20	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
21	Assessment of predicted enzymatic activity of α-<i>N</i>-acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
22	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
23	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
24	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
25	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
26	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
27	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
28	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
29	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
30	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
31	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
32	Gnathodiaphyseal dysplasia: Severe atypical presentation with novel heterozygous mutation of the anoctamin gene (ANO5). Bone, 2018, 107, 161-171.	2.9	23
33	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
34	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
35	Predicting phenotype from genotype: Improving accuracy through more robust experimental and computational modeling. Human Mutation, 2017, 38, 569-580.	2.5	36
36	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	2.5	17

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37	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
38	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
39	Objective assessment of the evolutionary action equation for the fitness effect of missense mutations across CAGI–blinded contests. Human Mutation, 2017, 38, 1072-1084.	2.5	26
40	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
41	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
42	Protein stabilization improves STAT3 function in autosomal dominant hyper-IgE syndrome. Blood, 2016, 128, 3061-3072.	1.4	28
43	Cdkn2asuppresses metastasis in squamous cell carcinomas induced by the gain-of-function mutantp53R172H. Journal of Pathology, 2016, 240, 224-234.	4.5	27
44	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. , 2016, , .		10
45	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
46	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
47	Wee-1 Kinase Inhibition Overcomes Cisplatin Resistance Associated with High-Risk *TP53* Mutations in Head and Neck Cancer through Mitotic Arrest Followed by Senescence. Molecular Cancer Therapeutics, 2015, 14, 608-619.	4.1	97
48	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
49	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
50	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
51	Single nucleotide variations: Biological impact and theoretical interpretation. Protein Science, 2014, 23, 1650-1666.	7.6	94
52	Negative Feedback in Genetic Circuits Confers Evolutionary Resilience and Capacitance. Cell Reports, 2014, 7, 1789-1795.	6.4	20
53	Prediction and redesign of protein–protein interactions. Progress in Biophysics and Molecular Biology, 2014, 116, 194-202.	2.9	25
54	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

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55	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
56	Molecular defects in human carbamoy phosphate synthetase I: mutational spectrum, diagnostic and protein structure considerations. Human Mutation, 2011, 32, 579-589.	2.5	67
57	Separation of Recombination and SOS Response in Escherichia coli RecA Suggests LexA Interaction Sites. PLoS Genetics, 2011, 7, e1002244.	3.5	71
58	Mitochondrial Neurogastrointestinal Encephalopathy Due to Mutations in RRM2B. Archives of Neurology, 2009, 66, 1028-32.	4.5	103
59	Metastable Liquid Clusters in Super- and Undersaturated Protein Solutions. Journal of Physical Chemistry B, 2007, 111, 3106-3114.	2.6	112
60	Corresponding-States Laws for Protein Solutions. Journal of Physical Chemistry B, 2006, 110, 17638-17644.	2.6	21