

# Olivier Lichtarge

## List of Publications by Year in descending order

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160  
papers

12,312  
citations

61984

43  
h-index

28297

105  
g-index

168  
all docs

168  
docs citations

168  
times ranked

20119  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
2	An Evolutionary Trace Method Defines Binding Surfaces Common to Protein Families. <i>Journal of Molecular Biology</i> , 1996, 257, 342-358.	4.2	1,169
3	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
4	Identification of a candidate therapeutic autophagy-inducing peptide. <i>Nature</i> , 2013, 494, 201-206.	27.8	669
5	$\beta$ -Arrestin-dependent, G Protein-independent ERK1/2 Activation by the $\beta$ 2 Adrenergic Receptor. <i>Journal of Biological Chemistry</i> , 2006, 281, 1261-1273.	3.4	651
6	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
7	Rhodopsin activation blocked by metal-ion-binding sites linking transmembrane helices C and F. <i>Nature</i> , 1996, 383, 347-350.	27.8	429
8	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	6.4	382
9	Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. <i>Annals of Neurology</i> , 2000, 47, 670-679.	5.3	314
10	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
11	Evolutionary predictions of binding surfaces and interactions. <i>Current Opinion in Structural Biology</i> , 2002, 12, 21-27.	5.7	256
12	Identity and Function of a Large Gene Network Underlying Mutagenic Repair of DNA Breaks. <i>Science</i> , 2012, 338, 1344-1348.	12.6	195
13	Structural clusters of evolutionary trace residues are statistically significant and common in proteins. <i>Journal of Molecular Biology</i> , 2002, 316, 139-154.	4.2	190
14	Evolutionary Trace of G Protein-coupled Receptors Reveals Clusters of Residues That Determine Global and Class-specific Functions. <i>Journal of Biological Chemistry</i> , 2004, 279, 8126-8132.	3.4	179
15	An Accurate, Sensitive, and Scalable Method to Identify Functional Sites in Protein Structures. <i>Journal of Molecular Biology</i> , 2003, 326, 255-261.	4.2	174
16	Evolutionary Action Score of TP53 Identifies High-Risk Mutations Associated with Decreased Survival and Increased Distant Metastases in Head and Neck Cancer. <i>Cancer Research</i> , 2015, 75, 1527-1536.	0.9	139
17	Prediction and confirmation of a site critical for effector regulation of RGS domain activity. <i>Nature Structural Biology</i> , 2001, 8, 234-237.	9.7	125
18	A formal perturbation equation between genotype and phenotype determines the Evolutionary Action of protein-coding variations on fitness. <i>Genome Research</i> , 2014, 24, 2050-2058.	5.5	122

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19	Deleterious Effect of RAS and Evolutionary High-risk TP53 Double Mutation in Colorectal Liver Metastases. <i>Annals of Surgery</i> , 2019, 269, 917-923.	4.2	121
20	C5a Receptor Activation. <i>Journal of Biological Chemistry</i> , 1999, 274, 15757-15765.	3.4	120
21	Supergenomic Network Compression and the Discovery of EXP1 as a Glutathione Transferase Inhibited by Artesunate. <i>Cell</i> , 2014, 158, 916-928.	28.9	113
22	Identification of functional surfaces of the zinc binding domains of intracellular receptors. <i>Journal of Molecular Biology</i> , 1997, 274, 325-337.	4.2	107
23	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. <i>Cell</i> , 2018, 172, 924-936.e11.	28.9	103
24	Wee-1 Kinase Inhibition Overcomes Cisplatin Resistance Associated with High-Risk TP53 Mutations in Head and Neck Cancer through Mitotic Arrest Followed by Senescence. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 608-619.	4.1	97
25	Single nucleotide variations: Biological impact and theoretical interpretation. <i>Protein Science</i> , 2014, 23, 1650-1666.	7.6	94
26	Distinct faces of the Ku heterodimer mediate DNA repair and telomeric functions. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 301-307.	8.2	88
27	Evolution-guided discovery and recoding of allosteric pathway specificity determinants in psychoactive bioamine receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7787-7792.	7.1	86
28	Automated hypothesis generation based on mining scientific literature. , 2014, , .		82
29	Evolutionary Action Score of TP53 Coding Variants Is Predictive of Platinum Response in Head and Neck Cancer Patients. <i>Cancer Research</i> , 2015, 75, 1205-1215.	0.9	78
30	Elucidation of G-protein and $\beta$ -arrestin functional selectivity at the dopamine D2 receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7097-7102.	7.1	75
31	Functional Rescue of $\beta$ 1 Adrenoceptor Dimerization and Trafficking by Pharmacological Chaperones. <i>Traffic</i> , 2009, 10, 1019-1033.	2.7	71
32	Separation of Recombination and SOS Response in Escherichia coli RecA Suggests LexA Interaction Sites. <i>PLoS Genetics</i> , 2011, 7, e1002244.	3.5	71
33	Prediction of enzyme function based on 3D templates of evolutionarily important amino acids. <i>BMC Bioinformatics</i> , 2008, 9, 17.	2.6	70
34	Molecular defects in human carbamoyl phosphate synthetase I: mutational spectrum, diagnostic and protein structure considerations. <i>Human Mutation</i> , 2011, 32, 579-589.	2.5	67
35	ET viewer: an application for predicting and visualizing functional sites in protein structures. <i>Bioinformatics</i> , 2006, 22, 2049-2050.	4.1	62
36	Evolutionary action and structural basis of the allosteric switch controlling $\beta$ 2AR functional selectivity. <i>Nature Communications</i> , 2017, 8, 2169.	12.8	61

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37	Evolution of neural precursor selection: functional divergence of proneural proteins. <i>Development (Cambridge)</i> , 2004, 131, 1679-1689.	2.5	59
38	Evolutionary Trace for Prediction and Redesign of Protein Functional Sites. <i>Methods in Molecular Biology</i> , 2012, 819, 29-42.	0.9	59
39	Graph sharpening plus graph integration: a synergy that improves protein functional classification. <i>Bioinformatics</i> , 2007, 23, 3217-3224.	4.1	57
40	Genetic Mapping of the Human C5a Receptor. <i>Journal of Biological Chemistry</i> , 2000, 275, 35393-35401.	3.4	55
41	Essential Helix Interactions in the Anion Transporter Domain of Prestin Revealed by Evolutionary Trace Analysis. <i>Journal of Neuroscience</i> , 2006, 26, 12727-12734.	3.6	52
42	Desmosterolosisâ€”phenotypic and molecular characterization of a third case and review of the literature. <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 1597-1604.	1.2	52
43	Role for the Regulator of G-Protein Signaling Homology Domain of G Protein-Coupled Receptor Kinases 5 and 6 in $\beta$ 2-Adrenergic Receptor and Rhodopsin Phosphorylation. <i>Molecular Pharmacology</i> , 2010, 77, 405-415.	2.3	47
44	Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. <i>Nature Medicine</i> , 2018, 24, 505-511.	30.7	47
45	PyETV: a PyMOL evolutionary trace viewer to analyze functional site predictions in protein complexes. <i>Bioinformatics</i> , 2010, 26, 2981-2982.	4.1	46
46	Type 2 diabetesâ€”associated variants of the MT <sub>2</sub> melatonin receptor affect distinct modes of signaling. <i>Science Signaling</i> , 2018, 11, .	3.6	45
47	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 87-108.	2.9	45
48	Protein function prediction: towards integration of similarity metrics. <i>Current Opinion in Structural Biology</i> , 2011, 21, 180-188.	5.7	42
49	Comprehensive Genomic Characterization of Parathyroid Cancer Identifies Novel Candidate Driver Mutations and Core Pathways. <i>Journal of the Endocrine Society</i> , 2019, 3, 544-559.	0.2	40
50	Targeting SARS-CoV-2 Nsp3 macrodomain structure with insights from human poly(ADP-ribose) glycohydrolase (PARG) structures with inhibitors. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 171-186.	2.9	39
51	Accurate and scalable identification of functional sites by evolutionary tracing. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 159-166.	1.2	38
52	Evolutionary Trace Annotation of Protein Function in the Structural Proteome. <i>Journal of Molecular Biology</i> , 2010, 396, 1451-1473.	4.2	38
53	Intramolecular allosteric communication in dopamine D2 receptor revealed by evolutionary amino acid covariation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3539-3544.	7.1	38
54	Prediction and experimental validation of enzyme substrate specificity in protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4195-202.	7.1	37

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55	Specific TP53 Mutants Overrepresented in Ovarian Cancer Impact CNV, TP53 Activity, Responses to Nutlin-3a, and Cell Survival. <i>Neoplasia</i> , 2015, 17, 789-803.	5.3	37
56	Predicting phenotype from genotype: Improving accuracy through more robust experimental and computational modeling. <i>Human Mutation</i> , 2017, 38, 569-580.	2.5	36
57	Evolutionary Traces of Functional Surfaces along G Protein Signaling Pathway. <i>Methods in Enzymology</i> , 2002, 344, 536-556.	1.0	35
58	Evolution: a guide to perturb protein function and networks. <i>Current Opinion in Structural Biology</i> , 2010, 20, 351-359.	5.7	35
59	Literature-based automated discovery of tumor suppressor p53 phosphorylation and inhibition by NEK2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10666-10671.	7.1	33
60	Differential Effects of Collagen Prolyl 3-Hydroxylation on Skeletal Tissues. <i>PLoS Genetics</i> , 2014, 10, e1004121.	3.5	31
61	UET: a database of evolutionarily-predicted functional determinants of protein sequences that cluster as functional sites in protein structures. <i>Nucleic Acids Research</i> , 2016, 44, D308-D312.	14.5	31
62	Exploring use of unsupervised clustering to associate signaling profiles of GPCR ligands to clinical response. <i>Nature Communications</i> , 2019, 10, 4075.	12.8	31
63	Recurrent use of evolutionary importance for functional annotation of proteins based on local structural similarity. <i>Protein Science</i> , 2006, 15, 1530-1536.	7.6	30
64	Rapid detection of similarity in protein structure and function through contact metric distances. <i>Nucleic Acids Research</i> , 2006, 34, e152-e152.	14.5	30
65	Mutational Landscape of the BAP1 Locus Reveals an Intrinsic Control to Regulate the miRNA Network and the Binding of Protein Complexes in Uveal Melanoma. <i>Cancers</i> , 2019, 11, 1600.	3.7	30
66	Evolutionary Trace-based Peptides Identify a Novel Asymmetric Interaction That Mediates Oligomerization in Nuclear Receptors. <i>Journal of Biological Chemistry</i> , 2005, 280, 31818-31829.	3.4	28
67	Character and evolution of protein-protein interfaces. <i>Physical Biology</i> , 2005, 2, S36-S43.	1.8	28
68	Evolutionary Trace Annotation Server: automated enzyme function prediction in protein structures using 3D templates. <i>Bioinformatics</i> , 2009, 25, 1426-1427.	4.1	28
69	The use of evolutionary patterns in protein annotation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 316-325.	5.7	28
70	Protein stabilization improves STAT3 function in autosomal dominant hyper-IgE syndrome. <i>Blood</i> , 2016, 128, 3061-3072.	1.4	28
71	FARS2 deficiency; new cases, review of clinical, biochemical, and molecular spectra, and variants interpretation based on structural, functional, and evolutionary significance. <i>Molecular Genetics and Metabolism</i> , 2018, 125, 281-291.	1.1	28
72	Cdkn2asuppresses metastasis in squamous cell carcinomas induced by the gain-of-function mutantp53R172H. <i>Journal of Pathology</i> , 2016, 240, 224-234.	4.5	27

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73	Objective assessment of the evolutionary action equation for the fitness effect of missense mutations across CAGI-blind contests. <i>Human Mutation</i> , 2017, 38, 1072-1084.	2.5	26
74	CAGI5: Objective performance assessments of predictions based on the Evolutionary Action equation. <i>Human Mutation</i> , 2019, 40, 1436-1454.	2.5	26
75	Genome interpretation using in silico predictors of variant impact. <i>Human Genetics</i> , 2022, 141, 1549-1577.	3.8	26
76	Prediction and redesign of protein-protein interactions. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 194-202.	2.9	25
77	Computational and Biochemical Identification of a Nuclear Pore Complex Binding Site on the Nuclear Transport Carrier NTF2. <i>Journal of Molecular Biology</i> , 2004, 344, 303-310.	4.2	23
78	Correlated Evolutionary Pressure at Interacting Transcription Factors and DNA Response Elements Can Guide the Rational Engineering of DNA Binding Specificity. <i>Journal of Molecular Biology</i> , 2005, 350, 402-415.	4.2	23
79	Regulation of Ras Localization and Cell Transformation by Evolutionarily Conserved Palmitoyltransferases. <i>Molecular and Cellular Biology</i> , 2014, 34, 374-385.	2.3	23
80	Gnathodiaphyseal dysplasia: Severe atypical presentation with novel heterozygous mutation of the anoctamin gene (ANO5). <i>Bone</i> , 2018, 107, 161-171.	2.9	23
81	Accounting for epistatic interactions improves the functional analysis of protein structures. <i>Bioinformatics</i> , 2013, 29, 2714-2721.	4.1	22
82	Predicting Future Scientific Discoveries Based on a Networked Analysis of the Past Literature. , 2015, , .		22
83	De-Orphaning the Structural Proteome through Reciprocal Comparison of Evolutionarily Important Structural Features. <i>PLoS ONE</i> , 2008, 3, e2136.	2.5	21
84	Negative Feedback in Genetic Circuits Confers Evolutionary Resilience and Capacitance. <i>Cell Reports</i> , 2014, 7, 1789-1795.	6.4	20
85	Determinants of Endogenous Ligand Specificity Divergence among Metabotropic Glutamate Receptors. <i>Journal of Biological Chemistry</i> , 2015, 290, 2870-2878.	3.4	20
86	Lysine 270 in the Third Intracellular Domain of the Oxytocin Receptor is an Important Determinant for G $\pm$ qCoupling Specificity. <i>Molecular Endocrinology</i> , 2002, 16, 814-823.	3.7	19
87	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. <i>Human Mutation</i> , 2019, 40, 1546-1556.	2.5	19
88	A method to delineate de novo missense variants across pathways prioritizes genes linked to autism. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	19
89	Evolutionary identification of a subtype specific functional site in the ligand binding domain of steroid receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1046-1057.	2.6	18
90	Rank information: A structure-independent measure of evolutionary trace quality that improves identification of protein functional sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 111-123.	2.6	17

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91	The Maternal-to-Zygotic Transition Targets Actin to Promote Robustness during Morphogenesis. <i>PLoS Genetics</i> , 2013, 9, e1003901.	3.5	17
92	Benchmarking predictions of allostery in liver pyruvate kinase in CAG14. <i>Human Mutation</i> , 2017, 38, 1123-1131.	2.5	17
93	Protein Kinase A and Phosphodiesterase-4D3 Binding to Coding Polymorphisms of Cardiac Muscle Anchoring Protein (mAKAP). <i>Journal of Molecular Biology</i> , 2013, 425, 3277-3288.	4.2	16
94	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAG15 challenge. <i>Human Mutation</i> , 2019, 40, 1392-1399.	2.5	16
95	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. <i>Human Mutation</i> , 2019, 40, 1495-1506.	2.5	16
96	Accurate Protein Structure Annotation through Competitive Diffusion of Enzymatic Functions over a Network of Local Evolutionary Similarities. <i>PLoS ONE</i> , 2010, 5, e14286.	2.5	16
97	Role of Transmembrane Domain/Transmembrane Domain Interfaces of PGlycoprotein (ABCB1) in Solute Transport. Convergent Information from Photoaffinity Labeling, Site Directed Mutagenesis and in Silico Importance Prediction. <i>Current Medicinal Chemistry</i> , 2006, 13, 793-805.	2.4	14
98	Selectivity and Evolutionary Divergence of Metabotropic Glutamate Receptors for Endogenous Ligands and G Proteins Coupled to Phospholipase C or TRP Channels. <i>Journal of Biological Chemistry</i> , 2014, 289, 29961-29974.	3.4	14
99	Multimodal network diffusion predicts future disease-gene-chemical associations. <i>Bioinformatics</i> , 2019, 35, 1536-1543.	4.1	14
100	Harnessing the paradoxical phenotypes of APOE $\epsilon$ 2 and APOE $\epsilon$ 4 to identify genetic modifiers in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, 831-846.	0.8	14
101	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAG1. <i>Human Mutation</i> , 2017, 38, 1042-1050.	2.5	13
102	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016, 21, 207-18.	0.7	13
103	ETAscape: analyzing protein networks to predict enzymatic function and substrates in Cytoscape. <i>Bioinformatics</i> , 2012, 28, 2186-2188.	4.1	12
104	Using interpretable deep learning to model cancer dependencies. <i>Bioinformatics</i> , 2021, 37, 2675-2681.	4.1	12
105	Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. <i>Annals of Neurology</i> , 2000, 47, 670-679.	5.3	12
106	Untangling complex networks: Risk minimization in financial markets through accessible spin glass ground states. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 3250-3253.	2.6	11
107	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAG15 intellectual disability challenge. <i>Human Mutation</i> , 2019, 40, 1330-1345.	2.5	11
108	Evolutionary action of mutations reveals antimicrobial resistance genes in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	11



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109	Getting past appearances: the many-fold consequences of remote homology. , 2001, 8, 918-920.		10
110	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
111	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
112	Assessment of predicted enzymatic activity of $\beta$ -acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
113	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
114	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
115	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. , 2016, , .		10
116	A statistical model to correct systematic bias introduced by algorithmic thresholds in protein structural comparison algorithms. , 2008, , .		9
117	Function prediction from networks of local evolutionary similarity in protein structure. BMC Bioinformatics, 2013, 14, S6.	2.6	9
118	Cooperativity of Negative Autoregulation Confers Increased Mutational Robustness. Physical Review Letters, 2016, 116, 258104.	7.8	9
119	Identification of Functionally Important Residues/Domains in Membrane Proteins Using an Evolutionary Approach Coupled with Systematic Mutational Analysis. Methods in Molecular Biology, 2009, 493, 287-297.	0.9	9
120	CRISPR-FRT targets shared sites in a knock-out collection for off-the-shelf genome editing. Nature Communications, 2018, 9, 2231.	12.8	8
121	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
122	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI. Human Mutation, 2019, 40, 1474-1485.	2.5	8
123	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
124	Recurrent high-impact mutations at cognate structural positions in class A G protein-coupled receptors expressed in tumors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
125	An Angiotensin II type 1 receptor activation switch patch revealed through Evolutionary Trace analysis. Biochemical Pharmacology, 2010, 80, 86-94.	4.4	7
126	DISCOVERY OF FUNCTIONAL AND DISEASE PATHWAYS BY COMMUNITY DETECTION IN PROTEIN-PROTEIN INTERACTION NETWORKS. , 2017, 22, 336-347.		7



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127	EPIMUTESTR: a nearest neighbor machine learning approach to predict cancer driver genes from the evolutionary action of coding variants. <i>Nucleic Acids Research</i> , 2022, 50, e70-e70.	14.5	7
128	A general calculus of fitness landscapes finds genes under selection in cancers. <i>Genome Research</i> , 2022, , gr.275811.121.	5.5	7
129	Potential role of <i>Plasmodium falciparum</i> exported protein 1 in the chloroquine mode of action. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 31-35.	3.4	6
130	Structure and evolutionary trace-assisted screening of a residue swapping the substrate ambiguity and chiral specificity in an esterase. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2307-2317.	4.1	6
131	Identification of evolutionarily stable functional and immunogenic sites across the SARS-CoV-2 proteome and greater coronavirus family. <i>Bioinformatics</i> , 2021, 37, 4033-4040.	4.1	6
132	Assessing computational predictions of the phenotypic effect of cystathionine $\beta$ -synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	2.5	5
133	Evolutionary action score identifies a subset of TP53 mutated myelodysplastic syndrome with favorable prognosis. <i>Blood Cancer Journal</i> , 2021, 11, 52.	6.2	5
134	COMPOSITE MOTIFS INTEGRATING MULTIPLE PROTEIN STRUCTURES INCREASE SENSITIVITY FOR FUNCTION PREDICTION. , 2007, , .		5
135	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. <i>PLoS ONE</i> , 2017, 12, e0174766.	2.5	4
136	Discovery of disease- and drug-specific pathways through community structures of a literature network. <i>Bioinformatics</i> , 2020, 36, 1881-1888.	4.1	4
137	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 1614-1627.	4.9	4
138	Graph-based information diffusion method for prioritizing functionally related genes in protein-protein interaction networks. , 2019, , .		4
139	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. <i>Methods in Enzymology</i> , 2021, 661, 407-431.	1.0	4
140	Decoding Cancer Variants of Unknown Significance for Helicase $\beta$ -Nuclease $\beta$ -RPA Complexes Orchestrating DNA Repair During Transcription and Replication. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 791792.	3.5	4
141	Residues and residue pairs of evolutionary importance differentially direct signaling bias of D2 dopamine receptors. <i>Journal of Biological Chemistry</i> , 2019, 294, 19279-19291.	3.4	3
142	Graph-based information diffusion method for prioritizing functionally related genes in protein-protein interaction networks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 439-450.	0.7	3
143	An Evolutionary Trace method defines functionally important bases and sites common to RNA families. <i>PLoS Computational Biology</i> , 2020, 16, e1007583.	3.2	2
144	PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPAR $\beta$ -DNMT1 Interactions in the Genome. <i>Cancers</i> , 2021, 13, 3993.	3.7	2

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145	COMPUTING THERAPY FOR PRECISION MEDICINE: COLLABORATIVE FILTERING INTEGRATES AND PREDICTS MULTI-ENTITY INTERACTIONS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 21-32.	0.7	2
146	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
147	Structural Elements Directing G Proteins and $\beta$ -Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2022, 5, 89-101.	4.9	2
148	HUMAN KINASES DISPLAY MUTATIONAL HOTSPOTS AT COGNATE POSITIONS WITHIN CANCER. , 2017, 22, 414-425.		1
149	COMPUTING THERAPY FOR PRECISION MEDICINE: COLLABORATIVE FILTERING INTEGRATES AND PREDICTS MULTI-ENTITY INTERACTIONS. , 2016, , .		1
150	Incidence of PI3K pathway aberrations and their impact on response to neoadjuvant chemotherapy (NACT) in triple-negative breast cancer (TNBC) subtypes.. Journal of Clinical Oncology, 2018, 36, 588-588.	1.6	1
151	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
152	Evolutionary Action Score of TP53 Analysis in Pathologically High-Risk Human Papillomavirus-Negative Head and Neck Cancer From a Phase 2 Clinical Trial: NRG Oncology Radiation Therapy Oncology Group 0234. Advances in Radiation Oncology, 2022, 7, 100989.	1.2	1
153	Evolutionary Trace of Protein Functional Determinants. , 2010, , 119-146.		0
154	Computational Approaches to Studying Molecular Phylogenetics. , 2018, , 173-190.		0
155	P4493: IDENTIFYING GENETIC MODIFIERS OF APOE VIA IMPUTATION OF DEVIATION IN EVOLUTIONARY ACTION LOAD IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2019, 15, P1502.	0.8	0
156	Integration of large-scale molecular networks and exomic data can identify Alzheimer's disease genes. Alzheimer's and Dementia, 2020, 16, e041965.	0.8	0
157	Identifying genetic modifiers of APOE in Alzheimer's disease using evolutionary information and regression analyses. Alzheimer's and Dementia, 2020, 16, e043497.	0.8	0
158	AN EVOLUTIONARY PERSPECTIVE ON THE DETERMINANTS OF PROTEIN FUNCTION AND ASSEMBLY. , 2004, , .		0
159	Network Analytics: Evolutionary Compression, Diffusion and the Action Equation for Mutations. FASEB Journal, 2016, 30, 255.1.	0.5	0
160	Evolutionary Action Score Identifies a Subset of TP53 Mutated Myelodysplastic Syndrome with Favorable Prognosis. Blood, 2020, 136, 4-5.	1.4	0