# Olivier Lichtarge

List of Publications by Year
in descending order

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|---|---|---|---|
| 160<br>papers | 12,312<br>citations | 61945<br>43<br>h-index | 28275<br>105<br>g-index |
| 168<br>all docs | 168<br>docs citations | 168<br>times ranked | 20119<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23. | 13.5 | 1,794 |
| 2 | An Evolutionary Trace Method Defines Binding Surfaces Common to Protein Families. Journal of Molecular Biology, 1996, 257, 342-358. | 2.0 | 1,169 |
| 3 | A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227. | 9.0 | 789 |
| 4 | Identification of a candidate therapeutic autophagy-inducing peptide. Nature, 2013, 494, 201-206. | 13.7 | 669 |
| 5 | $\beta_2$-Arrestin-dependent, G Protein-independent ERK1/2 Activation by the $\beta_2$ Adrenergic Receptor. Journal of Biological Chemistry, 2006, 281, 1261-1273. | 1.6 | 651 |
| 6 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14. | 13.5 | 620 |
| 7 | Rhodopsin activation blocked by metal-ion-binding sites linking transmembrane helices C and F. Nature, 1996, 383, 347-350. | 13.7 | 429 |
| 8 | Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5. | 2.9 | 382 |
| 9 | Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. Annals of Neurology, 2000, 47, 670-679. | 2.8 | 314 |
| 10 | The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244. | 3.8 | 261 |
| 11 | Evolutionary predictions of binding surfaces and interactions. Current Opinion in Structural Biology, 2002, 12, 21-27. | 2.6 | 256 |
| 12 | Identity and Function of a Large Gene Network Underlying Mutagenic Repair of DNA Breaks. Science, 2012, 338, 1344-1348. | 6.0 | 195 |
| 13 | Structural clusters of evolutionary trace residues are statistically significant and common in proteins. Journal of Molecular Biology, 2002, 316, 139-154. | 2.0 | 190 |
| 14 | Evolutionary Trace of G Protein-coupled Receptors Reveals Clusters of Residues That Determine Global and Class-specific Functions. Journal of Biological Chemistry, 2004, 279, 8126-8132. | 1.6 | 179 |
| 15 | An Accurate, Sensitive, and Scalable Method to Identify Functional Sites in Protein Structures. Journal of Molecular Biology, 2003, 326, 255-261. | 2.0 | 174 |
| 16 | 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. | 0.4 | 139 |
| 17 | Prediction and confirmation of a site critical for effector regulation of RGS domain activity. Nature Structural Biology, 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. Genome Research, 2014, 24, 2050-2058. | 2.4 | 122 |

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| 19 | Deleterious Effect of RAS and Evolutionary High-risk TP53 Double Mutation in Colorectal Liver Metastases. Annals of Surgery, 2019, 269, 917-923. | 2.1 | 121 |
| 20 | C5a Receptor Activation. Journal of Biological Chemistry, 1999, 274, 15757-15765. | 1.6 | 120 |
| 21 | Supergenomic Network Compression and the Discovery of EXP1 as a Glutathione Transferase Inhibited by Artesunate. Cell, 2014, 158, 916-928. | 13.5 | 113 |
| 22 | Identification of functional surfaces of the zinc binding domains of intracellular receptors. Journal of Molecular Biology, 1997, 274, 325-337. | 2.0 | 107 |
| 23 | A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. Cell, 2018, 172, 924-936.e11. | 13.5 | 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. Molecular Cancer Therapeutics, 2015, 14, 608-619. | 1.9 | 97 |
| 25 | Single nucleotide variations: Biological impact and theoretical interpretation. Protein Science, 2014, 23, 1650-1666. | 3.1 | 94 |
| 26 | Distinct faces of the Ku heterodimer mediate DNA repair and telomeric functions. Nature Structural and Molecular Biology, 2007, 14, 301-307. | 3.6 | 88 |
| 27 | Evolution-guided discovery and recoding of allosteric pathway specificity determinants in psychoactive bioamine receptors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7787-7792. | 3.3 | 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. Cancer Research, 2015, 75, 1205-1215. | 0.4 | 78 |
| 30 | Elucidation of G-protein and Î²-arrestin functional selectivity at the dopamine D2 receptor. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7097-7102. | 3.3 | 75 |
| 31 | Functional Rescue of Î²$_1$â€Adrenoceptor Dimerization and Trafficking by Pharmacological Chaperones. Traffic, 2009, 10, 1019-1033. | 1.3 | 71 |
| 32 | Separation of Recombination and SOS Response in Escherichia coli RecA Suggests LexA Interaction Sites. PLoS Genetics, 2011, 7, e1002244. | 1.5 | 71 |
| 33 | Prediction of enzyme function based on 3D templates of evolutionarily important amino acids. BMC Bioinformatics, 2008, 9, 17. | 1.2 | 70 |
| 34 | Molecular defects in human carbamoy phosphate synthetase I: mutational spectrum, diagnostic and protein structure considerations. Human Mutation, 2011, 32, 579-589. | 1.1 | 67 |
| 35 | ET viewer: an application for predicting and visualizing functional sites in protein structures. Bioinformatics, 2006, 22, 2049-2050. | 1.8 | 62 |
| 36 | Evolutionary action and structural basis of the allosteric switch controlling Î²2AR functional selectivity. Nature Communications, 2017, 8, 2169. | 5.8 | 61 |

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| 37 | Evolution of neural precursor selection: functional divergence of proneural proteins. Development (Cambridge), 2004, 131, 1679-1689. | 1.2 | 59 |
| 38 | Evolutionary Trace for Prediction and Redesign of Protein Functional Sites. Methods in Molecular Biology, 2012, 819, 29-42. | 0.4 | 59 |
| 39 | Graph sharpening plus graph integration: a synergy that improves protein functional classification. Bioinformatics, 2007, 23, 3217-3224. | 1.8 | 57 |
| 40 | Genetic Mapping of the Human C5a Receptor. Journal of Biological Chemistry, 2000, 275, 35393-35401. | 1.6 | 55 |
| 41 | Essential Helix Interactions in the Anion Transporter Domain of Prestin Revealed by Evolutionary Trace Analysis. Journal of Neuroscience, 2006, 26, 12727-12734. | 1.7 | 52 |
| 42 | 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. | 0.7 | 52 |
| 43 | Role for the Regulator of G-Protein Signaling Homology Domain of G Protein-Coupled Receptor Kinases 5 and 6 in Î²2-Adrenergic Receptor and Rhodopsin Phosphorylation. Molecular Pharmacology, 2010, 77, 405-415. | 1.0 | 47 |
| 44 | Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. Nature Medicine, 2018, 24, 505-511. | 15.2 | 47 |
| 45 | PyETV: a PyMOL evolutionary trace viewer to analyze functional site predictions in protein complexes. Bioinformatics, 2010, 26, 2981-2982. | 1.8 | 46 |
| 46 | Type 2 diabetesâ€"associated variants of the MT$_2$ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, . | 1.6 | 45 |
| 47 | Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. Progress in Biophysics and Molecular Biology, 2021, 163, 87-108. | 1.4 | 45 |
| 48 | Protein function prediction: towards integration of similarity metrics. Current Opinion in Structural Biology, 2011, 21, 180-188. | 2.6 | 42 |
| 49 | Comprehensive Genomic Characterization of Parathyroid Cancer Identifies Novel Candidate Driver Mutations and Core Pathways. Journal of the Endocrine Society, 2019, 3, 544-559. | 0.1 | 40 |
| 50 | 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. | 1.4 | 39 |
| 51 | Accurate and scalable identification of functional sites by evolutionary tracing. Journal of Structural and Functional Genomics, 2003, 4, 159-166. | 1.2 | 38 |
| 52 | Evolutionary Trace Annotation of Protein Function in the Structural Proteome. Journal of Molecular Biology, 2010, 396, 1451-1473. | 2.0 | 38 |
| 53 | Intramolecular allosteric communication in dopamine D2 receptor revealed by evolutionary amino acid covariation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3539-3544. | 3.3 | 38 |
| 54 | Prediction and experimental validation of enzyme substrate specificity in protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4195-202. | 3.3 | 37 |

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| 55 | Specific TP53 Mutants Overrepresented in Ovarian Cancer Impact CNV, TP53 Activity, Responses to Nutlin-3a, and Cell Survival. Neoplasia, 2015, 17, 789-803. | 2.3 | 37 |
| 56 | Predicting phenotype from genotype: Improving accuracy through more robust experimental and computational modeling. Human Mutation, 2017, 38, 569-580. | 1.1 | 36 |
| 57 | Evolutionary Traces of Functional Surfaces along G Protein Signaling Pathway. Methods in Enzymology, 2002, 344, 536-556. | 0.4 | 35 |
| 58 | Evolution: a guide to perturb protein function and networks. Current Opinion in Structural Biology, 2010, 20, 351-359. | 2.6 | 35 |
| 59 | Literature-based automated discovery of tumor suppressor p53 phosphorylation and inhibition by NEK2. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10666-10671. | 3.3 | 33 |
| 60 | Differential Effects of Collagen Prolyl 3-Hydroxylation on Skeletal Tissues. PLoS Genetics, 2014, 10, e1004121. | 1.5 | 31 |
| 61 | UET: a database of evolutionarily-predicted functional determinants of protein sequences that cluster as functional sites in protein structures. Nucleic Acids Research, 2016, 44, D308-D312. | 6.5 | 31 |
| 62 | Exploring use of unsupervised clustering to associate signaling profiles of GPCR ligands to clinical response. Nature Communications, 2019, 10, 4075. | 5.8 | 31 |
| 63 | Recurrent use of evolutionary importance for functional annotation of proteins based on local structural similarity. Protein Science, 2006, 15, 1530-1536. | 3.1 | 30 |
| 64 | Rapid detection of similarity in protein structure and function through contact metric distances. Nucleic Acids Research, 2006, 34, e152-e152. | 6.5 | 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. Cancers, 2019, 11, 1600. | 1.7 | 30 |
| 66 | Evolutionary Trace-based Peptides Identify a Novel Asymmetric Interaction That Mediates Oligomerization in Nuclear Receptors. Journal of Biological Chemistry, 2005, 280, 31818-31829. | 1.6 | 28 |
| 67 | Character and evolution of protein–protein interfaces. Physical Biology, 2005, 2, S36-S43. | 0.8 | 28 |
| 68 | Evolutionary Trace Annotation Server: automated enzyme function prediction in protein structures using 3D templates. Bioinformatics, 2009, 25, 1426-1427. | 1.8 | 28 |
| 69 | The use of evolutionary patterns in protein annotation. Current Opinion in Structural Biology, 2012, 22, 316-325. | 2.6 | 28 |
| 70 | Protein stabilization improves STAT3 function in autosomal dominant hyper-IgE syndrome. Blood, 2016, 128, 3061-3072. | 0.6 | 28 |
| 71 | 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. | 0.5 | 28 |
| 72 | Cdkn2a suppresses metastasis in squamous cell carcinomas induced by the gain-of-function mutant p53 R172H. Journal of Pathology, 2016, 240, 224-234. | 2.1 | 27 |

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| 73 | Objective assessment of the evolutionary action equation for the fitness effect of missense mutations across CAGIâ€blinded contests. Human Mutation, 2017, 38, 1072-1084. | 1.1 | 26 |
| 74 | CAGI5: Objective performance assessments of predictions based on the Evolutionary Action equation. Human Mutation, 2019, 40, 1436-1454. | 1.1 | 26 |
| 75 | Genome interpretation using in silico predictors of variant impact. Human Genetics, 2022, 141, 1549-1577. | 1.8 | 26 |
| 76 | Prediction and redesign of proteinâ€"protein interactions. Progress in Biophysics and Molecular Biology, 2014, 116, 194-202. | 1.4 | 25 |
| 77 | Computational and Biochemical Identification of a Nuclear Pore Complex Binding Site on the Nuclear Transport Carrier NTF2. Journal of Molecular Biology, 2004, 344, 303-310. | 2.0 | 23 |
| 78 | Correlated Evolutionary Pressure at Interacting Transcription Factors and DNA Response Elements Can Guide the Rational Engineering of DNA Binding Specificity. Journal of Molecular Biology, 2005, 350, 402-415. | 2.0 | 23 |
| 79 | Regulation of Ras Localization and Cell Transformation by Evolutionarily Conserved Palmitoyltransferases. Molecular and Cellular Biology, 2014, 34, 374-385. | 1.1 | 23 |
| 80 | Gnathodiaphyseal dysplasia: Severe atypical presentation with novel heterozygous mutation of the anoctamin gene (ANO5). Bone, 2018, 107, 161-171. | 1.4 | 23 |
| 81 | Accounting for epistatic interactions improves the functional analysis of protein structures. Bioinformatics, 2013, 29, 2714-2721. | 1.8 | 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. PLoS ONE, 2008, 3, e2136. | 1.1 | 21 |
| 84 | Negative Feedback in Genetic Circuits Confers Evolutionary Resilience and Capacitance. Cell Reports, 2014, 7, 1789-1795. | 2.9 | 20 |
| 85 | Determinants of Endogenous Ligand Specificity Divergence among Metabotropic Glutamate Receptors. Journal of Biological Chemistry, 2015, 290, 2870-2878. | 1.6 | 20 |
| 86 | Lysine 270 in the Third Intracellular Domain of the Oxytocin Receptor is an Important Determinant for GÎ±qCoupling Specificity. Molecular Endocrinology, 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. Human Mutation, 2019, 40, 1546-1556. | 1.1 | 19 |
| 88 | A method to delineate de novo missense variants across pathways prioritizes genes linked to autism. Science Translational Medicine, 2021, 13, . | 5.8 | 19 |
| 89 | Evolutionary identification of a subtype specific functional site in the ligand binding domain of steroid receptors. Proteins: Structure, Function and Bioinformatics, 2006, 64, 1046-1057. | 1.5 | 18 |
| 90 | Rank information: A structure-independent measure of evolutionary trace quality that improves identification of protein functional sites. Proteins: Structure, Function and Bioinformatics, 2006, 65, 111-123. | 1.5 | 17 |

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| 91 | The Maternal-to-Zygotic Transition Targets Actin to Promote Robustness during Morphogenesis. PLoS Genetics, 2013, 9, e1003901. | 1.5 | 17 |
| 92 | Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131. | 1.1 | 17 |
| 93 | Protein Kinase A and Phosphodiesterase-4D3 Binding to Coding Polymorphisms of Cardiac Muscle Anchoring Protein (mAKAP). Journal of Molecular Biology, 2013, 425, 3277-3288. | 2.0 | 16 |
| 94 | Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399. | 1.1 | 16 |
| 95 | Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506. | 1.1 | 16 |
| 96 | Accurate Protein Structure Annotation through Competitive Diffusion of Enzymatic Functions over a Network of Local Evolutionary Similarities. PLoS ONE, 2010, 5, e14286. | 1.1 | 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. Current Medicinal Chemistry, 2006, 13, 793-805. | 1.2 | 14 |
| 98 | Selectivity and Evolutionary Divergence of Metabotropic Glutamate Receptors for Endogenous Ligands and G Proteins Coupled to Phospholipase C or TRP Channels. Journal of Biological Chemistry, 2014, 289, 29961-29974. | 1.6 | 14 |
| 99 | Multimodal network diffusion predicts future disease–gene–chemical associations. Bioinformatics, 2019, 35, 1536-1543. | 1.8 | 14 |
| 100 | Harnessing the paradoxical phenotypes of APOE É›2 and APOE É›4 to identify genetic modifiers in Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, 831-846. | 0.4 | 14 |
| 101 | Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050. | 1.1 | 13 |
| 102 | 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 |
| 103 | ETAscape: analyzing protein networks to predict enzymatic function and substrates in Cytoscape. Bioinformatics, 2012, 28, 2186-2188. | 1.8 | 12 |
| 104 | Using interpretable deep learning to model cancer dependencies. Bioinformatics, 2021, 37, 2675-2681. | 1.8 | 12 |
| 105 | Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. Annals of Neurology, 2000, 47, 670-679. | 2.8 | 12 |
| 106 | Untangling complex networks: Risk minimization in financial markets through accessible spin glass ground states. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 3250-3253. | 1.2 | 11 |
| 107 | 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. | 1.1 | 11 |
| 108 | Evolutionary action of mutations reveals antimicrobial resistance genes in Escherichia coli. Nature Communications, 2022, 13, . | 5.8 | 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. | 1.5 | 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. | 1.1 | 10 |
| 112 | Assessment of predicted enzymatic activity of $\alpha$-$N$-acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529. | 1.1 | 10 |
| 113 | Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320. | 1.1 | 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. | 1.1 | 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. | 1.2 | 9 |
| 118 | Cooperativity of Negative Autoregulation Confers Increased Mutational Robustness. Physical Review Letters, 2016, 116, 258104. | 2.9 | 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. | 0.4 | 9 |
| 120 | CRISPR-FRT targets shared sites in a knock-out collection for off-the-shelf genome editing. Nature Communications, 2018, 9, 2231. | 5.8 | 8 |
| 121 | Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473. | 1.1 | 8 |
| 122 | Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. Human Mutation, 2019, 40, 1474-1485. | 1.1 | 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. | 1.1 | 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, . | 3.3 | 8 |
| 125 | An Angiotensin II type 1 receptor activation switch patch revealed through Evolutionary Trace analysis. Biochemical Pharmacology, 2010, 80, 86-94. | 2.0 | 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. Nucleic Acids Research, 2022, 50, e70-e70. | 6.5 | 7 |
| 128 | A general calculus of fitness landscapes finds genes under selection in cancers. Genome Research, 2022, , gr.275811.121. | 2.4 | 7 |
| 129 | Potential role of Plasmodium falciparum exported protein 1 in the chloroquine mode of action. International Journal for Parasitology: Drugs and Drug Resistance, 2018, 8, 31-35. | 1.4 | 6 |
| 130 | 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. | 1.9 | 6 |
| 131 | Identification of evolutionarily stable functional and immunogenic sites across the SARS-CoV-2 proteome and greater coronavirus family. Bioinformatics, 2021, 37, 4033-4040. | 1.8 | 6 |
| 132 | Assessing computational predictions of the phenotypic effect of cystathionineâ€beta€synthase variants. Human Mutation, 2019, 40, 1530-1545. | 1.1 | 5 |
| 133 | Evolutionary action score identifies a subset of TP53 mutated myelodysplastic syndrome with favorable prognosis. Blood Cancer Journal, 2021, 11, 52. | 2.8 | 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. PLoS ONE, 2017, 12, e0174766. | 1.1 | 4 |
| 136 | Discovery of disease- and drug-specific pathways through community structures of a literature network. Bioinformatics, 2020, 36, 1881-1888. | 1.8 | 4 |
| 137 | Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2021, 4, 1614-1627. | 2.5 | 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. Methods in Enzymology, 2021, 661, 407-431. | 0.4 | 4 |
| 140 | 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. | 1.6 | 4 |
| 141 | Residues and residue pairs of evolutionary importance differentially direct signaling bias of D2 dopamine receptors. Journal of Biological Chemistry, 2019, 294, 19279-19291. | 1.6 | 3 |
| 142 | Graph-based information diffusion method for prioritizing functionally related genes in protein-protein interaction networks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 439-450. | 0.7 | 3 |
| 143 | An Evolutionary Trace method defines functionally important bases and sites common to RNA families. PLoS Computational Biology, 2020, 16, e1007583. | 1.5 | 2 |
| 144 | PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPARÎ³â€"DNMT1 Interactions in the Genome. Cancers, 2021, 13, 3993. | 1.7 | 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. | 0.4 | 2 |
| 147 | Structural Elements Directing G Proteins and Î²-Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2022, 5, 89-101. | 2.5 | 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. | 0.8 | 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. | 0.6 | 1 |
| 153 | Evolutionary Trace of Protein Functional Determinants. , 2010, , 119-146. | | 0 |
| 154 | Computational Approaches to Studying Molecular Phylogenetics. , 2018, , 173-190. | | 0 |
| 155 | P4â€493: IDENTIFYING GENETIC MODIFIERS OF APOE VIA IMPUTATION OF DEVIATION IN EVOLUTIONARY ACTION LOAD IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2019, 15, P1502. | 0.4 | 0 |
| 156 | Integration of largeâ€scale molecular networks and exomic data can identify Alzheimer's disease genes. Alzheimer's and Dementia, 2020, 16, e041965. | 0.4 | 0 |
| 157 | Identifying genetic modifiers of APOE in Alzheimerâ€™s disease using evolutionary information and regression analyses. Alzheimer's and Dementia, 2020, 16, e043497. | 0.4 | 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. | 0.2 | 0 |
| 160 | Evolutionary Action Score Identifies a Subset of TP53 Mutated Myelodysplastic Syndrome with Favorable Prognosis. Blood, 2020, 136, 4-5. | 0.6 | 0 |