Olivier Lichtarge

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	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
2	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
3	A general calculus of fitness landscapes finds genes under selection in cancers. Genome Research, 2022, , gr.275811.121.	2.4	7
4	Genome interpretation using in silico predictors of variant impact. Human Genetics, 2022, 141, 1549-1577.	1.8	26
5	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
6	Evolutionary action of mutations reveals antimicrobial resistance genes in Escherichia coli. Nature Communications, 2022, 13, .	5.8	11
7	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
8	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
9	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
10	Evolutionary action score identifies a subset of TP53 mutated myelodysplastic syndrome with favorable prognosis. Blood Cancer Journal, 2021, 11, 52.	2.8	5
11	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
12	A method to delineate de novo missense variants across pathways prioritizes genes linked to autism. Science Translational Medicine, 2021, 13, .	5.8	19
13	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
14	Using interpretable deep learning to model cancer dependencies. Bioinformatics, 2021, 37, 2675-2681.	1.8	12
15	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
16	PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPARÎ³â€“DNMT1 Interactions in the Genome. Cancers, 2021, 13, 3993.	1.7	2
17	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
18	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

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19	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
20	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
21	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
22	Discovery of disease- and drug-specific pathways through community structures of a literature network. Bioinformatics, 2020, 36, 1881-1888.	1.8	4
23	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
24	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
25	An Evolutionary Trace method defines functionally important bases and sites common to RNA families. PLoS Computational Biology, 2020, 16, e1007583.	1.5	2
26	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
27	Evolutionary Action Score Identifies a Subset of TP53 Mutated Myelodysplastic Syndrome with Favorable Prognosis. Blood, 2020, 136, 4-5.	0.6	0
28	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	1.1	8
29	CAGI5: Objective performance assessments of predictions based on the Evolutionary Action equation. Human Mutation, 2019, 40, 1436-1454.	1.1	26
30	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
31	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. Human Mutation, 2019, 40, 1546-1556.	1.1	19
32	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
33	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
34	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5.	2.9	382
35	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	1.1	8
36	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

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37	Exploring use of unsupervised clustering to associate signaling profiles of GPCR ligands to clinical response. Nature Communications, 2019, 10, 4075.	5.8	31
38	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
39	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
40	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	1.1	16
41	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	1.1	10
42	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
43	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
44	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
45	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
46	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
47	Multimodal network diffusion predicts future diseaseâ€“geneâ€“chemical associations. Bioinformatics, 2019, 35, 1536-1543.	1.8	14
48	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
49	Graph-based information diffusion method for prioritizing functionally related genes in protein-protein interaction networks. , 2019, , .		4
50	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
51	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
52	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
53	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
54	Gnathodiaphyseal dysplasia: Severe atypical presentation with novel heterozygous mutation of the anoctamin gene (ANO5). Bone, 2018, 107, 161-171.	1.4	23

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55	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
56	Computational Approaches to Studying Molecular Phylogenetics. , 2018, , 173-190.		0
57	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
58	Type 2 diabetesâ€“associated variants of the MT ₂ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, .	1.6	45
59	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
60	CRISPR-FRT targets shared sites in a knock-out collection for off-the-shelf genome editing. Nature Communications, 2018, 9, 2231.	5.8	8
61	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
62	DISCOVERY OF FUNCTIONAL AND DISEASE PATHWAYS BY COMMUNITY DETECTION IN PROTEIN-PROTEIN INTERACTION NETWORKS. , 2017, 22, 336-347.		7
63	Predicting phenotype from genotype: Improving accuracy through more robust experimental and computational modeling. Human Mutation, 2017, 38, 569-580.	1.1	36
64	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	1.1	17
65	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13
66	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
67	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
68	HUMAN KINASES DISPLAY MUTATIONAL HOTSPOTS AT COGNATE POSITIONS WITHIN CANCER. , 2017, 22, 414-425.		1
69	Evolutionary action and structural basis of the allosteric switch controlling Î²2AR functional selectivity. Nature Communications, 2017, 8, 2169.	5.8	61
70	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
71	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
72	Protein stabilization improves STAT3 function in autosomal dominant hyper-IgE syndrome. Blood, 2016, 128, 3061-3072.	0.6	28

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73	Cdkn2asuppresses metastasis in squamous cell carcinomas induced by the gain-of-function mutantp53R172H. Journal of Pathology, 2016, 240, 224-234.	2.1	27
74	Cooperativity of Negative Autoregulation Confers Increased Mutational Robustness. Physical Review Letters, 2016, 116, 258104.	2.9	9
75	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
76	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
77	COMPUTING THERAPY FOR PRECISION MEDICINE: COLLABORATIVE FILTERING INTEGRATES AND PREDICTS MULTI-ENTITY INTERACTIONS. , 2016, , .		1
78	REPURPOSING GERMLINE EXOMES OF THE CANCER GENOME ATLAS DEMANDS A CAUTIOUS APPROACH AND SAMPLE-SPECIFIC VARIANT FILTERING. , 2016, , .		10
79	Network Analytics: Evolutionary Compression, Diffusion and the Action Equation for Mutations. FASEB Journal, 2016, 30, 255.1.	0.2	0
80	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
81	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
82	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
83	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
84	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.	1.9	97
85	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
86	Determinants of Endogenous Ligand Specificity Divergence among Metabotropic Glutamate Receptors. Journal of Biological Chemistry, 2015, 290, 2870-2878.	1.6	20
87	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
88	Predicting Future Scientific Discoveries Based on a Networked Analysis of the Past Literature. , 2015, , .		22
89	Differential Effects of Collagen Prolyl 3-Hydroxylation on Skeletal Tissues. PLoS Genetics, 2014, 10, e1004121.	1.5	31
90	Regulation of Ras Localization and Cell Transformation by Evolutionarily Conserved Palmitoyltransferases. Molecular and Cellular Biology, 2014, 34, 374-385.	1.1	23

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91	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
92	Single nucleotide variations: Biological impact and theoretical interpretation. Protein Science, 2014, 23, 1650-1666.	3.1	94
93	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
94	Automated hypothesis generation based on mining scientific literature. , 2014, , .		82
95	Supergenomic Network Compression and the Discovery of EXP1 as a Glutathione Transferase Inhibited by Artesunate. Cell, 2014, 158, 916-928.	13.5	113
96	Negative Feedback in Genetic Circuits Confers Evolutionary Resilience and Capacitance. Cell Reports, 2014, 7, 1789-1795.	2.9	20
97	Prediction and redesign of proteinâ€“protein interactions. Progress in Biophysics and Molecular Biology, 2014, 116, 194-202.	1.4	25
98	Function prediction from networks of local evolutionary similarity in protein structure. BMC Bioinformatics, 2013, 14, S6.	1.2	9
99	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
100	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
101	Identification of a candidate therapeutic autophagy-inducing peptide. Nature, 2013, 494, 201-206.	13.7	669
102	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
103	Accounting for epistatic interactions improves the functional analysis of protein structures. Bioinformatics, 2013, 29, 2714-2721.	1.8	22
104	The Maternal-to-Zygotic Transition Targets Actin to Promote Robustness during Morphogenesis. PLoS Genetics, 2013, 9, e1003901.	1.5	17
105	ETAscape: analyzing protein networks to predict enzymatic function and substrates in Cytoscape. Bioinformatics, 2012, 28, 2186-2188.	1.8	12
106	Identity and Function of a Large Gene Network Underlying Mutagenic Repair of DNA Breaks. Science, 2012, 338, 1344-1348.	6.0	195
107	The use of evolutionary patterns in protein annotation. Current Opinion in Structural Biology, 2012, 22, 316-325.	2.6	28
108	Evolutionary Trace for Prediction and Redesign of Protein Functional Sites. Methods in Molecular Biology, 2012, 819, 29-42.	0.4	59

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109	Protein function prediction: towards integration of similarity metrics. Current Opinion in Structural Biology, 2011, 21, 180-188.	2.6	42
110	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
111	Molecular defects in human carbamoy phosphate synthetase I: mutational spectrum, diagnostic and protein structure considerations. Human Mutation, 2011, 32, 579-589.	1.1	67
112	Separation of Recombination and SOS Response in Escherichia coli RecA Suggests LexA Interaction Sites. PLoS Genetics, 2011, 7, e1002244.	1.5	71
113	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
114	Evolution: a guide to perturb protein function and networks. Current Opinion in Structural Biology, 2010, 20, 351-359.	2.6	35
115	An Angiotensin II type 1 receptor activation switch patch revealed through Evolutionary Trace analysis. Biochemical Pharmacology, 2010, 80, 86-94.	2.0	7
116	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
117	PyETV: a PyMOL evolutionary trace viewer to analyze functional site predictions in protein complexes. Bioinformatics, 2010, 26, 2981-2982.	1.8	46
118	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
119	Evolutionary Trace of Protein Functional Determinants. , 2010, , 119-146.		0
120	Evolutionary Trace Annotation of Protein Function in the Structural Proteome. Journal of Molecular Biology, 2010, 396, 1451-1473.	2.0	38
121	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
122	Evolutionary Trace Annotation Server: automated enzyme function prediction in protein structures using 3D templates. Bioinformatics, 2009, 25, 1426-1427.	1.8	28
123	Functional Rescue of Î²₁â€Adrenoceptor Dimerization and Trafficking by Pharmacological Chaperones. Traffic, 2009, 10, 1019-1033.	1.3	71
124	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
125	Prediction of enzyme function based on 3D templates of evolutionarily important amino acids. BMC Bioinformatics, 2008, 9, 17.	1.2	70
126	A statistical model to correct systematic bias introduced by algorithmic thresholds in protein structural comparison algorithms. , 2008, , .		9

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127	De-Orphaning the Structural Proteome through Reciprocal Comparison of Evolutionarily Important Structural Features. PLoS ONE, 2008, 3, e2136.	1.1	21
128	Graph sharpening plus graph integration: a synergy that improves protein functional classification. Bioinformatics, 2007, 23, 3217-3224.	1.8	57
129	Distinct faces of the Ku heterodimer mediate DNA repair and telomeric functions. Nature Structural and Molecular Biology, 2007, 14, 301-307.	3.6	88
130	COMPOSITE MOTIFS INTEGRATING MULTIPLE PROTEIN STRUCTURES INCREASE SENSITIVITY FOR FUNCTION PREDICTION. , 2007, , .		5
131	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
132	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
133	Recurrent use of evolutionary importance for functional annotation of proteins based on local structural similarity. Protein Science, 2006, 15, 1530-1536.	3.1	30
134	Rapid detection of similarity in protein structure and function through contact metric distances. Nucleic Acids Research, 2006, 34, e152-e152.	6.5	30
135	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
136	ET viewer: an application for predicting and visualizing functional sites in protein structures. Bioinformatics, 2006, 22, 2049-2050.	1.8	62
137	Î²-Arrestin-dependent, G Protein-independent ERK1/2 Activation by the Î²2 Adrenergic Receptor. Journal of Biological Chemistry, 2006, 281, 1261-1273.	1.6	651
138	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
139	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
140	Character and evolution of proteinâ€“protein interfaces. Physical Biology, 2005, 2, S36-S43.	0.8	28
141	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
142	Evolution of neural precursor selection: functional divergence of proneural proteins. Development (Cambridge), 2004, 131, 1679-1689.	1.2	59
143	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
144	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

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145	AN EVOLUTIONARY PERSPECTIVE ON THE DETERMINANTS OF PROTEIN FUNCTION AND ASSEMBLY. , 2004, , .		0
146	Accurate and scalable identification of functional sites by evolutionary tracing. Journal of Structural and Functional Genomics, 2003, 4, 159-166.	1.2	38
147	An Accurate, Sensitive, and Scalable Method to Identify Functional Sites in Protein Structures. Journal of Molecular Biology, 2003, 326, 255-261.	2.0	174
148	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
149	Evolutionary Traces of Functional Surfaces along G Protein Signaling Pathway. Methods in Enzymology, 2002, 344, 536-556.	0.4	35
150	Structural clusters of evolutionary trace residues are statistically significant and common in proteins. Journal of Molecular Biology, 2002, 316, 139-154.	2.0	190
151	Evolutionary predictions of binding surfaces and interactions. Current Opinion in Structural Biology, 2002, 12, 21-27.	2.6	256
152	Prediction and confirmation of a site critical for effector regulation of RGS domain activity. Nature Structural Biology, 2001, 8, 234-237.	9.7	125
153	Getting past appearances: the many-fold consequences of remote homology. , 2001, 8, 918-920.		10
154	Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. Annals of Neurology, 2000, 47, 670-679.	2.8	314
155	Genetic Mapping of the Human C5a Receptor. Journal of Biological Chemistry, 2000, 275, 35393-35401.	1.6	55
156	Influence of mutation type and X chromosome inactivation on Rett syndrome phenotypes. Annals of Neurology, 2000, 47, 670-679.	2.8	12
157	C5a Receptor Activation. Journal of Biological Chemistry, 1999, 274, 15757-15765.	1.6	120
158	Identification of functional surfaces of the zinc binding domains of intracellular receptors. Journal of Molecular Biology, 1997, 274, 325-337.	2.0	107
159	An Evolutionary Trace Method Defines Binding Surfaces Common to Protein Families. Journal of Molecular Biology, 1996, 257, 342-358.	2.0	1,169
160	Rhodopsin activation blocked by metal-ion-binding sites linking transmembrane helices C and F. Nature, 1996, 383, 347-350.	13.7	429