Eyal Akiva

List of Publications by Year
in descending order

21 papers	**1,685** citations	687363 **13** h-index	713466 **21** g-index
23 all docs	**23** docs citations	**23** times ranked	**3247** citing authors

#	Article	IF	Citations
1	Global landscape of HIV–human protein complexes. Nature, 2012, 481, 365-370.	27.8	651
2	The Structure–Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	14.5	210
3	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9549-E9558.	7.1	111
4	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. Methods in Enzymology, 2018, 606, 1-71.	1.0	99
5	Evolutionary conservation of domain-domain interactions. Genome Biology, 2006, 7, R125.	9.6	96
6	Built-in loops allow versatility in domain–domain interactions: Lessons from self-interacting domains. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13292-13297.	7.1	86
7	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. ELife, 2014, 3, .	6.0	81
8	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. PLoS Biology, 2014, 12, e1001843.	5.6	79
9	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. Biochemistry, 2018, 57, 4651-4662.	2.5	58
10	Parallel molecular mechanisms for enzyme temperature adaptation. Science, 2021, 371, .	12.6	48
11	A Dynamic View of Domain-Motif Interactions. PLoS Computational Biology, 2012, 8, e1002341.	3.2	48
12	A global view of structure–function relationships in the tautomerase superfamily. Journal of Biological Chemistry, 2018, 293, 2342-2357.	3.4	39
13	Prediction of Mutational Tolerance in HIV-1 Protease and Reverse Transcriptase Using Flexible Backbone Protein Design. PLoS Computational Biology, 2012, 8, e1002639.	3.2	21
14	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 111-132.	0.9	14
15	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. Methods in Enzymology, 2019, 620, 315-347.	1.0	13
16	Preferential use of protein domain pairs as interaction mediators: order and transitivity. Bioinformatics, 2010, 26, 2564-2570.	4.1	11
17	Biocuration in the structure–function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
18	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. Biochemistry, 2019, 58, 2617-2627.	2.5	6

#	Article	IF	Citations
19	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. Molecular Biology and Evolution, 2021, 38, 545-556.	8.9	5
20	Biocuration in the structure–function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	2
21	Evolutionary Reprograming of Protein-Protein Interaction Specificity. Cell, 2015, 163, 535-537.	28.9	1