## Amir Aharoni

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8474653/publications.pdf

Version: 2024-02-01

66 papers

4,351 citations

236925 25 h-index 110387 64 g-index

74 all docs

74 docs citations

74 times ranked 5914 citing authors

#	Article	IF	CITATIONS
1	The 'evolvability' of promiscuous protein functions. Nature Genetics, 2005, 37, 73-76.	21.4	742
2	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. Nature Structural and Molecular Biology, 2004, 11, 412-419.	8.2	569
3	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. Molecular Cell, 2016, 63, 337-346.	9.7	363
4	Directed evolution of mammalian paraoxonases PON1 and PON3 for bacterial expression and catalytic specialization. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 482-487.	7.1	275
5	High-throughput screening methodology for the directed evolution of glycosyltransferases. Nature Methods, 2006, 3, 609-614.	19.0	211
6	High-Throughput Screening of Enzyme Libraries: Thiolactonases Evolved by Fluorescence-Activated Sorting of Single Cells in Emulsion Compartments. Chemistry and Biology, 2005, 12, 1281-1289.	6.0	197
7	High-throughput screens and selections of enzyme-encoding genes. Current Opinion in Chemical Biology, 2005, 9, 210-216.	6.1	187
8	Proliferating Cell Nuclear Antigen Is a Novel Inhibitory Ligand for the Natural Cytotoxicity Receptor NKp44. Journal of Immunology, 2011, 187, 5693-5702.	0.8	176
9	Covalent Inhibition of Bacterial Quorum Sensing. Journal of the American Chemical Society, 2009, 131, 10610-10619.	13.7	172
10	Fusion Peptides Derived from the HIV Type 1 Glycoprotein 41 Associate within Phospholipid Membranes and Inhibit Cell-Cell Fusion. Journal of Biological Chemistry, 1997, 272, 13496-13505.	3.4	152
11	Directed evolution of proteins for heterologous expression and stability. Current Opinion in Structural Biology, 2005, 15, 50-56.	5.7	122
12	Surface Display of Redox Enzymes in Microbial Fuel Cells. Journal of the American Chemical Society, 2009, 131, 12052-12053.	13.7	100
13	Fine-tuning of the Msn2/4–mediated yeast stress responses as revealed by systematic deletion of Msn2/4 partners. Molecular Biology of the Cell, 2011, 22, 3127-3138.	2.1	75
14	Pif1 is essential for efficient replisome progression through lagging strand G-quadruplex DNA secondary structures. Nucleic Acids Research, 2018, 46, 11847-11857.	14.5	75
15	Targeting Deubiquitinases Enabled by Chemical Synthesis of Proteins. Journal of the American Chemical Society, 2012, 134, 3281-3289.	13.7	67
16	Coevolution Predicts Direct Interactions between mtDNA-Encoded and nDNA-Encoded Subunits of Oxidative Phosphorylation Complex I. Journal of Molecular Biology, 2010, 404, 158-171.	4.2	66
17	The Molecular Basis for the Broad Substrate Specificity of Human Sulfotransferase 1A1. PLoS ONE, 2011, 6, e26794.	2,5	54
18	Inter-ring Communication is Disrupted in the GroEL Mutant Arg13 â†' Gly; Ala126 â†' Val with Known Crystal Structure. Journal of Molecular Biology, 1996, 258, 732-735.	4.2	48

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19	Conditionâ€specific genetic interaction maps reveal crosstalk between the <scp>cAMP</scp> / <scp>PKA</scp> and the <scp>HOG MAPK</scp> pathways in the activation of the general stress response. Molecular Systems Biology, 2015, 11, 829.	7.2	46
20	Sequential switching of binding partners on PCNA during in vitro Okazaki fragment maturation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14118-14123.	7.1	45
21	Subtle Alterations in PCNA-Partner Interactions Severely Impair DNA Replication and Repair. PLoS Biology, 2010, 8, e1000507.	5 <b>.</b> 6	39
22	Tight coevolution of proliferating cell nuclear antigen (PCNA)-partner interaction networks in fungi leads to interspecies network incompatibility. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E406-14.	7.1	37
23	Interplay of metagenomics and <i>in vitro</i> compartmentalization. Microbial Biotechnology, 2009, 2, 31-39.	4.2	29
24	A Live-Cell Imaging Approach for Measuring DNA Replication Rates. Cell Reports, 2018, 24, 252-258.	6.4	28
25	Bacteriorhodpsin Experiences Light-induced Conformational Alterations in Nonisomerizable C13=C14Pigments. Journal of Biological Chemistry, 2000, 275, 21010-21016.	3.4	27
26	Harnessing the Oxidation Susceptibility of Deubiquitinases for Inhibition with Small Molecules. Angewandte Chemie - International Edition, 2015, 54, 599-603.	13.8	27
27	The Transition of Human Estrogen Sulfotransferase from Generalist to Specialist Using Directed Enzyme Evolution. Journal of Molecular Biology, 2012, 416, 21-32.	4.2	23
28	Conserved Motifs in the Msn2-Activating Domain are Important for Msn2-Mediated Yeast Stress Response. Journal of Cell Science, 2012, 125, 3333-42.	2.0	22
29	A continuous kinetic assay for protein and DNA methyltransferase enzymatic activities. Epigenetics and Chromatin, 2015, 8, 56.	3.9	21
30	Marker-free genetic manipulations in yeast using CRISPR/CAS9 system. Current Genetics, 2018, 64, 1129-1139.	1.7	21
31	Proteinâ $^{}$ Î <sup>2</sup> -Ionone Ring Interactions Enhance the Light-Induced Dipole of the Chromophore in Bacteriorhodopsin. Journal of Physical Chemistry B, 2003, 107, 6221-6225.	2.6	20
32	Directed Evolution of a Soluble Human IL-17A Receptor for the Inhibition of Psoriasis Plaque Formation in a Mouse Model. Chemistry and Biology, 2013, 20, 202-211.	6.0	17
33	Novel Hybrid Esteraseâ€Haloacid Dehalogenase Enzyme. ChemBioChem, 2010, 11, 1975-1978.	2.6	16
34	Protein co-evolution: how do we combine bioinformatics and experimental approaches?. Molecular BioSystems, 2013, 9, 175-181.	2.9	16
35	CNN Based Yeast Cell Segmentation in Multi-modal Fluorescent Microscopy Data. , 2017, , .		16
36	Evolution in Microfluidic Droplet. Chemistry and Biology, 2012, 19, 929-931.	6.0	13

3

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37	The functional importance of co-evolving residues in proteins. Cellular and Molecular Life Sciences, 2014, 71, 673-682.	5.4	12
38	The evolution of a G1/S transcriptional network in yeasts. Current Genetics, 2018, 64, 81-86.	1.7	12
39	Transcription-replication coordination revealed in single live cells. Nucleic Acids Research, 2022, 50, 2143-2156.	14.5	12
40	Mining for new enzymes. Microbial Biotechnology, 2009, 2, 128-129.	4.2	11
41	Gene duplication and co-evolution of G1/S transcription factor specificity in fungi are essential for optimizing cell fitness. PLoS Genetics, 2017, 13, e1006778.	3.5	11
42	Directed evolution of SIRT6 for improved deacylation and glucose homeostasis maintenance. Scientific Reports, 2018, 8, 3538.	3.3	11
43	Point Mutation of a Non-Elastase-Binding Site in Human $\hat{l}\pm 1$ -Antitrypsin Alters Its Anti-Inflammatory Properties. Frontiers in Immunology, 2018, 9, 759.	4.8	11
44	Experimental analysis of co-evolution within protein complexes: The yeast exosome as a model. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1997-2006.	2.6	10
45	Light-Induced Hydrolysis and Rebinding of Nonisomerizable Bacteriorhodopsin Pigment. Biophysical Journal, 2002, 82, 2617-2626.	0.5	9
46	Computational protein design suggests that human PCNAâ€partner interactions are not optimized for affinity. Proteins: Structure, Function and Bioinformatics, 2013, 81, 341-348.	2.6	9
47	Increased Potency of a Bi-specific TL1A-ADAM17 (TACE) Inhibitor by Cell Surface Targeting. Frontiers in Molecular Biosciences, 2017, 4, 61.	3.5	8
48	Proteasome accessory factor A (PafA) transferase activity makes sense in the light of its homology with glutamine synthetase. Journal of Molecular Biology, 2018, 430, 668-681.	4.2	8
49	Employing directed evolution for the functional analysis of multi-specific proteins. Bioorganic and Medicinal Chemistry, 2013, 21, 3511-3516.	3.0	7
50	Dissecting the Roles of the N―and Câ€Flanking Residues of Acetyllysine Substrates for SIRT1 Activity. ChemBioChem, 2013, 14, 577-581.	2.6	7
51	Directed evolution of a soluble human DR3 receptor for the inhibition of TL1A induced cytokine secretion. PLoS ONE, 2017, 12, e0173460.	2.5	7
52	Cac1 WHD and PIP domains have distinct roles in replisome progression and genomic stability. Current Genetics, 2021, 67, 129-139.	1.7	7
53	Enhanced PKMT-substrate recognition through non active-site interactions. Biochemical and Biophysical Research Communications, 2018, 501, 1029-1033.	2.1	6
54	Photoreduction of Bacteriorhodopsin Schiff Base at Low Humidity. A Study with C13=C14 Nonisomerizable Artificial Pigments¶. Photochemistry and Photobiology, 2002, 75, 668.	2.5	6

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55	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. Molecular Biology and Evolution, 2021, 38, 545-556.	8.9	5
56	Directed evolution of recombinant serum paraoxonase (PON) variants. Discovery Medicine, 2004, 4, 120-4.	0.5	5
57	A bi-specific inhibitor targeting IL-17A and MMP-9 reduces invasion and motility in MDA-MB-231 cells. Oncotarget, 2018, 9, 28500-28513.	1.8	4
58	Engineering of Methylation State Specific 3xMBT Domain Using ELISA Screening. PLoS ONE, 2016, 11, e0154207.	2.5	3
59	Evolved to overcome Bt-toxin resistance. Nature, 2016, 533, 39-40.	27.8	2
60	A Bacterial Quorum Sensing Molecule Elicits a General Stress Response in Saccharomyces cerevisiae. Frontiers in Microbiology, 2021, 12, 632658.	3.5	2
61	Application of directed evolution and back-to-consensus algorithms to human alpha1-antitrypsin leads to diminished anti-protease activity and augmented anti-inflammatory activities. Cellular Immunology, 2020, 355, 104135.	3.0	2
62	Editorial overview: Engineering, evolving, andÂdesigning proteins. Current Opinion in Structural Biology, 2021, 69, iii-v.	5.7	1
63	Serum paraoxonase PON1 and its interactions with HDL. FASEB Journal, 2008, 22, 811.1.	0.5	1
64	High-throughput Screens and Selections of Enzyme-encoding Genes. , 2006, , 163-181.		0
65	Photoreduction of Bacteriorhodopsin Schiff Base at Low Humidity. A Study with C13=C14 Nonisomerizable Artificial Pigments¶. Photochemistry and Photobiology, 2007, 75, 668-674.	2.5	0
66	A KLK4 proteinase substrate capture approach to antagonize PAR1. Scientific Reports, 2021, 11, 16170.	3.3	0