

Julian D Langer

List of Publications by Year in descending order

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61
papers

3,118
citations

218381

26
h-index

174990

52
g-index

70
all docs

70
docs citations

70
times ranked

3991
citing authors

#	ARTICLE	IF	CITATIONS
1	The Structure of <i>cbb₃</i> Cytochrome Oxidase Provides Insights into Proton Pumping. Science, 2010, 329, 327-330.	6.0	244
2	Structure of the mycobacterial ATP synthase F _o rotor ring in complex with the anti-TB drug bedaquiline. Science Advances, 2015, 1, e1500106.	4.7	224
3	Local and global influences on protein turnover in neurons and glia. ELife, 2018, 7, .	2.8	168
4	Monosomes actively translate synaptic mRNAs in neuronal processes. Science, 2020, 367, .	6.0	166
5	Cell-type-specific metabolic labeling of nascent proteomes in vivo. Nature Biotechnology, 2017, 35, 1196-1201.	9.4	153
6	Structure of a bd oxidase indicates similar mechanisms for membrane-integrated oxygen reductases. Science, 2016, 352, 583-586.	6.0	143
7	Microscopic rotary mechanism of ion translocation in the F _o complex of ATP synthases. Nature Chemical Biology, 2010, 6, 891-899.	3.9	142
8	Cryo-EM Structure of the TOM Core Complex from Neurospora crassa. Cell, 2017, 170, 693-700.e7.	13.5	138
9	Nascent Proteome Remodeling following Homeostatic Scaling at Hippocampal Synapses. Neuron, 2016, 92, 358-371.	3.8	125
10	Structural insights into photosystem II assembly. Nature Plants, 2021, 7, 524-538.	4.7	102
11	Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. Science, 2019, 366, 100-104.	6.0	90
12	Engineering rotor ring stoichiometries in the ATP synthase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1599-608.	3.3	89
13	Heterotrimeric NADH-Oxidizing Methylenetetrahydrofolate Reductase from the Acetogenic Bacterium Acetobacterium woodii. Journal of Bacteriology, 2015, 197, 1681-1689.	1.0	83
14	Proteome dynamics during homeostatic scaling in cultured neurons. ELife, 2020, 9, .	2.8	79
15	Elucidating the control and development of skin patterning in cuttlefish. Nature, 2018, 562, 361-366.	13.7	72
16	Identification of potential mitochondrial CLPXP protease interactors and substrates suggests its central role in energy metabolism. Scientific Reports, 2015, 5, 18375.	1.6	68
17	Proteome Turnover in the Spotlight: Approaches, Applications, and Perspectives. Molecular and Cellular Proteomics, 2021, 20, 100016.	2.5	64
18	Neuronal ribosomes exhibit dynamic and context-dependent exchange of ribosomal proteins. Nature Communications, 2021, 12, 6127.	5.8	63

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19	Structural and energetic basis for H ⁺ versus Na ⁺ binding selectivity in ATP synthase Fo rotors. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 763-772.	0.5	58
20	Several ADP-ribosylation Factor (Arf) Isoforms Support COPI Vesicle Formation. <i>Journal of Biological Chemistry</i> , 2011, 286, 35634-35642.	1.6	53
21	Cell-type-specific metabolic labeling, detection and identification of nascent proteomes in vivo. <i>Nature Protocols</i> , 2019, 14, 556-575.	5.5	50
22	Time- and polarity-dependent proteomic changes associated with homeostatic scaling at central synapses. <i>ELife</i> , 2018, 7, .	2.8	49
23	Full-length transcriptome reconstruction reveals a large diversity of RNA and protein isoforms in rat hippocampus. <i>Nature Communications</i> , 2019, 10, 5009.	5.8	43
24	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018, 9, 1728.	5.8	38
25	Inhibition of Histone Deacetylases Permits Lipopolysaccharide-Mediated Secretion of Bioactive IL-1 β via a Caspase-1-Independent Mechanism. <i>Journal of Immunology</i> , 2015, 195, 5421-5431.	0.4	36
26	Ligand-induced conformational dynamics of the <i>Escherichia coli</i> Na ⁺ /H ⁺ antiporter NhaA revealed by hydrogen/deuterium exchange mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11691-11696.	3.3	36
27	Cryo-electron microscopy reveals two distinct type IV pili assembled by the same bacterium. <i>Nature Communications</i> , 2020, 11, 2231.	5.8	35
28	A Practical Guide to Small Protein Discovery and Characterization Using Mass Spectrometry. <i>Journal of Bacteriology</i> , 2022, 204, JB0035321.	1.0	30
29	The cation ion binding site of the ATP synthase from <i>Bacillus pseudofirmus</i> OF4 is adapted to alkaliphilic lifestyle. <i>Molecular Microbiology</i> , 2014, 92, 973-984.	1.2	27
30	A Conformational Change in the β -subunit of Coatamer Induced by Ligand Binding to β -COP Revealed by Single-pair FRET. <i>Traffic</i> , 2008, 9, 597-607.	1.3	26
31	Cysteine oxidation and disulfide formation in the ribosomal exit tunnel. <i>Nature Communications</i> , 2020, 11, 5569.	5.8	26
32	MEIS homeodomain proteins facilitate PARP1/ARTD1-mediated eviction of histone H1. <i>Journal of Cell Biology</i> , 2017, 216, 2715-2729.	2.3	25
33	Co-translational assembly orchestrates competing biogenesis pathways. <i>Nature Communications</i> , 2022, 13, 1224.	5.8	25
34	Characterizing a monotopic membrane enzyme. Biochemical, enzymatic and crystallization studies on <i>Aquifex aeolicus</i> sulfide:quinone oxidoreductase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010, 1798, 2114-2123.	1.4	24
35	The Xenobiotic Extrusion Mechanism of the MATE Transporter NorM_PS from <i>Pseudomonas stutzeri</i> . <i>Journal of Molecular Biology</i> , 2018, 430, 1311-1323.	2.0	24
36	Unusual N-terminal β -Fold of PilQ from <i>Thermus thermophilus</i> Mediates Ring Formation and Is Essential for Piliation. <i>Journal of Biological Chemistry</i> , 2012, 287, 8484-8494.	1.6	23

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37	A c Subunit with Four Transmembrane Helices and One Ion (Na ⁺)-binding Site in an Archaeal ATP Synthase. <i>Journal of Biological Chemistry</i> , 2012, 287, 39327-39337.	1.6	22
38	Dynamic bi-directional phosphorylation events associated with the reciprocal regulation of synapses during homeostatic up- and down-scaling. <i>Cell Reports</i> , 2021, 36, 109583.	2.9	21
39	An amiloride derivative is active against the F ₁ F ₀ -ATP synthase and cytochrome bd oxidase of <i>Mycobacterium tuberculosis</i> . <i>Communications Biology</i> , 2022, 5, 166.	2.0	21
40	Biochemical and Biophysical Characterization of the Two Isoforms of cbb3-Type Cytochrome c Oxidase from <i>Pseudomonas stutzeri</i> . <i>Journal of Bacteriology</i> , 2014, 196, 472-482.	1.0	20
41	Conformational changes of coat proteins during vesicle formation. <i>FEBS Letters</i> , 2007, 581, 2083-2088.	1.3	18
42	Identification and Characterization of the Novel Subunit CcoM in the cbb ₃ -Cytochrome c Oxidase from <i>Pseudomonas stutzeri</i> ZoBell. <i>MBio</i> , 2016, 7, e01921-15.	1.8	18
43	Na ⁺ Transport by the A1AO-ATP Synthase Purified from <i>Thermococcus onnurineus</i> and Reconstituted into Liposomes. <i>Journal of Biological Chemistry</i> , 2015, 290, 6994-7002.	1.6	16
44	Ligand binding and conformational dynamics in a flavin-based electron-bifurcating enzyme complex revealed by Hydrogen-Deuterium Exchange Mass Spectrometry. <i>FEBS Letters</i> , 2016, 590, 4472-4479.	1.3	16
45	Tumorigenic and Antiproliferative Properties of the TALE-Transcription Factors MEIS2D and MEIS2A in Neuroblastoma. <i>Cancer Research</i> , 2018, 78, 1935-1947.	0.4	11
46	Subunit CcoQ is involved in the assembly of the Cbb ₃ -type cytochrome c oxidases from <i>Pseudomonas stutzeri</i> ZoBell but not required for their activity. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 231-238.	0.5	10
47	Proteomic Characterization of the <i>Pseudomonas</i> sp. Strain phDV1 Response to Monocyclic Aromatic Compounds. <i>Proteomics</i> , 2021, 21, e2000003.	1.3	10
48	Molybdate pumping into the molybdenum storage protein via an ATP-powered piercing mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26497-26504.	3.3	8
49	Genetic analysis of MA4079, an aldehyde dehydrogenase homolog, in <i>Methanosarcina acetivorans</i> . <i>Archives of Microbiology</i> , 2012, 194, 75-85.	1.0	7
50	The membrane complexome of a new <i>Pseudomonas</i> strain during growth on lysogeny broth medium and medium containing glucose or phenol. <i>EuPA Open Proteomics</i> , 2014, 4, 1-9.	2.5	7
51	Top-Down Identification and Sequence Analysis of Small Membrane Proteins Using MALDI-MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 1293-1302.	1.2	7
52	Three multihaem cytochromes c from the hyperthermophilic archaeon <i>Ignicoccus hospitalis</i> : purification, properties and localization. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1278-1289.	0.7	6
53	Stoichiometry and deletion analyses of subunits in the heterotrimeric F ₁ ATP synthase c ring from the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>FEBS Journal</i> , 2016, 283, 510-520.	2.2	6
54	Proteome Analysis of Enriched Heterocysts from Two Hydrogenase Mutants from <i>Anabaena</i> sp. PCC 7120. <i>Proteomics</i> , 2019, 19, e1800332.	1.3	6

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55	Cell-free synthesis of isotopically labelled peptide ligands for the functional characterization of G protein-coupled receptors. <i>FEBS Open Bio</i> , 2016, 6, 90-102.	1.0	5
56	Larval Zebrafish Proteome Regulation in Response to an Environmental Challenge. <i>Proteomics</i> , 2019, 19, 1900028.	1.3	5
57	Role of the N-terminal signal peptide in the membrane insertion of <i>Aquifex aeolicus</i> F ₁ F ₀ ATP synthase c-subunit. <i>FEBS Journal</i> , 2013, 280, 3425-3435.	2.2	4
58	Site-Specific Detection of Arginine Methylation in Highly Repetitive Protein Motifs of Low Sequence Complexity by NMR. <i>Journal of the American Chemical Society</i> , 2020, 142, 7647-7654.	6.6	4
59	Production of fully assembled and active <i>Aquifex aeolicus</i> F ₁ F ₀ ATP synthase in <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 34-40.	1.1	1
60	Isolation, functional characterization and crystallization of Aq_1259, an outer membrane protein with porin features, from <i>Aquifex aeolicus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1358-1365.	1.1	0
61	Quantifying phosphorylation dynamics in primary neuronal cultures using LC-MS/MS. <i>STAR Protocols</i> , 2022, 3, 101063.	0.5	0