Anastassios Economou

List of Publications by Year in descending order

116 papers	6,264 citations	66234 42 h-index	76769 74 g-index
125 all docs	125 docs citations	125 times ranked	4539 citing authors

#	Article	IF	Citations
1	Bcl-xL acts as an inhibitor of IP3R channels, thereby antagonizing Ca2+-driven apoptosis. Cell Death and Differentiation, 2022, 29, 788-805.	5.0	41
2	Preproteins couple the intrinsic dynamics of SecA to its ATPase cycle to translocate via a catch and release mechanism. Cell Reports, 2022, 38, 110346.	2.9	5
3	Effective Small Molecule Antibacterials from a Novel Anti-Protein Secretion Screen. Microorganisms, 2021, 9, 592.	1.6	1
4	Sequence of proteome profiles in preclinical and symptomatic Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, 946-958.	0.4	16
5	Extensive Reannotation of the Genome of the Model Streptomycete Streptomyces lividans TK24 Based on Transcriptome and Proteome Information. Frontiers in Microbiology, 2021, 12, 604034.	1.5	5
6	Dynamics ante portas. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2110553118.	3.3	2
7	Chondrocyte protein co-synthesis network analysis links ECM mechanosensing to metabolic adaptation in osteoarthritis. Expert Review of Proteomics, 2021, 18, 623-635.	1.3	1
8	A nexus of intrinsic dynamics underlies translocase priming. Structure, 2021, 29, 846-858.e7.	1.6	17
9	Probing Universal Protein Dynamics Using Hydrogenâ€“Deuterium Exchange Mass Spectrometry-Derived Residue-Level Gibbs Free Energy. Analytical Chemistry, 2021, 93, 12840-12847.	3.2	16
10	Structural Dynamics of the Functional Nonameric Type III Translocase Export Gate. Journal of Molecular Biology, 2021, 433, 167188.	2.0	7
11	Structural dynamics in the evolution of a bilobed protein scaffold. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
12	Moderated Test Statistics to Detect Differential Deuteration in Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Analytical Chemistry, 2021, , .	3.2	2
13	Structural Insights into the Binding of Natural Pyrimidine-Based Inhibitors of Class II Aminoacyl-tRNA Synthetases. ACS Chemical Biology, 2020, 15, 407-415.	1.6	12
14	Trigger factor is a bona fide secretory pathway chaperone that interacts with SecB and the translocase. EMBO Reports, 2020, 21, e49054.	2.0	30
15	A Reporter System for Fast Quantitative Monitoring of Type 3 Protein Secretion in Enteropathogenic E. coli. Microorganisms, 2020, 8, 1786.	1.6	3
16	BDA-366, a putative Bcl-2 BH4 domain antagonist, induces apoptosis independently of Bcl-2 in a variety of cancer cell models. Cell Death and Disease, 2020, 11, 769.	2.7	15
17	The structural basis for an onâ€“off switch controlling Gî²î³-mediated inhibition of TRPM3 channels. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29090-29100.	3.3	17
18	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. Frontiers in Microbiology, 2019, 10, 1670.	1.5	25

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19	Inner Membrane Translocases and Insertases. Sub-Cellular Biochemistry, 2019, 92, 337-366.	1.0	14
20	Protein Transport Across the Bacterial Plasma Membrane by the Sec Pathway. Protein Journal, 2019, 38, 262-273.	0.7	30
21	The Preprotein Binding Domain of SecA Displays Intrinsic Rotational Dynamics. Structure, 2019, 27, 90-101.e6.	1.6	12
22	Secretome Dynamics in a Gram-Positive Bacterial Model. Molecular and Cellular Proteomics, 2019, 18, 423-436.	2.5	12
23	A double point mutation at residues Ile14 and Val15 of Bclâ€2 uncovers a role for the BH4 domain in both protein stability and function. FEBS Journal, 2018, 285, 127-145.	2.2	16
24	Structures of chaperone-substrate complexes docked onto the export gate in a type III secretion system. Nature Communications, 2018, 9, 1773.	5.8	72
25	Long-Lived Folding Intermediates Predominate the Targeting-Competent Secretome. Structure, 2018, 26, 695-707.e5.	1.6	44
26	Crossâ€linked peptide identification: A computational forest of algorithms. Mass Spectrometry Reviews, 2018, 37, 738-749.	2.8	27
27	Monitoring Protein Secretion in Streptomyces Using Fluorescent Proteins. Frontiers in Microbiology, 2018, 9, 3019.	1.5	11
28	Characterization of Sigma Factor Genes in Streptomyces lividans TK24 Using a Genomic Library-Based Approach for Multiple Gene Deletions. Frontiers in Microbiology, 2018, 9, 3033.	1.5	23
29	Transcriptomic and fluxomic changes in Streptomyces lividans producing heterologous protein. Microbial Cell Factories, 2018, 17, 198.	1.9	18
30	Streptomyces protein secretion and its application in biotechnology. FEMS Microbiology Letters, 2018, 365, .	0.7	22
31	Breaching the wall. Nature Microbiology, 2018, 3, 1192-1193.	5.9	0
32	Editorial: Thematic issue on bacterial protein export: from fundamentals to applications. FEMS Microbiology Letters, 2018, 365, .	0.7	0
33	Optimization of type 3 protein secretion in enteropathogenic Escherichia coli. FEMS Microbiology Letters, 2018, 365, .	0.7	5
34	Multi-Omics and Targeted Approaches to Determine the Role of Cellular Proteases in Streptomyces Protein Secretion. Frontiers in Microbiology, 2018, 9, 1174.	1.5	29
35	Comprehensive subcellular topologies of polypeptides in Streptomyces. Microbial Cell Factories, 2018, 17, 43.	1.9	19
36	Preprotein mature domains contain translocase targeting signals that are essential for secretion. Journal of Cell Biology, 2017, 216, 1357-1369.	2.3	67

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37	Fast and reliable strain characterization of Streptomyces lividans through microâ€scale cultivation. Biotechnology and Bioengineering, 2017, 114, 2011-2022.	1.7	37
38	Preprotein Conformational Dynamics Drive Bivalent Translocase Docking and Secretion. Structure, 2017, 25, 1056-1067.e6.	1.6	28
39	Analysis of Translocation-Competent Secretory Proteins by HDX-MS. Methods in Enzymology, 2017, 586, 57-83.	0.4	17
40	Hierarchical protein targeting and secretion is controlled by an affinity switch in the type <scp>III</scp> secretion system of enteropathogenic Escherichia coli. EMBO Journal, 2017, 36, 3517-3531.	3.5	54
41	MatureP: prediction of secreted proteins with exclusive information from their mature regions. Scientific Reports, 2017, 7, 3263.	1.6	33
42	Dynamics and ligand-induced conformational changes in human prolyl oligopeptidase analyzed by hydrogen/deuterium exchange mass spectrometry. Scientific Reports, 2017, 7, 2456.	1.6	20
43	Protein export through the bacterial Sec pathway. Nature Reviews Microbiology, 2017, 15, 21-36.	13.6	332
44	Quantitative Proteomics of the E. coli Membranome. Methods in Enzymology, 2017, 586, 15-36.	0.4	24
45	Large-scale production of a thermostable Rhodothermus marinus cellulase by heterologous secretion from Streptomyces lividans. Microbial Cell Factories, 2017, 16, 232.	1.9	40
46	Rapid labelâ€free quantitative analysis of the E. coli BL21(DE3) inner membrane proteome. Proteomics, 2016, 16, 85-97.	1.3	24
47	The E.coli Sec Pathway under a Single-Molecule Loupe. Biophysical Journal, 2016, 110, 45a-46a.	0.2	0
48	Proteome Changes during Transition from Human Embryonic to Vascular Progenitor Cells. Journal of Proteome Research, 2016, 15, 1995-2007.	1.8	10
49	A polysulfobetaine hydrogel for immobilization of a glucose-binding protein. RSC Advances, 2016, 6, 83890-83900.	1.7	11
50	Recognition and targeting mechanisms by chaperones in flagellum assembly and operation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9798-9803.	3.3	25
51	Protein Secretion in Gram-Positive Bacteria: From Multiple Pathways to Biotechnology. Current Topics in Microbiology and Immunology, 2016, 404, 267-308.	0.7	53
52	Xilmass: A New Approach toward the Identification of Cross-Linked Peptides. Analytical Chemistry, 2016, 88, 9949-9957.	3.2	25
53	Protein folding in the cell envelope of Escherichia coli. Nature Microbiology, 2016, 1, 16107.	5.9	75
54	Type III Secretion: Building and Operating a Remarkable Nanomachine. Trends in Biochemical Sciences, 2016, 41, 175-189.	3.7	146

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55	Comparative proteomic analysis of hypertrophic chondrocytes in osteoarthritis. Clinical Proteomics, 2015, 12, 12.	1.1	49
56	Identification of small-molecule inhibitors against SecA by structure-based virtual ligand screening. Journal of Antibiotics, 2015, 68, 666-673.	1.0	14
57	Complete genome sequence of Streptomyces lividans TK24. Journal of Biotechnology, 2015, 199, 21-22.	1.9	96
58	Proteome-wide Subcellular Topologies of E. coli Polypeptides Database (STEPdb). Molecular and Cellular Proteomics, 2014, 13, 3674-3687.	2.5	67
59	Antibiotic targeting of the bacterial secretory pathway. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1762-1783.	1.9	44
60	Structural Basis for Protein Antiaggregation Activity of the Trigger Factor Chaperone. Science, 2014, 344, 1250494.	6.0	254
61	Preface to special issue on protein trafficking and secretion in bacteria. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1427.	1.9	4
62	SecA-mediated targeting and translocation of secretory proteins. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1466-1474.	1.9	76
63	Substrate-Activated Conformational Switch on Chaperones Encodes a Targeting Signal in Type III Secretion. Cell Reports, 2013, 3, 709-715.	2.9	39
64	Quaternary Dynamics of the SecA Motor Drive Translocase Catalysis. Molecular Cell, 2013, 52, 655-666.	4.5	51
65	Breaking on through to the other side: protein export through the bacterial Sec system. Biochemical Journal, 2013, 449, 25-37.	1.7	64
66	The Escherichia coli Peripheral Inner Membrane Proteome. Molecular and Cellular Proteomics, 2013, 12, 599-610.	2.5	79
67	Quantitative analysis of energy transfer between fluorescent proteins in CFPâ€“GBPâ€“YFP and its response to Ca2+. Physical Chemistry Chemical Physics, 2011, 13, 17852.	1.3	3
68	Structural Instability Tuning as a Regulatory Mechanism in Protein-Protein Interactions. Molecular Cell, 2011, 44, 734-744.	4.5	31
69	Using nanoelectrospray ion mobility spectrometry (GEMMA) to determine the size and relative molecular mass of proteins and protein assemblies: a comparison with MALLS and QELS. Analytical and Bioanalytical Chemistry, 2011, 399, 2421-2433.	1.9	24
70	Development of a high-throughput screening assay for the discovery of small-molecule SecA inhibitors. Analytical Biochemistry, 2011, 413, 90-96.	1.1	22
71	SecA: a tale of two protomers. Molecular Microbiology, 2010, 76, 1070-1081.	1.2	65
72	In Vitro Assays to Analyze Translocation of the Model Secretory Preprotein Alkaline Phosphatase. Methods in Molecular Biology, 2010, 619, 157-172.	0.4	22

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73	Signal peptides are allosteric activators of the protein translocase. Nature, 2009, 462, 363-367.	13.7	125
74	Clamour for a kiss. Nature, 2008, 455, 879-880.	13.7	9
75	Assembly of the translocase motor onto the preproteinâ€conducting channel. Molecular Microbiology, 2008, 70, 311-322.	1.2	26
76	The P. CÃ‰ZANNE Project: Innovative Approaches to Continuous Glucose Monitoring. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 6061-4.	0.5	4
77	Structural Basis for Signal-Sequence Recognition by the Translocase Motor SecA as Determined by NMR. Cell, 2007, 131, 756-769.	13.5	381
78	Structure of Dimeric SecA, the Escherichia coli Preprotein Translocase Motor. Journal of Molecular Biology, 2007, 366, 1545-1557.	2.0	127
79	Bacterial protein secretion through the translocase nanomachine. Nature Reviews Microbiology, 2007, 5, 839-851.	13.6	210
80	Preprotein-controlled catalysis in the helicase motor of SecA. EMBO Journal, 2007, 26, 2904-2914.	3.5	56
81	Functional large-scale production of a novel Jonesia sp. xyloglucanase by heterologous secretion from Streptomyces lividans. Journal of Biotechnology, 2006, 121, 498-507.	1.9	54
82	Cloning, purification and characterization of a functional anthracycline glycosyltransferase. Journal of Biotechnology, 2006, 125, 425-433.	1.9	10
83	Double hexameric ring assembly of the type III protein translocase ATPase HrcN. Molecular Microbiology, 2006, 61, 119-125.	1.2	45
84	Secretion by numbers: protein traffic in prokaryotes. Molecular Microbiology, 2006, 62, 308-319.	1.2	129
85	Disorder-order folding transitions underlie catalysis in the helicase motor of SecA. Nature Structural and Molecular Biology, 2006, 13, 594-602.	3.6	73
86	Identification of the Preprotein Binding Domain of SecA. Journal of Biological Chemistry, 2005, 280, 43209-43217.	1.6	76
87	Escherichia coliSecA truncated at its termini is functional and dimeric. FEBS Letters, 2005, 579, 1267-1271.	1.3	39
88	Purification of a functional mature region from a SecA-dependent preprotein. Protein Expression and Purification, 2005, 40, 336-339.	0.6	6
89	Global Co-ordination of Protein Translocation by the SecA IRA1 Switch. Journal of Biological Chemistry, 2004, 279, 22490-22497.	1.6	47
90	Helicase Motif III in SecA is essential for coupling preprotein binding to translocation ATPase. EMBO Reports, 2004, 5, 807-811.	2.0	24

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91	Structure and function of SecA, the preprotein translocase nanomotor. Biochimica Et Biophysica Acta - Molecular Cell Research, 2004, 1694, 67-80.	1.9	105
92	Type III Protein Translocase. Journal of Biological Chemistry, 2003, 278, 25816-25824.	1.6	61
93	Allosteric Communication between Signal Peptides and the SecA Protein DEAD Motor ATPase Domain. Journal of Biological Chemistry, 2002, 277, 13724-13731.	1.6	49
94	The ATPase domain of SecA can form a tetramer in solution 1 1Edited by I. B. Holland. Journal of Molecular Biology, 2002, 315, 831-843.	2.0	27
95	Bacterial secretome: the assembly manual and operating instructions (Review). Molecular Membrane Biology, 2002, 19, 159-169.	2.0	46
96	Sec, drugs and rockâ€™nâ€™roll: antibiotic targeting of bacterial protein translocation. Expert Opinion on Therapeutic Targets, 2001, 5, 141-153.	1.0	12
97	NS5A mutations predict biochemical but not virological response to interferon-alpha treatment of sporadic hepatitis C virus infection in European patients. Journal of Viral Hepatitis, 2001, 8, 243-248.	1.0	7
98	Protein secretion biotechnology usingStreptomyces lividans: Large-scale production of functional trimeric tumor necrosis factor ?. Biotechnology and Bioengineering, 2001, 72, 611-619.	1.7	47
99	Cross-talk between catalytic and regulatory elements in a DEAD motor domain is essential for SecA function. EMBO Journal, 2001, 20, 961-970.	3.5	104
100	Indecisive M13 Procoat Protein Mutants Bind to SecA but Do Not Activate the Translocation ATPase. Journal of Biological Chemistry, 2001, 276, 37909-37915.	1.6	22
101	Bacterial protein translocase: a unique molecular machine with an army of substrates. FEBS Letters, 2000, 476, 18-21.	1.3	36
102	Analysis of Quorum-Sensing-Dependent Control of Rhizosphere-Expressed (rhi) Genes in Rhizobium leguminosarum bv. viciae. Journal of Bacteriology, 1999, 181, 3816-3823.	1.0	134
103	A molecular switch in SecA protein couples ATP hydrolysis to protein translocation. Molecular Microbiology, 1999, 34, 1133-1145.	1.2	124
104	Following the leader: bacterial protein export through the Sec pathway. Trends in Microbiology, 1999, 7, 315-320.	3.5	119
105	Bacterial preprotein translocase: mechanism and conformational dynamics of a processive enzyme. Molecular Microbiology, 1998, 27, 511-518.	1.2	80
106	Escherichia coliSecA shape and dimensions. FEBS Letters, 1998, 436, 277-282.	1.3	46
107	Separable ATPase and Membrane Insertion Domains of the SecA Subunit of Preprotein Translocase. Journal of Biological Chemistry, 1996, 271, 31580-31584.	1.6	51
108	The Câ€terminal domain of the Rhizobium leguminosarum chitin synthase NodC is important for function and determines the orientation of the Nâ€terminal region in the inner membrane. Molecular Microbiology, 1996, 19, 443-453.	1.2	40

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109	Greek needs. Nature, 1996, 382, 294-294.	13.7	0
110	SecYEG and SecA Are the Stoichiometric Components of Preprotein Translocase. Journal of Biological Chemistry, 1995, 270, 20106-20111.	1.6	126
111	SecA membrane cycling at SecYEG is driven by distinct ATP binding and hydrolysis events and is regulated by SecD and SecF. Cell, 1995, 83, 1171-1181.	13.5	305
112	SecA promotes preprotein translocation by undergoing ATP-driven cycles of membrane insertion and deinsertion. Cell, 1994, 78, 835-843.	13.5	550
113	Secretion of the Rhizobium leguminosarum nodulation protein NodO by haemolysin-type systems. Molecular Microbiology, 1992, 6, 231-238.	1.2	60
114	Transcription of rhiA, a gene on a Rhizobium leguminosarum bv. viciae Sym plasmid, requires rhiR and is repressed by flavanoids that induce nod genes. Molecular Microbiology, 1989, 3, 87-93.	1.2	41
115	Allosteric Cross-Talk between the Hydrophobic Cleft and the BH4 Domain of Bcl-2 in Control of IP3R Activity. SSRN Electronic Journal, 0, , .	0.4	0
116	Allosteric cross-talk between the hydrophobic cleft and the BH4 domain of Bcl-2 in control of inositol 1,4,5-trisphosphate receptor activity. Exploration of Targeted Anti-tumor Therapy, 0, , 375-391.	0.5	1