

Vassilis Koronakis

List of Publications by Year in descending order

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36271

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121
all docs

121
docs citations

121
times ranked

5811
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial Metal Resistance: Coping with Copper without Cooperativity?. MBio, 2021, 12, e0065321.	1.8	3
2	A kinase-independent function of PAK is crucial for pathogen-mediated actin remodelling. PLoS Pathogens, 2021, 17, e1009902.	2.1	7
3	Structural and functional diversity calls for a new classification of ABC transporters. FEBS Letters, 2020, 594, 3767-3775.	1.3	169
4	Arf6 Can Trigger Wave Regulatory Complex-Dependent Actin Assembly Independent of Arno. International Journal of Molecular Sciences, 2020, 21, 2457.	1.8	10
5	Structure of CYRI-B (FAM49B), a key regulator of cellular actin assembly. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1015-1024.	1.1	12
6	EPEC Recruits a Cdc42-Specific GEF, Frabin, To Facilitate PAK Activation and Host Cell Colonization. MBio, 2020, 11, .	1.8	4
7	Pathogenic Escherichia coli Hijacks GTPase-Activated p21-Activated Kinase for Actin Pedestal Formation. MBio, 2019, 10, .	1.8	11
8	Arf GTPase interplay with Rho GTPases in regulation of the actin cytoskeleton. Small GTPases, 2019, 10, 411-418.	0.7	32
9	Antibiotic Resistance Mediated by the MacB ABC Transporter Family: A Structural and Functional Perspective. Frontiers in Microbiology, 2018, 9, 950.	1.5	121
10	Insights into bacterial lipoprotein trafficking from a structure of LolA bound to the LolC periplasmic domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7389-E7397.	3.3	58
11	MYO6 is targeted by <i>Salmonella</i> virulence effectors to trigger PI3-kinase signaling and pathogen invasion into host cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3915-3920.	3.3	24
12	Structure and mechanotransmission mechanism of the MacB ABC transporter superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12572-12577.	3.3	114
13	Swiss Army Pathogen: The Salmonella Entry Toolkit. Frontiers in Cellular and Infection Microbiology, 2017, 7, 348.	1.8	73
14	Structures of Gate Loop Variants of the AcrB Drug Efflux Pump Bound by Erythromycin Substrate. PLoS ONE, 2016, 11, e0159154.	1.1	42
15	Inhibition of WAVE Regulatory Complex Activation by a Bacterial Virulence Effector Counteracts Pathogen Phagocytosis. Cell Reports, 2016, 17, 697-707.	2.9	32
16	The Arf GTPase-Activating Protein Family Is Exploited by Salmonella enterica Serovar Typhimurium To Invade Nonphagocytic Host Cells. MBio, 2015, 6, .	1.8	52
17	Structure of a bacterial toxin-activating acyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3058-66.	3.3	33
18	WAVE Regulatory Complex Activation. Methods in Enzymology, 2014, 540, 363-379.	0.4	9

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19	Structure of the periplasmic adaptor protein from a major facilitator superfamily (MFS) multidrug efflux pump. <i>FEBS Letters</i> , 2014, 588, 3147-3153.	1.3	40
20	Structure and Operation of Bacterial Tripartite Pumps. <i>Annual Review of Microbiology</i> , 2013, 67, 221-242.	2.9	100
21	Structure of an atypical periplasmic adaptor from a multidrug efflux pump of the spirochete <i>Borrelia burgdorferi</i> . <i>FEBS Letters</i> , 2013, 587, 2984-2988.	1.3	21
22	Arf6 coordinates actin assembly through the WAVE complex, a mechanism usurped by <i>Salmonella</i> to invade host cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16880-16885.	3.3	85
23	The Bacterial Cytoskeleton Modulates Motility, Type 3 Secretion, and Colonization in <i>Salmonella</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002500.	2.1	28
24	The <i>Drosophila</i> Arf1 homologue Arf79F is essential for lamellipodium formation. <i>Journal of Cell Science</i> , 2012, 125, 5630-5635.	1.2	24
25	<i>Salmonella</i> Virulence Effector SopE and Host GEF ARNO Cooperate to Recruit and Activate WAVE to Trigger Bacterial Invasion. <i>Cell Host and Microbe</i> , 2012, 11, 129-139.	5.1	84
26	Structures of sequential open states in a symmetrical opening transition of the TolC exit duct. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2112-2117.	3.3	72
27	WAVE regulatory complex activation by cooperating GTPases Arf and Rac1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14449-14454.	3.3	119
28	Enteropathogenic <i>Escherichia coli</i> Recruits the Cellular Inositol Phosphatase SHIP2 to Regulate Actin-Pedestal Formation. <i>Cell Host and Microbe</i> , 2010, 7, 13-24.	5.1	57
29	The assembled structure of a complete tripartite bacterial multidrug efflux pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7173-7178.	3.3	276
30	LuxS-Based Quorum Sensing Does Not Affect the Ability of <i>Salmonella enterica</i> Serovar Typhimurium To Express the SPI-1 Type 3 Secretion System, Induce Membrane Ruffles, or Invade Epithelial Cells. <i>Journal of Bacteriology</i> , 2009, 191, 7253-7259.	1.0	25
31	Clustering transfers the translocated <i>Escherichia coli</i> receptor into lipid rafts to stimulate reversible activation of c-Fyn. <i>Cellular Microbiology</i> , 2009, 11, 433-441.	1.1	20
32	The <i>Salmonella</i> Effector SptP Dephosphorylates Host AAA+ ATPase VCP to Promote Development of its Intracellular Replicative Niche. <i>Cell Host and Microbe</i> , 2009, 5, 225-233.	5.1	67
33	<i>Salmonella</i> takes control: effector-driven manipulation of the host. <i>Current Opinion in Microbiology</i> , 2009, 12, 117-124.	2.3	285
34	Mimicry Is the Sincerest Form of Flattery?. <i>Cell Host and Microbe</i> , 2008, 4, 411-412.	5.1	3
35	Repetitive N-WASP Binding Elements of the Enterohemorrhagic <i>Escherichia coli</i> Effector EspFU Synergistically Activate Actin Assembly. <i>PLoS Pathogens</i> , 2008, 4, e1000191.	2.1	47
36	Deciphering Interplay between <i>Salmonella</i> Invasion Effectors. <i>PLoS Pathogens</i> , 2008, 4, e1000037.	2.1	61

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37	A periplasmic coiled-coil interface underlying TolC recruitment and the assembly of bacterial drug efflux pumps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4612-4617.	3.3	125
38	Salmonella SPI1 Effector SipA Persists after Entry and Cooperates with a SPI2 Effector to Regulate Phagosome Maturation and Intracellular Replication. <i>Cell Host and Microbe</i> , 2007, 1, 63-75.	5.1	130
39	Flexibility in a Drug Transport Accessory Protein: Molecular Dynamics Simulations of MexA. <i>Biophysical Journal</i> , 2006, 91, 558-564.	0.2	65
40	Directed evolution of a bacterial efflux pump: Adaptation of the <i>E. coli</i> TolC exit duct to the <i>Pseudomonas</i> MexAB translocase. <i>FEBS Letters</i> , 2006, 580, 5339-5343.	1.3	56
41	Pathogens reWrite Rho's Rules. <i>Cell</i> , 2006, 124, 15-17.	13.5	7
42	Exploiting pathogenic <i>Escherichia coli</i> to model transmembrane receptor signalling. <i>Nature Reviews Microbiology</i> , 2006, 4, 358-370.	13.6	89
43	Cholesterol binding by the bacterial type III translocon is essential for virulence effector delivery into mammalian cells. <i>Molecular Microbiology</i> , 2005, 56, 590-603.	1.2	139
44	Structure of the periplasmic component of a bacterial drug efflux pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9994-9999.	3.3	243
45	Interactions underlying assembly of the <i>Escherichia coli</i> AcrAB-TolC multidrug efflux system. <i>Molecular Microbiology</i> , 2004, 53, 697-706.	1.2	184
46	The target cell plasma membrane is a critical interface for <i>Salmonella</i> cell entry effector-host interplay. <i>Molecular Microbiology</i> , 2004, 54, 887-904.	1.2	40
47	Reply: Complex kinase requirements for EPEC pedestal formation. <i>Nature Cell Biology</i> , 2004, 6, 795-796.	4.6	9
48	Phosphorylation of the enteropathogenic <i>E. coli</i> receptor by the Src-family kinase c-Fyn triggers actin pedestal formation. <i>Nature Cell Biology</i> , 2004, 6, 618-625.	4.6	113
49	Three's company: component structures bring a closer view of tripartite drug efflux pumps. <i>Current Opinion in Structural Biology</i> , 2004, 14, 741-747.	2.6	132
50	Structure and Function of TolC: The Bacterial Exit Duct for Proteins and Drugs. <i>Annual Review of Biochemistry</i> , 2004, 73, 467-489.	5.0	318
51	Structure of the Ligand-blocked Periplasmic Entrance of the Bacterial Multidrug Efflux Protein TolC. <i>Journal of Molecular Biology</i> , 2004, 342, 697-702.	2.0	53
52	Control of Actin Turnover by a <i>Salmonella</i> Invasion Protein. <i>Molecular Cell</i> , 2004, 13, 497-510.	4.5	116
53	Self-association of EPEC intimin mediated by the β -barrel-containing anchor domain: a role in clustering of the Tir receptor. <i>Molecular Microbiology</i> , 2003, 51, 73-87.	1.2	69
54	The purified <i>Shigella</i> IpaB and <i>Salmonella</i> SipB translocators share biochemical properties and membrane topology. <i>Molecular Microbiology</i> , 2003, 49, 425-439.	1.2	69

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55	Locking TolC Entrance Helices to Prevent Protein Translocation by the Bacterial Type I Export Apparatus. <i>Journal of Molecular Biology</i> , 2003, 327, 309-315.	2.0	57
56	TolC - the bacterial exit duct for proteins and drugs. <i>FEBS Letters</i> , 2003, 555, 66-71.	1.3	92
57	Transition to the open state of the TolC periplasmic tunnel entrance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11103-11108.	3.3	145
58	Hemolysin. , 2002, , 361-378.		3
59	Direct modulation of the host cell cytoskeleton by <i>Salmonella</i> actin-binding proteins. <i>Trends in Cell Biology</i> , 2002, 12, 15-20.	3.6	88
60	Processing of viable <i>Salmonella typhimurium</i> for presentation of a CD4 T cell epitope from the <i>Salmonella</i> invasion protein C (SipC). <i>European Journal of Immunology</i> , 2002, 32, 2664-2671.	1.6	26
61	An aspartate ring at the TolC tunnel entrance determines ion selectivity and presents a target for blocking by large cations. <i>Molecular Microbiology</i> , 2002, 44, 1131-1139.	1.2	83
62	Topology of the <i>Salmonella</i> invasion protein SipB in a model bilayer. <i>Molecular Microbiology</i> , 2002, 44, 1309-1321.	1.2	43
63	A <i>Salmonella</i> SipB-derived polypeptide blocks the "trigger"™ mechanism of bacterial entry into eukaryotic cells. <i>Molecular Microbiology</i> , 2002, 45, 1715-1727.	1.2	17
64	The <i>Salmonella</i> pathogenicity island 1 secretion system directs cellular cholesterol redistribution during mammalian cell entry and intracellular trafficking. <i>Cellular Microbiology</i> , 2002, 4, 153-165.	1.1	85
65	Substrate-triggered recruitment of the TolC channel-tunnel during type I export of hemolysin by <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2001, 313, 501-510.	2.0	116
66	Interaction of <i>Escherichia coli</i> hemolysin with biological membranes. <i>FEBS Journal</i> , 2001, 268, 800-808.	0.2	54
67	Protein export and drug efflux through bacterial channel-tunnels. <i>Current Opinion in Cell Biology</i> , 2001, 13, 412-416.	2.6	56
68	Channel-tunnels. <i>Current Opinion in Structural Biology</i> , 2001, 11, 403-407.	2.6	33
69	Membrane Interaction of <i>Escherichia coli</i> Hemolysin: Flotation and Insertion-Dependent Labeling by Phospholipid Vesicles. <i>Journal of Bacteriology</i> , 2001, 183, 5364-5370.	1.0	50
70	Membrane fusion activity of purified SipB, a <i>Salmonella</i> surface protein essential for mammalian cell invasion. <i>Molecular Microbiology</i> , 2000, 37, 727-739.	1.2	76
71	Crystal structure of the bacterial membrane protein TolC central to multidrug efflux and protein export. <i>Nature</i> , 2000, 405, 914-919.	13.7	1,013
72	Channel vision. <i>EMBO Reports</i> , 2000, 1, 313-318.	2.0	82

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73	An ordered reaction mechanism for bacterial toxin acylation by the specialized acyltransferase HlyC: formation of a ternary complex with acylACP and protoxin substrates. <i>Molecular Microbiology</i> , 1999, 34, 887-901.	1.2	19
74	Binding of extracellular matrix laminin to <i>Escherichia coli</i> expressing the <i>Salmonella</i> outer membrane proteins Rck and PagC. <i>FEMS Microbiology Letters</i> , 1999, 176, 495-501.	0.7	32
75	Binding of extracellular matrix laminin to <i>Escherichia coli</i> expressing the <i>Salmonella</i> outer membrane proteins Rck and PagC. <i>FEMS Microbiology Letters</i> , 1999, 176, 495-501.	0.7	1
76	<i>Salmonella</i> InvG forms a ring-like multimer that requires the InvH lipoprotein for outer membrane localization. <i>Molecular Microbiology</i> , 1998, 30, 47-56.	1.2	151
77	Acylation of <i>Escherichia coli</i> Hemolysin: A Unique Protein Lipidation Mechanism Underlying Toxin Function. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 309-333.	2.9	172
78	RfaH and the ops element, components of a novel system controlling bacterial transcription elongation. <i>Molecular Microbiology</i> , 1997, 26, 845-851.	1.2	195
79	Structure of TolC, the outer membrane component of the bacterial type I efflux system, derived from two-dimensional crystals. <i>Molecular Microbiology</i> , 1997, 23, 617-626.	1.2	117
80	Synthesis, maturation and export of the <i>E. coli</i> hemolysin. <i>Medical Microbiology and Immunology</i> , 1996, 185, 65-71.	2.6	25
81	Suppression of transcription polarity in the <i>Escherichia coli</i> haemolysin operon by a short upstream element shared by polysaccharide and DNA transfer determinants. <i>Molecular Microbiology</i> , 1996, 19, 705-713.	1.2	68
82	Increased distal gene transcription by the elongation factor RfaH, a specialized homologue of NusG. <i>Molecular Microbiology</i> , 1996, 22, 729-737.	1.2	63
83	Independent interaction of the acyltransferase HlyC with two maturation domains of the <i>Escherichia coli</i> toxin HlyA. <i>Molecular Microbiology</i> , 1996, 20, 813-822.	1.2	33
84	Protein exporter function and in vitro ATPase activity are correlated in ABC-domain mutants of HlyB. <i>Molecular Microbiology</i> , 1995, 16, 87-96.	1.2	84
85	Chapter 20 Secretion of hemolysin and other proteins out of the Gram-negative bacterial cell. <i>New Comprehensive Biochemistry</i> , 1994, 27, 425-446.	0.1	2
86	ATPase activity and ATP/ADP-induced conformational change in the soluble domain of the bacterial protein translocator HlyB. <i>Molecular Microbiology</i> , 1993, 8, 1163-1175.	1.2	100
87	Bacterial signal peptide-independent protein export: HlyB-directed secretion of hemolysin. <i>Seminars in Cell Biology</i> , 1993, 4, 7-15.	3.5	46
88	ATPase activity and ATP/ADP-induced conformational change in the bacterial toxin exporter hemolysin B. <i>Biochemical Society Transactions</i> , 1993, 21, 347S-347S.	1.6	1
89	Activation of <i>Escherichia coli</i> prohemolysin to the membrane-targeted toxin by HlyC-directed ACP-dependent fatty acylation. <i>FEMS Microbiology Letters</i> , 1992, 105, 37-43.	0.7	24
90	The HlyB/HlyD-dependent secretion of toxins by Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 1992, 105, 44-53.	0.7	7

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91	Escherichia coli HlyT protein, a transcriptional activator of haemolysin synthesis and secretion, is encoded by the rfaH (sfrB) locus required for expression of sex factor and lipopolysaccharide genes. Molecular Microbiology, 1992, 6, 1003-1012.	1.2	93
92	E.coli hemolysin interactions with prokaryotic and eukaryotic cell membranes. BioEssays, 1992, 14, 519-525.	1.2	44
93	Activation of Escherichia coli prohaemolysin to the mature toxin by acyl carrier protein-dependent fatty acylation. Nature, 1991, 351, 759-761.	13.7	346
94	Identification of the promoters directing in vivo expression of hemolysin genes in Proteus vulgaris and Escherichia coli. Molecular Genetics and Genomics, 1988, 213, 99-104.	2.4	45
95	Comparison of the haemolysin secretion protein HlyB from Proteus vulgaris and Escherichia coli; site-directed mutagenesis causing impairment of export function. Molecular Genetics and Genomics, 1988, 213, 551-555.	2.4	52
96	Expression of the E.coli hemolysin secretion gene hlyB involves transcript anti-termination within the hly operon. Nucleic Acids Research, 1988, 16, 4789-4800.	6.5	65
97	The sequences of the traJ gene and the 5' end of the traY gene of the resistance plasmid R1. Molecular Genetics and Genomics, 1986, 203, 137-142.	2.4	16
98	The Type I Export Mechanism. , 0, , 71-79.		2