

Arcady R Mushegian

List of Publications by Year in descending order

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136
papers

13,224
citations

23567

58
h-index

24982

109
g-index

199
all docs

199
docs citations

199
times ranked

16054
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . Science, 2006, 314, 941-952.	12.6	1,018
2	A minimal gene set for cellular life derived by comparison of complete bacterial genomes.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 10268-10273.	7.1	833
3	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). Archives of Virology, 2018, 163, 2601-2631.	2.1	567
4	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). Archives of Virology, 2017, 162, 2505-2538.	2.1	506
5	A Complex Oscillating Network of Signaling Genes Underlies the Mouse Segmentation Clock. Science, 2006, 314, 1595-1598.	12.6	418
6	G protein-coupled receptor kinases: More than just kinases and not only for GPCRs. , 2012, 133, 40-69.		368
7	Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli. Current Biology, 1996, 6, 279-291.	3.9	307
8	Comparison of archaeal and bacterial genomes: computer analysis of protein sequences predicts novel functions and suggests a chimeric origin for the archaea. Molecular Microbiology, 1997, 25, 619-637.	2.5	302
9	RDH10 is essential for synthesis of embryonic retinoic acid and is required for limb, craniofacial, and organ development. Genes and Development, 2007, 21, 1113-1124.	5.9	285
10	New dimensions of the virus world discovered through metagenomics. Trends in Microbiology, 2010, 18, 11-19.	7.7	282
11	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	2.1	263
12	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). Archives of Virology, 2019, 164, 2417-2429.	2.1	257
13	Natural history of S-adenosylmethionine-binding proteins. BMC Structural Biology, 2005, 5, 19.	2.3	256
14	Positionally cloned human disease genes: Patterns of evolutionary conservation and functional motifs. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5831-5836.	7.1	242
15	Detecting periodic patterns in unevenly spaced gene expression time series using Lomb-Scargle periodograms. Bioinformatics, 2006, 22, 310-316.	4.1	226
16	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	2.1	219
17	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	6.5	217
18	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. Bioinformatics, 2010, 26, 1481-1487.	4.1	213

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19	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	3.4	211
20	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	2.1	202
21	Gene order is not conserved in bacterial evolution. <i>Trends in Genetics</i> , 1996, 12, 289-290.	6.7	198
22	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. <i>Nature Microbiology</i> , 2020, 5, 668-674.	13.3	198
23	Three monophyletic superfamilies account for the majority of the known glycosyltransferases. <i>Protein Science</i> , 2003, 12, 1418-1431.	7.6	196
24	Large-scale isolation of candidate virulence genes of <i>Pseudomonas aeruginosa</i> by in vivo selection.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10434-10439.	7.1	175
25	Short Integuments1/suspensor1/carpel Factory, a Dicer Homolog, Is a Maternal Effect Gene Required for Embryo Development in Arabidopsis. <i>Plant Physiology</i> , 2002, 130, 808-822.	4.8	171
26	Evolutionary plasticity of segmentation clock networks. <i>Development (Cambridge)</i> , 2011, 138, 2783-2792.	2.5	166
27	Large-Scale Taxonomic Profiling of Eukaryotic Model Organisms: A Comparison of Orthologous Proteins Encoded by the Human, Fly, Nematode, and Yeast Genomes. <i>Genome Research</i> , 1998, 8, 590-598.	5.5	156
28	A putative nucleic acid-binding domain in Bloom's and Werner's syndrome helicases. <i>Trends in Biochemical Sciences</i> , 1997, 22, 417-418.	7.5	148
29	Cell-to-cell movement of plant viruses. <i>Archives of Virology</i> , 1993, 133, 239-257.	2.1	142
30	Eukaryotic translation elongation factor 1 ^β contains a glutathione transferase domain—Study of a diverse, ancient protein super family using motif search and structural modeling. <i>Protein Science</i> , 1994, 3, 2045-2055.	7.6	140
31	Are There 10 ³¹ Virus Particles on Earth, or More, or Fewer?. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	137
32	The Sad1-UNC-84 homology domain in Mps3 interacts with Mps2 to connect the spindle pole body with the nuclear envelope. <i>Journal of Cell Biology</i> , 2006, 174, 665-675.	5.2	133
33	NleB, a Bacterial Effector with Glycosyltransferase Activity, Targets GAPDH Function to Inhibit NF- κ B Activation. <i>Cell Host and Microbe</i> , 2013, 13, 87-99.	11.0	126
34	Biosynthesis of Isoprenoids via Mevalonate in Archaea: The Lost Pathway. <i>Genome Research</i> , 2000, 10, 1468-1484.	5.5	119
35	The minimal genome concept. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 709-714.	3.3	118
36	A family of lysozyme-like virulence factors in bacterial pathogens of plants and animals.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 7321-7326.	7.1	116

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37	Comparative Genomics of Ethanolamine Utilization. <i>Journal of Bacteriology</i> , 2009, 191, 7157-7164.	2.2	113
38	Sequencing and analysis of bacterial genomes. <i>Current Biology</i> , 1996, 6, 404-416.	3.9	104
39	Orthologous Gene Clusters and Taxon Signature Genes for Viruses of Prokaryotes. <i>Journal of Bacteriology</i> , 2013, 195, 941-950.	2.2	104
40	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	2.1	102
41	Conserved transactivation domain shared by interferon regulatory factors and Smad morphogens. <i>Journal of Molecular Medicine</i> , 1999, 77, 403-405.	3.9	95
42	Incomplete penetrance and phenotypic variability characterize Gdf6-attributable oculo-skeletal phenotypes. <i>Human Molecular Genetics</i> , 2009, 18, 1110-1121.	2.9	92
43	The sea urchin kinome: A first look. <i>Developmental Biology</i> , 2006, 300, 180-193.	2.0	84
44	Chalcone isomerase family and fold: No longer unique to plants. <i>Protein Science</i> , 2004, 13, 540-544.	7.6	82
45	The evolution of Runx genes I. A comparative study of sequences from phylogenetically diverse model organisms. <i>BMC Evolutionary Biology</i> , 2003, 3, 4.	3.2	81
46	Functional Specialization and Evolution of Leader Proteinases in the Family Closteroviridae. <i>Journal of Virology</i> , 2001, 75, 12153-12160.	3.4	80
47	A Novel Serine/Threonine Protein Kinase Homologue of <i>Pseudomonas aeruginosa</i> Is Specifically Inducible within the Host Infection Site and Is Required for Full Virulence in Neutropenic Mice. <i>Journal of Bacteriology</i> , 1998, 180, 6764-6768.	2.2	79
48	Prp8, the pivotal protein of the spliceosomal catalytic center, evolved from a retroelement-encoded reverse transcriptase. <i>Rna</i> , 2011, 17, 799-808.	3.5	78
49	Evolutionary perspective on innate immune recognition. <i>Journal of Cell Biology</i> , 2001, 155, 705-710.	5.2	77
50	Evidence for Selection in Evolution of Alpha Satellite DNA: The Central Role of CENP-B/ β Binding Region. <i>Journal of Molecular Biology</i> , 1996, 261, 334-340.	4.2	75
51	The Epithelium-specific ETS Protein EHF/ESE-3 Is a Context-dependent Transcriptional Repressor Downstream of MAPK Signaling Cascades. <i>Journal of Biological Chemistry</i> , 2001, 276, 20397-20406.	3.4	73
52	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	2.1	72
53	The alpha subunit of <i>E. coli</i> RNA polymerase activates RNA binding by NusA. <i>Genes and Development</i> , 2000, 14, 2664-2675.	5.9	71
54	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	28.9	66

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55	Complete genome sequences of cellular life forms: glimpses of theoretical evolutionary genomics. <i>Current Opinion in Genetics and Development</i> , 1996, 6, 757-762.	3.3	65
56	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. <i>Virology</i> , 2015, 476, 304-315.	2.4	65
57	Metagenomic analysis of hadopelagic microbial assemblages thriving at the deepest part of Mediterranean Sea, Matapanâ€Vavilov Deep. <i>Environmental Microbiology</i> , 2013, 15, 167-182.	3.8	64
58	Genome of Xanthomonas oryzae Bacteriophage Xp10: An Odd T-Odd Phage. <i>Journal of Molecular Biology</i> , 2003, 330, 735-748.	4.2	62
59	Genomic and Proteomic Analysis of phiEco32, a Novel Escherichia coli Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	4.2	61
60	Thermus thermophilus Bacteriophage Î•YS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	4.2	60
61	The Origin and Evolution of G Protein-Coupled Receptor Kinases. <i>PLoS ONE</i> , 2012, 7, e33806.	2.5	58
62	Genome Comparison and Proteomic Characterization of Thermus thermophilus Bacteriophages P23-45 and P74-26: Siphoviruses with Triplex-forming Sequences and the Longest Known Tails. <i>Journal of Molecular Biology</i> , 2008, 378, 468-480.	4.2	56
63	Organization of the 3â€²-Terminal Half of Beet Yellow Stunt Virus Genome and Implications for the Evolution of Closteroviruses. <i>Virology</i> , 1996, 221, 199-207.	2.4	55
64	Distinct Circular Single-Stranded DNA Viruses Exist in Different Soil Types. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3934-3945.	3.1	54
65	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	2.1	51
66	Quod erat demonstrandum? The mystery of experimental validation of apparently erroneous computational analyses of protein sequences. <i>Genome Biology</i> , 2001, 2, research0051.1.	9.6	48
67	Detection of evolutionarily stable fragments of cellular pathways by hierarchical clustering of phyletic patterns. <i>Genome Biology</i> , 2004, 5, R32.	9.6	48
68	Human Family with Sequence Similarity 60 Member A (FAM60A) Protein: a New Subunit of the Sin3 Deacetylase Complex. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1815-1828.	3.8	47
69	Gene content of LUCA, the last universal common ancestor. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 4657.	3.0	46
70	Displacements of Prohead Protease Genes in the Late Operons of Double-Stranded-DNA Bacteriophages. <i>Journal of Bacteriology</i> , 2004, 186, 4369-4375.	2.2	45
71	Evolutionarily Conserved Orthologous Families in Phages Are Relatively Rare in Their Prokaryotic Hosts. <i>Journal of Bacteriology</i> , 2011, 193, 1806-1814.	2.2	45
72	Sequence Analysis of Eukaryotic Developmental Proteins: Ancient and Novel Domains. <i>Genetics</i> , 1996, 144, 817-828.	2.9	44

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73	A putative FAD-binding domain in a distinct group of oxidases including a protein involved in plant development. <i>Protein Science</i> , 1995, 4, 1243-1244.	7.6	43
74	Genome Sequence and Gene Expression of <i>Bacillus anthracis</i> Bacteriophage Fah. <i>Journal of Molecular Biology</i> , 2005, 354, 1-15.	4.2	42
75	Protein repertoire of double-stranded DNA bacteriophages. <i>Virus Research</i> , 2006, 117, 68-80.	2.2	40
76	Comparison of Pattern Detection Methods in Microarray Time Series of the Segmentation Clock. <i>PLoS ONE</i> , 2008, 3, e2856.	2.5	38
77	Changes in the composition of the RNA virome mark evolutionary transitions in green plants. <i>BMC Biology</i> , 2016, 14, 68.	3.8	37
78	Conserved Phosphoprotein Interaction Motif Is Functionally Interchangeable between Ataxin-7 and Arrestins. <i>Biochemistry</i> , 2000, 39, 6809-6813.	2.5	34
79	A novel histone fold domain-containing protein that replaces TAF6 in <i>Drosophila</i> SAGA is required for SAGA-dependent gene expression. <i>Genes and Development</i> , 2009, 23, 2818-2823.	5.9	34
80	Unexpected sequence similarity between nucleosidases and phosphoribosyltransferases of different specificity. <i>Protein Science</i> , 1994, 3, 1081-1088.	7.6	33
81	Evolutionary history of bacteriophages with double-stranded DNA genomes. <i>Biology Direct</i> , 2007, 2, 36.	4.6	33
82	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	2.1	33
83	The putative movement domain encoded by nepovirus RNA-2 is conserved in all sequenced nepoviruses. <i>Archives of Virology</i> , 1994, 135, 437-441.	2.1	32
84	Detection of evolutionarily stable fragments of cellular pathways by hierarchical clustering of phyletic patterns. <i>Genome Biology</i> , 2004, 5, 1.	8.8	31
85	Molecular dissection of arginyltransferases guided by similarity to bacterial peptidoglycan synthases. <i>EMBO Reports</i> , 2006, 7, 800-805.	4.5	30
86	Models of gene gain and gene loss for probabilistic reconstruction of gene content in the last universal common ancestor of life. <i>Biology Direct</i> , 2013, 8, 32.	4.6	28
87	Discrete Regions of the Sensor Protein VirA Determine the Strain-Specific Ability of <i>Agrobacterium</i> to Agroinfect Maize. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 221-227.	2.6	27
88	Characterization of the large (L) RNA of peanut bud necrosis tospovirus. <i>Archives of Virology</i> , 1998, 143, 2381-2390.	2.1	27
89	Genome Sequence Analysis Indicates that the Model Eukaryote <i>Nematostella vectensis</i> Harbors Bacterial Consorts. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6868-6873.	3.1	27
90	The proposed plant connexin is a protein kinase-like protein.. <i>Plant Cell</i> , 1993, 5, 998-999.	6.6	26

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91	2DE identification of proteins exhibiting turnover and phosphorylation dynamics during sea urchin egg activation. <i>Developmental Biology</i> , 2008, 313, 630-647.	2.0	26
92	The choice of optimal distance measure in genome-wide datasets. <i>Bioinformatics</i> , 2005, 21, iii3-iii11.	4.1	25
93	Identification and Characterization of a <i>Schizosaccharomyces pombe</i> RNA Polymerase II Elongation Factor with Similarity to the Metazoan Transcription Factor ELL. <i>Journal of Biological Chemistry</i> , 2007, 282, 5761-5769.	3.4	25
94	Protein content of minimal and ancestral ribosome. <i>Rna</i> , 2005, 11, 1400-1406.	3.5	23
95	Is Protein Folding a Thermodynamically Unfavorable, Active, Energy-Dependent Process?. <i>International Journal of Molecular Sciences</i> , 2022, 23, 521.	4.1	23
96	Measuring gene expression divergence: the distance to keep. <i>Biology Direct</i> , 2010, 5, 51.	4.6	21
97	Modeling protein folding in vivo. <i>Biology Direct</i> , 2018, 13, 13.	4.6	21
98	A topological algorithm for identification of structural domains of proteins. <i>BMC Bioinformatics</i> , 2007, 8, 237.	2.6	20
99	A family of GFP-like proteins with different spectral properties in lancelet <i>Branchiostoma floridae</i> . <i>Biology Direct</i> , 2008, 3, 28.	4.6	20
100	Eukaryotic RNase H shares a conserved domain with caulimovirus proteins that facilitate translation of polycistronic RNA. <i>Nucleic Acids Research</i> , 1994, 22, 4163-4166.	14.5	19
101	Sequence analysis of malacoherpesvirus proteins: Pan-herpesvirus capsid module and replication enzymes with an ancient connection to "Megavirales". <i>Virology</i> , 2018, 513, 114-128.	2.4	18
102	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , 2016, 66, syw096.	5.6	17
103	Molecular Analysis of the Essential and Nonessential Genetic Elements in the Genome of Peanut Chlorotic Streak Caulimovirus. <i>Virology</i> , 1995, 206, 823-834.	2.4	15
104	Refining structural and functional predictions for secretosome components by comparative sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 69-74.	2.6	15
105	The SPO1 gene product required for meiosis in yeast has a high similarity to phospholipase B enzymes. <i>Gene</i> , 1996, 177, 253-255.	2.2	14
106	Intermediary metabolism in sea urchin: The first inferences from the genome sequence. <i>Developmental Biology</i> , 2006, 300, 282-292.	2.0	14
107	Prokaryotic genes in eukaryotic genome sequences: when to infer horizontal gene transfer and when to suspect an actual microbe. <i>Environmental Microbiology</i> , 2015, 17, 2203-2208.	3.8	13
108	The role of the backbone torsion in protein folding. <i>Biology Direct</i> , 2016, 11, 64.	4.6	11

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109	An ancient evolutionary connection between Ribonuclease A and EndoU families. <i>Rna</i> , 2020, 26, 803-813.	3.5	11
110	Identification of Elongin C and Skp1 Sequences That Determine Cullin Selection. <i>Journal of Biological Chemistry</i> , 2004, 279, 43019-43026.	3.4	10
111	Sequenceâ€“function analysis of the Sendai virus L protein domain VI. <i>Virology</i> , 2010, 405, 370-382.	2.4	10
112	The Drosophila Beat protein is related to adhesion proteins that contain immunoglobulin domains. <i>Current Biology</i> , 1997, 7, R336-R338.	3.9	9
113	Similarity searches in genome-wide numerical data sets. <i>Biology Direct</i> , 2006, 1, 13.	4.6	8
114	Detection of Biochemical Pathways by Probabilistic Matching of Phyletic Vectors. <i>PLoS ONE</i> , 2009, 4, e5326.	2.5	8
115	Rotational restriction of nascent peptides as an essential element of co-translational protein folding: possible molecular players and structural consequences. <i>Biology Direct</i> , 2017, 12, 14.	4.6	8
116	Reply to Kyrpides and Ouzounis. <i>Molecular Microbiology</i> , 2002, 35, 697-698.	2.5	7
117	Distribution of words with a predefined range of mismatches to a DNA probe in bacterial genomes. <i>Bioinformatics</i> , 2004, 20, 67-74.	4.1	7
118	Chordopoxvirus protein F12 implicated in enveloped virion morphogenesis is an inactivated DNA polymerase. <i>Biology Direct</i> , 2014, 9, 22.	4.6	7
119	Host-dependent Suppression of Temperature-sensitive Mutations in Tobacco Mosaic Virus Transport Gene. <i>Journal of General Virology</i> , 1989, 70, 3421-3426.	2.9	6
120	Grand Challenges in Bioinformatics and Computational Biology. <i>Frontiers in Genetics</i> , 2011, 2, 60.	2.3	6
121	A Metazoan ATAC Acetyltransferase Subunit That Regulates Mitogen-activated Protein Kinase Signaling Is Related to an Ancient Molybdopterin Synthase Component. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 90-99.	3.8	6
122	Minimal genome encoding proteins with constrained amino acid repertoire. <i>Nucleic Acids Research</i> , 2013, 41, 8444-8451.	14.5	5
123	Energy-dependent protein folding: modeling how a protein folding machine may work. <i>F1000Research</i> , 2021, 10, 3.	1.6	4
124	Florigen and its homologs of FT/CETS/PEBP/RKIP/Ybhb family may be the enzymes of small molecule metabolism: review of the evidence. <i>BMC Plant Biology</i> , 2022, 22, 56.	3.6	4
125	Refining structural and functional predictions for secretosome components by comparative sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 69-74.	2.6	4
126	Measuring similarity between gene interaction profiles. <i>BMC Bioinformatics</i> , 2019, 20, 435.	2.6	3

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127	Gene I mutants of peanut chlorotic streak virus, a caulimovirus, replicate in plants but do not move from cell to cell. <i>Journal of Virology</i> , 1995, 69, 5781-5786.	3.4	3
128	A Polynomial-Time Algorithm Computing Lower and Upper Bounds of the Rooted Subtree Prune and Regraft Distance. <i>Journal of Computational Biology</i> , 2011, 18, 743-757.	1.6	1
129	Michael Adams: new life member of the International Committee on Taxonomy of Viruses (ICTV). <i>Archives of Virology</i> , 2019, 164, 2221-2221.	2.1	1
130	RNAs That Behave Like Prions. <i>MSphere</i> , 2020, 5, .	2.9	1
131	Refining structural and functional predictions for secretasome components by comparative sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 69.	2.6	1
132	Evolution and Function of Processosome, the Complex That Assembles Ribosomes in Eukaryotes: Clues from Comparative Sequence Analysis. <i>Nucleic Acids and Molecular Biology</i> , 2008, , 191-219.	0.2	1
133	A Minimal Gene Complement for Cellular Life and Reconstruction of Primitive Life Forms by Analysis of Complete Bacterial Genomes. , 1998, , 478-488.		1
134	Thematic Minireview Series on Computational Systems Biology. <i>Journal of Biological Chemistry</i> , 2011, 286, 23621-23622.	3.4	0
135	NleB, a Bacterial Effector with Glycosyltransferase Activity, Targets GAPDH Function to Inhibit NF- κ B Activation. <i>Cell Host and Microbe</i> , 2013, 13, 371-372.	11.0	0
136	Abstract LB-267: A role for the Sin3 histone deacetylase complex in cell migration. , 2012, , .		0