

# Arcady R Mushegian

## List of Publications by Year in descending order

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136  
papers

13,224  
citations

23567

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199  
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199  
docs citations

199  
times ranked

16054  
citing authors

#	ARTICLE	IF	CITATIONS
1	Is Protein Folding a Thermodynamically Unfavorable, Active, Energy-Dependent Process?. International Journal of Molecular Sciences, 2022, 23, 521.	4.1	23
2	Florigen and its homologs of FT/CETS/PEBP/RKIP/YbhB family may be the enzymes of small molecule metabolism: review of the evidence. BMC Plant Biology, 2022, 22, 56.	3.6	4
3	Differentiating between viruses and virus species by writing their names correctly. Archives of Virology, 2022, 167, 1231-1234.	2.1	33
4	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
5	Energy-dependent protein folding: modeling how a protein folding machine may work. F1000Research, 2021, 10, 3.	1.6	4
6	Binomial nomenclature for virus species: a consultation. Archives of Virology, 2020, 165, 519-525.	2.1	51
7	An ancient evolutionary connection between Ribonuclease A and EndoU families. Rna, 2020, 26, 803-813.	3.5	11
8	RNAs That Behave Like Prions. MSphere, 2020, 5, .	2.9	1
9	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	2.1	202
10	Are There $10^{31}$ Virus Particles on Earth, or More, or Fewer?. Journal of Bacteriology, 2020, 202, .	2.2	137
11	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. Nature Microbiology, 2020, 5, 668-674.	13.3	198
12	Measuring similarity between gene interaction profiles. BMC Bioinformatics, 2019, 20, 435.	2.6	3
13	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). Archives of Virology, 2019, 164, 943-946.	2.1	102
14	Michael Adams: new life member of the International Committee on Taxonomy of Viruses (ICTV). Archives of Virology, 2019, 164, 2221-2221.	2.1	1
15	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
16	Sequence analysis of malacoherpesvirus proteins: Pan-herpesvirus capsid module and replication enzymes with an ancient connection to "Megavirales". Virology, 2018, 513, 114-128.	2.4	18
17	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
18	Modeling protein folding in vivo. Biology Direct, 2018, 13, 13.	4.6	21

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19	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. Archives of Virology, 2017, 162, 1441-1446.	2.1	72
20	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
21	Rotational restriction of nascent peptides as an essential element of co-translational protein folding: possible molecular players and structural consequences. Biology Direct, 2017, 12, 14.	4.6	8
22	Changes in the composition of the RNA virome mark evolutionary transitions in green plants. BMC Biology, 2016, 14, 68.	3.8	37
23	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	2.1	263
24	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. Systematic Biology, 2016, 66, syw096.	5.6	17
25	The role of the backbone torsion in protein folding. Biology Direct, 2016, 11, 64.	4.6	11
26	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. Virology, 2015, 476, 304-315.	2.4	65
27	Prokaryotic genes in eukaryotic genome sequences: when to infer horizontal gene transfer and when to suspect an actual microbe. Environmental Microbiology, 2015, 17, 2203-2208.	3.8	13
28	Distinct Circular Single-Stranded DNA Viruses Exist in Different Soil Types. Applied and Environmental Microbiology, 2015, 81, 3934-3945.	3.1	54
29	Chordopoxvirus protein F12 implicated in enveloped virion morphogenesis is an inactivated DNA polymerase. Biology Direct, 2014, 9, 22.	4.6	7
30	Metagenomic analysis of hadopelagic microbial assemblages thriving at the deepest part of Mediterranean Sea, Matapanâ€Vavilov Deep. Environmental Microbiology, 2013, 15, 167-182.	3.8	64
31	Genome Sequence Analysis Indicates that the Model Eukaryote Nematostella vectensis Harbors Bacterial Consorts. Applied and Environmental Microbiology, 2013, 79, 6868-6873.	3.1	27
32	Models of gene gain and gene loss for probabilistic reconstruction of gene content in the last universal common ancestor of life. Biology Direct, 2013, 8, 32.	4.6	28
33	NleB, a Bacterial Effector with Glycosyltransferase Activity, Targets GAPDH Function to Inhibit NF-Î²B Activation. Cell Host and Microbe, 2013, 13, 371-372.	11.0	0
34	NleB, a Bacterial Effector with Glycosyltransferase Activity, Targets GAPDH Function to Inhibit NF-Î²B Activation. Cell Host and Microbe, 2013, 13, 87-99.	11.0	126
35	Minimal genome encoding proteins with constrained amino acid repertoire. Nucleic Acids Research, 2013, 41, 8444-8451.	14.5	5
36	Orthologous Gene Clusters and Taxon Signature Genes for Viruses of Prokaryotes. Journal of Bacteriology, 2013, 195, 941-950.	2.2	104

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37	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
38	The Origin and Evolution of G Protein-Coupled Receptor Kinases. <i>PLoS ONE</i> , 2012, 7, e33806.	2.5	58
39	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
40	G protein-coupled receptor kinases: More than just kinases and not only for GPCRs. , 2012, 133, 40-69.		368
41	Abstract LB-267: A role for the Sin3 histone deacetylase complex in cell migration. , 2012, , .		0
42	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
43	Evolutionary plasticity of segmentation clock networks. <i>Development (Cambridge)</i> , 2011, 138, 2783-2792.	2.5	166
44	Computational methods for Gene Orthology inference. <i>Briefings in Bioinformatics</i> , 2011, 12, 379-391.	6.5	217
45	Grand Challenges in Bioinformatics and Computational Biology. <i>Frontiers in Genetics</i> , 2011, 2, 60.	2.3	6
46	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
47	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
48	Thematic Minireview Series on Computational Systems Biology. <i>Journal of Biological Chemistry</i> , 2011, 286, 23621-23622.	3.4	0
49	Measuring gene expression divergence: the distance to keep. <i>Biology Direct</i> , 2010, 5, 51.	4.6	21
50	Sequence-function analysis of the Sendai virus L protein domain VI. <i>Virology</i> , 2010, 405, 370-382.	2.4	10
51	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. <i>Bioinformatics</i> , 2010, 26, 1481-1487.	4.1	213
52	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	28.9	66
53	New dimensions of the virus world discovered through metagenomics. <i>Trends in Microbiology</i> , 2010, 18, 11-19.	7.7	282
54	Detection of Biochemical Pathways by Probabilistic Matching of Phyletic Vectors. <i>PLoS ONE</i> , 2009, 4, e5326.	2.5	8

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55	Comparative Genomics of Ethanolamine Utilization. <i>Journal of Bacteriology</i> , 2009, 191, 7157-7164.	2.2	113
56	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
57	Incomplete penetrance and phenotypic variability characterize Gdf6-attributable oculo-skeletal phenotypes. <i>Human Molecular Genetics</i> , 2009, 18, 1110-1121.	2.9	92
58	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
59	Genomic and Proteomic Analysis of phiEco32, a Novel <i>Escherichia coli</i> Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	4.2	61
60	Genome Comparison and Proteomic Characterization of <i>Thermus thermophilus</i> 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
61	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
62	Gene content of LUCA, the last universal common ancestor. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 4657.	3.0	46
63	Comparison of Pattern Detection Methods in Microarray Time Series of the Segmentation Clock. <i>PLoS ONE</i> , 2008, 3, e2856.	2.5	38
64	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
65	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
66	RDH10 is essential for synthesis of embryonic retinoic acid and is required for limb, craniofacial, and organ development. <i>Genes and Development</i> , 2007, 21, 1113-1124.	5.9	285
67	Evolutionary history of bacteriophages with double-stranded DNA genomes. <i>Biology Direct</i> , 2007, 2, 36.	4.6	33
68	A topological algorithm for identification of structural domains of proteins. <i>BMC Bioinformatics</i> , 2007, 8, 237.	2.6	20
69	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
70	A Complex Oscillating Network of Signaling Genes Underlies the Mouse Segmentation Clock. <i>Science</i> , 2006, 314, 1595-1598.	12.6	418
71	Similarity searches in genome-wide numerical data sets. <i>Biology Direct</i> , 2006, 1, 13.	4.6	8
72	<i>Thermus thermophilus</i> Bacteriophage $\phi$ YS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	4.2	60

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73	Protein repertoire of double-stranded DNA bacteriophages. <i>Virus Research</i> , 2006, 117, 68-80.	2.2	40
74	Intermediary metabolism in sea urchin: The first inferences from the genome sequence. <i>Developmental Biology</i> , 2006, 300, 282-292.	2.0	14
75	The sea urchin kinome: A first look. <i>Developmental Biology</i> , 2006, 300, 180-193.	2.0	84
76	Molecular dissection of arginyltransferases guided by similarity to bacterial peptidoglycan synthases. <i>EMBO Reports</i> , 2006, 7, 800-805.	4.5	30
77	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
78	Detecting periodic patterns in unevenly spaced gene expression time series using Lombâ€™Scargle periodograms. <i>Bioinformatics</i> , 2006, 22, 310-316.	4.1	226
79	Natural history of S-adenosylmethionine-binding proteins. <i>BMC Structural Biology</i> , 2005, 5, 19.	2.3	256
80	Protein content of minimal and ancestral ribosome. <i>Rna</i> , 2005, 11, 1400-1406.	3.5	23
81	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
82	The choice of optimal distance measure in genome-wide datasets. <i>Bioinformatics</i> , 2005, 21, iii3-iii11.	4.1	25
83	Genome Sequence and Gene Expression of Bacillus anthracis Bacteriophage Fah. <i>Journal of Molecular Biology</i> , 2005, 354, 1-15.	4.2	42
84	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
85	Identification of Elongin C and Skp1 Sequences That Determine Cullin Selection. <i>Journal of Biological Chemistry</i> , 2004, 279, 43019-43026.	3.4	10
86	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
87	Detection of evolutionarily stable fragments of cellular pathways by hierarchical clustering of phyletic patterns. <i>Genome Biology</i> , 2004, 5, 1.	8.8	31
88	Chalcone isomerase family and fold: No longer unique to plants. <i>Protein Science</i> , 2004, 13, 540-544.	7.6	82
89	Detection of evolutionarily stable fragments of cellular pathways by hierarchical clustering of phyletic patterns. <i>Genome Biology</i> , 2004, 5, R32.	9.6	48
90	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

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91	Three monophyletic superfamilies account for the majority of the known glycosyltransferases. <i>Protein Science</i> , 2003, 12, 1418-1431.	7.6	196
92	Genome of <i>Xanthomonas oryzae</i> Bacteriophage Xp10: An Odd T-Odd Phage. <i>Journal of Molecular Biology</i> , 2003, 330, 735-748.	4.2	62
93	Short Integuments1/suspensor1/carpel Factory, a Dicer Homolog, Is a Maternal Effect Gene Required for Embryo Development in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2002, 130, 808-822.	4.8	171
94	Reply to Kyrpides and Ouzounis. <i>Molecular Microbiology</i> , 2002, 35, 697-698.	2.5	7
95	Refining structural and functional predictions for secretasome components by comparative sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 69-74.	2.6	15
96	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
97	Refining structural and functional predictions for secretasome components by comparative sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 69-74.	2.6	4
98	Evolutionary perspective on innate immune recognition. <i>Journal of Cell Biology</i> , 2001, 155, 705-710.	5.2	77
99	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
100	Functional Specialization and Evolution of Leader Proteinases in the Family Closteroviridae. <i>Journal of Virology</i> , 2001, 75, 12153-12160.	3.4	80
101	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
102	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
103	Biosynthesis of Isoprenoids via Mevalonate in Archaea: The Lost Pathway. <i>Genome Research</i> , 2000, 10, 1468-1484.	5.5	119
104	Conserved Phosphoprotein Interaction Motif Is Functionally Interchangeable between Ataxin-7 and Arrestins. <i>Biochemistry</i> , 2000, 39, 6809-6813.	2.5	34
105	Conserved transactivation domain shared by interferon regulatory factors and Smad morphogens. <i>Journal of Molecular Medicine</i> , 1999, 77, 403-405.	3.9	95
106	The minimal genome concept. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 709-714.	3.3	118
107	Characterization of the large (L) RNA of peanut bud necrosis tospovirus. <i>Archives of Virology</i> , 1998, 143, 2381-2390.	2.1	27
108	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

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109	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
110	A Minimal Gene Complement for Cellular Life and Reconstruction of Primitive Life Forms by Analysis of Complete Bacterial Genomes. , 1998, , 478-488.		1
111	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
112	Positionally cloned human disease genes: Patterns of evolutionary conservation and functional motifs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5831-5836.	7.1	242
113	The <i>Drosophila</i> Beat protein is related to adhesion proteins that contain immunoglobulin domains. <i>Current Biology</i> , 1997, 7, R336-R338.	3.9	9
114	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
115	Comparison of archaeal and bacterial genomes: computer analysis of protein sequences predicts novel functions and suggests a chimeric origin for the archaea. <i>Molecular Microbiology</i> , 1997, 25, 619-637.	2.5	302
116	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
117	Evidence for Selection in Evolution of Alpha Satellite DNA: The Central Role of CENP-B/p1± Binding Region. <i>Journal of Molecular Biology</i> , 1996, 261, 334-340.	4.2	75
118	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
119	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
120	A minimal gene set for cellular life derived by comparison of complete bacterial genomes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10268-10273.	7.1	833
121	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
122	Gene order is not conserved in bacterial evolution. <i>Trends in Genetics</i> , 1996, 12, 289-290.	6.7	198
123	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
124	Metabolism and evolution of <i>Haemophilus influenzae</i> deduced from a whole-genome comparison with <i>Escherichia coli</i> . <i>Current Biology</i> , 1996, 6, 279-291.	3.9	307
125	Sequencing and analysis of bacterial genomes. <i>Current Biology</i> , 1996, 6, 404-416.	3.9	104
126	Sequence Analysis of Eukaryotic Developmental Proteins: Ancient and Novel Domains. <i>Genetics</i> , 1996, 144, 817-828.	2.9	44



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127	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
128	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
129	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
130	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
131	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
132	Unexpected sequence similarity between nucleosidases and phosphoribosyltransferases of different specificity. <i>Protein Science</i> , 1994, 3, 1081-1088.	7.6	33
133	Eukaryotic translation elongation factor 1 <sup>3</sup> 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
134	Cell-to-cell movement of plant viruses. <i>Archives of Virology</i> , 1993, 133, 239-257.	2.1	142
135	The proposed plant connexin is a protein kinase-like protein.. <i>Plant Cell</i> , 1993, 5, 998-999.	6.6	26
136	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