

Jade Forwood

List of Publications by Year in descending order

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116
papers

3,306
citations

172207

29
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168136

53
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119
all docs

119
docs citations

119
times ranked

4280
citing authors

#	ARTICLE	IF	CITATIONS
1	A conserved arginine in NS5 binds genomic 3' stem-loop RNA for primer-independent initiation of flavivirus RNA replication. <i>Rna</i> , 2022, 28, 177-193.	1.6	7
2	MERS-CoV ORF4b employs an unusual binding mechanism to target IMP1 and block innate immunity. <i>Nature Communications</i> , 2022, 13, 1604.	5.8	10
3	Selective Targeting of Protein Kinase C (PKC)- β , Nuclear Translocation Reduces Mesenchymal Gene Signatures and Reinvigorates Dysfunctional CD8+ T Cells in Immunotherapy-Resistant and Metastatic Cancers. <i>Cancers</i> , 2022, 14, 1596.	1.7	3
4	The Structural Features of Henipavirus Matrix Protein Driving Intracellular Trafficking. <i>Viral Immunology</i> , 2021, 34, 27-40.	0.6	5
5	Structural Perspectives of Beak and Feather Disease Virus and Porcine Circovirus Proteins. <i>Viral Immunology</i> , 2021, 34, 49-59.	0.6	9
6	Structural characterization of a GNAT family acetyltransferase from <i>Elizabethkingia anophelis</i> bound to acetyl-CoA reveals a new dimeric interface. <i>Scientific Reports</i> , 2021, 11, 1274.	1.6	9
7	Insights into <i>Acinetobacter baumannii</i> fatty acid synthesis 3-oxoacyl-ACP reductases. <i>Scientific Reports</i> , 2021, 11, 7050.	1.6	9
8	The <i>Vibrio cholerae</i> SpeG Spermidine/Spermine N-Acetyltransferase Allosteric Loop and 26-27 Structural Elements Are Critical for Kinetic Activity. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 645768.	1.6	1
9	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. <i>Cell Discovery</i> , 2021, 7, 37.	3.1	11
10	Structural characterization of a Type B chloramphenicol acetyltransferase from the emerging pathogen <i>Elizabethkingia anophelis</i> NUHP1. <i>Scientific Reports</i> , 2021, 11, 9453.	1.6	4
11	Genomic Characterisation of a Highly Divergent Siadenovirus (Psittacine Siadenovirus F) from the Critically Endangered Orange-Bellied Parrot (<i>Neophema chrysogaster</i>). <i>Viruses</i> , 2021, 13, 1714.	1.5	18
12	Structural basis for nuclear import selectivity of pioneer transcription factor SOX2. <i>Nature Communications</i> , 2021, 12, 28.	5.8	24
13	Structural characterization of the porcine adeno-associated virus Po1 capsid protein binding to the nuclear trafficking protein importin alpha. <i>FEBS Letters</i> , 2021, 595, 2793-2804.	1.3	3
14	Structural characterization of 2-oxoacyl ACP synthase I bound to platencin and fragment screening molecules at two substrate binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 47-56.	1.5	3
15	Molecular characterisation of a novel pathogenic avipoxvirus from the Australian magpie (<i>Gymnorhina tibicen</i>). <i>Virology</i> , 2020, 540, 1-16.	1.1	24
16	Molecular Characterisation of a Novel and Highly Divergent Passerine Adenovirus 1. <i>Viruses</i> , 2020, 12, 1036.	1.5	12
17	Beak and feather disease virus: biology and resultant disease. <i>Wikijournal of Science</i> , 2020, 3, 7.	0.1	2
18	REPEAT SPILLOVER OF BEAK AND FEATHER DISEASE VIRUS INTO AN ENDANGERED PARROT HIGHLIGHTS THE RISK ASSOCIATED WITH ENDEMIC PATHOGEN LOSS IN ENDANGERED SPECIES. <i>Journal of Wildlife Diseases</i> , 2020, 56, 896-906.	0.3	9

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19	The Intrinsically Disordered W Protein Is Multifunctional during Henipavirus Infection, Disrupting Host Signalling Pathways and Nuclear Import. <i>Cells</i> , 2020, 9, 1913.	1.8	12
20	Henipavirus W Proteins Interact with 14-3-3 To Modulate Host Gene Expression. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
21	SpeG polyamine acetyltransferase enzyme from <i>Bacillus thuringiensis</i> forms a dodecameric structure and exhibits high catalytic efficiency. <i>Journal of Structural Biology</i> , 2020, 210, 107506.	1.3	5
22	Targeting Nuclear LSD1 to Reprogram Cancer Cells and Reinvigorate Exhausted T Cells via a Novel LSD1-EOMES Switch. <i>Frontiers in Immunology</i> , 2020, 11, 1228.	2.2	49
23	Structural basis for disulphide-CoA inhibition of a butyryl-CoA hexameric thioesterase. <i>Journal of Structural Biology</i> , 2020, 210, 107477.	1.3	1
24	Protein complexes including PGRMC1 and actin-associated proteins are disrupted by AG-205. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 64-69.	1.0	26
25	Human importin β 3 and its N-terminal truncated form, without the importin- β 2-binding domain, are oligomeric species with a low conformational stability in solution. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129609.	1.1	11
26	Structure, function, and regulation of thioesterases. <i>Progress in Lipid Research</i> , 2020, 79, 101036.	5.3	16
27	Pigeon circoviruses from feral pigeons in Australia demonstrate extensive recombination and genetic admixture with other circoviruses. <i>Avian Pathology</i> , 2019, 48, 512-520.	0.8	12
28	Lysine-Specific Histone Demethylase 1A Regulates Macrophage Polarization and Checkpoint Molecules in the Tumor Microenvironment of Triple-Negative Breast Cancer. <i>Frontiers in Immunology</i> , 2019, 10, 1351.	2.2	60
29	Structural characterization of a short-chain dehydrogenase/reductase from multi-drug resistant <i>Acinetobacter baumannii</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 465-471.	1.0	5
30	Assessing circovirus gene flow in multiple spill-over events. <i>Virus Genes</i> , 2019, 55, 802-814.	0.7	5
31	The first complete mitogenome of Australia's largest raptor, the wedge-tailed eagle (<i>Aquila</i>) Tj ETQq1 1 0.784314 rgBT ₁ /Overlo	0.2	1
32	Novel Flavivirus Antiviral That Targets the Host Nuclear Transport Importin β 1/ β 2 Heterodimer. <i>Cells</i> , 2019, 8, 281.	1.8	31
33	Zika Virus NS5 Forms Supramolecular Nuclear Bodies That Sequester Importin- β and Modulate the Host Immune and Pro-Inflammatory Response in Neuronal Cells. <i>ACS Infectious Diseases</i> , 2019, 5, 932-948.	1.8	34
34	The first complete mitogenome of Indian ringneck <i>(Psittacula krameri)</i> demonstrates close phylogenetic relationship with Eclectus parrot. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3579-3581.	0.2	10
35	Characterization of the first mitochondrial genome of a little Corella (<i>Cacatua sanguinea</i>) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3792-3794.	0.2	6
36	The first complete mitogenome of red-bellied parrot (<i>Poicephalus rufiventris</i>) resolves phylogenetic status within Psittacidae. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 195-197.	0.2	1

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37	Structural basis for importin alpha 3 specificity of W proteins in Hendra and Nipah viruses. <i>Nature Communications</i> , 2018, 9, 3703.	5.8	50
38	Contribution of the residue at position 4 within classical nuclear localization signals to modulating interaction with importins and nuclear targeting. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 1114-1129.	1.9	22
39	Structural characterisation of the fatty acid biosynthesis enzyme FabF from the pathogen <i>Listeria monocytogenes</i> . <i>Scientific Reports</i> , 2017, 7, 39277.	1.6	5
40	A novel pathogenic aviadenovirus from red-bellied parrots (<i>Poicephalus rufiventris</i>) unveils deep recombination events among avian host lineages. <i>Virology</i> , 2017, 502, 188-197.	1.1	34
41	Mycobacteria Encode Active and Inactive Classes of TesB Fatty-Acyl CoA Thioesterases Revealed through Structural and Functional Analysis. <i>Biochemistry</i> , 2017, 56, 1460-1472.	1.2	3
42	Structural Basis for Importin- β Binding of the Human Immunodeficiency Virus Tat. <i>Scientific Reports</i> , 2017, 7, 1650.	1.6	21
43	Structural insights into GDP-mediated regulation of a bacterial acyl-CoA thioesterase. <i>Journal of Biological Chemistry</i> , 2017, 292, 20461-20471.	1.6	9
44	Nuclear import inhibitor N -(4-hydroxyphenyl) retinamide targets Zika virus (ZIKV) nonstructural protein 5 to inhibit ZIKV infection. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1555-1559.	1.0	41
45	Complete mitochondrial genome sequence of an Australian little penguin (<i>Eudyptula minor</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	0
46	Molecular and microscopic characterization of a novel Eastern grey kangaroopox virus genome directly from a clinical sample. <i>Scientific Reports</i> , 2017, 7, 16472.	1.6	26
47	Characterization of Beak and Feather Disease Virus Genomes from Wild Musk Lorikeets (<i>Glossopsitta</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	1
48	Whole-Genome Sequence of a Beak and Feather Disease Virus Isolate from a Fledgling Red-Capped Parrot (<i>Purpureicephalus spurius</i>). <i>Genome Announcements</i> , 2016, 4, .	0.8	1
49	Forensic genetic evidence of beak and feather disease virus infection in a Powerful Owl, <i>Ninox strenua</i> . <i>Emu</i> , 2016, 116, 71-74.	0.2	33
50	Molecular Characterization of a Beak and Feather Disease Virus Genome from a Purple Crowned Lorikeet (<i>Glossopsitta porphyrocephala</i>). <i>Genome Announcements</i> , 2016, 4, .	0.8	0
51	Evolution of circoviruses in lorikeets lags behind its hosts. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 281-291.	1.2	22
52	A comparison of PCR assays for beak and feather disease virus and high resolution melt (HRM) curve analysis of replicase associated protein and capsid genes. <i>Journal of Virological Methods</i> , 2016, 237, 47-57.	1.0	9
53	Structural insights into the assembly and regulation of distinct viral capsid complexes. <i>Nature Communications</i> , 2016, 7, 13014.	5.8	43
54	The complete mitochondrial genome sequence of an Endangered powerful owl (<i>Ninox strenua</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 722-723.	0.2	5

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55	Structural and Functional Characterization of the Paal Thioesterase from <i>Streptococcus pneumoniae</i> Reveals a Dual Specificity for Phenylacetyl-CoA and Medium-chain Fatty Acyl-CoAs and a Novel CoA-induced Fit Mechanism. <i>Journal of Biological Chemistry</i> , 2016, 291, 1866-1876.	1.6	6
56	Characterization of a beta-catenin nuclear localization defect in MCF-7 breast cancer cells. <i>Experimental Cell Research</i> , 2016, 341, 196-206.	1.2	7
57	Structural Biology and Regulation of Protein Import into the Nucleus. <i>Journal of Molecular Biology</i> , 2016, 428, 2060-2090.	2.0	204
58	The C-terminal 18 Amino Acid Region of Dengue Virus NS5 Regulates its Subcellular Localization and Contains a Conserved Arginine Residue Essential for Infectious Virus Production. <i>PLoS Pathogens</i> , 2016, 12, e1005886.	2.1	66
59	Evidence of a deep viral host switch event with beak and feather disease virus infection in rainbow bee-eaters (<i>Merops ornatus</i>). <i>Scientific Reports</i> , 2015, 5, 14511.	1.6	45
60	Structural Characterisation of the Beta-Ketoacyl-Acyl Carrier Protein Synthases, FabF and FabH, of <i>Yersinia pestis</i> . <i>Scientific Reports</i> , 2015, 5, 14797.	1.6	19
61	Beak and feather disease virus genotypes in <scp>Australian</scp> parrots reveal flexible hostâ€switching. <i>Australian Veterinary Journal</i> , 2015, 93, 471-475.	0.5	20
62	Structural Characterisation of FabG from <i>Yersinia pestis</i> , a Key Component of Bacterial Fatty Acid Synthesis. <i>PLoS ONE</i> , 2015, 10, e0141543.	1.1	15
63	An efficient approach for recombinant expression and purification of the viral capsid protein from beak and feather disease virus (BFDV) in <i>Escherichia coli</i> . <i>Journal of Virological Methods</i> , 2015, 215-216, 1-8.	1.0	10
64	The C-terminal 50 Amino Acid Residues of Dengue NS3 Protein Are Important for NS3-NS5 Interaction and Viral Replication. <i>Journal of Biological Chemistry</i> , 2015, 290, 2379-2394.	1.6	105
65	Structural and functional characterization of TesB from <i>Yersinia pestis</i> reveals a unique octameric arrangement of hotdog domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 986-995.	2.5	8
66	Mutability Dynamics of an Emergent Single Stranded DNA Virus in a NaÃve Host. <i>PLoS ONE</i> , 2014, 9, e85370.	1.1	54
67	Structural Characterization of a Gcn5-Related N-Acetyltransferase from <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2014, 9, e102348.	1.1	12
68	Structural Basis for Regulation of the Human Acetyl-CoA Thioesterase 12 and Interactions with the Steroidogenic Acute Regulatory Protein-related Lipid Transfer (START) Domain. <i>Journal of Biological Chemistry</i> , 2014, 289, 24263-24274.	1.6	22
69	Crystallization and preliminary X-ray diffraction analysis of FabG from <i>Yersinia pestis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 101-104.	0.4	4
70	Characterization of the Whole-Genome Sequence of a Beak and Feather Disease Virus Isolate from a Mallee Ringneck Parrot (<i>Barnardius zonarius barnardi</i>). <i>Genome Announcements</i> , 2014, 2, .	0.8	6
71	Purification, crystallization and preliminary X-ray diffraction analysis of the N-acetyltransferase SAV0826 from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 211-214.	0.4	0
72	Expression, purification, crystallization and preliminary X-ray analysis of the Paal-like thioesterase SAV0944 from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 244-247.	0.4	1

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73	Rapid genotyping of beak and feather disease virus using high-resolution DNA melt curve analysis. <i>Journal of Virological Methods</i> , 2014, 208, 47-55.	1.0	12
74	Functional disruption of yeast metacaspase, Mca1, leads to miltefosine resistance and inability to mediate miltefosine-induced apoptotic effects. <i>Fungal Genetics and Biology</i> , 2014, 67, 71-81.	0.9	15
75	Phylogeny of beak and feather disease virus in cockatoos demonstrates host generalism and multiple-variant infections within Psittaciformes. <i>Virology</i> , 2014, 460-461, 72-82.	1.1	55
76	Whole-Genome Sequence Characterization of a Beak and Feather Disease Virus in a Wild Regent Parrot (<i>Polytelis anthopeplus monarchoides</i>). <i>Genome Announcements</i> , 2014, 2, .	0.8	7
77	Molecular Characterization of Genome Sequences of Beak and Feather Disease Virus from the Australian Twenty-Eight Parrot (<i>Barnardius zonarius semitorquatus</i>). <i>Genome Announcements</i> , 2014, 2, .	0.8	8
78	Differential expression of two isolates of beak and feather disease virus capsid protein in <i>Escherichia coli</i> . <i>Journal of Virological Methods</i> , 2013, 189, 118-124.	1.0	14
79	Structural determination of importin alpha in complex with beak and feather disease virus capsid nuclear localization signal. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 680-685.	1.0	13
80	Characterization of the Complete Genome Sequence of a Beak and Feather Disease Virus from a Moluccan Red Lory (<i>Eos bornea</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	15
81	Whole-Genome Sequences of Two Beak and Feather Disease Viruses in the Endangered Swift Parrot (<i>Tj ETQq1 1 0,784314 rgBT /Ove</i>	0.8	17
82	Crystallization of the acyl-CoA thioesterase TesB from <i>Yersinia pestis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 188-190.	0.7	1
83	Expression, purification and crystallization of acetyl-CoA hydrolase from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1303-1306.	0.7	4
84	Structural Characterisation of the Nuclear Import Receptor Importin Alpha in Complex with the Bipartite NLS of Prp20. <i>PLoS ONE</i> , 2013, 8, e82038.	1.1	22
85	Altered mitogen-activated protein kinase signaling in dystrophic (<i>mdx</i>) muscle. <i>Muscle and Nerve</i> , 2012, 46, 374-383.	1.0	18
86	Structural Basis of High-Affinity Nuclear Localization Signal Interactions with Importin β . <i>Traffic</i> , 2012, 13, 532-548.	1.3	91
87	Homology Modelling and Structural Comparisons of Capsid-Associated Proteins from Circoviruses Reveal Important Virus-Specific Surface Antigens. <i>Crystal Structure Theory and Applications</i> , 2012, 01, 9-16.	0.3	7
88	Molecular basis for specificity of nuclear import and prediction of nuclear localization. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 1562-1577.	1.9	336
89	Ligand-induced Conformational Changes within a Hexameric Acyl-CoA Thioesterase. <i>Journal of Biological Chemistry</i> , 2011, 286, 35643-35649.	1.6	11
90	Calmodulin-dependent nuclear import of HMG-box family nuclear factors: importance of the role of SRY in sex reversal. <i>Biochemical Journal</i> , 2010, 430, 39-48.	1.7	38

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91	Quantitative Structural Analysis of Importin- β^2 Flexibility: Paradigm for Solenoid Protein Structures. <i>Structure</i> , 2010, 18, 1171-1183.	1.6	89
92	Functional and structural properties of mammalian acyl-coenzyme A thioesterases. <i>Progress in Lipid Research</i> , 2010, 49, 366-377.	5.3	128
93	Importin- β^2 Is a GDP-to-GTP Exchange Factor of Ran. <i>Journal of Biological Chemistry</i> , 2009, 284, 22549-22558.	1.6	27
94	Crystallization of the flexible nuclear import receptor importin- β^2 in the unliganded state. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 625-628.	0.7	3
95	Interaction between Plate Make and Protein in Protein Crystallisation Screening. <i>PLoS ONE</i> , 2009, 4, e7851.	1.1	2
96	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1142-1146.	1.5	28
97	Kap95p Binding Induces the Switch Loops of RanGDP to Adopt the GTP-Bound Conformation: Implications for Nuclear Import Complex Assembly Dynamics. <i>Journal of Molecular Biology</i> , 2008, 383, 772-782.	2.0	32
98	Crystallography and protein-protein interactions: biological interfaces and crystal contacts. <i>Biochemical Society Transactions</i> , 2008, 36, 1438-1441.	1.6	61
99	Protein Structure Determination Using a Combination of Cross-linking, Mass Spectrometry, and Molecular Modeling. <i>Methods in Molecular Biology</i> , 2008, 426, 459-474.	0.4	18
100	Overview of the Pipeline for Structural and Functional Characterization of Macrophage Proteins at the University of Queensland. <i>Methods in Molecular Biology</i> , 2008, 426, 577-587.	0.4	1
101	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10382-10387.	3.3	71
102	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. <i>Plant Cell</i> , 2007, 19, 2898-2912.	3.1	143
103	The use of Co ²⁺ for crystallization and structure determination, using a conventional monochromatic X-ray source, of flax rust avirulence protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 209-213.	0.7	14
104	Nuclear Import Properties of the Sex-Determining Factor SRY. , 2007, 390, 83-97.		5
105	Crystallization of the C-terminal domain of the mouse brain cytosolic long-chain acyl-CoA thioesterase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 133-135.	0.7	6
106	Focusing in on structural genomics: The University of Queensland structural biology pipeline. <i>New Biotechnology</i> , 2006, 23, 281-289.	2.7	14
107	Quantitative analysis of DNA-protein interactions using double-labeled native gel electrophoresis and fluorescence-based imaging. <i>Electrophoresis</i> , 2006, 27, 3166-3170.	1.3	12
108	Modelling the structure of latexin-carboxypeptidase A complex based on chemical cross-linking and molecular docking. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 9-16.	1.0	19

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109	Substrate specificity of protein kinases and computational prediction of substrates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1754, 200-209.	1.1	88
110	Nuclear Protein Import. , 2005, , 137-160.		1
111	Defective importin α recognition and nuclear import of the sex-determining factor SRY are associated with XY sex-reversing mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7045-7050.	3.3	143
112	Nuclear Import Pathway of the Telomere Elongation Suppressor TRF1: α Inhibition by Importin β . <i>Biochemistry</i> , 2002, 41, 9333-9340.	1.2	42
113	Nuclear Import of Creb and AP-1 Transcription Factors Requires Importin- β 1 and Ran but Is Independent of Importin- β . <i>Biochemistry</i> , 2001, 40, 5208-5217.	1.2	89
114	The C-terminal Nuclear Localization Signal of the Sex-determining Region Y (SRY) High Mobility Group Domain Mediates Nuclear Import through Importin β 1. <i>Journal of Biological Chemistry</i> , 2001, 276, 46575-46582.	1.6	104
115	The 37-Amino-Acid Interdomain of Dengue Virus NS5 Protein Contains a Functional NLS and Inhibitory CK2 Site. <i>Biochemical and Biophysical Research Communications</i> , 1999, 257, 731-737.	1.0	87
116	Nuclear Import Properties of the Sex-Determining Factor SRY. , 0, , 83-98.		0