Juan Antonio Lopez

List of Publications by Year
in descending order

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139 papers	8,120 citations	46918 47 h-index	56606 83 g-index
141 all docs	141 docs citations	141 times ranked	15090 citing authors

#	Article	IF	Citations
1	Comparative proteomic analysis of nuclear and cytoplasmic compartments in human cardiac progenitor cells. Scientific Reports, 2022, 12, 146.	1.6	3
2	The Influence of Coronary Artery Disease in the Development of Aortic Stenosis and the Importance of the Albumin Redox State. Antioxidants, 2022, 11, 317.	2.2	6
3	Clinical profile and outcome of cardiac amyloidosis in a Spanish referral center. Revista Espanola De Cardiologia (English Ed), 2021, 74, 149-158.	0.4	10
4	Perfil clÃnico y evoluciÃ³n de la amiloidosis cardiaca en un centro espaÃ±ol de referencia. Revista Espanola De Cardiologia, 2021, 74, 149-158.	0.6	33
5	Proteomic and Biological Analysis of an In Vitro Human Endothelial System in Response to Drug Anaphylaxis. Frontiers in Immunology, 2021, 12, 692569.	2.2	6
6	Early renal and vascular damage within the normoalbuminuria condition. Journal of Hypertension, 2021, 39, 2220-2231.	0.3	7
7	Cardiovascular Risk Stratification Based on Oxidative Stress for Early Detection of Pathology. Antioxidants and Redox Signaling, 2021, 35, 602-617.	2.5	9
8	p38Î³ and p38Î´ regulate postnatal cardiac metabolism through glycogen synthase 1. PLoS Biology, 2021, 19, e3001447.	2.6	8
9	Comprehensive Proteomic Profiling of Pressure Ulcers in Patients with Spinal Cord Injury Identifies a Specific Protein Pattern of Pathology. Advances in Wound Care, 2020, 9, 277-294.	2.6	5
10	Intracellular calcium mishandling leads to cardiac dysfunction and ventricular arrhythmias in a mouse model of propionic acidemia. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165586.	1.8	22
11	Improved integrative analysis of the thiol redox proteome using filter-aided sample preparation. Journal of Proteomics, 2020, 214, 103624.	1.2	14
12	Bone Marrow Mesenchymal Stem Cells Support Acute Myeloid Leukemia Bioenergetics and Enhance Antioxidant Defense and Escape from Chemotherapy. Cell Metabolism, 2020, 32, 829-843.e9.	7.2	122
13	Mammalian lipid droplets are innate immune hubs integrating cell metabolism and host defense. Science, 2020, 370, .	6.0	245
14	Effects of Growth Hormone Treatment and Rehabilitation in Incomplete Chronic Traumatic Spinal Cord Injury: Insight from Proteome Analysis. Journal of Personalized Medicine, 2020, 10, 183.	1.1	3
15	Novel molecular plasma signatures on cardiovascular disease can stratify patients throughout life. Journal of Proteomics, 2020, 222, 103816.	1.2	5
16	ECM deposition is driven by caveolin-1â€“dependent regulation of exosomal biogenesis and cargo sorting. Journal of Cell Biology, 2020, 219, .	2.3	58
17	The chaperonin CCT controls T cell receptorâ€“driven 3D configuration of centrioles. Science Advances, 2020, 6, .	4.7	23
18	Successful aging: insights from proteome analyses of healthy centenarians. Aging, 2020, 12, 3502-3515.	1.4	31

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19	Lamin A/C deficiency in CD4⁺ Tâ€cells enhances regulatory Tâ€cells and prevents inflammatory bowel disease. Journal of Pathology, 2019, 249, 509-522.	2.1	12
20	Exercise Benefits in Pulmonary Hypertension. Journal of the American College of Cardiology, 2019, 73, 2906-2907.	1.2	5
21	Definition of a cell surface signature for human cardiac progenitor cells after comprehensive comparative transcriptomic and proteomic characterization. Scientific Reports, 2019, 9, 4647.	1.6	17
22	p38Î³ is essential for cell cycle progression and liver tumorigenesis. Nature, 2019, 568, 557-560.	13.7	72
23	Arabidopsis YAF9 histone readers modulate flowering time through NuA4â€complexâ€dependent H4 and H2A.Z histone acetylation at FLC chromatin. New Phytologist, 2019, 222, 1893-1908.	3.5	39
24	Identification of six cardiovascular risk biomarkers in the young population: A promising tool for early prevention. Atherosclerosis, 2019, 282, 67-74.	0.4	14
25	Urine Haptoglobin and Haptoglobin-Related Protein Predict Response to Spironolactone in Patients With Resistant Hypertension. Hypertension, 2019, 73, 794-802.	1.3	6
26	Muscle molecular adaptations to endurance exercise training are conditioned by glycogen availability: a proteomicsâ€based analysis in the McArdle mouse model. Journal of Physiology, 2018, 596, 1035-1061.	1.3	26
27	Arabidopsis SWC4 Binds DNA and Recruits the SWR1 Complex to Modulate Histone H2A.Z Deposition at Key Regulatory Genes. Molecular Plant, 2018, 11, 815-832.	3.9	60
28	Potential role of new molecular plasma signatures on cardiovascular risk stratification in asymptomatic individuals. Scientific Reports, 2018, 8, 4802.	1.6	8
29	Caveolin-1 Modulates Mechanotransduction Responses to Substrate Stiffness through Actin-Dependent Control of YAP. Cell Reports, 2018, 25, 1622-1635.e6.	2.9	91
30	Differential proteomic and oxidative profiles unveil dysfunctional protein import to adipocyte mitochondria in obesity-associated aging and diabetes. Redox Biology, 2017, 11, 415-428.	3.9	40
31	miR-28 regulates the germinal center reaction and blocks tumor growth in preclinical models of non-Hodgkin lymphoma. Blood, 2017, 129, 2408-2419.	0.6	52
32	Proteomic footprint of myocardial ischemia/reperfusion injury: Longitudinal study of the at-risk and remote regions in the pig model. Scientific Reports, 2017, 7, 12343.	1.6	37
33	CXCL6 is an important paracrine factor in the pro-angiogenic human cardiac progenitor-like cell secretome. Scientific Reports, 2017, 7, 12490.	1.6	39
34	Immune system deregulation in hypertensive patients chronically RAS suppressed developing albuminuria. Scientific Reports, 2017, 7, 8894.	1.6	13
35	A clinical perspective on the utility of alpha 1 antichymotrypsin for the early diagnosis of calcific aortic stenosis. Clinical Proteomics, 2017, 14, 12.	1.1	14
36	A multicentric study to evaluate the use of relative retention times in targeted proteomics. Journal of Proteomics, 2017, 152, 138-149.	1.2	9

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37	Kalirin and CHD7: novel endothelial dysfunction indicators in circulating extracellular vesicles from hypertensive patients with albuminuria. Oncotarget, 2017, 8, 15553-15562.	0.8	20
38	Urinary exosomes reveal protein signatures in hypertensive patients with albuminuria. Oncotarget, 2017, 8, 44217-44231.	0.8	33
39	The intracellular bacterium Anaplasma phagocytophilum selectively manipulates the levels of vertebrate host proteins in the tick vector Ixodes scapularis. Parasites and Vectors, 2016, 9, 467.	1.0	33
40	Dissecting the proteome dynamics of the early heat stress response leading to plant survival or death in Arabidopsis. Plant, Cell and Environment, 2016, 39, 1264-1278.	2.8	94
41	Arabidopsis DNA polymerase Ïµ recruits components of Polycomb repressor complex to mediate epigenetic gene silencing. Nucleic Acids Research, 2016, 44, 5597-5614.	6.5	34
42	HEY1 functions are regulated by its phosphorylation at Ser-68. Bioscience Reports, 2016, 36, .	1.1	13
43	Vascular Proteomics. , 2016, , 105-122.		0
44	Proteome-wide alterations on adipose tissue from obese patients as age-, diabetes- and gender-specific hallmarks. Scientific Reports, 2016, 6, 25756.	1.6	61
45	Paraoxonase-1 overexpression prevents experimental abdominal aortic aneurysm progression. Clinical Science, 2016, 130, 1027-1038.	1.8	17
46	Interplay between hepatic mitochondria-associated membranes, lipid metabolism and caveolin-1 in mice. Scientific Reports, 2016, 6, 27351.	1.6	131
47	Plasma Molecular Signatures in Hypertensive Patients With Reninâ€“Angiotensin System Suppression. Hypertension, 2016, 68, 157-166.	1.3	18
48	Chemoproteomic Approach to Explore the Target Profile of GPCR ligands: Application to 5â€HT_{1A} and 5â€HT₆ Receptors. Chemistry - A European Journal, 2016, 22, 1313-1321.	1.7	15
49	p38Î³ and Î´ promote heart hypertrophy by targeting the mTOR-inhibitory protein DEPTOR for degradation. Nature Communications, 2016, 7, 10477.	5.8	68
50	A Novel Systems-Biology Algorithm for the Analysis of Coordinated Protein Responses Using Quantitative Proteomics. Molecular and Cellular Proteomics, 2016, 15, 1740-1760.	2.5	86
51	iTRAQ proteomic analysis of extracellular matrix remodeling in aortic valve disease. Scientific Reports, 2015, 5, 17290.	1.6	36
52	Intracellular expression of Tat alters mitochondrial functions in T cells: a potential mechanism to understand mitochondrial damage during HIV-1 replication. Retrovirology, 2015, 12, 78.	0.9	27
53	White matter injury restoration after stem cell administration in subcortical ischemic stroke. Stem Cell Research and Therapy, 2015, 6, 121.	2.4	52
54	ApoA-I/HDL-C levels are inversely associated with abdominal aortic aneurysm progression. Thrombosis and Haemostasis, 2015, 113, 1335-1346.	1.8	41

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55	Exploring analytical proteomics platforms toward the definition of human cardiac stem cells receptome. Proteomics, 2015, 15, 1332-1337.	1.3	14
56	Systems Biology of Tissue-Specific Response to Anaplasma phagocytophilum Reveals Differentiated Apoptosis in the Tick Vector Ixodes scapularis. PLoS Genetics, 2015, 11, e1005120.	1.5	139
57	Executioner Caspase-3 and 7 Deficiency Reduces Myocyte Number in the Developing Mouse Heart. PLoS ONE, 2015, 10, e0131411.	1.1	38
58	Phosphatidylcholineâ€Coated Iron Oxide Nanomicelles for In Vivo Prolonged Circulation Time with an Antibiofouling Protein Corona. Chemistry - A European Journal, 2014, 20, 16662-16671.	1.7	26
59	Diabetic nephropathy induces changes in the proteome of human urinary exosomes as revealed by label-free comparative analysis. Journal of Proteomics, 2014, 96, 92-102.	1.2	127
60	Proteomic characterization of human coronary thrombus in patients with ST-segment elevation acute myocardial infarction. Journal of Proteomics, 2014, 109, 368-381.	1.2	33
61	Identification ofCandida albicanswall mannoproteins covalently linked by disulphide and/or alkali-sensitive bridges. Yeast, 2014, 31, 137-144.	0.8	13
62	Labelâ€free proteomic analysis of red blood cell membrane fractions from abdominal aortic aneurysm patients. Proteomics - Clinical Applications, 2014, 8, 626-630.	0.8	11
63	Proteomic characterization of EPCs and CECs â€œin vivoâ€•from acute coronary syndrome patients and control subjects. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 3030-3053.	1.1	10
64	Differential Protein Expression Analysis of Degenerative Aortic Stenosis by iTRAQ Labeling. Methods in Molecular Biology, 2013, 1005, 109-117.	0.4	2
65	Secretome of Human Aortic Valves. Methods in Molecular Biology, 2013, 1005, 237-243.	0.4	4
66	Self-Renewing Human Bone Marrow Mesenspheres Promote Hematopoietic Stem Cell Expansion. Cell Reports, 2013, 3, 1714-1724.	2.9	128
67	Proteomic perspective of Quercus suber somatic embryogenesis. Journal of Proteomics, 2013, 93, 314-325.	1.2	32
68	Characterization and Analysis of Human Arterial Tissue Secretome by 2-DE and nLC-MS/MS. Methods in Molecular Biology, 2013, 1000, 81-90.	0.4	0
69	Identification of Novel Biomarkers of Abdominal Aortic Aneurysms by 2D-DIGE and MALDI-MS from AAA-Thrombus-Conditioned Media. Methods in Molecular Biology, 2013, 1000, 91-101.	0.4	3
70	Unraveling Biomarkers of Abdominal Aortic Aneurisms by iTRAQ Analysis of Depleted Plasma. Methods in Molecular Biology, 2013, 1000, 157-166.	0.4	2
71	Proteomic Analysis of Intraluminal Thrombus Highlights Complement Activation in Human Abdominal Aortic Aneurysms. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2013-2020.	1.1	50
72	The Presence of HIV-1 Tat Protein Second Exon Delays Fas Protein-mediated Apoptosis in CD4+ T Lymphocytes. Journal of Biological Chemistry, 2013, 288, 7626-7644.	1.6	47

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73	Severe acute respiratory syndrome coronavirus accessory proteins 6 and 9b interact in vivo. Virus Research, 2012, 169, 282-288.	1.1	10
74	Attenuated metabolism is a hallmark of obesity as revealed by comparative proteomic analysis of human omental adipose tissue. Journal of Proteomics, 2012, 75, 783-795.	1.2	39
75	Proteome changes in the myocardium of experimental chronic diabetes and hypertension. Journal of Proteomics, 2012, 75, 1816-1829.	1.2	33
76	The multi-reference contrast method: Facilitating set enrichment analysis. Computers in Biology and Medicine, 2012, 42, 188-194.	3.9	5
77	Zampanolide, a Potent New Microtubule-Stabilizing Agent, Covalently Reacts with the Taxane Luminal Site in Tubulin Î±,Î²-Heterodimers and Microtubules. Chemistry and Biology, 2012, 19, 686-698.	6.2	81
78	Uncovering Suitable Reference Proteins for Expression Studies in Human Adipose Tissue with Relevance to Obesity. PLoS ONE, 2012, 7, e30326.	1.1	25
79	PTRF/Cavin-1 and MIF Proteins Are Identified as Non-Small Cell Lung Cancer Biomarkers by Label-Free Proteomics. PLoS ONE, 2012, 7, e33752.	1.1	60
80	Cyclostreptin Derivatives Specifically Target Cellular Tubulin and Further Map the Paclitaxel Site. Biochemistry, 2012, 51, 329-341.	1.2	17
81	Metabolomic study of plasma of patients with abdominal aortic aneurysm. Analytical and Bioanalytical Chemistry, 2012, 403, 1651-1660.	1.9	22
82	Setae from the pine processionary moth (Thaumetopoea pityocampa) contain several relevant allergens. Contact Dermatitis, 2012, 67, 367-374.	0.8	47
83	Secretome analysis of atherosclerotic and non-atherosclerotic arteries reveals dynamic extracellular remodeling during pathogenesis. Journal of Proteomics, 2012, 75, 2960-2971.	1.2	56
84	Protein phosphorylation analysis in archival clinical cancer samples by shotgun and targeted proteomics approaches. Molecular BioSystems, 2011, 7, 2368.	2.9	35
85	Applying selected reaction monitoring to targeted proteomics. Expert Review of Proteomics, 2011, 8, 165-173.	1.3	46
86	Comparative NMR and MS studies on the mechanism of enantioseparation of propranolol with heptakis(2,3-diacetyl-6-sulfo)-Î²-cyclodextrin in capillary electrophoresis with aqueous and non-aqueous electrolytes. Electrophoresis, 2011, 32, 1156-1163.	1.3	44
87	Separation of enantiomers of ephedrine by capillary electrophoresis using cyclodextrins as chiral selectors: Comparative CE, NMR and high resolution MS studies. Electrophoresis, 2011, 32, 2640-2647.	1.3	42
88	Identification of Peroxiredoxin-1 as a Novel Biomarker of Abdominal Aortic Aneurysm. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 935-943.	1.1	75
89	Modeling Human Endometrial Decidualization from the Interaction between Proteome and Secretome. Journal of Clinical Endocrinology and Metabolism, 2011, 96, 706-716.	1.8	53
90	Proteomic Analysis of Polymorphonuclear Neutrophils Identifies Catalase as a Novel Biomarker of Abdominal Aortic Aneurysm: Potential Implication of Oxidative Stress in Abdominal Aortic Aneurysm Progression. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 3011-3019.	1.1	71

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91	SPARC Promotes Cathepsin B-Mediated Melanoma Invasiveness through a Collagen I/Î±2Î²1 Integrin Axis. Journal of Investigative Dermatology, 2011, 131, 2438-2447.	0.3	61
92	Proteomic and Metabolomic Profiles in Atherothrombotic Vascular Disease. Current Atherosclerosis Reports, 2010, 12, 202-208.	2.0	26
93	Proteomic Strategies in the Search of New Biomarkers in Atherothrombosis. Journal of the American College of Cardiology, 2010, 55, 2009-2016.	1.2	41
94	Proteomic Analysis of Annexin A2 Phosphorylation Induced by Microtubule Interfering Agents and Kinesin Spindle Protein Inhibitors. Journal of Proteome Research, 2010, 9, 4649-4660.	1.8	7
95	Protein A-Mediated Multicellular Behavior inStaphylococcus aureus. Journal of Bacteriology, 2009, 191, 832-843.	1.0	267
96	Proteomic analysis of the human receptive versus non-receptive endometrium using differential in-gel electrophoresis and MALDI-MS unveils stathmin 1 and annexin A2 as differentially regulated. Human Reproduction, 2009, 24, 2607-2617.	0.4	110
97	Nitric Oxide Increases Cardiac I K1 by Nitrosylation of Cysteine 76 of Kir2.1 Channels. Circulation Research, 2009, 105, 383-392.	2.0	61
98	Endothelial Nitric Oxide Deficiency Reduces MMP-13â€“Mediated Cleavage of ICAM-1 in Vascular Endothelium. Arteriosclerosis, Thrombosis, and Vascular Biology, 2009, 29, 27-32.	1.1	42
99	15-Deoxi-Î”12,14-prostaglandin J2 is a tubulin-binding agent that destabilizes microtubules and induces mitotic arrest. Biochemical Pharmacology, 2009, 78, 1330-1339.	2.0	21
100	Proteomic analysis from haploid and diploid embryos of Quercus suber L. identifies qualitative and quantitative differential expression patterns. Proteomics, 2009, 9, 4355-4367.	1.3	41
101	Proteomics: New insights into rheumatic diseases. Proteomics - Clinical Applications, 2009, 3, 226-241.	0.8	9
102	Tackling the human adipose tissue proteome to gain insight into obesity and related pathologies. Expert Review of Proteomics, 2009, 6, 353-361.	1.3	24
103	Vascular proteomics, a translational approach: from traditional to novel proteomic techniques. Expert Review of Proteomics, 2009, 6, 461-464.	1.3	8
104	Differential Proteomics of Omental and Subcutaneous Adipose Tissue Reflects Their Unalike Biochemical and Metabolic Properties. Journal of Proteome Research, 2009, 8, 1682-1693.	1.8	94
105	MALDI Profiling of Human Lung Cancer Subtypes. PLoS ONE, 2009, 4, e7731.	1.1	29
106	Application of proteomics technology for analyzing the interactions between host cells and intracellular infectious agents. Proteomics, 2008, 8, 852-873.	1.3	31
107	A study of the Candida albicans cell wall proteome. Proteomics, 2008, 8, 3871-3881.	1.3	88
108	Changes in Escherichia coli outer membrane subproteome under environmental conditions inducing the viable but nonculturable state. FEMS Microbiology Ecology, 2008, 64, 28-36.	1.3	75

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109	Differential proteome of bone marrow mesenchymal stem cells from osteoarthritis patients. Osteoarthritis and Cartilage, 2008, 16, 929-935.	0.6	23
110	Proteomic analysis of human omental adipose tissue in the polycystic ovary syndrome using two-dimensional difference gel electrophoresis and mass spectrometry. Human Reproduction, 2008, 23, 651-661.	0.4	108
111	Nitric oxide elicits functional MMPâ€13 proteinâ€tyrosine nitration during wound repair. FASEB Journal, 2008, 22, 3207-3215.	0.2	38
112	Differential Proteome of Articular Chondrocytes From Patients with Osteoarthritis. Journal of Proteomics and Bioinformatics, 2008, 01, 267-280.	0.4	10
113	Experimental validation of Haldane's hypothesis on the role of infection as an evolutionary force for Metazoans. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13728-13731.	3.3	33
114	Cyclostreptin binds covalently to microtubule pores and lumenal taxoid binding sites. , 2007, 3, 117-125.		130
115	Proteomic analysis of phytopathogenic fungus Botrytis cinerea as a potential tool for identifying pathogenicity factors, therapeutic targets and for basic research. Archives of Microbiology, 2007, 187, 207-215.	1.0	70
116	A proteomic approach to study pea (Pisum sativum) responses to powdery mildew (Erysiphe pisi). Proteomics, 2006, 6, S163-S174.	1.3	90
117	Proteomic and transcriptional characterization of aromatic degradation pathways in Rhodoccocus sp. strainâ€...TFB. Proteomics, 2006, 6, S119-S132.	1.3	49
118	Two-dimensional electrophoresis protein profile of the phytopathogenic fungus Botrytis cinerea. Proteomics, 2006, 6, S88-S96.	1.3	70
119	Modifications in the human Tâ€...cell proteome induced by intracellular HIV-1 Tat protein expression. Proteomics, 2006, 6, S63-S73.	1.3	66
120	Structural analysis of the human respiratory syncytial virus phosphoprotein: characterization of an Î±-helical domain involved in oligomerization. Journal of General Virology, 2006, 87, 159-169.	1.3	65
121	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	9.4	1,710
122	Phosphorylation and subcellular localization of transmissible gastroenteritis virus nucleocapsid protein in infected cells. Journal of General Virology, 2005, 86, 2255-2267.	1.3	52
123	Overexpression of the Multidrug Efflux Pumps MexCD-OprJ and MexEF-OprN Is Associated with a Reduction of Type III Secretion in Pseudomonas aeruginosa. Journal of Bacteriology, 2005, 187, 1384-1391.	1.0	151
124	Identification of Proteins Expressing Differences among Isolates ofMeloidogyne spp. (Nematoda:Â) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Proteome Research, 2005, 4, 1017-1021.	1.8	11
125	Protein Variability in Meloidogyne spp. (Nematoda:â€‰ Meloidogynidae) Revealed by Two-Dimensional Gel Electrophoresis and Mass Spectrometry. Journal of Proteome Research, 2002, 1, 421-427.	1.8	25
126	Cleavage of the human respiratory syncytial virus fusion protein at two distinct sites is required for activation of membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9859-9864.	3.3	193

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127	Evidence of Multiple Regulatory Functions for the PtsN (IIA Ntr) Protein of Pseudomonas putida. Journal of Bacteriology, 2001, 183, 1032-1037.	1.0	50
128	Selective identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry of different types of gluten in foods made with cereal mixtures. Journal of Chromatography A, 1998, 823, 299-306.	1.8	43
129	An innovative sandwich ELISA system based on an antibody cocktail for gluten analysis. FEBS Letters, 1998, 439, 46-50.	1.3	71
130	Conformational studies of a short linear peptide corresponding to a major conserved neutralizing epitope of human respiratory syncytial virus fusion glycoprotein. Biopolymers, 1998, 39, 537-548.	1.2	15
131	A point mutation in the F1 subunit of human respiratory syncytial virus fusion glycoprotein blocks its cell surface transport at an early stage of the exocytic pathway. Journal of General Virology, 1996, 77, 649-660.	1.3	12
132	Mutant forms of the F protein of human respiratory syncytial (RS) virus induce a cytotoxic T lymphocyte response but not a neutralizing antibody response and only transient resistance to RS virus infection. Journal of General Virology, 1996, 77, 1239-1248.	1.3	19
133	Characterization of a Human Astrovirus Serotype 2 Structural Protein (VP26) That Contains an Epitope Involved in Virus Neutralization. Virology, 1994, 201, 312-320.	1.1	94
134	Conformational constraints of conserved neutralizing epitopes from a major antigenic area of human respiratory syncytial virus fusion glycoprotein. Journal of General Virology, 1993, 74, 2567-2577.	1.3	51
135	Analysis of genetic variability in human respiratory syncytial virus by the RNase a mismatch cleavage method: Subtype divergence and heterogeneity. Virology, 1990, 174, 126-134.	1.1	78
136	Frame shift mutations as a novel mechanism for the generation of neutralization resistant mutants of human respiratory syncytial virus.. EMBO Journal, 1990, 9, 4181-4187.	3.5	90
137	Location of a highly conserved neutralizing epitope in the F glycoprotein of human respiratory syncytial virus. Journal of Virology, 1990, 64, 927-930.	1.5	59
138	Nucleotide sequence of the fusion and phosphoprotein genes of human respiratory syncytial (RS) virus Long strain: evidence of subtype genetic heterogeneity. Virus Research, 1988, 10, 249-261.	1.1	70
139	An antigen-binding assay to determine the specificity of monoclonal antibodies against influenza virus and mapping of epitopes. Journal of Virological Methods, 1986, 13, 255-264.	1.0	26