

Luis Menendez-Arias

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2994398/publications.pdf>

Version: 2024-02-01

136
papers

4,560
citations

109321

35
h-index

133252

59
g-index

143
all docs

143
docs citations

143
times ranked

4289
citing authors

#	ARTICLE	IF	CITATIONS
1	Update and latest advances in antiretroviral therapy. Trends in Pharmacological Sciences, 2022, 43, 16-29.	8.7	71
2	A Rapid, Highly Sensitive and Open-Access SARS-CoV-2 Detection Assay for Laboratory and Home Testing. Frontiers in Molecular Biosciences, 2022, 9, 801309.	3.5	29
3	Novel RNase H Inhibitors Blocking RNA-directed Strand Displacement DNA Synthesis by HIV-1 Reverse Transcriptase. Journal of Molecular Biology, 2022, 434, 167507.	4.2	9
4	Lethal Mutagenesis of RNA Viruses and Approved Drugs with Antiviral Mutagenic Activity. Viruses, 2022, 14, 841.	3.3	25
5	Design, synthesis, and biological evaluation of novel double-winged galloyl derivatives as HIV-1 RNase H inhibitors. European Journal of Medicinal Chemistry, 2022, 240, 114563.	5.5	4
6	Reverse Transcriptase: From Transcriptomics to Genome Editing. Trends in Biotechnology, 2021, 39, 194-210.	9.3	31
7	Novel indolylarylsulfone derivatives as covalent HIV-1 reverse transcriptase inhibitors specifically targeting the drug-resistant mutant Y181C. Bioorganic and Medicinal Chemistry, 2021, 30, 115927.	3.0	11
8	An Update on Antiretroviral Therapy. Advances in Experimental Medicine and Biology, 2021, 1322, 31-61.	1.6	1
9	Search, Identification, and Design of Effective Antiviral Drugs Against Pandemic Human Coronaviruses. Advances in Experimental Medicine and Biology, 2021, 1322, 219-260.	1.6	5
10	Analysis and Molecular Determinants of HIV RNase H Cleavage Specificity at the PPT/U3 Junction. Viruses, 2021, 13, 131.	3.3	2
11	Medicinal chemistry strategies for discovering antivirals effective against drug-resistant viruses. Chemical Society Reviews, 2021, 50, 4514-4540.	38.1	84
12	Decoding molnupiravir-induced mutagenesis in SARS-CoV-2. Journal of Biological Chemistry, 2021, 297, 100867.	3.4	38
13	Discovery, optimization, and target identification of novel coumarin derivatives as HIV-1 reverse transcriptase-associated ribonuclease H inhibitors. European Journal of Medicinal Chemistry, 2021, 225, 113769.	5.5	9
14	Nucleocapsid Protein Precursors NCp9 and NCp15 Suppress ATP-Mediated Rescue of AZT-Terminated Primers by HIV-1 Reverse Transcriptase. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	2
15	Discovery and optimization of benzenesulfonamides-based hepatitis B virus capsid modulators via contemporary medicinal chemistry strategies. European Journal of Medicinal Chemistry, 2020, 206, 112714.	5.5	26
16	Defective Strand-Displacement DNA Synthesis Due to Accumulation of Thymidine Analogue Resistance Mutations in HIV-2 Reverse Transcriptase. ACS Infectious Diseases, 2020, 6, 1140-1153.	3.8	3
17	Peptides Mimicking the β 27/ β 28 Loop of HIV-1 Reverse Transcriptase p51 as α -Hotspot-Targeted β -Dimerization Inhibitors. ACS Medicinal Chemistry Letters, 2020, 11, 811-817.	2.8	8
18	Design, synthesis and biological evaluation of 3-hydroxyquinazoline-2,4(1H,3H)-diones as dual inhibitors of HIV-1 reverse transcriptase-associated RNase H and integrase. Bioorganic and Medicinal Chemistry, 2019, 27, 3836-3845.	3.0	12

#	ARTICLE	IF	CITATIONS
19	2019 meeting of the global virus network. <i>Antiviral Research</i> , 2019, 172, 104645.	4.1	5
20	Ribonuclease H, an unexploited target for antiviral intervention against HIV and hepatitis B virus. <i>Antiviral Research</i> , 2019, 171, 104613.	4.1	39
21	Design, synthesis, and biologic evaluation of novel galloyl derivatives as HIV-1 RNase H inhibitors. <i>Chemical Biology and Drug Design</i> , 2019, 93, 582-589.	3.2	14
22	DNA-Dependent DNA Polymerases as Drug Targets in Herpesviruses and Poxviruses. , 2019, , 95-134.		2
23	Amino acid residues in HIV-2 reverse transcriptase that restrict the development of nucleoside analogue resistance through the excision pathway. <i>Journal of Biological Chemistry</i> , 2018, 293, 2247-2259.	3.4	9
24	Transcriptional inaccuracy threshold attenuates differences in RNA-dependent DNA synthesis fidelity between retroviral reverse transcriptases. <i>Scientific Reports</i> , 2018, 8, 627.	3.3	24
25	Template-primer binding affinity and RNase H cleavage specificity contribute to the strand transfer efficiency of HIV-1 reverse transcriptase. <i>Journal of Biological Chemistry</i> , 2018, 293, 13351-13363.	3.4	10
26	5-Hydroxypyrido[2,3-b]pyrazin-6(5H)-one derivatives as novel dual inhibitors of HIV-1 reverse transcriptase-associated ribonuclease H and integrase. <i>European Journal of Medicinal Chemistry</i> , 2018, 155, 714-724.	5.5	31
27	Update on Recent Developments in Small Molecular HIV-1 RNase H Inhibitors (2013-2016): Opportunities and Challenges. <i>Current Medicinal Chemistry</i> , 2018, 25, 1682-1702.	2.4	41
28	Viral polymerases. <i>Virus Research</i> , 2017, 234, 1-3.	2.2	8
29	Fidelity of classwide-resistant HIV-2 reverse transcriptase and differential contribution of K65R to the accuracy of HIV-1 and HIV-2 reverse transcriptases. <i>Scientific Reports</i> , 2017, 7, 44834.	3.3	13
30	SAMHD1 is active in cycling cells permissive to HIV-1 infection. <i>Antiviral Research</i> , 2017, 142, 123-135.	4.1	18
31	Viral reverse transcriptases. <i>Virus Research</i> , 2017, 234, 153-176.	2.2	77
32	1-Hydroxypyrido[2,3-d]pyrimidin-2(1H)-ones as novel selective HIV integrase inhibitors obtained via privileged substructure-based compound libraries. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 5779-5789.	3.0	16
33	Quasispecies and Drug Resistance. , 2017, , 123-147.		2
34	Characterization of two distinct early post-entry blocks to HIV-1 in common marmoset lymphocytes. <i>Scientific Reports</i> , 2016, 6, 37489.	3.3	6
35	HIV-1 Adapts To Replicate in Cells Expressing Common Marmoset APOBEC3G and BST2. <i>Journal of Virology</i> , 2016, 90, 725-740.	3.4	4
36	Ribonuclease H/DNA Polymerase HIV-1 Reverse Transcriptase Dual Inhibitor: Mechanistic Studies on the Allosteric Mode of Action of Isatin-Based Compound RMNC6. <i>PLoS ONE</i> , 2016, 11, e0147225.	2.5	45

#	ARTICLE	IF	CITATIONS
37	Effects of HIV-1 reverse transcriptase connection subdomain mutations on polypurine tract removal and initiation of (+)-strand DNA synthesis. <i>Nucleic Acids Research</i> , 2015, 43, 2259-2270.	14.5	22
38	Quasispecies and Drug Resistance. , 2014, , 1-22.		0
39	Temperature effects on the fidelity of a thermostable HIV reverse transcriptase. <i>FEBS Journal</i> , 2014, 281, 342-351.	4.7	11
40	Nucleoside/nucleotide analog inhibitors of hepatitis B virus polymerase: mechanism of action and resistance. <i>Current Opinion in Virology</i> , 2014, 8, 1-9.	5.4	131
41	Amino acid substitutions away from the RNase H catalytic site increase the thermal stability of Moloney murine leukemia virus reverse transcriptase through RNase H inactivation. <i>Biochemical and Biophysical Research Communications</i> , 2014, 454, 269-274.	2.1	8
42	Cell Cycle Control and HIV-1 Susceptibility Are Linked by CDK6-Dependent CDK2 Phosphorylation of SAMHD1 in Myeloid and Lymphoid Cells. <i>Journal of Immunology</i> , 2014, 193, 1988-1997.	0.8	118
43	Editorial overview: Antivirals and resistance: Advances and challenges ahead. <i>Current Opinion in Virology</i> , 2014, 8, iv-vii.	5.4	18
44	Antiretroviral therapy and drug resistance in human immunodeficiency virus type 2 infection. <i>Antiviral Research</i> , 2014, 102, 70-86.	4.1	88
45	Molecular basis of the association of H208Y and thymidine analogue resistance mutations M41L, L210W and T215Y in the HIV-1 reverse transcriptase of treated patients. <i>Antiviral Research</i> , 2014, 106, 42-52.	4.1	3
46	126 Questions and challenges in HIV drug resistance. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 65, 52.	2.1	0
47	Molecular basis of human immunodeficiency virus type 1 drug resistance: Overview and recent developments. <i>Antiviral Research</i> , 2013, 98, 93-120.	4.1	179
48	Equine Infectious Anemia Virus Retropepsin. , 2013, , 207-210.		0
49	Mouse Mammary Tumor Virus Retropepsin. , 2013, , 223-226.		0
50	Moloney Murine Leukemia Virus Retropepsin. , 2013, , 226-230.		0
51	Antiviral Agents: Structural Basis of Action and Rational Design. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 599-630.	2.4	23
52	Major Groove Binding Track Residues of the Connection Subdomain of Human Immunodeficiency Virus Type 1 Reverse Transcriptase Enhance cDNA Synthesis at High Temperatures. <i>Biochemistry</i> , 2013, 52, 9318-9328.	2.5	11
53	Altered error specificity of RNase H-deficient HIV-1 reverse transcriptases during DNA-dependent DNA synthesis. <i>Nucleic Acids Research</i> , 2013, 41, 4601-4612.	14.5	23
54	HIV Reverse Transcriptase Fidelity, Clade Diversity, and Acquisition of Drug Resistance. , 2013, , 225-252.		6

#	ARTICLE	IF	CITATIONS
55	Clinical, virological and biochemical evidence supporting the association of HIV-1 reverse transcriptase polymorphism R284K and thymidine analogue resistance mutations M41L, L210W and T215Y in patients failing tenofovir/emtricitabine therapy. <i>Retrovirology</i> , 2012, 9, 68.	2.0	7
56	Intrinsic DNA synthesis fidelity of xenotropic murine leukemia virus-related virus reverse transcriptase. <i>FEBS Journal</i> , 2012, 279, 1433-1444.	4.7	10
57	Thermostable HIV-1 group O reverse transcriptase variants with the same fidelity as murine leukaemia virus reverse transcriptase. <i>Biochemical Journal</i> , 2011, 436, 599-607.	3.7	27
58	A structural frame for understanding the role of thymidine analogue resistance mutations in resistance to zidovudine and other nucleoside analogues. <i>Antiviral Therapy</i> , 2011, 16, 943-946.	1.0	3
59	Identification of low-molecular weight inhibitors of HIV-1 reverse transcriptase using a cell-based high-throughput screening system. <i>Antiviral Research</i> , 2011, 91, 94-98.	4.1	9
60	HIV-1 reverse transcriptase connection subdomain mutations involved in resistance to approved non-nucleoside inhibitors. <i>Antiviral Research</i> , 2011, 92, 139-149.	4.1	38
61	Evidence and controversies on the role of XMRV in prostate cancer and chronic fatigue syndrome. <i>Reviews in Medical Virology</i> , 2011, 21, 3-17.	8.3	19
62	Thymidine Analogue Excision and Discrimination Modulated by Mutational Complexes Including Single Amino Acid Deletions of Asp-67 or Thr-69 in HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2011, 286, 20615-20624.	3.4	14
63	A376S in the Connection Subdomain of HIV-1 Reverse Transcriptase Confers Increased Risk of Virological Failure to Nevirapine Therapy. <i>Journal of Infectious Diseases</i> , 2011, 204, 741-752.	4.0	19
64	Molecular basis of human immunodeficiency virus drug resistance: An update. <i>Antiviral Research</i> , 2010, 85, 210-231.	4.1	150
65	Mechanisms Involved in the Selection of HIV-1 Reverse Transcriptase Thumb Subdomain Polymorphisms Associated with Nucleoside Analogue Therapy Failure. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4799-4811.	3.2	29
66	Thymidine Analogue Resistance Suppression by V75I of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2009, 284, 32792-32802.	3.4	14
67	HIV-1 reverse transcriptase thumb subdomain polymorphisms associated with virological failure to nucleoside drug combinations. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 251-258.	3.0	12
68	Mutation Rates and Intrinsic Fidelity of Retroviral Reverse Transcriptases. <i>Viruses</i> , 2009, 1, 1137-1165.	3.3	102
69	Effect of the Human Immunodeficiency Virus Type 1 Reverse Transcriptase Polymorphism Leu-214 on Replication Capacity and Drug Susceptibility. <i>Journal of Virology</i> , 2009, 83, 7434-7439.	3.4	12
70	Increased Thermostability and Fidelity of DNA Synthesis of Wild-Type and Mutant HIV-1 Group O Reverse Transcriptases. <i>Journal of Molecular Biology</i> , 2009, 392, 872-884.	4.2	49
71	A Mg ²⁺ -induced conformational switch rendering a competent DNA polymerase catalytic complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 565-574.	2.6	28
72	Viral Quasispecies: Dynamics, Interactions, and Pathogenesis**Dedicated to Manfred Eigen on the occasion of his 80th birthday, for the insights that his pioneer studies have represented for virology.. , 2008, , 87-118.		27

#	ARTICLE	IF	CITATIONS
73	Mechanistic Insights into the Role of Val75 of HIV-1 Reverse Transcriptase in Misinsertion and Mismatch Extension Fidelity of DNA Synthesis. <i>Journal of Molecular Biology</i> , 2008, 375, 1234-1248.	4.2	32
74	Mechanistic Basis of Zidovudine Hypersusceptibility and Lamivudine Resistance Conferred by the Deletion of Codon 69 in the HIV-1 Reverse Transcriptase Coding Region. <i>Journal of Molecular Biology</i> , 2008, 382, 327-341.	4.2	18
75	Mechanisms of resistance to nucleoside analogue inhibitors of HIV-1 reverse transcriptase. <i>Virus Research</i> , 2008, 134, 124-146.	2.2	122
76	Retroviral reverse transcription. <i>Virus Research</i> , 2008, 134, 1-3.	2.2	13
77	HIV-1 protease inhibitors: effects on HIV-2 replication and resistance. <i>Trends in Pharmacological Sciences</i> , 2008, 29, 42-49.	8.7	51
78	Ritonavir-boosted darunavir: a powerful option for treatment-experienced HIV-1-infected patients. <i>Future Virology</i> , 2008, 3, 423-434.	1.8	0
79	Relative Fitness and Replication Capacity of a Multinucleoside Analogue-Resistant Clinical Human Immunodeficiency Virus Type 1 Isolate with a Deletion of Codon 69 in the Reverse Transcriptase Coding Region. <i>Journal of Virology</i> , 2007, 81, 4713-4721.	3.4	23
80	Mutational Patterns Associated with the 69 Insertion Complex in Multi-drug-resistant HIV-1 Reverse Transcriptase that Confer Increased Excision Activity and High-level Resistance to Zidovudine. <i>Journal of Molecular Biology</i> , 2007, 365, 298-309.	4.2	29
81	HIV-1 Protease Dimer Interface Mutations that Compensate for Viral Reverse Transcriptase Instability in Infectious Virions. <i>Journal of Molecular Biology</i> , 2007, 372, 369-381.	4.2	14
82	Mutational patterns and correlated amino acid substitutions in the HIV-1 protease after virological failure to nelfinavir and lopinavir/ritonavir-based treatments. <i>Journal of Medical Virology</i> , 2007, 79, 1617-1628.	5.0	20
83	HIV protease cleaves poly(A)-binding protein. <i>Biochemical Journal</i> , 2006, 396, 219-226.	3.7	85
84	DR_SEQAN: a PC/Windows-based software to evaluate drug resistance using human immunodeficiency virus type 1 genotypes. <i>BMC Infectious Diseases</i> , 2006, 6, 44.	2.9	10
85	Insertions and Deletions in HIV-1 Reverse Transcriptase: Consequences for Drug Resistance and Viral Fitness. <i>Current Pharmaceutical Design</i> , 2006, 12, 1811-1825.	1.9	33
86	Nucleotide specificity of HIV-1 reverse transcriptases with amino acid substitutions affecting Ala-114. <i>Biochemical Journal</i> , 2005, 387, 221-229.	3.7	14
87	Suppression of Multidrug-resistant HIV-1 Reverse Transcriptase Primer Unblocking Activity by γ -Phosphate-modified Thymidine Analogues. <i>Journal of Molecular Biology</i> , 2005, 349, 451-463.	4.2	44
88	Molecular Mechanisms of Resistance to Nucleoside Analogue Inhibitors of Human Immunodeficiency Virus Reverse Transcriptase. <i>Drug Design Reviews Online</i> , 2005, 2, 101-113.	0.7	5
89	Molecular Determinants of Multi-nucleoside Analogue Resistance in HIV-1 Reverse Transcriptases Containing a Dipeptide Insertion in the Fingers Subdomain. <i>Journal of Biological Chemistry</i> , 2004, 279, 24569-24577.	3.4	42
90	Increased G \rightarrow A Transition Frequencies Displayed by Primer Grip Mutants of Human Immunodeficiency Virus Type 1 Reverse Transcriptase. <i>Journal of Virology</i> , 2004, 78, 1012-1019.	3.4	14

#	ARTICLE	IF	CITATIONS
91	Tryptophan scanning mutagenesis of aromatic residues within the polymerase domain of HIV-1 reverse transcriptase: critical role of Phe-130 for p51 function and second-site revertant restoring viral replication capacity. <i>Virology</i> , 2004, 324, 400-411.	2.4	10
92	Tryptophan scanning mutagenesis of aromatic residues within the polymerase domain of HIV-1 reverse transcriptase: critical role of Phe-130 for p51 function and second-site revertant restoring viral replication capacity. <i>Virology</i> , 2004, 324, 400-400.	2.4	0
93	Relative replication fitness of multi-nucleoside analogue-resistant HIV-1 strains bearing a dipeptide insertion in the fingers subdomain of the reverse transcriptase and mutations at codons 67 and 215. <i>Virology</i> , 2004, 326, 103-112.	2.4	35
94	Moloney murine leukemia virus retropepsin. , 2004, , 176-178.		2
95	HIV-Resistance to Viral Entry Inhibitors. <i>Current Pharmaceutical Design</i> , 2004, 10, 1845-1860.	1.9	27
96	Mouse mammary tumor virus retropepsin. , 2004, , 174-175.		0
97	Equine infectious anemia virus retropepsin. , 2004, , 160-163.		0
98	Curing of foot-and-mouth disease virus from persistently infected cells by ribavirin involves enhanced mutagenesis. <i>Virology</i> , 2003, 311, 339-349.	2.4	149
99	The Eukaryotic Translation Initiation Factor 4GI Is Cleaved by Different Retroviral Proteases. <i>Journal of Virology</i> , 2003, 77, 12392-12400.	3.4	73
100	Fitness Variations and their Impact on the Evolution of Antiretroviral Drug Resistance. <i>Current Drug Targets Infectious Disorders</i> , 2003, 3, 355-371.	2.1	37
101	Molecular basis of fidelity of DNA synthesis and nucleotide specificity of retroviral reverse transcriptases. <i>Progress in Molecular Biology and Translational Science</i> , 2002, 71, 91-147.	1.9	95
102	Insertions in the Reverse Transcriptase Increase both Drug Resistance and Viral Fitness in a Human Immunodeficiency Virus Type 1 Isolate Harboring the Multi-Nucleoside Reverse Transcriptase Inhibitor Resistance 69 Insertion Complex Mutation. <i>Journal of Virology</i> , 2002, 76, 10546-10552.	3.4	40
103	Multidrug-resistant HIV-1 Reverse Transcriptase: Involvement of Ribonucleotide-dependent Phosphorolysis in Cross-resistance to Nucleoside Analogue Inhibitors. <i>Journal of Molecular Biology</i> , 2002, 323, 181-197.	4.2	44
104	Targeting HIV: antiretroviral therapy and development of drug resistance. <i>Trends in Pharmacological Sciences</i> , 2002, 23, 381-388.	8.7	120
105	Investigation of the dNTP-binding site of HIV-1 reverse transcriptase using photoreactive analogs of dNTP. <i>Biochemistry (Moscow)</i> , 2001, 66, 999-1007.	1.5	6
106	Functional Characterization of Chimeric Reverse Transcriptases with Polypeptide Subunits of Highly Divergent HIV-1 Group M and O Strains. <i>Journal of Biological Chemistry</i> , 2001, 276, 27470-27479.	3.4	32
107	Virus population dynamics, fitness variations and the control of viral disease: an update. , 2001, 57, 77-115.		34
108	Coupling Ribose Selection to Fidelity of DNA Synthesis. <i>Journal of Biological Chemistry</i> , 2000, 275, 19759-19767.	3.4	73

#	ARTICLE	IF	CITATIONS
109	Dynamics of dominance of a dipeptide insertion in reverse transcriptase of HIV-1 from patients subjected to prolonged therapy. <i>Virus Research</i> , 2000, 66, 13-26.	2.2	34
110	Viral Quasispecies and Fitness Variations. , 1999, , 141-161.		46
111	Sequence analysis of the polymerase domain of HIV-1 reverse transcriptase in naive and zidovudine-treated individuals reveals a higher polymorphism in alpha-helices as compared with beta-strands. <i>Virus Genes</i> , 1999, 18, 203-210.	1.6	0
112	Mutational analysis of Phe160 within the "palm" subdomain of human immunodeficiency virus type 1 reverse transcriptase 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 290, 615-625.	4.2	27
113	Studies on the Effects of Truncating \pm -Helix E $\tilde{}$ of p66 Human Immunodeficiency Virus Type 1 Reverse Transcriptase on Template $\tilde{}$ Primer Binding and Fidelity of DNA Synthesis. <i>Biochemistry</i> , 1998, 37, 16636-16644.	2.5	33
114	Cytotoxic T-Lymphocyte Responses to HIV-1 Reverse Transcriptase (Review). <i>Viral Immunology</i> , 1998, 11, 167-181.	1.3	17
115	Mispair extension fidelity of human immunodeficiency virus type 1 reverse transcriptases with amino acid substitutions affecting Tyr115. <i>Nucleic Acids Research</i> , 1997, 25, 1383-1389.	14.5	51
116	Viral quasispecies and the problem of vaccine-escape and drug-resistant mutants. , 1997, 48, 99-128.		72
117	Characterization of the Reverse Transcriptase of a Human Immunodeficiency Virus Type 1 Group O Isolate. <i>Virology</i> , 1997, 236, 364-373.	2.4	60
118	RNA virus fitness. , 1997, 7, 87-96.		113
119	Sequence analysis of HIV-1vif gene in Spanish isolates. <i>Virus Genes</i> , 1995, 9, 283-288.	1.6	6
120	Mutational Analysis of the Substrate Binding Pocket of Murine Leukemia Virus Protease and Comparison with Human Immunodeficiency Virus Proteases. <i>Journal of Biological Chemistry</i> , 1995, 270, 29162-29168.	3.4	21
121	Purification and characterization of napin-like proteins from radish. <i>Journal of Experimental Botany</i> , 1994, 45, 1169-1176.	4.8	11
122	Moloney Murine Leukemia Virus Protease: Bacterial Expression and Characterization of the Purified Enzyme. <i>Virology</i> , 1993, 196, 557-563.	2.4	37
123	Isolation and Characterization of a Major Allergen from Oriental Mustard Seeds, <i>Bra j</i>. <i>International Archives of Allergy and Immunology</i> , 1991, 96, 263-270.	2.1	65
124	A BASIC microcomputer program for prediction of B and T cell epitopes in proteins. <i>Bioinformatics</i> , 1990, 6, 101-105.	4.1	4
125	$\hat{2}$ -Turns as structural motifs for the proteolytic processing of seed proteins. <i>FEBS Letters</i> , 1990, 263, 209-212.	2.8	26
126	Epitope mapping of the major allergen from yellow mustard seeds, Sin a l. <i>Molecular Immunology</i> , 1990, 27, 143-150.	2.2	50

#	ARTICLE	IF	CITATIONS
127	Engineering protein thermal stability. <i>Journal of Molecular Biology</i> , 1989, 206, 397-406.	4.2	290
128	A BASIC microcomputer program to calculate the secondary structure of proteins from their circular dichroism spectrum. <i>Bioinformatics</i> , 1988, 4, 479-482.	4.1	7
129	Primary structure of the major allergen of yellow mustard (<i>Sinapis alba</i> L.) seed, <i>Sin a</i> I. <i>FEBS Journal</i> , 1988, 177, 159-166.	0.2	34
130	Primary structure of the major allergen of yellow mustard (<i>Sinapis alba</i> L.) seed, <i>Sin a</i> I. <i>FEBS Journal</i> , 1988, 177, 159-166.	0.2	136
131	Structure of the pigeon lysozyme and its relationship with other type c lysozymes. <i>Comparative Biochemistry and Physiology Part B: Comparative Biochemistry</i> , 1987, 88, 791-796.	0.2	9
132	Relationship between hydrophobic variability and functional properties of β -lactalbumins and type c lysozymes. <i>Journal of Theoretical Biology</i> , 1987, 126, 91-100.	1.7	4
133	A structural comparison of type c lysozymes based on their hydrophobic profiles. <i>Journal of Theoretical Biology</i> , 1987, 127, 221-228.	1.7	0
134	Molecular and spectroscopic characterisation of a low molecular weight seed storage protein from yellow mustard (<i>Sinapis alba</i> L.). <i>International Journal of Biochemistry & Cell Biology</i> , 1987, 19, 899-907.	0.5	45
135	Amino acid sequence around the cysteine residues of pigeon egg-white lysozyme: Comparative study with other type c lysozymes. <i>Comparative Biochemistry and Physiology Part B: Comparative Biochemistry</i> , 1985, 82, 639-642.	0.2	2
136	Comparative study on the secondary structure of lysozymes from different sources. <i>Comparative Biochemistry and Physiology Part B: Comparative Biochemistry</i> , 1984, 77, 83-88.	0.2	18