

Andrew Cr Martin

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

2,353
citations

331670

21
h-index

501196

28
g-index

30
all docs

30
docs citations

30
times ranked

2763
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibody-antigen Interactions: Contact Analysis and Binding Site Topography. <i>Journal of Molecular Biology</i> , 1996, 262, 732-745.	4.2	456
2	Structural Families in Loops of Homologous Proteins: Automatic Classification, Modelling and Application to Antibodies. <i>Journal of Molecular Biology</i> , 1996, 263, 800-815.	4.2	257
3	Analysis of the Antigen Combining Site: Correlations Between Length and Sequence Composition of the Hypervariable Loops and the Nature of the Antigen. <i>Journal of Molecular Biology</i> , 2003, 325, 337-354.	4.2	244
4	Analysis and improvements to Kabat and structurally correct numbering of antibody variable domains. <i>Molecular Immunology</i> , 2008, 45, 3832-3839.	2.2	190
5	Accessing the Kabat antibody sequence database by computer. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 130-133.	2.6	159
6	abYsis: Integrated Antibody Sequence and Structure Management, Analysis, and Prediction. <i>Journal of Molecular Biology</i> , 2017, 429, 356-364.	4.2	141
7	Integrating mutation data and structural analysis of the TP53 tumor-suppressor protein. <i>Human Mutation</i> , 2002, 19, 149-164.	2.5	122
8	Accessing the Kabat antibody sequence database by computer. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 130-133.	2.6	97
9	Analyzing the "Degree of Humanness" of Antibody Sequences. <i>Journal of Molecular Biology</i> , 2007, 369, 852-862.	4.2	91
10	Functional and modelling studies of the binding of human monoclonal anti-DNA antibodies to DNA. <i>Molecular Immunology</i> , 1996, 33, 471-483.	2.2	62
11	Dihydrofolate reductase: a potential drug target in trypanosomes and leishmania. <i>Journal of Computer-Aided Molecular Design</i> , 1998, 12, 241-257.	2.9	55
12	[6] Molecular modeling of antibody combining sites. <i>Methods in Enzymology</i> , 1991, 203, 121-153.	1.0	53
13	Analysis of Void Volumes in Proteins and Application to Stability of the p53 Tumour Suppressor Protein. <i>Journal of Molecular Biology</i> , 2004, 344, 1199-1209.	4.2	52
14	The SAAPdb web resource: A large-scale structural analysis of mutant proteins. <i>Human Mutation</i> , 2009, 30, 616-624.	2.5	51
15	Germline VH/VL pairing in antibodies. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 523-530.	2.1	50
16	G6PDdb, an integrated database of glucose-6-phosphate dehydrogenase (G6PD) mutations. <i>Human Mutation</i> , 2002, 19, 217-224.	2.5	39
17	The SAAP pipeline and database: tools to analyze the impact and predict the pathogenicity of mutations. <i>BMC Genomics</i> , 2013, 14, S4.	2.8	35
18	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. <i>MAbs</i> , 2022, 14, 2020082.	5.2	35

#	ARTICLE	IF	CITATIONS
19	The Humanness of Macaque Antibody Sequences. <i>Journal of Molecular Biology</i> , 2010, 396, 1439-1450.	4.2	33
20	Molecular Characterization of a Novel Intracellular ADP-Ribosyl Cyclase. <i>PLoS ONE</i> , 2007, 2, e797.	2.5	29
21	Compensated Pathogenic Deviations: Analysis of Structural Effects. <i>Journal of Molecular Biology</i> , 2010, 396, 19-30.	4.2	27
22	A single backmutation in the human kV framework of a previously unsuccessfully humanized antibody restores the binding activity and increases the secretion in cos cells. <i>Molecular Immunology</i> , 1999, 36, 709-719.	2.2	18
23	Molecular characterization of a novel cell surface ADP-ribosyl cyclase from the sea urchin. <i>Cellular Signalling</i> , 2008, 20, 2347-2355.	3.6	15
24	Automatically extracting functionally equivalent proteins from SwissProt. <i>BMC Bioinformatics</i> , 2008, 9, 418.	2.6	13
25	Characterization of pathogenic germline mutations in human Protein Kinases. <i>BMC Bioinformatics</i> , 2011, 12, S1.	2.6	10
26	An integrated approach to the interpretation of Single Amino Acid Polymorphisms within the framework of CATH and Gene3D. <i>BMC Bioinformatics</i> , 2009, 10, S5.	2.6	9
27	Compensated pathogenic deviations. <i>Biomolecular Concepts</i> , 2011, 2, 281-292.	2.2	7
28	Extracting human antibody sequences from public databases for antibody humanization: high frequency of species assignment errors. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 403-408.	2.1	3
29	Modelling Antibodies: Approach and Perspective. <i>Lupus</i> , 1994, 3, 365-366.	1.6	0