Andrew Cr Martin

List of Publications by Year
in descending order

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	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. MAbs, 2022, 14, 2020082.	5.2	35
2	abYsis: Integrated Antibody Sequence and Structure—Management, Analysis, and Prediction. Journal of Molecular Biology, 2017, 429, 356-364.	4.2	141
3	Extracting human antibody sequences from public databases for antibody humanization: high frequency of species assignment errors. Protein Engineering, Design and Selection, 2016, 29, 403-408.	2.1	3
4	The SAAP pipeline and database: tools to analyze the impact and predict the pathogenicity of mutations. BMC Genomics, 2013, 14, S4.	2.8	35
5	Germline VH/VL pairing in antibodies. Protein Engineering, Design and Selection, 2012, 25, 523-530.	2.1	50
6	Characterization of pathogenic germline mutations in human Protein Kinases. BMC Bioinformatics, 2011, 12, S1.	2.6	10
7	Compensated pathogenic deviations. Biomolecular Concepts, 2011, 2, 281-292.	2.2	7
8	Compensated Pathogenic Deviations: Analysis of Structural Effects. Journal of Molecular Biology, 2010, 396, 19-30.	4.2	27
9	The Humanness of Macaque Antibody Sequences. Journal of Molecular Biology, 2010, 396, 1439-1450.	4.2	33
10	An integrated approach to the interpretation of Single Amino Acid Polymorphisms within the framework of CATH and Gene3D. BMC Bioinformatics, 2009, 10, S5.	2.6	9
11	The SAAPdb web resource: A large-scale structural analysis of mutant proteins. Human Mutation, 2009, 30, 616-624.	2.5	51
12	Automatically extracting functionally equivalent proteins from SwissProt. BMC Bioinformatics, 2008, 9, 418.	2.6	13
13	Molecular characterization of a novel cell surface ADP-ribosyl cyclase from the sea urchin. Cellular Signalling, 2008, 20, 2347-2355.	3.6	15
14	Analysis and improvements to Kabat and structurally correct numbering of antibody variable domains. Molecular Immunology, 2008, 45, 3832-3839.	2.2	190
15	Analyzing the "Degree of Humanness" of Antibody Sequences. Journal of Molecular Biology, 2007, 369, 852-862.	4.2	91
16	Molecular Characterization of a Novel Intracellular ADP-Ribosyl Cyclase. PLoS ONE, 2007, 2, e797.	2.5	29
17	Analysis of Void Volumes in Proteins and Application to Stability of the p53 Tumour Suppressor Protein. Journal of Molecular Biology, 2004, 344, 1199-1209.	4.2	52
18	Analysis of the Antigen Combining Site: Correlations Between Length and Sequence Composition of the Hypervariable Loops and the Nature of the Antigen. Journal of Molecular Biology, 2003, 325, 337-354.	4.2	244

#	Article	IF	Citations
19	Integrating mutation data and structural analysis of the TP53 tumor-suppressor protein. Human Mutation, 2002, 19, 149-164.	2.5	122
20	G6PDdb, an integrated database of glucose-6-phosphate dehydrogenase (G6PD) mutations. Human Mutation, 2002, 19, 217-224.	2.5	39
21	A single backmutation in the human kIV framework of a previously unsuccessfully humanized antibody restores the binding activity and increases the secretion in cos cells. Molecular Immunology, 1999, 36, 709-719.	2.2	18
22	Dihydrofolate reductase: a potential drug target in trypanosomes and leishmania. Journal of Computer-Aided Molecular Design, 1998, 12, 241-257.	2.9	55
23	Functional and modelling studies of the binding of human monoclonal anti-DNA antibodies to DNA. Molecular Immunology, 1996, 33, 471-483.	2.2	62
24	Antibody-antigen Interactions: Contact Analysis and Binding Site Topography. Journal of Molecular Biology, 1996, 262, 732-745.	4.2	456
25	Structural Families in Loops of Homologous Proteins: Automatic Classification, Modelling and Application to Antibodies. Journal of Molecular Biology, 1996, 263, 800-815.	4.2	257
26	Accessing the Kabat antibody sequence database by computer. Proteins: Structure, Function and Bioinformatics, 1996, 25, 130-133.	2.6	97
27	Accessing the Kabat antibody sequence database by computer. Proteins: Structure, Function and Bioinformatics, 1996, 25, 130-133.	2.6	159
28	Modelling Antibodies: Approach and Perspective. Lupus, 1994, 3, 365-366.	1.6	0
29	[6] Molecular modeling of antibody combining sites. Methods in Enzymology, 1991, 203, 121-153.	1.0	53