Darren R Flower

List of Publications by Year
in descending order

161 papers	13,605 citations	41323 49 h-index	22808 112 g-index
165 all docs	165 docs citations	165 times ranked	11817 citing authors

#	Article	IF	Citations
1	VaxiJen: a server for prediction of protective antigens, tumour antigens and subunit vaccines. BMC Bioinformatics, 2007, 8, 4.	1.2	1,740
2	The lipocalin protein family: structure and function. Biochemical Journal, 1996, 318, 1-14.	1.7	1,505
3	The lipocalin protein family: structural and sequence overview. BBA - Proteins and Proteomics, 2000, 1482, 9-24.	2.1	717
4	Bovine Î²-lactoglobulin at 1.8 Ã… resolution â€"Â still an enigmatic lipocalin. Structure, 1997, 5, 481-495.	1.6	674
5	AllerTOP v.2â€"a server for in silico prediction of allergens. Journal of Molecular Modeling, 2014, 20, 2278.	0.8	663
6	Pheromone binding to two rodent urinary proteins revealed by X-ray crystallography. Nature, 1992, 360, 186-188.	13.7	374
7	Structure and sequence relationships in the lipocalins and related proteins. Protein Science, 1993, 2, 753-761.	3.1	312
8	On the Properties of Bit String-Based Measures of Chemical Similarity. Journal of Chemical Information and Computer Sciences, 1998, 38, 379-386.	2.8	310
9	AllerTOP - a server for in silico prediction of allergens. BMC Bioinformatics, 2013, 14, S4.	1.2	293
10	Benchmarking B cell epitope prediction: Underperformance of existing methods. Protein Science, 2009, 14, 246-248.	3.1	272
11	Lipocalins: unity in diversity. BBA - Proteins and Proteomics, 2000, 1482, 1-8.	2.1	233
12	MHCPred: a server for quantitative prediction of peptide-MHC binding. Nucleic Acids Research, 2003, 31, 3621-3624.	6.5	228
13	Modelling G-protein-coupled receptors for drug design. BBA - Biomembranes, 1999, 1422, 207-234.	7.9	196
14	Determinants of Human Immunodeficiency Virus Type 1 Escape from the Primary CD8+ Cytotoxic T Lymphocyte Response. Journal of Experimental Medicine, 2004, 200, 1243-1256.	4.2	196
15	The lipocalin protein family: A role in cell regulation. FEBS Letters, 1994, 354, 7-11.	1.3	175
16	A Deletion in the Gene Encoding the CD45 Antigen in a Patient with SCID. Journal of Immunology, 2001, 166, 1308-1313.	0.4	174
17	Identifying candidate subunit vaccines using an alignment-independent method based on principal amino acid properties. Vaccine, 2007, 25, 856-866.	1.7	174
18	Harnessing bioinformatics to discover new vaccines. Drug Discovery Today, 2007, 12, 389-395.	3.2	174

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19	In Silico Identification of Supertypes for Class II MHCs. Journal of Immunology, 2005, 174, 7085-7095.	0.4	173
20	AntiJen: a quantitative immunology database integrating functional, thermodynamic, kinetic, biophysical, and cellular data. Immunome Research, 2005, 1, 4.	0.1	157
21	EpiJen: a server for multistep T cell epitope prediction. BMC Bioinformatics, 2006, 7, 131.	1.2	144
22	Mycobacterium tuberculosis Peptides Presented by HLA-E Molecules Are Targets for Human CD8+ T-Cells with Cytotoxic as well as Regulatory Activity. PLoS Pathogens, 2010, 6, e1000782.	2.1	141
23	JenPep: a database of quantitative functional peptide data for immunology. Bioinformatics, 2002, 18, 434-439.	1.8	137
24	Toward the Quantitative Prediction of T-Cell Epitopes: CoMFA and CoMSIA Studies of Peptides with Affinity for the Class I MHC Molecule HLA-A*0201. Journal of Medicinal Chemistry, 2001, 44, 3572-3581.	2.9	128
25	In silico identified CCR4 antagonists target regulatory T cells and exert adjuvant activity in vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10221-10226.	3.3	126
26	Identifiying Human MHC Supertypes Using Bioinformatic Methods. Journal of Immunology, 2004, 172, 4314-4323.	0.4	123
27	Benchmarking pK(a) prediction. BMC Biochemistry, 2006, 7, 18.	4.4	123
28	Lead Generation Using Pharmacophore Mapping and Three-Dimensional Database Searching: Application to Muscarinic M3 Receptor Antagonists. Journal of Medicinal Chemistry, 1999, 42, 3210-3216.	2.9	120
29	Beyond the superfamily: the lipocalin receptors. BBA - Proteins and Proteomics, 2000, 1482, 327-336.	2.1	116
30	Towards in silico prediction of immunogenic epitopes. Trends in Immunology, 2003, 24, 667-674.	2.9	110
31	Multiple molecular recognition properties of the lipocalin protein family. Journal of Molecular Recognition, 1995, 8, 185-195.	1.1	103
32	Quantitative prediction of mouse class I MHC peptide binding affinity using support vector machine regression (SVR) models. BMC Bioinformatics, 2006, 7, 182.	1.2	103
33	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. Trends in Biotechnology, 2008, 26, 190-200.	4.9	101
34	SVRMHC prediction server for MHC-binding peptides. BMC Bioinformatics, 2006, 7, 463.	1.2	93
35	Computer aided selection of candidate vaccine antigens. Immunome Research, 2010, 6, S1.	0.1	93
36	Additive Method for the Prediction of Protein-Peptide Binding Affinity. Application to the MHC Class I Molecule HLA-A*0201. Journal of Proteome Research, 2002, 1, 263-272.	1.8	89

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37	On the hierarchical classification of G protein-coupled receptors. Bioinformatics, 2007, 23, 3113-3118.	1.8	87
38	Experimentally determined lipocalin structures. BBA - Proteins and Proteomics, 2000, 1482, 46-56.	2.1	81
39	Peptide length significantly influences in vitro affinity for MHC class II molecules. Immunome Research, 2008, 4, 6.	0.1	78
40	JenPep:â€‰ A Novel Computational Information Resource for Immunobiology and Vaccinology. Journal of Chemical Information and Computer Sciences, 2003, 43, 1276-1287.	2.8	77
41	Optimizing amino acid groupings for GPCR classification. Bioinformatics, 2008, 24, 1980-1986.	1.8	70
42	Coupling In Silico and In Vitro Analysis of Peptide-MHC Binding: A Bioinformatic Approach Enabling Prediction of Superbinding Peptides and Anchorless Epitopes. Journal of Immunology, 2004, 172, 7495-7502.	0.4	67
43	MHCPred 2.0. Applied Bioinformatics, 2006, 5, 55-61.	1.7	65
44	Predicting Class II MHC-Peptide binding: a kernel based approach using similarity scores. BMC Bioinformatics, 2006, 7, 501.	1.2	62
45	Physicochemical explanation of peptide binding to HLA-A*0201 major histocompatibility complex: A three-dimensional quantitative structure-activity relationship study. Proteins: Structure, Function and Bioinformatics, 2002, 48, 505-518.	1.5	61
46	AntigenDB: an immunoinformatics database of pathogen antigens. Nucleic Acids Research, 2010, 38, D847-D853.	6.5	58
47	EpiTOPâ€"a proteochemometric tool for MHC class II binding prediction. Bioinformatics, 2010, 26, 2066-2068.	1.8	55
48	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. Bioinformatics, 2016, 32, 821-827.	1.8	55
49	Quantitative online prediction of peptide binding to the major histocompatibility complex. Journal of Molecular Graphics and Modelling, 2004, 22, 195-207.	1.3	54
50	Peptide binding prediction for the human class II MHC allele HLA-DP2: a molecular docking approach. BMC Structural Biology, 2011, 11, 32.	2.3	52
51	Towards the chemometric dissection of peptide â€" HLA-A*0201 binding affinity: comparison of local and global QSAR models. Journal of Computer-Aided Molecular Design, 2005, 19, 203-212.	1.3	51
52	Toward the Discovery of Vaccine Adjuvants: Coupling In Silico Screening and In Vitro Analysis of Antagonist Binding to Human and Mouse CCR4 Receptors. PLoS ONE, 2009, 4, e8084.	1.1	51
53	EpiDOCK: a molecular docking-based tool for MHC class II binding prediction. Protein Engineering, Design and Selection, 2013, 26, 631-634.	1.0	51
54	Toward an atomistic understanding of the immune synapse: Large-scale molecular dynamics simulation of a membrane-embedded TCRâ€"pMHCâ€"CD4 complex. Molecular Immunology, 2008, 45, 1221-1230.	1.0	48

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55	MHC Class I Bound to an Immunodominant Theileria parva Epitope Demonstrates Unconventional Presentation to T Cell Receptors. PLoS Pathogens, 2010, 6, e1001149.	2.1	48
56	Selection of Conserved Epitopes from Hepatitis C Virus for Pan-Populational Stimulation of T-Cell Responses. Clinical and Developmental Immunology, 2013, 2013, 1-10.	3.3	48
57	Structural relationship of streptavidin to the calycin protein superfamily. FEBS Letters, 1993, 333, 99-102.	1.3	47
58	Quantitative approaches to computational vaccinology. Immunology and Cell Biology, 2002, 80, 270-279.	1.0	46
59	Analysis of Peptideâˆ’Protein Binding Using Amino Acid Descriptors:â€‰ Prediction and Experimental Verification for Human Histocompatibility Complex HLA-A*0201. Journal of Medicinal Chemistry, 2005, 48, 7418-7425.	2.9	46
60	Towards the knowledge-based design of universal influenza epitope ensemble vaccines. Bioinformatics, 2016, 32, 3233-3239.	1.8	46
61	HLA-A3 supermotif defined by quantitative structureâ€"activity relationship analysis. Protein Engineering, Design and Selection, 2003, 16, 11-18.	1.0	43
62	Greater CD8+ TCR Heterogeneity and Functional Flexibility in HIV-2 Compared to HIV-1 Infection. Journal of Immunology, 2003, 171, 307-316.	0.4	42
63	PPD v1.0--an integrated, web-accessible database of experimentally determined protein pKa values. Nucleic Acids Research, 2006, 34, D199-D203.	6.5	42
64	Transporter Associated with Antigen Processing Preselection of Peptides Binding to the MHC: A Bioinformatic Evaluation. Journal of Immunology, 2004, 173, 6813-6819.	0.4	40
65	Proteomic applications of automated GPCR classification. Proteomics, 2007, 7, 2800-2814.	1.3	40
66	FIMM, a database of functional molecular immunology: update 2002. Nucleic Acids Research, 2002, 30, 226-229.	6.5	38
67	A comparative molecular similarity index analysis (CoMSIA) study identifies an HLA-A2 binding supermotif. Journal of Computer-Aided Molecular Design, 2002, 16, 535-544.	1.3	36
68	Evolutionary dynamics of hepatitis C virus envelope genes during chronic infection. Journal of General Virology, 2005, 86, 1931-1942.	1.3	36
69	Computational modelling approaches to vaccinology. Pharmacological Research, 2015, 92, 40-45.	3.1	35
70	The HLA-A2-supermotif: a QSAR definitionElectronic supplementary information (ESI) available: matrices for A*6802, A*0206, A*0203, A*0202 and A*0201. See http://www.rsc.org/suppdata/ob/b3/b300707c/. Organic and Biomolecular Chemistry, 2003, 1, 2648.	1.5	34
71	BPROMPT: a consensus server for membrane protein prediction. Nucleic Acids Research, 2003, 31, 3698-3700.	6.5	34
72	Large-scale molecular dynamics simulations of HLA-A*0201 complexed with a tumor-specific antigenic peptide: Can the ?3 and ?2m domains be neglected?. Journal of Computational Chemistry, 2004, 25, 1803-1813.	1.5	34

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73	GPCRTree: online hierarchical classification of GPCR function. BMC Research Notes, 2008, 1, 67.	0.6	33
74	Designing immunogenic peptides. Nature Chemical Biology, 2013, 9, 749-753.	3.9	33
75	Peptide recognition by the T cell receptor: comparison of binding free energies from thermodynamic integration, Poisson–Boltzmann and linear interaction energy approximations. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 2037-2053.	1.6	32
76	Peptide-Based Immunotherapeutics and Vaccines. Journal of Immunology Research, 2014, 2014, 1-2.	0.9	32
77	Quantitative structure–activity relationships and the prediction of MHC supermotifs. Methods, 2004, 34, 444-453.	1.9	31
78	Molecular Basis of Peptide Recognition by the TCR: Affinity Differences Calculated Using Large Scale Computing. Journal of Immunology, 2005, 175, 1715-1723.	0.4	31
79	SERF: A Program for Accessible Surface Area Calculations. Journal of Molecular Graphics and Modelling, 1997, 15, 238-244.	1.3	30
80	Class I T-cell epitope prediction: Improvements using a combination of proteasome cleavage, TAP affinity, and MHC binding. Molecular Immunology, 2006, 43, 2037-2044.	1.0	30
81	In silico design of Mycobacterium tuberculosis epitope ensemble vaccines. Molecular Immunology, 2018, 97, 56-62.	1.0	30
82	Proteomics in Vaccinology and Immunobiology: An Informatics Perspective of the Immunone. Journal of Biomedicine and Biotechnology, 2003, 2003, 267-290.	3.0	29
83	Statistical deconvolution of enthalpic energetic contributions to MHC-peptide binding affinity. BMC Structural Biology, 2006, 6, 5.	2.3	27
84	Peptide binding to the HLA-DRB1 supertype: A proteochemometrics analysis. European Journal of Medicinal Chemistry, 2010, 45, 236-243.	2.6	27
85	On the hydrophobicity of peptides: Comparing empirical predictions of peptide log P values. Bioinformation, 2006, 1, 237-241.	0.2	26
86	Toward Prediction of Class II Mouse Major Histocompatibility Complex Peptide Binding Affinity: in Silico Bioinformatic Evaluation Using Partial Least Squares, a Robust Multivariate Statistical Technique. Journal of Chemical Information and Modeling, 2006, 46, 1491-1502.	2.5	25
87	T-cell epitope prediction and immune complex simulation using molecular dynamics: state of the art and persisting challenges. Immunome Research, 2010, 6, S4.	0.1	25
88	VaxiJen Dataset of Bacterial Immunogens: An Update. Current Computer-Aided Drug Design, 2019, 15, 398-400.	0.8	25
89	The first prokaryotic lipocalins. Trends in Biochemical Sciences, 1995, 20, 498-499.	3.7	24
90	Microarrays in hematology. Current Opinion in Hematology, 2002, 9, 23-29.	1.2	22

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91	Predicting Class I Major Histocompatibility Complex (MHC) Binders Using Multivariate Statistics:â€‰ Comparison of Discriminant Analysis and Multiple Linear Regression. Journal of Chemical Information and Modeling, 2007, 47, 234-238.	2.5	22
92	A comparative molecular similarity indices (CoMSIA) study of peptide binding to the HLA-A3 superfamily. Bioorganic and Medicinal Chemistry, 2003, 11, 2307-2311.	1.4	21
93	LIPPRED: A web server for accurate prediction of lipoprotein signal sequences and cleavage sites. Bioinformation, 2006, 1, 176-179.	0.2	21
94	Using databases and data mining in vaccinology. Expert Opinion on Drug Discovery, 2007, 2, 19-35.	2.5	20
95	MHC Class II Binding Predictionâ€"A Little Help from a Friend. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	20
96	PIP-DB: the Protein Isoelectric Point database. Bioinformatics, 2015, 31, 295-296.	1.8	20
97	In silico design of knowledge-based Plasmodium falciparum epitope ensemble vaccines. Journal of Molecular Graphics and Modelling, 2017, 78, 195-205.	1.3	20
98	Modeling the Peptideâ^'T Cell Receptor Interaction by the Comparative Molecular Similarity Indices Analysisâ^'Soft Independent Modeling of Class Analogy Technique. Journal of Medicinal Chemistry, 2006, 49, 2193-2199.	2.9	19
99	Receptor-Ligand Binding Sites and Virtual Screening. Current Medicinal Chemistry, 2006, 13, 1283-1304.	1.2	19
100	EPIPOX: Immunoinformatic Characterization of the Shared T-Cell Epitome between Variola Virus and Related Pathogenic Orthopoxviruses. Journal of Immunology Research, 2015, 2015, 1-11.	0.9	19
101	Integrative bioinformatics for functional genome annotation: trawling for G protein-coupled receptors. Seminars in Cell and Developmental Biology, 2004, 15, 693-701.	2.3	19
102	In Silico Prediction of Peptide Binding Affinity to Class I Mouse Major Histocompatibility Complexes:â€‰ A Comparative Molecular Similarity Index Analysis (CoMSIA) Study. Journal of Chemical Information and Modeling, 2005, 45, 1415-1423.	2.5	18
103	Peptide binding to HLA-DP proteins at pH 5.0 and pH 7.0: a quantitative molecular docking study. BMC Structural Biology, 2012, 12, 20.	2.3	17
104	Systematic identification of small molecule adjuvants. Expert Opinion on Drug Discovery, 2012, 7, 807-817.	2.5	17
105	New horizons in mouse immunoinformatics: reliable in silico prediction of mouse class I histocompatibility major complex peptide binding affinity. Organic and Biomolecular Chemistry, 2004, 2, 3274.	1.5	16
106	HLAâ€ÐP2 binding prediction by molecular dynamics simulations. Protein Science, 2011, 20, 1918-1928.	3.1	16
107	Novel perforin mutation in a patient with hemophagocytic lymphohistiocytosis and CD45 abnormal splicing. American Journal of Medical Genetics Part A, 2003, 117A, 255-260.	2.4	15
108	Toward the atomistic simulation of T cell epitopes. Journal of Molecular Graphics and Modelling, 2008, 26, 957-961.	1.3	15

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109	Integrating In Silico and In Vitro Analysis of Peptide Binding Affinity to HLA-Cw*0102: A Bioinformatic Approach to the Prediction of New Epitopes. PLoS ONE, 2009, 4, e8095.	1.1	15
110	Peptide-Based Immunotherapeutics and Vaccines 2017. Journal of Immunology Research, 2018, 2018, 1-2.	0.9	15
111	A statistical physics perspective on alignment-independent protein sequence comparison. Bioinformatics, 2015, 31, 2469-2474.	1.8	14
112	The lipocalin website. BBA - Proteins and Proteomics, 2000, 1482, 351-352.	2.1	12
113	From 'perfect mix' to 'potion magique' â€" regulatory T cells and anti-inflammatory cytokines as adjuvant targets. Nature Reviews Microbiology, 2008, 6, 88-88.	13.6	12
114	Alignment-Independent Techniques for Protein Classification. Current Proteomics, 2008, 5, 217-223.	0.1	12
115	Advances in Predicting and Manipulating the Immunogenicity of Biotherapeutics and Vaccines. BioDrugs, 2009, 23, 231-240.	2.2	11
116	Peptide-Based Immunotherapeutics and Vaccines 2015. Journal of Immunology Research, 2015, 2015, 1-2.	0.9	11
117	Immunoinformatic evaluation of multiple epitope ensembles as vaccine candidates: E coli 536. Bioinformation, 2012, 8, 272-275.	0.2	10
118	Bioinformatics tools for identifying T-cell epitopes. Drug Discovery Today Biosilico, 2004, 2, 18-23.	0.7	9
119	Selectionâ€based design of in silico dengue epitope ensemble vaccines. Chemical Biology and Drug Design, 2019, 93, 21-28.	1.5	9
120	Computational assembly of a human Cytomegalovirus vaccine upon experimental epitope legacy. BMC Bioinformatics, 2019, 20, 476.	1.2	9
121	Histidine Hydrogen Bonding in MHC at pH 5 and pH 7 Modeled by Molecular Docking and Molecular Dynamics Simulations. Current Computer-Aided Drug Design, 2014, 10, 41-49.	0.8	9
122	TATPred: a Bayesian method for the identification of twin arginine translocation pathway signal sequences. Bioinformation, 2006, 1, 184-187.	0.2	9
123	Empirical prediction of peptide octanol-water partition coefficients. Bioinformation, 2006, 1, 257-259.	0.2	9
124	Present Perspectives on the Automated Classification of the G-Protein Coupled Receptors (GPCRs) at the Protein Sequence Level. Current Topics in Medicinal Chemistry, 2011, 11, 1994-2009.	1.0	8
125	In silico prediction of cancer immunogens: current state of the art. BMC Immunology, 2018, 19, 11.	0.9	8
126	Drug Discovery: Today and Tomorrow. Bioinformation, 2020, 16, 1-3.	0.2	8

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127	Beta barrel trans-membrane proteins: Enhanced prediction using a Bayesian approach. Bioinformation, 2006, 1, 231-3.	0.2	8
128	Î²-Sheet topology A new system of nomenclature. FEBS Letters, 1994, 344, 247-250.	1.3	7
129	Automating the identification and analysis of protein Î²-barrels. Protein Engineering, Design and Selection, 1994, 7, 1305-1310.	1.0	6
130	Identification of the HLA-DM/HLA-DR interface. Molecular Immunology, 2008, 45, 1063-1070.	1.0	6
131	Proteins accessible to immune surveillance show significant T-cell epitope depletion: Implications for vaccine design. Molecular Immunology, 2009, 46, 2699-2705.	1.0	6
132	A Cohesive and Integrated Platform for Immunogenicity Prediction. Methods in Molecular Biology, 2016, 1404, 761-770.	0.4	6
133	Combining algorithms to predict Bacterial protein sub-cellular location: Parallel versus concurrent implementations. Bioinformation, 2006, 1, 285-289.	0.2	6
134	ALTER: Eclectic management of molecular structure data. Journal of Molecular Graphics and Modelling, 1997, 15, 161-169.	1.3	5
135	West Nile Virus Vaccine Design by T Cell Epitope Selection: In Silico Analysis of Conservation, Functional Cross-Reactivity with the Human Genome, and Population Coverage. Journal of Immunology Research, 2020, 2020, 1-7.	0.9	5
136	Scrutinizing human MHC polymorphism: Supertype analysis using Poisson-Boltzmann electrostatics and clustering. Journal of Molecular Graphics and Modelling, 2017, 77, 130-136.	1.3	4
137	In Silico Adjuvant Design and Validation. Methods in Molecular Biology, 2017, 1494, 107-125.	0.4	4
138	Designing Epitope Ensemble Vaccines against TB by Selection: Prioritizing Antigens using Predicted Immunogenicity.. Bioinformation, 2017, 13, 220-223.	0.2	4
139	Toward bacterial protein sub-cellular location prediction: single-class discrimminant models for all gram- and gram+ compartments. Bioinformation, 2006, 1, 276-280.	0.2	4
140	Discriminating antigen and non-antigen using proteome dissimilarity: bacterial antigens. Bioinformation, 2010, 4, 445-447.	0.2	4
141	On the utility of alternative amino acid scripts. Bioinformation, 2012, 8, 539-542.	0.2	4
142	FOLD: Integrated analysis and display of protein secondary structure. Journal of Molecular Graphics, 1995, 13, 377-384.	1.7	3
143	Designing HIV gp120 Peptide Vaccines: Rhetoric or Reality for Neuro-AIDS. , 0, , 105-119.		3
144	Multi-class subcellular location prediction for bacterial proteins. Bioinformation, 2006, 1, 260-264.	0.2	3

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145	Discriminating antigen and non-antigen using proteome dissimilarity II: viral and fungal antigens. Bioinformation, 2010, 5, 35-38.	0.2	3
146	Discriminating antigen and non-antigen using proteome dissimilarity III: tumour and parasite antigens. Bioinformation, 2010, 5, 39-42.	0.2	3
147	DSD--an integrated, web-accessible database of Dehydrogenase Enzyme Stereospecificities. BMC Bioinformatics, 2005, 6, 283.	1.2	2
148	The Immune System as Drug Target. Immunology and Immunogenetics Insights, 2013, 5, III.S12145.	1.0	2
149	Alpha helical trans-membrane proteins: Enhanced prediction using a Bayesian approach. Bioinformation, 2006, 1, 234-6.	0.2	2
150	A predictor of membrane class: Discriminating alpha-helical and beta-barrel membrane proteins from non-membranous proteins. Bioinformation, 2006, 1, 208-13.	0.2	2
151	Databases and data mining for computational vaccinology. Current Opinion in Drug Discovery & Development, 2003, 6, 396-400.	1.9	2
152	Towards the Systematic Discovery of Immunomodulatory Adjuvants. , 2013, , 155-180.		1
153	Protein lipograms. Journal of Theoretical Biology, 2017, 430, 109-116.	0.8	1
154	A Benchmark Dataset Comprising Partition and Distribution Coefficients of Linear Peptides. Dataset Papers in Biology, 2013, 2013, 1-4.	0.5	1
155	Computational Chemistry, Informatics, and the Discovery of Vaccines. Current Computer-Aided Drug Design, 2005, 1, 377-395.	0.8	0
156	In Silico QSAR-Based Predictions of Class I and Class II MHC Epitopes. , 2008, , 63-89.		0
157	Chapter 15. The Impact of Genomics, Systems Biology, and Bioinformatics on Drug and Target Discovery: Challenge and Opportunity. RSC Drug Discovery Series, 0, , 397-439.	0.2	0
158	Computational design of a legacy-based epitope vaccine against Human Cytomegalovirus. , 2018, , .		0
159	Computational Vaccinology. , 2009, , 1-20.		0
160	Computational Epitope Mapping. , 2010, , 187-202.		0
161	In Silico Identification of Novel G Protein-Coupled Receptors. Neuromethods, 2011, , 3-18.	0.2	0