Darren R Flower

List of Publications by Year
in descending order

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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	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
2	Drug Discovery: Today and Tomorrow. Bioinformation, 2020, 16, 1-3.	0.2	8
3	Selectionâ€based design of in silico dengue epitope ensemble vaccines. Chemical Biology and Drug Design, 2019, 93, 21-28.	1.5	9
4	Computational assembly of a human Cytomegalovirus vaccine upon experimental epitope legacy. BMC Bioinformatics, 2019, 20, 476.	1.2	9
5	VaxiJen Dataset of Bacterial Immunogens: An Update. Current Computer-Aided Drug Design, 2019, 15, 398-400.	0.8	25
6	In silico design of Mycobacterium tuberculosis epitope ensemble vaccines. Molecular Immunology, 2018, 97, 56-62.	1.0	30
7	Computational design of a legacy-based epitope vaccine against Human Cytomegalovirus. , 2018, , .		0
8	In silico prediction of cancer immunogens: current state of the art. BMC Immunology, 2018, 19, 11.	0.9	8
9	Peptide-Based Immunotherapeutics and Vaccines 2017. Journal of Immunology Research, 2018, 2018, 1-2.	0.9	15
10	In silico design of knowledge-based Plasmodium falciparum epitope ensemble vaccines. Journal of Molecular Graphics and Modelling, 2017, 78, 195-205.	1.3	20
11	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
12	Protein lipograms. Journal of Theoretical Biology, 2017, 430, 109-116.	0.8	1
13	In Silico Adjuvant Design and Validation. Methods in Molecular Biology, 2017, 1494, 107-125.	0.4	4
14	Designing Epitope Ensemble Vaccines against TB by Selection: Prioritizing Antigens using Predicted Immunogenicity.. Bioinformation, 2017, 13, 220-223.	0.2	4
15	A Cohesive and Integrated Platform for Immunogenicity Prediction. Methods in Molecular Biology, 2016, 1404, 761-770.	0.4	6
16	Towards the knowledge-based design of universal influenza epitope ensemble vaccines. Bioinformatics, 2016, 32, 3233-3239.	1.8	46
17	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. Bioinformatics, 2016, 32, 821-827.	1.8	55
18	Peptide-Based Immunotherapeutics and Vaccines 2015. Journal of Immunology Research, 2015, 2015, 1-2.	0.9	11

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19	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
20	A statistical physics perspective on alignment-independent protein sequence comparison. Bioinformatics, 2015, 31, 2469-2474.	1.8	14
21	Computational modelling approaches to vaccinology. Pharmacological Research, 2015, 92, 40-45.	3.1	35
22	PIP-DB: the Protein Isoelectric Point database. Bioinformatics, 2015, 31, 295-296.	1.8	20
23	Peptide-Based Immunotherapeutics and Vaccines. Journal of Immunology Research, 2014, 2014, 1-2.	0.9	32
24	AllerTOP v.2â€"a server for in silico prediction of allergens. Journal of Molecular Modeling, 2014, 20, 2278.	0.8	663
25	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
26	AllerTOP - a server for in silico prediction of allergens. BMC Bioinformatics, 2013, 14, S4.	1.2	293
27	Designing immunogenic peptides. Nature Chemical Biology, 2013, 9, 749-753.	3.9	33
28	EpiDOCK: a molecular docking-based tool for MHC class II binding prediction. Protein Engineering, Design and Selection, 2013, 26, 631-634.	1.0	51
29	Towards the Systematic Discovery of Immunomodulatory Adjuvants. , 2013, , 155-180.		1
30	The Immune System as Drug Target. Immunology and Immunogenetics Insights, 2013, 5, III.S12145.	1.0	2
31	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
32	A Benchmark Dataset Comprising Partition and Distribution Coefficients of Linear Peptides. Dataset Papers in Biology, 2013, 2013, 1-4.	0.5	1
33	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
34	Systematic identification of small molecule adjuvants. Expert Opinion on Drug Discovery, 2012, 7, 807-817.	2.5	17
35	Immunoinformatic evaluation of multiple epitope ensembles as vaccine candidates: E coli 536. Bioinformation, 2012, 8, 272-275.	0.2	10
36	On the utility of alternative amino acid scripts. Bioinformation, 2012, 8, 539-542.	0.2	4

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37	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
38	HLAâ€DP2 binding prediction by molecular dynamics simulations. Protein Science, 2011, 20, 1918-1928.	3.1	16
39	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
40	In Silico Identification of Novel G Protein-Coupled Receptors. Neuromethods, 2011, , 3-18.	0.2	0
41	Peptide binding to the HLA-DRB1 supertype: A proteochemometrics analysis. European Journal of Medicinal Chemistry, 2010, 45, 236-243.	2.6	27
42	Computer aided selection of candidate vaccine antigens. Immunome Research, 2010, 6, S1.	0.1	93
43	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
44	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
45	MHC Class II Binding Predictionâ€"A Little Help from a Friend. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	20
46	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
47	AntigenDB: an immunoinformatics database of pathogen antigens. Nucleic Acids Research, 2010, 38, D847-D853.	6.5	58
48	EpiTOPâ€"a proteochemometric tool for MHC class II binding prediction. Bioinformatics, 2010, 26, 2066-2068.	1.8	55
49	Discriminating antigen and non-antigen using proteome dissimilarity: bacterial antigens. Bioinformation, 2010, 4, 445-447.	0.2	4
50	Discriminating antigen and non-antigen using proteome dissimilarity II: viral and fungal antigens. Bioinformation, 2010, 5, 35-38.	0.2	3
51	Discriminating antigen and non-antigen using proteome dissimilarity III: tumour and parasite antigens. Bioinformation, 2010, 5, 39-42.	0.2	3
52	Computational Epitope Mapping. , 2010, , 187-202.		0
53	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
54	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

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55	Benchmarking B cell epitope prediction: Underperformance of existing methods. Protein Science, 2009, 14, 246-248.	3.1	272
56	Proteins accessible to immune surveillance show significant T-cell epitope depletion: Implications for vaccine design. Molecular Immunology, 2009, 46, 2699-2705.	1.0	6
57	Advances in Predicting and Manipulating the Immunogenicity of Biotherapeutics and Vaccines. BioDrugs, 2009, 23, 231-240.	2.2	11
58	Computational Vaccinology. , 2009, , 1-20.		0
59	Peptide length significantly influences in vitro affinity for MHC class II molecules. Immunome Research, 2008, 4, 6.	0.1	78
60	Toward the atomistic simulation of T cell epitopes. Journal of Molecular Graphics and Modelling, 2008, 26, 957-961.	1.3	15
61	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
62	GPCRTree: online hierarchical classification of GPCR function. BMC Research Notes, 2008, 1, 67.	0.6	33
63	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. Trends in Biotechnology, 2008, 26, 190-200.	4.9	101
64	In Silico QSAR-Based Predictions of Class I and Class II MHC Epitopes. , 2008, , 63-89.		0
65	Identification of the HLA-DM/HLA-DR interface. Molecular Immunology, 2008, 45, 1063-1070.	1.0	6
66	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
67	Alignment-Independent Techniques for Protein Classification. Current Proteomics, 2008, 5, 217-223.	0.1	12
68	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
69	Optimizing amino acid groupings for GPCR classification. Bioinformatics, 2008, 24, 1980-1986.	1.8	70
70	Using databases and data mining in vaccinology. Expert Opinion on Drug Discovery, 2007, 2, 19-35.	2.5	20
71	Identifying candidate subunit vaccines using an alignment-independent method based on principal amino acid properties. Vaccine, 2007, 25, 856-866.	1.7	174
72	On the hierarchical classification of G protein-coupled receptors. Bioinformatics, 2007, 23, 3113-3118.	1.8	87

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73	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
74	Proteomic applications of automated GPCR classification. Proteomics, 2007, 7, 2800-2814.	1.3	40
75	VaxiJen: a server for prediction of protective antigens, tumour antigens and subunit vaccines. BMC Bioinformatics, 2007, 8, 4.	1.2	1,740
76	Harnessing bioinformatics to discover new vaccines. Drug Discovery Today, 2007, 12, 389-395.	3.2	174
77	MHCPred 2.0. Applied Bioinformatics, 2006, 5, 55-61.	1.7	65
78	Toward Prediction of Class II Mouse Major Histocompatibility Complex Peptide Binding Affinity:Â 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
79	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
80	Receptor-Ligand Binding Sites and Virtual Screening. Current Medicinal Chemistry, 2006, 13, 1283-1304.	1.2	19
81	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
82	Benchmarking pK(a) prediction. BMC Biochemistry, 2006, 7, 18.	4.4	123
83	Statistical deconvolution of enthalpic energetic contributions to MHC-peptide binding affinity. BMC Structural Biology, 2006, 6, 5.	2.3	27
84	EpiJen: a server for multistep T cell epitope prediction. BMC Bioinformatics, 2006, 7, 131.	1.2	144
85	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
86	SVRMHC prediction server for MHC-binding peptides. BMC Bioinformatics, 2006, 7, 463.	1.2	93
87	Predicting Class II MHC-Peptide binding: a kernel based approach using similarity scores. BMC Bioinformatics, 2006, 7, 501.	1.2	62
88	PPD v1.0–an integrated, web-accessible database of experimentally determined protein pKa values. Nucleic Acids Research, 2006, 34, D199-D203.	6.5	42
89	LIPPRED: A web server for accurate prediction of lipoprotein signal sequences and cleavage sites. Bioinformation, 2006, 1, 176-179.	0.2	21
90	TATPred: a Bayesian method for the identification of twin arginine translocation pathway signal sequences. Bioinformation, 2006, 1, 184-187.	0.2	9

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91	On the hydrophobicity of peptides: Comparing empirical predictions of peptide log P values. Bioinformation, 2006, 1, 237-241.	0.2	26
92	Empirical prediction of peptide octanol-water partition coefficients. Bioinformation, 2006, 1, 257-259.	0.2	9
93	Multi-class subcellular location prediction for bacterial proteins. Bioinformation, 2006, 1, 260-264.	0.2	3
94	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
95	Combining algorithms to predict Bacterial protein sub-cellular location: Parallel versus concurrent implementations. Bioinformation, 2006, 1, 285-289.	0.2	6
96	Alpha helical trans-membrane proteins: Enhanced prediction using a Bayesian approach. Bioinformation, 2006, 1, 234-6.	0.2	2
97	Beta barrel trans-membrane proteins: Enhanced prediction using a Bayesian approach. Bioinformation, 2006, 1, 231-3.	0.2	8
98	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
99	DSD--an integrated, web-accessible database of Dehydrogenase Enzyme Stereospecificities. BMC Bioinformatics, 2005, 6, 283.	1.2	2
100	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
101	AntiJen: a quantitative immunology database integrating functional, thermodynamic, kinetic, biophysical, and cellular data. Immunome Research, 2005, 1, 4.	0.1	157
102	Computational Chemistry, Informatics, and the Discovery of Vaccines. Current Computer-Aided Drug Design, 2005, 1, 377-395.	0.8	0
103	In Silico Identification of Supertypes for Class II MHCs. Journal of Immunology, 2005, 174, 7085-7095.	0.4	173
104	Evolutionary dynamics of hepatitis C virus envelope genes during chronic infection. Journal of General Virology, 2005, 86, 1931-1942.	1.3	36
105	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
106	Peptide recognition by the T cell receptor: comparison of binding free energies from thermodynamic integration, Poissonâ€“Boltzmann and linear interaction energy approximations. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 2037-2053.	1.6	32
107	Analysis of Peptideâ˜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
108	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

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109	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
110	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
111	Quantitative online prediction of peptide binding to the major histocompatibility complex. Journal of Molecular Graphics and Modelling, 2004, 22, 195-207.	1.3	54
112	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
113	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
114	Identifiying Human MHC Supertypes Using Bioinformatic Methods. Journal of Immunology, 2004, 172, 4314-4323.	0.4	123
115	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
116	Quantitative structureâ€“activity relationships and the prediction of MHC supermotifs. Methods, 2004, 34, 444-453.	1.9	31
117	Bioinformatics tools for identifying T-cell epitopes. Drug Discovery Today Biosilico, 2004, 2, 18-23.	0.7	9
118	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
119	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
120	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
121	Towards in silico prediction of immunogenic epitopes. Trends in Immunology, 2003, 24, 667-674.	2.9	110
122	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
123	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
124	BPROMPT: a consensus server for membrane protein prediction. Nucleic Acids Research, 2003, 31, 3698-3700.	6.5	34
125	HLA-A3 supermotif defined by quantitative structureâ€“activity relationship analysis. Protein Engineering, Design and Selection, 2003, 16, 11-18.	1.0	43
126	MHCPred: a server for quantitative prediction of peptide-MHC binding. Nucleic Acids Research, 2003, 31, 3621-3624.	6.5	228

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127	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
128	Proteomics in Vaccinology and Immunobiology: An Informatics Perspective of the Immunone. Journal of Biomedicine and Biotechnology, 2003, 2003, 267-290.	3.0	29
129	Databases and data mining for computational vaccinology. Current Opinion in Drug Discovery & Development, 2003, 6, 396-400.	1.9	2
130	FIMM, a database of functional molecular immunology: update 2002. Nucleic Acids Research, 2002, 30, 226-229.	6.5	38
131	JenPep: a database of quantitative functional peptide data for immunology. Bioinformatics, 2002, 18, 434-439.	1.8	137
132	Microarrays in hematology. Current Opinion in Hematology, 2002, 9, 23-29.	1.2	22
133	Additive Method for the Prediction of Proteinâ˜Peptide Binding Affinity. Application to the MHC Class I Molecule HLA-A*0201. Journal of Proteome Research, 2002, 1, 263-272.	1.8	89
134	Quantitative approaches to computational vaccinology. Immunology and Cell Biology, 2002, 80, 270-279.	1.0	46
135	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
136	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
137	Toward the Quantitative Prediction of T-Cell Epitopes:Â 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
138	A Deletion in the Gene Encoding the CD45 Antigen in a Patient with SCID. Journal of Immunology, 2001, 166, 1308-1313.	0.4	174
139	Lipocalins: unity in diversity. BBA - Proteins and Proteomics, 2000, 1482, 1-8.	2.1	233
140	Experimentally determined lipocalin structures. BBA - Proteins and Proteomics, 2000, 1482, 46-56.	2.1	81
141	The lipocalin protein family: structural and sequence overview. BBA - Proteins and Proteomics, 2000, 1482, 9-24.	2.1	717
142	The lipocalin website. BBA - Proteins and Proteomics, 2000, 1482, 351-352.	2.1	12
143	Beyond the superfamily: the lipocalin receptors. BBA - Proteins and Proteomics, 2000, 1482, 327-336.	2.1	116
144	Modelling G-protein-coupled receptors for drug design. BBA - Biomembranes, 1999, 1422, 207-234.	7.9	196

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145	Lead Generation Using Pharmacophore Mapping and Three-Dimensional Database Searching:â€‰Application to Muscarinic M3 Receptor Antagonists. Journal of Medicinal Chemistry, 1999, 42, 3210-3216.	2.9	120
146	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
147	Bovine Î²-lactoglobulin at 1.8 Ã… resolution â€”Â still an enigmatic lipocalin. Structure, 1997, 5, 481-495.	1.6	674
148	SERF: A Program for Accessible Surface Area Calculations. Journal of Molecular Graphics and Modelling, 1997, 15, 238-244.	1.3	30
149	ALTER: Eclectic management of molecular structure data. Journal of Molecular Graphics and Modelling, 1997, 15, 161-169.	1.3	5
150	The lipocalin protein family: structure and function. Biochemical Journal, 1996, 318, 1-14.	1.7	1,505
151	The first prokaryotic lipocalins. Trends in Biochemical Sciences, 1995, 20, 498-499.	3.7	24
152	Multiple molecular recognition properties of the lipocalin protein family. Journal of Molecular Recognition, 1995, 8, 185-195.	1.1	103
153	FOLD: Integrated analysis and display of protein secondary structure. Journal of Molecular Graphics, 1995, 13, 377-384.	1.7	3
154	Automating the identification and analysis of protein Î²-barrels. Protein Engineering, Design and Selection, 1994, 7, 1305-1310.	1.0	6
155	Î²-Sheet topology A new system of nomenclature. FEBS Letters, 1994, 344, 247-250.	1.3	7
156	The lipocalin protein family: A role in cell regulation. FEBS Letters, 1994, 354, 7-11.	1.3	175
157	Structure and sequence relationships in the lipocalins and related proteins. Protein Science, 1993, 2, 753-761.	3.1	312
158	Structural relationship of streptavidin to the calycin protein superfamily. FEBS Letters, 1993, 333, 99-102.	1.3	47
159	Pheromone binding to two rodent urinary proteins revealed by X-ray crystallography. Nature, 1992, 360, 186-188.	13.7	374
160	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
161	Designing HIV gp120 Peptide Vaccines: Rhetoric or Reality for Neuro-AIDS. , 0, , 105-119.		3