Chris Bailey-Kellogg

List of Publications by Year
in descending order

109 papers	3,099 citations	159585 30 h-index	197818 49 g-index
116 all docs	116 docs citations	116 times ranked	3694 citing authors

#	Article	IF	Citations
1	Polyfunctional HIV-Specific Antibody Responses Are Associated with Spontaneous HIV Control. PLoS Pathogens, 2016, 12, e1005315.	4.7	220
2	High-throughput, multiplexed IgG subclassing of antigen-specific antibodies from clinical samples. Journal of Immunological Methods, 2012, 386, 117-123.	1.4	197
3	Adjuvant-dependent innate and adaptive immune signatures of risk of SIVmac251 acquisition. Nature Medicine, 2016, 22, 762-770.	30.7	197
4	Multiplexed Fc array for evaluation of antigen-specific antibody effector profiles. Journal of Immunological Methods, 2017, 443, 33-44.	1.4	158
5	Pentavalent HIV-1 vaccine protects against simian-human immunodeficiency virus challenge. Nature Communications, 2017, 8, 15711.	12.8	137
6	Route of immunization defines multiple mechanisms of vaccine-mediated protection against SIV. Nature Medicine, 2018, 24, 1590-1598.	30.7	129
7	The two-faced T cell epitope. Human Vaccines and Immunotherapeutics, 2013, 9, 1577-1586.	3.3	88
8	The NOESY Jigsaw: Automated Protein Secondary Structure and Main-Chain Assignment from Sparse, Unassigned NMR Data. Journal of Computational Biology, 2000, 7, 537-558.	1.6	85
9	Learning context-aware structural representations to predict antigen and antibody binding interfaces. Bioinformatics, 2020, 36, 3996-4003.	4.1	79
10	Protein interaction interface region prediction by geometric deep learning. Bioinformatics, 2021, 37, 2580-2588.	4.1	67
11	Graphical Models of Residue Coupling in Protein Families. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 183-197.	3.0	59
12	Antibody humanization by structure-based computational protein design. MAbs, 2015, 7, 1045-1057.	5.2	58
13	Structure-Guided Deimmunization of Therapeutic Proteins. Journal of Computational Biology, 2013, 20, 152-165.	1.6	54
14	Machine Learning Methods Enable Predictive Modeling of Antibody Feature:Function Relationships in RV144 Vaccinees. PLoS Computational Biology, 2015, 11, e1004185.	3.2	50
15	Accounting for conformational entropy in predicting binding free energies of proteinâ€protein interactions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 444-462.	2.6	49
16	Optimization algorithms for functional deimmunization of therapeutic proteins. BMC Bioinformatics, 2010, 11, 180.	2.6	48
17	Depletion of T Cell Epitopes in Lysostaphin Mitigates Anti-Drug Antibody Response and Enhances Antibacterial Efficacy InÂVivo. Chemistry and Biology, 2015, 22, 629-639.	6.0	48
18	CHOPPI: A web tool for the analysis of immunogenicity risk from host cell proteins in CHOâ€based protein production. Biotechnology and Bioengineering, 2014, 111, 2170-2182.	3.3	47

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19	Divergent Antibody Subclass and Specificity Profiles but Not Protective HLA-B Alleles Are Associated with Variable Antibody Effector Function among HIV-1 Controllers. Journal of Virology, 2014, 88, 2799-2809.	3.4	46
20	Structure-based redesign of lysostaphin yields potent antistaphylococcal enzymes that evade immune cell surveillance. Molecular Therapy - Methods and Clinical Development, 2015, 2, 15021.	4.1	45
21	Diversity of Antiviral IgG Effector Activities Observed in HIV-Infected and Vaccinated Subjects. Journal of Immunology, 2016, 197, 4603-4612.	0.8	44
22	Design and engineering of deimmunized biotherapeutics. Current Opinion in Structural Biology, 2016, 39, 79-88.	5.7	43
23	HCV epitope, homologous to multiple human protein sequences, induces a regulatory T cell response in infected patients. Journal of Hepatology, 2015, 62, 48-55.	3.7	39
24	Structure determination of symmetric homo-oligomers by a complete search of symmetry configuration space, using NMR restraints and van der Waals packing. Proteins: Structure, Function and Bioinformatics, 2006, 65, 203-219.	2.6	38
25	Computationally-driven identification of antibody epitopes. ELife, 2017, 6, .	6.0	37
26	Highâ€resolution definition of humoral immune response correlates of effective immunity againstÂ HIV. Molecular Systems Biology, 2018, 14, e7881.	7.2	37
27	Design and analysis of immune-evading enzymes for ADEPT therapy. Protein Engineering, Design and Selection, 2012, 25, 613-624.	2.1	36
28	A divideâ€andâ€conquer approach to determine the Pareto frontier for optimization of protein engineering experiments. Proteins: Structure, Function and Bioinformatics, 2012, 80, 790-806.	2.6	34
29	Integrated assessment of predicted MHC binding and cross-conservation with self reveals patterns of viral camouflage. BMC Bioinformatics, 2014, 15, S1.	2.6	34
30	Gaussian Processes for Active Data Mining of Spatial Aggregates. , 2005, , .		33
31	Analysis of self-associating proteins by singular value decomposition of solution scattering data. Biophysical Journal, 2008, 94, 4906-4923.	0.5	32
32	Computationally optimized deimmunization libraries yield highly mutated enzymes with low immunogenicity and enhanced activity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5085-E5093.	7.1	32
33	Gene and Protein Sequence Optimization for High-Level Production of Fully Active and Aglycosylated Lysostaphin in Pichia pastoris. Applied and Environmental Microbiology, 2014, 80, 2746-2753.	3.1	30
34	Protein deimmunization via structureâ€based design enables efficient epitope deletion at high mutational loads. Biotechnology and Bioengineering, 2015, 112, 1306-1318.	3.3	29
35	Optimization of Combinatorial Mutagenesis. Journal of Computational Biology, 2011, 18, 1743-1756.	1.6	28
36	Graphical models of proteinâ€“protein interaction specificity from correlated mutations and interaction data. Proteins: Structure, Function and Bioinformatics, 2009, 76, 911-929.	2.6	24

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37	Hypergraph Model of Multi-Residue Interactions in Proteins: Sequentially-Constrained Partitioning Algorithms for Optimization of Site-Directed Protein Recombination. Journal of Computational Biology, 2007, 14, 777-790.	1.6	23
38	Mapping the Pareto Optimal Design Space for a Functionally Deimmunized Biotherapeutic Candidate. PLoS Computational Biology, 2015, 11, e1003988.	3.2	23
39	A Random Graph Approach to NMR Sequential Assignment. Journal of Computational Biology, 2005, 12, 569-583.	1.6	22
40	EpiSweep: Computationally Driven Reengineering of Therapeutic Proteins to Reduce Immunogenicity While Maintaining Function. Methods in Molecular Biology, 2017, 1529, 375-398.	0.9	22
41	Globally deimmunized lysostaphin evades human immune surveillance and enables highly efficacious repeat dosing. Science Advances, 2020, 6, .	10.3	22
42	OPTIMIZATION OF THERAPEUTIC PROTEINS TO DELETE T-CELL EPITOPES WHILE MAINTAINING BENEFICIAL RESIDUE INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2011, 09, 207-229.	0.8	21
43	Computationally driven deletion of broadly distributed T cell epitopes in a biotherapeutic candidate. Cellular and Molecular Life Sciences, 2014, 71, 4869-4880.	5.4	21
44	Site-directed combinatorial construction of chimaeric genes: General method for optimizing assembly of gene fragments. Proteins: Structure, Function and Bioinformatics, 2006, 64, 629-642.	2.6	19
45	Contact replacement for NMR resonance assignment. Bioinformatics, 2008, 24, i205-i213.	4.1	18
46	Structureâ€based redesign of proteins for minimal Tâ€cell epitope content. Journal of Computational Chemistry, 2013, 34, 879-891.	3.3	18
47	Balancing sensitivity and specificity in distinguishing TCR groups by CDR sequence similarity. BMC Bioinformatics, 2019, 20, 241.	2.6	18
48	A complete algorithm to resolve ambiguity for intersubunit NOE assignment in structure determination of symmetric homo-oligomers. Protein Science, 2006, 16, 69-81.	7.6	17
49	Antibody Fabâ€Fc properties outperform titer in predictive models of <scp>SIV</scp> vaccineâ€induced protection. Molecular Systems Biology, 2019, 15, e8747.	7.2	17
50	An efficient randomized algorithm for contact-based NMR backbone resonance assignment. Bioinformatics, 2006, 22, 172-180.	4.1	16
51	A High Throughput MHC II Binding Assay for Quantitative Analysis of Peptide Epitopes. Journal of Visualized Experiments, 2014, , .	0.3	16
52	Development and validation of an epitope prediction tool for swine (PigMatrix) based on the pocket profile method. BMC Bioinformatics, 2015, 16, 290.	2.6	16
53	Fine epitope signature of antibody neutralization breadth at the HIV-1 envelope CD4-binding site. JCI Insight, 2018, 3, .	5.0	16
54	Comprehensive analysis of lectin-glycan interactions reveals determinants of lectin specificity. PLoS Computational Biology, 2021, 17, e1009470.	3.2	16

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55	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
56	Influence-based model decomposition for reasoning about spatially distributed physical systems. Artificial Intelligence, 2001, 130, 125-166.	5.8	15
57	Probabilistic cross-link analysis and experiment planning for high-throughput elucidation of protein structure. Protein Science, 2009, 13, 3298-3313.	7.6	15
58	Protein Design by Sampling an Undirected Graphical Model of Residue Constraints. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 506-516.	3.0	15
59	Structureâ€based design of combinatorial mutagenesis libraries. Protein Science, 2015, 24, 895-908.	7.6	15
60	DisruPPI: structure-based computational redesign algorithm for protein binding disruption. Bioinformatics, 2018, 34, i245-i253.	4.1	15
61	Algorithms for Joint Optimization of Stability and Diversity in Planning Combinatorial Libraries of Chimeric Proteins. Journal of Computational Biology, 2009, 16, 1151-1168.	1.6	14
62	Computationally driven antibody engineering enables simultaneous humanization and thermostabilization. Protein Engineering, Design and Selection, 2016, 29, 419-426.	2.1	14
63	Smarter vaccine design will circumvent regulatory T cell-mediated evasion in chronic HIV and HCV infection. Frontiers in Microbiology, 2014, 5, 502.	3.5	13
64	Reducing Mass Degeneracy in SAR by MS by Stable Isotopic Labeling. Journal of Computational Biology, 2001, 8, 19-36.	1.6	12
65	MHCEpitopeEnergy, a Flexible Rosetta-Based Biotherapeutic Deimmunization Platform. Journal of Chemical Information and Modeling, 2021, 61, 2368-2382.	5.4	12
66	Building blocks and blueprints for bacterial autolysins. PLoS Computational Biology, 2021, 17, e1008889.	3.2	11
67	ALGORITHMS FOR SELECTING BREAKPOINT LOCATIONS TO OPTIMIZE DIVERSITY IN PROTEIN ENGINEERING BY SITE-DIRECTED PROTEIN RECOMBINATION. , 2007, , .		11
68	Robotic Hierarchical Mixing for the Production of Combinatorial Libraries of Proteins and Small Molecules. ACS Combinatorial Science, 2008, 10, 63-68.	3.3	10
69	Analysis of sequence-reactivity space for protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2004, 58, 661-671.	2.6	9
70	A graphical method for analyzing distance restraints using residual dipolar couplings for structure determination of symmetric protein homo-oligomers. Protein Science, 2011, 20, 970-985.	7.6	9
71	Towards conformational fidelity of a quaternary HIV-1 epitope: computational design and directed evolution of a minimal V1V2 antigen. Protein Engineering, Design and Selection, 2018, 31, 121-133.	2.1	8
72	A subgroup algorithm to identify cross-rotation peaks consistent with non-crystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1057-1067.	2.5	7

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73	Protein Fragment Swapping: A Method for Asymmetric, Selective Site-Directed Recombination. Journal of Computational Biology, 2010, 17, 459-475.	1.6	7
74	Diverse antiviral IgG effector activities are predicted by unique biophysical antibody features. Retrovirology, 2021, 18, 35.	2.0	7
75	A Geometric Arrangement Algorithm for Structure Determination of Symmetric Protein Homo-Oligomers from NOEs and RDCs. Journal of Computational Biology, 2011, 18, 1507-1523.	1.6	6
76	Algorithms for optimizing cross-overs in DNA shuffling. BMC Bioinformatics, 2012, 13, S3.	2.6	6
77	Hit-and-run, hit-and-stay, and commensal bacteria present different peptide content when viewed from the perspective of the T cell. Vaccine, 2015, 33, 6922-6929.	3.8	6
78	Pareto Optimization of Combinatorial Mutagenesis Libraries. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1143-1153.	3.0	6
79	Algorithms for selecting breakpoint locations to optimize diversity in protein engineering by site-directed protein recombination. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 31-40.	0.4	6
80	A Hierarchical Grow-and-Match Algorithm for Backbone Resonance Assignments Given 3D Structure. , 2007, , .		5
81	NMR Structural Inference of Symmetric Homo-Oligomers. Journal of Computational Biology, 2011, 18, 1757-1775.	1.6	5
82	Learning Sequence Determinants of Protein:Protein Interaction Specificity with Sparse Graphical Models. Journal of Computational Biology, 2015, 22, 474-486.	1.6	5
83	Characterizing Epitope Binding Regions of Entire Antibody Panels by Combining Experimental and Computational Analysis of Antibody: Antigen Binding Competition. Molecules, 2020, 25, 3659.	3.8	5
84	Induction of cross-reactive HIV-1 specific antibody responses by engineered V1V2 immunogens with reduced conformational plasticity. Vaccine, 2020, 38, 3436-3446.	3.8	5
85	Hypergraph Model of Multi-residue Interactions in Proteins: Sequentiallyâ€“Constrained Partitioning Algorithms for Optimization of Site-Directed Protein Recombination. Lecture Notes in Computer Science, 2006, , 15-29.	1.3	5
86	Stoichiometries and affinities of interacting proteins from concentration series of solution scattering data: decomposition by least squares and quadratic optimization. Journal of Applied Crystallography, 2014, 47, 899-914.	4.5	4
87	Computer-guided binding mode identification and affinity improvement of an LRR protein binder without structure determination. PLoS Computational Biology, 2020, 16, e1008150.	3.2	4
88	A Chimeric Antigen Receptor That Binds to a Conserved Site on MICA. ImmunoHorizons, 2020, 4, 597-607.	1.8	4
89	Learning Sequence Determinants of Protein: Protein Interaction Specificity with Sparse Graphical Models. Lecture Notes in Computer Science, 2014, 8394, 129-143.	1.3	4
90	Combinatorial Resurfacing of Dengue Envelope Protein Domain III Antigens Selectively Ablates Epitopes Associated with Serotype-Specific or Infection-Enhancing Antibody Responses. ACS Combinatorial Science, 2020, 22, 446-456.	3.8	3

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91	A multi-resolution graph convolution network for contiguous epitope prediction. , 2021, , .		3
92	Structure-Guided Deimmunization of Therapeutic Proteins. Lecture Notes in Computer Science, 2012, , 184-198.	1.3	3
93	OPTIMIZING BAYES ERROR FOR PROTEIN STRUCTURE MODEL SELECTION BY STABILITY MUTAGENESIS. , 2008, , .		3
94	Intelligent simulation tools for mining large scientific data sets. New Generation Computing, 1999, 17, 333-347.	3.3	2
95	Functional evolution within a protein superfamily. Proteins: Structure, Function and Bioinformatics, 2006, 63, 697-708.	2.6	2
96	Bioinformaticsâ€driven discovery of novel Clostridioides difficile lysins and experimental comparison with highly active benchmarks. Biotechnology and Bioengineering, 2021, 118, 2482-2492.	3.3	2
97	A Geometric Arrangement Algorithm for Structure Determination of Symmetric Protein Homo-oligomers from NOEs and RDCs. Lecture Notes in Computer Science, 2011, , 222-237.	1.3	2
98	Algorithms for Joint Optimization of Stability and Diversity in Planning Combinatorial Libraries of Chimeric Proteins. , 2008, , 300-314.		2
99	Computational epitope binning reveals functional equivalence of sequence-divergent paratopes. Computational and Structural Biotechnology Journal, 2022, 20, 2169-2180.	4.1	2
100	Planning combinatorial disulfide cross-links for protein fold determination. BMC Bioinformatics, 2011, 12, S5.	2.6	1
101	Structure Discovery from Massive Spatial Data Sets Using Intelligent Simulation Tools. Lecture Notes in Computer Science, 2007, , 158-174.	1.3	1
102	Simultaneous determination of subunit and complex structures of symmetric homo-oligomers from ambiguous NMR data. , 2013, , .		0
103	OCoM-SOCoM. , 2016, , .		0
104	Extended Abstract: Structure Determination of Symmetric Protein Complexes by a Complete Search of Symmetry Configuration Space Using NMR Distance Restraints. Springer Tracts in Advanced Robotics, 2008, , 335-340.	0.4	0
105	Protein Fragment Swapping: A Method for Asymmetric, Selective Site-Directed Recombination. Lecture Notes in Computer Science, 2009, , 321-338.	1.3	0
106	Title is missing!. , 2020, 16, e1008150.		0
107	Title is missing!. , 2020, 16, e1008150.		0
108	Title is missing!. , 2020, 16, e1008150.		0

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109	Title is missing!. , 2020, 16, e1008150.		0