

Brian G Pierce

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

8,209
citations

66234

42
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54797

84
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97
all docs

97
docs citations

97
times ranked

11831
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | ZDOCK server: interactive docking prediction of protein-protein complexes and symmetric multimers. <i>Bioinformatics</i> , 2014, 30, 1771-1773. | 1.8 | 1,313 |
| 2 | Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812. | 2.4 | 762 |
| 3 | Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680. | 9.0 | 513 |
| 4 | Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. <i>PLoS ONE</i> , 2011, 6, e24657. | 1.1 | 490 |
| 5 | ZRANK: Reranking protein docking predictions with an optimized energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1078-1086. | 1.5 | 401 |
| 6 | Updates to the Integrated Protein-Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. <i>Journal of Molecular Biology</i> , 2015, 427, 3031-3041. | 2.0 | 348 |
| 7 | Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. <i>Nucleic Acids Research</i> , 2013, 41, D171-D176. | 6.5 | 274 |
| 8 | Integrating statistical pair potentials into protein complex prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 511-520. | 1.5 | 273 |
| 9 | Protein-protein docking benchmark 2.0: An update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 214-216. | 1.5 | 254 |
| 10 | Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 705-709. | 1.5 | 224 |
| 11 | M-ZDOCK: a grid-based approach for Cn symmetric multimer docking. <i>Bioinformatics</i> , 2005, 21, 1472-1478. | 1.8 | 160 |
| 12 | Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348. | 1.5 | 148 |
| 13 | Benchmarking <code><scp>AlphaFold</scp></code> for protein complex modeling reveals accuracy determinants. <i>Protein Science</i> , 2022, 31, . | 3.1 | 133 |
| 14 | Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302. | 2.0 | 131 |
| 15 | A combination of rescoring and refinement significantly improves protein docking performance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 270-279. | 1.5 | 126 |
| 16 | ZDOCK and RDOCK performance in CAPRI rounds 3, 4, and 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 207-213. | 1.5 | 102 |
| 17 | Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221. | 1.5 | 99 |
| 18 | Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1980-1987. | 1.5 | 87 |

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|----|---|-----|-----------|
| 19 | Global mapping of antibody recognition of the hepatitis C virus E2 glycoprotein: Implications for vaccine design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6946-E6954. | 3.3 | 86 |
| 20 | A flexible docking approach for prediction of T cell receptor-peptide-MHC complexes. <i>Protein Science</i> , 2013, 22, 35-46. | 3.1 | 75 |
| 21 | Prediction of protein-protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404. | 3.1 | 74 |
| 22 | Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823. | 1.5 | 73 |
| 23 | Performance of ZDOCK and ZRANK in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3104-3110. | 1.5 | 72 |
| 24 | Structural Basis for Penetration of the Glycan Shield of Hepatitis C Virus E2 Glycoprotein by a Broadly Neutralizing Human Antibody. <i>Journal of Biological Chemistry</i> , 2015, 290, 10117-10125. | 1.6 | 69 |
| 25 | TCR3d: The T cell receptor structural repertoire database. <i>Bioinformatics</i> , 2019, 35, 5323-5325. | 1.8 | 69 |
| 26 | ATLAS: A database linking binding affinities with structures for wild-type and mutant TCR-pMHC complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 908-916. | 1.5 | 68 |
| 27 | Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. <i>PLoS Computational Biology</i> , 2014, 10, e1003478. | 1.5 | 67 |
| 28 | Structure-based design of a T cell receptor leads to nearly 100-fold improvement in binding affinity for pepMHC. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 948-960. | 1.5 | 66 |
| 29 | An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. <i>Structure</i> , 2021, 29, 606-621.e5. | 1.6 | 65 |
| 30 | Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. <i>Journal of Immunology</i> , 2012, 188, 5819-5823. | 0.4 | 63 |
| 31 | TCRmodel: high resolution modeling of T cell receptors from sequence. <i>Nucleic Acids Research</i> , 2018, 46, W396-W401. | 6.5 | 62 |
| 32 | Cellular origins and genetic landscape of cutaneous gamma delta T cell lymphomas. <i>Nature Communications</i> , 2020, 11, 1806. | 5.8 | 62 |
| 33 | The performance of ZDOCK and ZRANK in rounds 6-11 of CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 719-725. | 1.5 | 61 |
| 34 | Affinity maturation of a broadly neutralizing human monoclonal antibody that prevents acute hepatitis C virus infection in mice. <i>Hepatology</i> , 2016, 64, 1922-1933. | 3.6 | 60 |
| 35 | CoV3D: a database of high resolution coronavirus protein structures. <i>Nucleic Acids Research</i> , 2021, 49, D282-D287. | 6.5 | 58 |
| 36 | Crystal structure of <i>Streptococcus pyogenes</i> EndoS, an immunomodulatory endoglycosidase specific for human IgG antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6714-6719. | 3.3 | 56 |

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|----|---|-----|-----------|
| 37 | Hepatitis C virus vaccine candidates inducing protective neutralizing antibodies. <i>Expert Review of Vaccines</i> , 2016, 15, 1535-1544. | 2.0 | 55 |
| 38 | How structural adaptability exists alongside HLA-A2 bias in the human $\hat{I}\hat{H}^2$ TCR repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1276-85. | 3.3 | 55 |
| 39 | Antigenicity and Immunogenicity of Differentially Glycosylated Hepatitis C Virus E2 Envelope Proteins Expressed in Mammalian and Insect Cells. <i>Journal of Virology</i> , 2019, 93, . | 1.5 | 51 |
| 40 | Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632. | 1.5 | 50 |
| 41 | Structure-Based Design of Hepatitis C Virus Vaccines That Elicit Neutralizing Antibody Responses to a Conserved Epitope. <i>Journal of Virology</i> , 2017, 91, . | 1.5 | 50 |
| 42 | Vaccination with Cancer- and HIV Infection-Associated Endogenous Retrotransposable Elements Is Safe and Immunogenic. <i>Journal of Immunology</i> , 2012, 189, 1467-1479. | 0.4 | 46 |
| 43 | Peptideâ€MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. <i>Journal of Biological Chemistry</i> , 2018, 293, 15991-16005. | 1.6 | 45 |
| 44 | Broadly neutralizing antibodies from an individual that naturally cleared multiple hepatitis C virus infections uncover molecular determinants for E2 targeting and vaccine design. <i>PLoS Pathogens</i> , 2019, 15, e1007772. | 2.1 | 45 |
| 45 | Viral evasion and challenges of hepatitis C virus vaccine development. <i>Current Opinion in Virology</i> , 2016, 20, 55-63. | 2.6 | 44 |
| 46 | Designing a B Cell-Based Vaccine against a Highly Variable Hepatitis C Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 2692. | 1.5 | 43 |
| 47 | Zika virus NS5 protein antagonizes type I interferon production via blocking TBK1 activation. <i>Virology</i> , 2019, 527, 180-187. | 1.1 | 43 |
| 48 | Structural Basis for Clonal Diversity of the Public T Cell Response to a Dominant Human Cytomegalovirus Epitope. <i>Journal of Biological Chemistry</i> , 2015, 290, 29106-29119. | 1.6 | 41 |
| 49 | Structural basis for oligoclonal T cell recognition of a shared p53 cancer neoantigen. <i>Nature Communications</i> , 2020, 11, 2908. | 5.8 | 40 |
| 50 | Evaluating template-based and template-free protein-protein complex structure prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 169-176. | 3.2 | 35 |
| 51 | Mapping Determinants of Virus Neutralization and Viral Escape for Rational Design of a Hepatitis C Virus Vaccine. <i>Frontiers in Immunology</i> , 2018, 9, 1194. | 2.2 | 34 |
| 52 | Exploring the DNA-recognition potential of homeodomains. <i>Genome Research</i> , 2012, 22, 1889-1898. | 2.4 | 26 |
| 53 | High-Throughput Sequencing Analysis of Post-Liver Transplantation HCV E2 Glycoprotein Evolution in the Presence and Absence of Neutralizing Monoclonal Antibody. <i>PLoS ONE</i> , 2014, 9, e100325. | 1.1 | 23 |
| 54 | Anti-CfaE nanobodies provide broad cross-protection against major pathogenic enterotoxigenic <i>Escherichia coli</i> strains, with implications for vaccine design. <i>Scientific Reports</i> , 2021, 11, 2751. | 1.6 | 23 |

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|----|---|-----|-----------|
| 55 | Performance of ZDOCK in CAPRI rounds 20â€“26. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2175-2182. | 1.5 | 22 |
| 56 | Resolving self-association of a therapeutic antibody by formulation optimization and molecular approaches. <i>MAbs</i> , 2014, 6, 1533-1539. | 2.6 | 20 |
| 57 | An Antigenically Diverse, Representative Panel of Envelope Glycoproteins for Hepatitis C Virus Vaccine Development. <i>Gastroenterology</i> , 2022, 162, 562-574. | 0.6 | 20 |
| 58 | Structural assessment of HLA-A2-restricted SARS-CoV-2 spike epitopes recognized by public and private T-cell receptors. <i>Nature Communications</i> , 2022, 13, 19. | 5.8 | 20 |
| 59 | Proteinâ€“Protein Docking: Overview and Performance Analysis. , 2008, 413, 283-314. | | 19 |
| 60 | Design of a native-like secreted form of the hepatitis C virus E1E2 heterodimer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 19 |
| 61 | Mutational analysis of the latency-associated nuclear antigen DNA-binding domain of Kaposi's sarcoma-associated herpesvirus reveals structural conservation among gammaherpesvirus origin-binding proteins. <i>Journal of General Virology</i> , 2010, 91, 2203-2215. | 1.3 | 19 |
| 62 | Structure-Based Design of Hepatitis C Virus E2 Glycoprotein Improves Serum Binding and Cross-Neutralization. <i>Journal of Virology</i> , 2020, 94, . | 1.5 | 17 |
| 63 | Backbone Flexibility of CDR3 and Immune Recognition of Antigens. <i>Journal of Molecular Biology</i> , 2014, 426, 1583-1599. | 2.0 | 16 |
| 64 | A generalized framework for computational design and mutational scanning of T-cell receptor binding interfaces. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 595-606. | 1.0 | 16 |
| 65 | <i>In Vivo</i> and <i>In Vitro</i> Potency of Polyphosphazene Immunoadjuvants with Hepatitis C Virus Antigen and the Role of Their Supramolecular Assembly. <i>Molecular Pharmaceutics</i> , 2021, 18, 726-734. | 2.3 | 16 |
| 66 | Geometrical characterization of T cell receptor binding modes reveals classâ€“specific binding to maximize access to antigen. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 503-513. | 1.5 | 15 |
| 67 | Bioinformatic Requirements for Protein Database Searching Using Predicted Epitopes from Disease-associated Antibodies. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 247-256. | 2.5 | 13 |
| 68 | Performance of ZDOCK and IRAD in CAPRI rounds 28â€“34. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 408-416. | 1.5 | 13 |
| 69 | High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. <i>Bioinformatics</i> , 2021, 36, 5377-5385. | 1.8 | 13 |
| 70 | Structural and energetic profiling of SARS-CoV-2 receptor binding domain antibody recognition and the impact of circulating variants. <i>PLoS Computational Biology</i> , 2021, 17, e1009380. | 1.5 | 13 |
| 71 | Computational Modeling of Hepatitis C Virus Envelope Glycoprotein Structure and Recognition. <i>Frontiers in Immunology</i> , 2018, 9, 1117. | 2.2 | 12 |
| 72 | Computational Modeling of T Cell Receptor Complexes. <i>Methods in Molecular Biology</i> , 2016, 1414, 319-340. | 0.4 | 11 |

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|----|---|-----|-----------|
| 73 | Combinations of Affinity-Enhancing Mutations in a T Cell Receptor Reveal Highly Nonadditive Effects within and between Complementarity Determining Regions and Chains. <i>Biochemistry</i> , 2010, 49, 7050-7059. | 1.2 | 10 |
| 74 | The Missing Heritability in T1D and Potential New Targets for Prevention. <i>Journal of Diabetes Research</i> , 2013, 2013, 1-10. | 1.0 | 9 |
| 75 | An extended motif in the SARS-CoV-2 spike modulates binding and release of host coatomer in retrograde trafficking. <i>Communications Biology</i> , 2022, 5, 115. | 2.0 | 9 |
| 76 | T cell receptors employ diverse strategies to target a p53 cancer neoantigen. <i>Journal of Biological Chemistry</i> , 2022, 298, 101684. | 1.6 | 9 |
| 77 | Molecular Basis of a Million-Fold Affinity Maturation Process in a Protein-Protein Interaction. <i>Journal of Molecular Biology</i> , 2011, 411, 321-328. | 2.0 | 7 |
| 78 | Structure-Based and Rational Design of a Hepatitis C Virus Vaccine. <i>Viruses</i> , 2021, 13, 837. | 1.5 | 7 |
| 79 | Molecular Determinants of Filament Capping Proteins Required for the Formation of Functional Flagella in Gram-Negative Bacteria. <i>Biomolecules</i> , 2021, 11, 1397. | 1.8 | 7 |
| 80 | Induction of broadly neutralizing antibodies using a secreted form of the hepatitis C virus E1E2 heterodimer as a vaccine candidate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112008119. | 3.3 | 7 |
| 81 | Structural Features of Antibody-Peptide Recognition. <i>Frontiers in Immunology</i> , 0, 13, . | 2.2 | 7 |
| 82 | Newcastle disease virus vectors expressing consensus sequence of the H7 HA protein protect broiler chickens and turkeys against highly pathogenic H7N8 virus. <i>Vaccine</i> , 2019, 37, 4956-4962. | 1.7 | 6 |
| 83 | Modeling T cell receptor recognition of CD1-lipid and MR1-metabolite complexes. <i>BMC Bioinformatics</i> , 2014, 15, 319. | 1.2 | 5 |
| 84 | Structural and Biophysical Characterization of the HCV E1E2 Heterodimer for Vaccine Development. <i>Viruses</i> , 2021, 13, 1027. | 1.5 | 5 |
| 85 | Structure Prediction of Protein Complexes. <i>Biological and Medical Physics Series</i> , 2007, , 109-134. | 0.3 | 5 |
| 86 | Modeling and Viewing T Cell Receptors Using TCRmodel and TCR3d. <i>Methods in Molecular Biology</i> , 2020, 2120, 197-212. | 0.4 | 4 |
| 87 | T Cell Receptor Genotype and Ubash3a Determine Susceptibility to Rat Autoimmune Diabetes. <i>Genes</i> , 2021, 12, 852. | 1.0 | 3 |
| 88 | Computational Reprogramming of T Cell Antigen Receptor Binding Properties. <i>Methods in Molecular Biology</i> , 2016, 1414, 305-318. | 0.4 | 2 |
| 89 | Biophysical Characterization of TCR Variants with Reengineered Specificity and Affinity. <i>FASEB Journal</i> , 2015, 29, 571.30. | 0.2 | 0 |