

Steven C Almo

List of Publications by Year in descending order

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Version: 2024-02-01

125
papers

6,925
citations

66343

42
h-index

69250

77
g-index

134
all docs

134
docs citations

134
times ranked

11719
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structural genomics: beyond the Human Genome Project. <i>Nature Genetics</i> , 1999, 23, 151-157. | 21.4 | 369 |
| 2 | Structural basis for co-stimulation by the human CTLA-4/B7-2 complex. <i>Nature</i> , 2001, 410, 604-608. | 27.8 | 323 |
| 3 | Immune responses to SARS-CoV-2 infection in hospitalized pediatric and adult patients. <i>Science Translational Medicine</i> , 2020, 12, . | 12.4 | 298 |
| 4 | Durable antitumor responses to CD47 blockade require adaptive immune stimulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2646-54. | 7.1 | 272 |
| 5 | A metabolic pathway for bile acid dehydroxylation by the gut microbiome. <i>Nature</i> , 2020, 582, 566-570. | 27.8 | 262 |
| 6 | GPRC5D is a target for the immunotherapy of multiple myeloma with rationally designed CAR T cells. <i>Science Translational Medicine</i> , 2019, 11, . | 12.4 | 229 |
| 7 | A naturally occurring antiviral ribonucleotide encoded by the human genome. <i>Nature</i> , 2018, 558, 610-614. | 27.8 | 225 |
| 8 | <scp>GBT</scp>440 increases haemoglobin oxygen affinity, reduces sickling and prolongs <scp>RBC</scp> half-life in a murine model of sickle cell disease. <i>British Journal of Haematology</i> , 2016, 175, 141-153. | 2.5 | 187 |
| 9 | Recent advances in mammalian protein production. <i>FEBS Letters</i> , 2014, 588, 253-260. | 2.8 | 179 |
| 10 | Structure of the profilin-poly-L-proline complex involved in morphogenesis and cytoskeletal regulation. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 953-960. | 8.2 | 154 |
| 11 | The 2.0 Å structure of human hypoxanthine-guanine phosphoribosyltransferase in complex with a transition-state analog inhibitor. <i>Nature Structural Biology</i> , 1999, 6, 588-593. | 9.7 | 148 |
| 12 | Structural genomics of protein phosphatases. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 121-140. | 1.2 | 148 |
| 13 | Discovery of GBT440, an Orally Bioavailable R-State Stabilizer of Sickle Cell Hemoglobin. <i>ACS Medicinal Chemistry Letters</i> , 2017, 8, 321-326. | 2.8 | 129 |
| 14 | Expression, Clinical Significance, and Receptor Identification of the Newest B7 Family Member HHLA2 Protein. <i>Clinical Cancer Research</i> , 2015, 21, 2359-2366. | 7.0 | 125 |
| 15 | The structure of an actin-crosslinking domain from human fimbrin. <i>Nature Structural Biology</i> , 1997, 4, 708-712. | 9.7 | 121 |
| 16 | Structural basis for cancer immunotherapy by the first-in-class checkpoint inhibitor ipilimumab. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4223-E4232. | 7.1 | 121 |
| 17 | Anti-CTLA-4 therapy requires an Fc domain for efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3912-3917. | 7.1 | 121 |
| 18 | Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. <i>Journal of the American Chemical Society</i> , 2017, 139, 11734-11744. | 13.7 | 119 |

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|----|--|------|-----------|
| 19 | Divergent Evolution in Enolase Superfamily: Strategies for Assigning Functions. <i>Journal of Biological Chemistry</i> , 2012, 287, 29-34. | 3.4 | 118 |
| 20 | Panoramic view of a superfamily of phosphatases through substrate profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1974-83. | 7.1 | 118 |
| 21 | Structure of EVH1, a novel proline-rich ligand-binding module involved in cytoskeletal dynamics and neural function. <i>Nature Structural Biology</i> , 1999, 6, 661-666. | 9.7 | 110 |
| 22 | Profilin binds proline-rich ligands in two distinct amide backbone orientations. <i>Nature Structural Biology</i> , 1999, 6, 666-671. | 9.7 | 102 |
| 23 | The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416. | 12.6 | 101 |
| 24 | PD-L1 is an activation-independent marker of brown adipocytes. <i>Nature Communications</i> , 2017, 8, 647. | 12.8 | 97 |
| 25 | Development and Evaluation of a Human Single Chain Variable Fragment (scFv) Derived Bcma Targeted CAR T Cell Vector Leads to a High Objective Response Rate in Patients with Advanced MM. <i>Blood</i> , 2017, 130, 742-742. | 1.4 | 92 |
| 26 | Trypanosomal Nucleoside Hydrolase. A Novel Mechanism from the Structure with a Transition-State Inhibitor. <i>Biochemistry</i> , 1998, 37, 6277-6285. | 2.5 | 89 |
| 27 | Structure Determination and Characterization of <i>Saccharomyces cerevisiae</i> Profilin. <i>Biochemistry</i> , 1998, 37, 11171-11181. | 2.5 | 85 |
| 28 | Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, . | 6.0 | 81 |
| 29 | Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843. | 5.6 | 79 |
| 30 | Development and Evaluation of an Optimal Human Single-Chain Variable Fragment-Derived BCMA-Targeted CAR T Cell Vector. <i>Molecular Therapy</i> , 2018, 26, 1447-1456. | 8.2 | 77 |
| 31 | Viperin Reveals Its True Function. <i>Annual Review of Virology</i> , 2020, 7, 421-446. | 6.7 | 76 |
| 32 | Biosynthesis of Squalene from Farnesyl Diphosphate in Bacteria: Three Steps Catalyzed by Three Enzymes. <i>ACS Central Science</i> , 2015, 1, 77-82. | 11.3 | 69 |
| 33 | Integrative Structure-Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2911-2926. | 3.8 | 67 |
| 34 | Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017, 25, 434-445. | 3.3 | 61 |
| 35 | Structure and Cancer Immunotherapy of the B7 Family Member B7x. <i>Cell Reports</i> , 2014, 9, 1089-1098. | 6.4 | 58 |
| 36 | Aptamer-targeted Antigen Delivery. <i>Molecular Therapy</i> , 2014, 22, 1375-1387. | 8.2 | 58 |

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|----|--|------|-----------|
| 37 | Better and faster: improvements and optimization for mammalian recombinant protein production. <i>Current Opinion in Structural Biology</i> , 2014, 26, 39-43. | 5.7 | 57 |
| 38 | Characterization of the SARS-CoV-2 S Protein: Biophysical, Biochemical, Structural, and Antigenic Analysis. <i>ACS Omega</i> , 2021, 6, 85-102. | 3.5 | 54 |
| 39 | Tissue-Expressed B7-H1 Critically Controls Intestinal Inflammation. <i>Cell Reports</i> , 2014, 6, 625-632. | 6.4 | 53 |
| 40 | Inhibition of SARS-CoV-2 polymerase by nucleotide analogs from a single-molecule perspective. <i>ELife</i> , 2021, 10, . | 6.0 | 53 |
| 41 | Structure-guided development of a high-affinity human Programmed Cell Death-1: Implications for tumor immunotherapy. <i>EBioMedicine</i> , 2017, 17, 30-44. | 6.1 | 52 |
| 42 | Structural Analysis of Adenine Phosphoribosyltransferase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2001, 40, 10800-10809. | 2.5 | 47 |
| 43 | Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4161-9. | 7.1 | 46 |
| 44 | A novel bifunctional transcriptional regulator of riboflavin metabolism in Archaea. <i>Nucleic Acids Research</i> , 2017, 45, gkw1331. | 14.5 | 44 |
| 45 | Synchrotron Protein Footprinting: A Technique to Investigate Protein-Protein Interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 19, 405-418. | 3.5 | 42 |
| 46 | Computational-guided discovery and characterization of a sesquiterpene synthase from <i>Streptomyces clavuligerus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5661-5666. | 7.1 | 42 |
| 47 | An essential bifunctional enzyme in <i>Mycobacterium tuberculosis</i> for itaconate dissimilation and leucine catabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15907-15913. | 7.1 | 42 |
| 48 | Substrate Distortion and the Catalytic Reaction Mechanism of 5-Carboxyvanillate Decarboxylase. <i>Journal of the American Chemical Society</i> , 2016, 138, 826-836. | 13.7 | 41 |
| 49 | Crystal Structure of the Complex of Human FasL and Its Decoy Receptor DcR3. <i>Structure</i> , 2016, 24, 2016-2023. | 3.3 | 39 |
| 50 | General principles of binding between cell surface receptors and multi-specific ligands: A computational study. <i>PLoS Computational Biology</i> , 2017, 13, e1005805. | 3.2 | 39 |
| 51 | Protein production from the structural genomics perspective: achievements and future needs. <i>Current Opinion in Structural Biology</i> , 2013, 23, 335-344. | 5.7 | 37 |
| 52 | Discovery of novel bacterial queuine salvage enzymes and pathways in human pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19126-19135. | 7.1 | 36 |
| 53 | Treatment of Severe COVID-19 with Convalescent Plasma in Bronx, NYC. <i>JCI Insight</i> , 2021, 6, . | 5.0 | 36 |
| 54 | CUE-101, a Novel E7-pHLA-IL2-Fc Fusion Protein, Enhances Tumor Antigen-Specific T-Cell Activation for the Treatment of HPV16-Driven Malignancies. <i>Clinical Cancer Research</i> , 2020, 26, 1953-1964. | 7.0 | 35 |

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|----|---|------|-----------|
| 55 | Diversity-Oriented Synthesis as a Strategy for Fragment Evolution against GSK3 ^{Δ2} . ACS Medicinal Chemistry Letters, 2016, 7, 852-856. | 2.8 | 34 |
| 56 | In vivo detection of antigen-specific CD8+ T cells by immuno-positron emission tomography. Nature Methods, 2020, 17, 1025-1032. | 19.0 | 34 |
| 57 | An HSV-2 single-cycle candidate vaccine deleted in glycoprotein D, gD-2, protects male mice from lethal skin challenge with clinical isolates of HSV-1 and HSV-2. Journal of Infectious Diseases, 2018, 217, 754-758. | 4.0 | 33 |
| 58 | Structural Basis of CD160:HVEM Recognition. Structure, 2019, 27, 1286-1295.e4. | 3.3 | 33 |
| 59 | Mechanism and Structure of ¹³ C-Resorcyate Decarboxylase. Biochemistry, 2018, 57, 3167-3175. | 2.5 | 30 |
| 60 | Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, . | 6.0 | 30 |
| 61 | Loss of quaternary structure is associated with rapid sequence divergence in the OSBS family. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8535-8540. | 7.1 | 29 |
| 62 | ATP-binding Cassette (ABC) Transport System Solute-binding Protein-guided Identification of Novel d-Altritol and Galactitol Catabolic Pathways in Agrobacterium tumefaciens C58. Journal of Biological Chemistry, 2015, 290, 28963-28976. | 3.4 | 29 |
| 63 | A General Strategy for the Discovery of Metabolic Pathways: d-Threitol, l-Threitol, and Erythritol Utilization in Mycobacterium smegmatis. Journal of the American Chemical Society, 2015, 137, 14570-14573. | 13.7 | 29 |
| 64 | Testing the Sulfotransferase Molecular Pore Hypothesis. Journal of Biological Chemistry, 2013, 288, 8619-8626. | 3.4 | 27 |
| 65 | Mechanistic Basis for Functional Promiscuity in the TNF and TNF Receptor Superfamilies: Structure of the LIGHT:DcR3 Assembly. Structure, 2014, 22, 1252-1262. | 3.3 | 27 |
| 66 | Functional assignment of multiple catabolic pathways for d-ribose. Nature Chemical Biology, 2018, 14, 696-705. | 8.0 | 26 |
| 67 | Structural Characterization of the Glycoprotein GP2 Core Domain from the CAS Virus, a Novel Arenavirus-Like Species. Journal of Molecular Biology, 2014, 426, 1452-1468. | 4.2 | 25 |
| 68 | Compensatory Mechanisms Allow Undersized Anchor-Deficient Class I MHC Ligands To Mediate Pathogenic Autoreactive T Cell Responses. Journal of Immunology, 2014, 193, 2135-2146. | 0.8 | 25 |
| 69 | Structural basis for tRNA methylthiolation by the radical SAM enzyme MiaB. Nature, 2021, 597, 566-570. | 27.8 | 25 |
| 70 | Orange Fluorescent Proteins: Structural Studies of LSSmOrange, PSmOrange and PSmOrange2. PLoS ONE, 2014, 9, e99136. | 2.5 | 24 |
| 71 | Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. Nucleic Acids Research, 2015, 43, 4602-4613. | 14.5 | 23 |
| 72 | Mechanistic dissection of the PD-L1:B7-1 co-inhibitory immune complex. PLoS ONE, 2020, 15, e0233578. | 2.5 | 23 |

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|----|--|------|-----------|
| 73 | Inhibition of Zinc-Dependent Histone Deacetylases with a Chemically Triggered Electrophile. <i>ACS Chemical Biology</i> , 2016, 11, 1844-1851. | 3.4 | 21 |
| 74 | Co-stimulate or Co-inhibit Regulatory T Cells, Which Side to Go?. <i>Immunological Investigations</i> , 2016, 45, 813-831. | 2.0 | 21 |
| 75 | A Binary Arginine Methylation Switch on Histone H3 Arginine 2 Regulates Its Interaction with WDR5. <i>Biochemistry</i> , 2020, 59, 3696-3708. | 2.5 | 21 |
| 76 | Structural Insight into the Substrate Scope of Viperin and Viperin-like Enzymes from Three Domains of Life. <i>Biochemistry</i> , 2021, 60, 2116-2129. | 2.5 | 21 |
| 77 | Stilbene epoxidation and detoxification in a <i>Photobacterium luminescens</i> -nematode symbiosis. <i>Journal of Biological Chemistry</i> , 2017, 292, 6680-6694. | 3.4 | 20 |
| 78 | Novel Metabolic Pathways and Regulons for Hexuronate Utilization in Proteobacteria. <i>Journal of Bacteriology</i> , 2019, 201, . | 2.2 | 19 |
| 79 | Photoswitchable Red Fluorescent Protein with a Large Stokes Shift. <i>Chemistry and Biology</i> , 2014, 21, 1402-1414. | 6.0 | 18 |
| 80 | Structural, mutational and biophysical studies reveal a canonical mode of molecular recognition between immune receptor TIGIT and nectin-2. <i>Molecular Immunology</i> , 2017, 81, 151-159. | 2.2 | 18 |
| 81 | A Small Protein Associated with Fungal Energy Metabolism Affects the Virulence of <i>Cryptococcus neoformans</i> in Mammals. <i>PLoS Pathogens</i> , 2016, 12, e1005849. | 4.7 | 17 |
| 82 | Tumor-expressed immune checkpoint B7x promotes cancer progression and antigen-specific CD8 T cell exhaustion and suppressive innate immune cells. <i>Oncotarget</i> , 2017, 8, 82740-82753. | 1.8 | 17 |
| 83 | Viperin triggers ribosome collision-dependent translation inhibition to restrict viral replication. <i>Molecular Cell</i> , 2022, 82, 1631-1642.e6. | 9.7 | 16 |
| 84 | Investigating the role of a backbone to substrate hydrogen bond in OMP decarboxylase using a site-specific amide to ester substitution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15066-15071. | 7.1 | 15 |
| 85 | HVEM structures and mutants reveal distinct functions of binding to LIGHT and BTLA/CD160. <i>Journal of Experimental Medicine</i> , 2021, 218, . | 8.5 | 15 |
| 86 | Active Site and Remote Contributions to Catalysis in Methylthioadenosine Nucleosidases. <i>Biochemistry</i> , 2015, 54, 2520-2529. | 2.5 | 14 |
| 87 | Identification of a novel tRNA wobble uridine modifying activity in the biosynthesis of 5-methoxyuridine. <i>Nucleic Acids Research</i> , 2018, 46, 9160-9169. | 14.5 | 13 |
| 88 | Computational Redesign of PD-1 Interface for PD-L1 Ligand Selectivity. <i>Structure</i> , 2019, 27, 829-836.e3. | 3.3 | 13 |
| 89 | Redesigning HVEM Interface for Selective Binding to LIGHT, BTLA, and CD160. <i>Structure</i> , 2020, 28, 1197-1205.e2. | 3.3 | 13 |
| 90 | A switch from parallel to antiparallel strand orientation in a coiled-coil X-ray structure via two core hydrophobic mutations. <i>Biopolymers</i> , 2015, 104, 178-185. | 2.4 | 12 |

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|-----|--|------|-----------|
| 91 | The active site of the Mycobacterium tuberculosis branched-chain amino acid biosynthesis enzyme dihydroxyacid dehydratase contains a 2Fe ²⁺ S cluster. <i>Journal of Biological Chemistry</i> , 2019, 294, 13158-13170. | 3.4 | 12 |
| 92 | HVEM signaling promotes protective antibody-dependent cellular cytotoxicity (ADCC) vaccine responses to herpes simplex viruses. <i>Science Immunology</i> , 2020, 5, . | 11.9 | 12 |
| 93 | Biochemical characterization of two haloalkane dehalogenases: DccA from <i>Caulobacter crescentus</i> and DsaA from <i>Saccharomonospora azurea</i> . <i>Protein Science</i> , 2016, 25, 877-886. | 7.6 | 11 |
| 94 | Single-Dilution COVID-19 Antibody Test with Qualitative and Quantitative Readouts. <i>MSphere</i> , 2021, 6, . | 2.9 | 11 |
| 95 | Chemical Synthesis of the Antiviral Nucleotide Analogue ddhCTP. <i>Journal of Organic Chemistry</i> , 2021, 86, 8843-8850. | 3.2 | 11 |
| 96 | Increased Heterologous Protein Expression in Drosophila S2 Cells for Massive Production of Immune Ligands/Receptors and Structural Analysis of Human HVEM. <i>Molecular Biotechnology</i> , 2015, 57, 914-922. | 2.4 | 10 |
| 97 | Narrow-Spectrum Antibiotic Targeting of the Radical SAM Enzyme MqnE in Menaquinone Biosynthesis. <i>Biochemistry</i> , 2020, 59, 2562-2575. | 2.5 | 10 |
| 98 | Longitudinally monitored immune biomarkers predict the timing of COVID-19 outcomes. <i>PLoS Computational Biology</i> , 2022, 18, e1009778. | 3.2 | 10 |
| 99 | INI1/SMARCB1 Rpt1 domain mimics TAR RNA in binding to integrase to facilitate HIV-1 replication. <i>Nature Communications</i> , 2021, 12, 2743. | 12.8 | 9 |
| 100 | CAR T Cell Therapy Targeting G Protein-Coupled Receptor Class C Group 5 Member D (GPC5D), a Novel Target for the Immunotherapy of Multiple Myeloma. <i>Blood</i> , 2018, 132, 589-589. | 1.4 | 9 |
| 101 | Can the propensity of protein crystallization be increased by using systematic screening with metals?. <i>Protein Science</i> , 2017, 26, 1704-1713. | 7.6 | 8 |
| 102 | T cell receptor ^α -targeted immunotherapeutics drive selective in vivo HIV- and CMV-specific T cell expansion in humanized mice. <i>Journal of Clinical Investigation</i> , 2021, 131, . | 8.2 | 8 |
| 103 | Temperature-induced conformational changes in prosomatostatin-II: implications for processing. <i>Biochemical Journal</i> , 1998, 334, 275-282. | 3.7 | 7 |
| 104 | Structural Determinants of the 5 ^α -Methylthioinosine Specificity of Plasmodium Purine Nucleoside Phosphorylase. <i>PLoS ONE</i> , 2014, 9, e84384. | 2.5 | 7 |
| 105 | Considerations for Combined Immune Checkpoint Modulation and Radiation Treatment. <i>Radiation Research</i> , 2014, 182, 230-238. | 1.5 | 7 |
| 106 | Identification of Mycobacterial Ribosomal Proteins as Targets for CD4 ⁺ T Cells That Enhance Protective Immunity in Tuberculosis. <i>Infection and Immunity</i> , 2018, 86, . | 2.2 | 7 |
| 107 | Purification, crystallization and structural elucidation of D-galactaro-1,4-lactone cycloisomerase from <i>Agrobacterium tumefaciens</i> involved in pectin degradation. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 36-41. | 0.8 | 7 |
| 108 | Structures of the L27 Domain of Disc Large Homologue 1 Protein Illustrate a Self-Assembly Module. <i>Biochemistry</i> , 2018, 57, 1293-1305. | 2.5 | 6 |

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|-----|--|-----|-----------|
| 109 | Structure of an ABC transporter solute-binding protein specific for the amino sugars glucosamine and galactosamine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 467-472. | 0.8 | 5 |
| 110 | The hidden treasure in your data: phasing with unexpected weak anomalous scatterers from routine data sets. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 184-195. | 0.8 | 5 |
| 111 | Substrate Profile of the Phosphotriesterase Homology Protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 6219-6227. | 2.5 | 5 |
| 112 | Function Discovery and Structural Characterization of a Methylphosphonate Esterase. <i>Biochemistry</i> , 2015, 54, 2919-2930. | 2.5 | 4 |
| 113 | Structures of FOX-4 Cephamycinase in Complex with Transition-State Analog Inhibitors. <i>Biomolecules</i> , 2020, 10, 671. | 4.0 | 4 |
| 114 | Structural and Functional Characterization of a Biliverdin-Binding Near-Infrared Fluorescent Protein From the Serpin Superfamily. <i>Journal of Molecular Biology</i> , 2022, 434, 167359. | 4.2 | 4 |
| 115 | Crystallization and preliminary crystallographic analysis of the N-terminal actin binding domain of human fimbrin. , 1997, 28, 452-453. | | 3 |
| 116 | Genetically modified hematopoietic stem/progenitor cells that produce IL-10-secreting regulatory T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2634-2639. | 7.1 | 3 |
| 117 | Peptide-HLA-based immunotherapeutics platforms for direct modulation of antigen-specific T cells. <i>Scientific Reports</i> , 2021, 11, 19220. | 3.3 | 2 |
| 118 | Structure of a single-chain H2A/H2B dimer. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 194-198. | 0.8 | 1 |
| 119 | Allosteric regulation of binding specificity of HVEM for CD160 and BTLA ligands upon G89F mutation. <i>Current Research in Structural Biology</i> , 2021, 3, 337-345. | 2.2 | 1 |
| 120 | Application of Novel T Cell Immunotherapeutics to Drive Antigen-Specific Activation, Expansion, and Differentiation of CD19 Chimeric Antigen Receptor T Cells (CAR T-cells). <i>Blood</i> , 2020, 136, 34-35. | 1.4 | 1 |
| 121 | Use of cMet Crystal Structures to Identify Potential Drug-Resistant Mutants. <i>FASEB Journal</i> , 2009, 23, . | 0.5 | 0 |
| 122 | Functional Annotation of Unknown Enzymes within the Amidohydrolase Superfamily. <i>FASEB Journal</i> , 2009, 23, 674.2. | 0.5 | 0 |
| 123 | Ultra High-throughput Screening Uncovers New Activities in Phosphatases of the Haloalkanoic Acid Dehalogenase Superfamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 571.1. | 0.5 | 0 |
| 124 | Type 1 Diabetes: A Promising Dialogue between Promiscuous T Cell Receptor and H ² D Peptide Complex. <i>FASEB Journal</i> , 2022, 36, . | 0.5 | 0 |
| 125 | HSMotifDiscover: identification of motifs in sequences composed of non-single-letter elements. <i>Bioinformatics</i> , 2022, 38, 4036-4038. | 4.1 | 0 |