

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 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
2	Longitudinally monitored immune biomarkers predict the timing of COVID-19 outcomes. <i>PLoS Computational Biology</i> , 2022, 18, e1009778.	3.2	10
3	Viperin triggers ribosome collision-dependent translation inhibition to restrict viral replication. <i>Molecular Cell</i> , 2022, 82, 1631-1642.e6.	9.7	16
4	Type 1 Diabetes: A Promising Dialogue between Promiscuous T Cell Receptor and H α 2D ^b Peptide Complex. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
5	HSMotifDiscover: identification of motifs in sequences composed of non-single-letter elements. <i>Bioinformatics</i> , 2022, 38, 4036-4038.	4.1	0
6	Treatment of Severe COVID-19 with Convalescent Plasma in Bronx, NYC. <i>JCI Insight</i> , 2021, 6, .	5.0	36
7	Single-Dilution COVID-19 Antibody Test with Qualitative and Quantitative Readouts. <i>MSphere</i> , 2021, 6, .	2.9	11
8	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
9	Chemical Synthesis of the Antiviral Nucleotide Analogue ddhCTP. <i>Journal of Organic Chemistry</i> , 2021, 86, 8843-8850.	3.2	11
10	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
11	Structural basis for tRNA methylthiolation by the radical SAM enzyme MiaB. <i>Nature</i> , 2021, 597, 566-570.	27.8	25
12	Inhibition of SARS-CoV-2 polymerase by nucleotide analogs from a single-molecule perspective. <i>ELife</i> , 2021, 10, .	6.0	53
13	Peptide-HLA-based immunotherapeutics platforms for direct modulation of antigen-specific T cells. <i>Scientific Reports</i> , 2021, 11, 19220.	3.3	2
14	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
15	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
16	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
17	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
18	Redesigning HVEM Interface for Selective Binding to LIGHT, BTLA, and CD160. <i>Structure</i> , 2020, 28, 1197-1205.e2.	3.3	13

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19	HVEM signaling promotes protective antibody-dependent cellular cytotoxicity (ADCC) vaccine responses to herpes simplex viruses. <i>Science Immunology</i> , 2020, 5, .	11.9	12
20	Immune responses to SARS-CoV-2 infection in hospitalized pediatric and adult patients. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	298
21	In vivo detection of antigen-specific CD8+ T cells by immuno-positron emission tomography. <i>Nature Methods</i> , 2020, 17, 1025-1032.	19.0	34
22	Mechanistic dissection of the PD-L1:B7-1 co-inhibitory immune complex. <i>PLoS ONE</i> , 2020, 15, e0233578.	2.5	23
23	A metabolic pathway for bile acid dehydroxylation by the gut microbiome. <i>Nature</i> , 2020, 582, 566-570.	27.8	262
24	Structures of FOX-4 Cephamycinase in Complex with Transition-State Analog Inhibitors. <i>Biomolecules</i> , 2020, 10, 671.	4.0	4
25	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
26	Viperin Reveals Its True Function. <i>Annual Review of Virology</i> , 2020, 7, 421-446.	6.7	76
27	Narrow-Spectrum Antibiotic Targeting of the Radical SAM Enzyme MqnE in Menaquinone Biosynthesis. <i>Biochemistry</i> , 2020, 59, 2562-2575.	2.5	10
28	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
29	Structure of a single-chain H2A/H2B dimer. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 194-198.	0.8	1
30	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
31	The active site of the Mycobacterium tuberculosis branched-chain amino acid biosynthesis enzyme dihydroxyacid dehydratase contains a 2Fe ²⁺ cluster. <i>Journal of Biological Chemistry</i> , 2019, 294, 13158-13170.	3.4	12
32	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
33	Structural Basis of CD160:HVEM Recognition. <i>Structure</i> , 2019, 27, 1286-1295.e4.	3.3	33
34	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
35	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
36	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

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37	Computational Redesign of PD-1 Interface for PD-L1 Ligand Selectivity. <i>Structure</i> , 2019, 27, 829-836.e3.	3.3	13
38	Novel Metabolic Pathways and Regulons for Hexuronate Utilization in Proteobacteria. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	19
39	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. <i>Journal of Infectious Diseases</i> , 2018, 217, 754-758.	4.0	33
40	Mechanism and Structure of β -Resorcylyate Decarboxylase. <i>Biochemistry</i> , 2018, 57, 3167-3175.	2.5	30
41	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
42	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
43	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
44	The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.	12.6	101
45	Substrate Profile of the Phosphotriesterase Homology Protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 6219-6227.	2.5	5
46	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018, 7, .	6.0	30
47	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
48	Functional assignment of multiple catabolic pathways for d-ribose. <i>Nature Chemical Biology</i> , 2018, 14, 696-705.	8.0	26
49	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
50	A naturally occurring antiviral ribonucleotide encoded by the human genome. <i>Nature</i> , 2018, 558, 610-614.	27.8	225
51	CAR T Cell Therapy Targeting G Protein-Coupled Receptor Class C Group 5 Member D (GPRC5D), a Novel Target for the Immunotherapy of Multiple Myeloma. <i>Blood</i> , 2018, 132, 589-589.	1.4	9
52	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. <i>Structure</i> , 2017, 25, 434-445.	3.3	61
53	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
54	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

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55	Structural basis for cancer immunotherapy by the first-in-class checkpoint inhibitor ipilimumab. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4223-E4232.	7.1	121
56	Can the propensity of protein crystallization be increased by using systematic screening with metals?. Protein Science, 2017, 26, 1704-1713.	7.6	8
57	The hidden treasure in your data: phasing with unexpected weak anomalous scatterers from routine data sets. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 184-195.	0.8	5
58	Stilbene epoxidation and detoxification in a Photobacterium luminescens-nematode symbiosis. Journal of Biological Chemistry, 2017, 292, 6680-6694.	3.4	20
59	Structural, mutational and biophysical studies reveal a canonical mode of molecular recognition between immune receptor TIGIT and nectin-2. Molecular Immunology, 2017, 81, 151-159.	2.2	18
60	PD-L1 is an activation-independent marker of brown adipocytes. Nature Communications, 2017, 8, 647.	12.8	97
61	Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. Journal of the American Chemical Society, 2017, 139, 11734-11744.	13.7	119
62	A novel bifunctional transcriptional regulator of riboflavin metabolism in Archaea. Nucleic Acids Research, 2017, 45, gkw1331.	14.5	44
63	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. Blood, 2017, 130, 742-742.	1.4	92
64	General principles of binding between cell surface receptors and multi-specific ligands: A computational study. PLoS Computational Biology, 2017, 13, e1005805.	3.2	39
65	Tumor-expressed immune checkpoint B7x promotes cancer progression and antigen-specific CD8 T cell exhaustion and suppressive innate immune cells. Oncotarget, 2017, 8, 82740-82753.	1.8	17
66	Structure of an ABC transporter solute-binding protein specific for the amino sugars glucosamine and galactosamine. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 467-472.	0.8	5
67	Biochemical characterization of two haloalkane dehalogenases: DccA from <i>Caulobacter crescentus</i> and DsaA from <i>Saccharomonospora azurea</i> . Protein Science, 2016, 25, 877-886.	7.6	11
68	Durable antitumor responses to CD47 blockade require adaptive immune stimulation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2646-54.	7.1	272
69	Inhibition of Zinc-Dependent Histone Deacetylases with a Chemically Triggered Electrophile. ACS Chemical Biology, 2016, 11, 1844-1851.	3.4	21
70	GBT440 increases haemoglobin oxygen affinity, reduces sickling and prolongs RBC half-life in a murine model of sickle cell disease. British Journal of Haematology, 2016, 175, 141-153.	2.5	187
71	Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4161-9.	7.1	46
72	Diversity-Oriented Synthesis as a Strategy for Fragment Evolution against GSK3 β . ACS Medicinal Chemistry Letters, 2016, 7, 852-856.	2.8	34

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73	Co-stimulate or Co-inhibit Regulatory T Cells, Which Side to Go?. Immunological Investigations, 2016, 45, 813-831.	2.0	21
74	Crystal Structure of the Complex of Human FasL and Its Decoy Receptor DcR3. Structure, 2016, 24, 2016-2023.	3.3	39
75	Substrate Distortion and the Catalytic Reaction Mechanism of 5-Carboxyvanillate Decarboxylase. Journal of the American Chemical Society, 2016, 138, 826-836.	13.7	41
76	Purification, crystallization and structural elucidation of <i>D</i> -galactaro-1,4-lactone cycloisomerase from <i>Agrobacterium tumefaciens</i> involved in pectin degradation. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 36-41.	0.8	7
77	A Small Protein Associated with Fungal Energy Metabolism Affects the Virulence of <i>Cryptococcus neoformans</i> in Mammals. PLoS Pathogens, 2016, 12, e1005849.	4.7	17
78	A switch from parallel to antiparallel strand orientation in a coiled-coil X-ray structure via two core hydrophobic mutations. Biopolymers, 2015, 104, 178-185.	2.4	12
79	Biosynthesis of Squalene from Farnesyl Diphosphate in Bacteria: Three Steps Catalyzed by Three Enzymes. ACS Central Science, 2015, 1, 77-82.	11.3	69
80	Function Discovery and Structural Characterization of a Methylphosphonate Esterase. Biochemistry, 2015, 54, 2919-2930.	2.5	4
81	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. Nucleic Acids Research, 2015, 43, 4602-4613.	14.5	23
82	Increased Heterologous Protein Expression in <i>Drosophila</i> S2 Cells for Massive Production of Immune Ligands/Receptors and Structural Analysis of Human HVEM. Molecular Biotechnology, 2015, 57, 914-922.	2.4	10
83	Active Site and Remote Contributions to Catalysis in Methylthioadenosine Nucleosidases. Biochemistry, 2015, 54, 2520-2529.	2.5	14
84	Computational-guided discovery and characterization of a sesquiterpene synthase from <i>Streptomyces clavuligerus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5661-5666.	7.1	42
85	Expression, Clinical Significance, and Receptor Identification of the Newest B7 Family Member HHLA2 Protein. Clinical Cancer Research, 2015, 21, 2359-2366.	7.0	125
86	Panoramic view of a superfamily of phosphatases through substrate profiling. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1974-83.	7.1	118
87	ATP-binding Cassette (ABC) Transport System Solute-binding Protein-guided Identification of Novel <i>d</i> -Altritol and Galactitol Catabolic Pathways in <i>Agrobacterium tumefaciens</i> C58. Journal of Biological Chemistry, 2015, 290, 28963-28976.	3.4	29
88	A General Strategy for the Discovery of Metabolic Pathways: <i>D</i> -Threitol, <i>L</i> -Threitol, and Erythritol Utilization in <i>Mycobacterium smegmatis</i> . Journal of the American Chemical Society, 2015, 137, 14570-14573.	13.7	29
89	Structural Determinants of the 5'-Methylthioinosine Specificity of Plasmodium Purine Nucleoside Phosphorylase. PLoS ONE, 2014, 9, e84384.	2.5	7
90	Orange Fluorescent Proteins: Structural Studies of LSSmOrange, PSmOrange and PSmOrange2. PLoS ONE, 2014, 9, e99136.	2.5	24

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91	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
92	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
93	Structure and Cancer Immunotherapy of the B7 Family Member B7x. <i>Cell Reports</i> , 2014, 9, 1089-1098.	6.4	58
94	Structural Characterization of the Glycoprotein GP2 Core Domain from the CAS Virus, a Novel Arenavirus-Like Species. <i>Journal of Molecular Biology</i> , 2014, 426, 1452-1468.	4.2	25
95	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
96	Recent advances in mammalian protein production. <i>FEBS Letters</i> , 2014, 588, 253-260.	2.8	179
97	Aptamer-targeted Antigen Delivery. <i>Molecular Therapy</i> , 2014, 22, 1375-1387.	8.2	58
98	Considerations for Combined Immune Checkpoint Modulation and Radiation Treatment. <i>Radiation Research</i> , 2014, 182, 230-238.	1.5	7
99	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
100	Mechanistic Basis for Functional Promiscuity in the TNF and TNF Receptor Superfamilies: Structure of the LIGHT:DcR3 Assembly. <i>Structure</i> , 2014, 22, 1252-1262.	3.3	27
101	Photoswitchable Red Fluorescent Protein with a Large Stokes Shift. <i>Chemistry and Biology</i> , 2014, 21, 1402-1414.	6.0	18
102	Compensatory Mechanisms Allow Undersized Anchor-Deficient Class I MHC Ligands To Mediate Pathogenic Autoreactive T Cell Responses. <i>Journal of Immunology</i> , 2014, 193, 2135-2146.	0.8	25
103	Loss of quaternary structure is associated with rapid sequence divergence in the OSBS family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8535-8540.	7.1	29
104	Tissue-Expressed B7-H1 Critically Controls Intestinal Inflammation. <i>Cell Reports</i> , 2014, 6, 625-632.	6.4	53
105	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, .	6.0	81
106	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
107	Testing the Sulfotransferase Molecular Pore Hypothesis. <i>Journal of Biological Chemistry</i> , 2013, 288, 8619-8626.	3.4	27
108	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

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109	Divergent Evolution in Enolase Superfamily: Strategies for Assigning Functions. <i>Journal of Biological Chemistry</i> , 2012, 287, 29-34.	3.4	118
110	Use of cMet Crystal Structures to Identify Potential Drug-Resistant Mutants. <i>FASEB Journal</i> , 2009, 23, .	0.5	0
111	Functional Annotation of Unknown Enzymes within the Amidohydrolase Superfamily. <i>FASEB Journal</i> , 2009, 23, 674.2.	0.5	0
112	Structural genomics of protein phosphatases. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 121-140.	1.2	148
113	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
114	Structural Analysis of Adenine Phosphoribosyltransferase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2001, 40, 10800-10809.	2.5	47
115	Structural basis for co-stimulation by the human CTLA-4/B7-2 complex. <i>Nature</i> , 2001, 410, 604-608.	27.8	323
116	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
117	Profilin binds proline-rich ligands in two distinct amide backbone orientations. <i>Nature Structural Biology</i> , 1999, 6, 666-671.	9.7	102
118	Structural genomics: beyond the Human Genome Project. <i>Nature Genetics</i> , 1999, 23, 151-157.	21.4	369
119	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
120	Trypanosomal Nucleoside Hydrolase. A Novel Mechanism from the Structure with a Transition-State Inhibitor. <i>Biochemistry</i> , 1998, 37, 6277-6285.	2.5	89
121	Structure Determination and Characterization of <i>Saccharomyces cerevisiae</i> Profilin. <i>Biochemistry</i> , 1998, 37, 11171-11181.	2.5	85
122	Temperature-induced conformational changes in prosomatostatin-II: implications for processing. <i>Biochemical Journal</i> , 1998, 334, 275-282.	3.7	7
123	The structure of an actin-crosslinking domain from human fimbrin. <i>Nature Structural Biology</i> , 1997, 4, 708-712.	9.7	121
124	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
125	Crystallization and preliminary crystallographic analysis of the N-terminal actin binding domain of human fimbrin. , 1997, 28, 452-453.		3