

Eric John Sundberg

List of Publications by Year in descending order

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100
papers

4,451
citations

71102

41
h-index

123424

61
g-index

108
all docs

108
docs citations

108
times ranked

6086
citing authors

#	ARTICLE	IF	CITATIONS
1	Sculpting therapeutic monoclonal antibody N-glycans using endoglycosidases. <i>Current Opinion in Structural Biology</i> , 2022, 72, 248-259.	5.7	7
2	Mechanism of cooperative N-glycan processing by the multi-modular endoglycosidase EndoE. <i>Nature Communications</i> , 2022, 13, 1137.	12.8	10
3	Bacterial protein domains with a novel Ig-like fold target human CEACAM receptors. <i>EMBO Journal</i> , 2021, 40, e106103.	7.8	16
4	Structural basis of the dynamic human CEACAM1 monomer-dimer equilibrium. <i>Communications Biology</i> , 2021, 4, 360.	4.4	6
5	Bacterial Flagellar Filament: A Supramolecular Multifunctional Nanostructure. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7521.	4.1	43
6	Insights into substrate recognition and specificity for IgG by Endoglycosidase S2. <i>PLoS Computational Biology</i> , 2021, 17, e1009103.	3.2	5
7	GH18 endo- β -N-acetylglucosaminidases use distinct mechanisms to process hybrid-type N-linked glycans. <i>Journal of Biological Chemistry</i> , 2021, 297, 101011.	3.4	6
8	Molecular Determinants of Filament Capping Proteins Required for the Formation of Functional Flagella in Gram-Negative Bacteria. <i>Biomolecules</i> , 2021, 11, 1397.	4.0	7
9	Molecular Basis of Selective Cytokine Signaling Inhibition by Antibodies Targeting a Shared Receptor. <i>Frontiers in Immunology</i> , 2021, 12, 779100.	4.8	9
10	Structural insights into the mechanisms and specificities of IgG-active endoglycosidases. <i>Glycobiology</i> , 2020, 30, 268-279.	2.5	24
11	Structure and dynamics of an α -fucosidase reveal a mechanism for highly efficient IgG transfucosylation. <i>Nature Communications</i> , 2020, 11, 6204.	12.8	29
12	Structural basis of mammalian high-mannose N-glycan processing by human gut <i>Bacteroides</i> . <i>Nature Communications</i> , 2020, 11, 899.	12.8	22
13	Hijacking antibody-induced CTLA-4 lysosomal degradation for safer and more effective cancer immunotherapy. <i>Cell Research</i> , 2019, 29, 609-627.	12.0	74
14	Structural Basis of IL-1 Family Cytokine Signaling. <i>Frontiers in Immunology</i> , 2019, 10, 1412.	4.8	194
15	Gastric Subserous Vaccination With <i>Helicobacter pylori</i> Vaccine: An Attempt to Establish Tissue-Resident CD4+ Memory T Cells and Induce Prolonged Protection. <i>Frontiers in Immunology</i> , 2019, 10, 1115.	4.8	24
16	Roles of Adhesion to Epithelial Cells in Gastric Colonization by <i>Helicobacter pylori</i> . <i>Advances in Experimental Medicine and Biology</i> , 2019, 1149, 57-75.	1.6	9
17	Direct CD137 costimulation of CD8 T cells promotes retention and innate-like function within nascent atherogenic foci. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2019, 316, H1480-H1494.	3.2	8
18	Molecular Basis of Broad Spectrum α -N-Glycan Specificity and Processing of Therapeutic IgG Monoclonal Antibodies by Endoglycosidase S2. <i>ACS Central Science</i> , 2019, 5, 524-538.	11.3	27

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19	The structure of PilA from <i>Acinetobacter baumannii</i> AB5075 suggests a mechanism for functional specialization in <i>Acinetobacter</i> type IV pili. <i>Journal of Biological Chemistry</i> , 2019, 294, 218-230.	3.4	59
20	Small-Molecule Inhibitor of FosA Expands Fosfomycin Activity to Multidrug-Resistant Gram-Negative Pathogens. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	11
21	The <i>Helicobacter pylori</i> adhesin protein HopQ exploits the dimer interface of human CEACAMs to facilitate translocation of the oncoprotein CagA. <i>EMBO Journal</i> , 2018, 37, .	7.8	47
22	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
23	High resolution X-ray and NMR structural study of human T-cell immunoglobulin and mucin domain containing protein-3. <i>Scientific Reports</i> , 2018, 8, 17512.	3.3	35
24	Structural basis for the recognition of complex-type N-glycans by Endoglycosidase S. <i>Nature Communications</i> , 2018, 9, 1874.	12.8	38
25	Getting oriented with antibodies. <i>Biochemical Journal</i> , 2017, 474, 517-519.	3.7	1
26	Infection-derived lipids elicit an immune deficiency circuit in arthropods. <i>Nature Communications</i> , 2017, 8, 14401.	12.8	103
27	Common Challenges in Studying the Structure and Function of Bacterial Proteins: Case Studies from <i>Helicobacter pylori</i> . <i>Methods in Molecular Biology</i> , 2017, 1535, 77-93.	0.9	0
28	A structural model of flagellar filament switching across multiple bacterial species. <i>Nature Communications</i> , 2017, 8, 960.	12.8	90
29	IL-1 Family Cytokines Use Distinct Molecular Mechanisms to Signal through Their Shared Co-receptor. <i>Immunity</i> , 2017, 47, 510-523.e4.	14.3	48
30	Structure and Dynamics of FosA-Mediated Fosfomycin Resistance in <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	28
31	Structure-Based Design of Hepatitis C Virus Vaccines That Elicit Neutralizing Antibody Responses to a Conserved Epitope. <i>Journal of Virology</i> , 2017, 91, .	3.4	50
32	<i>Helicobacter pylori</i> exploits human CEACAMs via HopQ for adherence and translocation of CagA. <i>Nature Microbiology</i> , 2017, 2, 16188.	13.3	134
33	Type IV pili promote early biofilm formation by <i>Clostridium difficile</i> . <i>Pathogens and Disease</i> , 2016, 74, ftw061.	2.0	86
34	Motility and adhesion through type IV pili in Gram-positive bacteria. <i>Biochemical Society Transactions</i> , 2016, 44, 1659-1666.	3.4	59
35	Some of the most interesting CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	2.6	16
36	The NEU1-selective sialidase inhibitor, C9-butyl-amide-DANA, blocks sialidase activity and NEU1-mediated bioactivities in human lung in vitro and murine lung in vivo. <i>Glycobiology</i> , 2016, 26, 834-849.	2.5	34

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37	The Tick Protein Sialostatin L2 Binds to Annexin A2 and Inhibits NLRC4-Mediated Inflammasome Activation. <i>Infection and Immunity</i> , 2016, 84, 1796-1805.	2.2	47
38	Structural Diversity in the Type IV Pili of Multidrug-resistant <i>Acinetobacter</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 22924-22935.	3.4	60
39	Bacterial flagellar capping proteins adopt diverse oligomeric states. <i>ELife</i> , 2016, 5, .	6.0	46
40	Structure of the N-terminal dimerization domain of CEACAM7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1169-1175.	0.8	9
41	Diverse oligomeric states of CEACAM IgV domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13561-13566.	7.1	33
42	Structural and Evolutionary Analyses Show Unique Stabilization Strategies in the Type IV Pili of <i>Clostridium difficile</i> . <i>Structure</i> , 2015, 23, 385-396.	3.3	45
43	A Decoy Peptide that Disrupts TIRAP Recruitment to TLRs Is Protective in a Murine Model of Influenza. <i>Cell Reports</i> , 2015, 11, 1941-1952.	6.4	58
44	An Intrinsically Disordered Region in the Proapoptotic ASPP2 Protein Binds to the <i>Helicobacter pylori</i> Oncoprotein CagA. <i>Biochemistry</i> , 2015, 54, 3337-3347.	2.5	9
45	Integrin Engagement by the Helical RGD Motif of the <i>Helicobacter pylori</i> CagL Protein Is Regulated by pH-induced Displacement of a Neighboring Helix. <i>Journal of Biological Chemistry</i> , 2015, 290, 12929-12940.	3.4	26
46	Severe Acute Respiratory Syndrome Coronavirus ORF7a Inhibits Bone Marrow Stromal Antigen 2 Virion Tethering through a Novel Mechanism of Glycosylation Interference. <i>Journal of Virology</i> , 2015, 89, 11820-11833.	3.4	133
47	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.	7.1	56
48	Crystal Structures of the Toll/Interleukin-1 Receptor (TIR) Domains from the <i>Brucella</i> Protein TcpB and Host Adaptor TIRAP Reveal Mechanisms of Molecular Mimicry. <i>Journal of Biological Chemistry</i> , 2014, 289, 669-679.	3.4	66
49	A Novel Multivalent, Single-Domain Antibody Targeting TcdA and TcdB Prevents Fulminant <i>Clostridium difficile</i> Infection in Mice. <i>Journal of Infectious Diseases</i> , 2014, 210, 964-972.	4.0	84
50	The Tick Salivary Protein Sialostatin L2 Inhibits Caspase-1-Mediated Inflammation during <i>Anaplasma phagocytophilum</i> Infection. <i>Infection and Immunity</i> , 2014, 82, 2553-2564.	2.2	51
51	Structure of <i>Clostridium difficile</i> PilJ Exhibits Unprecedented Divergence from Known Type IV Pilins. <i>Journal of Biological Chemistry</i> , 2014, 289, 4334-4345.	3.4	39
52	Molecular Determinants of Agonist and Antagonist Signaling through the IL-36 Receptor. <i>Journal of Immunology</i> , 2014, 193, 921-930.	0.8	65
53	Molecular Interactions in Interleukin and Toll-like Receptor Signaling Pathways. <i>Current Pharmaceutical Design</i> , 2014, 20, 1244-1258.	1.9	8
54	With an antibody whose duty's double, a step towards ending asthma trouble?. <i>Biochemical Journal</i> , 2013, 451, e1-e3.	3.7	1

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55	Recruitment of TLR adapter TRIF to TLR4 signaling complex is mediated by the second helical region of TRIF TIR domain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19036-19041.	7.1	47
56	Liquidâ€“liquid diffusion crystallization improves the X-ray diffraction of EndoS, an endo-Î²-N-acetylglucosaminidase from Streptococcus pyogenes with activity on human IgG. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1405-1410.	0.7	5
57	Characterization of the Translocation-competent Complex between the Helicobacter pylori Oncogenic Protein CagA and the Accessory Protein CagF. Journal of Biological Chemistry, 2013, 288, 32897-32909.	3.4	21
58	R753Q Polymorphism Inhibits Toll-like Receptor (TLR) 2 Tyrosine Phosphorylation, Dimerization with TLR6, and Recruitment of Myeloid Differentiation Primary Response Protein 88. Journal of Biological Chemistry, 2012, 287, 38327-38337.	3.4	63
59	Synthesis and Biophysical Study of Disassembling Nanohybrid Bioconjugates with a Cubic Octasilsesquioxane Core. Advanced Functional Materials, 2012, 22, 3191-3201.	14.9	36
60	Molecular Basis of a Million-Fold Affinity Maturation Process in a Proteinâ€“Protein Interaction. Journal of Molecular Biology, 2011, 411, 321-328.	4.2	7
61	HLA-DM captures partially empty HLA-DR molecules for catalyzed removal of peptide. Nature Immunology, 2011, 12, 54-61.	14.5	89
62	Dissecting Proteinâ€“Protein Interactions Using Directed Evolution. Biochemistry, 2011, 50, 2394-2402.	2.5	30
63	A highly tilted binding mode by a self-reactive T cell receptor results in altered engagement of peptide and MHC. Journal of Experimental Medicine, 2011, 208, 91-102.	8.5	77
64	The T Cell Receptor Î²-Chain Second Complementarity Determining Region Loop (CDR2Î²) Governs T Cell Activation and VÎ² Specificity by Bacterial Superantigens. Journal of Biological Chemistry, 2011, 286, 4871-4881.	3.4	17
65	A Single, Engineered Protein Therapeutic Agent Neutralizes Exotoxins from Both Staphylococcus aureus and Streptococcus pyogenes. Vaccine Journal, 2010, 17, 1781-1789.	3.1	18
66	Assessing Energetic Contributions to Binding from a Disordered Region in a Proteinâ€“Protein Interaction. Biochemistry, 2010, 49, 9256-9268.	2.5	17
67	HLA-B*35-Pxâ€“mediated acceleration of HIV-1 infection by increased inhibitory immunoregulatory impulses. Journal of Experimental Medicine, 2009, 206, 2959-2966.	8.5	92
68	Molecular Recognition of Diverse Ligands by T-Cell Receptors. Methods in Molecular Biology, 2009, 524, 347-359.	0.9	3
69	Neutralization of Multiple Staphylococcal Superantigens by a Singleâ€“Chain Protein Consisting of Affinityâ€“Matured, Variable Domain Repeats. Journal of Infectious Diseases, 2008, 198, 344-348.	4.0	20
70	Molecular Requirements for MHC Class II Î±-Chain Engagement and Allelic Discrimination by the Bacterial Superantigen Streptococcal Pyrogenic Exotoxin C. Journal of Immunology, 2008, 181, 3384-3392.	0.8	17
71	TCR recognition of peptide/MHC class II complexes and superantigens. Seminars in Immunology, 2007, 19, 262-271.	5.6	93
72	Recombinant expression and purification of the N-terminal extracellular domain of the parathyroid hormone receptor. Protein Expression and Purification, 2007, 54, 87-93.	1.3	6

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73	Crystal Structure of the Streptococcal Superantigen Spel and Functional Role of a Novel Loop Domain in T Cell Activation by Group V Superantigens. <i>Journal of Molecular Biology</i> , 2007, 367, 925-934.	4.2	34
74	A Novel Loop Domain in Superantigens Extends their T Cell Receptor Recognition Site. <i>Journal of Molecular Biology</i> , 2007, 371, 210-221.	4.2	41
75	Interactions between the Leucine-zipper Motif of cGMP-Dependent Protein Kinase and the C-terminal Region of the Targeting Subunit of Myosin Light Chain Phosphatase. <i>Journal of Molecular Biology</i> , 2007, 373, 1198-1212.	4.2	36
76	A viral CTL escape mutation leading to immunoglobulin-like transcript 4-mediated functional inhibition of myelomonocytic cells. <i>Journal of Experimental Medicine</i> , 2007, 204, 2813-2824.	8.5	95
77	Neutralization of staphylococcal enterotoxin B by soluble, high-affinity receptor antagonists. <i>Nature Medicine</i> , 2007, 13, 725-729.	30.7	88
78	Structural basis of T-cell specificity and activation by the bacterial superantigen TSST-1. <i>EMBO Journal</i> , 2007, 26, 1187-1197.	7.8	54
79	Surface Plasmon Resonance Biosensing in the Study of Ternary Systems of Interacting Proteins. , 2007, , 97-141.		6
80	Molecular Basis of TCR Selectivity, Cross-Reactivity, and Allelic Discrimination by a Bacterial Superantigen: Integrative Functional and Energetic Mapping of the SpeC-VI ^{2.1} Molecular Interface. <i>Journal of Immunology</i> , 2006, 177, 8595-8603.	0.8	20
81	Long-range cooperative binding effects in a T cell receptor variable domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9867-9872.	7.1	64
82	Molecular Recognition in the Immune System. , 2005, , 49-87.		0
83	Structural Basis of Affinity Maturation and Intramolecular Cooperativity in a Protein-Protein Interaction. <i>Structure</i> , 2005, 13, 1775-1787.	3.3	39
84	Crystal Structure of Human Peptidoglycan Recognition Protein S (PGRP-S) at 1.70Å... Resolution. <i>Journal of Molecular Biology</i> , 2005, 347, 683-691.	4.2	74
85	Characterization of T Cell Receptors Engineered for High Affinity Against Toxic Shock Syndrome Toxin-1. <i>Journal of Molecular Biology</i> , 2005, 353, 308-321.	4.2	52
86	Cloning, expression and interaction of human T cell receptors with the bacterial superantigen SSA. <i>FEBS Journal</i> , 2004, 271, 4075-4083.	0.2	23
87	Structural Mechanism Governing Cis and Trans Isomeric States and an Intramolecular Switch for Cis/Trans Isomerization of a Non-proline Peptide Bond Observed in Crystal Structures of Scorpion Toxins. <i>Journal of Molecular Biology</i> , 2004, 341, 1189-1204.	4.2	45
88	Structural, Energetic, and Functional Analysis of a Protein-Protein Interface at Distinct Stages of Affinity Maturation. <i>Structure</i> , 2003, 11, 1151-1161.	3.3	30
89	Functional Analysis of the TCR Binding Domain of Toxic Shock Syndrome Toxin-1 Predicts Further Diversity in MHC Class II/Superantigen/TCR Ternary Complexes. <i>Journal of Immunology</i> , 2003, 171, 1385-1392.	0.8	44
90	Dissecting Cooperative and Additive Binding Energetics in the Affinity Maturation Pathway of a Protein-Protein Interface. <i>Journal of Biological Chemistry</i> , 2003, 278, 50412-50421.	3.4	38

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91	Exploration of the P6/P7 Region of the Peptide-binding Site of the Human Class II Major Histocompatibility Complex Protein HLA-DR1. <i>Journal of Biological Chemistry</i> , 2003, 278, 44904-44912.	3.4	30
92	Quantifying the Energetics of Cooperativity in a Ternary Protein Complex. <i>Biochemistry</i> , 2002, 41, 5177-5184.	2.5	31
93	Molecular recognition in antibody-antigen complexes. <i>Advances in Protein Chemistry</i> , 2002, 61, 119-160.	4.4	214
94	Minor Structural Changes in a Mutated Human Melanoma Antigen Correspond to Dramatically Enhanced Stimulation of a CD4+ Tumor-infiltrating Lymphocyte Line. <i>Journal of Molecular Biology</i> , 2002, 319, 449-461.	4.2	32
95	Structures of Two Streptococcal Superantigens Bound to TCR β Chains Reveal Diversity in the Architecture of T Cell Signaling Complexes. <i>Structure</i> , 2002, 10, 687-699.	3.3	116
96	So many ways of getting in the way: diversity in the molecular architecture of superantigen-dependent T-cell signaling complexes. <i>Current Opinion in Immunology</i> , 2002, 14, 36-44.	5.5	81
97	Luxury accommodations: the expanding role of structural plasticity in protein-protein interactions. <i>Structure</i> , 2000, 8, R137-R142.	3.3	74
98	Estimation of the Hydrophobic Effect in an Antigen-Antibody Protein-Protein Interface. <i>Biochemistry</i> , 2000, 39, 15375-15387.	2.5	99
99	Effects of Cross-Linking on the Morphology of Structured Latex Particles. 2. Experimental Evidence for Lightly Cross-Linked Systems. <i>Macromolecules</i> , 1997, 30, 1028-1032.	4.8	58
100	Morphology development for three-component emulsion polymers: Theory and experiments. <i>Journal of Applied Polymer Science</i> , 1993, 47, 1277-1294.	2.6	68