

Brian J Sutton

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4485015/publications.pdf>

Version: 2024-02-01

73
papers

5,758
citations

87888

38
h-index

82547

72
g-index

74
all docs

74
docs citations

74
times ranked

6487
citing authors

#	ARTICLE	IF	CITATIONS
1	Reviving lost binding sites: Exploring calcium-binding site transitions between human and murine CD23. <i>FEBS Open Bio</i> , 2021, 11, 1827-1840.	2.3	2
2	Differences between Human and Mouse IgM Fc Receptor (Fc μ R). <i>International Journal of Molecular Sciences</i> , 2021, 22, 7024.	4.1	9
3	Mapping of the binding site for Fc γ 4R in human IgM-Fc. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140266.	2.3	8
4	Identification of Amino Acid Residues in Human IgM Fc Receptor (Fc μ R) Critical for IgM Binding. <i>Frontiers in Immunology</i> , 2020, 11, 618327.	4.8	11
5	Engineering the Fab fragment of the anti-IgE omalizumab to prevent Fab crystallization and permit IgE-Fc complex crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 116-129.	0.8	5
6	Interplay between Affinity and Valency in Effector Cell Degranulation: A Model System with Polcalcic Allergens and Human Patient-Derived IgE Antibodies. <i>Journal of Immunology</i> , 2019, 203, 1693-1700.	0.8	13
7	IgE Antibodies: From Structure to Function and Clinical Translation. <i>Antibodies</i> , 2019, 8, 19.	2.5	62
8	Crystal structures of murine and human Histamine-Releasing Factor (HRF/TCTP) and a model for HRF dimerisation in mast cell activation. <i>Molecular Immunology</i> , 2018, 93, 216-222.	2.2	15
9	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie</i> , 2018, 130, 17440-17445.	2.0	5
10	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 17194-17199.	13.8	39
11	The structure of PghL hydrolase bound to its substrate poly ϵ -glutamate. <i>FEBS Journal</i> , 2018, 285, 4575-4589.	4.7	2
12	Structure of a patient-derived antibody in complex with allergen reveals simultaneous conventional and superantigen-like recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8707-E8716.	7.1	29
13	Structural basis for selective inhibition of immunoglobulin E-receptor interactions by an anti-IgE antibody. <i>Scientific Reports</i> , 2018, 8, 11548.	3.3	22
14	Room temperature structure of human IgG4-Fc from crystals analysed in situ. <i>Molecular Immunology</i> , 2017, 81, 85-91.	2.2	7
15	Allosteric mechanism of action of the therapeutic anti-IgE antibody omalizumab. <i>Journal of Biological Chemistry</i> , 2017, 292, 9975-9987.	3.4	61
16	IgE binds asymmetrically to its B cell receptor CD23. <i>Scientific Reports</i> , 2017, 7, 45533.	3.3	25
17	<sc>IgY</sc>: a key isotype in antibody evolution. <i>Biological Reviews</i> , 2017, 92, 2144-2156.	10.4	87
18	IgE Trimers Drive SPE-7 Cytokinergic Activity. <i>Scientific Reports</i> , 2017, 7, 8164.	3.3	13

#	ARTICLE	IF	CITATIONS
19	Thermal sensitivity and flexibility of the C μ 3 domains in immunoglobulin E. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1336-1347.	2.3	10
20	Antibodies and superantibodies in patients with chronic rhinosinusitis with nasal polyps. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1195-1204.e11.	2.9	42
21	Antibody mimetics: promising complementary agents to animal-sourced antibodies. <i>Critical Reviews in Biotechnology</i> , 2016, 36, 268-275.	9.0	18
22	IgG4 Characteristics and Functions in Cancer Immunity. <i>Current Allergy and Asthma Reports</i> , 2016, 16, 7.	5.3	76
23	Mechanism of the Antigen-Independent Cytokinerigic SPE-7 IgE Activation of Human Mast Cells in Vitro. <i>Scientific Reports</i> , 2015, 5, 9538.	3.3	27
24	Structure and dynamics of IgE μ receptor interactions: Fc μ RI and μ CD23/Fc μ RII. <i>Immunological Reviews</i> , 2015, 268, 222-235.	6.0	85
25	Human IgG4: a structural perspective. <i>Immunological Reviews</i> , 2015, 268, 139-159.	6.0	119
26	Dynamics of Inter-heavy Chain Interactions in Human Immunoglobulin G (IgG) Subclasses Studied by Kinetic Fab Arm Exchange. <i>Journal of Biological Chemistry</i> , 2014, 289, 6098-6109.	3.4	76
27	A range of C μ 3 μ 4 interdomain angles in IgE Fc accommodate binding to its receptor CD23. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 305-309.	0.8	12
28	Structural Determinants of Unique Properties of Human IgG4-Fc. <i>Journal of Molecular Biology</i> , 2014, 426, 630-644.	4.2	96
29	Crystal structure of deglycosylated human IgG4-Fc. <i>Molecular Immunology</i> , 2014, 62, 46-53.	2.2	35
30	Human immunoglobulin E flexes between acutely bent and extended conformations. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 397-404.	8.2	52
31	Conformational plasticity at the IgE-binding site of the B-cell receptor CD23. <i>Molecular Immunology</i> , 2013, 56, 693-697.	2.2	16
32	Crystal structure of the human IgG4 CH3 dimer reveals the role of Arg409 in the mechanism of Fab-arm exchange. <i>Molecular Immunology</i> , 2013, 54, 1-7.	2.2	39
33	Allergy's Achilles' heel?. <i>Nature Chemical Biology</i> , 2013, 9, 757-759.	8.0	1
34	Ca ²⁺ -dependent Structural Changes in the B-cell Receptor CD23 Increase Its Affinity for Human Immunoglobulin E. <i>Journal of Biological Chemistry</i> , 2013, 288, 21667-21677.	3.4	27
35	Mapping of the CD23 Binding Site on Immunoglobulin E (IgE) and Allosteric Control of the IgE-Fc μ RI Interaction. <i>Journal of Biological Chemistry</i> , 2012, 287, 31457-31461.	3.4	21
36	Soluble CD23 Controls IgE Synthesis and Homeostasis in Human B Cells. <i>Journal of Immunology</i> , 2012, 188, 3199-3207.	0.8	67

#	ARTICLE	IF	CITATIONS
37	Crystal structure of IgE bound to its B-cell receptor CD23 reveals a mechanism of reciprocal allosteric inhibition with high affinity receptor Fc μ RI. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12686-12691.	7.1	82
38	A Fluorescent Biosensor Reveals Conformational Changes in Human Immunoglobulin E Fc. Journal of Biological Chemistry, 2012, 287, 17459-17470.	3.4	49
39	Synthesis and Incorporation into Cyclic Peptides of Tolan Amino Acids and Their Hydrogenated Congeners: Construction of an Array of A α B-loop Mimetics of the C μ 3 Domain of Human IgE. Journal of Organic Chemistry, 2012, 77, 3197-3214.	3.2	21
40	Synthesis of the C19 methyl ether of aspercyclide A via germyl-Stille macrocyclisation and ELISA evaluation of both enantiomers following optical resolution. Organic and Biomolecular Chemistry, 2011, 9, 6814.	2.8	10
41	Conformational changes in IgE contribute to its uniquely slow dissociation rate from receptor Fc ϵ RI. Nature Structural and Molecular Biology, 2011, 18, 571-576.	8.2	105
42	Mutations in an avian IgY-Fc fragment reveal the locations of monocyte Fc receptor binding sites. Developmental and Comparative Immunology, 2010, 34, 97-101.	2.3	18
43	Total synthesis of (\pm)-aspercyclide A and its C19 methyl ether. Chemical Communications, 2010, 46, 1824-1826.	4.1	31
44	The Crystal Structure of an Avian IgY-Fc Fragment Reveals Conservation with both Mammalian IgG and IgE. Biochemistry, 2009, 48, 558-562.	2.5	54
45	The crystal structure of rabbit IgG-Fc. Biochemical Journal, 2009, 417, 77-83.	3.7	25
46	IgE in allergy and asthma today. Nature Reviews Immunology, 2008, 8, 205-217.	22.7	947
47	Attenuation of IgE Affinity for Fc μ RI Radically Reduces the Allergic Response in Vitro and in Vivo. Journal of Biological Chemistry, 2008, 283, 29882-29887.	3.4	11
48	Asp-120 Locates Zn ²⁺ for Optimal Metallo- β -lactamase Activity. Journal of Biological Chemistry, 2007, 282, 18276-18285.	3.4	40
49	Soluble CD23 Monomers Inhibit and Oligomers Stimulate IGE Synthesis in Human B Cells. Journal of Biological Chemistry, 2007, 282, 24083-24091.	3.4	66
50	The Allergic March from Staphylococcus aureus Superantigens to Immunoglobulin E. , 2007, 93, 106-136.		51
51	Crystal Structure of a Human Autoimmune Complex between IgM Rheumatoid Factor RF61 and IgG1 Fc Reveals a Novel Epitope and Evidence for Affinity Maturation. Journal of Molecular Biology, 2007, 368, 1321-1331.	4.2	61
52	Three-colour flow cytometric method to measure antibody-dependent tumour cell killing by cytotoxicity and phagocytosis. Journal of Immunological Methods, 2007, 323, 160-171.	1.4	45
53	Role of IgE receptors in IgE antibody-dependent cytotoxicity and phagocytosis of ovarian tumor cells by human monocytic cells. Cancer Immunology, Immunotherapy, 2007, 57, 247-263.	4.2	65
54	Analysis of the interaction between RGD-expressing adenovirus type 5 fiber knob domains and α v β 3 integrin reveals distinct binding profiles and intracellular trafficking. Journal of General Virology, 2006, 87, 2497-2505.	2.9	19

#	ARTICLE	IF	CITATIONS
55	Disulfide Linkage Controls the Affinity and Stoichiometry of IgE Fc μ 3 γ 4 Binding to Fc μ R1. <i>Journal of Biological Chemistry</i> , 2005, 280, 16808-16814.	3.4	30
56	The structure of human CD23 and its interactions with IgE and CD21. <i>Journal of Experimental Medicine</i> , 2005, 202, 751-760.	8.5	127
57	Biased use of VH5 IgE-positive B cells in the nasal mucosa in allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2005, 116, 445-452.	2.9	61
58	The Biology of IgE and the Basis of Allergic Disease. <i>Annual Review of Immunology</i> , 2003, 21, 579-628.	21.8	576
59	The crystal structure of IgE Fc reveals an asymmetrically bent conformation. <i>Nature Immunology</i> , 2002, 3, 681-686.	14.5	152
60	Regulation of Cutaneous Malignancy by β 1 T Cells. <i>Science</i> , 2001, 294, 605-609.	12.6	895
61	Endocytosis and recycling of the complex between CD23 and HLA-DR in human B cells. <i>Immunology</i> , 2001, 103, 319-331.	4.4	61
62	The structure of the IgE Cepsilon2 domain and its role in stabilizing the complex with its high-affinity receptor FcepsilonR1alpha. <i>Nature Structural Biology</i> , 2001, 8, 437-441.	9.7	73
63	Complex between <i>Peptostreptococcus magnus</i> Protein L and a Human Antibody Reveals Structural Convergence in the Interaction Modes of Fab Binding Proteins. <i>Structure</i> , 2001, 9, 679-687.	3.3	121
64	The structure and origin of rheumatoid factors. <i>Trends in Immunology</i> , 2000, 21, 177-183.	7.5	90
65	Conformation of the Isolated C μ 3 Domain of IgE and Its Complex with the High-Affinity Receptor, Fc μ R1 α . <i>Biochemistry</i> , 2000, 39, 7406-7413.	2.5	40
66	The Structure of a Human Rheumatoid Factor Bound to IgG Fc. <i>Advances in Experimental Medicine and Biology</i> , 1998, 435, 41-50.	1.6	15
67	Participation of the N-Terminal Region of C μ 3 in the Binding of Human IgE to Its High-Affinity Receptor Fc μ R1 α . <i>Biochemistry</i> , 1997, 36, 15568-15578.	2.5	71
68	Interaction of the Low-Affinity Receptor CD23/Fc μ R1II Lectin Domain with the Fc μ 3 γ 4 Fragment of Human Immunoglobulin E α . <i>Biochemistry</i> , 1997, 36, 2112-2122.	2.5	62
69	Structure of human IgM rheumatoid factor Fab bound to its autoantigen IgG Fc reveals a novel topology of antibody α antigen interaction. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 374-381.	8.2	200
70	Cleavage of the low α affinity receptor for human IgE (CD23) by a mite cysteine protease: Nature of the cleaved fragment in relation to the structure and function of CD23. <i>European Journal of Immunology</i> , 1997, 27, 584-588.	2.9	86
71	Bent Domain Structure of Recombinant Human IgE-Fc in Solution by X-ray and Neutron Scattering in Conjunction with an Automated Curve Fitting Procedure. <i>Biochemistry</i> , 1995, 34, 14449-14461.	2.5	77
72	Secretion of recombinant human IgE-Fc by mammalian cells and biological activity of glycosylation site mutants. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 193-199.	2.1	51

#	ARTICLE	IF	CITATIONS
73	Prediction of domain organisation and secondary structure of thyroid peroxidase, a human autoantigen involved in destructive thyroiditis. FEBS Letters, 1990, 266, 133-141.	2.8	33