

Theodore S Jardetzky

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

5,831
citations

87888

38
h-index

79698

73
g-index

81
all docs

81
docs citations

81
times ranked

6883
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of functionally important domains of human cytomegalovirus gO that act after trimer binding to receptors. <i>PLoS Pathogens</i> , 2022, 18, e1010452.	4.7	1
2	The structural basis of herpesvirus entry. <i>Nature Reviews Microbiology</i> , 2021, 19, 110-121.	28.6	174
3	Bottom-up de novo design of functional proteins with complex structural features. <i>Nature Chemical Biology</i> , 2021, 17, 492-500.	8.0	65
4	EphrinB2 clustering by Nipah virus G is required to activate and trap F intermediates at supported lipid bilayerâ€‘cell interfaces. <i>Science Advances</i> , 2021, 7, .	10.3	18
5	Structure-guided design of ultrapotent disruptive IgE inhibitors to rapidly terminate acute allergic reactions. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1049-1060.	2.9	21
6	The role of allergenâ€‘specific IgE, IgG and IgA in allergic disease. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3627-3641.	5.7	100
7	Accuracy of serological testing for SARSâ€‘CoVâ€‘2 antibodies: First results of a large mixedâ€‘method evaluation study. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 853-865.	5.7	34
8	Cryo-Electron Microscopy Structure and Interactions of the Human Cytomegalovirus gH/gL/gO Trimer with Platelet-Derived Growth Factor Receptor Alpha. <i>MBio</i> , 2021, 12, e0262521.	4.1	2
9	Direct comparison of antibody responses to four SARS-CoV-2 vaccines in Mongolia. <i>Cell Host and Microbe</i> , 2021, 29, 1738-1743.e4.	11.0	61
10	Directed evolution of and structural insights into antibody-mediated disruption of a stable receptor-ligand complex. <i>Nature Communications</i> , 2021, 12, 7069.	12.8	6
11	The mechanistic and functional profile of the therapeutic anti-IgE antibody ligelizumab differs from omalizumab. <i>Nature Communications</i> , 2020, 11, 165.	12.8	123
12	Human B Cell Clonal Expansion and Convergent Antibody Responses to SARS-CoV-2. <i>Cell Host and Microbe</i> , 2020, 28, 516-525.e5.	11.0	219
13	Epstein-Barr Virus gH/gL and Kaposiâ€™s Sarcoma-Associated Herpesvirus gH/gL Bind to Different Sites on EphA2 To Trigger Fusion. <i>Journal of Virology</i> , 2020, 94, .	3.4	11
14	Defining the features and duration of antibody responses to SARS-CoV-2 infection associated with disease severity and outcome. <i>Science Immunology</i> , 2020, 5, .	11.9	404
15	IPSE, a urogenital parasite-derived immunomodulatory molecule, suppresses bladder pathogenesis and anti-microbial peptide gene expression in bacterial urinary tract infection. <i>Parasites and Vectors</i> , 2020, 13, 615.	2.5	2
16	IPSE, an abundant egg-secreted protein of the carcinogenic helminth <i>Schistosoma haematobium</i> , promotes proliferation of bladder cancer cells and angiogenesis. <i>Infectious Agents and Cancer</i> , 2020, 15, 63.	2.6	15
17	De novo protein design enables the precise induction of RSV-neutralizing antibodies. <i>Science</i> , 2020, 368, .	12.6	137
18	IPSE, a parasite-derived, host immunomodulatory infiltrin protein, alleviates resiniferatoxin-induced bladder pain. <i>Molecular Pain</i> , 2020, 16, 174480692097009.	2.1	1

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19	HCMV trimer- and pentamer-specific antibodies synergize for virus neutralization but do not correlate with congenital transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3728-3733.	7.1	42
20	Ephrin Receptor A4 is a New Kaposi's Sarcoma-Associated Herpesvirus Virus Entry Receptor. <i>MBio</i> , 2019, 10, .	4.1	34
21	IPSE, a urogenital parasite-derived immunomodulatory protein, ameliorates ifosfamide-induced hemorrhagic cystitis through downregulation of pro-inflammatory pathways. <i>Scientific Reports</i> , 2019, 9, 1586.	3.3	15
22	IPSE, a parasite-derived host immunomodulatory protein, is a potential therapeutic for hemorrhagic cystitis. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, F1133-F1140.	2.7	8
23	Ephrin receptor A2 is a functional entry receptor for Epstein-Barr virus. <i>Nature Microbiology</i> , 2018, 3, 172-180.	13.3	157
24	Therapeutic exploitation of IPSE, a urogenital parasite-derived host modulatory protein, for chemotherapy-induced hemorrhagic cystitis. <i>FASEB Journal</i> , 2018, 32, 4408-4419.	0.5	21
25	Structural basis for antibody cross-neutralization of respiratory syncytial virus and human metapneumovirus. <i>Nature Microbiology</i> , 2017, 2, 16272.	13.3	65
26	The COMPLEXity in herpesvirus entry. <i>Current Opinion in Virology</i> , 2017, 24, 97-104.	5.4	74
27	Monomeric ephrinB2 binding induces allosteric changes in Nipah virus G that precede its full activation. <i>Nature Communications</i> , 2017, 8, 781.	12.8	38
28	H-IPSE Is a Pathogen-Secreted Host Nucleus-Infiltrating Protein (Infiltrin) Expressed Exclusively by the <i>Schistosoma haematobium</i> Egg Stage. <i>Infection and Immunity</i> , 2017, 85, .	2.2	29
29	Inhibition of EBV-mediated membrane fusion by anti-gHgL antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8703-E8710.	7.1	27
30	Epstein-Barr Virus Fusion with Epithelial Cells Triggered by gB Is Restricted by a gL Glycosylation Site. <i>Journal of Virology</i> , 2017, 91, .	3.4	16
31	Editorial overview: Virus structure and functions. <i>Current Opinion in Virology</i> , 2017, 24, ix.	5.4	1
32	Immobilization of the N-terminal helix stabilizes prefusion paramyxovirus fusion proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3844-51.	7.1	4
33	Structural basis for Epstein-Barr virus host cell tropism mediated by gp42 and gHgL entry glycoproteins. <i>Nature Communications</i> , 2016, 7, 13557.	12.8	79
34	The Cytoplasmic Tail Domain of Epstein-Barr Virus gH Regulates Membrane Fusion Activity through Altering gH Binding to gp42 and Epithelial Cell Attachment. <i>MBio</i> , 2016, 7, .	4.1	14
35	Comparative Mutagenesis of Pseudorabies Virus and Epstein-Barr Virus gH Identifies a Structural Determinant within Domain III of gH Required for Surface Expression and Entry Function. <i>Journal of Virology</i> , 2016, 90, 2285-2293.	3.4	5
36	Structural basis for nonneutralizing antibody competition at antigenic site II of the respiratory syncytial virus fusion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6849-E6858.	7.1	38

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37	Structural basis of omalizumab therapy and omalizumab-mediated IgE exchange. <i>Nature Communications</i> , 2016, 7, 11610.	12.8	86
38	Mutagenesis of Paramyxovirus Hemagglutinin-Neuraminidase Membrane-Proximal Stalk Region Influences Stability, Receptor Binding, and Neuraminidase Activity. <i>Journal of Virology</i> , 2016, 90, 7778-7788.	3.4	16
39	Structure and stabilization of the Hendra virus F glycoprotein in its prefusion form. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1056-1061.	7.1	58
40	A Chimeric Pneumovirus Fusion Protein Carrying Neutralizing Epitopes of Both MPV and RSV. <i>PLoS ONE</i> , 2016, 11, e0155917.	2.5	14
41	Structural and Mechanistic Insights into the Tropism of Epstein-Barr Virus. <i>Molecules and Cells</i> , 2016, 39, 286-291.	2.6	47
42	On the Stability of Parainfluenza Virus 5 F Proteins. <i>Journal of Virology</i> , 2015, 89, 3438-3441.	3.4	6
43	Timing is everything: Fine-tuned molecular machines orchestrate paramyxovirus entry. <i>Virology</i> , 2015, 479-480, 518-531.	2.4	96
44	Membrane Anchoring of Epstein-Barr Virus gp42 Inhibits Fusion with B Cells Even with Increased Flexibility Allowed by Engineered Spacers. <i>MBio</i> , 2015, 6, .	4.1	6
45	Assembly and Architecture of the EBV B Cell Entry Triggering Complex. <i>PLoS Pathogens</i> , 2014, 10, e1004309.	4.7	68
46	The Epstein-Barr Virus (EBV) Glycoprotein B Cytoplasmic C-Terminal Tail Domain Regulates the Energy Requirement for EBV-Induced Membrane Fusion. <i>Journal of Virology</i> , 2014, 88, 11686-11695.	3.4	22
47	The Conserved Disulfide Bond within Domain II of Epstein-Barr Virus gH Has Divergent Roles in Membrane Fusion with Epithelial Cells and B Cells. <i>Journal of Virology</i> , 2014, 88, 13570-13579.	3.4	18
48	Activation of paramyxovirus membrane fusion and virus entry. <i>Current Opinion in Virology</i> , 2014, 5, 24-33.	5.4	120
49	Probing the Functions of the Paramyxovirus Glycoproteins F and HN with a Panel of Synthetic Antibodies. <i>Journal of Virology</i> , 2014, 88, 11713-11725.	3.4	9
50	Accelerated dissociation of IgE-Fc μ RI complexes by disruptive inhibitors actively desensitizes allergic effector cells. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1709-1719.e8.	2.9	122
51	Probing the paramyxovirus fusion (F) protein-refolding event from pre- to postfusion by oxidative footprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2596-605.	7.1	44
52	Fusion Activation through Attachment Protein Stalk Domains Indicates a Conserved Core Mechanism of Paramyxovirus Entry into Cells. <i>Journal of Virology</i> , 2014, 88, 3925-3941.	3.4	76
53	Mutations in the Parainfluenza Virus 5 Fusion Protein Reveal Domains Important for Fusion Triggering and Metastability. <i>Journal of Virology</i> , 2013, 87, 13520-13531.	3.4	62
54	A soluble form of Epstein-Barr virus gH/gL inhibits EBV-induced membrane fusion and does not function in fusion. <i>Virology</i> , 2013, 436, 118-126.	2.4	13

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55	An Engineered Disulfide Bond Reversibly Traps the IgE-Fc γ 4 in a Closed, Nonreceptor Binding Conformation. <i>Journal of Biological Chemistry</i> , 2012, 287, 36251-36257.	3.4	10
56	Accelerated disassembly of IgE γ receptor complexes by a disruptive macromolecular inhibitor. <i>Nature</i> , 2012, 491, 613-617.	27.8	89
57	Fusing structure and function: a structural view of the herpesvirus entry machinery. <i>Nature Reviews Microbiology</i> , 2011, 9, 369-381.	28.6	372
58	Structure of the Newcastle disease virus hemagglutinin-neuraminidase (HN) ectodomain reveals a four-helix bundle stalk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14920-14925.	7.1	147
59	Crystal structure of the Epstein-Barr virus (EBV) glycoprotein H/glycoprotein L (gH/gL) complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22641-22646.	7.1	141
60	Analysis of Epstein-Barr Virus Glycoprotein B Functional Domains via Linker Insertion Mutagenesis. <i>Journal of Virology</i> , 2009, 83, 734-747.	3.4	27
61	Structure of a trimeric variant of the Epstein γ Barr virus glycoprotein B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2880-2885.	7.1	199
62	Cleavage and Secretion of Epstein-Barr Virus Glycoprotein 42 Promote Membrane Fusion with B Lymphocytes. <i>Journal of Virology</i> , 2009, 83, 6664-6672.	3.4	32
63	Class III viral membrane fusion proteins. <i>Current Opinion in Structural Biology</i> , 2009, 19, 189-196.	5.7	123
64	Structure of Epstein-Barr Virus Glycoprotein 42 Suggests a Mechanism for Triggering Receptor-Activated Virus Entry. <i>Structure</i> , 2009, 17, 223-233.	3.3	56
65	Conformational Flexibility in Immunoglobulin E-Fc γ 4 Revealed in Multiple Crystal Forms. <i>Journal of Molecular Biology</i> , 2009, 393, 176-190.	4.2	35
66	Binding-Site Interactions between Epstein-Barr Virus Fusion Proteins gp42 and gH/gL Reveal a Peptide That Inhibits both Epithelial and B-Cell Membrane Fusion. <i>Journal of Virology</i> , 2007, 81, 9216-9229.	3.4	50
67	Hydrophobic Residues That Form Putative Fusion Loops of Epstein-Barr Virus Glycoprotein B Are Critical for Fusion Activity. <i>Journal of Virology</i> , 2007, 81, 9596-9600.	3.4	55
68	Structure of the parainfluenza virus 5 F protein in its metastable, prefusion conformation. <i>Nature</i> , 2006, 439, 38-44.	27.8	374
69	Structural Changes in the Lectin Domain of CD23, the Low-Affinity IgE Receptor, upon Calcium Binding. <i>Structure</i> , 2006, 14, 1049-1058.	3.3	36
70	Activation of a paramyxovirus fusion protein is modulated by inside-out signaling from the cytoplasmic tail. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9217-9222.	7.1	78
71	Mutational Analyses of Epstein-Barr Virus Glycoprotein 42 Reveal Functional Domains Not Involved in Receptor Binding but Required for Membrane Fusion. <i>Journal of Virology</i> , 2004, 78, 5946-5956.	3.4	46
72	Structure of the Epstein-Barr Virus gp42 Protein Bound to the MHC Class II Receptor HLA-DR1. <i>Molecular Cell</i> , 2002, 9, 375-385.	9.7	138

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73	Structure of the Fc fragment of human IgE bound to its high-affinity receptor Fc γ RII \pm . Nature, 2000, 406, 259-266.	27.8	327
74	Structure of the Human IgE-Fc C γ 3-C γ 4 Reveals Conformational Flexibility in the Antibody Effector Domains. Immunity, 2000, 13, 375-385.	14.3	89
75	THE CRYSTAL STRUCTURE OF THE HUMAN HIGH-AFFINITY IgE RECEPTOR (Fc γ RII \pm). Annual Review of Immunology, 1999, 17, 973-976.	21.8	37
76	Structural basis for HLA-DQ binding by the streptococcal superantigen SSA. , 1999, 6, 123-129.		51
77	Structural Basis for Paramyxovirus-Mediated Membrane Fusion. Molecular Cell, 1999, 3, 309-319.	9.7	371