

Alexey Teplyakov

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

2,344
citations

236925

25
h-index

214800

47
g-index

61
all docs

61
docs citations

61
times ranked

3200
citing authors

#	ARTICLE	IF	CITATIONS
1	Surface salt bridges contribute to the extreme thermal stability of an FN3-like domain from a thermophilic bacterium. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 270-281.	2.6	5
2	Discovery and Functional Characterization of hPT3, a Humanized Anti-Phospho Tau Selective Monoclonal Antibody. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 1397-1416.	2.6	12
3	Antibody Structure and Function: The Basis for Engineering Therapeutics. <i>Antibodies</i> , 2019, 8, 55.	2.5	273
4	Crystal structure of cell co-receptor CD19 in complex with antibody B43 reveals an unexpected fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 495-500.	2.6	31
5	Structural insights into chemokine CCL17 recognition by antibody M116. <i>Biochemistry and Biophysics Reports</i> , 2018, 13, 27-31.	1.3	3
6	Structural insights into humanization of anti-tissue factor antibody 10H10. <i>MAbs</i> , 2018, 10, 269-277.	5.2	11
7	Cover Image, Volume 86, Issue 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C4-C4.	2.6	0
8	Abstract 3813: Development of JNJ-64164711, a low fucose anti-GITR antibody for enhanced depletion of tumor regulatory T cells (Tregs). , 2018, , .		0
9	Epitope-dependent mechanisms of CD27 neutralization revealed by X-ray crystallography. <i>Molecular Immunology</i> , 2017, 83, 92-99.	2.2	6
10	Crystal structure of CD27 in complex with a neutralizing noncompeting antibody. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 294-299.	0.8	9
11	Crystal structure of tissue factor in complex with antibody 10H10 reveals the signaling epitope. <i>Cellular Signalling</i> , 2017, 36, 139-144.	3.6	9
12	A coiled conformation of amyloid- β^2 recognized by antibody C706. <i>Alzheimer's Research and Therapy</i> , 2017, 9, 66.	6.2	2
13	Conformational flexibility of an anti-IL-13 DARPin. <i>Protein Engineering, Design and Selection</i> , 2016, 30, 31-37.	2.1	9
14	Structural diversity in a human antibody germline library. <i>MAbs</i> , 2016, 8, 1045-1063.	5.2	51
15	Epitope mapping and structural basis for the recognition of phosphorylated tau by the anti-tau antibody AT8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 427-434.	2.6	84
16	Development of a CD123xCD3 Bispecific Antibody (JNJ-63709178) for the Treatment of Acute Myeloid Leukemia (AML). <i>Blood</i> , 2016, 128, 2824-2824.	1.4	27
17	Abstract 1492: Development of a CD123xCD3 bispecific antibody to treat acute myeloid leukemia (AML). , 2016, , .		0
18	Induced conformational change in human IL-4 upon binding of a signal-neutralizing DARPin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1191-1197.	2.6	5

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19	Canonical structures of short CDR ϵ L3 in antibodies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1668-1673.	2.6	17
20	Second antibody modeling assessment (AMA ϵ). <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1553-1562.	2.6	129
21	Structural evidence for a constrained conformation of short CDR ϵ L3 in antibodies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1679-1683.	2.6	6
22	Structure and specificity of an antibody targeting a proteolytically cleaved IgG hinge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1656-1667.	2.6	15
23	Protein crystallization with microseed matrix screening: application to human germline antibody Fabs. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1107-1115.	0.8	17
24	An engineered Fc variant of an IgG eliminates all immune effector functions via structural perturbations. <i>Methods</i> , 2014, 65, 114-126.	3.8	127
25	Antibody modeling assessment II. Structures and models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1563-1582.	2.6	60
26	N ϵ -terminal \hat{I} ϵ -strand swapping in a consensus ϵ -derived alternative scaffold driven by stabilizing hydrophobic interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1527-1533.	2.6	4
27	C ϵ -terminal \hat{I} ϵ -strand swapping in a consensus ϵ -derived fibronectin Type III scaffold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1359-1369.	2.6	9
28	IgG2 Fc structure and the dynamic features of the IgG CH2 ϵ -CH3 interface. <i>Molecular Immunology</i> , 2013, 56, 131-139.	2.2	60
29	Mechanisms of self-association of a human monoclonal antibody CNTO607. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 531-538.	2.1	70
30	Design of novel FN3 domains with high stability by a consensus sequence approach. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 107-117.	2.1	69
31	Lateral Clustering of TLR3:dsRNA Signaling Units Revealed by TLR3ecd:3Fabs Quaternary Structure. <i>Journal of Molecular Biology</i> , 2012, 421, 112-124.	4.2	37
32	Structural basis for high selectivity of anti-CCL2 neutralizing antibody CNTO 888. <i>Molecular Immunology</i> , 2012, 51, 227-233.	2.2	23
33	Crystal structure of human germline antibody 3-23/B3. <i>Molecular Immunology</i> , 2011, 48, 1586-1588.	2.2	9
34	Antigen recognition by antibody C836 through adjustment of V _L /V _H packing. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1165-1167.	0.7	17
35	Crystallization of a challenging antigen ϵ -antibody complex: TLR3 ECD with three noncompeting Fabs. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1290-1295.	0.7	11
36	Antibody modeling assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3050-3066.	2.6	114

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37	His-tag binding by antibody C706 mimics amyloid recognition. <i>Journal of Molecular Recognition</i> , 2011, 24, 570-575.	2.1	5
38	On the domain pairing in chimeric antibodies. <i>Molecular Immunology</i> , 2010, 47, 2422-2426.	2.2	6
39	Synthesis by native chemical ligation and crystal structure of human CCL2. <i>Biopolymers</i> , 2010, 94, 350-359.	2.4	9
40	Promoting crystallization of antibody-antigen complexes via microseed matrix screening. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 927-933.	2.5	34
41	Noncanonical conformation of CDR L1 in the anti-IL-23 antibody CNTO4088. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 229-232.	0.7	1
42	Structure-based engineering of a monoclonal antibody for improved solubility. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 643-651.	2.1	187
43	Human Framework Adaptation of a Mouse Anti-Human IL-13 Antibody. <i>Journal of Molecular Biology</i> , 2010, 398, 214-231.	4.2	55
44	Structural Basis for the Dual Recognition of IL-12 and IL-23 by Ustekinumab. <i>Journal of Molecular Biology</i> , 2010, 402, 797-812.	4.2	93
45	Coevolution of Antibody Stability and CDR-L3 Canonical Structure. <i>Journal of Molecular Biology</i> , 2010, 402, 708-719.	4.2	38
46	Structure of the EMMPRIN N-terminal domain 1: Dimerization via strand swapping. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 1009-1014.	2.6	19
47	Epitope Mapping of Anti-Interleukin-13 Neutralizing Antibody CNTO607. <i>Journal of Molecular Biology</i> , 2009, 389, 115-123.	4.2	55
48	Structure of phosphorylated enzyme I, the phosphoenolpyruvate:sugar phosphotransferase system sugar translocation signal protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16218-16223.	7.1	71
49	Crystal Structure of the Bacterial YhcH Protein Indicates a Role in Sialic Acid Catabolism. <i>Journal of Bacteriology</i> , 2005, 187, 5520-5527.	2.2	21
50	Crystal Structure of the Petal Death Protein from Carnation Flower. <i>Biochemistry</i> , 2005, 44, 16377-16384.	2.5	14
51	Crystal Structure of the YgfZ Protein from <i>Escherichia coli</i> Suggests a Folate-Dependent Regulatory Role in One-Carbon Metabolism. <i>Journal of Bacteriology</i> , 2004, 186, 7134-7140.	2.2	33
52	Crystal structure of the YffB protein from <i>Pseudomonas aeruginosa</i> suggests a glutathione-dependent thiol reductase function. <i>BMC Structural Biology</i> , 2004, 4, 5.	2.3	6
53	Crystal structure of the <i>Escherichia coli</i> YcdX protein reveals a trinuclear zinc active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 315-318.	2.6	43
54	Crystal structure of the <i>Escherichia coli</i> Tas protein, an NADP(H)-dependent aldo-keto reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 323-325.	2.6	7

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55	Crystal structure of the Escherichia coli YjiA protein suggests a GTP-dependent regulatory function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 371-374.	2.6	22
56	Crystal Structure of the YchF Protein Reveals Binding Sites for GTP and Nucleic Acid. <i>Journal of Bacteriology</i> , 2003, 185, 4031-4037.	2.2	56
57	From Lobry de Bruyn to enzyme-catalyzed ammonia channelling: molecular studies of D-glucosamine-6P synthase. <i>Natural Product Reports</i> , 2002, 19, 60-69.	10.3	46
58	Crystal structure of the YjeE protein from Haemophilus influenzae: A putative Atpase involved in cell wall synthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 220-226.	2.6	40
59	Channeling of ammonia in glucosamine-6-phosphate synthase 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 313, 1093-1102.	4.2	115
60	Crystal Structure of Dephospho-Coenzyme A Kinase from Haemophilus influenzae. <i>Journal of Structural Biology</i> , 2001, 136, 119-125.	2.8	37