

Anthony A Kossiakoff

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8700823/anthony-a-kossiakoff-publications-by-year.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

77
papers

3,902
citations

30
h-index

62
g-index

95
ext. papers

4,716
ext. citations

13.8
avg, IF

5
L-index

#	Paper	IF	Citations
77	Synthetic antibody binders detect distinct cellular states of Chromosome Passenger Complex proteins.. <i>Journal of Molecular Biology</i> , 2022 , 167602	6.5	
76	Development of a universal nanobody-binding Fab module for fiducial-assisted cryo-EM studies of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
75	Engineered Ultra-High Affinity Synthetic Antibodies for SARS-CoV-2 Neutralization and Detection. <i>Journal of Molecular Biology</i> , 2021 , 433, 166956	6.5	4
74	Structural basis of omega-3 fatty acid transport across the blood-brain barrier. <i>Nature</i> , 2021 , 595, 315-319	50.4	14
73	Inhibition of Cancer Cell Adhesion, Migration and Proliferation by a Bispecific Antibody that Targets two Distinct Epitopes on α Integrins. <i>Journal of Molecular Biology</i> , 2021 , 433, 167090	6.5	1
72	Structure of an AMPK complex in an inactive, ATP-bound state. <i>Science</i> , 2021 , 373, 413-419	33.3	5
71	K29-linked ubiquitin signaling regulates proteotoxic stress response and cell cycle. <i>Nature Chemical Biology</i> , 2021 , 17, 896-905	11.7	12
70	Structures of rhodopsin in complex with G-protein-coupled receptor kinase 1. <i>Nature</i> , 2021 , 595, 600-605	50.4	20
69	Structures of ABCB4 provide insight into phosphatidylcholine translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
68	Synthetic antibodies against BRIL as universal fiducial marks for single-particle cryoEM structure determination of membrane proteins. <i>Nature Communications</i> , 2020 , 11, 1598	17.4	17
67	Structure and mechanism of the ER-based glucosyltransferase ALG6. <i>Nature</i> , 2020 , 579, 443-447	50.4	21
66	Structure of human Frizzled5 by fiducial-assisted cryo-EM supports a heterodimeric mechanism of canonical Wnt signaling. <i>ELife</i> , 2020 , 9,	8.9	23
65	Recognition of an Ehelical hairpin in P22 large terminase by a synthetic antibody fragment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 876-888	5.5	2
64	An engineered ultra-high affinity Fab-Protein G pair enables a modular antibody platform with multifunctional capability. <i>Protein Science</i> , 2020 , 29, 141-156	6.3	3
63	Rapid Discovery and Characterization of Synthetic Neutralizing Antibodies against Anthrax Edema Toxin. <i>Biochemistry</i> , 2019 , 58, 2996-3004	3.2	3
62	Development of "Plug and Play" Fiducial Marks for Structural Studies of GPCR Signaling Complexes by Single-Particle Cryo-EM. <i>Structure</i> , 2019 , 27, 1862-1874.e7	5.2	12
61	Structure and drug resistance of the Plasmodium falciparum transporter PfCRT. <i>Nature</i> , 2019 , 576, 315-320	32.4	59

60	Reply to Kang and Brooks: Comment on the calculations in protein thermodynamics. <i>Journal of Biological Chemistry</i> , 2018 , 293, 5063	5.4	
59	Locking the Elbow: Improved Antibody Fab Fragments as Chaperones for Structure Determination. <i>Journal of Molecular Biology</i> , 2018 , 430, 337-347	6.5	34
58	Engineered synthetic antibodies as probes to quantify the energetic contributions of ligand binding to conformational changes in proteins. <i>Journal of Biological Chemistry</i> , 2018 , 293, 2815-2828	5.4	15
57	The structure of the C-terminal domain of the nucleoprotein from the Bundibugyo strain of the Ebola virus in complex with a pan-specific synthetic Fab. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 681-689	5.5	5
56	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018 , 558, 553-558	50.4	153
55	Structural basis for activation of SAGA histone acetyltransferase Gcn5 by partner subunit Ada2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 10010-10015	11.5	23
54	Structural basis for activation of voltage sensor domains in an ion channel TPC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9095-E9104	11.5	25
53	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018 , 7,	8.9	27
52	Prolactin Receptor-Mediated Internalization of Imaging Agents Detects Epithelial Ovarian Cancer with Enhanced Sensitivity and Specificity. <i>Cancer Research</i> , 2017 , 77, 1684-1696	10.1	7
51	Generation of Synthetic Antibody Fragments to Detergent Solubilized Membrane Proteins. <i>Springer Protocols</i> , 2017 , 231-243	0.3	
50	Targeted rescue of cancer-associated IDH1 mutant activity using an engineered synthetic antibody. <i>Scientific Reports</i> , 2017 , 7, 556	4.9	4
49	Generating Conformation and Complex-Specific Synthetic Antibodies. <i>Methods in Molecular Biology</i> , 2017 , 1575, 93-119	1.4	9
48	Conformational Chaperones for Structural Studies of Membrane Proteins Using Antibody Phage Display with Nanodiscs. <i>Structure</i> , 2016 , 24, 300-9	5.2	35
47	A polar ring endows improved specificity to an antibody fragment. <i>Protein Science</i> , 2016 , 25, 1290-8	6.3	9
46	Specific Recognition of a Single-Stranded RNA Sequence by a Synthetic Antibody Fragment. <i>Journal of Molecular Biology</i> , 2016 , 428, 4100-4114	6.5	8
45	The Preserved HTH-Docking Cleft of HIV-1 Integrase Is Functionally Critical. <i>Structure</i> , 2016 , 24, 1936-1946	3.6	3
44	Protein targeting. Structure of the Get3 targeting factor in complex with its membrane protein cargo. <i>Science</i> , 2015 , 347, 1152-5	33.3	74
43	Engineering synthetic antibody binders for allosteric inhibition of prolactin receptor signaling. <i>Cell Communication and Signaling</i> , 2015 , 13, 1	7.5	21

42	A New Versatile Immobilization Tag Based on the Ultra High Affinity and Reversibility of the Calmodulin-Calmodulin Binding Peptide Interaction. <i>Journal of Molecular Biology</i> , 2015 , 427, 2707-25	6.5	16
41	Engineering Synthetic Antibody Inhibitors Specific for LD2 or LD4 Motifs of Paxillin. <i>Journal of Molecular Biology</i> , 2015 , 427, 2532-2547	6.5	6
40	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015 , 12, 725-31	21.6	86
39	Phage display selections for affinity reagents to membrane proteins in nanodiscs. <i>Methods in Enzymology</i> , 2015 , 557, 219-45	1.7	30
38	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2833-47	7.6	75
37	A YidC-like Protein in the Archaeal Plasma Membrane. <i>Structure</i> , 2015 , 23, 1715-1724	5.2	43
36	Architecture of the fungal nuclear pore inner ring complex. <i>Science</i> , 2015 , 350, 56-64	33.3	80
35	Scalable high throughput selection from phage-displayed synthetic antibody libraries. <i>Journal of Visualized Experiments</i> , 2015 , 51492	1.6	16
34	Optimizing Production of Antigens and Fabs in the Context of Generating Recombinant Antibodies to Human Proteins. <i>PLoS ONE</i> , 2015 , 10, e0139695	3.7	20
33	Nuclear pores. Architecture of the nuclear pore complex coat. <i>Science</i> , 2015 , 347, 1148-52	33.3	84
32	Validation of Recombinant Antibodies Against Human Transcription Factors. <i>FASEB Journal</i> , 2015 , 29, 571.13	0.9	
31	Structural mechanism of voltage-dependent gating in an isolated voltage-sensing domain. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 244-52	17.6	173
30	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46
29	Visualization of arrestin recruitment by a G-protein-coupled receptor. <i>Nature</i> , 2014 , 512, 218-222	50.4	349
28	Probing the functions of the paramyxovirus glycoproteins F and HN with a panel of synthetic antibodies. <i>Journal of Virology</i> , 2014 , 88, 11713-25	6.6	8
27	Applications for an engineered Protein-G variant with a pH controllable affinity to antibody fragments. <i>Journal of Immunological Methods</i> , 2014 , 415, 24-30	2.5	23
26	Cell biology. New tricks for an old dimer. <i>Science</i> , 2014 , 344, 703-4	33.3	10
25	Generating conformation-specific synthetic antibodies to trap proteins in selected functional states. <i>Methods</i> , 2013 , 60, 3-14	4.6	61

24	Structure of active β arrestin-1 bound to a G-protein-coupled receptor phosphopeptide. <i>Nature</i> , 2013 , 497, 137-41	50.4	310
23	Mechanism of activation gating in the full-length KcsA K ⁺ channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 11896-9	11.5	60
22	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 100-6	17.6	56
21	Allosteric control of ligand-binding affinity using engineered conformation-specific effector proteins. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 437-42	17.6	49
20	Characterization of engineered actin binding proteins that control filament assembly and structure. <i>PLoS ONE</i> , 2010 , 5, e13960	3.7	8
19	An engineered substance P variant for receptor-mediated delivery of synthetic antibodies into tumor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 11011-5	11.5	39
18	Crystal structure of full-length KcsA in its closed conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6644-9	11.5	191
17	Understanding mechanisms governing protein-protein interactions from synthetic binding interfaces. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 499-506	8.1	26
16	Synthetic antibodies for specific recognition and crystallization of structured RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 82-7	11.5	103
15	The 1.38 Å crystal structure of DmsD protein from <i>Salmonella typhimurium</i> , a proofreading chaperone on the Tat pathway. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 525-33	4.2	24
14	Toward chaperone-assisted crystallography: protein engineering enhancement of crystal packing and X-ray phasing capabilities of a camelid single-domain antibody (VHH) scaffold. <i>Protein Science</i> , 2008 , 17, 1175-87	6.3	54
13	Exploring and designing protein function with restricted diversity. <i>Current Opinion in Chemical Biology</i> , 2007 , 11, 347-54	9.7	45
12	High-throughput generation of synthetic antibodies from highly functional minimalist phage-displayed libraries. <i>Journal of Molecular Biology</i> , 2007 , 373, 924-40	6.5	262
11	Exploring the capacity of minimalist protein interfaces: interface energetics and affinity maturation to picomolar KD of a single-domain antibody with a flat paratope. <i>Journal of Molecular Biology</i> , 2007 , 373, 941-53	6.5	63
10	Comprehensive and quantitative mapping of energy landscapes for protein-protein interactions by rapid combinatorial scanning. <i>Journal of Biological Chemistry</i> , 2006 , 281, 22378-22385	5.4	96
9	Crystal structure and site 1 binding energetics of human placental lactogen. <i>Journal of Molecular Biology</i> , 2006 , 358, 773-84	6.5	18
8	Intramolecular cooperativity in a protein binding site assessed by combinatorial shotgun scanning mutagenesis. <i>Journal of Molecular Biology</i> , 2005 , 347, 489-94	6.5	26
7	Alternative views of functional protein binding epitopes obtained by combinatorial shotgun scanning mutagenesis. <i>Protein Science</i> , 2005 , 14, 2405-13	6.3	30

6	Shotgun alanine scanning shows that growth hormone can bind productively to its receptor through a drastically minimized interface. <i>Journal of Biological Chemistry</i> , 2005 , 280, 25524-32	5.4	30
5	The structural basis for biological signaling, regulation, and specificity in the growth hormone-prolactin system of hormones and receptors. <i>Advances in Protein Chemistry</i> , 2004 , 68, 147-69		35
4	The functional binding epitope of a high affinity variant of human growth hormone mapped by shotgun alanine-scanning mutagenesis: insights into the mechanisms responsible for improved affinity. <i>Journal of Molecular Biology</i> , 2003 , 332, 195-204	6.5	41
3	The X-ray structure of a growth hormone-prolactin receptor complex. <i>Nature</i> , 1994 , 372, 478-81	50.4	365
2	X-ray structures of the antigen-binding domains from three variants of humanized anti-p185HER2 antibody 4D5 and comparison with molecular modeling. <i>Journal of Molecular Biology</i> , 1993 , 229, 969-95	6.5	172
1	Architecture of the cytoplasmic face of the nuclear pore		6