

# Anthony A Kossiakoff

## List of Publications by Year in descending order

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85  
papers

5,435  
citations

101384

36  
h-index

88477

70  
g-index

95  
all docs

95  
docs citations

95  
times ranked

6905  
citing authors

#	ARTICLE	IF	CITATIONS
1	Visualization of arrestin recruitment by a G-protein-coupled receptor. <i>Nature</i> , 2014, 512, 218-222.	13.7	433
2	The X-ray structure of a growth hormone-prolactin receptor complex. <i>Nature</i> , 1994, 372, 478-481.	13.7	399
3	Structure of active $\beta^2$ -arrestin-1 bound to a G-protein-coupled receptor phosphopeptide. <i>Nature</i> , 2013, 497, 137-141.	13.7	393
4	High-throughput Generation of Synthetic Antibodies from Highly Functional Minimalist Phage-displayed Libraries. <i>Journal of Molecular Biology</i> , 2007, 373, 924-940.	2.0	315
5	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018, 558, 553-558.	13.7	230
6	Structural mechanism of voltage-dependent gating in an isolated voltage-sensing domain. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 244-252.	3.6	228
7	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, 6644-6649.	3.3	213
8	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, 969-995.	2.0	185
9	Architecture of the fungal nuclear pore inner ring complex. <i>Science</i> , 2015, 350, 56-64.	6.0	125
10	Structure and drug resistance of the Plasmodium falciparum transporter PfCRT. <i>Nature</i> , 2019, 576, 315-320.	13.7	123
11	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, 82-87.	3.3	119
12	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.	1.6	112
13	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	9.0	109
14	Architecture of the nuclear pore complex coat. <i>Science</i> , 2015, 347, 1148-1152.	6.0	104
15	Structure of the Get3 targeting factor in complex with its membrane protein cargo. <i>Science</i> , 2015, 347, 1152-1155.	6.0	100
16	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2833-2847.	2.5	100
17	Generating conformation-specific synthetic antibodies to trap proteins in selected functional states. <i>Methods</i> , 2013, 60, 3-14.	1.9	89
18	Structures of rhodopsin in complex with G-protein-coupled receptor kinase 1. <i>Nature</i> , 2021, 595, 600-605.	13.7	87

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19	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, 941-953.	2.0	82
20	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 100-106.	3.6	75
21	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	2.9	72
22	Structure of human Frizzled5 by fiducial-assisted cryo-EM supports a heterodimeric mechanism of canonical Wnt signaling. <i>ELife</i> , 2020, 9, .	2.8	68
23	Mechanism of activation gating in the full-length KcsA K <sup>+</sup> channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11896-11899.	3.3	65
24	A YidC-like Protein in the Archaeal Plasma Membrane. <i>Structure</i> , 2015, 23, 1715-1724.	1.6	65
25	Architecture of the cytoplasmic face of the nuclear pore. <i>Science</i> , 2022, 376, .	6.0	65
26	Allosteric control of ligand-binding affinity using engineered conformation-specific effector proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 437-442.	3.6	62
27	Toward chaperone-assisted crystallography: Protein engineering enhancement of crystal packing and X-ray phasing capabilities of a camelid single-domain antibody (V <sub>H</sub> ) scaffold. <i>Protein Science</i> , 2008, 17, 1175-1187.	3.1	61
28	Structural basis of omega-3 fatty acid transport across the blood-brain barrier. <i>Nature</i> , 2021, 595, 315-319.	13.7	61
29	Conformational Chaperones for Structural Studies of Membrane Proteins Using Antibody Phage Display with Nanodiscs. <i>Structure</i> , 2016, 24, 300-309.	1.6	57
30	Synthetic antibodies against BRIL as universal fiducial marks for single-particle cryoEM structure determination of membrane proteins. <i>Nature Communications</i> , 2020, 11, 1598.	5.8	57
31	Structure and mechanism of the ER-based glucosyltransferase ALG6. <i>Nature</i> , 2020, 579, 443-447.	13.7	52
32	Exploring and designing protein function with restricted diversity. <i>Current Opinion in Chemical Biology</i> , 2007, 11, 347-354.	2.8	50
33	Locking the Elbow: Improved Antibody Fab Fragments as Chaperones for Structure Determination. <i>Journal of Molecular Biology</i> , 2018, 430, 337-347.	2.0	50
34	Phage Display Selections for Affinity Reagents to Membrane Proteins in Nanodiscs. <i>Methods in Enzymology</i> , 2015, 557, 219-245.	0.4	46
35	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018, 7, .	2.8	45
36	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.	2.0	42

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37	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, 11011-11015.	3.3	42
38	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.	3.3	42
39	Structure of an AMPK complex in an inactive, ATP-bound state. <i>Science</i> , 2021, 373, 413-419.	6.0	42
40	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.	3.3	40
41	K29-linked ubiquitin signaling regulates proteotoxic stress response and cell cycle. <i>Nature Chemical Biology</i> , 2021, 17, 896-905.	3.9	40
42	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, .	3.3	40
43	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, 25524-25532.	1.6	38
44	A peroxisomal ubiquitin ligase complex forms a retrotranslocation channel. <i>Nature</i> , 2022, 607, 374-380.	13.7	36
45	The Structural Basis for Biological Signaling, Regulation, and Specificity in the Growth Hormone- $\alpha$ -Prolactin System of Hormones and Receptors. <i>Advances in Protein Chemistry</i> , 2004, 68, 147-169.	4.4	35
46	Alternative views of functional protein binding epitopes obtained by combinatorial shotgun scanning mutagenesis. <i>Protein Science</i> , 2005, 14, 2405-2413.	3.1	34
47	Structures of atypical chemokine receptor 3 reveal the basis for its promiscuity and signaling bias. <i>Science Advances</i> , 2022, 8, .	4.7	31
48	Understanding mechanisms governing protein-protein interactions from synthetic binding interfaces. <i>Current Opinion in Structural Biology</i> , 2008, 18, 499-506.	2.6	29
49	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, 525-533.	1.5	28
50	Engineering synthetic antibody binders for allosteric inhibition of prolactin receptor signaling. <i>Cell Communication and Signaling</i> , 2015, 13, 1.	2.7	28
51	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.	0.6	27
52	Intramolecular Cooperativity in a Protein Binding Site Assessed by Combinatorial Shotgun Scanning Mutagenesis. <i>Journal of Molecular Biology</i> , 2005, 347, 489-494.	2.0	26
53	Optimizing Production of Antigens and Fabs in the Context of Generating Recombinant Antibodies to Human Proteins. <i>PLoS ONE</i> , 2015, 10, e0139695.	1.1	26
54	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.	1.6	26

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55	Structural basis of lipopolysaccharide maturation by the O-antigen ligase. <i>Nature</i> , 2022, 604, 371-376.	13.7	25
56	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, .	3.3	24
57	Scalable High Throughput Selection From Phage-displayed Synthetic Antibody Libraries. <i>Journal of Visualized Experiments</i> , 2015, , 51492.	0.2	22
58	Crystal Structure and Site 1 Binding Energetics of Human Placental Lactogen. <i>Journal of Molecular Biology</i> , 2006, 358, 773-784.	2.0	21
59	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.	1.6	19
60	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, 2707-2725.	2.0	18
61	Prolactin Receptor-Mediated Internalization of Imaging Agents Detects Epithelial Ovarian Cancer with Enhanced Sensitivity and Specificity. <i>Cancer Research</i> , 2017, 77, 1684-1696.	0.4	16
62	Generating Conformation and Complex-Specific Synthetic Antibodies. <i>Methods in Molecular Biology</i> , 2017, 1575, 93-119.	0.4	15
63	Specific Recognition of a Single-Stranded RNA Sequence by a Synthetic Antibody Fragment. <i>Journal of Molecular Biology</i> , 2016, 428, 4100-4114.	2.0	11
64	New Tricks for an Old Dimer. <i>Science</i> , 2014, 344, 703-704.	6.0	10
65	A polar ring endows improved specificity to an antibody fragment. <i>Protein Science</i> , 2016, 25, 1290-1298.	3.1	10
66	Characterization of Engineered Actin Binding Proteins That Control Filament Assembly and Structure. <i>PLoS ONE</i> , 2010, 5, e13960.	1.1	9
67	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.	1.5	9
68	Engineering Synthetic Antibody Inhibitors Specific for LD2 or LD4 Motifs of Paxillin. <i>Journal of Molecular Biology</i> , 2015, 427, 2532-2547.	2.0	9
69	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.	1.1	9
70	Engineered Ultra-High Affinity Synthetic Antibodies for SARS-CoV-2 Neutralization and Detection. <i>Journal of Molecular Biology</i> , 2021, 433, 166956.	2.0	9
71	Recognition of an $\alpha$ -helical hairpin in P22 large terminase by a synthetic antibody fragment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 876-888.	1.1	5
72	Quaternary structure independent folding of voltage-gated ion channel pore domain subunits. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 537-548.	3.6	5

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73	The Preserved HTH-Docking Cleft of HIV-1 Integrase Is Functionally Critical. <i>Structure</i> , 2016, 24, 1936-1946.	1.6	4
74	Targeted rescue of cancer-associated IDH1 mutant activity using an engineered synthetic antibody. <i>Scientific Reports</i> , 2017, 7, 556.	1.6	4
75	Rapid Discovery and Characterization of Synthetic Neutralizing Antibodies against Anthrax Edema Toxin. <i>Biochemistry</i> , 2019, 58, 2996-3004.	1.2	4
76	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.	3.1	4
77	Inhibition of Cancer Cell Adhesion, Migration and Proliferation by a Bispecific Antibody that Targets two Distinct Epitopes on $\alpha$ v Integrins. <i>Journal of Molecular Biology</i> , 2021, 433, 167090.	2.0	2
78	Synthetic Antibodies Detect Distinct Cellular States of Chromosome Passenger Complex Proteins. <i>Journal of Molecular Biology</i> , 2022, 434, 167602.	2.0	2
79	Structure of the rhodopsin-rhodopsin kinase complex defines the rules of engagement between G protein-coupled receptors (GPCRs) and GPCR kinases. <i>FASEB Journal</i> , 2021, 35, .	0.2	1
80	Generation of Synthetic Antibody Fragments to Detergent Solubilized Membrane Proteins. <i>Springer Protocols</i> , 2017, , 231-243.	0.1	0
81	Reply to Kang and Brooks: Comment on the calculations in protein thermodynamics. <i>Journal of Biological Chemistry</i> , 2018, 293, 5063.	1.6	0
82	Structural Insights into PLC $\mu$ : Discovery of an Integrated RA1 Domain and Novel Regulatory Elements. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
83	Validation of Recombinant Antibodies Against Human Transcription Factors. <i>FASEB Journal</i> , 2015, 29, 571.13.	0.2	0
84	Engineering of a synthetic antibody fragment for structural and functional studies of K <sup>+</sup> channels. <i>Journal of General Physiology</i> , 2022, 154, .	0.9	0
85	Structural Insights into Phospholipase C $\mu$ . <i>FASEB Journal</i> , 2022, 36, .	0.2	0