Anthony A Kossiakoff

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77
papers3,902
citations30
h-index62
g-index95
ext. papers4,716
ext. citations13.8
avg, IF5
L-index

#	Paper	IF	Citations
77	The X-ray structure of a growth hormone-prolactin receptor complex. <i>Nature</i> , 1994 , 372, 478-81	50.4	365
76	Visualization of arrestin recruitment by a G-protein-coupled receptor. <i>Nature</i> , 2014 , 512, 218-222	50.4	349
75	Structure of active Earrestin-1 bound to a G-protein-coupled receptor phosphopeptide. <i>Nature</i> , 2013 , 497, 137-41	50.4	310
74	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
73	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
72	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
71	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, 969-9	5 ^{6.5}	172
7°	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018 , 558, 553-558	50.4	153
69	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
68	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
67	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
66	Nuclear pores. Architecture of the nuclear pore complex coat. <i>Science</i> , 2015 , 347, 1148-52	33.3	84
65	Architecture of the fungal nuclear pore inner ring complex. <i>Science</i> , 2015 , 350, 56-64	33.3	80
64	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2833-47	7.6	75
63	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
62	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
61	Generating conformation-specific synthetic antibodies to trap proteins in selected functional states. <i>Methods</i> , 2013 , 60, 3-14	4.6	61

60	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	
59	Structure and drug resistance of the Plasmodium falciparum transporter PfCRT. <i>Nature</i> , 2019 , 576, 315	-35204	59	
58	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	
57	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	
56	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	
55	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46	
54	Exploring and designing protein function with restricted diversity. <i>Current Opinion in Chemical Biology</i> , 2007 , 11, 347-54	9.7	45	
53	A YidC-like Protein in the Archaeal Plasma Membrane. <i>Structure</i> , 2015 , 23, 1715-1724	5.2	43	
52	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	
51	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	
50	Conformational Chaperones for Structural Studies of Membrane Proteins Using Antibody Phage Display with Nanodiscs. <i>Structure</i> , 2016 , 24, 300-9	5.2	35	
49	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	
48	Locking the Elbow: Improved Antibody Fab Fragments as Chaperones for Structure Determination. Journal of Molecular Biology, 2018 , 430, 337-347	6.5	34	
47	Phage display selections for affinity reagents to membrane proteins in nanodiscs. <i>Methods in Enzymology</i> , 2015 , 557, 219-45	1.7	30	
46	Alternative views of functional protein binding epitopes obtained by combinatorial shotgun scanning mutagenesis. <i>Protein Science</i> , 2005 , 14, 2405-13	6.3	30	
45	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	
44	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018 , 7,	8.9	27	
43	Understanding mechanisms governing protein-protein interactions from synthetic binding interfaces. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 499-506	8.1	26	

42	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
41	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
40	The 1.38 A crystal structure of DmsD protein from Salmonella typhimurium, a proofreading chaperone on the Tat pathway. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 525-33	4.2	24
39	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
38	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
37	Structural basis for activation of SAGA histone acetyltransferase Gcn5 by partner subunit Ada2. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10010-1001.	5 ^{11.5}	23
36	Engineering synthetic antibody binders for allosteric inhibition of prolactin receptor signaling. <i>Cell Communication and Signaling</i> , 2015 , 13, 1	7.5	21
35	Structure and mechanism of the ER-based glucosyltransferase ALG6. <i>Nature</i> , 2020 , 579, 443-447	50.4	21
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	Structures of rhodopsin in complex with G-protein-coupled receptor kinase 1. <i>Nature</i> , 2021 , 595, 600-60	05 0.4	20
32	Crystal structure and site 1 binding energetics of human placental lactogen. <i>Journal of Molecular Biology</i> , 2006 , 358, 773-84	6.5	18
31	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
30	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
29	Scalable high throughput selection from phage-displayed synthetic antibody libraries. <i>Journal of Visualized Experiments</i> , 2015 , 51492	1.6	16
28	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
27	Structural basis of omega-3 fatty acid transport across the blood-brain barrier. <i>Nature</i> , 2021 , 595, 315-3	8 15 0.4	14
26	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
25	K29-linked ubiquitin signaling regulates proteotoxic stress response and cell cycle. <i>Nature Chemical Biology</i> , 2021 , 17, 896-905	11.7	12

24	Cell biology. New tricks for an old dimer. <i>Science</i> , 2014 , 344, 703-4	33.3	10
23	Generating Conformation and Complex-Specific Synthetic Antibodies. <i>Methods in Molecular Biology</i> , 2017 , 1575, 93-119	1.4	9
22	A polar ring endows improved specificity to an antibody fragment. <i>Protein Science</i> , 2016 , 25, 1290-8	6.3	9
21	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
20	Characterization of engineered actin binding proteins that control filament assembly and structure. <i>PLoS ONE</i> , 2010 , 5, e13960	3.7	8
19	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
18	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
17	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
16	Architecture of the cytoplasmic face of the nuclear pore		6
15	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
14	Structure of an AMPK complex in an inactive, ATP-bound state. Science, 2021, 373, 413-419	33.3	5
13	Targeted rescue of cancer-associated IDH1 mutant activity using an engineered synthetic antibody. <i>Scientific Reports</i> , 2017 , 7, 556	4.9	4
12	Engineered Ultra-High Affinity Synthetic Antibodies for SARS-CoV-2 Neutralization and Detection. Journal of Molecular Biology, 2021 , 433, 166956	6.5	4
11	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
10	Rapid Discovery and Characterization of Synthetic Neutralizing Antibodies against Anthrax Edema Toxin. <i>Biochemistry</i> , 2019 , 58, 2996-3004	3.2	3
9	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
8	The Preserved HTH-Docking Cleft of HIV-1 Integrase Is Functionally Critical. Structure, 2016, 24, 1936-1	19 46	3
7	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

6	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
5	Inhibition of Cancer Cell Adhesion, Migration and Proliferation by a Bispecific Antibody that Targets two Distinct Epitopes on ☑ Integrins. <i>Journal of Molecular Biology</i> , 2021 , 433, 167090	6.5	1
4	Generation of Synthetic Antibody Fragments to Detergent Solubilized Membrane Proteins. <i>Springer Protocols</i> , 2017 , 231-243	0.3	
3	Reply to Kang and Brooks: Comment on the calculations in protein thermodynamics. <i>Journal of Biological Chemistry</i> , 2018 , 293, 5063	5.4	
2		5.4	