Shohei Koide

List of Publications by Year
in descending order

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97 papers	6,337 citations	71102 41 h-index	76900 74 g-index
107 all docs	107 docs citations	107 times ranked	7755 citing authors

#	Article	IF	Citations
1	High-valency Anti-CD99 Antibodies Toward the Treatment of T Cell Acute Lymphoblastic Leukemia. Journal of Molecular Biology, 2022, 434, 167402.	4.2	3
2	Identification of the nucleotide-free state as a therapeutic vulnerability for inhibition of selected oncogenic RAS mutants. Cell Reports, 2022, 38, 110322.	6.4	11
3	Crystal structures of bacterial small multidrug resistance transporter EmrE in complex with structurally diverse substrates. ELife, 2022, 11, .	6.0	13
4	Structural basis for inhibition of the drug efflux pump NorA from Staphylococcus aureus. Nature Chemical Biology, 2022, 18, 706-712.	8.0	23
5	Engineering Binders with Exceptional Selectivity. Methods in Molecular Biology, 2022, 2491, 143-154.	0.9	3
6	The ACE2-binding Interface of SARS-CoV-2 Spike Inherently Deflects Immune Recognition. Journal of Molecular Biology, 2021, 433, 166748.	4.2	12
7	Monobodies as tool biologics for accelerating target validation and druggable site discovery. RSC Medicinal Chemistry, 2021, 12, 1839-1853.	3.9	10
8	Multiplex bead binding assays using off-the-shelf components and common flow cytometers. Journal of Immunological Methods, 2021, 490, 112952.	1.4	10
9	Antibody isotype diversity against SARS-CoV-2 is associated with differential serum neutralization capacities. Scientific Reports, 2021, 11, 5538.	3.3	37
10	Conformational interconversion of MLKL and disengagement from RIPK3 precede cell death by necroptosis. Nature Communications, 2021, 12, 2211.	12.8	56
11	Targeting the KRAS Î±4-Î±5 allosteric interface inhibits pancreatic cancer tumorigenesis. Small GTPases, 2021, , 1-14.	1.6	11
12	Selective and noncovalent targeting of RAS mutants for inhibition and degradation. Nature Communications, 2021, 12, 2656.	12.8	51
13	Mechanism of disease and therapeutic rescue of Dok7 congenital myasthenia. Nature, 2021, 595, 404-408.	27.8	30
14	Zinc binding alters the conformational dynamics and drives the transport cycle of the cation diffusion facilitator YiiP. Journal of General Physiology, 2021, 153, .	1.9	14
15	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. Nature Microbiology, 2021, 6, 1245-1258.	13.3	101
16	SHP2 inhibition diminishes KRASG12C cycling and promotes tumor microenvironment remodeling. Journal of Experimental Medicine, 2021, 218, .	8.5	138
17	STEM-09. DEFINING THE ROLE OF CD97 IN GLIOBLASTOMA STEM CELL SELF-RENEWAL. Neuro-Oncology, 2021, 23, vi22-vi23.	1.2	0
18	The structural basis of promiscuity in small multidrug resistance transporters. Nature Communications, 2020, 11, 6064.	12.8	35

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19	Specific and direct modulation of the interaction between adhesion GPCR GPR56/ADGRG1 and tissue transglutaminase 2 using synthetic ligands. Scientific Reports, 2020, 10, 16912.	3.3	11
20	Selective inhibition of STAT3 signaling using monobodies targeting the coiled-coil and N-terminal domains. Nature Communications, 2020, 11, 4115.	12.8	36
21	Monobodies as enabling tools for structural and mechanistic biology. Current Opinion in Structural Biology, 2020, 60, 167-174.	5.7	31
22	Two Distinct Structures of Membraneâ€Associated Homodimers of GTPâ€•and GDPâ€Bound KRAS4B Revealed by Paramagnetic Relaxation Enhancement. Angewandte Chemie - International Edition, 2020, 59, 11037-11045.	13.8	62
23	Identification of MLKL membrane translocation as a checkpoint in necroptotic cell death using Monobodies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8468-8475.	7.1	64
24	Two Distinct Structures of Membraneâ€Associated Homodimers of GTPâ€•and GDPâ€Bound KRAS4B Revealed by Paramagnetic Relaxation Enhancement. Angewandte Chemie, 2020, 132, 11130-11138.	2.0	5
25	Structural basis for the reaction cycle of DASS dicarboxylate transporters. ELife, 2020, 9, .	6.0	43
26	BRAF inhibitors promote intermediate BRAF(V600E) conformations and binary interactions with activated RAS. Science Advances, 2019, 5, eaav8463.	10.3	25
27	Allosteric modulation of a human protein kinase with monobodies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13937-13942.	7.1	36
28	Broad-Spectrum Proteome Editing with an Engineered Bacterial Ubiquitin Ligase Mimic. ACS Central Science, 2019, 5, 852-866.	11.3	34
29	Repurposing off-the-shelf antihelix antibodies for enabling structural biology. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17611-17613.	7.1	4
30	Targeting the Î±4-Î±5 interface of RAS results in multiple levels of inhibition. Small GTPases, 2019, 10, 378-387.	1.6	29
31	Atomic structure of the eukaryotic intramembrane RAS methyltransferase ICMT. Nature, 2018, 553, 526-529.	27.8	33
32	Monobody-Mediated Alteration of Lipase Substrate Specificity. ACS Chemical Biology, 2018, 13, 1487-1492.	3.4	7
33	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. ELife, 2018, 7, .	6.0	45
34	A CLC-type F-/H+ antiporter in ion-swapped conformations. Nature Structural and Molecular Biology, 2018, 25, 601-606.	8.2	32
35	Facile target validation in an animal model with intracellularly expressed monobodies. Nature Chemical Biology, 2018, 14, 895-900.	8.0	27
36	Next-generation antibodies for post-translational modifications. Current Opinion in Structural Biology, 2018, 51, 141-148.	5.7	32

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37	An Overlapping Region between the Two Terminal Folding Units of the Outer Surface Protein A (OspA) Controls Its Folding Behavior. Journal of Molecular Biology, 2018, 430, 1799-1813.	4.2	5
38	Monobodies and other synthetic binding proteins for expanding protein science. Protein Science, 2017, 26, 910-924.	7.6	127
39	Targeted rescue of cancer-associated IDH1 mutant activity using an engineered synthetic antibody. Scientific Reports, 2017, 7, 556.	3.3	4
40	Selective Targeting of SH2 Domainâ€“Phosphotyrosine Interactions of Src Family Tyrosine Kinases with Monobodies. Journal of Molecular Biology, 2017, 429, 1364-1380.	4.2	25
41	A synthetic intrabody-based selective and generic inhibitor of GPCR endocytosis. Nature Nanotechnology, 2017, 12, 1190-1198.	31.5	42
42	Stachel -independent modulation of GPR56/ADGRG1 signaling by synthetic ligands directed to its extracellular region. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10095-10100.	7.1	61
43	Aromatic claw: A new fold with high aromatic content that evades structural prediction. Protein Science, 2017, 26, 208-217.	7.6	0
44	Inhibition of RAS function through targeting an allosteric regulatory site. Nature Chemical Biology, 2017, 13, 62-68.	8.0	237
45	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. Nature Communications, 2017, 8, 2101.	12.8	33
46	sNASP and ASF1A function through both competitive and compatible modes of histone binding. Nucleic Acids Research, 2017, 45, 643-656.	14.5	29
47	Allosteric Inhibition of Bcr-Abl Kinase by High Affinity Monobody Inhibitors Directed to the Src Homology 2 (SH2)-Kinase Interface. Journal of Biological Chemistry, 2016, 291, 8836-8847.	3.4	33
48	Specific Recognition of a Single-Stranded RNA Sequence by a Synthetic Antibody Fragment. Journal of Molecular Biology, 2016, 428, 4100-4114.	4.2	11
49	Structural Basis for Regulation of GPR56/ADGRG1 by Its Alternatively Spliced Extracellular Domains. Neuron, 2016, 91, 1292-1304.	8.1	92
50	Antigen clasping by two antigen-binding sites of an exceptionally specific antibody for histone methylation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2092-2097.	7.1	39
51	Comprehensive Analysis of the Structural, Biochemical and Signaling Differences of the p210 and p185 Isoforms of Bcr-Abl in CML and B-ALL. Blood, 2016, 128, 4238-4238.	1.4	0
52	Scalable High Throughput Selection From Phage-displayed Synthetic Antibody Libraries. Journal of Visualized Experiments, 2015, , 51492.	0.3	22
53	Optimizing Production of Antigens and Fabs in the Context of Generating Recombinant Antibodies to Human Proteins. PLoS ONE, 2015, 10, e0139695.	2.5	26
54	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. Nature Methods, 2015, 12, 725-731.	19.0	109

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55	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. Molecular and Cellular Proteomics, 2015, 14, 2833-2847.	3.8	100
56	Architecture of the fungal nuclear pore inner ring complex. Science, 2015, 350, 56-64.	12.6	125
57	Monobody-mediated alteration of enzyme specificity. Nature Chemical Biology, 2015, 11, 762-764.	8.0	25
58	Crystal structures of a double-barrelled fluoride ion channel. Nature, 2015, 525, 548-551.	27.8	105
59	ETO family protein Mtgr1 mediates Prdm14 functions in stem cell maintenance and primordial germ cell formation. ELife, 2015, 4, e10150.	6.0	51
60	Validation of Recombinant Antibodies Against Human Transcription Factors. FASEB Journal, 2015, 29, 571.13.	0.5	0
61	A Synthetic Antibody Fragment Targeting Nicastrin Affects Assembly and Trafficking of Î³-Secretase. Journal of Biological Chemistry, 2014, 289, 34851-34861.	3.4	6
62	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14631-14636.	7.1	39
63	Editorial overview: Engineering and design: Raising the bar through innovation and integration. Current Opinion in Structural Biology, 2014, 27, vi-viii.	5.7	0
64	Proof of dual-topology architecture of Fluc Fâ˜' channels with monobody blockers. Nature Communications, 2014, 5, 5120.	12.8	47
65	Visualization of arrestin recruitment by a G-protein-coupled receptor. Nature, 2014, 512, 218-222.	27.8	433
66	Directed Network Wiring Identifies a Key Protein Interaction in Embryonic Stem Cell Differentiation. Molecular Cell, 2014, 54, 1034-1041.	9.7	32
67	Generation of High-Performance Binding Proteins for Peptide Motifs by Affinity Clamping. Methods in Enzymology, 2013, 523, 285-302.	1.0	7
68	Recombinant antibodies to histone post-translational modifications. Nature Methods, 2013, 10, 992-995.	19.0	58
69	Generating conformation-specific synthetic antibodies to trap proteins in selected functional states. Methods, 2013, 60, 3-14.	3.8	89
70	Dissection of the BCR-ABL signaling network using highly specific monobody inhibitors to the SHP2 SH2 domains. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14924-14929.	7.1	85
71	Structures of a Na ⁺ -coupled, substrate-bound MATE multidrug transporter. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2099-2104.	7.1	127
72	Identification of a tetratricopeptide repeat-like domain in the nicastrin subunit of Î³-secretase using synthetic antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8534-8539.	7.1	32

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73	Broad Ranges of Affinity and Specificity of Anti-Histone Antibodies Revealed by a Quantitative Peptide Immunoprecipitation Assay. Journal of Molecular Biology, 2012, 424, 391-399.	4.2	67
74	Structural insights for engineering binding proteins based on non-antibody scaffolds. Current Opinion in Structural Biology, 2012, 22, 413-420.	5.7	84
75	Teaching an Old Scaffold New Tricks: Monobodies Constructed Using Alternative Surfaces of the FN3 Scaffold. Journal of Molecular Biology, 2012, 415, 393-405.	4.2	172
76	Target-Binding Proteins Based on the 10th Human Fibronectin Type III Domain (10Fn3). Methods in Enzymology, 2012, 503, 135-156.	1.0	71
77	T Cell Receptor-Like Recognition of Tumor In Vivo by Synthetic Antibody Fragment. PLoS ONE, 2012, 7, e43746.	2.5	81
78	Targeting the SH2-Kinase Interface in Bcr-Abl Inhibits Leukemogenesis. Cell, 2011, 147, 306-319.	28.9	122
79	A portable RNA sequence whose recognition by a synthetic antibody facilitates structural determination. Nature Structural and Molecular Biology, 2011, 18, 100-106.	8.2	75
80	Isoform-specific monobody inhibitors of small ubiquitin-related modifiers engineered using structure-guided library design. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7751-7756.	7.1	55
81	A potent and highly specific FN3 monobody inhibitor of the Abl SH2 domain. Nature Structural and Molecular Biology, 2010, 17, 519-527.	8.2	138
82	Accelerating phage-display library selection by reversible and site-specific biotinylation. Protein Engineering, Design and Selection, 2009, 22, 685-690.	2.1	19
83	Engineering of recombinant crystallization chaperones. Current Opinion in Structural Biology, 2009, 19, 449-457.	5.7	137
84	Generation of new protein functions by nonhomologous combinations and rearrangements of domains and modules. Current Opinion in Biotechnology, 2009, 20, 398-404.	6.6	33
85	Structural Basis for Exquisite Specificity of Affinity Clamps, Synthetic Binding Proteins Generated through Directed Domain-interface Evolution. Journal of Molecular Biology, 2009, 392, 1221-1231.	4.2	44
86	The Importance of Being Tyrosine: Lessons in Molecular Recognition from Minimalist Synthetic Binding Proteins. ACS Chemical Biology, 2009, 4, 325-334.	3.4	172
87	Raf kinase inhibitory protein protects cells against locostatinâ€mediated inhibition of migration. FASEB Journal, 2009, 23, 687.4.	0.5	0
88	A Dominant Conformational Role for Amino Acid Diversity in Minimalist Proteinâ€“Protein Interfaces. Journal of Molecular Biology, 2008, 381, 407-418.	4.2	72
89	Design of protein function leaps by directed domain interface evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6578-6583.	7.1	88
90	Monobodies: Antibody Mimics Based on the Scaffold of the Fibronectin Type III Domain. , 2007, 352, 95-110.		70

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91	High-affinity single-domain binding proteins with a binary-code interface. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6632-6637.	7.1	165
92	High-throughput Generation of Synthetic Antibodies from Highly Functional Minimalist Phage-displayed Libraries. Journal of Molecular Biology, 2007, 373, 924-940.	4.2	315
93	Phage display for engineering and analyzing protein interaction interfaces. Current Opinion in Structural Biology, 2007, 17, 481-487.	5.7	132
94	Helix, Sheet, and Polyproline II Frequencies and Strong Nearest Neighbor Effects in a Restricted Coil Library. Biochemistry, 2005, 44, 9691-9702.	2.5	165
95	Probing protein conformational changes in living cells by using designer binding proteins: Application to the estrogen receptor. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1253-1258.	7.1	127
96	NMR identification of epitopes of lyme disease antigen OspA to monoclonal antibodies. Journal of Molecular Biology, 1998, 281, 61-67.	4.2	39
97	The fibronectin type III domain as a scaffold for novel binding proteins. Journal of Molecular Biology, 1998, 284, 1141-1151.	4.2	482