

Annemarie Honegger

List of Publications by Year in descending order

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50
papers

4,745
citations

147566

31
h-index

197535

49
g-index

50
all docs

50
docs citations

50
times ranked

3947
citing authors

#	ARTICLE	IF	CITATIONS
1	Fully synthetic human combinatorial antibody libraries (HuCAL) based on modular consensus frameworks and CDRs randomized with trinucleotides 1 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 296, 57-86.	2.0	706
2	Reliable cloning of functional antibody variable domains from hybridomas and spleen cell repertoires employing a reengineered phage display system. <i>Journal of Immunological Methods</i> , 1997, 201, 35-55.	0.6	469
3	Biophysical Properties of Human Antibody Variable Domains. <i>Journal of Molecular Biology</i> , 2003, 325, 531-553.	2.0	329
4	Domain Interactions in the Fab Fragment: A Comparative Evaluation of the Single-chain Fv and Fab Format Engineered with Variable Domains of Different Stability. <i>Journal of Molecular Biology</i> , 2005, 347, 773-789.	2.0	257
5	The Human Combinatorial Antibody Library HuCAL GOLD Combines Diversification of All Six CDRs According to the Natural Immune System with a Novel Display Method for Efficient Selection of High-Affinity Antibodies. <i>Journal of Molecular Biology</i> , 2008, 376, 1182-1200.	2.0	251
6	Antibody scFv fragments without disulfide bonds, made by molecular evolution 1 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 275, 245-253.	2.0	242
7	Yet Another Numbering Scheme for Immunoglobulin Variable Domains: An Automatic Modeling and Analysis Tool. <i>Journal of Molecular Biology</i> , 2001, 309, 657-670.	2.0	221
8	Selection for improved protein stability by phage display 1 1 Edited by J. A. Wells. <i>Journal of Molecular Biology</i> , 1999, 294, 163-180.	2.0	204
9	Stability improvement of antibodies for extracellular and intracellular applications: CDR grafting to stable frameworks and structure-based framework engineering. <i>Methods</i> , 2004, 34, 184-199.	1.9	200
10	A natural antibody missing a cysteine in VH: consequences for thermodynamic stability and folding. <i>Journal of Molecular Biology</i> , 1997, 265, 161-172.	2.0	121
11	Correlation between in Vitro Stability and in Vivo Performance of Anti-GCN4 Intrabodies as Cytoplasmic Inhibitors. <i>Journal of Biological Chemistry</i> , 2000, 275, 2795-2803.	1.6	121
12	Structural Basis for Eliciting a Cytotoxic Effect in HER2-Overexpressing Cancer Cells via Binding to the Extracellular Domain of HER2. <i>Structure</i> , 2013, 21, 1979-1991.	1.6	111
13	DARPin Recognizing the Tumor-Associated Antigen EpCAM Selected by Phage and Ribosome Display and Engineered for Multivalency. <i>Journal of Molecular Biology</i> , 2011, 413, 826-843.	2.0	110
14	Structure-Based Improvement of the Biophysical Properties of Immunoglobulin VH Domains with a Generalizable Approach. <i>Biochemistry</i> , 2003, 42, 1517-1528.	1.2	103
15	Turnover-based in vitro selection and evolution of biocatalysts from a fully synthetic antibody library. <i>Nature Biotechnology</i> , 2003, 21, 679-685.	9.4	90
16	Direct in Vivo Screening of Intrabody Libraries Constructed on a Highly Stable Single-chain Framework. <i>Journal of Biological Chemistry</i> , 2002, 277, 45075-45085.	1.6	80
17	Development of a generic adenovirus delivery system based on structure-guided design of bispecific trimeric DARPin adapters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E869-77.	3.3	67
18	Efficient cell-specific uptake of binding proteins into the cytoplasm through engineered modular transport systems. <i>Journal of Controlled Release</i> , 2015, 200, 13-22.	4.8	66

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19	Adenoviral vector with shield and adapter increases tumor specificity and escapes liver and immune control. <i>Nature Communications</i> , 2018, 9, 450.	5.8	65
20	The influence of the framework core residues on the biophysical properties of immunoglobulin heavy chain variable domains. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 121-134.	1.0	63
21	Aggregation-induced activation of the epidermal growth factor receptor protein tyrosine kinase. <i>Biochemistry</i> , 1993, 32, 8742-8748.	1.2	55
22	The Importance of Framework Residues H6, H7 and H10 in Antibody Heavy Chains: Experimental Evidence for a New Structural Subclassification of Antibody VH Domains. <i>Journal of Molecular Biology</i> , 2001, 309, 701-716.	2.0	55
23	Generation of molecular surfaces for graphic display. <i>Journal of Molecular Graphics</i> , 1983, 1, 9-12.	1.7	50
24	The Influence of the Buried Glutamine or Glutamate Residue in Position 6 on the Structure of Immunoglobulin Variable Domains. <i>Journal of Molecular Biology</i> , 2001, 309, 687-699.	2.0	47
25	T-cell receptor gene transfer exclusively to human CD8+ cells enhances tumor cell killing. <i>Blood</i> , 2012, 120, 4334-4342.	0.6	47
26	Crystal Structure of the Anti-His Tag Antibody 3D5 Single-chain Fragment Complexed to its Antigen. <i>Journal of Molecular Biology</i> , 2002, 318, 135-147.	2.0	46
27	Stabilization and humanization of a single-chain Fv antibody fragment specific for human lymphocyte antigen CD19 by designed point mutations and CDR-grafting onto a human framework. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 135-147.	1.0	46
28	Intermolecular biparatopic trapping of ErbB2 prevents compensatory activation of PI3K/AKT via RAS/p110 crosstalk. <i>Nature Communications</i> , 2016, 7, 11672.	5.8	38
29	Folding Nuclei of the scFv Fragment of an Antibody. <i>Biochemistry</i> , 1996, 35, 8457-8464.	1.2	36
30	Selection, Characterization and X-ray Structure of Anti-ampicillin Single-chain Fv Fragments from Phage-displayed Murine Antibody Libraries. <i>Journal of Molecular Biology</i> , 2001, 309, 671-685.	2.0	36
31	Reproducing the natural evolution of protein structural features with the selectively infective phage (SIP) technology. the kink in the first strand of antibody kappa domains 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 283, 395-407.	2.0	35
32	Complexes of the neurotensin receptor 1 with small-molecule ligands reveal structural determinants of full, partial, and inverse agonism. <i>Science Advances</i> , 2021, 7, .	4.7	32
33	Affinity and folding properties both influence the selection of antibodies with the selectively infective phage (SIP) methodology. <i>FEBS Letters</i> , 1997, 415, 289-293.	1.3	30
34	The nature of antibody heavy chain residue H6 strongly influences the stability of a VH domain lacking the disulfide bridge. <i>Journal of Molecular Biology</i> , 1998, 283, 95-110.	2.0	30
35	DARPin-Based Crystallization Chaperones Exploit Molecular Geometry as a Screening Dimension in Protein Crystallography. <i>Journal of Molecular Biology</i> , 2016, 428, 1574-1588.	2.0	30
36	Rigidly connected multispecific artificial binders with adjustable geometries. <i>Scientific Reports</i> , 2017, 7, 11217.	1.6	30

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37	Engineering an anti-HER2 biparatopic antibody with a multimodal mechanism of action. <i>Nature Communications</i> , 2021, 12, 3790.	5.8	29
38	A mutation designed to alter crystal packing permits structural analysis of a tight-binding fluorescein-scFv complex. <i>Protein Science</i> , 2005, 14, 2537-2549.	3.1	27
39	Receptor-targeted lentiviral vectors are exceptionally sensitive toward the biophysical properties of the displayed single-chain Fv. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 93-106.	1.0	23
40	Fructose-1,6-bisphosphate aldolase from <i>Drosophila melanogaster</i> : Primary structure analysis, secondary structure prediction, and comparison with vertebrate aldolases. <i>Archives of Biochemistry and Biophysics</i> , 1988, 266, 10-31.	1.4	22
41	Dual-targeting triplebody 33-16-123 (SPM-2) mediates effective redirected lysis of primary blasts from patients with a broad range of AML subtypes in combination with natural killer cells. <i>Oncology</i> , 2018, 7, e1472195.	2.1	21
42	Construction of scFv Fragments from Hybridoma or Spleen Cells by PCR Assembly. , 2010, , 21-44.		19
43	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. <i>Journal of Molecular Biology</i> , 2016, 428, 4467-4489.	2.0	19
44	Structural Basis for the Selective Inhibition of c-Jun N-Terminal Kinase 1 Determined by Rigid DARPin-DARPin Fusions. <i>Journal of Molecular Biology</i> , 2018, 430, 2128-2138.	2.0	12
45	Expression of a human insulin-like growth factor II cDNA in NIH-3T3 cells. <i>Biochemical and Biophysical Research Communications</i> , 1990, 169, 832-839.	1.0	11
46	Rigid fusions of designed helical repeat binding proteins efficiently protect a binding surface from crystal contacts. <i>Scientific Reports</i> , 2019, 9, 16162.	1.6	11
47	Rigidity of the extracellular part of HER2: Evidence from engineering subdomain interfaces and shared-helix DARPin-DARPin fusions. <i>Protein Science</i> , 2017, 26, 1796-1806.	3.1	10
48	Regulation of the Flavin Redox Potential by Flavin-Binding Antibodies. <i>FEBS Journal</i> , 1997, 249, 393-400.	0.2	9
49	Insight into odorant perception: the crystal structure and binding characteristics of antibody fragments directed against the musk odorant traseolide. <i>Journal of Molecular Biology</i> , 1999, 292, 855-869.	2.0	7
50	A Combined NMR and Computational Approach to Investigate Peptide Binding to a Designed Armadillo Repeat Protein. <i>Journal of Molecular Biology</i> , 2015, 427, 1916-1933.	2.0	6