

Annemarie Honegger

List of Publications by Citations

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

50
papers

4,119
citations

31
h-index

50
g-index

50
ext. papers

4,491
ext. citations

7.1
avg, IF

4.9
L-index

#	Paper	IF	Citations
50	Fully synthetic human combinatorial antibody libraries (HuCAL) based on modular consensus frameworks and CDRs randomized with trinucleotides. <i>Journal of Molecular Biology</i> , 2000 , 296, 57-86	6.5	633
49	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	2.5	441
48	Biophysical properties of human antibody variable domains. <i>Journal of Molecular Biology</i> , 2003 , 325, 531-53	6.5	284
47	Antibody scFv fragments without disulfide bonds made by molecular evolution. <i>Journal of Molecular Biology</i> , 1998 , 275, 245-53	6.5	231
46	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, 773-89	6.5	227
45	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, 1182-200	6.5	214
44	Selection for improved protein stability by phage display. <i>Journal of Molecular Biology</i> , 1999 , 294, 163-80	6.5	184
43	Yet another numbering scheme for immunoglobulin variable domains: an automatic modeling and analysis tool. <i>Journal of Molecular Biology</i> , 2001 , 309, 657-70	6.5	177
42	Stability improvement of antibodies for extracellular and intracellular applications: CDR grafting to stable frameworks and structure-based framework engineering. <i>Methods</i> , 2004 , 34, 184-99	4.6	175
41	A natural antibody missing a cysteine in VH: consequences for thermodynamic stability and folding. <i>Journal of Molecular Biology</i> , 1997 , 265, 161-72	6.5	117
40	Correlation between in vitro stability and in vivo performance of anti-GCN4 intrabodies as cytoplasmic inhibitors. <i>Journal of Biological Chemistry</i> , 2000 , 275, 2795-803	5.4	103
39	Structure-based improvement of the biophysical properties of immunoglobulin VH domains with a generalizable approach. <i>Biochemistry</i> , 2003 , 42, 1517-28	3.2	97
38	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, 826-43	6.5	90
37	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, 1979-91	5.2	85
36	Turnover-based in vitro selection and evolution of biocatalysts from a fully synthetic antibody library. <i>Nature Biotechnology</i> , 2003 , 21, 679-85	44.5	78
35	Direct in vivo screening of intrabody libraries constructed on a highly stable single-chain framework. <i>Journal of Biological Chemistry</i> , 2002 , 277, 45075-85	5.4	68
34	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	11.7	54

33	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, 121-34	1.9	54
32	The importance of framework residues H6, H7 and H10 in antibody heavy chains: experimental evidence for a new structural subclassification of antibody V(H) domains. <i>Journal of Molecular Biology</i> , 2001 , 309, 701-16	6.5	53
31	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	11.5	52
30	Aggregation-induced activation of the epidermal growth factor receptor protein tyrosine kinase. <i>Biochemistry</i> , 1993 , 32, 8742-8	3.2	52
29	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, 687-99	6.5	45
28	Generation of molecular surfaces for graphic display. <i>Journal of Molecular Graphics</i> , 1983 , 1, 9-12		44
27	Adenoviral vector with shield and adapter increases tumor specificity and escapes liver and immune control. <i>Nature Communications</i> , 2018 , 9, 450	17.4	43
26	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, 135-47	1.9	41
25	T-cell receptor gene transfer exclusively to human CD8(+) cells enhances tumor cell killing. <i>Blood</i> , 2012 , 120, 4334-42	2.2	39
24	Crystal structure of the anti-His tag antibody 3D5 single-chain fragment complexed to its antigen. <i>Journal of Molecular Biology</i> , 2002 , 318, 135-47	6.5	37
23	Folding nuclei of the scFv fragment of an antibody. <i>Biochemistry</i> , 1996 , 35, 8457-64	3.2	35
22	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, 671-85	6.5	34
21	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. <i>Journal of Molecular Biology</i> , 1998 , 283, 395-407	6.5	33
20	Intermolecular biparatopic trapping of ErbB2 prevents compensatory activation of PI3K/AKT via RAS-p110 crosstalk. <i>Nature Communications</i> , 2016 , 7, 11672	17.4	32
19	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	6.5	30
18	Affinity and folding properties both influence the selection of antibodies with the selectively infective phage (SIP) methodology. <i>FEBS Letters</i> , 1997 , 415, 289-93	3.8	25
17	DARPin-Based Crystallization Chaperones Exploit Molecular Geometry as a Screening Dimension in Protein Crystallography. <i>Journal of Molecular Biology</i> , 2016 , 428, 1574-88	6.5	24
16	Rigidly connected multispecific artificial binders with adjustable geometries. <i>Scientific Reports</i> , 2017 , 7, 11217	4.9	21

15	A mutation designed to alter crystal packing permits structural analysis of a tight-binding fluorescein-scFv complex. <i>Protein Science</i> , 2005 , 14, 2537-49	6.3	19
14	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	4.1	19
13	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	1.9	17
12	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>Oncolmmunology</i> , 2018 , 7, e1472195	7.2	16
11	Construction of scFv Fragments from Hybridoma or Spleen Cells by PCR Assembly 2010 , 21-44		16
10	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. <i>Journal of Molecular Biology</i> , 2016 , 428, 4467-4489	6.5	12
9	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	6.5	10
8	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	6.3	9
7	Rigid fusions of designed helical repeat binding proteins efficiently protect a binding surface from crystal contacts. <i>Scientific Reports</i> , 2019 , 9, 16162	4.9	9
6	Expression of a human insulin-like growth factor II cDNA in NIH-3T3 cells. <i>Biochemical and Biophysical Research Communications</i> , 1990 , 169, 832-9	3.4	9
5	Engineering an anti-HER2 biparatopic antibody with a multimodal mechanism of action. <i>Nature Communications</i> , 2021 , 12, 3790	17.4	9
4	A combined NMR and computational approach to investigate peptide binding to a designed Armadillo repeat protein. <i>Journal of Molecular Biology</i> , 2015 , 427, 1916-33	6.5	6
3	Regulation of the flavin redox potential by flavin-binding antibodies. <i>FEBS Journal</i> , 1997 , 249, 393-400		6
2	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,	14.3	6
1	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, 855-69 ^{6.5}		4