

Annemarie Honegger

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/4013286/annemarie-honegger-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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 | Engineering an anti-HER2 biparatopic antibody with a multimodal mechanism of action. <i>Nature Communications</i> , 2021 , 12, 3790 | 17.4 | 9 |
| 49 | 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 |
| 48 | 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 |
| 47 | 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 |
| 46 | 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>Oncolmunology</i> , 2018 , 7, e1472195 | 7.2 | 16 |
| 45 | 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 |
| 44 | 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 |
| 43 | Rigidly connected multispecific artificial binders with adjustable geometries. <i>Scientific Reports</i> , 2017 , 7, 11217 | 4.9 | 21 |
| 42 | 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 |
| 41 | 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 |
| 40 | Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. <i>Journal of Molecular Biology</i> , 2016 , 428, 4467-4489 | 6.5 | 12 |
| 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 | 1.9 | 17 |
| 38 | 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 |
| 37 | 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 |
| 36 | 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 |
| 35 | 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 |
| 34 | T-cell receptor gene transfer exclusively to human CD8(+) cells enhances tumor cell killing. <i>Blood</i> , 2012 , 120, 4334-42 | 2.2 | 39 |

| | | | |
|----|--|------|-----|
| 33 | 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 |
| 32 | Construction of scFv Fragments from Hybridoma or Spleen Cells by PCR Assembly 2010 , 21-44 | | 16 |
| 31 | 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 |
| 30 | 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 |
| 29 | 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 |
| 28 | 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 |
| 27 | 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 |
| 26 | 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 |
| 25 | 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 |
| 24 | 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 |
| 23 | Biophysical properties of human antibody variable domains. <i>Journal of Molecular Biology</i> , 2003 , 325, 531-53 | 6.5 | 284 |
| 22 | 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 |
| 21 | 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 |
| 20 | 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 |
| 19 | 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 |
| 18 | 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 |
| 17 | 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 |
| 16 | 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 |

| | | | |
|----|--|-----|-----|
| 15 | 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 |
| 14 | 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 |
| 13 | Selection for improved protein stability by phage display. <i>Journal of Molecular Biology</i> , 1999 , 294, 163-80 | 6.5 | 184 |
| 12 | Antibody scFv fragments without disulfide bonds made by molecular evolution. <i>Journal of Molecular Biology</i> , 1998 , 275, 245-53 | 6.5 | 231 |
| 11 | 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 |
| 10 | 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 |
| 9 | 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 |
| 8 | 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 |
| 7 | Regulation of the flavin redox potential by flavin-binding antibodies. <i>FEBS Journal</i> , 1997 , 249, 393-400 | | 6 |
| 6 | 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 |
| 5 | Folding nuclei of the scFv fragment of an antibody. <i>Biochemistry</i> , 1996 , 35, 8457-64 | 3.2 | 35 |
| 4 | Aggregation-induced activation of the epidermal growth factor receptor protein tyrosine kinase. <i>Biochemistry</i> , 1993 , 32, 8742-8 | 3.2 | 52 |
| 3 | 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 |
| 2 | 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 |
| 1 | Generation of molecular surfaces for graphic display. <i>Journal of Molecular Graphics</i> , 1983 , 1, 9-12 | | 44 |