Andreas PlÃ¼ckthun

List of Publications by Year
in descending order

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444	36,269	1994 101	4645 170
papers	citations	h-index	g-index

467	467	467	23560
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	In vitro selection and evolution of functional proteins by using ribosome display. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 4937-4942.	7.1	1,040
2	Assembly of a functional immunoglobulin Fv fragment in Escherichia coli. Science, 1988, 240, 1038-1041.	12.6	999
3	Fully synthetic human combinatorial antibody libraries (HuCAL) based on modular consensus frameworks and CDRs randomized with trinucleotides 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 296, 57-86.	4.2	706
4	Induction and Exhaustion of Lymphocytic Choriomeningitis Virusâ€“specific Cytotoxic T Lymphocytes Visualized Using Soluble Tetrameric Major Histocompatibility Complex Class Iâ€“Peptide Complexes. Journal of Experimental Medicine, 1998, 187, 1383-1393.	8.5	688
5	High-affinity binders selected from designed ankyrin repeat protein libraries. Nature Biotechnology, 2004, 22, 575-582.	17.5	598
6	Engineering novel binding proteins from nonimmunoglobulin domains. Nature Biotechnology, 2005, 23, 1257-1268.	17.5	598
7	Stability engineering of antibody single-chain Fv fragments. Journal of Molecular Biology, 2001, 305, 989-1010.	4.2	554
8	In vitro generated antibodies specific for telomeric guanine-quadruplex DNA react with Stylonychia lemnae macronuclei. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 8572-8577.	7.1	554
9	Reproducibility: Standardize antibodies used in research. Nature, 2015, 518, 27-29.	27.8	530
10	Designing Repeat Proteins: Well-expressed, Soluble and Stable Proteins from Combinatorial Libraries of Consensus Ankyrin Repeat Proteins. Journal of Molecular Biology, 2003, 332, 489-503.	4.2	510
11	A comparison of strategies to stabilize immunoglobulin Fv-fragments. Biochemistry, 1990, 29, 1362-1367.	2.5	506
12	Reliable cloning of functional antibody variable domains from hybridomas and spleen cell repertoires employing a reengineered phage display system. Journal of Immunological Methods, 1997, 201, 35-55.	1.4	469
13	Designed Ankyrin Repeat Proteins (DARPins): Binding Proteins for Research, Diagnostics, and Therapy. Annual Review of Pharmacology and Toxicology, 2015, 55, 489-511.	9.4	468
14	Picomolar affinity antibodies from a fully synthetic naive library selected and evolved by ribosome display. Nature Biotechnology, 2000, 18, 1287-1292.	17.5	362
15	BIACORE Analysis of Histidine-Tagged Proteins Using a Chelating NTA Sensor Chip. Analytical Biochemistry, 1997, 252, 217-228.	2.4	337
16	Biophysical Properties of Human Antibody Variable Domains. Journal of Molecular Biology, 2003, 325, 531-553.	4.2	329
17	In-vitro protein evolution by ribosome display and mRNA display. Journal of Immunological Methods, 2004, 290, 51-67.	1.4	321
18	Sequence Statistics Reliably Predict Stabilizing Mutations in a Protein Domain. Journal of Molecular Biology, 1994, 240, 188-192.	4.2	320

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19	New protein engineering approaches to multivalent and bispecific antibody fragments. Immunotechnology: an International Journal of Immunological Engineering, 1997, 3, 83-105.	2.4	310
20	Miniantibodies: use of amphipathic helixes to produce functional, flexibly linked dimeric FV fragments with high avidity in Escherichia coli. Biochemistry, 1992, 31, 1579-1584.	2.5	305
21	Stable one-step technetium-99m labeling of His-tagged recombinant proteins with a novel Tc(I)â€“carbonyl complex. Nature Biotechnology, 1999, 17, 897-901.	17.5	293
22	Competition BIAcore for Measuring True Affinities: Large Differences from Values Determined from Binding Kinetics. Analytical Biochemistry, 1996, 234, 155-165.	2.4	292
23	Ribosome display efficiently selects and evolves high-affinity antibodies in vitro from immune libraries. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 14130-14135.	7.1	290
24	Ribosome display: selecting and evolving proteins in vitro that specifically bind to a target. Nature Methods, 2007, 4, 269-279.	19.0	271
25	Designed to be stable: Crystal structure of a consensus ankyrin repeat protein. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1700-1705.	7.1	262
26	A label-free immunosensor array using single-chain antibody fragments. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14587-14592.	7.1	259
27	Domain Interactions in the Fab Fragment: A Comparative Evaluation of the Single-chain Fv and Fab Format Engineered with Variable Domains of Different Stability. Journal of Molecular Biology, 2005, 347, 773-789.	4.2	257
28	Antigen binding forces of individually addressed single-chain Fv antibody molecules. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 7402-7405.	7.1	250
29	Increasing the secretory capacity of Saccharomyces cerevisiae for production of single-chain antibody fragments. Nature Biotechnology, 1998, 16, 773-777.	17.5	244
30	Antibody scFv fragments without disulfide bonds, made by molecular evolution 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 275, 245-253.	4.2	242
31	Functional and dynamic polymerization of the ALS-linked protein TDP-43 antagonizes its pathologic aggregation. Nature Communications, 2017, 8, 45.	12.8	242
32	Efficient Selection of DARPins with Sub-nanomolar Affinities using SRP Phage Display. Journal of Molecular Biology, 2008, 382, 1211-1227.	4.2	236
33	PtdIns(4,5)P2 stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. Nature, 2018, 559, 423-427.	27.8	236
34	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. Nature Methods, 2007, 4, 13-17.	19.0	231
35	Yet Another Numbering Scheme for Immunoglobulin Variable Domains: An Automatic Modeling and Analysis Tool. Journal of Molecular Biology, 2001, 309, 657-670.	4.2	221
36	Covalently circularized nanodiscs for studying membrane proteins and viral entry. Nature Methods, 2017, 14, 49-52.	19.0	221

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37	Engineered turns of a recombinant antibody improve its in vivo folding. Protein Engineering, Design and Selection, 1995, 8, 81-89.	2.1	219
38	Efficient Tumor Targeting with High-Affinity Designed Ankyrin Repeat Proteins: Effects of Affinity and Molecular Size. Cancer Research, 2010, 70, 1595-1605.	0.9	218
39	Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells. Nature Methods, 2015, 12, 773-779.	19.0	217
40	DARPins and other repeat protein scaffolds: advances in engineering and applications. Current Opinion in Biotechnology, 2011, 22, 849-857.	6.6	212
41	A Designed Ankyrin Repeat Protein Evolved to Picomolar Affinity to Her2. Journal of Molecular Biology, 2007, 369, 1015-1028.	4.2	211
42	Disrupting the hydrophobic patches at the antibody variable/constant domain interface: improved in vivo folding and physical characterization of an engineered scFv fragment. Protein Engineering, Design and Selection, 1997, 10, 435-444.	2.1	209
43	Selection for improved protein stability by phage display 1 1Edited by J. A. Wells. Journal of Molecular Biology, 1999, 294, 163-180.	4.2	204
44	The Functional Expression of Antibody Fv Fragments in Ischhuchia coli: Improved Vectors and a Generally Applicable Purification Technique. Nature Biotechnology, 1991, 9, 273-278.	17.5	203
45	Ribosome display: an in vitro method for selection and evolution of antibodies from libraries. Journal of Immunological Methods, 1999, 231, 119-135.	1.4	202
46	Stability improvement of antibodies for extracellular and intracellular applications: CDR grafting to stable frameworks and structure-based framework engineering. Methods, 2004, 34, 184-199.	3.8	200
47	Structure of signaling-competent neurotensin receptor 1 obtained by directed evolution in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E655-62.	7.1	197
48	Selecting proteins with improved stability by a phage-based method. Nature Biotechnology, 1998, 16, 955-960.	17.5	192
49	Signal sequences directing cotranslational translocation expand the range of proteins amenable to phage display. Nature Biotechnology, 2006, 24, 823-831.	17.5	191
50	The disulfide bonds in antibody variable domains: effects on stability, folding in vitro, and functional expression in Escherichia coli. Biochemistry, 1992, 31, 1270-1279.	2.5	190
51	Selection for a periplasmic factor improving phage display and functional periplasmic expression. Nature Biotechnology, 1998, 16, 376-380.	17.5	190
52	An in vivo library-versus-library selection of optimized proteinâ€“protein interactions. Nature Biotechnology, 1999, 17, 683-690.	17.5	182
53	Biophysical Properties of Camelid VHHDomains Compared to Those of Human VH3 Domainsâ€. Biochemistry, 2002, 41, 3628-3636.	2.5	182
54	Functional antibody production using cell-free translation: Effects of protein disulfide isomerase and chaperones. Nature Biotechnology, 1997, 15, 79-84.	17.5	179

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55	Protein folding in the periplasm of Escherichia coli. Molecular Microbiology, 1994, 12, 685-692.	2.5	177
56	Design of multivalent complexes using the barnaseÂ·barstar module. Nature Biotechnology, 2003, 21, 1486-1492.	17.5	177
57	Directed evolution of a G protein-coupled receptor for expression, stability, and binding selectivity. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14808-14813.	7.1	176
58	Circular Î²-lactamase: stability enhancement by cyclizing the backbone. FEBS Letters, 1999, 459, 166-172.	2.8	175
59	In vitro display technologies: novel developments and applications. Current Opinion in Biotechnology, 2001, 12, 400-405.	6.6	173
60	Folding and Unfolding Mechanism of Highly Stable Full-Consensus Ankyrin Repeat Proteins. Journal of Molecular Biology, 2008, 376, 241-257.	4.2	161
61	Directed in Vitro Evolution and Crystallographic Analysis of a Peptide-binding Single Chain Antibody Fragment (scFv) with Low Picomolar Affinity. Journal of Biological Chemistry, 2004, 279, 18870-18877.	3.4	160
62	Destabilization of the complete protein secondary structure on binding to the chaperone GroEL. Nature, 1994, 368, 261-265.	27.8	157
63	The Periplasmic Escherichia coli Peptidylprolyl cis,trans-Isomerase FkpA. Journal of Biological Chemistry, 2000, 275, 17100-17105.	3.4	156
64	Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA. Structure, 1999, 7, 711-722.	3.3	155
65	Direct identification of ligand-receptor interactions on living cells and tissues. Nature Biotechnology, 2012, 30, 997-1001.	17.5	154
66	Recent advances in producing and selecting functional proteins by using cell-free translation. Current Opinion in Biotechnology, 1998, 9, 534-548.	6.6	145
67	Protein PEGylation Decreases Observed Target Association Rates via a Dual Blocking Mechanism. Molecular Pharmacology, 2005, 68, 1439-1454.	2.3	145
68	Factors Influencing the Dimer to Monomer Transition of an Antibody Single-Chain Fv Fragmentâ€. Biochemistry, 1998, 37, 12918-12926.	2.5	144
69	Tetravalent Miniantibodies with High Avidity Assembling inEscherichia colo. Journal of Molecular Biology, 1995, 246, 28-34.	4.2	143
70	Structure of a kinesinâ€“tubulin complex and implications for kinesin motility. Nature Structural and Molecular Biology, 2013, 20, 1001-1007.	8.2	143
71	Engineered proteins as specific binding reagents. Current Opinion in Biotechnology, 2005, 16, 459-469.	6.6	142
72	Mono- and Bivalent Antibody Fragments Produced in Escherichia coli: Engineering, Folding and Antigen Binding. Immunological Reviews, 1992, 130, 151-188.	6.0	140

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73	Novel fold and capsid-binding properties of the lambda-phage display platform protein gpD. Nature Structural Biology, 2000, 7, 230-237.	9.7	140
74	Improving in vivo folding and stability of a single-chain Fv antibody fragment by loop grafting. Protein Engineering, Design and Selection, 1997, 10, 959-966.	2.1	139
75	Model and Simulation of Multivalent Binding to Fixed Ligands. Analytical Biochemistry, 1998, 261, 149-158.	2.4	135
76	Reprogramming Bacteriophage Host Range through Structure-Guided Design of Chimeric Receptor Binding Proteins. Cell Reports, 2019, 29, 1336-1350.e4.	6.4	135
77	The Escherichia coli SlyD Is a Metal Ion-regulated Peptidyl-prolyl cis/trans-Isomerase. Journal of Biological Chemistry, 1997, 272, 15697-15701.	3.4	133
78	A designed ankyrin repeat protein selected to bind to tubulin caps the microtubule plus end. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12011-12016.	7.1	133
79	Different Equilibrium Stability Behavior of ScFv Fragments:â€‰ Identification, Classification, and Improvement by Protein Engineering. Biochemistry, 1999, 38, 8739-8750.	2.5	132
80	Cyclic Green Fluorescent Protein Produced in Vivo Using an Artificially Split PI-PfuI Intein from Pyrococcus furiosus. Journal of Biological Chemistry, 2001, 276, 16548-16554.	3.4	131
81	The Periplasmic Escherichia coli Peptidylprolyl cis,trans-Isomerase FkpA. Journal of Biological Chemistry, 2000, 275, 17106-17113.	3.4	127
82	A novel strategy to design binding molecules harnessing the modular nature of repeat proteins. FEBS Letters, 2003, 539, 2-6.	2.8	127
83	[34] Expression of functional antibody Fv and Fab fragments in Escherichia coli. Methods in Enzymology, 1989, 178, 497-515.	1.0	126
84	Inhibition of Caspase-2 by a Designed Ankyrin Repeat Protein: Specificity, Structure, and Inhibition Mechanism. Structure, 2007, 15, 625-636.	3.3	125
85	Mutual Stabilization of V_Land V_Hin Single-Chain Antibody Fragments, Investigated with Mutants Engineered for Stability. Biochemistry, 1998, 37, 13120-13127.	2.5	124
86	Designing Repeat Proteins: Modular Leucine-rich Repeat Protein Libraries Based on the Mammalian Ribonuclease Inhibitor Family. Journal of Molecular Biology, 2003, 332, 471-487.	4.2	123
87	A natural antibody missing a cysteine in VH: consequences for thermodynamic stability and folding. Journal of Molecular Biology, 1997, 265, 161-172.	4.2	121
88	Correlation between in Vitro Stability and in Vivo Performance of Anti-GCN4 Intrabodies as Cytoplasmic Inhibitors. Journal of Biological Chemistry, 2000, 275, 2795-2803.	3.4	121
89	Docking small ligands in flexible binding sites. Journal of Computational Chemistry, 1998, 19, 21-37.	3.3	120
90	Crystal Structure of the Dimeric C-terminal Domain of TonB Reveals a Novel Fold. Journal of Biological Chemistry, 2001, 276, 27535-27540.	3.4	117

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91	The structural basis of phage display elucidated by the crystal structure of the N-terminal domains of g3p. Nature Structural Biology, 1998, 5, 140-147.	9.7	116
92	Beyond binding: using phage display to select for structure, folding and enzymatic activity in proteins. Current Opinion in Structural Biology, 1999, 9, 514-520.	5.7	116
93	Antigen recognition by conformational selection. FEBS Letters, 1999, 450, 149-153.	2.8	116
94	Intracellular Kinase Inhibitors Selected from Combinatorial Libraries of Designed Ankyrin Repeat Proteins. Journal of Biological Chemistry, 2005, 280, 24715-24722.	3.4	115
95	Structural Basis for Eliciting a Cytotoxic Effect in HER2-Overexpressing Cancer Cells via Binding to the Extracellular Domain of HER2. Structure, 2013, 21, 1979-1991.	3.3	111
96	An intrinsically stable antibody scFv fragment can tolerate the loss of both disulfide bonds and fold correctly. FEBS Letters, 1998, 427, 357-361.	2.8	110
97	Directed Evolution of an Anti-prion Protein scFv Fragment to an Affinity of 1 pM and its Structural Interpretation. Journal of Molecular Biology, 2006, 363, 75-97.	4.2	110
98	DARPins Recognizing the Tumor-Associated Antigen EpCAM Selected by Phage and Ribosome Display and Engineered for Multivalency. Journal of Molecular Biology, 2011, 413, 826-843.	4.2	110
99	PEGylation and Multimerization of the Anti-p185HER-2 Single Chain Fv Fragment 4D5. Journal of Biological Chemistry, 2006, 281, 35186-35201.	3.4	109
100	Designed Armadillo Repeat Proteins as General Peptide-Binding Scaffolds: Consensus Design and Computational Optimization of the Hydrophobic Core. Journal of Molecular Biology, 2008, 376, 1282-1304.	4.2	108
101	Ribosome Display: A Perspective. Methods in Molecular Biology, 2012, 805, 3-28.	0.9	106
102	Antibody Engineering: Advances From the Use of Escherichia coli Expression Systems. Nature Biotechnology, 1991, 9, 545-551.	17.5	105
103	Engineered proteins with desired specificity: DARPins, other alternative scaffolds and bispecific IgGs. Current Opinion in Structural Biology, 2014, 27, 102-112.	5.7	104
104	Structure-Based Improvement of the Biophysical Properties of Immunoglobulin VHDomains with a Generalizable Approachâ€. Biochemistry, 2003, 42, 1517-1528.	2.5	103
105	A heterodimeric coiled-coil peptide pair selected in vivo from a designed library- versus -library ensemble 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 2000, 295, 627-639.	4.2	101
106	Designed Ankyrin Repeat Proteins (DARPins). Methods in Enzymology, 2012, 503, 101-134.	1.0	101
107	Tailoring in vitro evolution for protein affinity or stability. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 75-80.	7.1	100
108	High-resolution crystal structure of parathyroid hormone 1 receptor in complex with a peptide agonist. Nature Structural and Molecular Biology, 2018, 25, 1086-1092.	8.2	99

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109	Consensus Design of Repeat Proteins. ChemBioChem, 2004, 5, 183-189.	2.6	96
110	From DARPins to LoopDARPins: Novel LoopDARPin Design Allows the Selection of Low Picomolar Binders in a Single Round of Ribosome Display. Journal of Molecular Biology, 2014, 426, 691-721.	4.2	94
111	[24] Selecting and evolving functional proteins in vitro by ribosome display. Methods in Enzymology, 2000, 328, 404-430.	1.0	93
112	DARPins: An Efficient Targeting Domain for Lentiviral Vectors. Molecular Therapy, 2011, 19, 686-693.	8.2	93
113	Effects of overexpressing folding modulators on the in vivo folding of heterologous proteins in Escherichia coli. Current Opinion in Biotechnology, 1995, 6, 507-516.	6.6	91
114	Selectively-infective phage (SIP): a mechanistic dissection of a novel in vivo selection for protein-ligand interactions. Journal of Molecular Biology, 1997, 268, 607-618.	4.2	91
115	Selection and Characterization of Her2 Binding-designed Ankyrin Repeat Proteins. Journal of Biological Chemistry, 2006, 281, 35167-35175.	3.4	91
116	Structural and functional analysis of phosphorylation-specific binders of the kinase ERK from designed ankyrin repeat protein libraries. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2248-57.	7.1	91
117	Off-target-free gene delivery by affinity-purified receptor-targeted viral vectors. Nature Communications, 2015, 6, 6246.	12.8	91
118	Turnover-based in vitro selection and evolution of biocatalysts from a fully synthetic antibody library. Nature Biotechnology, 2003, 21, 679-685.	17.5	90
119	Secretion and in vivo folding of the Fab fragment of the antibody McPC603 in Escherichia coli: influence of disulphides and cis-prolines. Protein Engineering, Design and Selection, 1991, 4, 971-979.	2.1	89
120	The Effect of Folding Catalysts on the In Vivo Folding Process of Different Antibody Fragments Expressed in Escherichia coli. Nature Biotechnology, 1993, 11, 77-83.	17.5	89
121	Bispecific Designed Ankyrin Repeat Proteins (DARPins) Targeting Epidermal Growth Factor Receptor Inhibit A431 Cell Proliferation and Receptor Recycling. Journal of Biological Chemistry, 2011, 286, 41273-41285.	3.4	89
122	Antitumor activity of an epithelial cell adhesion moleculeâ€“targeted nanovesicular drug delivery system. Molecular Cancer Therapeutics, 2007, 6, 3019-3027.	4.1	87
123	A Novel Fusion Toxin Derived from an EpCAM-Specific Designed Ankyrin Repeat Protein Has Potent Antitumor Activity. Clinical Cancer Research, 2011, 17, 100-110.	7.0	87
124	Atomic Force Microscopy Detects Changes in the Interaction Forces between GroEL and Substrate Proteins. Biophysical Journal, 1998, 74, 3256-3263.	0.5	86
125	EpCAM-targeted delivery of nanocomplexed siRNA to tumor cells with designed ankyrin repeat proteins. Molecular Cancer Therapeutics, 2009, 8, 2674-2683.	4.1	85
126	A recombinant immunotoxin derived from a humanized epithelial cell adhesion molecule-specific single-chain antibody fragment has potent and selective antitumor activity. Clinical Cancer Research, 2003, 9, 2837-48.	7.0	85

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127	Correctly Folded T-cell Receptor Fragments in the Periplasm of Escherichia coli. Journal of Molecular Biology, 1994, 242, 655-669.	4.2	83
128	Direct in Vivo Screening of Intrabody Libraries Constructed on a Highly Stable Single-chain Framework. Journal of Biological Chemistry, 2002, 277, 45075-45085.	3.4	80
129	Tumor Targeting of Mono-, Di-, and Tetravalent Anti-p185HER-2 Miniantibodies Multimerized by Self-associating Peptides. Journal of Biological Chemistry, 2001, 276, 14385-14392.	3.4	79
130	Epithelial cell adhesion molecule-targeted drug delivery for cancer therapy. Expert Opinion on Drug Delivery, 2013, 10, 451-468.	5.0	79
131	Functional antibody single-chain fragments from the cytoplasm of Escherichia coli: influence of thioredoxin reductase (TrxB). Gene, 1995, 159, 203-207.	2.2	78
132	Allosteric Inhibition of Aminoglycoside Phosphotransferase by a Designed Ankyrin Repeat Protein. Structure, 2005, 13, 1131-1141.	3.3	78
133	Characterization and Further Stabilization of Designed Ankyrin Repeat Proteins by Combining Molecular Dynamics Simulations and Experiments. Journal of Molecular Biology, 2008, 375, 837-854.	4.2	77
134	Evolution of Three Human GPCRs for Higher Expression and Stability. Journal of Molecular Biology, 2011, 408, 599-615.	4.2	77
135	Conformational dynamics of a G-protein Î± subunit is tightly regulated by nucleotide binding. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3629-38.	7.1	77
136	The first constant domain (CH1 and CL) of an antibody used as heterodimerization domain for bispecific miniantibodies. FEBS Letters, 1998, 422, 259-264.	2.8	76
137	In Vitro Selection for Catalytic Activity with Ribosome Display. Journal of the American Chemical Society, 2002, 124, 9396-9403.	13.7	76
138	Structural Determinants for Improved Stability of Designed Ankyrin Repeat Proteins with a Redesigned C-Capping Module. Journal of Molecular Biology, 2010, 404, 381-391.	4.2	76
139	Thermodynamic Partitioning Model for Hydrophobic Binding of Polypeptides by GroEL. Journal of Molecular Biology, 1994, 242, 165-174.	4.2	75
140	Tandem Immobilized Metal-Ion Affinity Chromatography/Immunoaffinity Purification of His-tagged Proteinsâ€" Evaluation of Two Anti-His-Tag Monoclonal Antibodies. Analytical Biochemistry, 1998, 259, 54-61.	2.4	75
141	Stabilizing membrane proteins through protein engineering. Current Opinion in Chemical Biology, 2013, 17, 427-435.	6.1	75
142	Thermodynamic Partitioning Model for Hydrophobic Binding of Polypeptides by GroEL. Journal of Molecular Biology, 1994, 242, 150-184.	4.2	74
143	Co-selection of cognate antibody-antigen pairs by selectively-infective phages. FEBS Letters, 1995, 377, 227-231.	2.8	73
144	Affinity-Matured Recombinant Antibody Fragments Analyzed by Single-Molecule Force Spectroscopy. Biophysical Journal, 2007, 93, 3583-3590.	0.5	73

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145	Protein interference applications in cellular and developmental biology using DARPins that recognize GFP and mCherry. Biology Open, 2014, 3, 1252-1261.	1.2	73
146	Characterization of the linker peptide of the single-chain Fv fragment of an antibody by NMR spectroscopy. FEBS Letters, 1993, 320, 97-100.	2.8	72
147	Stepwise Unfolding of Ankyrin Repeats in a Single Protein Revealed by Atomic Force Microscopy. Biophysical Journal, 2006, 90, L30-L32.	0.5	72
148	High enzymatic activity and chaperone function are mechanistically related features of the dimeric E. coli peptidyl-prolyl-isomerase FkpA. Journal of Molecular Biology, 2001, 310, 485-498.	4.2	71
149	Rapid Selection of High-Affinity Binders Using Ribosome Display. Methods in Molecular Biology, 2012, 805, 261-286.	0.9	71
150	Critical features for biosynthesis, stability, and functionality of a G protein-coupled receptor uncovered by all-versus-all mutations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9810-9815.	7.1	71
151	Direct Molecular Evolution of Detergent-Stable G Protein-Coupled Receptors Using Polymer Encapsulated Cells. Journal of Molecular Biology, 2013, 425, 662-677.	4.2	71
152	Cryo-EM structure of an activated GPCRâ€“G protein complex in lipid nanodiscs. Nature Structural and Molecular Biology, 2021, 28, 258-267.	8.2	71
153	Development of the designed ankyrin repeat protein (DARPin) G3 for HER2 molecular imaging. European Journal of Nuclear Medicine and Molecular Imaging, 2015, 42, 288-301.	6.4	70
154	Inclusion of an upstream transcriptional terminator in phage display vectors abolishes background expression of toxic fusions with coat protein g3p. Gene, 1996, 178, 71-74.	2.2	69
155	A dimeric bispecific miniantibody combines two specificities with avidity. FEBS Letters, 1998, 432, 45-49.	2.8	69
156	Crystal structures of the human neurokinin 1 receptor in complex with clinically used antagonists. Nature Communications, 2019, 10, 17.	12.8	68
157	Mapping and modification of an antibody hapten binding site: a site-directed mutagenesis study of McPC603. Biochemistry, 1991, 30, 3049-3054.	2.5	67
158	Development of a generic adenovirus delivery system based on structure-guided design of bispecific trimeric DARPin adapters. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E869-77.	7.1	67
159	A quantitative comparison of cytosolic delivery via different protein uptake systems. Scientific Reports, 2017, 7, 13194.	3.3	67
160	Crystal structure of the human oxytocin receptor. Science Advances, 2020, 6, eabb5419.	10.3	67
161	Efficient cell-specific uptake of binding proteins into the cytoplasm through engineered modular transport systems. Journal of Controlled Release, 2015, 200, 13-22.	9.9	66
162	DARPin-targeting of Measles Virus: Unique Bispecificity, Effective Oncolysis, and Enhanced Safety. Molecular Therapy, 2013, 21, 849-859.	8.2	65

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163	Adenoviral vector with shield and adapter increases tumor specificity and escapes liver and immune control. Nature Communications, 2018, 9, 450.	12.8	65
164	Rapid selection of specific MAP kinase-binders from designed ankyrin repeat protein libraries. Protein Engineering, Design and Selection, 2006, 19, 219-229.	2.1	63
165	The influence of the framework core residues on the biophysical properties of immunoglobulin heavy chain variable domains. Protein Engineering, Design and Selection, 2009, 22, 121-134.	2.1	63
166	Refined crystal structure of a recombinant immunoglobulin domain and a complementarity-determining region 1-grafted mutant. Journal of Molecular Biology, 1992, 225, 739-753.	4.2	62
167	Helix-stabilized fv (hsfv) antibody fragments: substituting the constant domains of a fab fragment for a heterodimeric coiled-coil domain 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 312, 221-228.	4.2	62
168	Flavonolâ€mediated stabilization of PIN efflux complexes regulates polar auxin transport. EMBO Journal, 2021, 40, e104416.	7.8	61
169	In vitro selection and characterization of DARPins and Fab fragments for the co-crystallization of membrane proteins: The Na+-citrate symporter CitS as an example. Journal of Structural Biology, 2007, 159, 206-221.	2.8	59
170	Ribosome Display: A Technology for Selecting and Evolving Proteins from Large Libraries. Methods in Molecular Biology, 2011, 687, 283-306.	0.9	58
171	Receptor-Targeted Nipah Virus Glycoproteins Improve Cell-Type Selective Gene Delivery and Reveal a Preference for Membrane-Proximal Cell Attachment. PLoS Pathogens, 2016, 12, e1005641.	4.7	58
172	Animal-free alternatives and the antibody iceberg. Nature Biotechnology, 2020, 38, 1234-1239.	17.5	58
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