Andreas Plückthun

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9188061/publications.pdf

Version: 2024-02-01

444 papers

36,269 citations

101 h-index 170

467 all docs

467 docs citations

467 times ranked

23560 citing authors

g-index

#	Article	IF	CITATIONS
1	Improved Repeat Protein Stability by Combined Consensus and Computational Protein Design. Biochemistry, 2023, 62, 318-329.	2.5	1
2	Modular peptide binders– development of a predictive technology as alternative for reagent antibodies. Biological Chemistry, 2022, 403, 535-543.	2.5	4
3	Crystal structure of the α1B-adrenergic receptor reveals molecular determinants of selective ligand recognition. Nature Communications, 2022, 13, 382.	12.8	21
4	Universal platform for the generation of thermostabilized GPCRs that crystallize in LCP. Nature Protocols, 2022, 17, 698-726.	12.0	5
5	Structural basis of adenylyl cyclase 9 activation. Nature Communications, 2022, 13, 1045.	12.8	19
6	Sortase-Mediated Site-Specific Conjugation and ⁸⁹ Zr-Radiolabeling of Designed Ankyrin Repeat Proteins for PET. Molecular Pharmaceutics, 2022, , .	4.6	5
7	Disrupting the HDAC6-ubiquitin interaction impairs infection by influenza and Zika virus and cellular stress pathways. Cell Reports, 2022, 39, 110736.	6.4	19
8	International nonproprietary names for monoclonal antibodies: an evolving nomenclature system. MAbs, 2022, 14, 2075078.	5.2	10
9	Designed Ankyrin Repeat Proteins as a tool box for analyzing p63. Cell Death and Differentiation, 2022, 29, 2445-2458.	11.2	3
10	Thermal Shift Assay for Small GTPase Stability Screening: Evaluation and Suitability. International Journal of Molecular Sciences, 2022, 23, 7095.	4.1	10
11	NK cells with tissue-resident traits shape response to immunotherapy by inducing adaptive antitumor immunity. Science Translational Medicine, 2022, 14, .	12.4	29
12	Structural basis for the activation and ligand recognition of the human oxytocin receptor. Nature Communications, 2022, 13, .	12.8	12
13	Probing the Conformation States of Neurotensin Receptor 1 Variants by NMR Siteâ€Directed Methyl Labeling. ChemBioChem, 2021, 22, 139-146.	2.6	18
14	Animal-versus <i>in vitro</i> -derived antibodies: avoiding the extremes. MAbs, 2021, 13, 1950265.	5.2	11
15	Complexes of the neurotensin receptor 1 with small-molecule ligands reveal structural determinants of full, partial, and inverse agonism. Science Advances, 2021, 7, .	10.3	32
16	Cryo-EM structure of an activated GPCR–G protein complex in lipid nanodiscs. Nature Structural and Molecular Biology, 2021, 28, 258-267.	8.2	71
17	An Approach for the Real-Time Quantification of Cytosolic Protein–Protein Interactions in Living Cells. ACS Sensors, 2021, 6, 1572-1582.	7.8	9
18	iMATCH: an integrated modular assembly system for therapeutic combination high-capacity adenovirus gene therapy. Molecular Therapy - Methods and Clinical Development, 2021, 20, 572-586.	4.1	21

#	Article	IF	Citations
19	Engineering of Challenging G Protein-Coupled Receptors for Structure Determination and Biophysical Studies. Molecules, 2021, 26, 1465.	3.8	5
20	Directed evolution for high functional production and stability of a challenging G protein-coupled receptor. Scientific Reports, 2021, 11, 8630.	3.3	11
21	The SHREAD gene therapy platform for paracrine delivery improves tumor localization and intratumoral effects of a clinical antibody. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15
22	Crystal structures of HER3 extracellular domain 4 in complex with the designed ankyrin-repeat protein D5. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 192-201.	0.8	4
23	Engineering an anti-HER2 biparatopic antibody with a multimodal mechanism of action. Nature Communications, 2021, 12, 3790.	12.8	29
24	Generation of ordered protein assemblies using rigid three-body fusion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118 , .	7.1	25
25	Apoptosis-inducing anti-HER2 agents operate through oligomerization-induced receptor immobilization. Communications Biology, 2021, 4, 762.	4.4	12
26	Thermodynamic Stability Is a Strong Predictor for the Delivery of DARPins to the Cytosol via Anthrax Toxin. Pharmaceutics, 2021, 13, 1285.	4.5	4
27	An automated iterative approach for protein structure refinement using pseudocontact shifts. Journal of Biomolecular NMR, 2021, 75, 319-334.	2.8	5
28	Engineering Single Pan-Specific Ubiquibodies for Targeted Degradation of All Forms of Endogenous ERK Protein Kinase. ACS Synthetic Biology, 2021, 10, 2396-2408.	3.8	10
29	Designed Ankyrin Repeat Proteins as Novel Binders for Ultrasound Molecular Imaging. Ultrasound in Medicine and Biology, 2021, 47, 2664-2675.	1.5	1
30	Purification of MBP fusion proteins using engineered DARPin affinity matrix. International Journal of Biological Macromolecules, 2021, 187, 105-112.	7.5	3
31	Half-life extension of efficiently produced DARPin serum albumin fusions as a function of FcRn affinity and recycling. European Journal of Pharmaceutics and Biopharmaceutics, 2021, 167, 104-113.	4.3	5
32	Flavonolâ€mediated stabilization of PIN efflux complexes regulates polar auxin transport. EMBO Journal, 2021, 40, e104416.	7.8	61
33	A structural model of a Ras–Raf signalosome. Nature Structural and Molecular Biology, 2021, 28, 847-857.	8.2	44
34	Asymmetric requirement of Dpp/BMP morphogen dispersal in the Drosophila wing disc. Nature Communications, 2021, 12, 6435.	12.8	22
35	Distinct conformations of the HIV-1 V3 loop crown are targetable for broad neutralization. Nature Communications, 2021, 12, 6705.	12.8	9
36	Structures of neurokinin 1 receptor in complex with G _q and G _s proteins reveal substance P binding mode and unique activation features. Science Advances, 2021, 7, eabk2872.	10.3	25

#	Article	IF	CITATIONS
37	The RGD-binding integrins $\hat{l}\pm v\hat{l}^26$ and $\hat{l}\pm v\hat{l}^28$ are receptors for mouse adenovirus-1 and -3 infection. PLoS Pathogens, 2021, 17, e1010083.	4.7	8
38	Chaperone-assisted structure elucidation with DARPins. Current Opinion in Structural Biology, 2020, 60, 93-100.	5.7	21
39	High-Throughput Generation of Bispecific Binding Proteins by Sortase A–Mediated Coupling for Direct Functional Screening in Cell Culture. Molecular Cancer Therapeutics, 2020, 19, 1080-1088.	4.1	12
40	Engineering Af1521 improves ADP-ribose binding and identification of ADP-ribosylated proteins. Nature Communications, 2020, 11, 5199.	12.8	49
41	Animal-free alternatives and the antibody iceberg. Nature Biotechnology, 2020, 38, 1234-1239.	17.5	58
42	Crystal structure of the human oxytocin receptor. Science Advances, 2020, 6, eabb5419.	10.3	67
43	Salmonella-based platform for efficient delivery of functional binding proteins to the cytosol. Communications Biology, 2020, 3, 342.	4.4	14
44	Malignant tissues produce divergent antibody glycosylation of relevance for cancer gene therapy effectiveness. MAbs, 2020, 12, 1792084.	5.2	7
45	Animal-derived-antibody generation faces strict reform in accordance with European Union policy on animal use. Nature Methods, 2020, 17, 755-756.	19.0	27
46	The Antibody Society's antibody validation webinar series. MAbs, 2020, 12, 1794421.	5.2	26
47	Optimizing the anti-tumor efficacy of protein-drug conjugates by engineering the molecular size and half-life. Journal of Controlled Release, 2020, 327, 186-197.	9.9	30
48	Reengineering anthrax toxin protective antigen for improved receptor-specific protein delivery. BMC Biology, 2020, 18, 100.	3.8	9
49	Optimizing the $\hat{l}\pm 1B$ -adrenergic receptor for solution NMR studies. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183354.	2.6	19
50	Photoinduced damage of AsLOV2 domain is accompanied by increased singlet oxygen production due to flavin dissociation. Scientific Reports, 2020, 10, 4119.	3.3	10
51	Structure-Guided Design of a Peptide Lock for Modular Peptide Binders. ACS Chemical Biology, 2020, 15, 457-468.	3.4	8
52	Reproducibility: bypass animals for antibody production. Nature, 2020, 581, 262-262.	27.8	17
53	Lactoferrin-Hexon Interactions Mediate CAR-Independent Adenovirus Infection of Human Respiratory Cells. Journal of Virology, 2020, 94, .	3.4	16
54	Influence of size and charge of unstructured polypeptides on pharmacokinetics and biodistribution of targeted fusion proteins. Journal of Controlled Release, 2019, 307, 379-392.	9.9	22

#	Article	IF	CITATIONS
55	Reprogramming Bacteriophage Host Range through Structure-Guided Design of Chimeric Receptor Binding Proteins. Cell Reports, 2019, 29, 1336-1350.e4.	6.4	135
56	Rigid fusions of designed helical repeat binding proteins efficiently protect a binding surface from crystal contacts. Scientific Reports, 2019, 9, 16162.	3.3	11
57	New views into class B GPCRs from the crystal structure of PTH1R. FEBS Journal, 2019, 286, 4852-4860.	4.7	3
58	Structural analysis of biological targets by host:guest crystal lattice engineering. Scientific Reports, 2019, 9, 15199.	3.3	17
59	Multispecific Targeting with Synthetic Ankyrin Repeat Motif Chimeric Antigen Receptors. Clinical Cancer Research, 2019, 25, 7506-7516.	7.0	43
60	Peptide binding affinity redistributes preassembled repeat protein fragments. Biological Chemistry, 2019, 400, 395-404.	2.5	3
61	Systemic analysis of tyrosine kinase signaling reveals a common adaptive response program in a HER2-positive breast cancer. Science Signaling, 2019, 12, .	3.6	26
62	Computational Modeling of Designed Ankyrin Repeat Protein Complexes with Their Targets. Journal of Molecular Biology, 2019, 431, 2852-2868.	4.2	6
63	Targeted delivery and endosomal cellular uptake of DARPin-siRNA bioconjugates: Influence of linker stability on gene silencing. European Journal of Pharmaceutics and Biopharmaceutics, 2019, 141, 37-50.	4.3	10
64	High-Throughput Quantification of Surface Protein Internalization and Degradation. ACS Chemical Biology, 2019, 14, 1154-1163.	3.4	14
65	Insight into microtubule nucleation from tubulin-capping proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9859-9864.	7.1	15
66	A survival selection strategy for engineering synthetic binding proteins that specifically recognize post-translationally phosphorylated proteins. Nature Communications, 2019, 10, 1830.	12.8	9
67	Trapped! A Critical Evaluation of Methods for Measuring Total Cellular Uptake versus Cytosolic Localization. Bioconjugate Chemistry, 2019, 30, 1006-1027.	3.6	53
68	Inhibition of the MET Kinase Activity and Cell Growth in MET-Addicted Cancer Cells by Bi-Paratopic Linking. Journal of Molecular Biology, 2019, 431, 2020-2039.	4.2	20
69	High-Throughput Fluorescence Polarization Assay to Identify Ligands Using Purified G Protein-Coupled Receptor. SLAS Discovery, 2019, 24, 915-927.	2.7	12
70	Mutations in sigma 70 transcription factor improves expression of functional eukaryotic membrane proteins in Escherichia coli. Scientific Reports, 2019, 9, 2483.	3.3	8
71	Rotational symmetry of the structured Chip/LDB-SSDP core module of the Wnt enhanceosome. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20977-20983.	7.1	10
72	Labeling surface proteins with high specificity: Intrinsic limitations of phosphopantetheinyl transferase systems. PLoS ONE, 2019, 14, e0226579.	2.5	5

#	Article	IF	CITATIONS
73	Unravelling Receptor and RGD Motif Dependence of Retargeted Adenoviral Vectors using Advanced Tumor Model Systems. Scientific Reports, 2019, 9, 18568.	3.3	14
74	Crystal structures of the human neurokinin 1 receptor in complex with clinically used antagonists. Nature Communications, 2019, 10, 17.	12.8	68
75	In vivo assembly and large-scale purification of a GPCR - Gl_{\pm} fusion with Gl^2l^3 , and characterization of the active complex. PLoS ONE, 2019, 14, e0210131.	2.5	8
76	Site-Selective Enzymatic Labeling of Designed Ankyrin Repeat Proteins Using Protein Farnesyltransferase. Methods in Molecular Biology, 2019, 2033, 207-219.	0.9	4
77	Facile Site-Specific Multiconjugation Strategies in Recombinant Proteins Produced in Bacteria. Methods in Molecular Biology, 2019, 2033, 253-273.	0.9	5
78	Peptideâ€Guided Assembly of Repeat Protein Fragments. Angewandte Chemie - International Edition, 2018, 57, 4576-4579.	13.8	10
79	Adenoviral vector with shield and adapter increases tumor specificity and escapes liver and immune control. Nature Communications, 2018, 9, 450.	12.8	65
80	Peptide-Guided Assembly of Repeat Protein Fragments. Angewandte Chemie, 2018, 130, 4666-4669.	2.0	1
81	Segmental isotopic labeling by asparaginyl endopeptidase-mediated protein ligation. Journal of Biomolecular NMR, 2018, 71, 225-235.	2.8	19
82	Determinants of Ligand Subtype-Selectivity at \hat{l}_{\pm} _{1A} -Adrenoceptor Revealed Using Saturation Transfer Difference (STD) NMR. ACS Chemical Biology, 2018, 13, 1090-1102.	3.4	26
83	Modification of the kinetic stability of immunoglobulin G by solvent additives. MAbs, 2018, 10, 607-623.	5.2	12
84	Structural Basis for the Selective Inhibition of c-Jun N-Terminal Kinase 1 Determined by Rigid DARPin–DARPin Fusions. Journal of Molecular Biology, 2018, 430, 2128-2138.	4.2	12
85	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
86	DARPins recognizing mTFP1 as novel reagents for <i>in vitro</i> and <i>in vivo</i> protein manipulations. Biology Open, 2018, 7, .	1.2	7
87	Rapid Selection of High-Affinity Antibody scFv Fragments Using Ribosome Display. Methods in Molecular Biology, 2018, 1827, 235-268.	0.9	11
88	Assessment of ab initio models of protein complexes by molecular dynamics. PLoS Computational Biology, 2018, 14, e1006182.	3.2	33
89	Ptdlns(4,5)P2 stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. Nature, 2018, 559, 423-427.	27.8	236
90	An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. ACS Synthetic Biology, 2018, 7, 2226-2235.	3.8	11

#	Article	IF	Citations
91	A Library-Based Screening Strategy for the Identification of DARPins as Ligands for Receptor-Targeted AAV and Lentiviral Vectors. Molecular Therapy - Methods and Clinical Development, 2018, 10, 128-143.	4.1	30
92	Lung macrophage scavenger receptor SR-A6 (MARCO) is an adenovirus type-specific virus entry receptor. PLoS Pathogens, 2018, 14, e1006914.	4.7	56
93	Curvature of designed armadillo repeat proteins allows modular peptide binding. Journal of Structural Biology, 2018, 201, 108-117.	2.8	12
94	A Biotin Ligase-Based Assay for the Quantification of the Cytosolic Delivery of Therapeutic Proteins. Methods in Molecular Biology, 2017, 1575, 223-236.	0.9	10
95	Changes to International Nonproprietary Names for antibody therapeutics 2017 and beyond: of mice, men and more. MAbs, 2017, 9, 898-906.	5.2	28
96	Rigidity of the extracellular part of HER2: Evidence from engineering subdomain interfaces and sharedâ€helix DARPinâ€DARPin fusions. Protein Science, 2017, 26, 1796-1806.	7.6	10
97	Ligand Discovery for a Peptide-Binding GPCR by Structure-Based Screening of Fragment- and Lead-Like Chemical Libraries. ACS Chemical Biology, 2017, 12, 735-745.	3.4	24
98	Personalised proteome analysis by means of protein microarrays made from individual patient samples. Scientific Reports, 2017, 7, 39756.	3.3	17
99	SPRi-MALDI MS: characterization and identification of a kinase from cell lysate by specific interaction with different designed ankyrin repeat proteins. Analytical and Bioanalytical Chemistry, 2017, 409, 1827-1836.	3.7	13
100	A quantitative comparison of cytosolic delivery via different protein uptake systems. Scientific Reports, 2017, 7, 13194.	3.3	67
101	Analysis of IgG kinetic stability by differential scanning calorimetry, probe fluorescence and light scattering. Protein Science, 2017, 26, 2229-2239.	7.6	14
102	Rigidly connected multispecific artificial binders with adjustable geometries. Scientific Reports, 2017, 7, 11217.	3.3	30
103	Structures of designed armadillo repeat proteins binding to peptides fused to globular domains. Protein Science, 2017, 26, 1942-1952.	7.6	10
104	Design and applications of a clamp for Green Fluorescent Protein with picomolar affinity. Scientific Reports, 2017, 7, 16292.	3.3	49
105	Functional and dynamic polymerization of the ALS-linked protein TDP-43 antagonizes its pathologic aggregation. Nature Communications, 2017, 8, 45.	12.8	242
106	Covalently circularized nanodiscs for studying membrane proteins and viral entry. Nature Methods, 2017, 14, 49-52.	19.0	221
107	Advances in the design and engineering of peptide-binding repeat proteins. Biological Chemistry, 2017, 398, 23-29.	2.5	16
108	SPR-based fragment screening with neurotensin receptor 1 generates novel small molecule ligands. PLoS ONE, 2017, 12, e0175842.	2.5	24

#	Article	IF	CITATIONS
109	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
110	Directed evolution of G protein-coupled receptors in yeast for higher functional production in eukaryotic expression hosts. Scientific Reports, 2016, 6, 21508.	3.3	55
111	DARPin-Based Crystallization Chaperones Exploit Molecular Geometry as a Screening Dimension in Protein Crystallography. Journal of Molecular Biology, 2016, 428, 1574-1588.	4.2	30
112	Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition. Journal of Molecular Biology, 2016, 428, 4467-4489.	4.2	19
113	Intermolecular biparatopic trapping of ErbB2 prevents compensatory activation of PI3K/AKT via RAS–p110 crosstalk. Nature Communications, 2016, 7, 11672.	12.8	38
114	Structures of designed armadillo-repeat proteins show propagation of inter-repeat interface effects. Acta Crystallographica Section D: Structural Biology, 2016, 72, 168-175.	2.3	12
115	Destabilizing an interacting motif strengthens the association of a designed ankyrin repeat protein with tubulin. Scientific Reports, 2016, 6, 28922.	3.3	27
116	A generic selection system for improved expression and thermostability of G protein-coupled receptors by directed evolution. Scientific Reports, 2016, 6, 21294.	3.3	25
117	Enhanced lysis by bispecific oncolytic measles viruses simultaneously using HER2 /neu or EpCAM as target receptors. Molecular Therapy - Oncolytics, 2016, 3, 16003.	4.4	20
118	Conformational dynamics of a G-protein \hat{l}_{\pm} 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
119	Generation of Fluorogen-Activating Designed Ankyrin Repeat Proteins (FADAs) as Versatile Sensor Tools. Journal of Molecular Biology, 2016, 428, 1272-1289.	4.2	22
120	Structure and Energetic Contributions of a Designed Modular Peptide-Binding Protein with Picomolar Affinity. Journal of the American Chemical Society, 2016, 138, 3526-3532.	13.7	27
121	The INNs and outs of antibody nonproprietary names. MAbs, 2016, 8, 1-9.	5.2	48
122	Advanced analyses of kinetic stabilities of iggs modified by mutations and glycosylation. Protein Science, 2015, 24, 1100-1113.	7.6	13
123	Comprehensive analysis of heterotrimeric G-protein complex diversity and their interactions with GPCRs in solution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1181-90.	7.1	41
124	Antibodies: validate recombinants once. Nature, 2015, 520, 295-295.	27.8	26
125	A Combined NMR and Computational Approach to Investigate Peptide Binding to a Designed Armadillo Repeat Protein. Journal of Molecular Biology, 2015, 427, 1916-1933.	4.2	6
126	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

#	Article	IF	Citations
127	Off-target-free gene delivery by affinity-purified receptor-targeted viral vectors. Nature Communications, 2015, 6, 6246.	12.8	91
128	Liposome functionalization with copper-free "click chemistry― Journal of Controlled Release, 2015, 202, 14-20.	9.9	47
129	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
130	Phase Behavior of a Designed Cyclopropyl Analogue of Monoolein: Implications for Lowâ€Temperature Membrane Protein Crystallization. Angewandte Chemie - International Edition, 2015, 54, 1027-1031.	13.8	29
131	Receptor-targeted lentiviral vectors are exceptionally sensitive toward the biophysical properties of the displayed single-chain Fv. Protein Engineering, Design and Selection, 2015, 28, 93-106.	2.1	23
132	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
133	Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells. Nature Methods, 2015, 12, 773-779.	19.0	217
134	Antibody–Drug Conjugates for Tumor Targeting—Novel Conjugation Chemistries and the Promise of non-IgG Binding Proteins. Bioconjugate Chemistry, 2015, 26, 2176-2185.	3.6	38
135	A cleavable ligand column for the rapid isolation of large quantities of homogeneous and functional neurotensin receptor 1 variants from E. coli. Protein Expression and Purification, 2015, 108, 106-114.	1.3	19
136	Getting to reproducible antibodies: the rationale for sequenced recombinant characterized reagents. Protein Engineering, Design and Selection, 2015, 28, 303-305.	2.1	50
137	Reproducibility: Standardize antibodies used in research. Nature, 2015, 518, 27-29.	27.8	530
138	Protein interference applications in cellular and developmental biology using DARPins that recognize GFP and mCherry. Biology Open, 2014, 3, 1252-1261.	1.2	73
139	The ErbB4 CYT2 variant protects EGFR from ligand-induced degradation to enhance cancer cell motility. Science Signaling, 2014, 7, ra78.	3.6	34
140	Novel Prodrug-Like Fusion Toxin with Protease-Sensitive Bioorthogonal PEGylation for Tumor Targeting. Bioconjugate Chemistry, 2014, 25, 2144-2156.	3.6	19
141	Crystal structures of designed armadillo repeat proteins: Implications of construct design and crystallization conditions on overall structure. Protein Science, 2014, 23, 1572-1583.	7.6	16
142	Structure of signaling-competent neurotensin receptor 1 obtained by directed evolution in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E655-62.	7.1	197
143	Co-Crystallization with Conformation-Specific Designed Ankyrin Repeat Proteins Explains the Conformational Flexibility of BCL-W. Journal of Molecular Biology, 2014, 426, 2346-2362.	4.2	15
144	Increasing the Antitumor Effect of an EpCAM-Targeting Fusion Toxin by Facile Click PEGylation. Molecular Cancer Therapeutics, 2014, 13, 375-385.	4.1	37

#	Article	IF	CITATIONS
145	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
146	Modular peptide binding: From a comparison of natural binders to designed armadillo repeat proteins. Journal of Structural Biology, 2014, 185, 147-162.	2.8	50
147	G-quadruplexes are specifically recognized and distinguished by selected designed ankyrin repeat proteins. Nucleic Acids Research, 2014, 42, 9182-9194.	14.5	16
148	Spontaneous Self-Assembly of Engineered Armadillo Repeat Protein Fragments into a Folded Structure. Structure, 2014, 22, 985-995.	3.3	19
149	Improving the apo-state detergent stability of NTS1 with CHESS for pharmacological and structural studies. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 2817-2824.	2.6	36
150	Amyloid-β Peptide-specific DARPins as a Novel Class of Potential Therapeutics for Alzheimer Disease. Journal of Biological Chemistry, 2014, 289, 27080-27089.	3.4	17
151	Engineered proteins with desired specificity: DARPins, other alternative scaffolds and bispecific IgGs. Current Opinion in Structural Biology, 2014, 27, 102-112.	5.7	104
152	A Universal Approach to Prepare Reagents for DNA-Assisted Protein Analysis. PLoS ONE, 2014, 9, e108061.	2.5	5
153	Structure of a kinesin–tubulin complex and implications for kinesin motility. Nature Structural and Molecular Biology, 2013, 20, 1001-1007.	8.2	143
154	Knowledge-Based Design of a Biosensor to Quantify Localized ERK Activation in Living Cells. Chemistry and Biology, 2013, 20, 847-856.	6.0	49
155	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
156	Orthogonal Assembly of a Designed Ankyrin Repeat Protein–Cytotoxin Conjugate with a Clickable Serum Albumin Module for Half-Life Extension. Bioconjugate Chemistry, 2013, 24, 1955-1966.	3.6	53
157	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
158	Directed Evolution of G-Protein-Coupled Receptors for High Functional Expression and Detergent Stability. Methods in Enzymology, 2013, 520, 67-97.	1.0	20
159	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
160	Stabilizing membrane proteins through protein engineering. Current Opinion in Chemical Biology, 2013, 17, 427-435.	6.1	75
161	Epithelial cell adhesion molecule-targeted drug delivery for cancer therapy. Expert Opinion on Drug Delivery, 2013, 10, 451-468.	5.0	79
162	Protein tag-mediated conjugation of oligonucleotides to recombinant affinity binders for proximity ligation. New Biotechnology, 2013, 30, 144-152.	4.4	33

#	Article	IF	CITATIONS
163	DARPin-targeting of Measles Virus: Unique Bispecificity, Effective Oncolysis, and Enhanced Safety. Molecular Therapy, 2013, 21, 849-859.	8.2	65
164	Conformation-Dependent Recognition of HIV gp120 by Designed Ankyrin Repeat Proteins Provides Access to Novel HIV Entry Inhibitors. Journal of Virology, 2013, 87, 5868-5881.	3.4	34
165	Structural Model for the Interaction of a Designed Ankyrin Repeat Protein with the Human Epidermal Growth Factor Receptor 2. PLoS ONE, 2013, 8, e59163.	2.5	17
166	Transfer of engineered biophysical properties between different antibody formats and expression systems. Protein Engineering, Design and Selection, 2012, 25, 485-506.	2.1	34
167	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
168	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
169	Rapid Selection of High-Affinity Binders Using Ribosome Display. Methods in Molecular Biology, 2012, 805, 261-286.	0.9	71
170	Design and Characterization of Modular Scaffolds for Tubulin Assembly. Journal of Biological Chemistry, 2012, 287, 31085-31094.	3.4	22
171	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
172	Direct identification of ligand-receptor interactions on living cells and tissues. Nature Biotechnology, 2012, 30, 997-1001.	17. 5	154
173	Facile Double-Functionalization of Designed Ankyrin Repeat Proteins using Click and Thiol Chemistries. Bioconjugate Chemistry, 2012, 23, 279-286.	3.6	54
174	Engineering Aggregation Resistance in IgG by Two Independent Mechanisms: Lessons from Comparison of Pichia pastoris and Mammalian Cell Expression. Journal of Molecular Biology, 2012, 417, 309-335.	4.2	43
175	Maximizing Detergent Stability and Functional Expression of a GPCR by Exhaustive Recombination and Evolution. Journal of Molecular Biology, 2012, 422, 414-428.	4.2	55
176	Ribosome Display: A Perspective. Methods in Molecular Biology, 2012, 805, 3-28.	0.9	106
177	Optimization of designed armadillo repeat proteins by molecular dynamics simulations and NMR spectroscopy. Protein Science, 2012, 21, 1298-1314.	7.6	34
178	Designed Armadillo Repeat Proteins: Library Generation, Characterization and Selection of Peptide Binders with High Specificity. Journal of Molecular Biology, 2012, 424, 68-87.	4.2	46
179	Designed Ankyrin Repeat Proteins (DARPins). Methods in Enzymology, 2012, 503, 101-134.	1.0	101
180	Beyond antibodies: advances from engineered binding proteins. New Biotechnology, 2012, 29, S34-S35.	4.4	0

#	Article	IF	Citations
181	Structureâ€based optimization of designed Armadilloâ€repeat proteins. Protein Science, 2012, 21, 1015-1028.	7.6	32
182	Designed Ankyrin Repeat Proteins (DARPins) as Novel Isoform-Specific Intracellular Inhibitors of c-Jun N-Terminal Kinases. ACS Chemical Biology, 2012, 7, 1356-1366.	3.4	56
183	DARPins: An Efficient Targeting Domain for Lentiviral Vectors. Molecular Therapy, 2011, 19, 686-693.	8.2	93
184	Her2-specific Multivalent Adapters Confer Designed Tropism to Adenovirus for Gene Targeting. Journal of Molecular Biology, 2011, 405, 410-426.	4.2	56
185	Evolution of Three Human GPCRs for Higher Expression and Stability. Journal of Molecular Biology, 2011, 408, 599-615.	4.2	77
186	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
187	Ribosome Display: A Technology for Selecting and Evolving Proteins from Large Libraries. Methods in Molecular Biology, 2011, 687, 283-306.	0.9	58
188	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
189	DARPins and other repeat protein scaffolds: advances in engineering and applications. Current Opinion in Biotechnology, 2011, 22, 849-857.	6.6	212
190	Individual filamentous phage imaged by electron holography. European Biophysics Journal, 2011, 40, 1197-1201.	2.2	24
191	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
192	Antibodies with a split personality. Nature, 2010, 467, 537-538.	27.8	8
193	Computational analysis of off-rate selection experiments to optimize affinity maturation by directed evolution. Protein Engineering, Design and Selection, 2010, 23, 175-184.	2.1	48
194	Knowledge-based design of reagentless fluorescent biosensors from a designed ankyrin repeat protein. Protein Engineering, Design and Selection, 2010, 23, 229-241.	2.1	16
195	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
196	Construction of scFv Fragments from Hybridoma or Spleen Cells by PCR Assembly. , 2010, , 21-44.		19
197	Residue-Resolved Stability of Full-Consensus Ankyrin Repeat Proteins Probed by NMR. Journal of Molecular Biology, 2010, 402, 241-258.	4.2	33
198	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

#	Article	IF	Citations
199	Designed ankyrin repeat proteins: a novel tool for testing epidermal growth factor receptor 2 expression in breast cancer. Modern Pathology, 2010, 23, 1289-1297.	5.5	39
200	Improving Expression of scFv Fragments by Co-expression of Periplasmic Chaperones., 2010,, 345-361.		11
201	Miniantibodies. , 2010, , 85-99.		1
202	EpCAM-targeted delivery of nanocomplexed siRNA to tumor cells with designed ankyrin repeat proteins. Molecular Cancer Therapeutics, 2009, 8, 2674-2683.	4.1	85
203	Crystal Structure and Function of a DARPin Neutralizing Inhibitor of Lactococcal Phage TP901-1. Journal of Biological Chemistry, 2009, 284, 30718-30726.	3.4	55
204	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. Protein Engineering, Design and Selection, 2009, 22, 135-147.	2.1	46
205	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
206	Selection and characterization of DARPins specific for the neurotensin receptor 1. Protein Engineering, Design and Selection, 2009, 22, 357-366.	2.1	33
207	Construction and characterization of protein libraries composed of secondary structure modules. Protein Science, 2009, 11, 2631-2643.	7.6	23
208	Folding of a designed simple ankyrin repeat protein. Protein Science, 2009, 13, 2864-2870.	7.6	37
209	Facile promoter deletion in Escherichia coli in response to leaky expression of very robust and benign proteins from common expression vectors. Microbial Cell Factories, 2009, 8, 8.	4.0	20
210	Alternative Scaffolds: Expanding the Options of Antibodies. , 2009, , 243-272.		4
211	Structure of the recombinant antibody Fab fragment f3p4. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 636-643.	2.5	5
212	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
213	Folding and Unfolding Mechanism of Highly Stable Full-Consensus Ankyrin Repeat Proteins. Journal of Molecular Biology, 2008, 376, 241-257.	4.2	161
214	Stabilizing Ionic Interactions in a Full-consensus Ankyrin Repeat Protein. Journal of Molecular Biology, 2008, 376, 232-240.	4.2	51
215	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
216	Efficient Selection of DARPins with Sub-nanomolar Affinities using SRP Phage Display. Journal of Molecular Biology, 2008, 382, 1211-1227.	4.2	236

#	Article	IF	CITATIONS
217	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
218	Antitumor activity of an epithelial cell adhesion molecule–targeted nanovesicular drug delivery system. Molecular Cancer Therapeutics, 2007, 6, 3019-3027.	4.1	87
219	Monovalent antibody scFv fragments selected to modulate T-cell activation by inhibition of CD86–CD28 interaction. Protein Engineering, Design and Selection, 2007, 20, 91-98.	2.1	4
220	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
221	A Designed Ankyrin Repeat Protein Evolved to Picomolar Affinity to Her2. Journal of Molecular Biology, 2007, 369, 1015-1028.	4.2	211
222	Affinity-Matured Recombinant Antibody Fragments Analyzed by Single-Molecule Force Spectroscopy. Biophysical Journal, 2007, 93, 3583-3590.	0.5	73
223	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. Nature Methods, 2007, 4, 13-17.	19.0	231
224	Ribosome display: selecting and evolving proteins in vitro that specifically bind to a target. Nature Methods, 2007, 4, 269-279.	19.0	271
225	The design of evolution and the evolution of design. Current Opinion in Structural Biology, 2007, 17, 451-453.	5 . 7	6
226	Inhibition of Caspase-2 by a Designed Ankyrin Repeat Protein: Specificity, Structure, and Inhibition Mechanism. Structure, 2007, 15, 625-636.	3.3	125
227	Stepwise Unfolding of Ankyrin Repeats in a Single Protein Revealed by Atomic Force Microscopy. Biophysical Journal, 2006, 90, L30-L32.	0.5	72
228	Isolation of Intracellular Proteinase Inhibitors Derived from Designed Ankyrin Repeat Proteins by Genetic Screening. Journal of Biological Chemistry, 2006, 281, 40252-40263.	3.4	43
229	PIN-bodies: A new class of antibody-like proteins with CD4 specificity derived from the protein inhibitor of neuronal nitric oxide synthase. Biochemical and Biophysical Research Communications, 2006, 343, 334-344.	2.1	7
230	GroEL Walks the Fine Line: The Subtle Balance of Substrate and Co-chaperonin Binding by GroEL. A Combinatorial Investigation by Design, Selection and Screening. Journal of Molecular Biology, 2006, 357, 411-426.	4.2	14
231	Direct Selection of Antibodies from Complex Libraries with the Protein Fragment Complementation Assay. Journal of Molecular Biology, 2006, 357, 427-441.	4.2	44
232	Directed Evolution of an Anti-prion Protein scFv Fragment to an Affinity of $1\mathrm{pM}$ and its Structural Interpretation. Journal of Molecular Biology, 2006, 363, 75-97.	4.2	110
233	Crystal structure of a consensus-designed ankyrin repeat protein: Implications for stability. Proteins: Structure, Function and Bioinformatics, 2006, 65, 280-284.	2.6	34
234	Molecular dynamics study of the stabilities of consensus designed ankyrin repeat proteins. Proteins: Structure, Function and Bioinformatics, 2006, 65, 285-295.	2.6	13

#	Article	IF	CITATIONS
235	Signal sequences directing cotranslational translocation expand the range of proteins amenable to phage display. Nature Biotechnology, 2006, 24, 823-831.	17.5	191
236	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
237	Selection and Characterization of Her2 Binding-designed Ankyrin Repeat Proteins. Journal of Biological Chemistry, 2006, 281, 35167-35175.	3.4	91
238	PEGylation and Multimerization of the Anti-p185HER-2 Single Chain Fv Fragment 4D5. Journal of Biological Chemistry, 2006, 281, 35186-35201.	3.4	109
239	Chemosensitization of carcinoma cells using epithelial cell adhesion molecule–targeted liposomal antisense against bcl-2/bcl-xL. Molecular Cancer Therapeutics, 2006, 5, 3170-3180.	4.1	45
240	A mutation designed to alter crystal packing permits structural analysis of a tight-binding fluorescein-scFv complex. Protein Science, 2005, 14, 2537-2549.	7.6	27
241	Engineering novel binding proteins from nonimmunoglobulin domains. Nature Biotechnology, 2005, 23, 1257-1268.	17.5	598
242	Allosteric Inhibition of Aminoglycoside Phosphotransferase by a Designed Ankyrin Repeat Protein. Structure, 2005, 13, 1131-1141.	3.3	78
243	Engineered proteins as specific binding reagents. Current Opinion in Biotechnology, 2005, 16, 459-469.	6.6	142
244	NMR solution structure of the monomeric form of the bacteriophage λ capsid stabilizing protein gpD. Journal of Biomolecular NMR, 2005, 31, 351-356.	2.8	16
245	Engineering and functional immobilization of opioid receptors. Protein Engineering, Design and Selection, 2005, 18, 153-160.	2.1	9
246	Intracellular Kinase Inhibitors Selected from Combinatorial Libraries of Designed Ankyrin Repeat Proteins. Journal of Biological Chemistry, 2005, 280, 24715-24722.	3.4	115
247	Protein PEGylation Decreases Observed Target Association Rates via a Dual Blocking Mechanism. Molecular Pharmacology, 2005, 68, 1439-1454.	2.3	145
248	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
249	Ribosome display of mammalian receptor domains. Protein Engineering, Design and Selection, 2005, 18, 285-294.	2.1	25
250	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
251	Identification of a Functional Epitope of the Nogo Receptor by a Combinatorial Approach Using Ribosome Display. Journal of Molecular Biology, 2005, 352, 229-241.	4.2	37
252	Construction and characterization of a kappa opioid receptor devoid of all free cysteines. Protein Engineering, Design and Selection, 2004, 17, 37-48.	2.1	11

#	Article	IF	Citations
253	High-affinity binders selected from designed ankyrin repeat protein libraries. Nature Biotechnology, 2004, 22, 575-582.	17.5	598
254	In-vitro protein evolution by ribosome display and mRNA display. Journal of Immunological Methods, 2004, 290, 51-67.	1.4	321
255	Letter to the Editor: Assignments of 1H and 15N resonances of the bacteriophage \hat{l} » capsid stabilizing protein gpD. Journal of Biomolecular NMR, 2004, 28, 89-90.	2.8	3
256	Letter to the Editor: Backbone HN, N, Cα, C′ and Cβchemical shift assignments and secondary structure of FkpA, a 245-residue peptidyl-prolyl cis/trans isomerase with chaperone activity. Journal of Biomolecular NMR, 2004, 28, 405-406.	2.8	4
257	Strategies for Selection from Protein Libraries Composed of de Novo Designed Secondary Structure Modules. Origins of Life and Evolution of Biospheres, 2004, 34, 151-157.	1.9	11
258	Crystal structure of a truncated version of the phage \hat{l} » protein gpD. Proteins: Structure, Function and Bioinformatics, 2004, 57, 866-868.	2.6	6
259	Combinatorial Approaches To Novel Proteins. ChemBioChem, 2004, 5, 177-182.	2.6	12
260	Consensus Design of Repeat Proteins. ChemBioChem, 2004, 5, 183-189.	2.6	96
261	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
262	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
263	Kinetic Stability and Crystal Structure of the Viral Capsid Protein SHP. Journal of Molecular Biology, 2004, 344, 179-193.	4.2	36
264	An antibody library for stabilizing and crystallizing membrane proteins - selecting binders to the citrate carrier CitS. FEBS Letters, 2004, 564, 340-348.	2.8	43
265	Turnover-based in vitro selection and evolution of biocatalysts from a fully synthetic antibody library. Nature Biotechnology, 2003, 21, 679-685.	17.5	90
266	Design of multivalent complexes using the barnase·barstar module. Nature Biotechnology, 2003, 21, 1486-1492.	17.5	177
267	Structure-Based Improvement of the Biophysical Properties of Immunoglobulin VHDomains with a Generalizable Approachâ€. Biochemistry, 2003, 42, 1517-1528.	2.5	103
268	Biophysical Properties of Human Antibody Variable Domains. Journal of Molecular Biology, 2003, 325, 531-553.	4.2	329
269	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
270	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

#	Article	IF	Citations
271	A novel strategy to design binding molecules harnessing the modular nature of repeat proteins. FEBS Letters, 2003, 539, 2-6.	2.8	127
272	Selection based on the folding properties of proteins with ribosome display. FEBS Letters, 2003, 539, 24-28.	2.8	49
273	Structural analysis of mycobacterial and murine hsp60 epitopes in complex with the class I MHC molecule H-2Db. FEBS Letters, 2003, 543, 11-15.	2.8	1
274	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
275	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
276	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
277	Self-Immobilizing Recombinant Antibody Fragments for Immunoaffinity Chromatography: Generic, Parallel, and Scalable Protein Purification. Protein Expression and Purification, 2002, 24, 313-322.	1.3	36
278	Crystal Structure of the Anti-His Tag Antibody 3D5 Single-chain Fragment Complexed to its Antigen. Journal of Molecular Biology, 2002, 318, 135-147.	4.2	46
279	Biophysical Properties of Camelid VHHDomains Compared to Those of Human VH3 Domainsâ€. Biochemistry, 2002, 41, 3628-3636.	2.5	182
280	In Vitro Selection for Catalytic Activity with Ribosome Display. Journal of the American Chemical Society, 2002, 124, 9396-9403.	13.7	76
281	Comparison of In Vivo Selection and Rational Design of Heterodimeric Coiled Coils. Structure, 2002, 10, 1235-1248.	3.3	51
282	Direct Screening for Phosphatase Activity by Turnover-Based Capture of Protein Catalysts This work was supported by BBSRC studentships (to J.B. and H.D.), by an EPSRC studentship (to J.H.R.), and by an EC TMR studentship (to S.CT.) Angewandte Chemie - International Edition, 2002, 41, 775.	13.8	36
283	Ligand binding of a ribosome-displayed protein detected in solution at the single molecule level by fluorescence correlation spectroscopy. European Biophysics Journal, 2002, 31, 179-184.	2.2	23
284	Structure of cyclized green fluorescent protein. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1400-1406.	2.5	7
285	A kinetic trap is an intrinsic feature in the folding pathway of single-chain Fv fragments. Biophysical Chemistry, 2002, 96, 273-284.	2.8	19
286	AFM structural study of the molecular chaperone GroEL and its two-dimensional crystals: an ideal "living―calibration sample. Ultramicroscopy, 2002, 93, 83-89.	1.9	19
287	Stability engineering of antibody single-chain Fv fragments. Journal of Molecular Biology, 2001, 305, 989-1010.	4.2	554
288	The scFv fragment of the antibody hu4d5-8: evidence for early premature domain interaction in refolding. Journal of Molecular Biology, 2001, 305, 1111-1129.	4.2	28

#	Article	IF	CITATIONS
289	Fast selection of antibodies without antigen purification: adaptation of the protein fragment complementation assay to select antigen-antibody pairs 1 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 308, 115-122.	4.2	57
290	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
291	Selection, Characterization and X-ray Structure of Anti-ampicillin Single-chain Fv Fragments from Phage-displayed Murine Antibody Libraries. Journal of Molecular Biology, 2001, 309, 671-685.	4.2	36
292	The Influence of the Buried Glutamine or Glutamate Residue in Position 6 on the Structure of Immunoglobulin Variable Domains. Journal of Molecular Biology, 2001, 309, 687-699.	4.2	47
293	The Importance of Framework Residues H6, H7 and H10 in Antibody Heavy Chains: Experimental Evidence for a New Structural Subclassification of Antibody VH Domains. Journal of Molecular Biology, 2001, 309, 701-716.	4.2	55
294	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
295	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
296	Zooming in on the hydrophobic ridge of H-2Db: implications for the conformational variability of bound peptides11Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 312, 1059-1071.	4.2	16
297	Forces and energetics of hapten-antibody dissociation: a biased molecular dynamics simulation study 1 1Edited by B. Honig. Journal of Molecular Biology, 2001, 314, 589-605.	4.2	46
298	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
299	In vitro selection and evolution of proteins. Advances in Protein Chemistry, 2001, 55, 367-403.	4.4	46
300	Imaging the native structure of the chaperone protein GroEL without fixation using atomic force microscopy. Journal of Microscopy, 2001, 203, 195-198.	1.8	16
301	In vitro display technologies: novel developments and applications. Current Opinion in Biotechnology, 2001, 12, 400-405.	6.6	173
302	Protein-fold evolution in the test tube. Trends in Biochemical Sciences, 2001, 26, 577-579.	7.5	14
303	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
304	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
305	Cyclic Green Fluorescent Protein Produced in Vivo Using an Artificially Split PI-Pful Intein from Pyrococcus furiosus. Journal of Biological Chemistry, 2001, 276, 16548-16554.	3.4	131
306	Construction of scFv Fragments from Hybridoma or Spleen Cells by PCR Assembly. , 2001, , 19-40.		12

#	Article	IF	CITATIONS
307	Miniantibodies., 2001,, 637-647.		2
308	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
309	Improving Expression of scFv Fragments by Coexpression of Periplasmic Chaperones., 2001,, 307-317.		0
310	[22] Selectively infective phage technology. Methods in Enzymology, 2000, 328, 364-388.	1.0	6
311	Production of recombinant human \hat{l}^2 2-microglobulin for scintigraphic diagnosis of amyloidosis in uremia and hemodialysis. FEBS Journal, 2000, 267, 627-633.	0.2	15
312	Novel fold and capsid-binding properties of the lambda-phage display platform protein gpD. Nature Structural Biology, 2000, 7, 230-237.	9.7	140
313	Picomolar affinity antibodies from a fully synthetic naive library selected and evolved by ribosome display. Nature Biotechnology, 2000, 18, 1287-1292.	17.5	362
314	Characterizing the functionality of recombinant T-cell receptors in vitro: a pMHC tetramer based approach. Journal of Immunological Methods, 2000, 236, 147-165.	1.4	11
315	The Periplasmic Escherichia coli Peptidylprolyl cis,trans-Isomerase FkpA. Journal of Biological Chemistry, 2000, 275, 17100-17105.	3.4	156
316	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
317	The Periplasmic Escherichia coli Peptidylprolyl cis,trans-Isomerase FkpA. Journal of Biological Chemistry, 2000, 275, 17106-17113.	3.4	127
318	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
319	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
320	Viral escape at the molecular level explained by quantitative T-cell receptor/peptide/MHC interactions and the crystal structure of a peptide/MHC complex. Journal of Molecular Biology, 2000, 302, 873-885.	4.2	40
321	[24] Selecting and evolving functional proteins in vitro by ribosome display. Methods in Enzymology, 2000, 328, 404-430.	1.0	93
322	Direct evidence by H/D exchange and ESIâ€MS for transient unproductive domain interaction in the refolding of an antibody scFv fragment. Protein Science, 2000, 9, 552-563.	7.6	11
323	The hierarchy of mutations influencing the folding of antibody domains in Escherichia coli. Protein Engineering, Design and Selection, 1999, 12, 605-611.	2.1	28
324	An in vivo library-versus-library selection of optimized protein–protein interactions. Nature Biotechnology, 1999, 17, 683-690.	17.5	182

#	Article	IF	Citations
325	Stable one-step technetium-99m labeling of His-tagged recombinant proteins with a novel Tc(I)–carbonyl complex. Nature Biotechnology, 1999, 17, 897-901.	17.5	293
326	Selectively infective phage (SIP) technology: scope and limitations. Journal of Immunological Methods, 1999, 231, 93-104.	1.4	35
327	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
328	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
329	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
330	Different Equilibrium Stability Behavior of ScFv Fragments:  Identification, Classification, and Improvement by Protein Engineering. Biochemistry, 1999, 38, 8739-8750.	2.5	132
331	Antigen recognition by conformational selection. FEBS Letters, 1999, 450, 149-153.	2.8	116
332	Comparison of Escherichia coliand rabbit reticulocyte ribosome display systems. FEBS Letters, 1999, 450, 105-110.	2.8	55
333	Circular Î ² -lactamase: stability enhancement by cyclizing the backbone. FEBS Letters, 1999, 459, 166-172.	2.8	175
334	Domain interactions in antibody Fv and scFv fragments: effects on unfolding kinetics and equilibria. FEBS Letters, 1999, 462, 307-312.	2.8	56
335	Folding, heterodimeric association and specific peptide recognition of a murine $\hat{l}\pm\hat{l}^2$ T-cell receptor expressed in Escherichia coli 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 285, 1831-1843.	4.2	32
336	Folding and assembly of an antibody Fv fragment, a heterodimer stabilized by antigen 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 285, 2005-2019.	4.2	44
337	Removal of the conserved disulfide bridges from the scfv fragment of an antibody: effects on folding kinetics and aggregation. Journal of Molecular Biology, 1999, 290, 535-546.	4.2	51
338	Insight into odorant perception: the crystal structure and binding characteristics of antibody fragments directed against the musk odorant traseolide. Journal of Molecular Biology, 1999, 292, 855-869.	4.2	7
339	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
340	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
341	Selection for a periplasmic factor improving phage display and functional periplasmic expression. Nature Biotechnology, 1998, 16, 376-380.	17.5	190
342	Increasing the secretory capacity of Saccharomyces cerevisiae for production of single-chain antibody fragments. Nature Biotechnology, 1998, 16, 773-777.	17.5	244

#	Article	IF	CITATIONS
343	Selecting proteins with improved stability by a phage-based method. Nature Biotechnology, 1998, 16, 955-960.	17.5	192
344	Parallel pathways in the folding of a short-term denatured scFv fragment of an antibody. Folding & Design, 1998, 3, 39-49.	4.5	15
345	Tandem Immobilized Metal-Ion Affinity Chromatography/Immunoaffinity Purification of His-tagged Proteins— Evaluation of Two Anti-His-Tag Monoclonal Antibodies. Analytical Biochemistry, 1998, 259, 54-61.	2.4	7 5
346	Model and Simulation of Multivalent Binding to Fixed Ligands. Analytical Biochemistry, 1998, 261, 149-158.	2.4	135
347	Docking small ligands in flexible binding sites. Journal of Computational Chemistry, 1998, 19, 21-37.	3.3	120
348	Recent advances in producing and selecting functional proteins by using cell-free translation. Current Opinion in Biotechnology, 1998, 9, 534-548.	6.6	145
349	Mutual Stabilization of V _L and V _H in Single-Chain Antibody Fragments, Investigated with Mutants Engineered for Stability. Biochemistry, 1998, 37, 13120-13127.	2.5	124
350	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
351	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
352	A dimeric bispecific miniantibody combines two specificities with avidity. FEBS Letters, 1998, 432, 45-49.	2.8	69
353	Factors Influencing the Dimer to Monomer Transition of an Antibody Single-Chain Fv Fragmentâ€. Biochemistry, 1998, 37, 12918-12926.	2.5	144
354	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
355	Identification of the Binding Surface on β-Lactamase for GroEL by Limited Proteolysis and MALDI-Mass Spectrometryâ€. Biochemistry, 1998, 37, 11660-11669.	2.5	23
356	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
357	Two conformational states of \hat{l}^2 -lactamase bound to GroEL: a biophysical characterization 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 275, 663-675.	4.2	25
358	The nature of antibody heavy chain residue H6 strongly influences the stability of a VH domain lacking the disulfide bridge. Journal of Molecular Biology, 1998, 283, 95-110.	4.2	30
359	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 1Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 283, 395-407.	4.2	35
360	Structural Changes of theEscherichia coliGroEL–GroES Chaperonins upon Complex Formation in Solution: A Neutron Small Angle Scattering Study. Journal of Structural Biology, 1998, 121, 30-40.	2.8	26

#	Article	IF	Citations
361	Atomic Force Microscopy Detects Changes in the Interaction Forces between GroEL and Substrate Proteins. Biophysical Journal, 1998, 74, 3256-3263.	0.5	86
362	Induction and Exhaustion of Lymphocytic Choriomeningitis Virus–specific Cytotoxic T Lymphocytes Visualized Using Soluble Tetrameric Major Histocompatibility Complex Class I–Peptide Complexes. Journal of Experimental Medicine, 1998, 187, 1383-1393.	8.5	688
363	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
364	Studying Protein Structure and Function by Directed Evolution. , 1998, , 37-57.		0
365	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
366	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
367	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
368	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
369	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
370	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
371	Multiple cycles of global unfolding of GroEL-bound cyclophilin A evidenced by NMR. Journal of Molecular Biology, 1997, 271, 803-818.	4.2	28
372	New protein engineering approaches to multivalent and bispecific antibody fragments. Immunotechnology: an International Journal of Immunological Engineering, 1997, 3, 83-105.	2.4	310
373	Folding intermediates of β-lactamase recognized by GroEL. FEBS Letters, 1997, 401, 138-142.	2.8	12
374	Comparison of the amide proton exchange behavior of the rapidly formed folding intermediate and the native state of an antibody scFv fragment. FEBS Letters, 1997, 407, 42-46.	2.8	19
375	Affinity and folding properties both influence the selection of antibodies with the selectively infective phage (SIP) methodology. FEBS Letters, 1997, 415, 289-293.	2.8	30
376	The rate-limiting steps for the folding of an antibody scFv fragment. FEBS Letters, 1997, 418, 106-110.	2.8	41
377	Selectively infective phage (SIP) technology: A novel method for in vivo selection of interacting protein–ligand pairs. Nature Medicine, 1997, 3, 694-696.	30.7	38
378	Functional antibody production using cell-free translation: Effects of protein disulfide isomerase and chaperones. Nature Biotechnology, 1997, 15, 79-84.	17.5	179

#	Article	IF	CITATIONS
379	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
380	Conformational changes and spatial arrangement of the E. coli chaperones GroEL and GroES. Physica B: Condensed Matter, 1997, 234-236, 220-222.	2.7	1
381	BIACORE Analysis of Histidine-Tagged Proteins Using a Chelating NTA Sensor Chip. Analytical Biochemistry, 1997, 252, 217-228.	2.4	337
382	Folding Nuclei of the scFv Fragment of an Antibodyâ€. Biochemistry, 1996, 35, 8457-8464.	2.5	36
383	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
384	Effect of single point mutations in citrate synthase on binding to GroEL. FEBS Letters, 1996, 380, 152-156.	2.8	11
385	beta-Lactamase binds to GroEL in a conformation highly protected against hydrogen/deuterium exchange Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 12189-12194.	7.1	45
386	Monovalent single-chain Fv fragments and bivalent miniantibodies bound to vesicular stomatitis virus protect against lethal infection. European Journal of Immunology, 1996, 26, 2801-2806.	2.9	33
387	Competition BIAcore for Measuring True Affinities: Large Differences from Values Determined from Binding Kinetics. Analytical Biochemistry, 1996, 234, 155-165.	2.4	292
388	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
389	Engineered turns of a recombinant antibody improve its in vivo folding. Protein Engineering, Design and Selection, 1995, 8, 81-89.	2.1	219
390	A Mouse Ig \hat{I}^{Ω} Domain of Very Unusual Framework Structure Loses Function when Converted to the Consensus. Journal of Biological Chemistry, 1995, 270, 12446-12451.	3.4	6
391	Functional antibody single-chain fragments from the cytoplasm of Escherichia coli: influence of thioredoxin reductase (TrxB). Gene, 1995, 159, 203-207.	2.2	78
392	Tetravalent Miniantibodies with High Avidity Assembling in Escherichia colo. Journal of Molecular Biology, 1995, 246, 28-34.	4.2	143
393	Electron Microscopy of the GroEL-GroES Filament. Journal of Structural Biology, 1995, 115, 68-77.	2.8	10
394	Co-selection of cognate antibody-antigen pairs by selectively-infective phages. FEBS Letters, 1995, 377, 227-231.	2.8	73
395	Destabilization of the complete protein secondary structure on binding to the chaperone GroEL. Nature, 1994, 368, 261-265.	27.8	157
396	Protein folding in the periplasm of Escherichia coli. Molecular Microbiology, 1994, 12, 685-692.	2.5	177

#	Article	IF	CITATIONS
397	Sequence Statistics Reliably Predict Stabilizing Mutations in a Protein Domain. Journal of Molecular Biology, 1994, 240, 188-192.	4.2	320
398	Thermodynamic Partitioning Model for Hydrophobic Binding of Polypeptides by GroEL. Journal of Molecular Biology, 1994, 242, 150-184.	4.2	74
399	Thermodynamic Partitioning Model for Hydrophobic Binding of Polypeptides by GroEL. Journal of Molecular Biology, 1994, 242, 165-174.	4.2	75
400	Correctly Folded T-cell Receptor Fragments in the Periplasm of Escherichia coli. Journal of Molecular Biology, 1994, 242, 655-669.	4.2	83
401	Transmission Electron Microscopy of GroEL, GroES, and the Symmetrical GroEL/ES Complex. Journal of Structural Biology, 1994, 112, 216-230.	2.8	42
402	Structural and Dynamic Properties of the Fv Fragment and the Single-Chain Fv Fragment of an Antibody in Solution Investigated by Heteronuclear 3D NMR Spectroscopy. Biochemistry, 1994, 33, 3296-3303.	2.5	51
403	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
404	Improved Bivalent Miniantibodies, with Identical Avidity as Whole Antibodies, Produced by High Cell Density Fermentation of Escherichia coli. Nature Biotechnology, 1993, 11, 1271-1277.	17.5	48
405	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
406	Two-dimensional Crystals of the Molecular Chaperone GroEL Reveal Structural Plasticity. Journal of Molecular Biology, 1993, 229, 579-584.	4.2	31
407	A versatile and highly repressible Escherichia coli expression system based on invertible promoters: expression of a gene encoding a toxic product. Gene, 1993, 136, 199-203.	2.2	18
408	Antibody Engineering to Study Protein-Ligand Interactions and Catalysis: The Phosphorylcholine Binding Antibodies. Bioorganic Chemistry Frontiers, 1993, , 25-66.	1.2	2
409	Stability of engineered antibody fragments. Studies in Organic Chemistry, 1993, 47, 81-90.	0.2	1
410	GroE prevents the accumulation of early folding intermediates of pre-betalactamase without changing the folding pathway. Biochemistry, 1992, 31, 3249-3255.	2.5	50
411	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
412	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
413	Mono- and Bivalent Antibody Fragments Produced in Escherichia coli: Engineering, Folding and Antigen Binding. Immunological Reviews, 1992, 130, 151-188.	6.0	140
414	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

#	Article	IF	CITATIONS
415	Strategies for the expression of antibody fragments in Escherichia coli. Methods, 1991, 2, 88-96.	3.8	19
416	Mapping and modification of an antibody hapten binding site: a site-directed mutagenesis study of McPC603. Biochemistry, 1991, 30, 3049-3054.	2.5	67
417	Comparison of the FvFragments of Different Phosphorylcholine Binding Antibodies Expressed in Escherichia coli. Annals of the New York Academy of Sciences, 1991, 646, 115-124.	3.8	8
418	Antibody engineering. Current Opinion in Biotechnology, 1991, 2, 238-246.	6.6	22
419	Foldingin vitroand transportin vivoof pre- \hat{l}^2 -lactamase are SecB independent. Molecular Microbiology, 1991, 5, 117-122.	2.5	22
420	The Rationality of Random Screening—Efficient Methods of Selection of Peptides and Oligonucleotide Ligands. Angewandte Chemie International Edition in English, 1991, 30, 296-298.	4.4	13
421	Biotechnological aspects of antibody production in E. coli. Acta Biotechnologica, 1991, 11, 449-456.	0.9	1
422	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
423	Antibody Engineering: Advances From the Use of Escherichia coli Expression Systems. Nature Biotechnology, 1991, 9, 545-551.	17.5	105
424	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
425	Catalytic Antibodies: Contributions from Engineering and Expression in $\langle i \rangle$ Escherichia Coli $\langle i \rangle$. Novartis Foundation Symposium, 1991, 159, 103-117.	1.1	0
426	Antibodies from Escherichia coli. Nature, 1990, 347, 497-498.	27.8	51
427	Wege zu neuen Enzymen: Protein Engineering und Katalytische Antikörper. Chemie in Unserer Zeit, 1990, 24, 182-198.	0.1	13
428	Crystallization and preliminary X-ray studies of the VL domain of the antibody McPC603 produced in Escherichia coli. Journal of Molecular Biology, 1990, 213, 613-615.	4.2	32
429	[11] Secretion of heterologous proteins in Escherichia coli. Methods in Enzymology, 1990, 182, 132-143.	1.0	30
430	A comparison of strategies to stabilize immunoglobulin Fv-fragments. Biochemistry, 1990, 29, 1362-1367.	2.5	506
431	Structural features of the McPC603 Fabfragment not defined in the X-ray structure. FEBS Letters, 1990, 271, 203-206.	2.8	10
432	Protein-Struktur und Funktion: Die Möglichkeiten und Probleme der Computersimulation aus der Sicht des Experimentators. Informatik-Fachberichte, 1990, , 258-274.	0.2	0

#	Article	IF	CITATIONS
433	[34] Expression of functional antibody Fv and Fab fragments in Escherichia coli. Methods in Enzymology, 1989, 178, 497-515.	1.0	126
434	Assembly of a functional immunoglobulin Fv fragment in Escherichia coli. Science, 1988, 240, 1038-1041.	12.6	999
435	Conformation of fatty acyl chains in \hat{l}_{\pm} - and \hat{l}_{\pm} -phosphatidylcholine and phosphatidylethanolamine derivatives in sonicated vesicles. Biochimica Et Biophysica Acta - Biomembranes, 1986, 856, 144-154.	2.6	3
436	Mechanism of Interaction of Phospholipase A2 with Phospholipid Substrates and Activators. , 1986 , , $121\text{-}132$.		2
437	Short-chain phosphatidylethanolamines: physical properties and susceptibility of the monomers to phospholipase A2 action. Biochemistry, 1985, 24, 4201-4208.	2.5	38
438	Phosphorus-31 NMR of Phospholipids in Micelles. , 1984, , 423-446.		16
439	The membrane attack complex of complement and its precursor proteins lack phospholipase activity. Molecular Immunology, 1983, 20, 377-382.	2.2	10
440	Role of monomeric activators in cobra venom phospholipase A2 action. Biochemistry, 1982, 21, 1750-1756.	2.5	41
441	Hemolytic assay for venom phospholipase A2. Analytical Biochemistry, 1981, 118, 262-268.	2.4	21
442	Cobra venom phospholipase A2: A review of its action toward lipid/water interfaces. Molecular and Cellular Biochemistry, 1981, 36, 37-45.	3.1	50
443	Docking small ligands in flexible binding sites. , 0, .		1
444	Modern Antibody Technology: The Impact on Drug Development., 0,, 1147-1186.		25