

Rudi Glockshuber

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8770119/rudi-glockshuber-publications-by-citations.pdf>

Version: 2024-04-24

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

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

118
papers

8,222
citations

49
h-index

90
g-index

120
ext. papers

8,822
ext. citations

8.1
avg, IF

5.71
L-index

#	Paper	IF	Citations
118	NMR structure of the mouse prion protein domain PrP(121-231). <i>Nature</i> , 1996 , 382, 180-2	50.4	1063
117	NMR characterization of the full-length recombinant murine prion protein, mPrP(23-231). <i>FEBS Letters</i> , 1997 , 413, 282-8	3.8	574
116	Influence of amino acid substitutions related to inherited human prion diseases on the thermodynamic stability of the cellular prion protein. <i>Biochemistry</i> , 1999 , 38, 3258-67	3.2	290
115	The structure of a cytolytic alpha-helical toxin pore reveals its assembly mechanism. <i>Nature</i> , 2009 , 459, 726-30	50.4	250
114	Amyloid-beta aggregation. <i>Neurodegenerative Diseases</i> , 2007 , 4, 13-27	2.3	244
113	Uroplakin Ia is the urothelial receptor for uropathogenic Escherichia coli: evidence from in vitro FimH binding. <i>Journal of Cell Science</i> , 2001 , 114, 4095-4103	5.3	244
112	Redox properties of protein disulfide isomerase (DsbA) from Escherichia coli. <i>Protein Science</i> , 1993 , 2, 717-26	6.3	239
111	Atomic-resolution three-dimensional structure of amyloid fibrils bearing the Osaka mutation. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 331-5	16.4	211
110	Exploring the 3D molecular architecture of Escherichia coli type 1 pili. <i>Journal of Molecular Biology</i> , 2002 , 323, 845-57	6.5	192
109	A single dipeptide sequence modulates the redox properties of a whole enzyme family. <i>Folding & Design</i> , 1998 , 3, 161-71		171
108	Characterization of Escherichia coli thioredoxin variants mimicking the active-sites of other thiol/disulfide oxidoreductases. <i>Protein Science</i> , 1998 , 7, 1233-44	6.3	158
107	Recombinant full-length murine prion protein, mPrP(23-231): purification and spectroscopic characterization. <i>FEBS Letters</i> , 1997 , 413, 277-81	3.8	151
106	ERp57 is a multifunctional thiol-disulfide oxidoreductase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 18274-87	5.4	151
105	Oligosaccharyltransferase: the central enzyme of N-linked protein glycosylation. <i>Journal of Inherited Metabolic Disease</i> , 2011 , 34, 869-78	5.4	150
104	The recombinant amyloid-beta peptide Abeta1-42 aggregates faster and is more neurotoxic than synthetic Abeta1-42. <i>Journal of Molecular Biology</i> , 2010 , 396, 9-18	6.5	133
103	A novel strategy for inhibition of alpha-amylases: yellow meal worm alpha-amylase in complex with the Ragi bifunctional inhibitor at 2.5 Å resolution. <i>Structure</i> , 1998 , 6, 911-21	5.2	118
102	Structural basis and kinetics of inter- and intramolecular disulfide exchange in the redox catalyst DsbD. <i>EMBO Journal</i> , 2004 , 23, 1709-19	13	114

101	Catch-bond mechanism of the bacterial adhesin FimH. <i>Nature Communications</i> , 2016 , 7, 10738	17.4	113
100	Extremely rapid folding of the C-terminal domain of the prion protein without kinetic intermediates. <i>Nature Structural Biology</i> , 1999 , 6, 550-3		112
99	Oxidoreductase activity of oligosaccharyltransferase subunits Ost3p and Ost6p defines site-specific glycosylation efficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 11061-6	11.5	111
98	Random circular permutation of DsbA reveals segments that are essential for protein folding and stability. <i>Journal of Molecular Biology</i> , 1999 , 286, 1197-215	6.5	110
97	Circularly permuted variants of the green fluorescent protein. <i>FEBS Letters</i> , 1999 , 457, 283-9	3.8	108
96	The redox properties of protein disulfide isomerase (DsbA) of <i>Escherichia coli</i> result from a tense conformation of its oxidized form. <i>Journal of Molecular Biology</i> , 1993 , 233, 559-66	6.5	105
95	Crystal structure of yellow meal worm alpha-amylase at 1.64 Å resolution. <i>Journal of Molecular Biology</i> , 1998 , 278, 617-28	6.5	104
94	Cytotoxin ClyA from <i>Escherichia coli</i> assembles to a 13-meric pore independent of its redox-state. <i>EMBO Journal</i> , 2006 , 25, 2652-61	13	96
93	Reconstitution of pilus assembly reveals a bacterial outer membrane catalyst. <i>Science</i> , 2008 , 320, 376-9	33.3	95
92	Pilus chaperones represent a new type of protein-folding catalyst. <i>Nature</i> , 2004 , 431, 329-33	50.4	94
91	Structural basis of chaperone-subunit complex recognition by the type 1 pilus assembly platform FimD. <i>EMBO Journal</i> , 2005 , 24, 2075-86	13	93
90	Determination of the three-dimensional structure of the bifunctional alpha-amylase/trypsin inhibitor from ragi seeds by NMR spectroscopy. <i>Biochemistry</i> , 1995 , 34, 8281-93	3.2	91
89	Pilus chaperone FimC-adhesin FimH interactions mapped by TROSY-NMR. <i>Nature Structural Biology</i> , 1999 , 6, 336-9		89
88	Bacterial protein disulfide isomerase: efficient catalysis of oxidative protein folding at acidic pH. <i>Biochemistry</i> , 1993 , 32, 12251-6	3.2	89
87	Structural analysis of three His32 mutants of DsbA: support for an electrostatic role of His32 in DsbA stability. <i>Protein Science</i> , 1997 , 6, 1893-900	6.3	79
86	Efficient catalysis of disulfide formation during protein folding with a single active-site cysteine. <i>Journal of Molecular Biology</i> , 1995 , 247, 28-33	6.5	76
85	Autonomous and reversible folding of a soluble amino-terminally truncated segment of the mouse prion protein. <i>Journal of Molecular Biology</i> , 1996 , 261, 614-9	6.5	72
84	Structural basis and kinetics of DsbD-dependent cytochrome c maturation. <i>Structure</i> , 2005 , 13, 985-93	5.2	70

83	Localization of uroplakin Ia, the urothelial receptor for bacterial adhesin FimH, on the six inner domains of the 16 nm urothelial plaque particle. <i>Journal of Molecular Biology</i> , 2002 , 317, 697-706	6.5	70
82	Identification and characterization of the chaperone-subunit complex-binding domain from the type 1 pilus assembly platform FimD. <i>Journal of Molecular Biology</i> , 2003 , 330, 513-25	6.5	67
81	Structural basis of substrate specificity of human oligosaccharyl transferase subunit N33/Tusc3 and its role in regulating protein N-glycosylation. <i>Structure</i> , 2014 , 22, 590-601	5.2	66
80	DsbL and Dsbl form a specific dithiol oxidase system for periplasmic arylsulfate sulfotransferase in uropathogenic <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2008 , 380, 667-80	6.5	66
79	The assembly dynamics of the cytolytic pore toxin ClyA. <i>Nature Communications</i> , 2015 , 6, 6198	17.4	64
78	Quenching of tryptophan fluorescence by the active-site disulfide bridge in the DsbA protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1997 , 36, 6391-400	3.2	64
77	DsbA and DsbC-catalyzed oxidative folding of proteins with complex disulfide bridge patterns in vitro and in vivo. <i>Journal of Molecular Biology</i> , 2003 , 325, 495-513	6.5	64
76	Importance of redox potential for the in vivo function of the cytoplasmic disulfide reductant thioredoxin from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999 , 274, 25254-9	5.4	64
75	Infinite kinetic stability against dissociation of supramolecular protein complexes through donor strand complementation. <i>Structure</i> , 2008 , 16, 631-42	5.2	60
74	<i>Staphylococcus aureus</i> DsbA does not have a destabilizing disulfide. A new paradigm for bacterial oxidative folding. <i>Journal of Biological Chemistry</i> , 2008 , 283, 4261-71	5.4	55
73	Characterization of recombinant, membrane-attached full-length prion protein. <i>Journal of Biological Chemistry</i> , 2004 , 279, 25058-65	5.4	54
72	Structure of reduced DsbA from <i>Escherichia coli</i> in solution. <i>Biochemistry</i> , 1998 , 37, 6263-76	3.2	53
71	Mechanism of fibre assembly through the chaperone-usher pathway. <i>EMBO Reports</i> , 2006 , 7, 734-8	6.5	51
70	Mechanism of the electron transfer catalyst DsbB from <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2003 , 22, 3503-13	3.3	49
69	Influence of the pK(a) value of the buried, active-site cysteine on the redox properties of thioredoxin-like oxidoreductases. <i>FEBS Letters</i> , 2000 , 477, 21-6	3.8	48
68	Chaperone-independent folding of type 1 pilus domains. <i>Journal of Molecular Biology</i> , 2002 , 322, 827-40	6.5	47
67	Elimination of all charged residues in the vicinity of the active-site helix of the disulfide oxidoreductase DsbA. Influence of electrostatic interactions on stability and redox properties. <i>Journal of Biological Chemistry</i> , 1997 , 272, 21692-9	5.4	45
66	FRET-based in vivo screening for protein folding and increased protein stability. <i>Journal of Molecular Biology</i> , 2003 , 327, 239-49	6.5	43

65	Quality control of disulfide bond formation in pilus subunits by the chaperone FimC. <i>Nature Chemical Biology</i> , 2012 , 8, 707-13	11.7	41
64	Binding of the Bacterial Adhesin FimH to Its Natural, Multivalent High-Mannose Type Glycan Targets. <i>Journal of the American Chemical Society</i> , 2019 , 141, 936-944	16.4	40
63	Uropathogenic E. coli adhesin-induced host cell receptor conformational changes: implications in transmembrane signaling transduction. <i>Journal of Molecular Biology</i> , 2009 , 392, 352-61	6.5	39
62	Crystal structure of the ternary FimC-FimF(t)-FimD(N) complex indicates conserved pilus chaperone-subunit complex recognition by the usher FimD. <i>FEBS Letters</i> , 2008 , 582, 651-5	3.8	39
61	A bacterial thioredoxin-like protein that is exposed to the periplasm has redox properties comparable with those of cytoplasmic thioredoxins. <i>Journal of Biological Chemistry</i> , 1995 , 270, 26178-83 ⁵⁻⁴		39
60	Structure, folding and stability of FimA, the main structural subunit of type 1 pili from uropathogenic Escherichia coli strains. <i>Journal of Molecular Biology</i> , 2011 , 412, 520-35	6.5	38
59	The Osaka FAD mutation E22 Δ leads to the formation of a previously unknown type of amyloid β fibrils and modulates A β neurotoxicity. <i>Journal of Molecular Biology</i> , 2011 , 408, 780-91	6.5	36
58	RBI, a one-domain alpha-amylase/trypsin inhibitor with completely independent binding sites. <i>FEBS Letters</i> , 1996 , 397, 11-6	3.8	36
57	Structural and functional characterization of the oxidoreductase alpha-DsbA1 from Wolbachia pipientis. <i>Antioxidants and Redox Signaling</i> , 2009 , 11, 1485-500	8.4	35
56	Architecture and function of human uromodulin filaments in urinary tract infections. <i>Science</i> , 2020 , 369, 1005-1010	33.3	34
55	Influence of acidic residues and the kink in the active-site helix on the properties of the disulfide oxidoreductase DsbA. <i>Journal of Biological Chemistry</i> , 1997 , 272, 189-95	5.4	34
54	High-resolution structures of Escherichia coli cDsbD in different redox states: A combined crystallographic, biochemical and computational study. <i>Journal of Molecular Biology</i> , 2006 , 358, 829-45	6.5	34
53	Preparation and structure of the charge-transfer intermediate of the transmembrane redox catalyst DsbB. <i>FEBS Letters</i> , 2008 , 582, 3301-7	3.8	33
52	The alpha-amylase from the yellow meal worm: complete primary structure, crystallization and preliminary X-ray analysis. <i>FEBS Letters</i> , 1997 , 409, 109-14	3.8	32
51	How periplasmic thioredoxin TlpA reduces bacterial copper chaperone Sca1 and cytochrome oxidase subunit II (CoxB) prior to metallation. <i>Journal of Biological Chemistry</i> , 2014 , 289, 32431-44	5.4	30
50	Replacement of Pro109 by His in TlpA, a thioredoxin-like protein from Bradyrhizobium japonicum, alters its redox properties but not its in vivo functions. <i>FEBS Letters</i> , 1997 , 406, 249-54	3.8	26
49	Thermodynamic aspects of DsbD-mediated electron transport. <i>Journal of Molecular Biology</i> , 2008 , 380, 783-8	6.5	26
48	The Cryoelectron Microscopy Structure of the Type 1 Chaperone-Usher Pilus Rod. <i>Structure</i> , 2017 , 25, 1829-1838.e4	5.2	25

47	Assembly mechanism of the Pore-forming toxin cytolysin A from. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	25
46	Folding dynamics and energetics of recombinant prion proteins. <i>Advances in Protein Chemistry</i> , 2001 , 57, 83-105		22
45	NMR structure of the Escherichia coli type 1 pilus subunit FimF and its interactions with other pilus subunits. <i>Journal of Molecular Biology</i> , 2008 , 375, 752-63	6.5	21
44	The PAPS-independent aryl sulfotransferase and the alternative disulfide bond formation system in pathogenic bacteria. <i>Antioxidants and Redox Signaling</i> , 2010 , 13, 1247-59	8.4	20
43	Prion protein structural features indicate possible relations to signal peptidases. <i>FEBS Letters</i> , 1998 , 426, 291-6	3.8	19
42	Direct evidence for self-propagation of different amyloid-fibril conformations. <i>Neurodegenerative Diseases</i> , 2014 , 14, 151-9	2.3	17
41	(4R)- and (4S)-fluoroproline in the conserved cis-prolyl peptide bond of the thioredoxin fold: tertiary structure context dictates ring puckering. <i>ChemBioChem</i> , 2013 , 14, 1053-7	3.8	17
40	Folding and intrinsic stability of deletion variants of PrP(121-231), the folded C-terminal domain of the prion protein. <i>Biophysical Chemistry</i> , 2002 , 96, 293-303	3.5	17
39	Solid-state NMR sequential assignment of Osaka-mutant amyloid-beta (A β -40 E22) fibrils. <i>Biomolecular NMR Assignments</i> , 2015 , 9, 7-14	0.7	16
38	Thioredoxin-like protein TlpA from Bradyrhizobium japonicum is a reductant for the copper metallochaperone Scol. <i>FEBS Letters</i> , 2012 , 586, 4094-9	3.8	16
37	Competition between DsbA-mediated oxidation and conformational folding of RTEM1 beta-lactamase. <i>Biochemistry</i> , 1996 , 35, 11386-95	3.2	16
36	Kinetics of the intramolecular disulfide exchange between the periplasmic domains of DsbD. <i>Journal of Molecular Biology</i> , 2007 , 367, 1162-70	6.5	15
35	Characterization of FimC, a periplasmic assembly factor for biogenesis of type 1 pili in Escherichia coli. <i>Biochemistry</i> , 2000 , 39, 11564-70	3.2	14
34	Structural basis and mechanism for metallochaperone-assisted assembly of the Cu center in cytochrome oxidase. <i>Science Advances</i> , 2019 , 5, eaaw8478	14.3	13
33	Characterization of variants of the pore-forming toxin ClyA from Escherichia coli controlled by a redox switch. <i>Biochemistry</i> , 2014 , 53, 6357-69	3.2	13
32	Acceleration of protein folding by four orders of magnitude through a single amino acid substitution. <i>Scientific Reports</i> , 2015 , 5, 11840	4.9	12
31	Die atomare dreidimensionale Struktur von Amyloid-fibrillen mit der Osaka-Mutation. <i>Angewandte Chemie</i> , 2015 , 127, 337-342	3.6	12
30	Quantitative analysis of nonequilibrium, denaturant-dependent protein folding transitions. <i>Journal of the American Chemical Society</i> , 2007 , 129, 8938-9	16.4	12

29	Randomization of the entire active-site helix alpha 1 of the thiol-disulfide oxidoreductase DsbA from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2002 , 277, 43050-7	5.4	12
28	The cryo-EM structure of the human uromodulin filament core reveals a unique assembly mechanism. <i>ELife</i> , 2020 , 9,	8.9	11
27	The Redox State Regulates the Conformation of Rv2466c to Activate the Antitubercular Prodrug TP053. <i>Journal of Biological Chemistry</i> , 2015 , 290, 31077-89	5.4	10
26	Acceleration of the Rate-Limiting Step of Thioredoxin Folding by Replacement of its Conserved cis-Proline with (4 S)-Fluoroproline. <i>ChemBioChem</i> , 2015 , 16, 2162-6	3.8	9
25	Intramolecular donor strand complementation in the <i>E. coli</i> type 1 pilus subunit FimA explains the existence of FimA monomers as off-pathway products of pilus assembly that inhibit host cell apoptosis. <i>Journal of Molecular Biology</i> , 2014 , 426, 542-9	6.5	9
24	Evidence for proton shuffling in a thioredoxin-like protein during catalysis. <i>Journal of Molecular Biology</i> , 2008 , 382, 978-86	6.5	9
23	Soluble Oligomers of the Pore-forming Toxin Cytolysin A from <i>Escherichia coli</i> Are Off-pathway Products of Pore Assembly. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5652-5663	5.4	8
22	Functional analyses of ancestral thioredoxins provide insights into their evolutionary history. <i>Journal of Biological Chemistry</i> , 2019 , 294, 14105-14118	5.4	8
21	A Plethora of Terminal Oxidases and Their Biogenesis Factors in <i>Bradyrhizobium japonicum</i> 2015 , 293-306		7
20	The most stable protein-ligand complex: applications for one-step affinity purification and identification of protein assemblies. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4474-8	16.4	7
19	Glycan-protein interactions determine kinetics of -glycan remodeling. <i>RSC Chemical Biology</i> , 2021 , 2, 917-931	3	5
18	Development of the Mitochondrial Intermembrane Space Disulfide Relay Represents a Critical Step in Eukaryotic Evolution. <i>Molecular Biology and Evolution</i> , 2019 , 36, 742-756	8.3	4
17	Alternative folding to a monomer or homopolymer is a common feature of the type 1 pilus subunit FimA from enteroinvasive bacteria. <i>Journal of Biological Chemistry</i> , 2019 , 294, 10553-10563	5.4	3
16	Biochemical pathway for the biosynthesis of the Cu center in bacterial cytochrome c oxidase. <i>FEBS Letters</i> , 2019 , 593, 2977-2989	3.8	3
15	Mechanism of the prokaryotic transmembrane disulfide reduction pathway and its in vitro reconstitution from purified components. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 6900-3	16.4	3
14	Structure of native glycolipoprotein filaments in honeybee royal jelly. <i>Nature Communications</i> , 2020 , 11, 6267	17.4	2
13	Der stabilste Protein-Liganden-Komplex: Anwendung für die Einzschritt-Affinitätsreinigung und Identifizierung von Proteinkomplexen. <i>Angewandte Chemie</i> , 2012 , 124, 4551-4555	3.6	2
12	Formation of Adhesive Pili by the Chaperone-Usher Pathway 965-986		2

11	A metabolite binding protein moonlights as a bile-responsive chaperone. <i>EMBO Journal</i> , 2020 , 39, e104231	2
10	Glycan-Protein Interactions Determine Kinetics of N-Glycan Remodeling	1
9	Accelerating the Association of the Most Stable Protein-Ligand Complex by More than Two Orders of Magnitude. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 9350-5	16.4 1
8	Donor strand sequence, rather than donor strand orientation, determines the stability and non-equilibrium folding of the type 1 pilus subunit FimA. <i>Journal of Biological Chemistry</i> , 2020 , 295, 12437-41	12448
7	Assemblierung des CuA-Zentrums in bakterieller Cytochrom-Oxidase. <i>BioSpektrum</i> , 2019 , 25, 603-606	0.1
6	Accelerating the Association of the Most Stable Protein-Ligand Complex by More than Two Orders of Magnitude. <i>Angewandte Chemie</i> , 2016 , 128, 9496-9501	3.6
5	Mechanism of the Prokaryotic Transmembrane Disulfide Reduction Pathway and Its In Vitro Reconstitution from Purified Components. <i>Angewandte Chemie</i> , 2012 , 124, 7006-7009	3.6
4	Innenrücktitelbild: Der stabilste Protein-Liganden-Komplex: Anwendung für die Einschritt-Affinitätsreinigung und Identifizierung von Proteinkomplexen (Angew. Chem. 18/2012). <i>Angewandte Chemie</i> , 2012 , 124, 4569-4569	3.6
3	Inside Back Cover: The Most Stable Protein-Ligand Complex: Applications for One-Step Affinity Purification and Identification of Protein Assemblies (Angew. Chem. Int. Ed. 18/2012). <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4491-4491	16.4
2	Struktur, Assemblierung und Stabilität von Typ-1-Pili. <i>BioSpektrum</i> , 2013 , 19, 492-495	0.1
1	The trans-to-cis proline isomerization in E. coli Trx folding is accelerated by trans prolines. <i>Biophysical Journal</i> , 2021 , 120, 5207-5218	2.9