

# Rudi Glockshuber

## List of Publications by Year in Descending Order

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

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	The trans-to-cis proline isomerization in E. coli Trx folding is accelerated by trans prolines. <i>Biophysical Journal</i> , <b>2021</b> , 120, 5207-5218	2.9	
117	Glycan-protein interactions determine kinetics of -glycan remodeling. <i>RSC Chemical Biology</i> , <b>2021</b> , 2, 917-931	3	5
116	Structure of native glycolipoprotein filaments in honeybee royal jelly. <i>Nature Communications</i> , <b>2020</b> , 11, 6267	17.4	2
115	Architecture and function of human uromodulin filaments in urinary tract infections. <i>Science</i> , <b>2020</b> , 369, 1005-1010	33.3	34
114	The cryo-EM structure of the human uromodulin filament core reveals a unique assembly mechanism. <i>ELife</i> , <b>2020</b> , 9,	8.9	11
113	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> , <b>2020</b> , 295, 12437-12448	5.4	12448
112	A metabolite binding protein moonlights as a bile-responsive chaperone. <i>EMBO Journal</i> , <b>2020</b> , 39, e104231	3.1	2
111	Assemblierung des CuA-Zentrums in bakterieller Cytochrom-Oxidase. <i>BioSpektrum</i> , <b>2019</b> , 25, 603-606	0.1	
110	Structural basis and mechanism for metallochaperone-assisted assembly of the Cu center in cytochrome oxidase. <i>Science Advances</i> , <b>2019</b> , 5, eaaw8478	14.3	13
109	Development of the Mitochondrial Intermembrane Space Disulfide Relay Represents a Critical Step in Eukaryotic Evolution. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 742-756	8.3	4
108	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> , <b>2019</b> , 294, 10553-10563	5.4	3
107	Functional analyses of ancestral thioredoxins provide insights into their evolutionary history. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 14105-14118	5.4	8
106	Biochemical pathway for the biosynthesis of the Cu center in bacterial cytochrome c oxidase. <i>FEBS Letters</i> , <b>2019</b> , 593, 2977-2989	3.8	3
105	Binding of the Bacterial Adhesin FimH to Its Natural, Multivalent High-Mannose Type Glycan Targets. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 936-944	16.4	40
104	The Cryoelectron Microscopy Structure of the Type 1 Chaperone-Usher Pilus Rod. <i>Structure</i> , <b>2017</b> , 25, 1829-1838.e4	5.2	25
103	Assembly mechanism of the Pore-forming toxin cytolysin A from. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2017</b> , 372,	5.8	25
102	Accelerating the Association of the Most Stable Protein-Ligand Complex by More than Two Orders of Magnitude. <i>Angewandte Chemie</i> , <b>2016</b> , 128, 9496-9501	3.6	

101	Soluble Oligomers of the Pore-forming Toxin Cytolysin A from Escherichia coli Are Off-pathway Products of Pore Assembly. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 5652-5663	5.4	8
100	Catch-bond mechanism of the bacterial adhesin FimH. <i>Nature Communications</i> , <b>2016</b> , 7, 10738	17.4	113
99	Accelerating the Association of the Most Stable Protein-Ligand Complex by More than Two Orders of Magnitude. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 9350-5	16.4	1
98	The assembly dynamics of the cytolytic pore toxin ClyA. <i>Nature Communications</i> , <b>2015</b> , 6, 6198	17.4	64
97	Solid-state NMR sequential assignment of Osaka-mutant amyloid-beta (A $\beta$ -40 E22) $\beta$ fibrils. <i>Biomolecular NMR Assignments</i> , <b>2015</b> , 9, 7-14	0.7	16
96	Atomic-resolution three-dimensional structure of amyloid $\beta$ fibrils bearing the Osaka mutation. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 331-5	16.4	211
95	A Plethora of Terminal Oxidases and Their Biogenesis Factors in <i>Bradyrhizobium japonicum</i> <b>2015</b> , 293-306		7
94	Acceleration of protein folding by four orders of magnitude through a single amino acid substitution. <i>Scientific Reports</i> , <b>2015</b> , 5, 11840	4.9	12
93	Die atomare dreidimensionale Struktur von Amyloid- $\beta$ Fibrillen mit der Osaka-Mutation. <i>Angewandte Chemie</i> , <b>2015</b> , 127, 337-342	3.6	12
92	Acceleration of the Rate-Limiting Step of Thioredoxin Folding by Replacement of its Conserved cis-Proline with (4 S)-Fluoroproline. <i>ChemBioChem</i> , <b>2015</b> , 16, 2162-6	3.8	9
91	The Redox State Regulates the Conformation of Rv2466c to Activate the Antitubercular Prodrug TP053. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 31077-89	5.4	10
90	Structural basis of substrate specificity of human oligosaccharyl transferase subunit N33/Tusc3 and its role in regulating protein N-glycosylation. <i>Structure</i> , <b>2014</b> , 22, 590-601	5.2	66
89	Characterization of variants of the pore-forming toxin ClyA from Escherichia coli controlled by a redox switch. <i>Biochemistry</i> , <b>2014</b> , 53, 6357-69	3.2	13
88	Direct evidence for self-propagation of different amyloid- $\beta$ fibril conformations. <i>Neurodegenerative Diseases</i> , <b>2014</b> , 14, 151-9	2.3	17
87	How periplasmic thioredoxin TlpA reduces bacterial copper chaperone Sca1 and cytochrome oxidase subunit II (CoxB) prior to metallation. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 32431-44	5.4	30
86	Intramolecular donor strand complementation in the E. coli 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> , <b>2014</b> , 426, 542-9	6.5	9
85	Struktur, Assemblierung und Stabilität von Typ-1-Pili. <i>BioSpektrum</i> , <b>2013</b> , 19, 492-495	0.1	
84	(4R)- and (4S)-fluoroproline in the conserved cis-prolyl peptide bond of the thioredoxin fold: tertiary structure context dictates ring puckering. <i>ChemBioChem</i> , <b>2013</b> , 14, 1053-7	3.8	17

83	Thioredoxin-like protein TlpA from Bradyrhizobium japonicum is a reductant for the copper metallochaperone Scl. <i>FEBS Letters</i> , <b>2012</b> , 586, 4094-9	3.8	16
82	Quality control of disulfide bond formation in pilus subunits by the chaperone FimC. <i>Nature Chemical Biology</i> , <b>2012</b> , 8, 707-13	11.7	41
81	Der stabilste Protein-Liganden-Komplex: Anwendung für die Einschnitt-Affinitätsreinigung und Identifizierung von Proteinkomplexen. <i>Angewandte Chemie</i> , <b>2012</b> , 124, 4551-4555	3.6	2
80	Mechanism of the Prokaryotic Transmembrane Disulfide Reduction Pathway and Its In Vitro Reconstitution from Purified Components. <i>Angewandte Chemie</i> , <b>2012</b> , 124, 7006-7009	3.6	
79	Innenrücktitelbild: Der stabilste Protein-Liganden-Komplex: Anwendung für die Einschnitt-Affinitätsreinigung und Identifizierung von Proteinkomplexen (Angew. Chem. 18/2012). <i>Angewandte Chemie</i> , <b>2012</b> , 124, 4569-4569	3.6	
78	The most stable protein-ligand complex: applications for one-step affinity purification and identification of protein assemblies. <i>Angewandte Chemie - International Edition</i> , <b>2012</b> , 51, 4474-8	16.4	7
77	Mechanism of the prokaryotic transmembrane disulfide reduction pathway and its in vitro reconstitution from purified components. <i>Angewandte Chemie - International Edition</i> , <b>2012</b> , 51, 6900-3	16.4	3
76	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> , <b>2012</b> , 51, 4491-4491	16.4	
75	The Osaka FAD mutation E22L leads to the formation of a previously unknown type of amyloid $\beta$ fibrils and modulates A $\beta$ neurotoxicity. <i>Journal of Molecular Biology</i> , <b>2011</b> , 408, 780-91	6.5	36
74	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> , <b>2011</b> , 412, 520-35	6.5	38
73	Oligosaccharyltransferase: the central enzyme of N-linked protein glycosylation. <i>Journal of Inherited Metabolic Disease</i> , <b>2011</b> , 34, 869-78	5.4	150
72	The recombinant amyloid-beta peptide Abeta1-42 aggregates faster and is more neurotoxic than synthetic Abeta1-42. <i>Journal of Molecular Biology</i> , <b>2010</b> , 396, 9-18	6.5	133
71	The PAPS-independent aryl sulfotransferase and the alternative disulfide bond formation system in pathogenic bacteria. <i>Antioxidants and Redox Signaling</i> , <b>2010</b> , 13, 1247-59	8.4	20
70	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> , <b>2009</b> , 106, 11061-6	11.5	111
69	Structural and functional characterization of the oxidoreductase alpha-DsbA1 from Wolbachia pipientis. <i>Antioxidants and Redox Signaling</i> , <b>2009</b> , 11, 1485-500	8.4	35
68	The structure of a cytolytic alpha-helical toxin pore reveals its assembly mechanism. <i>Nature</i> , <b>2009</b> , 459, 726-30	50.4	250
67	Uropathogenic E. coli adhesin-induced host cell receptor conformational changes: implications in transmembrane signaling transduction. <i>Journal of Molecular Biology</i> , <b>2009</b> , 392, 352-61	6.5	39
66	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> , <b>2008</b> , 582, 651-5	3.8	39

65	Preparation and structure of the charge-transfer intermediate of the transmembrane redox catalyst DsbB. <i>FEBS Letters</i> , <b>2008</b> , 582, 3301-7	3.8	33
64	Infinite kinetic stability against dissociation of supramolecular protein complexes through donor strand complementation. <i>Structure</i> , <b>2008</b> , 16, 631-42	5.2	60
63	NMR structure of the Escherichia coli type 1 pilus subunit FimF and its interactions with other pilus subunits. <i>Journal of Molecular Biology</i> , <b>2008</b> , 375, 752-63	6.5	21
62	DsbL and Dsbl form a specific dithiol oxidase system for periplasmic arylsulfate sulfotransferase in uropathogenic Escherichia coli. <i>Journal of Molecular Biology</i> , <b>2008</b> , 380, 667-80	6.5	66
61	Thermodynamic aspects of DsbD-mediated electron transport. <i>Journal of Molecular Biology</i> , <b>2008</b> , 380, 783-8	6.5	26
60	Evidence for proton shuffling in a thioredoxin-like protein during catalysis. <i>Journal of Molecular Biology</i> , <b>2008</b> , 382, 978-86	6.5	9
59	Staphylococcus aureus DsbA does not have a destabilizing disulfide. A new paradigm for bacterial oxidative folding. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 4261-71	5.4	55
58	Reconstitution of pilus assembly reveals a bacterial outer membrane catalyst. <i>Science</i> , <b>2008</b> , 320, 376-9	33.3	95
57	Quantitative analysis of nonequilibrium, denaturant-dependent protein folding transitions. <i>Journal of the American Chemical Society</i> , <b>2007</b> , 129, 8938-9	16.4	12
56	Amyloid-beta aggregation. <i>Neurodegenerative Diseases</i> , <b>2007</b> , 4, 13-27	2.3	244
55	Kinetics of the intramolecular disulfide exchange between the periplasmic domains of DsbD. <i>Journal of Molecular Biology</i> , <b>2007</b> , 367, 1162-70	6.5	15
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> , <b>2006</b> , 358, 829-45	6.5	34
53	Cytotoxin ClyA from Escherichia coli assembles to a 13-meric pore independent of its redox-state. <i>EMBO Journal</i> , <b>2006</b> , 25, 2652-61	13	96
52	Mechanism of fibre assembly through the chaperone-usher pathway. <i>EMBO Reports</i> , <b>2006</b> , 7, 734-8	6.5	51
51	Structural basis of chaperone-subunit complex recognition by the type 1 pilus assembly platform FimD. <i>EMBO Journal</i> , <b>2005</b> , 24, 2075-86	13	93
50	Structural basis and kinetics of DsbD-dependent cytochrome c maturation. <i>Structure</i> , <b>2005</b> , 13, 985-93	5.2	70
49	ERp57 is a multifunctional thiol-disulfide oxidoreductase. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 18237-47	3.4	151
48	Characterization of recombinant, membrane-attached full-length prion protein. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 25058-65	5.4	54

47	Structural basis and kinetics of inter- and intramolecular disulfide exchange in the redox catalyst DsbD. <i>EMBO Journal</i> , <b>2004</b> , 23, 1709-19	13	114
46	Pilus chaperones represent a new type of protein-folding catalyst. <i>Nature</i> , <b>2004</b> , 431, 329-33	50.4	94
45	Mechanism of the electron transfer catalyst DsbB from Escherichia coli. <i>EMBO Journal</i> , <b>2003</b> , 22, 3503-13	33	49
44	DsbA and DsbC-catalyzed oxidative folding of proteins with complex disulfide bridge patterns in vitro and in vivo. <i>Journal of Molecular Biology</i> , <b>2003</b> , 325, 495-513	6.5	64
43	FRET-based in vivo screening for protein folding and increased protein stability. <i>Journal of Molecular Biology</i> , <b>2003</b> , 327, 239-49	6.5	43
42	Identification and characterization of the chaperone-subunit complex-binding domain from the type 1 pilus assembly platform FimD. <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 513-25	6.5	67
41	Folding and intrinsic stability of deletion variants of PrP(121-231), the folded C-terminal domain of the prion protein. <i>Biophysical Chemistry</i> , <b>2002</b> , 96, 293-303	3.5	17
40	Randomization of the entire active-site helix alpha 1 of the thiol-disulfide oxidoreductase DsbA from Escherichia coli. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 43050-7	5.4	12
39	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> , <b>2002</b> , 317, 697-706	6.5	70
38	Chaperone-independent folding of type 1 pilus domains. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 827-406	6.5	47
37	Exploring the 3D molecular architecture of Escherichia coli type 1 pili. <i>Journal of Molecular Biology</i> , <b>2002</b> , 323, 845-57	6.5	192
36	Folding dynamics and energetics of recombinant prion proteins. <i>Advances in Protein Chemistry</i> , <b>2001</b> , 57, 83-105		22
35	Uroplakin Ia is the urothelial receptor for uropathogenic Escherichia coli: evidence from in vitro FimH binding. <i>Journal of Cell Science</i> , <b>2001</b> , 114, 4095-4103	5.3	244
34	Influence of the pK(a) value of the buried, active-site cysteine on the redox properties of thioredoxin-like oxidoreductases. <i>FEBS Letters</i> , <b>2000</b> , 477, 21-6	3.8	48
33	Characterization of FimC, a periplasmic assembly factor for biogenesis of type 1 pili in Escherichia coli. <i>Biochemistry</i> , <b>2000</b> , 39, 11564-70	3.2	14
32	Importance of redox potential for the in vivo function of the cytoplasmic disulfide reductant thioredoxin from Escherichia coli. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 25254-9	5.4	64
31	Pilus chaperone FimC-adhesin FimH interactions mapped by TROSY-NMR. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 336-9		89
30	Extremely rapid folding of the C-terminal domain of the prion protein without kinetic intermediates. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 550-3		112

29	Influence of amino acid substitutions related to inherited human prion diseases on the thermodynamic stability of the cellular prion protein. <i>Biochemistry</i> , <b>1999</b> , 38, 3258-67	3.2	290
28	Circularly permuted variants of the green fluorescent protein. <i>FEBS Letters</i> , <b>1999</b> , 457, 283-9	3.8	108
27	Random circular permutation of DsbA reveals segments that are essential for protein folding and stability. <i>Journal of Molecular Biology</i> , <b>1999</b> , 286, 1197-215	6.5	110
26	A single dipeptide sequence modulates the redox properties of a whole enzyme family. <i>Folding &amp; Design</i> , <b>1998</b> , 3, 161-71		171
25	A novel strategy for inhibition of alpha-amylases: yellow meal worm alpha-amylase in complex with the Ragi bifunctional inhibitor at 2.5 A resolution. <i>Structure</i> , <b>1998</b> , 6, 911-21	5.2	118
24	Characterization of Escherichia coli thioredoxin variants mimicking the active-sites of other thiol/disulfide oxidoreductases. <i>Protein Science</i> , <b>1998</b> , 7, 1233-44	6.3	158
23	Prion protein structural features indicate possible relations to signal peptidases. <i>FEBS Letters</i> , <b>1998</b> , 426, 291-6	3.8	19
22	Structure of reduced DsbA from Escherichia coli in solution. <i>Biochemistry</i> , <b>1998</b> , 37, 6263-76	3.2	53
21	Crystal structure of yellow meal worm alpha-amylase at 1.64 A resolution. <i>Journal of Molecular Biology</i> , <b>1998</b> , 278, 617-28	6.5	104
20	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> , <b>1997</b> , 272, 21692-9	5.4	45
19	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> , <b>1997</b> , 272, 189-95	5.4	34
18	Quenching of tryptophan fluorescence by the active-site disulfide bridge in the DsbA protein from Escherichia coli. <i>Biochemistry</i> , <b>1997</b> , 36, 6391-400	3.2	64
17	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> , <b>1997</b> , 406, 249-54	3.8	26
16	The alpha-amylase from the yellow meal worm: complete primary structure, crystallization and preliminary X-ray analysis. <i>FEBS Letters</i> , <b>1997</b> , 409, 109-14	3.8	32
15	NMR characterization of the full-length recombinant murine prion protein, mPrP(23-231). <i>FEBS Letters</i> , <b>1997</b> , 413, 282-8	3.8	574
14	Recombinant full-length murine prion protein, mPrP(23-231): purification and spectroscopic characterization. <i>FEBS Letters</i> , <b>1997</b> , 413, 277-81	3.8	151
13	Structural analysis of three His32 mutants of DsbA: support for an electrostatic role of His32 in DsbA stability. <i>Protein Science</i> , <b>1997</b> , 6, 1893-900	6.3	79
12	Competition between DsbA-mediated oxidation and conformational folding of RTEM1 beta-lactamase. <i>Biochemistry</i> , <b>1996</b> , 35, 11386-95	3.2	16



11	Autonomous and reversible folding of a soluble amino-terminally truncated segment of the mouse prion protein. <i>Journal of Molecular Biology</i> , <b>1996</b> , 261, 614-9	6.5	72
10	RBI, a one-domain alpha-amylase/trypsin inhibitor with completely independent binding sites. <i>FEBS Letters</i> , <b>1996</b> , 397, 11-6	3.8	36
9	NMR structure of the mouse prion protein domain PrP(121-231). <i>Nature</i> , <b>1996</b> , 382, 180-2	50.4	1063
8	Efficient catalysis of disulfide formation during protein folding with a single active-site cysteine. <i>Journal of Molecular Biology</i> , <b>1995</b> , 247, 28-33	6.5	76
7	Determination of the three-dimensional structure of the bifunctional alpha-amylase/trypsin inhibitor from ragi seeds by NMR spectroscopy. <i>Biochemistry</i> , <b>1995</b> , 34, 8281-93	3.2	91
6	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> , <b>1995</b> , 270, 26178-83 <sup>5.4</sup>		39
5	The redox properties of protein disulfide isomerase (DsbA) of Escherichia coli result from a tense conformation of its oxidized form. <i>Journal of Molecular Biology</i> , <b>1993</b> , 233, 559-66	6.5	105
4	Bacterial protein disulfide isomerase: efficient catalysis of oxidative protein folding at acidic pH. <i>Biochemistry</i> , <b>1993</b> , 32, 12251-6	3.2	89
3	Redox properties of protein disulfide isomerase (DsbA) from Escherichia coli. <i>Protein Science</i> , <b>1993</b> , 2, 717-26	6.3	239
2	Formation of Adhesive Pili by the Chaperone-Usher Pathway <sup>965-986</sup>		2
1	Glycan-Protein Interactions Determine Kinetics of N-Glycan Remodeling		1