B Martin Hallberg

List of Publications by Year in Descending Order

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53 papers	4,233 citations	30 h-index	57 g-index
57 ext. papers	4,841 ext. citations	11.7 avg, IF	5.15 L-index

#	Paper	IF	Citations
53	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo.. *Nature Communications*, **2022**, 13, 155	17.4	6
52	Structural basis for late maturation steps of the human mitoribosomal large subunit. *Nature Communications*, **2021**, 12, 3673	17.4	7
51	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. *Science*, **2021**, 371,	33.3	149
50	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. *Nature Communications*, **2020**, 11, 5588	17.4	73
49	Post-translational Regulation of DNA Polymerase □a Connection to Damage-Induced Cohesion in. *Genetics*, **2020**, 216, 1009-1022	4	2
48	An alpaca nanobody neutralizes SARS-CoV-2 by blocking receptor interaction. *Nature Communications*, **2020**, 11, 4420	17.4	151
47	The MRPP1/MRPP2 complex is a tRNA-maturation platform in human mitochondria. *Nucleic Acids Research*, **2017**, 45, 12469-12480	20.1	30
46	SnoN Stabilizes the SMAD3/SMAD4 Protein Complex. *Scientific Reports*, **2017**, 7, 46370	4.9	9
45	Structural basis for cellobiose dehydrogenase action during oxidative cellulose degradation. *Nature Communications*, **2015**, 6, 7542	17.4	153
44	Structure of mitochondrial poly(A) RNA polymerase reveals the structural basis for dimerization, ATP selectivity and the SPAX4 disease phenotype. *Nucleic Acids Research*, **2015**, 43, 9065-75	20.1	19
43	TEFM is a potent stimulator of mitochondrial transcription elongation in vitro. *Nucleic Acids Research*, **2015**, 43, 2615-24	20.1	58
42	Structure of the nuclease subunit of human mitochondrial RNase P. *Nucleic Acids Research*, **2015**, 43, 5664-72	20.1	37
41	Making proteins in the powerhouse. *Cell Metabolism*, **2014**, 20, 226-40	24.6	139
40	The amino terminal extension of mammalian mitochondrial RNA polymerase ensures promoter specific transcription initiation. *Nucleic Acids Research*, **2014**, 42, 3638-47	20.1	36
39	Structure of the human MTERF4-NSUN4 protein complex that regulates mitochondrial ribosome biogenesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 15253-8	11.5	87
38	MTERF4 regulates translation by targeting the methyltransferase NSUN4 to the mammalian mitochondrial ribosome. *Cell Metabolism*, **2011**, 13, 527-39	24.6	190
37	Structural basis of tumor suppressor in lung cancer 1 (TSLC1) binding to differentially expressed in adenocarcinoma of the lung (DAL-1/4.1B). *Journal of Biological Chemistry*, **2011**, 286, 4511-6	5.4	22

36	Structure of mitochondrial transcription termination factor 3 reveals a novel nucleic acid-binding domain. *Biochemical and Biophysical Research Communications*, **2010**, 397, 386-90	3.4	40
35	RNA-protein mutually induced fit: structure of Escherichia coli isopentenyl-tRNA transferase in complex with tRNA(Phe). *Journal of Biological Chemistry*, **2009**, 284, 6600-4	5.4	30
34	Crystal structure of human diphosphoinositol phosphatase 1. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77, 242-6	4.2	21
33	Protein production and purification. *Nature Methods*, **2008**, 5, 135-46	21.6	655
32	Structural and biophysical characterization of human myo-inositol oxygenase. *Journal of Biological Chemistry*, **2008**, 283, 15209-16	5.4	33
31	Crystal structure of YegS, a homologue to the mammalian diacylglycerol kinases, reveals a novel regulatory metal binding site. *Journal of Biological Chemistry*, **2007**, 282, 19644-52	5.4	29
30	Crystal structure of the major Malassezia sympodialis allergen Mala s 1 reveals a beta-propeller fold: a novel fold among allergens. *Journal of Molecular Biology*, **2007**, 369, 1079-86	6.5	21
29	Cellobiose dehydrogenase--a flavocytochrome from wood-degrading, phytopathogenic and saprotropic fungi. *Current Protein and Peptide Science*, **2006**, 7, 255-80	2.8	190
28	Structural basis for substrate binding and regioselective oxidation of monosaccharides at C3 by pyranose 2-oxidase. *Journal of Biological Chemistry*, **2006**, 281, 35104-15	5.4	70
27	First structure of a eukaryotic phosphohistidine phosphatase. *Journal of Biological Chemistry*, **2006**, 281, 33830-4	5.4	17
26	The structure of the RNA m5C methyltransferase YebU from Escherichia coli reveals a C-terminal RNA-recruiting PUA domain. *Journal of Molecular Biology*, **2006**, 360, 774-87	6.5	33
25	Crystallization and preliminary crystallographic study of the yeast Malassezia sympodialis allergen Mala s 1. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 97-9		2
24	Expression, purification, crystallization and preliminary diffraction studies of the mammalian DAG kinase homologue YegS from Escherichia coli. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 295-7		5
23	The closed structure of presequence protease PreP forms a unique 10,000 Angstroms3 chamber for proteolysis. *EMBO Journal*, **2006**, 25, 1977-86	13	85
22	Thermofluor-based high-throughput stability optimization of proteins for structural studies. *Analytical Biochemistry*, **2006**, 357, 289-98	3.1	666
21	Catalytic mechanism of limonene epoxide hydrolase, a theoretical study. *Journal of the American Chemical Society*, **2005**, 127, 14339-47	16.4	70
20	Crystallization and preliminary X-ray diffraction analysis of pyranose 2-oxidase from the white-rot fungus Trametes multicolor. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 197-9		7
19	Expression, purification, crystallization and preliminary diffraction studies of the tRNA pseudouridine synthase TruD from Escherichia coli. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 775-6		6

18	Ancestral gene fusion in cellobiose dehydrogenases reflects a specific evolution of GMC oxidoreductases in fungi. *Gene*, **2004**, 338, 1-14	3.8	76
17	X-ray structure of tRNA pseudouridine synthase TruD reveals an inserted domain with a novel fold. *FEBS Letters*, **2004**, 565, 59-64	3.8	29
16	Crystal structure of the 270 kDa homotetrameric lignin-degrading enzyme pyranose 2-oxidase. *Journal of Molecular Biology*, **2004**, 341, 781-96	6.5	107
15	Biophysical and structural analysis of a novel heme B iron ligation in the flavocytochrome cellobiose dehydrogenase. *Journal of Biological Chemistry*, **2003**, 278, 33224-31	5.4	16
14	Structure of Rhodococcus erythropolis limonene-1,2-epoxide hydrolase reveals a novel active site. *EMBO Journal*, **2003**, 22, 2583-92	13	125
13	The heme domain of cellobiose oxidoreductase: a one-electron reducing system. *Biochimica Et Biophysica Acta - Bioenergetics*, **2003**, 1604, 47-54	4.6	15
12	Moth chemosensory protein exhibits drastic conformational changes and cooperativity on ligand binding. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 5069-74	11.5	115
11	Mechanism of the reductive half-reaction in cellobiose dehydrogenase. *Journal of Biological Chemistry*, **2003**, 278, 7160-6	5.4	55
10	Cellobiose quinone oxidoreductase from the white rot fungus Phanerochaete chrysosporium is produced by intracellular proteolysis of cellobiose dehydrogenase. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2002**, 1576, 15-22		11
9	Crystal structure of the flavoprotein domain of the extracellular flavocytochrome cellobiose dehydrogenase. *Journal of Molecular Biology*, **2002**, 315, 421-34	6.5	122
8	Production and characterization of recombinant Phanerochaete chrysosporium cellobiose dehydrogenase in the methylotrophic yeast Pichia pastoris. *Bioscience, Biotechnology and Biochemistry*, **2001**, 65, 2050-7	2.1	53
7	A new scaffold for binding haem in the cytochrome domain of the extracellular flavocytochrome cellobiose dehydrogenase. *Structure*, **2000**, 8, 79-88	5.2	126
6	Structure of Aspergillus niger epoxide hydrolase at 1.8 A resolution: implications for the structure and function of the mammalian microsomal class of epoxide hydrolases. *Structure*, **2000**, 8, 111-22	5.2	161
5	Structural basis of Omicron neutralization by affinity-matured public antibodies		3
4	An alpaca nanobody neutralizes SARS-CoV-2 by blocking receptor interaction		19
3	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2		11
2	Structural basis for late maturation steps of the human mitoribosomal large subunit		1
1	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo		3