

B Martin Hallberg

List of Publications by Citations

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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	Thermofluor-based high-throughput stability optimization of proteins for structural studies. <i>Analytical Biochemistry</i> , 2006 , 357, 289-98	3.1	666
52	Protein production and purification. <i>Nature Methods</i> , 2008 , 5, 135-46	21.6	655
51	MTERF4 regulates translation by targeting the methyltransferase NSUN4 to the mammalian mitochondrial ribosome. <i>Cell Metabolism</i> , 2011 , 13, 527-39	24.6	190
50	Cellobiose dehydrogenase--a flavocytochrome from wood-degrading, phytopathogenic and saprotropic fungi. <i>Current Protein and Peptide Science</i> , 2006 , 7, 255-80	2.8	190
49	Structure of <i>Aspergillus niger</i> epoxide hydrolase at 1.8 Å resolution: implications for the structure and function of the mammalian microsomal class of epoxide hydrolases. <i>Structure</i> , 2000 , 8, 111-22	5.2	161
48	Structural basis for cellobiose dehydrogenase action during oxidative cellulose degradation. <i>Nature Communications</i> , 2015 , 6, 7542	17.4	153
47	An alpaca nanobody neutralizes SARS-CoV-2 by blocking receptor interaction. <i>Nature Communications</i> , 2020 , 11, 4420	17.4	151
46	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021 , 371,	33.3	149
45	Making proteins in the powerhouse. <i>Cell Metabolism</i> , 2014 , 20, 226-40	24.6	139
44	A new scaffold for binding haem in the cytochrome domain of the extracellular flavocytochrome cellobiose dehydrogenase. <i>Structure</i> , 2000 , 8, 79-88	5.2	126
43	Structure of <i>Rhodococcus erythropolis</i> limonene-1,2-epoxide hydrolase reveals a novel active site. <i>EMBO Journal</i> , 2003 , 22, 2583-92	13	125
42	Crystal structure of the flavoprotein domain of the extracellular flavocytochrome cellobiose dehydrogenase. <i>Journal of Molecular Biology</i> , 2002 , 315, 421-34	6.5	122
41	Moth chemosensory protein exhibits drastic conformational changes and cooperativity on ligand binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5069-74	11.5	115
40	Crystal structure of the 270 kDa homotetrameric lignin-degrading enzyme pyranose 2-oxidase. <i>Journal of Molecular Biology</i> , 2004 , 341, 781-96	6.5	107
39	Structure of the human MTERF4-NSUN4 protein complex that regulates mitochondrial ribosome biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15253-8	11.5	87
38	The closed structure of presequence protease PreP forms a unique 10,000 Å chamber for proteolysis. <i>EMBO Journal</i> , 2006 , 25, 1977-86	13	85
37	Ancestral gene fusion in cellobiose dehydrogenases reflects a specific evolution of GMC oxidoreductases in fungi. <i>Gene</i> , 2004 , 338, 1-14	3.8	76

36	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5588	17.4	73
35	Structural basis for substrate binding and regioselective oxidation of monosaccharides at C3 by pyranose 2-oxidase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 35104-15	5.4	70
34	Catalytic mechanism of limonene epoxide hydrolase, a theoretical study. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14339-47	16.4	70
33	TEFM is a potent stimulator of mitochondrial transcription elongation in vitro. <i>Nucleic Acids Research</i> , 2015 , 43, 2615-24	20.1	58
32	Mechanism of the reductive half-reaction in cellobiose dehydrogenase. <i>Journal of Biological Chemistry</i> , 2003 , 278, 7160-6	5.4	55
31	Production and characterization of recombinant <i>Phanerochaete chrysosporium</i> cellobiose dehydrogenase in the methylotrophic yeast <i>Pichia pastoris</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2001 , 65, 2050-7	2.1	53
30	Structure of mitochondrial transcription termination factor 3 reveals a novel nucleic acid-binding domain. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 397, 386-90	3.4	40
29	Structure of the nuclease subunit of human mitochondrial RNase P. <i>Nucleic Acids Research</i> , 2015 , 43, 5664-72	20.1	37
28	The amino terminal extension of mammalian mitochondrial RNA polymerase ensures promoter specific transcription initiation. <i>Nucleic Acids Research</i> , 2014 , 42, 3638-47	20.1	36
27	Structural and biophysical characterization of human myo-inositol oxygenase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 15209-16	5.4	33
26	The structure of the RNA m5C methyltransferase YebU from <i>Escherichia coli</i> reveals a C-terminal RNA-recruiting PUA domain. <i>Journal of Molecular Biology</i> , 2006 , 360, 774-87	6.5	33
25	The MRPP1/MRPP2 complex is a tRNA-maturation platform in human mitochondria. <i>Nucleic Acids Research</i> , 2017 , 45, 12469-12480	20.1	30
24	RNA-protein mutually induced fit: structure of <i>Escherichia coli</i> isopentenyl-tRNA transferase in complex with tRNA(Phe). <i>Journal of Biological Chemistry</i> , 2009 , 284, 6600-4	5.4	30
23	Crystal structure of YegS, a homologue to the mammalian diacylglycerol kinases, reveals a novel regulatory metal binding site. <i>Journal of Biological Chemistry</i> , 2007 , 282, 19644-52	5.4	29
22	X-ray structure of tRNA pseudouridine synthase TruD reveals an inserted domain with a novel fold. <i>FEBS Letters</i> , 2004 , 565, 59-64	3.8	29
21	Structural basis of tumor suppressor in lung cancer 1 (TSLC1) binding to differentially expressed in adenocarcinoma of the lung (DAL-1/4.1B). <i>Journal of Biological Chemistry</i> , 2011 , 286, 4511-6	5.4	22
20	Crystal structure of human diphosphoinositol phosphatase 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77, 242-6	4.2	21
19	Crystal structure of the major <i>Malassezia sympodialis</i> allergen Mala s 1 reveals a beta-propeller fold: a novel fold among allergens. <i>Journal of Molecular Biology</i> , 2007 , 369, 1079-86	6.5	21

18	Structure of mitochondrial poly(A) RNA polymerase reveals the structural basis for dimerization, ATP selectivity and the SPAX4 disease phenotype. <i>Nucleic Acids Research</i> , 2015 , 43, 9065-75	20.1	19
17	An alpaca nanobody neutralizes SARS-CoV-2 by blocking receptor interaction		19
16	First structure of a eukaryotic phosphohistidine phosphatase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 33830-4	5.4	17
15	Biophysical and structural analysis of a novel heme B iron ligation in the flavocytochrome cellobiose dehydrogenase. <i>Journal of Biological Chemistry</i> , 2003 , 278, 33224-31	5.4	16
14	The heme domain of cellobiose oxidoreductase: a one-electron reducing system. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2003 , 1604, 47-54	4.6	15
13	Cellobiose quinone oxidoreductase from the white rot fungus <i>Phanerochaete chrysosporium</i> is produced by intracellular proteolysis of cellobiose dehydrogenase. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002 , 1576, 15-22		11
12	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2		11
11	SnoN Stabilizes the SMAD3/SMAD4 Protein Complex. <i>Scientific Reports</i> , 2017 , 7, 46370	4.9	9
10	Crystallization and preliminary X-ray diffraction analysis of pyranose 2-oxidase from the white-rot fungus <i>Trametes multicolor</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 197-9		7
9	Structural basis for late maturation steps of the human mitoribosomal large subunit. <i>Nature Communications</i> , 2021 , 12, 3673	17.4	7
8	Expression, purification, crystallization and preliminary diffraction studies of the tRNA pseudouridine synthase TruD from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 775-6		6
7	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo.. <i>Nature Communications</i> , 2022 , 13, 155	17.4	6
6	Expression, purification, crystallization and preliminary diffraction studies of the mammalian DAG kinase homologue YegS from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 295-7		5
5	Structural basis of Omicron neutralization by affinity-matured public antibodies		3
4	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo		3
3	Crystallization and preliminary crystallographic study of the yeast <i>Malassezia sympodialis</i> allergen Mala s 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 97-9		2
2	Post-translational Regulation of DNA Polymerase β Connection to Damage-Induced Cohesion in. <i>Genetics</i> , 2020 , 216, 1009-1022	4	2
1	Structural basis for late maturation steps of the human mitoribosomal large subunit		1

