

Helen R Saibil

List of Publications by Year in descending order

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81
papers

10,684
citations

46918

47
h-index

58464

82
g-index

90
all docs

90
docs citations

90
times ranked

11148
citing authors

#	ARTICLE	IF	CITATIONS
1	Chaperone machines for protein folding, unfolding and disaggregation. Nature Reviews Molecular Cell Biology, 2013, 14, 630-642.	16.1	836
2	The protofilament structure of insulin amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9196-9201.	3.3	770
3	Cryo-electron microscopy structure of an SH3 amyloid fibril and model of the molecular packing. EMBO Journal, 1999, 18, 815-821.	3.5	487
4	Atomic structure and hierarchical assembly of a cross- β^2 amyloid fibril. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5468-5473.	3.3	479
5	Mechanism of GroEL action: Productive release of polypeptide from a sequestered position under groes. Cell, 1995, 83, 577-587.	13.5	431
6	The Chaperonin ATPase Cycle: Mechanism of Allosteric Switching and Movements of Substrate-Binding Domains in GroEL. Cell, 1996, 87, 241-251.	13.5	389
7	Structural Basis of Pore Formation by the Bacterial Toxin Pneumolysin. Cell, 2005, 121, 247-256.	13.5	369
8	Location of a folding protein and shape changes in GroEL-GroES complexes imaged by cryo-electron microscopy. Nature, 1994, 371, 261-264.	13.7	366
9	The structural basis for membrane binding and pore formation by lymphocyte perforin. Nature, 2010, 468, 447-451.	13.7	364
10	Human Hsp70 Disaggregase Reverses Parkinson's-Linked α -Synuclein Amyloid Fibrils. Molecular Cell, 2015, 59, 781-793.	4.5	336
11	GroEL-GroES Cycling. Cell, 1999, 97, 325-338.	13.5	308
12	Structure of an Hsp90-Cdc37-Cdk4 Complex. Molecular Cell, 2006, 23, 697-707.	4.5	288
13	ATP-Bound States of GroEL Captured by Cryo-Electron Microscopy. Cell, 2001, 107, 869-879.	13.5	274
14	A Liquid to Solid Phase Transition Underlying Pathological Huntingtin Exon1 Aggregation. Molecular Cell, 2018, 70, 588-601.e6.	4.5	252
15	Multivalent Binding of Nonnative Substrate Proteins by the Chaperonin GroEL. Cell, 2000, 100, 561-573.	13.5	183
16	Two Structural Transitions in Membrane Pore Formation by Pneumolysin, the Pore-Forming Toxin of Streptococcus pneumoniae. Cell, 1999, 97, 647-655.	13.5	174
17	Direct three-dimensional visualization of membrane disruption by amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20455-20460.	3.3	162
18	ATP-Triggered Conformational Changes Delineate Substrate-Binding and -Folding Mechanics of the GroEL Chaperonin. Cell, 2012, 149, 113-123.	13.5	160

#	ARTICLE	IF	CITATIONS
19	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
20	Structure and Allostery of the Chaperonin GroEL. <i>Journal of Molecular Biology</i> , 2013, 425, 1476-1487.	2.0	153
21	Chaperone machines in action. <i>Current Opinion in Structural Biology</i> , 2008, 18, 35-42.	2.6	147
22	Stepwise visualization of membrane pore formation by suliyisin, a bacterial cholesterol-dependent cytolysin. <i>ELife</i> , 2014, 3, e04247.	2.8	145
23	Allosteric signaling of ATP hydrolysis in GroEL-GroES complexes. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 147-152.	3.6	142
24	Processing of Plasmodium falciparum Merozoite Surface Protein MSP1 Activates a Spectrin-Binding Function Enabling Parasite Egress from RBCs. <i>Cell Host and Microbe</i> , 2015, 18, 433-444.	5.1	141
25	The mechanism of pore formation by bacterial toxins. <i>Current Opinion in Structural Biology</i> , 2006, 16, 230-236.	2.6	132
26	The Molecular Basis for Perforin Oligomerization and Transmembrane Pore Assembly. <i>Immunity</i> , 2009, 30, 684-695.	6.6	123
27	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	2.6	114
28	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	5.8	112
29	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. <i>Science Advances</i> , 2017, 3, e1701726.	4.7	112
30	Cryo-EM of amyloid fibrils and cellular aggregates. <i>Current Opinion in Structural Biology</i> , 2019, 58, 34-42.	2.6	112
31	Head-to-tail interactions of the coiled-coil domains regulate ClpB activity and cooperation with Hsp70 in protein disaggregation. <i>ELife</i> , 2014, 3, e02481.	2.8	111
32	Atypical AAA+ Subunit Packing Creates an Expanded Cavity for Disaggregation by the Protein-Remodeling Factor Hsp104. <i>Cell</i> , 2007, 131, 1366-1377.	13.5	107
33	Topologies of a Substrate Protein Bound to the Chaperonin GroEL. <i>Molecular Cell</i> , 2007, 26, 415-426.	4.5	96
34	A protease cascade regulates release of the human malaria parasite Plasmodium falciparum from host red blood cells. <i>Nature Microbiology</i> , 2018, 3, 447-455.	5.9	96
35	Structure of a bacterial type III secretion system in contact with a host membrane in situ. <i>Nature Communications</i> , 2015, 6, 10114.	5.8	92
36	Real-time visualization of perforin nanopore assembly. <i>Nature Nanotechnology</i> , 2017, 12, 467-473.	15.6	88

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37	Multiple Distinct Assemblies Reveal Conformational Flexibility in the Small Heat Shock Protein Hsp26. <i>Structure</i> , 2006, 14, 1197-1204.	1.6	87
38	Motor Mechanism for Protein Threading through Hsp104. <i>Molecular Cell</i> , 2009, 34, 81-92.	4.5	84
39	Parasitophorous vacuole poration precedes its rupture and rapid host erythrocyte cytoskeleton collapse in <i>Plasmodium falciparum</i> egress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3439-3444.	3.3	84
40	Cryo electron microscopy to determine the structure of macromolecular complexes. <i>Methods</i> , 2016, 95, 78-85.	1.9	82
41	Conformational changes studied by cryo-electron microscopy. , 2000, 7, 711-714.		78
42	ATP-driven molecular chaperone machines. <i>Biopolymers</i> , 2013, 99, 846-859.	1.2	76
43	Detection and separation of heterogeneity in molecular complexes by statistical analysis of their two-dimensional projections. <i>Journal of Structural Biology</i> , 2008, 162, 108-120.	1.3	75
44	Three conformations of an archaeal chaperonin, TF55 from <i>Sulfolobus shibatae</i> . <i>Journal of Molecular Biology</i> , 2000, 296, 813-819.	2.0	74
45	Folding with and without encapsulation by cis- and trans-only GroEL-GroES complexes. <i>EMBO Journal</i> , 2003, 22, 3220-3230.	3.5	70
46	2.7-Å cryo-EM structure of ex vivo RML prion fibrils. <i>Nature Communications</i> , 2022, 13, .	5.8	66
47	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. <i>Journal of Structural Biology</i> , 2010, 172, 161-168.	1.3	64
48	REMBI: Recommended Metadata for Biological Images enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021, 18, 1418-1422.	9.0	63
49	Elongated Oligomers Assemble into Mammalian PrP Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2006, 357, 975-985.	2.0	61
50	Domain rotations between open, closed and bullet-shaped forms of the thermosome, an archaeal chaperonin 11 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2000, 301, 323-332.	2.0	56
51	Ex vivo mammalian prions are formed of paired double helical prion protein fibrils. <i>Open Biology</i> , 2016, 6, 160035.	1.5	55
52	Subunit organisation and symmetry of pore-forming, oligomeric pneumolysin. <i>FEBS Letters</i> , 1995, 371, 77-80.	1.3	51
53	A novel and rapid method for obtaining high titre intact prion strains from mammalian brain. <i>Scientific Reports</i> , 2015, 5, 10062.	1.6	51
54	Cryo-EM in molecular and cellular biology. <i>Molecular Cell</i> , 2022, 82, 274-284.	4.5	49

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55	Macromolecular structure determination by cryo-electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1215-1222.	2.5	47
56	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47
57	Two-Step Activation Mechanism of the ClpB Disaggregase for Sequential Substrate Threading by the Main ATPase Motor. <i>Cell Reports</i> , 2019, 27, 3433-3446.e4.	2.9	46
58	The membrane attack complex, perforin and cholesterol-dependent cytolysin superfamily of pore-forming proteins. <i>Journal of Cell Science</i> , 2016, 129, 2125-33.	1.2	45
59	Methods for Three-Dimensional Reconstruction of Heterogeneous Assemblies. <i>Methods in Enzymology</i> , 2010, 482, 321-341.	0.4	38
60	Heritable yeast prions have a highly organized three-dimensional architecture with interfiber structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14906-14911.	3.3	38
61	Structural features distinguishing infectious ex vivo mammalian prions from non-infectious fibrillar assemblies generated in vitro. <i>Scientific Reports</i> , 2019, 9, 376.	1.6	37
62	Multiple States of a Nucleotide-Bound Group 2 Chaperonin. <i>Structure</i> , 2008, 16, 528-534.	1.6	32
63	Prion aggregate structure in yeast cells is determined by the Hsp104-Hsp110 disaggregase machinery. <i>Journal of Cell Biology</i> , 2015, 211, 145-158.	2.3	28
64	An Expanded Protein Folding Cage in the GroEL-gp31 Complex. <i>Journal of Molecular Biology</i> , 2006, 358, 905-911.	2.0	26
65	Electron Bio-Imaging Centre (eBIC): the UK national research facility for biological electron microscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 488-495.	1.1	24
66	A national facility for biological cryo-electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 127-135.	2.5	22
67	N-terminal Domain of Prion Protein Directs Its Oligomeric Association. <i>Journal of Biological Chemistry</i> , 2014, 289, 25497-25508.	1.6	20
68	Cryo electron microscopy structures of Hsp100 proteins: crowbars in or out? This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 89-96.	0.9	19
69	Atomic force microscopy of membrane pore formation by cholesterol dependent cytolysins. <i>Current Opinion in Structural Biology</i> , 2016, 39, 8-15.	2.6	17
70	Malaria Parasite Schizont Egress Antigen-1 Plays an Essential Role in Nuclear Segregation during Schizogony. <i>MBio</i> , 2021, 12, .	1.8	17
71	Cooperative amyloid fibre binding and disassembly by the Hsp70 disaggregase. <i>EMBO Journal</i> , 2022, 41, .	3.5	14
72	Making connections: snapshots of chlamydial type III secretion systems in contact with host membranes. <i>Current Opinion in Microbiology</i> , 2015, 23, 1-7.	2.3	12

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73	Machinery to Reverse Irreversible Aggregates. <i>Science</i> , 2013, 339, 1040-1041.	6.0	11
74	A two-domain folding intermediate of RuBisCO in complex with the GroEL chaperonin. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 671-675.	3.6	11
75	The pore conformation of lymphocyte perforin. <i>Science Advances</i> , 2022, 8, eabk3147.	4.7	10
76	Structural basis of pore formation by cholesterol-binding toxins. <i>International Journal of Medical Microbiology</i> , 2000, 290, 389-394.	1.5	9
77	The PDB and protein homeostasis: From chaperones to degradation and disaggregase machines. <i>Journal of Biological Chemistry</i> , 2021, 296, 100744.	1.6	9
78	Correlative light and electron microscopy suggests that mutant huntingtin dysregulates the endolysosomal pathway in presymptomatic Huntington's disease. <i>Acta Neuropathologica Communications</i> , 2021, 9, 70.	2.4	7
79	Perforin proteostasis is regulated through its C2 domain: supra-physiological cell death mediated by T431D-perforin. <i>Cell Death and Differentiation</i> , 2018, 25, 1517-1529.	5.0	4
80	Three-Dimensional Structural Analysis of Amyloid Fibrils by Electron Microscopy. , 2006, , 303-313.		2
81	Macromolecular assemblies. <i>Current Opinion in Structural Biology</i> , 2009, 19, 178-180.	2.6	0