Maya Schuldiner

List of Publications by Year
in descending order

153 papers	16,569 citations	28274 55 h-index	17105 122 g-index
195 all docs	195 docs citations	195 times ranked	16805 citing authors

#	Article	IF	Citations
1	Show your true color: Mammalian cell surface staining for tracking cellular identity in multiplexing and beyond. Current Opinion in Chemical Biology, 2022, 66, 102102.	6.1	4
2	Widespread use of unconventional targeting signals in mitochondrial ribosome proteins. EMBO Journal, 2022, 41, e109519.	7.8	12
3	Peroxisome function relies on organelle-associated mRNA translation. Science Advances, 2022, 8, eabk2141.	10.3	18
4	A Similarity-Based Method for Predicting Enzymatic Functions in Yeast Uncovers a New AMP Hydrolase. Journal of Molecular Biology, 2022, 434, 167478.	4.2	2
5	Pls1 Is a Peroxisomal Matrix Protein with a Role in Regulating Lysine Biosynthesis. Cells, 2022, 11, 1426.	4.1	3
6	Cvm1 is a component of multiple vacuolar contact sites required for sphingolipid homeostasis. Journal of Cell Biology, 2022, 221, .	5.2	13
7	Beyond rare disorders: A new era for peroxisomal pathophysiology. Molecular Cell, 2022, 82, 2228-2235.	9.7	19
8	The Fast and the Furious: Golgi Contact Sites. Contact (Thousand Oaks (Ventura County, Calif)), 2021, 4, 251525642110344.	1.3	12
9	The ER protein Ema19 facilitates the degradation of nonimported mitochondrial precursor proteins. Molecular Biology of the Cell, 2021, 32, 664-674.	2.1	18
10	The chaperone-binding activity of the mitochondrial surface receptor Tom70 protects the cytosol against mitoprotein-induced stress. Cell Reports, 2021, 35, 108936.	6.4	47
11	ER-SURF: Riding the Endoplasmic Reticulum Surface to Mitochondria. International Journal of Molecular Sciences, 2021, 22, 9655.	4.1	18
12	Post-ER degradation of misfolded GPI-anchored proteins is linked with microautophagy. Current Biology, 2021, 31, 4025-4037.e5.	3.9	14
13	Cnm1 mediates nucleusâ€"mitochondria contact site formation in response to phospholipid levels. Journal of Cell Biology, 2021, 220, .	5.2	29
14	The NADH Dehydrogenase Nde1 Executes Cell Death after Integrating Signals from Metabolism and Proteostasis on the Mitochondrial Surface. Molecular Cell, 2020, 77, 189-202.e6.	9.7	39
15	Pex14p Phosphorylation Modulates Import of Citrate Synthase 2 Into Peroxisomes in Saccharomyces cerevisiae. Frontiers in Cell and Developmental Biology, 2020, 8, 549451.	3.7	20
16	Cargo Release from Myosin V Requires the Convergence of Parallel Pathways that Phosphorylate and Ubiquitylate the Cargo Adaptor. Current Biology, 2020, 30, 4399-4412.e7.	3.9	11
17	Cytosolic Events in the Biogenesis of Mitochondrial Proteins. Trends in Biochemical Sciences, 2020, 45, 650-667.	7.5	79
18	A piggybacking mechanism enables peroxisomal localization of the glyoxylate cycle enzyme Mdh2 in yeast. Journal of Cell Science, 2020, 133, .	2.0	21

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19	Uncovering targeting priority to yeast peroxisomes using an in-cell competition assay. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21432-21440.	7.1	17
20	Double the Fun, Double the Trouble: Paralogs and Homologs Functioning in the Endoplasmic Reticulum. Annual Review of Biochemistry, 2020, 89, 637-666.	11.1	10
21	Noncanonical regulation of phosphatidylserine metabolism by a Sec14-like protein and a lipid kinase. Journal of Cell Biology, 2020, 219, .	5.2	16
22	New horizons in mitochondrial contact site research. Biological Chemistry, 2020, 401, 793-809.	2.5	24
23	Unbiased yeast screens identify cellular pathways affected in Niemannâ€“Pick disease type C. Life Science Alliance, 2020, 3, e201800253.	2.8	10
24	Protein Topology Prediction Algorithms Systematically Investigated in the Yeast <i>Saccharomyces cerevisiae</i>. BioEssays, 2019, 41, e1800252.	2.5	18
25	Compartmentalized Synthesis of Triacylglycerol at the Inner Nuclear Membrane Regulates Nuclear Organization. Developmental Cell, 2019, 50, 755-766.e6.	7.0	52
26	Disease-causing mutations in subunits of OXPHOS complex I affect certain physical interactions. Scientific Reports, 2019, 9, 9987.	3.3	7
27	High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. Journal of Cell Biology, 2019, 218, 2797-2811.	5.2	18
28	The mitochondrial intermembrane spaceâ€“facing proteins Mcp2 and Tgl2 are involved in yeast lipid metabolism. Molecular Biology of the Cell, 2019, 30, 2681-2694.	2.1	5
29	Transfer of the Septin Ring to Cytokinetic Remnants in ER Stress Directs Age-Sensitive Cell-Cycle Re-entry. Developmental Cell, 2019, 51, 173-191.e5.	7.0	6
30	Cytotoxicity of 1-deoxysphingolipid unraveled by genome-wide genetic screens and lipidomics in <i>Saccharomyces cerevisiae</i>. Molecular Biology of the Cell, 2019, 30, 2814-2826.	2.1	14
31	Assessment of GFP Tag Position on Protein Localization and Growth Fitness in Yeast. Journal of Molecular Biology, 2019, 431, 636-641.	4.2	49
32	Yeast ceramide synthases, Lag1 and Lac1, have distinct substrate specificity. Journal of Cell Science, 2019, 132, .	2.0	26
33	Coming together to define membrane contactÂsites. Nature Communications, 2019, 10, 1287.	12.8	435
34	Promethin Is a Conserved Seipin Partner Protein. Cells, 2019, 8, 268.	4.1	52
35	The Endoplasmic Reticulum-Mitochondria Encounter Structure Complex Coordinates Coenzyme Q Biosynthesis. Contact (Thousand Oaks (Ventura County, Calif)), 2019, 2, 251525641882540.	1.3	35
36	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation. PLoS Genetics, 2019, 15, e1008387.	3.5	21

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37	Translational Regulation of Pmt1 and Pmt2 by Bfr1 Affects Unfolded Protein O-Mannosylation. International Journal of Molecular Sciences, 2019, 20, 6220.	4.1	4
38	Overexpression of branched-chain amino acid aminotransferases rescues the growth defects of cells lacking the Barth syndrome-related gene TAZ1. Journal of Molecular Medicine, 2019, 97, 269-279.	3.9	4
39	YeastRGB: comparing the abundance and localization of yeast proteins across cells and libraries. Nucleic Acids Research, 2019, 47, D1245-D1249.	14.5	39
40	Novel Regulation of Lipid Metabolism by a Phosphatidylinositol Transfer Protein and a Phosphatidylinositol 4â€Kinase. FASEB Journal, 2019, 33, lb330.	0.5	0
41	Title is missing!. , 2019, 15, e1008387.		0
42	Title is missing!. , 2019, 15, e1008387.		0
43	Title is missing!. , 2019, 15, e1008387.		0
44	Title is missing!. , 2019, 15, e1008387.		0
45	The GET pathway can increase the risk of mitochondrial outer membrane proteins to be mistargeted to the ER. Journal of Cell Science, 2018, 131, .	2.0	34
46	Database for High Throughput Screening Hits (dHITS): a simple tool to retrieve gene specific phenotypes from systematic screens done in yeast. Yeast, 2018, 35, 477-483.	1.7	7
47	Mind the Organelle Gap â€“ Peroxisome Contact Sites in Disease. Trends in Biochemical Sciences, 2018, 43, 199-210.	7.5	36
48	Systematic mapping of contact sites reveals tethers and a function for the peroxisome-mitochondria contact. Nature Communications, 2018, 9, 1761.	12.8	222
49	Toolbox: Creating a systematic database of secretory pathway proteins uncovers new cargo for COPI. Traffic, 2018, 19, 370-379.	2.7	15
50	Identification of seipin-linked factors that act as determinants of a lipid droplet subpopulation. Journal of Cell Biology, 2018, 217, 269-282.	5.2	99
51	Validation of a yeast malate dehydrogenase 2 (Mdh2) antibody tested for use in western blots. F1000Research, 2018, 7, 130.	1.6	4
52	Defining the Mammalian Peroxisomal Proteome. Sub-Cellular Biochemistry, 2018, 89, 47-66.	2.4	26
53	An ER surface retrieval pathway safeguards the import of mitochondrial membrane proteins in yeast. Science, 2018, 361, 1118-1122.	12.6	129
54	Stepping outside the comfort zone of membrane contact site research. Nature Reviews Molecular Cell Biology, 2018, 19, 483-484.	37.0	21

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55	Natural genetic variation for expression of a <scp>SWEET</scp> transporter among wild species of <i>Solanum lycopersicum</i> (tomato) determines the hexose composition of ripening tomato fruit. Plant Journal, 2018, 96, 343-357.	5.7	74
56	Genome-wide SWAp-Tag yeast libraries for proteome exploration. Nature Methods, 2018, 15, 617-622.	19.0	134
57	Validation of a yeast malate dehydrogenase 2 (Mdh2) antibody tested for use in western blots. F1000Research, 2018, 7, 130.	1.6	5
58	Temporal profiling of redox-dependent heterogeneity in single cells. ELife, 2018, 7, .	6.0	27
59	Ground control to major TOM: mitochondriaâ€“nucleus communication. FEBS Journal, 2017, 284, 196-210.	4.7	75
60	A pathway of targeted autophagy is induced by DNA damage in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1158-E1167.	7.1	52
61	Incredibly closeâ€”A newly identified peroxisomeâ€“ER contact site in humans. Journal of Cell Biology, 2017, 216, 287-289.	5.2	14
62	Mitochatting â€“ If only we could be a fly on the cell wall. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 1469-1480.	4.1	27
63	Peroxisome Mini-Libraries: Systematic Approaches to Study Peroxisomes Made Easy. Methods in Molecular Biology, 2017, 1595, 305-318.	0.9	17
64	Heterosis as a consequence of regulatory incompatibility. BMC Biology, 2017, 15, 38.	3.8	31
65	Saccharomyces cerevisiae cells lacking Pex3 contain membrane vesicles that harbor a subset of peroxisomal membrane proteins. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 1656-1667.	4.1	28
66	A different kind of love â€“ lipid droplet contact sites. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2017, 1862, 1188-1196.	2.4	160
67	Pex35 is a regulator of peroxisome abundance. Journal of Cell Science, 2017, 130, 791-804.	2.0	34
68	Maya Schuldiner. Current Biology, 2017, 27, R982-R984.	3.9	0
69	Two novel effectors of trafficking and maturation of the yeast plasma membrane H⁺â€‹<scp>ATPase</scp>. Traffic, 2017, 18, 672-682.	2.7	13
70	Syp1 regulates the clathrin-mediated and clathrin-independent endocytosis of multiple cargo proteins through a novel sorting motif. Molecular Biology of the Cell, 2017, 28, 2434-2448.	2.1	13
71	Iron affects Ire1 clustering propensity and the amplitude of endoplasmic reticulum stress signaling. Journal of Cell Science, 2017, 130, 3222-3233.	2.0	35
72	Definition of a High-Confidence Mitochondrial Proteome at Quantitative Scale. Cell Reports, 2017, 19, 2836-2852.	6.4	346

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73	Combining Deep Sequencing, Proteomics, Phosphoproteomics, and Functional Screens To Discover Novel Regulators of Sphingolipid Homeostasis. Journal of Proteome Research, 2017, 16, 571-582.	3.7	11
74	APOL1â€"Mediated Cell Injury Involves Disruption of Conserved Trafficking Processes. Journal of the American Society of Nephrology: JASN, 2017, 28, 1117-1130.	6.1	88
75	Targeting and translocation of proteins to the endoplasmic reticulum at a glance. Journal of Cell Science, 2017, 130, 4079-4085.	2.0	111
76	Cellular Consequences of Diminished Protein O-Mannosyltransferase Activity in Bakerâ€™s Yeast. International Journal of Molecular Sciences, 2017, 18, 1226.	4.1	6
77	<scp>hS</scp>nd2 protein represents an alternative targeting factor to the endoplasmic reticulum in human cells. FEBS Letters, 2017, 591, 3211-3224.	2.8	55
78	Water-Transfer Slows Aging in Saccharomyces cerevisiae. PLoS ONE, 2016, 11, e0148650.	2.5	11
79	The SND proteins constitute an alternative targeting route to the endoplasmic reticulum. Nature, 2016, 540, 134-138.	27.8	168
80	Mice lacking WRB reveal differential biogenesis requirements of tail-anchored proteins in vivo. Scientific Reports, 2016, 6, 39464.	3.3	35
81	Characterization of proteome dynamics in oleate reveals a novel peroxisome targeting receptor. Journal of Cell Science, 2016, 129, 4067-4075.	2.0	63
82	Making Sense of the Yeast Sphingolipid Pathway. Journal of Molecular Biology, 2016, 428, 4765-4775.	4.2	41
83	An unrecognized function for COPII components in recruiting a viral replication protein to the perinuclear ER. Journal of Cell Science, 2016, 129, 3597-3608.	2.0	32
84	A Tether Is a Tether Is a Tether: Tethering at Membrane Contact Sites. Developmental Cell, 2016, 39, 395-409.	7.0	315
85	The Protease Ste24 Clears Clogged Translocons. Cell, 2016, 164, 103-114.	28.9	93
86	One library to make them all: streamlining the creation of yeast libraries via a SWAp-Tag strategy. Nature Methods, 2016, 13, 371-378.	19.0	171
87	No peroxisome is an island â€" Peroxisome contact sites. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 1061-1069.	4.1	126
88	Lipid Droplets Are Essential for Efficient Clearance of Cytosolic Inclusion Bodies. Developmental Cell, 2015, 33, 603-610.	7.0	92
89	Lam6 Regulates the Extent of Contacts between Organelles. Cell Reports, 2015, 12, 7-14.	6.4	173
90	Genome-Wide Screens in <i>Saccharomyces cerevisiae</i> Highlight a Role for Cardiolipin in Biogenesis of Mitochondrial Outer Membrane Multispan Proteins. Molecular and Cellular Biology, 2015, 35, 3200-3211.	2.3	30

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91	Peroxisystem: Harnessing systems cell biology to study peroxisomes. Biology of the Cell, 2015, 107, 89-97.	2.0	4
92	Starvation-Dependent Regulation of Golgi Quality Control Links the TOR Signaling and Vacuolar Protein Sorting Pathways. Cell Reports, 2015, 12, 1876-1886.	6.4	46
93	Editorial overview: Cell organelles: Organelle communication: new means and new views. Current Opinion in Cell Biology, 2015, 35, v-vi.	5.4	1
94	Accurate, Model-Based Tuning of Synthetic Gene Expression Using Introns in S. cerevisiae. PLoS Genetics, 2014, 10, e1004407.	3.5	31
95	Primersâ€4â€Yeast: a comprehensive web tool for planning primers for <i>Saccharomyces cerevisiae</i>. Yeast, 2014, 31, 77-80.	1.7	41
96	The Yeast ER-Intramembrane Protease Ypf1 Refines Nutrient Sensing by Regulating Transporter Abundance. Molecular Cell, 2014, 56, 630-640.	9.7	48
97	A defect in the RNA-processing protein HNRPDL causes limb-girdle muscular dystrophy 1G (LGMD1G). Human Molecular Genetics, 2014, 23, 4103-4110.	2.9	101
98	OM14 is a mitochondrial receptor for cytosolic ribosomes that supports co-translational import into mitochondria. Nature Communications, 2014, 5, 5711.	12.8	106
99	LoQAtEâ€"Localization and Quantitation ATlas of the yeast proteomE. A new tool for multiparametric dissection of single-protein behavior in response to biological perturbations in yeast. Nucleic Acids Research, 2014, 42, D726-D730.	14.5	74
100	Embracing the voidâ€"how much do we really know about targeting and translocation to the endoplasmic reticulum?. Current Opinion in Cell Biology, 2014, 29, 8-17.	5.4	34
101	The Back and Forth of Cargo Exit from the Endoplasmic Reticulum. Current Biology, 2014, 24, R130-R136.	3.9	75
102	The yeast oligopeptide transporter Opt2 is localized to peroxisomes and affects glutathione redox homeostasis. FEMS Yeast Research, 2014, 14, n/a-n/a.	2.3	29
103	The PH gene determines fruit acidity and contributes to the evolution of sweet melons. Nature Communications, 2014, 5, 4026.	12.8	100
104	Peroxisomes are juxtaposed to strategic sites on mitochondria. Molecular BioSystems, 2014, 10, 1742-1748.	2.9	95
105	The emergence of proteome-wide technologies: systematic analysis of proteins comes of age. Nature Reviews Molecular Cell Biology, 2014, 15, 453-464.	37.0	80
106	A Dynamic Interface between Vacuoles and Mitochondria in Yeast. Developmental Cell, 2014, 30, 95-102.	7.0	321
107	A cytosolic degradation pathway, prERAD, monitors pre-inserted secretory pathway proteins. Journal of Cell Science, 2014, 127, 3017-23.	2.0	40
108	Yeast phospholipid biosynthesis is linked to mRNA localization. Journal of Cell Science, 2014, 127, 3373-81.	2.0	11

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109	Get3 is a holdase chaperone and moves to deposition sites for aggregated proteins when membrane targeting is blocked. Journal of Cell Science, 2013, 126, 473-483.	2.0	50
110	The Contribution of Systematic Approaches to Characterizing the Proteins and Functions of the Endoplasmic Reticulum. Cold Spring Harbor Perspectives in Biology, 2013, 5, a013284-a013284.	5.5	12
111	From rags to riches â€" The history of the endoplasmic reticulum. Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 2389-2391.	4.1	18
112	All roads lead to Rome (but some may be harder to travel): SRP-independent translocation into the endoplasmic reticulum. Critical Reviews in Biochemistry and Molecular Biology, 2013, 48, 273-288.	5.2	34
113	A Network of Cytosolic Factors Targets SRP-Independent Proteins to the Endoplasmic Reticulum. Cell, 2013, 152, 1134-1145.	28.9	166
114	The Yeast P5 Type ATPase, Spf1, Regulates Manganese Transport into the Endoplasmic Reticulum. PLoS ONE, 2013, 8, e85519.	2.5	62
115	The Role of Djp1 in Import of the Mitochondrial Protein Mim1 Demonstrates Specificity between a Cochaperone and Its Substrate Protein. Molecular and Cellular Biology, 2013, 33, 4083-4094.	2.3	68
116	A novel single-cell screening platform reveals proteome plasticity during yeast stress responses. Journal of Cell Biology, 2013, 200, 839-850.	5.2	210
117	Characterization of an M28 metalloprotease family member residing in the yeast vacuole. FEMS Yeast Research, 2013, 13, 471-484.	2.3	9
118	Formation and dissociation of proteasome storage granules are regulated by cytosolic pH. Journal of Cell Biology, 2013, 201, 663-671.	5.2	76
119	A Systematic Approach to Pair Secretory Cargo Receptors with Their Cargo Suggests a Mechanism for Cargo Selection by Erv14. PLoS Biology, 2012, 10, e1001329.	5.6	87
120	Ergosterol content specifies targeting of tail-anchored proteins to mitochondrial outer membranes. Molecular Biology of the Cell, 2012, 23, 3927-3935.	2.1	119
121	Interactions of subunit CCT3 in the yeast chaperonin CCT/TRiC with Q/N-rich proteins revealed by high-throughput microscopy analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18833-18838.	7.1	32
122	Confinement to Organelle-Associated Inclusion Structures Mediates Asymmetric Inheritance of Aggregated Protein in Budding Yeast. Cell Reports, 2012, 2, 738-747.	6.4	173
123	Advanced Methods for High-Throughput Microscopy Screening of Genetically Modified Yeast Libraries. Methods in Molecular Biology, 2011, 781, 127-159.	0.9	101
124	Staying in touch: the molecular era of organelle contact sites. Trends in Biochemical Sciences, 2011, 36, 616-623.	7.5	195
125	Protein Degradation: BAGging Up the Trash. Current Biology, 2011, 21, R692-R695.	3.9	5
126	A mitochondrial-focused genetic interaction map reveals a scaffold-like complex required for inner membrane organization in mitochondria. Journal of Cell Biology, 2011, 195, 323-340.	5.2	402

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127	Organelle structure and biogenesis. Molecular Biology of the Cell, 2011, 22, 723-723.	2.1	1
128	Getting the whole picture: combining throughput with content in microscopy. Journal of Cell Science, 2011, 124, 3743-3751.	2.0	40
129	Using high content microscopy screening to uncover insertion pathways for transmembrane proteins. FASEB Journal, 2011, 25, 194.3.	0.5	0
130	The DNA Damage Road Map. Science, 2010, 330, 1327-1328.	12.6	1
131	The plasma membrane code. Nature Chemical Biology, 2010, 6, 487-488.	8.0	4
132	Modularity and directionality in genetic interaction maps. Bioinformatics, 2010, 26, i228-i236.	4.1	27
133	Rapid creation and quantitative monitoring of high coverage shRNA libraries. Nature Methods, 2009, 6, 443-445.	19.0	92
134	Weizmann Young PI Forum: The Power of Peer Support. Molecular Cell, 2009, 36, 913-915.	9.7	5
135	Comprehensive Characterization of Genes Required for Protein Folding in the Endoplasmic Reticulum. Science, 2009, 323, 1693-1697.	12.6	646
136	An ER-Mitochondria Tethering Complex Revealed by a Synthetic Biology Screen. Science, 2009, 325, 477-481.	12.6	1,129
137	Explorations in topologyâ€“delving underneath the surface of genetic interaction maps. Molecular BioSystems, 2009, 5, 1473.	2.9	12
138	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. Nature Methods, 2008, 5, 711-718.	19.0	473
139	The GET Complex Mediates Insertion of Tail-Anchored Proteins into the ER Membrane. Cell, 2008, 134, 634-645.	28.9	460
140	Identification of yeast proteins necessary for cell-surface function of a potassium channel. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18079-18084.	7.1	53
141	Backup without redundancy: genetic interactions reveal the cost of duplicate gene loss. Molecular Systems Biology, 2007, 3, 86.	7.2	143
142	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. Nature, 2007, 446, 806-810.	27.8	806
143	Genetic Interaction mapping of essential genes in <i>Saccharomyces cerevisiae</i>. FASEB Journal, 2007, 21, A1004.	0.5	0
144	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. Genome Biology, 2006, 7, R63.	9.6	287

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145	Exploration of the Function and Organization of the Yeast Early Secretory Pathway through an Epistatic Miniarray Profile. Cell, 2005, 123, 507-519.	28.9	804
146	Cotranscriptional Set2 Methylation of Histone H3 Lysine 36 Recruits a Repressive Rpd3 Complex. Cell, 2005, 123, 593-605.	28.9	712
147	Modeling for Lesch-Nyhan Disease by Gene Targeting in Human Embryonic Stem Cells. Stem Cells, 2004, 22, 635-641.	3.2	167
148	Selective Ablation of Human Embryonic Stem Cells Expressing a â€œSuicideâ€•Gene. Stem Cells, 2003, 21, 257-265.	3.2	267
149	Factors Controlling Human Embryonic Stem Cell Differentiation. Methods in Enzymology, 2003, 365, 446-461.	1.0	18
150	Characterization of the expression of MHC proteins in human embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9864-9869.	7.1	628
151	Induced neuronal differentiation of human embryonic stem cells. Brain Research, 2001, 913, 201-205.	2.2	410
152	Establishment of human embryonic stem cell-transfected clones carrying a marker for undifferentiated cells. Current Biology, 2001, 11, 514-518.	3.9	360
153	Differentiation of Human Embryonic Stem Cells into Embryoid Bodies Comprising the Three Embryonic Germ Layers. Molecular Medicine, 2000, 6, 88-95.	4.4	1,377