

Robert F Murphy

List of Publications by Year in descending order

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124
papers

5,575
citations

101543

36
h-index

95266

68
g-index

136
all docs

136
docs citations

136
times ranked

6048
citing authors

#	ARTICLE	IF	CITATIONS
1	Biological imaging software tools. <i>Nature Methods</i> , 2012, 9, 697-710.	19.0	462
2	Effect of Bafilomycin A1 and Nocodazole on Endocytic Transport in HeLa Cells: Implications for Viral Uncoating and Infection. <i>Journal of Virology</i> , 1998, 72, 9645-9655.	3.4	291
3	Automated Subcellular Location Determination and High-Throughput Microscopy. <i>Developmental Cell</i> , 2007, 12, 7-16.	7.0	255
4	Automated recognition of patterns characteristic of subcellular structures in fluorescence microscopy images. <i>Cytometry</i> , 1998, 33, 366-375.	1.8	212
5	Immunofluorescence and fluorescent-protein tagging show high correlation for protein localization in mammalian cells. <i>Nature Methods</i> , 2013, 10, 315-323.	19.0	209
6	Maturation models for endosome and lysosome biogenesis. <i>Trends in Cell Biology</i> , 1991, 1, 77-82.	7.9	169
7	A Framework for the Automated Analysis of Subcellular Patterns in Human Protein Atlas Images. <i>Journal of Proteome Research</i> , 2008, 7, 2300-2308.	3.7	144
8	Nuclear segmentation in microscope cell images: A hand-segmented dataset and comparison of algorithms. , 2009, 5193098, 518-521.		138
9	Kinetics and temperature dependence of exposure of endocytosed material to proteolytic enzymes and low pH: Evidence for a maturation model for the formation of lysosomes. <i>Journal of Cellular Physiology</i> , 1987, 131, 200-209.	4.1	132
10	Transferrin recycling and dextran transport to lysosomes is differentially affected by bafilomycin, nocodazole, and low temperature. <i>Cell and Tissue Research</i> , 2005, 320, 99-113.	2.9	123
11	Boosting accuracy of automated classification of fluorescence microscope images for location proteomics. <i>BMC Bioinformatics</i> , 2004, 5, 78.	2.6	118
12	Automated Image Analysis for High-Content Screening and Analysis. <i>Journal of Biomolecular Screening</i> , 2010, 15, 726-734.	2.6	117
13	Flow cytometric DNA analysis of Neuroblastoma and Ganglioneuroma. A 10-year retrospective study. <i>Cancer</i> , 1988, 62, 749-754.	4.1	110
14	Robust Numerical Features for Description and Classification of Subcellular Location Patterns in Fluorescence Microscope Images. <i>Journal of Signal Processing Systems</i> , 2003, 35, 311-321.	1.0	106
15	From quantitative microscopy to automated image understanding. <i>Journal of Biomedical Optics</i> , 2004, 9, 893.	2.6	101
16	A multiresolution approach to automated classification of protein subcellular location images. <i>BMC Bioinformatics</i> , 2007, 8, 210.	2.6	101
17	An active role for machine learning in drug development. <i>Nature Chemical Biology</i> , 2011, 7, 327-330.	8.0	101
18	Automated learning of generative models for subcellular location: Building blocks for systems biology. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2007, 71A, 978-990.	1.5	96

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19	Conserved non-AUG uORFs revealed by a novel regression analysis of ribosome profiling data. <i>Genome Research</i> , 2018, 28, 214-222.	5.5	93
20	Advances in molecular labeling, high throughput imaging and machine intelligence portend powerful functional cellular biochemistry tools. <i>Journal of Cellular Biochemistry</i> , 2002, 87, 194-210.	2.6	86
21	Deformation-based nuclear morphometry: Capturing nuclear shape variation in HeLa cells. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 341-350.	1.5	74
22	Automated image analysis of protein localization in budding yeast. <i>Bioinformatics</i> , 2007, 23, i66-i71.	4.1	70
23	Objective Clustering of Proteins Based on Subcellular Location Patterns. <i>Journal of Biomedicine and Biotechnology</i> , 2005, 2005, 87-95.	3.0	59
24	Determining the subcellular location of new proteins from microscope images using local features. <i>Bioinformatics</i> , 2013, 29, 2343-2349.	4.1	59
25	Opening of Size-Selective Pores in Endosomes during Human Rhinovirus Serotype 2 In Vivo Uncoating Monitored by Single-Organelle Flow Analysis. <i>Journal of Virology</i> , 2005, 79, 1008-1016.	3.4	56
26	Automated interpretation of subcellular patterns in fluorescence microscope images for location proteomics. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2006, 69A, 631-640.	1.5	55
27	Feature reduction for improved recognition of subcellular location patterns in fluorescence microscope images. , 2003, , .		54
28	Primary cell cultures from murine kidney and heart differ in endosomal pH. <i>Journal of Cellular Physiology</i> , 1998, 176, 216-222.	4.1	52
29	Mitotic Golgi is in a Dynamic Equilibrium Between Clustered and Free Vesicles Independent of the ER. <i>Traffic</i> , 2001, 2, 873-884.	2.7	52
30	Discrete cytosolic macromolecular <sc>BRAF</sc> complexes exhibit distinct activities and composition. <i>EMBO Journal</i> , 2017, 36, 646-663.	7.8	52
31	Image-derived, three-dimensional generative models of cellular organization. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2011, 79A, 383-391.	1.5	51
32	Location proteomics: building subcellular location trees from high-resolution 3D fluorescence microscope images of randomly tagged proteins. , 2003, 4962, 298.		49
33	Flow cytometric DNA analysis of adrenocortical tumors in children. <i>Cancer</i> , 1987, 59, 2059-2063.	4.1	42
34	Object type recognition for automated analysis of protein subcellular location. <i>IEEE Transactions on Image Processing</i> , 2005, 14, 1351-1359.	9.8	42
35	Evaluation of methods for generative modeling of cell and nuclear shape. <i>Bioinformatics</i> , 2019, 35, 2475-2485.	4.1	41
36	Determining the distribution of probes between different subcellular locations through automated unmixing of subcellular patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2944-2949.	7.1	40

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37	Automated interpretation of subcellular patterns from immunofluorescence microscopy. <i>Journal of Immunological Methods</i> , 2004, 290, 93-105.	1.4	39
38	Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. <i>Bioinformatics</i> , 2010, 26, i7-i12.	4.1	39
39	Growth inhibition of 3T3 fibroblasts by lysosomotropic amines: Correlation with effects on intravesicular pH but not vacuolation. <i>Journal of Cellular Physiology</i> , 1986, 129, 65-70.	4.1	38
40	Putting proteins on the map. <i>Nature Biotechnology</i> , 2006, 24, 1223-1224.	17.5	38
41	Objective Evaluation of Differences in Protein Subcellular Distribution. <i>Traffic</i> , 2002, 3, 61-65.	2.7	37
42	CellOrganizer: Image-Derived Models of Subcellular Organization and Protein Distribution. <i>Methods in Cell Biology</i> , 2012, 110, 179-193.	1.1	37
43	Automated Analysis and Reannotation of Subcellular Locations in Confocal Images from the Human Protein Atlas. <i>PLoS ONE</i> , 2012, 7, e50514.	2.5	37
44	Computer programs for analysis of nucleic acid hybridization, thermal denaturation, and gel electrophoresis data. <i>Nucleic Acids Research</i> , 1979, 6, 3911-3922.	14.5	36
45	Active machine learning-driven experimentation to determine compound effects on protein patterns. <i>ELife</i> , 2016, 5, e10047.	6.0	36
46	Testing models of the arrangement of DNA inside bacteriophage λ by crosslinking the packaged DNA. <i>Journal of Molecular Biology</i> , 1982, 159, 71-92.	4.2	35
47	Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using a Weighted Ensemble of Trajectories. <i>PLoS Computational Biology</i> , 2016, 12, e1004611.	3.2	35
48	Location proteomics: a systems approach to subcellular location. <i>Biochemical Society Transactions</i> , 2005, 33, 535-538.	3.4	34
49	Automated analysis of immunohistochemistry images identifies candidate location biomarkers for cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18249-18254.	7.1	34
50	Image-based systems biology. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 459-461.	1.5	33
51	Discriminative Motif Finding for Predicting Protein Subcellular Localization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 441-451.	3.0	32
52	Toward the virtual cell: Automated approaches to building models of subcellular organization learned from microscopy images. <i>BioEssays</i> , 2012, 34, 791-799.	2.5	32
53	Kinetics of hydrolysis of endocytosed substrates by mammalian cultured cells: Early introduction of lysosomal enzymes into the endocytic pathway. <i>Journal of Cellular Physiology</i> , 1990, 143, 110-117.	4.1	31
54	Toward Objective Selection of Representative Microscope Images. <i>Biophysical Journal</i> , 1999, 76, 2230-2237.	0.5	30

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55	A generative model of microtubule distributions, and indirect estimation of its parameters from fluorescence microscopy images. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 457-466.	1.5	30
56	Chapter 16 Flow-Cytometric Analysis of Endocytic Compartments. <i>Methods in Cell Biology</i> , 1989, 31, 293-317.	1.1	29
57	Efficient discovery of responses of proteins to compounds using active learning. <i>BMC Bioinformatics</i> , 2014, 15, 143.	2.6	29
58	Large-Scale Automated Analysis of Location Patterns in Randomly Tagged 3T3 Cells. <i>Annals of Biomedical Engineering</i> , 2007, 35, 1081-1087.	2.5	28
59	The actin-driven spatiotemporal organization of T cell signaling at the system scale. <i>Immunological Reviews</i> , 2013, 256, 133-147.	6.0	27
60	Automated Learning of Subcellular Variation among Punctate Protein Patterns and a Generative Model of Their Relation to Microtubules. <i>PLoS Computational Biology</i> , 2015, 11, e1004614.	3.2	27
61	Joint modeling of cell and nuclear shape variation. <i>Molecular Biology of the Cell</i> , 2015, 26, 4046-4056.	2.1	27
62	A Novel Graphical Model Approach to Segmenting Cell Images. , 2006, , .		26
63	Communicating subcellular distributions. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 686-692.	1.5	26
64	Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature. <i>Lecture Notes in Computer Science</i> , 2010, , 23-32.	1.3	26
65	Building cell models and simulations from microscope images. <i>Methods</i> , 2016, 96, 33-39.	3.8	26
66	Efficient Modeling and Active Learning Discovery of Biological Responses. <i>PLoS ONE</i> , 2013, 8, e83996.	2.5	26
67	Automated analysis of patterns in fluorescence-microscope images. <i>Trends in Cell Biology</i> , 1999, 9, 201-202.	7.9	25
68	Structured correspondence topic models for mining captioned figures in biological literature. , 2009, 2009, 39-48.		24
69	Computational spatiotemporal analysis identifies WAVE2 and cofilin as joint regulators of costimulation-mediated T cell actin dynamics. <i>Science Signaling</i> , 2016, 9, rs3.	3.6	24
70	Cytomics and location proteomics: Automated interpretation of subcellular patterns in fluorescence microscope images. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2005, 67A, 1-3.	1.5	23
71	A graphical model approach to automated classification of protein subcellular location patterns in multi-cell images. <i>BMC Bioinformatics</i> , 2006, 7, 90.	2.6	23
72	Improved recognition of figures containing fluorescence microscope images in online journal articles using graphical models. <i>Bioinformatics</i> , 2008, 24, 569-576.	4.1	23

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73	Processing of Endocytosed Material. <i>Advances in Molecular and Cell Biology</i> , 1988, 2, 159-180.	0.1	22
74	Automated Interpretation of Protein Subcellular Location Patterns: Implications for Early Cancer Detection and Assessment. <i>Annals of the New York Academy of Sciences</i> , 2004, 1020, 124-131.	3.8	22
75	Efficient framework for automated classification of subcellular patterns in budding yeast. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009, 75A, 934-940.	1.5	21
76	Estimating Microtubule Distributions from 2D Immunofluorescence Microscopy Images Reveals Differences among Human Cultured Cell Lines. <i>PLoS ONE</i> , 2012, 7, e50292.	2.5	20
77	Automated analysis of Human Protein Atlas immunofluorescence images. , 2009, 5193229, 1023-1026.		19
78	Location Proteomics: Systematic Determination of Protein Subcellular Location. <i>Methods in Molecular Biology</i> , 2009, 500, 313-332.	0.9	19
79	Characterization of the TGN exit signal of the human mannose 6-phosphate uncovering enzyme. <i>Journal of Cell Science</i> , 2005, 118, 2949-2956.	2.0	17
80	Instance-based generative biological shape modeling. , 2009, 5193141, 690-693.		15
81	A new era in bioimage informatics. <i>Bioinformatics</i> , 2014, 30, 1353-1353.	4.1	15
82	PD-1 suppresses the maintenance of cell couples between cytotoxic T cells and target tumor cells within the tumor. <i>Science Signaling</i> , 2020, 13, .	3.6	15
83	Automated comparison of protein subcellular location patterns between images of normal and cancerous tissues. , 2008, 4540993, 304-307.		14
84	Intelligent Acquisition and Learning of Fluorescence Microscope Data Models. <i>IEEE Transactions on Image Processing</i> , 2009, 18, 2071-2084.	9.8	14
85	Structured literature image finder: Parsing text and figures in biomedical literature. <i>Web Semantics</i> , 2010, 8, 151-154.	2.9	14
86	Learning complex subcellular distribution patterns of proteins via analysis of immunohistochemistry images. <i>Bioinformatics</i> , 2020, 36, 1908-1914.	4.1	14
87	Deformation-based nonlinear dimension reduction: Applications to nuclear morphometry. , 2008, , .		13
88	Detection of Protein-Protein Interactions Through Vesicle Targeting. <i>Genetics</i> , 2009, 182, 33-39.	2.9	13
89	Learning Generative Models of Tissue Organization with Supervised GANs. , 2018, 2018, 682-690.		12
90	Learning the sequence of influenza A genome assembly during viral replication using point process models and fluorescence in situ hybridization. <i>PLoS Computational Biology</i> , 2019, 15, e1006199.	3.2	12

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91	Automated Interpretation of Protein Subcellular Location Patterns. International Review of Cytology, 2006, 249, 193-227.	6.2	10
92	Automated analysis of protein subcellular location in time series images. Bioinformatics, 2010, 26, 1630-1636.	4.1	10
93	Point process models for localization and interdependence of punctate cellular structures. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 633-643.	1.5	10
94	Automated estimation of microtubule model parameters from 3-D live cell microscopy images. , 2011, 2011, 1330-1333.		9
95	High-Content Analysis with Cellular and Tissue Systems Biology. , 2015, , 369-392.e7.		9
96	Systems Imaging of the Immune Synapse. Methods in Molecular Biology, 2017, 1584, 409-421.	0.9	9
97	A STACKED GRAPHICAL MODEL FOR ASSOCIATING SUB-IMAGES WITH SUB-CAPTIONS. , 2006, , .		9
98	Principles of Bioimage Informatics: Focus on Machine Learning of Cell Patterns. Lecture Notes in Computer Science, 2010, , 8-18.	1.3	8
99	Image-derived models of cell organization changes during differentiation and drug treatments. Molecular Biology of the Cell, 2020, 31, 655-666.	2.1	7
100	Transient protein accumulation at the center of the T cell antigen-presenting cell interface drives efficient IL-2 secretion. ELife, 2019, 8, .	6.0	7
101	Deciding when to stop: efficient experimentation to learn to predict drug-target interactions. BMC Bioinformatics, 2015, 16, 213.	2.6	6
102	CellOrganizer: Learning and Using Cell Geometries for Spatial Cell Simulations. Methods in Molecular Biology, 2019, 1945, 251-264.	0.9	6
103	Consistency and variation of protein subcellular location annotations. Proteins: Structure, Function and Bioinformatics, 2021, 89, 242-250.	2.6	5
104	Cell cycle dependence of protein subcellular location inferred from static, asynchronous images. , 2009, 2009, 1016-9.		4
105	Automated recognition of patterns characteristic of subcellular structures in fluorescence microscopy images. Cytometry, 1998, 33, 366-375.	1.8	4
106	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Journal of Computational Biology, 2011, 18, 1709-1722.	1.6	3
107	A method for characterizing phenotypic changes in highly variable cell populations and its application to high content screening of <i>Arabidopsis thaliana</i> protoplasts. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 326-335.	1.5	3
108	Flow Cytometric Analysis of Ligand Binding and Endocytosis. , 1989, , 363-376.		3

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109	Automated proteome-wide determination of subcellular location using high throughput microscopy. , 2008, 2008, 308-311.		2
110	Bioengineering and Imaging Research Opportunities Workshop V: A white paper on imaging and characterizing structure and function in native and engineered tissues. Medical Physics, 2008, 35, 3428-3435.	3.0	2
111	(3) The CellOrganizer project: An open source system to learn image-derived models of subcellular organization over time and space. , 2012, , .		2
112	Design Automation for Biological Models. , 2015, , .		2
113	Evaluation of categorical matrix completion algorithms: toward improved active learning for drug discovery. Bioinformatics, 2021, 37, 3538-3545.	4.1	2
114	Automated Interpretation of Subcellular Location Patterns from Three-Dimensional Confocal Microscopy. , 2006, , 818-828.		1
115	Determination of protein location diversity via analysis of immunohistochemical images from the Human Protein Atlas. , 2011, , .		1
116	Image-based spatiotemporal causality inference for protein signaling networks. Bioinformatics, 2017, 33, i217-i224.	4.1	1
117	Automated, Systematic Determination of Protein Subcellular Location using Fluorescence Microscopy. , 2007, 43, 263-276.		1
118	Location Proteomics. , 2007, , 196-214.		1
119	Integration of Heterogeneous Experimental Data Improves Global Map of Human Protein Complexes. , 2019, 2019, 144-153.		1
120	Identifying Subcellular Locations from Images of Unknown Resolution. Communications in Computer and Information Science, 2008, , 235-242.	0.5	1
121	Pattern Analysis Meets Cell Biology. Microscopy and Microanalysis, 1999, 5, 510-511.	0.4	0
122	Efficient Acquisition and Learning of Fluorescence Microscope Data Models. , 2007, , .		0
123	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Lecture Notes in Computer Science, 2011, , 204-221.	1.3	0
124	Deciding When to Stop: Efficient Experimentation to Learn to Predict Drug-Target Interactions (Extended Abstract). Lecture Notes in Computer Science, 2015, , 323-325.	1.3	0