Robert F Murphy

List of Publications by Year
in descending order

124 papers	5,575 citations	101384 36 h-index	95083 68 g-index
136 all docs	136 docs citations	136 times ranked	6048 citing authors

#	Article	IF	Citations
1	Consistency and variation of protein subcellular location annotations. Proteins: Structure, Function and Bioinformatics, 2021, 89, 242-250.	1.5	5
2	Evaluation of categorical matrix completion algorithms: toward improved active learning for drug discovery. Bioinformatics, 2021, 37, 3538-3545.	1.8	2
3	Learning complex subcellular distribution patterns of proteins via analysis of immunohistochemistry images. Bioinformatics, 2020, 36, 1908-1914.	1.8	14
4	Image-derived models of cell organization changes during differentiation and drug treatments. Molecular Biology of the Cell, 2020, 31, 655-666.	0.9	7
5	PD-1 suppresses the maintenance of cell couples between cytotoxic T cells and target tumor cells within the tumor. Science Signaling, 2020, 13, .	1.6	15
6	CellOrganizer: Learning and Using Cell Geometries for Spatial Cell Simulations. Methods in Molecular Biology, 2019, 1945, 251-264.	0.4	6
7	Learning the sequence of influenza A genome assembly during viral replication using point process models and fluorescence in situ hybridization. PLoS Computational Biology, 2019, 15, e1006199.	1.5	12
8	Evaluation of methods for generative modeling of cell and nuclear shape. Bioinformatics, 2019, 35, 2475-2485.	1.8	41
9	Integration of Heterogeneous Experimental Data Improves Global Map of Human Protein Complexes. , 2019, 2019, 144-153.		1
10	Transient protein accumulation at the center of the T cell antigen-presenting cell interface drives efficient IL-2 secretion. ELife, 2019, 8, .	2.8	7
11	Conserved non-AUG uORFs revealed by a novel regression analysis of ribosome profiling data. Genome Research, 2018, 28, 214-222.	2.4	93
12	Learning Generative Models of Tissue Organization with Supervised GANs. , 2018, 2018, 682-690.		12
13	Discrete cytosolic macromolecular <scp>BRAF</scp> complexes exhibit distinct activities and composition. EMBO Journal, 2017, 36, 646-663.	3.5	52
14	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.	1.1	3
15	Systems Imaging of the Immune Synapse. Methods in Molecular Biology, 2017, 1584, 409-421.	0.4	9
16	Image-based spatiotemporal causality inference for protein signaling networks. Bioinformatics, 2017, 33, i217-i224.	1.8	1
17	Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using a Weighted Ensemble of Trajectories. PLoS Computational Biology, 2016, 12, e1004611.	1.5	35
18	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.	1.1	10

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19	Computational spatiotemporal analysis identifies WAVE2 and cofilin as joint regulators of costimulation-mediated T cell actin dynamics. Science Signaling, 2016, 9, rs3.	1.6	24
20	Building cell models and simulations from microscope images. Methods, 2016, 96, 33-39.	1.9	26
21	Active machine learning-driven experimentation to determine compound effects on protein patterns. ELife, 2016, 5, e10047.	2.8	36
22	Image–based systems biology. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 459-461.	1.1	33
23	Automated Learning of Subcellular Variation among Punctate Protein Patterns and a Generative Model of Their Relation to Microtubules. PLoS Computational Biology, 2015, 11, e1004614.	1.5	27
24	Joint modeling of cell and nuclear shape variation. Molecular Biology of the Cell, 2015, 26, 4046-4056.	0.9	27
25	High-Content Analysis with Cellular and Tissue Systems Biology. , 2015, , 369-392.e7.		9
26	Deciding when to stop: efficient experimentation to learn to predict drug-target interactions. BMC Bioinformatics, 2015, 16, 213.	1.2	6
27	Design Automation for Biological Models. , 2015, , .		2
28	Deciding When to Stop: Efficient Experimentation to Learn to Predict Drug-Target Interactions (Extended Abstract). Lecture Notes in Computer Science, 2015, , 323-325.	1.0	0
29	Automated analysis of immunohistochemistry images identifies candidate location biomarkers for cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18249-18254.	3.3	34
30	Efficient discovery of responses of proteins to compounds using active learning. BMC Bioinformatics, 2014, 15, 143.	1.2	29
31	A new era in bioimage informatics. Bioinformatics, 2014, 30, 1353-1353.	1.8	15
32	The actin–driven spatiotemporal organization of T–cell signaling at the system scale. Immunological Reviews, 2013, 256, 133-147.	2.8	27
33	Immunofluorescence and fluorescent-protein tagging show high correlation for protein localization in mammalian cells. Nature Methods, 2013, 10, 315-323.	9.0	209
34	Determining the subcellular location of new proteins from microscope images using local features. Bioinformatics, 2013, 29, 2343-2349.	1.8	59
35	Efficient Modeling and Active Learning Discovery of Biological Responses. PLoS ONE, 2013, 8, e83996.	1.1	26
36	CellOrganizer: Image-Derived Models of Subcellular Organization and Protein Distribution. Methods in Cell Biology, 2012, 110, 179-193.	0.5	37

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37	(3) The CellOrganizer project: An open source system to learn image-derived models of subcellular organization over time and space. , 2012, , .		2
38	Estimating Microtubule Distributions from 2D Immunofluorescence Microscopy Images Reveals Differences among Human Cultured Cell Lines. PLoS ONE, 2012, 7, e50292.	1.1	20
39	Automated Analysis and Reannotation of Subcellular Locations in Confocal Images from the Human Protein Atlas. PLoS ONE, 2012, 7, e50514.	1.1	37
40	Biological imaging software tools. Nature Methods, 2012, 9, 697-710.	9.0	462
41	Toward the virtual cell: Automated approaches to building models of subcellular organization â€œlearnedâ€•from microscopy images. BioEssays, 2012, 34, 791-799.	1.2	32
42	An active role for machine learning in drug development. Nature Chemical Biology, 2011, 7, 327-330.	3.9	101
43	Imageâ€derived, threeâ€dimensional generative models of cellular organization. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2011, 79A, 383-391.	1.1	51
44	Determination of protein location diversity via analysis of immunohistochemical images from the Human Protein Atlas. , 2011, , .		1
45	Discriminative Motif Finding for Predicting Protein Subcellular Localization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 441-451.	1.9	32
46	Automated estimation of microtubule model parameters from 3-D live cell microscopy images. , 2011, 2011, 1330-1333.		9
47	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Journal of Computational Biology, 2011, 18, 1709-1722.	0.8	3
48	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Lecture Notes in Computer Science, 2011, , 204-221.	1.0	0
49	A generative model of microtubule distributions, and indirect estimation of its parameters from fluorescence microscopy images. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 457-466.	1.1	30
50	Communicating subcellular distributions. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2010, 77A, 686-692.	1.1	26
51	Structured literature image finder: Parsing text and figures in biomedical literature. Web Semantics, 2010, 8, 151-154.	2.2	14
52	Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. Bioinformatics, 2010, 26, i7-i12.	1.8	39
53	Determining the distribution of probes between different subcellular locations through automated unmixing of subcellular patterns. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2944-2949.	3.3	40
54	Principles of Bioimage Informatics: Focus on Machine Learning of Cell Patterns. Lecture Notes in Computer Science, 2010, , 8-18.	1.0	8

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55	Automated analysis of protein subcellular location in time series images. Bioinformatics, 2010, 26, 1630-1636.	1.8	10
56	Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature. Lecture Notes in Computer Science, 2010, , 23-32.	1.0	26
57	Automated Image Analysis for High-Content Screening and Analysis. Journal of Biomolecular Screening, 2010, 15, 726-734.	2.6	117
58	Instance-based generative biological shape modeling. , 2009, 5193141, 690-693.		15
59	Automated analysis of Human Protein Atlas immunofluorescence images. , 2009, 5193229, 1023-1026.		19
60	Nuclear segmentation in microscope cell images: A hand-segmented dataset and comparison of algorithms. , 2009, 5193098, 518-521.		138
61	Structured correspondence topic models for mining captioned figures in biological literature. , 2009, 2009, 39-48.		24
62	Detection of Protein–Protein Interactions Through Vesicle Targeting. Genetics, 2009, 182, 33-39.	1.2	13
63	Efficient framework for automated classification of subcellular patterns in budding yeast. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 934-940.	1.1	21
64	Cell cycle dependence of protein subcellular location inferred from static, asynchronous images. , 2009, 2009, 1016-9.		4
65	Intelligent Acquisition and Learning of Fluorescence Microscope Data Models. IEEE Transactions on Image Processing, 2009, 18, 2071-2084.	6.0	14
66	Location Proteomics: Systematic Determination of Protein Subcellular Location. Methods in Molecular Biology, 2009, 500, 313-332.	0.4	19
67	Deformation–based nuclear morphometry: Capturing nuclear shape variation in HeLa cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 341-350.	1.1	74
68	A Framework for the Automated Analysis of Subcellular Patterns in Human Protein Atlas Images. Journal of Proteome Research, 2008, 7, 2300-2308.	1.8	144
69	Automated proteome-wide determination of subcellular location using high throughput microscopy. , 2008, 2008, 308-311.		2
70	Deformation-based nonlinear dimension reduction: Applications to nuclear morphometry. , 2008, , .		13
71	Automated comparison of protein subcellular location patterns between images of normal and cancerous tissues. , 2008, 4540993, 304-307.		14
72	Improved recognition of figures containing fluorescence microscope images in online journal articles using graphical models. Bioinformatics, 2008, 24, 569-576.	1.8	23

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73	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.	1.6	2
74	Identifying Subcellular Locations from Images of Unknown Resolution. Communications in Computer and Information Science, 2008, , 235-242.	0.4	1
75	Automated image analysis of protein localization in budding yeast. Bioinformatics, 2007, 23, i66-i71.	1.8	70
76	Automated Subcellular Location Determination and High-Throughput Microscopy. Developmental Cell, 2007, 12, 7-16.	3.1	255
77	Efficient Acquisition and Learning of Fluorescence Microscope Data Models. , 2007, , .		0
78	Automated learning of generative models for subcellular location: Building blocks for systems biology. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2007, 71A, 978-990.	1.1	96
79	A multiresolution approach to automated classification of protein subcellular location images. BMC Bioinformatics, 2007, 8, 210.	1.2	101
80	Large-Scale Automated Analysis of Location Patterns in Randomly Tagged 3T3 Cells. Annals of Biomedical Engineering, 2007, 35, 1081-1087.	1.3	28
81	Automated, Systematic Determination of Protein Subcellular Location using Fluorescence Microscopy. , 2007, 43, 263-276.		1
82	Location Proteomics. , 2007, , 196-214.		1
83	A Novel Graphical Model Approach to Segmenting Cell Images. , 2006, , .		26
84	Putting proteins on the map. Nature Biotechnology, 2006, 24, 1223-1224.	9.4	38
85	Automated Interpretation of Subcellular Location Patterns from Three-Dimensional Confocal Microscopy. , 2006, , 818-828.		1
86	A graphical model approach to automated classification of protein subcellular location patterns in multi-cell images. BMC Bioinformatics, 2006, 7, 90.	1.2	23
87	Automated interpretation of subcellular patterns in fluorescence microscope images for location proteomics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2006, 69A, 631-640.	1.1	55
88	Automated Interpretation of Protein Subcellular Location Patterns. International Review of Cytology, 2006, 249, 193-227.	6.2	10
89	A STACKED GRAPHICAL MODEL FOR ASSOCIATING SUB-IMAGES WITH SUB-CAPTIONS. , 2006, , .		9
90	Location proteomics: a systems approach to subcellular location. Biochemical Society Transactions, 2005, 33, 535-538.	1.6	34

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91	Cytomics and location proteomics: Automated interpretation of subcellular patterns in fluorescence microscope images. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2005, 67A, 1-3.	1.1	23
92	Transferrin recycling and dextran transport to lysosomes is differentially affected by bafilomycin, nocodazole, and low temperature. Cell and Tissue Research, 2005, 320, 99-113.	1.5	123
93	Objective Clustering of Proteins Based on Subcellular Location Patterns. Journal of Biomedicine and Biotechnology, 2005, 2005, 87-95.	3.0	59
94	Characterization of the TGN exit signal of the human mannose 6-phosphate uncovering enzyme. Journal of Cell Science, 2005, 118, 2949-2956.	1.2	17
95	Opening of Size-Selective Pores in Endosomes during Human Rhinovirus Serotype 2 In Vivo Uncoating Monitored by Single-Organelle Flow Analysis. Journal of Virology, 2005, 79, 1008-1016.	1.5	56
96	Object type recognition for automated analysis of protein subcellular location. IEEE Transactions on Image Processing, 2005, 14, 1351-1359.	6.0	42
97	From quantitative microscopy to automated image understanding. Journal of Biomedical Optics, 2004, 9, 893.	1.4	101
98	Automated interpretation of subcellular patterns from immunofluorescence microscopy. Journal of Immunological Methods, 2004, 290, 93-105.	0.6	39
99	Automated Interpretation of Protein Subcellular Location Patterns: Implications for Early Cancer Detection and Assessment. Annals of the New York Academy of Sciences, 2004, 1020, 124-131.	1.8	22
100	Boosting accuracy of automated classification of fluorescence microscope images for location proteomics. BMC Bioinformatics, 2004, 5, 78.	1.2	118
101	Robust Numerical Features for Description and Classification of Subcellular Location Patterns in Fluorescence Microscope Images. Journal of Signal Processing Systems, 2003, 35, 311-321.	1.0	106
102	Feature reduction for improved recognition of subcellular location patterns in fluorescence microscope images. , 2003, , .		54
103	Location proteomics: building subcellular location trees from high-resolution 3D fluorescence microscope images of randomly tagged proteins. , 2003, 4962, 298.		49
104	Advances in molecular labeling, high throughput imaging and machine intelligence portend powerful functional cellular biochemistry tools. Journal of Cellular Biochemistry, 2002, 87, 194-210.	1.2	86
105	Objective Evaluation of Differences in Protein Subcellular Distribution. Traffic, 2002, 3, 61-65.	1.3	37
106	Mitotic Golgi is in a Dynamic Equilibrium Between Clustered and Free Vesicles Independent of the ER. Traffic, 2001, 2, 873-884.	1.3	52
107	Pattern Analysis Meets Cell Biology. Microscopy and Microanalysis, 1999, 5, 510-511.	0.2	0
108	Automated analysis of patterns in fluorescence-microscope images. Trends in Cell Biology, 1999, 9, 201-202.	3.6	25

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109	Toward Objective Selection of Representative Microscope Images. Biophysical Journal, 1999, 76, 2230-2237.	0.2	30
110	Automated recognition of patterns characteristic of subcellular structures in fluorescence microscopy images. Cytometry, 1998, 33, 366-375.	1.8	212
111	Primary cell cultures from murine kidney and heart differ in endosomal pH. Journal of Cellular Physiology, 1998, 176, 216-222.	2.0	52
112	Automated recognition of patterns characteristic of subcellular structures in fluorescence microscopy images. , 1998, 33, 366.		4
113	Effect of Bafilomycin A1 and Nocodazole on Endocytic Transport in HeLa Cells: Implications for Viral Uncoating and Infection. Journal of Virology, 1998, 72, 9645-9655.	1.5	291
114	Maturation models for endosome and lysosome biogenesis. Trends in Cell Biology, 1991, 1, 77-82.	3.6	169
115	Kinetics of hydrolysis of endocytosed substrates by mammalian cultured cells: Early introduction of lysosomal enzymes into the endocytic pathway. Journal of Cellular Physiology, 1990, 143, 110-117.	2.0	31
116	Chapter 16 Flow-Cytometric Analysis of Endocytic Compartments. Methods in Cell Biology, 1989, 31, 293-317.	0.5	29
117	Flow Cytometric Analysis of Ligand Binding and Endocytosis. , 1989, , 363-376.		3
118	Flow cytometric DNA analysis of Neuroblastoma and Ganglioneuroma. A 10-year retrospective study. Cancer, 1988, 62, 749-754.	2.0	110
119	Processing of Endocytosed Material. Advances in Molecular and Cell Biology, 1988, 2, 159-180.	0.1	22
120	Flow cytometric DNA analysis of adrenocortical tumors in children. Cancer, 1987, 59, 2059-2063.	2.0	42
121	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. Journal of Cellular Physiology, 1987, 131, 200-209.	2.0	132
122	Growth inhibition of 3T3 fibroblasts by lysosomotropic amines: Correlation with effects on intravesicular pH but not vacuolation. Journal of Cellular Physiology, 1986, 129, 65-70.	2.0	38
123	Testing models of the arrangement of DNA inside bacteriophage λ by crosslinking the packaged DNA. Journal of Molecular Biology, 1982, 159, 71-92.	2.0	35
124	Computer programs for analysis of nucleic acid hybridization, thermal denaturation, and gel electrophoresis data. Nucleic Acids Research, 1979, 6, 3911-3922.	6.5	36