Ulrike Korf

List of Publications by Year
in descending order

53 papers	1,895 citations	279798 23 h-index	265206 42 g-index
57 all docs	57 docs citations	57 times ranked	3305 citing authors

#	Article	IF	Citations
1	High-Throughput Profiling of Colorectal Cancer Liver Metastases Reveals Intra- and Inter-Patient Heterogeneity in the EGFR and WNT Pathways Associated with Clinical Outcome. Cancers, 2022, 14, 2084.	3.7	5
2	Disentangling ERBB Signaling in Breast Cancer Subtypes—A Model-Based Analysis. Cancers, 2022, 14, 2379.	3.7	4
3	Integrating proteomics into precision oncology. International Journal of Cancer, 2021, 148, 1438-1451.	5.1	15
4	Coordinated regulation of WNT/β-catenin, c-Met, and integrin signalling pathways by miR-193b controls triple negative breast cancer metastatic traits. BMC Cancer, 2021, 21, 1296.	2.6	4
5	Integrative analysis of multi-platform reverse-phase protein array data for the pharmacodynamic assessment of response to targeted therapies. Scientific Reports, 2020, 10, 21985.	3.3	9
6	Functional Proteomics of Breast Cancer Metabolism Identifies GLUL as Responder during Hypoxic Adaptation. Journal of Proteome Research, 2019, 18, 1352-1362.	3.7	9
7	Reconstruction of Different Modes of WNT Dependent Protein Networks from Time Series Protein Quantification. Studies in Health Technology and Informatics, 2019, 267, 175-180.	0.3	1
8	PI3K: A master regulator of brain metastasis-promoting macrophages/microglia. Glia, 2018, 66, 2438-2455.	4.9	59
9	Coordinated Pulses of mRNA and of Protein Translation or Degradation Produce EGF-Induced Protein Bursts. Cell Reports, 2017, 18, 3129-3142.	6.4	19
10	Liquid-phase electron microscopy of molecular drug response in breast cancer cells reveals irresponsive cell subpopulations related to lack of HER2 homodimers. Molecular Biology of the Cell, 2017, 28, 3193-3202.	2.1	19
11	Proteomic profiling of breast cancer metabolism identifies SHMT2 and ASCT2 as prognostic factors. Breast Cancer Research, 2017, 19, 112.	5.0	75
12	Role of Heterogeneity in Cancer Cells Examined through Quantitative Analysis of Single HER2 Protein Distribution and Activation Status. Microscopy and Microanalysis, 2016, 22, 26-27.	0.4	0
13	Reconstruction of Protein Networks Using Reverse-Phase Protein Array Data. Methods in Molecular Biology, 2016, 1362, 227-246.	0.9	1
14	Multi-omic profiles of human non-alcoholic fatty liver disease tissue highlight heterogenic phenotypes. Scientific Data, 2015, 2, 150068.	5.3	48
15	Visualizing the Distribution and Stoichiometry of Growth Factor Receptors in Intact Cells in Liquid Phase with Correlative Fluorescence and Scanning Transmission Electron Microscopy. Microscopy and Microanalysis, 2015, 21, 213-214.	0.4	0
16	Analysis of Reverse Phase Protein Array Data: From Experimental Design towards Targeted Biomarker Discovery. Microarrays (Basel, Switzerland), 2015, 4, 520-539.	1.4	14
17	Dynamic Bayesian Network Modeling of the Interplay between EGFR and Hedgehog Signaling. PLoS ONE, 2015, 10, e0142646.	2.5	15
18	Local variations of HER2 dimerization in breast cancer cells discovered by correlative fluorescence and liquid electron microscopy. Science Advances, 2015, 1, e1500165.	10.3	90

#	Article	IF	Citations
19	Subtyping of breast cancer using reverse phase protein arrays. Expert Review of Proteomics, 2014, 11, 757-770.	3.0	17
20	Boolean ErbB network reconstructions and perturbation simulations reveal individual drug response in different breast cancer cell lines. BMC Systems Biology, 2014, 8, 75.	3.0	36
21	Realizing the Promise of Reverse Phase Protein Arrays for Clinical, Translational, and Basic Research: A Workshop Report. Molecular and Cellular Proteomics, 2014, 13, 1625-1643.	3.8	152
22	Activation of AMP-activated protein kinase sensitizes lung cancer cells and H1299 xenografts to erlotinib. Lung Cancer, 2014, 86, 151-157.	2.0	12
23	Evaluation of reverse phase protein array (RPPA)-based pathway-activation profiling in 84 non-small cell lung cancer (NSCLC) cell lines as platform for cancer proteomics and biomarker discovery. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 950-959.	2.3	44
24	Reverse phase protein array based tumor profiling identifies a biomarker signature for risk classification of hormone receptor-positive breast cancer. Translational Proteomics, 2014, 2, 52-59.	1.2	19
25	Unbiased RNAi screen for hepcidin regulators links hepcidin suppression to proliferative Ras/RAF and nutrient-dependent mTOR signaling. Blood, 2014, 123, 1574-1585.	1.4	62
26	RPPanalyzer Toolbox: An improved R package for analysis of reverse phase protein array data. BioTechniques, 2014, 57, 125-135.	1.8	36
27	Synergism between Hedgehog-GLI and EGFR Signaling in Hedgehog-Responsive Human Medulloblastoma Cells Induces Downregulation of Canonical Hedgehog-Target Genes and Stabilized Expression of GLI1. PLoS ONE, 2013, 8, e65403.	2.5	72
28	A Systems Biology Approach to Deciphering the Etiology of Steatosis Employing Patient-Derived Dermal Fibroblasts and iPS Cells. Frontiers in Physiology, 2012, 3, 339.	2.8	22
29	Global microRNA level regulation of EGFR–driven cell–cycle protein network in breast cancer. Molecular Systems Biology, 2012, 8, 570.	7.2	184
30	uPA and PAI-1-Related Signaling Pathways Differ between Primary Breast Cancers and Lymph Node Metastases. Translational Oncology, 2012, 5, 98-IN3.	3.7	29
31	Peroxiredoxins 3 and 4 Are Overexpressed in Prostate Cancer Tissue and Affect the Proliferation of Prostate Cancer Cells in Vitro. Journal of Proteome Research, 2012, 11, 2452-2466.	3.7	46
32	Triplex DNA-binding proteins are associated with clinical outcomes revealed by proteomic measurements in patients with colorectal cancer. Molecular Cancer, 2012, 11, 38.	19.2	25
33	Quantitative Analysis of Phosphoproteins Using Microspot Immunoassays. Methods in Molecular Biology, 2011, 785, 191-201.	0.9	1
34	Utilization of RNAi to Validate Antibodies for Reverse Phase Protein Arrays. Methods in Molecular Biology, 2011, 785, 45-54.	0.9	3
35	Antibody-Mediated Signal Amplification for Reverse Phase Protein Array-Based Protein Quantification. Methods in Molecular Biology, 2011, 785, 55-64.	0.9	5
36	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. Proteome Science, 2010, 8, 36.	1.7	17

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37	QuantProReloaded: quantitative analysis of microspot immunoassays. Bioinformatics, 2010, 26, 2480-2481.	4.1	5
38	RPPanalyzer: Analysis of reverse-phase protein array data. Bioinformatics, 2010, 26, 2202-2203.	4.1	63
39	Dynamic deterministic effects propagation networks: learning signalling pathways from longitudinal protein array data. Bioinformatics, 2010, 26, i596-i602.	4.1	28
40	RNAi-based validation of antibodies for reverse phase protein arrays. Proteome Science, 2010, 8, 69.	1.7	18
41	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. BMC Systems Biology, 2009, 3, 1.	3.0	242
42	Reverse‐phase protein arrays for application‐orientated cancer research. Proteomics - Clinical Applications, 2009, 3, 1140-1150.	1.6	6
43	Contact spotting of protein microarrays coupled with spike-in of normalizer protein permits time-resolved analysis of ERBB receptor signaling. Proteomics, 2008, 8, 1586-1594.	2.2	13
44	Quantitative protein microarrays for time‐resolved measurements of protein phosphorylation. Proteomics, 2008, 8, 4603-4612.	2.2	30
45	Automated production of recombinant human proteins as resource for proteome research. Proteome Science, 2008, 6, 4.	1.7	20
46	Antibody Microarrays as an Experimental Platform for the Analysis of Signal Transduction Networks. Advances in Biochemical Engineering/Biotechnology, 2008, 110, 153-175.	1.1	7
47	Infrared-based protein detection arrays for quantitative proteomics. Expert Opinion on Drug Discovery, 2008, 3, 273-283.	5.0	2
48	Combinatorial RNAi for quantitative protein network analysis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6579-6584.	7.1	55
49	Infrared-based protein detection arrays for quantitative proteomics. Proteomics, 2007, 7, 558-564.	2.2	77
50	Large-scale protein expression for proteome research. Proteomics, 2005, 5, 3571-3580.	2.2	53
51	Systematic comparison of surface coatings for protein microarrays. Proteomics, 2005, 5, 4705-4712.	2.2	42
52	Protein microarrays as a discovery tool for studying protein–protein interactions. Expert Review of Proteomics, 2005, 2, 13-26.	3.0	20
53	From ORFeome to Biology: A Functional Genomics Pipeline. Genome Research, 2004, 14, 2136-2144.	5.5	44