Ashraf Dallol

List of Publications by Year
in descending order

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70 papers	4,356 citations	136950 32 h-index	106344 65 g-index
72 all docs	72 docs citations	72 times ranked	5726 citing authors

#	Article	IF	Citations
1	Prognostic value of TP53 expression and MGMT methylation in glioblastoma patients treated with temozolomide combined with other chemotherapies. Journal of Neuro-Oncology, 2021, 152, 541-549.	2.9	1
2	A novel DOK7 mutation causing congenital myasthenic syndrome with limb-girdle weakness: case series of three family members. Heliyon, 2021, 7, e06869.	3.2	6
3	Klotho promoter methylation status and its prognostic value in ovarian cancer. Molecular and Clinical Oncology, 2021, 15, 181.	1.0	2
4	Leptin Protein Expression and Promoter Methylation in Ovarian Cancer: A Strong Prognostic Value with Theranostic Promises. International Journal of Molecular Sciences, 2021, 22, 12872.	4.1	8
5	Molecular characterisation in tongue squamous cell carcinoma reveals key variants potentially linked to clinical outcomes. Cancer Biomarkers, 2020, 28, 213-220.	1.7	4
6	The Effect Sizes of PPARÎ³ rs1801282, FTO rs9939609, and MC4R rs2229616 Variants on Type 2 Diabetes Mellitus Risk among the Western Saudi Population: A Cross-Sectional Prospective Study. Genes, 2020, 11, 98.	2.4	17
7	Integration of Transcriptome and Metabolome Provides Unique Insights to Pathways Associated With Obese Breast Cancer Patients. Frontiers in Oncology, 2020, 10, 804.	2.8	36
8	Overlapping variants in the blood, tissues and cell lines for patients with intracranial meningiomas are predominant in stem cell-related genes. Heliyon, 2020, 6, e05632.	3.2	4
9	The prognostic impact of GSTM1/GSTP1 genetic variants in bladder Cancer. BMC Cancer, 2019, 19, 991.	2.6	12
10	MC4R variants rs12970134 and rs17782313 are associated with obese polycystic ovary syndrome patients in the Western region of Saudi Arabia. BMC Medical Genetics, 2019, 20, 144.	2.1	13
11	SLC22A1 And ATM Genes Polymorphisms Are Associated With The Risk Of Type 2 Diabetes Mellitus In Western Saudi Arabia: A Case-Control Study . The Application of Clinical Genetics, 2019, Volume 12, 213-219.	3.0	11
12	Ontology-based prediction of cancer driver genes. Scientific Reports, 2019, 9, 17405.	3.3	16
13	Membranous or Cytoplasmic HER2 Expression in Colorectal Carcinoma: Evaluation of Prognostic Value Using Both IHC & BDISH. Cancer Investigation, 2018, 36, 129-140.	1.3	6
14	Prognostic potential of KLOTHO and SFRP1 promoter methylation in head and neck squamous cell carcinoma. Journal of Applied Genetics, 2017, 58, 459-465.	1.9	9
15	Comprehensive molecular biomarker identification in breast cancer brain metastases. Journal of Translational Medicine, 2017, 15, 269.	4.4	80
16	Derivation and differentiation of bone marrow mesenchymal stem cells from osteoarthritis patients. Tissue Engineering and Regenerative Medicine, 2016, 13, 732-739.	3.7	7
17	Utilization of amplicon-based targeted sequencing panel for the massively parallel sequencing of sporadic hearing impairment patients from Saudi Arabia. BMC Medical Genetics, 2016, 17, 67.	2.1	11
18	Clinical significance of frequent somatic mutations detected by high-throughput targeted sequencing in archived colorectal cancer samples. Journal of Translational Medicine, 2016, 14, 118.	4.4	33

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19	Prognostic value of HER2 status in bladder transitional cell carcinoma revealed by both IHC and BDISH techniques. BMC Cancer, 2016, 16, 653.	2.6	36
20	Identification of novel genetic variations affecting osteoarthritis patients. BMC Medical Genetics, 2016, 17, 68.	2.1	18
21	Low expression of leptin and its association with breast cancer: A transcriptomic study. Oncology Reports, 2016, 36, 43-48.	2.6	17
22	Detection of Î²-Thalassemia Mutations Using TaqMan Single Nucleotide Polymorphism Genotyping Assays. Genetic Testing and Molecular Biomarkers, 2016, 20, 154-157.	0.7	1
23	Predictionof Anti-Diabetic Drugs as Dual Inhibitors Against Acetylcholinesterase and Beta-Secretase: A Neuroinformatics Study. CNS and Neurological Disorders - Drug Targets, 2016, 15, 1216-1221.	1.4	7
24	Enhancement of Pathologist's Routine Practice: Reuse of DNA Extracted from Immunostained Formalin-fixed Paraffin-embedded (FFPE) Slides in Downstream Molecular Analysis of Cancer. Cancer Genomics and Proteomics, 2016, 13, 399-406.	2.0	3
25	Characterization of familial breast cancer in Saudi Arabia. BMC Genomics, 2015, 16, S3.	2.8	15
26	Transcriptomics profiling study of breast cancer from Kingdom of Saudi Arabia revealed altered expression of Adiponectin and Fatty Acid Binding Protein4: Is lipid metabolism associated with breast cancer?. BMC Genomics, 2015, 16, S11.	2.8	34
27	Frequent methylation of the KLOTHO gene and overexpression of the FGFR4 receptor in invasive ductal carcinoma of the breast. Tumor Biology, 2015, 36, 9677-9683.	1.8	25
28	Exome Sequencing of Normal and Isogenic Transformed Human Colonic Epithelial Cells (HCECs) Reveals Novel Genes Potentially Involved in the Early Stages of Colorectal Tumorigenesis. BMC Genomics, 2015, 16, S8.	2.8	24
29	Individualized medicine enabled by genomics in Saudi Arabia. BMC Medical Genomics, 2015, 8, S3.	1.5	40
30	High fibroblast growth factor 19 (FGF19) expression predicts worse prognosis in invasive ductal carcinoma of breast. Tumor Biology, 2014, 35, 2817-2824.	1.8	29
31	Detection of rare single nucleotide variants affecting genes in the DNA repair pathways in hereditary breast cancer. BMC Genomics, 2014, 15, P20.	2.8	1
32	Identification of frequent MTNR1B methylation in breast cancer following the application of high-throughput methylome analysis. BMC Genomics, 2014, 15, P44.	2.8	4
33	Expression of matrix metalloproteinases (MMPs) in primary human breast cancer: MMP-9 as a potential biomarker for cancer invasion and metastasis. Anticancer Research, 2014, 34, 1355-66.	1.1	129
34	Identification of a novel SBF2 missense mutation associated with a rare case of thrombocytopenia using whole-exome sequencing. Journal of Thrombosis and Thrombolysis, 2013, 36, 501-506.	2.1	13
35	Functional epigenetic approach identifies frequently methylated genes in Ewing sarcoma. Epigenetics, 2013, 8, 1198-1204.	2.7	38
36	RASSF2methylation is a strong prognostic marker in younger age patients with Ewing sarcoma. Epigenetics, 2013, 8, 893-898.	2.7	27

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37	Methylation of the Polycomb Group Target Genes Is a Possible Biomarker for Favorable Prognosis in Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2069-2075.	2.5	24
38	Five novel glucose-6-phosphate dehydrogenase deficiency haplotypes correlating with disease severity. Journal of Translational Medicine, 2012, 10, 199.	4.4	12
39	Personalized medicine: a patient - centered paradigm. Journal of Translational Medicine, 2011, 9, 206.	4.4	21
40	Analysis of DNA Methylation in FFPE Tissues Using the MethyLight Technology. Methods in Molecular Biology, 2011, 724, 191-204.	0.9	21
41	RASSF1A methylation is predictive of poor prognosis in female breast cancer in a background of overall low methylation frequency. Anticancer Research, 2011, 31, 2975-81.	1.1	26
42	The neuronal repellent SLIT2 is a target for repression by EZH2 in prostate cancer. Oncogene, 2010, 29, 5370-5380.	5.9	75
43	A Genome-wide screen identifies frequently methylated genes in haematological and epithelial cancers. Molecular Cancer, 2010, 9, 44.	19.2	92
44	Identification of 5 novel genes methylated in breast and other epithelial cancers. Molecular Cancer, 2010, 9, 51.	19.2	83
45	Spectrum of GJB2 Mutations in a Cohort of Nonsyndromic Hearing Loss Cases from the Kingdom of Saudi Arabia. Genetic Testing and Molecular Biomarkers, 2010, 14, 79-83.	0.7	24
46	Abstract 165: MIRA (methylated CpG island recovery assay) assay identifies frequently methylated genes in breast cancer. , 2010, , .		0
47	Frequent epigenetic inactivation of the SLIT2 gene in chronic and acute lymphocytic leukemia. Epigenetics, 2009, 4, 265-269.	2.7	52
48	When RASSF1A RAN into tumor suppression: Ran GTPase is a RASSF1A effector involved in controlling microtubule organization. Cell Cycle, 2009, 8, 3796-3797.	2.6	4
49	RAN GTPase Is a RASSF1A Effector Involved in Controlling Microtubule Organization. Current Biology, 2009, 19, 1227-1232.	3.9	42
50	RASSF2 associates with and stabilizes the proapoptotic kinase MST2. Oncogene, 2009, 28, 2988-2998.	5.9	77
51	Epigenetic regulation of the ras effector/tumour suppressor RASSF2 in breast and lung cancer. Oncogene, 2008, 27, 1805-1811.	5.9	54
52	Raf kinase inhibitor protein: mechanism of loss of expression and association with genomic instability. Journal of Clinical Pathology, 2008, 61, 524-529.	2.0	68
53	Depletion of the Ras Association Domain Family 1, Isoform Aâ€“Associated Novel Microtubule-Associated Protein, C19ORF5/MAP1S, Causes Mitotic Abnormalities. Cancer Research, 2007, 67, 492-500.	0.9	42
54	The RASSF1A Tumor Suppressor Activates Bax via MOAP-1. Journal of Biological Chemistry, 2006, 281, 4557-4563.	3.4	122

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55	Involvement of the RASSF1A Tumor Suppressor Gene in Controlling Cell Migration. Cancer Research, 2005, 65, 7653-7659.	0.9	78
56	Epigenetic Disruption of the SLIT-ROBO Interactions in Human Cancer. , 2005, , 191-214.		3
57	A Role for the RASSF1A Tumor Suppressor in the Regulation of Tubulin Polymerization and Genomic Stability. Cancer Research, 2004, 64, 4244-4250.	0.9	139
58	RASSF1A Interacts with Microtubule-Associated Proteins and Modulates Microtubule Dynamics. Cancer Research, 2004, 64, 4112-4116.	0.9	127
59	SLIT2 promoter methylation analysis in neuroblastoma, Wilms' tumour and renal cell carcinoma. British Journal of Cancer, 2004, 90, 515-521.	6.4	51
60	Identification of the E1A-Regulated Transcription Factor p120E4F as an Interacting Partner of the RASSF1A Candidate Tumor Suppressor Gene. Cancer Research, 2004, 64, 102-107.	0.9	67
61	NORE1A, a homologue of RASSF1A tumour suppressor gene is inactivated in human cancers. Oncogene, 2003, 22, 947-954.	5.9	129
62	Epigenetic inactivation of the candidate 3p21.3 suppressor gene BLU in human cancers. Oncogene, 2003, 22, 1580-1588.	5.9	98
63	Frequent epigenetic inactivation of the SLIT2 gene in gliomas. Oncogene, 2003, 22, 4611-4616.	5.9	125
64	SLIT2 axon guidance molecule is frequently inactivated in colorectal cancer and suppresses growth of colorectal carcinoma cells. Cancer Research, 2003, 63, 1054-8.	0.9	107
65	Frequent 3p allele loss and epigenetic inactivation of the RASSF1A tumour suppressor gene from region 3p21.3 in head and neck squamous cell carcinoma. European Journal of Cancer, 2002, 38, 1585-1592.	2.8	86
66	Tumour specific promoter region methylation of the human homologue of the Drosophila Roundabout gene DUTT1 (ROBO1) in human cancers. Oncogene, 2002, 21, 3020-3028.	5.9	106
67	SLIT2, a human homologue of the Drosophila Slit2 gene, has tumor suppressor activity and is frequently inactivated in lung and breast cancers. Cancer Research, 2002, 62, 5874-80.	0.9	173
68	Gene Mutations in the Succinate Dehydrogenase Subunit SDHB Cause Susceptibility to Familial Pheochromocytoma and to Familial Paraganglioma. American Journal of Human Genetics, 2001, 69, 49-54.	6.2	1,021
69	Methylation associated inactivation of RASSF1A from region 3p21.3 in lung, breast and ovarian tumours. Oncogene, 2001, 20, 1509-1518.	5.9	341
70	RASSF1A promoter region CpG island hypermethylation in phaeochromocytomas and neuroblastoma tumours. Oncogene, 2001, 20, 7573-7577.	5.9	127