Brain Related?	Title	Author	Journal/Year	PubMed ID
Directly related	Soluble epoxide inhibition is protective against cerebral ischemia via vascular and neural protection.	Simpkins AN et al.	Am J Pathol. 2009	PMID:19435785
Directly related	Genomic deletions correlate with underexpression of novel candidate genes at six loci in pediatric pilocytic astrocytoma.	Potter N et al.	Neoplasia. 2008	PMID:18670637
	A genetic association analysis of cognitive ability and cognitive ageing using 325 markers for 109 genes associated with oxidative stress			
Directly related	or cognition.	Harris SE et al.	BMC Genet. 2007	PMID:17601350
Directly related	The commonality of protein interaction networks determined in neurodegenerative disorders (NDDs).	Limviphuvadh V et al.	Bioinformatics. 2007	PMID:17553855
Directly related	Adaptation of energy metabolism in breast cancer brain metastases.	Chen El et al.	Cancer Res. 2007	PMID:17308085
Directly related	Biomarker discovery: a proteomic approach for brain cancer profiling.	Khalil AA. et al.	Cancer Sci. 2007	PMID:17233837
Directly related	IFN-beta down-regulates the expression of DNA repair gene MGMT and sensitizes resistant glioma cells to temozolomide.	Natsume A et al.	Cancer Res. 2005	PMID:16140920
Directly related	Gene regulation and DNA damage in the ageing human brain.	Lu T et al.	Nature. 2004	PMID:15190254
Directly related	Incipient Alzheimer's disease: microarray correlation analyses reveal major transcriptional and tumor suppressor responses.	Blalock EM et al.	Proc Natl Acad Sci U S A. 2004	
Directly related	Genome-wide gene expression profiles of the developing mouse hippocampus.	Mody M et al.	Proc Natl Acad Sci U S A. 2001	
Indirectly related	Integrative analysis reveals the direct and indirect interactions between DNA copy number aberrations and gene expression changes.	Lee H et al.	Bioinformatics. 2008	PMID:18263644
Indirectly related	Transcriptional and phenotypic comparisons of Ppara knockout and siRNA knockdown mice.	De Souza AT et al.	Nucleic Acids Res. 2006	PMID:16945951
Indirectly related	Systematic identification of human mitochondrial disease genes through integrative genomics.	Calvo S et al.	Nat Genet. 2006	PMID:16582907
Indirectly related	Adaptation and increased susceptibility to infection associated with constitutive expression of misfolded SP-C.	Bridges JP et al.	J Cell Biol. 2006	PMID:16449190
manectly related	Differentiation stage-dependent preferred uptake of basolateral (systemic) glutamine into Caco-2 cells results in its accumulation in	bridges in et al.	J CCII BIOI. 2000	110110.10443130
Indirectly related	proteins with a role in cell-cell interaction.	Lenaerts K et al.	FEBS J. 2005	PMID:15978041
manectly related	Analysis of double-stranded RNA-induced apoptosis pathways using interferon-response noninducible small interfering RNA expression		1255. 2005	111111111111111111111111111111111111111
Indirectly related	vector library.	Matsumoto S et al.	J Biol Chem. 2005	PMID:15845550
Indirectly related	A transcriptional profile of aging in the human kidney.	Rodwell GE et al.	PLoS Biol. 2004	PMID:15562319
Indirectly related	Functional gene expression analysis of clonal plasma cells identifies a unique molecular profile for light chain amyloidosis.	Abraham RS et al.	Blood. 2005	PMID:15388584
Indirectly related	Microarray analysis of differentiation-specific gene expression during 3T3-L1 adipogenesis.	Burton GR et al.	Gene. 2004	PMID:15033539
Indirectly related	Identification of the apoptosis activation cascade induced in mammary carcinomas by energy restriction.	Thompson HJ et al.	Cancer Res. 2004	PMID:14973070
Indirectly related	Stemness": transcriptional profiling of embryonic and adult stem cells."	Ramalho-Santos M et al.		PMID:12228720
Indirectly related	Systematic screen for human disease genes in yeast.	Steinmetz LM et al.	Nat Genet. 2002	PMID:12134146
Indirectly related	Influences of aging and caloric restriction on the transcriptional profile of skeletal muscle from rhesus monkeys.	Kayo T et al.	Proc Natl Acad Sci U S A. 2001	
Liver	Genomic and proteomic analysis reveals a threshold level of MYC required for tumor maintenance.	Shachaf CM et al.	Cancer Res. 2008	PMID:18593912
2.70.	Epigenetics of gene expression in human hepatoma cells: expression profiling the response to inhibition of DNA methylation and	ondendi em ec an	Carreer riest 2000	111112110333311
Liver	histone deacetylation.	Dannenberg LO et al.	BMC Genomics. 2006	PMID:16854234
LIVEI	Integrating time-course microarray gene expression profiles with cytotoxicity for identification of biomarkers in primary rat hepatocyte:		Divic denomics. 2000	111111111111111111111111111111111111111
Liver	exposed to cadmium.	Tan Y et al.	Bioinformatics. 2006	PMID:16249259
	Integrated analysis of DNA methylation and gene expression reveals specific signaling pathways associated with platinum resistance in			
Unrelated cancer	ovarian cancer.	Li M et al.	BMC Med Genomics. 2009	PMID:19505326
Unrelated cancer	Genetic variants in apoptosis and immunoregulation-related genes are associated with risk of chronic lymphocytic leukemia.	Enjuanes A et al.	Cancer Res. 2008	PMID:19074885
Unrelated cancer	Evolutionary origins of human apoptosis and genome-stability gene networks.	Castro MA et al.	Nucleic Acids Res. 2008	PMID:18832373
Unrelated cancer	Ganoderma lucidum polysaccharides in human monocytic leukemia cells: from gene expression to network construction.	Cheng KC et al.	BMC Genomics. 2007	PMID:17996095
	Comparative analysis of genes regulated in acute myelomonocytic leukemia with and without inv(16)(p13a22) using microarray			
Unrelated cancer	techniques, real-time PCR, immunohistochemistry, and flow cytometry immunophenotyping.	Sun X et al.	Mod Pathol. 2007	PMID:17571080
Unrelated cancer	Analysis of gene expression identifies PLAB as a mediator of the apoptotic activity of fenretinide in human ovarian cancer cells.	Appierto V et al.	Oncogene. 2007	PMID:17213814
Unrelated cancer	The expression of FHIT, PCNA and EGFR in benign and malignant breast lesions.	Terry G et al.	Br J Cancer. 2007	PMID:17164758
Unrelated cancer	Identification of differentially expressed genes in cutaneous squamous cell carcinoma by microarray expression profiling.	Nindl I et al.	Mol Cancer. 2006	PMID:16893473
	Progress towards in vivo use of siRNAs.	Behlke MA. et al.	Mol Ther. 2006	PMID:16481219
	Global gene expression in human myocardium-oligonucleotide microarray analysis of regional diversity and transcriptional regulation in		2000	
Unrelated non-cancer		Kaab S et al.	J Mol Med (Berl). 2004	PMID:15103417
z zatea non cancer	······································		zz. mea (Ben). 200 /	