What is circAD?

CircAD (circRNAs associated with diseases) is a comprehensive, manually curated resource for dysregulated circRNAs in disease. This database provides the information including source PMID, genome locus, gene name, method of experimental validation, fold change and significance. In exception to other databases, we have also included the primer details for respective circRNAs available in the publication. For cases where primer details were not available, we have included suggested primers for the circRNAs. CircAD contains 930 circRNAs annotations including 850 circRNAs from human, 71 entries from mouse, 24 from rat and 4 from chicken.

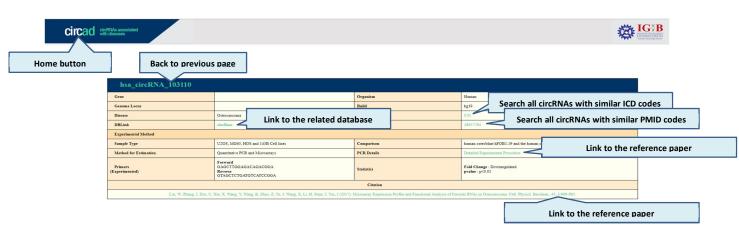
Home page



Search result page



Detailed circRNA information



Suggested primer page





hsa_circ_0000140/hsa_circ_002059										
Gene	KIAA0907	Organism	Human							
Genome Locus	chr1:155891165-155895634:-	Build	hg19							
Disease	Gastric cancer	ICD-10	C16.0							
DBLink	circBase	PMID	25689795							
Experimental Method										
Sample Type	Tissues	Comparison	101 paired gastric cancer tissues and adjacent nontumorous tissues from surgical gastric cancer patients and 36 paired plas a samples from preoperative and postoperative gastric cancer patients							
Method for Estimation	Quantitative PCR and Microarrays	PCR Details	Detailed Experimental Procedure							
Primers (Predicted)	Suggested Primers Link to the predi	cted primers	Fold Change: Downregulated pvalue: p<0.05							
Citation										
Li, P, Chen, S, Chen, H, Mo, X, Li, T, Shao, Y, Xiao, B, Oso, J (2015). Using circular RNA as a novel type of biomarder in the screening of gastric cancer. Clin. Clinn. Acta, 444:132-6.										

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	Locus:			chr1:155891165-155895634						
Product Size	Left Primers	Right Primers		Right GC	Left Tm	Right Tm	Left Position	Right Position		Right Size
233	AGGCTGGTCTCAAACTCCTG	CCTACCTCCACCTCCCAAAG	55	60	59.31	59.088	69	301	20	20
185	CCAGCTGATAGTGGGCAAC	AGCCTGGTCTCGAATTCCTA	57.895	50	58.214	57.839	152	336	19	20
120	CCGTGCCCAGCTGATAGT	ATGAGCCACTATGCCAGCC	61.111	57.895	59.097	59.85	146	265	18	19
148	CCTCGGCCTTCCAAAGTG	GCCAGCCCGTATTCTATATTCC	61.111	50	58.013	58.467	106	253	18	22
226	CGGCCTTCCAAAGTGCTG	CCTGGTCTCGAATTCCTAAGC	61.111	52.381	59.043	58.172	109	334	18	21
170	CTCGTGATCCACCTGCCTC	CCACTATGCCAGCCCGTAT	63.158	57.895	59.857	59.245	91	260	19	19
173	CTGACCTCGTGATCCACCTG	ACTATGCCAGCCCGTATTCT	60	50	59.826	58.575	86	258	20	20
279	GTCTCAAACTCCTGACCTCG	GTCTCACCATGTTTCTCAGCC	55	52.381	57.644	58.92	75	353	20	21
146	GTGGGCAACTCTTTTCTGGG	AAACTGCCTACCTCCACCTC	55	55	59.038	59.015	162	307	20	20
192	TCAAACTCCTGACCTCGTGA	AGTCATGAGCCACTATGCCA	50	50	58.3	58.793	78	269	20	20
233	TTGGTCAGGCTGGTCTCAAA	TCCACCTCCCAAAGTGCTAG	50	55	59.157	59.016	63	295	20	20