

Table S1: CircRNA-related databases and their useful functions

Databases	Year	Function	Website
RegRNA 2.0	2013	Predict miRNA-circRNA interactions	http://regrna2.mbc.nctu.edu.tw
Circ2Traits	2013	Collect disease-associated circRNAs	http://gyanxet-beta.com/circdb/
circBase	2014	Provide gene description, genomic position of circRNAs	http://www.circbase.org
circRNABase	2014	Predict miRNA-circRNA interactions	http://starbase.sysu.edu.cn/mirCircRNA.php
circinteractome	2016	Predict miRNA-circRNA interactions; Design junction-spanning primers of circRNAs; Design siRNAs for circRNA silencing; Identify potential internal ribosomal entry sites (IRES)	http://circinteractome.nia.nih.gov
CircNet	2016	Provide tissue-specific circRNA expression profiles; Provide circRNA-miRNA-gene regulatory networks	http://circnet.mbc.nctu.edu.tw/
deepbase v2.0	2016	Predict protein-circRNA co-expression networks	http://biocenter.sysu.edu.cn/deepBase/
circRNADb	2016	Predict protein-coding function of circRNAs	http://reprod.njmu.edu.cn/circrnadb
CSCD	2018	Predict the microRNA response element sites of circRNAs; Predict RNA binding protein sites of circRNAs; Predict potential open reading frames of circRNAs	http://gb.whu.edu.cn/CSCD
circIncRNAet	2018	Analyze expression profiles, co-expression networks and pathways, and molecular interactomes of circRNAs according to user-defined criteria.	http://app.cgu.edu.tw/circInc/