|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **Table S3: The fifty predicted target genes for hsa-miR-622 in miRDB** | | | | | | | **Target Rank** | **Target Score** | | **miRNA Name** | **Gene Symbol** | **Gene Description** | | 1 | 99 | hsa-miR-622 | | [DCUN1D1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=54165) | DCN1, defective in cullin neddylation 1, domain containing 1 | | 2 | 99 | hsa-miR-622 | | [INSIG2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=51141) | insulin induced gene 2 | | 3 | 98 | hsa-miR-622 | | [TXLNG](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=55787) | taxilin gamma | | 4 | 97 | hsa-miR-622 | | [NFYA](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=4800) | nuclear transcription factor Y, alpha | | 5 | 96 | hsa-miR-622 | | [APPL1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=26060) | adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 | | 6 | 96 | hsa-miR-622 | | [MIER1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=57708) | mesoderm induction early response 1, transcriptional regulator | | 7 | 96 | hsa-miR-622 | | [VMA21](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=203547) | VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) | | 8 | 95 | hsa-miR-622 | | [TOR1AIP2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=163590) | torsin A interacting protein 2 | | 9 | 95 | hsa-miR-622 | | [SRSF1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=6426) | serine/arginine-rich splicing factor 1 | | 10 | 94 | hsa-miR-622 | | [DYRK2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=8445) | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 | | 11 | 94 | hsa-miR-622 | | [SCN1A](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=6323) | sodium channel, voltage-gated, type I, alpha subunit | | 12 | 94 | hsa-miR-622 | | [SERAC1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=84947) | serine active site containing 1 | | 13 | 93 | hsa-miR-622 | | [VIPAS39](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=63894) | VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog | | 14 | 92 | hsa-miR-622 | | [CAMTA1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=23261) | calmodulin binding transcription activator 1 | | 15 | 92 | hsa-miR-622 | | [PEA15](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=8682) | phosphoprotein enriched in astrocytes 15 | | 16 | 91 | hsa-miR-622 | | [BOD1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=91272) | biorientation of chromosomes in cell division 1 | | 17 | 91 | hsa-miR-622 | | [TCAIM](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=285343) | T cell activation inhibitor, mitochondrial | | 18 | 90 | hsa-miR-622 | | [KIAA1211](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=57482) | KIAA1211 | | 19 | 90 | hsa-miR-622 | | [TRDN](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=10345) | triadin | | 20 | 89 | hsa-miR-622 | | [KCNA6](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=3742) | potassium voltage-gated channel, shaker-related subfamily, member 6 | | 21 | 89 | hsa-miR-622 | | [COL4A3BP](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=10087) | collagen, type IV, alpha 3 (Goodpasture antigen) binding protein | | 22 | 89 | hsa-miR-622 | | [MYL12A](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=10627) | myosin, light chain 12A, regulatory, non-sarcomeric | | 23 | 89 | hsa-miR-622 | | [NR3C1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=2908) | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) | | 24 | 89 | hsa-miR-622 | | [TBC1D14](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=57533) | TBC1 domain family, member 14 | | 25 | 88 | hsa-miR-622 | | [CDK8](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=1024) | cyclin-dependent kinase 8 | | 26 | 88 | hsa-miR-622 | | [SLC16A10](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=117247) | solute carrier family 16 (aromatic amino acid transporter), member 10 | | 27 | 88 | hsa-miR-622 | | [TMEM47](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=83604) | transmembrane protein 47 | | 28 | 88 | hsa-miR-622 | | [ING1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=3621) | inhibitor of growth family, member 1 | | 29 | 87 | hsa-miR-622 | | [FAM104A](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=84923) | family with sequence similarity 104, member A | | 30 | 87 | hsa-miR-622 | | [PTPN1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=5770) | protein tyrosine phosphatase, non-receptor type 1 | | 31 | 87 | hsa-miR-622 | | [CBLN2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=147381) | cerebellin 2 precursor | | 32 | 87 | hsa-miR-622 | | [DOT1L](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=84444) | DOT1-like histone H3K79 methyltransferase | | 33 | 87 | hsa-miR-622 | | [CCNJ](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=54619) | cyclin J | | 34 | 87 | hsa-miR-622 | | [GGT7](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=2686) | gamma-glutamyltransferase 7 | | 35 | 86 | hsa-miR-622 | | [MOB1B](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=92597) | MOB kinase activator 1B | | 36 | 86 | hsa-miR-622 | | [KDM6A](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=7403) | lysine (K)-specific demethylase 6A | | 37 | 86 | hsa-miR-622 | | [USP20](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=10868) | ubiquitin specific peptidase 20 | | 38 | 85 | hsa-miR-622 | | [EYA1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=2138) | eyes absent homolog 1 (Drosophila) | | 39 | 85 | hsa-miR-622 | | [MYL12B](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=103910) | myosin, light chain 12B, regulatory | | 40 | 85 | hsa-miR-622 | | [PLEKHM3](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=389072) | pleckstrin homology domain containing, family M, member 3 | | 41 | 85 | hsa-miR-622 | | [BNIP3](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=664) | BCL2/adenovirus E1B 19kDa interacting protein 3 | | 42 | 85 | hsa-miR-622 | | [SLAIN2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=57606) | SLAIN motif family, member 2 | | 43 | 85 | hsa-miR-622 | | [PNN](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=5411) | pinin, desmosome associated protein | | 44 | 85 | hsa-miR-622 | | [FRAS1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=80144) | Fraser syndrome 1 | | 45 | 84 | hsa-miR-622 | | [SARM1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=23098) | sterile alpha and TIR motif containing 1 | | 46 | 84 | hsa-miR-622 | | [SS18](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=6760) | synovial sarcoma translocation, chromosome 18 | | 47 | 84 | hsa-miR-622 | | [HEYL](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=26508) | hes-related family bHLH transcription factor with YRPW motif-like | | 48 | 84 | hsa-miR-622 | | [YTHDF1](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=54915) | YTH domain family, member 1 | | 49 | 84 | hsa-miR-622 | | [SLC38A2](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=54407) | solute carrier family 38, member 2 | | 50 | 84 | hsa-miR-622 | | [PRKAR2B](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=5577) | protein kinase, cAMP-dependent, regulatory, type II, beta | |