Songbird Brain Transcriptome Database

Address: http://songbirdtranscriptome.net/?view=cluster&freeze=2&clusterLevel=cluster&clusterUid=C7434086262E4EF1828E4C4C5137515E

Songbird Brain Transcriptome Database

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A

Cluster: H3 histone, family 3B (view this cluster in clustalw, dialign - or all clones in clustalw, dialign)

- **cluster: H3 histone, family 3B (zebra finch)** — *3 subclusters, 18 clones* View cluster evidence (6 blasts)
  - subcluster: H3 histone, family 3B, variant 1 (zebra finch) — *14 clones* View subcluster evidence (182 blasts)
    - clone 0061P0023D06: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0008A11: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0008G10: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0065P0013G06: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0063P0009E07: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0044A07: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0008F10: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0020G11: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0008B11: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0063P0006D07: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0006E06: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0061P0016F11: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0018B10: H3 histone, family 3B, variant 1, complete cds (zebra finch)
    - clone 0058P0050F10: H3 histone, family 3B, variant 1, complete cds (zebra finch)
  - subcluster: H3 histone, family 3B, variant 2 (zebra finch) — *3 clones* View subcluster evidence (6 blasts)
    - clone 0065P0009F02: H3 histone, family 3B, variant 2, complete cds (zebra finch)
    - clone 0063P0002B04: H3 histone, family 3B, variant 2, complete cds (zebra finch)
    - clone 0063P0003D04: H3 histone, family 3B, variant 2, complete cds (zebra finch)
  - subcluster: H3 histone, family 3B, variant 3 (zebra finch) — *1 clone*
    - clone 0061P0006D04: H3 histone, family 3B, variant 3, complete cds (zebra finch)

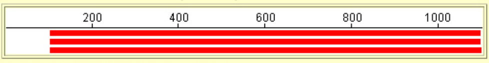
B

Primer annotations:
- **Species:** zebra finch (18)
- **Tissues:** whole brain (18)
- **Ages:** PH86 (3); adult (5); PH10 (1); PH64 (2); PH47 (6)
- **Sexes:** M (17)
- **Subject IDs:** 31 (3); 45 (4); 56 (2); 40 (1); 13 (1); 54 (6)
- **Conditions:** silence-male (3); development (1); sleep (4); seizure (1); learning (8)
- **Details:** sleep 2hr (4); juvenile rapid vocal learning minus juvenile singing control (4); seizure-kainate receptor activation 0.5h (1); silent male minus hearing female (3); post hatch development (1); rapid vocal learning-afternoon 7th day (2); juvenile rapid vocal learning minus adult singers 2hr,6hr (2)
- **Aviaries:** Jarvis-Duke (5); Sakaguchi-Tokyo (4); Tchernichovski-CUNY (8)
- **Library numbers:** 0058 (9); 0065 (2); 0063 (4); 0061 (3)
- **Library conditions:** Single male minus single female (3); Single juvenile learning minus 2 adult male singers (2); 50 mix pooled juveniles + adults (9); Single juvenile learning minus single juvenile untutored (4)
- **Library types:** subtracted (9); normalized (9)
- **Investigators:** Wada, Jarvis, Lints

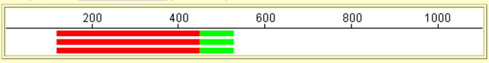
C

Database Sequence Searches:

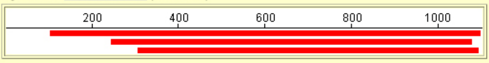
NCBI nucleotide nr: 91 total blastn hits (10/19/2004)



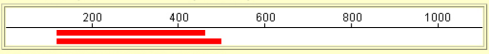
NCBI protein nr: 100 total blastx hits (11/29/2004)



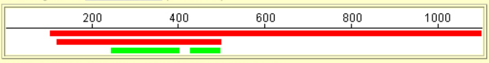
Tigr chicken: 20 total blastn hits (10/20/2004)



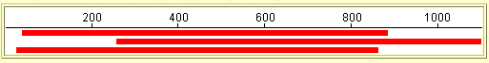
Chicken transcriptome: 2 total blastn hits (10/20/2004)



Chicken genome: 4 total blastn hits (10/22/2004)



ESTIMA zebrafinch database: 66 total blastn hits (1/25/2005)



D

Hs.180877: H3 histone, family 3B (H3.3B)

LocusLink: H3F3B

Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Two molecules of each of the four core histones (H2A, H2B, H3, and H4) form an octamer, around which approximately 146 bp of DNA is wrapped in repeating units, called nucleosomes. The linker histone, H1, interacts with linker DNA between nucleosomes and functions in the compaction of chromatin into higher order structures. This gene contains introns and its mRNA is poyadenylated, unlike most histone genes. The protein encoded is a member of the histone H3 family.

Annotated gene ontology:

molecular_function
- DNA binding
- molecular_function unknown

biological_process
- biological_process unknown
- chromosome organization and biogenesis (sensu Eukarya)
- nucleosome assembly

cellular_component
- chromosome
- nucleosome
- nucleus
- cellular_component unknown

Annotator's note: Variant 1 has unique deleltionin the ORF compared to varinant 2. Variant 3 has a long 5' UTR

C

Consensus Clone Sequence: (GenBank accession #: DQ217322) fasta format

```
   1 ggcagtgtgcggcgcggcggctgaagagcggctcgagtagcggcacggcgtaaaagcttcggcgcgcagcgctaccggcaccggcgcttccttctcttcc 100
 101 taccggtaagtgaggaaaaatggcccgtacaaagcagaccgcccgcaagtccaccgggggaaggcgccgcgcaagcagctggccacgaaggcggcccgg 200
 201 aaaagcgcccccctctaccggcggcgtcaagaagcctcaccgctacaggccgggaaccgtggcgctccgtgagatccggcgttaccagaaatccacggagc 300
 301 tgctgatccgcaagctgcccttccagcggctggtcagggaaatcgcccaagatttcaaaacagacttgaggttccagagcgcggccatcggggctctgca 400
 401 ggaggccagcgaggcatatctggtgggtctgtttgaagacacaaacctngtgtgccatccatgccaagagagtcaccatcatgcccaaagatatccagtt 500
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1001 aaaaacgtaaacctggcagctatagaatacactatgtgcatttataatagctattttatatattgtagtgtcaacattttaaattaaatgttttacatc 1100
1101 caaaaaaaaaaaaaaa                                                                                     1116
```
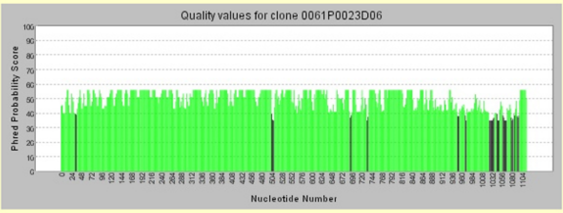

E



Unverified coding sequence: (bps 120 to 560, frame +3)

```
MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSAAIGALQEASEAY
LVGLFEDTNLVCHPCQESHHHAQRYPVGSQDTGREGLSEGCFYGVL*
```