







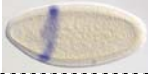




| Cluster number | Cyto-logical position | Flanking gene(s) | Cluster start position | Cluster end position | Annotated molecular function | Whole mount in-situ hybridization hour 0-4 | Embryonic DNA microarray | Known Regulators | References |
|----------------|-----------------------|------------------|------------------------|----------------------|---|--|--------------------------|-------------------------|------------|
| 1 | 3A | gt | -2,759 | -1,815 | RNA Polymerase II Transcription Factor |  | + | <i>bcd, cad, hb, Kr</i> | (1-6) |
| | | tko | +12,310 | +13,254 | structural protein of the ribosome | not available | + | | |
| 2 | 4B | CG12688 | +2,033 | +3,039 | none | not available | - | | |
| 3,4 | 5C | CG3011 | -1,966 | -1,341 | glycine hydroxymethyltransferase | not available | - | | |
| | | CG3726 | -4,038 | -3,344 | none | ubiquitous | + | | |
| 5 | 7A | CG9650 | +23,470 | +24,018 | transcription factor | ubiquitous | + | | |
| | | CG1958 | -11,100 | -10,552 | none | no staining | - | | |
| 6 | 7B | CG11368 | +46,957 | +47,595 | none | no staining | - | | |
| | | CG11369 | -75,488 | -74,850 | none | not available | inconclusive | | |
| 7 | 7F | otd | +37,924 | +38,583 | RNA Polymerase II Transcription Factor |  | + | <i>bcd, hb</i> | (7-9) |
| | | Caf1-180 | -6,195 | -5,536 | nucleosome assembly chaperone | ubiquitous | + | | |
| 8 | 8F | btd | -34,117 | -33,376 | RNA Polymerase II Transcription Factor |  | + | <i>bcd, hb</i> | (10, 11) |
| | | Sp1 | -34,117 | -33,376 | RNA Polymerase II Transcription Factor | not available | + | | |
| 9 | 12E | CG5291 | -9,253 | -8,590 | Immunoglobulin and major histocompatibility complex | not available | - | | |
| | | CG18313 | +34,741 | +35,404 | none | not available | - | | |
| 10 | 24A | odd | -3,394 | -2,634 | RNA Polymerase II Transcription Factor |  | + | | (12) |
| | | Dot | -10,102 | -9,342 | UDP glucuronosyl transferase | not available | inconclusive | | |
| 11 | 33E | pdm1 | -2,519 | -1,825 | RNA Polymerase II Transcription Factor |  | + | <i>hb, kni</i> | (13) |
| | | CG15488 | +2,688 | +3,382 | None | not available | - | | |
| 12 | 33F | pdm2 | -3,596 | -2,873 | RNA Polymerase II Transcription Factor |  | + | <i>hb</i> | (13) |
| | | CG15486 | +2,085 | +2,808 | None | not available | inconclusive | | |

| | | | | | | | | |
|----|-----|---------|----------|----------|--|--|--------------|-----------------------------|
| 13 | 34E | bgm | -6,635 | -5,785 | long-chain-fatty-acid-CoA-ligase | patterned (early gastrulation) | + | |
| | | rk | -14,492 | -13,642 | G-protein coupled receptor | no staining | - | |
| 14 | 36F | Fas3 | +39,849 | +40,550 | cell adhesion | not available | - | |
| | | RpS26 | +19,831 | +20,532 | structural protein of ribosome | not available | + | |
| 15 | 47A | psq | +45,838 | +46,493 | Transcription Factor |  | + | (14) |
| 16 | 55C | sbb | -2,637 | -1,934 | Zinc-finger C2H2 | ubiquitous | + | |
| | | CG14502 | -3,199 | -2,496 | none | no staining | + | |
| 17 | 56B | CG7097 | +24,150 | +24,783 | protein serine/threonine kinase | not available | + | |
| 18 | 59B | CG13534 | +5,589 | +6,305 | none | not available | + | |
| | | CG9898 | +32,094 | +32,810 | serine-type peptidase | no staining | - | |
| 19 | 67B | CG14178 | +19,239 | +19,905 | none | no staining | - | |
| | | CG17357 | -8,941 | -8,275 | none | not available | - | |
| 20 | 70F | CG17705 | +10,471 | +11,181 | none | no staining | inconclusive | |
| | | CG13473 | -12,244 | -11,534 | electron transfer/thioredoxin | no staining | - | |
| 21 | 75C | rpr | +6,616 | +7,368 | unknown |  | + | |
| | | grim | -87,688 | -86,936 | unknown | not available | inconclusive | |
| 22 | 76C | CG8786 | -2,356 | -1,652 | none | ubiquitous | + | |
| | | CG8782 | +4,833 | +5,537 | ornithine-oxo-acid aminotransferase | no staining | - | |
| 23 | 84A | Dfd | -22,070 | -21,370 | RNA Polymerase II Transcription Factor |  | + | <i>bcd, hb</i> (15-17) |
| | | Ama | +6,089 | +6,789 | Cell Adhesion | patterned | + | |
| 24 | 84B | Antp | +131,348 | +132,041 | RNA Polymerase II Transcription Factor |  | + | <i>hb, kr, kni</i> (17, 18) |
| | | ftz | +3,696 | +4,389 | RNA Polymerase II Transcription Factor |  | + | <i>cad</i> (19-21) |

| | | | | | | | |
|----|---------|---------|---------------|---------------|---------------------------|---------------|---------------|
| 25 | 85C | pum | +117,980 | +118,817 | RNA binding | ubiquitous | + |
| 26 | 88F-89A | CG18516 | -46,483 | -45,810 | none | not available | - |
| | | CG5302 | -35,010 | -34,328 | serine-type endopeptidase | not available | - |
| 27 | 91F | sqz | +10,124 | +10,933 | transcription factor | no staining | - |
| | | CG14282 | -2,691 | -1,882 | none | not available | not available |
| 28 | 95C | Gdh | +937 | +1,560 | glutamate dehydrogenase | ubiquitous | + |

Supporting Table 2: **Genes flanking 28 novel binding site clusters identified in genome-wide searches**

23 of the 28 novel binding site clusters described in the text were located in intergenic regions and we describe both flanking genes. The remaining 5 novel binding site clusters were located in introns, and for these we describe the gene containing the intron. Whole mount *in situ* images are available on the Berkeley Drosophila Genome Project website (22). DNA microarray expression levels for 0-3 hour old embryos were examined and categorized as either indicating expression during these stages (+), not indicating expression during these stages (-), or as inconclusive.

References for Supporting Table 2

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