

## GENSCAN predicted genes in sequence contig12

0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 kb



10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 kb



20.0 21.0 22.0 23.0 24.0 25.0 26.0 27.0 28.0 29.0 30.0 kb



30.0 31.0 32.0 33.0 34.0 35.0 36.0 37.0 38.0 39.0 40.0 kb



**Key:**



Initial  
exon



Internal  
exon



Terminal  
exon



Single-exon  
gene



Optimal exon



Suboptimal exon