

CLUSTAL W (1.83) multiple sequence alignment

```
mouse_chr18_NM_027350   CCAAGGCTTTGATGACAGTTGGAAAAGAGCCATTTCCCACCATTTATGTG
human_chr18             CCAAGGCTTTGATGACAGTAGGGAAAAGAACCATTTCTACCATTTACGTA
***** ** ***** ***** **

mouse_chr18_NM_027350   GACTCACAAAAGGAAAATGAGGTAGGGTGCACCAGAACCTTCTCGAGATT
human_chr18             GATTCACAAAAGAAAATGAG-----
** ***** *****

mouse_chr18_NM_027350   GTGTTTTGTGAAAATAACGTTTTCTGAGCACATAGAGGTATTGAAGATA
human_chr18             -----

mouse_chr18_NM_027350   ACACAGATCTTTGTGCTCTCTCTGTAGAGATGGGATGTTATTTCTAAGTC
human_chr18             -----AGGTGGAATGTTATTTCTAAATC
** ** ***** **

mouse_chr18_NM_027350   ACAGATGAAGAACATTA AAAAGATGTGGCACAGAGAACAGATGAAGAACG
human_chr18             ACAGTTGAAGAACATTA AAAAGATGTGGCATAGGGAACAAATGAAGAGTG
**** ***** ** ***** *

mouse_chr18_NM_027350   ACTCT
human_chr18             AATCC
* **
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CLUSTAL W (1.83) multiple sequence alignment

```
mouse_chr6_NM_008084
TCCCAGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTTCCCTACCCCAATGTGT
human_chr12
TCCCTGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTCCCCACTGCCAACGTGT
*****
****

mouse_chr6_NM_008084
CCGTCGTGGATCTGACGTGCCGCCTGGAGAACCTGTATGTATGGGGAGAGCTGGGCTTG
human_chr12
CAGTGGTGGACCTGACCTGCCGTCTAGAAAAACCT-----
-----
* ** *****

mouse_chr6_NM_008084
TCTCTGGTGTGACAGTGACTTGGGACAAGGATAGTCATTTTGGGGTTTGTTCATTATCAGG
human_chr12
-----G
-----G

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mouse_chr6_NM_008084
CCAAGTATGATGACATCAAGAAGGTGGTGAAGCAGGCATCTGAGGGCCCACTGAAGGGCA
human_chr12
CCAAATATGATGACATCAAGAAGGTGGTGAAGCAGGCATCTGAGGGCCCCCTCAAGGGCA
*****

mouse_chr6_NM_008084      TCTTGGGCT
human_chr12                TCCTGGGCT
** *****
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CLUSTAL W (1.83) multiple sequence alignment

```
mouse_chr11_NM_145370   CTGTTGAAACTGGAGAAGCTGGACACGGACTTGAAGAACTATAAGGGCAA
human_chr17             CTGCTGAAGCTGGAGAAGCTGGACACAGACCTGAAGAACTACAAGGGCAA
                        ***      *      *      *      *      *      *      *      *
mouse_chr11_NM_145370   TTCTATCAAAGAGAGCATCAGGTGCTGGGCTTCTCTGGGCAGGGGAGGTG
human_chr17             CTCCATCAAAGAGAGCATCCG-----
                        **      *      *      *      *      *      *
mouse_chr11_NM_145370   GGCAACCGGGCCCTAATGGCCCCTCGACCAGCATTCACTCACTGCCAGGC
human_chr17             -----
mouse_chr11_NM_145370   CTACAGGCGCGGCCACGATGACCTGGGTGATCACTACCTGGACTGTGGGG
human_chr17             -----GCGCGGCCACGACGACCTGGGCGACCACTACCTGGACTGTGGGG
                        *****      *      *      *      *      *
mouse_chr11_NM_145370   ACCTCAGCAATGCCCTCAAATGTTACTCACGAGCCCGA
human_chr17             ACCTCAGCAACGCCCTCAAGTGCTATTCCCGGGCCCGG
                        *****      *      *      *      *      *
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CLUSTAL W (1.83) multiple sequence alignment

```
mouse_chr15_NM_031170      AATCGCAGCCGAGCTGAGGCTGAAACCATGTACCAGATTAAGGTAAAGAG
human_chr12                AACCGCAGCCGGGCTGAGGCTGAGAGCATGTACCAGATCAAG-----
** ***** * ***** **

mouse_chr15_NM_031170      CAGGGGGGTCACAAGCCTGGGTCTCCCTTCCTGGCCCGTTCTGTGTCCTG
human_chr12                -----

mouse_chr15_NM_031170      GATCATTGAGGAGGGAGCAGAGAACCAAATCCCACGCTGCCTGCTGTGGA
human_chr12                -----

mouse_chr15_NM_031170      CTGGCTCCACACAATGGAGGCCTGGAGGTCTGGAAAGGGGCCTTCACTGG
human_chr12                -----

mouse_chr15_NM_031170      TGTGTGCATTGAGTGTGTGTGTGTGTCGGTGTGCACACGCAGGAGCTTGGTG
human_chr12                -----

mouse_chr15_NM_031170      GGTGAGATGTCAGCTGAACCCTCACCTCCCTTCTTGCCCCCTGCAGTATG
human_chr12                -----TATG
** **

mouse_chr15_NM_031170      AGGAATTGCAGACCCTGGCTGGGAAGCACGGGGATGATCTGCGCCGCACA
human_chr12                AGGAGCTGCAGAGCCTGGCTGGGAAGCACGGGGATGACCTGCGGCGCACA
***** *****

mouse_chr15_NM_031170      AA
human_chr12                AA
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