

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_032377      ----CACCAGTCCCTTCTCTTGGTCTGTTTTCAGGGACCGTGCCCCGAACA
mouse_chr9                  TCTCATGCATACCTACACCTTGTCTCACTGCAGGGACCGTGCTCGAAACA
                             **  **      ****      * ***** **  ****

human_chr19_NM_032377      CCGGAGTCATCTCTTGTACCGTGTGCCTAGAGGAATTCCAGACGCCATA
mouse_chr9                  CTGGAGTCATCTCCTGTACTGTGTGCCTAGAGGAATTCCAGACACCCATC
* ***** **  **** *****

human_chr19_NM_032377      ACGTGTATCCTTGAAACCTGGGCTTTTTCCAGAGGGTGGGGAGGGGGCT
mouse_chr9                  ACAT-----
** *

human_chr19_NM_032377      GGAGTCCGGACCCTGCTCATCTGGCCCACTGTGTGCCCTGGTGCAGGGCC
mouse_chr9                  -----

human_chr19_NM_032377      AAAGCCGTCCAGAGGAACAGGTGCCACCTAGTGATTTCTGTGGGGTGAGA
mouse_chr9                  -----

human_chr19_NM_032377      AGATGCAGGGCAGGGTTCCAATGCCAATGATCGCCCTTGACCTAAGTGGC
mouse_chr9                  -----

human_chr19_NM_032377      CCAGATCTGTGAGAACCCGTGGATGTGTACAGTGATTGGATAGACGCCTG
mouse_chr9                  ----ACCTGTGAGAACCAGTGGATGTGTACAGCGACTGGATAGATGCCTG
* ***** **  **** *****

human_chr19_NM_032377      CGAGGCGGCCAATCAGTAGCGACACAGAGGACCCGCCCCCTGAGCAGCCC
mouse_chr9                  CGAGGCAGCCAATCAGTAGCAAAGTCAGGGACCTGCTCCTCCACAGCCCC
***** ***** *          ***** **  **  *      ***

human_chr19_NM_032377      CGCG-
mouse_chr9                  CATCT
*
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr20_NM_000516    ---CCAGTCCCTCTGGAATAACCAGCTGTCCTCCTCCCCACCAGCATGTT
mouse_chr2               AGAGTGGTGGGCCAGGGTAACCCAGTATTTTCCGGTT--CCAGCATGTT
                        **      * * * ***** * * *** *****
human_chr20_NM_000516    TGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCA
mouse_chr2               CGATGTGGGCGGCCAGCGCGATGAGCGCCGCAAGTGGATCCAGTGCTTCA
                        ** ***** *****
human_chr20_NM_000516    ACGGTAGGATGCTGTGGGCTTGGCTGTTTCGTAAAGAACGCTTTGCTTCTG
mouse_chr2               ATG-----
                        * *
human_chr20_NM_000516    TGTTGTTAGGGATCAGGGTCGCTGCTCACGCTCTTGGCTTTGCTCTCTTT
mouse_chr2               -----
human_chr20_NM_000516    GGTTAAGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAA
mouse_chr2               -----ATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAA
                        *****
human_chr20_NM_000516    CATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGA
mouse_chr2               CATGGTCATTCGGGAGGACAACCAGACTAACCGCCTGCAGGAGGCTCTGA
                        *****
human_chr20_NM_000516    ACCTCTT----
mouse_chr2               ACCTCTTCAAG
                        *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr20_NM_005560      -CCGTGGCTGCGTCAAAGGCATCAAGGCCCTGGGCAAGTATGTGGACCTC
mouse_chr2                  TCCGTGGCTGCATCAAGGGTATTAAGGCTCTGGGCAAGTACGTGGACCTC
                             ***** ** * * * ***** *****
human_chr20_NM_005560      AAGCGGCTGAACACGACAGGCGTGAGCGCCGGCTGCACCGCCGACCTGCT
mouse_chr2                  AAACGGTTGAACACCACGGGCATCAGTTTCGGCTGCACCGCTGACCTGCT
                             ** ** * * * * * * * * * * * * * * * * * * * * * * * * *
human_chr20_NM_005560      GGTGAGCAGCCCTCCCCGGGCTGGGGGTGGCATCTGTGGACATGCAGGGG
mouse_chr2                  A-----
human_chr20_NM_005560      CACCCGCGGGCACTCAGGGATGGCCTCCCCGCAGGTGGGGCGCGCCATGA
mouse_chr2                  -----GTGGGACGCACCATGA
                             ***** ** * * * * *
human_chr20_NM_005560      CTTTCCATGGCCACGGCTTCCTTCGCCTGGCGCTCTCGAACGTGGCACCG
mouse_chr2                  CTTTTACGGCCACGGCTTCCTGCCCCTGGCACTTCCTGATGTGGCACCC
                             ***** ** * * * * * * * * * * * * * * * * * * * * *
human_chr20_NM_005560      CTCACTGGCAACGTCTACTCCGGCTTCGGCTTCC-
mouse_chr2                  ATCACCGAAGTGGTCTATTCTGGCTTTGGCTTTTCG
                             ***** * * * * * * * * * * * * * * * * *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr20_NM_033405      ----TGTGGTCAAGAATGAGCGGCTGCAAAACCTGGGTCTGGACCGGTCT
mouse_chr2                  GGCCTGTGGTCAAGAGTGAACAGCTGCAGAGTCTGGGGATGGATCGGTCT
                             ***** * * ***** * ***** * * * * *
human_chr20_NM_033405      CTGTTTCGAGCGGTACCACGAGGACGCACATATGCTGGACACTCAGTACCG
mouse_chr2                  CTCTTTGAGAGGTACCACAGGGATGCCATCATGCTGGACACACAGTACCG
                             ** ** * * * * * * * * * * * * * * * * * * * * * * * * *
human_chr20_NM_033405      CATGGTGAGCCCCGCCCACTCAGCCCCAGCCCACCTGCAGCCCCTGGGG
mouse_chr2                  TATG-----
                             ***
human_chr20_NM_033405      GGCCACAACCCCGCGTGGCAGCCTCTGACCAGCGCACATCCTTGCTGCA
mouse_chr2                  -----
human_chr20_NM_033405      GCATGAGGGCATCTGTGCCTTCCCCTCTGTGGCGTTCTACAAGAGCAAGC
mouse_chr2                  -CATAAGGACATCTGTTTCCTTCCCCTCCGTGGAGTTCTATGGGGGAAAGC
                             *** * * * * * * * * * * * * * * * * * * * * *
human_chr20_NM_033405      TGAAGACGTGGCAGGGCCTGAGGAGGCCGCCAGTGTCTGGGCCACGCT
mouse_chr2                  TAAAGACCTGGTCTGACCTGAGGCGTCTGCCTAGTATCCTGGGTCACT
                             * * * * * * * * * * * * * * * * * * * * * * * * *
human_chr20_NM_033405      G-
mouse_chr2                  GG
                             *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr22_NM_001670 -----GCAGCCTGGCCGCTGATGACGAGGGTGGCCCTGAGCTGGAGCC
mouse_chr16      GATACACGGAGCCTGGCTGCGGATGATGAGGGTGGCCCCGACCTGGAGCC
                  * ***** ** ***** ***** ** *****
human_chr22_NM_001670 TGA CTATGGCACGGCCACAAGGAGGAGGCCTGAGTGTGGGCGGGCCTTC
mouse_chr16      TGACTATAGCACGGCAACCCGGAGAAGACCTGAGTACGGGCGGGCCTTC
                  ***** ***** ** ***** ** ***** *****
human_chr22_NM_001670 ATACCAGGTGAGCTGCACCCCGTCCCCTGTGGCTACCTCCTCTGGGAAGT
mouse_chr16      GTGCCAG-----
                  * ****
human_chr22_NM_001670 CTGCCCTCCACCCCCCAACTACAGAGTGCCCCACTTGTCAAGTGGCGCAG
mouse_chr16      -----
human_chr22_NM_001670 TTGAGTTAGTCATGCATGTTAGTTTGAATTGGCCTTGGCTCTCGTCAGGG
mouse_chr16      -----
human_chr22_NM_001670 ACAGAAGAAAGGTGGACCCTGGGGTGGTAGGAGTTCGGCTGGGCACTGTC
mouse_chr16      -----
human_chr22_NM_001670 CTGCAGGCCCAGGGCCAGGAAAGCTGGGAAGAGTGCCGGCCACTGGCCT
mouse_chr16      -----
human_chr22_NM_001670 TGCTCCAGCCACACTCTGGGTAACCAGAACCCAGAGCCCTGGCCCTTGTC
mouse_chr16      -----
human_chr22_NM_001670 ACAGCCCCTGGTTCTGTCCCCATTGCCCTCAGTTTCTGCATCTCTGGAGT
mouse_chr16      -----
human_chr22_NM_001670 GGGGATGTGACCACAGCCCGGGTCAGGATTTTGTGTGTGACCCTGGCCA
mouse_chr16      -----
human_chr22_NM_001670 AGTCACCTGACCGTCACTCCTAGCCTCAGGGCAGGCGGTTTGATGACAGC
mouse_chr16      -----
human_chr22_NM_001670 AACCCACAGGGCTACTGAGAGCTAAGGAGATCTTGTGCCCAAGGGGCTG
mouse_chr16      -----
human_chr22_NM_001670 GTGGCCTGAATACTCCTCAGGTGGTCCTACTGGGATGGCTTCATGCGGAG
mouse_chr16      -----
human_chr22_NM_001670 AGGGCCATTTACTCCCCCTACATCCTGGCACAGCCAGAGATGGGCCTCAT
mouse_chr16      -----
```

human_chr22_NM_001670 GGAAGATGGGGTGGTTTTGTGGAAGGGAGGTGAGACGGTCTCTCCAGCAG
mouse_chr16 -----

human_chr22_NM_001670 CCATAGCAGATGTCTCACAGAACTTGTTTTGCTCGGGATTGGGAACTG
mouse_chr16 -----

human_chr22_NM_001670 CCCGGTGACAGCAGTGAGTGAGTTTGCTGTCCTGGGAGGGTTGCCTGGGT
mouse_chr16 -----

human_chr22_NM_001670 CCTGGTAGCCGCTGGCTGGGGTTTTGGCATTGGCTCTGAATTGGTTCTCA
mouse_chr16 -----

human_chr22_NM_001670 CTGGGCTGGTGCATGACTCTCTGTGTCCCCACCATGCTCCGGGCCAAGAT
mouse_chr16 -----

human_chr22_NM_001670 ACAGGTGCTCTCAGCCCAGCGCTGCTGGGTGAGTTTGCAGTCCTGAAGAA
mouse_chr16 -----

human_chr22_NM_001670 GGTGTGATGGGGCAGCTCAGAGGCAGGGCTGGCGGCTGCTGTGACGATGT
mouse_chr16 -----

human_chr22_NM_001670 CCACGCGCCCCACTTGCCCTGTGCAGGGCCTACGAGGACACAGCAGATGAT
mouse_chr16 -----GGCCTTTGAAGACACAGCAGATGAT
***** ** *****

human_chr22_NM_001670 GCGGCGAGCTGGCGGACGAGCGGCCTGCGTTCCCAATGGTGACGGCGCC
mouse_chr16 GCTGGTGAGCTGATAGAAGAGCGTCCCCATTTCCAGCAGCAACAGCCCC
* ** ***** ** ***** ** * ** * * * * ** * ** * * *

human_chr22_NM_001670 CCTGGCCCAGCCTGAACGGGGCAGC-
mouse_chr16 TCTGGCCCAGCCTGAGAGGGGCAGCC
***** *****

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr1_NM_004550      -
AATCACACGTTTGTGTTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGG
mouse_chr1
AGATCACACGGATTTTAAACCATATCATGGCTGTCACCACACATGCCCTGGACATCGGTG
***** * ** ***** *****
* ** *
```

```
human_chr1_NM_004550
CCATGACCCCTTTCTTCTGGCTGTTTGAAGAAAGGGAGAAGGTAAGAGTGGGAGGAAAGG
mouse_chr1                CCATGACTCCTTTCTTCTGGATGTTTGAAGAAAGAGAGAAG-----
-----
***** ***** ***** *****
```

```
human_chr1_NM_004550
ATAGGAATAGGGAAGGAAGTGCAGGAAGTAGAGAAGGTATAAAGGAGACAGGAGATTTAA
mouse_chr1                -----
-----
```

```
human_chr1_NM_004550
AGAAGAGAGAGAACATGGGAGAACATTTAGAGGGGGAAGGTATGTTTAACTTGGGTTATA
mouse_chr1                -----
-----
```

```
human_chr1_NM_004550
TTTGTAGAAACTATATCATGAGGGGTTGGTTGGGCACAAGAAGGCAGAAAGTGGGGGAGT
mouse_chr1                -----
-----
```

```
human_chr1_NM_004550
AGGCCATCATAGGACCTGGGGCCTGGGACTTTGACACTAATTCCCAGCACGTTCTATGA
mouse_chr1                -----
-----
```

```
human_chr1_NM_004550
AGATGTTTGTGAGTTCTACGAGCGAGTGTCTGGAGCCCGAATGCATGCTGCTTATATCCGGC
mouse_chr1                --
ATGTTTCGAGTTCTATGAGCGGGTGTCTGGGGCCCGGATGCACGCGGCGTATATCCGAC
***** ***** ***** ***** ***** ***** ** **
***** *
```

```
human_chr1_NM_004550      CAGGAGGAGTGCACCAGGTGAGCAGGTCCCCGGCTTCCCCAA----
mouse_chr1                CTGGAGGAGTGCACCAGGTGAGTGTGAGCTGCTCTCTGGCCTCTCTCC
* ***** ***** * * ** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr1_NM_006600      -
GGAGGAAGATGAGAAGGACAAAGGAAAAGCTGAAGCCCAACCTAGGCAACGGGGCAGACC
mouse_chr4
ACGAGGAGGATGAGAAGGACAAAGGAAAAGCTGAAGCCCAACCTAGGCAATGGGGCTGACC
*****
*****

human_chr1_NM_006600
TGCCCAATTACCGCTGGACCCAGACCCTGTCTGGAGCTGGACGTGAGTGTGAGGGACCAGA
mouse_chr4                TGCCCAACTACCGCTGGACCCAGACCCTGGCAGAACTGGAT-----
-----
*****

human_chr1_NM_006600
GGTAAAGCTTAGGGGGCCAGCCTGGGGTACCAGCAGCACTTAGTGGCCTCTTCTGACTGC
mouse_chr4                -----
-----

human_chr1_NM_006600
CTCTGCCCTATGCAGCTGGCGGTCCCTTTCTGTGTGAACTTCCGGCTGAAAGGGAAGGAC
mouse_chr4                -----
CTGGCAGTGCCTTCCGGGTGAGCTTCCGGCTGAAGGGAAGGAT
*****

human_chr1_NM_006600
ATGGTGGTGGACATCCAGCGGCGGCACCTCCGGGTGGGGCTCAAGGGGCAGCCAG----
mouse_chr4
GTGGTGGTGGACATCCAGCGGCGGCATCTCCGGGTGGGCCTTAAAGGACAGCCACCAGT
*****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr1_NM_007122      -----
CACAGTGGAGCGTCGCCGCCGAGACAAGATCAACAACCTGGATCGTGCAGCTCT
mouse_chr1
TCTGCCCCACAGTGGAGCGCCGCCCGGGACAAGATCAACAACCTGGATTGTACAGCTGT
*****
***** *

human_chr1_NM_007122
CCAAGATAATCCCAGACTGCTCTATGGAGAGCACCAAGTCTGGCCAGGTCATGGAAAGAC
mouse_chr1                CCAAAATCATCCCAGACTGCTCTATGGAGAGCACCAAGTCTGGCCAG-----
-----
***** ** *****

human_chr1_NM_007122
CCTGGTAGTGGGCAGGATGCCTGAATTCTGCCTCCTGGTATTGTTTCCAGAAATGGTAGA
mouse_chr1                -----
-----

human_chr1_NM_007122
GAGAGGGGCACACATGACAGTAGTCTTATCTCTCCCTGAGGTTCTGTATCCCTGGGAGA
mouse_chr1                -----
-----

human_chr1_NM_007122
TATTATACCACCTTCTTAGATGAAAATGAGGTCCAAAGTGTGAACCTACTTTTGGAAAG
mouse_chr1                -----
-----

human_chr1_NM_007122
CAAGCTGGGTATCTGAAATCCTAGTTCTCATTTTTGTTGACCTTATCTTGCAGAGTAAAGG
mouse_chr1                -----
AGTAAAGG

*****

human_chr1_NM_007122
TGGGATTCTATCCAAAGCTTGTGATTATATCCAGGAGCTTCGGCAGAGTAACCACCGCTT
mouse_chr1
TGGAATCCTGTCCAAAGCCTGTGATTATATCCAGGAGCTGCGGCAGAGCAACCACCGGCT
*** ** * *****
***** *

human_chr1_NM_007122      GTCTGAAGAAGTGCAGGGACTTGACCAACTGC-
mouse_chr1                GTCTGAAGAGCTGCAGGGGTTAGATCAGTTGCA
***** ***** * ** * **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr1_NM_024319      ---
GGCGCCATGTTTCGGCTCCAGTCGTGGAGGCGTGC GCGGCGGGCAGGACCAGTTCAAC
mouse_chr11
TCCAGCGCCATGTTTCGGCTCCAATCGCGGTGGCGTGC GTGGCGGACAAGACCAGTTCAAT
*****
*****

human_chr1_NM_024319
TGGGAGGACGTGAAGACTGACAAGCAGCGGGAGAACTACCTGGGTGGGTGCGCGCGGTGG
mouse_chr11              TGGGAGGACGTGAAGACTGACAAGCAGAGGGAGAACTACTTGG-----
-----
*****

human_chr1_NM_024319
GCGGGCTCCGGGCTCCGGGCTCCGGGATCCCGGGCGGGCGCTGGACTCACAGCGTCTACG
mouse_chr11              -----
-----

human_chr1_NM_024319
TCCGCAGGCAACTCGCTGATGGCGCCGGTAGGCCGCTGGCAGAAGGGCCGCGACCTCACC
mouse_chr11              -----
GCAACTCGCTGATGGCGCCAGTAGGCCGCTGGCAGAAGGGCCGCGACCTCACC
*****
*****

human_chr1_NM_024319      TGGTACGCCAAGGGCCGGGCGCCATGCGCGGGCCCCGAGCCGCGAGGA-
mouse_chr11              TGGTACGCGAAGGACCGCGCGCCGTGTACCGCCCCGAGCCGTGAGGAA
***** ***** ***** ** * ***** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr1_NM_182752      -
GCGGCCGGGGGCGGGGACGCCGCTGCGCCAGACACTCTGGCCTCTCAGCATCCACGACC
mouse_chr4
GCCGGCCTGGGGCGGGCACACCGCTGCGCCAGACGTTGTGGCCGCTGAACGTCCACGACC
                    ***** ***** ** ***** ***** * ***** ** * *
*****

human_chr1_NM_182752
CCACGCGCCGCGCCCGCGTCAAGGAGTACTTCGTGTTCCGGGTGAGGCAGGGGCCAGGGC
mouse_chr4              CTACACGCCGCGCCCGCGTCAAGGAGTACTTCGTGTTCCGG-----
-----
                    * ** ***** ***** ***** *****

human_chr1_NM_182752
CGGGGCGGGGCGGAGGGCGCGGGGCGGGATGGGGGCGGGTGGGGTCCGGAGGCGGGCGCC
mouse_chr4              -----
-----

human_chr1_NM_182752
GGGCGGTCCCGCAGGGAGCGAGCTGTGACCTGTGATCTTTGCCCCCGTCCCCACCCCGC
mouse_chr4              -----
-----

human_chr1_NM_182752
AACCCGCCAGCCCGGCAGCATCGAGCAGGCAGTGGAGGAGATCCGCGTGGTGGTGCGGC
mouse_chr4              -----
CCCGGCACCATCGAGCAGGCGGTGAGGAGATCCGCGCCGTGGTACGGC
                    ***** ***** ** ***** *****
***** *****

human_chr1_NM_182752      CCGTGGAGGACGGCGAGATCCAGGGAGTGTGGCTGCTTACCGAGTAAGCCG---
-
mouse_chr4
CCGTGGAGGACGGCGAGATCCAGGGGTTGTGGCTGCTGACCGAGTAAGCCGGCGC
                    ***** ***** ***** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr2_NM_006773      -
GATAATGGGTGGCAGTAACAGATCTGCTGAAGCACAGAACTTGGTAATGGGATCAACA
mouse_chr1
TGATCATGGGCGGCAGCAACAGGTCTGCTGAAGTGCAGAAGCTCCTCAATGGGATCAACA
                                *** ***** **
*****

human_chr2_NM_006773
TCATTGTGGCCACACCAGGCCGTCTGCTGGACCATATGCAGGTAAGAGATGTAGTGCTTG
mouse_chr1                    TCATCGTGGCCACGCCCGCCGGCTCCTGGACCACATGCAG-----
-----
                                **** ***** ** ***** **

human_chr2_NM_006773
TCTCATTGTCTTGTATGAAACATAAACTGACAACATAATGGTTGTTCTTTGTCCTTTGTTT
mouse_chr1                    -----
-----

human_chr2_NM_006773
TGTTAGAATACCCAGGATTTATGTATAAAAACCTGCAGTGTCTGGTTATTGATGAAGCT
mouse_chr1                    -----
AACACGCCAGGGTTTATGTACAAGAACCTGCAGTGTCTGGTTATTGATGAGGCT
                                ** ** ***** **
*****

human_chr2_NM_006773      GATCGTATCTTGGATGTGGGTTTGAAGAGGAATTAAGCAAATTA--
mouse_chr1                  GACCGTATCTTGGATGTTGGGTTTGAAGAAGAATTAAGCAAATTATT
                                ** ***** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr2_NM_012290      ----  
AATCCTAGGCTTTTGACCTTTATGAACAAAGATATGCTGCTGTGAAGATACATCAG  
mouse_chr2  
CTTGAATTGTAGGCATTCGACTTGTATGAGCAAAGATACGCTGCTGTGAAGATCCACCAG  
***  ***** ** ** * ***** ***** *****  
**  ***
```

```
human_chr2_NM_012290  
CTTAATAAAAGCTGGAGAGATGAGAAGAAAGAAAACCTACCACAAGTAAATACTAATACTT  
mouse_chr2                CTTAATAAGAGCTGGAGAGACGAGAAGAAAGAAAACCTACCACAA-----  
-----  
***** ***** ***** ***** *****
```

```
human_chr2_NM_012290  
TATGGTTTTTTTAAATTGAATATTTTTTTGAATGATCATGGAGAATTAATACACTGTCTTC  
mouse_chr2                -----  
-----
```

```
human_chr2_NM_012290  
TCATAGACATGCCTGCAGAGAGTATAGAATACACAAAGAACTGGATCACCCAGAATAGT  
mouse_chr2                -----  
ACACGCTTGCCGAGAGTATCGAATACACAAGGAACTGGACCACCCAGAATAGT  
***  ** ** ***** ***** *****  
*****
```

```
human_chr2_NM_012290      TAAACTCTATGATTATTTCTCCTTGGATACAGATACGTAAGTGAAT-  
mouse_chr2                TAAACTCTATGATTACTTCTCCTTGGATACAGATACGTAAGTAAAGA  
***** ***** ***** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr2_NM_014763      -
GCGGCCTGCATTGCAGCGGGGCACTGGGCTGCAATGGGCCTAGGCCGGAGTTTCCAAGC
mouse_chr6
GGCGGCCTCCATGGCAGAAAGTTGTAGGGCGTCCCTGTACCTGGCCCCGGAGCGTCCGAAT
***** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
*** *

human_chr2_NM_014763
CGCCAGGACTCTGCTCCCCCGCCGGCCTCTATCGCCTGCAGTAAGTGGAGCCGGACTTG
mouse_chr6                GGCCAGGCCACGGCTTGCTGCCTTCGCATCTGATGCCTGCC-----
-----
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human_chr2_NM_014763
CGAGCTGGGGCGCGTTAGGGGCCAGGGTCAGGATGGGGGAGGCGAACCTGGAGATCAGA
mouse_chr6                -----
-----

human_chr2_NM_014763
GGCAACCCAGCGTTGGTCCCCCGTGGGACGCCGGGTTGGGGGAGATTGCGGGGCTCTGC
mouse_chr6                -----
-----

human_chr2_NM_014763
GGGATCTCAGGGTTGGCACGAGAGTTCTGACCTCCGTCGTCCGCTCCCGCAGGGGTCCAC
mouse_chr6                -----
GTGTCTGC

*** *

human_chr2_NM_014763
GCGGGCCTGTCCGGCAGCAGAGCACTGGGCCTTCCGAGCCCGGTGCGTTCCAACCGCCG
mouse_chr6
ACGGGCCCAAGCCGATTTAGAGCACCGGGCCTTACAGAGCCCGGTGGGTTCAAGCCACCG
***** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
** ***

human_chr2_NM_014763      CCGAAACCGGTCATCGTGGACAAGCACCGCC-----
mouse_chr6                CCGAAACCTGTCATCGTGGACCGGCGCCGAGTCCCGGA
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr2_NM_016252      -
CAGAATATCTTGCTTTGGGTCTGGGGAGCTGCCCTCATTCTTAGCTGCTGCAACTAAAC
mouse_chr17
ACAGAATAGCTTTGCTTTGGGTCTGGGAGCTGTCCTCAGTTTCTAGCTGCTGCAACCAAAC
*****
*****
*****

human_chr2_NM_016252
GAGGAAAGATCTGCATATGGGATGTTTCCAAACTTATGAAGGTATGTTTGAATTTGAAG
mouse_chr17                GTGGGAAGATCTGCATATGGGACGTCTCCAAACTCATGAAG-----
-----
* * *****

human_chr2_NM_016252
TAACAAATTAGTAATTGAAAAAAGATCAGTTGTAAACTTAGGCTTTTCATTTGTTTAGGT
mouse_chr17                -----
----GT

**

human_chr2_NM_016252
GCACTTAAAGTTTGAATTAATGCCTATGATCCAGCAATTGTACAACAGCTTATTCTATC
mouse_chr17
GCACTTGAAGTTTGAATTAATGCCTATGACCCAGCAATCGTGCAACAGCTGATCCTATC
*****
*****

human_chr2_NM_016252      AGGAGACCCAAGCTCAGGAGTTGATTCAAGGAGACCAA--
mouse_chr17                AGGAGACCCAAGTTCAGGAGTTGATTCAAGGAGACCCACT
*****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr2_NM_145212      -
CGTTGCTTTGTTGTTGTTGTTTCACAGGCACATACCCCTCAAGTTCACAAGAATATCCCT
mouse_chr1
CTGTGATATTGCTCCTCTTGTTCCTAGGCACACAGCCCTCAAATTCACAAGAACATCCCA
                **      *** *  * *****  ***** *  *****  *****
*****
```

```
human_chr2_NM_145212
TCAGTGAATGCAAATTGAAAGTAGTTAAGCATTGATAAGGTTTGTGTTTCTTCTCAG
mouse_chr1          TCGGTGAATGCAAAGCTGAAAGTGGTTAAACACTTGATACG-----
-----
                ** *****  *****  *****  ** ***** *
```

```
human_chr2_NM_145212
CTCTTTTTTAAAATGTATTGCCTAGTGTAAATCTAAATGCATTTTTCTTTTTTCGTTAATG
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
TTCTGAAAAAACTTTTTAAAAAACTAAAATTTATTTTGTTTTTTTTTTAATTGACACAT
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
AATAATTGTACATATTTATGGGGTACATAGTGACGTTTCAATATATATAAAGTATAGTGA
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
TCCGATCAGGGTAATTGGCATATCCATCATCTCAGACATTTACCATTTCTTCATGTTGGG
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
AACATTCAACATCCTCCTCCTAGCTATTTGAAACTATGTGTTATTGTTAACTGTAGTTAT
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
CCTGCGGGGATATAGAACGCTAGAACGTATTCTCCTATCTAAACGCATTTTCTTGTGTC
mouse_chr1          -----
-----
```

```
human_chr2_NM_145212
ACAGAATCAAGCCCTTGAAGTTGCCACAAGGACTTCCAGCAGAGGAGAACATGTCTAACA
mouse_chr1          ----
CATCCAGCCTCTGAAGCTGCCACAGGGACTTCCCACAGAAGAGACCATGTCCAGCA
                *** *****  *****  *****  *****  *****
***** * **
```

human_chr2_NM_145212
mouse_chr1

CGTGCCTCAAAGCACTGGGGAGTTAGTAGTGCAGTGGCATCTG-----
CATGCCTCAAGAGCACTGGGGAGTTGGTCGTGCAGTGGCATCTGAAGCC
* ***** ***** ** *****

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr5_NM_153188      -
TTCAGTTGCCACAGCACTGCAGTCTGGATTCTTCCGTAAGTGTGAACCTGTGTATCAGC
mouse_chr13
CGTCTGTTGCCACAGCCTTGCAGTCTGGCTTCCTTCCATATTGTGAACCTGTATATCAGC
                ** ***** ** ***** ** *****
*****
```

```
human_chr5_NM_153188
GTTGTGTAAACCTAGTACAGAAGACTCTTGACAAGCCATGGTAATTTTTTTAAAATGTC
mouse_chr13          GTTGCGTAAACCTAGTTCAGAAGACTCTGGCACAAGCCATG-----
-----
                **** ***** ***** *****
```

```
human_chr5_NM_153188
TTCCTCTTCTTGACATGGTGGACATTTTTCTAAAGATAGGTATAATGTATACAGACTTTT
mouse_chr13          -----
-----
```

```
human_chr5_NM_153188
TAAGTAGTTAATTAACCAAACCTTACAAAAACATTGTGTCTAATTTTCAGCTAAACAAT
mouse_chr13          -----
CTAAACAAT
*****
```

```
human_chr5_NM_153188
GCTCAACCAGATCAATATGAAGCTCCAGATAAAGATTTTATGATAGTGGCTCTTGATTTA
mouse_chr13
GCTCAACCAGAACAGTATGAAGCTCCAGATAAAGATTTTATGATTGTGGCTCTTGACTTA
                ***** ** *****
***** **
```

```
human_chr5_NM_153188      CTGAGTGGCCTGGCTGAAGGACTTGGAGGCA----
mouse_chr13              CTCAGCGGCCTGGCTGAGGGCCTGGGAGGCAACAT
                ** ** ***** ** ** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr6_NM_001090      -
TGGAGAAGTTCAGCATCTCCGCTCATGGCAAGGAGCTGTTTCGTCAATGCAGACCTGTAC
mouse_chr17
TTGGAAAAGTTCAGCATCTCCGCCACGGCAAGGAGCTATTCGTCAATGCTGACCTGTAC
*****
*****

human_chr6_NM_001090
ATTGTAGCCGGCCCGCTACGGGCTGGTAGGACCCAATGGGTGAGAAGAGGAGGGAGCT
mouse_chr17      ATAGTAGCCGGCCCGCTATGGGCTGGTGGGACCCAACGG-----
-----
** *****

human_chr6_NM_001090
GGAGGCAAAAAGGGCCTGGAGGGAAAAGAAGAGATTTCTCAGTGGTGGCCAGGTCCTAA
mouse_chr17      -----
-----

human_chr6_NM_001090
TAGCTTTTATTCCCCAGCAAGGGCAAGACCACACTCCTCAAGCACATTGCCAACCGAGCC
mouse_chr17      -----
CAAAGGCAAAACCACGCTTCTGAAGCACATTGCCAACCGTGCC
***** ***** ** **

*****

human_chr6_NM_001090
CTGAGCATCCCTCCCAACATTGATGTGTTGCTGTGTGAGCAGGGTGAGACCACTGGG---
mouse_chr17
CTGAGCATCCCCCTAACATTGACGTGCTGCTGTGCGAGCAGGGTGAGGCTGGGGAGTGG
***** ** ***** ** ***** ***** *
* *
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr6_NM_001634      -
GCCAGATCAAACCTTGAAATTCTGATGAGTGAGCTTGACCCAGCAGTTATGGACCAGT
mouse_chr10
AGCCAGATCAAACACTGGAAATTCTGATGAGTGAGCTTGACCCAGCAGTTATGGACCAGT
*****
*****

human_chr6_NM_001634
TCTACATGAAAGATGGTGTACTGCAAAGGATGTCACTCGTGTAAAGCATTTTTAGTAATA
mouse_chr10      TCTACATGAAAGATGGTGTACTGCAAAGGATGTCACTCGT-----
-----
*****

human_chr6_NM_001634
ATTGTTGCTGGACTCTTCTGCGTGGGGACTAAATTTTATTTTTCATTCTGTAACCTTTTAA
mouse_chr10      -----
-----

human_chr6_NM_001634
GTTTCAGGGTAACAAGTGCTAGTTTGTACATAGGTAACTTGTGTCATGGGGGTTTGTCG
mouse_chr10      -----
-----

human_chr6_NM_001634
TACACAGTATTTTCGTCACCCAGGTGTTAAGCCTAGTACCCATTAGTTATTTTTCCTGGTC
mouse_chr10      -----
-----

human_chr6_NM_001634
CTCTCCCTTCTCCCACCCTGGGACTAAATTTTGGACTCAATTGAAGTTTATTTGTCAAAC
mouse_chr10      -----
-----

human_chr6_NM_001634
CCTTGTTAAACTCGGTCTTTTTCCCCCCCCAGGAGAGTGGAATTCGTGACCTGATACCAG
mouse_chr10      -----
GAGAGTGGAATTCGTGACCTGATACCAG

*****

human_chr6_NM_001634
GTTCTGTCATTGATGCCACAATGTTCAATCCTTGTGGGTATTTCGATGAATGGAATGAAAT
mouse_chr10
GTTCTGTCATTGATGCCACACTGTTCAATCCTTGTGGCTACTCGATGAATGGAATGAAAT
*****
*****

human_chr6_NM_001634      CGGATGTGAGTA-----
mouse_chr10      CGGATGTGAGTAGCTGT
*****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr6_NM_007355      -
GACCTTTTTGAGAACAAGAAGAAAAGAACAACATCAAACCTCTATGTCCGCCGTGTGTT
mouse_chr17
CGACCTTTTTGAGAACAAGAAGAAGAACAACATCAAATTGTATGTCCGCCGTGTGTT
*****
*****

human_chr6_NM_007355
CATCATGGACAGCTGTGATGAGTTGATAACCAGAGTATCTCAGTGAGTATCTCCTTGGCCT
mouse_chr17              CATCATGGACAGCTGTGACGAGCTGATACCTGAGTACCTCA-----
-----
*****

human_chr6_NM_007355
AATTTAGTTGGGTGAAGTCTTGGGAGGTTTTAGGCATTCTGCTAGGATATTCTAAGGTAA
mouse_chr17              -----
-----

human_chr6_NM_007355
CAGTTTTCTGCAATACATAGTAGGTGTAAGGGTTCAGGAGGCTATTAGAGCCTTCTGTTT
mouse_chr17              -----
-----

human_chr6_NM_007355
GAATCTGGGGACCAGGTCTGGTCTAGCTGTTTTTTACTGAGCTTTCTCACCCCTGGTTGAT
mouse_chr17              -----
-----

human_chr6_NM_007355
GGCAGATTTTATCCGTGGTGTGGTTGACTCTGAGGATCTGCCCTGAACATCTCCCGAGA
mouse_chr17              -----
ACTTTATCCGCGGTGTGGTTGACTCCGAGGACCTGCCCTGAACATCTCCCGGGA
*****
*****

human_chr6_NM_007355      AATGCTCCAGCAGAGCAAAATCTTGAAAGTCATTTCGAAAAACAT----
mouse_chr17              GATGCTGCAGCAGAGCAAGATCCTGAAGGTCATCCGCAAGAACATCGTC
*****
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr6_NM_022551      -
TCACTTCATT CAGGGTGTGGGCCGAAGATATGCTCATGTGGTGTGAGGAAAGCAGACA
mouse_chr17
ACTTTTGACCTCAGGGCGTGGGGCGGAGATATGCTCATGTGGTGTGAGGAAAGCAGACA
                        *   *   *   *   *   *   *
*****

human_chr6_NM_022551
TTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGAGGACAAGGAAGGGGG
mouse_chr17              TCGACCTCACCAAGAGGGCTGGAGAACTCACGGAGGATGAG-----
-----
                        *   *   *   *   *   *   *

human_chr6_NM_022551
CTGGGGGTGGGGT CAGCCTCAGAAAGGGGTCCATCTAGATCTGACCTTGGTCTGCCTGCC
mouse_chr17              -----
-----

human_chr6_NM_022551
AGGTGGAACGTGTGATCACCATTATGCAGAATCCACGCCAGTACAAGATCCCAGACTGGT
mouse_chr17              --
GTGGAGCGAGTGATCACCATCATGCAGAACCCACGACAGTACAAGATCCCAGACTGGT
                        *****
*****

human_chr6_NM_022551      TCTTGAACAGACAGAAGGATGTAAAGGATGGAAAATACAGCC--
mouse_chr17              TCCTGAACAGACAGAAGGATGTGAAGGATGGGAAGTACAGCCAG
                        ** ***** ** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr6_NM_138419      -----
ATTATAGTCATCATTCAAAAAGCCAGAGAAATAAAGATATTCCAAACATGTTGG
mouse_chr10
AGACCGATGACAGCCATCATTCAAAAAGCCAGAGACTTCGTGATGTCCCAAACATGCTGG
                                ** * ** ***** *      *** *
***** **

human_chr6_NM_138419
ACGTTCTAAAGGATATGAATAAGGTTAAGCTTCGTGCAATTGAGCGGTATGTTGTTGTAA
mouse_chr10                ATGTTCTGAAGGACGTGAACAAGGTCAGACTTCGGCCTGTGAAAG-----
-----
                                * ***** *      * * * *
                                * * * * * * * * * * * * * * * *

human_chr6_NM_138419
TTTGAAAAGTGAAGTGAATTTTGTCAATTTTATGTTTAGAAAAATTATTATGTTTATGA
mouse_chr10                -----
-----

human_chr6_NM_138419
AAATTAACATATATGTCTTTTTTCTTATTCTTCTTCCACCCTGAATACCTCTCCTAGAGA
mouse_chr10                -----
-----

human_chr6_NM_138419
TAATGACATTCAATTATTTTGTACTATTTCTTCTTCTAGTCTCTTATCACCATATTTTGT
mouse_chr10                -----
-----

human_chr6_NM_138419
AAACAACATACTTATTTGCTATTTCTTGATATTTTAATTATGTTGACTTCCAATTGTAGG
mouse_chr10                -----
-----

human_chr6_NM_138419
ATATTAGGAATATATTTTCTTAGATACTCTACCCAGGACACACACACATCTTGCCACG
mouse_chr10                -----
-----

human_chr6_NM_138419
TCTTCCTGAAATAGTTAAACCACAATCTTTAGTTAAATGAGTATTCAGAATTAATATCCT
mouse_chr10                -----
-----

human_chr6_NM_138419
TATTATAACAGTGAACATCCACAGTAAGCCATTTCTCATATTGTAACCCAGGCTGTAGGG
mouse_chr10                -----
-----
```

human_chr6_NM_138419
CAGTGTGGAAATTACAGCTCACTGCAGCCTCGACCTCCTGGGCTCAAGTGATCCTCCCAC
mouse_chr10 -----

human_chr6_NM_138419
CTCAGCTTCCTTAGTAGCTGGGACTATAGGCATGTGCCACCATGCCTGGCTAATTTTTTGT
mouse_chr10 -----

human_chr6_NM_138419
ATTTTTTTGTAGAGATGGGGTTTTCGCCATGTTGCCAGGCTGGTCTCTAACTCCTGAGCT
mouse_chr10 -----

human_chr6_NM_138419
CAAGCGATCTGCCCATGTTGGCCTCCCAAAGCGCTGGGATTACAGGTGTGAGCCACTGTG
mouse_chr10 -----

human_chr6_NM_138419
CCTGGCCCCATTTTCATATATTTTTGACTACATTTTTATTTGTTGAATAATTTTTTTAGAGTT
mouse_chr10 -----

human_chr6_NM_138419
AATAATTGCCTCTCTGAGTTCCATGTGTGTGTGTGTGTGTGTGTGTGTGGTGAAAA
mouse_chr10 -----

human_chr6_NM_138419
AACATAATGAGCTCTATTCTGTAAACAAATTTTTATGTGTATAATACAGTATCGTTAAGC
mouse_chr10 -----

human_chr6_NM_138419
ACAATGTTGTACAACAGATCTCTAGAGCTTTTTTCATCTTGCATAACTGAAATTTTATACT
mouse_chr10 -----

human_chr6_NM_138419
CACTGAACAGTAATCATTTCCTCTCCCCTCATCCCCTGGCAACTGCCATTCTTCTTTCT
mouse_chr10 -----

human_chr6_NM_138419
ACTTCTATAGTTTTGATTACTTTATTTTTTATTTTATCTTATTAATAAAAAAATAGAGACAGG
mouse_chr10 -----

human_chr6_NM_138419
ATTTCACTGTGTTGCCAGGCTGGTCTTGAAGCTCGGCTCAAGTGATCCTCCTGCCTCGGT
mouse_chr10 -----

human_chr6_NM_138419
CTCTCAAAGTACTGGGATTACAGGCAAGAGCCACTGTGTCTGGCCCAGTTTGATTACTTT
mouse_chr10 -----

human_chr6_NM_138419
AGATGCCTCATATAAGTGAATCATGCAGCATTATCTTTTTGTGACTGGCTTATTTCACT
mouse_chr10 -----

human_chr6_NM_138419
TAGCATGCTGTATATTGTATGTATATATCCCATTTCTTAATCCATTCATCTGTTGATAGA
mouse_chr10 -----

human_chr6_NM_138419
CATTTAGTTTGCTTCCATGTCTTGTCTATTGTAAATAGCACTGCAATGAATGTGGGTGTG
mouse_chr10 -----

human_chr6_NM_138419
CAGATATCTCTTTGAGATGCTGATTTCACTTCTTTTTGGATAAGTACCCAGAAGTGGGATT
mouse_chr10 -----

human_chr6_NM_138419
GCTGGATCATAGGGTAGTTCTATTTCTAATTTTTGGATGACCCTCCATTTAGTTCTTGGT
mouse_chr10 -----

human_chr6_NM_138419
GATTCTCCTCAAGGATCCCTCTGTGCCTGAAGGATTTCTTCGCTTACCTCTTGAGCATT
mouse_chr10 -----

human_chr6_NM_138419
CTTGCCCCCTTTTTCTATGCTGCATCACTGATTTCTAAATGTCATATCTTCCTATAGC
mouse_chr10 -----

human_chr6_NM_138419
TTCCTGAGAAACATAAAGGGTAGATTAGTTTACTACTTTGCATGTCCAAAAATGTTCTTT
mouse_chr10 -----

human_chr6_NM_138419
TATTCTTTTTTTTTTTAGATGGAGTCTGGCTCTGTGCGCCCGGGCTGGAGTGCAGTGGCA
mouse_chr10 -----

human_chr6_NM_138419
TGATCTTGGCTCACTGCAGCTTCTGCCTCCTGGGTCTTGGTTCAAGCAATTCTTTTGCTG
mouse_chr10 -----

human_chr6_NM_138419
CAGCCTCCCGAGTAGCTGGGATTACAGGCACGTGCCACCATGCCAGCTAATTTTTGTAG
mouse_chr10 -----

human_chr6_NM_138419
TTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCATGAACTCCTGACCTTGT
mouse_chr10 -----

human_chr6_NM_138419
GATCTGCCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCACACCTGG
mouse_chr10 -----

human_chr6_NM_138419
CCCACATTTTTAATTTTTAAGAGCTGTTTCTTTTTCTTCAAATGCTTCTTGTAAATCT
mouse_chr10 -----

human_chr6_NM_138419
TTTTGGTTTTGTTGGTCTTATCCCACTGACAGTATTAAGTGTAGGTTTGTTTAAAGTT
mouse_chr10 -----

human_chr6_NM_138419
TCCTCTGTTCTTGAATACTGTATTTTTGTGAGTTTCTTTTTCTTTTAGCTTTGATC
mouse_chr10 -----

human_chr6_NM_138419
TCTATCTTTAGTTTTGTAGCCTTGGGTAAGCATCTGGTGATTCTTATTTAAATGAGGCA
mouse_chr10 -----

human_chr6_NM_138419
AGGAAAAGCTGATCGCATGTTCTTTGTGTGAGGTGGGCTTATCAACTTGGGAGCTTCACA

mouse_chr10 -----

human_chr6_NM_138419
GTTTAGTGATTAGGGAGAGGACCATTTTGTGGCCACACCCAGAGCTGTATGTCTTTTC
mouse_chr10 -----

human_chr6_NM_138419
TTTTGGGCTACAGGATTTTCCTTAGAAAGTTCTTCATTCTCCCTTGTGGTCAGGAGGGAT
mouse_chr10 -----

human_chr6_NM_138419
GGGGATTACACAGCGGGTGCAAGTCAGGTCATTGGAGAGCTGAGTGGGGAAAGAGGAGCA
mouse_chr10 -----

human_chr6_NM_138419
AGAGAGAAGTGTCTTATTTAGCACACGCCCTGTGTTTCAGCAGGGCGCCCACGCCCCATGC
mouse_chr10 -----

human_chr6_NM_138419
TCTCACTTTTCATCAGCTTTCCAGCTTCCGGCATCTGGTTGCAATTCTTATCTCCTGTCTC
mouse_chr10 -----

human_chr6_NM_138419
CCCTTCTAATCTCTTTGTCCTTGTGGATATATAGATCTTTTTTCATTTCTTTACTGTCATT
mouse_chr10 -----

human_chr6_NM_138419
TTAGTAGGATTTTACAAGGGATTTGCCATGCTTACTTGGAAATCCCTCAGTGAGGTTTTTC
mouse_chr10 -----

human_chr6_NM_138419
GGTGAGAAAATAGATATATTTTCTGTATGATAGTCCTGGGACAGATAAGTCAGTTCTGTT
mouse_chr10 -----

human_chr6_NM_138419
TTTAATGAGGTTGTGAGTTTGATCCTTGCAACGATGCAGAAGGGCTCATTTTAAGTGAAA
mouse_chr10 -----

human_chr6_NM_138419
TCCTTGTGAAGAGGAAAGAGAAGGGAAACCAGTAACCACAGGAAGAGCATGAGGCAGCTT
mouse_chr10 -----

human_chr6_NM_138419
GTTGAGAAGAATCTCATGGCTGTAGGTGCATGCTTGGTCCCAACTAGATCTTGTACTTGT
mouse_chr10 -----

human_chr6_NM_138419
GTTGTCGGGCTTAGTATCAAGTGGCAACTCTGTGACTGTTACCATCACTGGAAAAACAAC
mouse_chr10 -----

human_chr6_NM_138419
TAAAAGGCCAGTAGCCTCTGCCTCCTGTCCCCCTATTCTCTCCTGAGTTGCCTCTACAGC
mouse_chr10 -----

human_chr6_NM_138419
TAAC TTTG TTTTGTACGTTGCTGAGGAATCAGATGAGCTCTCTCACCTCTTTACACCTAC
mouse_chr10 -----

human_chr6_NM_138419
AGATTCCCCGTGCAGATTCTCTGCCTTCCATCTTGCTGTTGGGAGCCAAGTGTCATCATT
mouse_chr10 -----

human_chr6_NM_138419
CATGGCCAGGCTCTTCCTTTGGTTACTGGTTTCCCTTCTCTTTCTCTTCCACAAGGATTT
mouse_chr10 -----

human_chr6_NM_138419
CACTTAAAATGAGCCCTTCTGCATCACTGAGTCTTCCTTCTATACTTCATCCTTCTCCTC
mouse_chr10 -----

human_chr6_NM_138419
ACACCTGAGTACTTCCCACCTTCAAACACATGTA CTCTCAGCCGTTGTTCTGTTGTTCT
mouse_chr10 -----

human_chr6_NM_138419
GCTCCCCTTTCTGATATGAATTCTTGAAGTCGTCTATAATTTGTTTCTGTCTATCGCTGC
mouse_chr10 -----

human_chr6_NM_138419
TGCCTTCTACCCATGAAAACCTCCATTGAAAACCTGCTTCACCAGTGACTCCATGTGGCTAA
mouse_chr10 -----

human_chr6_NM_138419
ATCCACTGGTCTCTTAGCATTGCTCGTCTTAGTTGACCTCTTGGCAGCATTGATAACAGC
mouse_chr10 -----

human_chr6_NM_138419
CTATGGTCCCCACCTCCTTGGAGCACTTTCTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTG
mouse_chr10 -----

human_chr6_NM_138419
TTGCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAACCTCTGCCTCCTGGATT
mouse_chr10 -----

human_chr6_NM_138419
CAAGTGATTCTCCTGCCTCGGCCTCCCGAGTAGCTGGGACTACAGGCATGTGCCACCATG
mouse_chr10 -----

human_chr6_NM_138419
CTCAGCTAATTTTTGTATTTTTAGTAGAGATAGGGTTTCACCGTATTGGCCAGGATGGTC
mouse_chr10 -----

human_chr6_NM_138419
TCGATCTCTTGACCGCATGATCCGACCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGC
mouse_chr10 -----

human_chr6_NM_138419
ATGAGCCACTGCGCCTAGCCTGGAGCACTTTCTTTACTTGGTTTCTGGGAAAGCATAACC
mouse_chr10 -----

human_chr6_NM_138419
CCAGGTTTCCTCTGACCTCATCAGCTATTCTTTCTTATTCTTAAACTCTTCCCCCTGGG
mouse_chr10 -----

human_chr6_NM_138419
CCTGGTCTTTAAATGTTGAAATACCTGGTTTCAGACCTCAGCCCCCTCTCTTCTCTGTCCA
mouse_chr10 -----

human_chr6_NM_138419
TGCTGTTTCCTTTGGTGAGCTCACCTAGTCCTATGACTCTAAATACCAGCTGTATGCTTA
mouse_chr10 -----

human_chr6_NM_138419
TGACTCAAACGTTTATTTTTCTAGCCCTGACCTCTCCTCTTGAGCCCAGATGCACATACT
mouse_chr10 -----

human_chr6_NM_138419
GAAATGCCTACTTGACATCTTTATTTGCCTGTCTCACAGGTATCTCGTTTCACAGGTCCA
mouse_chr10 -----

human_chr6_NM_138419
AAACAGGACTTTTCCTTCTACCTGTTCTTTTCCGCCACCTTGAAAACCTGTTCTTTCCC
mouse_chr10 -----

human_chr6_NM_138419
ACGTCTTTTGCATATTAGCAAATGGCAACACGATCACCCGGTTGCTTAAGATCTAGGAAT
mouse_chr10 -----

human_chr6_NM_138419
CAGGCCAGGTGCGGTGGCTCACACCAGTAAACACAGCACTTTGAGAGGCTGAGGTGGGCA
mouse_chr10 -----

human_chr6_NM_138419
GATCACTCGAGGTGAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCAGTCTCTA
mouse_chr10 -----

human_chr6_NM_138419
CTAAAAATACAAAAATTACCCTGACATGATGGCGCACACCTGTAATCCCAGCTACTAGGA
mouse_chr10 -----

human_chr6_NM_138419
GGCTGAGGCAGGAGAATTAATTGTTTGGAGCCCGGGAGGCGGAGGTTGCAGTGAGCCACTA
mouse_chr10 -----

human_chr6_NM_138419
TACTCCAGCCTTGGTGACAAAGCGAGACTCCGTCTCAAAAAACAAAAACAAATATCTAG

mouse_chr10 -----

human_chr6_NM_138419
GAATCATCCTTCATCTTTATTTTCCATTCTATCTCCCACCGTTCCCATCAGCACATAGCT
mouse_chr10 -----

human_chr6_NM_138419
CAATTCTGTGGACCTCTTGACCTCCACTGCCAACTCCCCAGGCTAAGCCCATTCTTATCT
mouse_chr10 -----

human_chr6_NM_138419
AGCTTAGACTTCCGCAGCAGCCTCCTCAGTGATCTGTTTTTCATTCTTGCCCTCCTTATTTA
mouse_chr10 -----

human_chr6_NM_138419
TTCTGCAGATAGTGACCAGAAGTCAGATCAGGCCATTCTCCTGCTTCAGACTCTTCTGTG
mouse_chr10 -----

human_chr6_NM_138419
GGTTTCCGTTGTGCTTGAATCAGTTCTAGAGCCCTTGCTGTGTCCGTAGGCCCTCCAGG
mouse_chr10 -----

human_chr6_NM_138419
AGCCAGCCCTCACTTCTCTCGCTGAGCTCCTCTCCTATGCCCATGTTTGCCCACTGCAC
mouse_chr10 -----

human_chr6_NM_138419
TCCAGCTGCAGTTGCTTTCTTTTTTCCGTTTCTCACACATGCCAAGCTCCTTCCTGATGC
mouse_chr10 -----

human_chr6_NM_138419
AGCCCCAGATGTTTACTAAAAGTACCCTTGTCAATTTCTTAAAGAGGATGTTGCTT
mouse_chr10 -----

human_chr6_NM_138419
CCTTAAAGAGGCTTTTTTCTGATCATATCTAAAGTGCTTCTGTCCCTAATCACTATTAC
mouse_chr10 -----

human_chr6_NM_138419
ATTTCCCTATTTTTTATTTTTTAATTTAGTTTTTTTTTTTTTTTTTTTGGAGACAGGGTGTT
mouse_chr10 -----

human_chr6_NM_138419
GCTCTGTCACCCAGGCTGGAGTGTAGTGGTGCCATGACTTGCTGCAGGCTTGACCTCCTT
mouse_chr10 -----

human_chr6_NM_138419
GGCTCAAGTGATCCTCCTGCCTTAACCTCCCAAGTAGTTGCCTGGCTAATTTTTAAATTT
mouse_chr10 -----

human_chr6_NM_138419
TTTCTAGAGATGGGGTCTCGCTATGTTACCCAAGCTGCTCTCGAACTCCTGGGCTCAGGC
mouse_chr10 -----

human_chr6_NM_138419
AGTCCTCCCACCTTGGCCTCCTAAAGTGTGGGATTATAGGCATGAGCTACCGTGCCCAG
mouse_chr10 -----

human_chr6_NM_138419
CCTCTGTTTTGTTTTATTACAGCTCTTATTACCAGCCAAATGATCTTACTTGTATATTG
mouse_chr10 -----

human_chr6_NM_138419
ATGATAATCTTGCTGTAAGAATTGGGAGCAGAATACTCCCAAAGCATAAAATGGAGTCGG
mouse_chr10 -----

human_chr6_NM_138419
ATGTGGTAGTGGGCATTCAATGAAGATTAATGAATGAACAACCAAACAAATGAACAATT
mouse_chr10 -----

human_chr6_NM_138419
TGCCTAATTTTTTTTTTTTTGGCATGAACTCTCGTCCTTTTAAAAGTTCTTATTTATTTG
mouse_chr10 -----

human_chr6_NM_138419
AATTTTCCTACCCATTAGGAAATTAGAAAATTACCATAATAAAGATCTTCAGCATAGTGA
mouse_chr10 -----

human_chr6_NM_138419
CATCTGACAAATCTCAGGTATAACAAGGTTATGGCAGAGTCTCAAGTCACATGGGTTCT
mouse_chr10 -----

human_chr6_NM_138419
TGGTTTTCTGATTCTTCATTCATTGTGCCTTCCTTATTTTCATTGCGAAAATTTCTTGAAG
mouse_chr10 -----

human_chr6_NM_138419
ATTAGATTATTTTCAATCTCTTGAAGACTAATTAATTTGTAAGATATGCTTGTATTCCTG
mouse_chr10 -----

human_chr6_NM_138419
CCATGTTTGTCAACAAGGAGCTAAAATTACATCCAAGTTTTAATAAATTCAATTTTTTTTT
mouse_chr10 -----

human_chr6_NM_138419
TTTTAAAAATAGGTCACCTGGCGGTAGACCCATTCATAAGAGGAAAAGACAGAATTCACA
mouse_chr10 -----
GTCACCAGGTGGCAGACCCGTTTCAGAAGAGGAAGAGACGGAGTTTCAGA
***** ** ** ***** ** *
**** *

human_chr6_NM_138419
mouse_chr10 TTGGGATCCAGTTTCTTTAATATCTCATGCACTTAAACAGAAATTTGCATTT-
ATGGGATCCAGTGTCTTTAATATCTAATGCACTGAAGCAGAAGTTTGCATTT
***** ***** ***** ** ***** *****

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr8_NM_006421      -----
GTGTTCTTTTAAAGAAATTTTCTTATACATTTTGGAAACTTCTACCAGCTCATT
mouse_chr1
GTCACAGGTATTCTTTAAAGAAATCTTCTGTACATTTTGGAAACGTCTACAAGCTCATT
                                     ** ***** ** * *****
*****

human_chr8_NM_006421
TGATCACAAATGGATGGTTATTCAGACACTGACGAGGATTTGTGCAGGTATTTTAAATTA
mouse_chr1                      TGACCATAAGTGGATGGTTATTCAGACACTGACAAGGATCTGTGCAG-----
-----
                                     *** ** * ***** *****

human_chr8_NM_006421
TCCTTTTTTATTATCTCTTTCTTATTATTAGATATTTAAAAGGCCAAATGTACTCATATCC
mouse_chr1                      -----
-----

human_chr8_NM_006421
TAGATGTACTTTGTTGAAATTAATGTTATATTGTTACAGATGCTCAGAGTGTAGTGGATA
mouse_chr1                      -----
ATGCTCAGAGTGTGGTGGACA
                                     *****

***** *

human_chr8_NM_006421
TTTATGTAAACTATGACTGTGACTTAAATGCAGCCAATATATTTGAAAGACTAGTAAATG
mouse_chr1
TTTATGTAAATTATGACTGTGACCTAAATGCAGCAAATATATTTGAAAGACTAGTAAATG
                                     *****
*****

human_chr8_NM_006421      ATCTATCAAAAATTGCTCA-
mouse_chr1                ACCTGTCGAAAATTGCCCAA
                           * ** * ***** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr9_NM_001010      -----  
GCAGCACAAACGGCGGCGTATTGCTCTGAAGAAGCAGCGTACCAAGAAAAATAA  
mouse_chr4  
TGTCCTGCAACACAAACGCCGACGTATTGCTCTGAAGAAGCAACGCACTAAGAAGAACAA  
*** ***** ** ***** ** ** *****  
** **
```

```
human_chr9_NM_001010  
AGAAGAGGCTGCAGAATATGCTAAACTTTTGGCCAAGAGAATGAAGGTTAGTCTAAGATG  
mouse_chr4                GGAGGAGGCTGCAGAATACGCTAAACTTTTGGCCAAGAGAATGAAG-----  
-----  
** ***** *****
```

```
human_chr9_NM_001010  
ATTTGAGGGGTGGGAGGAGTTCGACCTGGCTTTGGATTTGCGTCTTTAACCCAGAAAGG  
mouse_chr4                -----  
-----
```

```
human_chr9_NM_001010  
CCTTAACTGTTTGCTGTTTTGTTTTGTTTAGGAGGCTAAGGAGAAGCGCCAGGAACAAAT  
mouse_chr4                -----  
GAAGCCAAAGAAAAGCGCCAGGAACAGAT  
** ** ** **  
***** **
```

```
human_chr9_NM_001010  
TGCGAAGAGACGCAGACTTTCCTCTCTGCGAGCTTCTACTTCTAAGTCTGAATCCAGTCA  
mouse_chr4  
TGCCAAGAGACGTAGGCTGTCCTCACTGAGAGCTTCTACTTCTAAGTCTGAGTCCAGTCA  
*** ***** ** ** ***** ** *****  
*****
```

```
human_chr9_NM_001010      GAAATAAGATT-  
mouse_chr4                AAAATGAGTCTT  
***** ** *
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr11_NM_000920 -----TCACTGCTGGCCACTCGTGTGCGCACCCACGATCTCAAAAAGAT
mouse_chr19      CACCAGTCACTACTGGCCACTAGAGTGCGCACACATGATCTCAAAAAGAT
                  *****
human_chr11_NM_000920 CGCCCCCTATGTTGCCCACTTTCAGCAAGCTCTTCAGCATGGAGAACT
mouse_chr19      TGCGCCCTATGTTGCCCACTTCAACAAGCTCTTCAGCATGGAGAACT
                  **
human_chr11_NM_000920 GGGGAGGTAGGCTGGCATGCTGCGCAGCGCCTGGTAGGAATGGGCGCCCG
mouse_chr19      GGGGAG-----
                  *****
human_chr11_NM_000920 CTCTGTGGCCAGTCCCACAGGCTTAGGCCACTGGGGACAAGCTAGAGACG
mouse_chr19      -----
human_chr11_NM_000920 CTGACACGAAGAACACCAAAGAGGAAGGACCGAAGAAGGCACAGCGCCCT
mouse_chr19      -----
human_chr11_NM_000920 CTCCGGCCAGGCCTGGTGCCGGCACGAGGTTGCAGAGCTGAGACCAGGTG
mouse_chr19      -----
human_chr11_NM_000920 CATCCTGGGAGGTCCAGGGTCAGGAGGAGACACCTGCCTGTTAATTATAG
mouse_chr19      -----
human_chr11_NM_000920 CACAGAGAGGTAGAGGAGAAGATGGGATTATAAAGGGGGCATAGAAGGGA
mouse_chr19      -----
human_chr11_NM_000920 CACAAATGAGCCTGGTCTCCCCCTTAGAGATCAGACAAGGGAAAAATCTG
mouse_chr19      -----
human_chr11_NM_000920 TGGGGGTTGGAGCAGGGAACACAGGTATGGCGAAGATGAGCAGGACCTGG
mouse_chr19      -----
human_chr11_NM_000920 TATTGGGGCCAGAGGCTTGTGCTGCAGAGCTAGCTCCAAGGCCTGGTGG
mouse_chr19      -----
human_chr11_NM_000920 GTTCCCCAGGCATGCAGAGCTGATCTGGGCCTCTCGGTTCTGTGCAGGA
mouse_chr19      -----GC
                  *
human_chr11_NM_000920 GCCACGTTTGACGTGCGCATGCGCTTCCTGTATGAGTGCCCTGGCGGGCG
mouse_chr19      GCCACGTTGACGTTGCCATGCGCTTCCTGTACGAGTGCCCTGGCGGGCG
                  *****
human_chr11_NM_000920 GCTGCAGGAGCTCCGGGAGCTCATCCCCAACATCCCTTTCCAGATGCT-
mouse_chr19      GCTCCAGGAGCTCCGGGAGCTTATCCCGAACATCCCGTTCCAGATGCTA
                  ***
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr11_NM_004357      -CCGCGCCCCGCAGGGCGGCTGCATCACCAAGTTGGAGACCTTCATCCAG
mouse_chr7                 TTCTCTCCCACTAGGGTGGCTGTATCACTAAGCTGGAGACCTTCATTCAG
                          * * ***      ***** ***** ***** *** ***** *****
human_chr11_NM_004357      GAGCACCTGAGGGTCATTGGGGCTGTGGGGATCGGCATTGCCTGTGTGCA
mouse_chr7                 GAGCACCTGCGGGTCATTGGGGCGGTGGGCATTGGCATCGCCTGTGTGCA
                          ***** ***** ***** ** ***** *****
human_chr11_NM_004357      GGTGAGGGCACATGGGGGTGGCGGTCATCTTGTTGGGGACACGGGGCAGG
mouse_chr7                 G-----
                          *
human_chr11_NM_004357      GCGGTGGCTGGTGGCCCCATGACGTCTGCTTACGCCACCCGGCTCTGCA
mouse_chr7                 -----
human_chr11_NM_004357      CACAGGTCTTTGGCATGATCTTCACGTGCTGCCTGTACAGGAGTCTCAAG
mouse_chr7                 -----GTCTTCGGCATGATCTTCACCTGCTGCTTGTACCGAAGCCTCAAG
                          ***** ***** ***** ***** * ** *****
human_chr11_NM_004357      CTGGAGCACTACTGACCCTGCCTTGGGCCTTGCTGCTGCTGCACCCAACT
mouse_chr7                 CTGGAACACTACTGACCACGATGATGTCAGGCCGGGCGGCCAGCCTTGCA
                          ***** ***** *      * *      * * *      ** *
human_chr11_NM_004357      ACTGA-
mouse_chr7                 CTACTG
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr11_NM_015104 -----CCAGGCGCCGCCGGTGGACGTGCATCAGCCGCCTGCCTT
mouse_chr19      CGGGACCCCAGCCAGGCCCCACCTGTGGACGTGCACCAGCCGCCTGCCTT
                  ***** ** ** *****
human_chr11_NM_015104 CCTGCACAAGCTGCTGCAGCTGGCAGGGGTCCGCCTGCACTACGAGGAGC
mouse_chr19      CCTGCACAAGCTGCTGCAGCTGAGTGGGGTCTGCCTATACTTTGAGGAGC
                  ***** ***** ** ** *****
human_chr11_NM_015104 TCCCGGCACAGGTGAGCGGGCTCTGATTCCCACAGCCCCTGTCTCCTCTC
mouse_chr19      TGCCCTCCCAG-----
                  * ** * **
human_chr11_NM_015104 CCTTGAGCCCATTGAGCCCCTCCCATCCTTTCTGACCATCTCTGACTCCA
mouse_chr19      -----
human_chr11_NM_015104 TTTTCTCAACCTTTCCCTCTTGTATCCTCCCGTCTCCAGGAAGAGCCTC
mouse_chr19      -----GCAGACCCAC
                  * ** ** *
human_chr11_NM_015104 CAGAGCCCCCCTTGAGATCGGCAGCTGCTCAGGGTACATGGAGCTGATG
mouse_chr19      CACAGCCACCTCTGCAAATCGGCAGCTGCACGGGGTACGTGGAGCTCATG
                  ** ** ** ** ** ** ** ** ** ** ** ** * ** ** ** ** ** ** **
human_chr11_NM_015104 GTGAAGTTGAAGCAAAATGAGGCCTTCCCTGGCCCCAAGG-
mouse_chr19      GTGAGGCTGAAGCAGAACGAGGCCTTTCCAGGCCCAAGGT
                  ***** * ***** ** ***** ** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr11_NM_020680      -GACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGAGAGTGGAG
mouse_chr19                TGACAGAGGCTGTGACCCCCCTGGGAACATACCTCAAGGCACGAGCAGAA
                        *****
human_chr11_NM_020680      GCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGT
mouse_chr19                GCAGGTGGCCTGAAGGAGCAGGAGCTGTCATGGGGGTTACACCAGATCGT
                        ** *****
human_chr11_NM_020680      GGTGAGGTGGGGGCAGTGGTGATGAGAGCAGGGATGGGGGTTGCAGGT
mouse_chr19                G-----
                        *
human_chr11_NM_020680      GCTGGGGCGTGATGGCTCCTTTTGCCCCAGAAAGCCCTCAGCTTCCTGG
mouse_chr19                -----AAAGCCCTCAGCTTCCTGG
                        *****
human_chr11_NM_020680      TCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCGCGTGTTC
mouse_chr19                TCAACGACTGCAACCTCATCCACAATAATGTCTGCATGGCCGCTGTGTTT
                        *****
human_chr11_NM_020680      GTGGACCGAGCTGGCGAGTGAAGCTTGGGG---
mouse_chr19                GTGGACAGGGCTGGCGAGTGGAACTTGGGGGTC
                        *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_001273      -----CATTGCCCGAATTCCCCCAGTTGCTGTGAGGTTACAGATGTCAG
mouse_chr6                  AGCCACCATTGCCCGCATCCCCCAGTCGCTGTGAGGTTACAGATGTCAG
                             ***** ** ***** *****
human_chr12_NM_001273      AGCGTAACATTCTCAGCCGCCTGGCAAACCGGGCACCCGAACCTACCCCA
mouse_chr6                  AGCGGAACATTCTCAGCCGCCTGGCAAACAGGGCGCCAGAACCTCCCCCA
                             ***** *****
human_chr12_NM_001273      CAGCAGGTAGGACCATTTTCTTCTTGACACCACCTCTTCCTGCAGAACCA
mouse_chr6                  CAGCAG-----
                             *****
human_chr12_NM_001273      TTCTGGAGCTTGTAACTTTGCTGTATGTCCCTAGCTTTACATACTGGGTG
mouse_chr6                  -----
human_chr12_NM_001273      GGTGGCCTATCAGTGAATTCCCTTGAGATTGGGTGGATTCCCTATCATCTG
mouse_chr6                  -----
human_chr12_NM_001273      GAATTCTGACTCCTCGGGTCTCCTTCTCTAGGTAGCCAGCAGCAGTGAA
mouse_chr6                  -----GTAGCCAGCAGCAGTGAA
                             *****
human_chr12_NM_001273      GATGC--AGACTGATACCACCTCCACCGCTGAGCAGTGACCTTCCTCACT
mouse_chr6                  AGACCCAGAGTGATATCCACCTCCACCACTCAGCAGTGACCTTCCTCACT
                             *          ***** ** *****
human_chr12_NM_001273      TTCTCTTGTCAGCTTCTCCCCTGGGGGCCTG
mouse_chr6                  TTCTCTTGTCAGCTTCTCCCCTGGGGGCCAGA-
                             ***** ** * ** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_002046      -ATTTGGTCGTATTGGGCGCCTGGTCACCAGGGCTGCTTTTAACTCTGGT
mouse_chr6                 GATTTGGCCGTATTGGGCGCCTGGTCACCAGGGCTGCCATTTGCAGTGGC
                          ***** ** * ***

human_chr12_NM_002046      AAAGTGGATATTGTTGCCATCAATGACCCCTTCATTGACCTCAACTACAT
mouse_chr6                 AAAGTGGAGATTGTTGCCATCAACGACCCCTTCATTGACCTCAACTACAT
                          *****

human_chr12_NM_002046      GGTGAGTGCTACATGGTGAGCCCCAAAGCTGGTGTGGGAGGAGCCACCTG
mouse_chr6                 G-----
                          *

human_chr12_NM_002046      GCTGATGGGCAGCCCTTCATACCCTCACGTATTCCCCAGGTTTACATG-
mouse_chr6                 -----GTCTACATGG
                          *

human_chr12_NM_002046      TTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTCAAGGCTGA
mouse_chr6                 TTCCAGTATGACTCCACTCACGGCAAATTCAACGGCACAGTCAAGGCCGA
                          ***** **

human_chr12_NM_002046      GAACGGGAAGCTTGTCATCAATGGAAATCCCATCACCATCT--
mouse_chr6                 GAATGGGAAGCTTGTCATCAACGGGAAGCCCATCACCATCTTC
                          *** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_002046      -TGTTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTCAAGGC
mouse_chr6                 TGGTTCAGTATGACTCCACTCACGGCAAATTCAACGGCACAGTCAAGGC
                           ***** **
human_chr12_NM_002046      TGAGAACGGGAAGCTTGTTCATCAATGGAAATCCCATCACCATCTTCCAGG
mouse_chr6                 CGAGAATGGGAAGCTTGTTCATCAACGGGAAGCCCATCACCATCTTCCAGG
                           ***** **
human_chr12_NM_002046      AGTGAGTGAAGACAGAATGGAAGAAATGTGCTTTGGGGAGGCAACTAGG
mouse_chr6                 A-----
                           *
human_chr12_NM_002046      ATGGTGTGGCTCCCTTGGGTATATGGTAACCTTGTGTCCCTCAATATGGT
mouse_chr6                 -----
human_chr12_NM_002046      CCTGTCCCCTCTCCCCCCCACCCCATAGGCGAGATCCCTCCAAAATCA
mouse_chr6                 -----GCGAGACCCCACTAACATCA
                           ***** **
human_chr12_NM_002046      AGTGGGGCGATGCTGGCGCTGAGTACGTCGTGGAGTCCACTGGCGTCTTC
mouse_chr6                 AATGGGGTGAGGCCGGTGCTGAGTATGTCGTGGAGTCTACTGGTGTCTTC
                           * ***** **
human_chr12_NM_002046      ACCACCATGGAGAAGGCTGGGGTGAGTGCA-----
mouse_chr6                 ACCACCATGGAGAAGGCCGGGTAAGTGGCCGGAA
                           ***** **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_002046      -GAGCCAAAAGGGTCATCATCTCTGCCCCCTCTGCTGATGCCCCCATGTT
mouse_chr6                 GGAGCCAAAAGGGTCATCATCTCCGCCCCTTCTGCCGATGCCCCCATGTT
                             *****
human_chr12_NM_002046      CGTCATGGGTGTGAACCATGAGAAGTATGACAACAGCCTCAAGATCATCA
mouse_chr6                 TGTGATGGGTGTGAACCACGAGAAATATGACAACTCACTCAAGATTGTCA
                             ** *****
human_chr12_NM_002046      GGTGAGGAAGGCAGGGCCCGTGGAGAAGCGGCCAGCCTGGCACCCCTATGG
mouse_chr6                 G-----
                             *
human_chr12_NM_002046      ACACGCTCCCCTGACTTGCGCCCCGCTCCCTCTTTCTTTGCAGCAATGCC
mouse_chr6                 -----CAATGCA
                             *****
human_chr12_NM_002046      TCCTGCACCACCAACTGCTTAGCACCCCTGGCCAAGGTCATCCATGACAA
mouse_chr6                 TCCTGCACCACCAACTGCTTAGCCCCCTGGCCAAGGTCATCCATGACAA
                             *****
human_chr12_NM_002046      CTTTGGTATCGTGAAGGACTCATGGTATGAGAGCTGGGGAAT-
mouse_chr6                 CTTTGGCATTGTGAAGGGCTCATGGTATGTAGGCAGTGGGGAG
                             ***** ** ***** ** * **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_006191 -CTTTCTCTCTATTCCCTTTTAGGAAGGACCATGAAAAAGCTGAATTTGAG
mouse_chr10          GTTCCTTCTCTGTTCCCTTTTAGGAAGGACCATGAAAAGGCAGAATTTGAG
                    *      *****
human_chr12_NM_006191 GTACATGAAGTATATGCTGTGGATGTTCTCGTCAGCTCAGGAGAGGGCAA
mouse_chr10          GTGCATGAGGTTTATGCTGTAGATGTCCTCGTCAGCTCAGGAGAAGGCAA
                    ** ***** ** ***** *****
human_chr12_NM_006191 GGTGAGGAGAGTACCAGAGTTGGCAAAGAGGGGTGACTGAGAGTGTTTAC
mouse_chr10          G-----
                    *
human_chr12_NM_006191 CAGACCAAATGTTACTTAAATTACTCTTTCAGGCCAAGGATGCAGGACAG
mouse_chr10          -----GCCAAAGATGCAGGACAG
                    *****
human_chr12_NM_006191 AGAACCACTATTTACAAACGAGACCCCTCTAAACAGTATGGACTGAAAAT
mouse_chr10          AGAACCACTATTTACAAACGAGACCCCTCTAAACAATATGGCCTGAAAAT
                    ***** ** ***** *****
human_chr12_NM_006191 GAAAACTTCACGTGCCTTCTTCAGTGAGGTGG--
mouse_chr10          GAAAACTTCACGTGCCTTTTTCAGTGAGGTGGAA
                    *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr12_NM_053275      ----GCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACAC
mouse_chr5                  ATCCGCATGTCGCTCCGAGGGAAGGCCGTGGTGCTGATGGGCAAGAACAC
                             ***** ** ** ***** *****
human_chr12_NM_053275      CATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGG
mouse_chr5                  CATGATGCGCAAGGCTATCAGGGGCCACCTGGAGAACAACCCAGCTCTGG
                             ***** ** * ** ***** *****
human_chr12_NM_053275      AGAAGTCAGTTCCTGCGAGTTTTGTCCTTTCTCCCCAGTGCCCGTCTC
mouse_chr5                  AGAA-----
                             ****
human_chr12_NM_053275      CCTCTTCCTGGAGAATGGTGCTGAAAGGTGATTGTCTCCATAAACTTCT
mouse_chr5                  -----
human_chr12_NM_053275      CTTTGCAGACTGCTGCCTCATATCC-GGGGAA-TGTGGGCTTTGTGTTTAC
mouse_chr5                  -----ACTGCTGCCTCACATCCCGGGGAAACGTGGGCTTCGTGTTTAC
                             ***** ** * ** ***** *****
human_chr12_NM_053275      CAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTAA
mouse_chr5                  CAAGGAGGACCTCACTGAGATTCGGGATATGCTGTTGGCCAATAAGGTAA
                             ***** ** * ** ***** *****
human_chr12_NM_053275      GGGGACAA
mouse_chr5                  GGGGCTG-
                             ****
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr14_NM_004184    ---TCCTGCCATCCAGGCTGCTCCCTCCTTCAGCAACTCATTCCCACAGA
mouse_chr12              TTTTCCTGCTGTCCAGGCCGCGCCATCGTTCAGCAACTCTTTCCCGAAGA
                        *****  *****  ** ** *  *****  *****  ***

human_chr14_NM_004184    TCTTCCGAGACAGGACGGATATCCAGTGCCTTATCCCATGTGCCATTGAC
mouse_chr12              TCTTCCGAGACAGGACAGATATCCAGTGCCTCATCCCGTGTGCCATTGAC
                        *****  *****  *****  *****  *****

human_chr14_NM_004184    CAGGTCAGCAGGCAGAAAAGCAAGGCTCTCTAAGTCTGGGGCATTGACAG
mouse_chr12              CAG-----
                        ***

human_chr14_NM_004184    CAGGTTCTCTTACTCTTCAGCGGGGAGAGGTATTGAAAGATATGATGGG
mouse_chr12              -----

human_chr14_NM_004184    CAGCCAGGCAGGGTGGCTCACGCCTGTAATACCAGCACTCTGGGAGGCCA
mouse_chr12              -----

human_chr14_NM_004184    AGGCAGGCGGATCACTTGAGGCCAGGAGTTCAAGACCAGCCTGGCCAACA
mouse_chr12              -----

human_chr14_NM_004184    TGGCGAAACCCCGTCTCTACTAAAAATACAAAATTTAGCCACATGTGGTG
mouse_chr12              -----

human_chr14_NM_004184    GCAGGCGCCTGTAATCCCAGCTACTCGCCTCGCTTGAACCCAGAGGCAG
mouse_chr12              -----

human_chr14_NM_004184    AGGTTGCAGCGAGAGCGCATCACTGCACTCTAGCCTGGGCGACAGAGCAA
mouse_chr12              -----

human_chr14_NM_004184    GGCTCTGTCTCAAAAAAAGGAAAGAAAGTTGGGGAGTGGGGCAAGGGGA
mouse_chr12              -----

human_chr14_NM_004184    GGGAGAGCATTAGGACAAATACCTAATGCATGCGGGGCTTAAACCTAGA
mouse_chr12              -----

human_chr14_NM_004184    TGACGGGTTGATGGGTGCAGCAAACCACCATGGCACATGTATACCTATGT
mouse_chr12              -----

human_chr14_NM_004184    AACAAACCTGCGTGTTCTGTACATGTATCCAGAACTGGAAGTAAAATTT
mouse_chr12              -----

human_chr14_NM_004184    AAAAAAAAAAAGGAAAAGATGAAGGGGAGGAGGGAGTGAATTTCTTTGG
mouse_chr12              -----
```

human_chr14_NM_004184 TTGGAAGCATGAGAGCCTTCTGGGAAGATGCTCACAGGGACTGCTCATGG
mouse_chr12 -----

human_chr14_NM_004184 CTGAAAGCTGGCATGTTTTCTGGCCGCCCTCATCAGGGTCCTTACTCTCC
mouse_chr12 -----

human_chr14_NM_004184 CCACAGGATCCTTACTTTAGAAATGACAAGGGACGTGCGCCCCCAGGATCGG
mouse_chr12 -----GATCCGTACTTCAGAATGACAAGGGACGTGGCCCCCAGGATCGG

human_chr14_NM_004184 CTATCCTAAACCAGCCCTGCTGCACTCCACCTTCTTCCCAGCCCTGCAGG
mouse_chr12 CCATCCTAAACCTGCCCTGCTGCACTCGACCTTCTTCCCTGCCCTGCAGG
* *****

human_chr14_NM_004184 GCGCCC-
mouse_chr12 GCGCTCA
**** *

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr15_NM_001003      -ATTGGGAGCCTCATCTGCAATGTAGGGGCCGGTGGACCTGCTCCAGCAG
mouse_chr9                 CATTGGGAGCCTCATCTGCAATGTAGGGGCTGGTGGGCCCGCTCCAGCAG
                             ***** ** *****

human_chr15_NM_001003      CTGGTGCTGCACCAGCAGGAGGTCCTGCCCCCTCCACTGCTGCTGCTCCA
mouse_chr9                 CTGGAGCTGCGCCTGCTGGTGGTGGTCTGCTCCATCCACTGCCGCCGCCCA
                             **** * ** * * * * * * * * * * * * * * * * * * * *

human_chr15_NM_001003      GGTAGGAAACATGGAGTTTTTAGTATTGGGAGGAGTGTAGAGATTTTTTA
mouse_chr9                 G-----
                             *

human_chr15_NM_001003      AAAAATAGTATTATAGACAAAATTGCCATTAATTTTTTACAAGTATATGA
mouse_chr9                 -----

human_chr15_NM_001003      AGTATGGAAATCCTAACACCTGATTGACTTTTTTTTTCTAGCTGAGGAGA
mouse_chr9                 -----CTGAGGAGA
                             *****

human_chr15_NM_001003      AGAAAGTGAAGCAAAGAAAGAAGAATCCGAGGAGTCTGATGATGACATG
mouse_chr9                 AGAAAGTGGAGGCAAAGAAGGAAGAGTCCGAGGAGTCTGAAGATGACATG
                             ***** ** * * * * * * * * * * * * * * * *

human_chr15_NM_001003      G-GCTTTGGTCTTTTTGACTAAACCTCTTTTATAACATGTTC-
mouse_chr9                 GAGCTTCGGTCTTTTTGACTAAACTGCTTTTGTAAAGTTGGCT
                             * * * * * * * * * * * * * * * * * * * * *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr16_NM_002952  --CATCCGTGGGGCCATCATCCTGGCCAAGCTCTCCATCGTCCCCGTGCG
mouse_chr17            GCCATCCGAGGGGCCATCATCTTGGCCAAGCTTTCCATCGTCCCTGTGCG
                        *****
human_chr16_NM_002952  CAGAGGCTACTGGGGGAACAAGATCGGCAAGCCCCACACTGTCCCTTGCA
mouse_chr17            GAGAGGCTACTGGGGGAACAAGATTGGCAAGCCCCACACTGTTCCATGCA
                        *****
human_chr16_NM_002952  AGGTAGGCTGGTGGCAGGTGATGGGCCTGCCGTGGGGCAGGCTCCCTCGG
mouse_chr17            AG-----
                        **
human_chr16_NM_002952  GCCCCCGTCTCCTGACTCCTTCCCTCACCAGGTGACAGGCCGCTGCGGCT
mouse_chr17            -----GTGACAGGCCGCTGTGGCT
                        *****
human_chr16_NM_002952  CTGTGCTGGTACGCCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCC
mouse_chr17            CTGTGCTGGTGCCTCATCCCTGCCCCAGAGGCACTGGCATTGTCTCT
                        *****
human_chr16_NM_002952  GCACCTGTGCCTAAGAAGCTGCTCATGATGG-
mouse_chr17            GCTCCTGTGCCCAAGAAGCTCCTGATGATGGC
                        **
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr17_NM_002230      -----GCAGGAGGCAGCGGTCATCCCCGCCTCGTCCAAGTCTGGTGAA
mouse_chr11                CCTCTGCAGGAGGCCGCGGTCATTCCCCGCCTCGTCCAGCTGTTGGTCAA
                        *****
human_chr17_NM_002230      GGCCCACCAGGATGCCCAGCGCCACGTAGCTGCAGGCACACAGCAGCCCT
mouse_chr11                GGCCCACCAGGACGCCAGCGCCATGTGGCTGCAGGCACCCAGCAGCCCT
                        *****
human_chr17_NM_002230      ACACGGTATGTGAGCTGGTGGTGCCTCTGACAGCCTTCCTGGGGGGTCAG
mouse_chr11                ACACG-----
                        *****
human_chr17_NM_002230      GGTGTCCTCTGTGGGTGTGTGTGTGAATGGGGAGGTCAGTTGCAACTGAT
mouse_chr11                -----
human_chr17_NM_002230      GCCAATTCCAAGAACCTGTGAAGTTCATTTCGGCTGTTCATGGGGAGGAGTT
mouse_chr11                -----
human_chr17_NM_002230      GTGGCCATGTCCAAGGCACCTGTCCCATGCCCCCTGCCTCCTCTCACACA
mouse_chr11                -----
human_chr17_NM_002230      GGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTGC
mouse_chr11                -GATGGTGTGAGGATGGAGGAGATCGTGGAAGGCTGCACCGGAGCCCTGC
                        *****
human_chr17_NM_002230      ACATCCTCGCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAAC
mouse_chr11                ACATCCTCGCCCGGGATCCCATGAACCGCATGGAGATCTTCCGGCTCAAC
                        *****
human_chr17_NM_002230      A-
mouse_chr11                AC
                        *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr17_NM_002805      -TTTGGTGGCTGTCAAGGAAGGTCATGAGCCCTTGTTTCTTTAGGTACAT
mouse_chr11                TGCTGACCACCGAGGGAGATCATAGCCCATTATTATTTCTCAGGTCCAT
                          **      * *      **      *      ** ***  * ***** **

human_chr17_NM_002805      CCTGAAGGTAAATTTGTTGTAGACGTGGACAAAAACATTGACATCAATGA
mouse_chr11                CCTGAGGGCAAATTTGTTGTTGATGTGGACAAGAACATTGATATCAACGA
                          ***** ** ***** ** ***** ** ***** **

human_chr17_NM_002805      TGTGAGTGTAGCAGGTGAGGTGGTGGTGGTGGGGTCAGCTCTTACTG
mouse_chr11                T-----
                          *

human_chr17_NM_002805      TACCACTTCTGAAACTCGCCCCCTTACCCAGGTGACACCCAATTGCCGG
mouse_chr11                -----GTGACGCCCAATTGTCGG
                          ***** ***** **

human_chr17_NM_002805      GTGGCTCTAAGGAATGACAGCTTACTCTGCACAAGATCCTGCCCAACAA
mouse_chr11                GTCGCTCTAAGAAATGACAGCTTACTCTGCATAAGATCTTACCTAACAA
                          ** ***** ***** ***** ***** * ** *****

human_chr17_NM_002805      GGTAGACCCATTAGTGTCACTGATGATGGTGG----
mouse_chr11                GGTGGACCCTTTGGTGTCACTAATGATGGTGGAGAA
                          *** ***** ** ***** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr17_NM_014030      ----GGAGCTGAAGAAGGCCCTGGCTACATCGGAGGCAAAGGTGCAGCAG
mouse_chr11                 ACCTGGAGCTGAAGAAGGCTCTGGCTACCTCCGAGGCCAAGGTGCAACAG
                             ***** ** ***** **
human_chr17_NM_014030      CTCATGAAGGTCAACAGTAGCCTGAGCGACGAGCTCCGGAGGCTGCAGCG
mouse_chr11                 CTCATGAAGGTCAACAGCAGCCTGAGTGACGAGCTGCGGCGGCTGCAAAG
                             ***** ** ***** **
human_chr17_NM_014030      AGAGGTGAGGGTGCAGCCTCGGTGGGAGGGGAGCCCCAGGACTCCAGGG
mouse_chr11                 GGAG-----
                             ***
human_chr17_NM_014030      GGTTGACAGCACTTTGCACCCATAGATCCACAAGCTGCAGGCGGAGAACC
mouse_chr11                 -----ATCCACAAATTGCAGGCAGAGAACC
                             ***** ** ***** **
human_chr17_NM_014030      TGCAGCTCCGGCAGCCTCCAGGGCCGGTGCCACACCTCCACTCCCCAGT
mouse_chr11                 TGCAGCTTCGGCAGCCACCCGACCAGTGCCTCCACCCTCACTTCCCAGT
                             ***** ** ** ** ***** **
human_chr17_NM_014030      GAACGGGCGGAACACACCCCATGG-
mouse_chr11                 GAACGGGCAGAACACACCCTCATGGG
                             ***** ** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr18_NM_024805 -CTTATGTAAC TTTTGGACTTTGCCATCACTAACATAATGCTTATTTTCT
mouse_chr18          CCACTGAGCTACTTCTCCAGCCGCCCCCTCCCAACCCAATCTTGTTTTCT
                      *          ** *          *** * * *          *          *** *****

human_chr18_NM_024805 CCCCAGAAAAAGGTTTGGTATGAAAGTCCTTCCTTGGGTTCTCACTC
mouse_chr18          TGATCTAGGAAGAAGTTTTGGTATGAAGTCCCTCCCTGGGGTCTCACTT
                      ** ** *** ***** ***** ** * ** * ** * **

human_chr18_NM_024805 GGTGAGTATAAGCCATGAGCCACTTTATAATCTTGATGGGAGTGAGGGTT
mouse_chr18          G-----
                      *

human_chr18_NM_024805 TAAAAGTTGGCAAACTCTTACCTGGAGGTCTTCCATTTCTGTATTGGA
mouse_chr18          -----

human_chr18_NM_024805 GGGGATAGTGTCTATGTGGATGCGACTGGATGCCATTGGCAACATGGAGT
mouse_chr18          -----

human_chr18_NM_024805 TTTGATCTTTTCAAAAAAATGTACTGACATTAATGTTTTCTGGAAAGT
mouse_chr18          -----

human_chr18_NM_024805 CATATCTTTTATCAAATTATAATATGGTAATATCCATTGTTTTTAGTG
mouse_chr18          -----

human_chr18_NM_024805 TGTGTGTAAGTGTAAAAGTTTATAACAATATATGGCTCCCATTCTGAAAAAT
mouse_chr18          -----

human_chr18_NM_024805 AAATACATCAGTTTTCAAAAAAATTACTGAATTATCCCTTTAGCACGGT
mouse_chr18          -----

human_chr18_NM_024805 GAACTTTATGGTATGTGAATTATATCTCAACAAAAACTTTTTTTGAGAAA
mouse_chr18          -----

human_chr18_NM_024805 ATATTTACTGGCAGTACTTTTAATCTTGAGGGTTACCAGGTAAAATTTA
mouse_chr18          -----

human_chr18_NM_024805 AAAGGATCCCGGTTTATAAACTTTATCTTAATGAAAGCTGAGGCAGCTG
mouse_chr18          -----

human_chr18_NM_024805 AGAGTGATAGCTGCTGTTGATCTGGTTGCCCATCCAGCCCTCCCCAGCC
mouse_chr18          -----

human_chr18_NM_024805 CCTGCTGTGTGACTTGGTGAGTTTGGAGTTGTAACGCTGCCCTTGGGGTG
mouse_chr18          -----
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_000979 -----CGGGCCCGCAGCCGCATCCTCAGGGCAGGGGGCAAGAT
mouse_chr7      CGGGTGAGCAGCCGGGCCCCGGAGTCGCATCCTCAAGGCTGGGGGTAAGAT
                  ***** ** ***** ** *
human_chr19_NM_000979 CCTCACTTTTCGACCAGCTGGCCCTGGACTCCCCTAAGGGCTGTGGCACTG
mouse_chr7      CCTCACCTTTGACCAGCTGGCCCTGGAGTCTCCCAAGGGCCGGGGCACTG
                  ***** ** ***** ** *
human_chr19_NM_000979 TCCTGCTCTCCGGTGAGTGATACGTGGTTCGACGGTTTGGACTGAGCTGT
mouse_chr7      TGCTCCTGTCTG-----
                  * ** ** *
human_chr19_NM_000979 GTGGCTACTGGCAGCCTTACCCTCCTGGATCTGGGAGGCCAGAAGCTGG
mouse_chr7      -----
human_chr19_NM_000979 GCGCCAGATCCCTGTCTACCCGGTTCTCCTTCCCCTTCCCTAGGTCCTC
mouse_chr7      -----GTCCTC
                  *****
human_chr19_NM_000979 GCAAGGGCCGAGAGGTGTACCGCATTTTCGGCAAGGCCCCAGGAACCCCG
mouse_chr7      GGAAGGGCCGAGAGGTGTACCGACATTTTGGCAAGGCCCCAGGAACCCCA
                  * ***** **
human_chr19_NM_000979 CACAGCCACACCAAGTGAGTATCAGGCCCCAGCCCTGCCCTCT-
mouse_chr7      CACAGCCATACCAAGTGAGTATCAGAGCTTTGGCTTCAGGTAGTT
                  ***** ** *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_001379 -----CGGGAACCGGCACAACCACTGGGCTGGCCTCTATGGAAGGCTC
mouse_chr9      CGCACACTGGGAACCGGCACAACCACTGGGCTGGCCTCTACGGGCGTCTG
                  ***** ** * **

human_chr19_NM_001379 GAGTGGGACGGCTTCTTCAGCACAACCGTCACCAACCCCGAGCCCATGGG
mouse_chr9      GAGTGGGATGGCTTCTTCAGCACCCTGTACCAACCCTGAGCCCATGGG
                  ***** ** *****

human_chr19_NM_001379 CAAGCAGGTAGGTGGGGAGGGGCATCCGAGGGCCTGGGTGAGGCCCTGT
mouse_chr9      CAAGCAG-----
                  *****

human_chr19_NM_001379 ACTTGGCGGCCTAACTAGGTGGAAGTGTGGGTTTAGCCAAGTGGGGGACA
mouse_chr9      -----

human_chr19_NM_001379 GCACCCAGGACCCAGGCACCTGGCCTCTGCCTCCTGCCCTCCACGTC
mouse_chr9      -----

human_chr19_NM_001379 CACGGGACAAGCTCATAGGCCAAGGCCATGGCCGTATGCTGTACAGTGC
mouse_chr9      -----

human_chr19_NM_001379 CATTTCCCTCCCTGTCCCCGACGGTGACCCGGCCTGGGTGCTACTGCCCT
mouse_chr9      -----

human_chr19_NM_001379 CGCCCACCGCGCCTCTTTCCCCCAGGGCCGCGTGCTCCACCCAGAGCAGC
mouse_chr9      -----GGTCGGGTGCTCCACCCGAGCAGC
                  ** ** *****

human_chr19_NM_001379 ACCGTGTGGTGAGCGTGCGGGAGTGTGCCCGCTCCCAGGGCTTCCCTGAC
mouse_chr9      ACCGGGTCGTGAGTGTTTCGGGAATGTGCCCGCTCCCAGGGCTTCCAGAT
                  **** * ***** **

human_chr19_NM_001379 ACCTACCGGCTCTTCGGCAACATCC-
mouse_chr9      AGCTACCGGTTCTTCGGCAACATCCT
                  * *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_001961 -----CATGAATTTCAAGAAAGAGGAGACAGCAAAACTGATAGAGAAAC
mouse_chr10      CGCCATCATGAACTTCAGGAAGGAGGAGACAGCCAAGCTGATCGAGAAGC
                  *****  ****  ***  *****  *****  **  *****  *****  *

human_chr19_NM_001961 TGGACATCAAACCTGGACAGCGAGGACAAGGACAAAGAAGGCAAACCCCTG
mouse_chr10      TGGACATCAAGCTGGACAGCGAGGACAAGGACAAGGAGGGCAAGCCATTG
                  *****  *****  *****  *****  **  *****  **  **

human_chr19_NM_001961 CTGAAGGTGCGGCCTGGGCCAGCCCTCGGGGTGGAGGGAACACAGGCTG
mouse_chr10      CTCAAG-----
                  **  ***

human_chr19_NM_001961 CTGTTTCCGGATGCTCTGACAGCCCAGGCCTGGGGGCTGAAGTCCTCAGC
mouse_chr10      -----

human_chr19_NM_001961 TGGGCAGGGACAGCTGCTGCCCCTTTTCGCTTTAGACTCTGGGTGCTGCTG
mouse_chr10      -----

human_chr19_NM_001961 GAGACACATCCCAGCAGCCAGCCCCATCCGGGACAGGTGTGGGTGAGGGC
mouse_chr10      -----

human_chr19_NM_001961 CTTGGCAGGAGTGTGCATGGCCTTTGCCGCCTTCCAGAAGGGACTGTGCT
mouse_chr10      -----

human_chr19_NM_001961 TTGGAGAACGTTAGTCCTGACTTTGGCTTCCTTGGCTTCAAGAGAGGAAG
mouse_chr10      -----

human_chr19_NM_001961 CGTGTACGGGGTGGGGCCATCCTGGGCTCCCCAGGTGTCTCATGCACCGC
mouse_chr10      -----

human_chr19_NM_001961 TCTCTGCCCCCGCAGGCTGTGATGCGCCGCTGGCTGCCTGCCGGAGACGC
mouse_chr10      -----GCTGTGATGCGCCGCTGGCTGCCTGCAGGGGACGC
                  *****  *****  **  *****

human_chr19_NM_001961 CTTGTTGCAGATGATCACCATCCACCTGCCCTCCCCTGTGACGGCCCAGA
mouse_chr10      CCTCCTGCAGATGATCACCATCCACTTACCATCCCCGTCCTACTGCACAGA
                  *  *  *****  *  *  *****  **  **  **  **

human_chr19_NM_001961 AGTACCGCTGCGAGC-
mouse_chr10      AGTACCGTTGTGAGCT
                  *****  **  ****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_002695      ----CATCAAGACCATCAAGGTGTACTGCCAGCGCATGCAGGAGGAGAAC
mouse_chr10                 TGGGCATCAAGACCATCAAGGTATACTGCCAGCGCATGCAGGAGGAAAAC
                             *****
human_chr19_NM_002695      ATCACACGGGCTCTCATCGTGGTGCAGCAGGGCATGACACCCTCCGCCAA
mouse_chr10                 ATCACACGGGCGCTGATTGTGGTGCAGCAGGGCATGACGCCCTCCGCCAA
                             ***** ** ** *****
human_chr19_NM_002695      GCAGGTGGGCACCCCTGCCCCACCCCGCCAGCCTCTCCCCCTCCCCAGCC
mouse_chr10                 GCAG-----
                             ****
human_chr19_NM_002695      TCCTCCCGCAAGCAGTACCCACAGGCGGCCACGTGCCTTGGGCTTTGGG
mouse_chr10                 -----
human_chr19_NM_002695      CCAGGCCAGCCAGGGTGCCCTGGAGGATGTGGCCGGGATGTCCGGCAAGC
mouse_chr10                 -----
human_chr19_NM_002695      CCCGACCGCCTCCCTCCCACCGCGTCCATGGGCCCCACCCAGGCAGCCG
mouse_chr10                 -----
human_chr19_NM_002695      CCGTCTCCCCCAGCTCTCAGGAGGGGCGTCAGGGCGGAGGGCACTGTGC
mouse_chr10                 -----
human_chr19_NM_002695      CTCTCGCCAGCTCCTGTGGGCTCCAGCCCTCGGCCTGGTGCAGATTCCAG
mouse_chr10                 -----
human_chr19_NM_002695      GAGCCGGAGGTTCTTTATCCTGAGCTGATGTCCAGGGGGACTTGCAGAGG
mouse_chr10                 -----
human_chr19_NM_002695      AGGCCCGGCACGGGGTCTCCAGGGGCCTATCCGTGTTCCCCGTCTGTCT
mouse_chr10                 -----
human_chr19_NM_002695      GTCGGAACTCTGGAGCCAGGCTGCTGTGCTGTGACGGGCAGTCAGCAGA
mouse_chr10                 -----
human_chr19_NM_002695      GCAGTTTAGTCCCTGGCCCACCAGCTGTGGGGTTCACGCAGCCACACAGA
mouse_chr10                 -----
human_chr19_NM_002695      GCAGCACCCCTGTATGGGGAAGAGGTCGCCCTGCCAGCTCTGAGGGCCGC
mouse_chr10                 -----
human_chr19_NM_002695      CCCTGGAAGCGTGTGATGGATGGAAACACATCCGAGTTTCCACGGCCACT
mouse_chr10                 -----
```

human_chr19_NM_002695 TCACTGCTGGATGAGGCTCTCGATGAGCAGAGAGGCTGGGGAGGGGCGGG
mouse_chr10 -----

human_chr19_NM_002695 CTGTTGAAGGCTCCTGGGCTGGCGGTGGGGTTTTCTGATTACGACGTGG
mouse_chr10 -----

human_chr19_NM_002695 GTGTGTTGTTGGGGCACACGAGTAAGCCCCAGGTAGCTTGAGGCAGGAAA
mouse_chr10 -----

human_chr19_NM_002695 TGGGGTTGGGGTTGTCTGGGCCCCTCCGGGCCGTGCCTTAGAGCCGCTCT
mouse_chr10 -----

human_chr19_NM_002695 CTTCCAGTCCCTGGTCGACATGGCCCCAAGTACATCCTGGAGCAGTTTC
mouse_chr10 -----TCCCTGGTGGACATGGCCCCGAAGTATGTGCTGGAACAGTTTC
***** ***** ***** * ***** *****

human_chr19_NM_002695 TGCAGCAGGAGCTGCTCATCAACATCACGGAGCACGAGGTGGGCGCGCGC
mouse_chr10 TACAGCAGGAGCTGCTCATCAATATCACAGAGCACGAGGTGTGTGTGGTG
* ***** ***** ***** * * *

human_chr19_NM_002695 CGCGGAA-
mouse_chr10 GGGTGGGG
* *

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_003333      -CCACCCTGCACCTGGTGTGCGCCTGCGAGGTGGCATTATTGAGCCTTC
mouse_chr8                 TCCACCTTGCACCTGGTGCTGCGTCTGCGCGGTGGCATCATTGAGCCATC
                          *****
human_chr19_NM_003333      TCTCCGCCAGCTTGCCCAGAAATACAACCTGCGACAAGATGATCTGCCGCA
mouse_chr8                 CCTTCGTCAGCTTGCCCAGAAGTACAACCTGTGACAAGATGATCTGCCGCA
                          ** **
human_chr19_NM_003333      AGTATGTGTGCTCCGATGCTTGGGGGGCTGTGGGGGGCTGCCGGAGTCGGG
mouse_chr8                 A-----
                          *
human_chr19_NM_003333      GTATGCCCTCACCCACCCCTCCTGTCTCTGTGCAGGTGCTATGCTCGCCT
mouse_chr8                 -----GTGCTACGCACGCCT
                          ***** **
human_chr19_NM_003333      TCACCCTCGTGCTGTCAACTGCCGCAAGAAGAAGTGTGGTACACCAACA
mouse_chr8                 GCACCCTCGTGCAGTCAACTGCCGCAAGAAGAAGTGCGGCCATACCAACA
                          ***** **
human_chr19_NM_003333      ACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTGGT----
mouse_chr8                 ACCTGCGCCCCAAGAAGAAGGTCAAATAAAGCTGTGGTC
                          ***** * **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_003685 -----TGACGGGACAGGGCCCGAGAAGATTGCTCATATAATGGGGCCC
mouse_chr17      ATTCAGATGATGGGACCGGCCCTGAGAAGATTGCTCACATCATGGGGCCT
                  ***  *****  **  **  *****  *****  **  *****

human_chr19_NM_003685 CCAGACAGGTGCGAGCACGCAGCCCGGATCATCAACGACCTCCTCCAGAG
mouse_chr17      CCAGATCGGTGTGAACACGCAGCCCGGATCATCAATGACCTCCTCCAGAG
                  *****  *****  **  *****  *****  *****

human_chr19_NM_003685 CCTCAGGGTAGGTGGCCCCGGGTGCTGAAGGGGCTGGCAGGGCCTCCAGG
mouse_chr17      TCTTCGG-----
                  **   **

human_chr19_NM_003685 GGAGTGCAAGACCAGACCGGCTTCCAGGGTTCATCATCCTCCTCCTCCTC
mouse_chr17      -----

human_chr19_NM_003685 TTGTCTTGCAGAGTGGTCCCCCAGGTCTCCTCCAGGGGGTCCAGGCATGCCC
mouse_chr17      -----AGTGGGCCCCCGGGTCTCCTCCAGGGGCCCTGGCATGCCC
                  *****  *****  *****  *****  **  *****

human_chr19_NM_003685 CCGGGGGGCCGAGGCCGAGGAAGAGGCCAAGGCAATTGGGGTCCCCCTGG
mouse_chr17      CCTGGGGGCAGGGGCCGGGGCCGAGGCCAAGGCAACTGGGGCCCTCCTGG
                  **  *****  *  *****  **  *****  *****  *****  *****

human_chr19_NM_003685 CGGGGAGATGA-
mouse_chr17      AGGGGAGATGAC
                  *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_003938      --TAGACAAGGCAGAGGGTACCACCTACCGTGACGAGCTGCTCACCAAGA
mouse_chr10                CGTGGACAAGGCTGAGGGCACCACCTATCGCGATGAACTGCTCACCAAGA
                             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
human_chr19_NM_003938      TCATTGACATCTGCAGCCAGTCCAACCTACCAGTACATCACCAACTTCGAG
mouse_chr10                TCATTGACATCTGTAGCCAGTCCAACCTACCAGCACATCACCAACTTCGAG
                             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
human_chr19_NM_003938      TGGTGCGTCCCGCTCCCAGGGGTGTGGCCGGGGGTTCCGTGGCGCCGCTC
mouse_chr10                TG-----
                             **
human_chr19_NM_003938      ACTCACCCTCTGCCCCACAGGTACATCAGCATCCTGGTGGAGCTGACC
mouse_chr10                -----GTACATCAGCATCCTTGTGGAGCTGACA
                             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
human_chr19_NM_003938      CGGCTGGAGGGCACACGGCACGGCCACCTCATCGCCGCCCAAATGCTGGA
mouse_chr10                AGGCTGGAGGGCACCCGCCATGGCCACCTCATTGCTGCACAGATGCTGGA
                             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
human_chr19_NM_003938      CGTGGCCATCCGCGTGAAGGCC-
mouse_chr10                CGTGGCTATCCGGGTCAAGGCCA
                             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_005498      ----AGGAGAGCATCCGGGACAACCTTTGTCATCGTCTACGAGTTGCTGGA
mouse_chr9                 GAGGAGGAGAGCATCCGGGACAACCTTCGTCATCGTGTACGAGCTGCTGGA
                             *****
human_chr19_NM_005498      CGAGCTCATGGACTTTGGCTTCCCGCAGACCACCGACAGCAAGATCCTGC
mouse_chr9                 TGAGCTCATGGACTTTCGGCTTTCCGCAGACCACAGACAGCAAGATCCTGC
                             *****
human_chr19_NM_005498      AGGAGTGAGTGGACCCCTGGAGGCAGCCATGGGCTGGACTGTGGGTGTAA
mouse_chr9                 AGGA-----
                             ****
human_chr19_NM_005498      GGAACTGGAGGAGGTCCACGGAGGTGTCCCTGGGTCCAGCTGCTTGTCCC
mouse_chr9                 -----
human_chr19_NM_005498      TGCCGCCCTCCCTCCAGGTACATCACTCAGCAGAGCAACAAGCTGGAGAC
mouse_chr9                 -----GTACATCACACAACAGGGCAACAAGCTGGAGAC
                             ***** ** ***
human_chr19_NM_005498      GGGCAAGTCACGGGTGCCACCCACTGTCACCAACGCTGTGTCCTGGCGCT
mouse_chr9                 TGGCAAATCTCGTGTACCACCTACAGTCACCAATGCGGTGTTCGTGGCGCT
                             ***** ** ** *
human_chr19_NM_005498      CCGAGGGTATCAAGTAT-
mouse_chr9                 CTGAGGGCATTAAGTACA
                             * ***** ** *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_015965      -CCACCCCCACCATCGGCCCCATCCCCACAGGACCTTGCAGATGCTTCGG
mouse_chr8                  CCTTGAGCTTAGCCATGCCTCGTGGCCACAGGACCCTGCAGATTCTCCGG
                             *      *      *** * *      ***** ***** ** **

human_chr19_NM_015965      GAGAACCTGGAGGAGGAGGCCATCATCATGAAGGACGTGCCCCACTGGAA
mouse_chr8                  GAAAACCTGGAGGAGGAAGCCATCATCATGAAGGATGTGCCCAACTGGAA
                             ** ***** ***** ***** ***** *****

human_chr19_NM_015965      GGTGGGTCCCGGCTGGGAGGGCAGAGGTGCCAGCCACGGCAGAGACAGGG
mouse_chr8                  G-----
                             *

human_chr19_NM_015965      CCTGGGGTTGGGGAGCTCCCACAGCTTTCTATAGAAACCCAGGACCAAG
mouse_chr8                  -----

human_chr19_NM_015965      GGGGTGGTGGGTGCCAGGTCCCACAAGGGAAGGCTGTAGCGCCTGCCACG
mouse_chr8                  -----

human_chr19_NM_015965      CACAGGGGCCACTGATCCTGGGGGATGGGTCTTAGCAGGCTGTATATGGG
mouse_chr8                  -----

human_chr19_NM_015965      TGGCTGTGCCTCTACCCATACCCCACTGTCCCCACAGGTGGGGGAGTCTG
mouse_chr8                  -----GTGGGCGAGTCTG
                             ***** *****

human_chr19_NM_015965      TGTTCCACACAACCCGCTGGGTGCCCCCCTTGATCGGGGAGCTGTACGGG
mouse_chr8                  TGTTCCATAACCACACGATGGGTGCCACCCCTCATTGGCGAGATGTATGGG
                             ***** ** ** * ***** ** * ** * ** * ** *

human_chr19_NM_015965      CTGCGCACACAGAGGAGGCTCTCCATGCCAGCCACG-----
mouse_chr8                  TTGCGCACCAAGGAGGAGATGAGCAATGCCAACTTCGGCTTCACCTG
                             ***** ***** * ***** * **
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_020170      -CCTGGACACCGTGGGCCGGGGCAGCAGCCTGCACCTGCACGTGTCCAAG
mouse_chr10                 GCCTGGACACTGTGGGACGTGGCAGCCACCTGCGCCTGCATGTGTCCAAG
                             *****  *****  *  *****  *****  *****  *****

human_chr19_NM_020170      CCGCCTCGGGAGGGCACCCTGCAGCACGCCTTCCTGCGGGAGCTGGAGAC
mouse_chr10                 CCTCCACGGGAAGGGACACTGCAGCATGCCTTCCTGCGAGAGCTGGAGAC
                             **  **  *****  **  **  *****  *****  *****  *****

human_chr19_NM_020170      GGTGGGTGCCCTTTCATGGATGGGTCCGGAGCTCTGCGGAGCACACACA
mouse_chr10                 G-----
                             *

human_chr19_NM_020170      TCGGGGCCGGGTTGGGGCATCCTGTCCCAGGGTGTCTTGCTGTCCGCC
mouse_chr10                 -----

human_chr19_NM_020170      CTCAGGCTCTGAGGGCCACACTGTGTCTGGGGTCTGGGCTGGGGTGTCTGT
mouse_chr10                 -----

human_chr19_NM_020170      CCTGGGGTGTCTTGCTGTCCAACCCGGGGCTCTGAGGGGCACACTGCG
mouse_chr10                 -----

human_chr19_NM_020170      TCAGGGCCGGGCTGGGGTGTCTGTCCCAGAGTGTCCCCTTGTCCCTCCT
mouse_chr10                 -----

human_chr19_NM_020170      TACCCACTGCTCATTGCCCGCCGGGGCTCCAGCAGGCCTTAGGGGGACCC
mouse_chr10                 -----

human_chr19_NM_020170      CGGGGGCAGGTGGATTTCTCCTCATTTTGCACCCTCGGGGGTTCTGGGAG
mouse_chr10                 -----

human_chr19_NM_020170      GCCCCTGGAGCATTTGGGGAATGGGCTGGGGTGGCCGCCATCCCCGCTG
mouse_chr10                 -----

human_chr19_NM_020170      CCCTCTGCTAATGGCGCCTCCGGCTGCAGGTGGCCGCGCACCAGTTCCT
mouse_chr10                 -----GTGGCTGCGCACCAGTTCCT
                             *****  *****

human_chr19_NM_020170      GAGGTACGGTTCTCCATGGTGCACAAGCGGATCAACCTGGCGGAGGACGT
mouse_chr10                 GATGTCAGCTTCTCCATGGTACACAAGAAGATCAATCTAGCGGATGACGT
                             **  **  *  *****  *****  *****  **  *****  *****

human_chr19_NM_020170      GCTGGCCTGGGAGCACGAGCGCTTCGCCA-----
mouse_chr10                 GCTTGCCTGGGAACACGAGCGCTTTGCCATCCGAAGG
                             ***  *****  *****  *****
```

CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_020230      -TCCTGGAAGCCAAGGAGAAGAAGCTGCGGCTGAAGGCGCAGAGGCAGGC
mouse_chr9                  ATCCTGGCAGCCAAGGAGGAGAAGCTCCGGCTGAAGGCACAGCGTCAGAA
                          *****
human_chr19_NM_020230      CCAGCAGGCCCAAGAATGTGCAGCGCAAGCAGGAGCAGCGGGAGGCCACA
mouse_chr9                  CCAACAGGCAGAGAACTTGCAGCGCAAGCAGGAGCTGCGCGAGGCCACA
                          ***
human_chr19_NM_020230      GGTCCAGGCAGAGCTGGGAAGGGCAGGGCCAAGGGGGGTCCCTGGGATG
mouse_chr9                  A-----
human_chr19_NM_020230      GGCGGCTATGTTGACCCCCACGCCCTCCTCCAGAAAGAAGAGCCTGGAGG
mouse_chr9                  -----GAAGAAGAGCCTGGCAG
                          *****
human_chr19_NM_020230      GCATGAAGAAGGCACGGGTCGGGGGTAGTGATGAAGAGGCCTCTGGGATC
mouse_chr9                  GCATAAAGCGAGCCCGTGCAAGGGCCGACGGTGACAGTGATGCTGAGGAC
                          ****
human_chr19_NM_020230      CCTTCAAGGACGGCGAGCCTGGAGTTGGGTGAG----
mouse_chr9                  CCAGGGGCACCGCCAGAGGCAGTGGGGGCAGGTCAGC
                          **
```


CLUSTAL W (1.83) multiple sequence alignment

```
human_chr19_NM_032285      -CTCCCTGCAGATCCTAGACCAGCTGCTGCTGCCCAAGCAGAGCCGCTAC
mouse_chr8                  GCTCGCTGCAGATCCTCGACCAGCTGCAGCTGCCAGAGCACTGCCACTAT
                             *** *****
human_chr19_NM_032285      GAGGCGGTGGGCTCGGTGCACCAGGCCTGGGAGGCCATCCGCGCCATGAA
mouse_chr8                  GAGGCACTGAGCTCCGTGCAGCAGGCTAGTGAAGCCATCCGCGCCATGAA
                             ***** ** ***** ***** ***** * ** *****
human_chr19_NM_032285      GGTGCAGCGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGGG
mouse_chr8                  G-----
                             *
human_chr19_NM_032285      GGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCCGGGTTGGAGGT
mouse_chr8                  -----
human_chr19_NM_032285      GGGAGTGCGCCCGCGCCTGCAGCTTCCGACGCCCAAATCCCTGCCCCGCA
mouse_chr8                  -----
human_chr19_NM_032285      GGTGCGGGGCGCCCCGGCCATAGCCCTGGTGGGCTGTCTCAGCCTCGCCG
mouse_chr8                  -GTGCGCGGAGCCCCGGCCATCGCGCTGGTTCGGCTGCCTCAGCCTGGCCG
                             ***** ** ***** ***** ** ***** ***** ***** *****
human_chr19_NM_032285      TGGAGCTGCAGGCGGGCGCCGGGGACCGGGACTCGCCGCGCTCGTGGCC
mouse_chr8                  TGGAGCTGCGGGCCGGCGCCGGCGGTCCCGGACTCGCTGCTCTGGTGGCC
                             ***** ***** ***** ** ** ***** ** ** *****
human_chr19_NM_032285      T-----
mouse_chr8                  TTCGTGCGA
                             *
```