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CLUSTAL W (1.83) multiple sequence alignment

```
1prev      ATGATAACCAGCCAACTCTCTGTCTTCTTCATGCTCATCTATATGCTCGA
1seq      -----

1prev      GTTCTTGACAATAACTGGGCAGAGCAGCCTGATTGTCATAGTGCTGGGCA
1seq      -----

1prev      GAGAGTGGGTGCAGACTCAAAGGCTGCCGCCTGTGGACATGATTCTCACC
1seq      -----CCTGTGGACATGATTCTCACC
                      *****

1prev      AGCCTGGGCATCTGCCGCTTCTGTCAACTGTGGTCATCGATGCTGCACAA
1seq      AGCCTGGGCATCTGCCGCTTCTGTCAACTGTGGTCATCGATGCTGCACAA
                      *****

1prev      CTTCGGCTCCCACTTCCACCTGAATTACAATTTTGGTGTTTGGGATCA
1seq      CTTCGGCTCCCACTTCCACCTGAATTACAATTTTGGTGTTTCGGGATCA
                      *****

1prev      TCTGGCAGTTTACTAACATCCTTTCCTTCTGGTTAACCAGCTTGCTTGCT
1seq      TCTGGCAATTTACTAACATCCTTTCCTTCTGGTTGACCAGCTTGCTTGCT
                      *****

1prev      GTCTTCTACTGTGTCAAAGTCTCCTTCTTCAGCCACCCCATCTTCCTCTG
1seq      GTCTTCTACTGTGTCAAAGTCTCCTTCTTCAGCCACCCCATCTTCCTCTG
                      *****

1prev      GATGAAGTGGAGAATTGTGAGATGGGTTCCCTCAGCTGCTGCTGGGCTCTC
1seq      GATGAAGTGGAGAATTGTGAGATGGGTTCCCTCGGCTGCTGCTGGGCTCTC
                      *****

1prev      TGCTGGTTTCTTGTTGTGTCTACCATCTTTTCAGCGACTAGTTATTACATC
1seq      TGCTGGTTTCTTGTTGTGTCTACCATCTTTTCAGCGACTAGTTATTACATC
                      *****

1prev      ATCATTCAATTCATCTCCATGAAGGATTTCCCTAGGAACAGCACCATGCT
1seq      ATCATTCAATTCATCTCCATGAAGGATTTCCCTAGGAACAGCACCATGCT
                      *****

1prev      TGAGAGACTGGAGGCGTTCCTGTGGGATTTTCCACACTGCGGAAAGTGG
1seq      TGAGAGACTAGAGGCGTTCCTGTGGGATTTTCCACACTGCGGCAAGTAG
                      *****

1prev      TTGTATTGGTTATTTCCTTTCCTCCTGTTCCCTGGCCTCCACAGTCTTGCTC
1seq      TTGTATTGGTTATTTCCTTTCCTCCTGTTTCTGGCCTCCACAGTCTTGCTC
                      *****

1prev      ATGGCCTTATTATCCCGACATCTGAAGCAGATGAAAGACCTTCACACAGG
1seq      ATGGCCTTATTATCCCGACATCTGAAGCAGATGAAAGACCTTCACACAGG
                      *****

1prev      CCGCCCCATCTCCAGCCGGGAAGCTCACTCTGCCGCCCTGAGGTCTCTTG
1seq      CCACCCCATCTCCAGCCCGGAAGCTCACTCTGCCGCCCTGAGGTCTCTTG
                      ** *****

1prev      GCATCTTCCTCATCTTGTTACCTTTTATTTTCTGACCGTGCTCGTCTCC
1seq      GCATCTTCCTCATCTTGTTACCTTTTATTTTCTGACCGTGCTCGTCTCC
                      *****
```

```
1prev      ATCTTGGATGTCCTATTTAATAAAGAGTCTTGGTTCTGGGCCTGGGAAGC
1seq      ATCTTGGATGTCCTATTTAATAAAGAGTCTTGGTTCTGGGCCTGGGAAGC
          *****

1prev      TATCATCTATGCATTAGTCTCTATTCATTCTACTTTACTAATGCTGAGCA
1seq      TATCATCTATGCATTAGTCTCTATTCATTCTACTTTACTAATGCTGAGCA
          *****

1prev      GTGCCAAACTGAAAAGAGTTTTAAAGGCAAGGTGCTGGAGCCTAGAAGCT
1seq      GTGCCAA-----
          *****

1prev      GCCTGA
1seq      -----A
          *
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CLUSTAL W (1.83) multiple sequence alignment

```
2prev      ATGCTGAGTACAGTGGGAAGGCCTCCTAATTTATGTAGCAGTTAGTGAATC
2seq      -----

2prev      AGTATTGGGGGTCTTAGGGAATGGATTTATTGGAGTTGTAAGCTGCATTG
2seq      --TATTGGGGGTCTTAGGGAATGGATTTATTGGAGTTGTAAGCTGCATTG
          *****

2prev      ATTGTGTGAAAAGCAAGAAGATCCCTACTGTCAGCCTTATTCTCACTGGC
2seq      ATTGTGTGAAAAGCAAGAAGATCCCTACTGTCAGCCTTATTCTCACTGGC
          *****

2prev      TTAGCTTCTTCCAGATTTTGCCTGATATGGATAATAATTACAGATGCATA
2seq      TTAGCTTCTTCCAGATTTTGCCTGATATGGATAATAATTACAGATGCATA
          *****

2prev      TGTGAGGATGTTTTTCCAGATACATATTTGTCTGGTAATCTAAGTCAAA
2seq      TGTGAGGATGTTTTTCCAGATACATATTTGTCTGGTAATCTAAGTCAAA
          *****

2prev      ATATAGCTCACTTTTGGATAATTATGAATCAGTCAAGTATCTGGTTTGCC
2seq      ATATAGCTCACTTTTGGATAATTATGAATCAGTCAAGTATCTGGTTTGCC
          *****

2prev      ACCAGCCTCAACATCTTCTATTTTCCTGAAGATAGCCAATTATTCCTACTG
2seq      ACCAGCCTCAACATCTTCTATTTTCCTGAAGATAGCCAATTATTCCTACTG
          *****

2prev      CATTTTTCTCTGGCTGAAGGGTCACATCAACAGGGTTCTTCTCCTTTTCA
2seq      CATTTTTCTCTGGCTGAAGGGTCACATCAACAGGGTTCTTCTCCTTTTCA
          *****

2prev      TGGGGTCTTTGCTTATTTTCATGGTTATTTGCTTTTCCAAGCATTGCAAAG
2seq      TGGGGTCTTTGCTTATTTTCATGGTTATTTGCTTTTCCAAGCATTGCAAAG
          *****

2prev      CCTAGTATTAATGATATTATGAAGAACAGAAGCTCAACCTGGCTGATCGC
2seq      CCTAGTATTAATGATATTATGAAGAACAGAAGCTCAACCTGGCTGATCGC
          *****

2prev      CCTGCATAAAAGGGAATACTTGACAAATCATATTCTGCTCAATATTGGAG
2seq      CCTGCATAAAAGGGAATACTTGACAAATCATATTCTGCTCAATATTGGAG
          *****

2prev      TCATTCTTGTCTTTGTGCTATGCCTGATTACATGTTTCTTATTAATCACT
2seq      TCATTCTTGTCTTTGTGCTATGCCTGATTACATGTTTCTTATTAATCACT
          *****

2prev      TCCCTTTGGAGACACAACAGAAAGATGCAATTGAATGCCACAGGATTTCAG
2seq      TCCCTTTGGAGACACAACAGAAAGATGCAATTGAATGCCACAGGATTTCAG
          *****

2prev      AGATCCCAGCACTGAAGCACATATCAAAGCAATGAAGACTTTGGTGTCTT
2seq      AGATCCCAGCACTGAAGCACATATCAAAGCAATGAAGACTTTGGTGTCTT
          *****

2prev      TTATCATCCTCTTTATCTTGTATTTTGTAGGCACTGCCATACAAATATCA
2seq      TTATCATCCTCTTTATCTTGTATTTTGTAGGCACTGCCATACAAATATCA
          *****
```

```
2prev      GGTAGTACTATGCCTGAAAACAACCTGTTGCTCATTATTGGTATAACAAC
2seq      AGTAGTACTATGCCTGAAAACAACCTGTTGCTCATTATTGGTATAACAAC
          *****

2prev      CAGACTCCTCTATCCCTGTGGACACTCGTTGATCCTAATTCTAGGAAACA
2seq      CAGACTCCTCTATCCCTGTGGACACTCGTTGATCCTAATTCTAGGAAACA
          *****

2prev      GGAAGCTGAAGCAAGACTTTTTGAGGGTACTGAAGCCATTAAAGTGCTGG
2seq      GGAAGCTGAAGCAAGACTTTTTGAGGGTACTGAAGCCATTAAAGTGCTGG
          *****

2prev      GGAAAAGAGAAACTTCTTAGAATTCCATGA
2seq      G-----GA
          *                      **
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CLUSTAL W (1.83) multiple sequence alignment

```
3prev      ATGGAGAGAACTGAACAATATACTTATGATCATTTCTGCTGGAGAATT
3seq      -----TT
              **

3prev      CTTACTGGGTATTTTGGGAAATGGATTCATTGTCCTGGTTAACTGTATTG
3seq      CTTACTGGGTATTTTGGGAAATGGATTCATTGTCCTGGTTAACTGTATTG
              *****

3prev      ATTGGATCAGGAGCAGGAAGTTCTCCCTGATTGACTTTATTCTCACCTGC
3seq      ATTGGATCAGGAGCAGGAAGTTCTCCCTGATTGACTTTATTCTCACCTGC
              *****

3prev      TTGGCTATTTCCAGAATATTTGTGCTGTGCATAATGATTTCAAGTACAGG
3seq      TTGGCTATTTCCAGAATATTTGTGCTGTGCATAATGATTTCAAGTACAGG
              *****

3prev      TTTATATGTAATCTCTGAGGAAATACAGTACAACAAGAATCTCCTGATAA
3seq      TTTATATGTAATCTCTGAGGAAATACAGTACAACAAGAATCTCCTGATAA
              *****

3prev      ATTTGGGGTTCCTCTGGACAGGATCCAATTATTTCTCCATAGCCTGCACC
3seq      ATTTGGGGTTCCTCTGGACAGGATCCAATTATTTCTCCATAGCCTGCACC
              *****

3prev      ACCTGCATCAGTGTCTTCTATCTCCTCAGAATAGCTAACTTTTCTAATTT
3seq      ACCTGCATCAGTGTCTTCTATCTCCTCAGAATAGCTAACTTTTCTAATTT
              *****

3prev      CCTTTTCTCTGGATGAAACGGAGAATTCAACAAGGTGCTTCTCATTATTG
3seq      CCTTTTCTCTGGATGAAACGGAGAATTCAACAAGGTGCTTCTCATTATTG
              *****

3prev      CACTGGGGGCTGTCTTCTCTTTCTGCTTGTGCCTTCTTCAAAAGAATATG
3seq      CACTGGGGGCTGTCTTCTCTTTCTGCTTGTGCCTTCTTCAAAAGAATATG
              *****

3prev      GCAGTTGAAATCCTGTTCCAAAACCGGTAAACAGCAAAAAAATGTGAC
3seq      GCAGTTGAAATCCTGTTCCAAAACCGGTAAACAGCAAAAAAATGTGAC
              *****

3prev      ATTGGACTTTCTAATGATAAGATACGATTTGTTCTTTGCCATAATGTTCC
3seq      ATTGGACTTTCTAATGATAAGATACAATTGTTCTTTGCCATAATGTTCC
              *****

3prev      TCATCCCCTTTGTAGTGTCCCTGGCCTCCTTTCTCCTTTTAAATCCTCTCC
3seq      TCATCCCCTTTGTAGTGTCCCTGGCCTCCTTTCTCCTTTTAAATCCTCTCC
              *****

3prev      TTATGTGGTCATCTCAGGCGTATGAAGGGTGTAGACTGTAGCTCGGAAGC
3seq      TTATGTGGTCATCTCAGGCGTATGAAGGGTGTAGACTGTAGCTCGGAAGC
              *****

3prev      CCATGTGAGAGCCCTGAAGGCTATGATTTTCATTCCTACTCCTCTTCATTC
3seq      CCATGTGAGAGCCCTGAAGGCTATGATTTTCATTCCTACTCCTCTTCATTC
              *****

3prev      TACACTATTTGAGCAATATTATGACAGTGTGGGCCAATCACATTCTCGGT
3seq      TACACTATTTGAGCAATATTATGACAGTGTGGGCCAATCACATTCTCGGT
              *****
```

```
3prev      AGTTTTGTGGCAAAGATTTTGTGAACATGCTGTTATTTTCTGTCCTTC
3seq      AGTTTTGTGGCAAAGATTTTGTGAACATGCTGTTATTTTCTGTCCTTC
          *****

3prev      TGGCCACCCTTTGCTTCTGATTTTGTGGAACAGCAAATTGAAAAAGGCTT
3seq      TGGCCACCCTTTGCTTCTGATTTTGTGGAACAGCAAATTGAAAAAGGCTT
          *****

3prev      CACTCTGTGTCCTAAGGAAGCTGAGGGGTTACATGAATCTAAGAAACTC
3seq      CACTCTGTGTCCTAAGGAAGCTGAGG-----
          *****

3prev      TTCCAAAAATAAGCCTGAAGTGATGA
3seq      -----GG
          *
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CLUSTAL W (1.83) multiple sequence alignment

```
4prev      ATGTTGAGACTCAGCAATTTGGGGTTTCTGGTTCTGACCGCCATTTCAGTT
4seq      -----

4prev      CATCCTGGGAATGCTGGGGAATGGTTTCATAGGGTGGGTCAATGGCAGCA
4seq      -----TGGTTTCATAGGGTGGGTCAATGGCAGCA
                      *****

4prev      GCTGGTTCAAGAGCAAGAGGATCTCTTTGCATGACTTCATTATCACTAAC
4seq      GCTGGTTCAAGAGCAAGAGGATCTCTTTGCATGACTTCATTATCACTAAC
                      *****

4prev      CTGGCTGTCTCCAGGATTGTTTTGCTGTGGATTCTCTTGATCGATGGTGT
4seq      CTGGCTGTCTCCAGGATTGTTTTGCTGTGGATTCTCTTGATCGATGGTGT
                      *****

4prev      TTTACTGGTGTTCTCTCCCAAACCTACATGATGAAGGGATAATCATGCAAA
4seq      TTTACTGGTGTTCTCTCCCAAACCTACACGATGAAGGGATAATCATGCAAA
                      *****

4prev      TTATTGATGTGTTCTGGACATTTACAAACCATCTGAGCATTTGGCTTACC
4seq      TTATTGATGTGTTCTGGACATTTACAAACCATCTGAGCATTTGGCTTACC
                      *****

4prev      ACCTGTGTCAGTGTCTTCTACTGCCTGAAAGTGGCCAGTTTCTCCCATCC
4seq      ACCTGTGTCAGTGTCTTCTACTGCCTGAAAGTGGCCAGTTTCTCCCATCC
                      *****

4prev      TATGTTCTCTGGCTCAAATGGAGAGTTTCCAGGGTGGTTGTATGGATGC
4seq      TATGTTCTCTGGCTCAAATGGAGAGTTTCCAGGGTGGTTGTATGGATGC
                      *****

4prev      TGTTGAGTACCCTGCTGTTATCATGTGGCAGTGCCATCTCTCTGATCCGA
4seq      TGTTGAGTACCCTGCTGTTATCATGTGGCAGTGCCATCTCTCTGATCCGA
                      *****

4prev      GAATTTAAGATCTATTCTGTTCTCGGTGGAATTGATAGAACCGGGAATAT
4seq      GAATTTAAGATCTATTCTGTTCTCGGTGGAATTGATAGAACCGGGAATAT
                      *****

4prev      GACTGAGCTCTTTAGAAGGAAGGAAAAAGAATATAAACTGATCCATGTTT
4seq      GACTGAGCTCTTTAGAAGGAAGGAAAAAGAATATAAACTGATCCATGTTT
                      *****

4prev      TTGGGACTCTGTGGGACCTCCCTCCCCTAGTCGTATCTCTGATCTCCTAC
4seq      TTGGGACTCTGTGGGACCTCCCTCCCCTAGTCGTATCTCTGATCTCCTAC
                      *****

4prev      TTTCTGCTTATCCTCTCCCTGGGGAGGCACGTGCGGCAGATGCATCAAGA
4seq      TTTCTGCTTATCCTCTCCCTGGGGAGGCACGTGCGGCAGATGCATCAAGA
                      *****

4prev      CTGTGGCAGCTCCAGAGATCCCAGTACCGAGGCCCCACAGGAGGGCCATCA
4seq      CTGTGGCAGCTCCAGAGATCCCAGTACCGAGGCCCCACAGGAGGGCCATCA
                      *****

4prev      GAGTCATCCTCTCCTTCCTCTTCCTCTTCTACTCTACTATCTTTTCCTTT
4seq      GAGTCATCCTCTCCTTCCTCTTCCTCTTCTACTCTACTATCTTTTCCTTT
                      *****
```

4prev	TCTGTTTTTAACATCCAGTTATTTTCCTACCAGCAACTAAGATGATTGCGAA
4seq	TCTGTTTTTAACATCCAGTTATTTTCCTACCAGCAACTAAGATGATTGCGAA *****
4prev	GATCGGAGAAGTAATTACAATGTTCTATCTTGCTGGCCACTCCTATGTTC
4seq	GATCGGAGAAGTAATTACAATGTTCTATCTTGCTGGCCACTCCTATGTTC *****
4prev	TCATTCTGGGAAATAGCAAGCTGAAGCAGATGTTTGTGGCGATGCTCCGG
4seq	TCATTCTGGGAAATAGCAAGCTGAAGCAGATGTTTGTGGCGATGCTCCGG *****
4prev	TGTGAGCCTGGTTGTCTGAAGCCTGGATCCAAGGGATCTGTTTATCCATA
4seq	TGTGAGCCTGGTTGTCTGAAGCCTGGATCCAAGGGATCTGTTTATCC---

4prev	G
4seq	A

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CLUSTAL W (1.83) multiple sequence alignment

```
5prev      ATGCTTCGGATAGTCTTTTTTCTTCTATCGTTGTCTCTGAAATTATAAC
5seq      -----

5prev      TTTTGTAGGACTCATTGTGAATCTCTTCATTGTAGTGGTCAGTTACAAGA
5seq      -----TCTCTTCATTGTAGTGGTCAGTTACAAGA
                    *****

5prev      CTTGCATCAAAAGCCACAGGATCTCTTCTTCTGACAGACTCCTGTTTCAGT
5seq      CTTGCATCAAAAGCCACAGGATCTCTTCTTCTGACAGACTCCTGTTTCAGT
                    *****

5prev      TTGGGCATCACCAGATTTTTTATACTGTTACTGAATGTTGTTGTCATCAT
5seq      TTGGGCATCACCAGATTTTTTATACTGTTACTGAATGTTGTTGTCATCAT
                    *****

5prev      CTCTCCAAATGTGGAAAGGTCAGTCTCCTTATCCTCTTTCTTCCTGTCAT
5seq      CTCTCCAAATGTGGAAAGGTCAGTCTCCTTATCCTCTTTCTTCCTGTCAT
                    *****

5prev      GTTGGATGTTTTTGGACTCTAGTAGTCTTTGGTTTGTAACCTTGCTCAAC
5seq      GTTGGATGTTTTTGGACTCTAGTAGTCTTTGGTTTGTAACCTTGCTCAAC
                    *****

5prev      GTCTTGATTGTGTGAAGATTGCTAACTACCAACACTCCGTGTTTCTCCT
5seq      GTCTTGATTGTGTGAAGATTGCTAACTACCAACACTCCGTGTTTCTCCT
                    *****

5prev      GCTGAAACGAAATCTCTCCACCAGGATGCCCGGCTGCTGCTGGTCTGTA
5seq      GCTGAAACGAAATCTCTCCACCAGGATGCCCGGCTGCTGCTGGTCTGTA
                    *****

5prev      TGCTCCTTTCTGTCTTCACCACTCTCCTGTATGTTATGCTCAGACAGTTG
5seq      TGCTCCTTTCTGTCTTCACCACTCTCCTGTATGTTATGCTCAGACAGTTG
                    *****

5prev      GCACCCCGTCTTGAATTTGTGACTGTGAGAAATGGCACAGTATTTGACAT
5seq      GCACCCCGTCTTGAATTTGTGACTGTGAGAAATGGCACAGTATTTGACAT
                    *****

5prev      CAATGAGGGACTCCTGTCTTTGGTGACTCCTTTGGTCTTGAGCTCATTTT
5seq      CAATGAGGGACTCCTGTCTTTGGTGACTCCTTTGGTCTTGAGCTCATTTT
                    *****

5prev      TCCAATTCATCATTAATGTGACTTCTGCTTCTTTGTTGATCAATTCCTTG
5seq      TCCAATTCATCATTAATGTGACTTCTGCTTCTTTGTTGATCAATTCCTTG
                    *****

5prev      AAGAGACATGTACGGAAGATGCAGAGAAGCGCCACTGTTCTTTGGAATCC
5seq      AAGAGACATGTACGGAAGATGCAGAGAAGCGCCACTGTTCTTTGGAATCC
                    *****

5prev      CCAGACTGAAGCTCATGTGGGTGCTATGAAGCTGATGATCTGTTTCCTCA
5seq      CCAGACTGAAGCTCATGTGGGTGCTATGAAGCTGATGATCTGTTTCCTCA
                    *****

5prev      TACTCTACATTCCATATTCAGTTGCTACCTTGCTCCATTATCTCCCTTCT
5seq      TACTCTACATTCCATATTCAGTTGCTACCTTGCTCCATTATCTCCCTTCT
                    *****
```

```
5prev      TCTATAGGGATGGATTTGAGAACCAAGTCTATTTATGTTATTATGTCCAC
5seq       TCTATAGGGATGGATTTGAGAACCAAGTCTATTTATGTTATTATGTCCAC
          *****

5prev      CATTTACCTCCAGGACATTCTCTTCTTATTATTCTCACACATCCTAAAC
5seq       CATTTACCTCCAGGACATTCTCTTCTTATTATTCTCACACATC-----
          *****

5prev      TGAAAACAAAAGCAAAGAATATTCTTTGTTTCAGTAAATAG
5seq       -----C
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CLUSTAL W (1.83) multiple sequence alignment

```
6prev      ATGCCATCTGGAATTGAAAATACTTTTCTAGTAGTAACAATAGGAGGATT
6seq      -----

6prev      TGTGATTGGAATGTTGGGGAATGGGTTTCATTGTACTAGTTAACTGCATTG
6seq      -----ATGTTGGGGAATGGGTTTCATTGTACTAGTTAACTGCATTG
                *****

6prev      ACCTGGTGAAGAGACAAAAGCTCTCATCAGCTGACTGCATCCTCACAGGC
6seq      ACCTGGTGAAGAGACAAAAGCTCTCATCAGCTGACTGCATCCTCACAGGC
                *****

6prev      CTGGCTATCTCCAGAATCAGTCAACTTTGGGCAATACTATGTGACTCATT
6seq      CTGGCTATCTCCAGAATCAGTCAACTTTGGGCAATACTATGTGACTCATT
                *****

6prev      TTTATTGGTACTATGGCCACACCTATATGCCATTGATAAACTAACAAAGG
6seq      TTTATTGGTACTATGGCCACACCTATATGCCATTGATAAACTAACAAAGG
                *****

6prev      TTGTTAATAGTTTTTGGATACTGTCCAATCACCTAGCTACCTGGTTTGCC
6seq      TTGTTAATATTTTTTGGATATTGTCCAATCACCTAACTACCTGGTTTGCC
                *****

6prev      ACCTGTCTAAGTGTTTTCTACTTCTTTAAAGTAGCCAACCTTCTCCCACCC
6seq      ACCTGTCTAAGTGTTTTCTACTTCTTTAAAGTAGCCAACCTTCTCCCACCC
                *****

6prev      CTGCTTCACTTGGCTGCGGTGGCGAATTCGTAGTGTTGGTACTGGTGCTTC
6seq      CTGCTTCACTTGGCTGCGGTGGCGAATTCGTAGTGTTGGTACTGGTGCTTC
                *****

6prev      TCTTGGGGTCTTTGTCCTTACTGTTTTTGAATTCTGAATCAATATATATG
6seq      TCTTGGGGTCTTTGTCCTTACTGTTTTTGAATTCTGAATCAATATATATG
                *****

6prev      TTTAGTCATATCTCAACTAACAGCTACAAAATATATGCAAGAACTCAAC
6seq      TTTAGTCATATCTCAACTAACAGCTACAAAATATATGCAAGAACTCAAC
                *****

6prev      GTGGTCCCCAAATGTAAGTGAAACTCATTATCTTCACCAGTTGATTGTTT
6seq      GTGGTCCCCAAATGTAAGTGAAACTCATGATCTTCACCAGTTGATTGTTT
                *****

6prev      TTAACCTCATCAACTTAATCCCCTTTCTTCTGTCCCTGACCTCACTGCTC
6seq      TTAACCTCATCAACTTAATCCCCTTTCTTCTGTCCCTGACCTCACTGCTC
                *****

6prev      CTCTTAGTCCTCTCCTTGATGAGGCACATCAGGAATTTGCAGCTCAACCC
6seq      CTCTTAGTCCTCTCCTTGATGAGGCACATCAGGAATTTGCAGCTCAACCC
                *****

6prev      CAGCTCAAAGGATCTCAGCACAGAGGCCCATAAAAGAGCCATGAAAATGG
6seq      CAGCTCAAAGGATCTCAGCACAGAGGCCCATAAAAGAGCCATGAAAATGG
                *****

6prev      TGATGTCTTTCTCTTCTCTTCGTCATTCATGTTTCTTCCGTCCTATTA
6seq      TGATGTCTTTCTCTTCTCTTCGTCGTTTCATGTTTCTTCCATCCTGTTA
                *****
```

```
6prev      ACAGGTTGGGTTTTTCCTTAAACTGCAGGGACGTCTGGCCAAATTGGTGGT
6seq      ACAGGTTGGGTTTTTCCTTAAACTGCAGGGACGTCTGGCCAAATTGGTGGT
          *****

6prev      TGTGTAACTTCGACTGTTTTTCCTTCAAGCCACTCATTTATCCTAATTT
6seq      TGTGTAACTTCGACTGTTTTTCCTTCAAGCCACTCATTTATCCTAATTT
          *****

6prev      TGGGAAATAGCAAGCTGAGACAAAATGCCATAGGACTACTGTGGTATCTT
6seq      TGGGAAATAGCAAGCTGAGACAAAATGCCATAGGACTATTGTGGTATCTT
          *****

6prev      AACTGCCGCCTGAAAAGAGTGAAATCTTTAGCTTCATAG
6seq      AACTG-----C
          *****
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CLUSTAL W (1.83) multiple sequence alignment

```
7prev      ATGGCAGATTCTTTGGAAAACATCTTTATCATTTTAAATAAATTCAGCATT
7seq      -----TT
              **

7prev      CATAATTGGTATTCTGGGGAATGGATTCATAGCACTGGTGAACGTCATTG
7seq      CATAATTGGTATTCTGGGGAATGGATTCATAGCACTGGTGAACGTCATTG
              *****

7prev      ACTGGATCAAGATGCAAAAGGTCTCCTTGGCTGATCGAATCCTCACTGCT
7seq      ACTGGATCAAGATGCAAAAGGTCTCCTTGGCTGATCGAATCCTCACTGCT
              *****

7prev      TTGGCAATTTTCAGAATTGGTCTGATTTTGGTAATGATGGTGAGTTGGTT
7seq      TTGGCAATTTTCAGAATTGGTCTGATTTTGGTAATGATGGTGAGTTGGTT
              *****

7prev      TACAAAGGAGTCTTATCCATTTTCTTCTTTAGACATAAAGGGAAATAAAG
7seq      TACAAAGGAGTCTTATCCATTTTCTTCTTTAGACATAAAGGGAAATAAAG
              *****

7prev      TCATACTTTTTAGTATTGCTGGGCTCTTGGCCAATTATTTTAGTGCTGG
7seq      TCATACTTTTTAGTATTGCTGGGCTCTTGGCCAATTATTTTAGTGCTGG
              *****

7prev      CTTGCCACAGGCCTCAGCCTCTTTTATTTCCCTCAAGATAGCCAATTTTTC
7seq      CTTGCCACAGGCCTCAGCCTCTTTTATTTCCCTCAAGATAGCCAATTTTTC
              *****

7prev      AAATGCTGTTTTCTTCACCTAAAAGTTTAGAATTGGAATGGTATTTATGG
7seq      AAATGCTGTTTTCTTCACCTAAAAGTTTAGAATTGGAATGGTATTTATGG
              *****

7prev      TAATGTTTCTGGGGACATTAGTATTGCTGCCTCTAAGTCTTACTTTGGTG
7seq      TAATGTTTCTGGGGACATTAGTATTGCTGCCTCTAAGTCTTACTTTGGTG
              *****

7prev      AGCATCTATATTAATATCAAGATACATCCATATGAAAGAAATATGACTTT
7seq      AGCATCTATATTAATATCAAGATACATCCATATGAAAGAAATATGACTTT
              *****

7prev      AAGTTCTAAAAGAAGTGACACTGAAACCTTTTCCAAATTGATCATATTCA
7seq      AAGTTCTAAAAGAAGTGACACTGAAACCTTTTCCAAATTGATCATATTCA
              *****

7prev      CCATGGGATCTTTCTCATCCTTTTATTATATCCCTGAGTTGTTTTCTCCTG
7seq      CCATGGGATCTTTCTCACCTTTTATTATATCCCTGAGTTGTTTTCTCCTG
              *****

7prev      TTAATGTTCTCCCTACGGAATCATGTCTAGAAGATGAGGAGCCAGGGTTC
7seq      TTAATGTTCTCCCTACGGAATCATGTCTAGAAGATGAGGAGCCAGGGTTC
              *****

7prev      AAGAGATCCCAGCAGCAAAGCCACGTCAGAGCCATGATCATGGCGATGC
7seq      AAGAGATCCCAGCAGCAAAGCCACGTCAGAGCCATGATCATGGCGATGC
              *****

7prev      CTTTCCTCATACTACTTGCCATTCACCTCCTATCTCATCTCATGACAACT
7seq      CTTTCCTCATACTACTTGCCATTCACCTCCTATCTCATCTCATGACAACT
              *****
```

7prev	TTTCATCACAATGTGATGCAGAGTGAAGTGGCCTTTATGCTTGCTGAAGC
7seq	TTTCATCACAATGTGATGCAGAGTGAAGTGGCCTTTATGCTTGCTGAAGC

7prev	TCTTGGAAGTATTTATCCTTCAGTCCACTCATTGTCTTGATTCTGGGAA
7seq	TCTTGGAAGTATTTATCCTTCAGTCCACTCATTGTCTTGATTCTGGGAA

7prev	ATGACAAGCTAAGAAAAGCTTCACTTTTGGTGCTGTGGCAGTTGAGGTGT
7seq	ATGACAAGCTAAGAAAAGCTTCACTT-----

7prev	GGCTGA
7seq	-----T

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CLUSTAL W (1.83) multiple sequence alignment

```
8prev      ATGATCCAAACCTGCAGTTCCTCAGAAAAGGATCTGTCACCATCTCTTGT
8seq      -----

8prev      CACTTTGATGTTAATAATTATCGGCACGGAATGCATCCTTGGTATTCTCG
8seq      ---TTGATGTTAATAATTATCGGCACGGAATGCATCCTTGGTATTCTCG
          *****

8prev      CAAATGGGTTCATTGCAGCGATAAACACAGCTGAATGGATTACAAATAAG
8seq      CAAATGGGTTCATTGCAGCGATAAACACAGCTGAATGGATTACAAATAAG
          *****

8prev      GTACTCTCCACCAGTGGCAAGATCTTGCTTTTCCTGGGTGTATCCAGAAT
8seq      GTACTCTCCACCAGTGGCAAGATCTTGCTTTTCCTGGGTGTATCCAGAAT
          *****

8prev      AGTTCTACAAAGCTTCATGATGCTAGAACTTACCTTAAGCTCAACATCCC
8seq      AGTTCTACAAAGCTTCATGATGCTAGAACTTACCTTAAGCTCAACATCCC
          *****

8prev      CACAGTTTTATAATGACGACATCACGTATCACACATTCAGAGGATGTTTC
8seq      CACAGTTTTATAATGACGACATCACGTATCACACATTCAGAGGATGTTTC
          *****

8prev      ATGTTCTTAAATCACTGCAGCCTCTGGTTTGCTGCCTGGCTCAGTGTCTT
8seq      ATGTTCTTAAATCACTGCAGCCTCTGGTTTGCTGCCTGGCTCAGTGTCTT
          *****

8prev      CTACTTCGTGAAGGTGGCGGATTTCTCCTACCCCCTTTTCCTCAAGCTGA
8seq      CTACTTCGTGAAGGTGGCGAATTTCTCCTACCCCCTTTTCCTCAAGCTGA
          *****

8prev      AGTGGAGAATTTCCAGACTGATGCCCTGGCTTCTGCAGCTTTCAGTGTTT
8seq      AGTGGAGAATTTCCAGACTGATGCCCTGGCTTCTGCAGCTTTCAGTGTTT
          *****

8prev      GTTTCCTTGGGCCAGAGTGTGCTCTTCTTCCAAAACATCTATACTATGAA
8seq      GTTTCCTTGGGCCAGAGTGTGCTCTTCTTCCAAAACATCTATACTATGAA
          *****

8prev      TTGTAACAATCTTTTTTCTCTCCCCTCCTTCAACTCCACTAAGAAAAAGT
8seq      TTGTAACAATCTTTTTTCTCTCCCCTCCTTCAACTCCACTAAGAAAAAGT
          *****

8prev      CCTTCTCGGAGGCCACTGTGATCAACCTGGTTCTTTTCCTTAACCTGGGG
8seq      CCTTCTCGGAGGCCACTGTGATCAACCTGGTTCTTTTCCTTAACCTGGGG
          *****

8prev      ATCTTCATCCCTCTGATCATGTTTATCCTGGCAGCCACCCTGCTGATCAT
8seq      ATCTTCATCCCTCTGATCATGTTTATCCTGGCAGCCACCCTGCTGATCAT
          *****

8prev      CTCTCTCAAAAGACACATCTTCCACATGAAAAGCAATGCCACTGGCTCCA
8seq      CTCTCTCAAAAGACACATCTTCCACATGAAAAGCAATGCCACTGGCTCCA
          *****

8prev      GAGATCCCAGCACGGAGGCTCACCTGGGGGCCATCAGAGCTATCAGCTAC
8seq      GAGATCCCAGCACGGAGGCTCACCTGGGGGCCATCAGAGCTATCAGCTAC
          *****
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8prev	TTTCTCATTCTCTATATTTTCCAAGTACTTGCTCTTTTCTCTACATGTC
8seq	TTTCTCATTCTCTATATTTTCCAAGTACTTGCTCTTTTCTCTACATGTC *****
8prev	CAACTTCTTTGACATCAATAGTCCCTTGAATATTTTGTGCAAAATCATCA
8seq	CAACTTCTTTGACATCAATAGTCCCTTGAATATTTTGTGCAAAATCATCA *****
8prev	TGGCTACCTACCCTGTGGCCCATTCCATTCTACTGATTCAGGACAACCCCT
8seq	TGGCTACCTACCCTGTGGCCCATTCCATTCTACTGATTCAGGACAACCCCT *****
8prev	GGGCTGAAAAGAGCCTGGAAGAGGCTTCAGGCTCAAGTCCACCTTTATTT
8seq	GGGCTGAAAAGAGCCTGGAAGAGGCTTCAGGCTCAANNCCACCTTTATTT *****
8prev	TAAAAAGTAG
8seq	TAA-----A ***