Alignment of rat and mouse *Chaer* homologs:

Score	**Expect**	**Identities**	**Gaps**	**Strand**
2425 bits(2688)	0.0	2184/2731(80%)	177/2731(6%)	Plus/Plus

Query = rat Chaer
Sbjct = mouse Chaer

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Query  1      CATTTGCAGGGGCCTCACGGAGTGCAGACTCGGTGTTACATCAGGCAGTTCTCCATAATC  60
              ||||| | |||||||||||||||||||||||||| || |||| ||||||||||  |||||
Sbjct  107    CATTTACTGGGGCCTCACGGAGTGCAGACTCGGTATTCCATCGGGCAGTTCTCGGTAATC  166

Query  61     TGGTAGCCCATGTCTGACGCCAATTCTGGTTCTCTG----AATCTGATAGGTGCAGATCC  116
              ||||| | | |||| || |||| |||  ||||||||    |||||||||||| |||||||
Sbjct  167    TGGTAACACGTGTCCGATGCCAGTTCCAGTTCTCTGGTTGAATCTGATAGGTACAGATCC  226

Query  117    CAAACTGATCTTGAACATGGTGTGGGCAGGATCACCTAGCAGGC-TGAAAGTCATGTGAA  175
              |||||  || ||| |||||||||||||||||| |||| |||||| ||  |||||  ||||
Sbjct  227    CAAACCCATGTTGGACATGGTGTGGGCAGGATAACCTGGCAGGCCTGGGAGTCAAATGAA  286

Query  176    GAGAAGAGCGGAGGGTTTGTTGCAAA-GTCTCAGGATGGCTAACTTGTCTCCTTCCGAGG  234
              |||| |||| ||||| | | |||||| |||||||||||||| ||||||||||||| || |
Sbjct  287    GAGAGGAGCTGAGGGCT-GCTGCAAAAGTCTCAGGATGGCTGACTTGTCTCCTTCTGAAG  345

Query  235    CTTCTAGAAATGGCTCTGACACAAAGGCCTTTGGGAGAGCAGGCTCAAGTGACAAGAGA-  293
               |||||||  || ||||||||||||||||||||||||| ||| |||||| |||||| |
Sbjct  346    TTTCTAGACTTGACTCTGACACAAAGGCCTTTGGGAGAACAGACTCAAGGGACAAGGGGT  405

Query  294    -------CCCTTCTCTCATTTGAGCCCCATTCAGAGGGGGACACCCACAGGCAGGAACAT  346
                     | |||| |||||| ||||||| |||||||||| | || ||||||||||||| |
Sbjct  406    GATGCTTCGCTTCCCTCATTGGAGCCCCTTTCAGAGGGGAAAACTCACAGGCAGGAACCT  465

Query  347    GTGTGCCAGCCCTGACC-AGAGCAACAGTGAACAGTCACTGCTGTGTTTGACAGCATCCA  405
              | ||||||||||||||| ||||||||||||||||||| | ||||||||  |||||   ||
Sbjct  466    GCGTGCCAGCCCTGACCCAGAGCAACAGTGAACAGTCCCCGCTGTGTTCCACAGCGCTCA  525

Query  406    TCCAGAAACACTTGTGGTTTTCCATCACATTCTAGAATCCACAGGAGACCTGGAAGCTGA  465
              ||||||||||||   || |||||||||||||||  | ||||||||| |||||||||||||
Sbjct  526    TCCAGAAACACTGCGGGGTTTCCATCACATTCTGCAGTCCACAGGAAACCTGGAAGCTGA  585

Query  466    CTCTTTCTCTTCTGTGATCTCCGCCTCCCCTGCTGGCCTGTGCTCTGTGGGAACTCATTA  525
               ||||| |||||||||||||| |||||||||||||||||||||||| ||||| |||||||
Sbjct  586    GTCTTTTTCTTCTGTGATCTCTGCCTCCCCTGCTGGCCTGTGCTCTATGGGAGCTCATTA  645

Query  526    GCTGAACCCT-GGAC-AAGGACAAGCAAGCAGGGCTGAAAAGAGACTTTATGAACAACTG  583
              |||||||||  |||| ||||||||||||||||||||||| |||||||||||||||| |||
Sbjct  646    GCTGAACCCCAGGACCAAGGACAAGCAAGCAGGGCTGAATAGAGACTTTATGAACAGCTG  705

Query  584    -TGGTC-----TGCTGTCTCCTTGTGAAGAAA--------CCTG-AACTAGAAAGCAGGG  628
               |  ||     || ||||||||||||||||||        |||| || ||||||||||||
Sbjct  706    CTACTCCGTGGTGTTGTCTCCTTGTGAAGAAAGGGGTGAGCCTGGAAGTAGAAAGCAGGG  765

Query  629    AGTTTGGCTTTGTTATTGT----TATTCCTGGAAGGGAtgtgtgtgtgtgtgtgtgtgtg  684
                ||||| ||||||||||     | |||||||||||   | | | |
Sbjct  766    GATTTGGTTTTGTTATTGCGTAATCTTCCTGGAAGGCGGGCGAGGG--------------  811

Query  685    tgtgtgtgtgtgtgtgtAGGGGGGTAATAACAGCATTTGTCACTTTTACTGCCTGGTTGT  744
                                ||| ||||| || ||||||||||||||  |||| ||| |||
Sbjct  812    ------------------GGGTGGTAAGAAGAGCATTTGTCACTTGAACTGTCTGCTTGG  853

Query  745    GATAGTAGTCCCTGACCCCTTTCCAGGACTTCCATAACTTGGCTCAGAGTTGGCCCTTAG  804
              || |||| ||||||||||||||||||||||||||||||||||| | |||||||||||||
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Sbjct  854   GACAGTATTCCCTGACCCCTTTCCAGGACTTCCATAACTTGGCACTGAGTTGGCCCTTAA  913

Query  805   ATTGGCAAACCAAAGTTGGCACTGAGCAACACATAAGAAGTAGAAAGAATTTTTTCATGA  864
              ||||||||| ||  ||||||||||||||||| ||||| ||||||||||| ||||||||
Sbjct  914   GTTGGCAAACAAACCTTGGCACTGAGCAACACTTAAGAGGTAGAAAGAATGTTTTCATGC  973

Query  865   CTTCAGCAGCTCCAACAGACTCTGAAGGGAGAGAGGTACCAGTCCTATTGCTTACCATCC  924
             |||||||||||||| |||||||||||||  ||| |||| |||| |||| || | ||||||
Sbjct  974   CTTCAGCAGCTCCAGCAGACTCTGAAGGCTGAGCGGTAGCAGTTCTATCGCCTGCCATCC  1033

Query  925   AGTCCCAGAGCAGCAGGGTCCTTAGACCTGCATCTCAAGCCAGGTAGCCTGCACATCAGA  984
             || ||||||| || |||||||        ||||||| |||||||||||||| |  ||||
Sbjct  1034  AGCCCCAGAGTAGAAGGGTCCG-------GCATCTCCAGCCAGGTAGCCTGTATGTCAGG  1086

Query  985   CTCACACAGGATATG----GGATCTCCATCTTGGGAGAACA-GCATTGATGCTTCAGCTC  1039
             |||||| ||| ||||    | |||||||||| ||||||||| || |||||||||||| ||
Sbjct  1087  CTCACATAGGCTATGTATGGCATCTCCATCTCGGGAGAACAAGCGTTGATGCTTCAGTTC  1146

Query  1040  TGGCCTAGTCATTGCCAATGTCCATTGACGGTTCATCTTCACTCTGAGGGGAGCAGAAAA  1099
             |||||| |||||| ||||||||| |  | ||| | |||| ||||||||||||||||||||
Sbjct  1147  TGGCCTCGTCATTACCAATGTCCTTCAATGGTCCCTCTTTACTCTGAGGGGAGCAGAAAA  1206

Query  1100  AGGGGGGTCTCATTCGGATGCTAAGAGATGA-CAAATTTCTAGAACCTTCTCTCTCTTCT  1158
               |||||||||||| |||||| | ||||| | | ||||||||||||||||||| ||||||
Sbjct  1207  --GGGGGTCTCATTTGGATGCCATGAGATAAGCTAATTTCTAGAACCTTCTCTATCTTCT  1264

Query  1159  GTCAATTCTAGCTTGGATGAGCAATTAGCAGTCAGAAGCAGACG----ACTCTACTCAGA  1214
             |||| |||||| |||||| ||| |||||| ||||||| |||||     ||||||||||||
Sbjct  1265  GTCAGTTCTAGTTTGGATTAGCGATTAGCTGTCAGAACCAGACAGACAACTCTACTCAGA  1324

Query  1215  CAAGTTCCAGAAGGTGAGAGCCGGGTCCTTGA-TGCCAAAGGAACCTCAGACGATTCCTG  1273
             ||||| ||||| || ||| || | ||||| |  |||| |||| |||||||| |||||||
Sbjct  1325  CAAGTACCAGATGGGGAGCGCTGAGTCCTCGGGTGCCGAAGGGACCTCAGATGATTCCTA  1384

Query  1274  CCGGGTCTGCGTTTCCTTCCCTTGCTTAGATAACAGCACATGGGTCCTTAGGAGCTTGCA  1333
             | ||| ||| | || |||||| |||||||| |||||||||| |||||||||  |||||||
Sbjct  1385  CAGGGCCTGTGCTTTCTTCCCCTGCTTAGAGAACAGCACATAGGTCCTTAGCGGCTTGCA  1444

Query  1334  CATAAAAATAAATGAAAGATTTTTGTTTACCCTCATCTATCTTTAGCCCCATAGGAAAGa  1393
             |||||| |||||||||||||                    ||||||||||||| ||||||
Sbjct  1445  CATAAACATAAATGAAAGAT--------------------CTTTAGCCCCATAAGAAAGA  1484

Query  1394  aaaaaaCAAGCAAACAAAATAGGCCTGGGCAGTCTGGTTTGGAATAAAAACACAAGCGGT  1453
             |||||      |||||||| |  |||| |||| ||||||||| |||||||||   || ||
Sbjct  1485  AAAAAT-----AAACAAAAAAC-CCTGAGCAGCCTGGTTTGGGATAAAAACAT--GCAGT  1536

Query  1454  GTACACGATTTTTGTAAAAATTAACTTTGGCTAAAGCATTTCGGAAGTCAGCAGCATCTA  1513
             ||||| ||||||||||||||||||||||||| | |||| || |||||  |||||||||||
Sbjct  1537  GTACATGATTTTTGTAAAAATTAACTTTGGCCAGAGCACTTGGGAAGCAAGCAGCATCTA  1596

Query  1514  AGCTTAGTCAGGCAGATTCATGGGTGAAAGCCTGTGTAGTTGACAAGCGTTTGCAGATGA  1573
             |||| || |||||||  |||||  ||||| ||||| |||||||||||| | |||| ||||
Sbjct  1597  AGCTGAGACAGGCAG--TCATGCCTGAAAACCTGTCTAGTTGACAAGCATATGCAAATGA  1654

Query  1574  GAAAAGAGAGAAGTCTCTGTAGTCCTAGTGAGAAGCCTTGGCTGACT-CCATGACAGGCT  1632
             | |||||| || | |||  | |||||||| || || || |||||||  ||||||||||||
Sbjct  1655  GGAAAGAGGGAGGCCTCCCTGGTCCTAGTCAGCAGGCTAGGCTGACGGCCATGACAGGCT  1714

Query  1633  TCAAACTGGCAGTTCAGGAGACTAGGCCTAAATCTCTTTTTCCAAGAACTGGACAATTCC  1692
             |||||||| ||||| ||||||||||||||||| |||| ||||||||| ||||  |||||
Sbjct  1715  TCAAACTGACAGTTAAGGAGACTAGGCCTAAACCTCTGTTTCCAAGACCTGGGAAATTCT  1774

Query  1693  AGGCTAGTTCAGGCCT----CAGAAGCTTCCCTGCCATCTGGCCTGAGGCAAGGACAATG  1748
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              ||| ||| |||||||    |||||| | |||  ||| ||||||||||||||||||||||
Sbjct  1775  TGGCGAGTCCAGGCCTGCCTCAGAAGGTGCCCCACCACCTGGCCTGAGGCAAGGACAATG  1834

Query  1749  GGGTCAGCAGCCATTTCCAGACTTCCTCAGCTACTTCCTCAGCGGCAGTTTCCAGACC--  1806
             |                         | ||        ||||| |||||||||||| |
Sbjct  1835  GA------------------------TGAG--------TCAGCTGCAGTTTCCAGATCGA  1862

Query  1807  -TCCCC--AGCAAGTTTCCAGCCCC-CACACTTCAGTAATGGA-TGTCGGTAGAGATGGA  1861
              |||||  ||||||||||||||||| ||||| ||||||||||| ||||  ||||||||||
Sbjct  1863  CTCCCCCTAGCAAGTTTCCAGCCCCTCACACCTCAGTAATGGAATGTCTATAGAGATGGA  1922

Query  1862  CCCAACAGATTAACATAGACGTCATCTACCCTGGAATTCCCTAACGTGCTTTAATTCAGG  1921
             |||||||||||||| |||| |||| ||||||  ||||||||||| ||||||||| |||||
Sbjct  1923  CCCAACAGATTAACGTAGAGGTCACCTACCCCAGAATTCCCTAATGTGCTTTAAATCAGG  1982

Query  1922  CCTGCAAGCTCTCTTGGT-GACTCTCTAT--TCTGGTAACGGGAAACCGCAGCACGCTGG  1978
             |||| |||||| |||||| |||||||| |  |||||||| |||| | | ||||| |||||
Sbjct  1983  CCTGTAAGCTCACTTGGTTGACTCTCTCTGTTCTGGTAATGGGAGAGCCCAGCATGCTGG  2042

Query  1979  ACTTCTACAGAATAAAACACT--TTGTGGTTATATACTATTTAAGTCCGGG-TATCATTC  2035
             |||   |||||||||||||||  |||||  ||||||||||| ||||||||| | || |||
Sbjct  2043  ACT---ACAGAATAAAACACTCTTTGTGTCTATATACTATTCAAGTCCGGGCTTTCGTTC  2099

Query  2036  TTCAGTGAATCATGGACCCTTACACTAGGAAGGAGATATCCCAGCACAGTGTAAGGTATT  2095
             ||    |||  ||||||||||||| |||||||||| || || ||||  |||| ||||| |
Sbjct  2100  TTTGTGGAAATATGGACCCTTACAGTAGGAAGGAGGTAGCCTAGCATGGTGTGAGGTACT  2159

Query  2096  GGAACAGAACA--GAGTCTCCCAGAGAGGAGGGCCAGAAGAGACTCCTGGCTCCATGAAA  2153
             || ||||| ||  |||||| ||||||| |||||  ||||||||||| |||||||||||||
Sbjct  2160  GGGACAGAGCAAAGAGTCTTCCAGAGAAGAGGGTGAGAAGAGACTCTTGGCTCCATGAAA  2219

Query  2154  AAACTAAAGATGGCAAGAACACAAGGCAGGAACTTGGACAGTATCAGAGCTGCGAGCTGT  2213
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Sbjct  2220  AAGCTAAAGCCAGCAAGAACATAAGGCGGGAACTTGAACAGTGTCAGAGCTGTGAGCTGA  2279

Query  2214  TCTGAAGGGTTTCTGCCCCTGGTTACTGACATAGCCTACAGGAGTTCTT-CCACCTATGC  2272
             ||||  |||||||||||||||| || |||| |||||   |||||| ||| ||||| ||||
Sbjct  2280  TCTGTGGGGTTTCTGCCCCTGGCTAGTGACGTAGCCCGGAGGAGTCCTTGCCACCCATGC  2339

Query  2273  CTTTGAGTAGAGGAGGTGTAGGATCTGCAGAACATCCAGAGCCTTGTTCTGGAACAAAAG  2332
             ||| | |||||||||| ||||||| |||||| | | |||||| |  | |||| || || |
Sbjct  2340  CTTCGGGTAGAGGAGGAGTAGGATTTGCAGAGCGTTCAGAGCTTCATCCTGGTACCAAGG  2399

Query  2333  CTCTAACCCACAGCTGTGTGGTGCTTGCAGTTATGTACCCACAGTAAACCACAGTCCAAA  2392
             | || |||||||||| || ||||||||   ||||||||||||||||||||||| ||||||
Sbjct  2400  CCCTTACCCACAGCTTTGCGGTGCTTGTCATTATGTACCCACAGTAAACCACAATCCAAA  2459

Query  2393  AGTATTAAATGGAAAACTCTAAAAATAAATAACCCATGGTCTTTAAATTGCAGCCTGTGT  2452
             ||||| |||||| |||||||||||||||||||| || |  ||| | ||||| |||| |||
Sbjct  2460  AGTATCAAATGGGAAACTCTAAAAATAAATAACTCAAGAACTTGACATTGCGGCCTCTGT  2519

Query  2453  CGGGAACTCTGGTCCCATCAGCTCCCTCTGGCCCCTGCATGTGAACTGTTCCCTCAAGCA  2512
             | ||||||||| |||||||||||||||||| | || | ||| ||| | |||||||  |||
Sbjct  2520  CAGGAACTCTGCTCCCATCAGCTCCCTCTGACTCCCGGATGGGAATTATTCCCTCGTGCA  2579

Query  2513  GTCTACCCCATCCCTGCACATTAGCCCTGGTTTCCTTCCCAGCCATTTCA-CTCTCAGGC  2571
             || || ||   |||||| ||| ||| ||   ||| ||||||||| ||||| |||||||||
Sbjct  2580  GTATAACCTCACCCTGCCCATCAGCGCTTACTTCGTTCCCAGCCGTTTCAGCTCTCAGGC  2639

Query  2572  CCGCTGTGGTGGCACAGTAATTTAGATCTACATTAAGTTTATGTTGTTGGTCTTGAGCTG  2631
             |  |||||| |  |||||||| |||||| |||||| ||||||||||||| ||||||| ||
Sbjct  2640  CTACTGTGGGGTTACAGTAATCTAGATCCACATTATGTTTATGTTGTTGATCTTGAGTTG  2699
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Query  2632  GGCTTAA-TTTATGAATTAAACTTATTCTTA  2661
              |||||| ||||   ||||||||||||||||
Sbjct  2700  TGCTTAATTTTACTTATTAAACTTATTCTTA  2730
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