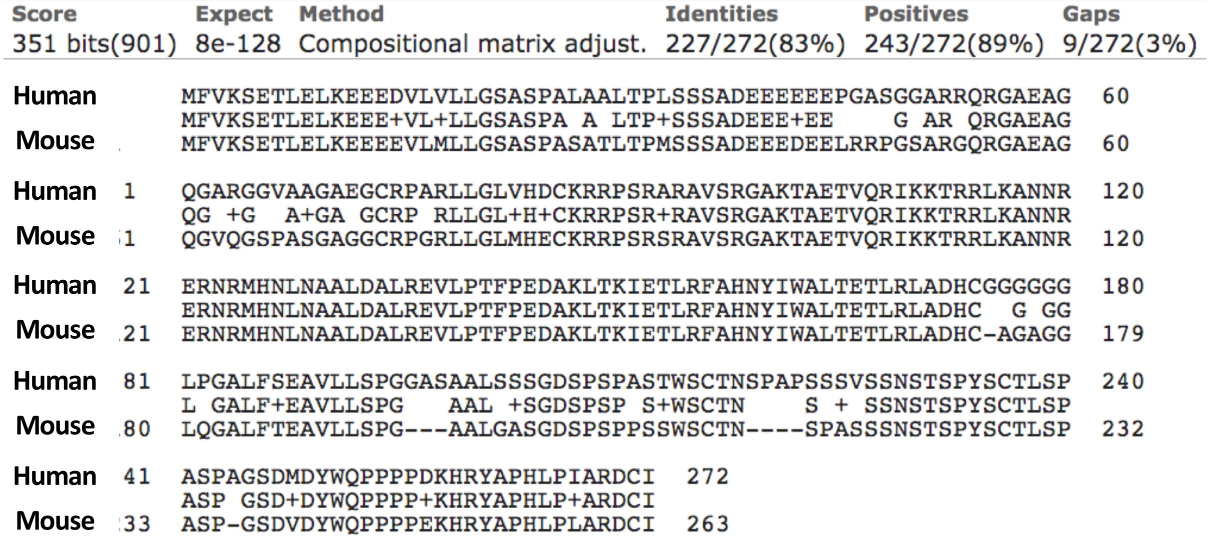
Neurogenin 2



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Score        Expect  Method                        Identities     Positives      Gaps
351 bits(901) 8e-128 Compositional matrix adjust.  227/272(83%)   243/272(89%)   9/272(3%)

Human         MFVKSETLELKEEEDVLVLLGSASPALAALTPLSSSADEEEEEEPGASGGARRQRGAEAG   60
              MFVKSETLELKEEE+VL+LLGSASPA A LTP+SSSADEEE+EE    G AR QRGAEAG
Mouse         MFVKSETLELKEEEEVLMLLGSASPASATLTPMSSSADEEEDEELRRPGSARGQRGAEAG   60

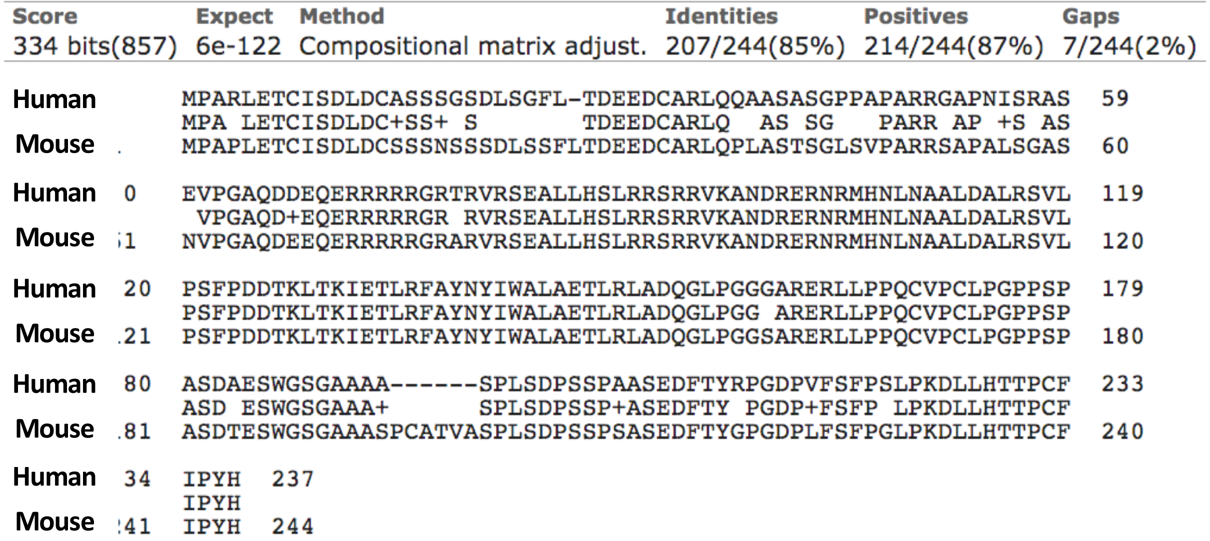
Human     1   QGARGGVAAGAEGCRPARLLGLVHDCKRRPSRARAVSRGAKTAETVQRIKKTRRLKANNR   120
              QG +G  A+GA GCRP RLLGL+H+CKRRPSR+RAVSRGAKTAETVQRIKKTRRLKANNR
Mouse     1   QGVQGSPASGAGGCRPGRLLGLMHECKRRPSRSRAVSRGAKTAETVQRIKKTRRLKANNR   120

Human    21   ERNRMHNLNAALDALREVLPTFPEDAKLTKIETLRFAHNYIWALTETLRLADHCGGGGGG   180
              ERNRMHNLNAALDALREVLPTFPEDAKLTKIETLRFAHNYIWALTETLRLADHC  G GG
Mouse    21   ERNRMHNLNAALDALREVLPTFPEDAKLTKIETLRFAHNYIWALTETLRLADHC-AGAGG   179

Human    81   LPGALFSEAVLLSPGGASAALSSSGDSPSPASTWSCTNSPAPSSSVSSNSTSPYSCTLSP   240
              L GALF+EAVLLSPG   AAL +SGDSPSP S+WSCTN    S + SSNSTSPYSCTLSP
Mouse    80   LQGALFTEAVLLSPG---AALGASGDSPSPPSSWSCTN----SPASSSNSTSPYSCTLSP   232

Human    41   ASPAGSDMDYWQPPPPDKHRYAPHLPIARDCI   272
              ASP GSD+DYWQPPPP+KHRYAPHLP+ARDCI
Mouse    33   ASP-GSDVDYWQPPPPEKHRYAPHLPLARDCI   263
```

Neurogenin 1



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Score        Expect  Method                        Identities     Positives      Gaps
334 bits(857) 6e-122 Compositional matrix adjust.  207/244(85%)   214/244(87%)   7/244(2%)

Human         MPARLETCISDLDCASSSGSDLSGFL-TDEEDCARLQQAASASGPPAPARRGAPNISRAS   59
              MPA LETCISDLDC+SS+ S       TDEEDCARLQ  AS SG   PARR AP +S AS
Mouse         MPAPLETCISDLDCSSSNSSSDLSSFLTDEEDCARLQPLASTSGLSVPARRSAPALSGAS   60

Human     0   EVPGAQDDEQERRRRRGRTRVRSEALLHSLRRSRRVKANDRERNRMHNLNAALDALRSVL   119
               VPGAQD+EQERRRRRGR RVRSEALLHSLRRSRRVKANDRERNRMHNLNAALDALRSVL
Mouse     1   NVPGAQDEEQERRRRRGRARVRSEALLHSLRRSRRVKANDRERNRMHNLNAALDALRSVL   120

Human    20   PSFPDDTKLTKIETLRFAYNYIWALAETLRLADQGLPGGGARERLLPPQCVPCLPGPPSP   179
              PSFPDDTKLTKIETLRFAYNYIWALAETLRLADQGLPGG ARERLLPPQCVPCLPGPPSP
Mouse    21   PSFPDDTKLTKIETLRFAYNYIWALAETLRLADQGLPGGSARERLLPPQCVPCLPGPPSP   180

Human    80   ASDAESWGSGAAAA------SPLSDPSSPAASEDFTYRPGDPVFSFPSLPKDLLHTTPCF   233
              ASD ESWGSGAAA+      SPLSDPSSP+ASEDFTY PGDP+FSFP LPKDLLHTTPCF
Mouse    81   ASDTESWGSGAAASPCATVASPLSDPSSPSASEDFTYGPGDPLFSFPGLPKDLLHTTPCF   240

Human    34   IPYH   237
              IPYH
Mouse    41   IPYH   244
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Supplemental Figure 5