

Supplementary figure S1: The predicted *Monosiga brevicollis* teneurin aligned with teneurin sequences.

The intracellular domain (ICD) does not align well with any of the teneurins. Here it is shown aligned with the ICD of chicken (*Gallus gallus*) teneurin-1:

```

Mb          1 MDSGDNDNDYLNVS AEPDPF DAADDEALYGFNKPFPAMPAS 40
Gg  MEQMDCKPYQPLSKVKHEVDLTYTSSSDESEDGRKQRQSYDSRETLNEYSQELRLNYSQ 60
          :   ...* :   : : : * :   :   :
Mb  TGKTVVSNP-----AYASSINPLFDGGDADEEGAYADLDAPS----- 77
Gg  SRKRKNTDQSTQDMEFCETPHILCSGYQTDLHGVSEHSYPLEVGSVDVTETEGGASPDHA 120
          : *   : :   . * : : : . . * * : . * : : .
Mb  -----GFGGAATTAFGTNSDNGTYFDPTHNFAG-----PATQSAEYMFDPDASPDAGS 124
Gg  LRMWMRGMKSEHSSCLSSRANSALS LTDTDHERKSDGENDMPGSPHNQFTFRPLPPPPPP 180
          * : .   : : : : : : : :   : * : :   * : :   *   . * . .
Mb  SKAGASNKVAPFQIDDGMDKSPGTNASRN----- 153
Gg  PHACTCTRKPPPAADSLQRRSMTTRS QPSPAAPTPTSTQDSVHLHNSWVLNSNIPLPTR 240
          . : * : : : . *   * .   : *   * : : . .
Mb  ----DKGRGR 159
Gg  HFLFKHGS GSSAIFSAASQNYPLTSNTVYSPPPRPLPRNTFSRPAFTFSKPYRCCNWKCT 300
          . : * *
Gg  ALSATA 306

```

Here is the 23aa transmembrane domain (upper case) of the *Monosiga brevicollis* teneurin, as predicted by SMART, followed by the ECD found between the transmembrane domain and the EGFs (lower case):

```

Mb  LYIIIIAILLAIILALIVVIVLAgggssgnatngtass
     agsegsqassqntkpppttipptttpaptttgd      230

```

Monosiga brevicollis teneurin has 8 EGF repeats. Here they are shown aligned with the 8 EGF repeats of Drosophila melanogaster (Dm) ten-m and Gallus gallus (Gg) teneurin-1. The conserved cysteines are in bold.

```

Mb  VPCGTGFCTHGICCHEAKGVCWCLDGYFGDACD-
Dm  QNCPNGCSGNGQCLLGH--CQCNPGFGGDDCSE
Gg  DDCSTNCNGNGECISGH--CHCFPGFLGPDCAK
      *  ..   : * *   . :   * *   * : *   * .

Mb  QECPGLCTDNSRGLCGTQGSCLCFPGFAGDACQNTT 298
Dm  SVCPVLCSQHGE---YTNGECICNPGWKGKECSLRH
Gg  DSCPVLCSGNGE---YEKGHCVCRNGWKGPECDVPE
      .  ** **: :..   : * * : * : *   * .   :

Mb  dsvwmrfrdslgpledfdfdqflanidllfpddsfavegcshndglvceis
     vstsqdagavvtqilnmaeannidlfnlgveavtdsqggnwssels 395

Mb  AQCLN-DCSGHGRCLETTQCECYSGWDGEDCSREVVF
Dm  DECEVADCSGHGHCVSG-KCQCMRGYKGKFCEE---
Gg  EQCIDPTCFGHGTCIMG-VCICVPGYKGEICEE---
      : *      * * * * :      * *   * : . * : * .

Mb  KSCE-NDCSGNGYCFDGTCECDEGWSGSACDALL---
Dm  VDCPHPNCSGHGFCADGTCICKKGWKGPDCATMDQDA
Gg  EDCLDPMCSGHGVCVQGECHCSAGWGGVNCETSL---
      ..* .   *** : * * : * * * . * * *   * :

Mb  VPCTDDCNGRGTCDQTTGICNCTQGYIGDACEE
Dm  LQCLPDCSGHGTFDLDTQTCTCEAKWSGDDCSK
Gg  PICQEHCSGHGTFLLDVGLCSCEPQWTGSDCST
      *  . * . * : * *   .   * . *   : * . * .

Mb  RICLAGCGDHGVCRSGVCDCDDGFTGETCSE
Dm  ELCDLDCGQHGRCEGDACACDPEWGGEYCNT
Gg  ELCTLDCGSHGVCSRGICQCEEGWVGPTCEE
      . : *   . * * . * *   .   * * :   : *   * .

Mb  ISCTLDCGDHGYCSNNTCVCSTGWNGEYCDV
Dm  RLCDVRCNEHGQCKNGTCLCVTGWNGKHCTI
Gg  RTCHSHCAEHGQCKDGKCECSPGWEGDHCTI
      *   * : * * * . : . * *   . * * : * : * :

Mb  QGCRKDCSNGACVQNSETAIWSCQCQSGWQGDACQA 596
Dm  EGCPNSCAGHGQCR-VSGEGQWECRCYEGWDGPDCGI
Gg  DGCPLCYGNGRCT-LDQNG-WHCVCQVGWSGSGCV
      : * *   * * : * *   .   .   * * *   * * *   *

```

Adjacent to the EGFs is a 38aa-long cysteine-rich domain, aligned here with the cysteine-rich domains of *Drosophila melanogaster* ten-m and *Gallus gallus* teneurin-1:

```
Mb  GIELNCNDGIDNDNDRVTDCNDADCCSSPACQDHPSCQ 634
Dm  ALELNCGDSKDNDKDGLVDCEDPECCASHVCKTSQLCV
Gg  VMEMACGDNLNDNDGDGLTDCVDPDCCQQNNCYASPLCQ
    **: *.*. *** * :.*. * :.*. . * *
```

The next 1015aa includes the NHL repeats. The two complete NHL repeats are shown below in upper case:

```
Mb  tvpdaddvvtkvnltapidevdpieeesfleqwwplvdgdsatqmevdtstqldearval
vtgtvldtnlipvtgkvqilghpefgytmmtatgafnmvvnngggylsirfarddfmes
qrtpyipenertiipavvmqpvsniktevelgtgssedsvvasgdavedesgsrtarml
ffgnntatvqnmtdgtnstlpsmnlriteftvgsagpeampselpansgytyaveislde
eatvnsdtnvqfgspvpfytenflgfpvgsvvpgsynrqaqawmpesdgrvieivrie
kvngvdtavlnlrpnaadfgdiasepilsadieagcddeafqqvnahrnptavdelsde
elshfqislaekqrlaelygagaqiwrvlvphatpwcndwpygppldgcspaqcnpnp
ddpednddpdpdcakagsiihpstqtlseainiagsnmnlvyssnrmpgyhvaidvp
atsanppdsllgvivtlkiagrefsrtfdsgkpnlkarfvwdrdnrgalvlgqidytv
trqytyplyypsrnsnfaaafgrfsgsvtvpstgsgtanqmanrtiavsneyqgtlqg
rrdirrlkmggwsldvhhrynpsstmlhrgdgtrtqfyaskgvtttilggnnrrstsc
eclegntsslypsvsvahhpsgslfigdynviyrretngtvtiaytfppgseptstyy
lavhptwgdlvsipsrrqvfrltsagalepiigtgeacdpsdlvqqaracgdgglavn
aalMMPRGLTVLKDGDIIYLADgtrivhvtpdgvigthvgatefmqgmlpayvpdvpltd
ailvqptylaysaveslyildgasaliyritsanlmqvvagypnsqgraepyqddki
gitetvaaltplqdprglaisatgtvfvveasmyrvrevtaegmirtlagstslcsss
ssscpgiggtqapdaalfKAPADVSIHRGLVYVADEGNRAIrslgvrtdfaygtelavp
em 1639
```

The next 790aa includes 26 YD repeats that can be aligned with the 26 YD repeats of *Gallus gallus* teneurin-1:

1 2
 Mb GTTLVYVFDNNGRHLTTRSTITN | QPILTFQYDATNPELLTGLTTAF | GDEIVFARDAAT
 Gg ADQELYQFTINGTHLHTLNLITR | DYIYNFTYSGE--GDVATITSSN | GNSVHIRRDTSG
 . : * * * * * . * . : * . * * . : : : : * : : : * : : :

3
 Mb GRLTRITANGVVTDVEIDESGYLRTIRQPNDRSYYFAYRMTMPGIPDGLLEEQIDAE | GR
 Gg LPLWVVVPPGQVYWLTISSNGVLKRVAQG---YNLALMTYPG--NTGLLATKSDEN | GW
 * : . . . * * : * . . . * * : : . * : * * * * : * : *

Mb LHSYVYNSEGRLTADSGPR | GGTTKLSRRQNNETGEYQIVVTLPELQVQKLSFAPLSSAT
 Gg TTVYEYDSDGHLTNATFPT | GEVSSFHSDVEKLT-----RVELDTSNRENMTATNFSAT
 * * : * : * : * * . : : : : * * * : : : : * . * * *

Mb GTRTTATNEHGGVGITDVPDGSWNEYNPDGSSLTALVSPHPVWKGQARVVTQQRMRVPS
 Gg STIYTLKQDN-TQNIYRVSPDGLRVTFASGMEITLNTEPHILAGVVSPTLGKCNISLPG
 . * * . : : : . * * * * * . . . * . : * . . * * : : : : : * .

4 5
 Mb GSALVTSYAYSVTQTDVTPFVSPTSLSLTKQTTIA | GRLAHTVTRDVVNRQ-VTSE | VPGLG
 Gg ---EHNSNLIWRQRREQTKGNISTFERRLAH | NRNLLSIDFDHVTRTGKIYD | DHRKF
 . * . * . : : : : : . * : : * * * * :

6 7
 Mb QFVMAYDGFGRITITQTFPGS | NLDAIETSYHSNGQVNETRR | GNYYVRYTYDASGAVTSW
 Gg TLRIMYDQTRPVLWS-PIS | KYNEVNITYSHSGLVTYIQR | GTWTEKMEYDPSGNIISR
 : : * * * * : : * * : : : : * . * * . : * * . : : * * * * : *

8 9
 Mb VSSS | GLSAHYSQENLGSLARRNVSY | SGRTVSFDVDTLGRRL | QVTLPSGSAHVVMGY
 Gg TWAD | GKIWSYTYLEKSVMLLLH----- | SQRRYIFEYDQSDYLL | SVTMPSMVRHALQT
 . : . | * * : : . * : : * * * * * * . * * * * * * . :

10 11
 Mb ADHIGEDTDYTPED | -HVMMQTLRLDNKIKSITLP-S | GRTIQHEFSEGGLVTRKID |
 Gg MLSVGYRNIYTPPDS | GAAFIQDVTRDGRLLQTLYPGT | GRRVLYKYSKQSRLLSEILY |
 : * : * * * . : : : : * : : . * : | * * : : : : : . : : : :

12 13 14
 Mb GDQFLDLDYIPGLARPSLLRYGT | GHEEVQSTFVWDGPLLQR---WT | TDAGSVSSYYQ
 Gg DTTQVTFTYEESGVIKTIHLMHD | GFICTIR-YRQTGPLIGRQIFRF | SEEGLVNARFD
 . : : * . . . : : * . . : * * * * * : : * * . : :

15 16 17
 Mb LDYESSWRVQDYDVYYNN | NRLYNTRVYRDSNGLVYQV | DDFPLTYSPNRDELTVR | RSD
 Gg YSYNNFRVTSMQAMINET | PLPIDLYRYVDVSGRTEQF | GKFSVINYDLNQVITTT | VMK
 . * : . . : : . : * * * * . * . . * . : : : * . .

18 19
 Mb GLGYWSLDNSLGLPAERKAYVTTG | STPVFQEELLYAQGDNLVSGWLH | QLPGSSNTVNT
 Gg HTKIFSANG----QVIEVQYEILK | SIAYWMTIQYDNMGRMVICDIRV | GVD--ANITRY
 : * : . . * * . : * : : . : : : : : : * : .

20 21
 Mb TFVYDVGDLTQVLED | GAEVESYSYDVNG--NRVAW | NVRGAAHSATYGADDAVFTV |
 Gg FYEYDRDGQLQTVSVN | DKTQWRYSYDLNGNINLLSH | GNSARLTPLRYDLRDRITRL |
 : * * * * * * : . * * * * * * : : . . * . * : :

22 23 24
 Mb DGQSYAVDVGFLTSV | RGMSLAYSGRGELLSATLPSG | AGTVRYRYDGFRRIMRISPL
 Gg GEIQYKMDDEDGFLRQR | GNEIFEYNSGLLNKAYNKVS | GWTVQYCYDGLGRRVASKSSL
 . * : * * * * . . : * . . * * . . * * * * * * * * : * *

25 26
 Mb | EEVTTYMYNDPGQIHLVTDIYMPT | GKHMR-FRHDPNGRLAVIHYDN | 2429
 Gg | GQHLQFFYADLSNP IRVTHLYNHS | SSEITSLYYDLQGHLIAMELSS
 : : : * * . : * * . : * . : : : * * * * . : . .

The next 79aa includes an RHS core domain. It's shown here aligned with the same region of Gallus gallus teneurin-1 and the RHS core domain of E. coli (Ec) RhsA:

```
Mb VDYIVVTTHVGTPLAVVEESSGTVVLARTYDAYGHLQSETG--TFDLPIGFAGGIADDEAT
Gg EEEYVACDNTGTPLAVFS-SRGQVIKEILYTPYGEIYQDTNP-DFQVVIGFHGGLYDSL
Ec KIHLYHCDHRGLPLALIS-KEGATEWCAEYDEWGNLLNEENPHQLQQLIRLPGQYDEES
   :      : * ***:.. . * .      * :*: .: . : : * : * * . :
```

```
Mb GLVNFFRRDYDPVVGFRCAKD 2508
Gg KLVHLGQRDYDVIAGRWTTPN
Ec GLYYNRHRYDPLQGRYITQ-
   *      :* ** : ** : :
```

The C-terminal 191aa are shown here:

```
Mb plvfgggspnlfayvfndpvnfkdpplglfciglgagfifgsgfefcadydsdrgfeasv
   cvkkyvgfgggvdiidlfgdakaskmkaygkvygslnagpaqlggelsggydftpenmpg
   rnpckggwsgeagveahvggygkwnsddgfdamytrdmndfdrdktvkdwgkfkakag
   aeagvelcagngqn 2699
```