Supplementary information

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Details of RNA preparation, nucleotide sequencing, and bioinformatics.

The whole CNS was dissected from the snails (n=15) and homogenized using a TissueLyser LT (QIAGEN) in TRI reagent (#93289, Sigma-Aldrich). RNA was isolated with Direct-zol™ RNA MiniPrep (#R2050, Zymo Research) following the instructions of manufacturer. The RNA was quantified by Qubit BR RNA Kit (#Q10211, ThermoFisher) and the quality was checked on Agilent Bioanalyzer 2100 using RNA 6000 Nano Kit (#5067-1511, Agilent).

Nanopore sequencing was used to identify evolutionary conserved sequences involved aging, aging-related memory loss, and (neurodegenerative) diseases. The library was prepared using cDNA-PCR Kit (#SQK-PCS108, Oxford Nanopore Technologies) according to the description of manufacturer. The sample was sequenced on a MinION device with R9.4.1 flowcells (#FLO-MIN106). Base calling was performed using Guppy v3.2.2 software. Previous findings on relevant sequences of *A. californica* (Moroz et al. 2006; Moroz and Kohn 2010) were used as search queries. Adapters were trimmed with Porechop v0.2.4 (Wick, 2018), moreover sequences with internal adapters, which were indicating chimera reads, were also splitted with Porechop. Reads were assembled with CLC Genomimcs Workbench v12.0.3 software *de novo* pipeline (QIAGEN). Consensus sequence was called and manually corrected also within CLC Genomics Workbench.

Figure S1. Identified nucleotide and deduced protein sequences of *L. stagnalis* homologs of human genes relevant to aging, aging-related memory loss, and neurodegenerative diseases

>Lymnaea stagnalis_klotho_mRNA

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>Lymnaea stagnalis_fragile X mental retardation protein_protein

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IVNGAE

>Lymnaea stagnalis_Parkinson disease protein 7/Protein deglycase DJ-1 (PARK7/DJ-1)_mRNA

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>Lymnaea stagnalis_Parkinson disease protein 7/Protein deglycase DJ-1 (PARK7/DJ-1)_protein

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>Lymnaea stagnalis_ alpha-secretase (ADAM10)_mRNA

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>Lymnaea stagnalis_ alpha-secretase (ADAM10)_protein

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>Lymnaea stagnalis_ apolipoprotein E (apoE) receptor_mRNA

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>Lymnaea stagnalis_ apolipoprotein E (apoE) receptor_protein

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780 QVVHPLRQTAVLDKYNMSPCDYQQCTHLCLLRPGENGVGVQAVCACPESHYLANDSRSCISNCTSSQILCSSTSKCIP
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786 IAKECTRPSFLCDSLTKCVHQNQMCDDVTDCVDGSDEDKAFCDSLKSVNCSVRNGGCEHHCNTTSNGAKCSCKKNYIL
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796 GPTCAAHTEGSKEQSTADTNPLMIAVPIAIALIVIAVIVILIFVMKRRNRRSSQYGHKRMDERGGNMNVTNPVYMRRD
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798

799

>Lymnaea stagnalis_choline acetyltransferase (ChAT)_mRNA

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>Lymnaea stagnalis_choline acetyltransferase (ChAT)_protein

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>Lymnaea stagnalis_ amyloid precursor protein (APP)_mRNA

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Lymnaea stagnalis_ amyloid precursor protein (APP)_protein

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>Lymnaea stagnalis_presenilin 1 (PSEN1)_mRNA

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>Lymnaea stagnalis_presenilin 1 (PSEN1)_protein

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997 **>Lymnaea stagnalis_notch receptor 3_mRNA**

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>Lymnaea stagnalis_notch receptor 3_protein

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DECASSPCINNGTCTDYVDSYTCSCKQGFSGVHCQVNDNDCSRSSCLNNGRCIDQVNGFTCECAKGYTGSNCQYNINP
CDSNPCLNGGSCYNKPGNSYMCYCPYGLTGSRCESFVDWCSLSPNPCQNKATCEQIANDFRCTCASSWSGKLCDVQMV
SCSLAAQNKGVDLNSLCQNGGTCSNVDSGRSHICSCRKGFEGSYCEIDVNECLSAPCQNGATCNDLIGKYSCQCARGF
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VMLVFGVIVMLKRKRVYGLTWYPENSKKSSAEGAKSGLNRKGPDGEEMQDKMDKMDANDNHTSPPPSIEHWQEDDDDD
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AEDSTGRTPLHTAVAADAQGVFQILLRNRSTNLNARMHCGTTPLILACRLAIEETVEELISADADIEATDNNGRTALH
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LLDTYKVASASTVHLGGGVTSPNHHSNMGYMHQTKQSKAKSRKKSTTVKDPGAISPPGGAVPATVTNGKVSKPRKKKG
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>Lymnaea stagnalis_potassium voltage-gated channel subfamily KQT member 2 isoform-e (KCNQ2)_mRNA

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>Lymnaea stagnalis_potassium voltage-gated channel subfamily KQT member 2 isoform-e (KCNQ2)_protein

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GSVIYLHRQELITTLYIGFLGLIFSSYFVYLAEREDGRKDFSSYADALWWGVITVMTIGYGDKVPQTWMGKIVASCFA
VFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAATLIQCLWRCHAAEPHSNSEATWRIHIHDPSSEETVFARM
ARRASLSLRKRRMSRLDSTSTVPNHLYRESMSSSMSYADDRLGRTQTSCLF

>Lymnaea stagnalis_aldehyde dehydrogenase family 3 member A2 isoform 2 (ALDH3A2)_mRNA

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CACAGTCGCTTTGTATTATAATAATAATATTAATAAAGCTGTTTCTTCAAAATAATTTTTTTTTT

>Lymnaea stagnalis_aldehyde dehydrogenase family 3 member A2 isoform 2 (ALDH3A2)_protein

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YLDNDCVRVINGGVKETTALLQVRFDHIFYTGNSVVGKIVMEAAAKYLTPVILELGGKSPVYVDKGTDLEIVARRLSW
GKFCNAGQTCIAPDYVMCPKDIQEGLVEKVKSAIEEFYTKDPKSSDSYGRIINERHFQRLQRLKKGATAAYEGEDDEK
ERYIAPTVIPNVKLSDPIMQDEIFGPLMPIVPVTDHKEAIEIINGREKPLSLYVFTNNKSIGQEFRDRTSSGALLIND
TVVHAGLTTLPFGGVGNSGIGSYHGKHSFNAFSHDKPVMEKSLALDQVNSMRYPPYTEKKLGWVKWLMAKKVKRQGFF
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>Lymnaea stagnalis_copper-transporting ATPase 2 isoform-a (ATP7B)_mRNA

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1292 AC

1293

1294

1295

>Lymnaea stagnalis_copper-transporting ATPase 2 isoform a (ATP7B)_protein

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>Lymnaea stagnalis_ubiquitin-protein ligase E3A (UBE3A)_mRNA

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>Lymnaea stagnalis_ubiquitin-protein ligase E3A (UBE3A)_protein

MSSIQNTGSLDGQESASDLTVEHSLSGKVPKVSESTENMSKRGAAQQVIFQYFNQLTEGCGNESCTNENCASSRTFRF
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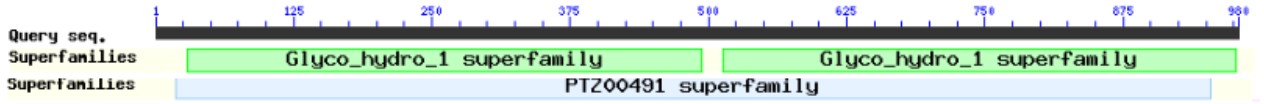
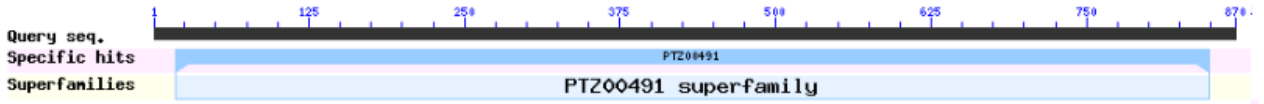
GPDSDRLPTSHTCFNVLLLPEYPTVEKLQDRLLKAINYSKGFGML

Figure S2. Identified conserved domains (specific hits) within the *L. stagnalis* homolog protein sequences (query sequence) for *in silico* validation. Conserved domain search was performed with NCBI CDD/SPARCLE (Lu et al. 2020; Marchler-Bauer et al. 2017).

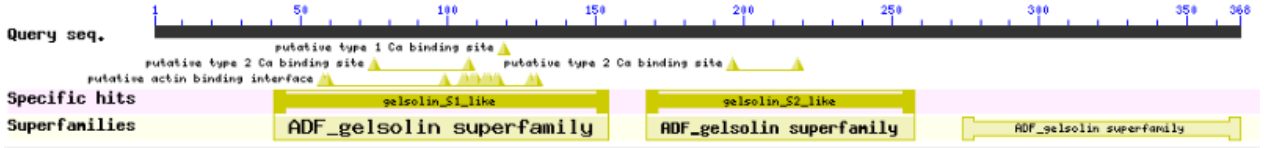
>*L. stagnalis*_klotho



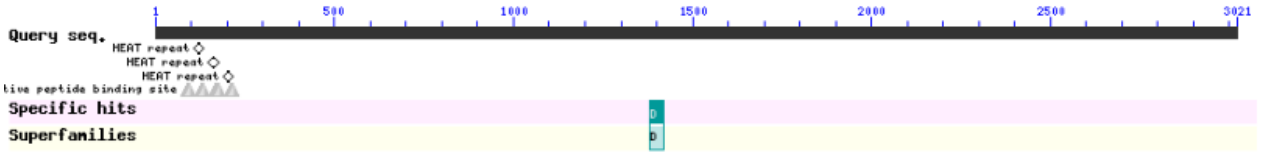
>*L. stagnalis*_ major vault 1



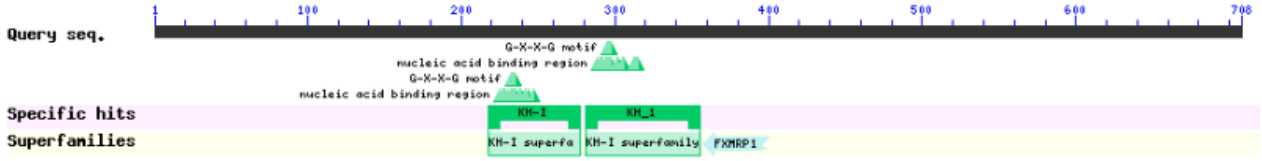
>*L. stagnalis*_ gelsolin



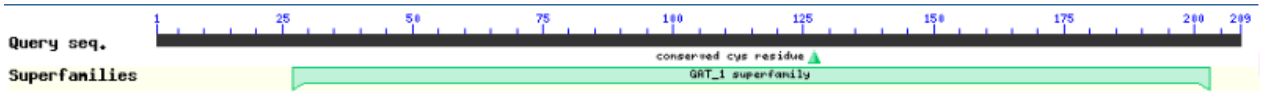
>*L. stagnalis*_ huntingtin



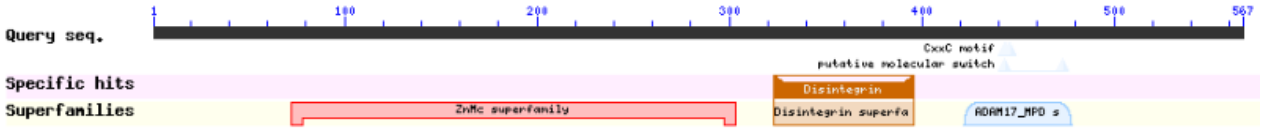
>*L. stagnalis*_ **fragile X mental retardation protein**



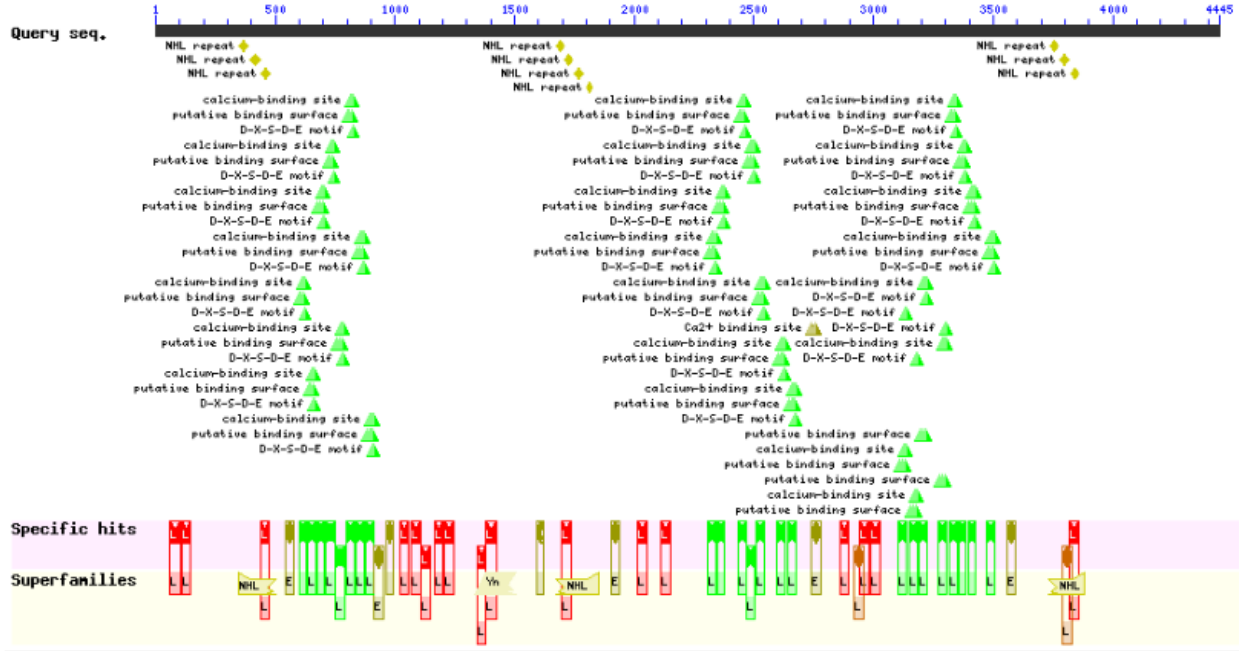
>*L. stagnalis*_ **Parkinson disease protein 7/Protein deglycase DJ-1 (PARK7/DJ-1)**



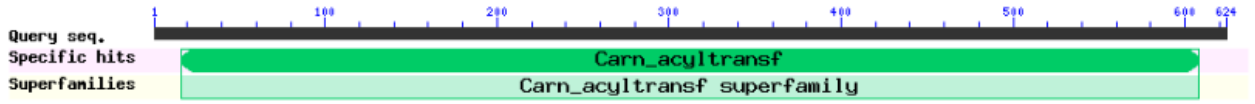
>*L. stagnalis*_ **alpha-secretase (ADAM10)**



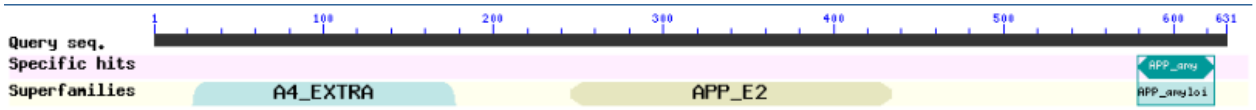
>*L. stagnalis*_ **apolipoprotein E (apoE) receptor**



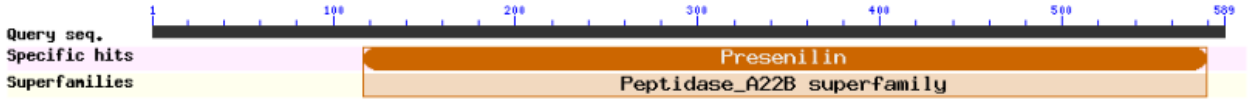
>*L. stagnalis*_ **choline acetyltransferase (ChAT)**



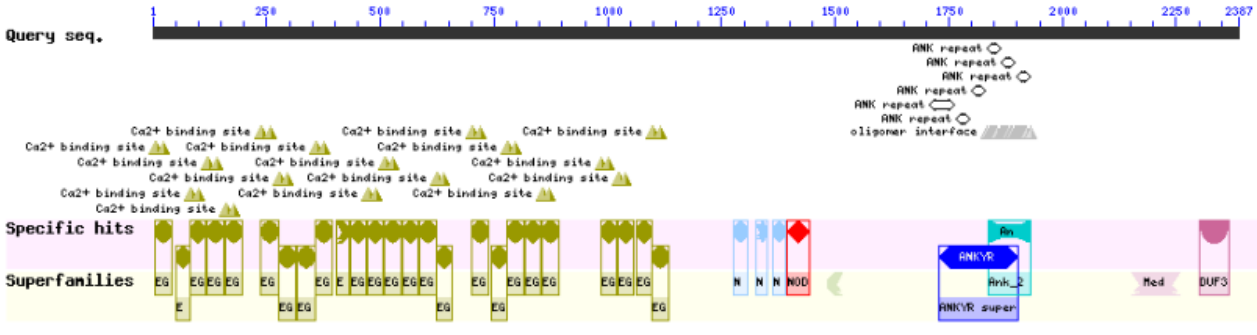
>*L. stagnalis*_ **amyloid precursor protein (APP)**



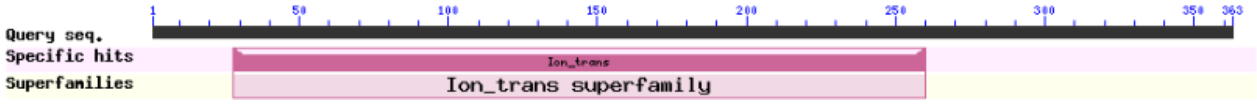
>*L. stagnalis*_ **presenilin 1 (PSEN1)**



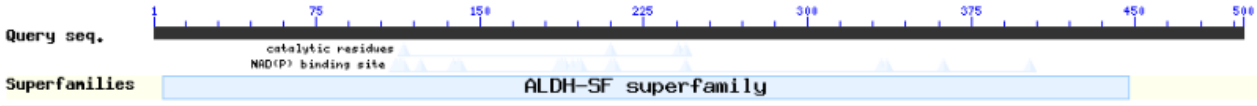
>*L. stagnalis*_ notch receptor 3



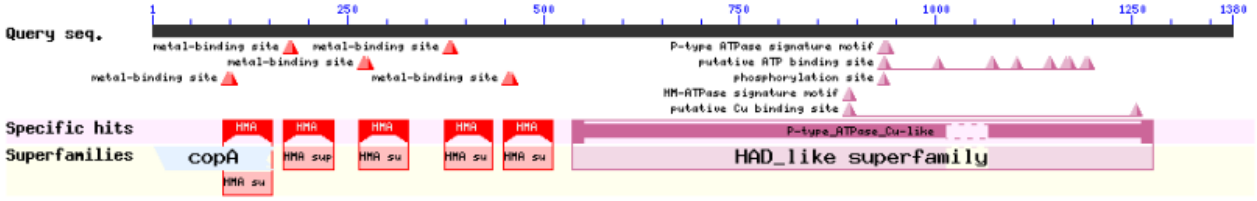
>*L. stagnalis*_potassium voltage-gated channel subfamily KQT member 2 isoform-e (KCNQ2)



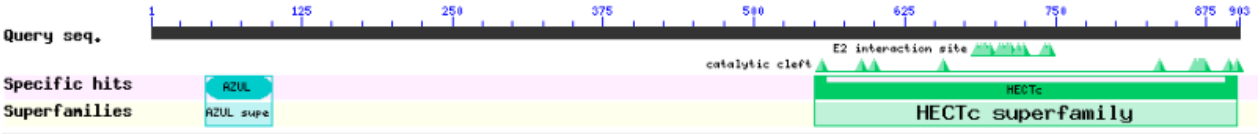
>*L. stagnalis*_ aldehyde dehydrogenase family 3 member A2 isoform 2 (ALDH3A2)



>*L. stagnalis*_ copper-transporting ATPase 2 isoform a (ATP7B)



>*L. stagnalis*_ ubiquitin-protein ligase E3A (UBE3A)



Lu, S., Wang, J., Chitsaz, F., Derbyshire, M. K., Geer, R. C., Gonzales, N. R., et al. (2020). CDD/SPARCLE: the conserved domain database in 2020. *Nucleic Acids Res, 48*(D1), D265-D268, doi:10.1093/nar/gkz991.

Marchler-Bauer, A., Bo, Y., Han, L., He, J., Lanczycki, C. J., Lu, S., et al. (2017). CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. *Nucleic Acids Res, 45*(D1), D200-D203, doi:10.1093/nar/gkw1129.

Figure S3. Sequence comparisons between some chosen sequences from *L. stagnalis* and *A. californica*.

```
# Fragile X mental retardation protein
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 730
# Identity:     550/730 (75.3%)
# Similarity:   609/730 (83.4%)
# Gaps:          40/730 ( 5.5%)
# Score: 2795.5
#
#
#=======================================

Lymnaea            1 MEDLSVEVGGSN--GVYYKAYLKSFYEDEVLVSFENNWQADKRVKLTNVR     48
                     |||||||:.|::  |.:||.|:|.|:|||.||||||||..|:.||.:.:|
Aplysia            1 MEDLSVEISGNDGYGTFYKGYIKCFFEDEALVSFENNWLPDRTVKFSLIR     50

Lymnaea           49 LPPKSGATKPEFREDERVEVF--GKVKDEEGLAWYPAKIKMLKGEFAVVA     96
                     |||..|..||||||||:|||:  ||.||:||.|||||:||||||||||.
Aplysia           51 LPPTPGQAKPEFREDEKVEVYTKGKDKDDEGPAWYPARIKMLKGEFAVVD    100

Lymnaea           97 SPWDANDILPLDKIRSVNHNPPITKESFFQFVLEVPPDLREGCQEELAIQ    146
                     .|||.||||||||||.||.||||||:||.||:|||||||||||||||:|||
Aplysia          101 FPWDQNDILPLDKIRMVNLNPPITKDSFCQFLLEVPPDLREGCQEEVAIQ    150

Lymnaea          147 EFRKHIGGAMVSYNPEDKSLHVLSTSPSVIKRASMIGDMFLRNMRQKVLL    196
                     |||||||||:|:|.|||:|:||:::..:|:||||||||||||||||||||
Aplysia          151 EFRKHIGGAVVTYCPEDRSIHVVTSDQTVVKRASMIGDMFLRNMRQKVLL    200

Lymnaea          197 KQRTEEAAKKLQSTKIRSGYMEEFQVRDELMGLAIGTHGANIQQARKVDG    246
                     |||||||||||||||:||||||||||||||||||||||||||||||||:|
Aplysia          201 KQRTEEAAKKLQSTKVRSGYMEEFQVRDELMGLAIGTHGANIQQARKVEG    250

Lymnaea          247 ITGIELDEGSCTFKVYGETQEAVKSARGLLEFSEETFQVPRDLVAKVIGK    296
                     ||||||||.||||||||||.|||:||||||||||||||||||||||||||
Aplysia          251 ITGIELDEASCTFKVYGETLEAVRSARGLLEFSEETFQVPRDLVAKVIGK    300

Lymnaea          297 NGRNIQDIVDKSGVVRVKIEGDNEHETEREE--FFASFQGQVPFIFVGTM    344
                     |||||||||||||||||||||||||||||||  ||...:|||||||||||
Aplysia          301 NGRNIQDIVDKSGVVRVKIEGDNEHETEREEASFFCPMKGQVPFIFVGTM    350
```

```
Lymnaea          345 ESISNAKLLLEYHLDHLKEVEQLRQAKLEIDQQLKSLSGPQPGSYFPPPR    394
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Aplysia          351 ESISNAKLLLEYHLDHLKEVEQLRQAKLEIDQQLKSLSGPQPGSYFPPPR    400

Lymnaea          395 DRRWGYPEQFDDRRGRGSRGGRGTGRGRRWNTDRHGDDPSMPAAMVGDWS    444
                     :|||||.:.::||||||.|||||.|||||:..||||||||||.:||.|||
Aplysia          401 ERRWGYQDSYEDRRGRGGRGGRGAGRGRRFGMDRHGDDPSMPTSMVADWS    450

Lymnaea          445 AEVDEEKRQAGYLTDSILSGRGRAGGAYRRGSRGGGMRGGRGGLPPRG--    492
                     ||.:||||.|||||||||:|||..|| ||||:|||||||...||||||
Aplysia          451 AEGEEEKRDAGYLTDSILTGRGGRGG-YRRGARGGGMRGRGDGLPPRGPV    499

Lymnaea          493 -AGYDDDESRDPRSRRRMTDDDDTVLDNASVTSQDQDYDQQDRQRRPRRK    541
                      .||::|::||.|||||:|||||||||||||||||||..|||| ||:
Aplysia          500 MGGYEEDDNRDSRSRRRLTDDDDTVLDNASVTSQDQDYDQHARQRR-RRR    548

Lymnaea          542 KNRPRGNGGQASGTETDTSVSNFRGDRSRGRGGRGGGYNQRGHESDSGRG    591
                     ||||||:.|..||||||||:||:|.:  ||.||||||...|      |.|
Aplysia          549 KNRPRGSYGTHSGTETDTSISNYRSE--RGSGGRGGGRQGR------GAG    590

Lymnaea          592 GYRG-NESDSGHPPSVSASGVGRSSVSPGMQTVNGGGGDRPTKQEPPPKD    640
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Aplysia          591 AYSGPRDADSAPVPSGSVSTAGRSSVSPGVQTVNGGSGDRSLKQDGGPKE    640

Lymnaea          641 QRDGRPPRDTRPRGSNNNSSVPPS------------GSTQPPKQMVGNHH    678
                     ||:||||||.||||||||||...|            |:.||     |:||
Aplysia          641 QREGRPPRDPRPRGSNNNSSATASATSGAGGNSSQLGTKQP-----GSHH    685

Lymnaea          679 SGSDSDSKLAKSKMNNNSAKAKEHIVNGAE    708
                     |||||.|||||:|:||  :|.|||||||.
Aplysia          686 SGSDSGSKLAKNKLNN--SKTKEHIVNGE-    712


#---------------------------------------
#---------------------------------------
```

#**Gelsolin**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 369
# Identity:     233/369 (63.1%)
# Similarity:   288/369 (78.0%)
# Gaps:           3/369 ( 0.8%)
# Score: 1256.0
#
#
#=======================================

Lymnaea            1 MAGRGLVKAKKYDWKDSNLALFGSDLEKNVKKASAATEVAWKGAGTQPGV     50
                       ..||||||||||||||||||||:||||||.||..|.|||.||:|.|:
Aplysia            1 --MSGLVKAKKYDWKDSNLALFGSDVEKNVKKESAEQEPAWKNAGSQVGI     48

Lymnaea           51 QVWRIVQFKVTPWPKEDYGKFFSGDSYIVLNTYKEEGNDQLLYDVHFWIG    100
                     |:||||:|||.||||||||||.||||||:||||||:..||||||||||||
Aplysia           49 QIWRIVKFKVQPWPKEDYGKFFEGDSYIILNTYKEQDTDQLLYDVHFWIG     98
```

```
Lymnaea          101 KESTQDEYGTAAYKTVELDTFLNDVPVQHREVQDHESDLFKSYFKTITIM    150
                     :.||||||||||||||||||.|:||||||||||.|||:|||||||:||||
Aplysia           99 RHSTQDEYGTAAYKTVELDTLLDDVPVQHREVQGHESELFKSYFKSITIM    148

Lymnaea          151 KGGAQTGFRHVEEEKYKPRLFHFSGQRKNVVVSEVPLCKDRIKSDDVFIL    200
                     ||||:||||||:.|:||.||...:|.:::|.|:||||.|:|:.:.|||:|
Aplysia          149 KGGAETGFRHVKPEEYKQRLLQITGNKQSVTVTEVPLNKNRVTAKDVFVL    198

Lymnaea          201 DLGKKIYQWNGRGSNKDERFKAGQFCQQLESERSGRAKADVLEEDTTDRS    250
                     |.|.:|:||||....|:|::||.|..||:.|||.|:...:|.::::.|.|
Aplysia          199 DNGLEIFQWNGEECAKEEKYKAVQVVQQIRSERGGKPSVEVFDQNSDDGS    248

Lymnaea          251 HLFYQSLTEDDSDDDSEFDAKDLQ-KELFRLSDSSGNMTFKVEKKGTVSK    299
                     ..|......:|.|||||::..|.: .||:|||||||...|:..|:|.|.|
Aplysia          249 TFFDHFNDNEDDDDDSEYEDNDNKTPELYRLSDSSGEFEFERTKEGRVFK    298

Lymnaea          300 SDFDTKDVFILDAKKSLFVWIGQGTTAGEKKLALQYAHEYLQKTDHPLIP    349
                     .||.:||||||.|.||.:|||||:..:..|.:.||.|||:|||.|.|||:|
Aplysia          299 DDFSSKDVFIFDNKKEVFVWIGKSASKSENQNALSYAHKYLQGTQHPLLP    348

Lymnaea          350 VTCLKEGQESRDFAAAIAA    368
                     :||:|||:|::.|.:||||
Aplysia          349 ITCVKEGKENKFFRSAIAA    367


#---------------------------------------
#---------------------------------------
```

#**Choline acetyltransferase**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 732
# Identity:     446/732 (60.9%)
# Similarity:   508/732 (69.4%)
# Gaps:         108/732 (14.8%)
# Score: 2348.0
#
#
#=======================================

Lymnaea            1 --------------------------------------------------      0

Aplysia            1 MDHRNGDETSCSSSTHSNNNSRSSSNTASNNSIISDAGGITKQTPFNQNS     50

Lymnaea            1 -------------------------------------------------M      1
                                                                     .
Aplysia           51 SSGQHPDQQEQDQQQQQQKRQSLNGGISNGGSGGLSSPANQKATVNGSNK    100

Lymnaea            2 GKTTECPFSPRKF----PLPKLPVPDLQGTMEKYLSLIKTVVSPQEYSRT     47
                     |.||....|...:    ||||||||:||.||||||||:|||:||.|:|||
Aplysia          101 GTTTRTNGSQVYYDLSQPLPKLPVPELQSTMEKYLSLVKTVMSPHEFSRT    150

Lymnaea           48 KYTVDEFCKPGGVGHELQEYLLKRQQCMDNWANEWWLNDMYLNVRIPVLI     97
                     ||.||||||....||||||:||||||.||||||:.|::|||||:::|:.|
Aplysia          151 KYIVDEFCKTQAQGHELQEHLLKRQQGMDNWANDLWIHDMYLNIQVPLTI    200
```

```
Lymnaea           98 NPNPAAVFPYQGFPSHREQIRFAAKFIRGMLDFKHLTDTRTLPIERCKYK    147
                     |.|.||:||||.|||.|||:||.|||.||:||||.||||||||||||:||
Aplysia          201 NSNAAAMFPYQAFPSQREQLRFTAKFARGLLDFKRLTDTRTLPIERCRYK    250

Lymnaea          148 EKGQPLCMDQHYRLFTSYREPGRERDVQRTDLGFMGREYIVVACNNQFYK    197
                     |||||:||:||||||||||||||||||.|:|.|..||::|:|||.|||||
Aplysia          251 EKGQPMCMEQHYRLFTSYREPGRERDVMRSDTGTPGRDFIIVACRNQFYK    300

Lymnaea          198 VDVQREGDELTEADICLQLSRVLNMAEQESNQSEPVGLLTSQKRTLWAEQ    247
                     |||.:||.||:||||.|||:||:..|:|..::..|||:||||.|.:|||.
Aplysia          301 VDVIQEGQELSEADIFLQLNRVMTSAQQSVDKPAPVGILTSQARNIWAEH    350

Lymnaea          248 RERLQLDATNRANLHILENCLFLLCLDKPTVPSRCGIQGGMLNDMTARTH    297
                     ||||..||||||||..|||||||:|||..|:||.....|||..||.||||
Aplysia          351 RERLLQDATNRANLFALENCLFLVCLDLTTLPSGRDGDGGMAGDMAARTH    400

Lymnaea          298 HIIHGQGVHNNSANRWMDKTIQVIVSEDGTCGINMEHSVAEGIALGHMIE    347
                     .|:||||||..|:||||||||:|.||:||||||:||||||.||||||...:|
Aplysia          401 QILHGQGVERNTANRWMDKTVQFIVAEDGTCGVNMEHSVVEGIALCSAVE    450

Lymnaea          348 HAFGVMGKEKIQDGPRDPNSLPHPKCLQWSLSAHSLADIEQAKESVDNMV    397
                     |||.||||:...|...||.||..||||||:|:..||.|||.|||:|..:|
Aplysia          451 HAFSVMGKDNFSDKICDPASLALPKCLQWNLTTQSLRDIEVAKENVARLV    500

Lymnaea          398 NDFDLTVFRFEGYGREFIKTQGMSPDAYIQLALQLTYYKIHGTLTSTYES    447
                     :||||.||||..|||||||.|||||||||||||||||||||..||||||
Aplysia          501 DDFDLAVFRFPRYGREFIKAQGMSPDAYIQLALQLTYYKIHGCSTSTYES    550

Lymnaea          448 ASVRRYRQGRVDVIRANSPPALTWIKAMLGQTEATEEDKLRLFTEAVHWQ    497
                     |||||||.||||.||||||.||.||||||||||||:|||.||.||||.||
Aplysia          551 ASVRRYRHGRVDNIRANSPAALAWIKAMLGQTEATDEDKRRLLTEAVQWQ    600

Lymnaea          498 QDYMLDTILGYGIDLHLLGLREAAKEMGIPTPEFFNDPSYKELNTFRLST    547
                     ||.||:||||.|.|||:|||||||.|:|:|||:.|.|.|||..|.|:|||
Aplysia          601 QDNMLETILGNGTDLHILGLREAAAELGLPTPDLFQDASYKAFNCFKLST    650

Lymnaea          548 SQVPTVSDYWMGYGAVVPDGYGCCYNPK-PDSIIFSVATFNTCQDTSSEM    596
                     ||||..||:||||||||||||||||||: ||||:||||:|.:|.||||||
Aplysia          651 SQVPMTSDFWMGYGAVVPDGYGCCYNPQAPDSIVFSVASFLSCYDTSSEM    700

Lymnaea          597 FAHSLESSLLQMAELCTYDP----ETATIKQR    624
                     |..||||||||||||:||.:.    :....|:|
Aplysia          701 FTQSLESSLLQMAEICTVESDVKVQNPNSKER    732


#---------------------------------------
#---------------------------------------
```

#**Amyloid precursor protein**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 683
# Identity:     423/683 (61.9%)
# Similarity:   516/683 (75.5%)
# Gaps:          67/683 ( 9.8%)
# Score: 2232.0
```

```
#
#
#=======================================

Lymnaea            1 -------------------------MRHLFQVG-----ALF-ALIQVLFS     19
                                          :.:..::|     |:| .|:|||::
Aplysia            1 MNATLRPLTEYGKFEAEDLKYLLLGLDYTAEMGLVTNCAIFLGLLQVLYA     50

Lymnaea           20 ASLEDKYEPMVAFICERPAMHRGVNGWIADKSTDCLDRMEDILAYCKAMY     69
                     ||:||||||||||||||||||||||||||||||||||:||||||:||:.||
Aplysia           51 ASVEDKYEPMVAFICERPAMHRGVNGWIADKSTDCLNRMEDILSYCQRMY    100

Lymnaea           70 PDHNITNVVESSYLVTISDWPMGNAERQHPHRVRPFRCLVGGFQSDALLV    119
                     ||||||||||:||||||.||||.:|:|.||||||||||||||||||||||
Aplysia          101 PDHNITNVVEASYLVTIKDWPMTSADRMHPHRVRPFRCLVGGFQSDALLV    150

Lymnaea          120 PQHCEFDHRHDQTQCEGFAHWNVIADDACDKKGMHLESFGMLLNCNLGKF    169
                     ||||.|||||||..|:||:||||:||::|..|.||||||||||||.||.|
Aplysia          151 PQHCVFDHRHDQRVCQGFSHWNVVADESCRSKDMHLESFGMLLNCKLGMF    200

Lymnaea          170 SGVEYVCCPVETETKYHQPQTDDKPDSWVNTHDDMDKEEKTNASKSSTD-    218
                     |||||||||.:.:..||.||||||||.|   ||...:||.....|...|
Aplysia          201 SGVEYVCCPNQNKPNYHPPQTDDKPDDW---HDSSAEEEDEEEEKEGEDS    247

Lymnaea          219 -PAAATSSSS---------SSSEEVLIFVCSLLQEAD--ENTVDLYEAYL    256
                      |.|..|:||         |:|:..:     .:.|.|  |:.:|.|||||
Aplysia          248 NPTAPQSTSSEESSDSGATSNSDSAV-----TINEDDLEEDVMDFYEAYL    292

Lymnaea          257 RGQEFPQKYNNEHKKFVAARDRMKKNQQHKVTKLLQEWQAARDHVNEVRK    306
                     ||||||.|||||||||:||:||||||||||.|||||:||.|||||:||||
Aplysia          293 RGQEFPSKYNNEHKKFLAAKDRMKKNQQHKTTKLLQQWQVARDHVDEVRK    342

Lymnaea          307 SDPKTADTMAKEITARFQNLYAAYEQEDDSEKEQLTSLHQQHVQAALNER    356
                     .|.|.||:::.||.:|||.|||:|||||.:||:||.:||||||||||||
Aplysia          343 VDTKKADSLSGEIASRFQKLYASYEQEDAAEKQQLMALHQQHVQAALNER    392

Lymnaea          357 KRDAMDKYMRALEKGDADKIIKYLRAYIKAEEKDRMHTVNHFEHVKYSSP    406
                     ||||||.||:||||||.:||||.||:|.:...|||||||||||||||:.
Aplysia          393 KRDAMDNYMKALEKGDVEKIIKDLRSYSRRRRKDRMHTVNHFEHVKYSNA    442

Lymnaea          407 SQAKALQPHIKDHLSLTEKRIEQALQLLSRYPDIEAKNKPEIYEFLKRFE    456
                     .:|..:.|.|.:||.|:|:|||:|||::||||||||.:.:||:.||:|||:
Aplysia          443 REALRIHPFIINHLRLSEQRIDQALEMLSRYPDIEVQVRPEVEEFMKRFD    492

Lymnaea          457 SIANSIRDVV--LPEIVEESESEESEEVTEVPQNI---VNNNDEINLDDN    501
                     :|||||::||  ||::.||.:::.:.:  |.||:.   |:.:|:|.:||.
Aplysia          493 AIANSIKNVVLPLPKVEEEPQTKSASQ--EAPQDASDSVSPDDDIRIDDA    540

Lymnaea          502 NDFDVSKQEIDTQGDDVVENEHDYEKKNAFVANRMEDTHHIQQGFVESAA    551
                     .|||:|.:::|.:||||.|:|||||:.:.|:|:||:|..|::|||.||||
Aplysia          541 GDFDLSSEQVDEEGDDVSEDEHDYERGSQFIAHRMDDKMHVRQGFAESAA    590

Lymnaea          552 TSSQVGSTIGIALGSVSVFVIIVVAIIMLKRNKTRQSVTHGYVEVDPSAS    601
                     ||||:|||||||||.||||||||||:.|:||....|..:.||||||||||
Aplysia          591 TSSQMGSTIGIALGGVSVFVIIVVAVFMVKRKNRNQYPSPGYVEVDPSAS    640

Lymnaea          602 PEERHLANMQMNGYENPTYKYFEVQNNPKA---    631
                     |||||:||||||||||||||||     |.
Aplysia          641 PEERHVANMQMNGYENPTYKYFE-----KGEFV    668


#---------------------------------------
#---------------------------------------
```

#**Presenilin**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 626
# Identity:     372/626 (59.4%)
# Similarity:   436/626 (69.6%)
# Gaps:          82/626 (13.1%)
# Score: 1782.0
#
#
#
#=======================================

Lymnaea            1 --MSSHSKTSGAVFATDDSPTERTSLMSSFV-NEAARDGGSTSVFGPVPS     47
                       ...:|.||..|   |.||||||.|||:.. .|.|.:.|:   |.||
Aplysia            1 MNPQRNSTTSVGV---DSSPTERTGLMSNLTGGEWAGESGN---FSPV--     42

Lymnaea           48 SPNTNRITTIEDGSATPAIPETSVIIPNANNTGQVSGAPRDSHRRRRRNP     97
                         .|.:..:|.:.|  :|||||:.|:.|:|  .:..|:....||....
Aplysia           43 ----RRYSAADDEATT--VPETSVVTPSTNST--TNQQPQSQRTRRGEGS     84

Lymnaea           98 SQRS--------------------------------AHQQQEEEEDEETLL    116
                     ..||                                :.||:||::.|||||
Aplysia           85 QNRSDGDGAAATRGGGAQPAAAARQEAGRGSGGAVSGQQEEEDDGEETLL    134

Lymnaea          117 YGAKHVIMLFVPVTLCMAVVVATISTVNYYTDTGTYLIYTPFHDKTDNTG    166
                     |||||||||||||||||.|||||||::.|||..|||.:||||||||::||
Aplysia          135 YGAKHVIMLFVPVTLCMVVVVATISSITYYTTKGTYFLYTPFHDKTEDTG    184

Lymnaea          167 TKIWQSLANSLIMLGGIVVMTIVLLLLYKYKCYKIIHGWLVLSSVMLLFF    216
                     ||:|||:||:||:||.|:||||||||||||:|||||:||||:||||||||
Aplysia          185 TKLWQSMANALILLGAIIVMTIVLLLLYKYECYKIINGWLVMSSVMLLFF    234

Lymnaea          217 FSYIYMEQILRSYNTPIDYITVAIIMWNFGVGGMFCIHWKGPLLLQQAYL    266
                     |||||:|||||:||.|:||||||||||||||||:||||||||||||||||
Aplysia          235 FSYIYLEQILRAYNVPMDYITVAIIMWNFGVGGLFCIHWKGPLLLQQAYL    284

Lymnaea          267 IMVSSLVALMFIKYLPDWTAWTVLGVMVVWDLVAVLCPKGPLRMLVETAQ    316
                     |.:|:||||||||:|||||.|.||||||||||||||||||||||||||||
Aplysia          285 ISISALVALMFIKFLPDWTTWAVLGVMVVWDLVAVLCPKGPLRMLVETAQ    334

Lymnaea          317 TRNEPIFPALIYSSTMVWLITMADDESSSKKGKRGTSQGTGVSGTSGGAR    366
                     .||||||||||||||||||.|||||.:.:.||.::...|.|..:..|  |.
Aplysia          335 NRNEPIFPALIYSSTMVWTITMADGDPNKKKNQKKKKQETTTAEES--AN    382

Lymnaea          367 GASEIHESD-DEGGFREHLSNGTNRANELTASSDSQTARRAVQALGEMSH    415
                     ||.....:| |:|||:||:.||.:|:..|::.|:|.:||.||.|||:||.
Aplysia          383 GAQASGGADEDDGGFQEHIQNGGSRSRGLSSGSESNSARTAVAALGDMSQ    432

Lymnaea          416 G-NPNPHRHIAGSSSDPVQNPTETSAVVPKKKKTPKPR-QRAAAPQENSA    463
                     . :|...|    :..|.|....||:.||  .:..|:|| ||||..|:|..
Aplysia          433 ADSPRQQR----AKVDTVAVDAETTVVV--NRNPPRPRAQRAATDQQNRQ    476

Lymnaea          464 EEDEENNIVRFQKFERKHICNYYLFPKLLTHHFILFAGGVKLGLGDFIFY    513
                     ..:.|.::...:..|.:                     ||||||||||||
Aplysia          477 RNESETDVASSEADEDR--------------------GVKLGLGDFIFY    505
```

```
Lymnaea          514 GVLVGKASSKGDWNTTLACFVAILIGLCCTLLLLAIFRKALPALPISLTF    563
                     |||||||||.||||||||||||||||||.||||||||||||||||||||
Aplysia          506 GVLVGKASSNGDWNTTLACFVAILIGLCFTLLLLAIFRKALPALPISLTF    555

Lymnaea          564 GLVFNFATSALVRPFMDSLASEQVYI    589
                     |||||||||||||||||||||||||||
Aplysia          556 GLVFNFATSALVRPFMDSLASEQVYI    581


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#---------------------------------------
```

#**Huntingtin**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 3045
# Identity:    2384/3045 (78.3%)
# Similarity:  2698/3045 (88.6%)
# Gaps:          45/3045 ( 1.5%)
# Score: 12328.5
#
#
#=======================================

Lymnaea            1 MATIEKLIKAFEGLKVFQPNAQTVEDPKKKDQNLPTKKDKMLHCNIVADC     50
                     |||||||||||||||:|||||||..:|.||||||:||||||:||||:||||
Aplysia            1 MATIEKLIKAFEGLRVFQPNAQAADDSKKKDQNVPTKKDKILHCNVVADC     50

Lymnaea           51 MCSPNMRTIADFPKFLGIAMESFLTLCDDPEADVRMVADECLNRTIKVLL    100
                     ||:||||.:||||||||||||:||.||||||||||||||||||||||||
Aplysia           51 MCAPNMRGVADFPKFLGIAMEAFLALCDDPEADVRMVADECLNRTIKVLL    100

Lymnaea          101 ETNLGRLQVELYKELKKNGPSRSLRAALWRFADMCHLIRPQKCRPYIVNL    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Aplysia          101 ETNLGRLQVELYKELKKNGPSRSLRAALWRFADMCHLIRPQKCRPYIVNL    150

Lymnaea          151 LPCVARICRREEEAVQDTLSMAMPKICSALMPFANDTEVKALLKSFLPNL    200
                     |||||||||||||||||:|||.||||||||||||||||||||||||||.|
Aplysia          151 LPCVARICRREEEAVQETLSSAMPKICSALMPFANDTEVKALLKSFLPTL    200

Lymnaea          201 KSNSAVCRRMSASSLALICQHSRAPLSFFNYLIGVLLEMILPVDIDHEVP    250
                     ::.||||||||||||||||||||||||||||||:.||||||||||||:|:||
Aplysia          201 RATSAVCRRMSASSLALICQHSRAPLSFFNYLVSVLLEMILPVDIEHDVP    250

Lymnaea          251 TLLGVILCLRHSIPHLVPSNNKDQGLKDSFGYRESEAEQAIGEEKMVKIL    300
                     |||||||||||||||||.|:.|||.||||||||||.||||||..::::|||
Aplysia          251 TLLGVILCLRHSIPHLAPTTNKDLGLKDSFGYREVEAEQAIHVDQIIKIL    300

Lymnaea          301 QALLHYSGHSDHNVVTAALESLQQLLRTPPPILRKMLLTRGSISRTYIFI    350
                     ||||||:||||||||||:||||||||||||||.|.::||.:||||||:||.
Aplysia          301 QALLHYTGHSDHNVVTASLESLQQLLRTPPPALLRLLLKKGSISRTFIFS    350

Lymnaea          351 HDFEEEDQARIESVVDLTSMSDDANLDED-ADLGYTNSHPSARKSNTSGL    399
                     .||.||:||||:||.||....|::.||:| .|:  :....::..|:.|..
Aplysia          351 QDFNEEEQARIDSVTDLALTVDESGLDDDPGDV--SGQSVASGGSDNSTF    398
```

```
Lymnaea          400 MSEFEAKSATSQSRLAASLTESNVGYNELVNND---AILVTDGTDYSGVE    446
                     .|::...|.|||.  ::.:..::.|..::|..|   .|:|||||||||||
Aplysia          399 ASDYGTGSFTSQQ--SSDVEAASAGLTKIVIGDEGEMIVVTDGTDYSGVE    446

Lymnaea          447 IGDLNEERSEMSATSGMSHSDSIETLQSVRSISPHLAYTPPVQLLGHDMN    496
                     ||||||||||:||.|.:|||||||||||||||:|||   ..|:||..||||
Aplysia          447 IGDLNEERSELSAASCISHSDSIETLQSVRSLSPH---PGPLQLPSHDMN    493

Lymnaea          497 GNPQIVVYPGEDAAPPLSPNPALGEPLEQINIEHESLQEDEVPLLFYLRL    546
                     ||||:.|...|::. |.||||||.|:.::||.:|.|||:|||||||||||
Aplysia          494 GNPQLPVEQEEESV-PASPNPATGDTVQQIEVEPESLKEDEVPLLFYLRL    542

Lymnaea          547 LCKRFLLTGVTDGLVTDKQVRVSLKSLALGCVSCSLALCPRLFLFKLCPT    596
                     ||||||||||.:|||:||||||||||||||||||:.|:|:||||||||:|||
Aplysia          543 LCKRFLLTGVPEGLVSDKQVRVSLKSLALGCVAHSVAICPRLFLFKVCPT    592

Lymnaea          597 ANNAGNDQNLQDTTLYASHPDHQLKGQTAVVIGSFIRAALIEGRGNFHQW    646
                     |..||:||||||.||||.|.|||||||||:|:||||||||:|||.:|.||
Aplysia          593 ATGAGSDQNLQDLTLYAGHSDHQLKGQTALVLGSFIRAALLEGRADFSQW    642

Lymnaea          647 IDSHKPPEQSVLSLEALLKIIINILEDESAVAVRAALMALQMCLSYLMDS    696
                     :..|.|.||:|||||.||:||:|||.|||||||||.|:||||||||:|:||
Aplysia          643 VMEHLPSEQNVLSLEDLLRIIVNILGDESAVAVRAGLVALQMCLSHLLDS    692

Lymnaea          697 CHGRLGFRILLDLLIVKTNPYWLVKVELLELIAGLNFKVISYLESISPDI    746
                     ||||||..||||||.:..||||||||||||||:||||||||||:|||||||
Aplysia          693 CHGRLGLSILLDLLCIHNNPYWLVKVELLELMAGLNFKVISYMESISPDI    742

Lymnaea          747 ARGDHNFLGRMCLQEHIFQEIVIQLLGDEDPRVRAAASAAILRMVPTLFF    796
                     .||:||:||:||||:|..|||::.||||||.|||.||:.|.||::|.||:
Aplysia          743 TRGEHNYLGKMCLQQHCIQEILLPLLGDEDARVRTAAANAFLRLIPKLFY    792

Lymnaea          797 GSDSPQQDPVLSVASDLTQHLLTPIMNPIMAGQLPPLVQGLMKPYAFDIL    846
                     .||||||||||:||||.|::|||||:|:|:::||||||||||:.||..|.|
Aplysia          793 ASDSPQQDPVLAVASDQTRYLLTPMMSPVLSGQLPPLVQGLVGPYKHDEL    842

Lymnaea          847 QEIDPSTESALSRVVQQLLHTLLMSQSKFVTSGCCLALCRLSEEYLVTQY    896
                     .::.|:||||||||||.|||.||:|.|:::||||||.||||||||||||||
Aplysia          843 AQVCPATESALSRVVQMLLHNLLVSNSRYITSGCCNALCRLSEEYLVTQY    892

Lymnaea          897 ASSWSCGPAKPIASKERVEKLGMRRPPSRSLSASSMDELTSASGGGPLPI    946
                     |:||.|||||||..||..|:.|:||||||||||||||||||:|||||||||
Aplysia          893 AASWGCGPAKPIVPKESEERFGIRRPPSRSLSASSMDELTAASGGGPLPI    942

Lymnaea          947 VLSLMLSSQAGLELTTHQDLLELAGNLVCGAAYKNLRPSEDTEKLSGSGD    996
                     |:||||||||||||||||||||:||||||.|||||||:.|::.:|.  |||
Aplysia          943 VMSLMLSSQAGLELTTHQDLLQLAGNLVAGAAYKNLKNSDELDKT--SGD    990

Lymnaea          997 DGHWAAVADRFLVPMIVQLFTHTARLLNACTHAIEETMPGPPQVKPSLPS   1046
                     |..|:||:||.|:|:|.||||||||||||||||||||.||||||||||||
Aplysia          991 DVSWSAVSDRLLLPIIEQLFTHTARLLNACTHAIEETNPGPPQVKPSLPS   1040

Lymnaea         1047 LPNAATLSPVRRKMKGEKETNPPGPGASPDQKSGQKTPGKDQKDSEKDRN   1096
                     ||||:||||||||||||||:.:|..|..|||.|:||||||||.||||||:
Aplysia         1041 LPNASTLSPVRRKMKGEKDASPQAPVGSPDPKTGQKTPGKDSKDSEKDK-   1089

Lymnaea         1097 RKDGIGSFYNIPQYVKLFEVLRGSYSNFKTSLDLTSSDKFCTMLRTTLTV   1146
                     :|||||:|||||||:|||:||||||||||||||||||||||:||:.|.|
Aplysia         1090 KKDGIGAFYNIPQYMKLFDVLRGSYSNFKTSLDLTSSDKFCTILRSALRV   1139
```

```
Lymnaea         1147 LSQLLEIATLYDVGKVTDEILGYLKVTMALEPTWTVLCVQQLLKALFGTN   1196
                     ||||||:|||.||||||:|:||||||||||||||||||||||||||||||
Aplysia         1140 LSQLLEVATLQDVGKVTEEMLGYLKVTMALEPTWTVLCVQQLLKALFGTN   1189

Lymnaea         1197 MASQWDSNSQSATSLTSDLGARVAGGSSPGLYYYCLNKPYAQLAHCLVGA   1246
                     :||||:.:.|||..:.::::..||..|:|||||::|||:||||||||||.|
Aplysia         1190 LASQWEPSKQSAAPILAEVSTRVTAGTSPGLYHHCLNRPYAQLAHCLVAA   1239

Lymnaea         1247 ACRATLPADEAHGSLLWLKQRVDRKLPAILKPTSKVDKAVIGSYIRLFEP   1296
                     ||||||||||||.||||||||||||||||||||:|||||:||||||||||||
Aplysia         1240 ACRATLPADEAHSSLLWLKQRVDRKLPAILKPSSKVDKSVIGSYIRLFEP   1289

Lymnaea         1297 LVIKALKQYTVTSSLDLQCQVLALLAQLIQLRVNYCLLDSDQIFIGFVIK   1346
                     ||||:||||||||||:||||||||||||||||||||||||||||||||||:|
Aplysia         1290 LVIKSLKQYTVTSSLELQCQVLALLAQLIQLRVNYCLLDSDQIFIGFVLK   1339

Lymnaea         1347 QFEYIEEGQIRNSEVLIPHIFQFLVMLSYEKFHTKSIIDMPRIIHRCDGI   1396
                     ||||||||||||||:||||||||||||||||||:||||||||||||||||
Aplysia         1340 QFEYIEEGQIRNSELLIPHIFQFLVMLSYEKFHSKSIIDMPRIIHRCDGI   1389

Lymnaea         1397 MASGLQPTTHAIPALRPVVYDLFLLRGTVKSEVGKDLETQREVVVSMLLR   1446
                     ||||||||||||||||||||:||||||||||||||||||||||||||||||
Aplysia         1390 MASGLQPTTHAIPALRPVVYELFLLRGTVKSEVGKDLETQREVVVSMLLR   1439

Lymnaea         1447 LVQYYQALDMFTLVLQQCHRESEERWKRLSRQVMDAVLPALAKQQINLES   1496
                     |||||||:|||.||||||||||||||||||||||||.||||||||.:||.|
Aplysia         1440 LVQYYQAVDMFVLVLQQCHRESEERWKRLSRQVMDVVLPALAKQTMNLCS   1489

Lymnaea         1497 QDALDVLHRLFESVSPSVFRPVDFLLKTLLAPPHDVSDVSSLQKWLCLVL   1546
                     |::||||||||||||||||||||||.||||||||||||:|.|.|||||:||||
Aplysia         1490 QESLDVLHRLFESVSPSVFRPVDTLLKTLLAPPHDISTVQSLQKWMCLVL   1539

Lymnaea         1547 IIVRVLISQSKEEVILSRLTELQLHVCLIRDLDNSGTSAANSVVELLRNL   1596
                     .||||||||||||:||||||:||||||||||||:||:.::|.:|::|:|:||
Aplysia         1540 TIVRVLISQSKEDVILSRLSELQLHVCLIRDVDNTDSAATSSMIEVLKNL   1589

Lymnaea         1597 APEETVAWFLLQVIGKCSEMLNKETSLLGSNYNGPSYSTSNGNGIIVSRC   1646
                     |||||:||:||||||||||||||:|||:|| |:..|.....|:|:|  .||.
Aplysia         1590 APEETLAWYLLQVIGKCSEMLDKETALL-SSAGGGGAGGSSGDG--ESRY   1636

Lymnaea         1647 HFLLQQTLHLMLYITHMFQSGSLFRRVATAAMGLLQLDSPACMYSVGEIN   1696
                     ||||||||||:||||||||||  |||||.||||.||||:||||:|||.:||
Aplysia         1637 HFLLQQTLHLLLYITHMFQSG-LFRRVVTAAMRLLQLESPACVYSVRQIN   1685

Lymnaea         1697 EHMVGVSSVCPALTLHWCNVLILLNFDDRGLWTRVVQSPPTYK-------   1739
                     :|||.||||||.||||||.||||||||||.||:.|||:|||||
Aplysia         1686 QHMVAVSSVCPTLTLHWCYVLILLNFDDRSLWSTVVQTPPTYKVMAHRSH   1735

Lymnaea         1740 ----ST---GTSVRHLPRSSECCGLEMLRRGGLILFCDYVCENLSDAEHM   1782
                         ||   ..::....|||:||||||||||||||||||||||||||||
Aplysia         1736 QYSQSTEDHDATLTPQQRSSQCCGLEMLRRGGLILFCDYVCENLSDAEHM   1785

Lymnaea         1783 TWLIINHVSDLILLSNESPVQDFIRQVAIHRNSAASSLFIQAIHARGDSI   1832
                     |||||||||||||||.||||||||.  |||||.||||||||||||||||||
Aplysia         1786 TWLIINHVSDLILLSQESPVQDFIG--AIHRNPAASSLFIQAIHARGDSI   1833

Lymnaea         1833 TKPSMVKRTLKCLDAIHISQSGSLVALLIDKFLGCHRLAITRMTDSIVCQ   1882
                     |||.:|||||:||:|:|.||||||||||:|.|||.|:|||.|:|||:|||.
Aplysia         1834 TKPHLVKRTLRCLEAVHSSQSGSLVALLVDTFLGSHQLAIARLTDAIVCH   1883

Lymnaea         1883 RLESLLGETAEEIAKQLPKEDIEKQLQFMKSNGLIQRHQRLASLLSKLCI   1932
                     |||:||||||.||.||||||||||.||||||.|||||||||.||||||..
Aplysia         1884 RLETLLGETAGEITKQLPKEDIEKLLQFMKSKGLIQRHQRLTSLLSKLGT   1933
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Lymnaea         1933 AAGSTAQIKLSPERSHPLSVVPVDVAKISIDKEFYLSIVKEQCFMATPNT   1982
                     |||||:|::||||||:|||....:||.::|||||||::||||||.|:||.
Aplysia         1934 AAGSTSQVRLSPERSNPLSGPVTNVANVTIDKEFYLAVVKEQCFQASPNI   1983

Lymnaea         1983 RECAFLLQRLDYPDILSITMTKEFNLSILEECMSLGAFRSVLRYNRDVDL   2032
                     ||||||||||:||||||||||.|||||:||||||||||||||||||.:.
Aplysia         1984 RECAFLLQRLEYPDILSITMTSEFNLSVLEECMSLGAFRSVLRYNRDAEA   2033

Lymnaea         2033 GSLSPQPASNEHTLDPLFQASQLTLFRHINNMVIQLPLPHQCLVFIDSAP   2082
                     |:|||..|..|..:||||.||:|||||||||:|.|||.|||||.|.|..|
Aplysia         2034 GTLSPLAAPGERIMDPLFLASELTLFRHINNVVNQLPTPHQCLSFTDCGP   2083

Lymnaea         2083 ASSLHYMDRIEELFTDAQWVDNNFCLASALVRYMVAIHQFPWRAELPPES   2132
                     |||||||||:|||||||.||..||.||:||||::||:..||||||||.:|
Aplysia         2084 ASSLHYMDRMEELFTDAAWVHANFNLAAALVRHLVALSHFPWRAELPADS   2133

Lymnaea         2133 LKDVASFVVLCAELIHWSVEHDMLPESEHIQNCLSCLSLLLQDPAVHALM   2182
                     ..|||.|.|||||||||||:.|:::|||||.||.||||||||||..:|:.:
Aplysia         2134 HHDVARFAVLCAELIHWSLRHELMPESEQIQTCLSCLSLLLQDGKLHSQL   2183

Lymnaea         2183 SQTEHATFVCSIVGFLYQLLCSMAVLPGENVACLFQDDRRDDAEEEDVSL   2232
                     .|.|:|:.||:||..|||:|.|:||||||.||.|:.|:.|::|||:||||
Aplysia         2184 GQIENASCVCAIVAALYQVLSSLAVLPGEQVANLYHDEHREEAEEDDVSL   2233

Lymnaea         2233 SACLIRACDEISELVHCLHTRLDPNTSHEPRLPQFLASTFRNIIIAVARL   2282
                     ||||:|||::||||||||||||:||:.:.|||||.||||:||||:|:|:||
Aplysia         2234 SACLVRACEQISELVHCLHTRMDPSYTKEPRLPPFLASSFRNIVISVSRL   2283

Lymnaea         2283 PAVNTYARTPPLVWRLGWSPTPVGELRTCLPPLPVEYLQEKDVLKEFVTR   2332
                     |.||||||||||||||||||||.||||||||||||||||||||:|||.|
Aplysia         2284 PVVNTYARTPPLVWRLGWSPTPGGELRTCLPPLPVEYLQEKDVLREFVAR   2333

Lymnaea         2333 ISSLGWVNRQQFEESWMSLLGVLNPVSHTGHDLSAEEEIEQAQGMVIAVK   2382
                     |:.||||||||||||||||||||||||||||||||.||||||||||:|||
Aplysia         2334 INFLGWVNRQQFEESWMSLLGVLNPVSHTGHDLSPEEEIEQAQGMVLAVK   2383

Lymnaea         2383 AITSLLLQSSMVPHAGNPSNSYYETRPRDKPLAFLHTRCGKKLSVIRGLI   2432
                     ||||||||:|:||.:||.:||.||||||||||||||||||||||||||||
Aplysia         2384 AITSLLLQASLVPTSGNTANSCYETRPRDKPLAFLHTRCGKKLSVIRGLI   2433

Lymnaea         2433 EKEIVNLCAARPDRLVPQAYSGSPSDKSSPNLFDGNLERELGVEDFSLGQ   2482
                     |:||:||||:||||||.|||.|:||||:|.:||:||||||:|.|::||||
Aplysia         2434 EQEIINLCASRPDRLVAQAYCGNPSDKASVSLFNGNLEREIGSEEYSLGQ   2483

Lymnaea         2483 ISIESTWSLVGSLDTNLSNSDTTDSLDSPTGRGDMAATSPSSASSSSG-G   2531
                     ||||||||||||:||..||.|::|||.||..|:. .|.|:||:.|.||| |
Aplysia         2484 ISIESTWSLVGNLDLPLSTSESTDSPDSTAGQA-AAETTPSATSPSSGSG   2532

Lymnaea         2532 RLS-----TARSVHHCGLDIHSCLQFLLELYGAWLHIDNNPKPPLMLLNS   2576
                     ..|     ::|||..||||||||||||||||||||:||:||||||||||
Aplysia         2533 SASSPEGVSSRSVSRCGLDIHSCLQFLLELYGAWLHVDNSPKPPLMLLNS   2582

Lymnaea         2577 VVKSMVCLSDLFMEREQFEFMQDILLDLLKGHPVEDELITQYLIVGMCKA   2626
                     ||||||.|||||:||||||||||||||||||||.||||:||||:||:||:
Aplysia         2583 VVKSMVSLSDLFVEREQFEFMQDILLDLLKGHPAEDELVTQYLVVGLCKS   2632

Lymnaea         2627 TAIVGTEALISERVVKLIESGLKSTHLPTKISSLHGALYLLEGGPSELNS   2676
                     ||:||||||::||:|||:||||||||||||||:||||||:||.|.|:|::
Aplysia         2633 TAVVGTEALVNERMVKLVESGLKSTHLPTKISALHGALYVLETGVSDLST   2682
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Lymnaea         2677 SLLPILTDFLSKHLAIVISQTCIISQQFVIIMWAVAFYIIENFSNELKDS   2726
                     :.||:|||||:|||||| ||.||||||||:.||||||||||||:||:||.
Aplysia         2683 AFLPVLTDFLAKHLAIV-SQVCIISQQFVVNMWAVAFYIIENFTNEIKDL   2731

Lymnaea         2727 DFTSKTIQLVVQTASGNEENVSTSVFLTVMKGTERLLLIDVLTQSDTETI   2776
                     ||:||.:.||||||||.||.|||:|||.||||||||||.|||||:|||||
Aplysia         2732 DFSSKIMPLVVQTASGTEETVSTAVFLVVMKGTERLLLTDVLTQTDTETI   2781

Lymnaea         2777 IKLSMDRLCLPNPQRALAALGLMFTCMYSGKSTDQYSPQPREEQMFGDSG   2826
                     ||||||||||||||||||||||||||||||||.|||||:|||||.||:.|
Aplysia         2782 IKLSMDRLCLPNPQRALAALGLMFTCMYSGKSVDQYSPRPREEQTFGEPG   2831

Lymnaea         2827 FQLLHQDPDSLILAMERVTVLFDRIKKGYPYEARVITRLLPAFLADFFPA   2876
                     |:||||||||||||||||||||||||||||||||||||||||||||||||
Aplysia         2832 FELLHQDPDSLILAMERVTVLFDRIKKGYPYEARVITRLLPAFLADFFPA   2881

Lymnaea         2877 QDIMNKVIGEFLSAHQPYPYLIAKVVFQVFTNLHQQKQQGLVKEWVMLSL   2926
                     |||||||||||||||||||||||||||||..||||:||.||:|||||||
Aplysia         2882 QDIMNKVIGEFLSAHQPYPYLIAKVVFQVFATLHQQQQQSLVREWVMLSL   2931

Lymnaea         2927 SNFTQRSPVSMAMWSLTLFFISASTNVWLRALFPHVLGRMGYMEPMDRRL   2976
                     ||||||||.:||||||:|||||||||:|||||||||||||||:||.:||:|
Aplysia         2932 SNFTQRSPPAMAMWSLSLFFISASTNIWLRALFPHVLGRMGHMESLDRQL   2981

Lymnaea         2977 FCLCAVDFYCQLTDDGHKRAFLATFQTIAAPDSPYSDLVQCITML   3021
                     |||||:|||.|||::|.:||||:|||.||||:|||||||.|:.
Aplysia         2982 FCLCALDFYRQLTEEGQRRAFLSTFQAIAAPESPYSDLVACLA--   3024


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Parkinson disease protein 7/Protein deglycase DJ-1

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 209
# Identity:     132/209 (63.2%)
# Similarity:   154/209 (73.7%)
# Gaps:          25/209 (12.0%)
# Score: 670.0
#
#
#=======================================

Lymnaea            1 MFNLCCNKAGHRLFYHSSRKNMASVSTALVFLAEGAEEMETVITVDVLRR     50
                                                :.:||||||||||||||||:||||||
Aplysia            1 ------------------------MPSALVFLAEGAEEMETVISVDVLRR     26

Lymnaea           51 GEVDVVLAGIDGDGPVKCSRNVKLVPDKSLRDALH-KEYDVLICPGGGLG     99
                     ..:||.|||:.|||||.|||||:|||||:|:.||. ..||||:.||||.|
Aplysia           27 AGIDVTLAGLGGDGPVLCSRNVRLVPDKNLKQALSAAPYDVLVLPGGGGG     76

Lymnaea          100 AENLCKSKEVGKALQEQEKRGGFIAAICAGPTALLAHNVGKGKKITSYPS    149
                     ::.|.:|:||.|||.|||.|||.|||:||.|||||||.:.||||:||:||
Aplysia           77 SKKLSESEEVRKALLEQENRGGLIAAVCAAPTALLAHGIAKGKKVTSHPS    126
```

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Lymnaea          150 MADKLKDAYKYSEDRVVVDGKFITSRGPGTCFEFALAIVEQLKGKEKAHA    199
                     :||||...|.||||||||||.||||||||||||||||.:|.|||||.:
Aplysia          127 VADKLSGDYSYSEDRVVVDGKLITSRGPGTCFEFALAIVTELMGKEKAES    176

Lymnaea          200 LVKPMLIKI    208
                     ||.|||:|:
Aplysia          177 LVDPMLVKL    185


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#**Ubiquitin-protein ligase E3A**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 927
# Identity:     638/927 (68.8%)
# Similarity:   749/927 (80.8%)
# Gaps:          39/927 ( 4.2%)
# Score: 3274.0
#
#=======================================

Lymnaea            1 MSSIQNTGSLDGQESASDLTVEHSLSGKVPKVSESTENMSKRGAAQQVIF     50
                     |||.....|||||:|||||:||:.::   .::|...||| ||.||:|:|.
Aplysia            1 MSSSNTNSSLDGQQSASDLSVENLIN---RRLSPPPENM-KRAAAKQLIE     46

Lymnaea           51 QYFNQLTEGCGNESCTNENCASSRTFRFKESDNNTLALEAITLSKAKATL    100
                     ||:.|||||||:|:|||||||||..|:|:::::.|.||||||.|||:||.|
Aplysia           47 QYYYQLTEGCGDENCTNENCASSSDFQFRDANRNKLALEAINLSKSKAPL     96

Lymnaea          101 CERRPRKISRLPTEQENGTLDTSVLVASKELGMRTKSKMLSPTA-SSSVD    149
                     |||||.|:||.||::|.....::...|.:.:|...:||:.|||: |||.|
Aplysia           97 CERRPNKLSRYPTQEEGAASSSTAASAGEPVGQGARSKIASPTSCSSSTD    146

Lymnaea          150 VG-------SSQSPHGSNSEIKEPNYLTEERLSAVIHDCQASNEWLKLIH    192
                     |.       ||.|..|:.::     :||||.|:.||.:|:|.|.|.||.|
Aplysia          147 VAAEAVSACSSSSSLGTATQ-----FLTEEILTKVIDECEARNSWSKLNH    191

Lymnaea          193 LIGSVFNNPESIIMSFRKSYPVSSPPKVNLVSPDDSSSP-----------    231
                     :||||||||||||::||||:.|.|.|......:.|:||:.
Aplysia          192 VIGSVFNNPESILLSFRKASPASEPVVDEAAATDESSATTSQASDGDSSG    241

Lymnaea          232 -----PISQPGIESPTVPTVSSIKDPDLTVDLPALRRAFKLLMDVPDQPY    276
                          |.||.|..|....|.....|.|::||||:||||::.|:||||||:
Aplysia          242 SNLPVPESQSGPASTDKVTTDGHHDDDMSVDLPSLRRAYQRLLDVPDQPF    291

Lymnaea          277 QGALINALTALSQTLEYETKYNKVLERQTDYINVFIVVMEIPMLHFPEYL    326
                     ||||:|||..||.||:.|.||...|.|:.||||||::||||||||:||||
Aplysia          292 QGALVNALMILSHTLDMELKYKDALARRPDYINVFVIVMEIPMLHWPEYL    341

Lymnaea          327 ETAFPGINKVIGLLPVSAQARLARIWSTFDQSRLKDMVQSLQQLITVKVI    376
                     ..|||.:.:.:|.:|:|.||||||||:|:...||::|||.|||:||||||
Aplysia          342 VNAFPCLCRALGSMPLSGQARLARIWATYGSGRLQEMVQGLQQMITVKVI    391
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Lymnaea          377 NYEGRWSANFRPSDDSAITSATRVLKILYYASMLGGHMDSTELVEEERRL    426
                     |.|||||.:|:|.||.:||||||||||::||||:|||||||.||:.||..|
Aplysia          392 NNEGRWSQSFQPGDDMSITSATRVLKVIYYASVLGGHMDSPELLREEAEL    441

Lymnaea          427 NDSESLLELMQGAFGYEPKESSPVKEDPLGKEVGVQVINCREPLIPYEDF    476
                     :..||:.|.||||||.|||:|:|.||||||||:||||||||||||:|:|||
Aplysia          442 SQRESIQEHMQGAFGMEPKDSTPPKEDPLGKELGVQVINCREPLVPFEDF    491

Lymnaea          477 INEPLNDNLDIGVDYTNHRLEPENKFSFVPYCFILTTASKHTSMYYDNRI    526
                     |||||||.::|..||||      ||||||||.|||||||||:||||:|||
Aplysia          492 INEPLNDTVNIYQDYTN------NKFSFVPYSFILTTASKHSSMYYENRI    535

Lymnaea          527 RMLHERRTAFVQTLVHGGPPNPFLRVRVRRDHIIDDALVNLEMIAMENPS    576
                     |||.||||||:||||.||||||||||||||:||||||||:|||.||||||
Aplysia          536 RMLSERRTAFIQTLVSGGPPNPFLRVRVRREHIIDDALVSLEMTAMENPS    585

Lymnaea          577 DLRKQLFVEFDGEQGLDEGGVSKEFFQLIVEELFNPDIGMFTYNEQSHHF    626
                     ||||||||||:||||||||||||||||||||||||||||.|||:||||
Aplysia          586 DLRKQLFVEFEGEQGLDEGGVSKEFFQLIVEELFNPDIGMFAYNEESHHF    635

Lymnaea          627 WFNSLSFENDAQFTLIGILLGLAIYNSCILDIHFPMVVYRKLMGKKGTFR    676
                     ||||||||||||||||||||||||||||||||||||||||||||||||||.
Aplysia          636 WFNSLSFENDAQFTLIGILLGLAIYNSCILDIHFPMVVYRKLMGKKGTFA    685

Lymnaea          677 DLYDVDPTLFASLKEMLEYKLEDFEEVFDQTFRIGYSDVFGNNHTYDLKE    726
                     ||||:||||..||::||:|:.||||:||.|:|.|||.||||:.||.:|||
Aplysia          686 DLYDLDPTLMHSLQDMLDYEGEDFEDVFAQSFSIGYHDVFGHCHTVELKE    735

Lymnaea          727 NGESTMVSQENKQEFVDLYADYLLNKSIDQQFRAFKRGFLMVTSESPLKQ    776
                     .|||..::|:||.||:.||||||||||||::||.|||||||||||||||:|
Aplysia          736 GGESLPLTQDNKHEFIKLYADYLLNKSIERQFLAFKRGFLMVTSESPLRQ    785

Lymnaea          777 LFRPEEIEMLVCGSQIFDFHALEEATEYDGGFTDDSATIRNFWTVVHAMS    826
                     ||||||||:|||||:|.||||||||||||||||.:|.||||||||||.|.
Aplysia          786 LFRPEEIEVLVCGSKILDFHALEEATEYDGGFTQESQTIRNFWTVVHDME    835

Lymnaea          827 EEDKKKLLQFTTGTDRVPVGGLSKLKMIIARNGPDSDRLPTSHTCFNVLL    876
                     |.:||||||||||||||||||||.||||||:||||||||||||||||||
Aplysia          836 ETEKKKLLQFTTGTDRVPVGGLSHLKMIIAKNGPDSDRLPTSHTCFNVLL    885

Lymnaea          877 LPEYPTVEKLQDRLLKAINYSKGFGML    903
                     |||||:||||:|||||||||||||||||
Aplysia          886 LPEYPSVEKLKDRLLKAINYSKGFGML    912


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```

#**Major vault 1**

```
#
# Aligned_sequences: 2
# 1: Lymnaea stagnalis
# 2: Aplysia californica
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
```

```
# Length: 872
# Identity:     658/872 (75.5%)
# Similarity:   749/872 (85.9%)
# Gaps:          21/872 ( 2.4%)
# Score: 3407.5
#
#
#=======================================

Lymnaea            1 MADPRKTRSDDPHSRWDKADNPIYRIPPYYYIHVMDQNSNVTRIELGPQT     50
                               ..||  |.||.|:|||||||||:|||:||||||:||||
Aplysia            1 -----------MTSR--KEDNAIFRIPPYYYIHVLDQNTNVTRIEIGPQT     37

Lymnaea           51 FVRQDNQRVTLGPEKMIIVPPRHYCTIENPVCRDKDGNVVVDRLGQIKLK    100
                     |:|||||||||||||::|||||||.|||||.|||||..|:|:|||.||:
Aplysia           38 FIRQDNQRVTLGPEKMVVVPPRHYCMIENPVFRDKDGKPVIDQLGQTKLQ     87

Lymnaea          101 HAELEIRLAQDPFPLYPGEILRHPVTALTVVQSNSALKILAVLDFKDGDV    150
                     ||:|||||.||||||:|||:|:.|||||.||.:|:||:|.||||::|.:.
Aplysia           88 HADLEIRLTQDPFPLFPGEVLKQPVTALKVVPANAALRIRAVLDYEDAEG    137

Lymnaea          151 D-RAAGDVWLFEGPGTYIPKKETVVKETVRATVIGPNQAIKLRATKEFED    199
                     : |.|||.||||||||||||:||.:::||:||||||||||||:|||.||..|
Aplysia          138 EKRTAGDEWLFEGPGTYIPRKECMIEETIRATVIGPNQAIRLRARKECID    187

Lymnaea          200 RDGNLRVTGEEWLVKQTGAYLPGVFEEVVDIVKAYVLTETKALHVRALKS    249
                     ||...||||||||||:|||||||.:|||||:|.||||||.||||:|||.:
Aplysia          188 RDNIRRVTGEEWLVKRTGAYLPGAYEEVVDLVNAYVLTEKKALHMRALMT    237

Lymnaea          250 FKDDFGVERKNGEEWLITMDDSEAHIPGVYEEVVGVVNITTLTNRQYAVI    299
                     ||||||:.||||||||||||.|:|.|||.||||||||||||.|:||||.||
Aplysia          238 FKDDFGIVRKNGEEWLITMTDTETHIPNVYEEVVGVVNITPLSNRQYCVI    287

Lymnaea          300 LDPVGADGKPQLGQKKLVRGEKSFFLLPGEKLEKGIQNIYILGEDEGLVL    349
                     ||||...|:|||||||||:|||||||:||||||||||:|||||||||:|
Aplysia          288 LDPVDDKGRPQLGQKKLVKGEKSFFLMPGEKLEKGIQNVYILGEDEGLIL    337

Lymnaea          350 RAIEQFKDGVSQRSPGDRWMIRGPLEYVPPVEIEVVMKRKAIPLDLNEGI    399
                     ||.|.|.||...|:|||||||:||.|||||||:|||:||:||||||.||||
Aplysia          338 RANESFMDGQINRNPGDRWMIKGPTEYVPPVEVEVVLKRQAIPLDENEGI    387

Lymnaea          400 YVRDIKTGKVRAITGATYMIKEDEELWEKELPETVEELIISERDPKSERY    449
                     ||||||:||||||.|.||||.:||||||.||||.|||.|:.:.:||.::|.
Aplysia          388 YVRDIKSGKVRAIQGETYMINQDEELWAKELPPTVESLLSAGKDPLADRS    437

Lymnaea          450 ATKGQDSKSKTRDKTRVVTFRVPHNAAVQIYDYKDKKSRVVFGPELVMLG    499
                     ..|..|...||||||||||||||||||||||||:||:||||||||||||
Aplysia          438 DRKSTDHSPKTRDKTRVVTFRVPHNAAVQIYDYKEKKARVVFGPELVMLG    487

Lymnaea          500 PDEQFTVLSLSGGKPKKNHAIKALCLLLGPDFATDIITVETADHARLSLQ    549
                     ||||||.||||||||||.:.||||||||||||.||||.||||||||||||
Aplysia          488 PDEQFTQLSLSGGKPKKPNLIKALCLLLGPDFCTDIIVVETADHARLSLQ    537

Lymnaea          550 LAYNWYFEVTGKTPEESAKLFSVPDFVGDSCKAIASRVRGAVAQVTFDDF    599
                     |:|||:||...|:|||:||:||||||.||||||||||||||||||.||||
Aplysia          538 LSYNWHFETLSKSPEEAAKIFSVPDFTGDSCKAIASRVRGAVAQVQFDDF    587

Lymnaea          600 HKNSAKIIRSSVFGF-KDGKVGSHLTFSQNNLVITNVDIQSVEPVDQRTR    648
                     ||||||||||||||| .:.||.....|.|||||||::||||||||||||||
Aplysia          588 HKNSAKIIRSSVFGFDPNNKVRDKFVFPQNNLVITSIDIQSVEPVDQRTR    637
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Lymnaea          649 DSLQKSVQLAIEITTNSQEATARHEAERLEQEAKGRLERQKIMDEAEAEK    698
                     |:|||||||||||||||||.||||||||||||||||||||||||||||||
Aplysia          638 DALQKSVQLAIEITTNSQEAAARHEAERLEQEAKGRLERQKIMDEAEAEK    687

Lymnaea          699 SRRELLELQANSAAVESTGQAKAEAQSRAEAARIEGEAAVQQAKLKAEAQ    748
                     :|:||||||||||||||||||||||||||||||:|||||||:||:||::|.
Aplysia          688 ARKELLELQANSAAVESTGQAKAEAQSRAEAAKIEGEAAVEQARLKSQAT    737

Lymnaea          749 TIEAESDLQRLTQARTAELAYLKEQNIMEIEKTTELTTIEVNKFRQMVES    798
                     .||:|::|:|||.||.|||.||.|||.||:||.||::.||..||::|||:
Aplysia          738 KIESEAELERLTSAREAELKYLSEQNRMELEKATEMSNIETTKFKEMVEA    787

Lymnaea          799 IGSGTLLAMATAGPDMQVRMLQALGLKSTLITDGTTPVNLFNTASGLIGD    848
                     ||:.||..|||||||||||||:||||||||||::|:||||||||||.
Aplysia          788 IGTQTLQTMATAGPDMQVRMLQSLGLKSTLITDGSSPINLFNTASGLIGG    837

Lymnaea          849 LVPSKRRRREKKEEEEESDSFA    870
                     |||.:.|.|:..:::|
Aplysia          838 LVPKRHRARDDDDDE------    853


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Table S1. Detailed functions of *L. stagnalis* findings in higher organisms.

***L. stagnalis* findings to genes linked to human aging/disease-related genes**	**Their normal and pathological functions in higher organisms**
klotho [MT153186]	A transmembrane protein mainly involved in the modulation of aging. Mice models revealed that a defect in Klotho gene expression accelerates the aging process, while its overexpression extends the life span.
major vault 1 [MT153187]	Major vault protein is the main component of ubiquitous cellular ribonucleoprotein particles called vaults. It is involved in intracellular signalling and cell survival. Due to its anti-apoptotic effect, it is considered to play a role in aging modulation.
gelsolin [MT153188]	A Ca^{2+}-dependent actin regulatory protein. It has an anti-aging function manifested in an age-related anti-apoptotic effect in mitochondria. Well-characterized point mutations of gelsolin gene will cause unfolded protein conformations and so systematically deposed gelsolin proteins leading to Gelsolin Amyloidosis disease.
huntingtin [MT153189]	The exact function of huntingtin protein is unknown, however, animal models revealed that it is necessary for development, memory consolidation, and it is linked to aging. The increased number (more than 36 copies) of repetitions of the tribasic CAG sequence at the 5' end of huntingtin gene is the main cause of Huntington's disease.
fragile X mental retardation protein [MT153190]	The protein is most commonly found in the brain and essentially responsible for normal cognitive development and female reproductive function. The increased number (more than 200 copies) of repetitions of the tribasic CGG sequence in the gene

	leads to fragile X mental retardation syndrome. Moreover, minor expansions of this repeat that do not cause fragile X syndrome are associated with an increased risk for premature ovarian aging.
Parkinson disease protein 7/Protein deglycase DJ-1 (PARK7/DJ-1) [MT153192]	PARK7/DJ-1 protein has a neuroprotection function acting as a chaperon to inhibit the aggregation of α-synuclein. Defect of the gene causes autosomal recessive early-onset Parkinson's disease.
α-secretase (ADAM10) [MT153191]	α-secretases are proteolytic enzymes that cleave APP in its transmembrane region. Since the α-secretase pathway is the predominant in APP processing, mutations can lead to β-amyloid production and so to Alzheimer's disease.
apolipoprotein E (apoE) receptor [MT137053]	Being involved in different neural signalling pathways, these receptors seem to play a protective role against β-amyloid production and tau phosphorylation.
choline acetyltransferase (ChAT) [MT153193]	A transferase enzyme responsible for the synthesis of neurotransmitter acetylcholine. Disturbances of ChAT and so the cholinergic system is associated with Alzheimer's disease.
amyloid precursor protein (APP) [MT153194]	An integral membrane protein expressed in many tissues and concentrated in the synapses of neurons. It is primary implicated as a regulator of synapse formation. Mutations of the protein as well as β-amyloid production from APP by secretases is one of the main cause of Alzheimer's disease.
presenilin 1 (PSEN1) [MT153195]	PSEN1 is a transmembrane protein which constitutes the catalytic subunits of the gamma-secretase intramembrane protease complex. Mutations of the gene or protein cause early onset forms of familial Alzheimer's disease manifested in, for example, an increased ratio of produced Aβ 42 / Aβ 40.
notch receptor 3 [MT153197]	Being as a part of notch signalling pathway, the receptor plays a key role in neuronal development. Mutations in the gene have been identified as the underlying cause of cerebral arteriopathy.
potassium voltage-gated channel subfamily KQT member 2 isoform e (KCNQ2) [MT153198]	Forming the so-called M channel by association with KCNQ3, KCNQ2 plays a critical role in the regulation of neuronal excitability. Defects of this gene cause epilepsy.
aldehyde dehydrogenase family 3 member A2 isoform 2 (ALDH3A2) [MT153199]	An aldehyde dehydrogenase enzyme what plays a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. Mutations of the gene will lead to Sjörger-Larsson syndrome.
copper-transporting ATPase 2 isoform a (ATP7B) [MT153200]	This protein is a member of the P-type ATPase family, a group of proteins that transport metals into and out of cells by using ATP. Mutations of the gene, manifested in protein structure changes what prevent copper-transporting, cause Wilson disease.
ubiquitin-protein ligase E3A (UBE3A) [MT153201]	Attaching ubiquitin as a marker to proteins that should be degraded, this enzyme is involved in targeting proteins for degradation within cells.

	Mutations of the gene, mostly resulted in non-functional proteins, are responsible for Angelman syndrome.